	wt.72 vs wt.0								
ID	Description	Gene Symb	AGI	FC	logFC	t	P.Value	adj.P.Val	B
257203_at	xyloglucan endotransglycosylase, p	---	AT3G23730	-34.26	-5.10	-48.42	8.22E-10	1.87E-05	11.51
254889_at	osmotin precursor ;supported by fu	ATOSM34	AT4G11650	346.86	8.44	43.69	1.64E-09	1.87E-05	11.20
253505_at	Cytochrome P450-like protein flavo	CYP82C2	AT4G31970	45.74	5.52	35.09	7.12E-09	4.06E-05	10.41
245393_at	beta-1,3-glucanase class I precurs	---	AT4G16260	187.96	7.55	30.12	1.98E-08	9.02E-05	9.76
256964_at	unknown protein ;supported by full-	AGP12	AT3G13520	-12.54	-3.65	-29.02	2.54E-08	9.64E-05	9.58
267592_at	unknown protein similar to GP 2245	---	AT2G39710	5.15	2.37	24.71	7.42E-08	0.000167	8.78
260592_at	cellulose synthase catalytic subuni	CSLE1	AT1G55850	12.59	3.65	24.47	7.92E-08	0.000167	8.73
259150_at	unknown protein similar to unknowr	---	AT3G10320	6.04	2.60	24.35	8.18E-08	0.000167	8.70
255360_at	putative protein ;supported by full-l	---	AT4G03960	6.87	2.78	24.21	8.50E-08	0.000167	8.67
254833_s_a	copper amine oxidase like protein (	---	AT4G12280	4.98	2.32	23.51	1.03E-07	0.000167	8.52
260101_at	putative trypsin inhibitor similar to tr	---	AT1G73260	15.06	3.91	23.12	1.15E-07	0.000167	8.43
249123_at	beta-ketoacyl-CoA synthase ; supp	KCS20	AT5G43760	-4.14	-2.05	-23.04	1.18E-07	0.000167	8.41
261728_at	pectinesterase, putative similar to p	sks5	AT1G76160	-23.08	-4.53	-22.92	1.22E-07	0.000167	8.38
267256_s_a	putative serine carboxypeptidase I	scpl10	AT2G23000	-10.07	-3.33	-22.81	1.27E-07	0.000167	8.35
263228_at	putative reticuline oxidase-like prot	---	AT1G30700	35.30	5.14	22.72	1.30E-07	0.000167	8.33
267200_at	hypothetical protein predicted by ge	---	AT2G31010	-8.06	-3.01	-22.51	1.38E-07	0.000167	8.28
264923_s_a	peroxiredoxin, putative similar to ty	---	AT1G60740	45.34	5.50	21.68	1.77E-07	0.000196	8.07
258975_at	putative WRKY-like transcriptional r	WRKY45	AT3G01970	7.65	2.93	21.62	1.81E-07	0.000196	8.05
258957_at	feebly-like protein contains similarit	DOX1	AT3G01420	11.34	3.50	21.04	2.17E-07	0.000206	7.90
267201_at	putative protein kinase contains a p	---	AT2G31010	-22.34	-4.48	-21.01	2.18E-07	0.000206	7.89
256598_at	cytochrome P450 homolog, putativ	BR6OX2	AT3G30180	-11.56	-3.53	-20.90	2.26E-07	0.000206	7.86
251323_at	delta-8 sphingolipid desaturase ;su	---	AT3G61580	-5.84	-2.55	-20.01	3.02E-07	0.000265	7.61
265305_at	putative tyrosine decarboxylase	---	AT2G20340	-7.51	-2.91	-19.67	3.38E-07	0.000277	7.51
260602_at	serine acetyltransferase identical t	ATSERAT2	AT1G55920	5.91	2.56	19.65	3.41E-07	0.000277	7.50
261020_at	hypothetical protein similar to reticu	---	AT1G26390	72.71	6.18	19.28	3.86E-07	0.000301	7.39
255885_at	sterol-C-methyltransferase identical	SMT2	AT1G20330	-4.45	-2.15	-18.91	4.39E-07	0.000301	7.27
263475_at	Expressed protein ; supported by fu	---	AT2G31945	5.72	2.52	18.90	4.40E-07	0.000301	7.27
257061_at	hypothetical protein predicted by ge	---	AT3G18250	15.09	3.92	18.79	4.58E-07	0.000301	7.23
245780_at	unknown protein ;supported by full-	---	AT1G45688	-5.65	-2.50	-18.76	4.62E-07	0.000301	7.23
259014_at	putative glucan endo-1-3-beta-gluc	---	AT3G07320	-10.57	-3.40	-18.70	4.72E-07	0.000301	7.21
252048_at	expressed protein supported by cDI	---	AT3G52500	-8.10	-3.02	-18.58	4.93E-07	0.000301	7.17
257202_at	receptor-like kinase, putative simila	---	AT3G23750	-6.15	-2.62	-18.52	5.03E-07	0.000301	7.15
264271_at	beta-glucosidase, putative similar t	BGLU6	AT1G60270	-14.31	-3.84	-18.46	5.14E-07	0.000301	7.13

261785_at	hypothetical protein contains simila	---	AT1G08230	3.74	1.90	18.31	5.43E-07	0.00031	7.08
258483_at	putative mannose-6-phosphate isor	MEE31	AT3G02570	-9.09	-3.18	-17.99	6.09E-07	0.000312	6.97
245275_at	beta-amylase ; supported by cDNA	BAM5	AT4G15210	-33.11	-5.05	-17.93	6.23E-07	0.000312	6.95
252414_at	putative protein sn-glycerol-3-phos	---	AT3G47420	8.97	3.17	17.91	6.29E-07	0.000312	6.95
267318_at	fatty acid hydroxylase (FAH1) ident	FAH1	AT2G34770	-4.96	-2.31	-17.88	6.36E-07	0.000312	6.94
245317_at	hypothetical protein ; supported by	---	AT4G15610	4.40	2.14	17.85	6.42E-07	0.000312	6.93
246200_at	putative protein ;supported by full-le	---	AT4G37240	-15.46	-3.95	-17.78	6.60E-07	0.000312	6.90
260686_at	unknown protein ; supported by cDI	---	AT1G17620	-22.26	-4.48	-17.72	6.75E-07	0.000312	6.88
260327_at	putative RING zinc finger protein P	---	AT1G63840	10.85	3.44	17.69	6.83E-07	0.000312	6.87
247183_at	putative protein strong similarity to	---	AT5G65440	-3.53	-1.82	-17.65	6.93E-07	0.000312	6.86
265233_s_a	hypothetical protein	---	AT2G07718	4.31	2.11	17.57	7.14E-07	0.000312	6.83
253382_at	putative protein AT.I.24, Arabidops	---	AT4G33040	6.05	2.60	17.50	7.33E-07	0.000312	6.80
260667_at	very-long-chain fatty acid condensi	KCS4	AT1G19440	-3.57	-1.84	-17.49	7.34E-07	0.000312	6.80
259958_at	leucine-rich repeat transmembrane	SRF6	AT1G53730	-4.39	-2.13	-17.48	7.37E-07	0.000312	6.80
256376_s_a	unknown protein	PXMT1	AT1G66690	82.21	6.36	17.48	7.38E-07	0.000312	6.80
265066_at	unknown protein location of ESTs	FLA9	AT1G03870	-10.58	-3.40	-17.39	7.62E-07	0.000313	6.77
263083_at	purple acid phosphatase precursor	PAP12	AT2G27190	3.93	1.97	17.37	7.69E-07	0.000313	6.76
261492_at	acid phosphatase, putative similar	SBH2	AT1G14290	-6.18	-2.63	-17.28	7.95E-07	0.000318	6.73
257071_at	unknown protein ; supported by cD	ATCSLC04	AT3G28180	-8.32	-3.06	-16.98	8.94E-07	0.000346	6.62
259072_at	unknown protein similar to unknowr	FLA18	AT3G11700	-6.60	-2.72	-16.92	9.16E-07	0.000348	6.60
265175_at	hypothetical protein similar to putati	ATCSLA03	AT1G23480	-9.58	-3.26	-16.83	9.49E-07	0.000355	6.56
264857_at	putative glycosyl transferase simila	LGT9	AT1G24170	-7.26	-2.86	-16.42	1.12E-06	0.000399	6.41
249093_at	putative protein similar to unknown	---	AT5G43880	-3.06	-1.61	-16.41	1.12E-06	0.000399	6.41
258250_at	putative delta 9 desaturase similar t	FAD5	AT3G15850	-3.07	-1.62	-16.38	1.13E-06	0.000399	6.40
249985_at	Ser/Thr specific protein kinase - lik	---	AT5G18500	-4.97	-2.31	-16.37	1.14E-06	0.000399	6.39
249309_at	homeotic protein BEL1 homolog ; s	BEL1	AT5G41410	4.69	2.23	16.24	1.20E-06	0.000414	6.34
260109_at	hypothetical protein predicted by ge	TET10	AT1G63260	-4.99	-2.32	-16.09	1.27E-06	0.000432	6.28
266184_s_a	phosphate transporter (AtPT2) iden	ATPT2	AT2G38940	15.63	3.97	16.07	1.29E-06	0.000432	6.27
253163_at	putative protein E1B 19K/Bcl-2-inte	---	AT4G35750	6.32	2.66	15.99	1.33E-06	0.000438	6.24
261926_at	unknown protein	PATL2	AT1G22530	-4.31	-2.11	-15.95	1.35E-06	0.000438	6.23
247794_at	phosphoinositide specific phospholi	PLC1	AT5G58670	-4.92	-2.30	-15.92	1.36E-06	0.000438	6.22
262733_s_a	lipase identical to lipase GB:AAA9	---	AT1G28660	4.36	2.12	15.82	1.43E-06	0.000442	6.17
253165_at	putative protein predicted protein, A	---	AT4G35320	-16.48	-4.04	-15.81	1.43E-06	0.000442	6.17
261722_at	acyl-(acyl carrier protein) thioestera	FATB	AT1G08510	-2.98	-1.58	-15.78	1.45E-06	0.000442	6.16
257985_at	hypothetical protein predicted by ge	---	AT3G20810	4.77	2.25	15.77	1.45E-06	0.000442	6.16

267364_at	unknown protein ;supported by full-	ELF4	AT2G40080	4.63	2.21	15.72	1.48E-06	0.000442	6.14
248419_at	putative protein similar to unknown	EXL3	AT5G51550	-9.83	-3.30	-15.67	1.51E-06	0.000442	6.12
253268_s_a	glucosyltransferase -like protein im	UGT73B2	AT4G34131	10.25	3.36	15.65	1.53E-06	0.000442	6.11
245262_at	predicted protein ; supported by cD	---	AT4G16563	-8.52	-3.09	-15.45	1.66E-06	0.000457	6.02
266296_at	putative glutathione S-transferase	ATGSTU7	AT2G29420	4.52	2.18	15.43	1.68E-06	0.000457	6.02
263662_at	ankyrin-like protein EST gb|ATTS0	---	AT1G04430	-8.15	-3.03	-15.42	1.68E-06	0.000457	6.01
253551_at	Expressed protein ; supported by c	---	AT4G30996	-3.91	-1.97	-15.31	1.77E-06	0.000461	5.97
247597_at	GTP-binding protein - like GTP-bin	AtRABA1f	AT5G60860	-17.08	-4.09	-15.29	1.78E-06	0.000461	5.96
261851_at	hexokinase, putative similar to chlo	HKL1	AT1G50460	-10.38	-3.38	-15.28	1.79E-06	0.000461	5.95
245276_at	DNA-binding homeotic protein Athb	ATHB-2	AT4G16780	-4.29	-2.10	-15.27	1.80E-06	0.000461	5.95
260391_at	putative strictosidine synthase extre	SS2	AT1G74020	4.34	2.12	15.19	1.86E-06	0.00047	5.92
261292_at	hypothetical protein predicted by ge	---	AT1G36940	-4.11	-2.04	-15.08	1.95E-06	0.000479	5.87
261242_at	subtilisin-like serine protease conta	SBT3.3	AT1G32960	8.23	3.04	15.04	1.99E-06	0.000479	5.85
266295_at	tubulin beta-7 chain identical to GB	TUB7	AT2G29550	-11.66	-3.54	-15.02	2.00E-06	0.000479	5.84
250102_at	receptor-like protein kinase	LRR1	AT5G16590	-4.10	-2.04	-14.98	2.04E-06	0.000479	5.83
260551_at	putative trypsin inhibitor ; supporte	ATTI1	AT2G43510	17.58	4.14	14.97	2.04E-06	0.000479	5.83
247186_at	putative protein contains similarity t	---	AT5G65470	-8.13	-3.02	-14.96	2.06E-06	0.000479	5.82
260431_at	putative zinc finger protein similar to	---	AT1G68190	-2.59	-1.37	-14.95	2.06E-06	0.000479	5.82
256243_at	basic chitinase identical to basic ch	ATHCHIB	AT3G12500	63.47	5.99	14.94	2.07E-06	0.000479	5.81
264449_at	hypothetical protein predicted by ge	NPGR1	AT1G27460	-8.54	-3.09	-14.93	2.08E-06	0.000479	5.81
258856_at	hypothetical protein predicted by ge	SRG3	AT3G02040	14.53	3.86	14.91	2.10E-06	0.00048	5.80
258676_at	hypothetical protein predicted by ge	---	AT3G08600	-3.99	-2.00	-14.81	2.19E-06	0.000491	5.75
257912_at	formin-like protein AHF1 identical to	AFH1	AT3G25500	-14.35	-3.84	-14.73	2.27E-06	0.000504	5.72
257299_at	unknown protein ;supported by full-	---	AT3G28050	3.74	1.90	14.69	2.31E-06	0.000507	5.70
253925_at	putative protein ; supported by cDN	SHV3	AT4G26690	-9.47	-3.24	-14.64	2.37E-06	0.000515	5.68
259611_at	GTP-binding protein RAB7D, putat	AtRABG3d	AT1G52280	-3.63	-1.86	-14.53	2.49E-06	0.000523	5.63
262603_at	hypothetical protein Is a member o	---	AT1G15380	15.94	3.99	14.52	2.50E-06	0.000523	5.63
258791_at	hevein-like protein precursor (PR-4	PR4	AT3G04720	23.75	4.57	14.48	2.54E-06	0.000527	5.61
262803_at	unknown protein Location of ESTs	---	AT1G21000	6.73	2.75	14.33	2.73E-06	0.000556	5.54
248060_at	putative protein contains similarity t	---	AT5G55560	3.16	1.66	14.25	2.82E-06	0.000556	5.51
255016_at	sucrose-phosphate synthase - like	ATSPS4F	AT4G10120	5.94	2.57	14.25	2.83E-06	0.000556	5.51
267497_at	putative glutaredoxin ;supported by	---	AT2G30540	-11.11	-3.47	-14.23	2.85E-06	0.000556	5.50
246932_at	ethylene-responsive element - like	---	AT5G25190	-14.94	-3.90	-14.23	2.85E-06	0.000556	5.50
247982_at	serine O-acetyltransferase (EC 2.3.	ATSERAT1	AT5G56760	-3.28	-1.71	-14.15	2.96E-06	0.000569	5.46
262930_at	hypothetical protein similar to hin1 (	---	AT1G65690	9.68	3.28	14.13	2.99E-06	0.000569	5.45

248704_at	putative protein pectinesterase-like;	sks3	AT5G48450	-4.65	-2.22	-14.07	3.07E-06	0.000576	5.42
253776_at	ADP,ATP carrier-like protein ADP,A	AAC3	AT4G28390	5.81	2.54	14.05	3.10E-06	0.000576	5.42
250110_at	putative protein many predicted pro	---	AT5G15350	-15.97	-4.00	-14.03	3.13E-06	0.000576	5.40
261346_at	putative aspartyl protease contains	---	AT1G79720	-3.29	-1.72	-14.03	3.13E-06	0.000576	5.40
261229_at	RAC-like GTP-binding protein ARA(	ROP2	AT1G20090	-2.52	-1.33	-13.99	3.18E-06	0.000581	5.39
258764_at	putative pectinesterase contains sir	---	AT3G10720	-11.69	-3.55	-13.97	3.22E-06	0.000582	5.38
247717_at	nonspecific lipid-transfer protein pr	LTP3	AT5G59320	-12.21	-3.61	-13.86	3.39E-06	0.000602	5.33
254759_at	short-chain alcohol dehydrogenase	---	AT4G13180	5.49	2.46	13.85	3.40E-06	0.000602	5.32
246682_at	putative protein EXOSTOSIN-1 (PU	XGD1	AT5G33290	3.61	1.85	13.80	3.49E-06	0.000602	5.30
255818_at	hypothetical protein predicted by ge	---	AT2G33570	-23.64	-4.56	-13.79	3.50E-06	0.000602	5.29
263680_at	unknown protein	---	AT1G26930	2.41	1.27	13.78	3.52E-06	0.000602	5.29
263989_at	putative MAP kinase ; supported by	ATMPK20	AT2G42880	-5.21	-2.38	-13.77	3.54E-06	0.000602	5.28
249071_at	putative protein similar to unknown	---	AT5G44050	-15.53	-3.96	-13.72	3.62E-06	0.000608	5.26
262137_at	transcription factor, putative similar	---	AT1G77920	2.85	1.51	13.71	3.64E-06	0.000608	5.25
263499_at	unknown protein ; supported by cD	TTL3	AT2G42580	-6.16	-2.62	-13.64	3.76E-06	0.000608	5.22
249101_at	unknown protein	---	AT5G43580	21.38	4.42	13.63	3.79E-06	0.000608	5.21
255411_at	putative ribonucleoprotein similarity	---	AT4G03110	-3.54	-1.82	-13.60	3.83E-06	0.000608	5.20
263981_at	unknown protein ;supported by full-	PAR1	AT2G42870	-36.61	-5.19	-13.59	3.85E-06	0.000608	5.20
251544_at	putative protein general stress prot	GAUT15	AT3G58790	-5.05	-2.34	-13.59	3.86E-06	0.000608	5.20
262452_at	hypothetical protein similar to hypot	---	AT1G11210	2.96	1.57	13.58	3.86E-06	0.000608	5.19
265414_at	nodulin-like protein	---	AT2G16660	-17.79	-4.15	-13.56	3.91E-06	0.000608	5.18
254363_at	pectinesterase like protein pectines	sks4	AT4G22010	-6.09	-2.61	-13.55	3.92E-06	0.000608	5.18
260581_at	MYB transcription factor (Atmyb2)	MYB2	AT2G47190	4.85	2.28	13.54	3.95E-06	0.000608	5.17
265610_at	unknown protein ;supported by full-	---	AT2G25430	-2.42	-1.27	-13.53	3.97E-06	0.000608	5.17
256293_at	pinhead-like protein similar to pinhe	AGO7	AT1G69440	5.05	2.34	13.44	4.15E-06	0.000618	5.12
257858_at	hypothetical protein predicted by ge	---	AT3G12920	-7.15	-2.84	-13.43	4.16E-06	0.000618	5.12
265444_s_a	aquaporin (plasma membrane intrin	RD28	AT2G37170	-8.79	-3.14	-13.42	4.19E-06	0.000618	5.11
249850_at	putative protein similar to unknown	---	AT5G23240	2.45	1.30	13.41	4.19E-06	0.000618	5.11
264209_at	RAS-related protein, RAB7 identica	RABG3B	AT1G22740	-3.65	-1.87	-13.40	4.22E-06	0.000618	5.11
267040_at	unknown protein	---	AT2G34300	-11.28	-3.50	-13.40	4.23E-06	0.000618	5.10
250657_at	steroid sulfotransferase-like protein	ST2B	AT5G07000	-9.69	-3.28	-13.38	4.26E-06	0.000619	5.10
267260_at	putative proline-rich protein ; suppo	AGP17	AT2G23130	-16.24	-4.02	-13.32	4.39E-06	0.000622	5.07
245025_at	ATPase I subunit	---	---	-2.20	-1.14	-13.31	4.42E-06	0.000622	5.06
248393_at	putative protein contains similarity t	ATBAG1	AT5G52060	-5.86	-2.55	-13.29	4.44E-06	0.000622	5.05
253405_at	transcription factor TINY homolog f	---	AT4G32800	-7.09	-2.82	-13.27	4.49E-06	0.000622	5.04

265771_at	unknown protein ;supported by full-	---	AT2G48030	-3.67	-1.88	-13.27	4.49E-06	0.000622	5.04
252102_at	dehydrin Xero2 ; supported by cDN	LTI30	AT3G50970	-24.86	-4.64	-13.26	4.53E-06	0.000622	5.03
245905_at	putative protein predicted proteins,	---	AT5G11090	3.04	1.61	13.23	4.59E-06	0.000622	5.02
252993_at	monooxygenase 2 (MO2)	---	AT4G38540	8.86	3.15	13.21	4.62E-06	0.000622	5.01
253407_at	putative protein	---	AT4G32920	3.09	1.63	13.20	4.64E-06	0.000622	5.01
265920_s_a	unknown protein	---	AT2G15120	14.20	3.83	13.20	4.67E-06	0.000622	5.00
252167_at	putative protein steroid dehydroger	---	AT3G50560	-3.31	-1.73	-13.18	4.70E-06	0.000622	5.00
267175_s_a	actin 3 identical to GB:U29480;supp	ACT1	AT2G37620	-4.49	-2.17	-13.18	4.71E-06	0.000622	5.00
259848_at	leucine-rich receptor-like protein ki	---	AT1G72180	-3.76	-1.91	-13.17	4.72E-06	0.000622	4.99
254815_at	putative pollen-specific protein poll	SKU5	AT4G12420	-6.91	-2.79	-13.17	4.72E-06	0.000622	4.99
254110_at	putative protein pectinesterase - C	---	AT4G25260	-13.84	-3.79	-13.16	4.75E-06	0.000623	4.99
251516_s_a	putative protein hypothetical protei	---	AT3G59310	-3.13	-1.65	-13.07	4.97E-06	0.000646	4.94
267162_s_a	putative phosphoribosylaminoimida	---	AT2G05140	4.99	2.32	13.06	4.99E-06	0.000646	4.94
258468_at	unknown protein predicted by gens	---	AT3G06070	-13.12	-3.71	-13.00	5.15E-06	0.000659	4.91
259598_at	sphingosine-1-phosphate lyase, pu	DPL1	AT1G27980	3.36	1.75	12.97	5.22E-06	0.000662	4.89
265057_at	unknown protein ;supported by full-	---	AT1G52140	-3.00	-1.58	-12.97	5.22E-06	0.000662	4.89
252265_at	putative protein SRG1 protein - Ara	DIN11	AT3G49620	69.59	6.12	12.91	5.39E-06	0.000672	4.86
246071_at	ids4-like protein ids-4 protein - Hor	SPX1	AT5G20150	16.08	4.01	12.89	5.42E-06	0.000672	4.85
260784_at	MYB-related protein identical to GE	ATMYB13	AT1G06180	8.39	3.07	12.89	5.42E-06	0.000672	4.85
263421_at	unknown protein ;supported by full-	EXL5	AT2G17230	-11.40	-3.51	-12.89	5.44E-06	0.000672	4.85
251791_at	expansin-like protein expansin At-E	ATEXPA16	AT3G55500	-11.84	-3.57	-12.88	5.45E-06	0.000672	4.85
266215_at	putative endoxyloglucan glycosyltra	EXGT-A1	AT2G06850	-23.00	-4.52	-12.80	5.69E-06	0.00069	4.80
257746_at	chorismate mutase identical to chor	CM1	AT3G29200	2.49	1.32	12.73	5.88E-06	0.000698	4.77
257196_at	AMP-binding protein, putative simil	---	AT3G23790	3.70	1.89	12.73	5.90E-06	0.000698	4.77
261727_at	S-adenosyl-methionine-sterol-C-m	SMT3	AT1G76090	-6.95	-2.80	-12.69	6.02E-06	0.0007	4.75
250505_at	cellulose synthase catalytic subunit	CESA5	AT5G09870	-4.34	-2.12	-12.68	6.05E-06	0.0007	4.74
247440_at	peptide transporter	---	AT5G62680	2.55	1.35	12.65	6.14E-06	0.000703	4.73
266962_at	hypothetical protein predicted by ge	---	AT2G39435	2.78	1.47	12.64	6.16E-06	0.000703	4.72
247360_at	cytochrome P450-like protein ;supp	CYP94B1	AT5G63450	-19.41	-4.28	-12.59	6.34E-06	0.000709	4.69
255064_at	putative phi-1-like phosphate-induc	EXO	AT4G08950	-50.23	-5.65	-12.58	6.37E-06	0.000709	4.69
262291_at	zinc finger and C2 domain protein,	---	AT1G70790	2.49	1.31	12.57	6.39E-06	0.000709	4.69
255714_at	contains weak similarity to S. cerev	---	AT4G00300	-3.09	-1.63	-12.57	6.41E-06	0.000709	4.68
256116_at	unknown protein contains similarity	CPuORF55	AT1G16858	-3.11	-1.64	-12.55	6.46E-06	0.000711	4.67
261005_at	hypothetical protein similar to reticu	---	AT1G26420	17.27	4.11	12.54	6.49E-06	0.000711	4.67
262970_at	unknown protein	---	AT1G75690	-2.72	-1.44	-12.49	6.68E-06	0.000729	4.64

252890_at	brassinosteroid insensitive 1 gene (	BRI1	AT4G39400	-2.53	-1.34	-12.47	6.73E-06	0.000731	4.63
251768_at	phosphoinositide-specific phospho	---	AT3G55940	-6.46	-2.69	-12.44	6.83E-06	0.000737	4.62
254667_at	glycine-rich cell wall protein-like gly	---	AT4G18280	-7.27	-2.86	-12.44	6.85E-06	0.000737	4.61
255433_at	putative xyloglucan endotransglyco	XTH9	AT4G03210	-9.91	-3.31	-12.42	6.92E-06	0.000738	4.60
250413_at	adenine phosphoribosyltransferase	APT5	AT5G11160	-4.40	-2.14	-12.41	6.96E-06	0.000738	4.60
263866_at	putative farnesylated protein ;supp	---	AT2G36950	4.98	2.32	12.40	6.99E-06	0.000738	4.59
264300_at	gamma glutamyl hydrolase, putativ	ATGGH3	AT1G78670	2.62	1.39	12.37	7.10E-06	0.000739	4.58
262229_at	unknown protein ; supported by cDI	---	AT1G68620	15.50	3.95	12.35	7.18E-06	0.000739	4.57
253879_s_a	UDP rhamnose--anthocyanidin-3-g	---	AT4G27560	-7.98	-3.00	-12.34	7.19E-06	0.000739	4.57
263867_at	putative aquaporin (tonoplast intrins	GAMMA-TI	AT2G36830	-7.41	-2.89	-12.34	7.19E-06	0.000739	4.56
261023_at	unknown protein similar to unknowr	---	AT1G12200	3.23	1.69	12.32	7.28E-06	0.000742	4.55
259132_at	putative auxin-independent growth	---	AT3G02250	-4.33	-2.11	-12.30	7.37E-06	0.000743	4.54
248466_at	putative protein similar to unknown	HVA22E	AT5G50720	-5.76	-2.53	-12.29	7.39E-06	0.000743	4.54
263948_at	similar to harpin-induced protein hir	YLS9	AT2G35980	16.76	4.07	12.29	7.41E-06	0.000743	4.53
266946_at	putative protein kinase contains a p	---	AT2G18890	-3.08	-1.62	-12.28	7.43E-06	0.000743	4.53
246595_at	formate dehydrogenase (FDH) ;su	FDH	AT5G14780	2.61	1.38	12.22	7.69E-06	0.000759	4.50
264770_at	unknown protein similar to unknowr	---	AT1G23030	-8.06	-3.01	-12.21	7.73E-06	0.00076	4.49
248721_at	putative protein strong similarity to	GAUT4	AT5G47780	-2.08	-1.06	-12.16	7.92E-06	0.00077	4.47
267212_at	similar to late embryogenesis abun	---	AT2G44060	-2.37	-1.25	-12.11	8.14E-06	0.00078	4.44
251036_at	putative protein ; supported by cDN	---	AT5G02160	-2.95	-1.56	-12.11	8.14E-06	0.00078	4.44
248701_at	ligand-gated ion channel protein-lik	GLR1.3	AT5G48410	2.70	1.43	12.03	8.52E-06	0.000802	4.39
260254_at	putative glycerophosphodiester pho	---	AT1G74210	2.53	1.34	12.01	8.58E-06	0.000802	4.38
265433_at	unknown protein	---	AT2G20950	3.66	1.87	12.01	8.59E-06	0.000802	4.38
256751_at	CLC-b chloride channel protein ide	CLC-B	AT3G27170	-7.25	-2.86	-11.98	8.74E-06	0.000804	4.36
263319_at	putative anion exchange protein ide	BOR1	AT2G47160	-6.67	-2.74	-11.97	8.78E-06	0.000804	4.36
251575_at	putative protein basic leucine zippe	BZIP61	AT3G58120	-14.36	-3.84	-11.96	8.81E-06	0.000804	4.36
261252_at	RAS-related protein ARA-1 identica	RABA5E	AT1G05810	-3.38	-1.76	-11.96	8.85E-06	0.000804	4.35
250180_at	early nodule-specific protein - like e	---	AT5G14450	-2.58	-1.37	-11.92	9.01E-06	0.000814	4.33
258386_at	hypothetical protein predicted by ge	---	AT3G15520	-4.00	-2.00	-11.90	9.14E-06	0.000821	4.32
247072_at	putative protein similar to unknown	---	AT5G66490	4.33	2.11	11.89	9.18E-06	0.000822	4.31
250665_at	unknown protein ;supported by full-	---	AT5G06980	-3.36	-1.75	-11.88	9.23E-06	0.000822	4.31
266424_at	unknown protein	---	AT2G41330	-4.93	-2.30	-11.86	9.32E-06	0.000822	4.30
250261_at	peptide transporter - like protein pe	---	AT5G13400	-7.58	-2.92	-11.85	9.37E-06	0.000822	4.29
260783_at	ethylene response factor, putative	ORA59	AT1G06160	18.53	4.21	11.83	9.49E-06	0.000823	4.28
245809_at	squalene monooxygenase, putativ	XF1	AT1G58440	-3.08	-1.62	-11.77	9.77E-06	0.000838	4.25

247005_at	adenylylsulfate kinase-like protein	---	AT5G67520	-3.61	-1.85	-11.76	9.81E-06	0.000838	4.25
247161_at	putative protein similar to unknown	---	AT5G65810	-3.26	-1.70	-11.73	9.99E-06	0.000843	4.23
259410_at	hypothetical protein predicted by ge	---	AT1G13340	11.29	3.50	11.73	1.00E-05	0.000843	4.22
264471_at	hypothetical protein predicted by ge	---	AT1G67120	5.46	2.45	11.72	1.00E-05	0.000843	4.22
263876_at	putative RAS superfamily GTP-binc	ATRAB7A	AT2G21880	-3.72	-1.90	-11.72	1.00E-05	0.000843	4.22
245018_at	hypothetical protein	---	---	-2.24	-1.16	-11.72	1.01E-05	0.000843	4.22
245193_at	F12A21.6 hypothetical protein	SUFE2	AT1G67810	30.52	4.93	11.68	1.03E-05	0.000843	4.20
261006_at	unknown protein similar to reticuline	---	AT1G26410	10.01	3.32	11.67	1.03E-05	0.000843	4.19
249454_at	expressed protein predicted protei	---	AT5G39520	24.02	4.59	11.67	1.03E-05	0.000843	4.19
249377_at	putative protein predicted proteins,	---	AT5G40690	5.67	2.50	11.67	1.04E-05	0.000843	4.19
259232_at	unknown protein similar to hypothet	---	AT3G11420	-4.49	-2.17	-11.66	1.04E-05	0.000843	4.19
246995_at	formin-like protein	---	AT5G67470	-4.72	-2.24	-11.66	1.04E-05	0.000843	4.19
254785_at	putative pollen surface protein end	FLA2	AT4G12730	-53.32	-5.74	-11.64	1.05E-05	0.000844	4.17
246510_at	cyclic nucleotide-gated cation chan	DND1	AT5G15410	-2.85	-1.51	-11.64	1.05E-05	0.000844	4.17
259671_at	protein kinase, putative similar to G	---	AT1G52290	-9.09	-3.18	-11.63	1.05E-05	0.000844	4.17
244926_s_a	maturase	---	AT2G07711	3.07	1.62	11.60	1.07E-05	0.000845	4.15
246098_at	ethylene-forming-enzyme-like diox	---	AT5G20400	4.65	2.22	11.58	1.08E-05	0.000845	4.14
264772_at	unknown protein location of EST g	---	AT1G22930	2.68	1.42	11.58	1.09E-05	0.000845	4.14
258750_at	putative pectinacetylesterase simila	---	AT3G05910	-9.47	-3.24	-11.57	1.09E-05	0.000845	4.13
246820_at	putative protein predicted proteins,	---	AT5G26910	-2.10	-1.07	-11.53	1.12E-05	0.000857	4.11
258158_at	acid phosphatase type 5 identical to	PAP17	AT3G17790	16.15	4.01	11.53	1.12E-05	0.000857	4.11
267127_at	putative acetone-cyanohydrin lyase	MES3	AT2G23610	-2.69	-1.43	-11.51	1.13E-05	0.00086	4.10
248046_at	receptor protein kinase-like protein	---	AT5G56040	-3.52	-1.81	-11.51	1.13E-05	0.00086	4.10
252940_at	receptor protein kinase - like protei	---	AT4G39270	4.67	2.22	11.49	1.14E-05	0.00086	4.09
266956_at	unknown protein	---	AT2G34510	-10.85	-3.44	-11.48	1.15E-05	0.000864	4.08
261762_at	hypothetical protein predicted by ge	---	AT1G15510	5.82	2.54	11.44	1.17E-05	0.000865	4.06
258467_at	unknown protein contains Pfam pro	---	AT3G06060	-2.87	-1.52	-11.44	1.18E-05	0.000865	4.06
254234_at	putative major latex protein major l	---	AT4G23680	15.71	3.97	11.42	1.19E-05	0.00087	4.05
267170_at	putative RING zinc finger protein	---	AT2G37585	-5.22	-2.39	-11.41	1.20E-05	0.000871	4.04
245947_at	spermine synthase (ACL5) ;suppor	ACL5	AT5G19530	-4.79	-2.26	-11.38	1.21E-05	0.00088	4.03
264313_at	carbonic anhydrase, putative simila	BCA4	AT1G70410	-2.10	-1.07	-11.37	1.22E-05	0.00088	4.02
249410_at	receptor-like protein kinase recepto	---	AT5G40380	-5.99	-2.58	-11.35	1.24E-05	0.000885	4.01
264479_at	hypothetical protein similar to recep	---	AT1G77280	2.82	1.50	11.35	1.24E-05	0.000885	4.01
247063_at	unknown protein	---	AT5G66820	3.97	1.99	11.34	1.25E-05	0.000888	4.00
261658_at	hypothetical protein predicted by ge	---	AT1G50040	-13.27	-3.73	-11.33	1.25E-05	0.00089	3.99

252000_at	hypothetical protein predicted prote	---	AT3G52710	3.11	1.64	11.30	1.27E-05	0.000897	3.98
248968_at	pectin acetylesterase ;supported b	---	AT5G45280	-6.35	-2.67	-11.28	1.29E-05	0.000903	3.96
261117_at	unknown protein	AUL1	AT1G75310	-4.34	-2.12	-11.27	1.30E-05	0.000908	3.96
266712_at	unknown protein	---	AT2G46750	3.02	1.59	11.21	1.34E-05	0.00092	3.92
250939_at	putative protein various predicted p	iqd2	AT5G03040	-4.15	-2.05	-11.20	1.34E-05	0.00092	3.92
255662_at	putative protein	GPAT8	AT4G00400	-6.24	-2.64	-11.20	1.35E-05	0.00092	3.92
244982_at	ribosomal protein L14	---	---	-2.84	-1.51	-11.20	1.35E-05	0.00092	3.92
251200_at	putative protein PrMC3, Pinus radi	GID1B	AT3G63010	3.24	1.69	11.19	1.35E-05	0.00092	3.91
259990_s_a	F-box protein FKF1/ADO3, AtFBX2	FKF1	AT1G68050	4.00	2.00	11.19	1.36E-05	0.00092	3.91
250125_at	biotin carboxyl carrier protein of ace	CAC1	AT5G16390	-2.48	-1.31	-11.19	1.36E-05	0.00092	3.91
254434_at	ethylene-regulated transcript 2 (ER	---	AT4G20880	2.28	1.19	11.18	1.36E-05	0.00092	3.91
245008_at	hypothetical protein	---	---	-2.20	-1.14	-11.17	1.37E-05	0.000921	3.90
261708_at	unknown protein similar to hypothet	---	AT1G32740	2.32	1.21	11.16	1.38E-05	0.000922	3.89
254484_at	hypothetical protein	---	AT4G20760	-2.29	-1.19	-11.16	1.38E-05	0.000922	3.89
248366_at	SCARECROW transcriptional regul	---	AT5G52510	2.88	1.52	11.15	1.39E-05	0.000922	3.89
248879_at	ornithine aminotransferase	DELTA-OA	AT5G46180	3.06	1.61	11.14	1.40E-05	0.000922	3.88
251141_at	Expressed protein ; supported by fu	---	AT5G01075	-5.37	-2.42	-11.11	1.42E-05	0.000924	3.87
265823_at	hypothetical protein predicted by ge	---	AT2G35760	-2.42	-1.27	-11.11	1.42E-05	0.000924	3.86
262868_at	unknown protein	---	AT1G64980	-4.06	-2.02	-11.10	1.43E-05	0.000924	3.86
247338_at	pyruvate kinase	---	AT5G63680	2.39	1.26	11.09	1.44E-05	0.000926	3.85
266682_at	putative disease resistance protein	---	AT2G19780	-4.83	-2.27	-11.07	1.45E-05	0.000931	3.84
262910_at	unknown protein ;supported by full-	---	AT1G59710	-3.38	-1.76	-11.05	1.47E-05	0.000939	3.83
253273_at	putative protein hypothetical protei	---	AT4G34180	2.21	1.14	11.05	1.47E-05	0.000939	3.83
250287_at	putative protein AP2 domain conta	Rap2.6L	AT5G13330	3.86	1.95	11.03	1.49E-05	0.000946	3.81
256441_at	unknown protein ;supported by full-	---	AT3G10940	-5.21	-2.38	-11.01	1.50E-05	0.000949	3.80
247979_at	pollen specific protein SF21 ;suppo	---	AT5G56750	-2.81	-1.49	-11.00	1.51E-05	0.000949	3.80
253489_at	monogalactosyldiacylglycerol synth	MGD1	AT4G31780	-3.69	-1.89	-11.00	1.51E-05	0.000949	3.80
249037_at	putative protein contains similarity t	FLA13	AT5G44130	-20.72	-4.37	-11.00	1.51E-05	0.000949	3.80
252365_at	Expressed protein ; supported by fu	---	AT3G48350	-8.54	-3.09	-10.99	1.52E-05	0.000949	3.79
250618_at	putative protein hypothetical protein	ATBAG3	AT5G07220	-2.25	-1.17	-10.95	1.56E-05	0.000963	3.77
253631_at	nucleotide sugar epimerase-like pr	GAE1	AT4G30440	-3.12	-1.64	-10.94	1.56E-05	0.000964	3.76
263606_at	putative beta-ketoacyl-CoA synthas	KCS9	AT2G16280	-3.72	-1.89	-10.93	1.58E-05	0.000966	3.75
245274_at	ankyrin like protein ; supported by c	---	AT4G14360	-2.68	-1.42	-10.93	1.58E-05	0.000966	3.75
259553_x_a	hypothetical protein	ATEXT3	AT1G21310	8.99	3.17	10.90	1.61E-05	0.000978	3.73
245528_at	pyruvate,orthophosphate dikinase	PPDK	AT4G15530	2.94	1.55	10.88	1.63E-05	0.00098	3.72

258264_at	unknown protein	MBD11	AT3G15790	-2.89	-1.53	-10.88	1.63E-05	0.00098	3.72
253891_at	putative protein ;supported by full-l	---	AT4G27720	-5.99	-2.58	-10.87	1.63E-05	0.00098	3.72
260914_at	beta-xylosidase, putative similar to	BXL2	AT1G02640	-9.61	-3.26	-10.85	1.65E-05	0.000986	3.71
254293_at	putative protein SF16 protein, Helia	IQD22	AT4G23060	-5.46	-2.45	-10.85	1.65E-05	0.000986	3.71
267319_at	ABC transporter (AtMRP2) identica	ATMRP2	AT2G34660	3.43	1.78	10.85	1.65E-05	0.000986	3.71
249765_at	putative protein contains similarity t	SLAH3	AT5G24030	-17.46	-4.13	-10.83	1.67E-05	0.000991	3.69
258751_at	low temperature and salt responsiv	RCI2B	AT3G05890	-19.22	-4.26	-10.82	1.68E-05	0.000992	3.69
255110_at	peroxidase C2 precursor like prote	---	AT4G08770	75.94	6.25	10.81	1.69E-05	0.000994	3.68
266168_at	putative protease inhibitor ;support	---	AT2G38870	14.72	3.88	10.81	1.69E-05	0.000996	3.68
245859_at	serine (threonine) protein kinase -	ATNEK3	AT5G28290	-4.07	-2.03	-10.80	1.70E-05	0.000996	3.67
245026_at	ATPase III subunit	---	---	-2.15	-1.11	-10.80	1.70E-05	0.000996	3.67
251864_at	pectate lyase - like protein pectate	PMR6	AT3G54920	-2.96	-1.56	-10.76	1.74E-05	0.001013	3.65
247461_at	putative protein various predicted p	ATBAG2	AT5G62100	-3.00	-1.58	-10.75	1.75E-05	0.001013	3.64
253994_at	protein phosphatase ABI1 ; suppor	ABI1	AT4G26080	2.41	1.27	10.75	1.76E-05	0.001014	3.64
249481_at	frnE protein - like frnE protein, Deir	---	AT5G38900	29.10	4.86	10.73	1.77E-05	0.001014	3.63
249008_at	putative protein contains similarity t	---	AT5G44680	-4.52	-2.18	-10.73	1.77E-05	0.001014	3.63
256578_at	peroxidase, putative similar to perc	---	AT3G28200	-5.43	-2.44	-10.73	1.78E-05	0.001015	3.63
261021_at	hypothetical protein similar to reticu	---	AT1G26380	52.43	5.71	10.70	1.81E-05	0.001028	3.61
266489_at	unknown protein ; supported by cD	NPSN11	AT2G35190	-4.20	-2.07	-10.68	1.83E-05	0.001029	3.60
245915_s_a	tubulin alpha-5 chain-like protein tu	TUA3	AT5G19770	-2.38	-1.25	-10.68	1.83E-05	0.001029	3.60
251413_at	bZIP protein ; supported by cDNA:	---	AT3G60320	-2.85	-1.51	-10.68	1.83E-05	0.001029	3.60
259010_at	unknown protein contains helix-loop	---	AT3G07340	-4.05	-2.02	-10.68	1.83E-05	0.001029	3.60
249383_at	putative protein putative DNA-bindi	PRE1	AT5G39860	-4.56	-2.19	-10.65	1.86E-05	0.001039	3.58
253811_at	hypothetical protein ;supported by	ULT1	AT4G28190	-5.61	-2.49	-10.62	1.90E-05	0.00105	3.56
255430_at	putative chloroplast protein import	tic20-IV	AT4G03320	5.47	2.45	10.60	1.91E-05	0.001054	3.55
246482_at	plant adhesion molecule 1 (PAM1)	PAM1	AT5G15930	-2.28	-1.19	-10.60	1.92E-05	0.001054	3.55
261017_at	UDP-glucose dehydrogenase, puta	UGD1	AT1G26570	-2.61	-1.38	-10.60	1.92E-05	0.001054	3.55
260856_at	TINY-like protein similar to TINY GE	---	AT1G21910	-33.68	-5.07	-10.58	1.94E-05	0.001059	3.54
259858_at	putative receptor kinase similar to r	---	AT1G68400	-4.88	-2.29	-10.56	1.96E-05	0.001066	3.52
253841_at	putative beta-glucosidase beta-glu	BGLU10	AT4G27830	3.45	1.78	10.56	1.97E-05	0.001067	3.52
254726_at	isoflavone reductase-like protein is	PRR2	AT4G13660	7.95	2.99	10.54	1.99E-05	0.001071	3.51
253224_at	invertase - like protein mRNA, Liliu	---	AT4G34860	3.71	1.89	10.52	2.02E-05	0.001082	3.50
261420_at	fatty acid elongase 3-ketoacyl-CoA	KCS3	AT1G07720	-6.29	-2.65	-10.51	2.03E-05	0.001082	3.49
261611_at	hypothetical protein predicted by ge	---	AT1G49730	-4.96	-2.31	-10.51	2.03E-05	0.001082	3.49
259642_at	hypothetical protein predicted by ge	---	AT1G69030	-3.58	-1.84	-10.50	2.03E-05	0.001082	3.49

259104_at	unknown protein ;supported by full-	LNG2	AT3G02170	-4.40	-2.14	-10.50	2.04E-05	0.001082	3.49
260000_at	unknown protein similar to C-termi	ATMAP70-	AT1G68060	-2.93	-1.55	-10.49	2.06E-05	0.001088	3.48
261563_at	polyphosphoinositide binding prote	---	AT1G01630	-2.52	-1.33	-10.45	2.10E-05	0.001106	3.45
248921_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G45950	-9.30	-3.22	-10.44	2.11E-05	0.00111	3.45
251601_at	Expressed protein ; supported by fu	---	AT3G57800	-3.92	-1.97	-10.43	2.12E-05	0.001114	3.44
253253_at	putative protein auxin-regulated ge	---	AT4G34750	-2.27	-1.18	-10.42	2.13E-05	0.001116	3.44
254770_at	extensin-like protein extensin-like p	---	AT4G13340	-7.84	-2.97	-10.42	2.14E-05	0.001116	3.43
253911_at	putative receptor protein kinase rec	---	AT4G27300	6.98	2.80	10.41	2.15E-05	0.001117	3.43
247123_at	unknown protein	---	AT5G66050	-3.38	-1.76	-10.39	2.18E-05	0.001119	3.41
246449_at	hypothetical protein	---	AT5G16810	-2.47	-1.31	-10.38	2.19E-05	0.001119	3.41
245740_at	amino acid permease, putative alm	AAP5	AT1G44100	2.92	1.54	10.38	2.19E-05	0.001119	3.41
253330_at	putative potassium transporter AtK	KUP5	AT4G33530	-2.19	-1.13	-10.37	2.20E-05	0.001119	3.40
263957_at	unknown protein ; supported by cD	---	AT2G35880	-2.10	-1.07	-10.34	2.24E-05	0.001129	3.38
264833_at	putative protein phosphatase simila	---	AT1G03590	-3.76	-1.91	-10.33	2.27E-05	0.001137	3.37
258515_at	ATP citrate lyase, putative similar t	ACLB-1	AT3G06650	-2.12	-1.09	-10.30	2.31E-05	0.001146	3.35
248179_at	receptor-protein kinase-like protein	THE1	AT5G54380	-6.97	-2.80	-10.29	2.32E-05	0.001146	3.35
259995_at	putative golgi transport complex pr	---	AT1G67930	-2.73	-1.45	-10.29	2.32E-05	0.001146	3.35
245816_at	hypothetical protein similar to hypot	---	AT1G26210	-6.24	-2.64	-10.27	2.34E-05	0.001146	3.34
257650_at	protein phosphatase, putative simil	---	AT3G16800	-3.04	-1.61	-10.27	2.34E-05	0.001146	3.34
264704_at	unknown protein similar to putative	LGT8	AT1G70090	-4.02	-2.01	-10.27	2.34E-05	0.001146	3.34
259766_at	unknown protein ;supported by full-	---	AT1G64360	4.45	2.15	10.27	2.35E-05	0.001146	3.33
258087_at	putative peroxiredoxin similar to per	ATPRX Q	AT3G26060	-3.50	-1.81	-10.27	2.35E-05	0.001146	3.33
246968_at	RING finger-like protein RING-H2 f	---	AT5G24870	2.99	1.58	10.23	2.41E-05	0.001165	3.31
253496_at	glutathione peroxidase - like protei	ATGPX7	AT4G31870	-12.08	-3.59	-10.21	2.44E-05	0.001175	3.29
260015_at	putative S-adenosyl-L-methionine:t	CCOAMT	AT1G67980	25.96	4.70	10.19	2.46E-05	0.001179	3.29
256930_at	O-acetylserine(thiol) lyase, putative	OASA2	AT3G22460	2.70	1.43	10.19	2.46E-05	0.001179	3.29
255283_at	putative symbiosis-related protein ;	ATG8B	AT4G04620	3.41	1.77	10.17	2.50E-05	0.001192	3.27
253428_at	cellulose synthase catalytic subunit	CESA1	AT4G32410	-3.06	-1.61	-10.16	2.52E-05	0.001192	3.26
256787_at	beta-fructofuranosidase 1 identical	ATBFRUC	AT3G13790	4.95	2.31	10.16	2.52E-05	0.001192	3.26
259915_at	unknown protein	---	AT1G72790	-7.44	-2.89	-10.16	2.52E-05	0.001192	3.26
248943_s_a	putative protein similar to unknown	---	AT5G45440	-6.24	-2.64	-10.15	2.53E-05	0.001195	3.26
250954_at	putative protein ;supported by full-l	ATRAB8C	AT5G03520	-2.91	-1.54	-10.14	2.55E-05	0.001197	3.25
257636_at	cytochrome P450, putative contain	CYP71B22	AT3G26200	6.93	2.79	10.14	2.55E-05	0.001197	3.25
246596_at	CARBONIC ANHYDRASE 2 ; supp	CA2	AT5G14740	-2.19	-1.13	-10.13	2.56E-05	0.001197	3.25
260877_at	unknown protein ; supported by full-	---	AT1G21500	-3.25	-1.70	-10.13	2.56E-05	0.001197	3.25

257772_at	unknown protein C-term similar to p	---	AT3G23080	-2.55	-1.35	-10.13	2.56E-05	0.001197	3.24
247954_at	beta-galactosidase (emb|CAB6474	BGAL4	AT5G56870	2.67	1.42	10.08	2.64E-05	0.001218	3.21
246843_at	putative protein various predicted p	---	AT5G26740	-2.09	-1.07	-10.08	2.64E-05	0.001218	3.21
248082_at	fimbrin	---	AT5G55400	-4.26	-2.09	-10.07	2.65E-05	0.001221	3.21
253099_s_a	peroxidase - like protein peroxidas	---	AT4G37520	2.58	1.37	10.06	2.67E-05	0.001223	3.20
259523_at	hypothetical protein	---	AT1G12500	-4.09	-2.03	-10.06	2.68E-05	0.001223	3.20
256396_at	unknown protein	---	AT3G06150	-4.19	-2.07	-10.05	2.69E-05	0.001225	3.19
251342_at	putative protein SAUR-AC1, Arabic	---	AT3G60690	3.07	1.62	10.05	2.69E-05	0.001225	3.19
253050_at	putative protein probable arabinoga	AGP18	AT4G37450	-13.47	-3.75	-10.05	2.70E-05	0.001225	3.19
261191_at	starch synthase, putative similar to	---	AT1G32900	-5.02	-2.33	-10.04	2.72E-05	0.001225	3.18
253519_at	predicted protein red-1 gene, M.mu	---	AT4G31240	4.89	2.29	10.03	2.72E-05	0.001225	3.18
250936_at	putative protein ;supported by full-l	---	AT5G03120	-5.03	-2.33	-10.03	2.73E-05	0.001225	3.18
245671_at	purine permease identical to purine	PUP1	AT1G28230	2.11	1.08	10.03	2.73E-05	0.001225	3.18
259058_at	putative cytochrome P450 similar to	CYP89A9	AT3G03470	6.36	2.67	10.03	2.73E-05	0.001225	3.18
247596_at	putative protein predicted protein, I	---	AT5G60840	-4.36	-2.12	-10.02	2.75E-05	0.001226	3.17
246097_at	putative protein CGI-45 protein - H	HHP1	AT5G20270	-7.99	-3.00	-10.01	2.75E-05	0.001226	3.17
263131_at	ribosomal protein L13, putative sim	emb1473	AT1G78630	-2.21	-1.14	-10.01	2.76E-05	0.001226	3.17
255969_at	Expressed protein ; supported by fu	---	AT1G22330	-5.05	-2.34	-9.99	2.79E-05	0.001234	3.15
259911_at	putative cinnamyl-alcohol dehydrog	CAD1	AT1G72680	3.25	1.70	9.99	2.79E-05	0.001234	3.15
253590_at	putative protein various predicted p	HHP2	AT4G30850	-3.01	-1.59	-9.97	2.83E-05	0.001239	3.14
257194_at	serine acetyltransferase (Sat-1) ide	ATSERAT2	AT3G13110	2.32	1.22	9.97	2.83E-05	0.001239	3.14
244901_at	hypothetical protein	---	ATMG00640	2.45	1.29	9.97	2.84E-05	0.001239	3.14
251701_at	putative protein hypothetical protei	---	AT3G56650	-2.35	-1.23	-9.96	2.86E-05	0.001239	3.13
252885_at	glycine-rich protein (clone AtGRP8)	GR-RBP8	AT4G39260	3.37	1.75	9.95	2.86E-05	0.001239	3.13
265471_at	putative peroxidase ATP2a ;suppo	---	AT2G37130	7.13	2.83	9.95	2.87E-05	0.001239	3.13
255889_at	ABC transporter, putative similar to	WBC11	AT1G17840	-3.10	-1.63	-9.95	2.87E-05	0.001239	3.12
249693_at	histidine kinase-like protein ; suppo	AHK2	AT5G35750	-3.82	-1.94	-9.90	2.96E-05	0.001264	3.09
261150_at	floral nectary-specific protein, putat	JMT	AT1G19640	-16.83	-4.07	-9.90	2.96E-05	0.001264	3.09
254016_at	putative transcription factor Arabid	CGA1	AT4G26150	-4.28	-2.10	-9.88	3.00E-05	0.001277	3.08
260347_at	DHHC-type zinc finger protein, put	---	AT1G69420	-3.60	-1.85	-9.87	3.02E-05	0.00128	3.07
253835_at	putative beta-glucosidase beta-glu	BGLU9	AT4G27820	2.44	1.29	9.86	3.03E-05	0.001283	3.07
247552_at	phytochelatin synthetase - like prot	COB	AT5G60920	-3.93	-1.98	-9.85	3.06E-05	0.001289	3.06
250569_at	myc-like protein myc-like regulatory	BIM1	AT5G08130	-4.63	-2.21	-9.85	3.07E-05	0.001291	3.05
252433_at	putative protein putative hydrolyse	---	AT3G47560	-3.33	-1.74	-9.84	3.07E-05	0.001291	3.05
263664_at	putative auxin-induced protein, IAA	AXR3	AT1G04250	-8.23	-3.04	-9.83	3.09E-05	0.001296	3.04

253974_at	receptor protein kinase - like protei	---	AT4G26540	-4.63	-2.21	-9.79	3.18E-05	0.00132	3.02
257074_at	unknown protein	---	AT3G19660	4.99	2.32	9.79	3.19E-05	0.00132	3.01
251402_at	SRG1 - like protein SRG1 protein,	---	AT3G60290	-6.90	-2.79	-9.79	3.19E-05	0.00132	3.01
245176_at	unknown protein similar to GP|2104	---	AT2G47440	-7.08	-2.82	-9.78	3.20E-05	0.001322	3.01
259741_at	unknown protein	---	AT1G71020	-2.98	-1.58	-9.78	3.21E-05	0.001322	3.01
251790_at	elicitor responsive/phloem -like pro	---	AT3G55470	2.45	1.29	9.77	3.22E-05	0.001322	3.00
255078_at	putative protein ascorbate peroxida	APX4	AT4G09010	-3.03	-1.60	-9.76	3.24E-05	0.00133	3.00
249120_at	unknown protein ;supported by full-	---	AT5G43750	-2.20	-1.13	-9.74	3.29E-05	0.001345	2.98
255298_at	putative protein similar to transcript	ATMSRB6	AT4G04840	-16.86	-4.08	-9.74	3.29E-05	0.001345	2.98
267565_at	putative cytochrome P450	CYP71A12	AT2G30750	25.35	4.66	9.72	3.33E-05	0.001352	2.97
245362_at	homeobox-leucine zipper protein H	HAT1	AT4G17460	-3.01	-1.59	-9.71	3.35E-05	0.001356	2.96
262396_at	unknown protein ;supported by full-	---	AT1G49470	5.24	2.39	9.70	3.38E-05	0.001365	2.95
254701_at	putative protein predicted protein,	---	AT4G18030	-4.20	-2.07	-9.69	3.40E-05	0.001369	2.95
261564_at	NAC domain protein, putative simil	ATAF1	AT1G01720	3.01	1.59	9.68	3.42E-05	0.00137	2.94
250645_at	putative protein strong similarity to	---	AT5G06700	-4.21	-2.07	-9.67	3.43E-05	0.00137	2.94
245698_at	phosphate/phosphoenolpyruvate tra	---	AT5G04160	-3.78	-1.92	-9.67	3.43E-05	0.00137	2.94
265824_at	putative glucosyltransferase ;suppo	ATCSLA07	AT2G35650	-2.87	-1.52	-9.67	3.44E-05	0.00137	2.93
264321_at	unknown protein Contains similarity	---	AT1G04200	-2.90	-1.54	-9.67	3.44E-05	0.00137	2.93
266963_at	unknown protein	MTP11	AT2G39450	-2.31	-1.21	-9.67	3.45E-05	0.00137	2.93
250408_at	serine/threonine protein kinase -lik	CIPK5	AT5G10930	3.92	1.97	9.66	3.47E-05	0.001377	2.92
249118_at	putative protein similar to unknown	---	AT5G43870	-2.63	-1.39	-9.64	3.50E-05	0.001381	2.91
256310_at	unknown protein ; supported by cDI	ERD4	AT1G30360	-3.20	-1.68	-9.64	3.51E-05	0.001381	2.91
259430_at	hypothetical protein similar to unkno	GPAT4	AT1G01610	-3.30	-1.72	-9.64	3.51E-05	0.001381	2.91
246371_at	unknown protein contains similarity	---	AT1G51940	-2.33	-1.22	-9.64	3.51E-05	0.001381	2.91
255590_at	cathepsin B-like cysteine protease,	---	AT4G01610	2.59	1.38	9.62	3.55E-05	0.001384	2.90
256417_s_a	omega-3 fatty acid desaturase, chl	FAD7	AT3G11170	-3.96	-1.99	-9.62	3.56E-05	0.001384	2.90
267078_at	unknown protein ;supported by full-	---	AT2G40960	-2.15	-1.10	-9.61	3.57E-05	0.001384	2.89
266884_at	phytocyanin identical to GB:U9042	UCC2	AT2G44790	8.63	3.11	9.59	3.62E-05	0.001395	2.88
252317_at	putative protein hypersensitivity-rel	---	AT3G48720	-17.99	-4.17	-9.57	3.67E-05	0.001408	2.86
263184_at	UDP-glucose:indole-3-acetate beta	UGT75B1	AT1G05560	3.08	1.62	9.56	3.69E-05	0.00141	2.86
250690_at	ABC transporter-like protein ; supp	---	AT5G06530	-3.32	-1.73	-9.55	3.73E-05	0.001419	2.85
263297_at	putative ADP-ribosylation factor ; s	ATARFB1A	AT2G15310	3.38	1.76	9.52	3.79E-05	0.001441	2.83
260900_s_a	branched-chain alpha keto-acid de	---	AT1G21400	4.28	2.10	9.51	3.82E-05	0.001441	2.82
267481_at	putative receptor-like protein kinase	---	AT2G02780	-6.82	-2.77	-9.51	3.83E-05	0.001441	2.82
261594_at	DNA-binding factor, putative simila	AT-GTL1	AT1G33240	-2.36	-1.24	-9.51	3.83E-05	0.001441	2.82

251996_at	beta-galactosidase precursor - like	BGAL2	AT3G52840	-2.46	-1.30	-9.50	3.84E-05	0.001441	2.82
257628_at	cytochrome P450, putative contain	CYP71B26	AT3G26290	5.25	2.39	9.49	3.86E-05	0.001443	2.81
253136_at	putative protein leucine-rich protein	---	AT4G35470	-2.24	-1.16	-9.49	3.88E-05	0.001443	2.81
252231_at	hypothetical protein ;supported by	---	AT3G49720	-2.46	-1.30	-9.48	3.89E-05	0.001446	2.80
258357_at	putative leucine-rich repeat transme	SRF7	AT3G14350	-3.89	-1.96	-9.45	3.97E-05	0.00147	2.78
259057_at	unknown protein ; supported by cD	---	AT3G03310	2.72	1.44	9.45	3.99E-05	0.001475	2.77
267005_at	unknown protein ; supported by cDI	---	AT2G34460	-2.12	-1.08	-9.44	4.00E-05	0.001476	2.77
258921_at	unknown protein N-terminus similar	anac053	AT3G10500	2.67	1.42	9.42	4.05E-05	0.001488	2.76
249823_s_a	putative protein contains similarity t	---	AT5G23350	-3.03	-1.60	-9.41	4.07E-05	0.001493	2.75
254300_at	Translation factor EF-1 alpha - like	ACR7	AT4G22780	3.10	1.63	9.41	4.10E-05	0.001493	2.75
247949_at	cytochrome P450	CYP81F2	AT5G57220	34.41	5.10	9.41	4.10E-05	0.001493	2.75
255552_at	S-adenosylmethionine synthase 2	SAM-2	AT4G01850	-2.22	-1.15	-9.37	4.19E-05	0.001514	2.72
259008_at	metallothionein-like protein similar t	MT2A	AT3G09390	2.28	1.19	9.37	4.19E-05	0.001514	2.72
263953_at	hypothetical protein predicted by ge	OFP15	AT2G36050	-4.13	-2.05	-9.37	4.19E-05	0.001514	2.72
264960_at	hypothetical protein contains simila	ATEXT4	AT1G76930	37.44	5.23	9.37	4.19E-05	0.001514	2.72
264916_at	ATP citrate-lyase, putative similar t	ACLA-2	AT1G60810	-2.89	-1.53	-9.36	4.24E-05	0.00152	2.71
266791_at	unknown protein	---	AT2G02960	-2.02	-1.01	-9.35	4.24E-05	0.00152	2.71
266735_at	putative pectinesterase ; supported	---	AT2G46930	-2.61	-1.38	-9.35	4.26E-05	0.001524	2.71
256569_at	hypothetical protein ; supported by	---	AT3G19550	8.86	3.15	9.34	4.29E-05	0.001528	2.70
267008_at	putative ABC transporter	---	AT2G39350	-3.31	-1.73	-9.33	4.30E-05	0.001528	2.70
258123_at	putative MAP kinase similar to blast	MPK9	AT3G18040	-4.36	-2.12	-9.33	4.32E-05	0.001531	2.69
259161_at	carbonic anhydrase, chloroplast pr	CA1	AT3G01500	-7.72	-2.95	-9.31	4.36E-05	0.00154	2.68
256891_at	hypothetical protein contains simila	---	AT3G19030	2.70	1.44	9.30	4.40E-05	0.001546	2.67
259592_at	lipid transfer protein, putative conta	LTPG1	AT1G27950	-9.71	-3.28	-9.30	4.41E-05	0.001547	2.67
258736_at	unknown protein	---	AT3G05900	-3.23	-1.69	-9.29	4.42E-05	0.001548	2.66
253740_at	Expressed protein ; supported by cl	---	AT4G28706	-2.41	-1.27	-9.29	4.43E-05	0.001548	2.66
260222_at	putative alpha galactosyltransferase	XXT5	AT1G74380	-4.34	-2.12	-9.27	4.49E-05	0.001559	2.65
259645_at	putative DNA-binding protein predi	BIM2	AT1G69010	-2.70	-1.43	-9.27	4.49E-05	0.001559	2.65
247251_at	cellulose synthase catalytic subunit	CESA6	AT5G64740	-2.88	-1.53	-9.26	4.51E-05	0.001565	2.64
266899_at	hypothetical protein predicted by ge	---	AT2G34620	-6.47	-2.69	-9.23	4.63E-05	0.001592	2.62
265884_at	unknown protein	---	AT2G42320	-2.53	-1.34	-9.22	4.65E-05	0.001593	2.61
261131_at	unknown protein	---	AT1G19835	-3.76	-1.91	-9.22	4.65E-05	0.001593	2.61
247573_at	anthocyanin 5-aromatic acyltransfe	AACT1	AT5G61160	57.15	5.84	9.22	4.66E-05	0.001593	2.61
252255_at	pectinesterase - like protein pectin	---	AT3G49220	-5.79	-2.53	-9.21	4.68E-05	0.001597	2.60
265405_at	putative protein kinase contains a p	---	AT2G16750	-3.90	-1.96	-9.20	4.70E-05	0.001597	2.60

245629_at	hypothetical protein predicted by ge	---	AT1G56580	-2.65	-1.41	-9.19	4.73E-05	0.001601	2.59
258982_at	putative serine/threonine protein ki	---	AT3G08870	3.27	1.71	9.17	4.81E-05	0.001615	2.58
244950_at	cytochrome c oxidase subunit 2	---	---	3.24	1.70	9.17	4.82E-05	0.001615	2.57
254665_at	beta-1,3-glucanase-like protein stro	---	AT4G18340	-3.79	-1.92	-9.16	4.83E-05	0.001615	2.57
259106_at	unknown protein ;supported by full-	RALFL22	AT3G05490	-5.87	-2.55	-9.16	4.84E-05	0.001615	2.57
255709_at	putative YABBY3 axial regulator ; s	YAB3	AT4G00180	-2.37	-1.24	-9.16	4.84E-05	0.001615	2.57
257076_at	unknown protein	---	AT3G19680	-5.15	-2.36	-9.15	4.89E-05	0.001618	2.56
254709_at	Expressed protein ; supported by cl	AGD8	AT4G17890	-2.48	-1.31	-9.14	4.91E-05	0.001618	2.55
250062_at	BCS1 - like protein h-bcs1, Homo s	---	AT5G17760	3.52	1.82	9.14	4.92E-05	0.001618	2.55
245011_at	photosystem II G protein	---	---	-2.08	-1.06	-9.14	4.92E-05	0.001618	2.55
251584_at	putative protein At2g42580 - Arabi	TTL4	AT3G58620	-6.19	-2.63	-9.13	4.93E-05	0.001618	2.55
254453_at	amino acid transport protein AAT1	AAT1	AT4G21120	3.14	1.65	9.13	4.95E-05	0.001618	2.54
262729_at	rac-like GTP binding protein (ARAC	ARAC5	AT1G75840	-2.67	-1.42	-9.13	4.96E-05	0.001618	2.54
252997_at	putative pollen allergen pollen aller	ATEXLA2	AT4G38400	-7.33	-2.87	-9.12	4.98E-05	0.00162	2.54
247884_at	lipid transfer protein; glossy1 homol	CER3	AT5G57800	-6.95	-2.80	-9.11	5.03E-05	0.001622	2.53
255543_at	predicted protein of unknown functi	---	AT4G01870	7.50	2.91	9.10	5.03E-05	0.001622	2.53
260493_at	hypothetical protein predicted by ge	---	AT2G41830	-3.70	-1.89	-9.10	5.03E-05	0.001622	2.53
248138_at	pyruvate decarboxylase (gb|AAB16	PDC2	AT5G54960	2.74	1.45	9.10	5.03E-05	0.001622	2.53
258179_at	integral membrane protein, putative	---	AT3G21690	2.98	1.58	9.10	5.03E-05	0.001622	2.53
251192_at	alpha galactosyltransferase-like pr	XT1	AT3G62720	-6.04	-2.59	-9.08	5.11E-05	0.001641	2.51
259790_s_a	auxin-induced protein, putative sim	---	AT1G29430	-9.62	-3.27	-9.08	5.13E-05	0.001643	2.51
245136_at	putative auxin-regulated protein	---	AT2G45210	6.19	2.63	9.06	5.19E-05	0.001652	2.50
266745_at	unknown protein ; supported by cD	PKS1	AT2G02950	-6.03	-2.59	-9.05	5.20E-05	0.001655	2.49
259586_at	unknown protein	---	AT1G28100	-2.00	-1.00	-9.05	5.24E-05	0.001662	2.48
266533_s_a	putative plasma membrane intrinsic	PIP2;8	AT2G16850	-2.84	-1.50	-9.03	5.29E-05	0.001666	2.47
255850_at	putative chloroplast 50S ribosomal	---	AT2G33450	-2.31	-1.21	-9.03	5.29E-05	0.001666	2.47
257686_at	unknown protein similar to unknowr	SDRB	AT3G12800	2.24	1.16	9.03	5.31E-05	0.001666	2.47
258371_at	hypothetical protein contains simila	---	AT3G14410	-2.20	-1.14	-9.01	5.36E-05	0.001673	2.46
246284_at	putative protein	---	AT4G36780	-2.18	-1.13	-9.00	5.40E-05	0.001682	2.45
256057_at	unknown protein contains similarity	NDA1	AT1G07180	-4.81	-2.27	-8.99	5.43E-05	0.001687	2.45
258239_at	putative chlorophyll A-B binding pro	LHCB2.3	AT3G27690	-29.66	-4.89	-8.98	5.47E-05	0.001693	2.44
244902_at	NADH dehydrogenase subunit 4L	---	ATMG00650	2.23	1.15	8.98	5.49E-05	0.001693	2.44
254764_at	putative protein ; supported by cDN	---	AT4G13250	4.92	2.30	8.97	5.51E-05	0.001699	2.43
256999_at	hypothetical protein predicted by ge	---	AT3G14200	-2.01	-1.01	-8.97	5.53E-05	0.001702	2.43
255626_at	coded for by A. thaliana cDNA T20(	---	AT4G00780	2.30	1.20	8.97	5.54E-05	0.001702	2.43

260009_at	unknown protein ;supported by full-	---	AT1G67950	-2.99	-1.58	-8.96	5.55E-05	0.001704	2.42
261822_at	unknown protein ;supported by full-	---	AT1G11380	-3.87	-1.95	-8.92	5.70E-05	0.001729	2.39
259143_at	calmodulin-like protein similar to ca	---	AT3G10190	2.68	1.42	8.91	5.74E-05	0.001737	2.39
266938_at	hypothetical protein predicted by ge	HPT1	AT2G18950	2.40	1.26	8.88	5.87E-05	0.001758	2.36
254445_at	3-hydroxyisobutyrate dehydrogena	---	AT4G20930	2.09	1.07	8.88	5.88E-05	0.001758	2.36
264954_at	carboxyphosphonoenolpyruvate m	---	AT1G77060	-2.71	-1.44	-8.87	5.92E-05	0.001766	2.35
245987_at	NAM-like protein hypothetical prote	ANAC083	AT5G13180	2.17	1.12	8.83	6.10E-05	0.001791	2.32
258813_at	NAM-like protein (no apical meriste	anac046	AT3G04060	2.73	1.45	8.83	6.11E-05	0.001791	2.32
260225_at	putative glutathione S-transferase s	GSTU10	AT1G74590	22.22	4.47	8.83	6.11E-05	0.001791	2.32
254332_at	leucine rich repeat receptor kinase	---	AT4G22730	-2.84	-1.51	-8.82	6.12E-05	0.001791	2.32
255732_at	fatty acid condensing enzyme CUT	KCS5	AT1G25450	-6.80	-2.77	-8.81	6.18E-05	0.001802	2.31
256865_at	NAD dependent epimerase, putativ	GAE6	AT3G23820	-3.89	-1.96	-8.81	6.20E-05	0.001806	2.30
247480_at	KED - like protein KED, Nicotiana t	ATBAG7	AT5G62390	-2.48	-1.31	-8.80	6.22E-05	0.001809	2.30
264910_at	resistance protein, putative similar	---	AT1G61100	-4.43	-2.15	-8.80	6.22E-05	0.001809	2.30
251922_at	protein kinase -like protein protein	---	AT3G54030	-3.96	-1.99	-8.79	6.28E-05	0.001813	2.29
262482_at	SRG1-like protein Strong homolog	SRG1	AT1G17020	11.65	3.54	8.78	6.30E-05	0.001813	2.29
247934_at	putative protein similar to unknown	---	AT5G57000	-2.04	-1.03	-8.78	6.32E-05	0.001813	2.28
254370_at	L1 specific homeobox gene ATML1	ATML1	AT4G21750	-2.49	-1.32	-8.77	6.34E-05	0.001818	2.28
260676_at	integral membrane protein, putative	---	AT1G19450	-3.91	-1.97	-8.77	6.38E-05	0.001822	2.27
267209_at	unknown protein ;supported by full-	---	AT2G30930	-2.46	-1.30	-8.75	6.43E-05	0.001827	2.27
257338_s_a	NADH dehydrogenase subunit 5 (na	---	AT2G07711	2.68	1.42	8.75	6.46E-05	0.001832	2.26
248914_at	Rab-type small GTP-binding protein	AtRABA1c	AT5G45750	-3.29	-1.72	-8.73	6.55E-05	0.001849	2.24
257216_at	4-methyl-5(b-hydroxyethyl)-thiazole	---	AT3G14990	4.68	2.23	8.73	6.56E-05	0.001849	2.24
263391_at	putative monogalactosyldiacylglyce	MGDC	AT2G11810	3.58	1.84	8.73	6.56E-05	0.001849	2.24
265817_at	histone H1 ;supported by full-lengt	HIS1-3	AT2G18050	6.56	2.71	8.72	6.59E-05	0.001852	2.24
256228_at	phosphoglycerate kinase, putative	---	AT1G56190	-2.48	-1.31	-8.72	6.60E-05	0.001852	2.24
245042_at	hypothetical protein predicted by ge	HEMD	AT2G26540	-3.51	-1.81	-8.69	6.73E-05	0.00187	2.22
251993_at	peroxiredoxin - like protein peroxire	---	AT3G52960	-2.27	-1.19	-8.69	6.74E-05	0.00187	2.21
266905_at	putative katanin ;supported by full-	---	AT2G34560	-2.73	-1.45	-8.69	6.76E-05	0.00187	2.21
253394_at	putative protein predicted protein,	VTE1	AT4G32770	-3.66	-1.87	-8.68	6.79E-05	0.001871	2.21
263382_at	putative anthranilate N-hydroxycinn	---	AT2G40230	-2.42	-1.27	-8.68	6.79E-05	0.001871	2.21
247069_at	pectinesterase like protein ;suppor	sks17	AT5G66920	-5.81	-2.54	-8.67	6.82E-05	0.001875	2.20
264307_at	hypothetical protein contains simila	---	AT1G61900	-2.30	-1.20	-8.66	6.88E-05	0.001886	2.19
263207_at	putative endoxyloglucan transferase	XTH33	AT1G10550	-17.37	-4.12	-8.66	6.89E-05	0.001887	2.19
261763_at	ABC transporter, putative similar to	PDR12	AT1G15520	20.13	4.33	8.65	6.91E-05	0.001888	2.19

254260_at	hypothetical protein	---	AT4G23440	-2.96	-1.56	-8.65	6.92E-05	0.001888	2.19
256456_at	unknown protein ; supported by full-	---	AT1G75180	-3.68	-1.88	-8.65	6.94E-05	0.001888	2.18
251855_at	sugar-phosphate isomerase - like p	---	AT3G54690	-4.10	-2.03	-8.64	6.97E-05	0.00189	2.18
246411_at	hypothetical protein contains simila	---	AT1G57770	-4.74	-2.24	-8.64	6.98E-05	0.00189	2.18
260746_at	glutathione transferase, putative si	ATGSTU19	AT1G78380	2.03	1.02	8.64	6.99E-05	0.00189	2.18
263851_at	putative retroelement pol polyprotei	---	---	6.22	2.64	8.62	7.06E-05	0.001901	2.17
265573_at	putative zinc-finger protein similar t	---	AT2G28200	4.23	2.08	8.62	7.07E-05	0.001902	2.16
254077_at	putative protein NorM, Vibrio parah	---	AT4G25640	2.34	1.23	8.62	7.10E-05	0.001908	2.16
253875_at	putative protein ENOD20 gene, Me	---	AT4G27520	-4.01	-2.00	-8.61	7.12E-05	0.001909	2.16
259020_at	unknown protein ; supported by cD	---	AT3G07470	-2.30	-1.20	-8.60	7.18E-05	0.001917	2.15
244937_at	NADH dehydrogenase 49KDa prote	---	---	-3.48	-1.80	-8.60	7.19E-05	0.001917	2.15
249493_at	acyltransferase -like protein Anthoc	---	AT5G39080	-3.07	-1.62	-8.60	7.19E-05	0.001917	2.14
249467_at	NAM / CUC2 - like protein CUC2, A	ATNAC6	AT5G39610	9.58	3.26	8.58	7.27E-05	0.001926	2.13
244953_s_a	NADH dehydrogenase subunit 6	---	AT2G07731	3.02	1.60	8.58	7.27E-05	0.001926	2.13
258565_at	unknown protein ; supported by cD	---	AT3G04350	2.86	1.52	8.58	7.30E-05	0.001927	2.13
261949_at	hypothetical protein predicted by ge	BDG1	AT1G64670	-5.67	-2.50	-8.58	7.30E-05	0.001927	2.13
247074_at	putative protein contains similarity t	---	AT5G66590	-2.64	-1.40	-8.57	7.32E-05	0.001931	2.13
256529_at	protein kinase, putative contains P	---	AT1G33260	-3.78	-1.92	-8.54	7.49E-05	0.001949	2.10
258033_at	unknown protein similar to MRP-like	MRP6	AT3G21250	3.51	1.81	8.54	7.50E-05	0.001949	2.10
265938_at	putative SF21 protein {Helianthus a	---	AT2G19620	-6.66	-2.74	-8.54	7.51E-05	0.001949	2.10
248487_at	ATP-dependent Clp protease ATP-	ERD1	AT5G51070	2.12	1.09	8.52	7.64E-05	0.001966	2.08
258632_s_a	putative MAP3K epsilon protein kin	MAPKKK7	AT3G07980	-2.55	-1.35	-8.51	7.66E-05	0.001969	2.08
246133_at	aldehyde oxidase AAO1 ; supporte	AAO1	AT5G20960	7.41	2.89	8.51	7.70E-05	0.001976	2.07
246368_at	light repressible receptor protein ki	---	AT1G51890	8.75	3.13	8.50	7.75E-05	0.00198	2.06
251661_at	putative protein NODULIN-26 - Gly	SIP2;1	AT3G56950	2.46	1.30	8.49	7.80E-05	0.001986	2.06
259237_at	putative 2-cys peroxiredoxin BAS1	---	AT3G11630	-2.59	-1.38	-8.48	7.87E-05	0.001988	2.05
258484_at	sterol-C5-desaturase identical to GI	STE1	AT3G02580	-2.00	-1.00	-8.47	7.87E-05	0.001988	2.05
253492_at	enoyl-CoA hydratase - like protein	---	AT4G31810	5.34	2.42	8.47	7.88E-05	0.001988	2.05
255674_at	probable plasma membrane intrinsi	PIP1;4	AT4G00430	-3.73	-1.90	-8.47	7.89E-05	0.001988	2.05
252441_at	putative protein ; supported by cDN	PTAC16	AT3G46780	-2.86	-1.52	-8.46	7.97E-05	0.002	2.04
267335_s_a	putative beta-1,3-glucanase	---	AT1G64760	-2.96	-1.56	-8.45	8.01E-05	0.002002	2.03
254638_at	hypothetical protein	---	AT4G18740	-2.84	-1.51	-8.45	8.02E-05	0.002002	2.03
251803_at	putative protein predicted proteins,	---	AT3G55350	-2.40	-1.26	-8.43	8.13E-05	0.002023	2.01
249073_at	vegetative storage protein-like ;sup	---	AT5G44020	-6.04	-2.59	-8.43	8.16E-05	0.002026	2.01
258719_at	putative pectate lyase simliar to pec	---	AT3G09540	-4.75	-2.25	-8.40	8.32E-05	0.002058	1.99

266993_at	nodulin-like protein ; supported by	---	AT2G39210	3.41	1.77	8.39	8.35E-05	0.002063	1.99
263513_at	unknown protein	---	AT2G12400	-3.12	-1.64	-8.38	8.47E-05	0.00208	1.97
252563_at	putative protein cim1 induced aller	ATEXLA1	AT3G45970	-8.14	-3.03	-8.34	8.72E-05	0.002123	1.94
245339_at	hypothetical protein ;supported by f	COBL7	AT4G16120	-3.44	-1.78	-8.33	8.77E-05	0.00213	1.93
245757_at	phosphate-induced (phi-1) protein,	PHI-1	AT1G35140	-33.33	-5.06	-8.33	8.77E-05	0.00213	1.93
247038_at	anthranilate N-hydroxycinnamoyl/be	EPS1	AT5G67160	2.49	1.32	8.32	8.80E-05	0.002136	1.93
256848_at	hypothetical protein similar to hypot	---	AT3G27960	-7.74	-2.95	-8.32	8.81E-05	0.002136	1.93
253571_at	putative calmodulin-binding protein	---	AT4G31000	-8.43	-3.07	-8.31	8.89E-05	0.002145	1.92
263676_at	putative RNA-binding protein Ident	CRB	AT1G09340	-2.47	-1.31	-8.31	8.90E-05	0.002145	1.92
248273_at	putative protein contains similarity t	---	AT5G53500	-3.38	-1.76	-8.29	9.02E-05	0.002169	1.90
264037_at	putative steroid sulfotransferase ;s	---	AT2G03750	-2.23	-1.16	-8.29	9.03E-05	0.002169	1.90
249818_at	Expressed protein ; supported by c	TUB8	AT5G23860	-3.39	-1.76	-8.29	9.06E-05	0.002172	1.90
253215_at	putative protein AT.I.24-7, Arabido	---	AT4G34950	-5.79	-2.53	-8.27	9.13E-05	0.002183	1.89
256076_at	unknown protein ; supported by cD	---	AT1G18060	-2.99	-1.58	-8.27	9.14E-05	0.002183	1.89
247817_at	Expressed protein ; supported by fu	---	AT5G58375	2.20	1.13	8.26	9.20E-05	0.002187	1.88
246952_at	putative protein similar to unknown	OFP13	AT5G04820	-2.27	-1.18	-8.26	9.20E-05	0.002187	1.88
250327_at	putative serine rich protein predicte	---	AT5G12050	-6.87	-2.78	-8.26	9.21E-05	0.002187	1.88
263823_s_a	AP2 domain transcription factor	---	AT2G40340	4.22	2.08	8.25	9.30E-05	0.002202	1.87
253022_at	putative protein	---	AT4G38060	3.73	1.90	8.25	9.33E-05	0.002204	1.87
250983_at	putative protein In2, Zea mays, EM	---	AT5G02780	12.53	3.65	8.24	9.35E-05	0.002204	1.86
253309_at	male sterility 2-like protein male ste	CER4	AT4G33790	-4.24	-2.08	-8.24	9.35E-05	0.002204	1.86
252711_at	lipid-transfer protein-like protein no	---	AT3G43720	-9.20	-3.20	-8.24	9.35E-05	0.002204	1.86
253046_at	cytochrome P450 - like protein cyt	CYP81D8	AT4G37370	14.47	3.86	8.24	9.37E-05	0.002205	1.86
264280_at	beta-glucosidase, putative similar t	BGLU46	AT1G61820	4.15	2.05	8.24	9.39E-05	0.002205	1.86
248153_at	cyclic nucleotide and calmodulin-re	ATCNGC4	AT5G54250	2.06	1.04	8.21	9.60E-05	0.002229	1.83
252117_at	mucin -like protein hemomucin, Dr	YLS2	AT3G51430	2.96	1.56	8.21	9.60E-05	0.002229	1.83
257204_at	Expressed protein ; supported by fu	RALFL24	AT3G23805	-5.68	-2.51	-8.21	9.61E-05	0.002229	1.83
256725_at	hypothetical protein predicted by ge	---	AT2G34070	-4.22	-2.08	-8.20	9.64E-05	0.002231	1.83
253197_at	putative protein Cyanophora parad	---	AT4G35250	-2.62	-1.39	-8.20	9.65E-05	0.002231	1.83
263545_at	unknown protein	---	AT2G21560	4.92	2.30	8.20	9.65E-05	0.002231	1.83
263553_at	putative purple acid phosphatase p	PAP10	AT2G16430	2.21	1.14	8.20	9.68E-05	0.002233	1.83
258421_at	MtN3-like protein similar to MtN3 G	---	AT3G16690	-3.76	-1.91	-8.20	9.69E-05	0.002233	1.83
257766_at	auxin-inducible gene (IAA2) identic	IAA2	AT3G23030	-2.84	-1.51	-8.20	9.69E-05	0.002233	1.82
258528_at	unknown protein contains Pfam pro	---	AT3G06770	-4.78	-2.26	-8.19	9.76E-05	0.002245	1.82
262225_at	pectinesterase, putative similar to p	ATPME1	AT1G53840	-4.06	-2.02	-8.18	9.78E-05	0.002245	1.82

252945_at	putative protein ;supported by full-l	---	AT4G39140	2.10	1.07	8.18	9.84E-05	0.002253	1.81
262314_at	unknown protein contains similarity	---	AT1G70810	2.17	1.12	8.17	9.85E-05	0.002253	1.81
256617_at	unknown protein ; supported by full	---	AT3G22240	5.13	2.36	8.16	9.98E-05	0.002269	1.79
267261_at	unknown protein ;supported by full-	---	AT2G23120	-3.43	-1.78	-8.15	9.99E-05	0.002269	1.79
244943_at	NADH dehydrogenase subunit 9	---	ATMG00070	2.42	1.27	8.15	0.0001	0.002269	1.79
251150_at	putative protein Sb34 (PREG-like p	CYCP1;1	AT3G63120	-2.07	-1.05	-8.15	0.0001	0.002269	1.79
255647_at	Ca2+-transporting ATPase - like pro	ECA2	AT4G00900	2.24	1.17	8.14	0.000101	0.002281	1.78
266650_at	unknown protein	---	AT2G25800	-2.24	-1.17	-8.14	0.000101	0.002281	1.78
253617_at	hypothetical protein	---	AT4G30410	-5.82	-2.54	-8.13	0.000102	0.00229	1.77
248608_at	ATP citrate lyase ; supported by cD	ACLB-2	AT5G49460	-2.16	-1.11	-8.13	0.000102	0.002291	1.77
262661_s_a	hypothetical protein	---	AT1G14230	-12.70	-3.67	-8.13	0.000102	0.002291	1.77
259660_at	unknown protein ; supported by full-	---	AT1G55260	-11.11	-3.47	-8.13	0.000102	0.002291	1.77
247399_at	putative protein similar to unknown	---	AT5G62960	-3.33	-1.74	-8.12	0.000103	0.002302	1.76
250213_at	H-protein promoter binding factor-1	TBP1	AT5G13820	2.52	1.33	8.11	0.000103	0.002307	1.76
254174_at	putative protein various predicted p	YSL1	AT4G24120	2.79	1.48	8.10	0.000104	0.002327	1.75
250300_at	putative protein various predicted p	---	AT5G11890	-2.65	-1.41	-8.09	0.000105	0.002331	1.74
256305_at	glutathione S-conjugate transportin	MRP1	AT1G30400	2.62	1.39	8.08	0.000106	0.002333	1.73
266140_at	nodulin-like protein ; supported by	---	AT2G28120	-2.44	-1.29	-8.07	0.000107	0.002352	1.72
258202_at	unknown protein	---	AT3G13940	2.98	1.57	8.07	0.000107	0.002354	1.72
257022_at	zinc finger protein, putative similar	AZF2	AT3G19580	2.30	1.20	8.06	0.000107	0.002357	1.71
254034_at	P-glycoprotein-2 (pgp2)	PGP2	AT4G25960	-2.58	-1.37	-8.06	0.000108	0.002357	1.71
261767_s_a	adenine nucleotide translocase, pu	NTT1	AT1G15500	2.12	1.09	8.05	0.000108	0.002365	1.70
261055_at	chloroplast nucleoid DNA binding p	---	AT1G01300	-2.12	-1.08	-8.05	0.000108	0.002365	1.70
266418_at	putative annexin ;supported by full-	ANNAT4	AT2G38750	-6.86	-2.78	-8.05	0.000108	0.002365	1.70
245349_at	cyanohydrin lyase like protein ;supp	MES16	AT4G16690	4.30	2.10	8.04	0.000109	0.002367	1.70
262902_x_a	hypothetical protein similar to putati	---	AT1G59930	-2.89	-1.53	-8.04	0.000109	0.002372	1.69
252400_at	hypothetical protein	---	AT3G48020	3.97	1.99	8.02	0.000111	0.002391	1.68
258901_at	putative protein phosphatase-2C si	---	AT3G05640	-19.30	-4.27	-8.02	0.000111	0.002392	1.68
251259_at	putative protein phosphoprotein ph	---	AT3G62260	2.85	1.51	8.01	0.000111	0.002396	1.68
260501_at	unknown protein ; supported by cD	---	AT2G41770	-2.44	-1.29	-8.01	0.000111	0.002396	1.67
263456_at	unknown protein	---	AT2G22125	-2.40	-1.26	-8.01	0.000111	0.002396	1.67
256855_at	30S ribosomal protein S20 contains	---	AT3G15190	-2.20	-1.13	-8.01	0.000112	0.002402	1.67
246792_at	putative protein predicted proteins,	---	AT5G27290	-4.01	-2.01	-8.00	0.000112	0.002402	1.67
258923_at	putative glucose acyltransferase sir	SCPL7	AT3G10450	4.10	2.04	8.00	0.000113	0.002411	1.66
259520_at	hypothetical protein	---	AT1G12320	2.99	1.58	7.98	0.000114	0.002425	1.65

259618_at	myb-related transcription factor (cp	MYB112	AT1G48000	2.51	1.33	7.98	0.000114	0.002427	1.65
248756_at	sodium-dicarboxylate cotransporter	TDT	AT5G47560	3.62	1.86	7.98	0.000114	0.002427	1.65
252866_at	putative protein	---	AT4G39840	-5.83	-2.54	-7.97	0.000115	0.002432	1.64
263947_at	unknown protein ;supported by full-	---	AT2G35820	3.20	1.68	7.95	0.000117	0.002457	1.62
246584_at	putative protein predicted protein, A	---	AT5G14730	10.01	3.32	7.95	0.000117	0.002457	1.62
251191_at	putative protein putative protein F1	---	AT3G62590	3.52	1.81	7.95	0.000117	0.002457	1.62
254805_at	pEARLI 1 ; supported by cDNA: gi_	pEARLI 1	AT4G12480	48.43	5.60	7.93	0.000118	0.002479	1.61
254189_at	putative protein cellulose synthase	CSLG2	AT4G24000	6.21	2.63	7.93	0.000118	0.002479	1.61
262665_at	xyloglucan fucosyltransferase, puta	FUT7	AT1G14070	5.47	2.45	7.92	0.000119	0.002493	1.60
250960_at	putative protein	---	AT5G02940	-3.31	-1.72	-7.92	0.00012	0.002497	1.60
251906_at	putative protein several hypothetica	ATCHX20	AT3G53720	2.34	1.22	7.92	0.00012	0.002497	1.59
259800_at	Expressed protein ; supported by fu	---	AT1G72175	-2.16	-1.11	-7.91	0.00012	0.0025	1.59
249941_at	putative protein similar to unknown	---	AT5G22270	2.32	1.22	7.91	0.000121	0.0025	1.59
251305_at	peptidylprolyl isomerase ROC4 ;su	ROC4	AT3G62030	-2.67	-1.42	-7.89	0.000122	0.002513	1.57
258395_at	putative jasmonic acid regulatory pr	ANAC055	AT3G15500	3.19	1.67	7.89	0.000123	0.002516	1.57
261758_at	hypothetical protein contains simila	ADT6	AT1G08250	2.82	1.50	7.89	0.000123	0.002516	1.57
261135_at	defensin AMP1, putative similar to	PDF1.4	AT1G19610	17.71	4.15	7.89	0.000123	0.002516	1.57
261240_at	subtilisin-like serine protease conta	SBT3.5	AT1G32940	5.30	2.41	7.87	0.000124	0.002533	1.56
249174_at	putative protein similar to unknown	---	AT5G42900	3.20	1.68	7.87	0.000124	0.002534	1.56
267279_at	hypothetical protein predicted by ge	---	AT2G19460	-3.95	-1.98	-7.87	0.000124	0.002534	1.56
257173_at	S-adenosyl-L-homocysteinas, puta	SAHH2	AT3G23810	-11.45	-3.52	-7.87	0.000124	0.002534	1.55
255794_at	putative NAM (no apical meristem)-	ANAC041	AT2G33480	4.22	2.08	7.84	0.000127	0.00256	1.53
251176_at	Ca2+-transporting ATPase -like pro	---	AT3G63380	9.99	3.32	7.84	0.000127	0.00256	1.53
256461_s_a	adenylosuccinate lyase - like protei	---	AT1G36280	-6.49	-2.70	-7.84	0.000127	0.002564	1.53
265228_s_a	hypothetical protein	---	AT2G07698	2.15	1.10	7.83	0.000128	0.002579	1.52
245976_at	WRKY-like protein WRKY DNA bin	WRKY75	AT5G13080	15.69	3.97	7.83	0.000129	0.002582	1.52
249847_at	serine carboxypeptidase II-like prot	SCPL34	AT5G23210	-2.65	-1.41	-7.82	0.000129	0.002584	1.52
250827_at	cellulose synthase catalytic subunit	CEV1	AT5G05170	-2.42	-1.28	-7.82	0.00013	0.002588	1.51
245148_at	putative pectinesterase ; supported	---	AT2G45220	16.55	4.05	7.82	0.00013	0.002588	1.51
245325_at	xyloglucan endotransglycosylase-re	XTR7	AT4G14130	-20.10	-4.33	-7.81	0.000131	0.002598	1.50
246446_at	putative protein hypothetical protei	---	AT5G17640	-2.19	-1.13	-7.80	0.000131	0.002602	1.50
252184_at	steroid 22-alpha-hydroxylase (DWF	DWF4	AT3G50660	-2.33	-1.22	-7.80	0.000132	0.002609	1.49
266000_at	putative cytochrome P450 identical	CYP71B6	AT2G24180	3.52	1.82	7.79	0.000132	0.002613	1.49
249807_at	pectinacetylesterase	---	AT5G23870	-2.52	-1.33	-7.79	0.000133	0.002622	1.48
255774_at	unknown protein	---	AT1G18620	-3.98	-1.99	-7.76	0.000136	0.002659	1.46

254085_at	abscisic acid-induced - like protein	HVA22D	AT4G24960	-3.71	-1.89	-7.74	0.000137	0.002679	1.45
258535_at	unknown protein ; supported by cD	---	AT3G06750	-3.23	-1.69	-7.74	0.000138	0.002682	1.44
246463_at	quinone oxidoreductase -like prote	AT-AER	AT5G16970	2.58	1.37	7.74	0.000138	0.002682	1.44
244983_at	ribosomal protein L16	---	---	-3.13	-1.64	-7.73	0.000138	0.002682	1.44
248683_at	putative protein similar to unknown	---	AT5G48490	-7.64	-2.93	-7.73	0.000138	0.002682	1.44
253281_at	predicted protein	UGT73B1	AT4G34138	3.89	1.96	7.73	0.000139	0.002682	1.44
254122_at	CER2 ;supported by full-length cDI	CER2	AT4G24510	-35.22	-5.14	-7.73	0.000139	0.002682	1.44
266254_at	putative membrane transporter	NAT12	AT2G27810	-2.24	-1.17	-7.73	0.000139	0.002682	1.44
257793_at	unknown protein ;supported by full-	---	AT3G26960	-12.16	-3.60	-7.71	0.000141	0.0027	1.42
245692_at	myc - like protein	BHLH101	AT5G04150	-2.39	-1.26	-7.71	0.000141	0.002701	1.42
259530_at	hypothetical protein	---	AT1G12450	-3.21	-1.68	-7.71	0.000141	0.002701	1.42
254485_at	cell-cell signaling protein csgA - lik	---	AT4G20760	-2.25	-1.17	-7.71	0.000141	0.002704	1.42
249065_at	putative protein similar to unknown	---	AT5G44260	-3.25	-1.70	-7.70	0.000142	0.002709	1.41
261315_at	AP2 domain containing protein, pu	ERF8	AT1G53170	3.77	1.92	7.70	0.000143	0.002712	1.41
253975_at	putative protein proliferating-cell nu	---	AT4G26600	4.18	2.06	7.69	0.000143	0.002712	1.41
247679_at	1-aminocyclopropane-1-carboxylat	---	AT5G59540	3.66	1.87	7.68	0.000144	0.002722	1.40
256327_at	unknown protein ;supported by full-	GAUT9	AT3G02350	-2.15	-1.10	-7.68	0.000144	0.002722	1.40
263433_at	putative myo-inositol 1-phosphate s	MIPS2	AT2G22240	-2.58	-1.37	-7.68	0.000145	0.002726	1.39
247162_at	xyloglucan endo-transglycosylase-l	---	AT5G65730	-5.57	-2.48	-7.68	0.000145	0.002726	1.39
254520_at	potassium transporter-like protein p	---	AT4G19960	2.36	1.24	7.67	0.000145	0.002731	1.39
248311_at	beta-carotene hydroxylase	BETA-OHA	AT5G52570	-2.87	-1.52	-7.67	0.000146	0.002733	1.38
267635_at	rhodanese-like family protein ;supp	---	AT2G42220	-2.88	-1.53	-7.67	0.000146	0.002733	1.38
258368_at	subtilisin-like serine protease conta	---	AT3G14240	-3.88	-1.95	-7.66	0.000146	0.002735	1.38
244981_at	ribosomal protein S8	---	---	-2.08	-1.05	-7.64	0.000149	0.002765	1.36
260812_at	nodulin-like protein similar to MtN2	---	AT1G43650	-2.74	-1.46	-7.63	0.000151	0.002794	1.35
254563_at	putative protein several hypothetica	ERD3	AT4G19120	-2.29	-1.20	-7.62	0.000152	0.002804	1.34
251365_at	putative DNA-binding protein At2g3	---	AT3G61310	-2.20	-1.14	-7.61	0.000152	0.002813	1.34
253794_at	putative protein dimethylaniline mo	---	AT4G28720	-5.67	-2.50	-7.61	0.000153	0.002813	1.33
263497_at	cold-regulated protein cor15a precu	COR15A	AT2G42540	-27.93	-4.80	-7.58	0.000157	0.002868	1.30
247488_at	putative protein MtN19, Medicago t	---	AT5G61820	2.54	1.35	7.57	0.000157	0.002869	1.30
265042_at	unknown protein Similar to acid ph	---	AT1G04040	-6.37	-2.67	-7.56	0.000159	0.002877	1.29
253039_at	squalene epoxidase - like protein s	SQE3	AT4G37760	-3.45	-1.79	-7.56	0.000159	0.002878	1.29
253493_at	putative protein various predicted p	ENP	AT4G31820	-2.84	-1.51	-7.56	0.000159	0.002878	1.29
259729_at	hypothetical protein predicted by ge	---	AT1G77640	-5.80	-2.54	-7.56	0.000159	0.00288	1.29
263467_at	unknown protein	---	AT2G31730	-3.76	-1.91	-7.56	0.00016	0.00288	1.29

249045_at	berberine bridge enzyme-like protei	---	AT5G44380	8.12	3.02	7.55	0.00016	0.002886	1.28
259437_at	protein serine/threonine kinase, pu	---	AT1G01540	-3.25	-1.70	-7.54	0.000161	0.002896	1.27
264746_at	unknown protein similar to putative	WRKY6	AT1G62300	5.64	2.50	7.54	0.000161	0.002896	1.27
252411_at	putative protein PMP31 protein - C	PEX11B	AT3G47430	3.51	1.81	7.54	0.000161	0.002896	1.27
261768_at	gibberellin 3 beta-hydroxylase, put	GA3OX1	AT1G15550	-2.04	-1.03	-7.54	0.000162	0.002898	1.27
264338_at	potassium transporter, putative sim	KUP6	AT1G70300	2.62	1.39	7.54	0.000162	0.0029	1.27
251796_at	synaptic glycoprotein SC2-like prot	---	AT3G55360	-2.74	-1.46	-7.53	0.000163	0.002912	1.26
260924_at	hypothetical protein similar to Pto ki	---	AT1G21590	2.51	1.33	7.52	0.000164	0.002918	1.26
255617_at	putative protein kinase	---	AT4G01330	-2.14	-1.09	-7.52	0.000164	0.002918	1.26
258997_at	hypothetical protein similar to unkno	---	AT3G01810	-2.86	-1.52	-7.52	0.000164	0.00292	1.25
253478_at	putative protein trichohyalin - huma	---	AT4G32350	-2.77	-1.47	-7.52	0.000165	0.00292	1.25
247126_at	protein phosphatase 2C-like protein	---	AT5G66080	-2.51	-1.33	-7.51	0.000165	0.002929	1.25
260898_at	plastid ribosomal protein L34 precu	---	AT1G29070	-2.23	-1.16	-7.51	0.000166	0.002929	1.24
248100_at	beta-1,3-glucanase-like protein ;su	---	AT5G55180	-5.99	-2.58	-7.51	0.000166	0.002933	1.24
255536_at	Expressed protein ; supported by fu	---	AT4G01575	-2.69	-1.43	-7.50	0.000168	0.002948	1.23
247819_at	MAP kinase ; supported by cDNA: g	WNK4	AT5G58350	2.45	1.29	7.49	0.000169	0.00296	1.23
258887_at	putative phospholipase D similar to	PLDP2	AT3G05630	2.41	1.27	7.49	0.000169	0.00296	1.23
257051_at	squamosa promoter binding protein	SPL5	AT3G15270	-6.35	-2.67	-7.48	0.00017	0.002972	1.22
267220_at	putative sugar nucleotide phosphor	ISPD	AT2G02500	-2.06	-1.04	-7.47	0.000171	0.00298	1.21
259664_at	unknown protein ; supported by full-	AGP21	AT1G55330	-38.51	-5.27	-7.47	0.000171	0.00298	1.21
259248_at	putative heat-shock protein similar t	---	AT3G07770	3.79	1.92	7.47	0.000172	0.002982	1.21
247925_at	TCH4 protein (gb|AAA92363.1) ; s	TCH4	AT5G57560	-12.58	-3.65	-7.46	0.000172	0.00299	1.20
253042_at	formamidase - like protein formami	---	AT4G37550	-2.76	-1.47	-7.45	0.000174	0.003005	1.19
247327_at	peroxidase (emb|CAA67551.1) ;su	---	AT5G64120	14.11	3.82	7.45	0.000174	0.003005	1.19
260302_at	putative sulfate transporter contains	---	AT1G80310	2.22	1.15	7.44	0.000176	0.00302	1.18
253424_at	putative protein ; supported by cDN	---	AT4G32330	-2.10	-1.07	-7.42	0.000179	0.003054	1.16
258684_at	putative protein kinase contains Pf	---	AT3G08680	-2.20	-1.14	-7.41	0.000179	0.003059	1.16
261769_at	plastocyanin identical to plastocyan	PETE1	AT1G76100	-2.05	-1.04	-7.41	0.00018	0.003063	1.16
248460_at	Expressed protein ; supported by fu	---	AT5G50915	-8.57	-3.10	-7.40	0.000181	0.003066	1.15
248085_at	putative protein similar to unknown	SVL1	AT5G55480	-3.40	-1.77	-7.39	0.000183	0.003077	1.14
258225_at	unknown protein ; supported by cD	---	AT3G15630	-4.28	-2.10	-7.38	0.000184	0.003095	1.13
263411_at	putative C2H2-type zinc finger prote	---	AT2G28710	3.13	1.65	7.38	0.000185	0.003095	1.13
246408_at	hypothetical protein predicted by ge	---	AT1G57680	-2.14	-1.10	-7.37	0.000185	0.003097	1.13
267377_at	beta-ketoacyl-CoA synthase (FIDD	KCS10	AT2G26250	-3.54	-1.82	-7.37	0.000185	0.003097	1.12
255904_at	lemir (miraculin), putative similar to	---	AT1G17860	2.14	1.10	7.37	0.000186	0.003098	1.12

263536_at	putative WRKY-type DNA binding p	WRKY60	AT2G25000	3.89	1.96	7.35	0.000189	0.003119	1.10
255479_at	coded for by A. thaliana cDNA T46	SAG21	AT4G02380	10.55	3.40	7.34	0.00019	0.003133	1.10
249052_at	antifungal protein-like (PDF1.2)	PDF1.2	AT5G44420	12.91	3.69	7.34	0.000191	0.00314	1.09
257157_at	syntaxin-like protein similar to synt	SYP32	AT3G24350	-2.26	-1.17	-7.33	0.000192	0.003159	1.08
251282_at	putative protein transcription factor	CRF6	AT3G61630	4.10	2.03	7.32	0.000193	0.003161	1.08
254210_at	putative protein zinc finger protein,	---	AT4G23450	3.19	1.67	7.32	0.000194	0.003161	1.08
254630_at	glycolate oxidase - like protein (S)-	---	AT4G18360	11.73	3.55	7.31	0.000195	0.003172	1.07
264078_at	putative beta-galactosidase	BGAL8	AT2G28470	-7.30	-2.87	-7.30	0.000197	0.0032	1.06
264788_at	putative DnaJ protein ;supported b	---	AT2G17880	-5.81	-2.54	-7.29	0.000198	0.003211	1.05
250668_at	unknown protein ; supported by ful	---	AT5G07020	-2.22	-1.15	-7.29	0.000198	0.003211	1.05
251105_at	putative protein unknown protein A	ATSCAR4	AT5G01730	-3.70	-1.89	-7.29	0.000199	0.003217	1.05
256981_at	brassinosteroid receptor kinase, pu	BRL3	AT3G13380	2.61	1.39	7.28	0.0002	0.003223	1.04
263809_at	putative GDSL-motif lipase/hydrola	---	AT2G04570	-3.98	-1.99	-7.28	0.0002	0.003227	1.04
261639_at	tubulin alpha-2/alpha-4 chain, puta	TUA2	AT1G50010	-5.87	-2.55	-7.26	0.000203	0.003268	1.02
257219_at	uroporphyrinogen decarboxylase, p	HEME1	AT3G14930	-2.29	-1.19	-7.26	0.000203	0.003268	1.02
265649_at	putative ferredoxin ; supported by f	ATFD3	AT2G27510	3.04	1.60	7.25	0.000206	0.003285	1.01
258076_at	50S ribosomal protein L15, chlorop	RPL15	AT3G25920	-2.30	-1.20	-7.24	0.000206	0.003289	1.01
252549_at	protein kinase - like receptor-like p	---	AT3G45860	-4.32	-2.11	-7.24	0.000206	0.003289	1.01
253855_at	senescence-associated protein -lik	TET7	AT4G28050	-4.71	-2.23	-7.24	0.000207	0.003292	1.01
251428_at	beta-glucosidase-like protein severa	DIN2	AT3G60140	54.80	5.78	7.24	0.000207	0.003295	1.00
266995_at	putative cytochrome P450	CYP710A1	AT2G34500	12.55	3.65	7.23	0.000208	0.003311	1.00
260345_at	receptor protein kinase, putative si	RPK1	AT1G69270	2.41	1.27	7.23	0.000208	0.003311	1.00
260933_at	hypothetical protein contains non-c	---	AT1G02470	8.92	3.16	7.22	0.00021	0.003323	0.99
255692_at	putative protein	GPAT8	AT4G00400	-6.46	-2.69	-7.21	0.000211	0.003333	0.98
259185_at	putative phosphate/phosphoenolpy	PPT2	AT3G01550	-9.69	-3.28	-7.21	0.000211	0.003333	0.98
264990_at	unknown protein supported by cDN	---	AT1G27210	-3.13	-1.65	-7.21	0.000212	0.003333	0.98
258351_at	hypothetical protein contains simila	CNBT1	AT3G17700	2.47	1.30	7.21	0.000212	0.003335	0.98
250054_at	potassium-dependent sodium-calc	CAX7	AT5G17860	4.67	2.22	7.20	0.000213	0.003346	0.97
248040_at	putative protein contains similarity t	---	AT5G55970	3.52	1.82	7.20	0.000214	0.003355	0.97
259773_at	auxin-induced protein, putative sim	---	AT1G29500	-7.92	-2.99	-7.19	0.000216	0.003363	0.96
246777_at	RING-H2 zinc finger protein-like RI	---	AT5G27420	15.22	3.93	7.18	0.000218	0.003389	0.95
265913_at	Expressed protein ; supported by fu	---	AT2G25625	4.52	2.18	7.17	0.000219	0.003402	0.94
247427_at	putative protein similar to unknown	---	AT5G62580	-2.83	-1.50	-7.17	0.000219	0.003402	0.94
264521_at	unknown protein Location of EST g	---	AT1G10020	-3.95	-1.98	-7.17	0.000219	0.003402	0.94
247101_at	apospory-associated protein C-like	---	AT5G66530	-2.15	-1.11	-7.17	0.00022	0.003402	0.94

247175_at	G protein-coupled receptor-like prot	GCL1	AT5G65280	-4.87	-2.28	-7.17	0.00022	0.003402	0.94
256114_at	unknown protein ; supported by cDI	---	AT1G16850	-6.43	-2.68	-7.16	0.000221	0.003421	0.93
263628_at	unknown protein ;supported by full-	FLA7	AT2G04780	-8.21	-3.04	-7.16	0.000222	0.003421	0.93
264424_at	unknown protein similar to hypothet	---	AT1G61740	-2.05	-1.04	-7.16	0.000222	0.003422	0.93
261717_at	helix-loop-helix protein homolog, p	BEE1	AT1G18400	-8.23	-3.04	-7.15	0.000222	0.003424	0.93
260005_at	unknown protein ;supported by full-	---	AT1G67920	6.78	2.76	7.14	0.000225	0.00344	0.92
265151_at	hypothetical protein similar to hypot	---	AT1G51340	2.05	1.04	7.14	0.000225	0.003447	0.91
255506_at	predicted glycosyl transferase simi	GATL6	AT4G02130	-3.21	-1.68	-7.13	0.000227	0.003462	0.91
251519_at	putative protein hypothetical protei	GUN4	AT3G59400	-2.12	-1.09	-7.13	0.000227	0.003462	0.90
248607_at	NaCl-inducible Ca2+-binding protei	ATCP1	AT5G49480	4.39	2.13	7.13	0.000227	0.003462	0.90
251503_at	ABC transporter-like protein putativ	ATMRP14	AT3G59140	2.77	1.47	7.13	0.000228	0.003464	0.90
258003_at	expansin At-EXP5 identical to expa	EXPA5	AT3G29030	-7.01	-2.81	-7.12	0.000228	0.003467	0.90
249027_at	ATP dependent copper transporter	RAN1	AT5G44790	2.06	1.04	7.12	0.00023	0.003479	0.89
250248_at	transporter-like protein	ZIF1	AT5G13740	-3.49	-1.80	-7.10	0.000232	0.0035	0.88
259788_at	lipase/hydrolase, putative contains	---	AT1G29670	-10.41	-3.38	-7.10	0.000233	0.003507	0.88
267339_at	unknown protein ; supported by cD	---	AT2G39870	-2.80	-1.48	-7.10	0.000234	0.003513	0.87
257339_s_a	ATP synthase subunit 9	---	AT2G07671	2.44	1.29	7.09	0.000234	0.003515	0.87
248812_at	palmitoyl-protein thioesterase precu	---	AT5G47330	-8.48	-3.08	-7.09	0.000235	0.003517	0.87
266071_at	unknown protein	---	AT2G18670	7.12	2.83	7.09	0.000235	0.003517	0.87
253412_at	putative protein (fragment) calcineu	CBL10	AT4G33000	-2.00	-1.00	-7.08	0.000237	0.003529	0.86
246724_at	putative protein CDPK substrate pr	---	AT5G29000	2.06	1.04	7.07	0.000238	0.003541	0.85
263509_s_a	hypothetical protein	---	AT2G07687	2.47	1.31	7.06	0.000241	0.003565	0.84
258472_at	unknown protein identical to unknov	---	AT3G06080	-2.54	-1.34	-7.05	0.000243	0.00357	0.83
249927_at	Glucose-1-phosphate adenylyltrans	APL1	AT5G19220	-2.55	-1.35	-7.05	0.000244	0.003578	0.83
248276_at	EspB-like protein	YSL3	AT5G53550	2.26	1.17	7.04	0.000245	0.003586	0.82
258338_at	putative L-asparaginase similar to L	---	AT3G16150	2.72	1.45	7.04	0.000245	0.003586	0.82
260685_at	Expressed protein ; supported by fu	GLYR2	AT1G17650	-2.28	-1.19	-7.03	0.000247	0.003604	0.81
251169_at	putative protein putative protein At2	MARD1	AT3G63210	3.53	1.82	7.00	0.000253	0.003649	0.79
256585_at	hypothetical protein	---	AT3G28760	-2.34	-1.23	-7.00	0.000253	0.003654	0.78
267116_at	unknown protein	---	AT2G32560	-2.97	-1.57	-6.99	0.000255	0.003665	0.78
253255_at	putative auxin-regulated protein au	---	AT4G34760	-8.97	-3.17	-6.99	0.000255	0.003665	0.78
266892_at	putative glycine dehydrogenase	AtGLDP2	AT2G26080	-2.06	-1.04	-6.99	0.000256	0.003674	0.77
253286_at	hypothetical protein	FUC95A	AT4G34260	-9.63	-3.27	-6.99	0.000257	0.003676	0.77
246911_at	transcription factor TINY	tny	AT5G25810	-3.94	-1.98	-6.98	0.000259	0.0037	0.76
246880_s_a	myrosinase TGG2 ; supported by c	TGG2	AT5G25980	-5.94	-2.57	-6.97	0.00026	0.003701	0.76

263591_at	unknown protein	ATMAP65-	AT2G01910	-6.92	-2.79	-6.97	0.000261	0.00371	0.75
257933_at	aminoalcoholphosphotransferase,	AAPT2	AT3G25585	2.54	1.35	6.96	0.000261	0.003714	0.75
248819_at	putative protein contains similarity t	---	AT5G47050	2.68	1.42	6.96	0.000262	0.003722	0.75
263348_at	cytoplasmic aconitate hydratase	---	AT2G05710	2.22	1.15	6.96	0.000263	0.003726	0.74
261192_at	NAM protein, putative similar to NA	ANAC13	AT1G32870	2.21	1.15	6.96	0.000263	0.003726	0.74
259892_at	germin-like protein similar to germin	GER1	AT1G72610	-12.28	-3.62	-6.95	0.000264	0.003735	0.74
265849_at	hypothetical protein predicted by ge	---	AT2G35736	2.21	1.15	6.95	0.000265	0.003737	0.74
248908_at	receptor kinase-like protein	MEE62	AT5G45800	5.05	2.34	6.93	0.00027	0.003794	0.71
250254_at	24-sterol C-methyltransferase ; sup	SMT1	AT5G13710	-2.25	-1.17	-6.92	0.000272	0.003807	0.71
261407_at	unknown protein ;supported by full-	---	AT1G18810	-2.44	-1.28	-6.92	0.000273	0.003814	0.71
250167_at	myb-related protein - like myb-relat	ATMYB16	AT5G15310	-2.28	-1.19	-6.91	0.000275	0.003829	0.70
259358_at	hypothetical protein similar to putati	GATL3	AT1G13250	-5.46	-2.45	-6.90	0.000276	0.003842	0.69
255462_at	hypothetical protein similar to A. th	---	AT4G02940	2.69	1.43	6.89	0.000279	0.003863	0.68
252515_at	heat shock protein 17 ; supported b	HSP17.4	AT3G46230	8.60	3.10	6.89	0.00028	0.003867	0.68
253688_at	putative protein ;supported by full-l	---	AT4G29590	-2.25	-1.17	-6.88	0.000281	0.003872	0.67
250351_at	heat shock protein 17.6A	AT-HSP17.	AT5G12030	4.66	2.22	6.88	0.000282	0.003881	0.67
249895_at	male sterility 2-like protein (emb|CA	FAR1	AT5G22500	-6.64	-2.73	-6.88	0.000282	0.003881	0.67
256793_at	unknown protein ;supported by full-	---	AT3G22160	3.58	1.84	6.87	0.000283	0.003881	0.66
257634_s_a	cytochrome P450, putative similar	CYP71B19	AT3G26170	3.02	1.60	6.86	0.000286	0.003901	0.65
248377_at	unknown protein ; supported by ful	---	AT5G51720	-3.14	-1.65	-6.86	0.000286	0.003901	0.65
251178_at	cytokinin oxidase -like protein cytol	CKX6	AT3G63440	-3.44	-1.78	-6.86	0.000287	0.003901	0.65
251406_at	putative protein various predicted p	---	AT3G60260	-2.72	-1.44	-6.85	0.000289	0.003921	0.64
258299_at	unknown protein contains GMC oxi	---	AT3G23410	-2.21	-1.14	-6.85	0.000289	0.003921	0.64
260820_at	receptor protein kinase, putative si	---	AT1G06840	2.79	1.48	6.84	0.00029	0.003937	0.64
264083_at	ethylene reponse factor-like AP2 do	ATERF15	AT2G31230	7.39	2.89	6.84	0.000292	0.003947	0.63
267611_at	unknown protein	SPX2	AT2G26660	2.70	1.43	6.84	0.000292	0.003947	0.63
246488_at	steroid 5alpha-reductase-like prote	---	AT5G16010	-2.75	-1.46	-6.83	0.000293	0.003955	0.63
256275_at	actin 11 (ACT11) identical to actin 1	ACT11	AT3G12110	-2.28	-1.19	-6.83	0.000293	0.003955	0.63
265716_at	unknown protein ;supported by full-	---	AT2G03350	-2.11	-1.08	-6.83	0.000295	0.003973	0.62
260362_at	putative protein kinase similar to C-	---	AT1G70530	3.63	1.86	6.82	0.000296	0.003977	0.62
261272_at	Expressed protein ; supported by c	---	AT1G26665	3.05	1.61	6.82	0.000296	0.003977	0.61
256453_at	GSH-dependent dehydroascorbate	DHAR2	AT1G75270	3.03	1.60	6.82	0.000297	0.003987	0.61
252363_at	lipase - like protein lipase Arab-1, A	---	AT3G48460	-5.34	-2.42	-6.81	0.000298	0.003989	0.61
253949_at	grpE like protein ;supported by full-	AR192	AT4G26780	4.17	2.06	6.81	0.000299	0.003998	0.60
245277_at	glucosyltransferase like protein ; su	IAGLU	AT4G15550	3.05	1.61	6.81	0.0003	0.004002	0.60

252859_at	putative protein AP2 domain conta	---	AT4G39780	2.49	1.32	6.81	0.0003	0.004002	0.60
250006_at	putative protein 2'-hydroxyisoflavor	PCB2	AT5G18660	-4.28	-2.10	-6.81	0.0003	0.004003	0.60
253066_at	1-aminocyclopropane-1-carboxylat	ACS8	AT4G37770	-11.29	-3.50	-6.79	0.000303	0.004034	0.59
259431_at	plasma membrane intrinsic protein	PIP1C	AT1G01620	-8.66	-3.11	-6.79	0.000303	0.004037	0.59
247214_at	putative protein similar to unknown	---	AT5G64850	-4.18	-2.06	-6.79	0.000304	0.004037	0.59
266291_at	putative tropinone reductase ;supp	---	AT2G29320	2.84	1.51	6.79	0.000305	0.004048	0.58
261570_at	fatty acid elongase 3-ketoacyl-CoA	KCS1	AT1G01120	-11.91	-3.57	-6.78	0.000307	0.004055	0.58
247079_at	Expressed protein ; supported by c	AKRP	AT5G66055	-2.20	-1.14	-6.78	0.000307	0.004056	0.58
265214_at	unkown protein ESTs gb|H36249,	---	AT1G05000	3.55	1.83	6.78	0.000308	0.004061	0.57
246926_at	putative protein	---	AT5G25240	-2.62	-1.39	-6.78	0.000308	0.004062	0.57
265499_at	putative glucosyltransferase	UGT73B5	AT2G15480	7.71	2.95	6.77	0.000309	0.004066	0.57
257206_at	putative lectin similar to lectin SP:P	---	AT3G16530	14.40	3.85	6.77	0.00031	0.004066	0.57
251973_at	nodulin / glutamate-ammonia ligas	---	AT3G53180	-2.66	-1.41	-6.77	0.00031	0.004066	0.57
255232_at	putative protein phosphatidylinosito	AGD13	AT4G05330	-2.11	-1.08	-6.77	0.000311	0.004074	0.56
264266_at	putative protein phosphatase 2C sir	---	AT1G09160	-2.17	-1.12	-6.77	0.000311	0.004077	0.56
260386_at	putative strictosidine synthase simil	---	AT1G74010	6.72	2.75	6.76	0.000312	0.004084	0.56
261801_at	hypothetical protein similar to hypot	AAE14	AT1G30520	-2.10	-1.07	-6.76	0.000314	0.004095	0.55
245662_at	hypothetical protein predicted by ge	---	AT1G28190	7.76	2.96	6.75	0.000316	0.004105	0.55
249750_at	unknown protein ;supported by full-	---	AT5G24570	-2.55	-1.35	-6.75	0.000316	0.004105	0.55
266721_at	unknown protein	FT1	AT2G03220	-2.07	-1.05	-6.74	0.000318	0.004124	0.54
258505_at	hypothetical protein predicted by ge	---	AT3G06530	4.73	2.24	6.73	0.000321	0.004152	0.53
252291_s_a	peroxidase ;supported by full-lengt	PRXCB	AT3G49110	2.78	1.48	6.73	0.000322	0.004154	0.53
248252_at	putative protein similar to unknown	AGP22	AT5G53250	-4.73	-2.24	-6.72	0.000323	0.004162	0.52
262093_at	receptor protein kinase, putative co	---	AT1G56145	2.37	1.24	6.72	0.000324	0.004162	0.52
251743_at	Yippee-like protein Yippee protein,	---	AT3G55890	3.30	1.72	6.71	0.000325	0.004177	0.51
266014_s_a	hypothetical protein	---	AT2G07722	3.06	1.61	6.71	0.000328	0.004202	0.50
255690_at	probable cytochrome P450	CYP86A2	AT4G00360	-13.52	-3.76	-6.71	0.000328	0.004202	0.50
253109_at	putative protein predicted protein A	MCA1	AT4G35920	-2.69	-1.43	-6.70	0.000328	0.004207	0.50
254250_at	serine/threonine kinase - like prote	---	AT4G23290	-3.00	-1.58	-6.70	0.000329	0.004209	0.50
259771_at	unknown protein	---	AT1G29470	-2.20	-1.14	-6.70	0.00033	0.004216	0.50
250490_at	pectin methylesterase - like protein	---	AT5G09760	-3.31	-1.73	-6.70	0.00033	0.004216	0.50
259878_at	putative catechol O-methyltransfera	---	AT1G76790	-3.34	-1.74	-6.70	0.00033	0.004216	0.50
246389_at	amino acid carrier, putative similar	AAP3	AT1G77380	2.14	1.09	6.69	0.000332	0.004217	0.49
252740_at	pectinesterase -like protein PECTI	---	AT3G43270	-2.37	-1.24	-6.69	0.000334	0.004231	0.49
258809_at	NAM-like protein (no apical meriste	anac047	AT3G04070	3.92	1.97	6.69	0.000334	0.004231	0.49

261216_at	catechol O-methyltransferase, puta	---	AT1G33030	5.64	2.50	6.67	0.000339	0.00426	0.47
245398_at	hydroxyproline-rich glycoprotein ho	---	AT4G14900	2.42	1.27	6.65	0.000344	0.004301	0.45
258415_at	putative s-adenosylmethionine synt	MTO3	AT3G17390	-3.18	-1.67	-6.64	0.000348	0.004333	0.44
246984_at	cytochrome P450	CYP81G1	AT5G67310	6.59	2.72	6.64	0.000349	0.004336	0.44
248028_at	putative protein similar to unknown	---	AT5G55620	-3.75	-1.91	-6.62	0.000352	0.00436	0.43
262237_at	hypothetical protein predicted by ge	---	AT1G48320	2.70	1.43	6.62	0.000354	0.004371	0.42
266481_at	unknown protein ; supported by cD	TCP10	AT2G31070	-2.03	-1.02	-6.61	0.000357	0.004397	0.41
255575_at	predicted protein of unknown funct	---	AT4G01430	4.41	2.14	6.61	0.000358	0.004404	0.41
266873_at	putative PREG1-like negative regul	CYCP4;1	AT2G44740	-6.42	-2.68	-6.60	0.000359	0.004416	0.40
253871_at	protochlorophyllide reductase precu	PORB	AT4G27440	-2.26	-1.18	-6.59	0.000362	0.004436	0.40
264315_at	aromatic rich glycoprotein, putative	---	AT1G70370	-6.37	-2.67	-6.58	0.000367	0.004463	0.38
262174_at	putative GDP-mannose pyrophosph	---	AT1G74910	-2.00	-1.00	-6.57	0.000369	0.004476	0.38
245078_at	putative AP2 domain transcription f	---	AT2G23340	-4.31	-2.11	-6.57	0.00037	0.004478	0.37
251494_at	protein kinase-like protein Pto kina	---	AT3G59350	-3.48	-1.80	-6.56	0.000373	0.004514	0.36
264708_at	putative ER6 protein similar to GB:	---	AT1G09740	2.06	1.04	6.55	0.000378	0.004553	0.35
254241_at	serine/threonine kinase - like prote	CRK11	AT4G23190	6.26	2.65	6.54	0.000379	0.004556	0.35
259661_at	Expressed protein ; supported by fu	---	AT1G55265	2.03	1.02	6.54	0.00038	0.004563	0.34
251017_at	protein phosphatase - like protein p	---	AT5G02760	-22.54	-4.49	-6.54	0.000382	0.004574	0.34
250656_at	putative protein contains similarity t	---	AT5G06970	-2.08	-1.06	-6.53	0.000385	0.004598	0.33
257129_at	cytochrome P450, putative contain	CYP705A1	AT3G20100	2.42	1.28	6.52	0.000389	0.004627	0.32
264837_at	unknown protein similar to ESTs er	---	AT1G03600	-2.53	-1.34	-6.51	0.00039	0.00463	0.32
253736_at	Proline-rich APG - like protein proli	---	AT4G28780	-2.39	-1.26	-6.51	0.000391	0.004632	0.31
264102_at	hypothetical protein predicted by ge	ECT8	AT1G79270	2.06	1.04	6.51	0.000391	0.004632	0.31
251157_at	mRNA binding protein precursor - I	CSP41A	AT3G63140	-2.13	-1.09	-6.50	0.000396	0.004672	0.30
251899_at	nucleoid DNA-binding - like protein	---	AT3G54400	-12.37	-3.63	-6.49	0.000399	0.004701	0.29
265260_at	NAM (no apical meristem)-like prote	anac042	AT2G43000	13.57	3.76	6.49	0.000399	0.004701	0.29
263656_at	putative auxin-induced protein AUX	SHY2	AT1G04240	-13.81	-3.79	-6.48	0.000401	0.004721	0.28
266155_at	cytochrome p450, putative similar t	CYP89A5	AT1G64950	3.36	1.75	6.47	0.000406	0.004755	0.27
258394_at	unknown protein ;supported by full-	---	AT3G15530	-2.73	-1.45	-6.46	0.000408	0.004769	0.27
247246_at	invertase inhibitor homolog (emb|C/	C/VIF2	AT5G64620	-2.53	-1.34	-6.45	0.000413	0.004803	0.25
249552_s_a	receptor serine/threonine protein ki	---	AT5G38240	2.56	1.36	6.45	0.000414	0.004804	0.25
256098_at	unknown protein similar to 6-phosp	---	AT1G13700	-2.78	-1.47	-6.43	0.000419	0.004842	0.24
250646_at	peroxidase (emb|CAA68212.1) ;su	---	AT5G06720	2.06	1.04	6.43	0.000419	0.004843	0.24
254543_at	putative chitinase chitinase (EC 3.2	---	AT4G19810	5.55	2.47	6.43	0.00042	0.004845	0.24
255230_at	ferredoxin--NADP+ reductase - like	ATRFNR1	AT4G05390	6.29	2.65	6.42	0.000423	0.004872	0.23

261356_at	predicted protein	---	AT1G79660	-2.11	-1.08	-6.42	0.000424	0.004884	0.22
254101_at	alpha-amylase - like protein alpha-	AMY1	AT4G25000	4.69	2.23	6.41	0.000428	0.00491	0.22
247037_at	putative protein similar to unknown	RALFL34	AT5G67070	-12.41	-3.63	-6.41	0.000429	0.00491	0.21
256655_at	hypothetical protein predicted by ge	---	AT3G18890	-2.23	-1.15	-6.40	0.00043	0.004915	0.21
248095_at	putative protein strong similarity to	ATMAP65-	AT5G55230	-2.00	-1.00	-6.40	0.000431	0.004915	0.21
252320_at	endoxyloglucan transferase-like pr	---	AT3G48580	3.46	1.79	6.39	0.000434	0.004945	0.20
258708_at	putative oxidoreductase similar to p	---	AT3G09580	-2.22	-1.15	-6.39	0.000437	0.004959	0.19
260267_at	very-long-chain fatty acid condensi	KCS6	AT1G68530	-3.09	-1.63	-6.37	0.000445	0.005023	0.17
261109_at	cytokinin oxidase, putative similar t	CKX5	AT1G75450	-9.81	-3.29	-6.37	0.000446	0.005029	0.17
263942_at	unknown protein	FLA16	AT2G35860	-17.79	-4.15	-6.36	0.000446	0.005029	0.17
254417_at	putative protein	ATFMN/FH	AT4G21470	2.14	1.10	6.35	0.000452	0.005063	0.15
257506_at	auxin-induced protein, putative sim	---	AT1G29440	-6.36	-2.67	-6.35	0.000453	0.005066	0.15
264318_at	putative beta-ketoacyl-CoA synthas	KCS2	AT1G04220	-2.74	-1.46	-6.34	0.000455	0.005072	0.15
255676_at	putative beta-amylase similar to the	BAM2	AT4G00490	-3.31	-1.73	-6.34	0.000455	0.005072	0.15
264836_at	unknown protein similar to hypothet	---	AT1G03610	-2.30	-1.20	-6.34	0.000456	0.005072	0.14
255962_at	glycine-rich RNA-binding protein, p	---	AT1G22330	-6.29	-2.65	-6.33	0.000462	0.005102	0.13
254553_at	TMV resistance protein N - like TM	---	AT4G19530	-2.64	-1.40	-6.33	0.000462	0.005102	0.13
259707_at	thylakoid-bound ascorbate peroxida	TAPX	AT1G77490	-2.09	-1.06	-6.33	0.000462	0.005102	0.13
260939_at	hypothetical protein contains simila	---	AT1G45180	-3.65	-1.87	-6.32	0.000467	0.005127	0.12
257805_at	sugar transport, putative similar to	ATPLT5	AT3G18830	2.78	1.48	6.31	0.000468	0.005137	0.12
257365_x_a	putative antifungal protein	PDF1.2b	AT2G26020	13.44	3.75	6.31	0.000471	0.005162	0.11
246831_at	hexose transporter - like protein he	MSS1	AT5G26340	2.40	1.26	6.30	0.000474	0.005187	0.10
256385_at	60S ribosomal protein L10, putative	---	AT1G66580	2.41	1.27	6.29	0.000477	0.005205	0.10
262119_s_a	glutathione S-transferase, putative	ATGSTF6	AT1G02920	5.46	2.45	6.27	0.000485	0.005255	0.08
251109_at	ferritin 1 precursor ;supported by fu	FER1	AT5G01600	2.92	1.55	6.25	0.000496	0.00533	0.05
264195_at	putative gibberellin-regulated protei	---	AT1G22690	-2.42	-1.28	-6.24	0.000499	0.005355	0.05
258393_at	unknown protein similar to unknown	---	AT3G15480	-2.25	-1.17	-6.24	0.000503	0.005385	0.04
254328_at	adenine phosphoribosyltransferase	APT3	AT4G22570	-2.68	-1.42	-6.24	0.000503	0.005385	0.04
254137_at	hypothetical protein	---	AT4G24930	-2.43	-1.28	-6.23	0.000504	0.005396	0.04
259015_at	unknown protein similar to hypothet	---	AT3G07350	-3.61	-1.85	-6.23	0.000507	0.005416	0.03
255561_at	putative hexose transporter similar	---	AT4G02050	2.15	1.11	6.23	0.000507	0.005418	0.03
250471_at	myo-inositol-1-phosphate synthase	MIPS3	AT5G10170	-2.20	-1.14	-6.22	0.00051	0.005431	0.02
258836_at	hypothetical protein predicted using	---	AT3G07210	-2.03	-1.03	-6.21	0.000515	0.005464	0.01
253044_at	hypothetical protein ;supported by f	---	AT4G37290	19.26	4.27	6.20	0.000518	0.005486	0.01
261618_at	unknown protein	---	AT1G33110	3.01	1.59	6.19	0.000524	0.005528	-0.01

252970_at	small auxin up RNA (SAUR-AC1) ;	SAUR15	AT4G38850	-2.31	-1.21	-6.19	0.000526	0.00554	-0.01
261309_at	phosphoethanolamine N-methyltra	CPuORF31	AT1G48598	-2.34	-1.23	-6.19	0.000527	0.005548	-0.01
245007_at	PSI P700 apoprotein A1	---	---	-2.46	-1.30	-6.18	0.000529	0.005557	-0.02
252852_at	hypothetical protein ;supported by	---	AT4G39900	-2.92	-1.55	-6.16	0.000538	0.005609	-0.04
263706_s_a	3-methyladenine DNA glycosylase	---	AT1G31180	-2.29	-1.20	-6.16	0.000539	0.00561	-0.04
261395_at	unknown protein similar to putative	---	AT1G79700	-3.37	-1.75	-6.16	0.00054	0.005611	-0.04
262935_at	hypothetical protein similar to putati	AtOCT5	AT1G79410	4.12	2.04	6.16	0.00054	0.005611	-0.04
257623_at	cytochrome P450, putative contain	CYP71B23	AT3G26210	4.57	2.19	6.16	0.000541	0.005613	-0.04
265620_at	unknown protein	---	AT2G27310	4.69	2.23	6.15	0.000543	0.005628	-0.05
257113_at	cytochrome P450, putative contain	CYP705A2	AT3G20130	-2.78	-1.48	-6.15	0.000543	0.005629	-0.05
256756_at	ATPase II, putative similar to GB:A	---	AT3G25610	3.16	1.66	6.15	0.000548	0.005658	-0.05
250233_at	putative protein weak homology wi	IQD11	AT5G13460	-5.46	-2.45	-6.14	0.00055	0.00567	-0.06
261740_at	hypothetical protein similar to unkn	---	AT1G47740	-2.03	-1.02	-6.14	0.000551	0.005682	-0.06
259403_at	unknown protein ; supported by full-	PGDH	AT1G17745	7.25	2.86	6.14	0.000553	0.005692	-0.07
263962_at	putative protein kinase contains a p	---	AT2G36350	-2.03	-1.02	-6.14	0.000553	0.005692	-0.07
AFFX-Athal-	Arabidopsis thaliana /REF=M64116	GAPC1	---	2.15	1.11	6.13	0.000555	0.005698	-0.07
259791_at	unknown protein ; supported by cDI	---	AT1G29700	-2.44	-1.28	-6.13	0.000557	0.005717	-0.07
255571_at	hypothetical protein ; supported by	---	AT4G01220	-2.25	-1.17	-6.13	0.000558	0.005719	-0.07
260744_at	hypothetical protein predicted by ge	---	AT1G15010	-8.94	-3.16	-6.12	0.00056	0.005722	-0.08
257624_at	cytochrome P450 monooxygenase	CYP71B3	AT3G26220	6.45	2.69	6.12	0.000563	0.00574	-0.08
247189_at	unknown protein ;supported by full-	AGP7	AT5G65390	-4.17	-2.06	-6.11	0.000565	0.005756	-0.09
249932_at	unknown protein	---	AT5G22390	-3.88	-1.96	-6.11	0.000566	0.005763	-0.09
264394_at	aminomethyltransferase-like precu	---	AT1G11860	-2.12	-1.09	-6.11	0.000569	0.005786	-0.10
264574_at	putative zinc transporter Similar to A	ZIP5	AT1G05300	2.78	1.47	6.10	0.000574	0.005821	-0.11
248656_at	fimbrin 2 (gb|AAB97844.1) ; suppo	---	AT5G48460	-4.03	-2.01	-6.10	0.000575	0.005822	-0.11
262744_at	anthranilate N-hydroxycinnamoyl/b	---	AT1G28680	2.38	1.25	6.09	0.000576	0.005828	-0.11
257556_at	hypothetical protein predicted by ge	---	AT3G28100	3.45	1.79	6.09	0.000579	0.005849	-0.12
254066_at	transcriptional activator CBF1-like	DREB1A	AT4G25480	4.01	2.00	6.08	0.000581	0.005853	-0.12
266163_at	hypothetical protein predicted by ge	---	AT2G28130	-2.16	-1.11	-6.08	0.000582	0.005858	-0.12
256883_at	unknown protein ; supported by cD	---	AT3G26440	4.41	2.14	6.08	0.000582	0.005859	-0.12
264611_at	putative pectate lyase A11 similar t	---	AT1G04680	-7.17	-2.84	-6.08	0.000585	0.005876	-0.13
254215_at	putative Na+/H+-exchanging prote	ATCHX17	AT4G23700	7.27	2.86	6.08	0.000585	0.005876	-0.13
261394_at	wall-associated kinase 2, putative s	---	AT1G79680	12.10	3.60	6.07	0.000587	0.00589	-0.13
247351_at	putative protein contains similarity t	ANAC102	AT5G63790	3.57	1.84	6.07	0.000587	0.00589	-0.13
249550_at	protein kinase - like protein wall-as	---	AT5G38210	2.64	1.40	6.07	0.000589	0.005908	-0.13

258879_at	unknown protein ; supported by ful	---	AT3G03270	2.77	1.47	6.07	0.000591	0.005921	-0.14
253638_at	cinnamoyl-CoA reductase - like pro	---	AT4G30470	-3.85	-1.95	-6.06	0.000597	0.005966	-0.15
245399_at	membrane channel like protein ;sup	TIP2;2	AT4G17340	-2.53	-1.34	-6.05	0.0006	0.005986	-0.15
256451_s_a	unknown protein	---	AT1G75170	3.84	1.94	6.05	0.000601	0.005989	-0.15
264645_at	unknown protein Similar to Saccha	---	AT1G08940	4.41	2.14	6.05	0.000601	0.005991	-0.16
261366_at	unknown protein	---	AT1G53100	3.67	1.87	6.05	0.000601	0.005991	-0.16
260203_at	NAM-like protein similar to NAM (no	ANAC019	AT1G52890	2.42	1.27	6.04	0.000604	0.006006	-0.16
249057_at	putative protein contains similarity t	DUR	AT5G44480	5.42	2.44	6.04	0.000606	0.006015	-0.16
252876_at	putative protein ;supported by full-l	---	AT4G39970	-2.19	-1.13	-6.04	0.000607	0.006018	-0.17
265342_at	hypothetical protein predicted by ge	---	AT2G18300	-2.50	-1.32	-6.03	0.000612	0.00606	-0.18
253372_at	pectinesterase - like protein pectin	PME44	AT4G33220	-3.54	-1.82	-6.03	0.000613	0.006065	-0.18
261459_at	O-methyltransferase, putative simil	---	AT1G21100	12.01	3.59	6.01	0.000622	0.006129	-0.19
267057_at	hypothetical protein predicted by ge	---	AT2G32500	-3.25	-1.70	-6.01	0.000622	0.006129	-0.19
254601_at	putative protein DNA (cytosine-5-)-	CMT2	AT4G19020	-2.08	-1.05	-6.01	0.000625	0.006151	-0.20
253829_at	Medicago nodulin N21-like protein	---	AT4G28040	5.14	2.36	6.00	0.000629	0.006172	-0.20
253423_at	Expressed protein ; supported by cl	IAA29	AT4G32280	-10.89	-3.45	-6.00	0.00063	0.006182	-0.21
245213_at	photosystem II 22kDa protein, puta	NPQ4	AT1G44575	-3.45	-1.79	-5.98	0.000641	0.006257	-0.23
251479_at	serine/threonine-specific kinase lec	ATHLECRK	AT3G59700	3.59	1.84	5.97	0.000651	0.006316	-0.24
256446_at	RING zinc finger protein contains R	---	AT3G11110	-2.31	-1.21	-5.96	0.000656	0.006347	-0.25
254041_at	Expressed protein ; supported by fu	---	AT4G25830	-4.75	-2.25	-5.96	0.000657	0.006353	-0.25
264024_at	hypothetical protein predicted by ge	---	AT2G21180	2.55	1.35	5.95	0.000658	0.006355	-0.25
249469_at	UDP-glucose dehydrogenase-like p	---	AT5G39320	-3.13	-1.65	-5.95	0.000661	0.006374	-0.26
254040_at	possible apospory-associated like p	---	AT4G25900	2.21	1.15	5.94	0.000665	0.006389	-0.27
261861_at	hypothetical protein predicted by ge	---	AT1G50450	-2.74	-1.45	-5.94	0.000666	0.006399	-0.27
259787_at	auxin-induced protein, putative sim	---	AT1G29460	-4.34	-2.12	-5.94	0.000671	0.006424	-0.28
248198_at	putative protein contains similarity t	---	AT5G54200	-2.63	-1.40	-5.93	0.000673	0.006441	-0.28
257323_at	hypothetical protein	---	AT2G07698	3.59	1.84	5.92	0.00068	0.006492	-0.29
245385_at	hypothetical protein ;supported by f	---	AT4G14020	2.01	1.01	5.91	0.000686	0.006524	-0.30
262682_at	anter-specific proline-rich -like prote	---	AT1G75900	-4.80	-2.26	-5.91	0.000688	0.006537	-0.30
266044_s_a	hypothetical protein	---	AT2G07725	2.55	1.35	5.91	0.00069	0.00655	-0.31
262235_at	ribosomal protein L18, putative sim	---	AT1G48350	-2.02	-1.01	-5.90	0.000693	0.006567	-0.31
261455_at	unknown protein ;supported by full-	---	AT1G21070	-2.17	-1.12	-5.89	0.000702	0.00662	-0.32
264261_at	putative nicotianamine synthase sin	NAS3	AT1G09240	6.39	2.68	5.88	0.000706	0.006633	-0.33
263410_at	predicted protein ;supported by full-	---	AT2G04039	-2.21	-1.14	-5.87	0.000711	0.006672	-0.34
265877_at	unknown protein ; supported by cD	BZIP34	AT2G42380	-2.39	-1.26	-5.87	0.000715	0.006699	-0.34

245460_at	disease resistance RPP5 like protei	RLM3	AT4G16990	-2.53	-1.34	-5.86	0.000722	0.00675	-0.36
257314_at	integral membrane protein, putative	---	AT3G26590	3.24	1.69	5.85	0.000728	0.006795	-0.37
256411_at	ATP-dependent Clp protease protei	CLPP3	AT1G66670	2.14	1.10	5.82	0.000747	0.006922	-0.39
253040_at	endo-xyloglucan transferase - like	---	AT4G37800	-5.03	-2.33	-5.81	0.000761	0.007018	-0.41
254221_at	putative polygalacturonase polygal	---	AT4G23820	-6.22	-2.64	-5.80	0.000762	0.007018	-0.41
262047_at	hypothetical protein predicted by ge	---	AT1G80160	6.64	2.73	5.80	0.000766	0.007046	-0.42
252023_at	putative protein various predicted p	---	AT3G52920	3.15	1.66	5.79	0.000775	0.007108	-0.43
253550_at	putative protein kinase serine/threo	SIP3	AT4G30960	2.27	1.18	5.78	0.000779	0.007135	-0.44
246011_at	putative protein auxin-induced bas	---	AT5G08330	-2.59	-1.37	-5.78	0.000783	0.007154	-0.44
263517_at	unknown protein ;supported by full-	RD2	AT2G21620	2.03	1.02	5.77	0.000789	0.007177	-0.45
254500_at	vacuolar sorting receptor-like prote	---	AT4G20110	2.83	1.50	5.76	0.000794	0.007197	-0.46
262496_at	unknown protein ; supported by full-	---	AT1G21790	-2.40	-1.26	-5.76	0.000794	0.007197	-0.46
266327_at	homeodomain transcription factor (	ATHB-7	AT2G46680	2.65	1.41	5.76	0.000795	0.007197	-0.46
250337_at	putative protein SF21 protein, Helia	---	AT5G11790	-4.47	-2.16	-5.75	0.000802	0.007243	-0.47
266167_at	unknown protein ;supported by full-	YLS5	AT2G38860	4.86	2.28	5.75	0.000805	0.007261	-0.47
249188_at	N-hydroxycinnamoyl benzoyltransfe	---	AT5G42830	3.31	1.73	5.75	0.000808	0.007276	-0.48
262850_at	signal response protein (GAI) identi	GAI	AT1G14920	-2.47	-1.30	-5.75	0.000808	0.007277	-0.48
265411_at	unknown protein	---	AT2G16630	-5.04	-2.33	-5.74	0.000809	0.007282	-0.48
262920_at	2-dehydro-3-deoxyphosphooctonat	---	AT1G79500	-2.85	-1.51	-5.74	0.00081	0.007282	-0.48
257880_at	AMP-binding protein, putative cont	AAE7	AT3G16910	2.32	1.21	5.74	0.000811	0.007282	-0.48
261526_at	protein kinase identical to protein ki	APK2A	AT1G14370	2.28	1.19	5.74	0.000812	0.007282	-0.48
258203_at	hypothetical protein predicted by ge	---	AT3G13950	8.62	3.11	5.73	0.000817	0.007311	-0.49
265183_at	unknown protein ;supported by full-	---	AT1G23750	-2.18	-1.12	-5.73	0.00082	0.007323	-0.49
267503_at	unknown protein ; supported by ful	---	AT2G45600	-2.15	-1.10	-5.73	0.000821	0.007328	-0.50
262357_at	jacalin, putative similar to jacalin G	---	AT1G73040	4.22	2.08	5.72	0.000828	0.007368	-0.50
245252_at	ethylene responsive element bindin	ATERF-1	AT4G17500	4.18	2.06	5.72	0.00083	0.007381	-0.51
259783_at	auxin-induced protein, putative sim	SAUR68	AT1G29510	-8.69	-3.12	-5.71	0.000837	0.007407	-0.52
254299_at	hypothetical protein ;supported by	NYE1	AT4G22920	2.51	1.33	5.71	0.000841	0.007431	-0.52
248402_at	dihydrodipicolinate reductase-like p	crr1	AT5G52100	-2.17	-1.12	-5.71	0.000841	0.007431	-0.52
256713_at	putative peroxidase	---	AT2G34060	-2.15	-1.10	-5.70	0.000844	0.007447	-0.53
260547_at	putative trypsin inhibitor ;supported	---	AT2G43550	-5.01	-2.33	-5.70	0.000844	0.007447	-0.53
257045_at	dynamin-like protein similar to phra	ARC5	AT3G19720	-2.10	-1.07	-5.70	0.000847	0.007459	-0.53
254598_at	xyloglucan endo-transglycosylase -	---	AT4G18990	2.68	1.42	5.70	0.000849	0.007466	-0.53
248962_at	putative protein contains similarity t	FKBP13	AT5G45680	-2.14	-1.10	-5.69	0.000857	0.007516	-0.54
249306_at	RING zinc finger protein-like ;suppo	---	AT5G41400	3.23	1.69	5.67	0.000871	0.00759	-0.56

252834_at	putative protein RING-H2 zinc finge	---	AT4G40070	-2.53	-1.34	-5.67	0.000872	0.007599	-0.56
265450_at	hypothetical protein predicted by ge	---	AT2G46620	2.09	1.06	5.66	0.000879	0.007641	-0.57
253263_at	abscisic acid responsive elements-l	ABF3	AT4G34000	2.76	1.47	5.66	0.000881	0.007651	-0.57
246212_at	putative protein ; supported by cDN	SPT	AT4G36930	4.00	2.00	5.66	0.000884	0.007653	-0.58
258277_at	putative cytochrome P450 similar to	PAD3	AT3G26830	26.78	4.74	5.65	0.000885	0.007653	-0.58
267034_at	unknown protein ;supported by full-	---	AT2G38310	-3.94	-1.98	-5.64	0.000897	0.007719	-0.59
251281_at	putative protein hypothetical protei	AGP20	AT3G61640	-3.19	-1.67	-5.64	0.000899	0.007729	-0.59
260930_at	GTP-binding protein Sar1, putative	---	AT1G02620	-2.48	-1.31	-5.64	0.000901	0.007735	-0.60
259103_at	unknown protein ; supported by cD	---	AT3G11690	-2.97	-1.57	-5.64	0.000901	0.007735	-0.60
256407_at	sucrose-proton symporter, putative	ATSUC7	AT1G66570	4.89	2.29	5.64	0.000903	0.007745	-0.60
254673_at	membrane-bound small GTP-bindi	AtRABA1e	AT4G18430	3.80	1.93	5.63	0.000905	0.00776	-0.60
251096_at	receptor like protein kinase recepto	LECRKA4.2	AT5G01550	2.19	1.13	5.61	0.000927	0.007877	-0.63
259970_at	putative chlorophyll A-B binding pro	---	AT1G76570	-2.09	-1.06	-5.60	0.000932	0.007905	-0.63
267607_s_a	epoxide hydrolase (ATsEH) identica	ATSEH	AT2G26740	-2.25	-1.17	-5.60	0.000933	0.007906	-0.64
247026_at	protein kinase-like protein	MAPKKK19	AT5G67080	11.32	3.50	5.60	0.000939	0.007947	-0.64
262980_at	endo-beta-1,4-glucanase, putative	AtGH9B7	AT1G75680	-6.86	-2.78	-5.59	0.000947	0.008002	-0.65
261025_at	Expressed protein ; supported by fu	---	AT1G01225	-2.26	-1.18	-5.57	0.000967	0.008115	-0.67
257264_at	hypothetical protein contains Pfam	---	AT3G22060	6.29	2.65	5.56	0.000972	0.008137	-0.68
257951_at	putative SGP1 monomeric G-protei	SGP2	AT3G21700	2.91	1.54	5.56	0.000977	0.008166	-0.69
246607_at	receptor-like protein kinase - like p	---	AT5G35370	2.81	1.49	5.55	0.000983	0.008197	-0.69
245861_at	GTL1 - like protein GTL1, Arabidop	---	AT5G28300	-2.56	-1.35	-5.53	0.001007	0.008345	-0.72
261129_at	tubulin alpha-2/alpha-4 chain identi	TUA4	AT1G04820	-3.16	-1.66	-5.52	0.001013	0.008384	-0.73
261425_at	peptide transporter, putative simila	---	AT1G18880	2.62	1.39	5.51	0.001027	0.008483	-0.74
267645_at	putative beta-glucosidase	BGLU33	AT2G32860	-3.43	-1.78	-5.50	0.00103	0.00849	-0.74
247215_at	Expressed protein ; supported by fu	PROPEP3	AT5G64905	12.09	3.60	5.50	0.001032	0.008497	-0.75
250847_at	putative protein predicted protein, A	---	AT5G04480	-2.46	-1.30	-5.50	0.001033	0.008504	-0.75
261413_at	unknown protein ;supported by full-	PLL5	AT1G07630	2.89	1.53	5.48	0.001056	0.008631	-0.77
267549_at	hypothetical protein predicted by ge	---	AT2G32640	-3.39	-1.76	-5.47	0.00107	0.008693	-0.78
253747_at	serine threonine-specific kinase like	---	AT4G29050	2.33	1.22	5.47	0.001072	0.008702	-0.79
266971_at	unknown protein	---	AT2G39580	-2.46	-1.30	-5.45	0.001086	0.008763	-0.80
257983_at	unknown protein	---	AT3G20790	-3.17	-1.66	-5.45	0.001095	0.0088	-0.81
265067_at	hypothetical protein predicted by ge	---	AT1G03850	4.09	2.03	5.44	0.001101	0.008836	-0.82
254448_at	fatty acid hydroxylase - like protein	FAH2	AT4G20870	-3.54	-1.82	-5.44	0.001105	0.008857	-0.82
257093_at	hypothetical protein ;supported by	---	AT3G20570	-2.10	-1.07	-5.43	0.001112	0.008881	-0.83
252624_at	Expressed protein ; supported by fu	PSK1	AT3G44735	-2.62	-1.39	-5.42	0.001124	0.008929	-0.84

264616_at	unknown protein	---	AT2G17740	12.63	3.66	5.41	0.001133	0.008953	-0.85
255719_at	unknown protein ;supported by full-	---	AT1G32080	-2.59	-1.38	-5.41	0.001134	0.008953	-0.85
251387_at	putative protein	---	AT3G60810	-2.04	-1.03	-5.41	0.001136	0.008964	-0.85
249677_at	DNA helicase-like	---	AT5G35970	-2.19	-1.13	-5.40	0.001146	0.009014	-0.86
248420_at	receptor-like protein kinase ;suppo	---	AT5G51560	-3.35	-1.74	-5.39	0.001157	0.009057	-0.87
264635_at	unknown protein ;supported by full-	---	AT1G65500	3.34	1.74	5.39	0.001158	0.009057	-0.87
264435_at	putative glutathione S-transferase T	ATGSTU18	AT1G10360	-2.16	-1.11	-5.39	0.001158	0.009057	-0.87
263126_at	hypothetical protein predicted by ge	---	AT1G78460	4.26	2.09	5.39	0.001163	0.009081	-0.88
253052_at	cytochrome P450-like protein ; supp	CYP81H1	AT4G37310	2.77	1.47	5.39	0.001164	0.009083	-0.88
259211_at	unknown protein identical to GB:AA	---	AT3G09020	4.71	2.24	5.38	0.001173	0.009124	-0.88
260542_at	putative FKBP type peptidyl-prolyl c	---	AT2G43560	-2.13	-1.09	-5.36	0.001192	0.00922	-0.90
261688_at	unknown protein contains similarity	---	AT1G47380	-3.56	-1.83	-5.35	0.001204	0.009259	-0.91
264324_at	myosin heavy chain MYA2 Strong s	XIB	AT1G04160	-2.32	-1.21	-5.35	0.001209	0.009285	-0.92
258815_at	putative short-chain type dehydroge	---	AT3G04000	2.18	1.12	5.34	0.001219	0.009331	-0.93
267169_at	putative oxidoreductase	---	AT2G37540	-2.48	-1.31	-5.34	0.001223	0.009345	-0.93
258662_at	unknown protein	---	AT3G02900	-2.48	-1.31	-5.34	0.001226	0.009363	-0.93
260438_at	putative bifunctional nuclease simila	ENDO 2	AT1G68290	-2.94	-1.56	-5.33	0.001229	0.009366	-0.94
252572_at	putative protein Mlo-h1 protein - Hc	MLO3	AT3G45290	2.11	1.08	5.33	0.00124	0.009419	-0.95
244995_at	ATPase a subunit	---	---	-2.26	-1.18	-5.32	0.001247	0.009453	-0.95
260490_at	ATP-dependent transmembrane tra	CER5	AT1G51500	-2.32	-1.21	-5.30	0.001269	0.009559	-0.97
251962_at	plasma membrane intrinsic protein	PIP2A	AT3G53420	-2.14	-1.10	-5.29	0.001289	0.009661	-0.99
252334_at	mitochondrial phosphate transporte	---	AT3G48850	6.93	2.79	5.29	0.001291	0.009661	-0.99
262263_at	auxin transport protein REH1, puta	PIN3	AT1G70940	-3.45	-1.79	-5.28	0.001295	0.00969	-0.99
250550_at	N-hydroxycinnamoyl benzoyltransf	---	AT5G07870	-2.49	-1.32	-5.28	0.001296	0.009697	-0.99
262796_at	cysteine proteinase XCP2 identical	XCP2	AT1G20850	-3.15	-1.66	-5.28	0.001298	0.009709	-1.00
267038_at	expressed protein supported by cD	---	AT2G38480	-2.86	-1.52	-5.28	0.001303	0.009734	-1.00
255177_at	strong similarity to 1-aminocyclopro	ACS11	AT4G08040	-3.78	-1.92	-5.28	0.001305	0.009737	-1.00
260371_at	unknown protein ; supported by cD	---	AT1G69690	-3.00	-1.59	-5.28	0.001306	0.009737	-1.00
250307_at	putative protein similar to unknown	---	AT5G12170	2.12	1.08	5.27	0.001313	0.009757	-1.01
245783_s_a	hypothetical protein similar to hypot	---	AT1G35170	-3.26	-1.70	-5.27	0.001314	0.00976	-1.01
251920_at	uracil phosphoribosyltransferase-lil	---	AT3G53900	-2.47	-1.30	-5.26	0.001326	0.009802	-1.02
251072_at	putative protein wound-inducible pr	---	AT5G01740	-2.40	-1.26	-5.26	0.001328	0.009805	-1.02
245657_at	unknown protein similar to receptor	---	AT1G56720	-3.07	-1.62	-5.26	0.001328	0.009805	-1.02
265740_at	RING-H2 finger protein RHA2b ider	RHA2B	AT2G01150	-2.64	-1.40	-5.24	0.001362	0.009973	-1.05
247199_at	DNA binding protein TGA1a homolo	TGA1	AT5G65210	2.31	1.21	5.23	0.001373	0.01003	-1.06

253987_at	pyrophosphate-dependent phosph	PFK3	AT4G26270	2.57	1.36	5.23	0.001378	0.010046	-1.06
251196_at	glutaredoxin -like protein glutaredo	---	AT3G62950	-3.62	-1.86	-5.23	0.001379	0.010046	-1.06
245352_at	indole-3-acetate beta-glucosyltrans	UGT84A3	AT4G15490	2.09	1.06	5.22	0.001385	0.010068	-1.07
258419_at	unknown protein	---	AT3G16670	-6.23	-2.64	-5.21	0.001395	0.010107	-1.07
265720_at	unknown protein	---	AT2G40110	2.41	1.27	5.21	0.001406	0.010167	-1.08
258682_at	putative ribosomal-protein S6 kinas	S6K2	AT3G08720	2.90	1.54	5.21	0.001407	0.010169	-1.08
250199_at	putative protein contains similarity t	MPL1	AT5G14180	4.23	2.08	5.21	0.001409	0.010179	-1.09
247166_at	unknown protein	---	AT5G65840	-2.25	-1.17	-5.20	0.00142	0.010216	-1.09
249361_at	protein kinase - like protein protein	---	AT5G40540	-2.35	-1.23	-5.20	0.001424	0.010231	-1.10
248162_at	1,4-benzoquinone reductase-like; T	FQR1	AT5G54500	2.04	1.03	5.19	0.001429	0.01026	-1.10
248687_at	ADPG pyrophosphorylase small su	ADG1	AT5G48300	-2.33	-1.22	-5.19	0.001431	0.010263	-1.10
250611_at	gibberellin 20-oxidase	GA20OX3	AT5G07200	-2.00	-1.00	-5.19	0.001434	0.010276	-1.10
259516_at	hypothetical protein ; supported by	ERD10	AT1G20450	-2.35	-1.23	-5.19	0.001438	0.010283	-1.11
262280_at	unknown protein	---	AT1G68580	-2.24	-1.16	-5.19	0.001439	0.010284	-1.11
248335_at	putative protein strong similarity to u	---	AT5G52450	2.05	1.04	5.18	0.001446	0.010326	-1.11
251100_at	aldose reductase-like protein aldos	---	AT5G01670	2.14	1.10	5.18	0.001448	0.010327	-1.12
266156_at	hypothetical protein predicted by ge	FRA8	AT2G28110	3.89	1.96	5.18	0.00145	0.01033	-1.12
260919_at	hypothetical protein predicted by ge	---	AT1G21520	4.69	2.23	5.16	0.001476	0.010462	-1.14
247478_at	DC1.2 homologue - like protein DC	---	AT5G62360	-3.64	-1.87	-5.16	0.00148	0.010478	-1.14
255926_at	AP2 domain containing protein RA	---	AT1G22190	2.43	1.28	5.15	0.00149	0.010539	-1.15
256112_at	guanine nucleotide regulatory prote	ATRABA1E	AT1G16920	-3.22	-1.69	-5.14	0.001509	0.010628	-1.16
267619_at	putative receptor-like protein kinase	---	AT2G26730	-2.15	-1.10	-5.14	0.00151	0.010636	-1.16
262309_at	phosphoglucomutase, putative sim	---	AT1G70820	-2.31	-1.21	-5.13	0.001522	0.01069	-1.17
250777_at	putative protein similar to unknown	---	AT5G05440	-5.42	-2.44	-5.13	0.00153	0.010724	-1.17
266368_at	putative embryo-abundant protein	---	AT2G41380	10.11	3.34	5.12	0.001546	0.010813	-1.19
261788_at	unknown protein ;supported by full-	NDF1	AT1G15980	-2.17	-1.12	-5.12	0.001546	0.010813	-1.19
265221_s_a	putative glutamate decarboxylase ;	GAD3	AT2G02000	4.59	2.20	5.11	0.001556	0.010858	-1.19
262195_at	allergen, putative similar to allergen	---	AT1G78040	-2.57	-1.36	-5.11	0.001566	0.0109	-1.20
256673_at	unknown protein	FLA15	AT3G52370	-5.10	-2.35	-5.10	0.001572	0.010917	-1.20
253207_at	putative protein small auxin up-reg	---	AT4G34770	-3.20	-1.68	-5.10	0.001578	0.010938	-1.21
260221_at	GAST1-like protein similar to GAST	---	AT1G74670	-7.40	-2.89	-5.10	0.001581	0.010952	-1.21
259297_at	putative disease resistance protein	AtRLP30	AT3G05360	2.85	1.51	5.09	0.001586	0.010963	-1.21
266292_at	putative tropinone reductase ;supp	SAG13	AT2G29350	13.90	3.80	5.09	0.001591	0.010984	-1.22
261032_at	unknown protein ;supported by full-	---	AT1G17430	-3.27	-1.71	-5.09	0.001594	0.010995	-1.22
254592_at	heat shock transcription factor - like	HSF A4A	AT4G18880	3.54	1.82	5.07	0.001623	0.011115	-1.24

253608_at	xyloglucan endo-1,4-beta-D-glucar	XTH19	AT4G30290	-3.80	-1.93	-5.07	0.00163	0.011136	-1.24
266856_at	putative ABC transporter related to	PDR4	AT2G26910	-2.20	-1.14	-5.04	0.001674	0.011359	-1.27
260982_at	chalcone isomerase, putative simil	---	AT1G53520	-3.66	-1.87	-5.04	0.001687	0.011412	-1.28
264400_at	glucose-6-phosphate/phosphate-tr	GPT2	AT1G61800	10.64	3.41	5.04	0.00169	0.011421	-1.28
266984_at	unknown protein ; supported by cD	---	AT2G39570	2.19	1.13	5.03	0.001693	0.011436	-1.29
251621_at	protein kinase - like protein wall-as	---	AT3G57700	2.08	1.06	5.03	0.001695	0.011436	-1.29
257333_at	cytochrome c oxidase subunit 1	---	---	2.24	1.16	5.02	0.001712	0.011496	-1.30
260153_at	putative lipase similar to monoglyce	---	AT1G52760	2.21	1.14	5.02	0.001725	0.011554	-1.31
252300_at	pyruvate kinase -like protein various	---	AT3G49160	2.12	1.08	5.02	0.001726	0.011555	-1.31
250012_x_a	auxin-induced protein-like	---	AT5G18060	-8.50	-3.09	-5.01	0.001735	0.011579	-1.31
266503_at	unknown protein	---	AT2G47780	-2.27	-1.19	-5.00	0.001758	0.011684	-1.33
246233_at	putative protein	---	AT4G36550	2.89	1.53	5.00	0.001763	0.011699	-1.33
250293_s_a	auxin reponsive - like protein Nt-gh	---	AT5G13360	2.53	1.34	4.99	0.001768	0.011716	-1.33
248344_at	hyaluronan mediated motility recep	---	AT5G52280	-2.09	-1.06	-4.99	0.00178	0.011773	-1.34
263287_at	Expressed protein ; supported by fu	---	AT2G36145	-3.10	-1.63	-4.98	0.001793	0.011826	-1.35
260704_at	glycine cleavage system H protein	---	AT1G32470	-3.26	-1.70	-4.97	0.001811	0.011883	-1.36
254384_at	heat shock protein - like heat shoc	---	AT4G21870	-3.33	-1.74	-4.97	0.00182	0.01191	-1.36
251665_at	responce reactor 4 ; supported by	ARR9	AT3G57040	-2.88	-1.53	-4.96	0.001834	0.011955	-1.37
260522_x_a	hypothetical protein predicted by ge	---	AT2G41730	8.17	3.03	4.96	0.001835	0.011955	-1.37
258871_at	putative 26S proteosome regulatory	---	AT3G03060	2.51	1.33	4.96	0.001846	0.012005	-1.38
260884_at	unknown protein similar to unknow	---	AT1G29240	2.59	1.37	4.95	0.001847	0.012011	-1.38
245906_at	putative protein ;supported by full-l	---	AT5G11070	-2.49	-1.32	-4.94	0.001872	0.012113	-1.39
258000_at	AIG2-like protein similar to AIG2 pr	---	AT3G28940	2.08	1.05	4.94	0.001877	0.012128	-1.40
262210_at	hypothetical protein predicted by ge	IQD31	AT1G74690	-2.52	-1.33	-4.94	0.001883	0.01215	-1.40
247393_at	unknown protein	---	AT5G63130	5.57	2.48	4.92	0.001921	0.012315	-1.42
258470_at	Expressed protein ; supported by fu	---	AT3G06035	-7.04	-2.82	-4.92	0.001923	0.012315	-1.42
249610_at	putative protein	---	AT5G37360	-2.24	-1.17	-4.91	0.001932	0.012347	-1.43
257337_at	NADH dehydrogenase subunit 5 (n	---	---	2.35	1.23	4.90	0.001957	0.012455	-1.44
248794_at	ethylene responsive element bindi	ERF2	AT5G47220	6.64	2.73	4.89	0.001984	0.012582	-1.46
266097_at	unknown protein ; supported by cD	SOUL-1	AT2G37970	2.50	1.32	4.89	0.001986	0.012587	-1.46
264757_at	receptor protein kinase (IRK1), put	---	AT1G61360	5.35	2.42	4.87	0.002033	0.012827	-1.49
258074_at	unknown protein	---	AT3G25890	2.88	1.53	4.86	0.002041	0.012843	-1.49
266172_at	putative aquaporin (water channel p	PIP2E	AT2G39010	-2.33	-1.22	-4.86	0.002048	0.012875	-1.49
262151_at	hypothetical protein predicted by ge	---	AT1G52510	-2.16	-1.11	-4.85	0.002066	0.012951	-1.50
266225_at	putative membrane channel protein	ATOEP16-	AT2G28900	-2.59	-1.37	-4.83	0.00212	0.013189	-1.53

258633_at	putative serine carboxypeptidase II	SCPL27	AT3G07990	-2.22	-1.15	-4.83	0.002122	0.013197	-1.53
264223_s_a	receptor kinase, putative similar to	---	AT1G67520	2.65	1.41	4.83	0.002131	0.013216	-1.54
258679_at	putative 2,3-bisphosphoglycerate-i	---	AT3G08590	2.13	1.09	4.82	0.00215	0.013311	-1.55
260179_at	unknown protein similar to hypothet	HWI1	AT1G70690	2.35	1.23	4.81	0.002161	0.013348	-1.55
267436_at	putative receptor-like protein kinase	FRK1	AT2G19190	3.61	1.85	4.81	0.002161	0.013348	-1.55
252214_at	putative protein EREBP-3 homolog	CEJ1	AT3G50260	2.59	1.37	4.81	0.002162	0.013348	-1.55
247314_at	3(2),5-bisphosphate nucleotidase (	SAL2	AT5G64000	2.83	1.50	4.81	0.002168	0.013376	-1.56
252366_at	Expressed protein ; supported by fu	---	AT3G48420	-2.46	-1.30	-4.81	0.002176	0.013403	-1.56
260028_at	unknown protein ; supported by cDI	---	AT1G29980	-4.66	-2.22	-4.81	0.002177	0.013405	-1.56
262518_at	putative glutathione transferase On	ATGSTU24	AT1G17170	20.64	4.37	4.80	0.002194	0.013483	-1.57
260882_at	DNA binding protein, putative simil	WRKY65	AT1G29280	2.11	1.08	4.78	0.002234	0.013662	-1.59
259730_at	unknown protein similar to hypothet	---	AT1G77660	2.80	1.49	4.78	0.002253	0.013729	-1.60
249996_at	glutaredoxin -like protein glutaredo	---	AT5G18600	-2.19	-1.13	-4.77	0.002268	0.013801	-1.60
258055_at	putative 2Fe-2S iron-sulfur cluster p	NDF4	AT3G16250	-2.99	-1.58	-4.77	0.002273	0.01382	-1.61
247912_at	putative protein contains similarity t	---	AT5G57480	2.26	1.17	4.77	0.002275	0.013824	-1.61
244934_at	NADH dehydrogenase ND6	---	---	-2.21	-1.15	-4.77	0.00228	0.013841	-1.61
267567_at	putative cytochrome P450	CYP71A13	AT2G30770	27.98	4.81	4.76	0.002282	0.013849	-1.61
262369_at	hypothetical protein predicted by ge	---	AT1G73010	5.12	2.36	4.76	0.002298	0.01392	-1.62
245760_s_a	receptor serine/threonine kinase P	---	AT1G66910	2.45	1.29	4.76	0.002303	0.013937	-1.62
246280_at	hypothetical protein	---	AT4G36660	-2.26	-1.18	-4.75	0.002318	0.013991	-1.63
255856_at	unknown protein identical to unknov	---	AT1G66940	-4.84	-2.27	-4.74	0.002347	0.014115	-1.64
266831_at	putative squalene epoxidase	SQE2	AT2G22830	-3.09	-1.63	-4.73	0.002373	0.014221	-1.65
254343_at	PRH26 protein ;supported by full-le	אפר-03	AT4G21990	3.26	1.70	4.73	0.002381	0.014248	-1.66
249755_at	unknown protein ;supported by full-	---	AT5G24580	-3.15	-1.65	-4.72	0.002405	0.014342	-1.67
258183_at	unknown protein ;supported by full-	---	AT3G21550	-3.50	-1.81	-4.72	0.002412	0.014368	-1.67
264301_at	hypothetical protein contains simila	---	AT1G78780	2.60	1.38	4.71	0.002438	0.014469	-1.68
254232_at	tyrosine transaminase like protein t	CORI3	AT4G23600	-3.73	-1.90	-4.70	0.002462	0.014584	-1.69
255437_at	putative oxidoreductase similar to I	AOP2	AT4G03060	-3.05	-1.61	-4.69	0.002485	0.014686	-1.70
250090_at	glutamate decarboxylase 1 (GAD 1	GAD	AT5G17330	5.60	2.49	4.69	0.002486	0.014686	-1.70
259180_at	unknown protein	---	AT3G01680	-2.88	-1.53	-4.68	0.002511	0.014768	-1.71
262488_at	unknown protein EST gb|AA58624	---	AT1G21830	-2.09	-1.06	-4.67	0.002529	0.014842	-1.72
261421_at	hypothetical protein similar to unkn	IQD30	AT1G18840	-2.44	-1.29	-4.67	0.002551	0.014925	-1.73
246863_at	nodulin - like protein early nodulin I	---	AT5G25940	2.21	1.14	4.66	0.002558	0.014949	-1.73
259166_at	unknown protein ; supported by cD	---	AT3G01670	-3.16	-1.66	-4.66	0.002568	0.014991	-1.74
246487_at	putative protein with poly glutamic	---	AT5G16030	-2.06	-1.04	-4.66	0.002577	0.015035	-1.74

247881_at	putative protein similar to unknown	---	AT5G57700	-2.47	-1.30	-4.65	0.002585	0.015066	-1.75
251058_at	putative protein	---	AT5G01790	-3.69	-1.88	-4.65	0.00259	0.015085	-1.75
260804_at	hypothetical protein predicted by ge	---	AT1G78410	15.99	4.00	4.64	0.002614	0.015184	-1.76
256366_at	protein kinase, putative contains P	---	AT1G66880	2.24	1.16	4.64	0.002634	0.015278	-1.77
262414_at	acyl CoA synthetase, putative simi	LACS2	AT1G49430	-4.26	-2.09	-4.64	0.00264	0.015304	-1.77
249515_at	tryptophan synthase beta chain	---	AT5G38530	3.55	1.83	4.62	0.002688	0.015487	-1.79
260243_at	hypothetical protein similar to putati	---	AT1G63720	2.54	1.34	4.62	0.002699	0.015527	-1.79
253343_at	putative protein	---	AT4G33540	2.59	1.37	4.61	0.002715	0.015562	-1.80
258897_at	unknown protein	---	AT3G05730	-12.36	-3.63	-4.61	0.002733	0.015638	-1.81
260867_at	hypothetical protein predicted by ge	TED6	AT1G43790	-3.40	-1.77	-4.60	0.002751	0.015702	-1.81
261814_at	unknown protein	---	AT1G08310	5.66	2.50	4.60	0.002762	0.015756	-1.82
258588_s_a	glyceraldehyde-3-phosphate dehyc	GAPC1	AT3G04120	2.17	1.12	4.59	0.002789	0.015899	-1.83
247768_at	I-box binding factor - like protein I-b	---	AT5G58900	-3.03	-1.60	-4.58	0.002823	0.016048	-1.84
248327_at	putative protein similar to unknown	---	AT5G52750	8.40	3.07	4.57	0.002831	0.016077	-1.85
267178_at	unknown protein ; supported by ful	---	AT2G37750	4.29	2.10	4.57	0.002859	0.016178	-1.86
257325_at	hypothetical protein	---	AT2G07798	2.40	1.26	4.56	0.002866	0.016207	-1.86
262288_at	unknown protein identical to residue	CRR23	AT1G70760	-2.56	-1.35	-4.56	0.002869	0.016212	-1.86
258877_at	putative expansin precursor similar	ATEXPA13	AT3G03220	-2.31	-1.21	-4.56	0.002888	0.016264	-1.87
258929_at	unknown protein Pfam HMM hit: FK	---	AT3G10060	-2.64	-1.40	-4.55	0.002904	0.016325	-1.87
254331_s_a	cytochrome P450 - like protein flav	CYP706A2	AT4G22690	2.82	1.50	4.55	0.002905	0.016325	-1.87
264402_at	HSP100/ClpB, putative similar to H	CLPB4	AT2G25140	2.05	1.03	4.55	0.002909	0.016325	-1.87
251304_at	putative protein several O-methyltra	---	AT3G61990	3.44	1.78	4.55	0.002917	0.016349	-1.88
255817_at	unknown protein ;supported by full-	PDLP3	AT2G33330	-2.11	-1.08	-4.54	0.002934	0.01642	-1.88
259507_at	unknown protein	---	AT1G43910	2.75	1.46	4.54	0.00294	0.016451	-1.89
249983_at	putative protein S-receptor kinase	---	AT5G18470	10.93	3.45	4.54	0.002943	0.016451	-1.89
251272_at	homeobox-leucine zipper protein A	ATHB-12	AT3G61890	2.82	1.50	4.53	0.002972	0.01656	-1.90
262634_at	unknown protein ; supported by cDI	---	AT1G06690	-2.53	-1.34	-4.53	0.002978	0.016568	-1.90
252950_at	putative protein phospholipase C (I	---	AT4G38690	-2.26	-1.18	-4.53	0.002979	0.016568	-1.90
266536_at	hypothetical protein predicted by ge	---	AT2G16900	2.93	1.55	4.53	0.00298	0.016568	-1.90
248448_at	putative protein contains similarity t	---	AT5G51190	5.35	2.42	4.53	0.002981	0.016568	-1.90
247213_at	unknown protein ; supported by ful	PROPEP1	AT5G64900	3.43	1.78	4.53	0.002989	0.016591	-1.90
245854_at	adenosine nucleotide translocator	AAC2	AT5G13490	6.12	2.61	4.50	0.003102	0.016985	-1.94
256186_at	4-coumarate:CoA ligase 1 identical	4CL1	AT1G51680	2.49	1.31	4.49	0.003107	0.017006	-1.95
250132_at	putative protein similar to unknown	KAN	AT5G16560	-2.03	-1.02	-4.49	0.003115	0.017038	-1.95
267610_at	K+ transporter, AKT1 identical to G	AKT1	AT2G26650	2.59	1.37	4.49	0.003135	0.017119	-1.96

246988_at	putative protein strong similarity to	---	AT5G67340	2.45	1.29	4.48	0.003172	0.017258	-1.97
266017_at	unknown protein ; supported by cD	---	AT2G18690	2.74	1.46	4.47	0.003182	0.017286	-1.97
261913_at	flavin-containing monooxygenase F	FMO GS-O	AT1G65860	-2.30	-1.20	-4.47	0.00319	0.017307	-1.97
262871_at	hypothetical protein predicted by ge	---	AT1G65010	-2.98	-1.57	-4.46	0.00322	0.017393	-1.99
245793_at	unknown protein ;supported by full-	---	AT1G32220	-2.11	-1.08	-4.46	0.00323	0.017414	-1.99
247729_at	1-aminocyclopropane-1-carboxylat	---	AT5G59530	2.02	1.01	4.46	0.003245	0.017439	-1.99
250680_at	putative protein similar to unknown	---	AT5G06570	-2.21	-1.14	-4.46	0.003245	0.017439	-1.99
264777_at	unknown protein similar to L-allo-th	THA1	AT1G08630	4.26	2.09	4.45	0.003266	0.017519	-2.00
247487_at	putative protein predicted protein,	---	AT5G62150	4.76	2.25	4.44	0.003295	0.017644	-2.01
251336_at	putative protein hypothetical protei	BAP1	AT3G61190	2.17	1.12	4.44	0.003305	0.017672	-2.01
246370_at	hypothetical protein predicted by ge	---	AT1G51920	4.50	2.17	4.44	0.003323	0.017728	-2.02
264524_at	tat-binding protein, putative Highly	ATBCAT-2	AT1G10070	4.45	2.16	4.44	0.003326	0.01774	-2.02
260754_at	unknown protein	---	AT1G49000	2.32	1.22	4.43	0.003343	0.017801	-2.03
251374_at	homeobox-leucine zipper protein H	HAT3	AT3G60390	-2.09	-1.06	-4.43	0.003358	0.017865	-2.03
247908_at	GS1-like protein ;supported by full-l	GS1	AT5G57440	-2.22	-1.15	-4.43	0.003365	0.017889	-2.03
260239_at	putative receptor protein kinase sir	---	AT1G74360	5.16	2.37	4.42	0.003387	0.017977	-2.04
255842_at	putative serine carboxypeptidase II	scpl46	AT2G33530	-2.38	-1.25	-4.42	0.003394	0.017992	-2.04
248676_at	putative protein similar to unknown	ATSDI1	AT5G48850	-3.57	-1.84	-4.42	0.003394	0.017992	-2.04
260368_at	AtHVA22c identical to AtHVA22c G	ATHVA22C	AT1G69700	-3.07	-1.62	-4.42	0.003409	0.018051	-2.05
252133_at	hypothetical protein hypothetical pr	---	AT3G50900	3.13	1.64	4.40	0.003455	0.018224	-2.06
250892_at	putative protein beta-(1-3)-glucosyl	ATCSLA09	AT5G03760	-10.98	-3.46	-4.40	0.003458	0.018235	-2.06
246251_at	cold acclimation protein homolog	---	AT4G37220	-2.56	-1.35	-4.39	0.003493	0.01838	-2.07
255546_at	putative CHP-rich zinc finger protei	---	AT4G01910	2.31	1.21	4.39	0.003515	0.018449	-2.08
254737_at	fatty acid elongase - like protein (c	---	AT4G13840	-2.61	-1.39	-4.39	0.003525	0.018487	-2.08
257923_at	hypothetical protein predicted by ge	---	AT3G23160	2.53	1.34	4.39	0.003531	0.01851	-2.09
248404_at	trehalose-6-phosphate phosphatas	ATTPPA	AT5G51460	-2.12	-1.08	-4.38	0.00355	0.018573	-2.09
260978_at	17.6 kDa heat shock protein (AA 1-	---	AT1G53540	2.29	1.20	4.37	0.003576	0.018667	-2.10
261480_at	phytochrome kinase substrate 1, p	PKS2	AT1G14280	-3.65	-1.87	-4.37	0.003578	0.018671	-2.10
264511_at	putative galactinol synthase similar	AtGolS3	AT1G09350	-3.15	-1.66	-4.36	0.003621	0.018837	-2.11
259979_at	unknown protein ;supported by full-	---	AT1G76600	2.19	1.13	4.36	0.003631	0.018866	-2.12
255065_s_a	putative arginase similar to arginas	---	AT4G08870	-3.39	-1.76	-4.36	0.003659	0.018982	-2.12
264147_at	receptor-like protein glossy1 (gl1),	CER1	AT1G02205	-13.77	-3.78	-4.35	0.003685	0.019084	-2.13
259244_at	unknown protein similar to zinc fing	COL9	AT3G07650	2.17	1.12	4.34	0.003705	0.019147	-2.14
250267_at	putative protein predicted proteins	---	AT5G12930	4.15	2.05	4.34	0.003722	0.019211	-2.14
252280_at	SF16 -like protein SF16 protein, pc	iqd21	AT3G49260	-2.45	-1.29	-4.34	0.003731	0.019242	-2.15

248932_at	peptide transporter	PTR3	AT5G46050	3.62	1.86	4.34	0.003739	0.019268	-2.15
263924_at	enolase (2-phospho-D-glycerate hy	LOS2	AT2G36530	2.16	1.11	4.34	0.003746	0.019294	-2.15
249783_at	calcium sensor homolog (gb|AAC2(	SOS3	AT5G24270	2.07	1.05	4.32	0.003802	0.019539	-2.17
259980_at	unknown protein ;supported by full-	---	AT1G76520	2.02	1.02	4.32	0.003808	0.019555	-2.17
265572_at	putative carbonic anhydrase	ATACA2	AT2G28210	8.70	3.12	4.32	0.003828	0.019623	-2.17
266775_at	putative SCARECROW gene regula	---	AT2G29060	2.04	1.03	4.31	0.003866	0.019778	-2.18
245336_at	Expressed protein ; supported by fu	---	AT4G16515	-4.36	-2.12	-4.31	0.003869	0.019787	-2.18
259033_at	putative pectinacetylesterase simila	---	AT3G09405	6.75	2.75	4.30	0.003893	0.01988	-2.19
255127_at	nodulin-like protein nodulin gene M	---	AT4G08300	3.43	1.78	4.28	0.003979	0.020196	-2.22
266132_at	hypothetical protein predicted by ge	SPX3	AT2G45130	2.14	1.10	4.27	0.004042	0.020446	-2.23
257938_at	cell elongation protein, Dwarf1 iden	DWF1	AT3G19820	-4.38	-2.13	-4.27	0.004047	0.020469	-2.23
248405_at	putative protein pectinesterase-like;	SKS2	AT5G51480	-5.07	-2.34	-4.27	0.004055	0.02049	-2.24
258362_at	unknown protein	---	AT3G14280	3.77	1.91	4.23	0.00423	0.021115	-2.28
254571_at	hypothetical protein	---	AT4G19370	3.79	1.92	4.22	0.004291	0.021291	-2.30
263565_at	unknown protein	FUT4	AT2G15390	3.10	1.63	4.22	0.004323	0.021388	-2.30
250443_at	Pto kinase interactor - like protein F	RBK1	AT5G10520	5.02	2.33	4.22	0.004326	0.021389	-2.31
247983_at	pyrophosphate-dependent phospho	PFK7	AT5G56630	2.45	1.29	4.21	0.004353	0.021488	-2.31
251183_at	putative protein putative protein At2	---	AT3G62630	-2.84	-1.51	-4.18	0.004516	0.022109	-2.35
263495_at	cold-regulated protein cor15b precu	COR15B	AT2G42530	-3.46	-1.79	-4.18	0.004537	0.022191	-2.36
245334_at	Expressed protein ; supported by fu	RALFL33	AT4G15800	-2.01	-1.01	-4.17	0.004548	0.022204	-2.36
253088_at	ferulate-5-hydroxylase (FAH1) ; su	FAH1	AT4G36220	2.10	1.07	4.17	0.004577	0.022294	-2.37
266516_at	putative glutaredoxin ;supported by	---	AT2G47880	-2.27	-1.18	-4.17	0.004583	0.02231	-2.37
266979_at	unknown protein ;supported by full-	PPL2	AT2G39470	-3.71	-1.89	-4.16	0.004599	0.022363	-2.37
249494_at	acyltransferase - like protein Antho	---	AT5G39050	2.23	1.16	4.16	0.004606	0.022382	-2.37
266150_s_a	hypothetical protein	---	AT2G12290	2.64	1.40	4.16	0.00463	0.022454	-2.38
258399_at	early auxin-induced protein, IAA19	IAA19	AT3G15540	-3.29	-1.72	-4.15	0.004653	0.022534	-2.38
264774_at	unknown protein	---	AT1G22890	2.32	1.22	4.15	0.004702	0.022729	-2.40
247444_at	putative protein strong similarity to (	HIPL2	AT5G62630	2.30	1.20	4.13	0.004792	0.023026	-2.42
259743_at	hypothetical protein predicted by ge	---	AT1G71140	3.65	1.87	4.12	0.004841	0.023212	-2.43
247816_at	similar to unknown protein (pir||S75	---	AT5G58260	-2.11	-1.08	-4.12	0.004851	0.023229	-2.43
257021_at	branched-chain amino acid aminot	BCAT4	AT3G19710	-2.07	-1.05	-4.12	0.004865	0.023271	-2.43
260477_at	Ser/Thr protein kinase isolog	---	AT1G11050	3.84	1.94	4.11	0.004915	0.023457	-2.44
261279_at	class I chitinase, putative similar to	POM1	AT1G05850	-4.76	-2.25	-4.11	0.004945	0.023534	-2.45
257058_at	Expressed protein ; supported by c	COX17	AT3G15352	3.47	1.79	4.09	0.005061	0.023874	-2.48
253274_at	Phosphoglycerate dehydrogenase	EDA9	AT4G34200	6.48	2.70	4.08	0.005072	0.023907	-2.48

264501_at	putative lipase Similar to nodulins a	---	AT1G09390	-2.53	-1.34	-4.07	0.005137	0.02412	-2.49
255502_at	contains similarity to a protein kina	---	AT4G02410	3.68	1.88	4.07	0.005151	0.024153	-2.49
265656_at	putative nonspecific lipid-transfer pr	---	AT2G13820	-2.18	-1.13	-4.06	0.005222	0.024413	-2.51
260857_at	unknown protein contains Pfam pro	LYM1	AT1G21880	-2.15	-1.10	-4.06	0.005233	0.024457	-2.51
263182_at	Expressed protein ; supported by fu	---	AT1G05575	7.99	3.00	4.05	0.005299	0.024679	-2.53
253414_at	putative protein	EDA39	AT4G33050	4.91	2.30	4.05	0.005308	0.024707	-2.53
257547_at	hypothetical protein predicted by ge	---	AT3G13000	-2.40	-1.27	-4.04	0.005335	0.024796	-2.53
249109_at	auxin-induced protein AUX2-11 (sp	ATAUX2-11	AT5G43700	-3.09	-1.63	-4.04	0.00536	0.024877	-2.54
255111_at	peroxidase C2 precursor like prote	---	AT4G08780	10.86	3.44	4.03	0.005389	0.024964	-2.54
262942_at	hypothetical protein similar to unkno	ALIS5	AT1G79450	2.28	1.19	4.03	0.005416	0.025029	-2.55
265853_at	putative RING zinc finger protein	---	AT2G42360	2.91	1.54	4.03	0.005423	0.025057	-2.55
267028_at	putative WRKY-type DNA binding p	WRKY33	AT2G38470	5.41	2.43	4.03	0.005428	0.025075	-2.55
246516_at	putative protein auxin-independent	---	AT5G15740	-3.02	-1.59	-4.03	0.005449	0.025151	-2.56
256933_at	unknown protein contains Pfam pro	---	AT3G22600	10.82	3.44	4.03	0.005453	0.025156	-2.56
256015_at	PSI type II chlorophyll a/b-binding p	LHCA6	AT1G19150	-3.76	-1.91	-4.02	0.005506	0.025314	-2.57
249986_at	putative protein predicted proteins,	---	AT5G18460	-2.10	-1.07	-4.01	0.005566	0.025484	-2.58
245744_at	unknown protein	---	AT1G51110	-2.32	-1.22	-4.01	0.005591	0.025549	-2.58
262882_at	cytochrome p450, putative similar t	CYP89A2	AT1G64900	2.52	1.33	4.00	0.0056	0.025578	-2.59
261248_at	calreticulin, putative similar to GB:A	---	AT1G20030	-2.29	-1.19	-4.00	0.005616	0.025645	-2.59
254408_at	serine/threonine kinase - like prote	B120	AT4G21390	6.51	2.70	4.00	0.00565	0.025737	-2.59
246858_at	receptor-like protein kinase - like re	---	AT5G25930	2.89	1.53	3.99	0.005707	0.025936	-2.61
264433_at	beta-glucosidase, putative similar t	BGLU45	AT1G61810	4.61	2.21	3.99	0.005721	0.025969	-2.61
248895_at	receptor protein kinase	FLS2	AT5G46330	-2.06	-1.04	-3.97	0.00582	0.026285	-2.63
258282_at	unknown protein	---	AT3G26910	2.31	1.21	3.93	0.006125	0.027265	-2.68
255011_at	cytochrome c several plant cytochr	CYTC-2	AT4G10040	2.79	1.48	3.93	0.006176	0.027408	-2.69
266270_at	putative glutathione S-transferase	ATGSTU3	AT2G29470	7.92	2.98	3.91	0.006255	0.027647	-2.70
261247_at	hypothetical protein predicted by ge	---	AT1G20070	-3.39	-1.76	-3.90	0.00634	0.027922	-2.72
261451_at	unknown protein	---	AT1G21060	-2.55	-1.35	-3.90	0.006353	0.02795	-2.72
249485_at	receptor protein kinase - like protei	---	AT5G39020	2.43	1.28	3.90	0.006408	0.028125	-2.73
255923_at	hypothetical protein contains Pfam	---	AT1G22180	2.33	1.22	3.89	0.006423	0.028153	-2.73
252908_at	putative protein	---	AT4G39670	5.54	2.47	3.89	0.006452	0.028232	-2.74
258002_at	AIG2-like protein similar to AIG2 pr	AIG2	AT3G28930	4.71	2.24	3.89	0.006464	0.028269	-2.74
252178_at	putative protein various predicted p	---	AT3G50750	-2.11	-1.07	-3.87	0.006585	0.028658	-2.76
260706_at	oxidase, putative similar to oxidase	AOX1D	AT1G32350	10.36	3.37	3.85	0.00676	0.029176	-2.79
248970_at	urea active transporter-like protein	---	AT5G45380	2.10	1.07	3.85	0.006797	0.029298	-2.79

247754_at	putative protein	---	AT5G59080	-2.14	-1.10	-3.85	0.006799	0.0293	-2.79
262649_at	unknown protein contains similarity	---	AT1G14040	2.29	1.20	3.84	0.006875	0.029555	-2.81
253203_at	arginine decarboxylase SPE2 ; sup	ADC2	AT4G34710	-2.38	-1.25	-3.83	0.00694	0.029761	-2.82
246919_at	putative protein hypothetical protei	---	AT5G25460	-9.93	-3.31	-3.82	0.007046	0.030071	-2.83
248382_at	peroxidase	---	AT5G51890	-3.02	-1.60	-3.80	0.007217	0.030589	-2.86
256300_at	unknown protein similar to N-term h	NAP	AT1G69490	3.02	1.60	3.80	0.007225	0.030611	-2.86
266581_at	putative desiccation related protein	---	AT2G46140	4.11	2.04	3.79	0.00728	0.03076	-2.87
256583_at	hypothetical protein	---	AT3G28850	2.04	1.03	3.79	0.007282	0.03076	-2.87
262801_at	unknown protein ;supported by full-	---	AT1G21010	2.16	1.11	3.77	0.007496	0.031359	-2.90
266290_at	putative glutathione S-transferase	ATGSTU1	AT2G29490	5.18	2.37	3.77	0.007518	0.031406	-2.90
255879_at	receptor-like kinase, putative simila	---	AT1G67000	2.00	1.00	3.77	0.007522	0.031418	-2.90
256185_at	dof zinc finger protein identical to d	ADOF1	AT1G51700	2.47	1.30	3.77	0.007532	0.031435	-2.90
255340_at	putative receptor-like protein kinase	---	AT4G04490	3.02	1.60	3.77	0.007537	0.031435	-2.91
266752_at	putative ABC transporter related to	ABCB4	AT2G47000	5.41	2.44	3.75	0.007668	0.031854	-2.92
246275_at	putative protein ; supported by full-l	BEE2	AT4G36540	-4.63	-2.21	-3.75	0.007709	0.031965	-2.93
257008_at	myrosinase-associated protein, put	ESM1	AT3G14210	-4.02	-2.01	-3.75	0.007745	0.032091	-2.93
251395_at	unknown protein ;supported by full-	FLA8	AT2G45470	-7.96	-2.99	-3.73	0.00786	0.032415	-2.95
256589_at	cytochrome P450, putative contain	CYP81D1	AT3G28740	4.57	2.19	3.73	0.007869	0.032439	-2.95
252939_at	NAD(P)H oxidoreductase, isoflavor	---	AT4G39230	2.82	1.49	3.73	0.007907	0.032549	-2.96
258140_at	Expressed protein ; supported by cl	ALDH2C4	AT3G24503	2.19	1.13	3.73	0.007927	0.032586	-2.96
266834_s_a	putative protein phosphatase 2C	---	AT2G05050	4.41	2.14	3.72	0.00802	0.032844	-2.97
266992_at	similar to Mlo proteins from H. vulga	MLO12	AT2G39200	3.47	1.79	3.71	0.008083	0.032983	-2.98
258641_at	unknown protein ;supported by full-	---	AT3G08030	-2.80	-1.49	-3.71	0.008085	0.032986	-2.98
262926_s_a	receptor kinase, putative similar to	ARK1	AT1G65790	2.26	1.18	3.71	0.008145	0.033139	-2.99
262366_at	disease resistance protein, putative	---	AT1G72890	2.13	1.09	3.70	0.00825	0.033432	-3.00
255999_at	DNA-binding protein, putative simil	WRKY71	AT1G29860	2.08	1.06	3.69	0.008297	0.033519	-3.01
266294_at	putative small heat shock protein ;s	---	AT2G29500	3.91	1.97	3.69	0.008315	0.033581	-3.01
252338_at	putative progesterone-binding prote	MAPR3	AT3G48890	2.65	1.41	3.69	0.008339	0.033621	-3.01
245929_at	alcohol dehydrogenase - like prote	---	AT5G24760	2.46	1.30	3.67	0.008497	0.034049	-3.03
248719_at	respiratory burst oxidase protein ; s	RBOHD	AT5G47910	2.75	1.46	3.67	0.00852	0.034093	-3.04
259439_at	1-aminocyclopropane-1-carboxylate	ACS2	AT1G01480	4.76	2.25	3.66	0.0086	0.034301	-3.05
261363_at	pectinesterase, putative similar to (	SKS6	AT1G41830	-6.13	-2.62	-3.66	0.008702	0.034613	-3.06
255753_at	myb factor, putative similar to myb	MYB51	AT1G18570	5.06	2.34	3.65	0.008715	0.034655	-3.06
261653_at	subtilisin-like serine protease, puta	SBTI1.1	AT1G01900	-2.07	-1.05	-3.65	0.008737	0.03473	-3.06
266311_at	hypothetical protein predicted by ge	---	AT2G27130	-2.49	-1.32	-3.65	0.008778	0.034817	-3.07

261663_at	hypothetical protein similar to hypot	EPR1	AT1G18330	-2.42	-1.28	-3.64	0.008819	0.034893	-3.07
253373_at	lysine-ketoglutarate reductase/sacc	---	AT4G33150	2.32	1.21	3.64	0.008853	0.034979	-3.08
246821_at	calmodulin-binding - like protein ca	CBP60G	AT5G26920	3.11	1.64	3.64	0.008904	0.035128	-3.08
AFFX-r2-At-	Arabidopsis thaliana /REF=M6411(	---	---	2.09	1.06	3.63	0.008963	0.035292	-3.09
257466_at	hypothetical protein predicted by ge	---	AT1G62840	2.11	1.08	3.63	0.008985	0.035354	-3.09
261375_at	transcription factor, putative similar	SPL4	AT1G53160	-3.37	-1.75	-3.62	0.009124	0.03568	-3.11
264773_at	putative disease resistance respons	---	AT1G22900	2.26	1.17	3.61	0.00917	0.035806	-3.12
246949_at	cytochrome P450-like protein CYT(	CYP71B13	AT5G25140	-2.45	-1.29	-3.60	0.009335	0.036318	-3.14
266464_at	glutathione-conjugate transporter A	ATMRP4	AT2G47800	4.29	2.10	3.60	0.009359	0.036383	-3.14
245251_at	calcineurin B-like protein 1 ; suppor	CBL1	AT4G17615	2.33	1.22	3.59	0.009429	0.036577	-3.15
245318_at	Expressed protein ; supported by fu	---	AT4G16980	-5.66	-2.50	-3.58	0.009559	0.03694	-3.16
260405_at	putative glutathione transferase sim	ATGSTU11	AT1G69930	6.10	2.61	3.57	0.009687	0.03732	-3.18
250798_at	peroxidase	---	AT5G05340	5.57	2.48	3.57	0.009743	0.037484	-3.18
259757_at	putative thioredoxin similar to prote	ATPDIL1-2	AT1G77510	2.55	1.35	3.56	0.009793	0.037598	-3.19
254926_at	ACC synthase (AtACS-6) ; support	ACS6	AT4G11280	4.45	2.15	3.55	0.009929	0.037983	-3.20
249872_at	unknown protein	---	AT5G23130	-2.35	-1.23	-3.54	0.010065	0.038315	-3.22
260693_at	peptide transporter PTR2-B, putati	NRT1.5	AT1G32450	2.09	1.06	3.54	0.010077	0.038348	-3.22
253627_at	low temperature and salt responsiv	---	AT4G30650	-5.16	-2.37	-3.53	0.01028	0.038901	-3.24
257925_at	unknown protein ;supported by full-	---	AT3G23170	3.81	1.93	3.52	0.010408	0.039207	-3.25
252604_at	high-affinity nitrate transporter - like	NRT2.6	AT3G45060	-2.50	-1.32	-3.50	0.010579	0.039682	-3.27
263231_at	putative indole-3-acetate beta-gluco	---	AT1G05680	11.60	3.54	3.48	0.010885	0.040491	-3.30
254229_at	hypothetical protein ; supported by	---	AT4G23610	2.45	1.29	3.48	0.010934	0.040634	-3.30
256442_at	hypothetical protein predicted by ge	---	AT3G10930	4.09	2.03	3.48	0.010961	0.040711	-3.31
261648_at	salt-tolerance zinc finger protein ide	STZ	AT1G27730	3.19	1.68	3.48	0.01098	0.040744	-3.31
259479_at	Expressed protein ; supported by fu	---	AT1G19020	3.25	1.70	3.47	0.011071	0.040967	-3.32
245038_at	similar to latex allergen from Hevea	PLA2A	AT2G26560	2.52	1.34	3.47	0.011116	0.041109	-3.32
250916_at	monodehydroascorbate reductase	ATMDAR2	AT5G03630	2.37	1.25	3.45	0.011433	0.041985	-3.35
260745_at	2,4-D inducible glutathione S-trans	ATGSTU20	AT1G78370	-2.12	-1.08	-3.45	0.011434	0.041985	-3.35
246912_at	putative protein various predicted p	---	AT5G25820	2.03	1.02	3.44	0.011521	0.042238	-3.36
260568_at	endochitinase isolog	---	AT2G43570	8.36	3.06	3.43	0.011645	0.042518	-3.37
264756_at	receptor protein kinase (IRK1), put	---	AT1G61370	2.76	1.47	3.43	0.011704	0.042655	-3.38
250415_at	putative protein GLUR3 ligand-gate	GLR2.5	AT5G11210	2.39	1.26	3.42	0.011827	0.042965	-3.39
265028_at	hypothetical protein predicted by ge	---	AT1G24530	-2.49	-1.32	-3.42	0.011836	0.042975	-3.39
267559_at	putative cytochrome P450	CYP76C2	AT2G45570	3.34	1.74	3.41	0.011931	0.043251	-3.40
259213_at	putative receptor ser/thr protein kina	---	AT3G09010	2.69	1.43	3.41	0.011979	0.043371	-3.40

266865_at	omega-3 fatty acid desaturase iden	FAD3	AT2G29980	-9.98	-3.32	-3.41	0.011985	0.04338	-3.40
245250_at	ethylene responsive element bindin	ATERF6	AT4G17490	4.66	2.22	3.41	0.011985	0.04338	-3.40
266267_at	putative glutathione S-transferase	ATGSTU4	AT2G29460	3.81	1.93	3.40	0.012107	0.043676	-3.41
261431_at	Myb-related transcription factor mi	AtMYB47	AT1G18710	2.48	1.31	3.40	0.012119	0.043691	-3.41
257137_at	P-glycoprotein, putative similar to P	ABCB19	AT3G28860	-2.55	-1.35	-3.38	0.012399	0.044347	-3.44
251297_at	germin-like protein (GLP10)	GLP10	AT3G62020	-2.06	-1.04	-3.36	0.012746	0.045216	-3.47
258947_at	hypothetical protein similar to calmo	---	AT3G01830	4.24	2.08	3.36	0.012864	0.045485	-3.48
249928_at	CCR4-associated factor-like protein	---	AT5G22250	4.46	2.16	3.34	0.01324	0.046469	-3.51
256093_at	predicted protein ; supported by cD	---	AT1G20823	2.46	1.30	3.31	0.013726	0.04766	-3.55
245749_at	proline-rich protein, putative similar	---	AT1G51090	-2.25	-1.17	-3.31	0.013739	0.0477	-3.55
254954_at	hypothetical protein ;supported by	---	AT4G10910	-2.09	-1.06	-3.30	0.013797	0.047828	-3.55
248896_at	putative protein contains similarity t	WRKY8	AT5G46350	2.56	1.36	3.30	0.013925	0.048161	-3.56
255959_at	phosphatidylinositol-4-phosphate 5	ATPIP5K1	AT1G21980	-2.55	-1.35	-3.29	0.013983	0.048267	-3.57
264514_at	putative cinnamyl alcohol dehydrog	---	AT1G09500	3.81	1.93	3.29	0.014161	0.048682	-3.58
258787_at	hypothetical protein predicted by ge	PUB24	AT3G11840	3.39	1.76	3.28	0.014213	0.048829	-3.58
251975_at	CDC48 - like protein transitional en	---	AT3G53230	2.29	1.20	3.28	0.014234	0.048856	-3.59
245711_at	putative c2h2 zinc finger transcriptio	ZAT6	AT5G04340	2.55	1.35	3.28	0.014243	0.048861	-3.59
262381_at	virus resistance protein, putative si	---	AT1G72900	2.92	1.54	3.27	0.014464	0.049342	-3.60
264415_at	AP2 domain containing protein, pu	RAP2.6	AT1G43160	-48.25	-5.59	-38.70	3.70E-09	2.81E-05	10.79
259942_at	unknown protein	ATWHY2	AT1G71260	4.28	2.10	23.71	9.78E-08	0.000167	8.56
251142_at	Expressed protein ; supported by fu	---	AT5G01015	-6.78	-2.76	-22.49	1.39E-07	0.000167	8.27
247030_at	putative protein similar to unknown	---	AT5G67210	-3.88	-1.96	-21.19	2.06E-07	0.000206	7.94
260235_at	putative SET protein, phospatase 2	NRP1	AT1G74560	3.58	1.84	19.02	4.23E-07	0.000301	7.31
262811_at	unknown protein ESTs gb|R65381 a	---	AT1G11700	4.83	2.27	18.50	5.08E-07	0.000301	7.14
261086_at	hypothetical protein predicted by ge	TRFL3	AT1G17460	3.29	1.72	17.03	8.78E-07	0.000345	6.63
263412_at	putative histone H2B ;supported by	---	AT2G28720	3.42	1.77	15.65	1.53E-06	0.000442	6.11
255604_at	hypothetical protein	---	AT4G01080	-7.00	-2.81	-15.62	1.55E-06	0.000442	6.09
249839_at	Expressed protein ; supported by cl	---	AT5G23405	3.94	1.98	15.46	1.66E-06	0.000457	6.03
245060_at	GDP-mannose pyrophosphorylase	CYT1	AT2G39770	-2.85	-1.51	-15.34	1.75E-06	0.000461	5.98
260496_at	putative ABC transporter	---	AT2G41700	2.70	1.43	14.86	2.15E-06	0.000485	5.78
253358_at	gamma-VPE (vacuolar processing e	GAMMA-VP	AT4G32940	3.12	1.64	14.57	2.45E-06	0.000523	5.65
250194_at	putative protein various predicted p	---	AT5G14550	3.13	1.65	14.53	2.49E-06	0.000523	5.63
246809_s_a	SAR DNA-binding protein - like SA	---	AT5G27120	2.44	1.29	14.29	2.77E-06	0.000556	5.53
249970_at	dermal glycoprotein precursor -like	---	AT5G19100	-8.12	-3.02	-14.27	2.80E-06	0.000556	5.51
264657_at	putative 26S protease regulatory s	RPT5B	AT1G09100	2.92	1.55	14.12	2.99E-06	0.000569	5.45

252123_at	flavanone 3-hydroxylase (FH3) ;su	F3H	AT3G51240	-2.80	-1.49	-13.81	3.46E-06	0.000602	5.30
249090_at	Expressed protein ; supported by cl	---	AT5G43745	-4.85	-2.28	-13.79	3.50E-06	0.000602	5.29
261772_at	hypothetical protein predicted by ge	---	AT1G76240	-8.52	-3.09	-13.60	3.83E-06	0.000608	5.20
255264_at	putative protein ethylene responsiv	---	AT4G05170	-3.32	-1.73	-13.59	3.84E-06	0.000608	5.20
251472_at	putative protein nodule inception p	---	AT3G59580	2.75	1.46	13.54	3.93E-06	0.000608	5.18
250545_at	serine/threonine protein kinase ;su	ATPK3	AT5G08160	-2.62	-1.39	-13.48	4.05E-06	0.000616	5.15
250663_at	putative protein prenylated rab acc	PRA1.B6	AT5G07110	-2.77	-1.47	-13.35	4.34E-06	0.000622	5.08
262996_at	hypothetical protein predicted by ge	---	AT1G54440	2.84	1.50	13.29	4.46E-06	0.000622	5.05
263929_at	hypothetical protein predicted by ge	URH1	AT2G36310	-3.21	-1.68	-13.02	5.08E-06	0.000655	4.92
257608_at	chaperonin, putative similar to CHA	HSP60-3A	AT3G13860	2.84	1.51	12.85	5.54E-06	0.000679	4.83
257164_at	mismatch binding protein, putative	MSH1	AT3G24320	2.88	1.52	12.80	5.68E-06	0.00069	4.81
257193_at	Expressed protein ; supported by fu	---	AT3G13160	2.42	1.28	12.78	5.75E-06	0.000694	4.79
245367_at	Expressed protein ; supported by fu	NRPB9B	AT4G16265	2.89	1.53	12.74	5.85E-06	0.000698	4.78
249354_at	nuclear pore protein -like nuclear p	EMB3012	AT5G40480	4.68	2.23	12.73	5.89E-06	0.000698	4.77
249540_at	4-coumarate--CoA ligase -like prot	---	AT5G38120	-8.44	-3.08	-12.70	5.99E-06	0.0007	4.75
264516_at	unknown protein	---	AT1G10090	-2.58	-1.37	-12.67	6.07E-06	0.0007	4.74
260605_at	hypothetical protein predicted by ge	---	AT2G43780	2.62	1.39	12.67	6.08E-06	0.0007	4.74
248753_at	acyl carrier protein-like	mtACP3	AT5G47630	2.59	1.38	12.61	6.26E-06	0.000709	4.71
266264_at	Expressed protein ; supported by fu	---	AT2G27775	2.52	1.33	12.59	6.34E-06	0.000709	4.69
261071_at	unknown protein	---	AT1G07380	3.38	1.76	12.40	6.97E-06	0.000738	4.60
261951_at	hypothetical protein predicted by ge	---	AT1G64490	2.73	1.45	12.38	7.05E-06	0.000739	4.59
252355_at	putative protein various predicted p	---	AT3G48250	2.62	1.39	12.36	7.15E-06	0.000739	4.57
258453_at	RNA polymerase I, II and III 24.3 k	NRPB5	AT3G22320	2.30	1.20	12.32	7.29E-06	0.000742	4.55
260364_at	putative alliinase similar to aliinase	TAA1	AT1G70560	4.12	2.04	12.27	7.47E-06	0.000745	4.53
245141_at	putative flavonol reductase	BEN1	AT2G45400	-3.06	-1.61	-12.24	7.60E-06	0.000753	4.51
263533_at	putative Rieske iron-sulfur protein ;	TIC55	AT2G24820	2.11	1.08	12.19	7.80E-06	0.000763	4.48
246603_at	copper amine oxidase, putative sim	---	AT1G31690	-4.03	-2.01	-12.16	7.93E-06	0.00077	4.46
255825_at	Expressed protein ; supported by fu	---	AT2G40475	-4.51	-2.17	-12.14	8.02E-06	0.000776	4.45
246057_at	putative protein predicted proteins,	---	AT5G08400	2.42	1.27	12.04	8.47E-06	0.000802	4.40
260500_at	Expressed protein ; supported by cl	---	AT2G41705	2.28	1.19	12.04	8.48E-06	0.000802	4.40
247434_at	Expressed protein ; supported by fu	---	AT5G62575	2.33	1.22	12.03	8.51E-06	0.000802	4.39
264257_at	unknown protein	---	AT1G09230	3.09	1.63	12.01	8.61E-06	0.000802	4.38
262379_at	hypothetical protein predicted by ge	---	AT1G73020	-2.35	-1.24	-11.98	8.74E-06	0.000804	4.36
254773_at	putative protein Cyclic beta-1-3-glu	ATCSLA15	AT4G13410	-12.05	-3.59	-11.96	8.81E-06	0.000804	4.36
253558_at	kinase binding protein - like Skb1 p	SKB1	AT4G31120	2.93	1.55	11.92	9.03E-06	0.000814	4.33

250598_at	transcription factor-like protein ; su	ATMYB29	AT5G07690	-4.41	-2.14	-11.86	9.31E-06	0.000822	4.30
256661_at	hypothetical protein similar to putati	---	AT3G11964	2.43	1.28	11.85	9.34E-06	0.000822	4.30
250529_at	RNA helicase-like protein	---	AT5G08610	3.81	1.93	11.83	9.45E-06	0.000823	4.28
257239_at	unknown protein	---	AT3G24100	2.67	1.42	11.83	9.48E-06	0.000823	4.28
257765_at	hypothetical protein contains Pfam	---	AT3G23020	2.29	1.20	11.79	9.69E-06	0.000837	4.26
246260_at	amino acid permease, putative con	---	AT1G31820	3.64	1.86	11.77	9.81E-06	0.000838	4.25
260089_at	putative ATPase contains Pfam pro	---	AT1G73170	2.16	1.11	11.69	1.02E-05	0.000843	4.20
265895_at	unknown protein ;supported by full-	---	AT2G15000	2.84	1.50	11.69	1.02E-05	0.000843	4.20
247386_at	putative protein similar to unknown	emb2746	AT5G63420	2.40	1.26	11.66	1.04E-05	0.000843	4.19
263679_at	RNA helicase, putative similar to R	---	AT1G59990	3.12	1.64	11.66	1.04E-05	0.000843	4.18
253976_at	putative protein kinase protein kina	D6PKL1	AT4G26610	-2.08	-1.05	-11.62	1.06E-05	0.000845	4.16
256489_at	unknown protein	---	AT1G31550	-2.10	-1.07	-11.60	1.07E-05	0.000845	4.15
257635_at	cytochrome P450 monooxygenase	CYP71B4	AT3G26280	3.09	1.63	11.60	1.08E-05	0.000845	4.15
261317_at	cytochrome C oxidase assembly p	---	AT1G53030	2.55	1.35	11.60	1.08E-05	0.000845	4.15
248219_at	unknown protein ; supported by ful	---	AT5G53650	2.00	1.00	11.59	1.08E-05	0.000845	4.15
245323_at	cysteine proteinase inhibitor like pro	---	AT4G16500	-3.22	-1.69	-11.57	1.09E-05	0.000845	4.14
263786_at	putative auxin-responsive protein ;	JAR1	AT2G46370	-1.99	-0.99	-11.54	1.11E-05	0.000856	4.12
259759_at	hypothetical protein similar to GB:(	---	AT1G77550	2.51	1.33	11.50	1.14E-05	0.00086	4.09
264344_at	putative aspartic proteinase similar	---	AT1G11910	2.05	1.04	11.50	1.14E-05	0.00086	4.09
250196_at	polynucleotide phosphorylase	---	AT5G14580	3.06	1.61	11.47	1.16E-05	0.000864	4.08
250484_at	asparagine synthetase ASN3 ; sup	ASN3	AT5G10240	2.42	1.28	11.46	1.16E-05	0.000865	4.07
247575_at	RNA-binding protein - like RNA-bin	GR-RBP3	AT5G61030	3.40	1.76	11.45	1.17E-05	0.000865	4.07
261796_at	non-phototropic hypocotyl, putative	---	AT1G30440	-2.47	-1.30	-11.44	1.17E-05	0.000865	4.06
251951_s_a	putative protein predicted proteins,	---	AT1G55710	2.54	1.35	11.42	1.19E-05	0.00087	4.05
267534_at	putative CCCH-type zinc finger prot	---	AT2G41900	2.33	1.22	11.39	1.21E-05	0.000879	4.03
263483_at	putative heat shock protein ; suppo	CR88	AT2G04030	2.59	1.38	11.37	1.22E-05	0.00088	4.02
258616_at	putative protein kinase contains Pf	---	AT3G02880	-3.14	-1.65	-11.31	1.27E-05	0.000897	3.98
248878_at	50S ribosomal protein L14	---	AT5G46160	2.33	1.22	11.28	1.29E-05	0.000903	3.97
247453_at	putative protein similar to unknown	---	AT5G62440	3.21	1.68	11.23	1.32E-05	0.00092	3.94
261872_s_a	hypthetical protein contains similari	---	AT1G11520	2.60	1.38	11.22	1.33E-05	0.00092	3.93
266419_at	putative annexin ;supported by full-	ANNAT3	AT2G38760	-3.68	-1.88	-11.21	1.34E-05	0.00092	3.92
249115_at	PINHEAD (gb|AAD40098.1); transla	ZLL	AT5G43810	2.12	1.08	11.20	1.34E-05	0.00092	3.92
253422_at	putative protein ;supported by full-l	---	AT4G32240	2.55	1.35	11.15	1.39E-05	0.000922	3.89
255365_at	putative phosphofructokinase beta	MEE51	AT4G04040	2.27	1.19	11.14	1.39E-05	0.000922	3.88
259422_at	unknown protein	---	AT1G13810	3.73	1.90	11.14	1.40E-05	0.000922	3.88

248739_at	DnaJ protein-like ;supported by full	GFA2	AT5G48030	2.22	1.15	11.13	1.40E-05	0.000922	3.88
264512_at	Expressed protein ; supported by cl	---	AT1G09575	-2.71	-1.44	-11.12	1.41E-05	0.000924	3.87
255651_at	putative protein	---	AT4G00940	2.49	1.32	11.11	1.42E-05	0.000924	3.86
245108_at	putative cytokinin oxidase	CKX1	AT2G41510	2.31	1.21	11.10	1.43E-05	0.000924	3.85
262505_at	unknown protein ESTs gb|N96028.	---	AT1G21680	2.73	1.45	11.03	1.49E-05	0.000946	3.81
266841_at	putative heat shock transcription fac	ATHSFA2	AT2G26150	-4.26	-2.09	-10.99	1.52E-05	0.000949	3.79
256092_at	Expressed protein ; supported by fu	HMGB3	AT1G20696	2.00	1.00	10.99	1.52E-05	0.000949	3.79
266480_at	unknown protein ; supported by cD	---	AT2G31130	2.13	1.09	10.96	1.55E-05	0.000962	3.77
248984_at	DNA-directed RNA polymerase sub	NRPC2	AT5G45140	3.03	1.60	10.96	1.55E-05	0.000962	3.77
253562_at	putative protein ;supported by full-l	---	AT4G31130	2.03	1.02	10.90	1.60E-05	0.000978	3.74
261838_at	heat shock protein hsp70, putative	Hsp70b	AT1G16030	2.39	1.26	10.90	1.61E-05	0.000978	3.73
264239_at	hypothetical protein predicted by ge	---	AT1G54770	2.12	1.08	10.88	1.62E-05	0.00098	3.72
254999_at	putative protein ; supported by full-	---	AT4G09830	3.13	1.65	10.84	1.66E-05	0.00099	3.70
259515_at	hypothetical protein ; supported by	---	AT1G20430	2.08	1.06	10.83	1.67E-05	0.000991	3.69
251278_at	putative protein hypothetical protei	emb1703	AT3G61780	2.69	1.43	10.77	1.74E-05	0.001013	3.65
263375_s_a	putative prohibitin ;supported by fu	ATPHB6	AT2G20530	2.69	1.43	10.75	1.75E-05	0.001013	3.65
262618_at	unknown protein	---	AT1G06560	2.03	1.02	10.74	1.77E-05	0.001014	3.63
259819_at	unknown protein ; supported by cDI	ATMTK	AT1G49820	2.00	1.00	10.72	1.78E-05	0.001015	3.63
247247_at	50S ribosomal protein L17 ;suppor	---	AT5G64650	2.20	1.14	10.68	1.83E-05	0.001029	3.60
264922_s_a	U2 snRNP auxiliary factor, large su	---	AT1G60830	2.06	1.04	10.67	1.84E-05	0.001029	3.59
255428_at	putative LRR receptor-like protein I	SRF3	AT4G03390	-2.29	-1.20	-10.65	1.86E-05	0.001039	3.58
256466_at	plastid protein, putative similar to G	---	AT1G32580	2.02	1.01	10.64	1.87E-05	0.00104	3.57
249971_at	dermal glycoprotein - like dermal g	---	AT5G19110	-4.23	-2.08	-10.63	1.89E-05	0.001047	3.57
248326_at	Notchless protein homolog	---	AT5G52820	3.03	1.60	10.61	1.90E-05	0.00105	3.56
245710_at	ferulate-5-hydroxylase	---	AT5G04330	-3.26	-1.71	-10.59	1.93E-05	0.001057	3.54
253973_at	Expressed protein ; supported by cl	---	AT4G26555	-1.89	-0.92	-10.58	1.94E-05	0.001059	3.53
251015_at	putative protein predicted protein, A	---	AT5G02480	2.10	1.07	10.55	1.97E-05	0.001067	3.52
266643_s_a	putative flavonol 3-O-glucosyltransf	---	AT2G29710	-3.04	-1.60	-10.54	1.98E-05	0.00107	3.51
263371_at	unknown protein ;supported by full-	NOP10	AT2G20490	2.89	1.53	10.50	2.04E-05	0.001082	3.48
265511_at	putative glycine-rich protein ; suppo	---	AT2G05540	3.50	1.81	10.47	2.07E-05	0.001092	3.47
260595_at	unknown protein	---	AT1G55890	2.60	1.38	10.42	2.14E-05	0.001116	3.43
263236_at	putative response regulator 3 simil	ARR4	AT1G10470	-4.07	-2.03	-10.40	2.17E-05	0.001119	3.42
264811_at	hypothetical protein predicted by ge	---	AT1G08640	2.02	1.02	10.39	2.17E-05	0.001119	3.42
265139_at	unknown protein	---	AT1G51310	2.68	1.42	10.39	2.18E-05	0.001119	3.41
258850_at	putative cellulose synthase catalytic	CSLD3	AT3G03050	-2.36	-1.24	-10.39	2.18E-05	0.001119	3.41

248362_at	fibrillarin 1 (AtFib1) identical to fibril	FIB1	AT5G52470	2.20	1.14	10.37	2.20E-05	0.001119	3.40
265147_at	hypothetical protein	---	AT1G51380	3.41	1.77	10.37	2.20E-05	0.001119	3.40
261927_at	RING-H2 zinc finger protein ATL5,	---	AT1G22500	6.71	2.75	10.37	2.21E-05	0.001122	3.40
262946_at	hypothetical protein predicted by ge	---	AT1G79390	2.32	1.22	10.35	2.23E-05	0.001127	3.39
261406_at	unknown protein contains similarity	NRP2	AT1G18800	3.69	1.88	10.35	2.24E-05	0.001129	3.39
252362_at	hypothetical protein	PDE312	AT3G48500	4.02	2.01	10.33	2.26E-05	0.001135	3.38
266466_at	hypothetical protein The first 3 exor	---	AT2G47790	2.23	1.16	10.32	2.28E-05	0.001139	3.37
266197_at	hypothetical protein predicted by ge	---	AT2G39120	2.19	1.13	10.31	2.28E-05	0.001139	3.37
254452_at	UV-damaged DNA-binding protein-	DDB1B	AT4G21100	2.87	1.52	10.30	2.30E-05	0.001146	3.36
257724_at	hypothetical protein predicted by ge	---	AT3G18510	2.60	1.38	10.29	2.31E-05	0.001146	3.35
249433_at	putative protein hypothetical protei	---	AT5G39940	3.13	1.65	10.27	2.34E-05	0.001146	3.34
264513_at	putative glucose-6-phosphate dehy	G6PD4	AT1G09420	2.27	1.18	10.26	2.36E-05	0.001148	3.33
256672_at	ABC transporter, putative contains	---	AT3G52310	-2.82	-1.50	-10.24	2.39E-05	0.001159	3.32
258059_at	NAM-like protein (No Apical Merist	ATNAC3	AT3G29035	3.69	1.88	10.23	2.41E-05	0.001165	3.31
250767_at	putative protein contains similarity t	ATNFXL2	AT5G05660	-2.04	-1.03	-10.22	2.42E-05	0.001169	3.30
246316_at	putative protein predicted proteins -	---	AT3G56890	1.89	0.92	10.17	2.50E-05	0.001192	3.27
255795_at	putative calcium-binding EF-hand p	RD20	AT2G33380	-7.38	-2.88	-10.17	2.50E-05	0.001192	3.27
255668_s_a	predicted protein ; supported by full	---	AT4G00238	2.79	1.48	10.11	2.60E-05	0.001209	3.23
253942_at	putative protein	---	AT4G27010	3.74	1.90	10.11	2.60E-05	0.001209	3.23
258009_at	unknown protein	---	AT3G19440	1.89	0.92	10.10	2.61E-05	0.001213	3.22
256091_at	Expressed protein ; supported by fu	HMGB2	AT1G20693	2.26	1.17	10.08	2.64E-05	0.001218	3.21
256064_at	Expressed protein ; supported by fu	---	AT1G07020	-2.22	-1.15	-10.08	2.64E-05	0.001218	3.21
261819_at	receptor-like kinase, putative simila	---	AT1G11410	2.16	1.11	10.06	2.67E-05	0.001223	3.20
261487_at	hypothetical protein predicted by ge	---	AT1G14340	2.12	1.09	10.03	2.73E-05	0.001225	3.18
248394_at	unknown protein	---	AT5G52070	2.11	1.08	10.03	2.73E-05	0.001225	3.18
247776_at	phosphoinositide-specific phospho	PLC4	AT5G58700	-2.75	-1.46	-10.01	2.76E-05	0.001226	3.17
260985_at	dTDP-D-glucose 4,6-dehydratase,	MUM4	AT1G53500	-2.42	-1.28	-10.00	2.78E-05	0.001232	3.16
258531_at	importin alpha identical to GB:AAC	IMPA-1	AT3G06720	2.01	1.00	9.99	2.81E-05	0.001237	3.15
256892_at	hypothetical protein contains simila	---	AT3G19000	4.18	2.06	9.98	2.81E-05	0.001237	3.15
264605_at	putative auxin-induced protein, IAA	IAA12	AT1G04550	2.30	1.20	9.98	2.82E-05	0.001239	3.14
267082_at	CPDK-related protein kinase CDPK	CRK1	AT2G41140	2.03	1.02	9.96	2.84E-05	0.001239	3.13
263200_at	hypothetical protein predicted by ge	---	AT1G05600	2.90	1.54	9.96	2.85E-05	0.001239	3.13
255008_at	putative protein hypothetical protei	---	AT4G10060	-2.24	-1.17	-9.95	2.87E-05	0.001239	3.12
250126_at	ubiquitin C-terminal hydrolase-like p	UCH1	AT5G16310	2.57	1.36	9.93	2.90E-05	0.001249	3.11
248510_at	Expressed protein ; supported by fu	---	---	1.91	0.93	9.91	2.94E-05	0.001261	3.10

253803_at	putative protein hypothetical protei	---	AT4G28200	2.13	1.09	9.90	2.96E-05	0.001264	3.09
253917_at	hypothetical protein ;supported by	---	AT4G27380	3.29	1.72	9.90	2.96E-05	0.001264	3.09
251699_at	cytochrome P450-like protein cytoc	CYP94D2	AT3G56630	2.30	1.20	9.88	3.01E-05	0.001277	3.08
254788_at	putative protein other predicted pro	---	AT4G12790	-2.00	-1.00	-9.85	3.05E-05	0.001289	3.06
260020_at	hydrophilic protein, putative similar	PDF6	AT1G29990	1.92	0.94	9.83	3.10E-05	0.001296	3.04
255749_at	p68 RNA helicase, putative similar	STRS1	AT1G31970	2.15	1.10	9.82	3.12E-05	0.001303	3.04
245019_at	hypothetical protein	---	---	-1.87	-0.90	-9.81	3.13E-05	0.001307	3.03
247132_at	putative protein strong similarity to	ARO2	AT5G66200	-2.89	-1.53	-9.79	3.18E-05	0.00132	3.02
251637_at	hypothetical protein	---	AT3G57570	2.33	1.22	9.78	3.21E-05	0.001322	3.01
267033_at	unknown protein ;supported by full-	---	AT2G38450	1.86	0.89	9.73	3.30E-05	0.001347	2.98
250513_at	protein kinase ;supported by full-le	---	AT5G09890	-2.14	-1.10	-9.72	3.32E-05	0.001352	2.97
260897_at	ER lumen protein retaining receptor	ERD2	AT1G29330	-2.16	-1.11	-9.72	3.33E-05	0.001353	2.97
254303_at	predicted protein	---	AT4G22830	-2.08	-1.06	-9.72	3.34E-05	0.001353	2.96
252942_at	putative protein ;supported by full-l	---	AT4G39300	2.43	1.28	9.68	3.41E-05	0.00137	2.94
261250_at	unknown protein	---	AT1G05890	2.09	1.06	9.67	3.44E-05	0.00137	2.93
267337_at	putative anthocyanin 5-aromatic ac	---	AT2G39980	-3.28	-1.71	-9.65	3.48E-05	0.001378	2.92
250863_at	F1F0-ATPase inhibitor - like protei	---	AT5G04750	1.89	0.92	9.64	3.52E-05	0.001381	2.91
260607_at	putative receptor protein kinase	---	AT2G43700	2.75	1.46	9.63	3.54E-05	0.001384	2.90
261102_at	unknown protein	---	AT1G62880	1.99	0.99	9.63	3.54E-05	0.001384	2.90
246457_at	WD40-repeat protein transducin ho	TOZ	AT5G16750	2.24	1.16	9.62	3.54E-05	0.001384	2.90
259347_at	putative GAR1 protein similar to GE	---	AT3G03920	2.07	1.05	9.62	3.56E-05	0.001384	2.90
258114_at	putative cytochrome P450 similar to	CYP72A13	AT3G14660	2.13	1.09	9.61	3.57E-05	0.001384	2.89
266127_s_a	putative mitochondrial translation el	---	AT1G45332	2.95	1.56	9.60	3.60E-05	0.001393	2.88
258812_at	unknown protein similar to GB:AAD	ECT1	AT3G03950	2.41	1.27	9.59	3.62E-05	0.001396	2.88
263774_at	unknown protein ; supported by cD	---	AT2G40280	-2.04	-1.03	-9.58	3.65E-05	0.001405	2.87
260688_at	hypothetical protein similar to dehyd	---	AT1G17665	2.28	1.19	9.57	3.68E-05	0.00141	2.86
262754_at	putative inosine-5-monophosphate	---	AT1G16350	2.42	1.28	9.56	3.69E-05	0.00141	2.86
246478_at	putative protein several hypothetica	---	AT5G15980	2.05	1.03	9.56	3.70E-05	0.001411	2.86
251478_at	putative protein SF16 protein, polle	IQD13	AT3G59690	1.91	0.93	9.52	3.80E-05	0.001441	2.83
250485_at	Expressed protein ; supported by fu	PROPEP5	AT5G09990	3.91	1.97	9.51	3.82E-05	0.001441	2.82
264142_at	hypothetical protein predicted by ge	---	AT1G78930	3.06	1.61	9.51	3.83E-05	0.001441	2.82
255573_at	hypothetical protein	---	AT4G01400	-1.81	-0.86	-9.50	3.84E-05	0.001441	2.82
248864_at	bHLH protein-like	---	AT5G46760	1.87	0.91	9.50	3.85E-05	0.001443	2.81
253926_at	hnRNP-like protein ; supported by	---	AT4G26650	-2.02	-1.02	-9.49	3.86E-05	0.001443	2.81
260696_at	unknown protein	---	AT1G32520	2.25	1.17	9.49	3.88E-05	0.001443	2.81

254026_at	putative calmodulin-binding protein	---	AT4G25800	1.85	0.89	9.48	3.91E-05	0.00145	2.80
256595_x_a	hypothetical protein	---	AT3G28530	2.42	1.27	9.44	4.01E-05	0.001476	2.77
254779_at	hypothetical protein	---	AT4G12760	1.95	0.96	9.43	4.03E-05	0.001483	2.76
248933_at	putative protein contains similarity t	---	AT5G46070	2.04	1.03	9.41	4.08E-05	0.001493	2.75
250314_at	putative protein contains similarity t	---	AT5G12190	1.93	0.95	9.41	4.09E-05	0.001493	2.75
266072_at	putative trehalose-6-phosphate syn	ATTPS11	AT2G18700	-3.66	-1.87	-9.40	4.12E-05	0.001499	2.74
262751_at	hypothetical protein predicted by ge	---	AT1G16310	1.94	0.96	9.38	4.18E-05	0.001514	2.73
266903_at	hypothetical protein predicted by ge	MEE21	AT2G34570	1.94	0.95	9.36	4.24E-05	0.00152	2.71
245483_at	cysteine proteinase contains similar	---	AT4G16190	1.93	0.95	9.36	4.24E-05	0.00152	2.71
262780_at	putative cytochrome P450 monoox	CYP71B28	AT1G13090	2.68	1.42	9.34	4.28E-05	0.001528	2.70
250356_at	clathrin binding protein - like Af10-p	---	AT5G11710	-1.76	-0.82	-9.34	4.29E-05	0.001528	2.70
258663_at	hypothetical protein	---	AT3G08670	-1.92	-0.94	-9.33	4.30E-05	0.001528	2.70
253386_at	sulfolipid biosynthesis protein SQD1	SQD1	AT4G33030	2.86	1.52	9.32	4.33E-05	0.001535	2.69
267123_at	putative acetone-cyanohydrin lyase	MES7	AT2G23560	-3.94	-1.98	-9.31	4.36E-05	0.00154	2.68
249335_at	putative protein contains similarity t	NRPB12	AT5G41010	2.11	1.08	9.31	4.37E-05	0.001541	2.68
247529_at	monosaccharide transporter STP3	---	AT5G61520	2.10	1.07	9.30	4.40E-05	0.001546	2.67
250424_at	bromodomain protein - like bromod	GTE2	AT5G10550	-1.90	-0.92	-9.30	4.40E-05	0.001546	2.67
254679_at	putative protein Mei2-like protein, A	AML3	AT4G18120	2.15	1.10	9.29	4.44E-05	0.001549	2.66
263711_at	putative protein phosphatase 2C ;s	---	AT2G20630	-2.13	-1.09	-9.27	4.48E-05	0.001559	2.65
249140_at	F-box protein family, AtFBX6 conta	---	AT5G43190	-2.82	-1.49	-9.25	4.54E-05	0.001572	2.64
255243_at	putative protein hypothetical protei	---	AT4G05590	2.04	1.03	9.25	4.55E-05	0.001572	2.64
255278_at	putative WD-repeat membrane prot	---	AT4G04940	3.21	1.68	9.24	4.59E-05	0.001583	2.63
250985_at	putative protein various predicted p	---	AT5G02830	1.93	0.95	9.23	4.61E-05	0.00159	2.62
256033_at	UDP-glucose glucosyltransferase,	UGT71C4	AT1G07250	-2.04	-1.03	-9.22	4.66E-05	0.001593	2.61
251320_at	3-methyl-2-oxobutanoate hydroxy-	PANB2	AT3G61530	1.90	0.93	9.21	4.68E-05	0.001597	2.61
257697_at	hypothetical protein predicted by ge	---	AT3G12700	-3.10	-1.63	-9.20	4.70E-05	0.001597	2.60
259272_at	unknown protein similar to hypothet	---	AT3G01290	-2.43	-1.28	-9.20	4.70E-05	0.001597	2.60
245502_at	hypothetical protein	---	AT4G15640	2.50	1.32	9.20	4.73E-05	0.001601	2.59
261034_s_a	hypothetical protein predicted by ge	---	AT1G17450	2.66	1.41	9.19	4.75E-05	0.001605	2.59
259593_at	nuclear transport factor 2, putative	NTF2B	AT1G27970	1.81	0.86	9.19	4.76E-05	0.001605	2.59
263532_s_a	putative protein RIO1 protein, Sacc	---	AT2G24990	2.77	1.47	9.18	4.78E-05	0.001612	2.58
251011_at	putative protein histone H2A, garde	HTA12	AT5G02560	1.92	0.94	9.16	4.83E-05	0.001615	2.57
265946_s_a	putative WD-40 repeat protein, MS	FVE	AT2G19520	1.92	0.94	9.16	4.84E-05	0.001615	2.57
261187_at	beta-1,3-glucanase precursor, puta	---	AT1G32860	-3.49	-1.80	-9.15	4.86E-05	0.001618	2.56
262026_at	calcium-dependent protein kinase i	ATCDPK2	AT1G35670	-2.50	-1.32	-9.15	4.89E-05	0.001618	2.56

266951_at	putative salt-inducible protein ; sup	---	AT2G18940	1.85	0.89	9.14	4.91E-05	0.001618	2.55
255600_s_a	putative protein predicted protein, A	---	AT4G01020	1.86	0.89	9.14	4.91E-05	0.001618	2.55
262307_at	heat shock protein DnaJ, putative s	---	AT1G71000	-2.66	-1.41	-9.13	4.92E-05	0.001618	2.55
266002_at	hypothetical protein predicted by ge	---	AT2G37310	2.10	1.07	9.13	4.95E-05	0.001618	2.55
262957_s_a	RNA polymerase II subunit, putativ	NRPB8A	AT1G54250	1.73	0.79	9.13	4.96E-05	0.001618	2.54
252921_at	putative protein DNA damage-indu	EDS5	AT4G39030	-5.10	-2.35	-9.12	4.96E-05	0.001618	2.54
265451_at	unknown protein	---	AT2G46490	-1.82	-0.87	-9.12	4.98E-05	0.00162	2.54
257007_at	Expressed protein ; supported by cl	---	AT3G14205	-1.85	-0.89	-9.12	4.99E-05	0.00162	2.54
258687_at	unknown protein	---	AT3G07860	2.76	1.47	9.10	5.03E-05	0.001622	2.53
249315_at	unknown protein	---	AT5G41190	1.88	0.91	9.09	5.08E-05	0.001634	2.52
252293_at	4-coumarate-CoA ligase -like prote	---	AT3G48990	1.96	0.97	9.08	5.13E-05	0.001643	2.51
258120_at	hypothetical protein predicted by ge	---	AT3G14730	1.86	0.90	9.07	5.14E-05	0.001643	2.51
254045_at	pumilio-like protein abdominal segr	APUM6	AT4G25880	1.92	0.94	9.07	5.15E-05	0.001643	2.50
259285_at	hypothetical protein similar to putati	---	AT3G11460	1.99	1.00	9.07	5.15E-05	0.001643	2.50
260519_at	unknown protein	---	AT1G51540	-1.82	-0.86	-9.05	5.21E-05	0.001655	2.49
257825_at	protein kinase, putative contains P	---	AT3G26700	-2.14	-1.10	-9.04	5.25E-05	0.001664	2.48
246947_at	cytochrome P450-like protein CYT	CYP71B11	AT5G25120	1.97	0.98	9.04	5.26E-05	0.001666	2.48
259426_at	hypothetical protein contains simila	LEA14	AT1G01470	-2.23	-1.16	-9.03	5.29E-05	0.001666	2.47
266259_at	unknown protein ;supported by full-	---	AT2G27830	2.04	1.03	9.03	5.30E-05	0.001666	2.47
258244_at	unknown protein ; supported by cD	---	AT3G27770	-1.96	-0.97	-9.03	5.31E-05	0.001666	2.47
259346_at	putative glutamate dehydrogenase	GDH3	AT3G03910	-1.88	-0.91	-9.02	5.35E-05	0.001673	2.46
252031_at	putative protein 150-kD protein clu	---	AT3G52140	1.96	0.97	9.01	5.35E-05	0.001673	2.46
265025_at	Expressed protein ; supported by fu	---	AT1G24575	2.20	1.14	9.01	5.36E-05	0.001673	2.46
264047_at	hypothetical protein predicted by ge	---	AT2G22410	2.03	1.02	8.99	5.43E-05	0.001687	2.45
245569_at	RNA polymerase II fifth largest subu	NRPE7	AT4G14660	1.80	0.85	8.99	5.44E-05	0.001687	2.45
264515_at	hypothetical protein similar to hypot	---	AT1G10090	-1.72	-0.78	-8.98	5.48E-05	0.001693	2.44
254635_at	extensin-like protein extensin-like p	---	AT4G18670	-2.26	-1.17	-8.98	5.48E-05	0.001693	2.44
256480_at	unknown protein	SAR1	AT1G33410	2.40	1.26	8.95	5.61E-05	0.001719	2.41
250495_at	ribsomal protein - like chloroplast r	---	AT5G09770	2.46	1.30	8.94	5.62E-05	0.001719	2.41
265258_at	hypothetical protein predicted by ge	---	AT2G20390	1.81	0.86	8.94	5.63E-05	0.001719	2.41
253396_at	putative protein RNA-binding prote	AtLa1	AT4G32720	2.02	1.01	8.94	5.63E-05	0.001719	2.41
264951_at	unknown protein contains similarity	---	AT1G76970	1.77	0.83	8.94	5.64E-05	0.001719	2.41
251221_at	putative protein ER6 protein - Lyco	---	AT3G62550	2.07	1.05	8.93	5.66E-05	0.001724	2.40
253480_at	putative protein ENOD16, Medicag	---	AT4G31840	-1.98	-0.99	-8.93	5.68E-05	0.001728	2.40
261073_at	hypothetical protein predicted by ge	---	AT1G07300	2.04	1.03	8.93	5.69E-05	0.001728	2.40

255305_at	putative ABC transporter similar to	ATABC1	AT4G04770	2.56	1.36	8.92	5.72E-05	0.001734	2.39
249727_at	putative protein similar to unknown	MRU1	AT5G35490	-1.88	-0.91	-8.91	5.76E-05	0.001737	2.38
266551_at	unknown protein ; supported by cD	---	AT2G35260	-1.72	-0.78	-8.91	5.76E-05	0.001737	2.38
261891_at	transcriptional regulator, putative s	---	AT1G80790	1.80	0.85	8.90	5.81E-05	0.001752	2.37
252980_at	putative protein Human multiple ex	---	AT4G38040	-1.80	-0.85	-8.89	5.85E-05	0.001758	2.37
266229_at	putative RING zinc finger ankyrin pr	---	AT2G28840	1.91	0.93	8.89	5.86E-05	0.001758	2.37
257451_at	hypothetical protein predicted by ge	BT3	AT1G05690	2.07	1.05	8.88	5.87E-05	0.001758	2.36
249581_at	glutamate--ammonia ligase ; suppo	GSR 1	AT5G37600	1.98	0.98	8.88	5.87E-05	0.001758	2.36
250987_at	putative protein crp1 protein, Zea r	---	AT5G02860	2.25	1.17	8.88	5.89E-05	0.001758	2.36
258512_at	beta-glucosidase, putative similar t	---	AT3G06510	1.72	0.78	8.86	5.96E-05	0.001776	2.35
259835_at	unknown protein	TRZ3	AT1G52160	1.96	0.97	8.86	5.98E-05	0.001776	2.34
260294_at	GMP synthase similar to GMP synt	---	AT1G63660	1.90	0.93	8.86	5.98E-05	0.001776	2.34
256797_at	DEAD box helicase protein, putativ	---	AT3G18600	3.04	1.60	8.85	6.00E-05	0.001781	2.34
244906_at	hypothetical protein	---	ATMG00690	1.96	0.97	8.84	6.04E-05	0.001789	2.33
250978_at	putative protein contains transmem	---	AT5G03080	-1.78	-0.83	-8.84	6.06E-05	0.00179	2.33
249475_at	putative protein CGI-108 protein, H	---	AT5G38890	2.56	1.36	8.84	6.06E-05	0.00179	2.33
256745_at	UDP-glucose dehydrogenase, puta	---	AT3G29360	-2.35	-1.24	-8.84	6.07E-05	0.00179	2.33
260292_at	putative UDP-N-acetylmuramoylala	MURE	AT1G63680	1.73	0.79	8.83	6.07E-05	0.00179	2.33
251686_at	putative protein hypothetical protein	ATATG18D	AT3G56440	-1.90	-0.93	-8.83	6.09E-05	0.001791	2.32
261576_at	unknown protein ;supported by full-	---	AT1G01070	5.12	2.35	8.82	6.13E-05	0.001791	2.32
257122_at	RNA-binding protein, putative cont	APUM5	AT3G20250	3.01	1.59	8.82	6.13E-05	0.001791	2.32
255132_at	inositol 1,3,4-trisphosphate 5/6-kin	---	AT4G08170	-2.38	-1.25	-8.80	6.24E-05	0.00181	2.30
264689_at	hypothetical protein predicted by ge	---	AT1G09900	2.79	1.48	8.79	6.25E-05	0.001812	2.30
260733_at	RNA-binding protein, putative simil	---	AT1G17640	2.35	1.23	8.79	6.28E-05	0.001813	2.29
248292_at	putative protein similar to unknown	---	AT5G53030	2.93	1.55	8.79	6.29E-05	0.001813	2.29
251740_at	peptidylprolyl isomerase	ROC2	AT3G56070	4.17	2.06	8.78	6.29E-05	0.001813	2.29
246623_at	nuM1 protein, putative similar to nu	ATNUC-L1	AT1G48920	2.59	1.37	8.78	6.30E-05	0.001813	2.29
264099_at	replicase, putative similar to replica	---	AT1G79050	2.08	1.06	8.78	6.32E-05	0.001813	2.28
260824_at	unknown protein	---	AT1G06720	4.02	2.01	8.77	6.37E-05	0.001822	2.28
261070_at	disease resistance protein, putative	AtRLP1	AT1G07390	2.42	1.28	8.76	6.41E-05	0.001827	2.27
259881_at	Expressed protein ; supported by cl	---	AT1G76820	2.86	1.52	8.76	6.42E-05	0.001827	2.27
249253_at	putative protein similar to unknown	---	AT5G42060	2.18	1.13	8.76	6.42E-05	0.001827	2.27
263049_at	unknown protein ;supported by full-	---	AT2G05260	-2.04	-1.03	-8.75	6.43E-05	0.001827	2.26
265826_at	hypothetical protein predicted by ge	---	AT2G35795	1.83	0.87	8.74	6.51E-05	0.001843	2.25
259393_at	trehalose-6-phosphate synthase, p	ATTPS7	AT1G06410	-2.08	-1.06	-8.73	6.52E-05	0.001846	2.25

259884_at	hypothetical protein predicted by ge	---	AT1G76390	1.88	0.91	8.72	6.58E-05	0.001852	2.24
248710_at	unknown protein ;supported by full-	---	AT5G48480	2.50	1.32	8.72	6.60E-05	0.001852	2.24
256570_at	unknown protein ; supported by cD	---	AT3G19540	-1.78	-0.84	-8.71	6.62E-05	0.001856	2.23
263122_at	prenyltransferase, putative similar	SPS1	AT1G78510	2.32	1.21	8.71	6.66E-05	0.001864	2.23
248192_at	IAA-amino acid hydrolase homolog	ILL3	AT5G54140	1.93	0.95	8.70	6.67E-05	0.001864	2.23
261839_at	unknown protein	---	AT1G16040	2.14	1.09	8.70	6.69E-05	0.001867	2.22
261303_at	unknown protein contains DNA-bin	HON5	AT1G48620	1.74	0.80	8.69	6.74E-05	0.00187	2.21
266824_at	homeodomain transcription factor (	HAT9	AT2G22800	1.90	0.92	8.69	6.74E-05	0.00187	2.21
261319_at	phytochrome A supressor spa1, pu	SPA4	AT1G53090	1.68	0.75	8.69	6.75E-05	0.00187	2.21
255176_s_a	putative DNA-directed RNA polyme	---	AT1G01210	1.95	0.97	8.69	6.76E-05	0.00187	2.21
267051_at	hypothetical protein predicted by ge	---	AT2G38500	-2.72	-1.44	-8.68	6.76E-05	0.00187	2.21
263104_at	unknown protein	---	AT2G05120	2.14	1.10	8.68	6.79E-05	0.001871	2.21
253393_at	Expressed protein ; supported by c	GLB3	AT4G32690	2.10	1.07	8.67	6.82E-05	0.001875	2.20
249375_at	putative protein predicted proteins,	AGP24	AT5G40730	-2.03	-1.02	-8.66	6.88E-05	0.001886	2.19
266194_at	unknown protein	---	AT2G39090	-1.69	-0.75	-8.66	6.90E-05	0.001887	2.19
263127_at	hypothetical protein predicted by ge	MSL6	AT1G78610	-2.24	-1.16	-8.65	6.94E-05	0.001888	2.18
252281_at	putative protein various predicted p	---	AT3G49320	2.58	1.37	8.65	6.95E-05	0.00189	2.18
246808_at	putative protein many predicted pro	---	AT5G27110	1.97	0.98	8.64	6.98E-05	0.00189	2.18
260486_at	F-box protein ZEITLUPE/FKF/LKP/	---	AT1G51550	2.03	1.02	8.64	6.99E-05	0.00189	2.18
265605_at	putative cellulose synthase catalytic	CESA10	AT2G25540	-1.69	-0.76	-8.63	7.04E-05	0.001897	2.17
250197_at	isocitrate dehydrogenase - like pro	---	AT5G14590	1.84	0.88	8.63	7.04E-05	0.001897	2.17
252868_at	putative protein tubulin-folding cofa	POR	AT4G39920	-1.81	-0.85	-8.61	7.12E-05	0.001909	2.16
247833_at	putative protein	---	AT5G58575	1.80	0.85	8.61	7.14E-05	0.00191	2.15
261044_at	molybdopterin biosynthesis CNX3	CNX3	AT1G01290	2.09	1.07	8.61	7.14E-05	0.00191	2.15
262656_at	unknown protein location of EST T	---	AT1G14200	-2.04	-1.03	-8.59	7.23E-05	0.001924	2.14
252619_at	putative protein several hypothetica	---	AT3G45210	3.66	1.87	8.59	7.26E-05	0.001926	2.14
267344_at	hypothetical protein predicted by ge	---	AT2G44230	-4.75	-2.25	-8.58	7.27E-05	0.001926	2.13
259551_at	hypothetical protein	---	AT1G21190	1.94	0.96	8.58	7.30E-05	0.001927	2.13
248307_at	selenium-binding protein-like	---	AT5G52850	2.16	1.11	8.56	7.38E-05	0.001943	2.12
265961_at	unknown protein ;supported by full-	---	AT2G37400	2.94	1.55	8.56	7.39E-05	0.001943	2.12
252677_at	nitrilase 3 ;supported by full-length	NIT3	AT3G44320	-3.38	-1.76	-8.56	7.39E-05	0.001943	2.12
254147_at	putative protein similarity Human m	---	AT4G24270	3.03	1.60	8.56	7.41E-05	0.001945	2.11
252824_at	histone H3.3 ; supported by cDNA:	---	AT4G40030	2.09	1.06	8.55	7.43E-05	0.001946	2.11
265326_at	unknown protein predicted by gens	---	AT2G18220	2.59	1.37	8.55	7.43E-05	0.001946	2.11
257477_at	unknown protein	---	AT1G10660	2.46	1.30	8.55	7.45E-05	0.001946	2.11

265011_at	putative chloroplast membrane pro	ALB4	AT1G24490	1.71	0.78	8.55	7.45E-05	0.001946	2.11
253061_at	putative protein SPOP, Homo sapi	BT5	AT4G37610	-3.49	-1.80	-8.54	7.48E-05	0.001949	2.10
250217_at	nodulin-like protein	---	AT5G14120	-2.55	-1.35	-8.54	7.49E-05	0.001949	2.10
264169_at	hypothetical protein predicted by ge	---	AT1G02020	1.64	0.72	8.54	7.51E-05	0.001949	2.10
250679_at	putative protein contains similarity t	---	AT5G06550	2.82	1.50	8.54	7.53E-05	0.001952	2.10
262769_at	actin-like protein strong similarity to	DIS1	AT1G13180	-2.24	-1.16	-8.53	7.56E-05	0.001958	2.09
253294_at	hypothetical protein	---	AT4G33740	2.02	1.01	8.53	7.57E-05	0.001959	2.09
256808_at	unknown protein	ALY3	AT3G21430	1.77	0.82	8.52	7.60E-05	0.001961	2.09
251961_at	inorganic pyrophosphatase -like pr	AtPPa4	AT3G53620	-3.61	-1.85	-8.52	7.61E-05	0.001961	2.08
253249_at	GATA transcription factor 3	---	AT4G34680	2.46	1.30	8.52	7.61E-05	0.001961	2.08
247818_at	contains similarity to GTP-binding p	---	AT5G58370	1.97	0.98	8.50	7.70E-05	0.001976	2.07
254133_at	putative protein various predicted A	---	AT4G24810	1.78	0.83	8.50	7.73E-05	0.001978	2.07
263249_at	delta 9 desaturase ALMOST identic	ADS2	AT2G31360	-1.83	-0.87	-8.50	7.73E-05	0.001978	2.07
260407_at	putative protein kinase Pfam HMM	---	AT1G69910	-1.78	-0.83	-8.50	7.74E-05	0.001978	2.07
267099_at	DNA-(apurinic or apyrimidinic site) l	ARP	AT2G41460	2.96	1.57	8.49	7.79E-05	0.001986	2.06
248573_at	cellulase homolog OR16pep precur	ATGH9A1	AT5G49720	-2.16	-1.11	-8.49	7.80E-05	0.001986	2.06
262943_at	inosine-5'-monophosphate dehydro	---	AT1G79470	1.92	0.94	8.48	7.84E-05	0.001988	2.05
265029_at	zinc finger protein 7, ZFP7 ; suppo	ZFP7	AT1G24625	2.58	1.37	8.48	7.85E-05	0.001988	2.05
252183_at	UTP-glucose glucosyltransferase -	UGT72E1	AT3G50740	2.39	1.26	8.48	7.86E-05	0.001988	2.05
245269_at	hypothetical protein ; supported by	---	AT4G14500	-2.05	-1.03	-8.48	7.86E-05	0.001988	2.05
260390_at	unknown protein ; supported by ful	---	AT1G73940	2.13	1.09	8.47	7.89E-05	0.001988	2.05
259174_at	hypothetical protein similar to putat	UNE7	AT3G03690	-1.67	-0.74	-8.47	7.91E-05	0.00199	2.04
255870_at	hypothetical protein predicted by ge	---	AT2G30280	1.90	0.92	8.47	7.91E-05	0.00199	2.04
266366_at	unknown protein	---	AT2G41420	-2.32	-1.22	-8.46	7.95E-05	0.001996	2.04
245388_at	hypothetical protein ;supported by f	---	AT4G16410	1.80	0.84	8.45	8.01E-05	0.002002	2.03
265712_s_a	unknown protein	---	AT2G03330	1.95	0.97	8.45	8.01E-05	0.002002	2.03
257300_at	unknown protein ; supported by ful	---	AT3G28080	3.41	1.77	8.45	8.03E-05	0.002002	2.03
251087_at	putative protein unknown protein T	---	AT5G01460	-1.82	-0.87	-8.45	8.03E-05	0.002002	2.03
261979_at	nitrate reductase, putative similar t	NIA2	AT1G37130	3.26	1.71	8.44	8.09E-05	0.002015	2.02
255670_at	Expressed protein ; supported by fu	RHB1A	AT4G00335	1.76	0.81	8.43	8.15E-05	0.002024	2.01
246152_at	IPP transferase - like protein tRNA	IPT9	AT5G20040	1.91	0.93	8.40	8.30E-05	0.002057	1.99
251267_at	putative protein hypothetical protei	---	AT3G62330	-2.19	-1.13	-8.40	8.32E-05	0.002058	1.99
248315_at	selenium-binding protein-like	MEF1	AT5G52630	2.01	1.01	8.39	8.37E-05	0.002067	1.98
250463_at	transcription factor OBF4	TGA4	AT5G10030	2.19	1.13	8.39	8.39E-05	0.002069	1.98
246789_at	long-chain-fatty-acid--CoA ligase-li	LACS7	AT5G27600	1.84	0.88	8.38	8.42E-05	0.002073	1.98

250721_at	putative protein contains similarity t	---	AT5G06210	1.85	0.88	8.38	8.43E-05	0.002073	1.98
254778_at	putative protein	---	AT4G12750	2.34	1.23	8.38	8.45E-05	0.002076	1.97
247459_at	putative protein embryo-specific pr	---	AT5G62200	1.97	0.98	8.37	8.48E-05	0.002081	1.97
267562_at	unknown protein similar to hypothet	---	AT2G39670	1.84	0.88	8.37	8.49E-05	0.002081	1.97
253585_at	putative protein hypothetical protei	---	AT4G30720	1.85	0.89	8.36	8.54E-05	0.002091	1.96
262354_at	H+-transporting ATPase protein, pu	VHA-E3	AT1G64200	-4.60	-2.20	-8.36	8.59E-05	0.002099	1.96
246124_at	putative protein acyl-protein thioest	---	AT5G20060	-1.67	-0.74	-8.35	8.61E-05	0.002102	1.95
261409_at	zinc finger protein OBP2 identical to	OBP2	AT1G07640	2.02	1.02	8.35	8.63E-05	0.002105	1.95
262168_at	unknown protein ;supported by full-	---	AT1G74730	-1.98	-0.99	-8.34	8.67E-05	0.002112	1.95
252901_at	putative protein various predicted p	---	AT4G39550	1.86	0.89	8.32	8.82E-05	0.002136	1.93
258245_at	hypothetical protein	---	AT3G29075	-1.94	-0.96	-8.32	8.86E-05	0.002142	1.92
266005_at	unknown protein	RSZ33	AT2G37340	2.42	1.27	8.31	8.87E-05	0.002142	1.92
266957_at	unknown protein	PTAC12	AT2G34640	2.20	1.14	8.31	8.92E-05	0.002149	1.91
254955_at	putative protein RNA polymerase I	KELP	AT4G10920	1.85	0.88	8.30	8.93E-05	0.00215	1.91
247550_at	putative protein many predicted pro	---	AT5G61370	1.74	0.80	8.28	9.07E-05	0.002172	1.90
245465_at	cellulose synthase like protein	ATCSLA01	AT4G16590	-13.42	-3.75	-8.27	9.15E-05	0.002183	1.89
247187_at	putative protein similar to unknown	---	AT5G65490	1.90	0.93	8.27	9.15E-05	0.002183	1.89
253996_at	nucleosome assembly protein I-like	NAP1;1	AT4G26110	2.11	1.07	8.27	9.16E-05	0.002184	1.89
262947_at	unknown protein ;supported by full-	GASA1	AT1G75750	-1.67	-0.74	-8.26	9.23E-05	0.002188	1.88
247355_at	unknown protein ; supported by ful	SPT42	AT5G63670	1.84	0.88	8.26	9.23E-05	0.002188	1.88
247155_at	2-oxoglutarate dehydrogenase, E1	---	AT5G65750	2.63	1.40	8.24	9.35E-05	0.002204	1.86
263449_at	unknown protein	AtRABA5d	AT2G31670	-1.85	-0.89	-8.24	9.39E-05	0.002205	1.86
253538_at	putative protein ribosomal protein Y	---	AT4G31460	1.75	0.81	8.23	9.41E-05	0.002205	1.86
266288_s_a	putative pumilio/Mpt5 family RNA-b	APUM1	AT2G29140	2.16	1.11	8.23	9.41E-05	0.002205	1.86
252875_at	GTP-binding protein GB3 ;supporte	RABA4B	AT4G39990	-1.80	-0.85	-8.22	9.49E-05	0.002222	1.85
267405_at	putative related to microbial divalen	CUTA	AT2G33740	1.80	0.84	8.22	9.50E-05	0.002222	1.85
253344_at	putative protein predicted protein, A	---	AT4G33550	-3.65	-1.87	-8.21	9.56E-05	0.002229	1.84
248197_at	NADPH:protochlorophyllide oxidore	PORA	AT5G54190	-1.90	-0.93	-8.21	9.56E-05	0.002229	1.84
266715_at	putative RNA-binding protein	---	AT2G46780	-2.14	-1.10	-8.21	9.56E-05	0.002229	1.84
265828_at	hypothetical protein predicted by ge	---	AT2G14520	1.79	0.84	8.21	9.57E-05	0.002229	1.84
248378_at	unknown protein ;supported by full-	---	AT5G51840	-1.82	-0.86	-8.21	9.58E-05	0.002229	1.84
257149_at	prohibitin, putative similar to prohib	ATPHB4	AT3G27280	3.93	1.97	8.21	9.62E-05	0.002229	1.83
245244_at	IAA-amino acid hydrolase, putative	ILL6	AT1G44350	-2.77	-1.47	-8.19	9.70E-05	0.002233	1.82
262094_at	SAR DNA binding protein, putative	NOP56	AT1G56110	4.16	2.06	8.18	9.78E-05	0.002245	1.81
256002_at	carbamoylphosphate synthetase, p	CARB	AT1G29900	1.97	0.98	8.18	9.80E-05	0.002246	1.81

259081_at	putative sodium proton exchanger s	NHX2	AT3G05030	2.24	1.16	8.17	9.91E-05	0.002265	1.80
261535_at	Expressed protein ; supported by fu	---	AT1G01725	2.21	1.15	8.16	9.95E-05	0.002269	1.80
247406_at	response regulator 6 (ARR6) ; sup	ARR6	AT5G62920	-5.37	-2.43	-8.16	9.95E-05	0.002269	1.80
250112_at	low density lipoprotein B-like protei	---	AT5G16300	-1.80	-0.85	-8.16	9.96E-05	0.002269	1.79
266557_at	unknown protein ; supported by cD	---	AT2G46080	1.64	0.71	8.16	9.97E-05	0.002269	1.79
267511_at	unknown protein	---	AT2G45670	-1.88	-0.91	-8.15	0.0001	0.002276	1.79
247641_at	imidazoleglycerol-phosphate synth	PDX2	AT5G60540	1.96	0.97	8.14	0.000101	0.002281	1.78
266589_at	hypothetical protein predicted by ge	---	AT2G46250	2.45	1.29	8.14	0.000101	0.002285	1.78
251927_at	hypothetical protein ER6 protein - l	---	AT3G53990	-1.80	-0.84	-8.13	0.000102	0.002291	1.77
266570_at	putative chloroplast ribosomal prote	---	AT2G24090	-1.82	-0.87	-8.13	0.000102	0.002291	1.77
253672_at	mRNA cleavage factor subunit - lik	CFIM-25	AT4G29820	2.27	1.18	8.12	0.000103	0.002302	1.76
256890_at	glycine-rich RNA binding protein, p	GRP4	AT3G23830	4.17	2.06	8.11	0.000103	0.002306	1.76
249821_at	putative protein contains similarity t	---	AT5G23690	3.09	1.63	8.11	0.000103	0.002307	1.76
259344_at	putative polynucleotide phosphoryl	RIF10	AT3G03710	2.19	1.13	8.09	0.000105	0.002329	1.74
257218_at	unknown protein similar to DAG pro	---	AT3G15000	1.82	0.86	8.09	0.000105	0.002329	1.74
254079_at	putative protein pmt2 methyltransfe	---	AT4G25730	3.42	1.77	8.09	0.000105	0.002329	1.74
253004_at	putative protein	---	AT4G38280	2.46	1.30	8.09	0.000105	0.002331	1.74
251678_at	putative protein conserved hypothe	EDA7	AT3G56990	1.78	0.83	8.09	0.000105	0.002331	1.74
254593_s_a	putative protein IEF SSP 9502, Ho	---	AT4G18900	2.16	1.11	8.08	0.000106	0.002333	1.73
252613_at	putative protein hypothetical protei	---	AT3G45190	1.70	0.77	8.08	0.000106	0.002333	1.73
256253_at	60S acidic ribosomal protein, putat	---	AT3G11250	2.02	1.02	8.08	0.000106	0.002342	1.73
254919_at	RING-H2 finger protein RHA1b ;su	RHA1B	AT4G11360	2.88	1.53	8.07	0.000106	0.002344	1.73
246173_s_a	putative protein hypothetical protei	---	AT3G61520	2.49	1.32	8.06	0.000107	0.002357	1.71
257674_at	translational inhibitor protein, putat	---	AT3G20390	-1.82	-0.87	-8.06	0.000107	0.002357	1.71
254187_at	putative protein hypothetical protei	---	AT4G23890	1.73	0.79	8.06	0.000107	0.002357	1.71
250329_at	putative potassium transport protei	KEA6	AT5G11800	-1.95	-0.96	-8.06	0.000108	0.002359	1.71
251256_at	putative protein hypothetical protein	---	AT3G62300	2.25	1.17	8.05	0.000108	0.002365	1.70
247907_at	unknown protein	---	AT5G57460	-1.75	-0.81	-8.04	0.000109	0.002367	1.70
252723_at	hypothetical protein ; supported by	---	AT3G43520	1.71	0.77	8.04	0.000109	0.002367	1.70
253388_at	putative protein ; supported by cDN	---	AT4G32910	2.59	1.38	8.04	0.000109	0.002367	1.70
256458_at	integral membrane protein, putative	---	AT1G75220	-2.96	-1.57	-8.04	0.000109	0.00237	1.70
262595_at	putative ethylene responsive eleme	SHN1	AT1G15360	-1.91	-0.93	-8.03	0.00011	0.002372	1.69
259846_at	peptide transporter PTR2-B, putati	---	AT1G72140	-2.04	-1.03	-8.03	0.00011	0.002387	1.69
265272_at	unknown protein	ARF10	AT2G28350	2.52	1.34	8.02	0.00011	0.002388	1.68
250510_at	15.9 kDa subunit of RNA polymeras	NRPB4	AT5G09920	1.80	0.85	8.02	0.000111	0.002393	1.68

255686_at	putative potassium/H+ antiporter	KEA2	AT4G00630	2.20	1.14	8.01	0.000112	0.0024	1.67
247763_at	RNA polymerase II	NRPB7	AT5G59180	1.89	0.92	8.00	0.000112	0.002407	1.67
250004_at	putative protein predicted proteins -	---	AT5G18750	2.37	1.24	7.99	0.000114	0.002425	1.65
263863_at	3-oxoacyl carrier protein synthase	---	AT2G04540	1.67	0.74	7.99	0.000114	0.002425	1.65
250743_at	phosphate/phosphoenolpyruvate tra	---	AT5G05820	-2.02	-1.02	-7.98	0.000114	0.002425	1.65
249785_at	soluble starch synthase	SSI1	AT5G24300	-1.98	-0.99	-7.98	0.000114	0.002425	1.65
266117_at	hypothetical protein ; supported by	---	AT2G02170	-1.78	-0.83	-7.98	0.000114	0.002425	1.65
259932_at	zinc finger protein, putative similar	STOP1	AT1G34370	1.95	0.96	7.98	0.000114	0.002425	1.65
251987_at	CYTOCHROME P450 71B5 ; supp	CYP71B5	AT3G53280	2.10	1.07	7.98	0.000114	0.002427	1.65
255338_at	PEROXISOMAL MEMBRANE PRO	PMP22	AT4G04470	1.72	0.79	7.97	0.000115	0.002436	1.64
263637_at	hypothetical protein predicted by ge	---	AT2G11890	1.78	0.83	7.97	0.000115	0.002436	1.64
265475_at	ferredoxin--nitrite reductase ; supp	NIR1	AT2G15620	2.62	1.39	7.97	0.000115	0.002439	1.64
249359_at	putative protein unnamed ORF, Ho	---	AT5G40470	2.18	1.13	7.96	0.000116	0.00245	1.63
265472_at	putative RING-H2 zinc finger protei	---	AT2G15580	2.17	1.12	7.96	0.000116	0.002453	1.63
247735_at	thymidylate kinase - like protein thy	ZEU1	AT5G59440	3.68	1.88	7.95	0.000117	0.002457	1.62
250753_at	glucuronosyl transferase-like protei	UGT76C2	AT5G05860	-2.29	-1.19	-7.94	0.000118	0.002472	1.61
258485_at	putative stearoyl-acyl carrier protein	---	AT3G02630	1.61	0.69	7.94	0.000118	0.002479	1.61
264924_at	RNA polymerase subunit identical t	ATRPAC43	AT1G60620	1.77	0.83	7.93	0.000119	0.002489	1.60
267044_at	nodulin-like protein	---	AT2G34357	3.05	1.61	7.92	0.00012	0.002497	1.60
252058_at	putative protein hin1 protein -Nicot	---	AT3G52470	-2.82	-1.50	-7.92	0.00012	0.002497	1.60
262402_at	unknown protein ; supported by cDI	TOM6	AT1G49410	2.29	1.19	7.92	0.00012	0.002497	1.59
252093_at	putative protein predicted protein, (	---	AT3G51500	1.96	0.97	7.91	0.00012	0.0025	1.59
255465_at	hypothetical protein similar to A. th	---	AT4G02990	2.16	1.11	7.91	0.000121	0.0025	1.59
262846_at	endomembrane protein, putative si	---	AT1G14670	-1.97	-0.97	-7.91	0.000121	0.0025	1.59
250028_at	putative protein similar to unknown	---	AT5G18130	1.88	0.91	7.91	0.000121	0.0025	1.59
253322_at	putative protein ;supported by full-l	---	AT4G33980	2.29	1.19	7.90	0.000121	0.002501	1.58
261803_at	transcription factor, putative similar	NF-YA7	AT1G30500	2.43	1.28	7.90	0.000121	0.002501	1.58
257211_at	exonuclease, putative contains Pfa	---	AT3G15080	2.32	1.21	7.90	0.000121	0.002505	1.58
257369_at	hypothetical protein predicted by ge	BPC7	AT2G35550	1.99	0.99	7.90	0.000122	0.00251	1.58
255819_s_a	40S ribosomal protein S26	---	AT2G40510	1.87	0.90	7.89	0.000122	0.002512	1.58
261954_at	plastid ribosomal protein S6, putati	---	AT1G64510	-1.89	-0.92	-7.89	0.000123	0.002516	1.57
265678_at	putative RAD50 DNA repair protein	RAD50	AT2G31970	2.75	1.46	7.89	0.000123	0.002516	1.57
248369_at	arginine/serine-rich splicing factor R	ATRSP41	AT5G52040	2.29	1.19	7.88	0.000123	0.002516	1.57
262714_s_a	unknown protein similar to gb|AJ22	---	AT1G07950	1.78	0.83	7.88	0.000124	0.002527	1.56
258953_at	hypothetical protein predicted by ge	---	AT3G01430	-2.10	-1.07	-7.87	0.000125	0.002534	1.55

248039_at	putative protein similar to unknown	---	AT5G55950	-1.68	-0.75	-7.87	0.000125	0.002537	1.55
247836_at	putative protein similar to unknown	---	AT5G57860	2.05	1.04	7.86	0.000125	0.002537	1.55
254763_at	ribosomal protein L13a like protein	---	AT4G13170	2.24	1.16	7.86	0.000125	0.002542	1.55
247261_at	ZW10-like protein ; supported by c	---	AT5G64460	-1.82	-0.87	-7.85	0.000126	0.002556	1.54
264436_at	putative glutathione S-transferase	ERD9	AT1G10370	-10.54	-3.40	-7.85	0.000126	0.002557	1.54
260160_at	putative RNA-binding protein conta	---	AT1G79880	1.79	0.84	7.85	0.000127	0.00256	1.54
246856_at	nucleic acid binding protein - like n	AL4	AT5G26210	1.68	0.75	7.84	0.000127	0.00256	1.53
259955_s_a	unknown protein ;supported by full-	BZR1	AT1G19350	1.98	0.99	7.84	0.000127	0.00256	1.53
266108_at	putative peptide/amino acid transpo	---	AT2G37900	-2.11	-1.08	-7.84	0.000127	0.00256	1.53
256979_at	Expressed protein ; supported by fu	PSBTN	AT3G09550	-1.99	-0.99	-7.84	0.000127	0.00256	1.53
246253_at	myb-related protein	MYB73	AT4G37260	-2.39	-1.26	-7.83	0.000129	0.002582	1.52
256675_at	putative protein DNA-binding prote	---	AT3G52170	3.34	1.74	7.82	0.000129	0.002584	1.52
256337_at	unknown protein	---	AT1G72060	6.28	2.65	7.82	0.000129	0.002584	1.52
247029_at	TINY-like protein	---	AT5G67190	-2.30	-1.20	-7.82	0.00013	0.002588	1.51
251355_at	putative protein hypothetical protei	---	AT3G61100	2.23	1.16	7.82	0.00013	0.002588	1.51
259859_at	putative protein phosphatase simila	---	AT1G68410	-4.74	-2.25	-7.81	0.000131	0.002598	1.50
257891_at	hypothetical protein predicted by ge	RFC3	AT3G17170	2.69	1.43	7.81	0.000131	0.002598	1.50
261547_at	protein kinase, putative contains P	---	AT1G63500	-1.90	-0.93	-7.80	0.000131	0.002605	1.50
257756_at	uridylate kinase, putative similar to	---	AT3G18680	2.03	1.02	7.80	0.000131	0.002606	1.50
252508_at	putative protein tRNA nucleotidyltra	---	AT3G46210	2.74	1.45	7.80	0.000131	0.002606	1.50
244980_at	ribosomal protein L36	---	---	-1.87	-0.90	-7.80	0.000132	0.002609	1.49
264633_at	step II splicing factor, putative simi	SMP1	AT1G65660	1.90	0.93	7.79	0.000132	0.002615	1.49
258079_at	hypothetical protein predicted by ge	---	AT3G25940	1.88	0.91	7.78	0.000133	0.002624	1.48
260995_at	unknown protein	---	AT1G12120	-1.85	-0.88	-7.77	0.000134	0.002643	1.47
265900_at	unknown protein	---	AT2G25730	1.59	0.67	7.77	0.000134	0.002643	1.47
250316_at	cystatin (emb|CAA03929.1) ; supp	ATCYS1	AT5G12140	-1.82	-0.86	-7.77	0.000135	0.002649	1.47
255481_at	T14P8.6 ; supported by cDNA: gi_	PMS1	AT4G02460	2.25	1.17	7.77	0.000135	0.002649	1.47
266822_at	60S ribosomal protein L30 ;suppor	---	AT2G44860	2.48	1.31	7.76	0.000135	0.002657	1.46
256279_at	protein phosphatase 2C, putative c	---	AT3G12620	-1.60	-0.68	-7.76	0.000135	0.002657	1.46
257948_at	hypothetical protein predicted by ge	APO4	AT3G21740	1.96	0.97	7.75	0.000137	0.002673	1.45
265722_at	putative chlorophyll a/b binding prot	LHCB4.3	AT2G40100	-2.87	-1.52	-7.75	0.000137	0.002674	1.45
262636_at	DEIH-box RNA/DNA helicase ident	NIH	AT1G06670	2.06	1.04	7.75	0.000137	0.002674	1.45
260915_at	hypothetical protein similar to hypot	---	AT1G02660	-4.33	-2.11	-7.75	0.000137	0.002674	1.45
260129_at	hypothetical protein similar to vanill	---	AT1G36380	1.73	0.79	7.74	0.000137	0.002679	1.45
255446_at	hypothetical protein similar to A. th	---	AT4G02750	1.98	0.98	7.74	0.000138	0.002682	1.45

245797_at	defective chloroplasts and leaves (	---	AT1G45230	1.58	0.66	7.73	0.000138	0.002682	1.44
267596_s_a	putative leucine-rich repeat disease	AtRLP26	AT2G33050	4.92	2.30	7.73	0.000139	0.002682	1.44
252990_at	putative protein	---	AT4G38440	3.56	1.83	7.73	0.000139	0.002682	1.44
250034_at	apyrase (gb|AAF00612.1) ; suppor	ATAPY2	AT5G18280	-1.99	-0.99	-7.73	0.000139	0.002682	1.44
263548_at	glycine-rich RNA binding protein 7	CCR2	AT2G21660	1.92	0.94	7.72	0.000139	0.002687	1.43
267036_at	Expressed protein ; supported by fu	---	AT2G38465	3.07	1.62	7.72	0.00014	0.002687	1.43
266888_s_a	putative thiamin pyrophosphokinase	TPK1	AT1G02880	1.79	0.84	7.72	0.00014	0.002687	1.43
246398_at	auxin-induced basic helix-loop-heli	---	AT1G58100	-1.61	-0.69	-7.72	0.00014	0.002691	1.43
247572_at	putative protein ; supported by full-	---	AT5G61220	1.73	0.79	7.72	0.00014	0.002692	1.43
253490_at	methyltransferase - like protein me	---	AT4G31790	3.45	1.79	7.72	0.00014	0.002692	1.43
249641_at	DegP protease contains similarity to	DegP10	AT5G36950	1.97	0.98	7.72	0.00014	0.002692	1.43
257016_at	protein kinase, putative similar to P	---	AT3G28690	1.99	0.99	7.70	0.000142	0.002709	1.41
264835_at	unknown protein similar to unknown	---	AT1G03550	1.60	0.68	7.70	0.000142	0.002709	1.41
251642_at	imbibition protein homolog probabl	AtSIP2	AT3G57520	-1.94	-0.96	-7.70	0.000142	0.002709	1.41
257154_at	unknown protein ; supported by cD	---	AT3G27210	2.21	1.15	7.70	0.000142	0.002711	1.41
258553_at	hypothetical protein ; supported by	PDE320	AT3G06960	1.74	0.80	7.69	0.000143	0.002712	1.41
247277_at	putative protein similar to unknown	---	AT5G64420	1.88	0.91	7.69	0.000143	0.002712	1.41
267081_at	putative phosphatidylinositol-4-phos	PIP5K5	AT2G41210	1.82	0.87	7.69	0.000143	0.002714	1.40
264953_at	alcohol dehydrogenase identical to	ADH1	AT1G77120	-2.30	-1.20	-7.69	0.000143	0.002714	1.40
256511_at	RNA helicase, putative similar to G	---	AT1G33390	1.75	0.81	7.69	0.000144	0.002717	1.40
256789_at	seven in absentia-like protein simila	---	AT3G13672	3.66	1.87	7.69	0.000144	0.00272	1.40
250148_at	putative protein various predicted p	---	AT5G14530	1.96	0.97	7.68	0.000144	0.002722	1.40
264094_at	unknown protein ;supported by full-	---	AT1G79200	1.96	0.97	7.68	0.000145	0.002726	1.39
266579_at	putative small nuclear ribonucleopr	SNRNP-G	AT2G23930	2.13	1.09	7.68	0.000145	0.002726	1.39
263912_at	starch branching enzyme II	SBE2.1	AT2G36390	2.23	1.16	7.67	0.000145	0.00273	1.39
261306_at	regulatory protein HAL3B similar to	---	AT1G48610	-1.86	-0.89	-7.67	0.000146	0.002735	1.38
248549_at	putative protein contains similarity t	---	AT5G50310	1.81	0.85	7.66	0.000146	0.002735	1.38
261062_at	transcription factor scarecrow-like	SCL14	AT1G07530	1.82	0.86	7.66	0.000146	0.002735	1.38
262590_at	putative RING-H2 zinc finger prote	RHA2A	AT1G15100	1.98	0.99	7.66	0.000147	0.00274	1.38
255010_at	lipase-like protein monoglyceride li	---	AT4G10050	1.75	0.81	7.66	0.000147	0.00274	1.38
259340_at	hypothetical protein predicted using	PYK10	AT3G03870	2.02	1.01	7.66	0.000147	0.00274	1.37
251959_at	putative protein KIAA0544 protein,	---	AT3G53410	1.78	0.83	7.65	0.000148	0.002756	1.37
259643_at	putative menaquinone biosynthesis	---	AT1G68890	-1.71	-0.77	-7.65	0.000149	0.002763	1.36
249330_at	putative protein similar to unknown	---	AT5G40970	1.86	0.90	7.64	0.000149	0.002769	1.36
257730_at	unknown protein contains Pfam pro	---	AT3G18420	2.38	1.25	7.63	0.00015	0.002785	1.35

262001_at	myrosinase binding protein, putativ	---	AT1G33790	-1.99	-0.99	-7.63	0.000151	0.002793	1.35
261069_at	small G protein, putative similar to	ATRABA2E	AT1G07410	-1.64	-0.71	-7.62	0.000151	0.002796	1.35
266284_at	putative pumilio/Mpt5 family RNA-b	APUM2	AT2G29190	1.94	0.95	7.62	0.000151	0.002797	1.34
256229_at	unknown protein	MSL3	AT1G58200	-2.26	-1.18	-7.61	0.000152	0.002813	1.34
254526_at	putative protein cyclin C homolog 1	CYCT1;4	AT4G19600	1.75	0.81	7.61	0.000153	0.002813	1.33
255572_at	hypothetical protein ; supported by	---	AT4G01050	-1.60	-0.68	-7.61	0.000153	0.002813	1.33
250627_at	putative amidase	---	AT5G07360	2.05	1.04	7.61	0.000153	0.002813	1.33
252548_at	kinesin-related protein - like kinesir	---	AT3G45850	-1.97	-0.98	-7.61	0.000153	0.002813	1.33
249997_at	chromatin remodelling complex AT	CHR17	AT5G18620	1.98	0.98	7.61	0.000153	0.002813	1.33
259130_at	putative ribosomal protein L39 simil	---	AT3G02190	1.98	0.99	7.61	0.000153	0.002813	1.33
250283_at	putative protein many hypothetical	---	AT5G13270	1.91	0.93	7.60	0.000154	0.002817	1.33
246943_at	putative protein kinase serine/threc	---	AT5G25440	-2.66	-1.41	-7.59	0.000155	0.002843	1.32
249947_at	FVT1 - like protein follicular lympho	---	AT5G19200	-1.68	-0.75	-7.58	0.000156	0.002854	1.31
260373_at	unknown protein	---	AT1G73970	1.81	0.86	7.58	0.000156	0.002854	1.31
247632_at	protein transport protein subunit - li	---	AT5G60460	2.00	1.00	7.58	0.000157	0.002863	1.31
251429_at	dynamin-like protein 4 (ADL4) ; sup	ADL1E	AT3G60190	1.91	0.94	7.57	0.000157	0.002868	1.30
266422_at	hypothetical protein predicted by ge	GAUT7	AT2G38650	-1.78	-0.84	-7.57	0.000158	0.002876	1.30
262931_at	small nuclear ribonucleoprotein, pu	---	AT1G65700	1.87	0.90	7.57	0.000158	0.002877	1.30
266490_at	unknown protein	---	AT2G07000	2.08	1.06	7.57	0.000158	0.002877	1.29
256204_at	DNA polymerase A family protein,	POLGAMM	AT1G50840	2.17	1.12	7.57	0.000158	0.002877	1.29
253964_at	putative protein qkI-7, Mus muscul	---	AT4G26480	-1.82	-0.86	-7.56	0.000159	0.002877	1.29
265768_at	putative sugar transporter ;support	---	AT2G48020	-1.74	-0.80	-7.56	0.000159	0.002878	1.29
257131_at	mitochondrial carrier protein, putati	---	AT3G20240	1.68	0.75	7.56	0.000159	0.002878	1.29
251421_at	enoyl-CoA-hydratase - like protein	---	AT3G60510	1.83	0.87	7.56	0.00016	0.00288	1.29
258489_at	14-3-3 protein GF14nu (grf7) identi	GRF7	AT3G02520	1.68	0.75	7.55	0.00016	0.002885	1.28
250087_at	putative protein contains similarity t	---	AT5G17270	2.86	1.51	7.55	0.00016	0.002885	1.28
246619_at	transmembrane protein FT27/PFT2	---	AT5G36290	-1.66	-0.73	-7.55	0.00016	0.002886	1.28
260289_at	CAD ATPase (AAA1) identical to C/	ERH3	AT1G80350	-1.57	-0.65	-7.54	0.000161	0.002896	1.27
262678_at	hypothetical protein ;supported by f	---	AT1G75810	2.28	1.19	7.54	0.000162	0.002898	1.27
260705_at	unknown protein ;supported by full-	TOM2A	AT1G32400	-1.71	-0.77	-7.54	0.000162	0.0029	1.27
253557_at	putative protein wall-associated kir	---	AT4G31110	1.65	0.72	7.53	0.000163	0.002903	1.27
245479_at	extensin like protein	---	AT4G16140	-1.86	-0.90	-7.53	0.000163	0.002905	1.27
264120_at	latex-abundant protein, putative sir	AtMC4	AT1G79340	-1.64	-0.72	-7.53	0.000163	0.002908	1.26
265483_at	hypothetical protein ; supported by	SQN	AT2G15790	2.38	1.25	7.52	0.000164	0.002918	1.26
259793_at	AP2-containing DNA-binding protei	---	AT1G64380	-5.53	-2.47	-7.52	0.000165	0.002921	1.25

252113_at	putative protein predicted protein, /	---	AT3G51620	1.67	0.74	7.52	0.000165	0.002921	1.25
261524_at	hypothetical protein predicted by ge	---	AT1G14300	1.97	0.98	7.51	0.000165	0.002925	1.25
254038_at	nitrogen fixation like protein nitroge	NFU3	AT4G25910	1.70	0.77	7.51	0.000166	0.002929	1.25
266986_at	putative dolichyl-phosphate beta-glu	---	AT2G39630	1.67	0.74	7.51	0.000166	0.002932	1.24
262231_at	putative receptor protein similar to	---	AT1G68740	4.20	2.07	7.50	0.000167	0.00294	1.24
255829_at	putative potassium transporter ; su	KT2	AT2G40540	-1.65	-0.72	-7.50	0.000167	0.002943	1.24
263064_at	putative bZIP transcription factor co	CPuORF1	AT2G18160	2.34	1.23	7.50	0.000168	0.002948	1.23
252625_at	putative histone deacetylase similar	HDA3	AT3G44750	5.29	2.40	7.49	0.000169	0.00296	1.23
249977_at	chaperonin 60 alpha chain - like pr	EMB3007	AT5G18820	2.25	1.17	7.49	0.000169	0.00296	1.23
255685_s_a	putative tetrahydrofolate synthase s	---	AT4G00600	2.62	1.39	7.49	0.000169	0.002961	1.22
246594_at	pyrroline-5-carboxylate reductase ;	P5CR	AT5G14800	2.13	1.09	7.48	0.000169	0.002966	1.22
255482_at	putative chloroplast outer envelope	TOC159	AT4G02510	1.76	0.82	7.48	0.00017	0.002967	1.22
251427_at	beta-glucosidase-like protein severa	BGLU16	AT3G60130	-2.37	-1.25	-7.48	0.00017	0.002975	1.22
249864_at	putative protein similar to unknown	ATMGT10	AT5G22830	-1.63	-0.71	-7.47	0.000171	0.002977	1.21
250787_at	meiotic check point regulator-like pr	EMB2771	AT5G05560	1.73	0.79	7.47	0.000171	0.00298	1.21
257799_at	protein kinase, putative similar to s	---	AT3G15890	1.85	0.89	7.47	0.000171	0.002982	1.21
251447_at	U6 snRNA-associated Sm-like prot	---	AT3G59810	1.63	0.71	7.46	0.000172	0.002992	1.20
246479_at	hypothetical protein	---	AT5G16060	1.83	0.87	7.46	0.000173	0.002999	1.20
248942_at	putative protein similar to unknown	---	AT5G45480	-1.98	-0.98	-7.46	0.000173	0.003	1.20
248920_at	magnesium chelatase subunit of pr	CHLI2	AT5G45930	-1.88	-0.91	-7.45	0.000173	0.003005	1.20
258861_at	putative helicase similar to C-termin	---	AT3G02060	2.30	1.20	7.45	0.000174	0.003005	1.19
254076_at	putative protein immunophilin FKB	---	AT4G25340	3.04	1.60	7.45	0.000174	0.003005	1.19
259945_at	unknown protein	---	AT1G71460	1.98	0.99	7.45	0.000174	0.003005	1.19
266338_at	putative ligand-gated ion channel su	GLR5	AT2G32400	2.11	1.08	7.45	0.000175	0.003009	1.19
253952_at	ubiquitin-like protein ubiquitin-like p	SUMO1	AT4G26840	1.79	0.84	7.44	0.000175	0.003011	1.19
263212_at	unknown protein similar to ribonucle	emb2004	AT1G10510	1.81	0.85	7.44	0.000175	0.003011	1.19
261124_at	hypothetical protein predicted by ge	---	AT1G04900	1.79	0.84	7.44	0.000175	0.003015	1.18
258999_at	putative D-ribulose-5-phosphate 3-e	---	AT3G01850	1.81	0.85	7.43	0.000176	0.003024	1.18
259838_at	unknown protein ;supported by full-	---	AT1G52220	-1.67	-0.74	-7.43	0.000176	0.003024	1.18
248515_at	putative protein strong similarity to u	---	AT5G50530	-1.95	-0.96	-7.43	0.000176	0.003024	1.18
246282_at	ATPase-like protein	---	AT4G36580	2.69	1.43	7.43	0.000177	0.003041	1.17
245106_at	unknown protein	---	AT2G41650	2.03	1.02	7.42	0.000178	0.003041	1.17
245981_at	putative protein ;supported by full-l	---	AT5G13100	-1.95	-0.96	-7.42	0.000178	0.003044	1.17
265484_at	unknown protein ; supported by cD	OTP51	AT2G15820	1.86	0.90	7.42	0.000178	0.003045	1.17
251593_at	DNA-directed RNA polymerase I 1	NRPA1	AT3G57660	2.71	1.44	7.42	0.000178	0.003045	1.17

266716_at	unknown protein ;supported by full-	PSI-P	AT2G46820	-1.85	-0.89	-7.42	0.000179	0.003054	1.16
261166_s_a	Expressed protein ; supported by fu	---	AT1G34570	2.21	1.14	7.41	0.00018	0.003065	1.16
252923_at	kinesin like protein kinesin motor p	---	AT4G39050	-2.26	-1.18	-7.41	0.00018	0.003065	1.15
249081_at	protein phosphatase 2A 62 kDa B r	---	AT5G44090	1.79	0.84	7.40	0.000181	0.003066	1.15
248492_at	putative protein similar to unknown	---	AT5G51040	1.68	0.75	7.40	0.000181	0.003066	1.15
265594_at	50S ribosomal protein L4 ;supporte	---	AT2G20060	2.62	1.39	7.40	0.000181	0.003066	1.15
248820_at	putative protein similar to unknown	---	AT5G47060	2.23	1.16	7.40	0.000181	0.003073	1.15
259882_at	unknown protein similar to hypothet	---	AT1G76670	-1.89	-0.92	-7.40	0.000181	0.003073	1.15
246052_at	putative protein predicted proteins,	---	AT5G08310	2.11	1.08	7.40	0.000182	0.003073	1.15
256603_at	unknown protein similar to At14a pr	---	AT3G28270	-4.03	-2.01	-7.40	0.000182	0.003073	1.15
258519_at	unknown protein	---	AT3G06760	-2.11	-1.08	-7.39	0.000182	0.003076	1.14
266055_at	hypothetical protein predicted by ge	---	AT2G40650	1.98	0.98	7.39	0.000182	0.003076	1.14
248442_at	DEAD-box protein abstrakt	---	AT5G51280	2.03	1.02	7.39	0.000183	0.003077	1.14
251892_at	putative protein	WRI1	AT3G54320	2.30	1.20	7.39	0.000183	0.003077	1.14
264928_at	auxin-induced protein, putative sim	ATB2	AT1G60710	-1.81	-0.86	-7.39	0.000183	0.003084	1.14
262207_at	hypothetical protein predicted by ge	PTAC2	AT1G74850	2.12	1.09	7.39	0.000183	0.003084	1.14
253900_at	translation initiation factor ; suppor	---	AT4G27130	1.78	0.83	7.38	0.000184	0.003091	1.13
249826_at	iron superoxide dismutase 3 (gb|AA	FSD3	AT5G23310	2.30	1.20	7.38	0.000184	0.003095	1.13
247748_at	putative protein ;supported by full-l	---	AT5G58920	1.82	0.86	7.38	0.000185	0.003096	1.13
258800_at	unknown protein predicted by gens	---	AT3G04550	1.98	0.99	7.38	0.000185	0.003096	1.13
249703_at	putative protein strong similarity to	---	AT5G35560	1.66	0.73	7.37	0.000186	0.003098	1.12
260250_at	putative phosphoribosylformylglycin	PUR4	AT1G74260	2.04	1.03	7.37	0.000186	0.003098	1.12
250896_at	putative protein ; supported by cDN	---	AT5G03560	2.34	1.23	7.37	0.000186	0.003099	1.12
256741_at	hypothetical protein predicted by ge	---	AT3G29375	2.35	1.23	7.37	0.000186	0.003101	1.12
261664_s_a	hypothetical protein contains simila	---	AT1G18320	2.37	1.24	7.37	0.000186	0.003101	1.12
247866_at	endoxyloglucan transferase (gb|AA	XTR3	AT5G57550	-6.82	-2.77	-7.36	0.000187	0.003101	1.12
245337_at	Expressed protein ; supported by fu	---	AT4G16566	-1.70	-0.77	-7.36	0.000187	0.003101	1.12
252602_at	putative protein KIAA1094 protein,	---	AT3G45040	-1.93	-0.95	-7.36	0.000187	0.003101	1.11
247525_at	pseudo-response regulator 1 ; sup	TOC1	AT5G61380	1.59	0.67	7.36	0.000187	0.003101	1.11
259082_at	unknown protein similar to hypothet	---	AT3G04820	2.69	1.43	7.36	0.000187	0.003101	1.11
266732_at	unknown protein	---	AT2G03240	-2.40	-1.26	-7.36	0.000187	0.003101	1.11
249933_at	rac GTPase activating protein	---	AT5G22400	-1.69	-0.76	-7.36	0.000187	0.003101	1.11
252593_at	putative protein tRNA intron endon	ATSEN1	AT3G45590	2.07	1.05	7.36	0.000187	0.003101	1.11
261750_at	hypothetical protein contains simila	---	AT1G76120	2.04	1.03	7.36	0.000188	0.003105	1.11
266705_at	40S ribosomal protein S30 ; suppo	---	AT2G19750	2.44	1.29	7.36	0.000188	0.003105	1.11

261223_at	hypothetical protein predicted by ge	HVA22H	AT1G19950	-1.58	-0.66	-7.35	0.00019	0.003126	1.10
260491_at	hypothetical protein predicted by ge	---	AT1G51440	-2.36	-1.24	-7.35	0.00019	0.003126	1.10
260062_at	hypothetical protein contains Pfam	---	AT1G73710	2.01	1.01	7.34	0.00019	0.003133	1.10
261335_at	nodulin protein, putative similar to (	---	AT1G44800	1.59	0.66	7.34	0.000191	0.00314	1.09
251039_at	putative protein hypothetical protei	---	AT5G02020	4.16	2.06	7.33	0.000192	0.003159	1.08
267068_at	unknown protein	---	AT2G41020	2.04	1.03	7.33	0.000193	0.003161	1.08
246249_at	salt-inducible like protein	---	AT4G36680	2.08	1.06	7.32	0.000193	0.003161	1.08
267129_at	curly leaf protein (polycomb-group)	CLF	AT2G23380	-1.70	-0.77	-7.32	0.000193	0.003161	1.08
262937_at	FtsH protease, putative contains si	FTSH12	AT1G79560	1.67	0.74	7.32	0.000193	0.003161	1.08
246064_at	DNA binding protein ACBF - like D	---	AT5G19350	1.80	0.85	7.32	0.000193	0.003161	1.08
258876_at	putative ADP-ribosylation factor sim	ATARFB1C	AT3G03120	1.65	0.72	7.32	0.000194	0.003161	1.08
246622_at	protein phosphatase-2C PP2C-like	---	AT5G36250	-1.63	-0.71	-7.32	0.000194	0.003168	1.07
262706_at	putative ATP-dependent RNA helic	---	AT1G16280	2.19	1.13	7.31	0.000195	0.003182	1.07
249201_at	putative protein similar to unknown	---	AT5G42370	2.16	1.11	7.31	0.000196	0.003186	1.06
248433_at	putative protein strong similarity to	---	AT5G51400	-1.69	-0.76	-7.31	0.000196	0.003186	1.06
247506_at	Mei2-like protein Mei2-like protein,	AML1	AT5G61960	1.63	0.71	7.31	0.000196	0.003186	1.06
264506_at	germin-like protein Identical to Aral	GLP5	AT1G09560	1.97	0.98	7.30	0.000196	0.003188	1.06
260100_at	Expressed protein ; supported by fu	BNS	AT1G73177	1.64	0.72	7.30	0.000197	0.0032	1.06
262456_at	glucose transporter almost identica	STP1	AT1G11260	-3.07	-1.62	-7.30	0.000197	0.0032	1.06
247918_at	putative protein contains similarity t	---	AT5G57610	2.10	1.07	7.29	0.000199	0.003217	1.05
261588_at	hypothetical protein predicted by ge	---	AT1G01670	1.60	0.67	7.29	0.000199	0.003217	1.05
259862_at	hypothetical protein ;supported by	TRFL6	AT1G72650	2.04	1.03	7.28	0.0002	0.003225	1.04
261984_at	TINY-like protein similar to TINY GI	---	AT1G33760	-2.12	-1.09	-7.28	0.0002	0.003227	1.04
248299_at	unknown protein ;supported by full-	---	AT5G53080	1.80	0.85	7.27	0.000201	0.003237	1.04
265314_at	hypothetical protein predicted by ge	---	AT2G20210	1.88	0.91	7.26	0.000204	0.003269	1.02
256401_at	putative guanylate kinase similar to	---	AT3G06200	1.55	0.63	7.26	0.000204	0.003269	1.02
246555_at	putative protein 68 kDa protein - C	GAUT14	AT5G15470	-2.44	-1.29	-7.26	0.000204	0.003272	1.02
255611_at	hypothetical protein	---	AT4G01210	-1.68	-0.75	-7.26	0.000204	0.003274	1.02
245712_at	pullulanase-like protein (starch deb	ATLDA	AT5G04360	-1.72	-0.78	-7.25	0.000205	0.003277	1.02
267492_at	histone H1 ;supported by full-length	---	AT2G30620	2.18	1.13	7.25	0.000205	0.003277	1.02
266471_at	putative GTP-binding protein	---	AT2G31060	2.61	1.39	7.25	0.000205	0.003285	1.01
254263_at	Expressed protein ; supported by fu	---	AT4G23493	1.71	0.77	7.25	0.000206	0.003289	1.01
253605_at	putative protein probable membran	---	AT4G30990	2.23	1.16	7.24	0.000207	0.003295	1.00
261076_at	unknown protein ;supported by full-	SMO2-1	AT1G07420	-1.66	-0.73	-7.23	0.000208	0.003311	1.00
251184_at	small nuclear ribonucleoprotein-like	---	AT3G62840	1.59	0.67	7.23	0.000209	0.003312	1.00

264107_s_a	putative receptor-like protein kinase	SERK5	AT2G13790	-1.88	-0.91	-7.23	0.000209	0.003316	0.99
263934_at	hypothetical protein predicted by ge	EDA12	AT2G35950	1.59	0.67	7.22	0.00021	0.00333	0.99
245612_at	carnitine racemase like protein	HCD1	AT4G14440	-6.40	-2.68	-7.22	0.000211	0.00333	0.99
265330_at	unknown protein	GUT15	---	1.92	0.94	7.22	0.000211	0.00333	0.99
246850_at	Lon protease homolog 2 precursor	LON1	AT5G26860	3.52	1.82	7.22	0.000211	0.00333	0.98
250822_at	unknown protein	---	AT5G05230	1.66	0.73	7.22	0.000211	0.00333	0.98
245422_at	putative protein	---	AT4G17470	-6.78	-2.76	-7.22	0.000211	0.003333	0.98
258755_at	hypothetical protein identical to hyp	---	AT3G11945	-1.93	-0.95	-7.21	0.000212	0.003335	0.98
253238_at	putative protein (fragment)	---	AT4G34480	-1.95	-0.97	-7.21	0.000213	0.003346	0.97
246302_at	Ca2+/H+-exchanging protein-like A	CAX3	AT3G51860	6.33	2.66	7.20	0.000213	0.003346	0.97
262653_at	dioxygenase-like protein very simil	---	AT1G14130	1.61	0.69	7.20	0.000213	0.003346	0.97
250512_at	Expressed protein ; supported by fu	---	AT5G09995	-1.93	-0.95	-7.20	0.000213	0.003346	0.97
251291_at	putative protein auxin-induced prot	---	AT3G61900	1.73	0.79	7.20	0.000214	0.003355	0.97
256436_at	hypothetical protein predicted by ge	---	AT3G11150	1.80	0.85	7.20	0.000214	0.003355	0.97
266718_at	putative zinc transporter ;supported	ZAT	AT2G46800	-1.80	-0.85	-7.19	0.000215	0.003361	0.96
263117_at	putative lipoamide dehydrogenase	---	AT1G03040	1.61	0.69	7.19	0.000215	0.003361	0.96
249403_at	putative protein intracellular protein	---	AT5G40270	2.09	1.06	7.19	0.000216	0.003363	0.96
250733_at	2-cys peroxiredoxin-like protein ;su	2-Cys Prx B	AT5G06290	-2.00	-1.00	-7.19	0.000216	0.003363	0.96
263636_at	unknown protein ; supported by ful	---	AT2G11910	1.87	0.90	7.19	0.000216	0.003363	0.96
256991_at	unknown protein	---	AT3G28600	-1.64	-0.72	-7.18	0.000218	0.003389	0.95
255631_at	hypothetical protein	BSK3	AT4G00710	-1.60	-0.68	-7.17	0.00022	0.003402	0.94
259505_at	hypothetical protein contains simila	---	AT1G15810	2.13	1.09	7.17	0.00022	0.003402	0.94
262056_at	Expressed protein ; supported by fu	---	AT1G80245	1.83	0.87	7.16	0.000221	0.003421	0.93
249089_at	ATPase, calcium-transporting	---	AT5G44240	1.56	0.64	7.16	0.000221	0.003421	0.93
254848_at	putative protein hypothetical protei	PGRL1B	AT4G11960	1.78	0.83	7.16	0.000222	0.003421	0.93
254951_at	putative protein various kinesin ligh	---	AT4G10840	-1.65	-0.72	-7.16	0.000222	0.003421	0.93
260805_at	glutathione transferase, putative si	ATGSTU23	AT1G78320	1.62	0.70	7.15	0.000222	0.003423	0.93
249307_s_a	DNA excision repair cross-complem	XPB1	AT5G41360	1.78	0.83	7.15	0.000223	0.003425	0.93
254418_at	glucose transporter glucose transp	---	AT4G21480	-1.79	-0.84	-7.15	0.000223	0.003429	0.92
261544_at	unknown protein	---	AT1G63540	2.17	1.12	7.15	0.000223	0.00343	0.92
258161_at	hypothetical protein predicted by ge	---	AT3G17930	1.88	0.91	7.15	0.000224	0.00343	0.92
249979_s_a	putative protein	---	AT5G18860	-3.98	-1.99	-7.15	0.000224	0.00343	0.92
250883_at	putative protein predicted proteins,	---	AT5G03970	2.12	1.09	7.14	0.000224	0.003435	0.92
245893_at	hypothetical protein ;supported by	---	AT5G09270	1.74	0.80	7.14	0.000225	0.00344	0.92
250079_at	putative protein similar to unknown	---	AT5G16650	-1.95	-0.96	-7.13	0.000227	0.003462	0.91

257265_at	PHD-finger protein, putative contai	---	AT3G14980	-1.87	-0.90	-7.13	0.000227	0.003462	0.90
251786_at	phosphatase - like protein DUAL S	MKP1	AT3G55270	1.68	0.74	7.13	0.000227	0.003462	0.90
265425_at	hypothetical protein	GCL2	AT2G20770	-2.04	-1.03	-7.13	0.000227	0.003462	0.90
249901_at	histone deacetylase-like protein no	HD2B	AT5G22650	2.26	1.17	7.12	0.000228	0.003467	0.90
266246_at	putative cytochrome P450	CYP94C1	AT2G27690	-5.79	-2.53	-7.12	0.000229	0.003473	0.90
259192_at	unknown protein ;supported by full-	---	AT3G01740	1.97	0.98	7.12	0.000229	0.003477	0.89
250139_at	putative protein de novo DNA meth	DRM2	AT5G14620	1.57	0.65	7.12	0.000229	0.003479	0.89
247800_at	Expressed protein ; supported by fu	---	AT5G58570	9.77	3.29	7.11	0.000231	0.003495	0.89
248956_at	unknown protein	---	AT5G45610	1.80	0.85	7.11	0.000231	0.003496	0.89
248093_at	putative protein similar to unknown	---	AT5G55210	1.92	0.94	7.11	0.000231	0.003496	0.88
262891_at	ent-kaurene synthase, putative sim	GA2	AT1G79460	-2.53	-1.34	-7.11	0.000232	0.003499	0.88
249886_at	unknown protein ; supported by cD	---	AT5G22320	2.39	1.26	7.11	0.000232	0.0035	0.88
252246_at	putative protein various predicted p	---	AT3G49725	1.82	0.87	7.10	0.000232	0.0035	0.88
261112_at	unknown protein	---	AT1G75420	1.94	0.95	7.10	0.000232	0.003505	0.88
267300_at	putative glucosyltransferase	---	AT2G30140	1.68	0.75	7.10	0.000233	0.003509	0.88
263875_at	unknown protein ;supported by full-	ספט-02	AT2G21970	2.43	1.28	7.10	0.000234	0.003513	0.87
246906_at	Expressed protein ; supported by fu	---	AT5G25475	1.73	0.79	7.09	0.000234	0.003513	0.87
260413_at	hypothetical protein predicted by ge	---	AT1G69800	2.18	1.13	7.09	0.000234	0.003515	0.87
256240_at	unknown protein ; supported by cDI	atnudt16	AT3G12600	-1.79	-0.84	-7.09	0.000234	0.003515	0.87
246958_at	putative protein similar to unknown	---	AT5G24690	2.18	1.12	7.09	0.000235	0.003517	0.87
253399_at	putative poly(A) polymerase polynu	nPAP	AT4G32850	1.66	0.73	7.09	0.000235	0.003517	0.87
246453_at	syntaxin homologue ;supported by	SYP21	AT5G16830	-1.85	-0.88	-7.09	0.000236	0.00352	0.86
260989_at	unknown protein ; supported by cDI	---	AT1G53450	2.11	1.08	7.09	0.000236	0.00352	0.86
252688_at	putative protein	---	AT3G44020	1.87	0.90	7.08	0.000236	0.00352	0.86
263142_at	unknown protein	---	AT1G65230	-1.85	-0.89	-7.08	0.000236	0.003521	0.86
252319_at	putative protein putative protein - A	---	AT3G48710	2.22	1.15	7.08	0.000236	0.003521	0.86
246614_at	serine/threonine protein kinase SOS	SOS2	AT5G35410	1.72	0.78	7.08	0.000237	0.003524	0.86
253703_at	putative protein origin recognition c	ORC5	AT4G29910	1.84	0.88	7.07	0.000238	0.003543	0.85
247668_at	pseudo-response regulator - like ps	APRR3	AT5G60100	1.59	0.67	7.07	0.000238	0.003543	0.85
250382_at	putative protein rjs protein, Mus mu	---	AT5G11580	1.56	0.64	7.07	0.000239	0.003546	0.85
259253_at	hypothetical protein predicted by ge	---	AT3G07640	1.56	0.64	7.07	0.00024	0.003554	0.85
255378_at	putative glucan synthase compone	ATGSL05	AT4G03550	-1.69	-0.76	-7.07	0.00024	0.003556	0.84
256528_at	C2H2-type zinc finger protein, puta	ZFP4	AT1G66140	2.37	1.24	7.06	0.00024	0.003556	0.84
260800_at	unknown protein	TSD2	AT1G78240	-2.26	-1.18	-7.06	0.00024	0.003556	0.84
249938_at	Ruv DNA-helicase-like protein ;sup	RIN1	AT5G22330	1.69	0.76	7.06	0.000241	0.003565	0.84

255799_at	Deetiolated1 (DET1) light signal tra	DET1	AT4G10180	1.83	0.87	7.06	0.000241	0.003565	0.84
253549_at	Expressed protein ; supported by fu	NFD1	AT4G30930	2.55	1.35	7.06	0.000242	0.003565	0.84
262610_at	putative mitochondrial uncoupling p	---	AT1G14140	-1.55	-0.63	-7.06	0.000242	0.003565	0.84
267545_at	unknown protein	GRP23	AT2G32690	-2.25	-1.17	-7.06	0.000242	0.003565	0.84
248065_at	putative protein similar to unknown	---	AT5G55580	2.15	1.10	7.06	0.000242	0.003565	0.84
256383_at	hypothetical protein ; supported by	---	AT1G66820	1.92	0.94	7.05	0.000242	0.003565	0.83
260343_at	fructokinase (Frk1), putative simila	---	AT1G69200	2.24	1.16	7.05	0.000242	0.003569	0.83
246083_at	zinc finger protein - like probable zi	AL5	AT5G20510	1.67	0.74	7.05	0.000243	0.00357	0.83
260774_at	serine-threonine protein kinase, pu	---	AT1G78290	4.67	2.22	7.05	0.000243	0.00357	0.83
260936_at	hypothetical protein predicted by ge	---	AT1G45150	1.81	0.85	7.05	0.000244	0.003577	0.83
245152_at	putative mitochondrial carrier protei	---	AT2G47490	-1.77	-0.82	-7.04	0.000244	0.003579	0.83
251611_at	putative protein several hypothetica	---	AT3G57940	2.21	1.15	7.04	0.000245	0.003586	0.82
249125_at	1-aminocyclopropane-1-carboxylate	---	AT5G43450	2.47	1.30	7.04	0.000245	0.003586	0.82
262756_at	putative transport protein may be a	אוק-06	AT1G16370	-7.36	-2.88	-7.04	0.000245	0.003586	0.82
258559_at	putative transcriptional regulator sir	ATCHR12	AT3G06010	2.01	1.01	7.04	0.000246	0.003588	0.82
264372_at	lactoylglutathione lyase-like protein	ATGLX1	AT1G11840	-2.36	-1.24	-7.03	0.000246	0.003597	0.82
249575_at	low-molecular-weight heat shock p	---	AT5G37670	2.35	1.23	7.03	0.000247	0.003598	0.81
261931_at	alcohol dehydrogenase ADH, putat	---	AT1G22430	-1.63	-0.71	-7.03	0.000247	0.003605	0.81
248177_at	putative protein strong similarity to	---	AT5G54630	-1.68	-0.75	-7.03	0.000248	0.00361	0.81
251967_at	putative protein DMR-N9 PROTEIN	---	AT3G53390	1.65	0.72	7.02	0.000248	0.003613	0.81
257700_at	unknown protein similar to unknown	ALIS1	AT3G12740	1.93	0.95	7.02	0.000248	0.003613	0.81
249975_s_a	ribosomal protein L33 - like riboson	---	AT3G06320	2.70	1.43	7.02	0.000249	0.003614	0.81
253462_at	synaptobrevin-like protein synaptol	ATVAMP71	AT4G32150	1.95	0.96	7.02	0.00025	0.003625	0.80
247586_at	mipC protein - like (aquaporin) mip	PIP2;4	AT5G60660	-1.76	-0.81	-7.02	0.00025	0.003628	0.80
257175_s_a	cyclopropane-fatty-acyl-phospholip	---	AT3G23470	-1.81	-0.85	-7.02	0.00025	0.003628	0.80
253897_at	putative protein	---	AT4G27120	1.69	0.75	7.02	0.00025	0.003628	0.80
250825_at	putative protein similar to unknown	---	AT5G05210	1.70	0.77	7.01	0.00025	0.003629	0.80
265909_at	unknown protein ;supported by full-	---	AT2G25720	1.83	0.87	7.01	0.000251	0.003629	0.80
260938_at	hypothetical protein contains simila	---	AT1G45170	1.96	0.97	7.01	0.000251	0.003629	0.80
261909_at	hypothetical protein predicted by ge	SAR3	AT1G80680	1.99	1.00	7.01	0.000251	0.003629	0.80
247464_at	putative protein various predicted p	IQD23	AT5G62070	-2.61	-1.38	-7.01	0.000251	0.003635	0.79
262592_at	unknown protein ESTs gb|H37295 a	---	AT1G15400	2.21	1.15	7.00	0.000253	0.003649	0.79
254102_at	acyl carrier - like protein acyl carrie	ACP4	AT4G25050	-1.94	-0.95	-7.00	0.000253	0.003649	0.79
245939_at	oxoglutarate/malate translocator-lik	---	AT5G19760	-1.76	-0.82	-6.99	0.000255	0.003665	0.78
255650_s_a	hypothetical protein	CIP4.1	AT4G00930	1.93	0.95	6.99	0.000255	0.003665	0.78

250504_at	putative protein similar to unknown	---	AT5G09840	2.00	1.00	6.99	0.000255	0.003665	0.78
262493_at	auxilin-like protein similar to GB:CA	---	AT1G21660	-1.69	-0.76	-6.99	0.000256	0.003676	0.77
261259_at	unknown protein	---	AT1G26660	1.80	0.85	6.99	0.000257	0.003676	0.77
264335_s_a	hypothetical protein contains simila	UPL1	AT1G55860	1.57	0.65	6.99	0.000257	0.003676	0.77
260157_at	unknown protein ; supported by cD	---	AT1G52930	3.46	1.79	6.98	0.000257	0.003681	0.77
267309_at	Expressed protein ; supported by fu	---	AT2G19385	2.29	1.19	6.98	0.000258	0.003699	0.76
250970_at	putative protein ; supported by cDN	---	AT5G02770	1.66	0.73	6.98	0.000259	0.0037	0.76
265270_at	putative ribose phosphate pyrophos	---	AT2G42910	1.71	0.77	6.97	0.000259	0.003701	0.76
265172_at	putative spermidine synthase	SPDS1	AT1G23820	1.60	0.68	6.97	0.000259	0.003701	0.76
262700_at	unknown protein	---	AT1G76020	-2.05	-1.03	-6.97	0.00026	0.003701	0.76
252479_at	small zinc finger-like protein TIM9 ;	TIM9	AT3G46560	2.25	1.17	6.97	0.00026	0.003705	0.76
262800_at	putative ATP-dependent RNA helic	emb1507	AT1G20960	1.79	0.84	6.97	0.000261	0.00371	0.75
261197_at	putative calcium-binding protein, ca	GAPA-2	AT1G12900	-1.85	-0.89	-6.97	0.000261	0.003712	0.75
266782_at	putative ligand-gated ion channel p	ATGLR2.7	AT2G29120	-1.69	-0.76	-6.96	0.000262	0.003714	0.75
260871_at	hypothetical protein predicted by ge	---	AT1G29040	-1.57	-0.65	-6.96	0.000262	0.003714	0.75
246494_at	putative protein putative cellulose s	CSLA11	AT5G16190	-1.88	-0.91	-6.95	0.000264	0.003733	0.74
256792_at	hypothetical protein predicted by ge	---	AT3G22150	3.43	1.78	6.95	0.000264	0.003735	0.74
263766_at	hypothetical protein predicted by ge	---	AT2G21440	2.09	1.06	6.95	0.000264	0.003735	0.74
255279_at	putative thioredoxin ; supported by	---	AT4G04950	2.42	1.28	6.95	0.000265	0.003737	0.74
248678_at	U6 snRNA-associated Sm-like prote	SAD1	AT5G48870	1.81	0.86	6.95	0.000265	0.003737	0.74
246295_at	calmodulin-binding protein ; suppo	CIP111	AT3G56690	2.08	1.06	6.95	0.000265	0.00374	0.73
247734_at	putative protein predicted protein, /	---	AT5G59400	1.82	0.86	6.95	0.000266	0.003745	0.73
250669_at	polygalacturonase inhibiting protein	PGIP2	AT5G06870	-5.20	-2.38	-6.94	0.000266	0.003746	0.73
255614_at	putative myb-related DNA-binding p	---	AT4G01280	1.66	0.74	6.94	0.000266	0.003749	0.73
245761_at	hypothetical protein predicted by ge	---	AT1G66890	1.76	0.81	6.94	0.000267	0.003757	0.73
251980_at	putative protein endopeptidase Clp	---	AT3G53270	1.58	0.66	6.93	0.000269	0.00378	0.72
265521_at	hypothetical protein predicted by ge	ORG4	AT2G06010	1.93	0.95	6.93	0.000269	0.003781	0.72
251771_at	putative protein cellulose synthase	CSLA14	AT3G56000	-1.82	-0.86	-6.93	0.00027	0.003793	0.72
252328_at	Expressed protein ; supported by cl	---	AT3G48570	-1.70	-0.77	-6.92	0.000271	0.003803	0.71
256406_at	unknown protein	---	AT1G50710	-1.83	-0.87	-6.92	0.000272	0.003805	0.71
266365_at	ferredoxin-dependent glutamate syn	GLU2	AT2G41220	2.15	1.10	6.92	0.000273	0.003814	0.71
250969_at	putative protein ;supported by full-l	---	AT5G02740	1.68	0.74	6.91	0.000273	0.003818	0.70
250711_at	cell division related protein-like	---	AT5G06110	1.71	0.78	6.91	0.000274	0.003822	0.70
250454_at	unknown protein ; supported by full	---	AT5G09830	1.52	0.60	6.91	0.000274	0.003829	0.70
266482_at	putative small nuclear ribonucleopro	---	AT2G47640	2.03	1.02	6.91	0.000275	0.003829	0.70

248605_at	putative protein similar to unknown	---	AT5G49410	2.45	1.30	6.91	0.000275	0.003829	0.70
254879_at	hypothetical protein	---	AT4G11670	1.76	0.82	6.90	0.000275	0.003832	0.70
251853_at	putative protein various Arabidopsis	---	AT3G54790	1.66	0.73	6.90	0.000276	0.003842	0.69
246131_at	MOLYBDOPTERIN BIOSYNTHESI	B73	AT5G20990	1.60	0.68	6.90	0.000276	0.003842	0.69
250613_at	putative protein SF16 protein, polle	IQD24	AT5G07240	-1.96	-0.97	-6.90	0.000277	0.003842	0.69
254624_at	hypothetical protein ;supported by	---	AT4G18580	1.73	0.79	6.90	0.000277	0.003843	0.69
248815_at	putative protein contains similarity t	---	AT5G46920	2.26	1.18	6.89	0.000278	0.003851	0.69
255619_s_a	putative CHP-rich zinc finger protei	---	AT4G01350	-2.11	-1.08	-6.89	0.000278	0.003851	0.69
264360_at	putative isoamylase Similar to gi|16	DBE1	AT1G03310	1.98	0.99	6.89	0.000279	0.003863	0.68
257587_at	3'-5' exonuclease, putative contain	---	AT1G56310	1.66	0.73	6.89	0.00028	0.003867	0.68
259666_at	unknown protein ; supported by cDI	SR33	AT1G55310	1.72	0.78	6.88	0.00028	0.00387	0.68
255681_at	predicted protein of unknown functi	DGD2	AT4G00550	1.91	0.93	6.88	0.00028	0.00387	0.68
247497_at	Peter Pan - like protein Peter Pan,	PPAN	AT5G61770	2.31	1.21	6.88	0.00028	0.00387	0.68
247891_at	GTP binding protein-like	---	AT5G57960	1.72	0.78	6.88	0.000281	0.003872	0.67
245161_at	putative myrosinase binding protein	NSP2	AT2G33070	-1.98	-0.98	-6.88	0.000281	0.003874	0.67
262162_at	unknown protein ;supported by full-	---	AT1G78020	2.09	1.07	6.88	0.000282	0.003881	0.67
259908_at	RNA polymerase subunit identical t	ATRPAC42	AT1G60850	2.17	1.11	6.87	0.000282	0.003881	0.67
256889_at	PHD-finger protein, putative contai	ING1	AT3G24010	1.57	0.65	6.87	0.000282	0.003881	0.67
264211_at	putative gigantea protein strong sim	GI	AT1G22770	1.59	0.66	6.87	0.000283	0.003881	0.67
255594_at	putative ABC transporter	ATABC1	AT4G01660	-1.69	-0.76	-6.87	0.000283	0.003881	0.66
245130_at	putative receptor-like protein kinase	---	AT2G45340	1.60	0.68	6.87	0.000283	0.003881	0.66
250119_at	putative protein similar to unknown	---	AT5G16470	1.65	0.72	6.87	0.000283	0.003881	0.66
258193_at	putative pectinesterase similar to pe	PME31	AT3G29090	1.62	0.69	6.87	0.000284	0.003882	0.66
250207_at	chalcone synthase (naringenin-cha	TT4	AT5G13930	-5.11	-2.35	-6.87	0.000284	0.003882	0.66
256860_at	hypothetical protein similar to acety	---	AT3G23840	-1.76	-0.81	-6.87	0.000284	0.003889	0.66
250477_at	putative protein CIS,CIS-MUCONA	---	AT5G10190	1.60	0.68	6.86	0.000285	0.003901	0.66
257932_at	unknown protein contains Pfam pro	HCF107	AT3G17040	-1.87	-0.91	-6.86	0.000286	0.003901	0.65
266521_at	unknown protein ; supported by cD	---	AT2G24020	-1.62	-0.69	-6.86	0.000286	0.003901	0.65
248508_at	histone acetyltransferase ;supporte	ELO3	AT5G50320	2.08	1.06	6.86	0.000286	0.003901	0.65
263082_at	putative nucleotide-binding protein	---	AT2G27200	1.55	0.63	6.86	0.000286	0.003901	0.65
255542_at	hypothetical protein	---	AT4G01860	1.90	0.93	6.86	0.000287	0.003903	0.65
267602_at	unknown protein ; supported by cD	---	AT2G32970	-2.11	-1.08	-6.85	0.000289	0.003921	0.64
262966_at	ER lumen protein retaining recepto	---	AT1G75760	-1.71	-0.78	-6.84	0.00029	0.003936	0.64
246070_at	ribosomal protein L7Ae-like NHP2/	---	AT5G20160	2.34	1.22	6.84	0.00029	0.003937	0.64
251583_at	putative protein several hypothetica	---	AT3G58590	2.23	1.16	6.84	0.000291	0.00394	0.63

254732_at	hypothetical protein	---	AT4G13750	2.23	1.16	6.84	0.000291	0.003942	0.63
247834_at	cinnamoyl-CoA reductase - like pro	---	AT5G58490	1.61	0.69	6.83	0.000292	0.003952	0.63
265510_at	putative microtubule-associated pro	ATG8D	AT2G05630	1.72	0.78	6.83	0.000293	0.003952	0.63
250141_at	protein kinase MSK-3 - like protein	SK13	AT5G14640	1.93	0.95	6.83	0.000294	0.003965	0.62
AFFX-Athal-	Arabidopsis thaliana /REF=M64116	GAPC1	---	2.11	1.08	6.82	0.000296	0.003977	0.62
245377_at	hypothetical protein	---	AT4G17700	-1.73	-0.79	-6.82	0.000296	0.003977	0.62
263939_at	hypothetical protein predicted by ge	ATTIM44-2	AT2G36070	1.71	0.77	6.82	0.000296	0.003977	0.61
250589_at	transcription factor (gb|AAD53097.1	MYB76	AT5G07700	-4.54	-2.18	-6.82	0.000296	0.003977	0.61
255451_at	putative protein similar to T5J8.17	---	AT4G02860	1.90	0.92	6.82	0.000296	0.003977	0.61
258104_at	hypothetical protein predicted by ge	---	AT3G23620	2.44	1.29	6.82	0.000298	0.003987	0.61
261919_at	type 2 peroxiredoxin, putative simil	TPX1	AT1G65980	1.88	0.91	6.81	0.000298	0.003987	0.61
251368_at	putative protein hypothetical protei	---	AT3G61380	-2.53	-1.34	-6.81	0.000298	0.003989	0.61
262433_s_a	DNA binding protein, putative simil	ATRBP47C	AT1G47490	1.63	0.71	6.81	0.0003	0.004003	0.60
258094_at	putative cytochrome P450 similar to	CYP72A15	AT3G14690	1.78	0.83	6.80	0.000303	0.004033	0.59
247696_at	MYB27 protein - like MYB27 protei	MYB59	AT5G59780	3.55	1.83	6.80	0.000303	0.004034	0.59
260290_at	hypothetical protein predicted by g	---	AT1G80510	-1.77	-0.82	-6.79	0.000304	0.004045	0.59
258390_at	unknown protein similar to leucine-r	---	AT3G15410	-1.69	-0.76	-6.79	0.000305	0.004048	0.58
263298_at	unknown protein ; supported by cD	TIC21	AT2G15290	-1.60	-0.68	-6.79	0.000305	0.004048	0.58
256455_at	unknown protein ;supported by full-	---	AT1G75190	-1.70	-0.77	-6.78	0.000306	0.004051	0.58
251760_at	Expressed protein ; supported by fu	---	AT3G55605	2.73	1.45	6.78	0.000306	0.004051	0.58
248102_at	putative protein contains similarity t	---	AT5G55140	2.14	1.10	6.78	0.000306	0.004053	0.58
259420_at	hypothetical protein similar to putati	---	AT1G13900	-1.49	-0.57	-6.78	0.000306	0.004053	0.58
266441_at	hypothetical protein predicted by ge	---	AT2G43250	1.70	0.77	6.78	0.000306	0.004053	0.58
259318_at	unknown protein similar to HYP1 G	HYP1	AT3G01100	1.99	1.00	6.78	0.000307	0.004055	0.58
265118_at	beta-fructosidase nearly identical to	---	AT1G62660	-2.50	-1.32	-6.78	0.000307	0.004056	0.58
245122_at	putative dimethyladenosine transfer	---	AT2G47420	1.81	0.86	6.78	0.000308	0.004061	0.57
267419_at	putative thioredoxin	ATO1	AT2G35010	1.74	0.80	6.77	0.000309	0.004066	0.57
266351_at	unknown protein ;supported by full-	---	AT2G01490	1.85	0.89	6.77	0.00031	0.004066	0.57
264467_at	unknown protein similar to EST gb|A	---	AT1G10140	1.80	0.85	6.77	0.00031	0.004066	0.57
249991_at	zinc finger -like protein zinc finger p	---	AT5G18550	-1.70	-0.76	-6.77	0.00031	0.004066	0.57
263180_at	unknown protein ;supported by full-	URH2	AT1G05620	-1.77	-0.82	-6.76	0.000311	0.004078	0.56
253096_at	cytochrome P450-like protein	CYP81D4	AT4G37330	1.82	0.87	6.76	0.000312	0.004083	0.56
256269_at	transcription factor HBP-1B-like nea	TGA6	AT3G12250	1.63	0.70	6.76	0.000312	0.004085	0.56
262708_at	UV-sensitive rad23, putative simila	---	AT1G16190	-1.57	-0.65	-6.76	0.000313	0.004092	0.56
261833_at	ATP citrate-lyase, putative similar t	ACLA-1	AT1G10670	-1.71	-0.77	-6.76	0.000314	0.004095	0.55

265453_at	putative cellular apoptosis susceptil	---	AT2G46520	-1.92	-0.94	-6.75	0.000314	0.004095	0.55
247027_at	subtilisin-like serine protease conta	---	AT5G67090	-1.57	-0.65	-6.75	0.000314	0.004098	0.55
251772_at	cyclophilin-like protein ROC7, cyclo	---	AT3G55920	-1.94	-0.95	-6.75	0.000315	0.004105	0.55
251242_at	ARGININE/SERINE-RICH SPLICIN	RSP31	AT3G61860	1.61	0.69	6.75	0.000315	0.004105	0.55
261322_at	hypothetical protein predicted by ge	ATPUP11	AT1G44750	1.81	0.86	6.75	0.000315	0.004105	0.55
266371_at	calmodulin-like protein identical to C	---	AT2G41410	3.06	1.61	6.75	0.000316	0.00411	0.54
262637_at	oxidoreductase, putative contains F	---	AT1G06640	-12.47	-3.64	-6.74	0.000317	0.004112	0.54
262351_at	beta-galactosidase (BGAL), putativ	BGAL17	AT1G72990	1.56	0.64	6.74	0.000318	0.004124	0.54
253410_at	putative protein various predicted p	---	AT4G32970	2.03	1.02	6.74	0.000318	0.004124	0.54
260873_at	hypothetical protein predicted by ge	---	AT1G21580	-1.55	-0.63	-6.74	0.000318	0.004127	0.54
262345_at	hypothetical protein similar to hypot	---	AT1G64180	1.79	0.84	6.74	0.000319	0.004129	0.54
263870_at	unknown protein	RKP	AT2G22010	1.78	0.83	6.74	0.000319	0.004129	0.53
253912_at	putative protein met-10+ protein, N	---	AT4G27340	1.89	0.92	6.73	0.00032	0.004139	0.53
246076_at	sucrose-phosphate synthase-like p	ATSPS1F	AT5G20280	1.75	0.81	6.73	0.000321	0.004151	0.53
266271_at	putative glutathione S-transferase	ATGSTU6	AT2G29440	-6.38	-2.67	-6.73	0.000322	0.004154	0.52
255317_at	putative vesicle transfer ATPase	---	AT4G04180	2.61	1.39	6.73	0.000322	0.004155	0.52
258673_at	unknown protein	---	AT3G08620	2.18	1.13	6.72	0.000323	0.004162	0.52
266461_at	glutathione S-transferase (GST6) i	ATGSTF8	AT2G47730	-2.61	-1.38	-6.72	0.000323	0.004162	0.52
252946_at	Expressed protein ; supported by fu	---	AT4G39235	2.38	1.25	6.72	0.000323	0.004162	0.52
249325_at	urophorphyrin III methylase (gb|AAI	UPM1	AT5G40850	2.00	1.00	6.72	0.000324	0.004162	0.52
251025_at	putative protein CND41, chloroplas	PCS1	AT5G02190	-2.00	-1.00	-6.72	0.000324	0.004163	0.52
258609_at	unknown protein ;supported by full-	---	AT3G02910	1.84	0.88	6.71	0.000327	0.004201	0.51
265187_at	putative ADP-ribosylation factor ; s	---	AT1G23490	-1.49	-0.57	-6.71	0.000327	0.004201	0.51
259034_at	putative pectinacetylesterase simila	---	AT3G09410	2.34	1.22	6.70	0.000329	0.004209	0.50
258766_at	galactokinase-like protein similar to	---	AT3G10700	-1.63	-0.70	-6.70	0.00033	0.004214	0.50
266414_at	mevalonate diphosphate decarboxy	MVD1	AT2G38700	-1.76	-0.82	-6.70	0.00033	0.004216	0.50
266977_at	putative phospholipase	---	AT2G39420	-3.79	-1.92	-6.70	0.000331	0.004216	0.50
255764_at	unknown protein	HCF173	AT1G16720	-1.96	-0.97	-6.69	0.000331	0.004217	0.49
250013_at	putative protein similar to unknown	---	AT5G18040	1.63	0.71	6.69	0.000331	0.004217	0.49
255535_at	putative RNaseP-associated protei	---	AT4G01790	2.18	1.12	6.69	0.000332	0.004217	0.49
246861_at	putative protein phytochrome-asso	IAA28	AT5G25890	1.73	0.79	6.69	0.000332	0.004217	0.49
253005_at	hypothetical protein ;supported by	---	AT4G38100	2.33	1.22	6.69	0.000332	0.004217	0.49
257227_at	monodehydroascorbate reductase s	MDAR4	AT3G27820	1.74	0.80	6.69	0.000332	0.004219	0.49
249427_at	40S ribosomal protein S9-like 40S	---	AT5G39850	4.20	2.07	6.69	0.000333	0.004224	0.49
265593_s_a	unknown protein ;supported by full-	LCV1	AT2G20120	-1.62	-0.69	-6.68	0.000334	0.004231	0.48

247972_at	histone acetyltransferase HAT B	HAG2	AT5G56740	2.12	1.08	6.68	0.000334	0.004231	0.48
266641_at	Expressed protein ; supported by fu	---	AT2G35605	1.73	0.79	6.68	0.000334	0.004231	0.48
256262_at	unknown protein	---	AT3G12150	-1.95	-0.97	-6.68	0.000334	0.004231	0.48
250358_at	putative protein gibberellin-respons	AGP15	AT5G11740	-2.02	-1.02	-6.68	0.000335	0.004232	0.48
262837_at	dynamin, putative similar to dynam	ADL1C	AT1G14830	-1.75	-0.81	-6.68	0.000335	0.004236	0.48
250718_at	unknown protein	emb2735	AT5G06240	1.69	0.76	6.68	0.000335	0.004237	0.48
265366_at	putative N-acetylglucosaminyltranst	---	AT2G13290	1.75	0.81	6.68	0.000336	0.00424	0.48
248418_at	cleavage and polyadenylation spec	CPSF160	AT5G51660	1.76	0.81	6.67	0.000337	0.004251	0.47
267174_at	60S ribosomal protein L36 ;suppor	---	AT2G37600	2.62	1.39	6.67	0.000337	0.004253	0.47
246708_at	putative protein various predicted p	---	AT5G28150	-1.98	-0.98	-6.67	0.000338	0.004257	0.47
257783_at	unknown protein	---	AT3G26950	-1.69	-0.76	-6.67	0.000338	0.004257	0.47
250704_at	Expressed protein ; supported by fu	---	AT5G06265	1.95	0.96	6.67	0.000339	0.00426	0.47
250647_at	putative protein contains similarity t	---	AT5G06770	-1.72	-0.79	-6.67	0.000339	0.00426	0.47
250246_at	polyamine oxidase	ATPAO1	AT5G13700	-1.55	-0.63	-6.67	0.000339	0.00426	0.47
252114_at	mucin -like protein hemomucin, Dr	---	AT3G51450	-4.99	-2.32	-6.66	0.00034	0.00427	0.47
247446_at	unknown protein ; supported by cD	---	AT5G62650	1.59	0.66	6.66	0.00034	0.00427	0.46
260775_at	14-3-3 protein GF14omega (grf2) ic	GRF2	AT1G78300	-1.98	-0.98	-6.66	0.000341	0.004274	0.46
256107_at	hypothetical protein predicted by ge	---	AT1G16830	1.60	0.67	6.66	0.000342	0.004288	0.46
260058_at	unknown protein ; supported by cD	---	AT1G78100	-1.78	-0.84	-6.66	0.000342	0.004288	0.46
259444_at	hypothetical protein predicted by ge	---	AT1G02370	3.39	1.76	6.66	0.000342	0.004288	0.46
264675_at	putative phosphoribosylglycinamid	---	AT1G09830	1.64	0.71	6.65	0.000343	0.004291	0.46
261334_at	unknown protein	---	AT1G44960	1.74	0.80	6.65	0.000343	0.004291	0.46
252986_at	putative protein T19C21.18 Arabid	---	AT4G38380	1.50	0.58	6.65	0.000345	0.004308	0.45
250784_at	unknown protein ; supported by cDI	---	AT5G05480	1.91	0.94	6.65	0.000345	0.004315	0.45
258868_at	putative exportin1 (XPO1) protein s	XPO1B	AT3G03110	1.78	0.83	6.64	0.000347	0.004333	0.44
256145_at	lipid transfer protein, putative simila	---	AT1G48750	-3.64	-1.86	-6.64	0.000347	0.004333	0.44
265596_at	hypothetical protein predicted by ge	CAF1	AT2G20020	3.05	1.61	6.64	0.000348	0.004333	0.44
259690_at	replication factor, putative similar to	---	AT1G63160	2.34	1.22	6.64	0.000348	0.004333	0.44
253775_at	putative protein T01B08.14 gene, E	---	AT4G28440	1.57	0.65	6.64	0.000348	0.004333	0.44
261700_at	hypothetical protein similar to hypot	---	AT1G32690	1.97	0.98	6.64	0.000348	0.004333	0.44
266774_at	hypothetical protein predicted by ge	ATRBL1	AT2G29050	-1.96	-0.97	-6.64	0.000349	0.004336	0.44
250662_at	steroid sulfotransferase-like protein	ST2A	AT5G07010	-3.37	-1.75	-6.63	0.000349	0.004339	0.44
261018_at	unknown protein contains similarity	---	AT1G26550	1.49	0.58	6.63	0.000349	0.004339	0.44
256255_at	MYB-family transcription factor, pu	---	AT3G11280	-1.52	-0.60	-6.63	0.00035	0.004342	0.43
266704_at	putative N-acetyl-gamma-glutamyl-	---	AT2G19940	-1.90	-0.93	-6.63	0.00035	0.004342	0.43

251733_at	copper homeostasis factor ;suppor	CCH	AT3G56240	1.77	0.82	6.63	0.00035	0.004342	0.43
246829_at	putative protein pyruvate water dik	ATGWD3	AT5G26570	1.62	0.69	6.63	0.000351	0.004351	0.43
251432_at	putative protein leucine zipper-EF-	---	AT3G59820	2.25	1.17	6.63	0.000351	0.004352	0.43
246593_at	putative protein predicted protein,	---	AT5G14790	-2.12	-1.09	-6.62	0.000352	0.00436	0.43
256852_at	unknown protein contains Pfam pro	ATRANGAI	AT3G18610	2.12	1.09	6.62	0.000353	0.004369	0.42
263824_at	putative WD-40 repeat protein	---	AT2G40360	2.55	1.35	6.62	0.000355	0.004385	0.42
254503_at	hypothetical protein ;supported by	PTAC9	AT4G20010	1.77	0.82	6.61	0.000356	0.00439	0.42
249264_s_a	disease resistance protein-like	---	AT5G41740	-2.67	-1.42	-6.61	0.000356	0.004395	0.41
259411_at	hypothetical protein contains Pfam	---	AT1G13410	1.69	0.76	6.61	0.000357	0.0044	0.41
263729_at	hypothetical protein predicted by ge	---	AT1G60080	1.52	0.61	6.61	0.000357	0.0044	0.41
264201_at	unknown protein ;supported by full-	---	AT1G22630	2.26	1.18	6.61	0.000358	0.004405	0.41
259105_at	stress related protein, putative simi	---	AT3G05500	-2.09	-1.06	-6.61	0.000358	0.004405	0.41
257207_at	hypothetical protein predicted by ge	---	AT3G14900	1.85	0.89	6.60	0.00036	0.004422	0.40
264712_at	unknown protein	ECT11	AT1G09810	2.06	1.04	6.60	0.00036	0.004424	0.40
258992_at	unknown protein similar to unknowr	---	AT3G08930	-1.51	-0.59	-6.60	0.000361	0.004433	0.40
253121_at	putative protein predicted protein,	---	AT4G35890	1.49	0.58	6.60	0.000361	0.004433	0.40
247345_at	putative protein contains similarity t	---	AT5G63760	1.84	0.88	6.59	0.000362	0.004436	0.40
262566_at	auxin response factor 1, putative si	ARF12	AT1G34310	-2.19	-1.13	-6.59	0.000362	0.004436	0.40
266065_at	phytochrome B Identical to GB:X17	PHYB	AT2G18790	-1.83	-0.88	-6.59	0.000363	0.004442	0.39
259154_at	unknown protein similar to unknowr	---	AT3G10260	-1.68	-0.75	-6.59	0.000363	0.004445	0.39
258728_at	unknown protein ; supported by cD	---	AT3G11800	-1.60	-0.68	-6.59	0.000364	0.004453	0.39
246953_at	unknown protein ;supported by full-	VPS60.2	AT5G04850	1.66	0.73	6.59	0.000365	0.004456	0.39
265931_at	unknown protein ;supported by full-	---	AT2G18520	1.99	0.99	6.58	0.000365	0.004456	0.39
245592_at	CCAAT-binding transcription factor	NF-YB3	AT4G14540	2.09	1.06	6.58	0.000365	0.004456	0.39
250938_at	putative protein various predicted p	---	AT5G03180	2.08	1.06	6.58	0.000365	0.004456	0.39
254758_at	putative protein dimethylaniline mo	YUC2	AT4G13260	-2.85	-1.51	-6.58	0.000366	0.004462	0.38
260041_at	unknown protein similar to hypothet	---	AT1G68780	-1.83	-0.87	-6.58	0.000366	0.004463	0.38
261695_at	Mg-chelatase, putative similar to M	CHLD	AT1G08520	-1.84	-0.88	-6.58	0.000367	0.004463	0.38
249843_at	putative protein similar to unknown	SGS3	AT5G23570	2.20	1.14	6.58	0.000367	0.004466	0.38
248785_at	unknown protein	---	AT5G47400	1.52	0.61	6.58	0.000367	0.004466	0.38
252529_at	putative protein several oxidases, r	---	AT3G46490	-4.77	-2.25	-6.58	0.000368	0.004472	0.38
267601_at	hypothetical protein predicted by ge	---	AT2G32980	-1.73	-0.79	-6.57	0.000368	0.004472	0.38
259295_at	hypothetical protein predicted by ge	---	AT3G05340	1.94	0.96	6.57	0.000369	0.004472	0.38
259708_at	lysophospholipase isolog, putative	---	AT1G77420	-1.98	-0.98	-6.57	0.000369	0.004472	0.38
259724_at	putative serine/threonine-protein kir	SNRK2.10	AT1G60940	2.00	1.00	6.57	0.000369	0.004476	0.38

246521_at	N2,N2-dimethylguanine tRNA meth	---	AT5G15810	1.97	0.98	6.57	0.00037	0.004484	0.37
259616_at	hypothetical protein contains simila	C/VIF1	AT1G47960	2.35	1.23	6.56	0.000372	0.0045	0.37
263574_at	putative tetracycline transporter pro	---	AT2G16990	-1.60	-0.67	-6.56	0.000373	0.004508	0.37
255716_at	coded for by A. thaliana cDNA R30	CRCK2	AT4G00330	-1.48	-0.57	-6.56	0.000375	0.004525	0.36
251260_at	putative protein ISOPENICILLIN N	---	AT3G62130	2.37	1.24	6.55	0.000376	0.004535	0.36
266280_at	putative tropinone reductase	---	AT2G29260	1.53	0.61	6.55	0.000376	0.00454	0.35
247311_at	DNA polymerase III catalytic subun	EMB2780	AT5G63960	1.74	0.80	6.55	0.000376	0.00454	0.35
263106_at	hypothetical protein predicted by ge	---	AT2G05160	-1.91	-0.93	-6.55	0.000377	0.004542	0.35
264219_at	unknown protein contains similarity	---	AT1G60420	2.19	1.13	6.55	0.000377	0.004542	0.35
247089_at	dimethyladenosine transferase-like	---	AT5G66360	1.80	0.85	6.55	0.000378	0.004555	0.35
258847_at	unknown protein ; supported by ful	---	AT3G03100	1.56	0.65	6.54	0.000379	0.004556	0.35
252081_at	putative heat shock transcription fa	HSFA7A	AT3G51910	3.28	1.71	6.54	0.000379	0.004556	0.35
255046_at	H+-transporting ATP synthase-like	ATPD	AT4G09650	-1.81	-0.86	-6.54	0.000379	0.004557	0.35
264100_at	lupeol synthase identical to lupeol s	LUP1	AT1G78970	-5.40	-2.43	-6.54	0.000381	0.004572	0.34
254051_at	putative protein other Arabidopsis p	---	AT4G25270	-1.68	-0.75	-6.54	0.000382	0.004574	0.34
257000_at	hypothetical protein predicted by ge	---	AT3G14120	2.28	1.19	6.54	0.000382	0.004574	0.34
257056_at	unknown protein similar to hypothet	---	AT3G15350	-1.73	-0.79	-6.53	0.000383	0.00458	0.34
266205_s_a	putative dTDP-glucose 4-6-dehydra	AXS2	AT1G08200	-1.83	-0.87	-6.53	0.000383	0.004581	0.34
250523_at	putative protein strong similarity to	---	AT5G08510	1.53	0.61	6.53	0.000383	0.004581	0.34
266808_at	Expressed protein ; supported by fu	---	AT2G29995	-1.98	-0.99	-6.53	0.000385	0.004604	0.33
266513_at	unknown protein	---	AT2G47700	-1.93	-0.95	-6.52	0.000386	0.004607	0.33
245821_at	hypothetical protein similar to putati	---	AT1G26270	-1.93	-0.95	-6.52	0.000386	0.004608	0.33
256207_at	GTP-binding protein, putative simil	---	AT1G50920	1.97	0.98	6.52	0.000386	0.004608	0.33
254911_at	putative protein ;supported by full-l	---	AT4G11100	-1.63	-0.70	-6.52	0.000386	0.004608	0.33
261136_at	ribokinase, putative similar to GB:A	---	AT1G19600	1.60	0.68	6.52	0.000387	0.004612	0.32
262941_at	hypothetical protein predicted by ge	EMB2217	AT1G79490	2.17	1.12	6.52	0.000387	0.004612	0.32
249167_at	putative protein similar to unknown	---	AT5G42860	-3.74	-1.90	-6.52	0.000388	0.004616	0.32
261893_at	unknown protein ;supported by full-	---	AT1G80690	-1.68	-0.75	-6.51	0.000389	0.004627	0.32
263259_at	putative zinc-binding protein similar	PUB18	AT1G10560	-2.65	-1.41	-6.51	0.000389	0.004629	0.32
263521_at	hypothetical protein predicted by ge	---	AT2G24960	2.07	1.05	6.51	0.00039	0.004632	0.31
246020_at	putative protein ; supported by cDN	---	AT5G10710	1.66	0.73	6.51	0.00039	0.004632	0.31
265575_at	proline iminopeptidase identical to	PIP	AT2G14260	1.61	0.69	6.51	0.000391	0.004632	0.31
252305_at	putative protein CRP1 protein, Zea	emb1796	AT3G49240	2.17	1.11	6.51	0.000391	0.004632	0.31
253438_at	glycine hydroxymethyltransferase	SHM3	AT4G32520	1.98	0.99	6.51	0.000392	0.004635	0.31
262118_at	beta-glucosidase, putative similar t	BGLU11	AT1G02850	5.35	2.42	6.51	0.000392	0.004636	0.31

263039_at	mak16-like protein-related similar t	---	AT1G23280	2.14	1.10	6.51	0.000392	0.004636	0.31
248217_at	cytochrome b5 (dbj|BAA74839.1) ;	CB5-E	AT5G53560	1.87	0.90	6.50	0.000394	0.004653	0.31
265100_at	hypothetical protein predicted by ge	OSB4	AT1G31010	2.11	1.08	6.49	0.000396	0.004678	0.30
254427_at	putative protein predicted protein, A	emb1417	AT4G21190	2.46	1.30	6.49	0.000397	0.004683	0.30
252136_at	calmodulin-like protein flagellar cal	---	AT3G50770	16.83	4.07	6.49	0.000398	0.004698	0.29
256281_at	myb-family transcription factor, put	TRFL9	AT3G12560	-1.89	-0.91	-6.48	0.000401	0.004716	0.29
259562_at	hypothetical protein ; supported by	---	AT1G21200	1.70	0.77	6.48	0.000401	0.00472	0.29
261053_at	hypothetical protein predicted by ge	---	AT1G01320	2.02	1.01	6.48	0.000402	0.004721	0.28
257019_at	unknown protein	---	AT3G19640	1.49	0.58	6.47	0.000403	0.004742	0.28
259746_at	hypothetical protein predicted by ge	---	AT1G71060	2.07	1.05	6.47	0.000404	0.004742	0.28
260453_s_a	unknown protein	---	AT1G72510	1.99	1.00	6.47	0.000404	0.004742	0.28
253175_at	WD-40 repeat protein (MSI3) ; sup	MSI3	AT4G35050	2.44	1.28	6.47	0.000404	0.004742	0.28
266166_at	putative glucosyltransferase ; supp	---	AT2G28080	-2.15	-1.10	-6.47	0.000405	0.004752	0.27
267411_at	putative disease resistance protein	---	AT2G34930	-16.62	-4.05	-6.47	0.000406	0.004761	0.27
259179_at	hypothetical protein similar to putati	---	AT3G01660	1.98	0.98	6.46	0.000407	0.004769	0.27
266934_at	unknown protein	---	AT2G18900	1.79	0.84	6.46	0.000408	0.004769	0.27
254213_at	tyrosine transaminase like protein t	---	AT4G23590	-1.63	-0.70	-6.46	0.000408	0.004769	0.27
261277_at	hypothetical protein predicted by ge	---	AT1G20230	1.84	0.88	6.46	0.000409	0.004774	0.27
255788_at	auxin regulated protein (IAA13) GB	IAA13	AT2G33310	2.03	1.02	6.46	0.000411	0.004792	0.26
255960_at	unknown protein ; supported by cDI	---	AT1G22140	1.94	0.96	6.46	0.000411	0.004792	0.26
252303_at	putative protein hypothetical protei	---	AT3G49210	1.60	0.68	6.46	0.000411	0.004792	0.26
260792_at	unknown protein ;supported by full-	---	AT1G06270	1.73	0.79	6.45	0.000411	0.004796	0.26
265192_at	hypothetical protein predicted by ge	---	AT1G05060	1.92	0.94	6.45	0.000412	0.004799	0.26
260069_at	unknown protein	---	AT1G73820	1.63	0.71	6.45	0.000412	0.004799	0.25
267406_at	unknown protein	MEE22	AT2G34780	1.83	0.87	6.45	0.000413	0.004799	0.25
259246_s_a	hypothetical protein predicted by ge	---	AT3G07730	1.96	0.97	6.45	0.000413	0.004799	0.25
248173_at	putative protein contains similarity t	---	AT5G54580	1.62	0.70	6.45	0.000413	0.004799	0.25
249443_at	putative protein ; supported by cDN	---	AT5G39600	1.99	1.00	6.45	0.000413	0.004803	0.25
264487_at	vacuolar protein sorting homolog al	VPS45	AT1G77140	-1.56	-0.64	-6.45	0.000414	0.004806	0.25
250856_at	putative protein salt-inducible prote	---	AT5G04810	1.91	0.93	6.44	0.000415	0.004811	0.25
256932_at	unknown protein	---	AT3G22520	1.61	0.69	6.44	0.000416	0.004825	0.25
258937_at	putative ribosomal protein S28 simi	---	AT3G10090	2.26	1.17	6.44	0.000417	0.004828	0.24
246681_at	chloride channel-like protein chlorid	---	AT5G33280	1.55	0.63	6.44	0.000417	0.004832	0.24
247855_at	similar to unknown protein (sp|P232	---	AT5G58210	1.98	0.98	6.44	0.000417	0.004832	0.24
260815_at	chloroplast inner envelope protein,	TIC110	AT1G06950	2.37	1.25	6.44	0.000418	0.004839	0.24

258215_at	phosphoprotein phosphatase, puta	atToc64-III	AT3G17970	2.14	1.10	6.43	0.000419	0.004845	0.24
256286_at	unknown protein	---	AT3G12180	1.74	0.80	6.43	0.000421	0.004859	0.23
259675_at	unknown protein similar to hypothet	---	AT1G77710	1.62	0.69	6.43	0.000421	0.00486	0.23
266410_at	unknown protein	EMB2765	AT2G38770	1.59	0.67	6.43	0.000422	0.004868	0.23
254852_at	putative disease resistance protein	WRKY19	AT4G12020	-1.50	-0.59	-6.42	0.000423	0.004872	0.23
248021_at	RuBisCO subunit binding-protein b	---	AT5G56500	2.63	1.39	6.42	0.000425	0.004888	0.22
262189_at	GTPase, putative similar to GTPas	---	AT1G78010	1.69	0.76	6.42	0.000426	0.004894	0.22
267429_at	putative UDP-galactose-4-epimeras	MEE25	AT2G34850	-2.14	-1.10	-6.42	0.000426	0.004894	0.22
253520_at	hypothetical protein ;supported by f	---	AT4G31410	1.56	0.64	6.41	0.000427	0.00491	0.22
253583_at	translation initiation factor-like prot	---	AT4G30680	-1.91	-0.93	-6.41	0.000428	0.00491	0.21
249400_at	putative protein MtN24 gene, Medi	---	AT5G40300	1.92	0.94	6.41	0.000428	0.00491	0.21
258993_at	putative chlorophyll a/b-binding pro	LHCB4.2	AT3G08940	-1.81	-0.86	-6.41	0.000429	0.00491	0.21
260258_at	putative ribosomal protein similar to	---	AT1G74270	2.03	1.02	6.41	0.000429	0.00491	0.21
252115_at	non-specific lipid transfer protein ;s	LTP5	AT3G51600	-1.87	-0.90	-6.41	0.000429	0.00491	0.21
258434_at	AP2 domain containing protein RAF	ATEBP	AT3G16770	2.18	1.12	6.41	0.000429	0.00491	0.21
267553_s_a	hypothetical protein predicted by ge	---	AT2G32180	2.18	1.12	6.41	0.000429	0.00491	0.21
263018_at	putative non-LTR retroelement reve	---	---	-1.48	-0.57	-6.41	0.00043	0.004914	0.21
247942_at	putative protein similar to unknown	---	AT5G57120	2.10	1.07	6.41	0.00043	0.004914	0.21
254827_at	putative protein KIAA0255 gene, H	---	AT4G12650	-1.71	-0.78	-6.40	0.000431	0.004916	0.21
246058_at	putative protein predicted proteins,	---	AT5G08430	1.73	0.79	6.40	0.000433	0.004935	0.20
259131_at	unknown protein similar to hypothet	SP1L3	AT3G02180	-1.63	-0.71	-6.40	0.000433	0.004939	0.20
250538_at	RNA helicase (emb|CAA09212.1) ;	STRS2	AT5G08620	2.36	1.24	6.39	0.000434	0.004945	0.20
258474_at	hypothetical protein predicted by ge	---	AT3G02650	2.18	1.13	6.39	0.000435	0.004945	0.20
251865_at	protein phosphatase 2A regulatory	---	AT3G54930	-1.55	-0.63	-6.39	0.000435	0.004945	0.20
262648_at	putative ribulose-1,5 bisphosphate	---	AT1G14030	1.64	0.71	6.39	0.000435	0.004945	0.20
263609_at	putative LRR receptor protein kinas	---	AT2G16250	-1.61	-0.68	-6.39	0.000435	0.004945	0.20
245314_at	Expressed protein ; supported by fu	---	AT4G16745	-1.69	-0.76	-6.39	0.000435	0.004945	0.20
263689_at	ribonuclease, RNS3 identical to rib	RNS3	AT1G26820	-2.42	-1.27	-6.39	0.000437	0.004959	0.19
265190_at	unknown protein ; supported by cD	---	AT1G23780	1.53	0.62	6.39	0.000438	0.004964	0.19
248795_at	Myb-related transcription activator-l	---	AT5G47390	-1.54	-0.62	-6.39	0.000438	0.004964	0.19
256972_at	unknown protein	---	AT3G21140	1.68	0.75	6.38	0.000439	0.004976	0.19
256223_at	unknown protein ;supported by full-	emb1303	AT1G56200	1.78	0.83	6.38	0.00044	0.004987	0.18
248938_at	receptor-like protein kinase	---	AT5G45780	1.57	0.65	6.38	0.000442	0.005001	0.18
256113_at	unknown protein ;supported by full-	---	AT1G16810	1.77	0.83	6.37	0.000442	0.005004	0.18
263692_at	unknown protein Location of ESTs	---	AT1G26850	-1.66	-0.73	-6.37	0.000443	0.005006	0.18

259673_at	putative phorbol ester / diacylglycer	---	AT1G77800	1.97	0.97	6.37	0.000444	0.005022	0.17
248603_at	WD-40 repeat protein-like	---	AT5G49430	1.54	0.62	6.37	0.000446	0.005029	0.17
264806_at	hypothetical protein predicted by ge	---	AT1G08610	2.73	1.45	6.37	0.000446	0.005029	0.17
264389_at	unknown protein similar to hypothet	---	AT1G11960	-2.38	-1.25	-6.37	0.000446	0.005029	0.17
261222_at	anter-specific proline-rich protein A	---	AT1G20120	1.59	0.67	6.36	0.000446	0.005029	0.17
260370_at	putative aminolevulinate dehydratas	HEMB1	AT1G69740	-1.64	-0.71	-6.36	0.000447	0.005035	0.17
249049_at	tubulin beta-4 chain (sp|P24636) ;	TUB4	AT5G44340	-2.12	-1.08	-6.36	0.000448	0.005043	0.16
252693_s_a	ribosomal protein S29 - like riboson	---	AT3G43980	1.61	0.69	6.36	0.000448	0.005043	0.16
258526_at	DAG protein, putative similar to DA	---	AT3G06790	1.69	0.76	6.36	0.000449	0.005043	0.16
246188_at	putative protein	---	AT5G21050	-1.51	-0.60	-6.36	0.000449	0.005044	0.16
267580_at	unknown protein	---	AT2G41990	-1.82	-0.86	-6.36	0.000449	0.005045	0.16
258621_at	zinc finger protein 1 (zfn1) identical	ZFN1	AT3G02830	-1.60	-0.68	-6.36	0.00045	0.005046	0.16
246496_at	putative protein KIAA1468 - Homo	---	AT5G16210	-1.73	-0.79	-6.36	0.00045	0.005046	0.16
254153_at	putative protein hypothetical protei	PWD	AT4G24450	2.68	1.42	6.36	0.00045	0.005046	0.16
253254_at	predicted protein	SQS2	AT4G34650	-2.80	-1.49	-6.35	0.000451	0.005056	0.16
249794_at	putative protein contains similarity t	AtCXE18	AT5G23530	-1.51	-0.60	-6.35	0.000452	0.00506	0.16
256894_at	PREG-like protein, putative similar	CYCP2;1	AT3G21870	1.51	0.60	6.35	0.000452	0.005063	0.15
265283_at	unknown protein predicted by gene	MUR3	AT2G20370	-2.14	-1.10	-6.35	0.000453	0.005066	0.15
250861_at	putative protein predicted proteins,	---	AT5G04740	1.79	0.84	6.35	0.000453	0.005066	0.15
247106_at	WD repeat protein-like ;supported b	---	AT5G66240	1.73	0.79	6.34	0.000455	0.005072	0.15
257403_at	hypothetical protein similar to hypot	---	AT1G62520	-1.67	-0.74	-6.34	0.000455	0.005072	0.15
260682_at	hypothetical protein predicted by ge	---	AT1G17510	1.65	0.72	6.34	0.000455	0.005072	0.15
252357_at	putative protein predicted proteins,	---	AT3G48410	2.13	1.09	6.34	0.000455	0.005072	0.15
249470_at	putative protein predicted proteins,	---	AT5G39350	1.85	0.88	6.34	0.000456	0.005072	0.15
253440_at	putative protein ;supported by full-le	TIFY8	AT4G32570	1.47	0.56	6.34	0.000456	0.005072	0.15
254306_at	putative protein ; supported by cDN	ATCES1	AT4G22330	-1.51	-0.60	-6.34	0.000456	0.005072	0.15
251206_at	putative protein various predicted p	---	AT3G63090	2.16	1.11	6.34	0.000456	0.005072	0.14
263707_at	hypothetical protein Similar to gi|15	---	AT1G09300	2.16	1.11	6.34	0.000456	0.005072	0.14
256887_at	hypothetical protein predicted by ge	---	AT3G15150	1.77	0.83	6.34	0.000457	0.005074	0.14
248579_at	mitotic checkpoint protein-like	---	AT5G49880	2.08	1.06	6.34	0.000457	0.005076	0.14
247449_at	putative protein swelling-induced c	---	AT5G62290	2.42	1.28	6.34	0.000458	0.005081	0.14
254527_at	putative protein KIAA0682 protein,	---	AT4G19610	1.49	0.58	6.34	0.000458	0.005081	0.14
246824_at	drought-induced protein - like non-	---	AT5G26990	-1.56	-0.64	-6.34	0.000459	0.005081	0.14
248765_at	MutT domain protein-like ; supporte	ATNUDT2	AT5G47650	-1.57	-0.65	-6.33	0.000459	0.005081	0.14
261743_s_a	protein serine/threonine phosphata	BSL2	AT1G08420	1.62	0.70	6.33	0.000459	0.005081	0.14

258097_at	transport protein, putative similar to	---	AT3G23660	-1.53	-0.61	-6.33	0.00046	0.005093	0.14
254493_at	DAG-like protein DAG precursor, A	---	AT4G20020	2.45	1.29	6.33	0.000461	0.005095	0.13
249862_at	PGPD14 protein ;supported by full-	---	AT5G22920	-2.94	-1.56	-6.33	0.000461	0.005098	0.13
255510_at	polycomb group - like protein simila	SWN	AT4G02020	1.99	0.99	6.33	0.000462	0.005102	0.13
251713_at	putative protein several hypothetica	---	AT3G56080	1.94	0.95	6.33	0.000463	0.005103	0.13
265206_at	putative protease belongs to eukary	---	AT2G36670	1.81	0.86	6.32	0.000463	0.005105	0.13
259899_at	hypothetical protein predicted by ge	---	AT1G71210	1.98	0.98	6.32	0.000463	0.005105	0.13
248951_at	putative protein similar to unknown	---	AT5G45550	-1.86	-0.89	-6.32	0.000464	0.005105	0.13
256542_at	unknown protein	PMI1	AT1G42550	1.92	0.94	6.32	0.000464	0.005105	0.13
251233_at	putative protein hypothetical protei	DRB4	AT3G62800	1.66	0.73	6.32	0.000465	0.005114	0.12
260087_at	hypothetical protein predicted by ge	---	AT1G73200	-1.99	-0.99	-6.32	0.000465	0.005114	0.12
260678_at	hypothetical protein predicted by ge	---	AT1G07970	1.49	0.58	6.32	0.000467	0.005127	0.12
257092_at	unknown protein	DDL	AT3G20550	1.93	0.95	6.31	0.000468	0.005137	0.12
259392_at	hypothetical protein similar to hypot	---	AT1G06380	1.57	0.65	6.31	0.000468	0.005137	0.12
258555_at	fatty acid multifunctional protein (At	MFP2	AT3G06860	1.76	0.82	6.31	0.000469	0.00514	0.12
267064_at	calmodulin (cam2)	CAM2	AT2G41110	-2.77	-1.47	-6.31	0.00047	0.005153	0.11
261422_at	unknown protein	NDF6	AT1G18730	-1.83	-0.88	-6.30	0.000472	0.00517	0.11
255061_at	putative protein disulfide isomerase	ATAPRL6	AT4G08930	-1.53	-0.61	-6.30	0.000473	0.005176	0.11
255891_at	hypothetical protein predicted by ge	EGY3	AT1G17870	-1.81	-0.86	-6.30	0.000475	0.005189	0.10
267211_at	Expressed protein ; supported by fu	---	AT2G44065	1.51	0.59	6.30	0.000475	0.005194	0.10
258538_at	putative tRNA pseudouridine syntha	---	AT3G06950	1.59	0.67	6.30	0.000475	0.005194	0.10
262074_at	glutathione S-transferase, putative	ATGSTU15	AT1G59670	2.45	1.29	6.29	0.000476	0.005202	0.10
247779_at	putative protein damage-specific D	DDB2	AT5G58760	1.84	0.88	6.29	0.000477	0.005205	0.10
266563_at	nodulin-like protein	---	AT2G23990	-1.62	-0.69	-6.29	0.000478	0.005214	0.09
260954_at	glyoxalase II isozyme, putative sim	GLX2-4	AT1G06130	1.81	0.85	6.29	0.00048	0.005227	0.09
265087_at	hypothetical protein predicted by ge	---	AT1G03760	2.47	1.31	6.29	0.00048	0.005227	0.09
261935_at	phosphoribosylanthranilate transfe	---	AT1G22610	-1.55	-0.63	-6.29	0.00048	0.005228	0.09
263222_at	putative protein kinase Strong simil	---	AT1G30640	-2.17	-1.12	-6.28	0.000481	0.005231	0.09
253659_at	hypothetical protein	---	AT4G30150	1.66	0.73	6.28	0.000481	0.005231	0.09
258925_at	unknown protein similar to hypothe	---	AT3G10420	1.82	0.87	6.28	0.000482	0.005236	0.09
251667_at	putative protein DYSKERIN (NUCL	NAP57	AT3G57150	3.23	1.69	6.28	0.000482	0.00524	0.08
250549_at	N-hydroxycinnamoyl benzoyltransf	---	AT5G07860	-2.21	-1.15	-6.28	0.000482	0.00524	0.08
256230_at	FKBP-type peptidyl-prolyl cis-trans	---	AT3G12340	1.89	0.92	6.28	0.000483	0.005242	0.08
265101_at	unknown protein similar to ESTs gb	---	AT1G30880	2.32	1.21	6.28	0.000483	0.005242	0.08
254353_s_a	putative protein probable membran	---	AT4G22285	2.02	1.01	6.28	0.000483	0.005242	0.08

261336_at	unknown protein ;supported by full-	---	AT1G44790	-2.17	-1.12	-6.28	0.000484	0.005243	0.08
263448_at	putative importin (nuclear transport	SAD2	AT2G31660	1.82	0.86	6.28	0.000484	0.005244	0.08
264621_at	putative protein kinase contains a p	---	AT2G17700	1.75	0.80	6.28	0.000484	0.005246	0.08
251879_at	putative protein hin1 protein, Nicoti	---	AT3G54200	-2.72	-1.44	-6.27	0.000487	0.005271	0.07
244936_at	NADH dehydrogenase ND1	---	---	-1.63	-0.70	-6.27	0.000488	0.005278	0.07
252374_at	response reactor 2 (ATRR2) ; supp	ARR5	AT3G48100	-2.41	-1.27	-6.27	0.000488	0.005278	0.07
256723_at	unknown protein ;supported by full-	---	AT2G34160	1.50	0.59	6.27	0.000489	0.005285	0.07
245926_at	VPS13 - like protein VPS13, Sacch	---	AT5G24740	1.68	0.74	6.26	0.00049	0.005288	0.07
262852_at	hypothetical protein predicted by ge	---	AT1G20910	1.61	0.69	6.26	0.000492	0.005308	0.06
265991_at	chloroplast single subunit DNA-dep	SCA3	AT2G24120	2.43	1.28	6.26	0.000492	0.005308	0.06
266045_s_a	hypothetical protein	---	AT2G07727	1.99	0.99	6.26	0.000493	0.005319	0.06
267147_at	putative anthocyanidin synthase ;s	---	AT2G38240	-8.39	-3.07	-6.26	0.000494	0.005319	0.06
250330_at	putative protein	---	AT5G11810	-1.73	-0.79	-6.26	0.000494	0.005319	0.06
265947_at	putative WD-40 repeat protein ; su	---	AT2G19540	2.30	1.20	6.26	0.000494	0.00532	0.06
246308_at	chlorophyll synthetase ; supported	G4	AT3G51820	-1.87	-0.90	-6.25	0.000495	0.005324	0.06
266076_at	ATP-dependent RNA helicase iden	---	AT2G40700	2.50	1.32	6.25	0.000495	0.005324	0.06
254784_at	growth factor like protein antisense	NUDT7	AT4G12720	-3.30	-1.72	-6.25	0.000498	0.005349	0.05
261591_at	protein kinase, putative similar to p	---	AT1G01740	1.96	0.97	6.25	0.000498	0.005349	0.05
249283_at	amino acid permease-like protein; p	---	AT5G41800	-2.04	-1.03	-6.25	0.000498	0.00535	0.05
262326_at	hypothetical protein similar to putati	---	AT1G64140	1.55	0.63	6.25	0.000498	0.00535	0.05
258845_at	unknown protein ; supported by ful	---	AT3G03150	-1.75	-0.81	-6.24	0.000502	0.005385	0.04
264920_at	hypothetical protein contains simila	ECHID	AT1G60550	-1.77	-0.82	-6.24	0.000503	0.005385	0.04
259794_at	unknown protein	---	AT1G64330	-1.73	-0.79	-6.24	0.000503	0.005385	0.04
266104_at	putative phosphatidate cytidylyltran	---	AT2G45150	1.73	0.79	6.23	0.000506	0.005412	0.03
255028_at	putative protein Arabidopsis thalian	PMP	AT3G24160	2.86	1.51	6.23	0.000508	0.005421	0.03
247173_at	poly(A)-binding protein II-like ; sup	---	AT5G65260	1.79	0.84	6.23	0.000508	0.005421	0.03
261016_at	beta-glucosidase, putative similar t	BGLU40	AT1G26560	-5.99	-2.58	-6.23	0.000508	0.005421	0.03
247032_at	putative protein strong similarity to	SDN3	AT5G67240	1.60	0.68	6.22	0.000509	0.005424	0.03
259278_at	hypothetical protein predicted by ge	---	AT3G01160	1.76	0.82	6.22	0.000512	0.005455	0.02
257125_at	t-complex polypeptide 1 homologue	ATTCP-1	AT3G20050	1.80	0.85	6.22	0.000512	0.005455	0.02
249960_at	squamosa promoter binding protein	SPL7	AT5G18830	1.63	0.70	6.22	0.000513	0.005455	0.02
254382_at	hypothetical protein	---	AT4G21890	-2.05	-1.04	-6.21	0.000513	0.005457	0.02
251130_at	oligopeptide transporter - like prote	PTR5	AT5G01180	-1.54	-0.62	-6.21	0.000513	0.005457	0.02
246262_at	hypothetical protein	---	AT1G31790	2.03	1.02	6.21	0.000514	0.005464	0.01
258380_at	PP1/PP2A phosphatases pleiotropi	---	AT3G16650	1.69	0.76	6.21	0.000514	0.005464	0.01

246490_at	S-adenosylmethionine decarboxyla	CPuORF10	AT5G15948	1.98	0.99	6.21	0.000515	0.005464	0.01
253208_at	putative protein	---	AT4G34830	1.59	0.67	6.21	0.000515	0.005467	0.01
247207_at	putative protein similar to unknown	---	AT5G65000	1.48	0.56	6.21	0.000516	0.005468	0.01
257892_at	unknown protein similar to ER6 pro	---	AT3G17020	1.64	0.71	6.21	0.000516	0.005474	0.01
254734_at	methionyl-tRNA synthetase - like p	---	AT4G13780	1.70	0.77	6.21	0.000517	0.005474	0.01
263693_at	hypothetical protein predicted by ge	ATPP2-A9	AT1G31200	3.50	1.81	6.21	0.000517	0.005474	0.01
249964_at	MAP kinase -like protein ATMPK9,	MPK16	AT5G19010	-1.62	-0.70	-6.21	0.000517	0.005474	0.01
265383_at	putative WD-40 repeat protein, MS	MSI2	AT2G16780	2.02	1.02	6.20	0.000519	0.005491	0.00
263599_at	putative histidine kinase ; supporte	WOL	AT2G01830	-2.19	-1.13	-6.20	0.000521	0.005507	0.00
247312_at	putative protein strong similarity to	---	AT5G63970	1.83	0.87	6.20	0.000522	0.005518	0.00
255580_at	putative water channel protein	TIP1;3	AT4G01470	-1.84	-0.88	-6.19	0.000523	0.005526	0.00
248495_at	putative protein strong similarity to	---	AT5G50780	1.77	0.83	6.19	0.000523	0.005526	-0.01
259172_at	O-acetylserine (thiol) lyase identica	CS26	AT3G03630	2.68	1.42	6.19	0.000525	0.00554	-0.01
264053_at	hypothetical protein predicted by ge	---	AT2G22560	-1.93	-0.95	-6.19	0.000526	0.005543	-0.01
247053_at	protein kinase ATN1-like protein	---	AT5G66710	-1.49	-0.57	-6.19	0.000527	0.005548	-0.01
248680_at	pantoate-beta-alanine ligase ;supp	PANC	AT5G48840	1.74	0.80	6.18	0.000528	0.005557	-0.01
253443_at	putative protein beta transducin-lik	LUG	AT4G32551	1.45	0.54	6.18	0.000529	0.005557	-0.02
248058_at	putative protein similar to unknown	---	AT5G55530	1.68	0.75	6.18	0.000529	0.005557	-0.02
253622_at	cyclic nucleotide and calmodulin-re	ATCNGC9	AT4G30560	-1.61	-0.69	-6.18	0.00053	0.005559	-0.02
262967_at	hypothetical protein predicted by ge	---	AT1G75730	-1.70	-0.76	-6.18	0.00053	0.005559	-0.02
260337_at	unknown protein	WRKY57	AT1G69310	1.78	0.83	6.18	0.00053	0.005559	-0.02
258716_at	unknown protein similar to a region	---	AT3G09700	2.22	1.15	6.18	0.000531	0.005565	-0.02
267628_at	unknown protein similar to GP|2262	---	AT2G42280	1.71	0.77	6.18	0.000531	0.005565	-0.02
246384_at	glutaredoxin, putative similar to glu	---	AT1G77370	1.53	0.61	6.18	0.000533	0.005577	-0.02
258292_at	hypothetical protein predicted by ge	---	AT3G23330	1.80	0.85	6.18	0.000533	0.005577	-0.02
265865_at	hypothetical protein predicted by ge	---	AT2G01740	1.52	0.60	6.18	0.000533	0.005577	-0.02
253980_at	sucrase-like protein sucrose cleava	---	AT4G26620	2.25	1.17	6.17	0.000534	0.005581	-0.03
245050_at	PSII K protein	---	---	-1.46	-0.55	-6.17	0.000534	0.005581	-0.03
260229_at	putative RING zinc finger protein c	---	AT1G74370	-1.88	-0.91	-6.17	0.000534	0.005581	-0.03
247625_at	zinc finger protein - like dof6 zinc fi	---	AT5G60200	-1.95	-0.97	-6.17	0.000536	0.005596	-0.03
250440_at	40S ribsomal protein S6 ; supporte	EMB3010	AT5G10360	2.01	1.01	6.17	0.000537	0.005604	-0.03
263880_at	unknown protein ;supported by full-	---	AT2G21960	-2.00	-1.00	-6.17	0.000537	0.005608	-0.03
245685_at	Expressed protein ; supported by cl	E2F1	AT5G22220	-1.50	-0.59	-6.17	0.000538	0.005608	-0.03
255742_at	DNA-binding protein RAV2, putativ	TEM1	AT1G25560	-1.57	-0.65	-6.17	0.000538	0.005608	-0.03
259489_at	unknown protein	---	AT1G15790	2.45	1.29	6.16	0.000538	0.005609	-0.04

252573_at	zinc finger protein zinc finger prote	---	AT3G45260	-1.64	-0.72	-6.16	0.000539	0.005609	-0.04
261190_at	ribosomal protein L11, putative sim	PRPL11	AT1G32990	-1.69	-0.75	-6.16	0.00054	0.005611	-0.04
259756_at	unknown protein ; supported by cD	---	AT1G71080	-1.56	-0.65	-6.16	0.00054	0.005611	-0.04
246045_at	putative protein predicted proteins,	---	AT5G19430	1.90	0.93	6.16	0.00054	0.005611	-0.04
249070_at	cellulose synthase catalytic subunit	CESA4	AT5G44030	-1.83	-0.87	-6.16	0.000542	0.005628	-0.04
248757_at	putative protein contains similarity t	---	AT5G47680	1.54	0.62	6.16	0.000543	0.005628	-0.04
246134_at	protein kinase tousled ; supported	TSL	AT5G20930	1.84	0.88	6.16	0.000543	0.005628	-0.04
249026_at	Expressed protein ; supported by fu	OSB3	AT5G44785	1.88	0.91	6.15	0.000545	0.005639	-0.05
247495_at	putative protein predicted protein, /	IPK2BETA	AT5G61760	1.81	0.85	6.15	0.000545	0.005642	-0.05
255443_at	sulfate transporter protein similar to	SULTR3;2	AT4G02700	-1.77	-0.82	-6.15	0.000546	0.005649	-0.05
250402_at	putative protein unnamed ORF cDI	---	AT5G10940	1.57	0.65	6.15	0.000546	0.00565	-0.05
247418_at	glutaredoxin-like protein ; supporte	---	AT5G63030	1.91	0.93	6.15	0.000547	0.005656	-0.05
246148_at	glycine-rich RNA-binding protein - I	---	AT5G19960	1.74	0.80	6.14	0.000548	0.005663	-0.06
258965_at	hypothetical protein similar to hypo	---	AT3G10530	2.66	1.41	6.14	0.000549	0.00567	-0.06
254943_at	putative protein predicted proteins,	---	AT4G10890	1.62	0.69	6.14	0.00055	0.00567	-0.06
260766_at	unknown protein similar to hypothet	---	AT1G48960	-1.67	-0.74	-6.14	0.000551	0.005682	-0.06
254398_at	photosystem II oxygen-evolving co	PSBQA	AT4G21280	-1.70	-0.76	-6.14	0.000552	0.005682	-0.06
266889_at	hypothetical protein predicted by ge	---	AT2G44640	1.71	0.78	6.13	0.000554	0.005693	-0.07
266932_s_a	putative RNA helicase	---	AT1G63250	2.20	1.14	6.13	0.000555	0.005698	-0.07
263978_at	unknown protein ;supported by full-	MBF1A	AT2G42680	1.56	0.64	6.13	0.000555	0.005701	-0.07
251859_at	putative protein proteophosphoglyc	---	AT3G54680	1.68	0.75	6.13	0.000556	0.005712	-0.07
250672_at	DnaJ homologue (gb|AAB91418.1|)	ATJ6	AT5G06910	1.48	0.57	6.13	0.000558	0.005719	-0.07
260425_at	hypothetical protein similar to CCA	EDA25	AT1G72440	3.22	1.69	6.13	0.000559	0.005719	-0.08
253958_at	putative protein RING zinc finger p	---	AT4G26400	-1.69	-0.76	-6.13	0.000559	0.005719	-0.08
256483_at	hypothetical protein	---	AT1G31410	-1.84	-0.88	-6.13	0.000559	0.005719	-0.08
246830_at	chaperonin gamma chain - like pro	---	AT5G26360	2.49	1.32	6.12	0.000559	0.005722	-0.08
265150_at	unknown protein ; supported by cD	---	AT1G51200	1.84	0.88	6.12	0.00056	0.005722	-0.08
248766_at	putative protein strong similarity to	---	AT5G47580	2.79	1.48	6.12	0.00056	0.005722	-0.08
263472_at	molybdopterin synthase (CNX2) ;s	CNX2	AT2G31955	1.85	0.89	6.12	0.00056	0.005723	-0.08
245405_at	hypothetical protein	---	AT4G17150	-1.49	-0.57	-6.12	0.000561	0.00573	-0.08
261398_at	hypothetical protein contains simila	NHX6	AT1G79610	1.64	0.72	6.12	0.000561	0.00573	-0.08
250757_at	tetrahydrofolylpolyglutamate syntha	ATDFB	AT5G05980	1.64	0.71	6.11	0.000564	0.005753	-0.09
249817_at	putative protein similar to unknown	---	AT5G23820	-13.09	-3.71	-6.11	0.000566	0.005763	-0.09
247718_at	nonspecific lipid-transfer protein pr	LTP4	AT5G59310	-1.94	-0.96	-6.11	0.000567	0.005768	-0.09
249128_at	1-aminocyclopropane-1-carboxylate	---	AT5G43440	1.60	0.68	6.11	0.000569	0.005786	-0.10

245702_at	calcium lipid binding protein - like G	SYTC	AT5G04220	2.04	1.03	6.10	0.00057	0.005789	-0.10
262044_s_a	hypothetical protein predicted by ge	---	AT1G80210	1.63	0.70	6.10	0.00057	0.005791	-0.10
249753_at	putative protein similar to unknown	---	AT5G24610	-1.48	-0.56	-6.10	0.000571	0.005791	-0.10
254190_at	Expressed protein ; supported by fu	---	AT4G23885	2.19	1.13	6.10	0.000571	0.005791	-0.10
260622_at	hypothetical protein predicted by ge	NF-YC10	AT1G07980	1.56	0.64	6.10	0.000571	0.005791	-0.10
257291_at	DNA-binding protein, putative simil	---	AT3G15590	3.00	1.58	6.10	0.000571	0.005792	-0.10
267268_at	hypothetical protein predicted by ge	---	AT2G02570	1.64	0.72	6.10	0.000574	0.005821	-0.11
258811_at	unknown protein similar to putative	---	AT3G03990	-2.16	-1.11	-6.09	0.000575	0.005825	-0.11
258445_at	putative lipoxygenase similar to lipo	LOX5	AT3G22400	-2.33	-1.22	-6.09	0.000577	0.005841	-0.11
264072_at	hypothetical protein	---	---	1.55	0.63	6.09	0.000578	0.005842	-0.11
251029_at	putative protein gene product of su	---	AT5G02050	2.75	1.46	6.09	0.000579	0.005849	-0.11
266939_at	plasma membrane proton ATPase	AHA1	AT2G18960	1.48	0.56	6.09	0.000579	0.005849	-0.12
267084_at	unknown protein ; supported by cD	---	AT2G41180	6.37	2.67	6.09	0.00058	0.005849	-0.12
259610_at	bZIP protein, putative similar to GI:	---	AT1G52320	1.52	0.61	6.09	0.00058	0.005851	-0.12
265662_at	putative C2H2-type zinc finger prote	FZF	AT2G24500	1.91	0.93	6.08	0.00058	0.005853	-0.12
261826_at	pectin methylesterase, putative sim	PMEPCRA	AT1G11580	-2.94	-1.55	-6.08	0.000581	0.005853	-0.12
261844_at	hypothetical protein predicted by ge	---	AT1G15940	2.30	1.20	6.08	0.000582	0.005859	-0.12
263843_at	translin-like protein ; supported by	---	AT2G37020	1.59	0.67	6.08	0.000583	0.005862	-0.12
261483_at	hypothetical protein predicted by ge	---	AT1G14270	-1.72	-0.78	-6.08	0.000583	0.005865	-0.12
256770_at	hypothetical protein predicted by g	---	AT3G13700	-1.89	-0.92	-6.07	0.000588	0.0059	-0.13
259273_s_a	serine/threonine specific protein kir	---	AT3G01300	1.61	0.69	6.07	0.000589	0.005908	-0.13
256205_at	hypothetical protein	---	AT1G50890	-1.59	-0.67	-6.06	0.000594	0.005945	-0.14
248063_at	RNA-binding protein-like ; supporte	---	AT5G55550	-1.57	-0.65	-6.06	0.000594	0.005947	-0.14
246400_at	hypothetical protein contains simila	---	AT1G57540	1.52	0.61	6.06	0.000595	0.005954	-0.15
249345_at	putative protein ; supported by cDN	---	AT5G40740	-1.68	-0.75	-6.06	0.000595	0.005954	-0.15
265340_at	putative AAA-type ATPase similar t	---	AT2G18330	2.45	1.29	6.05	0.000598	0.00597	-0.15
246286_at	unknown protein	---	AT1G31910	1.55	0.63	6.05	0.000599	0.005978	-0.15
259163_at	putative protein kinase similar to A	---	AT3G01490	-1.86	-0.89	-6.05	0.0006	0.005989	-0.15
254389_s_a	putative protein various predicted p	---	AT4G21903	-3.29	-1.72	-6.05	0.000601	0.005991	-0.16
245723_at	hypothetical protein predicted by ge	---	AT1G73400	1.86	0.90	6.05	0.000602	0.005997	-0.16
262341_at	E2, ubiquitin-conjugating enzyme,	UBC28	AT1G64230	1.76	0.81	6.05	0.000603	0.005997	-0.16
247886_at	branched-chain amino acid aminotr	---	AT5G57850	1.98	0.99	6.05	0.000603	0.005997	-0.16
259080_at	putative mitogen activated protein k	WNK1	AT3G04910	-1.77	-0.83	-6.04	0.000604	0.006006	-0.16
251935_at	fructokinase - like protein fructokina	---	AT3G54090	2.03	1.02	6.04	0.000605	0.006013	-0.16
253421_at	putative protein predicted proteins,	---	AT4G32340	1.88	0.91	6.04	0.000606	0.006015	-0.16

261337_at	unknown protein ; supported by cDI	---	AT1G44810	2.41	1.27	6.04	0.000606	0.006015	-0.17
259948_at	unknown protein similar to LIGATIN	---	AT1G71350	2.08	1.06	6.04	0.000608	0.006024	-0.17
250222_at	putative protein similar to unknown	---	AT5G14050	2.22	1.15	6.04	0.000608	0.006025	-0.17
252512_at	receptor protein kinase -like recept	---	AT3G46290	-1.60	-0.68	-6.03	0.000609	0.006035	-0.17
263920_at	unknown protein ;supported by full-	---	AT2G36410	-1.83	-0.87	-6.03	0.000613	0.006065	-0.18
253919_at	putative protein ; supported by full-	---	AT4G27350	-2.67	-1.42	-6.02	0.000617	0.0061	-0.18
251936_at	putative protein crp1 protein, Zea r	MEE40	AT3G53700	1.82	0.86	6.02	0.000617	0.006102	-0.19
245557_at	phosphatase like protein	PUX5	AT4G15410	-1.45	-0.54	-6.02	0.000618	0.006103	-0.19
258461_at	hypothetical protein predicted by ge	---	AT3G17340	-1.52	-0.60	-6.02	0.000618	0.006103	-0.19
245180_at	putative protein similarity to protein	---	AT5G12410	2.07	1.05	6.02	0.000619	0.006103	-0.19
256424_at	unknown protein ;supported by full-	---	AT1G33490	1.61	0.68	6.02	0.000619	0.006103	-0.19
245668_at	dormancy-associated protein, puta	DYL1	AT1G28330	1.90	0.92	6.01	0.000621	0.006127	-0.19
250602_s_a	unknown protein	---	AT5G07940	1.60	0.68	6.01	0.000623	0.006137	-0.20
259138_s_a	putative DNA gyrase subunit B simi	---	AT3G10270	1.66	0.73	6.01	0.000624	0.006142	-0.20
251265_at	ATP-dependent RNA helicase-like	---	AT3G62310	1.88	0.91	6.01	0.000625	0.006148	-0.20
251663_at	putative protein hypothetical protei	---	AT3G57070	-1.62	-0.69	-6.01	0.000626	0.006152	-0.20
246090_at	putative protein BEM46 bem1/bud5	WAV2	AT5G20520	2.47	1.31	6.01	0.000626	0.006152	-0.20
253715_at	RIBOSOMAL PROTEIN S30 homo	---	AT4G29390	1.69	0.76	6.00	0.000627	0.006161	-0.20
252886_at	cellulose synthase catalytic subunit	CESA2	AT4G39350	-1.72	-0.78	-6.00	0.000631	0.006191	-0.21
264818_at	hypothetical protein similar to hypot	NAF1	AT1G03530	2.85	1.51	5.99	0.000633	0.00621	-0.21
256225_at	unknown protein ; supported by full-	---	AT1G56220	1.98	0.99	5.99	0.000635	0.006222	-0.22
259665_at	unknown protein ; supported by cDI	---	AT1G55160	-1.87	-0.91	-5.99	0.000636	0.00623	-0.22
262525_at	putative cytochrome P450 41% ider	CYP72C1	AT1G17060	-2.30	-1.20	-5.99	0.000636	0.00623	-0.22
266253_at	unknown protein contains non-cons	HDT4	AT2G27840	2.58	1.37	5.99	0.000637	0.006235	-0.22
253445_at	putative protein pAFD103 mRNA, I	---	AT4G32605	1.71	0.77	5.99	0.000638	0.006248	-0.22
262932_at	glutathione-s-transferase, putative	---	AT1G65820	1.92	0.94	5.98	0.00064	0.006255	-0.22
246322_at	S-locus protein, putative similar to	---	AT1G16680	1.55	0.64	5.98	0.00064	0.006255	-0.22
249585_at	5-oxoprolinase -like protein 5-oxop	OXP1	AT5G37830	1.58	0.66	5.98	0.00064	0.006255	-0.22
258001_at	AIG2-like protein similar to AIG2 pr	---	AT3G28950	1.57	0.65	5.98	0.00064	0.006255	-0.22
253857_at	putative protein hypothetical chlor	---	AT4G27990	1.64	0.71	5.98	0.000641	0.006259	-0.23
265939_at	putative Ta11-like non-LTR retroele	---	AT2G19650	2.08	1.05	5.98	0.000642	0.00626	-0.23
252032_at	putative protein RNA-binding prote	---	AT3G52150	-1.50	-0.59	-5.98	0.000644	0.00628	-0.23
264322_at	unknown protein Contains similarity	---	AT1G04190	1.72	0.78	5.97	0.000646	0.006296	-0.23
259825_at	RNA and export factor binding prot	---	AT1G66260	-1.83	-0.87	-5.97	0.000646	0.006297	-0.23
264356_at	putative DNA repair protein Strong	UVH6	AT1G03190	1.59	0.67	5.97	0.000648	0.006305	-0.24

257685_at	unknown protein	---	AT3G12770	1.76	0.82	5.97	0.000648	0.006305	-0.24
252143_at	putative protein centromere protein	---	AT3G51150	-1.58	-0.66	-5.97	0.000648	0.006307	-0.24
264790_at	putative histidine kinase histidine ki	ATHK1	AT2G17820	1.80	0.85	5.97	0.000649	0.006314	-0.24
257771_at	SNF1 related protein kinase (ATSR	CIPK7	AT3G23000	4.43	2.15	5.97	0.00065	0.006316	-0.24
262385_at	root hair defective, putative similar	---	AT1G72960	-1.47	-0.55	-5.97	0.00065	0.006316	-0.24
251243_at	putative protein hypothetical protei	---	AT3G61870	-1.96	-0.97	-5.97	0.00065	0.006316	-0.24
259361_at	glyceraldehyde-3-phosphate dehyd	GAPC2	AT1G13440	1.69	0.76	5.97	0.000651	0.006316	-0.24
253808_at	predicted proline-rich protein hydro	---	AT4G28300	-1.83	-0.87	-5.97	0.000651	0.006316	-0.24
265776_at	hypothetical protein predicted by ge	---	AT2G07340	1.52	0.60	5.97	0.000651	0.006316	-0.24
248905_at	putative protein contains similarity t	---	AT5G46250	1.59	0.67	5.96	0.000653	0.006329	-0.25
245886_at	ribosomal protein S15-like ribosom	---	AT5G09510	1.48	0.57	5.96	0.000653	0.006329	-0.25
257044_at	hypothetical protein predicted by ge	ARC5	AT3G19720	-1.80	-0.85	-5.96	0.000654	0.006337	-0.25
250409_at	putative protein 110K5.11, unknow	---	AT5G10860	1.60	0.68	5.96	0.000656	0.006347	-0.25
249636_at	beta-glucosidase -like protein prun	BGLU42	AT5G36890	-1.63	-0.70	-5.96	0.000656	0.006347	-0.25
258396_at	unknown protein similar to unknowr	---	AT3G15460	2.53	1.34	5.96	0.000656	0.006347	-0.25
267388_at	putative beta-glucosidase	BGLU15	AT2G44450	-2.55	-1.35	-5.95	0.000659	0.00636	-0.26
256982_at	unknown protein	ECT2	AT3G13460	1.60	0.68	5.95	0.00066	0.006374	-0.26
254329_at	putative protein oxysterol-binding p	ORP2A	AT4G22540	-1.67	-0.74	-5.95	0.000661	0.006374	-0.26
254750_at	putative protein	---	AT4G13150	1.83	0.87	5.95	0.000661	0.006374	-0.26
262259_s_a	hypothetical protein predicted by ge	---	AT1G53870	2.13	1.09	5.95	0.000661	0.006374	-0.26
264076_at	unknown protein	---	AT2G28540	1.46	0.55	5.95	0.000662	0.006374	-0.26
257970_at	putative sucrose cleavage protein s	---	AT3G27570	1.67	0.74	5.95	0.000662	0.006374	-0.26
258647_at	unknown protein ; supported by cD	---	AT3G07870	1.66	0.73	5.95	0.000662	0.006374	-0.26
267208_at	putative shaggy-like protein kinase	ASKdZeta	AT2G30980	-1.46	-0.55	-5.95	0.000663	0.006374	-0.26
265718_at	putative WRKY DNA-binding protei	WRKY3	AT2G03340	1.67	0.74	5.95	0.000664	0.006382	-0.26
263480_at	putative root iron transporter protein	ZIP7	AT2G04032	-1.72	-0.78	-5.95	0.000664	0.006382	-0.26
264377_at	similar to early nodulins	---	AT2G25060	-1.51	-0.59	-5.94	0.000667	0.0064	-0.27
251943_at	splicing factor - like protein splicing	RSZ32	AT3G53500	1.47	0.55	5.94	0.000668	0.006413	-0.27
248748_at	putative protein contains similarity t	AMK2	AT5G47840	-1.62	-0.70	-5.94	0.000669	0.006418	-0.27
247593_at	ABC transporter homolog PnATH -	GCN1	AT5G60790	1.66	0.73	5.94	0.00067	0.006423	-0.27
260498_at	putative AP2 domain transcription f	---	AT2G41710	1.81	0.85	5.94	0.00067	0.006424	-0.27
245865_at	hypothetical protein contains simila	---	AT1G58025	1.57	0.65	5.93	0.000672	0.00643	-0.28
262824_at	putative DNA binding protein simila	RBP45B	AT1G11650	1.46	0.55	5.93	0.000672	0.006432	-0.28
248287_at	putative protein similar to unknown	---	AT5G52970	-1.99	-0.99	-5.93	0.000674	0.006449	-0.28
254301_at	predicted protein predicted protein,	---	AT4G22790	2.06	1.05	5.93	0.000675	0.006455	-0.28

249204_at	unknown protein ;supported by full-	---	AT5G42570	-1.57	-0.65	-5.93	0.000676	0.006458	-0.28
264597_at	unknown protein	---	AT1G04620	1.89	0.92	5.92	0.000678	0.006479	-0.29
266089_at	hypothetical protein predicted by ge	---	AT2G38010	-2.58	-1.37	-5.92	0.000679	0.006479	-0.29
264054_at	unknown protein	SVP	AT2G22540	1.72	0.78	5.92	0.000679	0.006479	-0.29
264258_at	hypothetical protein predicted by ge	---	AT1G09220	1.66	0.73	5.92	0.000681	0.006492	-0.29
246838_at	flap endonuclease - like protein Os	---	AT5G26680	1.62	0.70	5.92	0.000682	0.006499	-0.29
246432_at	RGA-like protein putative member	RGL3	AT5G17490	-2.31	-1.21	-5.92	0.000683	0.006505	-0.29
254457_at	putative protein various predicted p	---	AT4G21170	1.86	0.90	5.91	0.000685	0.006515	-0.30
253629_at	glycine-rich protein glycine-rich cel	---	AT4G30450	-1.78	-0.83	-5.91	0.000685	0.006515	-0.30
251094_at	putative protein ;supported by full-l	---	AT5G01350	1.68	0.75	5.91	0.000685	0.006515	-0.30
264254_at	unknown protein	---	AT1G09150	1.46	0.55	5.91	0.000687	0.006533	-0.30
259434_at	unknown protein	---	AT1G01490	1.55	0.63	5.91	0.000689	0.006542	-0.30
261011_at	cytochrome b5 similar to cytochrom	CB5-A	AT1G26340	1.70	0.77	5.90	0.000691	0.006561	-0.31
253698_at	nucleotide pyrophosphatase - like p	---	AT4G29680	1.57	0.65	5.90	0.000692	0.006562	-0.31
266874_at	unknown protein	---	AT2G44760	1.47	0.56	5.90	0.000692	0.006563	-0.31
265940_at	putative nucleosome assembly prot	NAP1;2	AT2G19480	1.59	0.67	5.90	0.000694	0.006575	-0.31
266348_at	putative MAP kinase	ATMPK17	AT2G01450	-1.83	-0.87	-5.90	0.000694	0.006575	-0.31
264152_at	Mago Nashi-like protein similar to M	MAGO	AT1G02140	1.62	0.70	5.90	0.000695	0.006583	-0.31
255017_at	hypothetical protein ;supported by	CNX7	AT4G10100	1.61	0.69	5.90	0.000697	0.00659	-0.32
246311_at	high mobility group protein 2-like ; s	HMGB1	AT3G51880	1.68	0.75	5.90	0.000697	0.00659	-0.32
251605_at	receptor-like protein kinase several	---	AT3G57830	-1.74	-0.80	-5.90	0.000697	0.00659	-0.32
260268_at	unknown protein ;supported by full-	---	AT1G68490	1.55	0.63	5.89	0.000698	0.006601	-0.32
255947_at	hypothetical protein contains Pfam	---	AT1G22040	1.59	0.67	5.89	0.000699	0.006603	-0.32
254144_at	putative protein	---	AT4G24690	1.62	0.69	5.89	0.0007	0.006612	-0.32
265896_at	unknown protein	emb2410	AT2G25660	1.62	0.70	5.89	0.000701	0.00662	-0.32
248709_at	unknown protein ;supported by full-	---	AT5G48470	2.28	1.19	5.89	0.000702	0.00662	-0.32
257209_at	hypothetical protein	---	AT3G14920	1.46	0.55	5.89	0.000702	0.006622	-0.33
246602_at	copper amine oxidase, putative sim	---	AT1G31710	-2.49	-1.32	-5.89	0.000703	0.006622	-0.33
253184_at	putative protein protein kinase APK	BSK1	AT4G35230	1.64	0.71	5.89	0.000703	0.006622	-0.33
250678_at	selenium-binding protein-like	---	AT5G06540	1.50	0.58	5.89	0.000703	0.006622	-0.33
261168_at	unknown protein	---	AT1G04940	2.35	1.23	5.88	0.000704	0.006624	-0.33
256324_at	MATE efflux family protein, putative	---	AT1G66760	-6.98	-2.80	-5.88	0.000704	0.006624	-0.33
251646_at	putative protein	---	AT3G57780	-5.35	-2.42	-5.88	0.000704	0.006624	-0.33
248700_at	ligand-gated ion channel protein-like	ATGLR1.2	AT5G48400	1.74	0.80	5.88	0.000706	0.006639	-0.33
265431_at	(1-4)-beta-mannan endohydrolase	---	AT2G20680	-1.57	-0.65	-5.88	0.000708	0.006654	-0.33

262791_at	unknown protein EST gb|F13926 co	---	AT1G10830	-1.75	-0.80	-5.88	0.00071	0.006666	-0.34
257062_at	zinc finger protein, putative contain	EMB2454	AT3G18290	-2.85	-1.51	-5.88	0.000711	0.006669	-0.34
245178_at	putative protein similarity to cDNA c	FIS1B	AT5G12390	1.52	0.60	5.88	0.000711	0.006669	-0.34
256336_at	unknown protein	---	AT1G72030	1.86	0.89	5.87	0.000713	0.006681	-0.34
247210_at	annexin ;supported by full-length c	ANNAT2	AT5G65020	-2.64	-1.40	-5.87	0.000715	0.006702	-0.35
256284_at	unknown protein	PSF2	AT3G12530	2.06	1.04	5.87	0.000717	0.006712	-0.35
263674_at	hypothetical protein predicted by ge	---	AT2G04790	1.66	0.73	5.86	0.000721	0.006746	-0.35
246191_at	T-complex protein 1, beta subunit T	---	AT5G20890	1.77	0.83	5.86	0.000721	0.006746	-0.35
246230_at	SCARECROW-like protein	---	AT4G36710	1.56	0.64	5.86	0.000722	0.006753	-0.36
262629_at	heat shock protein, putative contai	ACD32.1	AT1G06460	1.52	0.61	5.86	0.000723	0.006759	-0.36
252941_at	phenylalanyl-trna synthetase - like	---	AT4G39280	1.50	0.59	5.86	0.000724	0.006767	-0.36
262818_at	hypothetical protein predicted by ge	---	AT1G11755	1.59	0.67	5.86	0.000725	0.006767	-0.36
262964_at	hypothetical protein predicted by ge	---	AT1G54380	2.03	1.02	5.86	0.000725	0.006767	-0.36
266279_at	putative tropinone reductase	---	AT2G29290	-1.85	-0.88	-5.85	0.000729	0.006799	-0.37
258067_at	putative mitotic checkpoint protein	---	AT3G25980	-1.57	-0.65	-5.85	0.000729	0.006799	-0.37
266839_at	unknown protein	ELF3	AT2G25930	1.52	0.60	5.84	0.000735	0.006853	-0.38
257288_at	anthocyanin 5-aromatic acyltransfe	---	AT3G29670	-1.56	-0.64	-5.84	0.000737	0.006863	-0.38
253537_at	putative protein ; supported by full-	HCF153	AT4G31560	1.66	0.73	5.84	0.000739	0.006879	-0.38
265729_at	putative glucan synthase	ATGSL03	AT2G31960	1.83	0.87	5.84	0.000739	0.006879	-0.38
253035_at	glycosyltransferase like protein alp	CGL1	AT4G38240	1.52	0.61	5.84	0.000739	0.006879	-0.38
254286_at	putative MADS Box / AGL protein M	AGL19	AT4G22950	2.27	1.18	5.83	0.000741	0.006886	-0.38
252667_at	protein kinase-like protein MSTK2S	NEK6	AT3G44200	-1.86	-0.90	-5.83	0.000741	0.006886	-0.38
263799_at	unknown protein ; supported by cD	---	AT2G24550	-2.04	-1.03	-5.83	0.000741	0.006888	-0.38
251257_at	ADP-ribosylation factor-like protein	ATARFA1E	AT3G62290	1.93	0.95	5.83	0.000742	0.006891	-0.39
262058_at	Expressed protein ; supported by fu	---	AT1G79990	-1.44	-0.53	-5.83	0.000743	0.006893	-0.39
246476_at	putative protein predicted proteins -	---	AT5G16730	-1.96	-0.97	-5.83	0.000744	0.006907	-0.39
258054_at	delta tonoplast integral protein (del	DELTA-TIP	AT3G16240	-19.48	-4.28	-5.83	0.000746	0.006919	-0.39
265907_at	unknown protein ;supported by full-	---	AT2G25650	1.71	0.78	5.83	0.000746	0.006919	-0.39
245290_at	hypothetical protein ; supported by	---	AT4G16490	-1.94	-0.96	-5.82	0.000747	0.006922	-0.39
247996_at	putative protein contains similarity t	---	AT5G56170	-2.26	-1.18	-5.82	0.000748	0.006927	-0.39
251066_at	putative protein RING-H2 finger pr	---	AT5G01880	2.16	1.11	5.82	0.00075	0.006939	-0.40
261649_at	putative clathrin-coat assembly prot	---	AT1G27700	-1.57	-0.65	-5.82	0.000751	0.006945	-0.40
249778_at	Expressed protein ; supported by fu	---	AT5G24165	1.54	0.63	5.82	0.000751	0.006945	-0.40
260996_at	NBS/LRR disease resistance protei	RFL1	AT1G12210	1.86	0.90	5.81	0.000755	0.006977	-0.40
258689_at	putative GTPase activating protein	---	AT3G07940	-1.51	-0.59	-5.81	0.000755	0.006981	-0.41

260412_at	putative alpha-amylase similar to al	AMY3	AT1G69830	-1.46	-0.54	-5.81	0.000756	0.006981	-0.41
257875_at	hypothetical protein	---	AT3G17120	-1.62	-0.70	-5.81	0.000756	0.006985	-0.41
265831_at	unknown protein	---	AT2G14460	2.83	1.50	5.81	0.000758	0.006997	-0.41
245742_at	aldehyde dehydrogenase, putative	ALDH3H1	AT1G44170	2.08	1.06	5.81	0.000759	0.007	-0.41
254664_at	initiation factor-2Bepsilon-like prote	---	AT4G18300	1.67	0.74	5.81	0.00076	0.007011	-0.41
252426_at	putative protein proline transport h	---	AT3G47630	1.71	0.78	5.81	0.000762	0.007018	-0.41
251800_at	putative protein various predicted p	RBL	AT3G55510	2.57	1.36	5.80	0.000763	0.007024	-0.42
254650_at	hypothetical protein	---	---	-1.49	-0.58	-5.80	0.000764	0.007034	-0.42
259534_at	hypothetical protein	---	AT1G12290	1.73	0.79	5.80	0.000765	0.007038	-0.42
245868_at	hypothetical protein	CAT2	AT1G58030	1.74	0.80	5.80	0.000766	0.007046	-0.42
255455_at	mitochondrial elongation factor Tu	---	AT4G02930	2.59	1.37	5.80	0.000768	0.007058	-0.42
251240_at	putative protein	---	AT3G62450	1.52	0.60	5.79	0.000774	0.007108	-0.43
260886_at	hypothetical protein contains simila	---	AT1G29200	-1.48	-0.56	-5.79	0.000774	0.007108	-0.43
253174_at	catalase ; supported by cDNA: gi_1	CAT2	AT4G35090	-1.73	-0.79	-5.79	0.000775	0.007108	-0.43
246948_at	cytochrome P450-like protein CYT	CYP71B12	AT5G25130	-1.48	-0.56	-5.79	0.000776	0.00712	-0.43
255977_at	ribosomal protein S18, putative sim	---	AT1G34030	1.87	0.90	5.79	0.000777	0.007122	-0.44
258804_at	hypothetical protein similar to hypot	---	AT3G04760	1.89	0.92	5.78	0.000779	0.007135	-0.44
263226_at	unknown protein Contains the PF|0	---	AT1G30690	-1.46	-0.54	-5.78	0.000779	0.007135	-0.44
245512_at	hypothetical protein	---	AT4G15770	2.09	1.06	5.78	0.000781	0.007145	-0.44
261428_at	isochorismate synthase, putative s	ICS2	AT1G18870	-2.13	-1.09	-5.78	0.000781	0.007145	-0.44
252559_at	RNA binding protein -like COLD-IN	---	AT3G46020	1.47	0.55	5.78	0.000781	0.007145	-0.44
266635_at	unknown protein ;supported by full-	---	AT2G35470	-1.79	-0.84	-5.78	0.000782	0.007147	-0.44
250604_at	putative protein heparanase precu	PIP1B	AT2G45960	2.04	1.03	5.78	0.000782	0.007147	-0.44
257174_at	uracil phosphoribosyltransferase, p	---	AT3G27190	1.83	0.87	5.78	0.000783	0.00715	-0.44
253090_at	beta-galactosidase like protein ; sup	BGAL3	AT4G36360	-7.11	-2.83	-5.78	0.000784	0.007155	-0.45
250811_at	cysteine proteinase inhibitor-like pro	---	AT5G05110	2.36	1.24	5.77	0.000785	0.007163	-0.45
258783_at	unknown protein	---	AT3G11760	-1.65	-0.73	-5.77	0.000785	0.007163	-0.45
256908_at	hypothetical protein similar to mucin	---	AT3G24040	-1.64	-0.72	-5.77	0.000786	0.007167	-0.45
253992_at	putative protein ;supported by full-l	---	AT4G26060	1.63	0.70	5.77	0.000787	0.007167	-0.45
254649_at	pherophorin - like protein pherophc	---	AT4G18570	-1.66	-0.73	-5.77	0.000787	0.007167	-0.45
261418_at	mitochondrial ribosomal protein, pu	---	AT1G07830	2.01	1.01	5.77	0.000787	0.007168	-0.45
265984_at	putative limonene cyclase	TPS10	AT2G24210	-1.54	-0.62	-5.77	0.000788	0.007168	-0.45
261301_at	hypothetical protein predicted by ge	---	AT1G48570	2.99	1.58	5.77	0.000788	0.007168	-0.45
252066_at	receptor-protein kinase-like protein	FER	AT3G51550	-2.02	-1.01	-5.77	0.000789	0.007177	-0.45
266983_at	putative phospholipase ; supported	---	AT2G39400	2.05	1.04	5.77	0.00079	0.007183	-0.45

264894_at	unknown protein Location of EST g	---	AT1G23040	1.73	0.79	5.77	0.000791	0.007183	-0.45
262825_at	putative chloroplast prephenate deh	ADT1	AT1G11790	-2.27	-1.18	-5.76	0.000792	0.007195	-0.46
258276_at	putative signal peptidase 21kDa sul	---	AT3G15710	-1.74	-0.80	-5.76	0.000793	0.007195	-0.46
254228_at	putative protein ; supported by full-	---	AT4G23620	1.57	0.65	5.76	0.000793	0.007195	-0.46
251551_at	transcriptional coactivator - like pro	MBF1B	AT3G58680	1.43	0.51	5.76	0.000794	0.007197	-0.46
249672_at	nucleolar protein-like	---	AT5G35910	1.78	0.83	5.76	0.000795	0.007197	-0.46
247284_at	Isp4-like protein ; supported by full-	OPT4	AT5G64410	-2.84	-1.51	-5.76	0.000796	0.007201	-0.46
245291_at	Expressed protein ; supported by cl	---	AT4G16155	-1.58	-0.66	-5.76	0.000796	0.007203	-0.46
261900_at	unknown protein ;supported by full-	---	AT1G80940	1.58	0.66	5.76	0.000796	0.007203	-0.46
260830_at	histone H1, putative similar to histo	---	AT1G06760	2.25	1.17	5.76	0.000797	0.007203	-0.46
261435_at	GTP-binding protein, putative simil	---	AT1G07615	2.19	1.13	5.76	0.000799	0.007218	-0.47
267371_at	Expressed protein ; supported by cl	---	AT2G44510	2.08	1.06	5.76	0.0008	0.007229	-0.47
258333_at	myosin heavy chain-like protein sim	MFP1	AT3G16000	-1.60	-0.67	-5.75	0.000801	0.007237	-0.47
267314_at	putative myosin heavy chain	---	AT2G34730	1.87	0.90	5.75	0.000803	0.007247	-0.47
257017_at	beta-xylosidase, putative similar to	---	AT3G19620	-1.55	-0.63	-5.75	0.000807	0.007276	-0.48
259732_at	putative replication factor C similar	---	AT1G77470	1.64	0.71	5.75	0.000808	0.007276	-0.48
263712_at	Expressed protein ; supported by fu	NFD6	AT2G20585	1.98	0.98	5.74	0.000809	0.007282	-0.48
246747_at	ribosomal protein S21 - like riboson	---	AT5G27700	1.96	0.97	5.74	0.00081	0.007282	-0.48
261534_at	unknown protein ;supported by full-	PEX11C	AT1G01820	1.48	0.56	5.74	0.000811	0.007282	-0.48
246892_at	putative protein predicted protein, (	---	AT5G25500	1.62	0.70	5.74	0.000811	0.007282	-0.48
249210_at	unknown protein	---	AT5G42670	1.49	0.58	5.74	0.000811	0.007282	-0.48
259077_s_a	reversibly glycosylated polypeptide-	RGP1	AT3G02230	-2.44	-1.29	-5.74	0.000814	0.007299	-0.49
264052_at	putative cytochrome P450	CYP79B3	AT2G22330	-2.50	-1.32	-5.74	0.000815	0.007306	-0.49
258501_at	hypothetical protein predicted by ge	---	AT3G06780	-1.99	-1.00	-5.74	0.000815	0.007307	-0.49
261038_at	unknown protein ; supported by full-	---	AT1G17490	1.74	0.80	5.74	0.000816	0.007308	-0.49
249015_at	Dreg-2 like protein	---	AT5G44730	1.60	0.68	5.74	0.000816	0.007311	-0.49
262299_at	unknown protein Similar to gb|U04	---	AT1G27520	1.56	0.64	5.73	0.000817	0.007312	-0.49
260316_at	hypothetical protein similar to hypot	---	AT1G63810	1.79	0.84	5.73	0.000818	0.007315	-0.49
250897_at	putative protein ; supported by cDN	---	AT5G03430	1.57	0.65	5.73	0.000818	0.007315	-0.49
253826_s_a	E2, ubiquitin-conjugating enzyme 9	UBC9	AT4G27960	1.45	0.53	5.73	0.000819	0.007319	-0.49
253789_at	putative protein predicted proteins,	---	AT4G28570	1.76	0.82	5.73	0.00082	0.007323	-0.49
246559_at	putative protein YTM1 - Homo sapi	---	AT5G15550	2.11	1.08	5.73	0.00082	0.007323	-0.49
255957_at	unknown protein ;supported by full-	---	AT1G22160	3.33	1.74	5.73	0.000821	0.007325	-0.50
255231_at	F-box protein family, AtFBL20 cont	---	AT4G05460	1.51	0.59	5.73	0.000823	0.007342	-0.50
253920_at	histone H2A- like protein histone H	HTA2	AT4G27230	2.00	1.00	5.72	0.000826	0.007364	-0.50

266534_at	putative splicing factor ;supported b	---	AT2G16940	1.49	0.57	5.72	0.000827	0.007366	-0.50
263708_at	unknown protein	---	AT1G09320	1.56	0.64	5.72	0.000827	0.007368	-0.50
260398_at	putative RNA-binding domain conta	APUM23	AT1G72320	2.02	1.01	5.72	0.000829	0.007377	-0.51
261944_at	unknown protein	---	AT1G64650	-1.84	-0.88	-5.72	0.00083	0.007381	-0.51
256400_at	putative RING zinc finger protein c	---	AT3G06140	-1.83	-0.87	-5.72	0.00083	0.007381	-0.51
254010_at	putative protein ;supported by full-l	---	AT1G72125	1.53	0.61	5.71	0.000833	0.007405	-0.51
256786_at	unknown protein ;supported by full-	---	AT3G13740	-1.79	-0.84	-5.71	0.000834	0.007405	-0.51
259597_at	ATP-dependent RNA helicase, put	---	AT1G27900	1.67	0.74	5.71	0.000834	0.007405	-0.51
267278_at	unknown protein ; supported by ful	---	AT2G19350	1.41	0.49	5.71	0.000834	0.007405	-0.51
263098_at	Expressed protein ; supported by fu	---	AT2G16005	-1.49	-0.58	-5.71	0.000835	0.007405	-0.51
262419_at	hypothetical protein identical to hyp	---	AT1G50380	1.86	0.90	5.71	0.000835	0.007407	-0.51
251968_at	putative protein proline-rich protein	---	AT3G53100	-1.86	-0.90	-5.71	0.000836	0.007407	-0.52
265868_at	unknown protein ;supported by full-	PUX2	AT2G01650	1.86	0.90	5.71	0.000836	0.007407	-0.52
262565_at	hypothetical protein predicted by ge	---	AT1G34320	1.59	0.67	5.71	0.000837	0.007407	-0.52
249066_at	WD-repeat protein-like	---	AT5G43920	1.45	0.53	5.71	0.000837	0.007407	-0.52
256160_at	pyruvate dehydrogenase E1 beta s	PDH-E1 BE	AT1G30120	-1.90	-0.93	-5.71	0.000838	0.007412	-0.52
258356_at	unknown protein	---	AT3G14340	-1.72	-0.78	-5.71	0.000839	0.007417	-0.52
254956_at	putative protein various predicted p	---	AT4G10850	-1.49	-0.57	-5.70	0.000843	0.007445	-0.52
264188_at	histone H2A, putative similar to his	GAMMA-H2	AT1G54690	2.58	1.37	5.70	0.000843	0.007447	-0.53
256648_at	ribosomal protein, putative similar t	---	AT3G13580	1.90	0.93	5.70	0.000845	0.007447	-0.53
260323_at	putative U3 small nucleolar ribonuc	IMP4	AT1G63780	2.44	1.29	5.70	0.000845	0.007447	-0.53
263471_at	hypothetical protein predicted by ge	RAP	AT2G31890	1.66	0.73	5.70	0.000845	0.007447	-0.53
252245_at	putative protein various predicted p	---	AT3G49710	2.16	1.11	5.70	0.000845	0.007449	-0.53
252932_at	putative proton pump vacuolar prot	VHA-A3	AT4G39080	-1.58	-0.66	-5.70	0.000847	0.007459	-0.53
249786_at	putative protein strong similarity to	ABIL3	AT5G24310	2.40	1.26	5.70	0.000849	0.007466	-0.53
254116_at	hypothetical protein	---	AT4G24730	-1.52	-0.60	-5.70	0.000849	0.007466	-0.53
266325_at	putative extensin	---	AT2G46630	-4.58	-2.20	-5.69	0.000851	0.007483	-0.54
255081_at	MLH1 protein ; supported by cDNA	MLH1	AT4G09140	2.23	1.16	5.69	0.000852	0.00749	-0.54
267163_at	unknown protein	---	AT2G37520	1.82	0.86	5.69	0.000855	0.007508	-0.54
247801_at	putative protein ; supported by full-l	---	AT5G58560	-1.59	-0.67	-5.69	0.000855	0.007508	-0.54
252156_at	BCS1 protein-like protein BCS1 pr	---	AT3G50940	1.76	0.82	5.69	0.000855	0.007508	-0.54
252213_at	flavonol synthase - like protein SR	---	AT3G50210	1.75	0.81	5.69	0.000858	0.007522	-0.54
262953_at	hypothetical protein predicted by ge	---	AT1G75670	2.21	1.14	5.69	0.000858	0.007524	-0.54
264210_at	putative myb-related transcription f	MYB3	AT1G22640	1.98	0.98	5.68	0.00086	0.007535	-0.55
245428_at	putative protein	---	AT4G17570	1.58	0.66	5.68	0.00086	0.007535	-0.55

257495_at	unknown protein	ATPDIL5-1	AT1G07960	1.67	0.74	5.68	0.000861	0.007538	-0.55
251997_at	60S ribosomal protein - like 60S rib	STV1	AT3G53020	1.86	0.90	5.68	0.000861	0.00754	-0.55
260049_at	DNA-directed RNA polymerase sul	NRPA2	AT1G29940	2.43	1.28	5.68	0.000862	0.00754	-0.55
246214_at	heat shock transcription factor HSF	HSF4	AT4G36988	1.87	0.90	5.68	0.000863	0.007549	-0.55
258696_at	hypothetical protein predicted by ge	HCF152	AT3G09650	2.08	1.06	5.68	0.000865	0.007566	-0.55
248473_at	small zinc finger-like protein ;suppo	TIM8	AT5G50810	1.75	0.81	5.68	0.000866	0.007566	-0.55
265315_at	hypothetical protein predicted by ge	CLASP	AT2G20190	-1.56	-0.64	-5.68	0.000867	0.007571	-0.55
255452_at	hypothetical protein similar to A. th	---	AT4G02880	1.50	0.59	5.67	0.000869	0.007585	-0.56
252468_at	starch phosphorylase H (cytosolic	PHS2	AT3G46970	1.83	0.87	5.67	0.000869	0.007585	-0.56
248854_at	putative protein contains similarity t	---	AT5G46580	1.71	0.77	5.67	0.000869	0.007585	-0.56
261824_at	DAG protein, putative similar to DA	---	AT1G11430	1.47	0.56	5.67	0.00087	0.007587	-0.56
245574_at	hypothetical protein	IQD19	AT4G14750	-1.93	-0.95	-5.67	0.000871	0.00759	-0.56
265088_at	hypothetical protein similar to DNA	SWI2	AT1G03750	1.44	0.52	5.67	0.000871	0.00759	-0.56
249121_at	aluminum-induced protein-like ; su	---	AT5G43830	-1.59	-0.67	-5.67	0.000873	0.007601	-0.56
261952_at	unknown protein	---	AT1G64430	1.43	0.51	5.67	0.000874	0.007603	-0.56
248624_at	unknown protein ; supported by cD	---	AT5G48790	-1.53	-0.61	-5.67	0.000874	0.007603	-0.56
247720_at	dTDP-glucose 4-6-dehydratase - li	UXS3	AT5G59290	-1.69	-0.75	-5.66	0.000876	0.00762	-0.57
260372_at	unknown protein contains a region	---	AT1G73980	1.54	0.62	5.66	0.000877	0.007624	-0.57
245822_at	unknown protein ; supported by cDI	---	AT1G26110	1.72	0.78	5.66	0.000881	0.007653	-0.57
252913_at	AtRer1A ; supported by full-length	ATRER1A	AT4G39220	-1.55	-0.63	-5.66	0.000882	0.007653	-0.57
244979_at	ribosomal protein S11	---	---	-1.43	-0.52	-5.66	0.000882	0.007653	-0.57
266268_at	unknown protein predicted by gene	---	AT2G29510	-1.50	-0.59	-5.66	0.000883	0.007653	-0.58
262890_at	nucleoporin, putative similar to nuc	NUP155	AT1G14850	1.99	1.00	5.66	0.000883	0.007653	-0.58
247465_at	RNA helicase ; supported by cDNA	PRH75	AT5G62190	2.15	1.10	5.66	0.000884	0.007653	-0.58
267004_at	hypothetical protein predicted by ge	---	AT2G34260	4.02	2.01	5.66	0.000884	0.007653	-0.58
250555_at	putative protein ferredoxin (2Fe-2S	---	AT5G07950	1.91	0.94	5.65	0.000885	0.007653	-0.58
260620_at	unknown protein	---	AT1G08070	1.57	0.65	5.65	0.000885	0.007653	-0.58
250735_at	putative protein similar to unknown	---	AT5G06280	1.58	0.66	5.65	0.000885	0.007653	-0.58
250339_at	NADP dependent malic enzyme - I	ATNADP-M	AT5G11670	1.83	0.87	5.65	0.000886	0.007661	-0.58
251285_at	putative protein several hypothetica	---	AT3G61770	1.56	0.65	5.65	0.000888	0.007668	-0.58
265908_at	contains similarity to S. cerevisiae A	---	AT4G00270	1.95	0.96	5.65	0.000888	0.007668	-0.58
261119_at	chloroplast 50S ribosomal protein L	emb2184	AT1G75350	-1.39	-0.48	-5.65	0.000889	0.007673	-0.58
250326_at	putative protein strong similarity to	MSL10	AT5G12080	1.86	0.90	5.65	0.00089	0.007683	-0.58
267102_at	putative small nuclear ribonucleopr	LIS	AT2G41500	1.63	0.70	5.65	0.000891	0.007684	-0.58
254357_at	nifU-like protein nifU protein homol	ISU1	AT4G22220	1.40	0.49	5.65	0.000892	0.00769	-0.59

249257_at	unknown protein	---	AT5G41640	-1.41	-0.50	-5.65	0.000892	0.00769	-0.59
265675_at	70kD heat shock protein ;supporte	HSP70T-2	AT2G32120	1.86	0.90	5.64	0.000897	0.007719	-0.59
264476_at	hypothetical protein contains simila	PGSIP2	AT1G77130	1.68	0.75	5.64	0.000897	0.007719	-0.59
263332_at	putative snRNP splicing factor ;sup	---	AT2G03870	1.51	0.60	5.64	0.000897	0.007719	-0.59
259305_at	unknown protein ;supported by full-	---	AT3G05070	1.57	0.65	5.64	0.000897	0.007719	-0.59
261922_at	amp-binding protein, putative simil	AAE12	AT1G65890	-1.87	-0.90	-5.64	0.000899	0.007729	-0.59
247600_at	Myb transcription factor homolog (A	MYB34	AT5G60890	-3.28	-1.71	-5.64	0.000901	0.007735	-0.60
266302_at	ethylene-insensitive3-like1 (EIL1) ic	EIL1	AT2G27050	-1.75	-0.81	-5.64	0.000902	0.007744	-0.60
245983_at	5-formyltetrahydrofolate cyclo-ligas	5-FCL	AT5G13050	1.55	0.63	5.63	0.000908	0.007783	-0.61
258426_at	hypothetical protein predicted by ge	PLDP1	AT3G16785	-1.55	-0.64	-5.63	0.000909	0.00779	-0.61
245632_at	unknown protein contains similarity	ATRBL10	AT1G25290	-1.58	-0.66	-5.63	0.00091	0.007794	-0.61
263810_at	putative translation initiation factor e	---	AT2G04520	1.46	0.54	5.63	0.00091	0.007796	-0.61
255344_s_a	putative receptor-like protein kinase	---	AT4G04540	-3.46	-1.79	-5.63	0.000911	0.007796	-0.61
263132_at	unknown protein ;supported by full-	---	AT1G78560	-1.46	-0.54	-5.63	0.000911	0.007799	-0.61
253464_at	putative protein ; supported by full-	---	AT4G32030	-1.80	-0.85	-5.62	0.000913	0.007809	-0.61
248107_at	small Ras-like GTP-binding protein	RAN3	AT5G55190	1.46	0.54	5.62	0.000913	0.007809	-0.61
245933_at	putative protein KIAA1521 - Homo	VPS9B	AT5G09320	1.49	0.57	5.62	0.000913	0.007809	-0.61
262559_at	unknown protein similar to hypothet	---	AT1G31300	-1.64	-0.72	-5.62	0.000914	0.007813	-0.61
258298_at	unknown protein ; supported by cD	---	AT3G23300	-1.84	-0.88	-5.62	0.000915	0.007813	-0.61
262362_at	disease resistance protein, putative	---	AT1G72840	1.52	0.61	5.62	0.000915	0.007816	-0.61
258939_at	unknown protein predicted by gene	---	AT3G10020	-2.51	-1.33	-5.62	0.000917	0.007832	-0.62
262584_at	hypothetical protein Strong similari	---	AT1G15440	2.71	1.44	5.62	0.000918	0.007835	-0.62
264591_at	hypothetical protein contains simila	---	AT2G17670	1.58	0.66	5.62	0.000919	0.007837	-0.62
260981_at	hypothetical protein predicted by ge	---	AT1G53460	1.72	0.79	5.62	0.00092	0.007844	-0.62
266407_at	putative elongation factor	TFIIS	AT2G38560	1.54	0.62	5.62	0.00092	0.007844	-0.62
251915_at	putative protein peroxisomal Ca-de	---	AT3G53940	1.78	0.83	5.62	0.000921	0.007847	-0.62
251630_at	putative protein unknown protein -	---	AT3G57420	-1.48	-0.57	-5.61	0.000923	0.007863	-0.62
256062_at	unknown protein ;supported by full-	LSH6	AT1G07090	1.49	0.58	5.61	0.000925	0.007874	-0.63
263831_at	putative ferritin	ATFER4	AT2G40300	2.05	1.03	5.61	0.000925	0.007874	-0.63
250776_at	monooxygenase ;supported by full-	---	AT5G05320	1.47	0.55	5.61	0.000926	0.007874	-0.63
266298_at	unknown protein ;supported by full-	---	AT2G29590	1.70	0.76	5.61	0.000926	0.007874	-0.63
245745_at	unknown protein contains similarity	---	AT1G51110	-1.96	-0.97	-5.61	0.000927	0.007877	-0.63
248767_at	putative protein contains similarity t	---	AT5G47710	1.66	0.74	5.61	0.000927	0.007878	-0.63
259164_at	hypothetical protein contains brom	ATBET10	AT3G01770	1.86	0.90	5.61	0.000929	0.00789	-0.63
251117_at	putative protein predicted protein, (	---	AT3G63390	1.73	0.79	5.61	0.000929	0.00789	-0.63

246012_at	Pspzf zinc finger protein - like DNA	---	AT5G10650	1.97	0.98	5.60	0.000931	0.007901	-0.63
255567_at	hypothetical protein ; supported by	---	AT4G01150	-1.57	-0.65	-5.60	0.000933	0.007906	-0.63
251018_at	60S ribosomal protein - like 60S rib	---	AT5G02450	1.91	0.94	5.60	0.000934	0.007915	-0.64
260236_at	geranylgeranyl reductase identical	---	AT1G74470	-1.45	-0.53	-5.60	0.000937	0.00794	-0.64
245521_at	Expressed protein ;supported by cD	ESD4	AT4G15880	1.51	0.60	5.59	0.000941	0.007965	-0.64
247000_at	casein kinase II alpha subunit ; sup	CKA1	AT5G67380	1.70	0.77	5.59	0.000943	0.007979	-0.65
262051_at	putative coatomer protein complex	---	AT1G79990	-1.72	-0.78	-5.59	0.000944	0.007985	-0.65
255623_at	putative L5 ribosomal protein ;supp	---	AT4G01310	-1.52	-0.60	-5.59	0.000945	0.007988	-0.65
246378_at	integral membrane protein, putative	---	AT1G57620	-1.49	-0.57	-5.59	0.000947	0.008002	-0.65
266510_at	unknown protein	SWA1	AT2G47990	2.54	1.34	5.59	0.000949	0.008016	-0.65
256934_at	unknown protein contains Pfam pro	---	AT3G22530	1.68	0.75	5.58	0.000949	0.008016	-0.65
246613_at	acetyl-CoA carboxylase ;supported	CAC2	AT5G35360	-1.77	-0.83	-5.58	0.00095	0.00802	-0.66
247403_at	putative protein hypersensitive-indu	---	AT5G62740	1.55	0.63	5.58	0.000957	0.008073	-0.66
250297_at	putative protein predicted protein, l	---	AT5G11980	-1.66	-0.73	-5.58	0.000958	0.008074	-0.66
263482_at	putative GDSL-motif lipase/hydrolas	---	AT2G03980	-8.09	-3.02	-5.58	0.000958	0.008077	-0.66
258651_at	putative phosphatidylinositol-4-phos	PIP5K9	AT3G09920	-1.68	-0.75	-5.58	0.000959	0.008081	-0.67
250559_at	putative protein condensin subunit	---	AT5G08010	1.67	0.74	5.57	0.00096	0.008087	-0.67
263598_at	putative xyloglucan-specific glucana	EXGT-A3	AT2G01850	-1.62	-0.69	-5.57	0.000961	0.008087	-0.67
247075_at	putative protein contains similarity t	PLP3b	AT5G66410	-1.67	-0.74	-5.57	0.000961	0.008087	-0.67
249965_at	putative protein predicted proteins,	---	AT5G19020	1.40	0.48	5.57	0.000961	0.008087	-0.67
245137_at	unknown protein	---	AT2G45460	1.80	0.85	5.57	0.000962	0.008087	-0.67
260360_at	chorismate mutase, putative contai	CM3	AT1G69370	-1.86	-0.89	-5.57	0.000962	0.008091	-0.67
256249_at	26S proteasome regulatory subuni	MEE34	AT3G11270	1.59	0.67	5.57	0.000963	0.008091	-0.67
252496_at	putative protein several hypothetica	CRR2	AT3G46790	2.01	1.01	5.57	0.000963	0.008093	-0.67
249177_at	unknown protein ;supported by full-	---	AT5G42850	1.53	0.62	5.57	0.000966	0.008112	-0.67
252968_at	putative protein unknown mRNA, H	---	AT4G38890	1.94	0.96	5.57	0.000967	0.008115	-0.67
261149_s_a	GSH-dependent dehydroascorbate	DHAR1	AT1G19550	-2.14	-1.10	-5.57	0.000968	0.008118	-0.68
262940_at	unknown protein	---	AT1G79520	1.99	0.99	5.56	0.000969	0.008126	-0.68
249222_at	putative protein similar to unknown	---	AT5G42450	1.43	0.51	5.56	0.00097	0.008127	-0.68
264849_at	putative ribosomal protein S4 conta	---	AT2G17360	1.71	0.77	5.56	0.00097	0.008128	-0.68
261266_at	expansin 10 identical to GB:AAF61	ATEXPA10	AT1G26770	-1.89	-0.91	-5.56	0.00097	0.008128	-0.68
255789_at	60S ribosomal protein L23 ;suppor	---	AT2G33370	3.12	1.64	5.56	0.000973	0.008143	-0.68
254639_at	putative protein various predicted p	DOT4	AT4G18750	1.60	0.68	5.56	0.000974	0.008146	-0.68
265760_at	unknown protein	---	AT2G01220	1.58	0.66	5.56	0.000974	0.008146	-0.68
260819_at	b-Zip DNA binding protein, putative	AtbZIP52	AT1G06850	-2.33	-1.22	-5.56	0.000977	0.008166	-0.69

261972_at	hypothetical protein predicted by ge	---	AT1G64600	2.13	1.09	5.55	0.000979	0.008181	-0.69
264031_at	unknown protein	---	AT2G03780	1.70	0.77	5.55	0.000979	0.008181	-0.69
248289_at	unknown protein ; supported by cD	---	AT5G52880	1.51	0.59	5.55	0.00098	0.008184	-0.69
256398_at	putative major intrinsic protein conta	NIP7;1	AT3G06100	-1.42	-0.51	-5.55	0.000982	0.008192	-0.69
260852_at	transmembrane protein, putative si	---	AT1G21900	1.47	0.56	5.55	0.000983	0.008197	-0.69
246235_at	putative protein	---	AT4G36830	-1.70	-0.76	-5.55	0.000986	0.008213	-0.70
264086_at	unknown protein ;supported by full-	---	AT2G31190	1.77	0.82	5.55	0.000986	0.008213	-0.70
248049_at	putative protein contains similarity t	COX15	AT5G56090	2.66	1.41	5.55	0.000986	0.008213	-0.70
250244_at	putative protein similar to unknown	ABO1	AT5G13680	2.12	1.08	5.55	0.000988	0.008227	-0.70
247342_at	ARI-like RING zinc finger protein-lik	---	AT5G63730	-1.52	-0.61	-5.54	0.00099	0.008241	-0.70
244916_at	hypothetical protein	ORF187	ATMG00880	-1.49	-0.58	-5.54	0.000991	0.008248	-0.70
256430_at	DREB2B transcription factor identic	DREB2B	AT3G11020	1.53	0.62	5.54	0.000992	0.008252	-0.70
250818_at	Expressed protein ; supported by cl	ALA1	AT5G04930	1.84	0.88	5.54	0.000992	0.008252	-0.70
260760_at	hypothetical protein predicted by ge	---	AT1G49170	1.75	0.81	5.54	0.000993	0.008252	-0.70
267179_at	putative ADP ribosylation factor 1 G	AGD7	AT2G37550	-1.91	-0.93	-5.54	0.000996	0.008274	-0.71
256482_at	protein kinase, putative contains P	FEI1	AT1G31420	-1.55	-0.63	-5.54	0.000998	0.008287	-0.71
252633_x_a	putative protein HISTONE DEACE	hda17	AT3G44490	1.42	0.50	5.54	0.000999	0.008294	-0.71
264264_at	unknown protein ESTs gb|T04610,	---	AT1G09250	-2.67	-1.41	-5.53	0.001	0.008301	-0.71
264828_at	hypothetical protein predicted by ge	ATATG18G	AT1G03380	1.86	0.89	5.53	0.001001	0.008303	-0.71
260440_at	hypothetical protein predicted by ge	---	AT1G68160	1.52	0.60	5.53	0.001005	0.008332	-0.72
251676_at	hypothetical protein	---	AT3G57320	-1.92	-0.94	-5.53	0.001006	0.008341	-0.72
250832_at	nicotianamine synthase (dbj|BAA74	NAS1	AT5G04950	5.45	2.45	5.53	0.001008	0.008354	-0.72
261765_at	cyclin, putative similar to cyclin GI:	CYCA2;3	AT1G15570	-1.61	-0.69	-5.52	0.00101	0.008368	-0.72
245249_at	acyl-CoA oxidase like protein ; supp	ACX1	AT4G16760	-1.88	-0.91	-5.52	0.001011	0.008369	-0.72
261415_at	globulin-like protein similar to GB:7	---	AT1G07750	-2.33	-1.22	-5.52	0.001014	0.008384	-0.73
257984_at	putative cell differentiation protein	---	AT3G20800	1.80	0.85	5.52	0.001014	0.008384	-0.73
262633_at	Expressed protein ; supported by fu	---	AT1G06630	-1.48	-0.57	-5.52	0.001016	0.008396	-0.73
251945_at	dTDP-glucose 4-6-dehydratase -lik	UXS1	AT3G53520	-1.54	-0.62	-5.52	0.001019	0.008422	-0.73
253561_at	aspartate--tRNA ligase - like protei	---	AT4G31180	1.49	0.57	5.51	0.001028	0.008488	-0.74
257619_at	unknown protein	ICK3	AT3G24810	1.65	0.72	5.51	0.001029	0.00849	-0.74
254476_at	putative protein gamma-SNAP pro	GSNAP	AT4G20410	-1.50	-0.59	-5.51	0.001029	0.00849	-0.74
260523_at	putative salt-inducible protein	EMB2654	AT2G41720	1.88	0.91	5.51	0.00103	0.00849	-0.74
254333_at	predicted protein predicted protein	SMO1-3	AT4G22753	-3.77	-1.92	-5.51	0.00103	0.00849	-0.74
262049_at	unknown protein ;supported by full-	---	AT1G80180	1.63	0.70	5.51	0.00103	0.00849	-0.74
264484_at	hypothetical protein similar to ankyr	---	AT1G77260	-1.49	-0.58	-5.50	0.001031	0.00849	-0.74

250857_at	unknown protein	---	AT5G04790	-1.89	-0.92	-5.50	0.001034	0.008506	-0.75
261613_at	abscisic acid responsive elements-l	ABF1	AT1G49720	1.97	0.98	5.50	0.001035	0.008516	-0.75
261296_at	unknown protein	---	AT1G48460	2.28	1.19	5.50	0.001037	0.008526	-0.75
251469_at	putative protein strictosidine syntha	---	AT3G59530	-1.48	-0.57	-5.50	0.001037	0.008526	-0.75
258747_at	unknown protein ; supported by ful	---	AT3G05810	1.82	0.87	5.50	0.001038	0.008532	-0.75
265872_at	unknown protein ;supported by full-	atnudt17	AT2G01670	1.92	0.94	5.50	0.001039	0.008532	-0.75
258810_at	hypothetical protein similar to hypot	---	AT3G03970	-1.63	-0.71	-5.50	0.00104	0.008539	-0.75
247048_at	photoreceptor-interacting protein-lik	---	AT5G66560	-2.55	-1.35	-5.50	0.001041	0.008539	-0.75
253843_at	putative protein MLL protein, Gallu	SDG16	AT4G27910	-1.44	-0.53	-5.49	0.001041	0.008539	-0.75
252971_at	extensin - like protein proline-rich p	PRP4	AT4G38770	-16.95	-4.08	-5.49	0.001041	0.00854	-0.76
249047_at	berberine bridge enzyme-like protei	---	AT5G44410	1.62	0.69	5.49	0.001043	0.008554	-0.76
251683_at	putative protein several hypothetica	---	AT3G57120	-2.59	-1.37	-5.49	0.001046	0.008575	-0.76
263010_at	T76725 come from this gene.	---	AT1G23330	1.48	0.56	5.49	0.001048	0.008582	-0.76
247498_at	peroxisomal Ca-dependent solute (	---	AT5G61810	-1.77	-0.82	-5.49	0.001048	0.008582	-0.76
258355_at	hypothetical protein predicted by ge	---	AT3G14330	1.89	0.92	5.49	0.001048	0.008582	-0.76
260383_s_a	putative 60S ribosomal protein L6 s	---	AT1G74050	1.84	0.88	5.49	0.00105	0.008589	-0.76
260430_at	putative zinc finger protein similar to	---	AT1G68200	-1.45	-0.54	-5.49	0.00105	0.008589	-0.76
252737_at	putative protein KIAA0274 protein,	---	AT3G43220	-1.49	-0.58	-5.49	0.001051	0.008595	-0.77
255077_at	putative protein	---	AT4G09150	-2.00	-1.00	-5.48	0.001056	0.00863	-0.77
267515_at	putative PCF2-like DNA binding pro	---	AT2G45680	-1.70	-0.77	-5.48	0.001057	0.008639	-0.77
251860_at	Gluthatione reductase, chloroplast	GR	AT3G54660	-1.42	-0.50	-5.48	0.001059	0.008651	-0.77
256785_at	unknown protein ;supported by full-	PRA8	AT3G13720	-1.86	-0.89	-5.48	0.00106	0.008653	-0.77
259225_at	putative small nuclear ribonucleopro	---	AT3G07590	3.08	1.62	5.48	0.001061	0.008657	-0.78
251888_at	putative protein GTP-binding regula	---	AT3G54190	1.45	0.54	5.48	0.001062	0.008662	-0.78
266728_at	similar to late embryogenesis abun	---	AT2G03140	1.53	0.61	5.48	0.001062	0.008663	-0.78
265968_at	putative protein translocase ; supp	ATTIM17-2	AT2G37410	1.98	0.98	5.47	0.001063	0.008666	-0.78
256140_at	hypothetical protein contains simila	---	AT1G48650	1.92	0.94	5.47	0.001063	0.008666	-0.78
249016_at	putative protein contains similarity t	REV1	AT5G44750	1.76	0.82	5.47	0.001065	0.008672	-0.78
253777_at	SOF1 protein-like protein SOF1 (inv	---	AT4G28450	3.00	1.58	5.47	0.001065	0.008672	-0.78
251309_at	putative protein carbonyl reductase	---	AT3G61220	1.67	0.74	5.47	0.001066	0.008672	-0.78
261854_at	unknown protein	---	AT1G50670	-1.41	-0.50	-5.47	0.001066	0.008672	-0.78
246028_at	AKIN beta1 ; supported by full-leng	---	AT5G21170	-2.00	-1.00	-5.47	0.001067	0.008678	-0.78
265078_at	hypothetical protein contains simila	ECT4	AT1G55500	2.30	1.20	5.47	0.001067	0.008678	-0.78
250192_at	pescadillo - like protein embryonic	---	AT5G14520	2.00	1.00	5.47	0.001068	0.008678	-0.78
252095_at	epoxide hydrolase-like protein epo	---	AT3G51000	1.72	0.78	5.47	0.001071	0.008697	-0.79

263419_at	putative protein kinase contains a p	---	AT2G17220	1.90	0.92	5.47	0.001072	0.008701	-0.79
265735_at	putative aldolase ;supported by full	---	AT2G01140	1.92	0.94	5.47	0.001072	0.008702	-0.79
247249_at	putative protein similar to unknown	---	AT5G64670	1.86	0.90	5.46	0.001074	0.008709	-0.79
246196_at	hypothetical protein ;supported by f	---	AT4G37090	1.87	0.91	5.46	0.001074	0.00871	-0.79
265398_at	unknown protein	ATMAK10	AT2G11000	1.55	0.64	5.46	0.001075	0.008716	-0.79
251143_at	putative protein SqdX protein, Syn	SQD2	AT5G01220	2.37	1.24	5.46	0.001078	0.008732	-0.79
251617_at	putative protein hypothetical protei	---	AT3G58000	-1.49	-0.58	-5.46	0.001078	0.008732	-0.79
253668_at	snRNP Sm protein F - like Sm pro	RUXF	AT4G30220	1.66	0.73	5.46	0.00108	0.008741	-0.79
245002_at	PSII D2 protein	---	---	-1.72	-0.78	-5.46	0.00108	0.008743	-0.80
247398_at	putative protein predicted protein, A	---	AT5G62950	1.67	0.74	5.46	0.001082	0.008752	-0.80
253397_at	putative protein kinase protein kina	---	AT4G32710	-1.46	-0.54	-5.46	0.001082	0.008752	-0.80
255887_at	hypothetical protein contains Pfam	---	AT1G20370	1.45	0.54	5.46	0.001083	0.008752	-0.80
261973_at	hypothetical protein predicted by ge	---	AT1G64610	1.93	0.95	5.46	0.001083	0.008752	-0.80
267013_at	putative protein kinase contains a p	CCR2	AT2G39180	-1.57	-0.65	-5.46	0.001083	0.008755	-0.80
259912_at	hypothetical protein	iqd8	AT1G72670	-1.69	-0.76	-5.46	0.001084	0.008755	-0.80
260729_at	regulatory protein, putative contain	KU80	AT1G48050	1.44	0.53	5.45	0.001085	0.008763	-0.80
257515_at	zinc finger protein, putative similar	DOT5	AT1G13290	-1.49	-0.57	-5.45	0.001088	0.008777	-0.80
258478_at	unknown protein	---	AT3G02710	1.54	0.62	5.45	0.001088	0.008777	-0.80
265987_at	unknown protein	---	AT2G24240	1.98	0.99	5.45	0.00109	0.008784	-0.80
251391_at	putative protein weak homology wi	---	AT3G60910	1.68	0.75	5.45	0.00109	0.008784	-0.80
256853_at	hypothetical protein predicted by ge	---	AT3G18640	1.49	0.57	5.45	0.001092	0.0088	-0.81
253946_at	putative APG protein proline-rich p	---	AT4G26790	-1.99	-0.99	-5.45	0.001093	0.0088	-0.81
256568_at	hypothetical protein ;supported by	---	AT3G19520	1.51	0.59	5.45	0.001093	0.0088	-0.81
248237_at	receptor protein kinase-like protein	---	AT5G53890	1.73	0.79	5.45	0.001094	0.0088	-0.81
263621_at	putative DNA-directed RNA polyme	NRPB6B	AT2G04630	1.58	0.66	5.45	0.001094	0.0088	-0.81
265474_at	Expressed protein ; supported by cl	---	AT2G15690	2.09	1.07	5.45	0.001094	0.0088	-0.81
253679_at	cytidine deaminase 6 (CDA6)	---	AT4G29610	-2.88	-1.53	-5.45	0.001094	0.0088	-0.81
262534_at	unknown protein contains Pfam pro	SHA	AT1G17040	1.81	0.85	5.44	0.001096	0.008807	-0.81
255734_at	hypothetical protein similar to putati	---	AT1G25550	1.87	0.90	5.44	0.001097	0.008809	-0.81
264676_at	unknown protein EST gb|R64758 c	---	AT1G09870	1.45	0.53	5.44	0.001098	0.008816	-0.81
265344_at	unknown protein predicted by gene	---	AT2G22660	1.87	0.90	5.44	0.001101	0.008836	-0.82
245695_at	rec - like protein	---	AT5G04270	-1.57	-0.65	-5.44	0.001105	0.008857	-0.82
265325_at	putative integral membrane protein	---	AT2G18240	1.75	0.80	5.44	0.001105	0.008857	-0.82
261268_at	unknown protein similar to 50S ribo	---	AT1G26740	1.65	0.72	5.44	0.001105	0.008857	-0.82
248974_at	disease resistance protein-like	---	AT5G45060	1.50	0.59	5.43	0.001107	0.008868	-0.82

249067_at	putative protein similar to unknown	---	AT5G43960	1.55	0.63	5.43	0.001108	0.008871	-0.82
248625_at	3-keto-acyl-CoA thiolase 2 (gb|AAC	PKT2	AT5G48880	-2.43	-1.28	-5.43	0.001109	0.008876	-0.82
256397_at	putative dual-specificity protein pho	MKP2	AT3G06110	1.50	0.58	5.43	0.001109	0.008876	-0.82
255020_at	isoleucine-tRNA ligase - like protei	---	AT4G10320	1.40	0.48	5.43	0.00111	0.008876	-0.83
258323_at	unknown protein similar to putative	---	AT3G22750	1.84	0.88	5.43	0.00111	0.008876	-0.83
245486_x_a	glycine-rich protein homolog	---	AT4G16240	-1.54	-0.62	-5.43	0.001112	0.008881	-0.83
246034_at	putative protein FH protein interact	---	AT5G08350	-2.11	-1.07	-5.43	0.001112	0.008881	-0.83
264701_at	hypothetical protein similar to hypot	---	AT1G70160	1.59	0.67	5.43	0.001112	0.008881	-0.83
267219_at	putative transport protein ;supporte	---	AT2G02590	-1.82	-0.87	-5.43	0.001113	0.008886	-0.83
253143_at	putative protein	---	AT4G35530	1.72	0.78	5.43	0.001115	0.008897	-0.83
259193_at	putative thylakoid lumen rotamase	CYP38	AT3G01480	-1.87	-0.91	-5.43	0.001116	0.008897	-0.83
256117_at	unknown protein ; supported by cDI	---	AT1G16840	-1.46	-0.55	-5.43	0.001117	0.008901	-0.83
257444_at	hypothetical protein predicted by ge	---	AT2G12550	1.68	0.75	5.43	0.001117	0.008901	-0.83
252615_at	serine/proline-rich protein	---	AT3G45230	-1.98	-0.99	-5.43	0.001117	0.008901	-0.83
258568_at	unknown protein contains Pfam pro	---	AT3G04470	-1.54	-0.62	-5.43	0.001118	0.008905	-0.83
253733_at	hypothetical protein	ATMND1	AT4G29170	1.66	0.73	5.42	0.00112	0.008914	-0.83
264205_at	hypothetical protein identical to hyp	---	AT1G22790	1.46	0.54	5.42	0.00112	0.008917	-0.84
260656_at	hypothetical protein predicted by ge	---	AT1G19380	-5.21	-2.38	-5.42	0.001122	0.00892	-0.84
266359_at	putative phospholipid cytidylyltransf	CCT1	AT2G32260	1.49	0.57	5.42	0.001122	0.00892	-0.84
266661_at	TINY-like AP2 domain transcription	---	AT2G25820	-1.66	-0.73	-5.42	0.001122	0.00892	-0.84
264183_at	unknown protein	CLV2	AT1G65380	1.61	0.69	5.42	0.001123	0.008927	-0.84
262737_at	hypothetical protein	SRD2	AT1G28560	1.65	0.72	5.42	0.001125	0.008931	-0.84
262173_at	betaine aldehyde dehydrogenase,	ALDH10A8	AT1G74920	-1.59	-0.67	-5.42	0.001125	0.008931	-0.84
250353_at	putative protein predicted proteins,	---	AT5G11630	1.64	0.71	5.42	0.001125	0.008931	-0.84
250381_at	putative protein various predicted p	---	AT5G11610	2.26	1.18	5.42	0.001126	0.008935	-0.84
257835_at	cytochrome P450 monooxygenase	CYP82G1	AT3G25180	-3.83	-1.94	-5.42	0.001127	0.008935	-0.84
251174_at	putative protein latex protein allerg	PLP9	AT3G63200	-2.45	-1.29	-5.42	0.001128	0.00894	-0.84
255089_at	nucleoside-diphosphate kinase ;su	NDPK1	AT4G09320	1.88	0.91	5.42	0.001128	0.00894	-0.84
250470_at	(3R)-hydroxymyristoyl-[acyl carrier	---	AT5G10160	-1.71	-0.77	-5.42	0.001128	0.00894	-0.84
265724_at	hypothetical protein predicted by ge	OFP16	AT2G32100	-1.94	-0.96	-5.42	0.001129	0.008943	-0.84
252649_at	putative protein histone deacetylas	HDA9	AT3G44680	1.43	0.51	5.41	0.00113	0.008946	-0.84
262112_at	unknown protein ;supported by full-	---	AT1G02870	1.80	0.85	5.41	0.00113	0.008946	-0.84
261377_at	unknown protein ;supported by full-	---	AT1G18850	2.50	1.32	5.41	0.001132	0.008953	-0.85
253222_at	chalcone synthase - like protein ch	---	AT4G34850	-1.41	-0.49	-5.41	0.001132	0.008953	-0.85
264175_at	unknown protein Similar to rice cha	---	AT1G02050	1.70	0.76	5.41	0.001132	0.008953	-0.85

255527_at	putative protein	---	AT4G02360	-5.20	-2.38	-5.41	0.001134	0.008953	-0.85
260245_at	putative RNA-binding protein simila	GR-RBP5	AT1G74230	1.44	0.52	5.41	0.001134	0.008953	-0.85
249014_at	putative protein similar to unknown	---	AT5G44710	1.71	0.78	5.41	0.001134	0.008953	-0.85
257712_at	hypothetical protein predicted by ge	---	AT3G27420	-1.40	-0.49	-5.41	0.001135	0.008958	-0.85
259782_at	unknown protein	---	AT1G29680	-1.44	-0.52	-5.41	0.001138	0.008972	-0.85
253876_at	COP1-interacting protein 7 (CIP7)	CIP7	AT4G27430	-1.99	-1.00	-5.41	0.001138	0.008972	-0.85
255872_at	putative protein kinase contains a p	SIP4	AT2G30360	-3.03	-1.60	-5.41	0.001139	0.008976	-0.85
249164_at	U2 snRNP auxiliary factor, small su	U2AF35B	AT5G42820	1.66	0.73	5.41	0.00114	0.00898	-0.85
258814_at	putative short-chain type dehydroge	---	AT3G03980	-1.63	-0.71	-5.41	0.001141	0.008987	-0.86
245144_at	putative methionine aminopeptidase	MAP1A	AT2G45240	1.58	0.66	5.40	0.001144	0.009003	-0.86
262064_at	elongation factor, putative similar t	LOS1	AT1G56070	1.63	0.71	5.40	0.001144	0.009003	-0.86
265539_at	unknown protein	---	AT2G15830	3.04	1.60	5.40	0.001146	0.009014	-0.86
264027_at	putative AAA-type ATPase similar t	CDC48B	AT2G03670	1.79	0.84	5.40	0.00115	0.009042	-0.86
261392_at	hypothetical protein predicted by ge	---	AT1G79780	-1.46	-0.55	-5.40	0.001151	0.009044	-0.86
260665_at	unknown protein ;supported by full-	---	AT1G19360	1.59	0.67	5.40	0.001152	0.009044	-0.87
247325_at	putative protein contains similarity t	SC35	AT5G64200	1.47	0.56	5.40	0.001152	0.009044	-0.87
250518_at	Expressed protein ; supported by cl	---	AT5G08139	1.44	0.53	5.40	0.001152	0.009044	-0.87
262313_at	unknown protein ;supported by full-	---	AT1G70900	1.88	0.91	5.40	0.001153	0.009051	-0.87
264908_at	unknown protein	---	AT2G17440	1.53	0.62	5.39	0.001157	0.009057	-0.87
258134_at	rubisco expression protein, putative	---	AT3G24530	-1.84	-0.88	-5.39	0.001157	0.009057	-0.87
260545_at	putative glutathione peroxidase ;su	ATGPX3	AT2G43350	1.58	0.66	5.39	0.001157	0.009057	-0.87
248006_at	unknown protein	HAP8	AT5G56250	-1.52	-0.61	-5.39	0.001157	0.009057	-0.87
255087_at	putative protein proteins of this bac	---	AT4G09340	1.46	0.55	5.39	0.001158	0.009057	-0.87
250546_at	nhp2-like protein high mobility grou	---	AT5G08180	2.39	1.26	5.39	0.001158	0.009057	-0.87
249318_at	uridine kinase-like protein	AtUK/UPR	AT5G40870	1.53	0.62	5.39	0.001161	0.009078	-0.87
259763_at	unknown protein similar to GB:AAB	---	AT1G77630	-1.94	-0.96	-5.39	0.001161	0.009078	-0.87
248386_at	DNA-directed RNA polymerase II su	NRPB6A	AT5G51940	1.57	0.65	5.39	0.001162	0.009081	-0.88
263251_at	unknown protein ; supported by cD	---	AT2G31410	2.38	1.25	5.39	0.001163	0.009083	-0.88
258883_at	unknown protein predicted by gens	---	AT3G09970	1.61	0.69	5.39	0.001164	0.009083	-0.88
261782_at	unknown protein	---	AT1G76110	-1.74	-0.80	-5.39	0.001165	0.009087	-0.88
267096_at	unknown protein ; supported by cD	---	AT2G38180	2.30	1.20	5.38	0.001168	0.009102	-0.88
250666_at	SPF1-like protein SPF1 protein - Ip	WRKY26	AT5G07100	2.66	1.41	5.38	0.001168	0.009102	-0.88
249235_at	beta-1,3-glucanase-like protein ;su	BG_PPAP	AT5G42100	-1.38	-0.46	-5.38	0.001169	0.009111	-0.88
267378_at	hypothetical protein	---	AT2G26200	1.44	0.52	5.38	0.001169	0.009111	-0.88
258253_at	putative short chain alcohol dehydr	---	AT3G26760	-1.48	-0.56	-5.38	0.00117	0.009114	-0.88

259981_at	unknown protein ; supported by ful	---	AT1G76450	-1.67	-0.74	-5.38	0.001171	0.009118	-0.88
251536_at	ketol-acid reductoisomerase ; supp	---	AT3G58610	1.58	0.66	5.38	0.001173	0.009124	-0.89
258093_at	unknown protein ; supported by cD	---	AT3G14750	1.67	0.74	5.38	0.001173	0.009124	-0.89
247558_at	histone deacetylase - like histone d	HDA05	AT5G61060	1.54	0.62	5.38	0.001174	0.009124	-0.89
245010_at	NADH dehydrogenase subunit	---	---	-1.64	-0.72	-5.38	0.001174	0.009124	-0.89
255116_at	receptor protein kinase-like protein	---	AT4G08850	1.84	0.88	5.38	0.001174	0.009124	-0.89
258545_at	putative GTPase contains Pfam pro	---	AT3G07050	2.06	1.04	5.38	0.001175	0.009126	-0.89
258295_at	unknown protein ;supported by full	---	AT3G23400	-1.91	-0.93	-5.38	0.001177	0.009136	-0.89
262807_at	unknown protein strong similarity to	---	AT1G11740	-1.75	-0.81	-5.38	0.001178	0.009144	-0.89
256268_at	retinoblastoma-related protein, put	RBR1	AT3G12280	1.75	0.80	5.37	0.00118	0.009154	-0.89
252969_at	putative protein vsf-1 protein, Lyco	---	AT4G38900	-1.49	-0.58	-5.37	0.001181	0.009163	-0.89
246566_at	oligopeptide transporter -like protei	---	AT5G14940	2.25	1.17	5.37	0.001182	0.009164	-0.89
265825_at	ubiquitin-like (UBQ7), putative simi	UBQ7	AT2G35635	1.58	0.66	5.37	0.001186	0.009189	-0.90
258988_at	unknown protein similar to unknown	---	AT3G08890	-1.56	-0.64	-5.37	0.001186	0.009189	-0.90
264299_s_a	hypothetical protein predicted by ge	---	AT1G78850	-2.76	-1.46	-5.37	0.001187	0.009189	-0.90
251124_s_a	laccase -like protein lac110 laccase	LAC8	AT5G01040	-7.86	-2.97	-5.37	0.001187	0.009189	-0.90
246041_at	phospholipase - like protein various	---	AT5G19290	-1.42	-0.51	-5.37	0.001189	0.009201	-0.90
244944_s_a	ribosomal protein L16	---	---	1.86	0.90	5.36	0.001192	0.00922	-0.90
267338_at	26S proteasome regulatory subunit	EIF2	AT2G39990	1.64	0.71	5.36	0.001193	0.009224	-0.90
246976_s_a	putative protein UBIQUINONE BIO	---	AT5G24810	-1.98	-0.99	-5.36	0.001193	0.009224	-0.90
253578_at	putative protein diacylglycerol kina	ATDGK7	AT4G30340	-1.91	-0.93	-5.36	0.001194	0.009224	-0.90
258260_at	unknown protein ; supported by cD	---	AT3G26850	1.46	0.55	5.36	0.001195	0.009229	-0.91
253640_at	putative protein ;supported by full-l	---	AT4G30630	1.45	0.53	5.36	0.001196	0.009233	-0.91
260806_at	RNA recognition motif-containing pr	---	AT1G78260	-1.41	-0.50	-5.36	0.001197	0.009233	-0.91
252130_at	putative protein 1 photosystem II o	PSBO2	AT3G50820	-1.54	-0.63	-5.36	0.001197	0.009233	-0.91
249741_at	putative protein contains similarity t	APRR5	AT5G24470	1.39	0.47	5.36	0.001197	0.009233	-0.91
257072_at	myrosinase-associated protein, put	---	AT3G14220	-2.31	-1.21	-5.36	0.001197	0.009233	-0.91
258919_at	Expressed protein ; supported by fu	---	AT3G10525	-1.75	-0.80	-5.36	0.001198	0.009233	-0.91
259768_at	expressed protein supported by cD	COR314-TI	AT1G29390	-1.39	-0.47	-5.36	0.001198	0.009233	-0.91
250866_at	Expressed protein ; supported by fu	---	AT5G03905	1.57	0.65	5.36	0.001199	0.009237	-0.91
261655_at	hypothetical protein predicted by ge	---	AT1G01940	1.83	0.87	5.36	0.001199	0.009237	-0.91
248659_at	cyclin C-like protein	---	AT5G48640	1.63	0.71	5.36	0.001201	0.009238	-0.91
257794_at	hypothetical protein predicted by ge	---	AT3G27050	-1.75	-0.81	-5.36	0.001201	0.009238	-0.91
264327_at	putative translation initiation factor	EIF2 GAMM	AT1G04170	1.48	0.56	5.36	0.001201	0.009238	-0.91
266818_at	unknown protein	HUB1	AT2G44950	1.66	0.73	5.35	0.001207	0.009282	-0.92

247208_at	nodulin-like ;supported by full-lengt	---	AT5G64870	-1.60	-0.68	-5.35	0.001208	0.009285	-0.92
256524_at	glutamine synthetase, putative sim	ATGSR2	AT1G66200	1.58	0.66	5.35	0.001209	0.009285	-0.92
253889_at	forever young gene (FEY)	FEY	AT4G27760	-1.44	-0.53	-5.35	0.00121	0.009286	-0.92
246117_at	CAF-like protein CAF protein - Ara	DCL4	AT5G20320	1.89	0.92	5.35	0.00121	0.009286	-0.92
257271_at	Expressed protein ; supported by fu	---	AT3G28007	-3.90	-1.96	-5.35	0.00121	0.009286	-0.92
253909_at	putative protein LEDI-3 protein, Lit	---	AT4G27270	-1.67	-0.74	-5.35	0.001213	0.009305	-0.92
261154_at	unknown protein ;supported by full-	---	AT1G04970	1.76	0.82	5.35	0.001215	0.009316	-0.92
262539_at	unknown protein Location of est 13	---	AT1G17200	-1.86	-0.90	-5.34	0.001218	0.00933	-0.93
256803_at	cytochrome P450, putative similar	CYP705A3	AT3G20960	1.45	0.54	5.34	0.001218	0.00933	-0.93
265332_at	hypothetical protein predicted by ge	---	AT2G18410	1.66	0.73	5.34	0.001218	0.00933	-0.93
261585_at	NAC domain protein, putative simil	ANAC001	AT1G01010	2.05	1.04	5.34	0.001219	0.009332	-0.93
251688_at	putative protein hypothetical protei	---	AT3G56480	-2.55	-1.35	-5.34	0.00122	0.009334	-0.93
253247_at	Homeodomain - like protein similar	BLH6	AT4G34610	-2.11	-1.08	-5.34	0.00122	0.009334	-0.93
256118_at	hypothetical protein predicted by ge	KU70	AT1G16970	1.71	0.78	5.34	0.001222	0.009345	-0.93
251647_at	protein kinase - like protein wall-as	---	AT3G57770	1.65	0.73	5.34	0.001223	0.009345	-0.93
262853_at	unknown protein Location of ESTs	---	AT1G20890	1.56	0.64	5.34	0.001226	0.009363	-0.93
258910_at	putative RNA helicase similar to RI	---	AT3G06480	1.47	0.56	5.34	0.001227	0.009363	-0.93
254831_at	Ribosomal protein L7Ae -like variou	---	AT4G12600	2.54	1.34	5.34	0.001227	0.009366	-0.93
252075_at	putative protein saposin precursor	---	AT3G51730	1.80	0.85	5.34	0.001228	0.009366	-0.93
247357_at	receptor-like protein kinase ; suppo	---	AT5G63710	1.55	0.64	5.33	0.001229	0.009366	-0.94
253479_at	ferredoxin-NADP+ reductase - like	---	AT4G32360	1.45	0.54	5.33	0.001229	0.009366	-0.94
260291_at	putative protein kinase similar to MA	YDA	AT1G63700	-1.40	-0.48	-5.33	0.001232	0.009381	-0.94
248385_at	putative protein contains similarity t	---	AT5G51910	-1.69	-0.76	-5.33	0.001232	0.009381	-0.94
258649_at	putative transitional endoplasmic re	CDC48	AT3G09840	1.41	0.49	5.33	0.001232	0.009381	-0.94
261725_at	small nuclear ribonucleoprotein, pu	SmD3	AT1G76300	1.79	0.84	5.33	0.001234	0.009389	-0.94
262117_at	ribosomal protein L19, putative sim	emb2386	AT1G02780	1.71	0.77	5.33	0.001234	0.009389	-0.94
261019_at	unknown protein ; supported by cDI	---	AT1G26470	1.58	0.66	5.33	0.001236	0.009398	-0.94
258742_at	hypothetical protein predicted by ge	---	AT3G05800	-2.31	-1.21	-5.33	0.001238	0.009412	-0.94
245168_at	3-ketoacyl-CoA thiolase ;supported	PKT3	AT2G33150	1.69	0.76	5.33	0.00124	0.009419	-0.95
248798_at	putative protein contains similarity t	---	AT5G47190	-1.57	-0.65	-5.33	0.00124	0.009419	-0.95
257988_at	unknown protein ; supported by cD	---	AT3G20870	1.54	0.62	5.33	0.00124	0.009419	-0.95
266116_at	unknown protein ;supported by full-	TOM3	AT2G02180	-1.76	-0.82	-5.32	0.001243	0.009433	-0.95
247709_at	D-xylose-H+ symporter - like protei	---	AT5G59250	-1.69	-0.76	-5.32	0.001244	0.009436	-0.95
245145_at	putative dihydrodipicolinate synthas	DHDPS2	AT2G45440	2.07	1.05	5.32	0.001246	0.009452	-0.95
245693_at	thioredoxin - like protein	WCRKC2	AT5G04260	1.60	0.68	5.32	0.001247	0.009453	-0.95

265702_at	putative purple acid phosphatase c	PAP9	AT2G03450	1.60	0.68	5.32	0.001248	0.009454	-0.95
263995_at	putative MADS-box protein	SVP	AT2G22540	1.67	0.74	5.32	0.00125	0.00947	-0.95
247405_at	Arac10 ; supported by cDNA: gi_3	ARAC10	AT5G62880	-1.56	-0.65	-5.32	0.001251	0.009475	-0.96
257883_at	calmodulin-binding protein, putativ	---	AT3G16940	1.75	0.80	5.32	0.001252	0.009479	-0.96
265953_at	unknown protein	---	AT2G37478	1.49	0.57	5.32	0.001253	0.009479	-0.96
266916_at	hypothetical protein predicted by ge	---	AT2G45860	1.95	0.96	5.32	0.001254	0.00949	-0.96
258132_at	protein kinase, putative similar to G	ATPERK1	AT3G24550	-1.87	-0.90	-5.31	0.001255	0.009493	-0.96
267134_at	putative protein kinase contains a p	---	AT2G23450	1.38	0.46	5.31	0.001256	0.009493	-0.96
266109_at	putative mitochondrial carrier protei	---	AT2G37890	2.29	1.19	5.31	0.001257	0.009503	-0.96
257982_at	unknown protein similar to TYPE II	ATTOP6B	AT3G20780	-1.71	-0.77	-5.31	0.00126	0.009516	-0.96
257680_at	aspartate carbamoyltransferase pr	---	AT3G20330	1.75	0.81	5.31	0.00126	0.009516	-0.96
252056_at	ubiquitin extension protein (UBQ1)	UBQ1	AT3G52590	1.50	0.58	5.31	0.00126	0.009516	-0.96
266592_at	putative fatty acid desaturase/cytoc	---	AT2G46210	-1.50	-0.58	-5.31	0.001261	0.009518	-0.96
256747_at	unknown protein similar to CW14 G	---	AT3G29180	1.59	0.67	5.31	0.001264	0.009534	-0.97
258060_at	protein phosphatase 2A regulatory	ATB' DELT	AT3G26030	-1.44	-0.53	-5.31	0.001264	0.009538	-0.97
266767_at	Expressed protein ; supported by fu	---	AT2G46910	-1.75	-0.80	-5.31	0.001265	0.00954	-0.97
248403_at	arginine-aspartate-rich RNA bindin	---	AT5G51410	1.54	0.62	5.31	0.001266	0.00954	-0.97
252647_at	protein-tyrosine-phosphatase-like p	---	AT3G44620	-1.99	-0.99	-5.30	0.001269	0.009559	-0.97
251706_at	nodulin-like protein MtN21 - Medic	---	AT3G56620	1.64	0.72	5.30	0.00127	0.009566	-0.97
251598_at	AP2 transcription factor - like prote	---	AT3G57600	-1.46	-0.54	-5.30	0.001274	0.009588	-0.97
250671_at	transcription factor HBP-1b homolo	AHBP-1B	AT5G06950	1.47	0.56	5.30	0.001274	0.009588	-0.98
255636_at	homeodomain protein AHDP ; sup	ANL2	AT4G00730	1.65	0.72	5.30	0.001275	0.009595	-0.98
252464_at	RNA-binding protein-like protein va	---	AT3G47160	1.75	0.81	5.30	0.001276	0.009596	-0.98
248172_at	unknown protein ;supported by full	---	AT5G54660	2.17	1.12	5.30	0.001278	0.009609	-0.98
245781_at	S-ribonuclease binding protein SB	SBP1	AT1G45976	1.66	0.73	5.30	0.001279	0.009611	-0.98
245052_at	putative pectinesterase	---	AT2G26440	-1.72	-0.78	-5.29	0.001282	0.009628	-0.98
247268_at	putative protein contains similarity t	---	AT5G64080	-1.72	-0.79	-5.29	0.001282	0.00963	-0.98
250851_at	putative protein rngB protein, Dicty	---	AT5G04420	-1.67	-0.74	-5.29	0.001283	0.00963	-0.98
251356_at	putative protein hypothetical protei	AtPP2-A13	AT3G61060	1.68	0.74	5.29	0.001286	0.00965	-0.99
251837_s_a	spliceosomal - like protein spliceos	---	AT3G55200	1.66	0.73	5.29	0.001288	0.009661	-0.99
247627_at	cysteine proteinase AALP identical	AALP	AT5G60360	1.45	0.53	5.29	0.001289	0.009661	-0.99
254834_at	flavonoid 3,5-hydroxylase -like pro	CYP706A4	AT4G12300	1.73	0.79	5.29	0.001289	0.009661	-0.99
258934_at	putative RecA protein similar to Re	RECA3	AT3G10140	1.59	0.67	5.29	0.001289	0.009661	-0.99
260664_at	myb-related protein, putative simil	ATRL5	AT1G19510	2.45	1.29	5.29	0.00129	0.009661	-0.99
247156_at	lysosomal Pro-X carboxypeptidase	---	AT5G65760	1.55	0.63	5.29	0.001291	0.009661	-0.99

262888_at	RNA-directed RNA polymerase, pu	RDR1	AT1G14790	2.79	1.48	5.28	0.0013	0.009718	-1.00
256715_at	hypothetical protein predicted by g	MEE18	AT2G34090	-1.90	-0.93	-5.28	0.001301	0.009723	-1.00
251225_at	putative protein glycosyl transferas	GATL7	AT3G62660	-1.83	-0.87	-5.28	0.001303	0.009734	-1.00
252353_at	putative protein KIAA0226 gene pr	---	AT3G48200	-1.54	-0.63	-5.28	0.001304	0.009737	-1.00
245112_at	glycerol-3-phosphate dehydrogenas	GPDHC1	AT2G41540	-3.39	-1.76	-5.28	0.001304	0.009737	-1.00
261559_at	LIM domain protein, putative simila	---	AT1G01780	1.60	0.68	5.28	0.001306	0.009737	-1.00
249360_at	putative protein KIAA0409 protein,	---	AT5G40530	1.51	0.59	5.28	0.001307	0.009737	-1.00
265419_at	putative secretory carrier-associate	---	AT2G20840	-1.67	-0.74	-5.28	0.001307	0.009737	-1.00
246925_at	cytochrome P450 71B1 - like prote	CYP71B14	AT5G25180	1.48	0.57	5.28	0.001307	0.009737	-1.00
261569_at	DNA-binding protein, putative simil	LHY	AT1G01060	-1.62	-0.70	-5.28	0.001308	0.009742	-1.00
257294_at	non-phototropic hypocotyl protein,	---	AT3G15570	-1.95	-0.96	-5.27	0.001309	0.009745	-1.01
263922_s_a	putative pyruvate kinase ;supporte	---	AT2G36580	1.44	0.53	5.27	0.001309	0.009745	-1.01
255440_at	predicted protein of unknown functi	---	AT4G02530	-1.64	-0.72	-5.27	0.00131	0.009748	-1.01
247865_at	Expressed protein ; supported by fu	---	AT5G57815	1.48	0.56	5.27	0.001313	0.009757	-1.01
255821_at	putative initiator tRNA phosphoribos	---	AT2G40570	1.54	0.63	5.27	0.001313	0.009757	-1.01
255041_at	putative protein hypothetical protei	---	AT4G09620	1.66	0.73	5.27	0.001314	0.00976	-1.01
258966_at	putative DNA gyrase subunit A simi	---	AT3G10690	2.19	1.13	5.27	0.001314	0.00976	-1.01
267101_at	putative peroxidase	---	AT2G41480	1.80	0.85	5.27	0.001315	0.00976	-1.01
265742_at	putative ribose 5-phosphate isomer	---	AT2G01290	1.87	0.90	5.27	0.001316	0.009763	-1.01
266552_at	unknown protein ; supported by cDI	AGP16	AT2G46330	-1.86	-0.90	-5.27	0.001316	0.009765	-1.01
252271_s_a	putative protein CGI-141 protein- H	---	AT3G49420	1.42	0.51	5.27	0.001317	0.009768	-1.01
264323_at	putative dimethylaniline monooxyge	---	AT1G04180	-4.52	-2.18	-5.27	0.001318	0.009768	-1.01
245644_at	unknown protein similar to putative	---	AT1G25320	-1.64	-0.71	-5.27	0.001319	0.009772	-1.01
254073_at	splicing factor At-SRp40 contains E	RSP35	AT4G25500	1.56	0.64	5.27	0.001319	0.009772	-1.01
263785_at	unknown protein ; supported by cD	---	AT2G46390	1.56	0.64	5.26	0.001324	0.009802	-1.02
262558_at	Expressed protein ; supported by fu	---	AT1G31335	-1.59	-0.67	-5.26	0.001324	0.009802	-1.02
262531_at	putative leucine-rich receptor protei	---	AT1G17230	-1.78	-0.84	-5.26	0.001325	0.009802	-1.02
255557_at	hypothetical protein ; supported by	---	AT4G01990	1.96	0.97	5.26	0.001325	0.009802	-1.02
254002_at	steroid sulfotransferase - like prote	---	AT4G26280	-1.39	-0.48	-5.26	0.001326	0.009802	-1.02
256016_at	hypothetical protein predicted by ge	---	AT1G19240	1.63	0.71	5.26	0.001326	0.009802	-1.02
245730_at	unknown protein ;supported by full-	---	AT1G73470	-1.47	-0.56	-5.26	0.001326	0.009802	-1.02
258064_at	putative cytochrome P450 similar to	CYP72A14	AT3G14680	3.12	1.64	5.26	0.001327	0.009803	-1.02
253359_at	putative protein kinase protein kina	---	AT4G33080	1.67	0.74	5.26	0.001331	0.00982	-1.02
248594_at	unknown protein ; supported by full	---	AT5G49210	1.90	0.93	5.26	0.001331	0.00982	-1.02
264517_at	hypothetical protein predicted by ge	---	AT1G10120	-1.77	-0.82	-5.26	0.001333	0.009827	-1.02

266845_at	unknown protein	---	AT2G26110	-2.01	-1.01	-5.26	0.001334	0.009831	-1.03
248008_at	transcription factor NtWRKY4-like ;	WRKY2	AT5G56270	1.86	0.90	5.26	0.001335	0.009842	-1.03
265446_at	unknown protein ;supported by full-	---	AT2G37110	-1.54	-0.62	-5.26	0.001336	0.009842	-1.03
259047_at	unknown protein	DegP7	AT3G03380	1.40	0.49	5.25	0.001342	0.009884	-1.03
261230_at	beta tubulin 1, putative similar to G	TUB5	AT1G20010	-1.47	-0.56	-5.25	0.001345	0.009899	-1.03
245599_at	RING-H2 finger protein RHF1a	RHF1A	AT4G14220	1.93	0.95	5.25	0.001347	0.009911	-1.04
245084_at	putative MYB family transcription fa	AtMYB70	AT2G23290	-2.08	-1.06	-5.25	0.001348	0.009916	-1.04
260912_at	ATP-dependent Clp protease prote	CLPP5	AT1G02560	1.46	0.55	5.25	0.00135	0.009927	-1.04
245147_at	putative RAD51C-like DNA repair p	ATRAD51C	AT2G45280	2.25	1.17	5.24	0.001351	0.009931	-1.04
267523_at	unknown protein	---	AT2G30600	-1.57	-0.65	-5.24	0.001351	0.009931	-1.04
267620_at	putative beta-1,3-glucanase	---	AT2G39640	-1.46	-0.55	-5.24	0.001352	0.009931	-1.04
253954_at	putative aconitase Pumpkin mRNA	---	AT4G26970	1.96	0.97	5.24	0.001352	0.009931	-1.04
259984_at	putative RNA-binding protein conta	---	AT1G76460	1.61	0.69	5.24	0.001353	0.009935	-1.04
255743_at	unknown protein ; supported by cDI	---	AT1G25375	-1.53	-0.61	-5.24	0.001356	0.009953	-1.04
252925_at	ES43 like protein ES43 protein - ba	SHL1	AT4G39100	1.70	0.76	5.24	0.001357	0.009958	-1.04
253459_at	hypothetical protein	---	AT4G32080	-1.41	-0.49	-5.24	0.001358	0.009958	-1.04
250174_at	agp6	AGP6	AT5G14380	-1.45	-0.54	-5.24	0.001358	0.009958	-1.04
250829_at	disease resistance - like protein rp	ADR1-L2	AT5G04720	1.64	0.71	5.24	0.00136	0.009964	-1.05
260738_at	hypothetical protein predicted by ge	---	AT1G14990	1.48	0.56	5.24	0.00136	0.009964	-1.05
245986_at	protein kinase-like protein kinase 1	PBS1	AT5G13160	-1.42	-0.51	-5.24	0.00136	0.009964	-1.05
260548_at	biotin synthase (Bio B) ;supported	BIO2	AT2G43360	1.95	0.96	5.24	0.00136	0.009964	-1.05
254923_at	protein phosphatase type 1 PP1BG	TOPP7	AT4G11240	1.69	0.76	5.24	0.001363	0.009978	-1.05
252084_at	wax synthase-like protein wax synt	AtSAT1	AT3G51970	-1.68	-0.75	-5.24	0.001364	0.009979	-1.05
260895_at	unknown protein similar to unknown	---	AT1G29250	2.29	1.20	5.24	0.001364	0.00998	-1.05
249268_at	Expressed protein ; supported by cl	---	AT5G41685	1.46	0.55	5.23	0.001367	0.009994	-1.05
254080_at	fibrillarin 2 (AtFib2) identical to fibril	FIB2	AT4G25630	3.31	1.73	5.23	0.001369	0.010002	-1.05
245477_at	hypothetical protein	ARR2	AT4G16110	-1.54	-0.63	-5.23	0.001369	0.010002	-1.05
249529_at	putative protein predicted proteins,	---	AT5G38730	1.87	0.90	5.23	0.001369	0.010002	-1.05
245618_at	hypothetical protein	---	AT4G14510	1.64	0.71	5.23	0.001374	0.01003	-1.06
256149_at	zinc finger protein, putative similar	AtIDD7	AT1G55110	1.80	0.85	5.23	0.001374	0.010031	-1.06
249178_at	putative protein similar to unknown	SCP2	AT5G42890	1.47	0.56	5.23	0.001376	0.010043	-1.06
265816_s_a	putative elongation factor beta-1 ;s	---	AT1G30230	1.75	0.81	5.23	0.001377	0.010046	-1.06
262749_at	lipase, putative contains Pfam prof	---	AT1G28580	1.51	0.60	5.23	0.001379	0.010046	-1.06
250826_at	unknown protein ; supported by cDI	---	AT5G05220	-1.56	-0.64	-5.23	0.001379	0.010046	-1.06
257087_at	purple acid phosphatase, putative s	PAP18	AT3G20500	1.63	0.70	5.23	0.001379	0.010046	-1.06

255469_at	predicted OR23 protein of unknown	---	AT4G03030	1.55	0.63	5.22	0.001381	0.010056	-1.06
248985_at	GTP-binding protein-like; root hair d	---	AT5G45160	1.45	0.53	5.22	0.001382	0.010059	-1.06
266261_at	putative zinc finger protein ;suppor	---	AT2G27580	-1.39	-0.48	-5.22	0.001383	0.010059	-1.06
264803_at	hypothetical protein predicted by ge	---	AT1G08580	1.82	0.87	5.22	0.001383	0.010059	-1.06
245063_at	Expressed protein ; supported by fu	---	AT2G39795	2.69	1.43	5.22	0.001386	0.010074	-1.07
250928_at	putative protein	EIN2	AT5G03280	1.47	0.55	5.22	0.001386	0.010074	-1.07
258126_at	hypothetical protein predicted by ge	---	AT3G24490	1.58	0.66	5.22	0.001388	0.01008	-1.07
263136_at	trehalose-6-phosphate synthase, p	ATTPS1	AT1G78580	-1.53	-0.62	-5.22	0.00139	0.010093	-1.07
255933_at	membrane protein, putative similar	ATRBL6	AT1G12750	-1.95	-0.97	-5.22	0.001391	0.010093	-1.07
259895_at	unknown protein ;supported by full-	PFI	AT1G71440	-1.45	-0.53	-5.22	0.001391	0.010093	-1.07
247361_at	unknown protein ;supported by full-	---	AT5G63480	-1.72	-0.78	-5.22	0.001393	0.010107	-1.07
266561_at	unknown protein	---	AT2G23960	-1.43	-0.51	-5.22	0.001394	0.010107	-1.07
250554_at	unknown protein ;supported by full-	---	AT5G07900	1.52	0.61	5.21	0.001395	0.010107	-1.07
253019_at	putative protein crp1-hcf111 allele,	---	AT4G38010	1.49	0.58	5.21	0.001395	0.010107	-1.07
247885_at	putative protein similar to unknown	---	AT5G57830	-1.98	-0.99	-5.21	0.001398	0.010123	-1.08
246153_s_a	RAN1 small Ras-like GTP-binding r	RAN-1	AT5G20010	2.02	1.01	5.21	0.001399	0.010127	-1.08
255878_at	putative bZIP transcription factor co	---	AT2G40620	-1.88	-0.91	-5.21	0.001399	0.010127	-1.08
254087_at	brefeldin A-sensitive Golgi protein -	---	AT4G24840	-1.41	-0.50	-5.21	0.001403	0.010154	-1.08
256870_at	cytochrome P450, putative contain	CYP71B34	AT3G26300	2.19	1.13	5.21	0.001404	0.010158	-1.08
261566_at	unknown protein ;supported by full-	---	AT1G33230	-1.70	-0.77	-5.21	0.001409	0.010179	-1.08
261201_at	unknown protein ;supported by full-	---	AT1G12850	-1.54	-0.63	-5.20	0.00141	0.010179	-1.09
264248_at	hypothetical protein predicted by ge	---	AT1G78700	-1.78	-0.83	-5.20	0.00141	0.010179	-1.09
265149_at	unknown protein ; supported by full-	---	AT1G51400	-1.60	-0.67	-5.20	0.00141	0.010179	-1.09
246865_s_a	eukaryotic translation initiation fact	TIF3B1	AT5G25780	1.38	0.47	5.20	0.001411	0.010184	-1.09
259688_at	membrane protein, putative similar	ATRBL2	AT1G63120	-1.89	-0.92	-5.20	0.001412	0.010186	-1.09
246632_at	hypothetical protein similar to putati	---	AT1G29710	1.55	0.64	5.20	0.001415	0.010205	-1.09
255586_at	hypothetical protein ;supported by	MEE49	AT4G01560	2.05	1.03	5.20	0.001416	0.010205	-1.09
250769_at	putative protein similar to unknown	---	AT5G05680	2.12	1.08	5.20	0.001416	0.010206	-1.09
245242_at	chlorophyll a oxygenase identical to	CH1	AT1G44446	-1.73	-0.79	-5.20	0.001418	0.010213	-1.09
246447_at	putative protein SART-1 protein - H	DOT2	AT5G16780	1.58	0.66	5.20	0.001419	0.010213	-1.09
250891_at	fatty acid elongase - like protein K(	KCS19	AT5G04530	-1.67	-0.74	-5.20	0.001419	0.010213	-1.09
263930_at	hypothetical protein predicted by ge	---	AT2G36300	-1.52	-0.60	-5.20	0.001419	0.010213	-1.09
253812_at	putative wound induced protein wo	---	AT4G28240	-1.63	-0.70	-5.20	0.001421	0.01022	-1.09
259840_at	photosystem I subunit VI precursor	PSAH2	AT1G52230	-1.68	-0.75	-5.20	0.001423	0.01023	-1.10
258773_at	hypothetical protein predicted by ge	---	AT3G10730	-1.37	-0.46	-5.20	0.001423	0.01023	-1.10

262297_at	hypothetical protein similar to hypot	---	AT1G27600	-1.41	-0.50	-5.19	0.001425	0.010238	-1.10
259245_at	unknown protein predicted by gene	---	AT3G07660	1.62	0.69	5.19	0.001429	0.01026	-1.10
247549_at	putative transcription factor MYB28	MYB28	AT5G61420	1.97	0.98	5.19	0.00143	0.010263	-1.10
262770_at	hypothetical protein predicted by ge	---	AT1G13190	-1.92	-0.94	-5.19	0.00143	0.010263	-1.10
266228_at	unknown protein ; supported by ful	CXIP4	AT2G28910	1.64	0.71	5.19	0.001432	0.010265	-1.10
256873_at	cytochrome P450, putative contain	CYP71B34	AT3G26300	1.56	0.64	5.19	0.001434	0.010276	-1.10
253612_at	putative protein D-ribulokinase - Kl	---	AT4G30310	-1.47	-0.56	-5.19	0.001434	0.010276	-1.10
261628_at	hypothetical protein predicted by ge	---	AT1G50000	1.43	0.52	5.19	0.001435	0.010276	-1.11
248669_at	putative protein contains similarity t	---	AT5G48730	1.85	0.89	5.19	0.001436	0.010283	-1.11
254594_at	putative protein	---	AT4G18930	1.96	0.97	5.19	0.001437	0.010283	-1.11
256516_at	receptor protein kinase (TMK1), pu	TMK1	AT1G66150	-1.98	-0.99	-5.19	0.001438	0.010283	-1.11
260823_at	hypothetical protein predicted by g	DRIP1	AT1G06770	1.49	0.57	5.19	0.001438	0.010283	-1.11
259257_at	unknown protein ;supported by full-	---	AT3G07760	1.60	0.68	5.18	0.001443	0.010313	-1.11
259545_at	hypothetical protein ; supported by	AAE1	AT1G20560	1.53	0.62	5.18	0.001446	0.010326	-1.11
262055_at	unknown protein ; supported by full-	---	AT1G79970	1.45	0.53	5.18	0.001447	0.010326	-1.11
258379_at	putative decarboxilase similar to 5-	---	AT3G16700	-1.83	-0.87	-5.18	0.001447	0.010326	-1.11
255505_at	SAR1/GTP-binding secretory factor	ATSAR2	AT4G02080	1.50	0.59	5.18	0.001447	0.010327	-1.11
245639_at	unknown protein contains similarity	---	AT1G25260	2.11	1.08	5.18	0.001448	0.010327	-1.12
260968_at	hypothetical protein predicted by ge	---	AT1G12250	-1.63	-0.70	-5.18	0.001449	0.010327	-1.12
250355_at	putative protein predicted protein, A	---	AT5G11700	-1.63	-0.71	-5.18	0.001453	0.010353	-1.12
246120_at	tetratricopeptide repeat protein tetr	---	AT5G20360	1.65	0.72	5.18	0.001454	0.010353	-1.12
248255_at	ATP-dependent Clp protease ATP-	CLPX	AT5G53350	1.59	0.67	5.17	0.001455	0.010355	-1.12
260444_at	unknown protein ;supported by full-	---	AT1G68300	1.57	0.65	5.17	0.001455	0.010355	-1.12
257141_at	60S ribosomal protein L34, putative	---	AT3G28900	2.16	1.11	5.17	0.001456	0.010355	-1.12
267315_at	putative CCAAT-binding transcriptio	NF-YA4	AT2G34720	1.91	0.93	5.17	0.001456	0.010355	-1.12
257780_at	hypothetical protein predicted by ge	---	AT3G27100	1.64	0.71	5.17	0.001456	0.010355	-1.12
258656_at	putative Ras-like GTP-binding prote	ATRABE1E	AT3G09900	1.80	0.85	5.17	0.001458	0.01036	-1.12
255474_at	coded for by A. thaliana cDNA T75	---	AT4G02480	1.51	0.60	5.17	0.00146	0.010374	-1.12
253814_at	putative protein ;supported by full-l	---	AT4G28290	-1.91	-0.94	-5.17	0.00146	0.010374	-1.12
253782_at	hypothetical protein	---	AT4G28590	1.40	0.49	5.17	0.001463	0.010389	-1.13
258701_at	putative RNA helicase similar to RI	---	AT3G09720	2.04	1.03	5.17	0.001464	0.010397	-1.13
260283_at	hypothetical protein predicted by g	PTAC17	AT1G80480	1.39	0.47	5.17	0.001467	0.010412	-1.13
250421_at	putative protein	OCP3	AT5G11270	1.68	0.75	5.16	0.001471	0.010437	-1.13
256379_at	hypothetical protein predicted by ge	---	AT1G66840	1.80	0.85	5.16	0.001473	0.010445	-1.13
259735_at	Expressed protein ; supported by fu	---	AT1G64405	2.02	1.02	5.16	0.001476	0.010462	-1.14

247130_at	putative protein contains similarity t	---	AT5G66180	2.24	1.16	5.16	0.001477	0.010469	-1.14
266656_at	putative CCCH-type zinc finger prot	ATCTH	AT2G25900	-1.80	-0.85	-5.16	0.001478	0.010473	-1.14
259471_at	hypothetical protein contains simila	---	AT1G19040	-1.38	-0.47	-5.16	0.001482	0.010492	-1.14
255070_at	isoamylase-like protein probable is	ISA3	AT4G09020	1.45	0.54	5.16	0.001485	0.010513	-1.14
260441_at	unknown protein ;supported by full-	---	AT1G68260	-2.59	-1.37	-5.15	0.001488	0.010527	-1.14
256753_at	unknown protein contains Pfam pro	GHS1	AT3G27160	-1.66	-0.73	-5.15	0.001492	0.010549	-1.15
265530_at	12-oxophytodienoate-10,11-reduct	OPR3	AT2G06050	-3.09	-1.63	-5.15	0.001494	0.010563	-1.15
249700_at	40S ribosomal protein S3 ; support	---	AT5G35530	1.71	0.77	5.15	0.001495	0.010564	-1.15
266152_s_a	hypothetical protein predicted by ge	---	AT2G12050	-1.44	-0.52	-5.15	0.001495	0.010564	-1.15
258425_at	unknown protein	---	AT3G16760	-1.39	-0.47	-5.15	0.001497	0.010572	-1.15
251801_at	cytosolic triosephosphatisomerase	TPI	AT3G55440	-1.37	-0.46	-5.15	0.001498	0.010579	-1.15
259896_at	unknown protein ;supported by full-	---	AT1G71500	-1.56	-0.64	-5.15	0.0015	0.010585	-1.15
249466_at	ribosomal protein L5 - like ribosom	RPL5B	AT5G39740	1.93	0.95	5.15	0.001501	0.010589	-1.15
260566_at	cysteine synthase (cpACS1) ;supp	OASB	AT2G43750	-1.66	-0.73	-5.14	0.001502	0.010596	-1.16
254081_at	putative protein various predicted p	---	AT4G25660	-1.63	-0.70	-5.14	0.001503	0.010597	-1.16
260311_at	hypothetical protein predicted by ge	---	AT1G70570	1.38	0.47	5.14	0.001505	0.010608	-1.16
264946_at	hypothetical protein predicted by ge	---	AT1G77010	1.64	0.72	5.14	0.001508	0.010625	-1.16
262272_at	unknown protein ; supported by cDI	---	AT1G42440	1.39	0.48	5.14	0.001514	0.010658	-1.16
249553_at	receptor serine/threonine protein k	---	AT5G38260	1.79	0.84	5.14	0.001515	0.010663	-1.16
248103_at	ubiquitin-like protein SMT3-like ; su	SUMO2	AT5G55160	1.85	0.89	5.14	0.001516	0.010663	-1.16
261490_at	tumor suppressor, putative similar	SAC52	AT1G14320	1.75	0.81	5.14	0.001516	0.010663	-1.16
256513_at	unknown protein similar to phospho	SGR2	AT1G31480	1.47	0.56	5.14	0.001516	0.010663	-1.17
256404_at	unknown protein similar to far-red ir	FRS7	AT3G06250	1.76	0.81	5.13	0.00152	0.010683	-1.17
265141_at	hypothetical protein predicted by ge	---	AT1G51350	1.52	0.61	5.13	0.001522	0.01069	-1.17
250858_at	I-box binding factor - like protein I-b	---	AT5G04760	1.84	0.88	5.13	0.001522	0.010692	-1.17
247648_at	laccase - like protein laccase LAC2	LAC17	AT5G60020	-1.59	-0.67	-5.13	0.001523	0.010692	-1.17
247015_at	protease-like	---	AT5G66960	1.72	0.78	5.13	0.001524	0.010694	-1.17
265154_at	putative GTP-binding protein, ERG	---	AT1G30960	2.21	1.15	5.13	0.001525	0.010696	-1.17
260587_at	unknown protein ; supported by cDI	---	AT1G53210	-1.54	-0.62	-5.13	0.001525	0.010696	-1.17
266554_s_a	eukaryotic translation initiation facto	---	AT2G46280	1.67	0.74	5.13	0.001529	0.010721	-1.17
245123_at	unknown protein ; supported by cD	CAO	AT2G47450	-1.59	-0.67	-5.13	0.001531	0.010729	-1.18
264045_at	putative GTP cyclohydrolase	---	AT2G22450	1.46	0.55	5.13	0.001532	0.010731	-1.18
251327_at	prolyl aminopeptidase-like protein	---	AT3G61540	1.38	0.47	5.12	0.00154	0.010782	-1.18
245747_at	hypothetical protein predicted by ge	---	AT1G51100	1.77	0.83	5.12	0.001542	0.010797	-1.18
246436_at	putative protein cisplatin resistance	---	AT5G17440	1.42	0.50	5.12	0.001543	0.010799	-1.18

264878_at	unknown protein	---	AT2G17410	1.41	0.50	5.12	0.001544	0.010805	-1.19
246699_at	putative protein predicted proteins,	---	AT5G27990	1.80	0.85	5.12	0.001548	0.010815	-1.19
253867_at	putative protein tRNA nucleotidyltra	---	AT4G27490	1.97	0.98	5.12	0.001548	0.010815	-1.19
247013_at	putative protein strong similarity to (	BT4	AT5G67480	-2.07	-1.05	-5.12	0.001548	0.010815	-1.19
261864_s_a	10-formyltetrahydrofolate synthetas	THFS	AT1G50480	1.54	0.63	5.12	0.00155	0.010821	-1.19
257487_at	hypothetical protein predicted by ge	---	AT1G71850	2.17	1.12	5.12	0.00155	0.010821	-1.19
266237_at	DNA-directed RNA polymerase 14	ATRPC14	AT2G29540	1.93	0.95	5.11	0.001557	0.010862	-1.19
253717_at	putative protein putative suppresso	---	AT4G29440	-1.49	-0.58	-5.11	0.001558	0.01087	-1.20
255660_at	Expressed protein ; supported by fu	---	AT4G00755	1.58	0.66	5.11	0.001559	0.010872	-1.20
250716_at	sucrose transporter protein	ATSUC9	AT5G06170	-1.46	-0.54	-5.11	0.00156	0.010872	-1.20
253336_at	putative protein Caenorhabditis ele	EIF3K	AT4G33250	1.55	0.63	5.11	0.00156	0.010872	-1.20
248718_at	farnesyl diphosphate synthase pred	FPS1	AT5G47770	-1.93	-0.95	-5.11	0.001563	0.010891	-1.20
257816_at	glycosyl transferase, putative conta	QUA1	AT3G25140	-1.56	-0.65	-5.11	0.001564	0.010892	-1.20
258192_at	putative terpene synthase-related p	---	AT3G29110	-1.41	-0.49	-5.11	0.001565	0.010898	-1.20
251476_at	putative protein hypothetical protei	---	AT3G59670	1.99	0.99	5.11	0.001566	0.010898	-1.20
249811_at	unknown protein ;supported by full-	---	AT5G23760	1.42	0.51	5.11	0.001568	0.010908	-1.20
251037_at	putative protein oxysterol-binding p	UNE18	AT5G02100	1.88	0.91	5.10	0.00157	0.010914	-1.20
250609_at	peptide methionine sulfoxide reduct	PMSR3	AT5G07470	1.44	0.53	5.10	0.00157	0.010914	-1.20
261434_at	receptor-like serine/threonine kinas	---	AT1G07650	-1.85	-0.89	-5.10	0.001571	0.010917	-1.20
263351_at	hypothetical protein predicted by gr	---	AT2G22120	1.37	0.46	5.10	0.001571	0.010917	-1.20
245255_at	COP9 protein ; supported by cDNA	COP9	AT4G14110	1.52	0.61	5.10	0.001572	0.010917	-1.20
257832_at	light regulated protein, putative sim	CCL	AT3G26740	1.47	0.55	5.10	0.001573	0.010917	-1.21
266396_at	unknown protein	---	AT2G38790	1.82	0.87	5.10	0.001574	0.010922	-1.21
258455_at	unknown protein ;supported by full-	---	AT3G22440	1.82	0.87	5.10	0.001574	0.010922	-1.21
261088_at	DNA-binding protein, putative simil	---	AT1G07590	1.63	0.70	5.10	0.001576	0.010931	-1.21
250041_at	putative protein p53 inducible prote	PIR121	AT5G18410	-1.38	-0.47	-5.10	0.001578	0.010938	-1.21
266813_at	unknown protein	---	AT2G44920	-1.65	-0.72	-5.10	0.001581	0.010952	-1.21
255767_at	ribosomal protein L20, putative sim	---	AT1G16740	1.50	0.58	5.10	0.001582	0.010952	-1.21
261513_at	unknown protein contains Pfam pro	---	AT1G71840	1.57	0.65	5.10	0.001582	0.010953	-1.21
247335_at	RNA helicase	---	AT5G63630	1.52	0.60	5.10	0.001583	0.010957	-1.21
267506_at	unknown protein ;supported by full-	---	AT2G45520	1.44	0.53	5.10	0.001585	0.010963	-1.21
245773_at	hypothetical protein predicted by ge	---	AT1G30290	1.51	0.59	5.09	0.001585	0.010963	-1.21
262848_at	unknown protein ; supported by cDI	BPC2	AT1G14685	-1.52	-0.60	-5.09	0.001586	0.010963	-1.21
265295_at	putative DNA replication licensing fa	MCM9	AT2G14050	1.63	0.71	5.09	0.001587	0.010966	-1.21
255688_at	putative RNA helicase similar to AT	---	AT4G00660	1.49	0.57	5.09	0.001589	0.010975	-1.22

259889_at	predicted protein ; supported by cD	---	AT1G76405	1.79	0.84	5.09	0.001589	0.010975	-1.22
267011_at	unknown protein	---	AT2G39230	1.73	0.79	5.09	0.001591	0.010984	-1.22
257802_at	unknown protein	---	AT3G18770	1.71	0.77	5.09	0.001592	0.010985	-1.22
261578_at	acidic ribosomal protein, putative s	---	AT1G01100	1.71	0.77	5.09	0.001593	0.010986	-1.22
264913_at	hypothetical protein predicted by ge	---	AT1G60770	1.99	0.99	5.09	0.001596	0.010999	-1.22
264887_at	unknown protein similar to ripening	---	AT1G23120	1.87	0.91	5.09	0.001596	0.010999	-1.22
263334_at	putative nonsense-mediated mRNA	---	AT2G03820	1.50	0.59	5.09	0.001597	0.011004	-1.22
251658_at	putative protein strictosidine syntha	---	AT3G57020	-2.65	-1.41	-5.09	0.001599	0.011007	-1.22
252312_at	hypothetical protein SF16 protein,	iqd15	AT3G49380	-1.62	-0.69	-5.09	0.001599	0.011007	-1.22
249658_s_a	N-glyceraldehyde-2-phosphotransfe	---	AT5G36700	-1.79	-0.84	-5.08	0.001603	0.01103	-1.23
250457_at	splicing factor-like protein ; support	---	AT5G09880	1.54	0.63	5.08	0.001603	0.01103	-1.23
264568_at	putative O-GlcNAc transferase simi	---	AT1G05150	-1.67	-0.74	-5.08	0.001604	0.01103	-1.23
247206_at	putative protein similar to unknown	---	AT5G64950	1.35	0.43	5.08	0.001604	0.011031	-1.23
263438_at	unknown protein	---	AT2G28660	1.68	0.75	5.08	0.001606	0.011042	-1.23
245796_at	unknown protein similar to unknowr	RCD1	AT1G32230	1.51	0.59	5.08	0.001607	0.011046	-1.23
263431_at	unknown protein ;supported by full-	---	AT2G22170	-13.63	-3.77	-5.08	0.001608	0.011048	-1.23
248747_at	ribosomal protein S27 ;supported b	---	AT5G47930	1.76	0.81	5.08	0.001609	0.011054	-1.23
267259_at	Expressed protein ; supported by fu	---	AT2G23090	1.54	0.62	5.08	0.001612	0.011067	-1.23
259056_at	hypothetical protein similar to Ku70	---	AT3G03420	1.64	0.72	5.08	0.001612	0.011067	-1.23
250714_at	sorting nexin-like protein	SNX1	AT5G06140	1.58	0.66	5.08	0.001613	0.011068	-1.23
256094_at	hypothetical protein predicted by ge	SAUL1	AT1G20780	-1.50	-0.59	-5.08	0.001614	0.011068	-1.23
251858_at	aquaporin MIP - like protein aquap	PIP2;5	AT3G54820	-1.97	-0.98	-5.08	0.001614	0.011068	-1.23
245794_at	endoxyloglucan transferase, putati	XTR4	AT1G32170	-1.69	-0.76	-5.08	0.001614	0.011068	-1.23
251518_at	putative protein protein CG15643 -	---	AT3G59390	1.52	0.61	5.08	0.001616	0.011073	-1.23
258229_at	unknown protein contains Pfam pro	---	AT3G27700	1.44	0.53	5.08	0.001619	0.011095	-1.24
262703_at	putative auxin-induced protein simil	---	AT1G16510	1.85	0.89	5.07	0.001624	0.011119	-1.24
258726_at	Expressed protein ; supported by fu	---	AT3G11745	1.44	0.52	5.07	0.001625	0.011122	-1.24
249582_at	calmodulin 1 (CAM1) ; supported b	CAM1	AT5G37780	1.63	0.71	5.07	0.001626	0.011127	-1.24
250649_at	thioredoxin-like ; supported by cDN	WCRKC1	AT5G06690	-1.59	-0.67	-5.07	0.001626	0.011127	-1.24
261532_at	amino acid permease, putative sim	---	AT1G71680	-1.45	-0.54	-5.07	0.001627	0.011129	-1.24
251209_at	putative protein several hypothetica	---	AT3G62890	1.65	0.73	5.07	0.001628	0.011134	-1.24
255948_at	hypothetical protein predicted by ge	---	AT1G22060	-1.40	-0.48	-5.07	0.001629	0.011135	-1.24
250038_at	disease resistance protein -like dis	---	AT5G18360	-1.80	-0.85	-5.07	0.001632	0.011146	-1.25
266806_at	unknown protein ;supported by full-	---	AT2G30000	1.66	0.73	5.06	0.001643	0.011219	-1.25
265316_at	unknown protein	---	AT2G20400	1.82	0.86	5.06	0.001645	0.011232	-1.25

249999_at	triacylglycerol lipase-like protein tri	---	AT5G18640	2.14	1.10	5.06	0.001647	0.011242	-1.26
253275_at	Expressed protein ; supported by fu	---	AT4G34215	-1.57	-0.65	-5.06	0.001648	0.011246	-1.26
262701_at	hypothetical protein predicted by ge	---	AT1G16480	1.60	0.68	5.06	0.001649	0.011251	-1.26
257267_at	unknown protein similar to TCP3 G	TCP4	AT3G15030	-1.56	-0.64	-5.06	0.00165	0.011252	-1.26
251360_at	putative protein embryonic abunda	---	AT3G61210	-1.47	-0.55	-5.06	0.001651	0.011252	-1.26
263242_at	unknown protein	---	AT2G31400	1.54	0.62	5.06	0.001652	0.011261	-1.26
262068_at	splicing factor Prp8, putative simila	SUS2	AT1G80070	1.77	0.83	5.06	0.001654	0.011271	-1.26
258392_at	anther development protein, ATA2(	ATA20	AT3G15400	-1.70	-0.76	-5.05	0.001656	0.011274	-1.26
255929_at	hypothetical protein predicted by ge	---	AT1G12650	1.59	0.67	5.05	0.001656	0.011274	-1.26
252385_at	putative protein Vps29, Schizosacc	MAG1	AT3G47810	1.44	0.52	5.05	0.001656	0.011274	-1.26
266812_at	putative protein kinase contains a p	---	AT2G44830	-1.72	-0.78	-5.05	0.001657	0.011275	-1.26
245738_at	nucellin, putative similar to nucellin	---	AT1G44130	1.98	0.98	5.05	0.001658	0.011281	-1.26
246514_at	DNA-directed RNA polymerase (mit	---	AT5G15700	1.89	0.92	5.05	0.001659	0.011283	-1.26
246794_s_a	putative protein predicted proteins,	---	AT5G06350	2.20	1.14	5.05	0.00166	0.011283	-1.26
256173_at	unknown protein	---	AT1G51730	1.42	0.50	5.05	0.001666	0.011322	-1.27
259769_at	RNA-binding protein MEI2, putative	AML5	AT1G29400	1.89	0.92	5.05	0.001668	0.011334	-1.27
263534_at	putative steroid binding protein ;su	AtMAPR2	AT2G24940	1.57	0.65	5.05	0.001671	0.011352	-1.27
261684_at	hypothetical protein predicted by ge	---	AT1G47400	-4.11	-2.04	-5.04	0.001674	0.011359	-1.27
256008_s_a	allinase, putative similar to allinase	---	AT1G34040	1.50	0.59	5.04	0.001674	0.011359	-1.27
245899_at	putative protein	ALF4	AT5G11030	1.51	0.59	5.04	0.001675	0.011359	-1.27
256948_at	unknown protein	---	AT3G18930	1.45	0.54	5.04	0.001675	0.011359	-1.27
247265_at	putative protein strong similarity to (	CPuORF22	AT5G64550	2.45	1.30	5.04	0.001675	0.011359	-1.27
261720_at	hypothetical protein similar to hypot	HDA08	AT1G08460	1.99	1.00	5.04	0.001681	0.011395	-1.28
259700_at	unknown protein	---	AT1G68980	1.36	0.45	5.04	0.001684	0.01141	-1.28
256728_at	glutamyl-tRNA amidotransferase s	---	AT3G25660	-1.77	-0.83	-5.04	0.001685	0.01141	-1.28
252379_at	ABC-type transport protein-like pro	ATH1	AT3G47730	1.53	0.61	5.04	0.001685	0.01141	-1.28
253524_at	predicted protein ; supported by cD	---	AT4G31430	1.54	0.62	5.04	0.001686	0.011412	-1.28
257310_at	ATP-dependent RNA helicase, put	---	AT3G26560	1.56	0.64	5.04	0.001687	0.011412	-1.28
258381_at	kinesin-like protein similar to mitotic	KINESIN-1	AT3G16630	-1.56	-0.64	-5.04	0.001688	0.011412	-1.28
250426_at	ovule development protein - like ov	AIL6	AT5G10510	-1.43	-0.52	-5.04	0.001688	0.011412	-1.28
264996_at	nuclear matrix constituent protein 1	LINC1	AT1G67230	-1.61	-0.68	-5.04	0.001688	0.011412	-1.28
256125_at	pathogenesis-related group 5 prote	ATLP-1	AT1G18250	-1.79	-0.84	-5.04	0.00169	0.011421	-1.28
263847_at	putative glucosyltransferase ; supp	---	AT2G36970	4.44	2.15	5.03	0.001695	0.011436	-1.29
250190_at	ribosomal protein precursor - like ri	---	AT5G14320	-1.46	-0.54	-5.03	0.001695	0.011436	-1.29
265739_at	unknown protein ; supported by cD	AtQSOX2	AT2G01270	1.37	0.45	5.03	0.001695	0.011436	-1.29

248146_at	translation initiation factor-like prote	---	AT5G54940	1.48	0.57	5.03	0.001696	0.011436	-1.29
264295_at	hypothetical protein predicted by ge	---	AT1G78740	-1.38	-0.46	-5.03	0.001698	0.011446	-1.29
258143_at	hypothetical protein	---	AT3G18170	-1.89	-0.92	-5.03	0.001701	0.011462	-1.29
267130_at	hypothetical protein predicted by ge	---	AT2G23390	1.77	0.83	5.03	0.001701	0.011462	-1.29
247328_at	unknown protein ;supported by full-	---	AT5G64130	-1.88	-0.91	-5.03	0.001702	0.011462	-1.29
254549_at	putative protein various predicted p	---	AT4G19880	1.78	0.83	5.03	0.001702	0.011462	-1.29
262261_at	CLE17, putative CLAVATA3/ESR-l	CLE17	AT1G70895	-1.61	-0.69	-5.03	0.001703	0.011462	-1.29
250935_at	polyubiquitin (UBQ3) identical to Gl	UBQ3	AT5G03240	1.97	0.98	5.03	0.001704	0.011466	-1.29
263255_at	unknown protein similar to steroid r	---	AT1G10490	1.74	0.80	5.03	0.001704	0.011467	-1.29
264014_at	putative auxin-regulated protein	---	AT2G21210	3.67	1.87	5.03	0.001705	0.011467	-1.29
262625_at	hypothetical protein predicted by ge	---	AT1G06440	1.40	0.49	5.03	0.00171	0.011496	-1.30
250981_at	receptor like protein kinase recepto	---	AT5G03140	-1.75	-0.81	-5.02	0.001711	0.011496	-1.30
258285_at	photosystem I subunit VI precursor	PSAH-1	AT3G16140	-1.41	-0.50	-5.02	0.001711	0.011496	-1.30
264019_at	cyclophilin (CYP2) Same as GB: AF	---	AT2G21130	1.64	0.71	5.02	0.001712	0.011496	-1.30
247771_at	Ran binding protein 1 homolog - lik	RANBP1	AT5G58590	1.57	0.65	5.02	0.001712	0.011496	-1.30
251372_at	putative protein ;supported by full-l	---	AT3G60520	1.67	0.74	5.02	0.001713	0.011496	-1.30
266814_at	homeodomain transcription factor (A	ATHB4	AT2G44910	-1.36	-0.44	-5.02	0.001713	0.011496	-1.30
246923_at	putative multispanning membrane	---	AT5G25100	-1.63	-0.71	-5.02	0.001713	0.011496	-1.30
261286_at	unknown protein ; supported by cDI	---	AT1G35780	-1.68	-0.75	-5.02	0.001714	0.011498	-1.30
249028_at	DNA-damage-inducible protein P ;	POLH	AT5G44740	1.66	0.74	5.02	0.001718	0.01152	-1.30
261930_at	alcohol dehydrogenase ADH, putat	---	AT1G22440	1.79	0.84	5.02	0.00172	0.01153	-1.30
260029_at	endoplasmic reticulum alpha-mann	---	AT1G30000	-1.42	-0.51	-5.02	0.001724	0.01155	-1.30
258254_at	unknown protein contains Pfam pro	---	AT3G26780	1.72	0.78	5.02	0.001725	0.011554	-1.31
251007_at	ribosomal protein L35 - like riboson	---	AT5G02610	1.62	0.70	5.02	0.001726	0.011554	-1.31
247585_at	putative protein predicted proteins,	---	AT5G60680	-1.69	-0.76	-5.02	0.001727	0.011556	-1.31
261986_s_a	cytochrome P450, putative similar	CYP76C5	AT1G33720	-3.01	-1.59	-5.01	0.001729	0.011562	-1.31
262161_at	signal peptidase subunit, putative s	---	AT1G52600	1.45	0.53	5.01	0.001729	0.011562	-1.31
251500_at	receptor-like protein kinase recepto	---	AT3G59110	-1.46	-0.55	-5.01	0.001729	0.011562	-1.31
251270_at	putative protein	---	AT3G62370	-1.83	-0.87	-5.01	0.001731	0.011564	-1.31
260644_at	hypothetical protein contains simila	---	AT1G53290	-1.66	-0.73	-5.01	0.001731	0.011564	-1.31
266628_at	unknown protein	---	AT2G35330	1.40	0.49	5.01	0.001732	0.011565	-1.31
257144_at	glucose-6-phosphate 1-dehydroge	G6PD5	AT3G27300	1.45	0.54	5.01	0.001734	0.011577	-1.31
258979_at	heat-shock protein (At-hsc70-3) ide	---	AT3G09440	-2.22	-1.15	-5.01	0.001735	0.011579	-1.31
254145_at	hypothetical protein	---	AT4G24700	2.36	1.24	5.01	0.001739	0.011599	-1.31
247520_at	cytochrome c oxidase subunit - like	---	AT5G61310	2.07	1.05	5.01	0.00174	0.011604	-1.32

258139_at	heat shock transcription factor HSF	HSFC1	AT3G24520	1.68	0.75	5.01	0.001741	0.011608	-1.32
245307_at	gibberellin oxidase-like protein non-	---	AT4G16770	-1.59	-0.67	-5.01	0.001744	0.011621	-1.32
255759_at	hypothetical protein predicted by ge	---	AT1G16790	1.51	0.60	5.01	0.001744	0.011621	-1.32
261278_at	hypothetical protein predicted by ge	DGL	AT1G05800	-1.45	-0.53	-5.01	0.001745	0.011627	-1.32
248132_at	SGP1 monomeric G-protein (emb|C	SGP1	AT5G54840	1.85	0.88	5.01	0.001746	0.011629	-1.32
254711_at	putative protein	---	AT4G18060	-1.57	-0.65	-5.01	0.001747	0.011629	-1.32
254218_at	putative receptor kinase receptor-li	---	AT4G23740	-1.53	-0.61	-5.00	0.001751	0.011656	-1.32
261204_s_a	Eukaryotic peptide chain release fa	ERF1-2	AT1G12920	1.36	0.45	5.00	0.001755	0.011678	-1.32
262581_at	unknown protein ESTs gb|T22508,	---	AT1G15370	-1.38	-0.46	-5.00	0.001756	0.011683	-1.33
265974_at	unknown protein	---	---	-1.98	-0.98	-5.00	0.001757	0.011683	-1.33
262699_at	unknown protein	---	AT1G75980	1.51	0.59	5.00	0.001758	0.011684	-1.33
245438_at	growth regulator like protein	---	AT4G16650	1.47	0.55	5.00	0.001758	0.011684	-1.33
255603_at	hypothetical protein	---	AT4G01040	-1.42	-0.50	-5.00	0.001759	0.011684	-1.33
251308_at	putative protein several hypothetica	GAUT1	AT3G61130	-1.46	-0.55	-5.00	0.001761	0.011693	-1.33
264906_at	putative mitochondrial phosphate tr	---	AT2G17270	1.74	0.80	5.00	0.001761	0.011693	-1.33
252077_at	putative protein several putative my	---	AT3G51720	1.61	0.69	5.00	0.001764	0.011704	-1.33
250921_at	Expressed protein ; supported by fu	---	AT5G03460	1.69	0.76	5.00	0.001765	0.011704	-1.33
247612_at	ATPase - like protein ATPase, Sola	---	AT5G60730	1.53	0.62	5.00	0.001766	0.011709	-1.33
247775_at	phosphoinositide-specific phospho	PLC5	AT5G58690	-2.02	-1.02	-5.00	0.001767	0.011714	-1.33
250622_at	putative transcription factor AP2 do	---	AT5G07310	-1.43	-0.51	-4.99	0.001771	0.011731	-1.33
256419_at	RNA-binding protein similar to GI:82	---	AT1G33470	-1.55	-0.63	-4.99	0.001772	0.011733	-1.34
250083_at	glutathione S-transferase-like prote	ATGSTF12	AT5G17220	-1.57	-0.65	-4.99	0.001772	0.011733	-1.34
247004_at	putative protein similar to unknown	DG1	AT5G67570	1.54	0.62	4.99	0.001773	0.011734	-1.34
267524_at	unknown protein	---	AT2G30600	-1.81	-0.86	-4.99	0.001774	0.011739	-1.34
250268_s_a	putative protein putative secreted p	---	AT5G12950	1.74	0.80	4.99	0.001781	0.011778	-1.34
259051_at	unknown protein similar to CGI-86	---	AT3G03330	1.52	0.61	4.99	0.001782	0.011785	-1.34
258542_at	unknown protein	---	AT3G07030	1.60	0.68	4.99	0.001785	0.011796	-1.34
246199_at	putative protein ;supported by full-le	---	AT4G36530	-1.83	-0.87	-4.99	0.001785	0.011796	-1.34
261911_at	ribosomal protein L7, putative simil	---	AT1G80750	2.19	1.13	4.98	0.001787	0.011805	-1.34
257459_at	unknown protein	---	AT1G24040	1.49	0.57	4.98	0.001788	0.011807	-1.34
261208_at	unknown protein ; supported by cDI	---	AT1G12930	1.70	0.77	4.98	0.001789	0.01181	-1.35
245870_at	hypothetical protein similar to hypot	---	AT1G26300	-1.44	-0.53	-4.98	0.001791	0.011816	-1.35
246573_at	copper amine oxidase, putative sim	---	AT1G31690	-1.74	-0.80	-4.98	0.001791	0.011816	-1.35
245708_at	pectate lyase-like protein	---	AT5G04310	-1.61	-0.69	-4.98	0.001793	0.011826	-1.35
256146_at	delta-adaptin, putative similar to de	delta-ADR	AT1G48760	-1.44	-0.53	-4.98	0.001796	0.011838	-1.35

247124_at	prolyl 4-hydroxylase, alpha subunit	---	AT5G66060	-1.43	-0.51	-4.98	0.001796	0.011838	-1.35
264702_at	hypothetical protein contains simila	---	AT1G70190	1.56	0.64	4.98	0.001797	0.011838	-1.35
252377_at	putative peptide transporter peptid	---	AT3G47960	-1.68	-0.75	-4.98	0.001798	0.011846	-1.35
256220_at	unknown protein	---	AT1G56230	1.65	0.72	4.98	0.0018	0.011855	-1.35
265253_at	putative peptide/amino acid transpo	---	AT2G02020	-1.42	-0.50	-4.98	0.001802	0.011862	-1.35
250060_at	chromo domain protein polycomb-l	TFL2	AT5G17690	1.60	0.68	4.98	0.001803	0.011863	-1.35
260928_at	hypothetical protein similar to putati	GATL5	AT1G02720	-1.50	-0.58	-4.98	0.001803	0.011863	-1.35
250011_at	putative protein crp1 protein, maize	---	AT5G18475	-1.42	-0.51	-4.98	0.001804	0.011863	-1.35
255901_at	GDP-L-fucose synthetase, putative	GER2	AT1G17890	-1.85	-0.89	-4.98	0.001804	0.011863	-1.35
262298_at	unknown protein Similar to gb|AF15	---	AT1G27530	1.39	0.48	4.98	0.001806	0.011867	-1.36
254011_at	putative protein transcription termin	---	AT4G26370	1.55	0.63	4.98	0.001806	0.011867	-1.36
255000_at	S18.A ribosomal protein ;supported	RPS18C	AT4G09800	1.82	0.87	4.97	0.001807	0.011867	-1.36
267519_at	putative VP1/ABI3 family regulatory	HSI2	AT2G30470	-1.75	-0.80	-4.97	0.001807	0.011867	-1.36
247114_at	unknown protein ; supported by cD	---	AT5G65910	-1.58	-0.66	-4.97	0.001807	0.011867	-1.36
253820_at	hypothetical protein	---	AT4G28370	1.47	0.55	4.97	0.001809	0.011873	-1.36
266846_at	unknown protein	---	AT2G25970	1.42	0.51	4.97	0.00181	0.011877	-1.36
249426_at	putative RNA helicase putative ATI	---	AT5G39840	2.53	1.34	4.97	0.001814	0.0119	-1.36
256041_at	unknown protein	---	AT1G07230	1.68	0.75	4.97	0.001816	0.011906	-1.36
256622_at	unknown protein	AtHB34	AT3G28920	1.38	0.47	4.97	0.001819	0.01191	-1.36
250803_at	putative protein contains similarity t	---	AT5G04980	1.88	0.91	4.97	0.001819	0.01191	-1.36
247380_at	4-coumarate-CoA ligase-like protein	---	AT5G63380	-1.69	-0.75	-4.97	0.001819	0.01191	-1.36
249829_at	c-myc binding protein MM-1-like pro	PDF5	AT5G23290	1.47	0.56	4.97	0.001819	0.01191	-1.36
259110_at	unknown protein	---	AT3G05570	1.75	0.81	4.97	0.001819	0.01191	-1.36
249146_at	putative protein contains similarity t	---	AT5G43310	-1.45	-0.54	-4.97	0.001821	0.01191	-1.36
267161_at	hypothetical protein predicted by ge	---	AT2G37680	-1.42	-0.50	-4.97	0.001821	0.01191	-1.36
246193_at	Expressed protein ; supported by fu	---	---	1.47	0.55	4.97	0.001823	0.011916	-1.37
250418_at	putative protein predicted proteins,	---	AT5G11240	2.19	1.13	4.97	0.001823	0.011916	-1.37
256919_at	hypothetical protein predicted by ge	---	AT3G18970	1.55	0.63	4.97	0.001823	0.011916	-1.37
245597_at	salt-inducible protein homolog	---	AT4G14190	1.47	0.56	4.97	0.001824	0.011916	-1.37
258184_at	two-component phosphorelay med	AHP1	AT3G21510	-1.74	-0.80	-4.96	0.001828	0.011941	-1.37
261582_at	unknown protein ; supported by cDI	GIF2	AT1G01160	1.44	0.53	4.96	0.001829	0.011941	-1.37
260747_at	unknown protein ; supported by cDI	---	AT1G78420	1.40	0.48	4.96	0.001831	0.011955	-1.37
260619_at	glyoxalase I, putative similar to GB	---	AT1G08110	1.67	0.74	4.96	0.001833	0.011955	-1.37
251670_at	putative protein translation releasin	---	AT3G57190	1.64	0.72	4.96	0.001833	0.011955	-1.37
248952_at	putative protein similar to unknown	---	AT5G45410	1.56	0.64	4.96	0.001833	0.011955	-1.37

253956_at	fimbrin-like protein (ATFIM1) ; supp	FIM1	AT4G26700	-1.98	-0.98	-4.96	0.001834	0.011955	-1.37
248461_s_a	fumarate hydratase ; supported by	FUM1	AT2G47510	-1.58	-0.66	-4.96	0.001835	0.011955	-1.37
257797_at	hypothetical protein contains Pfam	---	AT3G15940	-1.55	-0.63	-4.96	0.001835	0.011955	-1.37
250406_at	enhancer of rudimentary ; supporte	ER	AT5G10810	1.76	0.82	4.96	0.001838	0.011968	-1.37
263761_at	putative fructose bisphosphate aldo	---	AT2G21330	-1.73	-0.79	-4.96	0.001839	0.01197	-1.38
254845_at	hydroxymethylglutaryl-CoA synthas	MVA1	AT4G11820	-1.70	-0.76	-4.96	0.001839	0.011971	-1.38
256071_at	ubiquitin, putative similar to ubiquit	---	AT1G13640	1.84	0.88	4.96	0.00184	0.011973	-1.38
251008_at	putative protein ;supported by full-le	---	AT5G02710	1.61	0.68	4.95	0.001849	0.01202	-1.38
251794_at	mannose-1-phosphate guanylyltran	---	AT3G55590	-1.42	-0.50	-4.95	0.001851	0.012026	-1.38
251098_at	light-inducible protein ATLS1	---	AT5G01650	1.38	0.47	4.95	0.001851	0.012026	-1.38
260946_at	hypothetical protein predicted by ge	---	AT1G06010	1.58	0.66	4.95	0.001854	0.012044	-1.38
267347_at	hypothetical protein predicted by ge	---	AT2G39950	1.44	0.52	4.95	0.001856	0.012049	-1.39
266587_at	unknown protein ; supported by ful	---	AT2G14880	1.57	0.66	4.95	0.00186	0.012073	-1.39
267214_at	unknown protein ; supported by cD	---	AT2G43970	1.70	0.76	4.95	0.001864	0.012095	-1.39
251078_at	putative protein hypothetical protein	---	AT5G01990	1.87	0.91	4.95	0.001865	0.012098	-1.39
257786_at	hypothetical protein predicted by ge	---	AT3G26990	1.71	0.77	4.95	0.001866	0.012099	-1.39
259816_at	RING-H2 finger protein RHY1a ide	---	AT1G49850	1.50	0.58	4.94	0.001867	0.012102	-1.39
260201_at	F12A21.27 hypothetical protein;sup	---	AT1G67600	2.28	1.19	4.94	0.001867	0.012102	-1.39
258270_at	putative lysophospholipase similar t	---	AT3G15650	-2.48	-1.31	-4.94	0.001868	0.012103	-1.39
258994_at	unknown protein similar to putative	RAPTOR1	AT3G08850	1.42	0.50	4.94	0.00187	0.012111	-1.39
267304_at	putative Fe(II) transport protein	ZIP6	AT2G30080	1.66	0.73	4.94	0.001871	0.012113	-1.39
257395_at	putative salt-inducible protein	---	AT2G15630	1.70	0.76	4.94	0.001872	0.012113	-1.39
250045_at	putative protein mRNA (orf04), Ara	---	AT5G17700	-1.86	-0.90	-4.94	0.001872	0.012113	-1.40
254965_at	putative protein other hypothetical p	---	AT4G11090	-1.41	-0.49	-4.94	0.001872	0.012113	-1.40
263320_at	putative galactinol synthase ;suppo	AtGolS1	AT2G47180	-3.61	-1.85	-4.94	0.001873	0.012114	-1.40
248410_at	putative protein similar to unknown	---	AT5G51570	1.46	0.55	4.94	0.001874	0.012116	-1.40
245195_at	F12A21.13 putative photosystem II	PSBY	AT1G67740	-1.47	-0.55	-4.94	0.001875	0.012116	-1.40
246021_at	ascorbate oxidase-like protein asc	---	AT5G21100	1.89	0.92	4.94	0.001876	0.01212	-1.40
254349_at	hypothetical protein	---	AT4G22250	1.56	0.64	4.94	0.00188	0.012141	-1.40
248969_at	unknown protein ; supported by cD	---	AT5G45310	2.38	1.25	4.94	0.001881	0.012141	-1.40
267298_at	putative homeodomain transcription	BLH4	AT2G23760	-1.75	-0.81	-4.94	0.001886	0.012168	-1.40
247065_s_a	disease resistance protein-like	---	AT5G66900	1.67	0.74	4.94	0.001886	0.012168	-1.40
267199_at	hypothetical protein predicted by ge	---	AT2G30990	-3.55	-1.83	-4.93	0.001888	0.012176	-1.40
248336_at	unknown protein ; supported by cD	---	AT5G52420	1.91	0.94	4.93	0.001889	0.012176	-1.40
255830_at	putative PRP19-like spliceosomal p	---	AT2G33340	2.12	1.08	4.93	0.00189	0.012176	-1.41

248797_at	putative protein similar to unknown	---	AT5G47210	1.57	0.65	4.93	0.00189	0.012176	-1.41
247541_at	structural protein - like glycine-rich	---	AT5G61660	-1.58	-0.66	-4.93	0.00189	0.012176	-1.41
264130_at	hypothetical protein predicted by ge	---	AT1G79160	1.64	0.71	4.93	0.001898	0.012226	-1.41
248746_at	NADH dehydrogenase 10.5K chain	---	AT5G47890	1.91	0.93	4.93	0.001899	0.012226	-1.41
250021_at	casein kinase-like protein	---	AT5G18190	-1.35	-0.43	-4.93	0.001907	0.012274	-1.42
251930_at	putative protein several hypothetica	ATRBL4	AT3G53780	1.62	0.69	4.92	0.00191	0.012284	-1.42
253092_at	putative protein various predicted p	---	AT4G37380	1.99	0.99	4.92	0.00191	0.012284	-1.42
250920_at	putative protein ;supported by full-l	---	AT5G03390	-2.03	-1.02	-4.92	0.00191	0.012284	-1.42
260359_at	hypothetical protein predicted by ge	---	AT1G69210	1.70	0.77	4.92	0.001911	0.012285	-1.42
247138_at	3-dehydroquinate synthase-like pro	---	AT5G66120	1.83	0.87	4.92	0.001911	0.012285	-1.42
251024_at	putative protein hypothetical protein	---	AT5G02180	-1.62	-0.69	-4.92	0.001915	0.012304	-1.42
252770_at	putative protein cellular nucleic aci	---	AT3G42860	1.55	0.63	4.92	0.001915	0.012304	-1.42
250522_at	cleft lip and palate associated trans	---	AT5G08500	1.44	0.52	4.92	0.001916	0.012304	-1.42
259152_at	hypothetical protein similar to putati	---	AT3G10210	1.37	0.45	4.92	0.001917	0.012309	-1.42
250852_at	putative protein BRL protein, Homo	---	AT5G04670	1.39	0.48	4.92	0.001918	0.012309	-1.42
267609_at	unknown protein similar to GP|5221	---	AT2G26780	1.33	0.42	4.92	0.001919	0.012309	-1.42
261077_at	protein phosphatase 2C, putative s	---	AT1G07430	1.87	0.90	4.92	0.001919	0.012309	-1.42
251177_at	cyclophylin -like protein CDC28/cd	---	AT3G63400	1.61	0.69	4.92	0.001921	0.012315	-1.42
257900_at	hypothetical protein predicted by ge	---	AT3G28420	-1.41	-0.50	-4.92	0.001922	0.012315	-1.42
257868_at	unknown protein	RIN4	AT3G25070	1.68	0.75	4.92	0.001922	0.012315	-1.42
264128_at	unknown protein	---	AT1G79190	1.46	0.55	4.92	0.001923	0.012315	-1.42
258449_s_a	putative RNA helicase similar to RN	PMH1	AT3G22310	1.80	0.84	4.92	0.001924	0.012315	-1.42
260176_at	unknown protein similar to Pi starva	---	AT1G71950	-1.52	-0.60	-4.92	0.001926	0.012328	-1.43
264351_at	unknown protein Contains similarity	---	AT1G03370	-1.51	-0.59	-4.92	0.001927	0.012328	-1.43
257509_at	unknown protein	---	AT1G63190	1.52	0.61	4.92	0.001929	0.012341	-1.43
264736_at	oligopeptide transporter, putative s	---	AT1G62200	1.70	0.76	4.91	0.001931	0.012345	-1.43
255946_at	glycine hydroxymethyltransferase,	SHM6	AT1G22020	1.35	0.43	4.91	0.001932	0.012347	-1.43
255635_at	Shaggy related protein kinase tetha	ATSK32	AT4G00720	1.54	0.62	4.91	0.001933	0.012349	-1.43
255216_s_a	putative peptidase	---	AT4G07670	2.12	1.09	4.91	0.001937	0.012374	-1.43
259761_at	putative acyl-CoA synthetase simila	LACS9	AT1G77590	-1.79	-0.84	-4.91	0.001939	0.012382	-1.43
259041_at	unknown protein similar to putative	ATCSLC6	AT3G07330	-1.79	-0.84	-4.91	0.00194	0.012385	-1.43
253762_at	putative protein conserved hypothe	---	AT4G28830	1.50	0.58	4.91	0.001945	0.012411	-1.44
255128_at	putative protein glutamic acid-rich	---	AT4G08310	1.65	0.72	4.91	0.001946	0.012415	-1.44
260679_at	unknown protein	---	AT1G07990	1.42	0.50	4.91	0.001947	0.012415	-1.44
267346_at	coronatine-insensitive 1 (COI1), At	COI1	AT2G39940	1.68	0.75	4.91	0.001947	0.012415	-1.44

259872_at	putative translation initiation factor I	---	AT1G76810	1.43	0.52	4.91	0.001947	0.012415	-1.44
247280_at	phi-1-like protein ;supported by full	EXL2	AT5G64260	-2.31	-1.21	-4.91	0.001949	0.012424	-1.44
263108_at	hypothetical protein similar to putati	---	AT1G65240	-3.60	-1.85	-4.90	0.001952	0.012436	-1.44
264131_at	unknown protein	---	AT1G79150	1.81	0.86	4.90	0.001956	0.012455	-1.44
264084_at	putative kinesin light chain	---	AT2G31240	1.48	0.57	4.90	0.001956	0.012455	-1.44
260190_at	putative lipoxygenase similar to 13-	---	AT1G67560	-1.96	-0.97	-4.90	0.001956	0.012455	-1.44
262172_at	ribosomal protein S9, putative simi	RPS9	AT1G74970	-1.47	-0.56	-4.90	0.001959	0.012467	-1.44
253001_at	Expressed protein ; supported by cl	---	AT4G38490	1.36	0.44	4.90	0.001961	0.012471	-1.45
262372_at	hypothetical protein predicted by ge	---	AT1G73130	1.95	0.96	4.90	0.001962	0.012471	-1.45
246435_at	hypothetical protein ; supported by	---	AT5G17460	1.39	0.47	4.90	0.001962	0.012471	-1.45
250808_at	putative protein contains similarity t	ATG18E	AT5G05150	-1.61	-0.68	-4.90	0.001962	0.012471	-1.45
266320_at	hypothetical protein predicted by ge	---	AT2G46640	-1.94	-0.96	-4.90	0.001963	0.012473	-1.45
260086_at	hypothetical protein predicted by ge	---	AT1G63240	-1.73	-0.79	-4.90	0.001965	0.012484	-1.45
250762_at	putative protein similar to unknown	---	AT5G05990	2.36	1.24	4.89	0.001975	0.012537	-1.45
263156_at	myrosinase-associated protein, put	---	AT1G54030	-2.20	-1.14	-4.89	0.001975	0.012537	-1.45
263759_at	hypothetical protein predicted by ge	---	AT2G21290	1.51	0.59	4.89	0.001978	0.012554	-1.45
261896_at	mRNA export protein, putative simi	---	AT1G80670	1.60	0.68	4.89	0.001983	0.012582	-1.46
261183_at	hypothetical protein predicted by ge	EMB2756	AT1G34550	-1.61	-0.69	-4.89	0.001984	0.012583	-1.46
249845_at	putative protein similar to unknown	---	AT5G23610	1.44	0.52	4.89	0.001985	0.012585	-1.46
264594_at	hypothetical protein ; supported by	ATSERAT3	AT2G17640	1.51	0.59	4.89	0.001989	0.012602	-1.46
245714_at	RNA-binding protein-like	---	AT5G04280	1.47	0.56	4.89	0.001991	0.012614	-1.46
253683_at	cytidine deaminase 4 (CDA4)	---	AT4G29650	-1.45	-0.53	-4.88	0.001996	0.012643	-1.47
248453_at	unknown protein	---	AT5G51340	1.46	0.55	4.88	0.001999	0.012656	-1.47
254350_at	putative protein hypothetical protei	---	AT4G22280	1.38	0.46	4.88	0.002003	0.012677	-1.47
245118_at	putative thioredoxin reductase The	NTRC	AT2G41680	-1.44	-0.53	-4.88	0.002004	0.012677	-1.47
248398_at	sorbitol dehydrogenase-like protein	---	AT5G51970	1.57	0.65	4.88	0.002005	0.012684	-1.47
260655_at	pathogenesis-related protein 5 pre	---	AT1G19320	-2.27	-1.18	-4.88	0.002013	0.012728	-1.47
266188_at	unknown protein	---	AT2G39000	1.56	0.64	4.88	0.002013	0.012728	-1.47
260423_at	unknown protein	ATEXO70D	AT1G72470	-2.50	-1.32	-4.88	0.002015	0.012734	-1.48
265306_at	unknown protein	---	AT2G20320	1.79	0.84	4.88	0.002016	0.012741	-1.48
246017_at	putative protein predicted proteins f	---	AT5G10730	1.41	0.50	4.87	0.002018	0.012748	-1.48
262417_at	hypothetical protein similar to hypot	ATSIRB	AT1G50170	1.36	0.45	4.87	0.002024	0.012783	-1.48
263076_at	putative protein kinase/endoribonuc	IRE1A	AT2G17520	-1.46	-0.55	-4.87	0.002025	0.012783	-1.48
247854_at	contains similarity to phosphoestera	---	AT5G58200	1.53	0.61	4.87	0.002026	0.012786	-1.48
256386_at	cytochrome P450, putative contain	---	AT1G66540	-1.39	-0.48	-4.87	0.002028	0.012798	-1.48

263193_at	acetyl-CoA carboxylase, putative s	---	AT1G36050	-1.44	-0.53	-4.87	0.002034	0.012828	-1.49
260103_at	unknown protein	---	AT1G35430	-1.46	-0.54	-4.87	0.002035	0.012831	-1.49
255094_at	putative zinc finger protein	ORTHL	AT4G08590	-1.91	-0.93	-4.87	0.002037	0.012838	-1.49
257504_at	dynein light chain, putative similar	ROPGEF1	AT1G52240	-2.18	-1.12	-4.87	0.002038	0.012839	-1.49
253027_at	putative protein leaf protein (PnC4(	---	AT4G38150	1.89	0.92	4.87	0.002039	0.012843	-1.49
262088_at	unknown protein	---	AT1G56020	-1.44	-0.53	-4.86	0.002039	0.012843	-1.49
265310_at	hypothetical protein predicted by ge	---	AT2G20280	1.44	0.53	4.86	0.002041	0.012843	-1.49
245304_at	hypothetical protein ; supported by	---	AT4G15630	-3.14	-1.65	-4.86	0.002041	0.012843	-1.49
252473_s_a	hypothetical protein several hypothe	---	AT3G46610	1.81	0.85	4.86	0.002043	0.012847	-1.49
265015_at	putative Ta11-1 reverse transcripta	---	---	-1.35	-0.43	-4.86	0.002043	0.012847	-1.49
254433_at	putative protein tripeptidyl-peptidas	TPP2	AT4G20850	1.38	0.47	4.86	0.002049	0.012877	-1.49
261858_at	Expressed protein ; supported by fu	---	AT1G50570	1.40	0.49	4.86	0.002052	0.012892	-1.49
262741_at	hypothetical protein	---	AT1G28760	1.42	0.50	4.86	0.002054	0.012905	-1.50
261701_at	hypothetical protein similar to hypot	HAF01	AT1G32750	1.35	0.43	4.86	0.002056	0.01291	-1.50
255992_at	unknown protein	---	AT1G29790	-1.55	-0.63	-4.86	0.002057	0.012917	-1.50
264200_at	putative invertase Similar to LIM17	---	AT1G22650	-1.89	-0.92	-4.86	0.002059	0.012919	-1.50
260060_at	feebly-like protein similar to feebly p	---	AT1G73680	1.63	0.71	4.86	0.002059	0.012919	-1.50
247933_at	putative protein non-consensus CC	---	AT5G56980	-2.78	-1.47	-4.86	0.002062	0.012935	-1.50
253691_at	putative protein predicted proteins,	EMB2752	AT4G29660	1.36	0.45	4.85	0.002064	0.012942	-1.50
256512_at	Expressed protein ; supported by fu	---	AT1G33265	1.59	0.67	4.85	0.002066	0.012951	-1.50
254181_at	FtsH protease, putative contains si	---	AT4G23940	-1.39	-0.47	-4.85	0.002068	0.012961	-1.50
258524_at	acetyl-coA dehydrogenase, putativ	IBR3	AT3G06810	1.56	0.64	4.85	0.002071	0.012972	-1.50
261254_at	Expressed protein ; supported by fu	---	AT1G05805	-1.51	-0.59	-4.85	0.002073	0.012982	-1.51
252475_s_a	putative protein several hypothetica	PCL1	AT3G46640	-1.63	-0.70	-4.85	0.002073	0.012982	-1.51
267396_at	hypothetical protein predicted by gr	---	AT2G44270	1.61	0.69	4.85	0.002078	0.013002	-1.51
255615_at	hypothetical protein	---	AT4G01290	1.34	0.42	4.85	0.002078	0.013002	-1.51
247659_at	DNA-directed RNA polymerase - li	NRPC1	AT5G60040	2.56	1.36	4.85	0.002079	0.013005	-1.51
266363_at	hypothetical protein predicted by ge	---	AT2G41250	2.03	1.02	4.85	0.002079	0.013005	-1.51
253319_at	putative protein various predicted p	EMB2758	AT4G33990	1.82	0.87	4.85	0.002083	0.013024	-1.51
259535_at	hypothetical protein	---	AT1G12280	1.77	0.82	4.84	0.002086	0.01304	-1.51
252507_at	putative protein predicted protein,	aTNUDT9	AT3G46200	-1.78	-0.83	-4.84	0.002091	0.013067	-1.52
262960_at	unknown protein ; supported by cDI	---	AT1G54320	1.48	0.56	4.84	0.002092	0.013068	-1.52
255826_at	putative uroporphyrinogen decarbo	HEME2	AT2G40490	-1.50	-0.58	-4.84	0.002094	0.013078	-1.52
250703_at	putative protein similar to unknown	---	AT5G06360	1.64	0.72	4.84	0.002097	0.013094	-1.52
249694_at	glucose-6-phosphate dehydrogenas	G6PD1	AT5G35790	-1.37	-0.45	-4.84	0.002098	0.013094	-1.52

263105_at	putative N-acetylglucosaminyltranst	---	AT2G05320	1.40	0.49	4.84	0.002098	0.013094	-1.52
266668_at	hypothetical protein predicted by gr	---	AT2G29760	2.18	1.13	4.84	0.002101	0.013108	-1.52
259928_at	DNA polymerase type I, putative si	---	AT1G34380	1.93	0.95	4.84	0.002107	0.013141	-1.52
247856_at	receptor-like protein kinase	---	AT5G58300	-1.71	-0.78	-4.84	0.002107	0.013141	-1.52
248555_at	DNA repair protein-like	---	AT5G50340	1.49	0.58	4.84	0.002108	0.013143	-1.52
252277_at	alpha NAC-like protein Nascent po	NACA2	AT3G49470	-1.36	-0.44	-4.83	0.00211	0.01315	-1.53
255724_at	hypothetical protein	BRCA2(IV)	AT4G00020	-1.41	-0.50	-4.83	0.002111	0.013155	-1.53
259227_at	putative 3 exoribonuclease contain	---	AT3G07750	2.81	1.49	4.83	0.002113	0.013158	-1.53
264705_at	putative leucyl-tRNA synthetase Str	---	AT1G09620	1.54	0.63	4.83	0.002113	0.013158	-1.53
247295_at	putative protein similar to unknown	---	AT5G64180	1.50	0.59	4.83	0.002115	0.013165	-1.53
250923_at	putative protein ; supported by full-	CDC25	AT5G03455	1.60	0.68	4.83	0.002118	0.013181	-1.53
248850_at	putative protein contains similarity t	---	AT5G46550	1.49	0.58	4.83	0.002126	0.013216	-1.53
246461_at	putative protein AAA family protein	---	AT5G16930	2.68	1.42	4.83	0.002126	0.013216	-1.53
247385_at	putative protein similar to unknown	emb2746	AT5G63420	1.74	0.80	4.83	0.002128	0.013216	-1.53
265647_at	hypothetical protein predicted by ge	---	AT2G27410	-1.46	-0.54	-4.83	0.002129	0.013216	-1.53
245729_at	unknown protein	---	AT1G73490	1.60	0.67	4.83	0.002129	0.013216	-1.54
253813_at	putative protein hypothetical protei	---	AT4G28150	-1.52	-0.60	-4.83	0.002129	0.013216	-1.54
262136_at	auxin response factor, putative sim	ARF17	AT1G77850	1.43	0.52	4.83	0.00213	0.013216	-1.54
253837_at	putative proline-rich protein extens	---	AT4G27850	-1.43	-0.51	-4.83	0.00213	0.013216	-1.54
259210_at	hypothetical protein nearly identical	HY2	AT3G09150	1.67	0.74	4.83	0.002131	0.013216	-1.54
267218_at	Expressed protein ; supported by fu	---	AT2G02515	-1.45	-0.54	-4.83	0.002131	0.013216	-1.54
248147_at	putative protein contains similarity t	ATRBP45A	AT5G54900	1.48	0.57	4.82	0.002137	0.01325	-1.54
263143_at	hypothetical protein Contains PF|00	---	AT1G03100	1.55	0.63	4.82	0.002138	0.013254	-1.54
245758_at	unknown protein contains similarity	KAN2	AT1G32240	1.84	0.88	4.82	0.002142	0.013271	-1.54
257618_at	protein kinase, putative similar to T	---	AT3G24715	-1.35	-0.43	-4.82	0.002145	0.013291	-1.54
263114_at	putative photosystem I reaction cer	PSAD-2	AT1G03130	-1.51	-0.59	-4.82	0.002147	0.013292	-1.54
246882_at	putative protein predicted proteins,	---	AT5G26180	1.39	0.48	4.82	0.002147	0.013292	-1.54
250404_at	CCR4-ASSOCIATED FACTOR -li	---	AT5G10960	1.38	0.46	4.82	0.002155	0.013335	-1.55
257407_at	unknown protein	---	AT1G27100	-1.45	-0.54	-4.81	0.002156	0.013341	-1.55
251833_at	putative protein various predicted p	---	AT3G55160	1.43	0.52	4.81	0.002157	0.013341	-1.55
254035_at	putative phosphatidylserine decarb	PSD3	AT4G25970	1.46	0.54	4.81	0.002159	0.013348	-1.55
252823_at	Expressed protein ; supported by fu	---	AT4G40045	-1.49	-0.58	-4.81	0.00216	0.013348	-1.55
256248_at	hypothetical protein	---	AT3G66652	1.77	0.83	4.81	0.00216	0.013348	-1.55
255133_at	putative protein (fragment) glutami	---	AT4G08320	1.55	0.64	4.81	0.002163	0.013353	-1.55
262164_at	unknown protein ; supported by cDI	---	AT1G78070	1.68	0.74	4.81	0.002164	0.013357	-1.55

259967_at	putative DNA-binding protein conta	---	AT1G76510	1.39	0.48	4.81	0.002166	0.013366	-1.55
251273_at	serine/threonine-protein kinase-like	---	AT3G61960	1.81	0.86	4.81	0.002169	0.013377	-1.56
263502_s_a	hypothetical protein	---	AT2G07675	1.86	0.89	4.81	0.002172	0.013393	-1.56
253280_at	poly(A)-binding protein non-conser	PAB2	AT4G34110	1.39	0.48	4.81	0.002174	0.013401	-1.56
255702_at	subtilisin-like serine protease XSP1	XSP1	AT4G00230	-1.78	-0.83	-4.81	0.002176	0.013403	-1.56
248690_at	acetyl-CoA C-acetyltransferase ; su	ACAT2	AT5G48230	1.38	0.46	4.81	0.002177	0.013405	-1.56
245289_at	Expressed protein ; supported by cl	---	AT4G15470	-1.36	-0.45	-4.80	0.002181	0.013422	-1.56
266347_at	putative ATP-dependent DNA helic	---	AT2G01440	1.66	0.73	4.80	0.00219	0.013473	-1.57
267187_s_a	putative methylenetetrahydrofolate	MTHFR2	AT2G44160	-1.75	-0.80	-4.80	0.002191	0.013477	-1.57
250526_at	pyruvate kinase	---	AT5G08570	1.45	0.54	4.80	0.002191	0.013477	-1.57
245575_at	centromere protein homolog	---	AT4G14760	-1.46	-0.54	-4.80	0.002193	0.013483	-1.57
253276_at	caffeoyl-CoA O-methyltransferase	---	AT4G34050	1.78	0.83	4.80	0.002201	0.013516	-1.57
253477_at	L-ascorbate peroxidase - like protei	APX6	AT4G32320	2.03	1.02	4.80	0.002201	0.013516	-1.57
262509_at	hypothetical protein similar to hypot	CRR22	AT1G11290	1.53	0.62	4.80	0.002201	0.013516	-1.57
265911_at	unknown protein ;supported by full-	---	AT2G25670	1.39	0.47	4.80	0.002202	0.013516	-1.57
261089_at	protein kinase APK1A identical to S	APK1A	AT1G07570	-1.83	-0.87	-4.80	0.002202	0.013516	-1.57
265356_at	putative TRAP protein	---	AT2G16595	1.65	0.72	4.80	0.002203	0.013518	-1.57
262686_at	proteasome regulatory subunit S3,	---	AT1G75990	-1.54	-0.63	-4.80	0.002204	0.013519	-1.57
263035_at	splicing factor, putative similar to R	RSZP21	AT1G23860	1.65	0.72	4.79	0.002205	0.013523	-1.57
245706_at	putative protein	---	AT5G04310	-1.47	-0.55	-4.79	0.002206	0.013526	-1.57
259071_at	unknown protein similar to hin1 GB	NHL2	AT3G11650	-1.92	-0.94	-4.79	0.002214	0.01357	-1.58
253674_at	UDP-N-acetylglucosamine O-acyltr	---	AT4G29540	1.46	0.55	4.79	0.002215	0.013575	-1.58
254694_at	putative protein	---	AT4G17900	1.71	0.77	4.79	0.002216	0.013575	-1.58
253873_at	hypothetical protein ;supported by f	PRA1.H	AT4G27540	1.44	0.52	4.79	0.002218	0.013586	-1.58
266599_at	unknown protein	---	AT2G46100	-1.41	-0.50	-4.79	0.002223	0.013615	-1.58
246290_at	calmodulin-3 ;supported by full-len	CAM3	AT3G56800	-1.40	-0.49	-4.79	0.002225	0.013623	-1.58
266299_at	glutathione S-transferase identical t	ATGSTU5	AT2G29450	-2.26	-1.18	-4.78	0.00223	0.013651	-1.59
263356_at	putative RNA-binding protein ; sup	UBA1A	AT2G22090	-1.39	-0.48	-4.78	0.002233	0.013657	-1.59
255784_at	hypothetical protein predicted by ge	---	AT1G19860	1.44	0.52	4.78	0.002233	0.013657	-1.59
258062_at	unknown protein ; supported by cD	---	AT3G26000	1.69	0.76	4.78	0.002235	0.013662	-1.59
248689_at	SCARECROW gene regulator-like	PAT1	AT5G48150	1.58	0.66	4.78	0.002236	0.013668	-1.59
250188_at	putative protein COP9 complex sul	COP13	AT5G14250	1.45	0.54	4.78	0.002239	0.01368	-1.59
248789_at	putative protein strong similarity to u	---	AT5G47440	-1.75	-0.81	-4.78	0.00224	0.013683	-1.59
253468_at	putative protein predicted gene T1(	---	AT4G32160	1.60	0.67	4.78	0.002241	0.013683	-1.59
250792_at	unknown protein ;supported by full-	---	AT5G05520	1.47	0.56	4.78	0.002244	0.013699	-1.59

247375_at	Expressed protein ; supported by fu	---	AT5G63135	1.34	0.42	4.78	0.002244	0.0137	-1.59
260949_at	F-box protein family contains simila	SKIP16	AT1G06110	1.47	0.56	4.78	0.002247	0.013712	-1.59
257215_at	RING zinc finger protein, putative c	---	AT3G15070	-1.46	-0.54	-4.78	0.002248	0.013714	-1.59
245330_at	hypothetical protein ;supported by f	---	AT4G14930	1.60	0.68	4.78	0.002252	0.013729	-1.60
261507_at	RIBOSOMAL PROTEIN, putative s	---	AT1G71720	-1.44	-0.53	-4.78	0.002253	0.013729	-1.60
264396_at	fumarylacetoacetate hydrolase-like	---	AT1G12050	1.40	0.48	4.78	0.002253	0.013729	-1.60
264583_at	putative AVR9 elicitor response pro	---	AT1G05170	1.62	0.70	4.77	0.002256	0.013746	-1.60
246469_at	putative protein predicted protein, l	---	AT5G17070	-1.43	-0.52	-4.77	0.00226	0.013765	-1.60
258700_at	putative SF16 protein similar to SF1	IQD1	AT3G09710	-1.45	-0.54	-4.77	0.002261	0.013765	-1.60
262029_at	50S ribosomal protein L21 chloropla	---	AT1G35680	-1.65	-0.72	-4.77	0.002264	0.013784	-1.60
262921_at	transfactor, putative similar to trans	APL	AT1G79430	1.46	0.55	4.77	0.002271	0.013812	-1.61
255568_at	putative DNA-binding protein ; sup	WRKY22	AT4G01250	-3.82	-1.93	-4.77	0.002271	0.013812	-1.61
259487_at	hypothetical protein contains simila	TRFL5	AT1G15720	-1.34	-0.43	-4.77	0.002275	0.013824	-1.61
264118_at	unknown protein	---	AT1G79150	2.40	1.26	4.77	0.002275	0.013824	-1.61
258964_at	putative 3-phosphoinositide-depend	---	AT3G10540	-1.47	-0.56	-4.77	0.002278	0.013837	-1.61
248477_at	putative protein similar to unknown	---	AT5G50900	-1.61	-0.69	-4.77	0.00228	0.013841	-1.61
267500_s_a	putative cytochrome P450	CYP704A1	AT2G44890	1.86	0.90	4.76	0.002281	0.013846	-1.61
256238_at	unknown protein ; supported by full-	ELC	AT3G12400	-1.65	-0.72	-4.76	0.002283	0.01385	-1.61
259603_at	Expressed protein ; supported by fu	---	AT1G56500	-1.80	-0.84	-4.76	0.002284	0.01385	-1.61
264551_at	unknown protein similar to beta-1,3	---	AT1G09460	-2.08	-1.05	-4.76	0.002286	0.013861	-1.61
265188_at	putative aldehyde dehydrogenase	ALDH2B7	AT1G23800	-1.66	-0.73	-4.76	0.002291	0.013885	-1.61
256274_at	GTPase, putative contains Pfam pr	emb2738	AT3G12080	1.41	0.50	4.76	0.002295	0.013907	-1.62
249441_at	avirulence induced gene (AIG) - lik	---	AT5G39730	-1.63	-0.70	-4.76	0.002298	0.01392	-1.62
248224_at	thylakoid lumenal 17.4 kD protein,	---	AT5G53490	-1.72	-0.79	-4.76	0.002299	0.01392	-1.62
261439_at	Expressed protein ; supported by fu	---	AT1G28395	2.09	1.06	4.76	0.0023	0.013922	-1.62
261857_at	hypothetical protein predicted by ge	---	AT1G50620	2.37	1.25	4.76	0.002304	0.013938	-1.62
255607_at	putative acetyltransferase similar to	---	AT4G01130	-1.93	-0.95	-4.76	0.002306	0.013942	-1.62
254980_at	putative ribosomal protein L9, cytos	---	AT4G10450	2.23	1.16	4.76	0.002306	0.013942	-1.62
249685_at	putative protein similar to unknown	CCB3	AT5G36120	-1.39	-0.47	-4.75	0.002314	0.013989	-1.63
263699_at	putative potassium transporter simi	KUP10	AT1G31120	1.77	0.83	4.75	0.002316	0.013989	-1.63
255695_at	putative protein	UNE11	AT4G00080	-1.40	-0.49	-4.75	0.002316	0.013989	-1.63
267089_at	unknown protein	---	AT2G38300	1.66	0.73	4.75	0.002316	0.013989	-1.63
250104_at	unknown protein	---	AT5G16610	1.71	0.77	4.75	0.002316	0.013989	-1.63
251110_at	putative protein various alpha amyla	---	AT5G01260	1.88	0.91	4.75	0.002317	0.013989	-1.63
246960_at	unknown protein	---	AT5G24710	-1.42	-0.50	-4.75	0.002319	0.013992	-1.63

249266_at	6-phosphogluconate dehydrogenas	---	AT5G41670	1.69	0.76	4.75	0.002325	0.014025	-1.63
256978_at	phosphoribosyamidoimidazole-suc	PUR7	AT3G21110	2.08	1.05	4.75	0.002327	0.014034	-1.63
255117_s_a	putative protein various hypothetica	ATPUP13	AT4G08700	1.35	0.44	4.75	0.002329	0.01404	-1.63
262198_at	pectin methylesterase (PMEU1), p	ATPME2	AT1G53830	-3.35	-1.75	-4.75	0.002331	0.01405	-1.63
247845_at	beta-1,3 glucanase - like protein be	---	AT5G58090	-1.44	-0.53	-4.74	0.002337	0.014076	-1.64
258316_at	unknown protein	---	AT3G22660	1.81	0.85	4.74	0.002337	0.014076	-1.64
251823_at	putative protein	---	AT3G55080	-1.37	-0.46	-4.74	0.002337	0.014076	-1.64
264308_at	hypothetical protein similar to hypot	---	AT1G61990	1.32	0.40	4.74	0.00234	0.014089	-1.64
254640_at	ion transporter - like protein integra	NRAMP5	AT4G18790	-1.46	-0.54	-4.74	0.002341	0.014094	-1.64
247706_at	putative ripening-related protein - lik	---	AT5G59480	-2.45	-1.29	-4.74	0.002343	0.014103	-1.64
253732_at	putative protein several hypothetica	---	AT4G29140	-1.46	-0.54	-4.74	0.002344	0.014106	-1.64
263054_at	putative cation transport protein	---	AT2G04620	1.45	0.53	4.74	0.002349	0.014125	-1.64
249900_at	unknown protein	emb1211	AT5G22640	1.43	0.52	4.74	0.00235	0.014127	-1.64
256696_at	unknown protein	---	AT3G20650	1.42	0.51	4.74	0.002353	0.014141	-1.64
248163_at	auxin-responsive-like protein ; supp	DFL1	AT5G54510	-6.05	-2.60	-4.74	0.002353	0.014141	-1.64
259380_at	putative ABC transporter similar to A	PDR1	AT3G16340	-1.59	-0.67	-4.74	0.002355	0.01415	-1.65
260395_at	homeobox gene 13 protein identica	ATHB13	AT1G69780	-2.37	-1.25	-4.74	0.002356	0.01415	-1.65
250988_at	putative protein thyroid receptor int	UPL4	AT5G02880	1.38	0.46	4.74	0.002357	0.01415	-1.65
246423_at	putative protein ribosomal protein L	---	AT5G16950	1.64	0.71	4.73	0.002359	0.01416	-1.65
260780_at	valyl-tRNA synthetase, putative sim	TWN2	AT1G14610	1.38	0.46	4.73	0.002362	0.014172	-1.65
258995_at	putative ribosomal protein L13 simil	---	AT3G01790	1.74	0.80	4.73	0.002365	0.014187	-1.65
250525_at	putative protein contains similarity t	ILP1	AT5G08550	1.43	0.52	4.73	0.002366	0.01419	-1.65
265773_at	unknown protein ; supported by cD	RPH1	AT2G48070	-1.51	-0.59	-4.73	0.002371	0.014216	-1.65
245841_s_a	ribosomal protein S2, putative simi	XW6	AT1G58380	1.84	0.88	4.73	0.002371	0.014216	-1.65
257843_at	hypothetical protein predicted by g	---	---	-1.39	-0.47	-4.73	0.002374	0.014221	-1.65
251537_at	putative protein several hypothetica	---	AT3G58470	1.97	0.98	4.73	0.002376	0.014229	-1.65
261427_at	protein kinase, putative similar to C	IBS1	AT1G18670	-2.04	-1.03	-4.73	0.002376	0.014229	-1.65
252663_at	putative protein several hypothetica	---	AT3G44070	-1.35	-0.44	-4.73	0.00238	0.014248	-1.66
250075_at	putative protein	---	AT5G17670	-2.00	-1.00	-4.73	0.002381	0.014248	-1.66
260350_at	Eukaryotic initiation factor 5A , put	ELF5A-3	AT1G69410	1.72	0.79	4.73	0.002383	0.014255	-1.66
245413_at	asparagine--tRNA ligase	NS1	AT4G17300	-1.45	-0.53	-4.73	0.002384	0.014255	-1.66
251185_at	60S RIBOSOMAL PROTEIN L7A p	---	AT3G62870	1.65	0.72	4.72	0.002386	0.014267	-1.66
248357_at	putative protein similar to unknown	---	AT5G52380	2.12	1.08	4.72	0.002388	0.014272	-1.66
251831_at	pectate lyase -like protein pectate l	---	AT3G55140	-1.35	-0.43	-4.72	0.002388	0.014272	-1.66
250231_at	AP2/EREBP-like transcription facto	LEP	AT5G13910	-1.40	-0.49	-4.72	0.002391	0.014283	-1.66

253850_at	pectinesterase like protein pectines	sks10	AT4G28090	-1.61	-0.69	-4.72	0.002394	0.014301	-1.66
260418_s_a	hypothetical protein predicted by ge	COX19-1	AT1G66590	2.47	1.31	4.72	0.002396	0.014302	-1.66
257687_at	hypothetical protein predicted by ge	SDRB	AT3G12800	1.45	0.54	4.72	0.002396	0.014302	-1.66
259311_at	putative SAR DNA-binding protein-	---	AT3G05060	2.08	1.06	4.72	0.002401	0.01433	-1.67
267055_at	unknown protein	PRA1.B4	AT2G38360	-2.73	-1.45	-4.72	0.002402	0.014332	-1.67
251526_at	putative protein several serine/thred	---	AT3G58640	-1.55	-0.63	-4.72	0.002405	0.014342	-1.67
264286_at	unknown protein ;supported by full-	PPR336	AT1G61870	1.94	0.96	4.72	0.002409	0.014361	-1.67
264164_at	Expressed protein ; supported by fu	---	AT1G65295	-1.58	-0.66	-4.72	0.00241	0.014361	-1.67
253988_at	putative protein elongation factor P	---	AT4G26310	1.41	0.50	4.72	0.00241	0.014361	-1.67
265390_at	unknown protein ; supported by full	---	AT2G20820	1.41	0.50	4.72	0.002413	0.014368	-1.67
258534_at	thioredoxin, putative similar to thior	---	AT3G06730	1.42	0.50	4.71	0.002415	0.01438	-1.67
255403_at	putative GH3-like protein similar to	DFL2	AT4G03400	-1.62	-0.70	-4.71	0.00242	0.014403	-1.67
264561_at	uracil phosphoribosyltransferase, p	---	AT1G55810	1.72	0.79	4.71	0.002421	0.014404	-1.68
267484_at	E2, ubiquitin-conjugating enzyme 2	ATUBC2	AT2G02760	1.45	0.54	4.71	0.002421	0.014404	-1.68
253453_at	protein phosphatase 2C - like prote	---	AT4G31860	1.37	0.45	4.71	0.002422	0.014404	-1.68
253213_at	RNA helicase (RH16)	---	AT4G34910	1.46	0.54	4.71	0.002425	0.01442	-1.68
248239_at	ribosomal protein L11 methyltransfe	---	AT5G53920	1.77	0.83	4.71	0.002427	0.014427	-1.68
247408_at	ZAP - like protein nuclear protein Z	---	AT5G62760	-1.36	-0.44	-4.71	0.002428	0.014427	-1.68
266614_at	unknown protein	---	AT2G14910	1.51	0.60	4.71	0.002428	0.014427	-1.68
259514_at	hypothetical protein ; supported by	OZS1	AT1G12480	-1.48	-0.56	-4.71	0.002431	0.014441	-1.68
255735_at	transmembrane protein, putative si	---	AT1G25520	2.01	1.00	4.71	0.002432	0.014441	-1.68
265037_at	putative prohibitin 2 B-cell receptor	ATPHB2	AT1G03860	1.56	0.64	4.71	0.002433	0.014443	-1.68
250817_at	SET-domain protein-like ; supporte	SUVH1	AT5G04940	1.43	0.52	4.70	0.002442	0.01449	-1.68
265230_s_a	hypothetical protein	---	AT2G07707	1.69	0.76	4.70	0.002449	0.01453	-1.69
260273_at	unknown protein	---	AT1G80550	1.56	0.64	4.70	0.002453	0.014547	-1.69
260537_at	hypothetical protein predicted by ge	---	AT2G43450	-1.34	-0.43	-4.70	0.002453	0.014547	-1.69
249238_at	GAMM1 protein-like ; supported by	---	AT5G41970	1.45	0.53	4.70	0.002456	0.014558	-1.69
265318_at	putative D-amino acid dehydrogena	---	AT2G22650	1.70	0.77	4.70	0.002461	0.014582	-1.69
248081_at	putative protein similar to unknown	EDM2	AT5G55390	1.38	0.46	4.70	0.002464	0.014593	-1.69
246630_at	hypothetical protein predicted by ge	---	AT1G50730	-1.93	-0.95	-4.70	0.002466	0.014601	-1.69
246198_at	geranylgeranyl pyrophosphate synt	GGPS1	AT4G36810	-1.66	-0.73	-4.70	0.002467	0.014607	-1.70
254224_at	calcium-dependent protein kinase (	CDPK6	AT4G23650	-1.41	-0.49	-4.69	0.002473	0.014639	-1.70
261817_at	hypothetical protein predicted by ge	---	AT1G08180	2.27	1.19	4.69	0.002474	0.014641	-1.70
255227_at	D123 -like protein protein D123, Ra	EDA35	AT4G05440	1.63	0.70	4.69	0.002477	0.014654	-1.70
252276_at	hypothetical protein ; supported by	---	AT3G49490	1.53	0.61	4.69	0.002478	0.014657	-1.70

258970_at	putative serine carboxypeptidase pr	scpl49	AT3G10410	1.66	0.73	4.69	0.002485	0.014686	-1.70
256367_at	C-x8-C-x5-C-x3-H type Zinc finger	---	AT1G66810	-1.49	-0.57	-4.69	0.002487	0.014686	-1.70
249434_at	putative protein GTP-binding protei	---	AT5G39960	1.68	0.75	4.69	0.002487	0.014686	-1.70
252406_at	putative protein pectinesterase - A	---	AT3G47670	-1.35	-0.44	-4.69	0.002487	0.014686	-1.70
263031_at	glucosyltransferase, putative simila	ATCSLA10	AT1G24070	-5.62	-2.49	-4.69	0.002488	0.014686	-1.70
256677_at	unknown protein contains Pfam pro	PHF1	AT3G52190	1.53	0.61	4.69	0.002492	0.014704	-1.71
261745_at	unknown protein identical to unknov	---	AT1G08500	-2.61	-1.38	-4.69	0.002494	0.01471	-1.71
250354_at	putative protein predicted proteins,	---	AT5G11640	-1.45	-0.53	-4.69	0.002496	0.01471	-1.71
266330_at	unknown protein ; supported by cD	MLP329	AT2G01530	1.80	0.85	4.69	0.002496	0.01471	-1.71
262154_at	unknown protein contains similarity	---	AT1G52700	-1.80	-0.85	-4.69	0.002496	0.01471	-1.71
263065_at	MAP kinase (ATMPK7) identical to	ATMPK7	AT2G18170	1.89	0.92	4.69	0.002496	0.01471	-1.71
253761_at	putative protein thyroid receptor int	---	AT4G28820	1.54	0.63	4.68	0.002497	0.01471	-1.71
262641_at	unknown protein ;supported by full-	---	AT1G62730	1.32	0.40	4.68	0.002497	0.01471	-1.71
253922_at	putative protein ; supported by cDN	VTC2	AT4G26850	1.79	0.84	4.68	0.0025	0.014726	-1.71
246733_at	serine protease-like protein serine	---	AT5G27660	1.51	0.59	4.68	0.002503	0.014735	-1.71
258138_at	Expressed protein GC donor splice	MSH7	AT3G24495	1.38	0.46	4.68	0.002504	0.014738	-1.71
258712_s_a	putative 40S ribosomal protein S23	---	AT3G09680	1.60	0.68	4.68	0.002505	0.014743	-1.71
247792_at	Expressed protein ; supported by fu	---	AT5G58787	1.89	0.92	4.68	0.00251	0.014768	-1.71
266158_at	putative ABC transporter	---	AT2G28070	1.69	0.75	4.68	0.002512	0.014769	-1.72
253186_at	putative protein predicted proteins,	---	AT4G35270	1.71	0.78	4.68	0.002515	0.014787	-1.72
248232_at	putative protein contains similarity t	MLO11	AT5G53760	-1.60	-0.68	-4.68	0.002521	0.014819	-1.72
262295_at	putative U2 snRNP auxiliary factor	ATU2AF35	AT1G27650	1.61	0.69	4.68	0.002522	0.014822	-1.72
264122_at	GTP-binding protein, ara-5 ras hon	ARA-5	AT1G02130	1.32	0.40	4.68	0.002524	0.014828	-1.72
245368_at	hypothetical protein ; supported by	---	AT4G15510	-1.86	-0.90	-4.67	0.002525	0.014831	-1.72
250905_at	protein kinase -like protein protein	---	AT5G03640	1.37	0.45	4.67	0.002526	0.014831	-1.72
249510_at	putative protein similar to unknown	---	AT5G38510	1.48	0.57	4.67	0.002529	0.014842	-1.72
266911_at	putative protein kinase contains a p	---	AT2G45910	1.65	0.72	4.67	0.00253	0.014842	-1.72
256771_at	unknown protein	---	AT3G13700	-1.39	-0.47	-4.67	0.002531	0.014843	-1.72
254991_at	putative protein conserved hypothe	---	AT4G10620	1.57	0.65	4.67	0.002534	0.01486	-1.72
253804_at	putative protein	---	AT4G28230	1.52	0.61	4.67	0.002538	0.014876	-1.73
246951_at	unknown protein	---	AT5G04880	2.19	1.13	4.67	0.002538	0.014876	-1.73
254655_s_a	ribosomal protein L32 -like protein	---	AT4G18100	1.87	0.90	4.67	0.002539	0.014876	-1.73
256607_at	unknown protein ; supported by cDI	---	AT3G32930	-1.39	-0.47	-4.67	0.00254	0.014876	-1.73
265442_at	hypothetical protein predicted by ge	---	AT2G20940	2.06	1.04	4.67	0.002543	0.01489	-1.73
261565_at	beta-1,3-glucanase, putative simila	---	AT1G33220	-1.34	-0.42	-4.67	0.002543	0.01489	-1.73

262777_at	hypothetical protein predicted by ge	---	AT1G13030	1.80	0.85	4.67	0.002544	0.014892	-1.73
267299_at	putative glucosyltransferase	---	AT2G30150	1.62	0.69	4.67	0.002548	0.014908	-1.73
255578_at	predicted protein of unknown funct	---	AT4G01450	2.29	1.20	4.67	0.002552	0.014925	-1.73
249144_at	squamosa promoter binding protein	SPL2	AT5G43270	-1.48	-0.56	-4.66	0.002554	0.014934	-1.73
264048_at	unknown protein	---	AT2G22400	1.72	0.78	4.66	0.002555	0.014939	-1.73
246879_at	endopeptidase - like protein O-sial	---	AT5G26110	1.46	0.54	4.66	0.002558	0.014949	-1.74
255240_at	coded for by A. thaliana cDNA Z18	IBR1	AT4G05530	1.43	0.52	4.66	0.00256	0.014954	-1.74
252286_at	putative protein	---	AT3G49070	-1.32	-0.40	-4.66	0.002561	0.014958	-1.74
245117_at	putative Ca2+-ATPase ; supported	ACA4	AT2G41560	1.71	0.77	4.66	0.002568	0.014991	-1.74
258963_at	putative myotubularin similar to myo	---	AT3G10550	-1.50	-0.59	-4.66	0.00257	0.014994	-1.74
250384_at	putative protein various predicted p	---	AT5G11500	1.42	0.50	4.66	0.002579	0.015044	-1.74
254573_at	putative pectinacetylesterase pecti	---	AT4G19420	2.16	1.11	4.66	0.002581	0.015047	-1.74
261607_at	unknown protein similar to putative	AtCXE5	AT1G49660	2.64	1.40	4.66	0.002582	0.01505	-1.75
259323_at	unknown protein	---	AT3G05280	-1.32	-0.40	-4.65	0.002588	0.015076	-1.75
266456_at	putative bHLH transcription factor	NAI1	AT2G22770	-1.50	-0.58	-4.65	0.002588	0.015077	-1.75
246965_at	methyltransferase-like protein meth	---	AT5G24840	1.81	0.86	4.65	0.002594	0.015105	-1.75
251881_at	DIPHOSPHOMEVALONATE DEC	---	AT3G54250	-2.07	-1.05	-4.65	0.002597	0.015114	-1.75
266057_at	putative methionyl-tRNA synthetase	---	AT2G40660	1.39	0.47	4.65	0.002598	0.015119	-1.75
251134_at	hypothetical protein RNA polymera	AtQSOX2	AT2G01270	1.46	0.55	4.65	0.0026	0.015126	-1.75
257990_at	putative myc-like DNA-binding prote	---	AT3G19860	-1.66	-0.73	-4.65	0.002606	0.015154	-1.76
260627_at	hypothetical protein predicted by ge	---	AT1G62310	-1.78	-0.83	-4.65	0.002607	0.015156	-1.76
251741_at	putative protein predicted protein,	UGP3	AT3G56040	2.17	1.12	4.65	0.002608	0.015163	-1.76
266746_s_a	putative glutathione S-transferase	ATGSTF3	AT2G02930	5.04	2.33	4.65	0.002612	0.01518	-1.76
257940_at	putative UDP-glucose glucosyltrans	---	AT3G21790	1.58	0.66	4.64	0.002613	0.015182	-1.76
247241_at	unknown protein	---	AT5G64680	1.98	0.99	4.64	0.002622	0.015228	-1.76
248196_at	putative protein similar to unknown	---	AT5G54150	-1.39	-0.48	-4.64	0.002623	0.015229	-1.76
266703_at	unknown protein predicted by gens	---	AT2G19880	-1.77	-0.82	-4.64	0.002626	0.015242	-1.76
253013_at	heat shock protein 70 like protein c	mtHsc70-1	AT4G37910	2.05	1.04	4.64	0.002627	0.015242	-1.76
260843_at	unknown protein similar to hypothet	---	AT1G29060	1.33	0.41	4.64	0.002628	0.015248	-1.76
259789_at	Expressed protein ; supported by fu	COR414-TI	AT1G29395	-1.51	-0.60	-4.64	0.002639	0.015303	-1.77
253815_at	putative beta-expansin/allergen pro	ATEXPB3	AT4G28250	-1.76	-0.82	-4.64	0.002641	0.015307	-1.77
257956_at	unknown protein	---	AT3G25400	1.62	0.69	4.63	0.002647	0.015335	-1.77
247705_at	putative protein ;supported by full-l	---	AT5G59460	1.44	0.52	4.63	0.002649	0.015342	-1.77
245957_at	putative protein predicted proteins -	---	AT5G19590	1.36	0.44	4.63	0.002653	0.015358	-1.77
262220_at	calcium-dependent protein kinase,	CPK30	AT1G74740	-1.39	-0.47	-4.63	0.002653	0.015358	-1.77

251538_at	putative protein PBK1 protein, Hom	---	AT3G58660	1.85	0.89	4.63	0.002656	0.015374	-1.78
258166_at	WD-repeat protein, putative contair	---	AT3G21540	2.12	1.09	4.63	0.002664	0.015413	-1.78
267533_at	unknown protein ;supported by full-	ATNUDX23	AT2G42070	1.48	0.57	4.63	0.002666	0.015425	-1.78
261606_at	peroxidase, putative similar to perc	---	AT1G49570	-1.60	-0.68	-4.63	0.00267	0.015438	-1.78
250453_at	putative protein predicted protein, I	---	AT5G10620	-1.60	-0.68	-4.63	0.002671	0.015438	-1.78
246074_at	hypothetical protein ; supported by	---	AT5G20130	1.40	0.49	4.63	0.002671	0.015438	-1.78
248242_at	aldo/keto reductase-like protein	---	AT5G53580	1.61	0.68	4.62	0.002674	0.015452	-1.78
261238_at	hypothetical protein predicted by ge	---	AT1G32810	1.46	0.55	4.62	0.002676	0.015462	-1.78
255495_at	predicted protein of unknown funct	---	AT4G02720	1.45	0.53	4.62	0.002678	0.015466	-1.78
257857_s_a	unknown protein contains an RNas	RRP45a	AT3G12990	1.76	0.82	4.62	0.002679	0.015467	-1.79
245565_at	hypothetical protein	---	AT4G14605	1.48	0.57	4.62	0.00268	0.015467	-1.79
260879_at	hypothetical protein predicted by ge	---	AT1G21480	-1.47	-0.55	-4.62	0.00268	0.015467	-1.79
259677_at	putative phosphatidylinositol-4-phos	---	AT1G77740	-1.63	-0.70	-4.62	0.00268	0.015467	-1.79
255226_at	UV-damaged DNA binding factor -	DDB1A	AT4G05420	1.39	0.47	4.62	0.002685	0.015486	-1.79
257002_at	oligouridylate binding protein, putat	---	AT3G14100	1.59	0.67	4.62	0.002685	0.015486	-1.79
259605_at	unknown protein	PUB45	AT1G27910	-1.95	-0.96	-4.62	0.002686	0.015486	-1.79
266064_at	expressed protein	---	AT2G18780	1.62	0.69	4.62	0.002686	0.015486	-1.79
261313_at	hypothetical protein predicted by ge	---	AT1G52970	-1.35	-0.44	-4.62	0.002688	0.015487	-1.79
265352_at	cytosolic cyclophilin (ROC3) ;suppo	ROC3	AT2G16600	1.48	0.57	4.62	0.002693	0.01551	-1.79
262342_at	unknown protein similar to hypothet	---	AT1G64150	-1.89	-0.92	-4.62	0.002693	0.01551	-1.79
264855_at	3-hydroxy-3-methylglutaryl-coenzy	HSK	AT2G17265	1.40	0.48	4.62	0.002695	0.015518	-1.79
257876_at	hypothetical protein predicted by ge	---	AT3G17130	-2.00	-1.00	-4.62	0.002696	0.015518	-1.79
255225_at	U3 snoRNP-associated -like protei	---	AT4G05410	2.33	1.22	4.62	0.002698	0.015527	-1.79
247197_at	receptor-like protein kinase	---	AT5G65240	2.32	1.22	4.62	0.002702	0.015541	-1.79
262594_at	putative 60s ribosomal protein L37	---	AT1G15250	2.75	1.46	4.61	0.002705	0.015544	-1.80
259292_at	unknown protein	---	AT3G11560	1.47	0.56	4.61	0.002705	0.015544	-1.80
254054_at	putative protein DNA-binding prote	---	AT4G25320	1.70	0.76	4.61	0.002706	0.015544	-1.80
249838_at	unknown protein ;supported by full-	---	AT5G23460	1.64	0.72	4.61	0.002706	0.015544	-1.80
247791_at	cyclophilin ROC7 ;supported by ful	ROC7	AT5G58710	1.65	0.72	4.61	0.002706	0.015544	-1.80
255018_at	hypothetical protein ; supported by	---	AT4G10090	1.62	0.69	4.61	0.002707	0.015544	-1.80
257652_at	unknown protein contains Pfam pro	APUM24	AT3G16810	2.02	1.02	4.61	0.002707	0.015544	-1.80
253825_at	Expressed protein ; supported by fu	---	AT4G28025	-1.68	-0.75	-4.61	0.00271	0.015557	-1.80
263384_at	hypothetical protein predicted by ge	---	AT2G40130	-1.51	-0.60	-4.61	0.002711	0.015558	-1.80
260645_at	hypothetical protein predicted by ge	TTL1	AT1G53300	-1.93	-0.95	-4.61	0.002712	0.015558	-1.80
255261_s_a	putative protein equilibrative nucle	FUR1	AT4G05110	-2.81	-1.49	-4.61	0.002713	0.015558	-1.80

257761_at	unknown protein	---	AT3G23090	-2.01	-1.01	-4.61	0.002713	0.015558	-1.80
254078_at	putative protein various predicted p	---	AT4G25710	1.50	0.58	4.61	0.002716	0.015565	-1.80
255224_at	putative protein hypothetical protei	---	AT4G05400	1.58	0.66	4.61	0.002717	0.015565	-1.80
245266_at	hypothetical protein ; supported by	---	AT4G17070	1.89	0.92	4.61	0.002718	0.015568	-1.80
245059_at	unknown protein ;supported by full-	RHC2A	AT2G39720	-1.38	-0.46	-4.61	0.002718	0.015568	-1.80
260984_at	Expressed protein ; supported by fu	---	AT1G53645	2.01	1.01	4.61	0.00272	0.015571	-1.80
251357_at	ribosomal protein S27 ; supported	ARS27A	AT3G61110	1.95	0.97	4.61	0.002727	0.015606	-1.80
265726_at	putative inositol polyphosphate 5'-p	---	AT2G32010	1.69	0.76	4.61	0.002727	0.015606	-1.80
266036_s_a	20S proteasome subunit (PAA2) ide	PAA2	AT2G05840	1.43	0.51	4.61	0.002735	0.015641	-1.81
260112_at	unknown protein similar to unknowr	---	AT1G63310	-1.61	-0.69	-4.60	0.002736	0.015643	-1.81
255249_at	3(2),5-BISPHOSPHATE NUCLEO1	---	AT4G05090	-1.83	-0.87	-4.60	0.00274	0.015665	-1.81
258996_at	putative ribosome recycling factor s	---	AT3G01800	1.61	0.69	4.60	0.002741	0.015665	-1.81
251784_at	putative protein photosystem II oxy	PPL1	AT3G55330	-1.84	-0.88	-4.60	0.002742	0.015667	-1.81
246775_at	putative protein GTP-binding protei	MIRO1	AT5G27540	1.36	0.44	4.60	0.002743	0.015667	-1.81
260786_s_a	unknown protein similar to Cryptosp	MEE5	AT1G06220	1.56	0.64	4.60	0.002746	0.015682	-1.81
248975_at	unknown protein ; supported by cD	---	AT5G45040	-1.46	-0.54	-4.60	0.002747	0.015682	-1.81
264731_at	hypothetical protein predicted by ge	---	AT1G62150	1.48	0.56	4.60	0.002751	0.015702	-1.81
258046_at	MAP kinase kinase 5 identical to GI	MKK5	AT3G21220	1.45	0.54	4.60	0.002763	0.015758	-1.82
259176_at	putative cell division control protein	CDC48C	AT3G01610	1.47	0.55	4.60	0.002764	0.015762	-1.82
245164_at	mitochondrial chaperonin (HSP60)	HSP60-2	AT2G33210	2.44	1.29	4.59	0.002785	0.015879	-1.83
245373_s_a	Expressed protein ; supported by fu	ATARD2	AT4G14710	1.45	0.54	4.59	0.00279	0.015899	-1.83
245999_at	putative protein predicted protein, /	COPT5	AT5G20650	1.38	0.47	4.59	0.002794	0.015918	-1.83
264064_at	hypothetical protein predicted by ge	---	AT2G27900	-1.42	-0.50	-4.59	0.002795	0.015918	-1.83
267093_at	high affinity Ca2+ antiporter identic	CAX1	AT2G38170	1.83	0.87	4.59	0.002798	0.015931	-1.83
245543_at	glucosyltransferase	---	AT4G15260	1.53	0.61	4.58	0.002799	0.015931	-1.83
266662_at	hypothetical protein predicted by ge	---	AT2G25830	-1.62	-0.70	-4.58	0.002799	0.015931	-1.83
260465_at	membrane-associated salt-inducible	---	AT1G10910	1.32	0.40	4.58	0.002811	0.015995	-1.84
266568_at	unknown protein	---	AT2G24070	-1.37	-0.46	-4.58	0.002817	0.016026	-1.84
266776_at	putative ubiquitin fusion-degradatio	---	AT2G29070	1.55	0.63	4.58	0.002822	0.016047	-1.84
254023_at	putative protein hypothetical protei	---	AT4G25770	-1.53	-0.62	-4.58	0.002827	0.016065	-1.84
253507_at	serine threonine protein kinase like	---	AT4G32000	-1.74	-0.80	-4.58	0.002827	0.016065	-1.84
259461_at	unknown protein	---	AT1G18900	1.81	0.86	4.58	0.002829	0.016074	-1.84
264670_s_a	unknown protein Similar to elongat	---	AT1G09640	1.56	0.64	4.58	0.00283	0.016074	-1.84
262395_at	hypothetical protein similar to hypot	---	AT1G49540	2.03	1.02	4.57	0.002833	0.01608	-1.85
262310_at	unknown protein contains similarity	MLP31	AT1G70840	-1.45	-0.54	-4.57	0.002835	0.016088	-1.85

252929_at	putative fructose-bisphosphate ald	---	AT4G38970	-1.43	-0.51	-4.57	0.002835	0.016089	-1.85
255593_at	hypothetical protein	---	AT4G01650	1.44	0.53	4.57	0.002837	0.016092	-1.85
245100_at	ubiquitin-specific protease 5 (UBP5	UBP5	AT2G40930	1.42	0.51	4.57	0.002841	0.016109	-1.85
253547_at	chloroplast omega-6 fatty acid desa	FAD6	AT4G30950	-1.42	-0.51	-4.57	0.002841	0.016109	-1.85
257775_at	short-chain alcohol dehydrogenase	---	AT3G29260	-1.48	-0.57	-4.57	0.002845	0.016117	-1.85
253072_at	putative protein ;supported by full-l	---	AT4G37830	1.36	0.45	4.57	0.002845	0.016117	-1.85
250133_at	thioredoxin f2 (gb|AAD35004.1) ; s	TRXF2	AT5G16400	-1.95	-0.96	-4.57	0.002846	0.016117	-1.85
261753_at	unknown protein	---	AT1G76340	-1.52	-0.61	-4.57	0.002846	0.016117	-1.85
256110_at	Ser Thr protein kinase, putative sin	---	AT1G16900	1.69	0.75	4.57	0.002847	0.016117	-1.85
246258_at	PPR-repeat protein, putative conta	---	AT1G31840	1.40	0.49	4.57	0.002847	0.016117	-1.85
259824_at	copper homeostasis factor, putativ	ATX1	AT1G66240	1.40	0.48	4.57	0.002847	0.016117	-1.85
258243_at	carbamoyl phosphate synthetase s	CARA	AT3G27740	1.73	0.79	4.57	0.002861	0.016186	-1.86
253849_at	putative protein 150-kD protein, Di	---	AT4G28080	-1.40	-0.49	-4.57	0.002862	0.016186	-1.86
252943_at	cinnamyl-alcohol dehydrogenase C	CAD9	AT4G39330	-12.83	-3.68	-4.56	0.002868	0.016212	-1.86
255677_at	putative calmodulin-binding heat sh	---	AT4G00500	1.75	0.81	4.56	0.00287	0.016212	-1.86
259682_at	transcription factor DREB1A, putat	---	AT1G63040	-1.67	-0.74	-4.56	0.00287	0.016212	-1.86
257060_at	unknown protein	---	AT3G18230	1.47	0.56	4.56	0.002872	0.016216	-1.86
254761_at	Expressed protein ; supported by fu	CLE44	AT4G13195	1.70	0.76	4.56	0.002872	0.016216	-1.86
257009_at	unknown protein ; supported by cD	---	AT3G14160	1.38	0.46	4.56	0.002874	0.016217	-1.86
259837_at	aquaporin, putative similar to delta	---	AT1G52180	-1.78	-0.83	-4.56	0.002874	0.016217	-1.86
265254_at	unknown protein ; supported by cD	DRB2	AT2G28380	-1.45	-0.54	-4.56	0.002878	0.016238	-1.86
248409_at	putative protein contains similarity t	LPA2	AT5G51540	-1.56	-0.64	-4.56	0.00288	0.016246	-1.86
248744_at	putative protein contains similarity t	---	AT5G48250	1.66	0.73	4.56	0.002883	0.016256	-1.87
250833_at	myotubularin - like protein myotubu	---	AT5G04540	1.41	0.50	4.56	0.002883	0.016256	-1.87
247410_at	putative protein similar to unknown	emb1692	AT5G62990	1.99	0.99	4.56	0.002887	0.016264	-1.87
256314_at	hypothetical protein	TOC75-I	AT1G35860	-1.45	-0.54	-4.56	0.002888	0.016264	-1.87
247608_at	replication protein A1 - like probabl	---	AT5G60990	1.56	0.64	4.56	0.002888	0.016264	-1.87
261634_at	ATP-dependent Clp protease prote	CLPR1	AT1G49970	1.61	0.69	4.56	0.002889	0.016264	-1.87
258904_at	putative ATPase (ISW2-like) simila	CHR11	AT3G06400	1.48	0.57	4.56	0.002889	0.016264	-1.87
259067_at	F-box protein family, AtFBL12 cont	---	AT3G07550	-1.38	-0.46	-4.56	0.00289	0.016267	-1.87
267550_at	putative protein kinase contains a p	AP4.3A	AT2G32800	-2.40	-1.26	-4.56	0.002892	0.016272	-1.87
246782_at	putative protein PrMC3 - Pinus rad	GID1C	AT5G27320	2.08	1.05	4.56	0.002893	0.016272	-1.87
258924_at	putative diadenosine 5',5'''-P1,P4-t	ATNUDX26	AT3G10620	-1.39	-0.48	-4.55	0.002903	0.016325	-1.87
246767_at	putative protein CG6949 - Drosoph	---	AT5G27395	2.55	1.35	4.55	0.002905	0.016325	-1.87
256078_at	hypothetical protein predicted by ge	---	AT1G20670	-1.45	-0.54	-4.55	0.002906	0.016325	-1.87

258041_at	Expressed protein ; supported by fu	ZML1	AT3G21175	1.46	0.55	4.55	0.002906	0.016325	-1.87
249748_at	thaumatin-like protein	---	AT5G24620	-1.48	-0.57	-4.55	0.002909	0.016325	-1.87
258226_at	putative phospholipase D similar to	PLDALPHA	AT3G15730	-1.45	-0.53	-4.55	0.002909	0.016325	-1.87
246565_at	biotin carboxyl carrier protein precu	BCCP2	AT5G15530	-1.46	-0.54	-4.55	0.00291	0.016325	-1.88
266671_at	anthranilate synthase, alpha subun	ASA2	AT2G29690	-1.49	-0.57	-4.55	0.00291	0.016325	-1.88
259754_at	hypothetical protein predicted by ge	---	AT1G71090	1.48	0.57	4.55	0.002911	0.016328	-1.88
267646_at	putative phosphate transporter	PHT5	AT2G32830	1.76	0.82	4.55	0.002916	0.016349	-1.88
255756_at	endo-beta-1,4-D-glucanase, putativ	AtGH9B5	AT1G19940	-1.47	-0.55	-4.55	0.002917	0.016349	-1.88
258974_at	unknown protein similar to brahma	---	AT3G01890	1.48	0.57	4.55	0.002925	0.016388	-1.88
246339_at	RP19 gene for chloroplast ribosoma	RPL9	AT3G44890	-1.48	-0.56	-4.54	0.002931	0.016414	-1.88
254262_at	putative protein annexin VII, Dictyo	---	AT4G23470	-1.57	-0.66	-4.54	0.002932	0.016414	-1.88
250234_at	transaldolase - like protein transald	---	AT5G13420	1.69	0.76	4.54	0.002932	0.016414	-1.88
259159_at	unknown protein contains Pfam pro	ACBP4	AT3G05420	-1.64	-0.71	-4.54	0.002934	0.01642	-1.88
259162_at	unknown protein similar to unknown	---	AT3G01640	-1.55	-0.63	-4.54	0.002943	0.016451	-1.89
264690_at	hypothetical protein similar to hypot	SNL4	AT1G70060	-1.58	-0.66	-4.54	0.002943	0.016451	-1.89
254945_at	putative RING finger protein ring fi	---	AT4G10940	-1.55	-0.64	-4.54	0.002943	0.016451	-1.89
267095_at	putative AMP deaminase ; support	FAC1	AT2G38280	1.51	0.60	4.54	0.002945	0.016455	-1.89
255494_at	predicted protein of unknown funct	---	AT4G02710	1.39	0.48	4.54	0.002951	0.016482	-1.89
251576_at	putative protein several hypothetica	---	AT3G58200	1.40	0.48	4.54	0.002951	0.016482	-1.89
266453_at	putative protein kinase contains a p	---	AT2G43230	-1.35	-0.43	-4.54	0.002956	0.016507	-1.89
260731_at	P-type ATPase, putative similar to	---	AT1G17500	-1.52	-0.60	-4.54	0.002958	0.016508	-1.89
255413_at	putative alcohol dehydrogenase sim	---	AT4G03140	-1.49	-0.58	-4.54	0.002959	0.016508	-1.89
254952_at	UDP-galactose 4-epimerase - like	UGE5	AT4G10955	1.52	0.61	4.54	0.002959	0.016508	-1.89
246294_at	ribosomal protein, chloroplast ribos	PSRP5	AT3G56910	-1.40	-0.48	-4.54	0.002959	0.016508	-1.89
258317_at	hypothetical protein predicted by ge	---	AT3G22670	1.40	0.49	4.54	0.002964	0.016528	-1.90
248228_at	unknown protein ;supported by full-	---	AT5G53800	1.63	0.70	4.53	0.002969	0.016552	-1.90
252223_at	MYB -like protein DNA-binding pro	TRB3	AT3G49850	1.72	0.78	4.53	0.002971	0.01656	-1.90
252118_at	putative protein various predicted p	---	AT3G51400	1.32	0.40	4.53	0.002974	0.016568	-1.90
258563_at	putative long-chain-fatty-acid--CoA	LACS6	AT3G05970	1.47	0.56	4.53	0.002978	0.016568	-1.90
248743_at	unknown protein	---	AT5G48240	1.81	0.85	4.53	0.002978	0.016568	-1.90
244985_at	ribosomal protein L22	---	---	-1.76	-0.81	-4.53	0.002978	0.016568	-1.90
258717_at	unknown protein ; supported by cD	SYP71	AT3G09740	-1.33	-0.41	-4.53	0.002978	0.016568	-1.90
257324_at	hypothetical protein	---	---	2.77	1.47	4.53	0.00298	0.016568	-1.90
248014_at	putative protein similar to unknown	---	AT5G56340	-1.60	-0.68	-4.53	0.002981	0.016568	-1.90
260585_at	unknown protein	EMB2777	AT2G43650	2.14	1.10	4.53	0.002982	0.016568	-1.90

264270_at	beta-glucosidase, putative similar t	---	---	-1.37	-0.45	-4.53	0.002984	0.016572	-1.90
253657_at	cadmium-transporting ATPase-like	HMA2	AT4G30110	2.57	1.36	4.53	0.002984	0.016572	-1.90
255886_at	plastocyanin, putative similar to pla	DRT112	AT1G20340	-1.39	-0.48	-4.53	0.002985	0.016573	-1.90
254867_at	hypothetical proteins	---	AT4G12240	1.68	0.75	4.53	0.002992	0.016606	-1.91
267530_at	putative receptor-like protein kinase	---	AT2G41890	2.32	1.21	4.53	0.002994	0.016613	-1.91
253589_at	puative protein membrane-associa	---	AT4G30825	1.67	0.74	4.53	0.002996	0.01662	-1.91
250235_s_a	ubiquinol--cytochrome-c reductase	---	AT5G13430	1.36	0.44	4.53	0.002998	0.016625	-1.91
260641_at	hypothetical protein predicted by ge	---	AT1G53200	1.98	0.99	4.52	0.003	0.016636	-1.91
263171_at	unknown protein	CCX4	AT1G54115	1.46	0.54	4.52	0.003006	0.016658	-1.91
254132_at	putative protein hypothetical protei	ATHB22	AT4G24660	1.77	0.82	4.52	0.003006	0.016658	-1.91
258217_at	unknown protein contains Pfam pro	XPL1	AT3G17998	-1.88	-0.91	-4.52	0.003007	0.016658	-1.91
265899_s_a	SKP1/ASK1 (At3), putative similar	ASK4	AT1G20140	1.48	0.56	4.52	0.003008	0.016659	-1.91
250321_at	zinc finger transcription factor -like	---	AT5G12850	-1.46	-0.55	-4.52	0.003012	0.016681	-1.91
252927_at	cysteine proteinase RD19A identic	RD19	AT4G39090	1.37	0.46	4.52	0.003014	0.016685	-1.91
264367_at	unknown protein ESTs gb|T21276,	---	AT1G03350	-1.40	-0.49	-4.52	0.003015	0.016687	-1.91
251710_at	putative protein several hypothetica	---	AT3G56930	-2.02	-1.01	-4.52	0.003016	0.016687	-1.91
261037_at	lipoxygenase identical to GB:CAB5	LOX3	AT1G17420	-5.47	-2.45	-4.52	0.003017	0.016687	-1.91
248303_at	FtsH protease, putative similar to A	FTSH11	AT5G53170	1.45	0.54	4.52	0.003017	0.016687	-1.91
259536_s_a	putative protein hypothetical protein	ATCOAB	AT1G12350	1.33	0.41	4.52	0.003018	0.016687	-1.91
265586_at	pathogenesis-related protein (PR-1	PR-1-LIKE	AT2G19990	-1.56	-0.64	-4.52	0.00302	0.016689	-1.92
256405_at	calcium-dependent protein kinase s	CPK33	AT1G50700	1.38	0.47	4.52	0.00302	0.016689	-1.92
253362_s_a	putative protein cyclopropane-fatty	---	AT4G33110	-1.66	-0.73	-4.52	0.00302	0.016689	-1.92
260148_at	putative oxidoreductase similar to g	---	AT1G52800	1.74	0.80	4.52	0.003021	0.016691	-1.92
246908_at	dehydration-induced protein RD22	RD22	AT5G25610	-4.93	-2.30	-4.52	0.003022	0.016693	-1.92
260575_at	hypothetical protein predicted by ge	---	AT2G47300	1.45	0.54	4.52	0.003028	0.016718	-1.92
256106_at	unknown protein	---	AT1G16870	1.40	0.48	4.52	0.003028	0.016718	-1.92
259277_at	putative glycogen synthase similar t	AtSS2	AT3G01180	-1.74	-0.80	-4.52	0.003031	0.016725	-1.92
246155_at	putative protein predicted proteins,	---	AT5G20030	-1.34	-0.42	-4.52	0.003032	0.01673	-1.92
253977_at	putative protein various Caenorhab	---	AT4G26630	1.73	0.79	4.52	0.003034	0.016738	-1.92
254819_at	pEARLI 1-like protein Arabidopsis t	---	AT4G12500	11.09	3.47	4.51	0.003036	0.016743	-1.92
260862_at	unknown protein	SEU	AT1G43850	1.42	0.50	4.51	0.00304	0.016756	-1.92
260632_at	homeobox protein, putative similar	STM	AT1G62360	-1.45	-0.54	-4.51	0.00304	0.016756	-1.92
263605_at	hypothetical protein predicted by ge	---	AT2G16485	1.56	0.64	4.51	0.003042	0.016763	-1.92
252504_at	telomere repeat-binding protein ho	TRFL1	AT3G46590	1.41	0.50	4.51	0.003044	0.016773	-1.92
258480_at	unknown protein ;supported by full-	---	AT3G02640	-1.47	-0.56	-4.51	0.003047	0.01678	-1.93

264952_at	Tub family protein, putative contain	AtTLP1	AT1G76900	-1.36	-0.45	-4.51	0.003047	0.01678	-1.93
266239_at	unknown protein ; supported by cD	---	AT2G29530	2.19	1.13	4.51	0.00305	0.016794	-1.93
257964_at	hypothetical protein similar to hypot	---	AT3G19850	-1.79	-0.84	-4.51	0.003053	0.016807	-1.93
249356_at	putative protein predicted proteins,	---	AT5G40520	1.84	0.88	4.51	0.003056	0.016809	-1.93
245925_at	bZIP transcription factor family prot	BZO2H3	AT5G28770	-1.68	-0.75	-4.51	0.003056	0.016809	-1.93
255021_at	hypothetical protein	---	AT4G10330	1.44	0.52	4.51	0.003056	0.016809	-1.93
250564_at	putative protein sigma factor F inhi	---	AT5G08060	1.34	0.42	4.51	0.003057	0.016809	-1.93
266701_at	profilin 1 ; supported by cDNA: gi_	PRF1	AT2G19760	-1.34	-0.42	-4.51	0.003057	0.016809	-1.93
249574_at	putative protein embryonic abunda	PDLP7	AT5G37660	-1.45	-0.54	-4.51	0.00306	0.016818	-1.93
246122_at	putative protein brain specific Na+-	PHT4;5	AT5G20380	1.51	0.59	4.51	0.003061	0.016818	-1.93
249828_at	succinyl-CoA synthetase, alpha su	---	AT5G23250	1.56	0.64	4.51	0.003061	0.016818	-1.93
260916_at	predicted protein ; supported by cD	---	AT1G02475	1.46	0.55	4.51	0.003067	0.016847	-1.93
260266_at	putative B-box zinc finger protein co	---	AT1G68520	-1.65	-0.72	-4.51	0.003068	0.016847	-1.93
264018_at	putative triosephosphate isomerase	TIM	AT2G21170	-1.42	-0.51	-4.51	0.00307	0.016852	-1.93
248886_at	phosphate/triose-phosphate translo	APE2	AT5G46110	-1.46	-0.55	-4.50	0.003071	0.016854	-1.93
263526_at	hypothetical protein predicted by ge	---	AT2G24830	1.39	0.47	4.50	0.003072	0.016854	-1.93
261561_at	unknown protein ;supported by full-	---	AT1G01730	1.69	0.76	4.50	0.003077	0.016878	-1.94
260616_at	hypothetical protein contains Pfam	---	AT1G53280	1.63	0.71	4.50	0.003082	0.016901	-1.94
255520_at	putative ribosomal protein L19 simil	---	AT4G02230	1.86	0.90	4.50	0.003085	0.016916	-1.94
249248_at	unknown protein	---	AT5G42320	-1.51	-0.60	-4.50	0.003087	0.016924	-1.94
257610_at	zinc finger protein, putative similar	AtIDD11	AT3G13810	2.33	1.22	4.50	0.003089	0.016929	-1.94
250156_at	putative protein predicted proteins,	---	AT5G15170	1.36	0.44	4.50	0.00309	0.016931	-1.94
253726_at	ribosomal protein S15a homolog ri	rps15ae	AT4G29430	2.18	1.12	4.50	0.003091	0.016931	-1.94
248833_at	Bax inhibitor-1 like ;supported by fu	ATBI1	AT5G47120	1.55	0.63	4.50	0.003093	0.016939	-1.94
254326_at	putative protein AIR1, Arabidopsis	---	AT4G22610	-1.46	-0.55	-4.49	0.003112	0.017033	-1.95
254765_at	hypothetical protein	---	AT4G13270	1.49	0.57	4.49	0.003114	0.017038	-1.95
263696_at	putative aspartate kinase-homoseri	AK-HSDH I	AT1G31230	1.79	0.84	4.49	0.00312	0.017061	-1.95
252527_at	dTDP-glucose 4-6-dehydratases-lil	UXS5	AT3G46440	1.53	0.62	4.49	0.00312	0.017061	-1.95
246211_at	G-box-binding factor 1 ; supported I	GBF1	AT4G36730	-2.00	-1.00	-4.49	0.003123	0.017069	-1.95
259348_at	hypothetical protein may contain C	---	AT3G03770	-1.82	-0.86	-4.49	0.003129	0.017099	-1.95
261553_at	hypothetical protein	---	AT1G63420	-1.50	-0.59	-4.49	0.003131	0.017108	-1.95
255979_at	hypothetical protein	UPF3	AT1G33980	1.43	0.52	4.49	0.003134	0.017119	-1.96
256510_at	ATP-dependent Clp protease ATP-	---	AT1G33360	1.48	0.57	4.49	0.003137	0.017126	-1.96
263120_at	cytochrome P450, putative similar	CYP708A3	AT1G78490	-7.43	-2.89	-4.49	0.003138	0.017128	-1.96
251092_at	putative protein ;supported by full-l	---	AT5G01470	-1.44	-0.53	-4.49	0.00314	0.017136	-1.96

264864_at	hypothetical protein predicted by ge	---	AT1G24310	1.80	0.85	4.48	0.003144	0.017149	-1.96
264693_at	hypothetical protein predicted by ge	CLE26	AT1G69970	-1.42	-0.50	-4.48	0.003144	0.017149	-1.96
266093_at	unknown protein ;supported by full-	---	AT2G37990	1.72	0.78	4.48	0.003149	0.017172	-1.96
260145_at	putative G protein-coupled receptor	GPCR	AT1G52920	1.33	0.41	4.48	0.003158	0.017215	-1.96
262005_at	ABC transporter protein, putative s	ATGCN3	AT1G64550	1.65	0.72	4.48	0.003159	0.017219	-1.96
262487_at	unknown protein ESTs gb|T42839 a	---	AT1G21610	1.30	0.38	4.48	0.003163	0.017232	-1.97
251841_at	putative protein CRP1, Zea mays,	---	AT3G54980	1.81	0.85	4.48	0.003163	0.017232	-1.97
259919_at	putative exportin, tRNA (nuclear ex	PSD	AT1G72560	1.63	0.70	4.48	0.003164	0.017232	-1.97
263600_at	hypothetical protein predicted by ge	DRD1	AT2G16390	-1.48	-0.57	-4.48	0.003168	0.017245	-1.97
259718_at	unknown protein	VIP5	AT1G61040	1.34	0.42	4.48	0.003168	0.017245	-1.97
257086_at	hypothetical protein predicted by ge	---	AT3G20490	1.70	0.77	4.48	0.003169	0.017245	-1.97
246817_at	putative protein various predicted p	---	AT5G27240	1.49	0.57	4.48	0.00317	0.017249	-1.97
259849_at	phosphoglycerate dehydrogenase,	---	AT1G72190	1.34	0.42	4.48	0.003173	0.017258	-1.97
264214_s_a	MADS-box transcription factor, put	AGL38	AT1G65300	-1.38	-0.47	-4.47	0.003179	0.017284	-1.97
245626_at	unknown protein ;supported by full-	---	AT1G56700	1.67	0.74	4.47	0.003179	0.017284	-1.97
253383_at	putative protein ;supported by full-l	---	AT4G32900	1.69	0.76	4.47	0.003181	0.017286	-1.97
245593_at	IAA7 like protein	IAA14	AT4G14550	-2.51	-1.33	-4.47	0.003182	0.017286	-1.97
258099_at	unknown protein similar to hypothet	---	AT3G23540	1.41	0.50	4.47	0.003183	0.017286	-1.97
258160_at	glutamine synthetase, putative sim	GLN1.3	AT3G17820	1.89	0.92	4.47	0.003187	0.017296	-1.97
247176_at	acyl-CoA oxidase (gb|AAC13497.1)	ACX2	AT5G65110	1.76	0.81	4.47	0.003187	0.017296	-1.97
253248_at	Putative S-phase-specific ribosoma	---	AT4G34670	2.47	1.30	4.47	0.003187	0.017296	-1.97
260590_at	phosphoenolpyruvate carboxylase	ATPPC1	AT1G53310	1.59	0.66	4.47	0.003195	0.017329	-1.98
253020_at	hypothetical protein	---	AT4G38020	1.61	0.68	4.47	0.003198	0.017335	-1.98
266574_at	hypothetical protein predicted by ge	---	AT2G23890	2.09	1.06	4.47	0.003198	0.017335	-1.98
250390_at	separation anxiety protein - like se	---	AT5G11340	1.32	0.40	4.47	0.003198	0.017335	-1.98
248491_at	unknown protein ;supported by full-	---	AT5G51010	1.67	0.74	4.47	0.003199	0.017335	-1.98
252849_at	Histon H3 ;supported by full-length	---	AT4G40040	1.41	0.50	4.47	0.0032	0.017335	-1.98
250350_at	putative protein predicted proteins,	---	AT5G12010	-2.09	-1.06	-4.47	0.003202	0.017345	-1.98
265284_at	unknown protein ;supported by full-	---	AT2G20230	1.48	0.56	4.47	0.003204	0.017345	-1.98
265384_at	unknown protein ;supported by full-	---	AT2G20760	-1.33	-0.41	-4.47	0.003204	0.017345	-1.98
246263_at	unknown protein	---	AT1G31780	-1.58	-0.66	-4.47	0.003205	0.017345	-1.98
264678_at	putative U2 small nuclear ribonucle	U2A'	AT1G09760	1.44	0.53	4.47	0.003206	0.017345	-1.98
254851_at	putative disease resistance protein	---	AT4G12010	1.92	0.94	4.47	0.003206	0.017345	-1.98
260480_at	Ser/Thr kinase ;supported by full-le	SNRK2.4	AT1G10940	1.32	0.40	4.47	0.003208	0.017349	-1.98
263243_at	putative glyoxalase II	GLX2-5	AT2G31350	1.50	0.59	4.47	0.003209	0.017349	-1.98

261207_at	peroxisomal targeting signal type 2	---	AT1G12830	1.74	0.80	4.47	0.003209	0.017349	-1.98
250571_at	hypothetical protein	---	AT5G08200	-1.66	-0.73	-4.47	0.003216	0.017381	-1.98
252186_at	putative protein	---	AT3G50810	1.52	0.60	4.46	0.003217	0.017386	-1.98
251249_at	putative protein 10-deacetylbaccat	---	AT3G62160	-1.45	-0.54	-4.46	0.00322	0.017393	-1.99
263386_at	unknown protein ; supported by cD	---	AT2G40150	-2.08	-1.06	-4.46	0.003222	0.017401	-1.99
258026_at	abscisic acid responsive elements-l	ABF4	AT3G19290	1.61	0.69	4.46	0.003224	0.017402	-1.99
251310_at	homeobox protein Anthocyaninless	HDG1	AT3G61150	-1.59	-0.67	-4.46	0.003225	0.017402	-1.99
252335_at	putative protein putative protein - A	---	AT3G48860	1.49	0.57	4.46	0.003225	0.017402	-1.99
259533_at	hypothetical protein	---	AT1G12530	1.33	0.41	4.46	0.003227	0.017402	-1.99
250625_at	calnexin homolog	---	AT5G07340	1.67	0.74	4.46	0.003227	0.017402	-1.99
264065_at	hypothetical protein predicted by ge	---	AT2G27900	-1.47	-0.55	-4.46	0.003227	0.017402	-1.99
254559_at	putative protein glycine/proline-rich	---	AT4G19200	-1.70	-0.76	-4.46	0.003232	0.017414	-1.99
251656_at	putative protein N-ACETYLGLUCO	---	AT3G57170	-1.44	-0.53	-4.46	0.003232	0.017414	-1.99
246244_at	receptor kinase-like protein	---	AT4G37250	-1.40	-0.48	-4.46	0.003232	0.017414	-1.99
258502_at	unknown protein	---	AT3G02490	1.86	0.89	4.46	0.003234	0.017416	-1.99
247607_at	putative protein various predicted p	---	AT5G60960	1.95	0.97	4.46	0.003235	0.01742	-1.99
245806_at	light-harvesting complex protein sim	LHCA5	AT1G45474	-1.85	-0.88	-4.46	0.003237	0.017426	-1.99
265119_at	flavin-containing monooxygenase,	FMO GS-O	AT1G62570	-2.16	-1.11	-4.46	0.003238	0.017426	-1.99
256288_at	arginine N-methyltransferase 3, pu	PRMT3	AT3G12270	2.23	1.16	4.46	0.00324	0.017435	-1.99
267442_at	unknown protein ;supported by full-	---	AT2G19080	1.37	0.45	4.46	0.003242	0.017437	-1.99
258297_at	Expressed protein ; supported by fu	---	AT3G23325	1.46	0.55	4.46	0.003243	0.017437	-1.99
258945_at	calmodulin-domain protein kinase (	CPK2	AT3G10660	-1.34	-0.42	-4.46	0.003243	0.017437	-1.99
256858_at	hypothetical protein predicted by ge	---	AT3G15140	1.69	0.76	4.46	0.003244	0.017437	-1.99
261709_at	RNA-binding protein, putative simil	CID11	AT1G32790	1.40	0.49	4.46	0.003247	0.017445	-1.99
265301_s_a	putative MYB family transcription fa	---	AT2G13960	1.45	0.53	4.46	0.003249	0.017451	-2.00
247271_at	nuclear protein-like	---	AT5G64270	1.50	0.59	4.46	0.00325	0.017452	-2.00
253648_at	pathogenesis related homeodomair	PRHA	AT4G29940	1.35	0.43	4.45	0.003257	0.017486	-2.00
257456_at	unknown protein predicted by gens	SRS4	AT2G18120	-1.45	-0.53	-4.45	0.00326	0.017497	-2.00
258174_at	hypothetical protein contains Pfam	---	AT3G21470	1.45	0.54	4.45	0.003262	0.017497	-2.00
250966_at	putative protein various predicted p	---	AT5G02910	1.54	0.62	4.45	0.003262	0.017497	-2.00
259723_at	putative iron-regulated transporter s	IRT3	AT1G60960	2.20	1.14	4.45	0.00327	0.017536	-2.00
266520_at	cyclic nucleotide and calmodulin-re	ATCNGC6	AT2G23980	1.51	0.59	4.45	0.003273	0.017543	-2.00
247601_at	zinc finger protein OBP4 - like zinc	OBP4	AT5G60850	-1.71	-0.78	-4.45	0.003276	0.017556	-2.00
263975_at	hypothetical protein predicted by ge	---	AT2G42710	1.47	0.56	4.45	0.003279	0.017571	-2.01
260331_at	hypothetical protein contains Pfam	---	AT1G80270	4.57	2.19	4.44	0.003294	0.017644	-2.01

252055_at	putative ribosomal protein S14 ribo	---	AT3G52580	1.56	0.64	4.44	0.003295	0.017644	-2.01
259648_at	hypothetical protein predicted by ge	---	---	-1.34	-0.42	-4.44	0.003298	0.017647	-2.01
261348_at	hypothetical protein contains simila	TED3	AT1G79810	1.37	0.46	4.44	0.003298	0.017647	-2.01
265032_at	ribosomal protein identical to riboso	RPL3B	AT1G61580	2.20	1.14	4.44	0.003298	0.017647	-2.01
250144_at	putative protein various predicted p	---	AT5G14680	1.86	0.90	4.44	0.003301	0.017659	-2.01
252566_at	cytoplasmic ribosomal protein S15	RPS15AD	AT3G46040	1.59	0.67	4.44	0.003305	0.017672	-2.01
258375_at	hypothetical protein predicted by ge	---	AT3G17470	-1.38	-0.46	-4.44	0.003313	0.017707	-2.02
246601_at	copper amine oxidase, putative sim	---	AT1G31710	-11.77	-3.56	-4.44	0.003313	0.017707	-2.02
245560_at	indole-3-acetate beta-glucosyltrans	UGT84A1	AT4G15480	-1.52	-0.60	-4.44	0.003316	0.017712	-2.02
253901_at	ribosomal protein L14 -like protein	---	AT4G27090	1.80	0.84	4.44	0.003316	0.017712	-2.02
245256_at	Expressed protein ; supported by cl	FAR1	AT4G15090	1.50	0.59	4.44	0.003317	0.017712	-2.02
261898_at	hypothetical protein predicted by ge	---	AT1G80720	2.08	1.06	4.44	0.003317	0.017712	-2.02
256986_at	unknown protein	---	AT3G28700	1.65	0.72	4.44	0.003319	0.017718	-2.02
259711_at	putative DNA-binding protein simila	---	AT1G77570	2.27	1.18	4.44	0.003322	0.017726	-2.02
248265_at	putative protein contains similarity t	SDG29	AT5G53430	1.63	0.71	4.44	0.003322	0.017726	-2.02
246549_at	putative protein predicted proteins,	---	AT5G15050	-2.00	-1.00	-4.44	0.003327	0.017742	-2.02
262986_at	unknown protein similar to hypothet	---	AT1G23390	-1.99	-0.99	-4.44	0.003331	0.017757	-2.02
257047_at	hypothetical protein predicted by ge	---	AT3G19570	-1.66	-0.73	-4.43	0.003333	0.017757	-2.02
254546_at	lectin like protein lectin 2, phloem-s	PP2-A2	AT4G19850	2.72	1.44	4.43	0.003333	0.017757	-2.02
246904_at	DNA methyltransferase PMT1 - like	DNMT2	AT5G25480	1.51	0.59	4.43	0.003342	0.017801	-2.03
246591_at	putative cation transport protein pu	---	AT5G14880	1.53	0.62	4.43	0.003343	0.017801	-2.03
260073_at	putative protein kinase contains Pfa	---	AT1G73660	1.59	0.67	4.43	0.003354	0.017851	-2.03
254615_at	RNase L inhibitor-like protein RNas	RLI2	AT4G19210	1.39	0.48	4.43	0.003357	0.017863	-2.03
251652_at	putative protein hypothetical protei	---	AT3G57380	1.75	0.81	4.43	0.003358	0.017865	-2.03
260868_at	unknown protein ;supported by full-	---	AT1G43860	1.58	0.66	4.43	0.003364	0.017889	-2.03
257755_at	unknown protein ; supported by full	---	AT3G18760	1.85	0.89	4.43	0.003367	0.0179	-2.03
262654_at	putative mandelonitrile lyase simila	---	AT1G14180	-1.59	-0.67	-4.43	0.003368	0.017901	-2.03
265676_at	putative CCR4-associated factor ;	---	AT2G32070	-1.38	-0.46	-4.42	0.003373	0.017922	-2.04
262284_at	hypothetical protein predicted by ge	---	AT1G68670	1.71	0.78	4.42	0.00338	0.017955	-2.04
260961_at	unknown protein similar to hypothet	---	AT1G05960	-1.33	-0.42	-4.42	0.003382	0.017963	-2.04
249525_at	putative protein similar to unknown	---	AT5G38650	1.38	0.47	4.42	0.003384	0.017966	-2.04
267186_at	unknown protein ; supported by cD	---	AT2G44090	-1.41	-0.50	-4.42	0.003387	0.017977	-2.04
258029_at	serine/threonine-protein kinase, PK	ATPK7	AT3G27580	1.36	0.45	4.42	0.00339	0.01799	-2.04
261049_at	hypothetical protein similar to hypot	---	AT1G01430	-1.74	-0.80	-4.42	0.003392	0.017991	-2.04
258011_at	putative homeobox protein, HAT3.	HAT3.1	AT3G19510	1.59	0.67	4.42	0.003392	0.017992	-2.04

266860_at	putative phospholipase C	---	AT2G26870	-1.98	-0.98	-4.42	0.003397	0.018004	-2.04
264799_at	putative violaxanthin de-epoxidase	NPQ1	AT1G08550	-1.53	-0.61	-4.42	0.0034	0.018016	-2.04
250673_at	serine threonine protein kinase-like	CIPK2	AT5G07070	-1.62	-0.70	-4.42	0.003402	0.018016	-2.04
266183_at	unknown protein	ATPT2	AT2G38940	1.57	0.65	4.42	0.003402	0.018016	-2.04
247349_at	putative protein similar to unknown	---	AT5G63820	-1.38	-0.47	-4.41	0.003411	0.018058	-2.05
245770_at	hypothetical protein predicted by ge	---	AT1G30240	1.83	0.87	4.41	0.003413	0.018061	-2.05
252998_at	probable H+-transporting ATPase I	---	AT4G38510	-1.48	-0.56	-4.41	0.003417	0.018081	-2.05
253947_at	putative protein hypothetical protei	MAP65-2	AT4G26760	1.50	0.58	4.41	0.003418	0.018081	-2.05
256534_at	unknown protein	---	AT1G33270	1.41	0.49	4.41	0.003422	0.018099	-2.05
249230_at	putative protein similar to unknown	---	AT5G42070	-1.55	-0.63	-4.41	0.003426	0.018115	-2.05
251437_at	putative protein hypothetical protei	---	AT3G59910	1.36	0.44	4.41	0.00343	0.018134	-2.05
262324_at	hypothetical protein similar to hypot	ATCHX16	AT1G64170	6.04	2.60	4.41	0.003432	0.01814	-2.05
254323_at	putative protein auxin-induced prot	---	AT4G22620	-2.27	-1.19	-4.41	0.003435	0.018149	-2.06
263638_at	unknown protein	---	AT2G25310	1.33	0.41	4.41	0.003438	0.018164	-2.06
266304_at	hypothetical protein	---	AT2G27090	1.39	0.48	4.41	0.003439	0.018164	-2.06
249040_at	eukaryotic translation initiation facto	---	AT5G44320	1.44	0.52	4.41	0.003441	0.018169	-2.06
250049_at	putative protein predicted proteins,	---	AT5G17780	-1.45	-0.54	-4.41	0.003442	0.018169	-2.06
250836_at	putative protein various predicted p	DME	AT5G04560	-1.33	-0.42	-4.41	0.003443	0.018172	-2.06
253190_at	UDP-galactose transporter - like pr	---	AT4G35335	-1.44	-0.53	-4.41	0.00345	0.018202	-2.06
256413_at	hypothetical protein predicted by ge	---	AT3G11100	1.45	0.53	4.40	0.003456	0.01823	-2.06
262969_at	unknown protein	---	AT1G75710	-1.62	-0.70	-4.40	0.003466	0.018269	-2.07
254438_at	translation initiation factor eIF3 - lik	---	AT4G20980	1.55	0.64	4.40	0.003467	0.018269	-2.07
259402_at	developmental protein, putative sin	VPS46.1	AT1G17730	-1.38	-0.47	-4.40	0.003467	0.018269	-2.07
251062_at	putative protein putative proteins - A	OFP1	AT5G01840	-1.44	-0.53	-4.40	0.00347	0.018281	-2.07
250748_at	AtPH1-like protein ;supported by fu	---	AT5G05710	1.50	0.59	4.40	0.003482	0.018337	-2.07
248998_at	unknown protein	---	AT5G45320	-1.37	-0.45	-4.40	0.003487	0.01836	-2.07
247830_at	putative protein predicted proteins,	---	AT5G58530	-1.74	-0.80	-4.40	0.003488	0.018361	-2.07
256486_at	chloroplast nucleoid DNA binding p	---	AT1G31450	-1.43	-0.52	-4.39	0.003493	0.01838	-2.07
267361_at	hypothetical protein predicted by ge	---	AT2G39920	1.81	0.86	4.39	0.003496	0.018389	-2.07
257750_at	unknown protein ;supported by full-	---	AT3G18800	-1.51	-0.59	-4.39	0.003499	0.018402	-2.08
253609_at	H+-transporting ATPase type 2, pla	AHA2	AT4G30190	1.51	0.60	4.39	0.003503	0.018419	-2.08
257352_at	putative RING3 protein	IMB1	AT2G34900	1.52	0.61	4.39	0.003504	0.018419	-2.08
250723_at	lysine decarboxylase-like protein	---	AT5G06300	-1.63	-0.70	-4.39	0.003505	0.018419	-2.08
254415_at	subtilisin-like serine protease conta	ATSBT3.12	AT4G21326	-1.34	-0.42	-4.39	0.003506	0.018422	-2.08
264722_at	unknown protein location of EST en	---	AT1G22970	1.59	0.67	4.39	0.003507	0.018422	-2.08

258529_at	hypothetical protein predicted by g	---	AT3G06740	-1.62	-0.70	-4.39	0.003511	0.018439	-2.08
250741_at	putative protein contains similarity t	---	AT5G05790	2.03	1.02	4.39	0.003515	0.018449	-2.08
248674_at	non-phototropic hypocotyl-like prote	---	AT5G48800	1.96	0.97	4.39	0.003515	0.018449	-2.08
258707_at	putative histone H2B similar to histo	---	AT3G09480	1.57	0.65	4.39	0.003522	0.018479	-2.08
254444_at	putative protein riboflavin biosynthe	---	AT4G20960	-1.89	-0.92	-4.39	0.003524	0.018487	-2.08
249237_at	putative protein similar to unknown	---	AT5G42050	1.72	0.78	4.39	0.003527	0.018492	-2.08
266370_at	hypothetical protein predicted by ge	---	AT2G41350	-1.33	-0.41	-4.39	0.003532	0.01851	-2.09
266087_at	putative alcohol dehydrogenase	---	AT2G37790	-1.53	-0.62	-4.38	0.003535	0.018523	-2.09
249386_at	disease resistance -like protein dov	---	AT5G40060	1.42	0.50	4.38	0.003536	0.018523	-2.09
251762_at	sedoheptulose-bisphosphatase pre	SBPASE	AT3G55800	-1.44	-0.53	-4.38	0.00354	0.018535	-2.09
257743_at	unknown protein	---	AT3G27390	1.64	0.71	4.38	0.003541	0.018535	-2.09
258432_at	unknown protein ;supported by full-	RALFL23	AT3G16570	-1.81	-0.85	-4.38	0.003541	0.018535	-2.09
263046_at	unknown protein ; supported by cD	GRP3S	AT2G05380	2.01	1.01	4.38	0.003541	0.018535	-2.09
252065_at	putative protein ;supported by full-l	---	AT3G51610	1.53	0.61	4.38	0.003546	0.018554	-2.09
257401_at	hypothetical protein identical to hyp	SRO2	AT1G23550	1.57	0.65	4.38	0.003552	0.018577	-2.09
246442_at	hypothetical protein ;supported by	---	AT5G17610	1.36	0.44	4.38	0.003554	0.018582	-2.09
256023_at	hypothetical protein predicted by ge	ZW2	AT1G58330	-1.51	-0.59	-4.38	0.003557	0.018599	-2.09
253183_at	putative protein predicted protein, A	---	AT4G35220	1.35	0.43	4.38	0.00356	0.018606	-2.09
251679_at	putative protein strictosidine syntha	---	AT3G57030	-1.95	-0.96	-4.38	0.003564	0.018624	-2.10
247555_at	putative protein various predicted p	ECT3	AT5G61020	1.81	0.86	4.38	0.003566	0.01863	-2.10
255537_at	protoporphyrinogen oxidase ; supp	PPOX	AT4G01690	-1.55	-0.63	-4.38	0.003567	0.018631	-2.10
266699_at	putative ribosomal protein L28 ; su	---	AT2G19730	1.76	0.82	4.38	0.003568	0.018631	-2.10
245229_at	putative protein contains EST gb:T4	---	AT4G25620	-1.90	-0.92	-4.37	0.003576	0.018667	-2.10
247454_at	unknown protein	---	AT5G62440	1.97	0.98	4.37	0.003579	0.018671	-2.10
254822_at	polyubiquitin-like protein polyubiqu	UPL5	AT4G12570	1.38	0.47	4.37	0.003581	0.018678	-2.10
247698_at	putative protein predicted proteins,	---	AT5G59830	1.47	0.56	4.37	0.003582	0.018679	-2.10
252359_at	putative protein predicted proteins,	---	AT3G48440	-1.59	-0.67	-4.37	0.00359	0.018715	-2.10
254508_at	putative protein gene F4P9.34 chro	---	AT4G20170	-1.52	-0.60	-4.37	0.00359	0.018715	-2.10
267375_at	G protein alpha subunit 1 (GPA1) id	GP ALPHA	AT2G26300	1.49	0.58	4.37	0.003593	0.018719	-2.10
249398_at	RING finger -like protein RING-H2	---	AT5G40250	1.47	0.56	4.37	0.003593	0.018719	-2.10
262188_at	Avr9 elicitor response protein, puta	---	AT1G77810	1.49	0.58	4.37	0.003594	0.018719	-2.10
245395_at	hypothetical protein ;supported by f	---	AT4G17420	-1.52	-0.61	-4.37	0.003597	0.018733	-2.11
257611_at	unknown protein	---	AT3G26580	1.60	0.68	4.37	0.003598	0.018734	-2.11
252408_at	putative transcription factor MYB94	ATMYB94	AT3G47600	-1.34	-0.42	-4.37	0.003614	0.018812	-2.11
261178_at	synaptobrevin 7B, putative similar t	ATVAMP72	AT1G04760	-1.35	-0.44	-4.36	0.003618	0.018829	-2.11

249331_at	50S ribosomal protein L27 ;support	RPL27	AT5G40950	-1.43	-0.52	-4.36	0.003621	0.018837	-2.11
261148_at	unknown protein ; supported by full-	GAMMA CA	AT1G19580	-1.35	-0.44	-4.36	0.003627	0.018853	-2.11
259121_at	unknown protein	---	AT3G02220	1.57	0.65	4.36	0.003627	0.018853	-2.11
252469_at	protein kinase - like protein Raf pro	---	AT3G46920	1.59	0.67	4.36	0.003627	0.018853	-2.11
262533_at	hypothetical protein Pfam	---	AT1G17090	1.45	0.54	4.36	0.003628	0.018853	-2.11
260533_at	putative U1 small nuclear ribonucle	---	AT2G43370	1.37	0.45	4.36	0.003639	0.018902	-2.12
257280_at	9-cis-epoxycarotenoid dioxygenase	NCED3	AT3G14440	-1.81	-0.85	-4.36	0.003641	0.01891	-2.12
256444_at	hypothetical protein predicted by ge	---	AT3G11060	-1.35	-0.44	-4.36	0.003645	0.018924	-2.12
249718_at	putative protein contains similarity	---	AT5G35740	-1.52	-0.60	-4.36	0.003655	0.018974	-2.12
250842_at	putative protein predicted proteins,	VTE5	AT5G04490	-1.61	-0.69	-4.36	0.003658	0.018982	-2.12
245673_at	hypothetical protein similar to putati	---	AT1G56690	1.49	0.57	4.36	0.003658	0.018982	-2.12
260593_at	poly(A)-specific ribonuclease, puta	AHG2	AT1G55870	1.57	0.65	4.36	0.00366	0.018985	-2.12
251444_at	putative protein ETHIONINE AMIN	MAP2B	AT3G59990	1.36	0.44	4.35	0.00367	0.019028	-2.13
248631_at	putative protein strong similarity to	---	AT5G49000	1.52	0.60	4.35	0.003672	0.019037	-2.13
255292_s_a	putative calcium dependent protein	CPK22	AT4G04710	1.56	0.64	4.35	0.003675	0.019047	-2.13
262428_at	hypothetical protein predicted by ge	---	AT1G47570	1.40	0.48	4.35	0.003676	0.019047	-2.13
265569_at	unknown protein ;supported by full-	PGR5	AT2G05620	1.42	0.51	4.35	0.00368	0.019064	-2.13
258776_at	putative T-complex protein 1, ETA	---	AT3G11830	1.49	0.58	4.35	0.003683	0.019076	-2.13
261351_at	hypothetical protein predicted by ge	---	AT1G79790	-1.47	-0.55	-4.35	0.003687	0.019087	-2.13
262455_at	Mlo protein, putative similar to Mlo	MLO2	AT1G11310	1.63	0.71	4.35	0.003694	0.019116	-2.13
247504_at	putative protein various predicted p	---	AT5G61990	1.65	0.72	4.35	0.003694	0.019116	-2.13
253798_at	predicted protein CUC2 (involved i	ANAC073	AT4G28500	-1.45	-0.54	-4.35	0.003695	0.019116	-2.13
248853_at	protein kinase-like protein	BSK2	AT5G46570	-1.55	-0.63	-4.35	0.003698	0.019127	-2.14
257315_at	proline oxidase, mitochondrial pred	ERD5	AT3G30775	-3.60	-1.85	-4.35	0.0037	0.019131	-2.14
260295_at	putative aminopeptidase similar to a	---	AT1G63770	1.51	0.60	4.35	0.0037	0.019131	-2.14
262098_at	transcription factor, putative similar	NF-YC2	AT1G56170	1.58	0.66	4.34	0.003704	0.019147	-2.14
265985_at	hypothetical protein predicted by ge	ATPUP5	AT2G24220	-1.36	-0.44	-4.34	0.003713	0.019184	-2.14
257073_at	hypothetical protein predicted by ge	---	AT3G19650	1.55	0.64	4.34	0.003717	0.019202	-2.14
255953_at	transcription factor identical to trans	TGA3	AT1G22070	1.60	0.67	4.34	0.00372	0.01921	-2.14
262134_at	sulfate transporter, putative similar	AST56	AT1G77990	1.96	0.97	4.34	0.003722	0.019211	-2.14
266898_at	unknown protein ; supported by cDI	---	AT2G45990	-1.51	-0.60	-4.34	0.003724	0.019219	-2.14
264450_s_a	unknown protein similar to hypothet	SNL6	AT1G10250	1.75	0.81	4.34	0.003726	0.019223	-2.14
253391_at	hypothetical protein ; supported by	---	AT4G32590	-1.69	-0.76	-4.34	0.00373	0.019242	-2.14
254878_at	heat shock transcription factor - like	AT-HSFB2I	AT4G11660	-1.82	-0.87	-4.34	0.003735	0.019258	-2.15
255770_at	hypothetical protein predicted by ge	---	AT1G18560	-1.41	-0.50	-4.34	0.003738	0.019268	-2.15

251446_at	Expressed protein ; supported by fu	---	AT3G59840	1.35	0.43	4.34	0.00374	0.019268	-2.15
262712_at	mercaptopyruvate sulfurtransferase	ATRDH2	AT1G16460	1.49	0.58	4.34	0.00374	0.019268	-2.15
265580_at	putative protein phosphatase 2C	---	AT2G20050	-1.53	-0.61	-4.33	0.003749	0.019304	-2.15
256309_at	photosystem I subunit X precursor i	PSAK	AT1G30380	-1.37	-0.45	-4.33	0.003762	0.019366	-2.15
257188_at	hypothetical protein contains Pfam	---	AT3G13150	1.47	0.56	4.33	0.003764	0.019374	-2.15
248749_at	eukaryotic release factor 1 homolog	ERF1-1	AT5G47880	1.35	0.43	4.33	0.003779	0.019443	-2.16
247415_at	unknown protein	---	AT5G63060	-1.96	-0.97	-4.33	0.003791	0.019502	-2.16
249528_at	putative protein predicted protein, l	---	AT5G38720	1.75	0.81	4.32	0.003794	0.019515	-2.16
250027_at	putative protein similar to unknown	---	AT5G18250	1.55	0.64	4.32	0.003796	0.01952	-2.16
254675_at	RNA helicase - like protein Cdc28p	---	AT4G18465	1.71	0.78	4.32	0.0038	0.019538	-2.17
262375_at	unknown protein ; supported by cDI	SUVH3	AT1G73100	1.50	0.58	4.32	0.003802	0.019539	-2.17
257235_at	ras-related GTP-binding protein cor	AtRABA1g	AT3G15060	-3.42	-1.77	-4.32	0.003805	0.019547	-2.17
257658_at	unknown protein ; supported by ful	---	AT3G13230	2.33	1.22	4.32	0.003806	0.019551	-2.17
258219_at	thioredoxin, putative similar to THI	ATTDX	AT3G17880	1.39	0.48	4.32	0.00381	0.019558	-2.17
258433_at	translationally controlled tumor prot	TCTP	AT3G16640	1.50	0.59	4.32	0.00381	0.019558	-2.17
266474_at	hypothetical protein predicted by gr	---	AT2G31110	2.86	1.51	4.32	0.003815	0.019575	-2.17
246756_at	protein phosphatase - like protein p	---	AT5G27930	-1.55	-0.64	-4.32	0.00382	0.019595	-2.17
249827_at	unknown protein ;supported by full-	---	AT5G23330	1.51	0.59	4.32	0.00382	0.019595	-2.17
259937_s_a	putative ABC transporter contains P	ATNAP5	AT1G71330	1.43	0.51	4.32	0.003823	0.019603	-2.17
248080_at	wax synthase-like protein	---	AT5G55380	-1.55	-0.64	-4.32	0.003828	0.019623	-2.17
254162_at	transcription factor IIA small subuni	---	AT4G24440	1.60	0.68	4.32	0.003832	0.019639	-2.17
266181_at	putative glutathione S-transferase	ATGSTZ1	AT2G02390	1.52	0.61	4.32	0.003834	0.019644	-2.17
260010_at	putative trehalose-6-phosphate syn	ATTPS6	AT1G68020	-1.74	-0.80	-4.31	0.003841	0.019675	-2.18
255508_at	putative zinc finger protein identical	---	AT4G02220	1.48	0.57	4.31	0.003843	0.019679	-2.18
245581_at	hypothetical protein	---	AT4G14840	-1.49	-0.58	-4.31	0.003845	0.019689	-2.18
254495_at	hypothetical protein	EMB1895	AT4G20060	1.69	0.76	4.31	0.003859	0.019754	-2.18
253172_at	putative protein ;supported by full-le	---	AT4G35060	-2.60	-1.38	-4.31	0.00386	0.019755	-2.18
245020_at	cytochrome f	---	---	-1.41	-0.50	-4.31	0.003863	0.019767	-2.18
264448_at	putative sensory transduction histid	AHK3	AT1G27320	1.34	0.42	4.31	0.003872	0.0198	-2.19
247429_at	putative protein strong similarity to	---	AT5G62620	1.60	0.68	4.31	0.003873	0.0198	-2.19
255816_at	unknown protein ;supported by full-	GLTP1	AT2G33470	1.33	0.42	4.31	0.003877	0.019815	-2.19
245993_at	putative protein predicted proteins,	---	AT5G20700	1.75	0.81	4.30	0.00389	0.019879	-2.19
265682_at	similar to avrRpt2-induced protein 2	---	AT2G24390	1.60	0.68	4.30	0.003891	0.019879	-2.19
266700_at	60S ribosomal protein L31 ; suppo	---	AT2G19740	1.62	0.69	4.30	0.003893	0.01988	-2.19
247545_at	putative protein rhoGAP, Homo sa	---	AT5G61530	1.36	0.45	4.30	0.003896	0.019892	-2.19

258617_at	putative calmodulin similar to calmo	---	AT3G03000	-1.33	-0.42	-4.30	0.003902	0.019914	-2.19
258881_at	unknown protein ; supported by ful	---	AT3G06310	1.43	0.52	4.30	0.003903	0.019918	-2.19
248189_at	DNA mismatch repair protein MutS2	---	AT5G54090	1.52	0.60	4.30	0.003905	0.019921	-2.19
259493_at	unknown protein	---	AT1G15840	-1.41	-0.50	-4.30	0.003906	0.019922	-2.19
251151_at	hypothetical protein ; supported by	---	AT3G63170	-1.51	-0.60	-4.30	0.003909	0.019935	-2.20
248958_at	unknown protein ; supported by ful	---	AT5G45590	-1.62	-0.70	-4.30	0.003913	0.019952	-2.20
251821_at	protein phosphatase 2C - like prote	---	AT3G55050	-2.03	-1.02	-4.30	0.003914	0.019952	-2.20
264848_at	unknown protein ;supported by full-	---	AT2G17350	1.32	0.40	4.30	0.003917	0.019961	-2.20
267557_at	unknown protein ; supported by cD	KRP4	AT2G32710	1.54	0.62	4.30	0.003924	0.019991	-2.20
257754_at	GTP binding protein, putative simil	ATRAB7B	AT3G18820	-1.37	-0.45	-4.30	0.003925	0.019991	-2.20
267269_at	unknown protein	CAND1	AT2G02560	1.45	0.53	4.30	0.003929	0.020007	-2.20
256836_at	pyruvate kinase, putative similar to	PKP-ALPH	AT3G22960	1.54	0.62	4.29	0.003933	0.020024	-2.20
254684_at	glycine-rich RNA-binding protein A	GR-RBP2	AT4G13850	1.67	0.74	4.29	0.003934	0.020026	-2.20
250584_at	WD-repeat protein-like	---	AT5G07590	-1.49	-0.58	-4.29	0.003935	0.020026	-2.20
257851_at	unknown protein	---	AT3G12940	-1.42	-0.51	-4.29	0.003942	0.020057	-2.20
254105_at	magnesium-protoporphyrin IX meth	CHLM	AT4G25080	-1.46	-0.55	-4.29	0.003947	0.020078	-2.21
261904_at	unknown protein contains similarity	---	AT1G65040	1.33	0.41	4.29	0.003949	0.020086	-2.21
251725_at	putative protein	---	AT3G56260	-1.73	-0.79	-4.29	0.003951	0.02009	-2.21
267115_s_a	putative cellulose synthase	ATCSLB04	AT2G32530	2.22	1.15	4.29	0.003953	0.020095	-2.21
265114_at	hypothetical protein contains simila	LRX2	AT1G62440	-1.95	-0.96	-4.29	0.003955	0.0201	-2.21
255118_at	nitrilase 1 like protein nitrilase 1 - M	---	AT4G08790	1.50	0.58	4.29	0.003961	0.020128	-2.21
253329_at	hypothetical protein	---	AT4G33480	1.35	0.43	4.29	0.00397	0.020166	-2.21
262680_at	anter-specific proline-rich -like prote	---	AT1G75880	1.76	0.82	4.29	0.003971	0.020168	-2.21
252595_at	putative transporter protein peptide	---	AT3G45690	-1.44	-0.52	-4.29	0.003973	0.020176	-2.21
265990_at	putative prolylcarboxypeptidase	---	AT2G24280	1.73	0.79	4.29	0.003976	0.020185	-2.21
256068_at	hypothetical protein contains simila	ATE1	AT1G13690	1.37	0.45	4.28	0.00398	0.020196	-2.22
266170_at	unknown protein ;supported by full-	---	AT2G39050	-1.89	-0.91	-4.28	0.003986	0.020223	-2.22
252202_at	anthranilate N-hydroxycinnamoyl/b	---	AT3G50300	-1.40	-0.49	-4.28	0.00399	0.02024	-2.22
251657_at	putative protein MULTICOPY SUP	---	AT3G57000	1.78	0.83	4.28	0.003993	0.020251	-2.22
245572_at	hypothetical protein	PPD2	AT4G14720	1.82	0.86	4.28	0.004	0.020278	-2.22
247694_at	GTP cyclohydrolase II / 3,4-dihydro	---	AT5G59750	1.44	0.53	4.28	0.004001	0.020278	-2.22
263921_at	putative fructose bisphosphate aldo	---	AT2G36460	1.55	0.64	4.28	0.004008	0.02031	-2.22
265043_at	Expressed protein ; supported by cl	ATNAP4	AT1G03900	1.44	0.53	4.28	0.004014	0.020338	-2.22
246443_at	hypothetical protein ;supported by	---	AT5G17620	-1.47	-0.55	-4.28	0.004016	0.020344	-2.23
248685_at	putative protein similar to unknown	---	AT5G48500	1.70	0.76	4.28	0.004022	0.02037	-2.23

258780_at	putative ubiquitin carboxyl-terminal	UBP13	AT3G11910	1.31	0.39	4.27	0.004036	0.020435	-2.23
260589_at	hypothetical protein predicted by ge	---	AT1G53400	-1.32	-0.41	-4.27	0.004037	0.020436	-2.23
267088_at	30S ribosomal protein S31 ;suppor	PSRP4	AT2G38140	-1.55	-0.63	-4.27	0.004038	0.020436	-2.23
264726_at	Expressed protein ; supported by fu	---	AT1G22985	1.56	0.64	4.27	0.00404	0.020444	-2.23
263415_at	hypothetical protein similar to GB:A	EMB2762	AT2G17250	1.61	0.69	4.27	0.004049	0.020476	-2.23
251795_at	putative protein MtN24, Medicago t	---	AT3G55390	1.68	0.75	4.27	0.004051	0.020479	-2.23
249147_at	cytosolic malate dehydrogenase ;su	---	AT5G43330	1.56	0.64	4.27	0.004054	0.02049	-2.24
250403_at	argininosuccinate lyase (AtArgH) ;	---	AT5G10920	1.90	0.93	4.27	0.00406	0.020511	-2.24
259528_at	hypothetical protein	---	AT1G12330	-1.66	-0.73	-4.27	0.004062	0.020518	-2.24
258699_at	unknown protein	---	AT3G09470	1.47	0.55	4.27	0.004065	0.020529	-2.24
245852_at	ribosomal protein L10-like ribosom	---	AT5G13510	-1.53	-0.61	-4.27	0.00407	0.020549	-2.24
257726_at	hypothetical protein predicted by ge	---	AT3G18360	-1.37	-0.46	-4.27	0.004071	0.020549	-2.24
265728_at	hypothetical protein predicted by ge	---	AT2G31990	1.60	0.68	4.27	0.004073	0.020555	-2.24
249076_at	putative protein similar to unknown	TOM22-V	AT5G43970	1.61	0.69	4.26	0.004075	0.020555	-2.24
260408_at	putative thioredoxin similar to thiore	ATH8	AT1G69880	1.50	0.59	4.26	0.004075	0.020555	-2.24
261804_at	UDP glucose:flavonoid 3-o-glucosy	UGT78D1	AT1G30530	-1.69	-0.76	-4.26	0.004078	0.020563	-2.24
263137_at	gamma glutamyl hydrolase, putativ	ATGGH1	AT1G78660	-2.04	-1.03	-4.26	0.004078	0.020563	-2.24
250135_at	putative protein	---	AT5G15360	1.41	0.49	4.26	0.004085	0.020591	-2.24
267446_s_a	putative tyrosyl-tRNA synthetase	---	AT1G28350	1.35	0.44	4.26	0.004086	0.020591	-2.24
249247_at	maize crp1 protein-like	---	AT5G42310	1.54	0.63	4.26	0.004089	0.020601	-2.24
261378_at	calcium-dependent protein kinase,	ATCDPK1	AT1G18890	-1.71	-0.77	-4.26	0.004089	0.020601	-2.24
251262_at	hypothetical protein ; supported by	---	AT3G62080	1.71	0.77	4.26	0.004092	0.020609	-2.25
247282_at	putative protein strong similarity to	AtMC3	AT5G64240	-1.45	-0.53	-4.26	0.004098	0.020634	-2.25
250906_at	1,4-alpha-glucan branching enzym	SBE2.2	AT5G03650	-1.45	-0.54	-4.26	0.004099	0.020634	-2.25
253302_at	Expressed protein ; supported by fu	---	AT4G33660	-1.63	-0.71	-4.26	0.0041	0.020636	-2.25
247339_at	unknown protein	---	AT5G63690	1.50	0.58	4.26	0.00411	0.020679	-2.25
263844_at	unknown protein ; supported by cD	---	AT2G36930	2.15	1.11	4.26	0.00411	0.020679	-2.25
260781_at	decoy identical to GB:AAB51588 G	DECOY	AT1G14620	2.73	1.45	4.26	0.004114	0.020692	-2.25
254032_at	predicted protein destination factor	---	AT4G25940	-1.56	-0.64	-4.26	0.004116	0.020697	-2.25
258608_at	unknown protein ;supported by full-	---	AT3G03020	-1.96	-0.97	-4.26	0.00412	0.020714	-2.25
264171_at	hypothetical protein predicted by ge	---	AT1G02100	1.50	0.59	4.26	0.004121	0.020714	-2.25
264875_at	putative glucanase	AKR2B	AT2G17390	1.30	0.38	4.25	0.004132	0.020764	-2.26
262522_at	putative amino acid transporter Ver	CAT8	AT1G17120	-1.44	-0.53	-4.25	0.004134	0.020768	-2.26
249134_at	unknown protein	---	AT5G43150	1.82	0.86	4.25	0.004134	0.020768	-2.26
246864_at	cytochrome P450 GA3 ; supported	GA3	AT5G25900	-1.92	-0.94	-4.25	0.004141	0.020797	-2.26

249742_at	putative protein contains similarity t	---	AT5G24490	-1.50	-0.59	-4.25	0.004143	0.0208	-2.26
258027_at	hypothetical protein predicted by ge	---	AT3G19515	1.40	0.49	4.25	0.004147	0.020818	-2.26
261350_at	hypothetical protein predicted by ge	---	AT1G79770	1.69	0.76	4.25	0.004155	0.020853	-2.26
258643_at	unknown protein ;supported by full-	ATAB2	AT3G08010	1.33	0.41	4.25	0.004163	0.020889	-2.26
252822_at	Expressed protein ; supported by fu	---	AT4G39955	1.48	0.57	4.25	0.004169	0.020914	-2.27
257806_at	hypothetical protein predicted by ge	---	AT3G18670	-1.39	-0.47	-4.24	0.004188	0.020998	-2.27
262245_at	unknown protein	NPSN12	AT1G48240	-1.55	-0.63	-4.24	0.004189	0.020998	-2.27
261601_at	ARP protein, putative similar to AR	NQR	AT1G49670	1.37	0.46	4.24	0.004189	0.020998	-2.27
262107_at	hypothetical protein predicted by ge	---	AT1G02750	1.36	0.44	4.24	0.004189	0.020998	-2.27
263705_at	unknown protein contains similarity	IMPL1	AT1G31190	-1.59	-0.67	-4.24	0.004191	0.021002	-2.27
259462_at	hypothetical protein contains simila	---	AT1G18940	-1.61	-0.68	-4.24	0.004193	0.021004	-2.27
251830_at	phosphoribosylformylglycinamidine	PUR5	AT3G55010	1.85	0.88	4.24	0.004194	0.021005	-2.27
248032_at	myosin heavy chain-like	---	AT5G55860	1.55	0.63	4.24	0.004199	0.021025	-2.27
250193_at	putative protein proline-rich protein	---	AT5G14540	-1.41	-0.49	-4.24	0.004201	0.021027	-2.27
259397_at	hypothetical protein predicted by ge	---	AT1G17680	1.37	0.46	4.24	0.004201	0.021027	-2.27
266556_at	hypothetical protein predicted by ge	---	AT2G46230	1.49	0.58	4.24	0.004203	0.021027	-2.27
247810_at	26S proteasome AAA-ATPase subu	RPT3	AT5G58290	1.36	0.45	4.24	0.004203	0.021027	-2.27
262624_at	CCR4-associated factor, putative s	---	AT1G06450	1.45	0.54	4.24	0.004204	0.021027	-2.27
258300_at	putative casein kinase I similar to ca	ckl10	AT3G23340	1.65	0.73	4.24	0.004205	0.021031	-2.27
267310_at	unknown protein	AIR9	AT2G34680	-2.51	-1.33	-4.24	0.00421	0.021051	-2.28
261694_at	60S ribosomal protein L10A, putati	---	AT1G08360	1.62	0.70	4.24	0.004215	0.021068	-2.28
247642_at	putative protein various predicted p	---	AT5G60590	1.37	0.46	4.24	0.004218	0.021078	-2.28
251246_at	auxin-induced protein homolog aux	IAA30	AT3G62100	-1.32	-0.40	-4.24	0.004218	0.021078	-2.28
267612_at	putative nitrate transporter	---	AT2G26690	-2.64	-1.40	-4.23	0.004225	0.021107	-2.28
263787_at	unknown protein ; supported by cD	---	AT2G46420	1.66	0.73	4.23	0.004228	0.021115	-2.28
247926_at	protein carboxyl methylase-like	---	AT5G57280	2.05	1.04	4.23	0.004229	0.021115	-2.28
247248_at	putative protein contains similarity t	---	AT5G64560	-1.83	-0.87	-4.23	0.00423	0.021115	-2.28
263432_at	putative beta-hydroxyacyl-ACP deh	---	AT2G22230	-1.55	-0.63	-4.23	0.004234	0.021121	-2.28
246038_s_a	putative protein thiamin pyrophosp	atnudt20	AT5G19460	-1.58	-0.66	-4.23	0.004234	0.021121	-2.28
264601_at	hypothetical protein similar to hypot	---	AT1G04540	-1.41	-0.50	-4.23	0.004234	0.021121	-2.28
266336_at	putative Fe(II) transporter identical	ZIP3	AT2G32270	-1.52	-0.61	-4.23	0.004235	0.021121	-2.28
259750_at	hypothetical protein predicted by g	---	AT1G71130	1.69	0.75	4.23	0.004237	0.021123	-2.28
260420_at	unknown protein	---	AT1G69610	1.41	0.49	4.23	0.004238	0.021123	-2.28
251321_at	RING finger protein ;supported by	BRH1	AT3G61460	-1.71	-0.78	-4.23	0.004239	0.021125	-2.28
265732_at	predicted by genscan and genefind	---	AT2G01300	-6.90	-2.79	-4.23	0.004241	0.021132	-2.28

247455_at	MYB96 transcription factor-like prot	MYB96	AT5G62470	-1.79	-0.84	-4.23	0.004243	0.021137	-2.28
246842_at	Expressed protein ; supported by fu	---	AT5G26731	1.80	0.85	4.23	0.004246	0.021146	-2.29
AFFX-Athal	Arabidopsis thaliana /REF=U37281	---	---	-1.51	-0.59	-4.23	0.004247	0.021146	-2.29
259519_at	hypothetical protein	---	AT1G12270	1.53	0.61	4.23	0.004248	0.021146	-2.29
247569_at	Cf-5 disease resistance protein - lik	---	AT5G61240	-1.64	-0.71	-4.23	0.004251	0.02116	-2.29
261304_at	unknown protein ;supported by full-	---	AT1G48440	-1.30	-0.38	-4.23	0.004253	0.021161	-2.29
267035_at	putative beta-alanine-pyruvate amir	AGT3	AT2G38400	-2.77	-1.47	-4.23	0.004254	0.021164	-2.29
259188_at	unknown protein ;supported by full-	---	AT3G01510	-1.62	-0.70	-4.23	0.004256	0.021169	-2.29
246877_at	putative protein various predicted p	---	AT5G26150	-1.31	-0.39	-4.23	0.004265	0.02121	-2.29
248136_at	RNA helicase-like protein	---	AT5G54910	1.84	0.88	4.23	0.00427	0.021229	-2.29
265400_at	unknown protein ;supported by full-	---	AT2G10940	-117.42	-6.88	-4.23	0.004272	0.021229	-2.29
259160_at	unknown protein	---	AT3G05410	1.45	0.54	4.23	0.004272	0.021229	-2.29
263735_s_a	hypothetical protein predicted by ge	AGL50	AT1G59810	-1.33	-0.41	-4.23	0.004273	0.021229	-2.29
259436_at	hypothetical protein predicted by ge	---	AT1G01500	1.39	0.47	4.22	0.004281	0.021254	-2.29
264692_at	DNA binding protein MybSt1, putat	---	AT1G70000	1.52	0.60	4.22	0.004281	0.021254	-2.29
250720_at	putative protein similar to unknown	---	AT5G06180	1.64	0.71	4.22	0.004281	0.021254	-2.29
247081_at	AtRAD17 (dbj|BAA90479.1) ; supp	ATRAD17	AT5G66130	1.48	0.57	4.22	0.004282	0.021254	-2.29
257171_at	unknown protein ; supported by ful	---	AT3G23760	-1.46	-0.55	-4.22	0.00429	0.021291	-2.30
259381_s_a	putative lectin contains Pfam profile	NSP1	AT3G16390	-4.10	-2.04	-4.22	0.004296	0.021313	-2.30
267062_at	putative spliceosome associated pr	---	AT2G32600	1.51	0.59	4.22	0.004298	0.021315	-2.30
265798_at	unknown protein ; supported by cDI	---	AT2G35790	1.67	0.74	4.22	0.004299	0.021316	-2.30
263333_at	unknown protein ; supported by cD	---	AT2G03890	1.59	0.67	4.22	0.0043	0.021316	-2.30
260096_at	hypothetical protein predicted by ge	---	AT1G73240	1.50	0.59	4.22	0.004302	0.021323	-2.30
257059_at	unknown protein ; supported by cD	---	AT3G15280	-1.35	-0.44	-4.22	0.004304	0.021328	-2.30
250009_at	putative protein nuclear FMRP inte	---	AT5G18440	2.05	1.03	4.22	0.004309	0.021348	-2.30
267135_at	cyclin-dependent kinase inhibitor pr	ICK1	AT2G23430	1.93	0.95	4.22	0.004311	0.021353	-2.30
248762_at	Expressed protein ; supported by fu	---	AT5G47455	1.75	0.80	4.22	0.004314	0.02136	-2.30
254259_s_a	putative protein rape mRNA, Brass	---	AT4G23420	-1.67	-0.74	-4.22	0.004314	0.02136	-2.30
254425_at	putative membrane associated pro	---	AT4G21450	1.33	0.41	4.22	0.004315	0.02136	-2.30
252938_at	hypothetical protein	---	AT4G39190	2.79	1.48	4.22	0.004322	0.021388	-2.30
261905_at	hypothetical protein contains simila	---	AT1G65070	1.39	0.47	4.22	0.004324	0.021388	-2.31
256426_at	hypothetical protein predicted by ge	---	AT1G33420	2.40	1.27	4.22	0.004324	0.021388	-2.31
266743_at	ribonuclease, RNS1 identical to rib	RNS1	AT2G02990	-5.41	-2.43	-4.22	0.004327	0.021389	-2.31
253903_at	kinesin-related protein katB ; suppo	ATK2	AT4G27180	1.29	0.37	4.21	0.004335	0.021427	-2.31
258678_at	E2, ubiquitin-conjugating enzyme 1	UBC11	AT3G08690	1.56	0.64	4.21	0.004337	0.021431	-2.31

257779_at	protein kinase, putative similar to P	CDG1	AT3G26940	-1.29	-0.37	-4.21	0.004339	0.021431	-2.31
256944_at	unknown protein similar to unknowr	VRN1	AT3G18990	1.61	0.69	4.21	0.00434	0.021431	-2.31
253566_at	DNA topoisomerase like- protein Ba	---	AT4G31210	2.53	1.34	4.21	0.00434	0.021431	-2.31
252313_at	RNA-binding - like protein RNA-bin	CID10	AT3G49390	1.82	0.86	4.21	0.004342	0.021435	-2.31
259113_at	hypothetical protein predicted by g	---	AT3G05510	1.47	0.55	4.21	0.004356	0.021496	-2.31
262407_at	hypothetical protein predicted by ge	---	AT1G34630	-1.82	-0.86	-4.21	0.004365	0.021536	-2.32
266673_at	putative thiamin biosynthesis protei	THIC	AT2G29630	1.73	0.79	4.21	0.004373	0.02157	-2.32
265941_s_a	recA, putative similar to GB:CAA39	---	AT2G19490	1.74	0.80	4.21	0.004376	0.02158	-2.32
264309_at	coatomer alpha subunit, putative si	---	AT1G62020	-1.33	-0.42	-4.21	0.004377	0.021584	-2.32
258832_at	putative protein kinase similar to AF	---	AT3G07070	-1.44	-0.52	-4.21	0.004379	0.021585	-2.32
246008_at	putative protein predicted proteins,	---	AT5G08320	-1.49	-0.57	-4.20	0.004382	0.021596	-2.32
255801_at	putative protein heat shock protein	---	AT4G10130	1.34	0.42	4.20	0.004384	0.021601	-2.32
249579_at	ADP-ribosylation factor - like protei	ATARLA1A	AT5G37680	1.40	0.48	4.20	0.00439	0.021626	-2.32
250823_at	putative protein similar to unknown	---	AT5G05180	-1.40	-0.49	-4.20	0.004391	0.021627	-2.32
258544_at	disease resistance gene (RPM1) id	RPM1	AT3G07040	-1.83	-0.87	-4.20	0.004394	0.021638	-2.32
267060_at	unknown protein ; supported by ful	---	AT2G32580	-1.68	-0.75	-4.20	0.004396	0.021642	-2.32
252181_at	Expressed protein ; supported by fu	---	AT3G50685	-1.37	-0.46	-4.20	0.004398	0.021648	-2.32
248861_at	senescence-associated protein 5-lik	TRN2	AT5G46700	-2.97	-1.57	-4.20	0.0044	0.021652	-2.32
266157_at	unknown protein	ATFUC1	AT2G28100	-1.29	-0.37	-4.20	0.004403	0.021662	-2.32
250066_at	unknown protein	---	AT5G17930	1.74	0.80	4.20	0.004405	0.021669	-2.33
267205_at	unknown protein	---	AT2G30820	-1.43	-0.52	-4.20	0.004408	0.021678	-2.33
263525_at	putative MADS-box protein	AGL61	AT2G24840	-1.52	-0.60	-4.20	0.00441	0.021683	-2.33
263199_at	hypothetical protein Similar to hexo	HEXO2	AT1G05590	-1.56	-0.64	-4.20	0.004411	0.021683	-2.33
266702_at	hexokinase (ATHXK2) ; supported	HXK2	AT2G19860	1.38	0.46	4.20	0.004413	0.02169	-2.33
258504_at	putative sterol-C5-desaturase ident	---	AT3G02590	-1.31	-0.39	-4.20	0.004429	0.021753	-2.33
258284_at	putative ribosomal protein similar to	---	AT3G16080	2.08	1.06	4.20	0.00443	0.021753	-2.33
265002_at	putative lysine/histidine-specific pe	LHT2	AT1G24400	1.65	0.72	4.20	0.00443	0.021753	-2.33
245296_at	isp4 like protein ; supported by cDN	ATOPT3	AT4G16370	-1.83	-0.87	-4.20	0.00443	0.021753	-2.33
262159_at	hypothetical protein predicted by ge	---	AT1G52720	-2.19	-1.13	-4.20	0.004431	0.021753	-2.33
257621_at	calmodulin-domain protein kinase C	CPK9	AT3G20410	1.87	0.90	4.19	0.004439	0.021788	-2.33
255839_at	putative CONSTANS-like B-box zin	---	AT2G33500	1.34	0.42	4.19	0.00447	0.021938	-2.34
245040_at	hypothetical protein predicted by ge	---	AT2G26520	-1.44	-0.53	-4.19	0.004473	0.021947	-2.34
260878_at	scarecrow-like 1 identical to scarec	SCL1	AT1G21450	1.62	0.69	4.19	0.004477	0.021958	-2.34
255864_at	putative pseudouridine synthase	---	AT2G30320	-1.46	-0.54	-4.19	0.004477	0.021958	-2.34
260858_at	hypothetical protein predicted by ge	---	AT1G43770	1.40	0.49	4.18	0.004487	0.022003	-2.35

245351_at	casein kinase II beta chain CKB2 ;s	CKB2	AT4G17640	-1.41	-0.50	-4.18	0.00449	0.022011	-2.35
254663_at	potassium channel protein KAT2	KAT2	AT4G18290	-1.60	-0.68	-4.18	0.004493	0.022021	-2.35
245616_at	kinase like protein	---	AT4G14480	1.89	0.92	4.18	0.004494	0.022021	-2.35
256724_at	unknown protein ;supported by full-	---	AT2G34040	1.44	0.53	4.18	0.004501	0.022049	-2.35
265599_at	unknown protein	AT2G1425	---	-1.39	-0.47	-4.18	0.004509	0.022087	-2.35
266003_at	hypothetical protein predicted by ge	---	AT2G37320	1.58	0.66	4.18	0.004511	0.022088	-2.35
256343_at	unknown protein ; supported by cDI	---	AT1G72090	1.47	0.56	4.18	0.004519	0.022119	-2.35
249479_at	germin - like protein probable germ	---	AT5G38960	-1.53	-0.61	-4.18	0.004524	0.02214	-2.35
264679_s_a	putative 60S ribosomal protein L21	---	AT1G09590	1.77	0.83	4.18	0.004529	0.022159	-2.36
251719_at	putative protein PUTATIVE PROTE	---	AT3G56140	1.49	0.57	4.18	0.004537	0.022191	-2.36
266588_at	putative proline-rich protein ; suppo	AGP9	AT2G14890	-5.86	-2.55	-4.18	0.00454	0.022194	-2.36
259012_at	hypothetical protein similar to hypot	PUB9	AT3G07360	-1.56	-0.64	-4.18	0.00454	0.022194	-2.36
246139_at	putative protein predicted protein, I	---	AT5G19900	1.48	0.56	4.17	0.004543	0.022202	-2.36
251353_at	putative protein hypothetical protei	---	AT3G61080	-1.54	-0.62	-4.17	0.004546	0.022204	-2.36
254796_at	putative protein protein kinase hom	---	AT4G13000	-1.48	-0.56	-4.17	0.004546	0.022204	-2.36
265438_at	hypothetical protein	---	AT2G20970	-1.32	-0.40	-4.17	0.004546	0.022204	-2.36
258313_at	unknown protein contains RanBP1	---	AT3G15970	1.35	0.43	4.17	0.004548	0.022204	-2.36
245635_at	zinc finger protein ID1, putative sim	AtIDD16	AT1G25250	-1.32	-0.40	-4.17	0.004552	0.022213	-2.36
257826_at	RING zinc finger protein, putative c	---	AT3G26730	1.37	0.46	4.17	0.004552	0.022213	-2.36
247670_at	putative protein predicted proteins,	---	AT5G60190	1.55	0.63	4.17	0.004558	0.022237	-2.36
253297_at	beta-xylan endohydrolase -like pro	---	AT4G33810	-1.38	-0.47	-4.17	0.004559	0.022237	-2.36
264157_at	xyloglucan endotransglycosylase,	XTH17	AT1G65310	-1.87	-0.90	-4.17	0.00456	0.022237	-2.36
257489_at	hypothetical protein predicted by ge	---	AT1G07330	-1.38	-0.47	-4.17	0.004562	0.022238	-2.36
250107_at	ids-4 protein - like ids-4 protein, Ho	SPX4	AT5G15330	-1.63	-0.71	-4.17	0.004563	0.022238	-2.36
252096_at	hypothetical protein ; supported by	---	AT3G51180	1.79	0.84	4.17	0.004563	0.022238	-2.36
259089_at	hypothetical protein similar to GB:C	---	AT3G04960	-1.38	-0.46	-4.17	0.004564	0.022238	-2.36
263516_at	AtRer1B ;supported by full-length c	ATRER1B	AT2G21600	-1.43	-0.52	-4.17	0.004576	0.022292	-2.37
251306_at	putative DNA-binding protein DNA-	---	AT3G61260	-1.54	-0.62	-4.17	0.004578	0.022294	-2.37
247815_at	ribosomal protein S4 - like ribosom	---	AT5G58420	1.65	0.73	4.17	0.004582	0.022308	-2.37
262722_at	sterol glucosyltransferase, putative	---	AT1G43620	-1.36	-0.44	-4.17	0.00459	0.022336	-2.37
247528_at	MIM protein ; supported by cDNA:	MIM	AT5G61460	1.47	0.55	4.17	0.004594	0.022351	-2.37
264748_at	hypothetical protein predicted by ge	EMB25	AT1G70070	1.32	0.40	4.17	0.004595	0.022352	-2.37
259531_at	hypothetical protein	---	AT1G12460	-1.66	-0.73	-4.17	0.004596	0.022354	-2.37
251840_at	protein disulfide-isomerase-like pro	ATPDIL1-3	AT3G54960	1.93	0.95	4.16	0.004603	0.022379	-2.37
246977_at	putative protein CONSTANS-like p	COL4	AT5G24930	-1.33	-0.41	-4.16	0.004607	0.022382	-2.37

259254_at	putative P-protein: chorismate mut	ADT2	AT3G07630	1.45	0.54	4.16	0.004608	0.022382	-2.37
246543_at	putative protein	---	AT5G15060	-1.30	-0.37	-4.16	0.004609	0.022382	-2.37
267181_at	putative alcohol dehydrogenase ; s	---	AT2G37760	1.89	0.92	4.16	0.004609	0.022382	-2.37
251119_at	putative protein nifR3 protein, Azos	---	AT3G63510	-1.60	-0.68	-4.16	0.004614	0.0224	-2.38
265225_at	putative PHD-type zinc finger protei	---	AT2G36720	1.39	0.47	4.16	0.004617	0.022413	-2.38
262916_at	glutathione S-transferase, putative	ATGSTU16	AT1G59700	1.75	0.80	4.16	0.004625	0.022443	-2.38
262572_at	unknown protein Contains a PF|001	---	AT1G15140	-1.52	-0.60	-4.16	0.004625	0.022443	-2.38
263090_at	hypothetical protein predicted by ge	---	AT2G16190	-1.34	-0.43	-4.16	0.004629	0.022454	-2.38
266274_at	putative protein phosphatase 2C	---	AT2G29380	-1.39	-0.47	-4.16	0.004632	0.02246	-2.38
249269_at	cell cycle control crn (crooked neck	---	AT5G41770	1.55	0.64	4.16	0.004649	0.022529	-2.38
248231_at	putative protein contains similarity t	---	AT5G53770	1.44	0.53	4.16	0.004649	0.022529	-2.38
259070_at	digalactosyldiacylglycerol synthase	DGD1	AT3G11670	1.95	0.96	4.16	0.004649	0.022529	-2.38
262575_at	putative ABC transporter Similar to	PDR7	AT1G15210	-1.41	-0.50	-4.16	0.00465	0.022529	-2.38
247731_at	glucuronosyl transferase - like prot	UGT76E2	AT5G59590	-1.39	-0.47	-4.16	0.004652	0.022534	-2.38
257423_at	hypothetical protein predicted by ge	---	AT1G62010	1.46	0.55	4.15	0.004658	0.022552	-2.39
253144_at	putative protein transcription factor	---	AT4G35540	1.37	0.46	4.15	0.004661	0.022563	-2.39
251376_at	scarecrow - like protein scarecrow-	---	AT3G60630	-1.71	-0.77	-4.15	0.004671	0.022605	-2.39
259823_at	beta-1,3-glucanase precursor, puta	---	AT1G66250	1.47	0.56	4.15	0.004673	0.02261	-2.39
261145_at	thioredoxin identical to GB:CAA84	ATTRX4	AT1G19730	1.40	0.48	4.15	0.004674	0.02261	-2.39
257147_at	unknown protein	---	AT3G27270	1.62	0.69	4.15	0.004687	0.022668	-2.39
260712_at	protein phosphatase 2C, putative s	HAB2	AT1G17550	1.57	0.66	4.15	0.00469	0.022678	-2.39
252107_at	sugar transporter-like protein sugar	TMT3	AT3G51490	-1.58	-0.66	-4.15	0.004696	0.022703	-2.39
249077_at	alcohol dehydrogenase (EC 1.1.1.1	HOT5	AT5G43940	1.43	0.51	4.15	0.004706	0.022741	-2.40
259994_at	putative C2H2-type zinc finger prot	AtIDD14	AT1G68130	-1.68	-0.75	-4.15	0.004708	0.022744	-2.40
266345_at	hypothetical protein predicted by ge	---	AT2G01410	-1.35	-0.44	-4.15	0.004708	0.022744	-2.40
249108_at	steroid sulfotransferase-like	---	AT5G43690	-1.29	-0.36	-4.14	0.004714	0.022764	-2.40
266514_at	putative zinc-finger protein (B-box z	---	AT2G47890	1.58	0.66	4.14	0.004718	0.022776	-2.40
256276_at	geranylgeranyl transferase type II b	---	AT3G12070	1.41	0.50	4.14	0.004719	0.022776	-2.40
259977_at	unknown protein ;supported by full-	---	AT1G76590	2.35	1.23	4.14	0.004719	0.022776	-2.40
265897_at	hypothetical protein predicted by ge	MOT1	AT2G25680	1.75	0.81	4.14	0.004722	0.022786	-2.40
249092_at	putative protein similar to unknown	---	AT5G43710	1.45	0.54	4.14	0.004723	0.022786	-2.40
253320_at	putative protein ThiJ protein, Esche	---	AT4G34020	1.39	0.47	4.14	0.004726	0.022786	-2.40
261213_at	unknown protein ; supported by cDI	---	AT1G12970	1.38	0.47	4.14	0.004726	0.022786	-2.40
246075_at	monogalactosyldiacylglycerol synth	MGD2	AT5G20410	2.71	1.44	4.14	0.004726	0.022786	-2.40
261832_at	S-ribonuclease binding protein SBF	---	AT1G10650	1.68	0.75	4.14	0.004738	0.022837	-2.40

265027_at	putative ribonuclease III similar to E	NFD2	AT1G24450	1.54	0.62	4.14	0.004739	0.022841	-2.40
253575_at	putative protein TINY, Arabidopsis	---	AT4G31060	-1.38	-0.47	-4.14	0.004744	0.022855	-2.41
250216_at	unknown protein	---	AT5G14090	-1.52	-0.60	-4.14	0.004744	0.022855	-2.41
260598_at	unknown protein	---	AT1G55930	1.62	0.70	4.14	0.004748	0.022866	-2.41
259373_at	hypothetical protein predicted by ge	---	AT1G69160	-2.29	-1.20	-4.14	0.004752	0.022882	-2.41
257112_at	cytochrome P450, putative contain	CYP705A2	AT3G20120	1.41	0.50	4.14	0.004755	0.022892	-2.41
245732_at	unknown protein contains similarity	---	AT1G73440	1.38	0.46	4.14	0.004759	0.022908	-2.41
246231_at	putative protein	---	AT4G37080	-1.57	-0.65	-4.14	0.004766	0.022933	-2.41
259379_at	putative MYB family transcription fa	---	AT3G16350	-2.10	-1.07	-4.13	0.004769	0.022945	-2.41
255444_at	LUMINIDEPENDENS protein ; sup	LD	AT4G02560	1.38	0.46	4.13	0.004772	0.022957	-2.41
249926_at	E1, ubiquitin-like activating enzyme	ECR1	AT5G19180	1.49	0.57	4.13	0.00478	0.022989	-2.41
254048_at	putative protein various predicted p	---	AT4G25680	-1.73	-0.79	-4.13	0.004786	0.02301	-2.41
265818_at	putative peptidyl-prolyl cis-trans iso	PIN1AT	AT2G18040	1.36	0.44	4.13	0.004789	0.023023	-2.42
246094_at	putative protein predicted proteins,	---	AT5G19300	1.72	0.78	4.13	0.004792	0.023026	-2.42
AFFX-r2-At-	Arabidopsis thaliana /REF=M6411	---	---	1.93	0.95	4.13	0.004813	0.023124	-2.42
254803_at	putative protein several hypothetica	---	AT4G13100	1.65	0.73	4.13	0.004822	0.023156	-2.42
264895_at	putative 10kd chaperonin strongly s	---	AT1G23100	2.24	1.16	4.13	0.004823	0.023156	-2.42
265998_at	putative NADP-dependent glyceralc	ALDH11A3	AT2G24270	1.42	0.51	4.13	0.004823	0.023156	-2.42
250752_at	cytochrome P450 90A1 (sp|Q42569	CPD	AT5G05690	-1.50	-0.59	-4.13	0.004824	0.023157	-2.42
249944_at	NAM (no apical meristem)-like prote	anac089	AT5G22290	2.24	1.16	4.12	0.004834	0.0232	-2.43
254346_at	symbiosis-related like protein symb	APG8A	AT4G21980	1.78	0.83	4.12	0.004836	0.023202	-2.43
264022_at	Expressed protein ; supported by fu	---	AT2G21185	1.54	0.62	4.12	0.00484	0.023212	-2.43
247407_at	putative protein predicted proteins,	---	AT5G62900	1.54	0.62	4.12	0.004841	0.023212	-2.43
258218_at	methyltransferase, putative similar	XPL1	AT3G17998	-1.64	-0.71	-4.12	0.004842	0.023212	-2.43
261581_at	serine/threonine kinase, putative si	CIPK9	AT1G01140	1.59	0.67	4.12	0.004847	0.023229	-2.43
260618_at	flower development protein cycloid	TCP3	AT1G53230	-1.48	-0.57	-4.12	0.004848	0.023229	-2.43
248027_at	outward rectifying potassium chann	ATKCO1	AT5G55630	-1.48	-0.56	-4.12	0.004849	0.023229	-2.43
260249_s_a	unknown protein similar to unknowr	---	AT1G74280	1.50	0.58	4.12	0.00485	0.023229	-2.43
258849_at	putative UDP-glucose pyrophospho	UGP	AT3G03250	1.53	0.62	4.12	0.004851	0.023229	-2.43
253948_at	Avr9 elicitor response like protein A	---	AT4G26940	-1.39	-0.47	-4.12	0.004858	0.023253	-2.43
255258_at	contains similarity to Arabidopsis th	---	AT4G05060	-1.44	-0.53	-4.12	0.004858	0.023253	-2.43
258240_at	oleosin isoform identical to oleosin i	OLEO4	AT3G27660	-1.42	-0.51	-4.12	0.004863	0.023267	-2.43
251186_at	putative protein unknown protein A	---	AT3G62790	1.29	0.37	4.12	0.004865	0.023271	-2.43
256226_at	unknown protein ; supported by cDI	ATDI19	AT1G56280	1.57	0.65	4.12	0.004867	0.023271	-2.43
250279_at	ABA-responsive protein - like ABA-	---	AT5G13200	-1.72	-0.78	-4.12	0.004867	0.023271	-2.43

245134_s_a	unknown protein	---	AT2G45250	1.39	0.47	4.12	0.004873	0.023294	-2.43
252110_at	disease resistance-like protein TM	---	AT3G51560	-1.33	-0.41	-4.11	0.004892	0.023378	-2.44
264285_at	symbiosis-related protein, putative	ATG8C	AT1G62040	1.43	0.51	4.11	0.004894	0.023385	-2.44
250073_at	unknown protein ; supported by cD	ENH1	AT5G17170	1.99	0.99	4.11	0.004898	0.023397	-2.44
264921_at	RNA binding protein, putative simil	---	AT1G60650	1.43	0.51	4.11	0.004904	0.023418	-2.44
266991_at	putative CDP-diacylglycerol--glycer	PGP1	AT2G39290	-1.30	-0.38	-4.11	0.004904	0.023418	-2.44
265481_at	unknown protein ; supported by cD	---	AT2G15960	1.41	0.49	4.11	0.004907	0.023425	-2.44
261206_at	heat shock factor protein hsf8, puta	---	AT1G12800	-1.50	-0.59	-4.11	0.004916	0.023457	-2.44
262981_at	unknown protein ;supported by full-	---	AT1G75590	-1.54	-0.63	-4.11	0.004917	0.023458	-2.44
265336_at	hypothetical protein predicted by ge	APC10	AT2G18290	1.35	0.43	4.11	0.004918	0.023459	-2.44
248955_at	putative protein contains similarity t	GAS41	AT5G45600	1.35	0.43	4.11	0.00492	0.023459	-2.44
247844_at	ARR2 - like protein ARR2 protein,	ARR18	AT5G58080	-1.33	-0.41	-4.11	0.004921	0.023459	-2.45
251392_at	dihydrodipicolinate synthase precur	DHDPS1	AT3G60880	1.36	0.44	4.11	0.004923	0.023459	-2.45
265388_s_a	unknown protein ;supported by full-	---	AT2G20990	-1.36	-0.45	-4.11	0.004923	0.023459	-2.45
245731_at	MAP kinase, putative similar to MA	MKK9	AT1G73500	1.98	0.98	4.11	0.004923	0.023459	-2.45
260889_at	hypothetical protein predicted by ge	---	AT1G29120	1.34	0.42	4.11	0.004933	0.023497	-2.45
245881_at	putative protein	---	AT5G09460	1.66	0.73	4.11	0.004933	0.023497	-2.45
266540_at	hypothetical protein predicted by ge	---	AT2G35310	-1.35	-0.43	-4.11	0.00494	0.023522	-2.45
259739_at	unknown protein supported by cDN	SEH1H	AT1G64350	1.40	0.48	4.11	0.004942	0.023529	-2.45
266500_at	Expressed protein ; supported by fu	PLA2-ALPH	AT2G06925	-1.79	-0.84	-4.10	0.004945	0.023534	-2.45
249993_at	GTP-binding protein obg -like GTP	---	AT5G18570	1.30	0.38	4.10	0.004948	0.02354	-2.45
250437_at	AtAGP4 ; supported by cDNA: gi_1	AGP4	AT5G10430	-3.77	-1.92	-4.10	0.004949	0.02354	-2.45
247099_at	putative protein contains similarity t	---	AT5G66500	1.45	0.54	4.10	0.00495	0.02354	-2.45
261108_at	1-aminocyclopropane-1-carboxylat	ACS10	AT1G62960	1.52	0.60	4.10	0.004951	0.023542	-2.45
265730_at	60S ribosomal protein L27	---	AT2G32220	2.89	1.53	4.10	0.004954	0.02355	-2.45
263237_at	hypothetical protein contains simila	---	AT1G10610	1.74	0.80	4.10	0.00496	0.023574	-2.45
252915_at	EF-Hand containing protein -like st	---	AT4G38810	-1.51	-0.59	-4.10	0.004964	0.023587	-2.45
246060_at	rev interacting protein mis3 - like re	---	AT5G08420	1.31	0.39	4.10	0.004966	0.023596	-2.46
254671_at	MuDR transposable element - like	---	---	-1.36	-0.44	-4.10	0.004969	0.023601	-2.46
255294_at	putative sugar transporter	---	AT4G04750	1.40	0.49	4.10	0.00497	0.023605	-2.46
254708_at	ubiquitin-specific protease 20 (UBP	UBP20	AT4G17895	-1.37	-0.45	-4.10	0.004971	0.023605	-2.46
259821_at	subtilisin-like serine protease conta	---	AT1G66220	-1.53	-0.62	-4.10	0.004973	0.023606	-2.46
248869_at	putative protein contains similarity t	---	AT5G46840	1.78	0.83	4.10	0.004978	0.023623	-2.46
246192_at	translation initiation factor eIF-2 be	EIF2 BETA	AT5G20920	1.33	0.41	4.10	0.004978	0.023623	-2.46
245991_at	24 kDa vacuolar protein - like 24 kI	---	AT5G20660	1.36	0.44	4.10	0.00498	0.023628	-2.46

257860_at	Expressed protein ; supported by cl	---	AT3G13062	1.65	0.72	4.10	0.004982	0.02363	-2.46
249849_at	putative protein similar to unknown	NIC2	AT5G23230	1.50	0.59	4.10	0.004983	0.023632	-2.46
258152_at	chaperonin subunit, putative simila	---	AT3G18190	1.45	0.54	4.10	0.004986	0.023638	-2.46
262067_at	hypothetical protein predicted by ge	---	AT1G80060	-1.49	-0.57	-4.10	0.004987	0.023638	-2.46
249322_at	protein import receptor TOM20, mi	TOM20-4	AT5G40930	1.32	0.40	4.10	0.004988	0.023641	-2.46
252912_at	ribosomal protein S25 ribosomal pr	---	AT4G39200	1.68	0.75	4.10	0.004992	0.023655	-2.46
245016_at	carboxytransferase beta subunit	---	---	-1.35	-0.44	-4.10	0.004998	0.023675	-2.46
248832_at	putative protein similar to unknown	---	AT5G47170	-1.32	-0.40	-4.10	0.004999	0.023675	-2.46
254830_at	putative protein predicted protein, S	---	AT4G12590	1.29	0.37	4.10	0.005004	0.023695	-2.46
263326_at	unknown protein ; supported by cD	---	AT2G04280	-1.62	-0.70	-4.10	0.005005	0.023696	-2.46
261270_at	initiation factor 5A-4, putative simila	FBR12	AT1G26630	1.34	0.42	4.09	0.005009	0.023709	-2.46
245054_at	unknown protein	---	AT2G26460	1.46	0.55	4.09	0.005012	0.023721	-2.47
264677_at	hypothetical protein predicted by ge	HYL1	AT1G09700	1.29	0.37	4.09	0.005016	0.023731	-2.47
259109_at	putative serine threonine protein ph	---	AT3G05580	-1.67	-0.74	-4.09	0.005021	0.023751	-2.47
251175_at	homocysteine S-methyltransferase	HMT2	AT3G63250	1.39	0.47	4.09	0.005024	0.02376	-2.47
249594_at	putative protein SIAH1 protein, Bra	---	AT5G37910	-1.34	-0.43	-4.09	0.005025	0.02376	-2.47
260126_at	putative hydroxymethyltransferase s	SHM7	AT1G36370	-1.68	-0.75	-4.09	0.005026	0.023762	-2.47
261923_at	UDP-glucose glucosyltransferase,	AtUGT85A1	AT1G22380	-1.44	-0.53	-4.09	0.005034	0.023792	-2.47
259668_at	hypothetical protein predicted by ge	---	AT1G52390	-1.37	-0.45	-4.09	0.005036	0.023797	-2.47
261742_at	hypothetical protein predicted by ge	---	AT1G08390	-1.34	-0.42	-4.09	0.005037	0.023798	-2.47
259544_at	hypothetical protein ; supported by	CAT3	AT1G20620	1.37	0.45	4.09	0.00504	0.023804	-2.47
257905_at	unknown protein	---	---	-1.44	-0.53	-4.09	0.005049	0.023841	-2.47
251471_at	putative protein GTPASE-ACTIVAT	---	AT3G59570	-1.42	-0.51	-4.09	0.00505	0.023841	-2.47
255968_at	Expressed protein ; supported by fu	---	AT1G22270	1.47	0.55	4.09	0.00505	0.023841	-2.47
266606_at	putative AP2 domain transcription f	CRF5	AT2G46310	1.80	0.85	4.09	0.005054	0.023851	-2.47
265779_at	unknown protein	---	AT2G07360	-1.67	-0.74	-4.09	0.00506	0.023874	-2.48
255136_s_a	putative protein chromatin structura	---	AT4G08350	1.45	0.54	4.09	0.005062	0.023875	-2.48
257317_at	hypothetical protein	AT2G0774	---	1.45	0.53	4.08	0.005071	0.023907	-2.48
249385_at	thioredoxin ; supported by full-leng	ATTRX2	AT5G39950	1.50	0.58	4.08	0.005071	0.023907	-2.48
249875_at	photosystem II stability/assembly fa	HCF136	AT5G23120	-1.70	-0.76	-4.08	0.005083	0.023951	-2.48
249286_at	transcription factor-like protein	---	AT5G41580	1.41	0.49	4.08	0.005083	0.023951	-2.48
255417_at	F-box protein GRR1-like protein 1,	GRH1	AT4G03190	-3.56	-1.83	-4.08	0.005089	0.023975	-2.48
258413_at	unknown protein ;supported by full-	---	AT3G17300	1.46	0.54	4.08	0.005093	0.023988	-2.48
262236_at	hypothetical protein similar to hypot	---	AT1G48330	-1.95	-0.96	-4.08	0.005107	0.024048	-2.49
250875_at	putative protein fimbriae-associate	---	AT5G04020	-2.29	-1.20	-4.08	0.005108	0.024049	-2.49

256612_at	hypothetical protein predicted by ge	---	AT3G29280	-1.47	-0.56	-4.08	0.005109	0.024049	-2.49
251502_at	putative protein several hypothetica	---	AT3G59130	-1.33	-0.41	-4.08	0.005112	0.024053	-2.49
248427_at	subtilisin-like serine protease simila	ATSBT1.3	AT5G51750	-1.54	-0.62	-4.08	0.005112	0.024053	-2.49
260692_at	hypothetical protein predicted by ge	---	AT1G32430	-1.36	-0.44	-4.08	0.005115	0.024061	-2.49
253083_at	aldehyde dehydrogenase like prote	ALDH3F1	AT4G36250	-1.96	-0.97	-4.08	0.005119	0.024073	-2.49
253360_at	aminopeptidase- like protein amino	APM1	AT4G33090	1.44	0.53	4.08	0.00512	0.024076	-2.49
250423_s_a	cytochrome P450 - like protein cyto	CYP81K2	AT5G10600	1.33	0.42	4.08	0.005124	0.024091	-2.49
266189_at	unknown protein	---	AT2G39020	-1.30	-0.38	-4.08	0.005127	0.024096	-2.49
246115_at	putative protein chloroplast outer e	---	AT5G20300	1.46	0.55	4.08	0.005129	0.024101	-2.49
260544_at	unknown protein predicted by gens	---	AT2G43540	1.62	0.70	4.08	0.00513	0.024101	-2.49
260654_at	hypothetical protein predicted by ge	---	AT1G19290	1.53	0.61	4.07	0.005132	0.024107	-2.49
253866_at	putative protein various putative pro	---	AT4G27480	1.45	0.53	4.07	0.005135	0.024114	-2.49
255394_at	hypothetical protein similar to A. th	---	---	-1.38	-0.47	-4.07	0.005139	0.024126	-2.49
258830_at	unknown protein	---	AT3G07090	-1.94	-0.96	-4.07	0.005141	0.024128	-2.49
259367_at	hypothetical protein predicted by ge	---	AT1G69070	1.67	0.74	4.07	0.005144	0.024137	-2.49
255627_at	Expressed protein ; supported by fu	---	AT4G00955	-1.33	-0.41	-4.07	0.005145	0.02414	-2.49
251379_at	putative protein various predicted A	---	AT3G60680	1.75	0.80	4.07	0.00515	0.024153	-2.49
252937_at	SEC14 - like protein phosphatidylin	SEC14	AT4G39180	-1.35	-0.44	-4.07	0.00515	0.024153	-2.49
250542_at	hypothetical protein (fragment at BA	---	AT5G08270	1.87	0.91	4.07	0.005153	0.024155	-2.50
246748_at	putative protein predicted protein, I	---	AT5G27730	1.39	0.47	4.07	0.005158	0.024172	-2.50
257844_at	prolyl 4-hydroxylase, putative simil	---	AT3G28480	1.56	0.64	4.07	0.005159	0.024172	-2.50
254327_at	RCc3- like protein RCc3 protein, O	---	AT4G22490	-2.07	-1.05	-4.07	0.00516	0.024172	-2.50
250429_at	putative protein TH65 protein, Arab	---	AT5G10470	1.39	0.48	4.07	0.005162	0.024179	-2.50
264475_s_a	hypothetical protein predicted by ge	---	AT1G77150	1.51	0.60	4.07	0.00517	0.024209	-2.50
252644_at	putative protein KIAA0073, Homo s	CYP71	AT3G44600	1.48	0.56	4.07	0.005191	0.024304	-2.50
262607_at	unknown protein ;supported by full-	---	AT1G13990	1.50	0.59	4.06	0.005195	0.024317	-2.50
256826_at	hypothetical protein predicted by ge	---	AT3G18540	-1.30	-0.38	-4.06	0.005202	0.024347	-2.51
264510_at	putative phytochrome-associated pi	PIF3	AT1G09530	1.82	0.87	4.06	0.005208	0.024366	-2.51
267584_at	putative protein kinase contains a p	---	AT2G41930	-1.38	-0.46	-4.06	0.005209	0.024366	-2.51
257269_at	unknown protein contains Pfam pro	NPSN13	AT3G17440	-1.61	-0.69	-4.06	0.005214	0.024384	-2.51
257863_at	hypothetical protein similar to GRA	anac057	AT3G17730	-1.30	-0.38	-4.06	0.005217	0.024394	-2.51
259868_at	thioredoxin-like protein similar to th	ATY1	AT1G76760	1.35	0.44	4.06	0.00523	0.024444	-2.51
246501_at	putative protein KIAA1012 protein -	---	AT5G16280	-1.37	-0.45	-4.06	0.005242	0.024494	-2.51
264822_at	putative ribonucleoprotein	---	AT1G03457	-1.83	-0.87	-4.06	0.005246	0.024506	-2.51
252650_at	putative protein	---	AT3G44690	1.34	0.42	4.06	0.005249	0.024513	-2.51

252207_at	putative protein mRNA of unknown	---	AT3G50370	1.40	0.48	4.06	0.00525	0.024516	-2.52
258345_at	unknown protein	---	AT3G22845	1.35	0.44	4.06	0.005252	0.024521	-2.52
265805_s_a	60S ribosomal protein L2	EMB2296	AT2G18020	1.58	0.66	4.06	0.005255	0.024522	-2.52
248035_at	sucrose cleavage protein-like ;supp	---	AT5G55900	1.36	0.44	4.06	0.005255	0.024522	-2.52
255706_at	putative ribosomal protein S13 simi	ATRPS13A	AT4G00100	1.64	0.72	4.06	0.005256	0.024522	-2.52
246001_at	putative protein predicted protein, /	---	AT5G20790	1.99	0.99	4.05	0.005262	0.024545	-2.52
249607_at	putative protein RING-H2 finger pr	---	AT5G37280	-1.34	-0.43	-4.05	0.005276	0.024604	-2.52
259294_at	hypothetical protein predicted by ge	ATN	AT3G05330	1.62	0.70	4.05	0.005282	0.024623	-2.52
264115_at	hypothetical protein	---	AT2G31290	1.48	0.57	4.05	0.005283	0.024623	-2.52
264884_at	unknown protein ;supported by full-	---	AT1G61170	-1.95	-0.97	-4.05	0.005283	0.024623	-2.52
264259_at	hypothetical protein This gene is co	---	AT1G09290	1.64	0.72	4.05	0.005289	0.024644	-2.52
253126_at	putative protein probable membran	---	AT4G36050	1.77	0.82	4.05	0.005295	0.024668	-2.52
263295_at	putative MADS-box protein ANR1	AGL44	AT2G14210	1.31	0.39	4.05	0.005296	0.024668	-2.52
250884_at	signal recognition particle 54CP pro	CPSRP54	AT5G03940	-1.34	-0.43	-4.05	0.005305	0.024702	-2.53
246489_at	14-3-3 protein GF14upsilon (grf5) ic	GRF5	AT5G16050	1.41	0.50	4.05	0.005309	0.024707	-2.53
255760_at	vacuolar-type H+-translocating inor	---	AT1G16780	1.39	0.47	4.05	0.005316	0.024735	-2.53
254061_at	putative protein several hypothetica	---	AT4G25360	-1.38	-0.47	-4.05	0.005318	0.024741	-2.53
261821_at	thioredoxin h, putative similar to thi	ATCXXS1	AT1G11530	1.40	0.49	4.05	0.005319	0.024741	-2.53
256807_at	unknown protein contains Pfam pro	NFU4	AT3G20970	1.38	0.47	4.05	0.005321	0.024742	-2.53
258789_at	Mutator-like transposase similar to I	---	---	1.39	0.47	4.04	0.005331	0.024784	-2.53
251023_at	putative protein amino acid transpo	---	AT5G02170	-1.44	-0.53	-4.04	0.005332	0.024785	-2.53
245927_at	sterol glucosyltransferase - like pro	---	AT5G24750	-1.28	-0.35	-4.04	0.005338	0.024804	-2.53
258141_at	hypothetical protein	HON4	AT3G18035	1.51	0.59	4.04	0.005351	0.024852	-2.54
261362_s_a	ribosomal protein identical to GB:CA	---	AT1G41880	1.75	0.81	4.04	0.005351	0.024852	-2.54
264587_at	putative ligand-gated ion channel p	ATGLR3.4	AT1G05200	2.95	1.56	4.04	0.005352	0.024852	-2.54
252327_at	MTN3-like protein MtN3 gene prod	---	AT3G48740	1.61	0.69	4.04	0.005356	0.024868	-2.54
253881_at	putative protein Ran_GTP binding	---	AT4G27640	1.35	0.43	4.04	0.00536	0.024877	-2.54
257937_at	hypothetical protein predicted by ge	---	AT3G19810	1.31	0.39	4.04	0.00537	0.02491	-2.54
248838_at	carnitine/acylcarnitine translocase-l	BOU	AT5G46800	-1.73	-0.79	-4.04	0.00537	0.02491	-2.54
266382_at	hypothetical protein predicted by ge	---	---	-1.31	-0.39	-4.04	0.005371	0.02491	-2.54
251506_at	putative protein ; supported by cDN	---	AT3G59090	-1.30	-0.38	-4.04	0.005372	0.02491	-2.54
253886_at	cytochrome P450 - like protein cyto	CYP709B3	AT4G27710	-1.34	-0.43	-4.04	0.005374	0.024915	-2.54
251882_at	peptide transport - like protein pept	PTR1	AT3G54140	-1.46	-0.55	-4.04	0.005381	0.024943	-2.54
258495_at	unknown protein ;supported by full-	---	AT3G02690	1.34	0.42	4.03	0.005389	0.024964	-2.54
258907_at	putative sodium proton exchanger s	NHX4	AT3G06370	-1.42	-0.51	-4.03	0.005389	0.024964	-2.54

265857_s_a	serine threonine protein phosphatas	PP2A-4	AT2G42500	1.42	0.51	4.03	0.005391	0.02497	-2.54
252622_at	cysteine proteinase AALP, putative	---	AT3G45310	1.42	0.51	4.03	0.005395	0.024979	-2.54
250414_at	putative protein Glr5, Arabidopsis t	GLR2.6	AT5G11180	-1.33	-0.41	-4.03	0.005396	0.024979	-2.54
245133_at	putative nucleotide sugar epimeras	GAE4	AT2G45310	-1.68	-0.75	-4.03	0.0054	0.024992	-2.55
245270_at	tubulin alpha-6 chain (TUA6) ; supp	TUA6	AT4G14960	-1.87	-0.90	-4.03	0.005401	0.024992	-2.55
249577_at	calmodulin-binding heat-shock prot	---	AT5G37710	-1.65	-0.73	-4.03	0.005402	0.024992	-2.55
252018_at	putative protein various predicted p	AtPP2-A15	AT3G53000	-1.57	-0.65	-4.03	0.005404	0.024996	-2.55
265602_at	putative retroelement pol polyprotei	---	---	-1.44	-0.52	-4.03	0.005405	0.024996	-2.55
257442_at	legumin-like protein contains a 11-S	---	AT2G28680	-1.59	-0.67	-4.03	0.005406	0.024996	-2.55
251194_at	putative protein	---	AT3G62920	1.69	0.75	4.03	0.005408	0.024996	-2.55
262491_at	putative SecA-type chloroplast prot	---	AT1G21650	1.43	0.51	4.03	0.005408	0.024996	-2.55
249320_at	disease resistance protein-like non-	---	AT5G40910	1.62	0.70	4.03	0.005436	0.025106	-2.55
253167_at	calmodulin-domain protein kinase C	CPK5	AT4G35310	-1.48	-0.57	-4.03	0.005437	0.025107	-2.55
253495_at	putative protein crp1 protein, Zea n	PGR3	AT4G31850	1.63	0.70	4.03	0.005449	0.025151	-2.56
251303_at	NAM-like protein no apical meriste	ANAC066	AT3G61910	-1.32	-0.40	-4.03	0.005452	0.025156	-2.56
262536_at	SOUL-like protein Similar to SOUL	---	AT1G17100	1.95	0.97	4.03	0.005454	0.025156	-2.56
265417_at	unknown protein	---	AT2G20920	1.74	0.80	4.02	0.005463	0.025189	-2.56
264805_at	unknown protein similar to putative	ATRX	AT1G08600	1.39	0.48	4.02	0.005463	0.025189	-2.56
246327_at	receptor-like serine/threonine kinas	---	AT1G16670	1.51	0.59	4.02	0.005468	0.025203	-2.56
264474_s_a	ribulose-bisphosphate carboxylase	RBCS1A	AT1G06820	-1.29	-0.36	-4.02	0.005468	0.025203	-2.56
262977_at	transcription factor, putative similar	---	AT1G75490	-1.44	-0.53	-4.02	0.005474	0.025224	-2.56
251552_at	ribosomal protein L11 -like ribosom	---	AT3G58700	1.81	0.86	4.02	0.005475	0.025224	-2.56
265958_at	putative adenylate kinase ;supporte	ADK	AT2G37250	1.75	0.81	4.02	0.005479	0.025236	-2.56
258265_at	putative beta-1,3-glucanase precur	---	AT3G15800	-1.40	-0.49	-4.02	0.005486	0.025267	-2.56
250794_at	putative protein contains similarity t	---	AT5G05270	-1.36	-0.44	-4.02	0.005489	0.025267	-2.56
256862_at	dihydroxyacid dehydratase, putativ	---	AT3G23940	2.15	1.11	4.02	0.00549	0.025267	-2.56
252392_s_a	putative protein various predicted p	---	AT3G47890	1.53	0.62	4.02	0.00549	0.025267	-2.56
258635_at	unknown protein	---	AT3G08020	1.30	0.38	4.02	0.005491	0.025267	-2.56
255924_at	unknown protein contains similarity	---	AT1G22170	-1.46	-0.55	-4.02	0.005492	0.025267	-2.56
257741_at	hypothetical protein predicted by ge	---	AT3G27340	1.58	0.66	4.02	0.0055	0.025299	-2.57
256957_at	hypothetical protein predicted by ge	---	AT3G13420	-1.38	-0.46	-4.02	0.005504	0.025313	-2.57
261122_at	ornithine carbamoyltransferase pre	OTC	AT1G75330	1.56	0.64	4.02	0.005508	0.025318	-2.57
259971_at	unknown protein similar to SPL1-re	---	AT1G76580	-1.61	-0.69	-4.02	0.00551	0.02532	-2.57
245851_at	putative protein HERC2 - Homo sa	KEG	AT5G13530	1.38	0.46	4.02	0.00551	0.02532	-2.57
260580_at	unknown protein	---	AT2G47390	1.30	0.38	4.02	0.005517	0.025345	-2.57

246524_at	Carboxylesterase-like protein sterd	ATPCME	AT5G15860	1.61	0.69	4.02	0.005518	0.025346	-2.57
254722_at	putative protein predicted protein, A	---	AT4G13530	1.80	0.85	4.02	0.005522	0.025359	-2.57
257293_at	unknown protein similar to symbios	APG8H	AT3G15580	1.59	0.67	4.01	0.005532	0.025393	-2.57
261426_at	unknown protein contains similarity	---	AT1G18680	-1.33	-0.42	-4.01	0.005532	0.025393	-2.57
251578_at	putative protein contains alternative	---	AT3G58180	1.36	0.44	4.01	0.005538	0.025417	-2.57
262544_at	hypothetical protein predicted by ge	---	AT1G15420	1.45	0.54	4.01	0.005539	0.025417	-2.57
254858_at	putative protein other predicted pro	---	AT4G12070	1.37	0.46	4.01	0.005543	0.025427	-2.57
247374_at	topoisomerase-like protein ;suppor	---	AT5G63190	1.64	0.71	4.01	0.005544	0.025427	-2.57
252759_at	putative protein hypothetical protein	---	AT3G42630	1.29	0.37	4.01	0.005545	0.025428	-2.57
253402_at	HD-zip transcription factor (athb-8)	ATHB-8	AT4G32880	-1.69	-0.75	-4.01	0.005546	0.025428	-2.57
255601_at	putative protein (fragment) various	---	AT4G01030	1.43	0.52	4.01	0.005551	0.025447	-2.58
252672_at	hypothetical protein	---	AT3G44230	-1.31	-0.39	-4.01	0.005554	0.025454	-2.58
265309_at	putative myosin heavy chain	XIG	AT2G20290	-1.61	-0.69	-4.01	0.005558	0.025466	-2.58
259013_at	unknown protein similar to putative	emb1990	AT3G07430	1.36	0.45	4.01	0.005563	0.025482	-2.58
266601_at	hypothetical protein predicted by ge	---	AT2G46060	1.73	0.79	4.01	0.005564	0.025482	-2.58
245253_at	hydroperoxide lyase (HPOL) like pr	HPL1	AT4G15440	-5.13	-2.36	-4.01	0.005564	0.025482	-2.58
264442_at	hypothetical protein similar to lecith	---	AT1G27480	1.67	0.74	4.01	0.005568	0.025487	-2.58
261761_at	hypothetical protein predicted by ge	CENP-C	AT1G15660	1.35	0.44	4.01	0.005569	0.025488	-2.58
260377_at	unknown protein	---	AT1G73930	-1.29	-0.37	-4.01	0.00557	0.025488	-2.58
255522_at	putative GTP pyrophosphokinase s	RSH1	AT4G02260	1.41	0.49	4.01	0.005571	0.025488	-2.58
248258_at	putative protein contains similarity t	---	AT5G53400	1.89	0.92	4.01	0.005575	0.025494	-2.58
245913_at	predicted protein	---	AT5G19860	1.41	0.50	4.01	0.005575	0.025494	-2.58
253116_at	putative protein CRP1, Zea mays,	---	AT4G35850	1.81	0.86	4.01	0.005576	0.025494	-2.58
261333_at	hypothetical protein predicted by ge	---	AT1G44910	1.62	0.69	4.01	0.005579	0.025503	-2.58
247221_at	Expressed protein ; supported by cl	LIP1	AT5G64813	-1.29	-0.37	-4.01	0.005584	0.025519	-2.58
251557_at	v-ATPase subunit D (vATPD) ; sup	---	AT3G58730	-1.37	-0.45	-4.00	0.005596	0.025565	-2.58
264685_at	endo-1,4-beta-glucanase, putative	KOR2	AT1G65610	-1.42	-0.51	-4.00	0.005628	0.025694	-2.59
248552_at	RNA-binding protein-like ; supporte	---	AT5G50250	1.38	0.46	4.00	0.00563	0.025694	-2.59
246536_at	putative protein KIAA0594 - Homo	---	AT5G15920	2.18	1.12	4.00	0.00563	0.025694	-2.59
245227_s_a	gunknown protein contains non-con	---	AT1G08410	1.64	0.71	4.00	0.005631	0.025694	-2.59
252899_at	putative protein leaf protein, Ipomo	---	AT4G39530	1.41	0.50	4.00	0.005634	0.025704	-2.59
247258_at	expressed protein similar to unknov	---	AT5G64816	1.45	0.53	4.00	0.005636	0.025706	-2.59
256961_at	transcription initiation factor TFIID-1	TBP1	AT3G13445	1.40	0.49	4.00	0.00564	0.025716	-2.59
257607_at	hypothetical protein predicted by ge	---	AT3G13880	1.29	0.37	4.00	0.00564	0.025716	-2.59
257050_at	putative protein phosphatase type 2	---	AT3G15260	1.51	0.60	4.00	0.005645	0.025732	-2.59

248681_at	pectate lyase non-consensus AG d	---	AT5G48900	-13.42	-3.75	-4.00	0.005649	0.025737	-2.59
260042_at	hypothetical protein C-term similar t	---	AT1G68820	1.71	0.77	4.00	0.005649	0.025737	-2.59
253293_at	Expressed protein ; supported by cl	---	AT4G33905	-1.65	-0.73	-4.00	0.005657	0.025768	-2.60
247182_at	putative protein contains similarity t	HB25	AT5G65410	-1.45	-0.53	-3.99	0.005662	0.025784	-2.60
252193_at	R2R3-MYB transcription factor ; su	MYB77	AT3G50060	-2.40	-1.26	-3.99	0.005664	0.025789	-2.60
253474_at	hypothetical protein	---	AT4G32270	1.46	0.55	3.99	0.005667	0.025792	-2.60
260840_at	hypothetical protein similar to hypot	---	AT1G29050	1.49	0.57	3.99	0.005668	0.025792	-2.60
262968_at	hypothetical protein predicted by ge	---	AT1G75720	-1.37	-0.46	-3.99	0.005669	0.025792	-2.60
265220_at	histidine transport protein (PTR2-B)	PTR2	AT2G02040	1.31	0.39	3.99	0.005669	0.025792	-2.60
255718_at	unknown protein ;supported by full-	ATNSI	AT1G32070	1.39	0.47	3.99	0.005676	0.025818	-2.60
251883_at	ribosomal protein L17 -like protein	---	AT3G54210	-1.37	-0.45	-3.99	0.00568	0.025829	-2.60
249924_at	kinase associated protein phosphat	KAPP	AT5G19280	1.49	0.57	3.99	0.005681	0.025829	-2.60
247376_at	nucleotide diphosphate kinase Ia (e	NDPK2	AT5G63310	-1.33	-0.41	-3.99	0.005686	0.025844	-2.60
250400_at	protein phosphatase 2C -like prote	---	AT5G10740	1.68	0.75	3.99	0.005709	0.025943	-2.61
259441_at	cathepsin B-like cysteine protease,	---	AT1G02300	1.49	0.58	3.99	0.005711	0.025947	-2.61
251333_at	putative protein putative protein F2	---	AT3G61690	1.28	0.35	3.99	0.005713	0.025948	-2.61
249619_at	stelar K+ outward rectifying channe	GORK	AT5G37500	-1.61	-0.69	-3.99	0.005717	0.02596	-2.61
248540_at	FRO1 and FRO2-like protein	FRO8	AT5G50160	1.29	0.37	3.99	0.005718	0.02596	-2.61
262108_at	unknown protein similar to unknowr	---	AT1G02740	1.46	0.54	3.99	0.005728	0.025996	-2.61
248010_at	peroxisomal targeting signal type 1	PEX5	AT5G56290	1.32	0.40	3.98	0.005742	0.026057	-2.61
257054_at	Expressed protein ; supported by fu	MT3	AT3G15353	1.28	0.36	3.98	0.00575	0.026081	-2.61
260361_at	unknown protein ; supported by cDI	---	AT1G69360	-1.55	-0.63	-3.98	0.005751	0.026081	-2.61
259102_at	unknown protein similar to hin1 GB	NHL1	AT3G11660	1.47	0.56	3.98	0.005751	0.026081	-2.61
266495_at	cycloartenol synthase identical to S	CAS1	AT2G07050	-1.42	-0.51	-3.98	0.005761	0.026114	-2.62
249628_at	putative protein tropomyosin gene	---	AT5G37590	1.48	0.56	3.98	0.005761	0.026114	-2.62
252332_at	putative protein	---	AT3G48810	-1.55	-0.63	-3.98	0.005762	0.026116	-2.62
263100_at	hypothetical protein predicted by ge	AtPOT1a	AT2G05210	-1.55	-0.63	-3.98	0.005764	0.02612	-2.62
247320_at	photosystem I reaction centre subu	PSAN	AT5G64040	-1.36	-0.45	-3.98	0.005767	0.026123	-2.62
250562_at	putative protein	TOM5	AT5G08040	1.46	0.55	3.98	0.005767	0.026123	-2.62
246480_at	TCP-1 chaperonin-like protein t-co	---	AT5G16070	1.54	0.62	3.98	0.00577	0.026126	-2.62
262616_at	oxidoreductase, putative contains I	---	AT1G06620	-1.88	-0.91	-3.98	0.005771	0.026126	-2.62
261883_at	protein kinase, putative similar to re	---	AT1G80870	-1.40	-0.49	-3.98	0.005772	0.026127	-2.62
250786_at	putative protein strong similarity to t	SDN2	AT5G05540	1.55	0.63	3.98	0.005775	0.026138	-2.62
245348_at	trehalose-6-phosphate synthase lik	ATTPS5	AT4G17770	1.57	0.65	3.98	0.005782	0.026162	-2.62
252105_at	protein phosphatase 2C-like protei	---	AT3G51470	-1.49	-0.57	-3.98	0.005792	0.026203	-2.62

261603_at	DNA binding protein ACBF, putativ	ATRBP47A	AT1G49600	1.90	0.93	3.98	0.005796	0.026216	-2.62
253138_at	ribosomal protein L11 homolog sev	MRPL11	AT4G35490	1.32	0.40	3.98	0.005802	0.026237	-2.62
261530_at	unknown protein contains Pfam pro	---	AT1G63460	1.52	0.60	3.97	0.005805	0.026247	-2.62
251255_at	putative protein early nodule-speci	---	AT3G62280	-1.31	-0.38	-3.97	0.00581	0.026263	-2.62
266526_at	putative tetracycline transporter pro	---	AT2G16980	-1.42	-0.50	-3.97	0.005811	0.026265	-2.63
246778_at	mevalonate kinase supported by fu	MK	AT5G27450	-1.43	-0.52	-3.97	0.005814	0.026273	-2.63
257792_at	TOM20, putative similar to TOM20	TOM20-3	AT3G27080	1.46	0.55	3.97	0.005817	0.02628	-2.63
260829_s_a	chloroplast thylakoidal processing	---	AT1G06870	1.58	0.66	3.97	0.005821	0.026285	-2.63
247691_at	heat shock protein 18 ;supported b	HSP18.2	AT5G59720	-1.39	-0.47	-3.97	0.005822	0.026285	-2.63
265627_at	Expressed protein ; supported by fu	---	AT2G27285	1.42	0.50	3.97	0.005824	0.026289	-2.63
257667_at	1,4-alpha-glucan branching enzym	EMB2729	AT3G20440	1.65	0.72	3.97	0.005826	0.026296	-2.63
247154_at	receptor protein kinase-like protein	HSL2	AT5G65710	-1.34	-0.42	-3.97	0.00583	0.026306	-2.63
263730_at	beta-glucosidase, putative similar t	BGLU4	AT1G60090	-1.33	-0.41	-3.97	0.005838	0.026337	-2.63
264783_at	putative calcium-dependent protein	PPCK1	AT1G08650	1.92	0.94	3.97	0.005851	0.02639	-2.63
253632_at	senescence-associated protein hor	TET9	AT4G30430	-1.28	-0.35	-3.97	0.005853	0.026393	-2.63
264141_at	hypothetical protein predicted by ge	---	AT1G79090	1.31	0.39	3.97	0.005854	0.026393	-2.63
260127_at	hypothetical protein similar to hypo	---	AT1G36320	1.57	0.65	3.97	0.005856	0.026393	-2.63
247209_at	putative protein contains similarity t	---	AT5G64830	1.35	0.44	3.97	0.005856	0.026393	-2.63
262985_s_a	60s ribosomal protein l27a. similar t	RPL27AB	AT1G23290	1.71	0.77	3.97	0.005858	0.026396	-2.63
248097_at	protein phosphatase X isoform 2 (g	PPX2	AT5G55260	1.46	0.54	3.97	0.005863	0.026411	-2.63
266344_at	hypothetical protein predicted by ge	---	AT2G01580	-1.34	-0.42	-3.97	0.005864	0.026411	-2.63
244945_at	cytochrome c biogenesis orf206	---	---	1.49	0.57	3.97	0.005865	0.026411	-2.63
254817_at	putative SWH1 protein SWH1 prote	ORP2B	AT4G12460	1.40	0.49	3.97	0.005866	0.026411	-2.64
256765_at	aminotransferase, putative similar t	POP2	AT3G22200	1.52	0.60	3.97	0.005875	0.026445	-2.64
262347_at	unknown protein similar to hypothet	---	AT1G64110	-1.42	-0.51	-3.96	0.005885	0.026487	-2.64
260004_at	unknown protein ;supported by full-	---	AT1G67860	1.75	0.80	3.96	0.005888	0.026493	-2.64
256468_at	ferredoxin, putative similar to GB:D	---	AT1G32550	-1.45	-0.53	-3.96	0.005889	0.026497	-2.64
260638_at	unknown protein similar to putative	---	AT1G62390	1.71	0.77	3.96	0.005897	0.026523	-2.64
262394_at	unknown protein	emb1273	AT1G49510	-1.66	-0.73	-3.96	0.005898	0.026525	-2.64
250651_at	cytochrome P450	CYP93D1	AT5G06900	-1.29	-0.36	-3.96	0.005899	0.026525	-2.64
262962_at	NADP-isocitrate dehydrogenase, p	ICDH	AT1G54340	1.28	0.35	3.96	0.005906	0.026549	-2.64
267435_at	30S ribosomal protein S5 ; support	---	AT2G33800	-1.32	-0.40	-3.96	0.005922	0.026608	-2.65
261113_at	hypothetical protein predicted by ge	---	AT1G75400	1.52	0.60	3.96	0.005922	0.026608	-2.65
251684_at	putative protein	---	AT3G56410	1.72	0.78	3.96	0.005922	0.026608	-2.65
248167_at	putative protein similar to unknown	---	AT5G54530	1.55	0.63	3.96	0.005929	0.026629	-2.65

253385_at	putative protein predicted protein, (	---	AT4G32930	1.33	0.41	3.96	0.005929	0.026629	-2.65
260651_at	hypothetical protein predicted by ge	---	AT1G32460	-1.35	-0.43	-3.96	0.005931	0.026629	-2.65
259834_at	H-protein promoter binding factor-2	---	AT1G69570	-1.81	-0.85	-3.96	0.005932	0.026629	-2.65
267539_at	putative RING zinc finger protein ;	---	AT2G42030	-1.42	-0.50	-3.96	0.00594	0.026659	-2.65
261098_at	unknown protein	---	AT1G62970	1.36	0.45	3.96	0.005947	0.026686	-2.65
258038_at	unknown protein ;supported by full-	---	AT3G21260	1.75	0.80	3.96	0.005948	0.026688	-2.65
246095_at	homeotic gene regulator - like prote	---	AT5G19310	1.66	0.73	3.96	0.00595	0.02669	-2.65
248620_at	putative protein similar to unknown	---	AT5G49320	-1.36	-0.44	-3.95	0.005952	0.026692	-2.65
254178_at	hypothetical protein	---	AT4G23880	3.70	1.89	3.95	0.005954	0.026692	-2.65
262157_at	unknown protein contains similarity	---	AT1G52670	-1.40	-0.49	-3.95	0.005954	0.026692	-2.65
261784_at	hypothetical protein predicted by ge	---	AT1G08220	1.34	0.43	3.95	0.005962	0.026721	-2.65
262380_at	threonine synthase, putative simila	---	AT1G72810	1.43	0.51	3.95	0.005981	0.026804	-2.66
260044_at	Expressed protein ; supported by fu	---	AT1G73655	-1.37	-0.46	-3.95	0.005993	0.026853	-2.66
249957_at	putative protein predicted proteins,	---	AT5G18900	1.47	0.56	3.95	0.006	0.026875	-2.66
262912_at	oligopeptide transporter, putative s	---	AT1G59740	-3.12	-1.64	-3.95	0.006001	0.026875	-2.66
252423_at	putative protein putative hydrolyse	---	AT3G47590	-1.34	-0.42	-3.95	0.006007	0.0269	-2.66
260579_at	putative cytochrome c oxidase Vc s	---	AT2G47380	1.40	0.48	3.95	0.006015	0.026929	-2.66
259657_at	phospholipase D alpha, putative si	PLDEPSIL(	AT1G55180	-1.34	-0.42	-3.95	0.006017	0.026932	-2.66
252080_at	putative protein polyphosphoinositi	---	AT3G51670	-1.71	-0.77	-3.94	0.006025	0.026965	-2.66
264364_at	unknown protein Similar to gb|U852	---	AT1G03330	1.32	0.40	3.94	0.006029	0.026976	-2.66
256227_at	unknown protein ; supported by cDI	---	AT1G56290	1.32	0.40	3.94	0.006035	0.026998	-2.67
252557_at	putative protein cim1 induced aller	ATEXLA3	AT3G45960	-1.34	-0.42	-3.94	0.006041	0.027017	-2.67
260749_at	hypothetical protein predicted by ge	---	AT1G49110	-1.43	-0.51	-3.94	0.006046	0.027037	-2.67
266713_at	unknown protein	---	AT2G46760	-1.36	-0.44	-3.94	0.006055	0.027069	-2.67
257447_at	hypothetical protein predicted by ge	---	AT2G04230	1.27	0.35	3.94	0.006057	0.027071	-2.67
253950_at	putative dihydrolipoamide succinylt	---	AT4G26910	1.71	0.77	3.94	0.006058	0.027071	-2.67
262062_s_a	hypothetical protein	emb1427	AT1G20570	1.39	0.47	3.94	0.006059	0.027071	-2.67
258283_at	hypothetical protein predicted by ge	---	AT3G26750	1.38	0.47	3.94	0.00606	0.027071	-2.67
259950_at	hypothetical protein predicted by g	---	AT1G71410	-1.41	-0.49	-3.94	0.006061	0.027071	-2.67
262859_at	hypothetical protein predicted by ge	---	AT1G64790	1.38	0.46	3.94	0.006062	0.027072	-2.67
254721_at	hypothetical protein ;supported by	SMAP1	AT4G13520	1.39	0.47	3.94	0.006064	0.027073	-2.67
250394_at	putative protein yllC, Enterococcus	---	AT5G10910	1.46	0.55	3.94	0.006065	0.027073	-2.67
249527_at	proline oxidase, mitochondrial prec	---	AT5G38710	1.60	0.68	3.94	0.006066	0.027073	-2.67
251926_at	60S RIBOSOMAL PROTEIN L36 h	---	AT3G53740	1.81	0.86	3.94	0.00607	0.027085	-2.67
247578_at	putative protein predicted protein, A	---	AT5G61300	-1.45	-0.53	-3.94	0.006072	0.027085	-2.67

259543_at	hypothetical protein ; supported by	---	AT1G20580	1.43	0.52	3.94	0.006073	0.027085	-2.67
262071_at	unknown protein ;supported by full-	CF9	AT1G59510	1.43	0.52	3.94	0.006074	0.027086	-2.67
259992_at	putative heat shock transcription fa	HSFA8	AT1G67970	1.70	0.76	3.94	0.006076	0.027088	-2.67
245660_at	unknown protein	---	AT1G28240	-1.68	-0.75	-3.94	0.006077	0.027088	-2.67
262963_at	dihydrolipoamide S-acetyltransfera	---	AT1G54220	-1.32	-0.40	-3.94	0.006079	0.027092	-2.67
251985_at	thioredoxin -like protein cop c2, C	---	AT3G53220	1.47	0.56	3.94	0.006083	0.027106	-2.67
252180_at	putative protein cyclin-dependent k	KRP2	AT3G50630	-1.63	-0.70	-3.94	0.00609	0.02713	-2.68
246305_at	putative protein protein At2g40060	---	AT3G51890	1.45	0.54	3.94	0.006094	0.027144	-2.68
253314_at	hypothetical protein	---	AT4G33890	1.31	0.39	3.93	0.006103	0.027179	-2.68
257190_at	30S ribosomal protein S10, putativ	---	AT3G13120	-1.63	-0.70	-3.93	0.006119	0.027244	-2.68
260055_at	unknown protein similar to putative	---	AT1G78150	1.32	0.40	3.93	0.006127	0.027268	-2.68
246954_at	unknown protein ; supported by cD	---	AT5G04830	-1.31	-0.39	-3.93	0.006128	0.027268	-2.68
258532_at	ribosomal protein L29, putative sim	---	AT3G06700	2.23	1.15	3.93	0.006132	0.027281	-2.68
259178_at	unknown protein similar to hypothe	RGLG1	AT3G01650	1.50	0.59	3.93	0.006135	0.027291	-2.68
256484_at	PPR-repeat protein contains multipl	---	AT1G31430	1.41	0.50	3.93	0.00614	0.027306	-2.68
258998_at	putative adenylate kinase similar to	---	AT3G01820	1.47	0.55	3.93	0.006141	0.027306	-2.68
247193_at	putative protein strong similarity to	---	AT5G65380	-1.54	-0.63	-3.93	0.006147	0.027325	-2.69
248786_at	unknown protein	---	AT5G47410	1.74	0.80	3.93	0.00615	0.027326	-2.69
248883_at	putative protein strong similarity to	---	AT5G46190	-1.34	-0.42	-3.93	0.00615	0.027326	-2.69
265377_at	putative beta-1,3-glucanase	---	AT2G05790	-4.85	-2.28	-3.93	0.006151	0.027326	-2.69
248589_at	von Hippel-Lindau binding protein (	PDF3	AT5G49510	1.33	0.41	3.93	0.006152	0.027326	-2.69
245790_at	glycerol-3-phosphate acyltransferas	ATS1	AT1G32200	-1.44	-0.53	-3.93	0.006155	0.027334	-2.69
264330_at	multi-drug resistance protein Strong	ATMRP5	AT1G04120	-1.35	-0.44	-3.93	0.006168	0.027384	-2.69
264661_at	hypothetical protein Similar to Nicot	---	AT1G09950	-1.75	-0.81	-3.93	0.006168	0.027384	-2.69
254052_at	UMP/CMP kinase like protein UMP	---	AT4G25280	-1.44	-0.53	-3.93	0.006173	0.0274	-2.69
253861_at	putative protein MSP1 protein, Sac	---	AT4G27680	1.36	0.44	3.92	0.006178	0.027408	-2.69
263466_at	hypothetical protein predicted by ge	---	AT2G31740	1.31	0.39	3.92	0.006179	0.027408	-2.69
257962_at	hypothetical protein predicted by ge	---	AT3G19790	-1.68	-0.75	-3.92	0.006185	0.027429	-2.69
258946_at	hypothetical protein predicted by ge	---	AT3G10650	1.46	0.54	3.92	0.006186	0.027429	-2.69
266880_at	hypothetical protein predicted by ge	---	AT2G44770	-1.44	-0.53	-3.92	0.006191	0.027447	-2.69
260526_at	putative WD-40 repeat protein	---	AT2G47410	-1.34	-0.42	-3.92	0.006197	0.027468	-2.69
245509_at	hypothetical protein	---	AT4G15730	1.45	0.54	3.92	0.006198	0.027468	-2.69
252108_at	putative protein various predicted p	---	AT3G51530	1.36	0.44	3.92	0.006199	0.027468	-2.69
258136_at	hypothetical protein predicted by ge	RSY3	AT3G24560	1.43	0.51	3.92	0.006202	0.027474	-2.70
255005_at	putative protein putative proteins Ar	---	AT4G09990	-1.42	-0.50	-3.92	0.006209	0.027499	-2.70

249231_at	putative protein similar to unknown	ABIL4	AT5G42030	1.41	0.49	3.92	0.006211	0.027503	-2.70
248941_s_a	putative protein similar to unknown	---	AT5G45460	-1.47	-0.55	-3.92	0.006213	0.027507	-2.70
265814_at	hypothetical protein similar to hypo	---	AT2G17930	1.37	0.45	3.92	0.006216	0.027517	-2.70
248547_at	putative protein contains similarity t	EMB1006	AT5G50280	1.68	0.75	3.92	0.00622	0.027527	-2.70
266792_at	putative sucrose/H+ symporter	SUT2	AT2G02860	-2.08	-1.06	-3.92	0.006227	0.027551	-2.70
253264_at	protein kinase - like protein protein	OST1	AT4G33950	-1.31	-0.39	-3.92	0.006232	0.02757	-2.70
248152_at	DNA repair and meiosis protein Mre	MRE11	AT5G54260	-1.55	-0.63	-3.92	0.006243	0.027615	-2.70
261938_at	hypothetical protein predicted by ge	---	AT1G22510	-1.88	-0.91	-3.92	0.006248	0.027632	-2.70
258090_at	putative 60S ribosomal protein L18	---	AT3G14600	1.54	0.62	3.92	0.00625	0.027634	-2.70
263716_at	26S proteasome regulatory subunit	RPN1A	AT2G20580	1.29	0.37	3.91	0.006255	0.027647	-2.70
265887_at	biotin holocarboxylase synthetase i	HCS1	AT2G25710	1.46	0.54	3.91	0.006272	0.027715	-2.71
254738_at	RNA-binding protein like	AT4G1386(	---	-1.39	-0.47	-3.91	0.006283	0.027758	-2.71
260875_at	hypothetical protein predicted by ge	SKP2A	AT1G21410	1.88	0.91	3.91	0.006285	0.027763	-2.71
245155_at	putative protein similarity to predict	---	AT5G12470	-1.61	-0.69	-3.91	0.006287	0.027766	-2.71
252805_at	putative protein	---	AT3G42380	-1.31	-0.39	-3.91	0.006296	0.027793	-2.71
258149_at	hypothetical protein contains Pfam	EMB1270	AT3G18110	1.46	0.55	3.91	0.006296	0.027793	-2.71
260332_at	hypothetical protein predicted by ge	---	AT1G70470	-1.27	-0.35	-3.91	0.006299	0.0278	-2.71
259063_at	putative 5B-anther specific protein s	---	AT3G07450	-1.28	-0.36	-3.91	0.006303	0.027812	-2.71
251319_at	putative protein POSSIBLE APOSI	---	AT3G61610	-1.56	-0.64	-3.91	0.006308	0.02783	-2.71
249181_at	putative protein contains similarity t	---	AT5G42920	1.38	0.46	3.91	0.00631	0.027832	-2.71
249842_at	putative protein contains similarity t	---	AT5G23550	1.32	0.40	3.91	0.006311	0.027832	-2.71
260053_at	hypothetical protein similar to unkno	---	AT1G78120	-1.48	-0.57	-3.91	0.006316	0.027849	-2.71
264046_at	putative non-LTR retroelement reve	---	AT2G22440	-1.37	-0.45	-3.91	0.006318	0.02785	-2.72
261036_at	developmentally regulated GTP-bi	ATDRG1	AT1G17470	1.31	0.39	3.91	0.006318	0.02785	-2.72
254776_at	3-hydroxyisobutyryl-coenzyme A h	---	AT4G13360	1.28	0.35	3.91	0.00632	0.027851	-2.72
253969_at	putative protein hypothetical protei	CSN6B	AT4G26430	1.73	0.79	3.90	0.006338	0.027922	-2.72
246460_at	cellulose synthase catalytic subuni	CSLD2	AT5G16910	-1.68	-0.75	-3.90	0.00634	0.027922	-2.72
258573_at	hypothetical protein contains Pfam	PTAC3	AT3G04260	1.30	0.38	3.90	0.006346	0.027937	-2.72
254617_s_a	ribosomal protein L11, cytosolic ;s	RPL16B	AT4G18730	1.63	0.70	3.90	0.006347	0.027937	-2.72
248388_at	putative protein contains similarity t	---	AT5G51980	1.42	0.50	3.90	0.006347	0.027937	-2.72
256394_at	unknown protein contains non-cons	---	AT3G06290	1.33	0.42	3.90	0.006349	0.02794	-2.72
258827_at	hypothetical protein predicted by ge	---	AT3G07150	1.55	0.63	3.90	0.006353	0.02795	-2.72
251076_at	putative protein putative protein At2	---	AT5G01970	-1.64	-0.72	-3.90	0.006356	0.027957	-2.72
260543_at	putative membrane transporter	INT1	AT2G43330	-1.63	-0.70	-3.90	0.006359	0.027963	-2.72
253285_at	fatty acid elongase - like protein fat	KCS16	AT4G34250	-1.83	-0.87	-3.90	0.006363	0.027976	-2.72

246307_at	putative nuclear DNA-binding prote	ATG2	AT3G51800	1.62	0.69	3.90	0.006366	0.027981	-2.72
251492_at	putative protein CGI-136 protein - I	TXR1	AT3G59280	1.29	0.36	3.90	0.006367	0.027981	-2.72
256575_at	dTDP-glucose 4,6-dehydratase, pu	RHM3	AT3G14790	-1.55	-0.64	-3.90	0.00638	0.028034	-2.73
260416_at	putative cullin similar to cullin 3 GB:	CUL3B	AT1G69670	1.35	0.43	3.90	0.006389	0.028067	-2.73
266707_at	hypothetical protein predicted by ge	---	AT2G03310	1.34	0.42	3.90	0.006394	0.028085	-2.73
262645_at	unknown protein similar to elongatic	SCO1	AT1G62750	1.49	0.57	3.90	0.006397	0.028094	-2.73
255296_at	hypothetical protein	---	AT4G04790	1.84	0.88	3.90	0.006399	0.028096	-2.73
266059_at	predicted protein ;supported by cDN	---	AT2G40765	1.87	0.90	3.90	0.006406	0.02812	-2.73
262775_at	unknown protein	---	AT1G13000	1.33	0.41	3.90	0.006411	0.028134	-2.73
247172_at	anthocyanidin-3-glucoside rhamnos	---	AT5G65550	-1.33	-0.41	-3.89	0.006414	0.028141	-2.73
248946_at	putative protein similar to unknown	---	AT5G45530	-1.31	-0.39	-3.89	0.00642	0.028153	-2.73
256311_at	auxin response factor 6 (ARF6) ide	ARF6	AT1G30330	-1.72	-0.78	-3.89	0.006422	0.028153	-2.73
251861_at	putative protein GATA transcription	BME3	AT3G54810	-2.68	-1.42	-3.89	0.006422	0.028153	-2.73
252294_at	60S ribosomal protein L13, BBC1 p	ATBBC1	AT3G49010	2.13	1.09	3.89	0.006423	0.028153	-2.73
259204_s_a	hypothetical protein predicted by g	---	---	-1.33	-0.41	-3.89	0.006424	0.028153	-2.73
263647_at	unknown protein	---	AT2G04690	1.51	0.60	3.89	0.006427	0.028161	-2.73
247218_at	asparagine synthetase (gb|AAC728	ASN2	AT5G65010	3.32	1.73	3.89	0.00643	0.028167	-2.73
262600_at	unknown protein ESTs gb|H37032.	MBD10	AT1G15340	1.56	0.64	3.89	0.006435	0.028185	-2.74
253232_at	hypothetical protein ;supported by	TAF8	AT4G34340	1.40	0.48	3.89	0.006444	0.028217	-2.74
261220_at	ER lumen protein-retaining recepto	---	AT1G19970	-2.05	-1.04	-3.89	0.006446	0.028217	-2.74
249295_at	putative protein contains similarity t	---	AT5G41280	-1.30	-0.37	-3.89	0.006446	0.028217	-2.74
260208_s_a	unknown protein similar to Ca+2-bi	---	AT1G70670	-1.84	-0.88	-3.89	0.006452	0.028232	-2.74
263134_at	dTDP-glucose 4,6-dehydratase, pu	RHM1	AT1G78570	-1.56	-0.65	-3.89	0.006455	0.028232	-2.74
253753_at	glycine-rich protein like glycine-rich	---	AT4G29030	-1.39	-0.47	-3.89	0.006455	0.028232	-2.74
261163_x_a	auxin response factor, putative sim	ARF21	AT1G34410	-1.28	-0.35	-3.89	0.006473	0.028303	-2.74
249906_at	unknown protein	---	AT5G22730	1.30	0.38	3.89	0.006475	0.028303	-2.74
247849_at	putative protein fibrinogen-binding	---	AT5G58130	1.48	0.56	3.89	0.006482	0.02833	-2.74
261012_at	CLE9, putative CLAVATA3/ESR-R	CLE9	AT1G26600	-1.27	-0.34	-3.89	0.00649	0.028357	-2.74
260768_at	Expressed protein ; supported by fu	---	AT1G49245	1.37	0.46	3.88	0.006503	0.028412	-2.75
246527_at	ribosomal protein-like 40S RIBOSO	---	AT5G15750	2.08	1.06	3.88	0.006517	0.028468	-2.75
257413_at	putative RNA-binding protein conta	---	AT1G22910	-1.60	-0.68	-3.88	0.006523	0.028477	-2.75
254049_at	putative ribosomal protein S10 40S	---	AT4G25740	1.80	0.85	3.88	0.006524	0.028477	-2.75
247041_at	floral homeotic protein apetala2-like	TOE3	AT5G67180	-1.42	-0.50	-3.88	0.006526	0.028477	-2.75
247400_at	putative protein ;supported by full-l	---	AT5G62840	-1.54	-0.63	-3.88	0.006526	0.028477	-2.75
257864_at	hypothetical protein predicted by ge	---	AT3G17740	1.55	0.63	3.88	0.006528	0.028477	-2.75

259036_at	putative laccase similar to laccase (	LAC7	AT3G09220	-1.31	-0.38	-3.88	0.006529	0.028477	-2.75
264987_at	unknown protein ; supported by cDI	---	AT1G27030	-1.99	-1.00	-3.88	0.00653	0.028477	-2.75
249138_at	putative protein contains similarity t	WPP1	AT5G43070	-1.35	-0.43	-3.88	0.00653	0.028477	-2.75
267532_at	unknown protein ;supported by full-	---	AT2G42040	-1.70	-0.77	-3.88	0.006531	0.028477	-2.75
247745_at	copper transport protein	COPT1	AT5G59030	1.29	0.37	3.88	0.006535	0.02849	-2.75
245866_s_a	unknown protein	---	AT1G57980	-3.55	-1.83	-3.88	0.006559	0.028589	-2.76
250914_at	myb -like protein telomeric DNA bir	TRFL10	AT5G03780	1.41	0.50	3.88	0.006561	0.028589	-2.76
265898_at	hypothetical protein predicted by ge	---	AT2G25690	1.72	0.79	3.88	0.006562	0.028589	-2.76
246852_at	putative protein various predicted b	---	AT5G26880	1.33	0.41	3.88	0.006562	0.028589	-2.76
250481_at	putative protein	---	AT5G10310	1.36	0.44	3.88	0.006572	0.028626	-2.76
263045_at	hypothetical protein predicted by ge	---	AT2G05370	-1.36	-0.44	-3.88	0.006575	0.028631	-2.76
262484_at	putative transcriptional regulatory p	ATSWI3C	AT1G21700	-1.26	-0.33	-3.87	0.006578	0.02864	-2.76
265858_at	putative ribophorin I	---	AT2G01720	1.45	0.54	3.87	0.006587	0.028658	-2.76
265005_at	Expressed protein ; supported by fu	---	AT1G61667	-1.74	-0.80	-3.87	0.006588	0.028658	-2.76
252295_at	signal recognition particle subunit 9	---	AT3G49100	1.54	0.63	3.87	0.006589	0.028658	-2.76
250874_at	putative protein	---	AT5G04010	-1.41	-0.49	-3.87	0.00659	0.028658	-2.76
245674_at	chitinase, putative similar to chitina	---	AT1G56680	-1.32	-0.40	-3.87	0.006592	0.028658	-2.76
259685_at	unknown protein	AtPP2-A11	AT1G63090	-1.70	-0.77	-3.87	0.006592	0.028658	-2.76
258851_at	glutathione S-transferase identical t	ATGSTF11	AT3G03190	-2.06	-1.04	-3.87	0.006592	0.028658	-2.76
255511_at	Expressed protein ; supported by cI	PIT1	AT4G02075	1.91	0.93	3.87	0.006602	0.028692	-2.76
260799_at	UDP-glucose glucosyltransferase,	AtUGT85A4	AT1G78270	1.44	0.53	3.87	0.006603	0.028692	-2.76
246232_at	hypothetical protein	EMB2754	AT4G36630	1.35	0.43	3.87	0.00663	0.028804	-2.77
248790_at	membrane channel protein-like; aqu	TIP2;3	AT5G47450	-1.58	-0.66	-3.87	0.006634	0.028816	-2.77
249430_at	GTP-binding protein-like GTP-bind	---	AT5G39900	1.60	0.68	3.87	0.006635	0.028816	-2.77
255458_at	small nuclear riboprotein Sm-D1-lik	---	AT4G02840	1.31	0.39	3.87	0.006636	0.028816	-2.77
264491_at	hypothetical protein predicted by ge	---	AT1G27410	1.34	0.42	3.87	0.006642	0.028837	-2.77
255582_at	putative DNA-binding protein simila	NGA4	AT4G01500	-1.32	-0.40	-3.87	0.006645	0.028845	-2.77
250729_at	ubiquitin activating enzyme 2 (UBA2	UBA 2	AT5G06460	1.36	0.44	3.87	0.006655	0.028882	-2.77
267206_at	putative dioxygenase	---	AT2G30830	-1.35	-0.44	-3.86	0.006662	0.028908	-2.77
257516_at	unknown protein	ACR4	AT1G69040	-1.64	-0.71	-3.86	0.006664	0.028911	-2.77
266980_at	60S ribosomal protein L35 ;suppor	---	AT2G39390	1.79	0.84	3.86	0.006669	0.028923	-2.77
251393_at	putative protein symbiosis-related p	ATG8G	AT3G60640	1.57	0.65	3.86	0.00667	0.028923	-2.77
252960_at	hypothetical protein	---	AT4G38750	1.72	0.78	3.86	0.006672	0.028926	-2.77
246758_at	60S ribosomal protein - like 60S rib	---	AT5G27850	1.74	0.80	3.86	0.006679	0.028949	-2.78
AFFX-Athal-	Arabidopsis thaliana /REF=M64116	GAPC1	---	1.87	0.90	3.86	0.006679	0.028949	-2.78

249523_at	cytochrome b-561 (gb|AAD45585.1	ACYB-1	AT5G38630	-1.36	-0.44	-3.86	0.006684	0.028962	-2.78
255656_at	putative protein (fragment) DNA-bi	---	AT4G00990	1.42	0.50	3.86	0.006685	0.028962	-2.78
251645_at	putative protein polygalacturonase	---	AT3G57790	-1.40	-0.49	-3.86	0.00669	0.028974	-2.78
252895_at	hypothetical protein	---	AT4G39450	1.33	0.41	3.86	0.006692	0.028974	-2.78
245120_at	hypothetical protein predicted by ge	HOS1	AT2G39810	1.45	0.53	3.86	0.006692	0.028974	-2.78
245967_at	proline-rich protein extensins	---	AT5G19800	-1.34	-0.42	-3.86	0.006693	0.028974	-2.78
249327_at	anion channel protein (gb|AAC0574	ATCLC-A	AT5G40890	-1.91	-0.93	-3.86	0.006699	0.028996	-2.78
247460_at	AtOXA1 ;supported by full-length c	OXA1	AT5G62050	1.26	0.33	3.86	0.006703	0.029006	-2.78
245844_at	hypothetical protein predicted by ge	---	AT1G26170	1.37	0.45	3.86	0.006708	0.029021	-2.78
247098_at	GTP-binding protein-like	---	AT5G66470	1.64	0.72	3.86	0.006709	0.029022	-2.78
247077_at	putative protein similar to unknown	---	AT5G66420	-1.44	-0.52	-3.86	0.006716	0.029048	-2.78
261175_at	unknown protein	---	AT1G04800	-1.38	-0.46	-3.86	0.00672	0.029058	-2.78
263004_at	hypothetical protein contains simila	ATNEK1	AT1G54510	1.40	0.49	3.86	0.006722	0.029061	-2.78
246910_at	exonuclease - like protein ribonucle	---	AT5G25800	1.60	0.68	3.86	0.006724	0.029063	-2.78
246434_at	root cap 1 (RCP1) ;supported by fu	RCP1	AT5G17520	-1.52	-0.60	-3.86	0.006725	0.029063	-2.78
259672_at	DNA-directed RNA polymerase ide	---	AT1G68990	2.17	1.12	3.86	0.006726	0.029063	-2.78
253029_at	hypothetical protein	FRS9	AT4G38170	1.92	0.94	3.86	0.006736	0.029099	-2.78
252484_at	glucuronosyl transferase-like prote	---	AT3G46690	1.45	0.54	3.86	0.006741	0.029118	-2.79
245877_at	unknown protein	---	AT1G26220	-1.53	-0.61	-3.85	0.006754	0.029163	-2.79
252015_at	putative protein growth-regulating f	AtGRF4	AT3G52910	1.27	0.34	3.85	0.006754	0.029163	-2.79
248059_at	putative protein similar to unknown	TRN1	AT5G55540	-1.80	-0.85	-3.85	0.006758	0.029174	-2.79
246114_at	seed imbitition protein-like seed im	DIN10	AT5G20250	-1.69	-0.75	-3.85	0.006762	0.02918	-2.79
251917_at	putative protein	---	AT3G53970	1.32	0.40	3.85	0.006782	0.02926	-2.79
258354_at	putative zinc finger protein similar t	---	AT3G14320	-1.29	-0.37	-3.85	0.006785	0.029269	-2.79
255221_at	putative protein various predicted p	---	AT4G05150	1.41	0.50	3.85	0.00679	0.029282	-2.79
245331_at	hypothetical protein ;supported by f	---	AT4G14410	1.34	0.42	3.85	0.006794	0.029292	-2.79
253463_at	Expressed protein ; supported by fu	---	AT4G32105	-1.35	-0.43	-3.85	0.006795	0.029292	-2.79
245771_at	hypothetical protein predicted by ge	---	AT1G30250	-5.08	-2.35	-3.85	0.006807	0.029329	-2.80
257374_at	hypothetical protein predicted by ge	---	AT2G43280	1.54	0.62	3.85	0.006814	0.029354	-2.80
248981_at	regulatory protein NPR1-like; transc	NPR3	AT5G45110	-1.36	-0.45	-3.85	0.006816	0.029355	-2.80
266894_at	hypothetical protein predicted by ge	---	AT2G26050	-1.28	-0.35	-3.85	0.006818	0.029355	-2.80
252764_at	nucleic acid binding protein-like nu	AL3	AT3G42790	1.35	0.44	3.85	0.006818	0.029355	-2.80
254192_at	acyl-CoA synthetase - like protein a	---	AT4G23850	-1.36	-0.45	-3.85	0.006823	0.029371	-2.80
253569_at	receptor kinase - like protein recep	---	AT4G31250	-1.45	-0.54	-3.84	0.006831	0.029397	-2.80
260178_at	hypothetical protein similar to unkn	---	AT1G70720	-1.37	-0.46	-3.84	0.006832	0.029397	-2.80

250303_at	putative protein similar to unknown	---	AT5G12100	1.77	0.82	3.84	0.006842	0.029433	-2.80
259936_at	putative UDP-glucose:glycoprotein	EBS1	AT1G71220	1.32	0.40	3.84	0.006845	0.029443	-2.80
244940_at	ribosomal protein S12 (trans-splice	---	---	-1.46	-0.54	-3.84	0.006861	0.029507	-2.80
250937_at	putative protein various predicted p	---	AT5G03230	1.71	0.77	3.84	0.006863	0.029509	-2.80
257856_at	hypothetical protein predicted by g	---	AT3G12930	-1.29	-0.37	-3.84	0.006899	0.029654	-2.81
247367_at	oxygen-independent coproporphyri	---	AT5G63290	1.66	0.73	3.84	0.006902	0.029656	-2.81
263038_at	conserved hypothetical protein prot	---	AT1G23270	-1.33	-0.41	-3.84	0.006902	0.029656	-2.81
259321_at	unknown protein	GAUT13	AT3G01040	-1.51	-0.60	-3.84	0.006904	0.029658	-2.81
247676_at	putative protein RNaseP protein p3	---	AT5G59980	1.72	0.78	3.84	0.00691	0.029678	-2.81
246390_at	1-aminocyclopropane-1-carboxylat	---	AT1G77330	-1.52	-0.60	-3.83	0.006916	0.029698	-2.81
255672_at	hypothetical protein ; supported by	EDA8	AT4G00310	-1.41	-0.49	-3.83	0.006919	0.029705	-2.81
259762_at	hypothetical protein predicted by ge	---	AT1G77600	1.40	0.49	3.83	0.006931	0.02975	-2.82
247043_at	protein kinase, 41K (EC 2.7.1.-) (pi	SNRK2.3	AT5G66880	1.65	0.72	3.83	0.006932	0.02975	-2.82
263311_at	hypothetical protein predicted by ge	---	AT2G10340	-1.41	-0.49	-3.83	0.006934	0.02975	-2.82
253189_at	putative protein	---	AT4G35335	-1.61	-0.69	-3.83	0.006935	0.02975	-2.82
254368_at	DNA-directed RNA polymerase (EC	NRPB2	AT4G21710	1.34	0.42	3.83	0.006937	0.029752	-2.82
250388_at	putative protein various predicted p	---	AT5G11310	2.01	1.01	3.83	0.006946	0.029781	-2.82
266119_at	protease inhibitor II identical to GB	LCR69	AT2G02100	-3.02	-1.60	-3.83	0.006949	0.029789	-2.82
264336_at	hypothetical protein contains simila	---	AT1G70360	1.42	0.51	3.83	0.00695	0.029789	-2.82
267237_s_a	unknown protein ;supported by full	---	AT2G44040	-1.96	-0.97	-3.83	0.006954	0.029797	-2.82
251854_at	putative protein various predicted p	---	AT3G54800	-1.33	-0.41	-3.83	0.006955	0.029797	-2.82
266125_at	putative GATA-type zinc finger tran	---	AT2G45050	-1.46	-0.55	-3.83	0.006958	0.029801	-2.82
256912_at	hypothetical protein predicted by ge	---	AT3G23850	-1.36	-0.44	-3.83	0.006958	0.029801	-2.82
267063_at	hypothetical protein predicted by ge	---	AT2G41120	1.51	0.60	3.83	0.006963	0.029817	-2.82
245345_at	proteinase like protein ;supported b	---	AT4G16640	-1.32	-0.40	-3.83	0.006965	0.029817	-2.82
265671_at	40S ribosomal protein S12 ;suppor	---	AT2G32060	1.97	0.98	3.83	0.006979	0.029867	-2.82
266950_at	expressed protein supported by full	---	AT2G18910	-1.60	-0.68	-3.83	0.006979	0.029867	-2.82
255585_at	putative NAM-like protein	anac069	AT4G01550	1.62	0.69	3.83	0.006998	0.029941	-2.83
254948_at	putative protein various predicted p	---	AT4G11000	-1.40	-0.48	-3.83	0.007003	0.029956	-2.83
259786_at	lipase/hydrolase, putative contains	---	AT1G29660	-13.89	-3.80	-3.82	0.007005	0.029956	-2.83
252272_at	receptor protein kinase - like protei	BAM2	AT3G49670	-1.92	-0.94	-3.82	0.007006	0.029956	-2.83
264192_at	hypothetical protein predicted by ge	ATATG18H	AT1G54710	1.28	0.35	3.82	0.007007	0.029956	-2.83
246769_at	hypothetical protein	---	AT5G27440	1.34	0.42	3.82	0.007008	0.029956	-2.83
253105_at	putative protein zinc finger protein,	---	AT4G35840	1.57	0.65	3.82	0.007009	0.029956	-2.83
255267_at	putative protein LpxD gene, Brucel	---	AT4G05210	-1.27	-0.35	-3.82	0.007012	0.029961	-2.83

244997_at	RNA polymerase beta' subunit-2	---	---	-1.38	-0.46	-3.82	0.007013	0.029962	-2.83
258151_at	beta-glucosidase, putative similar t	BGLU44	AT3G18080	1.82	0.87	3.82	0.007019	0.029983	-2.83
257522_at	Yippee-like protein similar to Yippee	---	AT3G08990	-1.30	-0.38	-3.82	0.007025	0.030003	-2.83
261133_at	DYW7 protein identical to DYW7 p	---	AT1G19715	-1.62	-0.69	-3.82	0.007041	0.030065	-2.83
253469_at	putative protein gene C42D8.3, Ca	ATPANK2	AT4G32180	1.35	0.44	3.82	0.007042	0.030065	-2.83
255488_at	putative serine/threonine protein kir	---	AT4G02630	1.49	0.58	3.82	0.007046	0.030071	-2.83
265205_at	putative poly(A) binding protein	PAB7	AT2G36660	-1.33	-0.41	-3.82	0.007058	0.030116	-2.83
245092_at	putative TGACG-sequence-specific	BZIP17	AT2G40950	1.44	0.52	3.82	0.007066	0.030142	-2.84
264637_at	allyl alcohol dehydrogenase, putati	---	AT1G65560	1.59	0.67	3.82	0.007067	0.030142	-2.84
252256_at	PRE-MRNA SPLICING FACTOR S	SRp34a	AT3G49430	1.47	0.55	3.82	0.007069	0.030143	-2.84
259124_at	floral homeotic protein AGL4 identi	ספט-02	AT3G02310	-1.27	-0.35	-3.82	0.007075	0.030165	-2.84
257381_at	unknown protein	---	AT2G37950	-1.76	-0.82	-3.82	0.007085	0.0302	-2.84
258914_at	hypothetical protein predicted by ge	AGP27	AT3G06360	-1.30	-0.37	-3.82	0.007088	0.030211	-2.84
251028_at	putative protein putative hydrolase	---	AT5G02230	1.42	0.51	3.81	0.007095	0.03023	-2.84
244999_at	RNA polymerase beta subunit	---	---	-1.64	-0.71	-3.81	0.007096	0.03023	-2.84
251669_at	putative protein hypothetical protei	---	AT3G57180	1.87	0.90	3.81	0.007097	0.030231	-2.84
261256_at	disease resistance protein RTM1 ic	RTM1	AT1G05760	-1.48	-0.56	-3.81	0.007101	0.030244	-2.84
260525_at	putative pre-mRNA splicing factor R	---	AT2G47250	1.31	0.39	3.81	0.007107	0.030263	-2.84
249224_at	mitochondrial carrier protein-like	---	AT5G42130	1.29	0.37	3.81	0.007111	0.030275	-2.84
257949_at	putative UDP-glucose glucosyltrans	UGT71B1	AT3G21750	-1.57	-0.65	-3.81	0.007113	0.030278	-2.84
249192_at	brain and reproductive organ-expre	---	AT5G42470	1.28	0.35	3.81	0.007117	0.030285	-2.84
256874_at	cytochrome P450, putative contain	CYP71B36	AT3G26320	1.41	0.49	3.81	0.007118	0.030285	-2.84
251851_at	structural maintenance of chromos	TTN8	AT3G54670	1.37	0.45	3.81	0.007119	0.030285	-2.84
253539_at	putative protein RING-finger protei	---	AT4G31450	1.39	0.48	3.81	0.007134	0.030341	-2.85
266310_at	putative PCI domain protein protea	FUS12	AT2G26990	1.39	0.48	3.81	0.007138	0.030351	-2.85
251322_at	cysteine synthase AtcysC1 ;suppo	CYSC1	AT3G61440	2.12	1.09	3.81	0.007139	0.030351	-2.85
257012_at	RNA-binding protein, putative simil	TEL1	AT3G26120	-1.31	-0.39	-3.81	0.007149	0.03039	-2.85
246558_at	putative protein IDN3-B - Homo sa	EMB2773	AT5G15540	1.44	0.52	3.81	0.007151	0.030391	-2.85
255857_at	unknown protein ;supported by full-	ABA4	AT1G67080	1.29	0.37	3.81	0.007155	0.030404	-2.85
248737_at	unknown protein	---	AT5G48120	1.56	0.64	3.81	0.007163	0.030431	-2.85
246807_at	ion channel - like protein ligand gat	GLR2.1	AT5G27100	-1.54	-0.62	-3.81	0.007167	0.030442	-2.85
248646_at	unknown protein ;supported by full-	---	AT5G49100	-1.86	-0.90	-3.81	0.007171	0.030453	-2.85
248111_at	wax synthase-like protein	---	AT5G55330	-1.32	-0.40	-3.81	0.007172	0.030453	-2.85
249054_at	unknown protein	---	AT5G02870	1.43	0.51	3.81	0.007178	0.030473	-2.85
255907_at	homeobox protein, putative similar	HDG12	AT1G17920	-1.31	-0.39	-3.80	0.007189	0.030515	-2.85

250912_at	histone deacetylase -like protein hi	HD2C	AT5G03740	1.83	0.87	3.80	0.007195	0.03053	-2.86
254430_at	reticuline oxidase - like protein retic	---	AT4G20820	2.07	1.05	3.80	0.007195	0.03053	-2.86
262710_at	unknown protein ESTs gb|T04357 a	---	AT1G16210	1.31	0.39	3.80	0.007199	0.030541	-2.86
254421_at	VP1 like protein transcription activa	VAL3	AT4G21550	1.55	0.64	3.80	0.007202	0.030548	-2.86
253447_at	hypothetical protein	---	AT4G32630	-1.28	-0.35	-3.80	0.007208	0.030567	-2.86
262504_at	putative protein disulfide isomerase	ATPDIL1-1	AT1G21750	1.61	0.68	3.80	0.007212	0.030575	-2.86
247847_at	putative protein predicted proteins,	---	AT5G58110	1.62	0.69	3.80	0.007216	0.030588	-2.86
257690_at	unknown protein contains similarity	---	AT3G12830	2.25	1.17	3.80	0.007223	0.030609	-2.86
262794_at	unknown protein EST gb|N37870 c	emb1745	AT1G13120	1.37	0.45	3.80	0.007236	0.030652	-2.86
258051_at	hypothetical protein predicted by ge	TRZ4	AT3G16260	1.49	0.58	3.80	0.007239	0.030659	-2.86
250306_at	putative protein similar to unknown	---	AT5G12170	1.58	0.66	3.80	0.007244	0.03067	-2.86
253932_at	putative protein other Arabidopsis p	---	AT4G26800	1.29	0.37	3.80	0.007245	0.03067	-2.86
258715_at	putative 60S ribosomal protein L1 s	---	AT3G09630	1.56	0.64	3.80	0.007251	0.030684	-2.86
255919_at	putative protein	---	---	-1.36	-0.44	-3.80	0.007252	0.030684	-2.86
250986_at	putative protein	---	AT5G02850	-1.34	-0.42	-3.80	0.007252	0.030684	-2.86
265347_at	similar to mammalian MHC III regio	SUVH6	AT2G22740	-1.27	-0.35	-3.80	0.007253	0.030684	-2.86
260095_at	putative transcription factor BTF3 (	---	AT1G73230	1.58	0.66	3.80	0.007264	0.030716	-2.87
266417_at	putative non-green plastid inner env	---	AT2G38550	1.44	0.53	3.80	0.007265	0.030716	-2.87
262685_at	unknown protein ; supported by cDI	---	AT1G76010	1.57	0.65	3.80	0.007265	0.030716	-2.87
245637_at	hypothetical protein similar to putati	---	AT1G25230	-2.45	-1.29	-3.80	0.007266	0.030716	-2.87
262052_at	hypothetical protein identical to hyp	---	---	1.38	0.47	3.79	0.007276	0.030752	-2.87
254574_at	expressed protein supported by cD	---	AT4G19430	3.42	1.77	3.79	0.007283	0.03076	-2.87
249285_at	unknown protein	---	AT5G41960	1.44	0.52	3.79	0.007283	0.03076	-2.87
263009_at	hypothetical protein contains simila	NHX5	AT1G54370	1.33	0.41	3.79	0.007291	0.030784	-2.87
250751_at	glucuronosyl transferase-like protei	---	AT5G05890	-1.41	-0.50	-3.79	0.007293	0.030784	-2.87
247721_at	elongin - like protein elongin C, Dro	---	AT5G59140	1.28	0.35	3.79	0.007294	0.030784	-2.87
261404_at	alpha galactosyltransferase, putativ	---	AT1G18690	1.69	0.75	3.79	0.007295	0.030784	-2.87
259363_at	methionine aminopeptidase I (MAF	MAP1C	AT1G13270	1.38	0.47	3.79	0.007296	0.030784	-2.87
252166_at	protein kinase SPK-2 ;supported b	SNRK2.2	AT3G50500	1.45	0.54	3.79	0.007299	0.030793	-2.87
258575_at	putative O-linked GlcNAc transferas	SEC	AT3G04240	1.32	0.41	3.79	0.007304	0.030808	-2.87
260976_at	hypothetical protein	CID8	AT1G53650	1.54	0.62	3.79	0.007317	0.030857	-2.87
263958_at	putative salt-inducible protein	---	AT2G36240	1.27	0.34	3.79	0.00732	0.030859	-2.87
250386_at	MYB like protein MYB like protein,	MYB3R-4	AT5G11510	-1.45	-0.54	-3.79	0.00732	0.030859	-2.87
255113_at	putative protein various hypothetica	---	---	-1.32	-0.40	-3.79	0.007324	0.030866	-2.87
257601_at	hypothetical protein predicted by ge	---	AT3G24820	1.32	0.40	3.79	0.007325	0.030866	-2.87

251929_at	sigma factor SigC ; supported by c	SIGC	AT3G53920	1.34	0.42	3.79	0.007334	0.030899	-2.88
256599_at	hypothetical protein predicted by ge	---	AT3G14760	-1.32	-0.40	-3.79	0.007338	0.03091	-2.88
258187_at	HSC70-interacting protein, putative	ATTDX	AT3G17880	1.34	0.43	3.79	0.007346	0.030938	-2.88
264460_at	hypothetical protein similar to trans	ATNFXL1	AT1G10170	1.47	0.55	3.79	0.007348	0.030943	-2.88
252044_at	outer envelope membrane protein-	OEP7	AT3G52420	1.29	0.37	3.79	0.007353	0.030952	-2.88
254088_at	putative protein snurportin1 m3G-c	---	AT4G24880	1.53	0.61	3.79	0.007353	0.030952	-2.88
257625_at	cytochrome P450, putative contain	CYP71B24	AT3G26230	4.42	2.14	3.79	0.007361	0.030977	-2.88
253025_at	hypothetical protein	---	AT4G38120	1.57	0.66	3.79	0.007362	0.030977	-2.88
267535_at	putative C2H2-type zinc finger prote	ZFP8	AT2G41940	-1.77	-0.82	-3.78	0.007371	0.031008	-2.88
250299_at	putative esterase - like protein cinI	---	AT5G11910	1.37	0.45	3.78	0.007374	0.031012	-2.88
259583_at	hypothetical protein	---	AT1G28070	1.41	0.50	3.78	0.007374	0.031012	-2.88
255434_at	predicted protein of unknown functi	---	AT4G03180	1.36	0.44	3.78	0.00738	0.03103	-2.88
247863_at	SKP1 interacting partner 1 (SKIP1)	---	AT5G57890	1.36	0.45	3.78	0.007392	0.031075	-2.88
266519_at	unknown protein ; supported by cD	---	AT2G35155	-1.40	-0.49	-3.78	0.007393	0.031075	-2.88
249161_at	20S proteasome subunit PAF1 (gb|	PAF1	AT5G42790	1.26	0.34	3.78	0.007395	0.031077	-2.88
253032_at	guanine nucleotide-exchange prote	---	AT4G38200	-1.31	-0.39	-3.78	0.007409	0.031121	-2.89
258259_s_a	unknown protein ; supported by cD	---	AT3G26820	1.37	0.45	3.78	0.007409	0.031121	-2.89
249200_at	5-3 exoribonuclease 2 ; supported b	XRN2	AT5G42540	1.47	0.55	3.78	0.00741	0.031121	-2.89
248564_at	putative protein contains similarity t	---	AT5G49700	1.53	0.61	3.78	0.007413	0.031131	-2.89
262070_at	far-red impaired response protein,	FRS8	AT1G80010	1.32	0.40	3.78	0.007418	0.031144	-2.89
258072_at	unknown protein	RGS1	AT3G26090	1.30	0.38	3.78	0.007421	0.03115	-2.89
248862_at	unknown protein	---	AT5G46730	-1.57	-0.65	-3.78	0.007422	0.03115	-2.89
248074_at	putative protein similar to unknown	FLA1	AT5G55730	-2.33	-1.22	-3.78	0.007428	0.03117	-2.89
247275_at	beta-ureidopropionase	BETA-UP	AT5G64370	1.69	0.76	3.78	0.007432	0.031178	-2.89
263145_at	hypothetical protein predicted by ge	ATEXO70D	AT1G54090	-1.50	-0.58	-3.78	0.007442	0.031214	-2.89
245198_at	Expressed protein ; supported by fu	---	AT1G67700	-1.34	-0.42	-3.78	0.007446	0.031229	-2.89
266484_at	putative putative sister-chromatide	SCC3	AT2G47980	1.37	0.46	3.78	0.00745	0.031236	-2.89
255683_at	putative malate oxidoreductase	---	AT4G00570	-1.41	-0.50	-3.78	0.007452	0.031236	-2.89
266182_at	hypothetical protein predicted by ge	---	AT2G02370	1.50	0.58	3.78	0.007454	0.031236	-2.89
254820_s_a	pEARLI 1-like protein Arabidopsis t	---	AT4G12510	-1.95	-0.96	-3.78	0.007454	0.031236	-2.89
264373_at	putative vesicle transport protein C	SEC22	AT1G11890	-1.50	-0.58	-3.78	0.007455	0.031237	-2.89
260463_at	DNA helicase isolog	RECQ4A	AT1G10930	-1.28	-0.35	-3.78	0.007459	0.031243	-2.89
258281_at	putative shikimate kinase similar to	---	AT3G26900	1.26	0.34	3.78	0.007459	0.031243	-2.89
258640_at	hypothetical protein predicted by ge	---	AT3G07930	1.46	0.55	3.77	0.007463	0.031251	-2.89
267065_at	hypothetical protein predicted by ge	---	AT2G41080	1.41	0.50	3.77	0.007477	0.031307	-2.90

265162_at	hypothetical protein predicted by ge	---	AT1G30910	1.39	0.48	3.77	0.007486	0.031332	-2.90
264146_at	hypothetical protein contains simila	CER1	AT1G02205	-16.94	-4.08	-3.77	0.007486	0.031332	-2.90
259075_at	putative N2,N2-dimethylguanosine	---	AT3G02320	1.39	0.48	3.77	0.007494	0.031359	-2.90
265460_at	putative caltractin ;supported by fu	---	AT2G46600	1.70	0.76	3.77	0.007497	0.031359	-2.90
266202_at	putative cinnamoyl-CoA reductase	---	AT2G02400	-1.31	-0.39	-3.77	0.007502	0.031375	-2.90
260012_at	Expressed protein ; supported by c	---	AT1G67865	1.78	0.84	3.77	0.007507	0.031389	-2.90
265440_at	pEARLI 4 protein Same as GB: L43	pEARLI4	AT2G20960	1.74	0.80	3.77	0.007509	0.031393	-2.90
250929_at	putative protein ; supported by cDN	---	AT5G03290	1.58	0.66	3.77	0.00751	0.031393	-2.90
259512_at	hypothetical protein ; supported by	KEU	AT1G12360	-1.28	-0.36	-3.77	0.007512	0.031393	-2.90
248877_at	putative protein similar to unknown	---	AT5G46140	-1.33	-0.41	-3.77	0.007516	0.031405	-2.90
258180_at	unknown protein	---	AT3G21480	1.67	0.74	3.77	0.007526	0.031424	-2.90
253368_at	myosin - like protein unconventiona	XI-I	AT4G33200	1.35	0.43	3.77	0.007526	0.031424	-2.90
248195_at	membrane associated protein ; sup	ATMAMI	AT5G54110	-1.45	-0.53	-3.77	0.007533	0.031435	-2.90
260683_at	ribosomal protein, putative similar t	HLL	AT1G17560	1.37	0.45	3.77	0.007536	0.031435	-2.91
246103_at	putative protein	AN3	AT5G28640	-1.26	-0.34	-3.77	0.007536	0.031435	-2.91
258855_at	unknown protein	---	AT3G02070	-1.67	-0.74	-3.77	0.007537	0.031435	-2.91
247955_at	nucleosome assembly protein	NAP1;3	AT5G56950	1.45	0.53	3.77	0.007546	0.031466	-2.91
252413_at	40S ribosomal protein S20-like pro	---	AT3G47370	1.84	0.88	3.77	0.007552	0.031487	-2.91
256231_at	unknown protein ; supported by full-	---	AT3G12630	1.33	0.41	3.76	0.007564	0.031531	-2.91
250664_at	putative protein 10-deacetylbaccati	---	AT5G07080	-1.97	-0.98	-3.76	0.007575	0.031563	-2.91
248787_at	putative protein similar to unknown	---	AT5G47420	-1.57	-0.65	-3.76	0.007575	0.031563	-2.91
256505_at	unknown protein	---	AT1G75200	1.52	0.60	3.76	0.007576	0.031563	-2.91
267416_at	putative phosphatidylinositol-glycan	SETH1	AT2G34980	-1.32	-0.40	-3.76	0.007578	0.031565	-2.91
259590_at	hypothetical protein contains simila	---	AT1G28160	-1.38	-0.46	-3.76	0.007581	0.031574	-2.91
261560_at	acyl CoA thioesterase, putative sim	---	AT1G01710	-1.28	-0.36	-3.76	0.007584	0.031579	-2.91
262249_at	root hairless 1 (RHL1) similar to roo	RHL1	AT1G48380	-1.38	-0.47	-3.76	0.007585	0.031579	-2.91
257817_at	putative RNA-binding protein conta	---	AT3G25150	-1.34	-0.42	-3.76	0.007595	0.031609	-2.91
259043_at	unknown protein similar to putative	---	AT3G03440	1.61	0.69	3.76	0.007595	0.031609	-2.91
248784_at	putative protein similar to unknown	---	AT5G47380	-1.58	-0.66	-3.76	0.0076	0.031621	-2.91
267604_at	hypothetical protein predicted by ge	ZFN2	AT2G32930	-1.84	-0.88	-3.76	0.007601	0.031621	-2.91
248436_at	putative protein contains similarity t	---	AT5G51220	1.33	0.41	3.76	0.007604	0.031629	-2.91
257046_at	ATPase, putative similar to spastin	---	AT3G19740	1.51	0.59	3.76	0.007613	0.031657	-2.92
245003_at	PSII 43 KDa protein	---	---	-1.37	-0.46	-3.76	0.007618	0.031674	-2.92
267561_at	putative protein kinase contains a p	---	AT2G45590	-1.68	-0.75	-3.76	0.007631	0.031721	-2.92
263435_at	putative ATP-dependent RNA helic	---	AT2G28600	1.73	0.79	3.76	0.007636	0.031737	-2.92

249866_at	2-isopropylmalate synthase-like; ho	MAM1	AT5G23010	-1.85	-0.89	-3.76	0.007651	0.031795	-2.92
247300_at	unknown protein	FCLY	AT5G63910	1.38	0.46	3.75	0.007658	0.031816	-2.92
257798_at	unknown protein	NAI2	AT3G15950	-1.52	-0.60	-3.75	0.007677	0.031883	-2.93
249810_at	unknown protein	---	AT5G23920	1.61	0.68	3.75	0.007681	0.031892	-2.93
248526_at	putative protein contains similarity t	---	AT5G50740	-1.55	-0.63	-3.75	0.007681	0.031892	-2.93
265449_at	putative arginine/serine-rich splicing	---	AT2G46610	1.57	0.65	3.75	0.007692	0.031931	-2.93
251581_at	putative protein CARBON CATABO	---	AT3G58560	1.42	0.51	3.75	0.007695	0.031936	-2.93
245378_at	GLABRA2 like protein	HDG4	AT4G17710	-1.30	-0.38	-3.75	0.007696	0.031936	-2.93
247281_at	immunophilin (gb|AAB57847.1) ;su	FKBP12	AT5G64350	1.30	0.38	3.75	0.007698	0.031937	-2.93
259659_at	hypothetical protein contains simila	---	AT1G55170	1.52	0.60	3.75	0.007706	0.031964	-2.93
246343_at	putative protein	---	AT3G56720	1.25	0.32	3.75	0.007708	0.031965	-2.93
252671_at	putative protein dehydrogenases of	---	AT3G44190	-1.47	-0.56	-3.75	0.007712	0.031972	-2.93
252586_at	dof6 zinc finger protein	---	AT3G45610	-1.38	-0.46	-3.75	0.007737	0.032071	-2.93
255397_at	putative transposon protein	---	---	-1.48	-0.56	-3.75	0.007745	0.032091	-2.93
256611_at	unknown protein similar to putative	---	AT3G29270	1.42	0.51	3.75	0.00775	0.032105	-2.94
248267_at	NADH-dependent glutamate syntha	GLT1	AT5G53460	1.56	0.64	3.74	0.007758	0.032133	-2.94
258822_s_a	unknown protein contains Pfam pro	---	AT3G07220	1.67	0.74	3.74	0.007762	0.032144	-2.94
262542_at	hypothetical protein similar to NAM-	anac016	AT1G34180	1.67	0.74	3.74	0.007764	0.032144	-2.94
257224_at	P-type ATPase, putative similar to	---	AT3G27870	-1.40	-0.49	-3.74	0.007765	0.032144	-2.94
263821_s_a	40S ribosomal protein S16 Same as	---	AT2G09990	1.55	0.63	3.74	0.007776	0.032181	-2.94
246955_at	calcium-dependent protein kinase	CPK1	AT5G04870	-2.06	-1.04	-3.74	0.007777	0.032181	-2.94
261314_at	putative GTP-binding protein simila	---	AT1G52980	1.56	0.64	3.74	0.007778	0.032182	-2.94
255723_at	hypothetical protein	AFP3	AT3G29575	-2.08	-1.06	-3.74	0.00778	0.032184	-2.94
253778_at	heat-shock protein heat-shock prot	---	AT4G28480	-1.43	-0.51	-3.74	0.007787	0.032201	-2.94
263607_at	unknown protein predicted by gens	---	AT2G16270	-1.49	-0.58	-3.74	0.007788	0.032201	-2.94
266583_at	Expressed protein ; supported by cl	---	AT2G46220	1.52	0.61	3.74	0.007788	0.032201	-2.94
258569_at	ribosomal protein L17, putative sim	emb2171	AT3G04400	1.55	0.63	3.74	0.007794	0.032217	-2.94
262224_at	hypothetical protein contains Pfam	OTP43	AT1G74900	1.29	0.37	3.74	0.007796	0.032219	-2.94
256992_at	hypothetical protein predicted by ge	---	AT3G28630	-1.37	-0.45	-3.74	0.007805	0.032253	-2.94
246220_at	putative protein ; supported by cDN	---	AT4G37210	1.31	0.39	3.74	0.00781	0.032263	-2.94
248816_at	prematurely terminated mRNA deca	LBA1	AT5G47010	1.31	0.39	3.74	0.007811	0.032263	-2.94
250428_at	putative protein phosphatase prote	PAS2	AT5G10480	-1.72	-0.78	-3.74	0.007824	0.032313	-2.95
252164_at	hypothetical protein nodH - Rhizob	---	AT3G50620	-1.91	-0.94	-3.74	0.007829	0.032329	-2.95
254846_at	Expressed protein ; supported by fu	PLDGAMM	AT4G11830	-1.45	-0.54	-3.74	0.007833	0.032336	-2.95
252481_at	putative protein DCL PROTEIN, CH	---	AT3G46630	-1.42	-0.50	-3.74	0.007834	0.032336	-2.95

265917_at	putative disease resistance protein	AtRLP19	AT2G15080	1.48	0.56	3.74	0.007835	0.032336	-2.95
260177_at	hypothetical protein predicted by ge	---	AT1G70650	1.60	0.68	3.74	0.007837	0.032336	-2.95
260666_at	unknown protein ;supported by full-	PARVUS	AT1G19300	-2.12	-1.08	-3.74	0.007853	0.032398	-2.95
246575_at	bystin, putative similar to bystin GI	---	AT1G31660	1.63	0.71	3.73	0.007855	0.032402	-2.95
254194_at	auxin response factor 9 (ARF9) ; s	ARF9	AT4G23980	1.56	0.64	3.73	0.007866	0.032433	-2.95
245319_at	Expressed protein ; supported by fu	---	AT4G16146	1.69	0.76	3.73	0.007879	0.032474	-2.95
247871_at	xyloglucan endotransglycosylase ;	---	AT5G57530	-1.28	-0.36	-3.73	0.00788	0.032475	-2.95
262622_at	hypothetical protein predicted by ge	---	AT1G06510	1.31	0.38	3.73	0.007882	0.032476	-2.95
259165_at	homeobox-leucine zipper protein H	ATHB-1	AT3G01470	1.84	0.88	3.73	0.007884	0.03248	-2.95
251104_at	F-box protein family, AtFBL3 conta	---	AT5G01720	1.48	0.57	3.73	0.007888	0.032487	-2.95
253486_at	putative protein KIAA0260 gene, h	---	AT4G31600	-1.34	-0.43	-3.73	0.007904	0.032548	-2.96
266074_at	putative small nuclear ribonucleopr	---	AT2G18740	1.63	0.71	3.73	0.007905	0.032548	-2.96
254360_at	CDP-diacylglycerol synthetase-like	---	AT4G22340	-1.33	-0.41	-3.73	0.00791	0.032556	-2.96
258052_at	putative hydrolase predicted by gen	---	AT3G16190	1.39	0.48	3.73	0.007913	0.032563	-2.96
260753_at	RING-H2 finger protein RHA3a, pu	---	AT1G49230	2.08	1.06	3.73	0.007918	0.032577	-2.96
248583_at	putative protein strong similarity to	emb1441	AT5G49930	1.42	0.50	3.73	0.007922	0.032586	-2.96
254290_at	hypothetical protein	---	AT4G23000	1.54	0.62	3.73	0.007926	0.032586	-2.96
252132_at	putative LEA protein Picea glauca	---	AT3G50790	-1.83	-0.87	-3.73	0.007926	0.032586	-2.96
256772_at	galactosidase, putative similar to B	BGAL1	AT3G13750	-2.77	-1.47	-3.73	0.007928	0.032586	-2.96
263579_at	hypothetical protein similar to hypot	---	AT2G17030	1.50	0.58	3.73	0.007929	0.032586	-2.96
262951_at	nodulin-like protein similar to MtN2	---	AT1G75500	-1.47	-0.56	-3.73	0.007933	0.032596	-2.96
247899_at	Expressed protein ; supported by fu	---	AT5G57345	-1.44	-0.52	-3.73	0.00794	0.032618	-2.96
254564_at	neoxanthin cleavage enzyme-like p	NCED4	AT4G19170	1.65	0.72	3.73	0.007941	0.032618	-2.96
246450_at	Heat Shock Factor 3	HSF3	AT5G16820	1.31	0.38	3.73	0.007953	0.032662	-2.96
260801_at	hypothetical protein predicted by ge	---	AT1G78430	-1.26	-0.33	-3.72	0.007955	0.032665	-2.96
251632_at	hypothetical protein	---	AT3G57440	-1.44	-0.53	-3.72	0.007965	0.032701	-2.96
264824_at	unknown protein similar to gb|T454	2A6	---	-1.63	-0.70	-3.72	0.007967	0.032702	-2.97
245775_at	serine/threonine kinase, putative si	CIPK23	AT1G30270	1.35	0.43	3.72	0.007972	0.032717	-2.97
267159_at	putative SCARECROW gene regula	---	AT2G37650	1.35	0.44	3.72	0.007974	0.032717	-2.97
247787_at	putative protein various predicted p	---	AT5G58640	1.30	0.37	3.72	0.007975	0.032717	-2.97
259491_at	chlorophyll binding protein, putative	LHCB6	AT1G15820	-1.39	-0.48	-3.72	0.007983	0.032746	-2.97
264821_at	hypothetical protein predicted by ge	---	AT1G03470	1.65	0.72	3.72	0.007985	0.032748	-2.97
264134_at	unknown protein contains similarity	---	AT1G79070	1.27	0.34	3.72	0.008005	0.032818	-2.97
264319_at	subtilisin-like serine protease, puta	SDD1	AT1G04110	-1.43	-0.51	-3.72	0.008005	0.032818	-2.97
252012_at	ubiquinol--cytochrome-c reductase	---	AT3G52730	1.33	0.41	3.72	0.008016	0.032844	-2.97

247388_s_a	transcription factor Hap5a-like prote	NF-YC1	AT3G48590	-1.83	-0.87	-3.72	0.008016	0.032844	-2.97
264984_at	unknown protein ;supported by full-	---	AT1G27000	1.27	0.35	3.72	0.00802	0.032844	-2.97
261558_at	unknown protein	---	AT1G01770	1.63	0.70	3.72	0.00802	0.032844	-2.97
245415_at	G2484-1 protein	ATG2484-1	AT4G17330	1.29	0.37	3.72	0.008022	0.032844	-2.97
257661_at	unknown protein contains Pfam pro	---	AT3G13340	1.26	0.34	3.72	0.008023	0.032844	-2.97
263918_at	putative proline transporter ;suppor	ProT3	AT2G36590	-2.99	-1.58	-3.72	0.008024	0.032844	-2.97
267236_at	GDP dissociation inhibitor identical	ATGDI1	AT2G44100	1.35	0.44	3.72	0.008025	0.032844	-2.97
258797_at	auxin-induced protein identical to G	IAA16	AT3G04730	-1.54	-0.62	-3.72	0.008026	0.032844	-2.97
257530_at	unknown protein	---	AT3G03040	1.32	0.40	3.72	0.008033	0.032867	-2.97
258576_at	putative 40S ribosomal protein S16	---	AT3G04230	1.51	0.60	3.72	0.008035	0.032867	-2.97
260687_at	inner mitochondrial membrane pro	ATTIM23-1	AT1G17530	1.58	0.66	3.72	0.008039	0.032876	-2.97
260336_at	putative protease IV similar to prote	SPPA	AT1G73990	-1.42	-0.51	-3.72	0.008039	0.032876	-2.97
260443_at	Expressed protein ; supported by fu	---	AT1G68185	1.27	0.34	3.72	0.008047	0.0329	-2.98
256866_at	unknown protein similar to alpha ga	---	AT3G26380	1.48	0.56	3.72	0.008051	0.03291	-2.98
247491_at	putative protein supported by cDNA	---	AT5G61880	1.80	0.85	3.71	0.008062	0.032948	-2.98
251324_at	plasma membrane intrinsic protein	PIP1A	AT3G61430	-1.43	-0.52	-3.71	0.008064	0.032951	-2.98
255682_at	putative dTDP-6-deoxy-L-mannose	---	AT4G00560	-1.35	-0.43	-3.71	0.008065	0.032951	-2.98
262721_at	thioredoxin, putative similar to thior	Aty2	AT1G43560	-1.43	-0.52	-3.71	0.008067	0.032951	-2.98
259123_at	unknown protein	---	AT3G02200	1.31	0.39	3.71	0.008068	0.032951	-2.98
264339_at	trehalose-6-phosphate synthase, p	TPS8	AT1G70290	-1.59	-0.67	-3.71	0.00807	0.032953	-2.98
259175_at	unknown protein	---	AT3G01560	-1.43	-0.51	-3.71	0.008071	0.032953	-2.98
261975_at	unknown protein	---	AT1G64640	-2.44	-1.29	-3.71	0.008079	0.032974	-2.98
254981_at	putative alpha NAC stong similarity	---	AT4G10480	1.68	0.75	3.71	0.008079	0.032974	-2.98
259068_at	unknown protein	PEX13	AT3G07560	1.37	0.45	3.71	0.008093	0.033004	-2.98
258725_at	putative RNA helicase similar to R	---	AT3G09620	-1.30	-0.38	-3.71	0.008093	0.033004	-2.98
266790_at	expansin AtEx6 identical to GB U30	ATEXPA6	AT2G28950	-4.02	-2.01	-3.71	0.008097	0.033017	-2.98
247882_at	Expressed protein ; supported by fu	---	AT5G57785	-2.73	-1.45	-3.71	0.008101	0.033024	-2.98
256402_at	hypothetical protein ; supported by	---	AT3G06130	-1.87	-0.90	-3.71	0.008102	0.033024	-2.98
254728_at	hypothetical protein	---	AT4G13690	-1.32	-0.40	-3.71	0.008104	0.033027	-2.98
257814_at	acyl-(acyl carrier protein) thioestera	AtFaTA	AT3G25110	-1.92	-0.94	-3.71	0.008112	0.033055	-2.98
255556_at	putative NifU-like metallocluster as	NFU1	AT4G01940	1.47	0.55	3.71	0.008115	0.033059	-2.98
249217_at	ubiquitin-like protein ; supported by	UBL5	AT5G42300	1.26	0.33	3.71	0.008119	0.033069	-2.99
258322_at	putative selenocysteine methyltrans	HMT3	AT3G22740	-2.54	-1.35	-3.71	0.008126	0.033091	-2.99
267454_at	putative U5 small nuclear ribonucle	---	AT2G33730	1.32	0.40	3.71	0.008131	0.033107	-2.99
261746_at	unknown protein ;supported by full-	PSAO	AT1G08380	-1.29	-0.37	-3.71	0.008136	0.033124	-2.99

245977_at	glucose-6-phosphate 1-dehydrogen	G6PD2	AT5G13110	1.78	0.83	3.71	0.008143	0.033138	-2.99
256628_at	membrane import protein, putative	TOM40	AT3G20000	1.62	0.69	3.71	0.008143	0.033138	-2.99
246576_at	hypothetical protein predicted by ge	ROPGEF14	AT1G31650	1.28	0.35	3.71	0.008151	0.033154	-2.99
267285_at	unknown protein	---	AT2G23690	-1.70	-0.76	-3.71	0.008151	0.033154	-2.99
247283_at	2-nitropropane dioxygenase-like pro	---	AT5G64250	1.38	0.46	3.70	0.008165	0.033203	-2.99
253002_at	phosphoinositide-specific phospholi	ATPLC1	AT4G38530	-1.40	-0.49	-3.70	0.008166	0.033203	-2.99
247188_at	14-3-3 protein GF14kappa (grf8) id	GRF8	AT5G65430	-1.38	-0.47	-3.70	0.008171	0.033212	-2.99
262918_at	hypothetical protein predicted by ge	---	AT1G65000	1.38	0.47	3.70	0.008171	0.033212	-2.99
261300_at	hypothetical protein predicted by ge	---	AT1G48560	1.40	0.48	3.70	0.008176	0.033225	-2.99
254869_at	protein kinase - like protein KI dom	---	AT4G11890	1.99	0.99	3.70	0.008181	0.033242	-2.99
259406_at	hypothetical protein predicted by ge	---	AT1G17690	1.29	0.37	3.70	0.008195	0.033292	-3.00
250739_at	putative protein similar to unknown	EGY2	AT5G05740	-1.55	-0.63	-3.70	0.008197	0.033292	-3.00
254159_at	putative DNA-binding protein DNA-	WRKY7	AT4G24240	1.85	0.89	3.70	0.0082	0.0333	-3.00
247831_at	putative protein serine/threonine-sp	---	AT5G58540	1.69	0.76	3.70	0.008203	0.033304	-3.00
254212_at	putative protein many putative prot	---	AT4G23580	-1.33	-0.41	-3.70	0.008204	0.033305	-3.00
256671_at	unknown protein	IQD3	AT3G52290	-1.56	-0.65	-3.70	0.008209	0.033316	-3.00
267246_at	putative WRKY-type DNA binding p	WRKY25	AT2G30250	-1.76	-0.82	-3.70	0.008213	0.033327	-3.00
254603_at	putative protein hypothetical protei	---	AT4G19045	-1.39	-0.47	-3.70	0.008221	0.033353	-3.00
259799_at	drought induced protein, putative s	---	AT1G72290	-1.27	-0.34	-3.70	0.008225	0.033366	-3.00
264138_at	beta-Amyrin Synthase, putative sin	---	AT1G78950	-1.39	-0.47	-3.70	0.008228	0.033368	-3.00
250039_at	disease resistance protein -like dis	---	AT5G18370	1.42	0.51	3.70	0.00823	0.033368	-3.00
266535_s_a	50S ribosomal protein L27 ;suppor	---	AT2G16930	1.47	0.56	3.70	0.00823	0.033368	-3.00
249059_at	subtilisin-like serine protease conta	---	AT5G44530	-1.61	-0.69	-3.70	0.008238	0.033394	-3.00
245219_at	viral resistance protein, putative sir	---	AT1G58807	1.33	0.41	3.70	0.008242	0.033404	-3.00
257987_at	fertilization-independent endosperm	FIE	AT3G20740	1.32	0.40	3.70	0.008257	0.033446	-3.00
267177_at	Expressed protein ; supported by fu	---	AT2G37580	-1.64	-0.72	-3.70	0.008257	0.033446	-3.00
260195_at	hypothetical protein predicted by ge	---	AT1G67540	-1.35	-0.43	-3.70	0.008258	0.033446	-3.00
250533_at	flavonol synthase (FLS) (sp|Q9633(	FLS	AT5G08640	-1.30	-0.38	-3.70	0.00826	0.033447	-3.00
248043_s_a	heat shock protein (emb|CAA72514	---	AT5G56000	-1.69	-0.76	-3.70	0.008262	0.03345	-3.00
264852_at	similar to Mlo proteins from H. vulga	MLO8	AT2G17480	-2.07	-1.05	-3.69	0.008266	0.033459	-3.00
246700_at	cysteine synthase - like cysteine sy	---	AT5G28030	1.82	0.86	3.69	0.008267	0.033459	-3.00
252618_at	lipoxygenase AtLOX2 ; supported l	LOX2	AT3G45140	-1.51	-0.60	-3.69	0.008272	0.033468	-3.01
265092_at	hypothetical protein predicted by ge	---	AT1G03910	1.28	0.36	3.69	0.008272	0.033468	-3.01
245342_at	ribosomal protein ;supported by full	---	AT4G16720	1.54	0.62	3.69	0.008275	0.033473	-3.01
253842_at	putative protein putative proteins fr	---	AT4G27860	-2.36	-1.24	-3.69	0.008276	0.033473	-3.01

260794_at	unknown protein ; supported by cDI	---	AT1G06210	1.37	0.46	3.69	0.008279	0.033475	-3.01
257788_at	unknown protein	TCP20	AT3G27010	1.46	0.55	3.69	0.00828	0.033475	-3.01
266472_at	unknown protein	---	AT2G31150	-1.27	-0.34	-3.69	0.008285	0.033488	-3.01
260564_at	putative small nuclear ribonucleopro	---	AT2G43810	1.41	0.49	3.69	0.008286	0.033488	-3.01
253470_s_a	putative protein dnaK-type molecul	SDH3-2	AT4G32210	1.30	0.38	3.69	0.008294	0.033512	-3.01
264133_at	hypothetical protein predicted by ge	---	AT1G79080	1.35	0.43	3.69	0.008298	0.033519	-3.01
258404_at	ribosomal protein L3	RPL3P	AT3G17465	1.43	0.51	3.69	0.00832	0.033593	-3.01
262230_at	alpha-xylosidase precursor identica	XYL1	AT1G68560	-1.99	-0.99	-3.69	0.008322	0.033598	-3.01
264429_at	hypothetical protein similar to meml	---	AT1G61670	-1.29	-0.37	-3.69	0.008326	0.033605	-3.01
261757_at	hypothetical protein similar to putati	---	AT1G08210	1.57	0.65	3.69	0.008327	0.033605	-3.01
264531_at	hypothetical protein predicted by ge	---	AT1G30790	-1.32	-0.40	-3.69	0.00833	0.033612	-3.01
258471_at	NPK1-related protein kinase 3 iden	ANP3	AT3G06030	-1.36	-0.44	-3.69	0.008336	0.033621	-3.01
249023_at	putative protein strong similarity to	---	AT5G44850	-1.90	-0.93	-3.69	0.008339	0.033621	-3.01
263186_at	lectin receptor kinase, putative sim	---	---	-1.51	-0.59	-3.69	0.008339	0.033621	-3.01
263347_at	putative U4/U6 small nuclear ribonu	---	AT2G05720	-1.47	-0.56	-3.69	0.00834	0.033621	-3.01
252034_at	putative protein ;supported by full-l	---	AT3G52040	1.78	0.83	3.69	0.008343	0.033623	-3.01
256221_at	DnaJ protein, putative contains Pfa	---	AT1G56300	1.31	0.39	3.69	0.008343	0.033623	-3.01
245756_at	hyoscyamine 6-dioxygenase hydro	---	AT1G35190	1.54	0.62	3.69	0.008353	0.033657	-3.02
254986_at	putative protein SF16 protein -Helia	IQD16	AT4G10640	-1.26	-0.34	-3.69	0.008355	0.033658	-3.02
260671_at	unknown protein ;supported by full-	---	AT1G19310	-1.42	-0.51	-3.69	0.008364	0.033688	-3.02
262277_at	transmembrane protein, putative si	---	AT1G68650	1.93	0.95	3.69	0.008367	0.033695	-3.02
260913_at	s-adenosylmethionine synthetase ic	SAM1	AT1G02500	1.66	0.73	3.69	0.008368	0.033695	-3.02
266927_at	aquaporin (plasma membrane intri	PIP1B	AT2G45960	-1.45	-0.54	-3.69	0.00837	0.033695	-3.02
267409_at	hypothetical protein predicted by ge	---	AT2G34910	-1.26	-0.34	-3.68	0.008381	0.033732	-3.02
250091_at	unknown protein	---	AT5G17340	-1.26	-0.33	-3.68	0.008382	0.033733	-3.02
246674_at	bcnt-like protein ; supported by full-	---	AT5G30490	1.34	0.42	3.68	0.008398	0.033789	-3.02
250585_at	putative protein contains similarity t	---	AT5G07620	-1.91	-0.93	-3.68	0.008399	0.033789	-3.02
267475_at	expressed protein ; supported by fu	---	AT2G02730	1.42	0.50	3.68	0.008414	0.033845	-3.02
255400_at	hypothetical protein	---	---	-1.38	-0.47	-3.68	0.008421	0.033859	-3.02
266578_at	putative cinnamoyl CoA reductase	---	AT2G23910	1.42	0.51	3.68	0.008423	0.033859	-3.02
253033_at	putative protein aminoacylase I - S	---	AT4G38220	-1.33	-0.41	-3.68	0.008423	0.033859	-3.02
259375_at	putative APG protein similar to ante	---	AT3G16370	-15.93	-3.99	-3.68	0.008425	0.033859	-3.03
255483_at	putative glycosyltransferase simila	XT2	AT4G02500	-1.54	-0.62	-3.68	0.008425	0.033859	-3.03
259513_at	hypothetical protein ; supported by	ARK3	AT1G12430	1.37	0.45	3.68	0.008428	0.033861	-3.03
246424_at	Exportin1 (XPO1) protein ; support	XPO1A	AT5G17020	1.40	0.49	3.68	0.008429	0.033861	-3.03

246396_at	carbonic anhydrase, putative simila	BCA6	AT1G58180	-1.57	-0.65	-3.68	0.00844	0.033899	-3.03
244939_at	ribosomal protein S12 (trans-splice	---	---	-1.63	-0.70	-3.68	0.008443	0.0339	-3.03
251595_at	putative protein galactose oxidase	---	AT3G57620	-1.36	-0.44	-3.68	0.008443	0.0339	-3.03
257372_at	hypothetical protein predicted by ge	---	AT2G43220	-1.31	-0.39	-3.68	0.008453	0.03393	-3.03
248241_at	unknown protein	---	AT5G53960	-1.31	-0.39	-3.68	0.008454	0.03393	-3.03
247368_at	putative protein contains similarity t	---	AT5G63320	1.42	0.51	3.68	0.008458	0.033941	-3.03
261903_at	chromomethylase identical to GB:A	CMT1	AT1G80740	-1.28	-0.35	-3.68	0.008459	0.033941	-3.03
253979_at	putative protein other putative prote	---	AT4G26680	1.36	0.44	3.68	0.008466	0.033961	-3.03
263037_at	conserved hypothetical protein	---	AT1G23230	1.42	0.51	3.68	0.008469	0.033968	-3.03
253769_at	putative protein (fragment) protein	RIC7	AT4G28560	-1.44	-0.53	-3.68	0.008471	0.033969	-3.03
249019_at	unknown protein	---	AT5G44780	2.03	1.02	3.67	0.008489	0.034037	-3.03
256620_at	disease resistance protein, putative	---	AT3G24480	-1.69	-0.76	-3.67	0.008491	0.034041	-3.03
259433_at	hypothetical protein predicted by ge	---	AT1G01570	-1.40	-0.49	-3.67	0.008495	0.034048	-3.03
261324_at	unknown protein	---	AT1G44770	1.49	0.58	3.67	0.008499	0.034053	-3.03
258642_at	unknown protein ;supported by full-	---	AT3G07910	1.30	0.37	3.67	0.008504	0.034068	-3.04
265266_at	putative RNA-binding protein ; sup	AML2	AT2G42890	1.43	0.51	3.67	0.008506	0.034068	-3.04
259307_at	unknown protein similar to MICROS	---	AT3G05230	-1.47	-0.55	-3.67	0.008511	0.034082	-3.04
257647_at	Expressed protein ; supported by cl	---	AT3G25805	-1.70	-0.76	-3.67	0.008517	0.034093	-3.04
250999_at	putative protein predicted proyeins	---	AT5G02630	1.48	0.57	3.67	0.008519	0.034093	-3.04
267400_at	unknown protein	---	AT2G26240	1.47	0.55	3.67	0.00852	0.034093	-3.04
260610_at	putative SF16 protein {Helianthus a	IQD14	AT2G43680	1.61	0.69	3.67	0.008521	0.034093	-3.04
264013_at	unknown protein	FIO1	AT2G21070	1.26	0.33	3.67	0.008526	0.034107	-3.04
260927_at	hypothetical protein predicted by ge	CAT9	AT1G05940	1.43	0.51	3.67	0.008529	0.034115	-3.04
257986_at	Expressed protein ; supported by fu	AGP40	AT3G20865	-1.59	-0.67	-3.67	0.008534	0.034123	-3.04
249612_at	putative protein CG14881, Drosopl	---	AT5G37290	1.76	0.81	3.67	0.008534	0.034123	-3.04
251664_at	leucine zipper-containing protein A	CRD1	AT3G56940	-1.40	-0.49	-3.67	0.008539	0.034137	-3.04
250007_at	beta-amylase-like proten beta-amy	BMY3	AT5G18670	-3.23	-1.69	-3.67	0.008543	0.034144	-3.04
246755_at	F-box protein family contains simila	---	AT5G27920	-1.92	-0.94	-3.67	0.008544	0.034144	-3.04
251295_at	putative protein several O-methyltra	---	AT3G62000	1.48	0.57	3.67	0.008548	0.034151	-3.04
257052_at	putative 3-hydroxybutyryl-CoA dehy	---	AT3G15290	-1.31	-0.39	-3.67	0.008549	0.034151	-3.04
245400_at	ATP-dependent Clp protease prote	---	AT4G17040	1.44	0.52	3.67	0.008553	0.034162	-3.04
251132_at	putative protein Myb-related transc	---	AT5G01200	1.50	0.58	3.67	0.008555	0.034162	-3.04
246437_at	putative protein hypersensitivity-rel	---	AT5G17540	-1.30	-0.38	-3.67	0.008556	0.034163	-3.04
257189_at	hypothetical protein	GIP1	AT3G13222	1.29	0.37	3.67	0.008563	0.034183	-3.04
255485_at	predicted protein of unknown funct	---	AT4G02550	1.33	0.41	3.67	0.008572	0.034214	-3.04

248367_at	actin depolymerizing factor-like ;su	ADF10	AT5G52360	-1.42	-0.50	-3.67	0.008583	0.034253	-3.05
266467_at	Not56-like protein ; supported by c	ALG3	AT2G47760	-1.39	-0.48	-3.67	0.008585	0.034254	-3.05
247439_at	plasma membrane proton ATPase-	AHA11	AT5G62670	-1.83	-0.87	-3.67	0.00859	0.034268	-3.05
260056_at	hypothetical protein predicted by ge	---	AT1G78140	-1.58	-0.66	-3.66	0.008614	0.034351	-3.05
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.80	-0.85	-3.66	0.008616	0.034353	-3.05
255820_at	putative protein kinase contains a p	---	AT2G40580	-1.39	-0.47	-3.66	0.00863	0.034401	-3.05
261539_at	hypothetical protein predicted by ge	---	AT1G01840	-1.38	-0.47	-3.66	0.008631	0.034401	-3.05
247644_s_a	translation elongation factor eEF-1	---	AT1G07920	1.33	0.41	3.66	0.008641	0.034435	-3.05
250238_at	unknown protein	DCP2	AT5G13570	1.32	0.40	3.66	0.008657	0.03449	-3.05
260948_at	delta 9 desaturase, putative similar	---	AT1G06100	-1.38	-0.46	-3.66	0.008659	0.03449	-3.05
256704_at	deacetylvindoline 4-O-acetyltransfe	---	AT3G30280	-1.30	-0.38	-3.66	0.00866	0.03449	-3.05
259670_at	protein kinase, putative similar to G	---	AT1G52310	1.42	0.51	3.66	0.00867	0.034527	-3.06
255583_at	hypothetical protein similar to C. el	ARV2	AT4G01510	1.39	0.47	3.66	0.008679	0.034555	-3.06
253662_at	transcription factor-like protein Ara	ARF16	AT4G30080	-1.36	-0.44	-3.66	0.008684	0.034569	-3.06
264615_at	unknown protein ; supported by cD	---	AT1G04590	1.60	0.67	3.66	0.008688	0.034579	-3.06
262991_at	hypothetical protein predicted by ge	BRX-LIKE3	AT1G54180	-1.27	-0.34	-3.66	0.008692	0.034588	-3.06
262887_at	hypothetical protein	---	AT1G14780	-2.64	-1.40	-3.66	0.008693	0.034588	-3.06
263950_at	hypothetical protein predicted by ge	HVA22J	AT2G36020	-1.25	-0.32	-3.66	0.008697	0.034597	-3.06
251195_at	glutaredoxin -like protein glutaredo	---	AT3G62930	-1.65	-0.72	-3.65	0.008727	0.034699	-3.06
263666_at	putative pre-mRNA splicing factor F	---	AT1G04510	1.52	0.60	3.65	0.008739	0.034734	-3.06
261085_at	hypothetical protein similar to hypot	IQD7	AT1G17480	-1.30	-0.38	-3.65	0.008746	0.03475	-3.07
254578_at	putative pectinacetylesterase prote	---	AT4G19400	-1.59	-0.67	-3.65	0.008748	0.03475	-3.07
261666_at	hypothetical protein contains simila	---	AT1G18440	-1.45	-0.54	-3.65	0.008749	0.03475	-3.07
261110_at	E2, ubiquitin-conjugating enzyme 1	UBC16	AT1G75440	-1.50	-0.58	-3.65	0.008752	0.03475	-3.07
260051_at	hypothetical protein	---	AT1G78210	-1.90	-0.92	-3.65	0.008752	0.03475	-3.07
253237_at	putative aldehyde dehydrogenase	ALDH3I1	AT4G34240	-1.60	-0.68	-3.65	0.008752	0.03475	-3.07
253205_at	putative cyclase associated protein	ATCAP1	AT4G34490	-1.70	-0.77	-3.65	0.008758	0.034769	-3.07
261823_at	hypothetical protein predicted by ge	PYM	AT1G11400	-1.33	-0.42	-3.65	0.008767	0.034795	-3.07
255667_at	phospholipase D, putative	PLDBETA2	AT4G00240	-1.32	-0.40	-3.65	0.00877	0.034802	-3.07
251525_at	putative protein several hypothetica	---	AT3G59000	1.39	0.48	3.65	0.008777	0.034817	-3.07
266421_at	putative nonspecific lipid-transfer pr	LP1	AT2G38540	-2.71	-1.44	-3.65	0.008778	0.034817	-3.07
253628_at	xyloglucan endo-1,4-beta-D-glucan	XTH18	AT4G30280	-7.92	-2.99	-3.65	0.008784	0.034835	-3.07
252754_at	putative protein hypothetical protei	---	---	1.66	0.73	3.65	0.008788	0.034838	-3.07
265391_at	Expressed protein ; supported by c	GAUT10	AT2G20810	-1.27	-0.35	-3.65	0.008788	0.034838	-3.07
250243_at	cobalamin biosynthesis protein	GUN5	AT5G13630	-1.50	-0.58	-3.65	0.008796	0.034861	-3.07

252417_at	putative calcium-binding protein cal	---	AT3G47480	4.31	2.11	3.65	0.008797	0.034861	-3.07
245211_at	putative protein similarity to sec10,	SEC10	AT5G12370	-1.26	-0.33	-3.65	0.008799	0.034861	-3.07
254442_at	putative protein predicted protein T	---	AT4G21060	1.32	0.40	3.65	0.008802	0.034861	-3.07
245196_at	F12A21.12 similar to pectate lyase	---	AT1G67750	-1.98	-0.98	-3.65	0.008802	0.034861	-3.07
267166_at	unknown protein	---	AT2G37720	-1.24	-0.31	-3.65	0.008803	0.034861	-3.07
250397_at	histon H3 protein HISTONE H3.2,	---	AT5G10980	1.24	0.31	3.65	0.008805	0.034863	-3.07
253216_at	cyclophilin - like protein cyclophilin	---	AT4G34960	1.42	0.50	3.65	0.008807	0.034864	-3.07
265544_at	putative cyclic nucleotide and calm	ATCNGC15	AT2G28260	-1.49	-0.57	-3.65	0.008812	0.034876	-3.07
263685_at	unknown protein similar to cell diffe	ATCUL3	AT1G26830	1.27	0.34	3.64	0.008818	0.034893	-3.07
258799_at	putative 40S ribosomal protein iden	RPSAb	AT3G04770	1.49	0.58	3.64	0.008821	0.034895	-3.07
263802_at	unknown protein ;supported by full-	---	AT2G40430	1.68	0.75	3.64	0.008823	0.034897	-3.07
256365_at	arginyl-tRNA synthetase nearly ider	---	AT1G66530	1.61	0.69	3.64	0.008827	0.034907	-3.08
251928_at	putative protein hypothetical protei	---	AT3G53980	-2.50	-1.32	-3.64	0.008829	0.034907	-3.08
245386_at	hypothetical protein ;supported by f	RALFL32	AT4G14010	-1.99	-0.99	-3.64	0.008843	0.034959	-3.08
248913_at	unknown protein ;supported by full-	---	AT5G45760	1.32	0.41	3.64	0.008849	0.034971	-3.08
247640_at	putative protein various predicted p	---	AT5G60610	1.34	0.42	3.64	0.008849	0.034971	-3.08
250591_at	alpha galactosyltransferase protein	---	AT5G07720	-1.42	-0.51	-3.64	0.008856	0.034985	-3.08
263428_at	ubiquitin-specific protease 4 (UBP4	ATUBP4	AT2G22310	1.37	0.45	3.64	0.008865	0.035012	-3.08
249198_s_a	putative protein similar to unknown	---	AT5G42350	-1.34	-0.42	-3.64	0.008867	0.035012	-3.08
252565_at	actin depolymerizing factor 2 (ADF2	ADF2	AT3G46000	1.27	0.35	3.64	0.008868	0.035012	-3.08
267092_at	unknown protein ;supported by full-	AUX1	AT2G38120	-1.97	-0.98	-3.64	0.008869	0.035012	-3.08
247134_at	putative protein similar to unknown	---	AT5G66230	-1.32	-0.40	-3.64	0.008881	0.035052	-3.08
267336_at	putative small heat shock protein ;s	---	AT2G19310	1.52	0.60	3.64	0.008892	0.035091	-3.08
253700_at	threonine synthase	MTO2	AT4G29840	1.56	0.64	3.64	0.008895	0.035096	-3.08
260497_at	40S ribosomal protein S2 ;supporte	---	AT2G41840	1.88	0.91	3.64	0.008912	0.035153	-3.09
266881_at	putative casein kinase II beta subur	CKB4	AT2G44680	1.34	0.42	3.64	0.008915	0.035159	-3.09
266542_at	unknown protein	ARAD1	AT2G35100	-1.29	-0.37	-3.64	0.008927	0.035199	-3.09
247333_at	1-aminocyclopropane-1-carboxylic a	FLS5	AT5G63600	1.90	0.92	3.63	0.008932	0.035213	-3.09
250168_at	putative protein predicted protein, A	---	AT5G15320	1.32	0.40	3.63	0.008935	0.035219	-3.09
252947_at	putative protein ubiquitin fusion deg	KAK	AT4G38600	1.27	0.34	3.63	0.008943	0.035243	-3.09
249482_at	putative protein ;supported by full-l	---	AT5G38980	2.00	1.00	3.63	0.008948	0.035253	-3.09
245303_at	hypothetical protein ; supported by	---	AT4G17010	1.29	0.37	3.63	0.008948	0.035253	-3.09
248717_at	Expressed protein ; supported by fu	---	AT5G48175	-1.26	-0.34	-3.63	0.00895	0.035253	-3.09
248586_at	putative protein similar to unknown	---	AT5G49610	1.36	0.44	3.63	0.008958	0.035279	-3.09
245005_at	ribosomal protein S14	---	---	-1.62	-0.70	-3.63	0.008975	0.035331	-3.09

258030_at	hypothetical protein predicted by ge	---	AT3G27590	-1.40	-0.49	-3.63	0.008979	0.035342	-3.09
247120_at	amino acid transporter protein-like	---	AT5G65990	1.33	0.41	3.63	0.008982	0.03535	-3.09
248523_s_a	ubiquitin activating enzyme ;suppo	SAE1B	AT5G50580	1.42	0.51	3.63	0.008987	0.035356	-3.09
257570_at	dirigent protein, putative similar to	---	AT3G13662	-1.32	-0.40	-3.63	0.008989	0.035358	-3.09
257638_at	terpene synthase-related protein co	ATTPS-CIN	AT3G25820	-1.31	-0.39	-3.63	0.008996	0.035378	-3.10
245411_at	hypothetical protein	---	AT4G17240	-1.67	-0.74	-3.63	0.009007	0.035414	-3.10
259286_at	hypothetical protein similar to hypot	BSMT1	AT3G11480	-11.30	-3.50	-3.63	0.009008	0.035414	-3.10
266948_at	unknown protein	---	AT2G18850	1.65	0.73	3.63	0.009012	0.03542	-3.10
250332_at	putative protein predicted proteins,	---	AT5G11680	-1.41	-0.50	-3.63	0.009013	0.03542	-3.10
246112_at	putative protein predicted proteins -	---	AT5G20200	1.41	0.49	3.63	0.00902	0.035441	-3.10
250284_at	protein kinase precursor - like rece	CRN	AT5G13290	1.55	0.63	3.63	0.009022	0.035446	-3.10
246130_at	putative protein various predicted p	---	---	-1.54	-0.62	-3.63	0.009035	0.035491	-3.10
246427_at	ADP/ATP translocase-like protein a	ER-ANT1	AT5G17400	-1.40	-0.49	-3.63	0.009046	0.035522	-3.10
267031_at	hypothetical protein predicted by ge	---	AT2G38420	1.30	0.38	3.62	0.009047	0.035522	-3.10
256055_at	mitochondrial carrier protein, putati	---	AT1G07030	1.31	0.39	3.62	0.009049	0.035522	-3.10
245425_at	carboxyl-terminal proteinase like pr	UCH3	AT4G17510	1.24	0.31	3.62	0.009051	0.035522	-3.10
246907_at	AtBgamma - like protein B' regulato	---	AT5G25510	-1.42	-0.50	-3.62	0.009051	0.035522	-3.10
262532_at	hypothetical protein predicted by ge	---	AT1G17210	1.34	0.42	3.62	0.009059	0.035545	-3.10
266164_at	putative salt-inducible protein	---	AT2G28050	-1.62	-0.70	-3.62	0.009065	0.035563	-3.10
251520_at	protein kinase like GCN2 - Saccha	---	AT3G59410	1.30	0.37	3.62	0.009067	0.035563	-3.10
250259_at	putative protein similar to unknown	---	AT5G13800	1.49	0.57	3.62	0.009068	0.035563	-3.10
247306_at	ser/thr protein phosphatase catalyti	PP7	AT5G63870	-1.42	-0.51	-3.62	0.009071	0.035569	-3.10
254633_at	putative protein (fragment)	MRH1	AT4G18640	-1.58	-0.66	-3.62	0.009074	0.035571	-3.10
254751_at	hypothetical protein	---	AT4G13150	1.30	0.38	3.62	0.009074	0.035571	-3.10
265403_at	putative Ta11-like non-LTR retroele	---	---	-1.38	-0.46	-3.62	0.009076	0.035571	-3.11
254019_at	putative protein mature-parasite-int	---	AT4G26190	1.24	0.32	3.62	0.009079	0.035576	-3.11
264562_at	hypothetical protein predicted by ge	---	AT1G55760	1.76	0.82	3.62	0.009081	0.035578	-3.11
255244_at	putative protein various hypothetica	---	AT4G05620	-1.33	-0.41	-3.62	0.009085	0.035588	-3.11
266257_at	putative chorismate mutase/prephe	PD1	AT2G27820	-1.48	-0.57	-3.62	0.0091	0.035641	-3.11
247178_at	Expressed protein ; supported by cl	---	AT5G65205	1.95	0.97	3.62	0.009107	0.03566	-3.11
265274_at	putative RNA methyltransferase	---	AT2G28450	1.41	0.50	3.62	0.009108	0.03566	-3.11
244929_at	NADH dehydrogenase subunit 4	---	---	1.58	0.66	3.62	0.009119	0.03568	-3.11
247299_at	putative protein contains similarity t	---	AT5G63900	-1.29	-0.36	-3.62	0.00912	0.03568	-3.11
262262_at	unknown protein identical to unknov	---	AT1G70780	1.63	0.70	3.62	0.009122	0.03568	-3.11
246433_at	glutamine-rich protein predicted pr	---	AT5G17510	1.52	0.60	3.62	0.009122	0.03568	-3.11

254890_at	phospholipid hydroperoxide glutath	ATGPX6	AT4G11600	1.34	0.43	3.62	0.009123	0.03568	-3.11
248329_at	putative protein similar to unknown	---	AT5G52780	1.52	0.60	3.62	0.009124	0.03568	-3.11
258587_at	hypothetical protein predicted by ge	---	AT3G04310	1.72	0.78	3.62	0.009126	0.035681	-3.11
252378_at	receptor kinase-like protein protein	---	AT3G47570	-1.58	-0.66	-3.62	0.009128	0.035684	-3.11
251533_at	putative protein several hypothetica	ATRBL15	AT3G58460	1.27	0.34	3.62	0.009141	0.035729	-3.11
254990_at	RNA-binding protein ;supported by	CID12	AT4G10610	1.26	0.33	3.62	0.00915	0.035756	-3.11
251214_at	putative protein hypothetical protein	---	AT3G62500	-1.32	-0.40	-3.62	0.00916	0.035791	-3.12
248531_at	putative protein contains similarity t	---	AT5G49950	1.35	0.43	3.61	0.009167	0.035806	-3.12
251834_at	ribosomal protein L35 -like various	---	AT3G55170	1.32	0.40	3.61	0.009169	0.035806	-3.12
264470_at	cytochrome P450, putative similar	CYP735A2	AT1G67110	-1.45	-0.54	-3.61	0.00917	0.035806	-3.12
250998_at	ankyrin - like protein ankyrin G119,	---	AT5G02620	1.52	0.61	3.61	0.009179	0.035834	-3.12
261999_at	hypothetical protein predicted by ge	---	AT1G33800	-1.42	-0.50	-3.61	0.009189	0.03586	-3.12
258514_at	unknown protein ; supported by ful	---	AT3G06610	1.29	0.37	3.61	0.009189	0.03586	-3.12
253555_at	putative protein predicted proetein,	---	AT4G31080	1.53	0.61	3.61	0.0092	0.035894	-3.12
251244_at	pectinacetylesterase precursor-like	---	AT3G62060	-1.37	-0.45	-3.61	0.009201	0.035894	-3.12
258448_at	unknown protein	---	AT3G22290	-1.27	-0.35	-3.61	0.009209	0.035919	-3.12
264108_at	hypothetical protein predicted by ge	CALS5	AT2G13680	-1.29	-0.37	-3.61	0.009211	0.035922	-3.12
258498_at	unknown protein similar to pollen co	---	AT3G02480	-1.93	-0.95	-3.61	0.00922	0.035949	-3.12
260565_at	unknown protein predicted by gene	---	AT2G43800	-1.67	-0.74	-3.61	0.009224	0.035961	-3.12
260950_s_a	delta 9 desaturase, putative similar	---	AT1G06090	-1.40	-0.49	-3.61	0.009236	0.036001	-3.12
246743_at	putative protein predicted proteins,	---	AT5G27750	1.38	0.46	3.61	0.009253	0.036059	-3.13
250131_at	unknown protein ; supported by cD	---	AT5G16550	-1.57	-0.65	-3.61	0.00926	0.036081	-3.13
252128_at	transcription factor-like protein Aral	MNP	AT3G50870	-1.30	-0.38	-3.61	0.009266	0.0361	-3.13
258430_at	phospholipase D, putative similar t	PLDP1	AT3G16785	-1.28	-0.36	-3.60	0.0093	0.036224	-3.13
264523_at	unknown protein Location of EST g	ERG28	AT1G10030	-1.29	-0.37	-3.60	0.009312	0.036264	-3.13
248865_at	putative protein similar to unknown	---	AT5G46790	1.47	0.55	3.60	0.009319	0.036285	-3.13
264163_at	Expressed protein ; supported by fu	---	AT1G65445	-1.39	-0.48	-3.60	0.009326	0.036294	-3.13
263274_at	putative protein kinase contains a p	CRCK3	AT2G11520	1.38	0.47	3.60	0.009326	0.036294	-3.13
251931_at	putative protein glyoxal oxidase (gl	---	AT3G53950	-1.61	-0.69	-3.60	0.009326	0.036294	-3.13
267207_at	putative dioxygenase	---	AT2G30840	2.02	1.01	3.60	0.009332	0.036314	-3.14
265614_at	Expressed protein ; supported by cl	---	AT2G25355	1.46	0.54	3.60	0.009345	0.036349	-3.14
251918_at	photoassimilate-responsive protein	---	AT3G54040	-1.30	-0.38	-3.60	0.009349	0.036358	-3.14
261620_s_a	ribosomal protein L9, putative simil	PGY2	AT1G33120	1.48	0.56	3.60	0.009354	0.036373	-3.14
257820_at	immunophilin (FKBP15-1) identical	FKBP15-1	AT3G25220	1.39	0.48	3.60	0.00936	0.036383	-3.14
250532_at	putative protein similar to unknown	---	AT5G08540	1.40	0.49	3.60	0.009362	0.036386	-3.14

257855_at	hypothetical protein predicted by ge	---	AT3G13040	1.31	0.39	3.60	0.009377	0.036436	-3.14
248999_at	putative protein contains similarity t	---	AT5G44970	-1.29	-0.37	-3.60	0.009381	0.036448	-3.14
264686_at	shaggy-like protien kinase, kappa I	ATSK41	AT1G09840	-1.26	-0.34	-3.60	0.009385	0.036456	-3.14
256920_at	hypothetical protein predicted by ge	---	AT3G18980	-1.27	-0.35	-3.60	0.009396	0.036492	-3.14
258358_at	unknown protein similar to unknowr	---	AT3G14380	-1.35	-0.44	-3.60	0.009398	0.036492	-3.14
259695_at	hypothetical protein predicted by ge	---	AT1G63170	-1.40	-0.48	-3.60	0.0094	0.036492	-3.14
261139_at	homeodomain protein, putative sim	BEL10	AT1G19700	1.29	0.37	3.60	0.009401	0.036492	-3.14
255468_at	putative WD-repeat protein similar	---	AT4G03020	1.31	0.39	3.60	0.009403	0.036497	-3.14
246503_at	40S ribosomal protein S7-like 40S	---	AT5G16130	1.75	0.81	3.59	0.009413	0.03653	-3.14
260165_at	30S ribosomal protein S17, chlorop	RPS17	AT1G79850	-1.49	-0.57	-3.59	0.009429	0.036577	-3.15
246759_at	putative protein kinesin heavy chai	---	AT5G27950	1.48	0.57	3.59	0.009432	0.036583	-3.15
245387_at	nuclear RNA binding protein A-like	---	AT4G17520	1.46	0.54	3.59	0.009447	0.036634	-3.15
263881_at	unknown protein ; supported by cD	---	AT2G21820	1.33	0.41	3.59	0.00945	0.036638	-3.15
264362_at	unknown protein ESTs gb|H36966,	---	AT1G03290	1.54	0.62	3.59	0.009462	0.036672	-3.15
250600_at	dimethylaniline monooxygenase-lik	---	AT5G07800	-1.31	-0.39	-3.59	0.009464	0.036672	-3.15
254089_at	putative protein apoptosis gene MA	---	AT4G24800	-1.35	-0.43	-3.59	0.009465	0.036672	-3.15
250420_at	HY5(bZIP transcription factor family	HY5	AT5G11260	1.40	0.48	3.59	0.009465	0.036672	-3.15
267215_at	hypothetical protein	---	AT2G02630	-1.25	-0.32	-3.59	0.00948	0.036721	-3.15
251041_at	ubiquitin-protein ligase E3-alpha -li	PRT6	AT5G02310	-1.49	-0.57	-3.59	0.009481	0.036721	-3.15
248497_at	putative protein strong similarity to	ATEXO70F	AT5G50380	1.56	0.64	3.59	0.009487	0.036737	-3.15
255319_at	putative disease resistance protein	AtRLP46	AT4G04220	1.84	0.88	3.59	0.009488	0.036737	-3.15
256479_at	unknown protein	---	AT1G33400	1.47	0.56	3.59	0.009496	0.036764	-3.15
245044_at	unknown protein Alternative splice t	---	AT2G26500	1.25	0.33	3.59	0.009513	0.036821	-3.16
261806_at	ferrodoxin NADP oxidoreductase, p	ATRFNR2	AT1G30510	1.74	0.80	3.59	0.00952	0.036841	-3.16
251136_at	mRNA capping enzyme - like prote	---	AT5G01290	1.27	0.35	3.59	0.009524	0.036848	-3.16
261305_at	glutamine synthetase, putative sim	GLN1;5	AT1G48470	1.27	0.34	3.59	0.009525	0.036848	-3.16
252713_at	calmodulin 7 ; supported by full-len	CAM7	AT3G43810	-1.35	-0.44	-3.59	0.009526	0.036848	-3.16
247058_at	dolichyl-di-phosphooligosaccharide	DGL1	AT5G66680	1.39	0.47	3.58	0.009529	0.036853	-3.16
252457_at	zinc-finger protein-like protein DNA	---	AT3G47180	-1.29	-0.37	-3.58	0.009533	0.036861	-3.16
250111_at	acetolactate synthase-like protein	---	AT5G16290	-1.54	-0.62	-3.58	0.009556	0.03694	-3.16
256485_at	unknown protein	---	AT1G31440	1.32	0.40	3.58	0.009559	0.03694	-3.16
263709_at	unknown protein ESTs gb|T20589,	---	AT1G09310	-4.60	-2.20	-3.58	0.00956	0.03694	-3.16
263067_at	hypothetical protein predicted by ge	---	AT2G17550	-1.64	-0.71	-3.58	0.00957	0.036971	-3.16
261624_at	nucleotide sugar epimerase, putati	GAE2	AT1G02000	-1.68	-0.75	-3.58	0.009571	0.036971	-3.16
257313_at	gamma tonoplast intrinsic protein n	TIP2	AT3G26520	-1.43	-0.52	-3.58	0.009573	0.036974	-3.16

245895_at	SIR2-family protein sirtuin type 4 (S	SRT2	AT5G09230	-1.35	-0.43	-3.58	0.00958	0.036994	-3.16
267456_at	E2, ubiquitin-conjugating enzyme,	PHO2	AT2G33770	1.89	0.92	3.58	0.009585	0.037007	-3.16
252616_at	serine threonine-protein kinase-like	GRIK1	AT3G45240	1.43	0.51	3.58	0.009595	0.037039	-3.16
259085_at	unknown protein similar to GB:CAB	---	AT3G05000	-1.33	-0.42	-3.58	0.009607	0.037078	-3.17
261846_at	hypothetical protein similar to hypot	---	AT1G11540	-1.36	-0.45	-3.58	0.00961	0.037085	-3.17
263239_at	amidophosphoribosyltransferase id	ATASE1	AT2G16570	-1.37	-0.45	-3.58	0.009615	0.037097	-3.17
260152_at	putative IAA6 protein similar to IAA	IAA6	AT1G52830	-1.92	-0.94	-3.58	0.009621	0.037116	-3.17
256332_at	trihelix DNA-binding protein (GT2)	GT2	AT1G76890	-1.93	-0.95	-3.58	0.009639	0.037178	-3.17
249119_at	unknown protein ;supported by full-	---	AT5G43720	1.25	0.32	3.58	0.009651	0.037217	-3.17
258312_at	putative long-chain acyl-CoA synthe	---	AT3G16170	1.51	0.59	3.57	0.009664	0.037261	-3.17
250634_at	putative protein 2-oxoglutarate-dep	---	AT5G07480	-1.29	-0.37	-3.57	0.009666	0.037263	-3.17
247595_at	ring finger protein - like ring finger p	---	AT5G60820	-1.45	-0.54	-3.57	0.009668	0.037263	-3.17
261265_at	hypothetical protein predicted by ge	---	AT1G26800	-1.67	-0.74	-3.57	0.00968	0.037302	-3.17
246837_at	pectin acetylesterase precursor - li	---	AT5G26670	-1.64	-0.72	-3.57	0.009682	0.037304	-3.17
257151_at	blue copper protein, putative simila	---	AT3G27200	-1.43	-0.52	-3.57	0.009696	0.037346	-3.18
254753_at	putative protein Pto kinase interact	---	AT4G13190	-1.28	-0.35	-3.57	0.009698	0.037348	-3.18
254602_at	hypothetical protein	EDR2	AT4G19040	1.32	0.40	3.57	0.009715	0.037407	-3.18
251992_at	putative protein myosin heavy chai	---	AT3G53350	1.48	0.57	3.57	0.009723	0.03743	-3.18
254481_at	hypothetical protein ; supported by	---	AT4G20480	1.55	0.63	3.57	0.009726	0.037432	-3.18
251461_at	putative protein	---	AT3G59780	-1.43	-0.52	-3.57	0.009726	0.037432	-3.18
259492_at	hypothetical protein predicted by ge	---	AT1G15830	-1.59	-0.67	-3.57	0.009741	0.037482	-3.18
267229_s_a	putative translation initiation factor e	---	AT2G44070	1.79	0.84	3.57	0.009753	0.037513	-3.18
249086_at	putative protein strong similarity to u	---	AT5G44180	1.34	0.42	3.57	0.009754	0.037513	-3.18
253198_at	putative protein various predicted p	---	AT4G35360	-1.34	-0.42	-3.57	0.009763	0.037542	-3.18
260732_at	myb-related DNA-binding protein, p	---	AT1G17520	1.30	0.37	3.57	0.009768	0.037549	-3.18
255019_at	putative protein IB1C3-1 protein, A	---	AT4G10210	-1.30	-0.38	-3.57	0.009768	0.037549	-3.18
262499_at	unknown protein EST gb|T41993 co	---	AT1G21770	1.48	0.57	3.57	0.009772	0.037559	-3.18
258657_at	hypothetical protein predicted by ge	---	AT3G09890	1.52	0.61	3.57	0.009774	0.037559	-3.18
266832_at	putative protein kinase contains a p	MAPKKK14	AT2G30040	1.57	0.65	3.57	0.009777	0.037562	-3.18
266847_at	hypothetical protein predicted by gr	emb1345	AT2G26060	1.42	0.51	3.56	0.009782	0.037578	-3.19
266122_at	putative helicase ; supported by cD	ETL1	AT2G02090	1.31	0.39	3.56	0.009786	0.037585	-3.19
264383_at	putative glutathione peroxidase Co	ATGPX1	AT2G25080	-1.43	-0.51	-3.56	0.009791	0.037598	-3.19
259795_at	hypothetical protein predicted by ge	---	AT1G64290	-1.37	-0.45	-3.56	0.009797	0.037602	-3.19
258201_at	hypothetical protein predicted by ge	---	AT3G13910	1.74	0.80	3.56	0.009797	0.037602	-3.19
247932_at	putative protein similar to unknown	---	AT5G56920	-1.27	-0.34	-3.56	0.009812	0.037651	-3.19

264840_at	unknown protein similar to leucine-r	---	AT1G03440	-1.30	-0.38	-3.56	0.009815	0.037658	-3.19
259924_at	putative DNA-binding protein simila	---	AT1G72740	1.37	0.46	3.56	0.009818	0.037665	-3.19
249265_at	E2, ubiquitin-conjugating enzyme 8	---	AT5G41080	1.25	0.33	3.56	0.009832	0.037713	-3.19
266807_at	hypothetical protein	---	AT2G29920	-1.41	-0.49	-3.56	0.009841	0.03774	-3.19
255384_at	hypothetical protein	---	AT4G03580	-1.26	-0.33	-3.56	0.009843	0.037742	-3.19
253559_at	1,3-beta-glucanase - like protein 1,	---	AT4G31140	-1.31	-0.39	-3.56	0.009884	0.037892	-3.20
249769_at	sigma-like factor (emb CAA77213.1	SIGE	AT5G24120	1.50	0.59	3.56	0.009889	0.037899	-3.20
255780_at	hypothetical protein contains Pfam	GAUT11	AT1G18580	-1.40	-0.49	-3.56	0.009891	0.037899	-3.20
260798_at	unknown protein contains similarity	---	AT1G78280	-1.58	-0.66	-3.56	0.009891	0.037899	-3.20
245149_at	putative SWI/SNF family transcriptic	ATSWI3A	AT2G47620	1.35	0.43	3.56	0.009894	0.037899	-3.20
263686_at	putative 60s ribosomal protein L10	---	AT1G26910	1.57	0.65	3.56	0.009894	0.037899	-3.20
253047_at	Expressed protein ; supported by fu	---	AT4G37295	1.67	0.74	3.56	0.009898	0.037904	-3.20
251804_at	beta-1,3-glucanase - like protein pr	---	AT3G55430	-1.50	-0.59	-3.56	0.009899	0.037904	-3.20
250109_at	GASA4 ; supported by cDNA: gi_9	GASA4	AT5G15230	-5.25	-2.39	-3.56	0.009907	0.037925	-3.20
261608_at	unknown protein similar to putative	---	AT1G49650	-1.36	-0.44	-3.55	0.009909	0.037925	-3.20
260264_at	hypothetical protein predicted by ge	---	AT1G68500	-1.50	-0.58	-3.55	0.009909	0.037925	-3.20
245358_at	PRL1 protein ;supported by full-leng	PRL1	AT4G15900	1.39	0.47	3.55	0.009911	0.037926	-3.20
258482_at	putative chaperonin similar to chape	---	AT3G02530	1.40	0.48	3.55	0.009918	0.037944	-3.20
251258_at	PECTINESTERASE-like protein PE	VGDH2	AT3G62170	-1.39	-0.48	-3.55	0.009935	0.037998	-3.20
247859_at	unknown protein	---	AT5G58410	1.24	0.32	3.55	0.009943	0.038021	-3.20
248199_at	membrane related protein-like ;sup	---	AT5G54170	-1.86	-0.90	-3.55	0.009954	0.038053	-3.20
255043_at	putative protein several hypothetica	---	AT4G09640	-1.65	-0.72	-3.55	0.009955	0.038053	-3.20
261199_at	unknown protein	---	AT1G12950	-1.26	-0.33	-3.55	0.009958	0.038062	-3.20
254422_at	putative protein hypothetical protei	VPS28-1	AT4G21560	-1.72	-0.78	-3.55	0.009961	0.038064	-3.20
266308_at	putative cytochrome P450	CYP705A9	AT2G27010	1.38	0.47	3.55	0.009962	0.038064	-3.21
253270_at	cyclin delta-3	CYCD3;1	AT4G34160	-1.53	-0.62	-3.55	0.009967	0.038077	-3.21
246897_at	putative protein predicted proteins,	---	AT5G25560	-1.40	-0.48	-3.55	0.009969	0.038078	-3.21
263687_at	unknown protein ;supported by full-	---	AT1G26940	1.50	0.58	3.55	0.009972	0.038083	-3.21
258551_at	hypothetical protein predicted by ge	---	AT3G06890	-1.25	-0.32	-3.55	0.009977	0.038087	-3.21
253567_at	protein kinase-like protein serine/th	---	AT4G31230	-1.45	-0.54	-3.55	0.009977	0.038087	-3.21
249472_at	hypothetical protein ;supported by	CRR7	AT5G39210	1.65	0.73	3.55	0.009993	0.038144	-3.21
245803_at	cysteine proteinase RD21A identica	RD21	AT1G47128	1.43	0.52	3.55	0.009998	0.038146	-3.21
249777_at	putative protein similar to unknown	---	AT5G24210	-1.47	-0.55	-3.55	0.009998	0.038146	-3.21
257362_at	hypothetical protein predicted by ge	---	AT2G45840	-1.26	-0.33	-3.55	0.009999	0.038146	-3.21
258906_at	unknown protein similar to C-termi	ATTLP9	AT3G06380	1.39	0.48	3.55	0.010003	0.038156	-3.21

254957_at	putative protein ; supported by full-	---	AT4G10970	1.37	0.45	3.55	0.010006	0.038161	-3.21
262586_at	hypothetical protein predicted by ge	---	AT1G15480	1.63	0.70	3.55	0.010008	0.038161	-3.21
267132_at	unknown protein	NAPRT2	AT2G23420	1.70	0.76	3.55	0.010018	0.03819	-3.21
260209_at	putative AP2 domain transcription f	CPuORF53	AT1G68550	1.37	0.46	3.55	0.010019	0.03819	-3.21
258329_at	putative protein disulfide isomerase	ATPDIL1-6	AT3G16110	1.32	0.40	3.54	0.01004	0.038263	-3.21
258860_at	putative potassium transporter simil	KUP3	AT3G02050	1.62	0.70	3.54	0.010047	0.038285	-3.21
264983_at	hypothetical protein predicted by ge	---	AT1G27240	-1.29	-0.37	-3.54	0.010049	0.038286	-3.21
259352_at	unknown protein	---	AT3G05170	-1.65	-0.72	-3.54	0.010051	0.038286	-3.21
246236_at	hypothetical protein	---	AT4G36470	-1.39	-0.47	-3.54	0.010053	0.038286	-3.21
265000_at	hypothetical protein predicted by ge	---	AT1G67410	-1.35	-0.44	-3.54	0.010054	0.038286	-3.21
263042_at	conserved hypothetical protein prot	---	AT1G23340	-1.37	-0.46	-3.54	0.010058	0.038295	-3.22
252878_at	mitochondrial carrier - like protein A	SAMC1	AT4G39460	-1.33	-0.41	-3.54	0.010075	0.038345	-3.22
260966_at	NBS/LRR disease resistance prote	RPS5	AT1G12220	1.33	0.41	3.54	0.01008	0.038354	-3.22
257187_at	hypothetical protein predicted by ge	---	AT3G13140	-1.31	-0.39	-3.54	0.010082	0.038354	-3.22
264283_at	hypothetical protein contains simila	---	AT1G61850	-1.33	-0.42	-3.54	0.010093	0.038388	-3.22
258550_at	putative mudrA protein similar to mu	---	---	1.37	0.45	3.54	0.010128	0.038513	-3.22
261002_at	hypothetical protein contains simila	---	AT1G26520	1.33	0.41	3.54	0.010129	0.038513	-3.22
246483_at	receptor protein kinase-like protein	NIK1	AT5G16000	-1.94	-0.96	-3.54	0.010137	0.038538	-3.22
257075_at	unknown protein contains Pfam pro	---	AT3G19670	1.46	0.54	3.54	0.010141	0.038548	-3.22
263793_at	putative glucosyltransferase	ATCSLC08	AT2G24630	-1.79	-0.84	-3.54	0.010143	0.038548	-3.22
262992_at	hypothetical protein predicted by ge	ATG12A	AT1G54210	1.48	0.56	3.54	0.01015	0.038566	-3.23
267355_at	putative LIM-domain protein	---	AT2G39900	-1.48	-0.57	-3.54	0.010154	0.038578	-3.23
256250_at	integral membrane protein, putative	---	AT3G11320	-1.46	-0.55	-3.54	0.010163	0.038604	-3.23
259368_at	aspartic protease, putative similar t	---	AT1G69100	-1.30	-0.38	-3.54	0.01017	0.038623	-3.23
252038_at	gamma response I protein ; suppor	---	AT3G52120	-1.46	-0.55	-3.53	0.010172	0.038623	-3.23
267009_at	unknown protein	---	AT2G39260	1.27	0.35	3.53	0.010174	0.038623	-3.23
266804_at	cyclophilin identical to GB:AF0204	CYP5	AT2G29960	1.35	0.43	3.53	0.010175	0.038623	-3.23
253734_at	putative serine/threonine-specific r	---	AT4G29180	-1.34	-0.42	-3.53	0.010179	0.038634	-3.23
248901_at	putative protein contains similarity t	---	AT5G46410	1.40	0.49	3.53	0.010186	0.038652	-3.23
246420_at	putative protein various predicted p	---	AT5G16870	-1.41	-0.49	-3.53	0.010187	0.038652	-3.23
255194_at	score=37.6, E=2.9e-07, N=3	---	AT4G07410	1.53	0.62	3.53	0.010193	0.038667	-3.23
245676_at	nodule-specific protein, putative sir	---	AT1G56670	-1.35	-0.43	-3.53	0.010197	0.038676	-3.23
259416_at	Expressed protein ; supported by cl	---	AT1G02305	1.44	0.52	3.53	0.010207	0.0387	-3.23
259202_at	putative mRNA capping enzyme, R	---	AT3G09100	1.35	0.44	3.53	0.010207	0.0387	-3.23
250461_at	hypothetical protein	---	AT5G10010	1.43	0.51	3.53	0.010211	0.038706	-3.23

253953_at	putative protein extensin precursor	---	AT4G26750	-1.57	-0.65	-3.53	0.010213	0.038706	-3.23
251759_at	tetrahydrofolylpolyglutamate syntha	ATDFD	AT3G55630	1.69	0.75	3.53	0.010214	0.038706	-3.23
251289_at	auxin response factor-like protein a	ARF18	AT3G61830	1.44	0.53	3.53	0.010215	0.038706	-3.23
263322_at	putative ribonuclease E	RNEE/G	AT2G04270	1.59	0.67	3.53	0.01022	0.038719	-3.23
246693_at	putative protein	---	AT5G29070	-1.30	-0.38	-3.53	0.010232	0.038758	-3.23
253527_at	pathogenesis-related protein homo	---	AT4G31470	-1.34	-0.42	-3.53	0.010234	0.038759	-3.23
246612_at	putative protein ;supported by full-l	---	AT5G35320	1.40	0.49	3.53	0.010245	0.038792	-3.24
252769_at	arabinose kinase - like protein puta	---	AT3G42850	-1.31	-0.39	-3.53	0.010256	0.038828	-3.24
249925_at	putative protein predicted proteins,	---	AT5G19150	1.50	0.58	3.53	0.01027	0.038875	-3.24
256645_at	hypothetical protein predicted by ge	---	AT3G24250	-1.27	-0.35	-3.53	0.010272	0.038875	-3.24
259119_at	transport protein SEC13, putative s	---	AT3G01340	-1.27	-0.34	-3.53	0.010292	0.038939	-3.24
255591_at	putative expansin	ATEXPA17	AT4G01630	-1.33	-0.41	-3.53	0.010296	0.038946	-3.24
265723_at	putative disease resistance protein	---	AT2G32140	-1.26	-0.34	-3.53	0.010302	0.038965	-3.24
267469_at	unknown protein ; supported by cD	WRKY21	AT2G30590	-1.36	-0.44	-3.52	0.010306	0.038971	-3.24
253017_at	cinnamyl alcohol dehydrogenase -l	CAD6	AT4G37970	-1.27	-0.34	-3.52	0.010309	0.038973	-3.24
258805_at	putative beta-1,3-glucanase similar	---	AT3G04010	1.52	0.60	3.52	0.01031	0.038973	-3.24
252456_at	hypersensitivity-related protein-like	---	AT3G47170	-1.34	-0.42	-3.52	0.010315	0.038988	-3.24
253037_at	putative protein other predicted Ara	GAUT3	AT4G38270	1.32	0.40	3.52	0.01032	0.038995	-3.24
257199_at	Tic22, putative similar to Tic22 GB	---	AT3G23710	1.38	0.47	3.52	0.010321	0.038995	-3.24
259055_at	unknown protein ;supported by full-	UNE6	AT3G03340	1.31	0.39	3.52	0.010322	0.038995	-3.24
259255_at	putative glycerol-3-phosphate dehy	---	AT3G07690	1.69	0.76	3.52	0.010328	0.03901	-3.24
250343_at	putative protein density regulated p	---	AT5G11900	1.32	0.40	3.52	0.010338	0.03904	-3.24
261050_at	transcription factor MYC7E, putativ	---	AT1G01260	-1.58	-0.66	-3.52	0.010339	0.03904	-3.24
259631_at	heat shock protein, putative similar	ERD2	AT1G56410	-1.27	-0.34	-3.52	0.010347	0.039062	-3.25
255928_at	unknown protein	---	AT1G12640	1.55	0.63	3.52	0.01036	0.039103	-3.25
259412_at	DNA binding protein GT-1, putative	---	AT1G13450	-1.32	-0.40	-3.52	0.010365	0.039113	-3.25
246040_at	peptidyl-prolyl cis-trans isomerase -	---	AT5G19370	-1.32	-0.40	-3.52	0.010366	0.039113	-3.25
253058_at	ribosomal - like protein ribosomal p	---	AT4G37660	1.52	0.60	3.52	0.010368	0.039115	-3.25
247637_at	putative protein gcpE protein, Chla	HDS	AT5G60600	1.46	0.55	3.52	0.010376	0.03914	-3.25
253619_at	glycine-rich protein glycine-rich cel	---	AT4G30460	-1.50	-0.59	-3.52	0.010382	0.039155	-3.25
254112_at	putative protein KIAA0136 gene, H	---	AT4G24970	1.32	0.40	3.52	0.010388	0.039165	-3.25
248708_at	putative protein contains similarity t	---	AT5G48560	-1.86	-0.89	-3.52	0.010388	0.039165	-3.25
257648_at	RNA helicase, putative similar to R	---	AT3G16840	1.65	0.72	3.52	0.010397	0.039194	-3.25
248558_at	permease	---	AT5G49990	1.58	0.66	3.52	0.010399	0.039194	-3.25
248792_at	ras-related small GTP-binding prote	ATRAB1A	AT5G47200	-1.34	-0.43	-3.52	0.010403	0.039203	-3.25

259327_at	putative lectin contains Pfam profile	---	AT3G16460	-3.38	-1.76	-3.52	0.010406	0.039207	-3.25
250318_at	dihydropyrimidinase ; supported by	---	AT5G12200	1.52	0.61	3.52	0.010413	0.03922	-3.25
246056_at	katanin p80 subunit - like protein ka	---	AT5G08390	-1.40	-0.48	-3.52	0.010416	0.039225	-3.25
266230_at	hypothetical protein predicted by ge	---	AT2G28830	1.74	0.80	3.52	0.010417	0.039225	-3.25
248720_at	protein kinase (EC 2.7.1.37) 5 (pir||	D6PKL2	AT5G47750	1.31	0.39	3.52	0.010427	0.039254	-3.25
252106_at	putative glutamate receptor putativ	ATGLR3.6	AT3G51480	-1.46	-0.55	-3.52	0.010439	0.039291	-3.26
261771_at	hypothetical protein contains simila	---	AT1G76150	1.24	0.31	3.51	0.010441	0.039293	-3.26
267157_at	putative MYB family transcription fa	AS1	AT2G37630	1.56	0.64	3.51	0.010451	0.039325	-3.26
250305_at	putative protein contains similarity t	---	AT5G12150	-1.41	-0.50	-3.51	0.010454	0.039325	-3.26
248298_at	putative protein similar to unknown	---	AT5G53110	1.59	0.67	3.51	0.010455	0.039325	-3.26
257707_at	hypothetical protein predicted by ge	---	AT3G12650	1.29	0.37	3.51	0.01046	0.03934	-3.26
255501_at	hypothetical protein	---	AT4G02400	1.54	0.62	3.51	0.010473	0.03938	-3.26
251885_at	fructose-bisphosphatase precursor	---	AT3G54050	-1.57	-0.65	-3.51	0.010485	0.039421	-3.26
266033_at	putative translation initiation factor e	---	AT2G05830	1.43	0.51	3.51	0.010488	0.039427	-3.26
247266_at	beta-xylosidase	XYL4	AT5G64570	1.63	0.71	3.51	0.010493	0.039439	-3.26
265123_at	hypothetical protein similar to putati	---	AT1G55440	-1.27	-0.35	-3.51	0.010495	0.039439	-3.26
266315_at	unknown protein ; supported by cD	SE	AT2G27100	1.27	0.34	3.51	0.010498	0.03944	-3.26
248019_at	putative protein similar to unknown	---	AT5G56480	-1.32	-0.40	-3.51	0.0105	0.03944	-3.26
267525_at	putative glycine-rich protein	---	AT2G30560	-1.24	-0.31	-3.51	0.010502	0.03944	-3.26
261370_at	cell division-related protein, putativ	---	AT1G53050	-1.30	-0.38	-3.51	0.010502	0.03944	-3.26
252450_s_a	receptor kinase-like protein recepto	---	AT3G47090	1.77	0.82	3.51	0.010504	0.039441	-3.26
257233_at	hypothetical protein similar to SF16	IQD10	AT3G15050	-1.30	-0.38	-3.51	0.010518	0.039485	-3.26
260734_at	disease resistance protein RPP1-W	---	AT1G17600	-1.41	-0.50	-3.51	0.010537	0.039552	-3.27
250483_at	alpha-hydroxynitrile lyase-like prote	MES5	AT5G10300	1.48	0.57	3.51	0.010552	0.039601	-3.27
248871_at	putative protein strong similarity to	---	AT5G46680	1.36	0.44	3.51	0.010558	0.039616	-3.27
259463_at	hypothetical protein predicted by ge	---	AT1G18950	1.63	0.71	3.51	0.010562	0.039626	-3.27
262900_at	hypothetical protein contains simila	SNL5	AT1G59890	1.39	0.47	3.50	0.010588	0.039708	-3.27
255665_at	hypothetical protein	CRP	AT4G00450	1.29	0.36	3.50	0.010595	0.03973	-3.27
247142_at	putative protein strong similarity to	---	AT5G65570	1.34	0.42	3.50	0.010604	0.039756	-3.27
248387_at	unknown protein	---	AT5G51960	1.38	0.47	3.50	0.010606	0.039756	-3.27
259566_at	hypothetical protein	---	AT1G20520	-1.27	-0.34	-3.50	0.010612	0.039775	-3.27
261626_at	unknown protein ; supported by cDI	---	AT1G01990	1.40	0.48	3.50	0.010636	0.039858	-3.28
255810_at	hypothetical protein ; supported by	---	AT4G10140	-1.32	-0.40	-3.50	0.010652	0.039909	-3.28
247744_at	putative protein various predicted p	---	AT5G59020	-1.45	-0.54	-3.50	0.010657	0.039922	-3.28
247970_at	cytosolic malate dehydrogenase	---	AT5G56720	-1.30	-0.38	-3.50	0.010663	0.039938	-3.28

246815_at	putative protein integrin analogue,	---	AT5G27220	1.27	0.35	3.50	0.010665	0.039939	-3.28
255982_at	hypothetical protein contains simila	OHP2	AT1G34000	-1.30	-0.38	-3.50	0.010669	0.039946	-3.28
259588_at	unknown protein ;supported by full-	---	AT1G27930	1.24	0.31	3.50	0.010673	0.039953	-3.28
253714_at	putative protein adaptor protein - H	---	AT4G29380	1.32	0.40	3.50	0.010674	0.039953	-3.28
246385_at	mitotic cyclin a2-type, putative simi	CYCA1;2	AT1G77390	-1.98	-0.98	-3.50	0.010686	0.039992	-3.28
257733_at	unknown protein ; supported by cD	---	AT3G18350	-1.36	-0.44	-3.50	0.010697	0.040026	-3.28
259395_at	GTP-binding protein(RAB11D), put	ARA-2	AT1G06400	-1.30	-0.38	-3.50	0.010699	0.040026	-3.28
265699_at	putative esterase (contains an este	---	AT2G03550	1.34	0.42	3.50	0.010713	0.040068	-3.28
265112_at	hypothetical protein predicted by ge	---	AT1G62530	-1.25	-0.32	-3.50	0.010713	0.040068	-3.28
260680_s_a	GATA transcription factor 3, putativ	---	AT1G08000	-1.26	-0.33	-3.50	0.010717	0.040073	-3.28
262476_at	phosphoprotein phosphatase identi	---	AT1G50370	1.30	0.38	3.49	0.010721	0.040081	-3.28
246240_at	nucleoporin-like protein	---	AT4G37130	1.25	0.32	3.49	0.010725	0.040092	-3.28
256573_at	hypothetical protein predicted by ge	---	AT3G14860	1.32	0.40	3.49	0.010733	0.040114	-3.28
259389_at	hypothetical protein predicted by ge	---	AT1G06320	-1.28	-0.36	-3.49	0.010735	0.040114	-3.29
246617_at	GSH-dependent dehydroascorbate	---	AT5G36270	-1.34	-0.42	-3.49	0.010741	0.040132	-3.29
255558_at	P II nitrogen sensing protein GLB I	GLB1	AT4G01900	-1.36	-0.45	-3.49	0.01075	0.04016	-3.29
258372_at	ubiquitin-specific protease 25 (UBP	UBP25	AT3G14400	1.29	0.37	3.49	0.010757	0.040179	-3.29
261852_at	unknown protein ;supported by full-	---	AT1G50440	-1.26	-0.33	-3.49	0.010761	0.040187	-3.29
264242_at	hypothetical protein predicted by ge	---	AT1G54640	-1.24	-0.31	-3.49	0.010765	0.040187	-3.29
261614_at	poly(A)-binding protein, putative sir	PAB8	AT1G49760	1.48	0.56	3.49	0.010766	0.040187	-3.29
262143_at	unknown protein	---	AT1G52630	-1.34	-0.43	-3.49	0.010767	0.040187	-3.29
247935_at	30S ribosomal protein S16 ; suppo	---	AT5G56940	1.46	0.54	3.49	0.010779	0.040223	-3.29
253366_at	putative protein predicted protein, A	---	AT4G33180	-1.44	-0.53	-3.49	0.01078	0.040223	-3.29
256914_at	hypothetical protein	---	AT3G23880	-1.57	-0.65	-3.49	0.010784	0.040232	-3.29
248429_at	putative protein contains similarity t	---	AT5G51770	1.79	0.84	3.49	0.010796	0.040271	-3.29
267445_at	hypothetical protein predicted by g	---	AT2G33680	1.36	0.44	3.49	0.010799	0.040271	-3.29
247158_at	branched-chain amino acid aminotr	ATBCAT-5	AT5G65780	1.29	0.37	3.49	0.010801	0.040271	-3.29
265012_at	putative b-keto acyl reductase simi	KCR2	AT1G24470	-1.33	-0.41	-3.49	0.010801	0.040271	-3.29
259706_at	unknown protein similar to GB:AAD	---	AT1G77540	1.38	0.46	3.49	0.01081	0.040293	-3.29
256587_at	histone-H4-like protein similar to H4	---	AT3G28780	-1.34	-0.43	-3.49	0.010811	0.040293	-3.29
248636_at	putative protein similar to unknown	---	---	-1.33	-0.41	-3.49	0.010814	0.040293	-3.29
258959_at	putative amino acid transporter sim	CAT7	AT3G10600	-1.31	-0.39	-3.49	0.010816	0.040293	-3.29
257198_at	DNA-binding protein, putative simil	---	AT3G23690	-1.38	-0.47	-3.49	0.010817	0.040293	-3.29
251480_at	putative protein inducible carbonyl	---	AT3G59710	-1.44	-0.53	-3.49	0.010818	0.040293	-3.29
246776_at	kinesin-like protein kinesin-like hea	---	AT5G27550	-1.49	-0.57	-3.49	0.010824	0.04031	-3.29

255792_at	AT-hook DNA-binding protein (AHP	---	AT2G33620	1.42	0.50	3.49	0.010833	0.040335	-3.29
255599_at	cyclic nucleotide gated channel (CI	ATCNGC1	AT4G01010	1.76	0.82	3.49	0.010834	0.040335	-3.29
252959_at	putative protein NADH dehydroger	---	AT4G38640	1.32	0.41	3.49	0.010838	0.040342	-3.30
263286_at	40S ribosomal protein S14 ;suppor	---	AT2G36160	1.54	0.62	3.49	0.010856	0.040402	-3.30
251730_at	N2,N2-dimethylguanosine tRNA m	---	AT3G56330	1.42	0.50	3.48	0.01088	0.040478	-3.30
247613_at	xABC transporter - like protein brea	---	AT5G60740	-1.39	-0.48	-3.48	0.01088	0.040478	-3.30
259466_at	response regulator 5, putative simi	ARR7	AT1G19050	-2.83	-1.50	-3.48	0.010899	0.040535	-3.30
266073_at	putative signal recognition particle r	---	AT2G18770	-1.31	-0.39	-3.48	0.010917	0.040597	-3.30
266511_at	putative ATP-dependent RNA helic	---	AT2G47680	1.40	0.48	3.48	0.010932	0.040634	-3.30
259198_at	hypothetical protein similar to F1N2	---	AT3G03610	-1.34	-0.42	-3.48	0.010932	0.040634	-3.30
249647_at	putative protein hypothetical protein	---	AT5G37040	-1.42	-0.51	-3.48	0.010934	0.040634	-3.30
252324_at	protein translocation complex sec6	---	AT3G48570	-1.36	-0.44	-3.48	0.010952	0.040693	-3.31
252135_at	putative cold acclimation protein co	COR413-P	AT3G50830	-1.48	-0.56	-3.48	0.010958	0.040707	-3.31
250955_at	putative protein various predicted p	CPUORF47	AT5G03190	-2.90	-1.54	-3.48	0.010963	0.040711	-3.31
257671_at	hypothetical protein predicted by ge	---	AT3G20450	-1.38	-0.47	-3.48	0.010964	0.040711	-3.31
260436_at	unknown protein	---	AT1G68140	1.41	0.50	3.48	0.01097	0.040726	-3.31
254790_at	probable photosystem I chain XI pr	PSAL	AT4G12800	-1.28	-0.36	-3.48	0.010977	0.040744	-3.31
260262_at	hypothetical protein similar to hypo	---	AT1G68470	-2.01	-1.01	-3.48	0.010979	0.040744	-3.31
266864_at	putative hydroxymethylglutaryl-CoA	---	AT2G26800	-1.43	-0.52	-3.48	0.010989	0.040765	-3.31
263909_at	hypothetical protein predicted by ge	DML1	AT2G36490	-1.59	-0.67	-3.48	0.010989	0.040765	-3.31
249279_at	SCARECROW gene regulator-like p	---	AT5G41920	-1.26	-0.33	-3.48	0.010992	0.04077	-3.31
246352_at	hypothetical protein	---	---	-1.25	-0.32	-3.48	0.010994	0.04077	-3.31
252298_at	putative protein various predicted p	---	AT3G49060	-1.28	-0.36	-3.48	0.010999	0.040781	-3.31
249580_at	putative protein predicted proteins,	---	AT5G37740	1.42	0.51	3.48	0.011001	0.040781	-3.31
260902_at	hypothetical protein similar to carbo	---	AT1G21440	-1.64	-0.71	-3.47	0.011017	0.040836	-3.31
255275_at	putative protein various ubiquitin-lik	---	AT4G05310	-1.23	-0.30	-3.47	0.01103	0.040876	-3.31
253577_at	putative protein	---	AT4G31080	1.60	0.67	3.47	0.011035	0.040888	-3.31
248694_at	unknown protein	---	AT5G48340	1.30	0.37	3.47	0.01104	0.040901	-3.32
247516_at	germin-like protein - like germin-lik	---	AT5G61750	-1.34	-0.43	-3.47	0.011044	0.040901	-3.32
252766_at	putative protein hypothetical protein	---	---	-1.45	-0.54	-3.47	0.011044	0.040901	-3.32
258127_at	unknown protein	---	AT3G24570	-1.28	-0.36	-3.47	0.011049	0.040915	-3.32
247533_at	putative protein kinase-like transme	---	AT5G61570	-1.95	-0.97	-3.47	0.011053	0.040916	-3.32
259029_at	putative oxysterol-binding protein si	ORP3B	AT3G09300	-1.39	-0.47	-3.47	0.011053	0.040916	-3.32
265495_at	unknown protein predicted by gens	---	AT2G15695	1.33	0.41	3.47	0.01106	0.040935	-3.32
267192_at	hypothetical protein predicted by gr	---	AT2G30890	-1.41	-0.50	-3.47	0.011082	0.041002	-3.32

246793_at	putative protein seven transmembr	---	AT5G27210	1.30	0.38	3.47	0.011084	0.041002	-3.32
249416_at	putative protein DNA DAMAGE-RE	---	AT5G39570	-1.33	-0.41	-3.47	0.011095	0.041038	-3.32
261925_at	oligopeptide transporter, putative s	---	AT1G22540	-1.32	-0.40	-3.47	0.01112	0.041115	-3.32
254865_s_a	putative protein, fragment other pre	---	AT4G05350	-1.28	-0.35	-3.47	0.011124	0.041125	-3.32
248397_at	unknown protein	---	AT5G52140	-1.32	-0.40	-3.47	0.011133	0.041144	-3.32
265252_at	putative Na+/H+ antiporter	SOS1	AT2G01980	1.26	0.34	3.47	0.011133	0.041144	-3.32
245980_at	putative protein ;supported by full-l	---	AT5G13140	-6.55	-2.71	-3.47	0.011136	0.041148	-3.32
264899_at	unknown protein similar to ripening	---	AT1G23130	1.75	0.81	3.47	0.01114	0.041158	-3.32
258698_at	unknown protein	---	AT3G09690	-1.36	-0.45	-3.47	0.011143	0.041161	-3.33
248976_at	putative protein strong similarity to	ARAD2	AT5G44930	1.41	0.50	3.47	0.011149	0.041172	-3.33
244931_at	hypothetical protein	---	---	1.50	0.58	3.47	0.01115	0.041172	-3.33
260094_at	GDP-4-keto-6-deoxy-D-mannose-3	GER1	AT1G73250	-1.42	-0.51	-3.46	0.011156	0.041189	-3.33
264228_at	hypothetical protein contains simila	GCS1	AT1G67490	1.32	0.40	3.46	0.011164	0.041211	-3.33
247080_at	20S proteasome subunit PAD2 (gb	PAD2	AT5G66140	1.34	0.42	3.46	0.011166	0.041214	-3.33
247790_at	putative PRL1 associated protein ;	---	AT5G58720	-1.35	-0.44	-3.46	0.011171	0.041225	-3.33
262464_at	hypothetical protein contains simila	---	AT1G50280	1.65	0.72	3.46	0.01118	0.041252	-3.33
255062_at	hypothetical protein	---	AT4G08940	1.39	0.48	3.46	0.011189	0.041273	-3.33
257721_at	hypothetical protein predicted by ge	---	AT3G18310	1.25	0.33	3.46	0.011189	0.041273	-3.33
252173_at	scarecrow-like 7 (SCL7)	---	AT3G50650	-1.67	-0.74	-3.46	0.011197	0.041295	-3.33
257178_at	hemolysin-like protein similar to her	---	AT3G13070	1.35	0.44	3.46	0.011222	0.041378	-3.33
266458_at	unknown protein ;supported by full-	---	AT2G47710	1.27	0.35	3.46	0.011224	0.041379	-3.33
258837_at	putative 60S ribosomal protein L13	---	AT3G07110	1.94	0.95	3.46	0.011228	0.041388	-3.33
262120_at	glutathione-S-transferase, putative	ATGSTF4	AT1G02950	-1.45	-0.54	-3.46	0.011238	0.041416	-3.33
256412_at	hypothetical protein predicted by ge	ELO1	AT3G11220	1.35	0.43	3.46	0.011239	0.041416	-3.33
254996_at	putative protein kinase CLV1 recep	---	AT4G10390	-1.43	-0.51	-3.46	0.01125	0.041443	-3.34
252665_at	valine-rich protein	---	AT3G44140	-1.36	-0.45	-3.46	0.011251	0.041443	-3.34
261060_at	unknown protein	---	AT1G17340	-1.40	-0.48	-3.46	0.011252	0.041443	-3.34
258018_at	hypothetical protein predicted by ge	---	AT3G19500	-1.46	-0.54	-3.46	0.011265	0.041484	-3.34
254577_at	putative protein ;supported by full-l	---	AT4G19450	1.51	0.59	3.46	0.011278	0.041526	-3.34
265122_at	similar to flavin-binding monooxyge	FMO GS-O	AT1G62540	-1.24	-0.31	-3.46	0.011291	0.041565	-3.34
254821_at	hypothetical protein	---	AT4G12540	-1.28	-0.36	-3.46	0.011292	0.041565	-3.34
245879_at	putative subunit of TOC complex c	ATTOC64-V	AT5G09420	2.07	1.05	3.46	0.011296	0.041572	-3.34
257226_at	hypothetical protein predicted by ge	---	AT3G27880	2.08	1.05	3.45	0.011298	0.041573	-3.34
252920_at	putative endo-1,4-beta-glucanase	AtGH9B17	AT4G39000	-1.36	-0.45	-3.45	0.011311	0.041615	-3.34
253337_at	putative protein acetylpolyamine ar	hda14	AT4G33470	-1.60	-0.68	-3.45	0.011322	0.041646	-3.34

264973_at	nitrate transporter, putative nitrate	---	AT1G27040	-1.40	-0.49	-3.45	0.011325	0.041652	-3.34
262602_at	unknown protein ESTs gb|AA6508	---	AT1G15270	1.26	0.34	3.45	0.011331	0.041668	-3.34
253916_at	hypothetical protein ;supported by	---	AT4G27240	-1.67	-0.74	-3.45	0.011366	0.04179	-3.35
249666_at	phytochrome C (sp|P14714)	PHYC	AT5G35840	1.41	0.50	3.45	0.011373	0.041809	-3.35
261273_at	unknown protein ; supported by cDI	---	AT1G26650	-1.53	-0.61	-3.45	0.011381	0.04183	-3.35
249782_at	dipeptidyl peptidase IV-like protein	---	AT5G24260	-1.32	-0.40	-3.45	0.011403	0.041904	-3.35
246568_at	E2F transcription factor -like protei	DEL2	AT5G14960	1.39	0.48	3.45	0.011412	0.041931	-3.35
245396_at	hypothetical protein ;supported by f	---	AT4G14870	-1.60	-0.67	-3.45	0.011422	0.041959	-3.35
248360_at	putative protein contains similarity t	---	AT5G52430	-1.49	-0.57	-3.45	0.011432	0.041985	-3.35
256897_at	hypothetical protein predicted by ge	---	AT3G24640	-1.26	-0.33	-3.44	0.011459	0.042068	-3.35
259524_at	hypothetical protein	---	AT1G12550	-1.49	-0.57	-3.44	0.011467	0.042091	-3.36
253381_at	Tic22 -like protein strong homology	---	AT4G33350	1.36	0.45	3.44	0.011469	0.042091	-3.36
249244_at	FtsH protease, putative similar to F	VAR1	AT5G42270	-1.33	-0.41	-3.44	0.01147	0.042091	-3.36
255596_at	putative DNA-binding protein simila	WRKY47	AT4G01720	1.93	0.95	3.44	0.011493	0.042168	-3.36
264825_at	hypothetical protein predicted by ge	---	AT1G03720	-1.35	-0.43	-3.44	0.011495	0.042168	-3.36
258241_at	hypothetical protein similar to hypot	LBD25	AT3G27650	-1.46	-0.54	-3.44	0.011504	0.042195	-3.36
255120_x_a	putative transposon protein similar	---	---	-1.27	-0.34	-3.44	0.01152	0.042238	-3.36
247511_at	Fdr1 Cen - like protein Fdr1, Oryza	---	AT5G62040	-1.37	-0.45	-3.44	0.011522	0.042238	-3.36
261682_at	unknown protein similar to hypothet	---	AT1G47330	1.38	0.47	3.44	0.011523	0.042238	-3.36
253413_at	putative protein Fe(II) transport pro	ZIP9	AT4G33020	1.22	0.29	3.44	0.011525	0.042238	-3.36
267462_at	Expressed protein ; supported by fu	---	AT2G33735	1.65	0.73	3.44	0.011531	0.042252	-3.36
249393_at	disease resistance - like protein res	AtRLP54	AT5G40170	1.74	0.80	3.44	0.011543	0.04229	-3.36
255966_at	14-3-3 protein GF14epsilon (grf10)	GRF10	AT1G22300	1.38	0.47	3.44	0.011556	0.042323	-3.36
245687_at	unknown protein	DEG15	AT1G28320	1.24	0.31	3.44	0.011557	0.042323	-3.36
258086_at	dihydrolipoamide S-acetyltransferas	LTA2	AT3G25860	-1.39	-0.47	-3.44	0.011558	0.042323	-3.36
265387_at	unknown protein ;supported by full-	---	AT2G20670	-2.10	-1.07	-3.44	0.01156	0.042324	-3.36
260119_at	AIG1-like protein similar to AIG1 pr	---	AT1G33930	-1.30	-0.38	-3.44	0.011562	0.042325	-3.36
245466_at	glucosyltransferase like protein	---	AT4G16600	-1.40	-0.48	-3.44	0.011566	0.042332	-3.36
249546_at	putative protein chromosome segre	PMI15	AT5G38150	1.57	0.65	3.44	0.011569	0.042338	-3.37
252292_at	RNA polymerase III subunit - like p	---	AT3G49000	1.35	0.43	3.44	0.011583	0.042381	-3.37
254832_at	pEARLI 1-like protein Arabidopsis	---	AT4G12490	5.15	2.36	3.44	0.011585	0.042383	-3.37
264332_at	hypothetical protein predicted by ge	---	AT1G61920	-1.29	-0.37	-3.44	0.011589	0.042389	-3.37
252090_at	5B protein like protein cysteine-rich	---	AT3G52130	-1.29	-0.36	-3.44	0.011591	0.042389	-3.37
246727_at	major latex protein homolog - like r	---	AT5G28010	1.44	0.53	3.43	0.011602	0.04242	-3.37
261195_at	transport inhibitor response 1 (TIR	AFB3	AT1G12820	1.33	0.41	3.43	0.011603	0.04242	-3.37

266207_at	unknown protein ; supported by cD	---	AT2G27680	-1.43	-0.52	-3.43	0.011606	0.042426	-3.37
248907_at	putative protein contains similarity t	---	AT5G46340	1.30	0.38	3.43	0.011612	0.04244	-3.37
248548_at	transmembrane transport protein-lik	---	AT5G50300	-1.27	-0.34	-3.43	0.011618	0.042456	-3.37
247580_at	putative protein traube, Mus muscu	---	AT5G61330	1.37	0.46	3.43	0.011634	0.042505	-3.37
252368_at	cytochrome P450-like protein cytoc	CYP94B3	AT3G48520	-1.94	-0.96	-3.43	0.011635	0.042505	-3.37
265888_at	putative cleavage and polyadenylat	RIE1	AT2G01735	-1.26	-0.34	-3.43	0.011641	0.042518	-3.37
250237_at	putative protein strong similarity to	---	AT5G13560	-1.40	-0.49	-3.43	0.011644	0.042518	-3.37
249324_at	cytochrome c1 precursor ; supporte	---	AT5G40810	1.26	0.33	3.43	0.011654	0.042545	-3.37
258911_at	unknown protein similar to hypothe	---	AT3G06470	-1.35	-0.43	-3.43	0.011657	0.042545	-3.37
267070_at	putative DnaJ protein	---	AT2G41000	1.53	0.61	3.43	0.011657	0.042545	-3.37
254933_at	putative RNA-directed RNA polyme	RDR2	AT4G11130	1.39	0.47	3.43	0.011669	0.04258	-3.37
252151_at	putative protein several hypothetica	---	AT3G51320	1.26	0.33	3.43	0.011675	0.042594	-3.37
263541_at	unknown protein ; supported by ful	---	AT2G24860	-1.30	-0.38	-3.43	0.011691	0.042643	-3.38
245332_at	isomerase like protein ;supported b	---	AT4G15940	1.23	0.30	3.43	0.011692	0.042643	-3.38
252472_at	GTP-binding protein Rab11 ; suppo	ATRABA2C	AT3G46830	-1.36	-0.45	-3.43	0.011696	0.042647	-3.38
265960_at	putative histone H2B ;supported by	---	AT2G37470	1.68	0.75	3.43	0.011698	0.042647	-3.38
266131_at	putative SCARECROW gene regula	---	AT2G45160	-1.52	-0.60	-3.43	0.011698	0.042647	-3.38
250674_at	laccase-like protein laccase - Popu	LAC13	AT5G07130	-1.56	-0.64	-3.43	0.011703	0.042655	-3.38
247450_at	ripening-related protein - like ripeni	---	AT5G62350	-1.42	-0.50	-3.43	0.01171	0.042668	-3.38
264644_at	hypothetical protein Similar to Caen	CAX11	AT1G08960	-1.37	-0.46	-3.43	0.011714	0.042677	-3.38
266922_s_a	SKP1/ASK1-related, putative simila	ASK20	AT2G45950	1.61	0.69	3.43	0.01172	0.042693	-3.38
244949_at	hypothetical protein	---	---	1.34	0.42	3.43	0.011742	0.042752	-3.38
251205_at	glutathione peroxidase -like protein	ATGPX5	AT3G63080	-1.41	-0.50	-3.43	0.011742	0.042752	-3.38
245719_at	DNA gyrase subunit B - like protein	---	AT5G04110	1.30	0.37	3.43	0.011743	0.042752	-3.38
260328_at	putative aspartate aminotransferase	---	AT1G80360	1.25	0.32	3.43	0.011744	0.042752	-3.38
246310_at	sulfate transporter ATST1 ; suppor	SULTR3;1	AT3G51895	1.59	0.67	3.43	0.01175	0.042765	-3.38
266501_at	unknown protein ; supported by cD	HEN2	AT2G06990	1.36	0.45	3.43	0.011754	0.042775	-3.38
262988_at	putative alanine aminotrans	GGT1	AT1G23310	1.27	0.35	3.42	0.01176	0.042788	-3.38
263075_at	hypothetical protein predicted by ge	---	AT2G17570	1.50	0.58	3.42	0.011769	0.042816	-3.38
263765_at	putative phosphatidylinositol phoph	SFH3	AT2G21540	-2.42	-1.28	-3.42	0.011772	0.042821	-3.38
256165_at	hypothetical protein predicted by ge	---	AT1G48780	-1.43	-0.51	-3.42	0.011778	0.042834	-3.38
249885_at	putative protein strong similarity to	F8H	AT5G22940	-1.67	-0.74	-3.42	0.011789	0.042869	-3.39
248165_at	putative protein similar to unknown	PHOS32	AT5G54430	1.39	0.47	3.42	0.011794	0.04288	-3.39
267465_at	subtilisin-like serine protease conta	SLP3	AT2G19170	-1.95	-0.96	-3.42	0.011802	0.042902	-3.39
258070_at	hypothetical protein predicted by ge	---	AT3G26040	-1.41	-0.50	-3.42	0.011806	0.04291	-3.39

251010_at	putative protein ;supported by full-l	---	AT5G02550	-1.42	-0.51	-3.42	0.011811	0.042919	-3.39
261116_at	sec14 cytosolic factor, putative sim	---	AT1G75370	-1.31	-0.39	-3.42	0.011829	0.042965	-3.39
264571_at	hypothetical protein predicted by ge	---	AT1G05330	-1.25	-0.32	-3.42	0.011829	0.042965	-3.39
255171_at	hypothetical protein	---	AT4G07990	1.28	0.36	3.42	0.011833	0.042971	-3.39
262124_at	nucleoporin 98-like protein similar t	---	AT1G59660	1.26	0.33	3.42	0.011837	0.042975	-3.39
263414_at	putative bZIP transcription factor co	---	AT2G21230	1.30	0.38	3.42	0.011851	0.043012	-3.39
246754_at	transcription factor - like protein Ha	NF-YC8	AT5G27910	-1.44	-0.52	-3.42	0.011851	0.043012	-3.39
266394_at	Ras-related GTP-binding protein (A	ARA4	AT2G43130	-1.32	-0.40	-3.42	0.011866	0.043058	-3.39
252375_at	rac GTP binding protein Arac8 ; su	ROP10	AT3G48040	-1.34	-0.43	-3.42	0.011868	0.043058	-3.39
246653_at	putative protein clathrin assembly p	---	AT5G35200	1.32	0.40	3.42	0.01189	0.043131	-3.39
247835_at	putative protein similar to unknown	---	AT5G57910	1.72	0.79	3.42	0.011908	0.043191	-3.40
248507_at	putative protein strong similarity to	---	AT5G50420	-1.40	-0.48	-3.41	0.011924	0.043239	-3.40
247540_at	ethylene responsive element bindi	---	AT5G61590	-1.88	-0.91	-3.41	0.011927	0.043244	-3.40
261550_at	hypothetical protein	---	AT1G63450	-1.29	-0.37	-3.41	0.011942	0.043285	-3.40
261592_at	double-stranded RNA-specific edita	---	AT1G01760	-1.34	-0.43	-3.41	0.011948	0.043302	-3.40
246572_at	putative protein predicted proteins,	---	AT5G15010	1.33	0.41	3.41	0.011955	0.043318	-3.40
248590_at	receptor protein kinase	---	AT5G49660	1.30	0.37	3.41	0.011957	0.043318	-3.40
265394_at	predicted protein ; supported by cD	---	AT2G20725	1.38	0.46	3.41	0.011964	0.043339	-3.40
266802_at	Expressed protein ; supported by c	---	AT2G22900	-3.26	-1.70	-3.41	0.011967	0.043341	-3.40
251983_at	putative protein MtN21, Medicago	---	AT3G53210	1.50	0.58	3.41	0.011976	0.043367	-3.40
265073_at	unknown protein similar to putative	---	AT1G55480	-1.68	-0.75	-3.41	0.011997	0.043417	-3.40
264357_at	hypothetical protein Similar to hypo	ATRRP4	AT1G03360	2.16	1.11	3.41	0.012002	0.043428	-3.40
253579_at	SERINE CARBOXYPEPTIDASE II	BRS1	AT4G30610	-1.94	-0.95	-3.41	0.012005	0.043432	-3.40
255449_at	hypothetical protein	---	AT4G02820	1.45	0.53	3.41	0.012014	0.043458	-3.41
252036_at	putative protein ;supported by full-l	---	AT3G52070	1.42	0.51	3.41	0.012021	0.043476	-3.41
257928_at	hypothetical protein contains Pfam	PPR40	AT3G16890	1.24	0.31	3.41	0.012024	0.043478	-3.41
266869_at	putative glucosyltransferase	---	AT2G44660	-1.53	-0.62	-3.41	0.012027	0.043484	-3.41
246206_at	Expressed protein ; supported by c	ATPBRP	---	-1.28	-0.36	-3.41	0.012034	0.043502	-3.41
263034_at	pollen allergen-like protein similar t	MLP423	AT1G24020	-1.73	-0.79	-3.41	0.012039	0.043511	-3.41
252874_at	putative protein ipiB1 gene, Phyto	---	---	-1.31	-0.39	-3.41	0.01204	0.043511	-3.41
258560_at	hypothetical protein predicted by ge	---	AT3G06020	-1.47	-0.55	-3.41	0.012043	0.043513	-3.41
260076_at	putative calmodulin similar to calmo	---	AT1G73630	1.54	0.63	3.41	0.01205	0.043532	-3.41
249506_at	putative protein	---	AT5G38880	-1.36	-0.44	-3.41	0.012055	0.043543	-3.41
256922_at	hypothetical protein contains simila	---	AT3G19010	1.88	0.91	3.41	0.012061	0.043552	-3.41
247524_at	thioredoxin-like 3 ; supported by cD	ACHT5	AT5G61440	-2.33	-1.22	-3.41	0.012061	0.043552	-3.41

262343_at	phosphoprotein phosphatase 1 ider	TOPP3	AT1G64040	1.28	0.36	3.40	0.012082	0.04362	-3.41
266968_at	putative protein kinase contains a p	---	AT2G39360	-1.91	-0.93	-3.40	0.012087	0.043628	-3.41
AFFX-r2-At-	/FEATURE=cds-2 /GENE= /LABEL	---	---	-1.32	-0.40	-3.40	0.012088	0.043628	-3.41
261203_at	Expressed protein ; supported by fu	---	AT1G12845	-2.88	-1.53	-3.40	0.012094	0.043643	-3.41
251644_at	putative protein putative DNA bindi	---	AT3G57540	1.70	0.76	3.40	0.012101	0.04366	-3.41
250250_at	putative protein similar to unknown	---	AT5G13610	1.34	0.42	3.40	0.01211	0.04368	-3.41
246042_at	cinnamyl-alcohol dehydrogenase -	---	AT5G19440	1.85	0.89	3.40	0.012114	0.043688	-3.41
260137_at	unknown protein ;supported by full-	---	AT1G66330	1.50	0.58	3.40	0.012119	0.043691	-3.41
266942_at	putative ATP binding protein	TXND9	AT2G18990	-1.55	-0.64	-3.40	0.01214	0.043758	-3.42
253754_at	glycine-rich protein like glycine-rich	---	AT4G29020	-2.64	-1.40	-3.40	0.01215	0.043788	-3.42
246957_at	unknown protein	---	AT5G24670	1.24	0.31	3.40	0.012152	0.04379	-3.42
245268_at	hypothetical protein ; supported by	PRMT7	AT4G16570	-1.63	-0.71	-3.40	0.012157	0.043798	-3.42
258164_at	surfeit 1 identical to GB:AAF19609	SURF1	AT3G17910	1.53	0.62	3.40	0.012158	0.043798	-3.42
251816_at	Expressed protein ; supported by cl	TON1B	AT3G55005	-1.45	-0.54	-3.40	0.012162	0.043805	-3.42
246921_at	putative protein small unique nucle	---	AT5G25080	1.51	0.59	3.40	0.01217	0.043824	-3.42
253218_at	subtilisin-like serine protease simila	SLP2	AT4G34980	1.71	0.78	3.40	0.012172	0.043824	-3.42
266012_s_a	predicted protein	---	AT2G07699	1.71	0.78	3.40	0.012174	0.043824	-3.42
256652_at	hypothetical protein similar to putati	LPAT5	AT3G18850	-1.96	-0.97	-3.40	0.012175	0.043824	-3.42
253729_at	beta-1,3-glucanase-like protein bet	---	AT4G29360	-1.39	-0.47	-3.40	0.012181	0.043837	-3.42
251751_at	putative protein predicted proteins,	---	AT3G55720	-1.24	-0.31	-3.40	0.012182	0.043837	-3.42
266895_at	hypothetical protein predicted by ge	---	AT2G26040	-1.29	-0.36	-3.40	0.012185	0.04384	-3.42
246583_at	protein kinase -like protein Ste-20 r	---	AT5G14720	-1.39	-0.48	-3.40	0.012193	0.043861	-3.42
253669_at	dihydropteroate synthase-like prote	---	AT4G30000	1.29	0.36	3.40	0.012196	0.043864	-3.42
263691_at	60s ribosomal protein L34 identical	---	AT1G26880	1.68	0.74	3.40	0.012198	0.043866	-3.42
249822_at	unknown protein	---	AT5G23710	1.33	0.41	3.40	0.012203	0.043873	-3.42
256089_at	hypothetical protein predicted by ge	---	AT1G20830	1.51	0.60	3.40	0.012204	0.043873	-3.42
247741_at	putative protein predicted proteins,	GIL1	AT5G58960	1.68	0.75	3.40	0.012217	0.043904	-3.42
258549_at	putative arginine methyltransferase	PRMT4B	AT3G06930	1.25	0.32	3.40	0.012219	0.043904	-3.42
265689_at	hypothetical protein predicted by ge	---	AT2G24310	-1.25	-0.32	-3.40	0.012221	0.043904	-3.42
253206_at	putative squalene synthase non-co	SQS1	AT4G34640	-1.34	-0.42	-3.40	0.012222	0.043904	-3.42
253757_at	rac GTP binding protein Arac7 ; su	ROP9	AT4G28950	-1.36	-0.45	-3.40	0.012223	0.043904	-3.42
249531_at	putative protein predicted protein, A	AtGDU7	AT5G38770	-1.29	-0.37	-3.40	0.012224	0.043904	-3.42
255925_at	unknown protein ;supported by full-	---	AT1G22200	1.41	0.50	3.39	0.012234	0.043934	-3.42
245665_at	unknown protein ;supported by full-	---	AT1G28250	-1.34	-0.42	-3.39	0.012246	0.043968	-3.43
248465_at	putative protein contains similarity t	---	AT5G51200	1.48	0.57	3.39	0.012248	0.04397	-3.43

256818_at	hypothetical protein contains Pfam	---	AT3G21420	-1.27	-0.35	-3.39	0.012261	0.044007	-3.43
251717_at	putative protein EXOENZYMES RE	LAF3	AT3G55850	1.43	0.51	3.39	0.012268	0.044022	-3.43
251163_at	putative protein S1R protein - Hom	---	AT3G63310	1.24	0.31	3.39	0.012269	0.044022	-3.43
261869_at	hypothetical protein predicted by ge	---	AT1G11470	-1.35	-0.43	-3.39	0.012272	0.044028	-3.43
255082_at	putative protein polyphosphoinositi	---	AT4G09160	-1.29	-0.37	-3.39	0.012275	0.044032	-3.43
247094_at	GDP-D-mannose 4,6-dehydratase;	GMD1	AT5G66280	-1.32	-0.40	-3.39	0.012282	0.044049	-3.43
246644_at	putative protein	---	AT5G35100	-1.49	-0.57	-3.39	0.012291	0.044068	-3.43
249344_at	prohibitin (gb AAC49691.1) ;suppor	ATPHB3	AT5G40770	1.61	0.69	3.39	0.012291	0.044068	-3.43
264882_at	NAM protein, putative similar to NA	anac025	AT1G61110	-1.28	-0.35	-3.39	0.012309	0.044117	-3.43
266401_s_a	putative cell division control protein	CDKB1;2	AT2G38620	-1.25	-0.32	-3.39	0.012311	0.044117	-3.43
249145_at	enoyl CoA hydratase-like protein	ATDCI1	AT5G43280	-1.27	-0.34	-3.39	0.012312	0.044117	-3.43
262489_at	unknown protein EST gb|T21171 co	---	AT1G21830	-1.45	-0.54	-3.39	0.012313	0.044117	-3.43
251711_at	phosphatidylinositol-4-phosphate 5	PIP5K4	AT3G56960	1.41	0.50	3.39	0.012315	0.04412	-3.43
250122_at	unknown protein	---	AT5G16520	1.33	0.41	3.39	0.01232	0.04413	-3.43
265090_at	putative protein phosphatase 2A H	---	AT1G03960	1.31	0.39	3.39	0.012333	0.044168	-3.43
264368_at	hypothetical protein Contains simila	---	AT1G03280	1.29	0.37	3.39	0.012347	0.044211	-3.43
246611_at	putative protein predicted proteins,	MBD02	AT5G35330	1.61	0.69	3.39	0.012354	0.044232	-3.44
265006_at	unknown protein similar to small zin	TIM13	AT1G61570	1.86	0.90	3.39	0.012357	0.044235	-3.44
264038_at	putative ubiquinone biosynthesis pr	---	AT2G03690	-1.42	-0.51	-3.39	0.01236	0.044238	-3.44
261667_at	unknown protein similar to putative	---	AT1G18460	-1.47	-0.55	-3.39	0.012364	0.044246	-3.44
245036_at	putative SF16 protein {Helianthus a	Iqd4	AT2G26410	-1.26	-0.34	-3.39	0.012395	0.044347	-3.44
263808_at	hypothetical protein predicted by ge	---	AT2G04340	1.30	0.38	3.38	0.012398	0.044347	-3.44
250761_at	ankyrin-like protein	---	AT5G06050	-1.34	-0.42	-3.38	0.012401	0.044347	-3.44
260325_at	putative monodehydroascorbate re	MDAR6	AT1G63940	1.44	0.53	3.38	0.012402	0.044347	-3.44
251059_at	serine/threonine protein kinase ATF	CIPK15	AT5G01810	-2.10	-1.07	-3.38	0.012406	0.044354	-3.44
248346_at	GTP-binding protein-like ;supporte	ATGB1	AT5G52210	-1.59	-0.67	-3.38	0.012418	0.044384	-3.44
260855_at	phosphatidylinositol-4-phosphate 5	---	AT1G21920	1.49	0.57	3.38	0.012418	0.044384	-3.44
265506_at	putative non-LTR retroelement reve	---	---	-1.38	-0.47	-3.38	0.012442	0.044463	-3.44
251756_at	putative protein	---	AT3G55820	-1.27	-0.35	-3.38	0.012453	0.044493	-3.44
266416_at	unknown protein ; supported by full	---	AT2G38710	1.48	0.56	3.38	0.012455	0.044494	-3.44
260787_at	Ring3-like bromodomain protein sir	GTE4	AT1G06230	1.33	0.41	3.38	0.01246	0.044505	-3.44
246548_at	putative protein ;supported by full-l	---	AT5G14910	-1.33	-0.42	-3.38	0.012464	0.044513	-3.44
253721_at	hypothetical protein ;supported by	---	AT4G29250	-1.43	-0.51	-3.38	0.01248	0.044555	-3.45
260299_at	putative gibberellin 3 beta-hydroxyl	GA3OX4	AT1G80330	-1.24	-0.31	-3.38	0.01248	0.044555	-3.45
265715_s_a	expressed protein non-consensus C	---	AT1G13860	-1.66	-0.73	-3.38	0.012482	0.044555	-3.45

262631_at	hypothetical protein predicted by ge	---	AT1G06500	1.29	0.37	3.38	0.012487	0.044568	-3.45
266731_at	unknown protein	---	AT2G03260	-1.26	-0.33	-3.38	0.012495	0.044588	-3.45
266636_at	glycine decarboxylase complex H-p	GDCH	AT2G35370	-1.36	-0.44	-3.38	0.012503	0.044611	-3.45
248535_at	putative protein contains similarity t	---	AT5G50120	-1.40	-0.48	-3.38	0.012513	0.044639	-3.45
251042_at	eceriferum3 (CER3)	PRT6	AT5G02310	1.28	0.36	3.38	0.012521	0.044661	-3.45
246961_at	unknown protein	---	AT5G24710	-1.62	-0.70	-3.38	0.012526	0.04467	-3.45
261747_at	unknown protein similar to putative	---	AT1G08350	1.43	0.51	3.38	0.012533	0.044688	-3.45
255412_at	auxin-binding protein 1 precursor ;s	ABP1	AT4G02980	1.31	0.39	3.38	0.012537	0.044697	-3.45
247917_at	putative protein similar to unknown	BIO1	AT5G57590	-1.28	-0.35	-3.38	0.012541	0.044703	-3.45
259117_at	unknown protein similar to hypothe	SNL1	AT3G01320	1.28	0.36	3.38	0.012543	0.044703	-3.45
259234_at	unknown protein similar to unknown	---	AT3G11620	-1.33	-0.41	-3.38	0.012549	0.04472	-3.45
258888_at	putative pectinesterase similar to pe	---	AT3G05620	-1.59	-0.67	-3.38	0.012561	0.044747	-3.45
247108_at	ReMembR-H2 protein JR700 (gb|A	RMR1	AT5G66160	1.36	0.44	3.38	0.012561	0.044747	-3.45
245968_at	proline-rich protein extensins	---	AT5G19800	-1.39	-0.47	-3.37	0.01257	0.044767	-3.45
261661_at	lysophospholipase homolog, putati	---	AT1G18360	-1.55	-0.63	-3.37	0.012571	0.044767	-3.45
252249_at	putative protein heat shock protein	---	AT3G49770	-1.38	-0.46	-3.37	0.012579	0.044789	-3.45
262793_at	putative cytochrome P450 monoox	CYP71B7	AT1G13110	1.89	0.92	3.37	0.012586	0.044804	-3.46
246462_at	putative protein predicted protein, I	---	AT5G16940	-1.54	-0.63	-3.37	0.012587	0.044804	-3.46
247110_at	putative protein contains similarity t	---	AT5G65830	-1.46	-0.54	-3.37	0.012592	0.044813	-3.46
260141_at	gibberellin regulatory protein, putat	RGL1	AT1G66350	-2.71	-1.44	-3.37	0.012594	0.044813	-3.46
257252_at	glutathione reductase, cytosolic ide	ATGR1	AT3G24170	1.69	0.76	3.37	0.012595	0.044813	-3.46
249732_at	6-phosphogluconolactonase-like pr	---	AT5G24420	-7.75	-2.95	-3.37	0.012602	0.044832	-3.46
247716_at	putative protein predicted protein, A	---	AT5G59350	1.53	0.61	3.37	0.012607	0.044839	-3.46
258438_at	hypothetical protein predicted by ge	---	AT3G17230	-1.24	-0.31	-3.37	0.012608	0.044839	-3.46
250621_at	membrane protein membrane prot	ATRBL3	AT5G07250	-1.33	-0.41	-3.37	0.012613	0.044849	-3.46
256210_at	hypothetical protein	---	AT1G50950	2.19	1.13	3.37	0.012627	0.044884	-3.46
258458_at	Expressed protein ; supported by cl	---	AT3G22435	1.50	0.59	3.37	0.012627	0.044884	-3.46
248171_at	putative protein similar to unknown	ILR3	AT5G54680	1.26	0.33	3.37	0.012634	0.0449	-3.46
245962_at	putative protein predicted proteins -	---	AT5G19700	-1.33	-0.41	-3.37	0.012636	0.044902	-3.46
256061_at	unknown protein ;supported by full-	---	AT1G07040	1.56	0.64	3.37	0.012644	0.044925	-3.46
264537_at	receptor kinase, putative similar to	BRL1	AT1G55610	1.50	0.59	3.37	0.012655	0.044957	-3.46
266100_at	similar to axi 1 protein from Nicotiar	---	AT2G37980	1.59	0.67	3.37	0.012657	0.044957	-3.46
253592_at	hypothetical protein ;supported by f	---	AT4G30840	1.28	0.35	3.37	0.012678	0.045017	-3.46
250256_at	GTP-binding protein typA (tyrosine	---	AT5G13650	1.29	0.37	3.37	0.01268	0.045017	-3.46
253758_at	Expressed protein ;supported by cD	emb2726	AT4G29060	1.38	0.47	3.37	0.01268	0.045017	-3.46

265374_at	hypothetical protein ;supported by	PSBX	AT2G06520	-1.25	-0.33	-3.37	0.012712	0.045122	-3.47
253009_at	glycine hydroxymethyltransferase I	SHM1	AT4G37930	-1.44	-0.53	-3.37	0.012717	0.045132	-3.47
256440_at	unknown protein ;supported by full-	---	AT3G10970	1.28	0.36	3.37	0.012725	0.045156	-3.47
253456_at	putative protein norbin, Rattus norv	---	AT4G32050	1.41	0.49	3.36	0.012742	0.045207	-3.47
254186_at	putative protein cellulose synthase	CSLG1	AT4G24010	-1.32	-0.40	-3.36	0.012757	0.045247	-3.47
265464_at	putative myosin heavy chain	---	AT2G37080	1.25	0.32	3.36	0.01276	0.045251	-3.47
253219_at	MYB-like protein myb-related prote	AtMYB32	AT4G34990	1.63	0.71	3.36	0.012767	0.045269	-3.47
261605_at	CDPK-related protein kinase, putat	---	AT1G49580	-1.40	-0.48	-3.36	0.012772	0.045278	-3.47
247202_at	GTP-binding protein ; supported by	AtRABA4a	AT5G65270	-1.37	-0.45	-3.36	0.012773	0.045278	-3.47
253010_at	ovule development protein aintegur	ANT	AT4G37750	-1.34	-0.42	-3.36	0.012779	0.045284	-3.47
258771_at	unknown protein ;supported by full-	---	AT3G10770	1.32	0.40	3.36	0.012781	0.045284	-3.47
246451_at	Inositol 1,3,4-Trisphosphate 5/6 kir	---	AT5G16760	1.24	0.31	3.36	0.012781	0.045284	-3.47
247184_at	putative protein contains similarity t	UBP17	AT5G65450	-1.41	-0.49	-3.36	0.012786	0.045294	-3.47
264101_at	unknown protein similar to putative	HAC1	AT1G79000	1.37	0.46	3.36	0.012795	0.045319	-3.47
245043_at	putative cyclin ;supported by full-le	RCY1	AT2G26430	1.57	0.65	3.36	0.012808	0.045356	-3.47
265714_at	putative integral membrane protein	ATUPS4	AT2G03520	-1.25	-0.33	-3.36	0.012809	0.045356	-3.47
265222_at	putative endosomal protein ; suppo	---	AT2G01970	-1.24	-0.32	-3.36	0.012813	0.045358	-3.47
251451_s_a	putative protein several hypothetica	---	AT3G60040	1.32	0.40	3.36	0.012814	0.045358	-3.47
265512_at	hypothetical protein predicted by ge	---	AT2G05590	-1.41	-0.49	-3.36	0.012817	0.04536	-3.47
267510_at	unknown protein ; supported by ful	SAP18	AT2G45640	1.43	0.52	3.36	0.012827	0.045389	-3.48
251758_at	transcription factor L2 ;supported b	---	AT3G55770	1.33	0.42	3.36	0.012836	0.045413	-3.48
248839_at	putative protein contains similarity t	bHLH071	AT5G46690	-2.03	-1.02	-3.36	0.012846	0.045445	-3.48
248187_at	zinc-binding protein-like ; supporte	---	AT5G53940	1.33	0.41	3.36	0.012853	0.045462	-3.48
251749_at	putative protein predicted proteins,	---	AT3G55690	-1.28	-0.35	-3.36	0.012858	0.045472	-3.48
257699_at	phosphoglycerate kinase, putative	PGK1	AT3G12780	-1.39	-0.47	-3.36	0.012867	0.045488	-3.48
245401_at	hypothetical protein ;supported by f	---	AT4G17670	2.03	1.02	3.36	0.012873	0.045504	-3.48
256752_at	hypothetical protein predicted by ge	---	AT3G27180	1.57	0.65	3.36	0.012876	0.045506	-3.48
246050_s_a	protein phosphatase 2A regulatory	---	AT5G28850	1.24	0.31	3.36	0.012881	0.045516	-3.48
254806_at	putative trehalose-6-phosphate pho	---	AT4G12430	1.32	0.40	3.36	0.01289	0.045538	-3.48
253955_at	putative DNA binding protein DNA	ATRBP45C	AT4G27000	1.50	0.59	3.36	0.012891	0.045538	-3.48
262170_at	hypothetical protein predicted by ge	---	AT1G74940	1.51	0.59	3.36	0.012895	0.045538	-3.48
264173_at	unknown protein	---	AT1G02160	1.28	0.36	3.36	0.012895	0.045538	-3.48
261895_at	metal ion transporter identical to GE	NRAMP1	AT1G80830	1.92	0.94	3.36	0.012901	0.045552	-3.48
251880_at	hypothetical protein ;supported by	---	AT3G54290	1.43	0.52	3.35	0.012909	0.045575	-3.48
247636_at	putative protein predicted proteins f	---	AT5G60570	-1.30	-0.38	-3.35	0.012915	0.045586	-3.48

266585_at	putative retroelement pol polyprotei	---	---	-1.37	-0.46	-3.35	0.012916	0.045586	-3.48
252911_at	cytochrome P450 -like protein cyto	CYP96A12	AT4G39510	-2.08	-1.05	-3.35	0.012927	0.045615	-3.48
254298_at	putative protein ;supported by full-l	PGR5-LIKE	AT4G22890	-1.42	-0.51	-3.35	0.012933	0.045627	-3.48
264999_at	hypothetical protein contains simila	---	AT1G67310	1.28	0.36	3.35	0.012934	0.045627	-3.48
261670_at	hypothetical protein contains simila	TET11	AT1G18520	-1.24	-0.31	-3.35	0.012942	0.045645	-3.48
250653_at	putative protein strong similarity to	---	AT5G06930	-1.87	-0.90	-3.35	0.012945	0.045645	-3.49
247628_at	putative protein	---	AT5G60400	-1.45	-0.53	-3.35	0.012945	0.045645	-3.49
266224_at	chloroplast membrane protein (ALB	ALB3	AT2G28800	-1.26	-0.33	-3.35	0.012961	0.045693	-3.49
247127_at	putative protein similar to unknown	---	AT5G66100	-1.29	-0.36	-3.35	0.012965	0.0457	-3.49
254042_at	xyloglucan endo-1,4-beta-D-glucar	XTR6	AT4G25810	-3.54	-1.82	-3.35	0.012974	0.045726	-3.49
246552_at	putative protein	---	AT5G15420	-1.71	-0.77	-3.35	0.012985	0.045759	-3.49
265959_at	unknown protein ;supported by full-	---	AT2G37240	-1.78	-0.83	-3.35	0.01299	0.045769	-3.49
266591_at	expressed protein supported by cD	ABIL1	AT2G46225	-1.55	-0.63	-3.35	0.012996	0.045784	-3.49
262148_at	chloroplast-localized small heat sh	---	AT1G52560	1.79	0.84	3.35	0.013009	0.045821	-3.49
249317_at	glutathione transferase	ATGSTT2	AT5G41240	-1.29	-0.37	-3.35	0.013018	0.045847	-3.49
263551_at	hypothetical protein contains NLS (	---	AT2G17110	1.75	0.81	3.35	0.013028	0.045873	-3.49
258189_at	unknown protein ;supported by full-	JAZ3	AT3G17860	-1.68	-0.75	-3.35	0.013032	0.045876	-3.49
258238_at	unknown protein	RST1	AT3G27670	1.25	0.32	3.35	0.013033	0.045876	-3.49
245792_at	pinoresinol-lariciresinol reductase,	PRR1	AT1G32100	-2.30	-1.20	-3.35	0.013044	0.04591	-3.49
260626_at	storage protein, putative similar to	---	AT1G08040	-1.35	-0.44	-3.35	0.013049	0.045921	-3.49
245949_at	elongation factor 1B alpha-subunit	---	AT5G19510	1.42	0.50	3.35	0.013056	0.045938	-3.49
252574_at	receptor like protein kinase recepto	---	AT3G45430	-1.33	-0.42	-3.35	0.013068	0.045972	-3.50
264625_at	hypothetical protein Contains simila	SNF4	AT1G09020	-1.30	-0.38	-3.34	0.013093	0.046052	-3.50
252716_at	putative protein CAF protein, Arabi	DCL3	AT3G43920	1.39	0.47	3.34	0.013119	0.046138	-3.50
263556_at	hypothetical protein predicted by ge	---	AT2G16365	1.36	0.44	3.34	0.013137	0.046193	-3.50
246929_at	putative protein ; supported by full-	---	AT5G25210	-1.43	-0.52	-3.34	0.013153	0.046243	-3.50
263158_at	CCAAT-binding factor B subunit, p	NF-YA5	AT1G54160	-1.30	-0.38	-3.34	0.013161	0.046264	-3.50
251251_at	serine/threonine protein kinase-like	---	AT3G62220	-1.34	-0.42	-3.34	0.013168	0.046281	-3.50
264535_at	Phosphatidylinositol Transfer Prote	---	AT1G55690	-1.99	-1.00	-3.34	0.013174	0.046293	-3.50
263570_at	aldehyde oxidase identical to GP:31	AAO3	AT2G27150	1.58	0.66	3.34	0.013185	0.046325	-3.50
250570_at	putative protein hypothetical bacter	EMB1873	AT5G08170	1.44	0.52	3.34	0.01319	0.046327	-3.51
257251_at	type 1 membrane protein, putative	PMP	AT3G24160	-1.31	-0.39	-3.34	0.013191	0.046327	-3.51
249208_at	allene oxide synthase (emb CAA73	AOS	AT5G42650	-2.12	-1.08	-3.34	0.013191	0.046327	-3.51
249088_at	selenium-binding protein-like	---	AT5G44230	1.45	0.54	3.34	0.0132	0.04635	-3.51
253095_at	putative protein ribonuclease III, Ba	---	AT4G37510	1.32	0.40	3.34	0.013218	0.046402	-3.51

259577_at	unknown protein	---	AT1G35340	-1.41	-0.50	-3.34	0.013219	0.046402	-3.51
265319_at	auxin-regulated protein (IAA8) ;sup	IAA8	AT2G22670	-1.72	-0.79	-3.34	0.013243	0.046472	-3.51
249911_at	glucosyltransferase-like protein ; su	CSLA02	AT5G22740	-2.67	-1.42	-3.33	0.013255	0.046506	-3.51
267362_at	hypothetical protein predicted by ge	---	AT2G39910	1.25	0.32	3.33	0.013276	0.046575	-3.51
245786_at	G-Box binding protein, putative sim	---	AT1G32150	-1.23	-0.30	-3.33	0.01328	0.04658	-3.51
252352_at	Expressed protein ; supported by fu	---	AT3G48185	1.41	0.50	3.33	0.013287	0.0466	-3.51
247654_at	cytoplasmic ribosomal protein S15	---	AT5G59850	1.94	0.96	3.33	0.013292	0.046609	-3.51
254628_at	Expressed protein ; supported by fu	---	AT4G18593	1.23	0.30	3.33	0.013302	0.046635	-3.51
261041_at	hypothetical protein contains simila	EER4	AT1G17440	1.31	0.39	3.33	0.013304	0.046635	-3.51
250395_at	putative protein cylicin II, bovine, P	---	AT5G10950	1.51	0.60	3.33	0.013305	0.046635	-3.51
265799_at	unknown protein ; supported by cD	---	AT2G35680	1.34	0.43	3.33	0.013316	0.046663	-3.52
260006_at	phosphatidylinositol synthase (PIS1	ATPIS1	AT1G68000	-1.23	-0.30	-3.33	0.013329	0.046702	-3.52
252575_at	receptor like protein kinase recepto	---	AT3G45440	-1.45	-0.54	-3.33	0.013341	0.046737	-3.52
248807_at	pectin methylesterase-like	---	AT5G47500	-1.22	-0.28	-3.33	0.013356	0.046783	-3.52
250950_at	putative protein	ATEXO70A	AT5G03540	-1.39	-0.47	-3.33	0.013359	0.046786	-3.52
249256_at	putative protein strong similarity to	---	AT5G41620	1.45	0.54	3.33	0.013362	0.046789	-3.52
260853_at	hypothetical protein predicted by ge	---	AT1G21950	-1.48	-0.57	-3.33	0.013366	0.046796	-3.52
248971_at	putative protein contains similarity t	---	AT5G45000	-1.53	-0.61	-3.33	0.01337	0.046803	-3.52
251445_at	putative protein hypothetical protei	---	AT3G59870	-1.25	-0.32	-3.33	0.013389	0.046857	-3.52
263209_at	Expressed protein ; supported by fu	---	AT1G10522	1.70	0.76	3.33	0.01339	0.046857	-3.52
256881_at	hypothetical protein ; supported by	---	AT3G26410	1.30	0.38	3.33	0.013398	0.046881	-3.52
245650_at	F5A9.20 similar to S-adenosyl-L-me	---	AT1G24735	-1.34	-0.42	-3.33	0.013404	0.046895	-3.52
249254_at	unknown protein	---	AT5G42110	-1.32	-0.40	-3.33	0.013407	0.046896	-3.52
260156_at	NAM-like protein similar to NAM (no	NAM	AT1G52880	1.58	0.66	3.33	0.01342	0.046933	-3.52
253425_at	putative protein myosin heavy chai	---	AT4G32190	-1.57	-0.65	-3.32	0.013429	0.046954	-3.52
261498_at	receptor kinase, putative similar to	HSL1	AT1G28440	-1.42	-0.50	-3.32	0.01343	0.046954	-3.52
261584_at	CAF protein identical to RNA helica	DCL1	AT1G01040	1.47	0.55	3.32	0.013445	0.046999	-3.53
249876_at	putative protein similar to unknown	CaS	AT5G23060	-1.38	-0.47	-3.32	0.013457	0.047037	-3.53
247025_at	zeaxanthin epoxidase precursor ; s	ABA1	AT5G67030	-1.40	-0.48	-3.32	0.013467	0.047062	-3.53
249734_at	putative protein strong similarity to	IRE1-1	AT5G24360	-1.24	-0.31	-3.32	0.013484	0.047113	-3.53
252241_at	putative protein CND41, chloroplas	---	AT3G50050	-1.31	-0.39	-3.32	0.013485	0.047113	-3.53
258196_at	hypothetical protein predicted by ge	---	AT3G13980	-2.24	-1.16	-3.32	0.013498	0.047145	-3.53
265195_at	hypothetical protein	---	AT2G36730	1.26	0.33	3.32	0.013499	0.047145	-3.53
253542_at	putative protein deubiquitinating en	UBP18	AT4G31670	1.29	0.37	3.32	0.013501	0.047145	-3.53
256155_at	MYB-family transcription factor, pu	MYB83	AT3G08500	-1.26	-0.33	-3.32	0.013508	0.047163	-3.53

263956_at	putative homeodomain transcriptior	BLH1	AT2G35940	1.62	0.69	3.32	0.013513	0.047172	-3.53
257809_at	ribonucleotide reductase small sub	TSO2	AT3G27060	-1.47	-0.56	-3.32	0.013518	0.047184	-3.53
253847_at	putative protein CRP1, Zea mays,	---	AT4G28010	1.29	0.36	3.32	0.01352	0.047184	-3.53
245627_at	water stress-induced protein, putat	AtGolS2	AT1G56600	1.77	0.83	3.32	0.013525	0.047194	-3.53
258570_at	phosphoenolpyruvate carboxylase	PPCK2	AT3G04530	1.39	0.47	3.32	0.013527	0.047194	-3.53
253098_at	cytochrome P450-like protein	CYP81D3	AT4G37340	-1.35	-0.44	-3.32	0.013532	0.047204	-3.53
255913_at	kinase, putative similar to leaf rust	---	AT1G66980	1.24	0.30	3.32	0.013541	0.047228	-3.53
247014_at	RuvB DNA helicase-like protein ; s	---	AT5G67630	1.72	0.78	3.32	0.013544	0.04723	-3.53
260929_at	transcription factor TFIID, putative	TAF13	AT1G02680	1.48	0.57	3.32	0.013549	0.04724	-3.53
264329_at	unknown protein Contains similarit	---	AT1G04140	1.26	0.34	3.32	0.013555	0.047257	-3.53
248364_at	fibrillarin 3 (AtFib3) similar to fibrilla	---	AT5G52490	-1.26	-0.33	-3.32	0.013568	0.047294	-3.54
259733_at	nucellin-like protein similar to nucell	---	AT1G77480	1.56	0.64	3.32	0.013576	0.047313	-3.54
258683_at	putative protein kinase contains Pfa	ATSIK	AT3G08760	1.61	0.69	3.32	0.01358	0.047319	-3.54
261678_at	disease resistance protein, putative	---	AT1G47370	-1.35	-0.44	-3.32	0.013585	0.04733	-3.54
246763_at	NHE1 Na+/H+ exchanger ; suppor	NHX1	AT5G27150	1.56	0.64	3.32	0.013588	0.047333	-3.54
247287_at	unknown protein ; supported by cD	---	AT5G64230	1.65	0.72	3.32	0.013595	0.047345	-3.54
265717_at	unknown protein ;supported by full-	---	AT2G03510	1.40	0.49	3.32	0.013596	0.047345	-3.54
260552_at	putative glyoxalase II ; supported b	GLX2-1	AT2G43430	-1.25	-0.32	-3.32	0.013598	0.047345	-3.54
261538_at	unknown protein ; supported by cDI	---	AT1G01830	1.74	0.80	3.32	0.0136	0.047345	-3.54
253792_at	ammonium transporter - like protei	AMT1;4	AT4G28700	-1.38	-0.47	-3.32	0.013603	0.047351	-3.54
251785_at	ABC transporter - like protein breas	ATWBC19	AT3G55130	-1.78	-0.83	-3.32	0.013608	0.047359	-3.54
248534_at	putative protein contains similarity t	---	AT5G50030	-1.28	-0.36	-3.31	0.013615	0.047376	-3.54
246513_at	hypothetical protein	---	AT5G15680	1.26	0.33	3.31	0.013623	0.047396	-3.54
264804_at	putative receptor kinase, CLV1 sim	---	AT1G08590	-1.37	-0.46	-3.31	0.013625	0.047396	-3.54
260684_at	transcription factor, putative similar	NF-YA8	AT1G17590	1.45	0.53	3.31	0.013637	0.047432	-3.54
252707_at	transporter-like protein multidrug-e	ZIFL2	AT3G43790	1.39	0.47	3.31	0.013645	0.047454	-3.54
245989_s_a	polyubiquitin (UBQ4) identical to GI	UBQ4	AT5G20620	1.33	0.41	3.31	0.013662	0.047504	-3.54
263853_at	putative mutT domain protein	---	AT2G04440	-1.47	-0.56	-3.31	0.013686	0.047579	-3.54
264560_at	hypothetical protein predicted by ge	---	AT1G55820	1.26	0.34	3.31	0.013691	0.047586	-3.54
255560_at	hypothetical protein similar to C. el	---	AT4G02030	-1.25	-0.32	-3.31	0.013694	0.047586	-3.55
247904_at	putative protein contains similarity t	AIL5	AT5G57390	-1.41	-0.49	-3.31	0.013696	0.047586	-3.55
264023_at	Expressed protein ; supported by fu	---	AT2G21195	1.58	0.66	3.31	0.013696	0.047586	-3.55
260527_at	unknown protein ;supported by full-	---	AT2G47270	2.58	1.37	3.31	0.013703	0.047605	-3.55
251528_at	putative protein hypothetical protei	---	AT3G58600	-1.37	-0.46	-3.31	0.013715	0.047639	-3.55
250740_at	t-SNARE SED5 (gb|AAC06291.1)	SYP31	AT5G05760	-1.25	-0.32	-3.31	0.013723	0.04766	-3.55

247977_at	putative protein similar to unknown	---	AT5G56850	-1.44	-0.53	-3.31	0.013743	0.047705	-3.55
250220_at	receptor protein kinase-like protein	---	AT5G14210	-1.80	-0.85	-3.31	0.013758	0.047744	-3.55
266323_at	putative calcium-dependent protein	CRK3	AT2G46700	-1.32	-0.40	-3.31	0.013758	0.047744	-3.55
261969_at	hypothetical protein contains simila	---	AT1G65950	1.26	0.34	3.31	0.01377	0.047777	-3.55
262459_at	hypothetical protein similar to hypot	---	AT1G50400	1.43	0.51	3.31	0.013775	0.047787	-3.55
260167_at	hypothetical protein predicted by ge	---	AT1G71970	1.36	0.44	3.31	0.013786	0.047818	-3.55
265550_at	hypothetical protein predicted by ge	---	---	-1.30	-0.37	-3.31	0.013789	0.047818	-3.55
260553_at	unknown protein similar to T11A07.	---	AT2G41800	-1.27	-0.35	-3.31	0.01379	0.047818	-3.55
260365_at	hypothetical protein predicted by ge	---	AT1G70630	-1.31	-0.39	-3.30	0.013795	0.047827	-3.55
261169_at	sucrose-phosphate synthase, puta	ATSPS3F	AT1G04920	-1.33	-0.42	-3.30	0.013799	0.047828	-3.55
248771_at	unknown protein	---	AT5G47790	1.37	0.45	3.30	0.013801	0.047828	-3.55
264775_at	putative endo-1,4-beta-D-glucanas	CEL5	AT1G22880	-1.38	-0.46	-3.30	0.01381	0.047851	-3.55
247747_at	putative protein predicted proteins,	---	AT5G59000	-1.43	-0.51	-3.30	0.01382	0.047875	-3.55
245064_at	Expressed protein ; supported by fu	---	AT2G39725	1.58	0.66	3.30	0.013821	0.047875	-3.55
255579_at	putative bHLH DNA-binding protein	---	AT4G01460	-1.75	-0.81	-3.30	0.013852	0.047976	-3.56
264168_at	unknown protein Similar to yeast ge	---	AT1G02080	1.33	0.41	3.30	0.013855	0.047977	-3.56
263756_at	putative ubiquitin fusion-degradatio	---	AT2G21270	1.24	0.32	3.30	0.013877	0.048047	-3.56
254492_at	endomembrane-associated protein	PCAP1	AT4G20260	1.33	0.41	3.30	0.013881	0.048054	-3.56
266450_s_a	hypothetical protein predicted by ge	---	AT2G43190	1.44	0.53	3.30	0.013887	0.048062	-3.56
259649_at	Serine/arginine-rich protein, putativ	TAF7	AT1G55300	-1.29	-0.36	-3.30	0.013888	0.048062	-3.56
251103_at	putative protein protein phosphatas	---	AT5G01700	-1.43	-0.52	-3.30	0.013893	0.04807	-3.56
253905_s_a	putative protein retrotransposon O	---	---	-1.23	-0.30	-3.30	0.013894	0.04807	-3.56
267172_at	unknown protein ;supported by full-	---	AT2G37660	-1.40	-0.49	-3.30	0.013905	0.048101	-3.56
258446_at	hypothetical protein predicted by ge	---	AT3G22430	1.28	0.36	3.30	0.013927	0.048163	-3.56
250042_at	putative protein non-consensus GC	---	AT5G18420	1.30	0.37	3.30	0.013938	0.048191	-3.56
259570_at	hypothetical protein	COR47	AT1G20440	-1.66	-0.73	-3.30	0.01395	0.048228	-3.56
245459_at	hypothetical protein	---	---	-1.49	-0.58	-3.30	0.013956	0.048237	-3.57
254362_at	Expressed protein ; supported by fu	---	AT4G22160	-1.44	-0.53	-3.30	0.013957	0.048237	-3.57
265038_at	putative protein kinase highly simila	---	AT1G03920	-1.31	-0.39	-3.30	0.013965	0.048248	-3.57
263000_at	hypothetical protein similar to hypot	---	AT1G54350	-1.34	-0.42	-3.30	0.013966	0.048248	-3.57
246061_at	RAN GTPase activating protein 2 ;	RANGAP2	AT5G19320	1.22	0.29	3.30	0.013968	0.048248	-3.57
250229_at	putative protein contains similarity t	NACA3	AT5G13850	1.56	0.64	3.30	0.013969	0.048248	-3.57
257954_at	putative UDP-glucose glucosyltrans	---	AT3G21760	1.35	0.43	3.30	0.013976	0.048263	-3.57
260134_at	Myb-related transcription factor, pu	MYB113	AT1G66370	-1.40	-0.49	-3.30	0.013977	0.048263	-3.57
263864_at	hypothetical protein predicted by ge	CPZ	AT2G04530	1.32	0.40	3.29	0.013982	0.048267	-3.57

266053_at	unknown protein	---	AT2G40730	-1.33	-0.41	-3.29	0.013987	0.048273	-3.57
255814_at	unknown protein	---	AT1G19900	-1.27	-0.34	-3.29	0.013994	0.048283	-3.57
261752_at	putative AMP-binding protein conta	---	AT1G76290	-1.31	-0.39	-3.29	0.013994	0.048283	-3.57
256939_at	multicatalytic endopeptidase comp	PBD1	AT3G22630	1.46	0.54	3.29	0.014011	0.048336	-3.57
254616_at	shaggy-like protein kinase etha (EC	BIN2	AT4G18710	-1.28	-0.36	-3.29	0.014034	0.048406	-3.57
249303_at	putative protein strong similarity to u	---	AT5G41460	-1.51	-0.60	-3.29	0.014048	0.048447	-3.57
264883_s_a	secretory carrier membrane protein	---	AT1G11180	1.29	0.37	3.29	0.014076	0.048539	-3.57
261676_at	Expressed protein ; supported by fu	---	AT1G18480	1.39	0.47	3.29	0.014083	0.048556	-3.57
246180_at	putative protein predicted proteins,	---	AT5G20840	-1.28	-0.35	-3.29	0.014094	0.048583	-3.58
261174_at	26S proteasome regulatory subuni	---	AT1G04810	1.37	0.45	3.29	0.014096	0.048583	-3.58
255931_at	hypothetical protein similar to putati	AtPP2-A12	AT1G12710	-1.56	-0.65	-3.29	0.014098	0.048583	-3.58
248268_at	importin beta	---	AT5G53480	-1.37	-0.45	-3.29	0.014105	0.0486	-3.58
249551_at	putative protein predicted proteins,	---	AT5G38220	1.39	0.47	3.29	0.014117	0.048618	-3.58
255739_at	unknown protein similar to hypothet	ANAC008	AT1G25580	1.44	0.53	3.29	0.014118	0.048618	-3.58
251414_at	hypothetical protein	---	AT3G60370	-1.39	-0.48	-3.29	0.014118	0.048618	-3.58
248472_at	cyclin-dependent protein kinase-like	---	AT5G50860	1.33	0.42	3.29	0.014119	0.048618	-3.58
262432_at	unknown protein	---	AT1G47530	1.65	0.72	3.29	0.014121	0.048621	-3.58
257804_at	protein kinase, putative similar to s	---	AT3G18810	-1.26	-0.34	-3.29	0.014124	0.048621	-3.58
255696_at	putative nucleotide sugar epimeras	GAE3	AT4G00110	-1.33	-0.41	-3.29	0.014131	0.048639	-3.58
264735_s_a	hypothetical protein similar to hypot	---	AT1G62000	-1.40	-0.49	-3.29	0.014144	0.048676	-3.58
246730_at	40S ribosomal protein S19 - like 40	---	AT5G28060	1.61	0.69	3.29	0.014151	0.048682	-3.58
258884_at	threonine dehydratase/deaminase	OMR1	AT3G10050	1.64	0.72	3.29	0.014152	0.048682	-3.58
245672_at	polygalacturonase, putative similar	---	AT1G56710	1.42	0.51	3.29	0.014154	0.048682	-3.58
252161_at	proline-rich protein	---	AT3G50580	-1.22	-0.29	-3.29	0.014157	0.048682	-3.58
258916_at	putative ABC transporter ATPase s	ATNAP7	AT3G10670	-1.28	-0.36	-3.29	0.014159	0.048682	-3.58
263223_at	coatomer-like protein, epsilon subu	---	AT1G30630	-1.34	-0.42	-3.29	0.01416	0.048682	-3.58
263804_at	putative protein kinase contains a p	---	AT2G40270	-1.39	-0.48	-3.29	0.014164	0.048685	-3.58
248064_at	unknown protein	---	AT5G55570	-1.93	-0.95	-3.28	0.014204	0.048815	-3.58
250688_at	transcription factor-like protein ;sup	NF-YA10	AT5G06510	1.27	0.34	3.28	0.014213	0.048829	-3.58
246015_at	putative protein predicted proteins,	---	AT5G10700	-1.28	-0.35	-3.28	0.014214	0.048829	-3.58
253457_at	putative protein C56A3.6,Caenorha	---	AT4G32060	-1.35	-0.43	-3.28	0.014222	0.04885	-3.59
255752_at	secretory carrier membrane protein	---	AT1G32050	-1.41	-0.50	-3.28	0.014232	0.048856	-3.59
252242_at	F-box protein family, AtFBL16 cont	VFB2	AT3G50080	1.32	0.40	3.28	0.014233	0.048856	-3.59
259215_at	unknown protein largely predicted b	DEX1	AT3G09090	1.27	0.35	3.28	0.014236	0.048856	-3.59
261699_at	hypothetical protein identical to hyp	---	AT1G32660	-1.33	-0.41	-3.28	0.014236	0.048856	-3.59

255003_at	AIG1-like protein AIG1 - Arabidops	---	AT4G09950	-1.26	-0.33	-3.28	0.014237	0.048856	-3.59
247793_at	putative protein ; supported by cDN	PSY1	AT5G58650	1.48	0.56	3.28	0.014242	0.048861	-3.59
245080_at	putative receptor-like protein kinase	---	AT2G23300	-1.44	-0.53	-3.28	0.014268	0.048941	-3.59
253738_at	photosystem I subunit PSI-E - like	PSAE-1	AT4G28750	-1.22	-0.29	-3.28	0.014274	0.048954	-3.59
256766_at	Expressed protein ; supported by cl	PCC1	AT3G22231	-13.63	-3.77	-3.28	0.014276	0.048954	-3.59
245116_at	unknown protein ; supported by cD	---	AT2G41620	1.72	0.78	3.28	0.014286	0.048978	-3.59
253755_at	26S proteasome subunit 4-like pro	RPT2a	AT4G29040	1.31	0.39	3.28	0.014288	0.048979	-3.59
245320_at	Expressed protein ; supported by fu	---	AT4G16444	1.27	0.35	3.28	0.014294	0.048994	-3.59
247965_at	putative protein similar to unknown	AGP14	AT5G56540	-1.53	-0.61	-3.28	0.014302	0.049013	-3.59
245458_at	kinase like protein	---	AT4G16970	-1.30	-0.38	-3.28	0.014308	0.049024	-3.59
265914_at	En/Spm-like transposon protein rela	---	---	-1.24	-0.31	-3.28	0.01431	0.049024	-3.59
246826_at	UTP-glucose glucosyltransferase -	UGT72E3	AT5G26310	-1.29	-0.37	-3.28	0.014319	0.04905	-3.59
251288_at	exonuclease RRP41 ; supported b	RRP41	AT3G61620	1.44	0.52	3.28	0.014322	0.049053	-3.59
245194_at	F12A21.5 similar to protein phospha	---	AT1G67820	1.61	0.69	3.28	0.014332	0.049077	-3.59
261500_at	hypothetical protein predicted by ge	---	AT1G28400	1.99	0.99	3.28	0.014335	0.049081	-3.59
251964_at	hypothetical protein ; supported by	---	AT3G53370	-1.53	-0.61	-3.28	0.014338	0.049083	-3.59
253482_at	Expressed protein ; supported by cl	---	AT4G31985	1.96	0.97	3.28	0.014342	0.049091	-3.59
245517_at	hypothetical protein	---	AT4G15840	1.22	0.28	3.28	0.014348	0.049102	-3.59
247517_at	100 kDa coactivator - like protein 1	---	AT5G61780	-1.38	-0.46	-3.28	0.014352	0.049111	-3.60
253921_at	glutamine amidotransferase/cyclase	AT-HF	AT4G26900	1.34	0.42	3.28	0.014359	0.049127	-3.60
265905_at	putative transcription elongation fac	---	AT2G25640	-1.24	-0.31	-3.27	0.01438	0.049188	-3.60
262730_at	putative transport protein may be a	ATOCT3	AT1G16390	-1.34	-0.42	-3.27	0.014384	0.049188	-3.60
262760_at	hypothetical protein contains simila	---	AT1G10770	2.38	1.25	3.27	0.014385	0.049188	-3.60
251820_at	putative protein In2-1 protein, Zea	GSTL2	AT3G55040	-1.72	-0.78	-3.27	0.014386	0.049188	-3.60
245930_at	transcriptional co-activator-like pro	---	AT5G09240	-1.53	-0.61	-3.27	0.014389	0.049188	-3.60
251723_at	putative protein speckle-type prote	---	AT3G56230	-1.36	-0.45	-3.27	0.01439	0.049188	-3.60
249958_at	plasma membrane associated prot	---	AT5G18970	-1.44	-0.52	-3.27	0.014398	0.049208	-3.60
258772_at	putative ubiquinol-cytochrome C re	---	AT3G10860	1.37	0.45	3.27	0.014403	0.04922	-3.60
248423_at	putative protein contains similarity t	---	AT5G51670	-1.51	-0.59	-3.27	0.014409	0.04923	-3.60
261933_at	3-deoxy-D-arabino-heptulosonate	---	AT1G22410	1.71	0.78	3.27	0.014419	0.049257	-3.60
253303_at	putative protein ; supported by full-	---	AT4G33780	1.31	0.39	3.27	0.014431	0.049291	-3.60
249094_at	dimethylaniline monooxygenase-lik	YUC5	AT5G43890	-1.38	-0.46	-3.27	0.01444	0.049314	-3.60
259653_at	unknown protein	---	AT1G55240	-1.24	-0.31	-3.27	0.014444	0.049322	-3.60
262588_at	unknown protein Similar to gb|AJ0	---	AT1G15130	-1.31	-0.39	-3.27	0.014455	0.049342	-3.60
255775_at	hypothetical protein predicted by ge	RBL12	AT1G18600	-1.28	-0.36	-3.27	0.014462	0.049342	-3.60

267461_at	putative auxin-regulated protein ;su	---	AT2G33830	1.37	0.45	3.27	0.014464	0.049342	-3.60
251562_at	putative protein hypothetical protei	---	AT3G57890	-1.28	-0.35	-3.27	0.014465	0.049342	-3.60
247508_at	auxin response factor - like protein	ARF2	AT5G62000	-1.46	-0.55	-3.27	0.014465	0.049342	-3.60
256060_at	hypothetical protein contains simila	---	AT1G07050	1.51	0.59	3.27	0.014465	0.049342	-3.60
254913_at	putative protein beta-transducin re	---	AT4G11270	1.28	0.36	3.27	0.014471	0.049353	-3.60
253160_at	putative protein predicted protein,	---	AT4G35760	1.50	0.59	3.27	0.014478	0.049373	-3.60
250812_at	putative protein similar to unknown	---	AT5G04900	1.27	0.35	3.27	0.014485	0.049386	-3.60
262923_at	Dhp1-like protein similar to Dhp1 pr	XRN3	AT1G75660	1.29	0.37	3.27	0.014488	0.04939	-3.61
251170_at	ATMRK1 ;supported by full-length	ATMRK1	AT3G63260	1.23	0.30	3.27	0.014495	0.049404	-3.61
253240_at	putative ketoacyl-CoA synthase fat	KCS17	AT4G34510	-1.25	-0.32	-3.27	0.014496	0.049404	-3.61
248890_at	disease resistance protein-like	---	AT5G46270	1.28	0.35	3.27	0.014516	0.049464	-3.61
246407_at	disease resistance protein RPS4, p	---	AT1G57670	-1.24	-0.31	-3.27	0.014518	0.049464	-3.61
264441_at	Expressed protein ; supported by fu	---	AT1G27435	1.36	0.44	3.27	0.014522	0.049464	-3.61
254096_at	acid phosphatase - like protein acid	---	AT4G25150	-1.33	-0.41	-3.27	0.014525	0.049464	-3.61
264289_at	hypothetical protein similar to hypot	---	AT1G61890	-1.98	-0.99	-3.27	0.014527	0.049464	-3.61
247107_at	senescence-associated protein alm	STR16	AT5G66040	1.53	0.61	3.27	0.014527	0.049464	-3.61
266604_at	E2, ubiquitin-conjugating enzyme 6	UBC6	AT2G46030	-1.63	-0.71	-3.27	0.014541	0.049504	-3.61
257973_at	unknown protein	---	AT3G20720	1.38	0.46	3.27	0.01455	0.049525	-3.61
257376_at	hypothetical protein predicted by ge	---	AT2G32350	-1.31	-0.39	-3.27	0.014552	0.049525	-3.61
251088_at	putative protein several hypothetica	---	AT5G01480	-1.48	-0.57	-3.27	0.014553	0.049525	-3.61
256876_at	hypothetical protein predicted by ge	---	AT3G26360	1.22	0.28	3.26	0.014557	0.049527	-3.61
248637_at	DNAJ-like protein	---	AT5G49060	1.28	0.35	3.26	0.014559	0.049527	-3.61
260313_at	putative disease resistance protein	---	AT1G63870	-1.39	-0.47	-3.26	0.014568	0.049548	-3.61
257679_at	glycine-rich protein, putative identic	GRP5	AT3G20470	-2.30	-1.20	-3.26	0.014569	0.049548	-3.61
264003_at	Expressed protein ; supported by fu	GEM	AT2G22475	-1.40	-0.49	-3.26	0.014593	0.049623	-3.61
245228_at	phytochelatin synthetase-like protei	COBL2	AT3G29810	-1.85	-0.89	-3.26	0.0146	0.049638	-3.61
250212_at	putative protein contains similarity t	SUVH4	AT5G13960	1.31	0.39	3.26	0.014608	0.049659	-3.61
251139_at	cell division - like protein JM23 pro	---	AT5G01230	1.38	0.46	3.26	0.014613	0.049661	-3.61
254483_at	putative protein CRP1, Zea mays,	---	AT4G20740	1.43	0.52	3.26	0.014613	0.049661	-3.61
257108_x_a	hypothetical protein	---	---	-1.25	-0.32	-3.26	0.014617	0.049667	-3.61
264025_at	AUX1-like amino acid permease ; s	---	AT2G21050	-2.44	-1.29	-3.26	0.014621	0.04967	-3.61
250895_at	RIBOSOMAL PROTEIN S28- like r	---	AT5G03850	1.51	0.60	3.26	0.014622	0.04967	-3.61
249290_at	putative protein strong similarity to u	---	AT5G41060	-1.58	-0.66	-3.26	0.014631	0.049692	-3.62
260334_at	homeotic protein (ATK1) identical to	KNAT2	AT1G70510	-1.26	-0.33	-3.26	0.014639	0.049712	-3.62
260999_at	hypothetical protein similar to putati	---	AT1G26580	1.26	0.33	3.26	0.014672	0.049816	-3.62

247289_at	2-oxoglutarate/malate translocator	DIT2.1	AT5G64290	-1.38	-0.46	-3.26	0.014676	0.049816	-3.62
262736_at	lipase, putative contains Pfam prof	---	AT1G28570	1.28	0.35	3.26	0.014676	0.049816	-3.62
248982_at	chloroplast nucleoid DNA-binding p	---	AT5G45120	-1.32	-0.40	-3.26	0.014682	0.049818	-3.62
264553_s_a	putative cinnamyl alcohol dehydrog	---	AT1G09480	1.36	0.45	3.26	0.014683	0.049818	-3.62
253684_at	nucleotide pyrophosphatase - like p	---	AT4G29690	-1.34	-0.42	-3.26	0.014683	0.049818	-3.62
264277_at	polygalacturonase isoenzyme 1 be	---	AT1G60390	-1.31	-0.39	-3.26	0.01469	0.049834	-3.62
253307_at	putative protein auxin-induced prot	---	AT4G33670	1.34	0.43	3.26	0.014699	0.049855	-3.62
259806_at	mysoin-like protein similar to GI:23	---	AT1G47900	-1.48	-0.56	-3.26	0.01471	0.049886	-3.62
259304_at	putative nucleotide repair protein si	ERCC1	AT3G05210	1.29	0.37	3.26	0.014729	0.049937	-3.62
259287_at	putative rac GTPase activating prot	---	AT3G11490	-1.36	-0.45	-3.26	0.014731	0.049937	-3.62
266171_at	putative CCAAT-binding transcriptio	NF-YB1	AT2G38880	1.39	0.47	3.26	0.014731	0.049937	-3.62
256050_at	leucine zipper protein, putative sim	ATEXO70B	AT1G07000	-1.31	-0.39	-3.26	0.014738	0.049953	-3.62
244921_s_a	hypothetical protein	---	AT2G07674	1.48	0.57	3.26	0.014741	0.049955	-3.62
252420_at	putative protein several hypothetica	---	AT3G47530	1.48	0.57	3.26	0.014744	0.049956	-3.62
249291_at	glutathione transferase AtGST 10 (e	ATGSTT1	AT5G41210	1.33	0.41	3.25	0.014755	0.049987	-3.62
257004_s_a	glycolate oxidase, putative similar t	---	AT3G14130	1.25	0.33	3.25	0.014762	0.050003	-3.62
263841_at	putative xyloglucan endo-transglyco	---	AT2G36870	-6.06	-2.60	-3.25	0.014766	0.050004	-3.63
253458_at	putative protein predicted protein, A	---	AT4G32070	1.53	0.61	3.25	0.014767	0.050004	-3.63
265050_at	jasmonate inducible protein, putativ	---	AT1G52070	-1.26	-0.33	-3.25	0.014796	0.050095	-3.63
251292_at	putative protein hypothetical protei	---	AT3G61920	-1.43	-0.52	-3.25	0.0148	0.050102	-3.63
253633_at	putative protein tetratricopeptide re	---	AT4G30480	1.35	0.44	3.25	0.01481	0.050127	-3.63
260279_at	putative DNA repair protein similar t	---	AT1G80420	-1.29	-0.37	-3.25	0.014813	0.05013	-3.63
255045_at	putative protein hypothetical protei	---	AT4G09690	-1.33	-0.41	-3.25	0.014817	0.050131	-3.63
262431_at	trypsin inhibitor 2, putative similar t	---	AT1G47540	-1.28	-0.35	-3.25	0.014817	0.050131	-3.63
246335_at	lethal leaf-spot 1 homolog Lls1	ACD1	AT3G44880	1.42	0.50	3.25	0.01482	0.050132	-3.63
251013_at	putative protein various predicted p	---	AT5G02540	-4.56	-2.19	-3.25	0.014827	0.050148	-3.63
262767_at	putative oxysterol-binding protein si	ORP1D	AT1G13170	-1.74	-0.80	-3.25	0.014836	0.050171	-3.63
252234_at	putative protein ; supported by full-	ATPSK4	AT3G49780	2.77	1.47	3.25	0.014849	0.050208	-3.63
263733_at	polyprotein, putative similar to poly	---	---	-1.22	-0.29	-3.25	0.014854	0.050215	-3.63
262664_at	hypothetical protein predicted by ge	---	AT1G13970	1.29	0.37	3.25	0.014855	0.050215	-3.63
265945_at	putative cytokinin oxidase ; suppor	CKX2	AT2G19500	-1.28	-0.36	-3.25	0.014877	0.050281	-3.63
252786_at	putative protein putative DNA-helic	CHR38	AT3G42670	1.65	0.72	3.25	0.014891	0.050321	-3.63
256045_at	MAP3K gamma protein kinase, put	MAPKKK13	AT1G07150	-1.33	-0.42	-3.25	0.014896	0.050325	-3.63
258366_at	DNA-binding protein contains AP2	RAP2.2	AT3G14230	1.33	0.41	3.25	0.014897	0.050325	-3.63
257881_at	putative serine carboxypeptidase II	scpl33	AT3G17180	-1.38	-0.46	-3.25	0.014899	0.050325	-3.63

259578_at	unknown protein	---	AT1G27990	-1.51	-0.59	-3.25	0.014904	0.050335	-3.64
254284_at	putative fizzy-related protein fizzy-r	FZR2	AT4G22910	-1.47	-0.55	-3.25	0.014911	0.050352	-3.64
251610_at	putative protein hypothetical protei	---	AT3G57930	-2.23	-1.16	-3.25	0.014921	0.050376	-3.64
262370_at	hypothetical protein predicted by ge	---	AT1G73090	1.42	0.51	3.25	0.014924	0.050376	-3.64
265863_at	putative membrane protein	VIT1	AT2G01770	-1.39	-0.48	-3.25	0.014925	0.050376	-3.64
265357_at	E2, ubiquitin-conjugating enzyme,	UBC29	AT2G16740	1.44	0.53	3.24	0.014972	0.050526	-3.64
249278_at	putative protein strong similarity to	---	AT5G41900	-5.67	-2.50	-3.24	0.014988	0.050573	-3.64
265943_at	putative cytidine deaminase ;suppo	CDA1	AT2G19570	-1.73	-0.79	-3.24	0.01499	0.050573	-3.64
261574_at	cytochrome P450, putative similar	CYP78A8	AT1G01190	-1.71	-0.78	-3.24	0.014996	0.050587	-3.64
258122_at	hypothetical protein contains simila	ATGSL04	AT3G14570	-1.57	-0.65	-3.24	0.015004	0.050599	-3.64
251487_at	cysteine synthase	OASC	AT3G59760	-1.68	-0.75	-3.24	0.015004	0.050599	-3.64
266633_at	putative DnaJ protein	---	AT2G35540	1.34	0.42	3.24	0.015009	0.050606	-3.64
246346_at	hypothetical protein	---	AT3G56810	-1.50	-0.58	-3.24	0.015016	0.050623	-3.64
262254_at	unknown protein similar to GDSL-m	GLIP5	AT1G53920	-1.72	-0.78	-3.24	0.015052	0.050738	-3.65
252025_at	putative protein chromosome asse	---	AT3G52900	-1.32	-0.40	-3.24	0.015071	0.05079	-3.65
259721_at	putative phosphatidylinositol-4-phos	---	AT1G60890	1.46	0.55	3.24	0.015072	0.05079	-3.65
261355_at	putative malate oxidoreductase sim	ATNADP-M	AT1G79750	1.35	0.43	3.24	0.015079	0.050801	-3.65
264581_at	hypothetical protein predicted by ge	---	AT1G05210	-1.75	-0.81	-3.24	0.01508	0.050801	-3.65
256754_at	unknown protein	CHUP1	AT3G25690	-1.33	-0.41	-3.24	0.015089	0.050826	-3.65
265246_at	putative pectinesterase	ATPMEPCI	AT2G43050	-1.36	-0.44	-3.24	0.015093	0.050828	-3.65
256653_at	hypothetical protein predicted by ge	---	AT3G18870	1.30	0.38	3.24	0.015095	0.050828	-3.65
260102_at	unknown protein	---	AT1G35470	1.34	0.43	3.24	0.015098	0.050828	-3.65
255943_at	UDP-glucose glucosyltransferase,	AtUGT85A	AT1G22370	2.23	1.16	3.24	0.015099	0.050828	-3.65
260065_at	putative RING zinc finger protein c	---	AT1G73760	1.33	0.41	3.24	0.015104	0.050836	-3.65
248243_at	unknown protein	CPuORF50	AT5G53588	1.24	0.31	3.24	0.015106	0.050837	-3.65
256438_s_a	ribosomal protein L41 identical to ri	---	AT2G40205	1.76	0.82	3.24	0.015109	0.050837	-3.65
246036_at	alpha-galactosidase - like protein a	AtAGAL2	AT5G08370	-1.73	-0.79	-3.24	0.015111	0.050837	-3.65
265850_at	putative DnaJ protein	---	AT2G35720	1.43	0.51	3.24	0.015113	0.050837	-3.65
245640_at	helix-loop-helix protein homolog, p	---	AT1G25330	-1.29	-0.36	-3.24	0.01512	0.050849	-3.65
267007_at	60S ribosomal protein L18A ; suppo	---	AT2G34480	1.54	0.62	3.24	0.015121	0.050849	-3.65
246944_at	ubiquinol--cytochrome-c reductase	---	AT5G25450	1.31	0.39	3.24	0.015146	0.050927	-3.65
249039_at	late embryogenesis abundant prote	---	AT5G44310	-1.33	-0.41	-3.24	0.015155	0.050949	-3.65
253312_s_a	putative protein (1,4)-beta-xylan en	---	AT4G33850	-1.28	-0.36	-3.23	0.015159	0.050953	-3.65
254238_at	putative protein probable membran	---	AT4G23540	1.39	0.48	3.23	0.015176	0.051003	-3.65
245946_at	putative protein glyoxal oxidase pre	---	AT5G19580	-1.39	-0.48	-3.23	0.015185	0.051018	-3.66

251884_at	embryonic abundant protein -like e	---	AT3G54150	3.51	1.81	3.23	0.015186	0.051018	-3.66
253200_at	vacuolar H+-transporting ATPase 1	AVA-P1	AT4G34720	-1.37	-0.45	-3.23	0.015187	0.051018	-3.66
254119_at	putative pectate lyase pectate lyas	---	AT4G24780	-2.81	-1.49	-3.23	0.015202	0.05106	-3.66
266761_at	putative alcohol dehydrogenase	---	AT2G47130	1.88	0.91	3.23	0.015205	0.051063	-3.66
252626_at	putative protein predicted protein, A	---	AT3G44940	-1.40	-0.48	-3.23	0.015224	0.051119	-3.66
262155_at	glycosyl transferase, putative simila	---	AT1G52420	1.34	0.42	3.23	0.01523	0.051133	-3.66
256885_at	chaperone-like ATPase contains Pf	---	AT3G15120	1.35	0.43	3.23	0.015238	0.051145	-3.66
252147_at	putative protein several hypothetica	---	AT3G51270	1.48	0.56	3.23	0.015238	0.051145	-3.66
253743_at	putative protein vegetative storage	---	AT4G28940	-1.21	-0.28	-3.23	0.015246	0.051164	-3.66
255553_at	predicted protein of unknown functi	---	AT4G01960	1.44	0.52	3.23	0.015257	0.051193	-3.66
252528_at	E2, ubiquitin-conjugating enzyme 1	UBC13	AT3G46460	-1.26	-0.33	-3.23	0.015261	0.051199	-3.66
252780_at	alcohol dehydrogenase (ATA1) ;su	ATA1	AT3G42960	-1.50	-0.58	-3.23	0.015286	0.051277	-3.66
248916_at	receptor protein kinase-like protein	---	AT5G45840	-1.87	-0.90	-3.23	0.015303	0.051321	-3.66
248421_at	unknown protein ;supported by full-	---	AT5G51510	1.31	0.38	3.23	0.015304	0.051321	-3.66
254074_at	transcriptional activator CBF1 CRT	CBF1	AT4G25490	1.78	0.83	3.23	0.015312	0.05134	-3.66
259738_at	predicted protein	---	AT1G64355	-1.31	-0.39	-3.23	0.015314	0.05134	-3.66
249870_at	unknown protein	TGH	AT5G23080	1.84	0.88	3.23	0.015324	0.051357	-3.66
245605_at	ribonucleoprotein like protein	---	AT4G14300	-1.23	-0.30	-3.23	0.015324	0.051357	-3.66
260832_at	unknown protein ; supported by cDI	GAUT6	AT1G06780	1.34	0.42	3.23	0.015358	0.051463	-3.67
265988_at	hypothetical protein predicted by ge	---	AT2G24255	-1.27	-0.34	-3.22	0.015377	0.051521	-3.67
251714_at	putative protein leucine-rich recept	---	AT3G56370	-1.84	-0.88	-3.22	0.015391	0.051558	-3.67
254014_at	NPR1 like protein regulatory protei	---	AT4G26120	1.88	0.91	3.22	0.015393	0.051558	-3.67
250531_at	GTP-binding protein LepA homolog	---	AT5G08650	-1.48	-0.57	-3.22	0.015399	0.051573	-3.67
255791_at	plastid protein identical to GB:Z860	DAL1	AT2G33430	1.42	0.51	3.22	0.015402	0.051575	-3.67
256063_at	Expressed protein ; supported by fu	STN1	AT1G07130	1.32	0.40	3.22	0.015409	0.051589	-3.67
247896_at	26S proteasome regulatory subuni	---	AT5G57950	1.25	0.32	3.22	0.015417	0.051609	-3.67
253139_at	ankyrin repeat-containing protein 2	AKR2	AT4G35450	-1.25	-0.32	-3.22	0.015426	0.051626	-3.67
249233_at	putative protein contains similarity t	---	AT5G42150	2.05	1.04	3.22	0.015427	0.051626	-3.67
263173_at	hypothetical protein predicted by ge	BRX-LIKE3	AT1G54180	-1.25	-0.32	-3.22	0.01543	0.05163	-3.67
247002_at	putative protein strong similarity to	HOS15	AT5G67320	1.34	0.42	3.22	0.015433	0.051632	-3.67
262870_at	alcohol dehydrogenase, putative si	---	AT1G64710	2.51	1.33	3.22	0.015445	0.051664	-3.67
263202_at	putative inositol 1,4,5-trisphosphat	5PTASE13	AT1G05630	-1.87	-0.91	-3.22	0.01545	0.05167	-3.67
248088_at	2-oxoglutarate dehydrogenase E2 s	---	AT5G55070	1.44	0.53	3.22	0.015453	0.05167	-3.67
267376_at	putative receptor-like protein kinas	ER	AT2G26330	-2.80	-1.48	-3.22	0.015453	0.05167	-3.67
263913_at	putative receptor-like protein kinase	---	AT2G36570	-1.54	-0.62	-3.22	0.015485	0.051763	-3.68

245356_at	adenosylhomocysteinase ;supporte	MEE58	AT4G13940	1.46	0.55	3.22	0.015486	0.051763	-3.68
247071_at	putative protein similar to unknown	DAR3	AT5G66640	-2.31	-1.21	-3.22	0.015491	0.051774	-3.68
252991_at	protein kinase like protein protein k	---	AT4G38470	-2.32	-1.21	-3.22	0.015498	0.051788	-3.68
257782_at	hypothetical protein predicted by ge	---	AT3G27120	-1.31	-0.39	-3.22	0.015503	0.051797	-3.68
264914_at	clathrin adaptor medium chain prot	HAP13	AT1G60780	-1.31	-0.39	-3.22	0.015511	0.051817	-3.68
246223_at	UDP-glucuronyltransferase-like pro	IRX14	AT4G36890	1.26	0.33	3.22	0.015515	0.051823	-3.68
245127_at	putative Na+/Ca2+ antiporter ; sup	ATMHX	AT2G47600	-1.60	-0.68	-3.22	0.015522	0.051837	-3.68
263129_at	unknown protein ;supported by full-	---	AT1G78620	-1.28	-0.36	-3.22	0.01553	0.051856	-3.68
259218_at	hypothetical protein similar to putat	---	AT3G03580	1.33	0.41	3.22	0.015537	0.051874	-3.68
262944_at	phosphoglycerate kinase, putative	PGK	AT1G79550	1.44	0.53	3.22	0.015549	0.051896	-3.68
259584_at	hypothetical protein predicted by ge	---	AT1G28080	-1.25	-0.32	-3.22	0.015552	0.051896	-3.68
266770_at	putative expansin Experimental evi	ATEXPA15	AT2G03090	-1.52	-0.61	-3.22	0.015554	0.051896	-3.68
263618_at	hypothetical protein predicted by ge	APC2	AT2G04660	1.37	0.46	3.22	0.015556	0.051896	-3.68
252440_at	aquaporin-like protein aquaporin -	TIP5;1	AT3G47440	-1.26	-0.33	-3.22	0.015557	0.051896	-3.68
263289_at	ubiquitin extension protein (UBQ2)	---	AT2G36170	1.61	0.69	3.22	0.015557	0.051896	-3.68
254816_at	putative adenine phosphoribosyltra	APT4	AT4G12440	-1.22	-0.29	-3.22	0.015562	0.051905	-3.68
259372_at	homeotic protein boi1AP1, putative	AP1	AT1G69120	-1.29	-0.37	-3.22	0.015566	0.051906	-3.68
253498_at	putative protein various predicted p	---	AT4G31890	-1.74	-0.80	-3.22	0.015567	0.051906	-3.68
256629_at	serine/threonine protein phosphata	ATFYPP3	AT3G19980	1.28	0.36	3.22	0.015571	0.051911	-3.68
256976_at	unknown protein similar to putative	---	---	1.46	0.55	3.21	0.015579	0.051931	-3.68
255544_at	predicted protein of unknown functi	---	AT4G01880	1.39	0.47	3.21	0.015594	0.051972	-3.68
252194_at	putative tyrosine phosphatase pho	ATPEN3	AT3G50110	-1.34	-0.42	-3.21	0.015603	0.051996	-3.68
259006_at	putative 60S acidic ribosomal prote	---	AT3G09200	1.54	0.63	3.21	0.01561	0.05201	-3.68
252587_at	putative protein Human (H326) tran	---	AT3G45620	1.64	0.71	3.21	0.015613	0.052012	-3.68
256006_at	hypothetical protein	---	AT1G34070	-1.25	-0.33	-3.21	0.015621	0.052031	-3.69
267277_at	putative protein transport protein SE	---	AT2G30050	-1.29	-0.37	-3.21	0.015625	0.052036	-3.69
249833_at	putative protein contains similarity t	---	AT5G23430	-1.37	-0.45	-3.21	0.015628	0.052041	-3.69
254207_at	putative protein Dof zinc finger prot	---	AT4G24060	-1.32	-0.40	-3.21	0.015644	0.052085	-3.69
263961_at	F-box protein family, AtFBL11 cont	---	AT2G36370	1.38	0.46	3.21	0.015648	0.052092	-3.69
255429_at	hypothetical protein	---	AT4G03410	-1.41	-0.50	-3.21	0.015657	0.052113	-3.69
258987_at	putative SCO1 protein similar to SC	---	AT3G08950	1.69	0.75	3.21	0.015667	0.052139	-3.69
245124_at	small nuclear ribonucleoprotein U1A	U1A	AT2G47580	1.31	0.38	3.21	0.015675	0.052157	-3.69
247164_at	NifS-like aminotranfserase ; suppo	NFS1	AT5G65720	1.30	0.38	3.21	0.015677	0.052157	-3.69
266981_at	60S ribosomal protein L23A identica	RPL23AA	AT2G39460	1.69	0.75	3.21	0.01569	0.052193	-3.69
266758_at	unknown protein	POL	AT2G46920	1.32	0.40	3.21	0.015693	0.052196	-3.69

267136_at	putative GTP-binding protein (extra	XLG1	AT2G23460	-1.31	-0.39	-3.21	0.015708	0.052238	-3.69
245621_at	AMP-binding protein	AAE15	AT4G14070	1.46	0.54	3.21	0.015715	0.052247	-3.69
247880_at	putative protein similar to unknown	---	AT5G57780	-2.55	-1.35	-3.21	0.015715	0.052247	-3.69
262886_at	hypothetical protein	KNATM	AT1G14760	-1.39	-0.47	-3.21	0.01572	0.052256	-3.69
247118_at	uridylyl transferases-like ; supporte	ACR1	AT5G65890	-1.53	-0.61	-3.21	0.015723	0.052257	-3.69
259662_at	Expressed protein ; supported by fu	HUB2	AT1G55250	1.41	0.50	3.21	0.015729	0.052269	-3.69
258417_at	Expressed protein ; supported by cl	---	AT3G17365	1.40	0.48	3.21	0.015734	0.052277	-3.69
257104_at	ER lumen retaining receptor (HDEI	---	AT3G25040	-1.28	-0.36	-3.21	0.015737	0.052282	-3.69
261412_at	L-ascorbate peroxidase identical to	APX1	AT1G07890	1.62	0.70	3.21	0.015744	0.052294	-3.69
252978_at	galactosidase like protein ss-1,4-ex	BGAL14	AT4G38590	-1.39	-0.47	-3.21	0.015745	0.052294	-3.69
251781_at	P-glycoprotein - like P-glycoprotein	PGP20	AT3G55320	1.30	0.37	3.21	0.015757	0.052325	-3.69
252199_at	anthranilate N-hydroxycinnamoyl/b	---	AT3G50270	1.35	0.43	3.21	0.01577	0.052361	-3.70
248274_at	isp4 protein	ATOPT9	AT5G53510	-1.26	-0.34	-3.20	0.015795	0.052434	-3.70
264522_at	putative xylan endohydrolase simil	---	AT1G10050	1.36	0.44	3.20	0.015817	0.0525	-3.70
266283_at	putative proline-rich protein	---	AT2G29210	1.31	0.39	3.20	0.015827	0.052527	-3.70
249988_at	putative protein predicted proteins,	---	AT5G18310	1.39	0.48	3.20	0.015842	0.052568	-3.70
255598_at	putative protein similar to nucleolin	---	AT4G00830	1.39	0.48	3.20	0.015866	0.052641	-3.70
257378_s_a	hypothetical protein predicted by ge	---	AT2G02290	-1.32	-0.40	-3.20	0.015869	0.052642	-3.70
256478_at	unknown protein	---	---	-1.32	-0.40	-3.20	0.015876	0.052658	-3.70
248334_s_a	unknown protein ; supported by cD	---	AT5G52370	1.57	0.65	3.20	0.015884	0.052678	-3.70
260276_at	unknown protein	---	AT1G80450	1.84	0.88	3.20	0.015895	0.052702	-3.70
245734_at	lysophospholipase homolog, putati	---	AT1G73480	-1.57	-0.65	-3.20	0.015897	0.052702	-3.70
251190_at	RING-H2 zinc finger protein ATL5	ATL5	AT3G62690	-1.64	-0.71	-3.20	0.015899	0.052702	-3.70
258181_at	nitrate transporter identical to nitrate	---	AT3G21670	-1.48	-0.56	-3.20	0.015901	0.052702	-3.70
263167_at	unknown protein Belongs to PF|01	---	AT1G03030	1.35	0.43	3.20	0.015908	0.052718	-3.70
259023_at	unknown protein ; supported by cD	---	AT3G07510	-1.53	-0.62	-3.20	0.015912	0.052723	-3.70
250886_at	putative protein	---	AT5G04440	1.33	0.41	3.20	0.015923	0.052752	-3.71
254873_at	putative protein a 162 kDa compor	EIF3A	AT4G11420	1.26	0.34	3.20	0.015936	0.052786	-3.71
265120_at	3-ketoacyl-acyl carrier protein synth	KAS III	AT1G62640	-1.37	-0.45	-3.20	0.015938	0.052786	-3.71
258817_at	hypothetical protein similar to hypo	---	AT3G04750	1.24	0.31	3.20	0.015941	0.05279	-3.71
254969_at	hypothetical protein ;supported by	---	AT4G10360	1.26	0.34	3.20	0.01597	0.052878	-3.71
254798_at	oleoyl-[acyl-carrier-protein] hydrola	---	AT4G13050	1.57	0.65	3.20	0.015984	0.052915	-3.71
246387_at	hypothetical protein predicted by ge	---	AT1G77400	1.41	0.49	3.19	0.016001	0.052966	-3.71
247846_at	putative protein	---	AT5G58100	1.29	0.37	3.19	0.016012	0.052995	-3.71
259546_at	unknown protein	---	AT1G35350	-1.91	-0.93	-3.19	0.016021	0.053015	-3.71

247624_at	aspartyl aminopeptidase - like prot	---	AT5G60160	1.22	0.29	3.19	0.016023	0.053015	-3.71
262116_at	Expressed protein ; supported by fu	---	AT1G02816	-1.71	-0.78	-3.19	0.016026	0.053017	-3.71
253333_at	2-dehydro-3-deoxyphosphoheptona	DHS2	AT4G33510	1.30	0.38	3.19	0.016049	0.053086	-3.71
246334_at	putative protein serine kinase SRP	---	AT3G44850	1.47	0.56	3.19	0.016061	0.053114	-3.71
250918_at	putative protein proline-rich protein	---	AT5G03610	3.07	1.62	3.19	0.016063	0.053114	-3.71
259609_at	myosin-like protein contains Pfam	TSA1	AT1G52410	-3.13	-1.65	-3.19	0.016066	0.053114	-3.71
250961_at	putative protein various predicted p	---	AT5G02980	-1.29	-0.37	-3.19	0.016067	0.053114	-3.72
254818_at	pEARLI 1-like protein Arabidopsis	---	AT4G12470	2.94	1.56	3.19	0.016069	0.053114	-3.72
246959_at	unknown protein	---	AT5G24690	1.68	0.75	3.19	0.016075	0.053122	-3.72
246871_at	extensin - like protein pAP8 protein	---	AT5G26070	-1.24	-0.32	-3.19	0.016079	0.053122	-3.72
256371_at	hypothetical protein	---	AT1G66770	-1.27	-0.35	-3.19	0.016079	0.053122	-3.72
255121_at	putative mitogen-activated protein k	MAPKKK9	AT4G08480	1.48	0.56	3.19	0.016081	0.053122	-3.72
254233_at	98b like protein 98b - Daucus carot	---	AT4G23800	-1.53	-0.62	-3.19	0.016096	0.053164	-3.72
259736_at	endo-beta-1,4-glucanase, putative	AtGH9C2	AT1G64390	-3.77	-1.91	-3.19	0.01611	0.053203	-3.72
251570_at	putative protein several hypothetica	---	AT3G58300	-1.31	-0.39	-3.19	0.01613	0.053258	-3.72
246868_at	protein phosphatase - like protein p	---	AT5G26010	-1.27	-0.35	-3.19	0.016132	0.053258	-3.72
246317_at	putative protein unnamed ORF - H	---	AT3G56900	1.46	0.54	3.19	0.016137	0.053265	-3.72
266460_at	unknown protein ; supported by cDI	AGP26	AT2G47930	-5.67	-2.50	-3.19	0.016138	0.053265	-3.72
266649_at	putative aquaporin (tonoplast intrins	TIP4;1	AT2G25810	-1.25	-0.33	-3.19	0.016144	0.053266	-3.72
246822_at	putative protein predicted proteins,	---	AT5G26960	-1.33	-0.41	-3.19	0.016145	0.053266	-3.72
250524_at	putative protein contains similarity t	---	AT5G08520	-1.27	-0.34	-3.19	0.016146	0.053266	-3.72
245347_at	ferredoxin ;supported by full-length	---	AT4G14890	1.40	0.49	3.19	0.016153	0.053275	-3.72
265200_s_a	putative glucosyl transferase an ES	UGT73C6	AT2G36790	1.96	0.97	3.19	0.016153	0.053275	-3.72
256301_at	unknown protein ;supported by full-	---	AT1G69510	1.28	0.36	3.19	0.016162	0.05329	-3.72
247959_at	unknown protein	---	AT5G57080	1.43	0.52	3.19	0.016165	0.05329	-3.72
248478_at	ubiquitin-conjugating enzyme-like p	UBC27	AT5G50870	-1.24	-0.31	-3.19	0.016166	0.05329	-3.72
247401_at	1-deoxy-D-xylulose 5-phosphate re	DXR	AT5G62790	-1.48	-0.56	-3.19	0.016168	0.05329	-3.72
257598_at	PRT1 identical to GB:CAA11891 fr	PRT1	AT3G24800	-1.39	-0.47	-3.19	0.016171	0.05329	-3.72
258385_at	putative jasmonic acid regulatory pr	ATNAC2	AT3G15510	1.45	0.54	3.19	0.016171	0.05329	-3.72
249020_at	helicase-like protein	CHR4	AT5G44800	1.33	0.42	3.19	0.016175	0.053293	-3.72
258592_at	hypothetical protein contains Pfam	---	AT3G04130	1.33	0.41	3.19	0.016177	0.053294	-3.72
258956_at	hypothetical protein predicted by ge	---	AT3G01440	2.14	1.10	3.19	0.016183	0.053303	-3.72
256272_at	unknown protein	---	AT3G12100	-1.28	-0.35	-3.19	0.016185	0.053303	-3.72
263248_at	putative endonuclease ;supported	ATNTH1	AT2G31450	1.28	0.35	3.19	0.016196	0.053325	-3.72
262065_at	hypothetical protein predicted by ge	---	AT1G56180	1.55	0.63	3.19	0.016198	0.053325	-3.72

265664_at	unknown protein predicted by gens	---	AT2G24420	1.34	0.42	3.19	0.016199	0.053325	-3.72
266876_at	hypothetical protein predicted by ge	---	AT2G44820	1.31	0.40	3.19	0.016207	0.053344	-3.72
247323_at	putative protein similar to unknown	---	AT5G64170	1.45	0.54	3.19	0.016211	0.05335	-3.72
249087_at	DNA binding protein EREBP-3-like	ERF9	AT5G44210	-1.50	-0.59	-3.19	0.016215	0.053355	-3.72
257894_at	unknown protein ; supported by cDI	---	AT3G17100	-1.64	-0.72	-3.18	0.016223	0.053376	-3.73
252275_at	ubiquitin-specific protease 26 (UBF	UBP26	AT3G49600	1.43	0.52	3.18	0.016242	0.053428	-3.73
251893_at	putative protein	---	AT3G54380	1.27	0.34	3.18	0.016244	0.053428	-3.73
258552_at	putative pectate lyase similar to pec	---	AT3G07010	-4.42	-2.15	-3.18	0.016255	0.05345	-3.73
260606_at	putative splicing factor	---	AT2G43770	1.48	0.56	3.18	0.016255	0.05345	-3.73
266106_at	putative microtubule-associated pro	ATATG8E	AT2G45170	-1.51	-0.59	-3.18	0.016262	0.053464	-3.73
265373_at	putative replication protein A1	RPA1A	AT2G06510	1.61	0.69	3.18	0.016265	0.053466	-3.73
255310_at	Expressed protein ; supported by fu	ATALN	AT4G04955	1.88	0.91	3.18	0.016273	0.053486	-3.73
257725_at	DNA mismatch repair protein MSH	MSH2	AT3G18524	1.43	0.51	3.18	0.016288	0.053526	-3.73
248342_at	unknown protein	MBD13	AT5G52230	1.24	0.31	3.18	0.016302	0.053564	-3.73
261518_at	peroxidase ATP4a identical to GB:(	---	AT1G71695	-1.36	-0.44	-3.18	0.016304	0.053565	-3.73
256899_at	putative kinase-like protein TMKL1	TMKL1	AT3G24660	1.31	0.38	3.18	0.016312	0.053581	-3.73
251026_at	hypothetical protein	FHL	AT5G02200	-2.64	-1.40	-3.18	0.016322	0.053602	-3.73
247989_at	pyruvate kinase ;supported by full-l	---	AT5G56350	1.44	0.52	3.18	0.016325	0.053602	-3.73
249334_at	putative protein strong similarity to	YSL4	AT5G41000	1.46	0.54	3.18	0.016325	0.053602	-3.73
262786_at	putative lipase similar to gb|X02844	---	AT1G10740	-1.43	-0.51	-3.18	0.016333	0.053622	-3.73
259861_at	unknown protein similar to ribosoma	---	AT1G80620	1.37	0.46	3.18	0.016338	0.053629	-3.73
256143_at	40S ribosomal protein S7 homolog	---	AT1G48830	1.39	0.47	3.18	0.01634	0.053629	-3.73
263396_at	unknown protein ;supported by full-	---	AT2G31710	1.31	0.39	3.18	0.016352	0.053657	-3.73
252188_at	putative clathrin coat assembly pro	---	AT3G50860	1.54	0.63	3.18	0.016354	0.053657	-3.73
248253_at	putative protein contains similarity t	CRF3	AT5G53290	-1.27	-0.34	-3.18	0.016356	0.053657	-3.73
256936_at	prefoldin-like protein similar to pref	PDF2	AT3G22480	1.29	0.36	3.18	0.016366	0.053682	-3.73
255424_at	putative glycosylation enzyme simi	---	AT4G03340	-1.28	-0.36	-3.18	0.016369	0.053684	-3.73
256757_at	membrane transporter, putative sir	---	AT3G25620	-1.30	-0.38	-3.18	0.016395	0.053762	-3.74
263066_at	unknown protein	---	AT2G17540	-1.23	-0.29	-3.18	0.016423	0.053845	-3.74
252424_at	putative protein activating signal co	---	AT3G47610	1.40	0.48	3.18	0.016428	0.053855	-3.74
264224_at	hypothetical protein predicted by ge	emb1688	AT1G67440	1.32	0.40	3.17	0.016447	0.053902	-3.74
258735_at	low temperature and salt responsiv	RCI2A	AT3G05880	-1.53	-0.61	-3.17	0.016447	0.053902	-3.74
255080_at	arabinogalactan-protein homolog a	AGP10	AT4G09030	-1.56	-0.65	-3.17	0.016461	0.05394	-3.74
245365_at	hypothetical protein ;supported by f	---	AT4G17720	1.54	0.63	3.17	0.016468	0.053956	-3.74
254608_at	major intrinsic protein (MIP)- like n	NIP1;2	AT4G18910	1.84	0.88	3.17	0.016493	0.054026	-3.74

253545_at	AIG2-like protein AIG2 protein, Ara	---	AT4G31310	1.40	0.48	3.17	0.016494	0.054026	-3.74
255994_at	hypothetical protein predicted by ge	---	AT1G29760	1.26	0.33	3.17	0.016497	0.054027	-3.74
250695_at	lectin-like protein kinase	---	AT5G06740	2.04	1.03	3.17	0.016513	0.054071	-3.74
252219_at	putative protein some putative prote	---	AT3G50160	-1.34	-0.42	-3.17	0.016518	0.05408	-3.74
259582_at	hypothetical protein	---	AT1G28060	1.35	0.43	3.17	0.016523	0.054089	-3.74
249835_s_a	putative protein similar to unknown	---	AT5G23490	1.66	0.73	3.17	0.016526	0.054091	-3.74
260404_at	unknown protein similar to activator	---	---	1.52	0.61	3.17	0.016534	0.05411	-3.75
265051_at	jasmonate inducible protein, putativ	---	AT1G52100	-1.40	-0.49	-3.17	0.016539	0.054119	-3.75
245932_at	3'(2'),5'-bisphosphate nucleotidase	---	AT5G09290	-1.77	-0.82	-3.17	0.016546	0.054131	-3.75
247447_at	nitrate transporter NTL1 - like prote	---	AT5G62730	-1.86	-0.90	-3.17	0.016548	0.054131	-3.75
256624_at	hypothetical protein predicted by ge	---	AT3G19990	1.26	0.34	3.17	0.016552	0.054138	-3.75
266040_at	hypothetical protein	---	AT2G07738	-1.24	-0.30	-3.17	0.016568	0.054182	-3.75
258705_at	hypothetical protein predicted by ge	---	AT3G09470	1.30	0.38	3.17	0.016573	0.05419	-3.75
260002_at	putative ABC transporter similar to	ATNAP3	AT1G67940	1.51	0.60	3.17	0.016579	0.054202	-3.75
264365_s_a	unknown protein Strong similarity t	---	AT1G03220	1.91	0.93	3.17	0.016588	0.054225	-3.75
264931_at	polygalacturonase, putative similar	---	AT1G60590	-1.30	-0.37	-3.17	0.016603	0.054266	-3.75
248474_at	pyruvate dehydrogenase E1 compo	MAB1	AT5G50850	1.36	0.44	3.17	0.016611	0.054278	-3.75
255691_at	hypothetical protein	ANTR2	AT4G00370	1.33	0.41	3.17	0.016612	0.054278	-3.75
246738_at	replication factor C - like replicatior	EMB2775	AT5G27740	1.28	0.36	3.17	0.016624	0.054303	-3.75
261369_at	protein kinase, putative similar to n	---	AT1G53060	-1.39	-0.48	-3.17	0.016624	0.054303	-3.75
267552_at	putative purple acid phosphatase pi	PAP13	AT2G32770	-1.25	-0.32	-3.17	0.01663	0.054316	-3.75
258175_at	FKBP-type peptidyl-prolyl cis-trans	TWD1	AT3G21640	1.29	0.36	3.17	0.016639	0.054335	-3.75
263856_at	unknown protein	---	AT2G04410	1.42	0.50	3.17	0.016652	0.054371	-3.75
246401_at	DNA-binding protein, putative simil	AtMYB50	AT1G57560	-1.52	-0.60	-3.16	0.016671	0.054424	-3.75
264420_at	hypothetical protein predicted by ge	---	AT1G43320	-1.24	-0.31	-3.16	0.016687	0.054468	-3.76
257460_at	auxin induced protein, putative sim	---	AT1G75580	-1.27	-0.34	-3.16	0.01669	0.05447	-3.76
266028_at	hypothetical protein predicted by ge	---	AT2G06000	1.42	0.51	3.16	0.016692	0.05447	-3.76
262211_at	AP2 domain containing protein, pu	ORA47	AT1G74930	2.58	1.36	3.16	0.016699	0.05448	-3.76
255059_at	putative protein downy mildew resi	---	AT4G09420	-1.81	-0.86	-3.16	0.0167	0.05448	-3.76
264456_at	unknown protein similar to T cell re	---	AT1G10390	1.29	0.37	3.16	0.016706	0.054491	-3.76
266079_at	unknown protein	LCD1	AT2G37860	1.37	0.45	3.16	0.016708	0.054492	-3.76
248647_at	sucrose synthase	SUS2	AT5G49190	-1.25	-0.32	-3.16	0.016713	0.054499	-3.76
245437_at	RNA helicase like protein	---	AT4G16630	1.46	0.55	3.16	0.016725	0.054531	-3.76
247435_at	glutathione S-transferase-like prote	ATGSTU9	AT5G62480	4.27	2.09	3.16	0.016728	0.054532	-3.76
267240_at	hypothetical protein predicted by ge	---	AT2G02680	-1.32	-0.41	-3.16	0.016754	0.054608	-3.76

247378_at	ATP-dependent RNA helicase-like	---	AT5G63120	-1.41	-0.50	-3.16	0.016761	0.054625	-3.76
259830_at	hypothetical protein predicted by ge	---	AT1G80630	-1.31	-0.38	-3.16	0.01677	0.054639	-3.76
266185_at	unknown protein	---	AT2G38950	1.26	0.33	3.16	0.016772	0.054639	-3.76
255608_at	hypothetical protein	---	AT4G01140	-1.39	-0.47	-3.16	0.016774	0.054639	-3.76
249899_at	putative protein similar to unknown	---	AT5G22620	-1.58	-0.66	-3.16	0.016775	0.054639	-3.76
252592_at	mitogen-activated protein kinase 3	NAXT1	AT3G45640	2.04	1.03	3.16	0.016787	0.054671	-3.76
253749_at	phytochrome-associated protein PA	PAP2	AT4G29080	-3.56	-1.83	-3.16	0.016803	0.054716	-3.76
255551_at	putative potassium channel ;suppo	KCO5	AT4G01840	1.23	0.30	3.16	0.016807	0.054721	-3.76
245481_at	hypothetical protein	---	AT4G16170	1.26	0.34	3.16	0.016822	0.054761	-3.76
267368_at	citrate synthase similar to GB:X175	ATCS	AT2G44350	1.33	0.41	3.16	0.016826	0.054766	-3.76
262278_at	transcription factor PERIANTHIA id	PAN	AT1G68640	-1.36	-0.44	-3.16	0.016871	0.054904	-3.77
265430_at	hypothetical protein predicted by ge	---	AT2G20700	-1.54	-0.62	-3.16	0.01688	0.054925	-3.77
260714_at	chaperonin CPN10 identical to SP:F	CPN10	AT1G14980	1.61	0.69	3.16	0.016891	0.054954	-3.77
254725_at	putative protein various predicted p	---	AT4G13650	1.34	0.43	3.15	0.0169	0.054968	-3.77
250984_at	protein kinase - like protein kinase	---	AT5G02800	1.23	0.30	3.15	0.0169	0.054968	-3.77
246426_at	ovule development protein aintegu	BBM	AT5G17430	-1.24	-0.32	-3.15	0.016905	0.05497	-3.77
258976_at	putative dehydrogenase contains F	---	AT3G01980	-1.24	-0.32	-3.15	0.016907	0.05497	-3.77
262570_at	unknown protein EST gb|H77143 c	---	AT1G15200	1.29	0.37	3.15	0.01691	0.05497	-3.77
258040_at	unknown protein ;supported by full-	---	AT3G21190	-3.84	-1.94	-3.15	0.01691	0.05497	-3.77
264866_at	putative metalloproteinase similar t	---	AT1G24140	4.08	2.03	3.15	0.016913	0.05497	-3.77
264293_at	cell division cycle protein, putative	APC6	AT1G78770	1.24	0.31	3.15	0.016938	0.055046	-3.77
246553_at	putative protein hypothetical protei	EDL1	AT5G15440	-1.31	-0.39	-3.15	0.016949	0.055073	-3.77
265026_at	putative 3-oxoacyl [acyl-carrier pro	---	AT1G24360	1.45	0.54	3.15	0.016981	0.055168	-3.77
264140_at	proteasome alpha subunit, putative	---	AT1G79210	1.26	0.33	3.15	0.016986	0.055169	-3.77
253060_at	putative protein predicted protein, A	---	AT4G37710	1.85	0.89	3.15	0.016986	0.055169	-3.77
250464_at	hypothetical protein	---	AT5G10040	-1.21	-0.28	-3.15	0.01699	0.055173	-3.77
249787_at	putative protein contains similarity t	---	AT5G24320	1.24	0.32	3.15	0.016996	0.05518	-3.77
266272_at	hypothetical protein predicted by ge	---	AT2G29600	-1.29	-0.37	-3.15	0.016997	0.05518	-3.77
265215_at	hypothetical protein predicted by ge	---	AT1G05040	-1.23	-0.30	-3.15	0.017007	0.055207	-3.78
263624_at	putative ferredoxin-thioredoxin redu	---	AT2G04700	-1.37	-0.45	-3.15	0.017015	0.055222	-3.78
248445_at	unknown protein ;supported by full-	---	AT5G51170	1.37	0.46	3.15	0.01702	0.055232	-3.78
260375_at	unknown protein	---	AT1G73950	1.30	0.37	3.15	0.017023	0.055234	-3.78
252351_at	putative protein ;supported by full-l	---	AT3G48210	1.37	0.46	3.15	0.017026	0.055234	-3.78
263379_at	putative CCCH-type zinc finger prot	CZF1	AT2G40140	2.83	1.50	3.15	0.017049	0.055302	-3.78
267595_at	putative glucanse	AtGH9B8	AT2G32990	-5.52	-2.46	-3.15	0.017054	0.055311	-3.78

255710_at	predicted protein of unknown functi	---	AT4G00030	-1.55	-0.64	-3.15	0.017062	0.055331	-3.78
266920_at	hypothetical protein predicted by ge	---	AT2G45750	-1.33	-0.41	-3.15	0.017075	0.055364	-3.78
262567_at	hypothetical protein contains simila	---	AT1G34300	1.50	0.58	3.15	0.01709	0.055405	-3.78
256776_at	multispanning membrane protein, p	---	AT3G13772	1.27	0.34	3.15	0.017093	0.055407	-3.78
259705_at	GRAB1-like protein similar to GRA	anac032	AT1G77450	1.54	0.62	3.15	0.017099	0.055418	-3.78
255466_at	putative protein similar to A. thalian	---	AT4G03000	1.30	0.38	3.15	0.017105	0.055424	-3.78
267358_at	proline transporter 1 ;supported by	PROT1	AT2G39890	1.36	0.44	3.15	0.017106	0.055424	-3.78
260309_at	putative alanine aminotransferase s	AOAT2	AT1G70580	-1.39	-0.48	-3.15	0.017111	0.055434	-3.78
246246_at	putative protein	---	AT4G37170	1.37	0.46	3.15	0.017115	0.055438	-3.78
246650_at	putative protein p76, Homo sapien	---	AT5G35160	-1.30	-0.38	-3.15	0.017117	0.055438	-3.78
254335_at	putative protein alternative oxidase	IM	AT4G22260	1.26	0.33	3.15	0.017121	0.05544	-3.78
253291_at	Expressed protein ; supported by fu	---	AT4G33865	1.42	0.50	3.14	0.017126	0.055445	-3.78
267317_at	putative proline-rich glycoprotein	---	AT2G34700	-1.27	-0.34	-3.14	0.017127	0.055445	-3.78
262132_at	ribosomal protein L22, putative sim	---	AT1G02830	-1.26	-0.33	-3.14	0.017147	0.055503	-3.78
261352_at	DNA repair protein RAD23, putativ	RAD23	AT1G79650	-1.30	-0.38	-3.14	0.017157	0.055525	-3.78
263538_at	hypothetical protein predicted by ge	---	AT2G25010	1.43	0.51	3.14	0.017165	0.055544	-3.79
252001_at	plastid division protein FtsZ-like Fts	FTSZ2-2	AT3G52750	-1.62	-0.70	-3.14	0.017197	0.055641	-3.79
264077_at	putative RAD51B-like DNA repair p	RAD51B	AT2G28560	-1.28	-0.35	-3.14	0.01721	0.055676	-3.79
250991_at	metallothionein 2b ; supported by f	MT2B	AT5G02380	1.31	0.39	3.14	0.017225	0.055715	-3.79
249589_at	pyridoxal kinase -like protein pyrido	SOS4	AT5G37850	1.22	0.29	3.14	0.017229	0.055721	-3.79
266355_at	hypothetical protein predicted by ge	---	AT2G01400	1.63	0.70	3.14	0.017263	0.055823	-3.79
247259_at	CPR5 protein, putative Constitutive	CPR5	AT5G64930	1.42	0.51	3.14	0.017266	0.055823	-3.79
250026_at	putative protein similar to unknown	---	AT5G18090	-1.32	-0.41	-3.14	0.01727	0.055823	-3.79
250170_at	putative protein ribulose-1,5-bispho	---	AT5G14260	-1.33	-0.41	-3.14	0.017271	0.055823	-3.79
262486_at	putative bzip-like transcription facto	---	AT1G21740	-1.44	-0.53	-3.14	0.017295	0.05589	-3.79
261105_at	unknown protein ;supported by full-	NRS/ER	AT1G63000	-1.39	-0.47	-3.14	0.017296	0.05589	-3.79
253361_at	putative protein various predicted p	---	AT4G33100	1.55	0.63	3.14	0.017305	0.055911	-3.79
264807_at	putative presenilin similar to presen	---	AT1G08700	1.40	0.48	3.14	0.017316	0.055937	-3.79
252121_at	GDP-D-mannose-4,6-dehydratase	MUR1	AT3G51160	-1.65	-0.72	-3.14	0.017333	0.055984	-3.80
251318_at	putative protein putative protein At2	GDAP1	AT3G61570	-1.25	-0.33	-3.14	0.01734	0.055993	-3.80
246818_at	putative protein crp1, Zea mays, P	EMB976	AT5G27270	1.68	0.75	3.14	0.01734	0.055993	-3.80
265074_at	hypothetical protein ; supported by	emb1011	AT1G55540	1.33	0.41	3.14	0.017344	0.055996	-3.80
251332_at	putative protein putative protein At2	---	AT3G61670	1.44	0.52	3.14	0.017347	0.055999	-3.80
251843_x_a	extensin precursor -like protein ext	ATHRGP1	AT3G54590	-1.61	-0.69	-3.14	0.017361	0.056036	-3.80
262066_at	hypothetical protein contains simila	---	AT1G79950	1.60	0.68	3.13	0.017364	0.056037	-3.80

252228_at	porin - like protein porin, Mesembry	VDAC5	AT3G49920	-1.24	-0.31	-3.13	0.017369	0.056047	-3.80
252680_at	putative protein predicted protein, (	---	AT3G44330	1.22	0.29	3.13	0.01738	0.056074	-3.80
267308_at	putative malonyl-CoA:Acyl carrier p	---	AT2G30200	1.34	0.42	3.13	0.017389	0.056093	-3.80
263488_at	hypothetical protein predicted by ge	---	AT2G31840	1.40	0.48	3.13	0.017391	0.056093	-3.80
254966_at	COP1 like protein photomorphoger	SPA2	AT4G11110	1.21	0.28	3.13	0.017397	0.056105	-3.80
257606_at	root hair defective 3 (RHD3) identi	RHD3	AT3G13870	-1.36	-0.44	-3.13	0.017402	0.056114	-3.80
249173_at	unknown protein	---	AT5G43000	-1.37	-0.45	-3.13	0.017406	0.056116	-3.80
258223_at	unknown protein ; supported by cD	PIFI	AT3G15840	1.33	0.41	3.13	0.017422	0.056159	-3.80
265415_at	unknown protein ;supported by full-	PSB29	AT2G20890	-1.31	-0.39	-3.13	0.017424	0.056159	-3.80
246259_at	amino acid permease, putative cor	---	AT1G31830	1.34	0.42	3.13	0.017426	0.05616	-3.80
264316_at	unknown protein ; supported by cDI	ENT1,AT	AT1G70330	-1.36	-0.44	-3.13	0.017429	0.05616	-3.80
265396_at	predicted protein	---	AT2G21040	-1.45	-0.53	-3.13	0.017433	0.056165	-3.80
264405_at	putative mitogen-activated protein	ATMPK1	AT1G10210	1.66	0.73	3.13	0.017436	0.056166	-3.80
260969_at	beta-fructosidase identical to beta-f	ATBETAFR	AT1G12240	-1.78	-0.83	-3.13	0.017454	0.056211	-3.80
247050_at	At14a protein-like	---	AT5G66660	-1.43	-0.51	-3.13	0.017455	0.056211	-3.80
259617_at	hypothetical protein predicted by ge	---	AT1G47970	1.34	0.42	3.13	0.017461	0.056222	-3.80
266192_at	unknown protein	---	AT2G39080	1.23	0.30	3.13	0.017493	0.056319	-3.81
265661_at	putative protein kinase contains a p	---	AT2G24360	1.34	0.42	3.13	0.017506	0.05635	-3.81
262495_at	unknown protein Contains similarit	---	AT1G21780	1.44	0.52	3.13	0.017508	0.05635	-3.81
255477_at	coded for by A. thaliana cDNA R64	---	AT4G02370	1.38	0.46	3.13	0.017512	0.056355	-3.81
251493_at	putative protein hypothetical protei	---	AT3G59300	1.36	0.44	3.13	0.017516	0.056362	-3.81
263965_at	putative retroelement pol polyprotei	---	---	-1.29	-0.37	-3.13	0.017519	0.056362	-3.81
251579_at	putative protein Bet1 homolog - Ra	BS14A	AT3G58170	1.26	0.33	3.13	0.017546	0.056438	-3.81
251639_at	acetylglutamate kinase-like protein	---	AT3G57560	-1.37	-0.45	-3.13	0.017548	0.056438	-3.81
250508_at	selenium-binding protein-like	---	AT5G09950	1.28	0.35	3.13	0.017563	0.056474	-3.81
264452_at	unknown protein similar to salt-indu	GRP23	AT1G10270	2.10	1.07	3.13	0.017564	0.056474	-3.81
254797_at	putative protein	---	AT4G13030	1.53	0.62	3.13	0.017582	0.056526	-3.81
248190_at	unknown protein	---	AT5G54130	1.29	0.36	3.13	0.017599	0.056572	-3.81
245454_at	disease resistance RPP5 like protei	---	AT4G16920	1.23	0.30	3.12	0.017603	0.056576	-3.81
256996_at	unknown protein similar to unknowr	---	AT3G25850	-1.23	-0.29	-3.12	0.01761	0.056591	-3.81
263980_at	hypothetical protein predicted by gr	---	AT2G42770	-1.37	-0.45	-3.12	0.017623	0.056604	-3.81
257452_at	hypothetical protein predicted by ge	---	AT1G05740	-1.24	-0.31	-3.12	0.017624	0.056604	-3.81
262929_at	hypothetical protein ;supported by f	---	AT1G65720	1.42	0.50	3.12	0.017624	0.056604	-3.81
256579_at	hypothetical protein	---	AT3G28720	1.24	0.31	3.12	0.017624	0.056604	-3.81
246691_at	putative protein predicted proteins -	---	---	-1.23	-0.30	-3.12	0.017641	0.056652	-3.81

267000_at	Expressed protein ; supported by fu	---	AT2G34310	-1.59	-0.67	-3.12	0.017655	0.056686	-3.81
261446_at	unknown protein	SEC5B	AT1G21170	-1.40	-0.48	-3.12	0.01766	0.056692	-3.82
250143_at	ADP-ribosylation factor - like protei	ATARFA1B	AT5G14670	-1.29	-0.37	-3.12	0.017664	0.056692	-3.82
262578_at	hypothetical protein Similar to gi|22	---	---	1.29	0.37	3.12	0.017664	0.056692	-3.82
254801_at	endoxyloglucan transferase-like pr	---	AT4G13080	-1.21	-0.27	-3.12	0.017687	0.056756	-3.82
245383_at	SUPERMAN like protein	---	AT4G17810	-1.58	-0.66	-3.12	0.017689	0.056756	-3.82
263842_at	Expressed protein ; supported by fu	---	AT2G36835	1.44	0.53	3.12	0.017691	0.056756	-3.82
245372_at	ribosomal protein ;supported by full	---	AT4G15000	1.63	0.71	3.12	0.017699	0.056773	-3.82
258981_at	hypothetical protein predicted by ge	---	AT3G08880	1.23	0.30	3.12	0.017701	0.056773	-3.82
262024_at	protein disulfide isomerase, putativ	ATPDIL5-2	AT1G35620	1.36	0.44	3.12	0.017728	0.056849	-3.82
265626_at	unknown protein ;supported by full-	---	AT2G27260	-1.31	-0.39	-3.12	0.017731	0.056849	-3.82
263164_at	putative glutamate/aspartate-bindin	---	AT1G03070	-1.29	-0.36	-3.12	0.017732	0.056849	-3.82
258211_at	hypothetical protein predicted by ge	---	AT3G17890	1.40	0.48	3.12	0.017755	0.056913	-3.82
256929_at	unknown protein	---	---	-1.32	-0.40	-3.12	0.017759	0.056916	-3.82
257435_at	putative RSZp22 splicing factor	---	AT2G24590	1.40	0.48	3.12	0.017763	0.056922	-3.82
258100_at	unknown protein	---	AT3G23550	3.52	1.81	3.12	0.017767	0.056927	-3.82
252026_at	serine protein kinase - like serine p	SRPK4	AT3G53030	-1.29	-0.37	-3.12	0.017771	0.056932	-3.82
260424_at	putative receptor-like protein kinas	---	AT1G72460	-1.27	-0.34	-3.12	0.017791	0.056989	-3.82
248391_at	putative protein similar to unknown	---	AT5G52030	-1.30	-0.38	-3.12	0.0178	0.057009	-3.82
246245_at	putative protein	---	AT4G36440	1.28	0.35	3.12	0.017808	0.057025	-3.82
262903_at	NADPH-dependent codeinone redu	---	AT1G59950	2.83	1.50	3.12	0.017812	0.057031	-3.82
266794_at	hypothetical protein	---	AT2G02980	1.25	0.33	3.12	0.01782	0.057048	-3.82
263028_at	protein kinase, putative similar to P	---	AT1G24030	-1.40	-0.48	-3.12	0.017829	0.05707	-3.83
251925_at	hypothetical protein ;supported by	---	AT3G54000	1.49	0.58	3.11	0.017854	0.05714	-3.83
252919_at	putative endo-1,4-beta-glucanase	AtGH9B16	AT4G38990	-1.39	-0.48	-3.11	0.017881	0.057219	-3.83
266921_at	putative cytochrome P450	CYP86A8	AT2G45970	-2.00	-1.00	-3.11	0.017904	0.057284	-3.83
257637_at	terpene synthase-related protein co	---	AT3G25810	-1.23	-0.30	-3.11	0.017907	0.057284	-3.83
245175_at	putative protein disulfide-isomerase	UNE5	AT2G47470	1.57	0.65	3.11	0.017908	0.057284	-3.83
248532_at	Expressed protein ; supported by cl	NFU2	AT5G49940	1.34	0.43	3.11	0.017916	0.057299	-3.83
246640_x_a	putative protein predicted proteins,	---	---	-1.29	-0.36	-3.11	0.017923	0.057311	-3.83
260624_at	high-affinity nitrate transporter ACH	NRT2.2	AT1G08100	-1.43	-0.52	-3.11	0.017925	0.057311	-3.83
259571_at	hypothetical protein	---	AT1G20410	1.40	0.48	3.11	0.01793	0.057319	-3.83
245608_at	protein kinase	---	AT4G14350	-1.43	-0.52	-3.11	0.017932	0.057319	-3.83
248587_at	Expressed protein ; supported by fu	---	AT5G49550	-1.29	-0.37	-3.11	0.01794	0.057335	-3.83
252304_at	hypothetical protein	---	AT3G49230	-1.22	-0.29	-3.11	0.017942	0.057335	-3.83

256196_at	hypothetical protein predicted by ge	---	---	-1.32	-0.40	-3.11	0.017949	0.05735	-3.83
253131_at	homeodomain - like protein several	WOX13	AT4G35550	-1.35	-0.43	-3.11	0.017962	0.057384	-3.83
262185_at	MADS box transcription factor, put	AGL67	AT1G77950	-1.22	-0.28	-3.11	0.01797	0.057394	-3.83
248222_at	GTPase activator protein of Rab-lik	---	AT5G53570	1.37	0.45	3.11	0.017971	0.057394	-3.83
256242_at	actin-like protein contains Pfam pro	ATARP5	AT3G12380	1.38	0.46	3.11	0.017975	0.057394	-3.83
251653_at	putative protein regulatory protein I	BOP1	AT3G57130	-1.34	-0.42	-3.11	0.017976	0.057394	-3.83
253272_at	putative protein ;supported by full-l	ספט-01	AT4G34190	-1.45	-0.54	-3.11	0.017985	0.057413	-3.83
246119_at	ankyrin-repeat protein patsas prote	TIP1	AT5G20350	1.34	0.42	3.11	0.017987	0.057413	-3.83
262060_at	polygalacturonase, putative similar	---	AT1G80170	-1.30	-0.38	-3.11	0.018011	0.057482	-3.84
266780_at	putative ligand-gated ion channel p	ATGLR2.8	AT2G29110	-1.48	-0.57	-3.11	0.018016	0.05749	-3.84
252198_x_a	putative protein predicted protein, A	---	AT3G50250	-1.46	-0.55	-3.11	0.018028	0.057521	-3.84
260937_at	hypothetical protein contains simila	---	AT1G45160	-1.22	-0.29	-3.11	0.018036	0.05754	-3.84
263160_at	oligouridylate binding protein, putat	UBP1A	AT1G54080	1.30	0.37	3.11	0.018043	0.057551	-3.84
251375_at	putative protein various predicted p	---	AT3G60410	-1.44	-0.53	-3.11	0.018045	0.057551	-3.84
254881_at	hypothetical protein	---	AT4G11700	-1.24	-0.31	-3.11	0.018047	0.057551	-3.84
249473_at	His-Asp Phosphotransfer Signal Tra	AHP3	AT5G39340	1.31	0.39	3.11	0.018062	0.057582	-3.84
253818_at	hypothetical protein	---	AT4G28330	-1.38	-0.47	-3.11	0.018062	0.057582	-3.84
247049_at	putative protein similar to unknown	---	AT5G66440	3.07	1.62	3.11	0.018067	0.057589	-3.84
249298_at	putative protein similar to unknown	---	AT5G41330	-1.27	-0.35	-3.11	0.018071	0.057595	-3.84
260215_at	unknown protein	---	AT1G74530	-1.28	-0.36	-3.11	0.018075	0.0576	-3.84
255859_at	putative protein embryonic abunda	---	AT5G34930	1.48	0.57	3.11	0.018083	0.057608	-3.84
255776_at	60S ribosomal protein L6, putative	---	AT1G18540	1.75	0.81	3.11	0.018083	0.057608	-3.84
258669_at	hypothetical protein predicted by ge	---	AT3G08800	1.25	0.32	3.10	0.018091	0.057614	-3.84
264823_at	putative serine/threonine protein ph	BSU1	AT1G03445	-1.41	-0.50	-3.10	0.018094	0.057614	-3.84
245941_at	putative protein karyopherin beta 3	emb2734	AT5G19820	-1.32	-0.40	-3.10	0.018095	0.057614	-3.84
250563_at	putative protein predicted protein, A	---	AT5G08050	-1.45	-0.54	-3.10	0.018095	0.057614	-3.84
256494_at	hypothetical protein predicted by ge	---	AT1G31520	-1.25	-0.32	-3.10	0.018121	0.057682	-3.84
247839_at	eukaryotic initiation factor 4, eIF4-li	---	AT5G57870	1.46	0.55	3.10	0.018121	0.057682	-3.84
259655_at	unknown protein	---	AT1G55210	2.17	1.12	3.10	0.018127	0.057692	-3.84
263589_at	hypothetical protein predicted by ge	---	AT2G25280	1.23	0.30	3.10	0.018144	0.057739	-3.84
246182_at	beta-1,3-glucanase - like protein pr	---	AT5G20870	-1.36	-0.44	-3.10	0.018154	0.057763	-3.84
256348_at	hypothetical protein predicted by ge	---	AT1G54880	-1.28	-0.35	-3.10	0.018163	0.057771	-3.84
264843_at	putative 1-aminocyclopropane-1-ca	---	AT1G03400	-1.53	-0.61	-3.10	0.018164	0.057771	-3.84
249368_at	putative protein predicted proteins,	---	AT5G40640	1.39	0.48	3.10	0.018165	0.057771	-3.85
251828_at	putative protein unnamed sequenc	---	AT3G55070	-1.30	-0.38	-3.10	0.018169	0.057778	-3.85

255865_at	unknown protein	---	AT2G30330	1.22	0.29	3.10	0.018175	0.057787	-3.85
267356_at	putative isoamylase	ISA1	AT2G39930	1.29	0.37	3.10	0.018182	0.057801	-3.85
265346_at	hypothetical protein	---	---	-1.27	-0.35	-3.10	0.018193	0.05783	-3.85
264957_at	F-box protein family, AtFBL5 conta	SKP2B	AT1G77000	1.55	0.63	3.10	0.018202	0.05785	-3.85
251522_at	hypothetical protein	---	AT3G59430	1.31	0.39	3.10	0.018247	0.057978	-3.85
259625_at	glyceraldehyde-3-phosphate dehyc	GAPB	AT1G42970	-1.37	-0.45	-3.10	0.018247	0.057978	-3.85
257426_at	hypothetical protein contains simila	---	AT1G54850	1.38	0.46	3.10	0.018254	0.057985	-3.85
253305_at	Expressed protein ; supported by fu	---	AT4G33666	-1.90	-0.93	-3.10	0.018257	0.057985	-3.85
246226_at	thiol-disulfide interchange like prote	HCF164	AT4G37200	1.41	0.50	3.10	0.018257	0.057985	-3.85
258447_at	hypothetical protein predicted by ge	---	AT3G22450	1.24	0.31	3.10	0.018269	0.058014	-3.85
264548_at	unknown protein ; supported by cDI	---	AT1G55680	1.28	0.35	3.10	0.018279	0.058036	-3.85
258648_at	putative auxin-independent growth	---	AT3G07900	-1.51	-0.60	-3.10	0.018281	0.058036	-3.85
252916_at	kinesin like protein kinesin-related	---	AT4G38950	-1.28	-0.35	-3.10	0.018286	0.058036	-3.85
262219_at	hypothetical protein predicted by ge	---	AT1G74750	1.49	0.57	3.10	0.018286	0.058036	-3.85
246511_at	UDP-glucose dehydrogenase-like p	---	AT5G15490	-1.79	-0.84	-3.10	0.018291	0.058044	-3.85
255728_at	unknown protein	---	AT1G25500	1.55	0.63	3.10	0.018314	0.058108	-3.85
267250_at	similar to hookless1 (HLS1)	---	AT2G23060	-1.24	-0.31	-3.10	0.018321	0.058123	-3.85
252905_at	putative protein predicted protein, A	---	AT4G39720	-1.37	-0.45	-3.10	0.018325	0.058125	-3.85
253278_at	receptor protein kinase - like protei	---	AT4G34220	-2.23	-1.16	-3.10	0.018327	0.058125	-3.85
264378_at	hypothetical protein predicted by ge	---	AT2G25220	-1.97	-0.98	-3.09	0.018367	0.058245	-3.86
262448_at	En/Spm-like transposon protein, pu	---	AT1G49450	-1.29	-0.36	-3.09	0.01837	0.058246	-3.86
264918_at	interferon-induced GTP-binding pro	---	AT1G60530	-1.27	-0.35	-3.09	0.018377	0.058259	-3.86
253719_at	putative protein, fragment prolidase	---	AT4G29490	1.22	0.28	3.09	0.018382	0.058261	-3.86
246086_at	beta-1,3-glucanase - like protein be	---	AT5G20560	-1.24	-0.31	-3.09	0.018382	0.058261	-3.86
261276_at	v-SNARE protein AtVTI1b, putative	VTI1B	AT1G26670	1.42	0.50	3.09	0.018387	0.058267	-3.86
266223_at	putative thaumatin ;supported by fu	---	AT2G28790	-2.47	-1.31	-3.09	0.018404	0.058308	-3.86
266838_at	similar to jasmonate-inducible prote	---	AT2G25980	-1.28	-0.35	-3.09	0.018405	0.058308	-3.86
247584_at	60S ribosomal protein L12 - like 60	---	AT5G60670	1.84	0.88	3.09	0.018423	0.058358	-3.86
259490_at	hypothetical protein preedicted by g	---	AT1G15800	-1.28	-0.35	-3.09	0.01844	0.058404	-3.86
266114_at	hypothetical protein predicted by ge	---	AT2G02150	-1.22	-0.28	-3.09	0.018446	0.058414	-3.86
247194_at	putative protein similar to unknown	---	AT5G65480	1.45	0.53	3.09	0.01845	0.058414	-3.86
245940_at	putative protein predicted proteins -	---	AT5G19630	-1.34	-0.42	-3.09	0.018451	0.058414	-3.86
260402_at	putative gamma-glutamyltransferas	GGT3	AT1G69820	-1.38	-0.47	-3.09	0.018461	0.058427	-3.86
247999_at	E2, ubiquitin-conjugating enzyme,	UBC30	AT5G56150	1.29	0.37	3.09	0.018462	0.058427	-3.86
246379_s_a	60S ribosomal protein L21, putative	---	AT1G57660	1.47	0.55	3.09	0.018465	0.058427	-3.86

267624_at	putative protein kinase	BIK1	AT2G39660	1.74	0.80	3.09	0.018466	0.058427	-3.86
254710_at	multidrug resistance protein/P-glyc	PGP9	AT4G18050	1.53	0.61	3.09	0.018481	0.058457	-3.86
267591_at	Expressed protein ; supported by fu	RTFL8	AT2G39705	2.02	1.01	3.09	0.018482	0.058457	-3.86
252129_at	putative protein hypothetical protei	AtHB28	AT3G50890	-1.31	-0.39	-3.09	0.018484	0.058457	-3.86
255259_at	coded for by A. thaliana cDNA W43	NDB2	AT4G05020	3.01	1.59	3.09	0.018485	0.058457	-3.86
264751_at	putative superoxide-generating NA	FRO3	AT1G23020	-2.24	-1.17	-3.09	0.01849	0.058465	-3.86
251615_at	putative protein hypothetical protei	---	AT3G57980	-1.46	-0.55	-3.09	0.018514	0.058531	-3.87
266438_at	putative carboxyphosphonoenolpyr	---	AT2G43180	1.36	0.45	3.09	0.018516	0.058531	-3.87
266913_at	hypothetical protein predicted by ge	ROPGEF4	AT2G45890	-1.22	-0.29	-3.09	0.018519	0.058532	-3.87
245246_at	hypothetical protein predicted by ge	---	AT1G44224	-1.25	-0.32	-3.09	0.018524	0.05854	-3.87
266796_at	predicted by genscan	---	AT2G02880	1.28	0.35	3.09	0.01854	0.058575	-3.87
258374_at	hypothetical protein predicted by ge	---	AT3G14360	-1.62	-0.70	-3.09	0.018541	0.058575	-3.87
246666_at	hypothetical protein	---	AT5G34830	-1.22	-0.28	-3.09	0.018568	0.058652	-3.87
250734_at	putative protein similar to unknown	---	AT5G06270	-1.88	-0.91	-3.09	0.018591	0.058716	-3.87
263979_at	En/Spm-like transposon protein rela	PDF1	AT2G42840	-1.42	-0.51	-3.08	0.018593	0.058717	-3.87
259423_at	unknown protein similar to putative	---	AT1G13880	-1.40	-0.49	-3.08	0.018599	0.058719	-3.87
249396_at	DegP protease contains similarity to	DegP9	AT5G40200	1.24	0.31	3.08	0.018599	0.058719	-3.87
245500_at	reverse transcriptase like protein	---	---	-1.25	-0.32	-3.08	0.018604	0.058727	-3.87
256263_at	5,10-methylenetetrahydrofolate de	---	AT3G12290	-1.30	-0.38	-3.08	0.018618	0.058755	-3.87
251431_at	protein synthesis initiation factor - I	EIF4G	AT3G60240	1.23	0.30	3.08	0.018618	0.058755	-3.87
256545_at	hypothetical protein predicted by ge	---	---	-1.29	-0.37	-3.08	0.018632	0.058789	-3.87
248305_at	putative protein similar to unknown	ATUSP	AT5G52560	-1.37	-0.45	-3.08	0.018634	0.058789	-3.87
261381_at	hypothetical protein predicted by ge	SDE3	AT1G05460	1.23	0.30	3.08	0.018638	0.058792	-3.87
264674_at	Expressed protein ; supported by fu	POLD4	AT1G09815	1.31	0.39	3.08	0.018646	0.058809	-3.87
247112_at	unknown protein	---	AT5G65950	1.29	0.37	3.08	0.018661	0.058849	-3.87
250698_at	putative protein similar to unknown	---	AT5G06810	1.25	0.32	3.08	0.018672	0.058875	-3.87
263150_at	heat-shock protein, putative similar	---	AT1G54050	-1.64	-0.71	-3.08	0.018674	0.058875	-3.87
250565_at	putative protein various predicted p	E13L3	AT5G08000	-1.37	-0.45	-3.08	0.018678	0.058878	-3.87
245081_at	unknown protein overlap with T20D	---	---	-1.47	-0.56	-3.08	0.018695	0.058923	-3.88
258213_at	hypothetical protein predicted by ge	---	AT3G17950	1.46	0.55	3.08	0.018697	0.058923	-3.88
246351_at	unknown protein contains similarity	---	AT1G16570	1.26	0.33	3.08	0.018706	0.058942	-3.88
260748_at	RING-H2 finger protein RHA3a, pu	---	AT1G49210	-2.52	-1.34	-3.08	0.018715	0.058962	-3.88
258388_at	putative expansin S2 precursor sim	ATEXPA12	AT3G15370	-1.23	-0.30	-3.08	0.018736	0.059019	-3.88
257420_at	hypothetical protein predicted by ge	---	AT1G77250	-1.34	-0.42	-3.08	0.018741	0.059029	-3.88
251754_at	beta-1,3-glucanase - like protein be	---	AT3G55780	-1.32	-0.40	-3.08	0.018761	0.059084	-3.88

255052_at	rab7 -like protein rab7 protein -Vigr	ATRABG3A	AT4G09720	-1.32	-0.40	-3.08	0.018776	0.05912	-3.88
266112_x_a	hypothetical protein predicted by ge	---	---	-1.33	-0.41	-3.08	0.018778	0.05912	-3.88
258697_at	putative minichromosome maintena	MCM8	AT3G09660	1.34	0.42	3.08	0.018794	0.059162	-3.88
263633_at	putative SCARECROW gene regula	SCL21	AT2G04890	1.35	0.44	3.08	0.018805	0.059189	-3.88
245688_at	prolin-rich protein, putative similar t	AGP31	AT1G28290	-3.73	-1.90	-3.08	0.018813	0.059207	-3.88
254688_at	DnaJ-like protein DnaJ-like protein	J20	AT4G13830	-1.27	-0.34	-3.08	0.018817	0.05921	-3.88
265498_at	putative C2H2-type zinc finger prote	---	AT2G15740	-1.23	-0.30	-3.08	0.018827	0.059233	-3.88
256969_at	unknown protein	---	AT3G21080	2.35	1.23	3.08	0.018831	0.059239	-3.88
259488_at	hypothetical protein preedicted by g	---	AT1G15780	1.37	0.46	3.08	0.018842	0.059263	-3.88
260951_at	hypothetical protein similar to hypot	---	AT1G06145	1.36	0.44	3.07	0.018851	0.059284	-3.88
263306_at	putative serine carboxypeptidase II	SCPL43	AT2G12480	-1.26	-0.33	-3.07	0.018854	0.059286	-3.88
262913_at	NADPH-dependent codeinone redu	---	AT1G59960	1.97	0.98	3.07	0.018875	0.059345	-3.89
257408_at	unknown protein similar to A. thalia	SON1	AT2G17310	-1.32	-0.40	-3.07	0.018891	0.059385	-3.89
262517_at	putative glutathione transferase Se	ATGSTU25	AT1G17180	4.22	2.08	3.07	0.018896	0.059388	-3.89
265375_at	unknown protein ;supported by full-	VPS2.1	AT2G06530	-1.37	-0.45	-3.07	0.018897	0.059388	-3.89
250932_s_a	putative protein MED7, Homo sapi	---	AT5G03220	1.26	0.33	3.07	0.018904	0.059402	-3.89
266598_at	3-methyl-2-oxobutanoate hydroxy-m	KPHMT1	AT2G46110	1.37	0.45	3.07	0.01891	0.059414	-3.89
249424_s_a	hypothetical protein ; supported by	---	AT5G39800	1.32	0.40	3.07	0.018919	0.059429	-3.89
256273_at	senescence-assocated protein, put	TET6	AT3G12090	1.33	0.42	3.07	0.01892	0.059429	-3.89
253531_at	putative protein tomato leucine zipp	ATEXO70G	AT4G31540	1.26	0.33	3.07	0.018928	0.059437	-3.89
259054_at	putative hypersensitivity-related ger	CHAT	AT3G03480	3.83	1.94	3.07	0.018928	0.059437	-3.89
263406_at	subtilisin-like serine protease AIR3	AIR3	AT2G04160	1.97	0.98	3.07	0.01894	0.059459	-3.89
247630_at	putative protein	SIZ1	AT5G60410	1.32	0.40	3.07	0.018941	0.059459	-3.89
250990_at	serine/threonine-specific protein kin	NAK	AT5G02290	1.60	0.68	3.07	0.018943	0.059459	-3.89
261084_at	tropinone reductase-I, putative sim	---	AT1G07440	1.51	0.60	3.07	0.018957	0.059494	-3.89
253864_at	hypothetical protein	---	AT4G27460	-1.35	-0.43	-3.07	0.018963	0.059507	-3.89
245374_at	hypothetical protein	---	AT4G17620	1.30	0.38	3.07	0.018973	0.059529	-3.89
251862_at	putative protein arm repeat contain	PUB14	AT3G54850	1.25	0.33	3.07	0.018981	0.059546	-3.89
245728_at	steroid 22-alpha-hydroxylase, puta	---	AT1G73340	-1.35	-0.43	-3.07	0.019016	0.059647	-3.89
262990_at	E2, ubiquitin-conjugating enzyme,	MMZ1	AT1G23260	-1.25	-0.32	-3.07	0.019038	0.059709	-3.89
247145_at	receptor protein kinase-like protein	---	AT5G65600	3.74	1.90	3.07	0.019056	0.059755	-3.90
252215_at	kinesin -like protein KINESIN-LIKE	KICP-02	AT3G50240	-2.02	-1.02	-3.07	0.019059	0.059756	-3.90
250385_at	aspartate aminotransferase (Asp3)	ASP3	AT5G11520	1.62	0.69	3.07	0.019067	0.059772	-3.90
245260_at	kinase like protein ; supported by cl	---	AT4G16360	1.23	0.30	3.07	0.019069	0.059772	-3.90
253079_s_a	putative protein F56F10.1, Caenorl	---	AT4G36190	1.39	0.48	3.06	0.019109	0.059891	-3.90

266736_at	putative cytochrome P450 ; suppor	CYP709B1	AT2G46960	-1.24	-0.31	-3.06	0.019115	0.0599	-3.90
266016_at	putative RING zinc finger protein ;	---	AT2G18670	1.30	0.37	3.06	0.019119	0.059903	-3.90
264654_s_a	putative sugar transport protein, EF	---	AT1G08890	-1.51	-0.59	-3.06	0.019121	0.059903	-3.90
246621_at	putative protein strong similarity to	---	AT5G36230	1.20	0.27	3.06	0.019124	0.059903	-3.90
266449_at	hypothetical protein predicted by ge	AT-P4H-1	AT2G43080	1.32	0.40	3.06	0.019128	0.059907	-3.90
262285_at	hypothetical protein predicted by ge	---	AT1G68680	1.26	0.34	3.06	0.019131	0.05991	-3.90
265948_at	1-aminocyclopropane-1-carboxylate	ACO1	AT2G19590	-1.30	-0.38	-3.06	0.019155	0.059968	-3.90
262574_at	unknown protein ESTs gb|R30529,	---	AT1G15230	1.53	0.61	3.06	0.019155	0.059968	-3.90
250298_at	putative protein NLI-interacting fac	---	AT5G11860	1.30	0.38	3.06	0.019173	0.060016	-3.90
256717_at	hypothetical protein predicted by ge	---	AT2G34110	-1.32	-0.40	-3.06	0.019177	0.060019	-3.90
250070_at	phosphoribosylanthranilate transfer	---	AT5G17980	-1.53	-0.61	-3.06	0.01918	0.060021	-3.90
261311_at	disease resistance protein RTM1, p	---	AT1G05770	-1.43	-0.51	-3.06	0.019192	0.060051	-3.90
246300_at	putative transmembrane protein GS	SAC8	AT3G51830	1.25	0.32	3.06	0.019209	0.060095	-3.90
259811_at	hypothetical protein predicted by ge	---	AT1G49830	-1.27	-0.35	-3.06	0.019235	0.060168	-3.91
246832_at	putative protein isopenicillin N epin	---	AT5G26600	1.32	0.40	3.06	0.019252	0.060212	-3.91
258525_at	hypothetical protein predicted by ge	IBR3	AT3G06810	1.41	0.49	3.06	0.019256	0.060212	-3.91
245505_at	glutaredoxin	---	AT4G15690	-1.93	-0.95	-3.06	0.019257	0.060212	-3.91
249568_at	glucosyltransferase-like protein UD	---	AT5G38040	1.33	0.41	3.06	0.019271	0.06025	-3.91
262854_at	unknown protein	---	AT1G20870	-1.28	-0.35	-3.06	0.019282	0.060273	-3.91
265041_at	unknown protein Contains similarity	TOM22-I	AT1G04070	1.48	0.57	3.06	0.019313	0.060362	-3.91
246849_at	putative protein various predicted p	---	AT5G26850	-1.75	-0.80	-3.06	0.019322	0.060383	-3.91
258273_at	unknown protein ;supported by full-	GRX4	AT3G15660	1.21	0.28	3.06	0.019334	0.060411	-3.91
263197_at	polyubiquitin, putative similar to po	---	AT1G53930	-1.32	-0.40	-3.06	0.01935	0.060447	-3.91
263826_at	hypothetical protein predicted by ge	---	AT2G40410	-1.40	-0.48	-3.06	0.01935	0.060447	-3.91
254984_s_a	putative protein Homo sapiens deu	UBP10	AT4G10570	1.20	0.26	3.06	0.019358	0.060464	-3.91
261511_at	polyadenylate-binding protein 5 ide	PAB5	AT1G71770	-1.31	-0.39	-3.06	0.019368	0.060485	-3.91
261414_at	Expressed protein ; supported by fu	---	AT1G07795	-1.44	-0.52	-3.05	0.019376	0.060498	-3.91
254922_at	RING-H2 finger protein RHA1a -like	RHA1A	AT4G11370	4.20	2.07	3.05	0.019377	0.060498	-3.91
262716_at	multicatalytic endopeptidase identi	PAB1	AT1G16470	1.38	0.46	3.05	0.019428	0.060648	-3.92
261460_at	MAP kinase, putative similar to GB	ATMPK13	AT1G07880	-1.21	-0.27	-3.05	0.019436	0.06066	-3.92
247843_at	aluminium tolerance associated - lik	SVL4	AT5G58050	-1.32	-0.40	-3.05	0.019437	0.06066	-3.92
258043_at	unknown protein ; supported by cD	---	AT3G21290	1.22	0.29	3.05	0.019441	0.060664	-3.92
258015_at	unknown protein	---	AT3G19340	-1.31	-0.39	-3.05	0.019444	0.060665	-3.92
264325_at	putative phosphoribosylanthranilate	---	AT1G04150	-1.37	-0.45	-3.05	0.019453	0.060683	-3.92
251113_at	hypothetical protein	---	AT5G01370	-1.35	-0.43	-3.05	0.019466	0.060718	-3.92

249464_at	putative protein crp1, Zea mays, P	EMB2745	AT5G39710	1.82	0.87	3.05	0.01948	0.060744	-3.92
247346_at	diacylglycerol kinase	ATDGK2	AT5G63770	1.44	0.53	3.05	0.01948	0.060744	-3.92
260601_at	Expressed protein ; supported by cI	ZIP11	AT1G55910	1.54	0.63	3.05	0.01949	0.060761	-3.92
259083_at	putative kinase similar to NIMA-rela	ATNEK2	AT3G04810	-1.26	-0.33	-3.05	0.019491	0.060761	-3.92
262175_at	unknown protein ; supported by cDI	NDH-O	AT1G74880	1.39	0.48	3.05	0.019494	0.060761	-3.92
245306_at	Expressed protein ; supported by fu	ELIP2	AT4G14690	-1.34	-0.42	-3.05	0.019512	0.06081	-3.92
266749_at	putative protein kinase contains a p	---	AT2G47060	-1.67	-0.74	-3.05	0.019519	0.060822	-3.92
259626_at	bZIP transcription factor, putative c	ATBZIP60	AT1G42990	2.44	1.29	3.05	0.01953	0.060849	-3.92
261712_at	alcohol dehydrogenase, putative si	---	AT1G32780	-1.30	-0.38	-3.05	0.019543	0.060881	-3.92
264341_at	hypothetical protein predicted by ge	---	AT1G70270	-1.22	-0.29	-3.05	0.01955	0.060896	-3.92
251631_at	putative protein several hypothetica	---	AT3G57430	1.31	0.39	3.05	0.019559	0.060915	-3.92
253506_at	putative protein EREBP-4 homolog	---	AT4G31980	-1.50	-0.59	-3.05	0.019597	0.061018	-3.93
263584_at	NAM (no apical meristem)-like prote	anac036	AT2G17040	2.16	1.11	3.05	0.019599	0.061018	-3.93
260297_at	unknown protein contains Pfam pro	---	AT1G80280	-1.30	-0.38	-3.05	0.019603	0.061018	-3.93
259118_at	unknown protein similar to unknow	---	AT3G01310	1.36	0.44	3.05	0.019604	0.061018	-3.93
254179_at	putative protein various predicted p	---	AT4G23910	1.42	0.50	3.05	0.019608	0.061018	-3.93
246989_at	unknown protein	---	AT5G67350	1.90	0.92	3.05	0.019608	0.061018	-3.93
257010_at	Expressed protein ; supported by cI	ATEXO70D	AT3G14090	-1.46	-0.55	-3.05	0.019617	0.061036	-3.93
253043_at	putative protein predicted protein, A	LBD39	AT4G37540	1.60	0.68	3.05	0.019619	0.061036	-3.93
250648_at	late embryogenesis abundant prote	---	AT5G06760	-1.30	-0.38	-3.05	0.01964	0.061092	-3.93
250764_at	putative protein similar to unknown	---	AT5G05960	-6.32	-2.66	-3.04	0.019649	0.061112	-3.93
266126_at	putative metalloproteinase ; suppo	---	AT2G45040	1.51	0.59	3.04	0.019652	0.061114	-3.93
254359_at	putative protein hypothetical protei	---	AT4G22360	-1.30	-0.38	-3.04	0.019688	0.061215	-3.93
251266_at	putative protein hypothetical protei	---	AT3G62320	-1.33	-0.41	-3.04	0.01969	0.061215	-3.93
247476_at	putative protein	---	AT5G62330	-1.26	-0.33	-3.04	0.019693	0.061216	-3.93
250944_at	putative protein	---	AT5G03380	2.40	1.26	3.04	0.019707	0.06125	-3.93
259552_at	hypothetical protein	---	AT1G21320	-1.32	-0.40	-3.04	0.019709	0.06125	-3.93
245700_at	carbonate dehydratase - like protei	ACA3	AT5G04180	-1.24	-0.31	-3.04	0.019721	0.061276	-3.93
245934_at	putative protein NAC1 - Medicago	anac082	AT5G09330	1.37	0.45	3.04	0.019724	0.061278	-3.93
252773_at	putative protein predicted proteins,	---	---	-1.23	-0.30	-3.04	0.019734	0.0613	-3.93
247131_at	ferredoxin-NADP+ reductase	FNR1	AT5G66190	-1.24	-0.31	-3.04	0.019739	0.061309	-3.93
265788_at	putative auxin-induced protein	IAA32	AT2G01200	-1.23	-0.29	-3.04	0.019749	0.06133	-3.93
260925_at	DNA-binding protein, putative cont	---	AT1G21340	-1.31	-0.39	-3.04	0.019771	0.061387	-3.93
261212_at	hypothetical protein predicted by ge	atnudt12	AT1G12880	1.46	0.54	3.04	0.019773	0.061387	-3.93
248852_at	unknown protein	---	AT5G46560	1.21	0.28	3.04	0.019776	0.061391	-3.93

262875_at	gamma-tocopherol methyltransfera	G-TMT	AT1G64970	1.32	0.40	3.04	0.019783	0.061404	-3.94
254265_s_a	serine threonine kinase - like prote	CRK6	AT4G23140	2.48	1.31	3.04	0.019806	0.061465	-3.94
264862_at	hypothetical protein predicted by ge	---	AT1G24330	-1.45	-0.53	-3.04	0.019813	0.061478	-3.94
249501_s_a	expansin-like protein expansin - Pr	ATEXP26	AT5G39270	-1.21	-0.28	-3.04	0.019834	0.061536	-3.94
259139_at	hypothetical protein similar to F16N	---	AT3G10240	-1.26	-0.34	-3.04	0.01984	0.061541	-3.94
252828_at	DnaJ - like protein DnaJ-like protei	---	AT4G39960	1.31	0.38	3.04	0.019841	0.061541	-3.94
247814_at	polyneuridine aldehyde esterase-lik	MES18	AT5G58310	-2.83	-1.50	-3.04	0.019854	0.061573	-3.94
245206_at	putative protein similarity to NCA2	DGS1	AT5G12290	1.31	0.39	3.04	0.019869	0.061607	-3.94
252470_at	protein kinase 6-like protein protein	---	AT3G46930	1.96	0.97	3.04	0.01987	0.061607	-3.94
266273_at	putative zinc transporter	MTPB1	AT2G29410	2.48	1.31	3.04	0.019877	0.061621	-3.94
265296_at	hypothetical protein predicted by ge	---	AT2G14060	-1.25	-0.32	-3.04	0.019882	0.061627	-3.94
251594_at	putative protein DOC4, Mus muscu	---	AT3G57630	2.12	1.08	3.04	0.019886	0.061631	-3.94
258296_at	putative ribosomal protein similar to	---	AT3G23390	1.72	0.78	3.04	0.019899	0.061663	-3.94
258214_at	amidase, putative similar to amidas	atToc64-III	AT3G17970	1.55	0.64	3.03	0.019939	0.061779	-3.94
252235_at	60S RIBOSOMAL PROTEIN - like	---	AT3G49910	1.60	0.67	3.03	0.019942	0.061779	-3.94
249221_at	serine/threonine protein kinase-like	---	AT5G42440	1.36	0.44	3.03	0.019962	0.061821	-3.94
250730_at	C3HC4-type RING zinc finger prote	---	AT5G06490	-1.28	-0.35	-3.03	0.019964	0.061821	-3.94
249974_at	putative protein predicted proteins,	---	AT5G18780	1.63	0.71	3.03	0.019964	0.061821	-3.94
265116_at	unknown protein ; supported by full-	---	AT1G62480	3.16	1.66	3.03	0.019967	0.061821	-3.94
251513_at	pirin-like protein pirin - Lycopersico	PRN	AT3G59220	-2.41	-1.27	-3.03	0.019972	0.061829	-3.95
255538_at	putative transcription factor ; suppo	MYB55	AT4G01680	-1.92	-0.94	-3.03	0.019984	0.061859	-3.95
248283_at	pyruvate kinase ;supported by full-	PKP-BETA	AT5G52920	1.54	0.62	3.03	0.020009	0.061921	-3.95
247874_at	101 kDa heat shock protein; HSP10	---	AT5G57710	-1.45	-0.53	-3.03	0.02001	0.061921	-3.95
245248_at	Expressed protein ; supported by c	ATB' GAMM	AT4G15415	1.19	0.26	3.03	0.020016	0.061933	-3.95
247643_at	auxin response factor 4 ; supported	ARF4	AT5G60450	1.47	0.56	3.03	0.02003	0.061967	-3.95
250072_at	putative protein similar to unknown	---	AT5G17210	-1.42	-0.50	-3.03	0.020049	0.062019	-3.95
245524_at	cytochrome c oxidoreductase like p	---	AT4G15920	-1.99	-1.00	-3.03	0.020062	0.062049	-3.95
250568_at	putative protein several putative AT	---	AT5G08110	1.28	0.35	3.03	0.020065	0.062049	-3.95
259985_at	unknown protein ; supported by cD	---	AT1G76620	-1.26	-0.34	-3.03	0.020073	0.062054	-3.95
248025_at	NOI protein, nitrate-induced	NOI	AT5G55850	-1.33	-0.42	-3.03	0.020074	0.062054	-3.95
255883_at	unknown protein similar to putative	---	AT1G20270	1.34	0.43	3.03	0.020074	0.062054	-3.95
256333_at	Sm-like protein contains Pfam profi	---	AT1G76860	1.47	0.56	3.03	0.020081	0.062068	-3.95
267350_at	putative DNA-directed RNA polyme	NRPD1B	AT2G40030	-1.34	-0.42	-3.03	0.020095	0.062084	-3.95
259313_at	hypothetical protein predicted by ge	---	AT3G05090	1.32	0.40	3.03	0.020097	0.062084	-3.95
266309_at	unknown protein ;supported by full-	---	AT2G27140	-1.41	-0.49	-3.03	0.020098	0.062084	-3.95

267017_at	unknown protein	SVR1	AT2G39140	1.71	0.77	3.03	0.020098	0.062084	-3.95
252037_at	putative calmodulin calmodulin - Te	CAM9	AT3G51920	1.47	0.56	3.03	0.0201	0.062084	-3.95
256261_at	ras-related GTP-binding protein cor	RABA4D	AT3G12160	-1.26	-0.34	-3.03	0.020124	0.062149	-3.95
259801_at	blue copper protein, putative simila	---	AT1G72230	-1.82	-0.87	-3.03	0.020145	0.062205	-3.95
260479_at	hypothetical protein predicted by ge	---	AT1G11020	1.23	0.30	3.03	0.020153	0.062222	-3.95
245359_at	carnitine racemase like protein ;sup	IBR10	AT4G14430	1.56	0.65	3.03	0.020167	0.062255	-3.96
267605_at	putative protein disulfide isomerase	ATPDIL2-3	AT2G32920	1.38	0.46	3.02	0.020192	0.062325	-3.96
258289_at	hypothetical protein predicted by ge	---	AT3G23450	-1.24	-0.31	-3.02	0.020195	0.062325	-3.96
257540_at	hypothetical protein	---	AT3G21520	-1.30	-0.38	-3.02	0.020202	0.062337	-3.96
248639_at	anthranilate N-benzoyltransferase	HCT	AT5G48930	1.48	0.57	3.02	0.020204	0.062337	-3.96
245264_at	Expressed protein ; supported by cl	---	AT4G17245	-2.09	-1.06	-3.02	0.020208	0.062341	-3.96
267579_at	metallothionein-like protein	---	AT2G42000	-1.22	-0.29	-3.02	0.020217	0.06236	-3.96
256614_at	hypothetical protein predicted by ge	---	AT3G29300	-1.26	-0.34	-3.02	0.020222	0.062367	-3.96
261402_at	wall-associated kinase 4, putative s	RFO1	AT1G79670	1.53	0.62	3.02	0.02024	0.062409	-3.96
253838_at	putative zinc finger protein zinc fing	---	AT4G27880	-1.45	-0.53	-3.02	0.020243	0.062409	-3.96
245532_at	cytochrome P450 like protein	CYP97B3	AT4G15110	-1.20	-0.27	-3.02	0.020244	0.062409	-3.96
261536_at	K Efflux antiporter KEA1 identical to	KEA1	AT1G01790	-1.39	-0.47	-3.02	0.020249	0.062415	-3.96
248799_at	ethylene responsive element bindin	ERF5	AT5G47230	3.63	1.86	3.02	0.020258	0.062437	-3.96
247177_at	unknown protein ; supported by cDI	---	AT5G65300	2.13	1.09	3.02	0.020265	0.062448	-3.96
261879_at	cytochrome P450, putative similar	CYP705A2	AT1G50520	-1.24	-0.31	-3.02	0.020285	0.062502	-3.96
253552_at	ubiquitin-specific protease 24 (UBF	UBP24	AT4G30890	1.25	0.33	3.02	0.02032	0.062595	-3.96
259784_at	auxin-induced protein, putative sim	---	AT1G29450	-1.67	-0.74	-3.02	0.020322	0.062595	-3.96
254752_at	putative protein IFA-binding protein	---	AT4G13160	1.28	0.36	3.02	0.020323	0.062595	-3.96
249790_at	putative protein similar to unknown	---	AT5G24290	-2.68	-1.42	-3.02	0.020332	0.062611	-3.96
251550_at	putative protein proline-rich protein	---	AT3G58800	-1.29	-0.37	-3.02	0.020381	0.062756	-3.97
249613_at	putative protein mDj10, Mus muscu	---	AT5G37380	1.35	0.43	3.02	0.020387	0.062766	-3.97
264314_at	unknown protein ; supported by cDI	---	AT1G70420	1.50	0.58	3.02	0.02039	0.062767	-3.97
247428_at	unknown protein	---	AT5G62600	1.22	0.29	3.02	0.020402	0.062792	-3.97
246283_at	putative protein	---	AT4G36860	-1.33	-0.42	-3.02	0.020404	0.062792	-3.97
248597_at	DNA (cytosine-5)-methyltransferase	MET1	AT5G49160	1.73	0.79	3.02	0.020445	0.062909	-3.97
262746_at	Expressed protein ; supported by fu	ATNUDX15	AT1G28960	1.21	0.28	3.02	0.020455	0.062933	-3.97
250862_s_a	40S ribosomal protein S17 -like 40	---	AT2G04390	1.51	0.60	3.02	0.020462	0.062936	-3.97
262050_at	unknown protein ;supported by full-	---	AT1G80130	-2.81	-1.49	-3.02	0.020463	0.062936	-3.97
265646_at	putative lipase	---	AT2G27360	1.30	0.38	3.02	0.020464	0.062936	-3.97
262768_at	putative beta-1,4-N-acetylglucosam	---	AT1G12990	-1.74	-0.80	-3.02	0.020469	0.06294	-3.97

246563_at	putative protein	---	AT5G15581	-1.33	-0.41	-3.01	0.020474	0.062949	-3.97
246655_at	hypothetical protein	---	AT5G35230	-1.26	-0.33	-3.01	0.020479	0.062952	-3.97
254225_at	putative major latex protein major l	---	AT4G23670	-2.90	-1.54	-3.01	0.020481	0.062952	-3.97
262260_at	major latex protein (MLP149), puta	MLP34	AT1G70850	-1.42	-0.51	-3.01	0.02049	0.062972	-3.97
246779_at	putative protein peroxisomal integra	PNC2	AT5G27520	-1.57	-0.65	-3.01	0.020512	0.063028	-3.97
261794_at	hypothetical protein contains simila	---	AT1G16060	-1.34	-0.43	-3.01	0.020514	0.063028	-3.97
254053_s_a	SRG1-like protein strong homology	---	AT4G25300	1.56	0.65	3.01	0.020555	0.063147	-3.98
260785_at	hypothetical protein predicted by ge	---	AT1G06200	1.26	0.34	3.01	0.020576	0.063203	-3.98
253476_at	S-receptor kinase -like protein seri	SD2-5	AT4G32300	-1.64	-0.71	-3.01	0.020607	0.063289	-3.98
253695_at	arginine methyltransferase (pam1)	PRMT11	AT4G29510	1.41	0.50	3.01	0.020615	0.063306	-3.98
263504_s_a	hypothetical protein	---	AT2G07677	1.24	0.31	3.01	0.020619	0.063308	-3.98
258437_at	unknown protein contains protein pl	---	AT3G16560	1.46	0.55	3.01	0.020627	0.063318	-3.98
260499_at	unknown protein ; supported by cD	---	AT2G41760	-1.24	-0.31	-3.01	0.020628	0.063318	-3.98
260944_at	beta-galactosidase, putative simila	BGAL5	AT1G45130	-4.32	-2.11	-3.01	0.020644	0.063358	-3.98
248591_at	xylulose kinase ; supported by cDN	---	AT5G49650	-1.31	-0.39	-3.01	0.020648	0.063358	-3.98
246323_at	hypothetical protein predicted by ge	---	AT1G16690	-1.33	-0.41	-3.01	0.020649	0.063358	-3.98
257279_at	unknown protein ;supported by full-	---	AT3G14430	1.27	0.34	3.01	0.020656	0.06337	-3.98
248889_at	unknown protein ;supported by full-	---	AT5G46230	1.50	0.59	3.01	0.020673	0.063415	-3.98
265770_at	Expressed protein ; supported by fu	---	AT2G48100	1.34	0.43	3.01	0.020687	0.063449	-3.98
245888_at	putative protein DNA-binding prote	---	AT5G09450	1.28	0.35	3.01	0.020691	0.063453	-3.98
261387_at	hypothetical protein predicted by ge	---	AT1G05410	1.52	0.61	3.01	0.02071	0.063504	-3.98
262441_at	hypothetical protein similar to hypot	OSB1	AT1G47720	1.32	0.40	3.01	0.020728	0.063548	-3.98
259120_at	unknown protein	---	AT3G02240	4.43	2.15	3.00	0.020761	0.063641	-3.99
256613_at	hypothetical protein predicted by ge	emb2076	AT3G29290	1.36	0.45	3.00	0.020802	0.06376	-3.99
258249_s_a	unknown protein ; supported by ful	---	AT3G15820	-1.43	-0.51	-3.00	0.020823	0.063815	-3.99
263585_at	60S ribosomal protein L39	---	AT2G25210	1.69	0.76	3.00	0.020837	0.063845	-3.99
266231_at	putative protein kinase	PSKR1	AT2G02220	2.21	1.14	3.00	0.020838	0.063845	-3.99
250163_at	putative protein various predicted p	---	AT5G15270	-1.30	-0.38	-3.00	0.020845	0.063857	-3.99
261698_at	unknown protein identical to hypoth	---	AT1G32630	1.34	0.42	3.00	0.020855	0.063878	-3.99
262046_at	hypothetical protein predicted by ge	OFP14	AT1G79960	-1.35	-0.44	-3.00	0.020882	0.063946	-3.99
263663_at	putative malate dehydrogenase sim	---	AT1G04410	1.26	0.34	3.00	0.020883	0.063946	-3.99
248818_at	Lon protease homolog 1 precursor	LON2	AT5G47040	-1.37	-0.46	-3.00	0.020887	0.063951	-3.99
247139_at	unknown protein ;supported by full-	---	AT5G66090	1.28	0.36	3.00	0.020892	0.063953	-3.99
246987_at	myb-related protein, 33.3K (pir |S7	MYBR1	AT5G67300	-1.58	-0.66	-3.00	0.020893	0.063953	-3.99
255104_at	Expressed protein ; supported by fu	SAH7	AT4G08685	-2.37	-1.24	-3.00	0.020907	0.063981	-3.99

260874_at	hypothetical protein predicted by ge	emb2170	AT1G21390	1.33	0.41	3.00	0.020908	0.063981	-3.99
248108_at	molybdopterin synthase sulphurylas	CNX5	AT5G55130	1.31	0.38	3.00	0.020914	0.063992	-3.99
247873_at	diacylglycerol kinase-like protein	---	AT5G57690	-1.24	-0.31	-3.00	0.020927	0.064021	-3.99
259753_at	putative isoprenylated protein simila	---	AT1G71050	-1.44	-0.52	-3.00	0.020939	0.064051	-4.00
250449_at	embryonic abundant protein -like e	---	AT5G10830	-1.69	-0.76	-3.00	0.020942	0.064051	-4.00
258350_at	unknown protein similar to serine/th	CIPK1	AT3G17510	-1.67	-0.74	-3.00	0.020951	0.064071	-4.00
262275_at	ATPase, putative similar to chroma	---	AT1G68710	1.30	0.38	3.00	0.020959	0.064084	-4.00
255385_at	putative hydrolase	---	AT4G03610	-1.36	-0.44	-3.00	0.020977	0.064131	-4.00
251207_at	putative protein ;supported by full-l	---	AT3G63050	1.57	0.65	3.00	0.020988	0.064157	-4.00
249601_at	quinone oxidoreductase -like prote	---	AT5G37980	-1.36	-0.45	-3.00	0.020997	0.064162	-4.00
266768_s_a	ubiquitin extension protein (UBQ6)	UBQ6	AT2G47110	1.44	0.53	3.00	0.020997	0.064162	-4.00
253317_at	putative protein	---	AT4G33960	1.74	0.80	3.00	0.020998	0.064162	-4.00
252502_at	copper transport protein - like prote	COPT2	AT3G46900	1.99	0.99	3.00	0.021008	0.064185	-4.00
253149_at	NAD+ dependent isocitrate dehydr	---	AT4G35650	-1.28	-0.36	-3.00	0.021016	0.064198	-4.00
266949_s_a	unknown protein ;supported by full-	---	AT2G18840	-1.34	-0.42	-3.00	0.021018	0.064198	-4.00
265792_at	predicted by genscan and genefind	---	AT2G01390	-1.31	-0.39	-3.00	0.021024	0.064202	-4.00
245514_at	OEP8 like protein	---	AT4G15810	-1.44	-0.53	-3.00	0.021025	0.064202	-4.00
255808_at	putative protein predicted protein, /	---	AT4G10280	1.29	0.36	3.00	0.021034	0.06422	-4.00
254164_at	putative protein ;supported by full-l	TIFY1	AT4G24470	1.28	0.35	2.99	0.021045	0.064245	-4.00
257102_at	endoxyloglucan transferase, putati	XTH3	AT3G25050	-1.21	-0.28	-2.99	0.021066	0.064296	-4.00
256452_at	hypothetical protein predicted by ge	AtHB33	AT1G75240	-2.32	-1.21	-2.99	0.021068	0.064296	-4.00
262593_at	putative ubiquinol--cytochrome-c re	---	AT1G15120	1.47	0.55	2.99	0.02107	0.064296	-4.00
253767_at	12S cruciferin seed storage protein	CRU3	AT4G28520	-1.27	-0.34	-2.99	0.021086	0.064334	-4.00
267030_at	unknown protein	SCAR2	AT2G38440	-1.24	-0.32	-2.99	0.021095	0.064353	-4.00
249720_at	fimbrin ; supported by cDNA: gi_15	FIM2	AT5G35700	1.25	0.33	2.99	0.021099	0.064359	-4.00
252833_at	Expressed protein ; supported by cl	AGP3	AT4G40090	-1.24	-0.31	-2.99	0.021111	0.064385	-4.00
257689_at	myb-related protein, putative myb-r	AtMYB10	AT3G12820	-1.28	-0.35	-2.99	0.02112	0.0644	-4.00
255704_at	putative proline-rich protein ;suppo	---	AT4G00170	1.22	0.28	2.99	0.021121	0.0644	-4.00
250676_at	harpin-induced protein-like ; suppo	NHL3	AT5G06320	-1.51	-0.59	-2.99	0.021129	0.0644	-4.00
255487_at	tryptophan synthase alpha 1-like p	---	AT4G02610	1.30	0.38	2.99	0.02113	0.0644	-4.00
253260_at	hypothetical protein	---	AT4G34420	-1.28	-0.36	-2.99	0.02113	0.0644	-4.00
260271_at	unknown protein similar to unknowr	---	AT1G63690	1.25	0.32	2.99	0.021134	0.064404	-4.00
252282_at	6-phosphogluconolactonase - like p	---	AT3G49360	1.23	0.30	2.99	0.021144	0.064428	-4.01
246084_at	putative protein predicted proteins,	ATBRXL4	AT5G20540	-1.29	-0.37	-2.99	0.021169	0.064492	-4.01
259027_at	hypothetical protein predicted by ge	---	AT3G09280	-1.21	-0.27	-2.99	0.021185	0.064534	-4.01

246760_at	putative protein predicted proteins,	---	AT5G27970	-1.24	-0.31	-2.99	0.021195	0.064548	-4.01
258936_s_a	hypothetical protein similar to hypo	---	---	-1.25	-0.32	-2.99	0.021196	0.064548	-4.01
245308_at	putative protein ; supported by cDN	---	AT4G17486	-1.23	-0.30	-2.99	0.021198	0.064548	-4.01
265184_at	unknown protein ;supported by full-	---	AT1G23710	2.55	1.35	2.99	0.021201	0.064548	-4.01
251986_at	putative protein various predicted p	---	AT3G53310	1.68	0.75	2.99	0.021222	0.064605	-4.01
245713_at	S-adenosyl-L-methionine:salicylic a	NAMT1	AT5G04370	-1.40	-0.49	-2.99	0.021228	0.064612	-4.01
266425_at	putative strictosidine synthase	---	AT2G41300	-1.29	-0.37	-2.99	0.021255	0.064685	-4.01
248521_s_a	nodulin-like protein ; supported by c	---	AT5G50520	1.27	0.34	2.99	0.021284	0.064766	-4.01
258983_at	putative aminotransferase similar t	---	AT3G08860	2.14	1.10	2.99	0.02132	0.064866	-4.01
264392_at	hypothetical protein Similar to salt-i	---	AT1G11900	1.34	0.42	2.98	0.021356	0.064966	-4.02
253984_at	isp4 like protein isp4 protein -Schiz	OPT5	AT4G26590	-1.29	-0.37	-2.98	0.021358	0.064966	-4.02
265441_at	unknown protein ;supported by full-	---	AT2G20870	-1.37	-0.46	-2.98	0.021378	0.065018	-4.02
256767_at	hypothetical protein predicted by ge	---	AT3G13680	-1.26	-0.33	-2.98	0.021389	0.065038	-4.02
265096_at	unknown protein Location of ESTs	---	AT1G04030	1.31	0.39	2.98	0.021391	0.065038	-4.02
257080_at	unknown protein	---	AT3G15240	-1.20	-0.27	-2.98	0.021413	0.065099	-4.02
249342_at	putative protein ATP12 protein pre	---	AT5G40660	1.30	0.38	2.98	0.021417	0.065102	-4.02
258737_at	unknown protein similar to unknowr	---	AT3G05940	-1.24	-0.32	-2.98	0.02143	0.065133	-4.02
246796_at	putative protein myosin heavy chai	---	AT5G26770	-1.38	-0.47	-2.98	0.021433	0.065133	-4.02
253756_at	Cdk-activating kinase CAK1At ; sup	CAK1AT	AT4G28980	-1.21	-0.28	-2.98	0.021444	0.065146	-4.02
251115_at	putative protein symplekin - Homo	ESP4	AT5G01400	1.27	0.35	2.98	0.021448	0.065146	-4.02
259604_at	20S proteasome beta subunit (PBG	PBG1	AT1G56450	1.25	0.33	2.98	0.021455	0.065146	-4.02
262952_at	hypothetical protein predicted by ge	---	AT1G75770	-1.34	-0.42	-2.98	0.021455	0.065146	-4.02
245504_at	glutaredoxin	---	AT4G15660	-1.49	-0.57	-2.98	0.021455	0.065146	-4.02
245346_at	putative beta-amylase ;supported b	CT-BMY	AT4G17090	-1.34	-0.42	-2.98	0.021456	0.065146	-4.02
265157_at	putative reverse transcriptase simila	---	---	-1.28	-0.35	-2.98	0.021462	0.065146	-4.02
262346_at	unknown protein similar to hypothet	---	AT1G63980	1.38	0.46	2.98	0.021462	0.065146	-4.02
264938_at	unknown protein contains similarity	---	AT1G60610	1.27	0.35	2.98	0.021463	0.065146	-4.02
264186_at	hypothetical protein predicted by ge	---	AT1G54570	1.86	0.90	2.98	0.021505	0.065257	-4.02
256543_at	unknown protein supported by full-l	---	AT1G42480	1.31	0.39	2.98	0.021506	0.065257	-4.02
261610_at	hypothetical protein predicted by ge	---	AT1G49560	1.49	0.57	2.98	0.021512	0.06527	-4.02
248884_at	putative protein similar to unknown	---	AT5G46030	1.22	0.29	2.98	0.021521	0.065286	-4.02
259909_at	unknown protein ; supported by full-	MEE9	AT1G60870	1.24	0.31	2.98	0.021527	0.065292	-4.02
260700_at	hypothetical protein identical to hyp	---	AT1G32260	1.31	0.39	2.98	0.021528	0.065292	-4.02
252583_at	putative protein several hypothetica	---	AT3G45540	-1.28	-0.35	-2.98	0.021546	0.065336	-4.03
244984_at	ribosomal protein S3	---	---	-1.43	-0.52	-2.98	0.02157	0.065402	-4.03

258110_at	putative cytochrome P450 similar to	CYP72A7	AT3G14610	1.35	0.43	2.98	0.021581	0.065425	-4.03
264440_at	unknown protein similar to fim prot	---	AT1G27340	1.24	0.31	2.98	0.021592	0.065451	-4.03
261365_at	proton pump interactor, putative sir	---	AT1G53110	1.88	0.91	2.98	0.021601	0.065469	-4.03
252590_at	putative protein kinase NPK1-relate	---	AT3G45670	-1.27	-0.35	-2.98	0.021611	0.06549	-4.03
256209_at	electron transport flavoprotein, puta	ETFALPHA	AT1G50940	1.27	0.34	2.98	0.021615	0.065491	-4.03
257705_at	unknown protein ; supported by cD	---	AT3G12760	1.19	0.26	2.98	0.021617	0.065491	-4.03
267599_at	putative serine/threonine protein kir	---	AT2G32850	-1.23	-0.30	-2.98	0.021622	0.065498	-4.03
249774_at	squalene monooxygenase	SQP1	AT5G24150	-1.53	-0.61	-2.97	0.021635	0.065529	-4.03
250366_at	putative protein predicted proteins	---	AT5G11420	-4.46	-2.16	-2.97	0.021638	0.065529	-4.03
255847_at	putative thioredoxin	ACHT3	AT2G33270	-1.21	-0.27	-2.97	0.021698	0.065701	-4.03
262933_at	polyamine oxidase, putative similar	ATPAO4	AT1G65840	-1.48	-0.57	-2.97	0.021707	0.065719	-4.03
246924_at	putative protein KIAA0332 - Homo	---	AT5G25060	1.21	0.28	2.97	0.021723	0.065759	-4.03
254231_at	putative protein AR411 - Arabidops	WRKY53	AT4G23810	3.75	1.91	2.97	0.021728	0.065759	-4.03
262711_at	hypothetical protein predicted by ge	---	AT1G16500	1.43	0.52	2.97	0.021733	0.065759	-4.03
250873_at	lipase -like protein lipase Arab-1, A	---	AT5G03980	-1.28	-0.36	-2.97	0.021734	0.065759	-4.03
257854_at	putative CREB-binding protein simil	HAC5	AT3G12980	-1.27	-0.34	-2.97	0.021739	0.065759	-4.03
246261_at	unknown protein	---	AT1G31810	1.29	0.36	2.97	0.02174	0.065759	-4.03
263254_x_a	hypothetical protein similar to hypot	---	---	-1.39	-0.48	-2.97	0.02174	0.065759	-4.03
248693_at	regulator of chromosome condensa	---	AT5G48330	1.42	0.51	2.97	0.021761	0.065815	-4.04
253076_at	NAM like protein P.hybrida NAM ge	ANAC076	AT4G36160	-1.26	-0.33	-2.97	0.021766	0.06582	-4.04
264446_at	putative nuclear transport factor sir	NTF2A	AT1G27310	1.28	0.36	2.97	0.02183	0.066004	-4.04
264221_s_a	unknown protein contains similarity	emb1220	AT1G60170	1.28	0.36	2.97	0.021843	0.066035	-4.04
256905_at	mitochondrial chaperonin hsp60 id	HSP60	AT3G23990	1.75	0.81	2.97	0.021874	0.066119	-4.04
264421_at	ribosomal protein identical to riboso	ARP1	AT1G43170	1.41	0.50	2.97	0.021876	0.066119	-4.04
253763_at	xyloglucan endotransglycosylase -	---	AT4G28850	-1.22	-0.29	-2.97	0.021899	0.066171	-4.04
250726_at	putative protein similar to unknown	---	AT5G06410	1.34	0.42	2.97	0.0219	0.066171	-4.04
257177_at	cyanate lyase (CYN) identical to cy	CYN	AT3G23490	1.42	0.50	2.97	0.021902	0.066171	-4.04
261595_at	hypothetical protein predicted by ge	---	AT1G33070	-1.21	-0.27	-2.97	0.021914	0.066196	-4.04
259342_at	unknown protein ;supported by full-	---	AT3G03890	1.39	0.48	2.97	0.021918	0.066196	-4.04
267569_at	putative photosystem II oxygen-evo	PSBP-2	AT2G30790	-1.52	-0.60	-2.97	0.021919	0.066196	-4.04
250105_at	putative protein contains similarity t	RAD4	AT5G16630	1.56	0.64	2.97	0.021936	0.066228	-4.04
258085_at	unknown protein ; supported by cD	---	AT3G26100	1.31	0.39	2.97	0.021936	0.066228	-4.04
261482_at	unknown protein ;supported by full-	THH1	AT1G14530	-1.28	-0.36	-2.96	0.021939	0.066228	-4.04
245874_at	unknown protein	---	AT1G26250	-1.29	-0.36	-2.96	0.021945	0.066235	-4.04
265922_at	putative sugar transporter	---	AT2G18480	-1.25	-0.32	-2.96	0.021947	0.066235	-4.04

260085_at	putative D-ribulose-5-phosphate sir	---	AT1G63290	1.24	0.31	2.96	0.021951	0.066239	-4.04
251788_at	putative protein	---	AT3G55420	-1.75	-0.80	-2.96	0.021957	0.066249	-4.05
266642_at	putative chloroplast RNA binding pr	---	AT2G35410	-1.28	-0.35	-2.96	0.021991	0.066343	-4.05
262715_at	putative myb-related transcription fa	MYB58	AT1G16490	-1.20	-0.26	-2.96	0.022018	0.066414	-4.05
265571_s_a	unknown protein	---	AT2G28020	1.24	0.31	2.96	0.022052	0.066508	-4.05
265707_at	unknown protein	---	AT2G03390	1.32	0.40	2.96	0.02206	0.066518	-4.05
259087_at	hypothetical protein, contains DnaJ	---	AT3G04980	1.21	0.27	2.96	0.022061	0.066518	-4.05
246846_at	putative protein	---	AT5G26760	1.23	0.30	2.96	0.022075	0.066542	-4.05
251199_at	transport inhibitor response 1 (TIR	TIR1	AT3G62980	-1.50	-0.59	-2.96	0.022075	0.066542	-4.05
259140_at	lycopene beta cyclase identical to ly	LYC	AT3G10230	1.23	0.30	2.96	0.022081	0.066551	-4.05
258291_at	putative protein kinase similar to pr	---	AT3G23310	-1.30	-0.38	-2.96	0.022109	0.066628	-4.05
258133_at	ethylene-responsive transcriptional	MBF1C	AT3G24500	1.40	0.48	2.96	0.022112	0.066629	-4.05
266915_at	hypothetical protein predicted by ge	---	AT2G45870	-1.24	-0.31	-2.96	0.022124	0.066654	-4.05
264343_at	unknown protein ; supported by ful	---	AT1G11850	-1.46	-0.55	-2.96	0.022144	0.066707	-4.05
260107_at	fructokinase, putative similar to fru	---	AT1G66430	-2.46	-1.30	-2.96	0.022155	0.066721	-4.05
254399_at	G10 - like protein Maternal G10 lik	---	AT4G21110	1.22	0.28	2.96	0.022156	0.066721	-4.05
246072_at	PISTILLATA ; supported by full-len	PI	AT5G20240	1.23	0.30	2.96	0.022157	0.066721	-4.05
246159_at	Expressed protein ; supported by fu	---	AT5G20935	1.56	0.64	2.96	0.022169	0.066746	-4.06
250877_at	putative protein predicted protein, A	SDP1	AT5G04040	-1.40	-0.48	-2.96	0.022176	0.066758	-4.06
256777_at	hypothetical protein predicted by ge	---	AT3G13780	1.25	0.33	2.96	0.022183	0.066771	-4.06
259419_at	acyl-CoA oxidase ACX3, putative s	ACX6	AT1G06310	-1.25	-0.32	-2.96	0.022192	0.06679	-4.06
246010_at	putative protein predicted proteins,	---	AT5G08440	1.21	0.28	2.96	0.022209	0.066831	-4.06
257297_at	unknown protein contains Pfam pr	---	AT3G28040	-1.79	-0.84	-2.96	0.022212	0.066831	-4.06
258063_at	putative cytochrome P450 similar to	CYP72A8	AT3G14620	2.07	1.05	2.96	0.022218	0.066837	-4.06
260459_at	hypothetical protein predicted by ge	---	AT1G68240	-1.28	-0.35	-2.96	0.022219	0.066837	-4.06
253296_at	putative protein inositol 1,3,4-trisph	---	AT4G33770	-1.25	-0.32	-2.96	0.022237	0.06688	-4.06
263760_at	unknown protein ; supported by cD	SULA	AT2G21280	-1.48	-0.57	-2.96	0.022239	0.06688	-4.06
254182_at	putative protein various npredicted	---	AT4G23950	1.32	0.40	2.95	0.022262	0.066928	-4.06
257729_at	histone deacetylase, putative conta	HDA15	AT3G18520	1.41	0.49	2.95	0.022263	0.066928	-4.06
252141_at	putative protein	---	AT3G51100	1.22	0.28	2.95	0.022266	0.066928	-4.06
254482_at	TWIN SISTER OF FT (TSF) termin	TSF	AT4G20370	-1.32	-0.40	-2.95	0.022267	0.066928	-4.06
256928_at	unknown protein	---	AT3G22590	-1.28	-0.35	-2.95	0.022275	0.066939	-4.06
264240_at	protein kinase, putative Simisimilar	---	AT1G54820	-2.60	-1.38	-2.95	0.022277	0.066939	-4.06
255833_at	unknown protein	---	AT2G33390	1.30	0.38	2.95	0.022282	0.066946	-4.06
251083_at	hypothetical protein ; supported by	---	AT5G01590	-1.27	-0.35	-2.95	0.022309	0.067018	-4.06

251707_at	protein kinase C inhibitor-like prote	---	AT3G56490	1.29	0.36	2.95	0.022317	0.067031	-4.06
262761_at	unknown protein ESTs gb|AA3957	---	AT1G10720	-1.40	-0.48	-2.95	0.022319	0.067031	-4.06
264071_at	putative carboxypeptidase ; suppor	SCPL51	AT2G27920	-1.53	-0.61	-2.95	0.022355	0.067128	-4.06
263665_at	putative putative 60S ribosomal pro	---	AT1G04480	1.54	0.62	2.95	0.022357	0.067128	-4.06
254810_at	putative protein pectinesterase - C	PME1	AT4G12390	1.73	0.79	2.95	0.022375	0.067168	-4.06
257461_at	hypothetical protein predicted by ge	ATPUP15	AT1G75470	-1.21	-0.27	-2.95	0.022377	0.067168	-4.07
255366_x_a	putative transposon protein	---	---	-1.27	-0.34	-2.95	0.022407	0.067252	-4.07
257841_at	nitrate transporter, putative similar	---	AT3G25260	-1.24	-0.31	-2.95	0.022429	0.067308	-4.07
267210_at	dihydroxypolyprenylbenzoate methy	ATCOQ3	AT2G30920	-1.20	-0.26	-2.95	0.022452	0.067368	-4.07
261731_s_a	hypothetical protein similar to hypot	---	AT1G47780	-1.21	-0.28	-2.95	0.022458	0.067378	-4.07
260813_at	VirE2-interacting protein VIP1 ident	VIP1	AT1G43700	1.40	0.48	2.95	0.022468	0.06739	-4.07
262467_at	hypothetical protein similar to hypot	FU	AT1G50240	-1.32	-0.40	-2.95	0.022468	0.06739	-4.07
262512_at	Expressed protein ; supported by fu	---	AT1G17145	1.69	0.76	2.95	0.022478	0.067412	-4.07
267603_at	unknown protein ; supported by cD	ATZW10	AT2G32900	-1.33	-0.41	-2.95	0.022485	0.067415	-4.07
247409_at	dihydroneopterin aldolase-like prote	---	AT5G62980	1.45	0.53	2.95	0.022492	0.067415	-4.07
262158_at	somatic embryogenesis receptor-li	---	AT1G52540	1.44	0.53	2.95	0.022493	0.067415	-4.07
251412_at	RING-H2 zinc finger protein ATL4	ATL4	AT3G60220	-1.72	-0.78	-2.95	0.022494	0.067415	-4.07
265369_s_a	putative retroelement pol polyprotei	---	---	-1.24	-0.31	-2.95	0.022494	0.067415	-4.07
249914_at	protease-like protein	---	AT5G22850	1.36	0.44	2.95	0.0225	0.067417	-4.07
258896_at	putative syntaxin protein, AtSNAP3	SYP43	AT3G05710	-1.29	-0.37	-2.95	0.022501	0.067417	-4.07
250123_at	putative protein contains similarity t	PIN5	AT5G16530	1.32	0.40	2.95	0.022519	0.067462	-4.07
263941_at	unknown protein	---	---	-1.33	-0.41	-2.95	0.022526	0.067474	-4.07
258049_at	hypothetical protein similar to CGI-1	---	AT3G16220	1.22	0.29	2.94	0.022558	0.067546	-4.07
263840_at	Expressed protein ; supported by fu	---	AT2G36885	-1.41	-0.50	-2.94	0.022558	0.067546	-4.07
247542_at	autophagocytosis protein - like aut	ATG3	AT5G61500	1.32	0.40	2.94	0.022559	0.067546	-4.07
263385_at	ABA-regulated gene (ATEM6) ; su	GEA6	AT2G40170	-1.33	-0.41	-2.94	0.022571	0.067575	-4.07
247383_at	putative protein contains similarity t	---	AT5G63410	1.56	0.64	2.94	0.022576	0.067576	-4.07
253431_at	putative protein predicted protein, A	---	AT4G32440	1.28	0.36	2.94	0.022578	0.067576	-4.07
264613_at	lipoyltransferase identical to GB:BA	LIP2	AT1G04640	-1.28	-0.36	-2.94	0.022596	0.067613	-4.08
260351_at	hypothetical protein predicated by g	---	AT1G69380	1.64	0.71	2.94	0.022596	0.067613	-4.08
247423_at	putative protein predicted proteins,	---	AT5G62830	-1.22	-0.29	-2.94	0.022606	0.067634	-4.08
249606_at	putative protein DNA-binding prote	RVE2	AT5G37260	1.28	0.35	2.94	0.022611	0.06764	-4.08
248684_at	Expressed protein ; supported by fu	DIR1	AT5G48485	1.99	0.99	2.94	0.022635	0.067702	-4.08
247073_at	33 kDa polypeptide of oxygen-evol	PSBO1	AT5G66570	-1.22	-0.29	-2.94	0.022654	0.067751	-4.08
255093_s_a	putative microfibril-associated prote	---	AT4G08580	1.22	0.29	2.94	0.022663	0.067765	-4.08

246047_at	putative protein predicted proteins,	---	---	-1.27	-0.34	-2.94	0.022664	0.067765	-4.08
258796_at	unknown protein ;supported by full-	WDL1	AT3G04630	-1.69	-0.76	-2.94	0.022675	0.067786	-4.08
248514_s_a	unknown protein	---	AT5G50510	-1.23	-0.30	-2.94	0.022684	0.067804	-4.08
247864_s_a	anthranilate synthase beta chain ;s	---	AT1G24807	2.38	1.25	2.94	0.022689	0.06781	-4.08
250172_at	putative protein	---	AT5G14330	-1.38	-0.46	-2.94	0.022692	0.06781	-4.08
249453_at	v-SNARE AtVTI1a	SGR4	AT5G39510	1.21	0.28	2.94	0.022713	0.067865	-4.08
261249_at	hypothetical protein predicted by ge	---	AT1G05880	-1.27	-0.35	-2.94	0.022731	0.06791	-4.08
257824_at	unknown protein ; supported by cD	---	AT3G25290	1.58	0.66	2.94	0.022734	0.06791	-4.08
258389_at	hypothetical protein predicted by ge	SDE5	AT3G15390	1.34	0.42	2.94	0.02274	0.067919	-4.08
249150_at	inorganic phosphate transporter (db	PHT6	AT5G43340	-1.23	-0.30	-2.94	0.022749	0.067938	-4.08
256043_at	hypothetical protein contains Pfam	---	AT1G07210	1.42	0.50	2.94	0.022773	0.068	-4.08
255185_at	hypothetical protein	---	AT4G07740	-1.27	-0.34	-2.94	0.022796	0.068061	-4.08
260596_at	unknown protein	TIM50	AT1G55900	1.49	0.58	2.94	0.022801	0.068066	-4.08
264069_at	putative rubisco subunit binding-pro	CPN60A	AT2G28000	1.45	0.53	2.94	0.022804	0.068066	-4.08
253704_at	X-Pro dipeptidase - like protein (fra	---	AT4G29490	1.28	0.35	2.94	0.022807	0.068066	-4.09
258691_at	unknown protein	---	AT3G08630	-1.88	-0.91	-2.94	0.022829	0.068123	-4.09
261068_at	tropinone reductase-I, putative sim	---	AT1G07450	-1.27	-0.34	-2.94	0.022869	0.068232	-4.09
264011_at	unknown protein	---	AT2G21090	1.29	0.36	2.93	0.022885	0.068269	-4.09
265694_at	hypothetical protein predicted by ge	---	AT2G24440	1.30	0.37	2.93	0.022887	0.068269	-4.09
254646_at	putative protein	---	AT4G18530	1.36	0.45	2.93	0.022902	0.068306	-4.09
260081_at	unknown protein	---	AT1G78170	-2.94	-1.56	-2.93	0.022907	0.06831	-4.09
255252_at	contains similarity to Gossypium hir	---	AT4G04990	-1.25	-0.32	-2.93	0.022912	0.068317	-4.09
267128_at	putative acetone-cyanohydrin lyase	MES1	AT2G23620	-1.33	-0.41	-2.93	0.022925	0.068348	-4.09
246889_at	putative protein various predicted p	---	AT5G25470	-1.32	-0.41	-2.93	0.02296	0.068439	-4.09
265861_at	hypothetical protein predicted by ge	---	AT2G01790	-1.27	-0.34	-2.93	0.022962	0.068439	-4.09
264700_at	hypothetical protein predicted by ge	---	AT1G70100	-1.33	-0.41	-2.93	0.022973	0.068464	-4.09
249898_at	alkaline/neutral invertase ; supporte	---	AT5G22510	1.40	0.48	2.93	0.022995	0.068516	-4.09
245679_at	clathrin-associated protein, putative	---	AT1G56590	-1.28	-0.36	-2.93	0.022997	0.068516	-4.09
262782_at	Expressed protein ; supported by fu	---	AT1G13195	1.24	0.31	2.93	0.023007	0.068538	-4.09
246971_at	Protein phosphatase 2C-like protei	---	AT5G24940	-1.24	-0.31	-2.93	0.023019	0.068563	-4.09
257965_at	unknown protein ;supported by full-	---	AT3G19900	1.44	0.52	2.93	0.023032	0.068595	-4.10
253572_at	hypothetical protein	---	AT4G31010	1.28	0.36	2.93	0.023058	0.068663	-4.10
265871_at	unknown protein ;supported by full-	---	AT2G01680	1.37	0.46	2.93	0.023064	0.068672	-4.10
250616_at	receptor-like protein kinase-like pro	EMS1	AT5G07280	-1.31	-0.39	-2.93	0.023078	0.068705	-4.10
247432_at	microtubule-associated protein EB1	ATEB1B	AT5G62500	-1.29	-0.36	-2.93	0.023088	0.068724	-4.10

246484_at	UVB-resistance protein-like UVB-re	---	AT5G16040	1.29	0.37	2.93	0.023111	0.068776	-4.10
247372_at	unknown protein ;supported by full-	---	AT5G63280	1.43	0.52	2.93	0.023111	0.068776	-4.10
258034_at	hypothetical protein predicted by ge	---	AT3G21300	1.76	0.81	2.93	0.023141	0.068845	-4.10
261262_at	hypothetical protein predicted by ge	SDG35	AT1G26760	-1.22	-0.29	-2.93	0.023141	0.068845	-4.10
246459_at	receptor protein kinase -like protein	---	AT5G16900	-1.25	-0.32	-2.93	0.023144	0.068845	-4.10
256856_at	Expressed protein ; supported by fu	---	AT3G15110	-1.41	-0.50	-2.93	0.023162	0.068892	-4.10
261438_at	metallothionein-like protein identica	---	AT1G07590	1.23	0.29	2.92	0.023211	0.069019	-4.10
256350_at	hypothetical protein contains simila	PGSIP4	AT1G54940	-1.22	-0.29	-2.92	0.023211	0.069019	-4.10
264967_at	unknown protein ;supported by full-	---	AT1G67250	1.22	0.29	2.92	0.023228	0.06906	-4.10
250806_at	putative protein similar to unknown	---	AT5G05070	-1.24	-0.31	-2.92	0.023243	0.069095	-4.10
261971_at	type 2 peroxiredoxin, putative simil	---	AT1G65990	-1.32	-0.40	-2.92	0.02326	0.069135	-4.11
252239_at	putative protein putative protein - D	---	AT3G49990	1.48	0.57	2.92	0.023262	0.069135	-4.11
266744_at	putative nucleoside triphosphatase	---	AT2G02970	-1.21	-0.27	-2.92	0.023284	0.069186	-4.11
252879_at	putative protein predicted proteins,	NST-K1	AT4G39390	-1.82	-0.87	-2.92	0.023286	0.069186	-4.11
256179_at	ubiquitin-specific protease 6 (UBP6	UBP6	AT1G51710	1.22	0.29	2.92	0.023294	0.069204	-4.11
266917_at	unknown protein	DTA2	AT2G45830	1.24	0.31	2.92	0.023307	0.069232	-4.11
251773_at	putative protein HSPC058, Homo s	---	AT3G55960	1.47	0.55	2.92	0.023318	0.069257	-4.11
250187_at	putative protein predicted proteins,	---	AT5G14370	-1.52	-0.60	-2.92	0.023326	0.06927	-4.11
265677_at	putative purine-rich single-stranded	PUR ALPH	AT2G32080	-1.23	-0.30	-2.92	0.023334	0.069286	-4.11
246162_at	actin interacting protein ; supported	---	AT4G36400	1.35	0.43	2.92	0.023339	0.069291	-4.11
264202_at	TINY-like transcription factor Conta	---	AT1G22810	-2.08	-1.06	-2.92	0.023357	0.069337	-4.11
255644_at	coded for by A. thaliana cDNA T43	---	AT4G00870	1.24	0.31	2.92	0.023361	0.069337	-4.11
266026_at	putative non-LTR retroelement reve	---	---	-1.29	-0.36	-2.92	0.023389	0.069388	-4.11
261052_at	hypothetical protein similar to hypot	---	AT1G01440	1.34	0.42	2.92	0.023391	0.069388	-4.11
266883_at	putative triacylglycerol lipase	DAD1	AT2G44810	-1.25	-0.32	-2.92	0.023393	0.069388	-4.11
255564_s_a	hypothetical protein T15B16.8	RGXT2	AT4G01750	1.29	0.36	2.92	0.023393	0.069388	-4.11
261920_at	isocitrate dehydrogenase, putative	---	AT1G65930	1.28	0.36	2.92	0.023395	0.069388	-4.11
259398_at	hypothetical protein predicted by ge	PRA1.F1	AT1G17700	-2.00	-1.00	-2.92	0.023396	0.069388	-4.11
258403_at	hypothetical protein predicted by ge	---	AT3G15380	1.25	0.33	2.92	0.023402	0.069397	-4.11
265276_at	hypothetical protein predicted by ge	---	AT2G28400	-1.45	-0.54	-2.92	0.023407	0.069398	-4.11
266853_at	putative salt-inducible protein	---	AT2G26790	1.23	0.30	2.92	0.023408	0.069398	-4.11
261433_s_a	endoplasmic reticulum-type calcium	---	AT1G07670	1.21	0.27	2.92	0.023424	0.069434	-4.11
260892_at	cysteine proteinase contains similar	---	AT1G29110	-1.29	-0.37	-2.92	0.023442	0.06948	-4.11
252210_at	DNA binding protein	OBP1	AT3G50410	-1.44	-0.53	-2.92	0.023456	0.069506	-4.11
247997_at	putative protein contains similarity t	ATARP8	AT5G56180	1.31	0.39	2.92	0.023457	0.069506	-4.11

261932_at	hypothetical protein predicted by ge	---	AT1G22420	-1.21	-0.28	-2.92	0.023462	0.069511	-4.11
262766_at	hypothetical protein predicted by ge	---	AT1G13160	1.52	0.60	2.92	0.023476	0.069544	-4.12
257345_s_a	pseudogene	---	---	-1.21	-0.28	-2.92	0.023489	0.069574	-4.12
266211_at	putative retroelement pol polyprotei	---	---	-1.26	-0.33	-2.92	0.023493	0.069577	-4.12
252163_at	hypothetical protein	---	AT3G50610	-1.27	-0.35	-2.92	0.023516	0.069635	-4.12
247703_at	putative protein predicted proteins,	SRR1	AT5G59560	1.29	0.37	2.91	0.023524	0.069639	-4.12
247307_at	UVB-resistance protein UVR8 (gb|A	---	AT5G21326	1.24	0.31	2.91	0.023528	0.069639	-4.12
254645_at	putative protein	---	AT4G18520	1.29	0.37	2.91	0.023529	0.069639	-4.12
267401_at	unknown protein	---	AT2G26210	1.26	0.33	2.91	0.023531	0.069639	-4.12
251627_at	glucan endo-1,3-beta-D-glucosidas	BG1	AT3G57270	-1.28	-0.35	-2.91	0.023532	0.069639	-4.12
266823_at	hypothetical protein predicted by ge	---	AT2G44930	-1.26	-0.34	-2.91	0.023543	0.06966	-4.12
245611_at	hypothetical protein	---	AT4G14390	-1.41	-0.50	-2.91	0.023546	0.069662	-4.12
254557_at	hypothetical protein ;supported by	---	AT4G19140	-1.58	-0.66	-2.91	0.023549	0.069662	-4.12
266538_at	hypothetical protein predicted by ge	---	AT2G35230	-1.26	-0.33	-2.91	0.023553	0.069663	-4.12
251229_at	beta-glucosidase-like protein severa	BGLU7	AT3G62740	-1.22	-0.29	-2.91	0.02356	0.069674	-4.12
246676_at	putative protein	---	---	-1.21	-0.27	-2.91	0.023575	0.069711	-4.12
266655_at	putative protein kinase contains a p	AtAUR2	AT2G25880	-1.35	-0.44	-2.91	0.023587	0.069737	-4.12
265109_s_a	NBS/LRR disease resistance prote	---	AT1G62630	1.47	0.56	2.91	0.023594	0.069749	-4.12
263369_at	unknown protein	---	AT2G20480	1.22	0.28	2.91	0.023607	0.069779	-4.12
257494_at	hypothetical protein predicted by ge	---	AT1G32375	-1.21	-0.27	-2.91	0.023629	0.069824	-4.12
267489_s_a	putative DNA2-NAM7 helicase fami	---	AT2G19120	1.43	0.51	2.91	0.023629	0.069824	-4.12
265963_s_a	40S ribosomal protein S5 identical t	ATRPS5B	AT2G37270	1.59	0.67	2.91	0.023636	0.069837	-4.12
264509_at	unknown protein Location of EST g	---	AT1G09520	1.28	0.36	2.91	0.023639	0.069837	-4.12
255699_at	putative pectinesterase	PME38	AT4G00190	-1.22	-0.29	-2.91	0.023646	0.069847	-4.12
245181_at	putative protein similarity to various	---	AT5G12420	1.89	0.92	2.91	0.023655	0.069865	-4.12
252954_at	putative thaumatin-like protein thau	---	AT4G38660	-2.28	-1.19	-2.91	0.023707	0.070011	-4.13
249111_at	unknown protein	---	AT5G43770	-1.21	-0.27	-2.91	0.023712	0.070015	-4.13
264298_at	hypothetical protein contains simila	---	AT1G78690	-1.27	-0.34	-2.91	0.023715	0.070015	-4.13
263296_at	unknown protein	---	AT2G38800	1.63	0.70	2.91	0.023735	0.070058	-4.13
266086_at	putative Na+-dependent inorganic p	PHT4;2	AT2G38060	-1.28	-0.35	-2.91	0.023736	0.070058	-4.13
254940_at	putative protein predicted proteins,	---	AT4G10820	-1.24	-0.32	-2.91	0.02376	0.070119	-4.13
248101_at	chaperone GrpE-like protein ;supp	---	AT5G55200	1.74	0.80	2.91	0.023762	0.070119	-4.13
245551_at	cytochrome P450 like protein	CYP705A2	AT4G15350	-1.22	-0.28	-2.91	0.023782	0.070166	-4.13
262203_at	transfactor-like protein similar to tra	---	AT2G01060	1.28	0.36	2.91	0.023784	0.070166	-4.13
265130_at	unknown protein similar to ESTs gb	---	AT1G30890	-1.19	-0.26	-2.91	0.023796	0.070192	-4.13

257406_at	hypothetical protein predicted by g	---	AT1G27060	1.33	0.41	2.91	0.023804	0.070205	-4.13
245873_at	bHLH transcription factor GBOF-1,	CIB5	AT1G26260	-1.34	-0.43	-2.91	0.023817	0.070235	-4.13
255837_at	unknown protein	RIC1	AT2G33460	-1.26	-0.33	-2.91	0.023829	0.07026	-4.13
265807_at	unknown protein	---	AT2G17990	1.27	0.35	2.90	0.023857	0.070335	-4.13
263422_s_a	putative ubiquitin-like protein ; supp	---	AT2G17190	1.22	0.29	2.90	0.023864	0.070347	-4.13
258989_at	rhodanese-like family protein contai	---	AT3G08920	-1.30	-0.38	-2.90	0.023881	0.070388	-4.13
256706_at	auxin-independent growth promote	---	AT3G30300	1.28	0.36	2.90	0.023898	0.070427	-4.13
263048_s_a	unknown protein ;supported by full-	---	AT2G05310	-1.31	-0.39	-2.90	0.023908	0.07045	-4.13
249859_at	serine protein kinase-like protein ;s	---	AT5G22840	1.54	0.62	2.90	0.023922	0.070479	-4.14
257950_at	putative UDP-glucose glucosyltrans	UGT71B6	AT3G21780	2.14	1.10	2.90	0.02395	0.070542	-4.14
261007_at	hypothetical protein similar to reticu	---	AT1G26400	1.19	0.25	2.90	0.023952	0.070542	-4.14
247216_at	4-alpha-glucanotransferase ; supp	DPE1	AT5G64860	1.37	0.46	2.90	0.023955	0.070542	-4.14
254129_at	putative tRNA isopentenyltransfera	IPT4	AT4G24650	-1.23	-0.30	-2.90	0.023955	0.070542	-4.14
259053_at	unknown protein similar to hypothet	---	AT3G03320	1.28	0.36	2.90	0.02399	0.070633	-4.14
267520_at	putative integral membrane protein	---	AT2G30460	-1.48	-0.56	-2.90	0.023992	0.070633	-4.14
261825_at	endo-xyloglucan transferase, putat	---	AT1G11545	-3.83	-1.94	-2.90	0.02401	0.070669	-4.14
250650_at	anthranilate phosphoribosyltransfer	---	AT5G06850	1.45	0.53	2.90	0.024011	0.070669	-4.14
258622_at	unknown protein contains Pfam pro	---	AT3G02720	-1.25	-0.32	-2.90	0.024024	0.070693	-4.14
255766_at	unknown protein ;supported by full-	---	AT1G16750	-1.35	-0.43	-2.90	0.024025	0.070693	-4.14
258466_at	hypothetical protein contains simila	---	AT3G06040	1.31	0.39	2.90	0.024044	0.070741	-4.14
261450_s_a	O-methyltransferase, putative simil	---	AT1G21110	5.53	2.47	2.90	0.02405	0.070747	-4.14
245602_at	Expressed protein ;supported by cD	---	AT4G14270	1.42	0.51	2.90	0.024057	0.070756	-4.14
262089_s_a	hypothetical protein predicted by ge	---	AT1G55980	-1.38	-0.46	-2.90	0.024059	0.070756	-4.14
261232_at	unknown protein ; supported by cDI	---	AT1G20220	-1.25	-0.32	-2.90	0.024069	0.070778	-4.14
249633_at	sucrose synthase-like protein sucr	SUS5	AT5G37180	-1.23	-0.30	-2.90	0.02409	0.070829	-4.14
260078_at	hypothetical protein predicted by ge	---	AT1G73790	1.29	0.36	2.90	0.024094	0.070833	-4.14
258798_at	hypothetical protein predicted by ge	---	AT3G04540	-1.28	-0.36	-2.90	0.024108	0.070864	-4.14
257886_at	pectinesterase, putative similar to p	---	AT3G17060	-1.26	-0.34	-2.90	0.024111	0.070865	-4.14
250497_at	putative protein predicted proteins,	---	AT5G09630	1.34	0.43	2.90	0.024121	0.070885	-4.14
267204_at	putative blue copper-binding protei	---	AT2G31050	-1.27	-0.35	-2.90	0.024141	0.070934	-4.14
249404_at	ankyrin repeat protein EMB506 ; su	EMB506	AT5G40160	1.36	0.45	2.90	0.024153	0.070959	-4.15
255880_at	hypothetical protein predicted by ge	---	AT1G67060	-1.24	-0.31	-2.90	0.024162	0.070976	-4.15
252322_at	putative protein putative zinc-finge	---	AT3G48550	-1.65	-0.72	-2.89	0.024191	0.071053	-4.15
257879_at	unknown protein	---	AT3G17160	1.47	0.56	2.89	0.024241	0.071192	-4.15
266238_at	phosphoprotein phosphatase, type	TOPP1	AT2G29400	1.45	0.53	2.89	0.024248	0.071201	-4.15

254854_at	putative protein hypothetical protei	---	AT4G12130	1.38	0.46	2.89	0.024265	0.071242	-4.15
AFFX-BioC-	E. coli /GEN=bioC /DB_XREF=gb:J	---	---	-1.54	-0.62	-2.89	0.024287	0.07128	-4.15
265761_at	putative stress protein	---	AT2G01330	1.25	0.32	2.89	0.024288	0.07128	-4.15
251623_at	MADS transcription factor-like prot	AGL18	AT3G57390	1.21	0.28	2.89	0.02429	0.07128	-4.15
250952_at	putative protein	ATIREG2	AT5G03570	-1.35	-0.43	-2.89	0.024293	0.07128	-4.15
246167_at	putative protein	---	---	-1.32	-0.40	-2.89	0.024293	0.07128	-4.15
245499_at	membrane transporter like protein	INT4	AT4G16480	-1.23	-0.30	-2.89	0.024311	0.071315	-4.15
259996_at	hypothetical protein predicted by ge	---	AT1G67910	-1.36	-0.44	-2.89	0.024311	0.071315	-4.15
261873_at	serine/threonine kinase, putative si	SD1-13	AT1G11350	-1.48	-0.57	-2.89	0.024315	0.071317	-4.15
251721_s_a	alpha-soluble NSF attachment prot	ALPHA-SN	AT3G56190	1.30	0.37	2.89	0.024327	0.071342	-4.15
255637_at	hypothetical protein	---	AT4G00750	1.41	0.49	2.89	0.024332	0.071348	-4.15
255346_at	hypothetical protein	---	---	-1.19	-0.25	-2.89	0.024338	0.071356	-4.15
248186_at	unknown protein ;supported by full	---	AT5G53880	-2.51	-1.32	-2.89	0.024353	0.07139	-4.15
259696_at	unknown protein ; supported by cDI	---	AT1G63150	1.26	0.34	2.89	0.024404	0.07151	-4.16
263906_at	plastid division protein (FtsZ) identi	FTSZ2-1	AT2G36250	1.30	0.38	2.89	0.024405	0.07151	-4.16
262033_at	terminal ear1, putative similar to te	MCT1	AT1G37140	-1.27	-0.35	-2.89	0.024406	0.07151	-4.16
266332_at	hypothetical protein predicted by ge	---	AT2G32415	-1.27	-0.34	-2.89	0.024406	0.07151	-4.16
247875_at	putative protein similar to unknown	---	AT5G57720	-1.28	-0.35	-2.89	0.024409	0.07151	-4.16
257818_at	hypothetical protein predicted by ge	---	AT3G25120	1.30	0.37	2.89	0.024418	0.071526	-4.16
256744_at	ATHP2, putative similar to ATHP2	AHP2	AT3G29350	1.32	0.40	2.89	0.024427	0.071542	-4.16
250805_at	unknown protein	---	AT5G05050	-1.23	-0.30	-2.89	0.02443	0.071542	-4.16
266901_at	hypothetical protein predicted by ge	JAZ7	AT2G34600	-2.01	-1.01	-2.89	0.024463	0.071629	-4.16
266620_at	unknown protein	---	AT2G35450	-1.32	-0.40	-2.89	0.024509	0.071756	-4.16
251797_at	putative protein AT-hook protein 1	AGF2	AT3G55560	1.36	0.45	2.88	0.024522	0.071776	-4.16
250455_at	unknown protein ; supported by ful	PROPEP4	AT5G09980	-1.39	-0.48	-2.88	0.024522	0.071776	-4.16
255916_at	putative protein	---	AT5G28550	-1.31	-0.39	-2.88	0.024528	0.071784	-4.16
262939_s_a	glyceraldehyde-3-phosphate dehyd	GAPCP-2	AT1G16300	2.57	1.36	2.88	0.024533	0.071785	-4.16
259396_at	shaggy-like kinase, putative similar	GSK1	AT1G06390	-1.22	-0.29	-2.88	0.024538	0.071785	-4.16
259366_at	allene oxide cyclase, putative simil	AOC4	AT1G13280	-1.41	-0.49	-2.88	0.024538	0.071785	-4.16
262072_at	hypothetical protein predicted by ge	ZCF37	AT1G59590	1.80	0.85	2.88	0.024551	0.071813	-4.16
245531_at	hydroxynitrile lyase like protein	scpl30	AT4G15100	-1.39	-0.48	-2.88	0.024572	0.071867	-4.16
245909_at	putative protein DNA-directed RNA	---	AT5G09380	1.33	0.41	2.88	0.024577	0.071873	-4.16
263112_at	unknown protein Strong similarity to	---	AT1G03080	1.29	0.37	2.88	0.024596	0.071918	-4.16
250191_at	kinase - like protein RING3 protein	ATBET9	AT5G14270	1.28	0.36	2.88	0.024599	0.071918	-4.16
254371_at	beta-glucosidase -like protein beta-	BGLU47	AT4G21760	-1.23	-0.30	-2.88	0.024606	0.071929	-4.16

265338_at	putative ribosomal protein L6 ; sup	---	AT2G18400	1.26	0.33	2.88	0.02461	0.071932	-4.16
257677_at	unknown protein contains Pfam pro	ATEHD1	AT3G20290	1.29	0.36	2.88	0.024638	0.072003	-4.17
247620_at	receptor like protein kinase recepto	---	AT5G60310	-1.28	-0.35	-2.88	0.024658	0.072053	-4.17
258690_at	putative phosphatidylinositol-4-phos	---	AT3G07960	-1.24	-0.31	-2.88	0.024675	0.072093	-4.17
265845_at	unknown protein	---	AT2G35610	1.19	0.24	2.88	0.024679	0.072097	-4.17
250136_at	putative protein de novo DNA meth	DRM1	AT5G15380	-1.52	-0.61	-2.88	0.024713	0.072187	-4.17
253696_at	cytokinin oxidase - like protein cyto	CKX4	AT4G29740	-1.78	-0.83	-2.88	0.024725	0.072213	-4.17
246891_at	putative protein various predicted p	---	AT5G25490	-1.21	-0.27	-2.88	0.024735	0.072234	-4.17
254167_at	serine/threonine kinase-like protein	CIPK8	AT4G24400	1.29	0.36	2.88	0.024753	0.072276	-4.17
265275_at	En/Spm-like transposon protein rela	---	AT2G28440	-1.50	-0.59	-2.88	0.024777	0.072336	-4.17
247310_at	putative protein contains similarity t	CHR24	AT5G63950	1.38	0.46	2.88	0.024789	0.072363	-4.17
261039_at	Expressed protein ; supported by fu	ELF4-L4	AT1G17455	-1.42	-0.51	-2.88	0.024798	0.072379	-4.17
253403_at	putative serine/threonine protein ki	AtAUR1	AT4G32830	-1.31	-0.39	-2.88	0.024803	0.072384	-4.17
247944_at	putative protein similar to unknown	---	AT5G57100	-1.31	-0.39	-2.88	0.024808	0.072389	-4.17
253607_at	small nuclear ribonucleoprotein ho	---	AT4G30330	1.37	0.45	2.88	0.024811	0.072389	-4.17
257532_at	hypothetical protein similar to hypot	---	AT3G04700	2.35	1.23	2.88	0.024819	0.072404	-4.17
257887_at	protein phosphatase-2c, putative s	---	AT3G17090	-1.32	-0.40	-2.88	0.024831	0.072429	-4.17
252967_at	amidophosphoribosyltransferase -	ATASE3	AT4G38880	-1.26	-0.34	-2.88	0.024854	0.072487	-4.18
253868_at	proton pump interactor non-consen	PPI1	AT4G27500	-1.29	-0.37	-2.88	0.024861	0.072497	-4.18
253475_at	putative protein predicted protein, A	---	AT4G32290	-1.56	-0.64	-2.87	0.024878	0.072532	-4.18
254431_at	reticuline oxidase - like protein retic	---	AT4G20840	1.47	0.55	2.87	0.024879	0.072532	-4.18
252975_s_a	putative protein other predicted pro	ROPGEF1	AT4G38430	-1.24	-0.31	-2.87	0.024888	0.07254	-4.18
255888_at	hypothetical protein contains simila	---	AT1G20300	1.87	0.91	2.87	0.024889	0.07254	-4.18
260971_at	hypothetical protein predicted by ge	---	AT1G53620	-1.24	-0.31	-2.87	0.024891	0.07254	-4.18
251149_at	putative protein CGI-77 protein, Ho	---	AT3G62940	1.19	0.26	2.87	0.024923	0.072612	-4.18
245897_at	potassium transport protein-like sev	KUP7	AT5G09400	-1.37	-0.46	-2.87	0.024924	0.072612	-4.18
267365_at	putative phosphoribosyl pyrophosph	---	AT2G44530	1.20	0.26	2.87	0.024926	0.072612	-4.18
252162_at	hypothetical protein	---	AT3G50590	-1.47	-0.55	-2.87	0.024937	0.072627	-4.18
246499_at	putative protein Tat-SF1 - Homo sa	---	AT5G16260	1.34	0.42	2.87	0.02494	0.072627	-4.18
250973_at	60S ribosomal protein - like 60S ro	---	AT5G02870	1.53	0.61	2.87	0.02494	0.072627	-4.18
248352_at	low-temperature-induced 65 kD pro	LTI65	AT5G52300	-2.21	-1.15	-2.87	0.024946	0.072633	-4.18
252887_at	putative protein various predicted p	---	AT4G39240	1.20	0.26	2.87	0.024949	0.072633	-4.18
256075_at	mitogen-activated protein kinase, p	ATMPK8	AT1G18150	1.32	0.40	2.87	0.024981	0.072719	-4.18
258200_at	putative ATPase similar to ATPase	---	AT3G13900	-1.32	-0.40	-2.87	0.025018	0.072804	-4.18
258606_at	unknown protein ;supported by full-	---	AT3G02840	4.84	2.27	2.87	0.025019	0.072804	-4.18

250441_at	oligopeptidase A - like protein oligo	---	AT5G10540	1.21	0.27	2.87	0.02502	0.072804	-4.18
249682_at	putative protein similar to unknown	---	AT5G36080	-1.22	-0.28	-2.87	0.025039	0.072849	-4.18
251470_at	putative protein hypothetical protei	---	AT3G59570	-1.33	-0.41	-2.87	0.02506	0.0729	-4.18
256577_at	unknown protein	---	AT3G28220	-2.39	-1.26	-2.87	0.025063	0.0729	-4.18
261132_at	hypothetical protein predicted by ge	TGD1	AT1G19800	-1.24	-0.31	-2.87	0.025085	0.072955	-4.19
256581_at	hypothetical protein	---	AT3G28830	-1.20	-0.26	-2.87	0.025094	0.072972	-4.19
246319_at	putative protein HYPOTHETICAL P	---	AT3G56680	-1.24	-0.31	-2.87	0.025105	0.072996	-4.19
260070_at	putative helix-loop-helix DNA-bindi	BEE3	AT1G73830	-2.81	-1.49	-2.87	0.025123	0.073026	-4.19
255208_at	see GB:AL022580	---	---	-1.25	-0.33	-2.87	0.025125	0.073026	-4.19
258391_at	hypothetical protein predicted by ge	---	AT3G15420	1.43	0.51	2.87	0.025126	0.073026	-4.19
262779_at	putative cytochrome P450 monooxy	---	AT1G13070	-1.20	-0.26	-2.87	0.025129	0.073026	-4.19
260198_at	F12A21.23 hypothetical protein	---	AT1G67635	-1.22	-0.28	-2.87	0.025147	0.073069	-4.19
255574_at	putative calcium-regulated protein	CBL5	AT4G01420	1.26	0.34	2.87	0.025172	0.073133	-4.19
262197_at	AP2 domain containing protein, pu	RAP2.12	AT1G53910	1.49	0.57	2.87	0.025175	0.073133	-4.19
253827_at	Expressed protein ; supported by c	---	AT4G28085	-1.99	-0.99	-2.87	0.025181	0.073142	-4.19
251866_at	putative protein MSP58 - nucleolar	emb1967	AT3G54350	1.21	0.28	2.86	0.025218	0.073235	-4.19
250958_at	laccase precursor - like laccase pr	LAC11	AT5G03260	-2.06	-1.04	-2.86	0.025225	0.073235	-4.19
255130_at	hypothetical protein ; supported by	---	AT4G08240	-1.29	-0.37	-2.86	0.025226	0.073235	-4.19
253404_at	putative pyrophosphate--fructose-6	PFK6	AT4G32840	-1.32	-0.40	-2.86	0.025226	0.073235	-4.19
248045_at	HEAT SHOCK PROTEIN 81-2 (HS	HSP81-2	AT5G56030	-1.80	-0.85	-2.86	0.025237	0.073257	-4.19
248057_at	putative protein strong similarity to	---	AT5G55520	-1.22	-0.28	-2.86	0.025248	0.073281	-4.19
247566_at	40S ribsomal protein S19 - like 40	---	AT5G61170	1.68	0.74	2.86	0.025268	0.073326	-4.19
263290_at	unknown protein	---	AT2G10930	-1.20	-0.26	-2.86	0.02527	0.073326	-4.19
260541_at	putative trypsin inhibitor	---	AT2G43530	-2.10	-1.07	-2.86	0.025275	0.073331	-4.19
266312_at	20S proteasome subunit C8 (PAG1	PAG1	AT2G27020	1.29	0.37	2.86	0.025285	0.07335	-4.19
252269_at	putative protein ;supported by full-l	LSU1	AT3G49580	1.91	0.93	2.86	0.025305	0.073397	-4.19
262687_at	PPR-repeat protein contains multip	---	AT1G62670	1.21	0.28	2.86	0.025308	0.073397	-4.19
258347_at	unknown protein identical to LEA-lik	---	AT3G17520	-1.28	-0.35	-2.86	0.025313	0.073404	-4.19
257752_at	hypothetical protein predicted by ge	---	AT3G18720	-1.27	-0.35	-2.86	0.025338	0.073449	-4.20
251958_at	putative protein predicted proteins,	---	AT3G53560	1.54	0.62	2.86	0.025338	0.073449	-4.20
253535_at	putaive DNA-binding protein DNA-	WRKY11	AT4G31550	2.37	1.25	2.86	0.02534	0.073449	-4.20
262717_s_a	putative cytochrome P450 similar to	CYP79F2	AT1G16400	-1.42	-0.50	-2.86	0.025342	0.073449	-4.20
265412_at	putative chloroplast outer membran	TOC132	AT2G16640	1.20	0.27	2.86	0.025352	0.07347	-4.20
253580_at	putative protein RING-H2 finger pr	---	AT4G30400	-1.67	-0.74	-2.86	0.025355	0.07347	-4.20
248205_at	cotton fiber expressed protein 1-like	---	AT5G54300	-2.05	-1.04	-2.86	0.025365	0.073489	-4.20

258025_at	putative D-3-phosphoglycerate deh	---	AT3G19480	-1.48	-0.56	-2.86	0.025369	0.073492	-4.20
267094_at	putative diphenol oxidase ; support	IRX12	AT2G38080	-2.20	-1.14	-2.86	0.025376	0.073502	-4.20
247556_at	putative protein predicted protein, A	---	AT5G61040	1.33	0.42	2.86	0.025383	0.073513	-4.20
263643_at	unknown protein predicted by gene	---	AT2G04740	1.42	0.50	2.86	0.025397	0.073543	-4.20
251218_at	CP12 protein precursor-like protein	CP12-2	AT3G62410	1.35	0.43	2.86	0.025414	0.073585	-4.20
256025_at	xylan endohydrolase, putative simi	RXF12	AT1G58370	-1.45	-0.54	-2.86	0.025418	0.073585	-4.20
266918_at	putative LIM-domain protein	---	AT2G45800	-1.22	-0.28	-2.86	0.025436	0.073627	-4.20
262589_s_a	hypothetical protein Strong similarit	---	AT1G15150	-1.24	-0.31	-2.86	0.025443	0.073627	-4.20
256815_at	unknown protein contains Pfam pro	---	AT3G21380	-1.24	-0.31	-2.86	0.025444	0.073627	-4.20
259484_at	calcium-dependent protein kinase,	PEPKR1	AT1G12580	-1.33	-0.41	-2.86	0.025447	0.073627	-4.20
264267_at	hypothetical protein contains simila	---	AT1G60200	-1.28	-0.36	-2.86	0.025448	0.073627	-4.20
263629_at	hypothetical protein predicted by ge	---	AT2G04850	-1.46	-0.54	-2.86	0.025463	0.073659	-4.20
255882_x_a	hypothetical protein contains simila	---	AT1G20280	1.28	0.36	2.86	0.025485	0.073715	-4.20
254692_at	putative protein predicted protein, A	---	AT4G17860	-1.25	-0.33	-2.86	0.025494	0.073731	-4.20
251317_at	putative protein polygalacturonase	---	AT3G61490	-1.43	-0.51	-2.86	0.025512	0.07377	-4.20
261397_at	hexose transporter, putative simila	SGB1	AT1G79820	-1.50	-0.58	-2.86	0.025514	0.07377	-4.20
245037_at	putative phosphatidylinositol-4-phos	PIP5K3	AT2G26420	-1.21	-0.27	-2.86	0.025523	0.073786	-4.20
255009_at	putative DNA-directed RNA polyme	---	AT4G10070	1.39	0.48	2.86	0.025528	0.073786	-4.20
256065_at	ribosomal protein, putative similar t	---	AT1G07070	1.58	0.66	2.86	0.025529	0.073786	-4.20
266049_at	putative translation initiation factor	---	AT2G40780	1.25	0.32	2.85	0.025573	0.073902	-4.21
257848_at	hypothetical protein predicted by ge	---	AT3G13030	1.33	0.41	2.85	0.025578	0.073902	-4.21
258653_at	hypothetical protein similar to auxir	---	AT3G09870	-1.32	-0.40	-2.85	0.025579	0.073902	-4.21
246725_at	putative protein various predicted p	---	AT5G29040	-1.41	-0.49	-2.85	0.025602	0.07396	-4.21
249273_at	unknown protein	---	AT5G41850	1.31	0.39	2.85	0.025608	0.073966	-4.21
250577_at	putative protein densin-180, Rattus	---	AT5G07910	-1.22	-0.28	-2.85	0.025615	0.073968	-4.21
245785_at	cellulose synthase catalytic subuni	ATCSLD6	AT1G32180	-1.26	-0.33	-2.85	0.025615	0.073968	-4.21
254315_at	putative glycine-rich protein glycine	---	---	-1.38	-0.47	-2.85	0.02562	0.073968	-4.21
246887_at	hexose transporter - like protein he	---	AT5G26250	-1.26	-0.33	-2.85	0.025621	0.073968	-4.21
259887_at	putative protein kinase similar to pr	---	AT1G76360	1.27	0.34	2.85	0.025627	0.073972	-4.21
263087_s_a	putative sugar transporter	---	AT2G16120	-1.26	-0.33	-2.85	0.025629	0.073972	-4.21
260770_at	RING-H2 finger protein RHA3a, pu	---	AT1G49200	-2.73	-1.45	-2.85	0.025646	0.074012	-4.21
250462_at	receptor protein kinase -like(fragme	---	AT5G10020	-1.19	-0.25	-2.85	0.025653	0.074022	-4.21
259409_at	hypothetical protein contains simila	---	AT1G13330	1.24	0.31	2.85	0.02569	0.074116	-4.21
251870_at	putative protein Various predicted p	---	AT3G54510	-1.24	-0.31	-2.85	0.025692	0.074116	-4.21
245716_at	Expressed protein ; supported by cl	NDC1	AT5G08740	-1.48	-0.57	-2.85	0.025697	0.074122	-4.21

259615_at	dessication-related protein, putativ	---	AT1G47980	-1.31	-0.38	-2.85	0.025731	0.07421	-4.21
262576_at	unknown protein ESTs gb|R90323	---	AT1G15280	1.21	0.28	2.85	0.025735	0.074212	-4.21
257536_at	unknown protein	---	AT3G02800	3.09	1.63	2.85	0.025749	0.074243	-4.21
251073_at	putative protein hypothetical protein	---	AT5G01750	-1.20	-0.26	-2.85	0.025768	0.074279	-4.21
256122_at	hypothetical protein predicted by ge	---	AT1G18180	-1.27	-0.35	-2.85	0.02577	0.074279	-4.21
258365_s_a	putative diaminopimelate decarboxy	---	AT3G14390	1.28	0.36	2.85	0.025772	0.074279	-4.21
255521_at	putative sucrose synthetase simila	SUS3	AT4G02280	1.45	0.53	2.85	0.025775	0.074279	-4.21
246207_at	RNA-binding like protein non-conse	---	AT4G36960	-1.24	-0.31	-2.85	0.025782	0.074287	-4.21
256994_s_a	limonene cyclase, putative similar t	ATTPS-CIN	AT3G25820	-1.24	-0.31	-2.85	0.025784	0.074287	-4.21
257396_at	predicted protein	EPF1	AT2G20875	-1.34	-0.42	-2.85	0.025847	0.07446	-4.22
246800_at	glycine hydroxymethyltransferase -	SHM2	AT5G26780	1.33	0.41	2.85	0.025869	0.074513	-4.22
251499_at	putative protein putative callose sy	ATGSL11	AT3G59100	-1.25	-0.32	-2.85	0.025873	0.074516	-4.22
249948_at	eIF-4AII - like protein EUKARYOTI	---	AT5G19210	1.35	0.43	2.85	0.02588	0.074528	-4.22
249143_at	putative protein strong similarity to	---	AT5G43230	-1.20	-0.27	-2.85	0.025886	0.074534	-4.22
257890_s_a	putative protein peroxidase - Lyco	---	AT3G17070	-1.36	-0.45	-2.85	0.025893	0.074545	-4.22
263133_at	hypothetical protein predicted by ge	---	AT1G78450	-2.45	-1.30	-2.85	0.025897	0.074546	-4.22
259485_at	ATP synthase gamma-subunit, put	ATPC2	AT1G15700	1.65	0.72	2.85	0.025902	0.074547	-4.22
246580_at	ABC transporter, putative contains	---	AT1G31770	1.33	0.41	2.85	0.025903	0.074547	-4.22
266675_s_a	hypothetical protein predicted by ge	---	AT2G29610	-1.19	-0.25	-2.85	0.025921	0.074588	-4.22
257312_at	Expressed protein ; supported by fu	AT3G2659(	---	1.22	0.29	2.85	0.025928	0.074594	-4.22
251650_at	hypothetical protein	---	AT3G57360	1.38	0.47	2.85	0.02593	0.074594	-4.22
258586_s_a	putative trypsin inhibitor similar to tr	---	AT3G04320	1.77	0.83	2.84	0.025934	0.074597	-4.22
254814_at	hypothetical protein ; supported by	---	AT4G12340	1.19	0.25	2.84	0.025939	0.074601	-4.22
255154_at	putative protein several hypothetica	---	---	1.20	0.27	2.84	0.025962	0.074659	-4.22
249722_at	putative protein similar to unknown	---	AT5G35430	-1.20	-0.26	-2.84	0.025973	0.074675	-4.22
251161_at	putative protein hypothetical protei	---	AT3G63290	1.27	0.35	2.84	0.025974	0.074675	-4.22
254377_at	subtilisin proteinase - like subtilisin	---	AT4G21650	-3.17	-1.66	-2.84	0.026001	0.074743	-4.22
263727_at	putative cap-binding protein ; supp	ABH1	AT2G13540	1.33	0.41	2.84	0.026013	0.074764	-4.22
259497_at	unknown protein	---	AT1G15860	1.20	0.26	2.84	0.026015	0.074764	-4.22
259608_at	unknown protein	ECT9	AT1G27960	-1.28	-0.36	-2.84	0.026024	0.07478	-4.22
265007_s_a	Expressed protein ; supported by fu	RALFL8	AT1G61563	-1.19	-0.25	-2.84	0.026035	0.074802	-4.22
265126_s_a	hypothetical protein similar to hypot	---	AT1G55380	-1.27	-0.35	-2.84	0.026071	0.074898	-4.23
250795_at	RING zinc finger protein-like	CPuORF64	AT5G05280	1.29	0.37	2.84	0.026092	0.074943	-4.23
245558_at	hypothetical protein	---	AT4G15430	-1.21	-0.27	-2.84	0.026094	0.074943	-4.23
245079_at	putative retroelement pol polyprotei	---	---	-1.21	-0.28	-2.84	0.026102	0.074957	-4.23

253426_at	putative protein polygalacturonase	---	AT4G32375	-1.23	-0.30	-2.84	0.026119	0.074997	-4.23
264652_at	putative sugar transport protein, EF	---	AT1G08920	-1.78	-0.83	-2.84	0.026127	0.075009	-4.23
249678_at	protein kinase-like	---	AT5G35980	-1.20	-0.26	-2.84	0.026161	0.0751	-4.23
260248_at	heat shock protein 101 (HSP101) ic	ATHSP101	AT1G74310	-1.59	-0.66	-2.84	0.026187	0.075163	-4.23
249635_at	putative glucan synthase glucan sy	ATGSL09	AT5G36870	-1.27	-0.34	-2.84	0.026199	0.075185	-4.23
248469_at	putative protein similar to unknown	anac097	AT5G50820	-1.34	-0.42	-2.84	0.026201	0.075185	-4.23
249524_at	putative protein similar to unknown	---	AT5G38520	-1.44	-0.53	-2.84	0.026211	0.075196	-4.23
267423_at	putative potassium transporter	KUP11	AT2G35060	1.50	0.59	2.84	0.026211	0.075196	-4.23
263888_at	unknown protein	---	AT2G37000	-1.35	-0.43	-2.84	0.026231	0.075242	-4.23
267029_at	unknown protein	ATIREG1	AT2G38460	-1.30	-0.38	-2.84	0.02625	0.075287	-4.23
250746_at	glucuronosyl transferase-like protei	---	AT5G05880	-1.22	-0.29	-2.84	0.026256	0.075296	-4.23
262131_at	hypothetical protein predicted by ge	RALF1	AT1G02900	-2.21	-1.14	-2.84	0.026279	0.075349	-4.23
255026_at	hypothetical protein	MES12	AT4G09900	1.55	0.63	2.84	0.026281	0.075349	-4.23
252550_at	putative protein MtN21, Medicago t	---	AT3G45870	-1.31	-0.39	-2.84	0.026293	0.075374	-4.23
253295_at	putative aspartate--tRNA ligase as	---	AT4G33760	1.41	0.49	2.83	0.02631	0.075405	-4.23
250502_at	heat shock protein 70 (Hsc70-5) ; s	MTHSC70-	AT5G09590	1.65	0.73	2.83	0.026311	0.075405	-4.23
248229_at	caffeic acid 3-O-methyltransferase-	---	AT5G53810	-1.32	-0.40	-2.83	0.026319	0.07542	-4.24
265564_s_a	hypothetical protein predicted by ge	---	---	-1.25	-0.33	-2.83	0.026334	0.07544	-4.24
260427_at	hypothetical protein predicted by ge	---	AT1G72430	-1.74	-0.80	-2.83	0.026336	0.07544	-4.24
256415_at	unknown protein ; supported by full-	---	AT3G11210	-1.95	-0.96	-2.83	0.026336	0.07544	-4.24
255107_at	hypothetical protein	---	AT4G08730	-1.33	-0.41	-2.83	0.026351	0.075473	-4.24
253065_at	putative protein predicted proteins,	AtGRF2	AT4G37740	-1.36	-0.45	-2.83	0.026362	0.075489	-4.24
258940_at	putative lipase acylhydrolase contai	---	AT3G09930	-1.20	-0.26	-2.83	0.026363	0.075489	-4.24
266262_at	hypothetical protein predicted by ge	---	AT2G27590	1.49	0.58	2.83	0.026374	0.075509	-4.24
263240_s_a	unknown protein ; supported by cD	---	AT1G72590	1.40	0.49	2.83	0.026379	0.075509	-4.24
250770_at	laccase (diphenol oxidase)	LAC12	AT5G05390	-1.37	-0.46	-2.83	0.02638	0.075509	-4.24
263931_at	unknown protein ;supported by full-	---	AT2G36220	1.79	0.84	2.83	0.026398	0.075552	-4.24
249009_at	unknown protein ; supported by ful	MAP18	AT5G44610	1.46	0.55	2.83	0.026439	0.075657	-4.24
264379_at	hypothetical protein predicted by gr	---	AT2G25200	-1.55	-0.63	-2.83	0.026444	0.075663	-4.24
253162_at	phosphoserine aminotransferase ;s	PSAT	AT4G35630	2.35	1.23	2.83	0.026479	0.075754	-4.24
263994_at	putative VSF-1-like b-ZIP transcript	---	AT2G12900	-1.20	-0.27	-2.83	0.026484	0.075758	-4.24
264599_at	putative myosin heavy chain similar	XIA	AT1G04600	-1.24	-0.31	-2.83	0.026503	0.075804	-4.24
260210_at	putative xyloglucan fucosyltransfer	FUT3	AT1G74420	-1.33	-0.41	-2.83	0.026528	0.075867	-4.24
260211_at	hypothetical protein similar to YGL0	---	AT1G74440	-2.05	-1.04	-2.83	0.026541	0.075892	-4.24
263216_s_a	putative reticuline oxidase-like prot	---	AT1G30720	3.33	1.73	2.83	0.026561	0.075941	-4.24

256152_at	ethylene-responsive RNA helicase	---	AT1G55150	1.20	0.27	2.83	0.026571	0.07596	-4.25
262764_at	putative cytochrome P450 monooxy	CYP86C3	AT1G13140	-1.24	-0.31	-2.83	0.026586	0.075993	-4.25
248911_at	tumor-related protein-like	DOG1	AT5G45830	-1.37	-0.45	-2.83	0.026597	0.076015	-4.25
263776_s_a	putative cyclic nucleotide-regulated	ATCNGC3	AT2G46430	2.74	1.46	2.83	0.026618	0.076066	-4.25
254100_at	hypothetical protein ;supported by	---	AT4G25020	1.53	0.61	2.83	0.026635	0.076105	-4.25
262386_at	hypothetical protein predicted by ge	---	AT1G49370	-1.34	-0.42	-2.83	0.026641	0.076112	-4.25
256720_at	putative DOF zinc finger protein	---	AT2G34140	-1.59	-0.67	-2.83	0.026645	0.076115	-4.25
246956_at	unknown protein ; supported by cD	RTM2	AT5G04890	-1.25	-0.33	-2.83	0.02665	0.076119	-4.25
251744_at	putative protein CHLOROPLAST 3	---	AT3G56010	1.32	0.40	2.82	0.026678	0.07619	-4.25
258557_at	hypothetical protein similar to recep	---	AT3G05990	-1.24	-0.31	-2.82	0.026685	0.076193	-4.25
260034_at	putative DNA-binding protein Pfam	---	AT1G68810	-1.91	-0.93	-2.82	0.026687	0.076193	-4.25
246888_at	putative protein	---	AT5G26270	-1.21	-0.27	-2.82	0.026689	0.076193	-4.25
258857_at	putative serine carboxypeptidase II	scpl25	AT3G02110	-2.17	-1.12	-2.82	0.026706	0.076232	-4.25
259137_at	unknown protein Pfam HMM hit: EF	---	AT3G10300	-1.45	-0.53	-2.82	0.026719	0.076258	-4.25
245067_at	S-like ribonuclease RNS2 identical	RNS2	AT2G39780	1.27	0.35	2.82	0.026726	0.07627	-4.25
256007_at	allinase, putative similar to allinase	SAMC2	AT1G34065	-1.36	-0.44	-2.82	0.026745	0.076314	-4.25
262392_at	hypothetical protein predicted by ge	---	AT1G49520	-1.39	-0.47	-2.82	0.026748	0.076314	-4.25
266289_at	putative C-4 sterol methyl oxidase	SMO2-2	AT2G29390	-1.24	-0.31	-2.82	0.026762	0.076342	-4.25
263569_at	putative chromosome associated pr	TTN7	AT2G27170	1.42	0.50	2.82	0.026775	0.07637	-4.25
246523_at	CONSTANS-like 1	COL1	AT5G15850	-1.44	-0.53	-2.82	0.026784	0.076388	-4.25
255037_at	DNA-binding protein ;supported by	ATMYB6	AT4G09460	-1.64	-0.71	-2.82	0.026802	0.07643	-4.25
267488_at	putative cadmium-transporting ATP	HMA4	AT2G19110	1.39	0.48	2.82	0.02682	0.076471	-4.26
251648_at	protein kinase - like protein S-recep	---	AT3G57720	-1.34	-0.42	-2.82	0.026841	0.076521	-4.26
245187_s_a	F12A21.17 similar to signal recogni	---	AT1G67650	1.24	0.31	2.82	0.026864	0.076573	-4.26
260940_at	26S proteasome regulatory particle	---	AT1G45000	1.30	0.38	2.82	0.026866	0.076573	-4.26
256321_at	lipoxygenase, putative similar to lip	LOX1	AT1G55020	2.72	1.44	2.82	0.026871	0.076577	-4.26
255300_at	putative phosphatidylglycerotransfe	CLS	AT4G04870	-1.37	-0.46	-2.82	0.026885	0.076602	-4.26
263871_at	hypothetical protein predicted by ge	RKP	AT2G22010	1.31	0.38	2.82	0.026886	0.076602	-4.26
251407_at	Arm repeat containing protein - like	---	AT3G60350	1.27	0.34	2.82	0.026907	0.076651	-4.26
257926_at	unknown protein contains Pfam pro	---	AT3G23280	1.19	0.26	2.82	0.026923	0.076688	-4.26
267182_at	unknown protein	---	AT2G23360	-1.32	-0.40	-2.82	0.026984	0.076852	-4.26
249642_at	putative protein	---	AT5G36960	-1.30	-0.38	-2.82	0.027026	0.076961	-4.26
249104_at	sucrose transporter protein	ATSUC6	AT5G43610	1.24	0.31	2.82	0.027032	0.076969	-4.26
255851_at	hypothetical protein predicted by ge	---	AT1G67040	-1.31	-0.39	-2.82	0.027036	0.07697	-4.26
258637_at	putative RHO GDP-dissociation inh	---	AT3G07880	-1.32	-0.40	-2.81	0.027095	0.077129	-4.27

262453_at	hypothetical protein predicted by ge	---	AT1G11240	1.20	0.27	2.81	0.027102	0.07714	-4.27
245376_at	peroxidase like protein	---	AT4G17690	-1.22	-0.28	-2.81	0.027111	0.077147	-4.27
255288_at	coded for by A. thaliana cDNA T41	---	AT4G04670	1.42	0.51	2.81	0.027111	0.077147	-4.27
247457_at	putative protein various predicted p	---	AT5G62170	-1.22	-0.29	-2.81	0.027128	0.077184	-4.27
260848_at	pectinesterase, putative similar to p	sks8	AT1G21850	-1.36	-0.44	-2.81	0.027144	0.07722	-4.27
255689_at	hypothetical protein	---	AT4G00670	-1.20	-0.26	-2.81	0.027154	0.077239	-4.27
247046_at	unknown protein ; supported by cD	---	AT5G66540	1.27	0.34	2.81	0.027186	0.077307	-4.27
257128_at	cytochrome P450, putative contain	CYP705A1	AT3G20080	1.33	0.41	2.81	0.027186	0.077307	-4.27
256681_at	unknown protein ; supported by cDI	SPP2	AT3G52340	1.97	0.98	2.81	0.027188	0.077307	-4.27
264236_at	hypothetical protein predicted by ge	---	AT1G54680	1.27	0.34	2.81	0.027204	0.077343	-4.27
245562_at	OBP33pep like protein contains nor	---	AT4G15520	1.33	0.41	2.81	0.02721	0.077349	-4.27
247958_at	putative protein similar to unknown	---	AT5G57070	-1.27	-0.35	-2.81	0.027215	0.077356	-4.27
253701_at	choline monooxygenase - like prote	---	AT4G29890	1.34	0.42	2.81	0.027227	0.077371	-4.27
255276_at	putative fatty acid desaturase simil	DES-1-LIKI	AT4G04930	-1.22	-0.29	-2.81	0.027227	0.077371	-4.27
260217_at	hypothetical protein contains Pfam	---	AT1G74600	1.21	0.27	2.81	0.027239	0.077395	-4.27
252844_at	putative protein several hypothetica	---	AT3G42140	-1.29	-0.37	-2.81	0.027265	0.077459	-4.27
259364_at	DNA-binding protein RAV1 identica	RAV1	AT1G13260	-1.30	-0.38	-2.81	0.027307	0.077568	-4.27
265397_at	hypothetical protein predicted by ge	---	---	-1.22	-0.28	-2.81	0.027321	0.077599	-4.27
260617_at	Expressed protein ; supported by fu	---	AT1G53345	1.30	0.38	2.81	0.027326	0.077599	-4.27
251173_at	putative protein hypothetical protei	---	AT3G63270	1.20	0.27	2.81	0.027332	0.077599	-4.27
262039_at	adenine phosphoribosyltransferase	APT2	AT1G80050	-1.35	-0.43	-2.81	0.027332	0.077599	-4.27
256252_at	glucosyl transferase, putative simil	---	AT3G11340	3.84	1.94	2.81	0.027336	0.077599	-4.27
259467_at	hypothetical protein predicted by ge	---	AT1G19060	-1.18	-0.24	-2.81	0.027338	0.077599	-4.28
257753_at	60S ribosomal protein, putative sim	---	AT3G18740	1.41	0.49	2.81	0.027359	0.077647	-4.28
258376_at	hypothetical protein similar to GB:A	---	AT3G17680	-1.21	-0.28	-2.81	0.027363	0.077649	-4.28
256506_at	unknown protein	---	AT1G75160	-1.29	-0.37	-2.81	0.027371	0.077664	-4.28
259456_s_a	unknown protein similar to putative	---	---	-1.26	-0.34	-2.81	0.027375	0.077665	-4.28
250166_at	putative protein many predicted pro	---	AT5G15300	1.23	0.30	2.81	0.027383	0.077676	-4.28
252596_at	receptor-like protein kinase recepto	---	AT3G45330	-1.21	-0.28	-2.81	0.027394	0.077686	-4.28
252709_at	putative protein predicted proteins,	---	AT3G43840	-1.19	-0.25	-2.81	0.027396	0.077686	-4.28
246272_at	hydroxynitrile lyase like protein	MES9	AT4G37150	1.88	0.91	2.81	0.027399	0.077686	-4.28
253945_at	putative protein gene F23F1.15 Ara	---	AT4G27050	1.20	0.26	2.81	0.027399	0.077686	-4.28
252127_at	putative protein ATP binding protei	PLP3a	AT3G50960	-1.35	-0.44	-2.81	0.027413	0.077706	-4.28
260442_at	unknown protein ; supported by full	---	AT1G68220	1.34	0.42	2.81	0.027415	0.077706	-4.28
250019_at	putative protein similar to unknown	---	AT5G18160	-1.30	-0.38	-2.81	0.027417	0.077706	-4.28

267171_at	putative DOF zinc finger protein	DOF2.4	AT2G37590	-1.32	-0.41	-2.81	0.027421	0.077708	-4.28
260308_at	putative ABC transporter contains P	ATTAP1	AT1G70610	-1.58	-0.66	-2.81	0.027429	0.077723	-4.28
262832_s_a	unknown protein	---	AT1G14870	7.19	2.85	2.80	0.027445	0.077757	-4.28
254524_at	hypothetical protein	---	AT4G20000	2.20	1.14	2.80	0.027461	0.077777	-4.28
252331_s_a	serine palmitoyltransferase-like prot	SPT1	AT3G48780	1.28	0.35	2.80	0.027462	0.077777	-4.28
261257_at	tat-binding protein, putative similar	---	AT1G05910	1.33	0.41	2.80	0.027462	0.077777	-4.28
254375_at	putative protein (fragment) ATP(GT	QQT2	AT4G21800	1.25	0.32	2.80	0.027482	0.077822	-4.28
266631_at	putative serpin	---	AT2G35570	-1.19	-0.25	-2.80	0.027486	0.077825	-4.28
267126_s_a	putative acetone-cyanohydrin lyase	ACL	AT2G23590	-1.44	-0.52	-2.80	0.02753	0.077939	-4.28
247645_at	late embryonic abundant protein - l	---	AT5G60530	-1.24	-0.31	-2.80	0.027539	0.077955	-4.28
265852_at	putative RING zinc finger protein	---	AT2G42350	1.50	0.58	2.80	0.02755	0.077978	-4.28
261101_at	transcription factor DREB1A, putat	ddf2	AT1G63030	-1.33	-0.41	-2.80	0.027557	0.077986	-4.28
250155_at	putative protein predicted proteins,	---	AT5G15160	-1.77	-0.82	-2.80	0.027578	0.078035	-4.28
246250_at	cysteine proteinase similar to cyste	CP1	AT4G36880	3.22	1.69	2.80	0.027581	0.078035	-4.28
262785_at	putative carboxyl-terminal peptidase	---	AT1G10750	-1.42	-0.50	-2.80	0.027616	0.078124	-4.29
249417_at	calcium-binding protein - like cbp1	---	AT5G39670	3.67	1.87	2.80	0.027628	0.078148	-4.29
255186_at	putative transposon protein similar t	---	---	-1.41	-0.50	-2.80	0.027632	0.078148	-4.29
246374_at	light repressible receptor protein ki	---	AT1G51840	-1.19	-0.26	-2.80	0.027634	0.078148	-4.29
262092_at	unknown protein	---	AT1G56150	1.99	0.99	2.80	0.027647	0.078175	-4.29
250846_at	sulphite reductase ; supported by c	SIR	AT5G04590	1.53	0.61	2.80	0.027652	0.078177	-4.29
260630_at	subtilisin-like serine protease conta	ALE1	AT1G62340	-1.34	-0.43	-2.80	0.027661	0.078194	-4.29
251070_at	translation initiation factor eIF-2 be	---	AT5G01940	1.47	0.56	2.80	0.027666	0.078197	-4.29
252995_at	hypothetical protein ;supported by f	---	AT4G38370	-1.32	-0.40	-2.80	0.027679	0.078226	-4.29
256530_at	unknown protein	---	AT1G33290	1.25	0.32	2.80	0.027699	0.078274	-4.29
248185_at	flavonol 3-O-glucosyltransferase-lik	UF3GT	AT5G54060	-1.24	-0.31	-2.80	0.027731	0.078352	-4.29
261144_s_a	unknown protein ;supported by full-	---	AT1G19660	1.26	0.33	2.80	0.027735	0.078353	-4.29
261715_at	hypothetical protein similar to hypot	---	AT1G18485	-1.26	-0.33	-2.80	0.027752	0.078393	-4.29
246055_at	alpha-galactosidase - like protein a	AtAGAL1	AT5G08380	1.66	0.73	2.80	0.027772	0.078439	-4.29
259965_at	transcriptional regulator, putative fc	MSRB1	AT1G53670	-1.32	-0.40	-2.80	0.027789	0.078478	-4.29
255473_at	putative protein similar to several pr	---	AT4G02450	1.21	0.28	2.80	0.0278	0.078498	-4.29
256649_at	serine/arginine-rich protein, putativ	SCL30A	AT3G13570	1.33	0.42	2.80	0.027803	0.078498	-4.29
249127_at	actin-like protein ; supported by cD	ATARP9	AT5G43500	1.29	0.37	2.80	0.027807	0.078498	-4.29
256904_at	unknown protein	---	AT3G23980	-1.20	-0.26	-2.79	0.027846	0.078599	-4.29
247821_at	WD-40 repeat protein MSI1 (sp|O22	MSI1	AT5G58230	1.28	0.35	2.79	0.027858	0.078625	-4.29
258899_at	Expressed protein ; supported by fu	---	AT3G05675	1.32	0.40	2.79	0.027866	0.078638	-4.30

258978_at	unknown protein ; supported by cD	---	AT3G09320	1.22	0.29	2.79	0.027881	0.078671	-4.30
262503_at	hypothetical protein predicted by ge	---	AT1G21670	1.58	0.66	2.79	0.027889	0.078683	-4.30
248458_at	putative protein contains similarity t	EYE	AT5G51430	-1.23	-0.30	-2.79	0.027904	0.078706	-4.30
262149_at	hypothetical protein predicted by ge	---	AT1G52530	-1.34	-0.42	-2.79	0.027904	0.078706	-4.30
266862_at	putative MYB family transcription fa	AtMYB104	AT2G26950	-1.20	-0.26	-2.79	0.027925	0.078755	-4.30
252643_at	acidic ribosomal protein P2 -like ac	---	AT3G44590	1.72	0.78	2.79	0.027939	0.078785	-4.30
248988_at	putative protein contains similarity t	---	AT5G45190	1.27	0.34	2.79	0.027958	0.078829	-4.30
263174_at	jasmonate inducible protein, putati	ESP	AT1G54040	-1.82	-0.87	-2.79	0.027973	0.078857	-4.30
257302_at	hypothetical protein predicted by ge	---	AT3G30220	-1.21	-0.27	-2.79	0.027975	0.078857	-4.30
247237_at	auxin-independent growth promoter	---	AT5G64600	-1.29	-0.36	-2.79	0.027982	0.078867	-4.30
263275_at	putative methylmalonate semi-alde	ALDH6B2	AT2G14170	1.38	0.46	2.79	0.027986	0.078868	-4.30
257553_at	unknown protein contains Pfam pro	TPR2	AT3G16830	1.43	0.51	2.79	0.02799	0.07887	-4.30
263130_at	hypothetical protein predicted by ge	POLD3	AT1G78650	1.52	0.60	2.79	0.028012	0.078921	-4.30
262258_at	20S proteasome subunit PAE1 iden	PAE1	AT1G53850	1.30	0.38	2.79	0.028018	0.078929	-4.30
259458_at	glycine-rich protein, putative simila	---	AT1G44085	-1.28	-0.35	-2.79	0.028034	0.078949	-4.30
260764_at	unknown protein	---	AT1G48950	1.31	0.39	2.79	0.028038	0.078949	-4.30
256669_s_a	hypothetical protein similar to hypot	---	AT3G32200	-1.29	-0.37	-2.79	0.028039	0.078949	-4.30
265965_at	putative glutamate/ornithine acetyltr	---	AT2G37500	1.26	0.34	2.79	0.028041	0.078949	-4.30
256304_at	Expressed protein ; supported by cl	---	AT1G69523	-1.48	-0.57	-2.79	0.028042	0.078949	-4.30
265778_at	unknown protein	---	AT2G07360	-1.21	-0.28	-2.79	0.028046	0.07895	-4.30
251649_at	Ca2+-transporting ATPase-like pro	ACA11	AT3G57330	1.46	0.55	2.79	0.028054	0.078962	-4.30
251486_at	60S RIBOSOMAL PROTEIN L38-li	---	AT3G59540	1.43	0.52	2.79	0.028065	0.078983	-4.30
250325_s_a	putative protein contains similarity t	---	AT5G12060	-1.20	-0.27	-2.79	0.028071	0.078991	-4.30
245240_at	polyprotein, putative similar to poly	---	---	-1.30	-0.37	-2.79	0.02816	0.079233	-4.31
267585_s_a	putative actin	ACT9	AT2G42090	-1.23	-0.30	-2.79	0.028165	0.079235	-4.31
262790_at	putative translation initiation factor s	TIF3H1	AT1G10840	1.18	0.24	2.79	0.028177	0.07926	-4.31
261499_at	cytochrome P450 (CYP93A1), puta	CYP705A2	AT1G28430	-1.27	-0.35	-2.79	0.028206	0.079327	-4.31
252510_at	putative protein serine/threonine-sp	---	AT3G46270	-1.24	-0.32	-2.79	0.028208	0.079327	-4.31
248248_at	spermidine synthase ;supported by	SPDS3	AT5G53120	-1.48	-0.57	-2.78	0.02822	0.079347	-4.31
248542_at	putative protein similar to unknown	AT5G5019(	---	-1.22	-0.29	-2.78	0.028222	0.079347	-4.31
245892_at	putative lipid transfer protein lipid tr	---	AT5G09370	-1.37	-0.46	-2.78	0.028237	0.079379	-4.31
261551_at	ATP dependent copper transporter	HMA5	AT1G63440	1.24	0.31	2.78	0.028285	0.079503	-4.31
267079_at	hypothetical protein predicted by ge	---	AT2G41200	1.21	0.28	2.78	0.028288	0.079503	-4.31
258905_at	unknown protein similar to hypothet	---	AT3G06390	-1.45	-0.54	-2.78	0.028291	0.079503	-4.31
264709_at	putative DNA-binding protein, Myb	ATCDC5	AT1G09770	1.44	0.52	2.78	0.028295	0.079504	-4.31

256102_at	unknown protein	---	AT1G13680	-1.21	-0.28	-2.78	0.028312	0.07954	-4.31
250480_at	protein serine/threonine kinase-like	---	AT5G10290	1.79	0.84	2.78	0.028322	0.079558	-4.31
259338_at	s-syntaxin-like protein similar to s-s	SYP131	AT3G03800	-1.21	-0.28	-2.78	0.028325	0.079558	-4.31
246354_at	hypothetical protein	---	AT1G38950	-1.27	-0.34	-2.78	0.028339	0.079582	-4.31
264797_at	unknown protein similar to ESTs gb	---	AT1G08710	1.27	0.34	2.78	0.02834	0.079582	-4.31
256219_at	hypothetical protein predicted by ge	---	AT1G56260	1.25	0.33	2.78	0.028346	0.079587	-4.31
254886_at	putative protein bp4A protein, Bras	LCR17	AT4G11760	-1.27	-0.34	-2.78	0.028352	0.079595	-4.31
264545_at	photosystem I subunit V precursor,	PSAG	AT1G55670	-1.19	-0.25	-2.78	0.028393	0.0797	-4.31
262879_at	plastid RNA polymerase sigma-sub	SIGA	AT1G64860	1.28	0.35	2.78	0.028427	0.079786	-4.32
248867_at	bHLH transcription factor	---	AT5G46830	-1.23	-0.30	-2.78	0.028457	0.07986	-4.32
261478_at	unknown protein	MIOX1	AT1G14520	-1.39	-0.47	-2.78	0.028472	0.079892	-4.32
258646_at	MATE efflux family protein, putative	FRD3	AT3G08040	-1.22	-0.29	-2.78	0.028503	0.079969	-4.32
250551_at	SNAP25 - like protein SNAP25A pr	SNAP29	AT5G07880	-1.26	-0.33	-2.78	0.028539	0.080062	-4.32
264156_at	unknown protein	---	AT1G65280	1.19	0.25	2.78	0.028547	0.080073	-4.32
255980_at	hypothetical protein ;supported by f	---	AT1G33970	1.27	0.35	2.78	0.028574	0.080141	-4.32
250725_at	putative protein similar to unknown	---	AT5G06400	1.30	0.38	2.77	0.028636	0.080303	-4.32
259229_at	unknown protein similar to transcrip	ADA2A	AT3G07740	1.33	0.41	2.77	0.028661	0.080357	-4.32
257952_at	putative peroxidase almost identica	---	AT3G21770	-1.39	-0.48	-2.77	0.028663	0.080357	-4.32
247740_at	receptor-like protein kinase precurs	CRCK1	AT5G58940	1.93	0.95	2.77	0.028666	0.080357	-4.32
247936_at	lycopene epsilon cyclase ; support	LUT2	AT5G57030	-1.38	-0.46	-2.77	0.028671	0.08036	-4.32
246144_at	dynein light chain - like protein dyn	---	AT5G20110	-1.45	-0.53	-2.77	0.028677	0.08036	-4.33
247686_at	receptor-like protein kinase precurs	---	AT5G59700	1.93	0.95	2.77	0.028681	0.08036	-4.33
247008_at	ADP-ribosylation factor-like protein	ATARLA1D	AT5G67560	-1.23	-0.30	-2.77	0.028681	0.08036	-4.33
264672_at	hypothetical protein predicted by ge	---	AT1G09750	-6.48	-2.70	-2.77	0.028712	0.080436	-4.33
251228_at	beta-D-glucan exohydrolase-like pr	---	AT3G62710	-1.23	-0.30	-2.77	0.028728	0.080474	-4.33
253533_at	putative protein cellulose synthase	ATCSLC5	AT4G31590	-2.02	-1.02	-2.77	0.028736	0.080485	-4.33
258658_at	putative adenosine kinase similar to	ADK1	AT3G09820	-1.64	-0.71	-2.77	0.028756	0.080531	-4.33
251755_at	putative protein predicted protein, A	---	AT3G55790	1.43	0.52	2.77	0.028783	0.080597	-4.33
255266_at	receptor protein kinase - like protei	---	AT4G05200	-1.25	-0.32	-2.77	0.028801	0.080628	-4.33
252673_at	CCR4-associated factor 1-like prot	---	AT3G44240	-1.24	-0.31	-2.77	0.028801	0.080628	-4.33
256861_at	beta-amylase, putative similar to be	BAM1	AT3G23920	1.51	0.60	2.77	0.028812	0.080649	-4.33
254904_at	putative translation initiation factor	---	AT4G11160	1.37	0.45	2.77	0.028834	0.0807	-4.33
247634_at	late embryonic abundant protein - l	---	AT5G60520	-1.19	-0.25	-2.77	0.028841	0.08071	-4.33
254249_at	serine /threonine kinase - like prote	---	AT4G23280	1.78	0.84	2.77	0.028856	0.08074	-4.33
260808_at	polyprotein, putative similar to poly	---	---	-1.21	-0.27	-2.77	0.028862	0.08074	-4.33

251955_at	putative protein predicted proteins,	---	AT3G53680	-1.25	-0.33	-2.77	0.028862	0.08074	-4.33
262892_at	succinic semialdehyde dehydroger	ALDH5F1	AT1G79440	1.23	0.29	2.77	0.028869	0.08074	-4.33
266801_at	putative nucleotide-binding protein	EMB2001	AT2G22870	1.57	0.65	2.77	0.02887	0.08074	-4.33
252263_at	putative protein several hypothetica	---	AT3G49520	-1.29	-0.37	-2.77	0.028885	0.080774	-4.33
245480_at	transcription factor like protein	---	AT4G16150	1.20	0.26	2.77	0.028892	0.080782	-4.33
248768_at	60S acidic ribosomal protein P1-like	---	AT5G47700	1.45	0.54	2.77	0.028898	0.080784	-4.33
260022_at	unknown protein	---	AT1G30020	-1.25	-0.32	-2.77	0.0289	0.080784	-4.33
255989_at	putative protein	---	AT5G35069	-1.30	-0.38	-2.77	0.028904	0.080786	-4.33
252742_at	putative protein glyceraldehyde-3-p	---	AT3G43290	-1.32	-0.40	-2.77	0.028944	0.080883	-4.33
254992_at	putative transcriptional regulator	SPT16	AT4G10710	1.36	0.44	2.77	0.028946	0.080883	-4.33
264021_at	putative auxin-regulated protein ;su	---	AT2G21200	-1.67	-0.74	-2.77	0.028956	0.080902	-4.34
259007_at	putative MYB family transcription fa	MYB3R-3	AT3G09370	-1.33	-0.41	-2.77	0.028961	0.080905	-4.34
262223_at	hypothetical protein predicted by ge	---	AT1G74680	1.44	0.53	2.77	0.028972	0.08092	-4.34
264340_at	unknown protein similar to hypothet	---	AT1G70280	-1.30	-0.37	-2.77	0.028974	0.08092	-4.34
250968_at	putative protein ;supported by full-l	---	AT5G02890	-1.67	-0.74	-2.77	0.028977	0.08092	-4.34
261572_at	unknown protein	---	AT1G01170	1.30	0.37	2.77	0.028997	0.080966	-4.34
251783_at	ribosomal L23a - like protein variou	RPL23AB	AT3G55280	1.61	0.69	2.77	0.029003	0.080974	-4.34
264929_at	auxin-induced protein, putative sim	---	AT1G60730	2.63	1.39	2.77	0.029007	0.080977	-4.34
255777_at	glycine-rich RNA-binding protein, p	GR-RBP6	AT1G18630	1.34	0.42	2.77	0.029013	0.080982	-4.34
262810_at	putative salt-inducible protein simila	---	AT1G11710	1.40	0.49	2.76	0.029019	0.080989	-4.34
265595_at	26S proteasome subunit 4 ;suppor	---	AT2G20140	-1.30	-0.38	-2.76	0.029029	0.081004	-4.34
262232_at	unknown protein ; supported by cDI	---	AT1G68600	-1.42	-0.50	-2.76	0.029032	0.081004	-4.34
245746_at	bHLH transcription factor, putative	---	AT1G51070	-1.32	-0.40	-2.76	0.029055	0.081054	-4.34
265129_at	putative zinc finger protein similar t	SUF4	AT1G30970	-1.26	-0.33	-2.76	0.029057	0.081054	-4.34
255727_at	hypothetical protein similar to unkno	---	AT1G25510	-1.27	-0.34	-2.76	0.029069	0.081079	-4.34
252225_at	ADP-RIBOSYLATION FACTOR -li	ATARLA1C	AT3G49870	-1.22	-0.29	-2.76	0.029086	0.081114	-4.34
254405_at	putative protein arm repeat contain	PUB8	AT4G21350	1.40	0.48	2.76	0.02909	0.081114	-4.34
265590_at	SKP1/ASK1 (At17), putative simila	MEO	AT2G20160	-1.23	-0.30	-2.76	0.029092	0.081114	-4.34
247591_at	high-affinity nitrate transporter ACH	NRT2.4	AT5G60770	-1.23	-0.29	-2.76	0.029107	0.081145	-4.34
252101_at	rac-like GTP binding protein Arac11	ROP1	AT3G51300	-1.25	-0.32	-2.76	0.029123	0.08118	-4.34
248517_at	St12p protein	---	AT5G50550	-1.24	-0.31	-2.76	0.029132	0.081195	-4.34
264538_at	hypothetical protein predicted by ge	WRKY10	AT1G55600	-1.30	-0.38	-2.76	0.029148	0.081221	-4.34
259982_at	putative RING zinc finger protein c	ATL8	AT1G76410	-1.86	-0.90	-2.76	0.029151	0.081221	-4.34
247436_at	dehydrogenase ; supported by cDN	ALDH12A1	AT5G62530	1.35	0.43	2.76	0.029152	0.081221	-4.34
264279_s_a	glycoprotein(EP1), putative similar	---	AT1G78820	-1.36	-0.44	-2.76	0.029157	0.081224	-4.34

256435_at	putative leucoanthocyanidin dioxyg	---	AT3G11180	-1.26	-0.33	-2.76	0.029167	0.081244	-4.34
265889_at	hypothetical protein predicted by ge	---	AT2G15130	-1.29	-0.36	-2.76	0.029179	0.081267	-4.34
248230_at	putative protein similar to unknown	---	AT5G53830	1.56	0.64	2.76	0.02919	0.081289	-4.34
253135_at	cytoplasmatic aconitate hydratase (	---	AT4G35830	1.38	0.46	2.76	0.029199	0.081301	-4.34
261775_at	hypothetical protein predicted by ge	---	AT1G76280	1.27	0.35	2.76	0.029205	0.081308	-4.34
251969_at	Cytochrom P450 -like protein CYT	LUT1	AT3G53130	-1.33	-0.41	-2.76	0.029215	0.081328	-4.34
248359_at	unknown protein	---	AT5G52410	-1.29	-0.36	-2.76	0.029243	0.081394	-4.35
247746_at	uncoupling protein AtUCP2 ;suppo	ATUCP2	AT5G58970	-1.35	-0.43	-2.76	0.029251	0.081407	-4.35
252552_at	putative protein	---	AT3G45900	1.36	0.45	2.76	0.029261	0.081425	-4.35
265216_at	putative NPK1-related MAP kinase	MAPKKK18	AT1G05100	-1.46	-0.55	-2.76	0.029273	0.081448	-4.35
252350_at	ataxia-telangiectasia mutated prote	ATM	AT3G48190	1.21	0.27	2.76	0.02928	0.081458	-4.35
261008_at	hypothetical protein contains simila	---	AT1G26370	1.32	0.40	2.76	0.029316	0.081548	-4.35
255877_at	putative PTR2 family peptide transp	---	AT2G40460	-1.82	-0.87	-2.76	0.029347	0.081624	-4.35
255988_at	putative protein	---	---	-1.24	-0.31	-2.76	0.02935	0.081624	-4.35
254157_at	putative protein protein induced up	VEP1	AT4G24220	-1.26	-0.33	-2.76	0.029361	0.081644	-4.35
252848_at	putative protein several hypothetica	---	---	-1.28	-0.36	-2.76	0.029381	0.081676	-4.35
258157_at	putative MYB family transcription fa	MYB4R1	AT3G18100	1.40	0.49	2.76	0.029382	0.081676	-4.35
254744_at	Expressed protein ; supported by cl	MEE55	AT4G13345	1.38	0.46	2.76	0.029384	0.081676	-4.35
267244_at	putative reverse transcriptase	---	AT2G02650	-1.22	-0.29	-2.76	0.029387	0.081676	-4.35
251527_at	putative protein hypothetical protei	---	AT3G58650	-1.23	-0.30	-2.76	0.029394	0.081687	-4.35
252891_at	putative WRKY DNA-binding prote	WRKY13	AT4G39410	-1.36	-0.44	-2.76	0.029402	0.081697	-4.35
257427_at	hypothetical protein predicted by ge	---	AT1G79060	-1.44	-0.53	-2.76	0.029412	0.081715	-4.35
245800_at	heat shock transcription factor, put	HSFB4	AT1G46264	-1.24	-0.31	-2.75	0.029442	0.081789	-4.35
267061_at	unknown protein ;supported by full-	---	AT2G32480	1.24	0.31	2.75	0.029461	0.081832	-4.35
260722_at	protein phosphatase-2C, putative s	---	AT1G48040	1.45	0.53	2.75	0.029465	0.081835	-4.35
257787_at	actin related protein, putative simila	ARP2	AT3G27000	1.19	0.25	2.75	0.029488	0.081886	-4.35
262468_at	alanine--tRNA ligase, putative simi	ALATS	AT1G50200	1.35	0.43	2.75	0.029492	0.081888	-4.35
265389_at	putative riboflavin synthase alpha c	---	AT2G20690	1.29	0.36	2.75	0.029507	0.081917	-4.35
250165_at	putative protein many predicted pro	---	AT5G15290	-1.24	-0.31	-2.75	0.02951	0.081917	-4.35
248528_at	putative protein similar to unknown	---	AT5G50760	3.72	1.90	2.75	0.029513	0.081917	-4.35
252830_at	putative protein 70K peroxisomal m	PXA1	AT4G39850	1.20	0.26	2.75	0.029534	0.081965	-4.36
255843_at	unknown protein	CPL3	AT2G33540	-1.20	-0.27	-2.75	0.029561	0.08203	-4.36
247783_at	light harvesting pigment - like prote	---	AT5G58800	1.54	0.62	2.75	0.029566	0.082035	-4.36
249301_at	putative protein similar to unknown	---	AT5G41440	-1.30	-0.38	-2.75	0.029608	0.082133	-4.36
264371_at	pEARLI 1-like protein may be induc	ELP	AT1G12090	-1.55	-0.63	-2.75	0.029609	0.082133	-4.36

251685_at	putative protein unknown protein A	---	AT3G56430	1.64	0.71	2.75	0.029631	0.082185	-4.36
256877_at	unknown protein ;supported by full-	---	AT3G26470	1.83	0.87	2.75	0.029676	0.082299	-4.36
264569_at	unknown protein EST gb|ATTS113(	---	---	-1.21	-0.28	-2.75	0.029697	0.082349	-4.36
252212_at	protein kinase -like protein NTPK1	MAPKKK2(	AT3G50310	1.72	0.78	2.75	0.029718	0.08239	-4.36
248651_at	unknown protein	---	AT5G49260	-1.21	-0.27	-2.75	0.02972	0.08239	-4.36
255525_at	coded for by A. thaliana cDNA T042	---	AT4G02340	-1.28	-0.36	-2.75	0.029731	0.08241	-4.36
252343_at	putative protein hypothetical protei	---	AT3G48610	-2.03	-1.02	-2.75	0.029743	0.082434	-4.36
250208_at	unknown protein ;supported by full-	anac084	AT5G14000	1.93	0.95	2.75	0.029746	0.082434	-4.36
247713_at	putative protein nonspecific lipid-tra	---	AT5G59330	-1.24	-0.31	-2.75	0.029758	0.082456	-4.36
260955_at	unknown protein contains similarity	---	AT1G06000	-1.64	-0.71	-2.75	0.029829	0.082638	-4.37
259371_at	unknown protein ;supported by full-	---	AT1G69080	-1.96	-0.97	-2.75	0.029831	0.082638	-4.37
248777_at	putative protein similar to unknown	---	AT5G47920	-1.27	-0.34	-2.74	0.029865	0.082723	-4.37
261557_at	kinesin-like protein C-terminal regio	---	AT1G63640	1.35	0.44	2.74	0.029889	0.08278	-4.37
249130_at	putative protein contains similarity t	---	AT5G43100	1.21	0.27	2.74	0.029911	0.082826	-4.37
248576_at	methionine S-methyltransferase (gb	MMT	AT5G49810	1.23	0.30	2.74	0.029913	0.082826	-4.37
251876_at	TATA box binding protein (TBP) as	RGD3	AT3G54280	1.26	0.33	2.74	0.029924	0.082836	-4.37
264879_at	cotton fiber expressed protein, puta	---	AT1G61260	-1.67	-0.74	-2.74	0.029924	0.082836	-4.37
265022_at	putative agp1 similar to GB:CAA48	BCP1	AT1G24520	-1.34	-0.42	-2.74	0.029933	0.082847	-4.37
257172_at	hypothetical protein predicted by g	---	AT3G23700	-1.32	-0.40	-2.74	0.029935	0.082847	-4.37
259206_at	hypothetical protein similar to putati	---	AT3G09040	1.29	0.37	2.74	0.029948	0.082872	-4.37
249406_at	putative protein MtN21, Medicago t	---	AT5G40210	-1.30	-0.38	-2.74	0.029957	0.082879	-4.37
247822_at	putative protein sorting nexin 2, Ho	SNX2a	AT5G58440	-1.29	-0.37	-2.74	0.029959	0.082879	-4.37
248682_at	cytochrome b5 (dbj|BAA74840.1) ;	CB5-D	AT5G48810	1.23	0.30	2.74	0.029961	0.082879	-4.37
262014_at	unknown protein	---	AT1G35660	1.51	0.59	2.74	0.030002	0.082982	-4.37
254566_at	hypothetical protein	---	AT4G19240	1.32	0.40	2.74	0.030021	0.083018	-4.37
247291_at	unknown protein	---	AT5G64480	-1.25	-0.32	-2.74	0.030023	0.083018	-4.37
245678_at	unknown protein	---	AT1G56610	1.35	0.43	2.74	0.030031	0.083023	-4.37
251138_at	putative protein various predicted p	---	AT5G01160	1.27	0.34	2.74	0.030032	0.083023	-4.37
256824_at	hypothetical protein predicted by ge	AT3G2212	---	-1.46	-0.55	-2.74	0.030049	0.083062	-4.37
263181_at	unknown protein ;supported by full-	---	AT1G05720	1.22	0.28	2.74	0.030053	0.083062	-4.37
245606_at	hypothetical protein	---	AT4G14310	-1.26	-0.34	-2.74	0.030092	0.083154	-4.38
264901_at	putative sulphate transporter prote	AST91	AT1G23090	2.00	1.00	2.74	0.030094	0.083154	-4.38
251388_at	putative protein protein regulating c	MAP65-4	AT3G60840	-1.27	-0.34	-2.74	0.030107	0.083181	-4.38
254201_at	putative protein predicted proteins	---	AT4G24130	-1.34	-0.43	-2.74	0.030121	0.08321	-4.38
250349_at	putative receptor - like kinase rece	---	AT5G12000	-1.27	-0.34	-2.74	0.030149	0.083275	-4.38

257972_at	putative protein kinase, ATN1 almo	ATN1	AT3G27560	1.27	0.34	2.74	0.030155	0.083282	-4.38
261043_at	hypothetical protein similar to unkno	---	AT1G01220	1.31	0.38	2.74	0.030177	0.083334	-4.38
251660_at	Expressed protein ; supported by fu	---	AT3G57160	-1.36	-0.45	-2.74	0.03026	0.083552	-4.38
266206_at	unknown protein ; supported by ful	---	AT2G27730	1.33	0.41	2.73	0.030313	0.083678	-4.38
260175_at	neutral invertase, putative similar t	---	AT1G72000	-1.21	-0.27	-2.73	0.030313	0.083678	-4.38
248396_at	unknown protein	---	AT5G52130	-1.28	-0.36	-2.73	0.030324	0.083679	-4.38
264226_at	hypothetical protein similar to putati	---	AT1G67510	-1.25	-0.32	-2.73	0.030326	0.083679	-4.38
255632_at	putative actin-depolymerizing factor	ADF8	AT4G00680	-1.19	-0.25	-2.73	0.030326	0.083679	-4.38
264112_at	putative 1,3-beta-D-glucan synthas	CALS5	AT2G13680	-1.28	-0.36	-2.73	0.030328	0.083679	-4.38
265263_at	putative DNA binding protein	---	AT2G42940	-1.23	-0.30	-2.73	0.030363	0.083766	-4.38
262492_at	unknown protein Contains similarity	---	AT1G21630	-1.25	-0.32	-2.73	0.030396	0.083849	-4.39
264255_at	putative SF2/ASF splicing modulat	---	AT1G09140	1.35	0.43	2.73	0.030443	0.083967	-4.39
255402_at	Expressed protein	hemf2	AT4G03205	-1.54	-0.63	-2.73	0.030466	0.08402	-4.39
259469_at	hypothetical protein predicted by ge	---	AT1G19100	1.22	0.29	2.73	0.030478	0.084039	-4.39
244951_s_a	cytochrome c biogenesis orf452	---	AT2G07723	1.56	0.64	2.73	0.03048	0.084039	-4.39
253790_at	photosystem II protein W - like pho	PSB28	AT4G28660	-1.45	-0.54	-2.73	0.030506	0.084094	-4.39
248759_at	putative protein similar to unknown	---	AT5G47610	1.66	0.73	2.73	0.03051	0.084094	-4.39
259384_at	putative lectin contains Pfam profile	---	AT3G16450	-1.31	-0.39	-2.73	0.030511	0.084094	-4.39
265563_s_a	hypothetical protein predicted by ge	---	---	-1.18	-0.24	-2.73	0.030548	0.084173	-4.39
258824_at	unknown protein	---	AT3G07190	1.34	0.42	2.73	0.030551	0.084173	-4.39
267447_at	putative GTP-binding protein	ArRABA1h	AT2G33870	-1.19	-0.26	-2.73	0.030551	0.084173	-4.39
266440_at	unknown protein	---	AT2G43235	1.23	0.30	2.73	0.030631	0.084383	-4.39
257963_at	hypothetical protein predicted by ge	---	AT3G19840	1.49	0.57	2.73	0.030636	0.084388	-4.39
254469_at	hypothetical protein	---	AT4G20470	-1.23	-0.30	-2.73	0.030648	0.084402	-4.39
247456_at	iron-regulated transporter - like pro	AtZIP12	AT5G62160	-1.23	-0.30	-2.73	0.030649	0.084402	-4.39
255426_at	putative protein	---	AT4G03370	-1.23	-0.30	-2.73	0.030657	0.084413	-4.39
258517_at	galactose kinase identical to GB:A	GALK	AT3G06580	-1.25	-0.32	-2.72	0.030707	0.084542	-4.40
252974_at	putative protein ; supported by cDN	MTN1	AT4G38800	1.22	0.29	2.72	0.030721	0.08457	-4.40
254588_at	putative protein hypothetical protein	---	AT4G18840	1.23	0.30	2.72	0.030729	0.084574	-4.40
255058_s_a	putative protein various hypothetica	---	---	-1.19	-0.25	-2.72	0.030731	0.084574	-4.40
259453_at	gibberelin 20-oxidase, putative, 5' p	ATGA20OX	AT1G44090	-1.35	-0.43	-2.72	0.030734	0.084574	-4.40
262521_at	unknown protein Location of est 27	---	AT1G17130	1.25	0.32	2.72	0.030756	0.084614	-4.40
246002_at	ripening-related protein - like grip2	---	AT5G20740	-1.60	-0.68	-2.72	0.030759	0.084614	-4.40
261685_at	3-beta-hydroxysteroid dehydrogena	AT3BETAH	AT1G47290	-1.61	-0.69	-2.72	0.030763	0.084614	-4.40
260397_at	hypothetical protein predicted by ge	---	AT1G69680	1.25	0.32	2.72	0.030766	0.084614	-4.40

263086_at	putative non-LTR retrolelement reve	---	AT2G16110	-1.24	-0.31	-2.72	0.030769	0.084614	-4.40
254847_at	putative phospholipase D-gamma	PLDGAMM	AT4G11850	1.72	0.79	2.72	0.030771	0.084614	-4.40
254961_at	putative acyl-CoA synthetase acyl-	---	AT4G11030	-1.25	-0.32	-2.72	0.030774	0.084614	-4.40
250301_at	putative protein predicted proteins,	---	AT5G11970	-1.36	-0.45	-2.72	0.030788	0.084641	-4.40
262787_at	putative clathrin-coat assembly prot	---	AT1G10730	1.42	0.50	2.72	0.030794	0.084649	-4.40
254789_at	blue copper-binding protein, 15K (I	---	AT4G12880	-3.59	-1.85	-2.72	0.030805	0.08467	-4.40
247254_at	CLE21, putative CLAVATA3/ESR-I	CLE21	AT5G64800	1.51	0.59	2.72	0.030846	0.084756	-4.40
266240_at	putative RNA-binding protein ; sup	---	AT2G29580	1.18	0.24	2.72	0.030847	0.084756	-4.40
253467_at	putative protein hypothetical protei	---	AT4G32140	-1.28	-0.35	-2.72	0.030848	0.084756	-4.40
250178_at	putative protein various unknown c	---	AT5G14430	1.21	0.27	2.72	0.030899	0.084883	-4.40
247898_at	F-box protein ZTL/LFK1/ADO1, AtF	ZTL	AT5G57360	1.25	0.32	2.72	0.030902	0.084883	-4.40
264123_at	unknown protein ; supported by cDI	---	AT1G02270	1.28	0.35	2.72	0.030928	0.084936	-4.40
250274_at	putative protein predicted protein, A	---	AT5G13020	1.27	0.35	2.72	0.030929	0.084936	-4.40
248635_at	unknown protein	---	AT5G49050	-1.22	-0.29	-2.72	0.030933	0.084936	-4.40
266275_at	putative tropinone reductase	---	AT2G29370	-1.31	-0.39	-2.72	0.030936	0.084936	-4.40
254393_at	putative NADPH quinone oxidored	---	AT4G21580	1.24	0.31	2.72	0.03094	0.084936	-4.40
257946_at	hypothetical protein predicted by ge	---	AT3G21710	1.23	0.30	2.72	0.030984	0.085035	-4.41
262938_at	hypothetical protein predicted by ge	---	AT1G79540	1.27	0.34	2.72	0.030985	0.085035	-4.41
252064_at	putative protein various predicted p	---	AT3G51520	1.23	0.30	2.72	0.03099	0.085035	-4.41
248612_at	putative protein contains similarity t	---	AT5G49530	1.40	0.49	2.72	0.030991	0.085035	-4.41
251489_at	putative protein putative proteins - A	---	AT3G59460	-1.28	-0.35	-2.72	0.031001	0.085054	-4.41
257829_at	unknown protein	SNM1	AT3G26680	1.47	0.56	2.72	0.031017	0.085087	-4.41
262246_at	leaf development protein Argonaute	AGO1	AT1G48410	-1.27	-0.35	-2.72	0.031042	0.085145	-4.41
252179_at	putative protein UDP-glucose:(gluc	GATL2	AT3G50760	-1.39	-0.48	-2.72	0.031054	0.085169	-4.41
252863_at	myo-inositol-1-phosphate synthase	MIPS1	AT4G39800	-2.95	-1.56	-2.72	0.031077	0.085219	-4.41
258918_at	putative cytochrome P450 similar to	UNE9	AT3G10560	-1.38	-0.47	-2.72	0.031083	0.085219	-4.41
255199_at	coded for by A. thaliana cDNA N64	---	AT4G07390	1.22	0.28	2.72	0.031084	0.085219	-4.41
259998_at	hypothetical protein similar to unkno	BPC3	AT1G68120	-1.36	-0.44	-2.72	0.031115	0.085295	-4.41
254429_at	Expressed protein ; supported by fu	---	AT4G21105	1.24	0.31	2.72	0.031132	0.085325	-4.41
261654_at	hypothetical protein contains simila	---	AT1G01920	1.34	0.42	2.72	0.031134	0.085325	-4.41
262415_at	40S ribosomal protein S17, putativ	emb1129	AT1G49400	1.32	0.40	2.71	0.03115	0.085361	-4.41
262353_at	hypothetical protein similar to hypot	---	AT1G64210	-1.19	-0.25	-2.71	0.03116	0.085377	-4.41
250816_at	coatomer delta subunit (delta-coat p	---	AT5G05010	-1.33	-0.41	-2.71	0.031178	0.085415	-4.41
246597_at	L-aspartate oxidase -like protein L-	AO	AT5G14760	2.03	1.02	2.71	0.031227	0.085531	-4.41
249808_at	unknown protein	---	AT5G23890	1.52	0.61	2.71	0.031228	0.085531	-4.41

265500_at	putative non-LTR retroelement reve	---	---	-1.42	-0.50	-2.71	0.031244	0.085565	-4.41
253497_at	putative protein microtubule-associ	---	AT4G31880	1.28	0.36	2.71	0.031255	0.085586	-4.41
253045_at	Expressed protein ; supported by fu	---	AT4G37445	-1.42	-0.51	-2.71	0.031262	0.085595	-4.41
260634_at	initiation factor isozyme 4F p82 sub	---	AT1G62410	-1.25	-0.32	-2.71	0.031272	0.085611	-4.42
262127_at	hypothetical protein predicted by ge	---	AT1G52550	1.34	0.42	2.71	0.031277	0.085615	-4.42
252297_at	cytosolic ribosomal protein S11 ;su	EMB1080	AT3G48930	1.52	0.61	2.71	0.031284	0.085624	-4.42
248530_at	putative protein strong similarity to	---	AT5G49945	-1.30	-0.38	-2.71	0.031296	0.085647	-4.42
252087_at	putative protein putative Na+/H+-e	chx28	AT3G52080	-1.22	-0.29	-2.71	0.031306	0.085663	-4.42
248213_at	putative protein similar to unknown	AtGRF7	AT5G53660	-1.26	-0.33	-2.71	0.031312	0.085669	-4.42
246627_s_a	5-enolpyruvylshikimate-3-phosphat	---	AT1G48860	1.74	0.80	2.71	0.03132	0.08568	-4.42
256998_at	hypothetical protein predicted by ge	---	AT3G14180	-1.32	-0.40	-2.71	0.031338	0.08572	-4.42
246564_at	putative protein hypothetical protei	---	AT5G15610	1.19	0.26	2.71	0.031346	0.085731	-4.42
255219_at	hypothetical protein	---	AT4G07720	-1.21	-0.28	-2.71	0.0314	0.085868	-4.42
248961_at	subtilisin-like protease	---	AT5G45650	1.89	0.92	2.71	0.031425	0.085927	-4.42
256509_at	NADPH oxidoreductase, putative s	---	AT1G75300	-1.49	-0.58	-2.71	0.031442	0.085937	-4.42
265019_at	putative myosin heavy chain similar	---	AT1G24560	1.20	0.26	2.71	0.031443	0.085937	-4.42
245103_at	putative Ta11-like non-LTR retroele	---	AT2G41590	-1.21	-0.27	-2.71	0.031446	0.085937	-4.42
266265_at	putative tropinone reductase ; supp	---	AT2G29340	-1.42	-0.50	-2.71	0.031446	0.085937	-4.42
251389_at	putative protein	---	AT3G60850	1.22	0.28	2.71	0.031447	0.085937	-4.42
246413_at	unknown protein	---	AT1G77310	1.26	0.33	2.71	0.031475	0.085991	-4.42
246099_at	blue copper binding protein ;suppo	ATBCB	AT5G20230	1.49	0.58	2.71	0.031475	0.085991	-4.42
262397_at	hypothetical protein predicted by ge	---	AT1G49380	-1.45	-0.54	-2.71	0.031482	0.085991	-4.42
252014_at	putative protein predicted proteins,	---	AT3G52870	-1.91	-0.93	-2.71	0.031482	0.085991	-4.42
249572_at	chromosome condensation protein	EMB2656	AT5G37630	-1.30	-0.38	-2.71	0.031496	0.086019	-4.42
264399_at	postsynaptic protein CRIPT, putativ	---	AT1G61780	1.18	0.24	2.71	0.031553	0.086165	-4.42
248112_at	wax synthase-like protein	---	AT5G55350	-1.31	-0.39	-2.71	0.03157	0.086194	-4.43
262514_at	NAM(no apical meristem) protein,	anac017	AT1G34190	1.20	0.26	2.71	0.031572	0.086194	-4.43
261111_at	homeodomain protein BELL1, puta	BLH11	AT1G75430	-1.20	-0.26	-2.70	0.031594	0.086244	-4.43
260689_at	hypothetical protein predicted by ge	---	AT1G32290	-1.31	-0.39	-2.70	0.031605	0.086255	-4.43
266525_at	putative tetracycline transporter pro	MEE15	AT2G16970	-1.28	-0.36	-2.70	0.031609	0.086255	-4.43
253187_at	putative zinc-finger protein PEThy;	---	AT4G35280	-1.20	-0.26	-2.70	0.031609	0.086255	-4.43
266571_at	unknown protein	---	AT2G23830	1.56	0.64	2.70	0.031624	0.086284	-4.43
260461_at	membrane protein PTM1 precursor	---	AT1G10980	-1.26	-0.33	-2.70	0.03163	0.086289	-4.43
266815_at	F-box protein family, AtFBX5 conta	---	AT2G44900	-1.28	-0.36	-2.70	0.031633	0.086289	-4.43
262025_at	growth regulator, putative similar to	---	AT1G35510	-1.28	-0.36	-2.70	0.031642	0.086303	-4.43

253444_at	putative protein ring finger protein,	---	AT4G32600	1.21	0.28	2.70	0.031647	0.086306	-4.43
256193_at	hypothetical protein similar to hypot	---	AT1G30200	-1.22	-0.29	-2.70	0.031674	0.086369	-4.43
252451_at	hypothetical protein	---	AT3G47100	-1.21	-0.27	-2.70	0.031678	0.086371	-4.43
250924_at	putative protein ;supported by full-l	---	AT5G03440	-1.25	-0.32	-2.70	0.031693	0.086401	-4.43
264798_at	putative myosin MYA1, class V (Z2	XIC	AT1G08730	-1.23	-0.30	-2.70	0.031702	0.086413	-4.43
264588_at	unknown protein contains similarity	---	AT2G17730	1.59	0.67	2.70	0.031705	0.086413	-4.43
266297_at	putative proliferating cell nuclear a	PCNA2	AT2G29570	2.12	1.09	2.70	0.03171	0.086417	-4.43
258973_at	putative cytochrome P450 similar to	CYP94B2	AT3G01900	-1.26	-0.33	-2.70	0.031718	0.086427	-4.43
262109_at	hypothetical protein similar to cellul	ATCSLD5	AT1G02730	-1.51	-0.60	-2.70	0.031739	0.086475	-4.43
257884_at	hypothetical protein predicted by ge	---	AT3G16960	-1.24	-0.32	-2.70	0.031755	0.086508	-4.43
248308_at	putative protein similar to unknown	---	AT5G52530	1.22	0.29	2.70	0.031764	0.086522	-4.43
252914_at	putative protein dehydrin, Glycine r	---	AT4G39130	-1.32	-0.40	-2.70	0.031781	0.086559	-4.43
264253_at	putative kinesin similar to GB:AAB6	---	AT1G09170	-1.39	-0.48	-2.70	0.03179	0.086572	-4.43
262163_at	ribosomal protein L30, putative sim	---	AT1G77940	1.63	0.71	2.70	0.031803	0.086588	-4.43
263408_at	predicted protein	---	AT2G04060	-1.21	-0.28	-2.70	0.031803	0.086588	-4.43
255153_at	putative protein several hypothetica	---	AT4G08210	-1.31	-0.39	-2.70	0.031809	0.086592	-4.43
256256_at	unknown protein ; supported by full-	---	AT3G11230	1.25	0.32	2.70	0.031849	0.086686	-4.43
261408_s_a	histone H4 identical to GB:M36659	---	AT1G07660	1.35	0.43	2.70	0.031851	0.086686	-4.43
260143_at	sucrose transport protein SUC1 ide	SUC1	AT1G71880	1.68	0.75	2.70	0.031861	0.086689	-4.43
256127_at	small GTP-binding protein (RAB11	AtRABA6b	AT1G18200	-1.28	-0.36	-2.70	0.031862	0.086689	-4.43
262325_at	dirigent protein, putative similar to	---	AT1G64160	1.60	0.67	2.70	0.031863	0.086689	-4.43
258601_at	putative histidyl tRNA synthetase si	---	AT3G02760	1.28	0.36	2.70	0.03188	0.086724	-4.44
259694_at	uridine diphosphate glucose epime	UGE3	AT1G63180	1.86	0.90	2.70	0.031902	0.086773	-4.44
262611_at	Expressed protein ; supported by fu	---	AT1G14060	1.44	0.52	2.70	0.031907	0.086776	-4.44
256761_at	hypothetical protein predicted by ge	---	AT3G25670	-1.32	-0.40	-2.70	0.031918	0.086795	-4.44
264490_at	putative protein import receptor sim	TOM20-2	AT1G27390	1.43	0.52	2.70	0.031931	0.086822	-4.44
247732_at	putative protein various predicted p	---	AT5G59600	1.19	0.26	2.70	0.031964	0.086902	-4.44
261003_at	hypothetical protein predicted by ge	---	AT1G26500	1.29	0.37	2.70	0.031986	0.086942	-4.44
259910_at	putative P-type transporting ATPas	---	AT1G72700	-1.53	-0.61	-2.70	0.031987	0.086942	-4.44
256191_at	unknown protein similar to hypothet	---	AT1G30130	-1.27	-0.34	-2.70	0.031991	0.086943	-4.44
252796_at	putative protein predicted proteins,	---	---	-1.37	-0.45	-2.70	0.031996	0.086947	-4.44
254376_at	putative protein ; supported by cDN	TOM1	AT4G21790	-1.18	-0.24	-2.70	0.032018	0.086995	-4.44
249659_s_a	putative protein similar to unknown	---	AT5G36710	-1.33	-0.42	-2.70	0.032034	0.087029	-4.44
251895_at	class IV chitinase (CHIV)	ATEP3	AT3G54420	1.78	0.84	2.69	0.032038	0.08703	-4.44
248207_at	tyrosine aminotransferase	---	AT5G53970	1.89	0.91	2.69	0.032042	0.08703	-4.44

266924_at	unknown protein ;supported by full-	---	AT2G45730	1.30	0.38	2.69	0.032047	0.087033	-4.44
250953_at	putative protein ;supported by full-l	DPB	AT5G03415	1.38	0.47	2.69	0.032056	0.087048	-4.44
260074_at	putative ras-related GTP-binding pr	AtRABA6a	AT1G73640	-1.22	-0.29	-2.69	0.032082	0.0871	-4.44
248127_at	transport protein particle componen	---	AT5G54750	-1.21	-0.28	-2.69	0.032083	0.0871	-4.44
251641_at	protease-like protein INSULIN-DEC	---	AT3G57470	-1.36	-0.45	-2.69	0.032113	0.087172	-4.44
260138_at	calmodulin-4 identical to GB:Q035	CAM4	AT1G66410	1.29	0.37	2.69	0.032155	0.087268	-4.44
257534_at	hypothetical protein predicted by ge	---	AT3G09670	1.22	0.28	2.69	0.032157	0.087268	-4.44
254170_at	LG27/30-like gene LG27/30 gene -	---	AT4G24430	-1.19	-0.26	-2.69	0.03216	0.087268	-4.44
247316_at	ankyrin-like protein	---	AT5G64030	-1.22	-0.29	-2.69	0.032169	0.087282	-4.44
258269_at	putative acetyl-CoA carboxylase bio	---	AT3G15690	-1.23	-0.29	-2.69	0.032182	0.087295	-4.45
261225_at	unknown protein ;supported by full-	---	AT1G20100	1.22	0.28	2.69	0.032187	0.087295	-4.45
246772_at	putative protein unknown protein T	---	AT5G27490	-1.51	-0.59	-2.69	0.032187	0.087295	-4.45
263677_at	unknown protein	PDLP2	AT1G04520	-1.25	-0.33	-2.69	0.03219	0.087295	-4.45
265423_at	unknown protein	---	AT2G20790	-1.44	-0.53	-2.69	0.032193	0.087295	-4.45
254121_at	putative protein putative protein F6	---	AT4G24760	1.48	0.56	2.69	0.032203	0.087311	-4.45
258596_at	unknown protein	LSH2	AT3G04510	-1.28	-0.35	-2.69	0.032218	0.087341	-4.45
245288_at	transcriptional adaptor like protein ;	ADA2B	AT4G16420	1.23	0.30	2.69	0.032235	0.087372	-4.45
260987_at	hypothetical protein predicted by ge	NTMC2T6.	AT1G53590	1.31	0.39	2.69	0.032237	0.087372	-4.45
259628_at	hypothetical protein contains Pfam	---	AT1G56440	1.36	0.45	2.69	0.032241	0.087373	-4.45
255325_at	putative membrane trafficking facto	PUX4	AT4G04210	1.23	0.30	2.69	0.032247	0.087378	-4.45
255454_at	hypothetical protein	---	AT4G02910	-1.20	-0.27	-2.69	0.032273	0.087438	-4.45
246586_at	putative protein predicted protein, /	---	AT5G14770	1.34	0.42	2.69	0.032313	0.087536	-4.45
254619_at	myb - like protein transforming prot	MYB98	AT4G18770	-1.23	-0.30	-2.69	0.032345	0.087613	-4.45
264907_at	unknown protein similar to S.pombe	---	AT2G17280	-1.81	-0.86	-2.69	0.032351	0.087619	-4.45
253854_at	putative protein zinc-finger protein	---	AT4G27900	1.80	0.85	2.69	0.03236	0.087634	-4.45
254754_at	pectate lyase like protein pectate ly	---	AT4G13210	-1.20	-0.26	-2.69	0.032368	0.087644	-4.45
263900_at	unknown protein ;supported by full-	---	AT2G36290	1.31	0.39	2.69	0.032388	0.087687	-4.45
265056_at	mitochondrial processing peptidase	---	AT1G51980	1.33	0.41	2.69	0.032391	0.087687	-4.45
245024_at	ATPase alpha subunit	---	---	-1.20	-0.26	-2.69	0.032407	0.087718	-4.45
258727_at	ethylene-responsive protein, putati	---	AT3G11930	1.29	0.36	2.69	0.032413	0.087725	-4.45
263510_s_a	hypothetical protein	---	AT2G07681	1.20	0.26	2.69	0.032422	0.087735	-4.45
253788_at	aromatic amino-acid decarboxylase	---	AT4G28680	-1.27	-0.35	-2.69	0.032425	0.087735	-4.45
265257_at	succinyl-CoA ligase beta subunit ;s	---	AT2G20420	1.51	0.60	2.69	0.032436	0.087756	-4.45
262802_at	putative cell division control protein	CDKB2;2	AT1G20930	-1.19	-0.25	-2.69	0.032473	0.087846	-4.45
251774_at	nematode resistance protein-like p	---	AT3G55840	-2.24	-1.16	-2.68	0.032507	0.087926	-4.46

265381_at	putative non-LTR retroelement reve	---	---	-1.34	-0.42	-2.68	0.032517	0.087945	-4.46
250479_at	GTP-binding protein GTP-binding p	AtRABH1e	AT5G10260	-1.25	-0.32	-2.68	0.032551	0.088024	-4.46
253236_at	putative protein ARI protein, Droso	ARI1	AT4G34370	1.20	0.26	2.68	0.03258	0.088093	-4.46
251563_at	anthranilate phosphoribosyltransfe	---	AT3G57880	-1.48	-0.56	-2.68	0.032598	0.088131	-4.46
247988_at	putative protein similar to unknown	---	AT5G56910	1.40	0.48	2.68	0.032603	0.088135	-4.46
262540_at	hypothetical protein predicted by ge	---	AT1G34260	-1.41	-0.50	-2.68	0.032622	0.088174	-4.46
266428_at	putative protein kinase contains a p	---	AT2G07180	1.30	0.38	2.68	0.032653	0.088247	-4.46
256825_at	unknown protein similar to cell wall-	CWLP	AT3G22120	-5.47	-2.45	-2.68	0.032658	0.088252	-4.46
263904_at	putative ABC transporter related to	PDR6	AT2G36380	1.88	0.91	2.68	0.032674	0.088285	-4.46
250880_at	putative protein Ube-1a, Mus musc	---	AT5G04070	1.20	0.26	2.68	0.032705	0.088334	-4.46
260642_at	plastid protein, putative similar to p	---	AT1G53260	-1.37	-0.45	-2.68	0.032709	0.088334	-4.46
249961_at	putative protein predicted proteins,	---	AT5G18770	1.27	0.35	2.68	0.03271	0.088334	-4.46
266411_at	putative peptidyl-prolyl cis-trans iso	---	AT2G38730	-1.32	-0.40	-2.68	0.032713	0.088334	-4.46
263539_at	putative tyrosine aminotransferase	TAT3	AT2G24850	-3.95	-1.98	-2.68	0.032715	0.088334	-4.46
251254_at	putative protein anion exchanger 3	---	AT3G62270	1.29	0.37	2.68	0.032716	0.088334	-4.46
260880_at	hypothetical protein similar to unkn	---	AT1G21380	-1.25	-0.32	-2.68	0.032722	0.088339	-4.46
260455_at	hypothetical protein predicted by ge	---	AT1G72500	-1.72	-0.78	-2.68	0.032741	0.088382	-4.46
256072_at	WD-40 repeat protein identical to W	ATARCA	AT1G18080	1.56	0.64	2.68	0.032748	0.088389	-4.46
249000_at	putative protein contains similarity t	---	AT5G44980	-1.25	-0.32	-2.68	0.032756	0.088397	-4.46
250900_at	putative protein ; supported by cDN	ATB' ALPH	AT5G03470	1.34	0.42	2.68	0.032759	0.088397	-4.46
255785_at	sulfate adenylyltransferase identica	APS2	AT1G19920	1.25	0.32	2.68	0.032774	0.08843	-4.46
258101_at	unknown protein	RFR1	AT3G23590	-1.52	-0.61	-2.68	0.032827	0.088551	-4.47
248948_at	putative protein strong similarity to	---	AT5G45560	-1.36	-0.44	-2.68	0.032827	0.088551	-4.47
258056_at	hypothetical protein similar to GB:A	---	AT3G29010	-1.33	-0.42	-2.68	0.032832	0.088554	-4.47
246304_at	acyl-coA dehydrogenase Mus musc	ACX4	AT3G51840	1.35	0.44	2.68	0.032846	0.08858	-4.47
255435_at	putative component of cytochrome	PETC	AT4G03280	-1.25	-0.33	-2.68	0.032854	0.088591	-4.47
247147_at	putative protein contains similarity t	GTE7	AT5G65630	-1.34	-0.43	-2.68	0.032863	0.088605	-4.47
262135_at	AP2 domain containing protein, pu	RAP2.4	AT1G78080	1.53	0.61	2.68	0.032925	0.088762	-4.47
257248_at	hypothetical protein predicted by ge	---	AT3G24150	-1.34	-0.42	-2.68	0.032933	0.088773	-4.47
249229_at	putative protein similar to unknown	---	AT5G42090	1.24	0.31	2.68	0.032948	0.088798	-4.47
260695_at	RNA helicase, putative similar to G	ESP3	AT1G32490	1.18	0.24	2.68	0.03295	0.088798	-4.47
246301_at	calcium-dependent protein kinase	CPK13	AT3G51850	1.22	0.29	2.68	0.03296	0.088809	-4.47
258718_at	unknown protein ; supported by cD	---	AT3G09760	1.25	0.32	2.67	0.032962	0.088809	-4.47
265238_s_a	hypothetical protein	---	AT2G07696	1.38	0.46	2.67	0.032993	0.088883	-4.47
253918_at	putative protein ; supported by full-	PHOS34	AT4G27320	1.24	0.32	2.67	0.032997	0.088883	-4.47

262795_at	hypothetical protein predicted by ge	---	AT1G13130	-1.36	-0.44	-2.67	0.033031	0.088965	-4.47
261226_at	expansin S2 precursor, putative sir	ATEXPA11	AT1G20190	-4.05	-2.02	-2.67	0.033078	0.089079	-4.47
256711_at	unknown protein contains Pfam pro	---	AT3G30390	1.42	0.50	2.67	0.033085	0.089088	-4.47
254893_at	putative phospholipase D-gamma	PLDGAMM	AT4G11830	-1.44	-0.53	-2.67	0.033092	0.089097	-4.47
252571_at	putative protein syntaxin 8 - Homo	SYP72	AT3G45280	-1.27	-0.34	-2.67	0.033109	0.089133	-4.47
261669_at	unknown protein similar to hypothet	---	AT1G18490	-1.18	-0.23	-2.67	0.033135	0.089193	-4.48
262872_at	hypothetical protein predicted by ge	---	AT1G64690	-1.36	-0.45	-2.67	0.033155	0.089235	-4.48
245057_at	En/Spm-like transposon protein rela	---	AT2G26490	-1.18	-0.23	-2.67	0.033164	0.08924	-4.48
263788_at	putative sarcosine oxidase	---	AT2G24580	1.42	0.50	2.67	0.033165	0.08924	-4.48
253097_at	cytochrome P450-like protein	CYP81D5	AT4G37320	1.79	0.84	2.67	0.033176	0.08926	-4.48
247151_at	unknown protein ;supported by full-	bHLH093	AT5G65640	-1.43	-0.52	-2.67	0.033185	0.089275	-4.48
247538_at	ABC family transporter - like protei	ATH16	AT5G61700	-1.18	-0.24	-2.67	0.033197	0.089295	-4.48
262338_at	Expressed protein ; supported by fu	---	AT1G64185	1.35	0.43	2.67	0.033233	0.08938	-4.48
253923_at	hypothetical protein Arabidopsis th	TOR1	AT4G27060	-1.24	-0.31	-2.67	0.033241	0.089384	-4.48
245453_at	disease resistance RPP5 like protei	---	AT4G16900	-1.24	-0.31	-2.67	0.033242	0.089384	-4.48
267472_at	putative basic blue protein (plantac	ARPN	AT2G02850	-1.26	-0.33	-2.67	0.033251	0.089399	-4.48
251055_at	putative protein putative protein F4	---	AT5G01710	-1.22	-0.28	-2.67	0.033272	0.089445	-4.48
266096_at	putative vacuolar protein sorting-as	VCL1	AT2G38020	1.22	0.28	2.67	0.033276	0.089446	-4.48
260166_at	homeobox protein (GLABRA2) iden	GL2	AT1G79840	-1.20	-0.27	-2.67	0.033306	0.089508	-4.48
267578_at	Expressed protein ; supported by c	---	AT2G30695	-1.51	-0.59	-2.67	0.033308	0.089508	-4.48
246997_at	putative protein similar to unknown	---	AT5G67390	1.37	0.46	2.67	0.033324	0.089542	-4.48
AFFX-Athal-	Arabidopsis thaliana /REF=U84969	---	---	1.18	0.24	2.67	0.033331	0.089549	-4.48
250903_at	putative protein coil protein PO22,	---	AT5G03600	-1.32	-0.41	-2.67	0.033385	0.089682	-4.48
248126_at	protein translation factor Sui1 homo	ROC5	AT4G34870	1.18	0.24	2.67	0.03339	0.089682	-4.48
248502_at	putative protein strong similarity to	---	AT5G50450	-1.33	-0.41	-2.67	0.033392	0.089682	-4.48
267455_at	hypothetical protein predicted by g	---	AT2G33760	1.31	0.39	2.67	0.033396	0.089682	-4.48
247470_at	putative protein various predicted p	---	AT5G62220	-1.95	-0.97	-2.67	0.033424	0.089748	-4.48
254339_at	glucosidase like protein furostanol	BGLU3	AT4G22100	-1.22	-0.29	-2.66	0.033442	0.089785	-4.48
247042_at	putative protein similar to unknown	---	AT5G67220	-1.22	-0.28	-2.66	0.033451	0.089798	-4.49
251160_at	inositol-1,4,5-trisphosphate 5-Phos	---	AT3G63240	-1.26	-0.33	-2.66	0.033462	0.089817	-4.49
261160_at	hypothetical protein	---	AT1G34480	-1.23	-0.30	-2.66	0.033469	0.089825	-4.49
266234_at	SKP1 interacting partner 3 (SKIP3)	SKIP3	AT2G02350	1.26	0.34	2.66	0.033473	0.089827	-4.49
267373_at	unknown protein	CID7	AT2G26280	1.24	0.31	2.66	0.033493	0.089869	-4.49
264012_at	hypothetical protein predicted by ge	---	AT2G21080	-1.30	-0.38	-2.66	0.033505	0.08989	-4.49
251054_at	receptor like protein kinase recepto	LECRKA4.	AT5G01540	2.71	1.44	2.66	0.033514	0.089905	-4.49

250893_at	putative protein predicted proteins -	EMB175	AT5G03795	-1.20	-0.27	-2.66	0.033519	0.089908	-4.49
264390_at	putative DNA-binding protein Conta	---	AT1G11950	1.29	0.37	2.66	0.033538	0.089938	-4.49
248330_at	putative protein contains similarity t	---	AT5G52810	1.52	0.60	2.66	0.033542	0.089938	-4.49
252369_at	putative protein deoxycytidylate de	---	AT3G48540	-1.22	-0.29	-2.66	0.033542	0.089938	-4.49
259614_at	dioxygenase, putative similar to dic	ATGA2OX4	AT1G47990	-1.25	-0.32	-2.66	0.033555	0.08996	-4.49
258330_at	unknown protein	ROPGEF1	AT3G16130	-1.25	-0.32	-2.66	0.033565	0.089978	-4.49
257105_at	unknown protein	---	AT3G15300	1.38	0.46	2.66	0.033573	0.089989	-4.49
266260_at	putative ATPase skd1 family; suppo	SKD1	AT2G27600	-1.20	-0.26	-2.66	0.033591	0.090025	-4.49
247141_at	putative protein strong similarity to	---	AT5G65560	1.38	0.46	2.66	0.033605	0.090053	-4.49
260057_at	putative protein phosphatase 2C sir	---	AT1G78200	1.21	0.27	2.66	0.033612	0.090062	-4.49
258752_at	hypothetical protein predicted by ge	ATEXO70H	AT3G09520	1.55	0.63	2.66	0.033632	0.090105	-4.49
253764_s_a	protein kinase - like protein ADK1 p	ckl4	AT4G28860	1.29	0.37	2.66	0.033639	0.090113	-4.49
245121_at	60S ribosomal protein L7A ;suppor	---	AT2G47610	1.51	0.60	2.66	0.033689	0.090234	-4.49
262753_at	putative 3-deoxy-D-manno-2-octulo	ATKDSA2	AT1G16340	1.23	0.29	2.66	0.033695	0.09024	-4.49
245506_at	glutaredoxin homolog	---	AT4G15700	-1.61	-0.69	-2.66	0.033713	0.09027	-4.49
264408_at	hypothetical protein predicted by ge	FRS11	AT1G10240	1.22	0.29	2.66	0.033714	0.09027	-4.49
263806_at	hypothetical protein predicted by ge	---	AT2G04305	-1.61	-0.69	-2.66	0.033749	0.090345	-4.49
254681_at	putative protein HYA22 protein, Ho	---	AT4G18140	-1.40	-0.49	-2.66	0.03375	0.090345	-4.49
251350_at	cytochrome P450 monooxygenase	CYP76C7	AT3G61040	-1.40	-0.49	-2.66	0.03376	0.090362	-4.49
267110_at	hypothetical protein predicted by ge	---	AT2G14800	1.30	0.38	2.66	0.033791	0.090432	-4.50
254931_at	serine/threonine kinase-like protein	---	AT4G11460	-1.33	-0.41	-2.66	0.033796	0.090432	-4.50
257135_at	hypothetical protein similar to oxido	---	AT3G12900	-1.30	-0.38	-2.66	0.033798	0.090432	-4.50
267108_at	hypothetical protein predicted by ge	---	AT2G14830	-1.20	-0.26	-2.66	0.033818	0.090476	-4.50
266653_at	hypothetical protein predicted by ge	---	AT2G25740	1.26	0.33	2.66	0.033835	0.09051	-4.50
258722_at	putative pathogenesis-related prote	---	AT3G09590	-1.23	-0.30	-2.66	0.03384	0.090514	-4.50
263279_x_a	hypothetical protein predicted by ge	---	---	-1.25	-0.32	-2.66	0.033872	0.090588	-4.50
255268_at	putative protein ubiquitin, Tetrahym	---	AT4G05230	-1.26	-0.34	-2.66	0.033906	0.090668	-4.50
263115_at	Expressed protein ; supported by cl	---	AT1G03055	-1.48	-0.57	-2.65	0.033925	0.090709	-4.50
261219_at	hypothetical protein predicted by ge	---	AT1G19980	1.28	0.35	2.65	0.033932	0.090716	-4.50
252416_at	chromosome assembly protein hor	ATSMC2	AT3G47460	-1.17	-0.23	-2.65	0.033974	0.090816	-4.50
260261_at	unknown protein	---	AT1G68450	2.24	1.17	2.65	0.033979	0.09082	-4.50
265844_at	putative receptor-like protein kinase	FEI2	AT2G35620	-1.36	-0.44	-2.65	0.034014	0.090885	-4.50
246108_at	putative protein retinal glutamic aci	---	AT5G28630	-1.63	-0.71	-2.65	0.034014	0.090885	-4.50
256070_at	hypothetical protein predicted by ge	---	AT1G13730	1.22	0.28	2.65	0.034015	0.090885	-4.50
251220_at	cytochrome c oxidase subunit 5c-li	---	AT3G62400	1.35	0.43	2.65	0.034026	0.090904	-4.50

256432_at	hypothetical protein similar to hypot	---	AT3G10990	-1.20	-0.26	-2.65	0.034036	0.090904	-4.50
248310_at	putative protein similar to unknown	CPuORF14	AT5G52550	1.22	0.28	2.65	0.034037	0.090904	-4.50
247317_at	putative protein contains similarity t	anac103	AT5G64060	-1.26	-0.34	-2.65	0.034038	0.090904	-4.50
267393_at	similar to axi 1 protein from Nicotiar	---	AT2G44500	-1.48	-0.56	-2.65	0.034043	0.090905	-4.50
247723_at	protein phosphatase 2C - like ABA	---	AT5G59220	1.50	0.59	2.65	0.034072	0.09097	-4.50
252922_at	putative protein	---	AT4G39040	-1.23	-0.30	-2.65	0.034076	0.09097	-4.50
250520_at	putative protein contains similarity t	PEX1	AT5G08470	1.18	0.24	2.65	0.034079	0.09097	-4.50
253171_at	putative protein ;supported by full-l	---	AT4G35040	1.27	0.35	2.65	0.034107	0.09103	-4.51
252174_at	putative protein APRIL protein, Hor	---	AT3G50690	1.19	0.26	2.65	0.034109	0.09103	-4.51
250158_at	putative protein	---	AT5G15190	-1.45	-0.54	-2.65	0.034147	0.091101	-4.51
252458_at	putative protein various predicted p	---	AT3G47210	-1.22	-0.29	-2.65	0.034147	0.091101	-4.51
249830_at	dihydroorotate dehydrogenase prec	PYRD	AT5G23300	1.50	0.59	2.65	0.034148	0.091101	-4.51
260426_at	putative 40S ribosomal protein SA (	P40	AT1G72370	1.48	0.57	2.65	0.034152	0.091101	-4.51
248158_at	unknown protein	---	AT5G54440	-1.19	-0.25	-2.65	0.034156	0.091101	-4.51
265045_s_a	putative protein kinase, ADK1 dual	ADK1	AT1G03930	-1.50	-0.58	-2.65	0.034164	0.091113	-4.51
259482_at	receptor-like serine/threonine kinas	RKF2	AT1G19090	-1.25	-0.32	-2.65	0.03417	0.091113	-4.51
257644_at	unknown protein ;supported by full-	AOC3	AT3G25780	-2.34	-1.23	-2.65	0.034172	0.091113	-4.51
261310_at	hypothetical protein predicted by ge	PDE247	AT1G05750	1.31	0.39	2.65	0.034238	0.091273	-4.51
263430_at	unknown protein ;supported by full-	---	AT2G22270	-1.28	-0.36	-2.65	0.03424	0.091273	-4.51
259399_at	hypothetical protein similar to putati	---	AT1G17710	1.32	0.40	2.65	0.034296	0.091411	-4.51
257827_at	unknown protein contains Pfam pro	---	AT3G26630	1.43	0.52	2.65	0.0343	0.091411	-4.51
258012_at	unknown protein similar to GB:CAB	---	AT3G19310	-1.18	-0.24	-2.65	0.034329	0.091462	-4.51
249212_at	putative protein strong similarity to	---	AT5G42690	-1.25	-0.32	-2.65	0.03433	0.091462	-4.51
261271_at	Expressed protein ; supported by fu	---	AT1G26795	-1.26	-0.33	-2.65	0.034331	0.091462	-4.51
259377_at	putative poly(A) binding protein sim	PAB6	AT3G16380	-1.32	-0.40	-2.65	0.034343	0.091483	-4.51
256308_s_a	ABC transporter, putative contains	ATMRP13	AT1G30410	1.43	0.51	2.65	0.034349	0.091487	-4.51
264230_at	hypothetical protein predicted by ge	---	AT1G67460	-1.22	-0.29	-2.65	0.034363	0.091507	-4.51
264539_at	hypothetical protein predicted by ge	---	AT1G55590	-1.26	-0.33	-2.65	0.034364	0.091507	-4.51
257719_at	unknown protein	AtALMT9	AT3G18440	1.34	0.42	2.65	0.034385	0.091551	-4.51
266990_at	putative ABC transporter	ATATH8	AT2G39190	-1.51	-0.59	-2.65	0.034389	0.091551	-4.51
254963_at	putative protein single strand DNA-	MTSSB	AT4G11060	1.27	0.34	2.64	0.034466	0.091736	-4.52
251004_at	putative protein predicted protein, A	---	AT5G02720	-1.24	-0.31	-2.64	0.034466	0.091736	-4.52
254460_at	putative protein sigma70 operon, S	ATRP1	AT4G21210	-1.32	-0.40	-2.64	0.034474	0.091745	-4.52
266978_at	putative disease resistance respons	---	AT2G39430	-1.23	-0.30	-2.64	0.034478	0.091745	-4.52
249554_at	CRS2 -like protein CRS2, Zea may	---	AT5G38290	-1.68	-0.75	-2.64	0.034511	0.091823	-4.52

245540_at	ABC transporter like protein	PDR2	AT4G15230	-1.95	-0.96	-2.64	0.034525	0.091849	-4.52
258405_at	unknown protein almost identical to	BSH	AT3G17590	1.36	0.45	2.64	0.034553	0.091914	-4.52
254840_at	hypothetical protein	---	AT4G11930	-1.34	-0.42	-2.64	0.034561	0.091924	-4.52
267577_at	unknown protein ; supported by cD	---	AT2G30710	-1.18	-0.24	-2.64	0.034591	0.091994	-4.52
257537_at	hypothetical protein predicted by ge	---	AT3G22350	-1.32	-0.40	-2.64	0.034608	0.09201	-4.52
261042_at	GTP-binding protein, putative simil	ATRABA3	AT1G01200	-1.28	-0.35	-2.64	0.03461	0.09201	-4.52
258493_at	Expressed protein ; supported by fu	---	AT3G02555	1.25	0.32	2.64	0.03461	0.09201	-4.52
245357_at	putative protein ;supported by full-le	---	AT4G17560	-1.33	-0.41	-2.64	0.034615	0.09201	-4.52
258198_at	putative transcription factor similar t	NF-YA6	AT3G14020	1.27	0.34	2.64	0.034618	0.09201	-4.52
251886_at	putative protein various predicted p	---	AT3G54260	-1.42	-0.51	-2.64	0.034643	0.092066	-4.52
263218_at	putative serine/threonine protein ki	---	AT1G30570	-1.32	-0.40	-2.64	0.034668	0.092122	-4.52
251453_at	putative protein hypothetical protei	---	AT3G60070	-1.24	-0.32	-2.64	0.034681	0.092141	-4.52
265637_at	unknown protein	ATCOAE	AT2G27490	1.23	0.30	2.64	0.034683	0.092141	-4.52
250756_at	putative protein strong similarity to	ROPGEF5	AT5G05940	-1.24	-0.32	-2.64	0.034689	0.092146	-4.52
245516_at	hypothetical protein	---	AT4G15820	1.29	0.37	2.64	0.034726	0.092234	-4.52
257458_at	hypothetical protein predicted by ge	---	AT2G05400	-1.18	-0.24	-2.64	0.034756	0.092302	-4.52
258078_at	unknown protein ;supported by full-	---	AT3G25870	1.56	0.64	2.64	0.034774	0.092332	-4.53
250617_at	Mei2-like protein Mei2-like protein -	AML4	AT5G07290	1.28	0.35	2.64	0.034775	0.092332	-4.53
264640_at	pollen allergen, putative similar to p	ATEXPB2	AT1G65680	-1.39	-0.47	-2.64	0.034788	0.092335	-4.53
267213_at	60S ribosomal protein L7 ;supporte	---	AT2G44120	1.51	0.59	2.64	0.034792	0.092335	-4.53
250828_at	unknown protein ; supported by cDI	---	AT5G05250	-3.13	-1.65	-2.64	0.034794	0.092335	-4.53
257150_at	unknown protein ;supported by full-	---	AT3G27230	-1.30	-0.38	-2.64	0.034795	0.092335	-4.53
249220_at	putative protein strong similarity to	---	AT5G42420	-1.27	-0.35	-2.64	0.034797	0.092335	-4.53
258902_at	putative pyruvate dehydrogenase k	PDK	AT3G06483	-1.20	-0.26	-2.64	0.034827	0.092404	-4.53
250887_at	putative protein	---	---	1.26	0.33	2.64	0.034842	0.092434	-4.53
255832_at	hypothetical protein predicted by ge	---	AT2G33360	1.34	0.42	2.64	0.034848	0.09244	-4.53
246745_at	60S ribosomal protein L22 - like rib	---	AT5G27770	1.46	0.54	2.64	0.034869	0.092479	-4.53
256520_at	hypothetical protein	CYP96A14	AT1G66030	-1.22	-0.29	-2.64	0.034871	0.092479	-4.53
247288_at	non-phototropic hypocotyl 3 (gb|AA	NPH3	AT5G64330	-1.96	-0.97	-2.64	0.034881	0.092495	-4.53
245397_at	auxin-responsive protein IAA1 ;sup	IAA1	AT4G14560	-1.81	-0.86	-2.63	0.034891	0.092508	-4.53
257067_at	unknown protein contains Pfam pro	CYP77A5P	AT3G18270	1.27	0.34	2.63	0.034896	0.092508	-4.53
264664_at	putative elongation factor similar to	---	AT1G09660	1.37	0.46	2.63	0.034899	0.092508	-4.53
246574_at	copper amine oxidase, putative sim	---	AT1G31670	-1.49	-0.58	-2.63	0.034914	0.092539	-4.53
247334_at	cdc2-like protein kinase-like protein	CDKE;1	AT5G63610	-1.18	-0.23	-2.63	0.034949	0.092621	-4.53
258383_at	hypothetical protein predicted by ge	---	AT3G15440	1.60	0.68	2.63	0.034961	0.092635	-4.53

260549_at	Expressed protein ; supported by fu	---	AT2G43535	-1.90	-0.92	-2.63	0.034962	0.092635	-4.53
264638_at	flowering signals mediating protein	FT	AT1G65480	1.79	0.84	2.63	0.034969	0.092642	-4.53
265708_at	unknown protein member of a large	---	AT2G03380	1.22	0.28	2.63	0.034989	0.092685	-4.53
248644_at	disease resistance protein-like	---	AT5G49140	-1.18	-0.24	-2.63	0.034997	0.092693	-4.53
253635_at	putative protein hypothetical protei	---	AT4G30620	1.20	0.27	2.63	0.035031	0.092772	-4.53
247553_at	MAD box containing protein NAP1-	AGL8	AT5G60910	1.50	0.59	2.63	0.035038	0.092774	-4.53
253102_at	Expressed protein ; supported by fu	---	AT4G36105	-1.35	-0.43	-2.63	0.035039	0.092774	-4.53
247507_at	putative protein predicted protein, A	APO3	AT5G61930	1.52	0.60	2.63	0.03505	0.092791	-4.53
262273_at	hypothetical protein predicted by ge	---	AT1G68730	-1.20	-0.27	-2.63	0.03506	0.092805	-4.53
245880_at	putative hydrolase EtbD1 - Rhodoc	---	AT5G09430	-1.31	-0.39	-2.63	0.035063	0.092805	-4.53
258933_at	unknown protein similar to unknow	---	AT3G09980	-1.24	-0.31	-2.63	0.03509	0.09286	-4.53
254537_at	putative protein chitinase / lysozym	---	AT4G19730	-1.25	-0.32	-2.63	0.035092	0.09286	-4.53
265577_at	unknown protein	---	AT2G20100	1.21	0.28	2.63	0.035097	0.092861	-4.54
260247_at	putative disease resistance protein	AtRLP16	AT1G74200	-1.19	-0.26	-2.63	0.035106	0.092874	-4.54
255303_at	predicted protein of unknown functi	DER2.2	AT4G04860	1.24	0.31	2.63	0.03512	0.092897	-4.54
247762_at	cell wall protein	---	AT5G59170	-1.64	-0.71	-2.63	0.035122	0.092897	-4.54
259003_at	hypothetical protein similar to hypo	---	AT3G02010	1.37	0.46	2.63	0.035131	0.092909	-4.54
267434_at	3-beta-hydroxysteroid dehydrogena	AT3BETAH	AT2G26260	-1.28	-0.35	-2.63	0.035141	0.092923	-4.54
261541_at	unknown protein contains Pfam pro	---	AT1G63600	-1.25	-0.32	-2.63	0.035169	0.092989	-4.54
251712_at	putative protein non-consensus TT	---	AT3G56120	1.19	0.25	2.63	0.035176	0.092996	-4.54
245216_at	Expressed protein non-consensus (	IMPA-2	AT4G16143	-1.17	-0.23	-2.63	0.03521	0.093055	-4.54
250309_at	putative protein similar to unknown	---	AT5G12220	1.33	0.41	2.63	0.035211	0.093055	-4.54
247253_at	beta-1,3-glucanase	---	AT5G64790	1.86	0.90	2.63	0.035211	0.093055	-4.54
245778_at	RNA-binding glycine-rich protein, p	---	AT1G73530	-1.36	-0.44	-2.63	0.035257	0.093165	-4.54
263400_s_a	40S ribosomal protein; contains C-t	---	AT2G31610	1.28	0.36	2.63	0.035271	0.093191	-4.54
252383_at	ABC-type transport protein-like pro	ATH6	AT3G47780	1.81	0.85	2.63	0.035275	0.093191	-4.54
264160_at	hypothetical protein predicted by ge	---	AT1G65450	-1.28	-0.36	-2.63	0.03529	0.093209	-4.54
263797_at	putative WRKY-type DNA binding p	WRKY17	AT2G24570	2.09	1.06	2.63	0.03529	0.093209	-4.54
262778_at	hypothetical protein predicted by ge	---	AT1G13050	1.19	0.25	2.63	0.035294	0.093209	-4.54
253852_at	putative protein diacylglycerol kina	---	AT4G28130	-1.21	-0.27	-2.63	0.035315	0.093255	-4.54
257083_s_a	non-race specific disease resistanc	---	AT3G20590	1.47	0.56	2.63	0.035322	0.093264	-4.54
253995_at	Col-0 casein kinase I-like protein ;	CK1	AT4G26100	-1.32	-0.40	-2.63	0.035343	0.093281	-4.54
263882_at	putative ribonucleoside-diphosphat	RNR1	AT2G21790	1.65	0.72	2.63	0.035344	0.093281	-4.54
261484_at	E2, ubiquitin-conjugating enzyme 1	UBC1	AT1G14400	1.21	0.28	2.63	0.035344	0.093281	-4.54
266546_at	putative AT-hook DNA-binding prot	---	AT2G35270	-1.20	-0.26	-2.63	0.035346	0.093281	-4.54

259486_at	embryo abundance protein (EMB2(	---	AT1G15710	-1.27	-0.34	-2.63	0.035351	0.093285	-4.54
261372_at	zinc finger protein, putative similar	---	AT1G53010	-1.27	-0.35	-2.62	0.035393	0.093386	-4.54
262840_at	linker histone protein, putative cont	HMGA	AT1G14900	1.26	0.34	2.62	0.035405	0.093406	-4.54
267568_at	hypothetical protein predicted by ge	---	AT2G30780	1.25	0.32	2.62	0.035425	0.093449	-4.54
252449_at	FtsH protease, putative contains si	ftsh7	AT3G47060	1.18	0.24	2.62	0.035439	0.093474	-4.55
261162_at	hypothetical protein predicted by ge	---	AT1G34440	-1.28	-0.35	-2.62	0.035443	0.093474	-4.55
255042_at	putative protein hypothetical protei	---	AT4G09630	-1.23	-0.30	-2.62	0.03547	0.093533	-4.55
267598_at	hypothetical protein predicted by ge	---	AT2G33010	-1.29	-0.36	-2.62	0.035492	0.093573	-4.55
249505_at	putative protein	---	---	-1.53	-0.61	-2.62	0.035493	0.093573	-4.55
262306_s_a	asparaginyl-tRNA synthetase(SYN	SYNC3	AT1G70980	1.31	0.38	2.62	0.035523	0.093632	-4.55
245324_at	lactate dehydrogenase (LDH1) ;sup	---	AT4G17260	-1.66	-0.73	-2.62	0.035524	0.093632	-4.55
261589_at	hypothetical protein predicted by ge	---	AT1G01690	-1.29	-0.37	-2.62	0.035535	0.093646	-4.55
265479_at	hypothetical protein ;supported by	---	AT2G15760	2.60	1.38	2.62	0.035537	0.093646	-4.55
253564_at	protein kinase - like protein protein	---	AT4G31170	-1.25	-0.32	-2.62	0.035553	0.093675	-4.55
245350_at	nuclear antigen homolog ;supporte	---	AT4G16830	1.27	0.34	2.62	0.035556	0.093675	-4.55
249951_at	S-adenosyl-L-methionine decarbox	BUD2	AT5G18930	-1.39	-0.48	-2.62	0.035619	0.093829	-4.55
261816_at	unknown protein	CHX6B	AT1G08135	-1.22	-0.29	-2.62	0.035625	0.093831	-4.55
266638_at	putative fibrillin ;supported by full-le	---	AT2G35490	-1.25	-0.32	-2.62	0.035628	0.093831	-4.55
263092_at	hypothetical protein predicted by ge	---	AT2G16210	-1.20	-0.26	-2.62	0.035649	0.093858	-4.55
253673_at	putative protein putative phosphata	---	AT4G29530	-1.26	-0.33	-2.62	0.035649	0.093858	-4.55
253560_at	putative protein KIAA0800 protein,	DCAF1	AT4G31160	1.25	0.32	2.62	0.03565	0.093858	-4.55
265952_at	unknown protein supported by cDN	---	AT2G37478	1.23	0.30	2.62	0.035659	0.093869	-4.55
262121_at	endo-1,4-beta-glucanase precurso	ATCEL2	AT1G02800	-1.29	-0.36	-2.62	0.035676	0.093903	-4.55
248691_at	putative protein strong similarity to	---	AT5G48310	-1.22	-0.29	-2.62	0.035698	0.093951	-4.55
252086_at	hypothetical protein	---	AT3G52030	1.24	0.31	2.62	0.035717	0.09399	-4.55
250845_at	rna binding protein - like rna bindin	---	AT5G04600	1.36	0.45	2.62	0.035757	0.094085	-4.55
245138_at	unknown protein predicted by gens	AFO	AT2G45190	-1.42	-0.50	-2.62	0.03582	0.094238	-4.56
266081_at	putative protein kinase contains a p	---	AT2G37840	-1.22	-0.28	-2.62	0.035827	0.094248	-4.56
250701_at	bZIP transcription factor-like protein	---	AT5G06839	-1.26	-0.33	-2.62	0.035837	0.094263	-4.56
256169_at	receptor protein kinase, putative co	---	AT1G51800	2.52	1.33	2.62	0.035843	0.094266	-4.56
265304_at	putative AP2 domain transcription f	---	AT2G20350	-1.19	-0.25	-2.62	0.035896	0.094386	-4.56
267508_at	hypothetical protein predicted by ge	---	AT2G45700	1.22	0.29	2.62	0.035896	0.094386	-4.56
262914_at	auxin response factor 1 identical to	ARF1	AT1G59750	-1.25	-0.32	-2.61	0.03593	0.094453	-4.56
247437_at	AtHVA22b-like protein ; supported	HVA22B	AT5G62490	-1.29	-0.36	-2.61	0.035933	0.094453	-4.56
250885_at	ABC transporter -like protein ABC-	ATH12	AT5G03910	-1.21	-0.28	-2.61	0.035934	0.094453	-4.56

260033_at	putative mutT protein contains Pfa	ATNUDX1	AT1G68760	-1.27	-0.35	-2.61	0.035947	0.094466	-4.56
262883_at	ammonium transporter, puitative si	ATAMT1;2	AT1G64780	-1.44	-0.52	-2.61	0.035947	0.094466	-4.56
253759_at	AIM1 protein ; supported by cDNA:	AIM1	AT4G29010	1.19	0.25	2.61	0.035986	0.094557	-4.56
263742_at	predicted protein	---	AT2G20625	-1.20	-0.27	-2.61	0.035993	0.094564	-4.56
266600_at	putative mitogen-activated protein k	MPK12	AT2G46070	1.41	0.50	2.61	0.036018	0.094618	-4.56
260389_at	Expressed protein ; supported by fu	---	AT1G74055	-1.37	-0.45	-2.61	0.036031	0.094641	-4.56
261051_at	cytochrome P450, putative similar	CYP703A2	AT1G01280	-1.22	-0.28	-2.61	0.036036	0.094645	-4.56
256518_at	hypothetical protein	---	AT1G66080	-1.28	-0.36	-2.61	0.036044	0.094647	-4.56
261958_at	peptide transporter, putative predic	---	AT1G64500	1.53	0.61	2.61	0.036046	0.094647	-4.56
246425_at	cellulose synthase catalytic subunit	IRX3	AT5G17420	-1.60	-0.68	-2.61	0.036057	0.094666	-4.56
262516_at	putative glutathione transferase On	ATGSTU26	AT1G17190	-1.24	-0.32	-2.61	0.036064	0.094668	-4.56
247890_at	cyclic nucleotide and calmodulin-re	ATCNGC5	AT5G57940	-1.28	-0.35	-2.61	0.036067	0.094668	-4.56
255051_at	RNA-directed DNA polymerase -lik	---	---	-1.39	-0.47	-2.61	0.03607	0.094668	-4.56
262227_s_a	26S proteasome ATPase subunit,	---	AT1G53750	1.20	0.26	2.61	0.036079	0.094679	-4.56
250101_at	putative protein contains similarity t	BGLU2	AT5G16580	-1.47	-0.56	-2.61	0.036089	0.094695	-4.56
258972_at	hypothetical protein predicted by ge	---	AT3G01920	-1.40	-0.48	-2.61	0.036094	0.094697	-4.56
264354_s_a	unknown protein similar to Lambda-	---	AT1G03200	1.24	0.31	2.61	0.03616	0.09486	-4.57
256533_at	unknown protein	---	AT1G33250	-1.34	-0.42	-2.61	0.03619	0.094927	-4.57
247191_at	homeobox-leucine zipper protein A	ATHB5	AT5G65310	-1.44	-0.52	-2.61	0.036212	0.094976	-4.57
260106_at	unknown protein ;supported by full-	---	AT1G35420	-1.24	-0.31	-2.61	0.036229	0.095008	-4.57
260988_at	MAP3K alpha protein kinase, putat	MAP3KA	AT1G53570	-1.38	-0.46	-2.61	0.036254	0.095055	-4.57
246005_at	lipoic acid synthase - like protein lip	---	AT5G08415	1.35	0.43	2.61	0.036255	0.095055	-4.57
259039_at	unknown protein ;supported by full-	---	AT3G09250	1.22	0.29	2.61	0.03626	0.095056	-4.57
255291_at	putative calcium dependent protein	CPK27	AT4G04700	-1.26	-0.33	-2.61	0.036281	0.095101	-4.57
261987_at	hypothetical protein predicted by ge	---	AT1G33710	-1.17	-0.23	-2.61	0.036298	0.095135	-4.57
257600_at	hypothetical protein predicted by ge	CLE41	AT3G24770	-1.29	-0.37	-2.61	0.036319	0.095178	-4.57
256909_at	hypothetical protein predicted by ge	---	AT3G24060	-1.28	-0.36	-2.61	0.036324	0.095181	-4.57
266340_at	similar to axi 1 protein from Nicotiar	---	AT2G01480	1.18	0.24	2.61	0.036334	0.095195	-4.57
246018_at	Expressed protein ; supported by fu	---	AT5G10695	-1.95	-0.96	-2.61	0.03634	0.095201	-4.57
258125_s_a	hypothetical protein contains Pfam	---	AT3G23510	-1.71	-0.78	-2.61	0.036373	0.095276	-4.57
250683_x_a	putative protein similar to unknown	---	AT5G06640	-1.37	-0.45	-2.61	0.036381	0.095286	-4.57
253845_at	putative protein myosin heavy chai	---	AT4G27980	-1.17	-0.23	-2.60	0.03642	0.095379	-4.57
260970_at	unknown protein	---	AT1G53640	-1.27	-0.34	-2.60	0.036426	0.095381	-4.57
267504_at	unknown protein ;supported by full-	---	AT2G45530	1.29	0.37	2.60	0.036457	0.095453	-4.57
265989_at	unknown protein	---	AT2G24260	1.21	0.28	2.60	0.036467	0.095469	-4.57

257484_at	unknown protein	---	AT1G01650	-1.20	-0.27	-2.60	0.036491	0.095521	-4.58
261224_at	subtilisin-like serine protease simila	ATSBT5.2	AT1G20160	-1.74	-0.80	-2.60	0.036505	0.095544	-4.58
264737_at	unknown protein	---	AT1G62210	-1.33	-0.42	-2.60	0.036538	0.095622	-4.58
257221_at	MYB family transcription factor (GL	ATMYB0	AT3G27920	-1.31	-0.39	-2.60	0.036547	0.095633	-4.58
254693_at	bHLH protein - like bHLH protein, A	---	AT4G17880	1.91	0.94	2.60	0.036585	0.095713	-4.58
266799_at	unknown protein	ATPSK2	AT2G22860	-1.50	-0.59	-2.60	0.036586	0.095713	-4.58
248501_at	golgi SNARE protein	MEMB12	AT5G50440	-1.28	-0.36	-2.60	0.036596	0.095729	-4.58
249176_at	thioredoxin (clone GIF1) (pir||S581	ATTRX3	AT5G42980	1.19	0.25	2.60	0.036608	0.095749	-4.58
250359_at	putative protein predicted proteins,	---	AT5G11350	1.21	0.28	2.60	0.036619	0.095757	-4.58
266047_at	unknown protein	---	AT2G40800	-1.29	-0.37	-2.60	0.036619	0.095757	-4.58
260730_at	lipoamide dehydrogenase precurso	mtLPD1	AT1G48030	-1.33	-0.41	-2.60	0.036645	0.095807	-4.58
250159_at	40S ribosomal protein - like 40S rib	---	AT5G15200	1.37	0.46	2.60	0.036647	0.095807	-4.58
248110_at	wax synthase-like protein	---	AT5G55320	-1.18	-0.24	-2.60	0.036654	0.095816	-4.58
267193_at	hypothetical protein predicted by gr	---	AT2G30900	-1.23	-0.29	-2.60	0.036673	0.095853	-4.58
248499_at	putative protein contains similarity t	PAP27	AT5G50400	1.19	0.25	2.60	0.036711	0.095935	-4.58
258786_at	putative syntaxin contains Pfam pro	SYP121	AT3G11820	-1.60	-0.67	-2.60	0.036713	0.095935	-4.58
248613_at	phytoene dehydrogenase-like	---	AT5G49555	-1.34	-0.42	-2.60	0.036721	0.095946	-4.58
258521_at	ribosomal protein L29, putative sim	---	AT3G06680	1.68	0.75	2.60	0.03674	0.095983	-4.58
259725_at	Expressed protein ; supported by fu	---	AT1G61065	1.39	0.48	2.60	0.036754	0.096002	-4.58
255518_at	putative pectinesterase similar to se	---	AT4G02300	-1.24	-0.32	-2.60	0.036755	0.096002	-4.58
253326_at	putative protein polygalacturonase	---	AT4G33440	-1.24	-0.31	-2.60	0.036784	0.096056	-4.58
257602_at	hydrolase, putative similar to Metal	---	AT3G13800	-1.23	-0.29	-2.60	0.036785	0.096056	-4.58
248361_at	putative protein similar to unknown	EDA41	AT5G52460	-1.25	-0.33	-2.60	0.036789	0.096056	-4.58
254486_at	putative protein crp1 protein, Zea m	---	AT4G20770	1.26	0.33	2.60	0.036819	0.096125	-4.58
263769_at	5S ribosomal RNA	---	---	-1.27	-0.34	-2.60	0.036824	0.096127	-4.58
264550_at	hypothetical protein predicted by ge	---	AT1G09450	-1.40	-0.49	-2.60	0.036841	0.09616	-4.59
245907_at	ubiquitin-like protein ubiquitins - diff	---	AT5G09340	1.18	0.24	2.60	0.036848	0.096167	-4.59
258318_at	unknown protein	---	AT3G22680	1.44	0.52	2.60	0.036867	0.096206	-4.59
253239_at	putative serine/threonine protein ki	---	AT4G34500	-1.39	-0.47	-2.60	0.036872	0.096207	-4.59
246901_at	putative protein Leaf protein, Phar	---	AT5G25630	1.22	0.28	2.60	0.036881	0.096221	-4.59
266854_at	putative C2H2-type zinc finger prote	---	AT2G26940	-1.31	-0.39	-2.60	0.036898	0.096254	-4.59
259090_at	putative ribosomal protein s19 or s2	---	AT3G04920	1.43	0.52	2.60	0.036914	0.096283	-4.59
260252_at	putative mitochondrial carrier protei	---	AT1G74240	1.34	0.42	2.60	0.036921	0.096283	-4.59
259331_at	putative auxin-induced protein simil	---	AT3G03840	-1.32	-0.40	-2.60	0.036922	0.096283	-4.59
258894_at	putative disease resistance protein	AtRLP32	AT3G05650	-1.62	-0.69	-2.59	0.036959	0.096369	-4.59

247232_at	ABC transporter-like	ATH13	AT5G64940	-1.31	-0.39	-2.59	0.036985	0.096426	-4.59
252491_at	disease resistance protein RPP8-li	---	AT3G46730	1.18	0.24	2.59	0.037005	0.096466	-4.59
248939_at	tyrosine-specific protein phosphatas	---	AT5G45790	1.24	0.31	2.59	0.03702	0.096495	-4.59
261390_at	hypothetical protein similar to hypot	---	AT1G35040	-1.20	-0.26	-2.59	0.03709	0.096665	-4.59
261612_at	fucosyltransferase c3 protein, puta	FUT12	AT1G49710	1.21	0.28	2.59	0.03716	0.096839	-4.59
250850_at	putative protein ; supported by cDN	---	AT5G04550	-1.29	-0.37	-2.59	0.037172	0.096859	-4.59
263440_at	unknown protein predicted by gens	ATEXO70H	AT2G28640	-1.17	-0.23	-2.59	0.037181	0.096865	-4.59
247652_at	histone H2B - like protein histone H	HTB4	AT5G59910	1.29	0.37	2.59	0.037185	0.096865	-4.59
259774_at	plasma membrane associated prot	---	AT1G29520	-1.36	-0.44	-2.59	0.037187	0.096865	-4.59
247068_at	putative protein similar to unknown	---	AT5G66800	-1.27	-0.34	-2.59	0.037217	0.096919	-4.60
250263_at	putative protein	---	AT5G13470	1.28	0.36	2.59	0.037219	0.096919	-4.60
267470_at	cinnamate-4-hydroxylase molecular	C4H	AT2G30490	1.79	0.84	2.59	0.037221	0.096919	-4.60
261681_at	hypothetical protein similar to hypot	---	AT1G47340	1.40	0.48	2.59	0.037238	0.096951	-4.60
251798_at	putative RNA binding protein Serin	SCL30	AT3G55460	1.22	0.29	2.59	0.037242	0.096952	-4.60
265531_at	hypothetical protein predicted by ge	AtGRF6	AT2G06200	-1.23	-0.30	-2.59	0.037267	0.097005	-4.60
251638_at	40S ribosomal protein S2 homolog	---	AT3G57490	1.52	0.60	2.59	0.037276	0.097011	-4.60
257081_at	RING zinc finger protein contains R	---	AT3G30460	-1.21	-0.28	-2.59	0.037278	0.097011	-4.60
262095_at	hypothetical protein predicted by ge	---	AT1G56090	1.32	0.40	2.59	0.037285	0.097016	-4.60
259283_at	putative transcription factor similar t	MYB65	AT3G11440	-1.24	-0.31	-2.59	0.037288	0.097016	-4.60
248223_at	unknown protein ; supported by cD	---	AT5G53620	1.17	0.23	2.59	0.037304	0.097045	-4.60
263519_at	40S ribosomal protein S25 ; suppo	---	AT2G21580	1.49	0.58	2.59	0.03731	0.097045	-4.60
253647_at	putative protein KIAA0210 gene, H	---	AT4G29950	-1.28	-0.35	-2.59	0.037312	0.097045	-4.60
251056_at	putative protein KIAA1303 protein	RAPTOR2	AT5G01770	1.30	0.38	2.59	0.037353	0.09714	-4.60
266748_at	putative squamosa-promoter bindin	SPL1	AT2G47070	-1.40	-0.48	-2.59	0.037391	0.097228	-4.60
266488_at	putative pectinesterase ; supported	---	AT2G47670	1.38	0.47	2.59	0.037397	0.097234	-4.60
253321_at	putative protein prolyl 4-hydroxylas	---	AT4G33910	1.21	0.28	2.59	0.037412	0.097261	-4.60
246003_at	chloroplast Cpn21 protein ; suppor	CPN20	AT5G20720	1.26	0.33	2.59	0.037445	0.097336	-4.60
262866_at	cytochrome p450, putative similar t	CYP89A6	AT1G64940	-1.19	-0.25	-2.59	0.037461	0.097365	-4.60
255419_at	putative receptor kinase	---	AT4G03230	-1.25	-0.32	-2.58	0.037468	0.097373	-4.60
251586_at	zinc finger-like protein several zinc	GIS	AT3G58070	-1.31	-0.39	-2.58	0.037513	0.097479	-4.60
249596_s_a	glucuronosyl transferase-like prote	---	AT5G37950	-1.39	-0.48	-2.58	0.037518	0.097482	-4.60
266607_at	hypothetical protein predicted by ge	---	AT2G46300	-1.26	-0.33	-2.58	0.037527	0.097494	-4.60
255387_at	putative nodulin similar to M. trunca	---	AT4G03630	-1.30	-0.38	-2.58	0.037536	0.097496	-4.60
252206_at	centrin	ATCEN2	AT3G50360	-1.24	-0.31	-2.58	0.037537	0.097496	-4.60
251396_at	transketolase - like protein transke	---	AT3G60750	1.21	0.28	2.58	0.03759	0.097613	-4.61

255861_at	putative vacuolar sorting receptor	---	AT2G30290	-1.19	-0.25	-2.58	0.03759	0.097613	-4.61
260189_at	putative urease similar to urease G	URE	AT1G67550	1.27	0.35	2.58	0.037601	0.097631	-4.61
262695_at	vacuolor sorting protein 35, putativ	VPS35B	AT1G75850	1.21	0.27	2.58	0.037613	0.097645	-4.61
257994_at	unknown protein	---	AT3G19920	1.34	0.43	2.58	0.037615	0.097645	-4.61
257651_at	polygalacturonase, putative similar	---	AT3G16850	-1.51	-0.60	-2.58	0.037679	0.097786	-4.61
263659_at	unknown protein EST gb|ATTS567	---	AT1G04470	-1.23	-0.30	-2.58	0.037683	0.097786	-4.61
260410_at	putative peptide transporter similar	---	AT1G69870	-1.51	-0.59	-2.58	0.037684	0.097786	-4.61
264540_at	hypothetical protein predicted by ge	---	AT1G55630	1.24	0.31	2.58	0.037687	0.097786	-4.61
264728_at	unknown protein location of EST gb	---	AT1G22850	-1.28	-0.35	-2.58	0.037709	0.097832	-4.61
248730_at	putative protein similar to unknown	---	AT5G48050	-1.30	-0.38	-2.58	0.037722	0.097854	-4.61
252097_at	putative protein hypothetical protein	---	AT3G51090	1.20	0.27	2.58	0.037747	0.097909	-4.61
256590_at	recombination signal sequence rec	ATHMG	AT3G28730	1.31	0.39	2.58	0.037768	0.097951	-4.61
262742_at	GTP-binding protein, putative simil	AtRABA1i	AT1G28550	-1.21	-0.28	-2.58	0.037824	0.098086	-4.61
267054_at	hypothetical protein	---	AT2G38370	1.40	0.49	2.58	0.037858	0.098164	-4.61
266448_s_a	unknown protein ;supported by full	---	AT2G43210	-1.22	-0.28	-2.58	0.037876	0.098199	-4.61
266679_at	putative helicase ; supported by cD	---	AT2G03270	1.25	0.32	2.58	0.037883	0.098205	-4.61
251944_at	ABC transporter -like protein breas	---	AT3G53510	-1.32	-0.40	-2.58	0.037898	0.098234	-4.61
257655_at	unknown protein contains Pfam pr	---	AT3G13350	1.53	0.62	2.58	0.037902	0.098234	-4.61
265705_at	unknown protein related to MO25 (r	---	AT2G03410	1.75	0.80	2.58	0.037915	0.098255	-4.61
248312_at	unknown protein	---	AT5G52580	-1.25	-0.33	-2.58	0.037938	0.098304	-4.62
258829_at	putative Sec24-like COPII protein s	---	AT3G07100	1.17	0.23	2.58	0.037982	0.098391	-4.62
245824_at	hypothetical protein predicted by ge	ATPUP17	AT1G57943	-1.37	-0.45	-2.58	0.037988	0.098391	-4.62
257524_at	hypothetical protein similar to putati	DEL3	AT3G01330	-1.25	-0.33	-2.58	0.037989	0.098391	-4.62
249969_at	putative protein glycine-rich protein	---	AT5G19090	-1.47	-0.55	-2.58	0.037989	0.098391	-4.62
261760_at	hypothetical protein similar to putati	---	AT1G15600	-1.33	-0.41	-2.58	0.037993	0.098391	-4.62
259760_at	hypothetical protein similar to GB:A	---	AT1G77580	-1.18	-0.24	-2.57	0.038022	0.098447	-4.62
267594_at	hypothetical protein predicted by ge	---	AT2G33000	-1.21	-0.28	-2.57	0.038024	0.098447	-4.62
266772_s_a	predicted by genefinder	---	AT2G03020	-1.38	-0.47	-2.57	0.038028	0.098447	-4.62
252934_at	Inositol monophosphatase - like pr	IMPL2	AT4G39120	1.31	0.39	2.57	0.038039	0.098453	-4.62
245578_at	RNA helicase like protein	ATSUV3	AT4G14790	1.29	0.36	2.57	0.038039	0.098453	-4.62
257270_at	unknown protein ; supported by ful	---	AT3G28140	1.19	0.25	2.57	0.038044	0.098454	-4.62
248148_at	putative protein similar to unknown	---	AT5G54930	1.39	0.47	2.57	0.038052	0.098464	-4.62
250774_at	ATP-dependent RNA helicase-like	---	AT5G05450	-1.33	-0.41	-2.57	0.038069	0.098498	-4.62
246151_at	putative protein predicted proteins f	---	AT5G19950	1.26	0.33	2.57	0.038074	0.0985	-4.62
262820_at	putative obtusifoliol 14-alpha deme	CYP51G1	AT1G11680	1.22	0.29	2.57	0.038078	0.0985	-4.62

246522_at	bZIP DNA-binding protein-like puta	AtbZIP3	AT5G15830	1.71	0.78	2.57	0.038102	0.098545	-4.62
247730_at	glucuronosyl transferase - like prot	UGT76E1	AT5G59580	-1.41	-0.50	-2.57	0.038105	0.098545	-4.62
262673_at	unknown protein	EMB1793	AT1G76060	1.23	0.30	2.57	0.038111	0.098551	-4.62
266982_at	unknown protein ; supported by cD	---	AT2G39500	1.30	0.38	2.57	0.038136	0.098603	-4.62
250412_at	putative protein synaptobrevin-like	ATVAMP71	AT5G11150	1.30	0.38	2.57	0.038158	0.098641	-4.62
246026_at	putative protein predicted protein - (	---	AT5G21070	-1.22	-0.29	-2.57	0.038159	0.098641	-4.62
262880_at	hypothetical protein contains simila	---	AT1G64880	1.68	0.75	2.57	0.038169	0.098654	-4.62
262867_at	hypothetical protein predicted by ge	---	AT1G64960	1.24	0.31	2.57	0.038196	0.09871	-4.62
258145_at	integral membrane protein, putative	---	AT3G18200	-1.28	-0.35	-2.57	0.038199	0.09871	-4.62
253494_at	putative protein	---	AT4G31830	-1.23	-0.30	-2.57	0.03822	0.098751	-4.62
254894_at	putative phospholipase D-gamma	PLDGAMM	AT4G11840	1.36	0.45	2.57	0.038223	0.098751	-4.62
248957_at	26S proteasome subunit-like protei	---	AT5G45620	-1.22	-0.29	-2.57	0.038228	0.098751	-4.62
259496_at	hypothetical protein predicted by ge	---	AT1G15900	-1.22	-0.29	-2.57	0.038234	0.098755	-4.62
261443_at	glutaredoxin, putative similar to glu	GRX480	AT1G28480	1.87	0.90	2.57	0.038263	0.098819	-4.62
247990_at	unknown protein ;supported by full-	---	AT5G56360	1.20	0.26	2.57	0.038277	0.098845	-4.62
265480_at	similar to cold acclimation protein W	COR413-P	AT2G15970	-1.42	-0.51	-2.57	0.038322	0.098949	-4.63
247534_at	pyrophosphate-dependent phosph	PFK4	AT5G61580	1.19	0.25	2.57	0.038336	0.098975	-4.63
256052_at	spliceosomal protein (U2B), putativ	---	AT1G06960	-1.24	-0.31	-2.57	0.03834	0.098975	-4.63
256910_at	hypothetical protein	---	AT3G24080	1.29	0.36	2.57	0.038345	0.098977	-4.63
253107_at	putative protein predicted proteins,	---	AT4G35880	-1.30	-0.38	-2.57	0.038363	0.09901	-4.63
248584_at	putative protein similar to unknown	---	AT5G49960	-1.38	-0.46	-2.57	0.038374	0.09902	-4.63
265467_at	putative receptor-like protein kinase	---	AT2G37050	-1.36	-0.44	-2.57	0.038378	0.09902	-4.63
249063_at	NBD-like protein (gb|AAD20643.1)	POP1	AT5G44110	-1.33	-0.41	-2.57	0.038379	0.09902	-4.63
260017_at	hypothetical protein predicted by ge	---	---	-1.40	-0.48	-2.57	0.038396	0.099048	-4.63
263583_at	putative NAD+ dependent isocitrat	IDH2	AT2G17130	1.36	0.45	2.57	0.038401	0.099048	-4.63
258866_at	unknown protein	---	AT3G03180	1.20	0.26	2.57	0.038403	0.099048	-4.63
249888_s_a	zinc finger protein-like ; supported	---	AT5G22480	1.23	0.30	2.57	0.038442	0.099135	-4.63
257236_at	hypothetical protein	---	AT3G15095	-1.30	-0.38	-2.57	0.038446	0.099135	-4.63
264505_at	putative nodulin protein, N21 Simila	---	AT1G09380	-1.36	-0.45	-2.57	0.038452	0.099141	-4.63
259450_at	hypothetical protein predicted by ge	DRL1	AT1G13870	-1.26	-0.33	-2.57	0.038465	0.099162	-4.63
246633_at	hypothetical protein ; supported by	---	AT1G29720	-1.84	-0.88	-2.57	0.038492	0.099219	-4.63
255570_at	putative carrier protein similar to mi	ADNT1	AT4G01100	1.24	0.31	2.57	0.038496	0.099219	-4.63
262922_at	hypothetical protein predicted by ge	---	AT1G79420	-1.31	-0.39	-2.57	0.038501	0.099221	-4.63
253819_at	receptor protein kinase like protein	---	AT4G28350	2.86	1.51	2.57	0.038534	0.099295	-4.63
252421_at	endochitinase-like protein BASIC E	---	AT3G47540	3.13	1.65	2.57	0.038548	0.099313	-4.63

254850_at	putative protein predicted proteins A	---	AT4G12000	-1.34	-0.42	-2.57	0.03855	0.099313	-4.63
246835_at	putative protein putative APC11 an	---	AT5G26640	-1.27	-0.35	-2.56	0.038557	0.099314	-4.63
260707_s_a	Expressed protein ; supported by fu	---	AT1G32410	-1.30	-0.38	-2.56	0.038559	0.099314	-4.63
253118_at	ras-related small GTP-binding prot	ARAC6	AT4G35950	-1.30	-0.38	-2.56	0.038563	0.099315	-4.63
250266_at	histone H3 -like protein histone H3	---	AT5G12910	-1.25	-0.32	-2.56	0.038577	0.099338	-4.63
248193_at	homogentisate 1,2-dioxygenase ;s	HGO	AT5G54080	1.48	0.56	2.56	0.03859	0.099356	-4.63
265916_at	hypothetical protein similar to En/Sp	---	---	-1.21	-0.28	-2.56	0.038592	0.099356	-4.63
264942_at	unknown protein ; supported by cDI	---	AT1G67340	1.32	0.40	2.56	0.038612	0.099396	-4.63
253584_at	putative protein several hypothetica	---	AT4G30700	1.22	0.29	2.56	0.038645	0.099468	-4.63
252909_at	putative protein	---	AT4G39680	1.20	0.26	2.56	0.038655	0.099483	-4.63
252785_at	putative protein AND-1 protein - Ho	---	AT3G42660	-1.46	-0.55	-2.56	0.038662	0.099491	-4.64
261672_at	unknown protein contains similarity	ATARP4	AT1G18450	1.32	0.40	2.56	0.038676	0.099498	-4.64
264845_at	putative thioredoxin-m similar to thi	ATHM1	AT1G03680	-1.25	-0.32	-2.56	0.038678	0.099498	-4.64
254475_at	putative snRNP protein small nucle	smB	AT4G20440	1.45	0.53	2.56	0.038682	0.099498	-4.64
249001_at	putative protein strong similarity to u	---	AT5G44990	1.95	0.96	2.56	0.038682	0.099498	-4.64
248831_at	putative protein contains similarity t	---	AT5G47160	1.25	0.32	2.56	0.038723	0.09959	-4.64
250247_at	unknown protein	---	AT5G13720	1.20	0.26	2.56	0.03876	0.099675	-4.64
255471_at	putative oxidoreductase similar to A	AOP3	AT4G03050	-1.23	-0.30	-2.56	0.038767	0.099682	-4.64
251341_at	ribosomal protein S13 -like AtRPS1	---	AT3G60770	1.50	0.58	2.56	0.038802	0.099762	-4.64
261094_at	hypothetical protein predicted by ge	---	AT1G62920	-1.35	-0.43	-2.56	0.038816	0.099786	-4.64
245825_at	protein kinase, putative similar to p	ATSK42	AT1G57870	-1.23	-0.30	-2.56	0.038838	0.099818	-4.64
262234_at	putative G protein coupled receptor	GCR1	AT1G48270	-1.34	-0.43	-2.56	0.038841	0.099818	-4.64
257276_at	disease resistance protein, putative	---	AT3G14460	-1.19	-0.25	-2.56	0.038842	0.099818	-4.64
258578_at	germin-like protein contains Pfam p	---	AT3G04200	-1.38	-0.47	-2.56	0.038853	0.099836	-4.64
248099_at	DNA topoisomerase I (sp P30181)	TOP1ALPH	AT5G55300	1.20	0.26	2.56	0.038876	0.099883	-4.64
264859_at	glucose-6-phosphate 1-dehydroge	G6PD3	AT1G24280	1.90	0.93	2.56	0.038888	0.099891	-4.64
253610_at	putative protein ; supported by cDN	VEL1	AT4G30200	1.27	0.34	2.56	0.038888	0.099891	-4.64
255478_at	putative protein ;supported by full-l	EID1	AT4G02440	-1.25	-0.32	-2.56	0.038894	0.099896	-4.64
248779_at	acetoacyl-CoA-thiolase ;supported	---	AT5G47720	1.43	0.51	2.56	0.038904	0.099901	-4.64
265103_at	UDP-N-acetylglucosamine pyrophc	---	AT1G31070	-1.29	-0.37	-2.56	0.038905	0.099901	-4.64
247474_at	putative protein predicted proteins,	---	AT5G62280	-3.49	-1.80	-2.56	0.038928	0.099948	-4.64
245156_at	calcium-dependent protein kinase-	CPK7	AT5G12480	1.23	0.30	2.56	0.038946	0.099976	-4.64
250684_at	zinc finger-like protein	GIS2	AT5G06650	-1.23	-0.30	-2.56	0.038947	0.099976	-4.64
258744_at	hypothetical protein similar to plant	---	AT3G05830	1.27	0.34	2.56	0.038972	0.100029	-4.64
254428_at	putative protein Human mRNA for	ZAC	AT4G21160	1.22	0.29	2.56	0.038991	0.100065	-4.64

266388_at	hypothetical protein predicted by ge	---	AT2G32340	1.27	0.35	2.56	0.039008	0.100097	-4.64
256199_at	unknown protein	SAB	AT1G58250	1.30	0.38	2.56	0.039025	0.10011	-4.64
245075_at	putative cytochrome P450	CYP96A1	AT2G23180	1.24	0.31	2.56	0.039028	0.10011	-4.64
257255_at	hypothetical protein contains Pfam	---	AT3G21960	-1.23	-0.30	-2.56	0.039029	0.10011	-4.64
260697_at	unknown protein	---	AT1G32530	1.37	0.45	2.56	0.03903	0.10011	-4.64
254547_at	putative protein	---	AT4G19860	1.37	0.46	2.56	0.039039	0.10012	-4.65
264557_at	putative pectinacetylesterase precu	---	AT1G09550	-1.34	-0.42	-2.56	0.039045	0.10012	-4.65
255781_at	unknown protein	---	AT1G19880	-1.20	-0.27	-2.56	0.039047	0.10012	-4.65
267273_at	putative non-LTR retroelement reve	---	AT2G02520	-1.18	-0.23	-2.56	0.039065	0.100155	-4.65
267590_at	putative expansin ;supported by ful	ATEXPA4	AT2G39700	-1.51	-0.59	-2.56	0.039074	0.100165	-4.65
258456_at	putative protein kinase similar to mi	WNK2	AT3G22420	1.74	0.80	2.55	0.03911	0.100247	-4.65
267564_at	putative protein kinase contains a p	---	AT2G30740	-1.26	-0.33	-2.55	0.039118	0.100257	-4.65
264238_at	hypothetical protein predicted by ge	---	AT1G54740	-1.60	-0.67	-2.55	0.039148	0.100322	-4.65
260064_at	ethylene-insensitive3-like3 (EIL3) i	EIL3	AT1G73730	1.31	0.39	2.55	0.039153	0.100323	-4.65
258670_at	unknown protein	---	AT3G08810	-1.28	-0.36	-2.55	0.039191	0.100393	-4.65
251910_at	serine/threonine-specific kinase lik	---	AT3G53810	2.16	1.11	2.55	0.039191	0.100393	-4.65
263061_at	putative AAA-type ATPase	---	AT2G18190	-1.25	-0.33	-2.55	0.039193	0.100393	-4.65
257789_at	unknown protein ;supported by full-	YSL6	AT3G27020	1.39	0.48	2.55	0.039208	0.100419	-4.65
256697_at	hypothetical protein contains simila	AtOCT4	AT3G20660	1.55	0.64	2.55	0.039212	0.100419	-4.65
263404_s_a	hypothetical protein similar to hypot	---	AT2G04090	1.95	0.97	2.55	0.039239	0.100476	-4.65
252751_at	putative protein RING-H2 zinc finge	---	AT3G43430	-1.54	-0.62	-2.55	0.039287	0.100588	-4.65
248802_at	Expressed protein ; supported by cl	---	AT5G47435	1.24	0.31	2.55	0.039317	0.100654	-4.65
261793_at	unknown protein ; supported by cDI	---	AT1G16080	-1.59	-0.67	-2.55	0.03933	0.100674	-4.65
254184_at	hypothetical protein	---	AT4G23970	-1.22	-0.29	-2.55	0.039343	0.100697	-4.65
260088_at	tonoplast intrinsic protein, alpha (al	TIP3;1	AT1G73190	-1.27	-0.34	-2.55	0.03936	0.100726	-4.65
247660_at	ankyrin-like protein ankyrin 3, Mus	---	AT5G60070	-1.20	-0.27	-2.55	0.039363	0.100726	-4.65
259351_at	putative sugar transporter similar to	---	AT3G05150	-1.22	-0.29	-2.55	0.039371	0.100734	-4.65
254126_at	RNA-binding protein RNP-T precurs	RBP31	AT4G24770	-1.24	-0.31	-2.55	0.03938	0.100746	-4.65
248529_at	protein kinase ;supported by full-len	---	AT5G50000	-1.35	-0.43	-2.55	0.039407	0.100804	-4.65
251805_at	putative protein RING-H2 finger pro	SDIR1	AT3G55530	1.21	0.27	2.55	0.039415	0.100814	-4.65
249036_at	nuclear cap-binding protein; CBP2(	CBP20	AT5G44200	1.26	0.34	2.55	0.039444	0.100877	-4.66
262209_at	hypothetical protein contains simila	---	AT1G74720	1.28	0.35	2.55	0.039454	0.100891	-4.66
266478_at	putative cysteinyl-tRNA synthetase	SYCO ARA	AT2G31170	-1.39	-0.47	-2.55	0.039461	0.100898	-4.66
258991_at	unknown protein contains Pfam pro	---	AT3G08820	1.23	0.30	2.55	0.039474	0.100919	-4.66
250291_at	aspartate kinase ;supported by full-	AK-LYS1	AT5G13280	1.37	0.45	2.55	0.039503	0.100983	-4.66

261835_at	hypothetical protein contains simila	---	AT1G16040	1.24	0.31	2.55	0.039514	0.100999	-4.66
249674_at	unknown protein	---	AT5G35930	1.19	0.25	2.55	0.039537	0.101047	-4.66
257263_at	unknown protein ;supported by full-	---	AT3G22070	-1.44	-0.52	-2.55	0.039547	0.101053	-4.66
255952_at	MADS-box protein (ZAP1), putative	AGL104	AT1G22130	1.18	0.24	2.55	0.039555	0.101053	-4.66
246051_at	epimerase/dehydratase - like prote	GME	AT5G28840	1.29	0.37	2.55	0.039557	0.101053	-4.66
262609_at	unknown protein ;supported by full-	---	AT1G13930	1.26	0.34	2.55	0.039558	0.101053	-4.66
266518_at	hypothetical protein predicted by ge	---	AT2G35170	-1.25	-0.32	-2.55	0.039562	0.101053	-4.66
265179_at	unknown protein predicted by gene	---	AT1G23650	-1.30	-0.38	-2.55	0.039577	0.101079	-4.66
255301_at	putative protein similar to transcript	ATMSRB3	AT4G04800	1.46	0.54	2.55	0.039588	0.101097	-4.66
246197_at	caltractin-like protein ;supported by	CEN2	AT4G37010	1.94	0.96	2.55	0.039603	0.101125	-4.66
248716_at	unknown protein ;supported by full-	---	AT5G48210	-1.29	-0.37	-2.55	0.039608	0.101125	-4.66
253928_at	phosphoprotein phosphatase (PPX-	PPX1	AT4G26720	1.23	0.29	2.55	0.039633	0.101177	-4.66
259405_at	Expressed protein ; supported by cl	---	AT1G17744	1.35	0.44	2.55	0.039645	0.101197	-4.66
257373_at	hypothetical protein predicted by ge	---	AT2G43140	1.30	0.38	2.55	0.039668	0.101246	-4.66
255013_at	putative protein ;supported by full-l	---	AT4G10000	1.26	0.34	2.54	0.039692	0.101296	-4.66
265010_at	T-complex chaperonin protein , eps	---	AT1G24510	1.36	0.44	2.54	0.039701	0.101307	-4.66
245439_at	hypothetical protein	---	AT4G16670	1.53	0.61	2.54	0.039726	0.10136	-4.66
257914_at	Expressed protein ; supported by cl	---	AT3G25545	1.28	0.35	2.54	0.039734	0.101367	-4.66
247285_at	putative protein similar to unknown	---	AT5G64400	1.20	0.27	2.54	0.039743	0.101379	-4.66
258607_at	thioredoxin f1 identical to thioredoxi	TRXF1	AT3G02730	-1.30	-0.38	-2.54	0.039794	0.101497	-4.66
259093_at	unknown protein similar to putative	---	AT3G04860	-1.49	-0.58	-2.54	0.03982	0.101543	-4.67
265312_at	unknown protein	---	AT2G20240	-1.52	-0.60	-2.54	0.039824	0.101543	-4.67
254222_at	hypothetical protein	---	AT4G23840	-1.25	-0.32	-2.54	0.039825	0.101543	-4.67
259415_at	hypothetical protein contains simila	---	AT1G02330	-1.30	-0.38	-2.54	0.039831	0.101547	-4.67
254683_at	hypothetical protein ;supported by	---	AT4G13800	-1.24	-0.31	-2.54	0.039887	0.101678	-4.67
247292_at	unknown protein	---	AT5G64490	1.25	0.32	2.54	0.039891	0.101679	-4.67
253125_at	DnaJ-like protein DnaJ-like protein	---	AT4G36040	1.30	0.38	2.54	0.039939	0.101789	-4.67
264593_at	putative GTP-binding protein ; supp	ARAC1	AT2G17800	-1.23	-0.30	-2.54	0.039974	0.101844	-4.67
258503_at	unknown protein	---	AT3G02500	-1.28	-0.36	-2.54	0.039974	0.101844	-4.67
245338_at	Expressed protein ; supported by fu	---	AT4G16442	-1.32	-0.40	-2.54	0.039981	0.101844	-4.67
263225_at	putative DNA-binding protein simila	WRKY14	AT1G30650	-1.25	-0.32	-2.54	0.039984	0.101844	-4.67
257274_at	geranylgeranyl pyrophosphate syn	---	AT3G14510	-1.25	-0.32	-2.54	0.039987	0.101844	-4.67
245272_at	hypothetical protein ; supported by	---	AT4G17250	1.51	0.59	2.54	0.039988	0.101844	-4.67
245736_at	Dr4(protease inhibitor) identical to D	ATDR4	AT1G73330	-1.60	-0.68	-2.54	0.04	0.101864	-4.67
248449_at	putative protein similar to unknown	---	AT5G51110	-1.19	-0.25	-2.54	0.040007	0.10187	-4.67

246345_at	calcium-dependent protein kinase-	---	AT3G56760	1.29	0.37	2.54	0.040027	0.101909	-4.67
246519_at	proline-rich protein other proline-ric	---	AT3G23750	-3.01	-1.59	-2.54	0.040031	0.101909	-4.67
260597_at	hypothetical protein predicted by ge	---	AT1G55915	1.36	0.44	2.54	0.040036	0.10191	-4.67
252059_at	E2, ubiquitin-conjugating enzyme,	UEV1D-4	AT3G52560	1.21	0.28	2.54	0.040072	0.10199	-4.67
258667_at	hypothetical protein	---	AT3G08750	-1.21	-0.28	-2.54	0.040099	0.102043	-4.67
248990_at	disease resistance protein-like	---	AT5G45210	-1.22	-0.28	-2.54	0.040101	0.102043	-4.67
249816_at	cleavage and polyadenylation spec	CPSF100	AT5G23880	1.32	0.40	2.54	0.040114	0.102063	-4.67
245150_at	photolyase/blue-light receptor (PHR	PHR2	AT2G47590	-1.27	-0.34	-2.54	0.040122	0.102071	-4.67
260193_at	putative amino acid permease simil	---	AT1G67640	-1.31	-0.39	-2.54	0.040126	0.102071	-4.67
265128_at	hypothetical protein predicted by ge	---	AT1G30860	-1.30	-0.38	-2.54	0.040135	0.102071	-4.67
263895_at	hypothetical protein predicted by ge	---	AT2G21920	-1.18	-0.23	-2.54	0.040139	0.102071	-4.67
261586_at	hypothetical protein predicted by g	---	AT1G01640	1.56	0.64	2.54	0.040139	0.102071	-4.67
251856_at	Peptidase - like protein ileal peptid	AMP1	AT3G54720	-1.41	-0.49	-2.54	0.040145	0.102075	-4.67
245656_at	hypothetical protein predicted by ge	---	AT1G56620	-1.22	-0.29	-2.54	0.040154	0.102086	-4.67
247198_at	unknown protein	---	AT5G65290	-1.20	-0.27	-2.54	0.04018	0.102131	-4.67
260979_at	MAP kinase ATMPK9, putative sim	ATMPK18	AT1G53510	-1.21	-0.27	-2.54	0.040181	0.102131	-4.67
259621_at	unknown protein	---	AT1G42710	-1.19	-0.25	-2.54	0.040221	0.102222	-4.68
256296_at	hypothetical protein	---	AT1G69480	1.19	0.26	2.54	0.040231	0.102235	-4.68
267173_at	origin recognition complex protein i	ORC2	AT2G37560	-1.41	-0.50	-2.53	0.040297	0.102373	-4.68
249326_at	unknown protein ; supported by cD	SYN2	AT5G40840	1.23	0.30	2.53	0.0403	0.102373	-4.68
250181_at	tRNA synthase - like protein tRNA	---	AT5G14460	1.23	0.30	2.53	0.040303	0.102373	-4.68
262084_at	hypothetical protein predicted by ge	---	AT1G56080	-1.25	-0.33	-2.53	0.040303	0.102373	-4.68
260556_at	putative endochitinase	---	AT2G43620	3.34	1.74	2.53	0.040311	0.102381	-4.68
265843_at	putative acyl-CoA oxidase possibly	ACX5	AT2G35690	-1.23	-0.30	-2.53	0.040315	0.102381	-4.68
254242_at	serine /threonine kinase - like prote	---	AT4G23200	-1.94	-0.96	-2.53	0.040319	0.102381	-4.68
249994_at	putative protein cell polarity protein	---	AT5G18590	1.24	0.31	2.53	0.040326	0.102381	-4.68
264380_at	unknown protein predicted by gens	---	AT2G25190	-1.17	-0.22	-2.53	0.040328	0.102381	-4.68
253048_at	formamidase - like protein formami	---	AT4G37560	1.74	0.80	2.53	0.040345	0.102402	-4.68
252864_at	putative protein regulatory protein	---	AT4G39740	1.46	0.54	2.53	0.040351	0.102402	-4.68
260449_at	unknown protein	---	AT1G72390	1.18	0.23	2.53	0.040352	0.102402	-4.68
247220_at	cdc2-like protein kinase ; supporte	CDKC2	AT5G64960	1.23	0.29	2.53	0.040355	0.102402	-4.68
266473_at	unknown protein	---	AT2G31110	1.81	0.85	2.53	0.040362	0.102409	-4.68
259236_at	unknown protein ; supported by ful	---	AT3G11530	1.20	0.27	2.53	0.0404	0.102494	-4.68
265160_at	unknown protein similar to EST gb|	---	AT1G31050	-1.28	-0.36	-2.53	0.040437	0.102576	-4.68
246746_at	putative protein predicted proteins,	---	AT5G27820	1.26	0.33	2.53	0.040497	0.102716	-4.68

256784_at	hypothetical protein predicted by ge	---	AT3G13674	-1.20	-0.26	-2.53	0.040508	0.102734	-4.68
245864_at	hypothetical protein predicted by ge	---	AT1G58070	-1.42	-0.50	-2.53	0.040526	0.102755	-4.68
262133_at	high affinity sulphate transporter, p	SULTR1;2	AT1G78000	1.95	0.97	2.53	0.040529	0.102755	-4.68
257791_at	unknown protein contains Pfam pro	---	AT3G27110	1.32	0.40	2.53	0.04053	0.102755	-4.68
244932_at	PSI 9KDa protein	---	---	-1.26	-0.34	-2.53	0.040572	0.102851	-4.68
267587_at	unknown protein	---	AT2G42080	-1.33	-0.41	-2.53	0.040577	0.102851	-4.68
246660_at	putative protein predicted protein, A	---	AT5G35180	-1.22	-0.29	-2.53	0.040585	0.10286	-4.69
251845_at	Expressed protein ; supported by fu	ATGCN4	AT3G54540	1.32	0.40	2.53	0.040619	0.102935	-4.69
262166_at	myb-related transcription activator,	---	AT1G74840	-1.30	-0.38	-2.53	0.040654	0.103012	-4.69
259421_at	disease resistance protein, putative	---	AT1G13910	1.28	0.36	2.53	0.040718	0.103162	-4.69
267448_at	putative protein phosphatase 2C	---	AT2G33700	1.18	0.23	2.53	0.040723	0.103164	-4.69
259715_at	hypothetical protein predicted by g	---	AT1G60990	1.28	0.36	2.53	0.040728	0.103165	-4.69
261134_at	cytochrome P450, putative similar	CYP722A1	AT1G19630	-1.21	-0.28	-2.53	0.040784	0.103295	-4.69
262632_at	23 kDa polypeptide of oxygen-evolv	PSBP-1	AT1G06680	-1.22	-0.29	-2.53	0.040805	0.103324	-4.69
255549_at	predicted protein of unknown functi	GPAT3	AT4G01950	-2.65	-1.41	-2.53	0.040807	0.103324	-4.69
263690_at	putative DNA-binding protein Simil	AtHB23	AT1G26960	-1.44	-0.52	-2.53	0.040809	0.103324	-4.69
251776_at	eukaryotic translation initiation fact	emb1624	AT3G55620	1.32	0.40	2.52	0.04084	0.103382	-4.69
257545_at	hypothetical protein predicted by ge	---	AT3G23200	1.35	0.43	2.52	0.040841	0.103382	-4.69
263601_s_a	dihydrofolate reductase-thymidylate	THY-1	AT2G16370	1.30	0.38	2.52	0.040854	0.103395	-4.69
259309_at	putative cyclin-dependent protein ki	---	AT3G05050	1.31	0.39	2.52	0.040856	0.103395	-4.69
262208_at	hypothetical protein predicted by ge	---	AT1G74800	-1.26	-0.34	-2.52	0.040864	0.103395	-4.69
266835_at	putative NADH dehydrogenase (ub	NDA2	AT2G29990	1.77	0.82	2.52	0.040864	0.103395	-4.69
248559_at	unknown protein	---	AT5G50010	-1.23	-0.30	-2.52	0.040893	0.103456	-4.69
254545_at	putative protein FKBP-type peptidy	---	AT4G19830	-1.42	-0.51	-2.52	0.040922	0.103512	-4.69
251293_at	hypothetical protein	---	AT3G61930	3.58	1.84	2.52	0.040924	0.103512	-4.69
256708_at	hypothetical protein predicted by ge	---	AT3G30320	-1.19	-0.26	-2.52	0.040933	0.103523	-4.69
265535_at	hypothetical protein predicted by g	---	AT2G15900	1.20	0.27	2.52	0.040945	0.103542	-4.69
262215_at	hypothetical protein contains simila	---	AT1G74790	-1.59	-0.66	-2.52	0.040954	0.103553	-4.69
264904_s_a	putative thioredoxin reductase	NTRA	AT2G17420	1.31	0.39	2.52	0.040965	0.103569	-4.69
261948_at	unknown protein ;supported by full-	---	AT1G64680	-1.43	-0.52	-2.52	0.04099	0.103622	-4.70
262640_at	hypothetical protein	---	AT1G62760	4.83	2.27	2.52	0.041023	0.103694	-4.70
254660_at	receptor serine/threonine kinase-lik	---	AT4G18250	1.41	0.50	2.52	0.041049	0.103745	-4.70
258321_at	early light-induced protein identical	ELIP1	AT3G22840	-1.25	-0.32	-2.52	0.041052	0.103745	-4.70
249624_at	putative protein predicted proteins,	---	AT5G37570	1.30	0.38	2.52	0.041079	0.1038	-4.70
261326_s_a	aminoacylase, putative similar to a	---	AT1G44180	1.37	0.45	2.52	0.041102	0.103848	-4.70

263911_at	hypothetical protein predicted by ge	---	AT2G36560	-1.19	-0.26	-2.52	0.041126	0.103898	-4.70
258156_at	unknown protein ; supported by cD	---	AT3G18050	-1.49	-0.58	-2.52	0.041163	0.103979	-4.70
246383_at	hypothetical protein predicted by ge	---	AT1G77360	1.42	0.50	2.52	0.041202	0.104067	-4.70
263073_at	unknown protein ;supported by full-	---	AT2G17500	4.78	2.26	2.52	0.041214	0.104083	-4.70
260451_at	putative AP2 domain transcription f	---	AT1G72360	-2.06	-1.04	-2.52	0.041222	0.104092	-4.70
249702_at	axi 1 (auxin-independent growth pr	---	AT5G35570	-1.66	-0.73	-2.52	0.041226	0.104092	-4.70
262361_at	unknown protein contains similarity	GTE3	AT1G73150	1.22	0.28	2.52	0.041241	0.104119	-4.70
255289_at	score=11/3, E=0.23, N=1 contains	---	AT4G04690	-1.23	-0.30	-2.52	0.041262	0.10416	-4.70
250252_at	transporter-like protein ;supported b	ZIFL1	AT5G13750	2.03	1.02	2.52	0.041277	0.104186	-4.70
250173_at	MYB40 - putative transcription facto	AtMYB40	AT5G14340	-1.25	-0.33	-2.52	0.041293	0.104214	-4.70
255442_at	predicted NADH dehydrogenase 2	---	AT4G02580	-1.20	-0.26	-2.52	0.0413	0.104221	-4.70
267156_at	hypothetical protein predicted by ge	---	AT2G37610	-1.23	-0.30	-2.52	0.04131	0.104233	-4.70
245787_at	unknown protein	---	AT1G32130	1.24	0.31	2.52	0.041314	0.104233	-4.70
259596_at	auxin-regulated GH3 protein, putat	GH3.17	AT1G28130	-1.57	-0.66	-2.52	0.04132	0.104237	-4.70
253982_at	calcineurin B-like protein 3 ;suppor	ATCBL3	AT4G26570	-1.36	-0.44	-2.52	0.041349	0.104295	-4.70
262017_at	elongation factor, putative similar t	---	AT1G35550	1.34	0.42	2.52	0.041352	0.104295	-4.70
245039_at	putative beta-1,3-glucanase ;supp	---	AT2G26600	1.23	0.29	2.52	0.041367	0.104321	-4.70
247486_at	putative protein	---	AT5G62140	-1.36	-0.45	-2.51	0.041431	0.104471	-4.71
260849_at	pectinesterase, putative similar to p	sks7	AT1G21860	-1.18	-0.24	-2.51	0.041436	0.104471	-4.71
262658_at	ribonuclease contains similarity to S	---	AT1G14220	-1.19	-0.25	-2.51	0.041476	0.104562	-4.71
264986_at	glutathione transferase, putative si	ATGSTU13	AT1G27130	2.22	1.15	2.51	0.041494	0.104595	-4.71
264526_at	putative calcium ATPase very simi	ECA3	AT1G10130	1.26	0.33	2.51	0.041519	0.104642	-4.71
253890_s_a	putative protein contains similarity t	---	AT4G27585	1.61	0.69	2.51	0.041522	0.104642	-4.71
263794_at	similar to S-locus glycoproteins	---	AT2G24620	-1.18	-0.24	-2.51	0.041532	0.104656	-4.71
260414_at	nitrate transporter (NTL1) identical	ATNRT1:2	AT1G69850	-1.26	-0.33	-2.51	0.041547	0.104656	-4.71
251908_at	putative protein late embryogenis a	---	AT3G53770	-1.24	-0.31	-2.51	0.04155	0.104656	-4.71
258494_at	cell division protein FtsH-like protei	---	AT3G02450	1.28	0.36	2.51	0.04155	0.104656	-4.71
263590_at	putative receptor-like protein kinase	---	AT2G01820	-1.20	-0.27	-2.51	0.04155	0.104656	-4.71
256678_at	RNA-binding protein (cp33) identic	CP33	AT3G52380	1.24	0.31	2.51	0.041558	0.104664	-4.71
257977_at	hypothetical protein predicted by ge	---	AT3G20850	-1.22	-0.28	-2.51	0.041587	0.104726	-4.71
260825_at	hypothetical protein predicted by ge	---	AT1G06810	-1.21	-0.27	-2.51	0.041597	0.104738	-4.71
245333_at	Expressed protein ; supported by fu	---	AT4G14615	1.17	0.22	2.51	0.04162	0.104786	-4.71
267075_at	putative bZIP transcription factor co	EEL	AT2G41070	1.19	0.25	2.51	0.041625	0.104786	-4.71
254623_at	protein ch-42 precursor, chloroplas	CHLI1	AT4G18480	-1.32	-0.40	-2.51	0.041643	0.104817	-4.71
266943_at	putative reverse transcriptase	---	---	-1.34	-0.43	-2.51	0.041646	0.104817	-4.71

266868_at	hypothetical protein predicted by ge	---	AT2G44630	1.21	0.28	2.51	0.041672	0.10487	-4.71
264972_at	meiotic asynaptic mutant asy1, put	ASY1	AT1G67370	1.36	0.44	2.51	0.041682	0.104874	-4.71
248012_at	putative protein strong similarity to	---	AT5G56310	1.29	0.37	2.51	0.041683	0.104874	-4.71
245468_at	pectinesterase like protein	---	AT4G15980	-1.20	-0.26	-2.51	0.041694	0.104891	-4.71
251933_at	putative protein mucin MUC3, Hom	---	AT3G54060	-1.28	-0.35	-2.51	0.041712	0.104911	-4.71
265796_at	Expressed protein ; supported by fu	---	AT2G35730	2.97	1.57	2.51	0.041713	0.104911	-4.71
256083_at	hypothetical protein predicted by ge	---	AT1G20730	-1.17	-0.23	-2.51	0.041716	0.104911	-4.71
264148_at	NAM (no apical meristem)-like prot	ANAC003	AT1G02220	5.32	2.41	2.51	0.041722	0.104915	-4.71
265039_at	unknown protein Location of ESTs	---	AT1G04000	-1.21	-0.28	-2.51	0.041728	0.104917	-4.71
258928_at	unknown protein similar to hypothet	TAF12	AT3G10070	1.30	0.38	2.51	0.041793	0.10507	-4.72
249631_at	sen1-like protein SEN1 - Saccharo	---	AT5G37160	-1.22	-0.29	-2.51	0.041824	0.105135	-4.72
250835_at	putative protein various predicted p	DME	AT5G04560	-1.26	-0.34	-2.51	0.041834	0.10515	-4.72
249836_at	unknown protein ;supported by full-	HMGB6	AT5G23420	1.53	0.62	2.51	0.041847	0.10517	-4.72
245985_at	peptidylprolyl isomerase-like protei	---	AT5G13120	-1.29	-0.36	-2.51	0.04186	0.105192	-4.72
250323_at	putative protein hydroxyproline-rich	---	AT5G12880	2.10	1.07	2.51	0.041877	0.105222	-4.72
249333_at	GDSL-motif lipase/hydrolase-like pr	GLIP1	AT5G40990	2.19	1.13	2.51	0.041881	0.105222	-4.72
263341_at	hypothetical protein predicted by ge	---	---	-1.24	-0.31	-2.51	0.041917	0.1053	-4.72
266447_at	putative calcium binding protein ;su	MSS3	AT2G43290	-1.70	-0.77	-2.51	0.041926	0.105302	-4.72
263020_at	unknown protein	---	AT1G23880	-1.21	-0.27	-2.51	0.041931	0.105302	-4.72
250859_at	cytochrom P450 - like protein cytoc	CYP77A4	AT5G04660	-1.16	-0.22	-2.51	0.041932	0.105302	-4.72
264044_at	putative pyrophosphate--fructose-6-	PFK5	AT2G22480	1.22	0.28	2.51	0.041956	0.105352	-4.72
262978_at	tubulin beta-1 chain identical to GB	TUB1	AT1G75780	-3.54	-1.82	-2.50	0.042042	0.105557	-4.72
254464_at	putative protein retinoblastoma bin	---	AT4G20400	1.33	0.41	2.50	0.042076	0.105631	-4.72
251032_at	putative homeodomain protein seve	RPL	AT5G02030	1.63	0.71	2.50	0.042115	0.105715	-4.72
264361_at	unknown protein Strong similarity to	---	AT1G03300	-1.23	-0.30	-2.50	0.04216	0.105819	-4.72
247895_at	putative protein bHLH transcription	---	AT5G58010	-1.21	-0.28	-2.50	0.042169	0.105827	-4.72
257922_at	ethylene receptor, putative (ETR2)	ETR2	AT3G23150	1.49	0.57	2.50	0.042189	0.105868	-4.72
266994_at	MADS-box protein (AGL29)	AGL29	AT2G34440	-1.25	-0.33	-2.50	0.042198	0.105878	-4.73
263355_at	putative RNA-binding protein ;supp	---	AT2G22100	1.28	0.36	2.50	0.042205	0.105884	-4.73
265680_at	putative hydrolase ; supported by c	---	AT2G32150	-1.43	-0.51	-2.50	0.042219	0.105908	-4.73
245392_at	glutaredoxin ;supported by full-leng	---	AT4G15680	-2.15	-1.11	-2.50	0.042224	0.105908	-4.73
262644_at	beta-VPE nearly identical to beta-V	BETA-VPE	AT1G62710	-1.23	-0.30	-2.50	0.042269	0.106006	-4.73
248668_at	putative protein similar to unknown	XRI1	AT5G48720	1.40	0.49	2.50	0.042272	0.106006	-4.73
252884_at	SEC14 - like protein phosphatidylin	---	AT4G39170	-1.26	-0.33	-2.50	0.042305	0.106076	-4.73
254579_at	hypothetical protein ;supported by	---	AT4G19400	-1.27	-0.35	-2.50	0.042312	0.106083	-4.73

256215_at	unknown protein ;supported by full-	---	AT1G50900	-1.24	-0.31	-2.50	0.042318	0.106085	-4.73
256819_at	unknown protein contains Pfam pro	---	AT3G21390	-1.21	-0.27	-2.50	0.042338	0.106124	-4.73
251825_at	ABC transporter - like protein ATP-	---	AT3G55100	-1.23	-0.30	-2.50	0.042372	0.106197	-4.73
248075_at	selenium-binding protein-like	CRR21	AT5G55740	1.37	0.45	2.50	0.042381	0.106208	-4.73
247149_at	unknown protein ;supported by full-	---	AT5G65660	-1.53	-0.62	-2.50	0.042411	0.106271	-4.73
253836_at	putative protein hypothetical protei	---	AT4G27840	1.22	0.28	2.50	0.042455	0.10637	-4.73
260509_at	natural resistance-associated macr	NRAMP2	AT1G47240	-1.17	-0.23	-2.50	0.042469	0.106393	-4.73
267464_at	putative pectinesterase	---	AT2G19150	-1.23	-0.30	-2.50	0.042481	0.106413	-4.73
251539_at	serine/threonine-specific protein ki	---	AT3G58690	-1.30	-0.38	-2.50	0.042504	0.106457	-4.73
259832_at	transfactor, putative similar to GI:4	---	AT1G69580	-1.67	-0.74	-2.50	0.04251	0.106461	-4.73
264819_at	hypothetical protein similar to mem	---	AT1G03510	1.37	0.46	2.50	0.042517	0.106467	-4.73
259612_at	60S ribosomal protein L37, putative	---	AT1G52300	1.51	0.60	2.50	0.042541	0.106516	-4.73
246994_at	putative protein similar to unknown	---	AT5G67460	-1.64	-0.71	-2.50	0.04255	0.106527	-4.73
262804_at	putative RNA-binding protein simila	---	AT1G20880	1.28	0.36	2.50	0.042575	0.106577	-4.73
262580_at	hypothetical protein Similar to gb|U	---	AT1G15330	-1.32	-0.40	-2.50	0.042592	0.106604	-4.73
260518_at	cinnamyl alcohol dehydrogenase, p	---	AT1G51410	-1.18	-0.24	-2.50	0.042598	0.106604	-4.73
253419_at	putative protein predicted proteins,	---	AT4G32780	-1.26	-0.33	-2.50	0.0426	0.106604	-4.73
245191_at	F12A21.10 similar to terminal ear1	TEL2	AT1G67770	-1.37	-0.46	-2.50	0.042612	0.106624	-4.74
263839_at	putative cis-Golgi SNARE protein ;	MEMB11	AT2G36900	1.35	0.44	2.49	0.042629	0.106654	-4.74
250431_at	cyclin protein - like cyclin D2.1 prot	CYCD4;2	AT5G10440	-1.21	-0.28	-2.49	0.042634	0.106654	-4.74
266084_at	hypothetical protein predicted by ge	---	AT2G37810	-1.29	-0.37	-2.49	0.042644	0.106669	-4.74
261004_at	hypothetical protein similar to putat	---	AT1G26450	-1.38	-0.46	-2.49	0.042709	0.10682	-4.74
264716_at	matrix metalloproteinase, putative	MMP	AT1G70170	1.73	0.79	2.49	0.042752	0.106915	-4.74
264349_at	putative Proline synthetase associa	---	AT1G11930	1.16	0.22	2.49	0.042757	0.106915	-4.74
249711_at	putative protein contains similarity t	---	AT5G35680	1.28	0.35	2.49	0.042775	0.106947	-4.74
264098_at	hypothetical protein predicted by ge	---	AT1G79260	-1.41	-0.49	-2.49	0.042779	0.106947	-4.74
256392_at	putative glycosyl transferase contai	GATL4	AT3G06260	-1.24	-0.31	-2.49	0.042785	0.10695	-4.74
263893_at	putative WRKY-type DNA binding p	WRKY59	AT2G21900	-1.31	-0.39	-2.49	0.04286	0.107127	-4.74
250361_at	putative protein various predicted p	---	AT5G11370	-1.18	-0.24	-2.49	0.042912	0.107245	-4.74
253858_at	carbohydrate kinase - like protein p	---	AT4G27600	1.19	0.25	2.49	0.042923	0.10726	-4.74
259689_x_a	unknown protein	---	AT1G63130	-1.42	-0.51	-2.49	0.042939	0.10729	-4.74
247397_at	Dof zinc finger protein - like Dof zin	---	AT5G62940	-1.40	-0.48	-2.49	0.043024	0.107488	-4.75
264519_at	putative reverse transcriptase simila	---	AT1G10000	-1.27	-0.35	-2.49	0.043032	0.107497	-4.75
251313_at	putative protein several hypothetica	---	AT3G61360	1.23	0.30	2.49	0.043042	0.10751	-4.75
246774_at	polygalacturonase-like protein poly	---	AT5G27530	-1.22	-0.28	-2.49	0.043055	0.10753	-4.75

248575_at	ATP-dependent Clp protease ATP-	---	AT5G49840	1.19	0.25	2.49	0.043064	0.107543	-4.75
247902_at	plasma membrane ATPase 3 (proto	AHA3	AT5G57350	1.26	0.34	2.49	0.043086	0.107586	-4.75
253793_at	myosin heavy chain - like protein (f	XIH	AT4G28710	-1.18	-0.24	-2.49	0.043118	0.107652	-4.75
255135_at	putative protein several hypothetica	---	---	-1.22	-0.29	-2.49	0.043122	0.107652	-4.75
263626_at	transcription factor ZAP1 identical t	ZAP1	AT2G04880	1.18	0.24	2.49	0.043129	0.107658	-4.75
245098_at	ethylene response sensor (ERS) id	ERS1	AT2G40940	-1.56	-0.64	-2.49	0.043148	0.107692	-4.75
262327_at	hypothetical protein similar to hypot	---	AT1G64130	-1.21	-0.28	-2.49	0.043163	0.107705	-4.75
250661_at	nucleoid DNA-binding-like protein ;	---	AT5G07030	-3.32	-1.73	-2.49	0.043173	0.107705	-4.75
253690_at	putative protein various predicted p	---	AT4G29550	-1.33	-0.41	-2.49	0.043173	0.107705	-4.75
258926_s_a	unknown protein N-terminus similar	anac052	AT3G10480	1.30	0.38	2.49	0.043178	0.107705	-4.75
263177_at	hypothetical protein predicted by ge	---	AT1G05540	-1.21	-0.27	-2.49	0.04318	0.107705	-4.75
265966_at	putative RNA-binding protein ; sup	---	AT2G37220	1.29	0.37	2.49	0.043185	0.107705	-4.75
248007_at	S-adenosylmethionine:2-demethyln	---	AT5G56260	1.18	0.24	2.49	0.043186	0.107705	-4.75
254993_at	putative protein kinase	---	AT4G10730	1.20	0.26	2.49	0.043193	0.10771	-4.75
254859_at	putative protein Arabidopsis thalian	---	AT4G12060	-1.29	-0.37	-2.49	0.043228	0.107787	-4.75
256879_at	unknown protein similar to auxin-in	---	AT3G26370	1.17	0.23	2.48	0.043238	0.107801	-4.75
261343_s_a	putative protein hypothetical protein	---	---	-1.19	-0.25	-2.48	0.043278	0.107886	-4.75
255420_at	putative frataxin-like protein similar	FH	AT4G03240	1.18	0.24	2.48	0.043289	0.107903	-4.75
251328_at	putative protein putative protein At2	ATPOB1	AT3G61600	-1.18	-0.24	-2.48	0.043306	0.107934	-4.75
245704_at	glycine-rich protein	KTF1	AT5G04290	1.18	0.24	2.48	0.043356	0.108047	-4.75
251662_at	putative protein DNA-DIRECTED R	NRPE5	AT3G57080	1.28	0.36	2.48	0.043389	0.108118	-4.75
250438_at	putative protein predicted protein, A	---	AT5G10580	-1.19	-0.25	-2.48	0.043413	0.108164	-4.75
260168_at	unknown protein contains zinc fing	---	AT1G71980	1.29	0.37	2.48	0.04344	0.10822	-4.75
248170_at	ankyrin-repeat-containing protein-lik	---	AT5G54620	-1.30	-0.38	-2.48	0.043456	0.108249	-4.76
258479_at	hypothetical protein predicted by ge	---	AT3G02440	-1.23	-0.29	-2.48	0.043503	0.108353	-4.76
252701_at	hypothetical protein SPOP protein,	ATBPM6	AT3G43700	1.28	0.36	2.48	0.043516	0.108375	-4.76
257770_at	unknown protein ;supported by full-	LFR	AT3G22990	1.23	0.30	2.48	0.043537	0.108404	-4.76
264688_at	hypothetical protein similar to LG27	---	AT1G09890	-1.32	-0.41	-2.48	0.043542	0.108404	-4.76
247592_at	high affinity nitrate transporter prot	NRT2.3	AT5G60780	-1.19	-0.25	-2.48	0.043542	0.108404	-4.76
253221_at	peptidylprolyl isomerase (cyclophilin	ROC5	AT4G34870	1.29	0.37	2.48	0.043593	0.108519	-4.76
262434_at	lysine and histidine specific transpo	---	AT1G47670	-1.46	-0.55	-2.48	0.043604	0.108534	-4.76
246348_at	putative protein putative glycerol-3-	---	AT3G56840	1.16	0.21	2.48	0.043616	0.108551	-4.76
248585_at	unknown protein	---	AT5G49640	1.22	0.28	2.48	0.043641	0.108602	-4.76
253824_at	putative protein protein kinase LeP	MTM1	AT4G27940	1.93	0.95	2.48	0.043663	0.108636	-4.76
265488_at	hypothetical protein predicted by ge	---	AT2G15610	-1.23	-0.29	-2.48	0.043664	0.108636	-4.76

248616_at	putative protein contains similarity t	---	AT5G49580	1.30	0.38	2.48	0.043669	0.108636	-4.76
258523_at	pectin methylesterase, putative sim	---	AT3G06830	-1.16	-0.22	-2.48	0.043683	0.10866	-4.76
247256_at	putative protein contains similarity t	---	AT5G64730	1.18	0.24	2.48	0.043688	0.108661	-4.76
248835_at	NBS/LRR disease resistance protei	---	AT5G47250	1.42	0.50	2.48	0.043709	0.108696	-4.76
246985_at	putative protein contains similarity t	---	AT5G67290	1.24	0.31	2.48	0.043712	0.108696	-4.76
250215_at	putative protein similar to unknown	---	AT5G14080	1.21	0.28	2.48	0.043755	0.108791	-4.76
260941_at	peroxidase, putative similar to perc	---	AT1G44970	-1.35	-0.43	-2.48	0.04377	0.108807	-4.76
263668_at	putative 1-aminocyclopropane-1-ca	---	AT1G04350	1.25	0.33	2.48	0.043771	0.108807	-4.76
262557_at	photosystem I subunit III precursor	---	AT1G31330	-1.22	-0.29	-2.48	0.043781	0.108821	-4.76
251948_at	diaminopimelate epimerase - like p	---	AT3G53580	1.25	0.32	2.48	0.043801	0.108852	-4.76
260400_at	putative peptide transporter similar	---	AT1G69860	-1.18	-0.24	-2.48	0.043803	0.108852	-4.76
266572_at	unknown protein	---	AT2G23840	1.34	0.42	2.48	0.04382	0.108883	-4.76
266909_at	hypothetical protein predicted by ge	BRM	AT2G46020	-1.27	-0.35	-2.48	0.043855	0.108957	-4.76
248353_at	cytochrome P450	CYP96A4	AT5G52320	-1.20	-0.26	-2.47	0.043866	0.108971	-4.76
249931_at	putative protein similar to unknown	QQT1	AT5G22370	1.32	0.40	2.47	0.043875	0.108983	-4.77
257833_at	transcriptional regulator protein, pu	LWD2	AT3G26640	-1.18	-0.24	-2.47	0.043896	0.109022	-4.77
245341_at	Expressed protein ; supported by fu	---	AT4G16447	1.71	0.78	2.47	0.0439	0.109022	-4.77
249251_at	putative protein similar to unknown	---	AT5G42000	-1.29	-0.36	-2.47	0.043927	0.109077	-4.77
251505_at	putative protein polyamine oxidase	CPuORF18	AT3G59050	-1.38	-0.47	-2.47	0.04394	0.109098	-4.77
257468_at	hypothetical protein contains simila	---	AT1G47470	-1.18	-0.24	-2.47	0.04397	0.10915	-4.77
259349_at	unknown protein ; supported by cD	ATAPRL5	AT3G03860	1.19	0.25	2.47	0.043971	0.10915	-4.77
250160_at	putative protein various predicted p	ATHB30	AT5G15210	1.60	0.68	2.47	0.043979	0.109158	-4.77
267083_at	calmodulin-like protein identical to C	TCH3	AT2G41100	-1.52	-0.60	-2.47	0.044	0.109199	-4.77
262129_at	mutM homologue-1 identical to mut	ATMMH-1	AT1G52500	1.28	0.35	2.47	0.044009	0.109208	-4.77
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281	---	---	-1.18	-0.24	-2.47	0.044023	0.109232	-4.77
260025_at	unknown protein ;supported by full-	---	AT1G30070	1.38	0.47	2.47	0.044032	0.109242	-4.77
254695_at	putative protein predicted protein, S	ATL4H	AT4G17905	-1.25	-0.32	-2.47	0.044057	0.109293	-4.77
259074_at	putative protein kinase contains Pfa	RPK2	AT3G02130	-1.35	-0.44	-2.47	0.04408	0.109337	-4.77
249990_at	hypothetical protein	---	AT5G18540	1.20	0.26	2.47	0.044113	0.109397	-4.77
264057_at	putative AP2 domain transcription fa	RAP2.7	AT2G28550	-1.37	-0.45	-2.47	0.044116	0.109397	-4.77
245183_at	putative protein similarity to predict	---	AT5G12440	1.30	0.38	2.47	0.044118	0.109397	-4.77
255763_at	hypothetical protein predicted by ge	---	AT1G16730	1.27	0.34	2.47	0.044211	0.109614	-4.77
259606_at	hypothetical protein predicted by ge	MAP65-8	AT1G27920	-1.18	-0.24	-2.47	0.044233	0.109657	-4.77
262059_at	DnaJ protein, putative similar to Dr	---	AT1G80030	-1.32	-0.40	-2.47	0.044252	0.109693	-4.77
246785_at	glutathione synthetase gsh2 non-c	GSH2	AT5G27380	1.48	0.56	2.47	0.044286	0.10976	-4.77

267296_at	hypothetical protein predicted by ge	LBD10	AT2G23660	-1.22	-0.28	-2.47	0.044289	0.10976	-4.77
245975_at	putative protein CGI-107 protein - h	---	AT5G13070	1.27	0.34	2.47	0.044312	0.109806	-4.78
260669_at	hypothetical protein predicted by ge	---	AT1G19340	1.22	0.29	2.47	0.044348	0.109882	-4.78
244978_at	RNA polymerase alpha subunit	---	---	-1.20	-0.26	-2.47	0.044355	0.109887	-4.78
251449_at	Rab GDP dissociation inhibitor ; su	ATGDI2	AT3G59920	1.28	0.35	2.47	0.044363	0.109895	-4.78
251690_at	putative protein TATA-binding prot	---	AT3G56510	1.22	0.28	2.47	0.044371	0.109904	-4.78
254131_at	protein kinase (AFC2) ; supported	AFC2	AT4G24740	1.25	0.32	2.47	0.04438	0.109904	-4.78
266738_at	unknown protein predicted by gene	---	AT2G47010	-1.33	-0.41	-2.47	0.044381	0.109904	-4.78
250347_at	putative protein	---	AT5G11960	-1.20	-0.27	-2.47	0.044387	0.109907	-4.78
266465_at	putative auxin-responsive protein ;	GH3.9	AT2G47750	-1.24	-0.31	-2.47	0.044406	0.109942	-4.78
265973_at	putative non-LTR retroelement reve	---	---	-1.18	-0.23	-2.47	0.044419	0.109944	-4.78
249207_at	C2H2-type zinc finger protein-like	---	AT5G42640	-1.21	-0.28	-2.47	0.044431	0.109944	-4.78
252415_at	glutamine-dependent asparagine sy	ASN1	AT3G47340	-3.76	-1.91	-2.47	0.044433	0.109944	-4.78
264968_at	stress related protein, putative simi	---	AT1G67360	1.60	0.68	2.47	0.044435	0.109944	-4.78
262909_at	serine/threonine protein phosphata	PP2A-1	AT1G59830	-1.23	-0.30	-2.47	0.044436	0.109944	-4.78
264856_at	3-hydroxy-3-methylglutaryl-coenzy	HMG2	AT2G17370	-1.31	-0.39	-2.47	0.044442	0.109944	-4.78
256921_at	unknown protein ;supported by full-	---	AT3G18940	1.23	0.30	2.47	0.044443	0.109944	-4.78
253212_s_a	xanthine dehydrogenase - like prot	XDH1	AT4G34890	1.30	0.38	2.47	0.044445	0.109944	-4.78
252784_at	putative protein predicted proteins,	---	---	-1.17	-0.22	-2.47	0.044453	0.109953	-4.78
261233_at	hypothetical protein similar to hypot	---	AT1G32810	1.24	0.32	2.47	0.044479	0.110003	-4.78
266988_at	putative myrosinase-binding protein	JAL22	AT2G39310	-1.36	-0.45	-2.46	0.044502	0.110048	-4.78
257153_at	unknown protein ; supported by cD	---	AT3G27220	1.34	0.42	2.46	0.044512	0.110061	-4.78
247009_at	unknown protein ;supported by full-	---	AT5G67600	1.49	0.58	2.46	0.044536	0.110109	-4.78
250459_at	unknown protein ; supported by cD	---	AT5G09860	1.22	0.29	2.46	0.044573	0.110188	-4.78
266548_at	unknown protein ;supported by full-	RPA	AT2G35210	-1.34	-0.43	-2.46	0.044578	0.110188	-4.78
261357_at	hypothetical protein predicted by ge	---	---	-1.18	-0.24	-2.46	0.044594	0.110216	-4.78
264802_at	putative syntaxin-related protein (U	SYP111	AT1G08560	-1.50	-0.59	-2.46	0.044601	0.110223	-4.78
261512_at	actin capping protein beta-2, putati	---	AT1G71790	-1.36	-0.45	-2.46	0.044612	0.110238	-4.78
262745_at	lipase, putative contains Pfam prof	---	AT1G28600	-1.29	-0.36	-2.46	0.044619	0.110243	-4.78
262483_at	putative translation initiation factor	FUG1	AT1G17220	1.20	0.26	2.46	0.044641	0.110284	-4.78
255263_at	4-coumarate--CoA ligase - like prot	---	AT4G05160	1.18	0.24	2.46	0.044651	0.110297	-4.78
263268_at	unknown protein	---	---	-1.22	-0.29	-2.46	0.044657	0.110301	-4.78
247987_at	putative protein similar to unknown	---	AT5G56900	1.23	0.30	2.46	0.04467	0.11031	-4.78
250466_at	putative protein TETRATRICOPEP	---	AT5G10090	-1.19	-0.25	-2.46	0.044671	0.11031	-4.78
255373_s_a	putative protein	---	---	-1.24	-0.31	-2.46	0.044678	0.110316	-4.78

249030_at	putative protein similar to unknown	---	---	-1.19	-0.25	-2.46	0.044689	0.110316	-4.78
264656_at	unknown protein Contains similarity	---	AT1G09010	1.20	0.26	2.46	0.044691	0.110316	-4.78
261269_at	unknown protein ; supported by full-	---	AT1G26690	1.26	0.33	2.46	0.044692	0.110316	-4.78
261159_s_a	cyclin, putative similar to GB:AAB0	CYCB1;5	AT1G34460	1.27	0.34	2.46	0.044741	0.110424	-4.79
257734_at	unknown protein contains Pfam pro	ATSYTF	AT3G18370	1.17	0.23	2.46	0.044787	0.110514	-4.79
264555_at	hypothetical protein predicted by ge	---	AT1G09360	-1.21	-0.28	-2.46	0.044787	0.110514	-4.79
255516_at	hypothetical protein similar to exter	---	AT4G02270	-1.33	-0.42	-2.46	0.044817	0.110577	-4.79
264233_at	ribosomal protein, putative similar t	---	AT1G67430	1.50	0.59	2.46	0.044822	0.110577	-4.79
255012_at	putative protein ;supported by full-l	---	AT4G10030	-1.41	-0.49	-2.46	0.04486	0.110659	-4.79
259474_at	unknown protein ;supported by full-	---	AT1G19130	1.60	0.68	2.46	0.044867	0.110664	-4.79
257023_at	RNA helicase, putative similar to R	---	AT3G19760	1.22	0.28	2.46	0.044872	0.110664	-4.79
260560_at	putative endochitinase	---	AT2G43590	1.38	0.46	2.46	0.044914	0.110751	-4.79
257505_at	hypothetical protein	---	AT1G47940	-1.16	-0.22	-2.46	0.044918	0.110751	-4.79
248811_at	putative protein contains similarity t	---	AT5G47310	-1.24	-0.31	-2.46	0.044922	0.110751	-4.79
251371_at	putative protein CGI-94 protein, Ho	EDA14	AT3G60360	1.41	0.49	2.46	0.04493	0.110757	-4.79
249704_at	Myb-related transcription factor LBM	TT2	AT5G35550	-1.29	-0.37	-2.46	0.044937	0.110757	-4.79
257597_at	protein kinase, putative similar to p	---	AT3G24790	-1.19	-0.25	-2.46	0.04494	0.110757	-4.79
264832_at	unknown unknown	---	AT1G03660	1.30	0.38	2.46	0.044944	0.110757	-4.79
263986_at	putative citrate synthase ;supporte	CSY3	AT2G42790	1.30	0.38	2.46	0.04497	0.110809	-4.79
257260_at	hypothetical protein predicted by ge	---	AT3G22104	1.32	0.40	2.46	0.044978	0.110817	-4.79
262115_at	Expressed protein ; supported by fu	---	AT1G02813	-1.22	-0.28	-2.46	0.044988	0.11083	-4.79
254247_at	putative protein receptor protein kir	---	AT4G23260	1.51	0.59	2.46	0.045021	0.110899	-4.79
258232_at	unknown protein	---	AT3G27750	1.34	0.42	2.46	0.045031	0.110902	-4.79
254985_x_a	putative reverse-transcriptase -like	---	---	-1.28	-0.36	-2.46	0.045032	0.110902	-4.79
264546_at	Expressed protein ; supported by cl	---	AT1G55805	1.45	0.54	2.46	0.04507	0.110981	-4.79
251283_at	seven in absentia-like protein SINA	---	AT3G61790	1.21	0.27	2.46	0.045073	0.110981	-4.79
252092_at	mucin-like protein hemomucin, Dro	SSL4	AT3G51420	1.41	0.49	2.46	0.045099	0.111024	-4.79
264370_at	hybrid proline-rich protein, putative	---	AT1G12100	-1.22	-0.29	-2.46	0.045101	0.111024	-4.79
256157_at	longevity assurance protein, putati	LAG13	AT1G13580	-1.30	-0.38	-2.45	0.045141	0.111108	-4.79
267111_s_a	hypothetical protein predicted by ge	---	---	-1.27	-0.35	-2.45	0.045145	0.111108	-4.79
258013_at	unknown protein	---	AT3G19320	-1.29	-0.36	-2.45	0.04517	0.111136	-4.80
265983_at	putative homeodomain transcription	HB-2	AT2G18550	-1.19	-0.26	-2.45	0.045171	0.111136	-4.80
258334_at	hypothetical protein predicted by ge	---	AT3G16010	-1.22	-0.29	-2.45	0.045173	0.111136	-4.80
267341_at	hypothetical protein predicted by ge	---	AT2G44200	1.31	0.38	2.45	0.045176	0.111136	-4.80
258146_at	putative WD-repeat protein (WDR1	---	AT3G18060	-1.25	-0.32	-2.45	0.045195	0.111171	-4.80

264454_at	unknown protein similar to U2 smal	---	AT1G10320	1.25	0.33	2.45	0.045253	0.111302	-4.80
254177_at	putative protein gene T22C1.1, Ca	---	AT4G23860	1.32	0.40	2.45	0.045258	0.111302	-4.80
266836_at	hypothetical protein predicted by gr	---	AT2G26000	1.30	0.38	2.45	0.045295	0.111382	-4.80
259241_at	unknown protein similar to unknowr	---	AT3G33530	-1.18	-0.24	-2.45	0.045301	0.111385	-4.80
253331_at	nucellin -like protein nucellin - Horc	---	AT4G33490	1.34	0.42	2.45	0.045327	0.111437	-4.80
252401_at	putative protein predicted proteins,	---	AT3G48030	-1.26	-0.33	-2.45	0.045339	0.111446	-4.80
251118_at	putative chloroplast inner envelope	APG1	AT3G63410	-1.29	-0.37	-2.45	0.045341	0.111446	-4.80
245951_at	aspartate aminotransferase Asp2 ;	ASP2	AT5G19550	1.41	0.50	2.45	0.045407	0.111597	-4.80
254455_at	hypothetical protein	---	AT4G21140	1.36	0.44	2.45	0.04543	0.111628	-4.80
257038_at	longevity factor-like protein similar	LOH2	AT3G19260	1.44	0.52	2.45	0.045431	0.111628	-4.80
259812_at	unknown protein	---	AT1G49840	-1.34	-0.43	-2.45	0.045434	0.111628	-4.80
245681_at	alkaline/neutral invertase, putative	---	AT1G56560	1.18	0.24	2.45	0.045446	0.111645	-4.80
265182_at	putative auxin-induced protein ;sup	---	AT1G23740	-1.33	-0.41	-2.45	0.045466	0.111683	-4.80
261786_at	cyclic nucleotide and calmodulin-re	ATCNGC7	AT1G15990	-1.21	-0.27	-2.45	0.045483	0.111706	-4.80
255675_at	MYC1 transcription factor	ATMYC1	AT4G00480	-1.23	-0.30	-2.45	0.045486	0.111706	-4.80
265264_at	hypothetical protein predicted by ge	---	AT2G42930	-1.19	-0.25	-2.45	0.045499	0.111711	-4.80
263260_at	putative protein-tyrosine phosphata	OTS2	AT1G10570	-1.19	-0.25	-2.45	0.045502	0.111711	-4.80
253306_at	dynamin-like protein ADL2	DRP3A	AT4G33650	1.19	0.26	2.45	0.045505	0.111711	-4.80
263673_at	unknown protein	---	AT2G04800	-1.36	-0.44	-2.45	0.045507	0.111711	-4.80
257319_at	hypothetical protein	---	---	1.32	0.40	2.45	0.045513	0.111714	-4.80
250183_at	putative protein various predicted p	---	AT5G14510	-1.34	-0.43	-2.45	0.045537	0.111749	-4.80
250765_at	unknown protein ;supported by full-	---	AT5G05930	-1.34	-0.42	-2.45	0.045537	0.111749	-4.80
253745_at	putative protein the C-terminus of t	---	AT4G29090	-1.20	-0.27	-2.45	0.045562	0.111797	-4.80
258820_at	putative tryptophanyl-tRNA syntheta	---	AT3G04600	1.18	0.24	2.45	0.04558	0.111817	-4.80
265541_at	hypothetical protein predicted by ge	SQN	---	-1.19	-0.25	-2.45	0.045584	0.111817	-4.80
254283_s_a	anthocyanidin synthase - like prote	---	AT4G22870	-1.29	-0.36	-2.45	0.045585	0.111817	-4.80
263899_at	hypothetical protein predicted by ge	EMB2219	AT2G21710	1.27	0.35	2.45	0.045594	0.111828	-4.80
250682_x_a	putative protein similar to unknown	---	AT5G06630	-1.59	-0.66	-2.45	0.045633	0.111911	-4.81
255624_at	MAP kinase 4 (MPK4) ;supported b	ATMPK4	AT4G01370	1.29	0.37	2.45	0.045644	0.111926	-4.81
265447_at	putative laccase (diphenol oxidase)	LAC6	AT2G46570	-1.28	-0.35	-2.45	0.045672	0.111983	-4.81
247315_at	unknown protein	---	AT5G64010	1.22	0.28	2.45	0.045691	0.112018	-4.81
263684_at	hypothetical protein predicted by ge	---	AT1G26900	1.23	0.30	2.45	0.04572	0.112076	-4.81
265736_at	putative ribosomal protein L7 ;supp	---	AT2G01250	1.48	0.56	2.45	0.045737	0.112106	-4.81
266825_at	unknown protein	---	AT2G22890	-1.49	-0.57	-2.45	0.045765	0.112163	-4.81
245921_at	putative protein predicted protein, /	---	AT5G28800	-1.18	-0.23	-2.45	0.045783	0.112191	-4.81

245484_at	enoyl-CoA hydratase like protein	ECHIA	AT4G16210	-1.21	-0.28	-2.45	0.045786	0.112191	-4.81
262176_at	3-ketoacyl-ACP synthase, putative	FAB1	AT1G74960	-1.26	-0.33	-2.44	0.0458	0.112213	-4.81
248245_at	MtN3 protein-like	---	AT5G53190	-1.26	-0.33	-2.44	0.045808	0.11222	-4.81
257065_at	diacylglycerol pyrophosphate phos	---	AT3G18220	-1.35	-0.43	-2.44	0.04584	0.112275	-4.81
253615_at	cyclic nucleotide and calmodulin-re	CNGC17	AT4G30360	1.33	0.41	2.44	0.04584	0.112275	-4.81
254358_at	putative protein light induced prote	---	AT4G22310	1.16	0.21	2.44	0.045922	0.112463	-4.81
247564_at	RNA helicase - like protein RNA he	---	AT5G61140	1.23	0.30	2.44	0.045995	0.112627	-4.81
267270_at	hypothetical protein predicted by ge	---	AT2G02550	-1.29	-0.37	-2.44	0.045999	0.112627	-4.81
257463_at	phosphatidylinositol/phosphatidylch	---	AT1G14820	-1.28	-0.36	-2.44	0.046016	0.112647	-4.81
245224_at	gene_id:K17E7.8~unknown protein	---	AT3G29796	-1.18	-0.24	-2.44	0.04602	0.112647	-4.81
248069_at	unknown protein	---	AT5G55650	-1.23	-0.30	-2.44	0.046022	0.112647	-4.81
248725_at	acetyl-CoA:benzylalcohol acetyltran	---	AT5G47980	-1.22	-0.29	-2.44	0.046049	0.112702	-4.81
259822_at	myb-related transcription factor, pu	MYB20	AT1G66230	-1.46	-0.55	-2.44	0.046056	0.112706	-4.81
258190_at	hypothetical protein predicted by ge	---	AT3G29080	-1.19	-0.25	-2.44	0.046065	0.112708	-4.82
259897_at	putative beta-glucanase similar to b	ATCEL3	AT1G71380	-1.21	-0.27	-2.44	0.046066	0.112708	-4.82
258980_at	putative reversibly glycosylatable p	RGP3	AT3G08900	-1.20	-0.27	-2.44	0.046099	0.112767	-4.82
263138_at	hypothetical protein predicted by ge	---	AT1G65090	-1.18	-0.24	-2.44	0.0461	0.112767	-4.82
263731_at	metalloproteinase, putative similar	---	AT1G59970	-1.83	-0.88	-2.44	0.046115	0.11279	-4.82
251546_at	putative protein predicted proteins,	---	AT3G58830	1.36	0.44	2.44	0.046148	0.112859	-4.82
266137_at	unknown protein ;supported by full-	---	AT2G45010	-1.21	-0.27	-2.44	0.046168	0.112897	-4.82
258582_at	germin-like protein contains Pfam p	---	AT3G04150	-1.16	-0.22	-2.44	0.046191	0.112941	-4.82
264978_at	unknown protein contains Pfam pro	---	AT1G27120	-1.46	-0.55	-2.44	0.046244	0.113057	-4.82
252747_at	putative protein retrotransposon fin	---	---	-1.24	-0.31	-2.44	0.046252	0.113057	-4.82
249530_at	putative protein asparaginyl-tRNA s	---	AT5G38750	-1.18	-0.24	-2.44	0.046254	0.113057	-4.82
258756_at	hypothetical protein similar to hypot	---	AT3G11960	1.23	0.30	2.44	0.046295	0.113146	-4.82
253822_at	hypothetical protein	---	AT4G28410	-1.20	-0.26	-2.44	0.046308	0.113157	-4.82
261983_at	protein kinase, putative similar to c	---	AT1G33770	-1.38	-0.46	-2.44	0.046309	0.113157	-4.82
245584_at	amine oxidase like protein	ATAO1	AT4G14940	-1.17	-0.23	-2.44	0.046314	0.113157	-4.82
250561_at	glycerophosphodiester phosphodie	---	AT5G08030	-1.27	-0.35	-2.44	0.046325	0.113171	-4.82
263661_at	unknown protein EST gb|T45093 co	---	AT1G04290	-1.40	-0.48	-2.44	0.046338	0.113185	-4.82
264058_at	F-box protein family, AtFBX7 conta	---	AT2G03560	-1.19	-0.25	-2.44	0.046341	0.113185	-4.82
260374_at	unknown protein	TAF2	AT1G73960	1.21	0.27	2.44	0.04636	0.11322	-4.82
261575_at	hypothetical protein contains simila	---	AT1G01130	-1.36	-0.44	-2.44	0.046369	0.11323	-4.82
264384_at	putative chromodomain-helicase-D	PKL	AT2G25170	1.17	0.23	2.44	0.046394	0.11328	-4.82
248106_at	putative protein similar to unknown	---	AT5G55100	-1.18	-0.24	-2.44	0.046429	0.113352	-4.82

246205_at	hypothetical protein ; supported by	---	AT4G36970	1.45	0.53	2.43	0.046466	0.11343	-4.82
264870_at	hypothetical protein ;supported by	---	AT1G24210	1.24	0.31	2.43	0.046475	0.113439	-4.82
247007_at	porin-like protein ;supported by full	VDAC2	AT5G67500	-1.27	-0.35	-2.43	0.046492	0.113468	-4.82
257350_x_a	hypothetical protein predicted by ge	RALFL12	AT2G19040	-1.22	-0.28	-2.43	0.046503	0.113484	-4.82
254905_at	RPP1-WsA-like disease resistance	---	AT4G11170	1.91	0.94	2.43	0.046535	0.113539	-4.83
263027_at	hypothetical protein predicted by ge	---	AT1G24010	-1.17	-0.23	-2.43	0.04654	0.113539	-4.83
264059_at	Expressed protein ; supported by fu	INH3	AT2G31305	1.22	0.29	2.43	0.046546	0.113539	-4.83
246686_at	putative protein predicted proteins -	---	---	-1.29	-0.37	-2.43	0.046551	0.113539	-4.83
263770_at	Mutator-like transposase similar to	---	---	-1.32	-0.40	-2.43	0.046555	0.113539	-4.83
245111_at	putative Ta11-like non-LTR retroele	---	---	-1.22	-0.29	-2.43	0.046557	0.113539	-4.83
254270_at	gamma-glutamylcysteine synthetas	GSH1	AT4G23100	1.65	0.72	2.43	0.046565	0.113539	-4.83
247366_at	putative protein contains similarity t	---	AT5G63260	-1.26	-0.34	-2.43	0.046566	0.113539	-4.83
250583_at	zinc finger transcription factor ; sup	PEI1	AT5G07500	-1.20	-0.26	-2.43	0.046597	0.113592	-4.83
247892_at	putative protein contains similarity t	---	AT5G57970	-1.38	-0.47	-2.43	0.046597	0.113592	-4.83
253796_at	hypothetical protein	---	AT4G28460	2.78	1.47	2.43	0.046617	0.113627	-4.83
251031_at	one helix protein (OHP) ;supported	OHP	AT5G02120	-1.25	-0.32	-2.43	0.046639	0.113671	-4.83
254868_at	copper amine oxidase like protein (	---	AT4G12270	1.27	0.35	2.43	0.046678	0.113752	-4.83
264050_at	putative non-LTR retroelement reve	---	---	-1.30	-0.38	-2.43	0.046703	0.113796	-4.83
263424_at	putative RING zinc finger protein	---	AT2G31510	1.21	0.28	2.43	0.046706	0.113796	-4.83
247229_at	putative protein contains similarity t	---	AT5G65160	-1.34	-0.43	-2.43	0.046729	0.11384	-4.83
258106_at	ribonucleoside-diphosphate reducta	RNR2A	AT3G23580	1.27	0.34	2.43	0.046737	0.113843	-4.83
259902_at	disease resistance protein, putative	AtRLP13	AT1G74170	1.54	0.62	2.43	0.046741	0.113843	-4.83
266695_at	putative CCCH-type zinc finger prot	---	AT2G19810	-1.59	-0.67	-2.43	0.046745	0.113843	-4.83
252883_at	GTP-binding - like protein GTP-bin	---	AT4G39520	1.29	0.37	2.43	0.046804	0.113965	-4.83
249954_at	putative protein ;supported by full-l	---	AT5G18920	1.16	0.21	2.43	0.046805	0.113965	-4.83
256641_at	hypothetical protein similar to putati	---	---	-1.26	-0.34	-2.43	0.046854	0.114068	-4.83
260727_at	polygalacturonase PG1, putative s	---	AT1G48100	-1.29	-0.37	-2.43	0.046857	0.114068	-4.83
256239_at	hypothetical protein predicted by ge	---	AT3G12470	-1.24	-0.31	-2.43	0.046907	0.114167	-4.83
246127_s_a	putative protein	---	---	-1.16	-0.22	-2.43	0.046908	0.114167	-4.83
253882_at	pelota (PEL1)	PEL1	AT4G27650	-1.26	-0.34	-2.43	0.046933	0.114204	-4.83
267548_at	putative disease resistance protein	AtRLP22	AT2G32660	1.77	0.82	2.43	0.046933	0.114204	-4.83
251548_at	putative protein predicted protein, A	---	---	-1.27	-0.34	-2.43	0.046987	0.114322	-4.84
253797_at	putative protein 55.11 protein hom	RPN1B	AT4G28470	1.16	0.21	2.43	0.047006	0.114357	-4.84
251675_at	helicase-like protein DNA helicase	INO80	AT3G57300	1.18	0.24	2.43	0.047049	0.114448	-4.84
263868_at	hypothetical protein predicted by ge	---	AT2G36840	1.24	0.31	2.43	0.047081	0.114516	-4.84

252220_at	putative protein hypothetical protei	LBD38	AT3G49940	-1.38	-0.47	-2.43	0.047089	0.114522	-4.84
252389_at	Expressed protein ; supported by fu	---	AT3G47833	1.44	0.53	2.43	0.047097	0.114528	-4.84
262698_at	AMP-binding protein, putative cont	---	AT1G75960	-1.60	-0.68	-2.42	0.047136	0.114611	-4.84
265363_at	hypothetical protein predicted by ge	---	---	-1.18	-0.23	-2.42	0.047147	0.114619	-4.84
258613_at	putative myo-inositol monophospha	VTC4	AT3G02870	-1.43	-0.51	-2.42	0.047149	0.114619	-4.84
253828_at	putative protein predicted protein, A	SLAH2	AT4G27970	-1.28	-0.36	-2.42	0.047159	0.11462	-4.84
255286_at	see T14P8.10 (GB:AF069298)	---	AT4G04650	-1.32	-0.40	-2.42	0.04716	0.11462	-4.84
245467_at	hypothetical protein	---	AT4G16610	-1.35	-0.44	-2.42	0.047191	0.114684	-4.84
251826_at	ABC transporter - like protein ATP-	---	AT3G55110	-1.24	-0.31	-2.42	0.047239	0.114788	-4.84
265256_at	hypothetical protein predicted by ge	---	AT2G28390	-1.16	-0.22	-2.42	0.0473	0.114924	-4.84
267262_at	putative serine carboxypeptidase I	SNG1	AT2G22990	-1.33	-0.41	-2.42	0.047314	0.114946	-4.84
257654_at	DnaJ protein, putative contains Pfa	---	AT3G13310	1.85	0.89	2.42	0.047359	0.115043	-4.84
253353_at	pathogenesis-related protein - like	---	AT4G33730	-1.18	-0.24	-2.42	0.047396	0.115121	-4.84
252252_at	putative protein GTP-binding prote	RID3	AT3G49180	1.45	0.54	2.42	0.047413	0.115139	-4.84
250175_at	putative protein CGI-67, Homo sap	---	AT5G14390	1.42	0.51	2.42	0.047413	0.115139	-4.84
259125_at	unknown protein Pfam HMM hit: Re	---	AT3G02300	-1.18	-0.24	-2.42	0.047429	0.115156	-4.84
257632_at	cytochrome P450, putative similar	CYP71B21	AT3G26190	1.44	0.53	2.42	0.047431	0.115156	-4.84
246642_s_a	putative protein predicted proteins,	---	---	-1.16	-0.22	-2.42	0.047486	0.115277	-4.85
266664_at	hypothetical protein predicted by gr	---	AT2G29800	-1.21	-0.28	-2.42	0.047501	0.115304	-4.85
264464_at	putative heat-shock protein similar t	---	AT1G10350	-1.24	-0.31	-2.42	0.047527	0.115354	-4.85
253706_at	putative protein D-threonine dehyd	---	AT4G29120	1.20	0.27	2.42	0.047539	0.115366	-4.85
266193_at	unknown protein	---	AT2G39080	-1.25	-0.32	-2.42	0.047542	0.115366	-4.85
245316_at	hypothetical protein ;supported by f	---	AT4G14000	1.23	0.30	2.42	0.047552	0.115376	-4.85
249559_at	putative protein	---	AT5G38320	1.31	0.39	2.42	0.047574	0.115407	-4.85
255731_at	phosphoprotein phosphatase 2A, r	RCN1	AT1G25490	-1.17	-0.22	-2.42	0.047574	0.115407	-4.85
255004_at	putative protein	---	AT4G09970	1.28	0.36	2.42	0.047632	0.115535	-4.85
261860_at	scarecrow-like protein similar to SC	SCL5	AT1G50600	1.26	0.34	2.42	0.047714	0.115722	-4.85
256773_at	hypothetical protein predicted by ge	---	AT3G13630	-1.23	-0.30	-2.42	0.047724	0.115732	-4.85
254463_at	putative protein transcription initiati	TAF11	AT4G20280	1.26	0.33	2.42	0.047731	0.115738	-4.85
264246_at	trehalose-6-phosphate synthase, p	ATTPS10	AT1G60140	-1.77	-0.82	-2.42	0.047749	0.115767	-4.85
264026_at	glycine-rich protein (AtGRP2) Same	ATGRP2B	AT2G21060	1.44	0.52	2.42	0.047753	0.115767	-4.85
248760_at	unknown protein ;supported by full-	---	AT5G47570	1.30	0.38	2.42	0.047773	0.1158	-4.85
248302_at	putative protein similar to unknown	---	AT5G53160	1.31	0.39	2.42	0.047777	0.1158	-4.85
265455_at	hypothetical protein predicted by ge	---	AT2G46560	1.20	0.26	2.41	0.047839	0.115939	-4.85
261289_at	hypothetical protein predicted by ge	---	AT1G37000	1.18	0.24	2.41	0.047845	0.115939	-4.85

258536_at	Rab escort protein, putative similar	---	AT3G06540	1.24	0.31	2.41	0.047871	0.115991	-4.85
260952_at	hypothetical protein predicted by ge	---	AT1G06140	1.31	0.39	2.41	0.047876	0.115991	-4.85
266300_at	putative auxin transport protein ; su	PIN4	AT2G01420	-1.95	-0.97	-2.41	0.047909	0.116048	-4.86
248773_at	kinesin-like protein	FRA1	AT5G47820	-1.28	-0.35	-2.41	0.04791	0.116048	-4.86
266218_s_a	putative cytochrome P450	CYP710A4	AT2G28850	-1.20	-0.26	-2.41	0.047937	0.116102	-4.86
263416_at	hypothetical protein contains protei	---	AT2G17170	-1.21	-0.28	-2.41	0.047949	0.116117	-4.86
255053_at	putative protein RNA helicase -Mus	---	AT4G09730	1.62	0.70	2.41	0.04797	0.116156	-4.86
251330_at	putative protein putative protein At2	---	AT3G61550	-1.32	-0.40	-2.41	0.04805	0.116338	-4.86
264606_at	unknown protein ;supported by full-	---	AT1G04660	-1.31	-0.39	-2.41	0.048065	0.116354	-4.86
265084_at	hypothetical protein contains Cys3H	SOM	AT1G03790	-1.21	-0.27	-2.41	0.048067	0.116354	-4.86
247960_at	N-myristoyl transferase ;supported	NMT1	AT5G57020	-1.18	-0.23	-2.41	0.048075	0.116361	-4.86
264624_at	zinc finger protein ATZF1, putative	ERD6	AT1G08930	-1.31	-0.39	-2.41	0.048095	0.116387	-4.86
251504_at	putative protein putative multidrug	TT12	AT3G59030	-1.24	-0.31	-2.41	0.048096	0.116387	-4.86
247023_at	putative protein similar to unknown	HEC1	AT5G67060	-1.30	-0.38	-2.41	0.048111	0.116411	-4.86
264212_at	putative tRNA adenylyltransferase S	---	AT1G22660	1.35	0.43	2.41	0.048127	0.116439	-4.86
267507_at	putative ribosomal protein S27 ;sup	---	AT2G45710	1.34	0.43	2.41	0.048171	0.116532	-4.86
249640_at	cationic amino acid transporter -like	CAT3	AT5G36940	-1.36	-0.44	-2.41	0.048199	0.116587	-4.86
260583_x_a	putative polyribonucleotide phospho	---	AT2G47220	1.31	0.38	2.41	0.048233	0.116658	-4.86
267527_at	unknown protein	---	AT2G45610	-1.25	-0.32	-2.41	0.04825	0.116685	-4.86
248309_at	putative protein contains similarity t	---	AT5G52540	-1.72	-0.79	-2.41	0.048255	0.116685	-4.86
256935_at	unknown protein ;supported by full-	---	AT3G22570	-1.18	-0.24	-2.41	0.048314	0.116815	-4.86
248463_at	putative protein contains similarity t	---	AT5G51130	1.57	0.66	2.41	0.048356	0.116905	-4.86
247364_at	putative protein similar to unknown	---	AT5G63200	1.18	0.24	2.41	0.048361	0.116905	-4.86
252436_x_a	putative protein several hypothetica	---	---	-1.42	-0.51	-2.41	0.048412	0.117017	-4.87
260563_at	putative glucosyltransferase	UGT74F1	AT2G43840	1.25	0.32	2.41	0.048428	0.117042	-4.87
258874_at	hypothetical protein similar to unkno	---	AT3G03230	-1.27	-0.35	-2.41	0.048453	0.117089	-4.87
252480_at	putative protein methyl-CpG-bindin	MBD5	AT3G46580	-1.17	-0.22	-2.41	0.048484	0.11714	-4.87
266693_at	unknown protein predicted by gens	MIOX2	AT2G19800	-2.80	-1.49	-2.41	0.048484	0.11714	-4.87
245971_at	putative protein ; supported by cDN	NPH4	AT5G20730	-1.20	-0.27	-2.41	0.048505	0.117178	-4.87
260039_at	CLE12 CLAVATA3/ESR-Related 12	CLE12	AT1G68795	-1.26	-0.33	-2.40	0.048535	0.117238	-4.87
264729_at	putative metal-binding protein highl	---	AT1G22990	-1.41	-0.49	-2.40	0.048569	0.117302	-4.87
254529_at	ATP binding protein - like nucleotid	INDL	AT4G19540	-1.19	-0.25	-2.40	0.048575	0.117302	-4.87
255711_at	putative WD repeat membrane prot	---	AT4G00090	1.25	0.33	2.40	0.048577	0.117302	-4.87
246405_at	disease resistance protein RPP1-W	---	AT1G57630	2.71	1.44	2.40	0.048614	0.117379	-4.87
254669_at	HhoA protease precursor, putative	DEG5	AT4G18370	-1.30	-0.38	-2.40	0.048621	0.117384	-4.87

257497_at	hypothetical protein predicted by ge	---	AT1G51430	-1.36	-0.44	-2.40	0.048645	0.117429	-4.87
248029_at	beta-amylase ; supported by cDNA	BAM4	AT5G55700	1.23	0.30	2.40	0.048657	0.117445	-4.87
267352_at	hypothetical protein predicted by ge	---	AT2G40050	-1.18	-0.24	-2.40	0.048683	0.117489	-4.87
246313_at	PPR-repeat protein, putative conta	---	AT1G31920	1.54	0.62	2.40	0.048685	0.117489	-4.87
264082_at	unknown protein ;supported by full-	---	AT2G28570	-1.21	-0.27	-2.40	0.048706	0.117513	-4.87
265104_at	unknown protein 3'-end of protein c	ATO2	AT1G31020	1.21	0.28	2.40	0.048707	0.117513	-4.87
261674_at	unknown protein	---	AT1G18270	1.41	0.49	2.40	0.04871	0.117513	-4.87
246525_at	CONSTANS ;supported by full-leng	CO	AT5G15840	1.23	0.30	2.40	0.048766	0.117633	-4.87
245544_at	UTP-glucose glucosyltransferase lik	---	AT4G15270	-1.24	-0.31	-2.40	0.04879	0.117681	-4.87
258952_at	putative RNase H contains Pfam pr	---	AT3G01410	-1.25	-0.32	-2.40	0.048799	0.117681	-4.87
253140_at	RING-H2 finger protein RHA3b ;su	RHA3B	AT4G35480	-1.27	-0.35	-2.40	0.048804	0.117681	-4.87
261083_at	unknown protein ; supported by cDI	---	AT1G07310	-1.25	-0.32	-2.40	0.048806	0.117681	-4.87
266088_at	hypothetical protein predicted by ge	---	AT2G37780	-1.28	-0.36	-2.40	0.04882	0.117704	-4.87
253986_at	putative protein predicted protein, A	---	AT4G26210	1.39	0.48	2.40	0.048872	0.117807	-4.88
263470_at	putative unconventional myosin	XIF	AT2G31900	-1.19	-0.25	-2.40	0.048874	0.117807	-4.88
264103_at	unknown protein	---	AT2G13660	1.23	0.30	2.40	0.048931	0.117932	-4.88
263089_at	putative retroelement pol polyprotei	---	---	-1.27	-0.35	-2.40	0.048949	0.117963	-4.88
262726_at	hypothetical protein similar to putati	AtTLP5	AT1G43640	-1.26	-0.33	-2.40	0.04899	0.11805	-4.88
250478_at	non-phototropic hypocotyl 3-like pr	DOT3	AT5G10250	-1.27	-0.34	-2.40	0.049053	0.118191	-4.88
254191_at	hypothetical protein ;supported by	---	AT4G23900	-1.27	-0.34	-2.40	0.049104	0.118293	-4.88
249780_at	ubiquitin	---	AT5G24240	1.26	0.34	2.40	0.049107	0.118293	-4.88
259060_at	hypothetical protein predicted by ge	---	AT3G07400	-1.29	-0.36	-2.40	0.049119	0.118311	-4.88
254891_at	putative protein Fly Fas-associated	SAY1	AT4G11740	1.18	0.24	2.40	0.049172	0.118416	-4.88
258508_at	protein kinase, putative similar to S	---	AT3G06640	-1.16	-0.22	-2.40	0.049173	0.118416	-4.88
265062_at	receptor kinase, putative similar to	---	AT1G61550	1.39	0.48	2.40	0.049185	0.118432	-4.88
254631_at	putative protein predicted proteins,	LSH9	AT4G18610	-1.53	-0.62	-2.40	0.049208	0.118474	-4.88
251507_at	putative protein CND41, chloroplas	---	AT3G59080	-2.33	-1.22	-2.39	0.049221	0.118484	-4.88
252542_at	nuclear receptor binding factor-like	---	AT3G45770	1.18	0.23	2.39	0.049222	0.118484	-4.88
250189_at	putative protein ;supported by full-l	---	AT5G14410	-1.37	-0.46	-2.39	0.049241	0.118518	-4.88
246561_at	putative protein hypothetical protei	---	AT5G15570	1.21	0.28	2.39	0.049253	0.118534	-4.88
246288_at	unknown protein	---	AT1G31850	-1.29	-0.37	-2.39	0.049265	0.118549	-4.88
254656_at	putative protein ;supported by full-l	---	AT4G18070	-1.32	-0.40	-2.39	0.049274	0.118559	-4.88
253998_at	putative peroxidase peroxidase AT	---	AT4G26010	-1.17	-0.23	-2.39	0.049304	0.11862	-4.88
259289_at	hypothetical protein predicted by ge	---	AT3G11350	-1.24	-0.31	-2.39	0.049343	0.118689	-4.89
250031_at	transfactor-like protein ; supported	MYR1	AT5G18240	-1.32	-0.40	-2.39	0.049346	0.118689	-4.89

248845_at	disease resistance protein-like	---	AT5G46470	-1.27	-0.34	-2.39	0.049357	0.118689	-4.89
245389_at	putative protein ;supported by full-le	---	AT4G17480	-1.27	-0.34	-2.39	0.049359	0.118689	-4.89
267566_at	unknown protein predicted by gens	---	AT2G30760	-1.16	-0.21	-2.39	0.049359	0.118689	-4.89
246410_at	hypothetical protein predicted by ge	---	AT1G57760	-1.18	-0.24	-2.39	0.049411	0.118801	-4.89
265774_at	hypothetical protein predicted by ge	---	AT2G07240	-1.29	-0.37	-2.39	0.049433	0.118842	-4.89
258816_at	putative T-complex protein 1, theta	---	AT3G03960	1.32	0.41	2.39	0.049448	0.118865	-4.89
250717_at	putative protein similar to unknown	---	AT5G06200	-1.28	-0.36	-2.39	0.049479	0.118926	-4.89
258853_at	unknown protein similar to GB:AAD	---	AT3G06440	-1.20	-0.27	-2.39	0.049521	0.119007	-4.89
246135_at	putative protein non-consensus do	---	AT5G20885	-1.45	-0.54	-2.39	0.049523	0.119007	-4.89
256433_at	unknown protein	SAG20	AT3G10985	1.32	0.41	2.39	0.049531	0.119014	-4.89
252165_at	hypothetical protein ;supported by	---	AT3G50550	1.25	0.32	2.39	0.049539	0.119021	-4.89
252972_at	auxin-induced protein - like auxin-i	---	AT4G38840	-1.59	-0.67	-2.39	0.049553	0.119041	-4.89
258863_at	unknown protein similar to RNA hel	DCL2	AT3G03300	1.38	0.46	2.39	0.04957	0.119069	-4.89
258429_at	putative GTP-binding protein simila	TOC120	AT3G16620	1.21	0.28	2.39	0.049633	0.119209	-4.89
261364_at	dynamin-like protein similar to GB:U	---	AT1G53140	-1.23	-0.30	-2.39	0.049648	0.119232	-4.89
252182_at	U1 snRNP 70K protein ; supported	U1-70K	AT3G50670	1.20	0.27	2.39	0.049659	0.119247	-4.89
256014_at	hypothetical protein predicted by ge	---	AT1G19200	1.77	0.83	2.39	0.049696	0.119322	-4.89
261383_at	hypothetical protein predicted by ge	---	AT1G05380	1.23	0.30	2.39	0.049718	0.119362	-4.89
258457_at	Expressed protein ; supported by fu	IGPD	AT3G22425	1.29	0.36	2.39	0.049727	0.119373	-4.89
245751_s_a	hypothetical protein contains simila	---	AT1G25682	-1.41	-0.50	-2.39	0.04974	0.119391	-4.89
253544_at	hypothetical protein	---	AT4G31280	-1.18	-0.24	-2.39	0.049835	0.119604	-4.90
247962_at	protein kinase MEK1 homolog	MKK6	AT5G56580	-1.20	-0.26	-2.39	0.049839	0.119604	-4.90
256544_at	Mlo-like protein similar to Mlo [Hord	MLO9	AT1G42560	-1.24	-0.31	-2.39	0.049857	0.119627	-4.90
249608_at	multispanning membrane protein -	---	AT5G37310	1.24	0.31	2.39	0.04986	0.119627	-4.90
265663_at	unknown protein predicted by gens	---	AT2G24290	1.24	0.31	2.39	0.049869	0.119639	-4.90
261058_at	histone, putative similar to histone	HTR12	AT1G01370	-1.18	-0.23	-2.39	0.049885	0.119662	-4.90
264687_at	cysteine protease XBCP3 identical	XBCP3	AT1G09850	-1.17	-0.23	-2.39	0.049894	0.119672	-4.90
253653_at	hypothetical protein	---	AT4G30050	-1.22	-0.28	-2.39	0.049907	0.11968	-4.90
253313_at	putative peroxidase peroxidase AT	---	AT4G33870	-1.22	-0.29	-2.39	0.049908	0.11968	-4.90
262569_at	hypothetical protein Strong similarit	---	AT1G15180	-1.36	-0.44	-2.39	0.049929	0.119715	-4.90
266148_x_a	En/Spm-like transposon protein rela	---	---	-1.24	-0.31	-2.38	0.049938	0.119715	-4.90
251847_at	tryptophan synthase alpha chain ; s	TSA1	AT3G54640	2.31	1.21	2.38	0.049938	0.119715	-4.90
257169_at	Expressed protein ; supported by fu	AtSec20	AT3G24315	-1.24	-0.31	-2.38	0.049954	0.119741	-4.90
264826_at	putative 1-aminocyclopropane-1-ca	2A6	AT1G03410	1.28	0.36	2.38	0.049969	0.119763	-4.90
257168_at	mrp protein, putative similar to mrp	HCF101	AT3G24430	-1.52	-0.61	-2.38	0.049988	0.119798	-4.90

253028_at	putative protein	pde191	AT4G38160	1.21	0.27	2.38	0.05004	0.11991	-4.90
267509_at	MADS-box protein (AGL20) ; supp	AGL20	AT2G45660	1.32	0.40	2.38	0.050057	0.119938	-4.90
265545_at	putative protein kinase contains a p	NCRK	AT2G28250	-1.24	-0.31	-2.38	0.050105	0.12004	-4.90
245709_at	putative protein	---	AT5G04320	1.28	0.35	2.38	0.050128	0.120081	-4.90
262819_at	putative cytochrome P450 strong si	CYP77B1	AT1G11600	-1.18	-0.24	-2.38	0.050135	0.120086	-4.90
256597_at	acidic ribosomal protein P2b (rpp2	---	AT3G28500	1.60	0.68	2.38	0.050199	0.120215	-4.90
248271_at	putative protein similar to unknown	---	AT5G53420	1.57	0.65	2.38	0.050199	0.120215	-4.90
265170_at	putative carbonic anhydrase	BCA3	AT1G23730	2.95	1.56	2.38	0.050219	0.120238	-4.90
256222_at	hypothetical protein predicted by ge	---	AT1G56210	-1.34	-0.43	-2.38	0.050219	0.120238	-4.90
256974_at	unknown protein similar to putative	---	---	-1.17	-0.23	-2.38	0.050233	0.120257	-4.90
260401_at	unknown protein similar to hypothet	---	AT1G69840	-1.26	-0.33	-2.38	0.05025	0.120264	-4.90
258436_at	putative RING zinc finger protein si	ATL2	AT3G16720	1.71	0.77	2.38	0.050251	0.120264	-4.90
248638_at	fatty acid elongase; beta-ketoacyl-C	KCS21	AT5G49070	-1.16	-0.21	-2.38	0.050252	0.120264	-4.90
262474_at	hypothetical protein identical to hyp	FU	AT1G50240	-1.23	-0.30	-2.38	0.050272	0.120302	-4.90
247780_at	dehydrodolichyl diphosphate - like	---	AT5G58770	1.71	0.77	2.38	0.050301	0.12035	-4.90
252930_at	putative endo-1,4-beta-glucanase	AtGH9B18	AT4G39010	-1.26	-0.34	-2.38	0.050303	0.12035	-4.91
251535_at	hypothetical protein ;supported by	---	AT3G58540	1.32	0.40	2.38	0.050328	0.120397	-4.91
262949_at	pectinesterase, putative similar to p	sks18	AT1G75790	-1.21	-0.28	-2.38	0.05035	0.120438	-4.91
266060_at	unknown protein unusual splice site	---	AT2G18630	-1.30	-0.38	-2.38	0.050362	0.120453	-4.91
262959_at	protein translation factor Sui1 hom	---	AT1G54290	1.24	0.31	2.38	0.050384	0.120492	-4.91
256104_at	trehalose-6-phosphate synthase, p	ATTPS2	AT1G16980	-1.18	-0.24	-2.38	0.050393	0.120502	-4.91
246662_at	putative protein	---	AT5G35290	-1.21	-0.27	-2.38	0.05042	0.120541	-4.91
265307_at	hypothetical protein predicted by ge	RIN13	AT2G20310	1.23	0.30	2.38	0.05042	0.120541	-4.91
259404_at	type 2A protein serine/threonine ph	ATB BETA	AT1G17720	1.16	0.21	2.38	0.050485	0.120674	-4.91
265297_at	putative disease resistance protein	---	AT2G14080	1.18	0.24	2.38	0.050486	0.120674	-4.91
255290_at	coded for by A. thaliana cDNA AA0	ATPC1	AT4G04640	-1.16	-0.21	-2.38	0.050528	0.120762	-4.91
246279_at	homeodomain protein	ATHB40	AT4G36740	-1.30	-0.38	-2.38	0.050536	0.120768	-4.91
254531_at	putative protein predicted protein,	---	AT4G19650	1.30	0.38	2.38	0.050576	0.120851	-4.91
246068_at	putative protein ribosomal protein S	---	AT5G20290	1.44	0.53	2.38	0.050627	0.12096	-4.91
246088_at	putative protein	---	AT5G20600	1.31	0.39	2.38	0.050638	0.120971	-4.91
264480_at	hypothetical protein predicted by ge	EFS	AT1G77300	-1.22	-0.29	-2.38	0.050647	0.120971	-4.91
252736_at	kinesin -like protein kinesin-like pro	TES	AT3G43210	-1.20	-0.26	-2.38	0.050648	0.120971	-4.91
253768_at	putative protein	---	AT4G28550	-1.35	-0.43	-2.37	0.050663	0.120995	-4.91
257344_s_a	pseudogene, putative mutator-like	---	---	-1.31	-0.39	-2.37	0.050691	0.121049	-4.91
248536_at	ankyrin-like protein	---	AT5G50140	-1.20	-0.27	-2.37	0.050796	0.121287	-4.91

265359_at	putative MYB family transcription fa	MYB7	AT2G16720	1.68	0.75	2.37	0.050812	0.121307	-4.92
251742_at	putative protein kinase serine threo	---	AT3G56050	1.20	0.26	2.37	0.050815	0.121307	-4.92
249462_at	putative protein predicted proteins,	EMB2744	AT5G39680	1.23	0.30	2.37	0.050864	0.121413	-4.92
249968_at	putative protein predicted proteins,	---	AT5G19070	-1.51	-0.60	-2.37	0.050889	0.121459	-4.92
248067_at	unknown protein	---	AT5G55600	1.26	0.33	2.37	0.050903	0.121479	-4.92
260905_at	hypothetical protein predicted by ge	---	AT1G02710	-1.16	-0.21	-2.37	0.050921	0.121509	-4.92
267425_at	putative berberine bridge enzyme	---	AT2G34810	-1.80	-0.85	-2.37	0.050976	0.121627	-4.92
AFFX-Athal-	Arabidopsis thaliana /REF=X52320	---	---	-1.30	-0.37	-2.37	0.051015	0.121709	-4.92
264977_at	unknown protein	---	AT1G27090	-1.37	-0.46	-2.37	0.051066	0.121816	-4.92
265197_at	putative glucosyl transferase	UGT73C1	AT2G36750	-1.16	-0.22	-2.37	0.051088	0.121857	-4.92
267311_at	hypothetical protein	---	AT2G34670	-1.16	-0.22	-2.37	0.051125	0.121933	-4.92
248005_at	unknown protein	---	AT5G56240	1.27	0.34	2.37	0.051133	0.121938	-4.92
260030_at	putative bZIP transcription factor sir	AtbZIP	AT1G68880	-1.20	-0.26	-2.37	0.051144	0.121952	-4.92
252862_at	putative L-ascorbate oxidase L-asc	---	AT4G39830	-1.66	-0.74	-2.37	0.051164	0.121987	-4.92
255783_at	hypothetical protein contains Pfam	iqd32	AT1G19870	1.33	0.41	2.37	0.05117	0.121989	-4.92
255890_at	rhodanese-like family protein predic	---	AT1G17850	1.39	0.47	2.37	0.051193	0.122023	-4.92
265203_at	unknown protein	---	AT2G36630	-1.25	-0.33	-2.37	0.051195	0.122023	-4.92
259517_at	hypothetical protein ; supported by	CAT1	AT1G20630	-1.35	-0.43	-2.37	0.051221	0.122064	-4.92
245494_at	salt-inducible protein homolog	---	AT4G16390	1.23	0.30	2.37	0.051223	0.122064	-4.92
257055_at	Expressed protein ; supported by fu	---	AT3G15351	1.20	0.27	2.37	0.051277	0.122179	-4.92
261165_at	dihydrolipoamide S-acetyltransfera	EMB3003	AT1G34430	-1.21	-0.28	-2.37	0.051326	0.122284	-4.93
261193_at	unknown protein ; supported by cDI	---	AT1G32920	1.75	0.80	2.37	0.051336	0.122291	-4.93
256259_at	hypothetical protein predicted by ge	---	AT3G12460	-1.29	-0.36	-2.37	0.05134	0.122291	-4.93
261457_at	Expressed protein ; supported by fu	---	AT1G21065	-1.23	-0.29	-2.37	0.051361	0.122328	-4.93
254872_at	putative protein several hypothetica	---	AT4G11560	1.19	0.25	2.37	0.051366	0.122329	-4.93
257234_at	hypothetical protein predicted by ge	---	AT3G14880	-1.28	-0.36	-2.36	0.05141	0.12242	-4.93
261411_at	histone H2B identical to GB:CAA7	HTB1	AT1G07790	1.33	0.42	2.36	0.051426	0.122441	-4.93
265942_at	putative casein kinase I ;supported	ckl5	AT2G19470	1.20	0.26	2.36	0.051429	0.122441	-4.93
248175_at	histone H2A (gb|AAF64418.1) ; su	RAT5	AT5G54640	1.22	0.29	2.36	0.05144	0.122454	-4.93
257571_at	hypothetical protein predicted by g	---	AT3G16870	1.43	0.51	2.36	0.051452	0.12247	-4.93
249710_at	glutamate-ammonia ligase (EC 6.3	GS2	AT5G35630	-1.22	-0.28	-2.36	0.051484	0.122523	-4.93
266068_at	putative geranylgeranyl pyrophosph	GGPS4	AT2G18640	-1.25	-0.32	-2.36	0.051485	0.122523	-4.93
254013_at	putative leucine-rich-repeat protein	---	AT4G26050	-1.33	-0.41	-2.36	0.051494	0.12253	-4.93
260182_at	unknown protein similar to IFA-bind	---	AT1G70750	1.23	0.29	2.36	0.051505	0.122544	-4.93
264438_at	putative 60S ribosomal protein L17	---	AT1G27400	1.39	0.47	2.36	0.05152	0.122568	-4.93

247975_at	putative protein similar to unknown	---	AT5G56800	-1.17	-0.23	-2.36	0.051532	0.122583	-4.93
257214_at	hypothetical protein ;supported by	---	AT3G15040	-1.25	-0.33	-2.36	0.051538	0.122584	-4.93
247759_at	copper transport protein - like ;supp	COPT3	AT5G59040	-1.18	-0.23	-2.36	0.051606	0.122734	-4.93
250519_at	GDSL-motif lipase/acylhydrolase-lik	---	AT5G08460	-1.24	-0.30	-2.36	0.051623	0.12276	-4.93
255138_at	extensin-like protein extensin class	---	AT4G08380	-1.18	-0.24	-2.36	0.051635	0.122776	-4.93
251508_at	putative protein mitochondrial RNA	---	AT3G58970	1.26	0.33	2.36	0.051643	0.122782	-4.93
261956_at	oxidoreductase, putative similar to	---	AT1G64590	-1.40	-0.48	-2.36	0.051673	0.122841	-4.93
250659_at	MtN21 nodulin protein-like	---	AT5G07050	-1.25	-0.32	-2.36	0.051682	0.122847	-4.93
250164_at	putative protein various predicted p	---	AT5G15280	-1.28	-0.36	-2.36	0.051689	0.122847	-4.93
253834_at	protein phosphatase homolog (PPH	---	AT4G27800	1.24	0.31	2.36	0.051692	0.122847	-4.93
251530_at	putative protein several hypothetica	---	AT3G58520	1.30	0.38	2.36	0.051723	0.122909	-4.93
249908_at	putative protein similar to unknown	---	AT5G22760	1.19	0.26	2.36	0.051741	0.122939	-4.93
246814_at	acyl carrier protein precursor - like	ACP5	AT5G27200	-1.18	-0.24	-2.36	0.051746	0.122939	-4.93
254107_at	putative protein putative glycerol-3-	---	AT4G25220	-1.27	-0.34	-2.36	0.051758	0.122954	-4.93
252787_at	putative protein several En/Spm-like	---	---	-1.15	-0.20	-2.36	0.05177	0.122969	-4.93
259974_at	putative phosphate transporter simi	---	AT1G76430	-1.26	-0.34	-2.36	0.051781	0.122983	-4.93
265681_at	putative protein kinase contains a p	---	AT2G24370	-1.18	-0.24	-2.36	0.051792	0.122995	-4.93
250226_at	putative protein contains similarity t	---	AT5G13780	1.24	0.31	2.36	0.051797	0.122996	-4.93
264060_at	hypothetical protein predicted by ge	---	AT2G27980	1.18	0.24	2.36	0.051812	0.123008	-4.94
261711_at	unknown protein similar to hypothet	---	AT1G32700	1.22	0.29	2.36	0.051813	0.123008	-4.94
262247_at	unknown protein contains similarity	D-CDES	AT1G48420	1.20	0.26	2.36	0.051819	0.123008	-4.94
258915_at	unknown protein similar to hypothet	VPS60.1	AT3G10640	-1.26	-0.34	-2.36	0.051824	0.123008	-4.94
263350_at	alanine-glyoxylate aminotransferase	AGT	AT2G13360	1.34	0.42	2.36	0.051864	0.123089	-4.94
259674_at	thaumatin-like protein similar to tha	---	AT1G77700	-1.23	-0.30	-2.36	0.051876	0.123106	-4.94
259966_at	unknown protein	SOB3	AT1G76500	-1.22	-0.29	-2.36	0.051888	0.123122	-4.94
250530_at	unknown protein	---	AT5G08630	1.22	0.29	2.36	0.05191	0.123148	-4.94
261179_at	unknown protein	---	AT1G04985	-1.24	-0.31	-2.36	0.05191	0.123148	-4.94
258556_at	UDP-glucose:sterol glucosyltransfe	---	AT3G07020	1.24	0.31	2.36	0.051959	0.123242	-4.94
253063_at	plasma membrane-type calcium AT	ACA2	AT4G37640	1.41	0.49	2.36	0.051962	0.123242	-4.94
266306_at	hypothetical protein predicted by gr	---	AT2G26970	1.23	0.30	2.36	0.05197	0.123242	-4.94
261959_s_a	polyprotein, putative similar to poly	---	---	-1.24	-0.31	-2.36	0.051972	0.123242	-4.94
244948_at	hypothetical protein	---	---	1.18	0.24	2.36	0.051976	0.123242	-4.94
258931_at	hypothetical protein similar to hypo	DML2	AT3G10010	1.38	0.46	2.36	0.052029	0.123352	-4.94
254454_at	hypothetical protein	EMB2271	AT4G21130	-1.21	-0.28	-2.36	0.052034	0.123353	-4.94
251082_at	chlorophyll a/b-binding protein CP2	---	AT5G01530	-1.15	-0.20	-2.36	0.052046	0.123368	-4.94

246874_at	arabinosidase - like protein arabinc	ASD2	AT5G26120	-1.22	-0.29	-2.36	0.052063	0.123394	-4.94
260844_at	peroxisomal targeting signal type 2	PEX7	AT1G29260	1.19	0.25	2.36	0.05209	0.123447	-4.94
245302_at	Expressed protein ; supported by cl	KAN3	AT4G17695	1.38	0.46	2.36	0.052106	0.123473	-4.94
256823_at	hypothetical protein predicted by ge	---	AT3G22220	1.24	0.31	2.36	0.052139	0.123529	-4.94
265335_at	Expressed protein ; supported by fu	---	AT2G18245	-1.16	-0.21	-2.35	0.052141	0.123529	-4.94
253989_at	uncharacterized protein ;supported	---	AT4G26130	1.35	0.43	2.35	0.052189	0.12363	-4.94
256525_at	unknown protein ;supported by full-	---	AT1G66180	-1.47	-0.55	-2.35	0.052199	0.123636	-4.94
245033_at	putative disease resistance protein	---	AT2G26380	-1.19	-0.26	-2.35	0.052202	0.123636	-4.94
245429_at	Bax inhibitor-1-like protein	---	AT4G17580	-1.16	-0.22	-2.35	0.052208	0.123636	-4.94
255074_at	putative protein RING-H2 zinc finge	---	AT4G09100	-1.22	-0.28	-2.35	0.052229	0.123668	-4.94
257084_at	unknown protein	---	AT3G20620	1.34	0.43	2.35	0.052232	0.123668	-4.94
255461_at	ent-kaurene synthetase A - like pro	GA1	AT4G02780	-1.22	-0.29	-2.35	0.052244	0.123671	-4.94
245694_at	EF - hand Calcium binding protein -	---	AT5G04170	-1.19	-0.25	-2.35	0.052244	0.123671	-4.94
247677_at	oxysterol-binding protein - like oxys	ORP3C	AT5G59420	1.18	0.24	2.35	0.052254	0.12368	-4.94
258900_at	putative 60S ribosomal protein L18	RPL18	AT3G05590	1.40	0.49	2.35	0.052288	0.12375	-4.94
256184_at	epsilon subunit of mitochondrial F1-	---	AT1G51650	1.31	0.39	2.35	0.052303	0.12377	-4.94
263834_at	hypothetical protein	---	AT2G40316	-1.23	-0.30	-2.35	0.052317	0.123791	-4.94
262373_at	hypothetical protein predicted by ge	---	AT1G73120	-1.53	-0.61	-2.35	0.052333	0.123813	-4.95
251778_at	putative protein various predicted p	ROPGEF6	AT3G55660	-1.26	-0.33	-2.35	0.052342	0.123813	-4.95
255918_at	putative protein	---	---	-1.17	-0.23	-2.35	0.052342	0.123813	-4.95
253338_at	somatic embryogenesis receptor-li	BAK1	AT4G33430	-1.21	-0.28	-2.35	0.052353	0.123826	-4.95
261543_at	unknown protein contains Pfam pro	---	AT1G63550	-1.26	-0.33	-2.35	0.052376	0.123866	-4.95
250094_at	2-hydroxyphytanoyl-CoA lyase-like	---	AT5G17380	1.61	0.68	2.35	0.052395	0.1239	-4.95
247701_at	putative protein many predicted pro	---	AT5G59900	1.19	0.25	2.35	0.052402	0.123902	-4.95
246749_at	putative protein ; supported by cDN	---	AT5G27830	1.31	0.39	2.35	0.05242	0.123917	-4.95
252042_at	putative serine/threonine protein ki	---	AT3G51990	-1.25	-0.33	-2.35	0.052425	0.123917	-4.95
249721_at	Expressed protein ; supported by fu	LSU4	AT5G24655	1.16	0.22	2.35	0.052429	0.123917	-4.95
262400_at	unknown protein ; supported by cDI	RTV1	AT1G49480	1.16	0.22	2.35	0.05243	0.123917	-4.95
265422_at	putative NADH-ubiquinone oxiredu	NDB4	AT2G20800	-1.23	-0.30	-2.35	0.052439	0.123926	-4.95
264542_at	hypothetical protein predicted by ge	---	AT1G55830	1.17	0.23	2.35	0.05252	0.124106	-4.95
254724_at	putative protein IFA-binding protein	---	AT4G13630	1.25	0.32	2.35	0.052529	0.124113	-4.95
253204_at	GTP binding protein beta subunit ;	AGB1	AT4G34460	1.16	0.22	2.35	0.052535	0.124115	-4.95
249133_at	putative protein strong similarity to	TAF4	AT5G43130	1.17	0.22	2.35	0.052544	0.124123	-4.95
245515_at	hypothetical protein	---	AT4G15810	1.41	0.49	2.35	0.052553	0.124131	-4.95
256390_at	putative MAP kinase similar to MAP	ATMKK8	AT3G06230	-1.18	-0.24	-2.35	0.052559	0.124132	-4.95

254340_at	putative protein hypothetical protei	---	AT4G22120	1.54	0.62	2.35	0.052581	0.124171	-4.95
253427_at	putative protein phosphate/phosph	---	AT4G32390	-1.20	-0.26	-2.35	0.052586	0.124171	-4.95
249048_at	auxin-repressed protein-like ;suppo	---	AT5G44300	-1.21	-0.27	-2.35	0.052659	0.124331	-4.95
264886_at	S-linalool synthase, putative simila	TPS04	AT1G61120	-4.07	-2.03	-2.35	0.052673	0.124349	-4.95
259652_at	unknown protein	HUB2	AT1G55250	1.30	0.38	2.35	0.052684	0.124362	-4.95
264567_s_a	putative peroxidase ATP12a Strong	---	AT1G05240	-1.23	-0.30	-2.35	0.052699	0.124385	-4.95
266329_at	unknown protein ; supported by cD	CRR3	AT2G01590	-1.47	-0.55	-2.35	0.052709	0.124396	-4.95
260701_at	heat shock transcription factor HSF	ATHSFA1D	AT1G32330	1.25	0.32	2.35	0.052715	0.124399	-4.95
249793_at	putative protein contains similarity t	---	AT5G23680	1.31	0.39	2.35	0.052767	0.124508	-4.95
260223_at	putative exonuclease contains Pfan	---	AT1G74390	1.20	0.27	2.35	0.052781	0.124527	-4.95
264320_at	unknown protein	---	AT1G04090	-1.16	-0.22	-2.35	0.052798	0.124554	-4.95
249310_at	putative protein contains similarity t	---	AT5G41520	1.23	0.30	2.35	0.052803	0.124554	-4.95
259559_at	hypothetical protein	WAK3	AT1G21240	1.34	0.42	2.35	0.052848	0.124646	-4.96
260894_at	hypothetical protein contains simila	---	AT1G29220	1.19	0.25	2.34	0.052957	0.124891	-4.96
264113_at	unknown protein	APG9	AT2G31260	1.25	0.32	2.34	0.052993	0.124964	-4.96
256657_at	unknown protein contains similarity	---	AT3G18860	1.20	0.26	2.34	0.05301	0.124991	-4.96
260793_at	unknown protein ;supported by full-	---	AT1G06190	1.21	0.27	2.34	0.053125	0.12525	-4.96
250023_at	beta-1,3-glucanase-like protein	---	AT5G18220	-1.24	-0.31	-2.34	0.053136	0.125261	-4.96
247255_at	putative protein similar to unknown	---	AT5G64780	1.43	0.52	2.34	0.053151	0.125285	-4.96
266960_at	putative retroelement pol polyprotei	---	---	-1.24	-0.31	-2.34	0.053177	0.125333	-4.96
246990_at	subtilisin-like serine protease ARA1	ARA12	AT5G67360	-1.37	-0.45	-2.34	0.053203	0.125381	-4.96
247905_at	unknown protein	---	AT5G57400	-1.16	-0.22	-2.34	0.053218	0.125403	-4.96
256266_at	unknown protein ; supported by cDI	---	AT3G12320	1.45	0.53	2.34	0.053276	0.125511	-4.96
246392_at	hypothetical protein predicted by ge	---	AT1G58120	-1.17	-0.23	-2.34	0.053279	0.125511	-4.96
261092_at	unknown protein	---	AT1G62870	-1.16	-0.21	-2.34	0.053283	0.125511	-4.96
260154_at	putative histone H2A similar to histo	HTA9	AT1G52740	1.30	0.38	2.34	0.053286	0.125511	-4.96
262204_at	unknown protein ; supported by ful	---	AT2G01100	1.20	0.26	2.34	0.053305	0.125542	-4.96
257143_at	cytochrome P450, putative contain	CYP705A2	AT3G20110	1.24	0.31	2.34	0.053331	0.125591	-4.96
256779_at	beta-fructofuranosidase, putative s	AtcwINV5	AT3G13784	-1.16	-0.21	-2.34	0.053351	0.125625	-4.96
264085_at	putative glutamyl tRNA reductase	HEMA3	AT2G31250	-1.18	-0.24	-2.34	0.053357	0.125626	-4.96
258230_s_a	hypothetical protein similar to hypo	ARI13	AT3G27710	-1.17	-0.23	-2.34	0.05343	0.125785	-4.97
260677_at	translation elongation factor EF-1 a	RNL	AT1G07910	1.38	0.47	2.34	0.053458	0.12582	-4.97
248480_at	ATP-dependent Clp protease ATP-I	CLPC1	AT5G50920	1.19	0.25	2.34	0.053461	0.12582	-4.97
260505_at	Cyclin, putative similar to GB:CAB7	CYCA3;4	AT1G47230	-1.19	-0.24	-2.34	0.053461	0.12582	-4.97
265502_at	putative poly(A) binding protein	---	AT2G15500	-1.25	-0.32	-2.34	0.053567	0.126045	-4.97

263085_at	hypothetical protein predicted by ge	ARI12	AT2G16090	1.28	0.36	2.34	0.053568	0.126045	-4.97
253282_at	putative protein hypothetical protei	LEJ1	AT4G34120	1.16	0.22	2.34	0.053618	0.126139	-4.97
267370_at	unknown protein ;supported by full-	---	AT2G44525	1.16	0.21	2.34	0.053619	0.126139	-4.97
246600_at	putative protein disease resistance	SAG101	AT5G14930	-1.43	-0.51	-2.34	0.053624	0.126139	-4.97
267614_at	putative cytochrome P450	BAS1	AT2G26710	-1.79	-0.84	-2.34	0.053635	0.126143	-4.97
262409_at	hypothetical protein predicted by ge	---	---	-1.25	-0.33	-2.34	0.053637	0.126143	-4.97
267141_at	putative MYB family transcription fa	---	AT2G38090	1.28	0.36	2.34	0.053649	0.126158	-4.97
249956_at	putative protein CGI-66 protein, Ho	---	AT5G18940	1.20	0.26	2.33	0.053671	0.126196	-4.97
266590_at	hypothetical protein predicted by ge	BAG6	AT2G46240	-1.38	-0.47	-2.33	0.05369	0.126229	-4.97
263828_at	putative GDSL-motif lipase/hydrolas	---	AT2G40250	-1.27	-0.34	-2.33	0.053723	0.126293	-4.97
249401_at	putative protein LIM7, Lily, EMBL:L	---	AT5G40260	-1.17	-0.23	-2.33	0.053749	0.126341	-4.97
263359_at	putative lysosomal acid lipase	ATLIP1	AT2G15230	1.25	0.32	2.33	0.053762	0.126358	-4.97
263567_at	hypothetical protein predicted by ge	---	AT2G15440	-1.24	-0.31	-2.33	0.05383	0.126499	-4.97
262128_at	late embryogenesis-abundant prote	---	AT1G52690	-3.17	-1.66	-2.33	0.053833	0.126499	-4.97
249255_at	Na+/H+ antiporter-like protein	CHX18	AT5G41610	1.24	0.31	2.33	0.053846	0.126507	-4.97
257518_at	hypothetical protein	---	AT3G03880	1.16	0.22	2.33	0.053847	0.126507	-4.97
245305_at	Expressed protein ; supported by fu	---	AT4G17215	1.96	0.97	2.33	0.053871	0.126543	-4.97
263971_at	hypothetical protein predicted by ge	AtRLP29	AT2G42800	-1.26	-0.33	-2.33	0.053874	0.126543	-4.97
262200_at	unknown protein similar to membra	---	AT2G01070	-1.26	-0.34	-2.33	0.053884	0.126555	-4.97
249788_at	putative protein contains similarity t	ATXR6	AT5G24330	-1.32	-0.40	-2.33	0.053893	0.126562	-4.98
267143_at	putative peptide/amino acid transpo	---	AT2G38100	-1.21	-0.28	-2.33	0.053901	0.126568	-4.98
249372_at	glucose-6-phosphate dehydrogenas	G6PD6	AT5G40760	1.43	0.52	2.33	0.053922	0.126604	-4.98
260888_at	hypothetical protein similar to allerg	---	AT1G29140	-1.19	-0.26	-2.33	0.053931	0.126612	-4.98
263938_at	hypothetical protein predicted by ge	---	AT2G35900	1.20	0.26	2.33	0.053941	0.126622	-4.98
256077_at	hypothetical protein contains simila	---	AT1G18090	-1.26	-0.33	-2.33	0.053951	0.12663	-4.98
259408_at	protein phosphatase 2A 65 kDa reg	PP2AA2	AT3G25800	1.17	0.23	2.33	0.053955	0.12663	-4.98
245034_at	putative serpin	---	AT2G26390	-1.27	-0.35	-2.33	0.053991	0.126702	-4.98
246364_at	hypothetical protein	---	---	-1.17	-0.23	-2.33	0.054005	0.126711	-4.98
260577_at	hypothetical protein predicted by ge	---	AT2G47340	-1.20	-0.26	-2.33	0.054007	0.126711	-4.98
264302_at	ATPase 70 kDa subunit, putative s	VHA-A	AT1G78900	-1.23	-0.30	-2.33	0.054032	0.126745	-4.98
246138_at	putative protein predicted proteins f	---	AT5G19870	-1.16	-0.21	-2.33	0.054032	0.126745	-4.98
261057_at	hypothetical protein predicted by ge	---	AT1G01230	-1.21	-0.27	-2.33	0.054104	0.126894	-4.98
262898_at	hypothetical protein predicted by ge	---	AT1G59850	-1.23	-0.30	-2.33	0.054107	0.126894	-4.98
260660_at	hypothetical protein contains Pfam	---	AT1G19485	1.26	0.33	2.33	0.054117	0.126905	-4.98
267165_at	putative receptor-like protein kinase	RLK	AT2G37710	1.59	0.67	2.33	0.054123	0.126906	-4.98

262671_at	calcium-dependent protein kinase,	CPK29	AT1G76040	1.28	0.36	2.33	0.054136	0.126925	-4.98
263148_at	ubiquitin, putative similar to ubiquit	---	AT1G53950	-1.22	-0.28	-2.33	0.054166	0.126982	-4.98
261942_at	unknown protein similar to putative	AGL87	AT1G22590	-1.44	-0.52	-2.33	0.054201	0.127049	-4.98
267437_at	hypothetical protein predicted by ge	---	AT2G19200	-1.20	-0.26	-2.33	0.054212	0.127057	-4.98
258794_at	ankyrin-like protein similar to ankyr	---	AT3G04710	1.51	0.60	2.33	0.054215	0.127057	-4.98
245649_at	F5A9.21 unknown protein; similar t	---	AT1G24706	1.25	0.32	2.33	0.054296	0.127233	-4.98
263352_at	En/Spm-like transposon protein rela	---	AT2G22080	1.32	0.41	2.33	0.054308	0.127233	-4.98
261403_at	unknown protein ;supported by full-	SYP52	AT1G79590	-1.17	-0.23	-2.33	0.054312	0.127233	-4.98
262646_at	aspartate aminotransferase nearly	ASP4	AT1G62800	-1.46	-0.54	-2.33	0.054325	0.127233	-4.98
264643_at	unknown protein	PGSIP5	AT1G08990	-1.18	-0.23	-2.33	0.054326	0.127233	-4.98
254341_at	serine/threonine protein kinase like	SRF8	AT4G22130	-1.65	-0.72	-2.33	0.054328	0.127233	-4.98
253783_at	putative protein predicted protein, A	NPGR2	AT4G28600	-1.22	-0.29	-2.33	0.054333	0.127233	-4.98
262253_s_a	unknown protein contains similarity	---	AT1G53880	1.23	0.30	2.33	0.054339	0.127233	-4.98
257795_at	hypothetical protein predicted by ge	---	AT3G15910	-1.27	-0.34	-2.33	0.05434	0.127233	-4.98
250292_at	putative protein predicted proteins,	JAZ10	AT5G13220	-2.34	-1.23	-2.33	0.054398	0.127355	-4.98
250869_at	Terminal flower1 (TFL1) ; supported	TFL1	AT5G03840	-1.20	-0.26	-2.33	0.054413	0.127377	-4.98
254877_at	putative protein threonine dehydrat	ATSR	AT4G11640	-1.23	-0.29	-2.33	0.054422	0.127384	-4.99
265044_at	hypothetical protein Similar to hum	VPS2.3	AT1G03950	-1.26	-0.34	-2.33	0.054435	0.127402	-4.99
266970_at	hypothetical protein predicted by ge	---	AT2G39560	-1.21	-0.28	-2.33	0.054448	0.127419	-4.99
248020_at	putative protein strong similarity to	---	AT5G56490	-1.17	-0.22	-2.32	0.054499	0.127513	-4.99
261802_at	hypothetical protein similar to hypot	---	AT1G30550	1.21	0.27	2.32	0.054502	0.127513	-4.99
252765_at	putative protein hypothetical protein	---	AT3G42800	-1.42	-0.50	-2.32	0.054505	0.127513	-4.99
260274_at	putative glycerol kinase similar to G	NHO1	AT1G80460	1.27	0.34	2.32	0.054534	0.127556	-4.99
260385_at	putative flavonol sulfotransferase si	SOT18	AT1G74090	1.26	0.33	2.32	0.054534	0.127556	-4.99
254092_at	respiratory burst oxidase - like prot	---	AT4G25090	-1.15	-0.21	-2.32	0.054541	0.127558	-4.99
258540_at	hypothetical protein predicted by ge	---	AT3G06990	-1.20	-0.26	-2.32	0.054552	0.127565	-4.99
251146_at	neoxanthin cleavage enzyme nc1	CCD1	AT3G63520	1.29	0.37	2.32	0.054555	0.127565	-4.99
252540_at	putative protein CDP-alcohol phosp	---	AT3G45740	-1.19	-0.25	-2.32	0.054599	0.127655	-4.99
253720_at	acid phosphatase-like protein acid	---	AT4G29270	-1.18	-0.24	-2.32	0.054634	0.127708	-4.99
259914_at	hypothetical protein predicted by ge	---	AT1G72640	-1.26	-0.34	-2.32	0.054643	0.127708	-4.99
258008_at	putative late embryogenesis abund	---	AT3G19430	-1.20	-0.26	-2.32	0.054646	0.127708	-4.99
247752_at	putative protein	---	AT5G59060	-1.16	-0.21	-2.32	0.054649	0.127708	-4.99
248843_at	homeobox protein	HB-7	AT5G46880	-1.23	-0.30	-2.32	0.05465	0.127708	-4.99
245312_at	Expressed protein ; supported by fu	---	AT4G14600	1.27	0.34	2.32	0.054661	0.127721	-4.99
255060_at	putative protein TMV resistance pr	---	AT4G09430	-1.23	-0.30	-2.32	0.054674	0.127739	-4.99

267526_at	photosystem II reaction center 6.1K	PSBW	AT2G30570	-1.15	-0.21	-2.32	0.054687	0.127756	-4.99
252454_at	putative protein various predicted p	---	AT3G47130	-1.16	-0.22	-2.32	0.054707	0.12779	-4.99
266391_at	putative strictosidine synthase ident	---	AT2G41290	-1.27	-0.35	-2.32	0.054725	0.127815	-4.99
264585_at	auxin-resistance protein AXR1 E1 u	AXR1	AT1G05180	1.16	0.21	2.32	0.054731	0.127815	-4.99
253840_at	putative acyl-CoA binding protein s	ACBP2	AT4G27780	1.27	0.34	2.32	0.054735	0.127815	-4.99
254056_at	putative protein Group I Pectineste	---	AT4G25250	-1.21	-0.28	-2.32	0.054766	0.127875	-4.99
250539_at	WD-repeat protein-like ; supported	---	AT5G08560	1.26	0.33	2.32	0.054776	0.127885	-4.99
264185_at	unknown protein ;supported by full-	---	AT1G54780	-1.19	-0.25	-2.32	0.054795	0.127916	-4.99
254273_at	glycoprotein endopeptidase - like p	---	AT4G22720	1.32	0.40	2.32	0.054808	0.127935	-4.99
266252_at	hypothetical protein predicted by ge	---	AT2G27520	-1.21	-0.27	-2.32	0.054866	0.128056	-4.99
246550_at	putative protein predicted protein, A	---	AT5G14920	-2.08	-1.06	-2.32	0.05489	0.128099	-4.99
255036_at	putative protein similarity RING zin	---	AT4G09560	-1.38	-0.47	-2.32	0.054913	0.12814	-4.99
256970_at	ABC transporter, putative similar to	---	AT3G21090	-1.22	-0.28	-2.32	0.054983	0.128289	-5.00
266439_s_a	hypothetical protein predicted by gr	---	AT2G43200	1.21	0.27	2.32	0.054992	0.128298	-5.00
262206_at	putative ubiquinol-cytochrome c red	---	AT2G01090	-1.25	-0.33	-2.32	0.055011	0.128329	-5.00
265189_at	unknown protein ; supported by cD	---	AT1G23840	1.49	0.57	2.32	0.055028	0.128355	-5.00
262668_at	flavin-containing amine oxidase cor	LDL1	AT1G62830	1.21	0.27	2.32	0.055044	0.12838	-5.00
260489_at	hypothetical protein ; supported by	---	AT1G51610	-1.19	-0.25	-2.32	0.05506	0.128405	-5.00
245908_at	laccase-like protein laccase - Acer	LAC14	AT5G09360	-1.34	-0.42	-2.32	0.05507	0.128413	-5.00
255701_at	predicted protein of unknown functi	JLO	AT4G00220	-1.18	-0.23	-2.32	0.055075	0.128413	-5.00
246546_at	voltage-dependent anion-selective c	VDAC3	AT5G15090	1.31	0.39	2.32	0.055121	0.128507	-5.00
259755_at	unknown protein similar to glucosar	---	AT1G71070	-1.24	-0.32	-2.32	0.055144	0.128548	-5.00
250575_at	putative protein	---	AT5G08240	1.39	0.48	2.32	0.055166	0.128586	-5.00
264486_at	hypothetical protein contains simila	---	AT1G77180	1.24	0.31	2.32	0.055184	0.12861	-5.00
253516_at	hypothetical protein	---	AT4G31360	-1.34	-0.42	-2.32	0.055188	0.12861	-5.00
265950_s_a	putative protein kinase contains a p	---	AT2G18530	-1.21	-0.27	-2.31	0.055307	0.128874	-5.00
247092_at	putative protein contains similarity t	ATFOLT1	AT5G66380	-1.25	-0.32	-2.31	0.055329	0.128908	-5.00
246651_at	adenylate kinase -like protein aden	---	AT5G35170	-1.29	-0.37	-2.31	0.055333	0.128908	-5.00
263635_at	hypothetical protein predicted by ge	---	---	-1.16	-0.21	-2.31	0.055376	0.128995	-5.00
255142_at	stromal ascorbate peroxidase ; sup	SAPX	AT4G08390	2.03	1.03	2.31	0.055381	0.128995	-5.00
266771_s_a	unknown protein	---	AT2G03010	1.19	0.25	2.31	0.055401	0.129028	-5.00
266010_at	putative C2H2-type zinc finger prote	---	AT2G37430	3.64	1.87	2.31	0.055413	0.129043	-5.00
257528_at	hypothetical protein predicted by ge	---	AT3G02125	-1.18	-0.24	-2.31	0.05542	0.129046	-5.00
247548_at	putative protein various predicted p	---	AT5G61400	1.28	0.36	2.31	0.055436	0.129059	-5.00
259752_at	spore coat protein-like protein simila	LPR2	AT1G71040	1.30	0.38	2.31	0.055437	0.129059	-5.00

257290_at	hypothetical protein predicted by ge	---	AT3G15550	-1.18	-0.24	-2.31	0.055449	0.129074	-5.00
251726_at	protein kinase NPK1-related protei	---	AT3G56280	-1.15	-0.20	-2.31	0.055464	0.129095	-5.00
257691_at	hypothetical protein predicted by ge	FLA14	AT3G12660	-1.30	-0.38	-2.31	0.055509	0.129187	-5.01
247103_at	putative protein similar to unknown	DAR7	AT5G66610	-1.19	-0.25	-2.31	0.05554	0.129246	-5.01
266121_at	unknown protein ; supported by cD	---	AT2G02160	1.28	0.35	2.31	0.05555	0.129257	-5.01
266930_at	hypothetical protein predicted by ge	---	AT2G45930	-1.25	-0.33	-2.31	0.055557	0.129258	-5.01
266054_at	hypothetical protein predicted by ge	---	AT2G40640	1.26	0.34	2.31	0.055584	0.129302	-5.01
251048_at	putative protein potassium channel	---	AT5G02410	1.23	0.30	2.31	0.055587	0.129302	-5.01
260205_at	hypothetical protein predicted by ge	TIFY7	AT1G70700	-1.56	-0.65	-2.31	0.055619	0.129365	-5.01
245935_at	hypothetical protein	---	AT5G19840	1.18	0.24	2.31	0.055626	0.129367	-5.01
253485_at	Expressed protein ; supported by fu	WRKY18	AT4G31800	-1.50	-0.59	-2.31	0.055642	0.129391	-5.01
252808_at	putative protein various predicted p	---	---	-1.23	-0.30	-2.31	0.055657	0.129391	-5.01
248897_at	KCO-like protein 3 (emb|CAB40380	KCO3	AT5G46360	-1.22	-0.29	-2.31	0.055658	0.129391	-5.01
255846_at	putative SWI/SNF complex subunit	ATSWI3B	AT2G33610	1.27	0.34	2.31	0.055659	0.129391	-5.01
258039_at	unknown protein ;supported by full-	---	AT3G21200	-1.20	-0.26	-2.31	0.055668	0.129398	-5.01
261718_at	wall-associated kinase, putative sir	---	AT1G18390	1.76	0.81	2.31	0.055675	0.129403	-5.01
261710_at	hypothetical protein identical to hyp	---	AT1G32730	1.24	0.30	2.31	0.055705	0.129418	-5.01
251107_at	putative protein several hypothetica	---	AT5G01610	1.25	0.32	2.31	0.055706	0.129418	-5.01
256130_at	unknown protein contains Pfam pro	---	AT1G18170	1.24	0.31	2.31	0.055706	0.129418	-5.01
247825_at	RNA/ssDNA-binding protein - like F	TAF15b	AT5G58470	-1.22	-0.29	-2.31	0.055706	0.129418	-5.01
264418_at	nuclear ribonucleoprotein, putative	---	AT1G43190	-1.30	-0.38	-2.31	0.055714	0.129418	-5.01
255628_at	coded for by A. thaliana cDNA T45	GIF3	AT4G00850	1.20	0.27	2.31	0.055716	0.129418	-5.01
245911_at	oligosaccharyl transferase STT3-lik	STT3A	AT5G19690	1.17	0.23	2.31	0.055725	0.129425	-5.01
264860_at	hypothetical protein contains ATP/G	---	AT1G24290	-1.17	-0.23	-2.31	0.05578	0.12954	-5.01
257713_at	succinate dehydrogenase iron-prot	SDH2-1	AT3G27380	1.37	0.45	2.31	0.055801	0.129575	-5.01
260237_at	putative MYB family transcription fa	MYB95	AT1G74430	-1.58	-0.66	-2.31	0.055846	0.129667	-5.01
253392_at	potassium channel protein AtKC po	ATKC1	AT4G32650	1.81	0.86	2.31	0.055858	0.129681	-5.01
255436_at	Expressed protein ; supported by cl	---	AT4G03150	1.15	0.21	2.31	0.055869	0.129692	-5.01
266199_at	putative calcium-dependent protein	CPK20	AT2G38910	-1.18	-0.24	-2.31	0.055874	0.129692	-5.01
262364_at	disease resistance protein, putative	---	AT1G72860	-1.18	-0.23	-2.31	0.055889	0.129714	-5.01
245310_at	hypothetical protein ;supported by f	RALFL31	AT4G13950	-1.56	-0.64	-2.31	0.055924	0.129783	-5.01
259158_at	hypothetical protein predicted by g	---	AT3G05430	-1.16	-0.22	-2.31	0.055941	0.129809	-5.01
256828_at	unknown protein	---	AT3G22968	1.46	0.55	2.31	0.055961	0.12984	-5.01
259873_s_a	putative translation initiation factor I	---	AT1G76720	-1.28	-0.36	-2.31	0.056013	0.129949	-5.01
262623_at	integral membrane protein, putative	---	AT1G06470	-1.24	-0.31	-2.31	0.05604	0.129997	-5.01

259378_at	unknown protein supported by full-	---	AT3G16310	1.47	0.56	2.30	0.056066	0.130045	-5.02
258665_at	thioredoxin-like protein similar to thi	ATH9	AT3G08710	1.41	0.49	2.30	0.056108	0.13013	-5.02
257889_at	S1 self-incompatibility protein, puta	---	AT3G17080	-1.25	-0.32	-2.30	0.056142	0.130196	-5.02
252200_at	anthranilate N-hydroxycinnamoyl/b	---	AT3G50280	1.74	0.80	2.30	0.056174	0.130257	-5.02
253357_at	Dem -like protein Dem (defective e	---	AT4G33400	-1.19	-0.26	-2.30	0.056189	0.130277	-5.02
244917_at	hypothetical protein	---	---	-1.19	-0.25	-2.30	0.056209	0.13031	-5.02
245091_at	unknown protein	---	AT2G40910	-1.21	-0.28	-2.30	0.056242	0.130374	-5.02
256664_at	DNA-3-methlyadenine glycosylase	---	AT3G12040	1.27	0.35	2.30	0.056254	0.130388	-5.02
249907_at	putative protein DNA repair protein	RAD5	AT5G22750	1.18	0.24	2.30	0.056284	0.130431	-5.02
262643_at	unknown protein ;supported by full-	---	AT1G62770	-1.39	-0.48	-2.30	0.056287	0.130431	-5.02
257078_at	putative MAP kinase very similar to	---	AT3G15220	1.19	0.26	2.30	0.05629	0.130431	-5.02
252268_at	kinesin-like protein several kinesin-	---	AT3G49650	-1.29	-0.36	-2.30	0.056314	0.130473	-5.02
250607_at	putative protein mammalian inosito	IPK2a	AT5G07370	1.15	0.21	2.30	0.056351	0.130547	-5.02
246508_at	sugar transporter-like protein putat	PGLCT	AT5G16150	-1.25	-0.33	-2.30	0.05636	0.130547	-5.02
248234_at	putative protein contains similarity t	---	AT5G53850	-1.17	-0.23	-2.30	0.056362	0.130547	-5.02
247056_at	SWI2/SNF2-like protein (gb|AAD28	CHR1	AT5G66750	1.20	0.26	2.30	0.056373	0.130559	-5.02
249168_at	putative protein strong similarity to	---	AT5G42870	1.23	0.30	2.30	0.056478	0.130789	-5.02
264653_at	unknown protein Contains similarit	AMI1	AT1G08980	-1.30	-0.38	-2.30	0.05649	0.130802	-5.02
258859_at	Expressed protein ; supported by fu	---	AT3G02120	-1.16	-0.21	-2.30	0.056507	0.130817	-5.02
264397_at	hypothetical protein	---	AT1G11820	-1.30	-0.38	-2.30	0.056508	0.130817	-5.02
250685_at	kinesin heavy chain-like protein	---	AT5G06670	1.15	0.20	2.30	0.05655	0.130901	-5.02
260513_at	cyanogenic beta-glucosidase, puta	BGLU36	AT1G51490	-1.19	-0.25	-2.30	0.056567	0.130928	-5.02
263963_at	putative DNA-binding protein RAV2	---	AT2G36080	-1.32	-0.40	-2.30	0.056594	0.130978	-5.02
259717_at	putative cleavage and polyadenylat	CPSF73-I	AT1G61010	1.24	0.31	2.30	0.056627	0.131029	-5.03
248997_at	beta-amylase-like	BMY2	AT5G45300	1.31	0.39	2.30	0.056628	0.131029	-5.03
262659_at	putative nucleoside triphosphatase	---	AT1G14240	-1.20	-0.26	-2.30	0.056638	0.131039	-5.03
262605_at	hypothetical protein Strong similarit	---	AT1G15170	1.82	0.86	2.30	0.056651	0.131055	-5.03
267486_at	putative protein kinase contains a p	APK2B	AT2G02800	1.33	0.41	2.30	0.056701	0.131158	-5.03
250116_at	putative protein similar to unknown	---	AT5G16430	-1.27	-0.34	-2.30	0.056718	0.131178	-5.03
260388_at	hypothetical protein predicted by g	---	AT1G74070	-1.46	-0.54	-2.30	0.056721	0.131178	-5.03
247321_s_a	phosphatidylinositol 4-kinase (emb|	PI-4KBETA	AT5G09350	1.28	0.35	2.30	0.056743	0.131216	-5.03
248406_at	pectinesterase	---	AT5G51490	-1.30	-0.38	-2.30	0.056761	0.131239	-5.03
253682_at	cytidine deaminase 5 (CDA5)	---	AT4G29640	-1.25	-0.33	-2.30	0.056765	0.131239	-5.03
256270_at	unknown protein ; supported by cDI	---	AT3G12300	1.20	0.27	2.30	0.056842	0.131393	-5.03
260027_at	unknown protein	CPuORF34	AT1G29950	1.29	0.37	2.30	0.056843	0.131393	-5.03

260965_s_a	hypothetical protein predicted by ge	---	---	-1.17	-0.22	-2.29	0.056868	0.131439	-5.03
260162_at	unknown protein	GC5	AT1G79830	1.15	0.21	2.29	0.056901	0.13149	-5.03
263291_at	unknown protein	---	AT2G10920	1.20	0.26	2.29	0.056904	0.13149	-5.03
249583_at	CALMODULIN-RELATED PROTE	TCH2	AT5G37770	-1.93	-0.95	-2.29	0.056909	0.13149	-5.03
263597_at	hypothetical protein predicted by ge	---	AT2G01870	-1.59	-0.66	-2.29	0.056914	0.13149	-5.03
248249_at	protein phosphatase 2C-like ; supp	---	AT5G53140	1.19	0.25	2.29	0.056935	0.13152	-5.03
244915_s_a	hypothetical protein	---	---	-1.19	-0.25	-2.29	0.056938	0.13152	-5.03
256302_at	Expressed protein ; supported by fu	---	AT1G69526	-1.25	-0.32	-2.29	0.056949	0.131532	-5.03
266470_at	putative non-LTR retroelement reve	---	---	-1.38	-0.47	-2.29	0.056956	0.131536	-5.03
264893_at	unknown protein similar to unknowr	---	AT1G23140	1.26	0.33	2.29	0.056973	0.131561	-5.03
260535_at	hypothetical protein predicted by ge	---	AT2G43390	-1.16	-0.22	-2.29	0.057009	0.131631	-5.03
263033_s_a	unknown protein ; supported by full-	---	AT1G23950	-1.34	-0.42	-2.29	0.057021	0.131634	-5.03
265386_at	unknown protein ;supported by full-	---	AT2G20930	-1.18	-0.24	-2.29	0.057022	0.131634	-5.03
249648_at	putative protein hypothetical protei	---	AT5G37050	-1.30	-0.38	-2.29	0.057053	0.131689	-5.03
263885_at	unknown protein	---	AT2G36940	-1.19	-0.25	-2.29	0.057058	0.131689	-5.03
267164_at	CER1-like protein may be involved	---	AT2G37700	-1.20	-0.26	-2.29	0.057071	0.131708	-5.03
258990_at	unknown protein ;supported by full-	---	AT3G08840	1.35	0.44	2.29	0.057086	0.131728	-5.03
249025_at	putative protein contains similarity t	---	AT5G44720	-1.40	-0.49	-2.29	0.0571	0.131746	-5.03
256020_at	glutamyl-tRNA reductase, putative	HEMA1	AT1G58290	-1.32	-0.40	-2.29	0.057113	0.131765	-5.03
256799_at	unknown protein ; supported by cD	---	AT3G18560	1.57	0.65	2.29	0.057127	0.131778	-5.03
252567_at	zinc finger -like protein zinc finger p	---	AT3G46070	-1.18	-0.24	-2.29	0.057136	0.131778	-5.03
250706_at	deoxyhypusine synthase ;supporte	DHS	AT5G05920	1.24	0.31	2.29	0.057137	0.131778	-5.03
261170_at	growth regulator protein similar to G	---	AT1G04910	-1.20	-0.27	-2.29	0.057173	0.131849	-5.04
249945_at	60S ribosomal protein L10A ; supp	---	AT5G22440	1.50	0.58	2.29	0.057184	0.13186	-5.04
264668_at	putative 2,3-bisphosphoglycerate-i	---	AT1G09780	1.27	0.35	2.29	0.057196	0.131875	-5.04
248096_at	embryo-specific protein 1; Ca2+-bir	---	AT5G55240	-1.19	-0.25	-2.29	0.057221	0.131918	-5.04
250221_at	protoporphyrinogen oxidase - like p	HEMG2	AT5G14220	1.33	0.41	2.29	0.057241	0.131945	-5.04
258410_at	putative ribosomal protein similar to	---	AT3G16780	1.57	0.65	2.29	0.057244	0.131945	-5.04
250422_at	putative protein KIAA0255 gene, H	---	AT5G10840	-1.35	-0.43	-2.29	0.057255	0.131958	-5.04
246063_at	putative protein predicted proteins,	---	AT5G19340	-1.18	-0.24	-2.29	0.057274	0.131982	-5.04
259495_at	NBS/LRR disease resistance prote	---	AT1G15890	-1.23	-0.30	-2.29	0.057281	0.131982	-5.04
255178_at	may be a pseudogene	---	---	-1.17	-0.23	-2.29	0.057283	0.131982	-5.04
258753_at	hypothetical protein predicted by ge	ATEXO70H	AT3G09530	-1.15	-0.20	-2.29	0.05729	0.131983	-5.04
264297_at	hypothetical protein similar to hypot	---	AT1G78710	-1.15	-0.20	-2.29	0.057295	0.131983	-5.04
260756_at	hypothetical protein contains simila	---	AT1G48970	1.17	0.23	2.29	0.057327	0.132038	-5.04

267463_at	Expressed protein ; supported by fu	---	AT2G33845	1.41	0.49	2.29	0.057334	0.132038	-5.04
265071_at	transcription initiation factor TFIID-2	TBP2	AT1G55520	1.20	0.27	2.29	0.057336	0.132038	-5.04
259079_at	unknown protein	---	AT3G04950	1.28	0.36	2.29	0.057349	0.132045	-5.04
247981_at	putative protein similar to unknown	MIOX5	AT5G56640	-1.17	-0.23	-2.29	0.057353	0.132045	-5.04
245715_s_a	Expressed protein ; supported by cl	---	AT5G08670	1.22	0.29	2.29	0.057357	0.132045	-5.04
263490_at	F-box protein ORE9, AtFBL7 identi	MAX2	AT2G42620	-1.43	-0.51	-2.29	0.057367	0.132055	-5.04
245919_at	putative protein various predicted p	---	AT5G28780	-1.16	-0.21	-2.29	0.05739	0.132094	-5.04
251155_at	putative protein outer envelope me	---	AT3G63160	1.17	0.23	2.29	0.05742	0.13215	-5.04
264256_at	putative importin alpha similar to GI	IMPA-4	AT1G09270	-1.17	-0.23	-2.29	0.057451	0.132209	-5.04
246154_at	putative protein predicted protein, A	---	AT5G19940	-1.20	-0.26	-2.29	0.057458	0.132213	-5.04
246916_at	disease resistance protein - like dis	AtRLP52	AT5G25910	-1.16	-0.22	-2.29	0.057496	0.132276	-5.04
257562_at	hypothetical protein	---	---	-1.24	-0.31	-2.29	0.057497	0.132276	-5.04
256742_at	transcription initiation factor IIB, pu	---	AT3G29380	-1.19	-0.25	-2.29	0.057549	0.132381	-5.04
264126_at	hypothetical protein predicted by ge	NUA	AT1G79280	1.16	0.22	2.29	0.057556	0.132384	-5.04
253913_at	myosin heavy chain - like protein m	VIIIB	AT4G27370	-1.18	-0.24	-2.29	0.057572	0.132408	-5.04
245417_at	phosphoribosylglycinamide formyltr	---	AT4G17360	1.34	0.42	2.29	0.057583	0.132411	-5.04
247298_at	glucosidase II alpha subunit	RSW3	AT5G63840	1.19	0.25	2.29	0.057585	0.132411	-5.04
254291_at	putative protein UDP-galactose tra	UTR2	AT4G23010	1.33	0.41	2.28	0.057705	0.132666	-5.04
261065_at	hypothetical protein predicted by ge	---	AT1G07500	-1.27	-0.35	-2.28	0.057712	0.132666	-5.04
255680_at	hypothetical protein	---	AT4G00530	1.26	0.34	2.28	0.057713	0.132666	-5.04
252131_at	BCS1 protein-like protein Homo sa	BCS1	AT3G50930	2.38	1.25	2.28	0.057758	0.132755	-5.05
257701_at	unknown protein contains similarity	---	AT3G12710	-2.12	-1.09	-2.28	0.057769	0.132767	-5.05
254047_at	hypothetical protein	---	AT4G26040	-1.26	-0.34	-2.28	0.057781	0.13278	-5.05
265145_at	unknown protein similar to GB:CAA	PLT2	AT1G51190	-1.21	-0.28	-2.28	0.057794	0.132797	-5.05
256690_at	hypothetical protein predicted by ge	---	AT3G32160	-1.24	-0.31	-2.28	0.057848	0.132907	-5.05
261902_at	unknown protein ; supported by full	PLMT	AT1G80860	1.18	0.24	2.28	0.057874	0.132955	-5.05
252485_at	disease resistance protein RPP13-	RPP13	AT3G46530	1.20	0.26	2.28	0.057894	0.132987	-5.05
264292_at	hypothetical protein predicted by ge	---	AT1G78790	1.24	0.31	2.28	0.05792	0.133034	-5.05
249055_at	calmodulin-like protein	---	AT5G44460	-1.16	-0.21	-2.28	0.057929	0.13304	-5.05
258194_at	unknown protein ; supported by ful	---	AT3G29170	-1.28	-0.36	-2.28	0.057936	0.133044	-5.05
260231_at	putative RING zinc finger protein c	---	AT1G74410	1.27	0.34	2.28	0.057959	0.133079	-5.05
263324_at	hypothetical protein predicted by ge	---	AT2G04220	-1.18	-0.24	-2.28	0.057964	0.133079	-5.05
267477_at	putative receptor-like protein kinase	PLPB	AT2G02710	-1.42	-0.51	-2.28	0.057969	0.133079	-5.05
262908_at	pyruvate dehydrogenase e1 alpha	AT-E1 ALP	AT1G59900	1.19	0.25	2.28	0.057978	0.133087	-5.05
265934_at	unknown protein	EER5	AT2G19560	1.16	0.21	2.28	0.058001	0.133113	-5.05

249626_at	putative protein nucleoid DNA-bind	---	AT5G37540	-1.43	-0.52	-2.28	0.058001	0.133113	-5.05
266923_at	unknown protein ;supported by full-	---	AT2G45980	1.20	0.27	2.28	0.058007	0.133113	-5.05
245031_at	putative mitochondrial carrier protei	---	AT2G26360	-1.17	-0.22	-2.28	0.05802	0.13313	-5.05
254636_at	putative protein kinase ; supported	CIPK12	AT4G18700	1.17	0.23	2.28	0.058044	0.13317	-5.05
253967_at	putative protein probable membran	---	AT4G26550	-1.31	-0.39	-2.28	0.058052	0.133175	-5.05
251814_at	chlorophyll a/b-binding protein ; su	LHCA1	AT3G54890	-1.15	-0.20	-2.28	0.05812	0.133319	-5.05
252843_at	glycine-rich protein other glycine-ric	---	AT3G42130	-1.26	-0.34	-2.28	0.058226	0.133549	-5.05
260008_at	putative RING zinc finger protein c	---	AT1G68070	1.18	0.24	2.28	0.058254	0.133599	-5.05
262214_at	germin subunit, putative similar to g	---	AT1G74820	-1.18	-0.24	-2.28	0.058266	0.13361	-5.05
260174_at	unknown protein ;supported by full-	---	AT1G71940	-1.18	-0.24	-2.28	0.058271	0.13361	-5.05
257368_at	hypothetical protein predicted by ge	---	AT2G29860	-1.18	-0.24	-2.28	0.058289	0.133638	-5.05
249566_at	cytochrome P450-like protein	CYP735A1	AT5G38450	-1.19	-0.25	-2.28	0.058301	0.133652	-5.05
248072_at	unknown protein	---	AT5G55680	-1.21	-0.28	-2.28	0.058311	0.133663	-5.05
262738_at	hypothetical protein	---	AT1G28530	1.25	0.32	2.28	0.058343	0.133712	-5.06
258128_at	chloroplast thylakoidal processing	PLSP1	AT3G24590	-1.25	-0.33	-2.28	0.058349	0.133712	-5.06
252789_s_a	hypothetical protein ; supported by	---	AT1G21930	1.17	0.23	2.28	0.05835	0.133712	-5.06
250108_at	homeobox-leucine zipper protein HA	ATHB-3	AT5G15150	-1.26	-0.33	-2.28	0.058397	0.133806	-5.06
249662_s_a	putative protein hypothetical protein	---	AT5G36680	-1.15	-0.20	-2.28	0.058529	0.134095	-5.06
261440_at	hypothetical protein predicted by ge	---	AT1G28510	-1.19	-0.25	-2.27	0.058575	0.134187	-5.06
255038_at	neutral invertase like protein Daucu	CINV2	AT4G09510	-1.51	-0.60	-2.27	0.058608	0.13425	-5.06
248874_at	putative protein strong similarity to	---	AT5G46460	1.32	0.40	2.27	0.058621	0.134266	-5.06
246080_at	putative protein	---	AT5G20460	1.19	0.25	2.27	0.058631	0.134274	-5.06
256420_at	unknown protein	---	AT1G33475	-1.26	-0.34	-2.27	0.058637	0.134275	-5.06
260572_at	putative molybdopterin synthase lar	---	AT2G43760	-1.18	-0.24	-2.27	0.058653	0.134297	-5.06
267327_at	putative protein kinase contains a p	---	AT2G19410	-1.18	-0.23	-2.27	0.058695	0.134373	-5.06
258882_at	unknown protein ; supported by ful	---	AT3G06330	1.22	0.28	2.27	0.058697	0.134373	-5.06
259256_at	putative coated vesicle membrane p	---	AT3G07680	1.19	0.25	2.27	0.058716	0.134391	-5.06
254065_at	gibberellin 20-oxidase - Arabidopsis	GA20OX1	AT4G25420	-1.59	-0.67	-2.27	0.058717	0.134391	-5.06
251201_at	putative protein predicted protein, A	---	AT3G63020	-1.16	-0.21	-2.27	0.058755	0.134463	-5.06
252318_at	glutamate-1-semialdehyde aminotra	GSA2	AT3G48730	-1.33	-0.42	-2.27	0.058786	0.134519	-5.06
256067_at	unknown protein ;supported by full-	---	AT1G07170	1.28	0.35	2.27	0.058791	0.134519	-5.06
246885_at	putative protein predicted protein, A	---	AT5G26230	-1.62	-0.70	-2.27	0.058808	0.134544	-5.06
254456_at	putative protein ribophorin II precu	HAP6	AT4G21150	1.24	0.31	2.27	0.058835	0.134592	-5.06
251475_at	putative protein other hypothetical p	---	AT3G59660	1.36	0.44	2.27	0.058889	0.134703	-5.06
264641_at	ATP-dependent Clp protease prote	---	AT1G09130	1.23	0.29	2.27	0.0589	0.134714	-5.07

267239_at	unknown protein	---	AT2G02510	1.21	0.27	2.27	0.058927	0.134751	-5.07
260723_at	unknown protein	---	AT1G48070	-1.17	-0.23	-2.27	0.058928	0.134751	-5.07
257550_at	hypothetical protein similar to GB:A	---	AT3G18460	-1.24	-0.31	-2.27	0.058958	0.134807	-5.07
255056_at	putative protein helix-loop-helix pro	TT8	AT4G09820	-1.16	-0.21	-2.27	0.059014	0.134921	-5.07
246043_at	putative protein predicted protein, A	---	AT5G19380	-1.41	-0.49	-2.27	0.059024	0.13493	-5.07
266709_at	unknown protein ;supported by full-	ATSPP	AT2G03120	1.29	0.37	2.27	0.059037	0.13493	-5.07
261462_at	hypothetical protein predicted by ge	---	AT1G07850	-1.23	-0.30	-2.27	0.059041	0.13493	-5.07
250946_at	putative protein	---	AT5G03420	1.18	0.24	2.27	0.059042	0.13493	-5.07
254410_at	serine/threonine kinase - like protei	---	AT4G21410	1.63	0.71	2.27	0.059069	0.134979	-5.07
246867_at	putative protein various predicted p	---	AT5G25990	1.16	0.22	2.27	0.059086	0.134993	-5.07
253119_at	Expressed protein ; supported by fu	---	AT4G35980	1.18	0.24	2.27	0.059087	0.134993	-5.07
266848_at	unknown protein ;supported by full-	---	AT2G25950	1.29	0.36	2.27	0.059117	0.135047	-5.07
245869_at	hypothetical protein predicted by ge	---	AT1G26330	-1.18	-0.24	-2.27	0.059162	0.135137	-5.07
245074_at	putative protein kinase contains a p	---	AT2G23200	1.87	0.91	2.27	0.0592	0.1352	-5.07
256144_at	guanine nucleotide-binding protein	RACK1B_A	AT1G48630	1.68	0.75	2.27	0.059207	0.1352	-5.07
249676_at	serine/threonine protein kinase-like	---	AT5G35960	-1.23	-0.30	-2.27	0.059207	0.1352	-5.07
250789_at	putative protein contains similarity t	---	AT5G05630	1.21	0.27	2.27	0.059231	0.135242	-5.07
254009_at	pyruvate kinase like protein pyruva	---	AT4G26390	-1.33	-0.42	-2.27	0.05925	0.135271	-5.07
262798_at	putative SPL1-related protein simil	SPL14	AT1G20980	1.21	0.27	2.27	0.059288	0.135323	-5.07
262126_at	disease resistance protein, putative	CW9	AT1G59620	1.29	0.37	2.27	0.05929	0.135323	-5.07
247806_at	ABC transporter-like protein ; suppo	STA1	AT5G58270	-1.18	-0.24	-2.27	0.059291	0.135323	-5.07
259112_at	putative 60S ribosomal protein L22	---	AT3G05560	1.44	0.53	2.27	0.059357	0.13546	-5.07
257182_s_a	crn-like protein similar to crn GB:CA	---	AT3G13210	1.28	0.36	2.27	0.059372	0.135482	-5.07
264766_at	receptor kinase, putative similar to	---	AT1G61420	1.50	0.58	2.26	0.059394	0.135508	-5.07
251817_at	small GTP-binding protein - like (fra	ARA6	AT3G54840	1.17	0.23	2.26	0.059395	0.135508	-5.07
265986_at	putative receptor-like protein kinase	---	AT2G24230	-1.31	-0.38	-2.26	0.059406	0.135519	-5.07
260521_at	putative villin 2	VLN2	AT2G41740	-1.33	-0.41	-2.26	0.059426	0.13555	-5.07
255796_at	similar to mammalian MHC III regio	SUVH2	AT2G33290	1.20	0.27	2.26	0.059456	0.135606	-5.07
265099_at	unknown protein Location of EST 2	---	AT1G03990	-1.60	-0.68	-2.26	0.059495	0.135676	-5.08
260257_at	putative dolichyl-phosphate mannos	---	AT1G74340	-1.18	-0.24	-2.26	0.059499	0.135676	-5.08
247664_at	APETALA2 protein - like APETALA	TOE2	AT5G60120	-1.20	-0.26	-2.26	0.059512	0.135693	-5.08
253176_at	putative protein Human (H326) mR	---	AT4G35140	1.32	0.40	2.26	0.059542	0.135747	-5.08
252524_at	putative protein mitochondrial ATP	---	AT3G46430	1.23	0.29	2.26	0.059556	0.135766	-5.08
265445_at	60S ribosomal protein L12 ;suppor	---	AT2G37190	1.62	0.70	2.26	0.059565	0.135772	-5.08
245485_at	proline-rich, APG like protein	---	AT4G16230	-1.22	-0.29	-2.26	0.059606	0.135844	-5.08

250655_at	transcription factor HBP-1b (gb|AAD	OBF5	AT5G06960	1.17	0.23	2.26	0.05961	0.135844	-5.08
263573_at	unknown protein similar to A. thalia	---	AT2G17150	1.28	0.36	2.26	0.059614	0.135844	-5.08
245006_at	PSI P700 apoprotein A2	---	---	-1.15	-0.20	-2.26	0.059631	0.135868	-5.08
262523_at	ubiquitin-specific protease 15 (UBP	UBP15	AT1G17110	-1.16	-0.21	-2.26	0.059652	0.135899	-5.08
265454_at	putative ARF1 family auxin respons	ARF11	AT2G46530	1.76	0.82	2.26	0.059656	0.135899	-5.08
265670_s_a	unknown protein ;supported by full-	---	AT2G32190	1.76	0.81	2.26	0.059683	0.135946	-5.08
266694_at	putative clathrin assembly protein ;	---	AT2G19790	-1.16	-0.21	-2.26	0.059708	0.135989	-5.08
256048_at	hypothetical protein contains simila	---	AT1G07025	-1.18	-0.24	-2.26	0.059744	0.136057	-5.08
253057_at	putative protein amino-acid N-acet	---	AT4G37670	1.66	0.73	2.26	0.059759	0.13607	-5.08
265885_at	hypothetical protein predicted by ge	---	AT2G42330	-1.28	-0.36	-2.26	0.059761	0.13607	-5.08
262781_s_a	proteasome epsilon chain precurso	PBE1	AT1G13060	1.24	0.32	2.26	0.059867	0.136297	-5.08
247797_at	predicted protein	---	AT5G58780	-1.23	-0.30	-2.26	0.059876	0.136304	-5.08
254512_at	terpene cyclase like protein vetispi	---	AT4G20230	-1.21	-0.28	-2.26	0.059901	0.136347	-5.08
260448_at	hypothetical protein predicted by ge	---	AT1G72410	-1.22	-0.29	-2.26	0.059914	0.136364	-5.08
246166_at	putative protein	---	---	-1.20	-0.26	-2.26	0.059991	0.136525	-5.08
246415_at	putative protein (fragment) predicte	---	AT5G17160	-1.33	-0.41	-2.26	0.060087	0.136729	-5.09
245476_at	hypothetical protein	---	AT4G16090	-1.21	-0.27	-2.26	0.060098	0.136742	-5.09
245421_at	hypothetical protein	---	AT4G17430	1.16	0.21	2.26	0.060179	0.136901	-5.09
251878_at	putative protein predicted protein, A	---	AT3G54310	-1.16	-0.22	-2.26	0.06018	0.136901	-5.09
256049_at	unknown protein	---	AT1G07010	1.27	0.34	2.26	0.060195	0.136921	-5.09
265697_at	hypothetical protein predicted by ge	---	AT2G32170	1.18	0.24	2.26	0.060232	0.136991	-5.09
260341_at	squamosa-promoter binding protei	---	AT1G69170	1.28	0.36	2.26	0.060239	0.136993	-5.09
261766_at	auxin-induced protein IAA5, putativ	IAA5	AT1G15580	-1.69	-0.76	-2.25	0.060292	0.1371	-5.09
250572_at	putative protein	MIR834A	---	1.28	0.35	2.25	0.060302	0.137111	-5.09
255129_at	nodulin-like protein nodulin gene M	---	AT4G08290	1.56	0.64	2.25	0.060341	0.137186	-5.09
264607_at	putative K+ channel, beta subunit s	KAB1	AT1G04690	1.15	0.21	2.25	0.060369	0.137224	-5.09
262390_at	hypothetical protein predicted by ge	---	AT1G49260	-1.22	-0.29	-2.25	0.06037	0.137224	-5.09
252422_at	putative protein PIT1 - Arabidopsis	---	AT3G47550	-1.31	-0.39	-2.25	0.060422	0.137328	-5.09
257659_at	Expressed protein ; supported by fu	---	AT3G13226	1.16	0.22	2.25	0.060442	0.137361	-5.09
257432_at	unknown protein	---	AT2G21850	-1.25	-0.32	-2.25	0.060489	0.137452	-5.09
261072_at	hexose transporter, putative simila	ATSTP2	AT1G07340	-1.24	-0.31	-2.25	0.060502	0.137456	-5.09
255729_at	hypothetical protein similar to putati	---	AT1G25470	1.20	0.26	2.25	0.060502	0.137456	-5.09
245407_at	GTP-binding RAB2A like protein	RABB1C	AT4G17170	-1.19	-0.25	-2.25	0.060523	0.13749	-5.09
260584_at	putative beta-1,3-glucanase, C terr	---	AT2G43660	-1.18	-0.23	-2.25	0.060534	0.137501	-5.09
261531_at	RB-binding protein -like similar to re	---	AT1G63490	1.30	0.38	2.25	0.060549	0.137508	-5.09

265785_at	hypothetical protein predicted by ge	---	AT2G07290	-1.16	-0.21	-2.25	0.060549	0.137508	-5.09
258459_at	hypothetical protein predicted by g	---	---	-1.21	-0.27	-2.25	0.060579	0.137556	-5.09
267474_at	hypothetical protein predicted by ge	WHY3	AT2G02740	1.22	0.29	2.25	0.060585	0.137556	-5.09
250416_at	putative protein predicted proteins,	---	AT5G11220	-1.19	-0.26	-2.25	0.060588	0.137556	-5.09
263097_at	hypothetical protein predicted by ge	PDV2	AT2G16070	1.25	0.33	2.25	0.060648	0.137677	-5.09
248994_at	disease resistance protein-like	RPS4	AT5G45250	1.26	0.33	2.25	0.060658	0.137686	-5.09
252606_at	carboxypeptidase precursor-like pr	scpl48	AT3G45010	-1.60	-0.68	-2.25	0.060706	0.137782	-5.10
261164_at	hypothetical protein ;supported by f	---	AT1G34470	-1.21	-0.28	-2.25	0.060743	0.137838	-5.10
248527_at	putative protein contains similarity t	---	AT5G50740	-1.21	-0.27	-2.25	0.060743	0.137838	-5.10
256988_s_a	adenosine triphosphatase, putative	---	AT3G28710	-1.16	-0.21	-2.25	0.060766	0.137875	-5.10
255260_at	score=63.7, E=3.9e-15, N=8 ; sup	---	AT4G05040	1.25	0.33	2.25	0.060774	0.137875	-5.10
251463_at	hypothetical protein	---	AT3G59800	-1.21	-0.27	-2.25	0.060782	0.137875	-5.10
248972_at	putative protein similar to unknown	ATDSS1(V	AT5G45010	1.35	0.43	2.25	0.060784	0.137875	-5.10
254960_at	predicted protein	---	AT4G10845	-1.22	-0.28	-2.25	0.060814	0.13793	-5.10
253851_at	putative transcription factor MYB41	AtMYB41	AT4G28110	-1.23	-0.30	-2.25	0.06082	0.13793	-5.10
265337_at	putative ADP-ribosylation factor ;su	TTN5	AT2G18390	-1.32	-0.40	-2.25	0.060886	0.13806	-5.10
245876_at	chaperonin precursor, putative sim	---	AT1G26230	1.38	0.47	2.25	0.060889	0.13806	-5.10
254294_at	putative membrane protein membr	ATRBL7	AT4G23070	-1.40	-0.48	-2.25	0.060903	0.138077	-5.10
256108_at	hypothetical protein predicted by ge	---	AT1G16940	-1.28	-0.36	-2.25	0.060911	0.138081	-5.10
245965_at	pectin methylesterase-like protein	---	AT5G19730	-1.39	-0.47	-2.25	0.060916	0.138081	-5.10
262290_at	Expressed protein ; supported by fu	---	AT1G70985	-1.31	-0.38	-2.25	0.060926	0.138089	-5.10
245900_at	putative protein predicted proteins,	---	AT5G11040	-1.23	-0.30	-2.25	0.060948	0.138124	-5.10
265486_at	unknown protein predicted by gens	---	AT2G15560	1.25	0.32	2.25	0.060964	0.138147	-5.10
252463_at	putative protein ;supported by full-l	---	AT3G47070	-1.43	-0.52	-2.25	0.060971	0.138148	-5.10
259096_at	putative 40S ribosomal protein S3A	---	AT3G04840	1.50	0.59	2.25	0.061017	0.138237	-5.10
262612_at	unknown protein location of ESTs	---	AT1G14150	-1.58	-0.66	-2.25	0.061022	0.138237	-5.10
264994_at	hypothetical protein contains simila	---	AT1G67270	-1.18	-0.23	-2.25	0.061045	0.138275	-5.10
264945_at	MADS-box protein (MADS2), putat	MAF1	AT1G77080	-1.44	-0.53	-2.25	0.061082	0.138333	-5.10
253888_at	hypothetical protein	ISI1	AT4G27750	-1.17	-0.23	-2.25	0.061087	0.138333	-5.10
249239_at	MAP kinase ; supported by cDNA:	CPuORF58	AT5G41990	1.17	0.23	2.25	0.061089	0.138333	-5.10
263917_at	putative AP2 domain transcription f	HRD	AT2G36450	-1.30	-0.38	-2.25	0.061101	0.138347	-5.10
262348_at	unknown protein similar to transcrip	---	AT2G48160	1.17	0.23	2.25	0.061131	0.138403	-5.10
266569_at	unknown protein	---	AT2G24080	-1.17	-0.23	-2.24	0.061167	0.138465	-5.10
260288_at	nodulin-like protein similar to nodule	---	AT1G80530	1.32	0.40	2.24	0.061171	0.138465	-5.10
253598_at	ribosomal protein S11 - like riboson	---	AT4G30800	1.66	0.73	2.24	0.061178	0.138468	-5.10

248337_at	low-temperature-induced protein 78	LTI78	AT5G52310	-2.50	-1.32	-2.24	0.061226	0.138562	-5.10
256497_at	ORF1, putative similar to ORF1 GI	ECS1	AT1G31580	-1.44	-0.52	-2.24	0.061261	0.138626	-5.10
251602_at	Expressed protein ; supported by fu	---	AT3G57785	1.19	0.25	2.24	0.061268	0.13863	-5.10
265660_at	putative disease resistance protein	AtRLP21	AT2G25470	1.30	0.38	2.24	0.061295	0.138674	-5.11
253865_at	putative RING zinc finger protein A	---	AT4G27470	-1.32	-0.40	-2.24	0.0613	0.138674	-5.11
262876_at	unknown protein ;supported by full-	ATDSS1(I)	AT1G64750	1.26	0.33	2.24	0.06132	0.138705	-5.11
265951_at	hypothetical protein predicted by ge	OFP7	AT2G18500	-1.35	-0.43	-2.24	0.061328	0.13871	-5.11
256277_at	omega-6 fatty acid desaturase, enc	FAD2	AT3G12120	-1.37	-0.45	-2.24	0.061356	0.13876	-5.11
252699_at	hypothetical protein predicted prote	---	---	-1.36	-0.44	-2.24	0.061499	0.139068	-5.11
250964_at	putative protein various predicted p	---	AT5G03010	-1.24	-0.31	-2.24	0.061515	0.139091	-5.11
259169_at	unknown protein similar to unknowr	---	AT3G03520	1.75	0.80	2.24	0.061533	0.139118	-5.11
265588_at	putative pathogenesis-related prote	---	AT2G19970	-1.96	-0.97	-2.24	0.061543	0.13912	-5.11
260305_at	putative ADP-ribosylation factor 1 n	ARFA1D	AT1G70490	-1.23	-0.30	-2.24	0.061546	0.13912	-5.11
266851_at	similar to avrRpt2-induced protein 1	ATPP2-A3	AT2G26820	-1.15	-0.20	-2.24	0.061584	0.139193	-5.11
247761_at	phosphoprotein phosphatase 1 cata	TOPP2	AT5G59160	-1.20	-0.27	-2.24	0.06162	0.139261	-5.11
257908_at	unknown protein contains Pfam pro	---	AT3G25410	1.21	0.28	2.24	0.061649	0.139306	-5.11
253087_at	purple acid phosphatase like protei	PAP25	AT4G36350	-1.22	-0.28	-2.24	0.061653	0.139306	-5.11
257336_at	hypothetical protein	---	---	1.16	0.22	2.24	0.061668	0.139317	-5.11
250460_at	putative protein similar to unknown	---	AT5G09850	-1.17	-0.23	-2.24	0.06167	0.139317	-5.11
260555_at	hypothetical protein predicted by ge	---	AT2G41780	1.63	0.71	2.24	0.061685	0.139338	-5.11
260128_at	hypothetical protein similar to Yml0	---	AT1G36310	1.21	0.28	2.24	0.061703	0.139364	-5.11
251580_at	putative protein ethylene-responsiv	---	AT3G58450	-1.30	-0.38	-2.24	0.061746	0.139449	-5.11
255086_at	putative protein chromosome I BAC	---	AT4G09300	-1.22	-0.29	-2.24	0.061811	0.13958	-5.11
254607_at	hypothetical protein ;supported by	---	AT4G18920	-1.18	-0.23	-2.24	0.061841	0.139634	-5.11
253103_at	putative auxin-induced protein high	---	AT4G36110	-2.39	-1.25	-2.24	0.061857	0.139657	-5.11
266398_at	hypothetical protein predicted by ge	---	AT2G38680	-1.49	-0.57	-2.24	0.061877	0.139689	-5.11
250444_at	beta-xylosidase - like protein beta-	---	AT5G10560	-1.21	-0.28	-2.24	0.061888	0.139699	-5.12
250588_at	SMC-like protein	---	AT5G07660	-1.18	-0.24	-2.24	0.061944	0.139812	-5.12
245045_at	unknown protein similar to glycopro	---	AT2G26590	1.16	0.22	2.24	0.061958	0.139819	-5.12
260603_at	membrane related protein CP5, pu	---	AT1G55960	1.32	0.40	2.24	0.061959	0.139819	-5.12
250927_at	lysine decarboxylase - like protein	---	AT5G03270	-1.26	-0.33	-2.24	0.061978	0.139844	-5.12
252337_at	CELL DIVISION CONTROL PROTE	CDC2	AT3G48750	1.34	0.42	2.24	0.061983	0.139844	-5.12
248340_at	putative protein similar to unknown	---	AT5G52180	-1.19	-0.25	-2.24	0.061998	0.139865	-5.12
246512_at	putative phytochelatin synthetase p	IRX6	AT5G15630	-1.25	-0.33	-2.24	0.062009	0.139874	-5.12
252216_at	putative protein several hypothetica	---	AT3G50420	1.24	0.32	2.24	0.062014	0.139874	-5.12

246909_at	putative protein predicted protein, (	---	AT5G25770	1.54	0.63	2.23	0.062069	0.139973	-5.12
252640_at	acyl CoA reductase -like protein ac	FAR8	AT3G44560	-1.17	-0.23	-2.23	0.062071	0.139973	-5.12
265291_at	unknown protein predicted by gens	---	AT2G22720	-1.20	-0.27	-2.23	0.062145	0.140105	-5.12
265102_at	putative peroxidase similar to catior	---	AT1G30870	-1.21	-0.28	-2.23	0.062147	0.140105	-5.12
253258_at	putative protein NF-180, Petromyz	---	AT4G34400	-1.23	-0.30	-2.23	0.062151	0.140105	-5.12
263372_at	60S ribosomal protein L14 ;suppor	---	AT2G20450	1.48	0.57	2.23	0.062165	0.140105	-5.12
254146_at	endo-1,4-beta-glucanase like prote	ATGH9A3	AT4G24260	-1.24	-0.31	-2.23	0.062172	0.140105	-5.12
254391_at	putative bifunctional nuclease bifur	ENDO3	AT4G21590	-1.17	-0.23	-2.23	0.062179	0.140105	-5.12
252260_at	putative protein several hypothetica	---	AT3G49480	-1.28	-0.36	-2.23	0.062188	0.140105	-5.12
257421_at	hypothetical protein predicted by ge	---	AT1G12030	-1.37	-0.46	-2.23	0.062194	0.140105	-5.12
257869_at	ER lumen protein retaining recepto	---	AT3G25160	-1.16	-0.21	-2.23	0.062195	0.140105	-5.12
254977_s_a	subtilisin-like serine protease conta	---	AT4G10520	-1.15	-0.20	-2.23	0.062198	0.140105	-5.12
253968_at	putative calcineurin B-like protein c	CBL7	AT4G26560	-1.18	-0.24	-2.23	0.062202	0.140105	-5.12
255242_at	putative protein putative retrotrans	---	---	-1.18	-0.23	-2.23	0.062205	0.140105	-5.12
264718_at	receptor-like kinase, putative simila	---	AT1G70130	-1.16	-0.22	-2.23	0.062209	0.140105	-5.12
263522_at	hypothetical protein	---	AT2G24950	-1.16	-0.21	-2.23	0.06222	0.140116	-5.12
249245_at	putative protein contains similarity t	---	AT5G42280	-1.29	-0.36	-2.23	0.06229	0.140247	-5.12
258730_at	putative GTP-binding protein (ATFF	ATFP8	AT3G11730	1.15	0.20	2.23	0.062292	0.140247	-5.12
264485_at	unknown protein ; supported by cDI	---	AT1G77220	-1.19	-0.25	-2.23	0.0623	0.140247	-5.12
260702_at	calmodulin, putative similar to calm	---	AT1G32250	-1.18	-0.24	-2.23	0.062303	0.140247	-5.12
254202_at	putative protein hydroxymuconic se	---	AT4G24140	-1.34	-0.42	-2.23	0.062328	0.140289	-5.12
264410_s_a	hypothetical protein predicted by ge	---	---	1.15	0.21	2.23	0.062339	0.140302	-5.12
261505_at	carboxypeptidase, putative similar	SOL1	AT1G71696	-1.26	-0.33	-2.23	0.062351	0.140306	-5.12
259407_at	protein phosphatase 2A regulatory	PP2AA3	AT1G13320	-1.16	-0.21	-2.23	0.062357	0.140306	-5.12
263328_at	hypothetical protein similar to hypot	---	AT2G15280	-1.25	-0.33	-2.23	0.06236	0.140306	-5.12
246834_at	putative protein homeotic protein b	---	AT5G26630	-1.21	-0.27	-2.23	0.0624	0.140382	-5.12
245184_at	F12A21.8 hypothetical protein	---	AT1G67790	-1.22	-0.28	-2.23	0.062483	0.140556	-5.12
250473_at	annexin -like protein annexin (Ann/	ANN6	AT5G10220	-1.15	-0.21	-2.23	0.062498	0.140565	-5.12
257684_s_a	unknown protein contains Pfam pro	VCS	AT3G13290	1.23	0.30	2.23	0.062499	0.140565	-5.12
263667_at	putative 40S ribosomal protein S15	RPS15	AT1G04270	1.27	0.34	2.23	0.062535	0.140612	-5.13
265685_at	NAM (no apical meristem)-like prote	ANAC038	AT2G24430	-1.24	-0.31	-2.23	0.062536	0.140612	-5.13
263196_at	hypothetical protein predicted by ge	---	AT1G36070	1.34	0.42	2.23	0.062541	0.140612	-5.13
258444_at	expressed protein supported by cDI	TIC	AT3G22380	1.19	0.26	2.23	0.062548	0.140612	-5.13
259170_at	hypothetical protein similar to putati	---	AT3G03510	-1.17	-0.23	-2.23	0.062551	0.140612	-5.13
250637_at	glycine-rich protein atGRP-7	GRP17	AT5G07530	-1.20	-0.27	-2.23	0.062573	0.140648	-5.13

263702_at	hypothetical protein identical to hyp	---	AT1G31240	-1.19	-0.25	-2.23	0.062585	0.14066	-5.13
253709_at	pyrophosphate-dependent phosph	PFK1	AT4G29220	1.27	0.35	2.23	0.062591	0.140661	-5.13
263887_at	hypothetical protein predicted by ge	---	AT2G36980	1.26	0.33	2.23	0.062608	0.140684	-5.13
248551_at	putative protein similar to unknown	WR3	AT5G50200	1.66	0.73	2.23	0.062717	0.140916	-5.13
264179_at	hypothetical protein predicted by ge	---	AT1G02180	-1.32	-0.40	-2.23	0.06274	0.140954	-5.13
263157_at	aldehyde dehydrogenase homolog	ALDH7B4	AT1G54100	1.38	0.46	2.23	0.062787	0.141038	-5.13
247638_at	arabinogalactan protein - like arabi	FLA12	AT5G60490	-1.48	-0.56	-2.23	0.06279	0.141038	-5.13
254240_at	Expressed protein ; supported by fu	SP1L5	AT4G23496	-1.19	-0.25	-2.23	0.062849	0.141157	-5.13
253660_at	putative protein proline-rich protein	---	AT4G30140	-1.18	-0.24	-2.23	0.062856	0.141158	-5.13
255961_at	UDP-glucose glucosyltransferase,	AtUGT85A1	AT1G22340	-1.37	-0.45	-2.23	0.062869	0.141174	-5.13
262312_at	hypothetical protein similar to putati	MLP28	AT1G70830	-4.52	-2.18	-2.23	0.062929	0.141282	-5.13
259702_at	putative endo-1,3-beta-glucanase s	---	AT1G77780	-1.18	-0.24	-2.23	0.06293	0.141282	-5.13
262759_at	unknown protein	---	AT1G10800	-1.18	-0.23	-2.22	0.062962	0.14134	-5.13
248174_at	50S ribosomal protein L24, chlorop	---	AT5G54600	-1.20	-0.26	-2.22	0.062972	0.14135	-5.13
256237_at	leucine rich repeat protein, putative	DRT100	AT3G12610	-6.11	-2.61	-2.22	0.062997	0.141391	-5.13
260047_at	putative UDP-N-acetylglucosamine-	---	AT1G73740	-1.19	-0.25	-2.22	0.063023	0.141436	-5.13
256280_at	unknown protein	---	AT3G12590	-1.22	-0.29	-2.22	0.063046	0.141471	-5.13
263195_at	non-specific lipid transfer protein, p	---	AT1G36150	-1.28	-0.35	-2.22	0.063051	0.141471	-5.13
261945_at	unknown protein	---	AT1G64530	-1.38	-0.47	-2.22	0.063065	0.141483	-5.13
249913_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G22810	-1.22	-0.28	-2.22	0.063069	0.141483	-5.13
263253_at	bZIP transcription factor (POSF21)	---	AT2G31370	-1.25	-0.32	-2.22	0.06308	0.141493	-5.13
266372_at	putative two-component response	ATRR3	AT2G41310	1.22	0.29	2.22	0.063096	0.141508	-5.13
251047_at	putative protein mature-parasite-int	---	AT5G02390	-1.23	-0.29	-2.22	0.063098	0.141508	-5.13
249214_at	beta-1,3-glucanase-like protein	---	AT5G42720	-1.42	-0.51	-2.22	0.063114	0.141516	-5.13
256682_at	putative protein dihydrolipoamide S	LTA3	AT3G52200	1.16	0.22	2.22	0.063115	0.141516	-5.13
259765_at	unknown protein ;supported by full-	---	AT1G64370	1.30	0.37	2.22	0.063122	0.141518	-5.13
259024_at	hypothetical protein predicted by ge	---	---	-1.26	-0.33	-2.22	0.063186	0.141648	-5.14
257238_at	unknown protein ; supported by cD	---	AT3G17430	-1.28	-0.35	-2.22	0.063215	0.14169	-5.14
261974_at	protein kinase, putative similar to m	CPuORF57	AT1G64628	1.19	0.25	2.22	0.063217	0.14169	-5.14
267265_at	putative serine carboxypeptidase I	SCPL13	AT2G22980	-1.30	-0.38	-2.22	0.063237	0.14172	-5.14
246517_at	ribosomal protein 3 precursor-like p	---	AT5G15760	-1.23	-0.30	-2.22	0.063257	0.141751	-5.14
245132_at	hypothetical protein predicted by ge	---	AT2G45320	1.30	0.38	2.22	0.063289	0.14181	-5.14
267289_at	putative protein kinase contains a p	---	AT2G23770	-1.17	-0.22	-2.22	0.063324	0.141875	-5.14
261892_at	transcription factor, putative similar	WRKY40	AT1G80840	3.02	1.60	2.22	0.063334	0.141883	-5.14
261211_at	uridine diphosphate glucose epime	UGE1	AT1G12780	1.37	0.45	2.22	0.063392	0.141999	-5.14

262221_at	hypothetical protein predicted by ge	ARC3	AT1G75010	1.26	0.33	2.22	0.06342	0.142048	-5.14
AFFX-r2-At-	Arabidopsis thaliana /REF=U84969	---	---	1.17	0.23	2.22	0.06344	0.142068	-5.14
266180_at	putative PHD-type zinc finger protei	AL6	AT2G02470	1.26	0.33	2.22	0.063442	0.142068	-5.14
250820_at	receptor-like protein kinase	---	AT5G05160	-1.23	-0.30	-2.22	0.063453	0.142079	-5.14
248142_at	putative protein similar to unknown	---	AT5G55040	-1.17	-0.23	-2.22	0.063515	0.142205	-5.14
252197_at	receptor protein kinase -like protein	---	AT3G50230	-1.16	-0.21	-2.22	0.063551	0.142271	-5.14
251340_at	actin - like protein actin 3, Drosoph	ATARP7	AT3G60830	1.19	0.25	2.22	0.063581	0.142324	-5.14
253089_at	putative protein hypothetical protei	---	AT4G36290	1.17	0.22	2.22	0.06364	0.142441	-5.14
257028_at	hypothetical protein predicted by g	---	AT3G19230	-1.36	-0.45	-2.22	0.063646	0.142441	-5.14
260896_at	flower pigmentation protein ATAN1	---	AT1G29310	-1.42	-0.50	-2.22	0.06366	0.142456	-5.14
246704_at	putative protein	---	AT5G28090	-1.19	-0.25	-2.22	0.063665	0.142456	-5.14
258176_at	B regulatory subunit of PP2A, puta	---	AT3G21650	1.40	0.48	2.22	0.063703	0.142526	-5.14
259629_at	disease resistance protein contains	WRR4	AT1G56510	-1.27	-0.35	-2.22	0.063722	0.142549	-5.14
246562_at	putative protein unknown protein F	LNG1	AT5G15580	-2.72	-1.44	-2.22	0.063725	0.142549	-5.14
251802_at	E2, ubiquitin-conjugating enzyme 1	UBC14	AT3G55380	1.17	0.23	2.22	0.063777	0.14265	-5.15
256900_at	pectate lyase, putative similar to pe	---	AT3G24670	-1.23	-0.30	-2.22	0.063791	0.142668	-5.15
244933_at	NADH dehydrogenase ND4L	---	---	-1.21	-0.27	-2.22	0.063822	0.142724	-5.15
251916_at	transporter-like protein oligopeptide	---	AT3G53960	-1.31	-0.39	-2.22	0.063835	0.142726	-5.15
253862_at	NOZZLE/SPOROCYTELESS ; sup	SPL	AT4G27330	-1.26	-0.34	-2.22	0.063835	0.142726	-5.15
267420_at	hypothetical protein predicted by gr	---	AT2G35030	1.44	0.52	2.21	0.063929	0.142921	-5.15
251703_at	putative protein hypothetical protein	---	AT3G56670	-1.26	-0.34	-2.21	0.063941	0.142934	-5.15
248509_at	Expressed protein ; supported by fu	---	AT5G50335	-5.51	-2.46	-2.21	0.063953	0.142946	-5.15
256602_at	unknown protein	---	AT3G28310	-1.27	-0.34	-2.21	0.063959	0.142946	-5.15
255150_at	putative xylan endohydrolase	---	AT4G08160	-1.35	-0.44	-2.21	0.063975	0.142968	-5.15
245979_at	putative protein leucine zipper-con	ATEXO70C	AT5G13150	-1.15	-0.20	-2.21	0.063985	0.142976	-5.15
263294_at	hypothetical protein predicted by ge	---	---	-1.26	-0.33	-2.21	0.064033	0.143067	-5.15
259871_at	nodulin-like protein similar to noduli	---	AT1G76800	1.53	0.61	2.21	0.064044	0.143067	-5.15
264649_at	hypothetical protein Similar to Vicia	---	AT1G09060	-1.24	-0.30	-2.21	0.064045	0.143067	-5.15
267016_at	hypothetical protein predicted by ge	---	AT2G39160	-1.19	-0.25	-2.21	0.064063	0.143086	-5.15
245449_at	retrotransposon like protein	---	---	-1.35	-0.43	-2.21	0.064069	0.143086	-5.15
256538_x_a	hypothetical protein predicted by ge	---	---	-1.17	-0.23	-2.21	0.064074	0.143086	-5.15
258454_at	putative 40S ribosomal protein S10	RPS10	AT3G22300	1.28	0.36	2.21	0.064078	0.143086	-5.15
262457_at	hypothetical protein similar to hypot	---	AT1G11200	1.36	0.45	2.21	0.064121	0.143167	-5.15
262182_at	hypothetical protein predicted by ge	---	AT1G77890	-1.18	-0.24	-2.21	0.064129	0.14317	-5.15
246673_at	ribosomal protein S1 ;supported by	RPS1	AT5G30510	-1.17	-0.23	-2.21	0.064138	0.14317	-5.15

265083_at	hypothetical protein predicted by ge	---	AT1G03820	-1.44	-0.53	-2.21	0.064141	0.14317	-5.15
260834_at	sugar kinase, putative similar to rib	---	AT1G06730	1.24	0.32	2.21	0.06416	0.143198	-5.15
249963_at	putative protein SPECKLE-TYPE F	ATBPM1	AT5G19000	-1.24	-0.31	-2.21	0.064167	0.1432	-5.15
253621_at	putative protein component of anili	---	AT4G30540	-1.20	-0.26	-2.21	0.06419	0.143229	-5.15
263848_at	putative reverse transcriptase	---	---	-1.22	-0.28	-2.21	0.064193	0.143229	-5.15
258848_at	Expressed protein ; supported by fu	DCL2	AT3G03300	1.18	0.24	2.21	0.064202	0.143237	-5.15
252177_at	protein kinase ATN1 - like protein p	---	AT3G50730	-1.23	-0.30	-2.21	0.064211	0.143242	-5.15
254084_at	ubiquitin activating enzyme - like p	SAE1A	AT4G24940	1.37	0.45	2.21	0.06426	0.143338	-5.15
261991_at	hypothetical protein predicted by ge	---	AT1G33700	-1.26	-0.33	-2.21	0.064269	0.143344	-5.15
245952_at	putative protein predicted proteins,	---	AT5G28500	1.25	0.32	2.21	0.064401	0.143624	-5.16
248553_at	putative protein strong similarity to	---	AT5G50170	1.44	0.52	2.21	0.064421	0.143655	-5.16
249892_at	unknown protein	---	AT5G22600	-1.16	-0.21	-2.21	0.06445	0.143704	-5.16
254235_at	putative Ap2 domain protein DNA-I	CRF2	AT4G23750	-1.18	-0.24	-2.21	0.064458	0.143708	-5.16
257646_at	methionine aminopeptidase, putati	MAP1B	AT3G25740	-1.41	-0.50	-2.21	0.064469	0.14372	-5.16
266509_at	DegP2 protease identical to DegP2	DEGP2	AT2G47940	-1.22	-0.29	-2.21	0.064482	0.143728	-5.16
253191_at	cysteine protease XCP1 identical to	XCP1	AT4G35350	-1.84	-0.88	-2.21	0.06449	0.143728	-5.16
260191_at	putative protein kinase Pfam HMM	---	AT1G67580	1.17	0.22	2.21	0.064497	0.143728	-5.16
257744_at	hypothetical protein contains Pfam	---	AT3G29230	1.24	0.31	2.21	0.064498	0.143728	-5.16
256154_at	hypothetical protein predicted by ge	---	AT3G08490	-1.23	-0.29	-2.21	0.064548	0.143824	-5.16
260837_at	fructose 1,6-bisphosphatase, putat	---	AT1G43670	-1.39	-0.48	-2.21	0.064559	0.143836	-5.16
267380_at	putative thromboxane-A synthase ;	CYP711A1	AT2G26170	1.47	0.56	2.21	0.06458	0.143856	-5.16
266493_at	Mutator-like transposase similar to	---	---	-1.18	-0.24	-2.21	0.064581	0.143856	-5.16
265996_at	putative leucine aminopeptidase ide	---	AT2G24200	1.47	0.56	2.21	0.064594	0.143858	-5.16
246035_at	succinyl-CoA-ligase alpha subunit	---	AT5G08300	1.54	0.62	2.21	0.064594	0.143858	-5.16
258566_at	putative glutamate receptor (GLR1)	GLR1.1	AT3G04110	1.36	0.45	2.21	0.064618	0.143884	-5.16
245755_at	hypothetical protein predicted by ge	---	AT1G35210	2.87	1.52	2.21	0.064619	0.143884	-5.16
246762_at	cyclin H-like protein cycH (CAK ass	CYCH;1	AT5G27620	1.32	0.40	2.21	0.064661	0.143964	-5.16
248735_at	laccase (diphenol oxidase)	TT10	AT5G48100	-1.18	-0.24	-2.21	0.064702	0.144042	-5.16
250232_at	unknown protein	---	AT5G13950	-1.18	-0.23	-2.21	0.06471	0.144045	-5.16
251383_at	beta-tubulin cofactor - like protein b	TTN1	AT3G60740	1.32	0.40	2.21	0.064723	0.144056	-5.16
262690_at	PPR-repeat protein contains multipl	---	AT1G62720	1.18	0.24	2.21	0.064727	0.144056	-5.16
258775_at	hydroxyacylglutathione hydrolase c	GLY2	AT3G10850	1.19	0.25	2.21	0.06475	0.144065	-5.16
252492_at	chloroplast import-associated chan	TOC75-III	AT3G46740	1.22	0.29	2.21	0.064755	0.144065	-5.16
261568_at	DNA-binding protein, putative simil	NGA3	AT1G01030	-1.20	-0.26	-2.21	0.064756	0.144065	-5.16
250265_at	putative protein predicted proteins,	---	AT5G12900	-1.30	-0.37	-2.21	0.064761	0.144065	-5.16

263403_at	hypothetical protein similar to hypot	TX1	AT2G04040	2.51	1.33	2.21	0.064763	0.144065	-5.16
250975_at	putative protein	---	AT5G03050	-1.24	-0.31	-2.20	0.064839	0.144219	-5.16
265348_at	putative RNA-binding protein	---	AT2G22600	-1.21	-0.27	-2.20	0.064858	0.144247	-5.16
252869_at	putative protein	---	AT4G39930	-1.18	-0.24	-2.20	0.064883	0.144249	-5.16
261171_at	unknown protein	---	AT1G04880	-1.19	-0.24	-2.20	0.064886	0.144249	-5.16
248706_at	unknown protein	---	AT5G48530	-1.22	-0.29	-2.20	0.064886	0.144249	-5.16
246741_at	glycine rich protein - like glycine ric	emb1644	AT5G27720	1.23	0.30	2.20	0.064889	0.144249	-5.16
265385_at	putative diacylglycerol kinase ;supp	---	AT2G20900	1.36	0.45	2.20	0.064896	0.144249	-5.16
259875_s_a	12-oxophytodienoate reductase (OI	OPR1	AT1G76680	1.68	0.75	2.20	0.064896	0.144249	-5.16
267041_at	unknown protein	---	AT2G34315	-1.15	-0.20	-2.20	0.064909	0.144263	-5.16
255645_at	coded for by A. thaliana cDNA T43	---	AT4G00880	1.34	0.42	2.20	0.064919	0.144266	-5.16
253460_at	hypothetical protein	---	AT4G32130	1.24	0.31	2.20	0.064926	0.144266	-5.16
258088_at	hypothetical protein predicted by ge	---	AT3G14580	1.18	0.24	2.20	0.064934	0.144266	-5.16
263503_s_a	hypothetical protein	---	AT2G07676	1.17	0.23	2.20	0.064935	0.144266	-5.16
245295_at	hypothetical protein ; supported by	---	AT4G16100	1.23	0.30	2.20	0.064955	0.144295	-5.16
267026_at	DREB-like AP2 domain transcriptio	---	AT2G38340	1.75	0.80	2.20	0.064978	0.144322	-5.16
255894_at	nuclear poly(A) polymerase, putati	---	AT1G17980	-1.20	-0.26	-2.20	0.06498	0.144322	-5.16
267292_at	hypothetical protein predicted by ge	---	AT2G23740	-1.20	-0.26	-2.20	0.064988	0.144327	-5.16
246266_at	30S ribosomal protein S11, putativ	NFD3	AT1G31817	1.28	0.36	2.20	0.065019	0.144373	-5.16
262547_at	hypothetical protein predicted by ge	---	AT1G31270	-1.15	-0.20	-2.20	0.065022	0.144373	-5.16
248673_at	putative protein contains similarity t	---	AT5G48780	-1.17	-0.22	-2.20	0.065031	0.144376	-5.16
253957_at	putative protein ; supported by cDN	AGP13	AT4G26320	-1.30	-0.38	-2.20	0.065036	0.144376	-5.16
246913_at	GATA transcription factor - like GA	---	AT5G25830	-1.26	-0.34	-2.20	0.065047	0.144386	-5.17
248151_at	Lhcb3 chlorophyll a/b binding prote	LHCB3	AT5G54270	-1.39	-0.48	-2.20	0.06506	0.144397	-5.17
252030_at	hypothetical protein predicted prote	---	AT3G52690	-1.16	-0.21	-2.20	0.065064	0.144397	-5.17
260635_at	unknown protein	---	AT1G62420	-1.25	-0.33	-2.20	0.065098	0.144459	-5.17
263572_at	putative disease resistance protein	---	AT2G17060	-1.17	-0.22	-2.20	0.065121	0.144496	-5.17
249518_at	putative protein similar to unknown	---	AT5G38610	-1.19	-0.25	-2.20	0.065128	0.144497	-5.17
247509_at	heat shock factor 6	HSFB2A	AT5G62020	1.23	0.30	2.20	0.065156	0.144532	-5.17
265164_at	putative OBP32pep protein	---	AT1G23600	-1.17	-0.23	-2.20	0.065157	0.144532	-5.17
263021_at	hypothetical protein predicted by ge	---	AT1G23910	-1.15	-0.20	-2.20	0.065167	0.144541	-5.17
246702_at	putative cytidine deaminase - like p	---	AT5G28050	-1.63	-0.71	-2.20	0.065239	0.144687	-5.17
262193_at	eukaryotic initiation factor 5 (eIF-5)	---	AT1G77840	1.29	0.36	2.20	0.065251	0.144699	-5.17
267185_at	unknown protein ; supported by cD	OEP37	AT2G43950	1.21	0.28	2.20	0.065264	0.144714	-5.17
258869_at	hypothetical protein similar to xylos	AtVGT1	AT3G03090	-1.23	-0.30	-2.20	0.065403	0.144982	-5.17

258650_at	putative protein kinase similar to pr	---	AT3G09830	1.37	0.46	2.20	0.065404	0.144982	-5.17
248950_at	ATP-dependent Clp protease prote	CLPP4	AT5G45390	-1.22	-0.29	-2.20	0.065404	0.144982	-5.17
267518_at	unknown protein	---	AT2G30500	1.64	0.71	2.20	0.065459	0.145089	-5.17
251399_at	putative protein	---	AT3G60590	-1.23	-0.30	-2.20	0.065478	0.145119	-5.17
247971_at	zinc protease PQQL-like protein	---	AT5G56730	1.18	0.24	2.20	0.065494	0.14514	-5.17
262748_at	lipase, putative contains Pfam prof	---	AT1G28610	1.37	0.45	2.20	0.065539	0.145225	-5.17
249287_at	putative protein strong similarity to	---	AT5G41250	-1.22	-0.28	-2.20	0.065551	0.145237	-5.17
253340_s_a	WD-repeat protein -like protein WD	CDC20.2	AT4G33260	1.19	0.25	2.20	0.065584	0.145296	-5.17
258222_at	putative zinc finger protein contains	---	AT3G15680	-1.39	-0.48	-2.20	0.065613	0.145337	-5.17
261419_at	hypothetical protein predicted by ge	---	AT1G07840	1.15	0.20	2.20	0.065615	0.145337	-5.17
244914_at	hypothetical protein	---	---	-1.19	-0.25	-2.20	0.065677	0.14546	-5.17
265570_at	unknown protein	---	AT2G28310	1.24	0.32	2.20	0.065715	0.145529	-5.18
264779_at	putative thioredoxin similar to EST	ACHT4	AT1G08570	-1.49	-0.57	-2.20	0.065728	0.145544	-5.18
258842_at	unknown protein similar to putative	CLPS3	AT3G04680	1.26	0.33	2.19	0.065748	0.145575	-5.18
262279_at	hypothetical protein predicted by ge	---	AT1G68630	1.45	0.54	2.19	0.065805	0.145686	-5.18
262178_at	membrane protein, putative similar	KOM	AT1G77860	-1.28	-0.35	-2.19	0.06587	0.145818	-5.18
262809_at	putative glycogen synthase strong s	ATSS3	AT1G11720	-1.56	-0.64	-2.19	0.065913	0.145898	-5.18
249420_at	NAC domain/ NAM like protein NA	anac094	AT5G39820	-1.18	-0.24	-2.19	0.065922	0.145904	-5.18
265468_at	hypothetical protein predicted by ge	---	AT2G37210	-1.19	-0.26	-2.19	0.065962	0.145977	-5.18
265927_at	hypothetical protein	---	AT2G18590	-1.23	-0.30	-2.19	0.065974	0.14599	-5.18
253779_at	receptor-like protein kinase 5 precu	HAE	AT4G28490	1.46	0.55	2.19	0.066015	0.146066	-5.18
258496_at	putative plant adhesion molecule si	---	AT3G02460	-1.29	-0.37	-2.19	0.066071	0.146177	-5.18
258660_at	hypothetical protein predicted by ge	---	AT3G09850	1.21	0.28	2.19	0.066078	0.146177	-5.18
253129_at	glycine-rich protein glycine-rich pro	CSDP1	AT4G36020	1.29	0.37	2.19	0.066134	0.146287	-5.18
250982_at	putative protein zinc finger protein,	JKD	AT5G03150	-1.36	-0.44	-2.19	0.066155	0.146306	-5.18
253220_s_a	putative protein phospholipase C,	---	AT4G34920	-1.28	-0.35	-2.19	0.066155	0.146306	-5.18
263113_at	unknown protein Belongs to PF|005	---	AT1G03150	-1.16	-0.21	-2.19	0.06617	0.146325	-5.18
245444_at	limonene cyclase like protein	ATTPS03	AT4G16740	-1.25	-0.32	-2.19	0.066212	0.146403	-5.18
267412_at	putative vacuolar sorting receptor	---	AT2G34940	-1.71	-0.77	-2.19	0.066224	0.146415	-5.18
255813_at	hypothetical protein contains Pfam	---	AT1G19930	-1.20	-0.26	-2.19	0.06627	0.146502	-5.18
257398_at	hypothetical protein predicted by ge	---	AT2G01990	1.15	0.21	2.19	0.066284	0.14652	-5.18
253196_at	NAD+ dependent isocitrate dehydro	IDH1	AT4G35260	1.27	0.34	2.19	0.066359	0.146667	-5.19
252434_s_a	putative protein mudrA protein - ma	---	---	-1.20	-0.26	-2.19	0.066367	0.146667	-5.19
267286_at	putative seed maturation protein	---	AT2G23640	-1.16	-0.21	-2.19	0.06637	0.146667	-5.19
263024_at	hypothetical protein predicted by ge	---	AT1G23980	-1.25	-0.32	-2.19	0.066386	0.146689	-5.19

249856_at	serine carboxypeptidase	scpl47	AT5G22980	-1.31	-0.39	-2.19	0.066397	0.146699	-5.19
257176_s_a	cyclopropane-fatty-acyl-phospholip	---	AT3G23510	-1.80	-0.85	-2.19	0.06642	0.146735	-5.19
246014_at	putative protein	---	AT5G10680	-1.19	-0.25	-2.19	0.066438	0.14676	-5.19
251998_at	putative protein KIAA0010 protein,	UPL7	AT3G53090	1.19	0.25	2.19	0.066478	0.146825	-5.19
253387_at	P-Protein - like protein P-Protein pr	AtGLDP1	AT4G33010	-1.46	-0.54	-2.19	0.066484	0.146825	-5.19
250745_at	putative protein strong similarity to	---	AT5G05850	1.31	0.39	2.19	0.066486	0.146825	-5.19
260851_at	nodulin-like protein similar to MtN2	---	AT1G21890	-1.20	-0.26	-2.19	0.066513	0.14687	-5.19
266077_at	putative non-LTR retroelement reve	---	---	-1.21	-0.27	-2.19	0.066526	0.146884	-5.19
253112_at	putative ascorbate peroxidase asc	APX5	AT4G35970	-1.31	-0.39	-2.19	0.066541	0.146902	-5.19
246883_at	putative protein many predicted pr	---	AT5G26190	-1.16	-0.21	-2.19	0.066615	0.147053	-5.19
263155_at	transcriptional activation factor TAF	TAFII21	AT1G54140	-1.22	-0.28	-2.19	0.066658	0.147133	-5.19
249544_at	anti-silencing factor 1-like protein S	ASF1B	AT5G38110	-1.28	-0.36	-2.19	0.066672	0.14715	-5.19
262915_at	response regulator 3 identical to res	ARR3	AT1G59940	-1.23	-0.29	-2.19	0.066697	0.14719	-5.19
259541_at	protein kinase, putative similar to p	---	AT1G20650	-1.33	-0.41	-2.18	0.066719	0.147224	-5.19
249690_at	acyl-peptide hydrolase-like	---	AT5G36210	1.18	0.24	2.18	0.066741	0.147259	-5.19
267554_at	E2, ubiquitin-conjugating enzyme,	---	AT2G32790	-1.23	-0.30	-2.18	0.06678	0.147331	-5.19
252657_at	hypothetical protein	---	AT3G44780	-1.15	-0.20	-2.18	0.066816	0.147395	-5.19
263321_at	ADP-ribosylation factor 1 ;supporte	ARF1A1C	AT2G47170	-1.18	-0.24	-2.18	0.066835	0.147423	-5.19
263283_at	hypothetical protein predicted by ge	---	AT2G36090	1.18	0.24	2.18	0.066844	0.14743	-5.19
253591_at	putative protein hypothetical protei	MUS81	AT4G30870	1.29	0.36	2.18	0.066883	0.147501	-5.19
266235_at	putative phloem-specific lectin	AtPP2-B10	AT2G02360	1.26	0.34	2.18	0.066926	0.147582	-5.19
251767_at	putative protein U4/U6 small nucle	---	AT3G55930	1.15	0.20	2.18	0.066982	0.14769	-5.19
254696_at	hypothetical protein	---	AT4G17930	-1.16	-0.22	-2.18	0.066993	0.1477	-5.19
250506_at	ABC transporter, ATP-binding prot	GCN2	AT5G09930	-1.21	-0.28	-2.18	0.067005	0.147713	-5.19
259141_at	putative cytoskeleton-associated pr	---	AT3G10220	1.19	0.25	2.18	0.067024	0.147741	-5.20
266933_at	putative Ta11-like non-LTR retroele	---	AT2G07760	-1.24	-0.31	-2.18	0.067041	0.147764	-5.20
247471_at	putative protein receptor-like protei	ERL1	AT5G62230	-1.21	-0.27	-2.18	0.067057	0.147779	-5.20
263429_at	putative aspartate aminotransferase	AAT	AT2G22250	1.81	0.86	2.18	0.067061	0.147779	-5.20
259580_at	oxidoreductase, putative contains F	---	AT1G28030	-1.25	-0.32	-2.18	0.067102	0.147855	-5.20
261114_at	bZIP transcription factor ATB2, put	AtbZIP44	AT1G75388	2.71	1.44	2.18	0.06712	0.14787	-5.20
253408_at	putative protein phosphoprotein ph	---	AT4G32950	-1.16	-0.21	-2.18	0.067122	0.14787	-5.20
264172_at	unknown protein	VAD1	AT1G02120	1.30	0.37	2.18	0.067188	0.147994	-5.20
247708_at	putative protein COP1-interacting p	---	AT5G59550	1.94	0.96	2.18	0.067191	0.147994	-5.20
253938_at	putative homeodomain protein hon	---	AT4G26920	-1.21	-0.27	-2.18	0.067206	0.148013	-5.20
261677_at	unknown protein ;supported by full-	---	AT1G18470	1.31	0.39	2.18	0.067221	0.148028	-5.20

254837_at	putative protein	---	AT4G12360	-1.22	-0.29	-2.18	0.067226	0.148028	-5.20
261327_at	transcription factor, putative contai	---	AT1G44830	-2.69	-1.43	-2.18	0.067278	0.148128	-5.20
261950_at	zinc finger protein, putative similar	---	AT1G64620	-1.31	-0.39	-2.18	0.067301	0.148162	-5.20
253935_at	putative aspartate-tRNA ligase asp	---	AT4G26870	1.51	0.60	2.18	0.06731	0.148162	-5.20
245903_at	CLB1 - like protein CLB1 protein, L	SYTD	AT5G11100	-1.19	-0.25	-2.18	0.067313	0.148162	-5.20
262398_at	hypothetical protein predicted by ge	---	AT1G49350	1.15	0.21	2.18	0.067321	0.148165	-5.20
267529_at	putative protein kinase contains a p	AtAUR3	AT2G45490	-1.24	-0.31	-2.18	0.067378	0.148274	-5.20
265131_at	putative polygalacuronase isoenzyn	JP630	AT1G23760	-1.51	-0.59	-2.18	0.067383	0.148274	-5.20
259989_at	hypothetical protein predicted by ge	---	---	-1.21	-0.28	-2.18	0.067392	0.148279	-5.20
249910_at	chorismate mutase/prephenate deh	ADT5	AT5G22630	-1.68	-0.75	-2.18	0.067414	0.148309	-5.20
254188_at	UDPglucose 4-epimerase - like pro	UGE2	AT4G23920	1.46	0.55	2.18	0.06742	0.148309	-5.20
262202_at	TATC-like protein similar to GB:AAI	APG2	AT2G01110	-1.30	-0.38	-2.18	0.067425	0.148309	-5.20
254689_at	putative pectate lyase A11 ; suppo	---	AT4G13710	-1.28	-0.35	-2.18	0.067436	0.14832	-5.20
259209_at	putative RNA-binding protein ident	---	AT3G09160	-1.14	-0.19	-2.18	0.06749	0.148424	-5.20
256449_at	mutator transposase MUDRA, puta	---	---	-1.18	-0.24	-2.18	0.067511	0.148455	-5.20
246201_at	minor allergen ;supported by full-ler	---	AT4G36750	-1.15	-0.21	-2.18	0.067527	0.148471	-5.20
249766_at	peroxidase-like protein	---	AT5G24070	-1.20	-0.26	-2.18	0.067531	0.148471	-5.20
258257_at	putative short chain alcohol dehydr	---	AT3G26770	-1.16	-0.21	-2.18	0.067644	0.148705	-5.20
253209_at	putative protein membrane-associa	---	AT4G34830	1.25	0.32	2.17	0.067698	0.14881	-5.21
247820_at	serine/threonine protein kinase ; su	SIP1	AT5G58380	1.26	0.33	2.17	0.067713	0.148827	-5.21
258206_at	hypothetical protein predicted by ge	CID4	AT3G14010	1.19	0.25	2.17	0.067741	0.148875	-5.21
252537_at	putative transporter protein peptide	---	AT3G45710	-1.19	-0.26	-2.17	0.067755	0.148891	-5.21
262672_at	RNA pseudouridylate synthase, pu	---	AT1G76050	-1.19	-0.25	-2.17	0.067793	0.148959	-5.21
249512_at	DNA repair protein RAD23 homolog	---	AT5G38470	1.14	0.20	2.17	0.067829	0.149022	-5.21
251316_s_a	putative protein putative protein Bo	---	AT3G61480	1.19	0.26	2.17	0.067835	0.149022	-5.21
249643_at	putative transposase putative trans	---	---	-1.23	-0.30	-2.17	0.067841	0.149022	-5.21
251301_at	cytochrome p450 (CYP78A9) ;supp	CYP78A9	AT3G61880	1.22	0.29	2.17	0.067852	0.149033	-5.21
248919_at	putative protein contains similarity t	---	AT5G45920	-1.21	-0.27	-2.17	0.067863	0.149041	-5.21
264458_at	unknown protein similar to ESTs gb	---	AT1G10410	1.19	0.25	2.17	0.06789	0.149088	-5.21
254134_at	argininosuccinate synthase -like pr	---	AT4G24830	-1.38	-0.46	-2.17	0.068011	0.14934	-5.21
265008_at	Mlo protein, putative similar to Mlo	MLO6	AT1G61560	1.90	0.93	2.17	0.068021	0.149347	-5.21
254441_at	prolamin box binding protein - like	---	AT4G21050	-1.16	-0.21	-2.17	0.068042	0.149368	-5.21
259938_at	hypothetical protein predicted by ge	---	AT1G71310	1.20	0.26	2.17	0.068044	0.149368	-5.21
263420_at	unknown protein ; supported by ful	---	AT2G17240	1.17	0.23	2.17	0.068123	0.149528	-5.21
249713_at	putative protein contains similarity t	---	AT5G35690	-1.23	-0.30	-2.17	0.068132	0.149532	-5.21

252315_at	putative protein PrMC3 - Pinus rad	CXE12	AT3G48690	1.24	0.31	2.17	0.068195	0.149656	-5.21
247097_at	mannan endo-1,4-beta-mannosida	---	AT5G66460	1.28	0.36	2.17	0.06823	0.149718	-5.21
264623_at	putative NPK1-related protein kinas	ANP1	AT1G09000	-1.16	-0.21	-2.17	0.06825	0.149748	-5.21
249691_at	translation releasing factor RF-2 ;s	HCF109	AT5G36170	1.15	0.20	2.17	0.068291	0.149824	-5.21
266094_at	Expressed protein ; supported by fu	---	AT2G37975	-1.21	-0.27	-2.17	0.0683	0.149826	-5.21
253940_at	putative protein other Arabidopsis h	---	AT4G26950	1.22	0.29	2.17	0.068305	0.149826	-5.21
258320_at	hypothetical protein predicted by ge	---	AT3G22710	-1.17	-0.22	-2.17	0.068325	0.149838	-5.21
265854_at	hypothetical protein predicted by ge	---	AT2G42370	1.16	0.22	2.17	0.068328	0.149838	-5.21
247560_at	putative protein predicted proteins,	---	AT5G61090	-1.24	-0.31	-2.17	0.06833	0.149838	-5.21
245032_at	En/Spm-like transposon protein rela	---	---	-1.29	-0.37	-2.17	0.068351	0.149852	-5.21
258806_at	unknown protein	---	AT3G04020	1.35	0.43	2.17	0.068355	0.149852	-5.21
256710_at	hypothetical protein predicted by ge	---	AT3G30350	-1.34	-0.43	-2.17	0.068357	0.149852	-5.21
262463_at	hexose transporter, putative simila	STP9	AT1G50310	-1.37	-0.46	-2.17	0.068369	0.149864	-5.22
258779_at	putative protein kinase contains Pfa	---	AT3G11870	-1.15	-0.20	-2.17	0.068377	0.149869	-5.22
253599_at	putative protein ash1 protein, Dros	SDG4	AT4G30860	-1.30	-0.37	-2.17	0.068422	0.149948	-5.22
255639_at	putative protein	APRR8	AT4G00760	-1.24	-0.32	-2.17	0.068427	0.149948	-5.22
259880_at	hypothetical protein similar to hypo	---	AT1G76730	-1.30	-0.38	-2.17	0.068436	0.149955	-5.22
264162_at	acyl carrier protein, putative similar	mtACP2	AT1G65290	1.23	0.29	2.17	0.068448	0.149967	-5.22
264590_at	unknown protein ;supported by full-	---	AT2G17710	2.20	1.13	2.17	0.068461	0.149981	-5.22
260574_at	hypothetical protein predicted by ge	---	AT2G47300	-1.21	-0.28	-2.17	0.068471	0.149988	-5.22
250239_at	ABC transporter-like protein	---	AT5G13580	-1.27	-0.35	-2.17	0.068616	0.150281	-5.22
247682_at	serine/threonine-specific protein ki	---	AT5G59650	-1.21	-0.27	-2.17	0.068618	0.150281	-5.22
262500_at	unknown protein Contains PF|0064	FBP7	AT1G21760	1.18	0.23	2.17	0.06863	0.150293	-5.22
262283_at	unknown protein ;supported by full-	---	AT1G68590	-1.26	-0.33	-2.16	0.068719	0.150474	-5.22
259424_at	hypothetical protein contains simila	---	AT1G13830	1.29	0.37	2.16	0.06875	0.150526	-5.22
263093_at	putative replication protein A1	---	---	-1.17	-0.22	-2.16	0.068781	0.15058	-5.22
263377_at	AP2 domain transcription factor (AB	ABI4	AT2G40220	-1.16	-0.21	-2.16	0.068804	0.150617	-5.22
267540_at	hypothetical protein predicted by ge	---	AT2G32760	-1.16	-0.22	-2.16	0.068813	0.150622	-5.22
260908_at	maternal embryogenesis control pr	MEA	AT1G02580	1.38	0.47	2.16	0.068827	0.150637	-5.22
248208_at	unknown protein	ATHB52	AT5G53980	-1.28	-0.35	-2.16	0.068837	0.150645	-5.22
245701_at	ferredoxin-dependent glutamate syn	GLU1	AT5G04140	-1.29	-0.36	-2.16	0.068844	0.150646	-5.22
247939_at	putative protein contains similarity t	ATLIG4	AT5G57160	1.18	0.24	2.16	0.068917	0.150792	-5.22
254115_at	putative protein binding protein HP	---	AT4G24710	-1.17	-0.23	-2.16	0.068957	0.150864	-5.22
251995_at	nuclear envelope membrane protei	FK	AT3G52940	-1.16	-0.22	-2.16	0.069001	0.150917	-5.22
260263_at	hypothetical protein predicted by ge	JAG	AT1G68480	-1.15	-0.20	-2.16	0.069003	0.150917	-5.22

249604_x_a	putative protein RING-H2 finger pr	---	AT5G37230	-1.20	-0.26	-2.16	0.069007	0.150917	-5.22
255055_at	hypothetical protein	---	AT4G09810	1.25	0.33	2.16	0.069008	0.150917	-5.22
257639_at	hypothetical protein	---	AT3G25720	-1.20	-0.26	-2.16	0.069041	0.150976	-5.22
252089_at	putative protein	---	AT3G52110	-1.28	-0.35	-2.16	0.06914	0.151177	-5.23
264763_at	hypothetical protein contains simila	---	AT1G61450	-1.15	-0.21	-2.16	0.069156	0.151188	-5.23
260573_at	putative pectinesterase	---	AT2G47280	-1.20	-0.27	-2.16	0.069159	0.151188	-5.23
247610_at	putative protein predicted protein, A	---	AT5G60630	2.60	1.38	2.16	0.069165	0.151188	-5.23
266462_at	unknown protein ; supported by cD	---	AT2G47770	-1.67	-0.74	-2.16	0.069212	0.151277	-5.23
265343_at	unknown protein ; supported by full-	NIC1	AT2G22570	1.37	0.45	2.16	0.069227	0.151277	-5.23
249064_at	putative protein contains similarity t	---	AT5G44250	-1.16	-0.21	-2.16	0.06923	0.151277	-5.23
248041_at	unknown protein ;supported by full-	emb2731	AT5G55940	-1.15	-0.21	-2.16	0.069232	0.151277	-5.23
252514_at	GTP-binding protein ara-3 ; suppor	ATRAB8A	AT3G46060	1.16	0.22	2.16	0.069317	0.151448	-5.23
251403_at	putative protein RING finger protei	---	AT3G60300	1.27	0.35	2.16	0.069361	0.151531	-5.23
265289_at	unknown protein predicted by gens	---	AT2G22690	1.15	0.20	2.16	0.069417	0.151638	-5.23
250715_at	splicing factor 3a ; supported by cD	ATO	AT5G06160	1.27	0.34	2.16	0.069446	0.151686	-5.23
259300_at	hypothetical protein predicted by ge	---	AT3G05100	-1.18	-0.24	-2.16	0.069467	0.151719	-5.23
264218_at	unknown protein	---	AT1G60200	1.15	0.20	2.16	0.069568	0.151924	-5.23
253155_at	putative protein predicted protein, A	---	AT4G35720	-1.20	-0.27	-2.16	0.069602	0.151971	-5.23
245361_at	hypothetical protein ;supported by f	---	AT4G17790	1.40	0.48	2.16	0.069603	0.151971	-5.23
263376_at	putative surface protein ; supporte	FLA6	AT2G20520	-1.15	-0.20	-2.16	0.069618	0.151989	-5.23
263074_at	putative HMG protein ;supported b	HMGB4	AT2G17560	1.23	0.30	2.16	0.069661	0.152064	-5.23
258050_at	unknown protein	---	AT3G16200	-1.23	-0.29	-2.16	0.069666	0.152064	-5.23
263224_at	putative GTP-binding protein Simila	---	AT1G30580	1.26	0.33	2.15	0.069782	0.152304	-5.24
261537_at	carbonyl reductase, putative simila	---	AT1G01800	1.15	0.20	2.15	0.069796	0.15232	-5.24
258620_at	putative MYB family transcription fa	MYB107	AT3G02940	-1.14	-0.18	-2.15	0.069814	0.152344	-5.24
261651_at	unknown protein similar to unknowr	SAT32	AT1G27760	1.41	0.49	2.15	0.069847	0.152403	-5.24
261013_at	fatty acid elongase 3-ketoacyl-CoA	ATUPS5	AT1G26440	1.28	0.35	2.15	0.069871	0.15244	-5.24
254141_at	glucose-6-phosphate isomerase gl	PGI1	AT4G24620	-1.18	-0.24	-2.15	0.069888	0.152462	-5.24
261749_at	dehydrin, putative similar to dehydr	ERD14	AT1G76180	-1.18	-0.23	-2.15	0.069904	0.152483	-5.24
263558_at	putative phosphatidylinositol/phospl	---	AT2G16380	-1.27	-0.34	-2.15	0.069912	0.152486	-5.24
251938_at	60S RIBOSOMAL PROTEIN L12 -	---	AT3G53430	1.26	0.33	2.15	0.069939	0.152529	-5.24
247725_at	putative Rab5-interacting protein -	---	AT5G59410	1.31	0.39	2.15	0.069946	0.152531	-5.24
254243_at	serine/threonine kinase - like prote	CRK13	AT4G23210	2.21	1.15	2.15	0.069975	0.152559	-5.24
250687_at	putative protein similar to unknown	---	AT5G06660	1.15	0.20	2.15	0.06999	0.152559	-5.24
246402_at	jasmonate inducible protein, putati	---	AT1G57570	-1.16	-0.21	-2.15	0.069991	0.152559	-5.24

265169_x_a	unknown protein	---	AT1G23720	-1.19	-0.25	-2.15	0.070001	0.152559	-5.24
256459_at	acetyl-CoA carboxylase, putative s	ACC2	AT1G36180	1.24	0.31	2.15	0.070002	0.152559	-5.24
264520_at	putative amino acid permease GC	AAP8	AT1G10010	-1.32	-0.40	-2.15	0.070003	0.152559	-5.24
246541_at	ubiquitin-fusion degradation protein	---	AT5G15400	1.18	0.24	2.15	0.070006	0.152559	-5.24
253351_at	putative protein hemolysin, 38K, Sy	---	AT4G33700	1.19	0.26	2.15	0.070018	0.15257	-5.24
246740_at	putative protein	---	AT5G27810	-1.15	-0.21	-2.15	0.070037	0.152585	-5.24
244910_s_a	hypothetical protein	---	---	-1.19	-0.25	-2.15	0.070038	0.152585	-5.24
250469_at	pollen allergen -like protein SAH7 p	---	AT5G10130	-1.25	-0.32	-2.15	0.070062	0.152622	-5.24
245725_at	sucrose synthase, putative similar	SUS6	AT1G73370	-1.45	-0.53	-2.15	0.070089	0.152666	-5.24
263743_at	coatomer alpha subunit	---	AT2G21390	-1.16	-0.21	-2.15	0.070101	0.152678	-5.24
259934_at	unknown protein	---	AT1G71340	1.29	0.37	2.15	0.070111	0.152687	-5.24
251420_at	transcription factor - like protein tra	---	AT3G60490	-1.27	-0.34	-2.15	0.070139	0.152731	-5.24
257668_at	sugar transporter, putative similar t	---	AT3G20460	-1.28	-0.36	-2.15	0.07016	0.152763	-5.24
267106_s_a	putative vacuolar sorting receptor id	ATVSR3	AT2G14720	1.24	0.31	2.15	0.070185	0.152802	-5.24
246217_at	APETALA2 protein ; supported by c	AP2	AT4G36920	-1.37	-0.45	-2.15	0.07022	0.152866	-5.24
259259_at	spindly (gibberellin signal transduct	SPY	AT3G11540	1.19	0.25	2.15	0.070234	0.15288	-5.24
258017_at	unknown protein	---	AT3G19370	-1.40	-0.48	-2.15	0.070252	0.152906	-5.24
261323_at	hypothetical protein predicted by ge	---	AT1G44760	1.33	0.41	2.15	0.07027	0.152919	-5.24
254862_at	putative transport protein Na(+) de	---	AT4G12030	-1.36	-0.45	-2.15	0.070272	0.152919	-5.24
265567_at	unknown protein predicted by gene	---	AT2G05580	-1.22	-0.29	-2.15	0.070283	0.15293	-5.24
267025_at	unknown protein predicted by gens	---	AT2G38350	-1.14	-0.19	-2.15	0.070292	0.152933	-5.24
249497_at	putative protein predicted proteins -	---	AT5G39220	-1.22	-0.29	-2.15	0.070337	0.153012	-5.24
245525_at	dynein light chain like protein	---	AT4G15930	1.14	0.19	2.15	0.070341	0.153012	-5.24
255641_at	contains region of similarity to beta	---	AT4G00800	-1.19	-0.25	-2.15	0.070363	0.153046	-5.24
252958_at	putative transcription factor (MYB4)	MYB4	AT4G38620	-1.58	-0.66	-2.15	0.070404	0.153117	-5.24
247144_at	DOF zinc finger protein-like	---	AT5G65590	-1.30	-0.38	-2.15	0.070418	0.153117	-5.24
256360_at	hypothetical protein	---	AT1G66440	-1.27	-0.34	-2.15	0.070422	0.153117	-5.24
254811_at	putative protein 2-hydroxy-6-oxohe	---	AT4G12230	1.21	0.27	2.15	0.070423	0.153117	-5.24
252694_at	nodulin -like protein nodulin-21, Gly	---	AT3G43630	-1.19	-0.25	-2.15	0.070453	0.153167	-5.25
266357_at	putative beta-amylase	BAM6	AT2G32290	1.64	0.72	2.15	0.070473	0.153196	-5.25
252669_at	putative protein hypothetical protei	---	AT3G44100	1.18	0.24	2.15	0.070506	0.153253	-5.25
249537_at	cysteine-tRNA ligase -like protein c	---	AT5G38830	1.25	0.32	2.15	0.070557	0.153345	-5.25
264274_at	disease resistance protein RPS4, p	---	AT1G60320	-1.18	-0.24	-2.15	0.070561	0.153345	-5.25
247684_at	serine/threonine-specific protein ki	---	AT5G59670	-2.84	-1.50	-2.15	0.070604	0.153423	-5.25
264395_at	putative GDP-dissociation inhibitor	---	AT1G12070	-1.25	-0.32	-2.15	0.070612	0.153426	-5.25

257885_at	S1 self-incompatibility protein, puta	---	AT3G16970	-1.17	-0.23	-2.15	0.070628	0.153434	-5.25
257042_s_a	hypothetical protein predicted by ge	---	AT3G28640	1.17	0.22	2.15	0.07063	0.153434	-5.25
260636_at	hypothetical protein contains simila	ATCDS1	AT1G62430	-1.37	-0.45	-2.15	0.070636	0.153434	-5.25
265245_at	unknown protein	---	AT2G43060	1.38	0.47	2.14	0.070694	0.153544	-5.25
251718_at	putative protein hypothetical protein	MRLK	AT3G56100	-1.25	-0.32	-2.14	0.070721	0.153589	-5.25
257626_s_a	hypothetical protein	---	AT3G26240	-1.20	-0.26	-2.14	0.070752	0.153642	-5.25
258986_at	putative heat shock protein similar	---	AT3G08910	-1.19	-0.26	-2.14	0.070765	0.153655	-5.25
267015_at	unknown protein	---	AT2G39340	-1.23	-0.30	-2.14	0.070791	0.153697	-5.25
262647_at	putative growth regulator protein si	---	AT1G14020	-1.28	-0.36	-2.14	0.070833	0.153761	-5.25
257865_at	protein kinase, putative contains P	---	AT3G17750	-1.15	-0.20	-2.14	0.070834	0.153761	-5.25
262251_at	hypothetical protein predicted by ge	---	AT1G53760	1.36	0.44	2.14	0.070844	0.153767	-5.25
262657_at	ribonuclease contains similarity to R	---	AT1G14210	-1.51	-0.59	-2.14	0.070876	0.153824	-5.25
256965_at	branched chain alpha-keto acid de	DIN4	AT3G13450	1.46	0.54	2.14	0.070914	0.153892	-5.25
265969_at	En/Spm-like transposon protein rela	---	---	-1.18	-0.24	-2.14	0.070922	0.153893	-5.25
263940_at	putative calcium-dependent protein	CPK25	AT2G35890	-1.16	-0.21	-2.14	0.070941	0.153919	-5.25
245699_at	putative protein ;supported by full-le	---	AT5G04250	1.37	0.45	2.14	0.070947	0.153919	-5.25
254976_at	subtilisin-like serine protease conta	---	AT4G10510	-1.18	-0.23	-2.14	0.070973	0.153961	-5.25
261141_at	unknown protein contains Pfam pro	---	AT1G19740	1.21	0.28	2.14	0.071004	0.154014	-5.25
260110_at	hypothetical protein similar to NBS/	---	AT1G63350	-1.16	-0.22	-2.14	0.071019	0.154031	-5.25
264964_at	hypothetical protein predicted by ge	---	AT1G60460	-1.23	-0.30	-2.14	0.071037	0.154056	-5.25
248629_at	mitochondrial carrier protein-like	---	AT5G48970	-1.26	-0.34	-2.14	0.071097	0.154171	-5.25
258729_at	putative amino acid transporter prot	ANT1	AT3G11900	1.16	0.22	2.14	0.071132	0.154232	-5.25
247726_at	telomere repeat-binding protein	TRP1	AT5G59430	1.24	0.31	2.14	0.07115	0.154242	-5.25
258652_at	putative Ras-like GTP-binding prote	ATRABC2E	AT3G09910	-1.37	-0.45	-2.14	0.071153	0.154242	-5.25
258694_at	putative non-phototropic hypocotyl	---	AT3G08660	-1.39	-0.47	-2.14	0.071157	0.154242	-5.26
248484_at	carbonyl reductase-like protein	---	AT5G51030	1.15	0.20	2.14	0.071164	0.154243	-5.26
250134_at	Expressed protein ; supported by cl	---	---	1.22	0.29	2.14	0.071183	0.154269	-5.26
251386_at	putative protein rec, Homo sapiens	---	AT3G60800	-1.15	-0.20	-2.14	0.071196	0.154282	-5.26
252951_at	disease resistance response like p	---	AT4G38700	-1.32	-0.40	-2.14	0.07121	0.154299	-5.26
258462_at	unknown protein	---	AT3G17350	-1.48	-0.57	-2.14	0.071218	0.154302	-5.26
249532_at	AtPP - like protein AtPP protein, Br	---	AT5G38780	1.48	0.57	2.14	0.071232	0.154317	-5.26
251614_at	hypothetical protein	---	AT3G57970	-1.23	-0.30	-2.14	0.071246	0.154332	-5.26
252046_at	putative protein extensin -Nicotiana	---	AT3G52460	-1.21	-0.28	-2.14	0.071281	0.154395	-5.26
251400_at	putative protein prib5, Ribes nigrun	---	AT3G60420	-2.03	-1.02	-2.14	0.071296	0.154411	-5.26
262037_at	hypothetical protein predicted by ge	---	---	-1.19	-0.25	-2.14	0.071302	0.154411	-5.26

250341_at	MAP3K delta-1 protein kinase	---	AT5G11850	-1.15	-0.21	-2.14	0.071325	0.154445	-5.26
251659_at	hypothetical protein ;supported by	BIGYIN	AT3G57090	1.19	0.26	2.14	0.071376	0.15454	-5.26
254176_at	hypothetical protein hypothetical pr	---	AT4G24200	1.18	0.24	2.14	0.071399	0.154575	-5.26
247059_at	UTP-glucose glucosyltransferase ;	UGT72E2	AT5G66690	1.18	0.24	2.14	0.071422	0.154597	-5.26
246428_at	spindle pole body protein-like spinc	---	AT5G17410	1.24	0.30	2.14	0.071425	0.154597	-5.26
246059_at	putative protein KED, Nicotiana tab	---	AT5G08450	1.17	0.23	2.14	0.071429	0.154597	-5.26
245624_at	glucosyltransferase like protein	---	AT4G14090	-1.25	-0.32	-2.14	0.07148	0.154692	-5.26
255359_at	putative glucose-6-phosphate/phos	---	AT4G03950	-1.19	-0.25	-2.14	0.071525	0.154776	-5.26
248297_at	protochlorophyllide reductase; oxid	---	AT5G53100	-1.15	-0.20	-2.14	0.071532	0.154776	-5.26
250942_at	putative protein	---	AT5G03350	-4.36	-2.12	-2.14	0.071557	0.154811	-5.26
248037_at	sexual differentiation process prote	OPT1	AT5G55930	-1.51	-0.59	-2.14	0.071562	0.154811	-5.26
265999_at	unknown protein ; supported by cD	---	AT2G24100	-1.26	-0.33	-2.14	0.071598	0.154875	-5.26
245547_at	cytochrome P450 like protein	CYP702A2	AT4G15300	-1.16	-0.21	-2.14	0.071605	0.154875	-5.26
248282_at	unknown protein ;supported by full-	---	AT5G52900	-1.78	-0.84	-2.14	0.071646	0.154938	-5.26
261689_at	hypothetical protein contains simila	---	AT1G50140	1.26	0.33	2.14	0.071648	0.154938	-5.26
260715_at	hypothetical protein predicted by ge	---	AT1G48200	1.38	0.46	2.14	0.07167	0.154968	-5.26
260356_at	unknown protein ; supported by ful	ATMINE1	AT1G69390	-1.18	-0.24	-2.14	0.071675	0.154968	-5.26
260816_at	hypothetical protein predicted by ge	---	AT1G06930	-1.25	-0.32	-2.14	0.07169	0.154986	-5.26
246535_at	putative protein several hypothetica	---	AT5G15900	-1.27	-0.34	-2.14	0.071717	0.155028	-5.26
265630_at	unknown protein similar to ovarian t	---	AT2G27350	1.16	0.21	2.13	0.071739	0.155062	-5.26
260735_at	disease resistance protein, putative	---	AT1G17610	-1.39	-0.48	-2.13	0.071759	0.155089	-5.26
260863_at	hypothetical protein predicted by ge	---	---	-1.29	-0.37	-2.13	0.071769	0.155097	-5.26
247157_at	nuclear matrix constituent protein 1	LINC4	AT5G65770	1.19	0.25	2.13	0.071841	0.155239	-5.26
261130_at	unknown protein ; supported by cDI	PRMT10	AT1G04870	1.39	0.47	2.13	0.071894	0.155298	-5.27
264792_at	hypothetical protein similar to hypot	---	AT1G08620	1.18	0.24	2.13	0.071898	0.155298	-5.27
244942_at	hypothetical protein	---	---	-1.17	-0.22	-2.13	0.071899	0.155298	-5.27
250198_at	expressed protein contains similari	NAP14	AT5G14100	1.30	0.38	2.13	0.0719	0.155298	-5.27
265754_x_a	En/Spm transposon protein (mosaic	---	---	-1.16	-0.21	-2.13	0.071903	0.155298	-5.27
258423_at	hypothetical protein predicted by ge	---	AT3G16730	1.16	0.21	2.13	0.07193	0.155343	-5.27
266531_at	putative plasma membrane intrinsi	---	AT2G16835	-1.15	-0.20	-2.13	0.071968	0.155404	-5.27
254230_at	polyprenyltransferase like protein p	AtPPT1	AT4G23660	1.19	0.25	2.13	0.071972	0.155404	-5.27
261652_at	dimethyladenosine transferase, pu	PFC1	AT1G01860	1.21	0.28	2.13	0.071991	0.15543	-5.27
259252_at	hypothetical protein similar to hypo	IBM1	AT3G07610	1.17	0.22	2.13	0.072022	0.155471	-5.27
255327_at	putative malonyl-CoA decarboxylas	---	AT4G04320	1.15	0.20	2.13	0.072024	0.155471	-5.27
265492_at	hypothetical protein	AGL95	AT2G15660	-1.18	-0.24	-2.13	0.072039	0.155488	-5.27

255507_at	AtKAP alpha similar to AtKAP, Ger	MOS6	AT4G02150	1.15	0.20	2.13	0.072046	0.155489	-5.27
265136_at	hypothetical protein similar to disea	---	AT1G51270	-1.14	-0.19	-2.13	0.072056	0.155496	-5.27
265847_at	unknown protein	---	AT2G35750	1.16	0.22	2.13	0.072106	0.155582	-5.27
252160_at	proline-rich protein	---	AT3G50570	-1.25	-0.32	-2.13	0.072109	0.155582	-5.27
263465_at	hypothetical protein predicted by ge	---	AT2G31940	-1.23	-0.30	-2.13	0.072129	0.15561	-5.27
250202_at	putative protein similar to unknown	---	AT5G13970	1.21	0.28	2.13	0.072138	0.155615	-5.27
259428_at	MAP kinase, putative similar to MA	ATMPK11	AT1G01560	2.42	1.28	2.13	0.072158	0.15564	-5.27
248390_at	importin alpha subunit	IMPA-8	AT5G52000	-1.14	-0.19	-2.13	0.072166	0.15564	-5.27
266565_at	putative serine carboxypeptidase II	scpl23	AT2G24010	-1.20	-0.27	-2.13	0.07217	0.15564	-5.27
266595_at	hypothetical protein predicted by ge	GC4	AT2G46180	-1.20	-0.27	-2.13	0.0722	0.15569	-5.27
252158_at	CDPK-related protein kinase	CRK	AT3G50530	1.22	0.29	2.13	0.072214	0.155705	-5.27
254123_at	Bnm1 like protein pollen-specific pr	APPB1	AT4G24640	-1.18	-0.24	-2.13	0.072249	0.155765	-5.27
246764_s_a	putative protein At2g27780 and At2	---	AT2G13640	-1.15	-0.21	-2.13	0.072268	0.155782	-5.27
252506_at	putative protein UDP-galactose tra	UTR5	AT3G46180	1.21	0.27	2.13	0.07227	0.155782	-5.27
254643_at	putative protein DNA polymerase I	---	AT4G18820	-1.19	-0.26	-2.13	0.072284	0.155796	-5.27
263172_at	hypothetical protein predicted by ge	CID3	AT1G54170	-1.14	-0.19	-2.13	0.072292	0.155798	-5.27
252690_at	putative protein	---	---	-1.25	-0.32	-2.13	0.072346	0.155893	-5.27
259883_at	putative ribophorin I (dolichyl-dipho	---	AT1G76400	1.23	0.30	2.13	0.072349	0.155893	-5.27
254106_at	geranylgeranylated protein ATGP4	ATGP4	AT4G24990	1.23	0.29	2.13	0.072429	0.15605	-5.27
252253_at	Expressed protein ; supported by fu	---	AT3G49300	-1.14	-0.19	-2.13	0.072496	0.156179	-5.27
257903_at	unknown protein	---	AT3G28460	-1.18	-0.23	-2.13	0.072545	0.156272	-5.27
252965_at	putative auxin-induced protein aux	---	AT4G38860	-1.54	-0.62	-2.13	0.072591	0.156349	-5.27
262662_at	hypothetical protein similar to hypot	---	AT1G13920	-1.22	-0.28	-2.13	0.072595	0.156349	-5.28
259852_at	disulfide bond formation protein, pu	AERO1	AT1G72280	1.46	0.55	2.13	0.072649	0.156438	-5.28
258367_at	putative protein kinase similar to pr	WAG2	AT3G14370	-1.20	-0.26	-2.13	0.072651	0.156438	-5.28
265021_at	unknown protein ;supported by full-	---	AT1G24610	-1.15	-0.20	-2.13	0.072657	0.156438	-5.28
261906_at	hypothetical protein predicted by ge	---	AT1G65080	1.34	0.42	2.13	0.072712	0.156528	-5.28
261837_s_a	transcriptional regulator, putative s	---	AT1G15910	1.25	0.33	2.13	0.072712	0.156528	-5.28
251651_at	putative protein transcription initiati	---	AT3G57370	1.14	0.19	2.13	0.072746	0.156586	-5.28
252685_at	disease resistence - like protein RF	---	AT3G44410	-1.36	-0.44	-2.13	0.07276	0.156602	-5.28
249966_at	putative protein COLD-INDUCIBLE	---	AT5G19030	1.38	0.47	2.12	0.072863	0.1568	-5.28
266092_at	hypothetical protein predicted by ge	---	AT2G37880	-1.19	-0.25	-2.12	0.072866	0.1568	-5.28
261829_at	P-glycoprotein, putative similar to P	PGP10	AT1G10680	-1.23	-0.30	-2.12	0.072874	0.156801	-5.28
250147_at	putative protein predicted proteins,	---	AT5G14600	1.30	0.37	2.12	0.072891	0.156824	-5.28
246537_at	putative protein protochlorophyllide	---	AT5G15940	-1.20	-0.26	-2.12	0.072899	0.156825	-5.28

266210_at	60S ribosomal protein L10A ; supp	PGY1	AT2G27530	1.36	0.44	2.12	0.072906	0.156827	-5.28
250574_at	putative protein putative transcripti	---	AT5G08230	1.16	0.22	2.12	0.072918	0.156838	-5.28
256864_at	topoisomerase II identical to topois	TOPII	AT3G23890	-1.25	-0.32	-2.12	0.072947	0.156884	-5.28
251681_at	putative protein hypothetical protei	---	AT3G57100	-1.21	-0.28	-2.12	0.072975	0.156931	-5.28
252553_at	putative protein	---	AT3G45910	-1.18	-0.23	-2.12	0.073035	0.157045	-5.28
252396_at	hypothetical protein	---	AT3G47980	1.17	0.22	2.12	0.073046	0.157053	-5.28
254223_at	putative protein Pennisetum ciliare	---	AT4G23730	1.15	0.20	2.12	0.073092	0.157138	-5.28
265439_at	senescence-associated protein con	---	AT2G21045	1.97	0.98	2.12	0.073168	0.157285	-5.28
267426_at	hypothetical protein predicted by ge	---	AT2G34820	-1.17	-0.23	-2.12	0.073224	0.157377	-5.28
252126_at	putative disease resistance protein	---	AT3G50950	-1.27	-0.35	-2.12	0.073224	0.157377	-5.28
246886_at	CLC-d chloride channel protein	CLC-D	AT5G26240	1.19	0.26	2.12	0.073242	0.157387	-5.28
264549_at	putative ser/thr protein kinase simila	---	AT1G09440	-1.17	-0.23	-2.12	0.073245	0.157387	-5.28
258124_at	Expressed protein ; supported by cl	---	AT3G18215	1.31	0.39	2.12	0.07325	0.157387	-5.28
251793_at	regulator of chromosome condensa	---	AT3G55580	-1.14	-0.19	-2.12	0.073284	0.157446	-5.28
260983_at	hypothetical protein predicted by ge	---	AT1G53560	-1.37	-0.45	-2.12	0.073364	0.157604	-5.29
246030_at	Expressed protein genomic sequer	---	AT5G21105	-1.18	-0.24	-2.12	0.073391	0.157648	-5.29
259128_at	unknown protein similar to pushove	BIG	AT3G02260	1.30	0.38	2.12	0.073434	0.157723	-5.29
245321_at	Expressed protein ; supported by fu	---	AT4G15545	1.15	0.20	2.12	0.073462	0.157768	-5.29
265842_at	putative AP2 domain transcription fa	ERF38	AT2G35700	-1.45	-0.54	-2.12	0.073479	0.157789	-5.29
261734_at	hypothetical protein similar to hypot	---	AT1G47790	-1.16	-0.22	-2.12	0.073487	0.157789	-5.29
257596_at	unknown protein	---	AT3G24760	1.21	0.27	2.12	0.073492	0.157789	-5.29
259226_at	unknown protein similar to hypothe	---	AT3G07700	-1.24	-0.31	-2.12	0.073543	0.157883	-5.29
261046_at	flavonol 3-o-glucosyltransferase, p	---	AT1G01390	1.30	0.38	2.12	0.073612	0.157997	-5.29
262620_at	hypothetical protein predicted by ge	---	AT1G06540	-1.16	-0.21	-2.12	0.073615	0.157997	-5.29
248928_at	Rac-like gtp binding protein ARAC2	ARAC2	AT5G45970	-1.13	-0.18	-2.12	0.073616	0.157997	-5.29
261638_at	Expressed protein ; supported by fu	---	AT1G49975	-1.41	-0.49	-2.12	0.073638	0.158028	-5.29
251722_at	putative protein neuronal glutamine	---	AT3G56200	1.37	0.45	2.12	0.073652	0.158044	-5.29
267640_at	photomorphogenesis repressor (CO	COP1	AT2G32950	1.24	0.31	2.12	0.073661	0.158048	-5.29
248264_at	putative protein similar to unknown	---	AT5G53310	-1.21	-0.27	-2.12	0.073706	0.15812	-5.29
261405_at	unknown protein ;supported by full-	---	AT1G18740	-1.41	-0.50	-2.12	0.073709	0.15812	-5.29
249989_at	putative protein FACTOR ASSOCI	---	AT5G18525	1.21	0.27	2.12	0.073739	0.158172	-5.29
246757_at	Expressed protein ; supported by fu	WPP3	AT5G27940	-1.15	-0.20	-2.12	0.073786	0.158257	-5.29
265538_at	unknown protein predicted by gens	---	AT2G15860	1.26	0.33	2.11	0.073838	0.158354	-5.29
264412_at	hypothetical protein similar to putati	---	AT1G43260	-1.16	-0.22	-2.11	0.073901	0.158474	-5.29
252340_at	myb-like protein	AtMYB45	AT3G48920	1.30	0.38	2.11	0.073945	0.158552	-5.29

245769_at	hypothetical protein similar to putati	INT2	AT1G30220	1.16	0.21	2.11	0.073955	0.158559	-5.29
251071_at	putative protein receptor protein kin	---	AT5G01950	1.33	0.41	2.11	0.073969	0.158559	-5.29
258023_at	cinnamyl alcohol dehydrogenase id	ATCAD4	AT3G19450	1.53	0.61	2.11	0.073973	0.158559	-5.29
259177_at	hypothetical protein similar to putati	---	AT3G01630	-1.16	-0.22	-2.11	0.073976	0.158559	-5.29
265308_at	putative protein kinase contains a p	ALE2	AT2G20300	-1.14	-0.19	-2.11	0.07399	0.158576	-5.29
266850_at	unknown protein	---	AT2G26850	-1.16	-0.21	-2.11	0.074009	0.1586	-5.29
250065_at	putative protein predicted proteins,	---	AT5G17910	-1.27	-0.34	-2.11	0.074027	0.158623	-5.29
252254_at	hypothetical protein ; supported by	DMS3	AT3G49250	-1.16	-0.21	-2.11	0.074079	0.15872	-5.30
255033_at	putative protein phosphonopyruvat	---	AT4G09520	-1.23	-0.30	-2.11	0.074162	0.158884	-5.30
248945_at	putative protein strong similarity to	---	AT5G45510	-1.22	-0.29	-2.11	0.074183	0.158901	-5.30
263889_at	putative ABC transporter	ATNAP12	AT2G37010	-1.21	-0.27	-2.11	0.074184	0.158901	-5.30
256081_at	hypothetical protein contains Pfam	WOX14	AT1G20700	-1.20	-0.27	-2.11	0.074263	0.159056	-5.30
267284_at	unknown protein predicted by gens	---	AT2G23700	-1.24	-0.31	-2.11	0.074297	0.159092	-5.30
267058_at	putative protein kinase contains a p	MAPKKK17	AT2G32510	-1.31	-0.39	-2.11	0.074302	0.159092	-5.30
264854_at	putative RING zinc finger protein ; s	RHA3A	AT2G17450	-1.21	-0.28	-2.11	0.074307	0.159092	-5.30
257160_at	hypothetical protein predicted by ge	---	---	-1.29	-0.37	-2.11	0.074308	0.159092	-5.30
251172_at	putative protein chloroplast riboson	RRF	AT3G63190	-1.17	-0.23	-2.11	0.074333	0.159132	-5.30
246544_at	auxin transport protein - like auxin	PIN8	AT5G15100	-1.16	-0.21	-2.11	0.074406	0.159272	-5.30
262830_at	purple acid phosphatase, putative	PAP3	AT1G14700	1.31	0.39	2.11	0.074423	0.159293	-5.30
262460_s_a	fructokinase, putative similar to fru	---	AT1G06030	1.16	0.22	2.11	0.074448	0.159331	-5.30
261287_at	hypothetical protein predicted by ge	---	AT1G37020	-1.14	-0.18	-2.11	0.074501	0.159419	-5.30
263047_at	putative phosphoserine aminotrans	---	AT2G17630	1.42	0.51	2.11	0.074503	0.159419	-5.30
253807_at	putative GPI-anchored protein GPI	---	AT4G28280	-1.25	-0.32	-2.11	0.074538	0.15948	-5.30
264684_at	unknown protein	HEXO3	AT1G65590	-1.40	-0.48	-2.11	0.074576	0.159542	-5.30
250387_at	putative protein predicted proteins,	---	AT5G11290	-1.15	-0.20	-2.11	0.074581	0.159542	-5.30
247477_at	putative protein 21K protein precur	---	AT5G62340	-1.26	-0.34	-2.11	0.074618	0.159606	-5.30
248181_at	cytochrome c biogenesis protein pr	---	AT5G54290	-1.27	-0.34	-2.11	0.074685	0.159735	-5.30
261156_s_a	hypothetical protein predicted by ge	---	AT1G34490	-1.17	-0.22	-2.11	0.074733	0.159821	-5.30
266278_at	putative tropinone reductase	---	AT2G29300	-1.56	-0.64	-2.11	0.07474	0.159821	-5.30
247808_at	contains similarity to unknown prote	ECT10	AT5G58190	-1.15	-0.21	-2.11	0.074796	0.159928	-5.30
265880_at	unknown protein	---	AT2G42300	1.28	0.36	2.11	0.074824	0.159971	-5.31
250077_at	putative protein	---	AT5G16680	1.16	0.21	2.11	0.074865	0.160045	-5.31
251752_at	proline transporter 2	PROT2	AT3G55740	-1.31	-0.39	-2.10	0.07492	0.160147	-5.31
255203_at	hypothetical protein	---	---	-1.25	-0.32	-2.10	0.074932	0.160154	-5.31
248084_at	sodium proton exchanger	NHX3	AT5G55470	-1.26	-0.33	-2.10	0.07494	0.160154	-5.31

250225_at	Expressed protein ; supported by fu	---	AT5G14105	1.25	0.32	2.10	0.074944	0.160154	-5.31
250296_at	heat shock protein 17.6-II ;supporte	HSP17.6II	AT5G12020	1.47	0.56	2.10	0.075119	0.160492	-5.31
251250_at	putative protein pectin methylester	---	AT3G62180	-1.25	-0.32	-2.10	0.07512	0.160492	-5.31
263221_at	UDP-galactose 4-epimerase-like pr	MUR4	AT1G30620	1.67	0.74	2.10	0.075124	0.160492	-5.31
265143_at	unknown protein	NFU5	AT1G51390	1.22	0.28	2.10	0.075201	0.160641	-5.31
253512_at	putative protein protein phosphatas	WIN2	AT4G31750	-1.18	-0.24	-2.10	0.075257	0.160732	-5.31
251466_at	putative protein hypothetical protei	---	AT3G59340	-1.22	-0.29	-2.10	0.075257	0.160732	-5.31
257609_at	Expressed protein ; supported by fu	---	AT3G13845	1.21	0.28	2.10	0.075266	0.160736	-5.31
264584_at	unknown protein Similar to Synecho	---	AT1G05140	1.21	0.27	2.10	0.075381	0.160958	-5.31
266384_at	hypothetical protein predicted by ge	---	AT2G14660	-1.21	-0.27	-2.10	0.075384	0.160958	-5.31
259435_at	hypothetical protein similar to putati	---	AT1G01450	-1.16	-0.21	-2.10	0.075454	0.161092	-5.31
259864_at	hypothetical protein predicted by ge	---	AT1G72800	1.36	0.44	2.10	0.075495	0.16114	-5.31
255985_at	putative protein contains similarity t	---	AT1G34150	1.15	0.21	2.10	0.075495	0.16114	-5.31
254282_at	hypothetical protein	---	AT4G22860	-1.17	-0.22	-2.10	0.075498	0.16114	-5.31
263678_at	hypothetical protein Similar to Babe	---	AT1G04420	-1.32	-0.40	-2.10	0.075505	0.16114	-5.31
264056_at	putative DOF zinc finger protein ;su	---	AT2G28510	-1.27	-0.34	-2.10	0.075513	0.16114	-5.31
264208_at	putative polyA-binding protein, PAE	PAB3	AT1G22760	-1.31	-0.39	-2.10	0.075519	0.16114	-5.31
263325_at	putative RING zinc finger protein ;	XERICO	AT2G04240	1.41	0.49	2.10	0.075527	0.161142	-5.31
246109_at	hypothetical protein (fragment?)	---	AT5G20120	-1.22	-0.29	-2.10	0.075592	0.16126	-5.32
264579_at	Expressed protein ; supported by fu	---	AT1G05205	1.26	0.34	2.10	0.075596	0.16126	-5.32
259440_at	hypothetical protein predicted by ge	BPS1	AT1G01550	1.17	0.22	2.10	0.075627	0.161311	-5.32
254972_at	putative protein more than 10 putati	---	AT4G10440	-1.20	-0.26	-2.10	0.075642	0.161327	-5.32
245435_at	hypothetical protein	AT4G1714(	---	-1.15	-0.20	-2.10	0.075665	0.161362	-5.32
248813_at	Expressed protein ; supported by fu	VAM3	AT5G46860	1.27	0.34	2.10	0.075697	0.161414	-5.32
254118_at	DNA polymerase III like protein DN	---	AT4G24790	1.16	0.22	2.10	0.075712	0.16143	-5.32
259587_at	unknown protein ;supported by full-	---	AT1G28120	1.19	0.25	2.10	0.075764	0.161527	-5.32
261027_at	cyclic nucleotide and calmodulin-re	ATCNGC1(	AT1G01340	1.64	0.71	2.10	0.075814	0.161619	-5.32
264061_at	putative cyclin-dependent kinase re	CKS2	AT2G27970	1.43	0.52	2.10	0.075843	0.161664	-5.32
255895_at	12-oxophytodienoate reductase, pu	---	AT1G17990	-1.82	-0.86	-2.10	0.075905	0.161767	-5.32
264016_at	putative auxin-regulated protein	---	AT2G21220	-1.19	-0.26	-2.10	0.075905	0.161767	-5.32
252526_at	putative protein ethylene-forming e	---	AT3G46480	-1.23	-0.30	-2.10	0.075926	0.161797	-5.32
259325_at	unknown protein	---	AT3G05320	-2.78	-1.47	-2.10	0.075936	0.161804	-5.32
249791_at	amino acid transporter ; supported	AAP7	AT5G23810	-1.32	-0.40	-2.09	0.076016	0.161958	-5.32
258497_at	putative flowering-time gene CONS	COL2	AT3G02380	-1.19	-0.25	-2.09	0.076028	0.161968	-5.32
257572_at	hypothetical protein predicted by ge	---	AT3G16880	-1.22	-0.28	-2.09	0.076043	0.161985	-5.32

247012_at	putative protein contains similarity t	TRB2	AT5G67580	1.19	0.25	2.09	0.076068	0.162024	-5.32
263219_at	putative serine proteinase Strong si	---	AT1G30600	-1.27	-0.34	-2.09	0.076095	0.162059	-5.32
261764_at	receptor lectin kinase, putative sim	---	AT1G15530	-1.20	-0.27	-2.09	0.076104	0.162059	-5.32
266426_x_a	hypothetical protein predicted by ge	---	AT2G07140	1.35	0.43	2.09	0.076106	0.162059	-5.32
261461_at	hypothetical protein predicted by ge	---	AT1G07860	-1.21	-0.27	-2.09	0.076139	0.162115	-5.32
250410_at	putative protein putative ATP/GTP-	---	AT5G11010	1.29	0.37	2.09	0.076156	0.162136	-5.32
249869_at	acetyl-CoA synthetase-like protein	AAE17	AT5G23050	1.28	0.36	2.09	0.076164	0.162138	-5.32
265086_at	hypothetical protein contains Zinc f	RING1B	AT1G03770	1.27	0.34	2.09	0.076232	0.162267	-5.32
258611_at	unknown protein ;supported by full-	---	AT3G02860	1.18	0.24	2.09	0.076259	0.162284	-5.32
257759_at	hypothetical protein	---	AT3G23070	1.29	0.37	2.09	0.076262	0.162284	-5.32
259792_at	unknown protein ; supported by cDI	CAD1	AT1G29690	-1.62	-0.70	-2.09	0.076266	0.162284	-5.32
258930_at	unknown protein predicted by gens	---	AT3G10040	-1.17	-0.23	-2.09	0.076269	0.162284	-5.32
252061_at	hypothetical protein phosphate act	---	AT3G52620	-1.16	-0.22	-2.09	0.076278	0.162284	-5.32
254706_at	putative protein DNA-binding prote	---	AT4G17950	-1.26	-0.33	-2.09	0.076283	0.162284	-5.32
252152_at	putative protein several hypothetica	---	AT3G51350	-1.17	-0.22	-2.09	0.076372	0.162458	-5.33
251590_at	pollen-specific protein BAN102-like	AGP23	AT3G57690	-1.27	-0.34	-2.09	0.07638	0.162461	-5.33
249223_at	receptor lectin kinase-like protein	---	AT5G42120	1.20	0.27	2.09	0.076554	0.162815	-5.33
248713_at	putative protein contains similarity t	NSP5	AT5G48180	1.45	0.54	2.09	0.07657	0.162834	-5.33
263079_at	putative retroelement pol polyprotei	---	---	-1.16	-0.22	-2.09	0.076612	0.162895	-5.33
257404_at	hypothetical protein predicted by ge	SUVR1	AT1G04050	-1.18	-0.24	-2.09	0.076615	0.162895	-5.33
246675_at	putative protein	---	AT5G30420	-1.19	-0.26	-2.09	0.07662	0.162895	-5.33
265457_at	unknown protein ; supported by ful	---	AT2G46550	1.24	0.30	2.09	0.076637	0.162907	-5.33
246125_at	Expressed protein ; supported by fu	---	AT5G19875	1.71	0.77	2.09	0.07664	0.162907	-5.33
267176_at	putative zinc finger protein	---	AT2G37730	-1.19	-0.26	-2.09	0.076672	0.16296	-5.33
251126_at	putative protein various predicted p	---	AT5G01070	-1.16	-0.22	-2.09	0.076685	0.162963	-5.33
251965_at	putative protein variety of predicted	---	AT3G53360	1.19	0.25	2.09	0.076688	0.162963	-5.33
251729_at	alpha-galactosidase-like protein alp	---	AT3G56310	1.36	0.44	2.09	0.076705	0.162984	-5.33
254989_at	retrotransposon like protein copia-l	---	---	-1.21	-0.27	-2.09	0.076745	0.163055	-5.33
261447_at	transcription factor, putative similar	---	AT1G21160	1.18	0.23	2.09	0.076755	0.163061	-5.33
262382_at	virus resistance protein, putative si	---	AT1G72920	2.31	1.21	2.09	0.076786	0.163112	-5.33
255271_at	putative protein (ubiquitin like) to va	---	AT4G05260	-1.20	-0.26	-2.09	0.07684	0.1632	-5.33
257941_at	putative UDP-glucose glucosyltrans	UGT71B8	AT3G21800	-1.17	-0.22	-2.09	0.076843	0.1632	-5.33
261125_at	zinc finger protein 2, putative simila	---	AT1G04990	1.37	0.45	2.09	0.076849	0.1632	-5.33
263058_at	putative non-LTR retrolelement reve	---	---	-1.19	-0.25	-2.09	0.07687	0.163228	-5.33
266781_at	putative protein kinase contains a p	---	AT2G28940	1.25	0.32	2.09	0.076918	0.163315	-5.33

246033_at	hydroxymethylbilane synthase ;sup	HEMC	AT5G08280	-1.26	-0.34	-2.09	0.076938	0.163344	-5.33
246507_at	lipase-like protein monoglyceride li	---	AT5G16120	-1.29	-0.37	-2.09	0.076999	0.163443	-5.33
245089_at	putative transketolase precursor ; s	---	AT2G45290	2.19	1.13	2.09	0.077	0.163443	-5.33
252267_at	putative protein NITROGEN REGU	---	AT3G49640	-1.27	-0.35	-2.09	0.077018	0.163466	-5.33
266285_at	unknown protein	---	AT2G29180	-1.39	-0.47	-2.09	0.077082	0.163587	-5.33
248295_at	putative protein contains similarity t	---	AT5G53070	1.20	0.26	2.09	0.077096	0.163588	-5.33
264001_at	putative peroxidase ;supported by	---	AT2G22420	-1.39	-0.47	-2.09	0.077096	0.163588	-5.33
266859_at	putative MADS-box protein	AGL41	AT2G26880	-1.21	-0.28	-2.09	0.077119	0.16362	-5.34
251224_at	hypothetical protein	---	AT3G62620	1.20	0.27	2.08	0.077128	0.163625	-5.34
252948_at	putative protein NLS receptor - Ory	KAK	AT4G38600	-1.20	-0.26	-2.08	0.07714	0.163634	-5.34
248380_at	phosphoglucomutase (emb|CAB64	PGM	AT5G51820	1.40	0.48	2.08	0.077179	0.163702	-5.34
260349_at	mitotic checkpoint protein, putative	---	AT1G69400	-1.20	-0.26	-2.08	0.077211	0.163751	-5.34
251624_at	hypothetical protein ;supported by	---	AT3G57280	1.23	0.30	2.08	0.077216	0.163751	-5.34
257999_at	hypothetical protein similar to hypot	---	AT3G27540	-1.37	-0.45	-2.08	0.077251	0.163805	-5.34
262086_at	GTP-binding protein, putative simil	---	AT1G56050	1.22	0.29	2.08	0.07726	0.163805	-5.34
248066_at	putative protein contains similarity t	QRT1	AT5G55590	-1.19	-0.25	-2.08	0.077263	0.163805	-5.34
252217_at	putative protein some putative prote	---	AT3G50140	-1.28	-0.35	-2.08	0.077275	0.163814	-5.34
265236_s_a	hypothetical protein	---	AT2G07714	-1.18	-0.24	-2.08	0.077286	0.163823	-5.34
262287_at	unknown protein ;supported by full-	---	AT1G68660	1.20	0.26	2.08	0.077297	0.16383	-5.34
250830_at	putative protein similar to unknown	---	AT5G04910	1.25	0.32	2.08	0.077316	0.163857	-5.34
247442_s_a	tubulin beta-2/beta-3 chain (sp|P29	TUB2	AT5G62690	-1.33	-0.42	-2.08	0.077333	0.163877	-5.34
248967_at	unknown protein ;supported by full-	---	AT5G45350	-1.24	-0.30	-2.08	0.077351	0.163877	-5.34
258022_at	hypothetical protein predicted by ge	---	AT3G19460	-1.14	-0.18	-2.08	0.077356	0.163877	-5.34
253929_s_a	putative protein H+-transporting AT	---	AT2G16030	-1.20	-0.26	-2.08	0.077363	0.163877	-5.34
250348_at	putative protein	---	AT5G11990	-1.22	-0.29	-2.08	0.077364	0.163877	-5.34
265542_at	putative SNF2 subfamily transcripti	SYD	AT2G28290	1.15	0.21	2.08	0.077369	0.163877	-5.34
259585_at	hypothetical protein contains simila	---	AT1G28090	1.17	0.22	2.08	0.077413	0.163954	-5.34
266609_at	unknown protein ; supported by cD	SRO1	AT2G35510	1.26	0.33	2.08	0.077483	0.164081	-5.34
251415_at	putative protein	---	AT3G60380	-1.17	-0.23	-2.08	0.077499	0.164081	-5.34
253594_at	Expressed protein ; supported by fu	---	AT4G30820	1.21	0.28	2.08	0.0775	0.164081	-5.34
246409_at	CRK1 protein, putative similar to C	---	AT1G57700	-1.26	-0.34	-2.08	0.077505	0.164081	-5.34
259647_at	acetyl-CoA synthetase, putative sir	---	AT1G55325	1.21	0.27	2.08	0.077509	0.164081	-5.34
245966_at	AP2 domain containing protein RAF	RAP2.11	AT5G19790	-1.19	-0.25	-2.08	0.077532	0.164116	-5.34
250154_at	putative aldose 1-epimerase - like	---	AT5G15140	-1.14	-0.19	-2.08	0.077553	0.164137	-5.34
249684_s_a	cytochrome P450-like	---	AT5G36110	-1.16	-0.21	-2.08	0.077557	0.164137	-5.34

265957_at	hypothetical protein predicted by ge	---	AT2G37300	-1.13	-0.18	-2.08	0.077583	0.164178	-5.34
264682_at	polygalacturonase, putative similar	---	AT1G65570	-1.15	-0.20	-2.08	0.077615	0.16423	-5.34
263619_at	putative GDP-mannose pyrophosp	---	AT2G04650	-1.18	-0.24	-2.08	0.077628	0.164241	-5.34
265777_at	hypothetical protein predicted by ge	---	AT2G07340	1.16	0.22	2.08	0.077637	0.164247	-5.34
258862_at	putative mitochondrial processing p	MPPBETA	AT3G02090	1.18	0.24	2.08	0.07765	0.164258	-5.34
255255_at	coded for by A. thaliana cDNA T447	---	AT4G05070	1.32	0.40	2.08	0.077666	0.164276	-5.34
257749_at	actin 2 identical to GB:AAB37098 f	ACT2	AT3G18780	-1.16	-0.21	-2.08	0.077733	0.164388	-5.34
266657_at	unknown protein ;supported by full	---	AT2G25910	-1.14	-0.18	-2.08	0.077733	0.164388	-5.34
245812_at	hypothetical protein predicted by ge	---	---	-1.16	-0.22	-2.08	0.077775	0.164462	-5.34
253934_at	putative beta-1,3-glucanase beta-1	---	AT4G26830	-1.17	-0.22	-2.08	0.077808	0.164501	-5.34
250336_at	alpha-glucosidase 1 ; supported by	---	AT5G11720	-1.22	-0.29	-2.08	0.077808	0.164501	-5.34
246325_at	hypothetical protein contains simila	ABA3	AT1G16540	1.50	0.58	2.08	0.077818	0.164507	-5.34
260663_at	hypothetical protein predicted by ge	NFD5	AT1G19520	1.32	0.40	2.08	0.077845	0.164548	-5.34
249959_at	NADH:ubiquinone oxidoreductase	---	AT5G18800	1.24	0.30	2.08	0.077853	0.16455	-5.34
260120_at	hypothetical protein	ATPP2-A4	AT1G33920	-1.18	-0.24	-2.08	0.077884	0.1646	-5.34
266301_at	putative MYB family transcription fa	AtMYB81	AT2G26960	-1.27	-0.34	-2.08	0.077892	0.164602	-5.35
259554_at	hypothetical protein	---	---	1.25	0.32	2.08	0.077929	0.164666	-5.35
248898_at	outward rectifying potassium chann	KCO2	AT5G46370	-1.21	-0.28	-2.08	0.077941	0.164676	-5.35
249162_at	Expressed protein ; supported by fu	---	AT5G42765	-1.26	-0.33	-2.08	0.077978	0.164739	-5.35
245204_at	1-AMINOCYCLOPROPANE-1-CAI	---	AT5G12270	-1.28	-0.36	-2.08	0.078047	0.164869	-5.35
245764_s_a	hypothetical protein contains simila	ATCSA-1	AT1G19750	-1.16	-0.21	-2.08	0.078107	0.16498	-5.35
251280_at	putative protein beta-1,3-glucanase	---	AT3G61810	-1.17	-0.23	-2.08	0.078171	0.1651	-5.35
245928_s_a	vegetative storage protein Vsp1 ;su	VSP1	AT5G24770	-3.02	-1.59	-2.08	0.078189	0.165124	-5.35
250658_at	C3HC4-type RING zinc finger prote	---	AT5G07040	-1.21	-0.27	-2.08	0.078206	0.165143	-5.35
267633_at	hypothetical protein predicted by ge	---	AT2G42180	-1.15	-0.20	-2.08	0.07823	0.16518	-5.35
254634_at	putative protein transcription factor	---	AT4G18650	-1.20	-0.26	-2.07	0.078284	0.165277	-5.35
246270_at	putative protein	---	AT4G36500	1.81	0.86	2.07	0.078309	0.165316	-5.35
254269_at	putative serine/threonine kinase M	---	AT4G23050	-1.22	-0.29	-2.07	0.078324	0.165327	-5.35
262490_at	hypothetical protein predicted by ge	UREF	AT1G21840	-1.23	-0.30	-2.07	0.078329	0.165327	-5.35
253233_at	putative protein various predicted p	---	AT4G34290	1.32	0.40	2.07	0.078353	0.165363	-5.35
262152_s_a	hypothetical protein predicted by ge	---	AT1G52430	1.17	0.22	2.07	0.078416	0.165479	-5.35
254108_at	putative protein	RIN2	AT4G25230	-1.21	-0.27	-2.07	0.078473	0.165584	-5.35
260163_at	putative carnitine/acylcarnitine trans	BAC2	AT1G79900	1.68	0.75	2.07	0.078512	0.165652	-5.35
263878_s_a	unknown protein	---	AT2G22040	1.22	0.28	2.07	0.078536	0.16568	-5.35
265016_at	unknown protein similar to deacety	---	AT1G24420	-1.14	-0.19	-2.07	0.07854	0.16568	-5.35

264158_at	hypothetical protein contains simila	PTAC4	AT1G65260	-1.22	-0.29	-2.07	0.078552	0.16569	-5.35
249069_at	unknown protein	---	AT5G44010	-1.44	-0.52	-2.07	0.078628	0.165836	-5.35
253766_at	putative protein ;supported by full-l	---	AT4G28770	-1.17	-0.23	-2.07	0.078652	0.16587	-5.35
249171_at	putative protein contains similarity t	---	AT5G42940	1.23	0.30	2.07	0.078707	0.16597	-5.36
249452_at	Sec7/gnom -like protein GNOM, Ar	---	AT5G39500	-1.17	-0.23	-2.07	0.078728	0.166	-5.36
261517_at	unknown protein ; supported by full-	---	AT1G71780	1.20	0.26	2.07	0.078754	0.166039	-5.36
256668_at	hypothetical protein similar to hypot	---	AT3G32190	-1.20	-0.27	-2.07	0.078806	0.166133	-5.36
265794_at	unknown protein	---	AT2G01310	1.15	0.20	2.07	0.078821	0.166149	-5.36
250317_at	tubulin beta-6 chain (sp|P29514) ;	TUB6	AT5G12250	-1.63	-0.70	-2.07	0.078864	0.166226	-5.36
250527_at	serine/threonine-protein kinase	SNRK2.1	AT5G08590	1.16	0.21	2.07	0.079074	0.166652	-5.36
259602_at	disease resistance protein, putative	---	AT1G56520	-1.15	-0.20	-2.07	0.079096	0.166683	-5.36
245170_at	60S ribosomal protein L18, 5'partia	---	AT2G47570	-1.18	-0.24	-2.07	0.079123	0.166724	-5.36
263757_at	cysteine proteinase similar to cyste	---	AT2G21430	1.30	0.38	2.07	0.079131	0.166725	-5.36
266317_at	calmodulin identical to GB:L18912;	CAM5	AT2G27030	-1.17	-0.23	-2.07	0.07916	0.166772	-5.36
251819_at	phosphatidylglycerophosphate syn	PGPS2	AT3G55030	-1.19	-0.25	-2.07	0.079169	0.166776	-5.36
253202_at	Expressed protein ; supported by fu	---	AT4G34555	1.40	0.49	2.07	0.07921	0.166846	-5.36
267354_at	putative MYB family transcription fa	MYB25	AT2G39880	-1.30	-0.38	-2.07	0.079236	0.166873	-5.36
250146_at	putative protein polypeptide deform	PDF1B	AT5G14660	-1.32	-0.40	-2.07	0.079237	0.166873	-5.36
247267_at	40S ribosomal protein S28 (sp|P34	RPS28	AT5G64140	1.42	0.50	2.07	0.079245	0.166873	-5.36
262451_at	receptor-associated kinase isolog	SUB	AT1G11130	-1.33	-0.41	-2.07	0.079263	0.166897	-5.36
266549_at	Expressed protein ; supported by fu	EXL1	AT2G35150	-1.19	-0.25	-2.07	0.079293	0.166944	-5.36
262356_at	hypothetical protein predicted by ge	---	AT1G73000	-1.16	-0.21	-2.07	0.079326	0.166997	-5.36
253898_s_a	tryptophan synthase beta-subunit (	TSB2	AT4G27070	1.65	0.72	2.07	0.079339	0.167008	-5.36
254404_at	hypothetical protein	B70	AT4G21340	-1.13	-0.18	-2.07	0.079345	0.167008	-5.36
255333_at	putative polyprotein	---	---	-1.16	-0.21	-2.07	0.079362	0.167028	-5.36
257823_at	integral membrane protein, putative	---	AT3G25190	-1.20	-0.26	-2.06	0.079413	0.16712	-5.36
264154_at	unknown protein	---	AT1G65430	-1.17	-0.23	-2.06	0.079443	0.167168	-5.36
252692_at	cysteine proteinase contains simila	---	AT3G43960	-1.48	-0.57	-2.06	0.079453	0.167173	-5.36
249775_at	squalene monooxygenase 1,2 (squ	SQE6	AT5G24160	1.32	0.40	2.06	0.079478	0.16721	-5.37
259076_at	hypothetical protein predicted by ge	TMAC2	AT3G02140	-2.00	-1.00	-2.06	0.079496	0.167211	-5.37
260011_at	hypothetical protein similar to hypo	---	AT1G68110	-1.22	-0.29	-2.06	0.079497	0.167211	-5.37
262305_at	hypothetical protein predicted by ge	---	AT1G70950	-1.17	-0.22	-2.06	0.0795	0.167211	-5.37
248741_at	putative protein similar to unknown	SLY2	AT5G48170	1.29	0.37	2.06	0.079526	0.167249	-5.37
259987_at	thaumatin-like protein (PR-5) simila	ATLP-3	AT1G75030	-1.24	-0.31	-2.06	0.079538	0.167256	-5.37
254927_at	putative protein hypothetical protei	---	AT4G11400	-1.21	-0.28	-2.06	0.079544	0.167256	-5.37

254281_at	predicted protein ileal sodium-depe	---	AT4G22840	1.68	0.74	2.06	0.079587	0.167331	-5.37
255101_at	putative lipid transfer protein simila	---	AT4G08670	-1.23	-0.30	-2.06	0.079716	0.167587	-5.37
246608_at	putative protein various predicted p	---	AT5G35380	-1.21	-0.27	-2.06	0.079809	0.167767	-5.37
250401_at	putative protein HSPC184, Homo s	---	AT5G10780	1.15	0.21	2.06	0.079816	0.167767	-5.37
263846_at	putative RNA polymerase sigma-70	SIGF	AT2G36990	1.27	0.35	2.06	0.079834	0.167789	-5.37
263381_at	putative MADS-box protein	AGL48	AT2G40210	-1.16	-0.21	-2.06	0.079948	0.168013	-5.37
247663_at	putative protein predicted proteins,	APUM18	AT5G60110	1.15	0.20	2.06	0.080007	0.168119	-5.37
259018_at	unknown protein similar to unknowr	AIR12	AT3G07390	1.72	0.79	2.06	0.080013	0.168119	-5.37
258977_s_a	putative aspartate kinase similar to	AK3	AT3G02020	-1.30	-0.37	-2.06	0.080035	0.168149	-5.37
247614_at	putative protein	---	AT5G60240	-1.16	-0.21	-2.06	0.080057	0.168177	-5.37
245631_at	tRNA-glutamine synthetase, putati	OVA9	AT1G25350	1.16	0.22	2.06	0.080063	0.168177	-5.37
254932_at	putative translation elongation fact	---	AT4G11120	1.29	0.37	2.06	0.080075	0.168187	-5.37
245017_at	PSI I protein	---	---	-1.20	-0.27	-2.06	0.080171	0.168374	-5.37
252660_at	putative protein	---	AT3G44440	-1.15	-0.21	-2.06	0.080213	0.168446	-5.37
252984_at	cinnamyl-alcohol dehydrogenase E	ELI3-2	AT4G37990	1.68	0.75	2.06	0.08023	0.168467	-5.37
245904_at	sucrose-phosphate synthase -like p	ATSPS2F	AT5G11110	1.21	0.28	2.06	0.080287	0.16857	-5.38
247554_at	putative protein leucine zipper-con	ATEXO70E	AT5G61010	1.55	0.63	2.06	0.080303	0.168579	-5.38
262861_at	hypothetical protein similar to hypot	---	AT1G64820	-1.18	-0.24	-2.06	0.080306	0.168579	-5.38
252918_at	putative protein	---	AT4G38980	1.14	0.19	2.06	0.080329	0.168613	-5.38
253665_at	hypothetical protein	---	AT4G30230	1.34	0.42	2.06	0.080361	0.168657	-5.38
252348_at	B12D-like protein B12D protein - H	---	AT3G48140	1.17	0.22	2.06	0.080365	0.168657	-5.38
253451_at	putative myb-protein transforming p	PC-MYB1	AT4G32730	-1.17	-0.22	-2.06	0.080382	0.168676	-5.38
261470_at	ethylene-responsive element bindi	ERF11	AT1G28370	2.17	1.12	2.06	0.08047	0.168839	-5.38
AFFX-r2-At-	Arabidopsis thaliana /REF=U84969	---	---	1.13	0.18	2.06	0.080479	0.168839	-5.38
248457_at	putative protein contains similarity t	---	AT5G51420	-1.25	-0.32	-2.06	0.080482	0.168839	-5.38
262293_at	heat-shock protein 90, putative ide	---	AT1G27640	-1.28	-0.35	-2.06	0.080509	0.16888	-5.38
267398_at	putative glucanase	AtGH9B11	AT2G44560	-1.20	-0.27	-2.06	0.08053	0.168896	-5.38
265803_at	hypothetical protein predicted by ge	---	AT2G18115	-1.23	-0.30	-2.06	0.080537	0.168896	-5.38
261627_at	arsA homolog (hASNA-I), putative	---	AT1G01910	-1.15	-0.21	-2.06	0.080539	0.168896	-5.38
254921_at	putative protein hypothetical protei	---	AT4G11300	1.29	0.37	2.05	0.080562	0.16893	-5.38
260344_at	polyneuridine aldehyde esterase, p	MES15	AT1G69240	-1.19	-0.25	-2.05	0.080571	0.168933	-5.38
264740_at	unknown protein	---	AT1G62070	-1.17	-0.23	-2.05	0.080581	0.168938	-5.38
248966_at	unknown protein ;supported by full-	---	AT5G45360	1.19	0.25	2.05	0.080607	0.168977	-5.38
255370_at	putative protein	---	---	-1.15	-0.20	-2.05	0.080624	0.168996	-5.38
248379_at	RAR1 (gb|AAF18433.1) non-conse	PBS2	AT5G51700	1.19	0.25	2.05	0.080654	0.168996	-5.38

263398_at	putative RAS superfamily GTP-bind	AtRABA5d	AT2G31680	-1.19	-0.25	-2.05	0.080657	0.168996	-5.38
249972_at	tRNA isopentenyltransferase -like p	IPT5	AT5G19040	-1.18	-0.23	-2.05	0.080661	0.168996	-5.38
262954_at	rubredoxin, putative similar to rubre	---	AT1G54500	-1.23	-0.30	-2.05	0.080663	0.168996	-5.38
265321_at	putative Tub family protein	AtTLP2	AT2G18280	-1.15	-0.20	-2.05	0.080666	0.168996	-5.38
265648_at	putative beta-1,3-glucanase ;supp	---	AT2G27500	1.45	0.54	2.05	0.080673	0.168996	-5.38
264177_at	hypothetical protein contains Pfam	---	AT1G02150	1.17	0.23	2.05	0.080675	0.168996	-5.38
262502_at	unknown protein similar to hypothet	PTAC6	AT1G21600	1.18	0.23	2.05	0.08075	0.169126	-5.38
259417_at	unknown protein contains similarity	HFR1	AT1G02340	-1.32	-0.40	-2.05	0.080752	0.169126	-5.38
264262_at	Expressed protein ; supported by fu	---	AT1G09200	-2.06	-1.04	-2.05	0.080788	0.169187	-5.38
261656_at	unknown protein similar to kinesin-l	ARK2	AT1G01950	-1.54	-0.62	-2.05	0.080822	0.169243	-5.38
253349_at	putative protein	---	---	1.15	0.20	2.05	0.080853	0.169283	-5.38
258144_at	hypothetical protein	---	AT3G18180	-1.15	-0.20	-2.05	0.080857	0.169283	-5.38
264151_at	hypothetical protein predicted by	---	AT1G02070	-1.19	-0.25	-2.05	0.080867	0.169289	-5.38
267617_at	heme oxygenase 1 (HO1) identical	TED4	AT2G26670	1.30	0.38	2.05	0.080891	0.169315	-5.38
252894_at	hypothetical protein	---	AT4G39440	-1.21	-0.27	-2.05	0.080894	0.169315	-5.38
263179_at	unknown protein similar to unknowr	---	AT1G05710	1.36	0.45	2.05	0.080902	0.169316	-5.38
261074_at	hypothetical protein predicted by ge	---	AT1G07290	-1.17	-0.23	-2.05	0.080926	0.16933	-5.38
248758_at	RNA-binding protein-like ;supporte	---	AT5G47620	1.21	0.28	2.05	0.080927	0.16933	-5.38
258111_at	putative cytochrome P450 similar to	CYP72A9	AT3G14630	-1.23	-0.30	-2.05	0.080931	0.16933	-5.38
261519_at	unknown protein ; supported by cDI	---	AT1G71810	-1.27	-0.34	-2.05	0.081003	0.169466	-5.38
260931_at	hypothetical protein predicted by ge	---	AT1G02550	-1.22	-0.29	-2.05	0.081028	0.169503	-5.38
248822_at	peroxidase ;supported by full-lengt	---	AT5G47000	-1.16	-0.21	-2.05	0.08111	0.169659	-5.39
250205_at	unknown protein	---	AT5G14020	-1.17	-0.22	-2.05	0.081236	0.169906	-5.39
246312_at	G-protein, putative contains Pfam p	XLG3	AT1G31930	1.46	0.55	2.05	0.081244	0.169906	-5.39
249801_at	calcium-dependent protein kinase (	CDPK9	AT5G23580	1.18	0.24	2.05	0.081277	0.16996	-5.39
254908_at	putative protein other hypothetical p	---	---	-1.20	-0.26	-2.05	0.081304	0.169976	-5.39
264642_at	putative CCAAT-binding transcriptio	NF-YB4	AT1G09030	-1.18	-0.24	-2.05	0.081305	0.169976	-5.39
245541_at	hypothetical protein	---	AT4G15240	1.28	0.35	2.05	0.081313	0.169976	-5.39
261476_at	hypothetical protein contains simila	---	AT1G14480	1.44	0.52	2.05	0.081314	0.169976	-5.39
249930_at	synaptobrevin-like protein	ATVAMP71	AT5G22360	-1.17	-0.22	-2.05	0.081325	0.169982	-5.39
255949_at	hypothetical protein predicted by ge	---	AT1G22080	-1.13	-0.18	-2.05	0.081353	0.170027	-5.39
248121_at	putative protein contains similarity t	GAUT12	AT5G54690	-1.28	-0.35	-2.05	0.08138	0.170065	-5.39
256100_at	unknown protein	---	AT1G13750	1.66	0.73	2.05	0.081386	0.170065	-5.39
253284_at	putative protein hydroxyproline-rich	---	AT4G34150	-1.42	-0.50	-2.05	0.081459	0.170201	-5.39
266522_at	putative ubiquitin-conjugating enzyr	UBC23	AT2G16920	1.20	0.26	2.05	0.081529	0.170323	-5.39

252229_at	putative protein lea32, Arabidopsis	---	AT3G49890	1.23	0.29	2.05	0.081532	0.170323	-5.39
258886_at	putative importin alpha similar to GI	IMPA-7	AT3G05720	-1.18	-0.24	-2.05	0.081597	0.170443	-5.39
250214_at	endoxyloglucan transferase (dbj|BA	EXGT-A4	AT5G13870	1.21	0.28	2.05	0.081653	0.170534	-5.39
261127_at	unknown protein ; supported by cDI	---	AT1G04790	1.24	0.31	2.05	0.08166	0.170534	-5.39
246917_at	serine-rich protein ;supported by fu	---	AT5G25280	1.37	0.46	2.05	0.081663	0.170534	-5.39
252538_at	putative transporter protein peptide	---	AT3G45720	-1.15	-0.20	-2.05	0.081689	0.170572	-5.39
252287_at	30S ribosomal protein S9 -like simil	---	AT3G49080	1.29	0.37	2.04	0.081788	0.170763	-5.39
259460_at	unknown protein ; supported by cDI	---	AT1G44000	-1.36	-0.45	-2.04	0.081814	0.170801	-5.39
266964_at	putative ABC transporter related to	PGP6	AT2G39480	-1.13	-0.18	-2.04	0.081827	0.170812	-5.39
257718_at	organ separation protein, putative s	anac058	AT3G18400	-1.19	-0.25	-2.04	0.081845	0.170834	-5.39
251093_at	putative protein several hypothetica	---	AT5G01360	-1.31	-0.39	-2.04	0.081908	0.170951	-5.39
257968_at	hypothetical protein predicted by ge	---	AT3G27550	1.28	0.36	2.04	0.081942	0.171006	-5.40
249943_at	putative protein similar to unknown	---	AT5G22280	1.39	0.48	2.04	0.081979	0.171057	-5.40
246118_at	beta-1,3-glucanase bg5	BG5	AT5G20340	-1.20	-0.26	-2.04	0.081981	0.171057	-5.40
258615_at	putative aspartyl protease contains	---	AT3G02740	1.23	0.30	2.04	0.082052	0.17119	-5.40
247823_at	putative protein predicted proteins	---	AT5G58450	1.14	0.19	2.04	0.082124	0.171302	-5.40
252273_at	putative WD-40 repeat - protein be	---	AT3G49660	1.19	0.25	2.04	0.08213	0.171302	-5.40
266506_at	unknown protein	---	AT2G47850	1.16	0.22	2.04	0.082145	0.171302	-5.40
266944_at	unknown protein predicted by gene	---	AT2G18870	-1.19	-0.25	-2.04	0.082147	0.171302	-5.40
257681_at	hypothetical protein predicted by ge	---	AT3G13370	-1.14	-0.19	-2.04	0.082151	0.171302	-5.40
248655_at	60S ribosomal protein L13a ;suppo	---	AT5G48760	1.26	0.33	2.04	0.082151	0.171302	-5.40
257474_at	DNA-3-methyladenine glycosidase	---	AT1G80850	-1.20	-0.27	-2.04	0.082246	0.171483	-5.40
249258_at	putative protein similar to unknown	---	AT5G41650	1.15	0.20	2.04	0.082276	0.17153	-5.40
253409_at	putative protein	---	AT4G32960	1.15	0.20	2.04	0.082299	0.171562	-5.40
258424_at	hypothetical protein predicted by ge	---	AT3G16750	1.20	0.26	2.04	0.082319	0.171589	-5.40
256013_at	unknown protein	DA1	AT1G19270	1.23	0.30	2.04	0.082363	0.171666	-5.40
260582_at	hypothetical protein predicted by ge	---	AT2G47200	1.20	0.26	2.04	0.082381	0.171679	-5.40
254605_at	protein kinase - like protein protein	---	AT4G18950	-1.48	-0.57	-2.04	0.082385	0.171679	-5.40
262828_at	major latex protein type1 identical t	---	AT1G14950	-1.31	-0.39	-2.04	0.082396	0.171687	-5.40
255990_at	glycyl tRNA synthetase, putative si	---	AT1G29870	-1.18	-0.24	-2.04	0.082507	0.171902	-5.40
246599_at	putative protein ATP-dependent RI	---	AT5G14900	-1.14	-0.19	-2.04	0.082522	0.171918	-5.40
264498_at	Expressed protein ; supported by fu	DIS2	AT1G30825	-1.20	-0.27	-2.04	0.082536	0.171927	-5.40
246744_at	putative protein predicted protein, A	---	AT5G27760	1.70	0.76	2.04	0.082542	0.171927	-5.40
264070_at	putative cyclin-dependent kinase re	CKS1	AT2G27960	1.27	0.35	2.04	0.082591	0.172015	-5.40
247527_at	leucine-rich receptor-like protein ki	---	AT5G61480	-1.28	-0.36	-2.04	0.082634	0.172089	-5.40

251812_at	hypothetical protein ;supported by	---	AT3G54970	-1.25	-0.32	-2.04	0.082645	0.172094	-5.40
251456_at	beta-glucosidase-like protein severa	BGLU27	AT3G60120	4.02	2.01	2.04	0.082727	0.17225	-5.40
255152_at	Rab-like protein Rab11 protein - Ar	---	AT4G08190	-1.13	-0.18	-2.04	0.082772	0.172329	-5.41
254365_at	putative protein hypothetical protei	---	AT4G22030	-1.17	-0.23	-2.04	0.082795	0.17236	-5.41
263361_at	putative senescence-associated pro	TET13	AT2G03840	-1.18	-0.24	-2.04	0.082813	0.172381	-5.41
246609_at	putative receptor-like protein kinas	---	AT5G35390	-1.15	-0.20	-2.04	0.082844	0.17243	-5.41
265287_at	putative photosystem I reaction cen	PSAE-2	AT2G20260	-1.14	-0.18	-2.04	0.08287	0.172469	-5.41
261353_at	hypothetical protein contains simila	---	AT1G79600	-1.28	-0.35	-2.04	0.08289	0.172495	-5.41
256161_at	unknown protein ; supported by cDI	---	AT1G30090	1.18	0.24	2.03	0.083012	0.172733	-5.41
245101_at	putative cytochrome P450 ; suppor	CYP98A3	AT2G40890	1.27	0.35	2.03	0.083024	0.172744	-5.41
256705_at	cytochrome P450, putative similar	CYP702A8	AT3G30290	-1.21	-0.28	-2.03	0.083045	0.172771	-5.41
246066_at	putative protein predicted proteins,	SMG7	AT5G19400	1.19	0.25	2.03	0.083054	0.172773	-5.41
253132_at	NAM / CUC2 -like protein nap gene	NTL9	AT4G35580	1.22	0.28	2.03	0.083157	0.172971	-5.41
265725_at	putative alanine acetyl transferase	---	AT2G32030	3.17	1.67	2.03	0.083171	0.172986	-5.41
245087_at	hypothetical protein predicted by ge	DAR2	AT2G39830	1.28	0.35	2.03	0.083187	0.173002	-5.41
254892_at	putative protein other hypothetical p	---	AT4G11800	1.21	0.27	2.03	0.083227	0.173055	-5.41
245471_at	probable ribosomal protein	---	AT4G16030	-1.15	-0.20	-2.03	0.083227	0.173055	-5.41
263002_at	hypothetical protein predicted by ge	---	AT1G54200	-1.46	-0.55	-2.03	0.083258	0.173104	-5.41
251337_at	proteasome component C5 ;suppo	PBF1	AT3G60820	1.14	0.19	2.03	0.083345	0.173269	-5.41
263314_at	putative membrane transporter	---	AT2G05760	-1.14	-0.19	-2.03	0.083359	0.17328	-5.41
267280_at	diacylglycerol O-acyltransferase ; s	TAG1	AT2G19450	-1.25	-0.33	-2.03	0.083384	0.17328	-5.41
264851_at	putative calmodulin-domain protein	CPK6	AT2G17290	-1.35	-0.44	-2.03	0.083384	0.17328	-5.41
255871_at	putative small nuclear ribonucleopro	U2B"	AT2G30260	1.19	0.25	2.03	0.083385	0.17328	-5.41
261126_at	TATA binding protein-associated fa	TAF6	AT1G04950	1.16	0.21	2.03	0.083389	0.17328	-5.41
261167_at	disulfide isomerase-related protein	ATPDIL2-2	AT1G04980	1.70	0.76	2.03	0.083441	0.173373	-5.41
246213_at	serine C-palmitoyltransferase like p	ATLCB1	AT4G36480	-1.22	-0.29	-2.03	0.083492	0.173463	-5.41
249942_at	Nitrilase 4 (sp|P46011) ; supported	GAPB	AT1G42970	2.96	1.56	2.03	0.083517	0.173489	-5.41
267072_at	unknown protein	---	AT2G41170	-1.22	-0.29	-2.03	0.083523	0.173489	-5.41
264106_at	unknown protein	SERK4	AT2G13790	-1.16	-0.21	-2.03	0.083527	0.173489	-5.41
246209_at	BEL1-like homeobox 2 protein (BLH	BLH2	AT4G36870	-1.31	-0.39	-2.03	0.083568	0.173557	-5.41
256447_at	nitrate transporter NTL1, putative s	---	AT1G33440	-1.22	-0.29	-2.03	0.083613	0.173635	-5.42
263728_at	gamma-adaptin, putative similar to	---	AT1G60070	-1.18	-0.24	-2.03	0.083639	0.173674	-5.42
267253_at	putative serine carboxypeptidase I	---	AT2G22960	-1.15	-0.20	-2.03	0.083703	0.173786	-5.42
262179_at	hypothetical protein predicted by ge	AGL66	AT1G77980	-1.21	-0.28	-2.03	0.083708	0.173786	-5.42
266203_at	putative phloem-specific lectin	AtPP2-B1	AT2G02230	1.50	0.59	2.03	0.083731	0.173812	-5.42

251940_at	putative protein lysine decarboxyla	---	AT3G53450	-1.17	-0.23	-2.03	0.083736	0.173812	-5.42
250089_at	homeobox protein	HDG9	AT5G17320	-1.21	-0.28	-2.03	0.083807	0.173944	-5.42
267301_at	ubiquitin activating enzyme 1 (UBA	ATUBA1	AT2G30110	1.18	0.24	2.03	0.083844	0.174004	-5.42
249622_at	putative protein	---	AT5G37550	-1.26	-0.33	-2.03	0.083999	0.174308	-5.42
259781_at	reverse transcriptase, putative simi	---	---	-1.20	-0.26	-2.03	0.084006	0.174308	-5.42
260348_at	PPR-repeat protein, putative conta	---	AT1G69350	1.26	0.33	2.03	0.084045	0.174375	-5.42
250127_at	putative protein similar to unknown	---	AT5G16380	-1.22	-0.29	-2.03	0.084066	0.174402	-5.42
252176_at	protein kinase ATN1 -like protein p	---	AT3G50720	-1.21	-0.27	-2.03	0.084105	0.174466	-5.42
246149_at	peroxidase ATP N ;supported by fu	---	AT5G19890	2.37	1.25	2.03	0.084119	0.17448	-5.42
257698_at	regulatory protein of P-starvation a	---	AT3G12730	1.18	0.24	2.03	0.084128	0.174482	-5.42
252611_at	oxidosqualene cyclase - like protei	LAS1	AT3G45130	-1.50	-0.58	-2.02	0.084166	0.174534	-5.42
266566_at	unknown protein	---	AT2G24040	1.20	0.26	2.02	0.084172	0.174534	-5.42
245766_at	En/Spm-like transposon protein, pu	---	---	-1.17	-0.23	-2.02	0.084176	0.174534	-5.42
256683_at	unknown protein ; supported by cDI	---	AT3G52220	-1.14	-0.19	-2.02	0.084195	0.174559	-5.42
253365_at	putative protein various predicted p	---	AT4G33170	1.17	0.23	2.02	0.084249	0.174653	-5.42
246654_s_a	putative protein predicted protein fr	EGY1	AT5G35210	1.13	0.18	2.02	0.084279	0.174701	-5.42
248417_at	unknown protein	---	AT5G51650	-1.14	-0.18	-2.02	0.084288	0.174704	-5.42
249806_at	putative protein contains similarity t	---	AT5G23850	-1.41	-0.49	-2.02	0.084321	0.174756	-5.42
258511_at	unknown protein ;supported by full-	---	AT3G06590	1.21	0.28	2.02	0.084329	0.174756	-5.42
258671_at	putative vacuolar ATP synthase sul	VHA-E2	AT3G08560	-1.23	-0.30	-2.02	0.084369	0.174823	-5.42
245659_at	hypothetical protein predicted by ge	---	AT1G28260	1.36	0.44	2.02	0.084376	0.174823	-5.42
250744_at	putative protein strong similarity to	---	AT5G05840	-1.22	-0.28	-2.02	0.084427	0.174913	-5.42
250080_at	translocon Tic40-like protein ; supp	TIC40	AT5G16620	1.14	0.19	2.02	0.084456	0.174956	-5.43
250854_at	aspartyl aminopeptidase -like prote	---	AT5G04710	1.22	0.29	2.02	0.084585	0.175187	-5.43
245607_at	kinesin like protein	---	AT4G14330	-1.18	-0.24	-2.02	0.084595	0.175187	-5.43
256011_at	respiratory burst oxidase protein, p	---	AT1G19230	-1.18	-0.24	-2.02	0.084596	0.175187	-5.43
263337_at	hypothetical protein predicted by ge	---	---	-1.13	-0.18	-2.02	0.084598	0.175187	-5.43
262410_at	MAGE protein, putative identical to	---	AT1G34770	1.31	0.39	2.02	0.084622	0.175212	-5.43
263610_at	putative beta-1,3-glucanase	---	AT2G16230	-1.21	-0.27	-2.02	0.084627	0.175212	-5.43
264251_at	hypothetical protein identical to GB	---	AT1G09190	1.25	0.32	2.02	0.084633	0.175212	-5.43
263413_at	unknown protein ;supported by full-	BPC4	AT2G21240	1.20	0.27	2.02	0.084641	0.175212	-5.43
245853_at	putative protein predicted protein A	---	AT5G13500	-1.24	-0.31	-2.02	0.084674	0.175261	-5.43
257210_at	hypothetical protein	TTL2	AT3G14950	-1.14	-0.19	-2.02	0.084682	0.175261	-5.43
245765_at	hypothetical protein similar to putati	---	AT1G33600	1.68	0.75	2.02	0.084688	0.175261	-5.43
244954_s_a	hypothetical protein	---	AT2G07732	1.40	0.49	2.02	0.08477	0.175415	-5.43

264963_at	hypothetical protein predicted by ge	ABC4	AT1G60600	-1.27	-0.35	-2.02	0.0848	0.175452	-5.43
251672_at	MADS-box transcription factor-like	AGL16	AT3G57230	-1.16	-0.21	-2.02	0.084803	0.175452	-5.43
247463_at	embryo-specific protein - like embr	---	AT5G62210	-1.19	-0.25	-2.02	0.084823	0.175477	-5.43
251957_at	putative protein predicted proteins,	---	AT3G53690	1.19	0.25	2.02	0.084835	0.175486	-5.43
245643_at	myb-related transcription factor (cp	MYB116	AT1G25340	-1.17	-0.23	-2.02	0.084849	0.175488	-5.43
263982_at	hypothetical protein predicted by ge	---	AT2G42860	-1.23	-0.29	-2.02	0.084859	0.175488	-5.43
265962_at	nodulin-like protein ;supported by f	---	AT2G37460	1.55	0.63	2.02	0.084865	0.175488	-5.43
257901_at	hypothetical protein predicted by ge	---	---	-1.17	-0.23	-2.02	0.084867	0.175488	-5.43
266212_at	putative retroelement pol polyprotei	---	---	-1.23	-0.29	-2.02	0.084893	0.175526	-5.43
251367_at	SKP1 interacting partner 4 (SKIP4)	SKIP4	AT3G61350	-1.21	-0.28	-2.02	0.084927	0.175576	-5.43
245964_at	putative protein C-terminus of gluta	---	AT5G19720	-1.21	-0.27	-2.02	0.084932	0.175576	-5.43
254007_s_a	putative protein RNA-directed DNA	---	AT1G60720	-1.16	-0.21	-2.02	0.085038	0.175779	-5.43
258431_at	hypothetical protein predicted by ge	---	AT3G16580	-1.15	-0.21	-2.02	0.085057	0.175801	-5.43
250972_at	putative protein various Myb relate	LCL1	AT5G02840	1.30	0.38	2.02	0.085072	0.175817	-5.43
257735_at	pectate lyase, putative similar to pe	---	AT3G27400	-1.33	-0.41	-2.02	0.085084	0.175826	-5.43
258159_at	receptor kinase, putative similar to	RLK902	AT3G17840	-1.38	-0.46	-2.02	0.085115	0.175866	-5.43
265529_at	hypothetical protein predicted by ge	---	---	-1.15	-0.20	-2.02	0.085119	0.175866	-5.43
254095_at	oleosin, 18.5K	OLEO1	AT4G25140	-1.18	-0.23	-2.02	0.085132	0.175877	-5.43
261097_at	protein kinase, putative contains pr	---	AT1G62950	-1.27	-0.35	-2.02	0.085168	0.175935	-5.43
267225_at	hypothetical protein predicted by ge	---	AT2G44000	-1.18	-0.24	-2.02	0.085188	0.17596	-5.43
260317_at	E2, ubiquitin-conjugating enzyme 5	UBC5	AT1G63800	1.31	0.39	2.02	0.085245	0.176056	-5.43
245095_at	putative protein kinase contains a p	---	AT2G40860	-1.27	-0.34	-2.02	0.085249	0.176056	-5.43
264457_at	puative glucosyl transferase similar	---	AT1G10400	-1.18	-0.24	-2.02	0.085291	0.176126	-5.43
252016_at	putative protein predicted protein, /	---	AT3G52950	1.17	0.23	2.02	0.085323	0.176177	-5.44
260287_at	unknown protein contains two Kelch	---	AT1G80440	1.31	0.39	2.02	0.085349	0.176213	-5.44
254037_at	hypothetical protein hypothetical pr	ATGDU2	AT4G25760	-1.16	-0.22	-2.01	0.085433	0.176371	-5.44
266098_at	hypothetical protein predicted by ge	---	AT2G37870	-1.26	-0.33	-2.01	0.085446	0.176383	-5.44
257676_at	unknown protein ;supported by full-	TGD2	AT3G20320	1.18	0.24	2.01	0.085497	0.176472	-5.44
265619_at	hypothetical protein	---	AT2G27320	-1.23	-0.30	-2.01	0.085522	0.176507	-5.44
245364_at	hypothetical protein ;supported by f	---	AT4G15790	-1.22	-0.29	-2.01	0.085567	0.176584	-5.44
266075_s_a	unknown protein	---	AT2G40710	1.22	0.29	2.01	0.085618	0.176673	-5.44
251394_at	endosperm specific protein - like er	FLA10	AT3G60900	-1.22	-0.29	-2.01	0.08565	0.176723	-5.44
267119_at	putative cellulose synthase	ATCSLB01	AT2G32610	-1.14	-0.19	-2.01	0.085671	0.176744	-5.44
253300_at	carbonate dehydratase - like protei	BCA5	AT4G33580	-1.29	-0.37	-2.01	0.085682	0.176744	-5.44
266130_at	putative transcription activator	---	AT2G44980	1.29	0.37	2.01	0.085683	0.176744	-5.44

263738_at	hypothetical protein predicted by ge	---	AT1G60060	-1.57	-0.65	-2.01	0.085719	0.176803	-5.44
258644_at	putative RNA-binding protein conta	---	AT3G07810	-1.14	-0.19	-2.01	0.085751	0.176839	-5.44
253289_at	putative protein F10M10_100, Arat	---	AT4G34320	-1.17	-0.23	-2.01	0.085753	0.176839	-5.44
260151_at	unknown protein ;supported by full	---	AT1G52910	-1.74	-0.80	-2.01	0.08578	0.176869	-5.44
254395_at	subtilisin-like protease subtilisin-lik	---	AT4G21640	-1.14	-0.19	-2.01	0.085782	0.176869	-5.44
266129_at	hypothetical protein predicted by ge	CCD7	AT2G44990	-1.67	-0.74	-2.01	0.085812	0.176902	-5.44
248947_at	putative protein similar to unknown	---	AT5G45540	-1.24	-0.30	-2.01	0.085814	0.176902	-5.44
249615_x_a	contains similarity to unknown prote	AGL105	AT5G37420	-1.18	-0.24	-2.01	0.085828	0.176914	-5.44
248633_at	arginine methyltransferase-like prot	PRMT4A	AT5G49020	1.19	0.25	2.01	0.085851	0.176947	-5.44
259532_at	hypothetical protein	---	AT1G12470	-1.14	-0.19	-2.01	0.085874	0.176977	-5.44
267153_at	glutathione S-transferase identical t	ATGSTF9	AT2G30860	1.25	0.33	2.01	0.085945	0.177108	-5.44
252977_at	Phospholipase like protein Arabido	---	AT4G38560	1.55	0.64	2.01	0.085955	0.177108	-5.44
254227_at	putative protein chS-Rex-b - Gallus	BTI1	AT4G23630	-1.26	-0.34	-2.01	0.085969	0.177108	-5.44
253113_at	putative protein physical impedanc	---	AT4G35985	-1.32	-0.40	-2.01	0.085973	0.177108	-5.44
260777_at	mitochondrial carrier protein, putati	---	AT1G14560	-1.18	-0.24	-2.01	0.085976	0.177108	-5.44
261881_at	nodulin-like protein similar to noduli	NIP6;1	AT1G80760	-1.31	-0.40	-2.01	0.086005	0.177141	-5.44
260246_at	hypothetical protein similar to GB:A	---	AT1G74220	-1.16	-0.22	-2.01	0.086008	0.177141	-5.44
246156_at	putative protein predicted proteins f	---	AT5G20090	1.20	0.26	2.01	0.086016	0.177141	-5.44
248400_at	putative protein contains similarity t	---	AT5G52020	-1.23	-0.30	-2.01	0.086025	0.177141	-5.44
267623_at	unknown protein	---	AT2G39650	1.95	0.96	2.01	0.086031	0.177141	-5.44
254915_s_a	cysteine proteinase contains simila	---	AT4G11310	-2.13	-1.09	-2.01	0.086054	0.177171	-5.44
244920_s_a	NADH dehydrogenase subunit 3 Pr	---	AT2G07751	1.20	0.26	2.01	0.086084	0.177218	-5.44
262526_at	putative prenyl transferase (prephy	SPS2	AT1G17050	1.54	0.63	2.01	0.086141	0.177319	-5.44
258083_at	Expressed protein ; supported by fu	---	AT3G25855	-1.20	-0.26	-2.01	0.086162	0.177341	-5.44
248703_at	dermal glycoprotein precursor, extr	---	AT5G48430	3.32	1.73	2.01	0.086167	0.177341	-5.44
256794_at	ribosomal protein L27, putative sim	---	AT3G22230	1.44	0.53	2.01	0.086185	0.177361	-5.45
246895_at	putative protein predicted protein, A	CID6	AT5G25540	-1.16	-0.22	-2.01	0.086196	0.177368	-5.45
265659_at	putative disease resistance protein	AtRLP20	AT2G25440	1.45	0.54	2.01	0.086216	0.177394	-5.45
251204_at	putative protein HMW prekininoger	AT3G6309	---	-1.19	-0.25	-2.01	0.086233	0.177413	-5.45
247086_at	GATA-binding transcription factor-li	---	AT5G66320	1.92	0.94	2.01	0.086253	0.177437	-5.45
252853_at	hypothetical protein ; supported by	---	AT4G39710	-1.45	-0.53	-2.01	0.086261	0.177437	-5.45
256626_at	hypothetical protein, 5' partial	---	AT3G20015	-1.49	-0.57	-2.01	0.086275	0.177451	-5.45
251408_at	palmitoyl-protein thioesterase prec	---	AT3G60340	1.22	0.29	2.01	0.086287	0.177456	-5.45
255602_at	Expressed protein ; supported by fu	---	AT4G01026	-1.20	-0.27	-2.01	0.086293	0.177456	-5.45
258353_s_a	unknown protein similar to GB:AAD	YSL5	AT3G17650	1.24	0.31	2.01	0.086332	0.177514	-5.45

260123_at	AIG1-like protein similar to AIG1 pr	---	AT1G33890	-1.17	-0.22	-2.01	0.086337	0.177514	-5.45
253853_at	putative diacylglycerol kinase (frag	---	AT4G28130	-1.16	-0.22	-2.01	0.086371	0.177568	-5.45
264863_at	putative peroxidase similar to pero	---	AT1G24110	-1.20	-0.26	-2.01	0.086389	0.177588	-5.45
249135_at	putative protein similar to unknown	---	AT5G43160	-1.37	-0.45	-2.01	0.086473	0.177745	-5.45
255262_at	putative protein equilibrative nuclec	---	AT4G05140	-1.16	-0.22	-2.01	0.086509	0.177787	-5.45
264927_at	phosphatidylinositol 3-kinase, puta	VPS34	AT1G60490	1.13	0.18	2.01	0.086525	0.177787	-5.45
267226_at	unknown protein	---	AT2G44010	1.46	0.54	2.01	0.086527	0.177787	-5.45
258073_at	putative auxin-resistance protein, A	---	AT3G25880	-1.16	-0.21	-2.01	0.086537	0.177787	-5.45
259454_at	unknown protein similar to hypothet	---	AT1G44050	-1.19	-0.25	-2.01	0.086538	0.177787	-5.45
260037_at	putative DNA-binding protein (RAV2	RAV2	AT1G68840	-1.87	-0.90	-2.01	0.08655	0.177787	-5.45
265802_at	predicted protein	---	AT2G35733	1.21	0.27	2.01	0.086555	0.177787	-5.45
245817_at	hypothetical protein similar to unkno	---	AT1G26160	1.14	0.19	2.01	0.086555	0.177787	-5.45
246136_at	peptide transporter - like protein pe	---	AT5G28470	-1.19	-0.25	-2.01	0.08657	0.177801	-5.45
267331_at	putative salt-inducible protein	---	AT2G19280	-1.21	-0.28	-2.00	0.086633	0.177915	-5.45
245441_at	decarboxylase like protein	PSD1	AT4G16700	1.23	0.30	2.00	0.086653	0.177939	-5.45
251902_at	uncoupling protein (ucp/PUMP) ; s	PUMP1	AT3G54110	1.46	0.54	2.00	0.086672	0.177962	-5.45
263477_at	putative glucosyltransferase ; supp	---	AT2G31790	-1.27	-0.35	-2.00	0.086704	0.178012	-5.45
260728_at	Pto kinase interactor 1, putative sir	---	AT1G48210	1.38	0.46	2.00	0.086722	0.178034	-5.45
255490_at	putative protein lysosomal trafficki	---	AT4G02660	-1.17	-0.23	-2.00	0.08675	0.178075	-5.45
254043_at	putative protein ; supported by cDN	CIL	AT4G25990	1.64	0.71	2.00	0.086782	0.17811	-5.45
248042_at	putative protein similar to unknown	---	AT5G55960	-1.22	-0.29	-2.00	0.086783	0.17811	-5.45
251286_at	putative protein Bcl-2-interacting pr	---	AT3G61710	1.16	0.21	2.00	0.086806	0.178141	-5.45
252171_at	hypothetical protein ; supported by	---	AT3G50590	-1.17	-0.22	-2.00	0.086814	0.178142	-5.45
246269_at	putative protein	---	AT4G37110	-1.40	-0.49	-2.00	0.086847	0.178193	-5.45
256254_at	hypothetical protein predicted by ge	---	AT3G11290	-1.23	-0.29	-2.00	0.086854	0.178193	-5.45
255175_at	putative glucosyltransferase ;suppo	ATCSLC12	AT4G07960	-1.18	-0.24	-2.00	0.08699	0.178456	-5.45
259959_at	hypothetical protein predicted by ge	CYP59	AT1G53720	1.20	0.27	2.00	0.087135	0.178728	-5.46
246590_at	cyclic nucleotide and calmodulin-re	CNGC18	AT5G14870	-1.14	-0.19	-2.00	0.087139	0.178728	-5.46
259930_at	hypothetical protein predicted by ge	---	AT1G34355	-1.18	-0.24	-2.00	0.087147	0.178728	-5.46
255184_at	putative athila transposon protein	---	---	-1.14	-0.19	-2.00	0.087175	0.17877	-5.46
246528_at	putative mitochondrial carrier prote	---	AT5G15640	-1.32	-0.40	-2.00	0.087215	0.178837	-5.46
263344_at	unknown protein ;supported by full-	---	AT2G04940	1.23	0.30	2.00	0.087266	0.178925	-5.46
255621_at	hypothetical protein	---	AT4G01390	1.99	0.99	2.00	0.087299	0.178965	-5.46
249319_s_a	putative protein similar to unknown	---	AT5G40880	1.20	0.27	2.00	0.087301	0.178965	-5.46
250736_s_a	putative protein contains similarity t	---	AT1G01350	1.25	0.32	2.00	0.087354	0.179038	-5.46

264527_at	putative reticuline oxidase-like prot	---	AT1G30760	-1.43	-0.52	-2.00	0.08736	0.179038	-5.46
251148_at	hypothetical protein	TKL	AT3G63180	1.17	0.22	2.00	0.087361	0.179038	-5.46
249483_at	Expressed protein ; supported by cl	---	AT5G38895	1.21	0.28	2.00	0.087392	0.179087	-5.46
260923_at	glycine-rich RNA-binding protein gr	---	AT1G21570	-1.18	-0.24	-2.00	0.087423	0.179134	-5.46
248520_at	11-beta-hydroxysteroid dehydrogen	AtHSD1	AT5G50600	-1.27	-0.35	-2.00	0.087529	0.179335	-5.46
255318_at	hypothetical protein	---	AT4G04190	1.20	0.26	2.00	0.087573	0.179409	-5.46
247784_at	subtilisin-like serine protease conta	---	AT5G58810	-1.16	-0.22	-2.00	0.087587	0.179417	-5.46
265543_at	unknown protein	---	AT2G28270	-1.13	-0.18	-2.00	0.087593	0.179417	-5.46
245630_at	hypothetical protein similar to putati	---	AT1G25360	1.17	0.23	2.00	0.087642	0.179502	-5.46
255996_s_a	receptor-like serine threonine kinas	---	AT1G29730	-1.21	-0.27	-2.00	0.087668	0.179539	-5.46
261828_at	unknown protein ; supported by cDI	---	AT1G11360	1.16	0.22	2.00	0.08772	0.17963	-5.46
256707_at	hypothetical protein predicted by ge	---	---	-1.15	-0.20	-2.00	0.087795	0.179768	-5.46
253348_at	putative protein SMT4 protein - Sa	---	AT4G33620	1.14	0.18	2.00	0.087816	0.179794	-5.46
250537_at	Expressed protein ; supported by fu	---	AT5G08565	1.30	0.37	2.00	0.087829	0.179804	-5.46
258583_at	putative SRF-type transcription fact	AGL57	AT3G04100	-1.15	-0.20	-2.00	0.087841	0.179814	-5.46
265020_at	putative cytochrome P450 similar t	CYP86C1	AT1G24540	-1.15	-0.20	-1.99	0.0879	0.179896	-5.46
267090_at	unknown protein ; supported by ful	CXIP2	AT2G38270	1.14	0.19	1.99	0.087901	0.179896	-5.46
259249_at	hypothetical protein predicted by ge	---	AT3G07790	-1.26	-0.34	-1.99	0.087914	0.179896	-5.46
264707_at	unknown protein	---	AT1G09730	1.16	0.22	1.99	0.087919	0.179896	-5.46
249277_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G41890	-1.54	-0.63	-1.99	0.087944	0.179896	-5.47
256731_at	hypothetical protein contains Pfam	---	AT3G30340	-1.16	-0.22	-1.99	0.087944	0.179896	-5.47
258821_at	putative wound-induced basic prote	---	AT3G07230	1.22	0.29	1.99	0.087944	0.179896	-5.47
251654_at	putative protein several hypothetica	SDP1-LIKE	AT3G57140	-1.15	-0.20	-1.99	0.087945	0.179896	-5.47
262684_s_a	vacuolar ATP synthase subunit B id	---	AT1G20260	-1.21	-0.27	-1.99	0.08797	0.179931	-5.47
257627_at	cytochrome P450, putative contain	CYP71B25	AT3G26270	1.19	0.25	1.99	0.087989	0.179954	-5.47
250595_at	unknown protein	---	AT5G07770	-1.28	-0.36	-1.99	0.088002	0.179964	-5.47
256087_at	hypothetical protein predicted by ge	---	AT1G20800	-1.16	-0.22	-1.99	0.08801	0.179964	-5.47
254310_at	putative protein predicted protein, A	---	AT4G22430	-1.13	-0.18	-1.99	0.088029	0.179988	-5.47
265098_at	unknown protein	---	AT1G04010	-1.39	-0.48	-1.99	0.088039	0.179993	-5.47
266717_at	Expressed protein ; supported by fu	---	AT2G46735	-1.17	-0.22	-1.99	0.088115	0.180131	-5.47
247536_at	PREG-like - like protein PREG-like	CYCP4;2	AT5G61650	-1.21	-0.28	-1.99	0.088139	0.180163	-5.47
255802_s_a	putative protein RING-H2 finger pr	---	AT4G10150	-1.15	-0.20	-1.99	0.088189	0.180251	-5.47
266666_at	hypothetical protein predicted by ge	---	AT2G29780	-1.17	-0.22	-1.99	0.088198	0.180253	-5.47
246178_s_a	putative protein predicted proteins -	---	---	1.22	0.28	1.99	0.088208	0.180257	-5.47
254967_at	putative protein various predicted p	---	AT4G10410	-1.16	-0.22	-1.99	0.088281	0.18039	-5.47

254345_at	hypothetical protein ;supported by	---	AT4G22000	1.29	0.37	1.99	0.088298	0.180408	-5.47
259810_at	Na+/H+ antiporter, putative similar	ATNHD2	AT1G49810	-1.15	-0.20	-1.99	0.088314	0.180425	-5.47
264592_at	putative prolyl 4-hydroxylase, alpha	---	AT2G17720	1.51	0.59	1.99	0.088369	0.18052	-5.47
245568_at	hypothetical protein	---	AT4G14650	-1.24	-0.31	-1.99	0.088468	0.180707	-5.47
256171_s_a	hypothetical protein similar to revers	---	---	-1.18	-0.24	-1.99	0.088559	0.180877	-5.47
251782_at	beta-N-acetylhexosaminidase -like	HEXO1	AT3G55260	-1.26	-0.33	-1.99	0.088576	0.180896	-5.47
258402_at	unknown protein very similar to unk	---	AT3G15450	-1.46	-0.55	-1.99	0.08859	0.180908	-5.47
264008_at	unknown protein	---	AT2G21120	-1.24	-0.30	-1.99	0.088643	0.181	-5.47
262323_at	6-phosphogluconate dehydrogenas	---	AT1G64190	1.14	0.19	1.99	0.088673	0.181044	-5.47
262989_at	F28C11.5 similar to INNER NO OU	INO	AT1G23420	-1.20	-0.27	-1.99	0.088698	0.18108	-5.47
261735_at	hypothetical protein similar to hypot	---	AT1G47765	-1.18	-0.24	-1.99	0.088766	0.181203	-5.47
246340_s_a	AtPP -like protein AtPP protein, Bra	---	AT3G44860	-1.41	-0.50	-1.99	0.08879	0.181236	-5.47
246306_at	putative protein hypothetical protei	ATBAG4	AT3G51780	1.13	0.18	1.99	0.088799	0.181238	-5.47
262924_s_a	vacuolar ATP synthase, putative si	AVA-P4	AT1G19910	1.20	0.27	1.99	0.088831	0.181271	-5.47
249381_at	acidic ribosomal protein P2 -like ac	---	AT5G40040	-1.21	-0.28	-1.99	0.088831	0.181271	-5.47
257935_at	unknown protein	---	AT3G25440	1.17	0.22	1.99	0.088844	0.181274	-5.48
263327_at	putative receptor-like protein kinase	---	AT2G15300	-1.14	-0.20	-1.99	0.088849	0.181274	-5.48
263518_at	Expressed protein ; supported by fu	---	AT2G21655	-1.17	-0.22	-1.99	0.088865	0.181292	-5.48
249687_at	putative protein oxidosqualene cyc	ATPEN3	AT5G36150	-1.16	-0.22	-1.99	0.0889	0.181346	-5.48
266256_at	60S acidic ribosomal protein P2 ;su	---	AT2G27710	1.34	0.42	1.99	0.088954	0.181439	-5.48
266893_at	hypothetical protein predicted by ge	RTE1	AT2G26070	-1.19	-0.25	-1.99	0.088969	0.181455	-5.48
260860_at	hypothetical protein predicted by ge	---	AT1G43810	-1.17	-0.23	-1.99	0.089002	0.181505	-5.48
264993_at	glyoxal oxidase (glx1), putative sim	---	AT1G67290	-1.32	-0.40	-1.99	0.089019	0.181523	-5.48
254895_at	hypothetical protein	---	AT4G11870	1.22	0.29	1.99	0.089128	0.18173	-5.48
248294_at	RNA-binding protein-like	---	AT5G53060	1.19	0.25	1.99	0.089136	0.18173	-5.48
256625_at	uteroglobin promoter-binding prote	---	AT3G20010	1.30	0.38	1.99	0.089158	0.181759	-5.48
251167_at	putative protein proteinase inhibito	---	AT3G63360	-1.15	-0.20	-1.99	0.08918	0.181786	-5.48
252907_at	putative gamma-glutamyltransferas	GGT2	AT4G39650	-1.15	-0.20	-1.98	0.089203	0.181818	-5.48
252513_at	putative protein KIAA0776 protein,	---	AT3G46220	1.17	0.23	1.98	0.089228	0.181838	-5.48
259745_at	unknown protein	SAG18	AT1G71190	1.19	0.24	1.98	0.089229	0.181838	-5.48
247231_at	transcription factor-like protein	AtMYB53	AT5G65230	-1.17	-0.22	-1.98	0.089244	0.181853	-5.48
261448_at	tonoplast intrinsic protein, alpha (a	---	AT1G21140	-1.29	-0.37	-1.98	0.089262	0.181873	-5.48
262073_at	unknown protein ;supported by full-	ZCW32	AT1G59640	1.36	0.45	1.98	0.089286	0.181905	-5.48
261644_s_a	hypothetical protein contains simila	ATCSA-1	AT1G19750	1.19	0.25	1.98	0.089314	0.181947	-5.48
265244_at	putative amine oxidase	ATPAO2	AT2G43018	-1.36	-0.45	-1.98	0.08933	0.181963	-5.48

255860_at	putative protein heparanase, Homo	AtGUS3	AT5G34940	3.12	1.64	1.98	0.089355	0.181992	-5.48
249757_at	Expressed protein ; supported by fu	---	AT5G24316	-1.20	-0.26	-1.98	0.08936	0.181992	-5.48
248563_at	anthocyanidin-3-glucoside rhamnos	---	AT5G49690	1.30	0.37	1.98	0.089385	0.182018	-5.48
247093_at	zinc finger protein SHI-like ; suppo	SHI	AT5G66350	1.25	0.32	1.98	0.089389	0.182018	-5.48
245225_at	mitochondrial protein-like; contains	---	AT3G29800	-1.23	-0.30	-1.98	0.089402	0.182028	-5.48
247653_at	transcriptional coactivator - like pro	---	AT5G59950	1.15	0.20	1.98	0.089423	0.182054	-5.48
252811_at	putative protein several hypothetica	---	---	-1.18	-0.24	-1.98	0.089445	0.182082	-5.48
262667_at	amine oxidase, putative similar to a	---	AT1G62810	1.28	0.36	1.98	0.089482	0.182142	-5.48
250709_at	putative protein similar to unknown	LBD33	AT5G06080	-1.17	-0.23	-1.98	0.089509	0.182181	-5.48
246604_at	putative protein	---	---	-1.17	-0.22	-1.98	0.089572	0.182285	-5.48
253581_at	stress responsive protein homolog	---	AT4G30660	-1.42	-0.50	-1.98	0.089576	0.182285	-5.48
260329_at	putative cyclin similar to cyclin GB:S	CYCA2;4	AT1G80370	-1.20	-0.26	-1.98	0.089601	0.18232	-5.48
249917_at	putative protein strong similarity to	---	AT5G22460	-2.19	-1.13	-1.98	0.089696	0.182497	-5.48
254180_at	putative protein hin1 protein homol	---	AT4G23930	-1.30	-0.38	-1.98	0.089737	0.18255	-5.48
257878_at	hypothetical protein predicted by ge	---	AT3G17150	-1.17	-0.23	-1.98	0.089738	0.18255	-5.48
267158_at	putative expansin	EXP3	AT2G37640	-2.27	-1.18	-1.98	0.089785	0.182629	-5.49
249456_at	unknown protein ;supported by full-	---	AT5G39410	1.18	0.24	1.98	0.089823	0.18269	-5.49
262442_at	unknown protein identical to hypoth	---	AT1G47420	1.15	0.20	1.98	0.089868	0.182765	-5.49
250894_s_a	putative protein proline-rich protein	---	AT5G03810	-1.19	-0.25	-1.98	0.089884	0.182779	-5.49
259813_at	glutathione S-transferase, putative	ATGSTF14	AT1G49860	-1.18	-0.24	-1.98	0.089899	0.182779	-5.49
258878_at	hypothetical protein predicted by ge	---	AT3G03170	1.15	0.20	1.98	0.089903	0.182779	-5.49
247842_at	SPP30 - like protein SPP30, Solan	---	AT5G58030	-1.14	-0.19	-1.98	0.089907	0.182779	-5.49
255955_at	hypothetical protein predicted by ge	---	AT1G22030	-1.33	-0.41	-1.98	0.089945	0.182833	-5.49
260628_at	hypothetical protein predicted by ge	---	AT1G62320	-1.15	-0.20	-1.98	0.08995	0.182833	-5.49
258117_at	hypothetical protein predicted by ge	---	AT3G14700	1.16	0.21	1.98	0.089966	0.182851	-5.49
249480_s_a	protein kinase - like protein recepto	---	AT5G38990	1.47	0.56	1.98	0.09003	0.182963	-5.49
254155_at	putative protein kinase putative pro	---	AT4G24480	-1.20	-0.26	-1.98	0.090093	0.183076	-5.49
251565_at	putative protein several hypothetica	LBD29	AT3G58190	-1.15	-0.20	-1.98	0.090111	0.183097	-5.49
253772_at	Expressed protein ; supported by fu	A7	AT4G28395	-1.13	-0.18	-1.98	0.090131	0.183119	-5.49
257919_at	myb-related transcription factor, pu	MYB15	AT3G23250	2.35	1.24	1.98	0.090203	0.18325	-5.49
250881_at	putative protein	---	AT5G04080	1.26	0.34	1.98	0.09031	0.18345	-5.49
259293_at	putative DNA binding protein simila	---	AT3G11580	1.32	0.40	1.98	0.090321	0.183456	-5.49
246164_at	putative protein predicted proteins,	---	---	-1.16	-0.22	-1.98	0.090353	0.183487	-5.49
263380_at	hypothetical protein	---	AT2G40200	-1.16	-0.22	-1.98	0.090359	0.183487	-5.49
257165_at	beta-1,3-glucanase, putative simila	---	AT3G24330	-1.26	-0.33	-1.98	0.09036	0.183487	-5.49

249004_at	unknown protein	---	AT5G44570	-1.22	-0.29	-1.98	0.090403	0.183535	-5.49
265703_at	putative ankyrin	---	AT2G03430	1.21	0.28	1.98	0.090407	0.183535	-5.49
259560_at	hypothetical protein	WAK2	AT1G21270	-1.64	-0.72	-1.98	0.090411	0.183535	-5.49
259712_at	putative 20S proteasome beta subu	PBC2	AT1G77440	1.15	0.20	1.98	0.090416	0.183535	-5.49
257622_at	hypothetical protein contains Pfam	---	AT3G20280	1.26	0.33	1.98	0.090428	0.183544	-5.49
246551_at	putative protein predicted proteins,	---	AT5G15070	-1.18	-0.24	-1.98	0.090438	0.183548	-5.49
258165_at	unknown protein ; supported by cD	---	AT3G17900	-1.18	-0.23	-1.98	0.090475	0.183606	-5.49
252218_at	putative protein some putative prote	---	AT3G50150	-1.16	-0.21	-1.97	0.090493	0.183615	-5.49
245056_at	putative glucosyltransferase	UGT76D1	AT2G26480	-1.26	-0.33	-1.97	0.090497	0.183615	-5.49
257029_at	dem-like protein similar to dem GE	---	AT3G19240	1.17	0.23	1.97	0.090504	0.183615	-5.49
262797_at	putative sugar transporter protein r	TMT1	AT1G20840	1.32	0.40	1.97	0.090515	0.183618	-5.49
259133_at	sugar transporter, putative similar t	---	AT3G05400	1.40	0.48	1.97	0.090521	0.183618	-5.49
251152_at	RAN GTPase activating protein 1 p	RANGAP1	AT3G63130	1.28	0.35	1.97	0.09053	0.183619	-5.49
250710_at	MYB family transcription factor-like	MYB33	AT5G06100	1.16	0.22	1.97	0.090544	0.183633	-5.49
245294_at	casein kinase I ; supported by cDN	CKI1	AT4G14340	-1.17	-0.22	-1.97	0.090674	0.18388	-5.50
245311_at	ribosomal protein ; supported by ful	---	AT4G14320	1.28	0.35	1.97	0.090708	0.183932	-5.50
253702_at	Ca2+-transporting ATPase - like pr	ACA10	AT4G29900	1.24	0.31	1.97	0.090729	0.183952	-5.50
249533_at	putative protein predicted protein, A	---	AT5G38790	-1.18	-0.24	-1.97	0.090734	0.183952	-5.50
245093_at	hypothetical protein predicted by ge	---	AT2G40815	-1.17	-0.23	-1.97	0.090746	0.183959	-5.50
261120_at	homeodomain protein BELL1, puta	BLH3	AT1G75410	1.27	0.35	1.97	0.090782	0.184006	-5.50
244989_s_a	hypothetical protein	---	---	-1.24	-0.31	-1.97	0.090785	0.184006	-5.50
245286_at	cytosolic O-acetylserine(thiol)lyase	OASA1	AT4G14880	-1.17	-0.23	-1.97	0.090844	0.18411	-5.50
257939_at	monosaccharide transport protein,	STP4	AT3G19930	-1.32	-0.40	-1.97	0.090889	0.184176	-5.50
257670_at	unknown protein	---	AT3G20340	-1.43	-0.52	-1.97	0.090893	0.184176	-5.50
259220_at	expressed protein predicted by ger	---	AT3G03550	-1.21	-0.27	-1.97	0.090934	0.184242	-5.50
257513_s_a	hypothetical protein	---	AT1G12340	1.18	0.24	1.97	0.09102	0.1844	-5.50
252455_at	putative protein various predicted p	---	AT3G47140	-1.13	-0.18	-1.97	0.091066	0.18447	-5.50
266795_at	unknown protein	---	AT2G03070	1.20	0.26	1.97	0.09107	0.18447	-5.50
252390_at	Expressed protein ; supported by cl	---	AT3G47836	1.19	0.26	1.97	0.091104	0.184522	-5.50
247812_at	peroxidase ;supported by full-length	---	AT5G58390	-1.61	-0.69	-1.97	0.091217	0.184733	-5.50
250815_s_a	putative protein similar to unknown	---	AT5G05040	-1.23	-0.29	-1.97	0.091249	0.184782	-5.50
265418_at	AP2 domain transcription factor	---	AT2G20880	-1.78	-0.83	-1.97	0.091289	0.184847	-5.50
266630_at	putative serpin	---	AT2G35580	-1.15	-0.20	-1.97	0.091303	0.184858	-5.50
246992_at	N-acetyltransferase hookless1-like	---	AT5G67430	-1.17	-0.22	-1.97	0.091384	0.185003	-5.50
265105_s_a	unknown protein contains similarity	---	AT1G62580	-1.13	-0.18	-1.97	0.091394	0.185003	-5.50

263623_at	hypothetical protein predicted by ge	---	AT2G04860	-1.14	-0.18	-1.97	0.091399	0.185003	-5.50
267572_at	3-hydroxyisobutyryl-coenzyme A hy	---	AT2G30660	-1.17	-0.23	-1.97	0.091485	0.185162	-5.50
256352_at	proline-rich protein, putative similar	ATPRP1	AT1G54970	-1.22	-0.29	-1.97	0.091507	0.18519	-5.50
261221_at	hypothetical protein predicted by ge	---	AT1G19960	2.98	1.58	1.97	0.091562	0.185284	-5.50
256647_at	unknown protein contains similarity	---	AT3G13610	3.67	1.87	1.97	0.091576	0.185297	-5.50
255687_at	hypothetical protein	KEA2	AT4G00630	1.37	0.45	1.97	0.091694	0.185504	-5.51
253637_at	putative protein ; supported by full-	---	AT4G30390	1.29	0.36	1.97	0.091696	0.185504	-5.51
248849_at	multidrug resistance p-glycoprotein	PGP7	AT5G46540	-1.15	-0.20	-1.97	0.09171	0.185504	-5.51
245533_at	putative phosphocholine cytidylyltra	CCT2	AT4G15130	-1.49	-0.57	-1.97	0.091711	0.185504	-5.51
258950_at	unknown protein contains Pfam pro	MBD9	AT3G01460	-1.13	-0.17	-1.97	0.091724	0.185513	-5.51
256951_at	hypothetical protein predicted by ge	---	AT3G19085	-1.13	-0.18	-1.97	0.091741	0.185513	-5.51
267024_s_a	putative aquaporin (plasma membra	NIP2;1	AT2G29870	-1.21	-0.27	-1.97	0.091743	0.185513	-5.51
245186_at	F12A21.15 hypothetical protein	ARR11	AT1G67710	-1.44	-0.53	-1.97	0.091754	0.185513	-5.51
254844_at	hypothetical protein supported by fu	---	AT4G11790	1.29	0.36	1.97	0.091756	0.185513	-5.51
259336_at	hypothetical protein C-term portion	SDG20	AT3G03750	-1.28	-0.36	-1.97	0.091788	0.185561	-5.51
253021_at	putative protein permease 1 - Mes	---	AT4G38050	-1.19	-0.25	-1.97	0.091804	0.185576	-5.51
252797_at	putative protein	---	---	-1.24	-0.31	-1.96	0.091822	0.185597	-5.51
252655_at	hypothetical protein with predicted h	---	AT3G44760	-1.15	-0.20	-1.96	0.091839	0.185614	-5.51
262752_at	putative mitotic cyclin similar to gb|[	CYCB3;1	AT1G16330	-1.21	-0.27	-1.96	0.091906	0.185734	-5.51
263364_at	unknown protein predicted by gens	---	AT2G20540	1.14	0.19	1.96	0.091927	0.185759	-5.51
258714_at	putative RING zinc finger protein c	---	AT3G09770	1.26	0.33	1.96	0.092003	0.18589	-5.51
266319_s_a	putative beta-ketoacyl-CoA synthas	KCS13	AT2G46720	1.28	0.36	1.96	0.092008	0.18589	-5.51
256955_at	L-ascorbate oxidase precursor, put	sks11	AT3G13390	-1.26	-0.33	-1.96	0.092021	0.1859	-5.51
267544_at	putative cytochrome b5	CB5-B	AT2G32720	1.50	0.58	1.96	0.092051	0.185935	-5.51
263405_s_a	hypothetical protein similar to hypot	---	AT2G04066	-1.14	-0.19	-1.96	0.09206	0.185935	-5.51
259168_at	unknown protein similar to hypothet	---	AT3G03570	-1.19	-0.25	-1.96	0.092063	0.185935	-5.51
261831_at	ADP-ribosylation factor, putative si	ATARFA1F	AT1G10630	-1.25	-0.33	-1.96	0.092074	0.185941	-5.51
256679_at	putative protein similar to ATP synth	ATPQ	AT3G52300	1.18	0.24	1.96	0.092105	0.185988	-5.51
261724_at	Expressed protein ; supported by fu	---	AT1G76185	1.16	0.22	1.96	0.092125	0.186012	-5.51
249365_at	putative protein predicted protein, A	---	AT5G40600	1.16	0.22	1.96	0.092248	0.186243	-5.51
257590_s_a	hypothetical protein predicted by ge	---	AT3G24870	1.22	0.28	1.96	0.092276	0.186283	-5.51
262538_at	Expressed protein ; supported by fu	---	AT1G17140	-1.35	-0.44	-1.96	0.092287	0.186289	-5.51
256694_at	hypothetical protein predicted gens	---	---	-1.18	-0.23	-1.96	0.092323	0.186345	-5.51
261961_at	hypothetical protein predicted by ge	---	AT1G36510	-1.19	-0.25	-1.96	0.092372	0.186412	-5.51
247082_at	putative protein contains similarity t	ATGRIP	AT5G66030	1.19	0.25	1.96	0.092372	0.186412	-5.51

255140_x_a	extensin-like protein hydroxyproline	---	AT4G08410	-1.28	-0.36	-1.96	0.092394	0.186439	-5.51
257769_at	indoleacetic acid (IAA)-inducible ge	IAA7	AT3G23050	-2.71	-1.44	-1.96	0.092427	0.186489	-5.51
266451_at	3-isopropylmalate dehydratase, sm	---	AT2G43090	1.16	0.22	1.96	0.092456	0.186532	-5.51
255762_at	unknown protein contains Pfam pro	HAC12	AT1G16710	-1.17	-0.23	-1.96	0.092467	0.186536	-5.51
245326_at	Expressed protein ; supported by fu	---	AT4G14100	1.23	0.30	1.96	0.092496	0.186578	-5.51
253390_at	hypothetical protein ;supported by	---	AT4G32750	1.23	0.30	1.96	0.092514	0.186598	-5.51
249154_at	Nicotiana EREBP-3 like	---	AT5G43410	1.95	0.97	1.96	0.092527	0.186609	-5.51
258709_at	putative 60S ribosomal protein L35	---	AT3G09500	1.37	0.45	1.96	0.092606	0.18675	-5.52
249584_s_a	Membrane integral protein (MIP) -li	NIP4;1	AT5G37810	-1.20	-0.26	-1.96	0.092666	0.186857	-5.52
244922_s_a	hypothetical protein	---	AT2G07674	1.21	0.28	1.96	0.092724	0.186957	-5.52
259136_at	unknown protein	---	AT3G05470	-1.25	-0.32	-1.96	0.092849	0.187191	-5.52
261780_at	cyclin, putative similar to B-like cyc	CYCB2;4	AT1G76310	-1.18	-0.24	-1.96	0.092876	0.187227	-5.52
267458_at	similar to Mlo proteins from H. vulga	MLO5	AT2G33670	-1.22	-0.28	-1.96	0.092883	0.187227	-5.52
245842_at	proline-rich protein, putative similar	RXF26	AT1G58430	-1.14	-0.19	-1.96	0.092897	0.187234	-5.52
256926_at	hypothetical protein predicted by ge	---	AT3G22540	-1.24	-0.31	-1.96	0.092903	0.187234	-5.52
252818_at	putative protein several hypothetica	---	---	-1.19	-0.25	-1.96	0.092912	0.187236	-5.52
257240_at	monooxygenase, putatve contains	---	AT3G24200	1.16	0.21	1.96	0.092967	0.187328	-5.52
263854_at	putative mutT domain protein	atnudt5	AT2G04430	-1.16	-0.21	-1.96	0.092976	0.187328	-5.52
261977_at	hypothetical protein contains simila	---	---	-1.15	-0.20	-1.96	0.092983	0.187328	-5.52
265644_at	hypothetical protein predicted by ge	ATEPR1	AT2G27380	-1.15	-0.21	-1.96	0.093017	0.187382	-5.52
266361_at	putative O-GlcNAc transferase	---	AT2G32450	-1.36	-0.44	-1.96	0.093039	0.187408	-5.52
251569_at	putative protein several hypothetica	---	AT3G58290	-1.20	-0.26	-1.96	0.093047	0.187409	-5.52
262355_at	unknown protein	---	AT1G72820	-1.24	-0.30	-1.96	0.093056	0.187409	-5.52
259891_at	putative Eukaryotic initiation factor	---	AT1G72730	-1.20	-0.26	-1.96	0.093077	0.187437	-5.52
262270_x_a	polyprotein, putative similar to poly	---	---	-1.13	-0.18	-1.95	0.093158	0.187581	-5.52
260538_at	60S ribosomal protein L38	---	AT2G43460	1.27	0.34	1.95	0.09319	0.18763	-5.52
245573_at	hypothetical protein	---	AT4G14730	-1.14	-0.18	-1.95	0.093203	0.187639	-5.52
265713_at	putative integral membrane protein	UPS2	AT2G03530	1.58	0.66	1.95	0.093223	0.187663	-5.52
265764_at	hypothetical protein predicted by ge	---	AT2G48060	-1.20	-0.27	-1.95	0.093258	0.187718	-5.52
257953_at	predicted protein supported by full-l	PEX22	AT3G21865	1.29	0.37	1.95	0.093366	0.187919	-5.52
249035_at	putative protein contains similarity t	GLK2	AT5G44190	-1.20	-0.27	-1.95	0.093411	0.187992	-5.52
256180_at	light repressible receptor protein ki	---	AT1G51810	-1.12	-0.17	-1.95	0.093441	0.188026	-5.52
245647_at	F5A9.22 hypothetical protein	---	AT1G24706	-1.13	-0.18	-1.95	0.093444	0.188026	-5.52
264143_at	latex-abundant protein, putative sir	ATMC5	AT1G79330	-1.16	-0.22	-1.95	0.09347	0.188062	-5.52
255207_at	Expressed protein ; supported by fu	---	AT4G07515	-1.13	-0.17	-1.95	0.093487	0.188078	-5.53

264033_at	hypothetical protein predicted by ge	---	AT2G03580	-1.20	-0.26	-1.95	0.093549	0.188187	-5.53
266637_at	hypothetical protein ;supported by	BRXL1	AT2G35600	-1.28	-0.36	-1.95	0.093576	0.188225	-5.53
256638_at	RNA-binding protein, putative simil	---	AT3G19090	-1.25	-0.32	-1.95	0.093599	0.188254	-5.53
264310_at	hypothetical protein similar to hypot	---	AT1G62030	1.19	0.25	1.95	0.093632	0.188304	-5.53
259650_at	leucoanthocyanidin dioxygenase 2	---	AT1G55290	-1.17	-0.23	-1.95	0.09364	0.188304	-5.53
247238_at	histone acetyltransferase	HAM1	AT5G64610	1.14	0.19	1.95	0.093652	0.188311	-5.53
256839_at	calmodulin, putative similar to calm	---	AT3G22930	1.19	0.26	1.95	0.093667	0.188325	-5.53
246939_at	AP2 domain containing protein AP	SHN2	AT5G25390	-1.17	-0.23	-1.95	0.093692	0.188352	-5.53
245619_at	hypothetical protein	---	AT4G13990	-1.26	-0.33	-1.95	0.093697	0.188352	-5.53
245884_at	branched-chain alpha keto-acid de	---	AT5G09300	1.25	0.33	1.95	0.093728	0.188398	-5.53
262439_at	hypothetical protein identical to hyp	---	AT1G47730	-1.13	-0.18	-1.95	0.093741	0.188408	-5.53
266303_at	putative receptor-like protein kinase	---	AT2G27060	-1.33	-0.41	-1.95	0.093754	0.188417	-5.53
247503_at	GCN4-complementing protein - like	AGD1	AT5G61980	-1.20	-0.26	-1.95	0.093778	0.188448	-5.53
265635_at	hypothetical protein predicted by ge	---	AT2G25360	-1.14	-0.18	-1.95	0.093812	0.188489	-5.53
247616_at	putative protein various predicted p	---	AT5G60260	-1.16	-0.22	-1.95	0.093822	0.188489	-5.53
254275_at	HSP associated protein like p48, H	AtHip1	AT4G22670	1.21	0.28	1.95	0.093823	0.188489	-5.53
250596_at	putative protein contains similarity t	---	AT5G07780	-1.26	-0.33	-1.95	0.093845	0.188516	-5.53
255356_x_a	putative transposon protein	---	---	-1.18	-0.24	-1.95	0.093868	0.188545	-5.53
265860_at	hypothetical protein predicted by ge	---	AT2G01810	-1.15	-0.20	-1.95	0.093936	0.188666	-5.53
259991_at	putative S-adenosyl-L-methionine:s	---	AT1G68040	-1.17	-0.22	-1.95	0.093948	0.188674	-5.53
253367_at	hypothetical protein	---	AT4G33180	-1.30	-0.37	-1.95	0.093969	0.188692	-5.53
249792_at	putative protein contains similarity t	PHS1	AT5G23720	1.15	0.20	1.95	0.093974	0.188692	-5.53
265585_at	CDC27/NUC2-like protein TPR-rep	HBT	AT2G20000	1.21	0.27	1.95	0.094001	0.188728	-5.53
251932_at	pasticcino 1 ; supported by cDNA:	PAS1	AT3G54010	1.16	0.21	1.95	0.094014	0.188728	-5.53
259630_at	peptide chain release factor 2, puta	---	AT1G56350	-1.27	-0.35	-1.95	0.094017	0.188728	-5.53
264002_at	putative DnaJ protein ;supported b	---	AT2G22360	1.23	0.30	1.95	0.094032	0.188728	-5.53
258922_at	putative 40S ribosomal protein S17	---	AT3G10610	1.49	0.57	1.95	0.094033	0.188728	-5.53
250085_at	unknown protein	---	AT5G17250	-1.22	-0.29	-1.95	0.094089	0.188825	-5.53
259224_at	putative thymidine kinase similar to	---	AT3G07800	-1.24	-0.31	-1.95	0.094116	0.188862	-5.53
266897_at	remorin identical to GB:M25268, a	---	AT2G45820	-1.30	-0.38	-1.95	0.094178	0.188958	-5.53
247623_at	receptor-like protein kinase recepto	---	AT5G60320	-1.16	-0.21	-1.95	0.094181	0.188958	-5.53
258255_at	hypothetical protein predicted by ge	---	AT3G26800	1.15	0.20	1.95	0.094217	0.189015	-5.53
244935_at	NADH dehydrogenase subunit	---	---	-1.16	-0.21	-1.95	0.094261	0.189071	-5.53
256938_at	LEA protein, putative similar to LEA	ATECP31	AT3G22500	-1.18	-0.24	-1.95	0.094262	0.189071	-5.53
267125_at	putative acetone-cyanohydrin lyase	MES4	AT2G23580	-1.14	-0.19	-1.95	0.094313	0.189156	-5.53

255779_at	unknown protein similar to beta-1,3	PDCB3	AT1G18650	-1.40	-0.49	-1.95	0.094372	0.189243	-5.53
258927_at	putative folylpolyglutamate syntheta	DFC	AT3G10160	1.16	0.22	1.95	0.094372	0.189243	-5.53
258628_at	unknown protein	---	AT3G02890	1.36	0.44	1.95	0.094389	0.189259	-5.53
254812_at	nucleotide sugar epimerase -like p	GAE5	AT4G12250	1.45	0.54	1.95	0.094425	0.189315	-5.53
244924_at	hypothetical protein	---	---	1.18	0.24	1.95	0.094437	0.189321	-5.53
246878_at	putative protein self-incompatibility	---	AT5G26060	-1.22	-0.28	-1.95	0.094507	0.189445	-5.54
245472_at	hypothetical protein	---	AT4G16040	-1.21	-0.27	-1.94	0.09461	0.189622	-5.54
248860_at	putative protein contains similarity t	---	AT5G46670	-1.16	-0.21	-1.94	0.094613	0.189622	-5.54
256782_at	dirigent protein, putative similar to	---	AT3G13660	-1.13	-0.18	-1.94	0.09462	0.189622	-5.54
258406_at	hypothetical protein similar to hypot	ATRBL14	AT3G17611	1.13	0.17	1.94	0.094643	0.189651	-5.54
248411_at	unknown protein	---	AT5G51580	-1.14	-0.19	-1.94	0.094658	0.189651	-5.54
263645_at	putative GTP-binding protein	---	AT2G04720	-1.13	-0.17	-1.94	0.094659	0.189651	-5.54
251035_at	Expressed protein ; supported by fu	---	AT5G02220	-1.26	-0.34	-1.94	0.094671	0.189658	-5.54
248649_at	putative protein contains similarity t	APRR4	AT5G49240	-1.19	-0.25	-1.94	0.094688	0.189674	-5.54
266204_at	hypothetical protein predicted by ge	---	AT2G02410	-1.24	-0.31	-1.94	0.094741	0.189765	-5.54
260435_at	putative transcription factor similar t	MYB62	AT1G68320	1.45	0.54	1.94	0.09475	0.189766	-5.54
252068_at	mucin -like protein hemomucin, Dr	---	AT3G51440	1.53	0.61	1.94	0.094805	0.189859	-5.54
246515_at	putative protein unusual floral orga	---	AT5G15710	-1.13	-0.17	-1.94	0.094826	0.189865	-5.54
261583_at	pyruvate dehydrogenase E1 alpha	PDH-E1 AL	AT1G01090	-1.16	-0.22	-1.94	0.094833	0.189865	-5.54
245053_at	putative pectinesterase	---	AT2G26450	-1.24	-0.31	-1.94	0.094835	0.189865	-5.54
256499_at	unknown protein	---	AT1G36640	1.34	0.42	1.94	0.094843	0.189865	-5.54
249563_at	similar to unknown protein (pir |T03	---	AT5G38360	-1.16	-0.21	-1.94	0.09485	0.189865	-5.54
256869_at	nodulin, putative similar to nodulin	---	AT3G26420	1.26	0.33	1.94	0.094865	0.189878	-5.54
251012_at	putative protein ;supported by full-l	---	AT5G02580	2.28	1.19	1.94	0.094872	0.189878	-5.54
246140_at	SOH1 - like protein SOH1, Saccha	---	AT5G19910	-1.13	-0.18	-1.94	0.094886	0.189888	-5.54
246918_at	putative protein hypothetical protei	---	AT5G25340	-1.22	-0.28	-1.94	0.094957	0.190014	-5.54
249006_at	putative protein similar to unknown	---	AT5G44650	1.26	0.33	1.94	0.094986	0.190056	-5.54
263739_at	putative CONSTANS-like B-box zin	---	AT2G21320	1.35	0.43	1.94	0.095031	0.190129	-5.54
245406_at	GTP-binding RAB2A like protein	ATRABB1A	AT4G17160	-1.14	-0.19	-1.94	0.095089	0.190217	-5.54
266871_at	unknown protein	---	AT2G44710	1.12	0.17	1.94	0.095092	0.190217	-5.54
250515_at	putative protein	---	AT5G09570	1.12	0.16	1.94	0.09513	0.19026	-5.54
267625_at	putative RNA-binding protein	---	AT2G42240	-1.17	-0.22	-1.94	0.095146	0.19026	-5.54
263459_at	ankyrin-like protein	---	AT2G31820	1.27	0.34	1.94	0.095148	0.19026	-5.54
254219_at	putative protein	---	AT4G23760	1.17	0.22	1.94	0.095156	0.19026	-5.54
267450_at	hypothetical protein predicted by ge	---	AT2G33720	-1.26	-0.33	-1.94	0.09516	0.19026	-5.54

267498_at	unknown protein	---	AT2G45720	1.24	0.31	1.94	0.095163	0.19026	-5.54
251966_at	receptor lectin kinase -like protein r	---	AT3G53380	-1.23	-0.30	-1.94	0.095191	0.190298	-5.54
258397_at	Expressed protein ; supported by fu	---	AT3G15357	1.15	0.21	1.94	0.09524	0.190381	-5.54
262862_at	hypothetical protein predicted by ge	---	AT1G64830	-1.26	-0.34	-1.94	0.095353	0.190575	-5.54
250201_at	ankyrin - like protein 270 kDa anky	---	AT5G14230	-1.47	-0.56	-1.94	0.095354	0.190575	-5.54
250558_at	flavonoid 3-hydroxylase - like prote	TT7	AT5G07990	-1.20	-0.26	-1.94	0.095366	0.190581	-5.54
257101_at	disease resistance protein, putative	AtRLP42	AT3G25020	1.17	0.23	1.94	0.095419	0.19067	-5.55
264042_at	putative steroid sulfotransferase ; s	ST	AT2G03760	-2.03	-1.02	-1.94	0.095484	0.190784	-5.55
258584_at	hypothetical protein predicted by ge	SIP1A	AT3G04090	-1.13	-0.17	-1.94	0.095567	0.190933	-5.55
247416_at	40S ribosomal protein S15-like prot	---	AT5G63070	-1.19	-0.25	-1.94	0.095672	0.191127	-5.55
265579_at	hypothetical protein predicted by ge	---	AT2G20070	-1.16	-0.21	-1.94	0.095684	0.191133	-5.55
256322_at	unknown protein ; supported by cDI	AXR4	AT1G54990	1.37	0.45	1.94	0.095701	0.191149	-5.55
246179_at	putative protein hypothetical protei	---	AT5G28440	-1.23	-0.30	-1.94	0.095716	0.191149	-5.55
248880_at	putative protein contains similarity t	---	AT5G46200	-1.15	-0.20	-1.94	0.095717	0.191149	-5.55
260040_at	Expressed protein ; supported by fu	IDA	AT1G68765	2.06	1.04	1.94	0.095748	0.191174	-5.55
246473_at	putative protein cathepsin L-like cy	---	AT5G17140	-1.18	-0.24	-1.94	0.095754	0.191174	-5.55
263954_at	unknown protein ; supported by cD	---	AT2G35840	-1.21	-0.28	-1.94	0.095755	0.191174	-5.55
266708_at	putative chloroplast nucleoid DNA b	---	AT2G03200	-1.24	-0.31	-1.94	0.095787	0.191208	-5.55
258004_at	unknown protein similar to putative	MYB110	AT3G29020	-1.17	-0.23	-1.94	0.095789	0.191208	-5.55
251919_at	putative protein Hsp70 binding prot	---	AT3G53800	-1.27	-0.35	-1.94	0.09581	0.191234	-5.55
265766_at	unknown protein	---	AT2G48080	-1.23	-0.30	-1.93	0.095932	0.191462	-5.55
249955_at	sugar transporter - like protein prob	---	AT5G18840	-1.47	-0.56	-1.93	0.095954	0.191489	-5.55
247226_at	putative protein contains similarity t	---	AT5G65100	-1.14	-0.18	-1.93	0.095988	0.19154	-5.55
249151_at	inorganic phosphate transporter (db	PHT3	AT5G43360	-1.17	-0.22	-1.93	0.09604	0.191627	-5.55
245938_at	putative protein protein phosphatas	---	AT5G19680	1.23	0.30	1.93	0.096107	0.191742	-5.55
251545_at	zinc transporter -like protein zinc tr	MTPA2	AT3G58810	-1.24	-0.32	-1.93	0.096145	0.191802	-5.55
254898_at	serine/threonine kinase-like protein	---	AT4G11480	1.85	0.89	1.93	0.096309	0.192113	-5.55
253085_s_a	putative protein hypothetical protei	---	AT4G36270	-1.29	-0.37	-1.93	0.096321	0.192119	-5.55
251276_at	putative protein hypothetical protei	SDG14	AT3G61740	1.15	0.20	1.93	0.096347	0.192154	-5.55
251448_at	allyl alcohol dehydrogenase-like pr	---	AT3G59845	-1.15	-0.21	-1.93	0.096383	0.192211	-5.55
261726_at	putative auxin-independent growth	---	AT1G76270	-1.31	-0.39	-1.93	0.096397	0.192221	-5.55
256842_at	hypothetical protein predicted by ge	---	---	-1.16	-0.21	-1.93	0.096413	0.192236	-5.56
247102_at	putative protein similar to unknown	---	AT5G66550	-1.19	-0.26	-1.93	0.09643	0.192253	-5.56
246505_at	putative protein hypothetical protei	---	AT5G16250	-1.32	-0.40	-1.93	0.096449	0.192274	-5.56
248485_at	calcium-binding transporter-like pro	---	AT5G51050	1.25	0.32	1.93	0.096473	0.192305	-5.56

246264_at	hypothetical protein	FRL2	AT1G31814	1.17	0.23	1.93	0.096503	0.192348	-5.56
260847_s_a	alanine aminotransferase, putative	AlaAT1	AT1G17290	1.16	0.22	1.93	0.096549	0.192422	-5.56
249708_at	unknown protein	---	AT5G35660	-1.35	-0.43	-1.93	0.096574	0.192456	-5.56
251732_at	putative protein prenylated Rab ac	PRA1.B1	AT3G56110	1.15	0.20	1.93	0.096617	0.192526	-5.56
262494_at	myosin-like protein similar to myosi	---	AT1G21810	-1.21	-0.28	-1.93	0.096706	0.192685	-5.56
264992_at	integral membrane protein, putativ	---	AT1G67300	-1.21	-0.28	-1.93	0.096742	0.192741	-5.56
267216_at	hypothetical protein	---	AT2G02620	-1.16	-0.22	-1.93	0.096798	0.192835	-5.56
247414_at	unknown protein	EMB2759	AT5G63050	1.21	0.27	1.93	0.096812	0.192846	-5.56
249038_at	putative protein contains similarity t	RING1A	AT5G44280	1.18	0.24	1.93	0.096884	0.192972	-5.56
263905_at	putative beta-fructofuranosidase (in	AtcwINV4	AT2G36190	-1.25	-0.32	-1.93	0.096942	0.193071	-5.56
258721_at	unknown protein similar to hypothet	---	AT3G09560	1.26	0.33	1.93	0.096982	0.193135	-5.56
264455_at	hypothetical protein predicted by ge	---	AT1G10330	1.20	0.26	1.93	0.097042	0.193236	-5.56
258416_at	hypothetical protein predicted by g	---	AT3G17310	1.17	0.23	1.93	0.097066	0.193267	-5.56
255902_at	transcription factor, putative similar	---	AT1G17880	1.16	0.22	1.93	0.097105	0.193326	-5.56
246771_at	putative protein putative replication	---	---	-1.14	-0.19	-1.93	0.097119	0.193326	-5.56
260079_s_a	helix-loop-helix protein 1A, putative	---	AT1G35460	-1.17	-0.22	-1.93	0.097121	0.193326	-5.56
266958_at	putative trans-prenyltransferase	GPS1	AT2G34630	1.25	0.32	1.93	0.097156	0.193379	-5.56
265611_at	unknown protein ;supported by full-	---	AT2G25510	-1.32	-0.41	-1.93	0.097209	0.193469	-5.56
260367_at	unknown protein ;supported by full-	---	AT1G69760	1.54	0.63	1.93	0.09723	0.193494	-5.56
256132_at	hypothetical protein similar to hypot	---	AT1G13610	-1.16	-0.21	-1.93	0.097261	0.193534	-5.56
265001_at	hypothetical protein contains simila	---	AT1G67350	1.16	0.21	1.93	0.097268	0.193534	-5.56
250380_at	putative protein	---	AT5G11600	1.16	0.22	1.92	0.097356	0.193694	-5.56
247998_at	unknown protein	---	AT5G56200	1.30	0.38	1.92	0.097373	0.19371	-5.56
262371_at	putative glycosyl transferase contai	---	AT1G73160	-1.15	-0.20	-1.92	0.09739	0.193727	-5.56
255609_s_a	hypothetical protein	---	AT4G01180	1.13	0.18	1.92	0.097562	0.194052	-5.57
246181_at	pectinesterase - like protein probab	---	AT5G20860	-1.14	-0.19	-1.92	0.097642	0.194178	-5.57
256317_at	hypothetical protein predicted by ge	---	AT1G35900	-1.27	-0.34	-1.92	0.097643	0.194178	-5.57
246790_at	putative protein unknown protein F	---	AT5G27610	-1.23	-0.30	-1.92	0.097685	0.194243	-5.57
254015_at	putative beta-galactosidase beta-g	BGAL12	AT4G26140	-1.27	-0.34	-1.92	0.097701	0.194243	-5.57
265886_at	putative protein phosphatase 2C ;	---	AT2G25610	1.36	0.45	1.92	0.097701	0.194243	-5.57
264888_at	hypothetical protein	---	AT1G23070	-1.17	-0.23	-1.92	0.097718	0.19426	-5.57
261985_at	terpene synthase, putative similar t	---	AT1G33750	-1.14	-0.18	-1.92	0.097798	0.194402	-5.57
257438_at	hypothetical protein similarity to pla	---	AT2G15325	-1.14	-0.19	-1.92	0.097836	0.194449	-5.57
263514_at	putative poly(ADP-ribose) glycohyd	---	AT2G31860	-1.17	-0.22	-1.92	0.097845	0.194449	-5.57
248505_at	putative protein similar to unknown	---	AT5G50360	-1.20	-0.27	-1.92	0.097847	0.194449	-5.57

249858_at	myb-related transcription factor-like	MYB37	AT5G23000	1.23	0.30	1.92	0.097869	0.194477	-5.57
257930_at	hypothetical protein	---	AT3G17010	-1.23	-0.30	-1.92	0.097934	0.194589	-5.57
263852_at	putative mutT domain protein	ATNUDT6	AT2G04450	-2.18	-1.13	-1.92	0.09801	0.194723	-5.57
251079_at	hypothetical protein	---	AT5G02000	-1.15	-0.20	-1.92	0.098035	0.194755	-5.57
248257_at	putative protein similar to unknown	---	AT5G53410	-1.23	-0.29	-1.92	0.098094	0.194855	-5.57
250328_at	putative protein	---	AT5G11780	-1.19	-0.25	-1.92	0.098118	0.194878	-5.57
266367_s_a	unknown protein	---	AT2G41390	-1.15	-0.20	-1.92	0.098122	0.194878	-5.57
257430_at	hypothetical protein similar to hypot	---	AT2G28580	-1.21	-0.28	-1.92	0.098175	0.194965	-5.57
260061_at	cell division protein kinase similar to	CDKD1;1	AT1G73690	-1.26	-0.33	-1.92	0.09819	0.194965	-5.57
262704_at	hypothetical protein predicted by ge	ASL9	AT1G16530	-1.42	-0.51	-1.92	0.098198	0.194965	-5.57
257107_at	transmembrane trafficking protein,	---	AT3G29070	-1.18	-0.24	-1.92	0.0982	0.194965	-5.57
246941_at	putative protein several hypothetica	---	AT5G25415	-1.16	-0.21	-1.92	0.098282	0.19511	-5.57
264576_at	unknown protein Similar to Arabido	---	AT1G05360	1.16	0.22	1.92	0.098293	0.195115	-5.57
252070_at	short-chain alcohol dehydrogenase	---	AT3G51680	-1.21	-0.27	-1.92	0.098302	0.195116	-5.57
250742_at	putative protein similar to unknown	---	AT5G05800	1.18	0.24	1.92	0.098338	0.19517	-5.57
255515_at	putative pistil-specific protein simila	---	AT4G02250	-1.14	-0.19	-1.92	0.09837	0.195207	-5.57
257031_at	fucosyltransferase, putative similar	FUT11	AT3G19280	1.17	0.23	1.92	0.098374	0.195207	-5.57
247223_at	MADS box transcription factor-like	MAF4	AT5G65070	-1.13	-0.17	-1.92	0.09839	0.195222	-5.57
254440_at	putative protein desiccation-related	---	AT4G21020	-1.15	-0.20	-1.92	0.098421	0.195267	-5.58
248128_at	thiazole biosynthetic enzyme precu	THI1	AT5G54770	1.22	0.28	1.92	0.098441	0.195289	-5.58
253522_at	predicted protein cation transport p	---	AT4G31290	-1.54	-0.63	-1.92	0.098467	0.195324	-5.58
263803_at	hypothetical protein predicted by ge	---	AT2G40440	-1.15	-0.20	-1.92	0.098476	0.195325	-5.58
252724_at	putative protein hypothetical protei	---	AT3G43540	1.20	0.27	1.92	0.098489	0.195334	-5.58
267517_at	unknown protein	RPT2	AT2G30520	1.19	0.25	1.92	0.098519	0.195377	-5.58
252019_at	late embryogenesis abundant prote	---	AT3G53040	-1.13	-0.18	-1.92	0.098558	0.195423	-5.58
257683_at	hypothetical protein predicted by ge	---	AT3G13280	-1.16	-0.21	-1.92	0.09856	0.195423	-5.58
245335_at	pore protein homolog ;supported by	ATOEP16-2	AT4G16160	-1.21	-0.27	-1.92	0.098585	0.195455	-5.58
251051_at	putative zinc finger protein zinc fing	---	AT5G02460	-1.18	-0.24	-1.92	0.098664	0.195586	-5.58
261996_at	AIG1-like protein similar to AIG1 pr	---	AT1G33830	1.13	0.18	1.92	0.098669	0.195586	-5.58
249844_at	putative protein similar to unknown	---	AT5G23590	1.19	0.25	1.92	0.098676	0.195586	-5.58
254987_s_a	hypothetical protein	---	AT4G10660	1.13	0.17	1.91	0.098756	0.195727	-5.58
250791_at	nucleic acid binding protein-like ;su	AL1	AT5G05610	1.15	0.21	1.91	0.098773	0.195732	-5.58
258153_at	Expressed protein ; supported by fu	MOS4	AT3G18165	1.20	0.27	1.91	0.098775	0.195732	-5.58
251677_at	putative protein hypothetical protei	BHLH039	AT3G56980	-1.64	-0.71	-1.91	0.098805	0.195761	-5.58
256644_at	unknown protein similar to hypothet	---	---	-1.15	-0.21	-1.91	0.098807	0.195761	-5.58

247278_at	fructose-bisphosphatase-like protei	---	AT5G64380	-1.20	-0.27	-1.91	0.098848	0.195814	-5.58
253817_at	hypothetical protein ;supported by	---	AT4G28310	-1.52	-0.60	-1.91	0.098851	0.195814	-5.58
264461_s_a	hypothetical protein	---	AT1G10190	-1.12	-0.17	-1.91	0.09892	0.195927	-5.58
265928_at	Ac-like transposase related to Ac/D	---	---	-1.20	-0.26	-1.91	0.098925	0.195927	-5.58
256699_at	hypothetical protein predicted by ge	---	AT3G20690	-1.20	-0.26	-1.91	0.098952	0.195958	-5.58
265030_at	receptor-like kinase, putative simila	---	AT1G61610	1.38	0.46	1.91	0.098958	0.195958	-5.58
246773_at	protein kinase-like protein MAP3Ka	---	AT5G27510	-1.24	-0.31	-1.91	0.098968	0.195961	-5.58
254853_at	putative DNA-binding protein AT-h	---	AT4G12080	1.22	0.29	1.91	0.099005	0.196017	-5.58
266529_at	putative salt-inducible protein	---	AT2G16880	1.19	0.25	1.91	0.099021	0.19603	-5.58
246356_x_a	hypothetical protein, 5' partial	---	---	-1.14	-0.19	-1.91	0.099039	0.19603	-5.58
257289_at	hypothetical protein	---	AT3G29690	-1.14	-0.19	-1.91	0.099043	0.19603	-5.58
246697_at	putative protein	---	AT5G29210	-1.18	-0.24	-1.91	0.099046	0.19603	-5.58
263755_at	unknown protein ;supported by full	---	AT2G21340	-1.23	-0.29	-1.91	0.099097	0.196111	-5.58
264858_at	hypothetical protein	SNL3	AT1G24190	-1.18	-0.24	-1.91	0.099104	0.196111	-5.58
260822_at	RNA polymerase, putative similar t	---	AT1G06790	1.16	0.21	1.91	0.099152	0.196175	-5.58
255664_at	putative protein	---	AT4G00440	-1.14	-0.19	-1.91	0.099154	0.196175	-5.58
248263_at	pectinesterase ; supported by cDN	PMEPCRF	AT5G53370	-1.37	-0.45	-1.91	0.099198	0.196244	-5.58
260284_at	unknown protein ; supported by ful	---	AT1G80380	-1.15	-0.20	-1.91	0.099262	0.196356	-5.58
248657_at	peptidylprolyl isomerase	ROF2	AT5G48570	-2.68	-1.42	-1.91	0.099297	0.196396	-5.58
257838_at	hypothetical protein contains Pfam	---	AT3G25210	1.15	0.20	1.91	0.099306	0.196396	-5.58
247087_at	putative protein contains similarity t	---	AT5G66330	-1.32	-0.40	-1.91	0.099312	0.196396	-5.58
255941_at	mitochondrial inner membrane tran	ATTIM17-1	AT1G20350	-1.28	-0.36	-1.91	0.099321	0.196396	-5.58
246638_at	putative protein predicted proteins,	---	---	-1.17	-0.22	-1.91	0.099326	0.196396	-5.58
259818_at	unknown protein ; supported by cDI	---	AT1G49890	-1.24	-0.32	-1.91	0.099419	0.196562	-5.59
250552_at	putative protein microtubule bindin	---	AT5G07890	1.15	0.20	1.91	0.099468	0.196616	-5.59
249679_at	unknown protein	---	AT5G35980	1.12	0.16	1.91	0.09947	0.196616	-5.59
262048_at	cytochrome c oxidase subunit, puta	---	AT1G80230	1.18	0.24	1.91	0.099472	0.196616	-5.59
247052_at	homeodomain transcription factor-li	HB53	AT5G66700	-1.18	-0.24	-1.91	0.099508	0.19667	-5.59
267006_at	putative membrane transporter ; su	---	AT2G34190	-1.18	-0.24	-1.91	0.099545	0.196716	-5.59
267307_at	putative laccase	LAC3	AT2G30210	-1.22	-0.29	-1.91	0.099548	0.196716	-5.59
255047_at	AX110P -like protein AX110P -Dau	---	AT4G09670	1.16	0.22	1.91	0.099608	0.196816	-5.59
250719_at	putative protein contains similarity t	---	AT5G06250	-1.20	-0.26	-1.91	0.09966	0.196904	-5.59
264075_at	envelope-like protein identical to GE	---	---	-1.23	-0.30	-1.91	0.099674	0.196914	-5.59
254477_at	zinc-finger protein Lsd1 ;supported	---	AT4G20380	-1.22	-0.29	-1.91	0.099786	0.197118	-5.59
261463_at	hypothetical protein predicted by ge	---	AT1G07730	1.14	0.19	1.91	0.099809	0.197147	-5.59

267241_at	hypothetical protein predicted by ge	---	AT2G02490	-1.14	-0.19	-1.91	0.099838	0.197187	-5.59
264137_at	lupeol synthase, putative similar to	ATLUP2	AT1G78960	1.27	0.34	1.91	0.099937	0.197365	-5.59
262784_at	unknown protein strong similarity to	SEX1	AT1G10760	1.27	0.35	1.91	0.100023	0.197518	-5.59
252370_at	putative protein	---	AT3G48600	-1.31	-0.38	-1.91	0.100119	0.19769	-5.59
258743_s_a	shaggy related protein kinase, ASK	ATSK12	AT3G05840	1.19	0.25	1.90	0.100169	0.197771	-5.59
246750_at	putative protein predicted proteins,	AT5G2786(	---	1.29	0.36	1.90	0.100327	0.198067	-5.59
252661_at	putative protein	---	AT3G44450	1.60	0.68	1.90	0.100367	0.198128	-5.59
254835_s_a	flavonoid 3,5-hydroxylase -like prot	CYP706A5	AT4G12310	1.35	0.43	1.90	0.100377	0.198132	-5.59
256340_at	DnaJ protein, putative contains Pfa	---	AT1G72070	-1.19	-0.25	-1.90	0.100391	0.198141	-5.59
252358_at	putative protein cfxY protein, Alcali	---	AT3G48425	1.15	0.20	1.90	0.100421	0.198178	-5.59
266696_at	copia-like retroelement pol polyprot	---	AT2G19680	1.20	0.26	1.90	0.100433	0.198178	-5.59
246268_at	cytochrome P450, putative contain	CYP97A3	AT1G31800	-1.21	-0.28	-1.90	0.100436	0.198178	-5.59
259269_at	putative pectate lyase similar to pec	---	AT3G01270	-1.17	-0.23	-1.90	0.100447	0.198178	-5.60
266882_at	unknown protein ;supported by full-	---	AT2G44670	1.48	0.56	1.90	0.100453	0.198178	-5.60
257371_at	putative CCAAT-box binding trancri	NF-YB5	AT2G47810	-1.20	-0.26	-1.90	0.100476	0.198206	-5.60
249855_at	unknown protein	---	AT5G22970	-1.17	-0.22	-1.90	0.100566	0.198367	-5.60
259815_at	hypothetical protein predicted by ge	---	AT1G49870	-1.16	-0.21	-1.90	0.100647	0.198509	-5.60
258612_at	putative replication factor A similar t	---	AT3G02920	-1.17	-0.23	-1.90	0.100656	0.19851	-5.60
262180_at	phosphoglycerate mutase, putative	PGM	AT1G78050	-1.15	-0.20	-1.90	0.100751	0.198681	-5.60
265829_at	unknown protein	---	AT2G14490	-1.14	-0.18	-1.90	0.100769	0.198697	-5.60
254809_at	putative protein auxin-induced prot	---	AT4G12410	-1.25	-0.32	-1.90	0.100802	0.198745	-5.60
255165_at	putative protein putative centromer	---	---	-1.30	-0.38	-1.90	0.100825	0.198775	-5.60
253770_at	protein kinase ADK1-like protein pr	CKL6	AT4G28540	1.14	0.19	1.90	0.100874	0.198853	-5.60
249299_at	E2, ubiquitin-conjugating enzyme 4	UBC4	AT5G41340	-1.20	-0.27	-1.90	0.100924	0.198934	-5.60
260164_at	putative D-isomer specific 2-hydrox	---	AT1G79870	1.16	0.22	1.90	0.100959	0.198986	-5.60
264355_at	unknown protein similar to PHZF, c	---	AT1G03210	-1.26	-0.34	-1.90	0.100976	0.199003	-5.60
259986_at	thaumatin-like protein similar to tha	---	AT1G75050	-1.18	-0.24	-1.90	0.101003	0.19904	-5.60
259191_at	unknown protein	---	AT3G01720	-1.21	-0.27	-1.90	0.101049	0.199098	-5.60
263099_at	putative non-LTR retroelement reve	---	---	-1.22	-0.29	-1.90	0.101051	0.199098	-5.60
246360_at	hypothetical protein	---	---	-1.16	-0.21	-1.90	0.10106	0.1991	-5.60
247941_at	putative protein strong similarity to	---	AT5G57200	-1.14	-0.19	-1.90	0.101098	0.199157	-5.60
259452_at	En/Spm-like transposon protein, pu	---	---	-1.17	-0.22	-1.90	0.101137	0.199217	-5.60
245215_at	F12A21.4 similar to iEP4 gb|AAD11	ATFXG1	AT1G67830	1.40	0.48	1.90	0.101156	0.199238	-5.60
251875_at	putative protein various predicted p	---	AT3G54270	-1.21	-0.27	-1.90	0.101168	0.199243	-5.60
254522_at	hypothetical protein	---	AT4G19980	-1.13	-0.17	-1.90	0.101181	0.199252	-5.60

251409_at	Expressed protein ; supported by fu	---	AT3G60245	1.46	0.54	1.90	0.101194	0.19926	-5.60
250800_at	ubiquinol-cytochrome C reductase (	HPR	AT1G68010	1.41	0.49	1.90	0.101254	0.199361	-5.60
245097_at	Expressed protein ; supported by fu	---	AT2G40935	1.13	0.18	1.90	0.101287	0.199409	-5.60
262110_at	SF2/ASF-like splicing modulator Sr	SR1	AT1G02840	1.21	0.27	1.90	0.101437	0.199687	-5.60
262040_at	receptor protein kinase, putative si	TMM	AT1G80080	-1.17	-0.23	-1.90	0.101476	0.199748	-5.61
248434_at	mitochondrial heat shock 22 kd prot	---	AT5G51440	2.25	1.17	1.90	0.101495	0.199766	-5.61
262082_s_a	wall-associated kinase 2, putative s	---	AT1G56120	1.52	0.60	1.90	0.101552	0.199847	-5.61
265808_at	hypothetical protein predicted by ge	---	AT2G17960	-1.15	-0.21	-1.90	0.101553	0.199847	-5.61
263426_at	putative glutathione peroxidase ;su	ATGPX2	AT2G31570	1.26	0.33	1.90	0.101585	0.199887	-5.61
263603_at	hypothetical protein	---	AT2G16340	-1.21	-0.27	-1.90	0.101591	0.199887	-5.61
251089_at	heat shock protein 40-like heat sho	---	AT5G01390	1.15	0.20	1.89	0.101636	0.199959	-5.61
264941_at	auxin-induced protein, putative sim	---	AT1G60680	-1.31	-0.39	-1.89	0.101658	0.199984	-5.61
256380_at	pheromone receptor, putative (AR4	AR401	AT1G66680	1.19	0.26	1.89	0.10168	0.20001	-5.61
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.57	-0.65	-1.89	0.101711	0.200055	-5.61
248800_at	40S ribosomal protein S19 ; suppo	RPS19	AT5G47320	1.17	0.22	1.89	0.101739	0.200093	-5.61
247635_at	serine/threonine-protein kinase - lik	GRIK2	AT5G60548	-1.14	-0.18	-1.89	0.101782	0.200158	-5.61
256997_at	subtilisin-like serine protease, puta	---	AT3G14067	1.27	0.35	1.89	0.101807	0.200192	-5.61
261374_at	hypothetical protein contains thiore	---	AT1G52990	-1.14	-0.19	-1.89	0.10188	0.200317	-5.61
252902_at	putative protein various predicted p	---	AT4G39560	1.16	0.22	1.89	0.101905	0.200349	-5.61
251696_at	putative protein	---	---	-1.20	-0.26	-1.89	0.101961	0.200443	-5.61
250779_at	eukaryotic translation initiation facto	EIF2 ALPH	AT5G05470	1.27	0.34	1.89	0.101982	0.200466	-5.61
248259_at	proline-rich cell wall protein-like ;su	---	AT5G53330	1.16	0.22	1.89	0.102008	0.200499	-5.61
254163_s_a	putative protein storage protein - P	---	AT4G24340	1.88	0.91	1.89	0.102049	0.200558	-5.61
256121_at	MAP kinase, putative similar to MA	---	AT1G18160	1.17	0.22	1.89	0.102055	0.200558	-5.61
246341_x_a	putative protein predicted proteins,	---	AT3G43150	-1.21	-0.28	-1.89	0.102114	0.200643	-5.61
253651_at	putative protein nucleoid DNA-bind	---	AT4G30030	-1.19	-0.26	-1.89	0.102116	0.200643	-5.61
246318_at	putative protein predicted protein B	---	AT3G56740	1.20	0.26	1.89	0.102128	0.200644	-5.61
263043_at	conserved hypothetical protein pred	---	AT1G23350	-1.19	-0.26	-1.89	0.102134	0.200644	-5.61
261294_at	dihydroxyacetone kinase, putative	---	AT1G48430	1.24	0.31	1.89	0.102149	0.200655	-5.61
259383_at	putative lectin contains Pfam profile	JR1	AT3G16470	-2.02	-1.01	-1.89	0.102166	0.200673	-5.61
266269_at	putative glutathione S-transferase	ATGSTU2	AT2G29480	1.54	0.62	1.89	0.102231	0.200783	-5.61
254020_at	beta-carotene hydroxylase ; suppo	BETA-OHA	AT4G25700	1.67	0.74	1.89	0.102254	0.20081	-5.61
254490_at	CTP synthase like protein CTP syn	---	AT4G20320	1.27	0.35	1.89	0.102284	0.200851	-5.61
262003_at	unknown protein	---	AT1G64460	1.17	0.23	1.89	0.102329	0.200922	-5.61
248568_at	receptor protein kinase-like	---	AT5G49760	1.20	0.26	1.89	0.10243	0.201104	-5.61

248489_at	unknown protein	---	AT5G51090	-1.14	-0.19	-1.89	0.102446	0.201119	-5.61
250002_at	proline-richh protein predicted prot	AGP25	AT5G18690	-1.58	-0.66	-1.89	0.102466	0.201139	-5.61
259876_at	putative DnaJ protein similar to dna	---	AT1G76700	-1.32	-0.40	-1.89	0.102538	0.201264	-5.62
254970_at	chlorophyll a/b-binding protein - like	LHCB5	AT4G10340	-1.15	-0.21	-1.89	0.102653	0.20146	-5.62
246157_at	cytochrome-b5 reductase - like pro	---	AT5G20080	-1.21	-0.28	-1.89	0.102656	0.20146	-5.62
253170_at	putative protein various predicted p	---	AT4G35130	1.13	0.18	1.89	0.102708	0.201546	-5.62
258274_at	putative cytochrome c oxidase subu	---	AT3G15640	1.19	0.26	1.89	0.102728	0.201568	-5.62
263639_at	unknown protein	---	AT2G25300	1.18	0.24	1.89	0.102749	0.201592	-5.62
245082_at	hypothetical protein predicted by ge	---	AT2G23270	2.64	1.40	1.89	0.102808	0.201689	-5.62
249085_at	putative protein similar to unknown	---	AT5G44170	-1.18	-0.23	-1.89	0.102899	0.201834	-5.62
246219_at	aminopeptidase-like protein ; suppo	APP1	AT4G36760	1.24	0.31	1.89	0.102899	0.201834	-5.62
263779_at	putative photomorphogenesis repre	SPA1	AT2G46340	1.19	0.25	1.89	0.102914	0.201846	-5.62
250819_at	putative protein strong similarity to	---	AT5G05100	1.18	0.24	1.89	0.102932	0.201864	-5.62
263390_at	hypothetical protein similar to Ta1-1	---	---	-1.14	-0.19	-1.89	0.10295	0.201883	-5.62
248924_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G45960	-1.14	-0.20	-1.89	0.103006	0.20196	-5.62
262365_at	disease resistance protein, putative	---	AT1G72870	-1.20	-0.26	-1.89	0.103008	0.20196	-5.62
265787_at	Mutator-like transposase similar to	---	---	-1.22	-0.29	-1.89	0.103035	0.201996	-5.62
261808_at	DNA damage repair protein, putati	DRT111	AT1G30480	1.15	0.20	1.89	0.103049	0.202006	-5.62
265748_at	putative Athila retroelement ORF1 p	---	---	-1.16	-0.22	-1.89	0.103086	0.202062	-5.62
246467_at	UDP glucose:flavonoid 3-o-glucosy	---	AT5G17040	-1.25	-0.33	-1.89	0.103103	0.202077	-5.62
252372_at	aldehyde dehydrogenase (NAD+)-l	ALDH2B4	AT3G48000	1.24	0.31	1.88	0.103118	0.202089	-5.62
255161_at	putative reverse transcriptase	---	---	1.15	0.20	1.88	0.103146	0.202128	-5.62
253288_at	hypothetical protein	---	AT4G34310	-1.17	-0.23	-1.88	0.103236	0.202287	-5.62
250511_at	putative protein similar to unknown	---	AT5G09960	-1.17	-0.22	-1.88	0.103339	0.202462	-5.62
266405_at	hypothetical protein predicted by ge	---	AT2G38580	-1.31	-0.39	-1.88	0.103344	0.202462	-5.62
248300_at	PP2A regulatory subunit ;supporte	TAP46	AT5G53000	-1.22	-0.28	-1.88	0.103361	0.202478	-5.62
261841_at	BTG1 binding factor 1, putative sim	---	AT1G15920	1.16	0.21	1.88	0.103444	0.202624	-5.62
254117_at	putative protein	---	AT4G24750	-1.23	-0.29	-1.88	0.103515	0.202735	-5.62
247992_at	unknown protein	---	AT5G56520	1.16	0.21	1.88	0.103518	0.202735	-5.62
245620_at	hypothetical protein	---	AT4G14050	1.18	0.24	1.88	0.103544	0.202765	-5.62
261914_at	dirigent protein, putative similar to	---	AT1G65870	-1.24	-0.31	-1.88	0.103552	0.202765	-5.62
266545_at	hypothetical protein predicted by ge	---	AT2G35290	-1.33	-0.42	-1.88	0.103593	0.202829	-5.63
255491_at	putative zinc finger protein similar t	AtIDD12	AT4G02670	-1.13	-0.17	-1.88	0.103608	0.20283	-5.63
259468_at	unknown protein	TTN10	AT1G19080	1.19	0.25	1.88	0.103611	0.20283	-5.63
264406_at	putative phragmoplastin similar to	ADL6	AT1G10290	1.18	0.24	1.88	0.103682	0.202951	-5.63

254239_at	water channel - like protein plasma	PIP1;5	AT4G23400	-1.30	-0.38	-1.88	0.103706	0.202981	-5.63
247588_at	protein disulfide isomerase precurs	ATPDIL1-4	AT5G60640	1.17	0.22	1.88	0.103733	0.203015	-5.63
253966_at	fructose-bisphosphate aldolase	---	AT4G26520	-1.22	-0.29	-1.88	0.103781	0.203092	-5.63
262628_at	glucan synthase, putative similar to	ATGSL07	AT1G06490	-1.21	-0.28	-1.88	0.103872	0.203253	-5.63
264004_at	Expressed protein ; supported by fu	---	AT2G22425	-1.19	-0.25	-1.88	0.10394	0.203357	-5.63
249645_at	thionin Thi2.2 ;supported by full-ler	THI2.2	AT5G36910	-1.23	-0.30	-1.88	0.103952	0.203357	-5.63
267160_at	putative WD-40 repeat protein	---	AT2G37670	-1.14	-0.18	-1.88	0.103952	0.203357	-5.63
252609_at	putative protein	---	AT3G45110	-1.16	-0.22	-1.88	0.103975	0.203385	-5.63
266333_at	putative ubiquitin activating enzyme	AXL	AT2G32410	1.19	0.25	1.88	0.104023	0.203461	-5.63
253697_at	nucleotide pyrophosphatase -like p	---	AT4G29700	2.24	1.16	1.88	0.104038	0.203472	-5.63
248980_at	putative protein similar to unknown	AtPP2-A7	AT5G45090	-1.21	-0.27	-1.88	0.10411	0.203597	-5.63
251727_at	putative protein	---	AT3G56290	-1.40	-0.49	-1.88	0.104128	0.203615	-5.63
266434_s_a	unknown protein	---	AT2G07120	-1.14	-0.19	-1.88	0.104148	0.203636	-5.63
247133_at	chalcone isomerase-like protein	---	AT5G66220	-1.32	-0.40	-1.88	0.104157	0.203637	-5.63
255500_at	NAD+ ADP-ribosyltransferase	APP	AT4G02390	1.21	0.28	1.88	0.104169	0.203642	-5.63
260791_at	lipase-like protein similar to lipase C	---	AT1G06250	-1.16	-0.21	-1.88	0.104212	0.203708	-5.63
263720_at	putative Na/H antiporter	ATCHX15	AT2G13620	-1.14	-0.19	-1.88	0.104227	0.203708	-5.63
259455_x_a	unknown protein	---	AT1G44030	-1.21	-0.28	-1.88	0.10423	0.203708	-5.63
266999_at	putative HMG protein ; supported b	---	AT2G34450	1.23	0.29	1.88	0.104242	0.203715	-5.63
257033_at	metalloprotease, putative similar to	ATPREP1	AT3G19170	-1.36	-0.44	-1.88	0.104259	0.203731	-5.63
257020_at	mitotic checkpoint protein, putative	---	AT3G19590	-1.18	-0.24	-1.88	0.104303	0.2038	-5.63
260899_at	hypothetical protein predicted by ge	---	AT1G21370	1.20	0.27	1.88	0.104325	0.203825	-5.63
261078_at	unknown protein identical to SP:O5	RPL4	AT1G07320	-1.16	-0.21	-1.88	0.104369	0.203894	-5.63
AFFX-BioDr	E. coli /GEN=bioD /DB_XREF=gb:J	---	---	-1.42	-0.50	-1.88	0.10438	0.203898	-5.63
250754_at	arginine-tRNA-protein transferase 1	ATE1	AT5G05700	-1.15	-0.20	-1.88	0.104447	0.20401	-5.63
246087_at	putative protein predicted protein, A	---	AT5G20580	1.26	0.33	1.88	0.104492	0.204082	-5.63
262257_at	hypothetical protein predicted by ge	---	AT1G53860	-1.17	-0.23	-1.88	0.104519	0.204116	-5.63
246538_at	40S RIBOSOMAL PROTEIN S19 -	---	AT5G15520	1.28	0.36	1.88	0.104532	0.204123	-5.63
247331_at	putative protein contains similarity t	FP3	AT5G63530	1.35	0.43	1.88	0.10454	0.204123	-5.63
246161_at	putative protein predicted proteins,	JAZ12	AT5G20900	-1.24	-0.31	-1.88	0.104574	0.204171	-5.63
256335_at	hypothetical protein predicted by ge	---	AT1G72110	-1.19	-0.25	-1.87	0.104657	0.204316	-5.63
248926_at	Ole e I (main olive allergen)-like pro	---	AT5G45880	-1.32	-0.40	-1.87	0.104777	0.204533	-5.64
267482_s_a	unknown protein	---	AT2G02770	-1.46	-0.55	-1.87	0.104799	0.20455	-5.64
249509_at	strong similarity to unknown protein	---	AT5G38390	-1.13	-0.17	-1.87	0.104804	0.20455	-5.64
267114_at	Expressed protein ; supported by fu	---	AT2G14835	-1.16	-0.21	-1.87	0.104816	0.204553	-5.64

265207_at	unknown protein	---	AT2G36680	-1.14	-0.19	-1.87	0.104823	0.204553	-5.64
262367_at	hypothetical protein contains simila	VPS46.2	AT1G73030	-1.20	-0.26	-1.87	0.104851	0.204589	-5.64
262399_at	unknown protein ;supported by full-	---	AT1G49500	1.25	0.33	1.87	0.10486	0.20459	-5.64
262349_at	unknown protein ;supported by full-	---	AT2G48130	-1.24	-0.31	-1.87	0.104981	0.204808	-5.64
252973_s_a	peptidylprolyl isomerase ROC1 ;su	ROC1	AT4G38740	1.25	0.32	1.87	0.105053	0.204932	-5.64
263984_at	hypothetical protein predicted by ge	---	AT2G42670	-1.16	-0.22	-1.87	0.10509	0.204984	-5.64
255297_x_a	hypothetical protein	---	---	-1.19	-0.25	-1.87	0.105098	0.204984	-5.64
261341_s_a	putative purple acid phosphatase si	PAP5	AT1G52940	-1.12	-0.17	-1.87	0.105136	0.205041	-5.64
250396_at	zinc finger -like protein CCHH finge	---	AT5G10970	-1.41	-0.50	-1.87	0.105169	0.205088	-5.64
253473_at	putative protein mixed-lineage prot	---	AT4G32250	1.33	0.41	1.87	0.105194	0.205118	-5.64
263631_at	unknown protein ; supported by ful	---	AT2G04900	1.14	0.19	1.87	0.105224	0.205159	-5.64
255736_at	unknown protein contains similarity	---	AT1G25380	1.17	0.22	1.87	0.10525	0.205193	-5.64
247350_at	unknown protein	---	AT5G63830	1.17	0.23	1.87	0.105388	0.205444	-5.64
252204_at	putative protein predicted protein, A	---	AT3G50340	-1.53	-0.62	-1.87	0.105419	0.205485	-5.64
263229_s_a	putative polygalacturonase similar t	---	AT1G05650	-1.14	-0.18	-1.87	0.105427	0.205485	-5.64
257544_at	putative DNA-binding protein simila	---	AT3G20880	-1.20	-0.27	-1.87	0.105454	0.20552	-5.64
245795_at	unknown protein contains similarity	---	AT1G32160	1.15	0.20	1.87	0.105486	0.205566	-5.64
258082_at	Expressed protein ; supported by fu	CLE27	AT3G25905	-1.34	-0.42	-1.87	0.105533	0.20562	-5.64
255228_at	F-box protein family, AtFBL21 cont	---	AT4G05470	-1.14	-0.19	-1.87	0.105539	0.20562	-5.64
266878_at	putative RING zinc finger protein	---	AT2G44580	-1.16	-0.22	-1.87	0.105541	0.20562	-5.64
264296_at	protein transport protein sec61 alpl	---	AT1G78720	-1.26	-0.33	-1.87	0.105589	0.205695	-5.64
248931_at	peptide transporter	---	AT5G46040	-1.13	-0.17	-1.87	0.105636	0.20574	-5.64
252612_at	hypothetical protein	---	AT3G45160	-2.15	-1.11	-1.87	0.105639	0.20574	-5.64
261809_at	rac GTPase activating protein, puta	---	AT1G08340	-1.24	-0.31	-1.87	0.105639	0.20574	-5.64
259802_at	thionin identical to GI:1181531 fron	THI2.1	AT1G72260	2.49	1.32	1.87	0.105659	0.205761	-5.64
254086_at	putative proteasome regulatory sub	---	AT4G24820	1.13	0.17	1.87	0.105675	0.205774	-5.64
262758_at	hypothetical protein predicted by ge	---	AT1G10780	1.17	0.23	1.87	0.105725	0.205851	-5.64
245394_at	hypothetical protein ;supported by f	---	AT4G16450	1.22	0.28	1.87	0.105732	0.205851	-5.64
258823_at	putative RING zinc finger protein c	---	AT3G07200	1.22	0.28	1.87	0.105753	0.205873	-5.65
254703_at	putative protein ; supported by full-	---	AT4G17960	1.23	0.30	1.87	0.105787	0.205913	-5.65
253515_at	auxin induced like-protein auxin-inc	---	AT4G31320	-1.21	-0.28	-1.87	0.105791	0.205913	-5.65
254786_at	putative protein gamma-interferon-	---	AT4G12890	-1.17	-0.23	-1.87	0.105822	0.205956	-5.65
264167_at	unknown protein Location of EST g	---	AT1G02060	1.23	0.30	1.87	0.10584	0.205973	-5.65
247781_at	dehydrodolichyl diphosphate synth	---	AT5G58784	-1.22	-0.29	-1.87	0.105853	0.205981	-5.65
253751_at	hypothetical protein ;supported by f	---	AT4G29070	1.33	0.42	1.87	0.105869	0.205994	-5.65

249650_at	Expressed protein ; supported by cl	SEF	AT5G37055	-1.19	-0.25	-1.87	0.105976	0.206186	-5.65
265075_at	hypothetical protein similar to embr	---	AT1G55450	1.74	0.80	1.87	0.106011	0.206235	-5.65
248827_at	calcium sensor protein, calcineurin	CBL9	AT5G47100	1.26	0.33	1.87	0.106088	0.206367	-5.65
263246_at	hypothetical protein predicted by ge	---	AT2G31460	-1.20	-0.26	-1.87	0.10612	0.206413	-5.65
250010_at	AP2-domain DNA-binding protein -	---	AT5G18450	-1.22	-0.29	-1.87	0.106131	0.206415	-5.65
267118_at	hypothetical protein	---	AT2G32590	-1.18	-0.24	-1.86	0.10627	0.206669	-5.65
262976_at	unknown protein	SRS5	AT1G75520	-1.20	-0.27	-1.86	0.106323	0.206755	-5.65
247876_at	unknown protein	---	AT5G57730	1.14	0.19	1.86	0.106348	0.206776	-5.65
260346_at	hypothetical protein predicted by ge	CLE10	AT1G69320	-1.19	-0.26	-1.86	0.106357	0.206776	-5.65
263121_at	receptor protein kinase, putative si	---	AT1G78530	-1.19	-0.25	-1.86	0.106362	0.206776	-5.65
256356_s_a	hypothetical protein	---	AT1G66500	-1.18	-0.24	-1.86	0.106468	0.206967	-5.65
252008_at	hypothetical protein ; supported by	---	AT3G52610	-1.17	-0.22	-1.86	0.106494	0.206998	-5.65
246711_at	putative protein	---	AT5G28190	-1.14	-0.19	-1.86	0.106529	0.207049	-5.65
261235_x_a	hypothetical protein predicted by ge	---	---	-1.14	-0.18	-1.86	0.106572	0.207114	-5.65
246860_at	putative protein various predicted p	---	AT5G25840	1.50	0.58	1.86	0.106673	0.207293	-5.65
258047_at	putative 4-coumarate:CoA ligase 2	4CL2	AT3G21240	1.77	0.82	1.86	0.10674	0.207406	-5.65
267639_at	putative squamosa-promoter bindin	SPL9	AT2G42200	1.14	0.19	1.86	0.10675	0.207408	-5.65
264189_s_a	hypothetical protein similar to acyl-c	ACP3	AT1G54580	-1.22	-0.29	-1.86	0.10685	0.207585	-5.66
265504_at	putative Ta11-like non-LTR retroele	---	---	-1.17	-0.22	-1.86	0.106964	0.207788	-5.66
249428_at	putative protein predicted protein K	---	AT5G39870	-1.12	-0.17	-1.86	0.106979	0.2078	-5.66
260458_at	unknown protein	---	AT1G68250	-1.16	-0.21	-1.86	0.106991	0.207805	-5.66
256189_at	hypothetical protein predicted by ge	---	AT1G30140	-1.14	-0.19	-1.86	0.107041	0.207878	-5.66
250868_at	malate synthase -like protein malat	MLS	AT5G03860	-1.25	-0.32	-1.86	0.107047	0.207878	-5.66
263345_s_a	putative chlorophyll a/b binding prot	LHCB2.1	AT2G05070	-1.47	-0.56	-1.86	0.107066	0.207897	-5.66
247715_at	putative protein predicted protein, A	---	AT5G59360	-1.26	-0.33	-1.86	0.107163	0.208069	-5.66
263718_at	putative CCAAT-box binding trancri	NF-YB7	AT2G13570	-1.19	-0.25	-1.86	0.107225	0.208172	-5.66
260675_at	unknown protein ; supported by cDI	---	AT1G19430	-1.20	-0.27	-1.86	0.107242	0.208187	-5.66
266201_at	similar to MtN3 protein ;supported	---	AT2G39060	-1.17	-0.23	-1.86	0.107255	0.208194	-5.66
252936_at	putative protein transcription initiati	---	AT4G39160	1.26	0.33	1.86	0.107269	0.208204	-5.66
249824_at	putative protein similar to unknown	---	AT5G23380	-1.15	-0.21	-1.86	0.10729	0.208227	-5.66
247841_at	putative protein predicted proteins,	ATFIP1[V]	AT5G58040	1.17	0.23	1.86	0.107304	0.208237	-5.66
266925_at	unknown protein ;supported by full-	PEX11D	AT2G45740	1.14	0.19	1.86	0.107397	0.208398	-5.66
257633_at	hypothetical protein	CYP86C2	AT3G26125	-1.14	-0.19	-1.86	0.107497	0.20857	-5.66
260809_at	hypothetical protein predicted by ge	---	AT1G43730	-1.13	-0.18	-1.86	0.107504	0.20857	-5.66
250782_at	SYN1 splice variant 1 (gb AAF0898	SYN1	AT5G05490	-1.16	-0.22	-1.86	0.107514	0.208573	-5.66

257132_at	hypothetical protein predicted by ge	---	AT3G20230	-1.15	-0.21	-1.86	0.107535	0.208595	-5.66
253965_at	hypothetical protein	---	AT4G26490	1.21	0.28	1.85	0.107697	0.208891	-5.66
247923_at	porin-like protein ;supported by full	VDAC4	AT5G57490	1.18	0.24	1.85	0.107904	0.209277	-5.66
263125_at	hypothetical protein predicted by ge	---	AT1G78470	-1.15	-0.21	-1.85	0.107938	0.209323	-5.66
247795_at	putative protein zinc finger transcri	---	AT5G58620	1.18	0.24	1.85	0.107965	0.209359	-5.67
254120_at	putative mitochondrial uncoupling p	DIC2	AT4G24570	2.80	1.49	1.85	0.108059	0.209523	-5.67
267387_at	hypothetical protein predicted by ge	---	AT2G44440	-1.12	-0.17	-1.85	0.108091	0.209567	-5.67
248987_at	dimethylaniline monooxygenase (N	---	AT5G45180	-1.14	-0.19	-1.85	0.108175	0.209706	-5.67
258858_at	putative 40S ribosomal protein S19	---	AT3G02080	1.31	0.39	1.85	0.108181	0.209706	-5.67
255836_at	putative splicing factor U2AF large	---	AT2G33440	1.23	0.30	1.85	0.10827	0.20986	-5.67
259350_at	putative serine/threonine protein kir	RBK2	AT3G05140	-1.18	-0.24	-1.85	0.108309	0.209917	-5.67
248061_at	putative protein contains similarity t	---	AT5G55340	-1.13	-0.17	-1.85	0.108385	0.210049	-5.67
263358_x_a	hypothetical protein similar to hypot	---	---	-1.17	-0.22	-1.85	0.108405	0.210069	-5.67
266135_at	putative transcription factor IIIB 70	---	AT2G45100	-1.28	-0.36	-1.85	0.108556	0.210344	-5.67
250242_at	putative protein similar to unknown	---	AT5G13620	-1.15	-0.20	-1.85	0.108613	0.210435	-5.67
257757_at	hypothetical protein predicted by ge	PGSIP1	AT3G18660	-1.15	-0.20	-1.85	0.108744	0.210672	-5.67
251524_at	3-isopropylmalate dehydratase-like	---	AT3G58980	1.39	0.47	1.85	0.108783	0.21073	-5.67
254502_at	hypothetical protein	PTAC14	AT4G20130	1.19	0.26	1.85	0.108854	0.21085	-5.67
259208_at	hypothetical protein similar to GB:A	---	AT3G09060	1.16	0.21	1.85	0.108875	0.210873	-5.67
248752_at	unknown protein	---	AT5G47600	-1.14	-0.19	-1.85	0.108902	0.210907	-5.67
257896_at	basic chitinase, putative similar to	---	AT3G16920	-1.70	-0.76	-1.85	0.108949	0.210979	-5.67
257247_at	helix-loop-helix DNA-binding protein	FMA	AT3G24140	1.23	0.30	1.85	0.108961	0.210984	-5.67
248666_at	cyclin C-like protein ;supported by	---	AT5G48630	-1.21	-0.27	-1.85	0.109011	0.211064	-5.67
263050_at	unknown protein ; supported by cD	ATVPS11	AT2G05170	-1.16	-0.21	-1.85	0.10904	0.211073	-5.67
251226_at	proline-rich protein proline-rich pro	PRP3	AT3G62680	-1.17	-0.22	-1.85	0.10904	0.211073	-5.67
265313_at	unknown protein	---	AT2G20210	1.18	0.24	1.85	0.109044	0.211073	-5.67
248490_at	putative protein similar to unknown	---	AT5G50940	-1.46	-0.54	-1.85	0.10908	0.211125	-5.68
246421_at	TOM (target of myb1) -like protein	---	AT5G16880	-1.19	-0.25	-1.85	0.109111	0.211168	-5.68
261106_at	homeodomain-containing protein H	KNAT7	AT1G62990	-1.14	-0.19	-1.85	0.109123	0.211173	-5.68
263907_at	abscisic acid insensitive 5 (ABI5) co	ABI5	AT2G36270	-1.21	-0.27	-1.85	0.109185	0.211276	-5.68
260681_at	hypothetical protein predicted by ge	AT1G0803(	---	1.14	0.19	1.84	0.109267	0.211415	-5.68
245027_at	heme oxygenase 2 (HO2)	HO2	AT2G26550	-1.15	-0.21	-1.84	0.109379	0.211614	-5.68
265589_at	hypothetical protein predicted by ge	---	AT2G20170	-1.17	-0.22	-1.84	0.109423	0.211683	-5.68
263946_at	hypothetical protein ;supported by	---	AT2G36000	-1.18	-0.24	-1.84	0.10957	0.211948	-5.68
255669_at	predicted protein	MBD3	AT4G00416	-1.12	-0.17	-1.84	0.109652	0.212088	-5.68

256151_at	multispanning membrane protein, p	---	AT1G55130	1.23	0.30	1.84	0.109703	0.212169	-5.68
255950_at	hypothetical protein predicted by ge	---	AT1G22110	-1.22	-0.28	-1.84	0.109719	0.212171	-5.68
245661_at	purine permease, putative similar t	ATPUP3	AT1G28220	-1.18	-0.23	-1.84	0.109723	0.212171	-5.68
257702_at	CTP-synthetase, putative similar to	emb2742	AT3G12670	1.19	0.25	1.84	0.109776	0.212257	-5.68
245804_at	hypothetical protein predicted by ge	---	AT1G46696	-1.13	-0.18	-1.84	0.109806	0.212296	-5.68
253137_at	protein kinase - like protein protein	---	AT4G35500	1.21	0.27	1.84	0.109861	0.212378	-5.68
247344_at	ARI-like RING zinc finger protein-lik	---	AT5G63750	-1.18	-0.24	-1.84	0.109867	0.212378	-5.68
249423_at	Expressed protein ; supported by fu	---	AT5G39785	1.21	0.28	1.84	0.109881	0.212388	-5.68
253528_s_a	putative protein bcop gene product	---	AT4G31480	-1.13	-0.18	-1.84	0.109919	0.212409	-5.68
256428_at	putative disease resistance protein	AtRLP35	AT3G11080	1.30	0.38	1.84	0.10992	0.212409	-5.68
258765_at	putative pectinesterase contains sir	---	AT3G10710	-1.16	-0.21	-1.84	0.10992	0.212409	-5.68
259839_at	peptide transporter, putative simila	---	AT1G52190	-2.25	-1.17	-1.84	0.109951	0.212452	-5.68
256566_at	hypothetical protein	---	AT3G19530	-1.14	-0.19	-1.84	0.109964	0.212458	-5.68
259946_at	putative TINY similar to TINY GB:C	---	AT1G71450	-1.12	-0.16	-1.84	0.110039	0.212585	-5.68
255214_at	hypothetical protein	---	---	-1.13	-0.18	-1.84	0.110184	0.212846	-5.68
246359_x_a	hypothetical protein	---	---	-1.21	-0.27	-1.84	0.110228	0.212914	-5.69
248702_at	unknown protein	---	AT5G48420	-1.14	-0.19	-1.84	0.110256	0.212942	-5.69
263753_at	putative dehydrin ;supported by ful	LEA	AT2G21490	-1.12	-0.16	-1.84	0.110261	0.212942	-5.69
253071_at	putative protein various predicted p	---	AT4G37880	-1.15	-0.20	-1.84	0.110306	0.213011	-5.69
260964_at	E2, ubiquitin-conjugating enzyme 1	ATUBC2-1	AT1G45050	1.13	0.17	1.84	0.110356	0.213074	-5.69
244976_at	cytochrome B6	---	---	1.14	0.19	1.84	0.110358	0.213074	-5.69
262205_at	hypothetical protein predicted by ge	---	AT2G01080	1.17	0.22	1.84	0.110406	0.213149	-5.69
255173_at	putative transposon protein similar	---	---	-1.18	-0.24	-1.84	0.110429	0.213176	-5.69
244988_s_a	ribosomal protein L23	---	---	-1.20	-0.26	-1.84	0.110444	0.213179	-5.69
251404_at	putative protein	---	AT3G60310	-1.17	-0.23	-1.84	0.110449	0.213179	-5.69
247651_at	histone H2A - like protein histone H	HTA6	AT5G59870	-1.81	-0.86	-1.84	0.110474	0.213209	-5.69
250573_at	putative protein	---	AT5G08220	1.19	0.25	1.84	0.11051	0.213261	-5.69
247313_at	3(2),5-bisphosphate nucleotidase	SAL1	AT5G63980	1.24	0.31	1.84	0.110554	0.213318	-5.69
250137_at	rRNA methylase - like protein rRNA	---	AT5G15390	-1.16	-0.22	-1.84	0.110559	0.213318	-5.69
258675_at	putative nonspecific lipid-transfer pr	LTP6	AT3G08770	-1.16	-0.22	-1.84	0.110584	0.213348	-5.69
262856_at	unknown protein contains Pfam pro	---	AT1G14910	-1.19	-0.25	-1.84	0.110633	0.213425	-5.69
249442_at	putative protein ; supported by cDN	---	AT5G39590	1.41	0.50	1.84	0.110717	0.213569	-5.69
248776_at	unknown protein	---	AT5G47900	-1.15	-0.20	-1.84	0.110733	0.213583	-5.69
263478_at	putative receptor-like protein kinase	---	AT2G31880	1.55	0.63	1.84	0.110748	0.213592	-5.69
245254_at	ATP-sulfurylase ; supported by cDN	APS3	AT4G14680	-1.80	-0.85	-1.84	0.110791	0.213658	-5.69

254012_at	putative ribosomal protein ribosom	---	AT4G26230	1.33	0.41	1.84	0.110808	0.213672	-5.69
265933_at	putative esterase contains esterase	---	AT2G19550	-1.18	-0.24	-1.84	0.110818	0.213674	-5.69
260092_at	putative serine carboxypeptidase s	scpl3	AT1G73280	-1.14	-0.18	-1.83	0.110925	0.213861	-5.69
250947_at	putative protein	---	AT5G03450	1.21	0.27	1.83	0.110934	0.213861	-5.69
267389_at	putative beta-glucosidase	BGLU28	AT2G44460	3.73	1.90	1.83	0.110966	0.213898	-5.69
253896_at	putative protein NBS/LRR disease	---	AT4G27190	-1.16	-0.22	-1.83	0.110972	0.213898	-5.69
245115_at	putative esterase D ;supported by	SFGH	AT2G41530	1.27	0.34	1.83	0.11099	0.213915	-5.69
248686_at	33 kDa secretory protein-like ; supp	---	AT5G48540	1.67	0.74	1.83	0.111012	0.213939	-5.69
247425_at	unknown protein	---	AT5G62550	-1.13	-0.18	-1.83	0.111064	0.214021	-5.69
260381_at	putative kinesin similar to kinesin-C	---	AT1G73860	-1.18	-0.24	-1.83	0.111113	0.214093	-5.69
245473_at	hypothetical protein	---	AT4G16050	1.13	0.18	1.83	0.11112	0.214093	-5.69
263053_at	similar to glucose inhibited division	---	AT2G13440	-1.16	-0.22	-1.83	0.111145	0.214107	-5.69
247269_at	alternative oxidase 2 (sp|O22049)	AOX2	AT5G64210	-1.14	-0.19	-1.83	0.111146	0.214107	-5.69
246291_at	hypothetical protein ; supported by	---	AT3G56820	1.17	0.23	1.83	0.111158	0.214113	-5.69
264445_at	unknown protein similar to ESTs gl	---	AT1G27290	-1.29	-0.37	-1.83	0.111208	0.21419	-5.69
262199_at	unknown protein ; supported by cDI	---	AT1G53800	-1.22	-0.29	-1.83	0.111245	0.214244	-5.69
245818_at	cytochrome b561, putative similar t	---	AT1G26100	-1.32	-0.40	-1.83	0.111263	0.214259	-5.69
248630_at	putative protein strong similarity to	---	AT5G48990	1.16	0.21	1.83	0.111295	0.214303	-5.69
248462_at	nucleotide-binding protein ; suppor	NBP35	AT5G50960	1.18	0.24	1.83	0.11131	0.214309	-5.69
264943_at	hypothetical protein predicted by ge	---	AT1G76910	-1.20	-0.26	-1.83	0.111316	0.214309	-5.69
248083_at	unknown protein	---	AT5G55420	1.63	0.70	1.83	0.111346	0.214348	-5.69
247914_at	xyloglucan endotransglycosylase	---	AT5G57540	-1.17	-0.23	-1.83	0.111395	0.214423	-5.70
248882_at	cullin ;supported by full-length cDNA	CUL4	AT5G46210	1.13	0.18	1.83	0.111422	0.214458	-5.70
266710_at	putative Ser/Thr protein kinase	---	AT2G46850	-1.16	-0.21	-1.83	0.11146	0.214508	-5.70
245963_at	putative protein HPt phosphotransr	---	AT5G19710	-1.13	-0.17	-1.83	0.111467	0.214508	-5.70
267180_at	unknown protein ; supported by cD	SLT1	AT2G37570	1.16	0.21	1.83	0.111484	0.214522	-5.70
246073_at	ribosomal protein L36-like ribosom	---	AT5G20180	-1.17	-0.23	-1.83	0.111504	0.214543	-5.70
262145_at	unknown protein contains similarity	---	AT1G52730	1.19	0.25	1.83	0.111537	0.214589	-5.70
254997_s_a	putative protein various predicted p	---	AT4G09920	1.14	0.19	1.83	0.11162	0.214708	-5.70
266783_at	putative laccase (diphenol oxidase)	LAC2	AT2G29130	-1.24	-0.31	-1.83	0.111624	0.214708	-5.70
257574_at	hypothetical protein predicted by ge	---	AT3G20710	-1.17	-0.23	-1.83	0.111628	0.214708	-5.70
265061_at	hypothetical protein contains simila	---	AT1G61640	1.41	0.50	1.83	0.111683	0.214796	-5.70
252525_at	putative protein hypothetical protein	---	AT3G46450	-1.16	-0.22	-1.83	0.111748	0.214904	-5.70
258548_at	hypothetical protein	ULP1A	AT3G06910	1.21	0.27	1.83	0.111781	0.214949	-5.70
254962_at	putative glucanase endo-beta-1,4-l	AtGH9C3	AT4G11050	-1.17	-0.22	-1.83	0.111845	0.215054	-5.70

265053_at	myrosinase binding protein, putativ	---	AT1G52000	-1.34	-0.42	-1.83	0.111861	0.215066	-5.70
258562_at	unknown protein ;supported by full-	---	AT3G05980	-1.13	-0.18	-1.83	0.111879	0.215083	-5.70
263577_at	putative protein kinase identical to h	SSP	AT2G17090	-1.19	-0.25	-1.83	0.111933	0.215169	-5.70
246376_at	auxin regulated protein IAA18, puta	IAA18	AT1G51950	-1.22	-0.29	-1.83	0.111966	0.215214	-5.70
245119_at	unknown protein ; supported by cD	---	AT2G41640	1.95	0.97	1.83	0.112019	0.215298	-5.70
253880_at	Expressed protein ;supported by cD	---	AT4G27590	-1.19	-0.25	-1.83	0.112066	0.215366	-5.70
258908_at	putative dehydroquinase shikimate	MEE32	AT3G06350	1.23	0.30	1.83	0.112074	0.215366	-5.70
256211_at	gibberellin 20-oxidase, putative sim	GA2OX7	AT1G50960	-1.13	-0.17	-1.83	0.112123	0.215443	-5.70
264796_at	unknown protein similar to ESTs gb	ZIGA4	AT1G08680	1.16	0.21	1.83	0.112164	0.215495	-5.70
245096_at	putative cysteine proteinase inhibito	ATCYSA	AT2G40880	1.18	0.23	1.83	0.112169	0.215495	-5.70
252762_at	putative protein hypothetical protei	---	AT3G42780	-1.22	-0.29	-1.83	0.112198	0.215532	-5.70
267230_at	unknown protein	ARL	AT2G44080	2.14	1.10	1.83	0.112282	0.215677	-5.70
266952_at	putative gibberellin 2-oxidase	ATGA2OX3	AT2G34555	-1.17	-0.23	-1.82	0.112493	0.216063	-5.70
245416_at	putative protein	---	AT4G17350	-1.19	-0.25	-1.82	0.112525	0.216101	-5.71
248437_at	putative protein similar to unknown	EMF2	AT5G51230	-1.22	-0.29	-1.82	0.112532	0.216101	-5.71
250697_at	putative protein contains similarity t	---	AT5G06800	1.18	0.24	1.82	0.112561	0.216139	-5.71
261100_at	RNA polymerase IIA large subunit,	NRPD1A	AT1G63020	-1.16	-0.22	-1.82	0.112709	0.216405	-5.71
254344_at	alcohol dehydrogenase like protein	---	AT4G22110	-1.26	-0.33	-1.82	0.112823	0.216607	-5.71
264124_at	hypothetical protein predicted by ge	ATOCT2	AT1G79360	-1.17	-0.23	-1.82	0.112844	0.216623	-5.71
250693_at	ubiquitin-specific protease 12 (UBP	UBP12	AT5G06600	1.14	0.19	1.82	0.112851	0.216623	-5.71
250050_at	putative protein predicted protein, A	VAR3	AT5G17790	1.17	0.22	1.82	0.112865	0.216629	-5.71
266697_at	profilin 4 ; supported by full-length	PRF5	AT2G19770	-1.20	-0.27	-1.82	0.112873	0.216629	-5.71
255750_at	hypothetical protein predicted by ge	---	AT1G31960	-1.15	-0.20	-1.82	0.112886	0.216636	-5.71
256021_at	unknown protein contains Pfam pro	ZW9	AT1G58270	-1.25	-0.32	-1.82	0.11298	0.216798	-5.71
264306_at	unknown protein predicted by gene	---	AT1G78890	1.18	0.24	1.82	0.113023	0.216861	-5.71
246100_at	putative protein predicted protein, A	---	---	-1.15	-0.21	-1.82	0.113064	0.216923	-5.71
248468_at	UDP-glucose:protein transglucosyla	RGP4	AT5G50750	-1.19	-0.25	-1.82	0.113094	0.216962	-5.71
266083_at	hypothetical protein predicted by ge	---	AT2G37820	-1.12	-0.16	-1.82	0.113121	0.216996	-5.71
260841_at	Expressed protein ; supported by fu	---	AT1G29195	1.19	0.25	1.82	0.113144	0.21702	-5.71
263820_at	hypothetical protein predicted by ge	---	---	-1.24	-0.32	-1.82	0.113163	0.217039	-5.71
249091_at	AtCLH2 (gb|AAF27046.1) ; suppor	CLH2	AT5G43860	1.16	0.22	1.82	0.113236	0.217156	-5.71
247243_at	nodulin-like protein	---	AT5G64700	-1.27	-0.34	-1.82	0.113251	0.217156	-5.71
249353_at	oleosin ; supported by cDNA: gi_72	OLEO2	AT5G40420	-1.20	-0.26	-1.82	0.113253	0.217156	-5.71
252465_x_a	putative protein several hypothetica	---	---	-1.15	-0.20	-1.82	0.113262	0.217156	-5.71
256126_at	hypothetical protein similar to MuDR	---	AT1G18050	-1.23	-0.30	-1.82	0.113308	0.217212	-5.71

255646_at	hypothetical protein	---	AT4G00890	-1.16	-0.22	-1.82	0.11331	0.217212	-5.71
250088_at	APG5 (autophagy 5)-like protein	APG5	AT5G17290	1.16	0.21	1.82	0.113331	0.217233	-5.71
255380_at	putative calcium channel ; supporte	ATTPC1	AT4G03560	-1.23	-0.30	-1.82	0.113384	0.217306	-5.71
251720_at	putative protein	---	AT3G56160	-1.34	-0.42	-1.82	0.113388	0.217306	-5.71
266248_at	hypothetical protein predicted by ge	---	AT2G27650	-1.12	-0.16	-1.82	0.113466	0.217438	-5.71
254068_at	putative protein similarity to multidr	NAP8	AT4G25450	1.17	0.22	1.82	0.113492	0.21747	-5.71
245456_at	disease resistance RPP5 like protei	RPP5	AT4G16950	1.19	0.25	1.82	0.11353	0.217523	-5.71
266941_at	peroxidase (ATP22a) identical to G	---	AT2G18980	-1.20	-0.26	-1.82	0.113568	0.217578	-5.71
246237_at	putative protein	---	AT4G36390	1.18	0.24	1.82	0.113594	0.21761	-5.71
250899_at	putative protein ; supported by cDN	---	AT5G03340	1.23	0.30	1.82	0.113677	0.217721	-5.71
262718_at	hypothetical protein similar to putati	---	---	-1.16	-0.21	-1.82	0.113685	0.217721	-5.71
263879_at	hypothetical protein predicted by ge	---	AT2G22030	-1.13	-0.18	-1.82	0.113688	0.217721	-5.71
253730_at	putative protein hypothetical protei	---	AT4G29480	1.29	0.36	1.82	0.113691	0.217721	-5.71
259239_at	putative 40S ribosomal protein s14	---	AT3G11510	1.46	0.55	1.82	0.113714	0.217749	-5.72
255044_at	putative protein	---	AT4G09680	1.17	0.22	1.82	0.113826	0.217944	-5.72
248150_at	kinesin-like protein ; supported by c	ATK3	AT5G54670	-1.41	-0.50	-1.82	0.113837	0.217947	-5.72
259527_at	hypothetical protein	---	AT1G12600	-1.12	-0.17	-1.82	0.113896	0.218041	-5.72
257527_at	hypothetical protein similar to hypo	---	AT3G01880	-1.15	-0.21	-1.82	0.113921	0.218072	-5.72
246382_at	hypothetical protein	---	---	-1.19	-0.25	-1.82	0.113959	0.218125	-5.72
251628_at	translation initiation factor 3 -like pr	EIF3E	AT3G57290	1.18	0.24	1.82	0.114053	0.218287	-5.72
267329_at	hypothetical protein	---	AT2G19250	1.15	0.21	1.81	0.114098	0.218355	-5.72
252652_at	putative chloroplast prephenate deh	ADT4	AT3G44720	1.70	0.77	1.81	0.114162	0.218458	-5.72
251459_at	putative protein hypothetical protei	---	AT3G60200	-1.50	-0.59	-1.81	0.114188	0.218491	-5.72
250033_at	eukaryotic cap-binding protein (gb|A	NCBP	AT5G18110	1.14	0.19	1.81	0.114206	0.218507	-5.72
259031_at	putative transcription factor similar t	---	AT3G09360	1.22	0.28	1.81	0.114223	0.218508	-5.72
246027_at	homoserine dehydrogenase-like pr	---	AT5G21060	-1.26	-0.33	-1.81	0.114226	0.218508	-5.72
265750_x_a	putative Athila retroelement ORF1 p	---	---	-1.25	-0.32	-1.81	0.114239	0.218514	-5.72
252022_at	fructose bisphosphate aldolase - lik	---	AT3G52930	1.24	0.31	1.81	0.114269	0.218553	-5.72
255190_x_a	may be a pseudogene similar to a	---	---	-1.13	-0.17	-1.81	0.114327	0.218647	-5.72
251188_at	putative protein DESSICATION-RE	---	AT3G62730	-1.16	-0.22	-1.81	0.114353	0.218664	-5.72
254613_at	ankyrin-like protein ankyrin 3, Mus	---	AT4G19150	-1.16	-0.22	-1.81	0.114355	0.218664	-5.72
249129_at	cyclin A-type	CYCA3;1	AT5G43080	-1.17	-0.22	-1.81	0.11438	0.21867	-5.72
264533_s_a	H+/Ca2+ antiporter, putative simila	CAX5	AT1G55720	-1.16	-0.21	-1.81	0.114381	0.21867	-5.72
248663_at	putative protein strong similarity to	---	AT5G48590	1.12	0.17	1.81	0.114387	0.21867	-5.72
262021_at	unknown protein	AT1G3554	---	1.17	0.23	1.81	0.114439	0.218751	-5.72

253603_at	putative protein SP8 binding protei	WRKY32	AT4G30935	1.13	0.18	1.81	0.114465	0.218783	-5.72
251153_at	putative protein predicted protein, A	NPL41	AT3G63000	1.18	0.24	1.81	0.114504	0.218839	-5.72
256005_at	hypothetical protein similar to putati	---	---	-1.15	-0.20	-1.81	0.114556	0.21891	-5.72
247031_at	UDP-glucuronyltransferase-like pro	---	AT5G67230	-1.23	-0.30	-1.81	0.11456	0.21891	-5.72
251766_at	putative protein PA26, p53 regulate	---	AT3G55890	1.15	0.21	1.81	0.114616	0.218965	-5.72
264462_at	putative transcription factor similar	WLIM1	AT1G10200	1.26	0.33	1.81	0.114624	0.218965	-5.72
257217_at	phosphoenolpyruvate carboxylase (	ATPPC3	AT3G14940	-1.23	-0.30	-1.81	0.114624	0.218965	-5.72
263807_at	putative indole-3-glycerol phosphat	---	AT2G04400	1.92	0.94	1.81	0.114636	0.218965	-5.72
256760_at	SKP1/ASK1 (At15), putative simila	ASK15	AT3G25650	-1.12	-0.16	-1.81	0.114637	0.218965	-5.72
261554_at	PPR-repeat protein contains multipl	---	AT1G63400	1.12	0.16	1.81	0.114683	0.219033	-5.72
261432_at	hypothetical protein predicted by ge	---	AT1G07680	-1.14	-0.19	-1.81	0.114696	0.219041	-5.72
262815_at	putative cytochrome P450 strong si	CYP71A18	AT1G11610	1.32	0.41	1.81	0.114762	0.219129	-5.72
248524_s_a	putative protein contains similarity t	---	AT5G50570	-1.63	-0.71	-1.81	0.114762	0.219129	-5.72
260773_at	gibberellin 2- oxidase identical to gi	ATGA2OX1	AT1G78440	-1.18	-0.24	-1.81	0.114825	0.219231	-5.72
258308_at	putative reverse transcriptase simila	---	---	-1.32	-0.40	-1.81	0.114834	0.219231	-5.72
267495_at	myb-like protein isolog	ETC2	AT2G30420	-1.34	-0.42	-1.81	0.114914	0.219364	-5.73
257448_s_a	putative protein various predicted p	---	AT2G11620	1.15	0.21	1.81	0.115043	0.219592	-5.73
245199_at	Expressed protein ; supported by fu	KCR1	AT1G67730	-1.19	-0.25	-1.81	0.115069	0.219617	-5.73
258398_at	thioredoxin m4 identical to GB:AAF	TRX-M4	AT3G15360	-1.14	-0.18	-1.81	0.115079	0.219617	-5.73
255798_at	unknown protein predicted by gene	---	AT2G33255	1.17	0.23	1.81	0.115085	0.219617	-5.73
257997_at	hypothetical protein similar to hypot	---	AT3G27500	-1.13	-0.18	-1.81	0.115188	0.219796	-5.73
257356_s_a	hypothetical protein predicted by ge	---	AT2G32490	-1.17	-0.22	-1.81	0.115242	0.21988	-5.73
263542_at	putative protein transport protein SE	---	AT2G21630	-1.23	-0.30	-1.81	0.115255	0.219887	-5.73
255934_at	cytochrome P450, putative similar	CYP87A2	AT1G12740	-1.14	-0.19	-1.81	0.115299	0.219953	-5.73
260959_at	unknown protein ;supported by full-	---	AT1G06050	1.15	0.21	1.81	0.115435	0.220193	-5.73
263378_at	protein phosphatase 2C (AthPP2C5	ATHPP2C5	AT2G40180	-1.25	-0.32	-1.81	0.115452	0.220207	-5.73
248493_at	putative protein contains similarity t	FSD2	AT5G51100	1.17	0.23	1.81	0.115493	0.220267	-5.73
251585_at	putative protein hypothetical protei	---	AT3G58630	-1.29	-0.37	-1.81	0.115532	0.220313	-5.73
262315_at	unknown protein ;supported by full-	---	AT1G70990	-1.36	-0.44	-1.81	0.115536	0.220313	-5.73
262677_at	unknown protein	---	AT1G75860	-1.30	-0.38	-1.81	0.115557	0.220334	-5.73
245994_at	putative protein various predicted p	---	---	-1.17	-0.23	-1.81	0.115697	0.220582	-5.73
246587_at	putative protein predicted proteins,	---	---	-1.16	-0.22	-1.81	0.115737	0.220626	-5.73
263013_at	knotted-like homeobox protein, put	KNAT6	AT1G23380	-1.18	-0.24	-1.81	0.115739	0.220626	-5.73
255693_s_a	putative BRCA2 homolog	BRCA2(IV)	AT4G00020	-1.16	-0.22	-1.80	0.115784	0.220693	-5.73
254953_at	Expressed protein ; supported by fu	---	AT4G10925	1.16	0.21	1.80	0.115822	0.220747	-5.73

253713_at	putative protein several hypothetica	---	AT4G29370	-1.14	-0.19	-1.80	0.115919	0.2209	-5.73
247379_at	unknown protein	---	---	-1.21	-0.28	-1.80	0.115929	0.2209	-5.73
249519_at	putative protein similar to unknown	APE1	AT5G38660	-1.20	-0.27	-1.80	0.115931	0.2209	-5.73
245233_at	putative protein similarity to low-ter	---	AT4G25580	-1.17	-0.23	-1.80	0.115995	0.221003	-5.73
257888_at	seed maturation protein, putative s	---	AT3G16990	1.29	0.37	1.80	0.116031	0.221036	-5.73
245832_at	chorismate synthase, putative simi	EMB1144	AT1G48850	1.54	0.63	1.80	0.116032	0.221036	-5.73
261800_at	HD-Zip protein identical to HD-Zip p	PHV	AT1G30490	-1.18	-0.24	-1.80	0.116048	0.221048	-5.73
266989_at	putative myrosinase-binding protein	JAL23	AT2G39330	-2.28	-1.19	-1.80	0.116095	0.22112	-5.74
252264_at	putative protein hypothetical protei	---	AT3G49590	-1.15	-0.20	-1.80	0.116136	0.221179	-5.74
246358_x_a	hypothetical protein	---	AT2G06570	-1.16	-0.21	-1.80	0.11616	0.221205	-5.74
255983_at	polyneuridine aldehyde esterase, p	MES14	AT1G33990	1.16	0.21	1.80	0.116172	0.221211	-5.74
261429_at	hypothetical protein contains simila	WRKY61	AT1G18860	1.15	0.20	1.80	0.116186	0.221219	-5.74
248204_at	myosin heavy chain	ATM2	AT5G54280	-1.20	-0.26	-1.80	0.1162	0.221227	-5.74
266475_at	putative lipase	---	AT2G31100	-1.15	-0.20	-1.80	0.116276	0.221354	-5.74
248000_at	WD-repeat protein-like ;supported	---	AT5G56190	-1.18	-0.23	-1.80	0.116353	0.221481	-5.74
246719_at	homology to many predicted putati	---	---	-1.12	-0.17	-1.80	0.116386	0.221514	-5.74
252746_at	sucrose synthase -like protein SUC	SUS4	AT3G43190	-1.15	-0.21	-1.80	0.11639	0.221514	-5.74
249463_s_a	putative protein predicted proteins,	anac064	AT3G56530	-1.16	-0.21	-1.80	0.116399	0.221514	-5.74
252775_s_a	putative protein various predicted p	---	---	1.15	0.20	1.80	0.116436	0.221556	-5.74
264965_at	hypothetical protein predicted by ge	---	AT1G60560	1.19	0.26	1.80	0.116444	0.221556	-5.74
254075_at	DRE CRT-binding protein DREB1C	CBF2	AT4G25470	1.28	0.36	1.80	0.116451	0.221556	-5.74
256774_at	hypothetical protein predicted by ge	---	AT3G13760	-1.12	-0.17	-1.80	0.116588	0.221799	-5.74
246571_at	putative protein	---	AT5G15000	-1.12	-0.16	-1.80	0.116598	0.221801	-5.74
264547_at	unknown protein ; supported by cDI	CLC-F	AT1G55620	-1.24	-0.31	-1.80	0.116611	0.221802	-5.74
252718_at	putative protein predicted proteins,	---	AT3G43940	-1.17	-0.23	-1.80	0.116618	0.221802	-5.74
251345_at	putative protein hypothetical protein	---	AT3G60940	-1.15	-0.21	-1.80	0.116729	0.221994	-5.74
256588_at	unknown protein	---	AT3G28790	-1.18	-0.24	-1.80	0.116756	0.222027	-5.74
251144_at	anthranilate N-benzoyltransferase	---	AT5G01210	1.33	0.41	1.80	0.116777	0.222049	-5.74
257100_at	disease resistance protein, putative	AtRLP41	AT3G25010	-1.19	-0.25	-1.80	0.116803	0.222074	-5.74
264861_at	putative glucosidase similar to a-gl	---	AT1G24320	-1.13	-0.18	-1.80	0.116811	0.222074	-5.74
258309_at	putative transposase related protein	---	---	-1.14	-0.19	-1.80	0.116823	0.222079	-5.74
258949_at	unknown protein	ATCFM2	AT3G01370	1.21	0.28	1.80	0.116864	0.222139	-5.74
264891_at	putative pectinesterase similar to G	---	AT1G23200	-1.26	-0.33	-1.80	0.116907	0.222202	-5.74
252610_x_a	putative protein putative MuDR pro	---	---	-1.12	-0.16	-1.80	0.11692	0.222209	-5.74
250840_at	putative protein predicted protein, A	---	---	-1.21	-0.28	-1.80	0.116938	0.222221	-5.74

253863_at	putative protein D.melanogaster P	---	AT4G27420	-1.18	-0.24	-1.80	0.116946	0.222221	-5.74
263560_s_a	unknown protein	FUT5	AT2G15350	-1.17	-0.23	-1.80	0.117041	0.222383	-5.74
253166_at	putative protein putative ligand-gat	GLUR2	AT4G35290	1.25	0.33	1.80	0.117078	0.222429	-5.74
248122_at	unknown protein	---	AT5G54700	-1.15	-0.20	-1.80	0.117085	0.222429	-5.74
266755_at	putative alcohol dehydrogenase	---	AT2G47150	-1.17	-0.23	-1.80	0.1171	0.222432	-5.74
246920_at	phytocyanin-related protein-like ph	---	AT5G25090	-1.13	-0.18	-1.80	0.117106	0.222432	-5.74
254787_at	putative protein hypothetical protein	---	AT4G12690	-1.27	-0.35	-1.80	0.117146	0.222489	-5.74
262169_at	hypothetical protein predicted by ge	---	AT1G74860	1.18	0.24	1.80	0.117239	0.222648	-5.74
248036_at	nucleolar protein-like	OLI2	AT5G55920	1.23	0.30	1.80	0.117295	0.222733	-5.74
246801_at	threonyl-tRNA synthetase ; suppor	---	AT5G26830	1.14	0.19	1.80	0.117305	0.222733	-5.74
267367_at	unknown protein ;supported by full-	---	AT2G44210	-1.23	-0.30	-1.80	0.117313	0.222733	-5.75
254517_at	putative protein conserved hypothe	---	AT4G20310	-1.15	-0.20	-1.80	0.117325	0.222738	-5.75
255805_at	zinc-finger - like protein zinc-finger	---	AT4G10240	-1.15	-0.21	-1.80	0.117371	0.222798	-5.75
253376_at	hypothetical protein Arabidopsis th	---	AT4G33290	-1.12	-0.16	-1.80	0.117377	0.222798	-5.75
261556_s_a	unknown protein	---	AT1G62600	-1.21	-0.27	-1.80	0.117391	0.222798	-5.75
249716_at	sterile apetala (emb|CAA11128.1)	SAP	AT5G35770	-1.16	-0.21	-1.80	0.117396	0.222798	-5.75
248034_at	serine threonine-specific protein kin	D6PK	AT5G55910	-1.17	-0.23	-1.80	0.11742	0.222825	-5.75
251069_at	(1-4)-beta-mannan endohydrolase-	---	AT5G01930	-1.38	-0.46	-1.79	0.11745	0.222862	-5.75
258477_at	hypothetical protein predicted by ge	NBS1	AT3G02680	1.13	0.18	1.79	0.117488	0.222902	-5.75
266175_at	NAM (no apical meristem)-like prote	ANAC035	AT2G02450	-1.15	-0.20	-1.79	0.117494	0.222902	-5.75
257155_at	hypothetical protein predicted by ge	---	AT3G27290	-1.19	-0.25	-1.79	0.1175	0.222902	-5.75
264468_at	unknown protein similar to daunoru	---	AT1G10310	1.20	0.26	1.79	0.117509	0.222902	-5.75
257584_at	hypothetical protein similar to putati	---	---	-1.24	-0.32	-1.79	0.117538	0.222937	-5.75
251994_at	protein kinase - like protein kinase,	KIPK	AT3G52890	1.32	0.40	1.79	0.117605	0.223046	-5.75
251102_at	putative transporter protein Na+/H+	CHX27	AT5G01690	-1.24	-0.31	-1.79	0.117696	0.2232	-5.75
246718_at	putative protein various predicted p	---	---	-1.17	-0.22	-1.79	0.117712	0.223211	-5.75
253563_at	putative protein predicted protein, S	---	AT4G31150	1.20	0.27	1.79	0.117737	0.22324	-5.75
255584_at	putative reverse transcriptase-like p	---	---	-1.14	-0.18	-1.79	0.117764	0.223274	-5.75
245750_at	histone H2A, putative similar to his	HTA10	AT1G51060	1.35	0.43	1.79	0.11783	0.223379	-5.75
262652_at	hypothetical protein One of a cluste	FUT9	AT1G14110	-1.14	-0.19	-1.79	0.117867	0.223431	-5.75
258400_at	unknown protein ; supported by cD	---	AT3G15470	-1.20	-0.26	-1.79	0.117906	0.223486	-5.75
262863_at	rhamnosyltransferase, putative sim	---	AT1G64910	-1.16	-0.21	-1.79	0.117976	0.2236	-5.75
265265_at	unknown protein	---	AT2G42900	-1.24	-0.31	-1.79	0.117993	0.223614	-5.75
260614_at	hypothetical protein contains Pfam	---	AT1G53390	1.13	0.17	1.79	0.118011	0.22363	-5.75
260259_at	unknown protein similar to unknowr	---	AT1G74300	-1.15	-0.21	-1.79	0.118034	0.223647	-5.75

264769_at	hypothetical protein predicted by ge	---	AT1G61350	1.36	0.45	1.79	0.11804	0.223647	-5.75
263529_at	ADP-ribosylation factor 3	ARF3	AT2G24765	-1.14	-0.19	-1.79	0.118051	0.22365	-5.75
256384_at	hypothetical protein	---	AT1G66660	1.17	0.23	1.79	0.118108	0.223739	-5.75
251467_at	putative protein putative proteins - A	---	AT3G59470	1.19	0.25	1.79	0.118154	0.223807	-5.75
251358_at	shaggy-like kinase beta	---	AT3G61160	1.39	0.48	1.79	0.118213	0.22389	-5.75
246855_at	putative protein various predicted p	---	AT5G26280	1.48	0.56	1.79	0.118217	0.22389	-5.75
249936_at	putative protein similar to unknown	---	AT5G22450	1.18	0.24	1.79	0.118313	0.224052	-5.75
262328_at	hypothetical protein similar to hypot	---	AT1G64100	-1.11	-0.16	-1.79	0.118397	0.224194	-5.75
252314_at	hypothetical protein	---	AT3G49400	1.16	0.22	1.79	0.118424	0.224226	-5.75
262728_at	receptor kinase (CLV1) identical to	CLV1	AT1G75820	-1.30	-0.38	-1.79	0.118435	0.224228	-5.75
260472_at	hypothetical protein predicted by ge	---	AT1G10990	2.29	1.20	1.79	0.118464	0.224256	-5.75
252187_at	putative protein UV inducible prote	---	AT3G50850	-1.18	-0.24	-1.79	0.118469	0.224256	-5.75
249476_at	germin - like protein probable germ	---	AT5G38910	-1.19	-0.25	-1.79	0.118507	0.224308	-5.75
255421_at	putative protein phosphatase regula	---	AT4G03260	1.17	0.23	1.79	0.118527	0.224328	-5.75
251275_at	putative protein anthranilate phosp	---	AT3G61720	-1.25	-0.32	-1.79	0.118578	0.224381	-5.76
252203_at	hypothetical protein	---	AT3G50320	-1.13	-0.18	-1.79	0.118583	0.224381	-5.76
255657_at	acidic ribosomal protein p1 similar t	---	AT4G00810	1.18	0.24	1.79	0.118585	0.224381	-5.76
266113_x_a	hypothetical protein predicted by ge	---	---	-1.18	-0.24	-1.79	0.118621	0.224432	-5.76
261597_at	hypothetical protein predicted by ge	PUB26	AT1G49780	-1.69	-0.76	-1.79	0.118653	0.224472	-5.76
251187_at	putative protein putative proteins - c	AtATG18a	AT3G62770	1.12	0.16	1.79	0.118662	0.224472	-5.76
257098_at	hypothetical protein	---	---	-1.14	-0.19	-1.79	0.118714	0.22455	-5.76
249095_at	myosin heavy chain MYA2 (pir||S51	MYA2	AT5G43900	-1.26	-0.34	-1.79	0.118723	0.22455	-5.76
256299_at	expansin (At-EXP1) identical to exp	ATEXPA1	AT1G69530	-1.87	-0.90	-1.79	0.118769	0.224604	-5.76
251354_at	putative protein hypothetical protei	---	AT3G61090	-1.13	-0.18	-1.79	0.118771	0.224604	-5.76
254196_at	putative protein	---	AT4G24030	-1.20	-0.27	-1.79	0.118783	0.224608	-5.76
249205_at	cycloartenol synthase	MRN1	AT5G42600	-1.28	-0.36	-1.79	0.118803	0.224627	-5.76
258948_at	putative sulfite oxidase similar to su	SOX	AT3G01910	1.13	0.18	1.79	0.118835	0.224669	-5.76
255610_at	putative phosphatidylinositol kinase	ATPIPK10	AT4G01190	-1.15	-0.20	-1.79	0.118856	0.22469	-5.76
263256_at	unknown protein similar to ESTs gb	ATCPISCA	AT1G10500	1.21	0.27	1.79	0.118938	0.224819	-5.76
250262_at	putative protein peptidyl-prolyl cis-t	---	AT5G13410	-1.29	-0.36	-1.79	0.118944	0.224819	-5.76
257449_at	hypothetical protein predicted by ge	---	AT2G31420	-1.16	-0.21	-1.79	0.118978	0.224864	-5.76
254604_at	cadmium-induced protein	---	AT4G19070	-1.17	-0.23	-1.79	0.119051	0.224983	-5.76
248408_at	ripening-related protein-like	---	AT5G51520	-1.13	-0.18	-1.79	0.119064	0.22499	-5.76
248645_at	unknown protein	GEX2	AT5G49150	-1.17	-0.23	-1.79	0.119094	0.225028	-5.76
253943_at	putative protein gene F19K23.12 o	---	AT4G27030	1.50	0.58	1.79	0.11913	0.225032	-5.76

253981_at	putative protein ;supported by full-le	---	AT4G26670	1.14	0.19	1.79	0.11914	0.225032	-5.76
267581_at	putative RING zinc finger protein	---	AT2G41980	-1.28	-0.35	-1.79	0.11914	0.225032	-5.76
248912_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G45670	-1.20	-0.26	-1.79	0.119142	0.225032	-5.76
255978_at	hypothetical protein	---	AT1G34010	-1.14	-0.18	-1.78	0.119146	0.225032	-5.76
245015_at	large subunit of riblose-1,5-bisphos	---	---	1.27	0.34	1.78	0.119188	0.225093	-5.76
245047_at	PSII 32 KDa protein	---	---	1.14	0.19	1.78	0.11923	0.225153	-5.76
257955_at	unknown protein ; supported by cD	---	AT3G21810	1.34	0.42	1.78	0.119266	0.225204	-5.76
256141_at	lysine and histidine specific transpo	---	AT1G48640	-1.12	-0.16	-1.78	0.119318	0.225283	-5.76
257573_at	putative SF16 protein {Helianthus a	iqd9	AT2G33990	-1.23	-0.30	-1.78	0.119357	0.225337	-5.76
267513_at	unknown protein ; supported by cD	---	AT2G45620	1.16	0.21	1.78	0.119402	0.225398	-5.76
267634_at	putative actin	---	AT2G42100	-1.13	-0.17	-1.78	0.119409	0.225398	-5.76
267493_at	unknown protein	OFP2	AT2G30400	-1.25	-0.32	-1.78	0.119433	0.225425	-5.76
250399_at	putative protein predicted proteins,	---	AT5G10750	-1.21	-0.27	-1.78	0.119469	0.225467	-5.76
250834_at	putative protein various predicted p	DME	AT5G04560	-1.21	-0.27	-1.78	0.119475	0.225467	-5.76
265219_at	unknown protein ; supported by ful	---	AT2G02050	1.19	0.25	1.78	0.119508	0.22551	-5.76
256123_at	hypothetical protein predicted by ge	GC2	AT1G18190	-1.12	-0.16	-1.78	0.119568	0.225606	-5.76
262614_at	putative pattern formation protein E	GN	AT1G13980	1.27	0.34	1.78	0.119579	0.225608	-5.76
262031_x_a	hypothetical protein similar to putati	---	---	-1.15	-0.20	-1.78	0.119603	0.225635	-5.76
265875_at	unknown protein ; supported by cD	---	AT2G01690	-1.19	-0.26	-1.78	0.119635	0.225646	-5.76
251401_at	stellacyanin (uclacyanin 3) - like pr	---	AT3G60270	-1.20	-0.26	-1.78	0.119643	0.225646	-5.76
263124_at	beta-Amyrin Synthase, putative sin	---	AT1G78480	1.21	0.28	1.78	0.119643	0.225646	-5.76
246234_at	putative protein	---	AT4G37280	-1.18	-0.23	-1.78	0.119649	0.225646	-5.76
253600_at	SERINE CARBOXYPEPTIDASE II	scpl29	AT4G30810	-1.15	-0.20	-1.78	0.119707	0.225736	-5.76
254521_at	putative protein similar to unknown	---	AT5G44820	1.16	0.21	1.78	0.119729	0.225759	-5.76
248541_at	protein kinase ATN1-like protein	---	AT5G50180	-1.22	-0.28	-1.78	0.11983	0.225931	-5.77
251325_s_a	Lhca2 protein ;supported by full-ler	LHCA2	AT3G61470	-1.11	-0.16	-1.78	0.119861	0.225941	-5.77
254148_at	hsp 70-like protein heat shock 70 p	cpHsc70-1	AT4G24280	1.15	0.21	1.78	0.119864	0.225941	-5.77
254501_at	hypothetical protein	PTAC14	AT4G20130	1.28	0.35	1.78	0.119865	0.225941	-5.77
266611_at	putative auxin-regulated protein	GH3.1	AT2G14960	-1.15	-0.20	-1.78	0.119894	0.225978	-5.77
245996_at	putative protein predicted non-LTR	---	---	-1.14	-0.19	-1.78	0.119922	0.226011	-5.77
266463_at	hypothetical protein predicted by ge	---	AT2G47840	-1.17	-0.23	-1.78	0.119969	0.226064	-5.77
250057_at	putative protein ; supported by full-	---	AT5G17840	-1.13	-0.18	-1.78	0.11997	0.226064	-5.77
254248_at	serine/threonine kinase serine/thre	---	AT4G23270	1.30	0.38	1.78	0.120031	0.22616	-5.77
262917_at	hypothetical protein contains simila	---	AT1G64800	-1.19	-0.25	-1.78	0.120072	0.226203	-5.77
252439_at	pectinesterase-like protein pectines	---	AT3G47400	-1.13	-0.17	-1.78	0.120073	0.226203	-5.77

251738_at	PROBABLE EUKARYOTIC TRANS	EIF3C	AT3G56150	1.14	0.19	1.78	0.1201	0.226235	-5.77
252676_at	putative protein	---	AT3G44280	1.12	0.16	1.78	0.120146	0.226304	-5.77
251989_at	RNA helicase -like protein RNA he	LOS4	AT3G53110	1.17	0.22	1.78	0.120164	0.226319	-5.77
249056_at	putative protein similar to unknown	---	AT5G44470	-1.14	-0.19	-1.78	0.120203	0.226372	-5.77
254561_at	putative protein ; supported by cDN	---	AT4G19160	-1.26	-0.33	-1.78	0.120255	0.226439	-5.77
266687_at	putative arginine N-methyltransfera	PRMT1A	AT2G19670	1.30	0.38	1.78	0.120267	0.226439	-5.77
255524_at	hypothetical protein similar to pectir	ATPMEPCI	AT4G02330	-1.95	-0.96	-1.78	0.120277	0.226439	-5.77
262302_at	hypothetical protein predicted by ge	---	AT1G70910	-1.17	-0.22	-1.78	0.120278	0.226439	-5.77
255967_at	protein phosphatase type 2C, puta	---	AT1G22280	-1.19	-0.25	-1.78	0.120309	0.22648	-5.77
247594_at	putative protein farnesylated protei	---	AT5G60800	-1.20	-0.27	-1.78	0.120334	0.226508	-5.77
263990_at	putative phosphoprotein phosphata	PP5.2	AT2G42810	1.15	0.20	1.78	0.120384	0.226572	-5.77
247947_at	auxin transport protein EIR1 (gb|AA	EIR1	AT5G57090	-1.19	-0.25	-1.78	0.120388	0.226572	-5.77
257025_at	hypothetical protein predicted by ge	ATG2	AT3G19190	-1.22	-0.29	-1.78	0.12051	0.226783	-5.77
253799_at	putative DNA-binding protein AP2 (	---	AT4G28140	-2.32	-1.21	-1.78	0.120526	0.226786	-5.77
248180_at	unknown protein ;supported by full-	AGD5	AT5G54310	-1.12	-0.17	-1.78	0.120532	0.226786	-5.77
252041_at	DNA-directed RNA polymerase II 1	NRPB11	AT3G52090	1.15	0.21	1.78	0.120558	0.226816	-5.77
252558_at	actin depolymerising like protein A(	---	AT3G45990	-1.14	-0.19	-1.78	0.120571	0.226823	-5.77
251827_at	chalcone isomerase ;supported by	TT5	AT3G55120	1.22	0.29	1.78	0.120606	0.22687	-5.77
260450_at	hypothetical protein predicted by ge	---	AT1G72390	-1.23	-0.30	-1.78	0.120628	0.226892	-5.77
262577_at	unknown protein ESTs gb|F20110 a	---	AT1G15290	1.21	0.28	1.78	0.120653	0.22691	-5.77
256363_at	unknown protein ; supported by cDI	---	AT1G66510	-1.31	-0.39	-1.78	0.120666	0.22691	-5.77
263771_at	putative Athila retroelement ORF1 p	---	---	-1.12	-0.16	-1.78	0.120667	0.22691	-5.77
267586_at	hypothetical protein predicted by ge	---	AT2G41950	1.21	0.28	1.78	0.120691	0.226937	-5.77
263188_at	hypothetical protein predicted by ge	---	AT1G36095	-1.16	-0.21	-1.78	0.120744	0.227018	-5.77
262334_at	hypothetical protein similar to putati	---	AT1G64010	-1.16	-0.21	-1.78	0.120758	0.227024	-5.77
254944_at	putative protein proliferation potent	---	AT4G10930	1.11	0.15	1.78	0.120774	0.227037	-5.77
264647_at	putative respiratory burst oxidase p	ATRBOHB	AT1G09090	-1.17	-0.23	-1.78	0.120804	0.227074	-5.77
253265_at	putative protein RING-finger protei	---	AT4G34040	1.13	0.17	1.78	0.120849	0.227139	-5.77
258645_s_a	exopolygalacturonase identical to e	---	AT3G07850	-1.16	-0.21	-1.77	0.120905	0.227227	-5.77
264294_at	hypothetical protein similar to heat s	---	AT1G78750	1.15	0.20	1.77	0.120987	0.227361	-5.77
254320_at	putative protein various predicted p	---	AT4G22580	-1.13	-0.18	-1.77	0.121002	0.227371	-5.77
264962_at	auxin transport protein EIR1, putat	PIN6	AT1G77110	-1.21	-0.28	-1.77	0.121092	0.227515	-5.78
251728_at	cysteine-tRNA ligase-like protein se	---	AT3G56300	-1.15	-0.20	-1.77	0.121099	0.227515	-5.78
246243_at	trichohyalin like protein	---	AT4G36520	-1.13	-0.17	-1.77	0.12112	0.227537	-5.78
266149_x_a	En/Spm-like transposon protein rela	---	---	-1.15	-0.20	-1.77	0.121145	0.227565	-5.78

253003_s_a	putative protein tapetum specific pr	---	AT4G38300	1.17	0.23	1.77	0.121222	0.227691	-5.78
256192_at	diadenosine 5,5-P1,P4-tetraphospl	ATNUDX25	AT1G30110	1.17	0.22	1.77	0.121285	0.227775	-5.78
265906_at	hypothetical protein predicted by ge	---	AT2G25565	-1.16	-0.21	-1.77	0.121287	0.227775	-5.78
255299_at	putative adenosine deaminase simi	---	AT4G04880	1.16	0.22	1.77	0.121325	0.227828	-5.78
262304_at	major latex protein (MLP149), puta	MLP43	AT1G70890	-2.06	-1.04	-1.77	0.121379	0.227911	-5.78
246847_at	putative protein ferroportin1, Mus r	ATIREG3	AT5G26820	-1.28	-0.36	-1.77	0.121427	0.227978	-5.78
265926_at	RUB1-conjugating enzyme, putativ	---	AT2G18600	1.24	0.31	1.77	0.121435	0.227978	-5.78
261059_at	transcription factor TINY, putative s	---	AT1G01250	-1.22	-0.28	-1.77	0.121446	0.227979	-5.78
262697_at	beta-glucosidase, putative similar t	ATA27	AT1G75940	-1.13	-0.18	-1.77	0.121476	0.228017	-5.78
264781_at	putative plastid RNA polymerase si	SIG2	AT1G08540	-1.21	-0.28	-1.77	0.121502	0.228048	-5.78
250766_at	putative protein similar to unknown	---	AT5G05550	-1.18	-0.23	-1.77	0.121518	0.228059	-5.78
258377_at	hypothetical protein contains simila	CNGC19	AT3G17690	-1.17	-0.22	-1.77	0.121538	0.228078	-5.78
261152_at	hypothetical protein predicted by ge	---	AT1G04930	-1.24	-0.31	-1.77	0.121563	0.228105	-5.78
260648_at	unknown protein	---	AT1G08050	1.28	0.36	1.77	0.121616	0.228187	-5.78
263003_at	protein phosphatase 2A 72 kDa reg	---	AT1G54450	-1.12	-0.17	-1.77	0.121674	0.228277	-5.78
257024_at	CDPK-related kinase identical to GI	---	AT3G19100	1.23	0.30	1.77	0.121694	0.228294	-5.78
255463_at	putative polyprotein of LTR transpo	---	---	-1.16	-0.21	-1.77	0.121795	0.228466	-5.78
267113_at	hypothetical protein predicted by ge	---	AT2G14850	1.13	0.17	1.77	0.121834	0.228521	-5.78
262501_at	putative replication factor Similar to	emb1968	AT1G21690	1.17	0.23	1.77	0.121937	0.228695	-5.78
250115_at	salt-inducible protein-like	---	AT5G16420	1.24	0.30	1.77	0.121978	0.228741	-5.78
262479_at	leucine-rich repeat transmembrane	SUB	AT1G11130	-1.13	-0.17	-1.77	0.121982	0.228741	-5.78
251960_at	GTPase AtRAB8 ;supported by full	HEMB1	AT1G69740	-1.15	-0.20	-1.77	0.122077	0.2289	-5.78
246472_at	putative protein predicted protein, A	---	AT5G17130	-1.12	-0.16	-1.77	0.122091	0.228908	-5.78
251380_at	putative protein	---	AT3G60700	-1.14	-0.19	-1.77	0.122112	0.228929	-5.78
247785_at	subtilisin-like serine protease conta	---	AT5G58820	-1.12	-0.16	-1.77	0.122129	0.228941	-5.78
257361_at	putative Ta11-like non-LTR retroele	---	---	-1.18	-0.24	-1.77	0.122209	0.229067	-5.78
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281	---	---	1.15	0.20	1.77	0.122216	0.229067	-5.78
260790_at	hypothetical protein predicted by ge	---	AT1G06240	1.25	0.33	1.77	0.122228	0.229071	-5.78
263681_at	hypothetical protein predicted by ge	ORC6	AT1G26840	1.22	0.29	1.77	0.122276	0.229141	-5.78
257969_at	hypothetical protein predicted by ge	---	AT3G27520	1.28	0.35	1.77	0.122345	0.229251	-5.79
266352_at	unknown protein	---	AT2G01610	-1.52	-0.61	-1.77	0.122433	0.229391	-5.79
260046_at	Expressed protein ; supported by cl	---	AT1G73805	-1.80	-0.85	-1.77	0.122439	0.229391	-5.79
249032_at	putative protein contains similarity t	---	AT5G44910	1.81	0.85	1.77	0.122449	0.229391	-5.79
248731_at	phosphoribosylanthranilate transfer	---	AT5G48060	-1.17	-0.23	-1.77	0.122513	0.229491	-5.79
253830_at	Expressed protein ; supported by fu	---	AT4G27652	1.85	0.89	1.77	0.122537	0.229518	-5.79

264203_at	putative 40S ribosomal protein S18	PFL	AT1G22780	1.36	0.44	1.77	0.122554	0.229531	-5.79
249673_at	cytochrome P450-like	CYP79A4P	AT5G35920	-1.11	-0.15	-1.77	0.122605	0.229607	-5.79
256241_at	nascent polypeptide associated co	---	AT3G12390	1.30	0.37	1.76	0.122648	0.229652	-5.79
247724_at	putative protein predicted protein, A	MBD6	AT5G59380	-1.14	-0.19	-1.76	0.122649	0.229652	-5.79
251666_at	CYSTATHIONINE BETA-LYASE P	CBL	AT3G57050	1.20	0.27	1.76	0.122691	0.229712	-5.79
252205_at	hypothetical protein various predict	---	AT3G50350	-1.20	-0.26	-1.76	0.122741	0.22976	-5.79
256663_at	unknown protein ;supported by full-	---	AT3G12050	-1.25	-0.33	-1.76	0.122745	0.22976	-5.79
262789_at	putative auxin-induced protein stron	---	AT1G10810	-1.13	-0.18	-1.76	0.122747	0.22976	-5.79
259335_s_a	unknown protein similar to unknown	---	AT3G03930	1.20	0.26	1.76	0.122789	0.229821	-5.79
264213_at	hypothetical protein contains simila	ATPP2-A5	AT1G65390	-2.06	-1.04	-1.76	0.12283	0.229877	-5.79
262130_at	hypothetical protein predicted by ge	---	AT1G02890	1.17	0.22	1.76	0.122894	0.229961	-5.79
257115_at	kinesin-like protein contains Pfam p	---	AT3G20150	-1.15	-0.21	-1.76	0.122895	0.229961	-5.79
262196_at	ubiquitin-fusion protein, putative sir	MUB5	AT1G77870	-1.33	-0.42	-1.76	0.122924	0.229998	-5.79
263926_at	hypothetical protein predicted by ge	ATEME1A	AT2G21800	-1.17	-0.23	-1.76	0.122963	0.230039	-5.79
259418_at	unknown protein ; supported by cDI	GPAT2	AT1G02390	-1.20	-0.27	-1.76	0.122966	0.230039	-5.79
258567_at	apyrase (Atapy1) identical to apyras	ATAPY1	AT3G04080	-1.20	-0.26	-1.76	0.122984	0.230044	-5.79
262587_at	unknown protein Contains PF|0056	---	AT1G15490	-1.29	-0.36	-1.76	0.12299	0.230044	-5.79
246292_at	putative protein hnRNP A/B related	UBA2A	AT3G56860	-1.18	-0.24	-1.76	0.123139	0.230304	-5.79
257296_at	hypothetical protein predicted by ge	---	AT3G28020	-1.15	-0.21	-1.76	0.123185	0.230371	-5.79
263675_x_a	En/Spm-like transposon protein rela	---	---	-1.22	-0.29	-1.76	0.123216	0.230401	-5.79
248440_at	acid phosphatase	---	AT5G51260	-1.18	-0.24	-1.76	0.12322	0.230401	-5.79
249915_at	putative protein similar to unknown	---	AT5G22870	-1.14	-0.18	-1.76	0.123252	0.230441	-5.79
253924_at	putative protein other hypothetical	COBL11	AT4G27110	-1.17	-0.23	-1.76	0.123269	0.230454	-5.79
266931_at	putative non-LTR retroelement reve	---	---	-1.15	-0.20	-1.76	0.123288	0.23047	-5.79
249511_at	putative protein contains similarity t	---	AT5G38500	-1.14	-0.18	-1.76	0.123335	0.230539	-5.79
253877_at	Expressed protein ; supported by cl	---	AT4G27435	-1.34	-0.42	-1.76	0.123365	0.230561	-5.79
264575_at	putative chloroplast 50S ribosomal	emb2394	AT1G05190	1.15	0.20	1.76	0.123372	0.230561	-5.79
245555_at	HSR201 like protein	---	AT4G15390	-1.14	-0.20	-1.76	0.123377	0.230561	-5.79
266050_at	putative SNF2/SWI2 family transcri	---	AT2G40770	-1.13	-0.18	-1.76	0.123442	0.230663	-5.79
252099_at	putative protein senescence-assoc	---	AT3G51250	1.18	0.24	1.76	0.123454	0.230667	-5.79
251857_at	RNA binding protein - like SEB4 pr	---	AT3G54770	-1.15	-0.20	-1.76	0.12347	0.230678	-5.79
261929_at	hypothetical protein similar to axi 1-	---	AT1G22460	-1.17	-0.23	-1.76	0.123491	0.230698	-5.79
264007_at	putative proline-rich protein	ATPRP2	AT2G21140	-2.30	-1.20	-1.76	0.123508	0.230712	-5.79
259308_at	putative nodulin similar to nodulin G	---	AT3G05180	1.28	0.36	1.76	0.123589	0.230818	-5.79
258893_at	putative disease resistance protein	AtRLP33	AT3G05660	-1.65	-0.72	-1.76	0.123593	0.230818	-5.79

250255_at	sigma-like factor (gb|AAC97954.1)	SIG4	AT5G13730	-1.33	-0.41	-1.76	0.123595	0.230818	-5.79
265879_at	hypothetical protein predicted by ge	---	AT2G42450	1.13	0.18	1.76	0.123606	0.230819	-5.80
254264_at	putative protein various predicted p	---	AT4G23510	-1.14	-0.19	-1.76	0.123627	0.230839	-5.80
257678_at	RNA helicase, putative contains Pf	RTL2	AT3G20420	1.18	0.24	1.76	0.123648	0.230852	-5.80
257261_s_a	hypothetical protein contains Pfam	---	AT3G21920	-1.12	-0.16	-1.76	0.123662	0.230852	-5.80
256467_at	copia-type polyprotein, putative sim	---	---	-1.14	-0.19	-1.76	0.123664	0.230852	-5.80
249340_at	putative protein contains similarity t	---	AT5G41140	-1.18	-0.24	-1.76	0.123754	0.231	-5.80
266293_at	putative tropinone reductase ;supp	---	AT2G29360	-1.14	-0.19	-1.76	0.123783	0.23102	-5.80
263546_at	putative dihydrofolate reductase-thy	---	AT2G21550	1.19	0.25	1.76	0.123784	0.23102	-5.80
256448_s_a	unknown protein	MED21	AT4G04780	-1.14	-0.19	-1.76	0.1238	0.23103	-5.80
258331_at	putative coatomer complex subunit	---	AT3G15980	-1.18	-0.23	-1.76	0.123842	0.23109	-5.80
248048_at	nicotianamine synthase	NAS2	AT5G56080	-1.15	-0.21	-1.76	0.123941	0.231255	-5.80
247078_at	unknown protein ; supported by cD	---	AT5G66000	-1.17	-0.22	-1.76	0.123973	0.231296	-5.80
257103_at	hypothetical protein contains Pfam	---	AT3G25060	1.17	0.22	1.76	0.123991	0.23131	-5.80
245315_at	proteasome chain protein ; supporte	PBD2	AT4G14800	1.13	0.18	1.76	0.124086	0.231469	-5.80
254274_at	putative DNA binding protein DNA-	---	AT4G22770	1.22	0.29	1.76	0.124223	0.231705	-5.80
259501_at	unknown protein ; supported by cDI	TPL	AT1G15750	1.18	0.24	1.76	0.124305	0.23184	-5.80
255937_at	transcriptional activator CBF1, puta	DDF1	AT1G12610	-1.34	-0.43	-1.76	0.124338	0.231882	-5.80
258205_at	unknown protein	---	AT3G13965	-1.14	-0.19	-1.76	0.124398	0.23197	-5.80
257082_at	hypothetical protein	COBL10	AT3G20580	-1.14	-0.19	-1.75	0.124414	0.23197	-5.80
262997_at	disease resistance protein, putative	RPP27	AT1G54470	-1.13	-0.17	-1.75	0.124416	0.23197	-5.80
267271_at	hypothetical protein predicted by ge	ATHB21	AT2G02540	-1.14	-0.19	-1.75	0.124492	0.232094	-5.80
257003_at	unknown protein ;supported by full-	FLU	AT3G14110	1.22	0.29	1.75	0.124526	0.232138	-5.80
265107_s_a	similar to glucose 1-dehydrogenase	---	AT1G62610	1.14	0.19	1.75	0.124568	0.232197	-5.80
264534_at	hypothetical protein predicted by ge	---	AT1G55700	-1.21	-0.28	-1.75	0.124595	0.232228	-5.80
265227_s_a	hypothetical protein	---	AT2G07695	-1.18	-0.24	-1.75	0.124632	0.232278	-5.80
254008_at	hypothetical protein various predict	---	AT4G26380	-1.15	-0.20	-1.75	0.124669	0.232303	-5.80
251362_at	DEAD box RNA helicase RH12	---	AT3G61240	1.15	0.21	1.75	0.124674	0.232303	-5.80
265469_at	unknown protein predicted by gens	---	AT2G37160	-1.12	-0.16	-1.75	0.124676	0.232303	-5.80
254907_at	putative disease resistance respon	---	AT4G11190	-1.15	-0.20	-1.75	0.124687	0.232306	-5.80
263423_at	hypothetical protein predicted by ge	---	AT2G31700	-1.14	-0.19	-1.75	0.124726	0.232359	-5.80
264933_at	hypothetical protein predicted by ge	---	AT1G61160	-1.17	-0.22	-1.75	0.124777	0.232435	-5.80
245992_at	receptor protein kinase - like recep	---	AT5G20690	-1.12	-0.16	-1.75	0.124794	0.232444	-5.80
254334_at	predicted protein	---	AT4G22760	1.17	0.23	1.75	0.124802	0.232444	-5.80
258659_at	B' regulatory subunit of PP2A (AtB	ATB' BETA	AT3G09880	1.15	0.21	1.75	0.124854	0.232521	-5.80

255330_s_a	putative polyprotein	---	---	-1.12	-0.16	-1.75	0.124869	0.23253	-5.80
245293_at	HSP like protein ; supported by cDN	---	AT4G16660	1.54	0.62	1.75	0.124892	0.232555	-5.80
246589_at	glucosyltransferase -like protein glu	---	AT5G14860	-1.15	-0.20	-1.75	0.12491	0.232568	-5.81
259265_at	hypothetical protein predicted by ge	---	AT3G01250	-1.13	-0.17	-1.75	0.125042	0.232796	-5.81
255457_at	putative photosystem I reaction cer	PSAD-1	AT4G02770	-1.12	-0.16	-1.75	0.125063	0.2328	-5.81
251311_at	FUSCA PROTEIN FUS6 ; supporte	FUS6	AT3G61140	1.14	0.19	1.75	0.125065	0.2328	-5.81
248304_at	polypyrimidine tract-binding RNA tra	PTB2	AT5G53180	1.12	0.17	1.75	0.125086	0.232819	-5.81
257106_at	unknown protein	---	AT3G29060	-1.13	-0.18	-1.75	0.125097	0.232822	-5.81
255927_at	transcriptional activator CBF1, puta	---	AT1G12630	-1.28	-0.36	-1.75	0.12511	0.232827	-5.81
251897_at	RING finger - like protein DNA-bind	---	AT3G54360	1.19	0.25	1.75	0.125134	0.232852	-5.81
254154_at	hypothetical protein	---	AT4G24460	-1.20	-0.26	-1.75	0.125157	0.232876	-5.81
261509_at	hypothetical protein predicted by ge	---	AT1G71740	-1.22	-0.29	-1.75	0.125171	0.232883	-5.81
248272_at	Expressed protein ; supported by fu	---	AT5G53480	-1.20	-0.27	-1.75	0.125304	0.233112	-5.81
248728_at	cytochrome P450-like protein	CYP708A2	AT5G48000	-1.16	-0.21	-1.75	0.125381	0.233223	-5.81
244904_at	hypothetical protein	---	---	-1.26	-0.33	-1.75	0.125384	0.233223	-5.81
261798_at	hypothetical protein similar to hypot	CPSF30	AT1G30460	1.17	0.22	1.75	0.125399	0.233231	-5.81
264096_at	Expressed protein ; supported by fu	---	AT1G78995	1.33	0.42	1.75	0.125413	0.233238	-5.81
266232_at	putative phloem-specific lectin	AtPP2-B6	AT2G02310	-1.12	-0.16	-1.75	0.125473	0.23333	-5.81
252040_at	putative protein hypothetical protei	---	AT3G52060	1.37	0.45	1.75	0.125493	0.23333	-5.81
261436_at	protein kinase, putative (fragment)	---	AT1G07870	-1.23	-0.29	-1.75	0.125495	0.23333	-5.81
260494_at	putative receptor-like protein kinase	---	AT2G41820	-1.19	-0.25	-1.75	0.125503	0.23333	-5.81
257640_at	hypothetical protein	---	AT3G25750	-1.19	-0.25	-1.75	0.125553	0.233403	-5.81
249953_at	FAR1 - like protein far-red impaired	FRS12	AT5G18960	1.17	0.23	1.75	0.125573	0.233414	-5.81
255079_s_a	14-3-3 protein GF14chi (grf1) ident	GF14 PHI	AT1G35160	1.13	0.17	1.75	0.125579	0.233414	-5.81
246567_at	alpha-mannosidase -like protein m	GMII	AT5G14950	1.12	0.17	1.75	0.125698	0.233617	-5.81
249637_at	hypothetical protein	---	AT5G36900	-1.14	-0.19	-1.75	0.125748	0.23369	-5.81
254256_at	serine/threonine kinase -like protei	CRK10	AT4G23180	1.25	0.32	1.75	0.125907	0.233966	-5.81
247777_at	putative protein MNUDC protein, H	---	AT5G58740	1.13	0.17	1.75	0.125991	0.234103	-5.81
249391_at	putative protein predicted proteins,	---	AT5G40140	1.22	0.28	1.74	0.126301	0.234661	-5.82
248494_at	putative protein contains similarity t	AtHSD6	AT5G50770	-1.16	-0.21	-1.74	0.126411	0.234845	-5.82
248672_at	disease resistance protein	---	AT5G48770	-1.17	-0.22	-1.74	0.126485	0.234965	-5.82
248105_at	cell division protein FtsZ chloroplas	FTSZ1-1	AT5G55280	-1.21	-0.27	-1.74	0.126501	0.234974	-5.82
253339_at	metal-transporting P-type ATPase	PAA1	AT4G33520	1.24	0.31	1.74	0.12652	0.234991	-5.82
260716_at	peroxiredoxin identical to SP:O040(	ATPER1	AT1G48130	-1.19	-0.25	-1.74	0.126544	0.235015	-5.82
249508_at	unknown protein	---	AT5G38380	1.14	0.19	1.74	0.126617	0.235133	-5.82

259483_at	hypothetical protein predicted by ge	---	AT1G43980	1.14	0.19	1.74	0.126705	0.235276	-5.82
246039_at	putative protein serine-arginine-rich	---	AT5G19480	1.14	0.18	1.74	0.126723	0.235291	-5.82
246669_at	galactinol synthase, putative	---	AT5G30500	-1.20	-0.26	-1.74	0.126734	0.235292	-5.82
254523_at	putative protein hypothetical protei	FRS1	AT4G19990	-1.23	-0.30	-1.74	0.126759	0.23532	-5.82
247373_at	unknown protein ;supported by full-	---	AT5G63150	1.18	0.24	1.74	0.126782	0.23533	-5.82
256265_at	serine carboxypeptidase, putative (	scpl16	---	-1.19	-0.25	-1.74	0.126785	0.23533	-5.82
249952_at	putative protein predicted proteins,	---	AT5G18950	1.17	0.22	1.74	0.126845	0.235422	-5.82
265465_at	hypothetical protein predicted by ge	---	AT2G37070	-1.40	-0.48	-1.74	0.126904	0.235512	-5.82
259016_at	unknown protein HMM hit: 2Fe-2S i	---	AT3G07480	-1.20	-0.26	-1.74	0.126917	0.235516	-5.82
255761_at	hypothetical protein predicted by ge	---	AT1G16770	-1.15	-0.20	-1.74	0.126968	0.235592	-5.82
246177_at	putative protein predicted proteins -	---	AT5G28420	-1.12	-0.17	-1.74	0.126981	0.235598	-5.82
248592_at	unknown protein ;supported by full-	---	AT5G49280	-1.42	-0.51	-1.74	0.126991	0.235598	-5.82
267541_at	hypothetical protein predicted by ge	---	AT2G32750	-1.18	-0.24	-1.74	0.127082	0.235747	-5.82
255638_at	predicted protein of unknown functi	---	AT4G00740	-1.20	-0.27	-1.74	0.127118	0.235795	-5.82
247559_at	histone deacetylase - like GR AF-1	HDA18	AT5G61070	-1.13	-0.17	-1.74	0.127198	0.235923	-5.82
244911_at	hypothetical protein	---	---	1.16	0.21	1.74	0.12728	0.236039	-5.82
250632_at	putative protein cyclin 2 - Trypanos	CYCP4;3	AT5G07450	-1.18	-0.23	-1.74	0.127281	0.236039	-5.82
252360_at	putative protein predicted protein, A	---	AT3G48480	1.18	0.24	1.74	0.127308	0.23607	-5.82
253271_s_a	SKP1/ASK1 (At11), putative simila	ASK12	AT4G34210	1.19	0.25	1.74	0.127331	0.236093	-5.82
249011_at	putative protein strong similarity to	---	AT5G44670	-1.38	-0.47	-1.74	0.127347	0.236104	-5.82
258604_at	putative N-acetlytransferase contair	---	AT3G02980	1.18	0.24	1.74	0.12739	0.236165	-5.82
252356_at	putative protein various predicted p	---	---	-1.20	-0.27	-1.74	0.127421	0.236203	-5.82
247055_at	putative protein similar to unknown	---	AT5G66740	-1.18	-0.24	-1.74	0.127528	0.236382	-5.82
251608_at	putative protein hypothetical protei	UVI4-LIKE	AT3G57860	-1.18	-0.24	-1.74	0.12758	0.236458	-5.83
264352_at	unknown protein Strong similarity to	---	AT1G03270	-1.25	-0.32	-1.74	0.127601	0.236473	-5.83
253604_at	hypothetical protein	---	AT4G30970	-1.13	-0.17	-1.74	0.127608	0.236473	-5.83
246438_at	putative protein non-phototropic hy	---	AT5G17580	1.12	0.16	1.74	0.127622	0.236478	-5.83
250755_at	DnaJ-like protein ; supported by cD	---	AT5G05750	-1.18	-0.24	-1.74	0.127674	0.236556	-5.83
256691_at	hypothetical protein predicted by ge	---	---	-1.12	-0.16	-1.74	0.127741	0.236661	-5.83
264478_at	hypothetical protein predicted by ge	---	AT1G77270	-1.13	-0.18	-1.74	0.127762	0.236664	-5.83
267636_at	hypothetical protein predicted by ge	---	AT2G42110	-1.13	-0.18	-1.74	0.127773	0.236664	-5.83
249758_at	putative protein similar to unknown	---	AT5G24350	1.20	0.26	1.74	0.127779	0.236664	-5.83
260802_at	exopolygalacturonase, putative sim	---	AT1G78400	-1.11	-0.16	-1.74	0.127784	0.236664	-5.83
257784_at	geranylgeranylated protein, putativ	MUB4	AT3G26980	-1.53	-0.62	-1.74	0.1278	0.236675	-5.83
258439_at	lipoamide dehydrogenase precurso	mtLPD2	AT3G17240	1.24	0.31	1.74	0.127861	0.236741	-5.83

251219_at	putative protein several hypothetica	---	AT3G62390	-1.31	-0.39	-1.74	0.127874	0.236741	-5.83
255915_at	putative protein	---	AT5G28620	-1.14	-0.19	-1.74	0.127876	0.236741	-5.83
248269_at	putative protein contains similarity t	ACBP1	AT5G53470	1.19	0.25	1.74	0.127877	0.236741	-5.83
251689_at	putative protein motif in hypothetica	---	AT3G56500	1.63	0.70	1.74	0.127894	0.236752	-5.83
260275_at	hypothetical protein predicted by gr	---	AT1G80610	-1.15	-0.20	-1.74	0.127924	0.236788	-5.83
247862_at	similar to unknown protein (sp|P727	---	AT5G58250	1.15	0.20	1.74	0.128032	0.236944	-5.83
252854_at	ubiquitin-specific protease 27 (UBF	UBP27	AT4G39370	1.12	0.17	1.74	0.128034	0.236944	-5.83
254674_at	EREBP - like protein EREBP-1 (Et	---	AT4G18450	-1.12	-0.16	-1.74	0.128039	0.236944	-5.83
255956_at	Expressed protein ; supported by fu	DD46	AT1G22015	-1.16	-0.22	-1.73	0.128054	0.236953	-5.83
250277_at	putative protein DRT100 protein pr	---	AT5G12940	-2.07	-1.05	-1.73	0.128076	0.236972	-5.83
246092_at	glutaredoxin ;supported by full-leng	---	AT5G20500	-1.16	-0.22	-1.73	0.128085	0.236972	-5.83
257877_at	hypothetical protein	---	AT3G17140	-1.15	-0.20	-1.73	0.128108	0.236994	-5.83
267384_at	unknown protein highly similar to G	---	AT2G44370	1.71	0.77	1.73	0.128132	0.237019	-5.83
247228_at	trehalose-6-phosphate phosphatase	---	AT5G65140	-1.56	-0.65	-1.73	0.128213	0.23715	-5.83
260379_at	putative glucosyltransferase similar	UGT89B1	AT1G73880	1.21	0.27	1.73	0.128358	0.2374	-5.83
257039_at	tRNA isopentenyl transferase, puta	ATIPT8	AT3G19160	-1.16	-0.22	-1.73	0.128409	0.237474	-5.83
263080_at	hypothetical protein predicted by ge	---	---	-1.17	-0.23	-1.73	0.128438	0.237508	-5.83
253809_at	putative (1-4)-beta-mannan endohy	---	AT4G28320	-1.21	-0.27	-1.73	0.128466	0.237542	-5.83
250434_at	histone H3 - like protein histone H3	---	AT5G10390	-1.83	-0.87	-1.73	0.128481	0.23755	-5.83
267391_at	putative beta-glucosidase	BGLU17	AT2G44480	1.23	0.30	1.73	0.12857	0.237696	-5.83
256606_at	hypothetical protein	---	AT3G32960	-1.14	-0.19	-1.73	0.128664	0.237841	-5.83
261227_at	proteasome regulatory subunit S3,	EMB2719	AT1G20200	1.13	0.18	1.73	0.128678	0.237841	-5.83
262472_at	hypothetical protein similar to putati	---	AT1G50160	-1.14	-0.19	-1.73	0.12868	0.237841	-5.83
247722_at	GTP-binding protein rab11 - like G	ATRABA2D	AT5G59150	-1.15	-0.20	-1.73	0.128727	0.237897	-5.83
265551_at	putative replication protein A1	---	---	-1.13	-0.18	-1.73	0.128737	0.237897	-5.83
261471_at	hypothetical protein contains simila	---	AT1G14460	-1.26	-0.33	-1.73	0.128742	0.237897	-5.83
252678_s_a	nitrilase 2 ;supported by full-length	NIT2	AT3G44300	1.13	0.18	1.73	0.128772	0.237921	-5.83
257445_x_a	hypothetical protein predicted by ge	---	---	-1.13	-0.18	-1.73	0.128775	0.237921	-5.83
259097_at	unknown protein similar to GB:AAD	---	AT3G04830	1.13	0.18	1.73	0.128887	0.238108	-5.83
245847_at	MYB DNA-binding - like protein my	MYB64	AT5G11050	-1.18	-0.24	-1.73	0.128912	0.238134	-5.84
253760_at	putative protein (fragment) predicte	AT4G2881	---	-1.19	-0.25	-1.73	0.128929	0.238146	-5.84
251735_at	putative protein ferritin 2 precursor	ATFER3	AT3G56090	1.39	0.47	1.73	0.128949	0.238165	-5.84
250639_at	oleosin-like protein oleosin - Brassi	GRP20	AT5G07560	-1.17	-0.23	-1.73	0.129027	0.238289	-5.84
261063_at	transcription factor scarecrow-like	---	AT1G07520	1.65	0.72	1.73	0.129037	0.238289	-5.84
265797_at	Expressed protein ; supported by fu	---	AT2G35710	-1.77	-0.82	-1.73	0.129129	0.238429	-5.84

265587_at	putative pathogenesis-related prote	---	AT2G19980	-1.15	-0.20	-1.73	0.129134	0.238429	-5.84
252519_at	hypothetical protein	---	AT3G46360	-1.15	-0.20	-1.73	0.129178	0.238483	-5.84
252405_at	putative protein RNA helicase HEL	---	AT3G48120	1.18	0.23	1.73	0.129184	0.238483	-5.84
266034_at	Expressed protein ; supported by fu	FIP1	AT2G06005	-1.13	-0.17	-1.73	0.129239	0.238564	-5.84
250785_at	unknown protein	---	AT5G05510	-1.21	-0.27	-1.73	0.129255	0.238576	-5.84
248561_at	unknown protein	---	AT5G49680	-1.21	-0.27	-1.73	0.129266	0.238576	-5.84
267037_at	hypothetical protein ; supported by	---	AT2G38320	-1.16	-0.21	-1.73	0.129459	0.238913	-5.84
248284_at	Expressed protein ; supported by fu	---	AT5G52975	-1.18	-0.24	-1.73	0.129564	0.239072	-5.84
261791_at	unknown protein ; supported by full-	---	AT1G16170	-1.38	-0.46	-1.73	0.129568	0.239072	-5.84
261308_at	protein kinase, putative contains si	RKL1	AT1G48480	-1.75	-0.81	-1.73	0.129577	0.239072	-5.84
255027_at	hypothetical protein F21E10.5 Arab	---	AT4G09880	-1.15	-0.21	-1.73	0.129611	0.239116	-5.84
263564_s_a	DNA-directed RNA polymerase II,	NRPB3	AT2G15400	1.15	0.20	1.73	0.129626	0.239124	-5.84
248050_at	unknown protein	---	AT5G56100	1.31	0.39	1.73	0.129658	0.239143	-5.84
267197_at	hypothetical protein predicted by ge	---	AT2G30960	-1.14	-0.19	-1.73	0.129662	0.239143	-5.84
246091_at	putative protein various predicted p	---	AT5G20590	1.18	0.24	1.73	0.129668	0.239143	-5.84
250342_at	putative protein predicted protein, A	---	AT5G11870	-1.21	-0.28	-1.73	0.129742	0.239261	-5.84
250240_at	unknown protein	---	AT5G13590	1.23	0.30	1.73	0.129753	0.239261	-5.84
251982_at	pectate lyase -like protein pectate l	---	AT3G53190	-1.22	-0.29	-1.73	0.129773	0.239278	-5.84
260717_at	serine/threonine phosphatase PP7	---	AT1G48120	1.20	0.26	1.73	0.129783	0.239278	-5.84
266680_s_a	hypothetical protein predicted by ge	---	AT2G19850	-1.12	-0.16	-1.73	0.129884	0.239446	-5.84
261396_at	hypothetical protein contains simila	---	AT1G79800	-1.15	-0.21	-1.72	0.129922	0.239496	-5.84
258045_at	ubiquitin-specific protease 7 (UBP7	UBP7	AT3G21280	-1.16	-0.21	-1.72	0.129945	0.239514	-5.84
252221_at	RuvB DNA helicase - like protein D	---	AT3G49830	-1.16	-0.21	-1.72	0.129953	0.239514	-5.84
247852_at	ATGP1 ; supported by cDNA: gi_1	YKT61	AT5G58060	1.14	0.19	1.72	0.129974	0.239515	-5.84
250489_s_a	putative protein predicted proteins,	---	AT5G09710	1.17	0.23	1.72	0.129974	0.239515	-5.84
247492_at	putative protein AP2 domain conta	---	AT5G61890	-1.47	-0.55	-1.72	0.130006	0.239554	-5.84
259847_at	unknown protein	---	AT1G72170	-1.18	-0.23	-1.72	0.130029	0.239577	-5.84
247279_at	arabinogalactan-protein (gb|AAC77	AGP1	AT5G64310	-1.74	-0.80	-1.72	0.130073	0.239638	-5.84
257599_at	60S ribosomal protein, putative sim	---	AT3G24830	1.35	0.43	1.72	0.130154	0.239768	-5.84
261533_at	hypothetical protein predicted by ge	---	AT1G71690	-1.20	-0.26	-1.72	0.13018	0.239797	-5.84
248809_at	GTP-binding protein-like	AtRABA5a	AT5G47520	-1.17	-0.23	-1.72	0.130229	0.239867	-5.84
254590_at	hypothetical protein	---	AT4G18860	-1.14	-0.18	-1.72	0.13027	0.239925	-5.84
247305_at	Expressed protein ; supported by fu	---	AT5G63905	-1.46	-0.54	-1.72	0.130284	0.23993	-5.85
257043_at	receptor-like protein kinase, putativ	IKU2	AT3G19700	-1.15	-0.20	-1.72	0.13032	0.239963	-5.85
246474_at	putative protein predicted protein, A	---	AT5G17150	-1.15	-0.20	-1.72	0.130323	0.239963	-5.85

253993_at	mitogen activated protein kinase kir	MEK1	AT4G26070	-1.29	-0.37	-1.72	0.130341	0.23997	-5.85
251443_at	putative protein unknown protein A	---	AT3G59940	-1.30	-0.38	-1.72	0.130347	0.23997	-5.85
250933_at	arabinogalactan protein - like arabi	FLA11	AT5G03170	-1.37	-0.46	-1.72	0.130426	0.240095	-5.85
254626_at	hypothetical protein ; supported by	---	AT4G18400	1.17	0.22	1.72	0.130459	0.240118	-5.85
266778_at	putative cytochrome P450	CYP707A2	AT2G29090	1.18	0.24	1.72	0.130459	0.240118	-5.85
258021_at	hypothetical protein predicted gene	PUB25	AT3G19380	1.52	0.61	1.72	0.1305	0.240173	-5.85
259386_at	hypothetical protein contains simila	NUB	AT1G13400	-1.16	-0.22	-1.72	0.130566	0.240275	-5.85
245863_s_a	hypothetical protein contains simila	---	AT1G58050	1.17	0.23	1.72	0.130577	0.240276	-5.85
258704_at	putative protein kinase similar to Pt	CCR1	AT3G09780	-1.22	-0.29	-1.72	0.130626	0.240346	-5.85
252407_at	chloroplast NAD-dependent malate	MDH	AT3G47520	1.19	0.26	1.72	0.130679	0.24041	-5.85
252466_x_a	putative protein several hypothetica	---	---	-1.14	-0.19	-1.72	0.130681	0.24041	-5.85
259841_at	unknown protein ; supported by full-	---	AT1G52200	1.20	0.26	1.72	0.13074	0.240492	-5.85
256056_at	hypothetical protein contains simila	---	AT1G07190	-1.12	-0.16	-1.72	0.130752	0.240492	-5.85
257840_at	protein kinase, putative contains P	AGC2-1	AT3G25250	1.99	0.99	1.72	0.130764	0.240492	-5.85
260244_at	putative choline kinase similar to Gl	---	AT1G74320	-1.15	-0.20	-1.72	0.130783	0.240492	-5.85
265370_s_a	unknown protein related to GB:AAD	---	AT3G30415	-1.13	-0.17	-1.72	0.130785	0.240492	-5.85
266560_at	putative LRR receptor protein kinas	---	AT2G23950	1.18	0.24	1.72	0.130789	0.240492	-5.85
257399_at	putative OBP32pep protein	---	AT1G23690	-1.11	-0.15	-1.72	0.130801	0.240495	-5.85
249776_at	unknown protein	---	AT5G24170	-1.20	-0.27	-1.72	0.130841	0.240548	-5.85
262421_at	hypothetical protein predicted by ge	---	AT1G50290	1.22	0.29	1.72	0.130859	0.240563	-5.85
263773_at	putative xylulose kinase	---	AT2G21370	-1.20	-0.27	-1.72	0.130909	0.240635	-5.85
251465_at	transporter-like protein UDP-galact	UTR6	AT3G59360	-1.12	-0.16	-1.72	0.130982	0.240738	-5.85
258327_at	unknown protein contains similarity	PAP85	AT3G22640	-1.12	-0.17	-1.72	0.130986	0.240738	-5.85
245850_at	ankyrin-repeat containing protein ar	KEG	AT5G13530	-1.21	-0.28	-1.72	0.131112	0.24095	-5.85
256292_at	unknown protein	---	AT1G69430	-1.17	-0.23	-1.72	0.131126	0.240956	-5.85
254195_at	putative protein various predicted p	NLP7	AT4G24020	-1.14	-0.19	-1.72	0.13114	0.240961	-5.85
261026_at	hypothetical protein predicted by ge	---	AT1G01240	-1.19	-0.25	-1.72	0.131184	0.241004	-5.85
264926_at	cytochrome b5, putative similar to (	CB5LP	AT1G60660	1.15	0.20	1.72	0.131184	0.241004	-5.85
258325_at	putative heat shock protein similar t	HSFA6B	AT3G22830	-1.14	-0.19	-1.72	0.131301	0.241199	-5.85
264572_at	unknown protein ESTs gb|AA0424	---	AT1G05320	1.16	0.21	1.72	0.131322	0.241199	-5.85
249142_at	putative protein similar to unknown	---	AT5G43230	-1.16	-0.22	-1.72	0.131322	0.241199	-5.85
257991_at	unknown protein	---	AT3G19870	-1.19	-0.25	-1.72	0.13142	0.241361	-5.85
255273_at	putative protein various predicted p	---	---	-1.12	-0.17	-1.72	0.131558	0.241576	-5.85
253746_at	putative protein hypothetical protei	---	AT4G29100	1.33	0.41	1.72	0.131559	0.241576	-5.85
254700_at	hypothetical protein	---	AT4G18000	-1.16	-0.21	-1.72	0.131623	0.241674	-5.85

258216_at	unknown protein contains Pfam pro	---	AT3G17980	1.19	0.25	1.72	0.131633	0.241674	-5.85
261719_at	hypothetical protein similar to hypot	---	AT1G18390	1.52	0.61	1.72	0.131659	0.241702	-5.86
256216_at	calreticulin (crt1) identical to calretic	CRT1	AT1G56340	1.32	0.40	1.72	0.131674	0.24171	-5.86
245430_at	hypothetical protein	FIP2	AT4G17060	-1.11	-0.15	-1.72	0.131727	0.241788	-5.86
251129_at	putative protein predicted protein, A	---	AT5G01150	-1.15	-0.20	-1.72	0.131759	0.241828	-5.86
245518_at	ATP-dependent RNA helicase like p	ATRH1	AT4G15850	1.26	0.33	1.72	0.131772	0.241832	-5.86
253623_at	GDP-mannose pyrophosphorylase	---	AT4G30570	-1.15	-0.20	-1.71	0.131823	0.241896	-5.86
260957_at	delta 9 desaturase identical to delta	ADS1	AT1G06080	-1.26	-0.34	-1.71	0.131828	0.241896	-5.86
252258_at	putative protein several hypothetica	---	AT3G49450	-1.18	-0.24	-1.71	0.131861	0.241936	-5.86
256759_at	hypothetical protein predicted by ge	---	AT3G25640	-1.20	-0.26	-1.71	0.13195	0.242073	-5.86
258452_at	alternative oxidase 1a precursor ide	AOX1A	AT3G22370	1.56	0.64	1.71	0.131957	0.242073	-5.86
264681_s_a	permease 1-like protein permease	---	AT1G65550	-1.18	-0.24	-1.71	0.132021	0.242171	-5.86
254006_at	putative protein various predicted p	---	AT4G26340	-1.14	-0.19	-1.71	0.132044	0.242195	-5.86
254423_at	Lsd1 like protein zinc-finger protein	LOL2	AT4G21610	1.20	0.26	1.71	0.132147	0.242363	-5.86
249538_at	kanadaptin - like protein unnamed	---	AT5G38840	1.14	0.19	1.71	0.132206	0.242452	-5.86
253821_at	extensin-like protein extensin-like p	---	AT4G28380	-1.15	-0.21	-1.71	0.132305	0.242613	-5.86
252675_at	putative protein hypothetical protein	---	---	-1.14	-0.19	-1.71	0.132323	0.242628	-5.86
256943_at	hypothetical protein similar to hypot	---	AT3G18910	1.13	0.17	1.71	0.132357	0.242671	-5.86
247135_at	auxin-induced protein-like	---	AT5G66260	-1.11	-0.16	-1.71	0.132389	0.24271	-5.86
248290_at	Ca2+-transporting ATPase-like prot	---	AT5G53010	1.17	0.22	1.71	0.132409	0.242727	-5.86
258854_at	putative UDP-glucosyl transferase	---	AT3G02100	-1.16	-0.21	-1.71	0.132443	0.242769	-5.86
250758_at	eukaryotic translation initiation facto	EIF3G2	AT5G06000	1.21	0.28	1.71	0.132464	0.242789	-5.86
246418_at	quinone oxidoreductase -like prote	---	AT5G16960	1.19	0.25	1.71	0.132484	0.242807	-5.86
260698_at	unknown protein contains similarity	---	AT1G32300	-1.12	-0.16	-1.71	0.132561	0.242927	-5.86
258547_at	unknown protein	---	AT3G06895	1.12	0.16	1.71	0.132627	0.243016	-5.86
248215_at	putative protein contains similarity t	---	AT5G53680	-1.22	-0.29	-1.71	0.132637	0.243016	-5.86
254114_at	putative protein (fragment) MtN21 (	---	AT4G24980	-1.19	-0.25	-1.71	0.132648	0.243016	-5.86
261384_at	hypothetical protein predicted by ge	---	AT1G05440	-1.15	-0.20	-1.71	0.132652	0.243016	-5.86
250608_at	pectin methyl-esterase-like protein	---	AT5G07420	-1.13	-0.17	-1.71	0.132691	0.243069	-5.86
262552_at	hypothetical protein similar to hypot	---	AT1G31350	-1.25	-0.33	-1.71	0.132765	0.243185	-5.86
265255_at	unknown protein ; supported by cD	---	AT2G28420	1.27	0.34	1.71	0.132881	0.243377	-5.86
253570_at	hypothetical protein	---	AT4G31260	-1.18	-0.24	-1.71	0.13292	0.24343	-5.86
257357_at	hypothetical protein predicted by ge	---	AT2G41050	-1.14	-0.19	-1.71	0.132954	0.243472	-5.86
261494_at	homeobox transcription factor Hox	HB-1	AT1G28420	1.17	0.22	1.71	0.133015	0.243563	-5.86
265848_at	putative sugar transporter	INT3	AT2G35740	-1.23	-0.30	-1.71	0.133069	0.243643	-5.87

255663_at	hypothetical protein	---	AT4G00420	-1.15	-0.20	-1.71	0.133103	0.243686	-5.87
265915_at	En/Spm-like transposon protein rela	---	---	1.12	0.17	1.71	0.133119	0.243696	-5.87
265691_at	unknown protein predicted by gens	---	AT2G24330	-1.24	-0.31	-1.71	0.13316	0.243751	-5.87
248522_at	predicted protein	---	AT5G50565	1.13	0.18	1.71	0.133201	0.243793	-5.87
254063_at	receptor kinase-like protein recepto	---	AT4G25390	-1.34	-0.43	-1.71	0.133207	0.243793	-5.87
252636_at	putative protein triacylglycerol lipas	---	AT3G44510	1.15	0.21	1.71	0.133215	0.243793	-5.87
248915_at	putative protein strong similarity to	---	AT5G45690	-1.17	-0.22	-1.71	0.133233	0.243795	-5.87
249655_at	putative helicase PIF1 protein - Ca	---	---	-1.14	-0.18	-1.71	0.133238	0.243795	-5.87
259316_at	unknown protein	---	AT3G01175	1.19	0.25	1.71	0.133249	0.243796	-5.87
260765_at	actin 8 almost identical to actin 8 G	ACT8	AT1G49240	1.35	0.44	1.71	0.133262	0.2438	-5.87
246579_at	hypothetical protein predicted by ge	---	AT1G31620	-1.18	-0.23	-1.71	0.13328	0.243815	-5.87
265331_at	similar to gibberellin-regulated prote	---	AT2G18420	-1.14	-0.19	-1.71	0.133298	0.243819	-5.87
249051_at	berberine bridge enzyme-like protei	---	AT5G44390	1.18	0.24	1.71	0.133304	0.243819	-5.87
256737_at	farnesyltranstransferase, putative (	---	AT3G29420	-1.13	-0.17	-1.71	0.133372	0.243924	-5.87
253646_at	MAP kinase kinase 2 ; supported b	ATMKK2	AT4G29810	-1.26	-0.33	-1.71	0.133457	0.24406	-5.87
245140_at	unknown protein predicted by gene	LBD18	AT2G45420	-1.12	-0.17	-1.71	0.133501	0.244121	-5.87
256812_at	hypothetical protein contains simila	---	AT3G21350	-1.13	-0.17	-1.71	0.133531	0.244142	-5.87
247045_at	putative protein similar to unknown	---	AT5G66930	1.18	0.24	1.71	0.133534	0.244142	-5.87
248900_at	putative protein strong similarity to	PRP39-2	AT5G46400	1.22	0.28	1.70	0.133758	0.244504	-5.87
259212_at	hypothetical protein predicted by ge	---	AT3G09180	1.16	0.21	1.70	0.133767	0.244504	-5.87
248834_at	unknown protein ;supported by full	---	AT5G47090	1.14	0.19	1.70	0.13377	0.244504	-5.87
266436_at	putative clathrin binding protein (ep	---	AT2G43160	-1.28	-0.36	-1.70	0.133775	0.244504	-5.87
263898_at	SKP1 interacting partner 6 (SKIP6)	SKIP6	AT2G21950	1.15	0.21	1.70	0.133834	0.244592	-5.87
267333_at	putative WD-40 repeat protein cont	---	AT2G19430	1.13	0.17	1.70	0.133851	0.244592	-5.87
259025_at	hypothetical protein predicted by ge	---	---	-1.19	-0.26	-1.70	0.133855	0.244592	-5.87
253613_at	PR-1-like protein gene PR-1 protei	---	AT4G30320	-1.17	-0.22	-1.70	0.133936	0.24471	-5.87
260776_at	zinc finger protein, putative similar	---	AT1G14580	-1.39	-0.47	-1.70	0.133942	0.24471	-5.87
252211_at	putative protein predicted proteins,	---	AT3G50220	-1.14	-0.19	-1.70	0.133981	0.244762	-5.87
245238_at	putative protein similarity to cytoch	ACYB-2	AT4G25570	-1.18	-0.24	-1.70	0.134037	0.244846	-5.87
250161_at	putative protein amino acid transpo	---	AT5G15240	1.27	0.35	1.70	0.134087	0.244917	-5.87
260406_at	putative glutathione transferase sim	ATGSTU12	AT1G69920	2.45	1.29	1.70	0.134108	0.244936	-5.87
258834_at	GTP cyclohydrolase I similar to GTI	---	AT3G07270	1.18	0.24	1.70	0.13415	0.244993	-5.87
250962_at	putative protein various predicted p	---	AT5G02990	-1.15	-0.20	-1.70	0.134192	0.245051	-5.87
250603_at	putative protein mature parasite-int	---	AT5G07820	1.16	0.21	1.70	0.134215	0.245072	-5.87
251691_at	putative protein hypothetical protei	---	AT3G56520	-1.17	-0.23	-1.70	0.13427	0.245154	-5.87

259898_at	hypothetical protein predicted by ge	---	AT1G71200	-1.14	-0.19	-1.70	0.134288	0.245166	-5.87
250813_at	GTP-binding protein (gb|AAD09203	TOC34	AT5G05000	1.18	0.24	1.70	0.134324	0.245202	-5.87
252063_at	lipid transfer protein-like protein lip	LTP12	AT3G51590	-1.15	-0.20	-1.70	0.134339	0.245202	-5.87
245537_at	hypothetical protein	---	AT4G15200	-1.12	-0.17	-1.70	0.13434	0.245202	-5.87
249439_at	thaumatin-like protein thaumatin-lik	---	AT5G40020	-1.31	-0.39	-1.70	0.134392	0.245261	-5.87
253576_at	putative protein various predicted p	---	AT4G31070	1.12	0.17	1.70	0.134398	0.245261	-5.87
262556_at	hypothetical protein	---	AT1G31370	-1.13	-0.17	-1.70	0.134404	0.245261	-5.87
249249_at	unknown protein	---	AT5G42330	1.16	0.21	1.70	0.134428	0.245285	-5.87
260158_at	unknown protein	---	AT1G79910	-1.16	-0.21	-1.70	0.134446	0.245298	-5.87
245767_at	hypothetical protein similar to putati	---	AT1G33610	-1.11	-0.15	-1.70	0.134466	0.245314	-5.87
257485_at	hypothetical protein contains Pfam	---	AT1G63580	-1.32	-0.40	-1.70	0.134519	0.24539	-5.88
262443_at	Expressed protein ; supported by fu	---	AT1G47655	-1.21	-0.27	-1.70	0.134532	0.24539	-5.88
264727_at	putative cytochrome C strong simila	CYTC-1	AT1G22840	1.34	0.43	1.70	0.13454	0.24539	-5.88
247568_at	putative protein predicted proteins,	---	AT5G61260	1.32	0.40	1.70	0.134572	0.245429	-5.88
254670_at	teosinte branched1 - like protein te	---	AT4G18390	1.26	0.34	1.70	0.134615	0.245471	-5.88
254568_x_a	hypothtetical protein	---	---	-1.17	-0.23	-1.70	0.134617	0.245471	-5.88
253075_at	putative disease resistance protein	---	AT4G36150	1.13	0.17	1.70	0.134642	0.245491	-5.88
245670_at	mitochondrial protein (AtJ1), putati	ATJ1	AT1G28210	1.30	0.38	1.70	0.134649	0.245491	-5.88
251417_at	putative protein prib5, Ribes nigrun	AT3G6042(	---	-1.12	-0.16	-1.70	0.134725	0.24561	-5.88
259969_at	putative pyrophosphate-dependent	---	AT1G76550	1.35	0.43	1.70	0.134748	0.245632	-5.88
250475_at	sulfate transporter ; supported by d	SULTR2;1	AT5G10180	-1.41	-0.50	-1.70	0.134762	0.245638	-5.88
266955_at	mitochondrial ribosomal protein S14	RPS14	AT2G34520	1.17	0.23	1.70	0.134909	0.245887	-5.88
266714_at	NAM (no apical meristem)-like prote	EMB2301	AT2G46770	-1.15	-0.20	-1.70	0.134951	0.245943	-5.88
257347_at	pseudogene, gene_id:K17E7.6	---	---	-1.12	-0.17	-1.70	0.134965	0.245946	-5.88
260339_at	putative serine/threonine kinase sin	SIK1	AT1G69220	-1.21	-0.28	-1.70	0.134974	0.245946	-5.88
253667_at	peroxidase ATP8a ;supported by fu	---	AT4G30170	-1.14	-0.18	-1.70	0.135006	0.245985	-5.88
264785_at	putative non-LTR retroelement reve	---	---	-1.15	-0.20	-1.70	0.135195	0.246309	-5.88
265612_at	hypothetical protein predicted by ge	---	AT2G25390	1.13	0.18	1.70	0.13525	0.24639	-5.88
259282_at	unknown protein similar to unknown	GPAT5	AT3G11430	-1.20	-0.26	-1.70	0.135354	0.24656	-5.88
248791_at	palmitoyl-protein thioesterase precu	---	AT5G47350	-1.11	-0.16	-1.70	0.135447	0.246697	-5.88
246019_at	putative protein predicted proteins,	---	AT5G10690	-1.19	-0.25	-1.70	0.135451	0.246697	-5.88
255496_at	putative protein similar to plant nucl	BZO2H1	AT4G02640	1.21	0.27	1.69	0.135717	0.247162	-5.88
248114_at	wax synthase-like protein	---	AT5G55370	-1.15	-0.20	-1.69	0.135731	0.247168	-5.88
262212_at	response regulator 7, putative simi	ARR15	AT1G74890	-1.20	-0.26	-1.69	0.135776	0.247231	-5.88
250130_at	amylogenin; reversibly glycosylatab	---	AT5G16510	-1.20	-0.27	-1.69	0.135915	0.247464	-5.89

249707_at	putative protein similar to unknown	---	AT5G35640	-1.22	-0.28	-1.69	0.135934	0.247477	-5.89
261210_at	vacuolar ATP synthase subunit C,	DET3	AT1G12840	-1.12	-0.16	-1.69	0.136002	0.24757	-5.89
261599_at	hypothetical protein similar to hypot	---	AT1G49700	-1.15	-0.21	-1.69	0.136006	0.24757	-5.89
248055_at	serine/threonine-specific kinase like	---	AT5G55830	-1.15	-0.20	-1.69	0.136024	0.247583	-5.89
254618_at	cellulose synthase - like protein cel	IRX1	AT4G18780	-1.27	-0.34	-1.69	0.136056	0.247616	-5.89
246393_at	phosphoglycerate kinase, putative	---	AT1G58150	-1.15	-0.20	-1.69	0.136064	0.247616	-5.89
257821_at	Expressed protein ; supported by fu	RALFL26	AT3G25170	-1.12	-0.16	-1.69	0.136079	0.247624	-5.89
266236_at	putative glutathione S-transferase	ATGSTZ2	AT2G02380	-1.13	-0.18	-1.69	0.136118	0.247674	-5.89
254318_at	putative protein embryo-abundant	---	AT4G22530	1.65	0.73	1.69	0.13615	0.247699	-5.89
257643_at	AP2 domain transcription factor co	---	AT3G25730	1.43	0.51	1.69	0.136173	0.247699	-5.89
257614_at	putative non-LTR retroelement reve	---	---	-1.17	-0.23	-1.69	0.136176	0.247699	-5.89
252395_at	H+-transporting ATPase - like prote	AHA4	AT3G47950	1.23	0.30	1.69	0.136182	0.247699	-5.89
248331_at	putative protein contains similarity t	---	AT5G52650	1.27	0.34	1.69	0.136193	0.247699	-5.89
260281_at	unknown protein	---	AT1G80500	-1.17	-0.22	-1.69	0.136197	0.247699	-5.89
246293_at	SigA binding protein ; supported by	SIB1	AT3G56710	1.82	0.87	1.69	0.136223	0.247727	-5.89
249630_s_a	sen1-like protein SEN1 - Saccharo	---	AT5G37150	-1.11	-0.15	-1.69	0.136272	0.247797	-5.89
265967_at	nodulin-like protein ; supported by	---	AT2G37450	-1.21	-0.27	-1.69	0.136421	0.248029	-5.89
258069_at	hypothetical protein predicted by ge	---	AT3G26010	-1.20	-0.26	-1.69	0.136421	0.248029	-5.89
254666_at	translation initiation factor eIF-2 ga	---	AT4G18330	-1.11	-0.15	-1.69	0.136455	0.248071	-5.89
254436_at	putative protein receptor kinase-lik	---	AT4G20940	-1.12	-0.17	-1.69	0.136473	0.248083	-5.89
262226_at	Expressed protein ; supported by fu	---	AT1G53885	-1.44	-0.53	-1.69	0.136545	0.248194	-5.89
247615_at	putative protein various predicted p	---	AT5G60250	-1.12	-0.16	-1.69	0.136663	0.24839	-5.89
267357_at	putative nematode-resistance prote	HSPRO2	AT2G40000	-1.41	-0.50	-1.69	0.136708	0.248451	-5.89
254715_at	putative protein hypothetical protei	---	AT4G13550	1.22	0.29	1.69	0.136905	0.248774	-5.89
263220_at	hypothetical protein predicted by ge	emb2279	AT1G30610	1.19	0.25	1.69	0.13691	0.248774	-5.89
264714_at	receptor-like protein kinase, putativ	---	AT1G69990	-1.16	-0.21	-1.69	0.136918	0.248774	-5.89
253133_at	DNA-directed RNA polymerase (EC	NRPB1	AT4G35800	1.15	0.20	1.69	0.137	0.248902	-5.89
266805_at	hypothetical protein ;supported by	---	AT2G30010	-2.26	-1.18	-1.69	0.137073	0.249015	-5.89
260121_at	AIG1-like protein similar to AIG1 pr	---	AT1G33910	-1.11	-0.15	-1.69	0.137117	0.249076	-5.89
262473_at	chloroplast FtsH protease almost id	FTSH1	AT1G50250	-1.19	-0.25	-1.69	0.137199	0.249199	-5.89
252924_at	putative zinc finger protein salt-tole	---	AT4G39070	-1.42	-0.50	-1.69	0.137207	0.249199	-5.89
250957_at	photoreceptor-interacting protein -	---	AT5G03250	1.12	0.16	1.69	0.137253	0.249252	-5.89
254103_at	putative protein ;supported by full-l	---	AT4G25030	1.41	0.50	1.69	0.137258	0.249252	-5.89
246761_at	embryonic abundant protein - like e	---	AT5G27980	-1.13	-0.18	-1.69	0.137317	0.249339	-5.89
246937_at	phospholipase D1-like protein phos	PLDALPHA	AT5G25370	-1.13	-0.18	-1.69	0.137331	0.249345	-5.89

248619_at	amino acid permease 6 (emb CAA6	AAP6	AT5G49630	-1.20	-0.27	-1.69	0.137379	0.249412	-5.90
254629_at	Expressed protein ; supported by fu	---	AT4G18425	-1.19	-0.26	-1.69	0.137406	0.249442	-5.90
246695_at	putative protein	---	---	-1.19	-0.25	-1.69	0.137502	0.249596	-5.90
248275_at	isp4 protein	ATOPT8	AT5G53520	-1.12	-0.16	-1.69	0.137518	0.249605	-5.90
262387_s_a	hypothetical protein contains simila	---	AT1G49340	1.14	0.19	1.69	0.137562	0.249665	-5.90
254620_at	pollen-specific protein - like 18.3K	---	AT4G18590	1.15	0.20	1.68	0.137655	0.249814	-5.90
250922_at	Expressed protein ; supported by fu	---	AT5G03345	-1.14	-0.19	-1.68	0.137701	0.249877	-5.90
258686_at	putative polygalacturonase similar	---	AT3G07840	-1.12	-0.17	-1.68	0.137754	0.249954	-5.90
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.26	-0.33	-1.68	0.137806	0.249992	-5.90
263845_at	phenylalanine ammonia lyase (PAL	pal1	AT2G37040	1.60	0.68	1.68	0.137807	0.249992	-5.90
253217_at	actin depolymerizing factor - like pr	ADF9	AT4G34970	-1.37	-0.45	-1.68	0.137818	0.249992	-5.90
260750_at	light repressible receptor protein ki	---	AT1G49100	-1.14	-0.19	-1.68	0.137819	0.249992	-5.90
265932_at	hypothetical protein predicted by gr	LBD8	AT2G19510	-1.11	-0.15	-1.68	0.13783	0.249993	-5.90
262301_at	ripening-induced protein, putative s	---	AT1G70880	-1.15	-0.21	-1.68	0.137867	0.25004	-5.90
258955_s_a	unknown protein ;supported by full-	---	AT3G01450	-1.19	-0.26	-1.68	0.137915	0.250107	-5.90
260392_at	putative enolase similar to ENOLAS	---	AT1G74030	2.04	1.03	1.68	0.137927	0.250109	-5.90
256822_at	unknown protein contains PF00612	IQD5	AT3G22190	-1.16	-0.22	-1.68	0.137982	0.250188	-5.90
253786_at	receptor protein kinase-like protein	---	AT4G28650	-1.15	-0.20	-1.68	0.138014	0.250227	-5.90
255498_at	putative vacuolar ATPase similar to	---	AT4G02620	-1.10	-0.14	-1.68	0.138094	0.250351	-5.90
248118_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G55050	-1.94	-0.96	-1.68	0.138199	0.250515	-5.90
258518_at	unknown protein ; supported by cD	---	AT3G06570	1.12	0.17	1.68	0.138206	0.250515	-5.90
247219_at	COP1-interacting protein CIP8 ; su	CIP8	AT5G64920	-1.15	-0.20	-1.68	0.138261	0.250594	-5.90
251298_at	hypothetical protein contains non-c	---	AT3G62040	1.33	0.41	1.68	0.138313	0.250669	-5.90
246492_at	CRS2-like protein CRS2 - Zea may	---	AT5G16140	-1.22	-0.28	-1.68	0.138347	0.250711	-5.90
259845_at	auxin transporter splice variant b, p	PIN1	AT1G73590	-1.22	-0.29	-1.68	0.138385	0.250746	-5.90
261687_at	hypothetical protein predicted by ge	---	AT1G47280	-1.13	-0.18	-1.68	0.138389	0.250746	-5.90
257041_at	unknown protein	---	AT3G28550	-1.20	-0.26	-1.68	0.1384	0.250746	-5.90
256416_at	ferritin subunit, putative similar to f	ATFER2	AT3G11050	-1.17	-0.23	-1.68	0.138418	0.25076	-5.90
250223_at	glutaredoxin-like protein ;supporte	ROXY2	AT5G14070	-1.13	-0.18	-1.68	0.13848	0.250853	-5.90
262675_at	anter-specific proline-rich -like prote	EXL6	AT1G75930	-1.16	-0.21	-1.68	0.138519	0.250887	-5.90
251223_at	putative transcription factor MYB11	ATMYB11	AT3G62610	-1.12	-0.16	-1.68	0.138521	0.250887	-5.90
259147_at	putative RNA binding protein simila	APUM4	AT3G10360	-1.25	-0.33	-1.68	0.138555	0.250918	-5.90
251549_at	putative protein predicted proteins,	---	AT3G58890	-1.13	-0.18	-1.68	0.138561	0.250918	-5.90
267056_at	hypothetical protein predicted by ge	---	AT2G32470	1.19	0.25	1.68	0.138699	0.251149	-5.90
262091_at	Myb-family transcription factor, put	MYB72	AT1G56160	-1.13	-0.18	-1.68	0.138796	0.25128	-5.90

259935_at	putative GDSL-motif lipase/acylhyd	---	AT1G71250	-1.17	-0.22	-1.68	0.138802	0.25128	-5.90
266494_at	putative receptor-like protein kinase	PRK2A	AT2G07040	-1.13	-0.18	-1.68	0.138805	0.25128	-5.90
257409_at	unknown protein predicted by gens	---	AT2G17470	-1.16	-0.22	-1.68	0.138829	0.251295	-5.91
253565_at	predicted protein DAN26, Homo sa	---	AT4G31200	1.18	0.24	1.68	0.138835	0.251295	-5.91
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=gb:J	---	---	-1.34	-0.42	-1.68	0.138854	0.251302	-5.91
267399_at	hypothetical protein predicted by ge	---	AT2G44195	-1.11	-0.16	-1.68	0.13886	0.251302	-5.91
263318_at	Expressed protein ; supported by fu	AtGDU4	AT2G24762	-1.81	-0.85	-1.68	0.138889	0.251333	-5.91
257183_at	ABC transporter contains Pfam prof	---	AT3G13220	-1.14	-0.19	-1.68	0.138903	0.251339	-5.91
263654_at	unknown protein	---	AT1G04300	1.14	0.19	1.68	0.138922	0.251342	-5.91
256496_at	hypothetical protein similar to hypot	---	AT1G31510	-1.15	-0.20	-1.68	0.138927	0.251342	-5.91
261805_at	hypothetical protein almost identica	---	AT1G30540	-1.15	-0.20	-1.68	0.138979	0.251398	-5.91
256763_at	unknown protein	COBL8	AT3G16860	-1.54	-0.62	-1.68	0.13898	0.251398	-5.91
259904_at	hypothetical protein predicted by ge	---	AT1G74150	-1.17	-0.22	-1.68	0.138998	0.25141	-5.91
262471_at	hypothetical protein similar to hypot	---	AT1G50140	-1.17	-0.23	-1.68	0.139036	0.25146	-5.91
260647_at	hypothetical protein predicted by ge	---	AT1G08030	1.17	0.23	1.68	0.139078	0.251516	-5.91
259740_at	phytochrome, putative similar to GI	---	AT1G64300	1.22	0.28	1.68	0.13922	0.251737	-5.91
263903_at	putative touch-induced calmodulin	---	AT2G36180	-1.12	-0.17	-1.68	0.139222	0.251737	-5.91
246007_at	Expressed protein ; supported by fu	FTRA2	AT5G08410	1.17	0.23	1.68	0.139328	0.251895	-5.91
255869_at	unknown protein	---	AT2G30270	-1.16	-0.21	-1.68	0.139332	0.251895	-5.91
259641_at	putative protease similar to proteas	---	AT1G69020	-1.18	-0.24	-1.68	0.139414	0.252023	-5.91
260818_at	unknown protein	---	AT1G06890	1.11	0.15	1.68	0.139453	0.252075	-5.91
261713_at	protein kinase, putative identical to	MYC2	AT1G32640	1.25	0.32	1.68	0.139482	0.252106	-5.91
253752_at	putative protein ;supported by full-l	---	AT4G28910	-1.18	-0.24	-1.68	0.139519	0.252154	-5.91
255754_at	auxin-induced protein, putative sim	---	AT1G43040	-1.11	-0.15	-1.67	0.139612	0.252301	-5.91
253433_s_a	nodulin - like protein nodulin (clone	---	AT4G28365	-1.17	-0.23	-1.67	0.139645	0.252339	-5.91
265231_s_a	hypothetical protein	---	AT2G07713	-1.14	-0.18	-1.67	0.139655	0.252339	-5.91
248125_at	2S storage protein-like	---	AT5G54740	-1.15	-0.20	-1.67	0.139697	0.252395	-5.91
251619_at	putative protein hypothetical protei	---	AT3G58050	-1.11	-0.15	-1.67	0.13978	0.252525	-5.91
260170_at	putative sucrose transport protein s	SUC5	AT1G71890	-1.22	-0.28	-1.67	0.139797	0.252532	-5.91
247168_at	putative protein contains similarity t	---	AT5G65860	1.18	0.24	1.67	0.139806	0.252532	-5.91
262813_at	unknown protein strong similarity to	---	AT1G11670	-1.48	-0.56	-1.67	0.139906	0.252692	-5.91
250322_at	putative transcription factor (MYB46	MYB46	AT5G12870	-1.11	-0.16	-1.67	0.140024	0.252886	-5.91
262945_at	unknown protein ;supported by full-	---	AT1G79510	1.29	0.36	1.67	0.140103	0.253009	-5.91
259720_at	hypothetical protein predicted by ge	---	AT1G61080	-1.16	-0.22	-1.67	0.140167	0.253104	-5.91
254313_at	extensin like protein extensin like p	---	AT4G22460	-1.17	-0.22	-1.67	0.140272	0.253273	-5.91

245867_at	ATP phosphoribosyl transferase ide	ATATP-PR	AT1G58080	1.16	0.21	1.67	0.140287	0.25328	-5.91
250289_at	putative protein ;supported by full-l	---	AT5G13190	-1.37	-0.46	-1.67	0.140393	0.253451	-5.92
251230_at	beta-glucosidase-like protein severa	BGLU8	AT3G62750	1.12	0.16	1.67	0.140473	0.253577	-5.92
262806_at	putative pyrophosphate-dependent	---	AT1G20950	1.23	0.30	1.67	0.140524	0.253648	-5.92
251064_at	putative zinc finger protein several	---	AT5G01860	-1.15	-0.20	-1.67	0.140551	0.253662	-5.92
252505_at	dehydrogenase -like protein alcoho	---	AT3G46170	-1.16	-0.21	-1.67	0.14056	0.253662	-5.92
260318_at	hypothetical protein predicted by ge	---	AT1G63960	-1.17	-0.23	-1.67	0.140565	0.253662	-5.92
252349_at	cell division cycle protein 23 homol	APC8	AT3G48150	1.24	0.31	1.67	0.14059	0.253687	-5.92
260922_at	hypothetical protein predicted by ge	---	AT1G21560	1.14	0.19	1.67	0.140669	0.253803	-5.92
267588_at	unknown protein	---	AT2G42060	-1.12	-0.17	-1.67	0.140677	0.253803	-5.92
265485_at	putative Ta11-like non-LTR retroele	---	---	-1.22	-0.29	-1.67	0.140689	0.253805	-5.92
245707_at	NAC2-like protein	anac077	AT5G04400	-1.16	-0.21	-1.67	0.140742	0.253881	-5.92
252094_at	multicatalytic endopeptidase compl	PAD1	AT3G51260	1.22	0.29	1.67	0.140813	0.253988	-5.92
250114_s_a	AMP-binding protein	AAE5	AT5G16340	-1.24	-0.31	-1.67	0.140826	0.253993	-5.92
247090_at	putative protein similar to unknown	---	AT5G66370	-1.14	-0.19	-1.67	0.14095	0.254196	-5.92
267494_at	TCP1-chaperonin cofactor A isolog	KIS	AT2G30410	-1.15	-0.20	-1.67	0.140974	0.254219	-5.92
266730_at	putative RNA-binding protein	---	AT2G03110	-1.15	-0.20	-1.67	0.141011	0.254259	-5.92
246367_at	light repressible receptor protein ki	---	AT1G51880	-1.13	-0.18	-1.67	0.141019	0.254259	-5.92
256326_at	RING zinc-finger protein, putative c	---	AT3G02340	-1.18	-0.24	-1.67	0.141111	0.254406	-5.92
265557_at	unknown protein	---	---	-1.16	-0.21	-1.67	0.141172	0.254495	-5.92
244919_at	cytochrome c biogenesis orf203 Pro	---	AT2G07768	1.15	0.20	1.67	0.141191	0.254497	-5.92
251235_at	putative protein lysophospholipase	---	AT3G62860	-1.26	-0.34	-1.67	0.141195	0.254497	-5.92
264970_at	glyoxalase I, putative similar to glyo	---	AT1G67280	1.13	0.18	1.67	0.141277	0.254624	-5.92
249719_at	Expressed protein ; supported by fu	---	AT5G35735	1.48	0.57	1.67	0.141304	0.254643	-5.92
256722_at	hypothetical protein predicted by ge	---	AT2G34050	1.29	0.37	1.67	0.14131	0.254643	-5.92
257906_at	ribosomal protein, putative similar t	ATL5	AT3G25520	1.39	0.48	1.67	0.141364	0.25472	-5.92
260218_at	putative RING zinc finger protein c	---	AT1G74620	-1.11	-0.15	-1.67	0.14139	0.254734	-5.92
265540_at	Mutator-like transposase similar to	---	---	-1.12	-0.16	-1.67	0.141394	0.254734	-5.92
267112_at	putative adenosine phosphosulfate	APK	AT2G14750	-1.34	-0.42	-1.67	0.141465	0.254842	-5.92
258339_at	putative dynein light chain protein s	---	AT3G16120	-1.11	-0.16	-1.67	0.141504	0.25489	-5.92
245813_at	hypothetical protein contains simila	---	AT1G49920	-1.20	-0.27	-1.67	0.141514	0.25489	-5.92
265578_at	unknown protein	---	AT2G20100	-1.17	-0.23	-1.67	0.141534	0.254906	-5.92
253054_at	probable N-acetyltransferase hookl	HLS1	AT4G37580	1.13	0.18	1.67	0.141562	0.254936	-5.92
260945_at	hypothetical protein predicted by ge	---	AT1G05950	-1.16	-0.22	-1.66	0.141607	0.254988	-5.92
265780_at	Mutator-like transposase similar to	---	---	-1.14	-0.19	-1.66	0.141613	0.254988	-5.92

255526_at	hypothetical protein	---	AT4G02350	-1.17	-0.22	-1.66	0.141717	0.255156	-5.92
263389_at	putative retroelement pol polyprotei	---	---	-1.13	-0.18	-1.66	0.141771	0.255232	-5.92
259002_at	putative glutaredoxin similar to gluta	ROXY1	AT3G02000	-1.21	-0.28	-1.66	0.141876	0.255402	-5.93
250593_at	putative protein similar to unknown	---	AT5G07740	-1.12	-0.17	-1.66	0.14189	0.255407	-5.93
249050_at	cyclin-dependent protein kinase-like	---	AT5G44290	1.15	0.21	1.66	0.141935	0.255466	-5.93
253374_at	hypothetical protein ; supported by	---	AT4G33140	1.12	0.17	1.66	0.141945	0.255466	-5.93
263486_at	AP2 domain transcription factor	---	AT2G22200	-1.13	-0.18	-1.66	0.141998	0.255541	-5.93
247066_at	DNA binding protein-like	---	AT5G66940	-1.12	-0.16	-1.66	0.14203	0.255578	-5.93
266626_at	hypothetical protein predicted by ge	---	AT2G35360	1.20	0.27	1.66	0.142121	0.255711	-5.93
259129_at	unknown protein predicted by gens	PTF1	AT3G02150	-1.36	-0.44	-1.66	0.14213	0.255711	-5.93
265097_at	unknown protein	BARD1	AT1G04020	-1.23	-0.30	-1.66	0.142138	0.255711	-5.93
251193_at	translation releasing factor RF-1 -li	APG3	AT3G62910	-1.22	-0.28	-1.66	0.142175	0.255758	-5.93
251423_at	regulatory protein - like regulatory	CYCP3;2	AT3G60550	-1.18	-0.24	-1.66	0.142235	0.255846	-5.93
263611_at	hypothetical protein predicted by ge	---	AT2G16450	-1.12	-0.16	-1.66	0.142301	0.255938	-5.93
263914_at	unknown protein	AtGRF3	AT2G36400	-1.27	-0.35	-1.66	0.142309	0.255938	-5.93
259059_at	hypothetical protein	---	AT3G07300	1.14	0.19	1.66	0.142328	0.255952	-5.93
249489_at	acyltransferase -like protein antho	---	AT5G39090	1.18	0.24	1.66	0.14238	0.256026	-5.93
253503_at	cytochrome P450-like protein cytoc	CYP82C3	AT4G31950	1.27	0.35	1.66	0.142453	0.256138	-5.93
265108_s_a	similar to flavin-binding monooxyge	---	AT1G62620	-1.18	-0.24	-1.66	0.142476	0.256158	-5.93
248031_at	unknown protein ; supported by cD	---	AT5G55640	1.11	0.15	1.66	0.142534	0.256242	-5.93
263339_at	Mutator-like transposase similar to	---	---	1.10	0.14	1.66	0.142556	0.256261	-5.93
254149_at	putative protein hypothetical protei	---	AT4G24300	-1.20	-0.27	-1.66	0.142575	0.256267	-5.93
261118_at	protease, putative similar to SP:P3	---	AT1G75460	-1.15	-0.20	-1.66	0.142581	0.256267	-5.93
259709_at	Expressed protein ; supported by fu	---	AT1G77655	-1.16	-0.22	-1.66	0.142603	0.256285	-5.93
266146_at	En/Spm-like transposon protein rela	---	---	-1.12	-0.16	-1.66	0.142642	0.256336	-5.93
252306_at	hypothetical protein	---	AT3G49270	-1.11	-0.15	-1.66	0.14277	0.256538	-5.93
264602_at	putative Ser/Thr protein kinase simi	---	AT1G04700	-1.14	-0.19	-1.66	0.142777	0.256538	-5.93
249539_at	putative protein AtPP - Brassica na	---	AT5G38100	-1.17	-0.23	-1.66	0.142827	0.256607	-5.93
250465_at	putative protein various predicted p	---	AT5G10070	1.11	0.15	1.66	0.142865	0.256656	-5.93
260511_at	anthranilate phosphoribosyltransfe	---	AT1G51570	-1.21	-0.27	-1.66	0.143016	0.256906	-5.93
249665_at	unknown protein	---	AT5G35830	-1.16	-0.21	-1.66	0.143221	0.257254	-5.93
245023_at	PSII I protein	---	---	-1.26	-0.33	-1.66	0.143241	0.257269	-5.93
264738_at	unknown protein contains similarity	---	AT1G62250	-1.18	-0.23	-1.66	0.14344	0.257596	-5.94
260639_at	hypothetical protein predicted by ge	---	AT1G53180	1.39	0.48	1.66	0.143447	0.257596	-5.94
266753_at	auxin-induced protein (IAA20) ident	IAA20	AT2G46990	-1.13	-0.18	-1.66	0.143458	0.257596	-5.94

248936_at	heat shock transcription factor	RHA1	AT5G45710	-1.21	-0.27	-1.66	0.143468	0.257596	-5.94
247563_at	putative protein various predicted p	PDCB1	AT5G61130	1.19	0.25	1.66	0.14349	0.257615	-5.94
265115_at	rho GDP-dissociation inhibitor, puta	---	AT1G62450	-1.14	-0.19	-1.66	0.143531	0.257669	-5.94
255287_at	see T10M13.1 (GB:AF001308) simi	---	AT4G04660	-1.15	-0.20	-1.66	0.143553	0.257688	-5.94
258636_at	putative GTPase activator protein c	---	AT3G07890	-1.15	-0.20	-1.66	0.143608	0.257766	-5.94
249595_at	putative protein SIAH1 protein, Bra	---	AT5G37930	-1.20	-0.26	-1.65	0.143676	0.257868	-5.94
246732_at	putative protein hypothetical protei	---	AT5G27650	1.18	0.24	1.65	0.14372	0.257927	-5.94
245257_at	calmodulin ; supported by cDNA: gi	CAM8	AT4G14640	1.14	0.19	1.65	0.14375	0.25796	-5.94
245623_s_a	hypothetical protein	---	AT4G14096	1.13	0.18	1.65	0.143832	0.258087	-5.94
261267_at	unknown protein ;supported by full-	---	AT1G26750	-1.15	-0.21	-1.65	0.143856	0.258111	-5.94
258344_at	hypothetical protein similar to hypot	CEG	AT3G22650	-1.14	-0.18	-1.65	0.143884	0.258141	-5.94
249252_at	putative protein contains similarity t	---	AT5G42010	1.58	0.66	1.65	0.143946	0.25823	-5.94
265409_at	unknown protein	PIP2;8	AT2G16830	-1.15	-0.20	-1.65	0.143981	0.258274	-5.94
249949_at	SAE1-S9-protein - like SAE1-S9-pr	---	AT5G18880	-1.14	-0.19	-1.65	0.144034	0.258349	-5.94
261522_at	RIBOSOMAL PROTEIN, putative s	---	AT1G71710	-1.31	-0.39	-1.65	0.144101	0.258448	-5.94
247861_at	strong similarity to unknown protein	---	AT5G58160	-1.17	-0.23	-1.65	0.144161	0.258536	-5.94
258597_x_a	hypothetical protein predicted by ge	---	AT3G04390	1.12	0.16	1.65	0.14427	0.258704	-5.94
258490_at	hypothetical protein predicted by ge	---	AT3G02670	-1.13	-0.18	-1.65	0.144278	0.258704	-5.94
262838_at	major latex protein, putative similar	---	AT1G14960	-1.15	-0.20	-1.65	0.144291	0.258707	-5.94
257924_at	unknown protein	---	AT3G23190	-1.20	-0.26	-1.65	0.144367	0.258823	-5.94
263717_at	malate oxidoreductase (malic enzyr	---	AT2G13560	-1.11	-0.15	-1.65	0.14441	0.25888	-5.94
260691_s_a	hypothetical protein predicted by ge	---	---	-1.14	-0.19	-1.65	0.144458	0.258947	-5.94
250055_at	NADH-cytochrome b5 reductase ;s	ATCBR	AT5G17770	1.37	0.46	1.65	0.144476	0.258959	-5.94
247329_at	putative protein similar to unknown	---	AT5G64150	1.27	0.34	1.65	0.144489	0.25896	-5.94
262271_x_a	hypothetical protein predicted by ge	---	---	-1.25	-0.32	-1.65	0.144518	0.258993	-5.94
255447_at	hypothetical protein similar to A. th	---	AT4G02790	1.28	0.35	1.65	0.144665	0.259229	-5.94
250790_at	putative protein similar to unknown	---	AT5G05640	-1.22	-0.28	-1.65	0.144678	0.259229	-5.94
263063_s_a	putative peroxidase	---	AT2G18140	-1.23	-0.30	-1.65	0.144684	0.259229	-5.94
260014_at	hydroxypyruvate reductase (HPR) i	HPR	AT1G68010	-1.17	-0.22	-1.65	0.144713	0.25925	-5.94
262027_at	DNA-binding protein, putative simil	HOS10	AT1G35515	-1.28	-0.36	-1.65	0.144718	0.25925	-5.94
256131_at	bZIP transcription factor, putative s	AtbZIP58	AT1G13600	-1.18	-0.24	-1.65	0.144802	0.259375	-5.94
255730_at	dihydroflavonol 4-reductase, putati	---	AT1G25460	-1.13	-0.18	-1.65	0.144817	0.259375	-5.94
249378_at	putative protein microtubule-associ	---	AT5G40450	-1.22	-0.28	-1.65	0.144822	0.259375	-5.94
252712_at	glutathione transferase-like protein	ATGSTU27	AT3G43800	-1.27	-0.34	-1.65	0.144881	0.259459	-5.95
264114_at	hypothetical protein predicted by ge	CDT1A	AT2G31270	-1.35	-0.44	-1.65	0.144975	0.259608	-5.95

256325_at	hypothetical protein	---	AT3G02330	1.17	0.22	1.65	0.145064	0.259727	-5.95
246890_at	Expressed protein ; supported by cI	---	AT5G25410	-1.15	-0.21	-1.65	0.145065	0.259727	-5.95
246736_at	putative protein hypothetical protei	---	AT5G27560	-1.15	-0.20	-1.65	0.145116	0.259798	-5.95
249894_at	unknown protein ; supported by cD	---	AT5G22580	-5.77	-2.53	-1.65	0.14513	0.259803	-5.95
254505_at	Expressed protein ; supported by fu	---	AT4G19985	-1.21	-0.28	-1.65	0.145164	0.259844	-5.95
251850_at	F-box protein family, AtFBL17 cont	FBL17	AT3G54650	-1.21	-0.28	-1.65	0.145179	0.25985	-5.95
246369_at	light repressible receptor protein ki	---	AT1G51910	-1.18	-0.24	-1.65	0.145192	0.259854	-5.95
257645_at	unknown protein ;supported by full-	---	AT3G25790	-1.18	-0.24	-1.65	0.145226	0.259894	-5.95
247786_at	putative protein various predicted p	PMR5	AT5G58600	1.12	0.17	1.65	0.145248	0.259902	-5.95
245218_s_a	viral resistance protein, putative, 5'	---	AT1G58848	-1.11	-0.15	-1.65	0.145257	0.259902	-5.95
246111_at	putative protein	---	AT5G20170	-1.15	-0.20	-1.65	0.145265	0.259902	-5.95
265013_at	unknown protein similar to EST gb|	---	AT1G24460	-1.13	-0.18	-1.65	0.145289	0.259926	-5.95
260080_at	putative RNA-binding protein conta	APUM7	AT1G78160	-1.11	-0.16	-1.65	0.145309	0.25994	-5.95
255595_at	putative chitinase similar to peanut	---	AT4G01700	1.59	0.67	1.65	0.145367	0.260023	-5.95
253068_at	putative protein Kaposi's sarcoma-	---	AT4G37820	1.14	0.19	1.65	0.145396	0.260054	-5.95
256748_x_a	En/Spm transposon protein, putativ	---	---	-1.15	-0.20	-1.65	0.145422	0.260082	-5.95
257720_at	hypothetical protein similar to GB:A	---	AT3G18450	-1.16	-0.21	-1.65	0.145455	0.260119	-5.95
263304_at	hypothetical protein predicted by ge	---	AT2G01920	-1.14	-0.18	-1.65	0.145488	0.260159	-5.95
250209_at	putative protein similar to unknown	---	AT5G14030	1.19	0.25	1.65	0.145534	0.26022	-5.95
252756_s_a	putative protein hypothetical protein	---	AT1G58520	-1.13	-0.18	-1.65	0.145556	0.260239	-5.95
261467_at	unknown protein	VOZ1	AT1G28520	1.22	0.29	1.65	0.145644	0.260376	-5.95
254044_at	putative xyloglucan endo-1,4-beta-	XTR9	AT4G25820	-1.13	-0.18	-1.64	0.145692	0.260442	-5.95
251937_at	putative protein predicted protein, A	CPuORF46	AT3G53400	-1.52	-0.60	-1.64	0.145766	0.260553	-5.95
246110_at	putative protein predicted proteins -	---	AT5G20140	-1.23	-0.30	-1.64	0.145783	0.260563	-5.95
255202_at	putative polyprotein	---	---	-1.13	-0.18	-1.64	0.145811	0.260593	-5.95
267502_at	putative cytochrome P450	CYP76C4	AT2G45550	-1.13	-0.17	-1.64	0.145837	0.260619	-5.95
259026_at	putative protein kinase similar to hy	---	AT3G09240	-1.15	-0.21	-1.64	0.145982	0.260858	-5.95
266111_at	unknown protein	---	AT2G02060	-1.14	-0.19	-1.64	0.146054	0.260966	-5.95
267573_at	putative tropinone reductase	---	AT2G30670	-1.11	-0.15	-1.64	0.146074	0.260982	-5.95
256523_at	unknown protein ;supported by full-	---	AT1G66070	1.15	0.21	1.64	0.146094	0.260996	-5.95
261479_at	unknown protein ;supported by full-	IQD28	AT1G14380	1.22	0.29	1.64	0.146204	0.261173	-5.95
249018_at	CHP-rich zinc finger protein-like	---	AT5G44770	-1.22	-0.29	-1.64	0.146233	0.261204	-5.95
250889_at	putative protein exostose-related p	---	AT5G04500	-1.14	-0.19	-1.64	0.14626	0.261232	-5.95
264136_at	leucine-rich repeat transmembrane	SRF5	AT1G78980	-1.20	-0.27	-1.64	0.146273	0.261235	-5.95
245370_at	Expressed protein ; supported by fu	---	AT4G16840	1.29	0.37	1.64	0.146308	0.261276	-5.95

246969_at	glutamic acid-rich protein other glut	---	AT5G24880	-1.15	-0.21	-1.64	0.14638	0.261385	-5.95
266877_at	putative glucanase	AtGH9B12	AT2G44570	-1.14	-0.19	-1.64	0.146416	0.261428	-5.96
256095_at	hypothetical protein contains Pfam	---	AT1G13630	1.28	0.36	1.64	0.146435	0.261442	-5.96
260761_at	hypothetical protein predicted by ge	---	AT1G49150	1.24	0.31	1.64	0.146502	0.261523	-5.96
252835_at	putative protein several hypothetica	---	AT3G42060	-1.16	-0.21	-1.64	0.146503	0.261523	-5.96
252581_at	hypothetical protein	---	AT3G45500	-1.15	-0.21	-1.64	0.146685	0.261826	-5.96
247900_at	60S acidic ribosomal protein P3 ; s	---	AT5G57290	1.31	0.39	1.64	0.146766	0.261951	-5.96
261697_at	hypothetical protein identical to hyp	---	AT1G32610	-1.25	-0.32	-1.64	0.146894	0.262159	-5.96
259326_at	putative mitochondrial processing p	MPPalpha	AT3G16480	1.12	0.17	1.64	0.146954	0.262245	-5.96
267048_at	hypothetical protein predicted by ge	---	AT2G34200	1.20	0.26	1.64	0.147016	0.262318	-5.96
248087_at	unknown protein	---	AT5G55060	-1.11	-0.15	-1.64	0.147018	0.262318	-5.96
254082_at	glutamine cyclotransferase precurs	QC	AT4G25720	1.31	0.39	1.64	0.147095	0.262436	-5.96
244909_at	hypothetical protein	---	---	-1.14	-0.19	-1.64	0.147115	0.262448	-5.96
261329_at	hypothetical protein predicted by ge	---	AT1G44890	-1.15	-0.20	-1.64	0.147125	0.262448	-5.96
245427_at	putative protein	---	AT4G17550	1.20	0.26	1.64	0.147181	0.262517	-5.96
253541_at	putative protein various predicted p	---	AT4G31630	-1.12	-0.16	-1.64	0.147187	0.262517	-5.96
267267_at	putative cytochrome P450	CYP71B9	AT2G02580	1.14	0.19	1.64	0.147244	0.262599	-5.96
264733_at	phloem serpin-1, putative similar to	---	AT1G62170	-1.12	-0.16	-1.64	0.147318	0.26271	-5.96
245088_at	subtilisin-like serine protease conta	---	AT2G39850	-1.35	-0.43	-1.64	0.147356	0.262757	-5.96
257629_at	cellulase, putative contains Pfam p	---	AT3G26140	-1.15	-0.21	-1.64	0.147398	0.262811	-5.96
245970_at	beta-galactosidase ; supported by	BGAL7	AT5G20710	-1.17	-0.23	-1.64	0.147504	0.262968	-5.96
254611_at	Expressed protein ; supported by fu	---	AT4G19095	-1.13	-0.17	-1.64	0.147509	0.262968	-5.96
256616_at	hypothetical protein similar to unkno	---	AT3G22260	1.23	0.30	1.64	0.147531	0.262988	-5.96
252503_at	putative protein hypothetical protei	---	AT3G46910	-1.15	-0.20	-1.64	0.147556	0.263012	-5.96
247574_at	putative protein predicted protein, A	---	AT5G61228	1.14	0.19	1.64	0.14758	0.263017	-5.96
260502_at	putative Tub family protein contains	AtTLP6	AT1G47270	1.16	0.21	1.64	0.147582	0.263017	-5.96
264699_at	unknown protein ;supported by full-	---	AT1G69980	1.11	0.15	1.64	0.147598	0.263025	-5.96
246900_at	putative protein flavin-containing m	YUC6	AT5G25620	-1.19	-0.25	-1.64	0.147644	0.263085	-5.96
245014_at	ATPase beta subunit	---	---	-1.11	-0.15	-1.64	0.147656	0.263086	-5.96
252116_at	putative protein ;supported by full-l	---	AT3G51510	-1.17	-0.22	-1.64	0.147706	0.263156	-5.96
249918_at	putative protein predicted protein, A	---	AT5G19240	-1.51	-0.60	-1.64	0.147777	0.263246	-5.96
247190_at	D-type cyclin (emb|CAB41347.1) ;s	CYCD4;1	AT5G65420	-1.15	-0.20	-1.64	0.14778	0.263246	-5.96
261528_at	pectate lyase, putative similar to pe	AT59	AT1G14420	-1.15	-0.20	-1.63	0.147825	0.263305	-5.96
264272_at	hypothetical protein contains simila	ANAC023	AT1G60280	-1.11	-0.16	-1.63	0.147863	0.263352	-5.96
253229_at	putative protein ;supported by full-l	---	AT4G34660	-1.10	-0.14	-1.63	0.147898	0.263388	-5.96

250692_at	putative protein strong similarity to	---	AT5G06560	1.15	0.20	1.63	0.147906	0.263388	-5.96
258227_at	6-4 photolyase (UVR3) identical to	UVR3	AT3G15620	1.63	0.70	1.63	0.147943	0.263434	-5.96
258324_at	putative DNA binding protein identic	TSO1	AT3G22780	-1.12	-0.16	-1.63	0.14804	0.263586	-5.97
261633_at	hypothetical protein predicted by ge	---	AT1G49930	1.13	0.17	1.63	0.14806	0.2636	-5.97
260921_at	amp-binding protein, putative simila	---	AT1G21540	-1.23	-0.30	-1.63	0.1481	0.263651	-5.97
265881_at	hypothetical protein predicted by ge	---	AT2G42480	-1.15	-0.21	-1.63	0.148129	0.263683	-5.97
263159_at	RSH3 (RelA/SpoT homolog) identic	RSH3	AT1G54130	-1.19	-0.25	-1.63	0.148144	0.263688	-5.97
263227_at	Expressed protein ; supported by cl	---	AT1G30750	-1.16	-0.22	-1.63	0.148165	0.263698	-5.97
255581_at	putative transposon protein similar	---	---	-1.17	-0.23	-1.63	0.148173	0.263698	-5.97
257666_at	bactericidal permeability-increasing	---	AT3G20270	-1.25	-0.32	-1.63	0.148239	0.263796	-5.97
261458_at	unknown protein contains DNA-J dc	---	AT1G21080	-1.17	-0.23	-1.63	0.148252	0.263799	-5.97
257980_at	hypothetical protein predicted by ge	---	AT3G20760	-1.14	-0.19	-1.63	0.148274	0.263817	-5.97
247146_at	unknown protein	---	AT5G65610	-1.23	-0.30	-1.63	0.148291	0.263827	-5.97
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb	---	---	1.49	0.58	1.63	0.148315	0.263848	-5.97
252149_at	putative protein hypothetical protei	---	AT3G51290	-1.11	-0.16	-1.63	0.148388	0.263923	-5.97
249625_at	hypothetical protein ;supported by	---	AT5G37480	-1.13	-0.18	-1.63	0.148392	0.263923	-5.97
258294_at	hypothetical protein predicted by ge	---	AT3G23350	-1.14	-0.18	-1.63	0.148392	0.263923	-5.97
258332_at	putative transport protein similar to	---	AT3G16180	-1.43	-0.52	-1.63	0.148465	0.264033	-5.97
259281_at	putative Myb-related transcription fa	MYB106	AT3G01140	-1.15	-0.21	-1.63	0.148656	0.264351	-5.97
261721_at	unknown protein ; supported by cDI	---	AT1G08480	1.12	0.17	1.63	0.148709	0.264425	-5.97
248191_at	putative protein similar to unknown	---	AT5G54130	1.16	0.21	1.63	0.148728	0.264439	-5.97
263580_at	hypothetical protein similar to hypot	---	AT2G17140	1.15	0.20	1.63	0.148948	0.264751	-5.97
254925_at	beta-adaptin - like protein beta-ada	---	AT4G11380	-1.16	-0.21	-1.63	0.148949	0.264751	-5.97
261424_at	unknown protein	---	AT1G18700	1.11	0.15	1.63	0.14895	0.264751	-5.97
247377_at	pectate lyase ; supported by cDNA	---	AT5G63180	-2.70	-1.43	-1.63	0.14895	0.264751	-5.97
264651_at	putative histone H2A Strong simila	H2AXA	AT1G08880	1.25	0.33	1.63	0.149017	0.26485	-5.97
258154_at	unknown protein ; supported by cD	---	AT3G18210	1.17	0.23	1.63	0.149107	0.264988	-5.97
246839_at	putative protein	---	AT5G26720	1.15	0.20	1.63	0.149194	0.26511	-5.97
245424_at	putative protein	---	AT4G17505	-1.13	-0.18	-1.63	0.149206	0.26511	-5.97
259956_at	unknown protein ;supported by full-	RRA2	AT1G75110	1.13	0.18	1.63	0.149221	0.26511	-5.97
255531_at	hypothetical protein similar to orf o	---	AT4G02160	-1.14	-0.19	-1.63	0.149221	0.26511	-5.97
264936_at	hypothetical protein predicted by ge	EDA16	AT1G61140	1.12	0.17	1.63	0.149275	0.265184	-5.97
254929_at	putative protein mitochondrial carri	---	AT4G11440	-1.14	-0.19	-1.63	0.149291	0.265191	-5.97
248432_at	putative protein similar to unknown	---	AT5G51390	-1.35	-0.43	-1.63	0.149355	0.265248	-5.97
261045_at	pathogenesis related protein, putat	---	AT1G01310	-1.11	-0.15	-1.63	0.149357	0.265248	-5.97

262561_at	late embryogenesis abundant prote	---	AT1G34340	-1.14	-0.19	-1.63	0.149357	0.265248	-5.97
256297_at	cytochrome P450, putative contain	---	AT1G69500	1.17	0.22	1.63	0.149387	0.26528	-5.97
260484_at	putative zinc finger protein similar to	---	AT1G68360	-1.15	-0.20	-1.63	0.149404	0.26529	-5.97
255834_at	putative RNA-binding protein	---	AT2G33410	1.11	0.14	1.63	0.149484	0.26541	-5.97
252071_at	putative protein DNA helicase hom	---	AT3G51690	-1.10	-0.14	-1.63	0.149621	0.265615	-5.98
251582_at	putative protein CARBON CATABO	---	AT3G58580	-1.13	-0.18	-1.63	0.149622	0.265615	-5.98
254654_at	translation initiation factor eIF4E ;s	EIF4E	AT4G18040	1.15	0.20	1.63	0.149719	0.265765	-5.98
246169_at	putative protein predicted protein, h	---	AT5G32470	-1.15	-0.20	-1.63	0.149732	0.265768	-5.98
253641_at	hypothetical protein ;supported by f	---	AT4G29980	-1.16	-0.22	-1.63	0.149896	0.266038	-5.98
266496_at	putative zinc finger protein	---	---	-1.15	-0.20	-1.62	0.14991	0.266044	-5.98
262639_at	calmodulin, putative similar to calm	---	AT1G62820	-1.22	-0.29	-1.62	0.149938	0.266072	-5.98
247617_at	receptor like protein kinase recepto	---	AT5G60270	1.35	0.44	1.62	0.150053	0.266255	-5.98
253664_at	NADPH-ferrihemoprotein reductase	ATR2	AT4G30210	-1.48	-0.57	-1.62	0.150121	0.266352	-5.98
246504_at	hypothetical protein ;supported by	---	AT5G16160	-1.11	-0.14	-1.62	0.150131	0.266352	-5.98
248923_at	putative protein similar to unknown	atnudt11	AT5G45940	-1.20	-0.27	-1.62	0.150164	0.26639	-5.98
259538_at	putative serine/threonine kinase ; su	---	AT1G12310	-1.17	-0.23	-1.62	0.150176	0.26639	-5.98
253848_at	putative protein regulator protein, F	---	AT4G28020	1.19	0.25	1.62	0.150196	0.266406	-5.98
257692_at	hypothetical protein contains simila	---	AT3G12840	-1.12	-0.17	-1.62	0.150268	0.266512	-5.98
247204_at	GTP binding protein-like	AtRABH1a	AT5G64990	1.15	0.20	1.62	0.150308	0.266545	-5.98
246999_at	photoreceptor-interacting protein-lik	NPY3	AT5G67440	-1.28	-0.35	-1.62	0.15032	0.266545	-5.98
267575_at	unknown protein predicted by gens	---	AT2G30690	-1.14	-0.19	-1.62	0.150322	0.266545	-5.98
262165_at	putative acyl-CoA:1-acylglycerol-3-p	LPAT4	AT1G75020	1.24	0.32	1.62	0.150333	0.266545	-5.98
249921_at	reverse-transcriptase - like protein p	---	AT5G19270	-1.13	-0.18	-1.62	0.150375	0.266599	-5.98
258539_at	putative RNA-binding protein conta	---	AT3G06970	-1.12	-0.16	-1.62	0.150389	0.266602	-5.98
249172_at	putative protein similar to unknown	---	AT5G42950	1.15	0.20	1.62	0.150491	0.266762	-5.98
258491_at	unknown protein ;supported by full-	---	AT3G02700	-1.22	-0.28	-1.62	0.150539	0.266827	-5.98
247250_at	FAS2 (dbj|BAA77766.1) ; supporte	FAS2	AT5G64630	-1.23	-0.30	-1.62	0.150566	0.266844	-5.98
266415_at	putative nonspecific lipid-transfer pr	LTP2	AT2G38530	-1.85	-0.89	-1.62	0.150574	0.266844	-5.98
266379_at	1,4-beta-xylan endohydrolase	---	AT2G14690	-1.15	-0.20	-1.62	0.150584	0.266844	-5.98
248626_at	receptor protein kinase-like protein	---	AT5G48940	-1.13	-0.18	-1.62	0.150656	0.266951	-5.98
248425_at	ACC synthase; 1-aminocyclopropan	ACS12	AT5G51690	1.18	0.24	1.62	0.150724	0.267051	-5.98
254916_at	putative protein hypothetical protei	---	AT4G11340	-1.14	-0.19	-1.62	0.150755	0.267084	-5.98
256521_at	AMP-binding enzyme, putative con	---	AT1G66120	-1.13	-0.18	-1.62	0.150778	0.267093	-5.98
250919_at	putative protein myosin heavy chai	---	AT5G03660	1.17	0.22	1.62	0.150783	0.267093	-5.98
264609_at	unknown protein ;supported by full-	---	AT1G04530	1.28	0.35	1.62	0.1508	0.267102	-5.98

265640_at	putative cysteine proteinase	---	AT2G27395	-1.11	-0.15	-1.62	0.150859	0.267153	-5.98
251296_at	putative protein paladin - Mus mus	---	AT3G62010	-1.15	-0.20	-1.62	0.150862	0.267153	-5.98
259240_at	unknown protein ; supported by cD	---	AT3G11590	-1.19	-0.26	-1.62	0.150863	0.267153	-5.98
250288_at	auxin-responsive - like protein Nt-g	---	AT5G13350	-1.15	-0.20	-1.62	0.150906	0.267207	-5.98
259747_at	putative dehydrogenase similar to D	---	AT1G71170	1.16	0.21	1.62	0.150919	0.26721	-5.98
256422_at	unknown protein	MOS2	AT1G33520	1.14	0.19	1.62	0.151021	0.267351	-5.98
251468_at	epsin-like protein Af10-protein - Av	---	AT3G59290	1.14	0.19	1.62	0.151022	0.267351	-5.98
245299_at	ras-related small GTP-binding prote	ATRAB1C	AT4G17530	-1.19	-0.25	-1.62	0.151106	0.267466	-5.98
256502_at	Eukaryotic translation initiation fact	---	AT1G36730	1.20	0.26	1.62	0.15112	0.267466	-5.98
267144_at	unknown protein	GPAT6	AT2G38110	1.36	0.45	1.62	0.151122	0.267466	-5.98
256898_at	abscisic acid-insensitive protein 3 i	ABI3	AT3G24650	-1.12	-0.17	-1.62	0.151149	0.267493	-5.98
266342_at	hypothetical protein predicted by gr	---	AT2G01540	1.20	0.26	1.62	0.151222	0.2676	-5.99
257902_at	receptor kinase, putative similar to	---	AT3G28450	1.24	0.31	1.62	0.151314	0.267743	-5.99
255270_at	putative protein (ubiquitin like) to va	---	AT4G05250	-1.11	-0.15	-1.62	0.151349	0.267772	-5.99
245590_at	hypothetical protein	---	AT4G15060	-1.13	-0.18	-1.62	0.151354	0.267772	-5.99
249904_at	unknown protein	---	AT5G22700	-1.13	-0.18	-1.62	0.151437	0.267888	-5.99
263996_at	unknown protein	---	AT2G22530	-1.16	-0.21	-1.62	0.151443	0.267888	-5.99
264459_at	putative reverse transcriptase simila	---	---	-1.23	-0.29	-1.62	0.151529	0.268019	-5.99
245774_at	hypothetical protein contains simila	TCP24	AT1G30210	-1.12	-0.17	-1.62	0.151577	0.268083	-5.99
259905_s_a	hypothetical protein predicted by ge	---	AT1G74130	-1.10	-0.14	-1.62	0.151667	0.268221	-5.99
258961_at	hypothetical protein similar to myb-	---	AT3G10580	1.11	0.15	1.62	0.151698	0.268252	-5.99
256388_at	unknown protein	---	AT3G06180	-1.14	-0.19	-1.62	0.151717	0.268252	-5.99
264105_x_a	hypothetical protein	---	AT2G13760	-1.16	-0.21	-1.62	0.151725	0.268252	-5.99
257910_at	hypothetical protein similar to hypot	---	AT3G25580	-1.16	-0.22	-1.62	0.151731	0.268252	-5.99
249712_at	eIF4Eiso protein (emb|CAA71579.1	LSP1	AT5G35620	1.20	0.26	1.62	0.151754	0.268272	-5.99
258006_at	cysteine proteinase non-consensus	---	AT3G19400	1.20	0.26	1.62	0.151822	0.268359	-5.99
251030_at	putative protein kinesin light chain	NDP1	AT5G02130	1.21	0.28	1.62	0.151832	0.268359	-5.99
256047_at	hypothetical protein predicted by ge	---	AT1G07060	-1.16	-0.22	-1.62	0.151838	0.268359	-5.99
262734_at	lipase, putative similar to lipase GE	---	AT1G28640	-1.12	-0.17	-1.62	0.151871	0.268364	-5.99
254090_at	MtN3 - like protein MtN3 (induced	---	AT4G25010	-1.17	-0.22	-1.62	0.151876	0.268364	-5.99
253073_at	cytochrome P450 monooxygenase	CYP81F4	AT4G37410	-1.16	-0.22	-1.62	0.151877	0.268364	-5.99
259874_at	unknown protein	---	AT1G76660	-1.20	-0.26	-1.62	0.151897	0.268378	-5.99
255284_at	5-adenylylsulfate reductase ;suppo	אפר-01	AT4G04610	1.54	0.62	1.62	0.151937	0.268428	-5.99
254648_at	lipase-like protein Pn47p, Ipomoea	---	AT4G18550	-1.13	-0.17	-1.62	0.151956	0.268435	-5.99
258610_at	IAA-amino acid hydrolase (ILR1) id	ILR1	AT3G02875	1.26	0.34	1.62	0.151964	0.268435	-5.99

266009_at	putative kinesin heavy chain	---	AT2G37420	1.14	0.18	1.61	0.152131	0.268709	-5.99
249376_at	Expressed protein ; supported by fu	---	AT5G40645	-1.11	-0.14	-1.61	0.152329	0.269038	-5.99
246025_at	zwille/pinhead-like protein GERp95	---	AT5G21150	-1.18	-0.23	-1.61	0.152349	0.269053	-5.99
265519_at	hypothetical protein	---	AT2G06040	1.13	0.18	1.61	0.15237	0.269069	-5.99
251990_at	putative protein MICRONUCLEAR	---	AT3G53320	-1.21	-0.28	-1.61	0.152385	0.269075	-5.99
255697_at	hypothetical protein	---	AT4G00130	-1.19	-0.25	-1.61	0.152435	0.269141	-5.99
261321_at	hypothetical protein predicted by ge	---	AT1G44740	-1.14	-0.19	-1.61	0.152446	0.269141	-5.99
255103_at	putative phosphoglyceride transfer	---	AT4G08690	-1.13	-0.18	-1.61	0.152507	0.269227	-5.99
249513_at	glucosyltransferase-like protein ; su	---	AT5G38460	-1.13	-0.18	-1.61	0.152547	0.269277	-5.99
252146_at	putative protein steroid sulfotransfe	---	AT3G51210	-1.11	-0.15	-1.61	0.152567	0.269277	-5.99
253342_at	Expressed protein ; supported by cl	PAA1	AT4G33520	-1.35	-0.43	-1.61	0.152571	0.269277	-5.99
259279_at	putative cystathionine gamma-synth	MTO1	AT3G01120	-1.13	-0.18	-1.61	0.152618	0.26934	-5.99
257526_s_a	hypothetical protein similar to putati	---	AT3G09330	-1.12	-0.16	-1.61	0.152722	0.269502	-5.99
262615_at	initiation factor 5A-4 identical to initi	ELF5A-1	AT1G13950	1.17	0.23	1.61	0.152747	0.269526	-5.99
262391_at	geranyl geranyl pyrophosphate syr	GGPS6	AT1G49530	-1.15	-0.20	-1.61	0.152791	0.269573	-5.99
261732_at	hypothetical protein predicted by ge	---	AT1G47770	-1.14	-0.19	-1.61	0.152797	0.269573	-5.99
AFFX-BioDr	E. coli /GEN=bioD /DB_XREF=gb:J	---	---	-1.36	-0.44	-1.61	0.152913	0.269732	-6.00
265949_at	putative vicilin storage protein (glob	---	AT2G18540	1.11	0.15	1.61	0.152921	0.269732	-6.00
245586_at	hypothetical protein	---	AT4G14980	-1.13	-0.18	-1.61	0.152923	0.269732	-6.00
257874_at	hypothetical protein	---	AT3G17110	-1.15	-0.20	-1.61	0.152964	0.269772	-6.00
261955_at	proteasome regulatory subunit, put	RPN12a	AT1G64520	1.12	0.16	1.61	0.152969	0.269772	-6.00
253080_at	hypothatical protein	---	---	-1.13	-0.17	-1.61	0.153003	0.269797	-6.00
245301_at	farnesyl-pyrophosphate synthetase	FPS2	AT4G17190	-1.30	-0.37	-1.61	0.153007	0.269797	-6.00
263144_at	unknown protein similar to putative	---	AT1G54070	-1.16	-0.22	-1.61	0.153047	0.269846	-6.00
257915_at	superman protein identical to super	SUP	AT3G23130	-1.16	-0.21	-1.61	0.153125	0.269962	-6.00
259001_at	hypothetical protein predicted by ge	---	AT3G01960	1.42	0.51	1.61	0.153178	0.270036	-6.00
263554_at	putative Ta11-like non-LTR retroele	---	---	-1.25	-0.33	-1.61	0.153214	0.270074	-6.00
267043_at	unknown protein	---	AT2G34330	-1.15	-0.20	-1.61	0.153223	0.270074	-6.00
253418_at	putative protein tom-1B protein, Ga	---	AT4G32760	-1.12	-0.16	-1.61	0.153379	0.270326	-6.00
252402_s_a	putative protein predicted proteins,	---	AT3G48050	1.12	0.16	1.61	0.153422	0.270382	-6.00
261181_at	monosaccharide transporter, putati	---	AT1G34580	-1.17	-0.23	-1.61	0.153607	0.270687	-6.00
263698_at	hypothetical protein similar to a mu	---	---	-1.17	-0.23	-1.61	0.153636	0.27071	-6.00
261865_at	sterol delta7 reductase identical to (	DWF5	AT1G50430	-1.23	-0.30	-1.61	0.153644	0.27071	-6.00
250667_at	40S ribosomal protein S4 ;supporte	---	AT5G07090	1.31	0.39	1.61	0.153655	0.27071	-6.00
265068_at	hypothetical protein Similar to Kines	---	AT1G55550	1.12	0.16	1.61	0.153697	0.270762	-6.00

258235_at	alternative oxidase 1c precursor ide	AOX1C	AT3G27620	-1.15	-0.20	-1.61	0.15373	0.2708	-6.00
251573_at	phenylalanine-tRNA synthetase-lik	---	AT3G58140	-1.15	-0.20	-1.61	0.153746	0.270806	-6.00
258057_at	unknown protein	AAR3	AT3G28970	1.12	0.16	1.61	0.153844	0.270959	-6.00
260586_at	unknown protein predicted by gene	---	AT2G43630	1.15	0.20	1.61	0.154027	0.271261	-6.00
262418_at	thioredoxin, putative similar to thior	ATHX	AT1G50320	-1.22	-0.28	-1.61	0.154077	0.271326	-6.00
248316_at	putative protein similar to unknown	---	AT5G52670	-1.19	-0.25	-1.61	0.154109	0.271363	-6.00
267402_at	putative SF16 protein {Helianthus a	IQD6	AT2G26180	-1.19	-0.26	-1.61	0.15413	0.271379	-6.00
246023_at	ethylene-insensitive3-like2 (EIL2)	EIL2	AT5G21120	-1.13	-0.18	-1.61	0.154149	0.271391	-6.00
255039_at	calmodulin-domain protein kinase C	CPK4	AT4G09570	1.16	0.21	1.60	0.154266	0.271576	-6.00
256315_at	hypothetical protein predicted by ge	---	AT1G35880	-1.13	-0.17	-1.60	0.154377	0.271743	-6.00
251168_at	putative protein several hypothetica	---	AT3G63370	-1.16	-0.21	-1.60	0.154388	0.271743	-6.00
246625_at	hypothetical protein predicted by ge	---	AT1G48880	-1.14	-0.19	-1.60	0.154398	0.271743	-6.00
250965_at	putative protein various predicted p	---	AT5G03020	-1.12	-0.16	-1.60	0.154409	0.271743	-6.00
245995_at	putative protein various predicted p	---	---	-1.20	-0.26	-1.60	0.154481	0.271844	-6.01
248782_at	palmitoyl-protein thioesterase precu	---	AT5G47340	-1.14	-0.19	-1.60	0.154501	0.271844	-6.01
249698_at	unknown protein	MIS12	AT5G35520	-1.20	-0.26	-1.60	0.154513	0.271844	-6.01
245418_at	putative protein	---	AT4G17370	1.19	0.25	1.60	0.154514	0.271844	-6.01
246456_at	telomerase reverse transcriptase ;	ATTERT	AT5G16850	-1.12	-0.16	-1.60	0.154537	0.271863	-6.01
255246_at	putative protein hypothetical protei	---	---	-1.16	-0.22	-1.60	0.154631	0.272008	-6.01
254768_at	hypothetical protein	---	AT4G13320	-1.15	-0.21	-1.60	0.154716	0.272137	-6.01
245340_at	elicitor like protein ; supported by fu	---	AT4G14420	1.21	0.28	1.60	0.154775	0.27222	-6.01
263613_at	unknown protein	---	AT2G25250	-1.30	-0.38	-1.60	0.154791	0.272226	-6.01
256689_at	hypothetical protein predicted by ge	---	AT3G32150	-1.12	-0.16	-1.60	0.154907	0.272397	-6.01
260998_at	CAF protein similar to C2H2 zinc fir	---	AT1G26590	-1.14	-0.18	-1.60	0.154912	0.272397	-6.01
249232_at	dynamin-like protein (pir||S59558)	ADL1	AT5G42080	1.20	0.26	1.60	0.154938	0.272423	-6.01
263367_at	putative retroelement pol polyprotei	---	---	-1.15	-0.21	-1.60	0.154972	0.272447	-6.01
265473_at	Expressed protein ; supported by fu	LCR10	AT2G15535	-1.14	-0.19	-1.60	0.154976	0.272447	-6.01
247789_at	putative protein various predicted p	---	AT5G58680	-1.16	-0.21	-1.60	0.155009	0.272484	-6.01
259654_at	hypothetical protein predicted by ge	---	AT1G55220	-1.15	-0.20	-1.60	0.155038	0.272513	-6.01
251629_at	villin 3 fragment ; supported by cDI	VLN3	AT3G57410	1.18	0.24	1.60	0.155095	0.272594	-6.01
265651_at	hypothetical protein predicted by ge	---	AT2G13900	1.12	0.17	1.60	0.155168	0.2727	-6.01
260286_at	putative acetylornithine transaminas	WIN1	AT1G80600	1.17	0.23	1.60	0.155199	0.272735	-6.01
247011_at	putative protein contains similarity t	FRO1	AT5G67590	1.24	0.31	1.60	0.155219	0.272748	-6.01
261693_at	hypothetical protein similar to hypot	DCP1	AT1G08370	1.11	0.15	1.60	0.155261	0.272801	-6.01
250514_at	GDP dissociation inhibitor GDP dis	---	AT5G09550	-1.12	-0.17	-1.60	0.155311	0.272867	-6.01

257057_at	hypothetical protein predicted by ge	---	---	-1.10	-0.13	-1.60	0.155384	0.272975	-6.01
248804_at	nodulin-like protein	---	AT5G47470	-1.14	-0.19	-1.60	0.155413	0.273005	-6.01
264543_at	hypothetical protein predicted by ge	---	AT1G55780	1.17	0.23	1.60	0.155473	0.273051	-6.01
259465_at	hypothetical protein similar to putati	---	AT1G19025	-1.15	-0.20	-1.60	0.155474	0.273051	-6.01
253283_at	hypothetical protein ; supported by	---	AT4G34090	-1.20	-0.27	-1.60	0.155475	0.273051	-6.01
265556_at	putative Athila retroelement ORF1-l	---	---	-1.14	-0.19	-1.60	0.155636	0.273313	-6.01
245142_at	putative O-sialoglycoprotein endope	---	AT2G45270	-1.14	-0.19	-1.60	0.155649	0.273315	-6.01
250051_at	MYB56 R2R3-MYB factor family me	AtMYB56	AT5G17800	-1.18	-0.24	-1.60	0.155716	0.273411	-6.01
245029_at	hypothetical protein predicted by ge	YAB5	AT2G26580	-1.36	-0.44	-1.60	0.155853	0.273618	-6.01
254021_at	putative protein cell death suppres	ACD1-LIKE	AT4G25650	-1.16	-0.22	-1.60	0.155858	0.273618	-6.01
258010_at	unknown protein similar to receptor	---	AT3G19300	-1.12	-0.17	-1.60	0.155884	0.273634	-6.01
250488_at	beta-glucosidase - like protein beta	---	AT5G09700	-1.13	-0.18	-1.60	0.155891	0.273634	-6.01
248688_at	indole-3-glycerol phosphate syntha	---	AT5G48220	-1.19	-0.25	-1.60	0.155944	0.273706	-6.01
247039_at	putative protein contains similarity t	ATEB1C	AT5G67270	-1.19	-0.25	-1.60	0.155974	0.273737	-6.01
247485_at	putative protein ARR1, Arabidopsis	ARR23	AT5G62120	-1.11	-0.15	-1.60	0.156078	0.273899	-6.01
253420_at	H+-transporting ATP synthase cha	---	AT4G32260	-1.16	-0.21	-1.60	0.156168	0.274031	-6.02
248347_at	putative protein contains similarity t	---	AT5G52250	-1.11	-0.16	-1.60	0.156177	0.274031	-6.02
245587_at	putative protein	---	AT4G15020	1.25	0.32	1.60	0.156237	0.274096	-6.02
254396_at	peptide transporter - like protein pe	---	AT4G21680	1.94	0.95	1.60	0.156239	0.274096	-6.02
266102_at	unknown protein	---	AT2G40720	1.14	0.19	1.60	0.156263	0.274119	-6.02
266376_at	putative endoxyloglucan glycosyltra	---	AT2G14620	-1.18	-0.23	-1.60	0.156302	0.274165	-6.02
246554_at	HSP100/ClpB, putative similar to H	CLPB3	AT5G15450	1.15	0.20	1.60	0.156314	0.274165	-6.02
262894_at	disease resistance protein, putative	---	AT1G59780	-1.15	-0.20	-1.59	0.156562	0.274579	-6.02
262739_at	lipase, putative contains Pfam prof	---	AT1G28650	1.25	0.33	1.59	0.15671	0.274818	-6.02
266099_at	putative alpha-carboxyltransferase	CAC3	AT2G38040	-1.20	-0.26	-1.59	0.156808	0.274969	-6.02
262142_at	hypothetical protein predicted by ge	---	AT1G52640	1.15	0.20	1.59	0.156842	0.275007	-6.02
259290_at	putative cyclin similar to cyclin cyc1	CYCB1;3	AT3G11520	-1.20	-0.26	-1.59	0.156902	0.27509	-6.02
266468_at	unknown protein ; supported by cDI	---	AT2G47960	1.16	0.21	1.59	0.15701	0.275259	-6.02
259250_at	unknown protein	---	AT3G07580	-1.22	-0.29	-1.59	0.157052	0.275312	-6.02
256608_at	hypothetical protein predicted by ge	---	AT3G30840	-1.10	-0.14	-1.59	0.157079	0.275321	-6.02
256619_at	hypothetical protein predicted by ge	---	AT3G24460	-1.13	-0.17	-1.59	0.157082	0.275321	-6.02
256258_at	unknown protein	NF-YC11	AT3G12480	1.11	0.15	1.59	0.157119	0.275346	-6.02
258314_at	putative RAS-related GTP-binding p	ATRABG3(	AT3G16100	1.15	0.20	1.59	0.15712	0.275346	-6.02
247764_at	subtilisin-like serine protease conta	---	AT5G59190	-1.14	-0.19	-1.59	0.157149	0.275376	-6.02
264359_at	hypothetical protein predicted by ge	---	AT1G03320	-1.15	-0.21	-1.59	0.157256	0.275531	-6.02

249304_at	folylpolyglutamate synthase-like pro	GLA1	AT5G41480	1.19	0.25	1.59	0.157266	0.275531	-6.02
249465_at	AIG2 - like protein AIG2, Arabidops	AIG2L	AT5G39720	-1.15	-0.20	-1.59	0.157274	0.275531	-6.02
251238_at	putative protein several hypothetica	---	AT3G62430	1.15	0.21	1.59	0.157303	0.275561	-6.02
259555_at	hypothetical protein	---	---	-1.12	-0.17	-1.59	0.157334	0.275594	-6.02
261338_at	hypothetical protein predicted by ge	---	AT1G44920	-1.16	-0.22	-1.59	0.157371	0.275639	-6.02
265242_at	hypothetical protein	---	AT2G07705	1.25	0.33	1.59	0.157473	0.275795	-6.02
255939_at	hypothetical protein predicted by ge	---	AT1G12730	1.20	0.27	1.59	0.157502	0.275824	-6.02
267415_at	putative translation initiation factor e	---	AT2G34970	1.11	0.15	1.59	0.157513	0.275824	-6.02
263293_x_a	hypothetical protein similar to hypot	---	---	-1.12	-0.16	-1.59	0.157549	0.275866	-6.02
258131_at	protein kinase, putative similar to G	---	AT3G24540	-1.19	-0.25	-1.59	0.157571	0.275882	-6.02
251977_at	putative protein auxin-induced prot	---	AT3G53250	-1.11	-0.15	-1.59	0.157607	0.275925	-6.02
249010_at	unknown protein ; supported by cD	---	AT5G44580	1.25	0.32	1.59	0.157632	0.275947	-6.02
255737_at	unknown protein ;supported by full-	---	AT1G25420	-1.14	-0.20	-1.59	0.157705	0.276043	-6.02
264366_at	unknown protein EST gb|N96383 c	---	AT1G03250	1.18	0.23	1.59	0.157719	0.276043	-6.02
264430_at	cineole synthase, putative similar t	TPS14	AT1G61680	1.13	0.17	1.59	0.157723	0.276043	-6.02
265641_at	putative RNA-binding glycine rich p	---	AT2G27330	1.16	0.21	1.59	0.157891	0.276315	-6.03
245628_at	anthocyanin2, putative similar to ar	PAP1	AT1G56650	1.22	0.29	1.59	0.15807	0.276608	-6.03
248506_at	adenylate kinase ;supported by full	---	AT5G50370	1.39	0.48	1.59	0.158153	0.276732	-6.03
265224_at	putative pectinesterase	---	AT2G36710	-1.13	-0.18	-1.59	0.158215	0.276819	-6.03
248009_at	transcription factor-like; similar to C	CSN6A	AT5G56280	-1.13	-0.18	-1.59	0.158325	0.27694	-6.03
267275_at	putative Na H antiporter	ATCHX13	AT2G30240	-1.18	-0.23	-1.59	0.15836	0.27694	-6.03
250276_at	putative protein mRNA, Moritella m	---	AT5G13030	1.14	0.18	1.59	0.158369	0.27694	-6.03
248476_at	putative protein similar to unknown	---	AT5G50890	-1.32	-0.40	-1.59	0.158384	0.27694	-6.03
265855_at	unknown protein ;supported by full-	---	AT2G42390	1.12	0.16	1.59	0.158391	0.27694	-6.03
248577_at	myrosinase binding protein-like ; su	---	AT5G49870	-1.11	-0.15	-1.59	0.158395	0.27694	-6.03
258941_at	putative monodehydroascorbate re	MDHAR	AT3G09940	-2.62	-1.39	-1.59	0.158396	0.27694	-6.03
258075_at	homocysteine S-methyltransferase	HMT-1	AT3G25900	1.82	0.86	1.59	0.158401	0.27694	-6.03
249751_at	putative protein similar to unknown	---	AT5G24650	1.17	0.23	1.59	0.158402	0.27694	-6.03
247242_at	unknown protein	---	AT5G64690	-1.11	-0.16	-1.59	0.158414	0.27694	-6.03
261031_at	hypothetical protein predicted by ge	---	AT1G17360	-1.28	-0.36	-1.59	0.158429	0.27694	-6.03
259978_at	putative cell division control protein	CDKB2;1	AT1G76540	-1.22	-0.28	-1.59	0.15843	0.27694	-6.03
258233_at	hypothetical protein contains simila	MYB118	AT3G27785	-1.14	-0.19	-1.59	0.158446	0.276946	-6.03
249165_at	putative protein similar to unknown	ATIPK1	AT5G42810	-1.20	-0.27	-1.59	0.158489	0.277	-6.03
247515_at	ABC family transporter - like protei	ATH14	AT5G61740	-1.11	-0.14	-1.59	0.158539	0.277067	-6.03
249113_at	putative protein similar to unknown	---	AT5G43790	1.19	0.25	1.58	0.158745	0.277406	-6.03

255589_s_a	hypothetical protein	---	AT4G01590	1.20	0.27	1.58	0.158795	0.277471	-6.03
256517_at	PHD-finger protein, putative contai	MMD1	AT1G66170	-1.11	-0.15	-1.58	0.15886	0.277563	-6.03
251090_at	putative protein ACR1-protein - Sa	---	AT5G01340	1.45	0.54	1.58	0.158913	0.277635	-6.03
263726_at	putative ABC transporter ;supporte	---	AT2G13610	-1.75	-0.81	-1.58	0.158926	0.277637	-6.03
247260_at	putative protein contains similarity t	---	AT5G64500	-1.20	-0.26	-1.58	0.159097	0.277914	-6.03
265176_at	OBP32pep protein, putative identic	---	AT1G23520	-1.12	-0.17	-1.58	0.159111	0.277918	-6.03
265262_at	putative chloroplast nucleoid DNA b	---	AT2G42980	1.17	0.23	1.58	0.159159	0.277979	-6.03
249804_at	galactinol synthase	AtGolS5	AT5G23790	-1.12	-0.16	-1.58	0.159198	0.278026	-6.03
254354_at	hypothetical protein	---	AT4G22370	-1.10	-0.14	-1.58	0.159261	0.278105	-6.03
247973_at	putative protein contains similarity t	---	AT5G56770	-1.12	-0.17	-1.58	0.159267	0.278105	-6.03
254882_s_a	putative protein various predicted r	---	---	-1.12	-0.17	-1.58	0.15933	0.278194	-6.03
263151_at	hypothetical protein predicted by ge	---	AT1G54120	1.38	0.47	1.58	0.159436	0.278357	-6.03
249288_at	unknown protein ;supported by full-	---	AT5G41050	1.47	0.55	1.58	0.15952	0.278457	-6.03
245114_at	transcription factor IIB (TFIIB) ident	TFIIB	AT2G41630	-1.24	-0.31	-1.58	0.15953	0.278457	-6.03
257212_at	zinc-binding dehydrogenase, putat	---	AT3G15090	1.19	0.25	1.58	0.15953	0.278457	-6.03
259274_at	putative homeobox-leucine zipper	ATHB20	AT3G01220	-1.12	-0.17	-1.58	0.159632	0.278614	-6.04
257642_at	putative HLH DNA-binding protein c	BHLH32	AT3G25710	-1.17	-0.23	-1.58	0.159654	0.278631	-6.04
256915_at	unknown protein	---	AT3G23900	1.16	0.21	1.58	0.159696	0.278682	-6.04
247711_at	receptor-like protein kinase recepto	---	AT5G59270	-1.14	-0.19	-1.58	0.159716	0.278687	-6.04
261609_at	unknown protein similar to MAP3K-	---	AT1G49740	-1.23	-0.30	-1.58	0.159723	0.278687	-6.04
261863_at	unknown protein ; supported by cDI	---	AT1G50630	-1.18	-0.24	-1.58	0.159735	0.278687	-6.04
251271_at	hypothetical protein ; supported by	---	AT3G62050	-1.19	-0.25	-1.58	0.159756	0.278702	-6.04
250579_at	putative protein terminal ear1, Zea	MCT2	AT5G07930	-1.12	-0.17	-1.58	0.159782	0.278727	-6.04
267439_at	putative GDSL-motif lipase/hydrolas	---	AT2G19060	-1.15	-0.20	-1.58	0.159858	0.278827	-6.04
261217_at	hypothetical protein contains simila	UBP11	AT1G32850	-1.11	-0.15	-1.58	0.159864	0.278827	-6.04
262320_at	hypothetical protein predicted by ge	---	AT1G27550	-1.13	-0.18	-1.58	0.15988	0.278833	-6.04
262123_at	hypothetical protein predicted by ge	---	AT1G59630	-1.16	-0.21	-1.58	0.159935	0.278909	-6.04
265566_at	hypothetical protein predicted by ge	---	AT2G05600	-1.15	-0.20	-1.58	0.159959	0.278929	-6.04
257079_at	unknown protein	---	AT3G15240	-1.12	-0.16	-1.58	0.16	0.278978	-6.04
258242_at	hypothetical protein predicted by ge	---	AT3G27640	-1.13	-0.17	-1.58	0.16005	0.279045	-6.04
246560_at	putative protein hypothetical protein	---	AT5G15560	-1.12	-0.17	-1.58	0.160067	0.279046	-6.04
255881_at	phosphomannose isomerase, puta	DIN9	AT1G67070	1.48	0.56	1.58	0.160082	0.279046	-6.04
255001_at	AIG1-like protein AIG1 - Arabidops	---	AT4G09930	-1.17	-0.23	-1.58	0.160087	0.279046	-6.04
262829_at	auxin-independent growth promote	---	AT1G14970	-1.26	-0.33	-1.58	0.16015	0.279127	-6.04
266133_at	putative C2H2-type zinc finger prote	---	AT2G45120	1.13	0.17	1.58	0.160158	0.279127	-6.04

263830_at	hypothetical protein predicted by ge	---	AT2G40260	-1.13	-0.18	-1.58	0.160191	0.279162	-6.04
255031_at	putative proteins various hypothetic	---	AT4G09490	1.18	0.23	1.58	0.160356	0.279428	-6.04
256735_at	hypothetical protein predicted by ge	ATEXO70E	AT3G29400	1.16	0.22	1.58	0.16039	0.279467	-6.04
253429_at	putative protein CDC28/cdc2-like k	---	AT4G32420	1.13	0.18	1.58	0.160403	0.279468	-6.04
253895_at	NWMU3 - 2S albumin 3 precursor	AT2S3	AT4G27160	-1.11	-0.16	-1.58	0.160479	0.279579	-6.04
248160_at	putative protein similar to unknown	---	AT5G54470	-1.20	-0.26	-1.58	0.160527	0.279642	-6.04
259579_at	P-glycoprotein, putative similar to F	PGP14	AT1G28010	-1.56	-0.65	-1.58	0.16058	0.279713	-6.04
260953_at	transcriptional activator RF2a, puta	---	AT1G06070	-1.14	-0.19	-1.58	0.16062	0.27976	-6.04
264659_at	unknown protein Similar to S. pomb	ATOPT2	AT1G09930	-1.12	-0.17	-1.58	0.160648	0.279789	-6.04
254062_at	putative protein zinc finger protein	---	AT4G25380	1.55	0.64	1.58	0.160778	0.279993	-6.04
266316_at	unknown protein ; supported by cD	---	AT2G27080	-1.85	-0.89	-1.58	0.160809	0.280005	-6.04
262548_at	unknown protein contains similarity	AGO2	AT1G31280	-1.16	-0.21	-1.58	0.16081	0.280005	-6.04
247878_at	unknown protein	---	AT5G57760	-2.91	-1.54	-1.58	0.160829	0.280018	-6.04
264717_at	hypothetical protein predicted by ge	ATFH8	AT1G70140	1.29	0.37	1.58	0.160854	0.280039	-6.04
265185_at	OBP32pep protein, putative identic	---	AT1G23670	-1.15	-0.20	-1.58	0.160874	0.280054	-6.04
249163_at	glucose-6-phosphate isomerase, c	---	AT5G42740	1.18	0.24	1.57	0.160984	0.280223	-6.04
263069_at	unknown protein	---	AT2G17590	-1.27	-0.35	-1.57	0.16101	0.280247	-6.04
249992_at	AP2 domain -like protein AP2/ERE	PUCHI	AT5G18560	-1.15	-0.20	-1.57	0.16111	0.2804	-6.04
256105_at	hypothetical protein predicted by ge	LSH8	AT1G16910	-1.15	-0.20	-1.57	0.161145	0.280418	-6.04
252944_at	hypothetical protein ;supported by	---	AT4G39320	-1.12	-0.17	-1.57	0.161145	0.280418	-6.04
257032_at	zinc finger protein, putative similar	---	AT3G19140	-1.10	-0.14	-1.57	0.161161	0.280425	-6.04
260387_at	putative flavonol sulfotransferase si	SOT16	AT1G74100	-1.36	-0.45	-1.57	0.161262	0.280578	-6.04
265509_at	putative retroelement pol polyprotei	---	---	-1.18	-0.24	-1.57	0.161324	0.280665	-6.05
259114_at	26S proteasome AAA-ATPase subu	RPT5A	AT3G05530	1.12	0.17	1.57	0.161336	0.280665	-6.05
256843_at	hypothetical protein predicted by ge	---	---	-1.13	-0.18	-1.57	0.161451	0.280844	-6.05
245520_at	delta-cadinene synthase like protein	ATTS1	AT4G15870	-1.13	-0.18	-1.57	0.161506	0.280913	-6.05
253692_at	putative protein Cs protein, Drosop	ATPAO5	AT4G29720	1.11	0.15	1.57	0.161516	0.280913	-6.05
248906_at	putative protein similar to unknown	---	AT5G46420	1.13	0.17	1.57	0.161549	0.280929	-6.05
258625_at	hypothetical protein predicted by ge	PDLP4	AT3G04370	-1.13	-0.18	-1.57	0.161549	0.280929	-6.05
264944_at	hypothetical protein similar to hypot	---	AT1G76940	-1.19	-0.25	-1.57	0.161612	0.281009	-6.05
258500_at	S-adenosylmethionine decarboxyla	CPuORF9	AT3G02468	1.14	0.19	1.57	0.161627	0.281009	-6.05
259004_at	putative protein kinase C-terminal	---	AT3G01840	-1.13	-0.18	-1.57	0.161632	0.281009	-6.05
255748_at	hypothetical protein predicted by ge	---	AT1G32000	-1.10	-0.14	-1.57	0.161704	0.281104	-6.05
256686_at	non-LTR reverse transcriptase, put	---	---	-1.10	-0.14	-1.57	0.161712	0.281104	-6.05
259951_at	unknown protein	---	AT1G71490	-1.12	-0.16	-1.57	0.161756	0.28116	-6.05

246221_at	step II splicing factor - like protein ;	SMP2	AT4G37120	1.14	0.18	1.57	0.161784	0.281166	-6.05
266397_at	unknown protein	---	AT2G38690	-1.12	-0.16	-1.57	0.161785	0.281166	-6.05
256164_at	terpene cyclase, putative similar to	---	AT1G48800	1.11	0.15	1.57	0.161799	0.281169	-6.05
249542_at	putative protein transcription factor	NF-YC12	AT5G38140	-1.19	-0.25	-1.57	0.161953	0.281416	-6.05
255852_at	unknown protein	SVL2	AT1G66970	-1.42	-0.50	-1.57	0.161985	0.281451	-6.05
265146_at	putative glucosyl transferase	---	AT1G51210	-1.27	-0.35	-1.57	0.162037	0.281518	-6.05
248627_at	putative protein similar to unknown	---	AT5G48950	-1.18	-0.24	-1.57	0.162158	0.281692	-6.05
261466_at	hypothetical protein predicted by ge	---	AT1G07690	-1.18	-0.24	-1.57	0.162161	0.281692	-6.05
252394_at	heat shock protein-like protein hea	---	AT3G47940	-1.19	-0.25	-1.57	0.162185	0.281711	-6.05
266161_at	hypothetical protein	ATCHX7	AT2G28170	-1.18	-0.24	-1.57	0.162208	0.281731	-6.05
246210_at	ribosomal protein ; supported by cD	---	AT4G36420	1.21	0.27	1.57	0.162226	0.281741	-6.05
258208_at	putative acetyltransferase similar to	---	AT3G13930	1.21	0.28	1.57	0.162276	0.281776	-6.05
264981_at	valyl- tRNA synthetase, putative si	---	AT1G27160	-1.15	-0.20	-1.57	0.162279	0.281776	-6.05
262560_at	hypothetical protein predicted by ge	---	AT1G34280	-1.15	-0.20	-1.57	0.162284	0.281776	-6.05
263620_at	hypothetical protein predicted by ge	---	---	-1.12	-0.17	-1.57	0.16243	0.281985	-6.05
256835_at	ATP sulfurylase, putative similar to	APS1	AT3G22890	-1.29	-0.36	-1.57	0.162441	0.281985	-6.05
248129_at	putative protein contains similarity t	---	AT5G54780	1.15	0.20	1.57	0.162446	0.281985	-6.05
255029_x_a	hypothetical protein	---	AT4G09470	-1.10	-0.14	-1.57	0.162454	0.281985	-6.05
245234_at	myb-like protein similarity to ATMY	AtMYB18	AT4G25560	-1.15	-0.20	-1.57	0.162473	0.281992	-6.05
256659_at	unknown protein similar to putative	---	AT3G12020	-1.14	-0.19	-1.57	0.162488	0.281992	-6.05
266483_at	unknown protein ;supported by full-	CRR6	AT2G47910	1.16	0.21	1.57	0.162495	0.281992	-6.05
264504_at	unknown protein similar to ATP-citr	ACLA-3	AT1G09430	1.13	0.17	1.57	0.162549	0.282047	-6.05
264719_at	receptor-like kinase, putative simila	---	AT1G70110	-1.20	-0.26	-1.57	0.162551	0.282047	-6.05
254070_at	hypothetical protein	---	AT4G25430	-1.20	-0.26	-1.57	0.162625	0.28209	-6.05
262799_at	hypothetical protein predicted by ge	---	AT1G20970	-1.22	-0.29	-1.57	0.162625	0.28209	-6.05
252544_at	respiratory burst oxidase - like prot	---	AT3G45810	-1.16	-0.21	-1.57	0.162628	0.28209	-6.05
247805_at	ATGP1-like protein	ATYKT62	AT5G58180	-1.21	-0.28	-1.57	0.162632	0.28209	-6.05
256501_at	hypothetical protein predicted by ge	---	AT1G36756	-1.13	-0.17	-1.57	0.162638	0.28209	-6.05
259216_at	hypothetical protein ; supported by	---	AT3G09000	1.30	0.38	1.57	0.162664	0.282114	-6.05
263858_at	hypothetical protein predicted by ge	---	AT2G04370	-1.12	-0.16	-1.57	0.162686	0.28213	-6.05
267621_at	unknown protein	---	---	1.16	0.22	1.57	0.162742	0.282206	-6.05
259511_at	unknown protein contains similarity	ATCCS	AT1G12520	1.47	0.56	1.57	0.162794	0.282275	-6.05
250974_at	meiosis specific - like protein Spo1	RHL2	AT5G02820	1.31	0.39	1.57	0.162812	0.282285	-6.05
258598_at	hypothetical protein predicted by ge	---	AT3G04410	-1.18	-0.24	-1.57	0.162854	0.282337	-6.05
247994_at	RNA-binding protein-like	---	AT5G56140	-1.16	-0.21	-1.57	0.162875	0.282351	-6.05

256990_at	hypothetical protein predicted by ge	---	AT3G28590	-1.19	-0.26	-1.57	0.162902	0.282377	-6.05
252725_at	putative protein mudrA transposas	---	---	-1.12	-0.17	-1.57	0.16295	0.282438	-6.05
264808_at	unknown protein similar to EST gb|	PRA1.E	AT1G08770	-1.13	-0.17	-1.57	0.163003	0.282509	-6.05
247115_at	kinesin-like calmodulin-binding prot	ZWI	AT5G65930	-1.17	-0.22	-1.57	0.16307	0.282599	-6.06
261445_at	unknown protein ; supported by cDI	NSL1	AT1G28380	-1.35	-0.43	-1.57	0.16308	0.282599	-6.06
257063_s_a	unknown protein ;supported by full-	---	AT3G18240	1.11	0.15	1.57	0.1631	0.282609	-6.06
260394_at	putative transcription factor similar t	MYB122	AT1G74080	1.87	0.90	1.57	0.16311	0.282609	-6.06
245498_at	hypothetical protein	---	AT4G16470	1.11	0.16	1.57	0.163217	0.282771	-6.06
265628_at	hypothetical protein predicted by ge	---	AT2G27290	-1.24	-0.31	-1.56	0.163305	0.282903	-6.06
260710_at	protein phosphatase 2C, putative s	---	AT1G17545	-1.11	-0.15	-1.56	0.163329	0.282923	-6.06
257455_s_a	hypothetical protein	---	AT1G27870	-1.11	-0.15	-1.56	0.163354	0.282945	-6.06
263701_at	putative protein kinase C inhibitor (2	---	AT1G31160	-1.11	-0.15	-1.56	0.163495	0.283168	-6.06
265395_at	putative LRR receptor protein kinas	SRF1	AT2G20850	1.19	0.25	1.56	0.163518	0.283186	-6.06
259893_at	putative disease resistance protein	AtRLP11	AT1G71390	-1.15	-0.20	-1.56	0.163611	0.283326	-6.06
245814_at	mitotic checkpoint protein, putative	---	AT1G49910	-1.16	-0.22	-1.56	0.163657	0.283383	-6.06
246067_at	membrane transporter - like protein	---	AT5G19410	-1.11	-0.16	-1.56	0.163686	0.283413	-6.06
251695_at	putative protein hypothetical protein	---	AT3G56590	-1.23	-0.30	-1.56	0.163777	0.283549	-6.06
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb	---	---	1.25	0.32	1.56	0.163803	0.283563	-6.06
252594_at	putative transporter protein peptide	---	AT3G45680	-1.24	-0.31	-1.56	0.163815	0.283563	-6.06
262583_at	putative phosphatidylserine synthas	---	AT1G15110	1.18	0.24	1.56	0.163823	0.283563	-6.06
260594_at	hypothetical protein predicted by ge	---	AT1G55880	1.10	0.14	1.56	0.163947	0.283753	-6.06
266737_at	putative alcohol dehydrogenase ; s	---	AT2G47140	-1.15	-0.20	-1.56	0.163957	0.283753	-6.06
266759_at	unknown protein predicted by gene	---	AT2G46915	-1.13	-0.18	-1.56	0.163986	0.283782	-6.06
253481_at	aspartate aminotransferase ;suppo	ASP5	AT4G31990	1.14	0.18	1.56	0.164023	0.283812	-6.06
251462_at	mitogen-activated protein kinase-li	ATMPK10	AT3G59790	-1.16	-0.22	-1.56	0.164029	0.283812	-6.06
255163_at	putative polyprotein	---	---	1.12	0.17	1.56	0.164067	0.283856	-6.06
266787_at	putative receptor-like protein kinase	---	AT2G28990	-1.11	-0.15	-1.56	0.164146	0.283972	-6.06
263960_at	putative kinesin-related cytokinesis	---	AT2G36200	-1.14	-0.18	-1.56	0.164198	0.28404	-6.06
264090_at	cytochrome P-450, putative similar	CYP79C1	AT1G79370	-1.13	-0.18	-1.56	0.164247	0.284103	-6.06
267189_at	putative methionine aminopeptidase	MAP2A	AT2G44180	1.32	0.40	1.56	0.164436	0.284409	-6.06
265523_at	putative Ty3-gypsy-like retroelemer	---	---	-1.11	-0.15	-1.56	0.164476	0.284453	-6.06
248030_at	transcription regulator Sir2-like prot	SRT1	AT5G55760	1.19	0.25	1.56	0.164486	0.284453	-6.06
250020_at	putative protein contains similarity t	---	AT5G18180	-1.16	-0.21	-1.56	0.164591	0.284574	-6.06
260637_at	ACC oxidase, putative similar to AC	ACO2	AT1G62380	1.46	0.55	1.56	0.164592	0.284574	-6.06
255285_at	putative protein A. thaliana hypothe	---	AT4G04630	-1.48	-0.57	-1.56	0.164594	0.284574	-6.06

253400_at	putative protein unknown protein T	---	AT4G32860	-1.12	-0.16	-1.56	0.164647	0.284645	-6.06
258745_at	unknown protein ; supported by full-	---	AT3G05920	-1.14	-0.19	-1.56	0.164829	0.284937	-6.07
245689_at	phosphoglycerate mutase - like pro	---	AT5G04120	-1.14	-0.19	-1.56	0.164897	0.285034	-6.07
248675_at	putative protein similar to unknown	ICK6	AT5G48820	-1.23	-0.30	-1.56	0.164928	0.285047	-6.07
252658_at	hypothetical protein	---	AT3G44800	-1.17	-0.23	-1.56	0.16493	0.285047	-6.07
262217_at	hypothetical protein predicted by ge	---	AT1G74770	-1.10	-0.14	-1.56	0.164964	0.285079	-6.07
249754_at	flavanone 3-hydroxylase-like protei	DMR6	AT5G24530	-1.82	-0.86	-1.56	0.164974	0.285079	-6.07
256586_at	hypothetical protein	---	AT3G28770	-1.11	-0.15	-1.56	0.164996	0.285097	-6.07
250796_at	putative protein similar to unknown	---	AT5G05300	1.78	0.83	1.56	0.165024	0.285122	-6.07
262028_at	DNA binding protein, putative simil	---	AT1G35560	1.12	0.17	1.56	0.165097	0.285228	-6.07
261146_at	hypothetical protein predicted by ge	---	AT1G19620	-1.18	-0.24	-1.56	0.165146	0.285291	-6.07
263270_at	putative replication protein A1	---	---	-1.12	-0.16	-1.56	0.165182	0.285331	-6.07
263974_at	hypothetical protein predicted by gr	---	AT2G42720	-1.13	-0.18	-1.56	0.16521	0.285358	-6.07
262007_at	hypothetical protein predicted by ge	---	AT1G64580	-1.13	-0.18	-1.56	0.16534	0.285561	-6.07
262833_at	cyclin, putative contains Pfam profi	SDS	AT1G14750	-1.11	-0.15	-1.56	0.165428	0.285691	-6.07
246224_at	putative MADS-box protein ;suppor	---	AT4G36590	-1.18	-0.24	-1.56	0.165542	0.285867	-6.07
247128_at	atfp6-like protein	---	AT5G66110	-1.19	-0.25	-1.55	0.165621	0.285962	-6.07
255233_at	putative protein ADRENODOXIN P	MFDX1	AT4G05450	1.14	0.19	1.55	0.165622	0.285962	-6.07
262337_at	hypothetical protein similar to hypot	---	AT1G64260	-1.16	-0.21	-1.55	0.165699	0.286073	-6.07
255997_s_a	photosystem II type I chlorophyll a	CAB3	AT1G29910	-1.20	-0.27	-1.55	0.165741	0.286124	-6.07
263672_at	putative retroelement pol polyprotei	---	---	-1.11	-0.15	-1.55	0.165785	0.286178	-6.07
267536_at	phospholipase D ; supported by cD	PLDBETA1	AT2G42010	-1.15	-0.20	-1.55	0.16586	0.286287	-6.07
258473_s_a	putative stearoyl-acyl carrier protein	---	AT3G02610	1.22	0.28	1.55	0.165933	0.286364	-6.07
267563_at	putative protein kinase contains a p	---	AT2G30730	-1.13	-0.17	-1.55	0.165936	0.286364	-6.07
265893_at	putative disease resistance protein	---	AT2G15040	1.39	0.47	1.55	0.165943	0.286364	-6.07
260980_at	hypothetical protein predicted by ge	---	AT1G53600	-1.19	-0.25	-1.55	0.165977	0.286402	-6.07
253718_at	serine/threonine-specific receptor p	---	AT4G29450	-1.15	-0.20	-1.55	0.166003	0.286423	-6.07
263307_at	hypothetical protein similar to myos	---	---	1.14	0.19	1.55	0.166039	0.286464	-6.07
262477_at	hypothetical protein contains simila	---	AT1G11220	-1.20	-0.27	-1.55	0.166076	0.286492	-6.07
250120_at	putative protein similar to unknown	RIC4	AT5G16490	-1.22	-0.28	-1.55	0.166082	0.286492	-6.07
245848_at	putative protein predicted proteins -	FY	AT5G13480	1.13	0.17	1.55	0.166093	0.286492	-6.07
264437_at	unknown protein EST gb|N65787 c	---	AT1G27510	1.14	0.19	1.55	0.166175	0.286613	-6.07
247656_at	actin depolymerizing factor 4 - like	ADF4	AT5G59890	-1.17	-0.22	-1.55	0.166234	0.286692	-6.07
259231_at	protein phosphatase 2C (PP2C) ide	PP2CA	AT3G11410	1.26	0.33	1.55	0.166377	0.286909	-6.07
260111_at	hypothetical protein similar to unkn	---	AT1G63320	1.10	0.14	1.55	0.166385	0.286909	-6.07

247980_at	putative protein similar to unknown	GNC	AT5G56860	-1.41	-0.50	-1.55	0.166482	0.287056	-6.07
249031_at	putative protein contains similarity t	---	AT5G44900	-1.15	-0.20	-1.55	0.166535	0.287123	-6.07
253536_at	RSZp22 splicing factor ;supported b	SRZ-22	AT4G31580	1.10	0.14	1.55	0.166546	0.287123	-6.07
254874_at	putative protein beta-phosphoglucc	---	AT4G11570	-1.18	-0.23	-1.55	0.16656	0.287124	-6.07
251511_at	putative protein several hypothetica	---	AT3G59180	-1.12	-0.16	-1.55	0.166588	0.287151	-6.07
254237_at	cysteine proteinase contains simila	---	AT4G23520	-1.11	-0.15	-1.55	0.166686	0.287279	-6.08
257727_at	unknown protein	---	AT3G18380	-1.13	-0.17	-1.55	0.166687	0.287279	-6.08
251835_at	lipase -like protein monoglyceride l	---	AT3G55180	-1.12	-0.16	-1.55	0.166774	0.287406	-6.08
249409_at	putative protein KED, Nicotiana tab	---	AT5G40340	-1.46	-0.54	-1.55	0.166789	0.287411	-6.08
267228_at	putative polygalacturonase	---	AT2G43890	-1.11	-0.15	-1.55	0.166865	0.287514	-6.08
257895_at	dihydrolipoamide dehydrogenase,	LPD1	AT3G16950	1.28	0.36	1.55	0.166877	0.287514	-6.08
267297_at	putative RING zinc finger protein ;s	---	AT2G23780	-1.14	-0.19	-1.55	0.166887	0.287514	-6.08
251344_at	putative protein beige-like protein ((	---	AT3G60920	-1.13	-0.18	-1.55	0.166924	0.287556	-6.08
254509_at	terpene cyclase like protein 5-epi-a	---	AT4G20200	-1.12	-0.16	-1.55	0.166977	0.287627	-6.08
265367_at	hypothetical protein predicted by ge	---	---	1.10	0.14	1.55	0.167017	0.287661	-6.08
252471_at	phosphoprotein phosphatase ;supp	TOPP5	AT3G46820	-1.14	-0.19	-1.55	0.167022	0.287661	-6.08
257414_at	hypothetical protein similar to hypot	---	AT1G62110	-1.13	-0.17	-1.55	0.167165	0.287885	-6.08
257478_at	hypothetical protein similar to putati	WAKL2	AT1G16130	-1.33	-0.41	-1.55	0.167319	0.28809	-6.08
262218_at	hypothetical protein contains simila	---	AT1G74770	-1.20	-0.27	-1.55	0.167328	0.28809	-6.08
257673_at	unknown protein similar to GB:BAA	---	AT3G20370	-1.17	-0.22	-1.55	0.167356	0.28809	-6.08
253504_at	hypothetical protein	---	AT4G31960	-1.09	-0.13	-1.55	0.16736	0.28809	-6.08
252419_at	putative protein	---	AT3G47510	-1.32	-0.40	-1.55	0.16736	0.28809	-6.08
264234_at	hypothetical protein contains simila	---	AT1G54720	-1.11	-0.15	-1.55	0.16736	0.28809	-6.08
266487_at	hypothetical protein predicted by ge	---	AT2G47660	-1.10	-0.14	-1.55	0.167439	0.288193	-6.08
246298_at	putative protein sequence in GenBa	ETO1	AT3G51770	-1.12	-0.16	-1.55	0.167456	0.288193	-6.08
264030_at	putative steroid sulfotransferase	---	AT2G03770	1.16	0.22	1.55	0.167457	0.288193	-6.08
250581_at	copine-like protein copine VII prote	BON2	AT5G07300	1.12	0.17	1.55	0.167519	0.288277	-6.08
246671_at	putative protein	---	---	-1.11	-0.15	-1.55	0.167559	0.288307	-6.08
261282_at	hypothetical protein predicted by ge	APUM10	AT1G35750	1.18	0.23	1.55	0.167562	0.288307	-6.08
245489_at	FCA gamma protein	FCA	AT4G16280	1.13	0.17	1.55	0.167627	0.288397	-6.08
266153_at	hypothetical protein	---	---	-1.11	-0.15	-1.55	0.167778	0.288635	-6.08
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=gb:J	---	---	-1.32	-0.40	-1.55	0.167909	0.288838	-6.08
266469_at	myb-related protein	MYB14	AT2G31180	1.13	0.18	1.55	0.167936	0.288864	-6.08
253041_at	phosphoenolpyruvate carboxykinas	PCK1	AT4G37870	1.27	0.35	1.55	0.167959	0.28888	-6.08
263370_at	hypothetical protein predicted by ge	---	AT2G20500	-1.28	-0.35	-1.54	0.167971	0.28888	-6.08

260762_at	I-box binding factor, putative simila	---	AT1G49015	-1.13	-0.17	-1.54	0.167987	0.288886	-6.08
254307_at	putative protein various predicted p	---	AT4G22400	-1.22	-0.29	-1.54	0.168081	0.289026	-6.08
260558_at	putative endochitinase	---	AT2G43600	-1.17	-0.23	-1.54	0.168142	0.289108	-6.08
250419_at	RPP1 disease resistance protein -	---	AT5G11250	1.19	0.25	1.54	0.168229	0.289215	-6.08
267467_at	putative C3HC4 zinc finger protein	DRIP2	AT2G30580	-1.14	-0.19	-1.54	0.168229	0.289215	-6.08
257437_s_a	hypothetical protein predicted by ge	---	AT2G16290	1.12	0.17	1.54	0.16829	0.289298	-6.08
264753_at	receptor kinase, putative similar to	---	AT1G61490	1.10	0.14	1.54	0.168307	0.289306	-6.08
246422_at	ADP-ribosylation factor -like protei	ATARFB1B	AT5G17060	-1.30	-0.38	-1.54	0.168387	0.289409	-6.08
251501_at	putative protein several hypothetica	---	AT3G59120	-1.13	-0.17	-1.54	0.168392	0.289409	-6.08
267453_at	putative homeodomain transcriptior	HB-3	AT2G33880	-1.19	-0.25	-1.54	0.168415	0.289426	-6.08
262528_at	H+-transporting ATPase AHA10 Ide	AHA10	AT1G17260	-1.17	-0.22	-1.54	0.168428	0.289426	-6.08
246712_at	putative protein various predicted p	---	---	-1.10	-0.14	-1.54	0.168458	0.289455	-6.09
261048_at	flavonol 3-o-glucosyltransferase, p	UGT72B3	AT1G01420	-1.15	-0.20	-1.54	0.168708	0.289863	-6.09
262847_at	unknown protein similar to myosin h	ATMAP70-4	AT1G14840	-1.29	-0.37	-1.54	0.168724	0.28987	-6.09
258469_at	unknown protein contains Pfam pro	PRXIIF	AT3G06050	-1.12	-0.16	-1.54	0.168834	0.290037	-6.09
260184_s_a	putative protein predicted proteins,	---	---	-1.10	-0.14	-1.54	0.168874	0.290083	-6.09
266356_at	putative uclacyanin I identical to GF	UCC1	AT2G32300	-1.11	-0.14	-1.54	0.168924	0.290146	-6.09
247824_at	putative protein Na+/H+-exchangin	CHX25	AT5G58460	-1.15	-0.20	-1.54	0.168959	0.290173	-6.09
245902_at	putative protein Scythe protein, Xe	---	AT5G11080	-1.20	-0.26	-1.54	0.16897	0.290173	-6.09
259094_at	putative cysteine synthase similar t	CYSD1	AT3G04940	1.20	0.27	1.54	0.168977	0.290173	-6.09
267385_at	unknown protein highly similar to G	---	AT2G44380	1.24	0.31	1.54	0.169031	0.290244	-6.09
260434_at	hypothetical protein predicted by ge	---	AT1G68330	-1.22	-0.29	-1.54	0.169077	0.290301	-6.09
261423_at	homeodomain transcription factor,	AGL65	AT1G18750	1.17	0.22	1.54	0.169145	0.290396	-6.09
255740_at	wall-associated kinase, putative sir	---	AT1G25390	1.38	0.46	1.54	0.169183	0.29044	-6.09
249740_at	unknown protein	---	AT5G24500	-1.20	-0.26	-1.54	0.169204	0.290453	-6.09
255768_at	Expressed protein ; supported by fu	---	AT1G16705	-1.12	-0.17	-1.54	0.169232	0.290479	-6.09
259429_at	cytochrome P450, putative similar t	CYP86A4	AT1G01600	-1.61	-0.69	-1.54	0.169259	0.290503	-6.09
251981_at	putative protein BETA-GALACTOS	---	AT3G53080	-1.13	-0.17	-1.54	0.169344	0.290595	-6.09
263247_at	unknown protein	---	AT2G31440	-1.11	-0.15	-1.54	0.169352	0.290595	-6.09
245284_at	phytoene dehydrogenase precurso	PDS3	AT4G14210	-1.20	-0.26	-1.54	0.169353	0.290595	-6.09
264782_at	putative transcription factor similar t	MYB60	AT1G08810	1.17	0.23	1.54	0.169363	0.290595	-6.09
264333_at	hypothetical protein similar to putati	AtTLP4	AT1G61940	-1.12	-0.16	-1.54	0.169379	0.2906	-6.09
263445_at	unknown protein	---	AT2G31590	-1.11	-0.16	-1.54	0.169432	0.290669	-6.09
256040_at	hypothetical protein similar to putati	---	AT1G07270	-1.12	-0.16	-1.54	0.169463	0.290701	-6.09
265153_at	unusual floral organ (UFO), AtFBX	UFO	AT1G30950	-1.14	-0.19	-1.54	0.169567	0.290857	-6.09

266872_at	unknown protein	---	AT2G44730	-1.15	-0.20	-1.54	0.169636	0.290953	-6.09
262727_at	thaumatin, putative contains Pfam	---	AT1G75800	-1.12	-0.16	-1.54	0.169672	0.290995	-6.09
254912_at	respiratory burst oxidase homolog	---	AT4G11230	-1.13	-0.17	-1.54	0.169697	0.291015	-6.09
248139_at	putative protein similar to unknown	---	AT5G54970	2.29	1.20	1.54	0.169777	0.29113	-6.09
247513_at	quinone oxidoreductase - like prote	---	AT5G61510	1.19	0.25	1.54	0.169843	0.291222	-6.09
246331_at	non-phototropic hypocotyl 3-like pr	---	AT3G44820	-1.16	-0.21	-1.54	0.169864	0.291236	-6.09
259391_s_a	delta 9 desaturase, putative similar	---	AT1G06350	-1.13	-0.18	-1.54	0.170102	0.291621	-6.09
262591_at	hypothetical protein Similar to gb|X8	CCMH	AT1G15220	-1.12	-0.16	-1.54	0.170148	0.291678	-6.09
254600_at	4-coumarate-CoA ligase - like 4-co	---	AT4G19010	1.24	0.31	1.54	0.170317	0.29194	-6.10
262233_at	hypothetical protein contains simila	CHR18	AT1G48310	1.12	0.16	1.54	0.170338	0.29194	-6.10
253114_at	GTP-binding protein GB2 ;supporte	ATGB2	AT4G35860	-1.15	-0.20	-1.54	0.170339	0.29194	-6.10
249272_at	geranylgeranyl transferase alpha su	---	AT5G41820	-1.20	-0.26	-1.53	0.170421	0.292059	-6.10
249860_at	prolylcarboxypeptidase-like protein	---	AT5G22860	2.02	1.01	1.53	0.170521	0.292209	-6.10
249982_at	putative protein predicted proteins,	---	AT5G18520	-1.13	-0.17	-1.53	0.170589	0.292303	-6.10
256886_at	hypothetical protein contains Pfam	---	AT3G15130	1.10	0.13	1.53	0.170619	0.292323	-6.10
262878_at	hypothetical protein predicted by ge	NDF2	AT1G64770	1.15	0.21	1.53	0.170633	0.292323	-6.10
248796_at	VAMP (vesicle-associated membra	---	AT5G47180	-1.22	-0.29	-1.53	0.170639	0.292323	-6.10
247755_at	subtilisin-like serine protease conta	ATSBT4.12	AT5G59090	-1.11	-0.15	-1.53	0.170695	0.292397	-6.10
254979_at	subtilisin-like serine protease conta	---	AT4G10550	1.13	0.18	1.53	0.170729	0.292433	-6.10
253188_at	putative sugar transporter protein s	TMT2	AT4G35300	1.14	0.19	1.53	0.17087	0.292652	-6.10
263056_at	Mutator-like transposase similar to	---	---	-1.10	-0.14	-1.53	0.170903	0.292656	-6.10
266477_at	CLE4 CLAVATA3/ESR-Related 4 (	CLE6	AT2G31085	-1.16	-0.21	-1.53	0.170919	0.292656	-6.10
258148_s_a	DNA-directed RNA polymerase II s	NRPD2B	AT3G18090	1.23	0.30	1.53	0.170927	0.292656	-6.10
248810_at	disease resistance protein-like	ADR1-L3	AT5G47280	-1.11	-0.15	-1.53	0.170933	0.292656	-6.10
253169_at	putative protein various predicted p	---	AT4G35120	-1.14	-0.19	-1.53	0.170936	0.292656	-6.10
256168_at	receptor protein kinase, putative co	---	AT1G51805	-1.33	-0.41	-1.53	0.170973	0.292697	-6.10
246964_at	putative protein crp1 protein - Zea	---	AT5G24830	-1.15	-0.21	-1.53	0.170996	0.292714	-6.10
255703_at	putative chalcone synthase similar t	---	AT4G00040	-1.22	-0.28	-1.53	0.171024	0.29274	-6.10
254466_at	subtilisin-like serine protease conta	---	AT4G20430	-1.18	-0.24	-1.53	0.171111	0.292855	-6.10
258960_at	hypothetical protein similar to myb-	---	AT3G10590	-1.12	-0.17	-1.53	0.171117	0.292855	-6.10
247443_at	putative protein predicted proteins,	---	AT5G62720	1.21	0.27	1.53	0.171133	0.292861	-6.10
248451_at	putative protein similar to unknown	---	AT5G51180	-1.10	-0.14	-1.53	0.171176	0.292895	-6.10
252792_at	hypothetical protein	---	---	-1.16	-0.21	-1.53	0.171179	0.292895	-6.10
253434_at	potassium channel - protein	AKT5	AT4G32500	-1.13	-0.17	-1.53	0.171276	0.293039	-6.10
247832_at	putative protein predicted proteins,	EOL2	AT5G58550	-1.15	-0.20	-1.53	0.171325	0.293101	-6.10

257561_at	hypothetical protein predicted by ge	APUM25	AT3G24270	-1.14	-0.18	-1.53	0.171347	0.293118	-6.10
267441_at	putative receptor-like protein kinase	---	AT2G19210	-1.11	-0.15	-1.53	0.171373	0.29314	-6.10
256158_at	hypothetical protein contains simila	ATPSK1	AT1G13590	-1.12	-0.17	-1.53	0.171522	0.293372	-6.10
263451_at	putative triacylglycerol lipase	---	AT2G31690	-1.10	-0.14	-1.53	0.171593	0.293448	-6.10
257762_at	hypothetical protein	XRCC4	AT3G23100	1.13	0.17	1.53	0.171597	0.293448	-6.10
261970_at	glutamate decarboxylase (gad), pu	GAD2	AT1G65960	1.18	0.24	1.53	0.171605	0.293448	-6.10
252608_at	putative protein 2-phosphoglycerat	---	AT3G45090	-1.15	-0.20	-1.53	0.171647	0.293499	-6.10
253124_at	putative protein unknown protein A	ARO3	AT4G36030	-1.43	-0.51	-1.53	0.171693	0.293555	-6.10
248141_at	unknown protein	---	AT5G55010	1.12	0.17	1.53	0.171748	0.293628	-6.10
248793_at	mutT domain protein-like ;supporte	atnudt8	AT5G47240	-1.33	-0.41	-1.53	0.171816	0.293721	-6.10
253262_at	putative serine threonine protein kir	---	AT4G34440	-1.12	-0.17	-1.53	0.171829	0.293721	-6.10
267100_at	unknown protein	---	AT2G41470	-1.12	-0.16	-1.53	0.171847	0.29373	-6.10
254704_at	putative protein predicted protein, A	APRR2	AT4G18020	1.14	0.19	1.53	0.171878	0.293762	-6.10
249644_at	putative serine-rich protein hypothe	---	AT5G37010	-1.16	-0.21	-1.53	0.171929	0.293827	-6.10
264388_at	hypothetical protein contains simila	---	AT1G11970	-1.16	-0.21	-1.53	0.171968	0.293871	-6.10
251364_at	anthranilate phosphoribosyltransfe	---	AT3G61300	-1.14	-0.18	-1.53	0.171984	0.293875	-6.10
259961_at	auxin-induced protein kinase, puta	WAG1	AT1G53700	-1.14	-0.19	-1.53	0.172024	0.293923	-6.10
250980_at	putative protein	---	AT5G03130	-1.32	-0.40	-1.53	0.172115	0.294056	-6.10
247122_at	putative protein non-consensus AT	ATSAC1B	AT5G66020	-1.18	-0.24	-1.53	0.172128	0.294056	-6.10
253051_at	cyclin cyc1 ; supported by cDNA: g	CYCB1;1	AT4G37490	-1.18	-0.24	-1.53	0.17222	0.294184	-6.11
245595_at	hypothetical protein	---	AT4G14170	1.11	0.16	1.53	0.172229	0.294184	-6.11
255812_at	potassium uptake transporter - like	HKT1	AT4G10310	1.24	0.31	1.53	0.172258	0.294193	-6.11
253748_at	putative protein RNA-binding prote	---	AT4G28990	-1.17	-0.22	-1.53	0.172267	0.294193	-6.11
255172_x_a	putative transposon protein similar	---	---	-1.17	-0.23	-1.53	0.172272	0.294193	-6.11
252247_at	putative protein various predicted p	---	AT3G49740	1.12	0.16	1.53	0.172301	0.294203	-6.11
246104_at	DNA-binding protein - like DNA-bin	WRKY74	AT5G28650	1.11	0.15	1.53	0.172304	0.294203	-6.11
262619_at	3-hydroxyisobutyryl-coenzyme A h	---	AT1G06550	1.46	0.55	1.53	0.172342	0.294232	-6.11
248052_at	putative protein contains similarity t	---	AT5G55800	-1.13	-0.18	-1.53	0.172347	0.294232	-6.11
265494_at	putative calmodulin-like protein	---	AT2G15680	-1.18	-0.23	-1.53	0.172432	0.294355	-6.11
254686_at	putative protein putative oncogene	---	AT4G13720	-1.15	-0.20	-1.53	0.17247	0.294398	-6.11
248279_at	putative protein similar to unknown	ATIM	AT5G52910	-1.31	-0.39	-1.53	0.172491	0.294404	-6.11
257431_at	unknown protein	---	AT2G36360	-1.13	-0.18	-1.53	0.172499	0.294404	-6.11
250106_at	putative protein strong similarity to	---	AT5G16640	1.12	0.16	1.53	0.172559	0.294469	-6.11
257244_at	receptor kinase, putative similar to	---	AT3G24240	-1.26	-0.33	-1.53	0.172563	0.294469	-6.11
264089_at	actin depolymerizing factor 6 ;supp	ADF6	AT2G31200	1.19	0.25	1.53	0.172615	0.294535	-6.11

257380_at	hypothetical protein predicted by ge	---	AT2G28090	-1.15	-0.20	-1.53	0.172639	0.294545	-6.11
247483_at	aldose reductase-like protein	---	AT5G62420	-1.17	-0.22	-1.53	0.172647	0.294545	-6.11
266006_at	putative ABC transporter	---	AT2G37360	-1.17	-0.23	-1.53	0.172665	0.294547	-6.11
248664_at	peptidyl-prolyl cis-trans isomerase-l	FKBP15-2	AT5G48580	1.20	0.26	1.53	0.172674	0.294547	-6.11
263265_at	hypothetical protein predicted by ge	---	AT2G38820	1.22	0.29	1.53	0.172742	0.294624	-6.11
265292_s_a	hypothetical protein predicted by ge	---	---	-1.10	-0.14	-1.53	0.172744	0.294624	-6.11
255867_at	hypothetical protein predicted by ge	---	AT2G30370	-1.12	-0.16	-1.53	0.172774	0.294652	-6.11
246430_at	calmodulin-like protein calmodulin-	---	AT5G17470	-1.12	-0.16	-1.52	0.172836	0.294736	-6.11
257472_at	hypothetical protein predicted by ge	---	AT1G56040	-1.11	-0.15	-1.52	0.17286	0.294756	-6.11
261998_at	putative gag-pol polyprotein similar	---	---	-1.13	-0.18	-1.52	0.172921	0.294838	-6.11
254947_at	putative retrotransposon polyprotei	---	---	-1.21	-0.27	-1.52	0.172951	0.294867	-6.11
248202_at	unknown protein	---	AT5G54220	-1.19	-0.25	-1.52	0.173022	0.294965	-6.11
250694_at	putative protein contains similarity t	HAT14	AT5G06710	1.17	0.23	1.52	0.173065	0.294999	-6.11
254171_at	PsRT17-1 like protein PsRT17-1, F	---	AT4G24530	-1.11	-0.15	-1.52	0.173068	0.294999	-6.11
251040_at	ribonuclease II-like protein ribonucl	EMB2730	AT5G02250	1.22	0.29	1.52	0.173161	0.295135	-6.11
245174_at	putative kinesin heavy chain	---	AT2G47500	-1.25	-0.33	-1.52	0.173231	0.2952	-6.11
260462_at	ZIP4, a putative zinc transporter pe	ZIP4	AT1G10970	1.25	0.32	1.52	0.173233	0.2952	-6.11
263791_at	putative plasma membrane proton A	AHA5	AT2G24520	1.22	0.28	1.52	0.173238	0.2952	-6.11
256443_at	hypothetical protein similar to hypot	---	AT3G10960	-1.26	-0.33	-1.52	0.17329	0.295267	-6.11
253491_at	RNA lariat debranching enzyme - li	---	AT4G31770	-1.24	-0.31	-1.52	0.17341	0.295449	-6.11
252779_at	putative protein	---	AT3G42990	-1.12	-0.17	-1.52	0.17346	0.295513	-6.11
246509_at	valine--tRNA ligase-like protein sev	EMB2247	AT5G16715	1.22	0.29	1.52	0.17349	0.295528	-6.11
259713_at	unknown protein similar to phospha	---	AT1G77610	1.19	0.25	1.52	0.173495	0.295528	-6.11
255612_at	hypothetical protein	---	AT4G01240	-1.17	-0.23	-1.52	0.173512	0.295536	-6.11
249570_at	hypothetical protein	---	AT5G38080	-1.15	-0.20	-1.52	0.173603	0.295668	-6.11
245363_at	hypothetical protein ;supported by f	---	AT4G15120	1.50	0.58	1.52	0.173616	0.295668	-6.11
267255_at	putative Ca2+-ATPase	---	AT2G22950	-1.17	-0.23	-1.52	0.173635	0.295679	-6.11
255588_at	hypothetical protein	---	AT4G01570	1.20	0.26	1.52	0.173664	0.295704	-6.11
263902_at	phosphoribosylformimino-5-aminoir	APG10	AT2G36230	-1.12	-0.17	-1.52	0.173676	0.295704	-6.11
258631_at	putative polygalacturonase similar t	QRT2	AT3G07970	1.47	0.55	1.52	0.173739	0.295789	-6.11
245167_s_a	putative synaptobrevin ;supported	ATVAMP72	AT2G33110	1.11	0.15	1.52	0.173806	0.295873	-6.11
253084_at	putative protein lateral root primord	STY2	AT4G36260	-1.20	-0.27	-1.52	0.173814	0.295873	-6.11
264482_at	sugar carrier protein, putative simil	---	AT1G77210	1.35	0.43	1.52	0.173853	0.295917	-6.11
256596_at	hypothetical protein predicted by ge	---	AT3G28540	1.26	0.33	1.52	0.173919	0.296008	-6.11
267627_at	putative ATP-dependent RNA helic	---	AT2G42270	1.26	0.33	1.52	0.173975	0.29608	-6.11

260457_at	unknown protein	---	AT1G72480	-1.13	-0.18	-1.52	0.173989	0.296082	-6.11
257533_at	putative alpha/beta hydrolase conta	---	AT3G10840	-1.24	-0.31	-1.52	0.174097	0.296244	-6.12
262772_at	puative calcium-transporting ATPas	ACA.I	AT1G13210	1.28	0.36	1.52	0.174111	0.296246	-6.12
247205_at	unknown protein ;supported by full-	PROPEP2	AT5G64890	1.81	0.86	1.52	0.174128	0.296253	-6.12
252871_at	proliferating-cell nucleolar antigen -	---	AT4G40000	-1.12	-0.17	-1.52	0.174291	0.296507	-6.12
254982_at	putative protein ; supported by cDN	---	AT4G10470	1.16	0.21	1.52	0.174375	0.296629	-6.12
263777_at	putative cyclic nucleotide-regulated	ATCNGC12	AT2G46450	1.62	0.69	1.52	0.174408	0.296648	-6.12
256746_at	alpha-glucan phosphorylase, putat	---	AT3G29320	-1.20	-0.26	-1.52	0.174412	0.296648	-6.12
247021_at	putative protein similar to unknown	---	AT5G67040	-1.14	-0.18	-1.52	0.174518	0.296805	-6.12
250848_at	3-phosphoinositide-dependent prote	PDK1	AT5G04510	-1.14	-0.19	-1.52	0.174546	0.296832	-6.12
258212_at	unknown protein contains Pfam pro	---	AT3G17920	-1.10	-0.13	-1.52	0.174604	0.296907	-6.12
252802_at	putative protein	---	---	1.09	0.13	1.52	0.174641	0.29694	-6.12
263508_s_a	hypothetical protein	---	---	-1.17	-0.23	-1.52	0.174649	0.29694	-6.12
251091_at	pyridoxine biosynthesis protein - lik	RSR4	AT5G01410	1.33	0.41	1.52	0.174677	0.296966	-6.12
257708_at	hypothetical protein predicted by ge	---	AT3G13330	-1.13	-0.17	-1.52	0.174758	0.297081	-6.12
254826_at	putative protein predicted protein, A	---	AT4G12640	1.16	0.21	1.52	0.174785	0.297105	-6.12
256172_at	hypothetical protein	---	AT1G51745	-1.11	-0.16	-1.52	0.174891	0.297262	-6.12
263206_at	unknown protein similar to ESTs gl	---	AT1G10590	1.10	0.14	1.52	0.174925	0.297287	-6.12
265791_at	putative transcription factor	MEE65	AT2G01280	-1.15	-0.20	-1.52	0.174931	0.297287	-6.12
256547_at	receptor-like serine/threonine kinas	---	AT3G14840	1.29	0.36	1.52	0.174976	0.297335	-6.12
261481_at	nucleoside triphosphatase, putative	---	AT1G14260	-1.17	-0.23	-1.52	0.174986	0.297335	-6.12
254658_at	putative protein predicted gene M0	---	AT4G18230	-1.13	-0.17	-1.52	0.175014	0.297361	-6.12
252546_at	DNA-binding protein - like DNA-bi	---	AT3G45830	1.12	0.17	1.52	0.175136	0.297546	-6.12
260814_at	histidine decarboxylase, putative s	emb1075	AT1G43710	1.12	0.16	1.52	0.175211	0.297652	-6.12
247020_at	putative protein strong similarity to	---	AT5G67020	-1.18	-0.24	-1.51	0.175289	0.297762	-6.12
261812_at	hypothetical protein contains simila	---	AT1G08270	-1.10	-0.14	-1.51	0.175381	0.297896	-6.12
259952_at	putative disease resistance protein	AtRLP12	AT1G71400	1.25	0.33	1.51	0.175398	0.297902	-6.12
250855_at	putative protein predicted proteins,	---	AT5G04730	-1.13	-0.17	-1.51	0.175459	0.297968	-6.12
265782_at	putative two-component response r	---	AT2G07440	-1.14	-0.18	-1.51	0.175463	0.297968	-6.12
258155_at	protein kinase C-receptor/G-protein	RACK1C_A	AT3G18130	1.45	0.54	1.51	0.175565	0.29812	-6.12
267618_at	putative cyclin ; supported by cDNA	CYCB1;4	AT2G26760	-1.15	-0.20	-1.51	0.175683	0.298298	-6.12
253093_at	putative protein SPINDLY protein,	SRFR1	AT4G37460	1.13	0.17	1.51	0.175714	0.298328	-6.12
245478_at	galactokinase like protein	ARA1	AT4G16130	1.32	0.40	1.51	0.175987	0.298768	-6.13
254004_at	arginyl-tRNA synthetase	emb1027	AT4G26300	1.10	0.13	1.51	0.176	0.298768	-6.13
259312_at	putative RING-H2 zinc finger protei	ATL6	AT3G05200	1.41	0.49	1.51	0.176068	0.298849	-6.13

257424_at	hypothetical protein predicted by ge	---	AT1G78840	-1.18	-0.24	-1.51	0.176073	0.298849	-6.13
249923_at	conglutin gamma - like protein con	---	AT5G19120	-1.26	-0.34	-1.51	0.176115	0.298889	-6.13
248395_at	putative protein contains similarity t	AtPP2-A14	AT5G52120	1.19	0.25	1.51	0.176123	0.298889	-6.13
246786_at	putative amino acid aminotransfera	---	AT5G27410	1.15	0.20	1.51	0.176174	0.298954	-6.13
246085_at	putative protein predicted proteins,	ATBRXL4	AT5G20540	-1.15	-0.21	-1.51	0.176193	0.298963	-6.13
254161_at	hypothetical protein ;supported by	---	AT4G24370	-1.13	-0.17	-1.51	0.176207	0.298965	-6.13
251763_at	MYB transcription factor - like prote	MYB109	AT3G55730	-1.15	-0.20	-1.51	0.176228	0.298979	-6.13
266222_at	hypothetical protein predicted by ge	---	AT2G28780	-1.12	-0.16	-1.51	0.176242	0.298979	-6.13
245104_at	hypothetical protein predicted by ge	---	AT2G41600	1.12	0.16	1.51	0.17627	0.299005	-6.13
248722_at	pyrophosphate-fructose-6-phospha	PFK2	AT5G47810	1.10	0.13	1.51	0.176326	0.299077	-6.13
255091_at	putative protein various predicted p	---	---	-1.10	-0.14	-1.51	0.176379	0.299145	-6.13
257123_at	hypothetical protein	---	AT3G20030	-1.10	-0.14	-1.51	0.176493	0.299316	-6.13
266048_at	putative thioredoxin H contains a th	ATCXXS2	AT2G40790	-1.14	-0.19	-1.51	0.17655	0.299392	-6.13
254325_at	putative protein various predicted p	---	AT4G22650	-1.19	-0.25	-1.51	0.176697	0.29961	-6.13
250967_at	putative protein In2, Zea mays, EM	---	AT5G02790	1.18	0.24	1.51	0.176706	0.29961	-6.13
264417_at	hypothetical protein contains simila	---	---	-1.20	-0.27	-1.51	0.176739	0.299629	-6.13
266244_at	unknown protein	---	AT2G27740	-1.38	-0.47	-1.51	0.176743	0.299629	-6.13
255806_at	fructokinase - like protein fructokina	---	AT4G10260	-1.09	-0.13	-1.51	0.176893	0.299861	-6.13
253395_at	protein kinase AME3 ; supported b	AME3	AT4G32660	-1.11	-0.15	-1.51	0.176913	0.299872	-6.13
266442_at	hypothetical protein	---	AT2G43260	1.10	0.14	1.51	0.176967	0.299942	-6.13
260320_at	hypothetical protein similar to putati	---	AT1G63930	-1.19	-0.25	-1.51	0.177004	0.299983	-6.13
264900_at	putative auxin transport protein stro	PIN7	AT1G23080	1.22	0.28	1.51	0.177112	0.300125	-6.13
253077_at	hypothetical protein	---	AT4G36170	1.10	0.14	1.51	0.177114	0.300125	-6.13
253487_at	ribosomal protein S6 - like ribosom	RPS6	AT4G31700	1.37	0.45	1.51	0.177242	0.300319	-6.13
259906_at	unknown protein	---	AT1G74120	1.11	0.15	1.51	0.177265	0.300335	-6.13
253723_at	extensin-like protein ;supported by	---	AT4G29240	-1.14	-0.19	-1.51	0.177311	0.30039	-6.13
247264_at	putative protein contains similarity t	XND1	AT5G64530	1.33	0.42	1.51	0.177414	0.300536	-6.13
254842_at	putative protein other hypothetical p	---	AT4G11950	-1.16	-0.21	-1.51	0.177432	0.300536	-6.13
267543_at	26S proteasome regulatory subunit	---	AT2G32730	1.10	0.14	1.51	0.177438	0.300536	-6.13
259863_at	hypothetical protein ;supported by	ELF4-L2	AT1G72630	-1.12	-0.16	-1.51	0.177449	0.300536	-6.13
265249_at	putative C2H2-type zinc finger prote	SGR5	AT2G01940	1.36	0.44	1.51	0.177466	0.300542	-6.13
250597_at	NAM (no apical meristem)-like prote	ANAC080	AT5G07680	1.28	0.36	1.51	0.177561	0.30068	-6.13
266766_at	hypothetical protein predicted by ge	PAP14	AT2G46880	-1.26	-0.33	-1.51	0.177697	0.300888	-6.13
264604_at	hypothetical protein predicted by ge	---	AT1G04650	1.18	0.23	1.51	0.17771	0.300888	-6.13
263397_s_a	putative GDSL-motif lipase/hydrolas	---	AT2G31540	-1.09	-0.13	-1.51	0.177724	0.300889	-6.13

247263_at	putative protein similar to unknown	---	AT5G64470	1.18	0.24	1.50	0.177821	0.301031	-6.13
254883_at	putative protein histidine-rich glyco	HAP2	AT4G11720	-1.16	-0.21	-1.50	0.177834	0.301031	-6.13
247054_at	zinc finger protein	---	AT5G66730	1.14	0.19	1.50	0.177864	0.30106	-6.13
262757_at	putative Na/H antiporter similar to g	ATCHX1	AT1G16380	-1.13	-0.18	-1.50	0.177903	0.301104	-6.13
262252_at	RING-H2 zinc finger protein ATL3,	---	AT1G53820	-1.12	-0.16	-1.50	0.177926	0.301119	-6.14
265429_at	hypothetical protein predicted by ge	---	AT2G20710	1.16	0.21	1.50	0.178054	0.301314	-6.14
259913_at	putative GTP-binding protein simila	---	AT1G72660	1.10	0.14	1.50	0.178173	0.301493	-6.14
253150_at	putative protein predicted protein, A	---	AT4G35660	-1.10	-0.13	-1.50	0.178239	0.301573	-6.14
252100_at	crooked neck-like protein crooked (	---	AT3G51110	1.24	0.31	1.50	0.178247	0.301573	-6.14
260122_at	AIG1-like protein similar to AIG1 pr	---	AT1G33900	-1.15	-0.20	-1.50	0.178303	0.301646	-6.14
249705_at	serine/threonine protein kinase-like	---	AT5G35580	1.20	0.27	1.50	0.178352	0.301696	-6.14
248562_at	putative protein strong similarity to (	---	AT5G49680	-1.32	-0.40	-1.50	0.178359	0.301696	-6.14
258778_s_a	hypothetical protein predicted by ge	---	AT3G11860	1.15	0.20	1.50	0.178435	0.301802	-6.14
246394_at	myrosinase binding protein, putativ	---	AT1G58160	-1.11	-0.15	-1.50	0.178449	0.301804	-6.14
245890_at	ribosomal protein S15-like ribosom	---	AT5G09490	-1.09	-0.13	-1.50	0.178485	0.301813	-6.14
261495_at	hypothetical protein predicted by ge	---	AT1G28410	1.13	0.18	1.50	0.17849	0.301813	-6.14
253675_at	hypothetical protein	---	AT4G29560	1.12	0.16	1.50	0.178494	0.301813	-6.14
262834_at	hypothetical protein predicted by ge	MAP65-7	AT1G14690	1.13	0.17	1.50	0.178545	0.301847	-6.14
261960_at	hypothetical protein similar to putati	---	---	1.10	0.13	1.50	0.17855	0.301847	-6.14
249153_s_a	putative protein strong similarity to (	---	AT5G43390	-1.14	-0.19	-1.50	0.178554	0.301847	-6.14
257558_s_a	hypothetical protein contains Pfam	---	AT3G22000	-1.12	-0.16	-1.50	0.178624	0.301943	-6.14
267576_at	putative Mutator-like transposase	---	---	1.16	0.22	1.50	0.178645	0.301956	-6.14
246677_at	putative protein predicted proteins -	---	---	-1.14	-0.19	-1.50	0.178664	0.301966	-6.14
245139_at	putative AT-hook DNA-binding prot	---	AT2G45430	-1.13	-0.18	-1.50	0.178755	0.302096	-6.14
261552_at	receptor protein kinase, putative co	---	AT1G63430	1.14	0.19	1.50	0.178767	0.302096	-6.14
251038_at	putative protein unknown protein A	---	AT5G02240	1.11	0.16	1.50	0.178823	0.302159	-6.14
250152_at	putative protein predicted proteins,	---	AT5G15120	-1.11	-0.15	-1.50	0.178831	0.302159	-6.14
251263_at	putative protein DNAJ PROTEIN -	---	AT3G62190	1.13	0.17	1.50	0.178845	0.30216	-6.14
265023_at	unknown protein weak similarity to (	---	AT1G24440	1.18	0.24	1.50	0.178861	0.302164	-6.14
251956_at	RNA-binding protein cp29 protein ;	CP29	AT3G53460	1.13	0.17	1.50	0.178904	0.302207	-6.14
262466_at	hypothetical protein similar to hypot	NTMC2T5.	AT1G50260	1.17	0.22	1.50	0.178913	0.302207	-6.14
264282_at	hypothetical protein similar to hypot	---	AT1G61840	-1.14	-0.18	-1.50	0.179094	0.30249	-6.14
261253_at	unknown protein ;supported by full-	---	AT1G05840	1.19	0.25	1.50	0.179124	0.302519	-6.14
246454_at	Expressed protein ; supported by fu	DHAR3	AT5G16710	-1.13	-0.17	-1.50	0.179204	0.302632	-6.14
257882_at	hypothetical protein predicted by ge	---	AT3G16930	-1.14	-0.18	-1.50	0.179264	0.302711	-6.14

261989_at	disease resistance protein, putative	---	AT1G33670	-1.14	-0.19	-1.50	0.179292	0.302711	-6.14
256601_s_a	At14a-1 protein identical to At14a p	AT14A	AT3G28290	-1.12	-0.16	-1.50	0.179302	0.302711	-6.14
254255_at	serine/threonine kinase - like prote	---	AT4G23220	-1.39	-0.47	-1.50	0.179304	0.302711	-6.14
264589_at	hypothetical protein	---	AT2G17650	1.16	0.22	1.50	0.179337	0.302744	-6.14
256028_at	poly(A)-binding protein, putative sir	PAB1	AT1G34140	-1.17	-0.23	-1.50	0.179355	0.302753	-6.14
256888_at	hypothetical protein predicted by ge	---	AT3G15160	-1.12	-0.16	-1.50	0.179383	0.302776	-6.14
256667_at	hypothetical protein predicted by ge	---	AT3G32180	-1.10	-0.13	-1.50	0.179435	0.302827	-6.14
249148_at	unknown protein ; supported by cD	---	AT5G43260	1.23	0.29	1.50	0.179439	0.302827	-6.14
256488_at	hypothetical protein	NFD4	AT1G31470	-1.12	-0.17	-1.50	0.179461	0.302841	-6.14
256684_at	geranylgeranyl pyrophosphate syn	---	AT3G32040	-1.17	-0.23	-1.50	0.179494	0.302862	-6.14
257223_at	50S ribosomal protein L12-B identi	RPL12-B	AT3G27840	-1.15	-0.20	-1.50	0.1795	0.302862	-6.14
258275_at	unknown protein ;supported by full-	---	AT3G15760	1.23	0.30	1.50	0.179537	0.302902	-6.14
260550_at	putative sterol dehydrogenase ; su	---	AT2G43420	1.19	0.25	1.50	0.179594	0.302972	-6.14
250100_at	Expressed protein ; supported by cl	GLN1;4	AT5G16570	1.39	0.47	1.50	0.179618	0.302972	-6.14
247319_at	glutamate-tRNA ligase ; supported	ERS	AT5G64050	1.13	0.18	1.50	0.179628	0.302972	-6.14
258692_at	unknown protein	---	AT3G08640	-1.24	-0.31	-1.50	0.179631	0.302972	-6.14
261623_at	hypothetical protein similar to reticu	ATSEC1A	AT1G01980	-1.13	-0.17	-1.50	0.179746	0.303143	-6.14
256159_at	Expressed protein ; supported by fu	JAZ8	AT1G30135	1.72	0.78	1.50	0.179829	0.303261	-6.14
263916_at	hypothetical protein predicted by ge	---	AT2G36440	-1.13	-0.18	-1.50	0.179917	0.303361	-6.15
257091_at	DNA polymerase, putative C-term s	POLGAMM	AT3G20540	-1.18	-0.24	-1.50	0.179934	0.303361	-6.15
250230_at	putative protein similar to unknown	---	AT5G13900	-1.22	-0.29	-1.50	0.179939	0.303361	-6.15
250486_at	putative protein predicted proteins,	---	AT5G09670	-1.13	-0.18	-1.50	0.179942	0.303361	-6.15
265838_at	putative spliceosome associated pr	---	AT2G14550	-1.11	-0.15	-1.50	0.179955	0.303361	-6.15
251416_at	putative protein various predicted p	---	AT3G60400	1.12	0.16	1.50	0.179972	0.303367	-6.15
251485_at	putative protein rad21 mitotic cohe	SYN3	AT3G59550	-1.11	-0.15	-1.50	0.18002	0.303426	-6.15
255944_at	putative protein	---	---	-1.14	-0.19	-1.50	0.180161	0.30364	-6.15
266444_at	putative extensin	---	AT2G43150	-1.16	-0.21	-1.50	0.180227	0.303729	-6.15
256027_at	putative protein	---	AT1G34160	1.10	0.14	1.49	0.180285	0.303805	-6.15
253593_at	putative protein hypothetical protei	---	AT4G30760	1.14	0.19	1.49	0.180339	0.303866	-6.15
257162_s_a	ammonium transporter, putative sir	AMT1;3	AT3G24290	-1.11	-0.15	-1.49	0.180348	0.303866	-6.15
255849_at	hypothetical protein predicted by ge	---	AT2G33320	-1.11	-0.16	-1.49	0.180369	0.303879	-6.15
258278_at	putative self-incompatibility protein	---	AT3G26860	-1.12	-0.16	-1.49	0.180453	0.303998	-6.15
256918_s_a	hypothetical protein similar to hypot	---	AT3G18960	-1.17	-0.23	-1.49	0.180516	0.304082	-6.15
262238_at	hypothetical protein predicted by ge	---	AT1G48300	1.22	0.28	1.49	0.180541	0.304101	-6.15
262282_at	hypothetical protein predicted by ge	---	AT1G68610	-1.15	-0.20	-1.49	0.180581	0.304146	-6.15

251458_at	putative protein several retrotranspo	---	---	-1.12	-0.16	-1.49	0.180629	0.304204	-6.15
266896_at	putative ATP-dependent RNA helic	---	AT2G45810	1.10	0.14	1.49	0.180685	0.304277	-6.15
254285_at	putative cdc2 kinase homolog cdc2	---	AT4G22940	1.16	0.22	1.49	0.18072	0.304312	-6.15
245237_at	putative protein similarity to ALR - H	SLK1	AT4G25520	1.12	0.16	1.49	0.18074	0.304324	-6.15
252760_x_a	putative protein several hypothetica	---	---	-1.11	-0.15	-1.49	0.180773	0.304356	-6.15
246024_at	putative protein predicted protein -	---	AT5G21130	-1.15	-0.20	-1.49	0.180802	0.304384	-6.15
257305_at	hypothetical protein predicted by ge	---	---	-1.15	-0.20	-1.49	0.18089	0.304509	-6.15
261604_at	unknown protein contains similarity	---	AT1G49590	1.14	0.19	1.49	0.180989	0.304649	-6.15
246116_at	putative protein predicted proteins -	---	AT5G20310	-1.14	-0.19	-1.49	0.181	0.304649	-6.15
256567_at	amino acid permease, putative cor	---	AT3G19553	-1.13	-0.18	-1.49	0.181038	0.304672	-6.15
256190_at	9-cis-epoxycarotenoid dioxygenase	NCED5	AT1G30100	-1.12	-0.17	-1.49	0.18104	0.304672	-6.15
251312_at	MADS-box protein AGL13 ; suppor	AGL13	AT3G61120	-1.12	-0.16	-1.49	0.181059	0.30468	-6.15
249729_at	6-phosphogluconolactonase-like pr	---	AT5G24410	-1.13	-0.18	-1.49	0.18108	0.30468	-6.15
260024_at	beta-1,3-glucanase precursor, puta	---	AT1G30080	-1.10	-0.14	-1.49	0.181085	0.30468	-6.15
250713_at	putative protein similar to unknown	---	AT5G06130	1.14	0.19	1.49	0.181176	0.30481	-6.15
250282_at	putative protein predicted protein, A	---	AT5G13260	-1.18	-0.24	-1.49	0.181232	0.304883	-6.15
251534_at	ATP-dependent RNA helicase-like	---	AT3G58510	1.23	0.29	1.49	0.181252	0.304894	-6.15
251787_at	2-oxoglutarate dehydrogenase, E1	---	AT3G55410	-1.15	-0.20	-1.49	0.18127	0.304902	-6.15
253261_at	putative protein mRNA, partial cds,	CHB3	AT4G34430	-1.14	-0.19	-1.49	0.181342	0.304997	-6.15
255250_at	MYB - like protein cM4 myb transc	AtMYB74	AT4G05100	-1.58	-0.66	-1.49	0.181356	0.304997	-6.15
259314_at	putative glucose and ribitol dehydro	---	AT3G05260	-1.21	-0.27	-1.49	0.181367	0.304997	-6.15
252251_at	hypothetical protein	---	AT3G49820	-1.11	-0.15	-1.49	0.181383	0.305	-6.15
255198_at	contains similarity to an Arabidopsi	---	---	-1.11	-0.15	-1.49	0.181395	0.305	-6.15
253823_at	putative protein ;supported by full-l	---	AT4G28030	1.10	0.14	1.49	0.181438	0.305044	-6.15
255406_at	hypothetical protein similar to hypo	---	AT4G03450	1.39	0.48	1.49	0.181448	0.305044	-6.15
257958_at	unknown protein similar to disease	---	AT3G25510	-1.15	-0.20	-1.49	0.181586	0.305253	-6.15
247671_at	putative protein slow myosin heavy	---	AT5G60210	-1.10	-0.14	-1.49	0.181766	0.305516	-6.15
250338_at	putative protein ; supported by cDN	---	AT5G11760	1.11	0.15	1.49	0.181769	0.305516	-6.15
259414_at	hypothetical protein contains Pfam	---	AT1G02420	1.15	0.21	1.49	0.181788	0.305524	-6.15
265072_at	hypothetical protein predicted by ge	LAS	AT1G55580	-1.17	-0.23	-1.49	0.18185	0.305606	-6.15
245984_at	putative protein predicted proteins -	---	AT5G13090	1.13	0.18	1.49	0.181989	0.305817	-6.16
259877_at	unknown protein C-terminal portion	SDG26	AT1G76710	-1.16	-0.21	-1.49	0.182012	0.305834	-6.16
257295_at	serine/threonine protein kinase, pu	GPK1	AT3G17420	-1.23	-0.29	-1.49	0.182125	0.306002	-6.16
264902_at	unknown protein Location of EST g	---	AT1G23060	1.28	0.36	1.49	0.182157	0.306017	-6.16
253846_at	putative protein MSP1, Saccharom	---	AT4G28000	-1.10	-0.14	-1.49	0.182161	0.306017	-6.16

260031_at	putative nuclear matrix constituent	LINC3	AT1G68790	1.13	0.18	1.49	0.182261	0.306162	-6.16
257097_at	hypothetical protein predicted by ge	---	---	-1.11	-0.15	-1.49	0.18231	0.306221	-6.16
264865_at	DNAJ-like heatshock protein similar	ARL1	AT1G24120	-1.11	-0.15	-1.49	0.182354	0.306273	-6.16
259337_at	putative cationic amino acid transpo	CAT4	AT3G03720	-1.12	-0.16	-1.49	0.182394	0.306317	-6.16
255717_at	coded for by A. thaliana cDNA H76	---	AT4G00350	-1.12	-0.16	-1.49	0.182473	0.306428	-6.16
263563_at	putative retroelement pol polyprotei	---	---	-1.12	-0.17	-1.49	0.182689	0.306767	-6.16
259155_at	transcription initiation factor IIB (TF	---	AT3G10330	1.16	0.21	1.49	0.182714	0.306777	-6.16
248430_at	putative protein similar to unknown	---	AT5G51800	-1.13	-0.18	-1.49	0.182729	0.306777	-6.16
264917_at	unknown protein contains Pfam pro	---	AT1G60500	-1.10	-0.14	-1.49	0.182734	0.306777	-6.16
254104_at	putative protein predicted protein, A	---	AT4G25040	-1.15	-0.20	-1.49	0.182807	0.306861	-6.16
245958_at	GNOM-like protein pattern-formatio	---	AT5G19610	-1.12	-0.16	-1.48	0.182812	0.306861	-6.16
263767_at	putative retroelement pol polyprotei	---	---	-1.10	-0.14	-1.48	0.182861	0.306922	-6.16
255126_at	putative protein hypothetical protei	---	AT4G08270	-1.10	-0.14	-1.48	0.182893	0.306952	-6.16
260355_at	transcription factor CRC identical to	CRC	AT1G69180	1.17	0.23	1.48	0.182926	0.306986	-6.16
257834_at	alpha-mannosidase, putative simila	---	AT3G26720	1.10	0.14	1.48	0.182954	0.30701	-6.16
265765_at	hypothetical protein predicted by ge	---	AT2G48060	1.14	0.18	1.48	0.183039	0.307129	-6.16
255773_at	flavonol 4'-sulfotransferase, putativ	SOT17	AT1G18590	1.42	0.51	1.48	0.183072	0.307163	-6.16
253246_at	putative protein	---	AT4G34600	1.15	0.20	1.48	0.18311	0.307203	-6.16
258626_at	transfactor, putative similar to trans	---	AT3G04450	1.14	0.19	1.48	0.183159	0.307263	-6.16
265522_at	putative TPR repeat nuclear phospl	ELF8	AT2G06210	1.14	0.19	1.48	0.183215	0.307334	-6.16
266875_at	putative flavonol synthase	---	AT2G44800	-1.15	-0.20	-1.48	0.183271	0.307405	-6.16
253791_at	early auxin-inducible protein 11 (IA	IAA11	AT4G28640	1.16	0.22	1.48	0.183343	0.307504	-6.16
264880_at	hypothetical protein contains simila	---	AT1G61210	-1.15	-0.20	-1.48	0.183358	0.307506	-6.16
250001_at	tub family-like protein tubby-like pr	AtTLP11	AT5G18680	-1.21	-0.27	-1.48	0.183397	0.307549	-6.16
251397_at	putative protein cim1 protein, Glyci	ATEXPB5	AT3G60570	-1.17	-0.23	-1.48	0.183453	0.30762	-6.16
251560_at	squamosa promoter-binding protei	SPL15	AT3G57920	-1.17	-0.23	-1.48	0.183592	0.307809	-6.16
263315_at	Expressed protein ; supported by fu	---	AT2G05755	-1.11	-0.15	-1.48	0.183593	0.307809	-6.16
254193_at	putative protein predicted proteins,	---	AT4G23870	1.42	0.51	1.48	0.183625	0.30782	-6.16
258077_at	unknown protein ;supported by full-	---	AT3G26110	-1.15	-0.20	-1.48	0.183626	0.30782	-6.16
247650_at	putative protein ;supported by full-l	---	AT5G59960	1.22	0.29	1.48	0.183771	0.308041	-6.16
253649_at	putative protein predicted protein, A	---	AT4G29790	1.25	0.32	1.48	0.18389	0.308217	-6.17
257593_at	phosphatidylinositol transfer protei	---	AT3G24840	-1.11	-0.15	-1.48	0.183911	0.308229	-6.17
259319_at	Snf1-related protein kinase KIN10	AKIN10	AT3G01090	1.10	0.14	1.48	0.184005	0.308364	-6.17
252865_at	Expressed protein ; supported by fu	---	AT4G39753	-1.18	-0.24	-1.48	0.184031	0.308386	-6.17
246972_s_a	cytochrome P-450-like protein cyto	CYP71A14	AT5G24950	1.29	0.37	1.48	0.18405	0.308395	-6.17

251609_at	putative protein hypothetical protei	---	AT3G57900	-1.10	-0.13	-1.48	0.184118	0.308461	-6.17
245768_at	hypothetical protein similar to putati	---	AT1G33590	1.31	0.39	1.48	0.184127	0.308461	-6.17
256477_at	unknown protein	---	---	-1.13	-0.17	-1.48	0.18413	0.308461	-6.17
257001_at	Sm protein, putative similar to GB:A	---	AT3G14080	1.13	0.18	1.48	0.184146	0.308464	-6.17
248194_at	Expressed protein ; supported by fu	---	AT5G54095	1.10	0.13	1.48	0.18416	0.308465	-6.17
250844_at	putative protein ;supported by full-l	SIM	AT5G04470	-1.29	-0.36	-1.48	0.184233	0.308566	-6.17
264121_at	putative GTP-binding protein Carb	TOC33	AT1G02280	1.15	0.20	1.48	0.184345	0.308731	-6.17
257266_at	RNA-binding protein contains Pfam	---	AT3G15010	1.11	0.15	1.48	0.184424	0.30883	-6.17
261815_at	leucine zipper protein, putative sim	---	AT1G08320	-1.16	-0.22	-1.48	0.184433	0.30883	-6.17
265135_at	unknown protein similar to unknowr	---	AT1G51270	-1.13	-0.17	-1.48	0.184445	0.30883	-6.17
247633_at	putative zinc finger protein finger p	---	AT5G60470	-1.21	-0.28	-1.48	0.184482	0.30887	-6.17
259046_at	calmodulin-like protein similar to ca	---	AT3G03400	-1.13	-0.17	-1.48	0.184538	0.30894	-6.17
245300_at	hypothetical protein ; supported by	CBL6	AT4G16350	1.11	0.14	1.48	0.184567	0.308965	-6.17
255963_at	unknown protein	MBD8	AT1G22310	-1.13	-0.17	-1.48	0.184651	0.309085	-6.17
262911_s_a	heat shock protein, putative similar	---	AT1G07400	-1.49	-0.57	-1.48	0.184682	0.309114	-6.17
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb	---	---	1.25	0.32	1.48	0.184765	0.309229	-6.17
254839_at	stress-induced protein sti1 -like pro	---	AT4G12400	-1.34	-0.43	-1.48	0.184812	0.309285	-6.17
262242_at	hypothetical protein predicted by ge	---	AT1G48360	-1.16	-0.21	-1.48	0.184838	0.309306	-6.17
250838_at	cytochrome P450 - like protein cyt	CYP77A9	AT5G04630	-1.10	-0.14	-1.48	0.184863	0.309326	-6.17
249405_at	beta subunit of protein farnesyl tran	ERA1	AT5G40280	1.12	0.16	1.48	0.184936	0.309425	-6.17
263993_at	hypothetical protein predicted by ge	---	---	-1.14	-0.19	-1.48	0.184996	0.309502	-6.17
260643_at	hypothetical protein contains simila	---	AT1G53270	-1.12	-0.16	-1.48	0.185019	0.309519	-6.17
250446_at	nucleoid DNA-binding protein cnd4	---	AT5G10770	1.25	0.32	1.48	0.185043	0.309536	-6.17
257539_at	hypothetical protein predicted by ge	---	AT3G29150	-1.11	-0.15	-1.48	0.185116	0.309632	-6.17
249591_at	putative protein predicted protein, A	---	---	-1.10	-0.14	-1.48	0.185129	0.309632	-6.17
246189_at	ABI3-interacting protein 2 ;supporte	---	AT5G20910	1.18	0.24	1.48	0.185148	0.309632	-6.17
266910_at	unknown protein	---	AT2G45920	1.32	0.41	1.48	0.185157	0.309632	-6.17
250311_at	unknown protein	---	AT5G12240	-1.10	-0.14	-1.48	0.185169	0.309632	-6.17
256099_at	cytochrome P450, putative similar	CYP78A5	AT1G13710	-1.20	-0.26	-1.48	0.185258	0.30976	-6.17
251824_at	ABC transporter - like protein ATP-	---	AT3G55090	-1.13	-0.18	-1.47	0.185411	0.309992	-6.17
249284_at	unknown protein ;supported by full-	---	AT5G41810	1.14	0.18	1.47	0.185483	0.310091	-6.17
AFFX-r2-Bs	B. subtilis /GEN=pheB /DB_XREF=	---	---	1.22	0.29	1.47	0.185702	0.310434	-6.17
265795_at	putative serine carboxypeptidase II	scpl26	AT2G35780	1.13	0.18	1.47	0.185789	0.310556	-6.17
247181_at	putative protein similar to unknown	---	AT5G65370	-1.12	-0.16	-1.47	0.186031	0.310938	-6.18
249080_at	putative protein strong similarity to	SUVR2	AT5G43990	-1.17	-0.23	-1.47	0.186087	0.311008	-6.18

245129_at	hypothetical protein predicted by ge	CRR4	AT2G45350	-1.10	-0.13	-1.47	0.186165	0.311116	-6.18
256791_at	hypothetical protein predicted by ge	---	---	-1.17	-0.23	-1.47	0.186218	0.311182	-6.18
262529_at	putative receptor protein kinase Apl	AtRLP3	AT1G17250	1.16	0.21	1.47	0.18625	0.311212	-6.18
266151_x_a	En/Spm transposon protein (mosaic	---	---	-1.13	-0.17	-1.47	0.186331	0.311326	-6.18
263644_at	hypothetical protein predicted by ge	---	AT2G04730	-1.13	-0.17	-1.47	0.186355	0.311343	-6.18
262857_at	major latex homologue type2 identi	---	AT1G14930	-1.11	-0.15	-1.47	0.18642	0.311425	-6.18
262156_at	hypothetical protein contains simila	---	AT1G52680	-1.14	-0.19	-1.47	0.186432	0.311425	-6.18
246973_at	putative protein UBIQUINONE BIO	---	AT5G24970	1.20	0.26	1.47	0.186622	0.31172	-6.18
263462_at	similar to Ariadne protein from Dros	ARI11	AT2G31780	-1.12	-0.16	-1.47	0.186636	0.311721	-6.18
AFFX-DapX	B. subtilis /GEN=jojG /DB_XREF=g	---	---	1.15	0.20	1.47	0.186655	0.311729	-6.18
246170_at	putative protein various predicted p	---	AT5G32450	-1.14	-0.19	-1.47	0.18668	0.311748	-6.18
255369_at	putative NifU-like metallocluster ass	ISU3	AT4G04080	-1.13	-0.18	-1.47	0.186709	0.311774	-6.18
245827_at	disease resistance protein RPS4, p	---	AT1G57830	-1.15	-0.20	-1.47	0.18673	0.31178	-6.18
260150_at	putative oxidoreductase similar to g	---	AT1G52820	-1.14	-0.18	-1.47	0.18674	0.31178	-6.18
261843_at	unknown protein	---	AT1G16180	1.11	0.15	1.47	0.186775	0.311816	-6.18
261946_at	unknown protein	---	AT1G64560	-1.16	-0.21	-1.47	0.1869	0.311996	-6.18
250700_at	CDK5 activator-binding protein-like	---	AT5G06830	1.13	0.18	1.47	0.18691	0.311996	-6.18
245105_at	hypothetical protein predicted by ge	---	AT2G41610	-1.22	-0.29	-1.47	0.186953	0.312023	-6.18
245675_at	hypothetical protein similar to putati	---	---	-1.18	-0.24	-1.47	0.186954	0.312023	-6.18
263783_at	putative WRKY-type DNA binding p	WRKY46	AT2G46400	1.64	0.72	1.47	0.186986	0.312038	-6.18
258228_at	unknown protein similar to unknown	---	AT3G27610	1.11	0.15	1.47	0.187001	0.312038	-6.18
250456_at	26S proteasome p55 protein-like ;	EMB2107	AT5G09900	1.17	0.23	1.47	0.187004	0.312038	-6.18
247467_at	putative protein predicted proteins,	---	AT5G62130	-1.27	-0.34	-1.47	0.187022	0.312046	-6.18
256896_at	hypothetical protein predicted by ge	---	AT3G24630	-1.26	-0.34	-1.47	0.18708	0.312119	-6.18
262125_at	heat shock protein, putative similar	EDA1	AT1G59680	-1.13	-0.17	-1.47	0.187097	0.312125	-6.18
256187_at	55 kDa B regulatory subunit of phos	ATB ALPH/	AT1G51690	1.15	0.20	1.47	0.18713	0.312145	-6.18
260447_at	hypothetical protein similar to N-ter	---	AT1G72410	-1.11	-0.14	-1.47	0.187138	0.312145	-6.18
256636_at	S-locus related protein SLR1 homo	---	AT3G12000	-1.11	-0.16	-1.47	0.18715	0.312145	-6.18
260640_at	viral resistance protein, putative sir	---	AT1G53350	1.30	0.38	1.47	0.187206	0.312215	-6.18
264896_at	Hypothetical protein similar to endo	AtGH9B6	AT1G23210	-1.12	-0.17	-1.47	0.187265	0.31229	-6.18
246481_s_a	cold and ABA inducible protein kin1	KIN1	AT5G15960	-1.88	-0.91	-1.47	0.18728	0.312292	-6.18
251123_at	putative protein predicted proteins,	---	AT5G01030	1.11	0.15	1.47	0.187293	0.312292	-6.18
264948_at	RNA helicase, putative similar to R	---	AT1G77030	1.11	0.16	1.47	0.18743	0.312497	-6.18
265925_at	hypothetical protein predicted by ge	---	AT2G18610	-1.12	-0.16	-1.47	0.187496	0.312584	-6.18
247337_at	putative protein similar to unknown	PDF2.5	AT5G63660	-1.10	-0.14	-1.47	0.18751	0.312585	-6.18

263593_at	hypothetical protein predicted by ge	EMB975	AT2G01860	1.16	0.21	1.47	0.187547	0.312593	-6.18
246330_at	aldehyde oxidase ; supported by cl	AAO2	AT3G43600	1.33	0.41	1.47	0.187577	0.312593	-6.18
247016_at	putative protein contains similarity t	---	AT5G66970	1.13	0.18	1.47	0.187584	0.312593	-6.18
266209_at	similar to terminal flower ; supporte	ATC	AT2G27550	-1.21	-0.28	-1.47	0.187587	0.312593	-6.18
257322_at	hypothetical protein	AT2G0766	---	-1.14	-0.19	-1.47	0.187596	0.312593	-6.18
260172_s_a	putative histidinol-phosphate amino	---	AT1G71920	1.17	0.23	1.47	0.18761	0.312593	-6.18
251971_at	glucosyltransferase - like protein gl	UGT73C7	AT3G53160	1.83	0.87	1.47	0.18761	0.312593	-6.18
257064_at	hypothetical protein predicted by ge	---	AT3G18260	1.16	0.21	1.47	0.187695	0.312711	-6.18
257273_at	hypothetical protein contains Pfam	UVH3	AT3G28030	1.15	0.20	1.47	0.187712	0.312716	-6.18
248053_at	putative protein similar to unknown	AtNMNAT	AT5G55810	1.14	0.19	1.47	0.187734	0.312731	-6.18
260510_at	hypothetical protein predicted by ge	---	AT1G51580	-1.22	-0.29	-1.47	0.187791	0.312784	-6.18
263407_at	bZIP protein (AtbZIP48) to be publis	AtbZIP48	AT2G04038	-1.12	-0.16	-1.47	0.187794	0.312784	-6.18
252601_s_a	40S ribsomomal protein 40S ribsor	---	AT3G45030	1.25	0.32	1.47	0.187821	0.312807	-6.18
245961_at	putative protein predicted proteins -	---	AT5G19670	1.15	0.20	1.47	0.187846	0.312807	-6.18
266644_at	unknown protein ;supported by full-	---	AT2G29660	1.16	0.22	1.47	0.187849	0.312807	-6.18
246678_at	putative protein predicted replicatio	---	---	1.14	0.18	1.47	0.187922	0.312906	-6.18
249191_at	putative protein similar to unknown	---	AT5G42760	-1.17	-0.22	-1.47	0.187979	0.312965	-6.18
245126_at	putative MYB family transcription fa	MYB12	AT2G47460	-1.11	-0.16	-1.47	0.187985	0.312965	-6.19
267264_at	putative serine carboxypeptidase II	SCPL11	AT2G22970	1.38	0.47	1.46	0.18807	0.313084	-6.19
250379_at	transcription factor like protein tran	TINY2	AT5G11590	-1.11	-0.15	-1.46	0.188086	0.313087	-6.19
257742_at	hypothetical protein predicted by ge	SDH2-1	AT3G27380	-1.12	-0.17	-1.46	0.188116	0.313115	-6.19
254111_at	putative protein acid phosphatase (	PAP24	AT4G24890	-1.20	-0.26	-1.46	0.188154	0.313155	-6.19
256462_at	hypothetical protein predicted by ge	---	AT1G36230	-1.14	-0.18	-1.46	0.188203	0.313213	-6.19
266020_at	hypothetical protein	SDG11	AT2G05900	-1.16	-0.21	-1.46	0.18827	0.313302	-6.19
249183_at	E2, ubiquitin-conjugating enzyme 1	UBC18	AT5G42990	1.11	0.15	1.46	0.188346	0.313407	-6.19
252682_at	putative protein AtOXA1, Arabidop	---	AT3G44370	-1.15	-0.20	-1.46	0.188376	0.313432	-6.19
256024_at	unknown protein contains Pfam pro	ZF14	AT1G58340	1.35	0.44	1.46	0.188389	0.313432	-6.19
262826_at	putative cytochrome P450 monoox	CYP71B2	AT1G13080	1.29	0.37	1.46	0.188505	0.313602	-6.19
255362_at	putative reverse transcriptase	---	---	-1.10	-0.14	-1.46	0.188645	0.313812	-6.19
248092_at	ubiquitin-like protein	SUMO3	AT5G55170	-1.44	-0.52	-1.46	0.188735	0.313939	-6.19
261598_at	unknown protein contains similarity	---	AT1G49750	-1.69	-0.75	-1.46	0.188815	0.31405	-6.19
251950_at	zinc finger - like protein Zat11 zinc	---	AT3G53600	1.92	0.94	1.46	0.188949	0.314249	-6.19
263588_s_a	unknown protein	---	AT2G25320	-1.12	-0.16	-1.46	0.189037	0.314373	-6.19
251080_at	putative protein hypothetical protein	ROPGEF7	AT5G02010	1.32	0.40	1.46	0.189092	0.314441	-6.19
255467_at	putative leucine-rich repeat protein	---	AT4G03010	-1.12	-0.17	-1.46	0.189135	0.314489	-6.19

265657_at	unknown protein ; supported by cD	---	AT2G13840	1.13	0.18	1.46	0.189156	0.314501	-6.19
253731_at	acid phosphatase-like protein acid	---	AT4G29260	1.10	0.14	1.46	0.189176	0.314512	-6.19
259478_at	germin, putative similar to germin G	---	AT1G18980	2.02	1.02	1.46	0.189198	0.314526	-6.19
260967_at	unknown protein contains similarity	---	AT1G12230	-1.16	-0.21	-1.46	0.189232	0.314537	-6.19
260757_at	phytocyanin, putative similar to phy	---	AT1G48940	-1.11	-0.15	-1.46	0.189233	0.314537	-6.19
249560_at	putative protein	LCR80	AT5G38330	-1.20	-0.26	-1.46	0.18928	0.314593	-6.19
258061_at	unknown protein ; supported by cD	---	AT3G25910	1.13	0.17	1.46	0.1893	0.314603	-6.19
263933_s_a	putative harpin-induced protein	---	AT2G35970	-1.13	-0.17	-1.46	0.189313	0.314603	-6.19
260068_at	putative calmodulin-binding protein	---	AT1G73805	-1.44	-0.53	-1.46	0.189398	0.314721	-6.19
260437_at	hypothetical protein predicted by ge	---	AT1G68380	-1.12	-0.17	-1.46	0.189469	0.314816	-6.19
267342_at	putative heme A:farnesyltransferase	COX10	AT2G44520	1.20	0.26	1.46	0.189503	0.31485	-6.19
262621_at	hypothetical protein	---	AT1G06530	1.12	0.17	1.46	0.189675	0.315109	-6.19
267583_at	unknown protein	---	AT2G41960	-1.10	-0.13	-1.46	0.189715	0.315109	-6.19
245432_at	putative serine protease-like protein	---	AT4G17100	-1.10	-0.14	-1.46	0.189719	0.315109	-6.19
257790_at	gda-1, putative similar to gda-1 GB	---	AT3G27090	1.16	0.22	1.46	0.189724	0.315109	-6.19
265737_at	putative phosphatidic acid phospha	ATPAP1	AT2G01180	-1.59	-0.67	-1.46	0.189735	0.315109	-6.19
258537_at	putative disease resistance protein	---	AT3G04210	-1.57	-0.65	-1.46	0.189742	0.315109	-6.19
245638_s_a	F5A9.10 unknown protein; similar t	---	AT1G24822	-1.12	-0.17	-1.46	0.189819	0.315214	-6.19
254533_at	putative protein ARI protein - Drosc	---	AT4G19670	1.19	0.25	1.46	0.189849	0.315241	-6.19
261095_at	unknown protein	---	AT1G62930	1.14	0.19	1.46	0.189971	0.31542	-6.19
249436_at	putative protein crp1 protein - Zea	---	AT5G39980	1.20	0.26	1.46	0.19007	0.315561	-6.19
248285_at	putative protein similar to unknown	---	AT5G52960	-1.09	-0.13	-1.46	0.190085	0.315563	-6.20
247484_at	putative protein predicted proteins,	---	AT5G62110	-1.12	-0.16	-1.46	0.190281	0.315866	-6.20
259918_at	putative AP2 domain transcription fa	---	AT1G72570	-1.11	-0.15	-1.46	0.1903	0.315874	-6.20
255497_at	hypothetical protein similar to A. th	UNE12	AT4G02590	1.12	0.16	1.46	0.190333	0.315905	-6.20
265762_at	hypothetical protein	---	AT2G01240	-1.18	-0.23	-1.46	0.190428	0.31604	-6.20
255343_at	hypothetical protein	---	---	-1.09	-0.13	-1.46	0.190468	0.316085	-6.20
246101_at	putative protein	---	---	-1.13	-0.18	-1.46	0.190486	0.316091	-6.20
254414_at	hypothetical protein	HSA32	AT4G21320	-1.16	-0.21	-1.46	0.190561	0.316193	-6.20
248319_at	unknown protein	---	AT5G52710	-1.11	-0.15	-1.46	0.190614	0.316257	-6.20
258844_at	hypothetical protein predicted by ge	SWP	AT3G04740	1.11	0.15	1.46	0.190629	0.316259	-6.20
248599_at	putative protein contains similarity t	---	AT5G49380	-1.20	-0.27	-1.45	0.19072	0.316367	-6.20
265801_at	fertilization-independent seed 2 pro	FIS2	AT2G35670	-1.12	-0.17	-1.45	0.190722	0.316367	-6.20
246862_at	E2, ubiquitin-conjugating enzyme,	PEX4	AT5G25760	1.12	0.16	1.45	0.190872	0.316589	-6.20
252354_at	betaine aldehyde dehydrogenase-l	ALDH10A9	AT3G48170	1.11	0.15	1.45	0.190884	0.316589	-6.20

260492_at	putative polygalacturonase	PGAZAT	AT2G41850	-1.18	-0.24	-1.45	0.190903	0.316589	-6.20
265324_at	hypothetical protein predicted by ge	ATCOAD	AT2G18250	1.15	0.20	1.45	0.190911	0.316589	-6.20
246145_at	peroxidase peroxidase, Lycopersic	---	AT5G19880	1.39	0.47	1.45	0.190931	0.316598	-6.20
252776_at	putative protein predicted proteins,	---	AT3G42940	-1.14	-0.19	-1.45	0.191065	0.316798	-6.20
258348_at	unknown protein ;supported by full-	---	AT3G17710	1.13	0.17	1.45	0.191083	0.316805	-6.20
260508_at	Unknown protein ; supported by cD	GAMMA CA	AT1G47260	-1.11	-0.15	-1.45	0.191175	0.316935	-6.20
255475_at	contains a short region of similarity	---	AT4G02480	-1.15	-0.20	-1.45	0.191248	0.317032	-6.20
259704_at	putative 3'-5' exoribonuclease simila	---	AT1G77680	-1.15	-0.21	-1.45	0.191268	0.317036	-6.20
259022_at	putative asparaginyl-tRNA syntheta	NS2	AT3G07420	-1.20	-0.26	-1.45	0.191278	0.317036	-6.20
246143_at	lipophosphoglycan biosynthetic pro	---	AT5G19980	-1.18	-0.24	-1.45	0.191317	0.317044	-6.20
263162_at	hypothetical protein predicted by ge	---	AT1G54150	-1.10	-0.14	-1.45	0.191321	0.317044	-6.20
247521_at	putative protein ATP/GTP nucleotic	---	AT5G61450	1.14	0.18	1.45	0.191325	0.317044	-6.20
260303_at	putative protein kinase similar to C	---	AT1G70520	1.28	0.35	1.45	0.191357	0.317069	-6.20
256834_at	cyclophilin, putative similar to cyclo	---	AT3G22920	-1.11	-0.15	-1.45	0.191367	0.317069	-6.20
261928_at	uclacyanin II, putative similar to ucl	---	AT1G22480	-1.19	-0.25	-1.45	0.191431	0.317144	-6.20
265210_at	60S ribosomal protein L24 ;suppor	RPL24A	AT2G36620	1.44	0.53	1.45	0.19144	0.317144	-6.20
259135_at	hypothetical protein predicted by ge	RAD9	AT3G05480	-1.19	-0.25	-1.45	0.19147	0.317171	-6.20
267487_at	putative non-LTR retroelement reve	---	---	-1.13	-0.18	-1.45	0.191685	0.317503	-6.20
245898_at	ser/thr specific protein kinase-like p	---	AT5G11020	-1.16	-0.21	-1.45	0.191708	0.317509	-6.20
246355_at	hypothetical protein	---	---	-1.26	-0.33	-1.45	0.191716	0.317509	-6.20
267032_at	putative protein kinase contains a p	CIPK22	AT2G38490	-1.20	-0.26	-1.45	0.191745	0.317531	-6.20
263955_at	putative E2F5 family transcription fa	E2F3	AT2G36010	-1.19	-0.25	-1.45	0.191758	0.317531	-6.20
256347_at	unknown protein similar to putative	---	---	1.13	0.17	1.45	0.191837	0.31764	-6.20
254584_at	putative protein probable membran	VPS54	AT4G19490	-1.11	-0.15	-1.45	0.19189	0.317682	-6.20
245051_at	putative WRKY-type DNA-binding p	WRKY15	AT2G23320	1.31	0.39	1.45	0.19189	0.317682	-6.20
266504_at	hypothetical protein predicted by ge	---	AT2G47820	1.15	0.20	1.45	0.191974	0.317797	-6.20
250068_at	CHP-rich zinc finger protein-like	---	AT5G17960	-1.15	-0.20	-1.45	0.19201	0.317834	-6.20
262250_at	Expressed protein predicted by gen	---	AT1G48280	-1.47	-0.56	-1.45	0.192057	0.317888	-6.20
252134_at	putative protein ; supported by cDN	---	AT3G50910	1.33	0.41	1.45	0.192252	0.318188	-6.21
257262_at	zinc finger protein, putative contain	---	AT3G21890	-1.24	-0.32	-1.45	0.1923	0.318244	-6.21
261261_at	putative aldehyde oxidase	---	AT1G26730	-1.54	-0.62	-1.45	0.192473	0.318508	-6.21
249114_at	putative protein similar to unknown	---	---	-1.16	-0.21	-1.45	0.192494	0.318519	-6.21
265554_at	hypothetical protein predicted by ge	---	AT2G07505	-1.10	-0.14	-1.45	0.192543	0.318578	-6.21
257501_at	hypothetical protein predicted by ge	---	---	-1.09	-0.13	-1.45	0.192583	0.318597	-6.21
256029_at	integral membrane protein, putative	STT3B	AT1G34130	1.26	0.33	1.45	0.192587	0.318597	-6.21

267293_at	hypothetical protein	TET8	AT2G23810	1.23	0.30	1.45	0.192608	0.318597	-6.21
248640_at	selenium-binding protein-like ; supp	---	AT5G48910	1.14	0.19	1.45	0.192611	0.318597	-6.21
259019_at	hypothetical protein similar to serol	CHIP	AT3G07370	1.13	0.17	1.45	0.192645	0.318631	-6.21
260520_at	mannosyl-oligosaccharide alpha-1,	---	AT1G51590	1.13	0.18	1.45	0.192771	0.318806	-6.21
249083_at	prohibitin non-consensus TT accep	ATPHB7	AT5G44140	1.12	0.16	1.45	0.192779	0.318806	-6.21
263703_at	unknown protein ;supported by full-	SRX	AT1G31170	1.14	0.19	1.45	0.192844	0.31889	-6.21
247017_at	putative protein similar to unknown	---	AT5G66980	-1.10	-0.13	-1.45	0.192987	0.319103	-6.21
260741_at	hypothetical protein contains Pfam	---	AT1G15040	2.56	1.36	1.45	0.193031	0.319153	-6.21
254128_at	ubiquitin-specific protease 16 (UBF	UBP16	AT4G24560	1.09	0.13	1.45	0.193051	0.319163	-6.21
249389_at	disease resistence like - protein do	---	AT5G40100	-1.15	-0.21	-1.45	0.193164	0.319307	-6.21
262144_at	hypothetical protein predicted by ge	---	AT1G52620	1.11	0.15	1.45	0.193166	0.319307	-6.21
257213_at	mitochondrial NAD-dependent mal	---	AT3G15020	1.23	0.29	1.44	0.193453	0.319756	-6.21
245833_at	transposon protein, putative similar	---	---	-1.13	-0.18	-1.44	0.193466	0.319756	-6.21
249771_at	receptor-like protein kinase ; suppo	---	AT5G24080	-1.20	-0.27	-1.44	0.193495	0.319782	-6.21
256206_at	hypothetical protein predicted by ge	---	AT1G50910	-1.17	-0.23	-1.44	0.193533	0.319821	-6.21
261867_at	unknown protein ; supported by cDI	---	AT1G50575	-1.14	-0.19	-1.44	0.193601	0.31991	-6.21
264303_s_a	E2, ubiquitin-conjugating enzyme,	UBC35	AT1G16890	1.12	0.16	1.44	0.193634	0.319941	-6.21
256854_at	hypothetical protein predicted by ge	---	AT3G15180	1.11	0.16	1.44	0.193693	0.320003	-6.21
246685_at	putative protein nucleoid DNA-bind	---	AT5G33350	-1.23	-0.30	-1.44	0.1937	0.320003	-6.21
253971_at	fructose-bisphosphate aldolase - lil	---	AT4G26530	1.28	0.36	1.44	0.19372	0.320015	-6.21
266969_at	similar to gibberellin-regulated prote	---	AT2G39540	-1.15	-0.20	-1.44	0.193782	0.320094	-6.21
255321_at	putative ES43-like protein	---	AT4G04260	1.13	0.17	1.44	0.193898	0.320261	-6.21
251591_at	carboxyl terminal protease - like pr	---	AT3G57680	1.23	0.30	1.44	0.193917	0.320271	-6.21
251034_at	putative protein ;supported by full-l	PRA1.A1	AT5G02040	1.13	0.17	1.44	0.193986	0.32036	-6.21
253483_at	putative protein anthranilate N-hyd	---	AT4G31910	-1.23	-0.30	-1.44	0.194103	0.320531	-6.21
263886_at	hypothetical protein predicted by ge	TKI1	AT2G36960	-1.10	-0.14	-1.44	0.1942	0.320659	-6.21
255092_s_a	putative protein various predicted p	---	---	-1.12	-0.16	-1.44	0.194209	0.320659	-6.21
254556_at	putative protein various predicted p	---	AT4G19220	1.18	0.24	1.44	0.194245	0.320696	-6.21
252498_at	putative protein several hypothetica	---	AT3G46810	-1.10	-0.14	-1.44	0.194404	0.320934	-6.22
258507_at	neutral invertase, putative similar t	---	AT3G06500	1.31	0.39	1.44	0.194512	0.32109	-6.22
262461_at	myosin, putative similar to myosin (	VIIIA	AT1G50360	1.23	0.30	1.44	0.19453	0.321097	-6.22
254098_at	superoxide dismutase (EC 1.15.1.1	FSD1	AT4G25100	1.16	0.21	1.44	0.194658	0.321284	-6.22
256032_at	polyprotein, putative similar to poly	---	---	-1.09	-0.12	-1.44	0.194686	0.321306	-6.22
250162_at	FtsH protease, putative similar to F	FTSH6	AT5G15250	-1.10	-0.14	-1.44	0.194768	0.321404	-6.22
256973_at	unknown protein similar to putative	---	AT3G20980	-1.12	-0.16	-1.44	0.194786	0.321404	-6.22

255942_at	UDP-glucose glucosyltransferase ic	AtUGT85A1	AT1G22360	-1.48	-0.56	-1.44	0.194787	0.321404	-6.22
267266_at	putative metal ion transporter (NRA	NRAMP3	AT2G23150	1.12	0.16	1.44	0.194827	0.321438	-6.22
254644_at	CLE2, putative CLAVATA3/ESR-R	CLE2	AT4G18510	-1.14	-0.18	-1.44	0.194835	0.321438	-6.22
253543_at	hypothetical protein	---	AT4G31270	-1.12	-0.16	-1.44	0.194878	0.321484	-6.22
259900_at	c-Jun coactivator-like protein (AJH2	CSN5B	AT1G71230	1.10	0.14	1.44	0.194918	0.321527	-6.22
266722_at	unknown protein	FUT2	AT2G03210	-1.13	-0.18	-1.44	0.194971	0.321591	-6.22
256680_at	unknown protein ; supported by full-	---	AT3G52230	-1.18	-0.24	-1.44	0.195008	0.321629	-6.22
254917_at	putative protein various hypothetica	---	AT4G11350	1.20	0.27	1.44	0.195039	0.321657	-6.22
263952_s_a	unknown protein ;supported by full-	---	AT2G35810	1.12	0.16	1.44	0.195203	0.321904	-6.22
245235_at	putative protein similarity to predict	---	AT4G25550	1.13	0.17	1.44	0.195244	0.321949	-6.22
264407_at	unknown protein similar to EST gb|	---	AT1G10180	1.15	0.20	1.44	0.195293	0.322007	-6.22
253620_at	receptor-like kinase homolog soma	---	AT4G30520	1.13	0.18	1.44	0.19536	0.322094	-6.22
248618_at	myb-related transcription factor	AtMYB78	AT5G49620	1.14	0.19	1.44	0.19541	0.322153	-6.22
251049_at	putative protein rab11 binding prote	---	AT5G02430	-1.13	-0.18	-1.44	0.195447	0.32219	-6.22
250186_at	putative protein apospory-associat	---	AT5G14500	1.15	0.20	1.44	0.19547	0.322204	-6.22
264767_at	hypothetical protein similar to putati	SD1-29	AT1G61380	1.35	0.44	1.44	0.195526	0.322274	-6.22
249234_at	putative protein similar to unknown	---	AT5G42200	-1.24	-0.31	-1.44	0.195598	0.32237	-6.22
256349_at	late embryogenesis protein, putativ	---	AT1G54890	2.72	1.44	1.44	0.195709	0.322529	-6.22
267131_at	hypothetical protein predicted by ge	---	AT2G23400	1.10	0.14	1.44	0.195791	0.32264	-6.22
258574_at	hypothetical protein	---	AT3G04250	-1.12	-0.16	-1.44	0.19588	0.322764	-6.22
249297_at	unknown protein	---	AT5G41320	-1.11	-0.15	-1.44	0.195987	0.322918	-6.22
258558_at	hypothetical protein predicted by ge	---	AT3G06000	-1.09	-0.12	-1.44	0.196004	0.322922	-6.22
248544_at	putative protein contains similarity t	PIMT2	AT5G50240	1.24	0.31	1.44	0.196026	0.322935	-6.22
248256_at	developmental protein SINA (seven	---	AT5G53360	-1.13	-0.18	-1.43	0.196136	0.323093	-6.22
264552_at	hypothetical protein predicted by ge	---	AT1G09470	-1.19	-0.26	-1.43	0.196198	0.323171	-6.22
246344_at	putative protein predicted proteins -	---	AT3G56730	1.24	0.32	1.43	0.196247	0.323229	-6.22
249609_at	putative protein predicted proteins,	---	---	-1.11	-0.15	-1.43	0.196281	0.323262	-6.22
245329_at	Expressed protein ; supported by fu	---	AT4G14365	-1.35	-0.43	-1.43	0.19631	0.323285	-6.22
256816_at	unknown protein	---	AT3G21400	1.13	0.18	1.43	0.196374	0.323367	-6.22
247532_at	putative protein disease resistance	---	AT5G61560	1.40	0.48	1.43	0.196453	0.323441	-6.22
247431_at	putative protein similar to unknown	SRO5	AT5G62520	-1.29	-0.37	-1.43	0.19647	0.323441	-6.22
256967_at	hypothetical protein predicted by g	---	AT3G21060	-1.13	-0.18	-1.43	0.196471	0.323441	-6.22
251716_at	anthranilate synthase alpha-1 chai	---	AT3G55870	-1.11	-0.15	-1.43	0.196494	0.323441	-6.22
246930_at	KNAT3 homeodomain protein ;sup	KNAT3	AT5G25220	1.15	0.20	1.43	0.196496	0.323441	-6.22
260962_at	pectin methylesterase, putative sim	PME7	AT1G44980	1.13	0.17	1.43	0.196508	0.323441	-6.22

263103_at	putative Ta11-like non-LTR retroele	---	---	-1.12	-0.17	-1.43	0.196528	0.323441	-6.23
252191_at	putative protein various predicted g	---	AT3G50180	-1.14	-0.18	-1.43	0.196532	0.323441	-6.23
263935_at	unknown protein	PUB23	AT2G35930	2.02	1.02	1.43	0.196612	0.323549	-6.23
254413_at	myb-related protein M4 ;supported	ATMYB102	AT4G21440	-1.21	-0.27	-1.43	0.196628	0.323552	-6.23
266007_at	unknown protein	---	AT2G37380	-1.15	-0.20	-1.43	0.196719	0.323679	-6.23
253523_at	putative protein myosin heavy chai	---	AT4G31340	-1.12	-0.17	-1.43	0.196771	0.323741	-6.23
265046_s_a	mutator-like transposase, putative	---	---	-1.12	-0.16	-1.43	0.196837	0.323826	-6.23
257384_at	unknown protein	---	AT2G15110	-1.12	-0.16	-1.43	0.196963	0.32401	-6.23
252953_at	putative phosphatidylinositol syntha	PIS2	AT4G38570	-1.12	-0.16	-1.43	0.197036	0.324107	-6.23
245048_at	orf within trnK intron orf within trnK	---	---	-1.18	-0.23	-1.43	0.1971	0.324189	-6.23
251352_at	putative protein hypothetical protei	PEX11E	AT3G61070	1.16	0.22	1.43	0.197265	0.324437	-6.23
246255_at	transcription initiation factor like pro	ATPBRP	AT4G36650	1.13	0.18	1.43	0.197427	0.32468	-6.23
252761_at	putative protein several hypothetica	---	AT3G42770	-1.20	-0.26	-1.43	0.197519	0.324808	-6.23
260795_at	CLE3, putative CLAVATA3/ESR-R	CLE3	AT1G06225	-1.12	-0.16	-1.43	0.197563	0.324838	-6.23
252310_at	GTPase activating -like protein GT	---	AT3G49350	-1.25	-0.32	-1.43	0.19759	0.324838	-6.23
247576_at	putative protein predicted protein, A	---	AT5G61280	-1.09	-0.13	-1.43	0.19759	0.324838	-6.23
246416_at	putative protein predicted proteins,	---	AT5G16920	-1.12	-0.16	-1.43	0.197603	0.324838	-6.23
264080_at	putative vacuolar proton-ATPase su	VHA-A1	AT2G28520	-1.10	-0.14	-1.43	0.197608	0.324838	-6.23
264268_at	hypothetical protein predicted by ge	ULP1D	AT1G60220	1.11	0.15	1.43	0.197667	0.324911	-6.23
261790_at	unknown protein ; supported by full-	---	AT1G16000	-1.20	-0.26	-1.43	0.197705	0.324949	-6.23
263928_at	hypothetical protein predicted by ge	---	AT2G36330	1.18	0.24	1.43	0.197731	0.324968	-6.23
264305_at	Expressed protein ; supported by fu	LSH7	AT1G78815	-1.11	-0.15	-1.43	0.197772	0.325014	-6.23
248910_at	serine threonine protein kinase ; su	CIPK20	AT5G45820	-1.23	-0.30	-1.43	0.197805	0.325044	-6.23
266061_at	putative translation initiation factor e	---	AT2G18720	-1.13	-0.17	-1.43	0.19784	0.325058	-6.23
247940_at	phosphatidylserine decarboxylase	PSD2	AT5G57190	1.40	0.48	1.43	0.197852	0.325058	-6.23
265052_at	caffeic acid O-methyltransferase, p	---	AT1G51990	-1.10	-0.14	-1.43	0.197857	0.325058	-6.23
250860_at	amino acid transport - like protein a	CAT6	AT5G04770	-1.28	-0.36	-1.43	0.197955	0.325197	-6.23
257363_at	hypothetical protein predicted by ge	BAP2	AT2G45760	-1.17	-0.22	-1.43	0.197987	0.325226	-6.23
266406_at	hypothetical protein predicted by ge	---	AT2G38570	-1.14	-0.19	-1.43	0.198103	0.325363	-6.23
254572_at	putative protein predicted protein M	---	AT4G19380	-1.12	-0.16	-1.43	0.198105	0.325363	-6.23
264496_at	putative polyprotein similar to GB:A	---	---	-1.14	-0.19	-1.43	0.198114	0.325363	-6.23
253959_at	putative protein	---	AT4G26410	1.11	0.15	1.43	0.198269	0.32552	-6.23
249611_at	putative protein unnamed ORF, Ho	ATSRL1	AT5G37370	1.15	0.20	1.43	0.198273	0.32552	-6.23
257873_at	P-glycoprotein, putative similar to P	PGP17	AT3G28380	-1.15	-0.20	-1.43	0.198275	0.32552	-6.23
262630_at	unknown protein ;supported by full-	GPAT1	AT1G06520	1.51	0.60	1.43	0.198278	0.32552	-6.23

256214_x_a	hypothetical protein predicted by ge	---	AT1G51000	-1.12	-0.16	-1.43	0.19829	0.32552	-6.23
254680_at	phytochrome E	PHYE	AT4G18130	1.16	0.21	1.43	0.198295	0.32552	-6.23
260769_at	Expressed protein ; supported by fu	---	AT1G49010	1.23	0.29	1.43	0.198393	0.325643	-6.23
253961_at	putative protein SPF1 protein, Ipon	WRKY34	AT4G26440	-1.10	-0.14	-1.43	0.198398	0.325643	-6.23
267606_at	putative beta-ketoacyl-CoA synthas	KCS11	AT2G26640	-1.10	-0.14	-1.43	0.198497	0.325763	-6.23
264580_at	unknown protein EST gb|ATTS029	---	AT1G05340	-1.28	-0.36	-1.43	0.1985	0.325763	-6.23
266929_at	putative AT-hook DNA-binding prot	---	AT2G45850	-1.12	-0.17	-1.43	0.198535	0.325798	-6.23
264711_at	hypothetical protein predicted by ge	---	AT1G09800	1.12	0.16	1.43	0.198572	0.325834	-6.23
AFFX-r2-Bs	B. subtilis /GEN=jojG /DB_XREF=g	---	---	1.21	0.27	1.43	0.198655	0.325947	-6.23
248452_at	putative protein contains similarity t	---	AT5G51300	1.09	0.13	1.42	0.198905	0.326334	-6.24
253859_at	Expressed protein ; supported by fu	---	AT4G27657	2.13	1.09	1.42	0.198991	0.326447	-6.24
247739_at	40S ribosomal protein S8 - like 40	---	AT5G59240	1.16	0.22	1.42	0.199003	0.326447	-6.24
257703_at	unknown protein ; supported by full	---	AT3G12640	1.10	0.14	1.42	0.199029	0.326466	-6.24
249852_at	monosaccharide transporter	STP11	AT5G23270	-1.13	-0.17	-1.42	0.199045	0.326469	-6.24
261936_at	seed maturation protein PM27, put	---	AT1G22600	-1.17	-0.23	-1.42	0.199074	0.326494	-6.24
266739_at	unknown protein predicted by gens	---	AT2G46730	1.12	0.16	1.42	0.199288	0.326821	-6.24
248965_at	nodulin-like protein	---	AT5G45370	-1.16	-0.21	-1.42	0.199327	0.32686	-6.24
262445_at	Expressed protein ; supported by fu	---	AT1G47485	-1.12	-0.16	-1.42	0.19934	0.32686	-6.24
264155_at	unknown protein	GTB1	AT1G65440	1.18	0.24	1.42	0.199358	0.326866	-6.24
249112_at	ATP sulfurylase precursor (gb|AAD	APS4	AT5G43780	1.24	0.32	1.42	0.19942	0.326944	-6.24
263208_at	zinc finger protein 5, ZFP5 possible	ZFP5	AT1G10480	-1.15	-0.21	-1.42	0.199548	0.32713	-6.24
254135_at	putative protein MSP1 protein, Sac	---	AT4G24860	-1.13	-0.17	-1.42	0.199579	0.327157	-6.24
249796_at	26S proteasome, non-ATPase regu	---	AT5G23540	1.12	0.16	1.42	0.199723	0.327348	-6.24
254138_at	hypothetical protein	---	AT4G24950	-1.11	-0.16	-1.42	0.199724	0.327348	-6.24
253100_at	cytochrome P450 monooxygenase	CYP81F3	AT4G37400	1.43	0.52	1.42	0.199802	0.327445	-6.24
266965_at	nodulin-like protein	---	AT2G39510	-1.12	-0.16	-1.42	0.199812	0.327445	-6.24
265515_at	hypothetical protein predicted by ge	---	---	-1.12	-0.16	-1.42	0.199853	0.327467	-6.24
253654_at	putative protein several hypothetica	---	AT4G30060	-1.28	-0.36	-1.42	0.199854	0.327467	-6.24
250904_at	subtilisin-like serine protease conta	---	AT5G03620	-1.11	-0.15	-1.42	0.199929	0.327567	-6.24
254748_at	unknown protein	---	---	-1.11	-0.16	-1.42	0.200022	0.327695	-6.24
249967_at	putative protein	---	AT5G19050	1.12	0.17	1.42	0.200037	0.327697	-6.24
258341_at	unknown protein similar to centrom	---	AT3G22790	-1.44	-0.52	-1.42	0.200186	0.327917	-6.24
251905_at	putative protein zinc finger protein	GAPB	AT1G42970	-1.13	-0.18	-1.42	0.200227	0.32796	-6.24
263951_at	putative harpin-induced protein ;su	NHL12	AT2G35960	-1.47	-0.56	-1.42	0.200425	0.328262	-6.24
262596_at	putative phosphatidic acid phospha	LPP2	AT1G15080	-1.14	-0.18	-1.42	0.200494	0.328348	-6.24

264876_at	hypothetical protein	---	AT2G17410	-1.13	-0.17	-1.42	0.200506	0.328348	-6.24
264422_at	unknown protein similar to unknowr	LCV2	AT1G43130	1.13	0.17	1.42	0.200577	0.328415	-6.24
264694_at	receptor serine/threonine kinase P	---	AT1G70250	1.10	0.14	1.42	0.2006	0.328415	-6.24
246770_at	putative protein DNA-binding prote	---	AT5G27460	1.16	0.21	1.42	0.200607	0.328415	-6.24
245513_at	SYBL1 like protein	ATVAMP72	AT4G15780	1.24	0.31	1.42	0.200632	0.328415	-6.24
246720_at	putative protein predicted proteins,	---	AT5G28950	-1.09	-0.12	-1.42	0.200638	0.328415	-6.24
249831_at	putative protein contains similarity t	---	AT5G23340	1.24	0.31	1.42	0.200669	0.328415	-6.24
253241_at	fatty acid elongase 1	KCS18	AT4G34520	-1.17	-0.23	-1.42	0.200669	0.328415	-6.24
245192_at	F12A21.9 hypothetical protein	---	AT1G67780	1.10	0.14	1.42	0.200669	0.328415	-6.24
260212_at	hypothetical protein predicted by ge	---	AT1G74480	-1.10	-0.13	-1.42	0.200677	0.328415	-6.24
260204_at	hypothetical protein predicted by ge	---	AT1G52900	-1.12	-0.16	-1.42	0.200757	0.328522	-6.24
247169_at	unknown protein	---	AT5G65520	-1.17	-0.23	-1.42	0.20091	0.328749	-6.24
261264_at	hypothetical protein predicted by ge	---	AT1G26710	-1.15	-0.20	-1.42	0.200975	0.328813	-6.25
261910_at	zinc finger protein identical to GB:A	ZFP1	AT1G80730	-1.10	-0.14	-1.42	0.200978	0.328813	-6.25
266634_at	putative G-box binding bZIP transcr	---	AT2G35530	-1.11	-0.15	-1.42	0.201043	0.328896	-6.25
249478_at	germin - like protein GLP6 germin -	---	AT5G38950	-1.12	-0.16	-1.42	0.2011	0.328961	-6.25
254958_at	nucleoside diphosphate kinase 3 (n	NDPK3	AT4G11010	1.17	0.23	1.42	0.201112	0.328961	-6.25
264566_at	hypothetical protein predicted by ge	---	AT1G05270	-1.13	-0.18	-1.42	0.201149	0.328998	-6.25
245285_s_a	selenium-binding protein like ; supp	SBP1	AT4G14030	-1.11	-0.15	-1.42	0.201396	0.329369	-6.25
264265_at	unknown protein ; supported by cD	---	AT1G09280	1.15	0.21	1.42	0.201425	0.329369	-6.25
261847_at	hypothetical protein predicted by ge	---	AT1G11560	-1.15	-0.20	-1.42	0.201457	0.329369	-6.25
263646_at	Ac-like transposase related to Ac/D	---	---	1.10	0.13	1.42	0.201458	0.329369	-6.25
263214_at	hypothetical protein predicted by ge	---	AT1G30660	1.14	0.19	1.42	0.20146	0.329369	-6.25
248885_at	putative protein similar to unknown	---	AT5G46150	-1.11	-0.15	-1.42	0.201463	0.329369	-6.25
251567_at	putative protein several hypothetica	---	AT3G58230	1.13	0.17	1.42	0.201477	0.329369	-6.25
265837_at	unknown protein	LURP1	AT2G14560	2.32	1.21	1.42	0.201521	0.329418	-6.25
247978_at	60S ribosomal protein L31 ;suppor	---	AT5G56710	1.31	0.39	1.42	0.201582	0.329493	-6.25
256373_at	hypothetical protein	SGA2	AT1G66740	1.16	0.21	1.42	0.201607	0.329497	-6.25
266221_at	putative nucleotide-sugar dehydrata	UXS6	AT2G28760	1.68	0.75	1.42	0.201613	0.329497	-6.25
245488_at	peroxidase like protein	---	AT4G16270	-1.12	-0.16	-1.42	0.201634	0.329507	-6.25
245344_at	F-box protein family, AtFBL4 conta	---	AT4G15475	-1.15	-0.20	-1.41	0.201744	0.329611	-6.25
260467_at	unknown protein	---	AT1G10890	-1.10	-0.13	-1.41	0.201746	0.329611	-6.25
245776_at	hypothetical protein predicted by ge	---	AT1G30260	1.23	0.30	1.41	0.201748	0.329611	-6.25
248781_at	putative protein similar to unknown	---	AT5G47870	-1.28	-0.36	-1.41	0.201755	0.329611	-6.25
266622_at	hypothetical protein predicted by ge	---	AT2G35430	1.14	0.19	1.41	0.201771	0.329613	-6.25

255905_at	tonoplast intrinsic protein, putative	BETA-TIP	AT1G17810	-1.22	-0.29	-1.41	0.201918	0.329831	-6.25
252860_at	putative protein bZIP protein, Arabi	---	AT4G39790	-1.10	-0.13	-1.41	0.201983	0.329913	-6.25
257014_at	hypothetical protein predicted by ge	---	AT3G26930	1.16	0.21	1.41	0.202016	0.329942	-6.25
265202_at	unknown protein	AT2G3681(	---	-1.13	-0.17	-1.41	0.202254	0.330307	-6.25
265329_at	putative succinate dehydrogenase f	SDH1-2	AT2G18450	-1.13	-0.17	-1.41	0.202336	0.330366	-6.25
245721_s_a	hypothetical protein similar to Ser-T	---	AT1G73450	1.17	0.23	1.41	0.202341	0.330366	-6.25
252727_s_a	putative protein predicted proteins,	---	---	1.10	0.13	1.41	0.202351	0.330366	-6.25
255460_at	hypothetical protein similar to A. tha	---	AT4G02800	-1.11	-0.15	-1.41	0.202359	0.330366	-6.25
262974_at	hypothetical protein predicted by ge	---	AT1G75550	1.12	0.16	1.41	0.202362	0.330366	-6.25
249819_at	unknown protein	---	AT5G23640	1.10	0.14	1.41	0.202452	0.330472	-6.25
262248_at	hypothetical protein predicted by ge	YSL8	AT1G48370	1.24	0.31	1.41	0.202463	0.330472	-6.25
259291_at	unknown protein similar to unknowr	---	AT3G11550	-1.15	-0.20	-1.41	0.202476	0.330472	-6.25
266241_s_a	hypothetical protein predicted by ge	---	AT2G27800	1.13	0.18	1.41	0.202485	0.330472	-6.25
249411_at	raffinose synthase -like protein raff	SIP1	AT5G40390	-1.34	-0.43	-1.41	0.20251	0.330489	-6.25
267287_at	putative pectinesterase	sks16	AT2G23630	-1.10	-0.14	-1.41	0.202539	0.3305	-6.25
245529_at	SEN1 like protein	MAA3	AT4G15570	1.22	0.29	1.41	0.202545	0.3305	-6.25
250061_at	chloroplast GrpE protein ; supporte	EMB1241	AT5G17710	1.15	0.20	1.41	0.202693	0.3307	-6.25
252788_at	putative protein several hypothetica	---	---	-1.11	-0.15	-1.41	0.202699	0.3307	-6.25
246502_at	stearoyl-acyl carrier protein desatu	---	AT5G16240	-1.17	-0.23	-1.41	0.202729	0.3307	-6.25
259644_at	unknown protein	---	AT1G68910	1.15	0.20	1.41	0.202733	0.3307	-6.25
257148_at	cytochrome c, putative similar to cy	---	AT3G27240	1.20	0.27	1.41	0.20274	0.3307	-6.25
260026_at	60S ribosomal protein L18A, putati	RPL18AA	AT1G29970	1.12	0.16	1.41	0.202839	0.330837	-6.25
267322_at	putative leucine-rich-repeat protein	---	AT2G19330	-1.10	-0.14	-1.41	0.202859	0.330842	-6.25
244972_at	PSII 47KDa protein	---	---	-1.34	-0.42	-1.41	0.202871	0.330842	-6.25
267133_at	unknown protein	---	AT2G23440	-1.13	-0.17	-1.41	0.202993	0.331018	-6.25
266967_at	unknown protein	---	AT2G39530	-1.10	-0.14	-1.41	0.203088	0.331148	-6.25
255200_at	hypothetical protein	---	---	-1.13	-0.17	-1.41	0.203138	0.331206	-6.25
255114_at	putative protein various putative rev	---	---	-1.18	-0.23	-1.41	0.203165	0.331226	-6.25
265199_s_a	putative glucosyl transferase	---	AT2G36770	1.20	0.27	1.41	0.203281	0.331393	-6.26
256054_at	unknown protein	---	AT1G07120	-1.09	-0.12	-1.41	0.203345	0.331472	-6.26
262004_at	calcineurin B-like protein similar to (	CBL8	AT1G64480	-1.17	-0.23	-1.41	0.203417	0.331566	-6.26
257146_at	unknown protein contains Pfam pro	GTE8	AT3G27260	1.09	0.13	1.41	0.203481	0.331648	-6.26
257751_at	hypothetical protein predicted by ge	MKS1	AT3G18690	1.47	0.56	1.41	0.203536	0.331687	-6.26
264897_at	dynein light subunit lc6, flagellar ou	---	AT1G23220	1.14	0.18	1.41	0.203551	0.331687	-6.26
248837_at	putative protein similar to unknown	---	AT5G47260	1.09	0.12	1.41	0.203566	0.331687	-6.26

250340_at	putative protein predicted proteins	---	AT5G11840	-1.17	-0.22	-1.41	0.20357	0.331687	-6.26
246029_at	leucine-rich repeat protein ; suppor	---	AT5G21090	1.11	0.16	1.41	0.203578	0.331687	-6.26
252010_at	hypothetical protein ; supported by	---	AT3G52740	-1.16	-0.21	-1.41	0.203627	0.331742	-6.26
257163_at	DNA-binding protein, putative simil	MYB305	AT3G24310	-1.12	-0.16	-1.41	0.203655	0.331742	-6.26
247887_at	unknown protein	---	AT5G57880	1.11	0.15	1.41	0.203655	0.331742	-6.26
250728_at	putative protein similar to unknown	---	AT5G06440	-1.14	-0.19	-1.41	0.203711	0.33179	-6.26
261198_at	nitrate transporter, putative similar	ATNRT2.5	AT1G12940	-1.10	-0.14	-1.41	0.203714	0.33179	-6.26
250890_at	3-oxoacyl-[acyl-carrier-protein] syn	---	AT5G04520	1.11	0.15	1.41	0.203741	0.331806	-6.26
252634_x_a	putative protein predicted proteins,	---	---	-1.13	-0.18	-1.41	0.203753	0.331806	-6.26
248504_at	transcription factor Hap5a-like	NF-YC6	AT5G50480	-1.18	-0.24	-1.41	0.203859	0.331955	-6.26
260445_at	ARG1 protein (Altered Response to	ARG1	AT1G68370	-1.14	-0.19	-1.41	0.203958	0.332093	-6.26
266658_at	Expressed protein ; supported by fu	---	AT2G25735	1.78	0.83	1.41	0.204064	0.33224	-6.26
250313_at	Rab geranylgeranyltransferase, be	---	AT5G12210	1.15	0.20	1.41	0.204136	0.332336	-6.26
249421_at	DegP protease contains similarity to	DEG8	AT5G39830	-1.13	-0.18	-1.41	0.204167	0.332347	-6.26
264432_at	hypothetical protein similar to hypot	---	AT1G61710	-1.11	-0.15	-1.41	0.204173	0.332347	-6.26
263559_at	putative non-LTR retroelement reve	---	---	-1.11	-0.15	-1.41	0.20427	0.332481	-6.26
249873_at	ATP-dependent Clp protease prote	NCLPP7	AT5G23140	-1.13	-0.17	-1.41	0.20437	0.332621	-6.26
251347_at	putative protein ferritin 1 precursor	---	AT3G61010	-1.21	-0.28	-1.41	0.204409	0.332661	-6.26
262606_at	hypothetical protein predicted by ge	---	AT1G15190	-1.15	-0.20	-1.41	0.204457	0.332715	-6.26
245845_at	Pto kinase interactor, putative simi	PERK10	AT1G26150	-1.12	-0.16	-1.40	0.204479	0.332726	-6.26
260082_at	putative mitochondrial carrier protei	---	AT1G78180	-1.16	-0.21	-1.40	0.204577	0.332863	-6.26
259475_at	unknown protein ;supported by full-	---	AT1G19140	1.21	0.27	1.40	0.204697	0.333034	-6.26
255951_at	unknown protein contains similarity	MUB6	AT1G22050	1.15	0.20	1.40	0.204769	0.333117	-6.26
252495_at	putative protein hypothetical protein	---	AT3G46770	-1.13	-0.17	-1.40	0.204795	0.333117	-6.26
262140_at	hypothetical protein predicted by ge	---	AT1G52470	-1.10	-0.14	-1.40	0.204803	0.333117	-6.26
255720_at	phosphoribulokinase precursor iden	PRK	AT1G32060	1.12	0.17	1.40	0.204806	0.333117	-6.26
264989_at	unknown protein ; supported by cDI	---	AT1G27200	-1.17	-0.23	-1.40	0.2049	0.333245	-6.26
248079_at	unknown protein	---	AT5G55790	-1.17	-0.23	-1.40	0.205051	0.333467	-6.26
255439_at	putative phospho-ser/thr phosphata	BSL1	AT4G03080	1.11	0.15	1.40	0.20515	0.333605	-6.26
260409_at	Expressed protein ; supported by fu	SHW1	AT1G69935	-1.21	-0.28	-1.40	0.205325	0.333866	-6.26
247690_at	putative protein	MBD7	AT5G59800	-1.23	-0.30	-1.40	0.205381	0.333931	-6.26
246898_at	putative protein	---	AT5G25580	1.09	0.13	1.40	0.205395	0.333931	-6.26
249825_at	putative protein similar to unknown	---	AT5G23390	1.11	0.16	1.40	0.205436	0.333975	-6.26
264376_at	putative protein phosphatase 2C ;s	---	AT2G25070	1.17	0.22	1.40	0.205481	0.334024	-6.26
249302_at	putative protein similar to unknown	---	AT5G41450	-1.14	-0.19	-1.40	0.205512	0.33405	-6.26

246652_at	extensin -like protein extensin, soy	---	AT5G35190	-1.11	-0.15	-1.40	0.205568	0.334118	-6.27
265077_at	hypothetical protein similar to RING	---	AT1G55530	-1.18	-0.24	-1.40	0.205721	0.334343	-6.27
255209_at	see GB:AF077408	---	---	-1.13	-0.18	-1.40	0.20576	0.334382	-6.27
250624_at	putative protein	---	AT5G07330	-1.13	-0.17	-1.40	0.205774	0.334382	-6.27
253304_at	putative protein ;supported by full-l	---	AT4G33640	-1.13	-0.17	-1.40	0.205792	0.334387	-6.27
246981_at	unknown protein	---	AT5G04840	-1.16	-0.22	-1.40	0.205874	0.334495	-6.27
256364_at	wrky-type DNA binding protein, put	WRKY67	AT1G66550	-1.13	-0.18	-1.40	0.205923	0.334551	-6.27
255725_at	hypothetical protein similar to putati	PFT1	AT1G25540	1.09	0.13	1.40	0.206009	0.334657	-6.27
244959_s_a	hypothetical protein	---	AT2G07708	1.16	0.21	1.40	0.206017	0.334657	-6.27
245273_at	hypothetical protein ; supported by	---	AT4G14950	1.14	0.19	1.40	0.206085	0.334743	-6.27
258509_at	protein kinase, putative similar to S	---	AT3G06620	1.20	0.27	1.40	0.20611	0.334759	-6.27
266251_s_a	unknown protein	---	AT2G18320	-1.10	-0.13	-1.40	0.206203	0.334886	-6.27
263309_at	putative replication protein A1	---	---	-1.18	-0.23	-1.40	0.206409	0.335198	-6.27
261400_at	protein phosphatase-2C, putative s	---	AT1G79630	1.18	0.24	1.40	0.206457	0.335252	-6.27
260866_at	polyprotein, putative similar to poly	---	---	-1.13	-0.17	-1.40	0.206477	0.33526	-6.27
249701_at	putative protein similar to unknown	---	AT5G35460	1.11	0.15	1.40	0.20658	0.335405	-6.27
260469_at	BRCA1-associated RING domain p	AGD4	AT1G10870	-1.15	-0.20	-1.40	0.206701	0.335577	-6.27
249296_at	kinesin-like protein	---	AT5G41310	-1.13	-0.18	-1.40	0.206745	0.335624	-6.27
266141_at	protease inhibitor II contains a gam	PDF2.1	AT2G02120	-1.10	-0.14	-1.40	0.206942	0.335905	-6.27
264937_at	hypothetical protein contains simila	SCPL32	AT1G61130	-1.12	-0.16	-1.40	0.206948	0.335905	-6.27
247501_at	putative protein predicted proteins,	---	AT5G61920	1.09	0.13	1.40	0.207097	0.336124	-6.27
248934_at	serine/threonine protein kinase-like	---	AT5G46080	1.56	0.64	1.40	0.207203	0.336272	-6.27
252201_at	putative protein anthranilate N-hyd	---	AT3G50295	-1.10	-0.14	-1.40	0.207287	0.336384	-6.27
245107_at	putative heat shock transcription fa	AT-HSFB3	AT2G41690	1.35	0.43	1.40	0.207315	0.336406	-6.27
266725_at	SKP1/ASK1 (At14), putative simila	ASK14	AT2G03170	-1.11	-0.15	-1.39	0.207361	0.336457	-6.27
259498_at	unknown protein similar to putative	GOS11	AT1G15880	-1.11	-0.15	-1.39	0.207484	0.336632	-6.27
265069_at	awaiting functional assignment simi	---	AT1G55545	-1.12	-0.16	-1.39	0.207561	0.336732	-6.27
245591_at	hypothetical protein	---	AT4G14530	-1.09	-0.13	-1.39	0.207593	0.33676	-6.27
254995_at	putative protein	---	AT4G10370	-1.14	-0.19	-1.39	0.207673	0.336867	-6.27
265668_at	putative alanine acetyl transferase	---	AT2G32020	1.49	0.58	1.39	0.207691	0.336872	-6.27
248073_at	pectate lyase	---	AT5G55720	-1.12	-0.16	-1.39	0.207726	0.336905	-6.27
267198_at	putative gibberellin-regulated protei	---	AT2G30810	1.10	0.13	1.39	0.207785	0.336976	-6.27
263813_s_a	putative TNP1-like transposon prote	---	---	-1.11	-0.16	-1.39	0.207903	0.337143	-6.28
265772_at	putative protein kinase contains a p	RKF3	AT2G48010	1.16	0.21	1.39	0.207917	0.337143	-6.28
245278_at	syntaxin ; supported by cDNA: gi_2	SYP23	AT4G17730	1.18	0.23	1.39	0.20797	0.337204	-6.28

251872_at	putative protein predicted protein A	---	AT3G54570	-1.10	-0.14	-1.39	0.208039	0.337293	-6.28
257675_at	ethylene responsive element bindi	ERF7	AT3G20310	-1.15	-0.20	-1.39	0.208088	0.337349	-6.28
245691_at	zinc finger protein - like	ELF6	AT5G04240	1.18	0.24	1.39	0.20811	0.33736	-6.28
252154_at	putative DNA-3-methyladenine gly	---	AT3G50880	1.17	0.22	1.39	0.208245	0.337555	-6.28
264749_at	hypothetical protein Contains simila	---	AT1G22830	1.21	0.27	1.39	0.208352	0.337704	-6.28
259594_at	unknown protein contains similarity	---	AT1G28140	1.11	0.15	1.39	0.208434	0.337812	-6.28
255828_at	hypothetical protein predicted by ge	---	AT2G40630	1.10	0.14	1.39	0.208466	0.33784	-6.28
247502_at	putative protein predicted proteins,	---	AT5G61940	1.11	0.15	1.39	0.208626	0.33804	-6.28
254209_at	Expressed protein ; supported by c	---	AT4G23490	-1.20	-0.26	-1.39	0.208628	0.33804	-6.28
256372_at	cell division protein kinase, putative	CAK4	AT1G66750	1.16	0.22	1.39	0.208634	0.33804	-6.28
251210_at	hypothetical protein ;supported by	---	AT3G62810	1.14	0.19	1.39	0.208667	0.33807	-6.28
261040_at	oligouridylate binding protein, puta	UBP1B	AT1G17370	-1.11	-0.16	-1.39	0.208804	0.338226	-6.28
247951_at	oxysterol-binding protein-like	ORP4C	AT5G57240	-1.11	-0.15	-1.39	0.208807	0.338226	-6.28
249535_at	transporter -like protein N system a	---	AT5G38820	-1.15	-0.20	-1.39	0.208808	0.338226	-6.28
260433_at	MtN21-like protein similar to MtN21	---	AT1G68170	-1.13	-0.17	-1.39	0.209025	0.338554	-6.28
261367_at	protein kinase, putative similar to n	---	AT1G53080	-1.81	-0.86	-1.39	0.209088	0.338633	-6.28
259144_at	putative kinesin-like centromere pro	---	AT3G10180	-1.11	-0.15	-1.39	0.20912	0.338655	-6.28
250273_at	pre-mRNA splicing factor ATP-dep	EMB3011	AT5G13010	1.10	0.14	1.39	0.209137	0.338655	-6.28
253711_at	hypothetical protein	DER1	---	-1.11	-0.15	-1.39	0.209152	0.338655	-6.28
255824_at	hypothetical protein predicted by ge	---	AT2G40530	-1.39	-0.47	-1.39	0.209172	0.338655	-6.28
256213_at	protein kinase, putative contains P	---	AT1G50990	-1.13	-0.17	-1.39	0.209179	0.338655	-6.28
252832_at	ubiquitin-specific protease 3 (UBP3	ATUBP3	AT4G39910	1.09	0.12	1.39	0.209196	0.338655	-6.28
255464_s_a	putative protein similar to T4I9.17	AT7SL-1	AT4G02970	-1.10	-0.14	-1.39	0.209206	0.338655	-6.28
250934_at	DNAJ protein - like DNAJ domain-c	---	AT5G03030	-1.20	-0.26	-1.39	0.209366	0.33889	-6.28
251559_at	putative protein hypothetical protei	---	AT3G58010	-1.16	-0.21	-1.39	0.209469	0.339032	-6.28
262336_at	hypothetical protein predicted be ge	TOM7-2	AT1G64220	1.10	0.13	1.39	0.209535	0.339106	-6.28
261660_at	kinesin heavy chain isolog, putative	HIK	AT1G18370	-1.10	-0.14	-1.39	0.209546	0.339106	-6.28
259238_at	putative eukaryotic translation initia	EIF3G1	AT3G11400	1.12	0.16	1.39	0.209561	0.339106	-6.28
255532_at	hypothetical protein similar to orf a	---	AT4G02170	-1.16	-0.22	-1.39	0.209574	0.339106	-6.28
246441_at	putative protein ;supported by full-l	---	AT5G17560	-1.11	-0.15	-1.39	0.209602	0.339124	-6.28
265404_at	putative beta-galactosidase	BGAL13	AT2G16730	-1.16	-0.22	-1.39	0.209615	0.339124	-6.28
254030_at	putative acidic ribosomal protein a	---	AT4G25890	1.32	0.40	1.39	0.209681	0.339208	-6.28
252771_at	receptor protein kinase -like protei	---	AT3G42880	-1.12	-0.16	-1.39	0.209708	0.339227	-6.28
249136_at	putative protein similar to unknown	---	AT5G43180	1.22	0.29	1.39	0.209795	0.339344	-6.28
246993_at	Cys2/His2-type zinc finger protein 1	AZF1	AT5G67450	1.45	0.54	1.39	0.209863	0.339429	-6.28

245663_at	steroid sulfotransferase, putative si	---	AT1G28170	-1.11	-0.15	-1.39	0.210044	0.339699	-6.28
246542_at	transcriptional regulatory - like prot	SNL2	AT5G15020	1.15	0.20	1.39	0.210082	0.339736	-6.28
265286_at	putative NADH-ubiquinone oxireduc	---	AT2G20360	-1.12	-0.16	-1.39	0.210118	0.339747	-6.28
265902_at	hypothetical protein predicted by ge	---	AT2G25590	-1.12	-0.16	-1.39	0.210119	0.339747	-6.28
262568_at	hypothetical protein contains simila	AtRLP5	AT1G34290	-1.13	-0.18	-1.39	0.210149	0.339756	-6.28
247857_at	peroxidase	---	AT5G58400	-1.13	-0.17	-1.39	0.21016	0.339756	-6.28
258349_at	Expressed protein ; supported by fu	HYH	AT3G17609	1.31	0.38	1.39	0.210169	0.339756	-6.28
255448_at	hypothetical protein	---	AT4G02810	-1.15	-0.21	-1.39	0.210189	0.339765	-6.28
258105_at	Expressed protein ; supported by fu	---	AT3G23605	1.24	0.30	1.38	0.210243	0.339814	-6.29
257546_s_a	hypothetical protein predicted by ge	---	AT3G28410	1.09	0.13	1.38	0.21025	0.339814	-6.29
256639_at	hypothetical protein predicted by ge	---	---	-1.14	-0.19	-1.38	0.210399	0.340031	-6.29
259032_at	hypothetical protein similar to hypo	---	AT3G09380	-1.10	-0.13	-1.38	0.210448	0.340085	-6.29
259045_at	calmodulin-like protein similar to ca	---	AT3G03410	1.11	0.15	1.38	0.210462	0.340085	-6.29
251923_at	reductase-like protein abscisic acid	---	AT3G53880	-1.27	-0.35	-1.38	0.210493	0.34011	-6.29
246634_at	epsilon-adaptin, putative similar to	---	AT1G31730	-1.11	-0.15	-1.38	0.210582	0.340231	-6.29
257960_at	S-adenosylmethionine decarboxyla	---	AT3G25570	-1.10	-0.13	-1.38	0.210672	0.340352	-6.29
256320_at	DnaJ protein, putative contains Pfa	---	AT3G12170	-1.14	-0.18	-1.38	0.210812	0.340553	-6.29
266452_at	hypothetical protein predicted by ge	---	AT2G43320	-1.19	-0.25	-1.38	0.210886	0.340649	-6.29
257612_at	unknown protein	ARO4	AT3G26600	1.31	0.39	1.38	0.210917	0.340676	-6.29
254800_at	putative protein several hypothetica	---	AT4G13070	1.19	0.25	1.38	0.211046	0.340859	-6.29
256868_at	eukaryotic translation initiation fact	EIF4B1	AT3G26400	1.21	0.28	1.38	0.211092	0.34091	-6.29
257392_at	hypothetical protein	FLA3	AT2G24450	-1.12	-0.16	-1.38	0.211169	0.341011	-6.29
256732_at	hypothetical protein predicted by ge	---	---	-1.10	-0.14	-1.38	0.211267	0.34114	-6.29
267222_at	putative polygalacturonase	---	AT2G43880	-1.10	-0.14	-1.38	0.21128	0.34114	-6.29
254266_at	protein kinase - like protein serine t	CRK5	AT4G23130	1.42	0.50	1.38	0.211315	0.341173	-6.29
259856_at	unknown protein ;supported by full-	---	AT1G68440	-1.31	-0.39	-1.38	0.211336	0.341183	-6.29
251264_at	multifunctional aminoacyl-tRNA liga	---	AT3G62120	-1.10	-0.14	-1.38	0.211352	0.341185	-6.29
245355_at	60S ribosomal protein L15 homolog	---	AT4G17390	1.28	0.35	1.38	0.211387	0.341218	-6.29
251335_at	1-aminocyclopropane-1-carboxylat	---	AT3G61400	-1.18	-0.24	-1.38	0.211535	0.341432	-6.29
265194_at	1-aminocyclopropane-1-carboxylat	EFE	AT1G05010	1.30	0.38	1.38	0.211577	0.341475	-6.29
266350_at	putative protein transport protein S	STL2P	AT2G01470	1.17	0.22	1.38	0.211688	0.34163	-6.29
246668_at	putative protein	---	---	-1.11	-0.15	-1.38	0.211713	0.341647	-6.29
264742_at	hypothetical protein similar to hypot	---	AT1G62130	-1.14	-0.20	-1.38	0.211858	0.341844	-6.29
248859_at	putative protein contains similarity t	---	AT5G46660	-1.13	-0.18	-1.38	0.211865	0.341844	-6.29
246141_at	TipD - like WD repeat protein TipD	---	AT5G19920	-1.14	-0.19	-1.38	0.211936	0.341934	-6.29

259537_at	hypothetical protein ; supported by	PHR1	AT1G12370	-1.14	-0.19	-1.38	0.21208	0.342142	-6.29
258428_at	unknown protein	---	AT3G16610	1.12	0.16	1.38	0.212194	0.342302	-6.29
251234_s_a	putative dTDP-glucose 4-6-dehydra	UXS4	AT2G47650	1.18	0.23	1.38	0.212226	0.342328	-6.29
252119_at	thioredoxin h ;supported by full-len	ATTRX1	AT3G51030	-1.22	-0.29	-1.38	0.212429	0.342632	-6.29
249747_at	putative protein similar to unknown	---	AT5G24600	-1.14	-0.18	-1.38	0.212467	0.342669	-6.29
245788_at	hypothetical protein similar to hypot	---	AT1G32120	1.30	0.37	1.38	0.212568	0.342808	-6.29
263857_at	unknown protein	---	AT2G04380	-1.09	-0.12	-1.38	0.212597	0.34283	-6.30
250228_at	cell cycle switch protein	FZR3	AT5G13840	-1.14	-0.18	-1.38	0.212616	0.342837	-6.30
259503_at	unknown protein ; supported by cDI	---	AT1G15870	1.17	0.23	1.38	0.212643	0.342856	-6.30
249388_at	putative protein downy mildew resi	---	AT5G40090	-1.13	-0.17	-1.38	0.212716	0.34295	-6.30
260255_at	putative protein kinase similar to p5	---	AT1G74330	-1.22	-0.29	-1.38	0.212733	0.342953	-6.30
246577_at	MADS box transcription factor, put	AGL92	AT1G31640	-1.11	-0.15	-1.38	0.212763	0.342958	-6.30
256328_at	6-phosphogluconate dehydrogenas	---	AT3G02360	1.23	0.30	1.38	0.212766	0.342958	-6.30
255917_at	putative protein	---	AT5G28560	-1.09	-0.13	-1.38	0.212922	0.343185	-6.30
250660_at	RNA-binding protein-like	---	AT5G07060	1.09	0.13	1.38	0.212964	0.343212	-6.30
262111_at	hypothetical protein predicted by ge	---	AT1G02960	-1.11	-0.15	-1.38	0.212969	0.343212	-6.30
259850_at	hypothetical protein predicted by ge	---	AT1G72240	-1.17	-0.22	-1.38	0.213058	0.343313	-6.30
249565_at	contains similarity to S1 self-incomp	---	AT5G38440	-1.12	-0.16	-1.38	0.213062	0.343313	-6.30
253101_at	cytochrome P450 monooxygenase	CYP91A2	AT4G37430	-1.24	-0.31	-1.38	0.213138	0.343388	-6.30
257476_at	unknown protein	---	AT1G80960	1.09	0.13	1.38	0.213139	0.343388	-6.30
257250_at	transfactor, putative similar to GB:E	---	AT3G24120	-1.12	-0.17	-1.37	0.213216	0.343474	-6.30
266907_at	Expressed protein ; supported by fu	ATGA2OX3	---	-1.14	-0.19	-1.37	0.213222	0.343474	-6.30
254838_at	hypothetical protein	---	AT4G12380	-1.16	-0.21	-1.37	0.213248	0.343491	-6.30
264787_at	putative senescence-associated pro	ERD7	AT2G17840	-1.22	-0.28	-1.37	0.213307	0.34354	-6.30
259382_s_a	jasmonate inducible protein isolog	JAL31	AT3G16420	-1.72	-0.78	-1.37	0.213323	0.34354	-6.30
245522_at	hypothetical protein	---	AT4G15890	-1.11	-0.15	-1.37	0.213323	0.34354	-6.30
257353_at	hypothetical protein predicted by ge	NPY4	AT2G23050	-1.12	-0.16	-1.37	0.213372	0.343595	-6.30
258177_at	ubiquitin-regulatory protein, putativ	---	AT3G21660	-1.11	-0.14	-1.37	0.2134	0.343613	-6.30
256952_at	mannosidase, putative similar to m	---	AT3G21160	1.14	0.19	1.37	0.213426	0.343613	-6.30
255548_at	putative CHP-rich zinc finger protei	---	AT4G01930	-1.09	-0.13	-1.37	0.213429	0.343613	-6.30
259011_s_a	unknown protein similar to putative	---	AT3G07380	-1.12	-0.16	-1.37	0.213445	0.343616	-6.30
266623_at	unknown protein	---	AT2G35390	-1.16	-0.21	-1.37	0.213491	0.34364	-6.30
254451_at	adrenodoxin - like protein adrenod	---	AT4G21090	1.09	0.13	1.37	0.213501	0.34364	-6.30
249962_at	pectin methyl esterase -like protein	---	AT5G18990	-1.19	-0.25	-1.37	0.213506	0.34364	-6.30
251616_at	putative protein	---	AT3G57990	1.10	0.14	1.37	0.213542	0.343675	-6.30

252679_at	CCR4-associated factor 1-like prot	---	AT3G44260	1.76	0.82	1.37	0.21357	0.343695	-6.30
254938_at	putative oligopeptide transporter si	OPT7	AT4G10770	-1.11	-0.15	-1.37	0.213685	0.343856	-6.30
249363_at	DegP protease contains similarity to	DegP13	AT5G40560	-1.09	-0.13	-1.37	0.213778	0.343941	-6.30
264697_at	cyclin, putative similar to cyclin D C	CYCD1;1	AT1G70210	-1.63	-0.70	-1.37	0.21378	0.343941	-6.30
249516_s_a	myrosinase binding protein-like; sim	---	AT5G38540	-1.12	-0.17	-1.37	0.213818	0.343941	-6.30
253860_at	hypothetical protein ;supported by	---	AT4G27700	-1.11	-0.14	-1.37	0.213818	0.343941	-6.30
257641_s_a	hypothetical protein	AOC1	AT3G25760	-1.24	-0.31	-1.37	0.213824	0.343941	-6.30
262934_s_a	hypothetical protein contains simila	---	AT1G16270	1.16	0.21	1.37	0.213828	0.343941	-6.30
261015_at	14-3-3 protein GF14iota (grf12) ider	GRF12	AT1G26480	1.11	0.15	1.37	0.213909	0.344046	-6.30
255848_at	hypothetical protein predicted by ge	---	AT2G33640	-1.13	-0.17	-1.37	0.213965	0.344113	-6.30
245094_at	4-alpha-glucanotransferase	DPE2	AT2G40840	-1.15	-0.20	-1.37	0.214025	0.344185	-6.30
256329_at	unknown protein	SEC5A	AT1G76850	-1.09	-0.12	-1.37	0.214047	0.344195	-6.30
253446_at	putative protein predicted protein T	---	AT4G32620	1.12	0.16	1.37	0.21409	0.344241	-6.30
248654_at	importin alpha	IMPA-5	AT5G49310	-1.11	-0.15	-1.37	0.214174	0.344351	-6.30
255771_at	hypothetical protein contains simila	---	AT1G18550	-1.12	-0.16	-1.37	0.214202	0.344372	-6.30
266817_at	hypothetical protein similar to hypot	HUB1	AT2G44950	1.16	0.21	1.37	0.214252	0.344429	-6.30
252499_s_a	subtilisin-like serine protease conta	---	AT3G46840	1.12	0.16	1.37	0.214483	0.344747	-6.30
249240_at	putative protein similar to unknown	---	AT5G42220	1.14	0.19	1.37	0.214486	0.344747	-6.30
250308_at	calcium-dependent protein kinase	CPK17	AT5G12180	-1.15	-0.20	-1.37	0.214496	0.344747	-6.30
258777_at	hypothetical protein predicted by ge	---	AT3G11850	1.15	0.21	1.37	0.21453	0.34477	-6.30
252073_at	hypothetical protein	---	AT3G51750	1.53	0.62	1.37	0.214541	0.34477	-6.30
260876_at	hypothetical protein contains simila	---	AT1G21460	-1.18	-0.24	-1.37	0.214818	0.345191	-6.30
265237_s_a	hypothetical protein	---	AT2G07706	-1.12	-0.17	-1.37	0.214856	0.345228	-6.30
252175_at	zinc finger protein zinc finger prote	AtIDD2	AT3G50700	1.09	0.13	1.37	0.214984	0.34541	-6.30
266505_at	unknown protein	---	AT2G47830	-1.11	-0.15	-1.37	0.215053	0.345497	-6.31
262877_at	unknown protein ;supported by full-	---	AT1G64850	1.15	0.20	1.37	0.215079	0.345514	-6.31
267629_at	putative DNA polymerase delta sma	POLD2	AT2G42120	1.16	0.22	1.37	0.21538	0.345974	-6.31
257360_at	unknown protein	---	AT2G39240	-1.10	-0.14	-1.37	0.215431	0.346031	-6.31
253053_at	putative protein beta-ketoadipate e	---	AT4G37470	-1.15	-0.20	-1.37	0.215447	0.346033	-6.31
251127_at	putative protein predicted protein, /	---	AT5G01080	1.13	0.18	1.37	0.215474	0.346051	-6.31
267328_at	putative receptor-like protein kinase	---	AT2G19230	-1.14	-0.18	-1.37	0.215507	0.346079	-6.31
252623_at	hypothetical protein	---	AT3G45320	-1.12	-0.16	-1.37	0.215583	0.346177	-6.31
265501_at	putative glucosyltransferase	UGT73B4	AT2G15490	1.37	0.45	1.37	0.215797	0.346496	-6.31
265458_at	unknown protein ;supported by full-	---	AT2G46580	-1.13	-0.18	-1.37	0.21592	0.346662	-6.31
266639_at	defender against cell death protein	DAD2	AT2G35520	1.11	0.15	1.37	0.215931	0.346662	-6.31

262171_at	unknown protein ;supported by full-	TIFY10B	AT1G74950	-1.19	-0.25	-1.37	0.215971	0.346703	-6.31
251237_at	bZIP transcription factor-like protei	CPuORF3	AT3G62420	-1.12	-0.16	-1.37	0.216028	0.34677	-6.31
256841_x_a	hypothetical protein predicted by ge	---	---	-1.18	-0.24	-1.36	0.216219	0.347053	-6.31
246742_at	TOPP8 serine/threonine protein pho	TOPP8	AT5G27840	1.09	0.12	1.36	0.216278	0.347122	-6.31
262814_at	putative heat-shock protein strong s	---	AT1G11660	1.10	0.14	1.36	0.216441	0.347358	-6.31
249218_at	pitrilysin	---	AT5G42390	1.16	0.22	1.36	0.216465	0.347358	-6.31
250636_at	glycine-rich protein atGRP	GRP18	AT5G07520	-1.12	-0.16	-1.36	0.21647	0.347358	-6.31
251911_at	putative C2H2-type zinc finger prote	---	AT3G53820	-1.12	-0.16	-1.36	0.216513	0.347381	-6.31
264413_s_a	hypothetical protein similar to hypot	---	---	-1.15	-0.20	-1.36	0.216515	0.347381	-6.31
265832_at	putative replication protein A1	---	---	-1.10	-0.14	-1.36	0.216646	0.347566	-6.31
260991_at	hypothetical protein predicted by ge	---	AT1G12160	1.10	0.13	1.36	0.216954	0.348019	-6.31
247192_at	histone H3 (sp|P05203) ; supporte	---	AT5G65360	-1.84	-0.88	-1.36	0.216959	0.348019	-6.31
266408_at	putative retroelement pol polyprotei	---	---	-1.14	-0.19	-1.36	0.21701	0.348049	-6.31
265784_at	hypothetical protein predicted by ge	---	AT2G07280	1.11	0.15	1.36	0.217022	0.348049	-6.31
260428_at	putative translation initiation factor I	---	AT1G72340	-1.16	-0.22	-1.36	0.217023	0.348049	-6.31
263581_at	hypothetical protein identical to hyp	---	AT2G17160	-1.14	-0.18	-1.36	0.217182	0.348279	-6.31
247018_at	AP2 domain transcription factor-like	---	AT5G67000	-1.09	-0.12	-1.36	0.217239	0.348347	-6.31
257672_at	unknown protein ;supported by full-	---	AT3G20300	-1.22	-0.28	-1.36	0.217294	0.34841	-6.31
250151_at	high affinity nitrate transporter - like	ATNRT2.7	AT5G14570	-1.23	-0.29	-1.36	0.21735	0.348475	-6.31
250708_at	Expressed protein ; supported by fu	RBE	AT5G06070	-1.11	-0.15	-1.36	0.217445	0.348555	-6.31
247270_at	ER66 protein-like	---	AT5G64220	-1.10	-0.14	-1.36	0.217452	0.348555	-6.31
254050_s_a	hypothetical protein ; supported by	---	AT4G25670	1.11	0.15	1.36	0.217459	0.348555	-6.31
250374_at	putative protein	EMF1	AT5G11530	1.22	0.29	1.36	0.217474	0.348555	-6.32
252478_at	putative protein mitotic phosphopro	---	AT3G46540	1.20	0.26	1.36	0.217476	0.348555	-6.32
263612_at	putative CDC21 protein	MCM4	AT2G16440	-1.43	-0.52	-1.36	0.217507	0.348576	-6.32
265901_at	putative selenium-binding protein	---	AT2G25580	1.14	0.18	1.36	0.21752	0.348576	-6.32
248935_at	salt-inducible protein-like	---	AT5G46100	1.13	0.18	1.36	0.217653	0.348765	-6.32
265524_at	hypothetical protein	---	---	-1.09	-0.13	-1.36	0.217678	0.34878	-6.32
251137_at	putative protein several hypothetica	---	AT5G01300	1.17	0.22	1.36	0.217749	0.348869	-6.32
257245_at	hypothetical protein contains Pfam	---	AT3G24110	-1.14	-0.19	-1.36	0.217852	0.349011	-6.32
265738_at	NADC homolog identical to GP|121	QPT	AT2G01350	1.12	0.17	1.36	0.217878	0.349026	-6.32
267107_at	hypothetical protein predicted by ge	---	---	-1.12	-0.16	-1.36	0.217893	0.349026	-6.32
264275_at	hypothetical protein predicted by ge	anac024	AT1G60350	-1.09	-0.12	-1.36	0.217953	0.349075	-6.32
254791_at	SERINE CARBOXYPEPTIDASE I	scpl20	AT4G12910	1.14	0.18	1.36	0.217954	0.349075	-6.32
248692_s_a	hypothetical protein	---	AT4G15070	1.12	0.16	1.36	0.218084	0.349239	-6.32

257525_at	hypothetical protein predicted by ge	---	AT3G04900	-1.13	-0.18	-1.36	0.218093	0.349239	-6.32
248634_at	isoleucyl-tRNA synthetase	OVA2	AT5G49030	-1.15	-0.20	-1.36	0.218102	0.349239	-6.32
254720_at	DNA (cytosine-5-)-methyltransferas	MEE57	AT4G13610	-1.12	-0.17	-1.36	0.218131	0.349261	-6.32
254127_at	NADPH-ferrihemoprotein reductase	ATR1	AT4G24520	1.14	0.19	1.36	0.218162	0.349285	-6.32
248578_at	putative protein contains similarity t	emb1879	AT5G49820	-1.16	-0.21	-1.36	0.218211	0.349336	-6.32
264401_at	dihydroflavonol 4-reductase, putati	BAN	AT1G61720	-1.09	-0.12	-1.36	0.218224	0.349336	-6.32
265741_at	putative membrane transporter ; su	---	AT2G01320	1.23	0.30	1.36	0.218377	0.349539	-6.32
260230_at	putative DNA-binding protein contai	---	AT1G74500	-1.11	-0.15	-1.36	0.218381	0.349539	-6.32
262294_at	hypothetical protein identical to hyp	---	AT1G27610	-1.11	-0.15	-1.36	0.21841	0.34954	-6.32
256743_at	Expressed protein ; supported by fu	---	AT3G29370	-1.36	-0.44	-1.36	0.218413	0.34954	-6.32
249543_at	Expressed protein ; supported by fu	---	---	-1.13	-0.17	-1.36	0.218526	0.349698	-6.32
264975_at	hypothetical protein predicted by ge	---	AT1G27070	1.12	0.16	1.36	0.218594	0.349776	-6.32
249929_at	unknown protein	---	AT5G22340	-1.14	-0.19	-1.36	0.218606	0.349776	-6.32
267571_at	3-hydroxyisobutyryl-coenzyme A hy	---	AT2G30650	-1.10	-0.14	-1.36	0.218652	0.349825	-6.32
254029_at	putative protein other hypothetical p	---	AT4G25870	1.13	0.18	1.36	0.218707	0.349888	-6.32
246296_at	putative protein hypothetical protei	---	AT3G56750	1.10	0.14	1.36	0.218723	0.349889	-6.32
262300_at	ripening-induced protein, putative s	---	AT1G70870	1.09	0.12	1.36	0.218754	0.349914	-6.32
251871_at	hypothetical protein	---	AT3G54520	-1.09	-0.12	-1.36	0.218778	0.349928	-6.32
256882_at	RNA-binding protein, putative simil	---	AT3G26420	1.15	0.20	1.36	0.218873	0.350055	-6.32
247438_at	unknown protein ; supported by cD	---	AT5G62460	-1.21	-0.28	-1.36	0.219019	0.350264	-6.32
267349_at	60S acidic ribosomal protein P0	---	AT2G40010	-1.10	-0.13	-1.36	0.219067	0.350316	-6.32
265615_at	putative dioxygenase ; supported b	---	AT2G25450	-1.13	-0.18	-1.35	0.219186	0.350482	-6.32
250909_at	S-receptor kinase - like protein S-r	---	AT5G03700	1.47	0.56	1.35	0.219299	0.350639	-6.32
248117_at	FH protein interacting protein FIP2	FIP2	AT5G55000	1.14	0.19	1.35	0.219353	0.350696	-6.32
259521_at	ATP-dependent Clp protease prote	CLP2	AT1G12410	-1.14	-0.19	-1.35	0.219377	0.350696	-6.32
254478_at	putative protein TRANSCRIPTION	---	AT4G20330	1.15	0.20	1.35	0.219381	0.350696	-6.32
251491_at	fructokinase-like protein fructokinas	---	AT3G59480	-1.17	-0.23	-1.35	0.219453	0.350787	-6.32
259927_at	unknown protein ; supported by cD	JAC1	AT1G75100	-1.19	-0.26	-1.35	0.219479	0.350804	-6.32
255991_at	unknown protein	---	AT1G29820	-1.20	-0.27	-1.35	0.219521	0.350846	-6.32
244947_at	hypothetical protein	---	---	1.14	0.19	1.35	0.219636	0.351005	-6.32
259686_at	transcription factor SCARECROW,	---	AT1G63100	-1.18	-0.24	-1.35	0.219654	0.35101	-6.32
261994_at	hypothetical protein contains simila	---	AT1G33640	-1.10	-0.14	-1.35	0.219714	0.35108	-6.32
261299_at	unknown protein	---	AT1G48550	1.15	0.20	1.35	0.2198	0.351194	-6.32
264391_at	pectate lyase-like protein Similar to	---	AT1G11920	-1.11	-0.16	-1.35	0.219888	0.35131	-6.32
251566_at	putative protein several hypothetica	---	AT3G58210	-1.09	-0.12	-1.35	0.22002	0.351496	-6.33

251216_at	putative protein hypothetical protei	---	---	-1.10	-0.14	-1.35	0.22012	0.35163	-6.33
262511_at	syntaxin-related protein At-SYR1, p	SYP125	AT1G11250	-1.15	-0.20	-1.35	0.220206	0.351731	-6.33
247753_at	hexosyltransferase - like protein	---	AT5G59070	1.32	0.41	1.35	0.220226	0.351731	-6.33
246046_at	putative protein predicted proteins,	---	---	-1.12	-0.17	-1.35	0.220229	0.351731	-6.33
254390_at	calcium-dependent protein kinase	CPK15	AT4G21940	1.12	0.16	1.35	0.220248	0.351738	-6.33
256971_at	unknown protein contains Pfam pro	---	AT3G21100	1.16	0.22	1.35	0.220266	0.351742	-6.33
245945_at	putative protein various predicted p	ROPGEF1(	AT5G19560	-1.09	-0.13	-1.35	0.220413	0.351951	-6.33
265058_s_a	myrosinase-binding protein homolo	MBP2	AT1G52030	-1.82	-0.86	-1.35	0.22045	0.351986	-6.33
260098_at	tumor-related protein, putative simi	---	AT1G73320	1.21	0.28	1.35	0.220492	0.352006	-6.33
265323_at	putative syntaxin	SYP112	AT2G18260	1.15	0.20	1.35	0.220494	0.352006	-6.33
257867_at	unknown protein	---	AT3G17780	-1.13	-0.18	-1.35	0.220527	0.352035	-6.33
267499_at	hypothetical protein predicted by ge	---	AT2G45500	1.12	0.16	1.35	0.220617	0.352135	-6.33
246303_at	putative carrier protein peroxisoma	---	AT3G51870	1.20	0.26	1.35	0.220621	0.352135	-6.33
250195_at	putative protein	---	AT5G14560	1.09	0.12	1.35	0.220657	0.352169	-6.33
262344_at	cytochrome b245 beta chain homo	ATRBOH F	AT1G64060	-1.36	-0.44	-1.35	0.220682	0.352183	-6.33
266689_at	hypothetical protein predicted by ge	---	AT2G19930	1.21	0.27	1.35	0.220705	0.352195	-6.33
264853_at	putative ligand-gated ion channel p	GLR2	AT2G17260	-1.14	-0.18	-1.35	0.22074	0.352227	-6.33
260358_at	unknown protein ; supported by cDI	---	AT1G69340	1.10	0.14	1.35	0.220799	0.352296	-6.33
248078_at	putative protein contains similarity t	---	AT5G55780	-1.10	-0.14	-1.35	0.220832	0.352324	-6.33
262038_at	invertase, putative similar to neutra	CINV1	AT1G35580	-1.20	-0.26	-1.35	0.220905	0.352415	-6.33
247062_at	putative protein similar to unknown	---	AT5G66810	1.25	0.32	1.35	0.220925	0.352418	-6.33
246893_at	PHD finger protein - like PHD finge	---	AT5G25520	-1.09	-0.12	-1.35	0.220937	0.352418	-6.33
266362_at	unknown protein	---	AT2G32430	1.14	0.19	1.35	0.22103	0.352542	-6.33
263671_at	hypothetical protein predicted by ge	---	AT2G04830	-1.11	-0.15	-1.35	0.221213	0.352785	-6.33
266403_at	putative acid phosphatase contains	---	AT2G38600	-1.13	-0.17	-1.35	0.221214	0.352785	-6.33
246000_at	putative protein predicted proteins,	---	AT5G20820	-1.22	-0.28	-1.35	0.221351	0.35298	-6.33
247769_at	laccase precursor - like protein lac	LAC16	AT5G58910	-1.10	-0.14	-1.35	0.221385	0.353009	-6.33
264439_at	adenine phosphoribosyltransferase	APT1	AT1G27450	1.12	0.16	1.35	0.221486	0.353145	-6.33
251351_s_a	CaLB protein	NTMC2T4	AT3G60950	-1.12	-0.16	-1.35	0.221861	0.353718	-6.33
256980_at	hypothetical protein contains Pfam	DRB3	AT3G26932	1.16	0.21	1.35	0.221923	0.353792	-6.33
245724_at	hypothetical protein predicted by ge	---	AT1G73390	1.20	0.26	1.35	0.222048	0.353967	-6.33
250176_at	putative protein cytochrome P450 (	CYP724A1	AT5G14400	-1.16	-0.21	-1.35	0.222094	0.35399	-6.33
251542_at	putative protein protein-tyrosine kir	---	AT3G58760	-1.14	-0.19	-1.35	0.222105	0.35399	-6.33
256609_at	hypothetical protein predicted by ge	---	---	-1.10	-0.13	-1.35	0.222112	0.35399	-6.33
261789_at	40S ribosomal protein S12, putativ	---	AT1G15930	1.26	0.34	1.35	0.22213	0.35399	-6.33

261347_at	unknown protein	ELF7	AT1G79730	1.13	0.17	1.35	0.22214	0.35399	-6.33
248399_at	putative protein strong similarity to	---	AT5G52010	1.11	0.14	1.34	0.222254	0.354146	-6.33
254739_at	putative disease resistance protein	AtRLP48	AT4G13880	-1.11	-0.15	-1.34	0.222285	0.354172	-6.33
263582_at	unknown protein similar to hypothet	LYM2	AT2G17120	-1.19	-0.25	-1.34	0.222418	0.354356	-6.33
254337_at	putative protein hypothetical protei	---	AT4G22060	-1.12	-0.16	-1.34	0.222432	0.354356	-6.33
245159_at	putative cellulose synthase	ATCSLD1	AT2G33100	-1.13	-0.18	-1.34	0.222487	0.354419	-6.34
246996_at	putative protein similar to unknown	LBD37	AT5G67420	-1.20	-0.26	-1.34	0.222526	0.354457	-6.34
266032_x_a	putative replication protein A1	---	---	-1.12	-0.16	-1.34	0.222589	0.354532	-6.34
246766_at	hypothetical protein	---	AT5G27340	-1.18	-0.24	-1.34	0.222657	0.354598	-6.34
257763_s_a	disease resistance protein, putative	AtRLP37	AT3G23110	1.38	0.47	1.34	0.222661	0.354598	-6.34
262150_at	hypothetical protein contains simila	FRS6	AT1G52520	-1.13	-0.18	-1.34	0.222732	0.354686	-6.34
261963_at	hypothetical protein predicted by ge	---	---	1.13	0.18	1.34	0.222782	0.354715	-6.34
250780_at	expansin At-EXP2 (gb|AAB38073.1	ATEXPA2	AT5G05290	-1.16	-0.22	-1.34	0.222794	0.354715	-6.34
247675_at	putative protein large number of pr	---	AT5G59940	-1.15	-0.20	-1.34	0.222797	0.354715	-6.34
250447_at	putative protein KIAA0332 gene, H	---	AT5G10800	-1.10	-0.13	-1.34	0.222893	0.354844	-6.34
249166_at	CHP-rich zinc finger protein-like	---	AT5G42840	1.12	0.16	1.34	0.222949	0.354908	-6.34
255673_at	Similar to receptor-like protein kina	RLK4	AT4G00340	-1.11	-0.15	-1.34	0.223011	0.354962	-6.34
253509_at	putative protein kainate receptor, R	GLR2.4	AT4G31710	-1.12	-0.16	-1.34	0.223015	0.354962	-6.34
251016_at	pathogenesis related protein - like	---	AT5G02730	-1.20	-0.26	-1.34	0.223049	0.354962	-6.34
254304_at	hypothetical protein ; supported by	---	AT4G22270	-1.14	-0.19	-1.34	0.223064	0.354962	-6.34
252645_at	bZIP transcription factor -like prote	DPBF2	AT3G44460	-1.12	-0.16	-1.34	0.223071	0.354962	-6.34
246853_at	putative protein	---	AT5G26890	-1.10	-0.14	-1.34	0.223077	0.354962	-6.34
260228_at	putative cytochrome P450 similar to	CYP98A8	AT1G74540	-1.12	-0.16	-1.34	0.223115	0.354998	-6.34
259595_at	CONSTANS family zinc finger prot	---	AT1G28050	1.18	0.24	1.34	0.223264	0.355183	-6.34
263658_at	unknown protein EST gb|T21788 co	---	AT1G04490	-1.10	-0.14	-1.34	0.223282	0.355183	-6.34
252637_at	WD repeat domain protein nuclear	HIRA	AT3G44530	1.13	0.18	1.34	0.223287	0.355183	-6.34
252949_at	putative thaumatin-like protein thau	---	AT4G38670	-1.23	-0.29	-1.34	0.223294	0.355183	-6.34
251789_at	serine/threonine-specific protein ki	---	AT3G55450	1.15	0.20	1.34	0.22331	0.355185	-6.34
257535_at	hypothetical protein predicted by ge	---	AT3G09490	-1.25	-0.33	-1.34	0.223506	0.355472	-6.34
257760_s_a	putative AC-like transposase simila	---	---	-1.11	-0.15	-1.34	0.223632	0.355647	-6.34
256235_at	cysteine proteinase inhibitor, putati	ATCYSB	AT3G12490	-1.09	-0.12	-1.34	0.2237	0.35573	-6.34
246238_at	sugar transporter like protein	---	AT4G36670	-1.31	-0.39	-1.34	0.22373	0.355753	-6.34
244957_at	hypothetical protein	AT2G0783	---	-1.12	-0.16	-1.34	0.223975	0.356117	-6.34
255197_x_a	contains similarity to Oryza sativa re	---	---	-1.13	-0.17	-1.34	0.224036	0.356181	-6.34
253310_at	hypothetical protein ; supported by	EX1	AT4G33630	1.10	0.14	1.34	0.224046	0.356181	-6.34

256176_at	hypothetical protein predicted by ge	ATEXO70G	AT1G51640	-1.10	-0.14	-1.34	0.224095	0.356223	-6.34
264443_at	Expressed protein ; supported by fu	---	AT1G27385	-1.16	-0.21	-1.34	0.224104	0.356223	-6.34
259091_at	hypothetical protein predicted by ge	---	AT3G04890	-1.12	-0.17	-1.34	0.224122	0.356228	-6.34
253111_at	putative protein glutamic acid-rich p	---	AT4G35940	1.16	0.22	1.34	0.224154	0.356253	-6.34
262269_at	hypothetical protein predicted by ge	---	---	-1.10	-0.14	-1.34	0.22417	0.356254	-6.34
259779_s_a	hypothetical protein predicted by ge	---	AT1G29620	1.11	0.16	1.34	0.224198	0.356274	-6.34
249159_at	Nicotiana lesion-inducing like ; sup	---	AT5G43460	1.16	0.22	1.34	0.224287	0.356391	-6.34
252054_at	hypothetical protein ;supported by	OFP18	AT3G52540	-1.13	-0.17	-1.34	0.224408	0.356558	-6.34
259853_at	leucine-rich receptor-like protein ki	---	AT1G72300	1.16	0.22	1.34	0.224442	0.356587	-6.34
262907_at	hypothetical protein predicted by ge	CRR28	AT1G59720	1.12	0.16	1.34	0.224574	0.356771	-6.34
250633_at	peptide methionine sulfoxide reduc	PMSR2	AT5G07460	-1.41	-0.49	-1.34	0.224739	0.356964	-6.34
258875_at	unknown protein ;supported by full-	---	AT3G03160	-1.16	-0.22	-1.34	0.224748	0.356964	-6.34
248356_at	putative protein strong similarity to	ATEXO70A	AT5G52350	1.09	0.13	1.34	0.224761	0.356964	-6.34
249219_at	putative protein contains similarity t	SDG25	AT5G42400	-1.14	-0.19	-1.34	0.224769	0.356964	-6.34
249940_at	NAC-domain protein-like ;supporte	anac090	AT5G22380	-1.12	-0.16	-1.34	0.224773	0.356964	-6.34
251131_at	laccase - like protein laccase precu	LAC10	AT5G01190	-1.09	-0.12	-1.34	0.224838	0.357042	-6.34
248537_at	putative protein similar to unknown	---	AT5G50100	-1.15	-0.20	-1.34	0.224866	0.357062	-6.34
265186_at	Expressed protein ; supported by fu	---	AT1G23560	1.15	0.20	1.34	0.224987	0.357191	-6.34
245475_at	hypothetical protein	---	AT4G16080	-1.10	-0.14	-1.34	0.224988	0.357191	-6.34
263968_s_a	PttA-like transposon protein no AT	---	---	-1.12	-0.16	-1.34	0.224994	0.357191	-6.34
250521_at	selenium-binding protein-like	---	AT5G08490	-1.11	-0.15	-1.34	0.22502	0.357197	-6.35
261897_at	hypothetical protein predicted by ge	---	AT1G80950	1.12	0.17	1.34	0.225046	0.357197	-6.35
267490_at	putative receptor-like protein kinase	---	AT2G19130	1.23	0.30	1.34	0.225058	0.357197	-6.35
244965_at	hypothetical protein	---	---	1.17	0.22	1.34	0.225061	0.357197	-6.35
257551_at	hypothetical protein contains simila	---	---	-1.12	-0.17	-1.34	0.225104	0.35724	-6.35
257785_at	geranylgeranylated protein, putativ	MUB4	AT3G26980	-1.45	-0.53	-1.34	0.225146	0.357266	-6.35
247174_at	unknown protein ; supported by cD	---	AT5G65250	1.10	0.14	1.34	0.225151	0.357266	-6.35
262383_at	disease resistance protein, putative	---	AT1G72940	1.68	0.75	1.34	0.22521	0.357334	-6.35
252488_at	glucuronosyl transferase-like prote	---	AT3G46700	-1.10	-0.14	-1.34	0.225252	0.357376	-6.35
256535_at	unknown protein	ANAC015	AT1G33280	-1.14	-0.19	-1.33	0.225324	0.357464	-6.35
249909_s_a	alpha-adaptin	---	AT5G22770	-1.14	-0.18	-1.33	0.225339	0.357464	-6.35
261030_at	unknown protein contains similarity	---	AT1G17410	1.13	0.18	1.33	0.225527	0.357717	-6.35
264846_at	senescence-associated protein con	---	AT2G17850	-1.11	-0.15	-1.33	0.22553	0.357717	-6.35
265482_at	hypothetical protein contains a dom	---	AT2G15780	2.28	1.19	1.33	0.225604	0.357776	-6.35
262181_at	xylosidase, putative similar to xylos	---	AT1G78060	-1.32	-0.40	-1.33	0.225611	0.357776	-6.35

246875_at	pathogenesis-related protein - like	---	AT5G26130	-1.11	-0.15	-1.33	0.225614	0.357776	-6.35
253831_at	Expressed protein ; supported by fu	---	AT4G27580	-1.12	-0.16	-1.33	0.225648	0.357805	-6.35
249236_at	putative protein similar to unknown	---	AT5G41950	-1.10	-0.13	-1.33	0.225802	0.358025	-6.35
248270_at	putative protein similar to unknown	ORG1	AT5G53450	-1.27	-0.35	-1.33	0.225837	0.358043	-6.35
265878_at	putative SUPERMAN-like C2H2 zin	ZFP11	AT2G42410	-1.09	-0.13	-1.33	0.225845	0.358043	-6.35
250867_at	putative protein predicted protein, /	---	AT5G03880	-1.17	-0.23	-1.33	0.225943	0.358173	-6.35
253872_at	putative protein Arabidopsis thalian	RD26	AT4G27410	1.19	0.25	1.33	0.225961	0.358176	-6.35
251022_at	putative protein Hsp70 binding prot	---	AT5G02150	1.13	0.17	1.33	0.225991	0.3582	-6.35
247667_at	putative protein predicted protein, /	---	AT5G60150	-1.13	-0.17	-1.33	0.226037	0.358247	-6.35
264658_at	hypothetical protein similar to LG27	---	AT1G09910	1.12	0.16	1.33	0.226109	0.358338	-6.35
260623_at	high-affinity nitrate transporter NRT	ATNRT2:1	AT1G08090	-1.13	-0.18	-1.33	0.226224	0.358489	-6.35
248401_at	putative protein similar to unknown	HCF208	AT5G52110	-1.23	-0.30	-1.33	0.226237	0.358489	-6.35
262009_at	hypothetical protein predicted by ge	---	AT1G35610	-1.13	-0.18	-1.33	0.226337	0.358623	-6.35
252804_at	putative protein	---	---	-1.09	-0.12	-1.33	0.226369	0.358637	-6.35
249597_at	putative protein probable quinone c	---	AT5G37960	-1.09	-0.12	-1.33	0.226377	0.358637	-6.35
264263_at	Expressed protein ; supported by fu	AtPP2-B15	AT1G09155	1.11	0.15	1.33	0.226527	0.35885	-6.35
246598_at	dolichyl-phosphate-mannose--glyc	---	AT5G14850	1.14	0.19	1.33	0.226556	0.358871	-6.35
259758_s_a	putative caffeic acid 3-O-methyltran	---	AT1G77520	-1.11	-0.15	-1.33	0.226578	0.358881	-6.35
245474_at	hypothetical protein	---	AT4G16060	-1.14	-0.18	-1.33	0.226603	0.358892	-6.35
250258_at	floral homeotic protein AGL15 (sp|C	AGL15	AT5G13790	-1.12	-0.16	-1.33	0.226616	0.358892	-6.35
267020_at	hypothetical protein predicted by ge	---	AT2G39320	-1.12	-0.16	-1.33	0.226736	0.359056	-6.35
266266_at	putative enolase (2-phospho-D-glyc	---	AT2G29560	-1.13	-0.18	-1.33	0.22682	0.359131	-6.35
255930_at	hypothetical protein predicted by ge	---	AT1G12660	-1.10	-0.14	-1.33	0.226826	0.359131	-6.35
256660_at	hypothetical protein similar to hypot	---	AT3G12060	-1.12	-0.16	-1.33	0.226857	0.359131	-6.35
252435_at	putative protein several hypothetica	---	---	-1.12	-0.17	-1.33	0.226861	0.359131	-6.35
250017_at	unknown protein	---	AT5G18140	-1.19	-0.25	-1.33	0.226876	0.359131	-6.35
264820_at	putative coproporphyrinogen III oxi	LIN2	AT1G03475	-1.09	-0.12	-1.33	0.226878	0.359131	-6.35
246175_s_a	putative protein hypothetical protei	---	AT5G28320	-1.11	-0.15	-1.33	0.226899	0.359139	-6.35
267086_at	putative salt-inducible protein	---	AT2G32630	1.14	0.19	1.33	0.226914	0.359139	-6.35
265532_at	hypothetical protein predicted by ge	---	---	-1.12	-0.16	-1.33	0.22695	0.359171	-6.35
263872_at	putative cellulose synthase catalyti	CESA9	AT2G21770	-1.13	-0.18	-1.33	0.227006	0.359235	-6.35
261540_at	unknown protein	---	AT1G63610	-1.13	-0.17	-1.33	0.227044	0.359269	-6.35
249728_at	GTPase activator-like protein of Ra	---	AT5G24390	1.13	0.17	1.33	0.227173	0.35945	-6.35
257657_at	Expressed protein ; supported by fu	---	AT3G13235	1.10	0.13	1.33	0.227202	0.359471	-6.35
246203_at	putative protein ; supported by full-l	---	AT4G36610	-1.22	-0.29	-1.33	0.227225	0.359482	-6.35

248726_at	RAS superfamily GTP-binding prote	ATRABA4C	AT5G47960	1.61	0.69	1.33	0.22727	0.359515	-6.35
258109_at	hypothetical protein contains Pfam	HGL1	AT3G23640	1.12	0.16	1.33	0.227278	0.359515	-6.35
263487_at	hypothetical protein predicted by ge	---	AT2G31850	-1.10	-0.14	-1.33	0.22747	0.359794	-6.35
258985_at	hypothetical protein similar to hypo	---	AT3G08960	-1.10	-0.14	-1.33	0.22751	0.359832	-6.35
260048_at	unknown protein contains Pfam pro	---	AT1G73750	-1.46	-0.54	-1.33	0.227541	0.359857	-6.35
245231_at	hypothetical protein	---	AT4G25600	1.13	0.18	1.33	0.227593	0.359891	-6.35
260600_at	hypothetical protein predicted by ge	---	AT1G55950	-1.12	-0.16	-1.33	0.227594	0.359891	-6.35
250270_at	putative protein FL10, EGF respon	---	AT5G12980	1.13	0.18	1.33	0.227719	0.360063	-6.36
257538_at	hypothetical protein predicted by ge	---	AT3G16160	-1.10	-0.13	-1.33	0.227736	0.360065	-6.36
256526_at	disease resistance protein, putative	---	AT1G66090	-1.12	-0.16	-1.33	0.227849	0.360219	-6.36
246664_at	putative protein predicted proteins -	---	---	-1.11	-0.15	-1.33	0.227918	0.360304	-6.36
258408_at	unknown protein similar to putative	ATCHX19	AT3G17630	1.10	0.14	1.33	0.228001	0.36041	-6.36
256377_at	hypothetical protein	---	AT1G66650	-1.09	-0.12	-1.33	0.228035	0.360438	-6.36
264055_at	putative protein kinase contains a p	---	AT2G28590	1.13	0.18	1.33	0.228071	0.360469	-6.36
256703_at	MADS-box transcription factor simi	AGL79	AT3G30260	1.08	0.11	1.33	0.228117	0.360517	-6.36
252248_at	putative protein resistance gene H	AtRLP44	AT3G49750	-1.21	-0.27	-1.33	0.228218	0.360651	-6.36
261442_at	Expressed protein ; supported by fu	---	AT1G28375	1.11	0.15	1.33	0.228273	0.360693	-6.36
258199_at	unknown protein	---	AT3G14030	-1.11	-0.15	-1.33	0.228277	0.360693	-6.36
248888_at	potassium channel protein KAT1 (p	KAT1	AT5G46240	-1.31	-0.39	-1.33	0.228291	0.360693	-6.36
259681_at	nitrate reductase 1 (NR1) identical t	NIA1	AT1G77760	-2.15	-1.10	-1.32	0.228469	0.360949	-6.36
260378_at	putative actin similar to actin GB:CA	ATARP4A	AT1G73910	-1.09	-0.12	-1.32	0.228558	0.361065	-6.36
265864_at	putative myosin heavy chain-like pr	ATMAP70-	AT2G01750	1.16	0.21	1.32	0.228789	0.361405	-6.36
254461_at	receptor kinase - like protein SRK3	---	AT4G21230	1.16	0.22	1.32	0.228871	0.361486	-6.36
262919_at	unknown protein ; supported by cDI	---	AT1G79380	-1.16	-0.21	-1.32	0.228875	0.361486	-6.36
254897_at	serine/threonine kinase-like protein	---	AT4G11470	1.37	0.45	1.32	0.228888	0.361486	-6.36
264017_s_a	putative ER lumen protein retaining	---	AT2G21190	1.10	0.14	1.32	0.22898	0.361591	-6.36
264959_at	hypothetical protein predicted by ge	---	AT1G77090	-1.13	-0.17	-1.32	0.228987	0.361591	-6.36
245960_at	subtilisin-like protein subtilisin/kexi	S1P	AT5G19660	1.09	0.12	1.32	0.229015	0.361611	-6.36
248376_at	unknown protein ; supported by full-	---	AT5G51880	-1.11	-0.15	-1.32	0.229087	0.361699	-6.36
265437_at	hypothetical protein predicted by ge	MCM10	AT2G20980	-1.12	-0.16	-1.32	0.229106	0.361705	-6.36
259833_at	MYB-family transcription factor, pu	MYB105	AT1G69560	-1.10	-0.13	-1.32	0.229174	0.361771	-6.36
251410_at	uclacyanin 3 ; supported by cDNA:	UCC3	AT3G60280	-1.10	-0.13	-1.32	0.22918	0.361771	-6.36
263278_at	dynamin-like protein	DRP3B	AT2G14120	1.13	0.17	1.32	0.229348	0.361995	-6.36
259719_at	unknown protein contains gamma-t	LCR66	AT1G61070	-1.10	-0.13	-1.32	0.229353	0.361995	-6.36
253031_at	putative protein cellulose synthase	CSLD4	AT4G38190	-1.12	-0.16	-1.32	0.229428	0.362069	-6.36

253693_at	Thioredoxin - like protein thioredoxi	ACHT2	AT4G29670	-1.19	-0.26	-1.32	0.229432	0.362069	-6.36
254668_at	neoxanthin cleavage enzyme - like	NCED2	AT4G18350	-1.14	-0.19	-1.32	0.229477	0.362116	-6.36
253644_at	putative protein predicted protein, A	---	AT4G29870	1.16	0.21	1.32	0.229508	0.362138	-6.36
265178_at	Pto kinase interactor, putative simil	---	AT1G23540	-1.12	-0.16	-1.32	0.229604	0.362265	-6.36
258311_at	transport inhibitor response 1 (TIR1	AFB2	AT3G26810	-1.12	-0.16	-1.32	0.229702	0.362394	-6.36
254718_at	putative protein disease resistance	---	AT4G13580	-1.11	-0.16	-1.32	0.2298	0.362524	-6.36
262403_s_a	mutator-like transposase, putative	---	---	1.09	0.13	1.32	0.22986	0.362595	-6.36
259116_at	putative peptide transporter similar	---	AT3G01350	1.21	0.27	1.32	0.229913	0.362652	-6.36
255517_at	putative endo-1,4-beta glucanase s	AtGH9B13	AT4G02290	-1.14	-0.19	-1.32	0.229947	0.362682	-6.36
257913_at	unknown protein ; supported by cD	LAG1	AT3G25540	1.12	0.16	1.32	0.230026	0.362781	-6.36
250095_at	phytoene synthase (gb|AAB65697.1	---	AT5G17230	-1.22	-0.29	-1.32	0.230073	0.36283	-6.36
255390_at	hypothetical protein similar to A. th	---	---	-1.11	-0.15	-1.32	0.230137	0.362892	-6.36
264898_at	Unknown protein ; supported by full	---	AT1G23205	-1.18	-0.24	-1.32	0.230156	0.362892	-6.36
256989_at	hypothetical protein predicted by ge	---	AT3G28580	1.85	0.89	1.32	0.230161	0.362892	-6.36
255892_at	hypothetical protein contains simila	---	AT1G17910	-1.10	-0.14	-1.32	0.230221	0.362963	-6.36
259443_at	chitinase, putative similar to chitina	---	AT1G02360	1.27	0.35	1.32	0.230249	0.362982	-6.37
258384_at	hypothetical protein predicted by ge	---	AT3G15490	-1.10	-0.14	-1.32	0.230294	0.363027	-6.37
255143_at	putative protein several hypothetica	---	AT4G08430	-1.08	-0.11	-1.32	0.230324	0.36305	-6.37
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.33	-0.41	-1.32	0.230344	0.363056	-6.37
252053_at	syntaxin-like protein synt4 ;support	SYP122	AT3G52400	1.40	0.49	1.32	0.230514	0.363277	-6.37
248496_at	MtN3-like protein ;supported by full	---	AT5G50790	-1.14	-0.18	-1.32	0.230516	0.363277	-6.37
244930_at	hypothetical protein	---	AT2G07809	1.10	0.13	1.32	0.230585	0.363361	-6.37
256942_at	hypothetical protein similar to unkn	LSH4	AT3G23290	-1.36	-0.44	-1.32	0.23067	0.363469	-6.37
263625_at	F-box protein family, AtFBX9 conta	---	AT2G04920	-1.10	-0.14	-1.32	0.230719	0.363519	-6.37
250949_at	putative protein	---	AT5G03510	-1.10	-0.13	-1.32	0.230733	0.363519	-6.37
250310_at	unknown protein	---	AT5G12230	1.15	0.20	1.32	0.230771	0.363553	-6.37
265565_at	putative retroelement pol polyprotei	---	---	-1.11	-0.15	-1.32	0.230943	0.363787	-6.37
265198_at	putative glucosyl transferase	UGT73C2	AT2G36760	-1.10	-0.13	-1.32	0.230952	0.363787	-6.37
259742_at	putative proline-rich APG protein si	GLIP6	AT1G71120	-1.17	-0.23	-1.32	0.230984	0.363814	-6.37
261469_at	unknown protein	AtRLP4	AT1G28340	-1.11	-0.15	-1.32	0.231096	0.363965	-6.37
247526_at	putative protein C2H2 zinc-finger p	---	AT5G61470	-1.10	-0.14	-1.32	0.231222	0.364139	-6.37
251668_at	putative protein strictosidine syntha	---	AT3G57010	-1.26	-0.34	-1.32	0.231271	0.36419	-6.37
262693_at	unknown protein	---	AT1G62780	-1.25	-0.32	-1.32	0.231311	0.364228	-6.37
251245_at	putative protein phytochrome-asso	PIL2	AT3G62090	1.37	0.46	1.32	0.231345	0.364257	-6.37
267290_at	putative SET-domain transcriptiona	---	AT2G23740	-1.13	-0.18	-1.32	0.231384	0.364271	-6.37

263128_at	zinc finger protein, putative similar	LZF1	AT1G78600	1.21	0.27	1.32	0.2314	0.364271	-6.37
257465_at	hypothetical protein predicted by ge	---	AT1G13040	1.09	0.12	1.32	0.231406	0.364271	-6.37
253624_at	putative protein 2-acylglycerophosp	ATS2	AT4G30580	1.14	0.19	1.32	0.231419	0.364271	-6.37
251761_at	glucuronosyl transferase - like prot	---	AT3G55700	1.15	0.21	1.32	0.2315	0.364374	-6.37
261777_at	hypothetical protein predicted by ge	---	AT1G76210	-1.11	-0.15	-1.32	0.231532	0.364383	-6.37
266101_at	unknown protein ; supported by cD	---	AT2G37940	1.35	0.43	1.32	0.231538	0.364383	-6.37
266334_at	hypothetical protein predicted by ge	---	AT2G32380	-1.19	-0.25	-1.31	0.231577	0.36442	-6.37
259370_at	hypothetical protein predicted by ge	---	AT1G69050	1.14	0.18	1.31	0.231727	0.364631	-6.37
267528_at	MADS-box protein (AGL6) ; suppo	AGL6	AT2G45650	-1.11	-0.15	-1.31	0.231743	0.364631	-6.37
261877_at	putative indole-3-acetate beta-gluc	---	AT1G50580	-1.11	-0.15	-1.31	0.23177	0.364649	-6.37
265360_s_a	putative Athila retroelement ORF1 p	---	---	-1.11	-0.15	-1.31	0.23186	0.364766	-6.37
249227_at	peroxidase (emb|CAA66960.1)	---	AT5G42180	-1.11	-0.14	-1.31	0.231902	0.364798	-6.37
247390_at	putative protein similar to unknown	---	AT5G63520	1.10	0.13	1.31	0.231913	0.364798	-6.37
246946_at	putative protein	---	AT5G25070	-1.09	-0.13	-1.31	0.231948	0.364827	-6.37
257229_at	putative calmodulin-binding protein	IQD26	AT3G16490	-1.14	-0.20	-1.31	0.231982	0.364842	-6.37
250278_at	2-oxoglutarate/malate translocator	DiT1	AT5G12860	1.20	0.27	1.31	0.231989	0.364842	-6.37
253147_at	protein kinase - like protein serine/	CONNEXIN	AT4G35600	1.21	0.27	1.31	0.232039	0.364895	-6.37
255134_at	putative protein	---	AT4G08330	1.12	0.16	1.31	0.232092	0.364954	-6.37
248978_at	putative protein contains similarity t	AtPP2-A8	AT5G45070	-1.15	-0.20	-1.31	0.23215	0.36502	-6.37
264671_at	unknown protein ; supported by ful	---	AT1G09920	1.13	0.17	1.31	0.23219	0.365045	-6.37
245834_at	transposon protein, putative similar	---	---	-1.09	-0.13	-1.31	0.232198	0.365045	-6.37
248280_at	putative protein similar to unknown	---	AT5G52950	-1.11	-0.15	-1.31	0.232221	0.365055	-6.37
245226_at	gene_id:K17E7.15~unknown protei	---	AT3G29970	1.63	0.71	1.31	0.23227	0.365104	-6.37
244923_s_a	orf153b orf153b	---	AT2G07674	-1.19	-0.26	-1.31	0.232283	0.365104	-6.37
251842_at	extensin precursor -like protein ext	---	AT3G54580	-1.30	-0.37	-1.31	0.232311	0.365122	-6.37
261542_at	unknown protein contains Pfam pro	---	AT1G63560	-1.13	-0.17	-1.31	0.232365	0.365182	-6.37
255353_at	putative transposon protein similar t	---	---	-1.09	-0.13	-1.31	0.232391	0.365197	-6.37
253011_at	putative protein retrotransposon -li	EDA40	AT4G37890	-1.23	-0.30	-1.31	0.232462	0.365255	-6.37
262187_at	hypothetical protein	---	AT1G77960	1.10	0.14	1.31	0.232465	0.365255	-6.37
244903_at	hypothetical protein	---	---	1.32	0.40	1.31	0.232476	0.365255	-6.37
247995_at	putative protein contains similarity t	---	AT5G56160	-1.15	-0.20	-1.31	0.232503	0.365272	-6.37
245455_at	disease resistance RPP5 like protei	---	AT4G16930	-1.10	-0.14	-1.31	0.232534	0.365272	-6.37
255707_at	predicted protein	MEE50	AT4G00231	1.09	0.13	1.31	0.232563	0.365272	-6.37
261915_at	amp-binding protein, putative simila	BZO1	AT1G65880	1.08	0.12	1.31	0.232573	0.365272	-6.37
252236_at	zinc-finger-like protein Cys2/His2-t	---	AT3G49930	1.11	0.15	1.31	0.232582	0.365272	-6.37

246506_at	putative protein hypothetical protei	---	AT5G16110	1.14	0.20	1.31	0.232593	0.365272	-6.37
263299_s_a	hypothetical protein predicted by ge	---	AT2G11570	-1.11	-0.14	-1.31	0.232599	0.365272	-6.37
247433_at	E2, ubiquitin-conjugating enzyme 3	UBC3	AT5G62540	-1.18	-0.23	-1.31	0.232644	0.365318	-6.37
253978_at	putative protein probable kinesin -	---	AT4G26660	-1.14	-0.18	-1.31	0.232675	0.365341	-6.37
257714_at	histone H3, putative similar to histo	---	AT3G27360	-1.13	-0.18	-1.31	0.232735	0.36541	-6.37
250015_at	N-acetylglucosamine-phosphate mu	DRT101	AT5G18070	-1.22	-0.29	-1.31	0.232886	0.365623	-6.37
259944_at	hypothetical protein predicted by ge	---	AT1G71470	-1.10	-0.14	-1.31	0.232998	0.365756	-6.38
266186_at	unknown protein	AERO2	AT2G38960	1.09	0.13	1.31	0.233003	0.365756	-6.38
252577_at	putative protein putative proteins - A	---	AT3G45460	-1.09	-0.12	-1.31	0.233076	0.365846	-6.38
267194_s_a	putative ARP2/3 protein complex su	ARPC1A	AT2G30910	-1.11	-0.15	-1.31	0.233203	0.366019	-6.38
258464_at	kinesin-like protein similar to KLP2	POK1	AT3G17360	-1.08	-0.12	-1.31	0.233271	0.366099	-6.38
248724_at	putative protein strong similarity to	---	AT5G47970	1.20	0.26	1.31	0.233291	0.366099	-6.38
264528_at	hypothetical protein similar to Huma	---	AT1G30810	1.09	0.12	1.31	0.233329	0.366099	-6.38
258554_at	putative DEAD/DEAH box helicase	---	AT3G06980	1.10	0.14	1.31	0.233332	0.366099	-6.38
266870_at	putative heterogeneous nuclear ribo	---	AT2G44710	1.17	0.23	1.31	0.233344	0.366099	-6.38
260963_at	hypothetical protein predicted by ge	---	AT1G44990	-1.11	-0.15	-1.31	0.233372	0.366099	-6.38
265166_at	putative OBP32pep protein	---	AT1G23640	1.09	0.13	1.31	0.233378	0.366099	-6.38
247489_at	carbonyl reductase - like protein in	---	AT5G61830	-1.12	-0.17	-1.31	0.233387	0.366099	-6.38
257565_at	hypothetical protein predicted by ge	---	AT3G28620	1.09	0.13	1.31	0.233398	0.366099	-6.38
250626_at	putative protein p100 co-activator -	---	AT5G07350	-1.11	-0.15	-1.31	0.233432	0.366128	-6.38
254001_at	putative protein PRE87 mRNA, Pir	MIOX4	AT4G26260	1.38	0.46	1.31	0.233531	0.366257	-6.38
255597_at	hypothetical protein	---	AT4G01730	-1.12	-0.16	-1.31	0.233554	0.366266	-6.38
249795_at	40S ribosomal protein S11 ;support	RPS11-BE	AT5G23740	1.22	0.29	1.31	0.233572	0.366266	-6.38
254406_at	putative transposable element reve	---	---	-1.09	-0.13	-1.31	0.233585	0.366266	-6.38
267641_at	Argonaute (AGO1)-like protein	AGO6	AT2G32940	-1.09	-0.13	-1.31	0.233736	0.366477	-6.38
247626_at	receptor like protein kinase recepto	---	AT5G60300	-1.38	-0.46	-1.31	0.23382	0.366584	-6.38
259803_at	cytosolic factor, putative similar to	PATL1	AT1G72150	-1.11	-0.14	-1.31	0.233858	0.366619	-6.38
266056_at	hypothetical protein predicted by ge	ATATG18C	AT2G40810	-1.09	-0.13	-1.31	0.233947	0.366733	-6.38
261465_at	unknown protein	---	AT1G07705	-1.10	-0.14	-1.31	0.233981	0.366758	-6.38
251901_at	putative protein axi1 protein, Nicoti	---	AT3G54100	-1.14	-0.19	-1.31	0.233995	0.366758	-6.38
245974_at	putative protein	---	---	-1.18	-0.24	-1.31	0.234087	0.366876	-6.38
252462_at	putative protein various predicted g	---	AT3G47250	-1.10	-0.14	-1.31	0.234103	0.366876	-6.38
256615_at	hypothetical protein predicted by ge	---	AT3G22250	-1.14	-0.19	-1.31	0.2342	0.367003	-6.38
260470_at	hypothetical protein predicted by ge	---	AT1G11120	-1.14	-0.18	-1.31	0.23428	0.367092	-6.38
262096_at	NAC1 identical to NAC1 GB:AAF21	NAC1	AT1G56010	1.26	0.34	1.31	0.234289	0.367092	-6.38

248621_at	putative protein similar to unknown	---	AT5G49350	-1.11	-0.15	-1.31	0.234329	0.367131	-6.38
247699_at	GTP-binding protein ara-3 GTP-bir	---	AT5G59840	1.20	0.26	1.31	0.23436	0.367154	-6.38
258602_at	putative protein phosphatase-2C (P	---	AT3G02750	-1.09	-0.12	-1.31	0.234639	0.367565	-6.38
257849_at	unknown protein	ECT5	AT3G13060	1.15	0.20	1.30	0.234755	0.367713	-6.38
246637_at	putative protein polymorphic memb	---	AT5G34870	-1.12	-0.16	-1.30	0.234772	0.367713	-6.38
256820_at	far-red impaired response protein,	FHY3	AT3G22170	1.09	0.13	1.30	0.234782	0.367713	-6.38
245412_at	hypothetical protein	---	AT4G17280	-1.18	-0.24	-1.30	0.234809	0.367731	-6.38
251904_at	Machado-Joseph disease MJD1a -	---	AT3G54130	1.15	0.20	1.30	0.234912	0.367867	-6.38
263792_at	putative retroelement pol polyprotei	---	---	-1.14	-0.19	-1.30	0.234952	0.367903	-6.38
266686_at	hypothetical protein	---	AT2G19700	-1.11	-0.15	-1.30	0.235002	0.367956	-6.38
252666_at	putative protein hypothetical protein	---	AT3G44180	-1.12	-0.16	-1.30	0.235055	0.367994	-6.38
262655_s_a	putative mandelonitrile lyase simila	---	AT1G14185	1.09	0.13	1.30	0.235058	0.367994	-6.38
256381_at	lipid transfer protein, putative conta	---	AT1G66850	-1.12	-0.17	-1.30	0.235172	0.368148	-6.38
252035_at	beta-ketoacyl-CoA synthase like pr	KCS15	AT3G52160	-1.13	-0.17	-1.30	0.235237	0.368224	-6.38
263439_at	hypothetical protein predicted by ge	ATEXO70H	AT2G28650	-1.12	-0.16	-1.30	0.235307	0.368285	-6.38
254513_at	cytochrome p450 like protein cytoc	CYP71A27	AT4G20240	-1.09	-0.13	-1.30	0.235308	0.368285	-6.38
264801_at	hypothetical protein gene overlaps	emb2411	AT1G08840	-1.11	-0.15	-1.30	0.235475	0.368516	-6.38
244991_s_a	NADH dehydrogenase ND2	---	---	-1.11	-0.14	-1.30	0.235499	0.368516	-6.38
256806_at	CCAAT-binding factor B chain, put	NF-YA9	AT3G20910	1.12	0.17	1.30	0.235516	0.368516	-6.38
258053_at	unknown protein similar to CGI-18 p	---	AT3G16230	1.09	0.12	1.30	0.23553	0.368516	-6.38
258835_at	putative RNA-binding protein conta	---	AT3G07250	-1.12	-0.17	-1.30	0.235537	0.368516	-6.38
264216_at	hypothetical protein similar to hypot	---	AT1G60180	-1.09	-0.13	-1.30	0.235619	0.368603	-6.39
247083_at	unknown protein	---	AT5G66290	1.10	0.14	1.30	0.235633	0.368603	-6.39
246377_at	low-temperature-specific protein, p	---	AT1G57550	-1.18	-0.24	-1.30	0.235656	0.368603	-6.39
254394_at	subtilisin-like serine protease conta	---	AT4G21630	-1.09	-0.12	-1.30	0.235657	0.368603	-6.39
245564_at	hypothetical protein	emb2739	AT4G14590	1.12	0.17	1.30	0.235694	0.368627	-6.39
252903_at	putative protein various predicted p	---	AT4G39570	1.19	0.25	1.30	0.235704	0.368627	-6.39
261799_at	unknown protein contains similarity	---	AT1G30473	-1.16	-0.21	-1.30	0.235747	0.368667	-6.39
258080_at	unknown protein ;supported by full-	---	AT3G25930	-1.09	-0.12	-1.30	0.235962	0.368972	-6.39
256361_at	formyl transferase, putative contain	pde194	AT1G66520	1.14	0.19	1.30	0.235991	0.368972	-6.39
265413_s_a	hypothetical protein predicted by ge	---	AT2G16650	-1.12	-0.16	-1.30	0.235992	0.368972	-6.39
252172_at	putative protein predicted proteins,	---	AT3G50640	-1.11	-0.15	-1.30	0.236006	0.368972	-6.39
258268_at	putative WD-repeat protein contain	WSIP2	AT3G15880	1.18	0.23	1.30	0.236132	0.369143	-6.39
265835_at	putative retroelement pol polyprotei	---	---	-1.13	-0.18	-1.30	0.236153	0.369151	-6.39
250498_at	microbody NAD-dependent malate	PMDH2	AT5G09660	-1.18	-0.24	-1.30	0.236252	0.369281	-6.39

253602_s_a	leucyl aminopeptidase - like protein	---	AT4G30910	1.10	0.14	1.30	0.236326	0.369348	-6.39
262550_at	hypothetical protein similar to hypot	---	AT1G31310	-1.10	-0.14	-1.30	0.236328	0.369348	-6.39
257077_at	PR-1 protein, putative similar to PR	---	AT3G19690	-1.16	-0.21	-1.30	0.236384	0.36941	-6.39
247551_at	ras-GTPase-activating protein SH3	---	AT5G60980	1.09	0.12	1.30	0.236472	0.369523	-6.39
AFFX-ThrX-	B. subtilis /GEN=thrC /DB_XREF=g	---	---	-1.23	-0.29	-1.30	0.236567	0.369647	-6.39
245366_at	Expressed protein ; supported by fu	AtMAPR4	AT4G14965	1.09	0.13	1.30	0.236733	0.369881	-6.39
254156_at	Rab geranylgeranyl transferase like	---	AT4G24490	-1.15	-0.21	-1.30	0.236751	0.369883	-6.39
244956_s_a	hypothetical protein	---	---	1.12	0.16	1.30	0.236806	0.369943	-6.39
260891_at	cysteine protease contains similarity	---	AT1G29080	-1.11	-0.16	-1.30	0.237085	0.370354	-6.39
254308_at	putative protein snRNP assembly f	---	AT4G22410	1.11	0.14	1.30	0.237144	0.37042	-6.39
247649_at	KED - like protein KED, Nicotiana t	---	AT5G60030	1.12	0.16	1.30	0.237254	0.370567	-6.39
247481_at	putative protein predicted protein, A	---	AT5G62400	-1.09	-0.13	-1.30	0.23729	0.370598	-6.39
266786_at	putative non-LTR retroelement reve	---	---	1.10	0.13	1.30	0.23744	0.370806	-6.39
248435_at	oleosin-like	OLEO3	AT5G51210	-1.13	-0.18	-1.30	0.237517	0.370901	-6.39
256712_at	unknown protein similar to T14G11	---	AT2G34020	-1.09	-0.12	-1.30	0.237651	0.371085	-6.39
256810_at	adenyl cyclase, putative similar to a	---	AT3G21465	1.12	0.17	1.30	0.237848	0.371368	-6.39
256387_at	hypothetical protein	---	AT3G06170	1.14	0.19	1.30	0.237895	0.371415	-6.39
254829_at	AIR1A-like protein putative cell wal	---	AT4G12530	-1.10	-0.13	-1.29	0.238017	0.371581	-6.39
251634_at	putative protein putative zinc finger	---	AT3G57480	-1.11	-0.15	-1.29	0.238225	0.371881	-6.39
251315_at	putative protein protein kinase hom	---	AT3G61410	-1.13	-0.17	-1.29	0.238349	0.372048	-6.40
257121_at	hypothetical protein similar to auxin	---	AT3G20220	-1.11	-0.15	-1.29	0.238432	0.372153	-6.40
248071_at	unknown protein	---	AT5G55670	1.11	0.15	1.29	0.238506	0.372237	-6.40
262670_s_a	transposase [Escherichia coli] must	---	---	-1.10	-0.14	-1.29	0.238519	0.372237	-6.40
261890_at	hypothetical protein predicted by ge	---	AT1G80970	-1.20	-0.26	-1.29	0.238613	0.372358	-6.40
245705_at	zinc finger transcription factor-like p	---	AT5G04390	1.10	0.13	1.29	0.238638	0.372372	-6.40
264947_at	heat shock protein DnaJ, putative s	---	AT1G77020	-1.14	-0.19	-1.29	0.238714	0.372465	-6.40
253130_at	putative protein ;supported by full-l	---	AT4G35510	-1.19	-0.25	-1.29	0.238818	0.372602	-6.40
264660_at	putative glutamyl-tRNA reductase 2	HEMA2	AT1G09940	1.33	0.41	1.29	0.238924	0.372742	-6.40
263401_at	hypothetical protein similar to hypot	---	AT2G04070	1.18	0.24	1.29	0.238944	0.372747	-6.40
252069_s_a	putative protein putative protein T18	---	AT3G51640	-1.10	-0.14	-1.29	0.239002	0.372812	-6.40
265448_at	putative DOF zinc finger protein	DAG2	AT2G46590	-1.14	-0.19	-1.29	0.239024	0.372822	-6.40
260075_at	putative integral membrane protein	---	AT1G73700	1.14	0.19	1.29	0.239177	0.373034	-6.40
265980_at	hypothetical protein predicted by ge	---	---	-1.12	-0.16	-1.29	0.239282	0.373149	-6.40
256224_at	GTP-binding protein (SAR1B) ident	ATSAR1B	AT1G56330	-1.16	-0.22	-1.29	0.239283	0.373149	-6.40
253739_at	putative protein predicted protein. A	---	AT4G28760	-1.14	-0.19	-1.29	0.239355	0.373236	-6.40

245309_at	putative protein ; supported by cDN	---	AT4G15140	1.19	0.25	1.29	0.239397	0.373275	-6.40
251874_at	putative protein (fragment) esteras	---	AT3G54240	-1.14	-0.19	-1.29	0.239428	0.373299	-6.40
256541_at	ligand-gated ion channel, putative (	GLR3.3	AT1G42540	1.15	0.20	1.29	0.239457	0.373318	-6.40
246534_at	putative protein several hypothetica	---	AT5G15890	-1.14	-0.19	-1.29	0.239597	0.373511	-6.40
248333_at	photoassimilate-responsive protein	---	AT5G52390	1.60	0.68	1.29	0.239746	0.373697	-6.40
267485_at	putative MYB family transcription fa	MYB88	AT2G02820	1.14	0.19	1.29	0.239749	0.373697	-6.40
254295_at	putative protein predicted protein, A	---	AT4G23080	-1.09	-0.12	-1.29	0.239811	0.373768	-6.40
265597_at	Expressed protein ; supported by cl	---	AT2G20142	1.39	0.47	1.29	0.239862	0.373822	-6.40
244973_at	PSII T protein	---	---	-1.27	-0.35	-1.29	0.240069	0.374118	-6.40
249061_at	putative protein similar to unknown	---	AT5G44550	-1.10	-0.14	-1.29	0.240089	0.374124	-6.40
256085_at	hypothetical protein predicted by ge	---	AT1G20760	-1.09	-0.12	-1.29	0.240288	0.374383	-6.40
264703_at	serine threonine protein phosphatas	PP2A	AT1G69960	1.09	0.13	1.29	0.240288	0.374383	-6.40
263213_at	unknown protein Strong similarity to	---	AT1G30560	-1.12	-0.17	-1.29	0.240317	0.374402	-6.40
247391_at	unknown protein	---	AT5G63540	-1.09	-0.12	-1.29	0.240343	0.374417	-6.40
256605_at	hypothetical protein predicted by ge	---	AT3G32940	1.12	0.16	1.29	0.240474	0.374596	-6.40
254361_at	Expressed protein ; supported by fu	---	AT4G22212	-1.14	-0.19	-1.29	0.240532	0.374661	-6.40
247930_at	putative protein similar to unknown	---	AT5G57060	1.17	0.22	1.29	0.240616	0.37476	-6.40
265355_at	hypothetical protein predicted by ge	---	AT2G16760	-1.18	-0.24	-1.29	0.240641	0.37476	-6.40
263118_at	putative 3-methylcrotonyl-CoA carb	MCCA	AT1G03090	-1.30	-0.37	-1.29	0.240645	0.37476	-6.40
250599_at	unknown protein ; supported by cD	---	AT5G07730	-1.15	-0.20	-1.29	0.240677	0.374783	-6.40
260403_at	hypothetical protein predicted by ge	WRKY36	AT1G69810	-1.09	-0.13	-1.29	0.240692	0.374783	-6.40
249099_at	putative protein similar to unknown	---	AT5G43550	-1.08	-0.11	-1.29	0.240747	0.374843	-6.40
256423_at	serine carboxypeptidase, putative s	scpl18	AT1G33540	-1.09	-0.12	-1.29	0.240844	0.374945	-6.40
246168_at	meristem protein - like reproductive	---	AT5G32460	1.17	0.23	1.29	0.240846	0.374945	-6.40
267369_at	unknown protein ;supported by full-	---	AT2G44420	1.12	0.17	1.29	0.240914	0.375026	-6.40
257653_at	hypothetical protein	---	AT3G13225	-1.13	-0.18	-1.29	0.241191	0.375394	-6.41
248115_at	putative protein strong similarity to u	---	AT5G54870	1.20	0.27	1.29	0.241197	0.375394	-6.41
260113_at	hypothetical protein predicted by ge	---	AT1G63300	-1.09	-0.12	-1.29	0.2412	0.375394	-6.41
255914_at	hypothetical protein predicted by ge	---	AT1G20290	-1.13	-0.17	-1.28	0.241265	0.375469	-6.41
254069_at	putative protein similarity to antiser	ATNUDT10	AT4G25434	1.16	0.21	1.28	0.241405	0.375661	-6.41
256857_at	NAM-like protein similar to NAM (no	CUC1	AT3G15170	-1.08	-0.12	-1.28	0.241442	0.375689	-6.41
257417_at	hypothetical protein predicted by ge	---	AT1G10110	-1.11	-0.16	-1.28	0.241456	0.375689	-6.41
252125_at	putative protein hypothetical protei	RTH	AT3G51040	-1.11	-0.15	-1.28	0.241494	0.375715	-6.41
261368_at	protein kinase, putative similar to m	---	AT1G53070	-1.15	-0.20	-1.28	0.241514	0.375715	-6.41
251222_at	putative membrane protein clone:2	---	AT3G62580	-1.19	-0.25	-1.28	0.24153	0.375715	-6.41

257904_at	myb transcription factor, putative s	TDF1	AT3G28470	-1.09	-0.12	-1.28	0.241538	0.375715	-6.41
245891_at	amino acid transport protein AAP2	AAP2	AT5G09220	-1.32	-0.40	-1.28	0.241562	0.375726	-6.41
247603_at	microtubule-associated motor - like	---	AT5G60930	-1.15	-0.20	-1.28	0.241677	0.37588	-6.41
260277_at	hypothetical protein predicted by ge	---	AT1G80520	1.24	0.31	1.28	0.241792	0.376033	-6.41
260238_at	AtHVA22a identical to AtHVA22a C	ATHVA22A	AT1G74520	-1.14	-0.19	-1.28	0.241836	0.376076	-6.41
247273_at	unknown protein	CPuORF40	AT5G64340	-1.18	-0.24	-1.28	0.241867	0.376099	-6.41
257967_at	hypothetical protein predicted by ge	---	AT3G19910	1.10	0.14	1.28	0.241887	0.376104	-6.41
251868_at	RNA polymerase 24kDa subunit -li	RPB5E	AT3G54490	-1.11	-0.16	-1.28	0.242258	0.37663	-6.41
249122_at	putative protein similar to unknown	ARD4	AT5G43850	1.16	0.22	1.28	0.242266	0.37663	-6.41
264348_at	putative NPK1-related protein kinas	NRT1.1	AT1G12110	-1.80	-0.85	-1.28	0.242275	0.37663	-6.41
255866_at	hypothetical protein predicted by ge	---	AT2G30350	-1.12	-0.16	-1.28	0.242403	0.376804	-6.41
251009_at	putative protein predicted proteins,	---	AT5G02640	-1.24	-0.32	-1.28	0.242443	0.376839	-6.41
263252_at	putative CONSTANS-like B-box zin	STH	AT2G31380	-1.19	-0.25	-1.28	0.24247	0.376856	-6.41
263141_at	hypothetical protein similar to unkno	---	AT1G65210	-1.09	-0.13	-1.28	0.2425	0.376877	-6.41
259332_at	putative auxin-induced protein simil	---	AT3G03830	-1.11	-0.15	-1.28	0.242656	0.377094	-6.41
249773_at	squalene monooxygenase 2 (squal	SQP2	AT5G24140	-1.11	-0.15	-1.28	0.242775	0.377253	-6.41
265819_at	Expressed protein ; supported by fu	---	AT2G17972	-1.13	-0.17	-1.28	0.24285	0.377344	-6.41
247290_at	putative protein similar to unknown	---	AT5G64450	1.22	0.29	1.28	0.242894	0.377387	-6.41
266785_at	putative receptor-like protein kinase	---	AT2G28970	-1.11	-0.15	-1.28	0.243045	0.377596	-6.41
261202_at	flower pigmentation protein ATAN1	ATAN11	AT1G12910	-1.11	-0.16	-1.28	0.24307	0.377608	-6.41
251060_at	putative protein serine/threonine pr	ATSR1	AT5G01820	1.50	0.58	1.28	0.243121	0.377662	-6.41
256344_at	C2H2-type zinc finger protein, puta	TFIIIA	AT1G72050	1.13	0.17	1.28	0.243172	0.377713	-6.41
253930_at	embryo-specific protein 1 (ATS1)	ATS1	AT4G26740	-1.11	-0.14	-1.28	0.243188	0.377713	-6.41
253878_at	trehalose-6-phosphate synthase - I	TPS4	AT4G27550	-1.09	-0.13	-1.28	0.243204	0.377713	-6.41
254317_at	hypothetical protein	---	AT4G22510	-1.09	-0.12	-1.28	0.243243	0.377746	-6.41
267392_at	putative beta-glucosidase	PEN2	AT2G44490	1.17	0.23	1.28	0.243267	0.377746	-6.41
245146_at	putative cis-Golgi SNARE protein ;	GOS12	AT2G45200	-1.12	-0.16	-1.28	0.243274	0.377746	-6.41
263052_at	unknown protein	---	AT2G13430	-1.10	-0.13	-1.28	0.243494	0.378061	-6.41
247044_at	MAP protein kinase ; supported by	MAPKKK5	AT5G66850	1.15	0.20	1.28	0.243521	0.378078	-6.41
261876_at	pirin-like protein similar to pirin GB:A	---	AT1G50590	1.30	0.38	1.28	0.243546	0.378091	-6.41
253894_at	NWMU2 - 2S albumin 2 precursor	---	AT4G27150	1.09	0.13	1.28	0.2436	0.378148	-6.41
250171_at	prohibitin - like protein prohibitin, A	ATPHB5	AT5G14300	-1.10	-0.14	-1.28	0.243646	0.378195	-6.41
248341_at	unknown protein	---	AT5G52220	-1.14	-0.19	-1.28	0.243755	0.378337	-6.41
265328_at	unknown protein	---	AT2G18200	-1.08	-0.11	-1.28	0.243816	0.378406	-6.41
248076_at	unknown protein	---	AT5G55750	-1.09	-0.13	-1.28	0.243933	0.378562	-6.42

254937_at	putative aldolase similar to 2,4-dihy	---	AT4G10750	1.09	0.13	1.28	0.244002	0.378644	-6.42
250831_at	unknown protein	---	AT5G04920	-1.10	-0.14	-1.28	0.244059	0.378706	-6.42
249160_at	putative protein similar to unknown	---	AT5G42660	1.10	0.13	1.28	0.244116	0.378769	-6.42
246694_at	putative protein	---	---	-1.10	-0.14	-1.28	0.244171	0.378811	-6.42
254994_at	putative methyltransferase	MTA	AT4G10760	1.20	0.27	1.28	0.244176	0.378811	-6.42
262141_s_a	hypothetical protein predicted by ge	---	AT1G52440	1.08	0.11	1.28	0.244245	0.378892	-6.42
265581_at	putative cAMP-dependent protein k	---	AT2G20050	-1.10	-0.14	-1.28	0.244308	0.378964	-6.42
254439_s_a	carbonic anhydrase -like protein ca	ACA6	AT4G20990	-1.08	-0.11	-1.28	0.244327	0.378967	-6.42
256073_at	terminal Flower 1 (TFL1), putative	E12A11	AT1G18100	-1.12	-0.17	-1.28	0.244345	0.37897	-6.42
255269_at	putative protein various predicted p	---	AT4G05240	-1.11	-0.15	-1.28	0.244443	0.379082	-6.42
250118_at	putative protein similar to unknown	---	AT5G16460	-1.11	-0.16	-1.28	0.244451	0.379082	-6.42
252195_at	putative protein various predicted p	---	AT3G50190	-1.12	-0.17	-1.28	0.244504	0.379139	-6.42
249768_at	receptor-like protein kinase	---	AT5G24100	-1.13	-0.18	-1.28	0.244558	0.379197	-6.42
246859_at	putative protein various predicted p	---	AT5G25950	-1.10	-0.14	-1.27	0.244586	0.379215	-6.42
245589_at	subtilisin-like serine protease conta	---	AT4G15040	-1.16	-0.21	-1.27	0.244637	0.379269	-6.42
262681_at	anter-specific proline-rich -like prote	---	AT1G75890	-1.09	-0.12	-1.27	0.244709	0.379354	-6.42
252459_s_a	1-phosphatidylinositol-4,5-bisphosp	PLC9	AT3G47220	-1.09	-0.13	-1.27	0.24476	0.379407	-6.42
264991_s_a	putative protein hypothetical protein	---	AT1G67400	-1.16	-0.22	-1.27	0.245004	0.379758	-6.42
252999_at	putative protein other Arabidopsis h	---	AT4G38500	-1.11	-0.15	-1.27	0.24502	0.379758	-6.42
250367_s_a	DEAD BOX RNA helicase RH15 ; s	---	AT5G11170	1.11	0.15	1.27	0.245037	0.37976	-6.42
266537_at	Expressed protein ; supported by fu	---	AT2G16860	1.11	0.15	1.27	0.24516	0.379919	-6.42
266596_at	hypothetical protein predicted by ge	---	AT2G46150	1.29	0.37	1.27	0.245174	0.379919	-6.42
262412_at	14-3-3 protein GF14omicron (grf11)	GRF11	AT1G34760	-1.13	-0.17	-1.27	0.245226	0.379975	-6.42
259975_at	putative cinnamoyl-CoA reductase	---	AT1G76470	1.37	0.45	1.27	0.245307	0.380074	-6.42
249671_at	putative protein similar to unknown	LBD35	AT5G35900	-1.11	-0.15	-1.27	0.245389	0.380175	-6.42
253091_at	cytochrome p450 - like protein cyto	CYP81D2	AT4G37360	-1.10	-0.14	-1.27	0.24549	0.380289	-6.42
251488_at	calmodulin-like protein calcium-bin	---	AT3G59440	-1.08	-0.11	-1.27	0.245496	0.380289	-6.42
264813_at	putative Ca2+-dependent ser/thr pr	CPK16	AT2G17890	-1.15	-0.20	-1.27	0.24559	0.38041	-6.42
245807_at	AP2 domain containing protein RAF	RAP2.1	AT1G46768	1.24	0.31	1.27	0.245739	0.380614	-6.42
244966_at	cytochrome b6-f complex, subunit `	---	---	-1.17	-0.22	-1.27	0.245845	0.380746	-6.42
252744_at	putative protein hypothetical protei	---	AT3G43310	-1.10	-0.14	-1.27	0.245857	0.380746	-6.42
250334_at	NADH dehydrogenase (ubiquinone	---	AT5G11770	1.11	0.15	1.27	0.245886	0.380764	-6.42
253616_at	blight-associated protein homolog I	EXLB2	AT4G30380	-1.09	-0.13	-1.27	0.245921	0.380792	-6.42
246970_at	cytochrome P450-like protein fatty	CYP714A2	AT5G24900	-1.18	-0.24	-1.27	0.246013	0.38091	-6.42
267059_at	putative carboxymethylenebutenolic	---	AT2G32520	1.11	0.14	1.27	0.246093	0.381007	-6.42

261024_at	hypothetical protein predicted by ge	---	AT1G12190	-1.09	-0.13	-1.27	0.246166	0.381094	-6.42
262844_at	unknown protein similar to pectines	---	AT1G14890	-1.32	-0.40	-1.27	0.246294	0.381247	-6.42
265547_at	hypothetical protein similar to hypot	---	AT2G28305	-1.24	-0.31	-1.27	0.246313	0.381247	-6.42
259330_at	hypothetical protein gene model pre	---	AT3G16270	-1.13	-0.18	-1.27	0.246315	0.381247	-6.42
258326_at	unknown protein similar to putative	SOL1	AT3G22760	-1.15	-0.20	-1.27	0.246418	0.381371	-6.42
253671_at	serine threonine-specific receptor p	---	AT4G29990	1.14	0.19	1.27	0.246428	0.381371	-6.42
247968_at	40S ribosomal protein S30 homolog	---	AT5G56670	1.26	0.33	1.27	0.246475	0.381411	-6.42
266618_at	unknown protein	---	AT2G35480	-1.27	-0.35	-1.27	0.246487	0.381411	-6.42
249124_at	disease resistance protein ; suppor	---	AT5G43740	-1.10	-0.14	-1.27	0.246508	0.381417	-6.42
262358_at	mandelonitrile lyase, putative simila	---	AT1G73050	-1.13	-0.17	-1.27	0.246627	0.381575	-6.42
256563_at	unknown protein	RALFL27	AT3G29780	-1.11	-0.15	-1.27	0.246689	0.381645	-6.42
245830_at	hypothetical protein predicted by ge	---	AT1G57790	-1.10	-0.13	-1.27	0.246928	0.381989	-6.43
257500_s_a	putative serine carboxypeptidase s	scpl2	AT1G73300	-1.08	-0.11	-1.27	0.247135	0.382283	-6.43
265894_at	putative lipid transfer protein	LTP	AT2G15050	-1.32	-0.40	-1.27	0.247175	0.382319	-6.43
261657_at	pathogenesis-related protein 1b pr	---	AT1G50050	-1.11	-0.15	-1.27	0.247358	0.382577	-6.43
262839_at	PhD-finger protein, putative contair	---	AT1G14770	1.19	0.25	1.27	0.247408	0.382628	-6.43
247967_at	putative protein similar to unknown	anac099	AT5G56620	-1.08	-0.12	-1.27	0.247453	0.382664	-6.43
264518_at	unknown protein	---	AT1G09980	-1.15	-0.20	-1.27	0.247465	0.382664	-6.43
256012_at	unknown protein similar to dimethyl	FMO1	AT1G19250	2.29	1.20	1.27	0.247555	0.382777	-6.43
251232_at	shock protein SRC2-like shock pro	---	AT3G62780	-1.38	-0.47	-1.27	0.247719	0.383005	-6.43
257364_at	hypothetical protein predicted by ge	---	AT2G45940	-1.08	-0.12	-1.27	0.247854	0.383188	-6.43
255441_at	putative cullin-like 1 protein similar	ATCUL1	AT4G02570	1.10	0.14	1.26	0.247954	0.383316	-6.43
248738_at	unknown protein ;supported by full-	---	AT5G48020	-1.11	-0.15	-1.26	0.248001	0.383363	-6.43
254462_at	putative protein ;supported by full-l	---	AT4G20150	1.09	0.12	1.26	0.248102	0.383492	-6.43
259167_at	putative oleosin similar to oleosin G	---	AT3G01570	1.09	0.13	1.26	0.248124	0.383501	-6.43
245625_at	transport protein	---	AT4G14160	1.10	0.14	1.26	0.248176	0.383556	-6.43
266532_at	putative glucosyltransferase ;suppo	---	AT2G16890	-1.67	-0.74	-1.26	0.248203	0.38356	-6.43
263865_at	putative ABC transporter related to	ABCB1	AT2G36910	-1.16	-0.21	-1.26	0.248212	0.38356	-6.43
252226_at	putative protein transcribed gene o	---	AT3G49880	-1.09	-0.13	-1.26	0.248387	0.383789	-6.43
263550_at	Expressed protein ; supported by cl	---	AT2G17033	-1.12	-0.17	-1.26	0.248394	0.383789	-6.43
266105_at	putative transport protein SEC61 be	SEC61 BE	AT2G45070	-1.15	-0.20	-1.26	0.248564	0.384002	-6.43
252067_at	protein phosphatase 2C -like prote	---	AT3G51370	1.12	0.16	1.26	0.248566	0.384002	-6.43
265024_at	Expressed protein ; supported by fu	---	AT1G24600	1.24	0.31	1.26	0.248598	0.384007	-6.43
254662_at	putative protein phospho-N-acetyln	TRANS11	AT4G18270	1.17	0.23	1.26	0.248603	0.384007	-6.43
266046_at	hypothetical protein	---	AT2G07728	-1.14	-0.19	-1.26	0.24879	0.384268	-6.43

257837_at	hypothetical protein predicted by ge	---	AT3G25200	-1.11	-0.16	-1.26	0.248805	0.384268	-6.43
248593_at	pectin methylesterase ;supported b	---	AT5G49180	-1.15	-0.20	-1.26	0.248868	0.384338	-6.43
257945_at	SKP1/ASK1 (At10), putative simila	ASK10	AT3G21860	-1.10	-0.14	-1.26	0.248939	0.384422	-6.43
249620_at	putative protein predicted proteins,	---	AT5G37520	-1.09	-0.13	-1.26	0.24901	0.384462	-6.43
253070_at	putative protein symbiotic ammoniu	---	AT4G37850	-1.11	-0.15	-1.26	0.249011	0.384462	-6.43
266263_at	putative flavonol sulfotransferase	---	AT2G27570	-1.10	-0.14	-1.26	0.249023	0.384462	-6.43
263778_at	putative cytochrome oxidase bioger	OXA1L	AT2G46470	1.12	0.16	1.26	0.249032	0.384462	-6.43
249832_at	disease resistance protein-like	---	AT5G23400	-1.13	-0.18	-1.26	0.249065	0.384487	-6.43
246458_at	putative protein various predicted p	---	AT5G16860	1.12	0.16	1.26	0.249104	0.384521	-6.43
257542_at	hypothetical protein predicted by ge	---	AT3G26050	-1.09	-0.12	-1.26	0.249158	0.384577	-6.43
245666_at	hypothetical protein predicted by ge	---	AT1G28280	1.23	0.29	1.26	0.249174	0.384577	-6.43
250707_at	putative protein similar to unknown	MEE60	AT5G05950	1.15	0.21	1.26	0.249303	0.38473	-6.43
263019_at	trehalose 6-phosphate synthase, p	ATTPS9	AT1G23870	1.34	0.43	1.26	0.249307	0.38473	-6.43
255920_at	putative protein	---	AT5G28590	-1.13	-0.18	-1.26	0.249388	0.384829	-6.43
255159_at	putative polyprotein	---	---	-1.14	-0.18	-1.26	0.249534	0.385028	-6.43
263634_at	putative retroelement gag/pol polyp	---	---	-1.10	-0.14	-1.26	0.249621	0.385137	-6.43
253832_at	Expressed protein ; supported by fu	---	AT4G27654	-1.34	-0.42	-1.26	0.249777	0.385351	-6.44
260300_at	gibberellin 3 beta-hydroxylase ident	GA3OX2	AT1G80340	-1.19	-0.25	-1.26	0.249805	0.385368	-6.44
258672_at	hypothetical protein	---	AT3G08570	-1.12	-0.16	-1.26	0.249851	0.385413	-6.44
251636_at	calcium-dependent protein kinase (	CPK32	AT3G57530	1.39	0.48	1.26	0.249873	0.385421	-6.44
255733_at	unknown protein similar to unknown	---	AT1G25400	-1.19	-0.25	-1.26	0.249915	0.385459	-6.44
264556_at	putative transcription factor contain	MYB61	AT1G09540	-1.08	-0.12	-1.26	0.250052	0.385645	-6.44
252629_at	cytochrome P450 - like protein cyto	---	AT3G44970	-1.09	-0.12	-1.26	0.250119	0.385697	-6.44
257327_at	hypothetical protein	---	---	-1.19	-0.25	-1.26	0.250134	0.385697	-6.44
250016_at	Cu/Zn superoxide dismutase-like pr	CSD3	AT5G18100	1.11	0.15	1.26	0.250143	0.385697	-6.44
257200_at	hypothetical protein predicted by ge	---	---	1.08	0.12	1.26	0.250154	0.385697	-6.44
251734_at	putative protein Centrosome- and (	---	AT3G56270	1.25	0.32	1.26	0.250171	0.385698	-6.44
265159_at	unknown protein similar to EST gb|	---	AT1G31060	-1.12	-0.17	-1.26	0.250211	0.385716	-6.44
261380_at	hypothetical protein predicted by ge	---	AT1G05400	-1.14	-0.19	-1.26	0.250216	0.385716	-6.44
264529_at	CTP synthase-like protein similar t	---	AT1G30820	1.26	0.33	1.26	0.250251	0.385742	-6.44
261093_at	non-LTR reverse transcriptase, put	AT1G6288(	---	-1.13	-0.18	-1.26	0.250284	0.385763	-6.44
261783_at	vacuolar assembly protein vps41, p	---	AT1G08190	-1.12	-0.17	-1.26	0.250298	0.385763	-6.44
257739_at	unknown protein	---	AT3G27470	1.15	0.20	1.26	0.250425	0.385932	-6.44
251745_at	putative protein zinc finger transcri	SZF1	AT3G55980	1.74	0.80	1.26	0.25046	0.385961	-6.44
250606_s_a	pectin methyl-esterase-like protein	PPME1	AT1G69940	1.09	0.13	1.26	0.250625	0.386189	-6.44

256827_at	hypothetical protein contains simila	---	AT3G18570	-1.09	-0.12	-1.26	0.250821	0.386464	-6.44
257620_at	hypothetical protein predicted by ge	---	AT3G24850	-1.12	-0.16	-1.26	0.250858	0.386496	-6.44
263354_at	hypothetical protein predicted by gr	---	AT2G22060	-1.08	-0.11	-1.26	0.250894	0.386525	-6.44
247964_at	profilin-like protein ; supported by fu	PRF3	AT5G56600	-1.16	-0.22	-1.26	0.250935	0.386562	-6.44
258168_at	hypothetical protein predicted by ge	---	AT3G21570	-1.09	-0.12	-1.26	0.25123	0.386973	-6.44
265137_at	F-box protein family, AtFBX10 cont	---	AT1G51290	-1.11	-0.14	-1.26	0.251244	0.386973	-6.44
255715_s_a	hypothetical protein	---	AT4G00320	1.09	0.13	1.26	0.251259	0.386973	-6.44
254569_s_a	hypothetical protein	---	---	-1.09	-0.12	-1.26	0.25127	0.386973	-6.44
260779_at	splicing factor, putative similar to h	---	AT1G14650	1.11	0.15	1.25	0.251315	0.387017	-6.44
251239_at	putative protein several hypothetica	---	AT3G62440	-1.14	-0.19	-1.25	0.25149	0.38726	-6.44
250995_at	dnaK-type molecular chaperone hs	HSC70-1	AT5G02500	-1.15	-0.21	-1.25	0.251607	0.387414	-6.44
257507_at	zinc finger protein, putative similar	---	AT1G29600	1.08	0.11	1.25	0.251836	0.387705	-6.44
264525_at	unknown protein Highly Similar to b	ATBCAT-1	AT1G10060	-1.46	-0.55	-1.25	0.251842	0.387705	-6.44
253008_at	expansin -like protein expansin (GI	ATEXPA20	AT4G38210	-1.16	-0.21	-1.25	0.251847	0.387705	-6.44
259306_at	unknown protein ;supported by full-	PNC1	AT3G05290	-1.10	-0.14	-1.25	0.251871	0.387715	-6.44
245969_at	putative protein nuclear gene for ch	---	AT5G19830	-1.20	-0.26	-1.25	0.251897	0.387725	-6.44
251655_at	hypothetical protein	AT3G5715	---	-1.14	-0.19	-1.25	0.251911	0.387725	-6.44
266354_at	putative homeodomain transcriptior	PFS2	AT2G01500	-1.10	-0.14	-1.25	0.25215	0.388067	-6.44
263178_at	hypothetical protein predicted by ge	---	AT1G05550	-1.12	-0.16	-1.25	0.25224	0.388179	-6.44
263552_x_a	unknown protein proline, tyrosine, a	---	AT2G24980	-1.15	-0.21	-1.25	0.25227	0.3882	-6.44
263190_at	mutator-like transposase, putative	---	---	-1.08	-0.11	-1.25	0.252373	0.388331	-6.44
261981_at	unknown protein	---	AT1G33811	-1.38	-0.46	-1.25	0.25249	0.388485	-6.44
245920_at	putative protein	---	---	-1.08	-0.11	-1.25	0.252547	0.388546	-6.44
255965_at	14-3-3 protein (grf14), putative sim	---	AT1G22290	-1.10	-0.13	-1.25	0.252638	0.38866	-6.45
265841_at	putative glycogenin	---	AT2G35710	-1.60	-0.68	-1.25	0.252668	0.388681	-6.45
262823_at	ATP-dependent Clp protease prote	CLPP6	AT1G11750	-1.10	-0.14	-1.25	0.252741	0.388768	-6.45
258352_at	putative auxin-induced protein simil	IAA31	AT3G17600	-1.13	-0.17	-1.25	0.252816	0.388841	-6.45
249262_at	putative protein similar to unknown	---	AT5G41720	-1.10	-0.14	-1.25	0.252831	0.388841	-6.45
267148_at	hypothetical protein predicted by ge	---	AT2G23470	1.13	0.18	1.25	0.252842	0.388841	-6.45
248439_at	putative protein similar to unknown	---	AT5G51250	-1.10	-0.13	-1.25	0.252858	0.388841	-6.45
255909_at	cdc2+/CDC28-related protein kinas	CDKD1;3	AT1G18040	-1.18	-0.23	-1.25	0.253071	0.389135	-6.45
253707_at	hypothetical protein	---	AT4G29200	-1.09	-0.13	-1.25	0.253082	0.389135	-6.45
263983_at	unknown protein ;supported by full-	---	AT2G42780	1.09	0.12	1.25	0.253178	0.38923	-6.45
256295_at	hypothetical protein	---	AT1G69470	-1.10	-0.14	-1.25	0.253179	0.38923	-6.45
264847_at	clathrin assembly protein AP19, sm	AP19	AT2G17380	-1.08	-0.11	-1.25	0.253285	0.389367	-6.45

257030_at	unknown protein	---	---	-1.10	-0.14	-1.25	0.253407	0.389529	-6.45
256552_at	hypothetical protein predicted by ge	---	AT3G31350	-1.12	-0.16	-1.25	0.253479	0.389613	-6.45
259390_at	hypothetical protein predicted by ge	---	AT1G06340	-1.11	-0.15	-1.25	0.253609	0.389786	-6.45
263238_at	putative auxin-induced protein	---	AT2G16580	-1.09	-0.12	-1.25	0.253663	0.389829	-6.45
254548_at	putative protein various predicted p	---	AT4G19865	-1.20	-0.26	-1.25	0.253671	0.389829	-6.45
266220_at	putative dTDP-glucose 4-6-dehydra	---	AT2G28755	1.13	0.18	1.25	0.253737	0.389904	-6.45
258186_s_a	protein kinase, putative similar to s	---	AT1G48490	1.10	0.13	1.25	0.253802	0.389978	-6.45
262427_s_a	thioglucosidase, putative similar to	BGLU34	AT1G47600	-1.09	-0.13	-1.25	0.253844	0.390017	-6.45
248953_at	serine/threonine-protein kinase Mak	---	AT5G45428	-1.10	-0.14	-1.25	0.2539	0.390076	-6.45
258838_at	unknown protein ; supported by cD	---	AT3G07140	1.09	0.13	1.25	0.253994	0.390192	-6.45
255986_x_a	putative protein predicted proteins,	---	---	-1.08	-0.11	-1.25	0.254025	0.390192	-6.45
267418_at	putative RING zinc finger protein	---	AT2G35000	-1.13	-0.17	-1.25	0.254027	0.390192	-6.45
260826_at	hypothetical protein predicted by ge	---	AT1G06710	1.10	0.14	1.25	0.254161	0.390359	-6.45
254532_at	putative protein regulatory protein I	NPR4	AT4G19660	1.18	0.24	1.25	0.254175	0.390359	-6.45
260759_at	hypothetical protein contains simila	---	AT1G49180	-1.19	-0.26	-1.25	0.254188	0.390359	-6.45
252715_x_a	putative protein predicted protein, A	---	AT3G43900	-1.12	-0.16	-1.25	0.254204	0.390359	-6.45
260529_at	putative chloroplast protein CP12 ;	CP12-1	AT2G47400	1.09	0.12	1.25	0.254274	0.390441	-6.45
265537_at	putative retroelement pol polyprotei	---	---	-1.12	-0.16	-1.25	0.254363	0.390549	-6.45
255654_at	Similar to receptor kinase	---	AT4G00970	-1.37	-0.45	-1.25	0.254379	0.390549	-6.45
250623_at	peroxisomal Ca-dependent solute (	---	AT5G07320	-1.10	-0.14	-1.25	0.25441	0.390565	-6.45
253939_at	putative myb-related protein myb-r	MYB97	AT4G26930	-1.15	-0.20	-1.25	0.254424	0.390565	-6.45
246429_at	farnesylated protein ATFP6-like pr	---	AT5G17450	1.29	0.37	1.25	0.254457	0.390586	-6.45
251217_at	Sar1-like GTP binding protein sma	---	AT3G62560	-1.11	-0.16	-1.25	0.254475	0.390586	-6.45
264227_at	hypothetical protein contains simila	ATREV3	AT1G67500	1.10	0.14	1.25	0.254489	0.390586	-6.45
264066_at	Argonaute (AGO1)-like protein	AGO5	AT2G27880	-1.11	-0.15	-1.25	0.254591	0.390717	-6.45
258301_at	hypothetical protein predicted by ge	---	---	1.08	0.11	1.25	0.254618	0.390732	-6.45
245563_at	SNF1 like protein kinase ; supporte	CIPK4	AT4G14580	1.32	0.40	1.25	0.254664	0.390776	-6.45
251006_at	putative protein predicted proteins,	---	AT5G02600	1.12	0.16	1.25	0.25471	0.39082	-6.45
251085_at	putative protein insulinase - Homo	---	AT5G01440	-1.11	-0.15	-1.24	0.25476	0.39083	-6.45
266887_at	unknown protein ; supported by cD	CHL-CPN1	AT2G44650	-1.13	-0.17	-1.24	0.25476	0.39083	-6.45
248940_at	replication protein A1-like	---	AT5G45400	1.12	0.16	1.24	0.254768	0.39083	-6.45
262765_at	putative cytochrome P450 monooxy	CYP86C4	AT1G13150	-1.11	-0.15	-1.24	0.254827	0.390895	-6.45
265747_s_a	hypothetical protein predicted by ge	---	AT2G06570	-1.11	-0.15	-1.24	0.254863	0.390923	-6.45
258401_at	unknown protein ; supported by cD	---	AT3G15430	-1.13	-0.17	-1.24	0.254886	0.390933	-6.45
267291_at	putative C2H2-type zinc finger prote	---	AT2G23740	-1.19	-0.26	-1.24	0.254982	0.391053	-6.45

250037_at	disease resistance protein -like dis	---	AT5G18350	-1.14	-0.19	-1.24	0.25509	0.391193	-6.45
262376_at	unknown protein contains similarity	HTH	AT1G72970	-1.10	-0.13	-1.24	0.255138	0.391215	-6.45
250839_at	MADS-box protein - like SLM3 MA	AGL99	AT5G04640	-1.09	-0.12	-1.24	0.255139	0.391215	-6.45
248133_at	unknown protein	---	AT5G54850	-1.15	-0.21	-1.24	0.255255	0.391368	-6.45
250992_at	expansin precursor - like protein ex	ATEXPA9	AT5G02260	1.28	0.36	1.24	0.255283	0.391372	-6.45
257694_at	nucleolar protein, putative nucleola	---	AT3G12860	1.10	0.13	1.24	0.255301	0.391372	-6.45
254782_at	putative calmodulin calmodulin - C	UNE14	AT4G12860	-1.12	-0.16	-1.24	0.255323	0.391372	-6.45
249367_at	putative protein predicted protein, A	---	AT5G40630	-1.11	-0.15	-1.24	0.255327	0.391372	-6.45
256059_at	hypothetical protein contains simila	---	AT1G06990	-1.13	-0.17	-1.24	0.255396	0.391452	-6.45
259993_at	unknown protein	---	AT1G67960	1.12	0.16	1.24	0.255509	0.391598	-6.45
265921_at	putative C2H2-type zinc finger prote	---	AT2G18490	-1.09	-0.13	-1.24	0.2556	0.391711	-6.46
248157_at	putative protein similar to unknown	---	AT5G54420	-1.10	-0.14	-1.24	0.25581	0.392006	-6.46
267408_at	putative CTP synthase	---	AT2G34890	-1.09	-0.13	-1.24	0.255889	0.392101	-6.46
255896_at	basic blue protein, putative similar	---	AT1G17800	-1.09	-0.12	-1.24	0.255917	0.392118	-6.46
260077_at	thaumatin-like protein contains Pfar	---	AT1G73620	-1.13	-0.18	-1.24	0.255963	0.392156	-6.46
261493_at	DNA-binding protein p24, putative	WHY1	AT1G14410	1.16	0.21	1.24	0.255976	0.392156	-6.46
245197_at	F12A21.7 hypothetical protein;supp	---	AT1G67800	1.10	0.14	1.24	0.256002	0.392161	-6.46
263819_x_a	putative TNP2-like transposon prote	---	---	-1.08	-0.11	-1.24	0.256018	0.392161	-6.46
254289_at	putative protein predicted protein, A	---	AT4G22980	1.53	0.61	1.24	0.256031	0.392161	-6.46
266198_at	unknown protein predicted by gens	---	AT2G38890	-1.10	-0.14	-1.24	0.256048	0.392161	-6.46
249082_at	legumin-like protein	CRA1	AT5G44120	-1.10	-0.14	-1.24	0.256177	0.392332	-6.46
257580_at	hypothetical protein	---	AT3G06210	-1.11	-0.15	-1.24	0.256201	0.392342	-6.46
260419_at	putative protein kinase contains Pfa	---	AT1G69730	1.29	0.37	1.24	0.256284	0.392443	-6.46
249152_s_a	inorganic phosphate transporter (db	APT1	AT5G43350	1.16	0.22	1.24	0.256454	0.392677	-6.46
255315_at	hypothetical protein	---	---	-1.09	-0.13	-1.24	0.256496	0.392716	-6.46
261899_at	cinnamoyl CoA reductase, putative	CCR2	AT1G80820	1.77	0.82	1.24	0.256518	0.392722	-6.46
257127_at	hypothetical protein predicted by ge	TTN9	AT3G20070	1.13	0.17	1.24	0.256577	0.392786	-6.46
262478_at	hypothetical protein similar to hypot	---	AT1G11170	1.11	0.15	1.24	0.256684	0.392924	-6.46
257184_at	ABC transporter, putative similar to	ATMRP8	AT3G13090	-1.09	-0.13	-1.24	0.256827	0.393117	-6.46
247963_at	beta-1,3-glucanase-like protein	---	AT5G56590	1.10	0.13	1.24	0.256867	0.393141	-6.46
267626_at	putative cytochrome P450	CYP712A1	AT2G42250	-1.17	-0.23	-1.24	0.256878	0.393141	-6.46
264768_at	hypothetical protein similar to putati	---	AT1G61410	-1.10	-0.14	-1.24	0.256929	0.393194	-6.46
246440_at	glycine/proline-rich protein glycine/	---	AT5G17650	-1.23	-0.30	-1.24	0.257001	0.393271	-6.46
256369_at	hypothetical protein predicted by ge	---	AT1G66790	-1.08	-0.11	-1.24	0.257014	0.393271	-6.46
254336_at	aspartic proteinase like protein ory	---	AT4G22050	-1.13	-0.18	-1.24	0.257103	0.393381	-6.46

251248_at	P-glycoprotein-like proetin P-glycor	PGP21	AT3G62150	1.54	0.62	1.24	0.257137	0.393406	-6.46
264508_at	putative phytochrome A similar to G	PHYA	AT1G09570	-1.19	-0.25	-1.24	0.257195	0.393468	-6.46
266476_at	unknown protein ;supported by full-	---	AT2G31090	-1.14	-0.19	-1.24	0.257217	0.393476	-6.46
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J	---	---	-1.26	-0.33	-1.24	0.257319	0.393606	-6.46
250643_at	putative protein similar to unknown	---	AT5G06780	-1.09	-0.12	-1.24	0.257431	0.393748	-6.46
259701_at	unknown protein similar to GB:AAC	---	AT1G77770	1.13	0.18	1.24	0.257447	0.393748	-6.46
255357_at	putative pectinesterase	---	AT4G03930	-1.09	-0.13	-1.24	0.257505	0.393786	-6.46
260342_at	hypothetical protein predicted by ge	---	AT1G69280	-1.12	-0.16	-1.24	0.257506	0.393786	-6.46
267476_at	putative pectate lyase	---	AT2G02720	-1.10	-0.13	-1.24	0.257551	0.393829	-6.46
254185_at	cellulose synthase catalytic subuni	CSLG3	AT4G23990	-1.17	-0.23	-1.24	0.257611	0.393893	-6.46
251331_s_a	tubulin gamma-1 chain	TUBG1	AT3G61650	1.28	0.36	1.24	0.257627	0.393893	-6.46
256162_at	hypothetical protein similar to hypot	---	AT1G55390	-1.09	-0.12	-1.24	0.257678	0.393944	-6.46
251924_at	histone H4-like protein several histo	---	AT3G53730	1.15	0.21	1.24	0.257786	0.394082	-6.46
250801_at	pectinesterase	---	AT5G04960	1.09	0.13	1.24	0.257821	0.394089	-6.46
251339_at	putative protein various predicted p	---	AT3G60780	-1.14	-0.18	-1.24	0.257825	0.394089	-6.46
266001_at	hypothetical protein predicted by ge	HHP3	AT2G24150	1.09	0.13	1.24	0.258003	0.394319	-6.46
267632_at	hypothetical protein predicted by ge	---	AT2G42160	1.16	0.21	1.24	0.25801	0.394319	-6.46
266358_at	hypothetical protein predicted by ge	---	AT2G32280	1.25	0.32	1.24	0.258042	0.394342	-6.46
245281_at	DEF (CLA1) protein ; supported by	CLA1	AT4G15560	-1.12	-0.16	-1.24	0.25806	0.394342	-6.46
266281_at	putative protein kinase contains a p	---	AT2G29250	-1.12	-0.16	-1.24	0.258101	0.39436	-6.46
257011_at	predicted protein	CAX9	AT3G14070	1.23	0.30	1.24	0.258106	0.39436	-6.46
244913_at	hypothetical protein	---	---	1.11	0.15	1.24	0.258137	0.394381	-6.46
251366_at	putative protein several hypothetica	---	AT3G61340	1.11	0.15	1.24	0.25817	0.394405	-6.46
265376_at	hypothetical protein predicted by ge	---	AT2G05810	-1.11	-0.15	-1.23	0.258448	0.394802	-6.46
264956_at	unknown protein similar to putative	ACR3	AT1G76990	1.31	0.39	1.23	0.258469	0.394809	-6.46
266961_at	Athila retroelement ORF1-like prote	---	---	-1.12	-0.16	-1.23	0.25852	0.394861	-6.46
266830_at	1-aminocyclopropane-1-carboxylate	ACS4	AT2G22810	-1.47	-0.55	-1.23	0.2587	0.395109	-6.47
249323_at	unknown protein	FLA20	AT5G40940	-1.10	-0.14	-1.23	0.258729	0.395126	-6.47
267242_at	hypothetical protein predicted by gr	---	AT2G02670	1.10	0.14	1.23	0.258786	0.395187	-6.47
259268_at	putative lamin similar to blue coppe	---	AT3G01070	-1.08	-0.11	-1.23	0.258812	0.3952	-6.47
266136_at	unknown protein ;supported by full-	---	AT2G45060	1.08	0.11	1.23	0.258893	0.395296	-6.47
251540_at	citrate synthase -like protein citrate	CSY1	AT3G58740	-1.08	-0.11	-1.23	0.258924	0.395296	-6.47
266067_s_a	hypothetical protein predicted by ge	---	AT2G18810	-1.08	-0.11	-1.23	0.258927	0.395296	-6.47
267551_at	ubiquitin-specific protease 1 (UBP1	UBP1	AT2G32780	-1.13	-0.17	-1.23	0.259006	0.395391	-6.47
246009_at	Expressed protein ; supported by cl	ATSTE14B	AT5G08335	1.14	0.19	1.23	0.259112	0.395525	-6.47

257480_at	hypothetical protein similar to putati	---	AT1G15640	-1.20	-0.27	-1.23	0.259172	0.39559	-6.47
252139_at	putative protein hypothetical protei	---	AT3G51050	1.10	0.13	1.23	0.259192	0.395596	-6.47
247974_at	putative protein contains similarity t	---	AT5G56780	-1.09	-0.13	-1.23	0.259252	0.395661	-6.47
254330_at	predicted protein predicted gene F	LBD32	AT4G22700	-1.10	-0.13	-1.23	0.259408	0.395836	-6.47
260562_at	putative protein kinase contains a p	---	AT2G43850	-1.15	-0.20	-1.23	0.259436	0.395836	-6.47
259233_at	hypothetical protein	---	AT3G11380	-1.08	-0.11	-1.23	0.259436	0.395836	-6.47
256313_s_a	RNA-binding protein, putative cont	APUM17	AT1G35850	1.08	0.12	1.23	0.259436	0.395836	-6.47
247152_at	oligopeptidase A ; supported by cD	---	AT5G65620	1.09	0.12	1.23	0.259491	0.395893	-6.47
267150_at	putative anthranilate N-hydroxycinn	SDT	AT2G23510	-1.08	-0.11	-1.23	0.259705	0.396192	-6.47
260240_at	putative tRNA isopentenyl transfera	ATIPT1	AT1G68460	-1.09	-0.13	-1.23	0.259732	0.396208	-6.47
254702_at	putative protein predicted protein,	---	AT4G17940	-1.11	-0.15	-1.23	0.259779	0.396244	-6.47
255102_s_a	putative MuDR-A-like transposon p	---	---	-1.12	-0.16	-1.23	0.259791	0.396244	-6.47
256916_at	GATA transcription factor 1 (AtGAT	---	AT3G24050	-1.13	-0.18	-1.23	0.259882	0.396357	-6.47
260827_at	mudrA-like protein similar to Mu tra	AT1G0675(	---	1.15	0.21	1.23	0.260018	0.396529	-6.47
261632_at	hypothetical protein predicted by ge	---	AT1G50120	1.12	0.16	1.23	0.260045	0.396529	-6.47
258252_at	putative polygalacturonase similar t	---	AT3G15720	1.22	0.29	1.23	0.260047	0.396529	-6.47
248519_at	11-beta-hydroxysteroid dehydrogen	AtHSD7	AT5G50590	-1.11	-0.15	-1.23	0.260089	0.396567	-6.47
257390_x_a	hypothetical protein predicted by ge	---	---	-1.14	-0.19	-1.23	0.260131	0.396604	-6.47
263740_at	hypothetical protein predicted by ge	RALFL14	AT2G20660	-1.13	-0.17	-1.23	0.260233	0.396733	-6.47
247233_at	mitochondrial carrier protein-like	---	AT5G64970	1.12	0.16	1.23	0.260389	0.396912	-6.47
261962_s_a	hypothetical protein predicted by ge	---	---	-1.11	-0.15	-1.23	0.260396	0.396912	-6.47
267105_at	hypothetical protein predicted by ge	---	AT2G14760	-1.13	-0.18	-1.23	0.260403	0.396912	-6.47
246914_at	putative protein various predicted p	---	AT5G25860	-1.14	-0.18	-1.23	0.260511	0.397051	-6.47
250149_at	cinnamoyl CoA reductase - like pro	---	AT5G14700	1.65	0.72	1.23	0.260561	0.397099	-6.47
253573_at	putative protein BEM46 PROTEIN,	---	AT4G31020	-1.12	-0.16	-1.23	0.260599	0.397132	-6.47
260960_at	calcium-binding protein, putative si	---	AT1G05990	-1.11	-0.16	-1.23	0.260646	0.397176	-6.47
266652_at	unknown protein	---	AT2G25760	1.09	0.13	1.23	0.260731	0.397266	-6.47
253553_at	putative protein LipB gene, Prochlo	---	AT4G31050	-1.11	-0.16	-1.23	0.260739	0.397266	-6.47
256473_at	unknown protein	---	---	-1.10	-0.14	-1.23	0.260785	0.397308	-6.47
258169_at	hypothetical protein	---	AT3G21590	-1.11	-0.15	-1.23	0.260833	0.397355	-6.47
263485_at	putative villin ; supported by cDNA	VLN1	AT2G29890	-1.11	-0.14	-1.23	0.260914	0.397452	-6.47
265040_at	G-box binding factor, GBF4 Identic	GBF4	AT1G03970	-1.14	-0.19	-1.23	0.260951	0.397482	-6.47
257979_at	unknown protein	---	AT3G20730	-1.10	-0.14	-1.23	0.260993	0.3975	-6.47
265144_at	putative serine/threonine protein kin	---	AT1G51170	-1.14	-0.19	-1.23	0.260997	0.3975	-6.47
258732_at	putative alkaline/neutral invertase s	---	AT3G05820	-1.10	-0.14	-1.23	0.261166	0.397723	-6.47

255652_at	putative protein	MEE47	AT4G00950	-1.36	-0.44	-1.23	0.261179	0.397723	-6.47
250864_at	putative protein predicted proteins,	---	AT5G03870	-1.11	-0.15	-1.23	0.261204	0.397734	-6.47
262805_at	putative DNA-binding protein simila	ESC	AT1G20900	-1.10	-0.13	-1.23	0.261232	0.397751	-6.47
264734_at	hypothetical protein predicted by ge	SLAH1	AT1G62280	-1.10	-0.13	-1.23	0.261281	0.397766	-6.47
245419_at	putative protein	MSH4	AT4G17380	-1.09	-0.12	-1.23	0.261302	0.397766	-6.47
249492_at	germin-like protein (GLP2a) copy1	GER2	AT5G39130	-1.09	-0.13	-1.23	0.261311	0.397766	-6.47
255539_at	putative actin polymerization factor	CRK	AT4G01710	1.11	0.15	1.23	0.261312	0.397766	-6.47
246827_at	copper binding - like protein mavicy	---	AT5G26330	-1.12	-0.16	-1.23	0.261347	0.397792	-6.47
261635_at	tubulin alpha-6 chain, putative iden	---	AT1G50020	1.14	0.18	1.23	0.261381	0.397819	-6.47
265688_at	putative calmodulin-binding protein	---	AT2G24300	1.08	0.11	1.23	0.261418	0.397823	-6.47
255329_at	hypothetical protein	---	AT4G04370	1.08	0.12	1.23	0.261419	0.397823	-6.47
251433_at	putative protein SERINE/THREON	---	AT3G59830	-1.08	-0.11	-1.23	0.261654	0.398154	-6.47
250286_at	auxin-responsive - like protein Nt-g	PBS3	AT5G13320	1.77	0.83	1.23	0.261711	0.398192	-6.48
265820_at	hypothetical protein predicted by ge	---	AT2G17940	-1.13	-0.18	-1.23	0.261714	0.398192	-6.48
249446_at	receptor protein kinase -like protein	---	AT5G39390	-1.10	-0.13	-1.22	0.261786	0.398255	-6.48
262994_at	hypothetical protein predicted by ge	---	AT1G54420	-1.08	-0.11	-1.22	0.26179	0.398255	-6.48
252155_at	putative protein	---	AT3G50920	1.14	0.18	1.22	0.261817	0.398269	-6.48
261885_at	unknown protein	---	AT1G80930	1.12	0.16	1.22	0.261838	0.398274	-6.48
261836_at	hypothetical protein contains simila	WAKL7	AT1G16090	1.45	0.54	1.22	0.262007	0.398476	-6.48
250642_at	receptor-like protein kinase several	ERL2	AT5G07180	1.08	0.12	1.22	0.262028	0.398476	-6.48
263015_at	hypothetical protein similar to hypot	---	AT1G23440	1.11	0.15	1.22	0.262045	0.398476	-6.48
255659_at	Expressed protein ; supported by fu	---	AT4G00895	1.22	0.29	1.22	0.262045	0.398476	-6.48
265173_at	unknown protein	---	AT1G23530	-1.10	-0.13	-1.22	0.262058	0.398476	-6.48
246635_at	hypothetical protein predicted by ge	---	AT1G31720	-1.16	-0.21	-1.22	0.262116	0.398538	-6.48
267537_at	putative guanylate kinase ; support	GK-1	AT2G41880	1.34	0.42	1.22	0.262183	0.398613	-6.48
262321_at	hypothetical protein predicted by ge	---	AT1G27570	-1.10	-0.14	-1.22	0.262251	0.398691	-6.48
247330_at	putative protein contains similarity t	GAMMA CA	AT5G63510	1.08	0.11	1.22	0.262506	0.39905	-6.48
248120_at	putative protein similar to unknown	---	AT5G54540	1.11	0.15	1.22	0.262546	0.399085	-6.48
246399_at	bZIP transcription factor similar to b	---	AT1G58110	-1.11	-0.15	-1.22	0.262667	0.399237	-6.48
246610_at	putative protein	---	AT5G35400	1.10	0.14	1.22	0.262681	0.399237	-6.48
256429_at	unknown protein	---	AT3G11040	-1.13	-0.18	-1.22	0.262721	0.399271	-6.48
256353_at	unknown protein ; supported by full-	---	AT1G55000	1.10	0.14	1.22	0.262771	0.399293	-6.48
248488_at	putative protein contains similarity t	---	AT5G51080	1.11	0.15	1.22	0.262778	0.399293	-6.48
250699_at	receptor-like protein kinase	SRF2	AT5G06820	-1.11	-0.15	-1.22	0.262802	0.399293	-6.48
252851_at	putative protein CLATHRIN COAT	---	AT4G40080	1.28	0.36	1.22	0.262805	0.399293	-6.48

265706_at	unknown protein	---	AT2G03390	1.14	0.19	1.22	0.262968	0.399514	-6.48
258819_at	unknown protein similar to putative	---	AT3G04590	1.13	0.17	1.22	0.262992	0.399524	-6.48
258781_at	hypothetical protein predicted by ge	---	AT3G11740	-1.08	-0.11	-1.22	0.263107	0.399671	-6.48
252250_at	putative protein predicted protein, A	---	AT3G49790	1.17	0.22	1.22	0.26317	0.399741	-6.48
260910_at	importin alpha, putative similar to ir	IMPA-6	AT1G02690	1.16	0.22	1.22	0.263229	0.399804	-6.48
254205_at	putative protein kinesin heavy chai	---	AT4G24170	-1.12	-0.16	-1.22	0.26325	0.399809	-6.48
258533_at	hypothetical protein	---	AT3G06670	1.11	0.15	1.22	0.263276	0.399822	-6.48
264489_at	putative squamosa-promoter bindin	---	AT1G27370	1.22	0.28	1.22	0.263294	0.399823	-6.48
254552_at	putative protein several hypothetica	---	AT4G19900	1.10	0.14	1.22	0.263416	0.39998	-6.48
261153_at	unknown protein ;supported by full-	---	AT1G04850	1.10	0.14	1.22	0.263433	0.39998	-6.48
256003_at	Ta11 non-LTR retroelement protein	---	AT3G31430	-1.11	-0.15	-1.22	0.263475	0.400018	-6.48
255863_s_a	putative GDSL-motif lipase/hydrolas	---	AT2G30220	-1.09	-0.12	-1.22	0.263543	0.400094	-6.48
258912_at	unknown protein similar to hypothe	---	AT3G06460	-1.15	-0.21	-1.22	0.26362	0.400105	-6.48
257027_at	DNA repair protein, putative similar	ATRAD54	AT3G19210	1.10	0.13	1.22	0.26363	0.400105	-6.48
245546_at	cellulose synthase like protein	ATCSLB05	AT4G15290	-1.16	-0.22	-1.22	0.263635	0.400105	-6.48
261291_at	hypothetical protein predicted by ge	---	AT1G36970	-1.16	-0.22	-1.22	0.263639	0.400105	-6.48
263796_at	unknown protein ;supported by full-	AFR	AT2G24540	-1.18	-0.24	-1.22	0.263654	0.400105	-6.48
255480_at	Expressed protein ; supported by fu	---	AT4G02485	1.09	0.13	1.22	0.263655	0.400105	-6.48
262405_at	hypothetical protein contains simila	HDG10	AT1G34650	-1.11	-0.16	-1.22	0.263903	0.400437	-6.48
248047_at	putative protein similar to unknown	---	AT5G56070	-1.10	-0.13	-1.22	0.263909	0.400437	-6.48
264667_s_a	hypothetical protein identical to hyp	ZW18	AT1G09980	-1.09	-0.13	-1.22	0.264086	0.400678	-6.48
247984_s_a	IAA-amino acid hydrolase homolog	ILL1	AT5G56650	1.15	0.20	1.22	0.264177	0.400791	-6.48
265036_at	unknown protein Contains similarity	PRP39	AT1G04080	1.09	0.13	1.22	0.264203	0.400796	-6.48
250587_at	putative protein contains similarity t	---	AT5G07640	-1.10	-0.13	-1.22	0.264216	0.400796	-6.48
265733_at	unknown protein ;supported by full-	---	AT2G01190	-1.12	-0.16	-1.22	0.264451	0.401126	-6.48
248260_at	putative protein similar to unknown	---	AT5G53240	-1.10	-0.13	-1.22	0.264858	0.401716	-6.49
252043_at	putative protein mttC protein, Esch	---	AT3G52390	1.12	0.16	1.22	0.264961	0.401846	-6.49
260304_at	unknown protein identical to most o	---	AT1G70480	-1.17	-0.23	-1.22	0.265156	0.402115	-6.49
251496_at	putative protein crp1 protein, involv	---	AT3G59040	1.09	0.13	1.22	0.265209	0.402168	-6.49
AFFX-BioC-	E. coli /GEN=bioC /DB_XREF=gb:J	---	---	-1.25	-0.33	-1.22	0.265261	0.40221	-6.49
263336_x_a	hypothetical protein predicted by ge	---	---	-1.09	-0.13	-1.21	0.265271	0.40221	-6.49
263688_at	unknown protein Location of EST 2	---	AT1G26920	-1.38	-0.46	-1.21	0.265334	0.402268	-6.49
266891_at	putative GTP-binding protein ; supp	ARAC9	AT2G44690	-1.12	-0.16	-1.21	0.265345	0.402268	-6.49
248022_at	putative protein contains similarity t	APUM12	AT5G56510	-1.08	-0.11	-1.21	0.265403	0.402316	-6.49
258801_at	unknown protein predicted by gens	---	AT3G04560	1.08	0.11	1.21	0.265412	0.402316	-6.49

258681_at	unknown protein ; supported by ful	---	AT3G08610	1.11	0.15	1.21	0.265513	0.402442	-6.49
253335_at	putative protein YHR077c (NMD2,I	---	AT4G33500	1.11	0.15	1.21	0.265578	0.402514	-6.49
245669_at	hypothetical protein contains simila	LEC2	AT1G28300	-1.13	-0.17	-1.21	0.265652	0.402599	-6.49
249903_at	disease resistance protein-like	---	AT5G22690	-1.36	-0.44	-1.21	0.265714	0.402636	-6.49
247024_at	Expressed protein ; supported by fu	---	AT5G66985	-1.12	-0.17	-1.21	0.265728	0.402636	-6.49
260471_at	hypothetical protein predicted by ge	---	AT1G11070	-1.09	-0.12	-1.21	0.265729	0.402636	-6.49
261737_at	hypothetical protein similar to putati	---	AT1G47885	1.11	0.16	1.21	0.26575	0.402641	-6.49
246128_at	putative protein predicted proteins,	---	---	-1.11	-0.15	-1.21	0.265773	0.402648	-6.49
264451_s_a	putative lectin receptor kinase very	---	---	1.10	0.14	1.21	0.265802	0.402657	-6.49
258266_at	hypothetical protein predicted by ge	---	AT3G15860	-1.13	-0.18	-1.21	0.265813	0.402657	-6.49
265609_at	hypothetical protein predicted by ge	---	AT2G25420	-1.17	-0.22	-1.21	0.265928	0.402803	-6.49
251484_at	putative protein putative protein At2	---	AT3G59640	1.09	0.12	1.21	0.266002	0.402888	-6.49
252279_at	1-aminocyclopropane-1-carboxylat	ACS9	AT3G49700	-1.11	-0.15	-1.21	0.266052	0.402907	-6.49
251140_at	lectin - like protein lectin precursor	---	AT5G01090	-1.11	-0.15	-1.21	0.266061	0.402907	-6.49
252877_at	hypothetical protein supported by fu	---	AT4G39630	-1.11	-0.15	-1.21	0.266084	0.402907	-6.49
267138_s_a	similar to SOR1 from the fungus Ce	PDX1.1	AT2G38210	-1.25	-0.33	-1.21	0.266084	0.402907	-6.49
247749_at	myb-related protein - like myb-relat	MYB119	AT5G58850	-1.13	-0.17	-1.21	0.266232	0.403104	-6.49
248246_at	putative protein contains similarity t	TRY	AT5G53200	-1.11	-0.15	-1.21	0.266307	0.40319	-6.49
262884_at	membrane related protein CP5, pu	CP5	AT1G64720	-1.10	-0.14	-1.21	0.266341	0.403209	-6.49
251521_at	putative protein receptor kinase ho	ACR4	AT3G59420	-1.13	-0.17	-1.21	0.266355	0.403209	-6.49
265507_s_a	Ac-like transposase related to Ac/D	---	---	1.10	0.13	1.21	0.266422	0.403271	-6.49
255804_at	putative protein IB1C3-1 protein, A	---	AT4G10220	-1.12	-0.16	-1.21	0.266439	0.403271	-6.49
249267_at	putative protein contains similarity t	BTI3	AT5G41600	-1.17	-0.23	-1.21	0.266449	0.403271	-6.49
263329_at	hypothetical protein contains C3HC	---	AT2G15260	1.09	0.13	1.21	0.266512	0.40334	-6.49
255550_at	putative raffinose synthase or seed	AtSTS	AT4G01970	-1.09	-0.12	-1.21	0.266555	0.403378	-6.49
261331_at	hypothetical protein predicted by ge	---	---	-1.11	-0.16	-1.21	0.266587	0.403384	-6.49
264165_at	hypothetical protein contains simila	ATNAP11	AT1G65410	1.09	0.12	1.21	0.266594	0.403384	-6.49
247384_at	protein kinase ; supported by cDNA	---	AT5G63370	-1.18	-0.24	-1.21	0.266655	0.403425	-6.49
267438_at	putative GDSL-motif lipase/hydrolas	---	AT2G19050	-1.16	-0.21	-1.21	0.266656	0.403425	-6.49
263014_at	unknown protein similar to hypothet	CAF2	AT1G23400	-1.10	-0.14	-1.21	0.266679	0.403429	-6.49
247599_at	putative protein	---	AT5G60880	-1.20	-0.27	-1.21	0.266695	0.403429	-6.49
257205_at	putative glucosyltransferase simila	UGT88A1	AT3G16520	1.10	0.13	1.21	0.26674	0.403471	-6.49
252002_at	hypothetical protein YIP1 protein, S	---	AT3G52760	-1.10	-0.13	-1.21	0.266904	0.403677	-6.49
267320_at	hypothetical protein predicted by ge	---	AT2G19300	-1.10	-0.14	-1.21	0.266912	0.403677	-6.49
266885_at	putative small GTP-binding protein	RAB6A	AT2G44610	1.12	0.16	1.21	0.266944	0.4037	-6.49

263161_at	myrosinase-associated protein, put	---	AT1G54020	-2.46	-1.30	-1.21	0.267232	0.404108	-6.49
247658_at	actin depolymerizing factor 3 - like	ADF3	AT5G59880	1.08	0.12	1.21	0.267311	0.404201	-6.49
263394_at	hypothetical protein predicted by ge	---	---	-1.10	-0.14	-1.21	0.267353	0.404238	-6.49
266997_at	hypothetical protein predicted by ge	---	AT2G34410	-1.17	-0.22	-1.21	0.267408	0.404277	-6.49
259968_at	unknown protein	---	AT1G76530	-1.11	-0.14	-1.21	0.267419	0.404277	-6.49
262651_at	hypothetical protein One of a cluste	FUT9	AT1G14100	-1.11	-0.16	-1.21	0.267433	0.404277	-6.49
252418_at	hypothetical protein	---	AT3G47490	1.13	0.18	1.21	0.267582	0.404477	-6.49
253802_at	putative protein	---	AT4G28180	-1.10	-0.14	-1.21	0.267673	0.404572	-6.49
251208_at	putative protein amino acid selectiv	ATOEP16-4	AT3G62880	1.10	0.14	1.21	0.267695	0.404572	-6.49
251075_at	putative protein leucine-rich recept	---	AT5G01890	-1.23	-0.30	-1.21	0.267699	0.404572	-6.49
266837_x_a	unknown protein	---	AT2G25990	-1.09	-0.12	-1.21	0.267738	0.404587	-6.49
253892_at	hypothetical protein ;supported by	---	AT4G27620	-1.10	-0.13	-1.21	0.267744	0.404587	-6.49
256282_at	unknown protein	---	AT3G12550	-1.12	-0.16	-1.21	0.267822	0.404661	-6.49
245410_at	putative protein	ATMAP70-4	AT4G17220	-1.09	-0.13	-1.21	0.267828	0.404661	-6.49
260846_at	unknown protein	---	AT1G17300	-1.10	-0.14	-1.21	0.268023	0.404928	-6.50
248351_at	unknown protein ; supported by cD	---	AT5G52200	-1.17	-0.22	-1.21	0.268101	0.405019	-6.50
262438_at	hypothetical protein identical to hyp	---	AT1G47410	-1.20	-0.26	-1.21	0.268157	0.405076	-6.50
266720_s_a	hypothetical protein predicted by ge	APRR9	AT2G46670	-1.21	-0.27	-1.21	0.268504	0.405573	-6.50
248733_at	unknown protein	ELP1	---	-1.12	-0.16	-1.21	0.268536	0.405577	-6.50
263425_at	putative preprotein translocase SEC	EMB2289	AT2G31530	1.12	0.16	1.21	0.268543	0.405577	-6.50
247343_at	unknown protein	---	AT5G63740	-1.09	-0.13	-1.21	0.268567	0.405577	-6.50
254253_at	serine/threonine kinase - like prote	---	AT4G23320	1.34	0.43	1.21	0.268577	0.405577	-6.50
254369_at	putative protein	---	AT4G21720	-1.14	-0.19	-1.21	0.268646	0.405654	-6.50
253347_at	putative protein	---	AT4G33610	-1.09	-0.13	-1.21	0.268677	0.405675	-6.50
247394_at	putative protein predicted proteins,	---	AT5G62860	-1.22	-0.29	-1.21	0.268784	0.405799	-6.50
261328_at	unknown protein	---	AT1G44835	-1.11	-0.15	-1.21	0.268795	0.405799	-6.50
265576_at	unknown protein	CLASP	AT2G20190	-1.09	-0.12	-1.20	0.268951	0.406007	-6.50
264507_at	Expressed protein ; supported by cl	NIMIN-3	AT1G09415	-1.14	-0.18	-1.20	0.269041	0.406085	-6.50
263736_at	nucleic acid-binding protein, putativ	---	AT1G60000	1.15	0.20	1.20	0.269067	0.406085	-6.50
257454_at	hypothetical protein predicted by ge	---	AT1G65170	-1.13	-0.18	-1.20	0.269069	0.406085	-6.50
251450_at	squamosa promoter binding protein	SPL12	AT3G60030	-1.12	-0.16	-1.20	0.269075	0.406085	-6.50
256267_at	unknown protein ; supported by cDI	---	AT3G12260	1.10	0.13	1.20	0.269105	0.406085	-6.50
263764_at	putative vacuolar proton-ATPase su	VHA-A2	AT2G21410	1.12	0.17	1.20	0.26911	0.406085	-6.50
265976_at	putative Athila retroelement ORF1 p	---	---	1.10	0.14	1.20	0.269321	0.406362	-6.50
254142_at	putative protein other predicted or l	---	AT4G24630	-1.10	-0.14	-1.20	0.269329	0.406362	-6.50

258654_at	unknown protein	---	AT3G09860	1.16	0.22	1.20	0.269372	0.4064	-6.50
259572_at	hypothetical protein	---	AT1G20400	-1.12	-0.16	-1.20	0.26949	0.406552	-6.50
257434_at	hypothetical protein predicted by ge	---	AT2G21740	-1.08	-0.12	-1.20	0.269652	0.406769	-6.50
253944_at	SNF8 like protein SNF8 protein - y	VPS22	AT4G27040	1.10	0.14	1.20	0.269695	0.406808	-6.50
261231_at	unknown protein ; supported by cDI	---	AT1G20110	-1.08	-0.11	-1.20	0.269767	0.406888	-6.50
256410_at	hypothetical protein	---	AT1G66630	-1.07	-0.10	-1.20	0.269841	0.406973	-6.50
258412_at	unknown protein similar to pop3 pe	HS1	AT3G17210	-1.11	-0.15	-1.20	0.269977	0.407152	-6.50
247419_at	unknown protein	---	AT5G63080	1.13	0.18	1.20	0.270033	0.407184	-6.50
258162_at	dehydrogenase, putative similar to	---	AT3G17810	-1.14	-0.19	-1.20	0.270034	0.407184	-6.50
257852_at	unknown protein	---	AT3G12950	1.13	0.17	1.20	0.270073	0.407216	-6.50
259073_at	unknown protein contains zinc fing	---	AT3G02290	-1.20	-0.26	-1.20	0.270199	0.407374	-6.50
250145_at	putative protein predicted protein, A	---	AT5G14690	-1.14	-0.18	-1.20	0.270214	0.407374	-6.50
250373_at	putative protein	---	AT5G11470	-1.08	-0.11	-1.20	0.270268	0.407429	-6.50
246962_s_a	transcription factor-like protein ligh	BZIP9	AT5G24800	-1.19	-0.25	-1.20	0.270296	0.407445	-6.50
253377_at	putative protein NBS/LRR disease	ADR1-L1	AT4G33300	1.11	0.15	1.20	0.270323	0.407459	-6.50
266107_at	hypothetical protein predicted by ge	---	AT2G37910	-1.16	-0.21	-1.20	0.270362	0.40749	-6.50
256504_at	cytosolic IMP-GMP specific 5'-nucl	---	AT1G75210	-1.10	-0.14	-1.20	0.270479	0.407639	-6.50
251547_at	putative protein predicted proteins,	---	AT3G58860	-1.10	-0.14	-1.20	0.270504	0.40765	-6.50
249449_at	unknown protein	---	AT5G39430	1.08	0.11	1.20	0.270561	0.40771	-6.50
255470_at	hypothetical protein	---	AT4G03040	-1.11	-0.15	-1.20	0.270612	0.407753	-6.50
259691_at	hypothetical protein predicted by ge	---	AT1G63200	-1.15	-0.20	-1.20	0.270626	0.407753	-6.50
255032_at	putative protein anthocyanin rhamr	---	AT4G09500	1.13	0.18	1.20	0.270765	0.407936	-6.50
266430_at	unknown protein	---	AT2G07200	-1.07	-0.10	-1.20	0.270821	0.407994	-6.50
257393_at	unknown protein	---	AT2G20080	-1.08	-0.11	-1.20	0.270994	0.408227	-6.50
255503_at	contains similarity to a protein kina	---	AT4G02420	-1.41	-0.49	-1.20	0.27106	0.408299	-6.50
255432_at	SYR1-like syntaxin ;supported by f	SYP123	AT4G03330	-1.09	-0.13	-1.20	0.2711	0.408333	-6.50
262874_at	hypothetical protein predicted by ge	---	AT1G65020	-1.13	-0.17	-1.20	0.27114	0.408365	-6.51
264385_at	unknown protein	---	AT1G12020	-1.16	-0.21	-1.20	0.271275	0.408542	-6.51
248829_at	putative protein contains similarity t	---	AT5G47130	-1.16	-0.22	-1.20	0.27135	0.408629	-6.51
251622_at	dnaJ-like protein DNAJ protein - Sc	---	AT3G57340	-1.09	-0.12	-1.20	0.271444	0.408742	-6.51
264630_at	hypothetical protein predicted by ge	FAS1	AT1G65470	-1.13	-0.17	-1.20	0.27153	0.408846	-6.51
266760_at	putative RAV-like B3 domain DNA b	NGA1	AT2G46870	-1.13	-0.18	-1.20	0.271576	0.408887	-6.51
264032_at	unknown protein	GEK1	AT2G03800	1.11	0.15	1.20	0.271655	0.408979	-6.51
262013_s_a	mudrA-like protein similar to Mu tra	---	---	-1.13	-0.17	-1.20	0.271776	0.409134	-6.51
260528_at	putative WRKY-type DNA binding p	WRKY23	AT2G47260	-1.26	-0.33	-1.20	0.271921	0.409326	-6.51

254794_at	putative protein	---	AT4G12970	-1.39	-0.48	-1.20	0.272041	0.40948	-6.51
263282_at	Expressed protein ; supported by fu	---	AT2G14095	-1.10	-0.14	-1.20	0.272251	0.409768	-6.51
248343_at	putative protein contains similarity t	AtMYB19	AT5G52260	-1.08	-0.11	-1.20	0.272274	0.409777	-6.51
254928_at	putative protein hypothetical protei	---	AT4G11410	1.10	0.14	1.20	0.272335	0.409842	-6.51
247473_at	putative protein AT-hook protein 2,	---	AT5G62260	-1.14	-0.18	-1.20	0.272494	0.410042	-6.51
267312_at	unknown protein	---	AT2G34750	1.13	0.18	1.19	0.272506	0.410042	-6.51
251482_s_a	receptor lectin kinase 3	---	AT3G59740	1.11	0.15	1.19	0.272522	0.410042	-6.51
257301_at	hypothetical protein predicted by ge	---	---	-1.09	-0.12	-1.19	0.272609	0.410129	-6.51
258065_at	putative pyruvate kinase similar to	---	AT3G25960	-1.11	-0.16	-1.19	0.272616	0.410129	-6.51
266492_at	putative protein kinase contains a p	---	AT2G07020	-1.11	-0.15	-1.19	0.272671	0.410184	-6.51
255456_at	hypothetical protein ;supported by f	---	AT4G02920	1.10	0.14	1.19	0.272786	0.410331	-6.51
264784_s_a	unknown protein similar to Arabido	---	AT2G17830	-1.11	-0.15	-1.19	0.272857	0.41039	-6.51
251531_at	putative protein hypothetical protei	---	AT3G58550	-1.11	-0.15	-1.19	0.272862	0.41039	-6.51
247669_at	putative protein transcriptional repr	---	AT5G60170	1.13	0.18	1.19	0.272927	0.410461	-6.51
263829_at	unknown protein	---	AT2G40435	-1.31	-0.39	-1.19	0.273124	0.41073	-6.51
265059_at	unknown protein ; supported by cDI	AR791	AT1G52080	1.14	0.19	1.19	0.27328	0.410938	-6.51
256750_at	unknown protein contains Pfam pro	---	AT3G27150	-1.13	-0.18	-1.19	0.273315	0.410963	-6.51
255835_at	unknown protein	---	AT2G33420	-1.10	-0.14	-1.19	0.273378	0.411031	-6.51
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.20	-0.27	-1.19	0.273494	0.411178	-6.51
251261_at	putative protein polygalacturonase	---	AT3G62110	-1.23	-0.30	-1.19	0.273634	0.411362	-6.51
264541_at	hypothetical protein predicted by ge	---	AT1G55660	-1.12	-0.16	-1.19	0.27366	0.411374	-6.51
262705_at	putative wall-associated kinase sim	---	AT1G16260	-1.42	-0.50	-1.19	0.273749	0.41148	-6.51
259146_at	putative glycerol-3-phosphate dehy	SDP6	AT3G10370	1.13	0.18	1.19	0.273828	0.411572	-6.51
264111_at	hypothetical protein predicted by ge	---	AT2G13690	-1.08	-0.12	-1.19	0.274081	0.411921	-6.51
261349_at	Expressed protein ; supported by fu	AT1G7961(	---	-1.08	-0.12	-1.19	0.274117	0.411921	-6.51
249242_at	alcohol dehydrogenase	---	AT5G42250	1.12	0.17	1.19	0.274121	0.411921	-6.51
262440_at	serpin, putative similar to serpin GE	---	AT1G47710	1.15	0.20	1.19	0.274132	0.411921	-6.51
264194_at	putative wall-associated kinase con	---	AT1G22720	-1.10	-0.13	-1.19	0.274153	0.411925	-6.51
255314_at	putative transposon protein	---	---	1.11	0.15	1.19	0.274215	0.411991	-6.51
260506_at	Cyclin, putative similar to GB:CAB7	CYCA3;2	AT1G47210	-1.21	-0.27	-1.19	0.27428	0.412062	-6.51
251189_at	putative protein putative mitochond	---	AT3G62650	1.14	0.19	1.19	0.274305	0.412071	-6.51
250264_at	glucosyltransferase -like protein glu	---	AT5G12890	1.08	0.10	1.19	0.274323	0.412071	-6.51
262061_at	hypothetical protein contains simila	ATPP2-B11	AT1G80110	1.10	0.14	1.19	0.274436	0.412213	-6.52
265085_at	hypothetical protein predicted by ge	TPX2	AT1G03780	-1.15	-0.20	-1.19	0.274478	0.412244	-6.52
252815_at	hypothetical protein	---	---	-1.12	-0.16	-1.19	0.274492	0.412244	-6.52

256987_at	hypothetical protein predicted by ge	---	AT3G28560	-1.09	-0.13	-1.19	0.27457	0.412333	-6.52
257541_at	hypothetical protein predicted by ge	---	AT3G25950	-1.25	-0.32	-1.19	0.274673	0.412434	-6.52
253127_at	putative Myc-type transcription fact	---	AT4G36060	-1.09	-0.12	-1.19	0.27468	0.412434	-6.52
257617_at	hypothetical protein	---	AT3G26550	-1.09	-0.13	-1.19	0.274691	0.412434	-6.52
254610_at	putative protein predicted protein, A	---	AT4G18890	1.10	0.14	1.19	0.274861	0.412662	-6.52
267422_at	putative protein kinase contains a p	---	AT2G35050	-1.08	-0.12	-1.19	0.274926	0.412733	-6.52
249803_at	putative protein similar to unknown	---	AT5G23780	-1.10	-0.14	-1.19	0.274969	0.41277	-6.52
253156_at	putative protein mRNA for KIAA01	---	AT4G35730	-1.11	-0.15	-1.19	0.275021	0.412789	-6.52
252731_at	putative protein predicted proteins,	---	---	-1.14	-0.18	-1.19	0.275035	0.412789	-6.52
257015_at	hypothetical protein predicted by ge	---	AT3G28680	-1.11	-0.15	-1.19	0.275036	0.412789	-6.52
263988_at	floral homeodomain transcription fa	SHP2	AT2G42830	-1.09	-0.13	-1.19	0.275082	0.41282	-6.52
265493_at	unknown protein predicted by gens	---	AT2G15670	-1.10	-0.13	-1.19	0.275093	0.41282	-6.52
251877_at	synaptobrevin -like protein vesicle-	ATVAMP72	AT3G54300	-1.12	-0.16	-1.19	0.275152	0.412882	-6.52
260232_at	unknown protein contains Pfam pro	---	AT1G74640	-1.19	-0.25	-1.19	0.275181	0.412898	-6.52
249854_at	putative protein contains similarity t	---	AT5G22960	-1.12	-0.16	-1.19	0.275237	0.412945	-6.52
255981_at	hypothetical protein ;supported by f	---	AT1G34020	-1.12	-0.16	-1.19	0.275264	0.412945	-6.52
251512_at	putative protein several hypothetica	---	AT3G59190	-1.10	-0.13	-1.19	0.275267	0.412945	-6.52
264536_at	hypothetical protein predicted by ge	PRA1.G1	AT1G55640	-1.16	-0.21	-1.19	0.275331	0.412982	-6.52
251473_at	putative protein myrosinase-bindin	---	AT3G59610	-1.14	-0.19	-1.19	0.275343	0.412982	-6.52
254097_at	putative Ser/Thr protein kinase ser	---	AT4G25160	1.08	0.11	1.19	0.275346	0.412982	-6.52
249840_at	unknown protein ; supported by cD	ATLCBK1	AT5G23450	-1.08	-0.11	-1.19	0.275379	0.413005	-6.52
264350_at	putative seryl-tRNA synthetase sim	SRS	AT1G11870	-1.16	-0.21	-1.19	0.275421	0.413042	-6.52
262982_at	unknown protein ;supported by full-	ING2	AT1G54390	-1.08	-0.12	-1.19	0.275494	0.413124	-6.52
253243_at	putative protein	---	AT4G34560	1.45	0.53	1.19	0.275561	0.413197	-6.52
265883_at	unknown protein	---	AT2G42310	1.09	0.13	1.19	0.275634	0.413279	-6.52
260718_at	unknown protein	ECT7	AT1G48110	1.08	0.10	1.19	0.275655	0.413283	-6.52
253159_at	HMG delta protein ;supported by fu	HMGB5	AT4G35570	1.09	0.12	1.19	0.275703	0.413328	-6.52
255307_at	hypothetical protein similar to A. th	RIC10	AT4G04900	-1.11	-0.15	-1.19	0.275733	0.413346	-6.52
255416_at	hypothetical protein	---	AT4G03170	1.08	0.11	1.19	0.2758	0.413357	-6.52
255755_s_a	polygalacturonase, putative similar	---	AT1G43050	-1.10	-0.14	-1.19	0.275801	0.413357	-6.52
247707_at	scarecrow-like 11 - like scarecrow-	---	AT5G59450	1.49	0.58	1.19	0.275816	0.413357	-6.52
253448_at	putative protein mRNA for KIAA00	---	AT4G32640	1.08	0.11	1.19	0.275816	0.413357	-6.52
259048_at	DegP protease contains similarity to	DegP7	AT3G03380	-1.10	-0.14	-1.19	0.275831	0.413357	-6.52
252597_at	putative protein several hypothetica	---	---	-1.12	-0.16	-1.19	0.27585	0.413359	-6.52
245582_at	hypothetical protein	LOI1	AT4G14850	1.14	0.19	1.19	0.27592	0.413436	-6.52

250417_at	putative protein predicted proteins,	---	AT5G11230	-1.12	-0.17	-1.19	0.275961	0.413471	-6.52
254774_at	hypothetical protein	---	AT4G13440	-1.18	-0.24	-1.19	0.276146	0.41372	-6.52
264473_at	hypothetical protein predicted by ge	---	AT1G67180	-1.20	-0.26	-1.18	0.276285	0.413902	-6.52
263300_at	Mutator-like transposase similar to	---	---	-1.08	-0.11	-1.18	0.276313	0.413904	-6.52
259242_at	putative actin similar to actin 1 GB:I	ATARP6	AT3G33520	1.09	0.13	1.18	0.276323	0.413904	-6.52
256135_at	hypothetical protein predicted by ge	---	AT1G48730	-1.11	-0.15	-1.18	0.27635	0.413917	-6.52
262860_at	unknown protein	APO1	AT1G64810	1.13	0.18	1.18	0.276421	0.413996	-6.52
252386_at	putative protein various predicted p	---	AT3G47840	1.13	0.17	1.18	0.276464	0.41402	-6.52
257277_at	disease resistance protein, putative	---	AT3G14470	-1.11	-0.16	-1.18	0.276491	0.41402	-6.52
258920_at	class 2 non-symbiotic hemoglobin i	---	AT1G04380	-1.22	-0.28	-1.18	0.276491	0.41402	-6.52
251227_at	ABC transporter-like protein glutath	ATMRP10	AT3G62700	-1.18	-0.24	-1.18	0.27659	0.41414	-6.52
254749_at	putative protein various predicted p	---	AT4G13130	-1.07	-0.10	-1.18	0.276646	0.414198	-6.52
253677_at	cytidine deaminase - like protein cy	---	AT4G29580	-1.12	-0.16	-1.18	0.276699	0.41424	-6.52
267560_at	putative cytochrome P450	CYP76C3	AT2G45580	-1.11	-0.15	-1.18	0.276714	0.41424	-6.52
253663_at	putative villin	VLN4	AT4G30160	-1.10	-0.14	-1.18	0.276729	0.41424	-6.52
254856_at	putative ribosomal protein (fragmer	---	AT4G12160	1.10	0.14	1.18	0.276752	0.414245	-6.52
263650_at	hypothetical protein predicted by ge	---	AT1G04360	-1.10	-0.14	-1.18	0.276769	0.414245	-6.52
263923_at	Expressed protein ; supported by cl	---	AT2G36485	1.14	0.19	1.18	0.276805	0.414249	-6.52
264598_at	putative dimethylaniline monooxyge	---	AT1G04610	-1.09	-0.12	-1.18	0.276807	0.414249	-6.52
245160_at	putative leucine-rich repeat disease	AtRLP28	AT2G33080	-1.08	-0.11	-1.18	0.276942	0.414405	-6.52
256330_at	hypothetical protein predicted by ge	---	AT1G76870	1.13	0.18	1.18	0.27696	0.414405	-6.52
245613_at	hypothetical protein	---	AT4G14450	1.65	0.73	1.18	0.276967	0.414405	-6.52
260200_at	unknown protein ; supported by full	---	AT1G67620	1.10	0.14	1.18	0.276988	0.414411	-6.52
255034_at	putative protein Phaseolus vulgaris	---	---	-1.09	-0.13	-1.18	0.277059	0.414482	-6.52
248384_at	mandelonitrile lyase-like protein	---	AT5G51930	-1.09	-0.12	-1.18	0.277073	0.414482	-6.52
250150_at	putative protein ;supported by full-le	---	AT5G14710	1.15	0.20	1.18	0.277233	0.414695	-6.52
261671_at	hypothetical protein similar to hypot	---	AT1G18340	1.17	0.23	1.18	0.27735	0.414802	-6.52
267294_at	hypothetical protein predicted by ge	YCF37	AT2G23670	-1.14	-0.19	-1.18	0.277358	0.414802	-6.52
264291_at	hypothetical protein contains simila	---	AT1G78800	1.11	0.15	1.18	0.277359	0.414802	-6.52
257732_at	unknown protein contains Pfam pro	AtCASP	AT3G18480	1.10	0.14	1.18	0.277383	0.414806	-6.52
261997_at	hypothetical protein similar C-term	---	---	-1.09	-0.12	-1.18	0.277398	0.414806	-6.52
258943_at	hypothetical protein predicted by g	---	AT3G10400	1.11	0.15	1.18	0.277456	0.414865	-6.52
252795_at	putative protein predicted proteins,	---	---	-1.09	-0.13	-1.18	0.27752	0.414934	-6.52
257142_at	cytochrome P450, putative contain	CYP705A1	AT3G20090	1.13	0.18	1.18	0.277639	0.415084	-6.52
258487_at	unknown protein ;supported by full-	LBD41	AT3G02550	1.48	0.56	1.18	0.277727	0.415166	-6.53

249987_at	putative protein predicted proteins,	---	AT5G18490	1.17	0.23	1.18	0.277735	0.415166	-6.53
249484_at	cytochrome P450 - like protein cyto	BR6OX1	AT5G38970	-1.09	-0.12	-1.18	0.277748	0.415166	-6.53
246715_at	putative protein glucose-6-phospha	---	AT5G28230	-1.13	-0.18	-1.18	0.277789	0.4152	-6.53
255940_at	prolyl endopeptidase, putative simi	---	AT1G20380	-1.08	-0.12	-1.18	0.277889	0.415322	-6.53
264903_at	putative phosphoglucomutase simi	---	AT1G23190	1.11	0.15	1.18	0.277982	0.415434	-6.53
266613_at	similar to gibberellin-regulated prote	---	AT2G14900	-2.41	-1.27	-1.18	0.278113	0.415602	-6.53
264198_at	unknown protein ESTs gb|Z34075,	---	AT1G22800	-1.14	-0.19	-1.18	0.278154	0.415637	-6.53
264049_at	putative GTP-binding protein	---	AT2G22390	-1.15	-0.20	-1.18	0.278212	0.415697	-6.53
265994_at	putative multispanning membrane p	---	AT2G24170	-1.23	-0.29	-1.18	0.278467	0.416041	-6.53
258516_at	myb-related protein, putative simila	MYB108	AT3G06490	1.35	0.43	1.18	0.278485	0.416041	-6.53
249555_at	putative protein predicted protein, r	---	AT5G38300	-1.10	-0.14	-1.18	0.278498	0.416041	-6.53
248868_at	putative protein similar to unknown	---	AT5G46780	1.24	0.31	1.18	0.278698	0.416314	-6.53
265285_at	hypothetical protein predicted by ge	---	AT2G20410	1.12	0.16	1.18	0.278795	0.416431	-6.53
253614_at	putative protein heat shock protein	---	AT4G30350	1.18	0.24	1.18	0.278816	0.416435	-6.53
245188_at	F12A21.19 unknown protein; simil	---	AT1G67660	1.10	0.14	1.18	0.278901	0.416535	-6.53
252757_at	putative protein several hypothetica	---	---	-1.11	-0.15	-1.18	0.279104	0.416811	-6.53
258843_at	putative protein kinase similar to hy	---	AT3G04690	-1.09	-0.13	-1.18	0.279173	0.416886	-6.53
260335_at	putative strictosidine synthase simil	SS3	AT1G74000	-1.26	-0.34	-1.18	0.279237	0.416955	-6.53
262743_at	unknown protein similar to unknowr	---	AT1G29020	-1.11	-0.14	-1.18	0.279266	0.416971	-6.53
255642_at	hypothetical protein	iqd17	AT4G00820	1.17	0.23	1.18	0.279346	0.417063	-6.53
264281_at	hypothetical protein similar to putati	---	AT1G61830	-1.12	-0.16	-1.18	0.279689	0.417528	-6.53
255822_at	putative expansin ;supported by ful	ATEXPA8	AT2G40610	-2.11	-1.08	-1.18	0.279694	0.417528	-6.53
246526_at	putative protein RXF26 - Arabidops	GLIP7	AT5G15720	-1.09	-0.12	-1.18	0.279865	0.417755	-6.53
259425_at	4,5 PIP kinase, putative similar to 4	PIPK11	AT1G01460	1.09	0.12	1.17	0.280062	0.418022	-6.53
258723_at	putative MYB-related protein simila	---	AT3G09600	1.10	0.13	1.17	0.280098	0.418049	-6.53
255910_at	unknown protein contains similarity	---	AT1G18030	-1.10	-0.14	-1.17	0.280218	0.4182	-6.53
246082_at	receptor protein kinase - like protei	EFR	AT5G20480	1.31	0.39	1.17	0.280273	0.418255	-6.53
250612_s_a	putative protein ARR2 protein - Ara	ARR13	AT2G27070	-1.13	-0.18	-1.17	0.280444	0.418483	-6.53
245648_at	F5A9.12 hypothetical protein	---	---	-1.10	-0.13	-1.17	0.280539	0.418598	-6.53
263393_at	hypothetical protein similar to hypot	---	---	-1.09	-0.12	-1.17	0.280582	0.418608	-6.53
266719_at	MYB-related transcription factor (C	CCA1	AT2G46830	-1.13	-0.17	-1.17	0.280583	0.418608	-6.53
258328_at	putative zinc finger protein similar to	---	AT3G16090	-1.08	-0.11	-1.17	0.280676	0.418719	-6.53
259983_at	3-hydroxy-3-methylglutaryl CoA red	HMG1	AT1G76490	-1.11	-0.15	-1.17	0.280863	0.418971	-6.53
262555_at	hypothetical protein	---	AT1G31400	-1.08	-0.11	-1.17	0.280974	0.419109	-6.53
263146_at	lipase, putative similar to lipase GI	GLIP2	AT1G53940	-1.12	-0.16	-1.17	0.281014	0.419141	-6.53

248652_at	putative protein contains similarity t	SHV2	AT5G49270	-1.16	-0.21	-1.17	0.281059	0.419181	-6.54
263305_at	unknown protein ;supported by full-	BPC1	AT2G01930	-1.14	-0.19	-1.17	0.281106	0.419224	-6.54
265613_at	putative DnaJ protein ; supported b	---	AT2G25560	1.12	0.16	1.17	0.281247	0.419407	-6.54
259388_at	steroid sulfotransferase, putative s	ST4B	AT1G13420	1.10	0.13	1.17	0.281271	0.419415	-6.54
266573_at	unknown protein	---	AT2G23860	-1.14	-0.18	-1.17	0.281304	0.419437	-6.54
250476_at	MADS box protein FLOWERING LO	FLC	AT5G10140	-1.10	-0.13	-1.17	0.281331	0.41945	-6.54
261820_at	hypothetical protein predicted by ge	---	AT1G11420	1.14	0.19	1.17	0.281386	0.419504	-6.54
247985_at	putative protein contains similarity t	---	AT5G56790	1.11	0.16	1.17	0.281419	0.419526	-6.54
263353_at	hypothetical protein predicted by ge	---	AT2G22070	1.10	0.14	1.17	0.281478	0.419564	-6.54
248288_at	unknown protein ; supported by cD	---	AT5G52840	-1.12	-0.17	-1.17	0.281492	0.419564	-6.54
254183_at	putative protein predicted protein, A	---	AT4G23960	1.11	0.15	1.17	0.2815	0.419564	-6.54
252208_at	putative protein hypothetical protei	---	AT3G50380	1.15	0.20	1.17	0.281625	0.419718	-6.54
248365_at	putative protein strong similarity to	---	AT5G52500	-1.10	-0.14	-1.17	0.28164	0.419718	-6.54
264182_at	MADS-box protein, putative similar	AGL23	AT1G65360	-1.09	-0.12	-1.17	0.28166	0.419721	-6.54
254885_at	putative protein various predicted p	---	AT4G11745	-1.13	-0.17	-1.17	0.281683	0.419728	-6.54
247185_at	putative protein contains similarity t	---	AT5G65460	-1.12	-0.16	-1.17	0.281725	0.419763	-6.54
261452_s_a	hypothetical protein predicted by ge	---	---	1.10	0.13	1.17	0.281871	0.419952	-6.54
251597_at	protein kinase - like protein wall-as	---	AT3G57750	1.23	0.30	1.17	0.281928	0.419995	-6.54
259504_at	inorganic pyrophosphatase, putativ	AVP1	AT1G15690	-1.12	-0.16	-1.17	0.281936	0.419995	-6.54
251556_at	putative protein predicted proteins,	---	AT3G58840	1.14	0.19	1.17	0.281959	0.420002	-6.54
251739_at	putative protein protein of unknowr	CAN	AT3G56170	-1.14	-0.18	-1.17	0.282043	0.420099	-6.54
247946_at	putative protein similar to unknown	CIA2	AT5G57180	1.28	0.36	1.17	0.282116	0.42018	-6.54
252662_at	putative protein Sec24A protein, H	CEF	AT3G44340	-1.10	-0.14	-1.17	0.282196	0.420273	-6.54
267558_at	unknown protein ; supported by cD	LUH	AT2G32700	-1.09	-0.12	-1.17	0.282242	0.420314	-6.54
244986_at	ribosomal protein S19	---	---	-1.16	-0.22	-1.17	0.28229	0.420341	-6.54
261917_at	hypothetical protein similar to TMV	---	AT1G65920	-1.22	-0.29	-1.17	0.282297	0.420341	-6.54
248609_at	unknown protein ; supported by cD	---	AT5G49440	1.11	0.15	1.17	0.28233	0.420348	-6.54
265229_s_a	hypothetical protein	---	AT2G07701	1.09	0.12	1.17	0.282339	0.420348	-6.54
251162_at	putative protein hypothetical protein	---	AT3G63300	-1.09	-0.13	-1.17	0.282502	0.42054	-6.54
247689_at	putative protein protein tyrosine ph	---	AT5G59770	-1.14	-0.19	-1.17	0.282505	0.42054	-6.54
252717_at	putative protein predicted proteins,	---	AT3G43930	1.19	0.25	1.17	0.282623	0.420688	-6.54
247853_at	non phototropic hypocotyl 1-like ; s	PHOT2	AT5G58140	1.11	0.15	1.17	0.282673	0.420735	-6.54
251839_at	putative protein patatin, Solanum t	PLA IIIA	AT3G54950	1.17	0.22	1.17	0.282712	0.420766	-6.54
253936_at	STIG1 like protein STIG1 protein -	---	AT4G26880	-1.09	-0.13	-1.17	0.282944	0.421077	-6.54
265218_at	putative transcription factor	GTF2H2	AT1G05055	1.08	0.11	1.17	0.282958	0.421077	-6.54

246751_at	pectin methyl-esterase - like protei	---	AT5G27870	-1.08	-0.11	-1.17	0.283071	0.421196	-6.54
252635_at	putative protein predicted proteins,	---	AT3G44510	1.11	0.16	1.17	0.283075	0.421196	-6.54
248623_at	putative protein similar to unknown	---	AT5G49170	-1.36	-0.45	-1.17	0.283123	0.421239	-6.54
261733_at	clathrin coat assembly protein AP1	---	AT1G47830	1.08	0.12	1.17	0.283143	0.421239	-6.54
257503_at	DAG-like protein similar to DAG pr	---	AT1G72530	1.13	0.18	1.17	0.283167	0.421239	-6.54
258135_at	Expressed protein ; supported by fu	---	AT3G24506	-1.10	-0.14	-1.17	0.283195	0.421239	-6.54
261580_at	unknown protein ;supported by full-	IQD18	AT1G01110	-1.16	-0.21	-1.17	0.283208	0.421239	-6.54
253327_at	putative transcription factor	MYB69	AT4G33450	-1.12	-0.17	-1.17	0.283218	0.421239	-6.54
260740_at	thioredoxin, putative contains Pfam	ATQSOX1	AT1G15020	-1.08	-0.11	-1.17	0.283233	0.421239	-6.54
264009_at	putative disease resistance respons	---	AT2G21110	-1.09	-0.13	-1.17	0.28332	0.421318	-6.54
264503_at	hypothetical protein Similar to Arab	---	AT1G09410	-1.09	-0.12	-1.17	0.283323	0.421318	-6.54
265247_at	50S ribosomal protein L3 ;supporte	---	AT2G43030	-1.09	-0.12	-1.17	0.283428	0.421439	-6.54
266258_at	60S acidic ribosomal protein P2 ;su	---	AT2G27720	1.18	0.24	1.17	0.283454	0.421439	-6.54
249592_at	putative protein SIAH1 protein, Bra	---	AT5G37890	-1.12	-0.16	-1.17	0.28346	0.421439	-6.54
249534_at	bZIP transcription factor - like prote	AtbZIP43	AT5G38800	-1.08	-0.12	-1.17	0.283508	0.421476	-6.54
250138_at	DRH1 DEAD box protein - like DRH	---	AT5G14610	-1.09	-0.13	-1.17	0.283522	0.421476	-6.54
263094_at	hypothetical protein predicted by ge	---	AT2G16020	-1.10	-0.14	-1.16	0.283701	0.421716	-6.54
249761_at	acetyl-CoA:benzylalcohol acetyltran	---	AT5G23970	-1.12	-0.17	-1.16	0.28374	0.421746	-6.54
259000_at	hypothetical protein predicted by ge	---	AT3G01860	1.22	0.29	1.16	0.283935	0.422008	-6.54
266733_at	similar to axi 1 protein from Nicotian	---	AT2G03280	-1.10	-0.13	-1.16	0.283976	0.422018	-6.54
246645_at	putative protein ;supported by full-l	---	AT5G35080	-1.12	-0.16	-1.16	0.283981	0.422018	-6.54
262274_at	deaminase, putative similar to cytic	TADA	AT1G68720	-1.08	-0.11	-1.16	0.283997	0.422018	-6.54
265836_at	Mutator-like transposase similar to	---	---	-1.10	-0.13	-1.16	0.284087	0.422085	-6.54
266429_at	hypothetical protein predicted by ge	---	AT2G07190	-1.10	-0.14	-1.16	0.284098	0.422085	-6.54
257311_at	phosphate transporter, putative co	PHT2;1	AT3G26570	-1.10	-0.14	-1.16	0.284098	0.422085	-6.54
254093_at	putative protein extensin, Catharan	AtMC2	AT4G25110	-1.29	-0.36	-1.16	0.284193	0.422199	-6.54
247113_at	unknown protein ;supported by full-	---	AT5G65960	-1.10	-0.13	-1.16	0.284238	0.422238	-6.54
249366_at	dihydroxyacetone 3-phosphate redu	---	AT5G40610	1.30	0.37	1.16	0.284291	0.422289	-6.54
260206_at	putative protein kinase contains Pfa	---	AT1G70740	-1.24	-0.31	-1.16	0.284351	0.422351	-6.54
263772_at	Expressed protein ; supported by fu	ELF4-L3	AT2G06255	-1.18	-0.24	-1.16	0.284379	0.422365	-6.54
254203_at	putative protein various predicted p	AtGRF8	AT4G24150	1.09	0.12	1.16	0.284404	0.422374	-6.54
247986_at	unknown protein	---	AT5G56880	-1.12	-0.16	-1.16	0.284464	0.422436	-6.55
252230_at	putative protein various predicted p	---	AT3G49810	1.36	0.44	1.16	0.284617	0.422636	-6.55
258450_at	hypothetical protein predicted by g	---	---	-1.09	-0.13	-1.16	0.284726	0.42277	-6.55
250615_at	putative protein ankyrins - different	---	AT5G07270	-1.12	-0.16	-1.16	0.284865	0.422919	-6.55

249726_at	unknown protein	---	AT5G35480	1.18	0.24	1.16	0.284874	0.422919	-6.55
255410_at	putative rac GTPase activating pro	---	AT4G03100	-1.10	-0.13	-1.16	0.284894	0.422919	-6.55
265687_s_a	hypothetical protein predicted by ge	---	AT2G24470	-1.09	-0.12	-1.16	0.2849	0.422919	-6.55
245754_at	hypothetical protein predicted by ge	---	AT1G35183	1.08	0.12	1.16	0.284922	0.422924	-6.55
249215_at	dihydroflavonol 4-reductase	DFR	AT5G42800	-1.16	-0.21	-1.16	0.284982	0.422985	-6.55
258668_at	hypothetical protein predicted by ge	---	AT3G08780	-1.09	-0.12	-1.16	0.285019	0.423013	-6.55
266625_at	putative peroxidase	---	AT2G35380	-1.10	-0.13	-1.16	0.285044	0.42302	-6.55
264626_at	unknown protein	AS2	AT1G65620	-1.16	-0.21	-1.16	0.285063	0.42302	-6.55
255320_at	putative transposon protein	---	---	-1.08	-0.11	-1.16	0.285098	0.42302	-6.55
251753_at	putative protein predicted protein, A	---	AT3G55760	-1.25	-0.33	-1.16	0.285101	0.42302	-6.55
248665_at	Expressed protein ; supported by fu	---	AT5G48655	1.08	0.11	1.16	0.285117	0.42302	-6.55
261359_at	hypothetical protein predicted by ge	---	---	-1.10	-0.14	-1.16	0.285191	0.423103	-6.55
247913_at	unknown protein	---	AT5G57510	1.67	0.74	1.16	0.285295	0.423229	-6.55
249202_at	cytochrome P450	CYP705A1	AT5G42580	-1.09	-0.12	-1.16	0.28536	0.423274	-6.55
255738_at	hypothetical protein predicted by ge	---	AT1G25570	-1.09	-0.12	-1.16	0.285368	0.423274	-6.55
264304_at	Expressed protein ; supported by fu	---	AT1G78895	1.12	0.16	1.16	0.285381	0.423274	-6.55
248567_at	putative protein contains similarity t	---	AT5G49750	-1.09	-0.12	-1.16	0.285477	0.42339	-6.55
264998_at	unknown protein similar to hypothet	---	AT1G67330	1.38	0.47	1.16	0.28554	0.423455	-6.55
249332_at	putative protein similar to unknown	---	AT5G40980	-1.12	-0.16	-1.16	0.285569	0.423471	-6.55
261399_at	receptor protein kinase, putative si	---	AT1G79620	-1.12	-0.16	-1.16	0.285588	0.423471	-6.55
245652_at	F-box protein family, putative	---	AT4G13960	-1.11	-0.15	-1.16	0.285642	0.423524	-6.55
258917_at	unknown protein C-terminal portion	---	AT3G10630	1.07	0.10	1.16	0.28568	0.423553	-6.55
262085_at	hypothetical protein predicted by ge	---	AT1G56060	1.53	0.61	1.16	0.285711	0.423571	-6.55
249663_s_a	unknown protein	---	---	-1.12	-0.16	-1.16	0.285765	0.423624	-6.55
249664_at	putative protein histone stem-loop	---	AT5G36722	-1.09	-0.13	-1.16	0.285815	0.423665	-6.55
261001_at	hypothetical protein similar to hypot	---	AT1G26530	1.12	0.16	1.16	0.28583	0.423665	-6.55
245495_at	hypothetical protein	---	AT4G16400	-1.07	-0.10	-1.16	0.285902	0.423745	-6.55
262723_at	hypothetical protein predicted by ge	---	AT1G43630	-1.13	-0.18	-1.16	0.285923	0.423748	-6.55
248596_at	putative protein contains similarity t	AtMYB111	AT5G49330	-1.24	-0.31	-1.16	0.286009	0.423848	-6.55
253437_at	putative protein mRNAs from Ricin	---	AT4G32460	-1.29	-0.37	-1.16	0.286053	0.423885	-6.55
245232_at	actin depolymerizing factor-like pro	ADF7	AT4G25590	-1.10	-0.14	-1.16	0.286117	0.423953	-6.55
249024_at	putative protein strong similarity to u	---	AT5G44860	1.09	0.13	1.16	0.28619	0.424034	-6.55
247195_at	putative protein contains similarity t	---	AT5G65500	-1.12	-0.16	-1.16	0.286262	0.424112	-6.55
254388_at	Expressed protein ; supported by fu	MSRB2	AT4G21860	1.10	0.13	1.16	0.286346	0.424205	-6.55
251302_at	RAV-like protein DNA-binding prote	NGA2	AT3G61970	-1.07	-0.10	-1.16	0.286362	0.424205	-6.55

246998_at	putative protein similar to unknown	---	AT5G67370	1.19	0.26	1.16	0.286395	0.424227	-6.55
259156_at	hypothetical protein predicted by ge	SEC8	AT3G10380	-1.09	-0.13	-1.16	0.286535	0.424407	-6.55
248233_at	F-box protein family, AtFBL13 cont	---	AT5G53840	-1.10	-0.14	-1.16	0.28657	0.424431	-6.55
257331_at	hypothetical protein	---	---	-1.12	-0.16	-1.16	0.286677	0.424561	-6.55
254723_at	ammonium transport protein (AMT1	AMT1;1	AT4G13510	1.14	0.18	1.16	0.286948	0.424906	-6.55
255381_at	RMA1 RING zinc finger protein ider	RMA1	AT4G03510	-1.20	-0.26	-1.16	0.287013	0.424906	-6.55
250304_at	elongation factor 1B alpha-subunit (	---	AT5G12110	-1.33	-0.41	-1.16	0.287016	0.424906	-6.55
255304_at	putative potassium transporter sim	KEA3	AT4G04850	-1.17	-0.23	-1.16	0.28702	0.424906	-6.55
263632_at	Expressed protein ; supported by cl	---	AT2G04795	-1.28	-0.36	-1.16	0.287046	0.424906	-6.55
252897_at	cytochrome P450 - like protein cyto	CYP96A9	AT4G39480	-1.10	-0.13	-1.16	0.287051	0.424906	-6.55
260487_at	RNA-binding protein, putative simil	Y14	AT1G51510	1.09	0.13	1.16	0.287056	0.424906	-6.55
249590_at	putative protein SIAH1, Brassica na	---	AT5G37870	-1.08	-0.12	-1.16	0.287058	0.424906	-6.55
262106_at	hypothetical protein similar to Wee1	WEE1	AT1G02970	-1.12	-0.16	-1.16	0.287213	0.425107	-6.55
264063_at	unknown protein	---	AT2G27900	-1.09	-0.13	-1.16	0.287292	0.425197	-6.55
259494_at	mitotic checkpoint protein, putative	---	AT1G15850	-1.12	-0.16	-1.16	0.287368	0.425282	-6.55
260131_at	unknown protein contains Pfam pro	---	AT1G66310	1.09	0.13	1.16	0.287402	0.425305	-6.55
252599_at	receptor-like protein kinase recepto	---	AT3G45390	-1.13	-0.18	-1.15	0.28745	0.425348	-6.55
251211_s_a	putative protein several hypothetica	---	AT3G62470	1.22	0.28	1.15	0.287551	0.425469	-6.55
247462_at	A9 protein precursor - like A9 prote	---	AT5G62080	-1.11	-0.15	-1.15	0.287616	0.425521	-6.55
254899_at	serine/threonine kinase-like protein	---	AT4G11490	-1.13	-0.17	-1.15	0.287623	0.425521	-6.55
259888_at	hypothetical protein similar to nodul	---	AT1G76350	1.27	0.35	1.15	0.287645	0.425526	-6.55
262498_at	8-oxoguanine DNA glycosylase-like	OGG1	AT1G21710	1.10	0.14	1.15	0.287746	0.425647	-6.55
253870_at	putative protein	---	AT4G27530	-1.10	-0.14	-1.15	0.287921	0.425879	-6.56
267330_at	unknown protein	---	AT2G19270	1.07	0.10	1.15	0.288012	0.425966	-6.56
252399_at	putative cyclic nucleotide-gated cha	CNGC16	AT3G48010	-1.08	-0.12	-1.15	0.288017	0.425966	-6.56
255418_at	predicted protein of unknown functi	---	AT4G03200	1.12	0.17	1.15	0.288084	0.426037	-6.56
249686_at	putative protein contains similarity t	CYP716A2	AT5G36140	-1.07	-0.10	-1.15	0.288253	0.42626	-6.56
259009_at	thioglucosidase 3D precursor identi	PYK10	AT3G09260	-1.17	-0.22	-1.15	0.28834	0.426361	-6.56
247060_at	succinate dehydrogenase flavoprot	SDH1-1	AT5G66760	1.33	0.41	1.15	0.288369	0.426376	-6.56
251439_at	putative protein unknown protein A	---	AT3G59950	1.11	0.15	1.15	0.288419	0.426387	-6.56
248002_at	Expressed protein ; supported by fu	ATARP8	AT5G56180	1.14	0.19	1.15	0.288465	0.426387	-6.56
253650_at	EST GB:N37377 spans last intron a	---	AT4G30020	-1.68	-0.75	-1.15	0.288468	0.426387	-6.56
258068_at	putative DNA-binding protein, GT-1	---	AT3G25990	1.09	0.12	1.15	0.288468	0.426387	-6.56
251363_at	putative transcription factor (MYB17	AtMYB17	AT3G61250	1.17	0.22	1.15	0.28847	0.426387	-6.56
248201_at	putative protein similar to unknown	PTAC15	AT5G54180	1.21	0.28	1.15	0.288537	0.426458	-6.56

258336_at	putative ethylene-inducible protein s	PDX1.2	AT3G16050	1.21	0.28	1.15	0.288716	0.426694	-6.56
245069_at	putative glucosyltransferase	UGT84B2	AT2G23250	-1.10	-0.13	-1.15	0.288788	0.426774	-6.56
261778_at	hypothetical protein predicted by ge	---	AT1G76220	-1.08	-0.10	-1.15	0.288811	0.42678	-6.56
267359_at	hypothetical protein predicted by ge	---	AT2G40020	1.13	0.18	1.15	0.2889	0.426884	-6.56
254876_at	putative phosphoribosylanthranilate	---	AT4G11610	-1.12	-0.17	-1.15	0.28892	0.426885	-6.56
255712_at	hypothetical protein similar to A. tha	---	AT4G00280	1.09	0.13	1.15	0.288952	0.426906	-6.56
248001_at	calcineurin B-like protein 2 (gb|AAC	CBL2	AT5G55990	1.13	0.17	1.15	0.288998	0.426945	-6.56
251181_at	putative protein pectinesterase hor	---	AT3G62820	-1.13	-0.17	-1.15	0.289078	0.427016	-6.56
263861_at	hypothetical protein	---	AT2G04560	-1.15	-0.20	-1.15	0.289085	0.427016	-6.56
258677_at	putative ribosomal-protein S6 kinas	PK1	AT3G08730	-1.11	-0.15	-1.15	0.289102	0.427016	-6.56
258852_at	unknown protein similar to C-termin	AT-P4H-2	AT3G06300	1.14	0.19	1.15	0.289196	0.427127	-6.56
252752_s_a	putative protein hypothetical protei	---	AT3G43470	-1.08	-0.12	-1.15	0.289312	0.427271	-6.56
260384_at	putative 2-isopropylmalate synthase	IMS1	AT1G74040	1.10	0.13	1.15	0.289446	0.427442	-6.56
266042_s_a	hypothetical protein	---	AT2G07734	1.15	0.21	1.15	0.289465	0.427442	-6.56
262069_at	hypothetical protein similar to SNF4	---	AT1G80090	-1.11	-0.15	-1.15	0.289546	0.427511	-6.56
256584_at	unknown protein	---	AT3G28750	-1.09	-0.12	-1.15	0.289549	0.427511	-6.56
252683_at	putative protein predicted proteins,	---	AT3G44380	-1.12	-0.17	-1.15	0.289686	0.427685	-6.56
264129_at	hypothetical protein predicted by ge	---	AT1G79170	-1.11	-0.15	-1.15	0.289739	0.427736	-6.56
255803_at	putative protein vesicle-associated	---	AT4G10170	1.09	0.12	1.15	0.289861	0.42788	-6.56
249981_at	putative protein predicted proteins,	---	AT5G18510	-1.12	-0.17	-1.15	0.289885	0.42788	-6.56
260524_at	unknown protein	---	AT2G47230	-1.09	-0.13	-1.15	0.289909	0.42788	-6.56
255844_at	putative protein kinase contains a p	---	AT2G33580	1.22	0.29	1.15	0.289912	0.42788	-6.56
248723_at	acetyl-CoA:benzylalcohol acetyltran	---	AT5G47950	-1.10	-0.14	-1.15	0.289944	0.4279	-6.56
260958_at	unknown protein identical to unknov	---	AT1G06060	-1.11	-0.15	-1.15	0.290184	0.428227	-6.56
250712_at	human RAN binding protein 16-like	---	AT5G06120	1.11	0.15	1.15	0.290334	0.42842	-6.56
245720_at	RNA binding protein - like	---	AT5G04210	-1.09	-0.12	-1.15	0.290393	0.428479	-6.56
259638_at	coatomer complex subunit, putative	---	AT1G52360	-1.11	-0.16	-1.15	0.290455	0.428543	-6.56
246915_at	malate dehydrogenase - like protei	ATNADP-M	AT5G25880	1.18	0.24	1.15	0.290477	0.428548	-6.56
251949_at	receptor protein kinase -like protein	---	AT3G53590	-1.12	-0.16	-1.15	0.290638	0.428758	-6.56
245554_at	cytochrome P450 like protein	CYP705A4	AT4G15380	-1.07	-0.10	-1.15	0.290736	0.428874	-6.56
255254_at	hypothetical protein	---	AT4G05030	-1.13	-0.17	-1.15	0.290798	0.428938	-6.56
255671_at	Expressed protein ; supported by fu	---	AT4G00355	1.11	0.15	1.15	0.290834	0.428964	-6.56
266445_at	unknown protein	---	AT2G43070	-1.13	-0.17	-1.15	0.290902	0.429037	-6.56
253735_at	putative protein SNF7 protein - Sac	SNF7.1	AT4G29160	1.09	0.13	1.15	0.290966	0.429103	-6.56
245882_at	mitochondrial carrier-like protein m	DIC3	AT5G09470	1.11	0.15	1.15	0.291056	0.429206	-6.56

267366_at	unknown protein ;supported by full-	---	AT2G44310	1.09	0.13	1.15	0.291073	0.429206	-6.56
247655_at	zinc finger protein Zat12 ;supporte	RHL41	AT5G59820	1.44	0.52	1.15	0.291113	0.429236	-6.56
245553_at	lupeol synthase like protein	BARS1	AT4G15370	-1.08	-0.11	-1.15	0.291182	0.429311	-6.56
259949_at	hypothetical protein predicted by ge	---	AT1G71420	1.10	0.14	1.14	0.291312	0.429474	-6.56
249764_at	septum site-determining MinD (dbj|	MIND	AT5G24020	1.12	0.17	1.14	0.291379	0.429526	-6.56
265079_at	hypothetical protein contains simila	---	AT1G55460	1.08	0.12	1.14	0.291384	0.429526	-6.56
265786_at	putative replication protein A1	---	---	1.07	0.10	1.14	0.29142	0.42955	-6.57
264184_at	early nodule-specific protein, putati	---	AT1G54790	-1.10	-0.13	-1.14	0.291529	0.429683	-6.57
263945_at	hypothetical protein predicted by ge	---	AT2G36030	-1.13	-0.17	-1.14	0.291615	0.429782	-6.57
248903_at	3-oxoacyl-[acyl-carrier-protein] synt	KAS I	AT5G46290	-1.18	-0.24	-1.14	0.291648	0.429804	-6.57
256490_at	unknown protein ;supported by full-	---	AT1G31460	1.14	0.19	1.14	0.291763	0.429945	-6.57
248323_at	unknown protein	---	AT5G52770	-1.07	-0.10	-1.14	0.291857	0.430054	-6.57
254130_at	MADS-box protein AGL24 ; suppor	AGL24	AT4G24540	1.17	0.23	1.14	0.291875	0.430054	-6.57
247033_at	SKP1 interacting partner 2 (SKIP2)	SKIP2	AT5G67250	-1.11	-0.15	-1.14	0.291932	0.43011	-6.57
254713_at	hypothetical protein	---	AT4G18090	-1.14	-0.18	-1.14	0.292051	0.430257	-6.57
264428_at	hypothetical protein predicted by ge	---	AT1G61790	1.15	0.20	1.14	0.292112	0.430294	-6.57
261184_at	pol polyprotein, putative similar to r	---	---	-1.11	-0.15	-1.14	0.292113	0.430294	-6.57
249541_at	anthranilate N-benzoyltransferase	---	AT5G38130	-1.10	-0.14	-1.14	0.292197	0.430321	-6.57
265476_at	putative thioredoxin M ; supported	ATHM3	AT2G15570	1.08	0.11	1.14	0.292225	0.430321	-6.57
256339_at	hypothetical protein	---	AT1G72080	-1.09	-0.12	-1.14	0.292258	0.430321	-6.57
255145_at	hypothetical protein	---	---	-1.11	-0.15	-1.14	0.29226	0.430321	-6.57
253800_at	putative protein probable cell wall p	---	AT4G28160	-1.11	-0.15	-1.14	0.292267	0.430321	-6.57
252753_at	hypothetical protein	---	AT3G43500	-1.10	-0.14	-1.14	0.292272	0.430321	-6.57
253151_at	putative polygalacturonase polygal	---	AT4G35670	-1.08	-0.11	-1.14	0.292295	0.430321	-6.57
265034_at	unknown protein ;supported by full-	---	AT1G61660	1.11	0.15	1.14	0.292323	0.430321	-6.57
258760_at	putative membrane protein similar	---	AT3G10780	1.19	0.25	1.14	0.292349	0.430321	-6.57
260885_at	protein kinase PK4, putative simila	CIPK18	AT1G29230	-1.12	-0.16	-1.14	0.292349	0.430321	-6.57
246054_at	putative protein predicted proteins,	---	AT5G08360	-1.09	-0.12	-1.14	0.292352	0.430321	-6.57
265393_at	unknown protein ; supported by cD	---	AT2G20830	-1.17	-0.23	-1.14	0.292358	0.430321	-6.57
263008_at	unknown protein	RPP27	AT1G54470	-1.08	-0.11	-1.14	0.2924	0.430355	-6.57
263360_at	unknown protein	---	AT2G03830	1.10	0.13	1.14	0.292451	0.430403	-6.57
258674_at	putative elongation factor P (EF-P)	---	AT3G08740	-1.16	-0.21	-1.14	0.292502	0.43045	-6.57
257560_at	galactosyltransferase, putative con	---	AT3G14960	1.08	0.11	1.14	0.292568	0.430519	-6.57
262773_at	putative nuclear matrix constituent	LINC2	AT1G13220	-1.11	-0.15	-1.14	0.29262	0.430568	-6.57
265745_at	hypothetical protein predicted by ge	---	---	-1.08	-0.11	-1.14	0.292712	0.430676	-6.57

254888_at	putative protein predicted protein, /	---	AT4G11780	-1.09	-0.13	-1.14	0.292737	0.430684	-6.57
257094_at	hypothetical protein similar to tetraa	---	AT3G20480	1.15	0.20	1.14	0.292911	0.430907	-6.57
253352_at	pathogenesis-related protein 1 pre	---	AT4G33710	-1.11	-0.15	-1.14	0.292926	0.430907	-6.57
262077_at	dynamin-like protein similar to dyna	ADL3	AT1G59610	1.09	0.12	1.14	0.293051	0.431063	-6.57
263500_s_a	hypothetical protein	---	AT2G07672	1.11	0.15	1.14	0.293284	0.431377	-6.57
250915_at	homeodomain -like protein homeo	HB51	AT5G03790	-1.16	-0.21	-1.14	0.29337	0.431457	-6.57
252224_at	putative protein various ADP-RIBO	ATARLA1B	AT3G49860	-1.11	-0.15	-1.14	0.293376	0.431457	-6.57
255281_at	contains similarity to glucan synthas	GSL1	AT4G04970	1.07	0.10	1.14	0.293398	0.431462	-6.57
267443_at	hypothetical protein predicted by ge	---	AT2G19000	-1.07	-0.10	-1.14	0.293428	0.431478	-6.57
257256_at	hypothetical protein contains Pfam	---	AT3G21970	-1.07	-0.10	-1.14	0.293459	0.431496	-6.57
255350_at	putative transposon protein similar t	---	---	1.08	0.11	1.14	0.293522	0.431561	-6.57
246615_at	putative protein similar to unknown	---	---	-1.10	-0.14	-1.14	0.293705	0.431789	-6.57
247629_at	putative protein	SIZ1	AT5G60410	-1.11	-0.15	-1.14	0.293715	0.431789	-6.57
247577_at	putative protein flavin-containing m	---	AT5G61290	1.10	0.14	1.14	0.293789	0.43187	-6.57
264710_at	putative phytochelatin synthetase s	COBL6	AT1G09790	-1.09	-0.13	-1.14	0.293888	0.431988	-6.57
246329_at	putative protein gamma-tubulin inte	---	AT3G43610	-1.11	-0.15	-1.14	0.294025	0.432161	-6.57
265935_at	putative senescence-associated pro	TET2	AT2G19580	-1.16	-0.22	-1.14	0.294159	0.432323	-6.57
264166_at	unknown protein ; supported by cDI	---	AT1G65370	-1.10	-0.14	-1.14	0.294173	0.432323	-6.57
262363_at	disease resistance protein, putative	---	AT1G72850	-1.09	-0.13	-1.14	0.29422	0.432365	-6.57
262099_s_a	auxin-regulated protein GH3, putat	GH3.4	AT1G59500	1.66	0.73	1.14	0.294249	0.43238	-6.57
250005_at	putative protein predicted proteins,	---	AT5G18760	1.08	0.12	1.14	0.2943	0.432427	-6.57
250814_at	E2, ubiquitin-conjugating enzyme,	UBC22	AT5G05080	1.11	0.15	1.14	0.294375	0.432508	-6.57
259061_at	putative GTP-binding protein simila	AtRABA5b	AT3G07410	1.20	0.26	1.14	0.29447	0.432599	-6.57
252988_at	putative cold-regulated protein cold	---	AT4G38410	-1.19	-0.25	-1.14	0.294475	0.432599	-6.57
258825_at	unknown protein	---	AT3G07180	1.08	0.11	1.14	0.294501	0.432609	-6.57
253346_at	hypothetical protein	---	AT4G33600	-1.09	-0.12	-1.14	0.29476	0.432962	-6.57
249638_at	acetyl-CoA synthetase ; supported	---	AT5G36880	1.26	0.33	1.14	0.294822	0.433011	-6.57
265632_at	hypothetical protein predicted by ge	---	AT2G14290	1.67	0.74	1.14	0.294831	0.433011	-6.57
248262_at	Avr9 elicitor response protein-like ;	---	AT5G53340	-1.13	-0.18	-1.14	0.294892	0.433073	-6.57
265869_at	putative two-component response r	ARR14	AT2G01760	-1.13	-0.17	-1.14	0.294929	0.433099	-6.57
252487_at	glucosyltransferase-like protein UD	UGT76E12	AT3G46660	1.51	0.60	1.14	0.294968	0.433128	-6.58
249514_at	14-3-3 protein GF14psi (grf3/RCI1)	GRF3	AT5G38480	1.11	0.14	1.14	0.295017	0.433173	-6.58
258932_at	hypothetical protein predicted by ge	PAP16	AT3G10150	1.09	0.12	1.14	0.295146	0.433334	-6.58
245875_at	hypothetical protein predicted by ge	---	AT1G26240	-1.12	-0.16	-1.14	0.295167	0.433336	-6.58
247943_at	light-inducible protein ATLS1-like ;s	---	AT5G57170	1.17	0.23	1.13	0.295293	0.433478	-6.58

266886_at	Expressed protein ; supported by fu	---	AT2G44745	-1.11	-0.15	-1.13	0.295334	0.433478	-6.58
259301_at	hypothetical protein predicted by ge	---	AT3G05110	1.13	0.18	1.13	0.295344	0.433478	-6.58
248808_at	putative protein contains similarity t	---	AT5G47510	-1.07	-0.10	-1.13	0.295357	0.433478	-6.58
265752_at	putative Athila retroelement ORF1 p	---	---	-1.09	-0.12	-1.13	0.295358	0.433478	-6.58
267019_at	hypothetical protein predicted by ge	---	AT2G39130	-1.11	-0.15	-1.13	0.295494	0.433649	-6.58
263284_at	unknown protein	---	AT2G36100	-1.09	-0.13	-1.13	0.295622	0.43381	-6.58
266031_at	hypothetical protein predicted by ge	---	---	-1.09	-0.12	-1.13	0.29569	0.433881	-6.58
259445_at	dioxygenase, putative similar to dio	GA2OX6	AT1G02400	-1.70	-0.77	-1.13	0.295761	0.433948	-6.58
252029_s_a	putative RNA binding protein heter	---	AT3G52660	1.08	0.11	1.13	0.295773	0.433948	-6.58
261056_at	hypothetical protein similar to hypot	---	AT1G01360	1.14	0.19	1.13	0.295871	0.434048	-6.58
260161_at	hypothetical protein similar to putati	ROPGEF12	AT1G79860	1.08	0.11	1.13	0.29588	0.434048	-6.58
246500_at	putative protein HR21spA protein i	SYN4	AT5G16270	1.10	0.14	1.13	0.295938	0.434087	-6.58
251300_at	hypothetical protein ;supported by	---	AT3G61980	-1.14	-0.18	-1.13	0.295944	0.434087	-6.58
264570_at	unknown protein Similar to Caenorh	---	AT1G05350	-1.11	-0.15	-1.13	0.296169	0.434389	-6.58
263544_at	putative ADP-glucose pyrophospho	APL4	AT2G21590	-1.11	-0.15	-1.13	0.296293	0.434543	-6.58
267190_at	putative N-myristoyltransferase ; su	NMT2	AT2G44170	-1.09	-0.13	-1.13	0.29632	0.434555	-6.58
255862_at	hypothetical protein predicted by ge	---	AT2G30300	-1.10	-0.13	-1.13	0.296371	0.434601	-6.58
255765_at	protein kinase, putative contains P	---	AT1G16760	-1.07	-0.10	-1.13	0.296446	0.434684	-6.58
246713_at	mRNA capping enzyme - like capp	---	AT5G28210	-1.12	-0.16	-1.13	0.296493	0.434725	-6.58
265859_at	hypothetical protein predicted by ge	---	---	-1.09	-0.13	-1.13	0.296549	0.434779	-6.58
249695_at	putative protein similar to unknown	---	---	1.09	0.12	1.13	0.296724	0.435007	-6.58
246273_at	globulin-like protein	---	AT4G36700	-1.08	-0.11	-1.13	0.296767	0.435041	-6.58
259480_at	hypothetical protein predicted by ge	---	AT1G19010	1.13	0.18	1.13	0.296877	0.435175	-6.58
249126_at	Expressed protein ; supported by cl	TOPP6	AT5G43380	1.22	0.29	1.13	0.296963	0.435274	-6.58
258224_at	LEA76 homologue type2 identical to	---	AT3G15670	-1.08	-0.12	-1.13	0.297017	0.435325	-6.58
255625_at	GBF2, G-box binding factor ;suppo	GBF2	AT4G01120	1.16	0.21	1.13	0.297043	0.435327	-6.58
259808_at	hypothetical protein contains Pfam	---	AT1G49790	-1.08	-0.11	-1.13	0.297057	0.435327	-6.58
246448_at	putative protein putative N-acetlytra	---	AT5G16800	-1.10	-0.14	-1.13	0.297159	0.435419	-6.58
258510_at	hypothetical protein predicted by ge	---	AT3G06600	-1.10	-0.14	-1.13	0.297164	0.435419	-6.58
265839_at	putative serpin	---	AT2G14540	-1.10	-0.13	-1.13	0.297177	0.435419	-6.58
256903_at	hypothetical protein	---	AT3G23960	-1.09	-0.13	-1.13	0.297253	0.435503	-6.58
255987_s_a	putative protein predicted proteins,	---	AT5G35050	1.08	0.11	1.13	0.297426	0.435729	-6.58
263077_at	putative mitotic control protein dis3	EMB2763	AT2G17510	1.08	0.11	1.13	0.297545	0.435875	-6.58
249756_at	Expressed protein ; supported by fu	---	AT5G24313	-1.08	-0.12	-1.13	0.297671	0.436031	-6.58
250534_at	NADH dehydrogenase ;supported	CI51	AT5G08530	-1.09	-0.12	-1.13	0.297735	0.436096	-6.58

253141_at	putative protein hypothetical protei	---	AT4G35430	1.11	0.15	1.13	0.29778	0.436122	-6.58
252342_at	endo-polygalacturonase - like prote	---	AT3G48950	-1.07	-0.10	-1.13	0.2978	0.436122	-6.58
251702_at	transcription factor-like protein mot	BZIP49	AT3G56660	-1.13	-0.17	-1.13	0.29782	0.436122	-6.58
251111_at	putative protein different hypothetic	---	AT5G01310	1.10	0.14	1.13	0.29784	0.436122	-6.58
249868_at	senescence-associated protein 5-lik	TET12	AT5G23030	-1.10	-0.13	-1.13	0.297848	0.436122	-6.58
254914_at	peroxidase ATP19a	---	AT4G11290	-1.51	-0.60	-1.13	0.297955	0.43625	-6.58
246228_at	peroxidase like protein	---	AT4G36430	1.43	0.51	1.13	0.298265	0.436677	-6.58
257929_at	RNA Polymerase II subunit 14.5 kD	NRPB9A	AT3G16980	1.10	0.14	1.13	0.298379	0.436816	-6.58
267023_at	putative protein transport protein SE	---	AT2G34250	-1.11	-0.16	-1.13	0.29845	0.436892	-6.58
257803_at	unknown protein	---	AT3G18790	1.09	0.12	1.13	0.298483	0.436902	-6.58
252238_at	peroxidase ATP21a	---	AT3G49960	-1.10	-0.13	-1.13	0.298496	0.436902	-6.58
251120_at	chloroplast ribosomal L1 - like prot	---	AT3G63490	-1.12	-0.16	-1.13	0.298564	0.436974	-6.58
AFFX-Athal-	Arabidopsis thaliana /REF=U84969	---	---	1.10	0.14	1.13	0.298785	0.43727	-6.59
258909_at	putative DnaJ protein Pfam HMM h	---	AT3G06340	1.08	0.10	1.13	0.298986	0.437536	-6.59
249399_at	putative protein intracellular protein	---	AT5G40290	-1.07	-0.10	-1.13	0.299036	0.43756	-6.59
248178_at	root cap protein 2-like protein	---	AT5G54370	-1.12	-0.17	-1.13	0.299041	0.43756	-6.59
245762_at	ATP-dependent DNA helicase Rec	---	AT1G27880	-1.07	-0.10	-1.12	0.299118	0.437644	-6.59
245633_at	unknown protein similar to putative	AtTLP10	AT1G25280	-1.07	-0.10	-1.12	0.299247	0.437782	-6.59
248051_at	Atmyb103 (gb|AAD40692.1)	ATMYB103	AT5G56110	-1.10	-0.13	-1.12	0.299264	0.437782	-6.59
258271_at	hypothetical protein predicted by ge	---	AT3G15605	-1.10	-0.14	-1.12	0.299269	0.437782	-6.59
246285_at	putative protein	---	AT4G36980	1.08	0.11	1.12	0.299351	0.437862	-6.59
250500_at	periaxin - like protein periaxin, Ratt	---	AT5G09530	-2.44	-1.28	-1.12	0.299362	0.437862	-6.59
262792_at	hypothetical protein predicted by ge	---	AT1G10710	-1.09	-0.13	-1.12	0.299434	0.437939	-6.59
258443_at	unknown protein	---	AT3G22290	1.11	0.15	1.12	0.299549	0.438043	-6.59
259680_at	putative AUX1-like permease simil	LAX3	AT1G77690	-1.50	-0.58	-1.12	0.299559	0.438043	-6.59
256562_at	Ty1/Copia-type retroelement polypr	---	---	1.09	0.12	1.12	0.299563	0.438043	-6.59
251571_at	putative protein several hypothetica	---	AT3G58330	-1.08	-0.12	-1.12	0.299615	0.438068	-6.59
265401_at	hypothetical protein predicted by ge	---	AT2G10970	-1.09	-0.12	-1.12	0.299618	0.438068	-6.59
260947_at	fructokinase, putative similar to fru	---	AT1G06020	-1.07	-0.10	-1.12	0.29968	0.43813	-6.59
256775_at	hypothetical protein predicted by ge	---	AT3G13770	1.16	0.21	1.12	0.299705	0.438139	-6.59
257549_at	hypothetical protein predicted by g	agl103	AT3G18650	-1.12	-0.16	-1.12	0.299751	0.438178	-6.59
251203_at	putative protein putative transcripti	---	AT3G63070	1.08	0.11	1.12	0.299824	0.438256	-6.59
265655_at	unknown protein contains weak PH	---	AT2G13920	-1.09	-0.13	-1.12	0.29987	0.438296	-6.59
246247_at	putative protein	---	AT4G36640	1.32	0.40	1.12	0.299911	0.438327	-6.59
254342_at	receptor like protein (fragment) ES	---	AT4G22140	-1.08	-0.11	-1.12	0.299967	0.438381	-6.59

262389_at	hypothetical protein contains simila	---	AT1G49270	-1.09	-0.12	-1.12	0.300038	0.438447	-6.59
254491_at	putative protein hypothetical protein	---	AT4G20300	-1.14	-0.18	-1.12	0.300069	0.438447	-6.59
266742_at	predicted by genefinder and gensca	---	AT2G03050	-1.09	-0.12	-1.12	0.30007	0.438447	-6.59
250580_at	glutamate dehydrogenase 2 ; supp	GDH2	AT5G07440	-1.23	-0.30	-1.12	0.300176	0.438575	-6.59
255363_x_a	hypothetical protein	---	---	-1.14	-0.19	-1.12	0.30026	0.438668	-6.59
245549_at	cellulose synthase like protein	ATCSLB06	AT4G15320	-1.09	-0.13	-1.12	0.300318	0.438726	-6.59
252259_at	putative protein acidic ribosomal pr	---	AT3G49460	-1.14	-0.19	-1.12	0.300382	0.438784	-6.59
261290_at	hypothetical protein predicted by ge	---	AT1G36990	1.14	0.19	1.12	0.300397	0.438784	-6.59
253634_at	putative protein ENOD20 gene pro	---	AT4G30590	-1.07	-0.10	-1.12	0.300419	0.438789	-6.59
258795_at	hypothetical protein similar to putat	---	AT3G04570	-1.12	-0.16	-1.12	0.300494	0.43887	-6.59
257096_at	hypothetical protein	---	AT3G30820	-1.09	-0.12	-1.12	0.300773	0.439225	-6.59
247347_at	putative protein similar to unknown	SHA1	AT5G63780	-1.24	-0.31	-1.12	0.300775	0.439225	-6.59
253784_at	putative protein WREBP-1, Nicotia	PHR1	AT4G28610	1.10	0.14	1.12	0.300832	0.439279	-6.59
262725_at	hypothetical protein predicted by ge	---	AT1G43580	1.18	0.24	1.12	0.300872	0.43931	-6.59
245535_at	cell wall protein like	---	AT4G15160	-1.11	-0.15	-1.12	0.300915	0.439343	-6.59
246357_x_a	hypothetical protein	---	---	-1.10	-0.13	-1.12	0.300985	0.439418	-6.59
261616_at	NAC domain containing protein, pu	ANAC014	AT1G33060	1.07	0.10	1.12	0.301033	0.43946	-6.59
260234_at	putative lipase/acylhydrolase contai	---	AT1G74460	-1.13	-0.18	-1.12	0.301063	0.439475	-6.59
254609_at	Expressed protein ; supported by fu	---	AT4G18970	-1.26	-0.34	-1.12	0.301111	0.439518	-6.59
264841_at	putative protein kinase similar to (Z	---	AT1G03740	1.23	0.29	1.12	0.301168	0.439564	-6.59
263894_at	putative cytochrome P450	CYP96A5	AT2G21910	-1.10	-0.14	-1.12	0.301181	0.439564	-6.59
245279_at	putative protein ; supported by cDN	---	AT4G17270	-1.09	-0.12	-1.12	0.301214	0.439584	-6.59
265804_at	putative peptide methionine sulfoxid	---	AT2G18030	-1.08	-0.11	-1.12	0.301267	0.439633	-6.59
260333_at	putative polygalacturonase similar t	---	AT1G70500	-1.15	-0.20	-1.12	0.301373	0.439744	-6.59
246289_at	putative protein predicted protein A	---	AT3G56880	-1.18	-0.24	-1.12	0.301419	0.439744	-6.59
267073_at	unknown protein	---	AT2G41160	1.12	0.17	1.12	0.30143	0.439744	-6.59
251757_at	Ca-dependent solute carrier - like p	---	AT3G55640	-1.15	-0.20	-1.12	0.301437	0.439744	-6.59
245682_at	Expressed protein ; supported by cl	---	AT5G08750	-1.10	-0.13	-1.12	0.30144	0.439744	-6.59
247683_at	serine/threonine-specific protein ki	---	AT5G59660	-1.11	-0.15	-1.12	0.301468	0.439757	-6.59
253177_s_a	O-methyltransferase - like protein c	---	AT4G35150	-1.15	-0.20	-1.12	0.301519	0.439794	-6.59
254416_at	receptor-like serine/threonine protei	ARK3	AT4G21380	1.34	0.42	1.12	0.301532	0.439794	-6.59
266242_at	hypothetical protein predicted by ge	---	AT2G27790	1.09	0.12	1.12	0.301644	0.43993	-6.59
253642_at	hypothetical protein ;supported by	---	AT4G29960	1.12	0.16	1.12	0.301837	0.44018	-6.59
258315_at	Expressed protein ; supported by fu	---	AT3G16175	1.10	0.14	1.12	0.301854	0.44018	-6.59
252570_at	isovaleryl-CoA-dehydrogenase prec	IVD	AT3G45300	1.22	0.28	1.12	0.301963	0.44031	-6.59

264741_at	aspartic protease, putative similar t	---	AT1G62290	-1.33	-0.41	-1.12	0.301999	0.440334	-6.59
267516_at	unknown protein	RPT2	AT2G30520	-1.11	-0.15	-1.12	0.302032	0.440341	-6.59
247475_at	IRE (root hair elongation)	IRE	AT5G62310	-1.09	-0.12	-1.12	0.302045	0.440341	-6.59
261508_at	unknown protein	---	AT1G71730	-1.10	-0.14	-1.12	0.302061	0.440341	-6.59
255643_at	hypothetical protein	---	AT4G00840	-1.09	-0.12	-1.12	0.302173	0.440477	-6.59
263683_at	putative NAM protein similar to GB	FEZ	AT1G26870	-1.10	-0.13	-1.12	0.302215	0.440508	-6.59
262885_at	alpha-tubulin, putative similar to alp	TUA1	AT1G64740	-1.11	-0.15	-1.12	0.302268	0.440558	-6.60
257649_at	predicted protein	ARR1	AT3G16857	-1.09	-0.12	-1.12	0.302289	0.440561	-6.60
263392_at	putative PttA-like transposon protei	---	---	-1.08	-0.11	-1.12	0.302317	0.440572	-6.60
265349_at	putative kinesin heavy chain	---	AT2G22610	-1.11	-0.15	-1.12	0.302339	0.440577	-6.60
259697_at	putative DNA-binding protein simila	---	AT1G68920	1.09	0.12	1.12	0.302476	0.440749	-6.60
258895_at	putative epoxide hydrolase similar t	---	AT3G05600	-1.08	-0.10	-1.12	0.302511	0.440771	-6.60
266409_at	hypothetical protein predicted by gr	---	AT2G38510	-1.11	-0.15	-1.12	0.302626	0.440911	-6.60
250993_at	putative protein HSPC172, Homo s	---	AT5G02280	-1.10	-0.14	-1.12	0.302665	0.44094	-6.60
261792_at	cinnamoyl CoA reductase, puitative	CCR1	AT1G15950	-1.11	-0.15	-1.12	0.302724	0.440988	-6.60
249736_at	unknown protein	---	AT5G24460	-1.07	-0.10	-1.12	0.302737	0.440988	-6.60
263264_at	histone H2A ; supported by full-len	HTA8	AT2G38810	1.17	0.23	1.12	0.302872	0.441156	-6.60
254280_at	Expressed protein ; supported by fu	SMO1-2	AT4G22756	1.14	0.19	1.12	0.302997	0.44131	-6.60
249688_at	putative protein tyrosine aminotrans	---	AT5G36160	-1.12	-0.17	-1.11	0.303088	0.441411	-6.60
251954_at	putative protein predicted protein, A	CPuORF51	AT3G53668	-1.22	-0.29	-1.11	0.303105	0.441411	-6.60
251780_s_a	beta-ketoacyl-ACP reductase - like	---	AT3G55290	-1.16	-0.22	-1.11	0.303149	0.441448	-6.60
252987_at	putative growth regulator protein a	---	AT4G38390	-1.11	-0.15	-1.11	0.303179	0.441463	-6.60
254459_at	gibberellin 20-oxidase - like protein	GA2OX8	AT4G21200	-1.08	-0.11	-1.11	0.303201	0.441467	-6.60
246799_at	putative protein various predicted b	---	AT5G26940	-1.13	-0.18	-1.11	0.303223	0.441471	-6.60
263444_at	putative MADS-box protein	AGL46	AT2G28700	-1.11	-0.15	-1.11	0.303302	0.441557	-6.60
258032_at	hypothetical protein predicted by ge	---	AT3G21170	-1.13	-0.18	-1.11	0.303346	0.441593	-6.60
246113_at	putative protein predicted proteins -	---	---	-1.08	-0.12	-1.11	0.303508	0.441801	-6.60
253869_at	hypothetical protein	---	AT4G27510	-1.12	-0.16	-1.11	0.303558	0.441845	-6.60
250224_at	putative protein similar to unknown	---	AT5G14150	-1.13	-0.17	-1.11	0.303714	0.442044	-6.60
260631_at	hypothetical protein predicted by ge	---	AT1G62350	1.11	0.15	1.11	0.303806	0.44215	-6.60
257665_at	unknown protein	---	AT3G20430	1.09	0.12	1.11	0.303889	0.442243	-6.60
267231_at	putative inositol polyphosphate 5'-p	---	AT2G43900	1.09	0.13	1.11	0.303986	0.442356	-6.60
264905_at	putative Mlo protein	MLO7	AT2G17430	-1.09	-0.12	-1.11	0.304021	0.442378	-6.60
266162_at	putative bHLH transcription factor	FRU	AT2G28160	-1.10	-0.13	-1.11	0.304156	0.442504	-6.60
263241_at	arginine decarboxylase identical to	ADC1	AT2G16500	1.33	0.41	1.11	0.304163	0.442504	-6.60

247084_at	NAM (no apical meristem)-like prote	NAC105	AT5G66300	1.09	0.12	1.11	0.304166	0.442504	-6.60
262650_at	lipoamide dehydrogenase, putative	---	AT1G14090	1.07	0.09	1.11	0.304203	0.44253	-6.60
260108_at	hypothetical protein similar to putati	---	AT1G63280	-1.10	-0.14	-1.11	0.304237	0.442551	-6.60
257748_at	hypothetical protein predicted by ge	PUB29	AT3G18710	1.77	0.83	1.11	0.304402	0.442763	-6.60
260142_at	unknown protein ; supported by cD	---	AT1G71900	-1.11	-0.15	-1.11	0.304485	0.442855	-6.60
265281_at	unknown protein ; supported by ful	---	AT2G28370	-1.11	-0.16	-1.11	0.304618	0.44302	-6.60
263292_at	putative Ta11-like non-LTR retroele	---	---	-1.09	-0.13	-1.11	0.304888	0.443386	-6.60
252428_at	putative protein rjs - Mus musculus	---	AT3G47660	-1.11	-0.14	-1.11	0.304947	0.443443	-6.60
252509_at	putative protein serine/threonine-sp	---	AT3G46240	-1.07	-0.10	-1.11	0.30498	0.443463	-6.60
250360_at	putative protein probable serine/thr	---	AT5G11360	-1.09	-0.12	-1.11	0.305212	0.443771	-6.60
252906_at	putative gamma-glutamyltransferas	GGT1	AT4G39640	-1.18	-0.24	-1.11	0.305255	0.443806	-6.60
255234_at	contains similarity to Medicago trun	---	AT4G05500	-1.09	-0.13	-1.11	0.305415	0.44401	-6.60
245680_at	hypothetical protein contains simila	---	AT1G56570	1.09	0.12	1.11	0.3057	0.444396	-6.60
248013_at	putative protein contains similarity t	ACA8	AT5G56330	-1.13	-0.18	-1.11	0.305793	0.444485	-6.60
263139_at	hypothetical protein similar to hypot	---	AT1G65110	-1.07	-0.10	-1.11	0.3058	0.444485	-6.60
253192_at	putative protein nuclear phosphopr	---	AT4G35370	-1.08	-0.11	-1.11	0.305874	0.444564	-6.60
255193_at	score=10.1, E=1.2, N=1 contains s	VFB3	AT4G07400	1.10	0.14	1.11	0.306148	0.444934	-6.61
259826_at	arm repeat-containing protein, puta	PUB17	AT1G29340	-1.15	-0.21	-1.11	0.306172	0.44494	-6.61
252800_at	putative protein	---	---	-1.09	-0.12	-1.11	0.306194	0.444944	-6.61
246963_at	putative protein nucleoid DNA-bind	---	AT5G24820	-1.11	-0.15	-1.11	0.3063	0.44507	-6.61
246828_at	putative protein hypothetical protei	---	---	-1.09	-0.12	-1.11	0.30632	0.44507	-6.61
250882_at	putative protein ;supported by full-l	---	AT5G04000	-1.09	-0.12	-1.11	0.306368	0.445111	-6.61
260709_at	hypothetical protein predicted by ge	ATNAP6	AT1G32500	-1.10	-0.14	-1.11	0.3064	0.445112	-6.61
248155_at	putative protein 3 (2'), 5'-bisphosph	AHL	AT5G54390	-1.11	-0.15	-1.11	0.306408	0.445112	-6.61
259767_s_a	unknown protein	---	AT1G29350	1.09	0.12	1.11	0.306426	0.445112	-6.61
245375_at	NAK like protein kinase	---	AT4G17660	-1.10	-0.14	-1.11	0.306479	0.44516	-6.61
258258_at	transcriptional regulator (FUSCA3)	FUS3	AT3G26790	-1.08	-0.11	-1.11	0.306534	0.445211	-6.61
245763_at	transposon protein, putative simila	---	AT1G27850	-1.08	-0.11	-1.11	0.306606	0.445288	-6.61
260536_at	putative electron transfer flavoprote	ETFQO	AT2G43400	1.17	0.23	1.11	0.306748	0.445441	-6.61
258890_at	putative transcription factor similar t	NF-YA2	AT3G05690	1.17	0.22	1.11	0.306751	0.445441	-6.61
256334_at	oligopeptide transporter, putative s	---	AT1G72120	-1.14	-0.18	-1.11	0.306837	0.445538	-6.61
265876_at	putative receptor-like protein kinase	---	AT2G42290	1.08	0.11	1.11	0.306894	0.445574	-6.61
254849_at	putative protein RNA splicing-relate	---	AT4G11970	1.07	0.10	1.11	0.306901	0.445574	-6.61
256565_at	hypothetical protein	AT3G1951	---	-1.09	-0.12	-1.11	0.307072	0.445793	-6.61
266035_at	enoyl-ACP reductase (enr-A)	MOD1	AT2G05990	-1.19	-0.25	-1.10	0.307105	0.445813	-6.61

267091_at	Expressed protein ; supported by fu	---	AT2G38185	1.15	0.20	1.10	0.307236	0.44595	-6.61
264393_at	unknown protein Contains similarity	---	AT1G11880	-1.09	-0.13	-1.10	0.307238	0.44595	-6.61
244961_at	hypothetical protein	---	---	1.08	0.11	1.10	0.307306	0.44602	-6.61
262627_at	hypothetical protein	---	AT1G06580	-1.10	-0.14	-1.10	0.307343	0.446045	-6.61
264116_at	putative poly (ADP-ribose) polymer	PARP2	AT2G31320	1.18	0.24	1.10	0.307473	0.446205	-6.61
259064_at	putative calmodulin similar to calm	AGD11	AT3G07490	-1.10	-0.14	-1.10	0.307598	0.446359	-6.61
260828_at	unknown protein	---	AT1G06750	1.09	0.12	1.10	0.307834	0.446672	-6.61
261180_at	hypothetical protein predicted by ge	---	---	-1.09	-0.12	-1.10	0.307864	0.446674	-6.61
265117_at	putative proline-rich cell wall protei	---	AT1G62500	-1.14	-0.19	-1.10	0.307874	0.446674	-6.61
263964_at	putative CCHC-type zinc finger prot	---	AT2G12880	-1.10	-0.14	-1.10	0.307905	0.44669	-6.61
252079_at	MAP kinase ; supported by cDNA:	CPuORF44	AT3G51630	1.08	0.11	1.10	0.308013	0.446818	-6.61
260887_at	ascorbate oxidase promoter-bindin	---	AT1G29160	-1.34	-0.42	-1.10	0.30818	0.447032	-6.61
263111_s_a	hypothetical protein contains simila	---	AT1G65190	1.13	0.18	1.10	0.308285	0.447139	-6.61
246735_at	histone H2A-like protein histone H2	HTA7	AT5G27670	-1.10	-0.14	-1.10	0.308292	0.447139	-6.61
247356_at	beta-galactosidase (emb|CAB6474	MUM2	AT5G63800	1.19	0.25	1.10	0.308335	0.447171	-6.61
265734_at	predicted by genscan and genefind	---	AT2G01260	1.09	0.12	1.10	0.308375	0.447185	-6.61
245545_at	UTP-glucose glucosyltransferase	UGT71B5	AT4G15280	1.12	0.16	1.10	0.308383	0.447185	-6.61
259972_at	unknown protein N-term similar to	CUC3	AT1G76420	-1.15	-0.20	-1.10	0.308552	0.447401	-6.61
267087_at	putative MYB family transcription fa	MYB101	AT2G32460	1.14	0.19	1.10	0.308648	0.447489	-6.61
250008_at	triacylglycerol lipase-like protein tri	---	AT5G18630	1.20	0.26	1.10	0.308652	0.447489	-6.61
249337_at	putative protein contains similarity t	---	AT5G41080	1.40	0.49	1.10	0.308676	0.447496	-6.61
250271_at	putative protein predicted protein, A	CLE40	AT5G12990	-1.08	-0.11	-1.10	0.308706	0.447511	-6.61
256893_x_a	unknown protein	---	---	1.07	0.10	1.10	0.30874	0.44752	-6.61
259151_at	kinesin-like protein similar to carbox	---	AT3G10310	-1.12	-0.16	-1.10	0.308751	0.44752	-6.61
248538_at	putative protein contains similarity t	---	AT5G50110	1.12	0.17	1.10	0.308835	0.447613	-6.61
255376_x_a	putative athila-like protein	---	---	-1.13	-0.17	-1.10	0.30891	0.447693	-6.61
254530_at	small GTP-binding protein - like GT	ARA7	AT4G19640	1.08	0.11	1.10	0.308965	0.447745	-6.61
254364_at	glycine-rich protein glycine-rich cel	---	AT4G22020	-1.11	-0.15	-1.10	0.308998	0.447764	-6.61
246938_at	cyclin 3a	CYCA2;1	AT5G25380	-1.11	-0.15	-1.10	0.309188	0.448011	-6.61
255900_at	hypothetical protein predicted by ge	---	AT1G17830	1.28	0.36	1.10	0.309279	0.448114	-6.61
254510_at	cadinene synthase like protein (+)-	---	AT4G20210	-1.12	-0.16	-1.10	0.309418	0.448287	-6.61
259831_at	hypothetical protein predicted by ge	ZFHD1	AT1G69600	-1.08	-0.12	-1.10	0.309493	0.448366	-6.61
259108_at	putative translationally controlled tu	---	AT3G05540	-1.08	-0.11	-1.10	0.309543	0.448411	-6.61
262724_s_a	PC-MYB2, putative similar to PC-M	---	AT1G43330	-1.08	-0.11	-1.10	0.309759	0.448696	-6.61
264812_at	putative thaumatin-like pathogenes	---	AT2G17860	1.08	0.11	1.10	0.309845	0.448768	-6.62

252430_at	CHLOROPHYLL A-B BINDING PR	LHCA4	AT3G47470	-1.11	-0.16	-1.10	0.309848	0.448768	-6.62
266043_at	hypothetical protein	---	AT2G07724	1.12	0.16	1.10	0.309872	0.448773	-6.62
265767_at	putative exonuclease contains zinc-	REF4	AT2G48110	1.10	0.14	1.10	0.310021	0.448942	-6.62
267085_at	putative cellulose synthase	ATCSLB02	AT2G32620	1.07	0.10	1.10	0.310028	0.448942	-6.62
250943_at	putative protein	---	AT5G03360	-1.08	-0.11	-1.10	0.310209	0.449151	-6.62
254558_at	Expressed protein ; supported by fu	---	AT4G19185	-1.08	-0.11	-1.10	0.310212	0.449151	-6.62
245313_at	UFD1 like protein ; supported by ful	---	AT4G15420	-1.11	-0.15	-1.10	0.31028	0.449222	-6.62
259065_at	unknown protein similar to putative	GLR1.4	AT3G07520	1.17	0.22	1.10	0.31031	0.449237	-6.62
257370_at	hypothetical protein predicted by ge	---	AT2G35080	-1.09	-0.13	-1.10	0.310427	0.449378	-6.62
247510_at	putative protein predicted proteins,	---	AT5G62030	1.11	0.16	1.10	0.31048	0.449426	-6.62
261099_at	expansin At-EXP6, putative similar	ATEXPA18	AT1G62980	-1.12	-0.16	-1.10	0.310522	0.449458	-6.62
253645_at	putative protein G protein beta sub	VIP3	AT4G29830	1.09	0.12	1.10	0.310621	0.449572	-6.62
258889_at	putative pectinesterase similar to pe	---	AT3G05610	-1.13	-0.17	-1.10	0.310658	0.449598	-6.62
257341_at	pseudogene, Mutator-like transpos	---	---	-1.08	-0.11	-1.10	0.310757	0.449712	-6.62
249884_at	Na+/H+ antiporter-like protein	CHX9	AT5G22910	-1.09	-0.13	-1.10	0.310819	0.449774	-6.62
263752_at	putative retroelement pol polyprotei	---	---	-1.12	-0.16	-1.10	0.3109	0.449862	-6.62
246267_at	Acyl CoA binding protein, putative	ACBP6	AT1G31812	1.08	0.11	1.10	0.311063	0.450053	-6.62
256170_at	receptor protein kinase, putative co	---	AT1G51790	-1.16	-0.22	-1.10	0.311071	0.450053	-6.62
262406_at	myb-related protein, putative simila	AtMYB93	AT1G34670	-1.11	-0.15	-1.09	0.311301	0.450357	-6.62
262422_at	hypothetical protein similar to hypot	---	AT1G23440	1.11	0.15	1.09	0.311364	0.450419	-6.62
255936_at	calcium dependent protein kinase,	---	AT1G12680	1.09	0.12	1.09	0.311403	0.450447	-6.62
248314_at	putative protein similar to unknown	---	AT5G52620	1.07	0.10	1.09	0.311471	0.450517	-6.62
257777_x_a	hypothetical protein	---	---	-1.10	-0.14	-1.09	0.311535	0.450552	-6.62
246578_at	MADS-box protein, putative similar	AGL86	AT1G31630	-1.08	-0.11	-1.09	0.311537	0.450552	-6.62
251970_at	glucosyltransferase - like protein gl	UGT73D1	AT3G53150	1.16	0.22	1.09	0.311554	0.450552	-6.62
266066_at	putative xyloglucan endo-transglyco	XTH21	AT2G18800	-1.13	-0.17	-1.09	0.31158	0.45056	-6.62
255921_at	hypothetical protein contains Pfam	APUM8	AT1G22240	1.09	0.13	1.09	0.311672	0.450665	-6.62
254383_at	hypothetical protein	---	AT4G21950	-1.09	-0.12	-1.09	0.311753	0.450754	-6.62
252311_at	calcium dependent protein kinase -	---	AT3G49370	1.23	0.30	1.09	0.311783	0.450762	-6.62
247034_at	cyclin D3-like protein ;supported by	CYCD3;2	AT5G67260	1.13	0.18	1.09	0.311826	0.450762	-6.62
246129_at	putative protein predicted protein, /	---	---	-1.07	-0.10	-1.09	0.311835	0.450762	-6.62
254866_at	putative protein other predicted pro	---	AT4G12220	1.07	0.10	1.09	0.311839	0.450762	-6.62
245259_at	kinesin like protein ; supported by c	PAKRP1	AT4G14150	-1.08	-0.11	-1.09	0.311858	0.450762	-6.62
248498_at	selenium-binding protein-like	---	AT5G50390	-1.09	-0.12	-1.09	0.312015	0.45096	-6.62
253225_at	Rho1Ps homolog Rac-like protein ;	ARAC3	AT4G35020	-1.10	-0.14	-1.09	0.312047	0.450978	-6.62

265378_at	putative GATA-type zinc finger tran	---	AT2G18380	-1.09	-0.12	-1.09	0.312084	0.451004	-6.62
260990_at	hypothetical protein predicted by ge	---	AT1G12180	-1.12	-0.16	-1.09	0.312296	0.451265	-6.62
246854_at	mitochondrial carrier - like protein r	---	AT5G26200	-1.10	-0.14	-1.09	0.312351	0.451265	-6.62
251848_at	Expressed protein ; supported by cl	BZIP25	AT3G54620	1.10	0.13	1.09	0.312356	0.451265	-6.62
247950_at	unknown protein	---	AT5G57230	1.09	0.12	1.09	0.312361	0.451265	-6.62
265213_at	clathrin protein family Similar to cla	---	AT1G05020	-1.13	-0.18	-1.09	0.312364	0.451265	-6.62
263587_at	putative synaptobrevin	ATVAMP71	AT2G25340	1.10	0.13	1.09	0.312422	0.45132	-6.62
245600_at	hypothetical protein	---	AT4G14230	-1.12	-0.16	-1.09	0.312493	0.451395	-6.62
266953_at	hypothetical protein predicted by ge	---	AT2G34540	-1.09	-0.12	-1.09	0.312551	0.45145	-6.62
258387_at	hypothetical protein predicted by ge	---	AT3G15550	-1.10	-0.14	-1.09	0.312753	0.451713	-6.62
250346_at	lysine decarboxylase - like protein	---	AT5G11950	1.27	0.34	1.09	0.312793	0.451742	-6.62
248363_at	nodulin-like protein	---	AT5G52480	-1.08	-0.11	-1.09	0.312917	0.451893	-6.62
254437_s_a	putative protein	---	AT3G06433	-1.15	-0.20	-1.09	0.313015	0.452005	-6.62
256128_at	laccase, putative similar to high-pl	LAC1	AT1G18140	-1.10	-0.14	-1.09	0.313113	0.452091	-6.62
245058_at	hypothetical protein predicted by ge	---	AT2G39790	-1.09	-0.12	-1.09	0.313114	0.452091	-6.62
250853_s_a	putative protein prtedicted prteins,	---	AT5G04680	-1.07	-0.10	-1.09	0.313136	0.452094	-6.62
254691_at	hypothetical protein ; supported by	---	AT4G17840	1.15	0.21	1.09	0.313163	0.452105	-6.62
250652_at	putative protein similar to unknown	FLA21	AT5G06920	-1.09	-0.12	-1.09	0.313268	0.452227	-6.62
266277_at	putative tropinone reductase	---	AT2G29310	1.10	0.14	1.09	0.313332	0.452291	-6.62
245001_at	PSII low MW protein	---	---	1.10	0.14	1.09	0.313362	0.452306	-6.62
259851_at	kinesin, putative	---	AT1G72250	-1.08	-0.11	-1.09	0.313616	0.452643	-6.63
250556_at	diacylglycerol kinase (ATDGK1) ; su	DGK1	AT5G07920	1.20	0.27	1.09	0.313659	0.452658	-6.63
252813_at	putative protein several hypothetica	---	---	-1.08	-0.12	-1.09	0.313666	0.452658	-6.63
252801_at	putative protein various predicted H	---	---	-1.08	-0.11	-1.09	0.313695	0.452672	-6.63
246753_at	putative protein	---	---	-1.11	-0.14	-1.09	0.313817	0.45282	-6.63
257859_at	Expressed protein ; supported by fu	---	AT3G12955	-1.10	-0.14	-1.09	0.313889	0.452894	-6.63
245369_at	Expressed protein ; supported by fu	---	AT4G15975	1.18	0.24	1.09	0.313947	0.452922	-6.63
257303_at	hypothetical protein predicted by ge	---	AT3G30230	-1.09	-0.12	-1.09	0.313948	0.452922	-6.63
249689_at	putative protein similar to unknown	---	AT5G36190	-1.07	-0.10	-1.09	0.314126	0.45315	-6.63
260099_at	unknown protein ;supported by full-	---	AT1G73180	1.08	0.11	1.09	0.314185	0.453182	-6.63
252296_at	putative protein GMFP7 isoprenyla	---	AT3G48970	-1.16	-0.22	-1.09	0.314188	0.453182	-6.63
248428_at	protein phosphatase-2C; PP2C-like	AHG1	AT5G51760	-1.08	-0.11	-1.09	0.314266	0.453266	-6.63
258019_at	hypothetical protein predicted by ge	---	AT3G19470	-1.08	-0.12	-1.09	0.314338	0.453342	-6.63
246902_at	putative protein	---	AT5G25640	-1.08	-0.11	-1.09	0.314432	0.453448	-6.63
250590_at	exonuclease-like protein	---	AT5G07710	-1.08	-0.12	-1.09	0.314474	0.45348	-6.63

257326_s_a	hypothetical protein	---	---	-1.11	-0.15	-1.09	0.314664	0.453725	-6.63
252274_at	branched-chain-amino-acid transar	BCAT3	AT3G49680	-1.09	-0.12	-1.09	0.314831	0.453921	-6.63
267139_s_a	hypothetical protein predicted by ge	---	AT2G38195	-1.08	-0.10	-1.09	0.314839	0.453921	-6.63
254246_at	protein kinase - like protein recepto	EMB1290	AT4G23250	-1.08	-0.11	-1.09	0.314923	0.454013	-6.63
250870_at	hypothetical protein	---	AT5G03920	-1.09	-0.12	-1.09	0.315061	0.454183	-6.63
246687_at	putative protein proline-rich protein	---	AT5G33370	-1.12	-0.16	-1.09	0.315081	0.454183	-6.63
263790_at	hypothetical protein predicted by ge	---	AT2G24530	1.12	0.16	1.09	0.31511	0.454196	-6.63
263016_at	ubiquitin extension protein, putative	---	AT1G23410	1.10	0.14	1.08	0.315261	0.454336	-6.63
250211_at	unknown protein ; supported by cD	---	AT5G13880	-1.09	-0.12	-1.08	0.315261	0.454336	-6.63
249107_at	unknown protein	---	AT5G43680	1.09	0.12	1.08	0.315267	0.454336	-6.63
254467_at	receptor protein kinase - like protei	---	AT4G20450	-1.10	-0.14	-1.08	0.315326	0.454393	-6.63
256291_at	protein kinase, putative contains P	AtNek7	AT3G12200	1.10	0.14	1.08	0.315358	0.45441	-6.63
253741_at	putative protein various hypothetica	---	AT4G28890	1.08	0.11	1.08	0.315439	0.454471	-6.63
254158_at	putative protein dihydrofolate reduc	---	AT4G24380	-1.45	-0.53	-1.08	0.315455	0.454471	-6.63
246202_at	methionyl aminopeptidase-like prote	MAP1D	AT4G37040	-1.13	-0.18	-1.08	0.315477	0.454471	-6.63
267203_at	hypothetical protein predicted by ge	---	AT2G31035	1.07	0.09	1.08	0.31548	0.454471	-6.63
253411_at	homeobox gene ATH1	ATH1	AT4G32980	1.19	0.25	1.08	0.315512	0.454488	-6.63
259669_at	short chain alcohol dehydrogenase	ABA2	AT1G52340	1.11	0.15	1.08	0.315549	0.454513	-6.63
262582_at	hypothetical protein Is a member of	---	AT1G15410	-1.27	-0.35	-1.08	0.315579	0.454528	-6.63
254756_at	putative protein late embryogenesi	EDA21	AT4G13235	-1.09	-0.12	-1.08	0.315698	0.454671	-6.63
247070_at	Expressed protein ; supported by fu	---	AT5G66815	-1.10	-0.13	-1.08	0.315739	0.454681	-6.63
247304_at	amino acid transporter AAP4 (pir||S	AAP4	AT5G63850	-1.14	-0.19	-1.08	0.315745	0.454681	-6.63
248922_at	putative protein contains similarity t	WOX8	AT5G45980	-1.08	-0.11	-1.08	0.315766	0.454683	-6.63
246690_at	hypothetical protein	---	---	-1.09	-0.13	-1.08	0.31585	0.454774	-6.63
257230_at	DegP protease contains similarity to	DegP11	AT3G16540	-1.07	-0.10	-1.08	0.315921	0.454848	-6.63
264940_at	galactinol synthase, putative simila	AtGolS4	AT1G60470	1.32	0.40	1.08	0.316033	0.454981	-6.63
249189_at	putative protein similar to unknown	AtHB27	AT5G42780	-1.14	-0.18	-1.08	0.316078	0.45499	-6.63
256017_at	unknown protein ;supported by full-	JAZ1	AT1G19180	-1.32	-0.40	-1.08	0.31608	0.45499	-6.63
265503_at	putative non-LTR retroelement reve	---	---	-1.12	-0.16	-1.08	0.316141	0.45503	-6.63
251241_s_a	putative protein hypothetical protein	---	AT3G62460	-1.13	-0.17	-1.08	0.316147	0.45503	-6.63
247105_at	putative protein similar to unknown	DAR5	AT5G66630	1.12	0.17	1.08	0.316297	0.455217	-6.63
245798_at	hypothetical protein predicted by ge	---	AT1G45545	1.07	0.10	1.08	0.316569	0.455579	-6.63
249603_at	putative protein predicted proteins,	---	AT5G37210	-1.08	-0.12	-1.08	0.316693	0.455703	-6.63
256906_at	hypothetical protein contains Pfam	---	AT3G24000	1.11	0.15	1.08	0.316694	0.455703	-6.63
248992_at	disease resistance protein RPS4	---	AT5G45230	-1.09	-0.13	-1.08	0.316784	0.455803	-6.63

250014_at	anthranilate phosphoribosyltransfe	TRP1	AT5G17990	-1.36	-0.44	-1.08	0.316919	0.455968	-6.63
261320_at	unknown protein ; supported by cDI	---	AT1G53120	1.08	0.11	1.08	0.316942	0.455972	-6.63
250275_at	putative protein mRNA, Moritella m	---	AT5G13030	-1.12	-0.17	-1.08	0.316979	0.455997	-6.63
263368_at	putative protein kinase contains a p	---	AT2G20470	-1.11	-0.15	-1.08	0.317044	0.456049	-6.63
249797_at	putative protein contains similarity t	---	AT5G23750	1.12	0.16	1.08	0.317055	0.456049	-6.63
256954_at	E2, ubiquitin-conjugating enzyme,	FUS9	AT3G13550	-1.10	-0.14	-1.08	0.317291	0.456352	-6.63
264444_at	putative squamosa-promoter bindin	---	AT1G27360	1.09	0.12	1.08	0.317306	0.456352	-6.63
265158_at	hypothetical protein predicted by ge	---	AT1G31040	-1.07	-0.10	-1.08	0.317341	0.456375	-6.63
265239_s_a	hypothetical protein	---	AT2G07692	-1.10	-0.14	-1.08	0.317422	0.456461	-6.63
245972_at	putative protein predicted proteins,	---	AT5G20680	-1.12	-0.16	-1.08	0.317529	0.456586	-6.63
249241_at	serine carboxypeptidase-II like	scpl41	AT5G42230	-1.08	-0.11	-1.08	0.317671	0.456755	-6.64
251269_at	putative protein Pm5 protein - Hom	---	AT3G62360	-1.11	-0.15	-1.08	0.317686	0.456755	-6.64
253750_at	putative transcription factor leghem	---	AT4G29000	1.12	0.17	1.08	0.317751	0.45682	-6.64
246626_at	hypothetical protein contains simila	---	AT1G48870	-1.13	-0.18	-1.08	0.317837	0.456896	-6.64
254474_at	putative protein predicted proteins,	---	AT4G20390	-1.13	-0.18	-1.08	0.317844	0.456896	-6.64
259310_s_a	Expressed protein ; supported by cI	---	AT3G05160	1.11	0.16	1.08	0.317913	0.456966	-6.64
267232_at	hypothetical protein predicted by ge	EDE1	AT2G44190	-1.09	-0.13	-1.08	0.318004	0.457068	-6.64
259988_at	Athila ORF 1, putative simlar to GI:	---	---	-1.07	-0.10	-1.08	0.318045	0.457098	-6.64
245718_at	putative protein	---	AT5G04110	1.11	0.15	1.08	0.318114	0.457143	-6.64
251338_at	putative protein VAP27, Nicotiana	VAP	AT3G60600	1.08	0.11	1.08	0.31812	0.457143	-6.64
258129_at	hypothetical protein predicted by ge	ROPGEF8	AT3G24620	-1.09	-0.13	-1.08	0.318163	0.457143	-6.64
251708_at	Expressed protein ; supported by cI	---	AT3G56580	-1.12	-0.16	-1.08	0.318167	0.457143	-6.64
246297_at	putative protein hypothetical protei	---	AT3G51760	1.13	0.18	1.08	0.318177	0.457143	-6.64
266550_s_a	Expressed protein ; supported by cI	---	AT2G35070	1.34	0.43	1.08	0.318253	0.457224	-6.64
253997_at	disease resistance protein RPS2 ;	RPS2	AT4G26090	1.31	0.39	1.08	0.318347	0.457331	-6.64
251693_at	putative protein several hypothetica	---	AT3G56550	1.10	0.13	1.08	0.318393	0.457367	-6.64
264079_at	putative seed storage protein (vicilir	---	AT2G28490	-1.09	-0.12	-1.08	0.318441	0.457408	-6.64
259879_at	putative calmodulin similar to calmo	CML38	AT1G76650	-1.48	-0.56	-1.08	0.318471	0.457422	-6.64
256666_at	histone H2A, putative similar to his	HTA13	AT3G20670	1.21	0.27	1.08	0.318681	0.457695	-6.64
248004_at	putative protein similar to unknown	PRA1.G2	AT5G56230	-1.19	-0.25	-1.08	0.318935	0.458031	-6.64
260724_at	unknown protein ;supported by full-	---	AT1G48140	1.09	0.12	1.08	0.319057	0.458177	-6.64
262265_at	hypothetical protein predicted by ge	---	---	-1.13	-0.17	-1.08	0.319241	0.458413	-6.64
261510_at	hypothetical protein predicted by ge	---	AT1G71760	-1.09	-0.12	-1.08	0.31927	0.458426	-6.64
253532_at	putative protein centromere protein	---	AT4G31570	-1.09	-0.12	-1.08	0.319346	0.458506	-6.64
259298_at	putative disease resistance protein	AtRLP31	AT3G05370	1.43	0.52	1.07	0.319517	0.458723	-6.64

254472_at	putative protein predicted proteins,	---	---	-1.07	-0.10	-1.07	0.319747	0.459007	-6.64
266747_at	predicted by genefinder and gensca	---	AT2G02870	1.11	0.15	1.07	0.319756	0.459007	-6.64
255811_at	heat shock protein 22.0 ; supported	ATHSP22.(	AT4G10250	-1.11	-0.15	-1.07	0.31996	0.459244	-6.64
264890_at	unknown protein	---	AT1G23180	1.13	0.17	1.07	0.319961	0.459244	-6.64
257192_at	unknown protein ;supported by full-	EMB2769	AT3G13200	1.10	0.14	1.07	0.320004	0.459262	-6.64
261934_at	UDP-glucose glucosyltransferase,	UGT85A1	AT1G22400	1.29	0.37	1.07	0.320013	0.459262	-6.64
245777_at	unknown protein contains similarity	atnudt21	AT1G73540	1.47	0.55	1.07	0.320038	0.459269	-6.64
252841_at	putative protein replication protein	---	---	-1.11	-0.15	-1.07	0.320101	0.45933	-6.64
263812_at	putative replication protein A1	---	---	-1.07	-0.10	-1.07	0.320123	0.459332	-6.64
247308_at	receptor-like protein kinase	---	AT5G63930	1.09	0.12	1.07	0.320199	0.459398	-6.64
248512_at	protein translocation complex Sec6	SIG2	AT1G08540	1.19	0.25	1.07	0.320209	0.459398	-6.64
265035_at	hypothetical protein contains Pfam	---	AT1G61620	1.10	0.13	1.07	0.320278	0.459468	-6.64
256802_at	cytochrome P450, putative similar	CYP705A3	AT3G20950	-1.08	-0.11	-1.07	0.320306	0.459479	-6.64
257486_at	unknown protein	---	AT1G63590	1.08	0.11	1.07	0.320548	0.459768	-6.64
263649_at	putative 1-aminocyclopropane-1-ca	---	AT1G04380	-1.07	-0.10	-1.07	0.320566	0.459768	-6.64
258731_at	unknown protein ; supported by cD	---	AT3G11880	1.09	0.12	1.07	0.320568	0.459768	-6.64
252371_at	putative protein finger protein SIG1	---	AT3G48070	1.10	0.14	1.07	0.320609	0.459798	-6.64
263748_at	putative protein kinase contains a p	---	AT2G21480	-1.09	-0.13	-1.07	0.320768	0.459968	-6.64
266214_at	putative retroelement integrase	---	---	-1.07	-0.10	-1.07	0.320785	0.459968	-6.64
255179_at	putative transposon protein	---	---	-1.07	-0.09	-1.07	0.320808	0.459968	-6.64
259699_at	hypothetical protein predicted by ge	---	AT1G68940	-1.08	-0.10	-1.07	0.320808	0.459968	-6.64
252190_at	putative protein various predicted g	---	AT3G50170	-1.08	-0.11	-1.07	0.320874	0.460033	-6.64
266118_at	protease inhibitor II ; supported by	LCR68	AT2G02130	-1.25	-0.32	-1.07	0.32093	0.460059	-6.64
247737_at	putative protein various predicted p	---	AT5G59200	1.07	0.09	1.07	0.320974	0.460059	-6.64
256082_at	hypothetical protein predicted by ge	---	AT1G20720	-1.16	-0.22	-1.07	0.320986	0.460059	-6.64
253681_at	cytidine deaminase 3 (CDA3)	---	AT4G29630	-1.09	-0.13	-1.07	0.320992	0.460059	-6.64
261389_s_a	hypothetical protein identical to hyp	---	---	1.07	0.10	1.07	0.320993	0.460059	-6.64
255415_at	hypothetical protein	---	AT4G03160	1.07	0.10	1.07	0.32102	0.46007	-6.64
265234_at	hypothetical protein	---	AT2G07721	-1.10	-0.14	-1.07	0.321102	0.460129	-6.64
254347_at	putative protein DNA-binding prote	WRKY31	AT4G22070	1.11	0.15	1.07	0.321102	0.460129	-6.64
264966_at	hypothetical protein predicted by ge	---	AT1G60570	-1.12	-0.17	-1.07	0.321197	0.460223	-6.64
254278_at	Expressed protein ; supported by fu	---	AT4G22740	-1.10	-0.13	-1.07	0.321216	0.460223	-6.64
263152_at	hypothetical protein predicted by ge	ASIL1	AT1G54060	-1.13	-0.18	-1.07	0.321228	0.460223	-6.64
248251_at	unknown protein	---	AT5G53220	1.08	0.11	1.07	0.321255	0.460233	-6.64
250783_at	cytochrome P450 ; supported by cl	CYP79A2	AT5G05260	-1.10	-0.14	-1.07	0.321309	0.460281	-6.64

266029_at	putative serine carboxypeptidase II	scpl38	AT2G05850	-1.09	-0.13	-1.07	0.321403	0.460366	-6.64
266740_at	hypothetical protein predicted by ge	---	AT2G46840	-1.09	-0.13	-1.07	0.321409	0.460366	-6.64
255328_at	putative leucyl tRNA synthetase	EMB2369	AT4G04350	-1.12	-0.17	-1.07	0.321481	0.460442	-6.64
246680_at	putative protein predicted proteins -	---	---	-1.10	-0.14	-1.07	0.321521	0.460469	-6.65
262535_at	trehalose-6-phosphate synthase, p	ATTPS3	AT1G17000	-1.07	-0.09	-1.07	0.321543	0.460473	-6.65
256218_at	hypothetical protein predicted by ge	---	AT1G56270	-1.11	-0.15	-1.07	0.321597	0.46052	-6.65
254935_at	putative disease resistance protein	---	AT4G10780	-1.11	-0.14	-1.07	0.321631	0.46054	-6.65
256051_at	hypothetical protein similar to putati	CHX14	AT1G06970	-1.11	-0.15	-1.07	0.321668	0.46056	-6.65
253999_at	1-aminocyclopropane-1-carboxylat	ACS7	AT4G26200	-1.20	-0.27	-1.07	0.321685	0.46056	-6.65
256867_at	hypothetical protein predicted by ge	---	AT3G26390	-1.08	-0.10	-1.07	0.321905	0.460835	-6.65
265526_x_a	putative Athila retroelement ORF1 p	---	---	-1.07	-0.10	-1.07	0.321918	0.460835	-6.65
248909_at	serine threonine protein kinase ; su	CIPK19	AT5G45810	-1.13	-0.17	-1.07	0.321954	0.460858	-6.65
249186_at	CHP-rich zinc finger protein-like	---	AT5G43040	-1.08	-0.11	-1.07	0.322021	0.460901	-6.65
259194_at	RNA helicase, DRH1 identical to R	DRH1	AT3G01540	1.07	0.10	1.07	0.322024	0.460901	-6.65
256548_at	hypothetical protein contains simila	---	AT3G14770	-1.57	-0.65	-1.07	0.322134	0.461023	-6.65
259203_at	hypothetical protein predicted by ge	---	AT3G09130	-1.09	-0.13	-1.07	0.32215	0.461023	-6.65
267288_at	similar to cold acclimation protein W	---	AT2G23680	1.32	0.40	1.07	0.32222	0.461093	-6.65
253568_at	putative protein receptor-like kinas	---	AT4G31230	1.09	0.13	1.07	0.322281	0.461153	-6.65
247354_at	flavonol synthase ;supported by ful	FLS3	AT5G63590	-1.07	-0.10	-1.07	0.322346	0.461216	-6.65
250911_at	SERINE/THREONINE-PROTEIN K	CTR1	AT5G03730	1.12	0.16	1.07	0.322371	0.461216	-6.65
252855_at	putative protein alpha-amino-epsilo	AGT2	AT4G39660	1.11	0.15	1.07	0.322386	0.461216	-6.65
252933_at	putative receptor-like protein kinas	---	AT4G39110	-1.10	-0.14	-1.07	0.322433	0.461253	-6.65
256917_at	unknown protein contains Pfam pro	---	AT3G18930	1.08	0.11	1.07	0.322479	0.461291	-6.65
259550_at	hypothetical protein ;supported by f	AGP5	AT1G35230	1.41	0.49	1.07	0.322516	0.461314	-6.65
249725_at	unknown protein	---	AT5G35470	1.08	0.11	1.07	0.322543	0.461325	-6.65
265525_at	putative Ty3-gypsy-like retroelemer	---	---	-1.10	-0.13	-1.07	0.322576	0.461343	-6.65
245858_at	CER1-like protein CER1-like, A.tha	---	AT5G28280	1.10	0.13	1.07	0.322639	0.461376	-6.65
266523_at	putative transportin	TRN1	AT2G16950	1.08	0.11	1.07	0.32264	0.461376	-6.65
247369_at	unknown protein	---	AT5G63340	-1.10	-0.14	-1.07	0.322718	0.461459	-6.65
251921_at	40S ribosomal protein S21 homolo	---	AT3G53890	1.23	0.29	1.07	0.322772	0.461508	-6.65
246006_at	putative protein DIM1 protein, Hom	YLS8	AT5G08290	1.08	0.12	1.07	0.322984	0.461782	-6.65
248161_at	unknown protein	---	AT5G54480	-1.09	-0.13	-1.07	0.323035	0.461799	-6.65
254208_at	Expressed protein ; supported by fu	---	AT4G24175	1.10	0.14	1.07	0.323036	0.461799	-6.65
244946_at	hypothetical protein	---	---	1.08	0.10	1.07	0.323079	0.461831	-6.65
259865_at	putative casein kinase I similar to ca	CKL2	AT1G72710	1.12	0.16	1.07	0.323104	0.461838	-6.65

266134_s_a	putative beta-expansin	---	AT1G65680	-1.09	-0.12	-1.07	0.323162	0.461892	-6.65
258594_at	hypothetical protein predicted by ge	---	AT3G04490	-1.09	-0.12	-1.07	0.323276	0.462025	-6.65
255166_at	putative protein putative centromer	---	---	-1.08	-0.11	-1.07	0.3233	0.462031	-6.65
245942_at	putative protein transcription regula	---	AT5G19490	1.07	0.10	1.07	0.32343	0.462187	-6.65
249213_at	unknown protein	---	AT5G42700	1.08	0.11	1.07	0.323462	0.46219	-6.65
252983_at	cinnamyl-alcohol dehydrogenase E	ELI3-1	AT4G37980	-1.17	-0.22	-1.07	0.323472	0.46219	-6.65
244927_at	hypothetical protein	---	AT2G07776	-1.11	-0.16	-1.06	0.323598	0.462341	-6.65
245857_at	putative protein various predicted p	---	---	-1.12	-0.16	-1.06	0.32362	0.462344	-6.65
249557_at	receptor serine/threonine kinase PF	PR5K	AT5G38280	1.17	0.22	1.06	0.323666	0.462379	-6.65
264603_at	hypothetical protein predicted by ge	---	AT1G04670	-1.07	-0.10	-1.06	0.323698	0.462396	-6.65
256312_x_a	hypothetical protein	---	AT1G35820	-1.08	-0.11	-1.06	0.32372	0.462399	-6.65
262079_at	unknown protein ; supported by cDI	ZCW7	AT1G59600	-1.13	-0.18	-1.06	0.323741	0.462401	-6.65
266502_at	hypothetical protein predicted by ge	---	AT2G47720	-1.08	-0.11	-1.06	0.323781	0.462429	-6.65
261506_at	choline kinase, putative similar to C	ATCK1	AT1G71697	-1.18	-0.24	-1.06	0.323813	0.462431	-6.65
247381_at	auxin-independent growth promoter	---	AT5G63390	-1.09	-0.13	-1.06	0.323823	0.462431	-6.65
263154_at	Expressed protein ; supported by fu	---	AT1G54110	1.11	0.15	1.06	0.323886	0.462491	-6.65
245810_at	axi 1 protein, putative similar to axi	---	AT1G38065	-1.10	-0.13	-1.06	0.324163	0.462858	-6.65
258121_s_a	putative geranylgeranyl pyrophosph	GGPS3	AT3G14530	1.10	0.14	1.06	0.32429	0.462984	-6.65
266159_at	putative chloroplast nucleoid DNA b	---	AT2G28030	-1.07	-0.10	-1.06	0.324292	0.462984	-6.65
250941_at	putative protein	---	AT5G03320	1.11	0.15	1.06	0.324377	0.463076	-6.65
256536_at	peptide chain release factor, putati	---	AT1G33330	1.08	0.11	1.06	0.324534	0.463272	-6.65
267146_at	hypothetical protein predicted by ge	---	AT2G38160	-1.08	-0.11	-1.06	0.324618	0.463363	-6.65
249602_at	porin -like protein porin, Prunus arr	---	AT5G37610	-1.09	-0.12	-1.06	0.324662	0.463397	-6.65
259698_at	hypothetical protein similar to hypo	---	AT1G68930	1.11	0.15	1.06	0.324941	0.463765	-6.65
257433_at	hypothetical protein predicted by ge	---	AT2G21990	1.08	0.11	1.06	0.325007	0.463831	-6.65
249371_at	hypothetical protein	---	AT5G40750	-1.07	-0.09	-1.06	0.325113	0.463953	-6.65
256610_at	hypothetical protein predicted by ge	---	AT3G30845	1.07	0.10	1.06	0.325163	0.463996	-6.65
253884_at	heat shock protein 21	HSP21	AT4G27670	-1.10	-0.14	-1.06	0.32521	0.464033	-6.65
260482_at	endomembrane protein EMP70 pre	---	AT1G10950	-1.09	-0.12	-1.06	0.325275	0.464071	-6.65
263081_at	putative homeodomain transcriptior	BLH5	AT2G27220	-1.07	-0.10	-1.06	0.325277	0.464071	-6.65
265259_at	putative WD-40 repeat protein simil	---	AT2G20330	1.09	0.13	1.06	0.325317	0.464079	-6.65
256740_at	hypothetical protein predicted by ge	---	AT3G29330	1.07	0.10	1.06	0.325323	0.464079	-6.65
265478_at	unknown protein ;supported by full-	MEE14	AT2G15890	1.08	0.12	1.06	0.325412	0.464176	-6.65
253991_at	putative nucleic acid binding protei	PEP	AT4G26000	-1.09	-0.12	-1.06	0.325466	0.464225	-6.65
247868_at	Myb-related transcription factor-like	MYB36	AT5G57620	-1.09	-0.12	-1.06	0.325507	0.464234	-6.65

258036_at	unknown protein	---	AT3G21210	-1.07	-0.10	-1.06	0.325513	0.464234	-6.65
254150_at	putative protein storage protein - P	---	AT4G24350	1.55	0.64	1.06	0.325593	0.464319	-6.66
265277_at	unknown protein ;supported by full	---	AT2G28410	-1.27	-0.35	-1.06	0.325759	0.464526	-6.66
266849_at	putative vacuolar processing enzym	ALPHA-VP	AT2G25940	1.08	0.12	1.06	0.32584	0.464612	-6.66
246684_at	putative protein nucleoid DNA-bind	CDR1	AT5G33340	-1.12	-0.16	-1.06	0.32593	0.464692	-6.66
255528_at	hypothetical protein	---	AT4G02090	-1.08	-0.11	-1.06	0.325936	0.464692	-6.66
250179_at	putative protein	---	AT5G14440	1.10	0.14	1.06	0.326154	0.464962	-6.66
249879_at	serine/threonine protein kinase-like	---	AT5G23170	-1.09	-0.12	-1.06	0.326166	0.464962	-6.66
250157_at	prx10 peroxidase - like protein prx1	---	AT5G15180	-1.09	-0.12	-1.06	0.326286	0.465104	-6.66
253502_at	Cytochrome P450-like protein cyto	CYP82C4	AT4G31940	1.08	0.11	1.06	0.326308	0.465105	-6.66
254380_at	putative protein	---	AT4G21865	1.32	0.40	1.06	0.326328	0.465105	-6.66
255306_at	putative calcium dependent protein	CPK23	AT4G04740	1.13	0.18	1.06	0.326357	0.465117	-6.66
263969_at	putative VSF-1-like b-ZIP transcript	UNE4	AT2G12940	-1.09	-0.13	-1.06	0.326443	0.465204	-6.66
260090_at	putative serine carboxypeptidase s	scpl4	AT1G73310	1.07	0.10	1.06	0.326458	0.465204	-6.66
246531_at	MADS box protein AGL2 ; supporte	ספס-01	AT5G15800	-1.11	-0.15	-1.06	0.326655	0.465454	-6.66
265674_at	unknown protein ; supported by ful	---	AT2G32190	1.31	0.39	1.06	0.326716	0.465487	-6.66
246649_at	putative protein predicted proteins,	---	---	-1.08	-0.11	-1.06	0.326718	0.465487	-6.66
261573_at	hypothetical protein identical to hyo	---	AT1G01180	-1.08	-0.11	-1.06	0.326743	0.465493	-6.66
252904_at	putative protein crp1 protein, Zea r	EMB2453	AT4G39620	-1.10	-0.13	-1.06	0.326849	0.465615	-6.66
252817_at	putative protein hypothetical protein	---	---	-1.11	-0.14	-1.06	0.326928	0.465678	-6.66
247276_at	putative protein contains similarity t	HEN4	AT5G64390	-1.15	-0.20	-1.06	0.326934	0.465678	-6.66
263310_s_a	hypothetical protein	---	---	-1.07	-0.10	-1.06	0.327	0.465743	-6.66
245717_at	Expressed protein ; supported by c	---	AT5G33390	1.09	0.13	1.06	0.327078	0.465805	-6.66
251314_at	putative protein several hypothetica	---	AT3G61180	-1.07	-0.09	-1.06	0.327094	0.465805	-6.66
259827_at	hypothetical protein	---	AT1G72270	-1.08	-0.11	-1.06	0.327105	0.465805	-6.66
252994_at	putative protein gene PC326 protei	---	AT4G38480	-1.23	-0.29	-1.06	0.327211	0.465927	-6.66
254864_at	putative reverse transcriptase other	---	---	-1.06	-0.09	-1.06	0.327346	0.466091	-6.66
256139_at	Nt-gh3 deduced protein, putative s	---	AT1G48660	-1.10	-0.14	-1.06	0.327462	0.466211	-6.66
256202_s_a	hypothetical protein	---	AT1G48150	-1.08	-0.11	-1.06	0.327472	0.466211	-6.66
258740_at	Lon protease, putative similar to Lo	LON3	AT3G05780	-1.12	-0.17	-1.06	0.327686	0.466487	-6.66
247140_at	putative protein similar to unknown	---	AT5G66250	1.08	0.11	1.05	0.327835	0.46667	-6.66
258251_at	unknown protein ; supported by ful	---	AT3G15810	1.09	0.12	1.05	0.32791	0.466747	-6.66
248569_at	receptor protein kinase-like	---	AT5G49770	-1.10	-0.14	-1.05	0.327982	0.46682	-6.66
264235_at	myosin, putative similar to myosin (	XIE	AT1G54560	-1.10	-0.14	-1.05	0.328037	0.46687	-6.66
246093_at	ethylene-forming-enzyme-like diox	---	AT5G20550	1.09	0.12	1.05	0.328063	0.466878	-6.66

247252_at	unknown protein	---	AT5G64770	1.39	0.48	1.05	0.328105	0.466908	-6.66
247490_at	LFY floral meristem identity control	LFY	AT5G61850	-1.08	-0.11	-1.05	0.328128	0.466911	-6.66
258954_at	unknown protein contains Pfam pro	---	AT3G01400	-1.07	-0.09	-1.05	0.328216	0.467006	-6.66
252104_at	putative protein KIAA0851 protein,	RHD4	AT3G51460	1.11	0.15	1.05	0.328235	0.467006	-6.66
260192_at	putative DNA polymerase alpha sul	POLA2	AT1G67630	-1.27	-0.35	-1.05	0.328455	0.467289	-6.66
244996_at	ribosomal protein S2	---	---	-1.10	-0.14	-1.05	0.328543	0.467387	-6.66
261953_at	UDP-galactose 4-epimerase, putat	RHD1	AT1G64440	1.18	0.23	1.05	0.328656	0.467489	-6.66
253500_at	predicted protein RegA gene, Dicty	ARR10	AT4G31920	1.14	0.19	1.05	0.328668	0.467489	-6.66
252257_at	putative protein several hypothetica	---	AT3G49440	-1.07	-0.10	-1.05	0.328694	0.467489	-6.66
263695_at	putative phosphoribosylglycinamid	---	AT1G31220	1.08	0.12	1.05	0.328698	0.467489	-6.66
250989_at	cytochrome P450 - like protein cyt	CYP96A13	AT5G02900	-1.07	-0.09	-1.05	0.328761	0.467516	-6.66
254762_at	Expressed protein ; supported by fu	---	AT4G13230	-1.09	-0.12	-1.05	0.328765	0.467516	-6.66
265638_at	similar to PIG-L	---	AT2G27340	1.08	0.11	1.05	0.328778	0.467516	-6.66
262350_at	putative glutathione peroxidase ;su	ATGPX4	AT2G48150	-1.08	-0.11	-1.05	0.32881	0.467533	-6.66
256621_at	unknown protein ; supported by ful	---	AT3G24450	-1.09	-0.13	-1.05	0.328894	0.467623	-6.66
256096_at	unknown protein	---	AT1G13650	-1.21	-0.27	-1.05	0.329003	0.467749	-6.66
251680_at	putative protein 13S condensin XC	---	AT3G57060	-1.08	-0.11	-1.05	0.329046	0.467781	-6.66
264619_at	putative chloroplast nucleoid DNA-b	---	AT2G17760	1.10	0.13	1.05	0.329138	0.467882	-6.66
264935_at	hypothetical protein predicted by ge	---	AT1G61150	1.14	0.19	1.05	0.329183	0.467917	-6.66
265672_at	putative cysteine proteinase inhibito	---	AT2G31980	1.39	0.47	1.05	0.329204	0.467917	-6.66
262465_at	hypothetical protein similar to hypot	---	AT1G50270	-1.07	-0.10	-1.05	0.329239	0.467932	-6.66
258287_at	putative sulfate transporter similar t	SULTR3;4	AT3G15990	1.25	0.33	1.05	0.329255	0.467932	-6.66
264949_at	unknown protein contains similarity	MAF1	AT1G77080	-1.07	-0.10	-1.05	0.329338	0.468021	-6.66
248857_at	putative protein contains similarity t	---	AT5G46640	1.18	0.24	1.05	0.32942	0.468098	-6.66
252329_at	putative protein several hypothetica	---	AT3G48760	-1.08	-0.11	-1.05	0.329437	0.468098	-6.66
253287_at	putative protein dJ69E11.3, Homo	---	AT4G34270	1.07	0.10	1.05	0.329454	0.468098	-6.66
253906_at	putative protein disease resistance	---	AT4G27220	-1.12	-0.17	-1.05	0.329529	0.468176	-6.66
261307_at	unknown protein similar to Glu-tRN	GATB	AT1G48520	-1.08	-0.11	-1.05	0.329565	0.468198	-6.66
252486_at	arm repeat containing protein hom	PUB13	AT3G46510	-1.09	-0.13	-1.05	0.329784	0.468458	-6.67
264544_s_a	unknown protein	---	AT1G55790	-1.08	-0.11	-1.05	0.32979	0.468458	-6.67
258738_at	hypothetical protein similar to hypot	---	AT3G05750	1.11	0.15	1.05	0.329828	0.468483	-6.67
256949_at	hypothetical protein predicted by ge	---	AT3G19070	-1.07	-0.10	-1.05	0.329881	0.46853	-6.67
255379_at	putative M-type thioredoxin similar	ATHM2	AT4G03520	1.07	0.10	1.05	0.329958	0.46861	-6.67
257415_at	hypothetical protein similar to hypot	---	AT1G70040	-1.10	-0.13	-1.05	0.330014	0.468646	-6.67
258420_at	putative RNA polymerase similar to	---	AT3G16680	-1.08	-0.11	-1.05	0.330024	0.468646	-6.67

245423_at	putative protein	---	AT4G17483	1.10	0.14	1.05	0.330166	0.468817	-6.67
259374_at	putative AP2 domain transcription f	---	AT3G16280	1.12	0.17	1.05	0.330272	0.468938	-6.67
263622_at	hypothetical protein predicted by ge	---	AT2G04870	-1.08	-0.12	-1.05	0.330407	0.469069	-6.67
266654_at	putative oleosin protein	---	AT2G25890	-1.12	-0.16	-1.05	0.33044	0.469069	-6.67
265743_s_a	En/Spm-like transposon protein rela	---	---	-1.08	-0.10	-1.05	0.330442	0.469069	-6.67
248930_at	unknown protein	---	AT5G46010	-1.09	-0.12	-1.05	0.330446	0.469069	-6.67
259222_at	putative phosphoribosylanthranilate	---	AT3G03680	1.11	0.15	1.05	0.330484	0.469094	-6.67
245390_at	putative protein ;supported by full-le	---	AT4G17650	1.18	0.24	1.05	0.330524	0.469122	-6.67
250807_at	helicase-like transcription factor-like	---	AT5G05130	1.11	0.15	1.05	0.330683	0.469317	-6.67
247404_at	permease 1 - like protein permease	---	AT5G62890	-1.19	-0.26	-1.05	0.330703	0.469317	-6.67
247167_at	unknown protein	---	AT5G65850	-1.11	-0.15	-1.05	0.330727	0.469322	-6.67
266627_at	putative pre-mRNA splicing factor R	MEE29	AT2G35340	-1.09	-0.13	-1.05	0.330808	0.469408	-6.67
255912_at	2,3-oxidosqualene-triterpenoid cyc	---	AT1G66960	-1.11	-0.16	-1.05	0.330874	0.469467	-6.67
264771_at	phosphomethylpyrimidine kinase p	TH1	AT1G22940	-1.07	-0.10	-1.05	0.330891	0.469467	-6.67
252060_at	putative protein other hypothetical p	PAD4	AT3G52430	1.34	0.42	1.05	0.331465	0.470253	-6.67
253501_at	predicted protein predicted protein (	HSL1	AT4G32010	1.09	0.12	1.05	0.331532	0.470319	-6.67
264127_at	serine/threonine protein kinase, pu	AGC1.7	AT1G79250	-1.07	-0.09	-1.05	0.331778	0.470633	-6.67
249060_at	putative protein similar to unknown	VPS2.2	AT5G44560	-1.07	-0.10	-1.05	0.331815	0.470633	-6.67
257517_at	unknown protein	---	AT3G16330	-1.34	-0.42	-1.05	0.331822	0.470633	-6.67
256849_at	hypothetical protein similar to hypot	---	---	-1.10	-0.13	-1.05	0.331836	0.470633	-6.67
264483_at	unknown protein	---	AT1G77230	1.11	0.15	1.05	0.331882	0.470668	-6.67
263071_at	putative retroelement pol polyprotei	---	---	-1.08	-0.11	-1.05	0.331919	0.470691	-6.67
261251_at	hypothetical protein predicted by ge	---	AT1G05920	-1.14	-0.18	-1.05	0.331968	0.470731	-6.67
257737_at	uridine kinase/uracil phosphoribosy	---	AT3G27440	1.08	0.12	1.05	0.331999	0.470747	-6.67
257491_at	hypothetical protein predicted by g	---	AT1G06170	-1.07	-0.09	-1.05	0.332057	0.470799	-6.67
252735_at	putative protein predicted proteins,	---	AT3G43170	1.08	0.11	1.04	0.332161	0.470918	-6.67
246142_at	putative protein	---	AT5G19970	1.07	0.10	1.04	0.332225	0.470979	-6.67
247893_at	RNA polymerase I, II and III 24.3 k	RPB5C	AT5G57980	-1.11	-0.15	-1.04	0.332386	0.471178	-6.67
265603_at	hypothetical protein predicted by ge	---	---	1.09	0.13	1.04	0.332508	0.471321	-6.67
245831_at	unknown protein	---	AT1G48840	-1.09	-0.13	-1.04	0.332679	0.471534	-6.67
262201_at	unknown protein	ORC4	AT2G01120	1.08	0.11	1.04	0.332711	0.471551	-6.67
254622_at	hypothetical protein contains simila	---	AT4G18375	1.15	0.20	1.04	0.332815	0.47165	-6.67
253354_at	putative protein RNA helicase DBP	---	AT4G33370	1.16	0.21	1.04	0.332848	0.47165	-6.67
257715_at	putative zinc transporter identical t	ZIP1	AT3G12750	1.18	0.23	1.04	0.332857	0.47165	-6.67
260515_at	ATP-dependent transmembrane tra	---	AT1G51460	-1.10	-0.13	-1.04	0.332864	0.47165	-6.67

256727_at	hypothetical protein	---	AT3G52240	-1.10	-0.14	-1.04	0.332899	0.471671	-6.67
255223_at	putative protein predicted proteins,	---	AT4G05370	-1.07	-0.10	-1.04	0.332995	0.471778	-6.67
255565_at	putative CHP-rich zinc finger protei	---	AT4G01760	-1.07	-0.10	-1.04	0.333114	0.471916	-6.67
263985_at	unknown protein ;supported by full-	---	AT2G42750	-1.15	-0.20	-1.04	0.333198	0.471999	-6.67
257473_at	unknown protein	---	AT1G33840	-1.12	-0.16	-1.04	0.333214	0.471999	-6.67
256439_at	putative [Mn] superoxide dismutase	MSD1	AT3G10920	1.10	0.14	1.04	0.333283	0.472068	-6.67
259401_at	hypothetical protein contains simila	CSTF77	AT1G17760	1.15	0.21	1.04	0.333373	0.472166	-6.67
253120_at	putative protein phospholipase D, /	PLDDELTA	AT4G35790	1.12	0.16	1.04	0.333404	0.472181	-6.67
247402_at	putative protein predicted proteins,	---	AT5G62750	-1.08	-0.11	-1.04	0.33352	0.472316	-6.67
248918_at	senescence-specific cysteine prote	SAG12	AT5G45890	-1.12	-0.16	-1.04	0.333604	0.472406	-6.67
267223_at	hypothetical protein predicted by gr	AtITPK4	AT2G43980	1.09	0.13	1.04	0.333649	0.472439	-6.67
249110_at	disease resistance protein	---	AT5G43730	1.07	0.10	1.04	0.333726	0.47252	-6.67
254204_at	putative protein CGI-58 protein - H	---	AT4G24160	-1.20	-0.26	-1.04	0.333758	0.472536	-6.67
256768_at	hypothetical protein predicted by g	LDL2	AT3G13682	1.07	0.10	1.04	0.333805	0.472573	-6.67
252794_at	putative protein predicted proteins,	---	---	-1.07	-0.10	-1.04	0.33388	0.47265	-6.68
264980_at	receptor kinase, putative similar to	---	AT1G27190	-1.10	-0.14	-1.04	0.333915	0.47267	-6.68
250996_at	putative protein BcDNA.LD24793,	---	AT5G02530	1.08	0.11	1.04	0.33399	0.472747	-6.68
259263_at	putative UDP-glucose 6-dehydroge	---	AT3G01010	-1.08	-0.12	-1.04	0.334054	0.472807	-6.68
261862_at	DNA-binding protein, putative simil	---	AT1G50410	1.11	0.15	1.04	0.334075	0.472809	-6.68
261549_at	DNA-binding protein, putative cont	---	AT1G63470	-1.11	-0.15	-1.04	0.334284	0.473074	-6.68
262972_at	unknown protein	---	AT1G75620	-1.09	-0.13	-1.04	0.334328	0.473108	-6.68
258035_at	putative Ca2+-transporting ATPase	ACA9	AT3G21180	-1.10	-0.13	-1.04	0.334401	0.473182	-6.68
251898_at	floral homeotic protein APETALA3 (	AP3	AT3G54340	1.07	0.10	1.04	0.334482	0.473267	-6.68
261115_at	hypothetical protein predicted by ge	---	AT1G75360	-1.07	-0.10	-1.04	0.334619	0.473412	-6.68
254027_at	putative mitochondrial protein Hom	---	AT4G25835	1.14	0.19	1.04	0.334626	0.473412	-6.68
249891_at	unknown protein	---	AT5G22590	1.06	0.09	1.04	0.334671	0.473446	-6.68
251268_at	putative protein hypothetical protein	---	AT3G62350	-1.09	-0.13	-1.04	0.334695	0.473451	-6.68
262506_at	unknown protein Similar to gb|X842	NADK2	AT1G21640	1.13	0.17	1.04	0.334719	0.473455	-6.68
254716_at	putative protein LEA protein , Cicer	UNE15	AT4G13560	-1.13	-0.18	-1.04	0.334804	0.473546	-6.68
256764_at	hypothetical protein predicted by ge	---	AT3G29310	1.11	0.15	1.04	0.334828	0.47355	-6.68
251145_at	putative protein predicted protein, /	---	AT3G63500	1.10	0.14	1.04	0.334848	0.47355	-6.68
266318_at	Mutator-like transposase similar to	FRS3	AT2G27110	1.06	0.09	1.04	0.334899	0.473592	-6.68
247518_at	putative protein many predicted pro	---	AT5G61800	1.10	0.13	1.04	0.335058	0.473788	-6.68
261246_at	unknown protein	SYTB	AT1G20080	-1.09	-0.12	-1.04	0.335141	0.473876	-6.68
263271_s_a	hypothetical protein predicted by ge	---	---	1.07	0.09	1.04	0.33538	0.474184	-6.68

247163_at	Expressed protein ; supported by cl	---	AT5G65685	1.10	0.14	1.04	0.335455	0.474261	-6.68
264386_at	putative pyrophosphate-fructose-6-	---	AT1G12000	1.19	0.25	1.04	0.335566	0.474389	-6.68
247239_at	pectin methylesterase-like protein s	---	AT5G64640	-1.09	-0.13	-1.04	0.335663	0.474497	-6.68
259230_at	unknown protein ; supported by cD	OBE1	AT3G07780	-1.11	-0.15	-1.04	0.335706	0.474528	-6.68
261176_at	hypothetical protein predicted by ge	---	AT1G04780	1.07	0.10	1.04	0.335835	0.474674	-6.68
266233_at	putative phloem-specific lectin	AtPP2-B8	AT2G02340	-1.07	-0.10	-1.04	0.335851	0.474674	-6.68
251147_at	kinesin heavy chain - like protein ki	---	AT3G63480	-1.09	-0.12	-1.04	0.33591	0.474728	-6.68
258247_at	hypothetical protein predicted by ge	---	AT3G29130	-1.06	-0.09	-1.04	0.33604	0.474882	-6.68
264241_at	hypothetical protein contains simila	---	AT1G54840	-1.07	-0.09	-1.04	0.336067	0.47489	-6.68
249250_at	arm repeat containing protein	---	AT5G42340	-1.07	-0.10	-1.04	0.33623	0.47505	-6.68
267431_at	unknown protein ;supported by full-	MEE26	AT2G34870	-1.09	-0.13	-1.04	0.336236	0.47505	-6.68
258115_at	hypothetical protein predicted by ge	---	AT3G14670	-1.09	-0.12	-1.04	0.336242	0.47505	-6.68
247760_at	subtilisin-like serine protease conta	---	AT5G59130	-1.40	-0.49	-1.04	0.336322	0.475133	-6.68
245404_at	putative protein	---	AT4G17610	1.11	0.15	1.04	0.336397	0.475204	-6.68
267452_at	auxin response transcription factor	ETT	AT2G33860	-1.09	-0.13	-1.04	0.336414	0.475204	-6.68
249820_at	putative protein contains similarity t	---	AT5G23650	-1.14	-0.19	-1.03	0.336531	0.47529	-6.68
256937_at	hypothetical protein predicted by ge	---	AT3G22620	-1.75	-0.80	-1.03	0.336543	0.47529	-6.68
252437_at	putative protein pectinesterase hor	---	AT3G47380	1.26	0.34	1.03	0.336549	0.47529	-6.68
256830_at	eukaryotic translation initiation fact	TIF3C2	AT3G22860	-1.10	-0.14	-1.03	0.336574	0.47529	-6.68
251939_at	putative protein MICRONUCLEAR	---	AT3G53440	-1.13	-0.18	-1.03	0.336578	0.47529	-6.68
262335_at	hypothetical protein predicted by ge	SPO11-2	AT1G63990	-1.07	-0.09	-1.03	0.336789	0.47554	-6.68
263944_at	hypothetical protein predicted by ge	---	---	-1.07	-0.10	-1.03	0.336797	0.47554	-6.68
264809_at	superoxidase dismutase identical to	CSD1	AT1G08830	1.31	0.39	1.03	0.336825	0.47555	-6.68
250206_at	mitochondrial phosphate translocat	---	AT5G14040	1.17	0.22	1.03	0.336947	0.475692	-6.68
247809_at	unknown protein	---	AT5G58280	-1.09	-0.13	-1.03	0.33699	0.475724	-6.68
252632_s_a	disease resistance protein -like dis	RPP1	AT3G44480	-1.09	-0.13	-1.03	0.337166	0.475942	-6.68
246455_at	putative protein predicted protein F	---	AT5G16790	1.09	0.13	1.03	0.337203	0.475953	-6.68
261194_at	unknown protein contains Pfam pro	---	AT1G12770	1.06	0.09	1.03	0.337215	0.475953	-6.68
256019_at	cytochrome P-450, putative similar	---	AT1G58260	-1.08	-0.11	-1.03	0.337262	0.475971	-6.68
265790_at	putative amino acid or GABA perme	BAT1	AT2G01170	-1.12	-0.16	-1.03	0.33727	0.475971	-6.68
262873_at	hypothetical protein predicted by ge	---	AT1G64700	-1.09	-0.12	-1.03	0.337295	0.475977	-6.68
256832_at	meiotic recombination protein (AtD	DMC1	AT3G22880	-1.14	-0.19	-1.03	0.337346	0.476019	-6.68
256427_at	hypothetical protein predicted by ge	LBD21	AT3G11090	1.18	0.23	1.03	0.337414	0.476064	-6.68
258221_at	Snf1-related protein kinase KIN11 (	AKIN11	AT3G29160	1.16	0.22	1.03	0.337419	0.476064	-6.68
258028_at	hypothetical protein	---	AT3G27473	-1.06	-0.09	-1.03	0.337452	0.476081	-6.68

247117_at	3-hydroxyisobutyryl-coenzyme A hy	CHY1	AT5G65940	1.12	0.16	1.03	0.337494	0.476112	-6.68
253023_at	hypothetical protein	---	AT4G38070	-1.12	-0.16	-1.03	0.337572	0.476188	-6.68
256476_at	TNP2-like transposon protein simila	---	---	-1.08	-0.11	-1.03	0.337591	0.476188	-6.68
245343_at	hypothetical protein ;supported by f	---	AT4G15830	-1.07	-0.10	-1.03	0.33787	0.476547	-6.68
248131_at	unknown protein	---	AT5G54830	1.18	0.24	1.03	0.337887	0.476547	-6.68
256800_at	hypothetical protein predicted by ge	---	AT3G20900	-1.09	-0.13	-1.03	0.337955	0.476596	-6.68
258014_at	hypothetical protein predicted by ge	---	AT3G19330	1.13	0.18	1.03	0.337972	0.476596	-6.68
246281_at	hypothetical protein	NAPRT1	AT4G36940	-1.14	-0.19	-1.03	0.337984	0.476596	-6.68
265273_at	unknown protein	---	AT2G28320	1.09	0.13	1.03	0.338089	0.476703	-6.68
255438_at	putative oxidoreductase	AOP1	AT4G03070	-1.21	-0.27	-1.03	0.338102	0.476703	-6.68
254401_at	putative protein various predicted p	---	AT4G21300	1.08	0.11	1.03	0.33814	0.476728	-6.69
247583_at	putative protein predicted protein, S	---	AT5G60750	1.08	0.11	1.03	0.338161	0.476728	-6.69
262709_at	unknown protein ESTs gb|F15498,	SYP51	AT1G16240	1.10	0.14	1.03	0.338199	0.476752	-6.69
261874_at	ethylene responsive element bindin	ERF3	AT1G50640	1.10	0.14	1.03	0.338317	0.476838	-6.69
263088_at	putative replication protein A1	---	---	1.08	0.11	1.03	0.33833	0.476838	-6.69
249139_at	Cys2/His2-type zinc finger protein 3	AZF3	AT5G43170	1.20	0.26	1.03	0.338357	0.476838	-6.69
245135_at	putative non-LTR retroelement reve	---	---	-1.10	-0.13	-1.03	0.338358	0.476838	-6.69
253833_at	putative calcium binding protein tai	---	AT4G27790	-1.14	-0.19	-1.03	0.338364	0.476838	-6.69
256656_at	hypothetical protein similar to hypot	---	AT3G18900	-1.08	-0.11	-1.03	0.338439	0.476913	-6.69
254746_at	putative protein hypothetical protei	---	AT4G12980	-1.17	-0.23	-1.03	0.338597	0.477101	-6.69
247937_at	Ca2+-transporting ATPase-like prot	ACA8	AT5G57110	1.17	0.22	1.03	0.338631	0.477101	-6.69
252482_at	glucosyltransferase-like protein UD	UGT76E11	AT3G46670	-1.33	-0.41	-1.03	0.338635	0.477101	-6.69
250686_at	gamma-tubulin interacting protein-li	SPC98	AT5G06680	1.13	0.17	1.03	0.338751	0.477235	-6.69
247565_at	putative protein Atu, Drosophila me	VIP4	AT5G61150	1.08	0.11	1.03	0.338847	0.47734	-6.69
266019_at	putative calmodulin-binding protein	---	AT2G18750	1.07	0.10	1.03	0.338922	0.477417	-6.69
247710_at	receptor-like protein kinase recepto	---	AT5G59260	-1.07	-0.09	-1.03	0.339032	0.477489	-6.69
260842_at	19S proteosome subunit 9, putative	ATS9	AT1G29150	1.09	0.12	1.03	0.339034	0.477489	-6.69
264639_at	unknown protein similar to ubiquitin	UCH2	AT1G65650	1.10	0.14	1.03	0.339036	0.477489	-6.69
260613_at	unknown protein	---	AT1G53380	1.09	0.13	1.03	0.339193	0.477681	-6.69
256755_at	calmodulin, putative similar to GB:I	---	AT3G25600	-1.18	-0.23	-1.03	0.339315	0.477823	-6.69
248137_at	putative protein contains similarity t	---	AT5G54950	-1.09	-0.12	-1.03	0.33949	0.478026	-6.69
257488_s_a	putative RING-finger protein	---	AT1G36950	1.06	0.09	1.03	0.339501	0.478026	-6.69
253153_at	hypothetical protein	---	AT4G35700	-1.08	-0.11	-1.03	0.339535	0.478044	-6.69
257382_at	hypothetical protein predicted by ge	WRKY54	AT2G40750	-1.76	-0.81	-1.03	0.339589	0.47809	-6.69
248426_at	putative protein contains similarity t	---	AT5G51740	1.07	0.10	1.03	0.339712	0.478235	-6.69

257575_at	hypothetical protein similar to hypot	---	---	-1.09	-0.12	-1.03	0.339914	0.478489	-6.69
267069_at	unknown protein	ATCAMBP2	AT2G41010	-1.31	-0.39	-1.03	0.339951	0.478501	-6.69
267053_s_a	peroxidase	---	AT2G38380	-1.19	-0.25	-1.03	0.339964	0.478501	-6.69
265810_at	unknown protein	---	AT2G18090	-1.14	-0.19	-1.03	0.340023	0.478535	-6.69
245353_at	hypothetical protein ;supported by f	---	AT4G16000	1.17	0.23	1.03	0.340031	0.478535	-6.69
249733_at	6-phosphogluconolactonase-like pr	emb2024	AT5G24400	1.08	0.12	1.03	0.340134	0.478624	-6.69
250631_at	pectin methyl-esterase-like protein	---	AT5G07430	-1.07	-0.10	-1.03	0.340136	0.478624	-6.69
258340_at	hypothetical protein predicted by ge	---	AT3G22770	-1.07	-0.10	-1.03	0.34018	0.478657	-6.69
257320_at	hypothetical protein	---	AT2G07749	1.10	0.13	1.03	0.340206	0.478663	-6.69
253687_at	putative protein ;supported by full-l	---	AT4G29520	1.46	0.54	1.03	0.340254	0.478692	-6.69
266402_at	hypothetical protein predicted by ge	---	AT2G38780	-1.14	-0.19	-1.03	0.340268	0.478692	-6.69
254698_at	NAM (no apical meristem) - like pro	anac071	AT4G17980	-1.06	-0.09	-1.03	0.340363	0.478796	-6.69
267451_at	putative AP2 domain transcription f	---	AT2G33710	1.54	0.63	1.03	0.34042	0.478847	-6.69
249003_at	putative protein contains similarity t	---	AT5G44500	-1.09	-0.13	-1.03	0.340518	0.478954	-6.69
246784_at	signal peptidase ; supported by cD	---	AT5G27430	1.07	0.10	1.03	0.340613	0.479059	-6.69
250605_at	glycine/proline-rich protein flagellifo	---	AT5G07570	-1.09	-0.13	-1.03	0.340776	0.479259	-6.69
251135_at	putative protein proteophosphoglyc	---	AT5G01280	1.08	0.11	1.02	0.340819	0.479261	-6.69
258306_at	putative transcription factor similar t	ATBZIP42	AT3G30530	-1.06	-0.09	-1.02	0.34082	0.479261	-6.69
244918_at	hypothetical protein	AT2G0774	---	-1.09	-0.12	-1.02	0.340905	0.479351	-6.69
252791_at	transposase - like protein putative t	---	---	1.08	0.10	1.02	0.341008	0.479467	-6.69
261260_at	hypothetical protein predicted by ge	---	AT1G26680	-1.08	-0.11	-1.02	0.341032	0.479471	-6.69
259190_at	unknown protein est hit, predicted	TPLATE	AT3G01780	-1.12	-0.16	-1.02	0.341106	0.479546	-6.69
250763_at	short chain alcohol dehydrogenase-	---	AT5G06060	-1.10	-0.13	-1.02	0.341164	0.479598	-6.69
266103_at	putative VAMP-associated protein	PVA12	AT2G45140	-1.09	-0.12	-1.02	0.341259	0.479702	-6.69
264419_s_a	hypothetical protein contains simila	---	AT1G43310	1.24	0.31	1.02	0.341298	0.479728	-6.69
263387_at	unknown protein ; supported by cD	---	AT2G40160	-1.09	-0.13	-1.02	0.34133	0.479743	-6.69
265822_at	putative SEC1 family transport prot	ATSLY1	AT2G17980	-1.08	-0.12	-1.02	0.341402	0.479814	-6.69
246466_at	sugar transporter - like protein D-X	---	AT5G17010	1.13	0.17	1.02	0.341451	0.479842	-6.69
249760_at	(+)-delta-cadinene synthase (d-cad	TPS21	AT5G23960	-1.07	-0.10	-1.02	0.341464	0.479842	-6.69
263095_at	Ac-like transposase related to Ac/D	---	AT2G16040	-1.08	-0.10	-1.02	0.341492	0.479852	-6.69
265435_s_a	putative major intrinsic (channel) pr	---	AT1G31885	-1.11	-0.15	-1.02	0.341633	0.480021	-6.69
246271_at	photosystem II oxygen-evolving cor	---	AT4G37230	-1.09	-0.12	-1.02	0.341727	0.480123	-6.69
254544_at	putative chitinase chitinase (EC 3.2	---	AT4G19820	-1.10	-0.14	-1.02	0.341785	0.480136	-6.69
255098_at	hypothetical protein	---	AT4G08640	-1.07	-0.09	-1.02	0.341785	0.480136	-6.69
258969_at	hypothetical protein predicted by g	---	AT3G10680	-1.07	-0.10	-1.02	0.341819	0.480136	-6.69

254412_at	putative protein chloroplast DNA-b	B160	AT4G21430	-1.14	-0.19	-1.02	0.341821	0.480136	-6.69
265180_at	putative OBP32pep protein ;suppo	---	AT1G23590	-1.06	-0.09	-1.02	0.341913	0.480236	-6.69
257557_at	terpene synthase-related protein, p	---	AT3G14490	-1.11	-0.15	-1.02	0.341947	0.480254	-6.69
245163_at	putative flavin-containing monooxyg	---	AT2G33230	-1.11	-0.15	-1.02	0.341989	0.480283	-6.69
246242_at	putative protein	---	AT4G36600	-1.12	-0.17	-1.02	0.342022	0.480301	-6.69
253355_at	putative protein	---	AT4G33380	1.07	0.10	1.02	0.342195	0.480514	-6.69
248539_at	ribitol dehydrogenase-like ; suppor	---	AT5G50130	1.11	0.15	1.02	0.34233	0.480674	-6.69
256134_at	aminoalcoholphosphotransferase id	AAPT1	AT1G13560	-1.08	-0.11	-1.02	0.342512	0.480899	-6.70
266928_at	putative phosphomannomutase ;su	PMM	AT2G45790	-1.12	-0.17	-1.02	0.342604	0.481	-6.70
256500_at	Ty1/copia-element polyprotein	---	---	-1.09	-0.12	-1.02	0.342626	0.481	-6.70
247673_at	tRNA intron endonuclease - like pr	SEN2	AT5G60230	-1.07	-0.09	-1.02	0.342715	0.481083	-6.70
256247_at	SRF-type transcription factor contai	AGL91	AT3G66656	-1.07	-0.10	-1.02	0.342727	0.481083	-6.70
266954_at	hypothetical protein predicted by ge	---	AT2G34530	-1.08	-0.10	-1.02	0.342779	0.481127	-6.70
252011_at	carbonic anhydrase (CAH1) ; supp	ACA1	AT3G52720	-1.12	-0.17	-1.02	0.34281	0.48114	-6.70
253887_at	putative protein isp4 protein, Schiz	OPT6	AT4G27730	-1.22	-0.28	-1.02	0.342893	0.481227	-6.70
251063_at	protein kinase ATN1-like protein pr	---	AT5G01850	1.08	0.12	1.02	0.342946	0.481233	-6.70
255405_s_a	hypothetical protein similar to A. tha	---	AT4G03440	-1.11	-0.15	-1.02	0.342964	0.481233	-6.70
262905_at	thioredoxin, putative similar to thior	ATH7	AT1G59730	-1.07	-0.10	-1.02	0.343002	0.481233	-6.70
264159_at	unknown protein ;supported by full-	---	AT1G65270	1.07	0.10	1.02	0.343002	0.481233	-6.70
264187_at	unknown protein ;supported by full-	---	AT1G54860	-1.07	-0.09	-1.02	0.343003	0.481233	-6.70
251577_at	putative protein several hypothetica	---	AT3G58350	-1.11	-0.15	-1.02	0.343027	0.481237	-6.70
265971_at	putative retroelement pol polyprotei	---	---	-1.08	-0.11	-1.02	0.343209	0.481463	-6.70
249474_s_a	germin-like protein (GLP2a) copy2	GER2	AT5G39130	1.10	0.14	1.02	0.34339	0.481688	-6.70
255562_at	G/T DNA mismatch repair enzyme	MSH6	AT4G02070	1.11	0.15	1.02	0.343413	0.48169	-6.70
254385_s_a	putative protein CGI-131 protein, H	ATMSRB7	AT4G21830	1.95	0.97	1.02	0.343652	0.481996	-6.70
245828_at	transcription factor, putative similar	VIM1	AT1G57820	-1.10	-0.14	-1.02	0.343867	0.482269	-6.70
259101_at	hypothetical protein predicted by ge	---	AT3G11640	-1.07	-0.10	-1.02	0.344083	0.482526	-6.70
245988_at	putative protein predicted protein,	---	AT5G20610	1.11	0.16	1.02	0.344093	0.482526	-6.70
257069_at	hypothetical protein predicted by ge	---	AT3G28170	-1.08	-0.11	-1.02	0.344161	0.482591	-6.70
248648_at	putative protein similar to unknown	---	AT5G49220	1.09	0.13	1.02	0.344346	0.482821	-6.70
259449_at	hypothetical protein similar to putati	---	AT1G13800	1.10	0.14	1.02	0.344369	0.482824	-6.70
256821_at	hypothetical protein predicted by g	---	AT3G22180	1.13	0.18	1.02	0.344414	0.482857	-6.70
250219_at	putative protein similar to unknown	MPL1	AT5G14180	1.22	0.28	1.02	0.344494	0.48294	-6.70
251438_s_a	putative protein hypothetical protei	---	AT3G59930	1.53	0.61	1.02	0.344534	0.482966	-6.70
264081_at	putative RING zinc finger transcript	---	AT2G28540	1.10	0.14	1.02	0.34462	0.483029	-6.70

257321_at	hypothetical protein	---	---	1.17	0.23	1.02	0.344638	0.483029	-6.70
249976_at	Serine/arginine rich protein - like S	SCL28	AT5G18810	-1.09	-0.12	-1.02	0.344643	0.483029	-6.70
249407_at	putative protein predicted proteins,	---	AT5G40320	-1.08	-0.10	-1.02	0.344667	0.483034	-6.70
251133_at	LAX1 / AUX1 -like permease	---	AT5G01240	1.13	0.18	1.02	0.344719	0.483076	-6.70
247903_at	unknown protein ; supported by cD	---	AT5G57340	1.11	0.15	1.02	0.344842	0.48322	-6.70
265288_at	putative glutaredoxin ;supported by	---	AT2G20270	-1.11	-0.15	-1.02	0.344949	0.483339	-6.70
249429_at	putative protein	---	AT5G39880	-1.06	-0.09	-1.02	0.345163	0.48361	-6.70
258261_at	putative RING zinc finger protein c	---	AT3G15740	1.15	0.21	1.01	0.345327	0.48381	-6.70
248368_at	mandelonitrile lyase-like protein ; s	---	AT5G51950	-1.08	-0.11	-1.01	0.345353	0.483816	-6.70
260778_at	splicing factor, putative similar to h	---	AT1G14640	-1.11	-0.15	-1.01	0.345388	0.483836	-6.70
258572_at	hypothetical protein	---	AT3G04270	1.07	0.09	1.01	0.34543	0.483865	-6.70
258903_at	hypothetical protein similar to zinc	---	AT3G06410	1.13	0.18	1.01	0.345583	0.48405	-6.70
250236_at	delta subunit of mitochondrial F1-A	---	AT5G13450	1.10	0.13	1.01	0.345609	0.484056	-6.70
263498_at	unknown protein ; supported by cD	LSH10	AT2G42610	-1.47	-0.56	-1.01	0.345685	0.484133	-6.70
264193_at	CRK1 protein, putative similar to C	---	AT1G54610	1.07	0.10	1.01	0.345761	0.48421	-6.70
261371_at	ubiquitin-conjugating enzyme, puta	UBC26	AT1G53020	-1.07	-0.10	-1.01	0.345914	0.484394	-6.70
258185_at	hypothetical protein similar to hypot	---	AT3G21580	-1.11	-0.15	-1.01	0.345941	0.484403	-6.70
265082_at	hypothetical protein predicted by ge	---	AT1G03830	1.08	0.11	1.01	0.346035	0.484504	-6.70
245013_at	ATPase epsilon subunit	---	---	-1.07	-0.09	-1.01	0.346162	0.484652	-6.70
253933_at	hypothetical protein	---	AT4G26820	-1.10	-0.13	-1.01	0.34622	0.484704	-6.70
251829_at	putative protein KIAA0882 protein,	---	AT3G55020	-1.20	-0.26	-1.01	0.346677	0.485314	-6.70
248801_at	homeobox-leucine zipper protein-lik	HAT2	AT5G47370	-1.28	-0.35	-1.01	0.346766	0.485396	-6.70
262881_at	unknown protein ; supported by cDI	---	AT1G64890	-1.16	-0.21	-1.01	0.346778	0.485396	-6.70
262420_at	hypothetical protein contains simila	TAF15	AT1G50300	-1.07	-0.09	-1.01	0.346862	0.485484	-6.71
258220_at	DnaJ, putative similar to DnaJ GB:	---	AT3G17830	1.12	0.16	1.01	0.346933	0.485554	-6.71
254217_at	putative protein other hypothetical	---	AT4G23720	-1.07	-0.10	-1.01	0.347055	0.485694	-6.71
265704_at	hypothetical protein predicted by ge	---	AT2G03420	-1.13	-0.17	-1.01	0.347087	0.485709	-6.71
248695_at	putative protein similar to unknown	---	AT5G48350	-1.12	-0.17	-1.01	0.347193	0.485828	-6.71
266360_at	Mutator-like transposase similar to	FRS2	AT2G32250	-1.19	-0.25	-1.01	0.347246	0.485852	-6.71
250204_at	leucine zipper protein-like	ATEXO70C	AT5G13990	-1.09	-0.13	-1.01	0.347253	0.485852	-6.71
249815_at	60S ribosomal protein L13 ; suppo	---	AT5G23900	1.13	0.18	1.01	0.347569	0.486263	-6.71
260782_at	unknown protein ; supported by cDI	---	AT1G14570	1.07	0.10	1.01	0.34768	0.486389	-6.71
254896_at	MADS-box protein AGL14	AGL14	AT4G11880	-1.07	-0.10	-1.01	0.347761	0.486449	-6.71
259153_at	unknown protein ;supported by full-	---	AT3G10250	1.10	0.14	1.01	0.347765	0.486449	-6.71
256805_at	unknown protein contains similarity	---	AT3G20930	1.19	0.25	1.01	0.347841	0.486507	-6.71

253737_at	Expressed protein ; supported by fu	---	AT4G28703	1.26	0.34	1.01	0.34785	0.486507	-6.71
247888_at	phytocyanin/early nodulin-like prote	---	AT5G57920	1.09	0.12	1.01	0.347895	0.486514	-6.71
246532_at	putative protein beta-glucan-elicito	---	AT5G15870	-1.38	-0.47	-1.01	0.347897	0.486514	-6.71
246980_at	peptidylprolyl isomerase (cyclophilir	---	AT5G67530	1.08	0.11	1.01	0.347993	0.486619	-6.71
252209_at	putative protein RXF26, Arabidops	---	AT3G50400	-1.16	-0.22	-1.01	0.348063	0.486686	-6.71
262507_at	receptor-like protein kinase, putativ	---	AT1G11330	-1.10	-0.14	-1.01	0.348089	0.486693	-6.71
251694_s_a	putative protein NAM (no apical me	anac063	AT3G55210	-1.07	-0.10	-1.01	0.348175	0.486783	-6.71
248168_at	beta-glucosidase	BGLU41	AT5G54570	-1.09	-0.12	-1.01	0.348238	0.486818	-6.71
247096_at	S-adenosyl-L-methionine:salicylic a	---	AT5G66430	1.06	0.09	1.01	0.348243	0.486818	-6.71
260233_at	putative cytochrome P450 similar to	CYP98A9	AT1G74550	-1.14	-0.19	-1.01	0.348308	0.48688	-6.71
255189_at	hypothetical protein	---	AT4G07350	-1.07	-0.10	-1.01	0.348407	0.486988	-6.71
257710_at	unknown protein ;supported by full-	---	AT3G27350	1.09	0.13	1.01	0.348446	0.487013	-6.71
246102_at	putative protein various predicted p	---	AT5G32590	-1.07	-0.10	-1.01	0.348605	0.487205	-6.71
245846_at	P-type transporting ATPase, putati	---	AT1G26130	1.11	0.15	1.01	0.348663	0.487239	-6.71
263261_at	putative pre-mRNA splicing factor s	---	AT1G10580	1.06	0.09	1.01	0.348699	0.487239	-6.71
248018_at	putative protein strong similarity to u	---	AT5G56470	-1.10	-0.14	-1.01	0.348707	0.487239	-6.71
266174_at	hypothetical protein predicted by ge	---	AT2G02440	-1.06	-0.09	-1.01	0.348714	0.487239	-6.71
247452_at	H-protein promoter binding factor-li	CDF1	AT5G62430	-1.13	-0.18	-1.01	0.348852	0.487353	-6.71
249184_at	receptor kinase-like protein	---	AT5G43020	-1.14	-0.19	-1.01	0.348856	0.487353	-6.71
256391_at	hypothetical protein predicted by ge	---	AT3G06090	-1.06	-0.09	-1.01	0.34886	0.487353	-6.71
256022_at	amino acid permease I identical to a	AAP1	AT1G58360	-1.24	-0.31	-1.01	0.348933	0.487425	-6.71
259050_at	hypothetical protein similar to GB:A	---	AT3G03356	-1.06	-0.09	-1.01	0.348961	0.487434	-6.71
262788_at	unknown protein ESTs gb|T75618 a	---	AT1G10690	1.12	0.16	1.01	0.349066	0.487551	-6.71
263366_at	unknown protein	---	AT2G20440	-1.09	-0.13	-1.01	0.349177	0.487677	-6.71
247948_at	putative protein strong similarity to u	---	AT5G57130	-1.10	-0.14	-1.01	0.349404	0.487963	-6.71
258150_at	hypothetical protein ;supported by	---	AT3G18160	1.17	0.23	1.01	0.349578	0.488177	-6.71
260870_at	GTP-binding protein(RAB1Y), puta	ATRAB18	AT1G43890	-1.10	-0.13	-1.00	0.349707	0.488326	-6.71
266670_at	putative flavonol 3-O-glucosyltransf	UGT71C2	AT2G29740	1.10	0.14	1.00	0.349728	0.488326	-6.71
262368_at	unknown protein ;supported by full-	---	AT1G73060	-1.14	-0.19	-1.00	0.349797	0.488393	-6.71
266373_x_a	putative retroelement pol polyprotei	---	---	-1.10	-0.13	-1.00	0.349898	0.488429	-6.71
265379_at	similar to late embryogenesis abun	---	AT2G18340	-1.08	-0.11	-1.00	0.349906	0.488429	-6.71
264586_at	putative cytochrome P450 Similar to	CYP88A3	AT1G05160	1.09	0.12	1.00	0.349907	0.488429	-6.71
259843_at	hypothetical protein predicted by ge	---	AT1G73570	-1.12	-0.16	-1.00	0.349908	0.488429	-6.71
244912_at	cytochrome c biogenesis orf382 Pro	---	AT2G07783	1.12	0.16	1.00	0.350014	0.488542	-6.71
257758_at	eukaryotic translation elongation fa	---	AT3G22980	1.09	0.13	1.00	0.350032	0.488542	-6.71

246647_at	putative protein predicted proteins f	---	---	-1.07	-0.10	-1.00	0.350109	0.488618	-6.71
265333_at	hypothetical protein predicted by ge	AtHB24	AT2G18350	-1.11	-0.15	-1.00	0.350237	0.488743	-6.71
254324_at	putative protein various predicted p	---	AT4G22640	-1.10	-0.14	-1.00	0.35024	0.488743	-6.71
254525_at	putative protein predicted protein, A	---	AT4G19580	-1.09	-0.12	-1.00	0.350262	0.488743	-6.71
263203_at	hypothetical protein predicted by ge	chr31	AT1G05490	-1.06	-0.09	-1.00	0.350476	0.489011	-6.71
259727_at	ferrodoxin precursor identical to FE	FED A	AT1G60950	-1.07	-0.10	-1.00	0.350691	0.489281	-6.71
263547_at	hypothetical protein predicted by ge	---	AT2G21680	-1.10	-0.13	-1.00	0.350714	0.489283	-6.71
263170_at	putative peroxisome assembly facto	PEX6	AT1G03000	1.06	0.09	1.00	0.350784	0.489333	-6.71
260322_at	unknown protein	---	AT1G63900	-1.08	-0.12	-1.00	0.350792	0.489333	-6.71
264669_at	putative RAS-related protein, RAB1	ATRAB11C	AT1G09630	-1.13	-0.18	-1.00	0.350999	0.489554	-6.71
262241_at	hypothetical protein predicted by ge	---	AT1G48390	-1.07	-0.09	-1.00	0.351005	0.489554	-6.71
258370_at	Expressed protein ; supported by fu	---	AT3G14395	-1.09	-0.13	-1.00	0.35103	0.489554	-6.71
256907_at	hydoxyethylthiazole kinase, putativ	---	AT3G24030	1.13	0.18	1.00	0.351037	0.489554	-6.71
248996_at	unknown protein	RRS1	AT5G45260	1.14	0.19	1.00	0.351133	0.489659	-6.71
264220_at	unknown protein similar to putative	ARPC3	AT1G60430	1.08	0.11	1.00	0.35133	0.489903	-6.72
262447_at	hypothetical protein contains simila	---	AT1G49250	-1.08	-0.11	-1.00	0.351447	0.490036	-6.72
264317_at	spermidine synthase, putative simi	SPDS2	AT1G70310	1.08	0.12	1.00	0.351741	0.490393	-6.72
254143_at	putative protein histidine-rich calciu	---	AT4G24680	1.07	0.09	1.00	0.351756	0.490393	-6.72
266139_at	Expressed protein ; supported by fu	---	AT2G28085	-1.18	-0.24	-1.00	0.351767	0.490393	-6.72
252144_at	ribosomal protein L8 homolog ribos	---	AT3G51190	1.07	0.10	1.00	0.3518	0.490409	-6.72
255030_at	putative protein retrovirus-related p	---	---	-1.08	-0.11	-1.00	0.352115	0.490817	-6.72
259432_at	myb-related protein, putative simila	---	AT1G01520	-1.11	-0.15	-1.00	0.352223	0.490938	-6.72
265280_at	Expressed protein ; supported by fu	LCR5	AT2G28355	-1.08	-0.11	-1.00	0.352391	0.491143	-6.72
260708_at	expressed protein ; supported by fu	---	AT1G32310	1.09	0.13	1.00	0.352673	0.491497	-6.72
256931_at	LEA protein, putative similar to LEA	---	AT3G22490	1.07	0.10	1.00	0.352688	0.491497	-6.72
266665_at	unknown protein	---	AT2G29790	-1.09	-0.12	-1.00	0.352713	0.491501	-6.72
249216_at	serine carboxypeptidase II-like ; su	scpl42	AT5G42240	-1.17	-0.23	-1.00	0.352831	0.491636	-6.72
255499_at	putative WD-repeat protein similar	---	AT4G02730	1.07	0.10	1.00	0.352883	0.491659	-6.72
262244_at	serine threonine kinase, putative si	CIPK17	AT1G48260	1.43	0.52	1.00	0.352899	0.491659	-6.72
258831_at	putative integral membrane protein	---	AT3G07080	1.07	0.09	1.00	0.352913	0.491659	-6.72
248247_at	putative protein contains similarity t	SPCH	AT5G53210	-1.08	-0.11	-1.00	0.353041	0.491808	-6.72
257225_s_a	50S ribosomal protein L12-C identi	RPL12-C	AT3G27830	-1.08	-0.10	-1.00	0.353168	0.491954	-6.72
259744_at	putative ketoacyl-CoA synthase sim	KCS7	AT1G71160	-1.08	-0.11	-1.00	0.353191	0.491957	-6.72
256053_at	UDP-glucose glucosyltransferase,	UGT71C3	AT1G07260	1.28	0.35	1.00	0.353468	0.492298	-6.72
255530_at	hypothetical protein	---	AT4G02140	-1.08	-0.11	-1.00	0.353479	0.492298	-6.72

262333_at	hypothetical protein similar to putati	---	AT1G64020	1.09	0.12	1.00	0.353655	0.492513	-6.72
250586_at	putative protein similar to unknown	---	AT5G07630	-1.10	-0.14	-1.00	0.353821	0.492714	-6.72
257512_at	unknown protein	---	AT1G35250	-1.07	-0.10	-1.00	0.353912	0.492811	-6.72
260352_at	Expressed protein ; supported by fu	PDCB4	AT1G69295	1.08	0.11	1.00	0.353985	0.492882	-6.72
256878_at	major latex protein, putative similar	---	AT3G26460	1.10	0.14	1.00	0.354055	0.49295	-6.72
260530_at	putative peptidyl-prolyl cis-trans iso	---	AT2G47320	1.07	0.10	0.99	0.354216	0.493143	-6.72
249770_at	unknown protein ;supported by full-	WRKY30	AT5G24110	1.57	0.65	0.99	0.354241	0.493149	-6.72
253257_at	extra-large G-protein - like extra-lar	XLG2	AT4G34390	1.10	0.14	0.99	0.354352	0.493272	-6.72
249328_at	AtRAD3 (dbj|BAA92828.1) ; suppo	ATR	AT5G40820	-1.09	-0.13	-0.99	0.354559	0.493531	-6.72
266640_at	Expressed protein ; supported by fu	---	AT2G35585	-1.10	-0.14	-0.99	0.354621	0.493587	-6.72
248322_at	putative protein similar to unknown	---	AT5G52760	1.85	0.89	0.99	0.35473	0.493709	-6.72
256298_at	DNA-binding protein contains Pfam	AGL94	AT1G69540	-1.08	-0.11	-0.99	0.354813	0.493794	-6.72
249012_at	flavonoid 3,5-hydroxylase-like; cyto	CYP706A3	AT5G44620	-1.08	-0.11	-0.99	0.354855	0.493798	-6.72
265634_at	hypothetical protein predicted by ge	---	AT2G25530	-1.08	-0.12	-0.99	0.354859	0.493798	-6.72
265251_at	unknown protein predicted by gens	TET14	AT2G01960	-1.08	-0.11	-0.99	0.354886	0.493805	-6.72
246493_at	putative protein hypothetical protein	CRS1	AT5G16180	-1.09	-0.13	-0.99	0.354971	0.493888	-6.72
254267_at	dihydroorotase ; supported by cDN	PYR4	AT4G22930	-1.09	-0.13	-0.99	0.354988	0.493888	-6.72
249499_at	hypothetical protein	---	AT5G39250	1.08	0.11	0.99	0.355356	0.494346	-6.72
257810_at	TOM20, putative similar to TOM20	TOM20-1	AT3G27070	1.08	0.12	0.99	0.355361	0.494346	-6.72
256924_at	Anthocyanin 5-aromatic acyltransfe	AT5MAT	AT3G29590	-1.09	-0.12	-0.99	0.355467	0.494455	-6.72
253639_at	putative protein component of anili	---	AT4G30550	1.13	0.17	0.99	0.355483	0.494455	-6.72
260633_at	protein kinase, putative similar to p	HT1	AT1G62400	-1.08	-0.11	-0.99	0.355608	0.494599	-6.72
250503_at	putative protein similar to unknown	---	AT5G09820	-1.12	-0.16	-0.99	0.355714	0.494716	-6.72
247894_at	putative protein similar to unknown	CPL4	AT5G58000	1.15	0.20	0.99	0.355822	0.494836	-6.72
261444_at	hypothetical protein predicted by ge	SYP61	AT1G28490	-1.08	-0.11	-0.99	0.355954	0.49499	-6.73
264723_at	putative salt-inducible protein simila	---	AT1G22960	1.08	0.11	0.99	0.356079	0.495134	-6.73
255272_at	putative protein (ubiquitin like) to va	---	AT4G05270	-1.07	-0.09	-0.99	0.356119	0.495158	-6.73
263561_at	unknown protein	---	AT2G15360	-1.06	-0.09	-0.99	0.356172	0.495202	-6.73
253038_at	homeobox protein HAT22 ;support	HAT22	AT4G37790	1.15	0.20	0.99	0.35636	0.495433	-6.73
266914_at	putative beta-amylase	BAM7	AT2G45880	-1.16	-0.21	-0.99	0.356408	0.49547	-6.73
265874_at	hypothetical protein predicted by ge	---	AT2G01640	1.09	0.13	0.99	0.356459	0.49551	-6.73
257411_s_a	hypothetical protein predicted by ge	---	AT1G61320	1.06	0.09	0.99	0.356496	0.495531	-6.73
266052_at	putative WRKY-type DNA binding p	WRKY55	AT2G40740	-1.16	-0.21	-0.99	0.356538	0.495539	-6.73
256730_at	floral homeotic protein AGL8, putat	AGL79	AT3G30260	-1.06	-0.09	-0.99	0.356545	0.495539	-6.73
247336_at	putative protein similar to unknown	---	AT5G63640	-1.11	-0.14	-0.99	0.356613	0.495549	-6.73

258846_at	unknown protein ; supported by ful	---	AT3G03070	1.07	0.10	0.99	0.35662	0.495549	-6.73
267251_at	putative casein kinase II catalytic (a	---	AT2G23070	-1.07	-0.10	-0.99	0.356621	0.495549	-6.73
251477_at	putative protein	---	AT3G59680	-1.07	-0.09	-0.99	0.356664	0.495549	-6.73
254321_at	trehalose-6-phosphate phosphatas	CPuORF27	AT4G22590	-1.15	-0.20	-0.99	0.356679	0.495549	-6.73
252710_at	cellulase-like protein cellulase, Sar	AtGH9A4	AT3G43860	-1.07	-0.10	-0.99	0.356682	0.495549	-6.73
256260_at	hypothetical protein	---	AT3G12440	1.07	0.10	0.99	0.356819	0.495709	-6.73
249346_at	amino acid permease	LTH1	AT5G40780	1.10	0.14	0.99	0.356861	0.495738	-6.73
253269_at	hypothetical protein	---	AT4G34140	-1.08	-0.11	-0.99	0.356968	0.495855	-6.73
247297_at	peroxidase ATP3a (emb|CAA6734(	---	AT5G64100	-1.24	-0.31	-0.99	0.357033	0.495915	-6.73
252483_at	scarecrow-like protein scarecrow-li	---	AT3G46600	1.21	0.27	0.99	0.357061	0.495924	-6.73
255324_s_a	putative reverse transcriptase	---	---	-1.06	-0.09	-0.99	0.357087	0.495929	-6.73
255845_at	putative cinnamoyl-CoA reductase	---	AT2G33600	1.13	0.18	0.99	0.357138	0.495971	-6.73
263725_at	unknown protein	---	AT2G13550	1.07	0.09	0.99	0.357405	0.496312	-6.73
246468_at	UDP glucose:flavonoid 3-o-glucosy	UGT78D2	AT5G17050	1.15	0.21	0.99	0.357443	0.496312	-6.73
248339_at	prolyl tRNA synthetase	OVA6	AT5G52520	-1.09	-0.12	-0.99	0.357449	0.496312	-6.73
266685_at	hypothetical protein	---	AT2G19710	-1.08	-0.12	-0.99	0.357547	0.496396	-6.73
AFFX-TrpnX	B. subtilis /GEN=trpC, trpF /DB_XR	---	---	-1.06	-0.09	-0.99	0.35756	0.496396	-6.73
257249_at	unknown protein	---	AT3G24180	1.12	0.16	0.99	0.357575	0.496396	-6.73
255911_at	receptor-like kinase, putative simila	---	AT1G66930	1.07	0.09	0.99	0.357665	0.496491	-6.73
252836_at	putative protein predicted polyprote	---	---	-1.07	-0.10	-0.99	0.357942	0.496845	-6.73
248184_at	CHP-rich zinc finger protein-like	---	AT5G54050	1.07	0.10	0.99	0.357982	0.49687	-6.73
254039_at	putative protein Human GS1 (prote	GPP1	AT4G25840	-1.11	-0.15	-0.99	0.358022	0.496896	-6.73
267012_at	similar to latex allergen from Hevea	PLP6	AT2G39220	1.23	0.30	0.99	0.358118	0.496999	-6.73
264776_at	unknown protein location of EST gb	---	AT1G22860	1.08	0.11	0.99	0.358167	0.497037	-6.73
252631_s_a	putative protein predicted proteins,	---	---	-1.07	-0.09	-0.99	0.358193	0.497042	-6.73
255253_at	contains similarity to S. cerevisiae v	VPS28-2	AT4G05000	1.08	0.11	0.99	0.358241	0.497042	-6.73
254653_at	polygalacturonase-like protein exo	---	AT4G18180	-1.06	-0.08	-0.99	0.358242	0.497042	-6.73
256695_at	unknown protein	---	AT3G32090	-1.09	-0.12	-0.99	0.358258	0.497042	-6.73
249343_at	succinate dehydrogenase iron-prot	SDH2-2	AT5G40650	1.11	0.15	0.99	0.358295	0.497063	-6.73
252642_at	putative protein predicted protein, A	---	AT3G44580	1.06	0.09	0.99	0.358359	0.497122	-6.73
249274_at	unknown protein	---	AT5G41860	-1.12	-0.16	-0.99	0.358451	0.497194	-6.73
262998_at	hypothetical protein predicted by ge	---	AT1G54280	-1.06	-0.09	-0.99	0.358455	0.497194	-6.73
247733_at	putative protein heat shock protein	---	AT5G59610	-1.13	-0.17	-0.99	0.358634	0.497412	-6.73
245614_at	retrovirus-related like polyprotein	---	---	-1.09	-0.13	-0.99	0.35869	0.49746	-6.73
247318_at	3(2),5-bisphosphate nucleotidase	---	AT5G63990	1.23	0.30	0.98	0.358856	0.497659	-6.73

254959_at	predicted protein	UGE5	AT4G10955	-1.13	-0.18	-0.98	0.358969	0.497786	-6.73
259737_at	acyl-CoA synthetase, putative simi	---	AT1G64400	1.28	0.36	0.98	0.359042	0.497857	-6.73
245610_at	hypothetical protein	---	AT4G14380	-1.09	-0.12	-0.98	0.359171	0.497944	-6.73
248769_at	putative protein strong similarity to	---	AT5G47730	1.30	0.38	0.98	0.35918	0.497944	-6.73
261818_at	similar to hypethetical 62.8 KD prot	---	AT1G11390	-1.09	-0.12	-0.98	0.359188	0.497944	-6.73
256474_at	unknown protein	---	---	-1.10	-0.14	-0.98	0.359192	0.497944	-6.73
250640_at	putative protein protein kinase Xa2	---	AT5G07150	1.16	0.21	0.98	0.359351	0.498107	-6.73
257379_x_a	Mutator-like transposase similar to	---	---	-1.08	-0.11	-0.98	0.359353	0.498107	-6.73
260213_at	putative protein kinase similar to pr	---	AT1G74490	1.07	0.09	0.98	0.359451	0.498187	-6.73
257287_at	hypothetical protein predicted by ge	---	---	1.07	0.09	0.98	0.359455	0.498187	-6.73
262889_at	hypothetical protein	---	AT1G14800	-1.11	-0.16	-0.98	0.35985	0.498705	-6.73
265930_at	putative spliceosome associated pr	emb2444	AT2G18510	-1.09	-0.12	-0.98	0.360057	0.498942	-6.73
249282_at	CMP-sialic acid transporter-like pro	---	AT5G41760	-1.11	-0.15	-0.98	0.360065	0.498942	-6.73
267468_at	unknown protein ; supported by cD	---	AT2G30530	1.10	0.13	0.98	0.36011	0.498973	-6.73
265618_at	hypothetical protein predicted by ge	---	AT2G25460	-1.09	-0.12	-0.98	0.360188	0.499052	-6.73
258267_at	putative delta 9 desaturase similar	---	AT3G15870	-1.07	-0.10	-0.98	0.360404	0.49932	-6.73
257068_at	non-LTR reverse transcriptase, put	---	---	1.06	0.09	0.98	0.360441	0.499341	-6.73
255398_at	hypothetical protein	---	AT4G03740	-1.08	-0.11	-0.98	0.36047	0.499349	-6.73
252931_at	putative ubiquitin-dependent protec	---	AT4G38930	1.08	0.11	0.98	0.360509	0.499349	-6.74
255427_at	hypothetical protein	---	AT4G03380	-1.06	-0.09	-0.98	0.360512	0.499349	-6.74
246366_at	light repressible receptor protein ki	---	AT1G51850	1.12	0.16	0.98	0.360644	0.499501	-6.74
264073_at	putative replication protein A1	---	---	1.09	0.12	0.98	0.360793	0.499677	-6.74
247412_at	unknown protein	---	AT5G63010	1.09	0.12	0.98	0.360907	0.499797	-6.74
253601_at	hypothetical protein	---	AT4G30900	-1.07	-0.09	-0.98	0.360923	0.499797	-6.74
246065_at	calcium-dependent protein kinase	CPK34	AT5G19360	-1.08	-0.11	-0.98	0.361033	0.499919	-6.74
257197_at	selenium binding protein, putative	SBP3	AT3G23800	-1.07	-0.10	-0.98	0.361065	0.499933	-6.74
265598_at	putative protein phosphatase 2C	---	AT2G14270	-1.08	-0.11	-0.98	0.361272	0.50019	-6.74
266082_at	hypothetical protein predicted by ge	---	AT2G37830	-1.12	-0.16	-0.98	0.361309	0.500199	-6.74
262437_at	hypothetical protein	---	---	-1.09	-0.13	-0.98	0.361323	0.500199	-6.74
249013_at	receptor-like protein kinase	GSO2	AT5G44700	-1.06	-0.09	-0.98	0.361414	0.500295	-6.74
255484_at	putative protein similar to A. thalian	---	AT4G02540	-1.10	-0.13	-0.98	0.361493	0.500373	-6.74
261593_at	unknown protein	---	AT1G33170	-1.57	-0.65	-0.98	0.361729	0.500669	-6.74
248550_at	putative protein similar to unknown	QS	AT5G50210	-1.14	-0.18	-0.98	0.36175	0.500669	-6.74
251599_at	adenylosuccinate synthetase ;supp	ADSS	AT3G57610	1.09	0.12	0.98	0.361795	0.500701	-6.74
254099_at	protein-methionine-S-oxide reducta	---	AT4G25130	-1.12	-0.17	-0.98	0.361844	0.50071	-6.74

256634_s_a	hypothetical protein predicted by ge	---	---	1.07	0.09	0.98	0.361846	0.50071	-6.74
251253_at	putative zinc-finger protein zinc-fin	---	AT3G62240	1.14	0.18	0.98	0.361932	0.500782	-6.74
245298_at	hypothetical protein ; supported by	---	AT4G15010	-1.08	-0.11	-0.98	0.36196	0.500782	-6.74
265669_at	unknown protein ;supported by full-	---	AT2G32040	-1.14	-0.19	-0.98	0.361963	0.500782	-6.74
249033_at	putative protein contains similarity t	---	AT5G44920	-1.08	-0.11	-0.98	0.362027	0.500839	-6.74
261014_at	unknown protein ;supported by full-	---	AT1G26460	1.08	0.11	0.98	0.362127	0.500948	-6.74
267168_at	putative alcohol dehydrogenase	---	AT2G37770	1.61	0.69	0.98	0.362161	0.500964	-6.74
266692_at	Ac-like transposase related to Ac D	---	AT2G19960	1.08	0.11	0.98	0.362373	0.501209	-6.74
264087_at	hypothetical protein predicted by ge	emb1381	AT2G31340	1.08	0.11	0.98	0.362382	0.501209	-6.74
262546_at	iron-regulated transporter protein,	ZIP10	AT1G31260	-1.18	-0.24	-0.98	0.362416	0.501225	-6.74
263149_at	unknown protein	---	AT1G53970	1.08	0.11	0.98	0.362702	0.50159	-6.74
257853_at	hypothetical protein predicted by g	---	AT3G12960	-1.08	-0.12	-0.98	0.362966	0.501926	-6.74
249314_at	receptor kinase-like protein	---	AT5G41180	-1.10	-0.13	-0.98	0.363107	0.502033	-6.74
245447_at	triacylglycerol lipase like protein	---	AT4G16820	1.28	0.36	0.98	0.363109	0.502033	-6.74
248516_at	unknown protein	---	AT5G50540	1.10	0.14	0.98	0.36311	0.502033	-6.74
259207_at	unknown protein	---	AT3G09050	1.10	0.14	0.97	0.363353	0.502339	-6.74
251498_at	putative protein hypothetical protein	---	AT3G59070	1.09	0.13	0.97	0.363491	0.502498	-6.74
249487_at	ABC transporter -like protein TAP-l	TAP2	AT5G39040	1.16	0.21	0.97	0.363527	0.502498	-6.74
256421_at	hypothetical protein predicted by ge	---	AT1G33500	-1.07	-0.10	-0.97	0.363535	0.502498	-6.74
256115_at	unknown protein ; supported by cDl	---	AT1G16880	1.13	0.17	0.97	0.363683	0.502673	-6.74
245726_at	homeobox protein, putative similar	HDG11	AT1G73360	-1.08	-0.11	-0.97	0.363749	0.502733	-6.74
245577_at	kinase like protein	---	AT4G14780	-1.09	-0.13	-0.97	0.363834	0.50282	-6.74
245937_at	putative protein 22kDa peroxisoma	---	AT5G19750	1.15	0.20	0.97	0.363946	0.502945	-6.74
264930_at	receptor-like kinase, putative simila	NIK3	AT1G60800	1.11	0.15	0.97	0.363972	0.502947	-6.74
267430_at	unknown protein	EDA3	AT2G34860	-1.12	-0.17	-0.97	0.363992	0.502947	-6.74
262808_at	Avr9 elicitor response-like protein s	---	AT1G11730	-1.08	-0.11	-0.97	0.36403	0.502969	-6.74
255958_at	high affinity sulphate transporter, p	SULTR1;3	AT1G22150	-1.10	-0.13	-0.97	0.36406	0.50298	-6.74
264243_at	hypothetical protein predicted by ge	---	AT1G54650	1.12	0.16	0.97	0.364165	0.503095	-6.74
260038_at	Expressed protein ; supported by fu	---	AT1G68875	1.07	0.10	0.97	0.364209	0.503125	-6.74
245205_at	putative protein similarity to splicing	---	AT5G12280	-1.11	-0.15	-0.97	0.364237	0.50313	-6.74
257578_x_a	unknown protein similar to hypothet	---	AT3G30160	-1.07	-0.10	-0.97	0.364256	0.50313	-6.74
254458_at	putative protein heat shock protein	ATERDJ2B	AT4G21180	1.14	0.19	0.97	0.364293	0.50315	-6.74
247743_at	protein kinase - like serine/threonir	---	AT5G59010	-1.10	-0.14	-0.97	0.364414	0.503257	-6.74
258543_at	unknown protein	---	AT3G06870	-1.09	-0.13	-0.97	0.364414	0.503257	-6.74
261630_at	hypothetical protein predicted by ge	---	AT1G50080	-1.07	-0.10	-0.97	0.364492	0.503333	-6.74

253899_at	putative protein protein disulfide-iso	ATPDIL5-4	AT4G27080	1.09	0.12	0.97	0.364539	0.503364	-6.74
263746_at	putative retroelement pol polyprotei	---	---	1.07	0.10	0.97	0.36456	0.503364	-6.74
264381_at	putative ribonuclease large subunit	---	AT2G25100	-1.13	-0.17	-0.97	0.36458	0.503364	-6.74
261755_at	histone H2B, putative similar to GB	---	AT1G08170	-1.11	-0.15	-0.97	0.364709	0.503493	-6.74
257831_at	unknown protein ;supported by full-	CCB1	AT3G26710	-1.10	-0.13	-0.97	0.364718	0.503493	-6.74
259062_at	unknown protein est hits to genscan	---	AT3G07440	1.12	0.16	0.97	0.364854	0.503651	-6.74
251021_at	thaumatin-like protein thaumatin-lik	---	AT5G02140	-1.16	-0.21	-0.97	0.364961	0.503768	-6.74
250383_at	putative GTP-binding protein GTP-	---	AT5G11480	1.12	0.16	0.97	0.365048	0.503857	-6.74
260454_at	RING-H2 zinc finger protein (ATL3)	ATL3	AT1G72310	-1.18	-0.23	-0.97	0.365132	0.503943	-6.74
256809_at	hypothetical protein predicted by ge	ALY3	AT3G21430	-1.10	-0.14	-0.97	0.365354	0.504218	-6.75
261714_at	hypothetical protein similar to hypot	TET16	AT1G18510	-1.11	-0.15	-0.97	0.365566	0.50448	-6.75
263713_at	Expressed protein ; supported by fu	---	AT2G20595	-1.09	-0.13	-0.97	0.365744	0.504696	-6.75
252653_at	putative kinesin-like protein similar	---	AT3G44730	1.09	0.12	0.97	0.365961	0.504965	-6.75
260901_at	flavin-containing monooxygenases	YUC11	AT1G21430	-1.10	-0.14	-0.97	0.366032	0.505031	-6.75
256257_at	arginine-tRNA-protein transferase,	ATE2	AT3G11240	1.07	0.10	0.97	0.366125	0.50513	-6.75
257110_x_a	hypothetical protein	---	---	-1.10	-0.13	-0.97	0.366338	0.505368	-6.75
251913_at	putative protein several malat dehy	---	AT3G53910	-1.07	-0.10	-0.97	0.366342	0.505368	-6.75
267074_s_a	hypothetical protein predicted by ge	---	AT2G40955	1.08	0.10	0.97	0.366428	0.505455	-6.75
265710_at	unknown protein	---	AT2G03370	-1.07	-0.10	-0.97	0.36646	0.505455	-6.75
253350_at	hypothetical protein	---	AT4G33690	1.07	0.10	0.97	0.366493	0.505455	-6.75
257351_at	putative mitochondrial carrier protei	MBAC1	AT2G33820	-1.10	-0.14	-0.97	0.366505	0.505455	-6.75
245172_at	hypothetical protein predicted by ge	---	AT2G47540	-1.06	-0.09	-0.97	0.366516	0.505455	-6.75
266904_at	putative pyruvate dehydrogenase E	---	AT2G34590	-1.16	-0.22	-0.97	0.366851	0.505887	-6.75
253006_at	putative amino acid transport prote	---	AT4G38250	1.09	0.13	0.97	0.366889	0.505908	-6.75
249578_at	putative protein predicted protein, A	---	AT5G37730	-1.06	-0.09	-0.97	0.366968	0.505987	-6.75
255162_at	putative transposon protein	---	---	-1.06	-0.09	-0.97	0.367	0.506001	-6.75
252739_at	putative protein mRNA, Homo sapi	---	AT3G43250	-1.08	-0.11	-0.97	0.367075	0.506072	-6.75
252490_at	glucuronosyl transferase-like prote	---	AT3G46720	-1.08	-0.11	-0.97	0.367096	0.506072	-6.75
246126_at	putative protein predicted protein, (	ATNUDX19	AT5G20070	-1.17	-0.23	-0.97	0.367151	0.506116	-6.75
244955_at	hypothetical protein	---	---	1.12	0.16	0.97	0.367211	0.506169	-6.75
251442_at	putative protein multisynthetase co	---	AT3G59980	-1.13	-0.18	-0.97	0.367242	0.506182	-6.75
262549_at	hypothetical protein similar to hypot	---	AT1G31290	-1.07	-0.10	-0.97	0.367273	0.506194	-6.75
254400_at	kinesin-related protein katA ; suppo	ATK1	AT4G21270	-1.07	-0.09	-0.97	0.367335	0.506224	-6.75
245217_at	retroelement pol polyprotein, putati	---	---	-1.11	-0.15	-0.97	0.36734	0.506224	-6.75
259770_s_a	phosphoribosylanthranilate isomera	PAI3	AT1G07780	1.13	0.18	0.97	0.367609	0.506565	-6.75

250517_at	serine-type carboxypeptidase II-like	scpl35	AT5G08260	-1.24	-0.31	-0.97	0.367691	0.506627	-6.75
262601_at	hypothetical protein similar to GB:P	ATHSRP54	AT1G15310	1.11	0.15	0.97	0.367699	0.506627	-6.75
259780_at	exonuclease, putative similar to GI	---	AT1G29630	1.08	0.11	0.97	0.367761	0.506682	-6.75
251052_at	DP-2 transcription factor - like trans	DPA	AT5G02470	-1.09	-0.12	-0.97	0.367799	0.506704	-6.75
254755_at	hypothetical protein	---	AT4G13220	-1.09	-0.12	-0.97	0.367879	0.506783	-6.75
264988_at	glutathione transferase, putative si	ATGSTU14	AT1G27140	1.11	0.15	0.96	0.368018	0.506926	-6.75
249259_at	putative protein similar to unknown	---	AT5G41660	1.33	0.41	0.96	0.368027	0.506926	-6.75
247479_at	NAC - like protein OsNAC7, Oryza	ANAC101	AT5G62380	-1.07	-0.10	-0.96	0.368211	0.507148	-6.75
248876_at	putative protein similar to unknown	---	---	-1.06	-0.08	-0.96	0.368275	0.507206	-6.75
245855_at	sulfate transporter ; supported by c	SULTR4;1	AT5G13550	1.12	0.16	0.96	0.368366	0.507286	-6.75
263168_at	putative glutaredoxin Strong similar	---	AT1G03020	-1.28	-0.36	-0.96	0.368377	0.507286	-6.75
264132_at	hypothetical protein predicted by ge	---	AT1G79100	-1.10	-0.13	-0.96	0.368429	0.507292	-6.75
266070_at	hypothetical protein predicted by ge	EXLB3	AT2G18660	2.30	1.20	0.96	0.368435	0.507292	-6.75
254536_at	putative protein chitinase / lysozym	---	AT4G19720	-1.08	-0.11	-0.96	0.368448	0.507292	-6.75
249156_s_a	putative protein similar to unknown	---	AT5G43490	-1.07	-0.09	-0.96	0.368608	0.507482	-6.75
258828_at	putative purple acid phosphatase si	PAP15	AT3G07130	-1.09	-0.12	-0.96	0.368726	0.507612	-6.75
250218_at	putative protein contains similarity t	CHC1	AT5G14170	1.11	0.15	0.96	0.368841	0.507741	-6.75
262999_at	NAM protein, putative similar to NA	ANAC020	AT1G54330	-1.11	-0.15	-0.96	0.368934	0.507817	-6.75
259940_at	hypothetical protein	---	AT1G71290	-1.07	-0.09	-0.96	0.368941	0.507817	-6.75
248960_at	subtilisin-like protease	---	AT5G45640	1.12	0.16	0.96	0.369021	0.507897	-6.75
260314_at	unknown protein similar to putative	---	AT1G63830	-1.14	-0.19	-0.96	0.369088	0.507936	-6.75
252474_at	putative protein several hypothetica	---	AT3G46620	1.25	0.32	0.96	0.369094	0.507936	-6.75
252758_at	putative protein several hypothetica	---	---	-1.09	-0.12	-0.96	0.369171	0.508011	-6.75
246132_at	Rad51-like protein ; supported by c	ATRAD51	AT5G20850	-1.06	-0.09	-0.96	0.36924	0.508075	-6.75
265809_at	unknown protein	---	AT2G18100	-1.09	-0.13	-0.96	0.369294	0.50812	-6.75
265152_s_a	hypothetical protein predicted by ge	---	AT1G30935	-1.07	-0.09	-0.96	0.369445	0.50827	-6.75
248317_at	unknown protein	---	AT5G52680	-1.08	-0.11	-0.96	0.369458	0.50827	-6.75
251164_s_a	putative protein protein phosphatas	---	AT3G63320	1.09	0.12	0.96	0.369471	0.50827	-6.75
265212_at	putative sugar transporter protein S	---	AT1G05030	-1.08	-0.11	-0.96	0.369597	0.508404	-6.75
259362_s_a	serin threonin-kinase, putative simi	---	AT1G13350	1.09	0.12	0.96	0.369613	0.508404	-6.75
259126_at	putative NADPH-ferrihemoprotein r	---	AT3G02280	1.07	0.10	0.96	0.369657	0.508434	-6.75
247519_at	NAM, no apical meristem, - like pro	ANAC100	AT5G61430	1.10	0.14	0.96	0.369698	0.50846	-6.75
262950_at	transcription initiation factor, putativ	---	AT1G75510	1.07	0.09	0.96	0.369762	0.508518	-6.75
264532_at	seed imbibition protein, putative sir	AtSIP1	AT1G55740	-1.08	-0.11	-0.96	0.36991	0.50869	-6.75
249044_at	Na+-dependent inorganic phosphat	PHT4;6	AT5G44370	-1.12	-0.16	-0.96	0.370024	0.508817	-6.75

265282_at	unknown protein	---	AT2G20380	-1.08	-0.11	-0.96	0.370107	0.5089	-6.76
259922_at	protein phosphatase 2C (AtP2C-H/	HAB1	AT1G72770	1.13	0.17	0.96	0.370134	0.508907	-6.76
254875_at	putative protein various predicted p	---	AT4G11590	1.08	0.11	0.96	0.370176	0.508934	-6.76
258984_at	putative DnaJ protein Pfam HMM h	ATERDJ3A	AT3G08970	-1.10	-0.13	-0.96	0.370536	0.509398	-6.76
265955_at	putative ABC transporter	PDR5	AT2G37280	1.08	0.11	0.96	0.370652	0.509498	-6.76
254488_at	putative protein receptor-like protei	---	AT4G20790	1.06	0.08	0.96	0.370653	0.509498	-6.76
256734_at	unknown protein	RIK	AT3G29390	-1.07	-0.10	-0.96	0.370791	0.509656	-6.76
247019_at	AP2 domain transcription factor-like	---	AT5G67010	-1.08	-0.11	-0.96	0.370875	0.50974	-6.76
264426_at	hypothetical protein similar to hypot	---	AT1G61760	-1.09	-0.12	-0.96	0.370958	0.509824	-6.76
249632_at	caffeic acid O-methyltransferase-lik	---	AT5G37170	-1.07	-0.10	-0.96	0.371036	0.509901	-6.76
266364_at	unknown protein	---	AT2G41230	1.39	0.48	0.96	0.371092	0.509947	-6.76
260293_at	unknown protein predicted by gens	---	AT1G63670	-1.10	-0.13	-0.96	0.371133	0.509948	-6.76
265211_at	late embryogenesis abundant prote	ATECP63	AT2G36640	-1.07	-0.09	-0.96	0.371138	0.509948	-6.76
259267_at	unknown protein ;supported by full-	---	AT3G01130	1.07	0.10	0.96	0.371258	0.510083	-6.76
246896_at	extensin - like protein Pex1 extensi	---	AT5G25550	-1.09	-0.12	-0.96	0.371406	0.510256	-6.76
247639_s_a	undecaprenyl diphosphate synthas	---	AT5G60500	-1.06	-0.08	-0.96	0.371508	0.510364	-6.76
253780_at	protein phosphatase 2C-like protei	---	AT4G28400	-1.19	-0.25	-0.96	0.371629	0.510501	-6.76
255815_at	histone H3, putative similar to histo	MGH3	AT1G19890	-1.09	-0.13	-0.96	0.371712	0.510584	-6.76
263110_at	unknown protein ;supported by full-	---	AT1G65220	-1.10	-0.14	-0.96	0.37178	0.510629	-6.76
267042_at	putative non-LTR retroelement reve	---	AT2G34320	-1.08	-0.11	-0.96	0.371814	0.510629	-6.76
263943_at	putative mitochondrial carrier protei	---	AT2G35800	-1.09	-0.13	-0.96	0.371819	0.510629	-6.76
254884_at	H+-transporting ATPase - like prote	---	AT4G11730	-1.06	-0.09	-0.96	0.371834	0.510629	-6.76
250994_at	dnaK-type molecular chaperone hs	---	AT5G02490	-1.24	-0.31	-0.96	0.371889	0.510673	-6.76
254000_at	galactinol synthase WSI76 protein	AtGolS6	AT4G26250	-1.06	-0.08	-0.96	0.371914	0.510676	-6.76
255678_at	predicted protein with unknown fun	AT4G0052(	---	-1.08	-0.12	-0.96	0.371958	0.510706	-6.76
247609_at	cleavage stimulation factor 50K ch	---	AT5G60940	-1.08	-0.11	-0.96	0.371999	0.510732	-6.76
256945_at	hypothetical protein similar to exten	---	AT3G19020	-1.08	-0.11	-0.96	0.372036	0.510752	-6.76
254236_at	putative protein VSG expression si	---	AT4G23840	-1.07	-0.10	-0.96	0.372089	0.510794	-6.76
247803_at	similar to unknown protein (gb|AAF	---	AT5G58340	-1.06	-0.08	-0.96	0.372135	0.510826	-6.76
253517_at	predicted protein hypothetical prote	---	AT4G31390	1.11	0.15	0.96	0.372422	0.511189	-6.76
251441_at	SKP1/ASK1 (At5), putative similar	ASK5	AT3G60020	1.07	0.10	0.96	0.372453	0.511202	-6.76
255605_at	hypothetical protein	---	AT4G01090	-1.13	-0.18	-0.96	0.372517	0.511227	-6.76
254740_s_a	glycine hydroxymethyltransferase -	---	AT2G42450	-1.26	-0.34	-0.96	0.37252	0.511227	-6.76
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J	---	---	-1.22	-0.29	-0.96	0.372559	0.511227	-6.76
247931_at	putative protein similar to unknown	---	AT5G57040	1.10	0.14	0.96	0.372561	0.511227	-6.76

249837_at	Expressed protein ; supported by fu	---	AT5G23480	-1.08	-0.11	-0.95	0.372694	0.511378	-6.76
246208_at	hypothetical protein ; supported by	SFH12	AT4G36490	-1.08	-0.11	-0.95	0.372972	0.511704	-6.76
267274_at	putative mitochondrial carrier protei	---	AT2G30160	1.11	0.15	0.95	0.372976	0.511704	-6.76
252330_at	hypothetical protein	---	AT3G48770	-1.11	-0.15	-0.95	0.373066	0.511796	-6.76
262281_at	peptide transporter, putative simila	---	AT1G68570	-1.22	-0.29	-0.95	0.37342	0.512251	-6.76
267547_at	putative synaptobrevin	ATVAMP72	AT2G32670	-1.10	-0.14	-0.95	0.373622	0.512497	-6.76
258958_at	vacuolar membrane ATPase subun	VMA10	AT3G01390	1.11	0.16	0.95	0.373771	0.512671	-6.76
265617_at	putative phosphate/phosphoenolpy	---	AT2G25520	1.16	0.21	0.95	0.373928	0.512855	-6.76
246414_at	hypothetical protein similar to hypot	---	AT1G77340	-1.07	-0.10	-0.95	0.374046	0.512986	-6.76
260063_at	unknown protein contains Pfam pro	---	AT1G73720	1.08	0.12	0.95	0.374081	0.513003	-6.76
264911_at	auxin-induced protein, putative sim	---	AT1G60690	1.11	0.15	0.95	0.374225	0.513154	-6.76
252278_at	NAC2-like protein NAC2 - Arabidop	anac062	AT3G49530	-1.21	-0.28	-0.95	0.374236	0.513154	-6.76
264834_at	unknown protein similar to ESTs gb	---	AT1G03730	-1.17	-0.22	-0.95	0.37426	0.513157	-6.76
264269_at	hypothetical protein predicted by ge	---	AT1G60240	-1.09	-0.13	-0.95	0.374381	0.513291	-6.76
252561_at	histone H2B ;supported by full-leng	HTB9	AT3G45980	1.12	0.16	0.95	0.374612	0.513578	-6.76
266335_at	putative cytochrome P450 ; suppor	KAO2	AT2G32440	1.14	0.19	0.95	0.374868	0.513893	-6.76
263402_at	hypothetical protein similar to hypot	---	AT2G04050	1.34	0.43	0.95	0.374888	0.513893	-6.76
247858_at	similar to unknown protein (pir||T34	TTL	AT5G58220	-1.09	-0.12	-0.95	0.37491	0.513893	-6.76
246974_at	putative protein	---	AT5G24980	1.10	0.13	0.95	0.374972	0.513947	-6.77
251497_at	putative protein phytochrome-asso	PIL6	AT3G59060	1.09	0.12	0.95	0.375048	0.513986	-6.77
260557_at	putative endochitinase	---	AT2G43610	-1.06	-0.09	-0.95	0.375061	0.513986	-6.77
261921_at	hypothetical protein predicted by ge	---	AT1G65900	-1.15	-0.20	-0.95	0.375068	0.513986	-6.77
266374_at	putative retroelement pol polyprotei	---	---	-1.10	-0.14	-0.95	0.375181	0.514092	-6.77
245594_at	acylaminoacyl-peptidase like protei	---	AT4G14570	-1.12	-0.16	-0.95	0.37519	0.514092	-6.77
252039_at	Expressed protein ; supported by cl	---	AT3G52155	-1.09	-0.13	-0.95	0.375376	0.514291	-6.77
246845_at	glutamyl-tRNA synthetase ; suppor	---	AT5G26710	1.07	0.09	0.95	0.37538	0.514291	-6.77
250566_at	putative helix-loop-helix DNA bindi	TCP17	AT5G08070	1.11	0.16	0.95	0.375465	0.51432	-6.77
256471_at	hypothetical protein predicted by ge	---	---	-1.07	-0.10	-0.95	0.375473	0.51432	-6.77
249447_at	PTEN -like protein PTEN/MMAC1,	PTEN1	AT5G39400	-1.12	-0.16	-0.95	0.375479	0.51432	-6.77
267104_at	ERD15 protein identical to GB D30	ERD15	AT2G41430	-1.09	-0.13	-0.95	0.375492	0.51432	-6.77
251490_at	putative protein	---	AT3G59490	-1.10	-0.14	-0.95	0.375517	0.514323	-6.77
263910_at	hypothetical protein predicted by ge	---	AT2G36550	-1.07	-0.10	-0.95	0.375686	0.514458	-6.77
248949_at	putative protein strong similarity to	---	AT5G45570	1.06	0.09	0.95	0.375693	0.514458	-6.77
266615_s_a	putative monooxygenase ;supporte	CTF2A	AT2G29720	1.31	0.39	0.95	0.375694	0.514458	-6.77
255341_at	putative receptor-like protein kinase	---	AT4G04500	1.57	0.65	0.95	0.375705	0.514458	-6.77

261520_at	unknown protein ; supported by cDI	SEC6	AT1G71820	-1.07	-0.10	-0.95	0.37577	0.514508	-6.77
260972_at	hypothetical protein contains simila	---	AT1G53530	-1.08	-0.11	-0.95	0.375787	0.514508	-6.77
261853_at	unknown protein	---	AT1G50660	-1.11	-0.15	-0.95	0.375875	0.514595	-6.77
246935_at	leucine-rich repeats containing prot	EBF2	AT5G25350	1.14	0.19	0.95	0.375896	0.514595	-6.77
265055_at	hypothetical protein similar to hypot	---	---	-1.08	-0.11	-0.95	0.375975	0.514653	-6.77
246165_at	putative protein	---	---	-1.07	-0.09	-0.95	0.375983	0.514653	-6.77
259353_at	putative branched-chain amino acid	---	AT3G05190	-1.07	-0.09	-0.95	0.376018	0.514669	-6.77
255906_at	hypothetical protein similar to RING	---	AT1G17790	-1.08	-0.11	-0.95	0.376127	0.514789	-6.77
267021_at	hypothetical protein predicted by ge	---	AT2G39300	1.06	0.09	0.95	0.376154	0.514795	-6.77
251361_at	LIM domain protein LIM domain pr	---	AT3G61230	-1.10	-0.14	-0.95	0.376193	0.514816	-6.77
249106_at	protein transport protein SEC23 ; su	---	AT5G43670	1.12	0.16	0.95	0.376278	0.514856	-6.77
250865_at	putative protein predicted protein, S	---	AT5G03900	-1.12	-0.16	-0.95	0.37628	0.514856	-6.77
259473_at	hypothetical protein predicted by ge	---	AT1G19025	-1.10	-0.13	-0.95	0.376289	0.514856	-6.77
252686_at	putative protein predicted protein, A	---	---	-1.07	-0.10	-0.95	0.376523	0.515145	-6.77
247363_at	unknown protein	---	AT5G63200	1.08	0.11	0.95	0.37656	0.515164	-6.77
259184_at	unknown protein ;supported by full-	---	AT3G01520	-1.08	-0.12	-0.95	0.376894	0.515561	-6.77
253245_at	bZIP transcription factor ATB2	GBF6	AT4G34588	1.22	0.29	0.95	0.376895	0.515561	-6.77
263749_at	putative phosphatidylinositol/phospl	---	AT2G21520	-1.09	-0.12	-0.95	0.377066	0.515753	-6.77
263123_at	beta-Amyrin Synthase, putative sim	---	AT1G78500	-1.08	-0.11	-0.95	0.377081	0.515753	-6.77
261472_at	hypothetical protein predicted by ge	---	AT1G14470	1.06	0.08	0.95	0.377109	0.515761	-6.77
249558_at	hypothetical protein	---	AT5G38310	1.30	0.38	0.95	0.377171	0.515815	-6.77
245642_at	Expressed protein ; supported by fu	---	AT1G25275	1.06	0.09	0.94	0.377357	0.516014	-6.77
245950_at	putative protein predicted protein, I	---	AT5G19570	-1.12	-0.17	-0.94	0.377362	0.516014	-6.77
263744_at	Mutator-like transposase similar to	---	AT2G21420	-1.08	-0.11	-0.94	0.377637	0.516359	-6.77
252232_at	bZIP transcription factor - like prote	AtbZIP5	AT3G49760	-1.06	-0.09	-0.94	0.377733	0.516455	-6.77
249651_at	auxin response factor 8 (ARF8) ; s	ARF8	AT5G37020	1.15	0.20	0.94	0.377773	0.516455	-6.77
252556_at	putative protein step II splicing fact	---	AT3G45950	1.06	0.08	0.94	0.377775	0.516455	-6.77
258084_at	putative B regulatory subunit of prot	---	AT3G26020	-1.12	-0.17	-0.94	0.377868	0.516537	-6.77
257387_s_a	putative receptor-like protein kinase	---	AT2G14440	1.09	0.12	0.94	0.37788	0.516537	-6.77
245576_at	hypothetical protein	TCX2	AT4G14770	-1.12	-0.16	-0.94	0.377914	0.516552	-6.77
262045_at	hypothetical protein predicted by ge	---	AT1G80240	-1.13	-0.17	-0.94	0.378027	0.516633	-6.77
252781_at	polygalacturonase -like protein poly	---	AT3G42950	1.08	0.11	0.94	0.378038	0.516633	-6.77
265759_at	putative membrane transporter	---	AT2G13100	1.07	0.09	0.94	0.378041	0.516633	-6.77
256200_at	hypothetical protein predicted by ge	EMB1674	AT1G58210	-1.08	-0.11	-0.94	0.378106	0.516691	-6.77
247010_at	60S ribosomal protein L26 ;suppor	---	AT5G67510	1.20	0.26	0.94	0.378146	0.516714	-6.77

246477_at	putative transcription factor (MYB9)	AtMYB9	AT5G16770	-1.14	-0.19	-0.94	0.378227	0.516773	-6.77
249599_at	putative protein AtPP protein, Bras	---	AT5G37990	-1.09	-0.12	-0.94	0.378249	0.516773	-6.77
247200_at	unknown protein ;supported by full	---	AT5G65120	1.10	0.13	0.94	0.378257	0.516773	-6.77
250876_at	hypothetical protein	---	AT5G04030	-1.07	-0.10	-0.94	0.378426	0.516972	-6.77
255336_at	putative transposon protein	---	---	-1.06	-0.08	-0.94	0.378489	0.517003	-6.77
267122_at	putative acetone-cyanohydrin lyase	MES6	AT2G23550	1.07	0.10	0.94	0.378493	0.517003	-6.77
250445_at	nucleoid DNA-binding protein cnd4	---	AT5G10760	1.70	0.76	0.94	0.378541	0.517038	-6.77
264363_at	hypothetical protein predicted by ge	---	AT1G03170	-1.09	-0.12	-0.94	0.378651	0.517156	-6.77
248826_at	casein kinase II beta chain ; suppor	CKB1	AT5G47080	1.10	0.14	0.94	0.378675	0.517158	-6.77
245166_at	putative receptor-like protein kinase	---	AT2G33170	-1.09	-0.12	-0.94	0.378862	0.517364	-6.77
261739_at	hypothetical protein similar to hypot	PEX11A	AT1G47750	-1.07	-0.09	-0.94	0.378871	0.517364	-6.77
252262_at	putative protein several hypothetica	---	AT3G49510	-1.06	-0.09	-0.94	0.378921	0.517394	-6.77
257349_at	unknown protein	---	AT2G30630	-1.07	-0.10	-0.94	0.378938	0.517394	-6.77
258173_at	putative protein kinase similar to se	CERK1	AT3G21630	-1.08	-0.11	-0.94	0.379005	0.517454	-6.77
257927_at	ethylene response factor 1 (ERF1)	ERF1	AT3G23240	1.78	0.83	0.94	0.379178	0.517659	-6.77
263308_at	hypothetical protein predicted by ge	---	---	1.07	0.10	0.94	0.379229	0.517698	-6.77
260539_at	putative peroxidase	---	AT2G43480	1.06	0.09	0.94	0.379296	0.517733	-6.77
248094_at	trigger factor-like protein	---	AT5G55220	1.10	0.14	0.94	0.379302	0.517733	-6.77
248775_at	receptor kinase-like protein	CCR4	AT5G47850	1.48	0.56	0.94	0.379323	0.517733	-6.77
251589_at	putative protein SINA2p zinc finger	SINAT2	AT3G58040	1.08	0.11	0.94	0.379354	0.517742	-6.77
249068_at	putative protein similar to unknown	PDLP1	AT5G43980	1.07	0.10	0.94	0.379375	0.517742	-6.77
265371_at	putative PttA-like transposon protei	---	---	-1.07	-0.09	-0.94	0.37952	0.517909	-6.77
266788_at	putative receptor-like protein kinase	---	AT2G29000	-1.06	-0.09	-0.94	0.379609	0.518	-6.77
256574_at	hypothetical protein similar to callos	---	AT3G14780	-1.14	-0.19	-0.94	0.379658	0.518035	-6.77
258414_at	unknown protein ;supported by full	---	AT3G17380	-1.08	-0.11	-0.94	0.379704	0.518065	-6.77
253384_at	Expressed protein ; supported by fu	---	AT4G32915	1.09	0.13	0.94	0.379725	0.518065	-6.77
255809_at	putative protein predicted protein, A	---	AT4G10300	-1.09	-0.12	-0.94	0.379779	0.518108	-6.77
263937_at	putative RING zinc finger protein	---	AT2G35910	1.08	0.12	0.94	0.37981	0.518119	-6.77
256454_at	NADPH oxidoreductase, putative s	---	AT1G75280	-1.23	-0.30	-0.94	0.37984	0.518129	-6.77
255884_at	hypothetical protein predicted by ge	---	AT1G20310	1.40	0.49	0.94	0.379977	0.518285	-6.78
253525_at	predicted protein ; supported by cD	---	AT4G31330	1.09	0.12	0.94	0.380194	0.518549	-6.78
259181_at	unknown protein similar to putative	---	AT3G01690	1.11	0.15	0.94	0.380313	0.518681	-6.78
252021_at	putative protein predicted protein, A	---	AT3G53070	-1.09	-0.12	-0.94	0.380525	0.518939	-6.78
247326_at	peroxidase ATP3a homolog ;suppo	---	AT5G64110	1.38	0.46	0.94	0.380572	0.518972	-6.78
264610_at	Expressed protein ; supported by fu	---	AT1G04645	1.08	0.11	0.94	0.380632	0.519023	-6.78

254268_at	putative protein FAF1, Mus muscu	---	AT4G23040	-1.09	-0.13	-0.94	0.380775	0.519187	-6.78
255509_at	hypothetical protein identical to T10	---	AT4G02210	-1.13	-0.17	-0.94	0.381033	0.519508	-6.78
264481_at	transcription factor TINY, putative s	---	AT1G77200	-1.09	-0.12	-0.94	0.381098	0.519565	-6.78
245579_at	hypothetical protein	---	AT4G14810	1.07	0.09	0.94	0.381294	0.519777	-6.78
262190_at	unknown protein	---	AT1G78030	-1.10	-0.14	-0.94	0.381299	0.519777	-6.78
264288_at	Expressed protein ; supported by fu	---	AT1G62045	-1.08	-0.11	-0.94	0.381438	0.519935	-6.78
245826_at	disease resistance protein RPS4, p	---	AT1G57850	-1.09	-0.12	-0.94	0.381464	0.51994	-6.78
245997_at	putative protein saur1 protein, Zea	---	AT5G20810	1.12	0.17	0.94	0.381555	0.520033	-6.78
245077_at	hypothetical protein predicted by ge	---	AT2G23160	1.11	0.15	0.94	0.38165	0.520131	-6.78
246225_at	putative protein ;supported by full-le	LEJ2	AT4G36910	-1.10	-0.14	-0.94	0.381869	0.520398	-6.78
261886_s_a	hypothetical protein predicted by ge	---	AT1G80700	1.06	0.09	0.94	0.381965	0.520472	-6.78
263837_at	unknown protein	---	AT2G04500	-1.06	-0.08	-0.94	0.381969	0.520472	-6.78
256676_at	putative protein ;supported by full-l	SEX4	AT3G52180	-1.13	-0.17	-0.94	0.38203	0.520524	-6.78
255239_at	contains similarity to Arabidopsis th	---	---	-1.06	-0.08	-0.93	0.382116	0.520579	-6.78
249547_at	lipid transfer - like protein P48h-10	---	AT5G38160	-1.10	-0.14	-0.93	0.382132	0.520579	-6.78
257254_at	salicylic acid carboxyl methyltransf	---	AT3G21950	-1.07	-0.10	-0.93	0.382138	0.520579	-6.78
260023_at	unknown protein	ATGA2OX2	AT1G30040	1.14	0.18	0.93	0.382166	0.520586	-6.78
265127_at	hypothetical protein similar to poller	sks14	AT1G55560	1.07	0.09	0.93	0.382203	0.520604	-6.78
257283_at	hypothetical protein predicted by ge	---	AT3G29750	-1.06	-0.09	-0.93	0.382231	0.520612	-6.78
265643_at	hypothetical protein predicted by ge	---	AT2G27390	1.15	0.21	0.93	0.382277	0.520643	-6.78
247567_at	putative protein various predicted p	---	AT5G61190	-1.10	-0.14	-0.93	0.382412	0.520797	-6.78
258102_at	unknown protein contains Pfam pro	---	AT3G23600	1.10	0.14	0.93	0.382587	0.521003	-6.78
266062_at	putative diacylglycerol kinase	---	AT2G18730	-1.06	-0.08	-0.93	0.382693	0.521117	-6.78
247976_at	unknown protein	---	---	-1.09	-0.13	-0.93	0.382752	0.521166	-6.78
251704_at	putative protein unknown protein 1	---	AT3G56360	-1.20	-0.26	-0.93	0.382865	0.521257	-6.78
246706_at	putative protein predicted proteins,	---	---	1.13	0.17	0.93	0.3829	0.521257	-6.78
267460_at	putative squamosa-promoter bindin	SPL3	AT2G33810	-1.31	-0.39	-0.93	0.382907	0.521257	-6.78
245735_at	myb-like transcription factor, putati	MYB54	AT1G73410	-1.06	-0.08	-0.93	0.38291	0.521257	-6.78
251171_at	putative protein several hypothetica	---	AT3G63220	-1.06	-0.09	-0.93	0.382957	0.521289	-6.78
262332_at	hypothetical protein similar to putati	---	AT1G64030	-1.08	-0.11	-0.93	0.382995	0.52131	-6.78
263862_at	putative protein phosphatase	IBR5	AT2G04550	1.07	0.10	0.93	0.383094	0.521414	-6.78
259500_at	unknown protein ; supported by cDI	---	AT1G15740	1.10	0.14	0.93	0.383126	0.521426	-6.78
246787_s_a	cdc20-like protein putative cdc20 p	---	AT5G27570	-1.06	-0.09	-0.93	0.383249	0.521562	-6.78
262842_at	xyloglucan endo-transglycosylase,	XTR2	AT1G14720	1.17	0.22	0.93	0.383394	0.521729	-6.78
260719_at	unknown protein	---	AT1G48090	-1.10	-0.13	-0.93	0.383481	0.521816	-6.78

247910_at	putative protein similar to unknown	---	AT5G57410	-1.10	-0.14	-0.93	0.383651	0.521975	-6.78
247766_at	FtsH protease, putative contains si	ftsh9	AT5G58870	1.09	0.12	0.93	0.383661	0.521975	-6.78
264573_at	putative pectin methylesterase Simi	---	AT1G05310	1.10	0.14	0.93	0.383666	0.521975	-6.78
245998_at	sucrose-UDP glucosyltransferase	SUS1	AT5G20830	-1.16	-0.22	-0.93	0.383731	0.522032	-6.78
254402_at	putative protein predicted protein, A	---	AT4G21310	-1.12	-0.17	-0.93	0.383778	0.52205	-6.78
250544_at	syntaxin-like protein syntaxin-relate	SYP132	AT5G08080	-1.10	-0.13	-0.93	0.38379	0.52205	-6.78
251889_at	putative protein probable lectin 2 p	---	AT3G54080	1.16	0.22	0.93	0.383953	0.522241	-6.78
256389_at	hypothetical protein predicted by ge	---	AT3G06220	1.08	0.11	0.93	0.384029	0.522312	-6.78
266051_at	rhodanese-like family protein	---	AT2G40760	1.11	0.15	0.93	0.384162	0.522444	-6.78
251001_at	putative protein	---	AT5G02670	1.10	0.14	0.93	0.384172	0.522444	-6.78
267077_at	unknown protein similar to cytoskel	---	AT2G40970	1.11	0.14	0.93	0.384487	0.522811	-6.78
265636_at	putative calcium binding protein	---	AT2G27480	1.09	0.12	0.93	0.384487	0.522811	-6.78
254166_at	HSP90-like protein HSP90 homolo	SHD	AT4G24190	1.25	0.32	0.93	0.384523	0.522828	-6.78
254305_at	potassium channel protein AKT3 ;	AKT2/3	AT4G22200	-1.06	-0.08	-0.93	0.38458	0.522875	-6.78
257917_at	ethylene responsive element bindi	---	AT3G23220	-1.06	-0.09	-0.93	0.384676	0.522974	-6.78
255566_s_a	hypothetical protein	---	AT3G48670	-1.08	-0.11	-0.93	0.384835	0.523159	-6.78
261600_x_a	hypothetical protein similar to hypot	---	AT1G49680	-1.06	-0.09	-0.93	0.384872	0.523178	-6.78
261779_at	hypothetical protein predicted by ge	---	AT1G76230	1.06	0.09	0.93	0.38498	0.523294	-6.78
255908_s_a	unknown protein ;supported by full-	---	AT1G18000	-1.08	-0.11	-0.93	0.385021	0.523318	-6.79
260559_at	putative polygalacturonase	---	AT2G43860	-1.09	-0.13	-0.93	0.385058	0.523337	-6.79
264199_at	unknown protein contains similarity	---	AT1G22700	1.09	0.12	0.93	0.385252	0.523571	-6.79
244964_at	PSII cytochrome b559	---	---	1.06	0.08	0.93	0.385377	0.523705	-6.79
254245_at	serine/threonine kinase - like prote	---	AT4G23240	-1.07	-0.10	-0.93	0.385397	0.523705	-6.79
265110_at	hypothetical protein predicted by ge	---	AT1G62490	-1.10	-0.14	-0.93	0.38559	0.523929	-6.79
257334_at	hypothetical protein	---	---	1.20	0.26	0.93	0.385608	0.523929	-6.79
265972_at	putative retroelement pol polyprotei	---	---	-1.06	-0.09	-0.93	0.38573	0.524064	-6.79
263970_at	putative cytochrome P450	CYP718	AT2G42850	-1.07	-0.10	-0.93	0.385857	0.524205	-6.79
249980_at	putative protein	---	AT5G18870	-1.08	-0.12	-0.93	0.386066	0.524431	-6.79
253963_at	putative protein probable calcium-d	---	AT4G26470	1.15	0.20	0.93	0.38607	0.524431	-6.79
246309_at	putative transmembrane protein G1	ATG1	AT3G51790	1.19	0.25	0.93	0.386174	0.524541	-6.79
255295_at	putative sugar transporter	---	AT4G04760	-1.07	-0.10	-0.93	0.386247	0.524591	-6.79
245214_at	F12A21.1 hypothetical protein	---	AT1G67855	-1.07	-0.09	-0.93	0.386257	0.524591	-6.79
264492_at	unknown protein similar to unknow	---	AT1G27430	1.06	0.08	0.93	0.386414	0.524749	-6.79
264578_at	hypothetical protein predicted by ge	---	AT1G05370	-1.06	-0.09	-0.93	0.386419	0.524749	-6.79
253554_at	putative protein predicted protein, (	---	AT4G30940	-1.11	-0.16	-0.93	0.386462	0.524777	-6.79

259640_at	beta-glucosidase, putative identica	BGLU18	AT1G52400	-1.18	-0.24	-0.93	0.386514	0.524788	-6.79
253676_at	cytidine deaminase - like protein cy	---	AT4G29570	-1.09	-0.13	-0.93	0.386516	0.524788	-6.79
259376_at	unknown protein C-terminus similar	CDC27a	AT3G16320	-1.08	-0.10	-0.93	0.386637	0.52492	-6.79
249564_at	unknown protein	---	AT5G38400	-1.09	-0.12	-0.93	0.386661	0.524922	-6.79
261729_s_a	hexokinase, putative similar to hex	HXK3	AT1G47840	-1.06	-0.08	-0.92	0.387007	0.525361	-6.79
262194_at	hypothetical protein similar to putati	---	AT1G77930	1.12	0.17	0.92	0.387096	0.52545	-6.79
263927_s_a	putative cinnamyl-alcohol dehydrog	CAD2	AT2G21730	1.10	0.14	0.92	0.387184	0.525538	-6.79
255629_at	stress-induced protein OZI1 precurs	ATOZI1	AT4G00860	1.12	0.16	0.92	0.387325	0.525699	-6.79
257412_at	unknown protein	---	AT1G22980	1.08	0.11	0.92	0.387668	0.526102	-6.79
253181_at	amino acid permease - like protein	LHT7	AT4G35180	1.37	0.46	0.92	0.387668	0.526102	-6.79
254518_at	downy mildew resistance-like prote	---	AT4G19910	-1.08	-0.11	-0.92	0.387746	0.526136	-6.79
261138_at	hypothetical protein contains Pfam	---	AT1G19710	1.08	0.12	0.92	0.387758	0.526136	-6.79
267224_at	hypothetical protein predicted by ge	---	AT2G43990	-1.09	-0.13	-0.92	0.387769	0.526136	-6.79
260917_at	unknown protein similar to hypothet	---	AT1G02700	-1.09	-0.12	-0.92	0.387786	0.526136	-6.79
253588_at	putative protein	---	AT4G30790	1.08	0.12	0.92	0.387954	0.526332	-6.79
260035_at	peroxidase ATP23a identical to per	---	AT1G68850	-1.14	-0.19	-0.92	0.387977	0.526332	-6.79
246873_at	putative protein	---	AT5G26100	-1.07	-0.10	-0.92	0.388135	0.526474	-6.79
249098_at	DNA repair protein-like	---	AT5G43530	1.07	0.10	0.92	0.388148	0.526474	-6.79
253148_at	cyclin 2b protein	CYCB2;2	AT4G35620	-1.09	-0.12	-0.92	0.388165	0.526474	-6.79
252584_at	putative protein several hypothetica	---	AT3G45560	-1.07	-0.10	-0.92	0.388174	0.526474	-6.79
255115_at	putative protein probable regulator	APUM11	AT4G08840	-1.07	-0.09	-0.92	0.388207	0.526488	-6.79
259345_s_a	hypothetical protein predicted by ge	---	AT3G03700	-1.18	-0.24	-0.92	0.388239	0.5265	-6.79
267570_at	putative RNA helicase A identical t	HVT1	AT2G30800	1.09	0.13	0.92	0.388319	0.526577	-6.79
246798_at	putative protein various predicted p	---	AT5G26930	-1.07	-0.09	-0.92	0.388357	0.526597	-6.79
255211_at	may be a pseudogene	---	---	-1.06	-0.09	-0.92	0.388458	0.526702	-6.79
263800_at	hypothetical protein predicted by ge	---	AT2G24600	-1.56	-0.64	-0.92	0.388546	0.526767	-6.79
252695_s_a	hypothetical protein predicted prote	---	---	1.06	0.08	0.92	0.388551	0.526767	-6.79
252518_at	receptor-like protein kinase homolo	---	AT3G46350	1.07	0.10	0.92	0.388598	0.526799	-6.79
253511_at	putative protein Sly1 protein, rat, P	---	AT4G31740	-1.07	-0.10	-0.92	0.388647	0.526834	-6.79
251509_at	pectinesterase precursor-like prote	---	AT3G59010	-1.23	-0.30	-0.92	0.389031	0.527324	-6.79
246419_at	UDP glucose:flavonoid 3-o-glucosy	UGT78D3	AT5G17030	-1.07	-0.09	-0.92	0.389107	0.527395	-6.79
248778_at	unknown protein	---	AT5G47940	-1.08	-0.11	-0.92	0.389236	0.527538	-6.79
252284_at	putative protein various predicted p	---	AT3G49020	-1.08	-0.11	-0.92	0.389276	0.527561	-6.79
250371_at	putative protein 23 kDa polypeptide	---	AT5G11450	1.09	0.12	0.92	0.389414	0.527717	-6.79
255158_s_a	hypothetical protein	---	---	1.07	0.10	0.92	0.389457	0.527745	-6.79

248238_at	putative protein similar to unknown	---	AT5G53900	1.11	0.15	0.92	0.389559	0.527851	-6.79
245487_at	phytochrome D	PHYD	AT4G16250	1.09	0.13	0.92	0.389731	0.528052	-6.79
254627_at	Expressed protein ; supported by fu	---	AT4G18395	-1.07	-0.09	-0.92	0.389771	0.528075	-6.79
AFFX-r2-Bs	B. subtilis /GEN=dapB, jojF /DB_XF	---	---	1.14	0.19	0.92	0.389799	0.528082	-6.79
264971_at	Expressed protein ; supported by fu	---	AT1G67210	1.06	0.08	0.92	0.38986	0.528133	-6.79
249141_at	putative protein similar to unknown	---	AT5G43200	-1.07	-0.09	-0.92	0.389907	0.528165	-6.79
255897_at	mutator-like transposase, putative	---	---	-1.06	-0.08	-0.92	0.389988	0.528244	-6.79
264595_at	putative vesicle-associated membr	VAMP721	AT1G04750	1.10	0.14	0.92	0.390017	0.528251	-6.79
252336_at	putative protein N7 protein - Medic	---	AT3G48880	-1.07	-0.10	-0.92	0.390087	0.528315	-6.79
261696_at	unknown protein similar to hypothet	---	AT1G08470	-1.12	-0.16	-0.92	0.390475	0.52881	-6.80
265775_at	Mutator-like transposase similar to	---	---	-1.12	-0.16	-0.92	0.390521	0.52884	-6.80
257577_at	hypothetical protein predicted by ge	---	---	1.08	0.11	0.92	0.390612	0.528932	-6.80
263615_at	putative MYB family transcription fa	MYB100	AT2G25230	-1.06	-0.08	-0.92	0.390668	0.528967	-6.80
256783_at	casein kinase, putative similar to ca	---	AT3G13670	1.06	0.09	0.92	0.390739	0.528967	-6.80
261741_at	transcription factor, putative similar	ATE2F2	AT1G47870	1.08	0.11	0.92	0.390748	0.528967	-6.80
264463_at	unknown protein similar to ESTs gl	---	AT1G10150	1.10	0.13	0.92	0.390751	0.528967	-6.80
245070_at	metallothionein-like protein identica	---	AT2G23240	-1.10	-0.14	-0.92	0.390754	0.528967	-6.80
265621_at	NAM (no apical meristem)-like prote	NTL8	AT2G27300	-1.07	-0.10	-0.92	0.390913	0.529075	-6.80
254244_at	putative protein S-receptor kinase	---	AT4G23230	1.09	0.12	0.92	0.39094	0.529075	-6.80
244990_s_a	hypothetical protein	---	---	1.18	0.24	0.92	0.39094	0.529075	-6.80
251942_at	ABC transporter - like protein PDR	PDR9	AT3G53480	1.23	0.30	0.92	0.390947	0.529075	-6.80
263317_s_a	similar to mammalian MHC III regio	SUVH7	AT1G17770	-1.11	-0.15	-0.92	0.39095	0.529075	-6.80
249195_s_a	disease resistance response protei	---	AT5G42500	-1.12	-0.16	-0.92	0.391015	0.529132	-6.80
254140_at	putative protein	---	AT4G24610	-1.11	-0.16	-0.92	0.391123	0.529247	-6.80
245503_at	kinase like protein	---	AT4G15650	-1.06	-0.09	-0.92	0.39133	0.529495	-6.80
259037_at	hypothetical protein predicted by ge	---	AT3G09350	-1.29	-0.36	-0.92	0.391399	0.529558	-6.80
246121_at	putative protein motif in PGPS/D10	---	AT5G20370	-1.08	-0.11	-0.92	0.391643	0.529856	-6.80
256345_at	hypothetical protein similar to hypot	---	AT1G55030	-1.07	-0.10	-0.92	0.391789	0.530022	-6.80
267449_at	hypothetical protein predicted by ge	---	AT2G33690	-1.06	-0.08	-0.91	0.391812	0.530022	-6.80
252003_at	hypothetical protein emm32, Strep	ZPR3	AT3G52770	1.07	0.10	0.91	0.392034	0.530291	-6.80
245384_at	glycoprotein homolog ;supported by	---	AT4G16790	-1.13	-0.17	-0.91	0.392215	0.530504	-6.80
260612_at	hypothetical protein similar to hypot	---	AT1G53360	-1.06	-0.09	-0.91	0.392312	0.530574	-6.80
256342_at	unknown protein ; supported by full-	---	AT1G72020	-1.08	-0.11	-0.91	0.392313	0.530574	-6.80
265631_at	putative helicase	---	---	-1.06	-0.08	-0.91	0.392382	0.530635	-6.80
259857_at	hypothetical protein predicted by ge	---	AT1G68430	-1.08	-0.11	-0.91	0.392641	0.530954	-6.80

259836_at	unknown protein	ROPGEF1	AT1G52240	-1.06	-0.08	-0.91	0.392784	0.531116	-6.80
252150_at	vacuolar sorting protein 35 homolo	VPS35C	AT3G51310	1.07	0.09	0.91	0.392812	0.531123	-6.80
262289_at	unknown protein identical to unknov	---	AT1G70770	1.07	0.09	0.91	0.392918	0.531235	-6.80
262688_at	PPR-repeat protein contains multip	---	AT1G62680	-1.07	-0.10	-0.91	0.393097	0.531445	-6.80
246934_at	putative protein several hypothetica	---	AT5G25290	-1.09	-0.13	-0.91	0.393142	0.531475	-6.80
246899_at	putative protein various predicted p	---	AT5G25590	-1.07	-0.10	-0.91	0.393199	0.53152	-6.80
259676_at	hypothetical protein similar to putati	---	AT1G77730	-1.07	-0.10	-0.91	0.393257	0.531542	-6.80
252856_at	putative protein ; supported by cDN	---	AT4G39690	1.07	0.09	0.91	0.393262	0.531542	-6.80
262339_at	WRKY DNA binding protein, putati	WRKY56	AT1G64000	1.07	0.09	0.91	0.393454	0.53177	-6.80
247445_at	putative protein similar to unknown	---	AT5G62640	1.08	0.11	0.91	0.3937	0.532045	-6.80
247774_at	putative protein fruit ripening expre	---	AT5G58660	-1.07	-0.09	-0.91	0.393705	0.532045	-6.80
265133_s_a	unknown protein similar to hypothet	---	AT1G51240	1.06	0.09	0.91	0.393727	0.532045	-6.80
267263_at	similar to late embryogenesis abun	---	AT2G23110	1.41	0.50	0.91	0.393758	0.532056	-6.80
264600_at	hypothetical protein predicted by ge	---	AT1G04730	-1.12	-0.16	-0.91	0.393796	0.532075	-6.80
256736_at	terpene synthase, putative similar t	---	AT3G29410	-1.07	-0.10	-0.91	0.393855	0.532123	-6.80
262122_at	polygalacturonase, putative similar	PGA4	AT1G02790	-1.08	-0.11	-0.91	0.393937	0.532202	-6.80
265753_at	putative Athila retroelement ORF1 p	---	---	1.06	0.08	0.91	0.393997	0.532252	-6.80
250536_at	Expressed protein ; supported by fu	---	AT5G08535	1.08	0.12	0.91	0.394119	0.532385	-6.80
260001_at	putative S-adenosyl-L-methionine:tr	TSM1	AT1G67990	-1.09	-0.13	-0.91	0.394142	0.532385	-6.80
256251_at	hypothetical protein predicted by ge	---	AT3G11330	1.10	0.14	0.91	0.394228	0.532469	-6.80
247788_at	putative protein carbohydrate kinas	---	AT5G58730	1.13	0.17	0.91	0.394387	0.532652	-6.80
256721_at	hypothetical protein predicted by g	WAVE1	AT2G34150	-1.09	-0.13	-0.91	0.394519	0.532799	-6.80
245923_at	putative protein predicted proteins,	---	AT5G28820	-1.08	-0.12	-0.91	0.394583	0.532826	-6.80
254067_at	hypothetical protein	NAP8	AT4G25450	-1.07	-0.09	-0.91	0.394617	0.532826	-6.80
265834_at	hypothetical protein predicted by ge	---	AT2G14410	-1.06	-0.08	-0.91	0.394633	0.532826	-6.80
262043_at	unknown protein	PSF1	AT1G80190	1.10	0.14	0.91	0.394636	0.532826	-6.80
267227_at	hypothetical protein predicted by ge	---	AT2G44030	-1.10	-0.13	-0.91	0.394655	0.532826	-6.80
264612_at	unknown protein similar to GB:AAC	---	AT1G04560	-1.10	-0.14	-0.91	0.394938	0.533176	-6.80
250096_at	putative protein similar to unknown	---	AT5G17190	1.08	0.11	0.91	0.394971	0.533189	-6.80
254351_at	putative protein probable membran	SOBER1	AT4G22300	-1.09	-0.12	-0.91	0.395012	0.533213	-6.80
259734_at	unknown protein similar to GB:AAD	---	AT1G77500	-1.18	-0.23	-0.91	0.395096	0.533295	-6.80
259356_at	unknown protein	---	AT3G05250	-1.07	-0.09	-0.91	0.395152	0.533338	-6.80
244963_at	PSII cytochrome b559	---	---	1.06	0.08	0.91	0.395201	0.533373	-6.80
261241_at	subtilisin-like serine protease conta	---	AT1G32950	1.07	0.10	0.91	0.395416	0.533609	-6.80
258581_at	hypothetical protein predicted by ge	---	AT3G04160	1.07	0.10	0.91	0.395423	0.533609	-6.80

254319_at	putative protein predicted proteins,	---	AT4G22560	-1.10	-0.14	-0.91	0.395538	0.533733	-6.81
266423_at	putative DNA-directed RNA polyme	RPB5D	AT2G41340	-1.10	-0.13	-0.91	0.39571	0.533933	-6.81
254443_at	putative protein (fragment) BRCA1	BRCA1	AT4G21070	-1.07	-0.10	-0.91	0.395776	0.533991	-6.81
248870_at	putative protein similar to unknown	---	AT5G46710	-1.28	-0.35	-0.91	0.395898	0.534124	-6.81
266544_at	similar to late embryogenesis abun	---	AT2G35300	-1.06	-0.09	-0.91	0.39604	0.534283	-6.81
250272_at	callose synthase catalytic subunit -	ATGSL12	AT5G13000	1.09	0.13	0.91	0.396125	0.534367	-6.81
261787_at	hypothetical protein predicted by ge	---	AT1G16020	1.08	0.11	0.91	0.396221	0.534459	-6.81
259581_at	RING zinc finger protein, putative c	---	AT1G28040	-1.08	-0.11	-0.91	0.396242	0.534459	-6.81
247225_at	inositol-1, 4, 5-trisphosphate 5-pho	BST1	AT5G65090	1.09	0.12	0.91	0.396264	0.534459	-6.81
262984_at	hypothetical protein predicted by ge	---	AT1G54460	-1.14	-0.19	-0.91	0.396294	0.534462	-6.81
248572_at	unknown protein	---	AT5G49800	-1.08	-0.11	-0.91	0.396323	0.534462	-6.81
261064_at	unknown protein	ftsh10	AT1G07510	1.09	0.13	0.91	0.396336	0.534462	-6.81
248220_at	26S proteasome regulatory particle	---	AT5G53540	1.08	0.11	0.91	0.396382	0.534493	-6.81
247482_at	chromosomal protein - like chromo	SMC2	AT5G62410	-1.08	-0.12	-0.91	0.396453	0.534542	-6.81
256153_at	ubiquitin-like (UBQ12), putative sin	UBQ12	AT1G55060	-1.09	-0.12	-0.91	0.396476	0.534542	-6.81
251154_at	tRNA isopentenyl transferase -like	ATIPT3	AT3G63110	1.21	0.27	0.91	0.396489	0.534542	-6.81
247850_at	receptor-like protein kinase	---	AT5G58150	-1.26	-0.34	-0.90	0.396841	0.534985	-6.81
249491_at	germin - like protein germin-like pr	---	AT5G39130	1.07	0.10	0.90	0.396899	0.535031	-6.81
255358_at	hypothetical protein	---	AT4G03940	-1.06	-0.09	-0.90	0.396938	0.535053	-6.81
250063_at	disease resistance protein - like dis	CSA1	AT5G17880	-1.10	-0.13	-0.90	0.396963	0.535054	-6.81
265477_at	hypothetical protein predicted by ge	GAUT2	AT2G46480	-1.08	-0.11	-0.90	0.397196	0.535337	-6.81
260831_at	glutaredoxin, putative similar to glu	---	AT1G06830	1.48	0.57	0.90	0.397287	0.535428	-6.81
248281_at	unknown protein	---	AT5G52980	1.06	0.09	0.90	0.39733	0.535454	-6.81
264817_at	hypothetical protein similar to meml	---	AT1G03540	-1.07	-0.09	-0.90	0.39747	0.535611	-6.81
267644_s_a	unknown protein highly similar to T2	---	AT2G32870	1.12	0.16	0.90	0.397522	0.535623	-6.81
247582_at	putative protein various predicted p	---	AT5G60760	-1.09	-0.12	-0.90	0.397526	0.535623	-6.81
262035_at	polyprotein, putative similar to poly	---	---	1.07	0.09	0.90	0.39771	0.53584	-6.81
251863_at	kinesin-like protein kinesin, Syncep	MRH2	AT3G54870	-1.06	-0.08	-0.90	0.397787	0.535906	-6.81
261496_at	ethylene responsive element bindi	ERF12	AT1G28360	-1.08	-0.12	-0.90	0.397836	0.535906	-6.81
245280_at	Expressed protein ; supported by cl	VRN2	AT4G16845	-1.08	-0.11	-0.90	0.397859	0.535906	-6.81
260591_at	predicted protein	---	AT1G53325	-1.06	-0.08	-0.90	0.397876	0.535906	-6.81
264191_at	integral membrane protein, putative	---	AT1G54730	-1.12	-0.16	-0.90	0.397877	0.535906	-6.81
255212_at	putative athila transposon protein	---	---	-1.06	-0.09	-0.90	0.39793	0.535946	-6.81
264041_at	MADS-box protein (AGL3) ; suppo	ספט-04	AT2G03710	-1.16	-0.22	-0.90	0.398027	0.536029	-6.81
263781_at	hypothetical protein predicted by ge	---	AT2G46360	-1.06	-0.08	-0.90	0.398039	0.536029	-6.81

263520_at	putative protein kinase contains a p	---	AT2G42640	1.07	0.10	0.90	0.398096	0.536075	-6.81
262019_s_a	hypothetical protein predicted by ge	---	---	-1.07	-0.10	-0.90	0.398253	0.536255	-6.81
248580_at	chloride channel (emb|CAA70310.1	CLC-C	AT5G49890	1.10	0.14	0.90	0.398283	0.536264	-6.81
253299_at	hypothetical protein ;supported by	---	AT4G33800	1.08	0.11	0.90	0.398347	0.536318	-6.81
255620_at	putative copper-containing glycopr	---	AT4G01380	-1.06	-0.09	-0.90	0.398425	0.536391	-6.81
260661_at	hypothetical protein predicted by ge	---	AT1G19500	-1.09	-0.12	-0.90	0.398561	0.536543	-6.81
246078_s_a	putative protein probable mitosis a	---	AT5G20430	-1.12	-0.17	-0.90	0.398664	0.536649	-6.81
265106_s_a	putative membrane-associated salt	---	AT1G62590	-1.06	-0.09	-0.90	0.398736	0.536714	-6.81
264215_at	cytochrome P450, putative similar	CYP96A3	AT1G65340	-1.07	-0.09	-0.90	0.398857	0.536836	-6.81
254214_at	putative potassium transport protei	TRH1	AT4G23640	1.09	0.12	0.90	0.398873	0.536836	-6.81
265891_at	putative thionin	---	AT2G15010	-1.07	-0.10	-0.90	0.39894	0.536888	-6.81
250702_at	peroxidase ;supported by full-lengt	---	AT5G06730	1.48	0.56	0.90	0.398959	0.536888	-6.81
255634_at	hypothetical protein ; supported by	FRI	AT4G00650	-1.06	-0.08	-0.90	0.399028	0.53695	-6.81
261391_at	hypothetical protein similar to hypot	---	AT1G35030	-1.08	-0.11	-0.90	0.399089	0.537	-6.81
253465_at	putative protein ATAC98, Arabidop	---	AT4G32120	-1.10	-0.13	-0.90	0.399538	0.537547	-6.81
259576_at	RING zinc finger protein, putative c	---	AT1G35330	-1.11	-0.14	-0.90	0.399543	0.537547	-6.81
256658_at	unknown protein	---	AT3G12010	-1.07	-0.10	-0.90	0.399601	0.537594	-6.81
266751_at	putative peptide chain release facto	---	AT2G47020	-1.07	-0.10	-0.90	0.399738	0.537746	-6.81
248116_at	putative protein contains similarity t	MYB120	AT5G55020	-1.09	-0.13	-0.90	0.399827	0.537822	-6.81
253142_at	putative protein methyl-directed mi	MLH3	AT4G35520	1.07	0.09	0.90	0.399841	0.537822	-6.81
266250_at	putative reverse transcriptase	---	---	-1.07	-0.10	-0.90	0.399996	0.537998	-6.81
263758_s_a	putative NADPH dependent manno	---	AT2G21250	-1.07	-0.09	-0.90	0.400106	0.538114	-6.81
257870_at	prolyl 4-hydroxylase, putative simil	---	AT3G28490	-1.06	-0.08	-0.90	0.40015	0.538142	-6.81
249696_at	copia-like retrotransposable elemer	---	---	1.06	0.09	0.90	0.400225	0.538182	-6.81
254900_at	hypothetical protein	RALFL28	AT4G11510	-1.06	-0.09	-0.90	0.400227	0.538182	-6.81
260307_at	unknown protein similar to unknowr	---	AT1G70620	1.06	0.08	0.90	0.400438	0.538433	-6.81
263102_at	unknown protein	---	AT2G05270	1.06	0.08	0.90	0.400482	0.538436	-6.81
249692_s_a	putative protein strong similarity to	---	AT5G36670	1.09	0.12	0.90	0.400498	0.538436	-6.81
261297_at	hypothetical protein predicted by ge	JAZ4	AT1G48500	-1.06	-0.09	-0.90	0.40051	0.538436	-6.81
258713_at	Expressed protein ; supported by fu	---	AT3G09735	1.07	0.09	0.90	0.40055	0.538458	-6.81
264000_at	putative mitochondrial dicarboxylate	UCP5	AT2G22500	1.31	0.39	0.90	0.40085	0.538828	-6.82
265436_at	putative retroelement pol polyprotei	---	---	1.06	0.08	0.90	0.400893	0.538854	-6.82
247712_at	E2, ubiquitin-conjugating enzyme 7	UBC7	AT5G59300	-1.08	-0.12	-0.90	0.40094	0.538886	-6.82
248677_at	unknown protein	---	AT5G48860	-1.08	-0.11	-0.90	0.401017	0.538959	-6.82
246031_at	putative protein KIAA0731 - Homo	---	AT5G21160	1.08	0.12	0.90	0.401088	0.539021	-6.82

264867_at	unknown protein	FH4	AT1G24150	-1.19	-0.25	-0.90	0.401196	0.539116	-6.82
249316_s_a	glutathione transferase-like ;suppor	ATGSTT2	AT5G41220	1.08	0.11	0.90	0.401205	0.539116	-6.82
262676_at	SKP1/ASK1 (At1) identical to Skp1	SKP1	AT1G75950	-1.06	-0.08	-0.90	0.401286	0.539193	-6.82
265113_at	hypothetical protein	---	---	-1.07	-0.10	-0.90	0.401572	0.539545	-6.82
266688_at	hypothetical protein	---	AT2G19660	-1.06	-0.08	-0.90	0.401613	0.539565	-6.82
252867_at	putative protein hypothetical protei	---	AT4G39870	1.09	0.12	0.90	0.401651	0.539565	-6.82
262835_at	Na+ H+ antiporter, putative similar	ATNHX8	AT1G14660	-1.07	-0.10	-0.90	0.401658	0.539565	-6.82
266390_at	hypothetical protein predicted by ge	---	AT2G32310	-1.07	-0.09	-0.89	0.401683	0.539568	-6.82
247695_at	putative protein Not2p, Homo sapie	VIP2	AT5G59710	1.06	0.09	0.89	0.40175	0.539626	-6.82
266528_at	putative disease resistance protein	---	AT2G16870	-1.06	-0.08	-0.89	0.401934	0.53984	-6.82
256088_at	putative FKBP-type peptidyl-prolyl c	---	AT1G20810	-1.11	-0.15	-0.89	0.401967	0.539853	-6.82
250393_at	serine/threonine protein phosphata	---	AT5G10900	-1.08	-0.11	-0.89	0.402032	0.539908	-6.82
256133_at	hypothetical protein predicted by ge	---	AT1G13570	-1.13	-0.18	-0.89	0.402249	0.540168	-6.82
262660_at	putative protein kinase	VIK	AT1G14000	-1.07	-0.10	-0.89	0.402296	0.5402	-6.82
247125_at	putative protein contains similarity t	---	AT5G66070	-1.21	-0.28	-0.89	0.402388	0.540291	-6.82
249905_at	unknown protein	---	AT5G22710	1.07	0.10	0.89	0.402442	0.540333	-6.82
255855_at	ABC transporter, putative similar to	PDR11	AT1G66950	-1.10	-0.13	-0.89	0.402478	0.540349	-6.82
260890_at	cysteine proteinase contains similar	---	AT1G29090	-1.11	-0.15	-0.89	0.402616	0.540475	-6.82
248183_at	CHP-rich zinc finger protein-like	---	AT5G54040	-1.06	-0.09	-0.89	0.402642	0.540475	-6.82
260130_s_a	beta-glucosidase, putative similar t	BGLU21	AT1G66270	1.06	0.08	0.89	0.402643	0.540475	-6.82
265956_at	hypothetical protein predicted by ge	---	AT2G37290	-1.06	-0.08	-0.89	0.402718	0.540543	-6.82
260312_at	putative disease resistance protein	---	AT1G63880	-1.10	-0.13	-0.89	0.402816	0.540643	-6.82
245247_at	scarecrow-like 13 (SCL13) ; suppor	SCL13	AT4G17230	-1.22	-0.28	-0.89	0.402861	0.540672	-6.82
256561_s_a	hypothetical protein similar to putati	---	---	1.06	0.09	0.89	0.402907	0.540702	-6.82
264614_s_a	putative aldehyde oxidase similar to	---	AT1G02590	-1.08	-0.11	-0.89	0.403024	0.540821	-6.82
255587_at	putative inorganic phosphatase ; su	AtPPa5	AT4G01480	1.10	0.14	0.89	0.403043	0.540821	-6.82
263479_x_a	hypothetical protein predicted by ge	---	---	-1.07	-0.10	-0.89	0.403078	0.540836	-6.82
260934_at	hypothetical protein predicted by ge	---	AT1G45100	-1.06	-0.08	-0.89	0.403266	0.541056	-6.82
264153_at	disease resistance protein RPS4, p	ATPP2-A5	AT1G65390	-1.18	-0.24	-0.89	0.403425	0.541238	-6.82
260609_at	putative receptor protein kinase	---	AT2G43690	-1.07	-0.10	-0.89	0.403484	0.541285	-6.82
248641_at	unknown protein	---	AT5G49110	1.07	0.10	0.89	0.403588	0.541388	-6.82
249193_at	putative protein similar to unknown	ARC6	AT5G42480	1.06	0.08	0.89	0.403615	0.541388	-6.82
252534_at	Myb DNA binding protein -like MYB	MYB111	AT3G46130	1.07	0.10	0.89	0.403646	0.541388	-6.82
246667_at	putative protein hypothetical protein	---	---	-1.07	-0.10	-0.89	0.403656	0.541388	-6.82
253618_at	nodulin-like protein MtN21 gene pr	---	AT4G30420	-1.06	-0.08	-0.89	0.403706	0.541424	-6.82

254316_at	putative protein glycine-rich cell wa	---	---	-1.08	-0.11	-0.89	0.403761	0.541466	-6.82
245609_at	disease resistance N like protein	---	AT4G14368	-1.09	-0.12	-0.89	0.403884	0.54156	-6.82
259142_at	unknown protein similar to ankyrin I	---	AT3G10200	-1.08	-0.11	-0.89	0.403884	0.54156	-6.82
248023_at	ADP/ATP translocase-like protein ;	---	AT5G56450	-1.08	-0.11	-0.89	0.403924	0.54156	-6.82
265364_at	putative retroelement pol polyprotei	---	---	1.06	0.09	0.89	0.403927	0.54156	-6.82
246585_at	myb transcription factor werewolf (W	ATMYB66	AT5G14750	-1.06	-0.09	-0.89	0.403981	0.541601	-6.82
248349_at	progesterone-binding protein-like ;	MSBP1	AT5G52240	1.10	0.14	0.89	0.404006	0.541603	-6.82
256984_at	hypothetical protein predicted by ge	---	AT3G13480	1.08	0.12	0.89	0.404059	0.541642	-6.82
249292_at	repair endonuclease (gb|AAF01274	UVH1	AT5G41150	-1.07	-0.09	-0.89	0.404258	0.541877	-6.82
252704_at	putative protein KIAA0161 gene, H	---	AT3G43750	1.07	0.10	0.89	0.40429	0.541888	-6.82
262146_at	membrane protein, putative similar	ATRBL5	AT1G52580	-1.13	-0.18	-0.89	0.404349	0.541935	-6.82
246582_at	hypothetical protein predicted by ge	---	AT1G31750	1.18	0.24	0.89	0.404377	0.541942	-6.82
257693_at	hypothetical protein predicted by ge	---	AT3G12850	-1.13	-0.17	-0.89	0.404405	0.541947	-6.82
249431_at	polygalacturonase-like protein poly	---	AT5G39910	-1.12	-0.16	-0.89	0.404442	0.541965	-6.82
257166_at	hypothetical protein similar to putati	---	AT3G24710	-1.07	-0.10	-0.89	0.404822	0.542441	-6.82
253364_at	F-box protein family, AtFBX13 cota	---	AT4G33160	1.06	0.08	0.89	0.405077	0.542743	-6.82
248842_at	unknown protein	---	AT5G46850	1.09	0.12	0.89	0.405094	0.542743	-6.82
256738_at	geranylgeranyl pyrophosphate syn	---	AT3G29430	-1.08	-0.11	-0.89	0.405125	0.542752	-6.82
259573_at	hypothetical protein	---	---	-1.07	-0.10	-0.89	0.405184	0.542799	-6.82
259804_at	cytosolic factor, putative similar to (	---	AT1G72160	-1.14	-0.19	-0.89	0.405254	0.542861	-6.82
252170_at	hypothetical protein ; supported by	HR4	AT3G26560	-1.09	-0.13	-0.89	0.405302	0.542893	-6.82
256519_at	hypothetical protein predicted by ge	---	AT1G66110	-1.11	-0.15	-0.89	0.405506	0.543113	-6.82
263070_at	unknown protein	---	AT2G17600	-1.07	-0.10	-0.89	0.405513	0.543113	-6.82
250153_at	putative protein TMV response-rela	WRKY72	AT5G15130	1.19	0.25	0.89	0.405664	0.543276	-6.82
266378_at	hypothetical protein predicted by ge	---	AT2G14700	-1.09	-0.12	-0.89	0.405683	0.543276	-6.82
262435_at	cytochrome P450, putative similar	CYP96A8	AT1G47620	-1.06	-0.08	-0.89	0.405801	0.543402	-6.82
261968_at	disease resistance protein RPP1-W	---	AT1G65850	-1.06	-0.08	-0.89	0.4059	0.543504	-6.82
249522_at	putative protein similar to unknown	---	AT5G38700	-1.07	-0.10	-0.89	0.405994	0.543597	-6.82
248929_at	myrosinase-binding protein-like; jas	---	AT5G46000	-1.08	-0.11	-0.89	0.406109	0.543716	-6.82
255408_at	hypothetical protein similar to A. th	---	AT4G03490	-1.13	-0.17	-0.89	0.406157	0.543716	-6.82
256079_at	hypothetical protein predicted by ge	---	AT1G20680	-1.06	-0.08	-0.89	0.40617	0.543716	-6.82
250047_at	BCS1 - like protein h-bcs1, Homo s	---	AT5G17730	-1.08	-0.12	-0.89	0.406178	0.543716	-6.82
260144_at	putative ABC transporter similar to	---	AT1G71960	1.10	0.14	0.89	0.406316	0.543868	-6.83
255721_at	unknown protein ;supported by full-	---	AT1G31940	-1.06	-0.09	-0.89	0.406347	0.543878	-6.83
250724_at	harpin-induced protein-like	---	AT5G06330	1.13	0.17	0.89	0.406554	0.544123	-6.83

247309_at	putative protein contains similarity t	---	AT5G63940	-1.11	-0.15	-0.88	0.406666	0.544241	-6.83
257308_at	unknown protein	---	AT3G28120	-1.06	-0.08	-0.88	0.406822	0.544418	-6.83
257457_at	hypothetical protein predicted by ge	---	AT2G05430	-1.07	-0.09	-0.88	0.407077	0.544727	-6.83
266176_at	lectin-like protein	AtPP2-B2	AT2G02250	-1.10	-0.14	-0.88	0.407148	0.544774	-6.83
248715_at	ATFP4, putative	---	AT5G48290	-1.11	-0.15	-0.88	0.407164	0.544774	-6.83
258746_at	germin-like protein similar to germir	---	AT3G05950	-1.08	-0.11	-0.88	0.40719	0.544774	-6.83
266593_at	hypothetical protein predicted by ge	---	AT2G46200	-1.08	-0.10	-0.88	0.407207	0.544774	-6.83
249950_at	protein kinase - like protein Pto kin	---	AT5G18910	-1.06	-0.09	-0.88	0.407329	0.544905	-6.83
264889_at	unknown protein	---	AT1G23050	-1.08	-0.12	-0.88	0.407525	0.545136	-6.83
262904_at	chaperone, putative similar to chap	---	AT1G59725	-1.09	-0.12	-0.88	0.407575	0.545171	-6.83
266247_at	hypothetical protein predicted by ge	---	AT2G27660	1.09	0.13	0.88	0.407624	0.545204	-6.83
266567_at	putative eukaryotic initiation factor	---	AT2G24050	-1.11	-0.15	-0.88	0.407677	0.545242	-6.83
248104_at	S-adenosyl-L-methionine:salicylic a	IAMT1	AT5G55250	-1.19	-0.25	-0.88	0.407705	0.545248	-6.83
258451_at	alternative oxidase 1b precursor ide	AOX1B	AT3G22360	-1.09	-0.12	-0.88	0.407791	0.545331	-6.83
255655_at	contains similarity to gag proteins	---	AT4G00980	1.13	0.17	0.88	0.407885	0.545422	-6.83
247838_at	ubiquitin-specific protease 23 (UBF	UBP23	AT5G57990	1.13	0.18	0.88	0.407907	0.545422	-6.83
261456_at	hypothetical protein predicted by ge	---	AT1G21050	-1.40	-0.49	-0.88	0.407934	0.545427	-6.83
265094_at	putative cruciferin 12S seed storag	---	AT1G03890	-1.06	-0.09	-0.88	0.407967	0.54543	-6.83
262638_at	oxidoreductase, putative contains F	---	AT1G06650	1.07	0.09	0.88	0.407984	0.54543	-6.83
247544_at	putative protein ;supported by full-l	---	AT5G61670	1.10	0.14	0.88	0.408019	0.545444	-6.83
261360_at	hypothetical protein predicted by ge	---	---	-1.08	-0.11	-0.88	0.408134	0.54555	-6.83
265399_at	hypothetical protein predicted by ge	---	AT2G11010	-1.16	-0.21	-0.88	0.408146	0.54555	-6.83
255935_at	hypothetical protein contains Pfam	---	AT1G12700	1.08	0.11	0.88	0.408329	0.54574	-6.83
265903_at	putative potassium transporter/char	SPIK	AT2G25600	-1.07	-0.09	-0.88	0.408338	0.54574	-6.83
252734_at	putative protein merozoite surface	MEE38	AT3G43160	-1.07	-0.10	-0.88	0.408372	0.54574	-6.83
261629_at	unknown protein	---	AT1G49980	1.07	0.09	0.88	0.408384	0.54574	-6.83
254771_at	hypothetical protein	MEE56	AT4G13380	-1.07	-0.09	-0.88	0.408413	0.545747	-6.83
246894_at	heat-shock protein - like heat-shoc	---	AT5G25530	-1.12	-0.16	-0.88	0.408493	0.545822	-6.83
256692_at	hypothetical protein predicted by ge	---	AT3G32050	-1.06	-0.08	-0.88	0.40852	0.545826	-6.83
252288_at	hypothetical protein	---	AT3G49080	1.11	0.14	0.88	0.408636	0.545891	-6.83
259040_at	putative glutathione transferase sim	ATGSTU8	AT3G09270	1.40	0.49	0.88	0.408659	0.545891	-6.83
263183_at	putative glucan synthase Highly sim	CALS1	AT1G05570	1.24	0.31	0.88	0.408677	0.545891	-6.83
253435_at	adenylate translocator (brittle-1) - l	SHS1	AT4G32400	-1.11	-0.15	-0.88	0.408679	0.545891	-6.83
264346_at	putative amino-cyclopropane-carbo	---	AT1G12010	-1.07	-0.10	-0.88	0.408688	0.545891	-6.83
249887_at	putative protein similar to unknown	---	AT5G22310	-1.24	-0.31	-0.88	0.40884	0.54604	-6.83

248098_at	unknown protein ; supported by cD	---	AT5G55290	1.07	0.10	0.88	0.408847	0.54604	-6.83
267428_at	putative coatomer epsilon subunit	---	AT2G34840	-1.08	-0.11	-0.88	0.408896	0.546054	-6.83
261441_at	NAM protein, putative similar to NA	ANAC010	AT1G28470	-1.13	-0.18	-0.88	0.408906	0.546054	-6.83
246811_at	putative protein	---	AT5G27170	1.07	0.10	0.88	0.409077	0.546224	-6.83
251020_at	ABC transporter -like protein NBD-	NAP9	AT5G02270	1.20	0.27	0.88	0.409082	0.546224	-6.83
250018_at	putative protein similar to unknown	---	AT5G18150	1.24	0.32	0.88	0.409218	0.546351	-6.83
263365_at	putative heat shock protein	---	AT2G20550	-1.12	-0.16	-0.88	0.409224	0.546351	-6.83
258204_at	hypothetical protein predicted by ge	AtGRF5	AT3G13960	-1.09	-0.12	-0.88	0.409264	0.546359	-6.83
260650_at	Expressed protein ; supported by fu	TOM2B	AT1G32370	-1.07	-0.09	-0.88	0.409278	0.546359	-6.83
247293_at	putative protein similar to unknown	---	AT5G64510	-1.27	-0.34	-0.88	0.409379	0.546461	-6.83
263443_at	putative fatty acid elongase ;suppo	KCS12	AT2G28630	-1.32	-0.40	-0.88	0.409512	0.546607	-6.83
252222_at	putative protein various predicted p	---	AT3G49840	-1.16	-0.21	-0.88	0.409599	0.546691	-6.83
256875_at	cytochrome P450, putative contain	CYP71B37	AT3G26330	-1.08	-0.11	-0.88	0.409665	0.546748	-6.83
262771_at	hypothetical protein predicted by ge	---	AT1G13200	-1.09	-0.12	-0.88	0.409891	0.547017	-6.83
258630_at	putative CCHC-type zinc finger pro	---	AT3G02820	-1.11	-0.15	-0.88	0.409952	0.547066	-6.83
246982_s_a	unknown protein	---	AT2G10560	1.16	0.21	0.88	0.410165	0.547318	-6.83
259890_at	inner mitochondrial membrane prot	ATTIM23-2	AT1G72750	1.13	0.18	0.88	0.41019	0.54732	-6.83
265294_at	Mutator-like transposase similar to	---	---	-1.08	-0.11	-0.88	0.410297	0.547431	-6.83
264760_at	syntaxin-related protein Nt-syr1, pu	SYP124	AT1G61290	-1.10	-0.14	-0.88	0.41078	0.548043	-6.83
255976_at	hypothetical protein predicted by ge	---	AT1G22010	-1.07	-0.09	-0.88	0.410812	0.548054	-6.83
256591_at	hypothetical protein	---	AT3G31910	-1.05	-0.08	-0.88	0.410839	0.548058	-6.83
246520_at	putative protein RING-H2 finger pr	---	AT5G15790	1.06	0.09	0.88	0.410889	0.548093	-6.83
250084_at	unknown protein	SDG40	AT5G17240	-1.11	-0.15	-0.88	0.411033	0.548252	-6.83
266750_s_a	putative pectinesterase	VGDH1	AT2G47030	1.06	0.09	0.88	0.411123	0.54834	-6.83
256959_at	methyltransferase, putative	---	AT3G13440	1.06	0.08	0.88	0.41118	0.548382	-6.83
248225_at	unknown protein	---	AT5G53740	-1.07	-0.10	-0.88	0.411203	0.548382	-6.83
254647_at	hypothetical protein	---	AT4G18540	1.06	0.08	0.88	0.411419	0.548639	-6.83
254705_at	putative protein ; supported by cDN	---	AT4G17870	-1.12	-0.16	-0.88	0.411467	0.548671	-6.83
247153_at	receptor protein kinase-like protein	BAM1	AT5G65700	-1.16	-0.21	-0.88	0.411597	0.548811	-6.83
248113_at	wax synthase-like protein	---	AT5G55360	-1.08	-0.11	-0.88	0.411697	0.548873	-6.83
254871_at	Srw1 -like protein WD repeat prote	CCS52A2	AT4G11920	-1.06	-0.08	-0.87	0.411714	0.548873	-6.83
253154_at	putative protein predicted protein, A	---	AT4G35710	-1.08	-0.11	-0.87	0.411715	0.548873	-6.83
262097_at	hypothetical protein predicted by ge	---	AT1G55990	-1.07	-0.10	-0.87	0.411936	0.549116	-6.84
245086_at	putative translation initiation factor	---	AT2G39820	1.07	0.09	0.87	0.411945	0.549116	-6.84
264558_at	putative protein kinase Similar to co	---	AT1G09600	-1.06	-0.09	-0.87	0.411999	0.549156	-6.84

245297_at	hypothetical protein ; supported by	---	AT4G16510	-1.09	-0.12	-0.87	0.412164	0.549344	-6.84
255577_at	putative hypoersensitive response	---	AT4G01410	-1.27	-0.35	-0.87	0.412288	0.549476	-6.84
253626_at	F-box protein family, AtFBL19 cont	---	AT4G30640	-1.12	-0.17	-0.87	0.412686	0.549975	-6.84
262961_at	exonuclease, putative similar to 5'-	XRN4	AT1G54490	1.07	0.10	0.87	0.41273	0.549993	-6.84
264950_at	peroxidase, putative similar to perc	---	AT1G77100	-1.07	-0.10	-0.87	0.412762	0.549993	-6.84
252460_at	putative protein predicted protein, /	---	---	1.05	0.08	0.87	0.412772	0.549993	-6.84
256576_at	zinc finger protein (PMZ), putative	PMZ	AT3G28210	1.26	0.33	0.87	0.412811	0.550013	-6.84
264961_at	unknown protein contains similarity	PRAF1	AT1G76950	-1.16	-0.21	-0.87	0.413045	0.550289	-6.84
251247_at	hypothetical protein	---	AT3G62140	1.09	0.12	0.87	0.413067	0.550289	-6.84
257567_at	hypothetical protein predicted by ge	---	AT3G23930	1.05	0.07	0.87	0.413111	0.550316	-6.84
253318_at	extensin-like protein extensin-like p	---	AT4G33970	1.06	0.08	0.87	0.413146	0.55033	-6.84
259749_at	putative ribose 5-phosphate isomer	RSW10	AT1G71100	-1.16	-0.21	-0.87	0.413296	0.550498	-6.84
264284_at	protein kinase, putative similar to p	---	AT1G61860	-1.07	-0.10	-0.87	0.413364	0.550556	-6.84
263302_at	hypothetical protein predicted by ge	---	---	1.06	0.08	0.87	0.413405	0.550579	-6.84
262213_at	hypothetical protein predicted by ge	---	AT1G74870	1.10	0.13	0.87	0.413455	0.550612	-6.84
264844_at	putative glycosylation enzyme ; su	---	AT1G03520	1.10	0.13	0.87	0.413512	0.550612	-6.84
257237_at	DNA nick sensor, putative contains	---	AT3G14890	-1.20	-0.26	-0.87	0.413539	0.550612	-6.84
246204_at	putative protein ; supported by cDN	---	AT4G37020	-1.07	-0.10	-0.87	0.413559	0.550612	-6.84
266011_at	unknown protein	---	AT2G37440	1.07	0.10	0.87	0.41356	0.550612	-6.84
254596_at	putative protein proline-rich protein	---	AT4G18975	1.07	0.10	0.87	0.413575	0.550612	-6.84
246158_at	Expressed protein ; supported by fu	---	AT5G19855	-1.12	-0.16	-0.87	0.41361	0.550627	-6.84
258071_s_a	unknown protein	---	AT3G26070	-1.11	-0.15	-0.87	0.413741	0.550693	-6.84
247224_at	MADS box transcription factor-like p	MAF5	AT5G65080	-1.12	-0.17	-0.87	0.413742	0.550693	-6.84
256408_at	hypothetical protein	---	AT1G66610	-1.09	-0.12	-0.87	0.413744	0.550693	-6.84
263185_at	transport protein, putative similar to	---	AT1G05520	1.06	0.08	0.87	0.413756	0.550693	-6.84
264181_at	ubiquitin, putative similar to ubiquit	UBQ13	AT1G65350	1.06	0.08	0.87	0.413831	0.550761	-6.84
249784_at	putative protein similar to unknown	---	AT5G24280	1.11	0.14	0.87	0.413872	0.550783	-6.84
265155_at	putative major latex protein type 1	---	AT1G30990	-1.07	-0.10	-0.87	0.413897	0.550784	-6.84
265592_at	hypothetical protein predicted by ge	---	AT2G20110	1.08	0.11	0.87	0.414071	0.550984	-6.84
249062_at	putative protein contains similarity t	---	AT5G44270	-1.08	-0.11	-0.87	0.414143	0.551047	-6.84
255183_at	hypothetical protein	---	AT4G08140	-1.08	-0.12	-0.87	0.414176	0.551058	-6.84
266498_at	1-aminocyclopropane-1-carboxylate	---	AT2G06960	-1.07	-0.10	-0.87	0.414199	0.551058	-6.84
256233_at	ankyrin-like protein contains Pfam p	ITN1	AT3G12360	-1.06	-0.09	-0.87	0.414477	0.551395	-6.84
267326_at	putative RNA-binding protein	---	AT2G19380	1.08	0.11	0.87	0.414515	0.551414	-6.84
250507_at	putative protein similar to unknown	---	AT5G09940	1.07	0.09	0.87	0.414548	0.551425	-6.84

261155_at	unknown protein ;supported by full-	---	AT1G04960	1.08	0.12	0.87	0.414622	0.55148	-6.84
254372_at	putative protein predicted proteins,	---	AT4G21620	-1.15	-0.20	-0.87	0.414638	0.55148	-6.84
263269_at	En/Spm-like transposon protein rela	---	---	1.07	0.09	0.87	0.414666	0.551486	-6.84
267501_at	unknown protein	---	AT2G45540	-1.09	-0.13	-0.87	0.414771	0.551593	-6.84
266030_x_a	hypothetical protein predicted by ge	---	---	-1.08	-0.11	-0.87	0.414813	0.551617	-6.84
254595_at	floral homeotic protein agamous (A	AG	AT4G18960	-1.06	-0.08	-0.87	0.414868	0.551638	-6.84
255790_at	hypothetical protein predicted by ge	---	AT2G33560	-1.07	-0.10	-0.87	0.414877	0.551638	-6.84
261430_at	hypothetical protein predicted by ge	---	AT1G18830	-1.10	-0.13	-0.87	0.41508	0.551876	-6.84
257180_at	sun protein (fmu protein), putative	---	AT3G13180	1.09	0.13	0.87	0.41514	0.551924	-6.84
252873_at	putative protein myosin heavy chai	---	AT4G40020	1.08	0.11	0.87	0.415265	0.552046	-6.84
245061_at	hypothetical protein ;supported by f	RCA	AT2G39730	-1.06	-0.08	-0.87	0.415281	0.552046	-6.84
260207_at	putative phosphoglucomutase simil	---	AT1G70730	1.10	0.14	0.87	0.415326	0.552073	-6.84
259035_at	hypothetical protein predicted by ge	---	AT3G09430	-1.06	-0.09	-0.87	0.415462	0.552173	-6.84
256066_at	hypothetical protein similar to hypot	---	AT1G06980	-1.22	-0.28	-0.87	0.415464	0.552173	-6.84
254946_at	putative protein proline-rich protein	---	AT4G10950	-1.07	-0.10	-0.87	0.415474	0.552173	-6.84
252168_at	putative protein pir7a protein - Ory	MES10	AT3G50440	-1.25	-0.32	-0.87	0.415678	0.552409	-6.84
264250_at	gamma glutamyl hydrolase, putativ	ATGGH2	AT1G78680	1.08	0.11	0.87	0.4157	0.552409	-6.84
246737_at	putative protein	---	AT5G27710	1.14	0.19	0.87	0.415789	0.552496	-6.84
246497_at	putative protein hypothetical protein	---	AT5G16220	-1.14	-0.19	-0.87	0.415853	0.552549	-6.84
257921_at	hypothetical protein contains Pfam	---	AT3G23270	-1.06	-0.08	-0.87	0.415882	0.552555	-6.84
259088_at	unknown protein, contains TNFR/N	---	AT3G04970	-1.11	-0.15	-0.87	0.416109	0.552825	-6.84
259557_at	hypothetical protein	WAK4	AT1G21210	1.06	0.09	0.87	0.416258	0.552991	-6.84
252806_at	putative protein	---	AT3G42390	-1.07	-0.10	-0.87	0.416364	0.553091	-6.84
245829_at	hypothetical protein predicted by ge	---	AT1G57780	-1.07	-0.10	-0.87	0.416382	0.553091	-6.84
245035_at	unknown protein similar to GP|2244	ATARD3	AT2G26400	-1.18	-0.24	-0.87	0.416442	0.553121	-6.84
250849_at	putative protein NAC2, Arabidopsis	NAC2	AT5G04410	1.07	0.10	0.87	0.416457	0.553121	-6.84
251436_at	putative protein hypothetical protei	ARGOS	AT3G59900	-1.39	-0.48	-0.87	0.416477	0.553121	-6.84
246372_at	hypothetical protein predicted by ge	---	AT1G51900	-1.07	-0.10	-0.87	0.416595	0.553237	-6.84
253983_at	putative protein SPF1 protein -Ipon	WRKY20	AT4G26640	-1.08	-0.12	-0.87	0.416614	0.553237	-6.84
251698_at	putative protein	---	AT3G56610	1.06	0.08	0.87	0.416652	0.553256	-6.84
262563_at	somatic embryogenesis receptor-li	SERK2	AT1G34210	1.09	0.13	0.87	0.416746	0.553349	-6.84
251422_at	transport protein subunit - like S61	---	AT3G60540	1.18	0.24	0.86	0.416812	0.553394	-6.84
261966_x_a	hypothetical protein similar to putati	---	---	1.07	0.09	0.86	0.416829	0.553394	-6.84
250058_at	plastid-specific ribosomal protein 6	PSRP6	AT5G17870	-1.09	-0.12	-0.86	0.416853	0.553394	-6.84
254504_at	putative protein RNPL, Homo sapie	---	AT4G20030	1.12	0.16	0.86	0.41688	0.553398	-6.84

250843_at	putative RNA-binding protein astro	BTR1L	AT5G04430	-1.06	-0.09	-0.86	0.416908	0.553403	-6.84
263476_at	putative poly(ADP-ribose) glycohyd	TEJ	AT2G31870	1.06	0.09	0.86	0.416958	0.553437	-6.84
261209_at	unknown protein ; supported by cDI	---	AT1G12810	1.10	0.13	0.86	0.417139	0.553625	-6.84
261080_at	proliferating cellular nuclear antigen	PCNA1	AT1G07370	-1.32	-0.40	-0.86	0.417162	0.553625	-6.84
265606_s_a	putative non-LTR retroelement reve	---	AT3G09510	-1.07	-0.09	-0.86	0.417173	0.553625	-6.84
254338_s_a	pectate lyase like protein pectate ly	---	AT4G22080	-1.06	-0.08	-0.86	0.417343	0.553791	-6.84
250738_at	anthranilate synthase component I-	ASA1	AT5G05730	1.24	0.32	0.86	0.417346	0.553791	-6.84
266018_at	putative preprotein translocase SE	SCY1	AT2G18710	-1.06	-0.09	-0.86	0.417415	0.55385	-6.84
261924_at	peptide transporter, putative simila	---	AT1G22550	-1.19	-0.25	-0.86	0.417497	0.553926	-6.84
266143_at	Expressed protein ; supported by cI	---	AT2G38905	-1.09	-0.12	-0.86	0.417558	0.553975	-6.84
262740_at	lipase, putative contains Pfam prof	---	AT1G28590	1.07	0.10	0.86	0.417794	0.554231	-6.85
255015_at	putative protein m6A methyltransfe	EMB1691	AT4G09980	1.11	0.16	0.86	0.417799	0.554231	-6.85
249789_at	putative protein similar to unknown	---	AT5G24340	1.08	0.12	0.86	0.417859	0.554278	-6.85
266154_at	putative cytochrome p450	---	AT2G12190	1.11	0.15	0.86	0.417906	0.554308	-6.85
259963_at	phosphate/phosphoenolpyruvate tr	---	AT1G53660	-1.07	-0.10	-0.86	0.417968	0.554357	-6.85
257569_at	hypothetical protein	---	AT3G26350	-1.10	-0.14	-0.86	0.418033	0.554412	-6.85
262286_at	Expressed protein ; supported by fu	---	AT1G68585	1.15	0.21	0.86	0.41829	0.554712	-6.85
255630_at	putative phosphoribosylanthranilate	---	AT4G00700	1.74	0.80	0.86	0.418307	0.554712	-6.85
256271_at	unknown protein	---	AT3G12140	1.10	0.14	0.86	0.418394	0.554794	-6.85
251405_at	plasma membrane H+-ATPase - lik	AHA7	AT3G60330	-1.06	-0.09	-0.86	0.418464	0.554854	-6.85
244992_s_a	ribosomal protein S7	---	---	-1.08	-0.11	-0.86	0.418744	0.55518	-6.85
256985_at	myb-related protein 5 identical to G	ATMYB5	AT3G13540	-1.10	-0.13	-0.86	0.41878	0.55518	-6.85
261090_at	protein kinase, putative contains P	---	AT1G07560	-1.08	-0.12	-0.86	0.418782	0.55518	-6.85
259183_at	hypothetical protein similar to putati	---	AT3G01580	1.10	0.14	0.86	0.418807	0.555181	-6.85
262153_at	unknown protein	---	AT1G52710	-1.06	-0.08	-0.86	0.418909	0.555273	-6.85
249437_at	putative protein predicted proteins -	---	AT5G39990	1.09	0.12	0.86	0.418925	0.555273	-6.85
245360_at	naringenin 3-dioxygenase like prote	---	AT4G16330	1.07	0.10	0.86	0.418964	0.555291	-6.85
257453_at	hypothetical protein predicted by ge	---	AT1G65130	-1.08	-0.11	-0.86	0.418994	0.555299	-6.85
263515_at	unknown protein	---	AT2G21640	1.27	0.34	0.86	0.419291	0.55566	-6.85
255191_at	may be a pseudogene	---	---	-1.06	-0.08	-0.86	0.41936	0.555719	-6.85
248925_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G45910	-1.09	-0.12	-0.86	0.419454	0.555788	-6.85
263873_at	unknown protein predicted by gens	---	AT2G21860	1.09	0.12	0.86	0.419461	0.555788	-6.85
248206_at	unknown protein	---	AT5G54350	-1.09	-0.12	-0.86	0.419523	0.55583	-6.85
248653_at	disease resistance protein-like	---	AT5G49290	-1.07	-0.10	-0.86	0.419541	0.55583	-6.85
266386_at	putative homeodomain transcriptior	HDG3	AT2G32370	-1.08	-0.11	-0.86	0.419608	0.555886	-6.85

246734_at	putative protein WRN (Werner syn	RECQSIM	AT5G27680	-1.07	-0.09	-0.86	0.419658	0.555921	-6.85
260576_at	putative FCA-related protein	---	AT2G47310	-1.10	-0.13	-0.86	0.419709	0.555956	-6.85
253210_at	putative protein predicted protein, A	MTN2	AT4G34840	-1.07	-0.10	-0.86	0.419875	0.556117	-6.85
250841_at	putative protein CGI-01 protein, Ho	---	AT5G04610	1.13	0.17	0.86	0.41989	0.556117	-6.85
257134_at	hypothetical protein similar to oxido	---	AT3G12870	-1.09	-0.12	-0.86	0.419904	0.556117	-6.85
245653_at	heat shock transcription factor like p	FBD1	AT4G13985	-1.07	-0.10	-0.86	0.420095	0.55631	-6.85
252028_at	hypothetical protein	---	AT3G52640	-1.12	-0.17	-0.86	0.4201	0.55631	-6.85
252963_at	putative protein	---	AT4G38820	-1.06	-0.09	-0.86	0.420123	0.55631	-6.85
246069_at	zinc finger protein ;supported by fu	---	AT5G20220	-1.12	-0.17	-0.86	0.420442	0.5567	-6.85
266337_at	putative ligand-gated ion channel su	ATGLR3.5	AT2G32390	1.07	0.09	0.86	0.420701	0.557012	-6.85
249043_at	berberine bridge enzyme	---	AT5G44360	-1.05	-0.08	-0.86	0.420922	0.557272	-6.85
248415_at	unknown protein	---	AT5G51620	1.06	0.09	0.86	0.421008	0.557353	-6.85
249228_at	SKP1/ASK1 (At2) identical to UIP2	ASK2	AT5G42190	-1.10	-0.13	-0.86	0.421045	0.55737	-6.85
259195_at	hypothetical protein predicted by ge	---	AT3G01730	-1.08	-0.11	-0.86	0.421111	0.557424	-6.85
266659_at	putative poly(A) polymerase ; supp	---	AT2G25850	-1.07	-0.10	-0.86	0.42118	0.557484	-6.85
267184_at	unknown protein ; supported by cD	ASHH3	AT2G44150	-1.06	-0.09	-0.86	0.421239	0.557529	-6.85
262329_at	hypothetical protein similar to hypot	---	AT1G64090	-1.06	-0.08	-0.86	0.421332	0.557599	-6.85
262183_at	unknown protein	---	AT1G77890	1.07	0.09	0.86	0.42134	0.557599	-6.85
257989_at	unknown protein ; supported by cDI	VPS9A	AT3G19770	1.07	0.10	0.86	0.421414	0.55766	-6.85
262425_at	hypothetical protein predicted by ge	---	AT1G47660	-1.06	-0.09	-0.86	0.421436	0.55766	-6.85
260282_at	putative N-terminal acetyltransferas	EMB2753	AT1G80410	1.07	0.10	0.86	0.421471	0.557675	-6.85
266527_at	hypothetical protein predicted by ge	---	---	-1.09	-0.12	-0.86	0.421506	0.557689	-6.85
247296_at	unknown protein ;supported by full-	---	AT5G64160	-1.09	-0.13	-0.86	0.421938	0.558228	-6.85
251979_at	caffeic acid O-methyltransferase -	LUT1	AT3G53130	1.07	0.10	0.85	0.421973	0.558241	-6.85
248277_at	ABC transporter-like protein	---	AT5G52860	-1.09	-0.12	-0.85	0.422013	0.558262	-6.85
265049_at	jasmonate inducible protein, putativ	---	AT1G52060	-1.06	-0.08	-0.85	0.422146	0.558406	-6.85
255396_at	hypothetical protein	---	---	-1.06	-0.09	-0.85	0.422345	0.558637	-6.85
246518_at	acetyltransferase-like protein Gluc	AtGNA1	AT5G15770	1.07	0.09	0.85	0.422484	0.558788	-6.85
250722_at	unknown protein ;supported by full-	---	AT5G06190	1.12	0.16	0.85	0.422558	0.558848	-6.85
251474_at	putative protein diphthamide synth	---	AT3G59630	1.07	0.10	0.85	0.422578	0.558848	-6.85
256303_at	disease resistance protein, putative	---	AT1G69550	1.09	0.12	0.85	0.422875	0.559207	-6.85
253972_at	putative protein Uvi31, Schizosacc	CPSUFE	AT4G26500	-1.05	-0.07	-0.85	0.422939	0.559261	-6.85
252979_at	Expressed protein ; supported by fu	---	AT4G38225	-1.12	-0.16	-0.85	0.422985	0.559289	-6.85
255049_at	gibberellin-regulated protein GASA2	GASA2	AT4G09610	-1.06	-0.08	-0.85	0.423072	0.559371	-6.85
245209_at	putative protein similarity to predict	---	AT5G12340	-1.27	-0.35	-0.85	0.423301	0.559642	-6.85

260503_at	proteasome, 30 kda subunit (ec 3.4	PAF2	AT1G47250	-1.07	-0.10	-0.85	0.423565	0.559959	-6.86
267027_at	hypothetical protein	---	AT2G38330	-1.10	-0.13	-0.85	0.423741	0.560138	-6.86
263493_at	putative ATP-dependent RNA helic	---	AT2G42520	1.10	0.14	0.85	0.42375	0.560138	-6.86
253062_at	putative protein predicted protein, A	NPY5	AT4G37590	-1.20	-0.26	-0.85	0.423813	0.56016	-6.86
250809_at	putative protein contains similarity t	---	AT5G05140	-1.16	-0.21	-0.85	0.423831	0.56016	-6.86
255205_at	putative transposon protein	---	---	-1.05	-0.07	-0.85	0.423841	0.56016	-6.86
250547_at	asparaginase ; supported by cDNA	---	AT5G08100	1.07	0.10	0.85	0.424155	0.560518	-6.86
260117_at	AIG1-like protein similar to AIG1 pr	---	AT1G33950	-1.05	-0.07	-0.85	0.424161	0.560518	-6.86
266754_at	hypothetical protein	---	AT2G46980	-1.09	-0.13	-0.85	0.424225	0.560556	-6.86
250956_at	putative protein	---	AT5G03210	1.11	0.15	0.85	0.424238	0.560556	-6.86
264650_at	putative transcription factor Similar	NF-YC9	AT1G08970	-1.07	-0.10	-0.85	0.424412	0.560753	-6.86
266455_at	putative bHLH transcription factor	---	AT2G22760	-1.17	-0.23	-0.85	0.42446	0.560784	-6.86
248236_at	putative protein contains similarity t	---	AT5G53870	-1.36	-0.45	-0.85	0.424506	0.560805	-6.86
265870_at	hypothetical protein predicted by ge	PDLP6	AT2G01660	1.06	0.09	0.85	0.424528	0.560805	-6.86
265353_at	unknown protein ;supported by full-	---	AT2G16800	1.06	0.08	0.85	0.42455	0.560805	-6.86
250493_at	putative protein various predicted p	---	AT5G09800	1.55	0.63	0.85	0.424966	0.561316	-6.86
261939_at	cytochrome c oxidase subunit, puta	COX6B	AT1G22450	-1.10	-0.13	-0.85	0.424986	0.561316	-6.86
265124_at	hypothetical protein similar to putati	---	AT1G55430	-1.08	-0.11	-0.85	0.425124	0.561466	-6.86
262541_at	hypothetical protein contains simila	---	---	-1.06	-0.08	-0.85	0.425238	0.561581	-6.86
256749_at	hypothetical protein similar to putati	---	---	-1.06	-0.09	-0.85	0.42526	0.561581	-6.86
247294_at	putative protein similar to unknown	XRCC2	AT5G64520	-1.06	-0.09	-0.85	0.42531	0.561588	-6.86
257531_at	putative RNA-binding protein conta	---	AT3G07250	-1.06	-0.08	-0.85	0.425315	0.561588	-6.86
244952_at	hypothetical protein	---	---	1.08	0.11	0.85	0.425348	0.561599	-6.86
255492_at	hypothetical protein similar to A. th	EOL1	AT4G02680	1.07	0.10	0.85	0.425409	0.561647	-6.86
250492_at	putative protein Requiem protein, X	ATXR5	AT5G09790	-1.07	-0.10	-0.85	0.425473	0.561688	-6.86
267473_at	hypothetical protein predicted by ge	---	AT2G02750	1.07	0.10	0.85	0.425489	0.561688	-6.86
250901_at	putative protein ; supported by cDN	RABC2A	AT5G03530	-1.25	-0.33	-0.85	0.425529	0.561708	-6.86
247217_s_a	MADS box transcription factors-like	MAF3	AT5G65050	-1.06	-0.08	-0.85	0.425613	0.561787	-6.86
258303_at	hypothetical protein predicted by ge	---	---	-1.06	-0.09	-0.85	0.425673	0.56183	-6.86
254804_at	putative protein putative oxidoredu	---	AT4G13010	-1.08	-0.11	-0.85	0.425704	0.56183	-6.86
251890_at	SCARECROW1 ; supported by cD	SCR	AT3G54220	1.07	0.10	0.85	0.42572	0.56183	-6.86
251613_at	hypothetical protein	---	AT3G57960	-1.08	-0.12	-0.85	0.425768	0.561861	-6.86
248887_at	Expressed protein ; supported by fu	---	AT5G46115	-1.08	-0.10	-0.85	0.425949	0.562068	-6.86
267120_at	hypothetical protein predicted by ge	---	AT2G23530	1.08	0.11	0.85	0.426105	0.562241	-6.86
264868_at	unknown protein	---	AT1G24090	1.16	0.21	0.85	0.42642	0.562624	-6.86

254589_at	hypothetical protein	---	AT4G18850	-1.08	-0.11	-0.85	0.426515	0.562716	-6.86
267252_at	hypothetical protein predicted by ge	---	AT2G23100	1.07	0.10	0.85	0.426632	0.562839	-6.86
262083_at	hypothetical protein predicted by ge	---	AT1G56100	-1.07	-0.10	-0.85	0.426847	0.563089	-6.86
259651_at	unknown protein	---	AT1G55280	1.17	0.22	0.85	0.426888	0.563111	-6.86
251705_at	DNA-binding protein-like DNA-bind	WRKY70	AT3G56400	-1.63	-0.70	-0.85	0.426963	0.563153	-6.86
262899_at	ABC transporter, putative similar to	PEN3	AT1G59870	1.08	0.11	0.85	0.426969	0.563153	-6.86
260975_at	receptor-like serine/threonine kinas	---	AT1G53430	1.19	0.26	0.85	0.427037	0.56321	-6.86
249995_at	protein kinase -like protein protein	---	AT5G18610	-1.06	-0.08	-0.85	0.427115	0.56328	-6.86
259921_at	putative protein kinase similar to pr	---	AT1G72540	1.30	0.37	0.84	0.427149	0.563292	-6.86
255751_at	terpene synthase family protein, pu	---	AT1G31950	1.08	0.11	0.84	0.427193	0.563318	-6.86
249355_at	hypothetical protein	---	AT5G40500	1.06	0.09	0.84	0.427259	0.563372	-6.86
244998_at	RNA polymerase beta' subunit-1	---	---	1.10	0.13	0.84	0.427347	0.563431	-6.86
262016_at	unknown protein	---	---	-1.05	-0.08	-0.84	0.427353	0.563431	-6.86
264563_s_a	unknown protein	---	AT1G55750	1.08	0.11	0.84	0.427536	0.563631	-6.86
245849_at	leukotriene-A4 hydrolase-like prote	---	AT5G13520	-1.16	-0.21	-0.84	0.427554	0.563631	-6.86
260147_at	putative oxidoreductase similar to a	---	AT1G52790	1.06	0.09	0.84	0.427688	0.563772	-6.86
253728_at	putative protein unknown protein c	---	AT4G29410	1.12	0.16	0.84	0.427711	0.563772	-6.86
253016_at	putative protein partial LG127/30 g	---	AT4G37950	-1.05	-0.07	-0.84	0.427811	0.563858	-6.86
246533_at	putative protein	---	AT5G15880	-1.09	-0.13	-0.84	0.427825	0.563858	-6.86
256306_at	lipase, putative contains Pfam prof	---	AT1G30370	1.62	0.69	0.84	0.427874	0.563889	-6.86
263883_at	hypothetical protein predicted by ge	---	AT2G21830	1.07	0.10	0.84	0.427942	0.563947	-6.86
256600_at	hypothetical protein predicted by ge	---	AT3G14850	-1.26	-0.33	-0.84	0.428008	0.564002	-6.86
246791_at	putative protein predicted proteins,	---	AT5G27280	-1.08	-0.11	-0.84	0.428187	0.564205	-6.86
256166_at	hypothetical protein	---	AT1G36920	-1.06	-0.08	-0.84	0.428491	0.564572	-6.86
255545_at	putative polygalacturonidase simila	---	AT4G01890	-1.06	-0.09	-0.84	0.428541	0.564605	-6.86
257018_at	unknown protein	---	AT3G19630	1.07	0.10	0.84	0.428618	0.564675	-6.86
258488_at	unknown protein ;supported by full-	---	AT3G02420	1.07	0.10	0.84	0.428894	0.564989	-6.86
266576_at	hypothetical protein predicted by ge	---	AT2G23940	1.07	0.09	0.84	0.428906	0.564989	-6.86
256995_at	protein kinase, putative contains si	---	AT3G25840	1.08	0.11	0.84	0.42899	0.565057	-6.86
251061_at	putative protein hypothetical protei	---	AT5G01830	-1.18	-0.24	-0.84	0.429007	0.565057	-6.86
251097_at	receptor like protein kinase recepto	LECRKA4.3	AT5G01560	1.30	0.38	0.84	0.429174	0.565227	-6.86
267140_at	putative GT-1-like transcription fact	---	AT2G38250	1.13	0.18	0.84	0.429186	0.565227	-6.86
257208_at	hypothetical protein predicted by ge	---	AT3G14910	-1.10	-0.14	-0.84	0.429309	0.565356	-6.86
262147_at	phospholipase D1, putative similar	PLDALPHA	AT1G52570	-1.06	-0.09	-0.84	0.429399	0.565443	-6.86
257220_at	MYB family transcription factor (Atr	ATMYB21	AT3G27810	-1.08	-0.12	-0.84	0.429537	0.565592	-6.87

251346_at	putative protein hypothetical protei	---	AT3G60980	-1.07	-0.10	-0.84	0.429616	0.565662	-6.87
264010_at	putative disease resistance respons	---	AT2G21100	-1.11	-0.16	-0.84	0.429749	0.565806	-6.87
251909_at	putative protein initiator-binding pr	TRFL4	AT3G53790	-1.08	-0.11	-0.84	0.429858	0.565916	-6.87
256962_at	glucan endo-1,3-beta-glucosidase	---	AT3G13560	1.20	0.26	0.84	0.429913	0.565955	-6.87
260569_at	putative signal recognition particle	---	AT2G43640	-1.08	-0.11	-0.84	0.430012	0.566053	-6.87
266128_at	hypothetical protein predicted by ge	EMB2766	---	-1.07	-0.10	-0.84	0.430049	0.566058	-6.87
267233_s_a	unknown protein	---	AT2G43910	1.10	0.14	0.84	0.430065	0.566058	-6.87
249460_at	v-SNARE - like protein v-SNARE A	---	AT5G39630	-1.07	-0.10	-0.84	0.430204	0.566208	-6.87
263323_at	putative receptor-like protein kinase	---	AT2G04300	1.07	0.10	0.84	0.430233	0.566213	-6.87
264499_at	Expressed protein ; supported by fu	---	AT1G30795	-1.08	-0.11	-0.84	0.43032	0.566276	-6.87
249717_at	unknown protein ;supported by full-	---	AT5G35730	-1.07	-0.09	-0.84	0.43033	0.566276	-6.87
252425_at	putative protein auxin-induced bas	AtTCP14	AT3G47620	-1.11	-0.15	-0.84	0.430652	0.566667	-6.87
260104_x_a	hypothetical protein predicted by ge	---	AT1G35410	1.08	0.11	0.84	0.430749	0.566762	-6.87
247064_at	putative protein contains similarity t	---	AT5G66890	1.13	0.17	0.84	0.430779	0.566769	-6.87
258666_at	hypothetical protein	KOB1	AT3G08550	-1.07	-0.09	-0.84	0.430875	0.566863	-6.87
257116_at	arginine methyltransferase, putativ	PRMT6	AT3G20020	1.08	0.11	0.84	0.431038	0.567032	-6.87
257966_at	unknown protein ;supported by full-	---	AT3G19800	-1.10	-0.14	-0.84	0.431054	0.567032	-6.87
265806_at	putative auxin-regulated protein	---	AT2G18010	-1.23	-0.30	-0.84	0.431226	0.567226	-6.87
256246_at	betaine aldehyde dehydrogenase,	ALDH22a1	AT3G66658	1.09	0.13	0.84	0.431301	0.567292	-6.87
262352_at	hypothetical protein similar to hypot	---	---	-1.12	-0.17	-0.84	0.431334	0.567302	-6.87
255684_at	putative glycosylasparaginase	---	AT4G00590	-1.11	-0.14	-0.84	0.431374	0.567323	-6.87
260115_at	AIG1-like protein similar to AIG1 pr	---	AT1G33870	-1.08	-0.11	-0.84	0.431422	0.567353	-6.87
261340_at	hypothetical protein predicted by ge	APUM9	AT1G35730	-1.08	-0.11	-0.84	0.431547	0.567484	-6.87
250499_at	beta-xylosidase - like protein beta-	BXL3	AT5G09730	1.07	0.09	0.84	0.431574	0.567488	-6.87
249504_at	disease resistance protein - like dis	---	AT5G38850	1.15	0.20	0.84	0.431618	0.567512	-6.87
256080_at	high mobility group protein (HMG1	---	AT1G20690	-1.06	-0.08	-0.84	0.431656	0.56753	-6.87
262222_at	unknown protein	TRZ1	AT1G74700	1.07	0.10	0.84	0.431721	0.567583	-6.87
262318_at	putative hypersensitivity-related pro	---	AT1G27620	-1.07	-0.10	-0.84	0.431876	0.567754	-6.87
260116_at	AIG1 identical to AIG1 (exhibits RF	AIG1	AT1G33960	-1.06	-0.09	-0.84	0.432028	0.567921	-6.87
263891_at	putative glucan synthase	GSL8	AT2G36850	-1.06	-0.09	-0.84	0.432157	0.568033	-6.87
260396_at	putative heme oxygenase similar to	ho3	AT1G69720	-1.12	-0.16	-0.84	0.432163	0.568033	-6.87
262378_at	CCAAT-binding factor B subunit ho	NF-YA3	AT1G72830	1.10	0.13	0.84	0.432259	0.568124	-6.87
265095_at	putative cruciferin 12S seed storag	CRU2	AT1G03880	-1.07	-0.10	-0.84	0.432283	0.568124	-6.87
264092_at	photosystem II polypeptide, putativ	PSBR	AT1G79040	1.06	0.09	0.83	0.432365	0.568199	-6.87
259751_at	putative transcription factor similar t	MYBL2	AT1G71030	-1.07	-0.10	-0.83	0.432398	0.56821	-6.87

265582_at	putative RING zinc finger protein	---	AT2G20030	1.08	0.11	0.83	0.432531	0.568353	-6.87
266765_at	putative inorganic pyrophosphatase	AtPPa3	AT2G46860	-1.06	-0.08	-0.83	0.432728	0.568566	-6.87
247036_at	putative protein contains similarity t	---	AT5G67130	1.10	0.13	0.83	0.432792	0.568566	-6.87
252142_at	putative protein hypothetical protei	---	AT3G51120	1.08	0.12	0.83	0.43281	0.568566	-6.87
249041_at	male sterility MS5; pollenless3	---	AT5G44330	-1.07	-0.10	-0.83	0.432822	0.568566	-6.87
260118_s_a	hypothetical protein predicted by ge	---	AT1G33940	1.09	0.13	0.83	0.432836	0.568566	-6.87
252453_at	putative RNA-binding protein variou	---	AT3G47120	-1.06	-0.08	-0.83	0.432843	0.568566	-6.87
251430_at	putative protein hypothetical protei	---	AT3G60110	1.07	0.10	0.83	0.432927	0.568643	-6.87
266647_at	hypothetical protein predicted by gr	---	AT2G25870	-1.09	-0.13	-0.83	0.433126	0.568849	-6.87
255192_at	hypothetical protein	---	AT4G07380	1.06	0.09	0.83	0.433133	0.568849	-6.87
263653_at	putative ethylene receptor (ERS2) E	ERS2	AT1G04310	1.09	0.12	0.83	0.433332	0.569077	-6.87
244905_at	hypothetical protein	---	---	-1.07	-0.10	-0.83	0.433389	0.569119	-6.87
254057_at	putative protein ;supported by full-l	---	AT4G25170	-1.13	-0.18	-0.83	0.433452	0.569158	-6.87
261703_at	OsNAC7 protein, putative similar to	ANAC012	AT1G32770	-1.06	-0.09	-0.83	0.433497	0.569158	-6.87
256264_at	unknown protein ; supported by full-	---	AT3G12210	-1.10	-0.14	-0.83	0.433515	0.569158	-6.87
258231_at	hypothetical protein contains Pfam	RCK	AT3G27730	-1.06	-0.08	-0.83	0.433518	0.569158	-6.87
248026_at	putative protein similar to unknown	---	AT5G55710	-1.08	-0.11	-0.83	0.433547	0.569164	-6.87
246698_at	putative protein	---	---	-1.06	-0.09	-0.83	0.433597	0.569196	-6.87
249653_at	putative protein REPLICATION PR	---	---	-1.06	-0.09	-0.83	0.433633	0.56921	-6.87
262388_at	unknown protein	---	AT1G49320	-1.07	-0.10	-0.83	0.433771	0.569359	-6.87
246905_at	putative protein ;supported by full-l	---	AT5G25570	1.15	0.20	0.83	0.433808	0.569374	-6.87
261645_at	hypothetical protein similar to hypot	---	---	1.06	0.09	0.83	0.434061	0.569673	-6.87
256136_s_a	lectin receptor kinase, putative sim	---	AT1G48720	1.06	0.08	0.83	0.434093	0.569684	-6.87
248407_at	pectinesterase	---	AT5G51500	-1.06	-0.09	-0.83	0.434297	0.569918	-6.87
249414_at	putative transcription factor MYB89	MYB89	AT5G39700	1.07	0.10	0.83	0.434333	0.569932	-6.87
251180_at	putative protein hypothetical protei	---	AT3G62640	1.11	0.15	0.83	0.434457	0.570062	-6.87
261473_at	hypothetical protein similar to putati	---	AT1G14490	-1.13	-0.17	-0.83	0.434668	0.570307	-6.87
253513_at	peroxidase - like protein peroxidas	---	AT4G31760	-1.06	-0.08	-0.83	0.434709	0.570327	-6.87
252290_at	putative protein various predicted p	---	AT3G49140	1.08	0.11	0.83	0.434893	0.570536	-6.87
263505_s_a	hypothetical protein	---	AT2G07678	1.14	0.19	0.83	0.435005	0.57065	-6.87
251348_at	putative protein hypothetical protei	---	AT3G61010	-1.10	-0.14	-0.83	0.435058	0.570675	-6.87
246870_at	ferrochelatase-I	FC1	AT5G26030	1.24	0.31	0.83	0.435074	0.570675	-6.87
259646_at	n-calpain-1 large subunit, putative	DEK1	AT1G55350	-1.06	-0.09	-0.83	0.435125	0.570709	-6.87
252827_at	cytochrome P450 - like protein cyt	CYP79B2	AT4G39950	1.33	0.41	0.83	0.435245	0.570833	-6.87
251799_at	putative protein P59 PROTEIN (HS	---	AT3G55520	-1.09	-0.13	-0.83	0.435392	0.570993	-6.87

257483_at	hypothetical protein contains simila	ICK5	AT1G49620	1.07	0.10	0.83	0.435647	0.571295	-6.88
248375_at	potassium/proton antiporter-like pro	KEA5	AT5G51710	-1.06	-0.08	-0.83	0.435698	0.5713	-6.88
245065_at	unknown protein ; supported by cD	---	AT2G39750	1.06	0.08	0.83	0.435708	0.5713	-6.88
257026_at	hypothetical protein predicted by ge	---	AT3G19200	-1.07	-0.10	-0.83	0.435726	0.5713	-6.88
254258_at	hypothetical protein	TET5	AT4G23410	-1.08	-0.11	-0.83	0.435854	0.571435	-6.88
255840_at	unknown protein	---	AT2G33520	-1.10	-0.14	-0.83	0.43596	0.571542	-6.88
263557_at	putative homeodomain transcriptior	BLH7	AT2G16400	1.09	0.12	0.83	0.436034	0.571606	-6.88
249882_at	putative protein contains similarity t	---	AT5G22890	-1.06	-0.08	-0.83	0.436137	0.571699	-6.88
246195_at	E2, ubiquitin-conjugating enzyme 1	UBC17	AT4G36410	1.31	0.39	0.83	0.436155	0.571699	-6.88
250474_at	annexin -like protein annexin (Ann/	ANNAT7	AT5G10230	-1.05	-0.08	-0.83	0.436187	0.571708	-6.88
249805_at	putative protein similar to unknown	---	AT5G23800	-1.06	-0.09	-0.83	0.4363	0.571823	-6.88
264039_at	putative cold-regulated protein ;sup	---	AT2G03740	-1.06	-0.09	-0.83	0.436365	0.571844	-6.88
252448_at	beta-D-glucan exohydrolase - like	---	AT3G47050	-1.07	-0.10	-0.83	0.436366	0.571844	-6.88
247211_at	unknown protein ; supported by ful	---	AT5G64880	-1.13	-0.18	-0.83	0.436472	0.571931	-6.88
260019_at	polyprotein, putative simlar to GI:4	---	---	-1.06	-0.08	-0.83	0.436483	0.571931	-6.88
256838_at	ADP-ribosylation factor, putative si	ATARFC1	AT3G22950	-1.08	-0.11	-0.83	0.436554	0.571992	-6.88
245072_s_a	putative cytochrome P450	CYP81D7	AT2G23190	1.08	0.11	0.83	0.43685	0.572338	-6.88
252308_at	putative protein sugar transporter 2	---	AT3G49310	1.06	0.09	0.83	0.43688	0.572338	-6.88
248054_at	unknown protein	---	AT5G55820	-1.10	-0.13	-0.83	0.436894	0.572338	-6.88
254172_at	clathrin coat assembly like protein	---	AT4G24550	-1.06	-0.08	-0.83	0.437	0.572444	-6.88
249576_at	putative protein predicted protein, /	---	AT5G37690	-1.06	-0.08	-0.83	0.437087	0.572462	-6.88
267249_at	hypothetical protein predicted by ge	---	AT2G23040	-1.06	-0.08	-0.83	0.437088	0.572462	-6.88
267191_at	similar to Mlo proteins from H. vulga	MLO15	AT2G44110	-1.10	-0.14	-0.83	0.437089	0.572462	-6.88
258623_at	unknown protein ; supported by cD	---	AT3G02790	1.15	0.20	0.83	0.43712	0.57247	-6.88
248774_at	unknown protein	---	AT5G47830	-1.06	-0.09	-0.83	0.437236	0.572558	-6.88
252659_at	putative protein	---	AT3G44430	1.08	0.11	0.83	0.43724	0.572558	-6.88
252346_at	hypothetical protein	---	AT3G48650	-1.06	-0.08	-0.83	0.437262	0.572558	-6.88
266773_at	hypothetical protein predicted by ge	---	AT2G29040	-1.06	-0.09	-0.83	0.437369	0.572664	-6.88
245741_at	hypothetical protein similar to unkn	---	AT1G44120	-1.07	-0.10	-0.83	0.437409	0.572684	-6.88
255096_at	hypothetical protein similar to T21E	---	---	-1.06	-0.09	-0.83	0.437547	0.572832	-6.88
256829_at	unknown protein similar to aluminur	---	AT3G22850	1.12	0.16	0.82	0.437644	0.572925	-6.88
260608_at	putative polygalacturonase	---	AT2G43870	1.70	0.77	0.82	0.437883	0.573206	-6.88
247611_at	putative protein predicted proteins	---	AT5G60710	1.06	0.08	0.82	0.437962	0.573277	-6.88
254586_at	TMV resistance protein N-like TMV	---	AT4G19510	-1.08	-0.10	-0.82	0.438025	0.573326	-6.88
249587_at	putative protein copper homeostas	---	AT5G37860	-1.05	-0.08	-0.82	0.438064	0.573344	-6.88

248582_at	heat shock protein 70 (gb|AAF2763	CPHSC70-	AT5G49910	-1.13	-0.17	-0.82	0.43814	0.573411	-6.88
248130_at	unknown protein	---	AT5G54790	-1.06	-0.09	-0.82	0.438189	0.573442	-6.88
245791_at	defender against cell death protein	ATDAD1	AT1G32210	1.08	0.11	0.82	0.438404	0.57369	-6.88
253587_at	hypothetical protein	---	AT4G30770	-1.07	-0.10	-0.82	0.438577	0.573884	-6.88
256643_at	unknown protein similar to putative	---	---	1.07	0.09	0.82	0.438663	0.573963	-6.88
267247_at	hypothetical protein predicted by ge	---	AT2G30170	1.08	0.11	0.82	0.438709	0.573991	-6.88
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281	---	---	-1.06	-0.08	-0.82	0.438783	0.574031	-6.88
252777_at	hypothetical protein	---	AT3G42970	-1.06	-0.09	-0.82	0.43879	0.574031	-6.88
266678_at	hypothetical protein predicted by gr	---	AT2G25870	-1.06	-0.09	-0.82	0.438816	0.574032	-6.88
256993_at	unknown protein ; supported by cD	---	AT3G28670	1.06	0.08	0.82	0.43886	0.574056	-6.88
262731_at	hypothetical protein similar to gb|AF	MC8	AT1G16420	1.62	0.70	0.82	0.439023	0.574236	-6.88
248986_at	putative protein similar to unknown	---	AT5G45170	-1.09	-0.12	-0.82	0.439083	0.574283	-6.88
247160_at	putative protein contains similarity t	---	AT5G65820	1.06	0.09	0.82	0.43922	0.574429	-6.88
260093_at	putative serine carboxypeptidase s	scpl6	AT1G73270	-1.06	-0.09	-0.82	0.43927	0.574429	-6.88
265995_at	hypothetical protein predicted by ge	---	AT2G24140	1.06	0.09	0.82	0.439271	0.574429	-6.88
254373_at	hypothetical protein ;supported by	---	AT4G21730	-1.06	-0.09	-0.82	0.439357	0.574508	-6.88
262080_at	unknown protein ; supported by cDI	CW14	AT1G59650	1.09	0.13	0.82	0.439416	0.574553	-6.88
264197_at	unknown protein Similar to hypothe	ATSAC1	AT1G22620	1.05	0.08	0.82	0.439441	0.574553	-6.88
252621_at	putative protein Ac-like transposase	---	---	1.07	0.10	0.82	0.439477	0.574567	-6.88
267332_at	hypothetical protein predicted by ge	---	AT2G19290	1.05	0.07	0.82	0.439716	0.574847	-6.88
263055_at	unknown protein	---	---	1.06	0.08	0.82	0.439818	0.574947	-6.88
254314_at	extensin - like protein hybrid proline	---	AT4G22470	1.57	0.65	0.82	0.439983	0.57513	-6.88
259635_at	purple acid phosphatase, putative s	PAP6	AT1G56360	-1.07	-0.10	-0.82	0.440064	0.575203	-6.88
256642_at	hypothetical protein similar to hypot	---	AT3G32280	-1.06	-0.08	-0.82	0.440107	0.575225	-6.88
264873_at	putative indole-3-acetate beta-gluco	UGT74B1	AT1G24100	1.20	0.26	0.82	0.440243	0.575371	-6.88
248456_at	putative protein similar to unknown	---	AT5G51380	-1.05	-0.07	-0.82	0.440373	0.575508	-6.88
261437_at	hypothetical protein predicted by ge	RAD51D	AT1G07745	-1.07	-0.10	-0.82	0.440438	0.57556	-6.88
256790_at	ARR1 protein, putative similar to A	ARR1	AT3G16857	-1.07	-0.10	-0.82	0.440536	0.575654	-6.88
245436_at	membrane protein homolog	---	AT4G16620	-1.07	-0.09	-0.82	0.440565	0.575659	-6.88
262776_at	unknown protein EST gb|T22808 co	---	AT1G13020	-1.08	-0.11	-0.82	0.440714	0.575812	-6.88
246342_at	putative protein male sterility protei	FAR6	AT3G56700	1.06	0.08	0.82	0.440733	0.575812	-6.88
246353_s_a	hypothetical protein	---	---	-1.06	-0.08	-0.82	0.440879	0.575971	-6.88
262965_at	hypothetical protein predicted by ge	---	AT1G54310	1.09	0.13	0.82	0.440993	0.576087	-6.88
260185_at	hypothetical protein similar to hypot	---	AT1G36030	-1.05	-0.07	-0.82	0.44116	0.576272	-6.88
267195_at	putative protein kinase contains a p	---	AT2G30940	-1.09	-0.13	-0.82	0.441364	0.576499	-6.88

247547_at	putative protein	---	AT5G61360	-1.11	-0.15	-0.82	0.441392	0.576499	-6.88
256709_at	hypothetical protein predicted by ge	---	---	1.06	0.08	0.82	0.44141	0.576499	-6.88
267582_at	putative protein kinase contains a p	---	AT2G41970	-1.06	-0.09	-0.82	0.44146	0.576531	-6.88
264691_s_a	putative reverse transcriptase	---	---	-1.07	-0.09	-0.82	0.441577	0.576652	-6.88
246768_at	putative protein hypothetical protein	---	AT5G27400	-1.05	-0.07	-0.82	0.441798	0.576906	-6.89
250280_at	putative protein many predicted pro	---	AT5G13230	1.08	0.11	0.82	0.441908	0.577018	-6.89
251426_at	URIDYLATE KINASE-like protein U	---	AT3G60180	1.07	0.10	0.82	0.441959	0.577051	-6.89
255168_at	putative protein hypothetical protei	---	---	-1.07	-0.10	-0.82	0.442036	0.577119	-6.89
AFFX-TrpnX	B. subtilis /GEN=trpE, trpD /DB_XR	---	---	-1.07	-0.10	-0.82	0.442085	0.577139	-6.89
264472_at	hypothetical protein predicted by ge	SWEETIE	AT1G67140	-1.09	-0.12	-0.82	0.442102	0.577139	-6.89
246229_at	pectinesterase like protein	sks15	AT4G37160	1.06	0.08	0.82	0.442142	0.577158	-6.89
263722_at	putative vanadate resistance protei	GONST1	AT2G13650	1.07	0.10	0.82	0.442207	0.577209	-6.89
245463_at	allergen like protein	ATEXLB1	AT4G17030	1.15	0.21	0.82	0.442299	0.577296	-6.89
257564_at	unknown protein	---	AT3G28610	-1.10	-0.13	-0.82	0.442362	0.577311	-6.89
265560_at	putative glycine-rich protein	GRP-3	AT2G05520	1.06	0.09	0.82	0.44237	0.577311	-6.89
261888_at	ribosomal protein, putative similar t	---	AT1G80800	1.07	0.10	0.82	0.442386	0.577311	-6.89
250907_at	putative protein predicted proteins,	---	AT5G03670	1.06	0.08	0.82	0.442504	0.577376	-6.89
267360_at	unknown protein ;supported by full-	---	AT2G40060	-1.08	-0.11	-0.82	0.442504	0.577376	-6.89
250097_at	putative protein similar to unknown	---	AT5G17280	-1.08	-0.11	-0.82	0.442511	0.577376	-6.89
257410_at	hypothetical protein similar to polyk	emb2421	AT1G24340	1.09	0.13	0.82	0.442565	0.577413	-6.89
253432_at	putative protein various predicted p	---	AT4G32450	1.06	0.08	0.82	0.442603	0.57743	-6.89
267124_at	putative acetone-cyanohydrin lyase	MES19	AT2G23570	-1.08	-0.10	-0.82	0.442728	0.577559	-6.89
262105_at	pectin esterase, putative similar to	---	AT1G02810	-1.09	-0.12	-0.82	0.44279	0.577559	-6.89
254322_at	hypothetical protein	---	AT4G22600	-1.10	-0.14	-0.82	0.442804	0.577559	-6.89
253308_at	putative protein aminotransferase (	AGD2	AT4G33680	-1.06	-0.09	-0.82	0.442804	0.577559	-6.89
254507_at	Glu-rich protein mature-parasite-int	---	AT4G20160	-1.06	-0.08	-0.82	0.442834	0.577565	-6.89
249373_at	putative protein vanilloid receptor g	---	AT5G40670	-1.07	-0.10	-0.81	0.443033	0.577777	-6.89
252103_at	putative protein various predicted p	---	AT3G51410	1.06	0.08	0.81	0.443047	0.577777	-6.89
248500_at	unknown protein	---	AT5G50410	1.08	0.11	0.81	0.443077	0.577784	-6.89
258486_at	putative 40S ribosomal protein simi	---	AT3G02560	1.17	0.23	0.81	0.443132	0.577823	-6.89
256197_at	hypothetical protein	---	---	-1.10	-0.13	-0.81	0.443196	0.577873	-6.89
258098_at	hypothetical protein similar to kines	KINESIN-1	AT3G23670	-1.10	-0.14	-0.81	0.443227	0.57788	-6.89
262322_at	hypothetical protein similar to hypot	---	AT1G27590	1.08	0.11	0.81	0.443458	0.578148	-6.89
252579_at	putative protein hypothetical protei	---	AT3G45510	-1.06	-0.08	-0.81	0.443624	0.578331	-6.89
260514_at	hypothetical protein predicted by ge	---	AT1G51480	1.06	0.09	0.81	0.443665	0.578352	-6.89

260758_at	endo-beta-1,4-glucanase, putative	AtGH9C1	AT1G48930	-1.09	-0.12	-0.81	0.443742	0.578419	-6.89
257037_at	nuclear acid binding protein, putati	ATRBP47B	AT3G19130	-1.14	-0.19	-0.81	0.443824	0.578493	-6.89
257090_at	protein kinase, putative contains P	---	AT3G20530	-1.07	-0.10	-0.81	0.443864	0.578513	-6.89
255746_at	heat shock transcription factor, put	---	AT1G32020	-1.06	-0.08	-0.81	0.444234	0.578962	-6.89
267466_at	putative GDSL-motif lipase/hydrolas	---	AT2G19010	-1.06	-0.08	-0.81	0.444711	0.57955	-6.89
255335_at	putative transposon protein	---	---	1.07	0.10	0.81	0.444765	0.579587	-6.89
257335_at	hypothetical protein	---	---	-1.06	-0.09	-0.81	0.444835	0.579615	-6.89
248154_at	putative protein strong similarity to	---	AT5G54400	1.28	0.35	0.81	0.444838	0.579615	-6.89
249874_at	putative protein contains similarity t	---	AT5G23070	1.12	0.17	0.81	0.444996	0.579788	-6.89
248699_at	putative protein similar to unknown	ATZIP4	AT5G48390	-1.09	-0.13	-0.81	0.445112	0.579906	-6.89
251807_at	methionyl-tRNA synthetase (AtcpM	OVA1	AT3G55400	1.08	0.12	0.81	0.445179	0.57996	-6.89
267407_at	unknown protein	MEE27	AT2G34880	-1.07	-0.10	-0.81	0.445263	0.580012	-6.89
261263_at	H-protein promoter binding factor-2	---	AT1G26790	-1.05	-0.08	-0.81	0.445269	0.580012	-6.89
254661_at	unknown protein multidrug resistan	---	AT4G18260	1.07	0.10	0.81	0.445339	0.58007	-6.89
257156_at	hypothetical protein predicted by ge	---	AT3G24260	1.06	0.08	0.81	0.44549	0.580233	-6.89
255355_at	hypothetical protein	---	---	-1.07	-0.10	-0.81	0.44562	0.580342	-6.89
250345_at	subtilisin-like serine protease conta	---	AT5G11940	-1.07	-0.10	-0.81	0.445642	0.580342	-6.89
256346_s_a	unknown protein	---	AT2G15040	1.05	0.07	0.81	0.445674	0.580342	-6.89
254540_s_a	putative protein chitinase / lysozym	---	AT4G19770	-1.06	-0.08	-0.81	0.445675	0.580342	-6.89
262057_at	unknown protein ;supported by full-	---	AT1G80040	1.07	0.09	0.81	0.445739	0.580357	-6.89
263399_at	unknown protein ; supported by full-	---	AT2G31490	1.07	0.09	0.81	0.445742	0.580357	-6.89
252185_at	putative protein	---	AT3G50780	1.09	0.12	0.81	0.445763	0.580357	-6.89
267154_at	glutathione S-transferase identical t	GSTF10	AT2G30870	1.22	0.29	0.81	0.445905	0.580509	-6.89
256236_at	hypothetical protein predicted by ge	---	AT3G12350	1.08	0.11	0.81	0.446035	0.580634	-6.89
256431_s_a	putative disease resistance protein	AtRLP34	AT3G11010	1.14	0.18	0.81	0.446077	0.580634	-6.89
250567_at	hypothetical protein	---	AT5G08090	-1.07	-0.10	-0.81	0.446078	0.580634	-6.89
266286_at	putative tropinone reductase	---	AT2G29160	-1.07	-0.10	-0.81	0.446309	0.580883	-6.89
257268_at	unknown protein	---	AT3G17450	1.10	0.13	0.81	0.446361	0.580883	-6.89
255251_at	see GB:U95973 similar to a family c	---	AT4G04980	-1.05	-0.08	-0.81	0.446363	0.580883	-6.89
255095_at	MEKK1/MAP kinase kinase kinase	MEKK1	AT4G08500	-1.10	-0.14	-0.81	0.446371	0.580883	-6.89
258870_at	putative NADP-dependent oxidored	---	AT3G03080	1.07	0.10	0.81	0.44647	0.580942	-6.89
264427_at	hypothetical protein predicted by ge	---	AT1G61770	1.08	0.11	0.81	0.446493	0.580942	-6.89
254707_at	putative protein inositol polyphosph	AT5PTASE	AT4G18010	-1.18	-0.24	-0.81	0.446516	0.580942	-6.89
263614_at	putative serpin	---	AT2G25240	-1.09	-0.12	-0.81	0.446532	0.580942	-6.89
254216_at	V-ATPase subunit G (vag2 gene)	VAG2	AT4G23710	1.13	0.18	0.81	0.446544	0.580942	-6.89

263896_at	hypothetical protein predicted by ge	---	AT2G21930	-1.08	-0.11	-0.81	0.446645	0.580979	-6.89
259506_at	protein phosphatase type 2C, puta	---	AT1G43900	1.06	0.09	0.81	0.446651	0.580979	-6.89
256195_at	hypothetical protein predicted by ge	---	---	1.05	0.07	0.81	0.446651	0.580979	-6.89
264196_at	putative RING zinc finger protein C	---	AT1G22670	1.06	0.09	0.81	0.446674	0.580979	-6.89
266858_at	unknown protein	GRV2	AT2G26890	1.06	0.09	0.81	0.446785	0.581054	-6.89
261103_s_a	O-methyltransferase 1, putative sir	---	AT1G62900	-1.07	-0.10	-0.81	0.44679	0.581054	-6.89
267202_s_a	putative oxysterol-binding protein	ORP1A	AT2G31020	1.12	0.16	0.81	0.446808	0.581054	-6.89
261172_at	hypothetical protein predicted by ge	---	AT1G04840	-1.07	-0.10	-0.81	0.44691	0.58111	-6.89
246848_at	putative protein	---	AT5G26840	-1.07	-0.10	-0.81	0.446913	0.58111	-6.89
261964_at	hypothetical protein similar to envel	---	---	-1.05	-0.07	-0.81	0.446927	0.58111	-6.89
248109_at	DNA topoisomerase I	TOP1BETA	AT5G55310	1.06	0.09	0.81	0.447021	0.581175	-6.89
255237_at	hypothetical protein	---	---	-1.06	-0.08	-0.81	0.447034	0.581175	-6.89
263562_at	hypothetical protein predicted by ge	---	AT2G15420	-1.05	-0.08	-0.81	0.447053	0.581175	-6.89
257332_at	hypothetical protein	---	---	-1.09	-0.12	-0.81	0.447092	0.581191	-6.89
266255_at	putative selenium-binding protein	---	AT2G27610	1.06	0.09	0.81	0.447314	0.581418	-6.89
248254_at	receptor protein kinase-like protein	---	AT5G53320	1.09	0.12	0.81	0.447324	0.581418	-6.89
255975_at	hypothetical protein	---	---	-1.08	-0.11	-0.81	0.447342	0.581418	-6.89
264810_at	putative GPI-anchor transamidase (	---	AT1G08750	-1.08	-0.11	-0.81	0.44742	0.581438	-6.89
254950_at	putative protein ;supported by full-l	---	AT4G10810	-1.05	-0.08	-0.81	0.447424	0.581438	-6.89
260474_at	lysophospholipase isolog	---	AT1G11090	-1.08	-0.11	-0.81	0.447435	0.581438	-6.89
251419_at	putative protein various predicted p	---	AT3G60470	-1.06	-0.09	-0.81	0.447736	0.581796	-6.89
254302_at	hypothetical protein	---	AT4G22800	1.05	0.07	0.81	0.447882	0.581953	-6.89
248959_at	putative protein similar to unknown	---	AT5G45630	-1.19	-0.25	-0.81	0.448057	0.582147	-6.90
257358_at	unknown protein predicted by gens	---	AT2G40990	-1.10	-0.14	-0.81	0.448105	0.582177	-6.90
246350_at	hypothetical protein predicted by ge	---	AT1G16650	1.08	0.11	0.80	0.448341	0.58245	-6.90
266307_at	putative cytochrome P450	CYP705A8	AT2G27000	1.07	0.10	0.80	0.448741	0.582937	-6.90
263026_at	hypothetical protein predicted by ge	---	AT1G24000	-1.06	-0.08	-0.80	0.448806	0.582987	-6.90
251587_at	hypothetical protein	---	AT3G58080	-1.11	-0.15	-0.80	0.448892	0.583065	-6.90
259199_at	putative signal peptidase similar to	---	AT3G08980	1.06	0.08	0.80	0.448917	0.583065	-6.90
259329_at	putative two-component phosphore	AHP4	AT3G16360	-1.18	-0.24	-0.80	0.449	0.583135	-6.90
251252_at	putative protein several hypothetica	---	AT3G62230	1.06	0.09	0.80	0.449022	0.583135	-6.90
262971_at	receptor-like protein kinase, putativ	---	AT1G75640	-1.09	-0.13	-0.80	0.449108	0.583214	-6.90
263651_at	unknown protein Similar to Nicotian	---	AT1G04340	-1.09	-0.12	-0.80	0.449137	0.583218	-6.90
250368_at	putative protein ; supported by cDN	---	AT5G11280	1.08	0.11	0.80	0.449272	0.58336	-6.90
259339_at	putative adenylylsulfate kinase simi	---	AT3G03900	-1.09	-0.12	-0.80	0.449375	0.583448	-6.90

246928_at	putative protein Scythe protein - Xe	---	AT5G25270	1.06	0.08	0.80	0.449395	0.583448	-6.90
264028_at	putative nitrilase-associated protein	SPR1	AT2G03680	-1.12	-0.16	-0.80	0.449416	0.583448	-6.90
246239_at	putative protein	---	AT4G36790	-1.06	-0.09	-0.80	0.449698	0.583781	-6.90
265833_at	Mutator-like transposase similar to	---	---	-1.06	-0.08	-0.80	0.449731	0.58379	-6.90
266530_at	bHLH transcription factor	AMS	AT2G16910	-1.05	-0.07	-0.80	0.449792	0.583837	-6.90
256953_at	flavonol 3-O-Glucosyltransferase, p	---	AT3G29630	-1.09	-0.13	-0.80	0.44984	0.583866	-6.90
265813_at	putative NAM (no apical meristem)	VND1	AT2G18060	1.06	0.08	0.80	0.44999	0.584027	-6.90
267608_at	hypothetical protein predicted by ge	---	AT2G26770	-1.07	-0.09	-0.80	0.450111	0.584138	-6.90
248698_at	receptor-like protein kinase ; suppo	---	AT5G48380	-1.11	-0.15	-0.80	0.45017	0.584138	-6.90
252882_at	Expressed protein ; supported by fu	---	AT4G39675	1.05	0.07	0.80	0.450175	0.584138	-6.90
267600_at	mitochondrial F1-ATPase, gamma	---	AT2G33040	-1.10	-0.14	-0.80	0.4502	0.584138	-6.90
261488_at	Expressed protein ; supported by fu	---	AT1G14345	-1.08	-0.11	-0.80	0.450204	0.584138	-6.90
261736_at	hypothetical protein simlar to hypotl	---	AT1G47810	-1.06	-0.09	-0.80	0.450284	0.584209	-6.90
254551_at	lectin like protein lectin phloem pro	ATPP2-A1	AT4G19840	1.08	0.11	0.80	0.450309	0.584209	-6.90
267167_at	putative C2H2-type zinc finger prote	ZFP10	AT2G37740	-1.07	-0.09	-0.80	0.450426	0.584327	-6.90
255155_at	hypothetical protein	---	AT4G08230	-1.08	-0.11	-0.80	0.450459	0.584337	-6.90
251603_at	putative protein wall-associated kin	---	AT3G57760	-1.18	-0.24	-0.80	0.450508	0.584366	-6.90
263464_at	putative ARI-like RING zinc finger p	---	AT2G31760	1.07	0.10	0.80	0.45057	0.584414	-6.90
245530_at	splicing factor like protein	---	---	-1.07	-0.10	-0.80	0.45068	0.584517	-6.90
265982_at	putative retroelement pol polyprotei	---	---	-1.05	-0.08	-0.80	0.450701	0.584517	-6.90
263267_at	putative vacuolar proton-ATPase 16	---	AT2G16510	1.07	0.09	0.80	0.450804	0.584617	-6.90
247148_at	auxin-induced protein IAA9 (pir |T05	IAA9	AT5G65670	-1.11	-0.14	-0.80	0.451024	0.584856	-6.90
253226_at	beta-galactosidase - like protein be	BGAL11	AT4G35010	1.06	0.08	0.80	0.451039	0.584856	-6.90
249536_at	pollen coat -like protein pollen coat	---	AT5G38760	1.05	0.07	0.80	0.451095	0.584895	-6.90
245158_at	hypothetical protein predicted by ge	RALFL18	AT2G33130	-1.10	-0.13	-0.80	0.451229	0.585025	-6.90
265690_at	hypothetical protein predicted by ge	---	AT2G24320	-1.08	-0.11	-0.80	0.451246	0.585025	-6.90
263859_at	hypothetical protein predicted by ge	---	AT2G04360	1.10	0.14	0.80	0.451455	0.585262	-6.90
258492_at	unknown protein	---	AT3G02390	1.06	0.08	0.80	0.451593	0.585398	-6.90
249709_at	putative protein similar to unknown	iqd33	AT5G35670	-1.08	-0.11	-0.80	0.451619	0.585398	-6.90
255352_at	putative transposon protein similar t	---	---	-1.07	-0.09	-0.80	0.451637	0.585398	-6.90
251775_s_a	delta-1-pyrroline-5-carboxylate synt	P5CS1	AT2G39800	1.15	0.20	0.80	0.451944	0.585763	-6.90
253201_at	putative ribosomal protein S16 ribo	SSR16	AT4G34620	-1.06	-0.09	-0.80	0.452036	0.58585	-6.90
251122_at	protein kinase -like protein serine/t	---	AT5G01020	1.10	0.13	0.80	0.452074	0.585865	-6.90
258522_at	hypothetical protein predicted by ge	---	AT3G06660	1.10	0.14	0.80	0.452178	0.585966	-6.90
246945_s_a	putative membrane protein hypothe	---	AT5G25040	-1.07	-0.10	-0.80	0.452203	0.585966	-6.90

255445_at	hypothetical protein	---	AT4G02740	-1.07	-0.10	-0.80	0.452342	0.58609	-6.90
259567_at	hypothetical protein	---	AT1G20500	-1.07	-0.10	-0.80	0.45235	0.58609	-6.90
245179_at	putative protein similarity to predict	---	AT5G12400	1.07	0.09	0.80	0.45262	0.586406	-6.90
254036_at	putative peroxidase peroxidase (E(	---	AT4G25980	-1.06	-0.09	-0.80	0.452841	0.586659	-6.90
254565_at	replication A protein-like replicatior	---	AT4G19130	-1.05	-0.07	-0.80	0.452866	0.586659	-6.90
249338_at	putative protein similar to unknown	anac095	AT5G41090	-1.05	-0.07	-0.80	0.453039	0.586849	-6.90
265873_at	putative beta-1,3-glucanase ;supp	---	AT2G01630	-1.08	-0.11	-0.80	0.453143	0.586917	-6.90
252050_at	hypothetical protein	---	AT3G52550	-1.08	-0.11	-0.80	0.453143	0.586917	-6.90
250435_at	putative protein various predicted p	RING1	AT5G10380	-1.14	-0.19	-0.80	0.45324	0.587009	-6.90
249392_at	peroxidase ATP26a	---	AT5G40150	-1.08	-0.11	-0.80	0.453406	0.587187	-6.90
254597_at	hypothetical protein	---	AT4G18980	1.10	0.14	0.80	0.453452	0.587187	-6.90
265466_at	putative CCAAT-box binding trancri	NF-YB8	AT2G37060	1.09	0.12	0.80	0.453455	0.587187	-6.90
252981_at	putative protein gene T10 protein -	---	AT4G38260	1.09	0.12	0.80	0.453488	0.587197	-6.90
251891_at	aintegumaenta-like protein ovule d	WRI1	AT3G54320	1.06	0.08	0.80	0.453551	0.587244	-6.90
265919_at	putative retroelement pol polyprotei	---	---	-1.07	-0.10	-0.80	0.453576	0.587244	-6.90
263669_at	putative cryptochrome 2 apoprotein	CRY2	AT1G04400	1.06	0.08	0.80	0.45372	0.587397	-6.90
263301_x_a	hypothetical protein predicted by ge	---	---	1.06	0.09	0.79	0.453801	0.587462	-6.90
255540_at	putative SecA-type chloroplast prot	---	AT4G01800	1.10	0.13	0.79	0.453821	0.587462	-6.90
263215_at	putative reticuline oxidase-like prot	---	AT1G30710	-1.07	-0.10	-0.79	0.453908	0.587509	-6.90
249461_at	putative protein predicted proteins,	---	AT5G39640	-1.06	-0.09	-0.79	0.453909	0.587509	-6.90
246780_at	seryl-tRNA synthetase ; supported	---	AT5G27470	1.07	0.10	0.79	0.453978	0.587557	-6.90
252398_at	putative protein RING-H2 finger pr	---	AT3G47990	1.07	0.09	0.79	0.453998	0.587557	-6.90
266947_at	hypothetical protein predicted by ge	---	AT2G18830	-1.08	-0.11	-0.79	0.454118	0.587679	-6.90
246190_at	hypothetical protein (fragment) ;sup	ATBPM5	AT5G21010	-1.05	-0.07	-0.79	0.454205	0.587759	-6.90
257581_s_a	RAV-like DNA-binding protein, puta	---	AT1G50680	-1.05	-0.07	-0.79	0.454507	0.588085	-6.90
267471_at	putative ferrochelatase precusor ; s	FC2	AT2G30390	1.12	0.16	0.79	0.454509	0.588085	-6.90
257872_at	P-glycoprotein, putative similar to F	PGP16	AT3G28360	1.05	0.07	0.79	0.454593	0.588153	-6.91
258638_at	unknown protein ;supported by full-	---	AT3G07950	1.06	0.08	0.79	0.454652	0.588153	-6.91
261047_at	hypothetical protein predicted by ge	APUM22	AT1G01410	-1.12	-0.16	-0.79	0.454652	0.588153	-6.91
259957_at	putative protein kinase C-terminal r	---	AT1G67890	-1.13	-0.17	-0.79	0.454665	0.588153	-6.91
260658_at	hypothetical protein predicted by ge	---	AT1G19410	-1.08	-0.11	-0.79	0.454765	0.588207	-6.91
264725_at	Expressed protein ; supported by fu	---	AT1G22885	-1.14	-0.19	-0.79	0.454782	0.588207	-6.91
257767_at	hypothetical protein predicted by ge	---	AT3G23040	1.08	0.11	0.79	0.454784	0.588207	-6.91
249397_at	putative protein MtN21, Medicago t	---	AT5G40230	-1.09	-0.13	-0.79	0.454876	0.588293	-6.91
262454_at	bifunctional nuclease bfn1 almost id	BFN1	AT1G11190	-1.37	-0.46	-0.79	0.455138	0.588598	-6.91

260306_at	hypothetical protein predicted by ge	EDA24	AT1G70540	-1.07	-0.09	-0.79	0.45539	0.588861	-6.91
260883_at	hypothetical protein predicted by ge	---	AT1G29270	-1.05	-0.07	-0.79	0.455406	0.588861	-6.91
248169_at	ankyrin-repeat-containing protein-lik	ANK	AT5G54610	-1.50	-0.59	-0.79	0.455419	0.588861	-6.91
253686_at	putative protein predicted proteins,	---	AT4G29750	1.08	0.11	0.79	0.455469	0.588893	-6.91
249573_at	ubiquitin-like protein (UBQ9), putat	UBQ9	AT5G37640	1.06	0.08	0.79	0.455617	0.589027	-6.91
255375_at	putative athila-like protein	---	---	-1.06	-0.08	-0.79	0.455643	0.589027	-6.91
247472_at	cytokinesis regulating protein - like	MAP65-9	AT5G62250	1.06	0.08	0.79	0.45565	0.589027	-6.91
245090_at	putative integral membrane protein	---	AT2G40900	1.10	0.14	0.79	0.45569	0.589045	-6.91
265235_s_a	hypothetical protein	---	AT2G07719	1.07	0.10	0.79	0.456084	0.589521	-6.91
250670_at	polygalacturonase inhibiting protein	PGIP1	AT5G06860	1.20	0.26	0.79	0.45612	0.589534	-6.91
254983_at	putative protein other hypothetical p	MEE53	AT4G10560	-1.06	-0.08	-0.79	0.456163	0.589556	-6.91
248729_at	cycloartenol synthase	THAS1	AT5G48010	-1.05	-0.07	-0.79	0.456292	0.58969	-6.91
248392_at	integral membrane protein-like	---	AT5G52050	-1.39	-0.48	-0.79	0.456326	0.5897	-6.91
251555_at	shatterproof 1 (SHP1)/ agamous -lik	SHP1	AT3G58780	-1.06	-0.09	-0.79	0.456383	0.589741	-6.91
257450_at	unknown protein similar to gb|AAD1	---	AT1G10530	-1.08	-0.11	-0.79	0.456512	0.589874	-6.91
263068_at	putative poly(A) polymerase	---	AT2G17580	1.08	0.11	0.79	0.456726	0.590065	-6.91
253856_at	hypothetical protein ;supported by	---	AT4G28100	-1.05	-0.08	-0.79	0.456757	0.590065	-6.91
250024_at	NAM (no apical meristem)-like prote	ANAC087	AT5G18270	-1.11	-0.15	-0.79	0.456759	0.590065	-6.91
260220_at	putative MYB family transcription fa	MYB31	AT1G74650	-1.10	-0.14	-0.79	0.456782	0.590065	-6.91
266936_at	hypothetical protein predicted by ge	---	AT2G18920	-1.05	-0.07	-0.79	0.456789	0.590065	-6.91
266906_at	Expressed protein ; supported by fu	---	AT2G34585	1.09	0.13	0.79	0.456889	0.590161	-6.91
257736_at	hypothetical protein predicted by ge	---	AT3G27410	1.07	0.10	0.79	0.456934	0.590184	-6.91
260330_at	putative RING zinc finger protein c	---	AT1G80400	1.06	0.09	0.79	0.456983	0.590215	-6.91
259941_s_a	putative DEAD/DEAH box helicase	---	AT1G71280	-1.06	-0.08	-0.79	0.457057	0.590277	-6.91
245883_at	ribosomal protein S15-like ribosom	---	AT5G09500	-1.06	-0.08	-0.79	0.457198	0.590425	-6.91
262585_at	hypothetical protein Is a member of	BOR4	AT1G15460	-1.09	-0.12	-0.79	0.457322	0.590552	-6.91
252543_at	nonphototropic hypocotyl 1 ; suppo	PHOT1	AT3G45780	-1.06	-0.08	-0.79	0.457478	0.590717	-6.91
261617_s_a	hypothetical protein predicted by ge	---	AT1G33090	1.06	0.08	0.79	0.457501	0.590717	-6.91
262973_at	histone H3, putative similar to HIS	---	AT1G75600	-1.06	-0.08	-0.79	0.45754	0.590724	-6.91
254499_at	putative protein probable membran	---	AT4G20100	-1.06	-0.09	-0.79	0.457559	0.590724	-6.91
260670_at	Expressed protein ; supported by fu	NFD5	AT1G19520	1.10	0.14	0.79	0.457847	0.591063	-6.91
250392_at	putative protein multifunctional ami	---	AT5G10880	-1.05	-0.08	-0.79	0.458179	0.591454	-6.91
253146_at	putative protein predicted protein, A	---	AT4G35590	1.06	0.09	0.79	0.458202	0.591454	-6.91
262696_at	hypothetical protein	---	AT1G75870	-1.06	-0.09	-0.79	0.458256	0.59149	-6.91
257971_at	unknown protein similar to hypothet	GC6	AT3G27530	1.10	0.14	0.79	0.458339	0.591564	-6.91

245539_at	ABC transporter homolog	PDR2	AT4G15230	-1.08	-0.11	-0.79	0.458386	0.591591	-6.91
260797_at	neoxanthin cleavage enzyme, puta	NCED9	AT1G78390	-1.07	-0.10	-0.79	0.458483	0.591618	-6.91
246581_at	hypothetical protein predicted by ge	---	AT1G31760	1.06	0.09	0.79	0.458497	0.591618	-6.91
256833_at	calmodulin-stimulated calcium-ATF	---	AT3G22910	-1.28	-0.36	-0.79	0.458497	0.591618	-6.91
249100_at	unknown protein	---	AT5G43560	1.07	0.09	0.79	0.45851	0.591618	-6.91
250689_at	putative protein similar to unknown	---	AT5G06610	1.18	0.23	0.79	0.458617	0.591722	-6.91
248459_at	putative protein similar to unknown	CRL	AT5G51020	1.06	0.09	0.79	0.458772	0.591888	-6.91
249880_at	putative protein similar to unknown	---	AT5G23180	-1.06	-0.09	-0.79	0.458874	0.591987	-6.91
262256_at	hypothetical protein similar to putati	---	---	-1.07	-0.10	-0.79	0.459002	0.592118	-6.91
263417_at	putative C2H2-type zinc finger prote	---	AT2G17180	-1.09	-0.12	-0.79	0.459146	0.592271	-6.91
248149_at	Expressed protein ; supported by fu	---	AT5G54855	1.06	0.08	0.78	0.459205	0.592313	-6.91
266412_at	hypothetical protein predicted by ge	MAP65-5	AT2G38720	1.06	0.08	0.78	0.459262	0.592348	-6.91
265261_at	putative APG isolog protein	---	AT2G42990	-1.22	-0.29	-0.78	0.459305	0.592348	-6.91
265757_x_a	putative PttA2-like transposon prote	---	---	-1.09	-0.12	-0.78	0.45931	0.592348	-6.91
253055_at	putative protein cyclin delta-1, Arab	CYCD5;1	AT4G37630	-1.09	-0.13	-0.78	0.459356	0.592374	-6.91
254496_at	hyuC-like protein 5-substituted hyd	ATAAH	AT4G20070	-1.18	-0.24	-0.78	0.459399	0.592396	-6.91
257340_at	pseudogene, retroelement pol poly	---	---	-1.07	-0.10	-0.78	0.459511	0.592474	-6.91
257377_at	unknown protein	PLL4	AT2G28890	1.14	0.19	0.78	0.459511	0.592474	-6.91
251809_at	putative protein predicted proteins,	---	AT3G55600	1.07	0.10	0.78	0.459678	0.592655	-6.91
250253_at	putative protein contains similarity t	PDAT	AT5G13640	1.07	0.10	0.78	0.459768	0.592737	-6.91
262266_at	mudrA-like protein similar to mudrA	---	---	1.07	0.10	0.78	0.460101	0.593133	-6.91
250029_at	galactose-1-phosphate uridyl transf	---	AT5G18200	1.08	0.11	0.78	0.4603	0.593324	-6.91
251373_at	GATA transcription factor 4 ; suppo	---	AT3G60530	-1.24	-0.31	-0.78	0.460301	0.593324	-6.91
261810_at	ligase I, putative similar to ligase I (	ATLIG1	AT1G08130	1.13	0.18	0.78	0.460672	0.593744	-6.91
257118_at	hypothetical protein	---	AT3G20180	1.06	0.08	0.78	0.460679	0.593744	-6.91
248598_at	putative protein contains similarity t	---	AT5G49370	-1.07	-0.10	-0.78	0.461055	0.594196	-6.91
267076_at	calcium binding protein (CaBP-22) i	---	AT2G41090	-1.37	-0.45	-0.78	0.461235	0.594363	-6.92
261104_at	unknown protein	---	AT1G62910	-1.07	-0.10	-0.78	0.461237	0.594363	-6.92
247170_at	putative protein contains similarity t	---	AT5G65530	-1.05	-0.07	-0.78	0.46128	0.594385	-6.92
250269_at	anthranilate phosphoribosyltransfe	---	AT5G12970	-1.07	-0.10	-0.78	0.461362	0.594452	-6.92
255265_at	kinesin - like protein kinesin like pr	ATK5	AT4G05190	-1.08	-0.12	-0.78	0.461384	0.594452	-6.92
265997_at	Expressed protein ; supported by cl	---	AT2G24250	-1.06	-0.08	-0.78	0.461556	0.59464	-6.92
248438_at	putative protein contains similarity t	EMF2	AT5G51230	-1.10	-0.13	-0.78	0.461609	0.594675	-6.92
257819_at	Expressed protein ; supported by fu	RALFL25	AT3G25165	-1.06	-0.08	-0.78	0.461733	0.5948	-6.92
259328_at	putative lectin contains Pfam profile	ATMLP-30(	AT3G16440	-1.08	-0.11	-0.78	0.461836	0.5949	-6.92

250285_at	putative protein GCN4-complemen	SFC	AT5G13300	1.10	0.14	0.78	0.461869	0.594908	-6.92
251633_at	putative protein metalloendopeptid	---	AT3G57460	-1.13	-0.18	-0.78	0.461938	0.594946	-6.92
254271_at	serine/threonine kinase - like prote	---	AT4G23150	1.15	0.20	0.78	0.46195	0.594946	-6.92
261884_at	myrosinase precursor, putative	---	AT1G80910	-1.07	-0.10	-0.78	0.462117	0.595096	-6.92
264231_at	hypothetical protein similar to hypot	---	AT1G67450	-1.05	-0.07	-0.78	0.462119	0.595096	-6.92
246816_at	putative protein	---	AT5G27230	1.06	0.08	0.78	0.462312	0.59531	-6.92
250364_at	putative protein serine threonine ty	---	AT5G11400	-1.07	-0.09	-0.78	0.462379	0.595334	-6.92
252825_at	small GTP-binding protein - like SF	AtRABH1c	AT4G39890	-1.16	-0.21	-0.78	0.462382	0.595334	-6.92
261982_at	hypothetical protein predicted by ge	---	AT1G33780	-1.06	-0.08	-0.78	0.462602	0.595583	-6.92
259703_at	putative endo-1,3-beta-glucanase s	---	AT1G77790	-1.06	-0.09	-0.78	0.462689	0.595662	-6.92
261637_at	DNA-binding protein PcMYB1, puta	TRB1	AT1G49950	-1.08	-0.11	-0.78	0.462816	0.595792	-6.92
264493_at	unknown protein similar to multiple	GUT2	AT1G27440	1.12	0.17	0.78	0.462928	0.595902	-6.92
255622_at	putative flavonol glucosyltransferas	GT72B1	AT4G01070	1.08	0.12	0.78	0.462982	0.595917	-6.92
263789_at	putative GDSL-motif lipase/hydrolas	---	AT2G24560	-1.09	-0.13	-0.78	0.462991	0.595917	-6.92
264997_at	hypothetical protein contains simila	HAC2	AT1G67220	-1.08	-0.11	-0.78	0.463245	0.59621	-6.92
255083_s_a	hypothetical protein	---	---	-1.08	-0.11	-0.78	0.463316	0.59623	-6.92
252138_at	peroxidase-like protein peroxidase	---	AT3G50990	1.08	0.11	0.78	0.46334	0.59623	-6.92
261449_at	putative ATPase similar to GB:AAF	---	AT1G21120	1.12	0.16	0.78	0.463371	0.59623	-6.92
264465_at	SKP1/ASK1 (At18), putative simila	ASK18	AT1G10230	-1.05	-0.07	-0.78	0.46339	0.59623	-6.92
258346_at	hypothetical protein predicted by ge	---	AT3G22690	1.07	0.10	0.78	0.463392	0.59623	-6.92
265698_at	hypothetical protein predicted by ge	---	AT2G32160	1.06	0.09	0.78	0.463425	0.59624	-6.92
250635_at	glycine-rich protein glycine-rich pro	GRP14	AT5G07510	-1.07	-0.10	-0.78	0.463565	0.596385	-6.92
248581_at	putative protein strong similarity to	---	AT5G49900	-1.09	-0.13	-0.78	0.463706	0.59649	-6.92
255090_at	putative protein disease resistance	---	AT4G09360	1.06	0.09	0.78	0.463722	0.59649	-6.92
266660_at	hypothetical protein predicted by ge	---	AT2G25920	1.11	0.15	0.78	0.463724	0.59649	-6.92
264795_at	unknown protein similar to ESTs er	ZIGA4	AT1G08680	1.13	0.18	0.78	0.463752	0.596492	-6.92
266457_at	putative glyoxysomal malate dehyd	PMDH1	AT2G22780	1.06	0.09	0.78	0.463901	0.59665	-6.92
251543_at	putative protein	---	AT3G58770	-1.07	-0.09	-0.78	0.464124	0.596903	-6.92
255945_at	putative protein	---	AT5G28610	-1.08	-0.11	-0.78	0.464174	0.596934	-6.92
245953_at	myrosinase - binding protein - like	---	AT5G28520	-1.09	-0.13	-0.78	0.464375	0.597159	-6.92
258758_at	putative RING zinc finger protein c	---	AT3G10810	-1.10	-0.14	-0.78	0.464491	0.597273	-6.92
266321_at	putative cytochrome P450	CYP78A6	AT2G46660	1.09	0.12	0.78	0.46452	0.597278	-6.92
258520_at	hypothetical protein predicted by ge	---	AT3G06710	1.09	0.12	0.78	0.464692	0.597464	-6.92
250056_at	putative protein predicted proteins,	---	AT5G17660	-1.15	-0.20	-0.77	0.464814	0.597587	-6.92
254570_s_a	puatative protein various predicted	---	AT4G19250	-1.07	-0.10	-0.77	0.464915	0.597684	-6.92

254160_at	putative protein ;supported by full-l	SLY1	AT4G24210	-1.08	-0.11	-0.77	0.465071	0.597843	-6.92
252410_at	putative protein br-1 protein (NITRI	NOA1	AT3G47450	1.08	0.11	0.77	0.465091	0.597843	-6.92
245667_at	FH protein interacting protein FIP1	FIP1	AT1G28200	1.06	0.08	0.77	0.465132	0.597862	-6.92
250638_at	glycine-rich protein atGRP-6	GRP16	AT5G07540	-1.08	-0.11	-0.77	0.465392	0.598163	-6.92
257589_at	hypothetical protein predicted by ge	---	AT1G55050	-1.08	-0.12	-0.77	0.465726	0.598527	-6.92
265339_at	putative inorganic pyrophosphatase	AtPPa2	AT2G18230	1.11	0.16	0.77	0.465745	0.598527	-6.92
258833_at	unknown protein	---	---	-1.07	-0.10	-0.77	0.465768	0.598527	-6.92
263657_at	putative casein kinase I similar to G	CKL13	AT1G04440	-1.12	-0.17	-0.77	0.465795	0.598527	-6.92
258209_at	expressed protein supported by cD	GAPC1	AT3G04120	1.16	0.21	0.77	0.465806	0.598527	-6.92
252541_at	putative protein hypothetical protei	---	AT3G45750	1.06	0.08	0.77	0.466139	0.598921	-6.92
251003_at	putative protein	---	AT5G02690	1.07	0.09	0.77	0.466222	0.598965	-6.92
267424_at	hypothetical protein predicted by ge	---	AT2G34800	1.05	0.07	0.77	0.466226	0.598965	-6.92
254168_at	Mlo-like protein Mlo protein - Horde	MLO13	AT4G24250	1.07	0.10	0.77	0.466432	0.599196	-6.92
251086_at	putative protein hypothetical protei	---	AT5G01450	-1.09	-0.12	-0.77	0.466505	0.599231	-6.92
265856_at	hypothetical protein predicted by ge	LBD16	AT2G42430	-1.09	-0.12	-0.77	0.466524	0.599231	-6.92
266147_at	putative C-1-tetrahydrofolate syntha	---	AT2G12230	-1.05	-0.07	-0.77	0.466538	0.599231	-6.92
254975_at	putative Fe(II)/ascorbate oxidase S	---	AT4G10500	-1.71	-0.78	-0.77	0.466574	0.599243	-6.92
253234_at	Expressed protein ; supported by fu	---	AT4G34265	-1.07	-0.09	-0.77	0.466639	0.599292	-6.92
262955_at	unknown protein ;supported by full-	---	AT1G54520	-1.08	-0.11	-0.77	0.466801	0.599467	-6.92
264871_at	pyruvate dehydrogenase E1 alpha s	IAR4	AT1G24180	1.12	0.16	0.77	0.466909	0.599572	-6.92
260224_at	hypothetical protein contains Pfam	---	AT1G74400	1.05	0.07	0.77	0.46706	0.599704	-6.92
258210_at	Eukaryotic initiation factor 4A, puta	EIF4A1	AT3G13920	-1.06	-0.08	-0.77	0.467064	0.599704	-6.92
257492_at	hypothetical protein contains simila	ARR19	AT1G49190	-1.05	-0.07	-0.77	0.467135	0.59976	-6.92
244968_at	ribosomal protein L33	---	---	-1.07	-0.10	-0.77	0.467247	0.59987	-6.92
247245_at	putative protein similar to unknown	---	AT5G64720	-1.06	-0.08	-0.77	0.467418	0.600027	-6.92
259620_s_a	Tam3-like transposon protein simil	---	---	-1.09	-0.13	-0.77	0.467421	0.600027	-6.92
257717_at	unknown protein	EMB1865	AT3G18390	-1.08	-0.11	-0.77	0.467487	0.600078	-6.92
246802_at	kinesin-like heavy chain non-conse	ATK4	AT5G27000	-1.08	-0.11	-0.77	0.467524	0.600091	-6.92
256445_at	hypothetical protein predicted by ge	---	AT3G11160	-1.07	-0.09	-0.77	0.467721	0.600295	-6.92
252703_at	leucine-rich repeat protein LRP -lik	---	AT3G43740	1.06	0.08	0.77	0.467735	0.600295	-6.92
265018_s_a	hypothetical protein predicted by ge	---	AT2G13770	-1.06	-0.08	-0.77	0.467823	0.600374	-6.92
257822_at	rotamase FKBP (ROF1) identical t	ROF1	AT3G25230	-1.17	-0.23	-0.77	0.467922	0.600409	-6.92
263116_s_a	unknown protein Similar to gb|U519	---	AT1G03140	-1.07	-0.10	-0.77	0.467922	0.600409	-6.92
247687_at	protein serine /threonine kinase - li	---	AT5G59740	-1.07	-0.10	-0.77	0.467929	0.600409	-6.92
247003_at	putative protein similar to unknown	---	AT5G67550	-1.08	-0.11	-0.77	0.467982	0.600441	-6.93

266341_at	hypothetical protein predicted by ge	---	AT2G01510	1.06	0.09	0.77	0.468007	0.600441	-6.93
253508_at	putative protein various predicted p	---	AT4G31680	-1.06	-0.09	-0.77	0.468143	0.600582	-6.93
262006_at	hypothetical protein predicted by ge	---	AT1G64570	1.06	0.09	0.77	0.468207	0.60063	-6.93
257099_s_a	disease resistance protein, putative	---	AT3G24982	1.05	0.07	0.77	0.468305	0.600722	-6.93
262429_at	polyprotein, putative similar to poly	---	---	1.07	0.10	0.77	0.468673	0.60116	-6.93
252850_at	putative protein ;supported by full-l	---	AT4G39880	1.08	0.11	0.77	0.4689	0.601404	-6.93
250290_at	putative protein ;supported by full-l	---	AT5G13310	1.06	0.08	0.77	0.468916	0.601404	-6.93
254198_at	hypothetical protein	---	AT4G24090	-1.07	-0.09	-0.77	0.469	0.601478	-6.93
249846_at	cation-transporting ATPase	---	AT5G23630	1.05	0.07	0.77	0.469075	0.60154	-6.93
262849_at	unknown protein ; supported by cDl	---	AT1G14710	-1.17	-0.22	-0.77	0.469132	0.60158	-6.93
256278_at	unknown protein ; supported by full-	---	AT3G12130	-1.06	-0.08	-0.77	0.469321	0.601789	-6.93
248670_at	receptor protein kinase-like protein	---	AT5G48740	-1.08	-0.11	-0.77	0.469414	0.601874	-6.93
AFFX-CreX-	Bacteriophage P1 /GEN=cre /DB_X	---	---	-1.14	-0.19	-0.77	0.469634	0.602122	-6.93
255238_at	see GB:AL022580)	---	---	1.05	0.07	0.77	0.469685	0.602154	-6.93
AFFX-Athal-	Arabidopsis thaliana /REF=U84969	---	---	1.07	0.10	0.77	0.469962	0.602458	-6.93
261621_at	hypothetical protein similar to guani	EDA10	AT1G01960	-1.06	-0.08	-0.77	0.469975	0.602458	-6.93
261850_at	hypothetical protein predicted by ge	---	AT1G50470	-1.09	-0.12	-0.77	0.470092	0.602574	-6.93
245200_at	F12A21.2 hypothetical protein; supp	---	AT1G67850	1.13	0.17	0.77	0.470202	0.60268	-6.93
266196_at	putative protein kinase contains a p	---	AT2G39110	-1.06	-0.09	-0.76	0.470353	0.60284	-6.93
255472_at	82.09 and 30.80) similar to alternati	---	AT4G02430	1.06	0.09	0.76	0.470434	0.602911	-6.93
264915_at	hypothetical protein predicted by ge	---	AT1G60790	1.05	0.07	0.76	0.470617	0.603111	-6.93
249294_at	unknown protein	---	AT5G41270	1.10	0.14	0.76	0.470656	0.603127	-6.93
253510_at	hypothetical protein	GDU1	AT4G31730	-1.14	-0.19	-0.76	0.470857	0.603351	-6.93
246752_at	putative protein predicted proteins,	---	AT5G27890	-1.07	-0.09	-0.76	0.470907	0.603368	-6.93
245154_at	putative protein similarity to predicte	---	AT5G12460	-1.07	-0.09	-0.76	0.470924	0.603368	-6.93
264353_at	hypothetical protein predicted by ge	---	AT1G03260	1.06	0.09	0.76	0.471063	0.60348	-6.93
245727_at	hypothetical protein contains simila	---	AT1G73350	1.07	0.10	0.76	0.471064	0.60348	-6.93
264245_at	galactinol synthase, putative simila	AtGolS7	AT1G60450	-1.06	-0.08	-0.76	0.471137	0.603541	-6.93
261571_at	hypothetical protein predicted by g	---	AT1G01150	-1.06	-0.08	-0.76	0.471258	0.603639	-6.93
247121_at	putative protein contains similarity t	---	AT5G66010	1.07	0.10	0.76	0.471268	0.603639	-6.93
249749_at	unknown protein	BIN4	AT5G24630	-1.07	-0.10	-0.76	0.471324	0.603649	-6.93
245431_at	hypothetical protein	---	AT4G17080	1.06	0.09	0.76	0.471328	0.603649	-6.93
264109_at	unknown protein	---	AT2G13720	-1.06	-0.08	-0.76	0.471394	0.6037	-6.93
256762_at	Expressed protein ; supported by fu	IDL1	AT3G25655	1.37	0.46	0.76	0.471536	0.603848	-6.93
252964_at	receptor-like protein kinase - like p	---	AT4G38830	-1.06	-0.09	-0.76	0.471565	0.603851	-6.93

264666_at	hypothetical protein Similar to N. ta	---	AT1G09680	1.08	0.11	0.76	0.471671	0.603953	-6.93
257682_at	hypothetical protein predicted by ge	---	AT3G13240	-1.05	-0.07	-0.76	0.471822	0.604091	-6.93
253546_at	hypothetical protein ;supported by	---	AT4G31030	-1.08	-0.11	-0.76	0.471839	0.604091	-6.93
263140_at	hypothetical protein predicted by ge	---	AT1G65120	1.05	0.07	0.76	0.471899	0.604091	-6.93
248751_at	putative protein similar to unknown	---	AT5G47540	-1.07	-0.10	-0.76	0.471904	0.604091	-6.93
257740_at	hypothetical protein predicted by g	---	AT3G27330	-1.05	-0.07	-0.76	0.471911	0.604091	-6.93
257391_at	hypothetical protein predicted by ge	---	AT2G32050	-1.05	-0.07	-0.76	0.472044	0.604227	-6.93
246183_at	beta-glucosidase - like protein beta	---	AT5G20940	1.07	0.10	0.76	0.472174	0.604328	-6.93
261754_at	alpha-amylase, putative similar to a	AMY2	AT1G76130	-1.18	-0.23	-0.76	0.472176	0.604328	-6.93
257514_at	hypothetical protein similar to putati	---	---	-1.09	-0.13	-0.76	0.472402	0.604584	-6.93
252530_at	putative protein several oxidases,	---	AT3G46500	-1.06	-0.09	-0.76	0.47271	0.604943	-6.93
265700_at	putative MYB family transcription fa	---	AT2G03470	1.05	0.07	0.76	0.472771	0.604959	-6.93
246277_at	hypothetical protein	---	AT4G36460	1.07	0.10	0.76	0.472775	0.604959	-6.93
247411_at	putative protein contains similarity t	---	AT5G63000	1.08	0.11	0.76	0.472893	0.605076	-6.93
255050_at	putative protein hypothetical protei	---	---	-1.08	-0.11	-0.76	0.473139	0.605357	-6.93
258364_at	unknown protein	GLIP4	AT3G14225	1.13	0.18	0.76	0.473257	0.605473	-6.93
265462_at	putative vetispiradiene synthase	---	AT2G37140	-1.07	-0.09	-0.76	0.473434	0.605666	-6.93
252500_at	proteinase inhibitor-like protein end	---	AT3G46860	-1.05	-0.08	-0.76	0.47349	0.605687	-6.93
265633_at	F-box protein family, AtFBL6 conta	EBF1	AT2G25490	1.08	0.10	0.76	0.473504	0.605687	-6.93
246545_at	pectate lyase -like protein pectate l	---	AT5G15110	-1.05	-0.08	-0.76	0.473545	0.605706	-6.93
265977_at	putative retroelement pol polyprotei	---	---	1.05	0.08	0.76	0.473911	0.60614	-6.93
246347_at	putative protein probable chloroplas	---	AT3G56830	1.06	0.09	0.76	0.474085	0.606329	-6.93
265054_x_a	mutator-like transposase, putative	---	---	-1.08	-0.11	-0.76	0.474228	0.606478	-6.93
263230_at	putative indole-3-acetate beta-gluc	---	AT1G05670	1.12	0.17	0.76	0.47426	0.606485	-6.93
248954_at	unknown protein ; supported by cD	---	AT5G45420	1.05	0.07	0.76	0.474299	0.606501	-6.93
266672_at	putative Na+-dependent inorganic p	PHT4;1	AT2G29650	-1.06	-0.08	-0.76	0.474377	0.606567	-6.93
260421_at	acid phosphatase, putative similar	SBH1	AT1G69640	1.06	0.09	0.76	0.474444	0.606595	-6.93
262101_at	hypothetical protein identical to hyp	---	AT1G59535	-1.05	-0.08	-0.76	0.474491	0.606595	-6.93
248711_at	putative protein similar to unknown	---	AT5G48270	1.07	0.10	0.76	0.474547	0.606595	-6.93
253636_at	putative protein predicted protein,	---	AT4G30500	1.29	0.37	0.76	0.474549	0.606595	-6.93
250804_at	putative protein contains similarity t	---	AT5G05030	-1.07	-0.10	-0.76	0.474552	0.606595	-6.93
251277_at	dynamin-like protein phragmoplast	ADL1B	AT3G61760	1.05	0.07	0.76	0.474559	0.606595	-6.93
245737_at	hypothetical protein similar to putati	---	AT1G44160	1.09	0.13	0.76	0.474629	0.606651	-6.93
253985_at	caffeoyl-CoA O-methyltransferase	---	AT4G26220	1.07	0.10	0.76	0.474676	0.606677	-6.93
252722_at	putative protein hypothetical protei	---	---	-1.05	-0.07	-0.76	0.474711	0.606687	-6.93

253094_at	putative protein DnaJ-like protein,	---	AT4G37480	1.05	0.07	0.76	0.474797	0.606763	-6.93
256549_at	hypothetical protein predicted by ge	---	---	-1.06	-0.08	-0.76	0.475087	0.6071	-6.94
257688_at	Snf2-related CBP activator protein,	PIE1	AT3G12810	1.05	0.07	0.76	0.475147	0.607143	-6.94
260321_at	putative RING zinc finger protein P	---	AT1G63900	1.06	0.09	0.76	0.475327	0.607324	-6.94
266328_at	unknown protein ; supported by ful	---	AT2G01600	1.05	0.07	0.76	0.475342	0.607324	-6.94
266213_s_a	Mutator-like transposase similar to	---	---	-1.06	-0.09	-0.76	0.475379	0.607336	-6.94
251737_at	40S ribosomal protein S26 homolog	---	AT3G56340	1.14	0.19	0.76	0.475591	0.607543	-6.94
259960_at	cell division control protein, putativ	---	AT1G53710	-1.08	-0.11	-0.76	0.475593	0.607543	-6.94
262936_at	hypothetical protein similar to putati	ATCHX2	AT1G79400	1.08	0.12	0.76	0.475647	0.607578	-6.94
255984_at	inositol polyphosphate 5-phosphata	IP5PI	AT1G34120	1.06	0.09	0.76	0.47581	0.607746	-6.94
250582_at	transcription factor-like protein ethy	---	AT5G07580	-1.13	-0.17	-0.76	0.475832	0.607746	-6.94
255088_at	putative protein heat shock protein	---	AT4G09350	1.11	0.15	0.75	0.475859	0.607746	-6.94
259923_at	putative protein kinase contains Pfa	---	AT1G72760	1.05	0.07	0.75	0.475902	0.607767	-6.94
262076_at	hypothetical protein identical to GB	ATMPK2	AT1G59580	-1.08	-0.11	-0.75	0.475967	0.607785	-6.94
252404_at	glycine--tRNA ligase precursor, chl	EDD1	AT3G48110	1.06	0.08	0.75	0.47597	0.607785	-6.94
249477_s_a	germin - like protein probable germ	---	AT5G38930	1.05	0.07	0.75	0.476007	0.6078	-6.94
260125_at	putative heat shock protein similar t	---	AT1G36390	1.09	0.12	0.75	0.476154	0.607859	-6.94
260911_at	hypothetical protein predicted by ge	---	AT1G02490	1.06	0.08	0.75	0.476159	0.607859	-6.94
256393_at	hypothetical protein	---	AT3G06280	-1.06	-0.08	-0.75	0.476166	0.607859	-6.94
261887_at	CCR4-associated factor, putative\0	---	AT1G80780	1.05	0.07	0.75	0.476171	0.607859	-6.94
246648_at	putative protein predicted proteins f	---	---	-1.06	-0.09	-0.75	0.476188	0.607859	-6.94
249598_at	putative protein AtPP protein, Bras	---	AT5G37970	-1.06	-0.08	-0.75	0.476329	0.608005	-6.94
256507_at	hypothetical protein predicted by ge	---	AT1G75150	-1.07	-0.10	-0.75	0.476373	0.608027	-6.94
259457_at	auxin response factor 1, putative s	ARF23	AT1G43950	-1.06	-0.08	-0.75	0.476405	0.608035	-6.94
259044_at	pollen allergen Bra r II identical to p	---	AT3G03430	-1.05	-0.08	-0.75	0.476756	0.608448	-6.94
261281_at	hypothetical protein predicted by ge	---	AT1G35740	1.05	0.07	0.75	0.476811	0.608485	-6.94
254775_at	hypothetical protein	---	AT4G13450	1.05	0.07	0.75	0.476878	0.608536	-6.94
253110_at	hypothetical protein	---	AT4G35930	-1.09	-0.13	-0.75	0.477047	0.608718	-6.94
261502_at	hypothetical protein predicted by ge	AtHB31	AT1G14440	-1.13	-0.17	-0.75	0.477107	0.608758	-6.94
262573_at	hypothetical protein Similar to gi|43	PDF1A	AT1G15390	1.07	0.10	0.75	0.477144	0.608758	-6.94
265645_at	unknown protein	---	AT2G27370	-1.06	-0.08	-0.75	0.477158	0.608758	-6.94
248355_at	putative protein strong similarity to	ATEXO70A	AT5G52340	-1.05	-0.07	-0.75	0.477201	0.608778	-6.94
250799_at	putative protein strong similarity to	---	AT5G05350	1.06	0.09	0.75	0.477278	0.608842	-6.94
267421_at	putative phosphoribosylaminoimida	---	AT2G35040	1.08	0.11	0.75	0.477436	0.60901	-6.94
248610_at	SRP54 (signal recognition particle 5	---	AT5G49500	1.05	0.08	0.75	0.477466	0.609014	-6.94

245062_at	hypothetical protein predicted by ge	BPM3	AT2G39760	1.05	0.07	0.75	0.477569	0.609081	-6.94
254432_at	reticuline oxidase -like protein retic	---	AT4G20830	1.22	0.29	0.75	0.477572	0.609081	-6.94
263535_at	hypothetical protein predicted by ge	---	AT2G24970	-1.07	-0.10	-0.75	0.477798	0.609336	-6.94
248846_at	putative protein similar to unknown	---	AT5G46500	-1.06	-0.08	-0.75	0.477917	0.609453	-6.94
246032_s_a	putative protein	---	---	-1.07	-0.09	-0.75	0.477971	0.609488	-6.94
254682_at	putative protein WERBP-1 - Nicotia	UNE16	AT4G13640	-1.07	-0.10	-0.75	0.478072	0.609581	-6.94
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.14	-0.19	-0.75	0.478097	0.609581	-6.94
252696_at	hypothetical protein predicted trans	---	---	-1.05	-0.07	-0.75	0.478169	0.609638	-6.94
251369_at	putative protein ;supported by full-l	---	AT3G60480	-1.07	-0.10	-0.75	0.47824	0.609695	-6.94
266726_at	SKP1/ASK1 (At19), putative simila	ASK19	AT2G03160	-1.09	-0.12	-0.75	0.478275	0.609705	-6.94
263374_at	putative heat shock protein ;suppo	---	AT2G20560	1.13	0.18	0.75	0.478309	0.609714	-6.94
266602_at	hypothetical protein predicted by ge	---	AT2G46050	-1.05	-0.07	-0.75	0.478405	0.609802	-6.94
249432_at	putative ATP/GTP-binding protein	CLPS5	AT5G39930	1.06	0.08	0.75	0.478505	0.609896	-6.94
254637_at	putative protein KIAA0244 gene, H	---	AT4G18720	-1.06	-0.09	-0.75	0.478704	0.610116	-6.94
260532_at	putative ATP-dependent RNA helic	---	AT2G47330	-1.05	-0.07	-0.75	0.478758	0.610151	-6.94
253652_at	putative protein nucleoid DNA-bind	---	AT4G30040	1.05	0.07	0.75	0.479009	0.610435	-6.94
259115_at	hypothetical protein predicted by ge	---	AT3G01360	1.07	0.10	0.75	0.479111	0.610531	-6.94
257328_s_a	hypothetical protein	---	---	-1.08	-0.12	-0.75	0.47916	0.610548	-6.94
252880_at	putative protein ;supported by full-le	---	AT4G39730	1.11	0.15	0.75	0.479177	0.610548	-6.94
248159_at	unknown protein	---	AT5G54460	-1.05	-0.07	-0.75	0.479238	0.610592	-6.94
258741_at	Lon protease, putative similar to Lo	LON4	AT3G05790	-1.05	-0.07	-0.75	0.47939	0.610751	-6.94
255125_at	putative protein SCARECROW - A	---	AT4G08250	-1.07	-0.10	-0.75	0.479427	0.610764	-6.94
245598_at	hypothetical protein	---	AT4G14200	1.08	0.12	0.75	0.479488	0.610807	-6.94
251846_at	histone H2A.F/Z ;supported by full-	HTA11	AT3G54560	-1.21	-0.27	-0.75	0.479702	0.611046	-6.94
252302_at	putative protein hypothetical protei	---	AT3G49190	1.05	0.07	0.75	0.479813	0.611154	-6.94
252323_at	putative protein probable transcript	KING1	AT3G48530	1.10	0.13	0.75	0.479923	0.611259	-6.94
249271_at	myosin heavy chain-like protein	CIP1	AT5G41790	1.10	0.14	0.75	0.479962	0.611275	-6.94
257343_s_a	pseudogene, polyprotein similar to	---	---	-1.05	-0.06	-0.75	0.480037	0.611315	-6.94
254450_at	putative protein prolamin box bindi	---	AT4G21080	-1.06	-0.09	-0.75	0.480048	0.611315	-6.94
263474_at	hypothetical protein predicted by ge	---	AT2G31725	-1.08	-0.11	-0.75	0.480074	0.611315	-6.94
253380_at	hypothetical protein hypothetical pr	PGSIP3	AT4G33330	-1.06	-0.09	-0.75	0.480196	0.611436	-6.94
254470_at	putative protein other hypothetical p	---	---	-1.08	-0.11	-0.75	0.480431	0.61167	-6.94
254781_at	putative protein putative protein F2	---	AT4G12840	1.06	0.08	0.75	0.480433	0.61167	-6.94
252576_s_a	clpC-like protein AtClpC - Arabidop	---	AT3G45450	1.10	0.14	0.75	0.480605	0.611854	-6.94
254091_at	hypothetical protein	---	AT4G25070	-1.11	-0.15	-0.75	0.480649	0.611877	-6.94

248742_at	unknown protein	---	AT5G48200	-1.07	-0.10	-0.75	0.480848	0.612077	-6.94
267414_at	putative berberine bridge enzyme	MEE23	AT2G34790	-1.11	-0.15	-0.75	0.48086	0.612077	-6.94
261410_at	metallothionein-like protein identica	MT1C	AT1G07610	-1.20	-0.26	-0.75	0.481123	0.612378	-6.94
256492_at	hypothetical protein contains simila	---	AT1G31490	-1.07	-0.10	-0.75	0.481374	0.612663	-6.94
257346_at	pseudogene, putative retroelement	---	---	-1.06	-0.09	-0.75	0.48144	0.612712	-6.94
267410_at	hypothetical protein predicted by ge	EDA18	AT2G34920	1.11	0.16	0.74	0.481543	0.612809	-6.94
250630_at	hypothetical protein	---	AT5G07400	1.08	0.11	0.74	0.481744	0.613031	-6.94
259885_at	hypothetical protein contains Pfam	---	AT1G76380	1.09	0.12	0.74	0.481862	0.613115	-6.94
248841_at	ubiquitin-specific protease 21 (UBP	UBP21	AT5G46740	1.10	0.13	0.74	0.481885	0.613115	-6.94
245559_at	glycine-rich protein like	---	AT4G15460	-1.05	-0.08	-0.74	0.481891	0.613115	-6.94
254612_at	putative protein hypothetical protei	---	AT4G19100	-1.05	-0.07	-0.74	0.482004	0.613224	-6.94
259947_at	putative protein kinase similar to pr	---	AT1G71530	1.07	0.10	0.74	0.482074	0.613279	-6.95
261555_s_a	hypothetical protein predicted by ge	---	AT1G63230	1.05	0.07	0.74	0.482113	0.613295	-6.95
255139_s_a	extensin-like protein hydroxyproline	---	AT4G08400	-1.05	-0.07	-0.74	0.482282	0.613476	-6.95
253298_at	putative protein ;supported by full-l	---	AT4G33560	-1.06	-0.09	-0.74	0.482344	0.61352	-6.95
267394_s_a	putative cellulase	AtGH9B9	AT2G44540	-1.06	-0.09	-0.74	0.482415	0.613576	-6.95
259360_at	hypothetical protein predicted by ge	---	AT1G13310	-1.06	-0.08	-0.74	0.482468	0.61361	-6.95
265846_at	putative serine carboxypeptidase II	scpl28	AT2G35770	-1.06	-0.09	-0.74	0.482675	0.613839	-6.95
264174_s_a	hypothetical protein	ANAC004	AT1G02230	1.09	0.12	0.74	0.48273	0.613874	-6.95
263543_at	putative pectinesterase	PE11	AT2G21610	1.05	0.07	0.74	0.482979	0.614157	-6.95
247530_at	glycosylasparaginase - like protein	---	AT5G61540	-1.09	-0.12	-0.74	0.483075	0.614245	-6.95
245752_at	hypothetical protein similar to Ac-lik	---	AT1G35150	-1.05	-0.07	-0.74	0.483104	0.614248	-6.95
259260_at	unknown protein similar to unknowr	---	AT3G11370	-1.07	-0.09	-0.74	0.483232	0.614376	-6.95
250541_at	putative proline-rich protein surface	---	AT5G09520	-1.11	-0.16	-0.74	0.483458	0.614609	-6.95
254870_at	KI domain interacting kinase 1 -like	---	AT4G11900	1.13	0.17	0.74	0.483469	0.614609	-6.95
260422_at	hypothetical protein predicted by ge	---	AT1G69630	-1.06	-0.08	-0.74	0.483583	0.614719	-6.95
260817_at	unknown protein	---	AT1G06900	-1.06	-0.09	-0.74	0.483686	0.614803	-6.95
266945_at	hypothetical protein predicted by ge	VEL2	AT2G18880	-1.05	-0.08	-0.74	0.483702	0.614803	-6.95
259173_at	beta-glucosidase identical to beta-g	BGLU25	AT3G03640	-1.11	-0.16	-0.74	0.48378	0.614867	-6.95
252845_at	vacuolar H(+)-ATPase subunit-like	---	AT3G42050	-1.05	-0.08	-0.74	0.483862	0.614906	-6.95
251067_at	hypothetical protein	---	AT5G01910	-1.09	-0.12	-0.74	0.483865	0.614906	-6.95
AFFX-Athal-	Arabidopsis thaliana /REF=M65137	---	---	1.05	0.08	0.74	0.483979	0.614991	-6.95
259547_at	gypsy/Ty3 element polyprotein, put	---	---	-1.06	-0.08	-0.74	0.483985	0.614991	-6.95
262948_at	DNA-binding protein similar to cellu	---	AT1G75560	1.06	0.09	0.74	0.484028	0.615011	-6.95
252799_at	putative protein various predicted H	---	---	1.05	0.06	0.74	0.4841	0.615068	-6.95

257828_at	unknown protein	---	AT3G26670	-1.11	-0.15	-0.74	0.484192	0.615151	-6.95
249569_at	putative protein Pit1 - Arabidopsis	---	AT5G38070	-1.08	-0.11	-0.74	0.484275	0.615222	-6.95
251307_at	putative protein ;supported by full-l	---	AT3G61200	1.07	0.10	0.74	0.48447	0.615387	-6.95
258873_at	hypothetical protein similar to unkno	---	AT3G03240	-1.08	-0.11	-0.74	0.484521	0.615387	-6.95
260578_at	unknown protein predicted by gens	---	AT2G47350	-1.06	-0.08	-0.74	0.484521	0.615387	-6.95
249075_at	putative protein similar to unknown	---	AT5G44000	-1.08	-0.11	-0.74	0.484535	0.615387	-6.95
258422_at	hypothetical protein predicted by ge	---	AT3G16710	-1.06	-0.08	-0.74	0.484539	0.615387	-6.95
246688_at	putative protein predicted proteins -	---	---	-1.05	-0.07	-0.74	0.484639	0.615479	-6.95
263710_at	unknown protein ;supported by full-	---	AT1G09330	-1.06	-0.09	-0.74	0.484816	0.615669	-6.95
266985_at	putative geranylgeranyl transferase	PGGT-I	AT2G39550	-1.07	-0.10	-0.74	0.484883	0.615721	-6.95
259299_at	unknown protein	---	AT3G05080	1.08	0.12	0.74	0.484976	0.615804	-6.95
266287_at	putative tropinone reductase	---	AT2G29150	1.07	0.10	0.74	0.485019	0.615825	-6.95
265148_at	unknown protein	---	AT1G51160	-1.06	-0.09	-0.74	0.48518	0.615994	-6.95
245182_at	putative protein similarity to TETRA	---	AT5G12430	1.09	0.12	0.74	0.485232	0.616007	-6.95
245208_at	lateral root primordia (LRP1)	LRP1	AT5G12330	-1.08	-0.10	-0.74	0.485244	0.616007	-6.95
261871_at	similar to serine/threonine protein k	---	AT1G11440	-1.07	-0.10	-0.74	0.48532	0.616069	-6.95
257304_at	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.74	0.485358	0.616084	-6.95
252839_at	putative protein PIF1 protein - Cae	---	---	-1.08	-0.12	-0.74	0.485557	0.616301	-6.95
262020_at	polyprotein, putative similar to gag-	---	---	1.05	0.07	0.74	0.485622	0.61635	-6.95
247587_at	putative protein predicted proteins,	---	AT5G60620	-1.06	-0.09	-0.74	0.485753	0.616482	-6.95
246077_at	putative protein XNP-1, Caenorhab	CHR42	AT5G20420	-1.09	-0.13	-0.74	0.485891	0.616587	-6.95
262735_at	hypothetical protein	---	AT1G28630	-1.06	-0.08	-0.74	0.485911	0.616587	-6.95
249196_at	unknown protein supported by full-	---	AT5G42560	1.06	0.09	0.74	0.485917	0.616587	-6.95
263801_at	putative Athila retroelement ORF1 p	---	---	1.05	0.08	0.74	0.48596	0.616607	-6.95
250888_at	putative protein trichohyalin, Oryct	---	AT5G04460	-1.10	-0.13	-0.74	0.486102	0.616753	-6.95
247359_at	acyltransferase-like protein ;suppor	---	AT5G63560	1.08	0.10	0.74	0.486165	0.616799	-6.95
259365_at	unknown protein ; supported by cDI	---	AT1G13300	1.27	0.34	0.74	0.486201	0.61681	-6.95
247324_at	putative protein strong similarity to	---	AT5G64190	-1.25	-0.32	-0.74	0.486269	0.616861	-6.95
260674_at	unknown protein ; supported by cDI	---	AT1G19370	-1.06	-0.08	-0.74	0.486295	0.616861	-6.95
263825_at	putative laccase (diphenol oxidase)	LAC5	AT2G40370	-1.14	-0.19	-0.74	0.486371	0.616922	-6.95
256630_at	unknown protein	---	AT3G28230	1.06	0.09	0.74	0.486403	0.616929	-6.95
256403_at	unknown protein similar to SPOP (r	BPM2	AT3G06190	-1.05	-0.07	-0.74	0.486495	0.617005	-6.95
267397_at	hypothetical protein predicted by ge	---	AT1G76170	-1.11	-0.15	-0.74	0.486517	0.617005	-6.95
249180_at	26S proteasome AAA-ATPase subu	RPT4A	AT5G43010	1.08	0.11	0.74	0.486557	0.617021	-6.95
265882_at	putative copper amine oxidase	---	AT2G42490	-1.09	-0.13	-0.74	0.486731	0.617207	-6.95

252477_at	glucosyltransferase-like protein UD	---	AT3G46680	1.08	0.11	0.74	0.486978	0.617487	-6.95
251114_at	transcription factor GT-3a	---	AT5G01380	-1.23	-0.30	-0.74	0.487039	0.61753	-6.95
258770_at	hypothetical protein	---	AT3G10830	-1.05	-0.08	-0.74	0.487146	0.617619	-6.95
245654_at	disease resistance protein, putative	---	AT1G56540	-1.06	-0.09	-0.73	0.487164	0.617619	-6.95
263017_at	putative cyclin 2	CYCB2;1	AT2G17620	-1.05	-0.08	-0.73	0.48724	0.617676	-6.95
260256_at	putative type II intron maturase con	---	AT1G74350	-1.07	-0.10	-0.73	0.487262	0.617676	-6.95
253134_at	putative protein procollagen-proline	---	AT4G35820	-1.05	-0.08	-0.73	0.487369	0.617735	-6.95
265408_at	Mutator-like transposase similar to	---	---	-1.05	-0.07	-0.73	0.48738	0.617735	-6.95
265142_at	unknown protein	DABB1	AT1G51360	1.05	0.08	0.73	0.487391	0.617735	-6.95
265508_at	hypothetical protein predicted by ge	---	AT2G15930	-1.05	-0.07	-0.73	0.487654	0.618034	-6.95
248600_at	putative protein contains similarity t	---	AT5G49390	-1.07	-0.10	-0.73	0.487681	0.618034	-6.95
249738_at	60s acidic ribosomal protein P1	---	AT5G24510	-1.05	-0.07	-0.73	0.487736	0.61807	-6.95
266734_at	hypothetical protein predicted by ge	---	AT2G46900	-1.07	-0.10	-0.73	0.48787	0.618179	-6.95
261668_at	2-isopropylmalate synthase, putati	MAML-4	AT1G18500	1.07	0.10	0.73	0.487894	0.618179	-6.95
252755_at	putative protein hypothetical protein	---	---	1.06	0.08	0.73	0.487904	0.618179	-6.95
254480_at	translation elongation factor EF-Tu	ATRABE1B	AT4G20360	1.07	0.09	0.73	0.488057	0.618339	-6.95
252227_at	putative protein various predicted p	---	AT3G49900	-1.05	-0.07	-0.73	0.488134	0.618379	-6.95
258170_at	unknown protein similar to senesce	---	AT3G21600	1.15	0.20	0.73	0.488143	0.618379	-6.95
246823_at	putative protein	---	AT5G26970	-1.05	-0.07	-0.73	0.488203	0.618422	-6.95
255476_at	hypothetical protein similar to rever	---	---	-1.07	-0.09	-0.73	0.488265	0.618466	-6.95
AFFX-r2-Bs	B. subtilis /GEN=thrB /DB_XREF=g	---	---	1.10	0.14	0.73	0.488448	0.618663	-6.95
258476_at	hypothetical protein predicted by ge	---	AT3G02400	-1.08	-0.11	-0.73	0.488564	0.618775	-6.95
248855_at	NAM-like	anac096	AT5G46590	-1.11	-0.15	-0.73	0.488617	0.618798	-6.95
258302_at	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.73	0.488636	0.618798	-6.95
256946_at	hypothetical protein contains Pfam	HAF2	AT3G19040	-1.10	-0.13	-0.73	0.488825	0.619002	-6.95
249395_at	putative protein	---	AT5G40190	-1.05	-0.07	-0.73	0.489055	0.61926	-6.95
261992_at	unknown protein	---	AT1G33680	1.06	0.09	0.73	0.489176	0.619378	-6.95
258435_at	unknown protein ;supported by full-	---	AT3G16740	-1.06	-0.09	-0.73	0.489214	0.619392	-6.95
250959_at	F-box protein family, AtFBL25 cont	---	AT5G02920	-1.06	-0.09	-0.73	0.489424	0.619624	-6.96
253228_at	putative protein ;supported by full-l	---	AT4G34630	-1.18	-0.24	-0.73	0.489532	0.619695	-6.96
257663_at	hypothetical protein predicted by ge	---	AT3G20260	1.06	0.08	0.73	0.489534	0.619695	-6.96
266723_at	SKP1/ASK1 (At16), putative simila	ASK16	AT2G03190	-1.05	-0.07	-0.73	0.489573	0.619706	-6.96
256871_at	WD-repeat protein, putative contai	---	AT3G26480	-1.12	-0.16	-0.73	0.489597	0.619706	-6.96
265047_at	hypothetical protein similar to unkn	IQD27	AT1G51960	-1.06	-0.09	-0.73	0.489737	0.619848	-6.96
263835_at	putative eukaryotic translation initia	---	AT2G40290	1.06	0.08	0.73	0.489816	0.619881	-6.96

245287_at	imidazoleglycerol-phosphate dehyd	---	AT4G14910	-1.09	-0.12	-0.73	0.489843	0.619881	-6.96
266683_at	hypothetical protein predicted by ge	GC1	AT2G19950	-1.06	-0.08	-0.73	0.489845	0.619881	-6.96
253115_at	putative protein ;supported by full-l	---	AT4G35910	1.06	0.08	0.73	0.48998	0.620018	-6.96
258618_at	Expressed protein ; supported by c	GASA5	AT3G02885	-1.08	-0.11	-0.73	0.490066	0.620061	-6.96
252646_at	protein kinase-like protein protein k	---	AT3G44610	1.05	0.08	0.73	0.490069	0.620061	-6.96
258624_at	unknown protein ; supported by cD	---	AT3G02950	1.07	0.10	0.73	0.490157	0.620132	-6.96
265420_s_a	hypothetical protein predicted by ge	BRX	AT1G31880	1.08	0.12	0.73	0.490179	0.620132	-6.96
246215_at	putative cytoskeletal protein ; suppo	---	AT4G37180	1.15	0.21	0.73	0.490449	0.620439	-6.96
258840_at	unknown protein similar to unknowr	---	AT3G04620	-1.05	-0.07	-0.73	0.490712	0.620737	-6.96
251033_at	hypothetical protein ;supported by	---	AT5G01960	-1.05	-0.07	-0.73	0.490894	0.620933	-6.96
244938_at	ribosomal protein S15	---	---	-1.11	-0.15	-0.73	0.49098	0.621008	-6.96
248991_at	putative protein contains similarity t	---	AT5G45220	-1.09	-0.13	-0.73	0.491176	0.621138	-6.96
266431_at	Mutator-like transposase similar to	---	---	1.06	0.08	0.73	0.491183	0.621138	-6.96
258286_at	kinesin-like protein similar to kinesir	---	AT3G16060	-1.07	-0.09	-0.73	0.491187	0.621138	-6.96
248414_at	50S ribosomal protein L11-like	---	AT5G51610	1.06	0.09	0.73	0.491192	0.621138	-6.96
256183_at	MAP kinase kinase 4 (ATMKK4) ide	MKK4	AT1G51660	1.17	0.22	0.73	0.491327	0.621275	-6.96
258304_at	hypothetical protein predicted by ge	---	---	-1.05	-0.06	-0.73	0.491369	0.621293	-6.96
264034_s_a	unknown protein	ATUPS1	AT2G03590	-1.06	-0.08	-0.73	0.491428	0.6213	-6.96
246287_at	unknown protein	---	AT1G31870	1.06	0.08	0.73	0.491429	0.6213	-6.96
252452_at	receptor protein kinase - like protei	---	AT3G47110	-1.05	-0.07	-0.73	0.491499	0.621345	-6.96
266025_at	putative retroelement pol polyprotei	---	---	1.06	0.08	0.73	0.491519	0.621345	-6.96
265351_at	putative MADS-box protein AGL17	AGL17	AT2G22630	-1.06	-0.09	-0.73	0.491628	0.621449	-6.96
255312_at	putative transposon protein	---	---	1.06	0.08	0.73	0.4918	0.621631	-6.96
253086_at	hypothetical protein	---	AT4G36370	-1.05	-0.07	-0.73	0.491847	0.621656	-6.96
251697_at	putative protein hypothetical protei	---	AT3G56600	-1.05	-0.07	-0.73	0.491902	0.621692	-6.96
248389_at	AP2 domain transcription factor-like	CBF4	AT5G51990	-1.06	-0.08	-0.73	0.491969	0.621742	-6.96
253914_at	putative protein late embryogenesi	---	AT4G27400	-1.09	-0.12	-0.73	0.492069	0.621833	-6.96
245442_at	hypothetical protein	---	AT4G16710	1.05	0.07	0.73	0.492131	0.621877	-6.96
256319_at	trehalose-phosphatase, putative co	---	AT1G35910	1.20	0.26	0.73	0.492277	0.622027	-6.96
264750_at	hypothetical protein predicted by ge	---	AT1G22870	-1.05	-0.07	-0.73	0.492319	0.622029	-6.96
249731_at	RNA-binding protein-like	CID13	AT5G24440	-1.08	-0.11	-0.73	0.492333	0.622029	-6.96
245604_at	hypothetical protein	---	AT4G14290	-1.06	-0.09	-0.73	0.492488	0.62219	-6.96
247057_at	SCARECROW gene regulator	---	AT5G66770	-1.17	-0.23	-0.73	0.492575	0.622266	-6.96
259148_at	putative ATPase similar to ATPase	---	AT3G10350	1.07	0.10	0.73	0.492622	0.622291	-6.96
253334_at	putative protein dihydrokaempferol	---	AT4G33360	-1.10	-0.13	-0.73	0.492739	0.622394	-6.96

267014_at	unknown protein	---	AT2G39170	-1.05	-0.06	-0.73	0.492758	0.622394	-6.96
251673_at	beta-1,3-glucanase	BG3	AT3G57240	-1.74	-0.80	-0.72	0.492898	0.622536	-6.96
245055_at	hypothetical protein predicted by ge	---	AT2G26470	1.07	0.10	0.72	0.492938	0.622552	-6.96
256846_at	pectin methylesterase, putative sim	---	AT3G27980	1.05	0.07	0.72	0.493013	0.622613	-6.96
262034_at	hypothetical protein predicted by ge	---	---	-1.06	-0.08	-0.72	0.493083	0.622666	-6.96
265867_at	unknown protein ;supported by full-	MEE11	AT2G01620	1.07	0.10	0.72	0.493162	0.622732	-6.96
252393_at	putative protein predicted proteins,	---	AT3G47910	1.07	0.09	0.72	0.493229	0.622782	-6.96
266413_at	unknown protein ;supported by full-	---	AT2G38740	1.07	0.09	0.72	0.493362	0.622904	-6.96
259634_at	hypothetical protein	---	AT1G56380	1.05	0.07	0.72	0.49338	0.622904	-6.96
250963_at	putative protein various predicted p	---	AT5G03000	-1.08	-0.11	-0.72	0.493463	0.622973	-6.96
257568_s_a	hypothetical protein	---	AT3G23950	-1.08	-0.11	-0.72	0.493695	0.623232	-6.96
247692_s_a	histone H4 - like protein histone H4	---	AT5G59690	1.12	0.17	0.72	0.493858	0.623403	-6.96
255661_at	hypothetical protein	ULP1B	AT4G00690	1.05	0.08	0.72	0.493894	0.623415	-6.96
267323_at	unknown protein	---	AT2G19340	-1.06	-0.08	-0.72	0.493975	0.623483	-6.96
253724_at	Expressed protein ; supported by fu	LCR24	AT4G29285	-1.05	-0.07	-0.72	0.494099	0.623604	-6.96
261236_at	importin alpha, putative similar to ir	---	AT1G32880	-1.06	-0.08	-0.72	0.494189	0.623684	-6.96
251279_at	hypothetical protein	---	AT3G61800	1.10	0.14	0.72	0.494359	0.623863	-6.96
251561_at	E2 ubiquitin-conjugating-like enzym	SCE1	AT3G57870	-1.05	-0.07	-0.72	0.494521	0.624033	-6.96
255898_at	hypothetical protein similar to hypot	---	AT1G17930	1.06	0.08	0.72	0.494808	0.624314	-6.96
256175_at	unknown protein	---	AT1G51670	1.05	0.07	0.72	0.494825	0.624314	-6.96
252562_s_a	Histone H4 - like protein histone H4	---	AT3G45930	1.06	0.09	0.72	0.494826	0.624314	-6.96
257316_at	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.72	0.494866	0.624331	-6.96
255414_at	hypothetical protein	---	AT4G03156	1.05	0.07	0.72	0.494956	0.624409	-6.96
259564_at	hypothetical protein	---	AT1G20540	1.05	0.07	0.72	0.495121	0.624582	-6.96
263233_at	hypothetical protein similar to Na/H	---	AT1G05577	-1.05	-0.07	-0.72	0.495223	0.624677	-6.96
262023_at	hypothetical protein predicted by ge	---	AT1G35500	-1.06	-0.08	-0.72	0.495263	0.624693	-6.96
261830_at	protein kinase, putative similar to p	---	AT1G10620	-1.06	-0.09	-0.72	0.495291	0.624694	-6.96
266844_at	hypothetical protein predicted by ge	---	AT2G26120	1.06	0.09	0.72	0.49536	0.624747	-6.96
246721_at	putative protein glycine-rich protein	---	---	1.05	0.07	0.72	0.49547	0.62485	-6.96
265517_at	putative S1 self-incompatibility prote	---	AT2G06090	-1.05	-0.07	-0.72	0.495541	0.624906	-6.96
256923_at	hypothetical protein	---	AT3G29635	1.07	0.10	0.72	0.495595	0.624939	-6.96
259526_at	hypothetical protein	---	AT1G12570	-1.13	-0.17	-0.72	0.49567	0.624999	-6.96
256475_s_a	myosin heavy chain ATM2, putative	---	AT1G42680	-1.06	-0.08	-0.72	0.495818	0.625151	-6.96
255858_at	zinc finger protein (ZFP6) identical t	ZFP6	AT1G67030	-1.08	-0.12	-0.72	0.495888	0.625204	-6.96
251736_at	putative protein acetyl-CoA carbox	---	AT3G56130	-1.11	-0.15	-0.72	0.49598	0.625287	-6.96

246726_at	putative protein predicted protein, /	---	AT5G29050	-1.05	-0.07	-0.72	0.496296	0.625649	-6.96
263568_at	hypothetical protein predicted by ge	---	AT2G27160	-1.08	-0.11	-0.72	0.496446	0.625805	-6.96
263869_at	unknown protein	PROPEP6	AT2G22000	1.05	0.07	0.72	0.496672	0.626054	-6.96
245382_at	hypothetical protein	---	AT4G17800	1.06	0.08	0.72	0.496932	0.626348	-6.97
261009_at	hypothetical protein similar to putati	MES13	AT1G26360	-1.07	-0.09	-0.72	0.496998	0.62639	-6.97
267325_at	unknown protein predicted by gens	---	AT2G19360	-1.06	-0.09	-0.72	0.49702	0.62639	-6.97
263630_at	Expressed protein ; supported by fu	---	AT2G04845	-1.05	-0.07	-0.72	0.497135	0.6265	-6.97
257836_at	hypothetical protein	---	---	-1.05	-0.08	-0.72	0.497213	0.626563	-6.97
261795_at	unknown protein ; supported by cDI	---	AT1G16010	1.05	0.07	0.72	0.497318	0.626652	-6.97
255772_at	calmodulin, putative similar to calm	---	AT1G18530	-1.06	-0.09	-0.72	0.497338	0.626652	-6.97
247512_at	putative protein predicted protein, /	---	AT5G61720	-1.05	-0.07	-0.72	0.497495	0.626815	-6.97
261454_at	hypothetical protein predicted by ge	---	AT1G21090	-1.06	-0.09	-0.72	0.497578	0.626885	-6.97
261081_at	transformer-SR ribonucleoprotein,	---	AT1G07350	1.10	0.13	0.72	0.497763	0.62702	-6.97
257976_at	putative transcription factor contain	PLT1	AT3G20840	1.06	0.08	0.72	0.497767	0.62702	-6.97
261662_at	MAP kinase kinase 5, putative simi	ATMKK7	AT1G18350	-1.06	-0.08	-0.72	0.497783	0.62702	-6.97
266144_at	hypothetical protein	---	AT2G12170	1.05	0.08	0.72	0.497795	0.62702	-6.97
260567_at	putative glucosyltransferase ;suppo	UGT74F2	AT2G43820	1.09	0.13	0.72	0.498431	0.627729	-6.97
252444_at	putative protein Na+-dependent inc	PHT4;3	AT3G46980	1.05	0.07	0.72	0.498442	0.627729	-6.97
265744_at	putative CENP-B/ARS binding prote	---	---	1.04	0.06	0.72	0.498455	0.627729	-6.97
255875_s_a	putative protein kinase contains a p	---	AT2G40500	-1.06	-0.09	-0.72	0.498468	0.627729	-6.97
252748_at	putative protein putative proteins - /	---	---	1.05	0.07	0.72	0.498514	0.62775	-6.97
257773_at	hypothetical protein predicted by ge	---	AT3G29185	1.06	0.09	0.72	0.498539	0.62775	-6.97
259866_at	putative calmodulin similar to calmo	---	AT1G76640	1.18	0.24	0.72	0.49858	0.627766	-6.97
248135_at	putative protein similar to unknown	---	AT5G54890	1.08	0.11	0.71	0.498671	0.627845	-6.97
255149_at	KNAT1 homeobox-like protein	KNAT1	AT4G08150	-1.07	-0.09	-0.71	0.49871	0.62786	-6.97
258042_at	hypothetical protein similar to hypot	---	AT3G21310	-1.05	-0.07	-0.71	0.498867	0.628024	-6.97
252517_at	receptor-like protein kinase homolo	---	AT3G46340	-1.07	-0.09	-0.71	0.498999	0.628155	-6.97
260181_at	endo-1,4-beta-glucanase identical	ATGH9B1	AT1G70710	1.14	0.19	0.71	0.499074	0.628195	-6.97
254599_at	putative protein hypothetical protei	---	AT4G19000	-1.06	-0.09	-0.71	0.499086	0.628195	-6.97
247828_at	putative protein KIAA0066, Homo s	---	AT5G58510	-1.05	-0.07	-0.71	0.499298	0.628428	-6.97
258171_at	unknown protein	---	AT3G21610	1.06	0.08	0.71	0.499493	0.628638	-6.97
261318_at	Expressed protein ; supported by fu	---	AT1G53035	1.27	0.35	0.71	0.499555	0.628677	-6.97
260588_at	unknown protein contains similarity	AtTLP7	AT1G53320	-1.07	-0.10	-0.71	0.499579	0.628677	-6.97
265548_s_a	putative helicase	---	---	1.04	0.06	0.71	0.499639	0.628718	-6.97
250501_at	carboxypeptidase - like protein GC	SCPL19	AT5G09640	-1.06	-0.08	-0.71	0.499799	0.628885	-6.97

257605_at	hypothetical protein predicted by ge	---	AT3G13840	-1.05	-0.06	-0.71	0.499833	0.628892	-6.97
248182_at	putative protein contains similarity t	---	AT5G54030	-1.05	-0.07	-0.71	0.499973	0.629034	-6.97
261811_at	DNA polymerase epsilon catalytic s	TIL1	AT1G08260	1.09	0.12	0.71	0.500002	0.629036	-6.97
262537_s_a	putative ubiquitin-conjugating enzyr	UBC34	AT1G17280	-1.09	-0.13	-0.71	0.500086	0.629106	-6.97
257521_at	hypothetical protein predicted by ge	---	AT3G09140	-1.05	-0.07	-0.71	0.500263	0.629295	-6.97
262515_at	unknown protein ; supported by cDI	---	AT1G34200	1.09	0.12	0.71	0.500362	0.629385	-6.97
265553_at	putative retroelement pol polyprotei	---	---	1.06	0.08	0.71	0.500398	0.629395	-6.97
255831_at	hypothetical protein predicted by ge	---	AT2G33350	1.06	0.08	0.71	0.500454	0.629431	-6.97
245102_at	putative non-LTR retroelement reve	---	---	1.09	0.12	0.71	0.500542	0.629506	-6.97
259568_at	hypothetical protein	---	AT1G20490	1.05	0.07	0.71	0.500581	0.629521	-6.97
265063_at	receptor kinase, putative similar to	---	AT1G61500	1.08	0.11	0.71	0.500685	0.629584	-6.97
252516_at	histidyl-tRNA synthetase ; supporte	ATHRS1	AT3G46100	-1.07	-0.09	-0.71	0.500733	0.629584	-6.97
245443_at	limonene cyclase like protein	---	AT4G16730	1.67	0.74	0.71	0.500756	0.629584	-6.97
265181_at	putative OBP32pep protein ;suppo	---	AT1G23510	-1.07	-0.10	-0.71	0.500761	0.629584	-6.97
264093_at	hypothetical protein predicted by ge	---	AT1G79220	1.06	0.08	0.71	0.500769	0.629584	-6.97
254206_at	thaumatin-like protein thaumatin-lik	---	AT4G24180	-1.07	-0.09	-0.71	0.500817	0.629609	-6.97
259591_at	unknown protein ;supported by full-	---	AT1G28150	1.04	0.06	0.71	0.501203	0.630059	-6.97
263780_at	hypothetical protein predicted by ge	SPA1	AT2G46340	1.11	0.15	0.71	0.501234	0.630059	-6.97
256688_at	non-LTR reverse transcriptase, put	---	AT3G32130	-1.05	-0.07	-0.71	0.501257	0.630059	-6.97
263721_at	hypothetical protein predicted by ge	---	AT2G13630	-1.06	-0.08	-0.71	0.501331	0.630116	-6.97
262543_at	Expressed protein ; supported by fu	---	AT1G34245	-1.06	-0.09	-0.71	0.501407	0.630147	-6.97
256316_at	hypothetical protein	---	AT1G35890	-1.05	-0.07	-0.71	0.501411	0.630147	-6.97
267386_at	unknown protein	---	AT2G44430	1.09	0.12	0.71	0.50146	0.630175	-6.97
247505_at	signal recognition particle - like pro	---	AT5G61970	1.05	0.07	0.71	0.501518	0.630214	-6.97
263936_at	putative ATP-dependent RNA helic	---	AT2G35920	1.07	0.10	0.71	0.501573	0.630247	-6.97
AFFX-r2-Bs	B. subtilis /GEN=thrC /DB_XREF=g	---	---	-1.13	-0.18	-0.71	0.501731	0.630411	-6.97
250871_at	putative protein	---	AT5G03930	-1.07	-0.09	-0.71	0.501833	0.630504	-6.97
263530_at	HSP100/ClpB, putative similar to H	---	AT2G25030	-1.06	-0.08	-0.71	0.501864	0.630509	-6.97
262340_at	Expressed protein ; supported by fu	ANAC027	AT1G64100	1.05	0.08	0.71	0.501944	0.630562	-6.97
266142_at	unknown protein ; supported by cD	---	AT2G39030	1.36	0.44	0.71	0.501962	0.630562	-6.97
250389_at	putative protein probable flavin-cor	YUC4	AT5G11320	-1.05	-0.07	-0.71	0.502113	0.630717	-6.97
252243_at	putative protein some putative prote	---	AT3G50120	-1.13	-0.18	-0.71	0.502345	0.63095	-6.97
258818_at	putative ethylene receptor (EIN4) s	EIN4	AT3G04580	-1.07	-0.10	-0.71	0.502354	0.63095	-6.97
250043_at	putative protein proline-rich protein	---	AT5G18430	-1.07	-0.10	-0.71	0.502422	0.631001	-6.97
257975_at	unknown protein similar to GB:AAD	---	AT3G20830	-1.09	-0.12	-0.71	0.502463	0.631017	-6.97

250375_at	putative protein L-gulono-gamma-l	---	AT5G11540	-1.06	-0.08	-0.71	0.50249	0.631017	-6.97
254887_at	putative protein various predicted p	---	AT4G11770	-1.06	-0.09	-0.71	0.50254	0.631045	-6.97
250036_at	putative protein predicted proteins,	---	AT5G18340	1.08	0.11	0.71	0.502597	0.631052	-6.97
263204_at	hypothetical protein contains simila	chr31	AT1G05490	1.04	0.06	0.71	0.502625	0.631052	-6.97
260136_at	hypothetical protein predicted by ge	---	AT1G66360	-1.06	-0.08	-0.71	0.502628	0.631052	-6.97
265666_at	putative rac GTPase activating prot	---	AT2G27440	-1.05	-0.06	-0.71	0.502731	0.631146	-6.97
267340_at	unknown protein	ACD11	AT2G34690	1.05	0.07	0.71	0.502867	0.631274	-6.97
263437_at	putative disease resistance respons	---	AT2G28670	-1.07	-0.09	-0.71	0.502888	0.631274	-6.97
252900_at	shikimate kinase - like protein shiki	---	AT4G39540	1.08	0.11	0.71	0.502949	0.631316	-6.97
262404_at	transposon-like ORF, putative simi	---	---	-1.06	-0.08	-0.71	0.503251	0.631643	-6.97
267521_at	hypothetical protein predicted by ge	---	AT2G30480	-1.08	-0.11	-0.71	0.503294	0.631643	-6.97
259976_at	hypothetical protein ;supported by	CP12-3	AT1G76560	1.10	0.14	0.71	0.503315	0.631643	-6.97
257298_at	hypothetical protein predicted by ge	---	AT3G28155	1.08	0.11	0.71	0.50332	0.631643	-6.97
248470_at	unknown protein	---	AT5G50830	-1.06	-0.08	-0.71	0.50338	0.631683	-6.97
257978_at	putative serine/threonine protein kir	ATNEK5	AT3G20860	1.20	0.27	0.71	0.503543	0.631852	-6.97
252840_at	putative protein various predicted h	---	---	-1.05	-0.07	-0.71	0.50361	0.631902	-6.97
252600_at	putative protein unknown protein C	VPS24.2	AT3G45000	-1.07	-0.10	-0.71	0.50367	0.631932	-6.97
264342_at	unknown protein ; supported by full-	---	AT1G12080	-1.29	-0.36	-0.71	0.503723	0.631932	-6.97
248993_at	putative protein contains similarity t	---	AT5G45240	-1.06	-0.08	-0.71	0.503743	0.631932	-6.97
267546_at	putative disease resistance protein	AtRLP23	AT2G32680	-1.32	-0.40	-0.71	0.50375	0.631932	-6.97
266564_at	putative serine carboxypeptidase II	scpl22	AT2G24000	-1.08	-0.11	-0.71	0.503805	0.631932	-6.97
247100_at	selenium-binding protein-like	---	AT5G66520	-1.06	-0.09	-0.71	0.503808	0.631932	-6.97
251434_at	polygalacturonase-like protein poly	---	AT3G59850	-1.06	-0.08	-0.71	0.503828	0.631932	-6.97
253816_at	hypothetical protein ;supported by	emb1923	AT4G28210	1.07	0.10	0.71	0.503934	0.632031	-6.97
257418_at	hypothetical protein predicted by ge	---	AT1G30850	-1.08	-0.11	-0.71	0.503999	0.632077	-6.97
260920_at	amp-binding protein, putative simila	---	AT1G21530	-1.05	-0.07	-0.71	0.504042	0.632097	-6.97
254055_at	hypothetical protein	---	AT4G25330	-1.05	-0.08	-0.71	0.504131	0.632173	-6.97
259687_at	unknown protein	---	AT1G63110	1.07	0.10	0.71	0.504385	0.632457	-6.97
249902_at	unknown protein	---	AT5G22680	-1.08	-0.12	-0.70	0.504483	0.632545	-6.97
245131_s_a	unknown protein	emb1067	AT2G45330	-1.05	-0.07	-0.70	0.504603	0.632657	-6.98
260016_at	Athila ORF 1, putative simlar to GI:	---	---	1.05	0.07	0.70	0.504628	0.632657	-6.98
245151_at	putative pectinesterase ;supported	---	AT2G47550	1.41	0.49	0.70	0.504829	0.632852	-6.98
258880_at	hypothetical protein similar to symb	ATG8H	AT3G06420	1.14	0.19	0.70	0.504838	0.632852	-6.98
256947_at	hypothetical protein contains Pfam	POK2	AT3G19050	1.04	0.06	0.70	0.504974	0.632986	-6.98
254621_at	gene 11-1 protein - like gene 11-1	WAVE5	AT4G18600	1.06	0.08	0.70	0.505065	0.633065	-6.98

264423_at	hypothetical protein predicted by ge	---	AT1G61690	1.07	0.10	0.70	0.505213	0.633216	-6.98
252545_at	putative protein	---	AT3G45820	1.07	0.09	0.70	0.505506	0.633549	-6.98
250092_at	putative protein	---	AT5G17360	1.05	0.06	0.70	0.505631	0.633671	-6.98
249623_at	putative protein Ariadne-2 protein (	---	AT5G37560	1.04	0.06	0.70	0.505696	0.633718	-6.98
247469_at	Expressed protein ; supported by cl	AGL42	AT5G62165	1.31	0.39	0.70	0.506024	0.634094	-6.98
250433_at	histone H3 - like protein histone H3	---	AT5G10400	-1.07	-0.09	-0.70	0.5062	0.63428	-6.98
250113_at	putative protein similar to unknown	FRL1	AT5G16320	-1.06	-0.08	-0.70	0.506292	0.63436	-6.98
254197_at	trehalase - like protein trehalase 1	TRE1	AT4G24040	-1.09	-0.12	-0.70	0.506382	0.634438	-6.98
257850_at	putative protein kinase leucine-rich	SRF4	AT3G13065	1.05	0.07	0.70	0.506429	0.634462	-6.98
265591_at	hypothetical protein predicted by ge	---	AT2G20150	-1.08	-0.11	-0.70	0.506475	0.634484	-6.98
260850_at	glucose 6 phosphate/phosphate tra	---	AT1G21870	-1.07	-0.10	-0.70	0.506604	0.634611	-6.98
265840_at	hypothetical protein predicted by ge	---	AT2G14530	-1.07	-0.10	-0.70	0.50665	0.634634	-6.98
247143_at	unknown protein	---	AT5G65580	-1.10	-0.14	-0.70	0.506869	0.634873	-6.98
261686_at	unknown protein ;supported by full-	---	AT1G47310	1.06	0.08	0.70	0.507012	0.635018	-6.98
263967_at	En/Spm-like transposon protein	---	---	1.05	0.07	0.70	0.507148	0.635153	-6.98
262177_at	isochorismate synthase (icsI) ident	EDS16	AT1G74710	1.19	0.25	0.70	0.507239	0.635232	-6.98
249158_at	electron transfer flavoprotein beta-s	ETFBETA	AT5G43430	-1.05	-0.07	-0.70	0.507367	0.635358	-6.98
250103_at	transcription factor (gb|AAD53095.1	MYB43	AT5G16600	-1.06	-0.08	-0.70	0.507746	0.635798	-6.98
258007_at	putative tyrosine phosphatase simil	ATPEN2	AT3G19420	-1.08	-0.12	-0.70	0.507837	0.635871	-6.98
260067_at	putative lipid transfer protein similar	---	AT1G73780	-1.06	-0.08	-0.70	0.507895	0.635871	-6.98
255679_at	putative acetyl CoA thioesterase	---	AT4G00520	1.08	0.11	0.70	0.507902	0.635871	-6.98
248543_at	putative protein similar to unknown	---	AT5G50230	-1.05	-0.06	-0.70	0.507916	0.635871	-6.98
259997_at	unknown protein similar to N-acetyl	---	AT1G67880	1.13	0.18	0.70	0.507998	0.635938	-6.98
261293_at	unknown protein ; supported by cDI	---	AT1G36980	1.05	0.07	0.70	0.508069	0.635958	-6.98
253744_s_a	putative protein hypothetical protei	---	---	-1.05	-0.07	-0.70	0.508069	0.635958	-6.98
253442_at	H+-transporting ATPase - like prote	---	AT4G32530	1.05	0.07	0.70	0.50825	0.636144	-6.98
267444_at	hypothetical protein predicted by ge	---	AT2G19180	-1.08	-0.11	-0.70	0.508274	0.636144	-6.98
246788_at	putative protein hypothetical protei	AGL89	AT5G27580	-1.05	-0.07	-0.70	0.508304	0.636147	-6.98
256338_at	hypothetical protein similar to seed	---	AT1G72100	-1.06	-0.08	-0.70	0.508554	0.636425	-6.98
245782_at	60S ribosomal protein (fragment),	---	AT1G35200	-1.08	-0.11	-0.70	0.508676	0.63652	-6.98
256956_at	expressed protein supported by cD	---	AT3G13410	-1.05	-0.07	-0.70	0.508686	0.63652	-6.98
257800_at	unknown protein ;supported by full-	---	AT3G15900	1.07	0.10	0.70	0.508856	0.636698	-6.98
257286_s_a	transposase, putative similar to tra	---	AT1G19260	-1.06	-0.09	-0.70	0.509016	0.636863	-6.98
254727_at	hypothetical protein	PTAC5	AT4G13670	1.05	0.07	0.70	0.509167	0.637017	-6.98
245510_at	hypothetical protein	---	AT4G15740	-1.09	-0.13	-0.70	0.509235	0.637068	-6.98

262906_at	unknown protein contains similarity	---	AT1G59760	1.07	0.10	0.70	0.50957	0.637451	-6.98
264985_at	unknown protein ;supported by full-	---	AT1G27150	1.10	0.14	0.70	0.509854	0.637757	-6.98
259470_at	unknown protein	---	AT1G19110	-1.05	-0.06	-0.70	0.50987	0.637757	-6.98
263023_at	unknown protein	---	AT1G23960	-1.12	-0.16	-0.70	0.509972	0.637849	-6.98
264730_at	hypothetical protein similar to putati	---	AT1G62085	1.06	0.08	0.70	0.510039	0.637898	-6.98
247236_at	putative protein similar to unknown	---	AT5G64590	-1.06	-0.08	-0.70	0.510093	0.637931	-6.98
249883_at	Na+/H+ antiporter-like protein	CHX3	AT5G22900	-1.05	-0.07	-0.70	0.510165	0.637986	-6.98
266996_at	putative cytochrome P450 ;support	CYP710A2	AT2G34490	-1.38	-0.46	-0.70	0.510248	0.638055	-6.98
265177_at	OBP32pep protein, putative identic	---	AT1G23640	-1.05	-0.07	-0.70	0.510314	0.638102	-6.98
258147_at	beta-glucosidase, putative similar t	BGLU43	AT3G18070	1.06	0.08	0.69	0.510444	0.638189	-6.98
252952_at	putative protein cylicin II - bovine, F	---	AT4G38710	1.08	0.11	0.69	0.510453	0.638189	-6.98
247370_at	putative protein similar to unknown	---	AT5G63320	1.11	0.15	0.69	0.510488	0.638189	-6.98
262530_at	putative receptor protein kinase Apı	AtRLP2	AT1G17240	1.07	0.10	0.69	0.510495	0.638189	-6.98
245664_at	hypothetical protein predicted by ge	---	AT1G28327	-1.05	-0.07	-0.69	0.510601	0.638287	-6.98
257846_at	unknown protein	---	AT3G12910	1.24	0.31	0.69	0.510644	0.638306	-6.98
254272_at	predicted protein hypothetical prote	---	AT4G22850	-1.05	-0.07	-0.69	0.510756	0.63841	-6.98
267343_at	hypothetical protein predicted by gr	---	AT2G44260	-1.32	-0.40	-0.69	0.510886	0.638538	-6.98
245570_at	heat shock protein 101 (HSP101),p	CLPB2	AT4G14670	1.06	0.08	0.69	0.510932	0.63856	-6.98
263594_at	putative purple acid phosphatase c	PAP7	AT2G01880	-1.14	-0.18	-0.69	0.511051	0.638654	-6.98
249336_at	putative protein similar to unknown	DRB5	AT5G41070	-1.10	-0.14	-0.69	0.511063	0.638654	-6.98
267001_at	putative urease accessory protein ;	UREG	AT2G34470	1.08	0.11	0.69	0.511177	0.638761	-6.98
257586_at	hypothetical protein predicted by ge	---	AT1G50760	-1.05	-0.06	-0.69	0.511383	0.638984	-6.98
260478_at	DnaJ isolog	---	AT1G11040	-1.05	-0.07	-0.69	0.511514	0.639112	-6.98
245482_at	hypothetical protein	---	AT4G16180	-1.08	-0.11	-0.69	0.511584	0.639165	-6.98
266497_at	putative retroelement pol polyprotei	---	---	-1.06	-0.09	-0.69	0.511804	0.639404	-6.98
258891_at	unknown protein	EMB2016	AT3G05680	1.05	0.07	0.69	0.51184	0.639414	-6.98
267491_at	unknown protein predicted by gens	---	---	-1.07	-0.10	-0.69	0.51192	0.639479	-6.98
256623_at	myosin identical to myosin GB:CAB	ATM1	AT3G19960	-1.06	-0.09	-0.69	0.512465	0.640115	-6.99
256359_at	protein kinase, putative contains P	---	AT1G66460	1.05	0.07	0.69	0.512485	0.640115	-6.99
265904_at	putative beta-glucosidase	BGLU14	AT2G25630	-1.06	-0.08	-0.69	0.512525	0.64013	-6.99
257664_at	hypothetical protein predicted by ge	EMB2743	AT3G20400	-1.07	-0.10	-0.69	0.51277	0.640372	-6.99
261545_at	unknown protein	---	AT1G63530	1.06	0.08	0.69	0.512775	0.640372	-6.99
252617_at	n-acetylglucosaminyl-phosphatidyli	SETH2	AT3G45100	-1.05	-0.07	-0.69	0.512805	0.640374	-6.99
252985_at	putative protein Niemann-Pick C di	---	AT4G38350	1.06	0.08	0.69	0.513003	0.640585	-6.99
259197_at	putative peroxidase similar to perox	---	AT3G03670	1.23	0.30	0.69	0.513029	0.640585	-6.99

265910_at	putative vacuolar ATP synthase pro	---	AT2G25610	1.06	0.08	0.69	0.513148	0.640652	-6.99
265111_at	similar to 14KD proline-rich protein	---	AT1G62510	1.33	0.42	0.69	0.513163	0.640652	-6.99
255640_at	hypothetical protein	---	AT4G00800	1.08	0.11	0.69	0.513168	0.640652	-6.99
248203_at	Myb-related transcription factor-like	MYB49	AT5G54230	-1.04	-0.06	-0.69	0.513196	0.640652	-6.99
248266_at	putative protein similar to unknown	---	AT5G53440	1.05	0.07	0.69	0.513231	0.640661	-6.99
258968_at	hypothetical protein similar to hypot	---	AT3G10460	1.06	0.08	0.69	0.513336	0.640757	-6.99
252778_at	putative protein replication protein	---	---	-1.05	-0.07	-0.69	0.513398	0.640799	-6.99
265937_at	putative RING zinc finger protein	---	AT2G19610	-1.06	-0.09	-0.69	0.513956	0.641438	-6.99
248863_at	zinc finger protein Glo3-like	AGD9	AT5G46750	-1.05	-0.07	-0.69	0.513966	0.641438	-6.99
250535_at	putative protein similar to unknown	---	AT5G08480	1.06	0.08	0.69	0.514264	0.641749	-6.99
259201_at	hypothetical protein predicted using	---	AT3G09080	-1.08	-0.11	-0.69	0.514271	0.641749	-6.99
267616_at	unknown protein ;supported by full-	---	AT2G26680	-1.06	-0.08	-0.69	0.514321	0.641775	-6.99
255040_at	putative protein hypothetical protei	---	AT4G09580	-1.06	-0.08	-0.69	0.514384	0.641819	-6.99
255592_s_a	hypothetical protein	---	AT2G34280	-1.06	-0.09	-0.69	0.51444	0.641854	-6.99
248221_at	vacuolar sorting protein-like; embry	VPS26A	AT5G53530	-1.05	-0.07	-0.69	0.514538	0.641941	-6.99
261228_at	C-8,7 sterol isomerase identical to	HYD1	AT1G20050	-1.07	-0.10	-0.69	0.514589	0.641948	-6.99
253036_at	putative protein other predicted pro	---	AT4G38340	-1.07	-0.10	-0.69	0.5146	0.641948	-6.99
263135_at	flavanone 3-hydroxylase, putative	---	AT1G78550	1.07	0.10	0.69	0.514648	0.641963	-6.99
252261_at	RNA-directed RNA polymerase RN	RDR6	AT3G49500	1.06	0.09	0.69	0.514684	0.641963	-6.99
255076_at	putative protein RING-H2 zinc finge	---	AT4G09130	1.05	0.07	0.69	0.51472	0.641963	-6.99
259400_at	receptor-like protein kinase, putativ	---	AT1G17750	1.28	0.35	0.69	0.514727	0.641963	-6.99
257257_at	hypothetical protein contains Pfam	---	AT3G22020	-1.04	-0.06	-0.69	0.514753	0.641963	-6.99
251329_at	putative protein hypothetical protei	SYP73	AT3G61450	1.08	0.11	0.69	0.515089	0.642347	-6.99
265490_s_a	putative polygalacturonase	---	AT2G15450	-1.05	-0.08	-0.69	0.515187	0.642412	-6.99
266515_at	putative tubby protein	AtTLP3	AT2G47900	1.08	0.11	0.69	0.515197	0.642412	-6.99
266219_at	putative para-aminobenzoate synth	emb1997	AT2G28880	-1.06	-0.08	-0.69	0.515323	0.642535	-6.99
265783_at	putative Athila retroelement ORF1 p	---	---	-1.06	-0.09	-0.69	0.515562	0.642797	-6.99
247772_at	putative protein various predicted p	---	AT5G58610	-1.07	-0.09	-0.69	0.515619	0.642832	-6.99
264958_at	unknown protein ; supported by cDI	---	AT1G76960	1.09	0.13	0.69	0.515759	0.642954	-6.99
264382_at	unknown protein similarity to strom	SDF2	AT2G25110	1.10	0.14	0.69	0.515773	0.642954	-6.99
256182_at	Expressed protein ; supported by fu	SYP81	AT1G51740	1.07	0.10	0.69	0.515982	0.64313	-6.99
264229_at	unknown protein	---	AT1G67480	1.09	0.13	0.69	0.515985	0.64313	-6.99
260417_at	putative chromomethylase similar to	CMT3	AT1G69770	1.12	0.16	0.69	0.515998	0.64313	-6.99
260382_at	unknown protein	---	AT1G73850	1.07	0.10	0.69	0.516042	0.643139	-6.99
266041_s_a	hypothetical protein	---	---	1.06	0.08	0.69	0.516062	0.643139	-6.99

258092_at	Expressed protein ; supported by fu	---	AT3G14595	1.09	0.13	0.68	0.516295	0.643378	-6.99
267505_at	putative cytochrome P450 ;support	CYP76C1	AT2G45560	-1.07	-0.09	-0.68	0.51631	0.643378	-6.99
255519_at	hypothetical protein	---	AT4G02310	-1.04	-0.06	-0.68	0.516456	0.643525	-6.99
258685_at	putative polygalacturonase similar t	---	AT3G07830	-1.07	-0.10	-0.68	0.51659	0.643622	-6.99
256983_at	chaperonin 60 beta, putative very s	---	AT3G13470	1.15	0.20	0.68	0.516591	0.643622	-6.99
252367_at	putative protein MEL-26, Caenorha	BT2	AT3G48360	-1.20	-0.26	-0.68	0.51663	0.643636	-6.99
257591_at	leucine-rich repeat disease resistar	AtRLP39	AT3G24900	-1.04	-0.06	-0.68	0.516676	0.643658	-6.99
249878_at	TATA-binding protein-associated ph	NF-YB13	AT5G23090	1.07	0.10	0.68	0.516784	0.643757	-6.99
264374_at	putative two-component response	ARR12	AT2G25180	-1.06	-0.08	-0.68	0.516812	0.643757	-6.99
260429_at	unknown protein ;supported by full-	JAZ6	AT1G72450	1.14	0.19	0.68	0.51686	0.643781	-6.99
264955_at	F-box protein family, AtFBX3 conta	---	AT1G76920	1.07	0.10	0.68	0.516888	0.643781	-6.99
254277_at	myb-like protein myb-related transc	MYB85	AT4G22680	1.19	0.25	0.68	0.517025	0.643898	-6.99
261234_x_a	hypothetical protein predicted by ge	---	---	-1.06	-0.08	-0.68	0.517064	0.643898	-6.99
245843_at	unknown protein	---	AT1G26180	-1.06	-0.09	-0.68	0.517067	0.643898	-6.99
249486_at	receptor protein kinase - like protei	---	AT5G39030	1.07	0.09	0.68	0.51713	0.643942	-6.99
267248_at	hypothetical protein predicted by ge	---	AT2G30120	1.07	0.10	0.68	0.517345	0.644164	-6.99
245046_at	putative membrane transporter ; su	PDE135	AT2G26510	1.06	0.08	0.68	0.517388	0.644164	-6.99
252893_at	hypothetical protein	---	AT4G39420	-1.04	-0.06	-0.68	0.517393	0.644164	-6.99
254113_at	hypothetical protein	---	AT4G24900	1.06	0.08	0.68	0.51746	0.644213	-6.99
251914_at	putative protein serine/threonine-sp	---	AT3G53930	-1.06	-0.08	-0.68	0.517549	0.644285	-6.99
254211_at	phosphatase like protein phosphop	SGT1A	AT4G23570	-1.09	-0.13	-0.68	0.517575	0.644285	-6.99
263724_at	putative Ta11-like non-LTR retroele	---	AT2G13510	-1.05	-0.07	-0.68	0.517618	0.644304	-6.99
263987_at	putative lipase ; supported by cDN	---	AT2G42690	1.08	0.11	0.68	0.517649	0.644307	-6.99
246570_at	putative protein nonmuscle myosin	---	AT5G14990	-1.06	-0.08	-0.68	0.517788	0.644414	-6.99
260534_at	hypothetical protein predicted by gr	---	---	-1.05	-0.07	-0.68	0.517797	0.644414	-6.99
264088_at	unknown protein	emb1381	AT2G31340	-1.06	-0.08	-0.68	0.51782	0.644414	-6.99
256129_at	calcium-binding protein, putative si	---	AT1G18210	-1.10	-0.14	-0.68	0.518182	0.644829	-6.99
254060_at	putative protein polytropic murine l	SHB1	AT4G25350	-1.11	-0.15	-0.68	0.518215	0.644836	-6.99
254175_at	putative protein CGI-82 protein - H	---	AT4G24050	1.05	0.08	0.68	0.518313	0.644923	-6.99
245207_at	RING finger-like protein similarity t	---	AT5G12310	-1.06	-0.08	-0.68	0.518367	0.644954	-6.99
245143_at	unknown protein ;supported by full-	ZPR1	AT2G45450	1.12	0.17	0.68	0.518515	0.645103	-6.99
255613_at	putative RING zinc finger protein	---	AT4G01270	-1.06	-0.09	-0.68	0.518549	0.645111	-6.99
260227_at	unknown protein similar to hypothe	---	AT1G74450	-1.15	-0.21	-0.68	0.518716	0.645283	-6.99
250140_at	putative protein	DRM2	AT5G14620	-1.07	-0.10	-0.68	0.518793	0.645343	-6.99
263091_at	unknown protein	---	AT2G16200	1.05	0.07	0.68	0.518863	0.645396	-6.99

254151_at	F-box protein family, AtFBX14 simi	---	AT4G24390	1.05	0.07	0.68	0.519009	0.645503	-6.99
257616_at	hypothetical protein contains Pfam	---	AT3G26540	1.07	0.10	0.68	0.519016	0.645503	-6.99
260646_at	hypothetical protein similar to CHP-	---	AT1G53340	1.08	0.12	0.68	0.519034	0.645503	-6.99
254538_at	putative protein chitinase / lysozym	---	AT4G19740	1.05	0.07	0.68	0.519349	0.645859	-6.99
245327_at	hypothetical protein ; supported by	---	AT4G16850	-1.05	-0.07	-0.68	0.519435	0.645931	-6.99
265193_at	unknown protein ESTs gb|T144077	---	AT1G05070	1.05	0.07	0.68	0.519498	0.645961	-6.99
262865_at	cytochrome p450, putative similar t	CYP89A7	AT1G64930	1.06	0.08	0.68	0.519516	0.645961	-6.99
262240_at	Pto kinase interactor 1, putative sir	---	AT1G48220	-1.06	-0.08	-0.68	0.51967	0.646084	-6.99
256531_at	cystathionine gamma-synthase, pu	---	AT1G33320	-1.05	-0.07	-0.68	0.519674	0.646084	-6.99
250099_at	unknown protein ; supported by cD	---	AT5G17300	-1.07	-0.10	-0.68	0.519699	0.646084	-6.99
260932_s_a	hypothetical protein contains simila	PGP12	AT1G02520	1.22	0.29	0.68	0.519878	0.646271	-6.99
255337_at	putative DNA-binding protein simila	WRKY42	AT4G04450	-1.07	-0.10	-0.68	0.519966	0.646297	-6.99
244969_at	ribosomal protein S18	---	---	-1.13	-0.18	-0.68	0.519976	0.646297	-6.99
251832_at	putative protein tomato leucine zip	ATEXO70H	AT3G55150	1.16	0.22	0.68	0.519984	0.646297	-6.99
247657_at	Expressed protein ; supported by fu	---	AT5G59845	-1.06	-0.09	-0.68	0.520324	0.646664	-6.99
249387_at	putative protein predicted proteins,	---	AT5G40070	-1.08	-0.11	-0.68	0.520336	0.646664	-6.99
252148_at	MS5-like protein	---	AT3G51280	-1.06	-0.09	-0.68	0.520369	0.646669	-6.99
247579_at	cytochrome P450 - like protein cyt	CYP89A3	AT5G61320	-1.05	-0.07	-0.68	0.520518	0.64682	-6.99
254386_at	peroxidase prxr1 ;supported by full	PRXR1	AT4G21960	1.11	0.15	0.68	0.520673	0.646976	-7.00
267514_at	putative glycerate dehydrogenase	---	AT2G45630	1.16	0.21	0.68	0.520738	0.647022	-7.00
248642_at	putative protein similar to unknown	---	AT5G49120	-1.06	-0.08	-0.68	0.520906	0.647196	-7.00
250177_at	putative protein copine I, Homo sa	RGLG2	AT5G14420	1.06	0.09	0.68	0.521129	0.647424	-7.00
264036_at	hypothetical protein similar to hypot	---	AT2G03810	-1.08	-0.11	-0.68	0.521146	0.647424	-7.00
265204_at	hypothetical protein predicted by ge	---	AT2G36650	-1.04	-0.06	-0.68	0.521248	0.647515	-7.00
266976_at	putative phospholipase	---	AT2G39410	1.09	0.12	0.68	0.521305	0.64755	-7.00
258475_at	putative tyrosyl-tRNA synthetase si	emb2768	AT3G02660	1.05	0.07	0.68	0.521376	0.647588	-7.00
265091_s_a	hypothetical protein similar to Anthc	---	AT1G03495	-1.07	-0.10	-0.68	0.521392	0.647588	-7.00
254769_at	hypothetical protein	---	AT4G13330	1.11	0.15	0.68	0.521705	0.647941	-7.00
264761_at	hypothetical protein predicted by ge	---	AT1G61280	1.05	0.07	0.68	0.521881	0.648125	-7.00
259271_at	Expressed protein ; supported by fu	---	AT3G01170	-1.06	-0.09	-0.68	0.521942	0.64816	-7.00
253844_at	hypothetical protein	---	AT4G27930	-1.06	-0.09	-0.68	0.52198	0.64816	-7.00
245808_at	RNA binding protein identical to RN	ATRBP1	AT1G58470	-1.07	-0.10	-0.68	0.521995	0.64816	-7.00
252743_at	guanine nucleotide-exchange - like	ATMIN7	AT3G43300	-1.05	-0.07	-0.68	0.522051	0.648195	-7.00
253540_at	putative protein various predicted p	---	AT4G31615	-1.05	-0.07	-0.68	0.522126	0.648252	-7.00
263576_at	hypothetical protein similar to hypot	---	AT2G17080	1.04	0.06	0.67	0.522217	0.648308	-7.00

248471_at	unknown protein	---	AT5G50840	-1.07	-0.10	-0.67	0.522227	0.648308	-7.00
263949_at	E2, ubiquitin-conjugating enzyme,	MMZ3	AT2G36060	1.05	0.06	0.67	0.522297	0.648359	-7.00
262311_at	homeodomain leucine zipper prote	ATHB18	AT1G70920	1.06	0.08	0.67	0.522419	0.648466	-7.00
250528_at	putative protein strong similarity to	---	AT5G08600	1.04	0.06	0.67	0.52244	0.648466	-7.00
248894_at	unknown protein	---	AT5G46320	-1.06	-0.08	-0.67	0.522473	0.648471	-7.00
259600_at	hypothetical protein predicted by ge	---	AT1G35220	1.07	0.10	0.67	0.522523	0.648499	-7.00
260546_at	putative trypsin inhibitor ;supported	ATTI2	AT2G43520	1.24	0.31	0.67	0.522724	0.648713	-7.00
257897_at	HAL3A protein identical to GB:AAD	HAL3A	AT3G18030	1.08	0.11	0.67	0.522905	0.648902	-7.00
265456_at	Expressed protein ; supported by fu	SDH4	AT2G46505	1.05	0.07	0.67	0.522983	0.648928	-7.00
256572_at	40S RIBOSOMAL PROTEIN S25,	---	AT3G30740	1.05	0.07	0.67	0.523004	0.648928	-7.00
254792_at	putative protein nucleoid DNA-bind	---	AT4G12920	-1.05	-0.08	-0.67	0.523012	0.648928	-7.00
257801_at	mitogen activated protein kinase ki	WNK6	AT3G18750	1.06	0.08	0.67	0.523099	0.648977	-7.00
259569_at	hypothetical protein	---	AT1G20480	1.06	0.09	0.67	0.523108	0.648977	-7.00
264745_at	5'-adenylylphosphosulfate reductas	אפר-02	AT1G62180	1.10	0.13	0.67	0.523315	0.649174	-7.00
261054_at	hypothetical protein predicted by ge	---	AT1G01320	-1.11	-0.15	-0.67	0.523324	0.649174	-7.00
258867_at	hypothetical protein predicted by ge	---	AT3G03130	-1.05	-0.08	-0.67	0.52349	0.649345	-7.00
261067_at	lectin, putative contains Pfam profi	---	AT1G07460	-1.05	-0.08	-0.67	0.523519	0.649346	-7.00
252790_at	putative protein various predicted tr	---	---	-1.05	-0.07	-0.67	0.523592	0.6494	-7.00
258108_at	unknown protein contains Pfam pro	---	AT3G23570	1.17	0.23	0.67	0.52368	0.64945	-7.00
246722_at	putative protein various predicted p	---	---	-1.07	-0.10	-0.67	0.523688	0.64945	-7.00
264874_at	unknown protein Location of EST g	---	AT1G24240	-1.05	-0.07	-0.67	0.523779	0.649527	-7.00
259394_at	hypothetical protein predicted by ge	---	AT1G06420	-1.05	-0.07	-0.67	0.523902	0.649644	-7.00
250432_at	putative protein various predicted p	---	AT5G10420	1.05	0.07	0.67	0.523967	0.64969	-7.00
245241_at	hypothetical protein contains simila	---	AT1G44478	-1.05	-0.07	-0.67	0.524076	0.649789	-7.00
249745_at	phloem-specific lectin-like protein	AtPP2-B12	AT5G24560	-1.06	-0.09	-0.67	0.524158	0.649856	-7.00
249946_at	putative protein predicted proteins,	---	AT5G19170	-1.12	-0.16	-0.67	0.524294	0.649989	-7.00
247257_at	proteasome regulatory subunit-like	RPN5B	AT5G64760	1.12	0.16	0.67	0.524328	0.649996	-7.00
253251_at	putative protein similarity predicted	---	AT4G34730	1.08	0.11	0.67	0.524385	0.650031	-7.00
263494_at	14-3-3 protein GF14mu (grf9) iden	GRF9	AT2G42590	1.05	0.07	0.67	0.524617	0.650283	-7.00
258942_at	unknown protein predicted by gens	---	AT3G09960	-1.06	-0.08	-0.67	0.524717	0.650372	-7.00
245931_at	major pollen allergen-like protein p	---	AT5G09280	-1.07	-0.10	-0.67	0.52478	0.650404	-7.00
263959_at	hypothetical protein predicted by ge	---	AT2G36210	-1.05	-0.07	-0.67	0.5248	0.650404	-7.00
266038_at	putative ABC transporter	ATMRP11	AT2G07680	1.10	0.14	0.67	0.524856	0.650417	-7.00
AFFX-DapX	B. subtilis /GEN=dapB /DB_XREF=	---	---	-1.12	-0.16	-0.67	0.524868	0.650417	-7.00
265533_at	putative replication protein A1	---	---	-1.04	-0.06	-0.67	0.525057	0.650616	-7.00

260278_at	hypothetical protein predicted by g	WRKY66	AT1G80590	-1.09	-0.13	-0.67	0.52552	0.651156	-7.00
247927_at	unknown protein	---	AT5G57310	-1.05	-0.08	-0.67	0.525564	0.651175	-7.00
261464_at	disease resistance response protei	---	AT1G07730	1.06	0.09	0.67	0.525636	0.651228	-7.00
261705_at	hypothetical protein predicted by ge	---	AT1G32670	-1.05	-0.08	-0.67	0.525679	0.651245	-7.00
245511_at	hypothetical protein	---	AT4G15755	-1.04	-0.06	-0.67	0.525775	0.651321	-7.00
247827_at	putative protein various predicted p	LSH5	AT5G58500	-1.07	-0.09	-0.67	0.525797	0.651321	-7.00
258234_at	hypothetical protein similar to myb-	MYB118	AT3G27785	-1.05	-0.07	-0.67	0.525932	0.651453	-7.00
251215_at	putative protein region within disulf	---	AT3G62510	-1.05	-0.08	-0.67	0.525994	0.651494	-7.00
259599_at	serine carboxypeptidase II, putative	SCPL45	AT1G28110	-1.19	-0.25	-0.67	0.526053	0.651503	-7.00
265981_s_a	putative replication protein A1	---	---	-1.07	-0.10	-0.67	0.526067	0.651503	-7.00
265470_at	putative protein with C-terminal RIN	---	AT2G37150	1.07	0.09	0.67	0.526087	0.651503	-7.00
257036_at	hypothetical protein predicted by ge	---	AT3G19120	1.05	0.07	0.67	0.526146	0.651516	-7.00
250124_at	putative protein contains similarity t	---	AT5G16480	-1.06	-0.09	-0.67	0.526154	0.651516	-7.00
246485_at	putative protein cell death associat	AtCXE17	AT5G16080	1.24	0.31	0.67	0.526203	0.651517	-7.00
255653_at	Similar to receptor kinase	---	AT4G00960	1.05	0.06	0.67	0.526212	0.651517	-7.00
248068_at	unknown protein	---	AT5G55610	-1.08	-0.11	-0.67	0.526344	0.651642	-7.00
256701_at	transcription initiation factor IIF, be	---	AT3G52270	-1.06	-0.08	-0.67	0.52637	0.651642	-7.00
254736_at	putative disease resistance protein	---	AT4G13820	1.10	0.14	0.67	0.5264	0.651644	-7.00
246836_s_a	putative protein MADS box protein	---	AT5G26650	-1.04	-0.06	-0.67	0.526538	0.651779	-7.00
250000_at	putative protein PGPD14 - Petunia	---	AT5G18650	1.08	0.11	0.67	0.526622	0.651847	-7.00
246931_at	putative protein apoptosis-related p	---	AT5G25170	1.18	0.24	0.67	0.526748	0.651966	-7.00
258256_at	unknown protein ; supported by cD	---	AT3G26890	-1.06	-0.08	-0.67	0.526787	0.651966	-7.00
245457_s_a	disease resistance RPP5 like protei	---	AT4G16940	-1.05	-0.08	-0.67	0.52681	0.651966	-7.00
256941_at	hypothetical protein	---	---	-1.06	-0.09	-0.67	0.52685	0.651966	-7.00
263901_at	unknown protein ;supported by full-	---	AT2G36320	-1.08	-0.11	-0.67	0.52686	0.651966	-7.00
251810_at	putative protein predicted pectate-l	---	AT3G55250	1.07	0.10	0.67	0.526995	0.652097	-7.00
260376_at	putative cytochrome P-450 similar t	CYP78A10	AT1G74110	-1.05	-0.07	-0.67	0.527089	0.652128	-7.00
252145_at	putative protein several putative pro	---	AT3G51200	-1.05	-0.07	-0.67	0.527095	0.652128	-7.00
251818_at	vacuolar protein sorting protein 33a	ATVPS33	AT3G54860	-1.06	-0.08	-0.67	0.527106	0.652128	-7.00
246812_at	putative protein predicted proteins,	---	---	-1.05	-0.07	-0.67	0.527283	0.652293	-7.00
256283_at	hypothetical protein	---	AT3G12540	-1.05	-0.07	-0.67	0.527309	0.652293	-7.00
259563_s_a	hypothetical protein	---	AT1G20590	1.05	0.07	0.67	0.527325	0.652293	-7.00
261173_at	hypothetical protein predicted by ge	---	AT1G04830	1.05	0.08	0.67	0.527382	0.652328	-7.00
266632_at	putative serpin	---	AT2G35570	-1.06	-0.08	-0.67	0.527463	0.652393	-7.00
255195_at	may be a pseudogene	---	---	-1.05	-0.07	-0.67	0.527629	0.652563	-7.00

253666_at	xyloglucan endo-1,4-beta-D-glucar	MERI5B	AT4G30270	-1.05	-0.07	-0.67	0.527724	0.65261	-7.00
261665_at	beta-glucan-elicitor receptor, putati	---	AT1G18310	1.05	0.07	0.67	0.527724	0.65261	-7.00
261022_at	unknown protein similar to NAM like	ANAC007	AT1G12260	-1.06	-0.08	-0.67	0.52779	0.652656	-7.00
253235_at	putative protein hypothetical protei	HDR	AT4G34350	1.11	0.15	0.67	0.527987	0.652865	-7.00
255399_at	hypothetical protein	---	---	-1.06	-0.09	-0.67	0.528036	0.652866	-7.00
263723_at	putative Ta11-like non-LTR retroele	---	AT2G13500	-1.05	-0.07	-0.67	0.528046	0.652866	-7.00
255072_at	outer envelope membrane protein	TOC75-IV	AT4G09080	1.06	0.09	0.66	0.528251	0.653084	-7.00
245677_at	hypothetical protein predicted by ge	---	AT1G56660	-1.04	-0.06	-0.66	0.528323	0.653138	-7.00
257815_at	unknown protein	---	AT3G25130	-1.05	-0.08	-0.66	0.528447	0.653238	-7.00
249370_at	zinc finger - like protein predicted p	---	AT5G40710	1.04	0.06	0.66	0.528462	0.653238	-7.00
247757_at	putative protein	---	AT5G59105	-1.04	-0.06	-0.66	0.528498	0.653248	-7.00
256150_at	beta-fructofuranosidase identical to	ATFRUCT5	AT1G55120	1.12	0.17	0.66	0.528683	0.653442	-7.00
264665_at	unknown protein ESTs gb|H37208.	---	AT1G09660	1.06	0.09	0.66	0.528809	0.653562	-7.00
246665_s_a	putative protein predicted proteins -	---	---	-1.06	-0.08	-0.66	0.528843	0.653568	-7.00
253014_at	MADS-box protein AGL17 -like pro	AGL21	AT4G37940	-1.04	-0.06	-0.66	0.528896	0.65357	-7.01
246967_at	FPF1 protein	FPF1	AT5G24860	1.09	0.13	0.66	0.528901	0.65357	-7.01
252283_at	60S ribosomal protein L13 (BBC1)	---	AT3G48960	1.05	0.08	0.66	0.529193	0.653895	-7.01
263506_s_a	hypothetical protein	---	---	-1.07	-0.09	-0.66	0.529356	0.654061	-7.01
264290_at	hypothetical protein predicted by ge	---	AT1G78810	-1.07	-0.10	-0.66	0.529405	0.654085	-7.01
254767_s_a	cytochrome p450 - like protein cyto	CYP71A19	AT4G13290	-1.05	-0.06	-0.66	0.529449	0.654104	-7.01
255569_at	putative CAAX prenyl protease ; su	ATSTE24	AT4G01320	1.05	0.07	0.66	0.529594	0.654249	-7.01
247537_s_a	ABC transport protein - like ABC tra	ATH15	AT5G61690	1.05	0.08	0.66	0.529648	0.654279	-7.01
258116_at	hypothetical protein similar to terpe	---	AT3G14520	-1.07	-0.09	-0.66	0.529687	0.654292	-7.01
249735_at	putative protein contains similarity	---	AT5G24450	-1.07	-0.10	-0.66	0.529774	0.654365	-7.01
257499_at	hypothetical protein similar to hypot	---	AT1G63850	1.11	0.15	0.66	0.529838	0.654408	-7.01
249275_at	polygalacturonase-like protein	---	AT5G41870	-1.06	-0.08	-0.66	0.530022	0.6546	-7.01
251941_at	putative protein ribosomal protein S	---	AT3G53470	-1.05	-0.08	-0.66	0.530129	0.654697	-7.01
245501_at	hypothetical protein	---	AT4G15620	-1.13	-0.18	-0.66	0.530247	0.654773	-7.01
248513_at	unknown protein	---	AT5G50500	-1.05	-0.06	-0.66	0.530255	0.654773	-7.01
246470_at	putative protein predicted proteins,	---	AT5G17080	1.05	0.07	0.66	0.5303	0.654773	-7.01
253081_at	putative protein F35D11.3, Caenor	---	AT4G36210	-1.07	-0.10	-0.66	0.530306	0.654773	-7.01
246278_at	tubulin-like protein	---	AT4G37190	-1.12	-0.16	-0.66	0.530373	0.654821	-7.01
266890_at	acyl carrier protein identical to GB:L	MTACP-1	AT2G44620	1.07	0.09	0.66	0.530434	0.65486	-7.01
263395_at	putative mitochondrial inner membr	ATTIM44-1	AT2G20500	-1.05	-0.07	-0.66	0.530525	0.654937	-7.01
266346_at	putative homeodomain transcriptior	ATHB17	AT2G01430	-1.07	-0.10	-0.66	0.530771	0.655206	-7.01

263427_at	hypothetical protein predicted by ge	---	AT2G22260	-1.05	-0.07	-0.66	0.530957	0.6554	-7.01
256198_at	Myb-family transcription factor, put	---	AT1G58220	1.08	0.11	0.66	0.531022	0.655444	-7.01
249669_at	putative protein similar to unknown	---	---	-1.05	-0.07	-0.66	0.531124	0.655513	-7.01
262054_s_a	putative heat-shock protein contain	---	AT1G79920	1.07	0.10	0.66	0.531159	0.655513	-7.01
245871_at	hypothetical protein predicted by ge	---	AT1G26290	-1.07	-0.10	-0.66	0.531164	0.655513	-7.01
259529_at	hypothetical protein	---	AT1G12400	1.05	0.07	0.66	0.53129	0.655627	-7.01
261035_at	hypothetical protein contains Pfam	---	---	1.05	0.06	0.66	0.531314	0.655627	-7.01
254659_at	starch synthase-like protein bacteri	SS4	AT4G18240	-1.09	-0.12	-0.66	0.531354	0.655641	-7.01
261525_at	hypothetical protein predicted by ge	---	AT1G14330	-1.07	-0.10	-0.66	0.531629	0.655945	-7.01
264387_at	putative growth regulator protein co	---	AT1G11990	-1.06	-0.08	-0.66	0.531689	0.655984	-7.01
251326_at	putative protein stamina pistilloidia	HWS	AT3G61590	-1.07	-0.10	-0.66	0.531736	0.656007	-7.01
257543_at	hypothetical protein predicted by ge	---	AT3G28960	-1.06	-0.08	-0.66	0.531912	0.656188	-7.01
249313_at	unknown protein	---	AT5G41560	1.05	0.07	0.66	0.532045	0.656316	-7.01
265165_at	putative OBP32pep protein	---	AT1G23610	-1.05	-0.07	-0.66	0.532118	0.656371	-7.01
257696_at	protein kinase, putative similar to p	AGC1.5	AT3G12690	-1.08	-0.11	-0.66	0.532257	0.656505	-7.01
251912_at	protein kinase-like protein wall-ass	---	AT3G53840	-1.06	-0.08	-0.66	0.532284	0.656505	-7.01
257114_at	cytochrome P450, putative contain	CYP705A2	AT3G20140	-1.07	-0.10	-0.66	0.532375	0.656581	-7.01
266558_at	putative polygalacturonase	---	AT2G23900	-1.05	-0.07	-0.66	0.532463	0.656654	-7.01
258463_at	putative protein kinase similar to Pt	---	AT3G17410	-1.06	-0.09	-0.66	0.532517	0.656685	-7.01
262713_at	unknown protein	---	AT1G16520	1.10	0.14	0.66	0.532609	0.656763	-7.01
262993_at	hypothetical protein contains simila	---	AT1G54230	-1.05	-0.07	-0.66	0.532653	0.656783	-7.01
261325_at	hypothetical protein predicted by ge	---	AT1G44780	1.04	0.06	0.66	0.532755	0.656842	-7.01
264029_at	unknown protein	MRH6	AT2G03720	-1.05	-0.08	-0.66	0.532759	0.656842	-7.01
246044_at	calcium-dependent protein kinase	CDPK19	AT5G19450	1.07	0.10	0.66	0.532984	0.657071	-7.01
250696_at	putative protein similar to unknown	---	AT5G06790	1.04	0.06	0.66	0.533002	0.657071	-7.01
246833_at	putative protein	---	AT5G26620	1.04	0.06	0.66	0.533138	0.657203	-7.01
251777_s_a	pyruvate kinase - like protein pyruv	---	AT3G55650	-1.06	-0.08	-0.66	0.533368	0.65745	-7.01
263627_at	Expressed protein ; supported by fu	---	AT2G04675	-1.06	-0.08	-0.66	0.533453	0.657498	-7.01
247879_at	unknown protein	---	AT5G57770	-1.04	-0.06	-0.66	0.533464	0.657498	-7.01
249413_at	ras - related GTP binding protein -	AtRABG1	AT5G39620	-1.05	-0.07	-0.66	0.533516	0.657527	-7.01
251197_at	glutaredoxin -like protein glutaredo	---	AT3G62960	1.12	0.16	0.66	0.533607	0.657603	-7.01
254930_at	putative protein hypothetical protei	---	AT4G11450	-1.10	-0.14	-0.66	0.533674	0.65765	-7.01
256640_at	hypothetical protein predicted by ge	---	AT3G32260	-1.06	-0.08	-0.66	0.533703	0.65765	-7.01
259107_at	hypothetical protein predicted by ge	---	AT3G05460	1.04	0.06	0.66	0.533893	0.65784	-7.01
246717_at	putative protein	---	AT5G28920	-1.05	-0.07	-0.66	0.533915	0.65784	-7.01

247496_at	putative protein predicted proteins,	GUT1	AT5G61840	1.05	0.07	0.66	0.534038	0.657957	-7.01
259622_at	hypothetical protein predicted by ge	---	AT1G43010	-1.05	-0.07	-0.66	0.534179	0.65809	-7.01
252380_at	ABC-type transport protein-like pro	ATH2	AT3G47740	-1.05	-0.07	-0.65	0.534214	0.65809	-7.01
256880_at	major latex protein, putative similar	---	AT3G26450	1.10	0.13	0.65	0.534252	0.65809	-7.01
259303_at	hypothetical protein predicted by ge	---	AT3G05130	-1.04	-0.06	-0.65	0.534262	0.65809	-7.01
265601_at	hypothetical protein predicted by ge	---	AT2G14390	-1.06	-0.08	-0.65	0.53446	0.658299	-7.01
255713_s_a	predicted protein	---	AT4G00234	-1.04	-0.06	-0.65	0.534489	0.658299	-7.01
252301_at	putative protein various predicted p	EMB2261	---	-1.07	-0.09	-0.65	0.534551	0.658339	-7.01
245583_at	hypothetical protein	---	AT4G14920	1.05	0.08	0.65	0.534668	0.658437	-7.01
247222_at	ABC transporter protein 1-like ; sup	ATGCN5	AT5G64840	1.09	0.13	0.65	0.534688	0.658437	-7.01
266322_at	putative auxin-regulated protein	---	AT2G46690	-1.11	-0.15	-0.65	0.53476	0.658491	-7.01
263694_at	putative reverse transcriptase stron	---	---	-1.04	-0.06	-0.65	0.535061	0.658802	-7.01
253106_at	putative protein predicted proteins,	---	AT4G35870	-1.05	-0.07	-0.65	0.535071	0.658802	-7.01
255745_at	hypothetical protein predicted by ge	---	AT1G32030	-1.04	-0.06	-0.65	0.535161	0.658836	-7.01
248750_at	putative protein similar to unknown	---	AT5G47530	-1.08	-0.12	-0.65	0.535166	0.658836	-7.01
249197_at	putative protein contains similarity t	CML37	AT5G42380	1.43	0.51	0.65	0.535185	0.658836	-7.01
252681_at	NAC domain -like protein Tobacco	anac061	AT3G44350	-1.06	-0.09	-0.65	0.535243	0.658872	-7.01
267556_at	putative beta-galactosidase ; suppo	BGAL9	AT2G32810	-1.06	-0.09	-0.65	0.535338	0.658901	-7.01
252403_at	hypothetical protein	---	AT3G48080	1.04	0.06	0.65	0.535351	0.658901	-7.01
249521_at	putative protein strong similarity to u	---	AT5G38690	1.05	0.07	0.65	0.535353	0.658901	-7.01
255170_at	hypothetical protein similar to A. tha	---	---	-1.05	-0.07	-0.65	0.535565	0.659126	-7.01
249471_at	putative protein predicted proteins,	EDL2	AT5G39360	-1.08	-0.11	-0.65	0.535622	0.65916	-7.01
246692_at	putative protein predicted protein, A	---	---	-1.07	-0.09	-0.65	0.535723	0.659249	-7.01
246641_s_a	Expressed protein ; supported by fu	---	AT5G34883	-1.05	-0.08	-0.65	0.535842	0.659325	-7.01
263062_at	putative phosphatidylinositol/phoph	---	AT2G18180	-1.05	-0.08	-0.65	0.535842	0.659325	-7.01
255280_at	score=179, E=5.7e-06, N=1)	---	AT4G04960	1.12	0.16	0.65	0.535999	0.659482	-7.01
246927_s_a	nodulin - like protein nodulin, Glyci	---	AT5G25250	1.09	0.13	0.65	0.536095	0.659548	-7.01
245978_at	putative protein MORC microrchidi	---	AT5G13130	-1.06	-0.08	-0.65	0.53611	0.659548	-7.01
264974_at	unknown protein contains Pfam pro	ATHB54	AT1G27050	-1.06	-0.08	-0.65	0.536171	0.659558	-7.01
260615_at	mitochondrial NAD-dependent mala	---	AT1G53240	1.11	0.15	0.65	0.536176	0.659558	-7.01
250644_at	protein phosphatase 2C-like ;suppo	---	AT5G06750	1.09	0.12	0.65	0.536348	0.6597	-7.01
252244_at	putative protein some putative prote	---	AT3G50130	-1.06	-0.09	-0.65	0.53635	0.6597	-7.01
267372_at	putative protein kinase contains a p	ARSK1	AT2G26290	1.21	0.27	0.65	0.536747	0.660153	-7.01
263450_at	putative calcium-dependent protein	CPK24	AT2G31500	-1.05	-0.06	-0.65	0.536852	0.660211	-7.01
261237_at	hypothetical protein contains simila	---	AT1G32980	-1.05	-0.07	-0.65	0.536852	0.660211	-7.01

256465_at	hypothetical protein predicted by ge	---	AT1G32570	-1.08	-0.11	-0.65	0.536958	0.660306	-7.01
259589_at	unknown protein	---	AT1G28135	1.07	0.09	0.65	0.537074	0.660389	-7.01
248565_at	putative protein similar to unknown	---	AT5G49710	1.08	0.11	0.65	0.5371	0.660389	-7.01
245452_at	retrotransposon like protein	---	---	-1.05	-0.07	-0.65	0.537112	0.660389	-7.01
256532_at	PPR-repeat protein, putative conta	---	AT1G33350	1.08	0.11	0.65	0.537166	0.660419	-7.01
246338_s_a	putative protein putative integral m	ATCHX10	AT3G44920	-1.04	-0.06	-0.65	0.537259	0.660498	-7.01
264287_at	hypothetical protein similar to hypot	---	AT1G61930	-1.06	-0.09	-0.65	0.537397	0.660608	-7.01
258627_at	unknown protein similar to peroxiso	PEX12	AT3G04460	1.07	0.09	0.65	0.537406	0.660608	-7.01
260052_at	14-3-3 protein (grf13), putative con	GRF13	AT1G78220	-1.05	-0.08	-0.65	0.537597	0.660758	-7.02
262527_at	SRG1-like protein Strong homolog	---	AT1G17010	-1.05	-0.07	-0.65	0.537602	0.660758	-7.02
258720_at	putative ankyrin similar to ankyrin G	---	AT3G09550	-1.06	-0.09	-0.65	0.537615	0.660758	-7.02
249498_at	putative protein motif in transcriptio	---	AT5G39230	-1.05	-0.07	-0.65	0.537805	0.660956	-7.02
257498_at	hypothetical protein predicted by ge	---	AT1G69660	1.05	0.07	0.65	0.537872	0.661002	-7.02
251894_at	putative protein predicted proteins,	---	AT3G54380	-1.06	-0.09	-0.65	0.53823	0.661406	-7.02
260196_at	hypothetical protein similar to hypot	---	AT1G67570	1.04	0.06	0.65	0.538536	0.661724	-7.02
258605_at	phi-1-like protein similar to phi-1 (ph	EXL6	AT3G02970	-1.06	-0.08	-0.65	0.538546	0.661724	-7.02
245856_at	putative protein predicted proteins,	---	---	-1.07	-0.10	-0.65	0.538585	0.661735	-7.02
257367_at	hypothetical protein predicted by ge	---	AT2G25780	-1.06	-0.08	-0.65	0.538678	0.661814	-7.02
264764_at	receptor kinase, putative similar to	---	AT1G61440	1.04	0.06	0.65	0.538882	0.661969	-7.02
245789_at	hypothetical protein similar to hypot	---	AT1G32090	-1.11	-0.15	-0.65	0.538889	0.661969	-7.02
248306_at	unknown protein ; supported by cD	WRKY27	AT5G52830	1.09	0.12	0.65	0.538891	0.661969	-7.02
250022_at	Brn1-like protein	---	AT5G18210	1.10	0.14	0.65	0.538991	0.662035	-7.02
259637_at	protein disulfide isomerase precurs	ATPDIL1-5	AT1G52260	-1.07	-0.10	-0.65	0.539002	0.662035	-7.02
252447_at	beta-D-glucan exohydrolase - like p	---	AT3G47040	-1.05	-0.07	-0.65	0.539206	0.662248	-7.02
265140_at	F-box protein family, AtFBX11 con	---	AT1G51320	-1.05	-0.07	-0.65	0.539278	0.662294	-7.02
259619_at	hypothetical protein	---	AT1G42980	1.06	0.09	0.65	0.539301	0.662294	-7.02
246922_at	serine/threonine protein kinase-like	CIPK25	AT5G25110	1.09	0.12	0.65	0.539367	0.66234	-7.02
253708_at	gamma-glutamyltransferase-like pr	GGT4	AT4G29210	1.12	0.17	0.65	0.539493	0.662454	-7.02
263745_at	hypothetical protein predicted by ge	CHR34	AT2G21450	-1.05	-0.07	-0.65	0.539518	0.662454	-7.02
264326_at	unknown protein	---	AT1G04230	-1.06	-0.09	-0.65	0.539606	0.662502	-7.02
259302_at	unknown protein	GID1A	AT3G05120	1.08	0.11	0.65	0.539615	0.662502	-7.02
255218_at	putative athila transposon protein	---	---	-1.04	-0.06	-0.65	0.539875	0.662785	-7.02
266539_at	similar to mammalian MHC III regio	SUVH5	AT2G35160	1.06	0.08	0.65	0.53992	0.662804	-7.02
260411_at	hypothetical protein similar to GB:A	---	AT1G69890	1.12	0.16	0.65	0.540277	0.6632	-7.02
246540_at	nitrilase associated protein-like nitr	SP1L4	AT5G15600	-1.08	-0.11	-0.64	0.5403	0.6632	-7.02

245490_at	hypothetical protein	LDL3	AT4G16310	-1.06	-0.08	-0.64	0.540335	0.663207	-7.02
265416_at	unknown protein ; supported by ful	---	AT2G37120	-1.13	-0.17	-0.64	0.540523	0.663402	-7.02
255407_at	hypothetical protein similar to A. th	---	AT4G03480	-1.07	-0.10	-0.64	0.540613	0.663477	-7.02
264793_at	unknown protein similar to beta-ga	---	AT1G08660	-1.08	-0.11	-0.64	0.540899	0.663792	-7.02
245403_at	putative protein	---	AT4G17590	-1.05	-0.07	-0.64	0.54093	0.663794	-7.02
261285_at	Ca2+-dependent membrane-bindin	ANNAT1	AT1G35720	-1.15	-0.20	-0.64	0.541018	0.663843	-7.02
261840_at	hypothetical protein contains simila	AtTLP8	AT1G16070	-1.05	-0.07	-0.64	0.541056	0.663843	-7.02
265789_at	putative receptor-like protein kinase	---	AT2G01210	-1.05	-0.07	-0.64	0.541057	0.663843	-7.02
255147_at	hypothetical protein	---	AT4G08460	1.05	0.08	0.64	0.541187	0.663968	-7.02
262002_at	hypothetical protein predicted by ge	---	AT1G64450	-1.04	-0.06	-0.64	0.541275	0.66398	-7.02
259809_at	hypothetical protein predicted by ge	---	AT1G49800	1.08	0.11	0.64	0.541284	0.66398	-7.02
253128_at	Calcium-dependent serine/threonir	CPK18	AT4G36070	-1.04	-0.06	-0.64	0.541301	0.66398	-7.02
266769_s_a	putative reverse transcriptase	---	---	1.06	0.08	0.64	0.541314	0.66398	-7.02
254841_at	putative protein predicted proteins A	---	AT4G11940	-1.06	-0.08	-0.64	0.541473	0.66414	-7.02
249746_at	NAC2-like protein	TIP	AT5G24590	1.06	0.09	0.64	0.541572	0.664203	-7.02
252698_at	amine oxidase -like protein amine	---	AT3G43670	1.06	0.09	0.64	0.541583	0.664203	-7.02
254479_at	putative protein hypothetical protei	---	AT4G20350	1.06	0.09	0.64	0.541783	0.664398	-7.02
257842_at	P-glycoprotein, putative similar to P	PGP18	AT3G28390	-1.05	-0.07	-0.64	0.541801	0.664398	-7.02
247921_at	CONSTANS-like B-box zinc finger p	COL5	AT5G57660	-1.08	-0.11	-0.64	0.541887	0.664454	-7.02
255106_at	putative protein hypothetical protein	---	---	-1.04	-0.06	-0.64	0.541904	0.664454	-7.02
260319_at	hypothetical protein predicted by ge	---	AT1G63950	-1.06	-0.09	-0.64	0.541936	0.664457	-7.02
247602_at	S-receptor kinase homolog 2 precu	RLK1	AT5G60900	1.16	0.22	0.64	0.542093	0.664614	-7.02
264631_at	DegP protease contains similarity to	DegP3	AT1G65630	-1.05	-0.08	-0.64	0.542313	0.664848	-7.02
267351_at	unknown protein	NRPD1B	AT2G40030	-1.05	-0.08	-0.64	0.542384	0.664899	-7.02
245267_at	major latex protein like ; supported	---	AT4G14060	-1.05	-0.07	-0.64	0.542519	0.665029	-7.02
248755_at	putative protein strong similarity to	---	AT5G47690	1.08	0.11	0.64	0.542689	0.665201	-7.02
252714_x_a	putative protein p97 homologous p	---	AT3G43880	-1.04	-0.06	-0.64	0.542732	0.665219	-7.02
258898_at	putative DNA helicase	RECQI1	AT3G05740	-1.09	-0.13	-0.64	0.542766	0.665224	-7.02
265746_at	hypothetical protein predicted by ge	---	---	1.05	0.07	0.64	0.542814	0.665248	-7.02
263555_at	unknown protein ;supported by full-	---	AT2G16460	-1.05	-0.07	-0.64	0.543024	0.66547	-7.02
250331_at	putative protein self-incompatibility	---	AT5G11820	-1.06	-0.08	-0.64	0.543129	0.665562	-7.02
265513_at	hypothetical protein	---	---	-1.04	-0.06	-0.64	0.543171	0.665578	-7.02
261386_at	unknown protein ;supported by full-	---	AT1G05430	1.06	0.09	0.64	0.543215	0.665596	-7.02
248200_at	O-methyltransferase ;supported by	ATOMT1	AT5G54160	-1.15	-0.20	-0.64	0.543331	0.665702	-7.02
252861_at	hypothetical protein	---	AT4G39820	1.09	0.12	0.64	0.543367	0.665711	-7.02

247756_at	subtilisin-like serine protease conta	---	AT5G59100	-1.05	-0.07	-0.64	0.543529	0.665873	-7.02
252523_at	putative protein light repressible re	---	AT3G46400	-1.06	-0.09	-0.64	0.543896	0.666276	-7.02
259607_at	P-glycoprotein, putative similar to P	PGP13	AT1G27940	-1.04	-0.06	-0.64	0.543916	0.666276	-7.02
257847_at	hypothetical protein predicted by ge	---	AT3G13020	1.05	0.08	0.64	0.544004	0.666348	-7.02
263349_at	putative chromodomain-helicase-DI	CHR5	AT2G13370	1.07	0.10	0.64	0.544245	0.666592	-7.02
248371_at	gibberellin 20-oxidase (emb|CAA58	GA20OX2	AT5G51810	1.14	0.19	0.64	0.544262	0.666592	-7.02
247303_at	histidinol dehydrogenase ;supporte	ATHDH	AT5G63890	1.07	0.10	0.64	0.544321	0.666609	-7.02
263051_s_a	En/Spm-like transposon protein rela	---	---	1.05	0.07	0.64	0.544334	0.666609	-7.02
253301_at	pathogenesis-related protein 1 pre	---	AT4G33720	-1.16	-0.22	-0.64	0.544366	0.666612	-7.02
261943_at	plasma membrane ATPase, putativ	AHA9	AT1G80660	1.05	0.08	0.64	0.544418	0.666641	-7.02
258803_at	unknown protein similar to elicitor re	WRKY39	AT3G04670	-1.06	-0.08	-0.64	0.544534	0.666746	-7.02
247840_at	putative protein protein x 0001, Ho	---	AT5G58020	1.04	0.06	0.64	0.544637	0.666837	-7.02
267003_at	hypothetical protein predicted by ge	---	AT2G34340	-1.05	-0.07	-0.64	0.544716	0.666898	-7.02
265489_at	hypothetical protein predicted by ge	---	AT2G15640	1.07	0.10	0.64	0.544794	0.666958	-7.02
264217_at	hypothetical protein predicted by ge	---	AT1G60190	-1.26	-0.34	-0.64	0.544836	0.666973	-7.02
246123_at	beta-1,3-glucanase-like protein bet	---	AT5G20390	1.04	0.06	0.64	0.544899	0.667014	-7.02
262103_at	glutathione S-transferase, putative	GSTF5	AT1G02940	1.09	0.12	0.64	0.544986	0.667085	-7.02
259601_s_a	CACTA-element transposase, puta	---	---	-1.05	-0.07	-0.64	0.545039	0.667115	-7.02
250824_at	putative protein contains similarity t	---	AT5G05200	-1.07	-0.10	-0.64	0.545196	0.667271	-7.02
265322_at	hypothetical protein predicted by ge	---	AT2G18270	-1.04	-0.06	-0.64	0.545323	0.66739	-7.02
256138_at	Nt-gh3 deduced protein, putative s	---	AT1G48670	1.07	0.10	0.64	0.54559	0.667654	-7.02
265299_at	putative retroelement pol polyprotei	---	---	-1.08	-0.11	-0.64	0.545618	0.667654	-7.02
262264_at	Niemann-Pick C disease protein-lik	---	AT1G42470	-1.14	-0.19	-0.64	0.545627	0.667654	-7.02
258661_at	unknown protein	---	AT3G02930	1.13	0.17	0.64	0.545666	0.667667	-7.02
254542_s_a	putative LTR retrotransposon Bras	---	---	-1.04	-0.06	-0.64	0.545945	0.667972	-7.02
257839_at	hypothetical protein	---	AT3G25080	1.04	0.06	0.64	0.545986	0.667984	-7.02
263107_at	putative cytochrome P450	CYP705A6	AT2G05180	1.05	0.06	0.64	0.546013	0.667984	-7.02
246274_at	transcription factor like protein	---	AT4G36620	-1.06	-0.09	-0.64	0.546106	0.668061	-7.02
255322_at	putative protein	---	---	-1.04	-0.06	-0.64	0.546397	0.668382	-7.03
252361_at	hypothetical protein	---	AT3G48490	-1.11	-0.15	-0.63	0.546546	0.668443	-7.03
262000_at	Expressed protein ; supported by fu	---	AT1G33810	1.06	0.08	0.63	0.54656	0.668443	-7.03
249289_at	N-hydroxycinnamoyl/benzoyltransfe	---	AT5G41040	-1.23	-0.29	-0.63	0.546562	0.668443	-7.03
247883_at	unknown protein	---	AT5G57790	-1.07	-0.10	-0.63	0.546565	0.668443	-7.03
248643_at	putative protein strong similarity to u	---	AT5G49130	-1.05	-0.07	-0.63	0.546595	0.668445	-7.03
248044_at	putative protein similar to unknown	---	AT5G56020	-1.05	-0.07	-0.63	0.546688	0.668523	-7.03

259481_at	germin, putative similar to germin (	GLP4	AT1G18970	-1.11	-0.15	-0.63	0.546741	0.668534	-7.03
251946_at	putative protein predicted proteins,	---	AT3G53540	1.20	0.27	0.63	0.546756	0.668534	-7.03
266282_at	putative protein kinase contains a p	---	AT2G29220	1.04	0.06	0.63	0.546837	0.668597	-7.03
248667_at	putative protein contains similarity t	---	AT5G48710	-1.04	-0.06	-0.63	0.547041	0.66881	-7.03
261245_at	anter-specific proline-rich protein AI	---	AT1G20130	1.04	0.06	0.63	0.547271	0.669057	-7.03
263011_at	conserved hypothetical protein prot	---	AT1G23250	-1.05	-0.07	-0.63	0.547499	0.6693	-7.03
253606_at	putative protein component of anili	---	AT4G30530	-1.11	-0.15	-0.63	0.547531	0.669302	-7.03
262975_at	zinc finger protein, putative similar	STH2	AT1G75540	-1.07	-0.10	-0.63	0.547617	0.669355	-7.03
254823_at	putative protein predicted protein	---	AT4G12580	1.04	0.06	0.63	0.547633	0.669355	-7.03
267018_at	unknown protein	SVR1	AT2G39140	1.09	0.12	0.63	0.547786	0.669507	-7.03
251612_at	putative protein hypothetical protei	---	AT3G57950	-1.05	-0.07	-0.63	0.547852	0.669552	-7.03
246616_at	aspartyl protease-like	---	AT5G36260	-1.08	-0.12	-0.63	0.547959	0.669647	-7.03
262139_at	mutator-like transposase, putative	AT1G5261	---	1.04	0.06	0.63	0.548093	0.669775	-7.03
267345_at	unknown protein ; supported by cD	---	AT2G44240	-1.17	-0.22	-0.63	0.548401	0.670086	-7.03
261995_at	unknown protein similar to N-termin	---	AT1G33850	-1.04	-0.06	-0.63	0.548407	0.670086	-7.03
249394_at	putative protein predicted protein, /	---	AT5G40180	-1.04	-0.06	-0.63	0.548572	0.670251	-7.03
256788_at	cytochrome P450, putative similar	CYP90D1	AT3G13730	-1.23	-0.29	-0.63	0.548692	0.670362	-7.03
249352_at	putative transcription factor MYB22	MYB22	AT5G40430	-1.04	-0.06	-0.63	0.549066	0.670716	-7.03
248024_at	putative protein contains similarity t	---	AT5G55840	1.06	0.09	0.63	0.549067	0.670716	-7.03
264559_at	unknown protein similar to hypothet	---	AT1G09610	-1.04	-0.06	-0.63	0.549087	0.670716	-7.03
266249_at	hypothetical protein predicted by ge	---	AT2G27630	1.04	0.06	0.63	0.549099	0.670716	-7.03
245328_at	Expressed protein ; supported by fu	---	AT4G14465	-1.05	-0.07	-0.63	0.549156	0.67075	-7.03
248446_at	putative protein similar to unknown	---	AT5G51140	-1.05	-0.07	-0.63	0.54926	0.670841	-7.03
265851_at	hypothetical protein predicted by ge	---	AT2G42340	-1.05	-0.07	-0.63	0.549344	0.670907	-7.03
261842_at	hypothetical protein contains simila	WAKL5	AT1G16160	-1.07	-0.09	-0.63	0.549414	0.670957	-7.03
264005_at	unknown protein ; supported by cD	AGP2	AT2G22470	1.32	0.40	0.63	0.549488	0.670996	-7.03
251999_at	hypothetical protein teichoic acid b	---	AT3G52700	-1.05	-0.06	-0.63	0.549532	0.670996	-7.03
254287_at	putative protein similaritry to hypotl	---	AT4G22960	-1.05	-0.07	-0.63	0.549554	0.670996	-7.03
256201_at	hypothetical protein predicted by ge	---	AT1G58230	-1.05	-0.07	-0.63	0.549564	0.670996	-7.03
260771_at	serine/threonine protein kinase, pu	WNK7	AT1G49160	-1.10	-0.13	-0.63	0.549746	0.671142	-7.03
255453_at	hypothetical protein similar to A. th	---	AT4G02900	1.07	0.10	0.63	0.549765	0.671142	-7.03
250951_at	putative protein	---	AT5G03550	-1.13	-0.18	-0.63	0.549772	0.671142	-7.03
260066_at	putative lipase/acylhydrolase contai	---	AT1G73610	-1.13	-0.17	-0.63	0.549831	0.671151	-7.03
267283_at	Mutator-like transposase similar to	---	---	1.04	0.06	0.63	0.549885	0.671151	-7.03
259869_at	putative heat shock protein predicte	---	AT1G76770	-1.05	-0.07	-0.63	0.549912	0.671151	-7.03

250040_at	putative protein predicted proteins,	---	AT5G18390	1.04	0.06	0.63	0.549919	0.671151	-7.03
250560_at	replication factor A - like protein rep	RPA70B	AT5G08020	-1.10	-0.14	-0.63	0.549926	0.671151	-7.03
259728_at	putative coatomer zeta subunit simi	---	AT1G60970	-1.05	-0.06	-0.63	0.550158	0.671398	-7.03
249744_at	beta-glucosidase	BGLU32	AT5G24550	-1.07	-0.10	-0.63	0.55036	0.671541	-7.03
259542_at	Expressed protein ; supported by fu	---	AT1G20575	-1.05	-0.07	-0.63	0.550376	0.671541	-7.03
261215_at	subtilase, putative similar to subtila	---	AT1G32970	-1.05	-0.06	-0.63	0.55041	0.671541	-7.03
265392_at	lipoic acid synthase (LIP1) ; suppo	LIP1	AT2G20860	1.05	0.06	0.63	0.550425	0.671541	-7.03
256147_at	hypothetical protein predicted by ge	---	AT1G55080	1.07	0.09	0.63	0.550425	0.671541	-7.03
263235_at	serine/threonine protein phosphata	PP2A-2	AT1G10430	1.05	0.08	0.63	0.550452	0.671541	-7.03
265232_s_a	hypothetical protein	---	AT2G07715	1.06	0.08	0.63	0.550514	0.671559	-7.03
260859_at	serine carboxypeptidase II, putative	scpl44	AT1G43780	-1.07	-0.09	-0.63	0.550543	0.671559	-7.03
252098_at	putative protein several hypothetica	---	AT3G51330	1.19	0.25	0.63	0.550555	0.671559	-7.03
267002_s_a	putative photosystem II type I chlor	LHB1B1	AT2G34420	1.04	0.06	0.63	0.550591	0.671568	-7.03
253582_at	Expressed protein ;supported by cD	---	AT4G30670	1.08	0.11	0.63	0.550701	0.671666	-7.03
263642_at	putative fimbrin	---	AT2G04750	-1.05	-0.07	-0.63	0.55146	0.672556	-7.03
267117_at	unknown protein	---	AT2G32560	-1.04	-0.06	-0.63	0.551514	0.672585	-7.03
248296_at	protochlorophyllide reductase; oxid	---	AT5G53090	1.07	0.09	0.63	0.55155	0.672585	-7.03
255164_at	hypothetical protein	---	---	-1.05	-0.06	-0.63	0.551572	0.672585	-7.03
245009_at	ribosomal protein S4	---	---	1.04	0.06	0.63	0.551632	0.672621	-7.03
263616_at	unknown protein	---	AT2G04680	1.06	0.08	0.63	0.551685	0.67265	-7.03
253455_at	putative protein	---	AT4G32020	-1.09	-0.13	-0.63	0.551727	0.672664	-7.03
248518_at	putative protein similar to unknown	---	AT5G50560	-1.08	-0.11	-0.63	0.551755	0.672664	-7.03
248697_at	putative protein contains similarity t	---	AT5G48370	1.10	0.13	0.63	0.551875	0.672759	-7.03
250448_at	putative protein lignostilbene-alpha	---	AT5G10820	-1.09	-0.13	-0.63	0.551892	0.672759	-7.03
249329_at	putative protein similar to unknown	---	AT5G40960	1.07	0.09	0.63	0.551995	0.672848	-7.03
255993_at	hypothetical protein contains simila	---	AT1G29770	-1.04	-0.06	-0.63	0.552087	0.672924	-7.03
266145_at	putative TNP2-like transposon prote	---	---	1.04	0.06	0.63	0.55238	0.673245	-7.03
246218_at	RUB1-conjugating enzyme RCE1,	RCE1	AT4G36800	1.08	0.11	0.63	0.55243	0.67327	-7.03
255838_at	unknown protein	---	AT2G33490	-1.05	-0.07	-0.62	0.552817	0.673707	-7.03
259870_at	putative heat shock protein predicte	---	AT1G76780	1.04	0.06	0.62	0.552877	0.673739	-7.03
258197_at	hypothetical protein predicted by ge	ATBRXL2	AT3G14000	-1.06	-0.08	-0.62	0.552903	0.673739	-7.03
259187_at	putative transcription factor similar t	AtMYB57	AT3G01530	-1.07	-0.09	-0.62	0.552943	0.673751	-7.03
249723_at	putative protein similar to unknown	---	AT5G35430	1.04	0.06	0.62	0.552993	0.673777	-7.03
259548_at	hypothetical protein similar to ripeni	MLP165	AT1G35260	1.13	0.17	0.62	0.553093	0.673862	-7.03
261189_at	hypothetical protein contains simila	NACA5	AT1G33040	-1.05	-0.07	-0.62	0.553159	0.673907	-7.03

246942_at	anion exchanger-like protein chlori	---	AT5G25430	-1.05	-0.08	-0.62	0.553353	0.674108	-7.03
251166_at	heat shock transcription factor-like	AT-HSFA7I	AT3G63350	-1.05	-0.07	-0.62	0.553484	0.674231	-7.03
258892_at	unknown protein	---	AT3G05670	-1.05	-0.07	-0.62	0.553572	0.674302	-7.03
265406_at	En/Spm-like transposon protein rela	---	---	-1.04	-0.05	-0.62	0.55367	0.674356	-7.03
250391_at	putative protein predicted proteins,	---	---	-1.05	-0.08	-0.62	0.553692	0.674356	-7.03
247798_at	subtilisin-like serine protease conta	---	AT5G58830	-1.04	-0.06	-0.62	0.553705	0.674356	-7.03
249079_at	putative protein contains similarity t	---	AT5G43930	1.07	0.10	0.62	0.554141	0.67485	-7.03
249502_s_a	expansin-like protein expansin - Pr	ATEXPA23	AT5G39280	-1.06	-0.08	-0.62	0.554183	0.674866	-7.03
245622_at	A6 anther-specific protein	MEE48	AT4G14080	-1.06	-0.08	-0.62	0.554341	0.675022	-7.03
247606_at	RNA helicase	---	AT5G61000	-1.15	-0.20	-0.62	0.554391	0.675047	-7.03
263578_at	F-box protein family, AtFBL10 cont	---	AT2G17020	-1.05	-0.07	-0.62	0.55463	0.675296	-7.03
266757_at	unknown protein	---	AT2G46940	-1.09	-0.13	-0.62	0.554658	0.675296	-7.03
245380_at	hypothetical protein	---	AT4G17760	-1.07	-0.10	-0.62	0.554704	0.675296	-7.03
261866_at	scarecrow-like 3 identical to GB:AA	SCL3	AT1G50420	1.22	0.29	0.62	0.554713	0.675296	-7.03
265527_at	putative Athila retroelement ORF1 p	---	---	1.04	0.06	0.62	0.555128	0.675764	-7.03
266517_at	glycine decarboxylase complex H-p	---	AT2G35120	1.12	0.16	0.62	0.555196	0.675811	-7.03
257695_at	hypothetical protein contains Pfam	HUA1	AT3G12680	1.05	0.08	0.62	0.555269	0.675864	-7.03
254031_at	putative protein other hypothetical p	---	AT4G25920	-1.05	-0.06	-0.62	0.555455	0.676054	-7.04
245408_at	putative protein	---	AT4G17180	-1.06	-0.09	-0.62	0.555598	0.67617	-7.04
249605_at	putative protein predicted protein, A	---	AT5G37240	1.06	0.08	0.62	0.55561	0.67617	-7.04
263060_s_a	hypothetical protein	---	AT2G07679	-1.07	-0.10	-0.62	0.555686	0.676227	-7.04
249096_at	putative protein similar to unknown	---	AT5G43910	-1.10	-0.13	-0.62	0.556	0.676538	-7.04
263187_at	athila ORF 1, putative similar to Atl	---	---	1.04	0.05	0.62	0.556001	0.676538	-7.04
255393_at	hypothetical protein	---	---	1.04	0.05	0.62	0.556051	0.676563	-7.04
245185_at	F12A21.11 similar to T-Complex pr	---	AT1G67760	1.07	0.09	0.62	0.556272	0.676795	-7.04
265424_at	putative sugar transporter	---	AT2G20780	1.06	0.08	0.62	0.556319	0.676817	-7.04
247680_s_a	glycine-rich protein - like glycine-ric	---	AT1G61210	1.05	0.07	0.62	0.556571	0.676991	-7.04
262430_s_a	unknown protein	---	AT1G47550	1.05	0.07	0.62	0.556578	0.676991	-7.04
249190_at	unknown protein ;supported by full-	BKI1	AT5G42750	1.06	0.08	0.62	0.556596	0.676991	-7.04
254918_at	putative protein phosphatase like p	SGT1B	AT4G11260	1.06	0.08	0.62	0.556604	0.676991	-7.04
258788_at	unknown protein ;supported by full-	---	AT3G11780	1.05	0.08	0.62	0.55661	0.676991	-7.04
255616_at	hypothetical protein	---	AT4G01290	-1.08	-0.11	-0.62	0.556843	0.677238	-7.04
247700_at	RNA-binding protein - like cold-indu	---	AT5G59860	-1.04	-0.06	-0.62	0.557045	0.677447	-7.04
261185_at	cytochrome p450, putative similar t	CYP94D1	AT1G34540	-1.05	-0.06	-0.62	0.557211	0.677612	-7.04
263511_at	En/Spm-like transposon protein rela	---	---	-1.05	-0.07	-0.62	0.557405	0.677812	-7.04

263850_at	hypothetical protein predicted by ge	---	AT2G04480	-1.08	-0.12	-0.62	0.557443	0.677823	-7.04
255348_at	hypothetical protein	---	AT4G03820	1.05	0.08	0.62	0.557561	0.677931	-7.04
261345_at	hypothetical protein predicted by ge	DTA4	AT1G79760	-1.06	-0.08	-0.62	0.557638	0.677987	-7.04
258095_at	dual-specificity protein phosphatase	---	AT3G23610	-1.06	-0.08	-0.62	0.557752	0.67809	-7.04
256084_at	hypothetical protein predicted by ge	---	AT1G20750	1.06	0.08	0.62	0.557811	0.678126	-7.04
251731_at	manganese superoxide dismutase	---	AT3G56350	-1.06	-0.09	-0.62	0.558057	0.678372	-7.04
261937_at	peptide transporter, putative simila	---	AT1G22570	-1.12	-0.17	-0.62	0.558073	0.678372	-7.04
258971_at	unknown protein similar to uridylyl	ACR6	AT3G01990	1.13	0.18	0.62	0.558208	0.6785	-7.04
252326_at	putative protein ferripyochelin bind	GAMMA CA	AT3G48680	1.05	0.08	0.62	0.558281	0.678552	-7.04
264979_s_a	disease resistance protein, putative	---	AT1G27170	-1.06	-0.09	-0.62	0.558341	0.678589	-7.04
262927_at	hypothetical protein shares similarit	---	AT1G65810	-1.05	-0.07	-0.62	0.558455	0.678691	-7.04
257443_at	hypothetical protein predicted by ge	---	AT2G22050	-1.05	-0.07	-0.62	0.558564	0.678727	-7.04
260625_at	storage protein, putative similar to	MOM	AT1G08060	1.04	0.06	0.62	0.558584	0.678727	-7.04
266826_at	putative amino acid acetyltransferas	---	AT2G22910	-1.11	-0.15	-0.62	0.558586	0.678727	-7.04
247035_at	putative protein similar to unknown	ALC	AT5G67110	-1.05	-0.06	-0.62	0.558603	0.678727	-7.04
250335_at	lysophospholipase - like protein lys	---	AT5G11650	-1.09	-0.12	-0.62	0.558656	0.678755	-7.04
247424_at	LIM7 - like protein LIM7, Lilium lon	AtVEX1	AT5G62850	-1.05	-0.07	-0.62	0.558712	0.678786	-7.04
258031_s_a	hypothetical protein similar to hypot	---	AT3G27480	-1.06	-0.09	-0.61	0.558899	0.678977	-7.04
260285_at	putative 3-isopropylmalate dehydro	---	AT1G80560	1.06	0.09	0.61	0.55903	0.6791	-7.04
256863_at	CCHC-type zinc finger protein, put	---	AT3G24070	-1.04	-0.06	-0.61	0.559099	0.679149	-7.04
253910_at	putative receptor like kinase recept	---	AT4G27290	1.04	0.06	0.61	0.559132	0.679152	-7.04
259052_at	unknown protein	PEX19-1	AT3G03490	1.05	0.07	0.61	0.559251	0.67926	-7.04
261477_at	unknown protein	---	AT1G14310	-1.06	-0.09	-0.61	0.559291	0.679274	-7.04
262858_at	major latex protein type3 identical t	---	AT1G14940	-1.05	-0.07	-0.61	0.559367	0.679329	-7.04
266491_at	putative retroelement pol polyprotei	---	---	-1.05	-0.06	-0.61	0.559399	0.679332	-7.04
254550_at	Fe(II) transport protein ;supported	IRT1	AT4G19690	1.04	0.06	0.61	0.559601	0.679532	-7.04
255797_at	putative steroid dehydrogenase ; s	---	AT2G33630	1.08	0.11	0.61	0.559623	0.679532	-7.04
265673_at	unknown protein ;supported by full	---	AT2G32090	-1.06	-0.09	-0.61	0.559726	0.67962	-7.04
259842_at	phosphoethanolamine N-methyltra	CPuORF32	AT1G73600	1.43	0.52	0.61	0.560164	0.680117	-7.04
253526_at	putative zinc finger protein hypothe	---	AT4G31420	-1.05	-0.07	-0.61	0.560195	0.680117	-7.04
249867_at	2-isopropylmalate synthase-like pro	IMS2	AT5G23020	-1.27	-0.35	-0.61	0.560235	0.68013	-7.04
257355_at	hypothetical protein predicted by ge	---	AT2G38150	1.05	0.07	0.61	0.560293	0.680164	-7.04
265290_at	putative anthocyanidin-3-glucoside	---	AT2G22590	-1.04	-0.06	-0.61	0.560428	0.680265	-7.04
261773_at	hypothetical protein predicted by ge	---	AT1G76250	-1.07	-0.10	-0.61	0.560452	0.680265	-7.04
259228_at	unknown protein similar to hypothet	---	AT3G07720	-1.06	-0.09	-0.61	0.560466	0.680265	-7.04

250771_at	NBS/LRR disease resistance protei	---	AT5G05400	-1.05	-0.07	-0.61	0.560532	0.680308	-7.04
257812_at	hypothetical protein	---	AT3G25090	-1.06	-0.08	-0.61	0.56056	0.680308	-7.04
256285_at	hypothetical protein predicted by ge	---	AT3G12510	1.07	0.10	0.61	0.5606	0.68032	-7.04
248588_at	unknown protein ; supported by cD	---	AT5G49540	-1.05	-0.06	-0.61	0.560663	0.680359	-7.04
255256_at	see GB:AC003952 similar to a fami	---	AT4G05080	1.06	0.08	0.61	0.560939	0.680621	-7.04
265345_at	copia-like retroelement pol polyprot	---	AT2G22680	-1.05	-0.07	-0.61	0.560946	0.680621	-7.04
260452_at	putative SRF-type transcription fact	---	AT1G72350	-1.08	-0.11	-0.61	0.560968	0.680621	-7.04
261901_at	J8-like protein similar to DnaJ homo	J8	AT1G80920	1.05	0.07	0.61	0.561354	0.681053	-7.04
255431_at	putative C-type U1 snRNP similar t	---	AT4G03120	-1.04	-0.05	-0.61	0.561452	0.681106	-7.04
259066_at	hypothetical protein predicted by ge	---	AT3G07530	-1.07	-0.10	-0.61	0.561457	0.681106	-7.04
252344_s_a	putative protein	---	AT3G44160	-1.05	-0.07	-0.61	0.561545	0.681176	-7.04
248320_at	putative protein similar to unknown	---	AT5G52720	-1.06	-0.08	-0.61	0.561588	0.681193	-7.04
260296_at	putative disease resistance protein	---	AT1G63750	-1.18	-0.24	-0.61	0.561665	0.68124	-7.04
262732_at	putative protein kinase similar to gb	---	AT1G16440	-1.06	-0.08	-0.61	0.561712	0.68124	-7.04
266324_at	putative rac GTPase activating prot	---	AT2G46710	-1.19	-0.25	-0.61	0.561734	0.68124	-7.04
262160_at	hypothetical protein predicted by ge	---	AT1G52590	1.09	0.13	0.61	0.561747	0.68124	-7.04
262401_at	small GTP-binding protein, putative	RABG3E	AT1G49300	1.04	0.06	0.61	0.56182	0.681293	-7.04
250436_at	RNA binding protein - like rna bindi	---	AT5G10350	-1.05	-0.08	-0.61	0.561922	0.681378	-7.04
253104_at	thaumatin-like protein thaumatin-lik	---	AT4G36010	1.18	0.24	0.61	0.56195	0.681378	-7.04
257013_at	hypothetical protein contains Pfam	---	AT3G26920	-1.05	-0.07	-0.61	0.562119	0.681547	-7.04
261214_at	Mutator-like protein similar to many	---	---	-1.07	-0.09	-0.61	0.562194	0.681601	-7.04
247422_at	putative protein	PEX14	AT5G62810	-1.05	-0.07	-0.61	0.562226	0.681604	-7.04
262958_at	water stress-induced protein, putat	---	AT1G54410	-1.06	-0.08	-0.61	0.56238	0.681754	-7.04
257145_at	esterase, putative similar to estera	---	AT3G27320	-1.07	-0.09	-0.61	0.562617	0.681975	-7.04
250003_at	hypothetical protein predicted prote	---	AT5G18710	-1.05	-0.07	-0.61	0.562622	0.681975	-7.04
265443_at	beta-expansin ;supported by full-le	ATEXPB1	AT2G20750	-1.07	-0.09	-0.61	0.562793	0.682147	-7.04
245836_at	hypothetical protein similar to hypot	---	---	-1.04	-0.06	-0.61	0.562966	0.682319	-7.04
259028_at	putative C2H2-type zinc finger prot	TAC1	AT3G09290	1.06	0.08	0.61	0.563072	0.682412	-7.04
255206_at	putative transposon protein	---	---	1.04	0.05	0.61	0.563129	0.682412	-7.04
248732_at	xyloglucan endo-1,4-beta-D-glucar	XTH20	AT5G48070	-1.06	-0.09	-0.61	0.563132	0.682412	-7.04
263805_at	unknown protein ; supported by cD	---	AT2G40400	1.04	0.06	0.61	0.563279	0.682554	-7.04
263715_at	unknown protein ; supported by cD	GPRI1	AT2G20570	1.05	0.07	0.61	0.563373	0.682631	-7.04
256069_at	hypothetical protein predicted by ge	AFP2	AT1G13740	-1.09	-0.13	-0.61	0.5636	0.682848	-7.04
252689_at	putative protein predicted proteins,	---	AT3G44030	-1.05	-0.07	-0.61	0.563612	0.682848	-7.04
249881_at	cytochrome P450-like protein	CYP86B1	AT5G23190	-1.04	-0.06	-0.61	0.563709	0.682913	-7.04

245878_at	hypothetical protein contains simila	---	AT1G26190	-1.06	-0.08	-0.61	0.563754	0.682913	-7.04
259354_at	unknown protein	---	AT3G05220	-1.08	-0.11	-0.61	0.563755	0.682913	-7.04
256968_at	unknown protein	NADK1	AT3G21070	1.26	0.34	0.61	0.563924	0.683082	-7.04
248622_at	xylosidase	---	AT5G01980	1.13	0.17	0.61	0.564361	0.683574	-7.04
246703_at	mitogen activated protein kinase -	WNK9	AT5G28080	-1.16	-0.22	-0.61	0.564459	0.683657	-7.04
256351_at	NPK1-related protein kinase, putat	ANP2	AT1G54960	-1.04	-0.06	-0.61	0.564506	0.683677	-7.04
260657_at	wall-associated kinase 2, putative s	---	AT1G19390	-1.05	-0.08	-0.61	0.564556	0.683679	-7.04
258163_at	aldose 1-epimerase, putative simila	---	AT3G17940	1.05	0.07	0.61	0.564586	0.683679	-7.04
264273_s_a	hypothetical protein contains simila	---	AT1G60300	-1.07	-0.10	-0.61	0.564597	0.683679	-7.04
258693_at	unknown protein	---	AT3G08650	-1.04	-0.06	-0.61	0.564978	0.684086	-7.05
258188_at	unknown protein ;supported by full	---	AT3G17800	1.06	0.09	0.61	0.564993	0.684086	-7.05
250750_at	glucuronosyl transferase-like protei	UGT76C2	AT5G05860	-1.05	-0.07	-0.60	0.565081	0.684152	-7.05
266200_at	hypothetical protein predicted by ge	---	AT2G38920	-1.08	-0.11	-0.60	0.565108	0.684152	-7.05
252898_at	cytochrome P450 -like protein simi	CYP96A11	AT4G39500	-1.04	-0.06	-0.60	0.565181	0.684176	-7.05
267483_at	unknown protein ;supported by full	UTR1	AT2G02810	-1.18	-0.24	-0.60	0.565188	0.684176	-7.05
258103_at	hypothetical protein contains Pfam	IPT7	AT3G23630	1.06	0.09	0.60	0.565245	0.684209	-7.05
247493_at	copine - like protein copine I, Homo	BON1	AT5G61900	-1.10	-0.14	-0.60	0.565351	0.684265	-7.05
248979_at	putative protein contains similarity t	AtPP2-A6	AT5G45080	-1.05	-0.07	-0.60	0.565351	0.684265	-7.05
258112_at	putative cytochrome P450 similar to	CYP72A10	AT3G14640	-1.05	-0.07	-0.60	0.565386	0.68427	-7.05
253902_at	NWMU4 - 2S albumin 4 precursor	---	AT4G27170	1.04	0.06	0.60	0.565429	0.684287	-7.05
263461_at	putative protein kinase contains a p	---	AT2G31800	1.06	0.08	0.60	0.565532	0.684359	-7.05
254903_at	H+-transporting ATPase chain E, v	TUF	AT4G11150	-1.06	-0.08	-0.60	0.565549	0.684359	-7.05
249311_at	disease resistance protein-like	---	AT5G41540	-1.06	-0.08	-0.60	0.565646	0.684441	-7.05
265684_at	unknown protein	---	AT2G24410	1.04	0.05	0.60	0.56572	0.684493	-7.05
244977_at	cytochrome b/f	---	---	-1.10	-0.14	-0.60	0.565881	0.684652	-7.05
251523_at	putative protein several hypothetica	---	AT3G58975	1.05	0.07	0.60	0.56598	0.684736	-7.05
253765_at	hypothetical protein ;supported by	---	AT4G28740	1.09	0.13	0.60	0.56614	0.684892	-7.05
250044_at	disease resistance protein RPP1-W	---	AT5G17680	1.07	0.10	0.60	0.566291	0.685039	-7.05
263342_at	putative helicase	---	---	-1.04	-0.05	-0.60	0.566551	0.685317	-7.05
257329_at	hypothetical protein	---	---	-1.08	-0.11	-0.60	0.566619	0.685353	-7.05
254988_at	putative protein Ran GTPase activa	GTC2	AT4G10670	-1.05	-0.07	-0.60	0.56664	0.685353	-7.05
257961_at	unknown protein	---	AT3G19780	-1.05	-0.06	-0.60	0.566828	0.685544	-7.05
246321_at	unknown protein	---	AT1G16640	1.05	0.07	0.60	0.566943	0.685646	-7.05
264618_at	hypothetical protein predicted by ge	---	AT2G17680	-1.04	-0.06	-0.60	0.567064	0.685735	-7.05
248817_at	putative protein strong similarity to	---	AT5G47020	-1.06	-0.08	-0.60	0.567077	0.685735	-7.05

247365_at	putative protein similar to unknown	---	AT5G63220	1.06	0.08	0.60	0.567128	0.685761	-7.05
254587_at	resistance protein RPP5 - like dow	---	AT4G19520	-1.06	-0.08	-0.60	0.56718	0.685787	-7.05
245819_at	cauliflower identical to CAULIFLOW	CAL	AT1G26310	-1.05	-0.07	-0.60	0.567261	0.685849	-7.05
256540_at	polyprotein, putative similar to poly	---	---	1.04	0.06	0.60	0.567521	0.686127	-7.05
250940_at	putative protein	---	AT5G03310	-1.04	-0.06	-0.60	0.567573	0.686153	-7.05
263463_at	putative ARI-like RING zinc finger p	---	AT2G31770	-1.04	-0.06	-0.60	0.567632	0.686188	-7.05
246903_at	putative protein	---	AT5G25750	-1.05	-0.08	-0.60	0.567702	0.686237	-7.05
265171_at	hypothetical protein	---	AT1G23790	-1.04	-0.05	-0.60	0.567736	0.686241	-7.05
254625_at	Expressed protein ; supported by fu	SNI1	AT4G18470	-1.06	-0.08	-0.60	0.567983	0.686503	-7.05
254690_at	N-acetylornithine deacetylase-like	---	AT4G17830	1.04	0.05	0.60	0.568232	0.686768	-7.05
256217_at	hypothetical protein predicted by ge	---	AT1G56320	1.10	0.14	0.60	0.568427	0.686967	-7.05
253586_s_a	putative protein hypothetical protei	---	AT4G30710	1.08	0.12	0.60	0.568556	0.687087	-7.05
255073_at	beta-1,3-glucanase-like protein pro	---	AT4G09090	-1.04	-0.06	-0.60	0.568644	0.687155	-7.05
263012_at	homeotic protein, putative similar t	KNAT6	AT1G23380	1.04	0.05	0.60	0.568694	0.687155	-7.05
246795_at	putative protein	---	AT5G27020	-1.05	-0.07	-0.60	0.568705	0.687155	-7.05
264565_at	hypothetical protein Similar to hypo	---	AT1G05280	-1.06	-0.09	-0.60	0.568733	0.687155	-7.05
262554_at	hypothetical protein similar to hypot	---	AT1G31380	-1.04	-0.06	-0.60	0.568809	0.687203	-7.05
253325_at	Expressed protein ; supported by fu	---	AT4G33925	-1.10	-0.14	-0.60	0.568833	0.687203	-7.05
258579_s_a	germin-like protein contains Pfam p	---	AT3G04180	-1.04	-0.06	-0.60	0.56889	0.687211	-7.05
260725_at	Expressed protein ; supported by fu	---	AT1G48170	1.05	0.07	0.60	0.5689	0.687211	-7.05
264119_at	myb-related protein, putative simila	MYB63	AT1G79180	-1.04	-0.06	-0.60	0.568993	0.687284	-7.05
258066_at	hypothetical protein predicted by ge	---	AT3G25970	-1.04	-0.05	-0.60	0.569021	0.687284	-7.05
250768_at	signal recognition particle receptor	---	AT5G05670	-1.07	-0.10	-0.60	0.569221	0.68749	-7.05
265267_at	hypothetical protein predicted by ge	---	AT2G42920	1.06	0.09	0.60	0.569257	0.687496	-7.05
251748_at	putative protein predicted protein,	---	AT3G55680	-1.06	-0.09	-0.60	0.569391	0.687622	-7.05
248250_at	cyclic nucleotide-regulated ion char	CNGC1	AT5G53130	1.10	0.14	0.60	0.569476	0.687689	-7.05
252585_s_a	putative protein UbcH 7-binding pro	---	AT3G45570	1.04	0.05	0.60	0.569612	0.687817	-7.05
260036_at	putative protein kinase Pfam HMM	STN7	AT1G68830	1.06	0.08	0.60	0.569684	0.687866	-7.05
246857_at	putative protein	---	AT5G25920	-1.05	-0.07	-0.60	0.569798	0.687968	-7.05
264646_at	hypothetical protein Similar to Hom	BON3	AT1G08860	-1.05	-0.07	-0.60	0.56985	0.687971	-7.05
256729_at	hypothetical protein predicted by ge	---	AT3G25680	1.05	0.07	0.60	0.569902	0.687971	-7.05
258785_at	unknown protein	---	---	-1.06	-0.08	-0.60	0.569943	0.687971	-7.05
251483_at	putative protein hypothetical protei	---	AT3G59650	1.06	0.08	0.60	0.56997	0.687971	-7.05
246380_at	cytochrome P450, putative similar	CYP96A15	AT1G57750	-1.07	-0.10	-0.60	0.569971	0.687971	-7.05
252982_at	Histone deacetylase ; supported by	HD1	AT4G38130	1.05	0.07	0.60	0.569981	0.687971	-7.05

247991_at	expansin ;supported by full-length (	ATEXPA14	AT5G56320	-1.04	-0.06	-0.60	0.570089	0.688065	-7.05
252745_at	putative protein Sh3yl1 mRNA, Mu	---	AT3G43230	1.05	0.07	0.60	0.570124	0.688071	-7.05
258768_at	hypothetical protein predicted by ge	---	AT3G10880	1.04	0.06	0.60	0.570395	0.688361	-7.05
248286_at	putative protein similar to unknown	---	AT5G52870	1.12	0.16	0.60	0.570537	0.688492	-7.05
248679_at	unknown protein ;supported by full-	---	AT5G48830	-1.08	-0.10	-0.60	0.570567	0.688492	-7.05
266935_at	F-box protein LKP2/ADO2, AtFBX2	LKP2	AT2G18915	1.05	0.06	0.60	0.570594	0.688492	-7.05
254379_at	putative protein calmodulin-binding	---	AT4G21820	-1.04	-0.05	-0.60	0.570685	0.688565	-7.05
256044_at	protein phosphatase 2C, putative s	---	AT1G07160	1.30	0.38	0.60	0.571046	0.688965	-7.05
254757_at	putative protein other putative or hy	ROPGEF9	AT4G13240	-1.05	-0.07	-0.60	0.571079	0.688967	-7.05
261474_at	anionic peroxidase, putative simila	---	AT1G14540	1.32	0.40	0.60	0.571145	0.689011	-7.05
263617_at	putative retroelement pol polyprotei	---	---	-1.06	-0.08	-0.60	0.571259	0.689112	-7.05
255827_at	unknown protein ; supported by cD	---	AT2G40600	-1.06	-0.08	-0.59	0.571329	0.68916	-7.05
261738_s_a	hypothetical protein identical to hyp	---	AT1G47813	1.08	0.11	0.59	0.571463	0.689285	-7.05
266577_at	predicted protein	---	AT2G23945	1.05	0.07	0.59	0.571712	0.68954	-7.05
265520_at	hypothetical protein predicted by ge	---	AT2G06020	-1.06	-0.09	-0.59	0.571735	0.68954	-7.05
262831_at	cytochrome B561, putative similar	---	AT1G14730	-1.09	-0.12	-0.59	0.571826	0.689613	-7.05
249593_at	putative protein SIAH1 protein, Bra	---	AT5G37900	1.05	0.06	0.59	0.571874	0.689635	-7.05
256637_at	unknown protein similar to membra	---	AT3G12030	1.07	0.10	0.59	0.572077	0.689844	-7.05
262836_at	hypothetical protein predicted by ge	---	AT1G14680	-1.04	-0.06	-0.59	0.572182	0.689934	-7.05
265070_at	branched-chain alpha-keto acid dec	BCDH BET	AT1G55510	1.12	0.16	0.59	0.572489	0.690267	-7.05
262012_s_a	integral membrane protein, putative	---	AT1G35625	1.05	0.06	0.59	0.572576	0.690336	-7.05
256038_at	hypothetical protein similar to polyg	---	AT1G19170	1.06	0.08	0.59	0.572697	0.690444	-7.05
252159_at	hypothetical protein	---	AT3G50540	-1.05	-0.06	-0.59	0.572835	0.690575	-7.05
265727_at	putative DNA topoisomerase III bet	---	AT2G32000	-1.05	-0.07	-0.59	0.57294	0.690664	-7.05
255309_at	hypothetical protein	SFR6	AT4G04920	1.04	0.06	0.59	0.573027	0.690733	-7.05
258407_at	unknown protein similar to unknown	---	AT3G17620	-1.07	-0.10	-0.59	0.573525	0.691297	-7.05
265402_at	hypothetical protein predicted by ge	---	AT2G10950	-1.05	-0.07	-0.59	0.573628	0.691384	-7.05
262042_at	polygalacturonase, putative similar	---	AT1G80140	-1.05	-0.07	-0.59	0.573704	0.69144	-7.05
255409_at	NDX1 homeobox protein homolog	---	AT4G03090	1.04	0.05	0.59	0.573827	0.691523	-7.05
252316_at	putative protein PrMC3 - Pinus rad	ATCXE13	AT3G48700	-1.05	-0.06	-0.59	0.573855	0.691523	-7.05
256781_at	dirigent protein, putative similar to (	---	AT3G13650	1.42	0.50	0.59	0.573864	0.691523	-7.05
254712_at	hypothetical protein	---	AT4G18080	-1.04	-0.05	-0.59	0.573962	0.691605	-7.05
255182_at	hypothetical protein	---	---	1.04	0.06	0.59	0.574171	0.691788	-7.05
259917_at	hypothetical protein predicted by ge	---	AT1G72580	1.05	0.07	0.59	0.574175	0.691788	-7.05
258774_at	putative alpha-L-arabinofuranosidas	ASD1	AT3G10740	1.15	0.20	0.59	0.574329	0.691933	-7.05

258195_at	myb protein(myb26) contains myb D	ATMYB26	AT3G13890	-1.05	-0.07	-0.59	0.574356	0.691933	-7.05
263798_at	putative ubiquitin carboxyl terminal	UBP19	AT2G24640	-1.04	-0.06	-0.59	0.574453	0.692013	-7.05
252442_at	dUTP pyrophosphatase-like protein	---	AT3G46940	-1.09	-0.13	-0.59	0.574583	0.692134	-7.06
252445_at	beta-D-glucan exohydrolase - like p	---	AT3G47000	-1.05	-0.07	-0.59	0.574669	0.692172	-7.06
250705_at	diadenosine 5,5-P1,P4-tetraphospl	ATNUDX27	AT5G06340	1.06	0.08	0.59	0.574676	0.692172	-7.06
264207_at	unknown protein strong similarity to	---	AT1G22750	1.06	0.09	0.59	0.574747	0.692221	-7.06
266479_at	unknown protein ; supported by cD	LSH3	AT2G31160	1.18	0.23	0.59	0.574962	0.692444	-7.06
257630_at	cytochrome P450, putative similar	CYP71B16	AT3G26150	-1.04	-0.06	-0.59	0.575018	0.692475	-7.06
257095_at	unknown protein ; supported by cD	ATPDIL5-3	AT3G20560	-1.06	-0.09	-0.59	0.575097	0.692534	-7.06
247872_at	putative protein similar to unknown	---	AT5G57670	-1.07	-0.10	-0.59	0.575379	0.692837	-7.06
253290_at	putative protein predicted protein F	---	AT4G34330	-1.04	-0.06	-0.59	0.575573	0.693033	-7.06
254378_at	putative protein NADH oxidoreduct	DER2.1	AT4G21810	1.09	0.13	0.59	0.575993	0.693502	-7.06
260621_at	carbonic anhydrase, putative	ACA5	AT1G08065	-1.05	-0.07	-0.59	0.576107	0.693603	-7.06
263005_at	hypothetical protein predicted by ge	---	AT1G54540	-1.08	-0.12	-0.59	0.576456	0.693987	-7.06
254498_at	membrane-associated salt-inducibl	EMB1025	AT4G20090	1.07	0.10	0.59	0.576717	0.694211	-7.06
260737_at	receptor-like serine threonine kinas	---	AT1G17540	1.06	0.08	0.59	0.576721	0.694211	-7.06
262022_at	hypothetical protein predicted by ge	---	AT1G35490	1.06	0.08	0.59	0.576764	0.694211	-7.06
246137_at	putative protein predicted proteins,	LSH1	AT5G28490	-1.13	-0.18	-0.59	0.576766	0.694211	-7.06
250411_at	putative protein	---	AT5G11120	-1.04	-0.06	-0.59	0.576795	0.694211	-7.06
252192_at	CASEIN KINASE II, ALPHA CHAIN	CKA2	AT3G50000	-1.04	-0.06	-0.59	0.57691	0.694313	-7.06
251377_at	putative protein	---	AT3G60650	-1.04	-0.06	-0.59	0.576999	0.694383	-7.06
256103_at	hypothetical protein similar to hypot	---	AT1G13540	-1.04	-0.05	-0.59	0.577052	0.694411	-7.06
255277_at	putative homeotic protein ; support	PDF2	AT4G04890	1.07	0.09	0.59	0.577189	0.694539	-7.06
265167_at	putative OBP32pep protein	---	AT1G23680	-1.05	-0.06	-0.59	0.577308	0.694646	-7.06
250352_at	beta-adaptin-like protein A ; suppo	---	AT5G11490	1.04	0.06	0.59	0.577403	0.694724	-7.06
246471_s_a	putative protein predicted proteins,	---	AT5G17100	1.04	0.06	0.59	0.577504	0.694776	-7.06
258427_at	putative DNA-binding protein simila	---	AT3G16600	-1.04	-0.06	-0.59	0.577508	0.694776	-7.06
256010_at	auxin response factor, putative sim	ARF19	AT1G19220	-1.05	-0.08	-0.58	0.57767	0.694876	-7.06
258807_at	transfactor-like similar to transfactor	---	AT3G04030	-1.08	-0.12	-0.58	0.577672	0.694876	-7.06
247957_at	protein phosphatase 2C ABI2 (PP2	ABI2	AT5G57050	-1.09	-0.13	-0.58	0.577682	0.694876	-7.06
245434_at	hypothetical protein	---	AT4G17140	-1.04	-0.06	-0.58	0.577715	0.694879	-7.06
267459_at	unknown protein ;supported by full-	---	AT2G33850	-1.04	-0.06	-0.58	0.577908	0.695074	-7.06
245534_at	hypothetical protein	---	AT4G15150	-1.05	-0.07	-0.58	0.577964	0.695105	-7.06
256357_at	hypothetical protein	---	AT1G66490	1.03	0.05	0.58	0.578006	0.695119	-7.06
256018_at	plastid heme oxygenase, putative s	ho4	AT1G58300	1.08	0.11	0.58	0.578107	0.695203	-7.06

252829_at	homeodomain - like protein ; suppo	ATHB16	AT4G40060	-1.06	-0.08	-0.58	0.578289	0.695386	-7.06
256651_at	hypothetical protein predicted by ge	---	AT3G18840	-1.06	-0.08	-0.58	0.57855	0.695663	-7.06
260909_at	hypothetical protein predicted by ge	---	AT1G02670	-1.05	-0.08	-0.58	0.578653	0.69575	-7.06
264663_at	unknown protein Similar to A. thalia	LRR XI-23	AT1G09970	-1.15	-0.20	-0.58	0.578689	0.695756	-7.06
250357_at	putative protein various predicted p	---	AT5G11730	1.05	0.07	0.58	0.578834	0.695894	-7.06
250093_at	hypothetical protein	---	AT5G17370	-1.04	-0.06	-0.58	0.579021	0.696082	-7.06
264204_at	putative sucrose transport protein,	SUC2	AT1G22710	-1.07	-0.10	-0.58	0.579084	0.696122	-7.06
253152_at	putative protein predicted proteins,	---	AT4G35690	-1.06	-0.08	-0.58	0.579157	0.696173	-7.06
248324_at	putative protein similar to unknown	---	AT5G52790	-1.05	-0.08	-0.58	0.579206	0.696195	-7.06
249503_at	expansin-like protein expansin - Pr	ATEXPA24	AT5G39310	-1.05	-0.07	-0.58	0.57942	0.696381	-7.06
266879_at	putative phragmoplastin	ADL1D	AT2G44590	-1.06	-0.08	-0.58	0.579422	0.696381	-7.06
261475_at	anionic peroxidase, putative simila	---	AT1G14550	-1.08	-0.11	-0.58	0.579513	0.696454	-7.06
261748_at	hypothetical protein predicted by ge	---	AT1G76070	-1.18	-0.24	-0.58	0.579554	0.696467	-7.06
245265_at	hypothetical protein ; supported by	ACD6	AT4G14400	-1.34	-0.43	-0.58	0.579664	0.696554	-7.06
247136_at	senescence-associated protein con	---	AT5G66170	-1.21	-0.27	-0.58	0.579688	0.696554	-7.06
254861_at	putative protein zinc finger protein	---	AT4G12040	-1.07	-0.09	-0.58	0.579777	0.696624	-7.06
266940_at	unknown protein	---	AT2G18970	-1.05	-0.07	-0.58	0.579868	0.696697	-7.06
266651_at	putative casein kinase I	---	AT2G25760	-1.05	-0.07	-0.58	0.579928	0.696732	-7.06
261965_at	athila ORF 1, putative similar to ath	---	---	1.04	0.05	0.58	0.580017	0.696803	-7.06
267589_at	hypothetical protein	---	---	1.04	0.05	0.58	0.580117	0.696854	-7.06
265132_at	unknown protein ; supported by cD	---	AT1G23830	1.09	0.13	0.58	0.580121	0.696854	-7.06
267538_at	putative DNA binding protein ; supp	---	AT2G41870	-1.04	-0.06	-0.58	0.580241	0.696952	-7.06
261602_at	hydrogenase protein, putative simil	ATPREP2	AT1G49630	-1.04	-0.06	-0.58	0.580264	0.696952	-7.06
246539_at	putative protein geranylgeranylated	MUB2	AT5G15460	1.04	0.05	0.58	0.580427	0.697108	-7.06
248479_at	unknown protein	---	AT5G50910	-1.04	-0.05	-0.58	0.580455	0.697108	-7.06
254747_at	serine/threonine-specific protein kin	MHK	AT4G13020	1.05	0.07	0.58	0.580671	0.697298	-7.06
267254_at	putative protein kinase contains a p	SNRK2.9	AT2G23030	1.16	0.21	0.58	0.580674	0.697298	-7.06
250281_at	putative protein prdeicted proteins,	---	AT5G13240	1.07	0.09	0.58	0.580808	0.697388	-7.06
249922_at	aluminium-induced protein - like alu	AILP1	AT5G19140	1.05	0.06	0.58	0.58081	0.697388	-7.06
259714_at	putative gibberellin 20-oxidase simi	ATGA20OX	AT1G60980	-1.05	-0.07	-0.58	0.580866	0.697418	-7.06
254028_s_a	putative protein N.crassa mRNA fo	ORP4B	AT4G25850	-1.04	-0.06	-0.58	0.580897	0.697418	-7.06
263640_at	hypothetical protein predicted by ge	---	AT2G25270	-1.05	-0.06	-0.58	0.580927	0.697418	-7.06
254033_at	V-ATPase G-subunit like protein G	VATG3	AT4G25950	-1.04	-0.05	-0.58	0.581183	0.697689	-7.06
260904_at	unknown protein	NIMIN1	AT1G02450	-1.18	-0.24	-0.58	0.581374	0.697847	-7.06
260561_at	putative endochitinase	---	AT2G43580	-1.06	-0.08	-0.58	0.581376	0.697847	-7.06

256817_at	F-box protein family, AtFBW1 conta	---	AT3G21410	-1.05	-0.08	-0.58	0.581498	0.697957	-7.06
252082_at	putative protein	---	AT3G51940	-1.04	-0.06	-0.58	0.581593	0.698034	-7.06
261342_at	putative replication protein similar to	---	AT1G52950	-1.04	-0.06	-0.58	0.581858	0.698315	-7.06
264260_at	putative calcium-binding protein, ca	---	AT1G09210	1.12	0.17	0.58	0.581954	0.698393	-7.06
264404_at	putative cytochrome P450	CYP82F1	AT2G25160	-1.06	-0.08	-0.58	0.582194	0.698645	-7.06
251873_at	putative protein KIAA0122 gene , H	---	AT3G54230	-1.04	-0.05	-0.58	0.582285	0.698718	-7.06
248431_at	auxin-responsive GH3-like protein	---	AT5G51470	-1.05	-0.07	-0.58	0.582429	0.698837	-7.06
250747_at	glucuronosyl transferase-like protei	---	AT5G05900	-1.04	-0.06	-0.58	0.582446	0.698837	-7.06
258044_at	Dof zinc finger protein identical to G	ADOF2	AT3G21270	-1.10	-0.14	-0.58	0.5825	0.698866	-7.06
267046_at	hypothetical protein	---	AT2G34360	-1.07	-0.09	-0.58	0.582697	0.699027	-7.06
264698_at	unknown protein	---	AT1G70200	-1.05	-0.07	-0.58	0.582732	0.699027	-7.06
247877_at	putative protein contains similarity t	XBAT32	AT5G57740	1.08	0.11	0.58	0.582743	0.699027	-7.06
250365_at	putative protein serine threonine ty	---	AT5G11410	-1.08	-0.11	-0.58	0.582785	0.699027	-7.06
245162_at	putative myosin heavy chain	XID	AT2G33240	-1.08	-0.11	-0.58	0.582789	0.699027	-7.06
265607_at	hypothetical protein predicted by ge	---	AT2G25370	1.04	0.06	0.58	0.582916	0.699143	-7.06
252720_at	putative protein predicted protein, A	---	AT3G43970	1.06	0.08	0.58	0.582977	0.69918	-7.06
265793_at	unknown protein	---	AT2G01220	-1.06	-0.09	-0.58	0.583188	0.699396	-7.06
260918_at	hypothetical protein predicted by ge	---	AT1G21510	-1.04	-0.06	-0.58	0.583256	0.699405	-7.06
260173_at	NAM-like protein similar to NAM GE	VND7	AT1G71930	-1.05	-0.07	-0.58	0.583257	0.699405	-7.06
260133_at	ethylene-response protein, ETR1 i	ETR1	AT1G66340	1.04	0.05	0.58	0.583487	0.699644	-7.06
246819_at	WD-repeat protein - like WD-repea	---	AT5G26900	1.05	0.07	0.58	0.583561	0.699697	-7.06
260903_at	polygalacturonase PG1, putative s	---	AT1G02460	-1.21	-0.28	-0.58	0.583658	0.699776	-7.06
252605_s_a	sulfotransferase-like protein FLAV	---	AT3G45070	1.04	0.05	0.58	0.583788	0.699896	-7.06
266779_at	putative ligand-gated ion channel p	ATGLR2.9	AT2G29100	-1.05	-0.07	-0.58	0.583848	0.69993	-7.06
267630_at	unknown protein predicted by gene	---	AT2G42130	-1.06	-0.08	-0.58	0.583879	0.69993	-7.06
251596_at	1-acylcerol-3-phosphate acyltransf	LPAT2	AT3G57650	-1.04	-0.05	-0.58	0.58394	0.699967	-7.06
247661_at	protein kinase - like protein kinase	---	AT5G60080	1.04	0.06	0.57	0.584244	0.700294	-7.06
252309_at	cysteine protease contains similarit	---	AT3G49340	1.05	0.07	0.57	0.584573	0.700652	-7.07
265549_at	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.57	0.584928	0.701031	-7.07
265208_at	putative giberellin beta-hydroxylase	---	AT2G36690	1.14	0.18	0.57	0.584951	0.701031	-7.07
247928_at	villin	---	AT5G57320	-1.06	-0.08	-0.57	0.585073	0.701141	-7.07
260803_at	glutathione transferase, putative si	ATGSTU22	AT1G78340	1.04	0.06	0.57	0.585169	0.70122	-7.07
264409_s_a	hypothetical protein similar to hypot	---	---	1.06	0.09	0.57	0.585217	0.70124	-7.07
258590_at	putative response regulator protein	ARR22	AT3G04280	1.04	0.06	0.57	0.585272	0.701269	-7.07
267479_at	hypothetical protein	---	AT2G02690	-1.04	-0.05	-0.57	0.585478	0.701479	-7.07

247159_at	1-aminocyclopropane-1-carboxylate	ACS5	AT5G65800	-1.04	-0.05	-0.57	0.585685	0.701658	-7.07
261107_at	unknown protein ; supported by cDI	---	AT1G63010	1.04	0.06	0.57	0.585701	0.701658	-7.07
261707_at	unknown protein	---	AT1G32650	1.04	0.06	0.57	0.58572	0.701658	-7.07
265528_at	hypothetical protein predicted by ge	---	---	-1.04	-0.05	-0.57	0.585867	0.701798	-7.07
248745_at	unknown protein	---	AT5G48250	1.06	0.08	0.57	0.585951	0.701861	-7.07
245446_at	enoyl-CoA hydratase	---	AT4G16800	-1.05	-0.07	-0.57	0.586155	0.702069	-7.07
266037_at	putative protein kinase contains a p	---	AT2G05940	-1.15	-0.20	-0.57	0.586216	0.702104	-7.07
251541_at	citrate synthase -like protein citrate	CSY2	AT3G58750	-1.06	-0.09	-0.57	0.586328	0.702189	-7.07
263998_at	unknown protein	---	AT2G22510	-1.10	-0.14	-0.57	0.586348	0.702189	-7.07
249419_s_a	putative protein MADS-box protein	AGL98	AT5G39750	-1.04	-0.06	-0.57	0.586387	0.702199	-7.07
256546_at	hypothetical protein contains simila	---	AT3G14820	-1.04	-0.06	-0.57	0.586449	0.702236	-7.07
260301_at	hypothetical protein ;supported by	---	AT1G80290	1.05	0.07	0.57	0.586503	0.702265	-7.07
250442_at	putative protein hypothetical bacteri	MSL2	AT5G10490	1.05	0.06	0.57	0.586559	0.702295	-7.07
248089_at	salt stress inducible small GTP bind	AtRAN4	AT5G55080	-1.05	-0.07	-0.57	0.586646	0.702362	-7.07
250908_at	GT2 -like protein GT2, Arabidopsis	PTL	AT5G03680	-1.04	-0.06	-0.57	0.586678	0.702363	-7.07
248557_at	transport inhibitor response 1 (TIR	AFB5	AT5G49980	1.05	0.07	0.57	0.586811	0.702469	-7.07
257943_at	SKP1/ASK1 (At7), putative similar	ASK7	AT3G21840	1.05	0.07	0.57	0.586828	0.702469	-7.07
257861_at	putative transporter similar to SV2 r	---	AT3G13050	-1.06	-0.08	-0.57	0.586925	0.702521	-7.07
250372_at	putative protein various predicted p	---	AT5G11460	1.06	0.08	0.57	0.586959	0.702521	-7.07
263795_at	putative cyclic nucleotide-regulated	ATCNGC14	AT2G24610	-1.04	-0.06	-0.57	0.586963	0.702521	-7.07
263832_at	putative polygalacturonase	---	AT2G40310	1.04	0.05	0.57	0.587168	0.702729	-7.07
261143_at	unknown protein	ATPUP14	AT1G19770	-1.09	-0.12	-0.57	0.587224	0.702733	-7.07
256685_at	hypothetical protein predicted by ge	---	AT3G32100	1.05	0.07	0.57	0.587258	0.702733	-7.07
248143_at	putative protein similar to unknown	---	AT5G55040	1.04	0.06	0.57	0.587264	0.702733	-7.07
260872_at	hypothetical protein predicted by ge	---	AT1G21350	-1.07	-0.10	-0.57	0.587319	0.702758	-7.07
251600_at	protein kinase - like protein wall-as	---	AT3G57710	1.04	0.05	0.57	0.587347	0.702758	-7.07
245585_at	hypothetical	---	AT4G14970	-1.05	-0.06	-0.57	0.58745	0.702844	-7.07
263641_at	putative non-LTR retroelement reve	---	---	-1.04	-0.06	-0.57	0.587556	0.702934	-7.07
246628_at	signal recognition particle 54 kDa p	---	AT1G48900	1.03	0.05	0.57	0.587624	0.702979	-7.07
252085_s_a	serine-type carboxypeptidase like p	scpl37	AT3G52000	-1.04	-0.05	-0.57	0.587929	0.703307	-7.07
260835_at	protein kinase interactor, putative s	---	AT1G06700	1.05	0.06	0.57	0.587991	0.703345	-7.07
256739_s_a	hypothetical protein similar to putati	---	---	1.04	0.05	0.57	0.588052	0.70338	-7.07
249384_at	putative protein hypothetical protei	---	AT5G39890	-1.04	-0.06	-0.57	0.588302	0.703622	-7.07
254426_at	putative protein predicted protein, /	---	AT4G21240	-1.04	-0.06	-0.57	0.588316	0.703622	-7.07
254641_at	ras-like GTP-binding protein strong	ATRABA1D	AT4G18800	-1.07	-0.10	-0.57	0.588441	0.703735	-7.07

249800_at	MtN3-like protein ; supported by cD	MTN3	AT5G23660	-1.05	-0.07	-0.57	0.588476	0.703741	-7.07
260772_at	unknown protein contains similarity	---	AT1G49050	-1.06	-0.08	-0.57	0.58912	0.704474	-7.07
261376_at	hypothetical protein contains simila	---	AT1G18660	-1.05	-0.07	-0.57	0.589172	0.704498	-7.07
260540_at	hypothetical protein predicted by ge	---	AT2G43500	1.04	0.06	0.57	0.589359	0.704685	-7.07
256631_at	At14a-like protein similar to At14a p	---	AT3G28320	-1.09	-0.13	-0.57	0.589432	0.704708	-7.07
255787_at	putative cinnamoyl-CoA reductase	---	AT2G33590	1.06	0.09	0.57	0.589439	0.704708	-7.07
261882_at	GTP-binding protein, putative simil	PDE318	AT1G80770	-1.05	-0.06	-0.57	0.58951	0.704755	-7.07
259200_at	unknown protein similar to hypothet	---	AT3G09070	1.05	0.06	0.57	0.58974	0.704993	-7.07
247448_at	putative protein predicted proteins,	---	AT5G62770	1.17	0.22	0.57	0.590092	0.705377	-7.07
248424_at	unknown protein	---	AT5G51680	-1.15	-0.21	-0.57	0.590155	0.705415	-7.07
266437_at	unknown protein	---	AT2G43160	-1.05	-0.07	-0.57	0.590317	0.705571	-7.07
260845_at	transcription factor, putative similar	---	AT1G17310	-1.05	-0.06	-0.57	0.59038	0.705585	-7.07
250945_at	putative protein	---	AT5G03400	-1.05	-0.06	-0.57	0.590394	0.705585	-7.07
260007_at	unknown protein contains non-cons	---	AT1G67870	1.09	0.13	0.56	0.590421	0.705585	-7.07
267022_at	hypothetical protein predicted by ge	---	AT2G34230	-1.04	-0.05	-0.56	0.590919	0.706143	-7.07
260439_at	hypothetical protein predicted by ge	---	AT1G68340	1.09	0.13	0.56	0.590973	0.706171	-7.07
255215_at	putative athila transposon protein	---	---	-1.03	-0.05	-0.56	0.591045	0.706219	-7.07
265250_at	putative receptor protein kinase sim	BRL2	AT2G01950	1.07	0.10	0.56	0.591106	0.706256	-7.07
247047_at	putative protein contains similarity t	---	AT5G66650	1.22	0.29	0.56	0.591153	0.706275	-7.07
248554_at	putative protein contains similarity t	---	AT5G50330	-1.06	-0.09	-0.56	0.591214	0.706311	-7.07
259038_at	unknown protein predicted by gens	PTAC13	AT3G09210	1.05	0.07	0.56	0.591314	0.706393	-7.07
257109_s_a	hypothetical protein	---	---	-1.04	-0.05	-0.56	0.591534	0.706619	-7.07
254447_at	berberine bridge enzyme - like prote	---	AT4G20860	1.17	0.23	0.56	0.591763	0.706855	-7.07
264494_at	hypothetical protein predicted by ge	---	AT1G27461	-1.07	-0.09	-0.56	0.591881	0.70696	-7.07
261128_at	ubiquitin-specific protease 2 (UBP2	UBP2	AT1G04860	1.05	0.06	0.56	0.591954	0.707009	-7.07
267281_at	putative protein kinase contains a p	---	AT2G19400	-1.06	-0.08	-0.56	0.591987	0.707012	-7.07
246624_at	flavin-containing monooxygenase,	YUC10	AT1G48910	-1.05	-0.07	-0.56	0.592161	0.707127	-7.07
249799_at	serine palmitoyltransferase ; suppo	LCB2	AT5G23670	1.04	0.05	0.56	0.592176	0.707127	-7.07
253970_at	putative uracil phosphoribosyl trans	---	AT4G26510	-1.05	-0.07	-0.56	0.592176	0.707127	-7.07
255302_at	putative protein similar to transcripti	ATMSRB5	AT4G04830	1.07	0.09	0.56	0.592291	0.707227	-7.07
251813_at	Expressed protein ; supported by fu	TON1A	AT3G55000	1.06	0.08	0.56	0.592418	0.707316	-7.07
253625_at	signal recognition particle receptor	---	AT4G30600	1.04	0.06	0.56	0.592428	0.707316	-7.07
259829_at	oligopeptide transporter, putative s	---	---	-1.06	-0.08	-0.56	0.592517	0.707367	-7.07
253439_at	dimethylaniline monooxygenase - I	YUC1	AT4G32540	-1.05	-0.07	-0.56	0.592532	0.707367	-7.07
248875_at	disease resistance protein-like	---	AT5G46470	-1.08	-0.11	-0.56	0.592612	0.707425	-7.07

260488_at	flowering protein CONSTANS, puta	TIFY2A	AT1G51600	-1.06	-0.08	-0.56	0.592678	0.707467	-7.07
247773_at	putative protein	---	AT5G58630	-1.05	-0.06	-0.56	0.592902	0.707697	-7.07
251382_at	pectinesterase - like protein pectine	---	AT3G60730	-1.04	-0.05	-0.56	0.59327	0.7081	-7.07
258792_at	hypothetical protein predicted by ge	---	AT3G04640	-1.16	-0.22	-0.56	0.593359	0.708143	-7.07
255741_at	tRNA isopentenyl transferase, puta	ATIPT6	AT1G25410	-1.05	-0.07	-0.56	0.593369	0.708143	-7.07
261590_at	hypothetical protein predicted by ge	ROPGEF2	AT1G01700	1.04	0.06	0.56	0.593681	0.708479	-7.07
259867_at	hypothetical protein predicted by ge	---	AT1G76740	-1.04	-0.05	-0.56	0.593751	0.708525	-7.07
252588_at	putative protein potential transcript	---	AT3G45630	-1.04	-0.06	-0.56	0.594022	0.708812	-7.07
252654_at	similar to glycyl tRNA synthetase	---	AT3G44740	1.04	0.05	0.56	0.594054	0.708812	-7.07
266187_at	putative retroelement pol polyprotei	---	AT2G38970	-1.08	-0.11	-0.56	0.594156	0.708898	-7.07
251057_at	putative protein alkB protein - Esch	---	AT5G01780	1.04	0.05	0.56	0.594214	0.708929	-7.07
263303_at	unknown protein ;supported by full-	---	AT2G15240	1.05	0.08	0.56	0.594286	0.708956	-7.07
251838_at	cysteine proteinase non-consensus	---	AT3G54940	1.05	0.07	0.56	0.594299	0.708956	-7.07
247196_at	putative protein similar to unknown	AIL7	AT5G65510	-1.04	-0.05	-0.56	0.594476	0.70913	-7.07
258680_at	adenylate translocator identical to a	AAC1	AT3G08580	1.08	0.11	0.56	0.594607	0.70925	-7.07
246194_at	putative protein ;supported by full-le	ACD2	AT4G37000	-1.06	-0.09	-0.56	0.59469	0.709312	-7.07
264786_at	putative Ta11-like non-LTR retroele	---	AT2G17920	-1.04	-0.06	-0.56	0.594774	0.709374	-7.07
254678_at	hypothetical protein	---	AT4G18500	1.04	0.06	0.56	0.594827	0.709374	-7.07
250654_at	receptor protein kinase-like protein	---	AT5G06940	-1.05	-0.07	-0.56	0.594836	0.709374	-7.07
260003_at	unknown protein ;supported by full-	IAR1	AT1G68100	1.04	0.05	0.56	0.595206	0.709778	-7.08
248805_at	putative protein similar to unknown	---	AT5G47480	1.04	0.06	0.56	0.595245	0.709788	-7.08
250802_at	pectinesterase	---	AT5G04970	-1.05	-0.06	-0.56	0.595311	0.709814	-7.08
260726_at	signal recognition particle 19 kDa p	---	AT1G48160	1.06	0.09	0.56	0.595329	0.709814	-7.08
265979_at	putative replication protein A1	---	---	1.05	0.07	0.56	0.595372	0.709828	-7.08
267152_at	hypothetical protein predicted by gr	---	AT2G31040	-1.07	-0.09	-0.56	0.595601	0.710065	-7.08
252266_at	putative protein ethylene-forming e	---	AT3G49630	1.07	0.09	0.56	0.595726	0.710176	-7.08
256464_at	late-embryogenesis abundant prote	---	AT1G32560	1.13	0.18	0.56	0.595841	0.710277	-7.08
257179_at	topoisomerase VIA (SPO11 gene 1	---	AT3G13160	1.04	0.05	0.56	0.595933	0.710349	-7.08
257439_at	hypothetical protein similar to hypot	---	AT2G17000	-1.04	-0.05	-0.56	0.596169	0.710592	-7.08
258593_at	unknown protein	---	AT3G04480	1.07	0.10	0.56	0.596223	0.71062	-7.08
257470_at	hypothetical protein predicted by ge	---	AT1G53770	-1.06	-0.08	-0.56	0.596311	0.710688	-7.08
262041_at	HPt phosphotransmitter, putative s	AHP6	AT1G80100	-1.05	-0.08	-0.56	0.596512	0.71089	-7.08
260072_at	unknown protein supported by cDN	---	AT1G73650	-1.05	-0.07	-0.56	0.596566	0.710894	-7.08
249293_at	protein kinase-like	---	AT5G41260	-1.06	-0.08	-0.56	0.596578	0.710894	-7.08
265629_at	unknown protein ; supported by cD	LHW	AT2G27228	-1.07	-0.10	-0.56	0.596793	0.711114	-7.08

265093_at	unknown protein similar to NBD-like	---	AT1G03905	1.06	0.08	0.55	0.59687	0.711169	-7.08
254843_at	putative protein TAK1 binding prote	---	AT4G11860	-1.04	-0.05	-0.55	0.596934	0.711208	-7.08
256368_at	cinnamyl alcohol dehydrogenase, p	---	AT1G66800	-1.04	-0.06	-0.55	0.5972	0.711488	-7.08
253597_at	putative protein translation initiation	---	AT4G30690	-1.08	-0.12	-0.55	0.597284	0.71155	-7.08
249243_s_a	beta-glucosidase	BGLU13	AT5G42260	-1.04	-0.05	-0.55	0.597471	0.711735	-7.08
261218_at	ferredoxin--NADP reductase precu	FNR2	AT1G20020	-1.08	-0.10	-0.55	0.597514	0.71175	-7.08
248606_at	putative protein contains similarity t	CPuORF4	AT5G49448	-1.08	-0.11	-0.55	0.597564	0.711773	-7.08
260935_at	hypothetical protein predicted by ge	---	AT1G45110	1.06	0.08	0.55	0.597664	0.711854	-7.08
264176_at	bZIP-like protein similar to bZIP (le	---	AT1G02110	1.08	0.11	0.55	0.597963	0.712173	-7.08
258759_at	putative bZIP transcription factor co	BZIP28	AT3G10800	-1.04	-0.06	-0.55	0.598104	0.712304	-7.08
250295_at	putative protein	NEF1	AT5G13390	1.05	0.08	0.55	0.598154	0.712326	-7.08
249074_at	putative protein contains similarity t	---	AT5G44080	1.05	0.06	0.55	0.598235	0.712386	-7.08
257111_x_a	hypothetical protein	---	---	-1.04	-0.06	-0.55	0.598322	0.712451	-7.08
254793_at	hypothetical protein	---	AT4G12930	-1.05	-0.07	-0.55	0.59867	0.712797	-7.08
266616_at	putative CDC6 protein ; supported	CDC6	AT2G29680	-1.04	-0.06	-0.55	0.598675	0.712797	-7.08
249440_at	protein kinase -like protein probabl	---	AT5G40030	-1.04	-0.06	-0.55	0.598777	0.712827	-7.08
253012_at	putative protein Caenorhabditis ele	---	AT4G37900	1.05	0.07	0.55	0.598785	0.712827	-7.08
262444_at	hypothetical protein similar to putati	---	AT1G47480	1.09	0.12	0.55	0.598793	0.712827	-7.08
257436_s_a	hypothetical protein predicted by ge	---	AT2G24650	1.06	0.08	0.55	0.598874	0.712886	-7.08
267183_at	hypothetical protein predicted by ge	---	AT2G44020	1.04	0.06	0.55	0.598928	0.712907	-7.08
267417_at	putative RING zinc finger protein	---	AT2G34990	1.04	0.05	0.55	0.598954	0.712907	-7.08
260171_at	hypothetical protein predicted by ge	---	AT1G71910	1.12	0.16	0.55	0.599161	0.713115	-7.08
260186_at	hypothetical protein predicted by ge	---	AT1G36020	-1.06	-0.08	-0.55	0.599248	0.713165	-7.08
263501_s_a	hypothetical protein	---	AT2G07673	1.05	0.07	0.55	0.59929	0.713165	-7.08
254828_at	putative cell wall-plasma membrane	AIR1	AT4G12550	1.04	0.06	0.55	0.599296	0.713165	-7.08
248235_at	unknown protein ;supported by full-	emb2737	AT5G53860	1.04	0.05	0.55	0.599471	0.713335	-7.08
264724_at	putative JUN kinase activator prote	CSN5A	AT1G22920	1.04	0.06	0.55	0.599576	0.713403	-7.08
254974_at	putative flavanone 3-beta-hydroxyl	---	AT4G10490	-1.04	-0.06	-0.55	0.59959	0.713403	-7.08
257585_at	hypothetical protein predicted by ge	---	AT3G12420	-1.05	-0.07	-0.55	0.59966	0.713445	-7.08
254374_at	hypothetical protein ;supported by	---	AT4G21780	1.04	0.06	0.55	0.599688	0.713445	-7.08
246079_at	putative protein unconventional my	---	AT5G20450	1.06	0.08	0.55	0.599874	0.713629	-7.08
248814_at	putative protein similar to unknown	---	AT5G46910	1.22	0.28	0.55	0.600061	0.713779	-7.08
261515_at	cleavage stimulation factor, putativ	---	AT1G71800	1.04	0.06	0.55	0.600104	0.713779	-7.08
245912_at	putative protein sulfate transporter	SULTR3;5	AT5G19600	-1.12	-0.17	-0.55	0.60011	0.713779	-7.08
256554_at	hypothetical protein similar to putati	---	---	1.06	0.08	0.55	0.600125	0.713779	-7.08

256811_at	serine/threonine-specific protein ki	---	AT3G21340	1.04	0.05	0.55	0.600191	0.71382	-7.08
259627_at	unknown protein ; supported by cDI	---	AT1G42960	1.05	0.07	0.55	0.600321	0.713921	-7.08
256120_at	hypothetical protein contains simila	---	AT1G18130	-1.04	-0.05	-0.55	0.600339	0.713921	-7.08
245684_at	Expressed protein ; supported by c	RHF2A	AT5G22000	-1.04	-0.06	-0.55	0.600408	0.713967	-7.08
263877_at	hypothetical protein predicted by ge	---	AT2G21780	-1.03	-0.05	-0.55	0.600503	0.714042	-7.08
255364_s_a	putative fibrillin ; supported by full-l	---	AT4G04020	-1.06	-0.08	-0.55	0.600576	0.714092	-7.08
262413_at	hypothetical protein contains simila	ATAPRL4	AT1G34780	1.06	0.08	0.55	0.600759	0.714273	-7.08
266926_at	unknown protein predicted by gens	---	AT2G46000	1.06	0.08	0.55	0.601005	0.714497	-7.08
253452_at	hypothetical protein ; supported by	---	AT4G31930	1.04	0.06	0.55	0.601011	0.714497	-7.08
267593_at	similar to disease resistance protein	AtRLP25	AT2G33030	1.04	0.05	0.55	0.601071	0.714531	-7.08
247966_at	putative protein contains similarity t	---	AT5G56610	-1.05	-0.06	-0.55	0.601182	0.714626	-7.08
248937_at	putative protein contains similarity t	AtRLP55	AT5G45770	-1.06	-0.09	-0.55	0.601252	0.714672	-7.08
245508_at	hypothetical protein	---	AT4G15720	1.04	0.05	0.55	0.601297	0.714689	-7.08
247095_at	dehydrin RAB18-like protein (sp P3	RAB18	AT5G66400	-1.11	-0.15	-0.55	0.60163	0.715047	-7.08
255903_at	myb-like protein, putative similar to	MYB52	AT1G17950	1.04	0.05	0.55	0.601668	0.715054	-7.08
246049_at	putative protein predicted proteins,	---	---	-1.05	-0.07	-0.55	0.601782	0.715124	-7.08
260690_at	RING finger protein, putative simila	NHL8	AT1G32340	-1.04	-0.05	-0.55	0.601789	0.715124	-7.08
255372_at	putative reverse transcriptase	---	---	-1.07	-0.10	-0.55	0.602124	0.715485	-7.08
258020_at	unknown protein ;supported by full-	NHD1	AT3G19490	1.05	0.06	0.55	0.602226	0.71554	-7.08
264872_at	putative floral homeotic protein, AG	סאפ-03	AT1G24260	-1.06	-0.09	-0.55	0.602233	0.71554	-7.08
256665_at	hypothetical protein predicted by ge	---	AT3G20700	1.06	0.08	0.55	0.602325	0.715612	-7.08
249072_at	putative protein similar to unknown	---	AT5G44060	1.15	0.20	0.55	0.602525	0.715779	-7.08
250450_at	putative transcription factor MYB92	ATMYB92	AT5G10280	1.03	0.05	0.55	0.602528	0.715779	-7.08
264337_at	hypothetical protein predicted by ge	---	AT1G70350	1.04	0.06	0.55	0.602661	0.715899	-7.08
248119_at	serine/threonine-specific protein kin	---	AT5G54590	-1.06	-0.08	-0.55	0.602861	0.7161	-7.08
259464_at	hypothetical protein predicted by ge	---	AT1G18990	1.04	0.06	0.55	0.602982	0.716205	-7.08
259624_at	hypothetical protein similar to unkno	---	AT1G43020	-1.05	-0.07	-0.55	0.603144	0.716361	-7.08
255382_at	putative pre-mRNA splicing factor s	EMB2770	AT4G03430	-1.04	-0.05	-0.54	0.603394	0.716621	-7.08
253370_at	pectinesterase - like protein pectin	---	AT4G33230	1.06	0.08	0.54	0.603464	0.716667	-7.08
250128_at	zinc finger protein 3 (gb|AAD27875	ZFN3	AT5G16540	-1.07	-0.10	-0.54	0.603587	0.716775	-7.08
251529_at	ATP-dependent RNA helicase-like	---	AT3G58570	-1.04	-0.06	-0.54	0.603755	0.716937	-7.08
255618_at	hypothetical protein	---	AT4G01340	-1.03	-0.05	-0.54	0.603801	0.716955	-7.08
262755_at	unknown protein	---	AT1G16360	-1.04	-0.06	-0.54	0.603837	0.71696	-7.08
255489_at	predicted protein destination factor	---	AT4G02650	-1.06	-0.08	-0.54	0.603873	0.716965	-7.08
257738_at	40S ribosomal subunit protein S21	---	AT3G27450	1.04	0.05	0.54	0.603917	0.716965	-7.08

250778_at	unknown protein ;supported by full-	---	AT5G05500	-1.04	-0.06	-0.54	0.603956	0.716965	-7.08
249865_at	unknown protein ; supported by cD	---	AT5G22820	1.06	0.08	0.54	0.603967	0.716965	-7.08
260751_at	unknown protein	SCD1	AT1G49040	1.07	0.10	0.54	0.60409	0.717074	-7.08
263084_at	hypothetical protein predicted by ge	---	AT2G27180	1.04	0.06	0.54	0.604186	0.717113	-7.08
246657_at	putative protein predicted proteins,	---	---	1.03	0.05	0.54	0.604189	0.717113	-7.08
261730_s_a	mutator-like transposase, putative	---	---	1.04	0.06	0.54	0.604218	0.717113	-7.08
255316_at	putative protein	---	---	-1.04	-0.05	-0.54	0.604275	0.717144	-7.08
266816_at	unknown protein identical to GB:AA	---	AT2G44970	-1.04	-0.06	-0.54	0.604518	0.717388	-7.08
260476_at	unknown protein	---	AT1G11060	1.06	0.08	0.54	0.604543	0.717388	-7.08
251510_at	putative protein several hypothetica	---	AT3G59170	-1.03	-0.05	-0.54	0.604601	0.71739	-7.08
251564_at	myosin heavy chain MYA3	XIJ	AT3G58160	-1.05	-0.07	-0.54	0.604608	0.71739	-7.08
256726_at	unknown protein	---	AT3G52210	-1.06	-0.09	-0.54	0.604664	0.717406	-7.08
253716_at	hypothetical protein	---	AT4G29420	1.05	0.07	0.54	0.604684	0.717406	-7.08
252547_at	putative protein many predicted pro	---	AT3G45840	-1.05	-0.07	-0.54	0.604751	0.717423	-7.08
258236_at	hypothetical protein predicted by ge	---	AT3G27800	1.04	0.06	0.54	0.604762	0.717423	-7.08
259134_at	hypothetical protein predicted by ge	---	AT3G05390	1.15	0.20	0.54	0.605077	0.71776	-7.08
261373_at	CMP-KDO synthetase, putative sin	---	AT1G53000	1.04	0.06	0.54	0.605246	0.717923	-7.08
256294_at	unknown protein	---	AT1G69450	1.05	0.07	0.54	0.605331	0.717986	-7.08
266663_at	putative receptor-like protein kinase	---	AT2G25790	1.07	0.10	0.54	0.60563	0.718304	-7.08
259931_at	hypothetical protein predicted by ge	---	AT1G34400	-1.05	-0.07	-0.54	0.605906	0.718552	-7.09
264469_at	hypothetical protein similar to hypot	LBD40	AT1G67100	-1.04	-0.06	-0.54	0.605962	0.718552	-7.09
257944_at	SKP1/ASK1 (At9), putative similar	ASK9	AT3G21850	1.04	0.06	0.54	0.605977	0.718552	-7.09
256840_x_a	unknown protein similar to putative	---	---	1.04	0.05	0.54	0.60602	0.718552	-7.09
259558_at	hypothetical protein	WAK5	AT1G21230	-1.05	-0.07	-0.54	0.60602	0.718552	-7.09
247778_at	wounding stress induced protein -	---	AT5G58750	-1.04	-0.05	-0.54	0.606028	0.718552	-7.09
254906_at	putative disease resistance respon	---	AT4G11180	1.04	0.06	0.54	0.606104	0.718558	-7.09
255169_x_a	hypothetical protein	---	AT4G07940	1.04	0.06	0.54	0.60611	0.718558	-7.09
252892_at	hypothetical protein	---	AT4G39420	-1.04	-0.05	-0.54	0.606129	0.718558	-7.09
247685_at	serine/threonine-specific protein ki	---	AT5G59680	1.13	0.18	0.54	0.60617	0.718558	-7.09
246465_at	quinone oxidoreductase - like prote	---	AT5G17000	1.08	0.11	0.54	0.606191	0.718558	-7.09
257158_at	3-hydroxyisobutyryl-coenzyme A h	---	AT3G24360	-1.05	-0.07	-0.54	0.606352	0.718711	-7.09
247622_at	putative protein	---	AT5G60350	-1.04	-0.06	-0.54	0.606448	0.718758	-7.09
258763_s_a	putative beta-mannan endohydrola	---	AT3G10900	-1.03	-0.05	-0.54	0.606454	0.718758	-7.09
255181_at	predicted protein of unknown functi	---	---	-1.05	-0.07	-0.54	0.607076	0.719361	-7.09
264416_at	hypothetical protein similar to putati	---	AT1G43140	1.05	0.06	0.54	0.607082	0.719361	-7.09

249652_at	putative protein hypothetical protein	---	AT5G37070	1.06	0.08	0.54	0.607091	0.719361	-7.09
258793_at	hypothetical protein supported by fu	---	AT3G04780	1.04	0.06	0.54	0.607097	0.719361	-7.09
264830_at	hypothetical protein predicted by ge	---	AT1G03710	-1.05	-0.07	-0.54	0.607144	0.719361	-7.09
259828_at	RING-H2 zinc finger protein ATL3,	---	AT1G72220	1.05	0.08	0.54	0.607181	0.719361	-7.09
262669_at	hypothetical protein	---	AT1G62850	-1.04	-0.06	-0.54	0.607184	0.719361	-7.09
253277_at	cinnamyl alcohol dehydrogenase -	ATCAD5	AT4G34230	-1.06	-0.09	-0.54	0.607283	0.719441	-7.09
263313_at	14-3-3 protein (grf15), putative con	---	AT2G10450	-1.04	-0.06	-0.54	0.607349	0.719483	-7.09
263036_at	hypothetical protein predicted by ge	---	AT1G23890	-1.05	-0.07	-0.54	0.607764	0.719936	-7.09
257959_at	somatic embryogenesis receptor-li	NIK2	AT3G25560	-1.09	-0.13	-0.54	0.607817	0.71995	-7.09
247322_at	unknown protein	---	AT5G64090	-1.04	-0.06	-0.54	0.607839	0.71995	-7.09
263586_at	unknown protein predicted by gens	---	AT2G25350	-1.06	-0.08	-0.54	0.607971	0.720069	-7.09
259078_at	unknown protein predicted by gene	HST	AT3G05040	1.04	0.06	0.54	0.608137	0.720219	-7.09
266400_at	methylenetetrahydrofolate dehydrog	---	AT2G38660	1.04	0.05	0.54	0.608161	0.720219	-7.09
257563_at	hypothetical protein predicted by ge	---	AT3G19610	-1.03	-0.05	-0.54	0.608192	0.720219	-7.09
259565_at	hypothetical protein	---	AT1G20530	1.03	0.05	0.54	0.608285	0.720265	-7.09
245860_at	putative protein predicted proteins,	---	AT5G28310	-1.05	-0.07	-0.54	0.608295	0.720265	-7.09
256037_at	hypothetical protein predicted by ge	---	AT1G19160	-1.05	-0.07	-0.54	0.608356	0.720265	-7.09
259264_at	putative aldose 1-epimerase shows	---	AT3G01260	-1.05	-0.07	-0.54	0.608357	0.720265	-7.09
249199_at	putative protein similar to unknown	BPC6	AT5G42520	1.04	0.06	0.54	0.608439	0.720324	-7.09
245212_at	hypothetical protein predicted by ge	AT1G4422	---	-1.06	-0.09	-0.54	0.608507	0.720367	-7.09
252691_at	kinesin -like protein KLP2 protein,	---	AT3G44050	1.04	0.05	0.54	0.608598	0.720418	-7.09
264043_at	putative cyclin D	CYCD2;1	AT2G22490	1.04	0.05	0.54	0.608612	0.720418	-7.09
250430_at	putative protein	---	AT5G10460	-1.04	-0.05	-0.54	0.608714	0.7205	-7.09
246991_at	peroxidase (emb|CAA66967.1)	---	AT5G67400	-1.04	-0.06	-0.54	0.608819	0.720559	-7.09
256635_at	hypothetical protein predicted by ge	---	AT3G28260	1.03	0.05	0.54	0.608843	0.720559	-7.09
266208_at	putative tRNA isopentenylpyrophos	ATIPT2	AT2G27760	-1.07	-0.10	-0.54	0.608878	0.720559	-7.09
255391_at	hypothetical protein similar to T6P5	---	---	1.04	0.05	0.54	0.60889	0.720559	-7.09
255108_at	hypothetical protein	---	AT4G08740	-1.06	-0.08	-0.54	0.609081	0.720719	-7.09
255658_at	hypothetical protein ;supported by	---	AT4G00770	-1.05	-0.07	-0.54	0.609109	0.720719	-7.09
250760_at	unknown protein	---	AT5G06040	-1.04	-0.06	-0.54	0.60912	0.720719	-7.09
258058_at	unknown protein	---	AT3G28980	-1.04	-0.06	-0.54	0.609264	0.720852	-7.09
246629_at	unknown protein similar to hypothet	---	AT1G50750	-1.06	-0.08	-0.54	0.609451	0.721037	-7.09
261503_at	hypothetical protein predicted by g	---	AT1G71691	-1.05	-0.07	-0.54	0.609633	0.72115	-7.09
257502_at	unknown protein	---	AT1G78110	-1.09	-0.13	-0.54	0.609654	0.72115	-7.09
266819_at	unknown protein ;supported by full	---	AT2G44870	1.06	0.08	0.54	0.609671	0.72115	-7.09

247906_at	putative protein similar to unknown	IAA33	AT5G57420	-1.06	-0.08	-0.54	0.609674	0.72115	-7.09
258591_at	hypothetical protein ; supported by	---	AT3G04360	-1.04	-0.06	-0.53	0.610004	0.721504	-7.09
248788_at	DNA-binding protein-like	---	AT5G47430	1.04	0.05	0.53	0.610227	0.721722	-7.09
263194_at	AP2 domain transcription factor, pu	---	AT1G36060	-1.07	-0.09	-0.53	0.610253	0.721722	-7.09
245171_at	hypothetical protein predicted by ge	---	AT2G47560	1.05	0.06	0.53	0.610294	0.721734	-7.09
253774_at	NAM / CUC2 -like protein No apica	anac074	AT4G28530	-1.08	-0.11	-0.53	0.61052	0.721964	-7.09
246186_at	PINHEAD - like protein PINHEAD,	---	AT5G21030	-1.06	-0.09	-0.53	0.610571	0.721987	-7.09
250184_at	putative protein various predicted p	---	AT5G14240	-1.04	-0.06	-0.53	0.610727	0.722134	-7.09
246216_at	cytochrome P450 like protein ; supp	ROT3	AT4G36380	-1.06	-0.09	-0.53	0.610822	0.722204	-7.09
265350_at	unknown protein predicted by gens	---	AT2G22620	-1.04	-0.06	-0.53	0.61085	0.722204	-7.09
261834_at	polygalacturonase PG1, putative si	---	AT1G10640	-1.04	-0.05	-0.53	0.611104	0.72244	-7.09
246315_at	hypothetical protein	---	AT3G56870	1.07	0.10	0.53	0.611113	0.72244	-7.09
258409_at	hypothetical protein similar to GB:A	---	AT3G17640	-1.09	-0.12	-0.53	0.61117	0.72247	-7.09
265993_at	putative disease resistance protein	---	AT2G24160	1.24	0.32	0.53	0.611394	0.722697	-7.09
249102_at	patatin-like protein	---	AT5G43590	1.03	0.05	0.53	0.611458	0.722736	-7.09
260711_at	myosin, putative similar to myosin	MYA1	AT1G17580	-1.05	-0.07	-0.53	0.611575	0.722824	-7.09
263528_at	putative peroxidase	---	AT2G24800	-1.05	-0.06	-0.53	0.611601	0.722824	-7.09
251952_at	histone H2B - like protein histone H	---	AT3G53650	1.03	0.05	0.53	0.611628	0.722824	-7.09
248740_at	putative protein contains similarity t	---	AT5G48130	-1.06	-0.08	-0.53	0.611783	0.722971	-7.09
255459_at	polyubiquitin (UBQ14) identical to	UBQ14	AT4G02890	1.04	0.06	0.53	0.611837	0.722997	-7.09
246176_at	putative protein DYNAMIN-LIKE PI	---	AT5G28410	-1.04	-0.05	-0.53	0.611883	0.723013	-7.09
253026_at	hypothetical protein	---	AT4G38120	-1.06	-0.09	-0.53	0.611938	0.723041	-7.09
262010_at	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.53	0.612189	0.7233	-7.09
264500_at	hypothetical protein predicted by ge	---	AT1G09370	-1.03	-0.05	-0.53	0.612248	0.723332	-7.09
257416_at	unknown protein	---	AT2G17750	1.05	0.07	0.53	0.61238	0.723418	-7.09
256895_at	zinc-finger protein, putative almost	---	---	-1.04	-0.06	-0.53	0.612384	0.723418	-7.09
252013_at	putative protein	---	AT3G52860	1.04	0.06	0.53	0.612631	0.723672	-7.09
251182_at	putative protein HIRA interacting p	ATERDJ3B	AT3G62600	1.15	0.20	0.53	0.61286	0.723905	-7.09
245076_at	unknown protein	GH3.3	AT2G23170	-1.29	-0.37	-0.53	0.612971	0.723999	-7.09
265652_x_a	hypothetical protein predicted by ge	---	---	-1.05	-0.07	-0.53	0.613465	0.724517	-7.09
252763_at	Expressed protein ; supported by c	---	AT3G42725	-1.05	-0.06	-0.53	0.613492	0.724517	-7.09
245220_at	hypothetical protein contains simila	---	AT1G59171	1.04	0.05	0.53	0.613515	0.724517	-7.09
249752_at	putative protein similar to unknown	LSU2	AT5G24660	1.05	0.08	0.53	0.613537	0.724517	-7.09
258441_at	hypothetical protein predicted by ge	AT3G1726	---	1.04	0.06	0.53	0.613818	0.724812	-7.09
266594_at	hypothetical protein	---	AT2G46190	1.03	0.05	0.53	0.613926	0.724866	-7.09

258951_at	putative phosphatidylinositolglycan	---	AT3G01380	1.05	0.06	0.53	0.613927	0.724866	-7.09
255726_at	lysine and histidine specific transpo	---	AT1G25530	-1.15	-0.21	-0.53	0.613968	0.724876	-7.09
252020_at	SKP1/ASK1 (At6), putative similar	ASK6	AT3G53060	1.03	0.04	0.53	0.614062	0.72495	-7.09
245914_at	putative protein outer membrane p	OEP80	AT5G19620	1.05	0.07	0.53	0.614262	0.725149	-7.09
245189_at	F12A21.18 hypothetical protein	---	AT1G67670	-1.03	-0.05	-0.53	0.614388	0.725222	-7.09
246495_at	putative protein hypothetical protei	---	AT5G16200	-1.16	-0.21	-0.53	0.614388	0.725222	-7.09
254296_at	hypothetical protein	---	AT4G23090	-1.06	-0.08	-0.53	0.614455	0.725264	-7.09
265608_at	hypothetical protein predicted by ge	---	AT2G25380	-1.03	-0.05	-0.53	0.614518	0.725265	-7.09
251212_at	putative protein hypothetical protei	---	---	1.04	0.06	0.53	0.61452	0.725265	-7.09
263833_at	hypothetical protein	---	AT2G40316	1.04	0.05	0.53	0.614572	0.725267	-7.09
248983_at	ras-related GTP-binding protein RH	RHA1	AT5G45130	-1.04	-0.05	-0.53	0.614617	0.725267	-7.09
259438_at	unknown protein similar to putative	AN	AT1G01510	1.06	0.09	0.53	0.614617	0.725267	-7.09
256181_at	light repressible receptor protein ki	---	AT1G51820	1.14	0.20	0.53	0.614904	0.725568	-7.09
245601_at	hypothetical protein	---	AT4G14240	1.05	0.07	0.53	0.614982	0.725623	-7.09
256564_at	alpha/beta hydrolase, putative cont	MES11	AT3G29770	1.11	0.15	0.53	0.6153	0.725961	-7.09
265781_at	putative Athila retroelement ORF1 p	---	---	-1.04	-0.05	-0.53	0.615534	0.726199	-7.09
265121_at	similar to flavin-containing monoox	FMO GS-O	AT1G62560	1.08	0.11	0.53	0.61565	0.726299	-7.09
254760_at	putative protein hypothetical protei	---	AT4G13200	1.04	0.06	0.53	0.615721	0.726344	-7.09
256514_at	oxidoreductase, putative contains F	---	AT1G66130	1.07	0.10	0.53	0.615932	0.726556	-7.09
254473_s_a	putative protein kinase like proteins	---	AT4G20520	1.04	0.05	0.53	0.616031	0.726635	-7.09
246881_at	putative protein histone deacetylas	HDA2	AT5G26040	1.07	0.10	0.53	0.616313	0.72693	-7.09
261151_at	sec14 cytosolic factor, putative sim	---	AT1G19650	-1.04	-0.06	-0.52	0.616488	0.727069	-7.09
245772_at	hypothetical protein similar to putati	---	AT1G30300	-1.07	-0.10	-0.52	0.616495	0.727069	-7.09
255144_at	putative protein predicted proteins -	---	---	1.03	0.05	0.52	0.616573	0.727124	-7.09
245823_at	hypothetical protein predicted by ge	---	AT1G57906	-1.05	-0.06	-0.52	0.616659	0.727188	-7.09
253839_at	putative protein prolactin-induced T	---	AT4G27890	-1.05	-0.07	-0.52	0.616711	0.727204	-7.09
252321_at	hypothetical protein ;supported by	---	AT3G48510	-1.05	-0.07	-0.52	0.61674	0.727204	-7.09
245887_at	putative protein CD2 cytoplasmic d	---	AT5G09390	1.03	0.05	0.52	0.616769	0.727204	-7.09
264431_at	RNA polymerase II subunit (hsRPB	---	AT1G61700	1.05	0.07	0.52	0.617056	0.727506	-7.10
255210_at	may be a pseudogene	---	---	-1.04	-0.05	-0.52	0.617114	0.727536	-7.10
263363_at	putative cold-regulated protein ;sup	---	AT2G03850	1.13	0.18	0.52	0.617197	0.727597	-7.10
246661_at	putative protein various predicted p	---	---	1.04	0.05	0.52	0.617259	0.727632	-7.10
250362_at	1-D-deoxyxylulose 5-phosphate sy	DXPS3	AT5G11380	1.04	0.05	0.52	0.617343	0.727693	-7.10
250997_at	putative protein histone H2B-2, ton	---	AT5G02570	1.04	0.06	0.52	0.617535	0.727882	-7.10
259785_at	unknown protein ;supported by full-	---	AT1G29490	-1.05	-0.07	-0.52	0.617744	0.72809	-7.10

263201_at	putative ADP-glucose pyrophospho	APS2	AT1G05610	-1.04	-0.06	-0.52	0.618095	0.728443	-7.10
246248_at	hypothetical protein	---	AT4G36560	1.04	0.05	0.52	0.618116	0.728443	-7.10
252088_at	putative protein	---	AT3G52100	1.05	0.07	0.52	0.618138	0.728443	-7.10
259182_at	hypothetical protein predicted by ge	---	AT3G01750	1.08	0.11	0.52	0.618696	0.729041	-7.10
248899_at	carboxy-terminal proteinase D1-like	---	AT5G46390	-1.05	-0.06	-0.52	0.61871	0.729041	-7.10
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb	---	---	1.11	0.15	0.52	0.618784	0.729091	-7.10
264334_at	calcium-dependent protein kinase,	CPK19	AT1G61950	-1.03	-0.05	-0.52	0.618837	0.729106	-7.10
256163_at	terpene cyclase, putative similar to	---	AT1G48820	1.03	0.05	0.52	0.61888	0.729106	-7.10
256571_at	hypothetical protein predicted by ge	---	AT3G30730	-1.03	-0.05	-0.52	0.618893	0.729106	-7.10
245924_at	Tha4 protein - like Tha4 protein, Pi	---	AT5G28750	-1.04	-0.05	-0.52	0.619125	0.729341	-7.10
246227_at	hypothetical protein	---	AT4G36510	-1.05	-0.07	-0.52	0.619239	0.729438	-7.10
252052_at	beta-fructofuranosidase	AtcwINV2	AT3G52600	-1.04	-0.05	-0.52	0.619457	0.729657	-7.10
258506_at	hypothetical protein predicted by ge	---	AT3G06520	1.06	0.08	0.52	0.619558	0.729738	-7.10
256030_at	hypothetical protein contains simila	---	AT1G34110	-1.04	-0.06	-0.52	0.619779	0.729953	-7.10
256814_at	beta-glucosidase, putative similar t	BGLU19	AT3G21370	-1.06	-0.09	-0.52	0.619824	0.729953	-7.10
253574_at	putative protein	---	AT4G31030	-1.06	-0.09	-0.52	0.619836	0.729953	-7.10
259639_at	unknown protein ;supported by full-	---	AT1G52380	1.05	0.07	0.52	0.619917	0.730011	-7.10
254742_at	putative protein various predicted 3	IIL1	AT4G13430	-1.03	-0.05	-0.52	0.62003	0.730106	-7.10
263566_at	hypothetical protein predicted by ge	---	AT2G15340	1.05	0.07	0.52	0.62021	0.730278	-7.10
265226_at	unknown protein ; supported by cD	---	AT2G28430	-1.04	-0.05	-0.52	0.620257	0.730278	-7.10
251158_at	rac-GTP binding protein -like RAC	MIRO2	AT3G63150	1.04	0.06	0.52	0.620272	0.730278	-7.10
263452_at	putative trehalose-6-phosphate pho	---	AT2G22190	1.08	0.11	0.52	0.620371	0.730317	-7.10
265584_at	unknown protein	PIL5	AT2G20180	-1.04	-0.05	-0.52	0.620393	0.730317	-7.10
253941_at	putative protein	---	AT4G26980	-1.04	-0.05	-0.52	0.620401	0.730317	-7.10
264696_at	unknown protein	---	AT1G70230	-1.11	-0.15	-0.52	0.620546	0.73045	-7.10
265459_at	unknown protein ; supported by ful	---	AT2G46540	1.04	0.05	0.52	0.620591	0.730456	-7.10
256539_at	hypothetical protein predicted by ge	---	---	-1.04	-0.05	-0.52	0.620615	0.730456	-7.10
261849_at	pectin methylesterase, putative sim	---	AT1G11370	-1.05	-0.07	-0.52	0.620731	0.730544	-7.10
261028_at	hypothetical protein predicted by ge	---	AT1G26620	-1.04	-0.06	-0.52	0.620754	0.730544	-7.10
262030_s_a	mutator-like transposase, putative	---	---	-1.04	-0.06	-0.52	0.620975	0.730766	-7.10
267097_at	unknown protein predicted by gens	---	AT2G41440	-1.04	-0.05	-0.52	0.621026	0.730788	-7.10
264636_at	hypothetical protein predicted by ge	---	AT1G65490	-1.10	-0.13	-0.52	0.621275	0.731043	-7.10
254901_at	serine/threonine kinase-like protein	---	AT4G11530	1.04	0.06	0.52	0.621327	0.731062	-7.10
262845_at	unknown protein ; supported by cDI	---	AT1G14740	1.08	0.11	0.52	0.621354	0.731062	-7.10
255174_at	putative Athila-like protein	---	---	-1.03	-0.05	-0.52	0.621467	0.731156	-7.10

252122_at	putative protein hypothetical protei	---	AT3G51140	1.05	0.06	0.52	0.621518	0.731179	-7.10
252598_at	putative protein putative proteins A	---	---	-1.03	-0.04	-0.52	0.621681	0.731332	-7.10
255007_at	putative oxidoreductase 11beta-hy	AtHSD5	AT4G10020	1.04	0.05	0.52	0.621829	0.731469	-7.10
246107_at	putative protein various predicted p	---	---	-1.04	-0.06	-0.52	0.621978	0.731607	-7.10
249680_s_a	putative protein strong similarity to	---	AT3G61730	-1.03	-0.04	-0.52	0.622038	0.731639	-7.10
249451_s_a	hypothetical protein	---	AT5G39480	-1.03	-0.05	-0.52	0.622114	0.731692	-7.10
250772_at	putative protein contains similarity t	---	AT5G05420	1.07	0.09	0.52	0.622402	0.731898	-7.10
262893_at	hypothetical protein contains simila	---	AT1G59790	-1.04	-0.05	-0.52	0.622438	0.731898	-7.10
256307_at	pectate lyase, putative contains Pfa	---	AT1G30350	-1.03	-0.05	-0.52	0.622453	0.731898	-7.10
256859_at	hypothetical protein	---	AT3G22940	-1.05	-0.07	-0.52	0.622478	0.731898	-7.10
248011_at	S-adenosyl-L-methionine:salicylic a	GAMT2	AT5G56300	1.03	0.05	0.52	0.622483	0.731898	-7.10
245354_at	Lil3 protein ;supported by full-length	LIL3:1	AT4G17600	-1.05	-0.07	-0.52	0.622511	0.731898	-7.10
251231_at	Glutathione transferase III-like prot	ATGSTF13	AT3G62760	1.04	0.06	0.52	0.622514	0.731898	-7.10
245239_at	putative homeodomain-protein sim	FWA	AT4G25530	-1.04	-0.06	-0.52	0.622547	0.731899	-7.10
253161_at	senescence-associated protein sen	SEN1	AT4G35770	1.12	0.16	0.52	0.622765	0.732112	-7.10
248145_at	unknown protein ;supported by full-	---	AT5G54880	1.05	0.06	0.52	0.622793	0.732112	-7.10
262895_at	hypothetical protein predicted by ge	---	AT1G59800	-1.05	-0.07	-0.51	0.623231	0.732589	-7.10
264062_at	unknown protein	---	AT2G27950	1.04	0.06	0.51	0.623306	0.73264	-7.10
252009_at	zinc finger - like protein zinc finger	---	AT3G52800	-1.06	-0.09	-0.51	0.623352	0.732656	-7.10
253250_at	hypothetical protein	---	AT4G34690	-1.03	-0.05	-0.51	0.623487	0.732778	-7.10
253375_at	hypothetical protein	---	AT4G33280	1.04	0.06	0.51	0.623773	0.733076	-7.10
261706_at	hypothetical protein similar to hypot	---	---	-1.03	-0.05	-0.51	0.623982	0.733284	-7.10
259807_at	hypothetical protein predicted by ge	---	AT1G47920	-1.04	-0.05	-0.51	0.624073	0.733323	-7.10
251869_at	putative protein	---	AT3G54500	-1.07	-0.10	-0.51	0.62408	0.733323	-7.10
263540_at	unknown protein	---	AT2G24780	1.04	0.06	0.51	0.624384	0.733615	-7.10
257845_at	unknown protein GC donor splice s	---	AT3G28430	1.04	0.06	0.51	0.624393	0.733615	-7.10
245113_at	hypothetical protein predicted by ge	MIZ1	AT2G41660	-1.06	-0.08	-0.51	0.624486	0.733686	-7.10
266629_at	putative serpin	---	AT2G35590	-1.04	-0.06	-0.51	0.624539	0.733711	-7.10
248705_at	putative protein similar to unknown	---	AT5G48520	1.06	0.08	0.51	0.624572	0.733713	-7.10
250059_at	peroxidase ATP13a ; supported by	---	AT5G17820	-1.04	-0.06	-0.51	0.624654	0.733747	-7.10
263418_at	putative selenium-binding protein	---	AT2G17210	1.04	0.06	0.51	0.624666	0.733747	-7.10
262983_at	hypothetical protein similar to unkno	---	AT1G54550	-1.05	-0.06	-0.51	0.624869	0.733948	-7.10
255293_at	putative zinc finger protein	---	AT4G04730	-1.04	-0.06	-0.51	0.625141	0.734229	-7.10
255332_at	predicted protein of unknown functi	---	AT4G04340	1.04	0.05	0.51	0.625253	0.734323	-7.10
255122_at	putative athila-like protein	---	---	1.06	0.08	0.51	0.625289	0.734328	-7.10

251671_at	putative protein hypothetical protei	---	AT3G57210	-1.04	-0.06	-0.51	0.625402	0.734401	-7.10
258639_at	polygalacturonase (PGA3) identica	---	AT3G07820	1.03	0.04	0.51	0.625442	0.734401	-7.10
267631_at	hypothetical protein predicted by ge	---	AT2G42150	-1.04	-0.05	-0.51	0.625448	0.734401	-7.10
267440_at	putative anthranilate N-hydroxycinn	SHT	AT2G19070	-1.04	-0.06	-0.51	0.625571	0.734508	-7.10
266326_at	putative cytochrome b5 ;supported	CB5-C	AT2G46650	1.16	0.21	0.51	0.625638	0.73454	-7.10
255541_s_a	P-glycoprotein-like protein pgp3 sim	PGP5	AT4G01820	1.04	0.05	0.51	0.625663	0.73454	-7.10
258962_at	putative cytochrome P450 similar to	CYP77A6	AT3G10570	-1.24	-0.31	-0.51	0.626026	0.734909	-7.10
255423_at	putative calmodulin	---	AT4G03290	-1.04	-0.05	-0.51	0.626042	0.734909	-7.10
251299_at	putative protein transcription factor	---	AT3G61950	-1.05	-0.06	-0.51	0.626099	0.734938	-7.10
253781_at	putative protein predicted protein, A	---	AT4G28580	-1.04	-0.05	-0.51	0.626223	0.735045	-7.10
247129_at	alpha-mannosidase	---	AT5G66150	-1.07	-0.09	-0.51	0.626363	0.735136	-7.10
267282_at	unknown protein ; supported by cD	---	AT2G19390	1.05	0.06	0.51	0.626364	0.735136	-7.10
256503_at	myb-related protein similar to GI:79	ATRL6	AT1G75250	-1.16	-0.22	-0.51	0.626746	0.735547	-7.10
247028_at	DNA polymerase alpha 1	ICU2	AT5G67100	-1.10	-0.13	-0.51	0.626779	0.735547	-7.10
265434_at	predicted protein	---	AT2G20805	-1.03	-0.05	-0.51	0.626899	0.73565	-7.10
245973_at	putative protein predicted proteins,	---	---	-1.03	-0.04	-0.51	0.626966	0.735676	-7.10
255705_at	hypothetical protein ;supported by	---	AT4G00160	1.03	0.05	0.51	0.626986	0.735676	-7.10
254560_at	kinase-like protein protein kinase r	---	AT4G19110	1.03	0.05	0.51	0.627329	0.736041	-7.10
257330_at	hypothetical protein	---	---	-1.04	-0.06	-0.51	0.627476	0.736176	-7.10
250629_at	respiratory burst oxidase protein A	ATRBOHA	AT5G07390	-1.04	-0.06	-0.51	0.627829	0.736552	-7.10
258418_at	unknown protein	---	AT3G16660	1.16	0.21	0.51	0.627949	0.736655	-7.10
260485_at	putative amp-binding protein simila	---	AT1G68270	1.04	0.06	0.51	0.628029	0.736711	-7.10
264190_at	heme activated protein, putative si	NF-YC3	AT1G54830	-1.03	-0.05	-0.51	0.628263	0.736948	-7.10
247531_at	putative protein protein kinase 1, P	---	AT5G61550	-1.05	-0.07	-0.51	0.628345	0.737006	-7.10
259901_at	disease resistance protein, putative	AtRLP14	AT1G74180	1.05	0.08	0.51	0.628431	0.737068	-7.10
256555_at	hypothetical protein similar to putati	---	---	-1.03	-0.05	-0.51	0.62853	0.737147	-7.10
261196_at	unknown protein	SCRM2	AT1G12860	-1.08	-0.12	-0.51	0.628704	0.737299	-7.11
252648_at	disease resistance protein homolo	---	AT3G44630	-1.04	-0.06	-0.51	0.628724	0.737299	-7.11
252189_at	cyclin D3-like protein Nicotiana tab	CYCD3;3	AT3G50070	1.06	0.09	0.51	0.62911	0.737667	-7.11
259722_at	putative DNA helicase similar to AT	ATRECQ4	AT1G60930	-1.03	-0.04	-0.51	0.629126	0.737667	-7.11
249349_at	putative transcription factor MYB24	MYB24	AT5G40350	-1.04	-0.06	-0.51	0.629135	0.737667	-7.11
265830_at	putative helicase	---	---	1.05	0.07	0.51	0.629256	0.737771	-7.11
250251_at	putative protein contains similarity t	---	AT5G13670	-1.04	-0.06	-0.51	0.629347	0.737805	-7.11
252551_at	phospholipase - like protein cytoso	---	AT3G45880	1.06	0.08	0.51	0.62935	0.737805	-7.11
250610_at	glycine-rich protein PUTG1 ;suppo	GRP19	AT5G07550	-1.07	-0.09	-0.51	0.629417	0.737846	-7.11

249270_at	putative protein similar to unknown	---	AT5G41780	1.03	0.05	0.51	0.629563	0.737979	-7.11
262679_at	unknown protein ; supported by cDI	LCR67	AT1G75830	-1.05	-0.07	-0.51	0.629661	0.738032	-7.11
245519_at	retrotransposon like protein	---	---	-1.03	-0.05	-0.50	0.629673	0.738032	-7.11
252111_at	propable disease resistance protei	---	AT3G51570	-1.06	-0.08	-0.50	0.629923	0.738287	-7.11
257446_at	hypothetical protein predicted by ge	---	AT2G10440	1.03	0.04	0.50	0.630066	0.738417	-7.11
251620_at	putative protein hypothetical protei	---	AT3G58060	-1.05	-0.07	-0.50	0.630374	0.73874	-7.11
249305_at	putative protein strong similarity to	---	AT5G41490	-1.05	-0.07	-0.50	0.630468	0.738775	-7.11
259678_at	putative 30S ribosomal protein S13	---	AT1G77750	-1.06	-0.09	-0.50	0.630469	0.738775	-7.11
266584_s_a	putative steroid sulfotransferase	ST4C	AT1G13430	-1.03	-0.04	-0.50	0.630523	0.7388	-7.11
252589_s_a	putative protein different transporte	NAXT1	AT3G45650	1.11	0.15	0.50	0.630838	0.739131	-7.11
262562_at	hypothetical protein predicted by ge	---	AT1G34220	1.03	0.05	0.50	0.631141	0.739449	-7.11
263512_at	hypothetical protein predicted by ge	---	---	-1.04	-0.05	-0.50	0.631217	0.739499	-7.11
265827_at	hypothetical protein predicted by ge	VOZ2	AT2G42400	1.03	0.05	0.50	0.63126	0.739512	-7.11
261880_at	unknown protein	HIT1	AT1G50500	-1.04	-0.06	-0.50	0.631351	0.739581	-7.11
249058_at	disease resistance protein-like	TAO1	AT5G44510	-1.05	-0.06	-0.50	0.631399	0.7396	-7.11
248556_at	unknown protein	---	AT5G50350	1.05	0.07	0.50	0.631595	0.739788	-7.11
255938_at	hypothetical protein contains Pfam	---	AT1G12620	-1.05	-0.07	-0.50	0.631636	0.739788	-7.11
253787_at	serine/threonine kinase-like protein	---	AT4G28670	-1.04	-0.06	-0.50	0.631658	0.739788	-7.11
253937_at	putative NPK1-related protein kina	MAPKKK16	AT4G26890	-1.07	-0.10	-0.50	0.631702	0.739802	-7.11
266855_at	unknown protein	---	AT2G26920	-1.05	-0.07	-0.50	0.632275	0.740435	-7.11
251398_at	zinc finger protein - like ZPT3-3, Pe	---	AT3G60580	1.05	0.07	0.50	0.632584	0.740759	-7.11
250553_at	putative protein PTD008, Homo sa	---	AT5G07960	1.05	0.07	0.50	0.632651	0.740799	-7.11
246363_at	hypothetical protein	---	AT1G40390	-1.05	-0.06	-0.50	0.63277	0.7409	-7.11
245901_at	HOMEOBOX PROTEIN KNOTTED	KNAT4	AT5G11060	1.06	0.09	0.50	0.632852	0.740958	-7.11
247647_at	respiratory burst oxidase protein - I	---	AT5G60010	-1.04	-0.06	-0.50	0.632901	0.740977	-7.11
257161_at	hypothetical protein predicted by ge	SMAP2	AT3G24280	-1.04	-0.05	-0.50	0.632933	0.740977	-7.11
245497_at	hypothetical protein	---	AT4G16460	-1.04	-0.06	-0.50	0.633068	0.741086	-7.11
254124_at	hypothetical protein ; supported by	---	AT4G24500	-1.04	-0.06	-0.50	0.633091	0.741086	-7.11
250117_at	isopentenyl pyrophosphate:dimethy	IPP1	AT5G16440	1.07	0.09	0.50	0.633191	0.741123	-7.11
261096_at	4-coumarate:coenzyme A ligase, p	ACOS5	AT1G62940	-1.04	-0.06	-0.50	0.633205	0.741123	-7.11
264869_at	hypothetical protein similar to hypot	---	AT1G24350	1.04	0.06	0.50	0.633248	0.741123	-7.11
254514_at	hypothetical protein	---	AT4G20250	-1.05	-0.07	-0.50	0.633253	0.741123	-7.11
255450_at	putative protein similar to T5J8.18	---	AT4G02850	-1.04	-0.06	-0.50	0.633335	0.741178	-7.11
259205_at	hypothetical protein similar to putati	---	AT3G09030	-1.04	-0.06	-0.50	0.633364	0.741178	-7.11
266645_at	hypothetical protein	---	AT2G29880	-1.04	-0.05	-0.50	0.633492	0.741182	-7.11

262191_at	hypothetical protein contains simila	---	---	-1.04	-0.06	-0.50	0.633511	0.741182	-7.11
262360_at	receptor protein kinase, putative si	---	AT1G73080	1.18	0.24	0.50	0.633522	0.741182	-7.11
251887_at	FKBP12 interacting protein (FIP37)	ATFIP37	AT3G54170	-1.06	-0.09	-0.50	0.633526	0.741182	-7.11
249097_at	putative protein strong similarity to	---	AT5G43520	1.05	0.06	0.50	0.633594	0.741182	-7.11
252289_at	putative protein pre-mRNA splicing	---	AT3G49130	-1.06	-0.09	-0.50	0.633595	0.741182	-7.11
246705_x_a	putative protein predicted resistanc	---	---	1.04	0.06	0.50	0.633628	0.741182	-7.11
264680_at	hypothetical protein predicted by ge	---	AT1G65510	1.09	0.12	0.50	0.633635	0.741182	-7.11
263714_at	putative tyrosine aminotransferase	SUR1	AT2G20610	1.08	0.11	0.50	0.63366	0.741182	-7.11
260251_at	putative heat shock protein similar t	---	AT1G74250	-1.06	-0.08	-0.50	0.63389	0.741398	-7.11
257440_at	unknown protein	---	AT2G24880	-1.03	-0.05	-0.50	0.63391	0.741398	-7.11
248858_at	AP47 50p (gb|AAB88283.1) ; suppo	---	AT5G46630	-1.04	-0.06	-0.50	0.634134	0.741622	-7.11
254309_s_a	putative protein predicted protein, A	---	AT4G22390	-1.05	-0.07	-0.50	0.634567	0.74209	-7.11
259247_at	unknown protein predicted by gene	---	AT3G07570	-1.05	-0.07	-0.50	0.634694	0.74218	-7.11
248383_at	putative protein contains similarity t	---	AT5G51900	-1.04	-0.05	-0.50	0.634709	0.74218	-7.11
256358_at	unknown protein	---	AT1G66470	-1.05	-0.07	-0.50	0.634779	0.742224	-7.11
265293_at	hypothetical protein predicted by ge	---	---	-1.04	-0.06	-0.50	0.634838	0.742255	-7.11
247750_at	protein kinase 6 - like protein kinas	---	AT5G58950	1.04	0.06	0.50	0.635095	0.742517	-7.11
249380_at	glutaredoxin -like protein glutaredo	---	AT5G40370	-1.04	-0.05	-0.50	0.63533	0.742703	-7.11
266433_at	unknown protein	---	AT2G07110	-1.04	-0.05	-0.50	0.635349	0.742703	-7.11
260380_at	hypothetical protein predicted by ge	---	AT1G73870	1.08	0.12	0.50	0.635352	0.742703	-7.11
251159_at	hypothetical protein	---	AT3G63230	1.06	0.08	0.50	0.635475	0.74281	-7.11
245944_at	putative protein various predicted p	MSL9	AT5G19520	-1.04	-0.06	-0.50	0.635562	0.742873	-7.11
265924_at	putative geranylgeranyl pyrophosph	---	AT2G18620	-1.03	-0.04	-0.50	0.635703	0.743	-7.11
263044_at	spore germination protein c2 simila	---	AT1G23360	1.04	0.06	0.50	0.635739	0.743004	-7.11
265696_at	putative molybdopterin biosynthesis	CNX2	AT2G31955	1.07	0.10	0.50	0.635834	0.743077	-7.11
245567_at	germin precursor oxalate oxidase	GLP9	AT4G14630	1.18	0.24	0.50	0.635873	0.743084	-7.11
253345_at	putative protein	BCA5	AT4G33580	-1.05	-0.08	-0.50	0.636306	0.743552	-7.11
247468_at	ARF1-binding protein ; supported b	ARF2	AT5G62000	1.04	0.06	0.49	0.636447	0.743679	-7.11
262308_at	unknown protein	---	AT1G71010	1.05	0.07	0.49	0.636494	0.743681	-7.11
261416_at	ribosomal protein S15 identical to C	RPS15A	AT1G07770	1.08	0.11	0.49	0.636514	0.743681	-7.11
262458_at	serine/threonine kinase, putative si	---	AT1G11280	-1.04	-0.06	-0.49	0.636561	0.743698	-7.11
251101_at	putative transporter protein Na+/H+	CHX26	AT5G01680	-1.03	-0.04	-0.49	0.636619	0.743728	-7.11
262642_at	hypothetical protein predicted by ge	---	AT1G62690	-1.04	-0.06	-0.49	0.636677	0.743757	-7.11
246373_at	receptor-like protein kinase, putativ	---	AT1G51860	-1.06	-0.09	-0.49	0.636715	0.743764	-7.11
253371_at	putative protein FAB1 protein, Sac	---	AT4G33240	-1.04	-0.06	-0.49	0.636895	0.743863	-7.11

260324_at	unknown protein similar to hypothet	ISPF	AT1G63970	-1.05	-0.07	-0.49	0.636901	0.743863	-7.11
263908_at	hypothetical protein predicted by ge	---	AT2G36480	-1.04	-0.06	-0.49	0.636919	0.743863	-7.11
260943_at	thioredoxin, putative similar to thior	ATTRX5	AT1G45145	1.06	0.08	0.49	0.636939	0.743863	-7.11
245990_at	putative protein predicted proteins,	---	AT5G20640	-1.06	-0.08	-0.49	0.637027	0.743863	-7.11
263897_at	putative shikimate kinase precursor	---	AT2G21940	1.07	0.10	0.49	0.637072	0.743863	-7.11
266039_s_a	hypothetical protein	---	AT2G07739	-1.05	-0.07	-0.49	0.637084	0.743863	-7.11
245894_at	putative protein ; supported by full-	---	AT5G09310	-1.04	-0.05	-0.49	0.637084	0.743863	-7.11
260415_at	putative protein kinase similar to pr	---	AT1G69790	1.07	0.10	0.49	0.637094	0.743863	-7.11
264715_at	hypothetical protein contains simila	---	AT1G70180	1.04	0.06	0.49	0.637419	0.744205	-7.11
266343_at	putative non-LTR retroelement reve	---	---	-1.05	-0.06	-0.49	0.637463	0.744218	-7.11
261516_at	hypoxanthine ribosyl transferase, p	---	AT1G71750	1.04	0.05	0.49	0.637601	0.744341	-7.11
262774_at	chloroplast nucleoid DNA binding p	---	AT1G13230	-1.03	-0.05	-0.49	0.637678	0.744392	-7.11
258734_at	putative DNA-binding protein simila	---	AT3G05860	-1.04	-0.05	-0.49	0.637999	0.74473	-7.11
252522_at	hypothetical protein	---	AT1G32337	-1.04	-0.05	-0.49	0.63831	0.745028	-7.11
252533_at	putative protein predicted proteins,	---	AT3G46110	-1.12	-0.16	-0.49	0.63832	0.745028	-7.11
249374_at	20S proteasome beta subunit PBB2	PBB2	AT5G40580	-1.04	-0.06	-0.49	0.638433	0.745122	-7.11
255964_at	hypothetical protein predicted by ge	ZYP1b	AT1G22275	-1.04	-0.05	-0.49	0.638528	0.745168	-7.11
266217_at	unknown protein	AT2G2883(	---	1.04	0.05	0.49	0.638538	0.745168	-7.11
259510_at	hypothetical protein predicted by ge	---	AT1G43970	-1.03	-0.04	-0.49	0.638722	0.745325	-7.11
266313_at	putative protein kinase contains a p	CIPK3	AT2G26980	1.07	0.10	0.49	0.638738	0.745325	-7.11
248016_at	putative protein similar to unknown	---	AT5G56380	1.05	0.07	0.49	0.639038	0.745636	-7.11
261691_at	branched-chain amino acid aminot	---	AT1G50060	-1.03	-0.05	-0.49	0.63907	0.745636	-7.11
255229_at	F-box protein family, AtFBL22 cont	---	AT4G05490	1.03	0.04	0.49	0.6392	0.74575	-7.11
249767_at	acidic endochitinase (dbj|BAA2186	---	AT5G24090	1.11	0.15	0.49	0.63933	0.745863	-7.11
254699_at	putative protein predicted protein, /	---	AT4G17990	-1.04	-0.06	-0.49	0.639363	0.745864	-7.11
256795_at	20S proteasome subunit PAC1 ide	PAC1	AT3G22110	-1.03	-0.05	-0.49	0.639532	0.746022	-7.11
245686_at	Expressed protein ; supported by c	J2	AT5G22060	1.08	0.12	0.49	0.639773	0.746254	-7.11
249422_at	putative protein predicted proteins,	AtHB23	AT5G39760	-1.05	-0.07	-0.49	0.639796	0.746254	-7.11
246618_at	putative protein similar to unknown	---	AT5G36280	-1.03	-0.05	-0.49	0.640031	0.746467	-7.11
262497_at	putative 20S proteasome beta sub	PBC1	AT1G21720	1.04	0.06	0.49	0.640044	0.746467	-7.11
251532_at	putative protein F-box protein Fbl2	---	AT3G58530	1.04	0.05	0.49	0.640262	0.746683	-7.11
254714_at	myb-like protein snapdragon myb p	AtMYB79	AT4G13480	-1.04	-0.05	-0.49	0.640322	0.746705	-7.11
249853_at	farnesyl cysteine carboxyl methyltra	ATSTE14A	AT5G23320	-1.04	-0.06	-0.49	0.640361	0.746705	-7.11
262228_at	protein kinase, putative similar to p	---	AT1G68690	-1.15	-0.20	-0.49	0.640379	0.746705	-7.11
257716_at	hypothetical protein predicted by ge	---	AT3G18300	-1.04	-0.06	-0.49	0.64046	0.746761	-7.11

264097_s_a	NADH dehydrogenase, putative sir	---	AT1G16700	1.04	0.05	0.49	0.640504	0.746775	-7.11
261075_at	unknown protein	---	AT1G07280	1.04	0.06	0.49	0.640549	0.746789	-7.11
254535_at	aspartate kinase-homoserine dehy	AK-HSDH I	AT4G19710	-1.04	-0.05	-0.49	0.640917	0.747179	-7.12
245743_at	hypothetical protein contains simila	---	AT1G51080	1.06	0.08	0.49	0.640949	0.747179	-7.12
266667_at	hypothetical protein predicted by ge	---	AT2G29770	1.03	0.05	0.49	0.641263	0.747507	-7.12
256167_at	hypothetical protein similar to putati	---	---	-1.04	-0.05	-0.49	0.641629	0.747895	-7.12
259613_at	hypothetical protein predicted by ge	---	AT1G48010	-1.03	-0.05	-0.49	0.641686	0.747924	-7.12
266486_at	hypothetical protein predicted by ge	---	AT2G47950	1.20	0.27	0.49	0.641756	0.747958	-7.12
249656_at	putative protein hypothetical protein	---	AT5G37130	1.03	0.04	0.49	0.641824	0.747958	-7.12
244941_at	hypothetical protein	---	---	-1.05	-0.07	-0.49	0.641826	0.747958	-7.12
259005_at	unknown protein similar to nodule-s	---	AT3G01930	-1.05	-0.07	-0.49	0.641847	0.747958	-7.12
260570_at	stearoyl-ACP desaturase ; support	SSI2	AT2G43710	1.06	0.08	0.49	0.642018	0.748119	-7.12
247916_at	adenosylmethionine-8-amino-7-oxo	BIO1	AT5G57590	-1.04	-0.06	-0.49	0.642153	0.748238	-7.12
250543_at	DR1-like protein TATA-binding pro	NF-YB12	AT5G08190	1.04	0.06	0.49	0.642325	0.7484	-7.12
251065_at	lipid-transfer protein-like lipid-trans	---	AT5G01870	1.05	0.07	0.49	0.642573	0.748623	-7.12
247420_at	unknown protein	---	AT5G63100	-1.06	-0.08	-0.49	0.642614	0.748623	-7.12
256434_at	putative 60S ribosomal protein L37a	---	AT3G10950	1.03	0.05	0.49	0.642614	0.748623	-7.12
266314_at	Argonaute (AGO1)-like protein ; su	AGO4	AT2G27040	-1.05	-0.08	-0.49	0.642904	0.748899	-7.12
259549_at	unknown protein ;supported by full-	---	AT1G35290	-1.04	-0.05	-0.49	0.642917	0.748899	-7.12
262424_at	hypothetical protein predicted by ge	---	AT1G47680	1.03	0.05	0.49	0.64298	0.748934	-7.12
264104_at	En/Spm-like transposon protein rela	---	---	-1.04	-0.06	-0.48	0.643728	0.749767	-7.12
249457_s_a	zinc finger -like protein transcriptior	VIM4	AT1G66040	1.05	0.08	0.48	0.643829	0.749846	-7.12
266605_at	putative SNF2 subfamily transcripti	BRM	AT2G46020	1.04	0.05	0.48	0.643894	0.749884	-7.12
246936_at	putative protein hypothetical protei	---	AT5G25360	1.04	0.05	0.48	0.643951	0.749912	-7.12
256580_s_a	hypothetical protein	---	AT3G28810	-1.03	-0.05	-0.48	0.644348	0.750336	-7.12
265583_at	unknown protein	---	AT2G20010	-1.03	-0.05	-0.48	0.644485	0.750457	-7.12
267245_at	hypothetical protein	---	AT2G02640	-1.03	-0.05	-0.48	0.644743	0.75072	-7.12
252614_at	serpin-like protein serpin - Hordeur	---	AT3G45220	-1.03	-0.04	-0.48	0.644867	0.750825	-7.12
245004_at	hypothetical protein	---	---	1.05	0.07	0.48	0.645123	0.751048	-7.12
266555_at	G-box binding bZIP transcription fa	GBF3	AT2G46270	1.09	0.13	0.48	0.645133	0.751048	-7.12
256341_at	deoxyguanosine kinase, putative s	---	AT1G72040	1.08	0.11	0.48	0.645169	0.751048	-7.12
264755_at	receptor kinase, putative similar to	---	AT1G61390	-1.04	-0.06	-0.48	0.64519	0.751048	-7.12
265892_at	hypothetical protein predicted by ge	---	AT2G15020	-1.08	-0.10	-0.48	0.645302	0.75114	-7.12
259084_at	putative inner mitochondrial membr	ATTIM23-3	AT3G04800	-1.04	-0.06	-0.48	0.645362	0.751171	-7.12
261756_at	Expressed protein ; supported by fu	---	AT1G08315	1.09	0.12	0.48	0.645687	0.751512	-7.12

253694_at	Expressed protein ; supported by fu	---	AT4G29735	1.04	0.06	0.48	0.645723	0.751515	-7.12
264622_at	putative vacuolar sorting protein 35	VPS35A	AT2G17790	1.04	0.06	0.48	0.645789	0.751522	-7.12
264732_at	serpin, putative similar to serpin GI	---	AT1G62160	-1.03	-0.05	-0.48	0.645813	0.751522	-7.12
244907_at	hypothetical protein	---	---	-1.03	-0.05	-0.48	0.645828	0.751522	-7.12
248902_at	unknown protein	---	AT5G46440	1.04	0.05	0.48	0.645913	0.751582	-7.12
252476_at	glucosyltransferase-like protein UD	---	AT3G46650	-1.05	-0.07	-0.48	0.646051	0.751705	-7.12
251692_s_a	serine carboxypeptidase-like protei	---	AT3G52020	1.04	0.05	0.48	0.646131	0.75176	-7.12
257520_at	hypothetical protein	---	AT3G07710	1.04	0.06	0.48	0.646223	0.75179	-7.12
253915_at	putative protein centrin, Marsilea v	---	AT4G27280	-1.19	-0.26	-0.48	0.646223	0.75179	-7.12
261907_at	4-coumarate:CoA ligase 3 identical	4CL3	AT1G65060	-1.11	-0.15	-0.48	0.646293	0.751834	-7.12
251046_at	kinesin -like protein kinesin, Xenop	---	AT5G02370	-1.03	-0.05	-0.48	0.64645	0.751977	-7.12
255744_at	hypothetical protein predicted by ge	---	---	1.03	0.04	0.48	0.6465	0.751997	-7.12
247618_at	receptor like protein kinase recepto	---	AT5G60280	1.04	0.06	0.48	0.6467	0.752177	-7.12
253315_at	putative protein various predicted p	---	AT4G33900	-1.04	-0.06	-0.48	0.64672	0.752177	-7.12
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=	---	---	1.08	0.11	0.48	0.646845	0.752283	-7.12
252237_at	putative protein lateral suppressor	---	AT3G49950	1.05	0.07	0.48	0.647163	0.752614	-7.12
247430_at	putative protein contains similarity t	---	AT5G62610	1.05	0.06	0.48	0.647199	0.752618	-7.12
251425_at	putative protein chloroplast Cpn21	---	AT3G60210	1.04	0.06	0.48	0.647262	0.752653	-7.12
246004_at	germin-like protein ; supported by c	GER3	AT5G20630	-1.43	-0.51	-0.48	0.647494	0.752851	-7.12
250200_at	peroxidase ATP20a (emb|CAA6733	---	AT5G14130	-1.05	-0.06	-0.48	0.647498	0.752851	-7.12
256960_at	unknown protein ;supported by full	---	AT3G13510	1.05	0.07	0.48	0.647604	0.752936	-7.12
253145_at	hypothetical protein	---	AT4G35560	-1.08	-0.10	-0.48	0.647654	0.752955	-7.12
261283_s_a	hypothetical protein predicted by ge	---	---	-1.03	-0.05	-0.48	0.64782	0.75311	-7.12
256001_at	unknown protein contains similarity	---	AT1G29850	-1.05	-0.07	-0.48	0.647922	0.75319	-7.12
267432_at	putative UDP-N-acetylglucosamine	---	AT2G35020	1.06	0.09	0.48	0.647979	0.753219	-7.12
266789_at	unknown protein ; supported by ful	---	AT2G29020	1.04	0.05	0.48	0.648043	0.753225	-7.12
261453_at	O-methyltransferase, putative simil	---	AT1G21130	1.09	0.13	0.48	0.648051	0.753225	-7.12
251050_at	putative protein	---	AT5G02440	-1.04	-0.06	-0.48	0.648156	0.753309	-7.12
260159_at	putative helicase similar to helicase	---	AT1G79890	-1.04	-0.06	-0.48	0.648265	0.753398	-7.12
263434_at	putative homeodomain transcriptior	PRS	AT2G28610	1.03	0.05	0.48	0.64831	0.753411	-7.12
245066_at	putative serine/threonine protein ph	TOPP4	AT2G39840	-1.04	-0.06	-0.48	0.64842	0.7535	-7.12
255392_at	hypothetical protein	---	---	-1.03	-0.04	-0.48	0.648501	0.753556	-7.12
260091_at	putative serine carboxypeptidase s	scpl5	AT1G73290	-1.04	-0.05	-0.48	0.648548	0.753572	-7.12
254783_at	hydrolase-like protein 2-hydroxy-6-	---	AT4G12830	1.09	0.13	0.48	0.648637	0.753637	-7.12
257704_at	myb-related transcription factor, pu	ATMYB67	AT3G12720	-1.03	-0.04	-0.48	0.64872	0.753696	-7.12

259844_at	lipid transfer protein, putative simila	---	AT1G73560	-1.04	-0.05	-0.48	0.648767	0.753712	-7.12
259508_at	hypothetical protein predicted by ge	---	---	-1.06	-0.08	-0.48	0.649007	0.753943	-7.12
265014_at	hypothetical protein similar to deac	---	AT1G24430	-1.06	-0.08	-0.48	0.649047	0.753943	-7.12
262032_at	biotin holocarboxylase synthetase,	HCS2	AT1G37150	1.03	0.05	0.48	0.649065	0.753943	-7.12
259266_at	hypothetical protein predicted by ge	---	AT3G01240	-1.03	-0.05	-0.48	0.649137	0.753978	-7.12
247802_at	putative protein RING-H2 zinc finge	ATL63	AT5G58580	1.04	0.06	0.48	0.649186	0.753978	-7.12
263855_at	putative non-LTR retrolelement reve	---	AT2G04420	-1.04	-0.06	-0.48	0.649228	0.753978	-7.12
262102_at	hypothetical protein contains simila	CUL2	AT1G02980	-1.03	-0.05	-0.48	0.649233	0.753978	-7.12
256203_at	hypothetical protein	---	AT1G50800	-1.04	-0.06	-0.48	0.649268	0.753978	-7.12
255873_at	hypothetical protein predicted by ge	LBD13	AT2G30340	-1.04	-0.06	-0.48	0.6493	0.753978	-7.12
245236_at	putative DNA mismatch repair prot	MSH3	AT4G25540	1.03	0.05	0.48	0.649326	0.753978	-7.12
263750_at	unknown protein	---	AT2G21530	1.05	0.07	0.48	0.649407	0.754033	-7.12
257529_at	hypothetical protein predicted by ge	---	AT3G03290	-1.04	-0.05	-0.48	0.649514	0.754118	-7.12
262508_at	serine/threonine kinase, putative si	---	AT1G11300	-1.09	-0.13	-0.48	0.649625	0.754202	-7.12
256318_s_a	hypothetical protein	---	---	1.03	0.05	0.48	0.649652	0.754202	-7.12
250302_at	fructosidase - like protein fructosida	AtcwINV6	AT5G11920	1.21	0.27	0.47	0.649884	0.754433	-7.12
246464_at	quinone oxidoreductase -like prote	---	AT5G16980	-1.04	-0.05	-0.47	0.649952	0.754452	-7.12
266512_at	unknown protein	---	AT2G47690	-1.03	-0.05	-0.47	0.649967	0.754452	-7.12
260050_at	hypothetical protein predicted by ge	AGL64	AT1G29960	-1.04	-0.06	-0.47	0.650148	0.754553	-7.12
266580_at	unknown protein ;supported by full-	---	AT2G46260	-1.04	-0.06	-0.47	0.650155	0.754553	-7.12
263022_s_a	gamma-adaptin, putative similar to	---	AT1G23900	1.05	0.08	0.47	0.650199	0.754553	-7.12
251005_at	putative protein various predicted p	---	AT5G02590	1.11	0.15	0.47	0.650209	0.754553	-7.12
265923_at	putative protein kinase contains a p	---	AT2G18470	-1.03	-0.05	-0.47	0.650246	0.754553	-7.12
257309_at	hypothetical protein predicted by ge	---	AT3G28150	-1.03	-0.04	-0.47	0.650252	0.754553	-7.12
248416_at	putative protein disease resistance	---	AT5G51630	-1.04	-0.06	-0.47	0.650343	0.754621	-7.12
266375_at	En/Spm-like transposon protein rela	---	---	-1.04	-0.06	-0.47	0.650381	0.754626	-7.12
261776_at	hypothetical protein similar to putati	---	AT1G76190	1.05	0.07	0.47	0.650423	0.754637	-7.12
257429_at	putative RING zinc finger protein	---	AT2G27940	-1.06	-0.08	-0.47	0.650603	0.754807	-7.12
262481_at	unknown protein Location of ests 1	---	AT1G17080	-1.04	-0.06	-0.47	0.650717	0.754901	-7.12
254381_at	putative protein membrane-associa	---	AT4G21880	1.05	0.06	0.47	0.650915	0.755092	-7.12
264466_at	Expressed protein ; supported by fu	---	AT1G10380	1.08	0.12	0.47	0.651111	0.755271	-7.12
245916_at	putative protein	---	AT5G28720	-1.04	-0.06	-0.47	0.651136	0.755271	-7.12
252560_at	histone H2B -like protein histone H	HTB11	AT3G46030	1.03	0.05	0.47	0.651252	0.755305	-7.12
263101_s_a	hypothetical protein predicted by ge	---	AT2G05230	1.04	0.05	0.47	0.65126	0.755305	-7.12
265421_s_a	predicted protein	---	AT2G20616	-1.04	-0.06	-0.47	0.651265	0.755305	-7.12

246765_at	glutamic acid-rich protein hypothet	---	AT5G27330	1.04	0.06	0.47	0.651338	0.755353	-7.12
260140_at	Myb-related transcription factor, pu	MYB90	AT1G66390	1.04	0.06	0.47	0.651415	0.755403	-7.12
259069_at	lysyl-tRNA synthetase identical to ly	ATKRS-1	AT3G11710	1.05	0.07	0.47	0.651565	0.755539	-7.12
248338_at	HCF106 (gb|AAD32652.1) ; suppo	HCF106	AT5G52440	-1.05	-0.06	-0.47	0.651642	0.755589	-7.12
248533_at	putative protein contains similarity t	---	AT5G50020	1.05	0.08	0.47	0.651907	0.755858	-7.12
252196_at	putative protein predicted protein, /	---	AT3G50200	-1.05	-0.07	-0.47	0.651984	0.75591	-7.12
248615_at	putative protein contains similarity t	AtPNG1	AT5G49570	1.06	0.09	0.47	0.652144	0.756032	-7.12
263818_at	putative retroelement pol polyprotei	---	---	-1.03	-0.04	-0.47	0.652157	0.756032	-7.12
267334_at	hypothetical protein predicted by ge	---	AT2G19420	-1.04	-0.06	-0.47	0.652364	0.756147	-7.12
259446_at	hypothetical protein contains simila	---	AT1G02410	1.05	0.07	0.47	0.652367	0.756147	-7.12
251077_at	putative protein COP1-interacting p	---	AT5G01980	-1.03	-0.04	-0.47	0.652371	0.756147	-7.12
260446_at	unknown protein	---	AT1G72420	1.04	0.06	0.47	0.652408	0.756147	-7.12
259964_at	glutathione transferase, putative si	ATGSTU28	AT1G53680	-1.04	-0.05	-0.47	0.652421	0.756147	-7.12
257307_at	myb-like transcription factor, putati	MYB121	AT3G30210	-1.05	-0.07	-0.47	0.652495	0.756194	-7.12
266827_at	putative serine carboxypeptidase I	SCPL12	AT2G22920	-1.03	-0.05	-0.47	0.652664	0.756352	-7.12
250496_at	inorganic pyrophosphatase - like p	AtPPa6	AT5G09650	-1.11	-0.14	-0.47	0.652825	0.756487	-7.12
265574_at	putative replication protein A1	---	---	-1.04	-0.05	-0.47	0.652847	0.756487	-7.12
248763_at	putative protein similar to unknown	---	AT5G47550	-1.31	-0.39	-0.47	0.653098	0.756721	-7.12
256142_at	hypothetical protein predicted by ge	---	AT1G48790	1.04	0.06	0.47	0.653116	0.756721	-7.12
259860_at	putative protein kinase similar to leu	---	AT1G80640	-1.05	-0.08	-0.47	0.653225	0.756809	-7.12
250129_at	S-adenosylmethionine:2-demethyln	---	AT5G16450	1.04	0.06	0.47	0.653359	0.756867	-7.12
266612_at	22 kDa peroxisomal membrane pro	---	AT2G14860	1.03	0.05	0.47	0.653397	0.756867	-7.12
264035_at	hypothetical protein predicted by ge	---	AT2G03630	1.04	0.06	0.47	0.653408	0.756867	-7.12
263816_at	putative CCHC-type zinc finger prot	---	---	-1.05	-0.07	-0.47	0.653408	0.756867	-7.12
254920_at	putative protein 24 kDa seed matu	BTI2	AT4G11220	-1.05	-0.06	-0.47	0.653573	0.757021	-7.12
263281_at	putative glycine-rich RNA-binding p	---	AT2G14160	1.04	0.05	0.47	0.653664	0.757088	-7.13
264135_at	S-locus protein, putative similar to	---	AT1G79030	-1.04	-0.05	-0.47	0.653831	0.757182	-7.13
260473_at	hypothetical protein predicted by ge	---	AT1G10880	1.04	0.05	0.47	0.65384	0.757182	-7.13
257195_at	hypothetical protein predicted by ge	---	AT3G23680	-1.04	-0.05	-0.47	0.653853	0.757182	-7.13
259920_at	putative phenylalanyl-tRNA synthet	---	AT1G72550	-1.04	-0.05	-0.47	0.653897	0.757182	-7.13
262078_at	hypothetical protein predicted by ge	CW7	AT1G59520	-1.03	-0.05	-0.47	0.653912	0.757182	-7.13
259100_at	DNA-damage-repair/toleration prote	DRT102	AT3G04880	-1.04	-0.06	-0.47	0.654046	0.757299	-7.13
266809_at	unknown protein ; supported by cD	---	AT2G29970	-1.07	-0.10	-0.47	0.654176	0.757411	-7.13
262956_at	eukaryotic translation initiation fact	EIF4A-2	AT1G54270	1.04	0.06	0.47	0.654312	0.75753	-7.13
252741_at	putative protein predicted protein, /	---	AT3G43280	1.03	0.05	0.47	0.654503	0.757712	-7.13

256399_at	hypothetical protein predicted by ge	---	AT3G06240	-1.04	-0.05	-0.47	0.654561	0.757741	-7.13
264095_at	mercaptopyruvate sulfurtransferase	MST1	AT1G79230	1.03	0.05	0.47	0.654682	0.757843	-7.13
264939_at	receptor kinase, putative similar to	---	AT1G60630	-1.04	-0.05	-0.47	0.654849	0.757998	-7.13
256901_at	hypothetical protein contains simila	---	---	-1.03	-0.04	-0.47	0.654935	0.758059	-7.13
262843_at	Expressed protein ; supported by fu	AtHB32	AT1G14687	1.06	0.08	0.47	0.655009	0.758106	-7.13
249890_at	putative protein contains similarity t	WRKY38	AT5G22570	-1.27	-0.35	-0.47	0.655098	0.758133	-7.13
255326_at	hypothetical protein	---	---	1.03	0.04	0.47	0.655109	0.758133	-7.13
266195_at	putative RING zinc finger protein	---	AT2G39100	-1.03	-0.05	-0.47	0.655132	0.758133	-7.13
266543_at	hypothetical protein predicted by ge	---	AT2G35075	-1.03	-0.04	-0.47	0.655195	0.758167	-7.13
245948_at	putative protein ;supported by full-l	---	AT5G19540	1.06	0.08	0.47	0.655239	0.75818	-7.13
260139_at	Myb-related transcription factor, pu	MYB114	AT1G66380	-1.03	-0.05	-0.47	0.655309	0.758223	-7.13
264892_at	GH3-like auxin-regulated protein hi	---	AT1G23160	-1.04	-0.05	-0.47	0.655456	0.758342	-7.13
247688_at	putative protein predicted proteins,	---	AT5G59760	-1.03	-0.05	-0.47	0.655484	0.758342	-7.13
246184_at	beta-D-glucan exohydrolase - like p	---	AT5G20950	1.06	0.09	0.47	0.655512	0.758342	-7.13
261000_at	hypothetical protein predicted by ge	---	AT1G26540	-1.03	-0.05	-0.47	0.655651	0.758426	-7.13
AFFX-TrpnX	B. subtilis /GEN=trpD, trpC /DB_XR	---	---	-1.03	-0.05	-0.47	0.655651	0.758426	-7.13
245839_at	disease resistance protein, putative	---	AT1G58390	-1.03	-0.04	-0.47	0.655704	0.758449	-7.13
262599_at	unknown protein ESTs gb|R65145.	---	AT1G15350	-1.04	-0.05	-0.47	0.655756	0.758471	-7.13
247678_at	putative zinc transporter ZIP2 - like	ZIP2	AT5G59520	1.07	0.10	0.47	0.655851	0.758542	-7.13
266863_at	putative ripening-associated protein	ATCDPME	AT2G26930	1.04	0.05	0.47	0.655964	0.758634	-7.13
263198_at	lipase, putative similar to lipase GI	GLIP3	AT1G53990	1.05	0.07	0.47	0.656033	0.758675	-7.13
245000_at	hypothetical protein	---	---	-1.04	-0.05	-0.47	0.656214	0.758846	-7.13
251514_at	pirin-like protein pirin - Lycopersico	---	AT3G59260	-1.04	-0.06	-0.47	0.656252	0.758852	-7.13
245552_at	cytochrome P450 like protein	CYP705A3	AT4G15360	-1.04	-0.05	-0.47	0.656316	0.758888	-7.13
264885_s_a	NBS/LRR disease resistance prote	---	AT1G61180	1.04	0.06	0.47	0.656484	0.759043	-7.13
267613_at	putative second messenger-depend	PID2	AT2G26700	1.04	0.05	0.46	0.656713	0.759269	-7.13
246397_at	hypothetical protein contains simila	AtRLP9	AT1G58190	1.03	0.05	0.46	0.656765	0.759269	-7.13
250594_at	putative protein contains similarity t	---	AT5G07760	1.04	0.05	0.46	0.65678	0.759269	-7.13
245641_at	Expressed protein ; supported by fu	---	AT1G25370	-1.16	-0.22	-0.46	0.65707	0.759566	-7.13
265298_s_a	putative retroelement pol polyprotei	---	---	-1.03	-0.05	-0.46	0.657194	0.759623	-7.13
245885_at	putative protein phi-1 - Nicotiana ta	EXL4	AT5G09440	-1.07	-0.10	-0.46	0.65721	0.759623	-7.13
256493_at	hypothetical protein predicted by ge	---	AT1G31600	-1.04	-0.06	-0.46	0.657219	0.759623	-7.13
255282_at	putative polyprotein	---	---	-1.03	-0.05	-0.46	0.657428	0.759826	-7.13
260219_at	hypothetical protein contains Pfam	---	AT1G74630	-1.04	-0.05	-0.46	0.657558	0.759938	-7.13
246739_at	putative protein predicted protein, A	---	AT5G27800	-1.04	-0.05	-0.46	0.657703	0.760038	-7.13

253049_at	putative protein ; supported by cDN	MEE59	AT4G37300	-1.08	-0.12	-0.46	0.657711	0.760038	-7.13
246475_at	putative protein IFA-binding protein	---	AT5G16720	1.05	0.07	0.46	0.657795	0.760097	-7.13
258865_at	NAM-like protein (no apical meriste	anac045	AT3G03200	1.03	0.04	0.46	0.658211	0.760538	-7.13
249934_at	peroxidase ATP14a homolog	---	AT5G22410	-1.03	-0.04	-0.46	0.658816	0.761199	-7.13
245683_at	ubiquitin-specific protease 8 (UBP8	UBP8	AT5G22030	-1.03	-0.05	-0.46	0.658873	0.761201	-7.13
259186_at	unknown protein similar to possible	---	AT3G01590	-1.04	-0.06	-0.46	0.658884	0.761201	-7.13
252285_at	calmodulin-binding heat-shock - lik	---	AT3G49050	-1.04	-0.05	-0.46	0.65898	0.761273	-7.13
261354_at	unknown protein ; supported by cDI	atnudt3	AT1G79690	1.04	0.05	0.46	0.659039	0.761302	-7.13
259442_at	(1-4)-beta-mannan endohydrolase	---	AT1G02310	1.07	0.09	0.46	0.65922	0.761473	-7.13
260789_s_a	acyl-CoA oxidase ACX3 identical to	ACX3	AT1G06290	-1.03	-0.04	-0.46	0.659285	0.76151	-7.13
249668_at	putative protein similar to unknown	---	AT5G35870	-1.05	-0.06	-0.46	0.65979	0.762054	-7.13
266353_at	unknown protein ;supported by full-	MLP328	AT2G01520	-1.07	-0.09	-0.46	0.659833	0.762065	-7.13
252768_at	putative protein hypothetical protein	---	---	-1.03	-0.05	-0.46	0.659908	0.762113	-7.13
259667_at	unknown protein ; supported by cDI	---	AT1G55270	1.04	0.06	0.46	0.659959	0.762134	-7.13
265161_at	putative vacuolar sorting receptor s	---	AT1G30900	1.16	0.21	0.46	0.660076	0.762225	-7.13
246361_s_a	hypothetical protein	---	---	-1.03	-0.05	-0.46	0.660104	0.762225	-7.13
246983_at	receptor protein kinase-like protein	---	AT5G67200	-1.05	-0.08	-0.46	0.660286	0.762395	-7.13
251381_at	secretory protein - like 33 kDa secr	PDLP8	AT3G60720	-1.07	-0.10	-0.46	0.660363	0.762427	-7.13
253773_s_a	Expressed protein ; supported by fu	---	AT1G52370	-1.04	-0.06	-0.46	0.66038	0.762427	-7.13
252467_at	putative protein predicted proteins,	---	AT3G47080	-1.05	-0.07	-0.46	0.660459	0.76248	-7.13
249490_s_a	germin -like protein germin -like pro	---	AT5G39110	-1.11	-0.15	-0.46	0.660517	0.762504	-7.13
265241_at	hypothetical protein	---	---	1.04	0.06	0.46	0.660547	0.762504	-7.13
265156_at	hypothetical protein predicted by ge	---	AT1G31000	-1.04	-0.06	-0.46	0.660791	0.762747	-7.13
263335_x_a	hypothetical protein	---	---	1.03	0.04	0.46	0.660829	0.762752	-7.13
253266_s_a	putative protein predicted protein, A	---	AT2G45260	1.04	0.06	0.46	0.660911	0.762808	-7.13
251455_at	citrate synthase-like protein citrate	CSY5	AT3G60100	-1.03	-0.04	-0.46	0.660986	0.762857	-7.13
258113_at	putative cytochrome P450 similar to	CYP72A11	AT3G14650	-1.06	-0.09	-0.46	0.661156	0.762978	-7.13
257548_s_a	hypothetical protein	LBD23	AT3G26620	1.03	0.04	0.46	0.661159	0.762978	-7.13
261770_at	prolyl endopeptidase, putative simi	---	AT1G76140	-1.03	-0.04	-0.46	0.661215	0.762991	-7.13
254494_at	putative protein C65DMY30S	QRT3	AT4G20050	-1.03	-0.05	-0.46	0.661237	0.762991	-7.13
251849_at	Expressed protein ; supported by cl	HAG1	AT3G54610	1.04	0.06	0.46	0.661281	0.762992	-7.13
266123_at	unknown protein identical to GB:AA	---	AT2G45180	1.03	0.04	0.46	0.661304	0.762992	-7.13
267433_at	putative peroxisome assembly prote	PEX10	AT2G26350	1.04	0.06	0.46	0.661348	0.763003	-7.13
248134_at	putative protein contains similarity t	---	AT5G54860	1.07	0.10	0.46	0.661424	0.76303	-7.13
265815_at	predicted protein	---	AT2G17975	-1.03	-0.04	-0.46	0.661461	0.76303	-7.13

265763_at	unknown protein	---	AT2G48060	1.03	0.04	0.46	0.661471	0.76303	-7.13
257911_at	hypothetical protein contains simila	GLYR1	AT3G25530	-1.03	-0.04	-0.46	0.661518	0.763046	-7.13
265033_at	PSI type III chlorophyll a/b-binding	LHCA3	AT1G61520	-1.03	-0.04	-0.46	0.661717	0.763237	-7.13
247920_at	putative protein contains similarity t	---	AT5G57670	-1.05	-0.07	-0.46	0.661881	0.763387	-7.13
254366_s_a	LTR retrotransposon like protein re	---	---	-1.03	-0.05	-0.46	0.661937	0.763413	-7.13
260807_at	hypothetical protein predicted by ge	---	AT1G78310	1.03	0.04	0.46	0.66229	0.763781	-7.13
257232_at	phytochrome-associated protein 1 (	PAP1	AT3G16500	1.05	0.06	0.46	0.662394	0.763863	-7.13
246631_at	unknown protein ; supported by full-	---	AT1G50740	1.03	0.05	0.46	0.662449	0.763887	-7.13
256232_at	unknown protein ; supported by full-	FYD	AT3G12570	1.03	0.04	0.46	0.662622	0.764049	-7.13
249724_at	disease resistance protein	---	AT5G35450	-1.03	-0.04	-0.46	0.662671	0.764067	-7.13
263357_s_a	Mutator-like transposase similar to	---	---	-1.03	-0.05	-0.46	0.662715	0.764078	-7.13
264608_at	putative acetyl-CoA acyltransferase	PKT4	AT1G04710	1.04	0.05	0.46	0.662803	0.764141	-7.13
247952_at	salt-inducible protein-like	CYP71B10	AT5G57250	1.04	0.06	0.46	0.66287	0.76418	-7.13
249105_at	40S ribosomal protein S15	---	AT5G43640	-1.04	-0.05	-0.46	0.662908	0.764186	-7.13
253656_at	putative protein hypothetical protei	emb1353	AT4G30090	-1.03	-0.05	-0.46	0.663257	0.764522	-7.13
255220_at	polyubiquitin (UBQ10) identical to G	UBQ10	AT4G05320	1.04	0.06	0.46	0.663267	0.764522	-7.13
245910_at	putative protein ER66 - Lycopersic	EICBP.B	AT5G09410	1.04	0.05	0.46	0.663357	0.764586	-7.13
250458_s_a	ACTIN 2/7 (sp|P53492) ; supporte	ACT7	AT5G09810	1.03	0.04	0.45	0.663542	0.764761	-7.13
248736_at	terpene synthase	---	AT5G48110	1.04	0.05	0.45	0.663576	0.764761	-7.13
250641_at	putative bZIP protein bZIP protein	---	AT5G07160	1.04	0.06	0.45	0.663823	0.765008	-7.13
257776_at	terpene synthase-related protein co	---	AT3G29190	-1.04	-0.06	-0.45	0.663959	0.765126	-7.13
262822_at	putative membrane-associated salt-	---	AT1G11630	-1.04	-0.05	-0.45	0.66402	0.765158	-7.13
263258_at	putative permease similar to putativ	---	AT1G10540	-1.05	-0.07	-0.45	0.664137	0.765254	-7.13
266959_at	putative DNA replication licensing f	MCM5	AT2G07690	1.12	0.16	0.45	0.664283	0.765384	-7.13
250451_at	cdc2-like protein kinase cdc2-like p	CDKC;1	AT5G10270	-1.04	-0.06	-0.45	0.664425	0.765509	-7.13
255793_at	Expressed protein ; supported by cl	---	AT2G33250	1.05	0.06	0.45	0.664693	0.765778	-7.13
247353_at	alcohol dehydrogenase-like protein	---	AT5G63620	1.05	0.06	0.45	0.664834	0.765902	-7.13
252140_at	putative protein several hypothetica	---	AT3G51070	-1.03	-0.04	-0.45	0.664894	0.765933	-7.13
251553_at	DNA-binding WRKY - like protein A	WRKY69	AT3G58710	-1.05	-0.07	-0.45	0.665044	0.766049	-7.13
252976_s_a	Phospholipase like protein Arabido	---	AT4G38550	-1.07	-0.09	-0.45	0.665062	0.766049	-7.13
246016_at	histidine kinase - like protein senso	AHK5	AT5G10720	-1.04	-0.06	-0.45	0.665307	0.766292	-7.13
249634_at	putative protein several hypothetica	---	---	1.04	0.06	0.45	0.66535	0.766303	-7.13
250917_at	fructose-bisphosphate aldolase -lik	---	AT5G03690	-1.05	-0.06	-0.45	0.665392	0.766313	-7.13
253680_at	cytidine deaminase 2 (CDA2)	---	AT4G29620	-1.03	-0.05	-0.45	0.665439	0.766328	-7.13
258564_at	poly(A) polymerase, putative simila	---	AT3G06560	-1.03	-0.05	-0.45	0.665526	0.76639	-7.13

255342_at	putative receptor-like protein kinase	---	AT4G04510	1.04	0.06	0.45	0.665739	0.766596	-7.13
260241_at	putative cytochrome P450 similar to	CYP86A7	AT1G63710	-1.05	-0.07	-0.45	0.665867	0.766706	-7.13
265604_s_a	hypothetical protein predicted by ge	---	---	-1.04	-0.05	-0.45	0.665931	0.76674	-7.13
261868_s_a	hypothetical protein contains simila	---	AT1G11450	1.03	0.04	0.45	0.665997	0.766745	-7.13
258595_at	unknown protein contains Pfam pro	---	AT3G04500	1.04	0.05	0.45	0.66601	0.766745	-7.13
248015_at	putative protein similar to unknown	---	AT5G56370	-1.04	-0.05	-0.45	0.666036	0.766745	-7.13
245799_at	disease resistance protein, putative	AtRLP6	AT1G45616	1.03	0.05	0.45	0.666159	0.766848	-7.13
259196_at	putative ribosomal protein S2 simila	RPS2	AT3G03600	1.05	0.07	0.45	0.666241	0.76688	-7.13
248856_at	putative protein similar to unknown	---	AT5G46620	1.03	0.05	0.45	0.666254	0.76688	-7.13
257934_at	serine carboxypeptidase, putative s	scpl21	AT3G25420	1.05	0.08	0.45	0.666335	0.766934	-7.13
252240_at	putative protein several hypothetica	---	AT3G50010	-1.04	-0.06	-0.45	0.666407	0.766958	-7.13
261587_at	hypothetical protein predicted by ge	---	AT1G01660	1.03	0.05	0.45	0.666423	0.766958	-7.13
247693_at	putative protein leucine zipper-con	ATEXO70H	AT5G59730	1.12	0.16	0.45	0.666681	0.767187	-7.13
264006_at	homeodomain transcription factor (	ATHB6	AT2G22430	1.06	0.08	0.45	0.666689	0.767187	-7.13
257493_at	unknown protein	---	AT1G48180	-1.06	-0.08	-0.45	0.666962	0.767463	-7.13
263976_at	unknown protein	---	AT2G42700	1.04	0.06	0.45	0.667076	0.767555	-7.14
260214_at	hypothetical protein contains Pfam	---	AT1G74510	-1.04	-0.05	-0.45	0.667187	0.767644	-7.14
260763_at	RING-H2 finger protein RHA3a, pu	---	AT1G49220	-1.03	-0.04	-0.45	0.667259	0.767688	-7.14
264358_at	hypothetical protein predicted by ge	---	AT1G03180	-1.05	-0.07	-0.45	0.667403	0.767814	-7.14
264620_at	putative bZIP transcription factor	ATBZIP27	AT2G17770	-1.04	-0.06	-0.45	0.667511	0.767901	-7.14
264276_at	hypothetical protein contains simila	---	AT1G60380	-1.03	-0.04	-0.45	0.6676	0.767932	-7.14
257228_at	NADPH:quinone oxidoreductase (N	NQR	AT3G27890	1.03	0.05	0.45	0.667643	0.767932	-7.14
264839_at	putative protochlorophyllide reduct	POR C	AT1G03630	-1.05	-0.07	-0.45	0.667652	0.767932	-7.14
252004_at	purple acid phosphatase-like prote	PAP20	AT3G52780	1.08	0.11	0.45	0.667673	0.767932	-7.14
254585_at	resistence protein - like downy mild	---	AT4G19500	1.03	0.05	0.45	0.667809	0.768049	-7.14
256769_at	protein kinase, putative similar to p	---	AT3G13690	-1.07	-0.10	-0.45	0.668227	0.768437	-7.14
247421_at	SIAH1 - like protein SIAH1, Brassic	---	AT5G62800	-1.04	-0.06	-0.45	0.66823	0.768437	-7.14
265303_at	hypothetical protein	---	---	1.04	0.05	0.45	0.668323	0.768437	-7.14
254497_at	Phosphoribosylanthranilate transfe	---	AT4G20080	-1.06	-0.08	-0.45	0.668338	0.768437	-7.14
251976_at	disease resistance - like protein dis	AtRLP45	AT3G53240	-1.04	-0.06	-0.45	0.668342	0.768437	-7.14
256831_at	hypothetical protein	---	AT3G22870	1.04	0.05	0.45	0.668349	0.768437	-7.14
262762_at	phosphoribosyl diphosphate syntha	---	AT1G10700	1.16	0.21	0.45	0.668418	0.768478	-7.14
263719_at	hypothetical protein predicted by ge	---	AT2G13600	-1.03	-0.04	-0.45	0.668571	0.768616	-7.14
247076_at	ferripyochelin-binding protein-like ;	GAMMA CA	AT5G66510	1.03	0.05	0.45	0.668741	0.768772	-7.14
248373_at	MADS box transcription factor-like p	---	AT5G51860	1.05	0.06	0.45	0.668797	0.768798	-7.14

267615_at	putative phytocyanin	---	AT2G26720	-1.05	-0.07	-0.45	0.669005	0.768999	-7.14
255841_at	putative tyrosine-specific transport	---	AT2G33260	-1.05	-0.07	-0.45	0.669138	0.769113	-7.14
250071_at	putative protein similar to unknown	---	AT5G18000	-1.03	-0.04	-0.45	0.669183	0.769126	-7.14
255493_at	putative glutamate-/aspartate-bindi	---	AT4G02690	-1.03	-0.05	-0.45	0.669271	0.769188	-7.14
249863_at	putative protein contains similarity t	VPS24.1	AT5G22950	1.03	0.04	0.45	0.669365	0.769194	-7.14
260977_at	hypothetical protein predicted by ge	---	AT1G53420	-1.03	-0.05	-0.45	0.669367	0.769194	-7.14
262087_at	hypothetical protein predicted by ge	---	AT1G56030	-1.03	-0.05	-0.45	0.669377	0.769194	-7.14
255523_at	pectinesterase - like protein similar	---	AT4G02320	1.04	0.05	0.45	0.669687	0.769478	-7.14
265407_at	F-box protein family, AtFBX8 conta	---	AT2G16810	-1.05	-0.08	-0.45	0.669692	0.769478	-7.14
261894_at	unknown protein ;supported by full-	MGT1	AT1G80900	1.03	0.05	0.45	0.669738	0.769491	-7.14
248348_at	putative protein similar to unknown	---	AT5G52190	-1.04	-0.05	-0.45	0.669784	0.769506	-7.14
257048_at	hypothetical protein predicted by ge	---	AT3G19740	-1.03	-0.05	-0.45	0.669835	0.769526	-7.14
257241_at	hypothetical protein contains Pfam	---	AT3G24210	-1.04	-0.06	-0.45	0.669963	0.769611	-7.14
257490_x_a	Myb homolog (CPC), putative simil	ETC1	AT1G01380	1.03	0.04	0.45	0.669977	0.769611	-7.14
253710_at	putative protein hypothetical protei	anac075	AT4G29230	-1.04	-0.06	-0.45	0.670113	0.769729	-7.14
255698_at	scarecrow-like 6 (SCL6)	---	AT4G00150	-1.05	-0.07	-0.45	0.670185	0.769773	-7.14
267413_at	putative amino acid transporter	CAT5	AT2G34960	1.06	0.08	0.44	0.670349	0.769922	-7.14
267512_at	hypothetical protein predicted by ge	SSE1	AT2G45690	1.04	0.06	0.44	0.670426	0.76995	-7.14
256382_at	unknown protein ;supported by full-	---	AT1G66860	-1.10	-0.14	-0.44	0.670441	0.76995	-7.14
264721_at	hypothetical protein predicted by ge	---	AT1G23000	1.04	0.05	0.44	0.670721	0.770233	-7.14
247758_at	subtilisin-like serine protease conta	ATSBT4.13	AT5G59120	-1.04	-0.06	-0.44	0.670828	0.770293	-7.14
254024_at	putative pathogenesis-related prote	---	AT4G25780	-1.06	-0.08	-0.44	0.67084	0.770293	-7.14
264145_at	latex-abundant protein, putative sir	AtMC7	AT1G79310	-1.03	-0.04	-0.44	0.671109	0.770562	-7.14
252826_at	hypothetical protein ; supported by	---	AT4G40050	-1.04	-0.05	-0.44	0.671207	0.770637	-7.14
263682_at	hypothetical protein similar to rever	AT5G4959(	---	1.03	0.04	0.44	0.671306	0.770712	-7.14
253471_at	hypothetical protein	---	---	1.04	0.05	0.44	0.671556	0.77096	-7.14
259656_at	protein kinase, putative contains P	---	AT1G55200	-1.03	-0.05	-0.44	0.671755	0.771111	-7.14
252627_at	putative protein	---	AT3G44950	-1.04	-0.06	-0.44	0.671756	0.771111	-7.14
261631_at	unknown protein contains similarity	---	AT1G49940	1.03	0.04	0.44	0.672108	0.771476	-7.14
248218_at	unknown protein ;supported by full-	---	AT5G53710	-1.05	-0.07	-0.44	0.672566	0.771917	-7.14
260460_at	unknown protein	---	AT1G68230	1.04	0.05	0.44	0.672586	0.771917	-7.14
265497_at	putative non-LTR retroelement reve	---	---	-1.09	-0.12	-0.44	0.672593	0.771917	-7.14
262449_at	hypothetical protein similar to hypot	---	AT1G11160	-1.03	-0.04	-0.44	0.672858	0.772162	-7.14
254555_at	putative protein curved DNA-bindi	---	AT4G19570	-1.03	-0.05	-0.44	0.672875	0.772162	-7.14
245210_at	putative protein similarity to UVB-re	---	AT5G12350	-1.03	-0.04	-0.44	0.67324	0.772542	-7.14

252966_at	putative protein various predicted p	---	AT4G38870	-1.04	-0.05	-0.44	0.673365	0.772647	-7.14
254575_at	putative protein various predicted p	---	AT4G19460	-1.09	-0.13	-0.44	0.673411	0.772661	-7.14
248209_at	flavonol 3-O-glucosyltransferase-lik	---	AT5G53990	1.05	0.07	0.44	0.673604	0.772844	-7.14
252137_at	dehydrin-like protein dehydrin Xer	XERO1	AT3G50980	1.04	0.06	0.44	0.673738	0.772932	-7.14
265125_at	hypothetical protein similar to putati	---	AT1G55410	-1.03	-0.04	-0.44	0.673749	0.772932	-7.14
257615_at	unknown protein	---	AT3G26510	-1.05	-0.07	-0.44	0.673847	0.773006	-7.14
252438_at	putative protein riboflavin biosynthe	---	AT3G47390	-1.03	-0.04	-0.44	0.673944	0.773042	-7.14
258359_s_a	putative glycolate oxidase similar to	---	AT3G14415	1.04	0.06	0.44	0.673946	0.773042	-7.14
246656_at	hypothetical protein	---	---	-1.04	-0.06	-0.44	0.67399	0.773053	-7.14
254407_at	receptor kinase - like protein recep	---	AT4G21370	1.04	0.05	0.44	0.674028	0.773058	-7.14
247382_at	adenylate kinase ;supported by full-	ADK1	AT5G63400	-1.05	-0.07	-0.44	0.674108	0.773111	-7.14
251084_at	putative protein putative proteins - A	---	AT5G01520	1.07	0.10	0.44	0.674254	0.773239	-7.14
258530_at	hypothetical protein predicted by ge	---	AT3G06840	-1.04	-0.06	-0.44	0.67443	0.773403	-7.14
245391_at	symbiosis-related like protein ;supp	ATG8F	AT4G16520	1.05	0.07	0.44	0.674503	0.773447	-7.14
251385_at	putative protein various predicted p	---	AT3G60790	-1.04	-0.05	-0.44	0.674596	0.773515	-7.14
248077_at	putative protein contains similarity t	---	AT5G55770	1.03	0.05	0.44	0.675067	0.773981	-7.14
247523_at	ribulose-5-phosphate-3-epimerase	RPE	AT5G61410	1.04	0.06	0.44	0.67507	0.773981	-7.14
247230_at	putative protein similar to unknown	---	AT5G65170	1.03	0.04	0.44	0.675232	0.77411	-7.14
257130_at	vacuolar processing enzyme/aspar	DELTA-VP	AT3G20210	-1.03	-0.04	-0.44	0.675251	0.77411	-7.14
252664_at	putative protein several hypothetica	---	AT3G44080	1.03	0.04	0.44	0.675415	0.77426	-7.14
256124_at	hypothetical protein predicted by ge	ATPUP9	AT1G18220	1.03	0.05	0.44	0.675543	0.774357	-7.14
245917_at	putative protein HCNP, Homo sapi	---	AT5G28740	1.04	0.05	0.44	0.675576	0.774357	-7.14
255035_at	putative protein	---	AT4G09550	-1.05	-0.07	-0.44	0.675641	0.774357	-7.14
266698_at	copia-like retroelement pol polyprot	SNF7.2	AT2G19830	1.04	0.05	0.44	0.675647	0.774357	-7.14
259772_at	hypothetical protein predicted by ge	---	AT1G29480	1.03	0.04	0.44	0.675686	0.774357	-7.14
266216_at	putative DOF zinc finger protein	---	AT2G28810	1.04	0.06	0.44	0.675704	0.774357	-7.14
267155_at	CLE7, putative CLAVATA3/ESR-re	---	AT2G30925	-1.04	-0.06	-0.44	0.675769	0.774392	-7.14
248836_at	NBS/LRR disease resistance protei	---	AT5G47260	-1.05	-0.06	-0.44	0.676094	0.774727	-7.14
259098_at	putative ribose 5-phosphate isome	---	AT3G04790	1.06	0.08	0.44	0.676191	0.774788	-7.14
266937_at	hypothetical protein predicted by ge	---	AT2G18930	-1.04	-0.05	-0.44	0.676215	0.774788	-7.14
262901_at	hypothetical protein predicted by ge	---	AT1G59910	-1.09	-0.12	-0.44	0.676249	0.774788	-7.14
257808_at	unknown protein, putative contains	---	AT3G26935	1.04	0.05	0.44	0.676363	0.774878	-7.14
244928_s_a	hypothetical protein	---	AT2G07716	-1.03	-0.05	-0.44	0.676636	0.775152	-7.14
258207_at	putative GTP pyrophosphokinase s	RSH2	AT3G14050	-1.08	-0.11	-0.44	0.676695	0.775181	-7.14
249699_at	putative protein similar to unknown	---	AT5G35540	-1.03	-0.04	-0.44	0.676793	0.77524	-7.14

256042_at	hypothetical protein predicted by ge	---	AT1G07220	1.03	0.04	0.44	0.676814	0.77524	-7.14
245068_at	putative glucosyltransferase	UGT84B1	AT2G23260	-1.04	-0.05	-0.44	0.677085	0.775511	-7.14
261673_at	lipid transfer protein, putative simila	---	AT1G18280	-1.15	-0.20	-0.43	0.677257	0.77567	-7.14
264877_at	putative obtusifoliol 14-alpha demet	CYP51G2	AT2G17330	1.03	0.04	0.43	0.677343	0.775728	-7.14
260199_at	unknown protein similar to putative	---	AT1G67590	1.03	0.04	0.43	0.677683	0.776079	-7.14
264706_at	hypothetical protein predicted by ge	---	AT1G09720	1.03	0.04	0.43	0.677735	0.7761	-7.14
258695_at	putative ascorbate peroxidase stron	APX2	AT3G09640	-1.04	-0.06	-0.43	0.677827	0.776166	-7.14
247813_at	NADP-dependent malate dehydrog	---	AT5G58330	-1.04	-0.05	-0.43	0.677916	0.776229	-7.14
265163_at	putative OBP32pep protein	---	AT1G23580	1.03	0.04	0.43	0.67798	0.776264	-7.14
257138_at	hypothetical protein predicted by ge	---	AT3G28870	-1.03	-0.04	-0.43	0.67802	0.77627	-7.14
255257_at	score=526.5, E=1.9e-154, N=3 ;su	UBQ11	AT4G05050	1.03	0.04	0.43	0.678143	0.776352	-7.14
249973_at	GPAA1 - like protein glycosylphosp	---	AT5G19130	-1.04	-0.06	-0.43	0.678169	0.776352	-7.14
248927_at	ubiquitin activating enzyme E1-like	APG7	AT5G45900	1.04	0.06	0.43	0.678193	0.776352	-7.14
263330_at	putative leucine-rich repeat disease	---	AT2G15320	1.08	0.10	0.43	0.678283	0.776377	-7.14
262186_at	hypothetical protein	---	AT1G77960	-1.08	-0.11	-0.43	0.678285	0.776377	-7.14
262817_at	putative reticuline oxidase strong si	---	AT1G11770	1.04	0.05	0.43	0.678318	0.776377	-7.14
245420_at	hypothetical protein	---	AT4G17410	-1.04	-0.05	-0.43	0.678666	0.776708	-7.14
256911_at	glutamine:fructose-6-phosphate an	---	AT3G24090	1.13	0.18	0.43	0.678675	0.776708	-7.14
248070_at	putative protein similar to unknown	---	AT5G55660	1.03	0.05	0.43	0.67873	0.776732	-7.14
256234_at	50S ribosomal protein L10, putative	---	AT3G12370	1.03	0.05	0.43	0.678988	0.776977	-7.14
258561_at	putative hexose transporter similar	STP6	AT3G05960	1.05	0.07	0.43	0.679036	0.776977	-7.14
266022_at	subtilisin-like serine protease, puta	---	AT2G05920	-1.05	-0.08	-0.43	0.679059	0.776977	-7.14
267622_at	hypothetical protein predicted by ge	---	AT2G39690	-1.03	-0.05	-0.43	0.67908	0.776977	-7.14
247807_at	similar to unknown protein (gb|AAB	OFP3	AT5G58360	-1.04	-0.06	-0.43	0.679209	0.777085	-7.14
256137_at	auxin-regulated protein, putative si	---	AT1G48690	1.03	0.04	0.43	0.679248	0.777091	-7.14
254717_at	histone H2A.F/Z - like protein histo	HTA4	AT4G13570	-1.04	-0.06	-0.43	0.679478	0.777315	-7.14
266115_at	protease inhibitor II ;supported by f	LCR72	AT2G02140	-1.06	-0.08	-0.43	0.679557	0.777366	-7.14
260045_at	putative MAP kinase similar to mito	ATMPK15	AT1G73670	-1.03	-0.04	-0.43	0.679793	0.777598	-7.14
263827_at	unknown protein	---	AT2G40420	-1.06	-0.08	-0.43	0.679915	0.777699	-7.14
250260_at	putative protein contains similarity t	---	AT5G13810	-1.04	-0.05	-0.43	0.679965	0.777717	-7.14
263700_at	unknown protein EST gb|Z33866 co	---	AT1G31150	-1.05	-0.07	-0.43	0.680058	0.777784	-7.14
267324_at	hypothetical protein predicted by ge	---	AT2G19360	-1.03	-0.04	-0.43	0.680151	0.777851	-7.14
247889_at	putative protein similar to unknown	APO2	AT5G57930	1.04	0.05	0.43	0.68041	0.778109	-7.14
263169_at	hypothetical protein similar to unkno	---	AT1G03010	-1.05	-0.07	-0.43	0.680452	0.778118	-7.14
249007_at	unknown protein ;supported by full-	---	AT5G44650	-1.06	-0.08	-0.43	0.680726	0.778392	-7.14

249621_at	putative protein predicted proteins,	---	AT5G37530	1.04	0.05	0.43	0.680913	0.778567	-7.14
250370_at	putative protein putative transcripti	---	AT5G11430	-1.03	-0.04	-0.43	0.680952	0.778573	-7.14
261280_at	hypothetical protein predicted by ge	---	AT1G05860	-1.05	-0.07	-0.43	0.681095	0.778697	-7.14
248727_at	cytochrome P450	CYP705A5	AT5G47990	-1.03	-0.04	-0.43	0.681201	0.778779	-7.15
257947_at	putative isocitrate lyase similar to G	ICL	AT3G21720	-1.04	-0.06	-0.43	0.68126	0.778793	-7.15
263782_at	hypothetical protein predicted by ge	---	AT2G46380	1.04	0.05	0.43	0.681282	0.778793	-7.15
261650_at	envelope Ca2+-ATPase identical to	ACA1	AT1G27770	1.06	0.09	0.43	0.681324	0.778803	-7.15
257774_at	short-chain alcohol dehydrogenase	---	AT3G29250	1.04	0.06	0.43	0.681402	0.778852	-7.15
258711_at	ubiquitin-like protein (UBQ8) identi	UBQ8	AT3G09790	1.03	0.05	0.43	0.6815	0.778921	-7.15
260997_at	zinc-finger protein (ZPT4-4), putati	---	AT1G26610	-1.03	-0.04	-0.43	0.68153	0.778921	-7.15
266684_at	40S ribosomal protein S15A	rps15ab	AT2G19720	1.03	0.04	0.43	0.68157	0.778928	-7.15
249402_at	Expressed protein ; supported by fu	---	AT5G40155	1.03	0.05	0.43	0.68176	0.779105	-7.15
250926_at	Expressed protein ; supported by fu	---	AT5G03555	-1.08	-0.11	-0.43	0.681982	0.77932	-7.15
252772_at	hypothetical protein	---	---	-1.03	-0.05	-0.43	0.68223	0.779535	-7.15
266078_at	putative two-component response r	ARR16	AT2G40670	1.03	0.05	0.43	0.682239	0.779535	-7.15
246825_at	putative protein various predicted p	---	AT5G26260	1.03	0.04	0.43	0.68232	0.779589	-7.15
245021_at	PSII component	---	---	1.05	0.06	0.43	0.682356	0.779591	-7.15
250082_at	polygalacturonase-like protein	---	AT5G17200	-1.04	-0.06	-0.43	0.682549	0.779733	-7.15
263697_at	hypothetical protein contains simila	---	AT1G31080	-1.04	-0.06	-0.43	0.682549	0.779733	-7.15
255141_at	putative protein several hypothetica	---	---	1.03	0.04	0.43	0.682583	0.779733	-7.15
245580_at	hypothetical protein	---	AT4G14820	-1.05	-0.07	-0.43	0.682697	0.779824	-7.15
248176_at	putative protein contains similarity t	Fh5	AT5G54650	1.07	0.10	0.43	0.68276	0.779858	-7.15
255188_at	contains similarity to Xenopus laevi	---	---	1.03	0.04	0.43	0.6829	0.779944	-7.15
247869_at	CCHH finger protein 2-like protein (	ZFP2	AT5G57520	-1.03	-0.04	-0.43	0.682924	0.779944	-7.15
246185_at	5-methyltetrahydropteroyltriglutama	ATMS3	AT5G20980	-1.03	-0.04	-0.43	0.682939	0.779944	-7.15
265174_s_a	polygalacturonase, putative similar	---	AT1G23460	-1.05	-0.07	-0.43	0.682993	0.779967	-7.15
251464_at	farnesyltransferase subunit A (FTA)	FTA	AT3G59380	-1.04	-0.06	-0.43	0.68304	0.779982	-7.15
261501_at	wall-associated kinase 1, putative s	---	AT1G28390	1.05	0.07	0.43	0.683092	0.780002	-7.15
263109_at	hypothetical protein similar to putati	---	AT1G65180	-1.04	-0.06	-0.43	0.683129	0.780006	-7.15
246979_s_a	putative protein hypothetical protein	---	AT5G24990	-1.04	-0.06	-0.43	0.683321	0.780186	-7.15
257152_at	Expressed protein ; supported by fu	PUX1	AT3G27310	-1.03	-0.04	-0.43	0.683445	0.780262	-7.15
248164_at	putative protein similar to unknown	PBP1	AT5G54490	1.22	0.28	0.43	0.683459	0.780262	-7.15
260974_at	receptor-like serine/threonine kinas	---	AT1G53440	1.07	0.10	0.43	0.683491	0.780262	-7.15
265711_at	unknown protein	---	AT2G03360	1.03	0.04	0.43	0.683651	0.780406	-7.15
258938_at	germin-like protein similar to germi	---	AT3G10080	-1.16	-0.22	-0.43	0.683878	0.780627	-7.15

262436_at	En/Spm-like transposon protein, pu	---	AT1G47610	1.07	0.10	0.43	0.683989	0.780715	-7.15
263244_at	hypothetical protein predicted by ge	---	AT2G31480	1.04	0.05	0.42	0.684106	0.780791	-7.15
255782_at	transcription factor identical to trans	MP	AT1G19850	1.07	0.10	0.42	0.684142	0.780791	-7.15
245840_at	hypothetical protein predicted by ge	---	AT1G58420	1.09	0.12	0.42	0.684159	0.780791	-7.15
257592_at	leucine-rich repeat disease resistar	---	AT3G24982	-1.03	-0.05	-0.42	0.684261	0.780869	-7.15
247458_at	putative protein PrMC3, Pinus radi	AtCXE20	AT5G62180	-1.07	-0.09	-0.42	0.684378	0.780963	-7.15
255633_at	Expressed protein ; supported by fu	---	AT4G00585	1.04	0.05	0.42	0.684416	0.780967	-7.15
256375_at	unknown protein	---	AT1G66720	-1.03	-0.04	-0.42	0.68471	0.781263	-7.15
247662_at	protein kinase - like protein kinase	---	AT5G60090	1.05	0.07	0.42	0.684766	0.781288	-7.15
265954_at	putative WRKY-type DNA binding p	TTG2	AT2G37260	1.03	0.05	0.42	0.684886	0.781385	-7.15
247371_at	histone deacetylase ;supported by	HDA6	AT5G63110	-1.03	-0.05	-0.42	0.684985	0.781423	-7.15
264398_at	unknown protein similar to hypothet	---	AT1G61730	1.03	0.05	0.42	0.684987	0.781423	-7.15
250081_at	unknown protein	---	AT5G17180	1.03	0.05	0.42	0.685139	0.781558	-7.15
253430_at	putative protein	---	AT4G32430	-1.04	-0.05	-0.42	0.685366	0.781777	-7.15
267478_at	hypothetical protein predicted by ge	---	AT2G02700	-1.03	-0.04	-0.42	0.68541	0.781788	-7.15
264925_at	hypothetical protein contains simila	---	AT1G60670	1.04	0.06	0.42	0.685461	0.781807	-7.15
261615_at	unknown protein	---	AT1G33050	1.04	0.05	0.42	0.685632	0.781943	-7.15
252708_at	putative protein amine oxidase, Ca	---	AT3G43820	1.04	0.06	0.42	0.685648	0.781943	-7.15
259017_at	unknown protein ; supported by ful	---	AT3G07310	-1.04	-0.05	-0.42	0.685836	0.782086	-7.15
256698_at	unknown protein	---	AT3G20680	1.04	0.06	0.42	0.685844	0.782086	-7.15
263932_at	unknown protein	---	AT2G35990	-1.03	-0.04	-0.42	0.685877	0.782086	-7.15
258037_at	putative 4-coumarate:CoA ligase 2	4CL5	AT3G21230	-1.20	-0.26	-0.42	0.686051	0.782246	-7.15
263741_at	hypothetical protein predicted by ge	---	AT2G20620	1.04	0.06	0.42	0.686359	0.782558	-7.15
256148_at	hypothetical protein similar to putati	---	AT1G55090	-1.03	-0.04	-0.42	0.686509	0.782689	-7.15
245012_at	NADH dehydrogenase D3	---	---	-1.04	-0.06	-0.42	0.686807	0.782957	-7.15
253548_at	Expressed protein ; supported by fu	---	AT4G30993	1.05	0.07	0.42	0.686813	0.782957	-7.15
261870_at	nuclear transport factor 2, putative	NTL	AT1G11570	-1.04	-0.05	-0.42	0.687061	0.783201	-7.15
251769_at	receptor kinase - like protein recep	CCR3	AT3G55950	1.20	0.26	0.42	0.687253	0.783381	-7.15
254780_s_a	auxilin-like protein auxilin - bovine,	---	AT4G12770	1.05	0.08	0.42	0.687343	0.783444	-7.15
257124_at	hexokinase, putative similar to hex	ATHXK4	AT3G20040	1.03	0.05	0.42	0.687434	0.783509	-7.15
263001_at	hypothetical protein contains simila	TAF6B4	AT1G54360	1.06	0.09	0.42	0.687573	0.783578	-7.15
259556_at	hypothetical protein	---	---	-1.03	-0.04	-0.42	0.687591	0.783578	-7.15
247539_at	putative protein predicted protein, A	---	AT5G61710	1.03	0.04	0.42	0.687598	0.783578	-7.15
247765_at	cytochrome P450 CYP86A1	CYP86A1	AT5G58860	-1.07	-0.09	-0.42	0.687802	0.783766	-7.15
249170_at	abscisic acid responsive elements-I	---	AT5G42910	-1.03	-0.04	-0.42	0.687855	0.783766	-7.15

253316_s_a	putative protein hyphally regulated	---	AT4G33930	1.06	0.08	0.42	0.687866	0.783766	-7.15
246696_at	putative protein predicted protein, /	---	---	1.03	0.05	0.42	0.688182	0.784087	-7.15
254022_at	putative membrane transporter Ba	---	AT4G25750	-1.04	-0.05	-0.42	0.688262	0.784109	-7.15
257481_at	hypothetical protein identical to hyp	ALMT1	AT1G08430	1.03	0.05	0.42	0.688269	0.784109	-7.15
257140_at	MYB family transcription factor (hs	MYB30	AT3G28910	-1.08	-0.11	-0.42	0.688348	0.784159	-7.15
255167_at	putative protein hypothetical prote	---	---	-1.03	-0.04	-0.42	0.688513	0.784308	-7.15
266559_at	unknown protein	---	AT2G23920	-1.04	-0.05	-0.42	0.688578	0.784324	-7.15
254978_at	subtilisin-like serine protease conta	---	AT4G10540	1.03	0.04	0.42	0.688596	0.784324	-7.15
265978_at	putative retroelement pol polyprotei	---	---	1.03	0.04	0.42	0.688759	0.784471	-7.15
259693_at	hypothetical protein predicted by ge	---	AT1G63060	-1.04	-0.05	-0.42	0.688926	0.784621	-7.15
249763_at	receptor-protein kinase-like protein	---	AT5G24010	-1.06	-0.08	-0.42	0.688984	0.78463	-7.15
267382_at	unknown protein	---	AT2G44300	-1.05	-0.08	-0.42	0.689003	0.78463	-7.15
265365_at	En/Spm-like transposon protein rela	---	---	-1.03	-0.04	-0.42	0.689264	0.784889	-7.15
261546_at	hypothetical protein	---	AT1G63520	-1.03	-0.05	-0.42	0.689422	0.785029	-7.15
247867_at	SNF1 related protein kinase-like pr	CIPK21	AT5G57630	1.06	0.08	0.42	0.689456	0.785029	-7.15
253658_at	cadmium-transporting ATPase-like	HMA3	AT4G30120	-1.03	-0.04	-0.42	0.689645	0.785205	-7.15
258603_at	putative heat shock transcription fa	ATHSFA1E	AT3G02990	1.05	0.07	0.42	0.689792	0.785333	-7.15
258802_at	unknown protein predicted by gens	---	AT3G04650	-1.05	-0.07	-0.42	0.689959	0.785484	-7.15
250516_at	putative protein predicted proteins,	---	AT5G09620	-1.03	-0.05	-0.42	0.690072	0.785533	-7.15
265452_at	putative bHLH transcription factor	ATAIB	AT2G46510	-1.11	-0.15	-0.42	0.69009	0.785533	-7.15
250601_at	putative protein contains similarity t	---	AT5G07810	-1.03	-0.04	-0.42	0.690105	0.785533	-7.15
256487_at	disease resistance gene, putative s	---	AT1G31540	-1.05	-0.07	-0.42	0.690177	0.785575	-7.15
247702_at	putative protein ;supported by full-l	---	AT5G59500	-1.04	-0.05	-0.42	0.690228	0.785594	-7.15
250245_at	alpha-N-acetylglucosaminidase	---	AT5G13690	1.04	0.06	0.42	0.690415	0.785768	-7.15
263288_at	cyclophilin-like protein ;supported b	---	AT2G36130	1.04	0.06	0.42	0.690858	0.786186	-7.15
251568_at	putative protein several hypothetica	---	AT3G58280	-1.04	-0.05	-0.42	0.69086	0.786186	-7.15
246081_s_a	myosin-like protein unconventional	---	AT5G20470	-1.05	-0.07	-0.42	0.690891	0.786186	-7.15
257359_x_a	putative protein kinase contains a p	---	AT2G34290	1.03	0.04	0.42	0.69092	0.786186	-7.15
265003_at	protein kinase, putative similar to p	---	AT1G26970	1.03	0.04	0.42	0.690974	0.786208	-7.15
265487_at	hypothetical protein	---	---	1.03	0.04	0.42	0.691011	0.786211	-7.15
258369_at	putative pectin methylesterase simi	ATPME3	AT3G14310	-1.04	-0.05	-0.41	0.691117	0.786293	-7.15
252607_at	xyloglucan endo-transglycosylase	XTR8	AT3G44990	-1.07	-0.09	-0.41	0.691258	0.786414	-7.15
247919_at	putative protein similar to unknown	---	AT5G57650	-1.04	-0.05	-0.41	0.691306	0.786429	-7.15
247811_at	leucine zipper-containing protein le	ATEXO70B	AT5G58430	-1.08	-0.11	-0.41	0.691388	0.786483	-7.15
257191_at	Expressed protein ; supported by fu	---	AT3G13175	-1.04	-0.05	-0.41	0.691437	0.7865	-7.15

251974_at	myb protein(MYB27) contains myb	AtMYB27	AT3G53200	-1.03	-0.04	-0.41	0.691548	0.786587	-7.15
250320_at	CCAAT box binding factor/ transcrip	NF-YA1	AT5G12840	1.04	0.05	0.41	0.691747	0.786762	-7.15
255786_at	unknown protein contains similarity	ATCLH1	AT1G19670	-1.09	-0.12	-0.41	0.691771	0.786762	-7.15
247227_at	putative protein contains similarity t	---	AT5G65130	-1.03	-0.05	-0.41	0.691913	0.786885	-7.15
247137_at	calcium-dependent protein kinase	CPK28	AT5G66210	-1.08	-0.11	-0.41	0.692034	0.786982	-7.15
250898_at	putative protein ; supported by cDN	ADK2	AT5G03300	-1.04	-0.06	-0.41	0.692305	0.787238	-7.15
257089_at	hypothetical protein	SVL3	AT3G20520	-1.03	-0.05	-0.41	0.692328	0.787238	-7.15
262987_at	conserved hypothetical protein prot	---	AT1G23240	-1.05	-0.07	-0.41	0.69258	0.78747	-7.15
252157_at	hypothetical protein	---	AT3G50430	-1.03	-0.05	-0.41	0.692631	0.78747	-7.15
248033_s_a	putative protein similar to unknown	---	AT5G54330	-1.03	-0.04	-0.41	0.692635	0.78747	-7.15
266226_at	histone H4 identical to GB:M17133	HIS4	AT2G28740	-1.06	-0.08	-0.41	0.692709	0.787514	-7.15
247546_at	Expressed protein ; supported by fu	---	AT5G61605	-1.04	-0.05	-0.41	0.693003	0.787778	-7.15
247728_at	putative protein	---	---	1.03	0.05	0.41	0.69301	0.787778	-7.15
248123_at	putative protein similar to unknown	---	AT5G54720	-1.03	-0.04	-0.41	0.69334	0.788114	-7.15
252732_at	putative protein predicted proteins,	---	---	-1.03	-0.05	-0.41	0.693585	0.788353	-7.15
252446_at	beta-D-glucan exohydrolase - like p	---	AT3G47010	-1.03	-0.04	-0.41	0.693694	0.788438	-7.15
258790_at	putative RNA-binding protein simila	FLK	AT3G04610	1.03	0.04	0.41	0.693783	0.7885	-7.15
245125_at	putative histidine kinase identical to	CKI1	AT2G47430	-1.04	-0.05	-0.41	0.693857	0.788544	-7.15
249500_at	expansin-like protein expansin - Pr	ATEXPA21	AT5G39260	-1.05	-0.07	-0.41	0.693891	0.788544	-7.15
250976_at	putative protein various predicted p	---	AT5G03060	-1.03	-0.04	-0.41	0.693939	0.78856	-7.15
254200_at	putative protein predicted proteins,	---	AT4G24110	1.16	0.21	0.41	0.694014	0.788605	-7.15
247738_at	putative protein myosin heavy chai	---	AT5G59210	1.04	0.05	0.41	0.694419	0.789026	-7.15
251867_at	SKP1 interacting partner 5 (SKIP5)	SKIP5	AT3G54480	1.03	0.04	0.41	0.694608	0.789163	-7.15
254387_at	putative protein CGI-131 protein, H	ATMSRB9	AT4G21850	1.24	0.31	0.41	0.694608	0.789163	-7.15
262750_at	unknown protein ; supported by cDI	---	AT1G28710	1.04	0.05	0.41	0.694659	0.789181	-7.15
255097_at	predicted transposon protein simila	---	---	1.04	0.06	0.41	0.694722	0.789213	-7.15
266777_at	putative AAA-type ATPase	ftsh3	AT2G29080	-1.03	-0.04	-0.41	0.694765	0.789223	-7.15
251988_at	CYTOCHROME P450-like protein	CYP71B31	AT3G53300	-1.03	-0.04	-0.41	0.694864	0.789295	-7.15
255112_at	casein kinase I - Arabidopsis thalia	---	AT4G08800	1.03	0.05	0.41	0.695105	0.78953	-7.15
260357_at	unknown protein ;supported by full-	AFP1	AT1G69260	1.04	0.06	0.41	0.695268	0.789672	-7.15
264791_at	predicted protein	---	AT2G17845	-1.03	-0.04	-0.41	0.695358	0.789672	-7.15
251002_at	putative protein predicted proteins,	---	AT5G02680	1.03	0.04	0.41	0.695373	0.789672	-7.15
249616_s_a	contains similarity to DnaJ protein	---	AT5G37440	1.03	0.04	0.41	0.695385	0.789672	-7.15
253406_at	putative protein GATA transcription	---	AT4G32890	-1.06	-0.09	-0.41	0.695403	0.789672	-7.15
260226_at	hypothetical protein predicted by ge	MIF1	AT1G74660	-1.04	-0.06	-0.41	0.695501	0.789744	-7.15

267151_at	aspartate aminotransferase (AAT1)	ASP1	AT2G30970	1.05	0.07	0.41	0.69559	0.789806	-7.15
262292_at	hypothetical protein similar to hypot	---	AT1G27595	1.04	0.05	0.41	0.695765	0.789965	-7.15
262104_at	hypothetical protein predicted by ge	LPA1	AT1G02910	-1.03	-0.05	-0.41	0.695852	0.790024	-7.15
257285_at	unknown protein	---	AT3G29760	-1.05	-0.07	-0.41	0.695916	0.790058	-7.15
262411_at	hypothetical protein predicted by ge	---	AT1G34640	-1.04	-0.05	-0.41	0.696064	0.7901	-7.16
263592_at	putative non-LTR retroelement reve	---	---	-1.05	-0.07	-0.41	0.696081	0.7901	-7.16
261980_at	hypothetical protein predicted by ge	---	AT1G33820	-1.03	-0.04	-0.41	0.696085	0.7901	-7.16
259189_at	unknown protein	AGP11	AT3G01700	-1.04	-0.06	-0.41	0.696091	0.7901	-7.16
254741_s_a	putative disease resistance protein	AtRLP49	AT4G13900	-1.03	-0.04	-0.41	0.696237	0.790225	-7.16
253416_at	pyruvate decarboxylase-1 (Pdc1)	---	AT4G33070	-1.05	-0.06	-0.41	0.69634	0.790303	-7.16
258481_at	putative phosphatidate phosphohyd	LPP3	AT3G02600	-1.04	-0.06	-0.41	0.696475	0.790362	-7.16
255876_at	hypothetical protein	---	AT2G40480	-1.07	-0.10	-0.41	0.696524	0.790362	-7.16
253341_at	putative protein ; supported by cDN	---	AT4G33410	1.04	0.05	0.41	0.696553	0.790362	-7.16
258733_at	unknown protein	---	---	-1.03	-0.04	-0.41	0.696565	0.790362	-7.16
255022_at	NAM/NAP like protein nap gene, A	ANAC070	AT4G10350	1.03	0.04	0.41	0.696635	0.790362	-7.16
247240_at	putative protein strong similarity to	CMPG2	AT5G64660	1.18	0.24	0.41	0.696658	0.790362	-7.16
257594_at	unknown protein	---	AT3G24740	-1.04	-0.06	-0.41	0.696674	0.790362	-7.16
255148_at	putative mitogen-activated protein k	MAPKKK1(	AT4G08470	1.08	0.11	0.41	0.696675	0.790362	-7.16
260504_at	Cyclin similar to GB:CAB77269 fron	CYCA3;3	AT1G47220	1.04	0.05	0.41	0.696731	0.790362	-7.16
254934_at	putative Ap2 domain protein DNA-l	CRF1	AT4G11140	1.04	0.06	0.41	0.696738	0.790362	-7.16
249103_at	N-carbamyl-L-amino acid amidohyd	UAH	AT5G43600	-1.03	-0.05	-0.41	0.696812	0.790406	-7.16
245221_s_a	polyprotein, putative similar to poly	---	---	1.03	0.04	0.41	0.696871	0.790434	-7.16
250376_at	putative protein	---	AT5G11550	1.06	0.08	0.41	0.696988	0.790503	-7.16
254254_at	hypothetical protein	---	AT4G23330	1.04	0.05	0.41	0.697001	0.790503	-7.16
266919_at	hypothetical protein predicted by ge	AT2G4578(	---	-1.03	-0.04	-0.41	0.697262	0.790737	-7.16
260253_at	disease resistance protein, putative	AtRLP15	AT1G74190	1.03	0.04	0.41	0.6973	0.790737	-7.16
257723_at	hypothetical protein predicted by ge	---	AT3G18500	-1.04	-0.06	-0.41	0.697312	0.790737	-7.16
265496_at	copia-like retroelement pol polyprot	---	---	1.03	0.04	0.41	0.697424	0.790825	-7.16
248844_s_a	extA (emb CAA47807.1)	---	AT5G46890	1.04	0.05	0.41	0.697668	0.791051	-7.16
252511_at	putative protein serine/threonine-sp	---	AT3G46280	1.09	0.12	0.41	0.697693	0.791051	-7.16
252820_at	plasma membrane H+-ATPase-like	AHA8	AT3G42640	1.05	0.08	0.41	0.697845	0.791185	-7.16
258279_at	putative self-incompatibility protein	---	AT3G26870	-1.02	-0.03	-0.41	0.697928	0.791239	-7.16
254863_at	putative protein predicted protein V	ATNUDX14	AT4G11980	-1.04	-0.05	-0.41	0.698033	0.791319	-7.16
263078_at	hypothetical protein predicted by ge	---	AT2G05350	-1.04	-0.05	-0.40	0.698068	0.791319	-7.16
247150_at	putative protein similar to unknown	---	AT5G65650	-1.04	-0.06	-0.40	0.698317	0.791562	-7.16

260512_at	unknown protein	---	AT1G51520	1.04	0.06	0.40	0.698463	0.791688	-7.16
249362_at	putative protein predicted protein, /	---	AT5G40550	1.08	0.12	0.40	0.698511	0.791703	-7.16
251764_at	putative protein exostose-related p	EPC1	AT3G55830	1.04	0.06	0.40	0.698704	0.791883	-7.16
265427_at	unknown protein	---	AT2G20740	1.04	0.06	0.40	0.698924	0.792093	-7.16
262377_at	rubisco activase, putative similar to	---	AT1G73110	1.06	0.09	0.40	0.698962	0.792095	-7.16
247109_at	putative protein similar to unknown	ATPSK5	AT5G65870	-1.07	-0.10	-0.40	0.698995	0.792095	-7.16
253015_at	hypothetical protein	---	AT4G37950	-1.03	-0.05	-0.40	0.699166	0.79225	-7.16
253415_at	putative protein peptidyl-prolyl cis-t	---	AT4G33060	1.05	0.07	0.40	0.699253	0.792308	-7.16
260432_at	putative DNA binding protein simila	WRKY9	AT1G68150	1.04	0.06	0.40	0.699601	0.792633	-7.16
261295_at	unknown protein	---	AT1G48450	1.03	0.04	0.40	0.699609	0.792633	-7.16
246689_at	putative protein predicted proteins -	---	---	1.02	0.04	0.40	0.699668	0.79266	-7.16
248293_at	unknown protein	---	AT5G53050	-1.05	-0.08	-0.40	0.699949	0.792939	-7.16
263442_at	hypothetical protein	---	AT2G28605	-1.03	-0.04	-0.40	0.70007	0.793037	-7.16
266562_at	unknown protein	---	AT2G23970	-1.05	-0.07	-0.40	0.700156	0.793096	-7.16
262827_at	putative cytochrome P450 monooxy	CYP71B29	AT1G13100	1.07	0.09	0.40	0.700336	0.79326	-7.16
250494_at	embryogenic callus protein - like er	HAM2	AT5G09740	-1.04	-0.06	-0.40	0.700381	0.793271	-7.16
264744_at	hypothetical protein predicted by ge	---	AT1G62050	-1.06	-0.08	-0.40	0.70044	0.793299	-7.16
259258_at	putative ribulose-1,5-bisphosphate	---	AT3G07670	1.06	0.08	0.40	0.700649	0.793479	-7.16
249871_at	putative protein similar to unknown	---	AT5G23110	1.05	0.07	0.40	0.700669	0.793479	-7.16
251112_s_a	pyruvate decarboxylase-like protei	PDC3	AT5G01320	1.05	0.07	0.40	0.700937	0.793743	-7.16
257511_at	hypothetical protein	---	AT1G43000	-1.03	-0.05	-0.40	0.701277	0.794089	-7.16
257893_at	E2, ubiquitin-conjugating enzyme,	UBC32	AT3G17000	1.05	0.08	0.40	0.701376	0.794162	-7.16
256074_at	unknown protein ; supported by cDI	---	AT1G18260	1.04	0.05	0.40	0.701491	0.794209	-7.16
263751_at	putative kinesin heavy chain	---	AT2G21300	-1.06	-0.08	-0.40	0.701522	0.794209	-7.16
267303_at	hookless1-like protein	---	AT2G30090	1.02	0.03	0.40	0.701522	0.794209	-7.16
260907_at	hypothetical protein predicted by ge	---	AT1G02570	1.03	0.04	0.40	0.701634	0.794296	-7.16
250294_at	auxin reponsive - like protein Nt-gh	---	AT5G13380	1.03	0.04	0.40	0.701688	0.794317	-7.16
265428_at	hypothetical protein predicted by gr	---	AT2G20720	1.07	0.10	0.40	0.701747	0.794345	-7.16
258808_at	putative pyruvate kinase similar to	---	AT3G04050	-1.03	-0.04	-0.40	0.70187	0.794445	-7.16
257747_at	hypothetical protein predicted by ge	---	AT3G18700	-1.03	-0.04	-0.40	0.702101	0.794667	-7.16
259683_at	unknown protein	---	AT1G63050	1.05	0.07	0.40	0.702236	0.794774	-7.16
264743_at	receptor-like protein kinase, putativ	---	AT1G62090	1.03	0.04	0.40	0.702289	0.794774	-7.16
263006_at	hypothetical protein contains simila	---	AT1G54240	-1.03	-0.05	-0.40	0.7023	0.794774	-7.16
248372_at	putative protein similar to unknown	---	AT5G51850	-1.03	-0.04	-0.40	0.702485	0.794943	-7.16
258319_at	hypothetical protein similar to hypot	---	AT3G22700	-1.03	-0.04	-0.40	0.702564	0.794978	-7.16

254581_at	putative protein membrane-associa	---	AT4G19440	-1.05	-0.06	-0.40	0.702618	0.794978	-7.16
260611_at	putative beta-1,3-glucanase, C terr	---	AT2G43670	-1.04	-0.05	-0.40	0.70262	0.794978	-7.16
265600_at	hypothetical protein predicted by ge	---	---	1.03	0.04	0.40	0.702708	0.795039	-7.16
246491_at	hypothetical protein	---	AT5G16100	1.03	0.04	0.40	0.703047	0.795369	-7.16
260114_at	AIG1-like protein similar to AIG1 pr	---	AT1G33880	1.03	0.04	0.40	0.703088	0.795369	-7.16
259916_at	hypothetical protein predicted by ge	---	AT1G72600	-1.03	-0.04	-0.40	0.703105	0.795369	-7.16
265463_at	unknown protein	IRX9	AT2G37090	-1.05	-0.07	-0.40	0.703268	0.795486	-7.16
258885_at	putative uridylate kinase similar to	---	AT3G10030	1.03	0.04	0.40	0.703281	0.795486	-7.16
265004_at	polyprotein, putative similar to poly	---	---	1.04	0.06	0.40	0.703313	0.795486	-7.16
261330_at	transcription factor, putative similar	MCM2	AT1G44900	-1.12	-0.16	-0.40	0.70343	0.795557	-7.16
246256_at	glucosyltransferase-like protein	---	AT4G36770	-1.05	-0.07	-0.40	0.703445	0.795557	-7.16
257419_at	hypothetical protein predicted by ge	---	AT1G30800	-1.03	-0.04	-0.40	0.70353	0.795613	-7.16
252580_at	putative protein putative proteins - A	---	AT3G45490	-1.03	-0.04	-0.40	0.703684	0.795748	-7.16
259796_at	hypothetical protein predicted by ge	---	---	-1.04	-0.05	-0.40	0.703782	0.79582	-7.16
263602_at	40S ribosomal protein S25	---	AT2G16360	1.03	0.04	0.40	0.703909	0.795924	-7.16
250067_at	unknown protein	---	AT5G17950	-1.03	-0.04	-0.40	0.704025	0.79601	-7.16
263571_at	putative disease resistance protein	---	AT2G17050	-1.03	-0.04	-0.40	0.704056	0.79601	-7.16
264497_at	hypothetical protein predicted by ge	ATPUP4	AT1G30840	1.05	0.07	0.40	0.704131	0.796057	-7.16
257385_at	hypothetical protein predicted by ge	---	AT2G01800	1.04	0.05	0.40	0.70447	0.796399	-7.16
262707_at	hypothetical protein	---	AT1G16290	-1.04	-0.05	-0.40	0.704504	0.796399	-7.16
254857_at	putative protein acetylcholine regul	SEC1B	AT4G12120	1.04	0.05	0.40	0.704597	0.796465	-7.16
253180_at	putative protein various predicted p	---	AT4G35210	-1.03	-0.04	-0.40	0.704784	0.796618	-7.16
250467_at	trehalose-6-phosphate phosphatas	---	AT5G10100	1.03	0.04	0.40	0.704802	0.796618	-7.16
246337_at	putative protein putative integral m	CHX12	AT3G44910	-1.04	-0.06	-0.40	0.704985	0.796785	-7.16
262090_at	CREB-binding protein, putative sim	HAC4	AT1G55970	1.03	0.05	0.39	0.705089	0.796863	-7.16
251014_at	putative protein fimbriae-associate	---	AT5G02520	-1.03	-0.04	-0.39	0.705147	0.796889	-7.16
262510_at	hypothetical protein similar to hypot	---	AT1G11270	-1.04	-0.05	-0.39	0.705196	0.796905	-7.16
247961_at	putative protein similar to unknown	---	AT5G56570	-1.03	-0.04	-0.39	0.705275	0.796954	-7.16
258664_at	E2, ubiquitin-conjugating enzyme,	UBC12	AT3G08700	1.03	0.05	0.39	0.705336	0.796984	-7.16
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb	---	---	1.05	0.07	0.39	0.705499	0.797127	-7.16
245041_at	AR781, similar to yeast pheromone	AR781	AT2G26530	1.16	0.22	0.39	0.705532	0.797127	-7.16
251440_at	SKP1/ASK1 (At13), putative simila	ASK13	AT3G60010	-1.05	-0.07	-0.39	0.705633	0.797167	-7.16
262571_at	hypothetical protein predicted by ge	---	AT1G15430	1.08	0.11	0.39	0.705638	0.797167	-7.16
260864_at	hypothetical protein predicted by ge	---	---	1.03	0.05	0.39	0.705759	0.797262	-7.16
266603_at	hypothetical protein predicted by ge	---	AT2G46040	-1.03	-0.04	-0.39	0.705804	0.797262	-7.16

248511_at	Expressed protein ; supported by cl	CPI1	AT5G50375	1.06	0.08	0.39	0.705831	0.797262	-7.16
267142_at	putative ammonium transporter	ATAMT2	AT2G38290	-1.06	-0.09	-0.39	0.705885	0.797262	-7.16
264068_at	putative homeodomain transcription	BLH8	AT2G27990	1.06	0.09	0.39	0.705917	0.797262	-7.16
250913_at	3-deoxy-D-manno-octulosonic acid	---	AT5G03770	1.03	0.04	0.39	0.705931	0.797262	-7.16
254614_at	putatative protein various predicted	---	AT4G19191	1.04	0.06	0.39	0.705992	0.797291	-7.16
253556_at	serine/threonine-specific protein ki	---	AT4G31100	-1.02	-0.04	-0.39	0.706067	0.797336	-7.16
264909_at	unknown protein	---	AT2G17300	1.03	0.05	0.39	0.706669	0.797977	-7.16
252388_at	putative protein ;supported by full-l	---	AT3G47850	-1.03	-0.05	-0.39	0.706895	0.798154	-7.16
263524_x_a	hypothetical protein predicted by ge	---	---	1.04	0.06	0.39	0.706896	0.798154	-7.16
259539_at	axi 1 protein, putative similar to axi	---	AT1G20550	1.04	0.05	0.39	0.706988	0.798218	-7.16
261087_at	hypothetical protein similar to unkn	---	AT1G17350	1.05	0.07	0.39	0.707038	0.798235	-7.16
251359_at	putative protein several hypothetica	---	AT3G61170	1.03	0.04	0.39	0.707428	0.798625	-7.16
258460_at	unknown protein	ECT6	AT3G17330	-1.04	-0.06	-0.39	0.707454	0.798625	-7.16
256719_at	En/Spm-like transposon protein rela	---	---	-1.03	-0.04	-0.39	0.70752	0.798661	-7.16
246174_s_a	putative protein hypothetical protei	---	AT5G28340	-1.03	-0.04	-0.39	0.708236	0.799405	-7.16
253661_at	putative protein bZIP protein - Arab	---	AT4G30130	1.03	0.05	0.39	0.70825	0.799405	-7.16
249379_at	putative protein predicted protein, A	---	AT5G40460	-1.07	-0.10	-0.39	0.708347	0.799475	-7.16
260752_at	unknown protein contains similarity	---	AT1G49030	-1.04	-0.05	-0.39	0.708631	0.799736	-7.16
255374_at	hypothetical protein	---	---	-1.03	-0.04	-0.39	0.708648	0.799736	-7.16
263383_at	putative protein kinase contains a p	---	AT2G40120	1.04	0.05	0.39	0.708708	0.799764	-7.16
265695_at	putative replication protein A1 ;sup	RPA2	AT2G24490	1.09	0.12	0.39	0.709093	0.800123	-7.16
247727_at	putative ripening-related protein - lik	---	AT5G59490	-1.04	-0.06	-0.39	0.709096	0.800123	-7.16
256592_at	hypothetical protein predicted by ge	---	---	1.03	0.04	0.39	0.709255	0.800263	-7.16
248156_at	unknown protein	---	AT5G54410	-1.02	-0.03	-0.39	0.709459	0.800453	-7.16
250121_at	protein kinase-like protein	---	AT5G16500	-1.03	-0.04	-0.39	0.709632	0.80057	-7.16
248325_at	unknown protein	---	AT5G52800	-1.03	-0.04	-0.39	0.709632	0.80057	-7.16
259939_s_a	ARE1-like protein similar to ARE1 (	---	AT1G71270	1.04	0.06	0.39	0.70973	0.800641	-7.16
265936_at	putative potassium/proton antiporte	ATKEA4	AT2G19600	-1.04	-0.05	-0.39	0.709826	0.800709	-7.16
263007_at	hypothetical protein contains simila	---	AT1G54260	1.03	0.04	0.39	0.709952	0.800812	-7.16
259472_at	hypothetical protein contains simila	---	AT1G18910	1.03	0.04	0.39	0.710291	0.801154	-7.16
265561_s_a	putative glycine-rich protein	---	AT1G47480	-1.04	-0.06	-0.39	0.710355	0.801187	-7.16
247514_at	peptide methionine sulfoxide reduc	PMSR1	AT5G61640	1.04	0.06	0.39	0.710405	0.801203	-7.16
247909_at	unknown protein ; supported by full	---	AT5G57370	1.04	0.05	0.39	0.710443	0.801206	-7.16
251349_s_a	putative protein several hypothetica	---	AT3G11030	-1.04	-0.06	-0.39	0.710805	0.801575	-7.16
265201_at	unknown protein	---	AT2G36810	1.03	0.04	0.39	0.710871	0.801604	-7.16

245956_s_a	luminal binding protein ; supported	BIP2	AT5G28540	1.10	0.14	0.39	0.7109	0.801604	-7.16
264222_at	hypothetical protein predicted by ge	---	AT1G60230	1.03	0.04	0.39	0.711015	0.801693	-7.16
263892_at	putative MYB family transcription fa	RAX2	AT2G36890	1.02	0.03	0.39	0.71113	0.801783	-7.16
252006_at	purple acid phosphatase-like prote	PAP22	AT3G52820	1.15	0.21	0.39	0.711222	0.801827	-7.16
250363_at	putative protein predicted proteins,	---	AT5G11390	1.06	0.08	0.39	0.711262	0.801827	-7.16
246670_at	putative protein	---	AT5G30520	-1.04	-0.06	-0.39	0.711274	0.801827	-7.16
261940_at	hypothetical protein predicted by ge	---	AT1G22520	1.04	0.06	0.39	0.711384	0.801911	-7.16
257731_at	unknown protein similar to CALCIN	---	AT3G18430	-1.03	-0.04	-0.39	0.711602	0.802117	-7.16
254165_at	putative protein hypothetical protei	---	AT4G24330	-1.04	-0.06	-0.39	0.711776	0.802221	-7.16
254745_at	putative protein G9A protein, Mus r	SUVH9	AT4G13460	1.02	0.03	0.39	0.711796	0.802221	-7.16
253164_at	Expressed protein ; supported by fu	---	AT4G35725	1.03	0.04	0.39	0.711819	0.802221	-7.16
248454_at	receptor protein kinase-like	---	AT5G51350	1.05	0.07	0.39	0.711835	0.802221	-7.16
245491_at	hypothetical protein	LDL3	---	1.04	0.05	0.39	0.711909	0.802265	-7.16
253611_at	RNase L inhibitor-like protein ribon	NAP15	AT4G30300	-1.03	-0.05	-0.39	0.711997	0.802324	-7.17
267049_at	putative transcription elongation fac	---	AT2G34210	-1.06	-0.08	-0.38	0.712126	0.8024	-7.17
254083_at	PROTEIN TRANSPORT PROTEIN	---	AT4G24920	1.05	0.06	0.38	0.712134	0.8024	-7.17
262359_at	disease resistance protein, putative	---	AT1G73060	-1.03	-0.05	-0.38	0.712361	0.802615	-7.17
253328_at	putative protein ABC-type transpor	ATNAP13	AT4G33460	-1.03	-0.04	-0.38	0.712487	0.802718	-7.17
247111_at	unknown protein	---	AT5G65880	1.05	0.07	0.38	0.712649	0.80286	-7.17
257133_at	hypothetical protein predicted by ge	---	AT3G17190	-1.02	-0.03	-0.38	0.712914	0.803097	-7.17
252926_at	H+-transporting ATPase 16K chain	ATVHA-C3	AT4G38920	1.03	0.05	0.38	0.712929	0.803097	-7.17
249812_at	putative protein similar to unknown	---	AT5G23830	-1.04	-0.06	-0.38	0.713061	0.803156	-7.17
260188_at	Mutator-like transposase similar to	---	---	-1.03	-0.04	-0.38	0.713063	0.803156	-7.17
245099_at	unknown protein ; supported by cD	RHC1A	AT2G40830	1.05	0.07	0.38	0.713087	0.803156	-7.17
251390_at	guanine nucleotide exchange facto	---	AT3G60860	-1.03	-0.05	-0.38	0.713175	0.803208	-7.17
255529_at	CTP synthase - like protein	---	AT4G02120	1.03	0.05	0.38	0.713203	0.803208	-7.17
257464_at	hypothetical protein predicted by ge	---	AT1G20940	-1.03	-0.04	-0.38	0.713439	0.803434	-7.17
253595_at	putative protein M1 protein, Strepto	---	AT4G30830	1.03	0.04	0.38	0.713688	0.803674	-7.17
266900_at	hypothetical protein predicted by ge	---	AT2G34610	-1.03	-0.04	-0.38	0.713873	0.803843	-7.17
252047_at	putative protein heat shock protein	---	AT3G52490	-1.04	-0.05	-0.38	0.71392	0.803856	-7.17
246639_x_a	adenylate kinase -like protein predi	---	---	1.03	0.04	0.38	0.714054	0.803967	-7.17
257996_at	unknown protein	---	AT3G19950	1.03	0.04	0.38	0.714308	0.804213	-7.17
264627_at	hypothetical protein similar to carnit	ECI1	AT1G65520	-1.03	-0.05	-0.38	0.714594	0.804456	-7.17
263973_at	60S ribosomal protein L11B	RPL16A	AT2G42740	-1.05	-0.08	-0.38	0.714594	0.804456	-7.17
248261_at	putative protein similar to unknown	PDV1	AT5G53280	-1.03	-0.04	-0.38	0.714753	0.804596	-7.17

256119_at	guanine nucleotide regulatory prote	---	AT1G18070	1.03	0.05	0.38	0.714945	0.804772	-7.17
266763_at	unknown protein	SPL1	AT2G47070	1.04	0.05	0.38	0.715119	0.804928	-7.17
265240_s_a	hypothetical protein	---	AT2G07691	1.04	0.05	0.38	0.715284	0.805036	-7.17
253417_at	putative protein	PC-MYB1	AT4G32730	1.03	0.04	0.38	0.715286	0.805036	-7.17
248650_at	putative protein similar to unknown	---	AT5G49250	1.04	0.06	0.38	0.71553	0.805235	-7.17
254419_at	NADH dehydrogenase like protein	NDB3	AT4G21490	-1.03	-0.04	-0.38	0.71555	0.805235	-7.17
255422_at	putative D-type cyclin	CYCD6;1	AT4G03270	-1.03	-0.04	-0.38	0.715568	0.805235	-7.17
263096_at	class 1 non-symbiotic hemoglobin (	AHB1	AT2G16060	-1.08	-0.11	-0.38	0.715618	0.805251	-7.17
246940_at	expressed protein glucose-6-phosp	---	AT5G25400	-1.03	-0.05	-0.38	0.715677	0.805278	-7.17
259324_at	unknown protein	MIRO3	AT3G05310	-1.04	-0.06	-0.38	0.715953	0.805516	-7.17
257425_at	hypothetical protein similar to heat s	---	AT1G60400	-1.04	-0.06	-0.38	0.715959	0.805516	-7.17
265721_at	putative ABC1 protein identical to E	ATATH9	AT2G40090	1.04	0.06	0.38	0.716144	0.805684	-7.17
264139_at	hypothetical protein contains similar	---	AT1G78940	-1.03	-0.04	-0.38	0.716323	0.805845	-7.17
249998_at	putative protein unnamed ORF, Mu	FASS	AT5G18580	1.03	0.04	0.38	0.716486	0.80599	-7.17
264934_at	hypothetical protein predicted by ge	---	AT1G61090	-1.03	-0.04	-0.38	0.716957	0.80648	-7.17
246813_at	putative protein various predicted p	---	---	-1.03	-0.04	-0.38	0.717424	0.806965	-7.17
259894_at	hypothetical protein predicted by ge	---	AT1G71430	-1.04	-0.05	-0.38	0.717467	0.806969	-7.17
253907_at	putative protein dihydrokaempferol	---	AT4G27250	-1.04	-0.06	-0.38	0.717628	0.806969	-7.17
248188_at	putative protein contains similarity t	HSFA9	AT5G54070	1.02	0.03	0.38	0.71763	0.806969	-7.17
245223_at	gene_id:K17E7.5~unknown protein	---	AT3G29791	-1.03	-0.04	-0.38	0.717641	0.806969	-7.17
260363_at	unknown protein similar to hypothet	---	AT1G70550	1.04	0.05	0.38	0.717697	0.806969	-7.17
249507_at	similar to unknown protein (pir||T02	---	AT5G38370	-1.02	-0.03	-0.38	0.717716	0.806969	-7.17
258619_at	isopentenyl diphosphate:dimethylall	IPP2	AT3G02780	1.04	0.05	0.38	0.717728	0.806969	-7.17
252333_at	putative protein N-terminus: severa	---	AT3G48830	1.03	0.04	0.38	0.717789	0.806969	-7.17
257388_at	putative non-LTR retroelement reve	---	---	-1.02	-0.03	-0.38	0.717812	0.806969	-7.17
256714_at	cysteine proteinase contains similar	---	AT2G34080	-1.03	-0.05	-0.38	0.717836	0.806969	-7.17
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_X	---	---	1.05	0.07	0.38	0.717854	0.806969	-7.17
260083_at	putative elicitor-responsive gene sir	---	AT1G63220	1.11	0.15	0.38	0.717874	0.806969	-7.17
263992_at	putative retroelement pol polyprotei	---	---	1.03	0.04	0.38	0.717888	0.806969	-7.17
245697_at	latex-abundant protein - like ;suppo	AtMC9	AT5G04200	-1.15	-0.20	-0.38	0.71795	0.807	-7.17
264150_at	unknown protein similar to FUS5 p	FUS5	AT1G02090	-1.03	-0.04	-0.38	0.718056	0.807078	-7.17
251724_at	putative protein	---	AT3G56250	1.03	0.04	0.38	0.718221	0.807225	-7.17
255068_at	Arabidopsis thaliana flavin-type blu	CRY1	AT4G08920	-1.02	-0.03	-0.38	0.71834	0.807287	-7.17
256331_at	GT-like trihelix DNA-binding protein	---	AT1G76880	1.03	0.04	0.38	0.718359	0.807287	-7.17
257088_at	unknown protein	---	AT3G20510	1.07	0.10	0.38	0.718383	0.807287	-7.17

246254_at	MAP kinase like protein	ATMPK14	AT4G36450	-1.05	-0.08	-0.38	0.718452	0.807311	-7.17
251746_at	mandelonitrile lyase-like protein AD	---	AT3G56060	1.04	0.05	0.38	0.718475	0.807311	-7.17
256662_at	male sterility protein 2 (MS2) nearly	MS2	AT3G11980	-1.03	-0.04	-0.38	0.718675	0.807496	-7.17
253472_at	hypothetical protein	---	AT4G32230	-1.03	-0.04	-0.38	0.7188	0.807597	-7.17
262666_at	xyloglucan fucosyltransferase, puta	FUT6	AT1G14080	-1.06	-0.09	-0.38	0.719051	0.8078	-7.17
249358_at	sucrose cleavage protein -like sucr	---	AT5G40510	1.03	0.05	0.38	0.719052	0.8078	-7.17
245820_at	allyl alcohol dehydrogenase, putati	---	AT1G26320	1.03	0.04	0.38	0.719147	0.807848	-7.17
262426_s_a	cytochrome P450, putative similar	---	AT1G47625	-1.04	-0.06	-0.37	0.7192	0.807848	-7.17
245190_at	F12A21.16 hypothetical protein	---	AT1G67690	1.04	0.06	0.37	0.719201	0.807848	-7.17
261382_at	hypothetical protein contains simila	CVP2	AT1G05470	1.04	0.06	0.37	0.719345	0.807956	-7.17
253712_at	putative protein putative NADH oxi	DER1	AT4G29330	-1.03	-0.05	-0.37	0.719382	0.807956	-7.17
264838_at	putative AHP2 similar to GB:BAA36	AHP5	AT1G03430	-1.02	-0.03	-0.37	0.71943	0.807956	-7.17
251517_at	putative protein hypothetical protei	---	AT3G59370	-1.02	-0.03	-0.37	0.719474	0.807956	-7.17
265912_at	hypothetical protein predicted by ge	---	AT2G25565	-1.03	-0.04	-0.37	0.719474	0.807956	-7.17
261137_at	auxin-induced protein, putative sim	---	AT1G19830	1.03	0.04	0.37	0.719615	0.808075	-7.17
265065_at	putative phytochelatin synthase	ATPCS2	AT1G03980	1.03	0.04	0.37	0.719801	0.808243	-7.17
253725_at	profilin 3 ;supported by full-length c	PRF4	AT4G29340	-1.03	-0.04	-0.37	0.719991	0.808417	-7.17
245426_at	hypothetical protein	---	AT4G17540	1.04	0.05	0.37	0.720311	0.808661	-7.17
265546_at	putative proline/hydroxyproline-rich	---	AT2G28240	1.03	0.05	0.37	0.720312	0.808661	-7.17
261091_at	protein kinase, putative contains P	---	AT1G07550	-1.03	-0.04	-0.37	0.720349	0.808661	-7.17
248450_at	putative protein contains similarity t	---	AT5G51290	-1.03	-0.05	-0.37	0.72035	0.808661	-7.17
266575_at	putative chloroplast initiation factor	---	AT2G24060	-1.03	-0.05	-0.37	0.720537	0.808831	-7.17
249131_at	putative protein contains similarity t	APUM14	AT5G43110	1.03	0.04	0.37	0.72059	0.808851	-7.17
247848_at	resistance protein - like disease res	---	AT5G58120	-1.04	-0.05	-0.37	0.720753	0.808995	-7.17
253785_s_a	ABC transporter - like protein ABC	ATM2	AT4G28620	1.03	0.04	0.37	0.720988	0.809218	-7.17
262674_at	anter-specific proline-rich -like prote	EXL4	AT1G75910	-1.03	-0.05	-0.37	0.72113	0.809338	-7.17
263860_at	hypothetical protein predicted by ge	---	---	-1.03	-0.04	-0.37	0.721236	0.809417	-7.17
260059_at	trehalose-6-phosphate phosphatas	ATTPPB	AT1G78090	-1.05	-0.08	-0.37	0.721464	0.809633	-7.17
263737_at	unknown protein ;supported by full-	---	AT1G60010	-1.04	-0.05	-0.37	0.721501	0.809634	-7.17
250548_at	myosin heavy chain-like protein ; s	MBP2C	AT5G08120	1.03	0.04	0.37	0.721561	0.809662	-7.17
265686_at	hypothetical protein predicted by ge	---	AT2G24460	-1.02	-0.04	-0.37	0.721951	0.81006	-7.17
257781_at	spastin protein, putative similar to s	---	AT3G27120	-1.02	-0.04	-0.37	0.722237	0.810324	-7.17
249802_at	putative protein similar to unknown	---	AT5G23770	1.03	0.04	0.37	0.722257	0.810324	-7.17
256650_at	hypothetical protein contains simila	---	AT3G13620	-1.03	-0.05	-0.37	0.722305	0.810337	-7.17
262864_at	anthocyanidin-3-glucoside rhamno	---	AT1G64920	-1.03	-0.05	-0.37	0.722364	0.810352	-7.17

265756_at	putative bZIP transcription factor sir	---	AT2G13150	1.02	0.03	0.37	0.722389	0.810352	-7.17
249920_at	putative protein various predicted p	---	AT5G19260	-1.08	-0.11	-0.37	0.722532	0.810472	-7.17
246096_at	beta-1,3-glucanase bg4 ;supporte	BETAG4	AT5G20330	1.03	0.05	0.37	0.722626	0.810537	-7.17
266124_at	putative PREG1-like negative regul	cycp3;1	AT2G45080	-1.03	-0.05	-0.37	0.722767	0.810656	-7.17
263455_at	hypothetical protein predicted by ge	---	AT2G22320	1.05	0.07	0.37	0.722851	0.81071	-7.17
251460_at	hypothetical protein	SAC9	AT3G59770	1.03	0.04	0.37	0.722906	0.810732	-7.17
247719_at	Expressed protein ; supported by fu	---	AT5G59305	1.03	0.04	0.37	0.722969	0.810764	-7.17
264252_at	putative GTP-binding protein, SAR	ATSARA1A	AT1G09180	-1.03	-0.04	-0.37	0.723377	0.811162	-7.17
250098_at	putative protein ;supported by full-l	---	AT5G17350	-1.20	-0.26	-0.37	0.723425	0.811162	-7.17
261514_at	hypothetical protein predicted by ge	---	AT1G71870	-1.04	-0.06	-0.37	0.723432	0.811162	-7.17
251558_at	putative protein ;supported by full-	---	AT3G57810	-1.06	-0.08	-0.37	0.723498	0.811172	-7.17
257397_at	hypothetical protein predicted by ge	RIC6	AT2G20430	1.04	0.06	0.37	0.723511	0.811172	-7.17
260662_at	2-hydroxyisoflavone reductase, put	---	AT1G19540	-1.03	-0.05	-0.37	0.723625	0.811219	-7.17
265751_at	putative retroelement pol polyprotei	---	---	-1.03	-0.04	-0.37	0.723649	0.811219	-7.17
255998_at	hypothetical protein contains simila	---	AT1G29780	-1.03	-0.04	-0.37	0.723685	0.811219	-7.17
267637_at	unknown protein predicted by gens	---	AT2G42190	-1.05	-0.06	-0.37	0.723696	0.811219	-7.17
263273_x_a	En/Spm-like transposon protein rela	---	---	-1.03	-0.04	-0.37	0.723782	0.811276	-7.17
257709_at	unknown protein similar to negative	---	AT3G27325	-1.04	-0.06	-0.37	0.723914	0.811341	-7.17
251128_at	putative protein crp1 protein, Zea r	---	AT5G01110	1.02	0.03	0.37	0.723974	0.811341	-7.17
263874_at	putative ATP synthase ;supported	---	AT2G21870	1.04	0.06	0.37	0.723974	0.811341	-7.17
255085_at	putative protein several hypothetica	---	---	1.03	0.04	0.37	0.724002	0.811341	-7.17
246529_at	serine/threonine-specific protein kin	---	AT5G15730	1.07	0.10	0.37	0.724018	0.811341	-7.17
260021_at	unknown protein	---	AT1G30010	-1.05	-0.07	-0.37	0.724188	0.811491	-7.17
246187_at	putative protein	AT5G2102(	---	1.04	0.06	0.37	0.724361	0.811557	-7.17
253074_at	putative disease resistance protein	---	AT4G36140	1.02	0.03	0.37	0.724365	0.811557	-7.17
254942_at	putative protein predicted proteins,	---	AT4G10880	1.02	0.03	0.37	0.724383	0.811557	-7.17
247180_at	histone H3	---	AT5G65350	1.02	0.04	0.37	0.724388	0.811557	-7.17
258096_at	hypothetical protein similar to putati	---	AT3G23650	-1.03	-0.04	-0.37	0.724459	0.811596	-7.17
255425_s_a	putative protein	---	AT4G02950	-1.04	-0.05	-0.37	0.724548	0.811656	-7.17
259561_at	hypothetical protein ; supported by	WAK1	AT1G21250	-1.18	-0.23	-0.37	0.724789	0.811886	-7.17
257706_at	Expressed protein ; supported by cl	---	AT3G12685	-1.05	-0.07	-0.37	0.724884	0.811952	-7.17
244975_at	PSII 10KDa phosphoprotein	---	---	1.03	0.05	0.37	0.725028	0.812074	-7.17
248571_at	putative protein similar to unknown	---	---	1.02	0.04	0.37	0.725108	0.812121	-7.17
259049_at	unknown protein	---	AT3G03370	-1.04	-0.05	-0.37	0.725141	0.812121	-7.17
245811_at	hypothetical protein similar to putati	---	---	-1.03	-0.04	-0.37	0.725351	0.8123	-7.17

257566_x_a	hypothetical protein predicted by ge	---	---	-1.03	-0.04	-0.37	0.725372	0.8123	-7.17
252819_at	putative protein several hypothetica	---	---	1.02	0.03	0.37	0.725507	0.812397	-7.17
260604_at	polyphosphoinositide binding prote	---	AT1G55840	-1.04	-0.06	-0.37	0.72553	0.812397	-7.17
251452_at	putative protein male sterility protei	---	AT3G60060	-1.02	-0.03	-0.37	0.725893	0.812763	-7.17
266004_at	unknown protein predicted by gens	ALS3	AT2G37330	-1.02	-0.03	-0.37	0.72603	0.81286	-7.17
260516_at	unknown protein	---	AT1G51450	1.03	0.05	0.37	0.726051	0.81286	-7.17
252816_at	putative protein several putative pro	---	AT3G42550	-1.02	-0.03	-0.37	0.726113	0.812891	-7.17
249984_at	putative protein rsc43, Dictyosteliu	---	AT5G18400	-1.06	-0.08	-0.37	0.726167	0.812911	-7.17
249321_at	disease resistance protein-like	---	AT5G40920	-1.04	-0.06	-0.37	0.726221	0.812922	-7.17
253530_at	putative protein hypothetical protei	---	AT4G31530	-1.05	-0.08	-0.37	0.726269	0.812922	-7.17
250439_at	14-3-3 protein GF14lambda (grf6/A	GRF6	AT5G10450	1.03	0.04	0.37	0.726284	0.812922	-7.17
263575_at	hypothetical protein similar to hypot	---	AT2G17070	1.03	0.04	0.36	0.726421	0.813036	-7.17
253157_at	putative protein DNA helicase TPS	RecQl3	AT4G35740	1.03	0.05	0.36	0.7267	0.813308	-7.17
246588_at	putative protein predicted protein, A	---	AT3G06433	-1.02	-0.03	-0.36	0.726899	0.813491	-7.17
246672_at	putative protein	---	---	-1.02	-0.03	-0.36	0.726994	0.813525	-7.17
255970_s_a	hypothetical protein predicted by ge	---	---	-1.02	-0.04	-0.36	0.727001	0.813525	-7.17
259387_at	histone H3 protein, putative similar	---	AT1G13370	1.03	0.04	0.36	0.727063	0.813555	-7.17
256354_at	dormancy related protein, putative	---	AT1G54870	-1.04	-0.05	-0.36	0.727158	0.813574	-7.17
263176_at	UDP-glucose:indole-3-acetate beta	UGT75B2	AT1G05530	1.03	0.04	0.36	0.727162	0.813574	-7.17
249851_at	MADS-box transcription factor-like p	TT16	AT5G23260	-1.02	-0.03	-0.36	0.727187	0.813574	-7.17
254468_at	UDP-glucose 4-epimerase - like pr	---	AT4G20460	-1.03	-0.04	-0.36	0.727235	0.813587	-7.17
244974_at	PSII low MW protein	---	---	-1.03	-0.04	-0.36	0.727426	0.813758	-7.17
257159_at	protein kinase, putative similar to p	---	AT3G24400	-1.05	-0.06	-0.36	0.727459	0.813758	-7.17
252989_at	putative pectinesterase pectinester	sks9	AT4G38420	1.13	0.17	0.36	0.727571	0.813843	-7.17
257519_at	unknown protein	---	AT3G01210	-1.03	-0.05	-0.36	0.728004	0.814288	-7.17
AFFX-ThrX-	B. subtilis /GEN=thrC, thrB /DB_XR	---	---	1.07	0.09	0.36	0.72812	0.814377	-7.17
254687_at	cytochrome P450 monooxygenase	CYP83A1	AT4G13770	-1.04	-0.06	-0.36	0.72841	0.814662	-7.17
250030_at	putative protein contains similarity t	ATAPRL7	AT5G18120	1.03	0.04	0.36	0.728495	0.814717	-7.17
260481_at	ferredoxin precusor isolog ;support	ATFD1	AT1G10960	-1.05	-0.07	-0.36	0.728601	0.814796	-7.17
253771_at	hypothetical protein ;supported by	---	AT4G28430	-1.03	-0.05	-0.36	0.728769	0.814944	-7.17
247499_at	predicted protein	---	AT5G61865	1.03	0.04	0.36	0.72888	0.815028	-7.17
257931_at	hypothetical protein predicted by ge	---	AT3G17030	1.03	0.04	0.36	0.728988	0.815109	-7.18
248851_s_a	disease resistance protein-like ; su	---	AT5G46260	1.03	0.04	0.36	0.729132	0.81523	-7.18
258130_at	unknown protein	---	AT3G24510	1.03	0.04	0.36	0.729263	0.815324	-7.18
255311_at	putative protein	---	---	-1.03	-0.04	-0.36	0.729288	0.815324	-7.18

264161_at	antigen receptor, putative similar to	---	AT1G65420	1.03	0.04	0.36	0.729387	0.815347	-7.18
265368_at	hypothetical protein identical to hyp	---	AT2G13350	-1.04	-0.06	-0.36	0.729405	0.815347	-7.18
261908_at	stig1-like protein similar to Stig1 GE	---	AT1G50650	-1.03	-0.05	-0.36	0.729442	0.815347	-7.18
256378_at	receptor protein kinase, putative co	---	AT1G66830	1.03	0.04	0.36	0.729465	0.815347	-7.18
258305_at	hypothetical protein predicted by ge	---	---	-1.02	-0.03	-0.36	0.729487	0.815347	-7.18
255071_at	putative protein putative chloroplas	---	AT4G09040	1.03	0.04	0.36	0.729588	0.81542	-7.18
260629_at	unknown protein	---	AT1G62330	-1.03	-0.05	-0.36	0.729641	0.815437	-7.18
260956_at	salt-tolerance protein identical to sa	STO	AT1G06040	-1.03	-0.04	-0.36	0.729675	0.815437	-7.18
262462_at	hypothetical protein predicted by ge	---	AT1G50350	1.03	0.04	0.36	0.729766	0.815497	-7.18
265800_at	similar to ch-TOG protein from Hom	MOR1	AT2G35630	1.03	0.04	0.36	0.7298	0.815497	-7.18
254420_at	hypothetical protein	---	AT4G21500	-1.04	-0.05	-0.36	0.730006	0.815687	-7.18
252078_at	putative protein brassinosteroid-ins	IMK2	AT3G51740	-1.02	-0.03	-0.36	0.730077	0.815727	-7.18
254813_at	putative transcription factor myb-re	MYB42	AT4G12350	-1.02	-0.03	-0.36	0.730226	0.815853	-7.18
252668_at	hypothetical protein	---	AT3G44210	-1.02	-0.03	-0.36	0.730315	0.815912	-7.18
266852_at	hypothetical protein predicted by ge	---	AT2G26810	1.03	0.04	0.36	0.73039	0.815956	-7.18
253267_at	putative protein TEB4 protein, Hom	---	AT4G34100	-1.03	-0.05	-0.36	0.730496	0.816035	-7.18
264564_at	hypothetical protein predicted by ge	---	AT1G05290	1.02	0.03	0.36	0.730639	0.816155	-7.18
250046_at	putative protein predicted proteins,	---	AT5G17720	-1.03	-0.04	-0.36	0.730779	0.816271	-7.18
257909_at	Expressed protein ; supported by fu	---	AT3G25480	-1.04	-0.05	-0.36	0.730937	0.816374	-7.18
266305_at	putative DNA polymerase epsilon c	TIL2	AT2G27120	-1.03	-0.04	-0.36	0.730943	0.816374	-7.18
250142_at	polygalacturonase - like protein pol	---	AT5G14650	1.06	0.09	0.36	0.730996	0.816393	-7.18
246381_at	hypothetical protein	---	---	1.05	0.07	0.36	0.731406	0.816812	-7.18
245872_at	hypothetical protein contains simila	---	AT1G26300	-1.03	-0.04	-0.36	0.731481	0.816853	-7.18
257554_at	synaptobrevin, putative similar to S	VAMP728	AT3G24890	1.03	0.04	0.36	0.731545	0.816853	-7.18
260869_at	stearoyl acyl carrier protein desatu	---	AT1G43800	-1.02	-0.03	-0.36	0.73155	0.816853	-7.18
253108_at	putative bZIP transcription factor D	FD	AT4G35900	-1.05	-0.08	-0.36	0.731666	0.816932	-7.18
251213_at	putative protein hypothetical protein	---	---	-1.03	-0.04	-0.36	0.731693	0.816932	-7.18
265505_at	putative RING zinc finger protein	---	AT2G15530	-1.03	-0.04	-0.36	0.731811	0.817024	-7.18
252493_at	hypothetical protein	---	AT3G46750	1.04	0.05	0.36	0.732075	0.817278	-7.18
261523_at	protein tyrosine phosphatase ident	PTP1	AT1G71860	-1.03	-0.04	-0.36	0.73212	0.817289	-7.18
261082_at	unknown protein ; supported by cDI	---	AT1G07360	-1.02	-0.03	-0.36	0.732292	0.817403	-7.18
247387_at	unknown protein	---	AT5G63460	-1.03	-0.04	-0.36	0.732294	0.817403	-7.18
266727_at	putative calmodulin	emb1579	AT2G03150	1.03	0.05	0.36	0.732336	0.81741	-7.18
261239_at	Avr9 elicitor response protein, puta	---	AT1G32930	1.03	0.04	0.36	0.732373	0.817411	-7.18
265278_at	hypothetical protein predicted by ge	---	AT2G28330	-1.04	-0.05	-0.36	0.732418	0.817421	-7.18

265354_at	actin depolymerizing factor 5 ;supp	ADF5	AT2G16700	-1.07	-0.09	-0.36	0.732548	0.817527	-7.18
263890_at	putative auxin-induced protein	---	AT2G37030	1.04	0.06	0.36	0.732602	0.817546	-7.18
251121_at	putative protein ; supported by cDN	AGG1	AT3G63420	1.04	0.06	0.36	0.733045	0.818	-7.18
256031_at	choline kinase (GmCK2p), putative	---	AT1G34100	-1.03	-0.04	-0.36	0.733161	0.818091	-7.18
255800_at	putative protein transposase, Ipom	---	AT4G10200	1.02	0.04	0.36	0.733215	0.81811	-7.18
261619_x_a	hypothetical protein	---	---	-1.03	-0.04	-0.36	0.733305	0.81817	-7.18
249549_at	lipid transfer - like protein lipid trans	---	AT5G38180	-1.03	-0.04	-0.36	0.733357	0.818188	-7.18
252857_at	putative protein various predicted p	---	AT4G39756	1.03	0.04	0.36	0.733447	0.818215	-7.18
246332_at	putative protein phosphatidylcholin	---	AT3G44830	1.04	0.05	0.36	0.733452	0.818215	-7.18
253810_at	putative NADH dehydrogenase NA	NDB1	AT4G28220	-1.08	-0.10	-0.35	0.733602	0.818342	-7.18
252955_at	multiubiquitin chain binding protein	RPN10	AT4G38630	-1.02	-0.03	-0.35	0.733748	0.818448	-7.18
267047_at	putative selenium-binding protein	---	AT2G34370	-1.03	-0.04	-0.35	0.733768	0.818448	-7.18
251765_at	putative protein	---	---	1.03	0.04	0.35	0.733817	0.818462	-7.18
254465_at	tapetum-specific A3 like protein Ara	---	AT4G20420	-1.03	-0.05	-0.35	0.733927	0.818545	-7.18
245451_at	disease resistance RPP5 like protei	SNC1	AT4G16890	1.02	0.03	0.35	0.734055	0.818647	-7.18
255069_s_a	Met2-type cytosine DNA-methyltra	---	AT4G08990	-1.05	-0.06	-0.35	0.734092	0.818648	-7.18
262100_s_a	hypothetical protein similar to hypot	---	AT1G59550	1.04	0.05	0.35	0.73422	0.818751	-7.18
258782_at	putative dihydroneopterin aldolase	---	AT3G11750	-1.04	-0.06	-0.35	0.734378	0.81886	-7.18
251715_at	putative protein putative WRKY-typ	---	AT3G56390	-1.02	-0.03	-0.35	0.734389	0.81886	-7.18
257957_at	wall-associated serine/threonine ki	---	AT3G25490	-1.04	-0.06	-0.35	0.734669	0.819131	-7.18
267234_x_a	putative protein kinase contains a p	---	AT2G43930	1.03	0.04	0.35	0.734916	0.819368	-7.18
247589_at	REVOLUTA or interfascicular fiberle	REV	AT5G60690	1.03	0.04	0.35	0.735114	0.819548	-7.18
263025_at	reverse transcriptase, putative simi	---	---	-1.03	-0.04	-0.35	0.735202	0.819606	-7.18
261147_at	unknown protein ;supported by full-	---	AT1G19690	-1.05	-0.07	-0.35	0.73526	0.81963	-7.18
263192_at	hypothetical protein putative acetyl	ACC1	AT1G36160	-1.04	-0.06	-0.35	0.735343	0.81966	-7.18
252578_at	putative protein Ariadne protein (Al	---	AT3G45480	1.02	0.04	0.35	0.735358	0.81966	-7.18
253801_at	hypothetical protein	---	AT4G28170	-1.03	-0.04	-0.35	0.735411	0.819678	-7.18
261875_at	receptor-like protein kinase, putativ	---	AT1G50610	1.03	0.04	0.35	0.73545	0.819682	-7.18
245523_at	drought-induced protein like	ATDI21	AT4G15910	-1.04	-0.06	-0.35	0.735527	0.819728	-7.18
260721_at	hypothetical protein predicted by ge	---	AT1G48060	1.03	0.04	0.35	0.735868	0.820068	-7.18
266404_at	hypothetical protein predicted by ge	---	AT2G38590	1.03	0.04	0.35	0.73607	0.820234	-7.18
264655_at	unknown protein Similar to Glycine	SRC2	AT1G09070	1.06	0.09	0.35	0.736089	0.820234	-7.18
258748_at	germin-like protein similar to germi	GLP8	AT3G05930	-1.03	-0.05	-0.35	0.736179	0.820287	-7.18
258411_at	hypothetical protein predicted by ge	---	AT3G17280	1.03	0.04	0.35	0.736209	0.820287	-7.18
245561_at	indole-3-acetate beta-glucosyltrans	UGT84A4	AT4G15500	1.04	0.05	0.35	0.736314	0.820365	-7.18

263454_at	putative cysteine proteinase	---	AT2G22160	1.03	0.04	0.35	0.736363	0.820379	-7.18
251179_at	putative protein ABP130 protein, H	---	AT3G63460	-1.02	-0.03	-0.35	0.736429	0.820403	-7.18
254058_at	putative protein cylicin II - human, I	---	AT4G25210	-1.03	-0.05	-0.35	0.736457	0.820403	-7.18
245733_at	hypothetical protein predicted by ge	---	AT1G73380	-1.04	-0.06	-0.35	0.736524	0.820438	-7.18
249415_at	promoter-binding protein like ascor	CDF2	AT5G39660	1.05	0.07	0.35	0.736647	0.820535	-7.18
246365_at	hypothetical protein	---	---	-1.03	-0.04	-0.35	0.736875	0.820749	-7.18
260456_at	hypothetical protein	---	AT1G72490	-1.03	-0.05	-0.35	0.736946	0.820783	-7.18
247235_at	putative protein contains similarity t	---	AT5G64580	1.05	0.07	0.35	0.736977	0.820783	-7.18
246106_at	receptor-like protein kinase precurs	---	AT5G28680	-1.02	-0.03	-0.35	0.737238	0.821034	-7.18
266063_at	putative SNF2/RAD54 family DNA r	CHR8	AT2G18760	1.03	0.04	0.35	0.737412	0.821187	-7.18
257366_s_a	unknown protein	---	AT2G03040	1.03	0.04	0.35	0.737526	0.821273	-7.18
254411_at	hypothetical protein	---	---	-1.03	-0.04	-0.35	0.737602	0.821299	-7.18
259099_at	unknown protein similar to GB:AAB	---	AT3G05010	1.03	0.04	0.35	0.737621	0.821299	-7.18
254199_at	putative protein Ste-20 related kina	---	AT4G24100	-1.03	-0.04	-0.35	0.737685	0.821306	-7.18
260097_at	putative transporter similar to organ	AtOCT1	AT1G73220	-1.18	-0.23	-0.35	0.737709	0.821306	-7.18
261643_at	hypothetical protein similar to hypot	TAF4B	AT1G27720	-1.04	-0.06	-0.35	0.737735	0.821306	-7.18
259540_at	nodule inception protein, putative s	---	AT1G20640	-1.05	-0.07	-0.35	0.737777	0.821313	-7.18
257582_at	hypothetical protein	---	AT1G50720	-1.02	-0.03	-0.35	0.738096	0.821627	-7.18
248464_at	putative protein similar to unknown	---	AT5G51160	-1.04	-0.06	-0.35	0.738132	0.821627	-7.18
259111_at	alpha subunit of F-actin capping pro	---	AT3G05520	-1.04	-0.05	-0.35	0.738237	0.821685	-7.18
260194_at	hypothetical protein similar to hypot	---	AT1G67530	1.05	0.07	0.35	0.738278	0.821685	-7.18
261976_at	hypothetical protein predicted by ge	---	---	1.03	0.04	0.35	0.738311	0.821685	-7.18
255274_at	putative protein various predicted p	---	---	1.03	0.05	0.35	0.738328	0.821685	-7.18
245784_at	hypothetical protein similar to hypot	---	AT1G32190	-1.03	-0.04	-0.35	0.738373	0.821695	-7.18
266798_at	putative embryo-abundant protein c	AtbZIP6	AT2G22850	-1.06	-0.08	-0.35	0.738671	0.821976	-7.18
261646_at	putative lipase similar to hypothetic	---	AT1G27690	1.03	0.04	0.35	0.738698	0.821976	-7.18
249737_at	putative protein similar to unknown	---	AT5G24480	-1.03	-0.04	-0.35	0.738757	0.822003	-7.18
266762_at	putative alcohol dehydrogenase	---	AT2G47120	-1.02	-0.03	-0.35	0.738796	0.822005	-7.18
251572_at	pelota-like protein pelota PEL1 - A	---	AT3G58390	-1.03	-0.04	-0.35	0.738886	0.822066	-7.18
262663_at	hypothetical protein identical to hyp	---	AT1G13940	1.03	0.04	0.35	0.73906	0.822219	-7.18
246386_at	beta-galactosidase, putative simila	BGAL16	AT1G77410	-1.04	-0.05	-0.35	0.739127	0.822254	-7.18
265749_at	putative retroelement pol polyprotei	---	---	-1.03	-0.04	-0.35	0.739308	0.822415	-7.18
265248_at	unknown protein ; supported by cD	PIF4	AT2G43010	1.05	0.07	0.35	0.739624	0.822726	-7.18
257807_at	glyceraldehyde 3-phosphate dehyd	GAPA	AT3G26650	-1.02	-0.04	-0.35	0.739817	0.822859	-7.18
248481_at	putative protein similar to unknown	---	AT5G50930	1.03	0.04	0.35	0.739862	0.822859	-7.18

256244_at	sulphate transporter, putative simil	SULTR4;2	AT3G12520	-1.03	-0.04	-0.35	0.739875	0.822859	-7.18
251043_s_a	putative protein various predicted p	---	AT5G02330	-1.03	-0.04	-0.35	0.739905	0.822859	-7.18
267109_at	hypothetical protein predicted by ge	---	AT2G14810	-1.03	-0.04	-0.35	0.739924	0.822859	-7.18
AFFX-Athal-	Arabidopsis thaliana /REF=U37281	ACT7	---	1.03	0.04	0.35	0.740009	0.822913	-7.18
246403_at	pectinacetylesterase precursor, pu	---	AT1G57590	1.04	0.06	0.35	0.740087	0.822961	-7.18
255649_at	contains region of similarity to mous	---	AT4G00920	1.03	0.04	0.35	0.740252	0.823104	-7.18
252961_at	putative protein KIAA0169 gene, H	---	AT4G38760	-1.03	-0.05	-0.35	0.740302	0.823119	-7.18
248944_at	putative protein similar to unknown	---	AT5G45500	1.04	0.05	0.35	0.740395	0.823166	-7.18
247751_at	putative protein	---	AT5G59050	1.06	0.08	0.35	0.740416	0.823166	-7.18
263460_at	putative acetolactate synthase	---	AT2G31810	-1.04	-0.05	-0.35	0.740586	0.823315	-7.18
252774_at	putative protein predicted proteins,	---	---	-1.03	-0.05	-0.34	0.740642	0.823337	-7.18
259903_at	unknown protein	---	AT1G74160	-1.05	-0.07	-0.34	0.740789	0.823429	-7.18
260495_at	unknown protein similar to T11A07.	---	AT2G41810	-1.04	-0.06	-0.34	0.740848	0.823429	-7.18
251435_at	putative protein hypothetical protein	---	---	1.03	0.04	0.34	0.740865	0.823429	-7.18
254562_at	cytochrome P450 cytochrome P45	CYP707A1	AT4G19230	-1.07	-0.09	-0.34	0.740869	0.823429	-7.18
264596_at	unknown protein similar to polygala	---	AT1G04625	1.03	0.05	0.34	0.740948	0.823476	-7.18
260269_at	putative disease resistance protein	---	AT1G63740	-1.03	-0.05	-0.34	0.741121	0.823628	-7.18
252702_at	putative protein predicted proteins,	---	---	-1.02	-0.03	-0.34	0.741285	0.823771	-7.18
245862_at	putative protein	---	AT5G01010	-1.03	-0.04	-0.34	0.741354	0.823802	-7.18
255893_at	threonyl-tRNA synthetase, putative	---	AT1G17960	-1.05	-0.07	-0.34	0.741385	0.823802	-7.18
257576_at	hypothetical protein predicted by ge	---	AT3G28280	1.03	0.04	0.34	0.741492	0.823844	-7.18
252555_at	putative protein alpha-xylosidase, /	---	AT3G45940	-1.02	-0.03	-0.34	0.741525	0.823844	-7.18
249261_at	putative protein similar to unknown	---	---	-1.04	-0.05	-0.34	0.741532	0.823844	-7.18
258739_s_a	unknown protein similar to hypothet	---	AT1G54300	-1.02	-0.03	-0.34	0.741709	0.823996	-7.18
251604_at	putative protein 60S RIBOSOMAL	---	AT3G57820	-1.02	-0.03	-0.34	0.741748	0.823996	-7.18
259235_at	hypothetical protein predicted by ge	---	AT3G11600	1.07	0.10	0.34	0.741801	0.823996	-7.18
261941_at	hypothetical protein contains simila	---	AT1G22490	1.07	0.09	0.34	0.741847	0.823996	-7.18
259385_at	hypothetical protein predicted by ge	---	AT1G13470	-1.22	-0.28	-0.34	0.741849	0.823996	-7.18
248595_at	drought-induced protein Di19-like p	HRB1	AT5G49230	-1.03	-0.04	-0.34	0.741934	0.824002	-7.18
256925_at	hypothetical protein predicted by ge	---	---	-1.02	-0.03	-0.34	0.741958	0.824002	-7.18
249661_x_a	putative protein similar to unknown	---	---	-1.03	-0.04	-0.34	0.741963	0.824002	-7.18
263991_at	putative retroelement pol polyprotei	---	---	-1.04	-0.05	-0.34	0.742105	0.824119	-7.18
248038_at	unknown protein	---	AT5G55980	-1.03	-0.04	-0.34	0.742168	0.824149	-7.18
248764_at	putative protein contains similarity t	NF-YB2	AT5G47640	-1.04	-0.05	-0.34	0.742371	0.824334	-7.18
246404_at	hypothetical protein contains simila	---	AT1G57600	-1.02	-0.04	-0.34	0.742461	0.824394	-7.18

265559_at	putative glycine-rich protein	---	AT2G05530	1.03	0.05	0.34	0.742539	0.824404	-7.18
254685_at	SAUR-AC - like protein (small auxi	---	AT4G13790	-1.07	-0.10	-0.34	0.742566	0.824404	-7.18
259217_at	unknown protein similar to F16N3.2	---	AT3G03620	1.03	0.04	0.34	0.742597	0.824404	-7.18
254554_at	hypothetical protein	---	AT4G19550	1.03	0.04	0.34	0.742614	0.824404	-7.18
247022_at	unknown protein	---	AT5G67050	-1.02	-0.04	-0.34	0.742696	0.824455	-7.18
259778_at	hypothetical protein predicted by ge	---	AT1G29610	-1.02	-0.04	-0.34	0.74298	0.824729	-7.18
265642_at	putative nitrilase ;supported by full-	NLP1	AT2G27450	1.04	0.05	0.34	0.743129	0.824855	-7.18
256963_at	lysyl-tRNA synthetase, putative sim	OVA5	AT3G13490	-1.04	-0.06	-0.34	0.743179	0.82487	-7.18
266393_at	late embryogenesis abundant M17	M17	AT2G41260	1.02	0.03	0.34	0.743364	0.825036	-7.18
247993_at	putative protein similar to unknown	---	AT5G56130	-1.03	-0.05	-0.34	0.743693	0.825343	-7.18
265196_at	hypothetical protein predicted by ge	SWC2	AT2G36740	1.04	0.05	0.34	0.743713	0.825343	-7.18
251588_at	putative protein several putative pro	---	AT3G58090	1.03	0.05	0.34	0.74383	0.825432	-7.18
247522_at	putative protein ; supported by cDN	---	AT5G61340	-1.04	-0.05	-0.34	0.743937	0.825462	-7.18
267050_at	putative RNA-binding protein ; sup	---	AT2G41060	-1.03	-0.04	-0.34	0.743971	0.825462	-7.18
253378_at	hypothetical protein	---	AT4G33310	-1.02	-0.03	-0.34	0.743974	0.825462	-7.18
257053_at	ethylene responsive element bindin	ERF4	AT3G15210	1.10	0.13	0.34	0.744001	0.825462	-7.18
248354_at	putative protein contains similarity t	---	AT5G52330	-1.03	-0.04	-0.34	0.744145	0.825582	-7.18
256851_at	hypothetical protein predicted by ge	---	AT3G27930	1.02	0.03	0.34	0.744348	0.825766	-7.18
262851_at	putative RNA helicase Contains DE	---	AT1G20920	1.03	0.05	0.34	0.744414	0.825799	-7.18
251806_at	zinc finger protein OBP3 ; supporte	OBP3	AT3G55370	-1.02	-0.04	-0.34	0.744473	0.825824	-7.18
264617_at	unknown protein	---	AT2G17660	-1.05	-0.08	-0.34	0.744556	0.825876	-7.18
248545_at	cysteine proteinase similar to cyste	---	AT5G50260	-1.03	-0.04	-0.34	0.744633	0.825916	-7.18
251625_at	beta-1,3-glucanase 2 (BG2) (PR-2	BGL2	AT3G57260	1.40	0.49	0.34	0.744664	0.825916	-7.18
264502_at	putative 12-oxophytodienoate redu	---	AT1G09400	-1.03	-0.05	-0.34	0.744741	0.825943	-7.18
245177_at	annexin-like protein genmodel sup	---	AT5G12380	-1.03	-0.04	-0.34	0.744761	0.825943	-7.18
261577_at	ribonucleoprotein, putative similar t	---	AT1G01080	-1.04	-0.06	-0.34	0.744891	0.825984	-7.18
266646_at	unknown protein ;supported by full-	ATPH1	AT2G29700	-1.03	-0.04	-0.34	0.744896	0.825984	-7.18
255024_at	hypothetical protein	---	AT4G09860	-1.02	-0.03	-0.34	0.744906	0.825984	-7.18
266085_at	hypothetical protein	---	AT2G37800	1.03	0.05	0.34	0.745	0.82602	-7.18
265944_at	putative SET-domain transcriptiona	ASHR2	AT2G19640	1.03	0.05	0.34	0.745011	0.82602	-7.18
256550_at	En/Spm-like transposon protein, pu	---	---	-1.02	-0.03	-0.34	0.745323	0.826325	-7.18
252821_at	putative protein ;supported by full-l	---	AT4G39860	-1.07	-0.10	-0.34	0.745447	0.826422	-7.18
245282_at	hypothetical protein ; supported by	---	AT4G14990	1.04	0.05	0.34	0.745535	0.82648	-7.18
248617_at	putative protein similar to unknown	---	AT5G49590	-1.02	-0.03	-0.34	0.745623	0.826537	-7.18
258710_s_a	putative coatomer zeta subunit (zet	---	AT3G09800	-1.02	-0.03	-0.34	0.745818	0.826659	-7.18

246592_at	putative protein predicted protein, A	---	AT5G14890	1.03	0.05	0.34	0.745834	0.826659	-7.18
263481_at	predicted protein	---	AT2G04025	-1.02	-0.03	-0.34	0.745866	0.826659	-7.18
255075_at	putative protein RING-H2 zinc finge	---	AT4G09110	-1.02	-0.03	-0.34	0.745936	0.826659	-7.18
258307_x_a	hypothetical protein predicted by g	---	---	1.03	0.04	0.34	0.745964	0.826659	-7.18
259262_at	unknown protein similar to nifU-like	ISU2	AT3G01020	-1.02	-0.03	-0.34	0.74599	0.826659	-7.18
261889_at	unknown protein	---	AT1G80810	-1.03	-0.04	-0.34	0.746001	0.826659	-7.18
249814_at	putative protein similar to unknown	---	AT5G23840	-1.02	-0.03	-0.34	0.746023	0.826659	-7.18
246781_at	sugar transporter-like protein putat	SFP1	AT5G27350	-1.06	-0.09	-0.34	0.746224	0.826842	-7.18
259926_at	putative DNA-3-methyladenine glyc	---	AT1G75090	1.02	0.03	0.34	0.746334	0.826924	-7.18
259502_at	unknown protein ; supported by cDI	---	AT1G15670	-1.06	-0.08	-0.34	0.746565	0.82714	-7.18
266138_at	unknown protein ; supported by ful	---	AT2G28060	1.03	0.04	0.34	0.746653	0.827197	-7.18
261859_at	E2, ubiquitin-conjugating enzyme,	UBC20	AT1G50490	1.03	0.05	0.34	0.746705	0.827214	-7.18
265410_at	putative protein kinase contains a p	---	AT2G16620	-1.02	-0.04	-0.34	0.746776	0.827253	-7.18
249021_at	putative protein similar to unknown	---	AT5G44820	1.05	0.06	0.34	0.746844	0.827287	-7.18
249978_at	putative protein	---	AT5G18850	1.03	0.04	0.34	0.74724	0.827686	-7.18
266395_at	3-isopropylmalate dehydratase, sm	---	AT2G43100	-1.08	-0.10	-0.34	0.747418	0.827829	-7.19
247796_at	Expressed protein ;supported by cD	---	AT5G58782	1.03	0.04	0.34	0.747441	0.827829	-7.19
246710_at	putative protein predicted proteins,	---	---	1.02	0.03	0.34	0.747547	0.827906	-7.19
256212_at	hypothetical protein	---	AT1G50970	-1.03	-0.04	-0.34	0.74771	0.828046	-7.19
247358_at	flavonol synthase	FLS2	AT5G63580	1.03	0.05	0.33	0.747907	0.828224	-7.19
255648_at	coded for by A. thaliana cDNA T20	---	AT4G00910	-1.02	-0.03	-0.33	0.748191	0.828498	-7.19
265268_at	putative protein kinase contains a p	---	AT2G42960	-1.03	-0.04	-0.33	0.748619	0.828933	-7.19
265320_at	unknown protein predicted by gens	---	AT2G18320	1.03	0.04	0.33	0.748711	0.828985	-7.19
253450_at	putative protein MUS308 gene, Dr	---	AT4G32700	1.02	0.03	0.33	0.748756	0.828985	-7.19
255196_x_a	see GB:AF058826	---	---	-1.02	-0.04	-0.33	0.748801	0.828985	-7.19
259731_at	unknown protein similar to unknow	---	AT1G77460	1.06	0.09	0.33	0.748812	0.828985	-7.19
257278_at	hypothetical protein predicted by ge	---	AT3G14480	-1.04	-0.05	-0.33	0.748899	0.82904	-7.19
262551_at	putative heat shock transcription fa	RUB1	AT1G31340	1.04	0.05	0.33	0.749367	0.829519	-7.19
261079_s_a	transcription factor IIA large subunit	---	AT1G07470	1.03	0.04	0.33	0.7496	0.829736	-7.19
267067_at	unknown protein	---	AT2G41020	1.04	0.05	0.33	0.749685	0.829782	-7.19
249260_at	Pto kinase interactor 1-like protein	---	AT5G41680	-1.03	-0.04	-0.33	0.749714	0.829782	-7.19
252564_at	actin depolymerizing factor 1 (ADF1	ADF1	AT3G46010	1.03	0.04	0.33	0.75011	0.830171	-7.19
263596_at	putative inositol polyphosphate-5-pl	---	AT2G01900	-1.02	-0.03	-0.33	0.750147	0.830171	-7.19
259333_at	putative auxin-independent growth	EDA30	AT3G03810	-1.03	-0.04	-0.33	0.750175	0.830171	-7.19
249348_at	unknown protein	---	AT5G40860	-1.03	-0.05	-0.33	0.750217	0.830178	-7.19

248227_at	ABA-inducible protein-like ;support	---	AT5G53820	-1.03	-0.04	-0.33	0.750278	0.830205	-7.19
253179_at	putative protein various predicted p	---	AT4G35200	1.02	0.03	0.33	0.750366	0.830254	-7.19
249053_at	berberine bridge enzyme-like protei	---	AT5G44440	-1.03	-0.04	-0.33	0.750395	0.830254	-7.19
254397_at	gibberellin 3 beta-hydroxylase - like	GA3OX3	AT4G21690	-1.05	-0.07	-0.33	0.750628	0.830471	-7.19
245073_at	putative glucosyltransferase	---	AT2G23210	-1.03	-0.04	-0.33	0.750708	0.830519	-7.19
252846_at	putative protein several pectin meth	---	AT3G42160	-1.02	-0.03	-0.33	0.750747	0.830522	-7.19
263762_at	putative kinesin heavy chain ; supp	---	AT2G21380	-1.04	-0.06	-0.33	0.750832	0.830576	-7.19
252812_at	putative protein hypothetical protein	---	---	1.02	0.03	0.33	0.750975	0.830683	-7.19
254772_at	extensin-like protein extensin class	---	AT4G13390	1.02	0.03	0.33	0.751002	0.830683	-7.19
263784_at	Expressed protein ; supported by fu	---	AT2G46375	1.03	0.04	0.33	0.751226	0.830871	-7.19
263040_at	conserved hypothetical protein pred	---	AT1G23300	-1.03	-0.04	-0.33	0.751244	0.830871	-7.19
249203_at	cytochrome P450	CYP71A16	AT5G42590	1.03	0.04	0.33	0.751302	0.830894	-7.19
248086_at	putative protein similar to unknown	GEX1	AT5G55490	1.02	0.03	0.33	0.751341	0.830898	-7.19
261622_at	hypothetical protein predicted by ge	---	AT1G01970	-1.03	-0.04	-0.33	0.751399	0.830921	-7.19
253064_at	bZIP transcription factor - like prote	AtbZIP7	AT4G37730	-1.03	-0.04	-0.33	0.751514	0.831008	-7.19
255700_at	putative transcription factor similar t	---	AT4G00200	-1.05	-0.07	-0.33	0.751717	0.831192	-7.19
255002_at	AIG1-like protein AIG1 - Arabidops	---	AT4G09940	-1.03	-0.04	-0.33	0.751851	0.8313	-7.19
260265_at	hypothetical protein similar to hypot	LBD42	AT1G68510	-1.03	-0.04	-0.33	0.752027	0.831455	-7.19
254729_at	putative protein purple acid phosph	PAP23	AT4G13700	-1.03	-0.04	-0.33	0.752206	0.831612	-7.19
254807_at	putative protein	---	AT4G12700	1.04	0.05	0.33	0.752322	0.8317	-7.19
258499_at	putative RAD23 similar to RAD23 p	RAD23-3	AT3G02540	1.03	0.04	0.33	0.752362	0.831704	-7.19
263343_at	putative replication protein A1	---	---	1.02	0.03	0.33	0.752441	0.831738	-7.19
252072_at	putative protein protein kinase PK1	---	AT3G51710	1.03	0.04	0.33	0.752466	0.831738	-7.19
252397_at	hypothetical protein	---	AT3G47980	-1.04	-0.06	-0.33	0.752785	0.832051	-7.19
251747_at	putative protein various predicted p	---	AT3G55670	-1.02	-0.03	-0.33	0.752856	0.832058	-7.19
245696_at	phytochrome kinase substrate 1 - li	PKS4	AT5G04190	1.08	0.11	0.33	0.752865	0.832058	-7.19
263527_at	putative thaumatin-like pathogenes	---	AT2G24810	-1.04	-0.06	-0.33	0.752998	0.832165	-7.19
249809_at	unknown protein	---	AT5G23910	-1.02	-0.03	-0.33	0.753145	0.832287	-7.19
260517_at	unknown protein	SPP1	AT1G51420	-1.02	-0.03	-0.33	0.753276	0.832391	-7.19
247561_at	putative protein	---	AT5G61110	-1.02	-0.03	-0.33	0.753338	0.832391	-7.19
248707_at	putative protein similar to unknown	---	AT5G48550	1.03	0.04	0.33	0.753348	0.832391	-7.19
251081_at	putative protein kinase wall-associa	---	AT5G02070	-1.04	-0.05	-0.33	0.753417	0.832427	-7.19
250759_at	unknown protein	---	AT5G06020	-1.02	-0.03	-0.33	0.753566	0.832514	-7.19
247451_at	MYB99 ; supported by cDNA: gi_1	ATMYB99	AT5G62320	-1.03	-0.04	-0.33	0.753569	0.832514	-7.19
261993_at	unknown protein	---	AT1G33860	-1.03	-0.04	-0.33	0.753639	0.83255	-7.19

263041_at	putative alliinase similar to alliinase	TAR1	AT1G23320	-1.03	-0.04	-0.33	0.753824	0.832708	-7.19
254735_at	putative disease resistance protein	AtRLP47	AT4G13810	1.03	0.04	0.33	0.753866	0.832708	-7.19
257907_at	hemolysin, putative similar to hemo	---	AT3G25470	1.02	0.03	0.33	0.753891	0.832708	-7.19
264969_at	hypothetical protein contains simila	---	AT1G67320	1.06	0.09	0.33	0.754045	0.832838	-7.19
244960_at	ribosomal protein L32	---	---	-1.06	-0.09	-0.33	0.754245	0.833019	-7.19
253484_at	Transcription factor II homolog ;sup	TAFII15	AT4G31720	-1.02	-0.03	-0.33	0.754364	0.83311	-7.19
266586_s_a	putative protein	---	---	-1.02	-0.03	-0.33	0.754634	0.833367	-7.19
250333_at	membrane translocase - like protei	TIM17-3	AT5G11690	1.05	0.07	0.33	0.754831	0.833544	-7.19
245507_at	hypothetical protein	---	AT4G15710	-1.04	-0.05	-0.33	0.754959	0.833645	-7.19
257034_at	hypothetical protein predicted by ge	---	AT3G19184	-1.02	-0.03	-0.32	0.755122	0.833786	-7.19
249496_s_a	putative protein predicted proteins -	---	AT5G39140	-1.03	-0.04	-0.32	0.755167	0.833794	-7.19
254677_at	chloroplast protein cs/ch-42	---	AT4G18490	-1.03	-0.04	-0.32	0.755233	0.833827	-7.19
257595_at	hypothetical protein predicted by ge	---	AT3G24750	-1.02	-0.04	-0.32	0.75544	0.834015	-7.19
246869_at	putative protein various predicted p	---	---	-1.02	-0.03	-0.32	0.755617	0.83417	-7.19
251574_at	putative protein GLUCAN ENDO-1	PDCB5	AT3G58100	-1.03	-0.04	-0.32	0.755745	0.834271	-7.19
254651_at	potassium channel - like protein kc	KCO6	AT4G18160	-1.03	-0.05	-0.32	0.755814	0.834306	-7.19
252767_at	ring-box protein-like ring-box protei	---	AT3G42830	1.03	0.04	0.32	0.756161	0.83465	-7.19
266190_at	unknown protein	---	AT2G38840	-1.02	-0.04	-0.32	0.756296	0.834735	-7.19
247116_at	Mlo protein-like ; supported by cDN	MLO10	AT5G65970	-1.03	-0.04	-0.32	0.756387	0.834735	-7.19
264244_at	pantothenate kinase, putative simil	ATPANK1	AT1G60440	1.03	0.04	0.32	0.756401	0.834735	-7.19
249618_at	putative protein predicted proteins,	---	AT5G37490	1.18	0.24	0.32	0.756413	0.834735	-7.19
264554_at	putative cinnamyl alcohol dehydrog	---	AT1G09510	1.03	0.05	0.32	0.756449	0.834735	-7.19
248291_at	putative protein similar to unknown	---	AT5G53020	-1.03	-0.04	-0.32	0.756458	0.834735	-7.19
250076_at	putative protein; similar to unknown	---	AT5G16660	1.03	0.04	0.32	0.756532	0.834746	-7.19
266784_at	putative receptor-like protein kinase	---	AT2G28960	-1.02	-0.03	-0.32	0.756541	0.834746	-7.19
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.06	-0.08	-0.32	0.756719	0.834902	-7.19
260699_at	MAP kinase, putative similar to MA	ATMKK10	AT1G32320	1.02	0.03	0.32	0.756896	0.835057	-7.19
255395_at	hypothetical protein	---	---	1.02	0.03	0.32	0.757007	0.835139	-7.19
258944_at	hypothetical protein similar to hypot	FLD	AT3G10390	1.03	0.05	0.32	0.757074	0.835172	-7.19
252494_at	receptor-like protein kinase recepto	---	AT3G46760	-1.03	-0.04	-0.32	0.757129	0.835193	-7.19
245748_at	unknown protein contains similarity	---	AT1G51140	1.05	0.07	0.32	0.757168	0.835195	-7.19
259855_at	putative asparaginyl-tRNA syntheta	---	AT1G68420	1.03	0.04	0.32	0.757283	0.835282	-7.19
248413_at	putative protein strong similarity to	PLE	AT5G51600	-1.03	-0.04	-0.32	0.757356	0.835313	-7.19
255137_at	extensin-like protein extensin precu	---	AT4G08370	-1.03	-0.04	-0.32	0.757385	0.835313	-7.19
246679_at	putative protein replication protein	---	---	1.02	0.03	0.32	0.757744	0.835669	-7.19

254632_at	putative protein predicted protein, A	---	AT4G18630	1.03	0.04	0.32	0.75817	0.836091	-7.19
257862_s_a	unknown protein similar to N-termin	---	AT3G17720	-1.02	-0.03	-0.32	0.7582	0.836091	-7.19
261157_at	peroxidase ATP13a, putative simila	---	AT1G34510	-1.02	-0.03	-0.32	0.758314	0.836165	-7.19
260742_at	putative glycerol kinase identical to	IAA34	AT1G15050	1.02	0.03	0.32	0.758345	0.836165	-7.19
266677_at	hypothetical protein predicted by ge	---	AT2G29820	-1.03	-0.04	-0.32	0.758377	0.836165	-7.19
261489_at	hypothetical protein contains simila	---	AT1G14450	1.02	0.03	0.32	0.758452	0.836168	-7.19
264829_at	hypothetical protein predicted by ge	ANAC006	AT1G03490	-1.02	-0.03	-0.32	0.758453	0.836168	-7.19
255757_at	putative protein	ROPGEF3	AT4G00460	-1.02	-0.03	-0.32	0.758532	0.836212	-7.19
253292_at	Expressed protein ; supported by fu	---	AT4G33985	-1.04	-0.06	-0.32	0.758567	0.836212	-7.19
250797_at	unknown protein	---	AT5G05310	1.03	0.04	0.32	0.758756	0.83638	-7.19
259145_at	hypothetical protein predicted by ge	---	AT3G10180	1.02	0.03	0.32	0.759034	0.836647	-7.19
257993_at	hypothetical protein similar to hypot	---	AT3G19890	1.02	0.03	0.32	0.759095	0.836673	-7.19
263531_s_a	hypothetical protein predicted by ge	---	AT2G25020	1.02	0.03	0.32	0.759303	0.836754	-7.19
263814_at	putative TNP2-like transposon prote	---	---	-1.03	-0.04	-0.32	0.759319	0.836754	-7.19
265679_at	putative myosin heavy chain ; supp	---	AT2G32235	-1.03	-0.04	-0.32	0.759319	0.836754	-7.19
247590_at	putative protein predicted proteins,	---	AT5G60720	-1.03	-0.04	-0.32	0.759329	0.836754	-7.19
250425_at	lectin-like protein kinase - like lectin	---	AT5G10530	-1.02	-0.03	-0.32	0.759351	0.836754	-7.19
266912_at	hypothetical protein predicted by ge	---	AT2G45900	-1.10	-0.13	-0.32	0.759683	0.837041	-7.19
256009_at	AP2 domain transcription factor, pu	---	AT1G19210	-1.10	-0.13	-0.32	0.759687	0.837041	-7.19
265060_at	HD-Zip protein, putative similar to H	ATHB-15	AT1G52150	1.06	0.08	0.32	0.759722	0.837041	-7.19
261182_at	hypothetical protein predicted by ge	---	AT1G34575	1.02	0.03	0.32	0.759796	0.837082	-7.19
261312_at	putative NPK1-related protein kinas	---	AT1G05790	1.03	0.04	0.32	0.759867	0.83712	-7.19
266385_at	pathogenesis-related PR-1-like prot	PR1	AT2G14610	1.41	0.50	0.32	0.759999	0.837211	-7.19
256966_at	pollen specific protein, putative sim	sks13	AT3G13400	1.02	0.03	0.32	0.760089	0.837211	-7.19
260994_at	hypothetical protein contains simila	---	AT1G12130	-1.03	-0.04	-0.32	0.760103	0.837211	-7.19
251635_at	endo-polygalacturonase	ADPG1	AT3G57510	-1.03	-0.05	-0.32	0.760104	0.837211	-7.19
246659_at	putative protein predicted proteins A	---	---	-1.03	-0.04	-0.32	0.760161	0.837211	-7.19
265862_at	putative S-locus glycoprotein	---	AT2G01780	-1.03	-0.04	-0.32	0.760225	0.837211	-7.19
264827_at	hypothetical protein similar to anthra	---	AT1G03390	-1.02	-0.03	-0.32	0.760257	0.837211	-7.19
247119_at	ATP-dependent RNA helicase-like	---	AT5G65900	1.02	0.03	0.32	0.760266	0.837211	-7.19
257583_at	hypothetical protein	PMI2	AT1G66480	1.11	0.15	0.32	0.760287	0.837211	-7.19
266015_at	putative carbonyl reductase	---	AT2G24190	-1.03	-0.04	-0.32	0.760327	0.837211	-7.19
265031_at	serine/threonine protein kinase, pu	---	AT1G61590	1.02	0.03	0.32	0.760354	0.837211	-7.19
253311_s_a	putative protein xylan endohydrola	---	AT4G33830	-1.02	-0.03	-0.32	0.760452	0.837279	-7.19
254276_at	predicted protein PVPR3 protein, P	---	AT4G22820	1.05	0.08	0.32	0.76055	0.837346	-7.19

247924_at	Expressed protein	---	AT5G57655	1.06	0.08	0.32	0.760758	0.837504	-7.19
249084_at	unknown protein	---	AT5G44150	-1.03	-0.04	-0.32	0.760766	0.837504	-7.19
267137_at	hypothetical protein predicted by ge	ACPT	AT2G23410	-1.02	-0.03	-0.32	0.760882	0.837554	-7.19
253518_at	hypothetical protein	---	AT4G31400	1.03	0.04	0.32	0.760886	0.837554	-7.19
249300_at	putative protein similar to unknown	---	AT5G41380	-1.03	-0.04	-0.32	0.761291	0.83796	-7.19
249562_at	disease resistance protein-like	---	AT5G38350	1.03	0.04	0.32	0.76158	0.838204	-7.19
258288_at	unknown protein	LSH4	---	-1.05	-0.08	-0.32	0.761622	0.838204	-7.19
262841_at	aspartate-semialdehyde dehydroge	---	AT1G14810	1.04	0.06	0.32	0.761623	0.838204	-7.19
249877_at	transcription factor-like protein (gb|	HUA2	AT5G23150	1.02	0.03	0.32	0.761837	0.838379	-7.19
249660_at	putative protein similar to unknown	---	AT5G36720	-1.03	-0.05	-0.32	0.761855	0.838379	-7.19
267395_at	unknown protein	---	AT2G44250	-1.02	-0.03	-0.32	0.762049	0.838511	-7.19
263057_at	hypothetical protein predicted by ge	---	AT2G09840	-1.03	-0.05	-0.32	0.762083	0.838511	-7.19
250319_at	putative protein strong similarity to	---	AT5G12120	-1.02	-0.03	-0.32	0.762091	0.838511	-7.19
261856_at	hypothetical protein	---	AT1G50530	-1.03	-0.04	-0.32	0.762122	0.838511	-7.19
258246_s_a	hypothetical protein similar to putati	---	---	-1.02	-0.03	-0.32	0.762194	0.83855	-7.19
247395_at	putative protein predicted proteins,	---	AT5G62910	1.03	0.04	0.31	0.762539	0.838813	-7.19
256463_s_a	unknown protein	---	---	1.02	0.04	0.31	0.762564	0.838813	-7.19
261275_at	Mlo protein, putative similar to GB:	MLO14	AT1G26700	1.02	0.03	0.31	0.762578	0.838813	-7.19
267238_at	unknown protein ;supported by full-	---	AT2G44130	-1.11	-0.15	-0.31	0.762581	0.838813	-7.19
256594_at	hypothetical protein similar to putati	---	AT3G28520	1.02	0.03	0.31	0.762802	0.839016	-7.19
265622_at	unknown protein	---	AT2G27280	-1.02	-0.03	-0.31	0.762915	0.8391	-7.19
265243_at	hypothetical protein predicted by ge	NPG1	AT2G43040	1.03	0.04	0.31	0.763003	0.839156	-7.19
260767_s_a	unknown protein ; supported by full-	---	AT1G49140	1.02	0.03	0.31	0.76313	0.839256	-7.19
263453_at	hypothetical protein predicted by ge	---	AT2G22180	-1.02	-0.03	-0.31	0.763261	0.839359	-7.19
246053_at	putative protein farnesyl cysteine c	---	AT5G08340	-1.03	-0.05	-0.31	0.763425	0.839499	-7.19
254731_at	hypothetical protein	---	AT4G13750	1.03	0.04	0.31	0.763515	0.839558	-7.19
255014_at	MADS-box protein AGL11 ; suppor	STK	AT4G09960	1.02	0.03	0.31	0.763627	0.839629	-7.19
267353_at	En/Spm-like transposon protein rela	---	AT2G40070	-1.03	-0.05	-0.31	0.763654	0.839629	-7.19
266013_s_a	hypothetical protein	---	AT2G07702	1.02	0.03	0.31	0.763736	0.839679	-7.19
252109_at	putative protein mucin 5AC, Homo	---	AT3G51540	1.06	0.08	0.31	0.763853	0.839741	-7.19
257866_at	dihydroxyacetone kinase, putative	---	AT3G17770	1.06	0.09	0.31	0.763866	0.839741	-7.19
246395_at	dirigent protein, putative similar to	---	AT1G58170	-1.02	-0.03	-0.31	0.764024	0.839874	-7.19
246844_at	transcription factor ATMYB4 ; supp	ATMYB86	AT5G26660	1.03	0.04	0.31	0.764078	0.839893	-7.19
255563_at	putative CHP-rich zinc finger protei	---	AT4G01740	-1.02	-0.03	-0.31	0.76425	0.840042	-7.19
252783_at	putative protein predicted proteins,	---	---	-1.02	-0.03	-0.31	0.764518	0.840283	-7.19

246362_at	hypothetical protein	---	---	1.02	0.03	0.31	0.764544	0.840283	-7.19
264720_at	hypothetical protein similar to vetisp	---	AT1G70080	-1.03	-0.04	-0.31	0.76465	0.840324	-7.19
255066_at	F-box protein family, AtFBW2 cont	---	AT4G08980	1.02	0.03	0.31	0.764654	0.840324	-7.19
255236_at	score=11.7, E=0.66,N=1	ATEHD2	AT4G05520	-1.04	-0.06	-0.31	0.764759	0.840398	-7.19
247413_at	NBS/LRR disease resistance protei	---	AT5G63020	1.03	0.04	0.31	0.764897	0.84051	-7.19
249445_at	putative protein predicted protein, A	---	AT5G39380	1.03	0.04	0.31	0.765036	0.840609	-7.19
254964_at	98b like protein 98b - Daucus carot	---	AT4G11080	-1.03	-0.04	-0.31	0.765061	0.840609	-7.19
260531_at	putative acyl-CoA synthetase ; sup	CER8	AT2G47240	1.03	0.05	0.31	0.765253	0.84078	-7.19
267374_at	putative uricase subunit similar to r	---	AT2G26230	1.02	0.03	0.31	0.765508	0.840946	-7.19
264180_at	hypothetical protein contains simila	---	AT1G02190	-1.02	-0.03	-0.31	0.76551	0.840946	-7.19
248313_at	putative protein contains similarity t	---	AT5G52580	1.02	0.03	0.31	0.765516	0.840946	-7.19
252017_at	cytochrome P450 - like protein cyto	CYP76G1	AT3G52970	-1.03	-0.04	-0.31	0.765583	0.84098	-7.19
246391_at	unknown protein ; supported by cDI	---	AT1G77350	-1.03	-0.04	-0.31	0.765804	0.841159	-7.19
249350_at	MYB -like protein MYB22, Arabidop	MYB115	AT5G40360	1.02	0.03	0.31	0.76582	0.841159	-7.19
252721_at	putative protein predicted proteins,	---	AT3G43990	-1.03	-0.05	-0.31	0.765886	0.841191	-7.19
264225_at	hypothetical protein predicted by ge	---	AT1G67420	1.04	0.06	0.31	0.766057	0.841338	-7.19
255222_at	putative protein Mitochondrial ATP	---	AT4G05340	-1.02	-0.03	-0.31	0.766168	0.84142	-7.19
265380_at	putative retroelement pol polyprotei	---	---	-1.03	-0.04	-0.31	0.766257	0.841477	-7.19
263030_at	hypothetical protein predicted by ge	---	AT1G24060	1.02	0.03	0.31	0.766392	0.841563	-7.19
251106_at	putative protein peroxisomal Ca-de	---	AT5G01500	-1.09	-0.12	-0.31	0.766467	0.841563	-7.19
257728_at	hypothetical protein predicted by ge	---	AT3G18295	1.03	0.04	0.31	0.766482	0.841563	-7.19
266178_at	putative phloem-specific lectin	AtPP2-B4	AT2G02280	-1.03	-0.04	-0.31	0.766482	0.841563	-7.19
261468_s_a	hypothetical protein predicted by ge	---	AT1G27860	1.03	0.05	0.31	0.766524	0.841568	-7.19
251984_at	phenylalanine ammonia-lyase ;sup	PAL2	AT3G53260	1.10	0.14	0.31	0.766645	0.841661	-7.19
262015_at	hypothetical protein predicted by ge	---	---	-1.02	-0.03	-0.31	0.76693	0.841933	-7.19
267321_at	hypothetical protein predicted by ge	---	AT2G19320	1.03	0.04	0.31	0.767002	0.841971	-7.19
246643_s_a	putative protein various predicted p	---	---	-1.02	-0.03	-0.31	0.767235	0.842186	-7.19
250910_at	heat shock transcription factor -like	HSFA3	AT5G03720	1.08	0.11	0.31	0.767455	0.842388	-7.20
263972_at	unknown protein	---	AT2G42760	1.09	0.12	0.31	0.767584	0.842488	-7.20
248166_at	putative protein contains similarity t	---	AT5G54520	-1.02	-0.03	-0.31	0.767731	0.842609	-7.20
247581_at	receptor-like protein kinase precurs	---	AT5G61350	-1.02	-0.03	-0.31	0.767797	0.842635	-7.20
266165_at	putative copper/zinc superoxide dis	CSD2	AT2G28190	1.14	0.18	0.31	0.767829	0.842635	-7.20
246172_s_a	fragment of 1-aminocyclopropane-	ACS1	AT3G61510	-1.03	-0.05	-0.31	0.767906	0.842657	-7.20
263280_x_a	hypothetical protein predicted by ge	---	---	1.02	0.04	0.31	0.767922	0.842657	-7.20
259633_at	hypothetical protein	---	AT1G56500	-1.03	-0.05	-0.31	0.767999	0.8427	-7.20

262138_at	NBS/LRR disease resistance prote	---	AT1G52660	1.03	0.04	0.31	0.768055	0.842722	-7.20
263032_at	unknown protein ;supported by full-	---	AT1G23850	-1.06	-0.09	-0.31	0.768218	0.84286	-7.20
265812_at	hypothetical protein predicted by ge	---	AT2G18070	-1.03	-0.04	-0.31	0.768634	0.843276	-7.20
252531_at	actin 12	ACT12	AT3G46520	1.02	0.03	0.31	0.768771	0.843385	-7.20
248226_at	putative protein strong similarity to	---	AT5G53750	-1.08	-0.11	-0.31	0.768868	0.843446	-7.20
266902_at	hypothetical protein predicted by ge	---	AT2G34580	1.02	0.03	0.31	0.7689	0.843446	-7.20
256498_at	hypothetical protein	---	---	1.02	0.03	0.31	0.769048	0.843567	-7.20
264632_at	DegP protease contains similarity to	DegP4	AT1G65640	-1.02	-0.03	-0.31	0.769215	0.84371	-7.20
259636_at	RNA pseudouridylate synthase, pu	---	AT1G56345	-1.05	-0.07	-0.31	0.76936	0.843813	-7.20
258688_at	putative eukaryotic translation initia	---	AT3G07920	1.02	0.03	0.31	0.769383	0.843813	-7.20
252842_at	putative protein hypothetical protein	---	---	1.03	0.04	0.30	0.769894	0.844333	-7.20
258293_at	unknown protein	PHO1	AT3G23430	-1.10	-0.13	-0.30	0.770073	0.844489	-7.20
250344_at	glutaredoxin - like protein glutaredo	---	AT5G11930	1.05	0.07	0.30	0.770177	0.844562	-7.20
258967_at	hypothetical protein predicted by g	---	AT3G10470	-1.03	-0.04	-0.30	0.770257	0.844609	-7.20
255559_at	putative NAK-like ser/thr protein kir	---	AT4G02010	-1.03	-0.04	-0.30	0.770343	0.844663	-7.20
263925_at	putative glycine-rich RNA binding p	---	AT2G21690	-1.02	-0.03	-0.30	0.770417	0.844704	-7.20
267348_at	unknown protein	---	AT2G39960	-1.02	-0.03	-0.30	0.770509	0.844764	-7.20
254506_at	leucine rich repeat-like protein Cf-2	GSO1	AT4G20140	1.03	0.05	0.30	0.770572	0.844792	-7.20
252847_at	putative transposase hypothetical p	---	AT3G42170	-1.03	-0.04	-0.30	0.770775	0.844974	-7.20
266243_at	hypothetical protein predicted by ge	---	AT2G27750	-1.02	-0.03	-0.30	0.770922	0.845087	-7.20
253244_at	putative protein SEC14 protein, Sa	COW1	AT4G34580	-1.03	-0.05	-0.30	0.770952	0.845087	-7.20
264488_s_a	unknown protein similar to EST gb|	---	AT1G27330	1.04	0.06	0.30	0.771058	0.845162	-7.20
261990_at	unknown protein	---	AT1G33660	-1.02	-0.03	-0.30	0.771266	0.845314	-7.20
255109_s_a	hypothetical protein	---	AT4G08760	-1.02	-0.03	-0.30	0.77127	0.845314	-7.20
267403_at	MADS-box protein (AGL33)	AGL33	AT2G26320	-1.02	-0.03	-0.30	0.771544	0.845526	-7.20
250677_at	putative protein similar to unknown	---	AT5G06520	1.03	0.04	0.30	0.771595	0.845526	-7.20
256716_at	hypothetical protein predicted by g	---	AT2G34100	-1.03	-0.04	-0.30	0.771616	0.845526	-7.20
254855_s_a	putative protein other predicted pro	---	AT4G12140	1.03	0.04	0.30	0.771629	0.845526	-7.20
252928_at	putative protein more than 30 pred	---	AT4G38940	1.05	0.07	0.30	0.771649	0.845526	-7.20
251045_s_a	putative protein various predicted p	---	AT2G13910	-1.02	-0.03	-0.30	0.771771	0.845619	-7.20
253323_at	putative protein protein phosphatas	---	AT4G33920	-1.07	-0.09	-0.30	0.772258	0.846111	-7.20
249545_at	putative transmembrane protein pu	---	AT5G38030	1.02	0.03	0.30	0.772303	0.84612	-7.20
266800_at	hypothetical protein predicted by ge	---	AT2G22880	1.18	0.24	0.30	0.77253	0.846329	-7.20
257669_at	DNA mismatch repair protein, puta	MSH5	AT3G20475	-1.02	-0.03	-0.30	0.772619	0.846385	-7.20
258089_at	hypothetical protein predicted by ge	---	AT3G14740	-1.05	-0.07	-0.30	0.772707	0.846441	-7.20

253962_at	hypothetical protein	---	AT4G26460	-1.03	-0.04	-0.30	0.772923	0.846637	-7.20
256627_at	unknown protein ; supported by cD	---	AT3G19970	-1.10	-0.14	-0.30	0.773221	0.846922	-7.20
254446_at	tubulin beta-9 chain ;supported by	TUB9	AT4G20890	1.02	0.03	0.30	0.773293	0.846961	-7.20
252700_at	hypothetical protein envelope-like,	---	---	1.03	0.04	0.30	0.773559	0.847212	-7.20
253389_at	hypothetical protein ;supported by	---	AT4G32680	-1.02	-0.03	-0.30	0.774039	0.847681	-7.20
259692_at	unknown protein	---	AT1G63080	-1.02	-0.03	-0.30	0.774062	0.847681	-7.20
256560_s_a	vetispiradiene synthase, putative, 5	---	AT3G31415	1.02	0.03	0.30	0.774099	0.847681	-7.20
256798_at	uracil-DNA glycosylase, putative si	---	AT3G18630	-1.03	-0.05	-0.30	0.774166	0.8477	-7.20
249762_at	putative protein contains similarity t	---	AT5G24000	1.02	0.03	0.30	0.774206	0.8477	-7.20
260084_at	chromatin structure regulator, puta	---	AT1G63210	-1.03	-0.04	-0.30	0.774256	0.8477	-7.20
251370_at	putative protein prib5, Ribes nigrun	---	AT3G60450	-1.07	-0.10	-0.30	0.774332	0.8477	-7.20
256582_at	unknown protein	---	AT3G28840	1.02	0.03	0.30	0.774338	0.8477	-7.20
257006_at	hypothetical protein predicted by ge	---	AT3G14075	-1.02	-0.03	-0.30	0.774339	0.8477	-7.20
266793_at	homeotic protein AGL30	AGL30	AT2G03060	1.04	0.06	0.30	0.774524	0.847862	-7.20
257259_at	hypothetical protein predicted by ge	---	AT3G22090	-1.02	-0.03	-0.30	0.774602	0.847906	-7.20
258589_at	putative GDSL-motif lipase/acylhyd	LTL1	AT3G04290	1.03	0.04	0.30	0.774656	0.847925	-7.20
258599_at	L-allo-threonine aldolase, putative	THA2	AT3G04520	1.04	0.06	0.30	0.774768	0.848007	-7.20
254591_at	heat shock transcription factor - like	---	AT4G18870	1.02	0.03	0.30	0.774811	0.848013	-7.20
253990_at	putative thioredoxin thioredoxin - L	ACHT1	AT4G26160	1.04	0.06	0.30	0.774999	0.848178	-7.20
267643_at	hypothetical protein predicted by ge	RALFL17	AT2G32890	-1.02	-0.03	-0.30	0.775103	0.848251	-7.20
256654_at	ribosomal protein, putative similar t	---	AT3G18880	1.04	0.05	0.30	0.775165	0.848279	-7.20
252733_at	putative protein INDOLE-3-ACETIC	---	AT3G43120	-1.02	-0.03	-0.30	0.775319	0.848401	-7.20
249556_at	Expressed protein ; supported by fu	---	AT5G38195	-1.02	-0.03	-0.30	0.775356	0.848401	-7.20
256733_at	hypothetical protein predicted by ge	---	AT3G30370	-1.02	-0.03	-0.30	0.775389	0.848401	-7.20
250737_at	putative protein similar to unknown	---	AT5G06370	1.03	0.05	0.30	0.775627	0.848621	-7.20
257995_at	putative monosaccharide transport	---	AT3G19940	-1.03	-0.04	-0.30	0.775728	0.84869	-7.20
252803_at	putative protein various predicted p	---	---	-1.03	-0.04	-0.30	0.775864	0.848799	-7.20
249681_s_a	putative protein strong similarity to u	---	---	1.03	0.04	0.30	0.776016	0.848925	-7.20
258048_at	FtsH protease, putative contains si	EMB2083	AT3G16290	1.02	0.04	0.30	0.776206	0.849091	-7.20
254576_at	putative protein ;supported by full-l	EMB3006	AT4G19350	-1.02	-0.03	-0.30	0.77629	0.849142	-7.20
267574_at	hypothetical protein predicted by ge	---	AT2G30680	-1.03	-0.05	-0.30	0.776379	0.8492	-7.20
259777_at	zinc finger protein, putative similar	---	AT1G29570	1.02	0.03	0.30	0.776437	0.849222	-7.20
252917_at	putative zinc finger protein zinc fing	---	AT4G38960	1.03	0.05	0.30	0.776516	0.849262	-7.20
249937_at	putative protein seed maturation pr	---	AT5G22470	1.03	0.05	0.30	0.776548	0.849262	-7.20
263822_at	hypothetical protein predicted by ge	---	AT2G40240	1.03	0.04	0.30	0.776722	0.849412	-7.20

246265_at	phosphoribosyl-ATP pyrophosphol	AT-IE	AT1G31860	-1.05	-0.07	-0.30	0.77677	0.849423	-7.20
261066_at	hypothetical protein predicted by ge	---	AT1G07485	-1.02	-0.03	-0.30	0.776845	0.849465	-7.20
252045_at	putative protein arm repeat contain	PUB22	AT3G52450	1.15	0.20	0.29	0.77692	0.849496	-7.20
265361_at	putative retroelement pol polyprotei	---	---	1.02	0.03	0.29	0.776985	0.849496	-7.20
256844_s_a	En/Spm transposon protein, putativ	---	---	-1.02	-0.03	-0.29	0.776985	0.849496	-7.20
264347_at	putative extensin strong similarity to	LRX1	AT1G12040	-1.02	-0.03	-0.29	0.777161	0.849648	-7.20
250369_at	cyclin 3b ; supported by cDNA: gi_	CYC3B	AT5G11300	-1.03	-0.04	-0.29	0.777227	0.849679	-7.20
253182_at	putative protein ctf, Mycobacterium	---	AT4G35190	1.04	0.06	0.29	0.777553	0.849994	-7.20
248881_at	unknown protein ;supported by full-	---	AT5G46020	1.02	0.03	0.29	0.777593	0.849998	-7.20
264982_at	hypothetical protein predicted by ge	---	AT1G27220	-1.03	-0.04	-0.29	0.777698	0.850049	-7.20
247570_at	putative protein heparanase, Homo	AtGUS1	AT5G61250	1.06	0.09	0.29	0.77775	0.850049	-7.20
253401_at	putative protein hypothetical protei	---	AT4G32870	1.15	0.20	0.29	0.777752	0.850049	-7.20
245802_at	hypothetical protein similar to hypot	---	AT1G46840	-1.02	-0.03	-0.29	0.777855	0.850121	-7.20
254516_at	putative protein	---	AT4G20290	-1.03	-0.04	-0.29	0.777916	0.850146	-7.20
245461_at	hypothetical protein	---	AT4G17000	1.02	0.04	0.29	0.777991	0.850188	-7.20
266191_at	putative peroxidase	---	AT2G39040	-1.02	-0.03	-0.29	0.778115	0.850282	-7.20
252443_at	putative helicase helicase SKI2W -	---	AT3G46960	1.03	0.04	0.29	0.778273	0.850294	-7.20
257462_at	hypothetical protein	---	AT1G65740	-1.02	-0.03	-0.29	0.778279	0.850294	-7.20
258465_at	unknown protein	PMEI2	AT3G17220	1.03	0.04	0.29	0.778289	0.850294	-7.20
259632_at	nicotianamine synathase, putative	NAS4	AT1G56430	1.06	0.09	0.29	0.77831	0.850294	-7.20
258767_at	putative (1-4)-beta-mannan endohy	---	AT3G10890	-1.02	-0.03	-0.29	0.778312	0.850294	-7.20
262303_at	homeobox protein, putative similar	ATHB18	AT1G70920	-1.04	-0.06	-0.29	0.778387	0.850336	-7.20
254094_at	putative protein ATP-dependent DI	---	AT4G25120	1.03	0.04	0.29	0.778569	0.850479	-7.20
252996_s_a	geranylgeranyl pyrophosphate synt	GGR	AT4G38460	1.03	0.04	0.29	0.778593	0.850479	-7.20
252807_at	putative replication protein various	---	---	1.02	0.03	0.29	0.778674	0.850527	-7.20
256156_at	phosphoinositide specific phospholi	ATPLC2	AT3G08510	-1.02	-0.03	-0.29	0.77887	0.8507	-7.20
258335_at	unknown protein	---	AT3G16020	-1.02	-0.03	-0.29	0.779048	0.850853	-7.20
254252_at	serine/threonine kinase - like prote	---	AT4G23310	-1.03	-0.05	-0.29	0.779284	0.851043	-7.20
253158_at	putative protein protein kinase 6, G	---	AT4G35780	1.03	0.04	0.29	0.779296	0.851043	-7.20
259623_at	hypothetical protein predicted by ge	---	AT1G42700	1.03	0.04	0.29	0.779523	0.851251	-7.20
249357_at	ribonucleoprotein -like ribonucleopi	---	AT5G40490	-1.03	-0.04	-0.29	0.779653	0.851352	-7.20
251074_at	putative protein hypothetical protei	---	AT5G01800	1.03	0.04	0.29	0.779841	0.851516	-7.20
258172_at	unknown protein similar to HYP1 G	---	AT3G21620	-1.02	-0.03	-0.29	0.779939	0.851563	-7.20
252749_at	putative protein several hypothetica	---	---	-1.02	-0.03	-0.29	0.779977	0.851563	-7.20
266485_at	putative phospholipase ;supported	---	AT2G47630	-1.05	-0.08	-0.29	0.779996	0.851563	-7.20

265223_at	putative pectinesterase	---	AT2G36700	-1.02	-0.03	-0.29	0.780136	0.851675	-7.20
255241_at	putative protein hypothetical protei	---	---	-1.02	-0.03	-0.29	0.780206	0.851711	-7.20
254109_at	Pollen-specific protein precursor lik	SKS1	AT4G25240	-1.02	-0.03	-0.29	0.780288	0.851728	-7.20
247067_at	putative protein strong similarity to	---	AT5G66950	1.03	0.05	0.29	0.780297	0.851728	-7.20
251343_at	phosphatidate cytidylyltransferase	---	AT3G60620	-1.04	-0.06	-0.29	0.780439	0.851843	-7.20
245634_at	MtN21 nodulin protein, putative sim	---	AT1G25270	-1.03	-0.04	-0.29	0.780569	0.851944	-7.20
266756_at	putative cytochrome P450	CYP709B2	AT2G46950	-1.12	-0.17	-0.29	0.780702	0.852048	-7.20
264311_at	hypothetical protein similar to hypot	---	AT1G70400	1.02	0.03	0.29	0.780841	0.852112	-7.20
245022_at	PSII L protein	---	---	1.03	0.05	0.29	0.780856	0.852112	-7.20
265701_at	unknown protein related to unchara	---	AT2G03460	-1.02	-0.03	-0.29	0.780872	0.852112	-7.20
260187_at	hypothetical protein	LBD5	AT1G36000	1.02	0.03	0.29	0.78098	0.852188	-7.20
246606_at	putative protein	---	---	1.02	0.03	0.29	0.781061	0.8522	-7.20
256674_at	unknown protein ;supported by full-	---	AT3G52360	-1.04	-0.05	-0.29	0.781091	0.8522	-7.20
247837_at	N-hydroxycinnamoyl/benzoyltransfe	---	AT5G57840	1.03	0.05	0.29	0.781102	0.8522	-7.20
253436_at	ubiquinol-cytochrome c reductase	---	AT4G32470	1.02	0.03	0.29	0.781173	0.852208	-7.20
247557_at	putative protein	---	AT5G61050	1.02	0.03	0.29	0.781185	0.852208	-7.20
259448_at	hypothetical protein similar to trans	---	AT1G13790	-1.03	-0.04	-0.29	0.781459	0.852426	-7.20
259315_at	unknown protein	AtRP2	AT3G01200	-1.02	-0.03	-0.29	0.781459	0.852426	-7.20
249116_at	putative protein similar to unknown	---	AT5G43820	-1.03	-0.04	-0.29	0.78193	0.85287	-7.20
263648_at	hypothetical protein predicted by ge	---	AT1G04390	1.03	0.04	0.29	0.781956	0.85287	-7.20
250731_at	putative protein contains similarity t	AGL96	AT5G06500	1.02	0.03	0.29	0.782012	0.85287	-7.20
265048_at	jasmonate inducible protein, putati	---	AT1G52050	-1.03	-0.04	-0.29	0.782015	0.85287	-7.20
253256_at	putative protein endothelin convert	---	AT4G34360	1.03	0.04	0.29	0.782136	0.852899	-7.20
248973_at	disease resistance protein-like	TTR1	AT5G45050	1.02	0.03	0.29	0.782138	0.852899	-7.20
264206_at	putative topoisomerase strong simil	---	AT1G22730	-1.03	-0.04	-0.29	0.782169	0.852899	-7.20
247826_at	beta 1-3 glucanase - like protein be	---	AT5G58480	-1.02	-0.03	-0.29	0.782192	0.852899	-7.20
264375_at	putative protein kinase contains a p	CIPK16	AT2G25090	1.07	0.10	0.29	0.78227	0.852944	-7.20
259953_at	putative anion exchanger contains l	BOR5	AT1G74810	1.03	0.05	0.29	0.782553	0.853211	-7.20
260942_s_a	hypothetical protein contains simila	---	AT1G45190	-1.02	-0.03	-0.29	0.782695	0.853293	-7.20
246412_at	phosphoglucomutase-like protein p	---	AT5G17530	1.04	0.06	0.29	0.782703	0.853293	-7.20
249017_at	C2 domain-containing protein-like	---	AT5G44760	-1.03	-0.04	-0.29	0.782745	0.853298	-7.20
260353_at	putative nitrilase-associated protein	SP1L2	AT1G69230	1.03	0.04	0.29	0.782808	0.853326	-7.20
245838_at	disease resistance protein, putative	---	AT1G58410	-1.02	-0.03	-0.29	0.783005	0.853501	-7.20
250315_at	putative protein contains similarity t	PDE149	AT5G12130	-1.04	-0.06	-0.29	0.783148	0.853615	-7.20
266975_at	hypothetical protein predicted by gr	ATEXO70H	AT2G39380	-1.05	-0.08	-0.29	0.783197	0.853628	-7.20

245896_at	putative transcriptional co-activator	KIWI	AT5G09250	1.03	0.04	0.29	0.783258	0.853639	-7.20
257467_at	hypothetical protein similar to hypot	LBD4	AT1G31320	-1.04	-0.06	-0.29	0.783282	0.853639	-7.20
246729_at	putative protein	---	AT5G28070	-1.02	-0.03	-0.29	0.78371	0.854058	-7.20
263191_at	polyprotein, putative similar to poly	---	---	-1.03	-0.04	-0.29	0.783741	0.854058	-7.20
261274_at	myb-related protein, putative simila	MYB117	AT1G26780	-1.02	-0.03	-0.29	0.783881	0.854169	-7.20
266619_at	similar to harpin-induced protein hir	---	AT2G35460	1.03	0.04	0.29	0.78393	0.854182	-7.20
249561_at	disease resistance - like protein dis	---	AT5G38340	-1.02	-0.03	-0.29	0.784182	0.854376	-7.20
246986_at	receptor-like protein kinase ;suppo	RLK	AT5G67280	-1.07	-0.10	-0.29	0.784191	0.854376	-7.20
256111_at	unknown protein	---	AT1G16820	-1.03	-0.04	-0.28	0.784249	0.854376	-7.20
253252_at	amidophosphoribosyltransferase 2	ATASE2	AT4G34740	1.04	0.05	0.28	0.784258	0.854376	-7.20
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_X	---	---	1.04	0.06	0.28	0.784533	0.854577	-7.20
256700_at	pseudouridine synthase, putative s	---	AT3G52260	1.02	0.03	0.28	0.784541	0.854577	-7.20
257005_at	hypothetical protein predicted by ge	---	AT3G14190	1.03	0.04	0.28	0.784555	0.854577	-7.20
247767_at	putative protein various predicted p	AGL82	AT5G58890	-1.02	-0.03	-0.28	0.784682	0.854661	-7.20
246452_at	putative protein predicted proteins -	BPA1	AT5G16840	-1.02	-0.03	-0.28	0.784724	0.854661	-7.20
259284_at	putative cell division related protein	---	AT3G11450	-1.03	-0.04	-0.28	0.784744	0.854661	-7.20
249435_at	putative protein tail-specific thyroid	---	AT5G39970	-1.02	-0.03	-0.28	0.784814	0.854696	-7.20
246324_at	arginine/serine-rich protein, putativ	SR45	AT1G16610	1.02	0.03	0.28	0.7849	0.854749	-7.20
267258_at	hypothetical protein predicted by ge	---	AT2G23140	-1.02	-0.03	-0.28	0.785018	0.854837	-7.20
266276_at	putative tropinone reductase	TRI	AT2G29330	-1.02	-0.03	-0.28	0.785183	0.854915	-7.20
263915_at	hypothetical protein predicted by ge	---	AT2G36430	1.07	0.10	0.28	0.785186	0.854915	-7.20
252376_at	L-galactono-1,4-lactone dehydroge	ATGLDH	AT3G47930	1.03	0.05	0.28	0.785203	0.854915	-7.20
262719_at	hypothetical protein predicted by ge	---	---	1.02	0.03	0.28	0.785291	0.854971	-7.20
247674_at	putative protein large number of pr	---	AT5G59930	-1.03	-0.04	-0.28	0.785598	0.855264	-7.20
246333_at	proteinkinase AtPP -like protein Atl	---	AT3G44840	-1.02	-0.03	-0.28	0.785641	0.85527	-7.20
252956_at	farnesylated protein (ATFP6) ; sup	ATFP6	AT4G38580	1.06	0.08	0.28	0.785739	0.855315	-7.20
260743_at	unknown protein	---	AT1G15030	1.04	0.06	0.28	0.785786	0.855315	-7.20
248503_at	putative protein contains similarity t	NF-YC7	AT5G50470	1.04	0.05	0.28	0.785795	0.855315	-7.20
265461_at	unknown protein similarity to ubiqui	---	AT2G46500	1.02	0.03	0.28	0.785878	0.855365	-7.20
256469_at	zinc-finger protein, putative similar	LOL1	AT1G32540	1.04	0.05	0.28	0.785939	0.855365	-7.20
262608_at	dioxygenase-like protein very simil	---	AT1G14120	-1.02	-0.04	-0.28	0.785953	0.855365	-7.20
252957_at	glycine-rich protein 2 (GRP2) ; sup	GRP2	AT4G38680	1.05	0.06	0.28	0.786126	0.855512	-7.20
251378_at	putative protein	---	AT3G60660	1.02	0.03	0.28	0.786182	0.855533	-7.20
255180_at	putative polyprotein	---	---	1.02	0.03	0.28	0.786294	0.855614	-7.20
267080_at	unknown protein ; supported by cD	---	AT2G41190	-1.06	-0.08	-0.28	0.78634	0.855622	-7.20

253795_at	tyrosine transaminase-like protein	---	AT4G28420	1.02	0.03	0.28	0.786649	0.855918	-7.20
259476_at	Myb-related transcription activator,	---	AT1G19000	-1.03	-0.04	-0.28	0.786914	0.856166	-7.20
252233_at	AtMYB84 ;supported by full-length	MYB84	AT3G49690	1.03	0.04	0.28	0.787034	0.856212	-7.20
254860_at	putative C-4 sterol methyl oxidase	SMO1-1	AT4G12110	-1.03	-0.04	-0.28	0.787064	0.856212	-7.20
259710_at	putative aminotransferase similar t	---	AT1G77670	1.06	0.09	0.28	0.78707	0.856212	-7.20
249526_at	putative protein contains similarity t	---	AT5G38560	-1.03	-0.04	-0.28	0.787316	0.85644	-7.20
267103_at	putative UDP-N-acetylglucosamine-	GPT	AT2G41490	-1.02	-0.03	-0.28	0.787442	0.856533	-7.20
261978_at	Athila retroelment ORF 1, putative	---	---	-1.02	-0.03	-0.28	0.787477	0.856533	-7.20
248614_at	putative protein similar to unknown	---	AT5G49560	-1.02	-0.03	-0.28	0.787621	0.856648	-7.20
249280_at	unknown protein	---	AT5G41940	-1.03	-0.04	-0.28	0.787754	0.856752	-7.20
260242_at	putative transcription factor similar t	EGL3	AT1G63650	-1.02	-0.03	-0.28	0.788018	0.856942	-7.20
254311_at	hypothetical protein	---	AT4G22440	1.02	0.04	0.28	0.788033	0.856942	-7.20
267638_at	unknown protein ; supported by ful	OEP16-3	AT2G42210	1.02	0.03	0.28	0.788041	0.856942	-7.20
257035_at	cytochrome P450, putative similar	CYP707A4	AT3G19270	-1.03	-0.04	-0.28	0.788105	0.856971	-7.20
260132_s_a	hypothetical protein	---	AT1G66320	1.02	0.03	0.28	0.788239	0.857076	-7.20
250182_at	putative protein predicted proteins,	---	AT5G14470	-1.07	-0.09	-0.28	0.788473	0.857289	-7.20
245371_at	hypothetical protein ;supported by f	---	AT4G15750	1.03	0.04	0.28	0.788574	0.857358	-7.20
AFFX-Athal-	Arabidopsis thaliana /REF=U37281	---	---	-1.02	-0.03	-0.28	0.788723	0.857479	-7.20
247088_at	unknown protein	---	AT5G66340	1.02	0.03	0.28	0.788826	0.857551	-7.20
266741_s_a	putative disease resistance protein	---	AT2G03030	-1.02	-0.03	-0.28	0.788892	0.85757	-7.20
249246_at	unknown protein	---	AT5G42290	-1.02	-0.03	-0.28	0.788919	0.85757	-7.20
256425_at	disease resistance protein, putative	ADR1	AT1G33560	1.03	0.05	0.28	0.788994	0.85761	-7.20
245440_at	RNA helicase	---	AT4G16680	1.02	0.03	0.28	0.78923	0.857826	-7.20
250749_at	26S proteasome regulatory subunit	RPN8A	AT5G05780	1.02	0.03	0.28	0.789326	0.857889	-7.20
254968_at	putative protein various predicted p	---	AT4G10420	1.02	0.03	0.28	0.789597	0.858143	-7.21
256718_at	hypothetical protein predicted by ge	---	AT2G34120	-1.02	-0.03	-0.28	0.78967	0.858181	-7.21
254909_at	putative disease resistance respon	---	AT4G11210	-1.02	-0.03	-0.28	0.789721	0.858196	-7.21
258600_at	putative protein kinase contains Pfa	---	AT3G02810	1.02	0.03	0.28	0.7898	0.858241	-7.21
265514_s_a	Mutator-like transposase similar to	---	---	1.02	0.03	0.28	0.789848	0.858252	-7.21
263670_at	hypothetical protein predicted by ge	---	AT2G04840	1.02	0.03	0.28	0.78993	0.858301	-7.21
260926_at	unknown protein	GLTP2	AT1G21360	1.02	0.03	0.28	0.790158	0.858507	-7.21
266507_at	unknown protein EST matches on	---	AT2G47860	-1.02	-0.03	-0.28	0.790325	0.858648	-7.21
251156_at	putative protein ZCF61, Arabidopsi	EDL3	AT3G63060	1.03	0.04	0.28	0.790421	0.858711	-7.21
260464_at	disease resistance protein RPM1 is	LOV1	AT1G10920	1.02	0.03	0.28	0.790691	0.858964	-7.21
256804_at	hypothetical protein predicted by ge	---	AT3G20920	-1.02	-0.02	-0.28	0.79091	0.859161	-7.21

261988_at	single-strand nucleic acid-binding p	---	AT1G33680	-1.03	-0.04	-0.28	0.791179	0.859412	-7.21
248821_at	protein serine threonine kinase-like	---	AT5G47070	1.05	0.07	0.28	0.791259	0.859425	-7.21
263492_at	putative seed maturation protein	---	AT2G42560	1.02	0.03	0.28	0.791266	0.859425	-7.21
260169_at	hypothetical protein predicted by g	FUT13	AT1G71990	1.04	0.06	0.28	0.791386	0.859478	-7.21
261188_at	hypothetical protein contains simila	---	---	-1.02	-0.03	-0.28	0.79139	0.859478	-7.21
254348_at	putative protein p47 - Homo sapien	PUX3	AT4G22150	-1.02	-0.03	-0.28	0.791469	0.859505	-7.21
256633_at	unknown protein	GATL10	AT3G28340	-1.11	-0.15	-0.28	0.791491	0.859505	-7.21
253805_at	putative protein	---	AT4G28260	1.03	0.04	0.27	0.791678	0.859668	-7.21
247782_at	putative protein predicted RNA bin	---	AT5G58790	1.02	0.03	0.27	0.791772	0.859729	-7.21
264582_at	putative ovule-specific homeotic pr	HDG2	AT1G05230	1.02	0.03	0.27	0.791872	0.859796	-7.21
255146_at	putative protein disease resistance	---	AT4G08450	-1.02	-0.02	-0.27	0.792134	0.86004	-7.21
265616_at	hypothetical protein predicted by ge	---	AT2G25500	1.02	0.03	0.27	0.792239	0.860113	-7.21
263234_at	hypothetical protein predicted by ge	---	AT1G10417	-1.02	-0.03	-0.27	0.792411	0.860259	-7.21
257066_at	lipid transfer protein, putative simila	---	AT3G18280	-1.06	-0.08	-0.27	0.792617	0.860441	-7.21
253670_at	putative protein ; supported by full-	---	AT4G30010	1.02	0.03	0.27	0.792673	0.860461	-7.21
264249_at	vacuolar-type H+-translocating inor	AVP2	AT1G78920	1.02	0.03	0.27	0.792845	0.860607	-7.21
260180_at	E2, ubiquitin-conjugating enzyme,	MMZ2	AT1G70660	1.03	0.05	0.27	0.79294	0.860669	-7.21
264976_at	peptide transporter, putative simila	NRT1.6	AT1G27080	-1.03	-0.04	-0.27	0.792991	0.860683	-7.21
254539_s_a	chitinase - like protein chitinase / ly	---	AT4G19750	-1.02	-0.03	-0.27	0.79323	0.860902	-7.21
262330_at	disease resistance protein, putative	RLM1	AT1G64070	1.02	0.03	0.27	0.793298	0.860934	-7.21
252935_at	dnaJ-like protein CAJ1 protein, Sa	---	AT4G39150	-1.02	-0.03	-0.27	0.793623	0.861232	-7.21
246714_at	putative protein predicted proteins,	---	AT5G28220	1.02	0.03	0.27	0.793674	0.861232	-7.21
256177_at	protein kinase, putative contains P	---	AT1G51620	-1.07	-0.09	-0.27	0.793685	0.861232	-7.21
258757_at	putative RING zinc finger protein c	---	AT3G10910	1.04	0.05	0.27	0.793753	0.861265	-7.21
253466_at	homeodomain containing protein 1	KNAT5	AT4G32040	-1.03	-0.04	-0.27	0.793948	0.861435	-7.21
258118_at	unknown protein	---	AT3G14710	-1.03	-0.04	-0.27	0.794293	0.861743	-7.21
261781_at	far-red impaired response protein,	FRS4	AT1G76320	1.03	0.04	0.27	0.794335	0.861743	-7.21
265279_at	hypothetical protein predicted by ge	---	AT2G28460	-1.03	-0.05	-0.27	0.794345	0.861743	-7.21
264447_at	hypothetical protein predicted by ge	---	AT1G27300	-1.05	-0.07	-0.27	0.794482	0.86185	-7.21
254312_s_a	hypothetical protein	---	---	1.03	0.04	0.27	0.794755	0.862106	-7.21
256558_at	hypothetical protein predicted by ge	---	---	1.02	0.03	0.27	0.794798	0.862111	-7.21
263775_at	putative MYB family transcription fa	CPC	AT2G46410	1.02	0.03	0.27	0.794908	0.862189	-7.21
250257_at	putative protein similar to unknown	---	AT5G13770	1.03	0.04	0.27	0.794971	0.862217	-7.21
262564_at	anionic peroxidase, putative simila	---	AT1G34330	-1.02	-0.03	-0.27	0.795215	0.862431	-7.21
257275_at	RNA-binding protein, putative cont	CID9	AT3G14450	-1.04	-0.06	-0.27	0.795244	0.862431	-7.21

265665_at	cysteine proteinase contains similar	---	AT2G27420	-1.02	-0.03	-0.27	0.795585	0.86276	-7.21
250491_at	putative protein predicted proteins,	---	AT5G09780	-1.03	-0.04	-0.27	0.795742	0.862889	-7.21
261680_at	hypothetical protein similar to hypot	---	AT1G47350	-1.02	-0.02	-0.27	0.795827	0.862941	-7.21
250977_at	importin alpha - like protein importi	IMPA-9	AT5G03070	-1.02	-0.03	-0.27	0.795929	0.86301	-7.21
259092_at	putative zeta-carotene desaturase p	ZDS	AT3G04870	1.02	0.02	0.27	0.796101	0.863155	-7.21
263147_at	polyubiquitin, putative similar to po	---	AT1G53980	1.02	0.03	0.27	0.79643	0.863472	-7.21
262113_at	late embryogenis abundant protein	---	AT1G02820	1.05	0.06	0.27	0.796481	0.863485	-7.21
263469_at	putative Na+/H+ antiporter	ATCHX21	AT2G31910	-1.02	-0.03	-0.27	0.796616	0.863559	-7.21
262626_at	FtsH protease, putative similar to z	FTSH8	AT1G06430	1.03	0.04	0.27	0.79666	0.863559	-7.21
256618_at	hypothetical protein	VRN5	AT3G24440	-1.05	-0.07	-0.27	0.796663	0.863559	-7.21
256109_at	hypothetical protein predicted by ge	---	AT1G16950	1.04	0.05	0.27	0.796831	0.863701	-7.21
265017_at	unknown protein similar to EST em	---	AT1G24390	-1.02	-0.03	-0.27	0.796891	0.863724	-7.21
252005_at	purple acid phosphatase-like prote	PAP21	AT3G52810	1.03	0.04	0.27	0.797006	0.863808	-7.21
257306_at	hypothetical protein contains regio	---	AT3G30200	1.02	0.03	0.27	0.797185	0.863933	-7.21
248381_at	fructokinase 1 ; supported by cDNA	---	AT5G51830	1.04	0.06	0.27	0.797197	0.863933	-7.21
248873_at	disease resistance protein-like	---	AT5G46450	1.07	0.10	0.27	0.797328	0.864034	-7.21
267305_at	high affinity K+ transporter (AtKUP1	ATKT1	AT2G30070	1.04	0.06	0.27	0.797396	0.864067	-7.21
245202_at	F12A21.14 similar to receptor prote	---	AT1G67720	1.03	0.04	0.27	0.79758	0.864225	-7.21
247897_at	unknown protein ;supported by full-	TET15	AT5G57810	1.02	0.03	0.27	0.79763	0.864239	-7.21
247362_at	putative protein strong similarity to u	ATPAP29	AT5G63140	-1.04	-0.06	-0.27	0.797702	0.864275	-7.21
248216_at	unknown protein	---	AT5G53690	1.02	0.03	0.27	0.797768	0.864292	-7.21
265653_at	hypothetical protein	---	---	1.02	0.03	0.27	0.797793	0.864292	-7.21
255974_at	hypothetical protein	---	---	-1.02	-0.04	-0.27	0.797999	0.864474	-7.21
265709_at	hypothetical protein predicted by ge	---	---	1.06	0.08	0.27	0.798067	0.864506	-7.21
253904_at	NWMU1 - 2S albumin 1 precursor	---	AT4G27140	-1.02	-0.03	-0.27	0.798175	0.86456	-7.21
262579_at	hypothetical protein predicted by ge	---	AT1G15320	1.02	0.03	0.27	0.798193	0.86456	-7.21
249425_at	putative protein 5'-AMP-ACTIVATE	---	AT5G39790	-1.04	-0.06	-0.27	0.79838	0.864722	-7.21
252881_at	putative protein predicted proteins,	---	AT4G39610	1.03	0.04	0.27	0.79846	0.864761	-7.21
253242_at	isoflavone reductase - like protein i	CIB1	AT4G34530	1.04	0.06	0.27	0.798492	0.864761	-7.21
252387_at	aldose 1-epimerase - like protein a	---	AT3G47800	-1.03	-0.04	-0.27	0.798645	0.864886	-7.21
263245_at	hypothetical protein predicted by ge	---	AT2G31470	-1.02	-0.02	-0.27	0.798815	0.865029	-7.21
252381_s_a	ABC-type transport protein-like pro	ABCA4	AT3G47750	-1.02	-0.03	-0.27	0.798918	0.8651	-7.21
247901_at	ubiquinone/menaquinone biosynthe	---	AT5G57300	-1.02	-0.03	-0.26	0.799054	0.865178	-7.21
249185_at	CHP-rich zinc finger protein-like	---	AT5G43030	-1.02	-0.03	-0.26	0.79908	0.865178	-7.21
250931_at	putative protein various predicted p	---	AT5G03200	1.06	0.08	0.26	0.799105	0.865178	-7.21

266711_at	unknown protein	---	AT2G46740	1.02	0.03	0.26	0.79915	0.865186	-7.21
256522_at	unknown protein ;supported by full-	CMPG1	AT1G66160	-1.12	-0.16	-0.26	0.79937	0.865383	-7.21
259251_at	unknown protein identical to residue	---	AT3G07600	-1.07	-0.09	-0.26	0.799423	0.8654	-7.21
260992_at	hypothetical protein predicted by ge	---	AT1G12150	-1.02	-0.03	-0.26	0.799467	0.865407	-7.21
262446_at	hypothetical protein predicted by ge	---	AT1G49310	-1.06	-0.08	-0.26	0.799597	0.865505	-7.21
262702_at	putative protein phosphatase 2C sir	---	AT1G16220	-1.02	-0.03	-0.26	0.79964	0.865511	-7.21
255708_at	predicted protein	---	AT4G00232	-1.02	-0.03	-0.26	0.79983	0.865676	-7.21
247681_at	serine/threonine-specific protein kir	---	---	-1.03	-0.04	-0.26	0.799895	0.865706	-7.21
265769_at	unknown protein weak similarity to (	---	AT2G48090	-1.02	-0.03	-0.26	0.799964	0.865713	-7.21
246556_at	putative protein hypothetical protei	---	AT5G15480	-1.02	-0.03	-0.26	0.799978	0.865713	-7.21
257318_at	hypothetical protein	---	AT2G07777	-1.02	-0.03	-0.26	0.80011	0.865814	-7.21
257796_at	hypothetical protein predicted by ge	---	AT3G15930	1.02	0.03	0.26	0.800304	0.865823	-7.21
255666_at	putative protein ;supported by full-l	---	AT4G00390	1.02	0.04	0.26	0.80034	0.865823	-7.21
260032_at	putative phosphoenolpyruvate carb	ATPPC4	AT1G68750	-1.02	-0.03	-0.26	0.800364	0.865823	-7.21
249670_at	unknown protein	---	AT5G35890	-1.02	-0.03	-0.26	0.800427	0.865823	-7.21
259243_at	unknown protein similar to unknow	---	AT3G07565	1.02	0.03	0.26	0.800435	0.865823	-7.21
265217_s_a	unknown protein ESTs gb|H76594 a	---	AT1G05090	1.03	0.04	0.26	0.800463	0.865823	-7.21
245959_at	peptide transport protein-like peptic	---	AT5G19640	-1.02	-0.03	-0.26	0.80047	0.865823	-7.21
261596_at	hypothetical protein predicted by ge	---	AT1G33080	1.02	0.03	0.26	0.800485	0.865823	-7.21
AFFX-r2-Bs	B. subtilis /GEN=thrC, thrB /DB_XR	---	---	-1.04	-0.06	-0.26	0.800489	0.865823	-7.21
263754_at	putative DnaJ protein ;supported b	---	AT2G21510	1.05	0.07	0.26	0.800498	0.865823	-7.21
261807_at	Expressed protein ; supported by fu	---	AT1G30515	1.02	0.03	0.26	0.800597	0.86586	-7.21
253024_at	putative protein	---	AT4G38080	-1.10	-0.14	-0.26	0.800608	0.86586	-7.21
255758_at	hypothetical protein predicted by ge	---	AT1G16800	1.02	0.03	0.26	0.800722	0.86593	-7.21
246731_at	putative protein RING finger rngB p	ACBP5	AT5G27630	-1.02	-0.03	-0.26	0.800748	0.86593	-7.21
266867_at	putative signal recognition particle r	CPFTSY	AT2G45770	1.02	0.03	0.26	0.800791	0.865936	-7.21
245722_at	unknown protein	---	AT1G73430	-1.03	-0.04	-0.26	0.800932	0.866047	-7.21
266840_at	hypothetical protein predicted by ge	---	AT2G26160	1.02	0.02	0.26	0.800998	0.866062	-7.21
252872_at	putative serine/threonine protein ki	SNRK2.7	AT4G40010	1.02	0.03	0.26	0.801022	0.866062	-7.21
255868_at	putative MYB family transcription fa	---	AT2G30380	-1.02	-0.04	-0.26	0.801249	0.866266	-7.21
248671_at	putative protein strong similarity to (	---	AT5G48750	-1.02	-0.03	-0.26	0.801584	0.866588	-7.21
257579_at	hypothetical protein predicted by ge	---	AT3G11000	-1.02	-0.03	-0.26	0.801835	0.866818	-7.21
256958_at	unknown protein contains Pfam pro	---	AT3G13430	-1.03	-0.05	-0.26	0.801939	0.866889	-7.21
249276_at	DNA polymerase alpha subunit IV (	POLA3	AT5G41880	-1.10	-0.14	-0.26	0.802063	0.866982	-7.21
262216_at	hypothetical protein contains simila	---	AT1G74780	-1.02	-0.04	-0.26	0.802204	0.867093	-7.21

259962_at	RNA polymerase II, putative simila	---	AT1G53690	1.02	0.03	0.26	0.80227	0.867099	-7.21
253117_at	Expressed protein ; supported by fu	---	AT4G35905	-1.03	-0.04	-0.26	0.802285	0.867099	-7.21
249912_at	putative protein similar to unknown	RER1	AT5G22790	-1.05	-0.07	-0.26	0.802372	0.867152	-7.21
253908_at	GH3 like protein GH3 protein, Glyc	WES1	AT4G27260	-1.10	-0.13	-0.26	0.802444	0.867185	-7.21
264842_at	hypothetical protein predicted by ge	---	AT1G03700	-1.02	-0.02	-0.26	0.802479	0.867185	-7.21
253596_s_a	hypothetical protein ; supported by	---	AT4G30730	-1.03	-0.05	-0.26	0.802517	0.867185	-7.21
249897_at	putative protein strong similarity to	---	AT5G22550	1.02	0.03	0.26	0.802581	0.867214	-7.21
264995_at	mutator-like transposase, putative	---	---	-1.03	-0.04	-0.26	0.802708	0.867309	-7.21
262925_at	hypothetical protein	YSL7	AT1G65730	1.02	0.03	0.26	0.802822	0.867392	-7.21
247736_at	actin 4 ;supported by full-length cD	ACT4	AT5G59370	-1.02	-0.03	-0.26	0.802891	0.867426	-7.21
249813_at	acyltransferase ; supported by full-	EMB3009	AT5G23940	-1.02	-0.02	-0.26	0.803068	0.867576	-7.21
261751_at	chloroplast drought-induced stress	CDSP32	AT1G76080	-1.02	-0.02	-0.26	0.803234	0.867713	-7.21
250691_at	glycolate oxidase subunit D-like; D-	---	AT5G06580	1.02	0.02	0.26	0.803297	0.86774	-7.21
255247_at	hypothetical protein	---	---	1.02	0.02	0.26	0.80352	0.86794	-7.21
249683_x_a	putative protein similar to unknown	---	---	-1.02	-0.03	-0.26	0.803951	0.868365	-7.21
245835_at	hypothetical protein similar to putati	---	AT1G42190	-1.02	-0.03	-0.26	0.804182	0.868573	-7.21
251844_at	putative protein retinoblastoma-ass	---	AT3G54630	-1.02	-0.03	-0.26	0.804398	0.868681	-7.21
251284_at	hypothetical protein	---	AT3G61840	-1.03	-0.04	-0.26	0.804399	0.868681	-7.21
256559_at	Athila ORF 1, putative similar to At	---	---	1.02	0.03	0.26	0.804424	0.868681	-7.21
257475_at	hypothetical protein predicted by ge	---	AT1G80880	-1.02	-0.02	-0.26	0.804435	0.868681	-7.21
247466_at	putative protein predicted proteins,	---	AT5G62090	1.03	0.04	0.26	0.804625	0.868806	-7.21
245445_at	apetala2 domain TINY like protein	---	AT4G16750	-1.05	-0.08	-0.26	0.804627	0.868806	-7.21
245703_at	S-adenosyl-L-methionine:salicylic a	---	AT5G04380	-1.02	-0.03	-0.26	0.805001	0.86917	-7.21
248611_at	putative protein contains similarity t	WRKY48	AT5G49520	-1.07	-0.10	-0.26	0.805042	0.869173	-7.21
256460_at	60S ribosomal protein L30, putative	---	AT1G36240	1.02	0.03	0.26	0.80511	0.869205	-7.21
248601_at	putative protein contains similarity t	---	AT5G49400	-1.02	-0.02	-0.26	0.805266	0.869332	-7.21
265358_at	putative HesB-like protein ; suppor	---	AT2G16710	-1.03	-0.04	-0.26	0.805343	0.869334	-7.21
253885_at	putative protein essential for embry	VPS26B	AT4G27690	-1.03	-0.04	-0.26	0.805344	0.869334	-7.21
261529_at	hypothetical protein contains simila	---	AT1G14430	-1.02	-0.03	-0.26	0.805663	0.869609	-7.21
246375_at	light repressible receptor protein ki	---	AT1G51830	1.03	0.04	0.26	0.805675	0.869609	-7.21
258178_at	hypothetical protein predicted by ge	---	AT3G21680	-1.02	-0.02	-0.26	0.805787	0.869646	-7.21
266160_at	hypothetical protein	ATCHX8	AT2G28180	-1.03	-0.04	-0.26	0.805807	0.869646	-7.21
248964_at	cytochrome P450	CYP707A3	AT5G45340	-1.06	-0.09	-0.26	0.805824	0.869646	-7.21
260788_at	cysteine proteinase contains simila	---	AT1G06260	-1.02	-0.03	-0.26	0.805926	0.869715	-7.21
253454_at	Expressed protein ; supported by cl	---	AT4G31875	1.04	0.05	0.26	0.805984	0.869725	-7.21

258280_at	putative self-incompatibility protein	---	AT3G26880	1.02	0.02	0.26	0.806011	0.869725	-7.21
257136_at	hypothetical protein predicted by ge	ASML2	AT3G12890	1.02	0.03	0.26	0.806138	0.869745	-7.21
266387_at	hypothetical protein predicted by ge	---	AT2G32360	-1.02	-0.03	-0.26	0.806139	0.869745	-7.21
262374_s_a	flax rust resistance protein, putative	TIR	AT1G72910	-1.08	-0.11	-0.26	0.806144	0.869745	-7.21
267066_at	hypothetical protein predicted by ge	---	AT2G41040	-1.03	-0.04	-0.26	0.80627	0.869832	-7.21
251554_at	putative protein predicted protein, A	---	AT3G58670	1.02	0.03	0.26	0.806301	0.869832	-7.21
255514_s_a	hypothetical protein similar to MNA	AGL78	AT5G65330	-1.02	-0.03	-0.25	0.806417	0.869875	-7.21
245492_at	putative protein	SPK1	AT4G16340	1.02	0.03	0.25	0.806417	0.869875	-7.21
256437_s_a	putative clathrin heavy chain similar	---	AT3G08530	-1.02	-0.02	-0.25	0.806892	0.870346	-7.21
260599_at	cytochrome P450, putative similar	CYP708A1	AT1G55940	-1.02	-0.02	-0.25	0.806981	0.870401	-7.21
261010_at	hypothetical protein predicted by ge	---	AT1G26350	-1.02	-0.03	-0.25	0.807262	0.870628	-7.21
263496_at	unknown protein ; supported by ful	---	AT2G42570	1.03	0.04	0.25	0.807268	0.870628	-7.21
250427_at	putative protein myosin heavy chai	---	AT5G10500	1.02	0.03	0.25	0.807311	0.870634	-7.21
266383_at	putative pathogenesis related-1 (PR	ATPRB1	AT2G14580	1.03	0.04	0.25	0.807361	0.870646	-7.21
249308_at	unknown protein ; supported by cD	---	AT5G41350	-1.02	-0.02	-0.25	0.807466	0.870677	-7.21
256174_at	NADP-specific glutatamate dehydr	---	AT1G51720	1.02	0.03	0.25	0.807488	0.870677	-7.21
253056_at	SHORT-ROOT (SHR)	SHR	AT4G37650	-1.04	-0.05	-0.25	0.807505	0.870677	-7.21
256687_x_a	hypothetical protein predicted by ge	---	AT3G32120	1.02	0.03	0.25	0.807673	0.870818	-7.21
249739_at	Ttg1 protein (emb CAB45372.1)	TTG1	AT5G24520	-1.02	-0.03	-0.25	0.807756	0.870866	-7.21
258541_at	hypothetical protein	---	AT3G07000	-1.02	-0.02	-0.25	0.807976	0.871056	-7.21
253356_at	putative protein myosin II heavy ch	---	AT4G33390	-1.02	-0.03	-0.25	0.808046	0.871056	-7.21
265811_at	unknown protein possibly related to	EDA2	AT2G18080	1.02	0.03	0.25	0.808047	0.871056	-7.21
262821_at	unknown protein EST gb|F14156 co	---	AT1G11800	1.01	0.02	0.25	0.808179	0.871158	-7.21
257441_at	putative GDSL-motif lipase/hydrolas	---	AT2G04020	1.02	0.03	0.25	0.808246	0.871189	-7.21
260393_at	putative lipase similar to lipase GB:	---	AT1G73920	-1.03	-0.04	-0.25	0.80831	0.871216	-7.21
265168_at	putative Ser/Thr protein kinase	---	AT1G23700	-1.02	-0.03	-0.25	0.809237	0.872138	-7.21
266820_at	putative AP2 domain transcription fa	---	AT2G44940	1.06	0.08	0.25	0.809241	0.872138	-7.21
266972_at	40S ribosomal protein S15A	---	AT2G39590	1.02	0.03	0.25	0.809341	0.872204	-7.21
258935_at	unknown protein predicted by gens	---	AT3G10120	-1.04	-0.05	-0.25	0.809495	0.872328	-7.21
246388_at	hypothetical protein predicted by ge	---	AT1G77405	1.03	0.04	0.25	0.809664	0.872469	-7.21
265821_at	putative homeodomain transcriptio	WUS	AT2G17950	1.03	0.04	0.25	0.809907	0.872678	-7.21
257281_s_a	hypothetical protein predicted by ge	---	AT3G29680	1.02	0.03	0.25	0.809934	0.872678	-7.21
261692_at	calreticulin, putative similar to calre	CRT3	AT1G08450	1.04	0.06	0.25	0.810125	0.872842	-7.21
246171_at	putative protein centrosomal Nek2-	---	AT5G32440	1.02	0.03	0.25	0.810176	0.872857	-7.21
263763_at	Expressed protein ; supported by cl	---	AT2G21385	-1.04	-0.05	-0.25	0.810297	0.872945	-7.21

262480_at	receptor kinase, putative similar to	---	AT1G11340	1.04	0.05	0.25	0.810563	0.873169	-7.21
246950_at	transcription initiation factor IID-ass	TAF5	AT5G25150	-1.02	-0.02	-0.25	0.810581	0.873169	-7.21
266597_at	putative WRKY-type DNA binding p	WRKY43	AT2G46130	1.02	0.02	0.25	0.810779	0.873341	-7.21
250793_at	leucoanthocyanidin dioxygenase-lik	---	AT5G05600	-1.05	-0.08	-0.25	0.81094	0.873474	-7.21
252674_at	cytochrome P450-like protein CYT	CYP71B38	AT3G44250	-1.02	-0.02	-0.25	0.811015	0.873513	-7.21
251626_at	UDP-GlcNAc:dolichol phosphate N	---	AT3G57220	-1.02	-0.03	-0.25	0.81107	0.873529	-7.21
262011_at	hypothetical protein predicted by ge	---	AT1G35614	-1.03	-0.04	-0.25	0.811107	0.873529	-7.21
251481_at	receptor lectin kinase-like protein (	---	AT3G59730	-1.02	-0.02	-0.25	0.811193	0.873581	-7.21
262683_at	anter-specific proline-rich -like prote	---	AT1G75920	-1.02	-0.02	-0.25	0.811314	0.873654	-7.21
245527_at	putative epoxide hydrolase	---	AT4G15955	-1.03	-0.04	-0.25	0.811338	0.873654	-7.21
261625_at	hypothetical protein predicted by ge	---	AT1G01930	1.02	0.02	0.25	0.811595	0.87389	-7.21
263457_at	unknown protein	SR1	AT2G22300	-1.04	-0.06	-0.25	0.812114	0.874408	-7.21
266857_at	putative Na+ dependent ileal bile ac	---	AT2G26900	-1.02	-0.03	-0.25	0.812173	0.87443	-7.21
246022_at	putative protein predicted protein -	---	AT5G21110	-1.02	-0.03	-0.25	0.812246	0.874466	-7.21
259459_at	En/Spm-like transposon protein, pu	---	---	-1.02	-0.03	-0.25	0.812366	0.874512	-7.21
252057_at	putative protein ;supported by full-l	---	AT3G52480	-1.04	-0.05	-0.25	0.812411	0.874512	-7.21
257631_at	cytochrome P450, putative similar	CYP71B17	AT3G26160	1.03	0.04	0.25	0.812436	0.874512	-7.21
265089_at	hypothetical protein similar to hypot	SUVR1	AT1G04050	-1.02	-0.03	-0.25	0.812441	0.874512	-7.21
259797_at	unknown protein	---	---	-1.02	-0.03	-0.25	0.812527	0.874544	-7.21
253018_at	putative protein Zn finger protein B	---	AT4G38000	1.02	0.03	0.25	0.812548	0.874544	-7.21
260468_at	transcription factor RUSH-1alpha is	---	AT1G11100	-1.03	-0.04	-0.25	0.812671	0.874636	-7.21
246707_at	putative protein	---	---	-1.02	-0.03	-0.25	0.812861	0.874799	-7.21
267188_at	6,7-dimethyl-8-ribityllumazine synth	COS1	AT2G44050	-1.02	-0.03	-0.25	0.812979	0.874867	-7.21
261158_at	hypothetical protein predicted by ge	---	AT1G34500	1.02	0.03	0.25	0.813001	0.874867	-7.21
245753_at	hypothetical protein similar to putati	---	---	1.02	0.02	0.25	0.813195	0.875034	-7.21
249281_at	GTPase activator protein of Rab-lik	---	AT2G36460	1.02	0.03	0.25	0.813253	0.875056	-7.21
248825_at	ATP synthase delta chain, mitocho	---	AT5G47030	-1.02	-0.03	-0.25	0.813349	0.875118	-7.21
249935_at	acyl CoA reductase-like protein	FAR7	AT5G22420	1.02	0.02	0.25	0.8137	0.875394	-7.21
261504_at	MADS-box protein identical to GB:	AGL12	AT1G71692	-1.03	-0.04	-0.25	0.813716	0.875394	-7.21
266432_s_a	putative gag-protease polyprotein	---	---	1.02	0.03	0.25	0.813721	0.875394	-7.21
261683_at	hypothetical protein similar to hypot	---	AT1G47300	-1.02	-0.02	-0.24	0.813776	0.875412	-7.21
257284_at	TNP1-like protein similar to TNP1 p	---	---	-1.01	-0.02	-0.24	0.813902	0.87549	-7.21
257656_at	Expressed protein ; supported by fu	---	AT3G13228	1.02	0.02	0.24	0.813926	0.87549	-7.21
249347_at	putative protein similar to unknown	---	AT5G40830	-1.04	-0.06	-0.24	0.814013	0.875542	-7.21
246933_at	ZFP3 zinc finger protein ; supporte	ZFP3	AT5G25160	-1.01	-0.02	-0.24	0.814063	0.875556	-7.21

259522_at	hypothetical protein	---	AT1G12490	1.02	0.02	0.24	0.814186	0.875615	-7.21
264634_at	cytochrome P450, putative	CYP702A1	AT1G65670	1.01	0.02	0.24	0.814195	0.875615	-7.21
256414_at	putative nucleic acid binding protein	AL2	AT3G11200	-1.02	-0.03	-0.24	0.814299	0.875685	-7.21
252810_at	putative protein several hypothetica	---	---	-1.02	-0.03	-0.24	0.814383	0.875716	-7.21
259341_at	unknown protein similar to hypothet	ATBPM4	AT3G03740	-1.02	-0.02	-0.24	0.814405	0.875716	-7.21
255371_at	putative RPP1-like disease resistan	---	AT4G04110	-1.02	-0.03	-0.24	0.814454	0.875729	-7.22
249187_at	cysteine proteinase RD21A similar	---	AT5G43060	-1.05	-0.07	-0.24	0.814773	0.87603	-7.22
249697_at	unknown protein	---	AT5G35510	-1.02	-0.03	-0.24	0.814859	0.876081	-7.22
258761_at	unknown protein	---	AT3G10760	-1.03	-0.04	-0.24	0.81491	0.876094	-7.22
264629_at	hypothetical protein similar to hypot	---	AT1G65540	1.02	0.03	0.24	0.81503	0.876182	-7.22
260105_at	hypothetical protein predicted by ge	---	---	1.02	0.03	0.24	0.815315	0.876447	-7.22
250930_at	putative protein P58 protein, Bos p	ATP58IPK	AT5G03160	-1.04	-0.06	-0.24	0.815497	0.876601	-7.22
251027_at	putative protein hypothetical protei	---	AT5G02210	1.02	0.02	0.24	0.815564	0.876633	-7.22
266690_at	malate oxidoreductase (malic enzyr	ATNADP-M	AT2G19900	-1.02	-0.03	-0.24	0.815806	0.876851	-7.22
249520_at	putative protein similar to unknown	---	AT5G38670	-1.02	-0.02	-0.24	0.81593	0.876943	-7.22
247494_at	calnexin - like protein calnexin hom	CNX1	AT5G61790	1.06	0.09	0.24	0.816068	0.87705	-7.22
256289_s_a	serine carboxypeptidase, putative (	scpl14	AT3G12230	-1.05	-0.07	-0.24	0.816127	0.877072	-7.22
259427_at	MADS-box transcription factor, put	AGL28	AT1G01530	-1.02	-0.03	-0.24	0.816177	0.877084	-7.22
264117_at	hypothetical protein predicted by ge	---	AT2G31210	-1.02	-0.02	-0.24	0.816266	0.877136	-7.22
265692_at	hypothetical protein predicted by ge	---	AT2G24340	-1.02	-0.03	-0.24	0.816311	0.877136	-7.22
256670_at	Athila ORF 1, putative similar to At	---	---	-1.02	-0.03	-0.24	0.816341	0.877136	-7.22
267196_at	FtsH protease (VAR2) identical to z	VAR2	AT2G30950	-1.02	-0.03	-0.24	0.816437	0.877177	-7.22
259684_at	unknown protein	---	AT1G63070	-1.02	-0.03	-0.24	0.816456	0.877177	-7.22
257722_at	putative chloroplast nucleoid DNA-	---	AT3G18490	1.03	0.05	0.24	0.816499	0.877183	-7.22
259369_s_a	hypothetical protein similar to putati	---	AT1G69150	-1.02	-0.03	-0.24	0.816538	0.877184	-7.22
266833_at	hypothetical protein predicted by ge	---	---	1.01	0.02	0.24	0.816769	0.877346	-7.22
263660_at	unknown protein ESTs gb|N65789.	MPI7	AT1G04260	1.02	0.03	0.24	0.8168	0.877346	-7.22
265334_at	putative lipid transfer protein ; supp	---	AT2G18370	1.04	0.06	0.24	0.816805	0.877346	-7.22
256780_at	RNase L inhibitor, putative similar t	ATRLI1	AT3G13640	1.02	0.03	0.24	0.816871	0.877376	-7.22
248056_at	unknown protein ; supported by cD	XYLT	AT5G55500	1.01	0.02	0.24	0.816921	0.877388	-7.22
265311_at	hypothetical protein predicted by ge	---	AT2G20250	1.03	0.05	0.24	0.817056	0.877492	-7.22
249042_at	ethylene-regulated nuclear protein I	---	AT5G44350	1.04	0.06	0.24	0.817201	0.877607	-7.22
252345_at	hypothetical protein	---	AT3G48640	-1.03	-0.04	-0.24	0.81756	0.87795	-7.22
252896_at	cytochrome P450 - like protein cyto	CYP96A9	AT4G39480	1.02	0.02	0.24	0.817624	0.87795	-7.22
253951_at	putative Proline synthetase associa	---	AT4G26860	1.03	0.04	0.24	0.817641	0.87795	-7.22

262469_s_a	hypothetical protein identical to hyp	---	AT1G50190	-1.02	-0.03	-0.24	0.817675	0.87795	-7.22
250732_at	putative protein contains similarity t	---	AT5G06480	-1.03	-0.05	-0.24	0.817863	0.87811	-7.22
259764_at	transcription factor inhibitor I kappa	NPR1	AT1G64280	-1.03	-0.04	-0.24	0.818025	0.878243	-7.22
261744_at	nitrogen fixation protein (nifS), puta	CPNIFS	AT1G08490	-1.02	-0.03	-0.24	0.818107	0.87829	-7.22
247165_at	transcription factor-like protein ; su	MYB68	AT5G65790	-1.02	-0.02	-0.24	0.818176	0.878323	-7.22
254424_at	hypothetical protein ;supported by	---	AT4G21510	1.03	0.05	0.24	0.818216	0.878324	-7.22
255347_at	putative retrotransposon protein	---	---	1.02	0.02	0.24	0.818259	0.878329	-7.22
246147_s_a	26S proteasome AAA-ATPase sub	RPT6A	AT5G19990	1.02	0.03	0.24	0.818495	0.878541	-7.22
247605_at	DNA binding protein - like putative	TCP5	AT5G60970	-1.02	-0.03	-0.24	0.818656	0.878595	-7.22
264815_at	hypothetical protein similar to hypot	---	AT1G03620	-1.04	-0.06	-0.24	0.818684	0.878595	-7.22
248412_at	putative protein contains similarity t	---	AT5G51590	-1.02	-0.03	-0.24	0.818735	0.878595	-7.22
255547_at	putative CHP-rich zinc finger protei	---	AT4G01920	-1.03	-0.04	-0.24	0.818766	0.878595	-7.22
263205_at	Ca2+-dependent lipid-binding prote	NTMC2T2.	AT1G05500	1.02	0.03	0.24	0.81877	0.878595	-7.22
259525_at	hypothetical protein	ATEXPA7	AT1G12560	1.02	0.03	0.24	0.818777	0.878595	-7.22
261255_at	hypothetical protein contains simila	ATNTH2	AT1G05900	-1.02	-0.03	-0.24	0.81886	0.878643	-7.22
260755_at	hypothetical protein predicted by ge	---	AT1G48980	1.02	0.03	0.24	0.818914	0.87865	-7.22
260146_at	putative non-phototropic hypocotyl	---	AT1G52770	1.05	0.07	0.24	0.818944	0.87865	-7.22
257523_at	hypothetical protein similar to putat	---	AT3G01620	-1.02	-0.03	-0.24	0.819059	0.878733	-7.22
263704_at	unknown protein similar to unknow	---	AT1G31130	-1.02	-0.03	-0.24	0.819105	0.878741	-7.22
263388_at	En/Spm-like transposon protein rela	---	---	-1.02	-0.03	-0.24	0.819252	0.878857	-7.22
252582_at	putative protein several hypothetica	---	AT3G45530	1.02	0.03	0.24	0.819346	0.878916	-7.22
263340_at	hypothetical protein predicted by ge	---	---	-1.02	-0.02	-0.24	0.819657	0.879209	-7.22
249382_at	putative protein predicted proteins,	---	AT5G40050	1.02	0.02	0.24	0.819964	0.879466	-7.22
251236_at	putative protein hypothetical protei	---	AT3G62380	1.01	0.02	0.24	0.819974	0.879466	-7.22
252670_at	dnaJ protein homolog atj3 ;support	ATJ3	AT3G44110	1.02	0.03	0.24	0.820132	0.879595	-7.22
250064_at	disease resistance protein - like do	DAR4	AT5G17890	-1.03	-0.04	-0.24	0.820181	0.879606	-7.22
253534_at	cytochrome P450 monooxygenase	CYP83B1	AT4G31500	1.05	0.06	0.24	0.820369	0.879738	-7.22
252910_at	putative protein various predicted p	---	AT4G39590	1.02	0.02	0.24	0.820383	0.879738	-7.22
246884_at	putative protein cation transport pr	---	AT5G26220	1.04	0.06	0.24	0.82042	0.879738	-7.22
251290_at	transcription factor BBFa	DAG1	AT3G61850	-1.02	-0.03	-0.24	0.820608	0.879898	-7.22
249225_at	TMV resistance protein-like	---	AT5G42140	1.03	0.04	0.24	0.820752	0.880011	-7.22
247571_at	snap25a ;supported by full-length c	SNAP33	AT5G61210	1.02	0.02	0.24	0.820998	0.880233	-7.22
259296_at	putative aminopeptidase similar to X	---	AT3G05350	-1.02	-0.03	-0.24	0.821117	0.880292	-7.22
254880_at	putative protein Crp1, Zea mays, A	---	AT4G11690	-1.02	-0.03	-0.24	0.82113	0.880292	-7.22
249137_at	putative protein contains similarity t	---	AT5G43140	1.03	0.04	0.23	0.821256	0.880332	-7.22

250048_s_a	BCS1 - like protein h-bcs1, Homo s	---	AT5G17740	-1.02	-0.03	-0.23	0.821275	0.880332	-7.22
252554_s_a	protein kinase - like receptor-like p	MEE39	AT3G45920	1.02	0.02	0.23	0.821283	0.880332	-7.22
265317_at	unknown protein	BRK1	AT2G22640	-1.02	-0.03	-0.23	0.821876	0.880901	-7.22
263072_at	putative protein kinase contains a p	---	AT2G17530	-1.02	-0.03	-0.23	0.821908	0.880901	-7.22
249175_at	COP8 (constitutive photomorphoge	COP8	AT5G42970	1.02	0.02	0.23	0.82193	0.880901	-7.22
258826_at	putative glucan synthase similar to	ATGSL10	AT3G07160	-1.01	-0.02	-0.23	0.822077	0.880976	-7.22
246146_at	receptor-like protein kinase - like p	---	AT5G20050	1.03	0.04	0.23	0.82209	0.880976	-7.22
249896_at	unknown protein ; supported by cD	---	AT5G22530	1.02	0.03	0.23	0.822115	0.880976	-7.22
266624_s_a	phosphoribosyl pyrophosphate synt	---	AT1G32380	1.04	0.06	0.23	0.82217	0.880992	-7.22
255954_at	hypothetical protein predicted by ge	emb2204	AT1G22090	-1.02	-0.03	-0.23	0.822226	0.880992	-7.22
259447_s_a	ADP-ribosylation factor, putative si	ATARFD1A	AT1G02430	1.02	0.03	0.23	0.822247	0.880992	-7.22
254059_at	Arabidopsis mitochondrion-localize	ATHSP23.6	AT4G25200	-1.02	-0.03	-0.23	0.822346	0.881058	-7.22
251674_at	hypothetical protein	---	AT3G57250	-1.02	-0.03	-0.23	0.822407	0.881059	-7.22
254924_at	MAP kinase (ATMPK5) possible in	ATMPK5	AT4G11330	1.03	0.04	0.23	0.822425	0.881059	-7.22
251424_at	putative protein 04.05.01.01	---	AT3G60560	-1.01	-0.02	-0.23	0.822637	0.881223	-7.22
251287_at	putative protein nucleoid DNA-bind	---	AT3G61820	1.03	0.04	0.23	0.822655	0.881223	-7.22
248803_at	selenium-binding protein-like	---	AT5G47460	1.02	0.03	0.23	0.822979	0.881456	-7.22
254802_at	endoxyloglucan transferase-like pr	---	AT4G13090	-1.02	-0.03	-0.23	0.822988	0.881456	-7.22
250578_at	proanthranilate N-benzoyltransfera	---	AT5G07850	1.02	0.02	0.23	0.823006	0.881456	-7.22
248848_at	disease resistance protein-like	---	AT5G46520	-1.01	-0.02	-0.23	0.823027	0.881456	-7.22
265302_at	Mutator-like transposase similar to	---	---	1.02	0.02	0.23	0.823163	0.88156	-7.22
245536_at	hypothetical protein	SDG2	AT4G15180	-1.02	-0.03	-0.23	0.823337	0.881705	-7.22
255995_at	receptor-like serine/threonine kinas	RKF1	AT1G29750	1.02	0.03	0.23	0.823407	0.881715	-7.22
253332_at	peroxidase ATP17a -like protein pe	---	AT4G33420	1.06	0.08	0.23	0.823424	0.881715	-7.22
260369_at	60S ribosomal protein L34, putative	RPL34	AT1G69620	1.03	0.04	0.23	0.823596	0.881859	-7.22
264051_at	hypothetical protein predicted by ge	---	AT2G22340	-1.02	-0.03	-0.23	0.823643	0.881867	-7.22
250837_at	8-amino-7-oxononanoate synthase	ATBIOF	AT5G04620	1.02	0.03	0.23	0.82403	0.88224	-7.22
252427_at	hypothetical protein	---	AT3G47640	-1.04	-0.06	-0.23	0.824353	0.882545	-7.22
255854_at	unknown protein ;supported by full-	---	AT1G67050	-1.05	-0.07	-0.23	0.824576	0.88273	-7.22
248963_at	unknown protein	---	AT5G45700	1.02	0.03	0.23	0.824604	0.88273	-7.22
256026_at	auxin response factor 1, putative si	---	AT1G34170	-1.02	-0.02	-0.23	0.824795	0.882893	-7.22
AFFX-ThrX-	B. subtilis /GEN=thrB /DB_XREF=g	---	---	1.03	0.05	0.23	0.824899	0.882924	-7.22
259929_at	transcription factor, putative similar	---	AT1G34360	1.02	0.03	0.23	0.82493	0.882924	-7.22
257998_at	hypothetical protein similar to hypot	---	AT3G27510	1.01	0.02	0.23	0.824977	0.882924	-7.22
254998_at	choline kinase GmCK2p -like prote	---	AT4G09760	1.03	0.05	0.23	0.824978	0.882924	-7.22

249468_at	putative protein predicted proteins,	---	AT5G39650	1.02	0.02	0.23	0.825084	0.882996	-7.22
245636_at	hypothetical protein similar to hypot	---	AT1G25240	-1.02	-0.03	-0.23	0.825566	0.88347	-7.22
266427_at	hypothetical protein predicted by ge	---	AT2G07170	-1.02	-0.03	-0.23	0.825635	0.883502	-7.22
255386_at	hypothetical protein	---	AT4G03620	-1.02	-0.02	-0.23	0.825815	0.883653	-7.22
257272_at	unknown protein ; supported by cD	---	AT3G28130	1.02	0.03	0.23	0.825879	0.88368	-7.22
261640_at	permease, putative similar to perm	---	AT1G49960	1.02	0.03	0.23	0.826127	0.883905	-7.22
248483_at	putative protein contains similarity t	---	AT5G50990	-1.03	-0.04	-0.23	0.826223	0.883966	-7.22
255807_at	probable wound-induced protein w	---	AT4G10270	-1.01	-0.02	-0.23	0.826419	0.884086	-7.22
259886_at	putative protein kinase similar to pr	---	AT1G76370	-1.02	-0.02	-0.23	0.82645	0.884086	-7.22
248332_at	heat-shock protein ; supported by c	ATHSP90.1	AT5G52640	1.08	0.11	0.23	0.826452	0.884086	-7.22
262896_at	chromaffin granule ATPase II hom	ALA3	AT1G59820	-1.02	-0.03	-0.23	0.826546	0.884145	-7.22
254973_at	putative retrotransposon Oryza aus	---	---	-1.02	-0.03	-0.23	0.826851	0.88443	-7.22
263849_at	putative retroelement pol polyprotei	---	---	-1.02	-0.03	-0.23	0.826905	0.884447	-7.22
264739_at	hypothetical protein predicted by ge	---	AT1G62260	-1.02	-0.03	-0.23	0.826956	0.88446	-7.22
247562_at	putative protein	---	AT5G61120	-1.02	-0.02	-0.23	0.827043	0.884511	-7.22
253806_at	putative protein Arabidopsis thalian	---	AT4G28270	-1.02	-0.03	-0.23	0.827083	0.884512	-7.22
249206_at	putative protein similar to unknown	ATS	AT5G42630	1.02	0.03	0.23	0.827318	0.884723	-7.22
246975_at	putative protein hypothetical protein	---	AT5G24890	-1.02	-0.04	-0.23	0.827472	0.884846	-7.22
258749_at	hypothetical protein predicted by ge	---	AT3G05760	-1.02	-0.03	-0.23	0.827654	0.884999	-7.22
261033_at	unknown protein ;supported by full-	JAZ5	AT1G17380	1.07	0.10	0.23	0.827706	0.885013	-7.22
246241_at	patatin-like protein	PLP4	AT4G37050	-1.02	-0.03	-0.23	0.827919	0.885143	-7.22
248780_at	4-nitrophenylphosphatase-like prote	ATPGLP2	AT5G47760	1.02	0.03	0.23	0.82795	0.885143	-7.22
265755_at	En/Spm transposon hypothetical pr	---	---	-1.02	-0.02	-0.23	0.827961	0.885143	-7.22
257778_at	hypothetical protein predicted by ge	---	---	-1.02	-0.03	-0.23	0.827983	0.885143	-7.22
261288_at	hypothetical protein predicted by ge	---	AT1G37010	1.02	0.03	0.23	0.828022	0.885143	-7.22
254528_at	hypothetical protein	---	AT4G19620	-1.02	-0.02	-0.23	0.828314	0.885376	-7.22
248443_at	gibberellin 20-oxidase-like protein	---	AT5G51310	1.02	0.02	0.23	0.828333	0.885376	-7.22
256515_at	terpene synthase, putative contains	---	AT1G66020	-1.02	-0.03	-0.23	0.828357	0.885376	-7.22
256796_at	hypothetical protein predicted by ge	---	AT3G22210	-1.03	-0.04	-0.23	0.82857	0.885562	-7.22
253223_at	L-ascorbate peroxidase ;supported	APX3	AT4G35000	1.02	0.02	0.22	0.828786	0.885752	-7.22
245173_at	putative AP2 domain transcription f	---	AT2G47520	-1.05	-0.06	-0.22	0.828917	0.88585	-7.22
252889_at	hypothetical protein	---	AT4G39380	-1.02	-0.03	-0.22	0.828962	0.885857	-7.22
251044_at	putative protein various predicted p	---	AT5G02350	-1.02	-0.02	-0.22	0.829011	0.885868	-7.22
251972_at	nodulin / glutamate-ammonia ligas	---	AT3G53170	-1.02	-0.03	-0.22	0.829625	0.886483	-7.22
255694_at	putative transcriptional regulator	UNE10	AT4G00050	1.02	0.03	0.22	0.829832	0.886663	-7.22

265624_at	CLAVATA3 CLE family of proteins;	CLV3	AT2G27250	1.02	0.03	0.22	0.829897	0.886682	-7.22
253168_at	putative protein various predicted p	---	AT4G35070	1.04	0.05	0.22	0.829965	0.886682	-7.22
250821_at	putative protein similar to unknown	---	AT5G05190	-1.02	-0.03	-0.22	0.829967	0.886682	-7.22
264759_at	receptor protein kinase (IRK1), put	---	AT1G61480	1.02	0.03	0.22	0.830331	0.886996	-7.22
250086_at	NAM (no apical meristem)-like prote	anac086	AT5G17260	-1.02	-0.03	-0.22	0.830347	0.886996	-7.22
266245_at	putative translation initiation factor I	---	AT2G27700	1.02	0.03	0.22	0.830377	0.886996	-7.22
256884_at	hypothetical protein contains Pfam	---	AT3G15200	1.03	0.04	0.22	0.830488	0.887072	-7.22
252628_at	putative protein	---	AT3G44960	1.01	0.02	0.22	0.830625	0.887177	-7.22
254136_at	putative protein various predicted p	---	AT4G24860	-1.02	-0.02	-0.22	0.830702	0.887186	-7.22
259907_at	GCN4-complementing protein, puta	AGD2	AT1G60860	1.03	0.05	0.22	0.830711	0.887186	-7.22
250035_at	putative protein contains similarity t	---	AT5G18230	1.02	0.02	0.22	0.830883	0.887328	-7.22
254367_at	hypothetical protein	---	AT4G21700	-1.02	-0.03	-0.22	0.831098	0.887476	-7.22
247348_at	beta-galactosidase (emb CAB6474(	BGAL10	AT5G63810	1.02	0.03	0.22	0.831099	0.887476	-7.22
260571_at	MAP kinase (ATMPK6) identical to	ATMPK6	AT2G43790	-1.02	-0.02	-0.22	0.831158	0.887497	-7.22
265562_at	hypothetical protein predicted by ge	---	AT2G05500	-1.01	-0.02	-0.22	0.831218	0.88752	-7.22
260298_at	putative oxidoreductase contains P	---	AT1G80320	1.02	0.02	0.22	0.831334	0.887601	-7.22
263884_at	hypothetical protein predicted by ge	---	AT2G36920	1.01	0.02	0.22	0.831689	0.887926	-7.22
245109_at	hypothetical protein predicted by ge	---	AT2G41520	1.02	0.03	0.22	0.831726	0.887926	-7.22
261161_at	hypothetical protein contains Pfam	---	AT1G34420	1.03	0.04	0.22	0.831755	0.887926	-7.22
254297_at	hypothetical protein	---	AT4G23110	1.01	0.02	0.22	0.831889	0.888028	-7.22
261690_at	branched-chain amino acid aminot	---	AT1G50090	1.02	0.02	0.22	0.832168	0.888285	-7.22
267243_at	hypothetical protein predicted by ge	---	AT2G02660	-1.01	-0.02	-0.22	0.832213	0.888291	-7.22
264831_at	hypothetical protein predicted by ge	---	AT1G03687	1.02	0.03	0.22	0.832341	0.888351	-7.22
249548_at	lipid transfer - like protein lipid trans	---	AT5G38170	1.02	0.02	0.22	0.832372	0.888351	-7.22
249714_at	unknown protein	---	---	-1.02	-0.03	-0.22	0.832386	0.888351	-7.22
245049_at	ribosomal protein S16	---	---	-1.03	-0.04	-0.22	0.832458	0.888386	-7.22
262239_at	unknown protein similar to putative	---	AT1G48230	-1.03	-0.04	-0.22	0.832522	0.888412	-7.22
257936_at	hypothetical protein contains simila	---	---	1.02	0.03	0.22	0.832642	0.8885	-7.22
259261_at	unknown protein similar to unknown	---	AT3G11390	-1.02	-0.03	-0.22	0.832906	0.888739	-7.22
266998_at	hypothetical protein predicted by ge	---	AT2G34400	1.02	0.03	0.22	0.833077	0.88888	-7.22
253211_at	amidase - like protein amidase, Ba	---	AT4G34880	1.02	0.02	0.22	0.833253	0.889027	-7.22
266621_at	unknown protein	---	AT2G35450	1.03	0.04	0.22	0.833421	0.889164	-7.22
258191_at	putative vesicle transport protein sir	VTI13	AT3G29100	-1.01	-0.02	-0.22	0.833501	0.889208	-7.22
264237_at	hypothetical protein predicted by ge	---	AT1G54700	-1.01	-0.02	-0.22	0.833735	0.889416	-7.22
255932_at	mutator-like transposase, putative	---	---	-1.02	-0.02	-0.22	0.833799	0.889443	-7.22

248090_at	putative protein contains similarity t	MAPKKK15	AT5G55090	-1.01	-0.02	-0.22	0.83384	0.889444	-7.22
250032_at	glutamate dehydrogenase (EC 1.4.	GDH1	AT5G18170	1.06	0.08	0.22	0.833965	0.889499	-7.22
252325_at	acetolactate synthase ; supported	CSR1	AT3G48560	-1.01	-0.02	-0.22	0.833991	0.889499	-7.22
253499_at	putative protein zinc-finger helicase	---	AT4G31900	-1.02	-0.02	-0.22	0.834008	0.889499	-7.22
258913_at	unknown protein similar to putative	---	AT3G06450	1.02	0.04	0.22	0.834268	0.889735	-7.22
261716_at	kinesin-related protein, putative sin	---	AT1G18410	1.01	0.02	0.22	0.834396	0.889829	-7.22
250620_at	embryo-specific protein 3 (ATS3) ;	ATS3	AT5G07190	-1.02	-0.02	-0.22	0.834646	0.890033	-7.22
249916_at	histone H2B like protein (emb|CAA	HTB2	AT5G22880	1.03	0.04	0.22	0.834664	0.890033	-7.22
258310_at	unknown protein	ICE1	AT3G26744	-1.02	-0.03	-0.22	0.834802	0.890138	-7.22
249182_at	putative protein similar to unknown	---	AT5G42960	-1.02	-0.02	-0.22	0.834853	0.890151	-7.22
259574_at	hypothetical protein	MLP168	AT1G35310	1.01	0.02	0.22	0.834993	0.890219	-7.22
264369_at	Ste-20 related kinase SPAK, putati	---	AT1G70430	-1.02	-0.03	-0.22	0.834995	0.890219	-7.22
252684_at	disease resistence - like protein RF	---	AT3G44400	1.02	0.02	0.22	0.835059	0.890222	-7.22
265134_at	putative acyl-CoA : 1-acylglycerol-3	LPAT3	AT1G51260	-1.02	-0.04	-0.22	0.835076	0.890222	-7.22
256086_at	hypothetical protein predicted by ge	---	AT1G20770	1.02	0.03	0.22	0.835116	0.890223	-7.22
255023_at	hypothetical protein	---	AT4G09850	1.02	0.03	0.22	0.835379	0.890437	-7.22
245203_at	hypothetical protein similar to protei	---	---	-1.01	-0.02	-0.22	0.835394	0.890437	-7.22
249893_at	Expressed protein ; supported by fu	---	AT5G22555	1.02	0.03	0.22	0.835911	0.890946	-7.22
255769_at	hypothetical protein predicted by ge	---	AT1G18610	1.02	0.02	0.22	0.836029	0.890992	-7.22
245538_at	p140mDia like protein	---	AT4G15200	1.02	0.03	0.22	0.836068	0.890992	-7.22
246805_at	putative protein various predicted t	AGL101	AT5G27050	-1.02	-0.02	-0.22	0.836071	0.890992	-7.22
254766_at	putative protein predicted protein, A	TPS12	AT4G13280	1.01	0.02	0.21	0.836251	0.891141	-7.22
257292_s_a	hypothetical protein contains Pfam	---	---	1.01	0.02	0.21	0.836354	0.891209	-7.22
260649_at	storage protein, putative similar to	ACA7	AT1G08080	-1.02	-0.02	-0.21	0.83641	0.891228	-7.22
251165_at	putative protein different MAP kinas	---	AT3G63330	1.02	0.03	0.21	0.83645	0.891229	-7.22
258571_at	hypothetical protein predicted by ge	anac048	AT3G04420	-1.02	-0.03	-0.21	0.83657	0.891274	-7.22
255401_at	hypothetical protein ;supported by	---	AT4G03600	1.02	0.03	0.21	0.836571	0.891274	-7.22
252373_at	disease resistance protein EDS1 ;	EDS1	AT3G48090	-1.05	-0.08	-0.21	0.836727	0.891399	-7.22
249706_at	histone deacetylase	HDA7	AT5G35600	-1.02	-0.02	-0.21	0.836868	0.891508	-7.22
254169_at	putative protein ; supported by cDN	---	AT4G24290	-1.02	-0.03	-0.21	0.836957	0.891561	-7.22
255747_s_a	hypothetical protein predicted by ge	---	AT1G32010	-1.02	-0.02	-0.21	0.837407	0.891975	-7.22
248661_at	putative protein contains similarity t	AGL80	AT5G48670	1.03	0.04	0.21	0.837424	0.891975	-7.22
246716_s_a	putative protein	---	AT5G28910	-1.01	-0.02	-0.21	0.837818	0.892353	-7.22
248144_at	glucose-6-phosphate/phosphate tra	GPT1	AT5G54800	-1.02	-0.03	-0.21	0.837949	0.892433	-7.22
250879_at	putative protein various predicted p	---	AT5G04060	-1.02	-0.03	-0.21	0.837972	0.892433	-7.22

246797_at	putative protein ;supported by full-l	---	AT5G26790	-1.01	-0.02	-0.21	0.83809	0.892518	-7.22
247085_at	kinesin heavy chain DNA binding pr	---	AT5G66310	-1.02	-0.03	-0.21	0.838196	0.892551	-7.22
246222_at	TINY-like protein ; supported by cD	RAP2.10	AT4G36900	-1.04	-0.05	-0.21	0.8382	0.892551	-7.22
256850_at	hypothetical protein similar to hypot	---	---	1.01	0.02	0.21	0.838404	0.892693	-7.22
257482_x_a	hypothetical protein contains simila	---	AT1G27820	-1.02	-0.04	-0.21	0.83845	0.892693	-7.22
261647_at	hypothetical protein similar to hypot	---	AT1G27740	-1.02	-0.03	-0.21	0.838451	0.892693	-7.22
252729_at	putative protein replication protein	---	---	-1.01	-0.02	-0.21	0.838537	0.892744	-7.22
257662_at	low affinity calcium antiporter CAX	CAX2	AT3G13320	-1.02	-0.02	-0.21	0.838787	0.892968	-7.22
257555_at	hypothetical protein predicted by ge	---	AT3G24780	1.02	0.03	0.21	0.839308	0.893423	-7.22
253521_at	multicatalytic endopeptidase comp	PBA1	AT4G31300	1.03	0.04	0.21	0.839318	0.893423	-7.22
255119_at	hypothetical protein	---	---	1.01	0.02	0.21	0.839332	0.893423	-7.22
256178_s_a	auxin conjugate hydrolase (ILL5) id	ILL5	AT1G51760	1.06	0.08	0.21	0.839518	0.89358	-7.22
264247_at	potassium transporter, putative sim	---	AT1G60160	-1.04	-0.05	-0.21	0.839628	0.893654	-7.22
247340_at	unknown protein	---	AT5G63700	-1.01	-0.02	-0.21	0.839701	0.89369	-7.22
257181_at	hypothetical protein	---	AT3G13190	1.02	0.03	0.21	0.840178	0.894157	-7.22
261258_at	unknown protein	---	AT1G26640	-1.02	-0.03	-0.21	0.840409	0.894361	-7.22
247500_at	putative protein B2 protein, Daucus	---	AT5G61910	1.03	0.04	0.21	0.84059	0.894477	-7.22
266008_at	hypothetical protein predicted by ge	---	AT2G37390	-1.02	-0.03	-0.21	0.840597	0.894477	-7.22
246431_at	calcium-binding protein calcium bir	APC1	AT5G17480	-1.01	-0.02	-0.21	0.840697	0.894543	-7.22
254657_s_a	putative protein W15DMY32F, W2	---	AT4G18210	-1.03	-0.05	-0.21	0.840917	0.894735	-7.22
246299_at	embryonic abundant protein AtEm1	EM1	AT3G51810	-1.01	-0.02	-0.21	0.841039	0.894823	-7.22
260475_at	Serine carboxypeptidase isolog	scpl31	AT1G11080	-1.04	-0.05	-0.21	0.841125	0.894831	-7.22
259575_at	unknown protein	---	AT1G35320	-1.01	-0.02	-0.21	0.841125	0.894831	-7.22
245462_at	transcription factor like protein	---	AT4G17020	-1.02	-0.03	-0.21	0.84145	0.895135	-7.22
263747_at	putative ubiquitin activating enzyme	SAE2	AT2G21470	-1.01	-0.02	-0.21	0.841606	0.895253	-7.22
264758_at	late embryogenesis abundant prote	---	AT1G61340	-1.08	-0.12	-0.21	0.841703	0.895253	-7.22
259021_at	hypothetical protein predicted by ge	---	AT3G07540	-1.03	-0.05	-0.21	0.84171	0.895253	-7.22
252992_at	putative protein phosphatase-2c pr	---	AT4G38520	-1.03	-0.04	-0.21	0.841719	0.895253	-7.22
266095_at	3-oxo-5-alpha-steroid 4-dehydroge	DET2	AT2G38050	1.02	0.03	0.21	0.841859	0.89536	-7.22
253398_at	putative protein retinal pigment mic	CCD8	AT4G32810	1.04	0.06	0.21	0.841927	0.895368	-7.22
253655_at	Expressed protein ;supported by cD	LCR59	AT4G30070	1.01	0.02	0.21	0.841944	0.895368	-7.22
267221_at	similar to prokaryotic DNA polymera	STI	AT2G02480	1.01	0.02	0.21	0.842268	0.89567	-7.22
253214_at	putative protein karyopherin alpha	ARO1	AT4G34940	1.02	0.02	0.21	0.842391	0.89576	-7.22
264814_at	putative SET-domain transcriptiona	SDG37	AT2G17900	1.02	0.03	0.21	0.842465	0.895797	-7.22
257186_at	hypothetical protein predicted by ge	---	AT3G13130	-1.02	-0.03	-0.21	0.84288	0.896196	-7.22

246646_at	putative protein ;supported by full-l	---	AT5G35090	1.02	0.02	0.21	0.842932	0.896209	-7.22
246089_at	ring-box protein - like ring-box prot	RBX1	AT5G20570	-1.01	-0.02	-0.21	0.842996	0.896236	-7.22
262553_at	hypothetical protein similar to hypot	RECQL2	AT1G31360	-1.02	-0.03	-0.21	0.843115	0.89632	-7.22
247091_at	peroxidase (emb CAA66964.1)	---	AT5G66390	1.02	0.03	0.21	0.84335	0.896528	-7.22
265975_at	putative citrate synthetase	---	AT2G11270	-1.02	-0.03	-0.21	0.84361	0.896748	-7.22
252074_at	putative protein DNA helicase hom	---	AT3G51700	1.02	0.02	0.20	0.843705	0.896748	-7.22
248214_at	putative protein similar to unknown	---	AT5G53670	-1.02	-0.03	-0.20	0.843708	0.896748	-7.22
253123_at	thaumatin-like protein thaumatin-lik	---	AT4G36000	-1.02	-0.03	-0.20	0.843713	0.896748	-7.22
252687_at	putative protein predicted protein, /	---	---	-1.02	-0.03	-0.20	0.843897	0.896901	-7.23
265191_at	hypothetical protein Similar to Sacc	---	AT1G05120	-1.02	-0.02	-0.20	0.843972	0.896904	-7.23
257258_at	hypothetical protein contains Pfam	---	AT3G22040	1.02	0.03	0.20	0.843978	0.896904	-7.23
249418_at	putative protein predicted protein, /	---	AT5G39785	-1.01	-0.02	-0.20	0.844131	0.897024	-7.23
256004_at	retroelement pol polyprotein, putati	---	---	-1.01	-0.02	-0.20	0.844379	0.897216	-7.23
247672_at	senescence-associated protein - lik	TET4	AT5G60220	-1.01	-0.02	-0.20	0.84439	0.897216	-7.23
254279_at	Expressed protein ; supported by fu	---	AT4G22750	-1.02	-0.02	-0.20	0.844487	0.897238	-7.23
245271_at	transcription factor like protein ; sup	---	AT4G16430	1.01	0.02	0.20	0.844495	0.897238	-7.23
245556_at	HSR201 like protein	---	AT4G15400	-1.01	-0.02	-0.20	0.844528	0.897238	-7.23
250407_at	chorismate mutase CM2 ; supporte	ATCM2	AT5G10870	1.02	0.02	0.20	0.844661	0.897336	-7.23
258248_at	hypothetical protein predicted by ge	---	AT3G29140	1.02	0.04	0.20	0.844965	0.897618	-7.23
246406_at	disease resistance protein RPP1-W	---	AT1G57650	-1.01	-0.02	-0.20	0.845035	0.897651	-7.23
247272_at	GTP cyclohydrolase II; 3,4-dihydro	---	AT5G14040	1.04	0.06	0.20	0.845081	0.897657	-7.23
267642_at	unknown protein	---	AT2G32905	1.01	0.02	0.20	0.845144	0.897683	-7.23
263604_s_a	putative replication protein A1	---	---	1.01	0.02	0.20	0.845205	0.897695	-7.23
261497_x_a	hypothetical protein contains simila	AGL59	AT1G28460	1.02	0.02	0.20	0.845235	0.897695	-7.23
264762_at	receptor kinase, putative similar to	---	AT1G61460	1.02	0.03	0.20	0.845516	0.897953	-7.23
266617_at	unknown protein ; supported by cD	---	AT2G29670	-1.04	-0.05	-0.20	0.845567	0.897965	-7.23
248560_at	putative protein contains similarity t	ATPPOX	AT5G49970	1.02	0.03	0.20	0.84592	0.898279	-7.23
246547_at	seed maturation -like protein seed	---	AT5G14970	-1.02	-0.03	-0.20	0.845942	0.898279	-7.23
256977_at	hypothetical protein predicted by g	---	---	-1.02	-0.02	-0.20	0.846031	0.898332	-7.23
254409_at	serine/threonine protein kinase - lik	---	AT4G21400	1.06	0.08	0.20	0.846099	0.89834	-7.23
260018_at	hypothetical protein predicted by ge	---	AT1G41820	-1.02	-0.02	-0.20	0.846117	0.89834	-7.23
247598_at	UVB-resistance protein UVR8 - like	---	AT5G60870	1.02	0.02	0.20	0.846436	0.898522	-7.23
266691_at	hypothetical protein predicted by ge	---	AT2G19890	-1.02	-0.03	-0.20	0.846442	0.898522	-7.23
260739_at	serine carboxypeptidase precursor	scpl50	AT1G15000	1.03	0.05	0.20	0.846458	0.898522	-7.23
256034_at	unknown protein ; supported by cDI	---	AT1G07080	1.01	0.02	0.20	0.84647	0.898522	-7.23

262689_at	unknown protein	ANAC026	AT1G62700	1.02	0.02	0.20	0.846509	0.898522	-7.23
245651_s_a	F5A9.18 unknown protein; similar t	---	AT1G24793	-1.02	-0.03	-0.20	0.846525	0.898522	-7.23
256323_at	unknown protein ; supported by cDI	---	AT1G54920	1.02	0.03	0.20	0.846749	0.898718	-7.23
264411_at	mutator-like transposase, putative	---	---	1.01	0.02	0.20	0.846796	0.898726	-7.23
247956_at	cytokinin oxidase ; supported by cI	CKX3	AT5G56970	1.02	0.02	0.20	0.846979	0.898878	-7.23
255157_at	hypothetical protein	---	---	-1.01	-0.02	-0.20	0.847018	0.898878	-7.23
247697_at	subtilisin-like protease - like protein	SBT5.4	AT5G59810	1.02	0.03	0.20	0.847319	0.899155	-7.23
254567_s_a	hypothetical protein	---	AT4G19260	-1.01	-0.02	-0.20	0.847419	0.89922	-7.23
266110_at	putative C2H2-type zinc finger prote	AtIDD4	AT2G02080	-1.02	-0.02	-0.20	0.847707	0.899483	-7.23
249517_at	putative protein similar to unknown	---	AT5G38580	1.01	0.02	0.20	0.847808	0.899549	-7.23
251095_at	putative protein hypothetical protei	---	AT5G01510	-1.02	-0.03	-0.20	0.848074	0.899766	-7.23
266729_at	50S ribosomal protein L7/L12	---	AT2G03130	-1.02	-0.02	-0.20	0.848092	0.899766	-7.23
262296_at	putative cyclin similar to cyclin GB:4	CYCT1;3	AT1G27630	1.01	0.02	0.20	0.848215	0.899855	-7.23
258361_at	unknown protein similar to hypothet	---	AT3G14270	-1.03	-0.04	-0.20	0.848356	0.899963	-7.23
262519_at	putative ribokinase Except for first	---	AT1G17160	1.03	0.04	0.20	0.848419	0.899988	-7.23
245409_at	putative protein	---	AT4G17200	-1.01	-0.02	-0.20	0.848652	0.900193	-7.23
263331_at	unknown protein ; supported by cD	---	AT2G15270	-1.02	-0.02	-0.20	0.84872	0.900224	-7.23
258382_at	hypothetical protein	UBC25	AT3G15355	-1.02	-0.03	-0.20	0.848949	0.900424	-7.23
262597_at	unknown protein Strong similarity t	---	AT1G15470	-1.02	-0.03	-0.20	0.849095	0.900538	-7.23
248017_at	protein kinase-like protein	---	AT5G56460	1.03	0.04	0.20	0.849378	0.900795	-7.23
265536_at	unknown protein contains a domain	---	AT2G15880	-1.04	-0.05	-0.20	0.849761	0.90116	-7.23
262816_at	alkylation repair-like protein	---	AT1G11780	-1.02	-0.03	-0.20	0.849911	0.901277	-7.23
258724_at	unknown protein	---	AT3G09600	1.01	0.02	0.20	0.850062	0.901395	-7.23
263029_at	unknown protein	---	AT1G24050	1.01	0.02	0.20	0.850151	0.901448	-7.23
254939_at	putative protein predicted proteins,	---	AT4G10800	-1.02	-0.03	-0.20	0.850288	0.901552	-7.23
252083_at	putative protein hypothetical protei	---	AT3G51960	1.04	0.05	0.20	0.850546	0.901783	-7.23
267145_at	putative acetyltransferase	ATMAK3	AT2G38130	-1.02	-0.02	-0.20	0.850743	0.90195	-7.23
252027_at	Spot 3 protein and vacuolar sorting	VSR1	AT3G52850	1.01	0.02	0.20	0.851047	0.90223	-7.23
248734_at	putative protein similar to unknown	ELP1	AT5G48090	-1.02	-0.03	-0.19	0.851195	0.902345	-7.23
261723_at	unknown protein ; supported by full-	---	AT1G76200	-1.01	-0.02	-0.19	0.851293	0.902378	-7.23
252270_at	putative protein ;supported by full-l	---	AT3G49560	-1.02	-0.03	-0.19	0.851305	0.902378	-7.23
266169_at	putative protease inhibitor ;support	---	AT2G38900	1.01	0.02	0.19	0.85143	0.902434	-7.23
254487_at	calcium-binding protein - like calciu	---	AT4G20780	-1.06	-0.09	-0.19	0.851437	0.902434	-7.23
266058_at	glycerol-3-phosphate dehydrogenas	GLY1	AT2G40690	1.02	0.03	0.19	0.851533	0.902494	-7.23
248847_at	disease resistance protein-like	---	AT5G46510	-1.01	-0.02	-0.19	0.851573	0.902495	-7.23

255331_at	hypothetical protein ; supported by	---	AT4G04330	1.02	0.02	0.19	0.851746	0.902635	-7.23
252347_at	ribosomal protein L13 homolog ribo	---	AT3G48130	1.02	0.02	0.19	0.851932	0.90279	-7.23
267052_at	unknown protein	---	AT2G38410	-1.02	-0.02	-0.19	0.851992	0.902812	-7.23
246636_at	acid phosphatase-like protein purp	PAP26	AT5G34850	1.02	0.03	0.19	0.852218	0.902975	-7.23
255388_at	hypothetical protein similar to A. th	---	---	-1.01	-0.02	-0.19	0.852225	0.902975	-7.23
260270_at	putative disease resistance protein	---	AT1G63730	1.02	0.02	0.19	0.852993	0.903747	-7.23
254642_at	putative protein hypothetical protei	---	AT4G18810	-1.03	-0.04	-0.19	0.853047	0.903763	-7.23
253960_at	putative protein various predicted p	GAMT1	AT4G26420	-1.02	-0.03	-0.19	0.853168	0.903849	-7.23
256758_at	hypothetical protein similar to Athila	---	---	1.02	0.02	0.19	0.853315	0.903962	-7.23
266843_at	hypothetical protein predicted by ge	---	AT2G26135	1.01	0.02	0.19	0.85348	0.904088	-7.23
255334_at	putative transposon protein	---	---	-1.01	-0.02	-0.19	0.853513	0.904088	-7.23
247341_at	unknown protein	---	AT5G63720	-1.01	-0.02	-0.19	0.853761	0.904302	-7.23
263458_at	putative GTP-binding protein	ATRABH1D	AT2G22290	-1.02	-0.02	-0.19	0.853826	0.904302	-7.23
255513_at	PROLIFERA similar to S. cerevisiae	PRL	AT4G02060	-1.07	-0.09	-0.19	0.853846	0.904302	-7.23
261642_at	ADP-glucose pyrophosphorylase, p	APL2	AT1G27680	1.02	0.03	0.19	0.853874	0.904302	-7.23
259954_at	cytochrome P450, putative similar	CYP721A1	AT1G75130	1.02	0.03	0.19	0.853995	0.904389	-7.23
248660_at	RNA-binding protein-like	---	AT5G48650	1.02	0.03	0.19	0.854398	0.90477	-7.23
267217_at	hypothetical protein	---	AT2G02610	-1.01	-0.02	-0.19	0.854434	0.90477	-7.23
247352_at	serine/threonine-protein kinase ;su	SNRK2.5	AT5G63650	-1.04	-0.06	-0.19	0.85468	0.904988	-7.23
249488_at	putative protein putative transposa	---	---	-1.01	-0.02	-0.19	0.854739	0.905008	-7.23
255377_at	hypothetical protein	---	AT4G03500	-1.02	-0.03	-0.19	0.854859	0.905094	-7.23
248628_at	putative protein contains similarity t	---	AT5G48960	1.02	0.02	0.19	0.855485	0.905631	-7.23
264754_at	receptor kinase, putative similar to	---	AT1G61400	1.02	0.02	0.19	0.855487	0.905631	-7.23
253173_at	putative protein pEARLI 4, Arabido	---	AT4G35110	-1.05	-0.06	-0.19	0.855498	0.905631	-7.23
259095_at	acyl carrier protein 1 precursor (AC	ACP1	AT3G05020	1.04	0.05	0.19	0.855526	0.905631	-7.23
258373_at	20S proteasome subunit PAE2 iden	PAE2	AT3G14290	-1.01	-0.02	-0.19	0.855595	0.905639	-7.23
258784_at	unknown protein	---	AT3G11770	1.03	0.04	0.19	0.855627	0.905639	-7.23
252051_at	putative protein similarity hypotheti	---	AT3G52570	1.01	0.02	0.19	0.855652	0.905639	-7.23
252697_at	nodulin - like protein nodulin-21, G	---	AT3G43660	1.02	0.02	0.19	0.856053	0.906021	-7.23
259814_at	zinc finger protein ATZF1, putative	---	AT1G49900	-1.03	-0.04	-0.19	0.856192	0.906126	-7.23
250979_at	putative protein	---	AT5G03090	-1.02	-0.03	-0.19	0.856236	0.906131	-7.23
248891_at	MCM3 homolog (emb|CAA03887.1	MCM3	AT5G46280	1.06	0.09	0.19	0.856399	0.906261	-7.23
248441_at	putative protein contains similarity t	---	AT5G51270	-1.01	-0.02	-0.19	0.856451	0.906274	-7.23
262692_at	hypothetical protein predicted by ge	---	---	-1.02	-0.02	-0.19	0.856677	0.906471	-7.23
266987_at	unknown protein	---	AT2G39280	-1.01	-0.02	-0.19	0.856984	0.906754	-7.23

245464_at	hypothetical protein	UGLYAH	AT4G17050	-1.02	-0.03	-0.19	0.857299	0.907045	-7.23
259776_s_a	eukaryotic translation initiation fact	---	AT1G29550	-1.01	-0.02	-0.19	0.857468	0.907182	-7.23
261967_at	En/Spm-like transposon protein, pu	---	---	-1.02	-0.03	-0.19	0.857522	0.907198	-7.23
246037_at	putative protein predicted chromos	---	AT5G19420	1.02	0.02	0.19	0.857563	0.907199	-7.23
244958_at	hypothetical protein	---	---	-1.01	-0.02	-0.19	0.857633	0.907231	-7.23
260893_at	hypothetical protein similar to hypot	---	AT1G29180	-1.01	-0.02	-0.19	0.857842	0.907378	-7.23
244908_at	hypothetical protein	---	---	-1.02	-0.04	-0.19	0.857911	0.907378	-7.23
263734_at	permease, putative similar to perm	NAT7	AT1G60030	-1.02	-0.03	-0.19	0.857919	0.907378	-7.23
255555_at	putative protein transport factor ; su	---	AT4G01810	1.02	0.02	0.19	0.857932	0.907378	-7.23
264091_at	hypothetical protein predicted by ge	---	AT1G79110	1.04	0.05	0.19	0.857989	0.90738	-7.23
266446_at	hypothetical protein predicted by ge	---	AT2G43310	-1.01	-0.02	-0.19	0.858013	0.90738	-7.23
255160_at	putative pathogenesis-related prote	---	AT4G07820	-1.01	-0.02	-0.19	0.858057	0.907384	-7.23
264331_at	hypothetical protein contains non-c	---	AT1G04130	1.02	0.02	0.19	0.858118	0.907407	-7.23
249730_at	calcium dependent protein kinase-li	---	AT5G24430	-1.03	-0.04	-0.19	0.858225	0.907419	-7.23
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb	---	---	-1.03	-0.04	-0.19	0.858247	0.907419	-7.23
245603_at	hypothetical protein	---	AT4G14280	1.02	0.02	0.19	0.8583	0.907419	-7.23
253067_at	myb transcription factor - like protei	MYB87	AT4G37780	-1.01	-0.02	-0.19	0.858301	0.907419	-7.23
257510_at	unknown protein	---	AT1G55360	1.04	0.06	0.19	0.858329	0.907419	-7.23
256813_at	unknown protein	---	AT3G21360	-1.02	-0.02	-0.19	0.858569	0.907631	-7.23
254941_s_a	putative protein various reverse tran	---	---	1.02	0.02	0.18	0.858729	0.907758	-7.23
255972_at	hypothetical protein similar to hypot	---	---	1.01	0.02	0.18	0.858796	0.907788	-7.23
249046_at	berberine bridge enzyme	---	AT5G44400	-1.03	-0.04	-0.18	0.859051	0.908015	-7.23
255067_at	putative phosphotyrosyl phosphatas	---	AT4G08960	1.01	0.02	0.18	0.859128	0.908054	-7.23
245566_at	disease resistance RPS2 like protei	---	AT4G14610	1.02	0.02	0.18	0.859243	0.908066	-7.23
263312_at	putative replication protein A1	---	---	-1.01	-0.02	-0.18	0.859248	0.908066	-7.23
257049_at	hypothetical protein predicted by ge	---	AT3G15250	1.02	0.03	0.18	0.859259	0.908066	-7.23
259275_at	unknown protin ;supported by full-l	---	AT3G01060	-1.03	-0.04	-0.18	0.859316	0.908084	-7.23
249364_at	putative protein predicted protein, A	---	AT5G40590	-1.01	-0.02	-0.18	0.859683	0.908352	-7.23
248658_at	chromosome condensation protein	ATSMC3	AT5G48600	-1.01	-0.02	-0.18	0.859692	0.908352	-7.23
260071_at	putative proline-rich protein precurs	ESP1	AT1G73840	1.01	0.02	0.18	0.859726	0.908352	-7.23
253259_at	putative protein ethylene-responsiv	RRTF1	AT4G34410	1.05	0.07	0.18	0.859728	0.908352	-7.23
250324_at	putative protein nitrilase/Fhit protei	---	AT5G12040	1.02	0.03	0.18	0.859793	0.908378	-7.23
263655_at	hypothetical protein predicted by ge	---	AT1G04500	1.01	0.02	0.18	0.859862	0.908409	-7.23
254471_s_a	putative protein parts of other prote	---	---	1.01	0.02	0.18	0.860221	0.908746	-7.23
245596_at	hypothetical protein	AtPRD1	AT4G14180	1.01	0.02	0.18	0.860346	0.908806	-7.23

252639_at	acyl CoA reductase -like protein ac	FAR5	AT3G44550	1.01	0.02	0.18	0.860358	0.908806	-7.23
252738_at	putative protein predicted protein, I	---	AT3G43240	-1.01	-0.02	-0.18	0.860727	0.909154	-7.23
252497_at	putative protein several putative pro	---	AT3G46800	-1.01	-0.02	-0.18	0.861007	0.909408	-7.23
254152_at	hypothetical protein	---	AT4G24410	1.01	0.02	0.18	0.861073	0.909435	-7.23
267071_at	unknown protein	---	AT2G40980	-1.01	-0.02	-0.18	0.861241	0.909554	-7.23
245028_at	unknown protein	---	AT2G26570	-1.02	-0.03	-0.18	0.861265	0.909554	-7.23
259820_at	subtilisin-like serine protease conta	---	AT1G66210	-1.02	-0.02	-0.18	0.861487	0.909705	-7.23
250781_at	DREB2A (dbj|BAA33794.1) ; suppo	DREB2A	AT5G05410	1.03	0.04	0.18	0.861488	0.909705	-7.23
261679_at	polyprotein, putative similar to poly	---	---	1.01	0.02	0.18	0.861536	0.909713	-7.23
267306_at	Ran binding protein (AtRanBP1b) ic	---	AT2G30060	-1.02	-0.02	-0.18	0.861612	0.909752	-7.23
247104_at	putative protein similar to unknown	DAR6	AT5G66620	-1.02	-0.03	-0.18	0.861729	0.909833	-7.23
265372_at	Ac-like transposase related to Ac/D	---	AT2G06500	-1.02	-0.02	-0.18	0.862057	0.910137	-7.23
258841_at	hypothetical protein similar to hypot	---	AT3G04660	1.01	0.02	0.18	0.862238	0.910286	-7.23
253722_at	putative protein zinc finger transcri	---	AT4G29190	-1.02	-0.03	-0.18	0.862584	0.910609	-7.23
260338_at	putative RNA-binding protein simila	---	AT1G69250	1.01	0.02	0.18	0.862778	0.910772	-7.23
244971_at	ATP-dependent protease subunit	---	---	1.01	0.02	0.18	0.862834	0.910789	-7.23
258262_at	hypothetical protein	---	AT3G15770	-1.02	-0.02	-0.18	0.86325	0.911186	-7.23
249715_at	putative protein similar to unknown	---	AT5G35760	-1.02	-0.02	-0.18	0.863554	0.911424	-7.23
254025_at	putative pathogenesis-related prote	---	AT4G25790	-1.01	-0.02	-0.18	0.863555	0.911424	-7.23
248447_at	putative protein contains similarity t	PABN1	AT5G51120	1.01	0.02	0.18	0.863601	0.91143	-7.23
256058_at	UDP-glucose glucosyltransferase,	UGT71C5	AT1G07240	-1.02	-0.03	-0.18	0.863878	0.911646	-7.23
251294_at	zinc transporter-like protein zinc tra	MTPA1	AT3G61940	1.01	0.02	0.18	0.863917	0.911646	-7.23
250592_at	putative protein contains similarity t	---	AT5G07740	1.02	0.02	0.18	0.863925	0.911646	-7.23
263523_at	hypothetical protein predicted by ge	---	---	1.01	0.02	0.18	0.864093	0.911781	-7.23
261302_at	hypothetical protein predicted by ge	---	AT1G48580	-1.02	-0.02	-0.18	0.864155	0.911796	-7.23
249654_at	putative protein hypothetical protein	---	---	-1.01	-0.02	-0.18	0.864188	0.911796	-7.23
263272_at	hypothetical protein predicted by ge	---	---	1.01	0.02	0.18	0.864284	0.911855	-7.23
258614_at	putative S-adenosylmethionine:2-de	---	AT3G02770	1.02	0.03	0.18	0.864578	0.912124	-7.23
249390_at	60S RIBOSOMAL PROTEIN L5 -lik	---	AT5G40130	-1.01	-0.02	-0.18	0.864766	0.912187	-7.23
262243_at	hypothetical protein predicted by ge	---	---	-1.02	-0.03	-0.18	0.864835	0.912187	-7.23
261298_at	cytochrome c oxidase assembly pr	---	AT1G48510	-1.01	-0.02	-0.18	0.864845	0.912187	-7.23
264453_at	putative GTP-binding protein simila	---	AT1G10300	1.01	0.02	0.18	0.864864	0.912187	-7.23
259805_at	disease resistance protein, putative	AtRLP7	AT1G47890	1.02	0.03	0.18	0.864869	0.912187	-7.23
260838_at	hypothetical protein predicted by ge	---	AT1G43680	-1.01	-0.02	-0.18	0.864878	0.912187	-7.23
250948_at	putative protein	---	AT5G03490	1.02	0.03	0.18	0.864973	0.912245	-7.23

254257_s_a	putative protein predicted proteins,	---	AT4G23350	1.01	0.02	0.18	0.865142	0.912381	-7.23
254261_at	beta adaptin - like protein beta-ada	---	AT4G23460	1.01	0.02	0.18	0.865314	0.91252	-7.23
252705_at	putative protein predicted proteins,	---	---	-1.02	-0.03	-0.18	0.865366	0.912533	-7.23
255606_at	hypothetical protein similar to T3F1	---	AT4G01110	1.02	0.03	0.18	0.865558	0.912693	-7.23
245936_at	putative protein predicted proteins -	---	AT5G19850	-1.02	-0.03	-0.18	0.865778	0.912883	-7.23
251000_at	putative protein	---	AT5G02650	-1.01	-0.02	-0.18	0.865827	0.912892	-7.23
259499_at	PRLI-interacting factor L, putative s	---	AT1G15730	-1.02	-0.03	-0.17	0.866409	0.913464	-7.23
265080_at	overlap with bases 100,099-109,16	sks12	AT1G55570	-1.02	-0.03	-0.17	0.866587	0.913609	-7.23
247286_at	2-oxoglutarate/malate translocator	DiT2.2	AT5G64280	1.01	0.02	0.17	0.866856	0.913851	-7.23
264752_at	unknown protein similar to Bacillus	LPR1	AT1G23010	1.01	0.02	0.17	0.867244	0.914195	-7.23
251815_at	putative protein thioredoxin-like pro	CXIP1	AT3G54900	-1.02	-0.02	-0.17	0.867263	0.914195	-7.23
259030_at	putative alpha-hemolysin similar to	---	AT3G09310	1.01	0.02	0.17	0.867719	0.914634	-7.23
245588_at	putative protein	---	AT4G15030	1.02	0.03	0.17	0.867944	0.914753	-7.23
254606_at	nodulin-26 - like protein major intrir	NLM1	AT4G19030	-1.01	-0.02	-0.17	0.867962	0.914753	-7.23
261527_at	hypothetical protein similar to putati	---	AT1G14390	-1.02	-0.03	-0.17	0.867966	0.914753	-7.23
249649_at	putative transporter protein Na+ H-	CHX24	AT5G37060	-1.01	-0.02	-0.17	0.868031	0.914753	-7.23
254910_at	translation initiation factor IF-1, put	---	AT4G11175	1.01	0.02	0.17	0.868033	0.914753	-7.23
253059_s_a	putative protein other predicted prot	HHP5	AT4G37680	1.02	0.03	0.17	0.868101	0.914776	-7.23
245450_at	disease resistance RPP5 like protei	---	AT4G16880	1.01	0.02	0.17	0.868135	0.914776	-7.23
259748_at	putative dehydrogenase similar to D	---	AT1G71180	1.02	0.02	0.17	0.868205	0.914808	-7.23
251852_at	putative protein	---	AT3G54750	-1.02	-0.03	-0.17	0.868339	0.914907	-7.23
266499_at	hypothetical protein predicted by ge	---	---	1.02	0.03	0.17	0.86838	0.914908	-7.23
246851_at	putative protein various predicted p	AGL26	AT5G26870	1.01	0.02	0.17	0.86858	0.915041	-7.23
247051_at	At14a protein-like	---	AT5G66670	-1.02	-0.02	-0.17	0.868587	0.915041	-7.23
259775_at	hypothetical protein predicted by ge	---	AT1G29530	1.02	0.03	0.17	0.868763	0.915184	-7.23
263549_at	unknown protein	MEE3	AT2G21650	1.06	0.08	0.17	0.868867	0.915251	-7.23
258081_at	Expressed protein ; supported by fu	---	AT3G26085	1.01	0.02	0.17	0.868974	0.915322	-7.23
245448_at	disease resistance RPP5 like protei	RPP4	AT4G16860	1.02	0.02	0.17	0.869139	0.915453	-7.23
257348_at	hypothetical protein predicted by ge	---	AT2G42140	1.02	0.04	0.17	0.869222	0.915499	-7.23
249614_at	putative protein predicted proteins,	WSD1	AT5G37300	1.01	0.02	0.17	0.869369	0.915611	-7.23
256472_at	unknown protein	---	---	-1.02	-0.02	-0.17	0.869439	0.915643	-7.23
246866_at	putative protein various predicted p	---	AT5G25960	-1.01	-0.02	-0.17	0.869623	0.915794	-7.23
256693_at	hypothetical protein predicted by ge	---	---	1.01	0.02	0.17	0.869757	0.915893	-7.23
259322_at	unknown protein	---	AT3G05270	1.02	0.02	0.17	0.870317	0.916441	-7.23
257942_at	SKP1/ASK1 (At8), putative similar	ASK8	AT3G21830	-1.02	-0.02	-0.17	0.870408	0.916481	-7.23

248482_at	unknown protein	---	AT5G50970	-1.01	-0.02	-0.17	0.870468	0.916481	-7.23
252719_at	putative protein predicted protein, /	---	AT3G43950	1.01	0.02	0.17	0.870476	0.916481	-7.23
257402_at	hypothetical protein similar to putati	---	AT1G23570	-1.01	-0.02	-0.17	0.870522	0.916487	-7.23
256702_at	unknown protein contains Pfam pro	---	AT3G30380	-1.02	-0.03	-0.17	0.870838	0.916761	-7.23
262545_at	prolin rich protein, putative similar t	---	AT1G31250	-1.01	-0.02	-0.17	0.870863	0.916761	-7.23
247804_at	strong similarity to unknown protein	SVL5	AT5G58170	-1.01	-0.02	-0.17	0.870974	0.916836	-7.23
255354_at	putative transposon protein	---	---	1.01	0.02	0.17	0.871033	0.916855	-7.23
254580_at	putative protein ; supported by cDN	---	AT4G19390	-1.01	-0.02	-0.17	0.87113	0.916915	-7.23
251903_at	putative protein 24 kDa seed matu	---	AT3G54120	1.03	0.05	0.17	0.871187	0.916933	-7.23
254824_s_a	origin recognition complex subunit	ORC1B	AT4G12620	-1.02	-0.03	-0.17	0.87128	0.916983	-7.23
257342_at	pseudogene, putative polyprotein s	---	---	1.02	0.03	0.17	0.871315	0.916983	-7.23
256872_at	non-phototropic hypocotyl, putative	---	AT3G26490	1.01	0.02	0.17	0.871402	0.917033	-7.23
252341_at	remorin -like protein remorin, Solar	---	AT3G48940	1.01	0.02	0.17	0.871578	0.917155	-7.23
261567_at	Expressed protein ; supported by c	---	AT1G33055	1.04	0.05	0.17	0.871599	0.917155	-7.23
249848_at	putative protein similar to unknown	NIC3	AT5G23220	1.01	0.02	0.17	0.871697	0.917183	-7.23
248455_at	unknown protein	---	AT5G51360	-1.01	-0.02	-0.17	0.871706	0.917183	-7.23
266377_at	Mutator-like transposase similar to	---	---	1.01	0.01	0.17	0.871808	0.917248	-7.23
259518_at	hypothetical protein ; supported by	OPCL1	AT1G20510	1.04	0.05	0.17	0.871879	0.91728	-7.23
264403_at	unknown protein similarity to HSR2	---	AT2G25150	-1.01	-0.02	-0.17	0.872582	0.917944	-7.23
249034_at	putative protein contains similarity t	NUC	AT5G44160	1.01	0.02	0.17	0.87259	0.917944	-7.23
258182_at	1-D-deoxyxylulose 5-phosphate sy	DXPS1	AT3G21500	-1.04	-0.06	-0.17	0.872794	0.918117	-7.23
260366_at	putative protein kinase similar to C-	---	AT1G70460	-1.01	-0.02	-0.17	0.872906	0.918192	-7.23
257916_at	unknown protein similar to hypothet	---	AT3G23210	-1.02	-0.03	-0.17	0.872971	0.918218	-7.23
245496_at	LET1 like protein	---	AT4G16440	1.01	0.02	0.17	0.873064	0.918273	-7.23
262075_at	hypothetical protein contains simila	ZCF61	AT1G59560	1.02	0.03	0.17	0.873259	0.918397	-7.23
247535_at	transcriptional activator - like protei	---	AT5G61620	-1.02	-0.03	-0.17	0.873263	0.918397	-7.23
250628_at	hypothetical protein	---	AT5G07380	-1.02	-0.02	-0.17	0.873317	0.918412	-7.23
245263_at	PSII D1 protein processing enzyme	---	AT4G17740	-1.01	-0.02	-0.17	0.873479	0.9185	-7.23
266339_s_a	hypothetical protein predicted by ge	---	AT2G01360	1.01	0.02	0.17	0.873481	0.9185	-7.23
258703_at	unknown protein	---	AT3G09750	1.02	0.02	0.16	0.874164	0.919176	-7.23
266610_at	Ac-like transposase related to Ac/D	---	---	1.01	0.02	0.16	0.87444	0.919423	-7.23
245617_at	hypothetical protein	---	AT4G14490	-1.01	-0.02	-0.16	0.874611	0.919561	-7.23
246810_at	putative protein many predicted pro	---	---	-1.01	-0.02	-0.16	0.874672	0.919583	-7.23
255486_at	AtMlo-h1-like protein	MLO1	AT4G02600	-1.01	-0.02	-0.16	0.874857	0.919735	-7.23
249157_at	unknown protein	---	AT5G43510	1.01	0.02	0.16	0.875022	0.919845	-7.23

264747_at	unknown protein	---	AT1G70150	1.02	0.02	0.16	0.875042	0.919845	-7.23
260861_at	hypothetical protein predicted by ge	---	---	-1.01	-0.02	-0.16	0.875131	0.919896	-7.23
264278_at	myrosinase binding protein, putativ	---	AT1G60130	-1.01	-0.02	-0.16	0.875227	0.919915	-7.23
251811_at	APETALA2 - like protein APETALA	SMZ	AT3G54990	1.02	0.03	0.16	0.87523	0.919915	-7.23
256188_at	unknown protein similar to hypothet	---	AT1G30160	1.03	0.04	0.16	0.875298	0.919944	-7.23
253449_at	putative protein hypothetical protei	---	AT4G32700	1.01	0.02	0.16	0.875339	0.919945	-7.23
249450_at	serine/threonine-specific protein ki	SnRK1.3	AT5G39440	1.01	0.02	0.16	0.875489	0.920037	-7.23
267480_at	putative retroelement pol polyprotei	---	---	1.01	0.02	0.16	0.875507	0.920037	-7.23
265654_s_a	En/Spm-like transposon protein rela	---	---	1.01	0.02	0.16	0.875626	0.92012	-7.23
260694_at	NAD+ dependent isocitrate dehydr	---	AT1G32480	-1.01	-0.02	-0.16	0.875695	0.92015	-7.23
251125_at	putative protein - kinase protein kin	---	AT5G01060	-1.01	-0.02	-0.16	0.875824	0.920242	-7.23
255201_at	putative transposon protein	---	---	1.01	0.01	0.16	0.875866	0.920245	-7.23
253324_at	Expressed protein ; supported by fu	---	AT4G33940	1.01	0.02	0.16	0.875945	0.920284	-7.23
251457_s_a	multi resistance protein homolog m	ATMRP9	AT3G60160	1.01	0.02	0.16	0.876088	0.920361	-7.23
251618_at	putative protein unknown protein A	---	AT3G58020	-1.02	-0.03	-0.16	0.876098	0.920361	-7.23
261916_at	jasmonic acid, putative similar to ja	anac028	AT1G65910	1.02	0.02	0.16	0.876281	0.92051	-7.23
262598_at	unknown protein EST gb|N65467 c	---	AT1G15260	-1.02	-0.03	-0.16	0.876353	0.920537	-7.23
266454_at	putative bHLH transcription factor	---	AT2G22750	1.01	0.02	0.16	0.876387	0.920537	-7.23
250788_at	putative protein similar to unknown	---	AT5G05570	1.02	0.02	0.16	0.876605	0.920724	-7.23
255722_at	hypothetical protein	---	AT3G29570	1.01	0.02	0.16	0.87674	0.920749	-7.23
252489_at	disease resistance protein RPP8-li	---	AT3G46710	1.02	0.02	0.16	0.876751	0.920749	-7.23
252539_at	putative protein	---	AT3G45730	1.02	0.02	0.16	0.876802	0.920749	-7.23
254220_at	putative protein Arabidopsis hypoth	---	AT4G23780	-1.01	-0.02	-0.16	0.87682	0.920749	-7.23
258363_at	putative pectin methylesterase simi	ATPMEPCI	AT3G14300	-1.01	-0.02	-0.16	0.876831	0.920749	-7.23
249667_at	unknown protein	---	---	-1.01	-0.01	-0.16	0.876936	0.920817	-7.23
249149_at	casein kinase I ; supported by cDN	ckl8	AT5G43320	-1.01	-0.01	-0.16	0.877052	0.920896	-7.23
264015_at	putative XAP-5 protein [Homo sapie	XCT	AT2G21150	1.01	0.02	0.16	0.877294	0.921064	-7.23
253000_at	putative protein other predicted prot	---	AT4G38360	-1.02	-0.02	-0.16	0.877329	0.921064	-7.23
250053_at	potassium-dependent sodium-calc	---	AT5G17850	1.02	0.02	0.16	0.877333	0.921064	-7.23
260326_at	putative MYB family transcription fa	AtMYB103	AT1G63910	1.01	0.02	0.16	0.877469	0.921165	-7.23
247244_at	putative protein similar to unknown	---	AT5G64710	1.01	0.02	0.16	0.877794	0.921464	-7.23
253363_at	hypothetical protein	---	AT4G33130	1.01	0.02	0.16	0.877972	0.921608	-7.23
261704_at	hypothetical protein identical to hyp	---	AT1G32600	-1.01	-0.02	-0.16	0.878272	0.921881	-7.23
263484_at	putative presenilin	---	AT2G29900	1.01	0.02	0.16	0.878896	0.922493	-7.23
252814_at	putative protein several hypothetica	---	---	1.01	0.02	0.16	0.879095	0.922617	-7.23

263473_at	putative glucosyltransferase ; supp	UGT74D1	AT2G31750	-1.04	-0.05	-0.16	0.879156	0.922617	-7.23
252888_at	glucose-1-phosphate adenylyltrans	APL3	AT4G39210	1.03	0.05	0.16	0.879157	0.922617	-7.23
248712_at	unknown protein	---	AT5G48280	-1.01	-0.02	-0.16	0.879183	0.922617	-7.23
258337_at	hypothetical protein predicted by ge	---	AT3G16040	1.02	0.03	0.16	0.879216	0.922617	-7.23
267379_at	unknown protein ; supported by cD	---	AT2G26340	1.02	0.03	0.16	0.879261	0.922622	-7.23
257559_at	hypothetical protein contains Pfam	---	AT3G22050	-1.01	-0.02	-0.16	0.879365	0.922664	-7.23
262485_at	kinesin-like protein Similar to gb|U0	---	AT1G21730	1.01	0.02	0.16	0.879387	0.922664	-7.23
259509_at	mutator-like transposase, putative	---	---	-1.01	-0.02	-0.16	0.879438	0.922664	-7.23
259716_at	unknown protein	---	AT1G60995	1.02	0.02	0.16	0.879504	0.922664	-7.23
247911_at	putative protein contains similarity t	XRCC3	AT5G57450	-1.01	-0.02	-0.16	0.879504	0.922664	-7.23
247938_at	putative protein similar to unknown	---	AT5G57140	-1.01	-0.02	-0.16	0.87959	0.922712	-7.23
253069_at	hexokinase - like protein hexokinas	HKL3	AT4G37840	-1.01	-0.02	-0.16	0.879653	0.922736	-7.23
247742_at	random slug protein - like random s	---	AT5G58980	1.01	0.02	0.16	0.879935	0.922988	-7.23
250398_at	putative protein predicted proteins,	---	AT5G11000	1.03	0.04	0.16	0.879985	0.922999	-7.23
265890_s_a	En/Spm-like transposon protein rela	---	---	-1.01	-0.02	-0.16	0.880049	0.923023	-7.23
258290_at	hypothetical protein predicted by ge	---	AT3G23460	1.01	0.01	0.16	0.880212	0.923152	-7.23
262812_at	hypothetical protein predicted by ge	---	AT1G11690	-1.01	-0.01	-0.16	0.880265	0.923165	-7.23
262393_at	hypothetical protein contains simila	---	AT1G49490	1.01	0.02	0.16	0.880507	0.923377	-7.23
263489_at	putative inositol polyphosphate 5'-p	---	AT2G31830	1.01	0.02	0.16	0.880625	0.923458	-7.24
265432_at	hypothetical protein predicted by gr	---	AT2G20650	-1.01	-0.02	-0.16	0.880704	0.923494	-7.24
246163_at	putative protein predicted proteins,	---	---	-1.02	-0.02	-0.16	0.88074	0.923494	-7.24
245815_at	unknown protein	---	AT1G26090	1.01	0.02	0.16	0.88092	0.92364	-7.24
248892_at	unknown protein	---	AT5G46300	1.01	0.02	0.16	0.880995	0.923676	-7.24
264345_at	Expressed protein ; supported by cl	---	AT1G11915	-1.02	-0.02	-0.16	0.88104	0.923681	-7.24
247301_at	DNA topoisomerase III	---	AT5G63920	1.02	0.03	0.16	0.881225	0.923832	-7.24
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J	---	---	-1.03	-0.04	-0.16	0.881319	0.923888	-7.24
266027_at	En/Spm-like transposon protein rela	---	---	1.01	0.01	0.15	0.88145	0.923983	-7.24
252461_at	putative protein predicted protein, A	---	---	1.01	0.02	0.15	0.881526	0.924021	-7.24
248662_at	unknown protein	---	AT5G48690	-1.01	-0.02	-0.15	0.881603	0.924057	-7.24
255383_at	hypothetical protein	---	AT4G03570	-1.01	-0.01	-0.15	0.881696	0.924057	-7.24
265076_at	Rubisco subunit binding-protein bet	CPN60B	AT1G55490	1.02	0.03	0.15	0.881723	0.924057	-7.24
262192_at	hypothetical protein predicted by ge	---	AT1G77830	-1.01	-0.02	-0.15	0.881725	0.924057	-7.24
261774_at	unknown protein	---	AT1G76260	1.02	0.03	0.15	0.881763	0.924057	-7.24
256208_at	hypothetical protein predicted by ge	---	AT1G50930	-1.01	-0.01	-0.15	0.881925	0.924148	-7.24
255131_at	putative protein hypothetical protei	---	AT4G08280	1.01	0.02	0.15	0.881932	0.924148	-7.24

257711_at	20S proteasome beta subunit (PBE	PBB1	AT3G27430	-1.01	-0.02	-0.15	0.88202	0.924198	-7.24
256035_at	Ran-binding protein (atranbp1a) ide	SIRANBP	AT1G07140	1.01	0.02	0.15	0.882082	0.924221	-7.24
261401_at	kinase, putative similar to Ste-20 re	---	AT1G79640	-1.02	-0.02	-0.15	0.882136	0.924235	-7.24
267390_at	putative beta-glucosidase	BGLU29	AT2G44470	-1.01	-0.02	-0.15	0.882249	0.924281	-7.24
260554_at	putative zinc protease member of ir	---	AT2G41790	1.01	0.01	0.15	0.882287	0.924281	-7.24
250025_at	putative protein similar to unknown	SIP1;2	AT5G18290	-1.02	-0.02	-0.15	0.882334	0.924281	-7.24
264713_at	hypothetical protein Similar to N. ta	---	AT1G09820	1.01	0.02	0.15	0.882342	0.924281	-7.24
251896_at	putative protein predicted proteins,	---	AT3G54390	1.02	0.02	0.15	0.882547	0.924453	-7.24
252651_at	putative protein several hypothetica	---	AT3G44700	1.01	0.02	0.15	0.882632	0.9245	-7.24
266821_at	putative ethylene response element	ERF13	AT2G44840	1.07	0.09	0.15	0.88275	0.924581	-7.24
249743_at	beta-glucosidase	BGLU31	AT5G24540	1.07	0.10	0.15	0.882791	0.924582	-7.24
263919_at	unknown protein ;supported by full-	---	AT2G36470	-1.04	-0.06	-0.15	0.882975	0.924681	-7.24
256097_at	unknown protein	---	AT1G13670	-1.01	-0.01	-0.15	0.882982	0.924681	-7.24
259320_at	putative DNA-binding protein simila	WRKY58	AT3G01080	1.04	0.05	0.15	0.883008	0.924681	-7.24
244987_s_a	ribosomal protein L2	---	---	-1.01	-0.01	-0.15	0.883169	0.924807	-7.24
263468_at	hypothetical protein predicted by ge	---	AT2G31930	-1.01	-0.02	-0.15	0.88342	0.925028	-7.24
255099_at	hypothetical protein	---	---	1.01	0.02	0.15	0.883551	0.925087	-7.24
261759_at	hypothetical protein similar to putati	---	AT1G15590	1.01	0.02	0.15	0.883557	0.925087	-7.24
257898_s_a	hypothetical protein predicted by ge	---	---	1.01	0.01	0.15	0.883633	0.925098	-7.24
247061_at	putative protein similar to unknown	---	AT5G66780	-1.02	-0.03	-0.15	0.883649	0.925098	-7.24
261061_at	DNA-binding protein, putative cont	TRFL2	AT1G07540	-1.01	-0.02	-0.15	0.883705	0.925114	-7.24
254652_at	DNA binding-like protein SPF1 pro	WRKY28	AT4G18170	1.06	0.08	0.15	0.883924	0.925301	-7.24
263537_at	CONSTANS-like B-box zinc finger p	COL3	AT2G24790	1.01	0.02	0.15	0.884057	0.925361	-7.24
259149_at	putative phenylalanine ammonia-lya	PAL4	AT3G10340	-1.06	-0.08	-0.15	0.884062	0.925361	-7.24
258634_at	putative RNA-binding protein conta	---	AT3G08000	-1.02	-0.03	-0.15	0.884122	0.925381	-7.24
257920_at	hypothetical protein predicted by ge	---	AT3G23260	1.01	0.01	0.15	0.88429	0.925514	-7.24
256508_at	unknown protein	---	AT1G75140	1.01	0.02	0.15	0.884544	0.925737	-7.24
250169_at	putative protein many predicted pro	---	AT5G15340	-1.02	-0.03	-0.15	0.884609	0.925763	-7.24
263811_at	putative acyl-CoA synthetase ; supp	---	AT2G04350	-1.01	-0.02	-0.15	0.884762	0.925841	-7.24
249841_at	unknown protein	---	AT5G23520	-1.01	-0.02	-0.15	0.884765	0.925841	-7.24
257389_at	hypothetical protein predicted by ge	---	AT2G17970	-1.01	-0.02	-0.15	0.885154	0.92619	-7.24
265568_s_a	hypothetical protein predicted by ge	---	---	1.02	0.02	0.15	0.885179	0.92619	-7.24
245153_at	putative protein similarity to predict	---	AT5G12450	1.01	0.01	0.15	0.885222	0.926192	-7.24
255105_at	putative sulfate transporter ; suppo	SULTR1;1	AT4G08620	-1.01	-0.02	-0.15	0.885572	0.926516	-7.24
253927_at	putative protein	---	AT4G26710	-1.01	-0.02	-0.15	0.885895	0.926811	-7.24

248211_at	flavonol 3-O-glucosyltransferase-lik	---	AT5G54010	-1.01	-0.01	-0.15	0.885971	0.926811	-7.24
251687_at	quinone reductase-like protein zeta	---	AT3G56460	-1.01	-0.02	-0.15	0.885976	0.926811	-7.24
257383_at	hypothetical protein predicted by ge	---	AT2G19630	-1.01	-0.02	-0.15	0.886085	0.926869	-7.24
251202_at	putative protein predicted protein, (	---	AT3G63040	-1.01	-0.01	-0.15	0.886133	0.926869	-7.24
253034_at	calcium-dependent protein kinase -	CPK26	AT4G38230	1.01	0.02	0.15	0.886154	0.926869	-7.24
258864_at	unknown protein	---	AT3G03210	1.02	0.02	0.15	0.886266	0.926944	-7.24
266091_at	hypothetical protein predicted by ge	emb1513	AT2G37920	-1.01	-0.02	-0.15	0.886463	0.927108	-7.24
247262_at	putative protein contains similarity t	AtFAAH	AT5G64440	1.01	0.02	0.15	0.886653	0.927264	-7.24
257496_s_a	hypothetical protein predicted by gr	---	AT2G43730	-1.01	-0.02	-0.15	0.886705	0.927276	-7.24
257185_at	ABC transporter, putative similar to	ATMRP7	AT3G13100	1.02	0.03	0.15	0.886891	0.927427	-7.24
254902_at	putative protein several hypothetica	---	AT4G11550	-1.01	-0.02	-0.15	0.886969	0.927467	-7.24
250482_at	putative protein	---	AT5G10320	1.01	0.02	0.15	0.887047	0.927506	-7.24
261243_at	hypothetical protein predicted by ge	---	AT1G20180	-1.03	-0.05	-0.15	0.887182	0.927604	-7.24
249211_at	putative protein similar to unknown	---	AT5G42680	1.03	0.04	0.15	0.887251	0.927634	-7.24
252630_at	putative protein	---	AT3G44980	1.01	0.02	0.15	0.887315	0.927659	-7.24
251682_s_a	hypothetical protein	---	AT3G57110	-1.01	-0.02	-0.15	0.887411	0.927717	-7.24
262869_s_a	putative protein predicted protein, (	GTG1	AT1G64990	1.01	0.02	0.15	0.88759	0.927861	-7.24
262747_at	hypothetical protein predicted by ge	---	AT1G28540	1.01	0.01	0.15	0.887993	0.928203	-7.24
252536_at	putative transporter protein peptide	---	AT3G45700	1.01	0.02	0.15	0.887999	0.928203	-7.24
246252_s_a	patatin-like protein ;supported by fu	PLP1	AT4G37060	1.01	0.01	0.15	0.888077	0.928243	-7.24
266842_at	FtsH protease, putative contains si	ftsh4	AT2G26140	1.01	0.02	0.15	0.888264	0.92836	-7.24
254949_at	hypothetical protein	---	AT4G11020	-1.01	-0.02	-0.15	0.88827	0.92836	-7.24
246320_at	unknown protein	---	AT1G16560	1.02	0.03	0.15	0.888523	0.928581	-7.24
252638_at	acyl CoA reductase - protein acyl (	FAR4	AT3G44540	-1.01	-0.02	-0.15	0.888592	0.928611	-7.24
253727_at	profilin 2 ; supported by full-length	PFN2	AT4G29350	-1.01	-0.02	-0.15	0.888637	0.928615	-7.24
266120_at	putative C2H2-type zinc finger prote	AtIDD5	AT2G02070	-1.01	-0.02	-0.15	0.888854	0.928768	-7.24
248212_at	CHP-rich zinc finger protein-like	---	AT5G54020	-1.01	-0.02	-0.15	0.888864	0.928768	-7.24
259359_at	B regulatory subunit of protein pho	---	AT1G13460	-1.01	-0.02	-0.14	0.889024	0.928853	-7.24
249571_at	putative protein predicted proteins,	---	AT5G37620	1.01	0.01	0.14	0.889027	0.928853	-7.24
251700_at	putative protein exocyst complex p	---	AT3G56640	-1.02	-0.03	-0.14	0.889259	0.928988	-7.24
251947_at	putative protein various predicted p	---	AT3G53550	1.01	0.01	0.14	0.889286	0.928988	-7.24
247969_at	putative protein similar to unknown	---	AT5G56700	1.02	0.03	0.14	0.889298	0.928988	-7.24
245169_at	unknown protein predicted by gene	---	AT2G33220	1.01	0.01	0.14	0.88932	0.928988	-7.24
266023_at	copia-like retroelement pol polyprot	---	---	1.01	0.02	0.14	0.8896	0.929239	-7.24
245779_at	hypothetical protein predicted by ge	---	AT1G73510	-1.01	-0.01	-0.14	0.889937	0.929511	-7.24

245615_at	reverse transcriptase like protein	---	---	-1.01	-0.02	-0.14	0.889942	0.929511	-7.24
249919_at	putative protein predicted protein, /	---	AT5G19250	-1.01	-0.02	-0.14	0.890362	0.929906	-7.24
246804_at	putative protein	---	---	-1.01	-0.01	-0.14	0.890652	0.930133	-7.24
247770_at	putative protein predicted proteins,	---	AT5G58930	1.03	0.04	0.14	0.89066	0.930133	-7.24
249779_at	putative protein similar to unknown	---	AT5G24230	1.01	0.01	0.14	0.890767	0.930201	-7.24
245433_at	hypothetical protein	---	AT4G17140	1.01	0.02	0.14	0.891005	0.930394	-7.24
262114_at	unknown protein contains similarity	NLA	AT1G02860	-1.02	-0.03	-0.14	0.891046	0.930394	-7.24
251334_at	putative protein several hypothetica	---	AT3G61390	-1.01	-0.02	-0.14	0.891073	0.930394	-7.24
257354_x_a	hypothetical protein predicted by ge	---	---	1.01	0.02	0.14	0.891275	0.930562	-7.24
257282_at	TNP2-like transposon protein, puta	---	---	-1.01	-0.02	-0.14	0.891704	0.930967	-7.24
267496_at	putative lipase ; supported by full-le	---	AT2G30550	1.02	0.02	0.14	0.891947	0.931178	-7.24
248754_at	putative protein contains similarity t	NF-YB6	AT5G47670	-1.01	-0.01	-0.14	0.892206	0.93138	-7.24
252569_at	receptor-like protein kinase recepto	---	AT3G45420	-1.01	-0.02	-0.14	0.892222	0.93138	-7.24
266392_at	late embryogenesis abundant M10	M10	AT2G41280	-1.01	-0.01	-0.14	0.892265	0.931382	-7.24
260973_at	hypothetical protein predicted by ge	---	AT1G53490	-1.01	-0.01	-0.14	0.892515	0.931601	-7.24
AFFX-r2-Bs	B. subtilis /GEN=dapB /DB_XREF=	---	---	-1.02	-0.03	-0.14	0.892712	0.931763	-7.24
252364_at	hypothetical protein ;supported by	---	AT3G48450	-1.04	-0.06	-0.14	0.892768	0.93178	-7.24
261358_s_a	hypothetical protein predicted by ge	---	AT1G41920	-1.01	-0.02	-0.14	0.892819	0.93179	-7.24
253742_at	putative protein retrofit - Oryza long	---	---	-1.01	-0.02	-0.14	0.893059	0.93197	-7.24
255351_x_a	putative transposon protein similar t	---	---	1.01	0.02	0.14	0.893081	0.93197	-7.24
267295_at	pregeranylgeranyl pyrophosphate s	GGPS2	AT2G23800	1.01	0.01	0.14	0.893151	0.93197	-7.24
254005_at	subtilisin-like serine protease conta	UNE17	AT4G26330	1.01	0.02	0.14	0.893155	0.93197	-7.24
262423_at	hypothetical protein predicted by ge	---	AT1G23450	-1.01	-0.01	-0.14	0.89322	0.931993	-7.24
261485_at	unknown protein ;supported by full-	UTR3	AT1G14360	-1.03	-0.04	-0.14	0.893258	0.931993	-7.24
261797_at	cation-chloride co-transporter, puta	---	AT1G30455	-1.01	-0.02	-0.14	0.893369	0.932066	-7.24
256902_s_a	HAPp48,5 protein identical to HAP	---	AT3G23910	-1.02	-0.02	-0.14	0.893456	0.932114	-7.24
256646_at	hypothetical protein predicted by ge	---	AT3G13590	-1.01	-0.02	-0.14	0.893528	0.932137	-7.24
245379_at	heat shock transcription factor HSF	HSF1	AT4G17750	1.01	0.02	0.14	0.893611	0.932137	-7.24
255404_at	predicted protein	---	AT4G03153	-1.01	-0.02	-0.14	0.89362	0.932137	-7.24
265382_at	putative gluconokinase ;supported	---	AT2G16790	1.02	0.03	0.14	0.893676	0.932137	-7.24
250468_at	transcription factor TEIL/ethylene-i	---	AT5G10120	1.01	0.01	0.14	0.893683	0.932137	-7.24
257242_at	9-cis-epoxycarotenoid dioxygenase	NCED6	AT3G24220	-1.01	-0.02	-0.14	0.893744	0.932158	-7.24
258005_at	cysteine proteinase contains simila	---	AT3G19390	1.04	0.06	0.14	0.893888	0.932253	-7.24
264932_at	hypothetical protein similar to hypot	---	AT1G61240	1.02	0.02	0.14	0.893917	0.932253	-7.24
252431_at	putative protein	MAG2	AT3G47700	1.02	0.02	0.14	0.893998	0.932273	-7.24

262694_at	unknown protein	---	AT1G62790	-1.02	-0.03	-0.14	0.894017	0.932273	-7.24
247922_at	putative protein similar to unknown	---	AT5G57500	-1.03	-0.04	-0.14	0.894194	0.932415	-7.24
246966_at	DNA photolyase - like protein DNA	CRY3	AT5G24850	-1.02	-0.02	-0.14	0.894647	0.932844	-7.24
252339_at	hypothetical protein	---	AT3G48900	1.01	0.01	0.14	0.894915	0.933081	-7.24
252409_at	putative protein bundle sheath defe	---	AT3G47650	-1.01	-0.02	-0.14	0.895052	0.933181	-7.24
257070_at	hypothetical protein predicted by ge	---	AT3G28190	-1.01	-0.01	-0.14	0.895173	0.933226	-7.24
266069_at	putative RING zinc finger protein	MEE16	AT2G18650	1.02	0.03	0.14	0.895198	0.933226	-7.24
259219_at	hypothetical protein predicted by ge	---	AT3G03560	-1.02	-0.02	-0.14	0.895244	0.933226	-7.24
248321_at	putative protein similar to unknown	---	AT5G52740	-1.01	-0.02	-0.14	0.895272	0.933226	-7.24
252730_at	putative protein	---	AT3G43110	1.02	0.02	0.14	0.895299	0.933226	-7.24
253461_at	cytochrome p450 - like protein cyto	CYP96A2	AT4G32170	-1.01	-0.01	-0.14	0.895525	0.933418	-7.24
250241_at	photoreceptor-interacting protein-lik	---	AT5G13600	1.01	0.02	0.14	0.895672	0.933529	-7.24
254046_at	hypothetical protein	---	AT4G26020	1.01	0.01	0.14	0.895745	0.933562	-7.24
248917_at	putative protein similar to unknown	---	AT5G45850	-1.01	-0.01	-0.14	0.89581	0.933587	-7.24
248828_at	Lil3 protein	---	AT5G47110	1.01	0.01	0.14	0.896092	0.933821	-7.24
257830_at	MutT-like protein contains Pfam pro	ATNUDX13	AT3G26690	-1.02	-0.03	-0.14	0.896116	0.933821	-7.24
262008_s_a	CACTA-element, putative similar to	---	---	1.01	0.02	0.14	0.8963	0.93397	-7.24
257552_at	cellulase, putative contains Pfam p	---	AT3G26130	-1.01	-0.01	-0.13	0.896597	0.934184	-7.24
260183_at	hypothetical protein similar to DNA	---	---	-1.01	-0.01	-0.13	0.896613	0.934184	-7.24
262167_at	putative RING zinc finger protein c	---	AT1G74990	-1.01	-0.02	-0.13	0.896662	0.934184	-7.24
248140_at	putative protein similar to unknown	---	AT5G54980	-1.01	-0.02	-0.13	0.896669	0.934184	-7.24
246062_at	putative protein VAC8 protein, Sac	---	AT5G19330	1.01	0.01	0.13	0.896806	0.934275	-7.24
254808_at	adenine DNA glycosylase like prote	---	AT4G12740	1.01	0.01	0.13	0.896839	0.934275	-7.24
251640_at	putative protein ;supported by full-l	---	AT3G57450	-1.04	-0.06	-0.13	0.897144	0.934551	-7.24
265992_at	putative receptor-like protein kinase	---	AT2G24130	-1.01	-0.01	-0.13	0.897273	0.934642	-7.24
261393_at	NAM (no apical meristem)-like prot	SMB	AT1G79580	-1.01	-0.01	-0.13	0.897401	0.934733	-7.24
267010_at	putative AP2 domain transcription f	SNZ	AT2G39250	-1.01	-0.02	-0.13	0.897566	0.934862	-7.24
266389_s_a	unknown protein	---	AT2G31580	-1.01	-0.01	-0.13	0.897781	0.935002	-7.24
252520_at	receptor-like protein kinase homolo	---	AT3G46370	-1.03	-0.04	-0.13	0.897782	0.935002	-7.24
248872_at	Expressed protein ; supported by fu	MSP2	AT5G46795	1.01	0.02	0.13	0.897915	0.935097	-7.24
259042_at	RGA1-like protein similar to RGA1	RGL2	AT3G03450	-1.02	-0.02	-0.13	0.898021	0.935165	-7.24
267381_at	unknown protein ; supported by cD	---	AT2G26190	1.05	0.07	0.13	0.898309	0.935422	-7.24
245982_at	senescence-associated protein (SA	SAG29	AT5G13170	-1.05	-0.08	-0.13	0.898426	0.935501	-7.24
256374_at	DNA ligase I, putative similar to DN	---	AT1G66730	1.01	0.02	0.13	0.898466	0.935501	-7.24
249675_at	putative protein myrosinase-binding	---	AT5G35940	-1.01	-0.01	-0.13	0.898569	0.935565	-7.24

261177_at	hypothetical protein predicted by ge	---	AT1G04770	-1.02	-0.03	-0.13	0.898735	0.935695	-7.24
252112_at	putative protein merozoite surface	---	AT3G51580	-1.01	-0.02	-0.13	0.899039	0.935969	-7.24
252535_at	hypothetical protein	---	AT3G46150	1.02	0.03	0.13	0.899099	0.935974	-7.24
258769_at	putative alpha-hydroxynitrile lyase s	MES17	AT3G10870	1.02	0.03	0.13	0.899144	0.935974	-7.24
249022_s_a	polygalacturonase-like protein	---	AT5G44830	-1.01	-0.01	-0.13	0.89918	0.935974	-7.24
266582_at	unknown protein ; supported by cD	---	AT2G46090	-1.01	-0.02	-0.13	0.899208	0.935974	-7.24
261029_at	unknown protein	---	AT1G17330	-1.01	-0.02	-0.13	0.899329	0.936057	-7.24
257375_at	unknown protein	---	AT2G38640	1.03	0.04	0.13	0.899448	0.936057	-7.24
263211_at	germin-like oxalate oxidase similar	GLP7	AT1G10460	-1.01	-0.02	-0.13	0.899475	0.936057	-7.24
249155_at	unknown protein	---	AT5G43480	-1.01	-0.01	-0.13	0.89948	0.936057	-7.24
253685_at	putative protein nucleotide pyrophc	---	AT4G29710	-1.01	-0.01	-0.13	0.899498	0.936057	-7.24
246445_at	glucose 6 phosphate/phosphate tra	---	AT5G17630	1.01	0.02	0.13	0.899534	0.936057	-7.24
252299_at	putative protein various predicted p	---	AT3G49150	1.01	0.02	0.13	0.899606	0.93609	-7.24
252726_at	putative protein predicted proteins,	---	---	-1.02	-0.02	-0.13	0.899731	0.936152	-7.24
258167_at	UDP-glucose:indole-3-acetate beta	UGT84A2	AT3G21560	-1.02	-0.03	-0.13	0.899748	0.936152	-7.24
263446_at	putative SET-domain transcriptiona	ATX1	AT2G31650	1.01	0.02	0.13	0.899871	0.936221	-7.24
256039_at	hypothetical protein contains simila	---	AT1G19190	-1.01	-0.02	-0.13	0.899897	0.936221	-7.24
248546_at	putative protein similar to unknown	---	AT5G50270	1.01	0.01	0.13	0.900013	0.936299	-7.24
248823_s_a	unknown protein ;supported by full-	---	AT5G46950	-1.08	-0.11	-0.13	0.900142	0.936391	-7.24
263316_s_a	putative ligand-gated ion channel p	ATGLR2.3	AT2G24710	1.01	0.01	0.13	0.90049	0.936686	-7.24
266349_at	unknown protein predicted by gens	---	AT2G01460	-1.01	-0.02	-0.13	0.900527	0.936686	-7.24
251978_at	CYTOCHROME P450 - like protein	CYP71B30	AT3G53290	1.01	0.02	0.13	0.900549	0.936686	-7.24
255576_at	predicted protein of unknown funct	---	AT4G01440	-1.02	-0.03	-0.13	0.90062	0.936712	-7.24
254449_at	putative protein predicted protein,	HEN1	AT4G20910	1.01	0.02	0.13	0.900656	0.936712	-7.24
248370_at	homeodomain transcription factor-li	HDG7	AT5G52170	-1.01	-0.02	-0.13	0.900785	0.936803	-7.24
256290_at	serine carboxypeptidase, putative	scpl17	AT3G12203	1.01	0.01	0.13	0.901037	0.937023	-7.24
249772_at	unknown protein	---	AT5G24130	-1.02	-0.03	-0.13	0.901151	0.937098	-7.24
248444_at	putative protein similar to unknown	---	---	1.01	0.01	0.13	0.901211	0.937118	-7.24
249194_at	kinesin heavy chain-like protein	---	AT5G42490	1.01	0.01	0.13	0.901297	0.93712	-7.24
251606_at	hypothetical protein	---	AT3G57840	1.01	0.02	0.13	0.901333	0.93712	-7.24
248806_at	putative protein contains similarity t	---	AT5G47490	-1.01	-0.01	-0.13	0.901336	0.93712	-7.24
253369_at	F-box protein family, AtFBL15 cont	---	AT4G33210	-1.01	-0.01	-0.13	0.901458	0.937204	-7.24
265426_at	hypothetical protein predicted by ge	---	AT2G20740	1.01	0.02	0.13	0.901803	0.93752	-7.24
265658_at	putative aspartate aminotransferase	ALD1	AT2G13810	1.04	0.06	0.13	0.90188	0.937544	-7.24
245128_at	unknown protein similar to gi23448	---	AT2G45380	-1.01	-0.02	-0.13	0.901909	0.937544	-7.24

260013_at	putative annexin similar to annexin	ANN5	AT1G68090	1.01	0.01	0.13	0.902108	0.937709	-7.24
262720_s_a	hypothetical protein similar to hypot	---	AT1G43600	-1.01	-0.01	-0.13	0.902236	0.937791	-7.24
247040_at	anthranilate N-hydroxycinnamoyl/be	---	AT5G67150	1.01	0.02	0.13	0.902269	0.937791	-7.24
258872_at	hypothetical protein similar to L1 sp	HDG8	AT3G03260	-1.01	-0.02	-0.13	0.902326	0.937807	-7.24
245955_at	hypothetical protein	BGLU24	AT5G28510	1.01	0.01	0.13	0.902497	0.937899	-7.24
247396_at	putative protein predicted proteins,	---	AT5G62930	1.01	0.01	0.13	0.902529	0.937899	-7.24
262613_at	putative DNA-binding protein simila	WRKY4	AT1G13960	1.01	0.01	0.13	0.902538	0.937899	-7.24
254355_at	Ribosomal protein L7Ae - like NHP	---	AT4G22380	-1.02	-0.02	-0.13	0.90282	0.93815	-7.24
263373_at	Expressed protein ; supported by fu	---	AT2G20515	-1.02	-0.02	-0.13	0.903077	0.938326	-7.24
266810_at	hypothetical protein predicted by ge	---	AT2G44880	1.01	0.01	0.13	0.903104	0.938326	-7.24
264850_at	unknown protein similar to F5J6.8 a	---	AT2G17340	-1.01	-0.01	-0.13	0.903113	0.938326	-7.24
251515_at	putative protein several hypothetica	---	AT3G59270	-1.01	-0.01	-0.13	0.903218	0.938359	-7.24
255874_at	hypothetical protein predicted by ge	ETG1	AT2G40550	1.03	0.05	0.13	0.903287	0.938359	-7.24
252793_at	hypothetical protein	---	---	-1.01	-0.01	-0.13	0.90329	0.938359	-7.24
246013_at	vacuolar calcium binding protein - l	---	AT5G10660	1.01	0.01	0.13	0.903322	0.938359	-7.24
260054_at	putative transporter contains Pfam (	UNE2	AT1G78130	1.02	0.03	0.13	0.90335	0.938359	-7.24
259679_at	putative protein kinase Pfam HMM	---	AT1G77720	-1.01	-0.01	-0.13	0.903521	0.938493	-7.24
251963_at	protein kinase (AME2/AFC1) ; supp	AFC1	AT3G53570	1.01	0.01	0.13	0.90366	0.938589	-7.24
258091_at	hypothetical protein predicted by ge	---	AT3G14560	1.03	0.05	0.13	0.903719	0.938589	-7.24
246683_at	putative protein chromokinesin KIF	---	AT5G33300	1.01	0.01	0.13	0.903737	0.938589	-7.24
247631_at	putative MADS box protein various	AGL62	AT5G60440	1.01	0.01	0.13	0.903855	0.938669	-7.24
255248_at	Oxygen-evolving enhancer protein	PSBQ-2	AT4G05180	1.01	0.01	0.13	0.903997	0.938727	-7.24
259317_at	hypothetical protein identical to hyp	HYP1	AT3G01100	-1.01	-0.02	-0.13	0.904	0.938727	-7.24
254356_at	hypothetical protein ;supported by	---	AT4G22190	-1.01	-0.02	-0.13	0.904074	0.938727	-7.24
256395_at	putative helix-loop-helix DNA-bindir	MUTE	AT3G06120	-1.01	-0.02	-0.13	0.904125	0.938727	-7.24
259798_at	hypothetical protein predicted by ge	---	AT1G64310	1.01	0.02	0.13	0.904141	0.938727	-7.24
257479_at	hypothetical protein contains simila	WAKL4	AT1G16150	-1.02	-0.02	-0.13	0.904158	0.938727	-7.24
255339_at	hypothetical protein similar to A. th	---	AT4G04480	1.02	0.03	0.12	0.904279	0.93881	-7.24
251900_at	putative protein lateral root primord	SRS6	AT3G54430	1.01	0.02	0.12	0.904389	0.938881	-7.24
256551_at	unknown protein	---	---	-1.01	-0.02	-0.12	0.90494	0.939377	-7.24
250487_at	putative protein MRS2 protein, Sac	---	AT5G09690	1.01	0.02	0.12	0.904948	0.939377	-7.24
262450_at	hypothetical protein identical to hyp	---	AT1G11320	1.01	0.02	0.12	0.905114	0.939506	-7.24
257811_at	nitrate transporter, putative similar	---	AT3G25280	-1.01	-0.01	-0.12	0.905493	0.939857	-7.24
252382_at	ABC-type transport protein-like pro	ATH5	AT3G47770	1.01	0.01	0.12	0.905638	0.939908	-7.24
265300_at	unknown protein contains weak PH	---	AT2G13950	-1.01	-0.02	-0.12	0.905752	0.939908	-7.24

250925_at	putative protein ; supported by full-	---	AT5G03370	1.01	0.02	0.12	0.905765	0.939908	-7.24
251116_at	serin carboxypeptidase - like protei	scpl40	AT3G63470	1.01	0.02	0.12	0.905765	0.939908	-7.24
248278_at	putative protein similar to unknown	---	AT5G52890	1.01	0.02	0.12	0.905778	0.939908	-7.24
244925_at	NADH dehydrogenase subunit 7	---	---	-1.01	-0.02	-0.12	0.905789	0.939908	-7.24
246723_at	putative protein various predicted p	---	AT5G29030	-1.01	-0.01	-0.12	0.906125	0.9402	-7.24
266974_at	unknown protein	---	AT2G39370	1.01	0.01	0.12	0.906153	0.9402	-7.24
263338_at	hypothetical protein predicted by ge	---	---	-1.01	-0.01	-0.12	0.906216	0.940222	-7.24
258263_at	unknown protein	---	AT3G15780	-1.02	-0.03	-0.12	0.906286	0.940253	-7.24
262276_at	hypothetical protein predicted by ge	---	AT1G68700	-1.01	-0.01	-0.12	0.906391	0.940277	-7.24
265650_at	hypothetical protein predicted by ge	---	AT2G27460	-1.01	-0.01	-0.12	0.906392	0.940277	-7.24
249458_at	putative protein predicted proteins,	---	AT5G39560	-1.01	-0.01	-0.12	0.90644	0.940284	-7.24
250576_at	cytochrome P450-like protein sever	---	AT5G08250	1.01	0.01	0.12	0.906836	0.94061	-7.24
261244_at	subtilisin-like serine protease simila	---	AT1G20150	1.01	0.01	0.12	0.906872	0.94061	-7.24
246336_at	putative protein putative integral m	ATCHX4	AT3G44900	-1.01	-0.01	-0.12	0.906878	0.94061	-7.24
252124_at	hypothetical protein ;supported by	---	AT3G51010	-1.01	-0.02	-0.12	0.907161	0.940861	-7.24
263999_at	hypothetical protein predicted by ge	---	AT2G22370	-1.01	-0.02	-0.12	0.907636	0.94131	-7.24
246326_at	unknown protein ; supported by cDI	REV7	AT1G16590	1.01	0.01	0.12	0.907964	0.941607	-7.24
260310_at	hypothetical protein predicted by ge	---	AT1G70590	-1.01	-0.02	-0.12	0.908014	0.941617	-7.24
257120_at	protein kinase, putative contains P	---	AT3G20200	-1.01	-0.01	-0.12	0.908055	0.941617	-7.24
260811_s_a	hypothetical protein predicted by ge	---	---	-1.01	-0.01	-0.12	0.908415	0.941903	-7.24
247945_at	putative protein contains similarity t	---	AT5G57150	-1.03	-0.04	-0.12	0.908441	0.941903	-7.24
249798_at	putative protein contains similarity t	---	AT5G23730	1.01	0.01	0.12	0.908521	0.941903	-7.24
250773_at	putative protein similar to unknown	---	AT5G05430	-1.02	-0.02	-0.12	0.90853	0.941903	-7.24
249586_at	putative protein predicted proteins,	---	AT5G37840	1.02	0.03	0.12	0.908538	0.941903	-7.24
260796_at	glutathione transferase, putative si	ATGSTU21	AT1G78360	1.01	0.02	0.12	0.908801	0.942133	-7.24
247201_at	50S ribosomal protein L29 ; suppo	---	AT5G65220	-1.01	-0.02	-0.12	0.908851	0.942142	-7.24
266090_at	unknown protein	---	AT2G38000	1.01	0.02	0.12	0.909015	0.942255	-7.24
261121_at	hypothetical protein predicted by ge	---	AT1G75340	1.01	0.01	0.12	0.909043	0.942255	-7.24
245402_at	putative protein	---	AT4G17585	1.01	0.01	0.12	0.909171	0.942345	-7.24
245083_at	putative integral membrane protein	ATRER1C1	AT2G23310	-1.01	-0.01	-0.12	0.909307	0.942405	-7.24
252591_at	putative protein senescence-assoc	TET3	AT3G45600	1.02	0.02	0.12	0.909311	0.942405	-7.24
266080_at	hypothetical protein predicted by ge	---	AT2G37840	1.01	0.01	0.12	0.909512	0.94257	-7.24
256000_at	glycyl tRNA synthetase, putative si	---	AT1G29880	-1.01	-0.01	-0.12	0.909581	0.942598	-7.24
264495_at	hypothetical protein predicted by ge	RIC2	AT1G27380	-1.01	-0.01	-0.12	0.909622	0.942598	-7.24
245646_x_a	F5A9.9 hypothetical protein	---	AT1G24851	-1.01	-0.01	-0.12	0.909689	0.942626	-7.24

264683_at	unknown protein similar to putative	FRA3	AT1G65580	-1.01	-0.01	-0.12	0.909764	0.94266	-7.24
257508_at	bZIP transcription factor, putative c	---	AT1G64320	1.01	0.01	0.12	0.909823	0.942678	-7.24
255349_at	hypothetical protein	---	AT4G03830	-1.01	-0.01	-0.12	0.910024	0.942844	-7.24
257085_at	ubiquitin-specific protease 14 (UBF	UBP14	AT3G20630	1.02	0.02	0.12	0.910373	0.943163	-7.24
261332_s_a	hypothetical protein contains simila	---	---	1.01	0.01	0.12	0.910433	0.943181	-7.24
263217_at	putative reticuline oxidase-like prot	---	AT1G30740	-1.01	-0.01	-0.12	0.910868	0.94359	-7.24
263732_at	hypothetical protein predicted by ge	ARL2	AT1G59980	-1.01	-0.01	-0.12	0.910948	0.94363	-7.24
245414_at	hypothetical protein	---	AT4G17310	1.01	0.02	0.12	0.911148	0.943794	-7.24
265518_at	hypothetical protein predicted by ge	---	AT2G06040	1.01	0.02	0.12	0.911248	0.943855	-7.24
260354_at	unknown protein ;supported by full-	---	AT1G69330	-1.01	-0.02	-0.12	0.911624	0.944198	-7.24
266803_at	putative protein kinase contains a p	APK1B	AT2G28930	-1.02	-0.03	-0.12	0.911663	0.944198	-7.24
253279_at	putative protein B subunit of propio	MCCB	AT4G34030	-1.02	-0.03	-0.12	0.91173	0.944225	-7.24
245739_at	mitotic cyclin a2-type, putative simi	CYCA1;1	AT1G44110	-1.01	-0.01	-0.11	0.911819	0.944274	-7.24
250509_at	cytochrome P450	CYP78A7	AT5G09970	-1.01	-0.02	-0.11	0.912158	0.944485	-7.24
249169_at	putative protein strong similarity to	---	AT5G42880	1.01	0.01	0.11	0.912167	0.944485	-7.24
252532_at	glucosidase-like protein GLUCAN I	---	AT3G46570	1.01	0.02	0.11	0.912182	0.944485	-7.24
255054_s_a	cellulase-like protein cellulase (EC	AtGH9B15	AT4G09740	1.01	0.01	0.11	0.912191	0.944485	-7.24
266369_at	hypothetical protein predicted by ge	BOP2	AT2G41370	1.01	0.02	0.11	0.912229	0.944485	-7.24
261491_at	hypothetical protein contains simila	FLP	AT1G14350	1.03	0.04	0.11	0.912289	0.944504	-7.24
250557_at	putative protein ankyrin, Rattus no	CPuORF16	AT5G07840	1.01	0.01	0.11	0.912396	0.944572	-7.24
265623_at	hypothetical protein predicted by ge	---	AT2G27270	-1.01	-0.01	-0.11	0.912452	0.944587	-7.24
246978_at	cytochrome P450-like protein fatty	CYP714A1	AT5G24910	-1.02	-0.02	-0.11	0.912528	0.944623	-7.24
266828_at	putative flavonol 3-O-glucosyltransf	---	AT2G22930	-1.01	-0.01	-0.11	0.912733	0.944792	-7.24
260839_at	unknown protein	---	AT1G43690	1.01	0.01	0.11	0.912774	0.944792	-7.24
261186_at	hypothetical protein predicted by ge	---	---	1.01	0.01	0.11	0.91285	0.944827	-7.24
245245_at	delta-aminolevulinic acid dehydrata	hemb2	AT1G44318	1.01	0.01	0.11	0.913139	0.945041	-7.24
260155_at	unknown protein	---	AT1G52870	-1.02	-0.03	-0.11	0.913175	0.945041	-7.24
267457_at	putative proline-rich protein	AGP30	AT2G33790	-1.01	-0.01	-0.11	0.913181	0.945041	-7.24
245550_at	cytochrome P450 like protein	CYP705A1	AT4G15330	-1.01	-0.01	-0.11	0.913251	0.945072	-7.24
256557_at	hypothetical protein similar to hypot	---	---	1.01	0.01	0.11	0.913352	0.945133	-7.24
248772_at	photoreceptor-interacting protein-lik	---	AT5G47800	-1.02	-0.03	-0.11	0.913572	0.945317	-7.24
255512_at	Expressed protein ; supported by c	SYP42	AT4G02195	-1.01	-0.02	-0.11	0.913887	0.945576	-7.24
264178_at	latex-abundant protein, putative sir	AMC1	AT1G02170	-1.01	-0.01	-0.11	0.913905	0.945576	-7.24
248893_at	unknown protein	---	AT5G46310	1.01	0.01	0.11	0.913984	0.945615	-7.24
AFFX-PheX	B. subtilis /GEN=pheB /DB_XREF=	---	---	-1.01	-0.02	-0.11	0.914159	0.945753	-7.24

245469_at	reverse transcriptase like protein	---	---	1.01	0.01	0.11	0.914324	0.945881	-7.24
267383_at	unknown protein	---	AT2G44360	1.01	0.01	0.11	0.914382	0.945898	-7.24
248824_at	putative protein contains similarity t	---	AT5G46940	-1.11	-0.15	-0.11	0.914548	0.946027	-7.24
254582_at	putative protein TMV resistance pr	---	AT4G19470	1.01	0.01	0.11	0.914723	0.946136	-7.24
247829_at	protein kinase - like protein kinase	---	AT5G58520	1.01	0.02	0.11	0.914815	0.946136	-7.24
262524_at	tuftelin-interacting-like protein Simil	---	AT1G17070	-1.01	-0.01	-0.11	0.914816	0.946136	-7.24
253630_at	putative protein putative ATPase -	---	AT4G30490	1.01	0.02	0.11	0.914819	0.946136	-7.24
248989_at	disease resistance protein RPS4	---	AT5G45200	-1.01	-0.01	-0.11	0.915037	0.946249	-7.24
260653_at	pyruvate kinase, plastid isozyme, p	PKp3	AT1G32440	1.01	0.01	0.11	0.915051	0.946249	-7.24
253874_at	putative protein stem-specific prote	---	AT4G27450	-1.02	-0.03	-0.11	0.915064	0.946249	-7.24
246663_at	putative protein	---	AT5G35300	-1.01	-0.01	-0.11	0.915094	0.946249	-7.24
264800_at	hypothetical protein similar to IFA-b	---	AT1G08800	-1.01	-0.02	-0.11	0.915345	0.946465	-7.24
245954_at	far-red impaired response protein (	FRS10	AT5G28530	1.01	0.01	0.11	0.915438	0.946472	-7.24
247860_at	bis(5'-adenosyl)-triphosphatase-like	---	AT5G58240	-1.01	-0.01	-0.11	0.915461	0.946472	-7.24
256362_at	hypothetical protein	---	AT1G66450	-1.01	-0.01	-0.11	0.9155	0.946472	-7.24
250878_at	maturase -like protein gene cob int	---	AT5G04050	1.01	0.02	0.11	0.915518	0.946472	-7.24
263175_at	hypothetical protein similar to unkno	---	AT1G05510	1.01	0.01	0.11	0.915565	0.946478	-7.24
254017_at	putative transcription factor	---	AT4G26170	-1.01	-0.01	-0.11	0.915623	0.946484	-7.24
247274_at	putative protein similar to unknown	---	AT5G64360	-1.01	-0.02	-0.11	0.915654	0.946484	-7.24
260483_at	Barley Mlo protein isolog ; supporte	MLO4	AT1G11000	-1.01	-0.02	-0.11	0.915723	0.946513	-7.24
257974_at	unknown protein similar to NA-DAM	---	AT3G20820	1.03	0.04	0.11	0.916047	0.946764	-7.24
261548_at	DNA-binding protein, putative cont	---	AT1G63480	1.01	0.02	0.11	0.916084	0.946764	-7.24
248422_at	putative protein strong similarity to	YLS7	AT5G51640	-1.01	-0.01	-0.11	0.916104	0.946764	-7.24
250540_at	unknown protein ; supported by cD	---	AT5G08580	-1.01	-0.02	-0.11	0.916133	0.946764	-7.24
263163_at	fructokinase, putative predicted by	FZL	AT1G03160	1.02	0.03	0.11	0.916208	0.9468	-7.24
265516_at	putative Athila retroelement ORF1 p	---	---	-1.01	-0.01	-0.11	0.916335	0.946818	-7.24
253185_at	putative protein bZIP protein - Arab	---	AT4G35240	-1.01	-0.02	-0.11	0.916374	0.946818	-7.24
244970_at	ribosomal protein L20	---	---	1.02	0.02	0.11	0.916387	0.946818	-7.24
257243_at	pectate lyase, putative similar to G	---	AT3G24230	1.01	0.01	0.11	0.916413	0.946818	-7.24
267257_at	putative casein kinase II catalytic (a	---	AT2G23080	-1.01	-0.01	-0.11	0.916433	0.946818	-7.24
249448_at	cdc2-like protein	cdc2cAt	AT5G39420	-1.01	-0.02	-0.11	0.916505	0.946849	-7.24
256847_at	early nodule-specific protein, putat	---	AT3G27950	-1.01	-0.01	-0.11	0.916906	0.94722	-7.24
264794_at	hypothetical protein predicted by ge	---	AT1G08670	-1.01	-0.01	-0.11	0.917028	0.947304	-7.24
266669_at	putative flavonol 3-O-glucosyltransf	UGT71C1	AT2G29750	1.01	0.01	0.11	0.917097	0.947327	-7.24
250452_at	putative protein KIAA1038 protein,	---	AT5G10630	-1.01	-0.01	-0.11	0.917134	0.947327	-7.24

265555_at	putative Mutator-like transposase re	---	---	-1.01	-0.01	-0.11	0.917656	0.947771	-7.24
265625_at	hypothetical protein predicted by ge	---	AT2G27240	1.01	0.02	0.11	0.917665	0.947771	-7.24
254743_at	potassium transporter - like protein	HAK5	AT4G13420	-1.06	-0.09	-0.11	0.917688	0.947771	-7.24
258577_at	putative disease resistance protein	---	AT3G04220	1.02	0.03	0.11	0.917864	0.947879	-7.24
251454_at	putative protein COP1-interacting p	---	AT3G60080	-1.01	-0.02	-0.11	0.917876	0.947879	-7.24
245493_at	hypothetical protein	---	---	-1.01	-0.01	-0.11	0.918048	0.948014	-7.24
258360_at	hypothetical protein predicted by ge	---	AT3G14250	-1.01	-0.01	-0.11	0.918166	0.948092	-7.24
246160_at	putative protein predicted protein, (	FBX2	AT5G21040	-1.01	-0.01	-0.11	0.918275	0.948141	-7.24
253230_at	putative protein ; supported by full-	---	AT4G34700	-1.01	-0.01	-0.11	0.918296	0.948141	-7.24
249438_at	putative protein BCS1 nuclear gen	AATP1	AT5G40010	1.01	0.02	0.11	0.918362	0.948166	-7.24
263276_at	putative cytochrome P450	CYP705A1	AT2G14100	-1.01	-0.01	-0.11	0.918543	0.94831	-7.24
246105_at	putative protein predicted helicase	---	---	-1.01	-0.01	-0.11	0.918686	0.948404	-7.24
259122_at	unknown protein similar to putative	COBL1	AT3G02210	1.01	0.01	0.11	0.918717	0.948404	-7.24
258546_at	hypothetical protein predicted by ge	emb1974	AT3G07060	1.01	0.01	0.11	0.918878	0.948463	-7.24
252501_at	hypothetical protein	---	AT3G46880	1.01	0.01	0.11	0.918878	0.948463	-7.24
255313_at	putative transposon protein	---	---	1.01	0.01	0.11	0.918899	0.948463	-7.24
266681_at	copia-like retroelement pol polyprot	---	---	-1.01	-0.01	-0.11	0.918983	0.948491	-7.24
246314_at	promoter-binding factor-like protein	AREB3	AT3G56850	1.01	0.01	0.11	0.919027	0.948491	-7.24
262520_at	putative polygalacturonase After fir	---	AT1G17150	-1.01	-0.01	-0.11	0.9191	0.948491	-7.24
252809_at	putative protein various predicted p	---	---	-1.01	-0.01	-0.11	0.919118	0.948491	-7.24
261123_at	hypothetical protein predicted by ge	---	AT1G62860	-1.01	-0.02	-0.11	0.919134	0.948491	-7.24
261361_at	hypothetical protein predicted by ge	---	---	-1.01	-0.01	-0.10	0.919466	0.948791	-7.24
249627_at	NADH dehydrogenase (ubiquinone	EMB1467	AT5G37510	1.01	0.01	0.10	0.919545	0.948829	-7.24
254799_at	putative protein various predicted p	---	AT4G13060	1.01	0.01	0.10	0.919745	0.948993	-7.24
255368_at	hypothetical protein	---	---	1.01	0.01	0.10	0.91982	0.94902	-7.24
249861_at	Expressed protein ; supported by fu	---	AT5G22875	-1.01	-0.01	-0.10	0.919855	0.94902	-7.24
262691_at	TPR-repeat protein contains multipl	---	AT1G62740	-1.01	-0.02	-0.10	0.919921	0.949045	-7.24
254971_at	major intrinsic protein (MIP) - like n	NIP5;1	AT4G10380	-1.01	-0.02	-0.10	0.920055	0.949141	-7.24
255853_at	hypothetical protein predicted by ge	---	AT1G67020	1.01	0.01	0.10	0.920222	0.94923	-7.24
252024_at	monodehydroascorbate reductase	ATMDAR1	AT3G52880	-1.01	-0.02	-0.10	0.920265	0.94923	-7.24
265719_at	unknown protein related to putative	---	AT2G03500	1.01	0.01	0.10	0.920323	0.94923	-7.24
256370_at	MATE efflux family protein, putative	---	AT1G66780	-1.01	-0.01	-0.10	0.920365	0.94923	-7.24
263441_at	putative kinesin-like spindle protein	---	AT2G28620	1.01	0.01	0.10	0.92037	0.94923	-7.24
260466_at	phosphatidylinositol-4-phosphate 5-	---	AT1G10900	-1.02	-0.03	-0.10	0.920391	0.94923	-7.24
251770_at	leucoanthocyanidin dioxygenase -l	---	AT3G55970	-1.04	-0.06	-0.10	0.920541	0.949342	-7.24

248003_at	putative protein contains similarity t	---	AT5G56220	-1.03	-0.04	-0.10	0.92092	0.949629	-7.24
262470_at	disease resistance protein, putative	---	AT1G50180	1.01	0.01	0.10	0.92094	0.949629	-7.24
266553_at	unknown protein ; supported by cD	---	AT2G46170	-1.01	-0.01	-0.10	0.920944	0.949629	-7.24
256837_at	hypothetical protein similar to DNA-	NRPD7	AT3G22900	-1.01	-0.02	-0.10	0.921159	0.949807	-7.24
265491_s_a	putative retroelement pol polyprotei	---	---	-1.01	-0.01	-0.10	0.921209	0.949815	-7.24
264778_at	unknown protein similar to C-1 (Hor	AIP3	AT1G08780	1.01	0.01	0.10	0.92129	0.949857	-7.24
255100_at	putative MuDR-like transposon prot	---	---	1.01	0.01	0.10	0.921412	0.94994	-7.24
264628_at	hypothetical protein contains simila	---	AT1G65540	-1.01	-0.01	-0.10	0.921509	0.949996	-7.24
265064_at	hypothetical protein contains simila	ENT7	AT1G61630	1.01	0.02	0.10	0.921626	0.95	-7.24
252568_at	receptor-like protein kinase recepto	---	AT3G45410	-1.01	-0.02	-0.10	0.921651	0.95	-7.24
259357_at	unknown protein ;supported by full-	---	AT1G13380	1.01	0.01	0.10	0.921685	0.95	-7.24
247389_at	putative protein strong similarity to	---	AT5G63490	-1.01	-0.02	-0.10	0.92169	0.95	-7.24
262331_at	unknown protein	---	AT1G64050	-1.01	-0.01	-0.10	0.92172	0.95	-7.24
251019_at	putative protein predicted proteins,	---	AT5G02420	1.01	0.01	0.10	0.92197	0.950194	-7.24
258702_at	hypothetical protein predicted by ge	---	AT3G09730	1.01	0.02	0.10	0.921992	0.950194	-7.24
246569_at	lysophospholipase -like protein lys	---	AT5G14980	1.01	0.01	0.10	0.922081	0.950243	-7.24
261417_at	Expressed protein ; supported by c	---	AT1G07700	-1.01	-0.01	-0.10	0.922152	0.950248	-7.24
251808_at	AP3-complex beta-3A adaptin subu	---	AT3G55480	-1.01	-0.01	-0.10	0.92217	0.950248	-7.24
259157_at	hypothetical protein predicted by ge	---	AT3G05440	-1.01	-0.01	-0.10	0.922275	0.950308	-7.24
261316_at	MAP kinase BnMAP4K alpha1, put	ATMAP4K	AT1G53165	1.01	0.01	0.10	0.922312	0.950308	-7.24
249005_at	terpene cyclase/synthase	---	AT5G44630	-1.01	-0.01	-0.10	0.922606	0.950569	-7.24
246349_at	Expressed protein ; supported by fu	---	AT1G51915	1.02	0.03	0.10	0.922725	0.950649	-7.24
247704_at	Expressed protein ; supported by fu	RTFL5	AT5G59510	1.02	0.03	0.10	0.92292	0.950784	-7.24
259943_at	unknown protein	---	AT1G71480	-1.01	-0.02	-0.10	0.922939	0.950784	-7.24
259451_at	synaptosomal associated protein (	SNAP30	AT1G13890	-1.01	-0.01	-0.10	0.923134	0.950907	-7.24
248602_s_a	MADS-box protein-like	---	AT5G38620	-1.01	-0.01	-0.10	0.923143	0.950907	-7.24
267039_at	hypothetical protein predicted by ge	---	AT2G34270	1.01	0.01	0.10	0.92323	0.950954	-7.24
253705_at	hexokinase ; supported by cDNA: g	HXK1	AT4G29130	1.01	0.02	0.10	0.923336	0.95102	-7.24
260216_at	hypothetical protein contains Pfam	---	AT1G74580	-1.01	-0.01	-0.10	0.923703	0.951355	-7.24
251495_at	putative protein RanBP7/importin 7	---	AT3G59020	1.01	0.02	0.10	0.923957	0.951574	-7.24
249759_at	putative protein contains similarity t	YSL2	AT5G24380	-1.01	-0.02	-0.10	0.924112	0.95169	-7.24
248301_at	DnaJ protein-like	---	AT5G53150	1.01	0.01	0.10	0.92419	0.951728	-7.24
267313_at	putative protein phosphatase 2C	---	AT2G34740	-1.01	-0.01	-0.10	0.924451	0.951953	-7.24
248244_at	heat shock transcription factor HSF	---	AT5G53640	-1.01	-0.01	-0.10	0.924665	0.952131	-7.24
263491_at	phosphoenolpyruvate carboxylase	ATPPC2	AT2G42600	-1.01	-0.01	-0.10	0.924769	0.952196	-7.24

245470_at	retrotransposon like protein	---	---	1.01	0.01	0.10	0.924958	0.952328	-7.24
266381_at	putative sucrose-proton symporter	ATSUC8	AT2G14670	-1.01	-0.01	-0.10	0.924982	0.952328	-7.24
266973_at	hypothetical protein predicted by gr	---	AT2G39620	-1.01	-0.01	-0.10	0.925167	0.952476	-7.24
261947_at	ubiquitin, putative similar to poly-ub	---	AT1G64470	1.01	0.01	0.10	0.925518	0.952727	-7.24
254534_at	putative Fe(II) transport protein Fe	IRT2	AT4G19680	1.01	0.01	0.10	0.925532	0.952727	-7.24
260315_at	hypothetical protein similar to C-ter	---	AT1G63820	1.01	0.01	0.10	0.925536	0.952727	-7.24
264074_at	putative retroelement pol polyprotei	---	---	1.01	0.01	0.10	0.925668	0.95282	-7.24
257117_at	geranyl geranyl pyrophosphate syn	---	AT3G20160	1.01	0.01	0.10	0.925853	0.952968	-7.24
246709_s_a	putative protein many predicted pro	---	AT5G28160	-1.01	-0.01	-0.10	0.92628	0.953364	-7.24
254072_at	putative protein ClpC protease - Sp	---	AT4G25370	-1.01	-0.01	-0.10	0.926331	0.953373	-7.24
256553_at	hypothetical protein contains simila	---	---	-1.01	-0.01	-0.10	0.926624	0.953631	-7.24
251822_at	centromere protein - like centrome	---	AT3G55060	-1.01	-0.01	-0.10	0.926873	0.953845	-7.24
249369_at	putative protein Kelch motif contair	---	AT5G40680	1.01	0.01	0.10	0.926921	0.953852	-7.24
266829_at	hypothetical protein predicted by ge	---	AT2G22940	1.01	0.01	0.10	0.926979	0.953868	-7.24
256470_at	hypothetical protein predicted by ge	---	AT1G42570	-1.01	-0.01	-0.10	0.927046	0.953894	-7.24
245690_at	phenylalanine ammonia-lyase PAL3	PAL3	AT5G04230	-1.01	-0.02	-0.09	0.927094	0.9539	-7.24
249588_at	protein kinase - like protein Pto kin	---	AT5G37790	-1.01	-0.02	-0.09	0.927224	0.953991	-7.24
258272_at	unknown protein similar to serine/tl	---	AT3G15610	-1.01	-0.02	-0.09	0.927375	0.95403	-7.24
245283_at	Expressed protein ; supported by c	AT-HSFA5	AT4G13980	1.01	0.01	0.09	0.927393	0.95403	-7.24
266908_at	putative protein kinase contains a p	PID	AT2G34650	1.02	0.03	0.09	0.92742	0.95403	-7.24
267302_at	putative unknown protein, leucine-r	---	AT2G30100	-1.01	-0.01	-0.09	0.92743	0.95403	-7.24
254226_at	putative disease resistance respon	---	AT4G23690	-1.04	-0.06	-0.09	0.927635	0.954184	-7.24
252429_at	H-protein promoter binding factor-2	CDF3	AT3G47500	1.01	0.02	0.09	0.927663	0.954184	-7.24
255823_at	unknown protein ;supported by full-	LBD15	AT2G40470	-1.02	-0.03	-0.09	0.927787	0.954253	-7.24
263507_s_a	hypothetical protein	---	---	-1.01	-0.02	-0.09	0.927868	0.954253	-7.24
266724_at	hypothetical protein predicted by ge	---	AT2G03180	1.01	0.01	0.09	0.927905	0.954253	-7.24
260124_at	E2, ubiquitin-conjugating enzyme,	UBC31	AT1G36340	1.01	0.01	0.09	0.927914	0.954253	-7.24
248714_at	polygalacturonase ;supported by fu	---	AT5G48140	-1.01	-0.01	-0.09	0.927939	0.954253	-7.24
255084_s_a	putative protein same aa sequence	---	AT4G09220	-1.01	-0.01	-0.09	0.928006	0.954279	-7.24
245071_at	putative vetispiradiene synthase	---	AT2G23230	-1.01	-0.01	-0.09	0.928186	0.954416	-7.24
263277_at	hypothetical protein predicted by ge	---	AT2G14110	-1.01	-0.01	-0.09	0.928223	0.954416	-7.24
267121_at	putative GDSL-motif lipase/hydrola	---	AT2G23540	-1.01	-0.02	-0.09	0.928373	0.954527	-7.24
263436_at	hypothetical protein	---	AT2G28690	-1.01	-0.01	-0.09	0.928464	0.954558	-7.24
256287_at	hypothetical protein	---	AT3G12190	-1.01	-0.01	-0.09	0.928534	0.954558	-7.24
247212_at	putative protein similar to unknown	---	AT5G65040	1.01	0.01	0.09	0.928565	0.954558	-7.24

246257_at	splicing factor-like protein	ATU2AF65	AT4G36690	-1.01	-0.01	-0.09	0.92857	0.954558	-7.24
253893_at	putative protein hypothetical protei	---	AT4G27390	1.01	0.01	0.09	0.92866	0.954607	-7.24
259127_at	putative translation initiation factor I	---	AT3G02270	-1.01	-0.01	-0.09	0.928723	0.954629	-7.24
255899_at	zinc-finger protein (C-terminal), put	---	AT1G17970	1.01	0.02	0.09	0.928824	0.95469	-7.24
257201_at	unknown protein	---	AT3G23740	-1.01	-0.01	-0.09	0.929384	0.955136	-7.24
260652_at	putative MYB family transcription fa	---	AT1G32360	-1.01	-0.01	-0.09	0.929395	0.955136	-7.24
248345_at	unknown protein	SHOC1	AT5G52290	1.01	0.01	0.09	0.929399	0.955136	-7.24
266021_at	unknown protein	---	AT2G05910	1.01	0.02	0.09	0.929442	0.955136	-7.24
249002_at	putative protein contains similarity t	---	AT5G44520	-1.01	-0.01	-0.09	0.929467	0.955136	-7.24
246530_at	Expressed protein ; supported by fu	---	AT5G15725	-1.01	-0.01	-0.09	0.929625	0.955255	-7.24
245658_at	hypothetical protein predicted by ge	RALFL4	AT1G28270	-1.01	-0.01	-0.09	0.929706	0.955295	-7.24
249339_at	putative protein similar to unknown	---	AT5G41100	1.02	0.03	0.09	0.929837	0.955364	-7.24
262317_at	unknown protein ;supported by full-	EDA4	AT2G48140	-1.01	-0.02	-0.09	0.929857	0.955364	-7.24
263838_at	putative s-adenosylmethionine synt	MAT3	AT2G36880	-1.02	-0.03	-0.09	0.929968	0.955435	-7.24
252728_at	putative protein various predicted p	---	---	1.01	0.01	0.09	0.930358	0.955793	-7.24
263262_at	unknown protein	---	AT2G38830	1.01	0.01	0.09	0.930409	0.955802	-7.24
253030_at	hypothetical protein	FRS5	AT4G38180	1.01	0.01	0.09	0.930798	0.956159	-7.24
254139_at	hypothetical protein	---	AT4G24600	-1.01	-0.01	-0.09	0.93097	0.956292	-7.24
260833_at	lipase, putative similar to lipase GE	---	AT1G06800	-1.02	-0.02	-0.09	0.931292	0.956537	-7.24
251792_at	probable serine/threonine-specific	---	AT3G55550	-1.01	-0.01	-0.09	0.931292	0.956537	-7.24
260149_at	putative oxidoreductase similar to a	---	AT1G52810	1.02	0.02	0.09	0.931467	0.956674	-7.24
252391_at	putative protein ; supported by cDN	---	AT3G47860	1.01	0.01	0.09	0.931564	0.956675	-7.24
255124_at	putative self-incompatability RNA-b	APUM15	AT4G08560	-1.01	-0.01	-0.09	0.93159	0.956675	-7.24
248210_at	ethylene-forming-enzyme-like dioxy	---	AT5G54000	1.01	0.01	0.09	0.931594	0.956675	-7.24
252153_at	putative protein several hypothetica	---	AT3G51360	1.01	0.01	0.09	0.931732	0.956774	-7.24
261200_at	60S ribosomal protein L27a, putati	---	AT1G12960	-1.01	-0.01	-0.09	0.931793	0.956793	-7.24
249834_at	putative protein contains similarity t	FTRA1	AT5G23440	-1.01	-0.01	-0.09	0.93196	0.956908	-7.24
264125_at	hypothetical protein predicted by ge	EMB1135	AT1G79350	1.01	0.01	0.09	0.932026	0.956908	-7.24
264919_at	hypothetical protein contains simila	---	AT1G60540	1.01	0.01	0.09	0.932046	0.956908	-7.24
245837_at	peptidylprolyl isomerase, putative s	---	AT1G58450	1.01	0.01	0.09	0.932073	0.956908	-7.24
265209_at	putative DNA binding protein with h	ATHB22	AT2G36610	-1.01	-0.01	-0.09	0.932434	0.957236	-7.24
246840_at	putative protein ;supported by full-l	---	AT5G26610	1.01	0.01	0.09	0.93256	0.957322	-7.24
249117_at	heat shock transcription factor-like p	AT-HSFA6A	AT5G43840	1.01	0.01	0.09	0.932605	0.957325	-7.24
258754_at	hypothetical protein similar to hypot	---	AT3G11920	1.01	0.01	0.09	0.932784	0.957428	-7.24
250074_at	UDP-glucose pyrophosphorylase ;	---	AT5G17310	-1.01	-0.01	-0.09	0.932789	0.957428	-7.24

245230_at	hypothetical protein Contains Zinc	---	AT4G25610	1.01	0.01	0.09	0.93302	0.957622	-7.24
259477_at	unknown protein ;supported by full-	---	AT1G19120	-1.01	-0.01	-0.09	0.93312	0.957681	-7.24
255057_at	hypothetical protein	---	AT4G09840	-1.01	-0.01	-0.09	0.933315	0.957838	-7.24
260668_at	unknown protein ;supported by full-	---	AT1G19530	-1.03	-0.04	-0.09	0.933527	0.958013	-7.24
264673_at	Expressed protein ; supported by fu	ATATP-PR	AT1G09795	1.01	0.01	0.09	0.933665	0.958049	-7.24
246806_at	putative cdc20 protein	---	AT5G27080	1.01	0.01	0.09	0.933689	0.958049	-7.24
266648_at	putative trytophanyl-tRNA synthetas	OVA4	AT2G25840	-1.01	-0.01	-0.09	0.933717	0.958049	-7.24
258629_at	stelar K+ outward rectifying channe	SKOR	AT3G02850	-1.01	-0.01	-0.09	0.93373	0.958049	-7.24
261385_at	lipid-transfer protein, putative simila	---	AT1G05450	-1.01	-0.01	-0.09	0.933829	0.958059	-7.24
263165_at	putataive transport protein Similar t	---	AT1G03060	-1.01	-0.01	-0.09	0.933859	0.958059	-7.24
247392_at	glutamate-1-semialdehyde 2,1-ami	GSA1	AT5G63570	1.01	0.02	0.09	0.933866	0.958059	-7.24
254733_at	putative polygalacturonase polygal	---	AT4G13760	1.01	0.01	0.09	0.933932	0.958084	-7.24
261142_at	cyclic nucleotide and calmodulin-re	ATCNGC8	AT1G19780	1.01	0.01	0.09	0.934142	0.958256	-7.24
255151_at	putative protein oxysterol-binding p	ORP1C	AT4G08180	1.01	0.01	0.09	0.934261	0.958335	-7.24
265639_at	putative reverse transcriptase	---	---	-1.01	-0.01	-0.09	0.934372	0.958405	-7.24
258527_at	branched chain alpha-keto acid de	BCE2	AT3G06850	-1.02	-0.03	-0.09	0.934524	0.958518	-7.24
259355_at	hypothetical protein predicted by ge	---	AT3G05240	-1.01	-0.01	-0.09	0.934599	0.958522	-7.24
261636_at	branched-chain amino acid aminot	---	AT1G50110	-1.01	-0.01	-0.09	0.934612	0.958522	-7.24
257603_at	unknown protein	---	AT3G13820	-1.01	-0.01	-0.09	0.934695	0.958529	-7.24
254541_at	putative LTR retrotransposon Bras	---	---	-1.01	-0.01	-0.09	0.934703	0.958529	-7.24
260659_s_a	hypothetical protein predicted by ge	---	AT1G19460	-1.01	-0.01	-0.08	0.934889	0.958678	-7.24
262783_at	receptor-kinase isolog	---	AT1G10850	1.01	0.02	0.08	0.934967	0.958714	-7.24
255534_at	CHP-rich hypothetical protein simila	---	AT4G02190	-1.01	-0.01	-0.08	0.935293	0.959006	-7.24
249312_at	disease resistance protein-like	---	AT5G41550	-1.01	-0.01	-0.08	0.935471	0.959145	-7.24
266676_s_a	hypothetical protein predicted by gr	---	AT2G29605	-1.01	-0.01	-0.08	0.93565	0.959285	-7.24
264232_at	putative protein kinase Pfam HMM	---	AT1G67470	1.02	0.03	0.08	0.935728	0.959322	-7.24
263966_s_a	putative TNP2-like transposon prote	---	---	-1.01	-0.01	-0.08	0.935798	0.959349	-7.24
264662_at	putative sucrose/H+ symporter simi	SUT4	AT1G09960	-1.01	-0.01	-0.08	0.935889	0.959349	-7.24
AFFX-CreX-	Bacteriophage P1 /GEN=cre /DB_X	---	---	-1.01	-0.02	-0.08	0.93593	0.959349	-7.24
248761_at	Expressed protein ; supported by fu	---	AT5G47635	1.01	0.02	0.08	0.93594	0.959349	-7.24
246605_at	putative protein predicted proteins,	---	---	1.01	0.01	0.08	0.935965	0.959349	-7.24
247915_at	putative protein similar to unknown	---	AT5G57570	-1.01	-0.01	-0.08	0.936129	0.95944	-7.24
256090_at	predicted protein	---	AT1G20816	-1.01	-0.01	-0.08	0.936137	0.95944	-7.24
259933_at	Expressed protein ; supported by fu	---	AT1G34350	-1.01	-0.01	-0.08	0.936222	0.959484	-7.24
249459_at	peroxidase ATP24a	---	AT5G39580	-1.04	-0.05	-0.08	0.936368	0.95959	-7.24

250727_at	putative protein similar to unknown	---	AT5G06430	-1.01	-0.01	-0.08	0.936547	0.95973	-7.25
247604_at	putative phytochelatin synthetase -	COBL5	AT5G60950	1.03	0.05	0.08	0.936685	0.959829	-7.25
266674_at	hypothetical protein predicted by ge	---	AT2G29620	1.01	0.01	0.08	0.936738	0.95984	-7.25
256495_at	hypothetical protein contains simila	---	AT1G31530	1.01	0.01	0.08	0.936868	0.959922	-7.25
253441_at	putative protein Fidipidine, Drosopl	---	AT4G32560	1.01	0.01	0.08	0.936969	0.959922	-7.25
265269_at	hypothetical protein predicted by ge	---	AT2G42950	-1.01	-0.01	-0.08	0.936973	0.959922	-7.25
264765_at	receptor kinase, putative similar to	---	AT1G61430	1.01	0.01	0.08	0.936996	0.959922	-7.25
245922_at	putative protein predicted proteins,	---	AT5G28810	-1.01	-0.01	-0.08	0.937028	0.959922	-7.25
252870_at	adenosine-5-phosphosulfate-kinase	AKN2	AT4G39940	-1.02	-0.03	-0.08	0.937112	0.959965	-7.25
253643_at	hypothetical protein ;supported by	---	AT4G29780	-1.02	-0.03	-0.08	0.937392	0.960184	-7.25
248091_at	putative protein strong similarity to	VTC5	AT5G55120	-1.02	-0.03	-0.08	0.937411	0.960184	-7.25
262763_at	hypothetical protein	---	AT1G28690	-1.01	-0.01	-0.08	0.937537	0.960238	-7.25
250377_at	putative protein predicted proteins,	---	AT5G11560	-1.01	-0.01	-0.08	0.937547	0.960238	-7.25
250681_at	unknown protein	---	AT5G06590	-1.01	-0.01	-0.08	0.937672	0.960315	-7.25
267597_at	putative leucine-rich repeat disease	AtRLP24	AT2G33020	-1.01	-0.02	-0.08	0.937707	0.960315	-7.25
250210_at	putative protein similar to unknown	---	AT5G13890	-1.01	-0.01	-0.08	0.937826	0.960394	-7.25
254583_at	hypothetical protein	---	AT4G19480	1.01	0.01	0.08	0.937947	0.960473	-7.25
254777_at	putative protein hypothetical protei	---	AT4G12960	1.01	0.01	0.08	0.937988	0.960473	-7.25
264816_at	hypothetical protein similar to meml	---	AT1G03560	-1.02	-0.02	-0.08	0.93808	0.960525	-7.25
266764_at	putative pectinesterase ;supported	---	AT2G47050	1.01	0.01	0.08	0.938253	0.960644	-7.25
248358_at	cytochrome P-450-like protein	CYP715A1	AT5G52400	-1.02	-0.02	-0.08	0.938285	0.960644	-7.25
267404_at	hypothetical protein predicted by ge	atnudt22	AT2G33980	1.01	0.01	0.08	0.938323	0.960644	-7.25
245918_at	putative protein various predicted p	---	---	1.01	0.01	0.08	0.938617	0.960901	-7.25
254489_at	putative protein berberine bridge e	---	AT4G20800	-1.01	-0.01	-0.08	0.938801	0.961047	-7.25
252641_at	putative protein predicted protein, A	---	AT3G44570	-1.01	-0.01	-0.08	0.938972	0.961157	-7.25
246783_at	sugar transporter-like protein putat	SFP2	AT5G27360	-1.02	-0.03	-0.08	0.938993	0.961157	-7.25
251779_at	putative protein various predicted p	---	---	1.01	0.01	0.08	0.939241	0.961368	-7.25
254125_at	putative alliin lyase alliin lyase (EC	TAR2	AT4G24670	1.01	0.02	0.08	0.939285	0.96137	-7.25
260836_at	hypothetical protein predicted by ge	---	---	1.00	0.01	0.08	0.939606	0.961627	-7.25
246498_at	stearoyl-acyl carrier protein desatu	---	AT5G16230	1.02	0.02	0.08	0.93969	0.961627	-7.25
250775_at	putative protein contains similarity t	---	AT5G05460	-1.01	-0.02	-0.08	0.939713	0.961627	-7.25
258137_at	Expressed protein ; supported by c	UBC37	AT3G24515	-1.01	-0.01	-0.08	0.939738	0.961627	-7.25
259413_at	hypothetical protein contains simila	---	AT1G02320	-1.01	-0.01	-0.08	0.939747	0.961627	-7.25
252412_at	Expressed protein ; supported by fu	---	AT3G47295	-1.01	-0.02	-0.08	0.940223	0.962064	-7.25
247870_at	calmodulin-binding protein ; suppo	---	AT5G57580	1.01	0.01	0.08	0.940258	0.962064	-7.25

249029_at	disease resistance protein-like	---	AT5G44870	-1.01	-0.01	-0.08	0.940352	0.962116	-7.25
255217_s_a	hypothetical protein	---	---	1.01	0.01	0.08	0.94061	0.962338	-7.25
254836_at	flavonoid 3,5-hydroxylase like prote	CYP706A7	AT4G12330	-1.01	-0.01	-0.08	0.940836	0.962525	-7.25
260135_at	calmodulin-related protein similar t	---	AT1G66400	-1.02	-0.03	-0.08	0.940934	0.962583	-7.25
254392_at	endonuclease, putative ; supported	ENDO5	AT4G21600	1.01	0.01	0.08	0.941024	0.962592	-7.25
267542_at	hypothetical protein predicted by ge	---	AT2G32740	-1.01	-0.01	-0.08	0.941028	0.962592	-7.25
246803_at	tSNARE AtTLG2a ; supported by c	SYP41	AT5G26980	1.01	0.01	0.08	0.941314	0.962842	-7.25
254515_at	CLV1 receptor kinase like protein C	BAM3	AT4G20270	1.01	0.01	0.08	0.94148	0.9629	-7.25
248350_at	putative protein similar to unknown	---	AT5G52160	-1.01	-0.01	-0.08	0.94149	0.9629	-7.25
254173_at	putative protein Kaposi's sarcoma-	REN1	AT4G24580	-1.01	-0.01	-0.08	0.941497	0.9629	-7.25
250675_at	putative protein contains similarity t	---	AT5G06260	-1.01	-0.01	-0.08	0.941617	0.962979	-7.25
250078_at	putative protein	ORC3	AT5G16690	1.01	0.01	0.08	0.941755	0.963077	-7.25
244994_at	NADH dehydrogenase ND5	---	---	1.01	0.01	0.08	0.941809	0.963089	-7.25
262475_at	hypothetical protein predicted by ge	---	AT1G50340	-1.01	-0.01	-0.08	0.942008	0.963249	-7.25
261339_at	protein kinase, putative similar to n	---	AT1G35710	1.01	0.02	0.08	0.942064	0.963264	-7.25
250614_at	putative protein homeodomain prot	---	AT5G07260	1.00	0.01	0.08	0.942201	0.963343	-7.25
259817_at	hypothetical protein predicted by ge	---	AT1G49880	-1.01	-0.01	-0.08	0.942246	0.963343	-7.25
255367_at	putative transposon protein	---	---	1.01	0.01	0.08	0.942299	0.963343	-7.25
260197_at	F12A21.25 hypothetical protein	---	AT1G67623	1.01	0.01	0.08	0.942311	0.963343	-7.25
261205_at	hypothetical protein predicted by ge	---	AT1G12790	1.01	0.01	0.08	0.942375	0.963365	-7.25
245759_at	hypothetical protein predicted by ge	---	AT1G66900	1.01	0.01	0.07	0.942816	0.963773	-7.25
252307_at	putative protein SAE1-S9-protein, I	---	---	-1.01	-0.01	-0.07	0.943209	0.964132	-7.25
258442_at	hypothetical protein predicted by ge	---	AT3G01015	-1.01	-0.01	-0.07	0.943308	0.96418	-7.25
252169_at	putative protein several bacterial ph	---	AT3G50520	-1.01	-0.01	-0.07	0.94334	0.96418	-7.25
259270_at	putative porin similar to outer mitoc	VDAC1	AT3G01280	1.01	0.01	0.07	0.943481	0.964275	-7.25
248574_at	putative protein strong similarity to u	---	AT5G49830	1.00	0.01	0.07	0.943518	0.964275	-7.25
244993_s_a	hypothetical protein	---	---	-1.01	-0.01	-0.07	0.94371	0.964427	-7.25
261912_s_a	unknown protein	---	AT1G66000	-1.01	-0.01	-0.07	0.943852	0.964489	-7.25
244962_at	NADH dehydrogenase ND4	---	---	-1.00	-0.01	-0.07	0.943855	0.964489	-7.25
255123_at	putative lipid transfer protein	---	AT4G08530	-1.01	-0.01	-0.07	0.943934	0.964504	-7.25
259854_at	RING-H2 zinc finger protein ATL3,	---	AT1G72200	-1.01	-0.01	-0.07	0.943953	0.964504	-7.25
264912_at	auxin-induced protein, putative sim	---	AT1G60750	-1.01	-0.01	-0.07	0.944201	0.964714	-7.25
264881_s_a	lysine and histidine specific transpo	---	AT1G61270	-1.00	-0.01	-0.07	0.944581	0.965022	-7.25
252837_at	putative protein hypothetical protein	---	---	1.00	0.01	0.07	0.944588	0.965022	-7.25
256975_at	unknown protein similar to putative	---	AT3G21000	1.01	0.01	0.07	0.944666	0.965029	-7.25

253678_at	cytidine deaminase 7	---	AT4G29600	1.01	0.01	0.07	0.944679	0.965029	-7.25
262384_at	disease resistance protein, putative	---	AT1G72950	1.01	0.01	0.07	0.944823	0.965124	-7.25
259999_at	hypothetical protein predicted by ge	---	AT1G68080	1.01	0.01	0.07	0.944857	0.965124	-7.25
261827_at	unknown protein contains similarity	---	AT1G11480	1.01	0.01	0.07	0.944966	0.965192	-7.25
259086_at	hypothetical protein predicted by ge	---	AT3G04990	1.00	0.01	0.07	0.945096	0.965266	-7.25
245943_at	putative protein permease family p	---	AT5G19500	1.01	0.01	0.07	0.945168	0.965266	-7.25
254719_at	putative protein beta 1,3-glucanase	---	AT4G13600	1.01	0.01	0.07	0.945217	0.965266	-7.25
246439_at	RING-H2 zinc finger protein-like RI	---	AT5G17600	-1.02	-0.02	-0.07	0.945239	0.965266	-7.25
260906_at	hypothetical protein predicted by ge	---	AT1G02540	-1.01	-0.01	-0.07	0.945292	0.965266	-7.25
263977_at	hypothetical protein predicted by ge	---	AT2G42660	-1.01	-0.01	-0.07	0.9453	0.965266	-7.25
263595_at	putative purple acid phosphatase c	PAP8	AT2G01890	1.06	0.08	0.07	0.945347	0.965266	-7.25
263266_at	hypothetical protein predicted by ge	---	AT2G16520	-1.01	-0.01	-0.07	0.945377	0.965266	-7.25
261521_at	protein kinase, putative similar to r	SERK1	AT1G71830	1.01	0.02	0.07	0.94548	0.965327	-7.25
256801_at	cytochrome P450, putative similar	CYP705A3	AT3G20940	1.01	0.01	0.07	0.945542	0.965327	-7.25
267235_at	unknown protein	---	AT2G43945	1.00	0.01	0.07	0.945563	0.965327	-7.25
257604_s_a	hypothetical protein predicted by ge	---	AT1G11810	1.01	0.01	0.07	0.945698	0.965421	-7.25
247426_at	putative protein contains similarity t	---	AT5G62570	1.01	0.02	0.07	0.945809	0.965486	-7.25
256036_at	fructose-2,6-bisphosphatase, putat	F2KP	AT1G07110	-1.01	-0.01	-0.07	0.945877	0.965486	-7.25
252603_at	putative protein	---	AT3G45050	-1.01	-0.01	-0.07	0.945889	0.965486	-7.25
260720_at	hypothetical protein predicted by ge	---	AT1G48095	1.01	0.01	0.07	0.94601	0.965567	-7.25
256481_at	elicitor response protein, putative s	---	AT1G33430	1.00	0.01	0.07	0.946104	0.96562	-7.25
253514_at	putative protein DNA-binding prote	---	AT4G31805	1.00	0.01	0.07	0.946405	0.965883	-7.25
248977_at	putative protein strong similarity to	---	AT5G45020	-1.01	-0.01	-0.07	0.946538	0.965923	-7.25
259276_at	putative peroxidase very similar to p	---	AT3G01190	1.00	0.01	0.07	0.946551	0.965923	-7.25
257040_at	unknown protein ; supported by cD	SCO2	AT3G19220	1.01	0.01	0.07	0.946574	0.965923	-7.25
263768_x_a	putative Athila retroelement ORF1 p	---	---	1.00	0.01	0.07	0.946613	0.965923	-7.25
245243_at	hypothetical protein predicted by ge	---	AT1G44414	1.00	0.01	0.07	0.94667	0.965937	-7.25
251274_at	putative protein hypothetical protei	---	AT3G61700	-1.01	-0.01	-0.07	0.946726	0.965952	-7.25
263059_at	putative non-LTR retrolelement reve	---	---	1.01	0.01	0.07	0.946781	0.965965	-7.25
256046_at	unknown protein	---	AT1G07135	-1.02	-0.03	-0.07	0.946958	0.966102	-7.25
266024_at	En/Spm-like transposon protein rela	---	---	1.00	0.01	0.07	0.947336	0.966445	-7.25
262604_at	unknown protein similar to unknow	---	AT1G15060	-1.00	-0.01	-0.07	0.947484	0.966514	-7.25
259343_s_a	putative methionine synthase simila	ATMS2	AT3G03780	-1.01	-0.01	-0.07	0.947488	0.966514	-7.25
249226_at	GDSL-motif lipase/hydrolase-like pr	---	AT5G42170	1.01	0.01	0.07	0.947547	0.96653	-7.25
249408_at	myb-related protein	MYB23	AT5G40330	1.01	0.01	0.07	0.947672	0.966615	-7.25

249617_at	receptor protein kinase-like protein	---	AT5G37450	1.01	0.01	0.07	0.947722	0.966622	-7.25
266459_at	unknown protein supported by full-l	---	AT2G47970	1.01	0.01	0.07	0.947933	0.966717	-7.25
263362_at	putative selenium-binding protein	---	AT2G03880	1.00	0.01	0.07	0.947937	0.966717	-7.25
257813_at	Cdc45-like protein similar to Cdc45	CDC45	AT3G25100	-1.00	-0.01	-0.07	0.947942	0.966717	-7.25
255922_at	trehalose-6-phosphate phosphatas	---	AT1G22210	1.00	0.01	0.07	0.948101	0.9668	-7.25
254795_at	putative protein	---	AT4G12990	-1.00	-0.01	-0.07	0.948108	0.9668	-7.25
253195_at	putative protein dihydroflavonol-4-r	---	AT4G35420	-1.01	-0.01	-0.07	0.948153	0.966802	-7.25
265138_at	hypothetical protein predicted by ge	---	AT1G51300	-1.01	-0.01	-0.07	0.948216	0.966824	-7.25
262928_at	hypothetical protein	---	AT1G65760	-1.01	-0.01	-0.07	0.948279	0.966844	-7.25
252091_at	putative protein NADH dehydroger	---	AT3G51390	1.00	0.01	0.07	0.948467	0.966975	-7.25
255235_at	contains similarity to transposases	---	---	-1.01	-0.01	-0.07	0.948492	0.966975	-7.25
253122_at	hypothetical protein	---	AT4G35987	-1.01	-0.01	-0.07	0.948627	0.96703	-7.25
260260_at	putative reductase similar to cinnar	---	AT1G68540	-1.01	-0.01	-0.07	0.94863	0.96703	-7.25
266706_at	hypothetical protein predicted by ge	---	AT2G03320	1.00	0.01	0.07	0.948739	0.967092	-7.25
255187_s_a	putative transposon protein	---	---	1.01	0.01	0.07	0.948776	0.967092	-7.25
246276_at	Cu2+-transporting ATPase-like prot	HMA1	AT4G37270	1.00	0.01	0.07	0.948863	0.96713	-7.25
258237_at	myb protein identical to ATMYB3 G	ATMYB21	AT3G27810	1.00	0.01	0.07	0.948899	0.96713	-7.25
248995_at	disease resistance protein-like	RRS1	AT5G45260	-1.01	-0.01	-0.07	0.949135	0.967328	-7.25
264477_at	amp-binding protein, putative simil	---	AT1G77240	1.01	0.01	0.07	0.949235	0.967387	-7.25
266399_at	putative phospholipid cytidylyltransf	PECT1	AT2G38670	1.01	0.01	0.07	0.949381	0.967492	-7.25
264144_at	latex-abundant protein, putative sir	AtMC6	AT1G79320	-1.00	-0.01	-0.07	0.949553	0.967592	-7.25
265341_at	hypothetical protein predicted by ge	---	AT2G18360	-1.01	-0.01	-0.07	0.949568	0.967592	-7.25
250312_at	unknown protein	---	AT5G12260	-1.01	-0.01	-0.07	0.949606	0.967592	-7.25
246728_at	putative protein various predicted p	---	AT5G28040	1.00	0.01	0.07	0.949789	0.967722	-7.25
262018_at	hypothetical protein predicted by ge	---	AT1G35617	-1.01	-0.01	-0.07	0.949818	0.967722	-7.25
256950_at	hypothetical protein similar to hypot	---	AT3G19080	1.01	0.01	0.07	0.94989	0.967751	-7.25
266524_at	putative importin, beta subunit	---	AT2G16960	1.01	0.01	0.07	0.949989	0.96781	-7.25
266420_at	putative RNA-binding protein ; sup	---	AT2G38610	1.00	0.01	0.07	0.950059	0.967834	-7.25
265866_at	unknown protein ;supported by full-	---	AT2G01710	1.01	0.01	0.06	0.950098	0.967834	-7.25
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=	---	---	1.01	0.02	0.06	0.950249	0.967944	-7.25
262979_s_a	unknown protein similar to histone h	---	AT1G13370	-1.01	-0.01	-0.06	0.950331	0.967984	-7.25
251750_at	glucuronosyl transferase - like prot	---	AT3G55710	1.01	0.01	0.06	0.950628	0.968244	-7.25
250810_at	putative protein contains similarity t	---	AT5G05090	-1.01	-0.01	-0.06	0.950759	0.968334	-7.25
248570_at	receptor protein kinase-like	---	AT5G49780	-1.00	-0.01	-0.06	0.950899	0.968427	-7.25
251934_at	putative protein delta-latroinsectotc	---	AT3G54070	1.01	0.01	0.06	0.950935	0.968427	-7.25

246658_at	putative protein predicted proteins,	---	---	1.00	0.01	0.06	0.951209	0.968663	-7.25
251099_at	putative protein KIAA0132 - Homo	---	AT5G01660	1.00	0.01	0.06	0.951354	0.968767	-7.25
245261_at	Expressed protein ; supported by cl	---	AT4G14385	1.00	0.01	0.06	0.951482	0.968854	-7.25
249639_at	disease resistance like protein TM	---	AT5G36930	-1.00	-0.01	-0.06	0.951625	0.968957	-7.25
249179_at	Expressed protein ; supported by fu	---	AT5G42955	-1.01	-0.01	-0.06	0.951678	0.968967	-7.25
261659_at	unknown protein contains similarity	TOR	AT1G50030	-1.00	-0.01	-0.06	0.952043	0.969295	-7.25
262063_at	unknown protein identical to unkno	---	AT1G80000	1.01	0.01	0.06	0.952189	0.969402	-7.25
257253_at	unknown protein ; supported by cD	---	AT3G24190	1.01	0.01	0.06	0.952317	0.969488	-7.25
267098_at	hypothetical protein predicted by ge	---	AT2G41451	1.01	0.01	0.06	0.952379	0.969505	-7.25
257222_at	DegP protease almost identical to	DEGP1	AT3G27925	-1.01	-0.01	-0.06	0.952442	0.969505	-7.25
246701_at	cysteine synthase ;supported by fu	CYSD2	AT5G28020	-1.01	-0.01	-0.06	0.952461	0.969505	-7.25
260673_at	unknown protein ; supported by full-	---	AT1G19330	-1.01	-0.01	-0.06	0.952731	0.969719	-7.25
252838_at	hypothetical protein	---	---	-1.00	-0.01	-0.06	0.952809	0.969719	-7.25
245085_at	putative poly(A) binding protein ; su	PAB4	AT2G23350	1.01	0.01	0.06	0.952836	0.969719	-7.25
258513_at	protein kinase, putative contains P	---	AT3G06630	1.00	0.01	0.06	0.952841	0.969719	-7.25
257428_at	hypothetical protein predicted by ge	---	AT1G78990	1.01	0.01	0.06	0.953046	0.969851	-7.25
256245_at	heat shock protein 70 identical to h	HSP70	AT3G12580	1.02	0.03	0.06	0.953072	0.969851	-7.25
252858_at	puative protein various predicted pr	---	AT4G39770	1.01	0.01	0.06	0.953099	0.969851	-7.25
257167_at	hypothetical protein predicted by g	chr40	AT3G24340	1.00	0.01	0.06	0.953197	0.969908	-7.25
257405_at	putative calmodulin similar to EST g	---	AT1G24620	1.00	0.01	0.06	0.953288	0.969957	-7.25
261579_at	soluble inorganic pyrophosphatase	AtPPa1	AT1G01050	-1.00	-0.01	-0.06	0.953579	0.97021	-7.25
247621_at	putative protein predicted proteins	---	AT5G60340	1.00	0.01	0.06	0.95364	0.970229	-7.25
256556_at	mutator-like transposase, putative	---	---	1.00	0.01	0.06	0.953697	0.970243	-7.25
250185_at	putative protein esterase HDE, Pet	AtCXE16	AT5G14310	-1.01	-0.01	-0.06	0.953779	0.970267	-7.25
253231_at	Nonclathrin coat protein gamma - I	---	AT4G34450	1.01	0.01	0.06	0.953805	0.970267	-7.25
266861_at	putative choline kinase ;supported	emb1187	AT2G26830	-1.01	-0.01	-0.06	0.954096	0.970519	-7.25
263346_at	En/Spm-like transposon protein rela	---	---	1.00	0.01	0.06	0.95426	0.970643	-7.25
246486_at	putative protein ;supported by full-l	---	AT5G15910	-1.00	-0.01	-0.06	0.954377	0.970682	-7.25
250619_at	A9 ;supported by full-length cDNA:	---	AT5G07230	-1.00	-0.01	-0.06	0.954383	0.970682	-7.25
256491_at	hypothetical protein contains simila	---	AT1G31500	1.01	0.01	0.06	0.954622	0.970881	-7.25
264789_at	putative glycine-rich, zinc-finger DN	---	AT2G17870	-1.00	-0.01	-0.06	0.955294	0.971521	-7.25
257660_at	unknown protein ; supported by cD	WIP3	AT3G13360	-1.00	-0.01	-0.06	0.955403	0.971589	-7.25
262268_at	hypothetical protein predicted by ge	---	---	-1.00	-0.01	-0.06	0.955448	0.971592	-7.25
263652_at	unknown protein EST gb|H76414 c	---	AT1G04330	1.00	0.01	0.06	0.955539	0.971641	-7.25
265758_at	hypothetical protein similar to myos	---	---	1.00	0.01	0.06	0.955715	0.971756	-7.25

247543_at	DNA binding protein - like DNA bin	---	AT5G61600	1.01	0.02	0.06	0.955738	0.971756	-7.25
266179_at	putative phloem-specific lectin	AtPP2-B5	AT2G02300	1.00	0.01	0.06	0.956126	0.972108	-7.25
246872_at	extensin - like protein hydroxyprolir	---	AT5G26080	-1.01	-0.01	-0.06	0.956257	0.972198	-7.25
260821_at	unknown protein contains Pfam pro	CRTISO	AT1G06820	1.01	0.01	0.06	0.956453	0.972353	-7.25
247646_at	putative protein various predicted p	---	AT5G59990	1.00	0.01	0.06	0.956711	0.972573	-7.25
260507_at	unknown protein contains similarity	WPP2	AT1G47200	1.01	0.01	0.06	0.957079	0.972897	-7.25
258440_at	putative protein phosphatase simila	---	AT3G17250	-1.00	-0.01	-0.06	0.957116	0.972897	-7.25
246048_at	putative protein	---	---	-1.00	-0.01	-0.06	0.95719	0.972912	-7.25
266331_at	putative RGA1, giberellin repsonse	RGA1	AT2G01570	1.01	0.01	0.06	0.957216	0.972912	-7.25
251108_at	putative protein several hypothetica	---	AT5G01620	1.01	0.01	0.06	0.957494	0.973151	-7.25
247666_at	putative protein various predicted p	---	AT5G60140	-1.00	-0.01	-0.06	0.957585	0.9732	-7.25
254403_at	subtilisin-like serine protease conta	---	AT4G21323	1.00	0.01	0.06	0.95768	0.973254	-7.25
267531_at	putative calcium-dependent protein	CPK14	AT2G41860	1.00	0.01	0.05	0.958012	0.973507	-7.25
245322_at	Expressed protein ; supported by fu	---	AT4G14815	-1.01	-0.01	-0.05	0.958025	0.973507	-7.25
260043_at	hypothetical protein predicted by ge	---	---	-1.01	-0.01	-0.05	0.958057	0.973507	-7.25
262513_at	unknown protein ; supported by cDI	---	AT1G34270	-1.00	-0.01	-0.05	0.958275	0.973568	-7.25
250249_at	putative protein similar to unknown	---	AT5G13760	-1.00	-0.01	-0.05	0.958298	0.973568	-7.25
245801_at	hypothetical protein similar to hypot	---	AT1G46912	-1.00	-0.01	-0.05	0.958298	0.973568	-7.25
263232_at	putative light repressible receptor p	---	AT1G05700	-1.00	-0.01	-0.05	0.95833	0.973568	-7.25
256593_at	hypothetical protein similar to putati	---	AT3G28510	-1.01	-0.02	-0.05	0.958331	0.973568	-7.25
266380_at	unknown protein	MEE13	AT2G14680	1.00	0.01	0.05	0.958401	0.973583	-7.25
248783_at	putative protein contains similarity t	---	AT5G47360	-1.01	-0.01	-0.05	0.958431	0.973583	-7.25
251418_at	putative protein prib5, Ribes nigrun	---	AT3G60440	-1.01	-0.01	-0.05	0.958486	0.973589	-7.25
248566_s_a	FRO2-like protein; NADPH oxidase	ATFRO7	AT5G49730	-1.01	-0.01	-0.05	0.95858	0.973589	-7.25
263608_at	putative glycine-rich RNA-binding p	---	---	1.01	0.01	0.05	0.958601	0.973589	-7.25
252831_at	2-dehydro-3-deoxyphosphoheptona	DHS1	AT4G39980	-1.01	-0.02	-0.05	0.958608	0.973589	-7.25
248840_at	unknown protein ; supported by cD	---	AT5G46770	1.01	0.01	0.05	0.958716	0.973656	-7.25
258119_at	putative MAP kinase similar to GB:A	MPK19	AT3G14720	1.00	0.01	0.05	0.958919	0.973819	-7.25
254519_at	putative protein W15DMY30S	---	AT4G19940	-1.01	-0.01	-0.05	0.959006	0.973864	-7.25
245292_at	Expressed protein ; supported by cI	---	AT4G15093	1.01	0.01	0.05	0.959203	0.97402	-7.25
252656_at	hypothetical protein	---	AT3G44770	1.01	0.01	0.05	0.959419	0.974174	-7.25
265558_at	putative non-LTR retroelement reve	---	---	1.00	0.00	0.05	0.95944	0.974174	-7.25
257918_at	ethylene responsive element bindir	---	AT3G23230	1.03	0.05	0.05	0.959491	0.974183	-7.25
259214_at	Expressed protein ; supported by fu	---	AT3G09085	1.00	0.01	0.05	0.959651	0.974302	-7.25
253379_at	putative protein glycogenin glucosy	PGSIP3	AT4G33330	-1.00	-0.01	-0.05	0.959846	0.974457	-7.25

247953_at	cytochrome P450	CYP71B10	AT5G57260	-1.00	0.00	-0.05	0.959973	0.974518	-7.25
266227_at	unknown protein ;supported by full-	---	AT2G28870	-1.00	0.00	-0.05	0.959992	0.974518	-7.25
260272_at	F-box protein family, AtFBL14 cont	---	AT1G80570	1.01	0.01	0.05	0.960434	0.974924	-7.25
253007_at	putative protein hypothetical protei	---	AT4G38090	-1.00	-0.01	-0.05	0.96086	0.975312	-7.25
254064_at	putative protein hypothetical protei	---	AT4G25410	1.00	0.00	0.05	0.961037	0.975448	-7.25
252798_at	putative protein	---	AT3G42310	-1.00	0.00	-0.05	0.961209	0.97558	-7.25
251068_at	putative protein several protein kina	STN8	AT5G01920	-1.01	-0.01	-0.05	0.961473	0.975805	-7.25
266811_at	unknown protein	---	AT2G44850	-1.00	-0.01	-0.05	0.961569	0.975859	-7.25
246150_at	putative protein predicted proteins f	---	AT5G19930	1.01	0.01	0.05	0.961761	0.97601	-7.25
254825_at	putative protein Pad-1, Neurospora	---	AT4G12640	-1.01	-0.01	-0.05	0.961807	0.976013	-7.25
252062_at	hypothetical protein KIAA0253 prot	---	AT3G52640	-1.01	-0.01	-0.05	0.961913	0.976077	-7.25
255504_at	drought-induced-19-like 1 similar to	---	AT4G02200	1.01	0.02	0.05	0.96221	0.976335	-7.25
254676_at	putative protein Hypothetical protein	---	AT4G18460	-1.00	-0.01	-0.05	0.962255	0.976337	-7.25
261675_at	hypothetical protein predicted by ge	---	AT1G18290	1.00	0.01	0.05	0.962408	0.976449	-7.25
260280_at	unknown protein contains AP2 DNA	---	AT1G80580	-1.01	-0.01	-0.05	0.96257	0.976535	-7.25
259171_at	hypothetical protein predicted by ge	---	AT3G03590	1.00	0.01	0.05	0.962578	0.976535	-7.25
251411_at	regulatory subunit of protein kinase	CKB3	AT3G60250	1.00	0.01	0.05	0.962811	0.976727	-7.25
254292_at	putative protein	---	AT4G23030	-1.01	-0.02	-0.05	0.962864	0.976738	-7.25
257422_at	hypothetical protein Contains simila	---	AT1G11940	1.00	0.01	0.05	0.962977	0.976807	-7.25
246876_at	putative protein various predicted l	---	AT5G26140	-1.00	-0.01	-0.05	0.963032	0.976807	-7.25
257400_s_a	hypothetical protein	---	AT1G23810	1.00	0.00	0.05	0.963089	0.976807	-7.25
248525_s_a	unknown protein	---	AT5G50610	-1.00	-0.01	-0.05	0.963104	0.976807	-7.25
260993_at	hypothetical protein predicted by ge	FMO GS-O	AT1G12140	1.00	0.00	0.05	0.963867	0.977464	-7.25
245571_at	light induced protein like	---	AT4G14695	-1.00	-0.01	-0.05	0.963888	0.977464	-7.25
256355_at	hypothetical protein predicted by ge	---	AT1G55040	1.00	0.01	0.05	0.96396	0.977464	-7.25
253883_at	hypothetical protein	---	AT4G27660	1.00	0.01	0.05	0.963966	0.977464	-7.25
257871_at	hypothetical protein predicted by ge	---	AT3G28350	-1.00	0.00	-0.05	0.963966	0.977464	-7.25
259280_at	putative polypyrimidine tract-bindin	PTB1	AT3G01150	-1.00	0.00	-0.05	0.964008	0.977464	-7.25
255006_at	putative protein kinase M.sativa mR	---	AT4G10010	1.00	0.00	0.05	0.964262	0.977678	-7.25
251198_at	putative protein PGP237-11, Petun	---	AT3G62970	1.00	0.00	0.05	0.964375	0.977749	-7.25
267522_at	hypothetical protein predicted by ge	---	AT2G30430	1.00	0.01	0.05	0.964727	0.978062	-7.25
247799_at	subtilisin-like serine protease conta	---	AT5G58840	1.01	0.01	0.05	0.965008	0.978303	-7.25
267427_at	putative WRKY-type DNA binding p	WRKY35	AT2G34830	1.00	0.00	0.05	0.965347	0.978604	-7.25
250227_at	FtsJ (dbj|BAA83750.1)	---	AT5G13830	1.00	0.01	0.04	0.965482	0.978698	-7.25
248696_at	putative protein similar to unknown	---	AT5G48360	-1.00	-0.01	-0.04	0.965619	0.978789	-7.25

264170_at	hypothetical protein	---	AT1G02260	1.00	0.01	0.04	0.965659	0.978789	-7.25
257139_at	disease resistance protein, putative	AtRLP43	AT3G28890	1.01	0.01	0.04	0.965701	0.978789	-7.25
261813_at	hypothetical protein contains simila	---	AT1G08280	1.01	0.01	0.04	0.965788	0.978833	-7.25
246444_at	putative protein predicted protein T	---	AT5G17570	-1.01	-0.01	-0.04	0.965869	0.978855	-7.25
245889_at	PEE-rich protein ;supported by full-	---	AT5G09480	1.01	0.01	0.04	0.965895	0.978855	-7.25
264149_at	NAM (no apical meristem)-like prot	anac005	AT1G02250	1.00	0.00	0.04	0.966081	0.978976	-7.25
265667_at	putative CCAAT-binding transcriptio	NF-YB11	AT2G27470	1.00	0.00	0.04	0.966101	0.978976	-7.25
245542_at	CONSTANS like protein	---	AT4G15250	1.00	0.01	0.04	0.966355	0.979191	-7.25
256913_at	unknown protein	---	AT3G23870	-1.01	-0.01	-0.04	0.966654	0.97945	-7.25
251907_at	putative protein 85p protein - Medi	---	AT3G53760	1.01	0.01	0.04	0.967027	0.979763	-7.25
263189_at	hypothetical protein similar to hypot	---	AT1G36100	-1.00	0.00	-0.04	0.967083	0.979763	-7.25
262855_at	putative inorganic phosphate transp	---	AT1G20860	1.00	0.01	0.04	0.967092	0.979763	-7.25
253082_at	putative glycine-rich cell wall protei	---	AT4G36230	1.01	0.01	0.04	0.967579	0.980175	-7.25
257745_at	unknown protein ;supported by full-	---	AT3G29240	1.01	0.01	0.04	0.967585	0.980175	-7.25
245201_at	F12A21.3 unknown protein; simila	CSK	AT1G67840	1.00	0.01	0.04	0.967989	0.980541	-7.25
255323_at	putative transposon protein	---	---	-1.00	0.00	-0.04	0.968063	0.980573	-7.25
246557_at	putative protein hypothetical protei	---	AT5G15510	1.00	0.00	0.04	0.968428	0.980899	-7.25
263153_s_a	myrosinase-associated protein, put	---	AT1G54000	-1.01	-0.01	-0.04	0.968486	0.980914	-7.25
249567_at	SAMT-like protein S-adenosyl-L-m	---	AT5G38020	1.00	0.00	0.04	0.968737	0.981088	-7.25
253529_at	putative protein hypothetical protei	---	AT4G31520	-1.00	0.00	-0.04	0.968744	0.981088	-7.25
262255_at	hypothetical protein similar to hypot	---	AT1G53790	-1.00	0.00	-0.04	0.968816	0.981099	-7.25
266173_at	unknown protein	---	AT2G02410	-1.00	0.00	-0.04	0.968841	0.981099	-7.25
267363_at	putative peroxisomal membrane ca	---	AT2G39970	1.00	0.00	0.04	0.968983	0.981199	-7.25
252521_at	hypothetical protein	---	AT3G46380	1.00	0.01	0.04	0.969072	0.981239	-7.25
248328_at	putative protein contains similarity t	---	AT5G52660	1.00	0.00	0.04	0.969108	0.981239	-7.25
256194_at	unknown protein	---	---	-1.00	-0.01	-0.04	0.969203	0.981292	-7.25
253178_at	putative protein predicted protein, A	---	AT4G35170	1.00	0.01	0.04	0.969265	0.981298	-7.25
256450_at	NADPH oxidoreductase, putative s	---	AT1G75290	1.00	0.00	0.04	0.969295	0.981298	-7.25
248318_at	unknown protein	---	AT5G52690	1.00	0.00	0.04	0.969367	0.981302	-7.25
250203_at	alpha-mannosidase	---	AT5G13980	1.01	0.01	0.04	0.969385	0.981302	-7.25
245157_at	putative polygalacturonase	---	AT2G33160	1.00	0.00	0.04	0.969686	0.981529	-7.25
254288_at	putative protein Human mRNA for	AESP	AT4G22970	-1.00	0.00	-0.04	0.969695	0.981529	-7.25
253488_at	putative protein reproductive meris	REM1	AT4G31610	1.00	0.01	0.04	0.969767	0.981551	-7.25
266547_at	similar to eyes absent protein ;sup	ATEYA	AT2G35320	-1.00	0.00	-0.04	0.969812	0.981551	-7.25
260703_at	syntaxin, putative similar to syntaxi	ATSYP24	AT1G32270	1.00	0.00	0.04	0.969847	0.981551	-7.25

265918_at	putative fatty acid elongase	KCS8	AT2G15090	-1.01	-0.02	-0.04	0.969956	0.981618	-7.25
255389_at	putative reverse transcriptase	---	---	1.00	0.00	0.04	0.970182	0.981803	-7.25
253931_at	putative CDP-diacylglycerol synthe	---	AT4G26770	-1.00	0.00	-0.04	0.970325	0.981887	-7.25
257119_at	receptor kinase protein, putative si	---	AT3G20190	1.00	0.00	0.04	0.970351	0.981887	-7.25
259658_at	hypothetical protein predicted by ge	NDF5	AT1G55370	-1.00	-0.01	-0.04	0.970524	0.981979	-7.25
247665_at	putative protein various predicted p	---	AT5G60130	1.00	0.00	0.04	0.970528	0.981979	-7.25
255345_at	putative aspartic protease ; suppor	---	AT4G04460	1.01	0.02	0.04	0.970717	0.982127	-7.25
245548_at	cytochrome P450 like protein	CYP702A3	AT4G15310	-1.00	0.00	-0.04	0.970828	0.982196	-7.25
254672_at	hypothetical protein	---	---	1.00	0.01	0.04	0.970974	0.9823	-7.25
255973_at	hypothetical protein predicted by ge	---	AT3G32400	-1.00	0.00	-0.04	0.971115	0.982399	-7.25
266508_at	hypothetical protein predicted by ge	---	AT2G47920	1.00	0.01	0.04	0.971385	0.9826	-7.25
258342_at	hypothetical protein similar to exten	---	AT3G22800	1.01	0.01	0.04	0.9714	0.9826	-7.25
252049_at	putative protein putative and hypoth	---	AT3G52510	-1.00	0.00	-0.04	0.971653	0.982798	-7.25
267149_s_a	Mutator-like transposase similar to	---	---	1.00	0.01	0.04	0.971686	0.982798	-7.25
266541_at	unknown protein	GRL	AT2G35110	-1.00	-0.01	-0.04	0.971725	0.982798	-7.25
263250_at	putative fructokinase ; supported b	---	AT2G31390	1.01	0.01	0.04	0.971866	0.982897	-7.25
257246_at	pectinesterase, putative contains P	---	AT3G24130	-1.00	0.00	-0.04	0.971998	0.982987	-7.25
247001_at	natural resistance-associated macr	NRAMP4	AT5G67330	-1.00	0.00	-0.04	0.972063	0.982996	-7.25
259334_at	unknown protein similar to hect don	---	AT3G03790	1.00	0.01	0.04	0.972219	0.982996	-7.25
261702_at	unknown protein similar to hypothet	---	AT1G32760	-1.00	0.00	-0.04	0.972221	0.982996	-7.25
252750_at	putative protein hypothetical protei	---	AT3G43420	1.00	0.00	0.04	0.972242	0.982996	-7.25
264110_at	unknown protein	---	---	-1.00	0.00	-0.04	0.972335	0.982996	-7.25
253078_at	putative receptor protein kinase Cf	---	AT4G36180	-1.00	-0.01	-0.04	0.972365	0.982996	-7.25
264312_at	putative protein kinase similar to pr	---	AT1G70450	1.00	0.00	0.04	0.972374	0.982996	-7.25
249889_at	putative protein strong similarity to	---	AT5G22540	1.01	0.01	0.04	0.972402	0.982996	-7.25
254435_at	putative protein	MS5	AT4G20900	-1.00	0.00	-0.04	0.972414	0.982996	-7.25
264425_at	serine/threonine protein kinase, pu	---	AT1G61750	-1.00	0.00	-0.04	0.972438	0.982996	-7.25
247417_at	putative protein similar to unknown	---	AT5G63040	-1.00	0.00	-0.04	0.97263	0.983147	-7.25
267276_at	hypothetical protein predicted by ge	ASL5	AT2G30130	1.00	0.00	0.04	0.973079	0.983557	-7.25
257386_at	hypothetical protein predicted by ge	---	AT2G42440	-1.00	0.00	-0.03	0.973156	0.983589	-7.25
262416_at	flavonol synthase, putative similar	---	AT1G49390	-1.00	0.00	-0.03	0.973197	0.983589	-7.25
255204_at	putative myosin-like protein	---	---	1.00	0.01	0.03	0.973263	0.983612	-7.25
249600_s_a	oxidoreductase-like protein zeta-cr	---	AT5G37940	-1.00	0.00	-0.03	0.973315	0.983617	-7.25
252076_at	LS1-like protein AT-LS1 product - A	---	AT3G51660	1.01	0.01	0.03	0.973354	0.983617	-7.25
248374_at	MADS box transcription factor-like	AGL71	AT5G51870	1.00	0.00	0.03	0.973399	0.983619	-7.25

264530_at	hypothetical protein	---	AT1G30780	1.00	0.00	0.03	0.973448	0.983625	-7.25
260713_at	disease resistance protein RPP1-V	---	AT1G17615	-1.00	0.00	-0.03	0.973529	0.983664	-7.25
266966_at	hypothetical protein predicted by ge	---	AT2G39520	1.00	0.00	0.03	0.973579	0.98367	-7.25
256537_at	unknown protein	---	AT1G33340	-1.01	-0.01	-0.03	0.973695	0.983744	-7.25
255063_at	putative transposon protein similar t	---	---	1.00	0.00	0.03	0.973786	0.983793	-7.25
262897_at	hypothetical protein predicted by ge	CCB4	AT1G59840	1.01	0.01	0.03	0.973842	0.983805	-7.25
267272_at	hypothetical protein predicted by ge	---	---	-1.00	0.00	-0.03	0.974035	0.983956	-7.25
262408_at	protein phosphatase type 2C, puta	---	AT1G34750	-1.01	-0.01	-0.03	0.974103	0.983981	-7.25
255361_at	hypothetical protein	---	---	-1.00	0.00	-0.03	0.974224	0.98406	-7.25
250405_at	ubiquitin-specific protease 22 (UBP	UBP22	AT5G10790	1.00	0.01	0.03	0.974393	0.984188	-7.25
264780_at	putative protein kinase similar to MA	EDR1	AT1G08720	1.00	0.00	0.03	0.974514	0.984241	-7.25
262316_at	pale cress protein identical to GB:C	PAC	AT2G48120	-1.00	-0.01	-0.03	0.974564	0.984241	-7.25
259973_at	hypothetical protein contains Pfam	---	AT1G76630	1.00	0.01	0.03	0.974576	0.984241	-7.25
258142_at	unknown protein	---	AT3G18120	1.00	0.00	0.03	0.974778	0.984396	-7.25
260340_at	putative dihydropterin pyrophospho	---	AT1G69190	-1.00	0.00	-0.03	0.974816	0.984396	-7.25
256418_at	hypothetical protein	---	AT3G06160	1.00	0.00	0.03	0.97493	0.984468	-7.25
261562_at	actin depolymerizing factor, putativ	ADF11	AT1G01750	-1.00	-0.01	-0.03	0.975052	0.984547	-7.25
246620_at	cytochrome P450 ; supported by cl	CYP81D1	AT5G36220	-1.00	-0.01	-0.03	0.975273	0.984727	-7.25
249444_at	putative protein S-locus-specific gly	---	AT5G39370	-1.00	0.00	-0.03	0.975606	0.98502	-7.25
250902_at	putative protein predicted proteins,	---	AT5G03590	1.00	0.00	0.03	0.975694	0.985065	-7.25
266797_at	unknown protein	AtGRF1	AT2G22840	1.01	0.01	0.03	0.97623	0.985563	-7.25
256457_at	3-methyladenine DNA glycosylase	---	AT1G75230	1.00	0.01	0.03	0.976348	0.985589	-7.25
261918_at	hypothetical protein	---	AT1G65940	1.00	0.00	0.03	0.976368	0.985589	-7.25
246328_at	putative protein hexamer-binding p	---	AT3G43590	1.00	0.00	0.03	0.976385	0.985589	-7.25
262081_at	kinesin motor protein (kin2), putativ	ZCF125	AT1G59540	-1.00	0.00	-0.03	0.976655	0.985817	-7.25
260854_at	CCAAT-box binding factor HAP3 h	LEC1	AT1G21970	1.00	0.00	0.03	0.977074	0.986196	-7.25
253699_at	putative protein patatin-like protein	PLP8	AT4G29800	-1.00	0.00	-0.03	0.977165	0.986245	-7.25
261855_at	unknown protein	---	AT1G50510	-1.00	0.00	-0.03	0.97722	0.986257	-7.25
256927_at	unknown protein	---	AT3G22550	1.00	0.00	0.03	0.977366	0.98636	-7.25
263263_at	putative guanylate binding protein	---	AT2G38840	1.00	0.00	0.03	0.977473	0.986425	-7.25
251836_at	lipase -like protein monoglyceride l	---	AT3G55190	1.00	0.00	0.03	0.977573	0.986482	-7.25
264648_at	putative luminal binding protein Sim	BIP3	AT1G09080	-1.00	0.00	-0.03	0.977634	0.9865	-7.25
266177_at	putative phloem-specific lectin	ATPP2-B3	AT2G02270	-1.00	0.00	-0.03	0.977715	0.986538	-7.25
252033_at	putative protein ;supported by full-l	---	AT3G51950	-1.00	-0.01	-0.03	0.977974	0.986756	-7.25
254251_at	serine/threonine kinase - like prote	---	AT4G23300	-1.00	0.00	-0.03	0.978131	0.986792	-7.25

264020_at	putative signal sequence receptor,	---	AT2G21160	1.00	0.00	0.03	0.978134	0.986792	-7.25
252706_at	putative protein predicted proteins,	---	---	1.00	0.00	0.03	0.97814	0.986792	-7.25
258585_at	unknown protein C-term similar to c	emb2458	AT3G04340	1.00	0.00	0.03	0.978272	0.986846	-7.25
265970_at	Mutator-like transposase similar to	---	---	1.00	0.00	0.03	0.97828	0.986846	-7.25
256778_at	nucleosome assembly protein, puta	NAP1;4	AT3G13782	1.00	0.00	0.03	0.978465	0.986955	-7.25
265271_at	hypothetical protein predicted by ge	---	AT2G28360	-1.00	0.00	-0.03	0.978475	0.986955	-7.25
261344_at	hypothetical protein similar to hypot	---	AT1G79710	-1.00	0.00	-0.03	0.978573	0.987011	-7.25
265964_at	putative RNA-binding protein ; sup	---	AT2G37510	1.00	0.00	0.03	0.978749	0.987145	-7.25
258706_at	unknown protein similar to putative	---	AT3G09570	-1.00	0.00	-0.03	0.978828	0.98718	-7.25
255048_at	gibberellin-regulated protein GASA3	GASA3	AT4G09600	-1.00	0.00	-0.03	0.979069	0.987288	-7.25
267555_at	Expressed protein ; supported by fu	SUMO5	AT2G32765	-1.00	0.00	-0.03	0.979074	0.987288	-7.25
257613_at	polygalacturonase, putative similar	---	AT3G26610	1.00	0.00	0.03	0.979087	0.987288	-7.25
260865_at	reverse transcriptase, putative simi	---	AT1G43760	1.00	0.00	0.03	0.979108	0.987288	-7.25
260736_at	hypothetical protein predicted by ge	---	AT1G17630	1.00	0.00	0.03	0.979281	0.987373	-7.25
247179_at	putative protein contains similarity t	---	AT5G65320	1.00	0.00	0.03	0.979304	0.987373	-7.25
249939_at	unknown protein ;supported by full-	---	AT5G22430	-1.00	0.00	-0.03	0.979358	0.987373	-7.25
259663_at	hypothetical protein predicted by ge	PRA7	AT1G55190	1.00	0.00	0.03	0.979407	0.987373	-7.25
261845_at	metal ion transporter, putative simi	NRAMP6	AT1G15960	-1.00	0.00	-0.03	0.979408	0.987373	-7.25
263257_at	putative DNA polymerase Beta simi	---	AT1G10520	1.00	0.00	0.03	0.979679	0.987602	-7.25
264067_x_a	putative chloroplast nucleoid DNA b	---	AT2G28010	1.00	0.00	0.03	0.979732	0.987612	-7.25
257899_at	P-glycoprotein, putative similar to P	---	AT3G28345	1.00	0.00	0.03	0.979899	0.987736	-7.25
253193_at	putative protein SEC7 protein, Sac	---	AT4G35380	1.00	0.00	0.03	0.980195	0.987992	-7.25
258839_at	unknown protein ; supported by cD	---	AT3G07170	1.00	0.00	0.03	0.980313	0.988067	-7.25
248604_at	protein kinase	---	AT5G49470	1.00	0.00	0.03	0.980381	0.988092	-7.25
258016_at	hypothetical protein similar to poly(A	MPC	AT3G19350	-1.00	0.00	-0.03	0.980519	0.988188	-7.25
253199_at	clathrin assembly protein AP19 hon	---	AT4G35410	1.00	0.01	0.02	0.980836	0.988463	-7.25
257588_x_a	En/Spm-like transposon protein, pu	---	---	1.00	0.00	0.02	0.981073	0.988638	-7.25
251592_at	zinc finger - like protein finger prote	NTT	AT3G57670	1.00	0.00	0.02	0.981097	0.988638	-7.25
257394_at	hypothetical protein predicted by ge	---	---	1.00	0.00	0.02	0.98116	0.988659	-7.25
254352_at	hypothetical protein	---	AT4G22320	1.00	0.00	0.02	0.981288	0.98874	-7.25
263997_at	hypothetical protein predicted by ge	---	AT2G22520	-1.00	0.00	-0.02	0.981328	0.98874	-7.25
247302_at	unknown protein ;supported by full-	VPS20.1	AT5G63880	-1.00	0.00	-0.02	0.981371	0.98874	-7.25
267045_at	putative protein kinase contains a p	CIPK13	AT2G34180	-1.00	0.00	-0.02	0.981466	0.988792	-7.25
255533_at	putative CHP-rich zinc finger protei	---	AT4G02180	-1.00	0.00	-0.02	0.981626	0.988909	-7.25
250052_at	putative protein predicted proteins,	---	AT5G17830	-1.00	0.00	-0.02	0.981827	0.989034	-7.25

260881_at	unknown protein contains similarity	---	AT1G21550	-1.01	-0.01	-0.02	0.981837	0.989034	-7.25
260202_at	hypothetical protein predicted by ge	---	---	-1.00	0.00	-0.02	0.981894	0.98904	-7.25
249209_at	major surface glycoprotein-like ; su	---	AT5G42620	-1.00	0.00	-0.02	0.981929	0.98904	-7.25
262036_at	ATP-dependent RNA helicase, put	---	AT1G35530	-1.00	0.00	-0.02	0.982162	0.98919	-7.25
251709_at	response regulator-like protein res	ARR17	AT3G56380	-1.00	0.00	-0.02	0.982165	0.98919	-7.25
260986_at	glyoxalase II, putative similar to Gl	GLY3	AT1G53580	-1.00	0.00	-0.02	0.98222	0.989202	-7.25
257170_at	beta-1,3-glucanase, putative simila	---	AT3G23770	1.00	0.00	0.02	0.98238	0.989318	-7.25
251053_at	Ca2+/H+ exchanger-like protein Ca	CAX4	AT5G01490	-1.00	0.00	-0.02	0.982421	0.989318	-7.25
263817_at	hypothetical protein predicted by ge	---	---	-1.00	0.00	-0.02	0.982507	0.98936	-7.25
256409_at	hypothetical protein	---	AT1G66620	1.00	0.00	0.02	0.982743	0.989554	-7.25
266435_s_a	hypothetical protein predicted by ge	---	AT2G07130	-1.00	0.00	-0.02	0.982895	0.989619	-7.25
262267_at	hypothetical protein predicted by ge	---	---	1.00	0.00	0.02	0.982929	0.989619	-7.25
252782_at	putative protein predicted proteins,	---	---	1.00	0.00	0.02	0.982938	0.989619	-7.25
248475_at	unknown protein	---	AT5G50880	-1.00	0.00	-0.02	0.983017	0.989655	-7.25
262053_at	putative DnaJ protein contains Pfa	ATERDJ2A	AT1G79940	-1.00	0.00	-0.02	0.983248	0.989844	-7.25
266866_at	putative ABC transporter	PDR3	AT2G29940	1.00	0.00	0.02	0.983314	0.989867	-7.25
256632_at	hypothetical protein	---	AT3G28330	-1.00	0.00	-0.02	0.983364	0.989874	-7.25
259221_s_a	putative phospholipase similar to u	NPC5	AT3G03530	1.01	0.01	0.02	0.983609	0.990077	-7.25
248866_s_a	putative protein contains similarity t	---	AT5G46810	-1.00	0.00	-0.02	0.983685	0.99011	-7.25
265327_at	unknown protein	---	AT2G18210	1.01	0.01	0.02	0.983774	0.990155	-7.25
244967_at	PSI J protein	---	---	1.00	0.00	0.02	0.983821	0.990159	-7.25
248062_at	unknown protein ;supported by full-	---	AT5G55450	1.01	0.02	0.02	0.983973	0.990268	-7.25
245165_at	unknown protein predicted by gens	---	AT2G33180	-1.00	-0.01	-0.02	0.984182	0.990402	-7.25
254071_at	hypothetical protein	---	AT4G25510	1.00	0.00	0.02	0.984193	0.990402	-7.25
249341_at	salt-inducible protein-like	---	AT5G41170	1.00	0.00	0.02	0.984299	0.990465	-7.25
258762_at	hypothetical protein	---	AT3G10750	-1.00	0.00	-0.02	0.984704	0.990829	-7.25
267316_at	homeodomain transcription factor (	PHB	AT2G34710	1.00	0.00	0.02	0.984769	0.990851	-7.25
252962_at	splicing factor - like protein splicing	---	AT4G38780	1.00	0.00	0.02	0.984964	0.991003	-7.25
251953_at	putative protein predicted protein, A	CPuORF51	AT3G53668	-1.00	0.00	-0.02	0.98507	0.991066	-7.25
249629_at	kinesin -like protein Krm protein, L.	---	AT5G37590	1.00	0.00	0.02	0.985159	0.99107	-7.25
253194_s_a	hypothetical protein	---	---	-1.00	0.00	-0.02	0.985161	0.99107	-7.25
252432_at	hypothetical protein	---	AT3G47675	-1.00	0.00	-0.02	0.985286	0.991152	-7.25
263119_at	hypothetical protein predicted by g	---	AT1G03110	-1.00	0.00	-0.02	0.985549	0.991373	-7.25
265081_at	hypothetical protein contains Zinc f	MGP	AT1G03840	1.00	0.00	0.02	0.985776	0.991558	-7.25
259288_at	putative small nuclear ribonucleopr	---	AT3G11500	1.00	0.00	0.02	0.985901	0.991617	-7.25

245381_at	MYB transcription factor like protein	MYB39	AT4G17785	-1.00	0.00	-0.02	0.985976	0.991617	-7.25
259925_at	thaumatin-like protein similar to tha	PR5	AT1G75040	-1.02	-0.02	-0.02	0.986023	0.991617	-7.25
261486_at	nucleic acid binding protein (alfin-1	AL7	AT1G14510	1.00	0.00	0.02	0.986057	0.991617	-7.25
251607_at	hypothetical protein	---	AT3G57850	-1.00	0.00	-0.02	0.986083	0.991617	-7.25
265534_at	En/Spm-like transposon protein rela	---	---	-1.00	0.00	-0.02	0.986096	0.991617	-7.25
251384_at	putative protein	---	AT3G60760	-1.00	0.00	-0.02	0.986143	0.991621	-7.25
255245_at	hypothetical protein	---	AT4G05630	-1.00	0.00	-0.02	0.986232	0.991667	-7.25
245110_at	hypothetical protein predicted by ge	---	AT2G41550	-1.00	0.00	-0.02	0.986397	0.991788	-7.25
263409_at	predicted protein	---	AT2G04063	-1.00	0.00	-0.02	0.986445	0.991793	-7.25
256527_at	thionin, putative similar to thionin [A	---	AT1G66100	1.00	0.00	0.02	0.986662	0.991968	-7.25
249781_at	unknown protein	---	AT5G24250	-1.00	0.00	-0.02	0.986925	0.992154	-7.25
250472_at	putative protein	---	AT5G10210	-1.00	0.00	-0.02	0.986934	0.992154	-7.25
247714_at	wuschel protein - like wuschel prot	WOX2	AT5G59340	1.00	0.00	0.02	0.987011	0.992187	-7.25
262635_at	4-hydroxyphenylpyruvate dioxygena	PDS1	AT1G06570	1.00	0.00	0.02	0.987514	0.992622	-7.25
247929_at	apospory-associated protein C	---	AT5G57330	1.00	0.00	0.02	0.987533	0.992622	-7.25
255308_at	putative component of vesicle-med	NSF	AT4G04910	1.00	0.00	0.02	0.987604	0.992622	-7.25
248904_at	Expressed protein ; supported by fu	---	AT5G46295	1.00	0.00	0.02	0.987618	0.992622	-7.25
255554_at	Expressed protein ; supported by fu	---	AT4G01897	1.00	0.00	0.02	0.987816	0.99274	-7.25
264434_at	hypothetical protein predicted by ge	---	AT1G10340	1.00	0.01	0.02	0.987822	0.99274	-7.25
249412_at	putative protein predicted proteins,	---	AT5G40410	-1.00	0.00	-0.02	0.987931	0.992798	-7.25
265731_at	putative RNA helicase A 3' end of t	---	AT2G01130	-1.00	0.00	-0.02	0.987977	0.992798	-7.25
265552_at	putative plasma membrane proton A	AHA6	AT2G07560	1.00	0.00	0.02	0.98801	0.992798	-7.25
254697_at	putative protein predicted protein, A	---	AT4G17970	-1.00	0.00	-0.02	0.9881	0.992802	-7.25
261284_at	hypothetical protein predicted by ge	---	---	1.00	0.00	0.02	0.988103	0.992802	-7.25
262184_at	hypothetical protein contains simila	---	AT1G77910	1.00	0.00	0.02	0.988144	0.992802	-7.25
263285_at	unknown protein	DOT1	AT2G36120	1.00	0.00	0.02	0.988289	0.992904	-7.25
264577_at	putative peroxidase Strong similarit	RCI3	AT1G05260	1.00	0.00	0.01	0.988687	0.993251	-7.25
262995_s_a	hypothetical protein predicted by ge	---	---	1.00	0.00	0.01	0.988731	0.993251	-7.25
247619_at	putative protein	---	AT5G60290	-1.00	0.00	-0.01	0.988766	0.993251	-7.25
259223_at	hypothetical protein	WOX11	AT3G03660	1.00	0.00	0.01	0.988851	0.993293	-7.25
247851_at	outer membrane lipoprotein - like p	TIL	AT5G58070	-1.00	0.00	-0.01	0.989027	0.993426	-7.25
249646_at	SEN1-like protein SEN1 - Sacchar	---	AT5G37030	1.00	0.00	0.01	0.989284	0.99364	-7.25
261848_at	pectin methylesterase, putative sim	---	AT1G11590	-1.00	0.00	-0.01	0.989393	0.993706	-7.25
262617_at	unknown protein	POR C	AT1G03630	-1.00	0.00	-0.01	0.989522	0.993792	-7.25
AFFX-DapX	B. subtilis /GEN=dapB, jojF /DB_XR	---	---	-1.00	0.00	-0.01	0.989627	0.993838	-7.25

264414_s_a	putative protein several hypothetica	---	---	1.00	0.00	0.01	0.989655	0.993838	-7.25
257469_at	hypothetical protein predicted by ge	---	AT1G49290	1.00	0.00	0.01	0.989701	0.99384	-7.25
253227_at	protein kinase - like leucine rich rep	---	AT4G35030	1.00	0.00	0.01	0.989781	0.993877	-7.25
247332_at	unknown protein ; supported by cD	---	AT5G63440	-1.00	0.00	-0.01	0.989833	0.993885	-7.25
249078_at	phytochelatin synthase (gb|AAD417	CAD1	AT5G44070	-1.00	0.00	-0.01	0.990156	0.994136	-7.25
248240_at	CUC2 (dbj|BAA19529.1)	CUC2	AT5G53950	-1.00	0.00	-0.01	0.990169	0.994136	-7.25
261878_at	cytochrome P450, putative similar	CYP705A2	AT1G50560	-1.00	0.00	-0.01	0.99034	0.994263	-7.25
247171_at	unknown protein	---	AT5G65540	-1.00	0.00	-0.01	0.990645	0.994525	-7.25
245526_at	putative protein	NRPD4	AT4G15950	1.00	0.00	0.01	0.990708	0.994545	-7.25
266608_at	hypothetical protein predicted by ge	---	AT2G35500	-1.00	0.00	-0.01	0.990822	0.994552	-7.25
248770_at	unknown protein	---	AT5G47740	1.00	0.00	0.01	0.990863	0.994552	-7.25
257764_at	disease resistance protein, putative	AtRLP36	AT3G23010	1.00	0.00	0.01	0.990868	0.994552	-7.25
246841_at	nectarin - like protein nectarin I pre	---	AT5G26700	-1.00	0.00	-0.01	0.990945	0.994552	-7.25
245655_at	hypothetical protein predicted by ge	---	AT1G56530	-1.00	0.00	-0.01	0.991007	0.994552	-7.25
257981_at	ethylene-insensitive 3 (EIN3) identi	EIN3	AT3G20770	-1.00	0.00	-0.01	0.991017	0.994552	-7.25
263836_at	unknown protein ;supported by full-	---	AT2G40330	-1.00	0.00	-0.01	0.991069	0.994552	-7.25
252007_at	hypothetical protein MobA, Pseudo	---	AT3G52830	-1.00	0.00	-0.01	0.991122	0.994552	-7.25
261388_at	Expressed protein ; supported by cl	---	AT1G05385	-1.00	0.00	-0.01	0.991144	0.994552	-7.25
247203_at	unknown protein ; supported by cD	---	AT5G65180	1.00	0.00	0.01	0.991151	0.994552	-7.25
247441_at	receptor - like protein kinase - like	---	AT5G62710	-1.00	0.00	-0.01	0.991302	0.99466	-7.25
249857_at	C2H2-type zinc finger protein-like	---	AT5G22990	1.00	0.00	0.01	0.991444	0.994759	-7.25
252620_at	hypothetical protein	---	---	-1.00	0.00	-0.01	0.991766	0.995038	-7.25
249455_s_a	putative protein predicted proteins,	---	AT1G50870	-1.00	0.00	-0.01	0.991896	0.995124	-7.25
254511_at	hypothetical protein	---	AT4G20220	-1.00	0.00	-0.01	0.992218	0.995372	-7.25
258107_at	unknown protein ; supported by cD	ALF5	AT3G23560	1.00	0.00	0.01	0.992245	0.995372	-7.25
261957_at	methionine/cystathionine gamma ly	ATMGL	AT1G64660	-1.00	0.00	-0.01	0.992274	0.995372	-7.25
249495_at	germin - like protein GLP6 exon 2 i	GLP6	AT5G39100	-1.00	0.00	-0.01	0.992472	0.995527	-7.25
252120_at	putative protein lin-10 protein - Rat	---	AT3G51130	-1.00	0.00	-0.01	0.992601	0.995581	-7.25
264328_at	putative IAA1 protein Match to IAA1	IAA10	AT1G04100	1.00	0.00	0.01	0.992613	0.995581	-7.25
245258_at	lupeol synthase like protein ; suppo	ATPEN1	AT4G15340	-1.00	0.00	-0.01	0.992676	0.9956	-7.25
254018_at	putative mitochondrial carrier prote	---	AT4G26180	-1.00	0.00	-0.01	0.992797	0.995641	-7.25
251991_at	transcription factor NF-Y, CCAAT-b	NF-YB10	AT3G53340	-1.00	0.00	-0.01	0.992804	0.995641	-7.25
262319_s_a	unknown protein similar to unknowr	---	AT1G27540	-1.00	0.00	-0.01	0.992864	0.995658	-7.25
248632_at	unknown protein	SLD5	AT5G49010	-1.00	0.00	-0.01	0.993107	0.995858	-7.25
263815_at	hypothetical protein predicted by ge	---	AT2G10020	-1.00	0.00	-0.01	0.993283	0.99599	-7.25

248467_at	MtN3-like protein ;supported by full-	---	AT5G50800	1.00	0.00	0.01	0.993363	0.996023	-7.25
259726_at	Expressed protein ; supported by fu	SCRL6	AT1G60985	-1.00	0.00	-0.01	0.993419	0.996023	-7.25
248124_at	putative protein contains similarity t	ATG18F	AT5G54730	1.00	0.00	0.01	0.993447	0.996023	-7.25
249351_at	MAP kinase kinase 3 (ATMKK3) 10	ATMKK3	AT5G40440	1.00	0.00	0.01	0.993632	0.996165	-7.25
246417_at	quinone oxidoreductase - like prote	---	AT5G16990	-1.00	0.00	-0.01	0.993942	0.996432	-7.25
250069_at	disease resistance protein-like	---	AT5G17970	1.00	0.00	0.01	0.994053	0.9965	-7.25
253689_at	hypothetical protein ;supported by f	---	AT4G29770	1.00	0.00	0.01	0.994178	0.99658	-7.25
257992_at	hypothetical protein similar to hypot	---	AT3G19880	-1.00	0.00	-0.01	0.994303	0.996662	-7.25
250971_at	putative protein ABI3-interacting pr	PRR7	AT5G02810	1.00	0.00	0.01	0.994353	0.996669	-7.25
258024_at	hypothetical protein predicted by ge	---	AT3G19360	-1.00	0.00	-0.01	0.994411	0.996682	-7.25
265009_at	putative protein kinase similar to G	---	AT1G24650	-1.00	0.00	-0.01	0.994516	0.996682	-7.25
264040_at	putative uridylyl transferase ; suppo	ACR5	AT2G03730	1.00	0.00	0.01	0.994538	0.996682	-7.25
256940_at	unknown protein	QQS	AT3G30720	1.00	0.00	0.01	0.994541	0.996682	-7.25
265929_s_a	putative flavonol 3-O-glucosyltransf	---	AT2G18560	1.00	0.00	0.01	0.994621	0.996719	-7.25
265683_at	putative auxin-regulated protein	---	AT2G24400	-1.00	0.00	-0.01	0.994692	0.996746	-7.25
263210_at	Expressed protein ; supported by cl	---	AT1G10585	1.00	0.01	0.01	0.994957	0.996967	-7.25
263166_at	putative protein destination factor S	---	AT1G03050	-1.00	0.00	-0.01	0.995229	0.997196	-7.25
255213_at	putative athila transposon protein	---	---	1.00	0.00	0.01	0.995538	0.997462	-7.25
255778_at	3-phosphoserine phosphatase iden	PSP	AT1G18640	-1.00	0.00	-0.01	0.995678	0.997559	-7.25
257471_at	G-box binding factor, putative simil	ATBZIP4	AT1G59530	1.00	0.00	0.01	0.995797	0.997592	-7.25
250378_at	putative oligopeptide transporter pr	---	AT5G11570	-1.00	0.00	-0.01	0.995799	0.997592	-7.25
245805_at	hypothetical protein predicted by ge	---	AT1G46336	-1.00	0.00	-0.01	0.995936	0.997653	-7.25
252384_at	ABC-type transport protein-like pro	ATH7	AT3G47790	1.00	0.00	0.01	0.995947	0.997653	-7.25
258655_at	putative isocitrate dehydrogenase (	---	AT3G09810	1.00	0.00	0.01	0.996012	0.997674	-7.25
260399_at	putative lipoxygenase similar to lipo	---	AT1G72520	-1.00	0.00	-0.01	0.996084	0.997703	-7.25
254936_at	predicted protein of unknown functi	---	AT4G10790	1.00	0.00	0.00	0.996188	0.997763	-7.25
257768_at	RING zinc finger protein, putative c	---	AT3G23060	-1.00	0.00	0.00	0.996292	0.997823	-7.25
261641_at	hypothetical protein similar to hypot	---	AT1G27670	1.00	0.00	0.00	0.996543	0.997887	-7.25
255025_at	putative host response protein pir7	MES12	AT4G09900	1.00	0.00	0.00	0.996544	0.997887	-7.25
245030_at	putative polygalacturonase	---	AT2G26620	1.00	0.00	0.00	0.996551	0.997887	-7.25
250872_at	putative protein SF16 protein, com	IQD12	AT5G03960	-1.00	0.00	0.00	0.99658	0.997887	-7.25
249657_at	sen1-like protein SEN1 - Saccharo	---	AT5G37140	1.00	0.00	0.00	0.996612	0.997887	-7.25
249263_at	putative protein contains similarity t	---	AT5G41730	-1.00	0.00	0.00	0.996619	0.997887	-7.25
255971_at	transposon related protein similar to	---	---	-1.00	0.00	0.00	0.996866	0.998091	-7.25
256604_at	hypothetical protein predicted by ge	---	---	-1.00	0.00	0.00	0.996991	0.998155	-7.25

256101_at	hypothetical protein predicted by ge	---	AT1G13760	-1.00	0.00	0.00	0.997036	0.998155	-7.25
254003_at	hypothetical protein	---	AT4G26290	-1.00	0.00	0.00	0.997061	0.998155	-7.25
245222_at	contains similarity to En/Spm transp	---	---	1.00	0.00	0.00	0.997125	0.998175	-7.25
258580_at	germin-like protein contains Pfam p	---	AT3G04170	-1.00	0.00	0.00	0.997381	0.998388	-7.25
265693_at	putative poly(A) binding protein	---	AT2G24350	-1.00	0.00	0.00	0.997448	0.9984	-7.25
265362_at	putative retroelement pol polyprotei	---	---	1.00	0.00	0.00	0.997516	0.9984	-7.25
260810_s_a	retroelement protein, putative simil	---	---	1.00	0.00	0.00	0.997525	0.9984	-7.25
263447_s_a	putative PHD-type zinc finger protei	ATX2	AT1G05830	1.00	0.00	0.00	0.997779	0.998596	-7.25
247006_at	unknown protein ;supported by full-	---	AT5G67490	1.00	0.00	0.00	0.997808	0.998596	-7.25
261140_at	unknown protein	---	AT1G19680	1.00	0.00	0.00	0.998071	0.998815	-7.25
247234_at	putative protein similar to unknown	---	AT5G64980	1.00	0.00	0.00	0.998178	0.998879	-7.25
249132_at	putative protein contains similarity t	---	AT5G43120	-1.00	0.00	0.00	0.998318	0.998975	-7.25
258378_at	hypothetical protein contains simila	---	AT3G17490	-1.00	0.00	0.00	0.998567	0.999179	-7.25
258343_at	unknown protein similar to hypothet	---	AT3G22810	1.00	0.00	0.00	0.998609	0.999179	-7.25
257126_at	E2, ubiquitin-conjugating enzyme,	UBC19	AT3G20060	1.00	0.00	0.00	0.998663	0.999188	-7.25
257231_at	DegP protease contains similarity to	DEGP12	AT3G16550	-1.00	0.00	0.00	0.998722	0.999204	-7.25
254730_at	putative protein GTPase activating	---	AT4G13730	-1.00	0.00	0.00	0.998814	0.999252	-7.25
256845_x_a	hypothetical protein similar to putati	---	---	-1.00	0.00	0.00	0.999012	0.999406	-7.25
255156_at	putative athila transposon protein	---	---	-1.00	0.00	0.00	0.999168	0.999519	-7.25
248830_at	putative protein contains similarity t	---	AT5G47150	-1.00	0.00	0.00	0.999275	0.999552	-7.25
251643_at	guanylate kinase-like protein guany	AGK2	AT3G57550	-1.00	0.00	0.00	0.999289	0.999552	-7.25
260672_at	Expressed protein ; supported by fu	---	AT1G19480	1.00	0.00	0.00	0.999393	0.999612	-7.25
245645_at	F5A9.19 unknown protein; similar t	ATMAP70-1	AT1G24764	1.00	0.00	0.00	0.999627	0.999763	-7.25
248486_at	respiratory burst oxidase protein	RHD2	AT5G51060	-1.00	0.00	0.00	0.999631	0.999763	-7.25
264695_at	lipid transfer protein, putative simila	---	AT1G70250	-1.00	0.00	0.00	0.999855	0.999943	-7.25
261379_at	unknown protein similar to YGL010	---	AT1G18720	1.00	0.00	0.00	0.999908	0.999952	-7.25
266443_at	putative myb-related transcription fa	---	AT2G43270	1.00	0.00	0.00	1	1	-7.25

	mut.72 vs mut.0								
ID	Description	Gene Symbo	AGI	FC	logFC	t	P.Value	adj.P.Val	B
257203_at	xyloglucan endotransglycosylase, puta	---	AT3G23730	-30.90	-4.95	-47.00	1.00E-09	2.29E-05	11.80
254889_at	osmotin precursor ;supported by full-le	ATOSM34	AT4G11650	183.85	7.52	38.95	3.54E-09	2.62E-05	11.11
253505_at	Cytochrome P450-like protein flavono	CYP82C2	AT4G31970	83.09	6.38	40.57	2.69E-09	2.62E-05	11.27
259150_at	unknown protein similar to unknown pr	---	AT3G10320	15.92	3.99	37.46	4.59E-09	2.62E-05	10.95
245393_at	beta-1,3-glucanase class I precursor ;	---	AT4G16260	163.30	7.35	29.31	2.37E-08	7.07E-05	9.82
258975_at	putative WRKY-like transcriptional regu	WRKY45	AT3G01970	15.50	3.95	29.12	2.48E-08	7.07E-05	9.79
258957_at	feebly-like protein contains similarity to	DOX1	AT3G01420	32.57	5.03	30.18	1.95E-08	7.07E-05	9.97
248701_at	ligand-gated ion channel protein-like; g	GLR1.3	AT5G48410	11.81	3.56	29.94	2.06E-08	7.07E-05	9.93
257774_at	short-chain alcohol dehydrogenase, p	---	AT3G29250	17.59	4.14	28.60	2.80E-08	7.09E-05	9.69
254833_s_	copper amine oxidase like protein (fra	---	AT4G12280 /	6.44	2.69	27.26	3.86E-08	8.80E-05	9.44
263228_at	putative reticuline oxidase-like protein	---	AT1G30700	67.52	6.08	26.86	4.26E-08	8.83E-05	9.36
260391_at	putative strictosidine synthase extreme	SS2	AT1G74020	12.61	3.66	26.22	5.00E-08	9.49E-05	9.24
264923_s_	peroxiredoxin, putative similar to type	---	AT1G60740 /	84.75	6.41	25.24	6.44E-08	0.00011	9.03
245317_at	hypothetical protein ; supported by full-	---	AT4G15610	8.01	3.00	25.07	6.74E-08	0.00011	8.99
260602_at	serine acetyltransferase identical to G	ATSERAT2;	AT1G55920	9.36	3.23	24.73	7.38E-08	0.000112	8.91
261242_at	subtilisin-like serine protease contains	SBT3.3	AT1G32960	29.85	4.90	24.23	8.47E-08	0.000121	8.80
257061_at	hypothetical protein predicted by gens	---	AT3G18250	30.64	4.94	23.68	9.84E-08	0.000132	8.67
267592_at	unknown protein similar to GP 224501	---	AT2G39710	4.56	2.19	22.86	1.25E-07	0.000137	8.47
260101_at	putative trypsin inhibitor similar to tryps	---	AT1G73260	15.21	3.93	23.21	1.13E-07	0.000137	8.56
250180_at	early nodule-specific protein - like earl	---	AT5G14450	-6.13	-2.62	-22.81	1.27E-07	0.000137	8.45
266117_at	hypothetical protein ; supported by cD	---	AT2G02170	-5.20	-2.38	-22.91	1.23E-07	0.000137	8.48
266712_at	unknown protein	---	AT2G46750	9.24	3.21	22.56	1.36E-07	0.000141	8.39
253268_s_	glucosyltransferase -like protein imme	UGT73B2	AT4G34131 /	26.08	4.70	21.92	1.65E-07	0.000155	8.22
260431_at	putative zinc finger protein similar to zi	---	AT1G68190	-4.04	-2.02	-21.95	1.63E-07	0.000155	8.23
260581_at	MYB transcription factor (Atmyb2)	MYB2	AT2G47190	12.73	3.67	21.81	1.70E-07	0.000155	8.19
266184_s_	phosphate transporter (AtPT2) identica	ATPT2	AT2G38940 /	39.28	5.30	21.45	1.90E-07	0.000167	8.09
247183_at	putative protein strong similarity to unk	---	AT5G65440	-4.35	-2.12	-20.57	2.51E-07	0.000172	7.84
265233_s_	hypothetical protein	---	AT2G07718	5.31	2.41	20.07	2.95E-07	0.000172	7.69
259958_at	leucine-rich repeat transmembrane pr	SRF6	AT1G53730	-5.52	-2.46	-20.20	2.83E-07	0.000172	7.73
262930_at	hypothetical protein similar to hin1 GB	---	AT1G65690	27.01	4.76	20.51	2.56E-07	0.000172	7.83
263680_at	unknown protein	---	AT1G26930	3.83	1.94	21.10	2.12E-07	0.000172	7.99
247440_at	peptide transporter	---	AT5G62680	4.44	2.15	20.13	2.90E-07	0.000172	7.71
262970_at	unknown protein	---	AT1G75690	-5.33	-2.42	-20.89	2.27E-07	0.000172	7.93

245008_at	hypothetical protein	---	---	-4.45	-2.15	-21.12	2.11E-07	0.000172	8.00
253273_at	putative protein hypothetical protein s	---	AT4G34180	4.20	2.07	20.01	3.02E-07	0.000172	7.67
245362_at	homeobox-leucine zipper protein HAT	HAT1	AT4G17460	-9.84	-3.30	-20.14	2.89E-07	0.000172	7.71
263184_at	UDP-glucose:indole-3-acetate beta-D	UGT75B1	AT1G05560	10.63	3.41	20.08	2.95E-07	0.000172	7.69
261335_at	nodulin protein, putative similar to GB	---	AT1G44800	3.63	1.86	20.51	2.56E-07	0.000172	7.83
256436_at	hypothetical protein predicted by gene	---	AT3G11150	5.33	2.41	20.38	2.67E-07	0.000172	7.79
248700_at	ligand-gated ion channel protein-like; g	ATGLR1.2	AT5G48400	7.09	2.83	20.90	2.26E-07	0.000172	7.94
267201_at	putative protein kinase contains a prot	---	AT2G31010	-18.10	-4.18	-19.59	3.47E-07	0.000178	7.54
258250_at	putative delta 9 desaturase similar to d	FAD5	AT3G15850	-3.82	-1.93	-19.55	3.52E-07	0.000178	7.53
264313_at	carbonic anhydrase, putative similar t	BCA4	AT1G70410	-3.62	-1.86	-19.76	3.28E-07	0.000178	7.60
266551_at	unknown protein ; supported by cDNA	---	AT2G35260	-3.29	-1.72	-19.61	3.45E-07	0.000178	7.55
252118_at	putative protein various predicted prot	---	AT3G51400	-3.35	-1.74	-19.55	3.52E-07	0.000178	7.53
262653_at	dioxygenase-like protein very similar t	---	AT1G14130	3.63	1.86	19.47	3.61E-07	0.000179	7.51
245276_at	DNA-binding homeotic protein Athb-2 ;	ATHB-2	AT4G16780	-6.33	-2.66	-19.34	3.78E-07	0.000179	7.47
254453_at	amino acid transport protein AAT1	AAT1	AT4G21120	11.34	3.50	19.38	3.73E-07	0.000179	7.48
244926_s_	maturase	---	AT2G07711 /	6.42	2.68	19.24	3.91E-07	0.000182	7.43
266296_at	putative glutathione S-transferase ;su	ATGSTU7	AT2G29420	6.50	2.70	19.15	4.04E-07	0.000184	7.40
260592_at	cellulose synthase catalytic subunit, p	CSLE1	AT1G55850	7.04	2.81	18.85	4.49E-07	0.000195	7.30
267318_at	fatty acid hydroxylase (FAH1) identical	FAH1	AT2G34770	-5.35	-2.42	-18.73	4.68E-07	0.000195	7.26
249377_at	putative protein predicted proteins, Ar	---	AT5G40690	16.57	4.05	18.87	4.44E-07	0.000195	7.31
262947_at	unknown protein ;supported by full-len	GASA1	AT1G75750	-3.21	-1.68	-18.72	4.70E-07	0.000195	7.26
266570_at	putative chloroplast ribosomal protein l	---	AT2G24090	-3.99	-2.00	-18.73	4.68E-07	0.000195	7.26
251323_at	delta-8 sphingolipid desaturase ;supp	---	AT3G61580	-5.15	-2.36	-18.57	4.94E-07	0.000201	7.21
263475_at	Expressed protein ; supported by full-l	---	AT2G31945	5.45	2.45	18.38	5.29E-07	0.000201	7.15
252048_at	expressed protein supported by cDNA	---	AT3G52500	-7.93	-2.99	-18.39	5.28E-07	0.000201	7.15
253382_at	putative protein AT.I.24, Arabidopsis t	---	AT4G33040	6.69	2.74	18.47	5.14E-07	0.000201	7.18
253973_at	Expressed protein ; supported by cDN	---	AT4G26555	-3.02	-1.60	-18.34	5.37E-07	0.000201	7.13
260408_at	putative thioredoxin similar to thioredo	ATH8	AT1G69880	5.79	2.53	18.38	5.29E-07	0.000201	7.15
267200_at	hypothetical protein predicted by gene	---	AT2G31010	-5.43	-2.44	-18.26	5.53E-07	0.000202	7.11
265920_s_	unknown protein	---	AT2G15120 /	39.15	5.29	18.24	5.58E-07	0.000202	7.10
261785_at	hypothetical protein contains similarity	---	AT1G08230	3.70	1.89	18.16	5.74E-07	0.000205	7.07
256598_at	cytochrome P450 homolog, putative s	BR6OX2	AT3G30180	-8.04	-3.01	-17.80	6.55E-07	0.000205	6.94
261020_at	hypothetical protein similar to reticuline	---	AT1G26390	52.75	5.72	17.84	6.45E-07	0.000205	6.96
245262_at	predicted protein ; supported by cDNA	---	AT4G16563	-11.73	-3.55	-17.75	6.66E-07	0.000205	6.93
254759_at	short-chain alcohol dehydrogenase lik	---	AT4G13180	9.04	3.18	17.92	6.26E-07	0.000205	6.99

263866_at	putative farnesylated protein ;supporte	---	AT2G36950	10.42	3.38	18.10	5.85E-07	0.000205	7.05
250327_at	putative serine rich protein predicted p	---	AT5G12050	-62.81	-5.97	-17.76	6.65E-07	0.000205	6.93
250646_at	peroxidase (emb|CAA68212.1) ;suppo	---	AT5G06720	7.52	2.91	18.00	6.07E-07	0.000205	7.02
246214_at	heat shock transcription factor HSF4 ;	HSF4	AT4G36988 /	7.10	2.83	17.79	6.56E-07	0.000205	6.94
267134_at	putative protein kinase contains a prot	---	AT2G23450	2.95	1.56	17.99	6.11E-07	0.000205	7.01
249527_at	proline oxidase, mitochondrial precurs	---	AT5G38710	8.37	3.07	17.73	6.72E-07	0.000205	6.92
264160_at	hypothetical protein predicted by gene	---	AT1G65450	-5.33	-2.41	-17.70	6.79E-07	0.000205	6.91
252097_at	putative protein hypothetical protein F1	---	AT3G51090	3.54	1.82	17.68	6.83E-07	0.000205	6.90
264209_at	RAS-related protein, RAB7 identical G	RABG3B	AT1G22740	-5.48	-2.45	-17.62	6.99E-07	0.000207	6.88
250287_at	putative protein AP2 domain containin	Rap2.6L	AT5G13330	8.62	3.11	17.59	7.07E-07	0.000207	6.87
245025_at	ATPase I subunit	---	---	-2.83	-1.50	-17.52	7.27E-07	0.000207	6.84
244997_at	RNA polymerase beta' subunit-2	---	---	-4.34	-2.12	-17.53	7.25E-07	0.000207	6.85
265066_at	unknown protein location of ESTs est	FLA9	AT1G03870	-10.70	-3.42	-17.48	7.38E-07	0.000208	6.83
252414_at	putative protein sn-glycerol-3-phospha	---	AT3G47420	8.36	3.06	17.33	7.82E-07	0.000212	6.77
261346_at	putative aspartyl protease contains Pfa	---	AT1G79720	-4.35	-2.12	-17.33	7.80E-07	0.000212	6.78
262229_at	unknown protein ; supported by cDNA	---	AT1G68620	47.02	5.56	17.35	7.76E-07	0.000212	6.78
265175_at	hypothetical protein similar to putative	ATCSLA03	AT1G23480	-10.20	-3.35	-17.29	7.92E-07	0.000213	6.76
260327_at	putative RING zinc finger protein Pfam	---	AT1G63840	10.18	3.35	17.21	8.17E-07	0.000213	6.73
256376_s_	unknown protein	PXMT1	AT1G66690 /	71.18	6.15	16.91	9.19E-07	0.000213	6.62
249093_at	putative protein similar to unknown pro	---	AT5G43880	-3.18	-1.67	-16.98	8.92E-07	0.000213	6.65
247717_at	nonspecific lipid-transfer protein precu	LTP3	AT5G59320	-21.36	-4.42	-16.96	9.02E-07	0.000213	6.63
263948_at	similar to harpin-induced protein hin1 f	YLS9	AT2G35980	50.72	5.66	17.12	8.48E-07	0.000213	6.69
245018_at	hypothetical protein	---	---	-3.23	-1.69	-17.06	8.65E-07	0.000213	6.68
250125_at	biotin carboxyl carrier protein of acetyl-	CAC1	AT5G16390	-3.98	-1.99	-17.01	8.83E-07	0.000213	6.66
257650_at	protein phosphatase, putative similar t	---	AT3G16800	-6.48	-2.70	-17.24	8.08E-07	0.000213	6.74
251096_at	receptor like protein kinase receptor li	LECRKA4.2	AT5G01550	10.84	3.44	17.08	8.59E-07	0.000213	6.68
255572_at	hypothetical protein ; supported by cD	---	AT4G01050	-2.86	-1.52	-16.99	8.92E-07	0.000213	6.65
261931_at	alcohol dehydrogenase ADH, putative	---	AT1G22430	-3.25	-1.70	-16.89	9.26E-07	0.000213	6.61
247718_at	nonspecific lipid-transfer protein precu	LTP4	AT5G59310	-6.29	-2.65	-16.90	9.20E-07	0.000213	6.61
256771_at	unknown protein	---	AT3G13700 /	-3.31	-1.73	-17.00	8.88E-07	0.000213	6.65
258259_s_	unknown protein ; supported by cDNA	---	AT3G26820 /	4.09	2.03	16.95	9.03E-07	0.000213	6.63
248721_at	putative protein strong similarity to unk	GAUT4	AT5G47780	-2.76	-1.46	-16.84	9.44E-07	0.000215	6.59
261229_at	RAC-like GTP-binding protein ARAC4	ROP2	AT1G20090	-3.03	-1.60	-16.79	9.63E-07	0.000215	6.57
246371_at	unknown protein contains similarity to	---	AT1G51940	-4.37	-2.13	-16.80	9.57E-07	0.000215	6.58
257202_at	receptor-like kinase, putative similar to	---	AT3G23750	-5.11	-2.35	-16.63	1.02E-06	0.000224	6.51

266962_at	hypothetical protein predicted by gens	---	AT2G39435 /	3.84	1.94	16.65	1.02E-06	0.000224	6.52
246200_at	putative protein ;supported by full-leng	---	AT4G37240	-12.87	-3.69	-16.59	1.04E-06	0.000225	6.49
247723_at	protein phosphatase 2C - like ABA ind	---	AT5G59220	12.86	3.68	16.59	1.04E-06	0.000225	6.49
249101_at	unknown protein	---	AT5G43580	40.35	5.33	16.45	1.10E-06	0.000226	6.44
261023_at	unknown protein similar to unknown pr	---	AT1G12200	4.80	2.26	16.47	1.09E-06	0.000226	6.45
246596_at	CARBONIC ANHYDRASE 2 ; support	CA2	AT5G14740	-3.60	-1.85	-16.52	1.07E-06	0.000226	6.47
251706_at	nodulin-like protein MtN21 - Medicago	---	AT3G56620	4.70	2.23	16.51	1.08E-06	0.000226	6.46
266967_at	unknown protein	---	AT2G39530	3.00	1.59	16.48	1.09E-06	0.000226	6.45
258386_at	hypothetical protein predicted by gens	---	AT3G15520	-6.78	-2.76	-16.42	1.11E-06	0.000227	6.43
261292_at	hypothetical protein predicted by gene	---	AT1G36940	-4.64	-2.21	-16.38	1.13E-06	0.000229	6.41
255885_at	sterol-C-methyltransferase identical to	SMT2	AT1G20330	-3.62	-1.86	-16.31	1.17E-06	0.000232	6.38
261926_at	unknown protein	PATL2	AT1G22530	-4.43	-2.15	-16.25	1.19E-06	0.000232	6.36
258676_at	hypothetical protein predicted by gens	---	AT3G08600	-4.58	-2.19	-16.26	1.19E-06	0.000232	6.37
246682_at	putative protein EXOSTOSIN-1 (PUTA	XGD1	AT5G33290	4.55	2.18	16.26	1.19E-06	0.000232	6.36
257636_at	cytochrome P450, putative contains P	CYP71B22	AT3G26200	22.19	4.47	16.24	1.20E-06	0.000232	6.35
251200_at	putative protein PrMC3, Pinus radiata	GID1B	AT3G63010	5.40	2.43	16.06	1.29E-06	0.000247	6.28
261728_at	pectinesterase, putative similar to pec	sks5	AT1G76160	-8.69	-3.12	-15.78	1.45E-06	0.000249	6.17
245780_at	unknown protein ;supported by full-len	---	AT1G45688	-4.22	-2.08	-15.59	1.57E-06	0.000249	6.09
259072_at	unknown protein similar to unknown pr	FLA18	AT3G11700	-5.75	-2.52	-15.67	1.51E-06	0.000249	6.12
257985_at	hypothetical protein predicted by gens	---	AT3G20810	4.86	2.28	15.95	1.35E-06	0.000249	6.24
248060_at	putative protein contains similarity to N	---	AT5G55560	3.59	1.84	15.83	1.42E-06	0.000249	6.19
252167_at	putative protein steroid dehydrogenas	---	AT3G50560	-4.23	-2.08	-15.89	1.38E-06	0.000249	6.22
257746_at	chorismate mutase identical to chorism	CM1	AT3G29200	3.14	1.65	15.96	1.35E-06	0.000249	6.24
257196_at	AMP-binding protein, putative similar t	---	AT3G23790	5.13	2.36	15.89	1.38E-06	0.000249	6.22
252890_at	brassinosteroid insensitive 1 gene (BR	BRI1	AT4G39400	-3.22	-1.69	-15.72	1.48E-06	0.000249	6.14
250665_at	unknown protein ;supported by full-ler	---	AT5G06980	-5.00	-2.32	-15.76	1.46E-06	0.000249	6.16
246820_at	putative protein predicted proteins, Ar	---	AT5G26910	-2.75	-1.46	-15.68	1.51E-06	0.000249	6.13
263131_at	ribosomal protein L13, putative similar	emb1473	AT1G78630	-3.46	-1.79	-15.70	1.50E-06	0.000249	6.13
249120_at	unknown protein ;supported by full-ler	---	AT5G43750	-3.51	-1.81	-15.56	1.58E-06	0.000249	6.08
267078_at	unknown protein ;supported by full-ler	---	AT2G40960	-3.46	-1.79	-15.62	1.55E-06	0.000249	6.10
267005_at	unknown protein ; supported by cDNA	---	AT2G34460	-3.44	-1.78	-15.56	1.59E-06	0.000249	6.08
245011_at	photosystem II G protein	---	---	-3.59	-1.85	-15.94	1.35E-06	0.000249	6.24
263851_at	putative retroelement pol polyprotein	---	---	28.24	4.82	15.77	1.46E-06	0.000249	6.16
263676_at	putative RNA-binding protein Identical	CRB	AT1G09340	-5.48	-2.46	-15.61	1.55E-06	0.000249	6.10
264280_at	beta-glucosidase, putative similar to b	BGLU46	AT1G61820	14.96	3.90	15.67	1.52E-06	0.000249	6.12

261768_at	gibberellin 3 beta-hydroxylase, putativ	GA3OX1	AT1G15550	-4.46	-2.16	-15.75	1.46E-06	0.000249	6.16
255462_at	hypothetical protein similar to A. thalia	---	AT4G02940	9.67	3.27	15.78	1.45E-06	0.000249	6.17
259884_at	hypothetical protein predicted by gens	---	AT1G76390	3.09	1.63	15.66	1.52E-06	0.000249	6.12
261954_at	plastid ribosomal protein S6, putative	---	AT1G64510	-3.61	-1.85	-15.85	1.41E-06	0.000249	6.20
250613_at	putative protein SF16 protein, pollen s	IQD24	AT5G07240	-4.56	-2.19	-15.57	1.58E-06	0.000249	6.08
255623_at	putative L5 ribosomal protein ;support	---	AT4G01310	-3.28	-1.71	-15.89	1.38E-06	0.000249	6.21
245010_at	NADH dehydrogenase subunit	---	---	-4.32	-2.11	-15.84	1.41E-06	0.000249	6.19
266247_at	hypothetical protein predicted by gens	---	AT2G27660	4.86	2.28	15.62	1.55E-06	0.000249	6.10
261492_at	acid phosphatase, putative similar to a	SBH2	AT1G14290	-5.13	-2.36	-15.51	1.62E-06	0.00025	6.05
250213_at	H-protein promoter binding factor-1 (gb	TBP1	AT5G13820	5.86	2.55	15.51	1.62E-06	0.00025	6.06
253740_at	Expressed protein ; supported by cDN	---	AT4G28706	-4.32	-2.11	-15.48	1.64E-06	0.000251	6.04
263662_at	ankyrin-like protein EST gb|ATTS0956	---	AT1G04430	-8.17	-3.03	-15.44	1.67E-06	0.000254	6.03
254638_at	hypothetical protein	---	AT4G18740	-6.73	-2.75	-15.43	1.68E-06	0.000254	6.02
258087_at	putative peroxiredoxin similar to perox	ATPRX Q	AT3G26060	-6.54	-2.71	-15.39	1.71E-06	0.000256	6.01
260667_at	very-long-chain fatty acid condensing	KCS4	AT1G19440	-3.04	-1.60	-15.27	1.79E-06	0.000265	5.96
250102_at	receptor-like protein kinase	LRR1	AT5G16590	-4.17	-2.06	-15.17	1.88E-06	0.000265	5.91
247186_at	putative protein contains similarity to a	---	AT5G65470	-8.47	-3.08	-15.25	1.81E-06	0.000265	5.95
267260_at	putative proline-rich protein ; supporte	AGP17	AT2G23130	-23.95	-4.58	-15.18	1.87E-06	0.000265	5.92
255433_at	putative xyloglucan endotransglycosyla	XTH9	AT4G03210	-16.47	-4.04	-15.17	1.88E-06	0.000265	5.91
260877_at	unknown protein ; supported by full-ler	---	AT1G21500	-5.88	-2.56	-15.23	1.83E-06	0.000265	5.94
255543_at	predicted protein of unknown function	---	AT4G01870	28.29	4.82	15.10	1.93E-06	0.000265	5.88
262314_at	unknown protein contains similarity to	---	AT1G70810	4.20	2.07	15.13	1.91E-06	0.000265	5.89
264195_at	putative gibberellin-regulated protein c	---	AT1G22690	-8.55	-3.10	-15.14	1.90E-06	0.000265	5.90
259838_at	unknown protein ;supported by full-len	---	AT1G52220	-2.85	-1.51	-15.12	1.92E-06	0.000265	5.89
250733_at	2-cys peroxiredoxin-like protein ;supp	2-Cys Prx B	AT5G06290	-4.31	-2.11	-15.16	1.88E-06	0.000265	5.91
263142_at	unknown protein	---	AT1G65230	-3.74	-1.90	-15.19	1.86E-06	0.000265	5.92
266279_at	putative tropinone reductase	---	AT2G29290	-4.90	-2.29	-15.16	1.89E-06	0.000265	5.90
248798_at	putative protein contains similarity to p	---	AT5G47190	-3.61	-1.85	-15.27	1.79E-06	0.000265	5.96
251701_at	putative protein hypothetical protein F	---	AT3G56650	-3.65	-1.87	-15.08	1.95E-06	0.000265	5.87
263226_at	unknown protein Contains the PF|006	---	AT1G30690	-2.66	-1.41	-15.08	1.95E-06	0.000265	5.87
257912_at	formin-like protein AHF1 identical to fo	AFH1	AT3G25500	-15.17	-3.92	-15.04	1.99E-06	0.000268	5.85
247312_at	putative protein strong similarity to unk	---	AT5G63970	4.34	2.12	15.01	2.01E-06	0.000269	5.84
264449_at	hypothetical protein predicted by gens	NPGR1	AT1G27460	-8.61	-3.11	-15.00	2.02E-06	0.00027	5.83
255818_at	hypothetical protein predicted by gene	---	AT2G33570	-30.93	-4.95	-14.96	2.05E-06	0.000272	5.82
263953_at	hypothetical protein predicted by gene	OFP15	AT2G36050	-9.62	-3.27	-14.95	2.06E-06	0.000272	5.82

251516_s_	putative protein hypothetical protein S	---	AT3G59310 /	-3.68	-1.88	-14.91	2.10E-06	0.000273	5.80
260784_at	MYB-related protein identical to GB:C	ATMYB13	AT1G06180	11.72	3.55	14.92	2.09E-06	0.000273	5.80
259014_at	putative glucan endo-1-3-beta-glucosic	---	AT3G07320	-6.53	-2.71	-14.88	2.12E-06	0.000274	5.79
258815_at	putative short-chain type dehydrogena	---	AT3G04000	8.77	3.13	14.90	2.11E-06	0.000274	5.79
253165_at	putative protein predicted protein, Ara	---	AT4G35320	-13.70	-3.78	-14.76	2.24E-06	0.000276	5.73
266938_at	hypothetical protein predicted by gene	HPT1	AT2G18950	4.29	2.10	14.77	2.23E-06	0.000276	5.73
245987_at	NAM-like protein hypothetical protein	ANAC083	AT5G13180	3.67	1.87	14.80	2.21E-06	0.000276	5.75
267220_at	putative sugar nucleotide phosphorylas	ISPD	AT2G02500	-4.18	-2.06	-14.81	2.20E-06	0.000276	5.75
256981_at	brassinosteroid receptor kinase, putat	BRL3	AT3G13380	7.10	2.83	14.85	2.16E-06	0.000276	5.77
245019_at	hypothetical protein	---	---	-2.58	-1.37	-14.83	2.17E-06	0.000276	5.76
252548_at	kinesin-related protein - like kinesin-re	---	AT3G45850	-3.72	-1.90	-14.77	2.24E-06	0.000276	5.73
261119_at	chloroplast 50S ribosomal protein L31	emb2184	AT1G75350	-2.37	-1.25	-14.80	2.21E-06	0.000276	5.75
251305_at	peptidylprolyl isomerase ROC4 ;suppo	ROC4	AT3G62030	-6.26	-2.65	-14.74	2.26E-06	0.000277	5.72
259848_at	leucine-rich receptor-like protein kinas	---	AT1G72180	-4.38	-2.13	-14.69	2.31E-06	0.000277	5.70
261006_at	unknown protein similar to reticuline ox	---	AT1G26410	18.25	4.19	14.72	2.29E-06	0.000277	5.71
255850_at	putative chloroplast 50S ribosomal pro	---	AT2G33450	-3.92	-1.97	-14.71	2.30E-06	0.000277	5.71
250975_at	putative protein	---	AT5G03050	-4.22	-2.08	-14.71	2.30E-06	0.000277	5.71
252265_at	putative protein SRG1 protein - Arabic	DIN11	AT3G49620	123.45	6.95	14.65	2.36E-06	0.000282	5.68
255360_at	putative protein ;supported by full-leng	---	AT4G03960	3.19	1.67	14.58	2.43E-06	0.000282	5.65
267364_at	unknown protein ;supported by full-ler	ELF4	AT2G40080	4.15	2.05	14.61	2.40E-06	0.000282	5.66
261005_at	hypothetical protein similar to reticuline	---	AT1G26420	27.68	4.79	14.62	2.39E-06	0.000282	5.67
252940_at	receptor protein kinase - like protein re	---	AT4G39270	7.10	2.83	14.60	2.41E-06	0.000282	5.66
261190_at	ribosomal protein L11, putative similar	PRPL11	AT1G32990	-3.44	-1.78	-14.57	2.45E-06	0.000282	5.64
255948_at	hypothetical protein predicted by gens	---	AT1G22060	-2.62	-1.39	-14.57	2.44E-06	0.000282	5.65
264458_at	unknown protein similar to ESTs gb|N9	---	AT1G10410	3.15	1.65	14.59	2.42E-06	0.000282	5.65
253551_at	Expressed protein ; supported by cDN	---	AT4G30996	-3.65	-1.87	-14.54	2.47E-06	0.000282	5.63
251519_at	putative protein hypothetical protein 2	GUN4	AT3G59400	-4.64	-2.21	-14.55	2.47E-06	0.000282	5.63
245671_at	purine permease identical to purine pe	PUP1	AT1G28230	2.94	1.56	14.50	2.52E-06	0.000286	5.61
246510_at	cyclic nucleotide-gated cation channel	DND1	AT5G15410	-3.66	-1.87	-14.42	2.61E-06	0.00029	5.58
256855_at	30S ribosomal protein S20 contains Pf	---	AT3G15190	-4.12	-2.04	-14.42	2.62E-06	0.00029	5.58
246001_at	putative protein predicted protein, Ara	---	AT5G20790	11.56	3.53	14.45	2.58E-06	0.00029	5.59
257824_at	unknown protein ; supported by cDNA	---	AT3G25290	9.45	3.24	14.42	2.62E-06	0.00029	5.57
253101_at	cytochrome P450 monooxygenase (CY	CYP91A2	AT4G37430	9.32	3.22	14.43	2.60E-06	0.00029	5.58
247338_at	pyruvate kinase	---	AT5G63680	3.10	1.63	14.39	2.65E-06	0.00029	5.56
254398_at	photosystem II oxygen-evolving comp	PSBQA	AT4G21280	-3.45	-1.79	-14.40	2.64E-06	0.00029	5.57

251864_at	pectate lyase - like protein pectate lya	PMR6	AT3G54920	-4.24	-2.08	-14.34	2.72E-06	0.000295	5.54
263957_at	unknown protein ; supported by cDNA	---	AT2G35880	-2.79	-1.48	-14.34	2.71E-06	0.000295	5.54
255078_at	putative protein ascorbate peroxidase	APX4	AT4G09010	-5.09	-2.35	-14.33	2.73E-06	0.000295	5.53
264614_s_	putative aldehyde oxidase similar to G	---	AT1G02590 /	3.21	1.68	14.29	2.77E-06	0.000298	5.52
252291_s_	peroxidase ;supported by full-length c	PRXCB	AT3G49110 /	8.77	3.13	14.27	2.80E-06	0.000299	5.51
249985_at	Ser/Thr specific protein kinase - like p	---	AT5G18500	-4.03	-2.01	-14.24	2.84E-06	0.000303	5.49
263180_at	unknown protein ;supported by full-ler	URH2	AT1G05620	3.32	1.73	14.21	2.87E-06	0.000305	5.48
254189_at	putative protein cellulose synthase ca	CSLG2	AT4G24000	26.08	4.70	14.17	2.93E-06	0.000309	5.46
263083_at	purple acid phosphatase precursor ide	PAP12	AT2G27190	3.05	1.61	14.16	2.95E-06	0.00031	5.45
255046_at	H+-transporting ATP synthase-like pro	ATPD	AT4G09650	-3.62	-1.86	-14.15	2.96E-06	0.00031	5.45
263499_at	unknown protein ; supported by cDNA	TTL3	AT2G42580	-6.56	-2.71	-14.11	3.01E-06	0.000314	5.43
263981_at	unknown protein ;supported by full-ler	PAR1	AT2G42870	-41.72	-5.38	-14.08	3.05E-06	0.000316	5.42
245528_at	pyruvate,orthophosphate dikinase	PPDK	AT4G15530	4.02	2.01	14.05	3.09E-06	0.000317	5.40
257194_at	serine acetyltransferase (Sat-1) identi	ATSERAT2;	AT3G13110	3.27	1.71	14.03	3.12E-06	0.000317	5.40
258921_at	unknown protein N-terminus similar to	anac053	AT3G10500	4.32	2.11	14.03	3.13E-06	0.000317	5.39
251336_at	putative protein hypothetical protein F	BAP1	AT3G61190	11.59	3.53	14.05	3.10E-06	0.000317	5.40
249727_at	putative protein similar to unknown pro	MRU1	AT5G35490	-2.70	-1.43	-14.06	3.09E-06	0.000317	5.41
266884_at	phytocyanin identical to GB:U90428; s	UCC2	AT2G44790	23.21	4.54	14.00	3.18E-06	0.000318	5.38
256979_at	Expressed protein ; supported by full-l	PSBTN	AT3G09550 /	-3.41	-1.77	-13.99	3.18E-06	0.000318	5.38
258993_at	putative chlorophyll a/b-binding protei	LHCB4.2	AT3G08940	-3.67	-1.87	-14.00	3.17E-06	0.000318	5.38
248920_at	magnesium chelatase subunit of proto	CHLI2	AT5G45930	-3.27	-1.71	-13.98	3.20E-06	0.000319	5.37
248419_at	putative protein similar to unknown pro	EXL3	AT5G51550	-7.63	-2.93	-13.94	3.27E-06	0.000323	5.35
261769_at	plastocyanin identical to plastocyanin (	PETE1	AT1G76100	-3.87	-1.95	-13.94	3.26E-06	0.000323	5.35
258751_at	low temperature and salt responsive p	RCI2B	AT3G05890	-44.51	-5.48	-13.90	3.33E-06	0.000324	5.33
265884_at	unknown protein	---	AT2G42320	-4.06	-2.02	-13.90	3.33E-06	0.000324	5.33
258167_at	UDP-glucose:indole-3-acetate beta-D	UGT84A2	AT3G21560	8.35	3.06	13.91	3.31E-06	0.000324	5.33
249008_at	putative protein contains similarity to D	---	AT5G44680	-7.01	-2.81	-13.86	3.38E-06	0.000326	5.31
244901_at	hypothetical protein	---	ATMG00640	3.48	1.80	13.86	3.38E-06	0.000326	5.31
255647_at	Ca2+-transporting ATPase - like protei	ECA2	AT4G00900	3.96	1.98	13.87	3.38E-06	0.000326	5.32
256617_at	unknown protein ; supported by full-le	---	AT3G22240	16.02	4.00	13.84	3.41E-06	0.000326	5.30
266716_at	unknown protein ;supported by full-ler	PSI-P	AT2G46820	-3.17	-1.66	-13.84	3.42E-06	0.000326	5.30
265724_at	hypothetical protein predicted by gens	OFP16	AT2G32100	-5.46	-2.45	-13.83	3.43E-06	0.000326	5.30
248918_at	senescence-specific cysteine protease	SAG12	AT5G45890	4.34	2.12	13.82	3.46E-06	0.000327	5.29
267266_at	putative metal ion transporter (NRAMP	NRAMP3	AT2G23150	2.91	1.54	13.80	3.48E-06	0.000328	5.28
249123_at	beta-ketoacyl-CoA synthase ; support	KCS20	AT5G43760	-2.34	-1.22	-13.76	3.55E-06	0.000329	5.26

246932_at	ethylene-responsive element - like pro	---	AT5G25190	-13.61	-3.77	-13.74	3.59E-06	0.000329	5.25
249850_at	putative protein similar to unknown pro	---	AT5G23240	2.50	1.32	13.71	3.63E-06	0.000329	5.24
267212_at	similar to late embryogenesis abundan	---	AT2G44060	-2.66	-1.41	-13.73	3.60E-06	0.000329	5.25
253994_at	protein phosphatase ABI1 ; supported	ABI1	AT4G26080	3.08	1.62	13.75	3.57E-06	0.000329	5.26
251790_at	elicitor responsive/phloem -like protei	---	AT3G55470	3.53	1.82	13.77	3.53E-06	0.000329	5.27
262482_at	SRG1-like protein Strong homology to	SRG1	AT1G17020	46.43	5.54	13.72	3.61E-06	0.000329	5.25
267435_at	30S ribosomal protein S5 ; supported	---	AT2G33800	-2.63	-1.40	-13.73	3.61E-06	0.000329	5.25
259399_at	hypothetical protein similar to putative	---	AT1G17710	4.23	2.08	13.72	3.62E-06	0.000329	5.24
254612_at	putative protein hypothetical protein s	---	AT4G19100	-2.47	-1.31	-13.76	3.55E-06	0.000329	5.26
260898_at	plastid ribosomal protein L34 precurso	---	AT1G29070	-4.32	-2.11	-13.69	3.66E-06	0.00033	5.23
257074_at	unknown protein	---	AT3G19660	9.44	3.24	13.67	3.70E-06	0.000333	5.22
245738_at	nucellin, putative similar to nucellin GI	---	AT1G44130	6.30	2.65	13.66	3.73E-06	0.000333	5.21
261252_at	RAS-related protein ARA-1 identical to	RABA5E	AT1G05810	-4.01	-2.00	-13.65	3.75E-06	0.000334	5.21
266993_at	nodulin-like protein ; supported by cDI	---	AT2G39210	7.31	2.87	13.60	3.83E-06	0.00034	5.19
256243_at	basic chitinase identical to basic chitin	ATHCHIB	AT3G12500	43.63	5.45	13.59	3.85E-06	0.00034	5.18
258483_at	putative mannose-6-phosphate isomer	MEE31	AT3G02570	-5.28	-2.40	-13.56	3.91E-06	0.000344	5.16
248046_at	receptor protein kinase-like protein	---	AT5G56040	-4.38	-2.13	-13.51	4.00E-06	0.000344	5.14
244982_at	ribosomal protein L14	---	---	-3.54	-1.82	-13.52	3.98E-06	0.000344	5.15
251413_at	bZIP protein ; supported by cDNA: gi_	---	AT3G60320	-3.76	-1.91	-13.50	4.01E-06	0.000344	5.14
249847_at	serine carboxypeptidase II-like protein	SCPL34	AT5G23210	-5.38	-2.43	-13.51	4.00E-06	0.000344	5.14
262168_at	unknown protein ;supported by full-len	---	AT1G74730	-3.03	-1.60	-13.51	4.01E-06	0.000344	5.14
253812_at	putative wound induced protein woun	---	AT4G28240	-3.56	-1.83	-13.52	3.98E-06	0.000344	5.15
256607_at	unknown protein ; supported by cDNA	---	AT3G32930	-2.57	-1.36	-13.52	3.99E-06	0.000344	5.14
245193_at	F12A21.6 hypothetical protein	SUFE2	AT1G67810	51.75	5.69	13.48	4.06E-06	0.000344	5.13
259237_at	putative 2-cys peroxiredoxin BAS1 pre	---	AT3G11630	-4.56	-2.19	-13.49	4.04E-06	0.000344	5.13
255521_at	putative sucrose synthetase similar to	SUS3	AT4G02280	5.74	2.52	13.48	4.06E-06	0.000344	5.13
251762_at	sedoheptulose-bisphosphatase precur	SBPASE	AT3G55800	-3.06	-1.61	-13.47	4.08E-06	0.000345	5.12
261708_at	unknown protein similar to hypothetica	---	AT1G32740	2.75	1.46	13.46	4.10E-06	0.000345	5.12
251478_at	putative protein SF16 protein, pollen s	IQD13	AT3G59690	2.50	1.32	13.44	4.13E-06	0.000347	5.11
254181_at	FtsH protease, putative contains simil	---	AT4G23940	-2.49	-1.31	-13.43	4.16E-06	0.000348	5.10
265228_s_	hypothetical protein	---	AT2G07698	3.70	1.89	13.41	4.19E-06	0.000348	5.09
246789_at	long-chain-fatty-acid--CoA ligase-like	LACS7	AT5G27600	2.65	1.41	13.42	4.19E-06	0.000348	5.09
246463_at	quinone oxidoreductase -like protein p	AT-AER	AT5G16970	5.13	2.36	13.37	4.29E-06	0.000354	5.07
260254_at	putative glycerophosphodiester phospl	---	AT1G74210	2.80	1.49	13.33	4.36E-06	0.000359	5.05
264857_at	putative glycosyl transferase similar to	LGT9	AT1G24170	-4.98	-2.32	-13.30	4.42E-06	0.000363	5.04

247074_at	putative protein contains similarity to p	---	AT5G66590	-4.50	-2.17	-13.28	4.47E-06	0.000366	5.03
265414_at	nodulin-like protein	---	AT2G16660	-16.72	-4.06	-13.27	4.50E-06	0.000366	5.02
258468_at	unknown protein predicted by genscan	---	AT3G06070	-13.77	-3.78	-13.24	4.56E-06	0.00037	5.01
257858_at	hypothetical protein predicted by gene	---	AT3G12920	-6.90	-2.79	-13.18	4.70E-06	0.000378	4.98
245809_at	squalene monooxygenase, putative si	XF1	AT1G58440	-3.52	-1.82	-13.18	4.71E-06	0.000378	4.97
250300_at	putative protein various predicted prot	---	AT5G11890	-4.89	-2.29	-13.18	4.71E-06	0.000378	4.97
256964_at	unknown protein ;supported by full-ler	AGP12	AT3G13520	-3.15	-1.65	-13.15	4.76E-06	0.000379	4.96
263989_at	putative MAP kinase ; supported by cl	ATMPK20	AT2G42880	-4.84	-2.28	-13.16	4.75E-06	0.000379	4.96
266557_at	unknown protein ; supported by cDNA	---	AT2G46080	2.21	1.14	13.16	4.74E-06	0.000379	4.97
256310_at	unknown protein ; supported by cDNA:	ERD4	AT1G30360	-4.88	-2.29	-13.14	4.79E-06	0.000379	4.96
258586_s_	putative trypsin inhibitor similar to tryps	---	AT3G04320 /	14.11	3.82	13.14	4.80E-06	0.000379	4.95
245026_at	ATPase III subunit	---	---	-2.54	-1.34	-13.10	4.89E-06	0.000381	4.94
253197_at	putative protein Cyanophora paradoxa	---	AT4G35250	-4.66	-2.22	-13.10	4.89E-06	0.000381	4.94
262610_at	putative mitochondrial uncoupling prot	---	AT1G14140	-2.26	-1.18	-13.12	4.85E-06	0.000381	4.94
261551_at	ATP dependent copper transporter, pu	HMA5	AT1G63440	2.75	1.46	13.10	4.89E-06	0.000381	4.93
249410_at	receptor-like protein kinase receptor-li	---	AT5G40380	-7.86	-2.98	-13.08	4.95E-06	0.000383	4.92
252441_at	putative protein ; supported by cDNA:	PTAC16	AT3G46780	-5.06	-2.34	-13.06	4.98E-06	0.000383	4.92
252032_at	putative protein RNA-binding protein 3	---	AT3G52150	-2.44	-1.29	-13.06	4.98E-06	0.000383	4.92
248298_at	putative protein similar to unknown pro	---	AT5G53110	5.64	2.50	13.06	4.98E-06	0.000383	4.92
250936_at	putative protein ;supported by full-leng	---	AT5G03120	-8.18	-3.03	-13.05	5.01E-06	0.000383	4.91
259766_at	unknown protein ;supported by full-len	---	AT1G64360	6.62	2.73	13.00	5.13E-06	0.000386	4.89
259161_at	carbonic anhydrase, chloroplast precu	CA1	AT3G01500	-17.34	-4.12	-13.00	5.14E-06	0.000386	4.88
255617_at	putative protein kinase	---	AT4G01330	-3.71	-1.89	-13.00	5.15E-06	0.000386	4.88
248607_at	NaCl-inducible Ca2+-binding protein-li	ATCP1	AT5G49480	14.86	3.89	13.01	5.12E-06	0.000386	4.89
248624_at	unknown protein ; supported by cDNA	---	AT5G48790	-2.64	-1.40	-13.00	5.14E-06	0.000386	4.88
251360_at	putative protein embryonic abundant p	---	AT3G61210	-2.68	-1.42	-13.02	5.09E-06	0.000386	4.89
246368_at	light repressible receptor protein kinas	---	AT1G51890	27.28	4.77	12.95	5.28E-06	0.000393	4.86
255440_at	predicted protein of unknown function	---	AT4G02530	-3.39	-1.76	-12.95	5.28E-06	0.000393	4.86
255016_at	sucrose-phosphate synthase - like pro	ATSPS4F	AT4G10120	5.04	2.33	12.93	5.33E-06	0.000395	4.85
266132_at	hypothetical protein predicted by gens	SPX3	AT2G45130	10.06	3.33	12.93	5.32E-06	0.000395	4.85
260686_at	unknown protein ; supported by cDNA:	---	AT1G17620	-9.60	-3.26	-12.91	5.38E-06	0.000397	4.84
253099_s_	peroxidase - like protein peroxidase, A	---	AT4G37520 /	3.36	1.75	12.89	5.44E-06	0.0004	4.83
264746_at	unknown protein similar to putative DN	WRKY6	AT1G62300	19.16	4.26	12.88	5.47E-06	0.000401	4.82
246792_at	putative protein predicted proteins, Ar	---	AT5G27290	-9.33	-3.22	-12.86	5.51E-06	0.000402	4.81
266521_at	unknown protein ; supported by cDNA	---	AT2G24020	-2.46	-1.30	-12.86	5.51E-06	0.000402	4.81

247794_at	phosphoinositide specific phospholipas	PLC1	AT5G58670	-3.60	-1.85	-12.81	5.66E-06	0.000402	4.78
250413_at	adenine phosphoribosyltransferase - l	APT5	AT5G11160	-4.62	-2.21	-12.82	5.63E-06	0.000402	4.79
251036_at	putative protein ; supported by cDNA:	---	AT5G02160	-3.14	-1.65	-12.81	5.66E-06	0.000402	4.78
259553_x_	hypothetical protein	ATEXT3	AT1G21310	13.30	3.73	12.84	5.57E-06	0.000402	4.80
247261_at	ZW10-like protein ; supported by cDN	---	AT5G64460	-2.67	-1.41	-12.81	5.66E-06	0.000402	4.78
245198_at	Expressed protein ; supported by full-l	---	AT1G67700	-2.69	-1.43	-12.84	5.58E-06	0.000402	4.80
248563_at	anthocyanidin-3-glucoside rhamnosyltr	---	AT5G49690	5.36	2.42	12.82	5.62E-06	0.000402	4.79
267496_at	putative lipase ; supported by full-leng	---	AT2G30550	4.05	2.02	12.82	5.63E-06	0.000402	4.79
258791_at	hevein-like protein precursor (PR-4) id	PR4	AT3G04720	16.38	4.03	12.78	5.73E-06	0.000406	4.77
251993_at	peroxiredoxin - like protein peroxiredo	---	AT3G52960	-3.34	-1.74	-12.77	5.78E-06	0.000408	4.76
254815_at	putative pollen-specific protein pollen-	SKU5	AT4G12420	-6.49	-2.70	-12.75	5.84E-06	0.000409	4.75
257940_at	putative UDP-glucose glucosyltransfer	---	AT3G21790	3.51	1.81	12.75	5.84E-06	0.000409	4.75
267088_at	30S ribosomal protein S31 ;supported	PSRP4	AT2G38140	-3.68	-1.88	-12.75	5.84E-06	0.000409	4.75
246952_at	putative protein similar to unknown pro	OFP13	AT5G04820	-3.53	-1.82	-12.71	5.95E-06	0.000413	4.73
257632_at	cytochrome P450, putative similar to c	CYP71B21	AT3G26190	6.89	2.78	12.72	5.93E-06	0.000413	4.74
249309_at	homeotic protein BEL1 homolog ; sup	BEL1	AT5G41410	3.33	1.74	12.65	6.13E-06	0.000425	4.70
266295_at	tubulin beta-7 chain identical to GB:M8	TUB7	AT2G29550	-7.90	-2.98	-12.64	6.18E-06	0.000426	4.69
256076_at	unknown protein ; supported by cDNA:	---	AT1G18060	-5.32	-2.41	-12.64	6.16E-06	0.000426	4.70
259132_at	putative auxin-independent growth pro	---	AT3G02250	-4.50	-2.17	-12.62	6.23E-06	0.000428	4.68
244979_at	ribosomal protein S11	---	---	-2.22	-1.15	-12.59	6.33E-06	0.000434	4.67
254101_at	alpha-amylase - like protein alpha-am	AMY1	AT4G25000	20.70	4.37	12.57	6.38E-06	0.000436	4.66
245136_at	putative auxin-regulated protein	---	AT2G45210	12.52	3.65	12.56	6.42E-06	0.000437	4.65
247819_at	MAP kinase ; supported by cDNA: gi_1	WNK4	AT5G58350	4.49	2.17	12.56	6.44E-06	0.000437	4.65
253841_at	putative beta-glucosidase beta-glucos	BGLU10	AT4G27830	4.35	2.12	12.55	6.46E-06	0.000437	4.65
260109_at	hypothetical protein predicted by gens	TET10	AT1G63260	-3.50	-1.81	-12.54	6.51E-06	0.000439	4.64
247597_at	GTP-binding protein - like GTP-bindin	AtRABA1f	AT5G60860	-10.20	-3.35	-12.51	6.59E-06	0.000441	4.63
249065_at	putative protein similar to unknown pro	---	AT5G44260	-6.79	-2.76	-12.50	6.62E-06	0.000441	4.62
252886_at	cellulose synthase catalytic subunit (A	CESA2	AT4G39350	-3.09	-1.63	-12.50	6.62E-06	0.000441	4.62
266832_at	putative protein kinase contains a prot	MAPKKK14	AT2G30040	4.91	2.30	12.51	6.59E-06	0.000441	4.63
251083_at	hypothetical protein ; supported by cD	---	AT5G01590	-2.79	-1.48	-12.48	6.70E-06	0.000446	4.61
260412_at	putative alpha-amylase similar to alpha	AMY3	AT1G69830	-2.24	-1.16	-12.47	6.73E-06	0.000446	4.60
246272_at	hydroxynitrile lyase like protein	MES9	AT4G37150	16.59	4.05	12.47	6.75E-06	0.000446	4.60
260551_at	putative trypsin inhibitor ; supported b	ATTI1	AT2G43510	10.86	3.44	12.46	6.77E-06	0.000447	4.60
258333_at	myosin heavy chain-like protein similar	MFP1	AT3G16000	-2.75	-1.46	-12.43	6.86E-06	0.00045	4.58
259418_at	unknown protein ; supported by cDNA:	GPAT2	AT1G02390	3.68	1.88	12.44	6.86E-06	0.00045	4.58

258179_at	integral membrane protein, putative c	---	AT3G21690	4.44	2.15	12.42	6.92E-06	0.00045	4.57
245712_at	pullulanase-like protein (starch debran	ATLDA	AT5G04360	-2.52	-1.33	-12.42	6.93E-06	0.00045	4.57
258253_at	putative short chain alcohol dehydroge	---	AT3G26760	-2.47	-1.30	-12.42	6.92E-06	0.00045	4.58
244950_at	cytochrome c oxidase subunit 2	---	---	4.91	2.30	12.40	6.99E-06	0.000453	4.56
245947_at	spermine synthase (ACL5) ;supported	ACL5	AT5G19530	-5.50	-2.46	-12.39	7.01E-06	0.000453	4.56
253136_at	putative protein leucine-rich protein - I	---	AT4G35470	-2.86	-1.52	-12.39	7.03E-06	0.000453	4.56
265771_at	unknown protein ;supported by full-ler	---	AT2G48030	-3.36	-1.75	-12.37	7.11E-06	0.000453	4.55
245195_at	F12A21.13 putative photosystem II C	PSBY	AT1G67740	-2.61	-1.38	-12.37	7.08E-06	0.000453	4.55
264523_at	unknown protein Location of EST gb|T	ERG28	AT1G10030	-2.41	-1.27	-12.37	7.10E-06	0.000453	4.55
245027_at	heme oxygenase 2 (HO2)	HO2	AT2G26550	-2.62	-1.39	-12.38	7.08E-06	0.000453	4.55
246831_at	hexose transporter - like protein hexos	MSS1	AT5G26340	5.56	2.47	12.34	7.21E-06	0.000457	4.53
248492_at	putative protein similar to unknown pro	---	AT5G51040	2.38	1.25	12.34	7.19E-06	0.000457	4.53
253428_at	cellulose synthase catalytic subunit (R	CESA1	AT4G32410	-3.89	-1.96	-12.33	7.24E-06	0.000457	4.53
259705_at	GRAB1-like protein similar to GRAB1	anac032	AT1G77450	5.37	2.43	12.32	7.28E-06	0.000459	4.52
245976_at	WRKY-like protein WRKY DNA bindin	WRKY75	AT5G13080	76.04	6.25	12.31	7.31E-06	0.000459	4.52
256116_at	unknown protein contains similarity to	CPuORF55	AT1G16858 /	-3.04	-1.61	-12.31	7.34E-06	0.00046	4.51
249581_at	glutamate--ammonia ligase ; supporte	GSR 1	AT5G37600	2.56	1.36	12.27	7.49E-06	0.000468	4.49
258515_at	ATP citrate lyase, putative similar to A	ACLB-1	AT3G06650	-2.45	-1.29	-12.26	7.53E-06	0.000469	4.49
249230_at	putative protein similar to unknown pro	---	AT5G42070	-3.38	-1.76	-12.25	7.54E-06	0.000469	4.48
245915_s_	tubulin alpha-5 chain-like protein tubu	TUA3	AT5G19770 /	-2.70	-1.44	-12.24	7.60E-06	0.000471	4.48
253811_at	hypothetical protein ;supported by full-	ULT1	AT4G28190	-7.28	-2.86	-12.23	7.65E-06	0.000471	4.47
260236_at	geranylgeranyl reductase identical to	---	AT1G74470	-2.24	-1.16	-12.22	7.67E-06	0.000471	4.47
256024_at	unknown protein contains Pfam profile	ZF14	AT1G58340	12.57	3.65	12.22	7.66E-06	0.000471	4.47
260023_at	unknown protein	ATGA2OX2	AT1G30040	5.29	2.40	12.23	7.65E-06	0.000471	4.47
249552_s_	receptor serine/threonine protein kina	---	AT5G38240 /	5.95	2.57	12.21	7.72E-06	0.000472	4.46
261564_at	NAC domain protein, putative similar t	ATAF1	AT1G01720	3.99	2.00	12.17	7.88E-06	0.000476	4.44
250863_at	F1F0-ATPase inhibitor - like protein F	---	AT5G04750	2.24	1.16	12.17	7.89E-06	0.000476	4.44
264951_at	unknown protein contains similarity to	---	AT1G76970	2.18	1.13	12.18	7.86E-06	0.000476	4.44
263114_at	putative photosystem I reaction cente	PSAD-2	AT1G03130	-2.83	-1.50	-12.18	7.84E-06	0.000476	4.44
250884_at	signal recognition particle 54CP protei	CPSRP54	AT5G03940	-2.43	-1.28	-12.18	7.85E-06	0.000476	4.44
262235_at	ribosomal protein L18, putative similar	---	AT1G48350	-4.26	-2.09	-12.16	7.92E-06	0.000476	4.43
253547_at	chloroplast omega-6 fatty acid desatur	FAD6	AT4G30950	-2.56	-1.36	-12.16	7.93E-06	0.000476	4.43
261727_at	S-adenosyl-methionine-sterol-C-meth	SMT3	AT1G76090	-6.39	-2.68	-12.14	8.02E-06	0.000477	4.42
261021_at	hypothetical protein similar to reticuline	---	AT1G26380	89.39	6.48	12.14	8.01E-06	0.000477	4.42
262729_at	rac-like GTP binding protein (ARAC5)	ARAC5	AT1G75840	-3.70	-1.89	-12.14	8.01E-06	0.000477	4.42

247101_at	apospory-associated protein C-like	---	AT5G66530	-3.67	-1.88	-12.15	7.97E-06	0.000477	4.43
256753_at	unknown protein contains Pfam profile	GHS1	AT3G27160	-3.31	-1.73	-12.13	8.06E-06	0.000477	4.42
256215_at	unknown protein ;supported by full-len	---	AT1G50900	-2.79	-1.48	-12.12	8.11E-06	0.000479	4.41
257044_at	hypothetical protein predicted by gens	ARC5	AT3G19720	-3.29	-1.72	-12.11	8.13E-06	0.000479	4.41
258856_at	hypothetical protein predicted by gene	SRG3	AT3G02040	8.78	3.13	12.10	8.20E-06	0.000481	4.40
255764_at	unknown protein	HCF173	AT1G16720	-3.38	-1.76	-12.10	8.20E-06	0.000481	4.40
264307_at	hypothetical protein contains similarity	---	AT1G61900	-3.19	-1.67	-12.09	8.24E-06	0.000482	4.39
258982_at	putative serine/threonine protein kinas	---	AT3G08870	4.76	2.25	12.07	8.33E-06	0.000485	4.38
250243_at	cobalamin biosynthesis protein	GUN5	AT5G13630	-3.83	-1.94	-12.07	8.31E-06	0.000485	4.38
264479_at	hypothetical protein similar to receptor	---	AT1G77280	3.01	1.59	12.05	8.39E-06	0.000487	4.37
263249_at	delta 9 desaturase ALMOST identical (	ADS2	AT2G31360	-2.36	-1.24	-12.05	8.42E-06	0.000487	4.37
257932_at	unknown protein contains Pfam profile	HCF107	AT3G17040	-3.01	-1.59	-12.05	8.43E-06	0.000487	4.37
251402_at	SRG1 - like protein SRG1 protein, Ara	---	AT3G60290	-10.74	-3.43	-12.03	8.48E-06	0.000488	4.36
263297_at	putative ADP-ribosylation factor ; supp	ATARFB1A	AT2G15310	4.65	2.22	12.00	8.62E-06	0.000488	4.35
260900_s_	branched-chain alpha keto-acid dehyd	---	AT1G21400 /	6.29	2.65	12.03	8.51E-06	0.000488	4.36
251259_at	putative protein phosphoprotein phosp	---	AT3G62260	4.82	2.27	12.02	8.54E-06	0.000488	4.35
251157_at	mRNA binding protein precursor - like	CSP41A	AT3G63140	-4.06	-2.02	-12.02	8.56E-06	0.000488	4.35
248095_at	putative protein strong similarity to unk	ATMAP65-1	AT5G55230	-3.67	-1.88	-12.02	8.56E-06	0.000488	4.35
255603_at	hypothetical protein	---	AT4G01040	-2.32	-1.21	-12.00	8.64E-06	0.000488	4.34
254724_at	putative protein IFA-binding protein, A	---	AT4G13630	3.07	1.62	12.01	8.60E-06	0.000488	4.35
252543_at	nonphototropic hypocotyl 1 ; supporte	PHOT1	AT3G45780	-2.26	-1.18	-12.00	8.63E-06	0.000488	4.34
248765_at	MutT domain protein-like ; supported	ATNUDT2	AT5G47650	-2.36	-1.24	-11.99	8.68E-06	0.000489	4.34
258736_at	unknown protein	---	AT3G05900	-4.54	-2.18	-11.98	8.71E-06	0.000489	4.33
266489_at	unknown protein ; supported by cDNA	NPSN11	AT2G35190	-4.99	-2.32	-11.97	8.76E-06	0.00049	4.33
256396_at	unknown protein	---	AT3G06150	-5.50	-2.46	-11.97	8.76E-06	0.00049	4.33
250954_at	putative protein ;supported by full-leng	ATRAB8C	AT5G03520	-3.52	-1.82	-11.95	8.89E-06	0.000496	4.31
251151_at	hypothetical protein ; supported by full-	---	AT3G63170	-3.15	-1.66	-11.94	8.91E-06	0.000496	4.31
256578_at	peroxidase, putative similar to peroxid	---	AT3G28200	-6.55	-2.71	-11.92	9.04E-06	0.000502	4.29
257805_at	sugar transport, putative similar to D-X	ATPLT5	AT3G18830	6.88	2.78	11.90	9.11E-06	0.000504	4.29
264467_at	unknown protein similar to EST gb|AA	---	AT1G10140	2.80	1.48	11.89	9.18E-06	0.000506	4.28
256255_at	MYB-family transcription factor, putati	---	AT3G11280	-2.11	-1.08	-11.89	9.18E-06	0.000506	4.28
259791_at	unknown protein ; supported by cDNA	---	AT1G29700	-5.62	-2.49	-11.88	9.23E-06	0.000507	4.27
249118_at	putative protein similar to unknown pro	---	AT5G43870	-3.28	-1.72	-11.86	9.30E-06	0.00051	4.26
260693_at	peptide transporter PTR2-B, putative	NRT1.5	AT1G32450	11.82	3.56	11.85	9.36E-06	0.000512	4.26
266946_at	putative protein kinase contains a prot	---	AT2G18890	-2.95	-1.56	-11.84	9.42E-06	0.000514	4.25

251172_at	putative protein chloroplast ribosome	RRF	AT3G63190	-2.41	-1.27	-11.83	9.45E-06	0.000514	4.25
267170_at	putative RING zinc finger protein	---	AT2G37585	-5.54	-2.47	-11.81	9.57E-06	0.000517	4.24
260746_at	glutathione transferase, putative simil	ATGSTU19	AT1G78380	2.63	1.40	11.81	9.55E-06	0.000517	4.24
248287_at	putative protein similar to unknown pro	---	AT5G52970	-3.95	-1.98	-11.82	9.54E-06	0.000517	4.24
252511_at	putative protein serine/threonine-spec	---	AT3G46280	12.14	3.60	11.81	9.59E-06	0.000517	4.23
248393_at	putative protein contains similarity to u	ATBAG1	AT5G52060	-4.80	-2.26	-11.80	9.62E-06	0.000518	4.23
253253_at	putative protein auxin-regulated gene,	---	AT4G34750	-2.52	-1.34	-11.80	9.65E-06	0.000518	4.23
261611_at	hypothetical protein predicted by gene	---	AT1G49730	-6.03	-2.59	-11.79	9.68E-06	0.000518	4.22
248927_at	ubiquitin activating enzyme E1-like pro	APG7	AT5G45900	2.83	1.50	11.78	9.71E-06	0.000519	4.22
262137_at	transcription factor, putative similar to	---	AT1G77920	2.46	1.30	11.77	9.77E-06	0.000519	4.21
245740_at	amino acid permease, putative almost	AAP5	AT1G44100	3.36	1.75	11.74	9.95E-06	0.000519	4.19
256930_at	O-acetylserine(thiol) lyase, putative si	OASA2	AT3G22460	3.14	1.65	11.75	9.92E-06	0.000519	4.20
257076_at	unknown protein	---	AT3G19680	-8.20	-3.04	-11.75	9.91E-06	0.000519	4.20
258338_at	putative L-asparaginase similar to L-AS	---	AT3G16150	5.33	2.41	11.76	9.86E-06	0.000519	4.20
263298_at	unknown protein ; supported by cDNA	TIC21	AT2G15290	-2.26	-1.18	-11.75	9.88E-06	0.000519	4.20
250190_at	ribosomal protein precursor - like ribos	---	AT5G14320	-2.41	-1.27	-11.74	9.94E-06	0.000519	4.20
253609_at	H+-transporting ATPase type 2, plasm	AHA2	AT4G30190	3.03	1.60	11.75	9.92E-06	0.000519	4.20
253264_at	protein kinase - like protein protein kin	OST1	AT4G33950	-2.23	-1.15	-11.75	9.90E-06	0.000519	4.20
252922_at	putative protein	---	AT4G39040	-2.51	-1.33	-11.75	9.88E-06	0.000519	4.20
261722_at	acyl-(acyl carrier protein) thioesterase	FATB	AT1G08510	-2.25	-1.17	-11.72	1.01E-05	0.000523	4.18
253407_at	putative protein	---	AT4G32920	2.72	1.44	11.72	1.01E-05	0.000523	4.18
254215_at	putative Na+/H+-exchanging protein N	ATCHX17	AT4G23700	45.57	5.51	11.70	1.02E-05	0.000526	4.17
259133_at	sugar transporter, putative similar to ir	---	AT3G05400	7.33	2.87	11.70	1.02E-05	0.000526	4.17
244983_at	ribosomal protein L16	---	---	-5.60	-2.49	-11.69	1.02E-05	0.000528	4.17
265433_at	unknown protein	---	AT2G20950	3.53	1.82	11.69	1.03E-05	0.000528	4.16
260420_at	unknown protein	---	AT1G69610	2.56	1.36	11.68	1.03E-05	0.000528	4.16
266424_at	unknown protein	---	AT2G41330	-4.80	-2.26	-11.65	1.04E-05	0.000528	4.14
244902_at	NADH dehydrogenase subunit 4L	---	ATMG00650	2.83	1.50	11.67	1.03E-05	0.000528	4.15
257022_at	zinc finger protein, putative similar to (	AZF2	AT3G19580	3.33	1.74	11.67	1.03E-05	0.000528	4.15
267635_at	rhodanese-like family protein ;supporte	---	AT2G42220	-5.00	-2.32	-11.66	1.04E-05	0.000528	4.15
263411_at	putative C2H2-type zinc finger protein	---	AT2G28710	6.05	2.60	11.64	1.05E-05	0.000528	4.14
265649_at	putative ferredoxin ; supported by full-	ATFD3	AT2G27510	5.97	2.58	11.65	1.05E-05	0.000528	4.14
249785_at	soluble starch synthase	SSI1	AT5G24300	-2.71	-1.44	-11.64	1.05E-05	0.000528	4.14
257294_at	non-phototropic hypocotyl protein, put	---	AT3G15570	-4.38	-2.13	-11.65	1.04E-05	0.000528	4.14
261230_at	beta tubulin 1, putative similar to GB:A	TUB5	AT1G20010	-2.35	-1.23	-11.64	1.05E-05	0.000528	4.14

254126_at	RNA-binding protein RNP-T precursor	RBP31	AT4G24770	-2.65	-1.41	-11.66	1.04E-05	0.000528	4.15
249235_at	beta-1,3-glucanase-like protein ;supp	BG_PPAP	AT5G42100	-2.01	-1.00	-11.63	1.06E-05	0.000529	4.13
252181_at	Expressed protein ; supported by full-l	---	AT3G50685	-2.40	-1.26	-11.63	1.06E-05	0.000529	4.13
261373_at	CMP-KDO synthetase, putative simila	---	AT1G53000	-2.39	-1.26	-11.61	1.07E-05	0.000533	4.12
266254_at	putative membrane transporter	NAT12	AT2G27810	-3.36	-1.75	-11.59	1.08E-05	0.000537	4.11
254110_at	putative protein pectinesterase - Citru	---	AT4G25260	-10.05	-3.33	-11.56	1.10E-05	0.00054	4.09
246995_at	formin-like protein	---	AT5G67470	-4.67	-2.22	-11.57	1.09E-05	0.00054	4.09
254726_at	isoflavone reductase-like protein isofla	PRR2	AT4G13660	9.70	3.28	11.55	1.10E-05	0.00054	4.08
259911_at	putative cinnamyl-alcohol dehydrogena	CAD1	AT1G72680	3.90	1.96	11.55	1.10E-05	0.00054	4.08
261758_at	hypothetical protein contains similarity	ADT6	AT1G08250	4.57	2.19	11.56	1.10E-05	0.00054	4.09
245745_at	unknown protein contains similarity to	---	AT1G51110	-3.98	-1.99	-11.55	1.11E-05	0.00054	4.08
260968_at	hypothetical protein predicted by gene	---	AT1G12250	-2.96	-1.57	-11.55	1.10E-05	0.00054	4.09
262029_at	50S ribosomal protein L21 chloroplast	---	AT1G35680	-3.35	-1.75	-11.56	1.10E-05	0.00054	4.09
255074_at	putative protein RING-H2 zinc finger p	---	AT4G09100	2.60	1.38	11.56	1.10E-05	0.00054	4.09
244906_at	hypothetical protein	---	ATMG00690	2.41	1.27	11.54	1.11E-05	0.000542	4.08
261594_at	DNA-binding factor, putative similar to	AT-GTL1	AT1G33240	-2.84	-1.50	-11.53	1.12E-05	0.000543	4.07
255904_at	lemir (miraculin), putative similar to le	---	AT1G17860	3.29	1.72	11.52	1.12E-05	0.000543	4.07
260041_at	unknown protein similar to hypothetica	---	AT1G68780	-2.88	-1.52	-11.52	1.12E-05	0.000543	4.06
258285_at	photosystem I subunit VI precursor ide	PSAH-1	AT3G16140	-2.20	-1.14	-11.52	1.12E-05	0.000543	4.07
259996_at	hypothetical protein predicted by gene	---	AT1G67910	-3.38	-1.76	-11.52	1.12E-05	0.000543	4.07
251996_at	beta-galactosidase precursor - like pr	BGAL2	AT3G52840	-2.98	-1.57	-11.50	1.14E-05	0.000546	4.05
246294_at	ribosomal protein, chloroplast ribosom	PSRP5	AT3G56910	-2.34	-1.23	-11.50	1.14E-05	0.000546	4.05
245016_at	carboxytransferase beta subunit	---	---	-2.33	-1.22	-11.49	1.14E-05	0.000546	4.05
248683_at	putative protein similar to unknown pro	---	AT5G48490	-20.42	-4.35	-11.48	1.15E-05	0.000551	4.04
260225_at	putative glutathione S-transferase simi	GSTU10	AT1G74590	56.28	5.81	11.47	1.16E-05	0.000552	4.04
259403_at	unknown protein ; supported by full-ler	PGDH	AT1G17745	40.51	5.34	11.46	1.16E-05	0.000553	4.03
261746_at	unknown protein ;supported by full-len	PSAO	AT1G08380	-2.20	-1.14	-11.46	1.17E-05	0.000553	4.03
259443_at	chitinase, putative similar to chitinase	---	AT1G02360	8.16	3.03	11.46	1.16E-05	0.000553	4.03
253871_at	protochlorophyllide reductase precurs	PORB	AT4G27440	-4.12	-2.04	-11.45	1.17E-05	0.000553	4.03
256309_at	photosystem I subunit X precursor ider	PSAK	AT1G30380	-2.29	-1.19	-11.45	1.17E-05	0.000553	4.02
259057_at	unknown protein ; supported by cDNA	---	AT3G03310	3.35	1.75	11.44	1.18E-05	0.000553	4.02
257686_at	unknown protein similar to unknown pr	SDRB	AT3G12800	2.77	1.47	11.44	1.18E-05	0.000553	4.02
244995_at	ATPase a subunit	---	---	-5.77	-2.53	-11.44	1.18E-05	0.000553	4.02
265823_at	hypothetical protein predicted by gens	---	AT2G35760	-2.48	-1.31	-11.42	1.19E-05	0.000555	4.01
245277_at	glucosyltransferase like protein ; supp	IAGLU	AT4G15550	6.49	2.70	11.42	1.19E-05	0.000555	4.01

247059_at	UTP-glucose glucosyltransferase ;sup	UGT72E2	AT5G66690	2.40	1.27	11.42	1.19E-05	0.000555	4.01
250723_at	lysine decarboxylase-like protein	---	AT5G06300	-3.56	-1.83	-11.41	1.20E-05	0.000556	4.00
247376_at	nucleotide diphosphate kinase Ia (emb	NDPK2	AT5G63310	-2.27	-1.18	-11.41	1.20E-05	0.000556	4.00
246843_at	putative protein various predicted prot	---	AT5G26740	-2.31	-1.21	-11.40	1.20E-05	0.000557	3.99
262671_at	calcium-dependent protein kinase, pu	CPK29	AT1G76040	3.35	1.74	11.40	1.20E-05	0.000557	3.99
254484_at	hypothetical protein	---	AT4G20760	-2.32	-1.22	-11.37	1.22E-05	0.000561	3.98
249693_at	histidine kinase-like protein ; supporte	AHK2	AT5G35750	-4.67	-2.22	-11.37	1.22E-05	0.000561	3.98
252433_at	putative protein putative hydrolyse - A	---	AT3G47560	-4.02	-2.01	-11.37	1.22E-05	0.000561	3.98
250415_at	putative protein GLUR3 ligand-gated c	GLR2.5	AT5G11210	18.19	4.18	11.38	1.22E-05	0.000561	3.98
259598_at	sphingosine-1-phosphate lyase, putat	DPL1	AT1G27980	2.89	1.53	11.36	1.23E-05	0.000563	3.97
251150_at	putative protein Sb34 (PREG-like prot	CYCP1;1	AT3G63120	-2.75	-1.46	-11.35	1.23E-05	0.000563	3.97
258805_at	putative beta-1,3-glucanase similar to	---	AT3G04010	3.83	1.94	11.36	1.23E-05	0.000563	3.97
254250_at	serine/threonine kinase - like protein s	---	AT4G23290	-6.41	-2.68	-11.35	1.24E-05	0.000563	3.96
260000_at	unknown protein similar to C-terminal	ATMAP70-1	AT1G68060	-3.19	-1.67	-11.34	1.25E-05	0.000566	3.96
266767_at	Expressed protein ; supported by full-l	---	AT2G46910	-3.28	-1.71	-11.32	1.26E-05	0.00057	3.94
250981_at	receptor like protein kinase receptor li	---	AT5G03140	-3.53	-1.82	-11.31	1.26E-05	0.00057	3.94
251883_at	ribosomal protein L17 -like protein rib	---	AT3G54210	-2.44	-1.29	-11.32	1.26E-05	0.00057	3.94
253277_at	cinnamyl alcohol dehydrogenase - like	ATCAD5	AT4G34230	3.65	1.87	11.31	1.26E-05	0.00057	3.94
251544_at	putative protein general stress protein	GAUT15	AT3G58790	-3.84	-1.94	-11.29	1.28E-05	0.000574	3.93
267565_at	putative cytochrome P450	CYP71A12	AT2G30750	42.74	5.42	11.29	1.28E-05	0.000574	3.93
260203_at	NAM-like protein similar to NAM (no ap	ANAC019	AT1G52890	5.19	2.38	11.28	1.29E-05	0.000577	3.92
255829_at	putative potassium transporter ; suppo	KT2	AT2G40540	-2.12	-1.08	-11.27	1.29E-05	0.000578	3.92
245357_at	putative protein ;supported by full-leng	---	AT4G17560	-3.36	-1.75	-11.27	1.30E-05	0.000578	3.92
247161_at	putative protein similar to unknown pro	---	AT5G65810	-3.11	-1.64	-11.26	1.30E-05	0.000579	3.91
266635_at	unknown protein ;supported by full-ler	---	AT2G35470	-3.09	-1.63	-11.25	1.31E-05	0.000581	3.90
251321_at	RING finger protein ;supported by full-	BRH1	AT3G61460	-4.19	-2.07	-11.25	1.31E-05	0.000581	3.91
259863_at	hypothetical protein ;supported by full-	ELF4-L2	AT1G72630	-2.34	-1.23	-11.25	1.31E-05	0.000581	3.90
259738_at	predicted protein	---	AT1G64355	-2.55	-1.35	-11.23	1.33E-05	0.000586	3.89
261131_at	unknown protein	---	AT1G19835	-5.00	-2.32	-11.21	1.34E-05	0.00059	3.88
261973_at	hypothetical protein predicted by gene	---	AT1G64610	3.86	1.95	11.21	1.34E-05	0.000591	3.88
256441_at	unknown protein ;supported by full-ler	---	AT3G10940	-5.36	-2.42	-11.20	1.35E-05	0.000591	3.87
245730_at	unknown protein ;supported by full-len	---	AT1G73470	-2.29	-1.19	-11.20	1.35E-05	0.000591	3.87
257903_at	unknown protein	---	AT3G28460	-2.35	-1.23	-11.19	1.35E-05	0.000592	3.87
255709_at	putative YABBY3 axial regulator ; sup	YAB3	AT4G00180	-2.87	-1.52	-11.19	1.36E-05	0.000593	3.87
249481_at	frnE protein - like frnE protein, Deinoc	---	AT5G38900	33.46	5.06	11.18	1.36E-05	0.000593	3.86

260015_at	putative S-adenosyl-L-methionine:tran	CCOAMT	AT1G67980	35.59	5.15	11.18	1.36E-05	0.000593	3.86
253424_at	putative protein ; supported by cDNA:	---	AT4G32330	-3.06	-1.61	-11.18	1.36E-05	0.000593	3.86
248952_at	putative protein similar to unknown pro	---	AT5G45410	2.73	1.45	11.17	1.37E-05	0.000593	3.86
258076_at	50S ribosomal protein L15, chloroplas	RPL15	AT3G25920	-3.60	-1.85	-11.15	1.38E-05	0.000599	3.85
247899_at	Expressed protein ; supported by full-l	---	AT5G57345	-2.96	-1.56	-11.15	1.39E-05	0.000599	3.84
256751_at	CLC-b chloride channel protein identi	CLC-B	AT3G27170	-6.32	-2.66	-11.14	1.39E-05	0.000599	3.84
261197_at	putative calcium-binding protein, calre	GAPA-2	AT1G12900	-2.68	-1.42	-11.14	1.39E-05	0.000599	3.84
264772_at	unknown protein location of EST gb|H	---	AT1G22930	2.58	1.37	11.11	1.42E-05	0.000608	3.82
245020_at	cytochrome f	---	---	-2.44	-1.29	-11.11	1.42E-05	0.000608	3.82
266899_at	hypothetical protein predicted by gene	---	AT2G34620	-9.46	-3.24	-11.10	1.43E-05	0.000609	3.81
261422_at	unknown protein	NDF6	AT1G18730	-2.91	-1.54	-11.10	1.42E-05	0.000609	3.82
253891_at	putative protein ;supported by full-leng	---	AT4G27720	-6.21	-2.63	-11.09	1.44E-05	0.00061	3.81
255719_at	unknown protein ;supported by full-len	---	AT1G32080	-7.05	-2.82	-11.09	1.44E-05	0.00061	3.81
248409_at	putative protein contains similarity to e	LPA2	AT5G51540 /	-2.96	-1.56	-11.09	1.44E-05	0.00061	3.81
257856_at	hypothetical protein predicted by gens	---	AT3G12930	-2.08	-1.06	-11.09	1.44E-05	0.00061	3.81
254952_at	UDP-galactose 4-epimerase - like pro	UGE5	AT4G10955 /	2.80	1.49	11.08	1.44E-05	0.00061	3.80
263902_at	phosphoribosylformimino-5-aminoimid	APG10	AT2G36230	-2.34	-1.23	-11.06	1.46E-05	0.000617	3.79
265405_at	putative protein kinase contains a prot	---	AT2G16750	-5.11	-2.35	-11.04	1.48E-05	0.00062	3.78
261763_at	ABC transporter, putative similar to AI	PDR12	AT1G15520	46.12	5.53	11.04	1.48E-05	0.00062	3.78
249876_at	putative protein similar to unknown pro	CaS	AT5G23060	-2.95	-1.56	-11.05	1.47E-05	0.00062	3.78
253480_at	putative protein ENOD16, Medicago t	---	AT4G31840	-2.33	-1.22	-11.03	1.48E-05	0.00062	3.77
259981_at	unknown protein ; supported by full-le	---	AT1G76450	-2.86	-1.51	-11.03	1.48E-05	0.00062	3.77
250690_at	ABC transporter-like protein ; supporte	---	AT5G06530	-4.00	-2.00	-11.03	1.49E-05	0.000621	3.77
250827_at	cellulose synthase catalytic subunit (gl	CEV1	AT5G05170	-3.48	-1.80	-11.02	1.49E-05	0.000621	3.77
259840_at	photosystem I subunit VI precursor ide	PSAH2	AT1G52230	-3.00	-1.59	-11.02	1.49E-05	0.000621	3.77
265610_at	unknown protein ;supported by full-ler	---	AT2G25430	-2.05	-1.04	-11.01	1.50E-05	0.000622	3.76
257772_at	unknown protein C-term similar to pho	---	AT3G23080	-2.77	-1.47	-11.02	1.50E-05	0.000622	3.76
254102_at	acyl carrier - like protein acyl carrier p	ACP4	AT4G25050	-2.83	-1.50	-11.01	1.50E-05	0.000622	3.76
260386_at	putative strictosidine synthase similar t	---	AT1G74010	22.18	4.47	11.00	1.51E-05	0.000626	3.75
248353_at	cytochrome P450	CYP96A4	AT5G52320	2.21	1.14	10.99	1.53E-05	0.000629	3.74
253631_at	nucleotide sugar epimerase-like prote	GAE1	AT4G30440	-3.14	-1.65	-10.98	1.53E-05	0.00063	3.74
255886_at	plastocyanin, putative similar to plasto	DRT112	AT1G20340	-2.23	-1.16	-10.97	1.54E-05	0.000633	3.73
257363_at	hypothetical protein predicted by gens	BAP2	AT2G45760	3.26	1.70	10.95	1.55E-05	0.000638	3.72
245852_at	ribosomal protein L10-like ribosomal p	---	AT5G13510	-2.96	-1.57	-10.95	1.56E-05	0.000638	3.72
260676_at	integral membrane protein, putative si	---	AT1G19450	-5.48	-2.45	-10.94	1.57E-05	0.000641	3.71

267300_at	putative glucosyltransferase	---	AT2G30140	2.22	1.15	10.93	1.57E-05	0.000641	3.71
251601_at	Expressed protein ; supported by full-l	---	AT3G57800	-4.18	-2.06	-10.92	1.59E-05	0.000645	3.70
246446_at	putative protein hypothetical protein T	---	AT5G17640	-2.99	-1.58	-10.92	1.59E-05	0.000645	3.70
259193_at	putative thylakoid lumen rotamase sim	CYP38	AT3G01480	-3.54	-1.82	-10.92	1.59E-05	0.000645	3.70
267335_s_	putative beta-1,3-glucanase	---	AT1G64760 /	-4.05	-2.02	-10.91	1.60E-05	0.000647	3.69
249331_at	50S ribosomal protein L27 ;supported	RPL27	AT5G40950	-2.45	-1.29	-10.90	1.60E-05	0.000648	3.69
248285_at	putative protein similar to unknown pro	---	AT5G52960	-1.94	-0.95	-10.90	1.60E-05	0.000648	3.69
263432_at	putative beta-hydroxyacyl-ACP dehydr	---	AT2G22230	-3.09	-1.63	-10.89	1.61E-05	0.000649	3.69
246366_at	light repressible receptor protein kinas	---	AT1G51850	3.38	1.76	10.89	1.62E-05	0.00065	3.68
259520_at	hypothetical protein	---	AT1G12320	4.46	2.16	10.88	1.63E-05	0.000652	3.68
259789_at	Expressed protein ; supported by full-l	COR414-TM	AT1G29395	-2.64	-1.40	-10.88	1.63E-05	0.000652	3.68
245050_at	PSII K protein	---	---	-1.95	-0.96	-10.83	1.67E-05	0.000667	3.65
253612_at	putative protein D-ribulokinase - Klebs	---	AT4G30310	-2.23	-1.16	-10.83	1.67E-05	0.000667	3.65
246339_at	RP19 gene for chloroplast ribosomal p	RPL9	AT3G44890	-2.53	-1.34	-10.83	1.67E-05	0.000667	3.65
255889_at	ABC transporter, putative similar to AB	WBC11	AT1G17840	-3.42	-1.77	-10.80	1.70E-05	0.000669	3.63
246284_at	putative protein	---	AT4G36780	-2.55	-1.35	-10.79	1.71E-05	0.000669	3.62
261240_at	subtilisin-like serine protease contains	SBT3.5	AT1G32940	9.89	3.31	10.81	1.69E-05	0.000669	3.63
254543_at	putative chitinase chitinase (EC 3.2.1.	---	AT4G19810	17.75	4.15	10.80	1.70E-05	0.000669	3.62
254598_at	xyloglucan endo-transglycosylase - lik	---	AT4G18990	6.50	2.70	10.81	1.69E-05	0.000669	3.63
261788_at	unknown protein ;supported by full-len	NDF1	AT1G15980	-5.15	-2.36	-10.82	1.68E-05	0.000669	3.64
258555_at	fatty acid multifunctional protein (AtMF	MFP2	AT3G06860	2.63	1.40	10.81	1.70E-05	0.000669	3.63
256468_at	ferredoxin, putative similar to GB:D90	---	AT1G32550	-2.75	-1.46	-10.80	1.70E-05	0.000669	3.63
250751_at	glucuronosyl transferase-like protein	---	AT5G05890	-2.66	-1.41	-10.81	1.69E-05	0.000669	3.64
245784_at	hypothetical protein similar to hypothet	---	AT1G32190	-2.54	-1.34	-10.81	1.69E-05	0.000669	3.63
245274_at	ankyrin like protein ; supported by cDN	---	AT4G14360	-2.65	-1.40	-10.79	1.71E-05	0.00067	3.62
258395_at	putative jasmonic acid regulatory prote	ANAC055	AT3G15500	4.88	2.29	10.78	1.72E-05	0.000671	3.62
257071_at	unknown protein ; supported by cDNA	ATCSLC04	AT3G28180	-3.83	-1.94	-10.76	1.75E-05	0.000673	3.60
263421_at	unknown protein ;supported by full-ler	EXL5	AT2G17230	-7.64	-2.93	-10.77	1.74E-05	0.000673	3.61
266956_at	unknown protein	---	AT2G34510	-9.37	-3.23	-10.77	1.73E-05	0.000673	3.61
256865_at	NAD dependent epimerase, putative c	GAE6	AT3G23820	-5.25	-2.39	-10.76	1.74E-05	0.000673	3.60
264318_at	putative beta-ketoacyl-CoA synthase S	KCS2	AT1G04220	-5.54	-2.47	-10.76	1.75E-05	0.000673	3.60
244936_at	NADH dehydrogenase ND1	---	---	-2.30	-1.20	-10.77	1.73E-05	0.000673	3.61
252353_at	putative protein KIAA0226 gene produ	---	AT3G48200	-2.42	-1.28	-10.76	1.75E-05	0.000673	3.60
264186_at	hypothetical protein predicted by gene	---	AT1G54570	9.43	3.24	10.76	1.74E-05	0.000673	3.60
250668_at	unknown protein ; supported by full-le	---	AT5G07020	-3.24	-1.69	-10.75	1.75E-05	0.000673	3.60

246595_at	formate dehydrogenase (FDH) ;suppo	FDH	AT5G14780	2.32	1.21	10.73	1.78E-05	0.000674	3.58
249037_at	putative protein contains similarity to s	FLA13	AT5G44130	-19.20	-4.26	-10.72	1.78E-05	0.000674	3.58
248179_at	receptor-protein kinase-like protein	THE1	AT5G54380	-7.59	-2.92	-10.74	1.77E-05	0.000674	3.59
253042_at	formamidase - like protein formamidas	---	AT4G37550	-4.31	-2.11	-10.72	1.78E-05	0.000674	3.58
260685_at	Expressed protein ; supported by full-l	GLYR2	AT1G17650	-3.51	-1.81	-10.72	1.78E-05	0.000674	3.58
256655_at	hypothetical protein predicted by gene	---	AT3G18890	-3.82	-1.93	-10.73	1.77E-05	0.000674	3.58
246988_at	putative protein strong similarity to unk	---	AT5G67340	8.60	3.10	10.73	1.77E-05	0.000674	3.58
251786_at	phosphatase - like protein DUAL SPE	MKP1	AT3G55270	2.18	1.12	10.74	1.76E-05	0.000674	3.59
262967_at	hypothetical protein predicted by gene	---	AT1G75730	-2.51	-1.33	-10.74	1.76E-05	0.000674	3.59
261077_at	protein phosphatase 2C, putative simi	---	AT1G07430	3.90	1.96	10.72	1.78E-05	0.000674	3.58
262925_at	hypothetical protein	YSL7	AT1G65730	2.52	1.33	10.72	1.78E-05	0.000674	3.58
248466_at	putative protein similar to unknown pro	HVA22E	AT5G50720	-4.59	-2.20	-10.70	1.80E-05	0.000677	3.56
253309_at	male sterility 2-like protein male sterili	CER4	AT4G33790	-6.53	-2.71	-10.71	1.80E-05	0.000677	3.57
253046_at	cytochrome P450 - like protein cytoch	CYP81D8	AT4G37370	32.15	5.01	10.70	1.80E-05	0.000677	3.56
262172_at	ribosomal protein S9, putative similar	RPS9	AT1G74970	-2.33	-1.22	-10.70	1.80E-05	0.000677	3.57
251575_at	putative protein basic leucine zipper tr	BZIP61	AT3G58120	-10.81	-3.43	-10.69	1.82E-05	0.000679	3.56
258244_at	unknown protein ; supported by cDNA	---	AT3G27770	-2.22	-1.15	-10.69	1.82E-05	0.000679	3.56
261443_at	glutaredoxin, putative similar to glutar	GRX480	AT1G28480	13.46	3.75	10.68	1.82E-05	0.000681	3.55
251743_at	Yippee-like protein Yippee protein, Ho	---	AT3G55890	6.68	2.74	10.68	1.83E-05	0.000681	3.55
256499_at	unknown protein	---	AT1G36640	4.97	2.31	10.68	1.83E-05	0.000681	3.55
261658_at	hypothetical protein predicted by gene	---	AT1G50040	-11.41	-3.51	-10.67	1.84E-05	0.000681	3.54
255110_at	peroxidase C2 precursor like protein p	---	AT4G08770	71.64	6.16	10.67	1.84E-05	0.000681	3.54
250563_at	putative protein predicted protein, Ara	---	AT5G08050	-3.63	-1.86	-10.67	1.84E-05	0.000681	3.54
258528_at	unknown protein contains Pfam profile	---	AT3G06770	-7.66	-2.94	-10.66	1.85E-05	0.000684	3.54
264192_at	hypothetical protein predicted by gene	ATATG18H	AT1G54710	1.98	0.99	10.65	1.86E-05	0.000685	3.53
256057_at	unknown protein contains similarity to	NDA1	AT1G07180	-6.43	-2.68	-10.65	1.87E-05	0.000688	3.53
258764_at	putative pectinesterase contains simila	---	AT3G10720	-6.50	-2.70	-10.64	1.88E-05	0.000691	3.52
245769_at	hypothetical protein similar to putative	INT2	AT1G30220	2.10	1.07	10.62	1.90E-05	0.000698	3.51
246071_at	ids4-like protein ids-4 protein - Hordeu	SPX1	AT5G20150	9.82	3.30	10.60	1.91E-05	0.0007	3.50
261055_at	chloroplast nucleoid DNA binding prot	---	AT1G01300	-2.69	-1.43	-10.60	1.91E-05	0.0007	3.50
253866_at	putative protein various putative protei	---	AT4G27480	2.62	1.39	10.60	1.91E-05	0.0007	3.50
264916_at	ATP citrate-lyase, putative similar to A	ACLA-2	AT1G60810	-3.33	-1.74	-10.60	1.92E-05	0.000702	3.50
248962_at	putative protein contains similarity to F	FKBP13	AT5G45680	-4.11	-2.04	-10.59	1.93E-05	0.000703	3.49
253925_at	putative protein ; supported by cDNA:	SHV3	AT4G26690	-5.06	-2.34	-10.56	1.97E-05	0.000714	3.47
255064_at	putative phi-1-like phosphate-induced	EXO	AT4G08950	-26.76	-4.74	-10.56	1.97E-05	0.000714	3.47

259586_at	unknown protein	---	AT1G28100	-2.25	-1.17	-10.55	1.97E-05	0.000714	3.47
258755_at	hypothetical protein identical to hypoth	---	AT3G11945 /	-2.62	-1.39	-10.56	1.97E-05	0.000714	3.47
262603_at	hypothetical protein Is a member of th	---	AT1G15380	7.43	2.89	10.51	2.02E-05	0.000714	3.44
262291_at	zinc finger and C2 domain protein, pu	---	AT1G70790	2.14	1.10	10.52	2.01E-05	0.000714	3.45
251768_at	phosphoinositide-specific phospholipa	---	AT3G55940	-4.84	-2.27	-10.51	2.02E-05	0.000714	3.44
250261_at	peptide transporter - like protein pepti	---	AT5G13400	-6.06	-2.60	-10.54	1.99E-05	0.000714	3.46
259995_at	putative golgi transport complex prote	---	AT1G67930	-2.79	-1.48	-10.51	2.02E-05	0.000714	3.44
247552_at	phytochelatin synthetase - like protein	COB	AT5G60920	-4.33	-2.11	-10.54	1.99E-05	0.000714	3.46
251176_at	Ca2+-transporting ATPase -like protei	---	AT3G63380	22.03	4.46	10.54	1.99E-05	0.000714	3.46
249807_at	pectinacetylesterase	---	AT5G23870	-3.49	-1.80	-10.53	2.00E-05	0.000714	3.45
254485_at	cell-cell signaling protein csgA - like c	---	AT4G20760	-3.03	-1.60	-10.52	2.01E-05	0.000714	3.45
265913_at	Expressed protein ; supported by full-le	---	AT2G25625	9.12	3.19	10.51	2.02E-05	0.000714	3.44
249188_at	N-hydroxycinnamoyl benzoyltransferas	---	AT5G42830	8.96	3.16	10.51	2.02E-05	0.000714	3.44
262369_at	hypothetical protein predicted by gene	---	AT1G73010	37.22	5.22	10.54	1.99E-05	0.000714	3.46
247506_at	Mei2-like protein Mei2-like protein, Ara	AML1	AT5G61960	2.02	1.01	10.51	2.02E-05	0.000714	3.44
249658_s_	N-glyceraldehyde-2-phosphotransferas	---	AT5G36700 /	-3.34	-1.74	-10.52	2.01E-05	0.000714	3.45
252823_at	Expressed protein ; supported by full-le	---	AT4G40045	-2.39	-1.26	-10.52	2.02E-05	0.000714	3.45
264163_at	Expressed protein ; supported by full-le	---	AT1G65445	-2.64	-1.40	-10.53	2.01E-05	0.000714	3.45
246133_at	aldehyde oxidase AAO1 ; supported b	AAO1	AT5G20960	11.85	3.57	10.50	2.04E-05	0.000718	3.44
263082_at	putative nucleotide-binding protein	---	AT2G27200	1.95	0.97	10.49	2.05E-05	0.000719	3.43
246308_at	chlorophyll synthetase ; supported by	G4	AT3G51820	-2.86	-1.52	-10.49	2.05E-05	0.000719	3.43
249765_at	putative protein contains similarity to u	SLAH3	AT5G24030	-15.92	-3.99	-10.48	2.06E-05	0.000722	3.42
254445_at	3-hydroxyisobutyrate dehydrogenase	---	AT4G20930	2.39	1.26	10.48	2.06E-05	0.000722	3.42
247934_at	putative protein similar to unknown pro	---	AT5G57000	-2.33	-1.22	-10.47	2.07E-05	0.000725	3.42
263410_at	predicted protein ;supported by full-len	---	AT2G04039	-4.11	-2.04	-10.47	2.08E-05	0.000725	3.41
259491_at	chlorophyll binding protein, putative si	LHCB6	AT1G15820	-2.54	-1.35	-10.47	2.07E-05	0.000725	3.42
251584_at	putative protein At2g42580 - Arabidop	TTL4	AT3G58620	-8.06	-3.01	-10.46	2.09E-05	0.000727	3.41
247648_at	laccase - like protein laccase LAC2-4,	LAC17	AT5G60020	-2.58	-1.37	-10.45	2.10E-05	0.000731	3.40
258033_at	unknown protein similar to MRP-like A	MRP6	AT3G21250	4.64	2.21	10.44	2.11E-05	0.000732	3.40
250645_at	putative protein strong similarity to unk	---	AT5G06700	-4.72	-2.24	-10.44	2.11E-05	0.000732	3.40
254040_at	possible apospory-associated like pro	---	AT4G25900	4.04	2.01	10.44	2.11E-05	0.000732	3.40
247320_at	photosystem I reaction centre subunit	PSAN	AT5G64040	-2.25	-1.17	-10.44	2.12E-05	0.000732	3.39
259010_at	unknown protein contains helix-loop-he	---	AT3G07340	-3.92	-1.97	-10.43	2.12E-05	0.000733	3.39
256756_at	ATPase II, putative similar to GB:AAD	---	AT3G25610	7.04	2.82	10.43	2.13E-05	0.000733	3.39
254911_at	putative protein ;supported by full-leng	---	AT4G11100	-2.18	-1.12	-10.43	2.13E-05	0.000733	3.39

263517_at	unknown protein ;supported by full-ler	RD2	AT2G21620	3.58	1.84	10.41	2.15E-05	0.00074	3.38
251031_at	one helix protein (OHP) ;supported by	OHP	AT5G02120	-2.56	-1.35	-10.40	2.16E-05	0.000742	3.37
247525_at	pseudo-response regulator 1 ; suppor	TOC1	AT5G61380	1.92	0.94	10.40	2.17E-05	0.000743	3.37
244978_at	RNA polymerase alpha subunit	---	---	-2.15	-1.10	-10.39	2.18E-05	0.000746	3.36
246926_at	putative protein	---	AT5G25240	-4.37	-2.13	-10.38	2.19E-05	0.000746	3.36
248449_at	putative protein similar to unknown pro	---	AT5G51110	-2.04	-1.03	-10.38	2.19E-05	0.000746	3.36
267319_at	ABC transporter (AtMRP2) identical to	ATMRP2	AT2G34660	3.25	1.70	10.37	2.21E-05	0.000752	3.35
244980_at	ribosomal protein L36	---	---	-2.29	-1.20	-10.36	2.22E-05	0.000754	3.35
259618_at	myb-related transcription factor (cpm1	MYB112	AT1G48000	3.30	1.72	10.35	2.23E-05	0.000754	3.34
255116_at	receptor protein kinase-like protein rec	---	AT4G08850	3.24	1.69	10.36	2.22E-05	0.000754	3.34
248749_at	eukaryotic release factor 1 homolog (g	ERF1-1	AT5G47880	2.04	1.03	10.35	2.23E-05	0.000754	3.34
267548_at	putative disease resistance protein	AtRLP22	AT2G32660	11.29	3.50	10.35	2.23E-05	0.000754	3.34
258887_at	putative phospholipase D similar to ph	PLDP2	AT3G05630	3.37	1.75	10.34	2.24E-05	0.000757	3.33
251243_at	putative protein hypothetical protein -	---	AT3G61870	-3.20	-1.68	-10.34	2.25E-05	0.000757	3.33
256793_at	unknown protein ;supported by full-ler	---	AT3G22160	6.82	2.77	10.33	2.26E-05	0.000759	3.33
250939_at	putative protein various predicted prot	iqd2	AT5G03040	-3.71	-1.89	-10.32	2.27E-05	0.000763	3.32
258512_at	beta-glucosidase, putative similar to b	---	AT3G06510 /	1.88	0.91	10.32	2.28E-05	0.000764	3.32
264920_at	hypothetical protein contains similarity	ECHID	AT1G60550	-2.56	-1.36	-10.32	2.28E-05	0.000764	3.32
266963_at	unknown protein	MTP11	AT2G39450	-2.44	-1.29	-10.31	2.29E-05	0.000764	3.31
250823_at	putative protein similar to unknown pro	---	AT5G05180	-2.29	-1.19	-10.31	2.29E-05	0.000764	3.31
259625_at	glyceraldehyde-3-phosphate dehydrog	GAPB	AT1G42970	-2.81	-1.49	-10.30	2.30E-05	0.000767	3.31
247069_at	pectinesterase like protein ;supported	sks17	AT5G66920	-8.09	-3.02	-10.30	2.30E-05	0.000767	3.30
263207_at	putative endoxyloglucan transferase si	XTH33	AT1G10550	-29.84	-4.90	-10.30	2.31E-05	0.000767	3.30
259645_at	putative DNA-binding protein predicte	BIM2	AT1G69010	-3.01	-1.59	-10.29	2.32E-05	0.000769	3.30
253630_at	putative protein putative ATPase - Ha	---	AT4G30490	2.86	1.51	10.29	2.32E-05	0.000769	3.30
266215_at	putative endoxyloglucan glycosyltranst	EXGT-A1	AT2G06850	-12.42	-3.63	-10.28	2.33E-05	0.00077	3.29
245705_at	zinc finger transcription factor-like prot	---	AT5G04390	2.09	1.07	10.28	2.33E-05	0.00077	3.29
248795_at	Myb-related transcription activator-like	---	AT5G47390	-2.00	-1.00	-10.28	2.34E-05	0.000772	3.29
253405_at	transcription factor TINY homolog tran	---	AT4G32800	-4.54	-2.18	-10.26	2.37E-05	0.000779	3.28
245629_at	hypothetical protein predicted by gene	---	AT1G56580	-2.97	-1.57	-10.26	2.37E-05	0.000779	3.28
265149_at	unknown protein ; supported by full-ler	---	AT1G51400	-2.51	-1.33	-10.25	2.38E-05	0.000781	3.27
253802_at	putative protein	---	AT4G28180	-2.23	-1.16	-10.22	2.42E-05	0.000794	3.25
259790_s_	auxin-induced protein, putative similar	---	AT1G29430 /	-12.76	-3.67	-10.21	2.44E-05	0.000795	3.24
246984_at	cytochrome P450	CYP81G1	AT5G67310	18.23	4.19	10.21	2.43E-05	0.000795	3.25
254137_at	hypothetical protein	---	AT4G24930	-4.29	-2.10	-10.21	2.44E-05	0.000795	3.24

261618_at	unknown protein	---	AT1G33110	6.15	2.62	10.21	2.44E-05	0.000795	3.24
251664_at	leucine zipper-containing protein AT10	CRD1	AT3G56940	-2.58	-1.36	-10.22	2.43E-05	0.000795	3.25
260264_at	hypothetical protein predicted by gene	---	AT1G68500	-3.19	-1.68	-10.21	2.43E-05	0.000795	3.25
259611_at	GTP-binding protein RAB7D, putative	AtRABG3d	AT1G52280	-2.47	-1.30	-10.20	2.45E-05	0.000796	3.24
258524_at	acetyl-coA dehydrogenase, putative s	IBR3	AT3G06810	2.54	1.34	10.20	2.46E-05	0.000796	3.24
252409_at	putative protein bundle sheath defecti	---	AT3G47650	-2.29	-1.20	-10.20	2.46E-05	0.000796	3.24
261117_at	unknown protein	AUL1	AT1G75310	-3.77	-1.92	-10.19	2.46E-05	0.000796	3.23
255626_at	coded for by A. thaliana cDNA T20615	---	AT4G00780	2.58	1.37	10.19	2.47E-05	0.000799	3.23
245338_at	Expressed protein ; supported by full-l	---	AT4G16442	-3.01	-1.59	-10.17	2.49E-05	0.000804	3.22
249750_at	unknown protein ;supported by full-ler	---	AT5G24570	-4.09	-2.03	-10.17	2.50E-05	0.000805	3.22
263553_at	putative purple acid phosphatase prec	PAP10	AT2G16430	2.67	1.42	10.17	2.50E-05	0.000806	3.21
267127_at	putative acetone-cyanohydrin lyase	MES3	AT2G23610	-2.39	-1.26	-10.16	2.52E-05	0.000808	3.21
264506_at	germin-like protein Identical to Arabid	GLP5	AT1G09560	2.57	1.36	10.16	2.52E-05	0.000808	3.21
256585_at	hypothetical protein	---	AT3G28760	-3.42	-1.77	-10.14	2.54E-05	0.00081	3.20
252320_at	endoxyloglucan transferase-like prote	---	AT3G48580	7.17	2.84	10.14	2.55E-05	0.00081	3.20
252303_at	putative protein hypothetical protein R	---	AT3G49210	2.10	1.07	10.14	2.54E-05	0.00081	3.20
247709_at	D-xylose-H+ symporter - like protein D	---	AT5G59250	-2.73	-1.45	-10.15	2.54E-05	0.00081	3.20
249685_at	putative protein similar to unknown pro	CCB3	AT5G36120	-2.02	-1.01	-10.14	2.54E-05	0.00081	3.20
264613_at	lipoyltransferase identical to GB:BAA7	LIP2	AT1G04640	-2.35	-1.23	-10.14	2.54E-05	0.00081	3.20
262803_at	unknown protein Location of ESTs 15	---	AT1G21000	3.85	1.95	10.14	2.55E-05	0.00081	3.20
260914_at	beta-xylosidase, putative similar to be	BXL2	AT1G02640	-8.26	-3.05	-10.13	2.57E-05	0.000811	3.19
257951_at	putative SGP1 monomeric G-protein s	SGP2	AT3G21700	7.01	2.81	10.13	2.56E-05	0.000811	3.19
251241_s_	putative protein hypothetical proteins -	---	AT3G62460 /	-3.09	-1.63	-10.13	2.56E-05	0.000811	3.19
260009_at	unknown protein ;supported by full-ler	---	AT1G67950	-3.44	-1.78	-10.12	2.57E-05	0.000812	3.19
254770_at	extensin-like protein extensin-like prot	---	AT4G13340	-7.39	-2.89	-10.12	2.58E-05	0.000813	3.18
267210_at	dihydroxypolyprenylbenzoate methyltra	ATCOQ3	AT2G30920	-1.87	-0.90	-10.12	2.58E-05	0.000813	3.18
263391_at	putative monogalactosyldiacylglycerol	MGDC	AT2G11810	4.38	2.13	10.11	2.59E-05	0.000814	3.18
256407_at	sucrose-proton symporter, putative sir	ATSUC7	AT1G66570	17.19	4.10	10.10	2.60E-05	0.000817	3.17
263014_at	unknown protein similar to hypothetica	CAF2	AT1G23400	-2.26	-1.18	-10.10	2.60E-05	0.000817	3.17
262288_at	unknown protein identical to residues 1	CRR23	AT1G70760	-7.98	-3.00	-10.10	2.61E-05	0.000818	3.17
247949_at	cytochrome P450	CYP81F2	AT5G57220	44.55	5.48	10.09	2.62E-05	0.000818	3.17
264394_at	aminomethyltransferase-like precurso	---	AT1G11860	-3.47	-1.80	-10.09	2.62E-05	0.000818	3.17
251839_at	putative protein patatin, Solanum tube	PLA IIIA	AT3G54950	3.77	1.92	10.10	2.61E-05	0.000818	3.17
258239_at	putative chlorophyll A-B binding protei	LHCB2.3	AT3G27690	-45.01	-5.49	-10.09	2.63E-05	0.000819	3.16
250006_at	putative protein 2'-hydroxyisoflavone r	PCB2	AT5G18660	-8.63	-3.11	-10.08	2.64E-05	0.000821	3.16

247826_at	beta 1-3 glucanase - like protein beta	---	AT5G58480	-2.25	-1.17	-10.08	2.64E-05	0.000821	3.16
258390_at	unknown protein similar to leucine-rich	---	AT3G15410	-2.18	-1.12	-10.07	2.65E-05	0.000823	3.15
252102_at	dehydrin Xero2 ; supported by cDNA:	LTI30	AT3G50970	-11.48	-3.52	-10.07	2.66E-05	0.000824	3.15
244981_at	ribosomal protein S8	---	---	-2.62	-1.39	-10.07	2.66E-05	0.000824	3.15
259410_at	hypothetical protein predicted by gene	---	AT1G13340	7.98	3.00	10.05	2.69E-05	0.000825	3.14
254701_at	putative protein predicted protein, Ara	---	AT4G18030	-4.43	-2.15	-10.05	2.68E-05	0.000825	3.14
258813_at	NAM-like protein (no apical meristem)	anac046	AT3G04060	3.13	1.65	10.05	2.69E-05	0.000825	3.14
257219_at	uroporphyrinogen decarboxylase, puta	HEME1	AT3G14930	-3.15	-1.65	-10.06	2.68E-05	0.000825	3.14
267178_at	unknown protein ; supported by full-le	---	AT2G37750	24.65	4.62	10.06	2.68E-05	0.000825	3.14
245793_at	unknown protein ;supported by full-len	---	AT1G32220	-5.38	-2.43	-10.06	2.68E-05	0.000825	3.14
262942_at	hypothetical protein similar to unknowr	ALIS5	AT1G79450	7.84	2.97	10.05	2.69E-05	0.000825	3.14
250857_at	unknown protein	---	AT5G04790	-3.19	-1.68	-10.06	2.68E-05	0.000825	3.14
259020_at	unknown protein ; supported by cDNA	---	AT3G07470	-2.64	-1.40	-10.05	2.70E-05	0.000826	3.13
248192_at	IAA-amino acid hydrolase homolog ILL	ILL3	AT5G54140	2.14	1.09	10.04	2.70E-05	0.000826	3.13
248879_at	ornithine aminotransferase	DELTA-OAT	AT5G46180	2.74	1.46	10.04	2.71E-05	0.000826	3.13
253776_at	ADP,ATP carrier-like protein ADP,ATP	AAC3	AT4G28390	3.51	1.81	10.03	2.73E-05	0.000832	3.12
262452_at	hypothetical protein similar to hypothet	---	AT1G11210	2.23	1.16	10.02	2.74E-05	0.000832	3.12
265057_at	unknown protein ;supported by full-len	---	AT1G52140	-2.34	-1.22	-10.02	2.74E-05	0.000832	3.12
248162_at	1,4-benzoquinone reductase-like; Trp	FQR1	AT5G54500	3.95	1.98	10.02	2.74E-05	0.000832	3.12
254218_at	putative receptor kinase receptor-like	---	AT4G23740	-2.33	-1.22	-10.02	2.75E-05	0.000832	3.12
247488_at	putative protein MtN19, Medicago trur	---	AT5G61820	3.44	1.78	10.02	2.75E-05	0.000832	3.11
259707_at	thylakoid-bound ascorbate peroxidase	TAPX	AT1G77490	-3.21	-1.68	-10.01	2.76E-05	0.000833	3.11
253121_at	putative protein predicted protein, Cae	---	AT4G35890	1.83	0.87	10.01	2.77E-05	0.000835	3.11
251652_at	putative protein hypothetical protein T	---	AT3G57380	3.53	1.82	10.00	2.78E-05	0.000836	3.10
254434_at	ethylene-regulated transcript 2 (ERT2)	---	AT4G20880	2.09	1.06	9.99	2.80E-05	0.00084	3.10
264424_at	unknown protein similar to hypothetica	---	AT1G61740	-2.73	-1.45	-9.99	2.80E-05	0.00084	3.10
267436_at	putative receptor-like protein kinase	FRK1	AT2G19190	14.37	3.84	9.99	2.80E-05	0.00084	3.10
267040_at	unknown protein	---	AT2G34300	-6.08	-2.60	-9.98	2.81E-05	0.000841	3.09
258203_at	hypothetical protein predicted by gene	---	AT3G13950	42.57	5.41	9.98	2.81E-05	0.000841	3.09
262607_at	unknown protein ;supported by full-len	---	AT1G13990	2.71	1.44	9.98	2.81E-05	0.000841	3.09
260856_at	TINY-like protein similar to TINY GB:C	---	AT1G21910	-27.53	-4.78	-9.97	2.83E-05	0.000843	3.09
245845_at	Pto kinase interactor, putative similar	PERK10	AT1G26150	-2.19	-1.13	-9.97	2.83E-05	0.000843	3.08
258484_at	sterol-C5-desaturase identical to GB:A	STE1	AT3G02580	-2.26	-1.18	-9.96	2.84E-05	0.000847	3.08
264514_at	putative cinnamyl alcohol dehydrogen	---	AT1G09500	57.63	5.85	9.96	2.85E-05	0.000847	3.08
266995_at	putative cytochrome P450	CYP710A1	AT2G34500	32.51	5.02	9.95	2.86E-05	0.000849	3.07

264344_at	putative aspartic proteinase similar to (	---	AT1G11910	1.86	0.90	9.95	2.86E-05	0.000849	3.07
248028_at	putative protein similar to unknown pro	---	AT5G55620	-7.28	-2.86	-9.95	2.87E-05	0.000851	3.07
251365_at	putative DNA-binding protein At2g336	---	AT3G61310	-2.80	-1.49	-9.94	2.88E-05	0.000852	3.07
253190_at	UDP-galactose transporter - like prote	---	AT4G35335	-2.29	-1.19	-9.94	2.89E-05	0.000855	3.06
255978_at	hypothetical protein	---	AT1G34010	-2.03	-1.02	-9.94	2.90E-05	0.000855	3.06
260058_at	unknown protein ; supported by cDNA	---	AT1G78100	-2.37	-1.25	-9.93	2.91E-05	0.000859	3.05
261078_at	unknown protein identical to SP:O500(	RPL4	AT1G07320	-2.20	-1.14	-9.92	2.92E-05	0.00086	3.05
247005_at	adenylylsulfate kinase-like protein ;su	---	AT5G67520	-2.95	-1.56	-9.92	2.93E-05	0.000862	3.05
264185_at	unknown protein ;supported by full-len	---	AT1G54780	-2.12	-1.09	-9.91	2.93E-05	0.000862	3.04
259937_s_	putative ABC transporter contains Pfar	ATNAP5	AT1G71330 /	2.26	1.17	9.91	2.94E-05	0.000863	3.04
266813_at	unknown protein	---	AT2G44920	-2.65	-1.40	-9.89	2.99E-05	0.000876	3.02
254649_at	pherophorin - like protein pherophorin	---	AT4G18570	-2.39	-1.25	-9.88	3.00E-05	0.000877	3.02
261351_at	hypothetical protein predicted by gene	---	AT1G79790	-2.39	-1.26	-9.87	3.01E-05	0.00088	3.02
260347_at	DHHC-type zinc finger protein, putativ	---	AT1G69420	-3.60	-1.85	-9.87	3.02E-05	0.000881	3.01
248132_at	SGP1 monomeric G-protein (emb|CAE	SGP1	AT5G54840	3.34	1.74	9.86	3.04E-05	0.000885	3.01
254347_at	putative protein DNA-binding protein A	WRKY31	AT4G22070	2.59	1.37	9.86	3.04E-05	0.000885	3.01
250618_at	putative protein hypothetical proteins -	ATBAG3	AT5G07220	-2.07	-1.05	-9.81	3.13E-05	0.000887	2.97
247954_at	beta-galactosidase (emb|CAB64740.1	BGAL4	AT5G56870	2.61	1.38	9.84	3.07E-05	0.000887	3.00
256891_at	hypothetical protein contains similarity	---	AT3G19030	2.87	1.52	9.85	3.06E-05	0.000887	3.00
254077_at	putative protein NorM, Vibrio parahae	---	AT4G25640	2.64	1.40	9.82	3.12E-05	0.000887	2.98
248273_at	putative protein contains similarity to u	---	AT5G53500	-4.24	-2.08	-9.84	3.08E-05	0.000887	2.99
261216_at	catechol O-methyltransferase, putativ	---	AT1G33030	12.78	3.68	9.82	3.12E-05	0.000887	2.98
266155_at	cytochrome p450, putative similar to c	CYP89A5	AT1G64950 /	6.27	2.65	9.81	3.14E-05	0.000887	2.97
262496_at	unknown protein ; supported by full-ler	---	AT1G21790	-4.46	-2.16	-9.84	3.09E-05	0.000887	2.99
259297_at	putative disease resistance protein sim	AtRLP30	AT3G05360	7.54	2.91	9.82	3.12E-05	0.000887	2.98
259882_at	unknown protein similar to hypothetica	---	AT1G76670	-2.32	-1.22	-9.83	3.10E-05	0.000887	2.99
249089_at	ATPase, calcium-transporting	---	AT5G44240	1.84	0.88	9.85	3.06E-05	0.000887	3.00
261483_at	hypothetical protein predicted by gene	---	AT1G14270	-2.40	-1.26	-9.82	3.13E-05	0.000887	2.98
256677_at	unknown protein contains Pfam profile	PHF1	AT3G52190	2.44	1.29	9.81	3.13E-05	0.000887	2.97
260165_at	30S ribosomal protein S17, chloroplas	RPS17	AT1G79850	-2.97	-1.57	-9.85	3.06E-05	0.000887	3.00
264383_at	putative glutathione peroxidase Conta	ATGPX1	AT2G25080	-2.67	-1.42	-9.82	3.12E-05	0.000887	2.98
251885_at	fructose-bisphosphatase precursor ; s	---	AT3G54050	-3.54	-1.82	-9.81	3.13E-05	0.000887	2.98
250483_at	alpha-hydroxynitrile lyase-like protein	MES5	AT5G10300	3.00	1.59	9.82	3.12E-05	0.000887	2.98
254790_at	probable photosystem I chain XI precu	PSAL	AT4G12800	-2.02	-1.01	-9.82	3.11E-05	0.000887	2.98
257699_at	phosphoglycerate kinase, putative sim	PGK1	AT3G12780	-2.60	-1.38	-9.83	3.10E-05	0.000887	2.99

254524_at	hypothetical protein	---	AT4G20000	15.70	3.97	9.81	3.13E-05	0.000887	2.97
267226_at	unknown protein	---	AT2G44010	6.31	2.66	9.83	3.09E-05	0.000887	2.99
253021_at	putative protein permease 1 - Mesem	---	AT4G38050	-2.38	-1.25	-9.83	3.10E-05	0.000887	2.99
267385_at	unknown protein highly similar to GP|2	---	AT2G44380	3.89	1.96	9.81	3.14E-05	0.000888	2.97
260179_at	unknown protein similar to hypothetica	HWI1	AT1G70690	5.72	2.52	9.81	3.15E-05	0.000889	2.97
256999_at	hypothetical protein predicted by gene	---	AT3G14200	-2.14	-1.10	-9.80	3.16E-05	0.000891	2.97
245003_at	PSII 43 KDa protein	---	---	-2.28	-1.19	-9.79	3.19E-05	0.000897	2.96
265335_at	Expressed protein ; supported by full-l	---	AT2G18245	-1.84	-0.88	-9.78	3.19E-05	0.000898	2.96
252000_at	hypothetical protein predicted protein,	---	AT3G52710	2.67	1.42	9.78	3.21E-05	0.000898	2.95
254563_at	putative protein several hypothetical pr	ERD3	AT4G19120	-2.90	-1.54	-9.78	3.21E-05	0.000898	2.95
254711_at	putative protein	---	AT4G18060	-2.40	-1.26	-9.78	3.21E-05	0.000898	2.95
257964_at	hypothetical protein similar to hypothet	---	AT3G19850	-3.54	-1.83	-9.78	3.21E-05	0.000898	2.95
251119_at	putative protein nifR3 protein, Azospir	---	AT3G63510	-3.04	-1.60	-9.78	3.20E-05	0.000898	2.95
245775_at	serine/threonine kinase, putative simil	CIPK23	AT1G30270	2.19	1.13	9.77	3.22E-05	0.000898	2.95
247596_at	putative protein predicted protein, Dro	---	AT5G60840	-4.20	-2.07	-9.77	3.22E-05	0.000898	2.94
248487_at	ATP-dependent Clp protease ATP-bin	ERD1	AT5G51070	2.37	1.25	9.77	3.23E-05	0.000898	2.94
252876_at	putative protein ;supported by full-leng	---	AT4G39970	-3.54	-1.82	-9.77	3.23E-05	0.000898	2.94
248177_at	putative protein strong similarity to unk	---	AT5G54630	-2.05	-1.04	-9.76	3.23E-05	0.000898	2.94
255567_at	hypothetical protein ; supported by cD	---	AT4G01150	-2.20	-1.13	-9.76	3.24E-05	0.000898	2.94
255411_at	putative ribonucleoprotein similarity to	---	AT4G03110	-2.47	-1.31	-9.76	3.25E-05	0.000899	2.94
259768_at	expressed protein supported by cDNA	COR314-TM	AT1G29390	-1.81	-0.86	-9.76	3.25E-05	0.000899	2.93
255403_at	putative GH3-like protein similar to so	DFL2	AT4G03400	-2.73	-1.45	-9.76	3.24E-05	0.000899	2.94
254034_at	P-glycoprotein-2 (pgp2)	PGP2	AT4G25960	-3.15	-1.65	-9.75	3.26E-05	0.000899	2.93
248402_at	dihydrodipicolinate reductase-like prote	crr1	AT5G52100	-3.76	-1.91	-9.75	3.26E-05	0.000899	2.93
267503_at	unknown protein ; supported by full-le	---	AT2G45600	-3.67	-1.88	-9.74	3.28E-05	0.000903	2.93
264619_at	putative chloroplast nucleoid DNA-bind	---	AT2G17760	2.37	1.25	9.74	3.28E-05	0.000903	2.93
262539_at	unknown protein Location of est 136A2	---	AT1G17200	-3.11	-1.64	-9.74	3.29E-05	0.000903	2.92
250505_at	cellulose synthase catalytic subunit	CESA5	AT5G09870	-3.09	-1.63	-9.73	3.30E-05	0.000905	2.92
266791_at	unknown protein	---	AT2G02960	-2.08	-1.05	-9.73	3.30E-05	0.000905	2.92
248153_at	cyclic nucleotide and calmodulin-regul	ATCNGC4	AT5G54250	2.35	1.23	9.73	3.31E-05	0.000907	2.92
247340_at	unknown protein	---	AT5G63700	-1.97	-0.98	-9.71	3.34E-05	0.000915	2.90
263419_at	putative protein kinase contains a prote	---	AT2G17220	3.12	1.64	9.71	3.36E-05	0.000917	2.90
258750_at	putative pectinacetylesterase similar to	---	AT3G05910	-6.58	-2.72	-9.70	3.37E-05	0.00092	2.90
247038_at	anthranilate N-hydroxycinnamoyl/benz	EPS1	AT5G67160	2.90	1.53	9.70	3.38E-05	0.000922	2.89
250110_at	putative protein many predicted protei	---	AT5G15350	-6.77	-2.76	-9.68	3.41E-05	0.000928	2.88

260542_at	putative FKBP type peptidyl-prolyl cis-t	---	AT2G43560	-3.91	-1.97	-9.67	3.43E-05	0.00093	2.88
253992_at	putative protein ;supported by full-leng	---	AT4G26060	2.26	1.18	9.68	3.43E-05	0.00093	2.88
258920_at	class 2 non-symbiotic hemoglobin iden	---	AT1G04380 /	-4.98	-2.32	-9.68	3.43E-05	0.00093	2.88
247251_at	cellulose synthase catalytic subunit	CESA6	AT5G64740	-3.01	-1.59	-9.66	3.47E-05	0.000936	2.87
252875_at	GTP-binding protein GB3 ;supported b	RABA4B	AT4G39990	-2.00	-1.00	-9.66	3.46E-05	0.000936	2.87
250141_at	protein kinase MSK-3 - like protein kin	SK13	AT5G14640	2.54	1.35	9.66	3.47E-05	0.000936	2.86
252130_at	putative protein 1 photosystem II oxyg	PSBO2	AT3G50820	-2.19	-1.13	-9.66	3.47E-05	0.000936	2.87
251461_at	putative protein	---	AT3G59780	-2.63	-1.40	-9.66	3.47E-05	0.000936	2.87
261695_at	Mg-chelatase, putative similar to Mg-c	CHLD	AT1G08520	-2.44	-1.29	-9.65	3.48E-05	0.000937	2.86
257225_s_	50S ribosomal protein L12-C identical	RPL12-C	AT3G27830 /	-2.02	-1.01	-9.65	3.48E-05	0.000937	2.86
254785_at	putative pollen surface protein endosp	FLA2	AT4G12730	-26.89	-4.75	-9.64	3.52E-05	0.000943	2.85
256787_at	beta-fructofuranosidase 1 identical to C	ATBFRUCT1	AT3G13790	4.56	2.19	9.64	3.52E-05	0.000943	2.85
253617_at	hypothetical protein	---	AT4G30410	-8.06	-3.01	-9.63	3.52E-05	0.000943	2.85
263937_at	putative RING zinc finger protein	---	AT2G35910	2.27	1.18	9.63	3.53E-05	0.000943	2.85
259526_at	hypothetical protein	---	AT1G12570	-5.01	-2.32	-9.63	3.53E-05	0.000943	2.85
253860_at	hypothetical protein ;supported by full-	---	AT4G27700	-2.02	-1.02	-9.62	3.55E-05	0.000947	2.84
251906_at	putative protein several hypothetical N	ATCHX20	AT3G53720	2.80	1.49	9.61	3.58E-05	0.000954	2.83
264708_at	putative ER6 protein similar to GB:AA	---	AT1G09740	2.89	1.53	9.61	3.58E-05	0.000954	2.83
266065_at	phytochrome B Identical to GB:X17342	PHYB	AT2G18790	-2.42	-1.28	-9.60	3.59E-05	0.000956	2.83
245642_at	Expressed protein ; supported by full-le	---	AT1G25275	1.88	0.91	9.60	3.59E-05	0.000956	2.83
253794_at	putative protein dimethylaniline monoc	---	AT4G28720	-8.89	-3.15	-9.58	3.65E-05	0.000968	2.81
248748_at	putative protein contains similarity to a	AMK2	AT5G47840	-2.18	-1.12	-9.57	3.67E-05	0.000974	2.80
264685_at	endo-1,4-beta-glucanase, putative sim	KOR2	AT1G65610	2.33	1.22	9.56	3.69E-05	0.000977	2.80
246548_at	putative protein ;supported by full-leng	---	AT5G14910	-2.26	-1.18	-9.56	3.69E-05	0.000977	2.80
252993_at	monooxygenase 2 (MO2)	---	AT4G38540	4.84	2.28	9.56	3.70E-05	0.000977	2.80
248366_at	SCARECROW transcriptional regulato	---	AT5G52510	2.47	1.30	9.54	3.75E-05	0.000977	2.78
254630_at	glycolate oxidase - like protein (S)-2-h	---	AT4G18360	24.88	4.64	9.55	3.73E-05	0.000977	2.79
247214_at	putative protein similar to unknown pro	---	AT5G64850	-7.46	-2.90	-9.54	3.75E-05	0.000977	2.78
251621_at	protein kinase - like protein wall-assoc	---	AT3G57700	4.01	2.00	9.54	3.73E-05	0.000977	2.79
262488_at	unknown protein EST gb|AA586241 co	---	AT1G21830	-4.49	-2.17	-9.54	3.74E-05	0.000977	2.78
252980_at	putative protein Human multiple exost	---	AT4G38040	-1.88	-0.91	-9.55	3.72E-05	0.000977	2.79
254105_at	magnesium-protoporphyrin IX methylt	CHLM	AT4G25080	-2.32	-1.21	-9.54	3.75E-05	0.000977	2.78
250444_at	beta-xylosidase - like protein beta-xylo	---	AT5G10560	-2.27	-1.18	-9.56	3.70E-05	0.000977	2.80
259417_at	unknown protein contains similarity to	HFR1	AT1G02340	-3.57	-1.84	-9.54	3.74E-05	0.000977	2.79
266293_at	putative tropinone reductase ;supporte	---	AT2G29360	-2.02	-1.01	-9.54	3.74E-05	0.000977	2.78

257064_at	hypothetical protein predicted by gene	---	AT3G18260	2.58	1.37	9.55	3.71E-05	0.000977	2.79
266747_at	predicted by genefinder and genscan	---	AT2G02870	2.49	1.31	9.55	3.72E-05	0.000977	2.79
265824_at	putative glucosyltransferase ;supporte	ATCSLA07	AT2G35650	-2.83	-1.50	-9.53	3.77E-05	0.000979	2.78
261086_at	hypothetical protein predicted by gene	TRFL3	AT1G17460	1.95	0.96	9.53	3.77E-05	0.000979	2.78
265728_at	hypothetical protein predicted by gens	---	AT2G31990	2.85	1.51	9.53	3.76E-05	0.000979	2.78
265021_at	unknown protein ;supported by full-ler	---	AT1G24610	-1.88	-0.91	-9.53	3.77E-05	0.000979	2.78
263509_s_	hypothetical protein	---	AT2G07687	3.40	1.76	9.53	3.78E-05	0.000979	2.77
261700_at	hypothetical protein similar to hypothet	---	AT1G32690	2.64	1.40	9.52	3.79E-05	0.00098	2.77
267256_s_	putative serine carboxypeptidase I ;su	scpl10	AT2G23000 /	-2.62	-1.39	-9.52	3.79E-05	0.000981	2.77
261822_at	unknown protein ;supported by full-len	---	AT1G11380	-4.22	-2.08	-9.51	3.83E-05	0.000987	2.76
266704_at	putative N-acetyl-gamma-glutamyl-pho	---	AT2G19940	-2.51	-1.33	-9.51	3.83E-05	0.000987	2.76
248943_s_	putative protein similar to unknown pro	---	AT5G45440 /	-5.54	-2.47	-9.50	3.85E-05	0.000991	2.75
245168_at	3-ketoacyl-CoA thiolase ;supported by	PKT3	AT2G33150	2.55	1.35	9.50	3.85E-05	0.000991	2.75
266671_at	anthranilate synthase, alpha subunit i	ASA2	AT2G29690	-2.30	-1.20	-9.50	3.85E-05	0.000991	2.75
252885_at	glycine-rich protein (clone AtGRP8) ; s	GR-RBP8	AT4G39260	3.19	1.67	9.50	3.86E-05	0.000991	2.75
245148_at	putative pectinesterase ; supported by	---	AT2G45220	30.22	4.92	9.49	3.87E-05	0.000992	2.75
261742_at	hypothetical protein predicted by gene	---	AT1G08390	-1.96	-0.97	-9.49	3.88E-05	0.000992	2.75
251021_at	thaumatin-like protein thaumatin-like p	---	AT5G02140	-4.10	-2.03	-9.49	3.87E-05	0.000992	2.75
261851_at	hexokinase, putative similar to chloro	HKL1	AT1G50460	-4.27	-2.09	-9.47	3.91E-05	0.000993	2.74
245905_at	putative protein predicted proteins, Ar	---	AT5G11090	2.22	1.15	9.48	3.91E-05	0.000993	2.74
257338_s_	NADH dehydrogenase subunit 5 (nad5	---	AT2G07711 /	2.91	1.54	9.47	3.91E-05	0.000993	2.74
257216_at	4-methyl-5(b-hydroxyethyl)-thiazole m	---	AT3G14990	5.34	2.42	9.48	3.91E-05	0.000993	2.74
252184_at	steroid 22-alpha-hydroxylase (DWF4)	DWF4	AT3G50660	-2.80	-1.49	-9.48	3.90E-05	0.000993	2.74
252515_at	heat shock protein 17 ; supported by	HSP17.4	AT3G46230	19.36	4.28	9.48	3.89E-05	0.000993	2.74
253688_at	putative protein ;supported by full-leng	---	AT4G29590	-3.05	-1.61	-9.48	3.91E-05	0.000993	2.74
259658_at	hypothetical protein predicted by gene	NDF5	AT1G55370	-3.05	-1.61	-9.48	3.89E-05	0.000993	2.74
263533_at	putative Rieske iron-sulfur protein ;su	TIC55	AT2G24820	1.79	0.84	9.47	3.93E-05	0.000997	2.73
251063_at	protein kinase ATN1-like protein prote	---	AT5G01850	2.11	1.08	9.46	3.94E-05	0.000997	2.73
258371_at	hypothetical protein contains similarity	---	AT3G14410	-2.29	-1.20	-9.46	3.95E-05	0.000998	2.73
252929_at	putative fructose-bisphosphate aldola	---	AT4G38970	-2.08	-1.06	-9.45	3.97E-05	0.001	2.72
253009_at	glycine hydroxymethyltransferase like	SHM1	AT4G37930	-2.80	-1.49	-9.46	3.96E-05	0.001	2.72
250580_at	glutamate dehydrogenase 2 ; support	GDH2	AT5G07440	5.70	2.51	9.46	3.96E-05	0.001	2.72
256293_at	pinhead-like protein similar to pinhead	AGO7	AT1G69440	3.13	1.64	9.45	3.97E-05	0.001	2.72
259143_at	calmodulin-like protein similar to calm	---	AT3G10190	2.84	1.51	9.45	3.98E-05	0.001	2.72
253976_at	putative protein kinase protein kinase	D6PKL1	AT4G26610	-1.81	-0.86	-9.45	3.99E-05	0.001002	2.71

252975_s_	putative protein other predicted protein	ROPGEF1	AT4G38430	-2.01	-1.01	-9.44	4.00E-05	0.001005	2.71
248230_at	putative protein similar to unknown pro	---	AT5G53830	4.55	2.19	9.44	4.01E-05	0.001005	2.71
267057_at	hypothetical protein predicted by gens	---	AT2G32500	-6.36	-2.67	-9.44	4.02E-05	0.001006	2.71
263867_at	putative aquaporin (tonoplast intrinsic	GAMMA-TIP	AT2G36830	-4.62	-2.21	-9.43	4.03E-05	0.001006	2.71
263761_at	putative fructose bisphosphate aldolas	---	AT2G21330	-2.82	-1.50	-9.43	4.03E-05	0.001006	2.70
256829_at	unknown protein similar to aluminum-i	---	AT3G22850	3.58	1.84	9.43	4.04E-05	0.001008	2.70
264645_at	unknown protein Similar to Saccharon	---	AT1G08940	10.09	3.33	9.42	4.06E-05	0.001011	2.70
265042_at	unknown protein Similar to acid phosp	---	AT1G04040	-10.03	-3.33	-9.42	4.07E-05	0.001013	2.69
266684_at	40S ribosomal protein S15A	rps15ab	AT2G19720	-1.90	-0.92	-9.41	4.07E-05	0.001013	2.69
253412_at	putative protein (fragment) calcineurin	CBL10	AT4G33000	-2.51	-1.33	-9.41	4.09E-05	0.001014	2.69
249927_at	Glucose-1-phosphate adenylyltransfer	APL1	AT5G19220	-3.50	-1.81	-9.41	4.08E-05	0.001014	2.69
254363_at	pectinesterase like protein pectinester	sks4	AT4G22010	-3.50	-1.81	-9.40	4.10E-05	0.001015	2.69
253330_at	putative potassium transporter AtKT5p	KUP5	AT4G33530	-2.03	-1.02	-9.41	4.10E-05	0.001015	2.69
255732_at	fatty acid condensing enzyme CUT1,	KCS5	AT1G25450 /	-7.74	-2.95	-9.40	4.10E-05	0.001015	2.69
259896_at	unknown protein ;supported by full-len	---	AT1G71500	-2.26	-1.18	-9.40	4.11E-05	0.001016	2.68
246482_at	plant adhesion molecule 1 (PAM1) ;su	PAM1	AT5G15930	-2.08	-1.06	-9.39	4.15E-05	0.001024	2.67
249677_at	DNA helicase-like	---	AT5G35970	-3.91	-1.97	-9.38	4.16E-05	0.001024	2.67
266480_at	unknown protein ; supported by cDNA	---	AT2G31130	1.91	0.93	9.38	4.16E-05	0.001024	2.67
249193_at	putative protein similar to unknown pro	ARC6	AT5G42480	-1.82	-0.87	-9.38	4.16E-05	0.001024	2.67
249742_at	putative protein contains similarity to ri	---	AT5G24490	-2.46	-1.30	-9.38	4.18E-05	0.001026	2.66
254710_at	multidrug resistance protein/P-glycopr	PGP9	AT4G18050	3.63	1.86	9.38	4.18E-05	0.001026	2.67
261771_at	hypothetical protein contains similarity	---	AT1G76150	1.78	0.83	9.37	4.18E-05	0.001026	2.66
266071_at	unknown protein	---	AT2G18670 /	13.39	3.74	9.37	4.20E-05	0.00103	2.66
266182_at	hypothetical protein predicted by gens	---	AT2G02370	2.72	1.44	9.37	4.21E-05	0.00103	2.66
265716_at	unknown protein ;supported by full-ler	---	AT2G03350	-2.79	-1.48	-9.36	4.21E-05	0.00103	2.66
264837_at	unknown protein similar to ESTs emb	---	AT1G03600	-3.79	-1.92	-9.36	4.23E-05	0.001032	2.65
264111_at	hypothetical protein predicted by gens	---	AT2G13690	-1.90	-0.92	-9.36	4.23E-05	0.001032	2.65
249694_at	glucose-6-phosphate dehydrogenase ;	G6PD1	AT5G35790	-1.83	-0.87	-9.35	4.25E-05	0.001036	2.65
246476_at	putative protein predicted proteins - Ar	---	AT5G16730	-2.93	-1.55	-9.35	4.27E-05	0.001039	2.64
259104_at	unknown protein ;supported by full-ler	LNG2	AT3G02170	-3.73	-1.90	-9.33	4.32E-05	0.001048	2.63
248864_at	bHLH protein-like	---	AT5G46760	1.85	0.89	9.33	4.32E-05	0.001048	2.63
259665_at	unknown protein ; supported by cDNA	---	AT1G55160	-2.66	-1.41	-9.33	4.32E-05	0.001048	2.63
265374_at	hypothetical protein ;supported by full-	PSBX	AT2G06520	-1.87	-0.90	-9.32	4.34E-05	0.001051	2.62
259370_at	hypothetical protein predicted by gens	---	AT1G69050	2.48	1.31	9.32	4.34E-05	0.001051	2.62
260754_at	unknown protein	---	AT1G49000	5.87	2.55	9.31	4.37E-05	0.001056	2.62

266207_at	unknown protein ; supported by cDNA	---	AT2G27680	-2.63	-1.40	-9.31	4.37E-05	0.001056	2.62
260302_at	putative sulfate transporter contains Pf	---	AT1G80310 /	2.71	1.44	9.31	4.38E-05	0.001058	2.61
257816_at	glycosyl transferase, putative contains	QUA1	AT3G25140	-2.26	-1.17	-9.29	4.43E-05	0.001067	2.60
249823_s_	putative protein contains similarity to A	---	AT5G23350 /	-2.99	-1.58	-9.29	4.43E-05	0.001068	2.60
254879_at	hypothetical protein	---	AT4G11670	2.14	1.10	9.28	4.46E-05	0.001073	2.60
263606_at	putative beta-ketoacyl-CoA synthase	KCS9	AT2G16280	-3.05	-1.61	-9.28	4.47E-05	0.001075	2.59
260493_at	hypothetical protein predicted by gens	---	AT2G41830	-3.79	-1.92	-9.27	4.49E-05	0.001077	2.59
257401_at	hypothetical protein identical to hypoth	SRO2	AT1G23550	2.61	1.38	9.27	4.49E-05	0.001077	2.59
257766_at	auxin-inducible gene (IAA2) identical t	IAA2	AT3G23030	-3.26	-1.70	-9.26	4.51E-05	0.00108	2.58
266578_at	putative cinnamoyl CoA reductase ;su	---	AT2G23910	2.43	1.28	9.26	4.52E-05	0.001081	2.58
260370_at	putative aminolevulinate dehydratase s	HEMB1	AT1G69740	-2.04	-1.03	-9.26	4.54E-05	0.001083	2.58
252277_at	alpha NAC-like protein Nascent polyp	NACA2	AT3G49470	-1.79	-0.84	-9.26	4.53E-05	0.001083	2.58
265444_s_	aquaporin (plasma membrane intrinsic	RD28	AT2G37170 /	-4.47	-2.16	-9.24	4.58E-05	0.001092	2.57
256305_at	glutathione S-conjugate transporting A	MRP1	AT1G30400	3.00	1.58	9.23	4.63E-05	0.001103	2.56
246199_at	putative protein ;supported by full-leng	---	AT4G36530	-3.06	-1.61	-9.22	4.63E-05	0.001103	2.55
264543_at	hypothetical protein predicted by gene	---	AT1G55780	2.51	1.33	9.21	4.67E-05	0.00111	2.55
244996_at	ribosomal protein S2	---	---	-2.29	-1.20	-9.21	4.67E-05	0.00111	2.55
250385_at	aspartate aminotransferase (Asp3) ; s	ASP3	AT5G11520	4.22	2.08	9.21	4.68E-05	0.00111	2.54
253790_at	photosystem II protein W - like photos	PSB28	AT4G28660	-3.53	-1.82	-9.21	4.69E-05	0.001111	2.54
259763_at	unknown protein similar to GB:AAB81	---	AT1G77630	-3.11	-1.64	-9.20	4.70E-05	0.001111	2.54
254931_at	serine/threonine kinase-like protein re	---	AT4G11460	-2.67	-1.42	-9.20	4.70E-05	0.001111	2.54
246673_at	ribosomal protein S1 ;supported by full	RPS1	AT5G30510	-1.95	-0.96	-9.20	4.70E-05	0.001111	2.54
264788_at	putative DnaJ protein ;supported by fu	---	AT2G17880	-9.21	-3.20	-9.20	4.72E-05	0.001113	2.53
247131_at	ferredoxin-NADP+ reductase	FNR1	AT5G66190	-1.93	-0.95	-9.20	4.72E-05	0.001113	2.53
249162_at	Expressed protein ; supported by full-l	---	AT5G42765	-2.77	-1.47	-9.20	4.72E-05	0.001113	2.53
248105_at	cell division protein FtsZ chloroplast ho	FTSZ1-1	AT5G55280	-2.68	-1.42	-9.19	4.73E-05	0.001113	2.53
249057_at	putative protein contains similarity to U	DUR	AT5G44480	13.06	3.71	9.19	4.75E-05	0.001116	2.53
260995_at	unknown protein	---	AT1G12120	-2.06	-1.05	-9.19	4.75E-05	0.001116	2.53
255607_at	putative acetyltransferase similar to D	---	AT4G01130	-3.56	-1.83	-9.18	4.76E-05	0.001117	2.52
245859_at	serine (threonine) protein kinase - like	ATNEK3	AT5G28290	-3.30	-1.72	-9.18	4.78E-05	0.001118	2.52
259523_at	hypothetical protein	---	AT1G12500	-3.62	-1.86	-9.18	4.77E-05	0.001118	2.52
245176_at	unknown protein similar to GP|210453	---	AT2G47440	-6.28	-2.65	-9.18	4.78E-05	0.001118	2.52
263774_at	unknown protein ; supported by cDNA	---	AT2G40280	-1.98	-0.98	-9.17	4.79E-05	0.001118	2.52
257700_at	unknown protein similar to unknown pr	ALIS1	AT3G12740	2.35	1.24	9.18	4.78E-05	0.001118	2.52
266045_s_	hypothetical protein	---	AT2G07727	2.74	1.45	9.17	4.79E-05	0.001118	2.52

251791_at	expansin-like protein expansin At-EXP	ATEXPA16	AT3G55500	-5.81	-2.54	-9.17	4.80E-05	0.001118	2.51
258123_at	putative MAP kinase similar to blast ar	MPK9	AT3G18040	-4.25	-2.09	-9.16	4.83E-05	0.001118	2.51
250983_at	putative protein In2, Zea mays, EMBL	---	AT5G02780	16.63	4.06	9.17	4.82E-05	0.001118	2.51
258682_at	putative ribosomal-protein S6 kinase (	S6K2	AT3G08720	6.52	2.71	9.16	4.83E-05	0.001118	2.51
262151_at	hypothetical protein predicted by gene	---	AT1G52510	-4.27	-2.10	-9.16	4.83E-05	0.001118	2.51
250306_at	putative protein similar to unknown pro	---	AT5G12170	3.03	1.60	9.17	4.81E-05	0.001118	2.51
259043_at	unknown protein similar to putative pro	---	AT3G03440	3.19	1.67	9.17	4.81E-05	0.001118	2.51
267181_at	putative alcohol dehydrogenase ; sup	---	AT2G37760	4.07	2.02	9.16	4.85E-05	0.001121	2.51
258684_at	putative protein kinase contains Pfam	---	AT3G08680	-2.65	-1.41	-9.15	4.86E-05	0.001124	2.50
261801_at	hypothetical protein similar to hypothet	AAE14	AT1G30520	-2.73	-1.45	-9.15	4.88E-05	0.001127	2.50
263319_at	putative anion exchange protein identi	BOR1	AT2G47160	-4.26	-2.09	-9.14	4.89E-05	0.001128	2.49
264704_at	unknown protein similar to putative gly	LGT8	AT1G70090	-3.45	-1.79	-9.14	4.90E-05	0.001128	2.49
248541_at	protein kinase ATN1-like protein	---	AT5G50180	-2.75	-1.46	-9.14	4.90E-05	0.001128	2.49
266302_at	ethylene-insensitive3-like1 (EIL1) iden	EIL1	AT2G27050	-2.48	-1.31	-9.13	4.93E-05	0.001134	2.49
265945_at	putative cytokinin oxidase ; supported	CKX2	AT2G19500	2.01	1.01	9.12	4.96E-05	0.001139	2.48
251766_at	putative protein PA26, p53 regulated I	---	AT3G55890 /	2.07	1.05	9.12	4.96E-05	0.001139	2.48
259528_at	hypothetical protein	---	AT1G12330	-2.95	-1.56	-9.12	4.99E-05	0.001144	2.47
255631_at	hypothetical protein	BSK3	AT4G00710	-1.82	-0.86	-9.11	5.01E-05	0.001145	2.47
247593_at	ABC transporter homolog PnATH - lik	GCN1	AT5G60790	2.18	1.12	9.11	5.01E-05	0.001145	2.47
260328_at	putative aspartate aminotransferase si	---	AT1G80360	1.81	0.86	9.11	5.00E-05	0.001145	2.47
260065_at	putative RING zinc finger protein cont	---	AT1G73760	2.22	1.15	9.11	5.02E-05	0.001145	2.47
255332_at	predicted protein of unknown function	---	AT4G04340	-1.86	-0.90	-9.11	5.02E-05	0.001145	2.47
254673_at	membrane-bound small GTP-binding	AtRABA1e	AT4G18430	8.65	3.11	9.10	5.03E-05	0.001146	2.47
246492_at	CRS2-like protein CRS2 - Zea mays,	---	AT5G16140	-2.89	-1.53	-9.10	5.04E-05	0.001148	2.46
246619_at	transmembrane protein FT27/PFT27-li	---	AT5G36290	-1.84	-0.88	-9.10	5.05E-05	0.001149	2.46
261525_at	hypothetical protein predicted by gene	---	AT1G14330	2.61	1.38	9.09	5.06E-05	0.00115	2.46
254667_at	glycine-rich cell wall protein-like glycir	---	AT4G18280	-4.26	-2.09	-9.09	5.08E-05	0.001153	2.45
246370_at	hypothetical protein predicted by gene	---	AT1G51920	21.76	4.44	9.09	5.09E-05	0.001153	2.45
266098_at	hypothetical protein predicted by gens	---	AT2G37870	2.82	1.50	9.09	5.09E-05	0.001153	2.45
260044_at	Expressed protein ; supported by full-l	---	AT1G73655	-2.07	-1.05	-9.08	5.10E-05	0.001155	2.45
247817_at	Expressed protein ; supported by full-l	---	AT5G58375	2.37	1.25	9.08	5.11E-05	0.001155	2.45
266000_at	putative cytochrome P450 identical to	CYP71B6	AT2G24180	4.33	2.11	9.07	5.16E-05	0.00116	2.44
264515_at	hypothetical protein similar to hypothet	---	AT1G10090	-1.73	-0.79	-9.07	5.16E-05	0.00116	2.44
249864_at	putative protein similar to unknown pro	ATMGT10	AT5G22830	-1.81	-0.86	-9.07	5.16E-05	0.00116	2.44
245644_at	unknown protein similar to putative rec	---	AT1G25320	-2.33	-1.22	-9.07	5.16E-05	0.00116	2.44

262558_at	Expressed protein ; supported by full-l	---	AT1G31335	-2.21	-1.15	-9.07	5.14E-05	0.00116	2.44
251784_at	putative protein photosystem II oxyge	PPL1	AT3G55330	-3.32	-1.73	-9.07	5.16E-05	0.00116	2.44
261942_at	unknown protein similar to putative DN	AGL87	AT1G22590	-4.09	-2.03	-9.07	5.16E-05	0.00116	2.44
255590_at	cathepsin B-like cysteine protease, pu	---	AT4G01610	2.45	1.30	9.06	5.17E-05	0.001161	2.43
254293_at	putative protein SF16 protein, Heliant	IQD22	AT4G23060	-4.12	-2.04	-9.06	5.19E-05	0.001163	2.43
258809_at	NAM-like protein (no apical meristem)	anac047	AT3G04070	6.35	2.67	9.06	5.20E-05	0.001164	2.43
267209_at	unknown protein ;supported by full-ler	---	AT2G30930	-2.54	-1.34	-9.05	5.22E-05	0.001166	2.43
256818_at	hypothetical protein contains Pfam pro	---	AT3G21420	1.91	0.93	9.05	5.22E-05	0.001166	2.43
265985_at	hypothetical protein predicted by gens	ATPUP5	AT2G24220	-1.89	-0.92	-9.05	5.22E-05	0.001166	2.42
256482_at	protein kinase, putative contains Pfam	FEI1	AT1G31420	-2.04	-1.03	-9.05	5.23E-05	0.001167	2.42
258218_at	methyltransferase, putative similar to	XPL1	AT3G17998 /	-2.96	-1.57	-9.04	5.24E-05	0.001168	2.42
259729_at	hypothetical protein predicted by gene	---	AT1G77640	-8.18	-3.03	-9.04	5.26E-05	0.00117	2.42
246842_at	Expressed protein ; supported by full-l	---	AT5G26731	3.52	1.82	9.04	5.27E-05	0.001171	2.42
263326_at	unknown protein ; supported by cDNA	---	AT2G04280	-2.89	-1.53	-9.03	5.30E-05	0.001176	2.41
261076_at	unknown protein ;supported by full-len	SMO2-1	AT1G07420	-1.88	-0.91	-9.03	5.31E-05	0.001177	2.41
266929_at	putative AT-hook DNA-binding protein	---	AT2G45850	-2.07	-1.05	-9.03	5.31E-05	0.001178	2.41
254300_at	Translation factor EF-1 alpha - like pr	ACR7	AT4G22780	2.96	1.57	9.02	5.34E-05	0.001182	2.40
247327_at	peroxidase (emb|CAA67551.1) ;suppo	---	AT5G64120	24.59	4.62	9.01	5.37E-05	0.001188	2.39
247351_at	putative protein contains similarity to N	ANAC102	AT5G63790	6.60	2.72	9.01	5.39E-05	0.001189	2.39
251500_at	receptor-like protein kinase receptor-li	---	AT3G59110	-1.98	-0.98	-9.01	5.38E-05	0.001189	2.39
246327_at	receptor-like serine/threonine kinase,	---	AT1G16670	2.50	1.32	9.00	5.40E-05	0.001192	2.39
253519_at	predicted protein red-1 gene, M.musc	---	AT4G31240	4.15	2.05	9.00	5.41E-05	0.001192	2.39
252366_at	Expressed protein ; supported by full-l	---	AT3G48420	-5.39	-2.43	-9.00	5.42E-05	0.001193	2.39
259858_at	putative receptor kinase similar to rece	---	AT1G68400	-3.86	-1.95	-8.99	5.45E-05	0.001197	2.38
245698_at	phosphate/phosphoenolpyruvate trans	---	AT5G04160	-3.44	-1.78	-8.98	5.47E-05	0.001197	2.38
244953_s_	NADH dehydrogenase subunit 6	---	AT2G07731	3.18	1.67	8.98	5.47E-05	0.001197	2.37
263456_at	unknown protein	---	AT2G22125	-2.67	-1.42	-8.98	5.47E-05	0.001197	2.37
256453_at	GSH-dependent dehydroascorbate re	DHAR2	AT1G75270	4.30	2.11	8.99	5.46E-05	0.001197	2.38
262055_at	unknown protein ; supported by full-ler	---	AT1G79970	1.90	0.92	8.99	5.46E-05	0.001197	2.38
257687_at	hypothetical protein predicted by gene	SDRB	AT3G12800	2.03	1.02	8.99	5.44E-05	0.001197	2.38
253163_at	putative protein E1B 19K/Bcl-2-interac	---	AT4G35750	2.82	1.49	8.98	5.48E-05	0.001197	2.37
265287_at	putative photosystem I reaction center	PSAE-2	AT2G20260	-1.76	-0.82	-8.98	5.48E-05	0.001197	2.37
261309_at	phosphoethanolamine N-methyltransf	CPuORF31	AT1G48598 /	-3.44	-1.78	-8.98	5.49E-05	0.001197	2.37
253849_at	putative protein 150-kD protein, Dicty	---	AT4G28080	-1.95	-0.96	-8.97	5.50E-05	0.001199	2.37
253736_at	Proline-rich APG - like protein proline-	---	AT4G28780	-3.33	-1.74	-8.97	5.53E-05	0.001202	2.36

260943_at	thioredoxin, putative similar to thiored	ATTRX5	AT1G45145	2.90	1.54	8.97	5.52E-05	0.001202	2.36
246154_at	putative protein predicted protein, Ara	---	AT5G19940	-2.03	-1.02	-8.96	5.54E-05	0.001204	2.36
265305_at	putative tyrosine decarboxylase	---	AT2G20340	-2.51	-1.33	-8.96	5.57E-05	0.001208	2.35
250133_at	thioredoxin f2 (gb|AAD35004.1) ; supp	TRXF2	AT5G16400	-3.70	-1.89	-8.96	5.57E-05	0.001208	2.36
257333_at	cytochrome c oxidase subunit 1	---	---	4.20	2.07	8.95	5.59E-05	0.001211	2.35
259008_at	metallothionein-like protein similar to m	MT2A	AT3G09390	2.20	1.14	8.95	5.61E-05	0.001212	2.35
245002_at	PSII D2 protein	---	---	-2.43	-1.28	-8.95	5.60E-05	0.001212	2.35
257236_at	hypothetical protein	---	AT3G15095	-2.51	-1.33	-8.95	5.61E-05	0.001212	2.35
264300_at	gamma glutamyl hydrolase, putative s	ATGGH3	AT1G78670	2.00	1.00	8.94	5.64E-05	0.001216	2.34
252334_at	mitochondrial phosphate transporter n	---	AT3G48850	26.37	4.72	8.94	5.64E-05	0.001217	2.34
246832_at	putative protein isopenicillin N epimer	---	AT5G26600	2.25	1.17	8.93	5.67E-05	0.001221	2.34
244940_at	ribosomal protein S12 (trans-splice pa	---	---	-2.40	-1.26	-8.93	5.68E-05	0.001223	2.33
265938_at	putative SF21 protein {Helianthus ann	---	AT2G19620	-7.25	-2.86	-8.93	5.69E-05	0.001224	2.33
253052_at	cytochrome P450-like protein ; suppor	CYP81H1	AT4G37310	5.42	2.44	8.92	5.70E-05	0.001225	2.33
260567_at	putative glucosyltransferase ;supporte	UGT74F2	AT2G43820	3.07	1.62	8.92	5.72E-05	0.001228	2.33
252115_at	non-specific lipid transfer protein ;sup	LTP5	AT3G51600	-2.38	-1.25	-8.91	5.75E-05	0.001232	2.32
256228_at	phosphoglycerate kinase, putative sim	---	AT1G56190	-2.53	-1.34	-8.91	5.77E-05	0.001235	2.32
247487_at	putative protein predicted protein, Ara	---	AT5G62150	22.84	4.51	8.91	5.77E-05	0.001235	2.32
264954_at	carboxyphosphonoenolpyruvate muta	---	AT1G77060	-2.72	-1.44	-8.89	5.84E-05	0.001248	2.30
251920_at	uracil phosphoribosyltransferase-like p	---	AT3G53900	-4.60	-2.20	-8.88	5.87E-05	0.001252	2.30
246613_at	acetyl-CoA carboxylase ;supported by	CAC2	AT5G35360	-2.49	-1.31	-8.88	5.87E-05	0.001252	2.30
252868_at	putative protein tubulin-folding cofacto	POR	AT4G39920	-1.84	-0.88	-8.88	5.88E-05	0.001254	2.30
252878_at	mitochondrial carrier - like protein AgF	SAMC1	AT4G39460	-2.05	-1.04	-8.87	5.91E-05	0.001259	2.29
252615_at	serine/proline-rich protein	---	AT3G45230	-3.06	-1.61	-8.87	5.94E-05	0.001262	2.29
260457_at	unknown protein	---	AT1G72480	-2.03	-1.02	-8.87	5.94E-05	0.001262	2.29
252400_at	hypothetical protein	---	AT3G48020	4.59	2.20	8.86	5.95E-05	0.001263	2.28
258997_at	hypothetical protein similar to unknown	---	AT3G01810	-3.45	-1.79	-8.86	5.96E-05	0.001264	2.28
258467_at	unknown protein contains Pfam profile	---	AT3G06060	-2.26	-1.18	-8.86	5.98E-05	0.001266	2.28
251428_at	beta-glucosidase-like protein several b	DIN2	AT3G60140	134.02	7.07	8.86	5.98E-05	0.001266	2.28
267237_s_	unknown protein ;supported by full-ler	---	AT2G44040 /	-4.75	-2.25	-8.86	5.98E-05	0.001266	2.28
263467_at	unknown protein	---	AT2G31730	-4.71	-2.24	-8.85	6.01E-05	0.001269	2.27
265415_at	unknown protein ;supported by full-ler	PSB29	AT2G20890	-2.15	-1.10	-8.85	6.00E-05	0.001269	2.27
250305_at	putative protein contains similarity to u	---	AT5G12150	-2.40	-1.26	-8.85	6.01E-05	0.001269	2.27
258324_at	putative DNA binding protein identical	TSO1	AT3G22780	-1.84	-0.88	-8.84	6.03E-05	0.001271	2.27
247461_at	putative protein various predicted prot	ATBAG2	AT5G62100	-2.47	-1.30	-8.84	6.05E-05	0.001275	2.26

266650_at	unknown protein	---	AT2G25800	-2.40	-1.26	-8.84	6.06E-05	0.001275	2.26
254303_at	predicted protein	---	AT4G22830	-1.95	-0.96	-8.84	6.06E-05	0.001275	2.26
265499_at	putative glucosyltransferase	UGT73B5	AT2G15480	14.29	3.84	8.82	6.15E-05	0.001293	2.25
253276_at	caffeoyl-CoA O-methyltransferase - lik	---	AT4G34050	2.88	1.53	8.81	6.17E-05	0.001294	2.24
251995_at	nuclear envelope membrane protein -	FK	AT3G52940	-1.84	-0.88	-8.81	6.18E-05	0.001296	2.24
261563_at	polyphosphoinositide binding protein,	---	AT1G01630	-2.18	-1.12	-8.81	6.19E-05	0.001297	2.24
255428_at	putative LRR receptor-like protein kina	SRF3	AT4G03390	-1.98	-0.99	-8.80	6.21E-05	0.001299	2.24
259300_at	hypothetical protein predicted by gens	---	AT3G05100	-1.97	-0.98	-8.80	6.22E-05	0.0013	2.24
245150_at	photolyase/blue-light receptor (PHR2)	PHR2	AT2G47590	-2.27	-1.19	-8.80	6.23E-05	0.0013	2.23
246968_at	RING finger-like protein RING-H2 fing	---	AT5G24870	2.56	1.36	8.80	6.24E-05	0.001301	2.23
253251_at	putative protein similarity predicted pr	---	AT4G34730	-2.70	-1.43	-8.79	6.25E-05	0.001301	2.23
245354_at	Lil3 protein ;supported by full-length cI	LIL3:1	AT4G17600	-2.27	-1.18	-8.80	6.24E-05	0.001301	2.23
255552_at	S-adenosylmethionine synthase 2 ;su	SAM-2	AT4G01850	-2.12	-1.08	-8.79	6.28E-05	0.001307	2.22
264037_at	putative steroid sulfotransferase ;supp	---	AT2G03750	-2.34	-1.23	-8.78	6.29E-05	0.001309	2.22
251934_at	putative protein delta-latroinsectotoxin	---	AT3G54070	-2.30	-1.20	-8.78	6.31E-05	0.001311	2.22
266745_at	unknown protein ; supported by cDNA	PKS1	AT2G02950	-5.71	-2.51	-8.78	6.32E-05	0.001312	2.22
257190_at	30S ribosomal protein S10, putative s	---	AT3G13120	-2.96	-1.57	-8.78	6.33E-05	0.001312	2.22
246015_at	putative protein predicted proteins, Dr	---	AT5G10700	-1.92	-0.94	-8.78	6.33E-05	0.001312	2.22
245007_at	PSI P700 apoprotein A1	---	---	-3.59	-1.85	-8.77	6.34E-05	0.001313	2.21
253489_at	monogalactosyldiacylglycerol synthas	MGD1	AT4G31780	-2.83	-1.50	-8.76	6.39E-05	0.001315	2.21
246411_at	hypothetical protein contains similarity	---	AT1G57770	-4.85	-2.28	-8.77	6.37E-05	0.001315	2.21
247213_at	unknown protein ; supported by full-le	PROPEP1	AT5G64900	10.84	3.44	8.77	6.37E-05	0.001315	2.21
245242_at	chlorophyll a oxygenase identical to ch	CH1	AT1G44446	-2.52	-1.33	-8.76	6.38E-05	0.001315	2.21
250906_at	1,4-alpha-glucan branching enzyme p	SBE2.2	AT5G03650	-2.16	-1.11	-8.77	6.36E-05	0.001315	2.21
258853_at	unknown protein similar to GB:AAD55	---	AT3G06440	-1.96	-0.97	-8.77	6.38E-05	0.001315	2.21
253283_at	hypothetical protein ; supported by cD	---	AT4G34090	-2.76	-1.46	-8.76	6.39E-05	0.001315	2.21
261315_at	AP2 domain containing protein, putati	ERF8	AT1G53170	4.54	2.18	8.76	6.40E-05	0.001315	2.20
255430_at	putative chloroplast protein import cor	tic20-IV	AT4G03320	4.07	2.02	8.75	6.44E-05	0.001317	2.20
248335_at	putative protein strong similarity to unk	---	AT5G52450	3.37	1.75	8.75	6.43E-05	0.001317	2.20
255573_at	hypothetical protein	---	AT4G01400	-1.73	-0.79	-8.76	6.42E-05	0.001317	2.20
252228_at	porin - like protein porin, Mesembryan	VDAC5	AT3G49920	-1.83	-0.87	-8.75	6.44E-05	0.001317	2.20
244993_s_	hypothetical protein	---	---	-2.39	-1.26	-8.75	6.43E-05	0.001317	2.20
262283_at	unknown protein ;supported by full-len	---	AT1G68590	-2.54	-1.34	-8.74	6.48E-05	0.001323	2.19
256186_at	4-coumarate:CoA ligase 1 identical to	4CL1	AT1G51680	5.88	2.56	8.74	6.50E-05	0.001326	2.19
246231_at	putative protein	---	AT4G37080	-2.60	-1.38	-8.74	6.51E-05	0.001329	2.19

263363_at	putative cold-regulated protein ;suppo	---	AT2G03850	7.78	2.96	8.73	6.52E-05	0.001329	2.18
265388_s_	unknown protein ;supported by full-ler	---	AT2G20990 /	-1.93	-0.95	-8.73	6.53E-05	0.00133	2.18
248460_at	Expressed protein ; supported by full-l	---	AT5G50915	-12.61	-3.66	-8.73	6.54E-05	0.00133	2.18
252231_at	hypothetical protein ;supported by full-	---	AT3G49720	-2.29	-1.20	-8.73	6.55E-05	0.001332	2.18
267606_at	putative beta-ketoacyl-CoA synthase	KCS11	AT2G26640	-1.84	-0.88	-8.73	6.56E-05	0.001333	2.18
266905_at	putative katanin ;supported by full-len	---	AT2G34560	-2.74	-1.45	-8.72	6.59E-05	0.001338	2.17
266194_at	unknown protein	---	AT2G39090	-1.69	-0.76	-8.72	6.60E-05	0.001338	2.17
250767_at	putative protein contains similarity to u	ATNFXL2	AT5G05660	-1.84	-0.88	-8.72	6.61E-05	0.001338	2.17
246454_at	Expressed protein ; supported by full-l	DHAR3	AT5G16710	-1.99	-1.00	-8.72	6.61E-05	0.001338	2.17
261165_at	dihydrolipoamide S-acetyltransferase,	EMB3003	AT1G34430	-2.03	-1.02	-8.71	6.62E-05	0.001339	2.17
255506_at	predicted glycosyl transferase similar	GATL6	AT4G02130	-4.15	-2.05	-8.71	6.65E-05	0.001341	2.16
247215_at	Expressed protein ; supported by full-l	PROPEP3	AT5G64905	51.67	5.69	8.71	6.64E-05	0.001341	2.16
263737_at	unknown protein ;supported by full-len	---	AT1G60010	-2.31	-1.21	-8.71	6.64E-05	0.001341	2.16
260215_at	unknown protein	---	AT1G74530	-2.01	-1.00	-8.70	6.67E-05	0.001344	2.16
251865_at	protein phosphatase 2A regulatory su	---	AT3G54930	-1.82	-0.86	-8.70	6.68E-05	0.001345	2.16
266275_at	putative tropinone reductase	---	AT2G29370	-2.36	-1.24	-8.70	6.70E-05	0.001347	2.16
249710_at	glutamate-ammonia ligase (EC 6.3.1.2	GS2	AT5G35630	-2.06	-1.05	-8.68	6.76E-05	0.001358	2.15
260289_at	CAD ATPase (AAA1) identical to CAD	ERH3	AT1G80350	-1.68	-0.75	-8.68	6.78E-05	0.001359	2.14
260566_at	cysteine synthase (cpACS1) ;supporte	OASB	AT2G43750	-2.34	-1.23	-8.68	6.78E-05	0.001359	2.14
247333_at	1-aminocyclopropane-1-carboxylic aci	FLS5	AT5G63600	4.61	2.21	8.68	6.78E-05	0.001359	2.14
253791_at	early auxin-inducible protein 11 (IAA11	IAA11	AT4G28640	-2.42	-1.28	-8.68	6.78E-05	0.001359	2.14
261394_at	wall-associated kinase 2, putative sim	---	AT1G79680	35.19	5.14	8.67	6.81E-05	0.001361	2.14
246708_at	putative protein various predicted prot	---	AT5G28150	-2.42	-1.28	-8.67	6.82E-05	0.001361	2.14
250075_at	putative protein	---	AT5G17670	-3.56	-1.83	-8.68	6.81E-05	0.001361	2.14
250656_at	putative protein contains similarity to u	---	AT5G06970	-2.64	-1.40	-8.67	6.82E-05	0.001362	2.13
263287_at	Expressed protein ; supported by full-l	---	AT2G36145	-7.17	-2.84	-8.67	6.83E-05	0.001362	2.13
258158_at	acid phosphatase type 5 identical to G	PAP17	AT3G17790	8.09	3.02	8.66	6.86E-05	0.001363	2.13
266225_at	putative membrane channel protein ;s	ATOEP16-1	AT2G28900	-5.52	-2.47	-8.67	6.84E-05	0.001363	2.13
247550_at	putative protein many predicted protei	---	AT5G61370	1.78	0.83	8.66	6.86E-05	0.001363	2.13
260812_at	nodulin-like protein similar to MtN21 G	---	AT1G43650	-3.14	-1.65	-8.66	6.88E-05	0.001368	2.13
259915_at	unknown protein	---	AT1G72790	-5.52	-2.47	-8.65	6.93E-05	0.001374	2.12
264887_at	unknown protein similar to ripening-in	---	AT1G23120	2.91	1.54	8.65	6.94E-05	0.001374	2.12
248507_at	putative protein strong similarity to unk	---	AT5G50420	-2.34	-1.23	-8.65	6.94E-05	0.001374	2.12
253458_at	putative protein predicted protein, Ara	---	AT4G32070	3.09	1.63	8.65	6.93E-05	0.001374	2.12
264938_at	unknown protein contains similarity to	---	AT1G60610	2.02	1.02	8.65	6.93E-05	0.001374	2.12

246389_at	amino acid carrier, putative similar to a	AAP3	AT1G77380	2.66	1.41	8.65	6.95E-05	0.001374	2.12
262966_at	ER lumen protein retaining receptor, p	---	AT1G75760	-1.97	-0.98	-8.64	6.98E-05	0.001374	2.11
245405_at	hypothetical protein	---	AT4G17150	-1.75	-0.81	-8.64	6.97E-05	0.001374	2.11
261286_at	unknown protein ; supported by cDNA	---	AT1G35780	-2.44	-1.29	-8.64	6.96E-05	0.001374	2.11
254623_at	protein ch-42 precursor, chloroplast ;	CHLI1	AT4G18480	-2.59	-1.37	-8.64	6.98E-05	0.001374	2.11
258086_at	dihydrolipoamide S-acetyltransferase i	LTA2	AT3G25860	-2.28	-1.19	-8.63	7.02E-05	0.001381	2.10
261540_at	unknown protein	---	AT1G63610	-2.16	-1.11	-8.63	7.03E-05	0.001381	2.10
265151_at	hypothetical protein similar to hypothet	---	AT1G51340	2.39	1.26	8.63	7.05E-05	0.001384	2.10
266097_at	unknown protein ; supported by cDNA	SOUL-1	AT2G37970	5.03	2.33	8.63	7.05E-05	0.001384	2.10
263922_s_	putative pyruvate kinase ;supported b	---	AT2G36580 /	1.82	0.86	8.62	7.07E-05	0.001386	2.10
252274_at	branched-chain-amino-acid transamin	BCAT3	AT3G49680	-1.95	-0.97	-8.62	7.07E-05	0.001386	2.10
252317_at	putative protein hypersensitivity-relate	---	AT3G48720	-13.49	-3.75	-8.62	7.08E-05	0.001387	2.09
258719_at	putative pectate lyase simliar to pectat	---	AT3G09540	-4.95	-2.31	-8.62	7.10E-05	0.001389	2.09
254167_at	serine/threonine kinase-like protein s	CIPK8	AT4G24400	2.13	1.09	8.61	7.11E-05	0.00139	2.09
254764_at	putative protein ; supported by cDNA:	---	AT4G13250	4.61	2.21	8.61	7.12E-05	0.00139	2.09
259990_s_	F-box protein FKF1/ADO3, AtFBX2a i	FKF1	AT1G68050 /	2.91	1.54	8.61	7.15E-05	0.001394	2.08
264635_at	unknown protein ;supported by full-len	---	AT1G65500	6.87	2.78	8.61	7.15E-05	0.001394	2.09
255243_at	putative protein hypothetical protein -	---	AT4G05590	1.94	0.96	8.61	7.16E-05	0.001394	2.08
247746_at	uncoupling protein AtUCP2 ;supporte	ATUCP2	AT5G58970	-2.53	-1.34	-8.60	7.18E-05	0.001397	2.08
256746_at	alpha-glucan phosphorylase, putative	---	AT3G29320	-2.77	-1.47	-8.60	7.19E-05	0.001399	2.08
244935_at	NADH dehydrogenase subunit	---	---	-1.90	-0.93	-8.59	7.21E-05	0.001401	2.08
261507_at	RIBOSOMAL PROTEIN, putative simi	---	AT1G71720	-1.93	-0.95	-8.59	7.22E-05	0.001401	2.07
247979_at	pollen specific protein SF21 ;supporte	---	AT5G56750	-2.24	-1.16	-8.59	7.24E-05	0.001402	2.07
258632_s_	putative MAP3K epsilon protein kinas	MAPKKK7	AT3G07980 /	-2.57	-1.36	-8.59	7.26E-05	0.001402	2.07
260936_at	hypothetical protein predicted by gene	---	AT1G45150	2.06	1.04	8.59	7.24E-05	0.001402	2.07
257794_at	hypothetical protein predicted by gens	---	AT3G27050	-2.46	-1.30	-8.59	7.25E-05	0.001402	2.07
251414_at	hypothetical protein	---	AT3G60370	-2.38	-1.25	-8.59	7.23E-05	0.001402	2.07
266575_at	putative chloroplast initiation factor 3 ;	---	AT2G24060	-2.12	-1.09	-8.59	7.25E-05	0.001402	2.07
250649_at	thioredoxin-like ; supported by cDNA:	WCRKC1	AT5G06690	-2.20	-1.14	-8.58	7.27E-05	0.001403	2.07
253738_at	photosystem I subunit PSI-E - like pro	PSAE-1	AT4G28750	-1.69	-0.76	-8.58	7.27E-05	0.001403	2.07
263010_at	T76725 come from this gene.	---	AT1G23330	1.84	0.88	8.58	7.29E-05	0.001404	2.06
249393_at	disease resistance - like protein resist	AtRLP54	AT5G40170	3.99	2.00	8.57	7.33E-05	0.00141	2.06
245138_at	unknown protein predicted by genscan	AFO	AT2G45190	-3.14	-1.65	-8.57	7.33E-05	0.00141	2.06
254234_at	putative major latex protein major late	---	AT4G23680	7.89	2.98	8.56	7.37E-05	0.001415	2.05
246408_at	hypothetical protein predicted by gene	---	AT1G57680	-2.43	-1.28	-8.56	7.38E-05	0.001415	2.05

256134_at	aminoalcoholphosphotransferase iden	AAPT1	AT1G13560	-1.85	-0.89	-8.56	7.37E-05	0.001415	2.05
265660_at	putative disease resistance protein	AtRLP21	AT2G25470	2.73	1.45	8.55	7.43E-05	0.001425	2.04
266509_at	DegP2 protease identical to DegP2 pr	DEGP2	AT2G47940	-2.17	-1.11	-8.55	7.44E-05	0.001425	2.04
248908_at	receptor kinase-like protein	MEE62	AT5G45800	7.39	2.89	8.55	7.45E-05	0.001425	2.04
247618_at	receptor like protein kinase receptor li	---	AT5G60280	2.08	1.06	8.55	7.45E-05	0.001425	2.04
257773_at	hypothetical protein predicted by gene	---	AT3G29185	-2.08	-1.06	-8.55	7.46E-05	0.001425	2.04
265260_at	NAM (no apical meristem)-like protein	anac042	AT2G43000	31.03	4.96	8.55	7.47E-05	0.001425	2.04
259952_at	putative disease resistance protein sim	AtRLP12	AT1G71400	3.60	1.85	8.55	7.47E-05	0.001425	2.04
253478_at	putative protein trichohyalin - human,	---	AT4G32350	-3.18	-1.67	-8.54	7.51E-05	0.001431	2.03
257175_s_	cyclopropane-fatty-acyl-phospholipid s	---	AT3G23470 /	-2.05	-1.04	-8.54	7.52E-05	0.001431	2.03
261398_at	hypothetical protein contains similarity	NHX6	AT1G79610	2.00	1.00	8.54	7.52E-05	0.001431	2.03
260648_at	unknown protein	---	AT1G08050	3.34	1.74	8.53	7.54E-05	0.001431	2.03
265873_at	putative beta-1,3-glucanase ;supporte	---	AT2G01630	-2.26	-1.18	-8.53	7.54E-05	0.001431	2.03
264018_at	putative triosephosphate isomerase ;s	TIM	AT2G21170	-1.95	-0.96	-8.53	7.55E-05	0.001434	2.02
265620_at	unknown protein	---	AT2G27310	8.51	3.09	8.53	7.57E-05	0.001435	2.02
266267_at	putative glutathione S-transferase ; su	ATGSTU4	AT2G29460	28.45	4.83	8.52	7.59E-05	0.001438	2.02
244943_at	NADH dehydrogenase subunit 9	---	ATMG00070	2.51	1.33	8.52	7.63E-05	0.001444	2.01
260222_at	putative alpha galactosyltransferase si	XXT5	AT1G74380	-3.85	-1.95	-8.51	7.66E-05	0.001444	2.01
253022_at	putative protein	---	AT4G38060	3.90	1.96	8.51	7.65E-05	0.001444	2.01
248100_at	beta-1,3-glucanase-like protein ;supp	---	AT5G55180	-7.62	-2.93	-8.51	7.66E-05	0.001444	2.01
245532_at	cytochrome P450 like protein	CYP97B3	AT4G15110	-1.69	-0.76	-8.52	7.64E-05	0.001444	2.01
252984_at	cinnamyl-alcohol dehydrogenase ELI3	ELI3-2	AT4G37990	8.60	3.10	8.51	7.66E-05	0.001444	2.01
256728_at	glutamyl-tRNA amidotransferase subu	---	AT3G25660	-2.63	-1.40	-8.50	7.70E-05	0.00145	2.00
256612_at	hypothetical protein predicted by gene	---	AT3G29280	-2.24	-1.17	-8.50	7.71E-05	0.00145	2.00
259771_at	unknown protein	---	AT1G29470	-2.72	-1.44	-8.50	7.73E-05	0.001453	2.00
250062_at	BCS1 - like protein h-bcs1, Homo sap	---	AT5G17760	3.22	1.69	8.50	7.74E-05	0.001454	2.00
245399_at	membrane channel like protein ;suppo	TIP2;2	AT4G17340	-3.69	-1.88	-8.50	7.75E-05	0.001455	2.00
247982_at	serine O-acetyltransferase (EC 2.3.1.3	ATSERAT1;	AT5G56760	-2.04	-1.03	-8.49	7.78E-05	0.001458	1.99
265073_at	unknown protein similar to putative tyr	---	AT1G55480	-3.62	-1.86	-8.49	7.78E-05	0.001458	1.99
266662_at	hypothetical protein predicted by gens	---	AT2G25830	-2.45	-1.29	-8.49	7.80E-05	0.00146	1.99
245861_at	GTL1 - like protein GTL1, Arabidopsis	---	AT5G28300	-4.23	-2.08	-8.48	7.81E-05	0.001462	1.99
267601_at	hypothetical protein predicted by gene	---	AT2G32980	-2.02	-1.02	-8.48	7.82E-05	0.001462	1.99
252117_at	mucin -like protein hemomucin, Droso	YLS2	AT3G51430	3.06	1.62	8.48	7.83E-05	0.001463	1.99
246622_at	protein phosphatase-2C PP2C-like ; s	---	AT5G36250	-1.76	-0.82	-8.48	7.84E-05	0.001463	1.98
254299_at	hypothetical protein ;supported by full-	NYE1	AT4G22920	3.93	1.98	8.48	7.86E-05	0.001466	1.98

257339_s_	ATP synthase subunit 9	---	AT2G07671	2.90	1.54	8.47	7.90E-05	0.001472	1.98
264893_at	unknown protein similar to unknown pr	---	AT1G23140	2.35	1.23	8.47	7.91E-05	0.001472	1.98
253856_at	hypothetical protein ;supported by full-	---	AT4G28100	-1.76	-0.81	-8.47	7.92E-05	0.001473	1.97
247884_at	lipid transfer protein; glossy1 homolog	CER3	AT5G57800	-6.07	-2.60	-8.46	7.94E-05	0.001476	1.97
248138_at	pyruvate decarboxylase (gb|AAB1685	PDC2	AT5G54960	2.55	1.35	8.45	8.00E-05	0.001479	1.96
263382_at	putative anthranilate N-hydroxycinnam	---	AT2G40230	-2.36	-1.24	-8.45	8.00E-05	0.001479	1.96
258879_at	unknown protein ; supported by full-le	---	AT3G03270	4.14	2.05	8.46	7.97E-05	0.001479	1.97
245939_at	oxoglutarate/malate translocator-like p	---	AT5G19760	-1.98	-0.99	-8.45	7.99E-05	0.001479	1.96
250234_at	transaldolase - like protein transaldola	---	AT5G13420	2.66	1.41	8.46	7.98E-05	0.001479	1.96
266370_at	hypothetical protein predicted by gens	---	AT2G41350	-1.73	-0.79	-8.45	8.01E-05	0.001479	1.96
261206_at	heat shock factor protein hsf8, putativ	---	AT1G12800	-2.30	-1.20	-8.45	8.00E-05	0.001479	1.96
248910_at	serine threonine protein kinase ; suppo	CIPK20	AT5G45820	-3.43	-1.78	-8.46	7.97E-05	0.001479	1.97
257911_at	hypothetical protein contains similarity	GLYR1	AT3G25530	-1.75	-0.81	-8.45	8.01E-05	0.001479	1.96
264266_at	putative protein phosphatase 2C simila	---	AT1G09160	-2.63	-1.39	-8.45	8.02E-05	0.001479	1.96
263706_s_	3-methyladenine DNA glycosylase, pu	---	AT1G31180 /	-3.12	-1.64	-8.45	8.03E-05	0.001479	1.96
260978_at	17.6 kDa heat shock protein (AA 1-15	---	AT1G53540	4.95	2.31	8.45	8.04E-05	0.001479	1.96
251225_at	putative protein glycosyl transferase lg	GATL7	AT3G62660	-2.62	-1.39	-8.45	8.03E-05	0.001479	1.96
248224_at	thylakoid lumenal 17.4 kD protein, chl	---	AT5G53490	-2.63	-1.39	-8.44	8.05E-05	0.001479	1.96
247176_at	acyl-CoA oxidase (gb|AAC13497.1) ;	ACX2	AT5G65110	2.89	1.53	8.44	8.05E-05	0.001479	1.96
260106_at	unknown protein ;supported by full-len	---	AT1G35420	-1.99	-0.99	-8.44	8.10E-05	0.001486	1.95
248975_at	unknown protein ; supported by cDNA	---	AT5G45040	-2.00	-1.00	-8.43	8.11E-05	0.001486	1.95
264340_at	unknown protein similar to hypothetica	---	AT1G70280	-2.20	-1.14	-8.43	8.11E-05	0.001486	1.95
251353_at	putative protein hypothetical protein -	---	AT3G61080	-2.39	-1.25	-8.43	8.13E-05	0.001489	1.94
263870_at	unknown protein	RKP	AT2G22010	2.06	1.04	8.43	8.14E-05	0.00149	1.94
249174_at	putative protein similar to unknown pro	---	AT5G42900	3.48	1.80	8.43	8.16E-05	0.00149	1.94
263502_s_	hypothetical protein	---	AT2G07675	2.96	1.57	8.43	8.15E-05	0.00149	1.94
245209_at	putative protein similarity to predicted	---	AT5G12340	10.84	3.44	8.42	8.20E-05	0.001496	1.94
266636_at	glycine decarboxylase complex H-prot	GDCH	AT2G35370	-2.13	-1.09	-8.42	8.22E-05	0.001499	1.93
264839_at	putative protochlorophyllide reductase	POR C	AT1G03630	-2.64	-1.40	-8.41	8.24E-05	0.0015	1.93
266181_at	putative glutathione S-transferase ; su	ATGSTZ1	AT2G02390	2.27	1.19	8.41	8.28E-05	0.001507	1.93
253039_at	squalene epoxidase - like protein squa	SQE3	AT4G37760	-3.95	-1.98	-8.39	8.38E-05	0.001522	1.91
250471_at	myo-inositol-1-phosphate synthase -li	MIPS3	AT5G10170	-2.90	-1.54	-8.39	8.39E-05	0.001522	1.91
256092_at	Expressed protein ; supported by full-l	HMGB3	AT1G20696	1.70	0.77	8.39	8.38E-05	0.001522	1.91
259038_at	unknown protein predicted by genscan	PTAC13	AT3G09210	-2.00	-1.00	-8.39	8.37E-05	0.001522	1.91
247026_at	protein kinase-like protein	MAPKKK19	AT5G67080	37.90	5.24	8.38	8.42E-05	0.001526	1.91

256327_at	unknown protein ;supported by full-len	GAUT9	AT3G02350	-2.30	-1.20	-8.38	8.46E-05	0.001533	1.90
258393_at	unknown protein similar to unknown pr	---	AT3G15480	-2.97	-1.57	-8.37	8.47E-05	0.001533	1.90
265593_s_	unknown protein ;supported by full-ler	LCV1	AT2G20120 /	-1.82	-0.87	-8.37	8.47E-05	0.001533	1.90
245840_at	hypothetical protein predicted by gene	---	AT1G58420	5.06	2.34	8.37	8.52E-05	0.001539	1.89
263433_at	putative myo-inositol 1-phosphate synt	MIPS2	AT2G22240	-2.81	-1.49	-8.37	8.53E-05	0.001539	1.89
251320_at	3-methyl-2-oxobutanoate hydroxy-me	PANB2	AT3G61530	1.79	0.84	8.37	8.53E-05	0.001539	1.89
248608_at	ATP citrate lyase ; supported by cDNA	ACLB-2	AT5G49460	-2.21	-1.14	-8.36	8.55E-05	0.001542	1.89
250351_at	heat shock protein 17.6A	AT-HSP17.6	AT5G12030	6.50	2.70	8.36	8.56E-05	0.001543	1.89
254417_at	putative protein	ATFMN/FHY	AT4G21470	2.72	1.44	8.36	8.59E-05	0.001546	1.89
264987_at	unknown protein ; supported by cDNA	---	AT1G27030	-4.42	-2.14	-8.35	8.60E-05	0.001547	1.88
261933_at	3-deoxy-D-arabino-heptulosonate 7-p	---	AT1G22410	3.96	1.98	8.35	8.61E-05	0.001548	1.88
263048_s_	unknown protein ;supported by full-ler	---	AT2G05310 /	-2.18	-1.13	-8.35	8.62E-05	0.001549	1.88
254520_at	potassium transporter-like protein puta	---	AT4G19960	2.55	1.35	8.35	8.65E-05	0.001552	1.88
267559_at	putative cytochrome P450	CYP76C2	AT2G45570	19.01	4.25	8.35	8.66E-05	0.001553	1.88
250663_at	putative protein prenylated rab accept	PRA1.B6	AT5G07110	-1.89	-0.92	-8.34	8.67E-05	0.001554	1.88
248659_at	cyclin C-like protein	---	AT5G48640	2.15	1.10	8.34	8.69E-05	0.001556	1.87
250584_at	WD-repeat protein-like	---	AT5G07590	-2.17	-1.12	-8.34	8.71E-05	0.001558	1.87
261651_at	unknown protein similar to unknown pr	SAT32	AT1G27760	3.74	1.90	8.34	8.72E-05	0.001559	1.87
245790_at	glycerol-3-phosphate acyltransferase i	ATS1	AT1G32200	-2.18	-1.12	-8.33	8.75E-05	0.001563	1.86
255817_at	unknown protein ;supported by full-ler	PDLP3	AT2G33330	-3.93	-1.97	-8.33	8.77E-05	0.001563	1.86
262326_at	hypothetical protein similar to putative	---	AT1G64140 /	1.79	0.84	8.33	8.77E-05	0.001563	1.86
266100_at	similar to axi 1 protein from Nicotiana t	---	AT2G37980	3.17	1.66	8.33	8.77E-05	0.001563	1.86
246443_at	hypothetical protein ;supported by full-	---	AT5G17620	-2.11	-1.07	-8.33	8.78E-05	0.001564	1.86
244937_at	NADH dehydrogenase 49KDa protein	---	---	-3.35	-1.74	-8.32	8.79E-05	0.001565	1.86
251796_at	synaptic glycoprotein SC2-like protein	---	AT3G55360	-3.05	-1.61	-8.32	8.83E-05	0.001565	1.86
261413_at	unknown protein ;supported by full-len	PLL5	AT1G07630	5.01	2.33	8.32	8.81E-05	0.001565	1.86
266126_at	putative metalloproteinase ; supported	---	AT2G45040	3.09	1.63	8.32	8.82E-05	0.001565	1.86
259541_at	protein kinase, putative similar to prot	---	AT1G20650	-2.99	-1.58	-8.32	8.82E-05	0.001565	1.86
244992_s_	ribosomal protein S7	---	---	-2.06	-1.04	-8.32	8.84E-05	0.001567	1.85
252997_at	putative pollen allergen pollen allerger	ATEXLA2	AT4G38400	-6.14	-2.62	-8.31	8.89E-05	0.001573	1.85
261526_at	protein kinase identical to protein kinas	APK2A	AT1G14370	3.29	1.72	8.31	8.88E-05	0.001573	1.85
253308_at	putative protein aminotransferase (As	AGD2	AT4G33680	-1.85	-0.89	-8.31	8.90E-05	0.001573	1.85
259751_at	putative transcription factor similar to n	MYBL2	AT1G71030	-1.97	-0.98	-8.31	8.91E-05	0.001574	1.85
265221_s_	putative glutamate decarboxylase ; su	GAD3	AT2G02000 /	11.89	3.57	8.30	8.94E-05	0.001579	1.84
254052_at	UMP/CMP kinase like protein UMP/CI	---	AT4G25280	-2.17	-1.12	-8.30	8.97E-05	0.001579	1.84

265200_s_	putative glucosyl transferase an EST r	UGT73C6	AT2G36790 /	5.76	2.53	8.30	8.97E-05	0.001579	1.84
247073_at	33 kDa polypeptide of oxygen-evolving	PSBO1	AT5G66570	-1.75	-0.81	-8.30	8.97E-05	0.001579	1.84
257132_at	hypothetical protein predicted by gene	---	AT3G20230	-1.90	-0.93	-8.30	8.96E-05	0.001579	1.84
253050_at	putative protein probable arabinogala	AGP18	AT4G37450	-8.56	-3.10	-8.30	8.99E-05	0.001581	1.84
255774_at	unknown protein	---	AT1G18620	-4.37	-2.13	-8.29	9.04E-05	0.001584	1.83
265067_at	hypothetical protein predicted by gene	---	AT1G03850	8.54	3.09	8.29	9.04E-05	0.001584	1.83
254229_at	hypothetical protein ; supported by cD	---	AT4G23610	8.45	3.08	8.29	9.01E-05	0.001584	1.83
250752_at	cytochrome P450 90A1 (sp|Q42569) ;	CPD	AT5G05690	-2.27	-1.18	-8.29	9.02E-05	0.001584	1.83
251207_at	putative protein ;supported by full-leng	---	AT3G63050	3.45	1.79	8.29	9.03E-05	0.001584	1.83
262157_at	unknown protein contains similarity to	---	AT1G52670	-2.04	-1.03	-8.28	9.07E-05	0.001587	1.83
246011_at	putative protein auxin-induced basic h	---	AT5G08330	-3.91	-1.97	-8.28	9.08E-05	0.001587	1.82
248174_at	50S ribosomal protein L24, chloroplas	---	AT5G54600	-1.95	-0.97	-8.28	9.08E-05	0.001587	1.82
258160_at	glutamine synthetase, putative similar	GLN1.3	AT3G17820	3.25	1.70	8.28	9.10E-05	0.001587	1.82
266202_at	putative cinnamoyl-CoA reductase	---	AT2G02400	-1.82	-0.86	-8.28	9.09E-05	0.001587	1.82
246131_at	MOLYBDOPTERIN BIOSYNTHESIS C	B73	AT5G20990	1.76	0.81	8.28	9.12E-05	0.00159	1.82
247177_at	unknown protein ; supported by cDNA	---	AT5G65300	7.92	2.99	8.28	9.12E-05	0.00159	1.82
263548_at	glycine-rich RNA binding protein 7 Alt	CCR2	AT2G21660 /	2.01	1.01	8.27	9.14E-05	0.001591	1.82
245213_at	photosystem II 22kDa protein, putative	NPQ4	AT1G44575	-5.54	-2.47	-8.27	9.18E-05	0.001597	1.81
250041_at	putative protein p53 inducible protein	PIR121	AT5G18410	-1.69	-0.76	-8.26	9.21E-05	0.001602	1.81
260519_at	unknown protein	---	AT1G51540	-1.72	-0.79	-8.26	9.24E-05	0.001605	1.81
253829_at	Medicago nodulin N21-like protein Mtl	---	AT4G28040	9.51	3.25	8.26	9.25E-05	0.001606	1.80
250803_at	putative protein contains similarity to ir	---	AT5G04980	2.86	1.51	8.25	9.29E-05	0.001611	1.80
263497_at	cold-regulated protein cor15a precurso	COR15A	AT2G42540	-37.54	-5.23	-8.25	9.31E-05	0.001613	1.80
258535_at	unknown protein ; supported by cDNA	---	AT3G06750	-3.49	-1.80	-8.24	9.33E-05	0.001616	1.79
251155_at	putative protein outer envelope memb	---	AT3G63160	-1.76	-0.81	-8.25	9.33E-05	0.001616	1.80
267497_at	putative glutaredoxin ;supported by fu	---	AT2G30540	-4.03	-2.01	-8.24	9.37E-05	0.001619	1.79
262850_at	signal response protein (GAI) identical	GAI	AT1G14920	-3.65	-1.87	-8.24	9.37E-05	0.001619	1.79
248634_at	isoleucyl-tRNA synthetase	OVA2	AT5G49030	-2.30	-1.20	-8.24	9.36E-05	0.001619	1.79
247393_at	unknown protein	---	AT5G63130	17.75	4.15	8.24	9.39E-05	0.00162	1.79
264770_at	unknown protein similar to unknown pr	---	AT1G23030	-4.09	-2.03	-8.23	9.43E-05	0.001622	1.78
260704_at	glycine cleavage system H protein pre	---	AT1G32470	-7.07	-2.82	-8.23	9.43E-05	0.001622	1.78
258663_at	hypothetical protein	---	AT3G08670	-1.78	-0.83	-8.23	9.41E-05	0.001622	1.79
246929_at	putative protein ; supported by full-len	---	AT5G25210	-2.42	-1.28	-8.23	9.43E-05	0.001622	1.78
260501_at	unknown protein ; supported by cDNA	---	AT2G41770	-2.50	-1.32	-8.23	9.45E-05	0.001625	1.78
265247_at	50S ribosomal protein L3 ;supported b	---	AT2G43030	-1.82	-0.86	-8.23	9.47E-05	0.001626	1.78

245017_at	PSI I protein	---	---	-2.10	-1.07	-8.22	9.48E-05	0.001628	1.78
255457_at	putative photosystem I reaction cente	PSAD-1	AT4G02770	-1.70	-0.77	-8.22	9.50E-05	0.001629	1.78
246620_at	cytochrome P450 ; supported by cDN	CYP81D1	AT5G36220	3.35	1.75	8.22	9.52E-05	0.001632	1.77
250833_at	myotubularin - like protein myotubular	---	AT5G04540	1.86	0.90	8.22	9.53E-05	0.001633	1.77
245024_at	ATPase alpha subunit	---	---	-1.75	-0.81	-8.21	9.58E-05	0.001639	1.77
261796_at	non-phototropic hypocotyl, putative si	---	AT1G30440	-1.91	-0.93	-8.20	9.64E-05	0.001648	1.76
251087_at	putative protein unknown protein T16	---	AT5G01460	-1.79	-0.84	-8.20	9.68E-05	0.001655	1.75
254332_at	leucine rich repeat receptor kinase-lik	---	AT4G22730	-2.64	-1.40	-8.19	9.71E-05	0.001658	1.75
255651_at	putative protein	---	AT4G00940	1.96	0.97	8.19	9.72E-05	0.001658	1.75
261017_at	UDP-glucose dehydrogenase, putativ	UGD1	AT1G26570	-2.10	-1.07	-8.18	9.80E-05	0.001669	1.74
266268_at	unknown protein predicted by genefinc	---	AT2G29510	-1.80	-0.85	-8.18	9.80E-05	0.001669	1.74
265024_at	Expressed protein ; supported by full-l	---	AT1G24600	4.01	2.00	8.18	9.80E-05	0.001669	1.74
253423_at	Expressed protein ; supported by cDN	IAA29	AT4G32280	-25.89	-4.69	-8.17	9.84E-05	0.001671	1.74
258988_at	unknown protein similar to unknown pr	---	AT3G08890	-1.97	-0.98	-8.18	9.83E-05	0.001671	1.74
259012_at	hypothetical protein similar to hypothet	PUB9	AT3G07360	-2.39	-1.26	-8.17	9.84E-05	0.001671	1.74
255436_at	Expressed protein ; supported by cDN	---	AT4G03150	-1.66	-0.73	-8.18	9.83E-05	0.001671	1.74
251803_at	putative protein predicted proteins, Ar	---	AT3G55350	-2.33	-1.22	-8.17	9.86E-05	0.001672	1.74
257634_s_	cytochrome P450, putative similar to c	CYP71B19	AT3G26170 /	3.74	1.90	8.17	9.87E-05	0.001673	1.73
253550_at	putative protein kinase serine/threonir	SIP3	AT4G30960	3.18	1.67	8.17	9.89E-05	0.001675	1.73
246487_at	putative protein with poly glutamic aci	---	AT5G16030	-3.54	-1.82	-8.16	9.95E-05	0.001683	1.73
266017_at	unknown protein ; supported by cDNA	---	AT2G18690	6.30	2.66	8.16	9.95E-05	0.001683	1.73
245325_at	xyloglucan endotransglycosylase-relat	XTR7	AT4G14130	-22.98	-4.52	-8.16	9.98E-05	0.001686	1.72
256275_at	actin 11 (ACT11) identical to actin 11 (	ACT11	AT3G12110	-2.67	-1.42	-8.16	9.98E-05	0.001686	1.72
253875_at	putative protein ENOD20 gene, Medic	---	AT4G27520	-3.72	-1.90	-8.15	0.0001	0.001689	1.72
254016_at	putative transcription factor Arabidops	CGA1	AT4G26150	-3.32	-1.73	-8.15	0.0001	0.001691	1.72
266950_at	expressed protein supported by full-ler	---	AT2G18910	-2.72	-1.44	-8.15	0.0001	0.001693	1.71
255249_at	3(2),5-BISPHOSPHATE NUCLEOTID	---	AT4G05090	-2.92	-1.54	-8.14	0.000101	0.001695	1.71
248713_at	putative protein contains similarity to ja	NSP5	AT5G48180	4.26	2.09	8.14	0.000101	0.001696	1.71
258919_at	Expressed protein ; supported by full-l	---	AT3G10525	-2.33	-1.22	-8.14	0.000101	0.001699	1.71
247126_at	protein phosphatase 2C-like protein	---	AT5G66080	-2.72	-1.44	-8.14	0.000101	0.001701	1.71
251037_at	putative protein oxysterol-binding prot	UNE18	AT5G02100	2.75	1.46	8.14	0.000101	0.001701	1.70
253722_at	putative protein zinc finger transcriptic	---	AT4G29190	-2.19	-1.13	-8.14	0.000101	0.001701	1.71
256055_at	mitochondrial carrier protein, putative	---	AT1G07030	1.82	0.87	8.13	0.000102	0.001701	1.70
263472_at	molybdopterin synthase (CNX2) ;supp	CNX2	AT2G31955	2.26	1.18	8.13	0.000102	0.001701	1.70
262868_at	unknown protein	---	AT1G64980	-2.79	-1.48	-8.13	0.000102	0.001709	1.70

246977_at	putative protein CONSTANS-like prote	COL4	AT5G24930	-1.74	-0.80	-8.12	0.000103	0.001717	1.69
260852_at	transmembrane protein, putative simil	---	AT1G21900	1.76	0.81	8.12	0.000103	0.001717	1.69
264728_at	unknown protein location of EST gb|T4	---	AT1G22850	-2.15	-1.10	-8.12	0.000103	0.001717	1.69
258989_at	rhodanese-like family protein contains	---	AT3G08920	-2.10	-1.07	-8.12	0.000103	0.001717	1.69
265450_at	hypothetical protein predicted by gene	---	AT2G46620	2.87	1.52	8.11	0.000103	0.001719	1.69
266368_at	putative embryo-abundant protein	---	AT2G41380	39.12	5.29	8.11	0.000103	0.001719	1.69
264321_at	unknown protein Contains similarity to	---	AT1G04200	-2.44	-1.29	-8.11	0.000103	0.00172	1.68
263962_at	putative protein kinase contains a prot	---	AT2G36350	-2.55	-1.35	-8.11	0.000104	0.001722	1.68
259596_at	auxin-regulated GH3 protein, putative	GH3.17	AT1G28130	4.32	2.11	8.10	0.000104	0.001726	1.68
250462_at	receptor protein kinase -like(fragment	---	AT5G10020	-1.65	-0.72	-8.10	0.000104	0.001728	1.68
255283_at	putative symbiosis-related protein ;su	ATG8B	AT4G04620	2.66	1.41	8.10	0.000104	0.001731	1.67
254597_at	hypothetical protein	---	AT4G18980	2.63	1.40	8.10	0.000104	0.001731	1.67
266327_at	homeodomain transcription factor (AT	ATHB-7	AT2G46680	3.93	1.97	8.09	0.000105	0.001735	1.67
259163_at	putative protein kinase similar to ATM	---	AT3G01490	-2.29	-1.19	-8.09	0.000105	0.001735	1.67
253855_at	senescence-associated protein -like s	TET7	AT4G28050	-5.64	-2.50	-8.09	0.000105	0.001736	1.67
246517_at	ribosomal protein 3 precursor-like prot	---	AT5G15760	-2.13	-1.09	-8.09	0.000105	0.001739	1.67
265817_at	histone H1 ;supported by full-length cl	HIS1-3	AT2G18050	5.72	2.52	8.09	0.000105	0.001739	1.66
248378_at	unknown protein ;supported by full-ler	---	AT5G51840	-1.80	-0.85	-8.09	0.000105	0.001739	1.66
260276_at	unknown protein	---	AT1G80450	4.68	2.23	8.08	0.000105	0.001739	1.66
249234_at	putative protein similar to unknown pro	---	AT5G42200	-3.28	-1.72	-8.08	0.000106	0.001741	1.66
246518_at	acetyltransferase-like protein Glucosa	AtGNA1	AT5G15770	-1.85	-0.89	-8.08	0.000106	0.001741	1.66
254271_at	serine/threonine kinase - like protein k	---	AT4G23150	4.33	2.11	8.08	0.000106	0.001741	1.66
257239_at	unknown protein	---	AT3G24100	1.96	0.97	8.08	0.000106	0.001745	1.66
253876_at	COP1-interacting protein 7 (CIP7) ; su	CIP7	AT4G27430	-2.80	-1.49	-8.08	0.000106	0.001745	1.66
251899_at	nucleoid DNA-binding - like protein nu	---	AT3G54400	-22.85	-4.51	-8.07	0.000107	0.00175	1.65
253608_at	xyloglucan endo-1,4-beta-D-glucanas	XTH19	AT4G30290	-8.38	-3.07	-8.07	0.000107	0.00175	1.65
253391_at	hypothetical protein ; supported by cD	---	AT4G32590	-2.65	-1.41	-8.07	0.000107	0.001754	1.65
245483_at	cysteine proteinase contains similarity	---	AT4G16190	1.76	0.82	8.06	0.000107	0.001755	1.65
254241_at	serine/threonine kinase - like protein s	CRK11	AT4G23190	9.56	3.26	8.06	0.000108	0.001762	1.64
255340_at	putative receptor-like protein kinase	---	AT4G04490	10.65	3.41	8.05	0.000108	0.001767	1.64
257204_at	Expressed protein ; supported by full-l	RALFL24	AT3G23805	-5.50	-2.46	-8.05	0.000108	0.001768	1.63
262188_at	Avr9 elicitor response protein, putative	---	AT1G77810	2.10	1.07	8.05	0.000108	0.001768	1.64
252562_s_	Histone H4 - like protein histone H4, Z	---	AT3G45930 /	-1.94	-0.95	-8.05	0.000108	0.001768	1.63
248252_at	putative protein similar to unknown pro	AGP22	AT5G53250	-6.43	-2.69	-8.05	0.000109	0.001771	1.63
261356_at	predicted protein	---	AT1G79660	-2.55	-1.35	-8.05	0.000109	0.001771	1.63

259800_at	Expressed protein ; supported by full-l	---	AT1G72175	-2.19	-1.13	-8.04	0.000109	0.001773	1.63
247628_at	putative protein	---	AT5G60400	-2.43	-1.28	-8.04	0.000109	0.001773	1.63
257506_at	auxin-induced protein, putative similar	---	AT1G29440	-10.39	-3.38	-8.03	0.00011	0.001786	1.62
248340_at	putative protein similar to unknown pro	---	AT5G52180	-1.88	-0.91	-8.03	0.00011	0.001786	1.62
266533_s_	putative plasma membrane intrinsic pr	PIP2;8	AT2G16850 /	-2.53	-1.34	-8.03	0.00011	0.001787	1.62
253255_at	putative auxin-regulated protein auxin	---	AT4G34760	-12.41	-3.63	-8.03	0.00011	0.001787	1.62
245701_at	ferredoxin-dependent glutamate synth	GLU1	AT5G04140	-2.55	-1.35	-8.02	0.00011	0.001792	1.61
251895_at	class IV chitinase (CHIV)	ATEP3	AT3G54420	5.60	2.49	8.02	0.000111	0.001796	1.61
253044_at	hypothetical protein ;supported by full-	---	AT4G37290	45.75	5.52	8.02	0.000111	0.001797	1.61
260933_at	hypothetical protein contains non-cons	---	AT1G02470	11.30	3.50	8.01	0.000112	0.001811	1.60
259979_at	unknown protein ;supported by full-ler	---	AT1G76600	4.21	2.07	8.01	0.000112	0.001811	1.60
249177_at	unknown protein ;supported by full-ler	---	AT5G42850	1.85	0.89	8.01	0.000112	0.001811	1.60
250058_at	plastid-specific ribosomal protein 6 pr	PSRP6	AT5G17870	-2.23	-1.16	-8.01	0.000112	0.001811	1.60
249964_at	MAP kinase -like protein ATMPK9, Ar	MPK16	AT5G19010	-1.86	-0.90	-8.00	0.000113	0.001819	1.59
266495_at	cycloartenol synthase identical to SP:P	CAS1	AT2G07050	-2.03	-1.02	-8.00	0.000113	0.00182	1.59
246861_at	putative protein phytochrome-associa	IAA28	AT5G25890	1.93	0.95	7.99	0.000113	0.001821	1.59
258607_at	thioredoxin f1 identical to thioredoxin f	TRXF1	AT3G02730	-2.28	-1.19	-7.99	0.000113	0.001821	1.59
261189_at	hypothetical protein contains similarity	NACA5	AT1G33040	-1.95	-0.96	-7.99	0.000113	0.001821	1.59
247747_at	putative protein predicted proteins, Ar	---	AT5G59000	-2.37	-1.24	-7.99	0.000113	0.001823	1.58
261480_at	phytochrome kinase substrate 1, puta	PKS2	AT1G14280	-10.65	-3.41	-7.99	0.000113	0.001823	1.58
248687_at	ADPG pyrophosphorylase small subur	ADG1	AT5G48300	-3.67	-1.87	-7.98	0.000114	0.00183	1.58
255969_at	Expressed protein ; supported by full-l	---	AT1G22330	-3.64	-1.86	-7.98	0.000114	0.001833	1.58
264717_at	hypothetical protein predicted by gene	ATFH8	AT1G70140	3.64	1.86	7.98	0.000114	0.001833	1.58
246449_at	hypothetical protein	---	AT5G16810	-2.00	-1.00	-7.98	0.000114	0.001836	1.57
258046_at	MAP kinase kinase 5 identical to GB:B	MKK5	AT3G21220	1.91	0.93	7.98	0.000115	0.001836	1.57
256205_at	hypothetical protein	---	AT1G50890	-1.83	-0.88	-7.97	0.000115	0.001841	1.57
246099_at	blue copper binding protein ;supporte	ATBCB	AT5G20230	3.25	1.70	7.97	0.000115	0.001843	1.57
259773_at	auxin-induced protein, putative similar	---	AT1G29500	-9.89	-3.31	-7.96	0.000116	0.001854	1.56
247400_at	putative protein ;supported by full-leng	---	AT5G62840	-2.43	-1.28	-7.96	0.000116	0.001856	1.56
262823_at	ATP-dependent Clp protease proteolyt	CLPP6	AT1G11750	-1.85	-0.88	-7.96	0.000116	0.001856	1.56
259701_at	unknown protein similar to GB:AAC28	---	AT1G77770	2.22	1.15	7.96	0.000116	0.001856	1.56
264107_s_	putative receptor-like protein kinase	SERK5	AT2G13790 /	2.01	1.00	7.95	0.000117	0.001862	1.55
262935_at	hypothetical protein similar to putative	AtOCT5	AT1G79410	6.21	2.63	7.95	0.000117	0.001865	1.55
247788_at	putative protein carbohydrate kinase,	---	AT5G58730	2.81	1.49	7.94	0.000118	0.001875	1.54
256883_at	unknown protein ; supported by cDNA	---	AT3G26440	6.92	2.79	7.93	0.000118	0.001885	1.54

245385_at	hypothetical protein ;supported by full-	---	AT4G14020	2.55	1.35	7.93	0.000118	0.001885	1.54
250885_at	ABC transporter -like protein ABC-typ	ATH12	AT5G03910	-1.80	-0.85	-7.93	0.000119	0.001887	1.53
258708_at	putative oxidoreductase similar to phyt	---	AT3G09580	-2.70	-1.43	-7.93	0.000119	0.00189	1.53
265670_s_	unknown protein ;supported by full-ler	---	AT2G32190 /	7.20	2.85	7.93	0.000119	0.00189	1.53
265059_at	unknown protein ; supported by cDNA	AR791	AT1G52080	2.37	1.24	7.92	0.000119	0.001891	1.53
250657_at	steroid sulfotransferase-like protein	ST2B	AT5G07000	-3.83	-1.94	-7.92	0.00012	0.001896	1.52
245525_at	dynein light chain like protein	---	AT4G15930	-1.63	-0.71	-7.92	0.00012	0.001896	1.52
258334_at	hypothetical protein predicted by gens	---	AT3G16010	-1.90	-0.93	-7.92	0.00012	0.001898	1.52
261638_at	Expressed protein ; supported by full-l	---	AT1G49975	-3.58	-1.84	-7.91	0.00012	0.0019	1.52
257763_s_	disease resistance protein, putative si	AtRLP37	AT3G23110 /	6.72	2.75	7.91	0.00012	0.001904	1.52
257299_at	unknown protein ;supported by full-ler	---	AT3G28050	2.03	1.02	7.91	0.000121	0.001909	1.51
247816_at	similar to unknown protein (pir||S7558	---	AT5G58260	-4.20	-2.07	-7.90	0.000121	0.001914	1.51
246124_at	putative protein acyl-protein thioestera	---	AT5G20060	-1.62	-0.70	-7.90	0.000121	0.001914	1.51
250423_s_	cytochrome P450 - like protein cytoch	CYP81K2	AT5G10600 /	1.75	0.81	7.90	0.000121	0.001914	1.51
251661_at	putative protein NODULIN-26 - Glycin	SIP2;1	AT3G56950	2.32	1.21	7.90	0.000122	0.001915	1.51
254210_at	putative protein zinc finger protein, Ar	---	AT4G23450	3.50	1.81	7.90	0.000122	0.001915	1.50
262379_at	hypothetical protein predicted by gens	---	AT1G73020	-1.76	-0.81	-7.90	0.000122	0.001915	1.50
259794_at	unknown protein	---	AT1G64330	-2.01	-1.01	-7.90	0.000122	0.001915	1.51
246420_at	putative protein various predicted prote	---	AT5G16870	-2.15	-1.10	-7.90	0.000122	0.001915	1.50
259085_at	unknown protein similar to GB:CAB05	---	AT3G05000	-1.89	-0.92	-7.89	0.000123	0.001928	1.50
257670_at	unknown protein	---	AT3G20340	4.23	2.08	7.89	0.000123	0.001928	1.50
258836_at	hypothetical protein predicted using ge	---	AT3G07210	-2.46	-1.30	-7.88	0.000123	0.001934	1.49
249494_at	acyltransferase - like protein Anthocya	---	AT5G39050	4.58	2.20	7.88	0.000123	0.001935	1.49
252945_at	putative protein ;supported by full-leng	---	AT4G39140	2.05	1.03	7.87	0.000124	0.001938	1.49
256583_at	hypothetical protein	---	AT3G28850	4.39	2.14	7.87	0.000124	0.001938	1.49
264799_at	putative violaxanthin de-epoxidase pre	NPQ1	AT1G08550	-2.13	-1.09	-7.87	0.000124	0.001938	1.48
247450_at	ripening-related protein - like ripening-	---	AT5G62350	-2.23	-1.16	-7.87	0.000124	0.001938	1.48
259287_at	putative rac GTPase activating protein	---	AT3G11490	-2.12	-1.08	-7.87	0.000124	0.001938	1.48
261674_at	unknown protein	---	AT1G18270	3.07	1.62	7.87	0.000124	0.001938	1.49
259741_at	unknown protein	---	AT1G71020	-2.41	-1.27	-7.87	0.000125	0.001939	1.48
247162_at	xyloglucan endo-transglycosylase-like	---	AT5G65730	-5.82	-2.54	-7.87	0.000124	0.001939	1.48
262632_at	23 kDa polypeptide of oxygen-evolving	PSBP-1	AT1G06680	-1.86	-0.89	-7.87	0.000125	0.001939	1.48
255714_at	contains weak similarity to S. cerevisia	---	AT4G00300	-2.03	-1.02	-7.86	0.000125	0.001946	1.47
260153_at	putative lipase similar to monoglyceric	---	AT1G52760	3.46	1.79	7.86	0.000125	0.001946	1.47
264513_at	putative glucose-6-phosphate dehydr	G6PD4	AT1G09420	1.88	0.91	7.86	0.000125	0.001946	1.47

262455_at	Mlo protein, putative similar to Mlo pro	MLO2	AT1G11310	2.42	1.28	7.86	0.000125	0.001946	1.47
264361_at	unknown protein Strong similarity to T	---	AT1G03300	-1.91	-0.93	-7.86	0.000125	0.001946	1.47
252214_at	putative protein EREBP-3 homolog, S	CEJ1	AT3G50260	4.72	2.24	7.85	0.000126	0.001951	1.47
248330_at	putative protein contains similarity to o	---	AT5G52810	3.43	1.78	7.85	0.000126	0.001951	1.47
263785_at	unknown protein ; supported by cDNA	---	AT2G46390	1.93	0.95	7.85	0.000126	0.001958	1.46
252178_at	putative protein various predicted prote	---	AT3G50750	-4.52	-2.18	-7.85	0.000127	0.001959	1.46
246584_at	putative protein predicted protein, Ara	---	AT5G14730	9.71	3.28	7.85	0.000127	0.00196	1.46
250384_at	putative protein various predicted prot	---	AT5G11500	1.80	0.85	7.84	0.000127	0.001964	1.46
250054_at	potassium-dependent sodium-calcium	CAX7	AT5G17860	5.35	2.42	7.84	0.000127	0.001966	1.46
248422_at	putative protein strong similarity to unk	YLS7	AT5G51640	1.62	0.70	7.84	0.000127	0.001966	1.46
260405_at	putative glutathione transferase simila	ATGSTU11	AT1G69930	52.72	5.72	7.84	0.000128	0.001971	1.45
257516_at	unknown protein	ACR4	AT1G69040	-2.71	-1.44	-7.83	0.000128	0.001973	1.45
245743_at	hypothetical protein contains similarity	---	AT1G51080	-2.44	-1.29	-7.83	0.000129	0.001983	1.44
260718_at	unknown protein	ECT7	AT1G48110	1.61	0.69	7.83	0.000129	0.001983	1.44
253590_at	putative protein various predicted prote	HHP2	AT4G30850	-2.37	-1.25	-7.82	0.000129	0.001983	1.44
264910_at	resistance protein, putative similar to r	---	AT1G61100	-3.75	-1.91	-7.82	0.000129	0.001987	1.44
266516_at	putative glutaredoxin ;supported by fu	---	AT2G47880	-4.65	-2.22	-7.82	0.000129	0.001987	1.44
256489_at	unknown protein	---	AT1G31550	-1.65	-0.72	-7.82	0.000129	0.001987	1.44
263880_at	unknown protein ;supported by full-ler	---	AT2G21960	-2.40	-1.27	-7.82	0.00013	0.00199	1.44
258025_at	putative D-3-phosphoglycerate dehydr	---	AT3G19480	-2.91	-1.54	-7.81	0.00013	0.001996	1.43
249071_at	putative protein similar to unknown pro	---	AT5G44050	-4.76	-2.25	-7.81	0.000131	0.001997	1.43
261250_at	unknown protein	---	AT1G05890	1.81	0.86	7.81	0.000131	0.001997	1.43
261306_at	regulatory protein HAL3B similar to GE	---	AT1G48610	-1.88	-0.91	-7.81	0.000131	0.001997	1.43
251823_at	putative protein	---	AT3G55080	-1.69	-0.75	-7.81	0.00013	0.001997	1.43
249929_at	unknown protein	---	AT5G22340	-2.12	-1.09	-7.81	0.000131	0.001997	1.43
247541_at	structural protein - like glycine-rich cel	---	AT5G61660	-2.07	-1.05	-7.81	0.000131	0.001998	1.43
263598_at	putative xyloglucan-specific glucanase	EXGT-A3	AT2G01850	-1.96	-0.97	-7.80	0.000131	0.002001	1.42
250490_at	pectin methylesterase - like protein pe	---	AT5G09760	-4.03	-2.01	-7.80	0.000132	0.002009	1.42
265034_at	unknown protein ;supported by full-len	---	AT1G61660	2.01	1.01	7.80	0.000132	0.002009	1.42
252737_at	putative protein KIAA0274 protein, Ho	---	AT3G43220	-1.77	-0.82	-7.79	0.000132	0.00201	1.42
258368_at	subtilisin-like serine protease contains	---	AT3G14240	-3.96	-1.99	-7.79	0.000133	0.002014	1.41
259942_at	unknown protein	ATWHY2	AT1G71260	1.61	0.69	7.79	0.000132	0.002014	1.41
259603_at	Expressed protein ; supported by full-l	---	AT1G56500	-2.60	-1.38	-7.79	0.000132	0.002014	1.41
255435_at	putative component of cytochrome B6-	PETC	AT4G03280	-1.93	-0.95	-7.79	0.000133	0.002014	1.41
256784_at	hypothetical protein predicted by gene	---	AT3G13674	-1.75	-0.81	-7.79	0.000133	0.002014	1.41

250137_at	rRNA methylase - like protein rRNA m	---	AT5G15390	-1.88	-0.91	-7.79	0.000133	0.002014	1.41
250057_at	putative protein ; supported by full-len	---	AT5G17840	-1.70	-0.77	-7.79	0.000133	0.002014	1.41
251970_at	glucosyltransferase - like protein gluc	UGT73D1	AT3G53150	2.96	1.56	7.79	0.000133	0.002014	1.41
261049_at	hypothetical protein similar to hypothet	---	AT1G01430	-2.64	-1.40	-7.78	0.000133	0.002016	1.41
259841_at	unknown protein ; supported by full-ler	---	AT1G52200	2.29	1.19	7.78	0.000134	0.002025	1.40
260266_at	putative B-box zinc finger protein conta	---	AT1G68520	-2.37	-1.25	-7.77	0.000134	0.002028	1.40
258475_at	putative tyrosyl-tRNA synthetase simil	emb2768	AT3G02660	-1.76	-0.82	-7.77	0.000134	0.002028	1.40
260243_at	hypothetical protein similar to putative	---	AT1G63720	4.79	2.26	7.76	0.000135	0.002041	1.39
247434_at	Expressed protein ; supported by full-l	---	AT5G62575	1.73	0.79	7.76	0.000135	0.002041	1.39
247401_at	1-deoxy-D-xylulose 5-phosphate reduc	DXR	AT5G62790	-2.59	-1.37	-7.76	0.000135	0.002041	1.39
264271_at	beta-glucosidase, putative similar to b	BGLU6	AT1G60270	-3.05	-1.61	-7.75	0.000137	0.002064	1.38
266290_at	putative glutathione S-transferase ;su	ATGSTU1	AT2G29490	29.33	4.87	7.74	0.000137	0.002065	1.37
257900_at	hypothetical protein predicted by gene	---	AT3G28420	-1.73	-0.79	-7.74	0.000137	0.002065	1.37
245093_at	hypothetical protein predicted by gens	---	AT2G40815 /	-1.87	-0.91	-7.74	0.000137	0.002065	1.37
249045_at	berberine bridge enzyme-like protein	---	AT5G44380	8.57	3.10	7.74	0.000138	0.002067	1.37
255290_at	coded for by A. thaliana cDNA AA041	ATPC1	AT4G04640	-1.60	-0.68	-7.74	0.000138	0.002071	1.37
249493_at	acyltransferase -like protein Anthocya	---	AT5G39080	-2.75	-1.46	-7.73	0.000138	0.002076	1.37
255878_at	putative bZIP transcription factor conta	---	AT2G40620	-2.55	-1.35	-7.73	0.000139	0.00208	1.36
262518_at	putative glutathione transferase One o	ATGSTU24	AT1G17170	130.90	7.03	7.73	0.000139	0.002085	1.36
258085_at	unknown protein ; supported by cDNA	---	AT3G26100	2.04	1.03	7.72	0.00014	0.00209	1.36
247845_at	beta-1,3 glucanase - like protein beta-	---	AT5G58090	-1.81	-0.86	-7.72	0.00014	0.002092	1.35
253835_at	putative beta-glucosidase beta-glucos	BGLU9	AT4G27820	2.01	1.01	7.72	0.00014	0.002093	1.35
258128_at	chloroplast thylakoidal processing pep	PLSP1	AT3G24590	-2.15	-1.10	-7.72	0.00014	0.002093	1.35
264078_at	putative beta-galactosidase	BGAL8	AT2G28470	-8.17	-3.03	-7.71	0.000141	0.002096	1.35
245632_at	unknown protein contains similarity to	ATRBL10	AT1G25290	-1.87	-0.91	-7.71	0.000141	0.002096	1.35
245368_at	hypothetical protein ; supported by full-	---	AT4G15510	-2.79	-1.48	-7.72	0.00014	0.002096	1.35
250428_at	putative protein phosphatase protein t	PAS2	AT5G10480	-3.06	-1.61	-7.72	0.000141	0.002096	1.35
254669_at	HhoA protease precursor, putative ide	DEG5	AT4G18370	-2.33	-1.22	-7.71	0.000141	0.002096	1.35
247673_at	tRNA intron endonuclease - like prote	SEN2	AT5G60230	-1.63	-0.71	-7.71	0.000141	0.002096	1.35
246701_at	cysteine synthase ;supported by full-le	CYSD2	AT5G28020	-2.07	-1.05	-7.72	0.00014	0.002096	1.35
258432_at	unknown protein ;supported by full-ler	RALFL23	AT3G16570	-2.83	-1.50	-7.71	0.000141	0.002097	1.35
265214_at	unkown protein ESTs gb|H36249, gb|	---	AT1G05000	4.23	2.08	7.71	0.000142	0.002098	1.34
245662_at	hypothetical protein predicted by gene	---	AT1G28190	10.37	3.38	7.71	0.000141	0.002098	1.34
267081_at	putative phosphatidylinositol-4-phosph	PIP5K5	AT2G41210	1.82	0.87	7.71	0.000142	0.002098	1.34
261457_at	Expressed protein ; supported by full-l	---	AT1G21065 /	-1.94	-0.95	-7.71	0.000142	0.002098	1.34

247862_at	similar to unknown protein (sp|P72777	---	AT5G58250	-1.85	-0.89	-7.71	0.000141	0.002098	1.34
251191_at	putative protein putative protein F15G	---	AT3G62590	3.38	1.76	7.70	0.000142	0.002102	1.34
248311_at	beta-carotene hydroxylase	BETA-OHAS	AT5G52570	-2.88	-1.53	-7.70	0.000142	0.002102	1.34
251479_at	serine/threonine-specific kinase lecRK	ATHLECRK	AT3G59700	5.19	2.38	7.70	0.000143	0.002109	1.33
261713_at	protein kinase, putative identical to bH	MYC2	AT1G32640	2.80	1.49	7.69	0.000143	0.002116	1.33
261334_at	unknown protein	---	AT1G44960	1.89	0.92	7.69	0.000144	0.00212	1.33
245349_at	cyanohydrin lyase like protein ;support	MES16	AT4G16690	4.03	2.01	7.68	0.000144	0.002125	1.32
252300_at	pyruvate kinase -like protein various py	---	AT3G49160	3.16	1.66	7.68	0.000144	0.002125	1.32
250818_at	Expressed protein ; supported by cDN	ALA1	AT5G04930	2.34	1.22	7.68	0.000144	0.002125	1.32
255982_at	hypothetical protein contains similarity	OHP2	AT1G34000	-1.77	-0.83	-7.68	0.000144	0.002125	1.32
247316_at	ankyrin-like protein	---	AT5G64030	-1.78	-0.83	-7.68	0.000144	0.002125	1.32
259131_at	unknown protein similar to hypothetica	SP1L3	AT3G02180	-1.80	-0.85	-7.68	0.000144	0.002126	1.32
257647_at	Expressed protein ; supported by cDN	---	AT3G25805	-3.03	-1.60	-7.68	0.000145	0.002128	1.32
262733_s_	lipase identical to lipase GB:AAA9326	---	AT1G28660 /	2.04	1.03	7.67	0.000145	0.002132	1.31
256033_at	UDP-glucose glucosyltransferase, put	UGT71C4	AT1G07250	-1.81	-0.85	-7.67	0.000145	0.002132	1.31
256060_at	hypothetical protein contains similarity	---	AT1G07050	2.63	1.39	7.67	0.000145	0.002132	1.31
252001_at	plastid division protein FtsZ-like FtsZ	FTSZ2-2	AT3G52750	-3.26	-1.70	-7.67	0.000145	0.002132	1.31
261696_at	unknown protein similar to hypothetica	---	AT1G08470	-2.57	-1.36	-7.67	0.000145	0.002132	1.31
265583_at	unknown protein	---	AT2G20010	1.66	0.73	7.67	0.000146	0.002132	1.31
250158_at	putative protein	---	AT5G15190	2.93	1.55	7.67	0.000146	0.002136	1.31
260930_at	GTP-binding protein Sar1, putative sir	---	AT1G02620	-3.43	-1.78	-7.66	0.000147	0.002148	1.30
250724_at	harpin-induced protein-like	---	AT5G06330	2.77	1.47	7.66	0.000147	0.002148	1.30
246197_at	caltractin-like protein ;supported by full	CEN2	AT4G37010	7.34	2.88	7.66	0.000147	0.002151	1.30
262263_at	auxin transport protein REH1, putative	PIN3	AT1G70940	-6.02	-2.59	-7.65	0.000147	0.002153	1.30
264400_at	glucose-6-phosphate/phosphate-trans	GPT2	AT1G61800	36.38	5.18	7.65	0.000148	0.002154	1.30
259437_at	protein serine/threonine kinase, putati	---	AT1G01540	-3.30	-1.72	-7.65	0.000148	0.002164	1.29
262962_at	NADP-isocitrate dehydrogenase, puta	ICDH	AT1G54340	1.60	0.68	7.64	0.000149	0.002166	1.29
254298_at	putative protein ;supported by full-leng	PGR5-LIKE	AT4G22890	-2.23	-1.16	-7.64	0.000149	0.002172	1.28
266892_at	putative glycine dehydrogenase	AtGLDP2	AT2G26080	-2.20	-1.14	-7.64	0.000149	0.002174	1.28
262902_x_	hypothetical protein similar to putative	---	AT1G59930	-2.74	-1.45	-7.64	0.00015	0.002178	1.28
260239_at	putative receptor protein kinase simila	---	AT1G74360	16.98	4.09	7.63	0.00015	0.002178	1.28
263136_at	trehalose-6-phosphate synthase, puta	ATTPS1	AT1G78580	-1.87	-0.90	-7.63	0.00015	0.002178	1.28
245275_at	beta-amylase ; supported by cDNA: gi	BAM5	AT4G15210	-4.43	-2.15	-7.63	0.00015	0.002182	1.28
253122_at	hypothetical protein	---	AT4G35987	-1.91	-0.93	-7.63	0.000151	0.002185	1.27
262721_at	thioredoxin, putative similar to thiored	Aty2	AT1G43560	-2.09	-1.06	-7.62	0.000152	0.002199	1.27

246097_at	putative protein CGI-45 protein - Hom	HHP1	AT5G20270	-4.85	-2.28	-7.61	0.000152	0.002207	1.26
258351_at	hypothetical protein contains similarity	CNBT1	AT3G17700	2.59	1.38	7.61	0.000152	0.002207	1.26
260982_at	chalcone isomerase, putative similar t	---	AT1G53520	-7.09	-2.83	-7.61	0.000153	0.002213	1.26
251013_at	putative protein various predicted prot	---	AT5G02540	-34.74	-5.12	-7.61	0.000153	0.002217	1.25
254502_at	hypothetical protein	PTAC14	AT4G20130	-2.07	-1.05	-7.61	0.000153	0.002217	1.25
265773_at	unknown protein ; supported by cDNA	RPH1	AT2G48070	-1.93	-0.95	-7.60	0.000154	0.002217	1.25
261669_at	unknown protein similar to hypothetica	---	AT1G18490	-1.59	-0.66	-7.60	0.000154	0.002217	1.25
254905_at	RPP1-WsA-like disease resistance pr	---	AT4G11170	7.59	2.92	7.60	0.000154	0.002218	1.25
251017_at	protein phosphatase - like protein prot	---	AT5G02760	-37.33	-5.22	-7.59	0.000155	0.002231	1.24
266018_at	putative preprotein translocase SECY	SCY1	AT2G18710	-1.70	-0.76	-7.59	0.000155	0.00224	1.24
265584_at	unknown protein	PIL5	AT2G20180	-1.70	-0.76	-7.59	0.000156	0.002242	1.24
260924_at	hypothetical protein similar to Pto kina	---	AT1G21590	2.53	1.34	7.58	0.000156	0.002244	1.24
261782_at	unknown protein	---	AT1G76110	-2.18	-1.13	-7.58	0.000156	0.002248	1.23
249875_at	photosystem II stability/assembly facto	HCF136	AT5G23120	-2.67	-1.42	-7.58	0.000157	0.002252	1.23
267298_at	putative homeodomain transcription fa	BLH4	AT2G23760	-2.36	-1.24	-7.58	0.000157	0.002254	1.23
245392_at	glutaredoxin ;supported by full-length c	---	AT4G15680	-10.23	-3.35	-7.58	0.000157	0.002255	1.23
259530_at	hypothetical protein	---	AT1G12450	-3.14	-1.65	-7.57	0.000157	0.002259	1.23
254890_at	phospholipid hydroperoxide glutathion	ATGPX6	AT4G11600	1.86	0.89	7.57	0.000158	0.002259	1.22
256014_at	hypothetical protein predicted by gene	---	AT1G19200	6.16	2.62	7.57	0.000158	0.002259	1.22
262952_at	hypothetical protein predicted by gene	---	AT1G75770	-2.09	-1.06	-7.57	0.000158	0.00226	1.22
266721_at	unknown protein	FT1	AT2G03220	-2.26	-1.18	-7.57	0.000158	0.002262	1.22
256483_at	hypothetical protein	---	AT1G31410	-2.12	-1.08	-7.56	0.000159	0.00227	1.22
259244_at	unknown protein similar to zinc finger p	COL9	AT3G07650	3.86	1.95	7.56	0.000159	0.00227	1.21
251755_at	putative protein predicted protein, Ara	---	AT3G55790	2.65	1.41	7.56	0.000159	0.00227	1.21
251497_at	putative protein phytochrome-associa	PIL6	AT3G59060	-1.94	-0.95	-7.56	0.000159	0.00227	1.21
260427_at	hypothetical protein predicted by gene	---	AT1G72430	-4.40	-2.14	-7.56	0.000159	0.002275	1.21
254877_at	putative protein threonine dehydratase	ATSR	AT4G11640	-1.94	-0.95	-7.55	0.00016	0.002277	1.21
261767_s_	adenine nucleotide translocase, putati	NTT1	AT1G15500 /	2.03	1.02	7.55	0.00016	0.002279	1.21
261191_at	starch synthase, putative similar to sta	---	AT1G32900	-3.37	-1.75	-7.55	0.00016	0.002279	1.20
265451_at	unknown protein	---	AT2G46490	-1.64	-0.72	-7.55	0.00016	0.002279	1.20
257809_at	ribonucleotide reductase small subuni	TSO2	AT3G27060	-2.41	-1.27	-7.55	0.00016	0.002279	1.21
253060_at	putative protein predicted protein, Ara	---	AT4G37710	4.36	2.12	7.55	0.00016	0.002279	1.21
256659_at	unknown protein similar to putative kin	---	AT3G12020	-1.86	-0.90	-7.55	0.00016	0.002279	1.21
265192_at	hypothetical protein predicted by gens	---	AT1G05060	2.14	1.10	7.55	0.000161	0.002283	1.20
256366_at	protein kinase, putative contains Pfam	---	AT1G66880	3.72	1.89	7.54	0.000161	0.002285	1.20

263000_at	hypothetical protein similar to hypothet	---	AT1G54350	-1.95	-0.96	-7.54	0.000161	0.002285	1.20
253635_at	putative protein hypothetical protein -	---	AT4G30620	-1.70	-0.77	-7.54	0.000161	0.002285	1.20
258610_at	IAA-amino acid hydrolase (ILR1) ident	ILR1	AT3G02875	2.96	1.57	7.54	0.000161	0.002285	1.20
249941_at	putative protein similar to unknown pro	---	AT5G22270	2.23	1.16	7.54	0.000162	0.002285	1.20
246777_at	RING-H2 zinc finger protein-like RING	---	AT5G27420	17.45	4.13	7.54	0.000162	0.002285	1.20
257198_at	DNA-binding protein, putative similar t	---	AT3G23690	-2.02	-1.02	-7.54	0.000162	0.002285	1.20
248573_at	cellulase homolog OR16pep precursor	ATGH9A1	AT5G49720	-1.98	-0.99	-7.54	0.000162	0.002286	1.19
258923_at	putative glucose acyltransferase simila	SCPL7	AT3G10450	3.78	1.92	7.54	0.000162	0.002288	1.19
265897_at	hypothetical protein predicted by gens	MOT1	AT2G25680	2.77	1.47	7.54	0.000162	0.002288	1.19
256698_at	unknown protein	---	AT3G20680	-2.06	-1.04	-7.53	0.000163	0.002294	1.19
265186_at	Expressed protein ; supported by full-l	---	AT1G23560	2.18	1.12	7.53	0.000163	0.0023	1.19
258525_at	hypothetical protein predicted by gene	IBR3	AT3G06810	2.32	1.22	7.53	0.000164	0.002304	1.18
256914_at	hypothetical protein	---	AT3G23880	-2.64	-1.40	-7.52	0.000164	0.002306	1.18
260414_at	nitrate transporter (NTL1) identical to r	ATNRT1:2	AT1G69850	-1.98	-0.99	-7.52	0.000164	0.002306	1.18
254571_at	hypothetical protein	---	AT4G19370	10.74	3.43	7.52	0.000164	0.002306	1.18
251195_at	glutaredoxin -like protein glutaredoxin	---	AT3G62930	-2.81	-1.49	-7.52	0.000164	0.002306	1.18
253282_at	putative protein hypothetical protein, A	LEJ1	AT4G34120	1.63	0.71	7.52	0.000164	0.002306	1.18
250189_at	putative protein ;supported by full-leng	---	AT5G14410	-2.71	-1.44	-7.52	0.000164	0.002308	1.18
245123_at	unknown protein ; supported by cDNA	CAO	AT2G47450	-1.97	-0.98	-7.52	0.000165	0.002311	1.17
266735_at	putative pectinesterase ; supported by	---	AT2G46930	-2.16	-1.11	-7.51	0.000165	0.002313	1.17
260112_at	unknown protein similar to unknown pr	---	AT1G63310	-2.18	-1.12	-7.51	0.000165	0.002313	1.17
267172_at	unknown protein ;supported by full-ler	---	AT2G37660	-2.16	-1.11	-7.51	0.000165	0.002313	1.17
262275_at	ATPase, putative similar to chromaffin	---	AT1G68710	1.94	0.96	7.51	0.000166	0.002315	1.17
251914_at	putative protein serine/threonine-spec	---	AT3G53930	1.82	0.86	7.51	0.000166	0.002315	1.17
253257_at	extra-large G-protein - like extra-large	XLG2	AT4G34390	2.05	1.04	7.51	0.000166	0.002318	1.17
266685_at	hypothetical protein	---	AT2G19710	1.83	0.88	7.51	0.000166	0.002318	1.17
258419_at	unknown protein	---	AT3G16670	-13.91	-3.80	-7.51	0.000166	0.002319	1.17
260783_at	ethylene response factor, putative sim	ORA59	AT1G06160	6.37	2.67	7.50	0.000167	0.002327	1.16
246736_at	putative protein hypothetical protein s	---	AT5G27560	-1.89	-0.92	-7.49	0.000169	0.002351	1.15
249282_at	CMP-sialic acid transporter-like protein	---	AT5G41760	-2.24	-1.16	-7.49	0.000169	0.002351	1.15
267175_s_	actin 3 identical to GB:U29480;support	ACT1	AT2G37620 /	-2.35	-1.23	-7.49	0.000169	0.002351	1.15
259106_at	unknown protein ;supported by full-ler	RALFL22	AT3G05490	-4.24	-2.09	-7.48	0.000169	0.002351	1.15
259970_at	putative chlorophyll A-B binding protei	---	AT1G76570	-2.68	-1.42	-7.48	0.00017	0.002351	1.14
255008_at	putative protein hypothetical protein s	---	AT4G10060	-1.84	-0.88	-7.48	0.000169	0.002351	1.15
253473_at	putative protein mixed-lineage protein	---	AT4G32250	3.15	1.66	7.48	0.000169	0.002351	1.15

262412_at	14-3-3 protein GF14omicron (grf11) si	GRF11	AT1G34760	-2.03	-1.02	-7.48	0.000169	0.002351	1.15
245492_at	putative protein	SPK1	AT4G16340	-1.85	-0.89	-7.48	0.00017	0.002351	1.14
263495_at	cold-regulated protein cor15b precurs	COR15B	AT2G42530	-9.24	-3.21	-7.48	0.00017	0.002351	1.14
248656_at	fimbrin 2 (gb|AAB97844.1) ; supporte	---	AT5G48460	-5.52	-2.46	-7.48	0.00017	0.002355	1.14
265819_at	Expressed protein ; supported by full-l	---	AT2G17972	-2.01	-1.00	-7.48	0.00017	0.002355	1.14
260220_at	putative MYB family transcription facto	MYB31	AT1G74650	-2.45	-1.29	-7.48	0.00017	0.002357	1.14
261118_at	protease, putative similar to SP:P367	---	AT1G75460	-1.84	-0.88	-7.47	0.000171	0.002364	1.13
246019_at	putative protein predicted proteins, Ar	---	AT5G10690	-2.17	-1.12	-7.47	0.000171	0.002366	1.13
257642_at	putative HLH DNA-binding protein con	BHLH32	AT3G25710	-2.11	-1.07	-7.47	0.000171	0.002366	1.13
257825_at	protein kinase, putative contains Pfam	---	AT3G26700	-1.88	-0.91	-7.47	0.000171	0.002367	1.13
263845_at	phenylalanine ammonia lyase (PAL1)	pal1	AT2G37040	7.96	2.99	7.46	0.000172	0.002372	1.13
256400_at	putative RING zinc finger protein cont	---	AT3G06140	-2.20	-1.14	-7.45	0.000174	0.002403	1.11
253493_at	putative protein various predicted prote	ENP	AT4G31820	-2.80	-1.48	-7.44	0.000175	0.002405	1.11
247786_at	putative protein various predicted prot	PMR5	AT5G58600	-1.68	-0.75	-7.45	0.000175	0.002405	1.11
245816_at	hypothetical protein similar to hypothet	---	AT1G26210	-3.77	-1.91	-7.44	0.000175	0.002407	1.11
256461_s_	adenylosuccinate lyase - like protein a	---	AT1G36280 /	-5.90	-2.56	-7.44	0.000175	0.002407	1.11
258929_at	unknown protein Pfam HMM hit: FKBP	---	AT3G10060	-4.88	-2.29	-7.44	0.000175	0.002407	1.11
246912_at	putative protein various predicted prot	---	AT5G25820	4.65	2.22	7.44	0.000175	0.002407	1.11
249081_at	protein phosphatase 2A 62 kDa B regu	---	AT5G44090	1.79	0.84	7.44	0.000175	0.002407	1.11
245273_at	hypothetical protein ; supported by cDI	---	AT4G14950	2.02	1.02	7.44	0.000176	0.002413	1.10
253795_at	tyrosine transaminase-like protein tyro	---	AT4G28420	1.89	0.92	7.43	0.000176	0.002413	1.10
247201_at	50S ribosomal protein L29 ; supporte	---	AT5G65220	-2.07	-1.05	-7.44	0.000176	0.002413	1.10
251183_at	putative protein putative protein At2g1	---	AT3G62630	-6.40	-2.68	-7.43	0.000177	0.002418	1.10
260996_at	NBS/LRR disease resistance protein i	RFL1	AT1G12210	2.21	1.15	7.43	0.000177	0.002418	1.10
245774_at	hypothetical protein contains similarity	TCP24	AT1G30210	-1.72	-0.78	-7.43	0.000177	0.002418	1.10
255342_at	putative receptor-like protein kinase	---	AT4G04510	1.99	0.99	7.43	0.000177	0.002423	1.10
259442_at	(1-4)-beta-mannan endohydrolase pre	---	AT1G02310	2.84	1.51	7.42	0.000178	0.002425	1.09
245332_at	isomerase like protein ;supported by fu	---	AT4G15940	1.57	0.65	7.42	0.000178	0.002431	1.09
246040_at	peptidyl-prolyl cis-trans isomerase - lik	---	AT5G19370	-1.78	-0.83	-7.42	0.000178	0.002432	1.09
259895_at	unknown protein ;supported by full-len	PFI	AT1G71440	-1.69	-0.76	-7.42	0.000178	0.002433	1.09
264845_at	putative thioredoxin-m similar to thiore	ATHM1	AT1G03680	-1.91	-0.93	-7.42	0.000179	0.002433	1.09
264832_at	unknown unknown	---	AT1G03660	2.22	1.15	7.42	0.000179	0.002433	1.09
262060_at	polygalacturonase, putative similar to	---	AT1G80170	-1.86	-0.89	-7.41	0.00018	0.002445	1.08
251118_at	putative chloroplast inner envelope pr	APG1	AT3G63410	-2.17	-1.11	-7.41	0.00018	0.002445	1.08
250821_at	putative protein similar to unknown pro	---	AT5G05190	1.97	0.98	7.41	0.00018	0.002445	1.08

252572_at	putative protein Mlo-h1 protein - Hord	MLO3	AT3G45290	2.83	1.50	7.41	0.00018	0.002448	1.08
246858_at	receptor-like protein kinase - like rece	---	AT5G25930	7.18	2.84	7.41	0.00018	0.002449	1.08
250621_at	membrane protein membrane protein	ATRBL3	AT5G07250	-1.86	-0.90	-7.40	0.000181	0.002452	1.07
262237_at	hypothetical protein predicted by gene	---	AT1G48320	3.03	1.60	7.39	0.000182	0.002457	1.07
245352_at	indole-3-acetate beta-glucosyltransfera	UGT84A3	AT4G15490	2.83	1.50	7.40	0.000182	0.002457	1.07
266979_at	unknown protein ;supported by full-ler	PPL2	AT2G39470	-10.28	-3.36	-7.39	0.000182	0.002457	1.07
261073_at	hypothetical protein predicted by gene	---	AT1G07300	1.81	0.85	7.40	0.000182	0.002457	1.07
263242_at	unknown protein	---	AT2G31400	1.88	0.91	7.39	0.000182	0.002457	1.07
248531_at	putative protein contains similarity to a	---	AT5G49950	1.84	0.88	7.40	0.000181	0.002457	1.07
262166_at	myb-related transcription activator, pu	---	AT1G74840	-2.15	-1.11	-7.40	0.000182	0.002457	1.07
259194_at	RNA helicase, DRH1 identical to RNA	DRH1	AT3G01540	1.61	0.69	7.40	0.000182	0.002457	1.07
261886_s_	hypothetical protein predicted by gens	---	AT1G80700 /	-1.60	-0.68	-7.39	0.000182	0.002457	1.07
261957_at	methionine/cystathionine gamma lyas	ATMGL	AT1G64660	3.48	1.80	7.39	0.000182	0.002457	1.07
261201_at	unknown protein ;supported by full-len	---	AT1G12850	-1.85	-0.89	-7.39	0.000182	0.00246	1.06
250879_at	putative protein various predicted prot	---	AT5G04060	-2.18	-1.12	-7.39	0.000183	0.00246	1.06
251196_at	glutaredoxin -like protein glutaredoxin	---	AT3G62950	-6.16	-2.62	-7.39	0.000183	0.002461	1.06
250842_at	putative protein predicted proteins, Ar	VTE5	AT5G04490	-2.24	-1.16	-7.39	0.000183	0.002465	1.06
250167_at	myb-related protein - like myb-related	ATMYB16	AT5G15310	-2.42	-1.27	-7.38	0.000184	0.002466	1.06
245252_at	ethylene responsive element binding fa	ATERF-1	AT4G17500	6.34	2.66	7.38	0.000183	0.002466	1.06
265182_at	putative auxin-induced protein ;suppo	---	AT1G23740	-2.34	-1.23	-7.39	0.000183	0.002466	1.06
254444_at	putative protein riboflavin biosynthesis	---	AT4G20960	-2.92	-1.55	-7.38	0.000185	0.002481	1.05
245118_at	putative thioredoxin reductase The las	NTRC	AT2G41680	-1.74	-0.80	-7.37	0.000185	0.002483	1.05
250569_at	myc-like protein myc-like regulatory R	BIM1	AT5G08130	-3.15	-1.66	-7.37	0.000185	0.002486	1.05
256796_at	hypothetical protein predicted by gens	---	AT3G22210	-2.77	-1.47	-7.37	0.000186	0.002496	1.04
261861_at	hypothetical protein predicted by gene	---	AT1G50450	-3.49	-1.80	-7.37	0.000186	0.002498	1.04
248243_at	unknown protein	CPuORF50	AT5G53588 /	1.62	0.70	7.36	0.000187	0.002498	1.04
254085_at	abscisic acid-induced - like protein ab	HVA22D	AT4G24960	-3.48	-1.80	-7.36	0.000187	0.0025	1.04
258947_at	hypothetical protein similar to calmodu	---	AT3G01830	23.71	4.57	7.36	0.000187	0.002501	1.04
251421_at	enoyl-CoA-hydratase - like protein en	---	AT3G60510	1.80	0.85	7.36	0.000188	0.002507	1.03
263624_at	putative ferredoxin-thioredoxin reducta	---	AT2G04700	-2.08	-1.06	-7.36	0.000188	0.00251	1.03
245155_at	putative protein similarity to predicted	---	AT5G12470	-2.45	-1.29	-7.35	0.000188	0.00251	1.03
263442_at	hypothetical protein	---	AT2G28605	-1.67	-0.74	-7.35	0.000189	0.002515	1.03
249899_at	putative protein similar to unknown pro	---	AT5G22620	-2.90	-1.54	-7.35	0.000189	0.002519	1.03
245042_at	hypothetical protein predicted by gene	HEMD	AT2G26540	-2.89	-1.53	-7.35	0.000189	0.00252	1.02
246982_s_	unknown protein	---	AT2G10560 /	3.37	1.75	7.35	0.000189	0.00252	1.02

253789_at	putative protein predicted proteins, Ar	---	AT4G28570	2.07	1.05	7.35	0.000189	0.00252	1.02
262373_at	hypothetical protein predicted by gene	---	AT1G73120	-3.74	-1.90	-7.35	0.00019	0.002522	1.02
250798_at	peroxidase	---	AT5G05340	34.32	5.10	7.34	0.00019	0.002525	1.02
245543_at	glucosyltransferase	---	AT4G15260	1.97	0.98	7.34	0.00019	0.002525	1.02
245605_at	ribonucleoprotein like protein	---	AT4G14300	-1.61	-0.69	-7.34	0.000191	0.002534	1.01
260229_at	putative RING zinc finger protein cont	---	AT1G74370	-2.12	-1.09	-7.33	0.000191	0.002539	1.01
250739_at	putative protein similar to unknown pro	EGY2	AT5G05740	-2.37	-1.25	-7.33	0.000192	0.002539	1.01
246944_at	ubiquinol--cytochrome-c reductase-lik	---	AT5G25450	1.85	0.89	7.33	0.000192	0.002539	1.01
247943_at	light-inducible protein ATLS1-like ;sup	---	AT5G57170	-2.80	-1.49	-7.33	0.000191	0.002539	1.01
266014_s_	hypothetical protein	---	AT2G07722	3.39	1.76	7.33	0.000193	0.002549	1.00
261107_at	unknown protein ; supported by cDNA	---	AT1G63010	1.73	0.79	7.33	0.000193	0.002549	1.00
253275_at	Expressed protein ; supported by full-l	---	AT4G34215	-1.92	-0.94	-7.32	0.000193	0.00255	1.00
253813_at	putative protein hypothetical protein -	---	AT4G28150	-1.88	-0.91	-7.32	0.000193	0.00255	1.00
255682_at	putative dTDP-6-deoxy-L-mannose-de	---	AT4G00560	-1.80	-0.85	-7.32	0.000193	0.00255	1.00
254244_at	putative protein S-receptor kinase 8 p	---	AT4G23230	1.98	0.99	7.32	0.000193	0.00255	1.00
246768_at	putative protein hypothetical proteins -	---	AT5G27400	-1.56	-0.64	-7.32	0.000193	0.00255	1.00
247079_at	Expressed protein ; supported by cDN	AKRP	AT5G66055	-2.35	-1.23	-7.32	0.000194	0.002551	1.00
266167_at	unknown protein ;supported by full-ler	YLS5	AT2G38860	7.48	2.90	7.32	0.000194	0.002551	1.00
260522_x_	hypothetical protein predicted by gene	---	AT2G41730	22.19	4.47	7.32	0.000194	0.002551	1.00
254709_at	Expressed protein ; supported by cDN	AGD8	AT4G17890	-2.07	-1.05	-7.32	0.000194	0.002558	1.00
252563_at	putative protein cim1 induced allergen	ATEXLA1	AT3G45970	-6.30	-2.65	-7.31	0.000194	0.002558	0.99
251642_at	imbibition protein homolog probable ir	AtSIP2	AT3G57520	1.88	0.91	7.31	0.000195	0.002558	0.99
265306_at	unknown protein	---	AT2G20320	2.39	1.26	7.31	0.000195	0.002558	0.99
264083_at	ethylene reponse factor-like AP2 doma	ATERF15	AT2G31230	8.47	3.08	7.30	0.000196	0.002577	0.98
267534_at	putative CCCH-type zinc finger protein	---	AT2G41900	1.72	0.78	7.30	0.000196	0.002577	0.98
257171_at	unknown protein ; supported by full-le	---	AT3G23760	-1.92	-0.94	-7.30	0.000197	0.002577	0.98
254247_at	putative protein receptor protein kinas	---	AT4G23260	3.40	1.76	7.30	0.000197	0.002577	0.98
264164_at	Expressed protein ; supported by full-l	---	AT1G65295	-2.03	-1.02	-7.30	0.000197	0.002581	0.98
266131_at	putative SCARECROW gene regulator	---	AT2G45160	-2.44	-1.28	-7.30	0.000197	0.002581	0.98
253215_at	putative protein AT.I.24-7, Arabidopsis	---	AT4G34950	-4.70	-2.23	-7.30	0.000197	0.002582	0.98
244985_at	ribosomal protein L22	---	---	-2.47	-1.31	-7.30	0.000197	0.002582	0.98
248889_at	unknown protein ;supported by full-len	---	AT5G46230	2.68	1.42	7.30	0.000198	0.002582	0.98
257990_at	putative myc-like DNA-binding protein	---	AT3G19860	-2.21	-1.14	-7.29	0.000198	0.002587	0.97
266481_at	unknown protein ; supported by cDNA	TCP10	AT2G31070	-2.19	-1.13	-7.29	0.000199	0.002591	0.97
247863_at	SKP1 interacting partner 1 (SKIP1) ide	---	AT5G57890 /	1.81	0.86	7.29	0.000199	0.002591	0.97

266761_at	putative alcohol dehydrogenase	---	AT2G47130	4.15	2.05	7.29	0.000199	0.002591	0.97
261307_at	unknown protein similar to Glu-tRNAG	GATB	AT1G48520	-1.73	-0.79	-7.28	0.000199	0.002597	0.97
246145_at	peroxidase peroxidase, Lycopersicon	---	AT5G19880	5.20	2.38	7.28	0.000199	0.002598	0.97
262580_at	hypothetical protein Similar to gb|U407	---	AT1G15330	-2.25	-1.17	-7.28	0.0002	0.002598	0.97
258565_at	unknown protein ; supported by cDNA	---	AT3G04350	2.44	1.29	7.28	0.0002	0.002598	0.97
246098_at	ethylene-forming-enzyme-like dioxyge	---	AT5G20400	2.63	1.39	7.28	0.0002	0.0026	0.96
247795_at	putative protein zinc finger transcriptic	---	AT5G58620	1.94	0.95	7.28	0.0002	0.0026	0.96
248756_at	sodium-dicarboxylate cotransporter-lik	TDT	AT5G47560	3.23	1.69	7.28	0.0002	0.002602	0.96
260871_at	hypothetical protein predicted by gene	---	AT1G29040	-1.60	-0.68	-7.28	0.000201	0.002607	0.96
249001_at	putative protein strong similarity to unk	---	AT5G44990	6.60	2.72	7.26	0.000203	0.002634	0.95
259655_at	unknown protein	---	AT1G55210	6.12	2.61	7.26	0.000203	0.002636	0.95
267014_at	unknown protein	---	AT2G39170	-1.57	-0.65	-7.26	0.000204	0.002639	0.94
251855_at	sugar-phosphate isomerase - like prot	---	AT3G54690	-3.27	-1.71	-7.26	0.000204	0.002641	0.94
245398_at	hydroxyproline-rich glycoprotein homo	---	AT4G14900	2.62	1.39	7.25	0.000205	0.002652	0.94
258277_at	putative cytochrome P450 similar to cy	PAD3	AT3G26830	67.70	6.08	7.25	0.000205	0.002654	0.94
251967_at	putative protein DMR-N9 PROTEIN, M	---	AT3G53390	1.67	0.74	7.25	0.000206	0.00266	0.93
259235_at	hypothetical protein predicted by gens	---	AT3G11600	4.07	2.03	7.24	0.000207	0.002678	0.93
258689_at	putative GTPase activating protein cor	---	AT3G07940	-1.66	-0.73	-7.24	0.000207	0.002678	0.92
247128_at	atfp6-like protein	---	AT5G66110	-2.26	-1.18	-7.24	0.000208	0.002679	0.92
250866_at	Expressed protein ; supported by full-le	---	AT5G03905	1.84	0.88	7.24	0.000208	0.00268	0.92
255298_at	putative protein similar to transcriptiona	ATMSRB6	AT4G04840	-8.15	-3.03	-7.23	0.000208	0.002681	0.92
262749_at	lipase, putative contains Pfam profile:	---	AT1G28580	1.77	0.83	7.23	0.000208	0.002681	0.92
267261_at	unknown protein ;supported by full-ler	---	AT2G23120	-2.98	-1.58	-7.23	0.000209	0.002687	0.92
246949_at	cytochrome P450-like protein CYTOC	CYP71B13	AT5G25140	-6.06	-2.60	-7.23	0.000209	0.002687	0.92
261949_at	hypothetical protein predicted by gene	BDG1	AT1G64670	-4.31	-2.11	-7.23	0.000209	0.00269	0.91
256848_at	hypothetical protein similar to hypothet	---	AT3G27960	-5.91	-2.56	-7.23	0.000209	0.00269	0.91
257147_at	unknown protein	---	AT3G27270	2.31	1.21	7.23	0.000209	0.00269	0.91
253097_at	cytochrome P450-like protein	CYP81D5	AT4G37320	4.81	2.27	7.23	0.000209	0.00269	0.91
259914_at	hypothetical protein predicted by gene	---	AT1G72640	-2.07	-1.05	-7.22	0.00021	0.002691	0.91
266422_at	hypothetical protein predicted by gens	GAUT7	AT2G38650	-1.74	-0.80	-7.22	0.00021	0.002695	0.91
253337_at	putative protein acetylpolyamine amin	hda14	AT4G33470	-2.68	-1.42	-7.22	0.00021	0.002698	0.91
255794_at	putative NAM (no apical meristem)-like	ANAC041	AT2G33480	3.77	1.91	7.22	0.000211	0.0027	0.91
265704_at	hypothetical protein predicted by gens	---	AT2G03420	-2.32	-1.21	-7.22	0.000211	0.0027	0.91
248377_at	unknown protein ; supported by full-le	---	AT5G51720	-3.33	-1.74	-7.22	0.000211	0.0027	0.91
256446_at	RING zinc finger protein contains Pfar	---	AT3G11110	-2.75	-1.46	-7.21	0.000212	0.002707	0.90

257783_at	unknown protein	---	AT3G26950	-1.76	-0.82	-7.21	0.000212	0.002707	0.90
247754_at	putative protein	---	AT5G59080	-4.16	-2.06	-7.21	0.000213	0.002718	0.90
247283_at	2-nitropropane dioxygenase-like protei	---	AT5G64250	1.87	0.90	7.20	0.000214	0.002731	0.89
258264_at	unknown protein	MBD11	AT3G15790	-2.02	-1.02	-7.20	0.000214	0.002732	0.89
265431_at	(1-4)-beta-mannan endohydrolase	---	AT2G20680	-1.74	-0.80	-7.20	0.000214	0.002732	0.89
267645_at	putative beta-glucosidase	BGLU33	AT2G32860	-5.02	-2.33	-7.20	0.000215	0.002737	0.89
264521_at	unknown protein Location of EST gb|T	---	AT1G10020	-3.96	-1.99	-7.19	0.000215	0.002741	0.88
256052_at	spliceosomal protein (U2B), putative s	---	AT1G06960	-1.82	-0.87	-7.19	0.000215	0.002743	0.88
253911_at	putative receptor protein kinase recep	---	AT4G27300	3.83	1.94	7.19	0.000216	0.002744	0.88
253174_at	catalase ; supported by cDNA: gi_154	CAT2	AT4G35090	-1.98	-0.98	-7.19	0.000216	0.002744	0.88
250531_at	GTP-binding protein LepA homolog	---	AT5G08650	-2.40	-1.26	-7.19	0.000216	0.00275	0.88
247480_at	KED - like protein KED, Nicotiana tab	ATBAG7	AT5G62390	-2.10	-1.07	-7.19	0.000216	0.00275	0.88
252463_at	putative protein ;supported by full-leng	---	AT3G47070	-3.14	-1.65	-7.18	0.000217	0.002752	0.88
257209_at	hypothetical protein	---	AT3G14920	1.59	0.67	7.18	0.000218	0.002763	0.87
263449_at	unknown protein	AtRABA5d	AT2G31670 /	-1.71	-0.77	-7.17	0.000219	0.002774	0.87
246724_at	putative protein CDPK substrate prote	---	AT5G29000	2.08	1.06	7.17	0.000219	0.002777	0.86
245575_at	centromere protein homolog	---	AT4G14760	-1.75	-0.81	-7.17	0.000219	0.002777	0.86
257172_at	hypothetical protein predicted by gene	---	AT3G23700	-2.08	-1.06	-7.17	0.000219	0.002777	0.86
245291_at	Expressed protein ; supported by cDN	---	AT4G16155	-1.76	-0.82	-7.17	0.00022	0.002787	0.86
254117_at	putative protein	---	AT4G24750	-2.17	-1.12	-7.16	0.000221	0.002792	0.86
248886_at	phosphate/triose-phosphate translocat	APE2	AT5G46110	-1.83	-0.87	-7.16	0.000221	0.002792	0.86
253571_at	putative calmodulin-binding protein ca	---	AT4G31000	-6.27	-2.65	-7.16	0.000222	0.0028	0.85
248276_at	EspB-like protein	YSL3	AT5G53550	2.29	1.19	7.15	0.000223	0.002814	0.84
253040_at	endo-xyloglucan transferase - like pro	---	AT4G37800	-7.31	-2.87	-7.15	0.000223	0.002814	0.84
256419_at	RNA-binding protein similar to GI:8292	---	AT1G33470	-1.88	-0.91	-7.15	0.000223	0.002814	0.84
256908_at	hypothetical protein similar to mucin c	---	AT3G24040	-1.85	-0.89	-7.15	0.000223	0.002815	0.84
263920_at	unknown protein ;supported by full-ler	---	AT2G36410	-2.04	-1.03	-7.15	0.000224	0.002822	0.84
248082_at	fimbrin	---	AT5G55400	-2.79	-1.48	-7.14	0.000224	0.002823	0.84
250861_at	putative protein predicted proteins, Ar	---	AT5G04740	1.92	0.94	7.14	0.000224	0.002824	0.84
255826_at	putative uroporphyrinogen decarboxyla	HEME2	AT2G40490	-1.82	-0.86	-7.14	0.000224	0.002824	0.84
263947_at	unknown protein ;supported by full-ler	---	AT2G35820	2.84	1.51	7.14	0.000225	0.002827	0.84
262001_at	myrosinase binding protein, putative s	---	AT1G33790	-1.90	-0.93	-7.14	0.000225	0.002828	0.83
256417_s_	omega-3 fatty acid desaturase, chloro	FAD7	AT3G11170 /	-2.78	-1.47	-7.14	0.000225	0.002829	0.83
257206_at	putative lectin similar to lectin SP:P028	---	AT3G16530	16.64	4.06	7.14	0.000226	0.002832	0.83
267184_at	unknown protein ; supported by cDNA	ASHH3	AT2G44150	-1.69	-0.76	-7.13	0.000226	0.00284	0.83

247429_at	putative protein strong similarity to unk	---	AT5G62620	2.19	1.13	7.13	0.000227	0.002841	0.83
256170_at	receptor protein kinase, putative conta	---	AT1G51790	2.66	1.41	7.13	0.000227	0.002841	0.83
250441_at	oligopeptidase A - like protein oligope	---	AT5G10540	-1.59	-0.67	-7.13	0.000227	0.002845	0.82
264549_at	putative ser/thr protein kinase similar t	---	AT1G09440	-1.70	-0.76	-7.13	0.000227	0.002846	0.82
245599_at	RING-H2 finger protein RHF1a	RHF1A	AT4G14220	2.45	1.29	7.13	0.000228	0.002848	0.82
247912_at	putative protein contains similarity to A	---	AT5G57480	3.37	1.75	7.12	0.000229	0.002854	0.82
248676_at	putative protein similar to unknown pro	ATSDI1	AT5G48850	-7.78	-2.96	-7.12	0.000228	0.002854	0.82
246008_at	putative protein predicted proteins, Ho	---	AT5G08320	-1.96	-0.97	-7.12	0.000229	0.002854	0.82
266073_at	putative signal recognition particle rece	---	AT2G18770	-1.75	-0.81	-7.12	0.000228	0.002854	0.82
252068_at	mucin -like protein hemomucin, Droso	---	AT3G51440	4.76	2.25	7.12	0.000229	0.002854	0.82
252740_at	pectinesterase -like protein PECTINE	---	AT3G43270	-2.51	-1.33	-7.12	0.000229	0.002855	0.82
253916_at	hypothetical protein ;supported by full-	---	AT4G27240	-2.88	-1.53	-7.12	0.000229	0.002855	0.82
247540_at	ethylene responsive element binding f	---	AT5G61590	-3.74	-1.90	-7.12	0.00023	0.002861	0.81
249454_at	expressed protein predicted protein, S	---	AT5G39520	6.93	2.79	7.11	0.000231	0.002872	0.80
258299_at	unknown protein contains GMC oxidor	---	AT3G23410	-2.27	-1.18	-7.11	0.000231	0.002872	0.80
258055_at	putative 2Fe-2S iron-sulfur cluster prot	NDF4	AT3G16250	-5.12	-2.36	-7.11	0.000231	0.002872	0.81
259534_at	hypothetical protein	---	AT1G12290	1.96	0.97	7.11	0.000231	0.002872	0.80
265676_at	putative CCR4-associated factor ; sup	---	AT2G32070	-1.67	-0.74	-7.11	0.000231	0.002872	0.81
252450_s_	receptor kinase-like protein receptor k	---	AT3G47090 /	3.17	1.66	7.11	0.000231	0.002872	0.81
261948_at	unknown protein ;supported by full-len	---	AT1G64680	-2.76	-1.46	-7.11	0.000231	0.002872	0.80
258814_at	putative short-chain type dehydrogena	---	AT3G03980	-1.90	-0.93	-7.11	0.000232	0.002875	0.80
263348_at	cytoplasmic aconitate hydratase	---	AT2G05710	2.26	1.18	7.10	0.000233	0.002883	0.80
254951_at	putative protein various kinesin light ch	---	AT4G10840	-1.64	-0.72	-7.10	0.000233	0.002886	0.80
248027_at	outward rectifying potassium channel k	ATKCO1	AT5G55630	-1.96	-0.97	-7.10	0.000233	0.002886	0.80
249027_at	ATP dependent copper transporter ; s	RAN1	AT5G44790	2.05	1.04	7.10	0.000233	0.002888	0.80
255571_at	hypothetical protein ; supported by cD	---	AT4G01220	-2.56	-1.35	-7.10	0.000234	0.00289	0.79
252133_at	hypothetical protein hypothetical prote	---	AT3G50900	6.27	2.65	7.09	0.000234	0.002896	0.79
250264_at	glucosyltransferase -like protein gluco	---	AT5G12890	1.54	0.62	7.09	0.000234	0.002896	0.79
245049_at	ribosomal protein S16	---	---	-2.46	-1.30	-7.09	0.000235	0.002897	0.79
259303_at	hypothetical protein predicted by gens	---	AT3G05130	-1.52	-0.60	-7.09	0.000235	0.002903	0.79
250257_at	putative protein similar to unknown pro	---	AT5G13770	-1.94	-0.96	-7.09	0.000235	0.002905	0.79
262882_at	cytochrome p450, putative similar to c	CYP89A2	AT1G64900	5.12	2.36	7.08	0.000236	0.00291	0.78
266991_at	putative CDP-diacylglycerol--glycerol-3	PGP1	AT2G39290	-1.57	-0.65	-7.08	0.000237	0.002918	0.78
267578_at	Expressed protein ; supported by cDN	---	AT2G30695	-2.96	-1.57	-7.08	0.000237	0.002918	0.78
254928_at	putative protein hypothetical protein -	---	AT4G11410	-1.79	-0.84	-7.08	0.000237	0.002918	0.78

250356_at	clathrin binding protein - like Af10-prot	---	AT5G11710	-1.54	-0.62	-7.08	0.000238	0.002923	0.78
261366_at	unknown protein	---	AT1G53100	4.57	2.19	7.07	0.000238	0.002926	0.77
264686_at	shaggy-like protien kinase, kappa Ider	ATSK41	AT1G09840	-1.59	-0.67	-7.07	0.000239	0.002931	0.77
250545_at	serine/threonine protein kinase ;suppo	ATPK3	AT5G08160	-1.66	-0.73	-7.07	0.000239	0.002932	0.77
261536_at	K Efflux antiporter KEA1 identical to G	KEA1	AT1G01790	-2.16	-1.11	-7.07	0.000239	0.002932	0.77
263053_at	similar to glucose inhibited division pro	---	AT2G13440	-1.79	-0.84	-7.07	0.00024	0.002938	0.77
255844_at	putative protein kinase contains a prot	---	AT2G33580	3.43	1.78	7.07	0.000239	0.002938	0.77
260261_at	unknown protein	---	AT1G68450	8.60	3.10	7.06	0.00024	0.002946	0.76
256015_at	PSI type II chlorophyll a/b-binding pro	LHCA6	AT1G19150	-10.27	-3.36	-7.06	0.00024	0.002946	0.76
264833_at	putative protein phosphatase similar to	---	AT1G03590	-2.47	-1.31	-7.06	0.000241	0.002946	0.76
249073_at	vegetative storage protein-like ;suppo	---	AT5G44020	-4.51	-2.17	-7.06	0.000241	0.002946	0.76
265183_at	unknown protein ;supported by full-ler	---	AT1G23750	-2.61	-1.38	-7.06	0.000241	0.002946	0.76
245337_at	Expressed protein ; supported by full-l	---	AT4G16566	-1.67	-0.74	-7.06	0.000241	0.002946	0.76
245383_at	SUPERMAN like protein	---	AT4G17810	-2.82	-1.49	-7.06	0.000241	0.002947	0.76
263705_at	unknown protein contains similarity to	IMPL1	AT1G31190	-2.16	-1.11	-7.06	0.000242	0.002949	0.76
249563_at	similar to unknown protein (pir |T0399	---	AT5G38360	-1.69	-0.76	-7.06	0.000242	0.002949	0.76
263656_at	putative auxin-induced protein AUX2-1	SHY2	AT1G04240	-17.40	-4.12	-7.05	0.000243	0.002957	0.75
262569_at	hypothetical protein Strong similarity to	---	AT1G15180	-2.48	-1.31	-7.05	0.000243	0.002957	0.75
267637_at	unknown protein predicted by genscan	---	AT2G42190	-2.36	-1.24	-7.05	0.000243	0.002957	0.75
259671_at	protein kinase, putative similar to GI:7	---	AT1G52290	-3.81	-1.93	-7.05	0.000244	0.002968	0.75
258356_at	unknown protein	---	AT3G14340	-1.95	-0.97	-7.05	0.000244	0.002968	0.75
261934_at	UDP-glucose glucosyltransferase, put	UGT85A1	AT1G22400	5.32	2.41	7.04	0.000244	0.002973	0.74
250254_at	24-sterol C-methyltransferase ; suppo	SMT1	AT5G13710	-2.28	-1.19	-7.04	0.000245	0.002981	0.74
265853_at	putative RING zinc finger protein	---	AT2G42360	6.47	2.69	7.04	0.000246	0.002986	0.74
266888_s_	putative thiamin pyrophosphokinase ;	TPK1	AT1G02880 /	1.70	0.77	7.04	0.000246	0.002986	0.74
252908_at	putative protein	---	AT4G39670	22.13	4.47	7.03	0.000246	0.002986	0.74
262775_at	unknown protein	---	AT1G13000	1.68	0.75	7.03	0.000246	0.002986	0.74
257168_at	mrp protein, putative similar to mrp pr	HCF101	AT3G24430	-3.46	-1.79	-7.03	0.000246	0.002986	0.74
247380_at	4-coumarate-CoA ligase-like protein	---	AT5G63380	-2.09	-1.07	-7.03	0.000246	0.002986	0.74
256181_at	light repressible receptor protein kinas	---	AT1G51820	6.07	2.60	7.03	0.000248	0.002999	0.73
251860_at	Gluthatione reductase, chloroplast pre	GR	AT3G54660	-1.56	-0.64	-7.03	0.000248	0.002999	0.73
247989_at	pyruvate kinase ;supported by full-len	---	AT5G56350	2.22	1.15	7.03	0.000248	0.002999	0.73
265742_at	putative ribose 5-phosphate isomerase	---	AT2G01290	2.30	1.20	7.03	0.000248	0.003	0.73
251645_at	putative protein polygalacturonase (E	---	AT3G57790	-1.85	-0.89	-7.02	0.000248	0.003	0.73
245924_at	Tha4 protein - like Tha4 protein, Pisur	---	AT5G28750	-1.63	-0.70	-7.02	0.000248	0.003	0.73

261833_at	ATP citrate-lyase, putative similar to A	ACLA-1	AT1G10670	-1.75	-0.80	-7.02	0.000249	0.003011	0.72
265581_at	putative cAMP-dependent protein kina	---	AT2G20050	-1.68	-0.74	-7.02	0.00025	0.003013	0.72
261192_at	NAM protein, putative similar to NAM	ANAC13	AT1G32870	2.23	1.16	7.02	0.00025	0.003014	0.72
260500_at	Expressed protein ; supported by cDN	---	AT2G41705	1.61	0.69	7.01	0.00025	0.003014	0.72
251028_at	putative protein putative hydrolase At2	---	AT5G02230	1.91	0.94	7.02	0.00025	0.003014	0.72
264365_s_	unknown protein Strong similarity to g	---	AT1G03220 /	4.18	2.06	7.02	0.00025	0.003014	0.72
248394_at	unknown protein	---	AT5G52070	1.69	0.75	7.01	0.000251	0.003019	0.72
262633_at	Expressed protein ; supported by full-l	---	AT1G06630	-1.65	-0.72	-7.01	0.000251	0.003025	0.71
246434_at	root cap 1 (RCP1) ;supported by full-l	RCP1	AT5G17520	-2.13	-1.09	-7.01	0.000252	0.003029	0.71
245985_at	peptidylprolyl isomerase-like protein c	---	AT5G13120	-2.02	-1.02	-7.01	0.000252	0.003029	0.71
262598_at	unknown protein EST gb|N65467 com	---	AT1G15260	-2.32	-1.22	-7.00	0.000253	0.003037	0.71
250408_at	serine/threonine protein kinase -like p	CIPK5	AT5G10930	2.69	1.43	7.00	0.000254	0.003045	0.70
246462_at	putative protein predicted protein, Dro	---	AT5G16940	-2.46	-1.30	-7.00	0.000254	0.003048	0.70
247907_at	unknown protein	---	AT5G57460	-1.63	-0.71	-6.99	0.000255	0.003051	0.70
253184_at	putative protein protein kinase APK1,	BSK1	AT4G35230	1.80	0.85	7.00	0.000255	0.003051	0.70
245064_at	Expressed protein ; supported by full-l	---	AT2G39725	2.62	1.39	6.99	0.000255	0.003051	0.70
246003_at	chloroplast Cpn21 protein ; supported	CPN20	AT5G20720	-1.86	-0.90	-7.00	0.000254	0.003051	0.70
253496_at	glutathione peroxidase - like protein g	ATGPX7	AT4G31870	-5.51	-2.46	-6.99	0.000255	0.003055	0.70
248040_at	putative protein contains similarity to u	---	AT5G55970	3.40	1.76	6.99	0.000256	0.003059	0.69
264959_at	hypothetical protein predicted by gene	---	AT1G77090	-1.89	-0.92	-6.99	0.000256	0.00306	0.69
247908_at	GS1-like protein ;supported by full-leng	GS1	AT5G57440	-3.53	-1.82	-6.99	0.000257	0.003066	0.69
263609_at	putative LRR receptor protein kinase	---	AT2G16250	-1.68	-0.75	-6.99	0.000257	0.003066	0.69
252711_at	lipid-transfer protein-like protein nonsp	---	AT3G43720	-6.56	-2.71	-6.98	0.000257	0.003069	0.69
267116_at	unknown protein	---	AT2G32560	-2.96	-1.57	-6.98	0.000257	0.003069	0.69
257314_at	integral membrane protein, putative c	---	AT3G26590	4.06	2.02	6.98	0.000257	0.003069	0.69
251573_at	phenylalanine-tRNA synthetase-like p	---	AT3G58140	-1.80	-0.85	-6.98	0.000258	0.003069	0.69
258728_at	unknown protein ; supported by cDNA	---	AT3G11800	-1.65	-0.72	-6.98	0.000258	0.003071	0.69
258472_at	unknown protein identical to unknown	---	AT3G06080	-2.51	-1.33	-6.98	0.000258	0.003075	0.68
245711_at	putative c2h2 zinc finger transcription f	ZAT6	AT5G04340	7.31	2.87	6.98	0.000259	0.003076	0.68
251780_s_	beta-ketoacyl-ACP reductase - like pr	---	AT3G55290 /	2.58	1.36	6.98	0.000259	0.003078	0.68
264053_at	hypothetical protein predicted by gens	---	AT2G22560	2.10	1.07	6.98	0.000259	0.003079	0.68
247856_at	receptor-like protein kinase	---	AT5G58300	-2.18	-1.12	-6.97	0.000259	0.00308	0.68
267308_at	putative malonyl-CoA:Acyl carrier prote	---	AT2G30200	-1.92	-0.94	-6.97	0.00026	0.003089	0.68
253820_at	hypothetical protein	---	AT4G28370	1.71	0.77	6.97	0.000261	0.003093	0.67
254526_at	putative protein cyclin C homolog 1, S	CYCT1;4	AT4G19600	1.67	0.74	6.97	0.000261	0.003096	0.67

253987_at	pyrophosphate-dependent phosphofru	PFK3	AT4G26270	3.51	1.81	6.96	0.000262	0.003108	0.67
245307_at	gibberellin oxidase-like protein non-cor	---	AT4G16770	-1.91	-0.94	-6.96	0.000262	0.003109	0.67
260362_at	putative protein kinase similar to C-terr	---	AT1G70530	3.72	1.90	6.96	0.000263	0.003109	0.67
247405_at	Arac10 ; supported by cDNA: gi_3702	ARAC10	AT5G62880	-1.80	-0.84	-6.96	0.000263	0.003115	0.66
260531_at	putative acyl-CoA synthetase ; suppor	CER8	AT2G47240	-2.13	-1.09	-6.96	0.000263	0.003115	0.66
258683_at	putative protein kinase contains Pfam	ATSIK	AT3G08760	2.73	1.45	6.95	0.000264	0.00312	0.66
245364_at	hypothetical protein ;supported by full-	---	AT4G15790	-1.99	-0.99	-6.95	0.000264	0.00312	0.66
258599_at	L-allo-threonine aldolase, putative sim	THA2	AT3G04520	2.48	1.31	6.95	0.000264	0.00312	0.66
248595_at	drought-induced protein Di19-like prote	HRB1	AT5G49230	-1.80	-0.85	-6.95	0.000265	0.003123	0.66
261559_at	LIM domain protein, putative similar to	---	AT1G01780	1.86	0.90	6.95	0.000265	0.003127	0.66
266224_at	chloroplast membrane protein (ALBIN	ALB3	AT2G28800	-1.60	-0.68	-6.95	0.000265	0.003128	0.65
259577_at	unknown protein	---	AT1G35340	-2.05	-1.03	-6.95	0.000266	0.003132	0.65
250170_at	putative protein ribulose-1,5-bisphosp	---	AT5G14260	-1.87	-0.90	-6.94	0.000266	0.003134	0.65
257831_at	unknown protein ;supported by full-ler	CCB1	AT3G26710	-1.94	-0.95	-6.94	0.000266	0.003134	0.65
253109_at	putative protein predicted protein A_T	MCA1	AT4G35920	-2.79	-1.48	-6.94	0.000267	0.003142	0.65
265720_at	unknown protein	---	AT2G40110	3.23	1.69	6.94	0.000268	0.003146	0.64
249345_at	putative protein ; supported by cDNA:	---	AT5G40740	-1.81	-0.86	-6.94	0.000268	0.003146	0.64
257713_at	succinate dehydrogenase iron-protein	SDH2-1	AT3G27380	2.56	1.36	6.94	0.000268	0.003146	0.64
264508_at	putative phytochrome A similar to GB:A	PHYA	AT1G09570	-2.61	-1.39	-6.94	0.000268	0.003147	0.64
252986_at	putative protein T19C21.18 Arabidops	---	AT4G38380	1.52	0.61	6.93	0.000268	0.003149	0.64
266285_at	unknown protein	---	AT2G29180	-2.98	-1.58	-6.93	0.000268	0.003149	0.64
253181_at	amino acid permease - like protein Lil	LHT7	AT4G35180	10.74	3.43	6.93	0.000269	0.003151	0.64
251859_at	putative protein proteophosphoglycan	---	AT3G54680	1.80	0.85	6.93	0.000269	0.003156	0.64
260004_at	unknown protein ;supported by full-ler	---	AT1G67860	2.65	1.41	6.93	0.000269	0.003156	0.64
254500_at	vacuolar sorting receptor-like protein E	---	AT4G20110	3.49	1.80	6.93	0.00027	0.003166	0.63
252852_at	hypothetical protein ;supported by full-	---	AT4G39900	-3.34	-1.74	-6.92	0.000271	0.003166	0.63
250107_at	ids-4 protein - like ids-4 protein, Hordε	SPX4	AT5G15330	-2.26	-1.18	-6.92	0.000271	0.00317	0.63
252255_at	pectinesterase - like protein pectineste	---	AT3G49220	-3.74	-1.90	-6.92	0.000272	0.003176	0.63
244934_at	NADH dehydrogenase ND6	---	---	-3.17	-1.66	-6.92	0.000272	0.003176	0.63
245744_at	unknown protein	---	AT1G51110	-4.29	-2.10	-6.92	0.000272	0.003176	0.63
249866_at	2-isopropylmalate synthase-like; homo	MAM1	AT5G23010	-3.10	-1.63	-6.92	0.000272	0.003176	0.63
245038_at	similar to latex allergen from Hevea br	PLA2A	AT2G26560	6.35	2.67	6.92	0.000272	0.003176	0.63
251193_at	translation releasing factor RF-1 -like	APG3	AT3G62910	-2.26	-1.18	-6.92	0.000272	0.003176	0.63
254174_at	putative protein various predicted prote	YSL1	AT4G24120	2.40	1.26	6.92	0.000273	0.003177	0.62
266340_at	similar to axi 1 protein from Nicotiana t	---	AT2G01480	1.56	0.64	6.92	0.000273	0.003178	0.62

265715_s_	expressed protein non-consensus GA	---	AT1G13860 /	-2.81	-1.49	-6.91	0.000273	0.003178	0.62
261740_at	hypothetical protein similar to unknowr	---	AT1G47740	-2.22	-1.15	-6.91	0.000273	0.003179	0.62
264102_at	hypothetical protein predicted by gene	ECT8	AT1G79270	2.16	1.11	6.91	0.000274	0.003183	0.62
262093_at	receptor protein kinase, putative conta	---	AT1G56145	2.43	1.28	6.91	0.000275	0.003194	0.62
259439_at	1-aminocyclopropane-1-carboxylate sy	ACS2	AT1G01480	18.90	4.24	6.91	0.000275	0.003194	0.62
247831_at	putative protein serine/threonine-spec	---	AT5G58540	2.67	1.42	6.91	0.000275	0.003194	0.62
262591_at	hypothetical protein Similar to gb|X825	CCMH	AT1G15220	-1.66	-0.73	-6.90	0.000276	0.003202	0.61
264516_at	unknown protein	---	AT1G10090	-1.68	-0.74	-6.90	0.000277	0.003208	0.61
253779_at	receptor-like protein kinase 5 precurso	HAE	AT4G28490	3.30	1.72	6.89	0.000278	0.003225	0.60
259927_at	unknown protein ; supported by cDNA	JAC1	AT1G75100	-2.47	-1.30	-6.89	0.000278	0.003225	0.60
246549_at	putative protein predicted proteins, Ar	---	AT5G15050	-2.93	-1.55	-6.89	0.000279	0.00323	0.60
248564_at	putative protein contains similarity to A	---	AT5G49700	2.16	1.11	6.89	0.000279	0.003232	0.60
251415_at	putative protein	---	AT3G60380	-1.68	-0.75	-6.89	0.000279	0.003232	0.60
257265_at	PHD-finger protein, putative contains	---	AT3G14980	-1.83	-0.87	-6.89	0.00028	0.003235	0.60
253063_at	plasma membrane-type calcium ATPa	ACA2	AT4G37640	2.71	1.44	6.88	0.00028	0.003239	0.60
263876_at	putative RAS superfamily GTP-binding	ATRAB7A	AT2G21880	-2.16	-1.11	-6.88	0.000281	0.003249	0.59
267126_s_	putative acetone-cyanohydrin lyase	ACL	AT2G23590 /	-2.44	-1.29	-6.88	0.000282	0.003256	0.59
262738_at	hypothetical protein	---	AT1G28530	-1.96	-0.97	-6.88	0.000282	0.003256	0.59
251192_at	alpha galactosyltransferase-like protei	XT1	AT3G62720	-3.90	-1.96	-6.88	0.000282	0.003258	0.59
255230_at	ferredoxin--NADP+ reductase - like pr	ATRFNR1	AT4G05390	7.16	2.84	6.87	0.000283	0.003258	0.59
262656_at	unknown protein location of EST TAT	---	AT1G14200	-1.77	-0.82	-6.87	0.000283	0.00326	0.58
256922_at	hypothetical protein contains similarity	---	AT3G19010	3.57	1.84	6.87	0.000284	0.00326	0.58
245365_at	hypothetical protein ;supported by full-	---	AT4G17720	2.56	1.35	6.87	0.000284	0.00326	0.58
260874_at	hypothetical protein predicted by gene	emb2170	AT1G21390	1.92	0.94	6.87	0.000283	0.00326	0.58
266235_at	putative phloem-specific lectin	AtPP2-B10	AT2G02360	2.09	1.07	6.87	0.000283	0.00326	0.58
246631_at	unknown protein ; supported by full-ler	---	AT1G50740	1.66	0.73	6.87	0.000283	0.00326	0.58
264026_at	glycine-rich protein (AtGRP2) Same as	ATGRP2B	AT2G21060	2.80	1.48	6.87	0.000284	0.003263	0.58
254010_at	putative protein ;supported by full-leng	---	AT1G72125 /	1.67	0.74	6.87	0.000285	0.00327	0.58
265656_at	putative nonspecific lipid-transfer prote	---	AT2G13820	-3.75	-1.91	-6.86	0.000285	0.003271	0.58
248932_at	peptide transporter	PTR3	AT5G46050	7.65	2.94	6.86	0.000285	0.003272	0.58
247585_at	putative protein predicted proteins, Ar	---	AT5G60680	-2.05	-1.04	-6.86	0.000286	0.003276	0.57
262357_at	jacalin, putative similar to jacalin GI:28	---	AT1G73040	5.62	2.49	6.86	0.000286	0.003281	0.57
251493_at	putative protein hypothetical protein T	---	AT3G59300	1.95	0.96	6.85	0.000288	0.003296	0.57
263701_at	putative protein kinase C inhibitor (Zin	---	AT1G31160	-1.59	-0.67	-6.85	0.000288	0.003296	0.57
249610_at	putative protein	---	AT5G37360	-3.08	-1.62	-6.85	0.000288	0.003298	0.56

256356_s_	hypothetical protein	---	AT1G66500 /	1.82	0.87	6.85	0.000288	0.003299	0.56
249606_at	putative protein DNA-binding protein (	RVE2	AT5G37260	1.76	0.82	6.85	0.000289	0.003302	0.56
266022_at	subtilisin-like serine protease, putative	---	AT2G05920	-2.33	-1.22	-6.85	0.000289	0.003302	0.56
250695_at	lectin-like protein kinase	---	AT5G06740	4.66	2.22	6.85	0.000289	0.003305	0.56
248704_at	putative protein pectinesterase-like; als	sks3	AT5G48450	-2.11	-1.08	-6.84	0.00029	0.003311	0.56
259213_at	putative receptor ser/thr protein kinase	---	AT3G09010	7.30	2.87	6.84	0.00029	0.003311	0.56
254635_at	extensin-like protein extensin-like prot	---	AT4G18670	-1.86	-0.90	-6.84	0.00029	0.003311	0.56
262581_at	unknown protein ESTs gb|T22508, gb	---	AT1G15370	-1.55	-0.63	-6.84	0.00029	0.003311	0.56
253665_at	hypothetical protein	---	AT4G30230	2.66	1.41	6.84	0.000291	0.003314	0.55
261715_at	hypothetical protein similar to hypothet	---	AT1G18485	-1.74	-0.80	-6.84	0.000292	0.003321	0.55
246927_s_	nodulin - like protein nodulin, Glycine	---	AT5G25250 /	2.57	1.36	6.84	0.000292	0.003323	0.55
253923_at	hypothetical protein Arabidopsis thalia	TOR1	AT4G27060	-1.74	-0.80	-6.83	0.000293	0.003331	0.55
266648_at	putative trytophanyl-tRNA synthetase	OVA4	AT2G25840	-1.64	-0.72	-6.83	0.000293	0.003331	0.55
260705_at	unknown protein ;supported by full-len	TOM2A	AT1G32400	-1.63	-0.70	-6.83	0.000293	0.003331	0.55
260959_at	unknown protein ;supported by full-len	---	AT1G06050	1.72	0.78	6.83	0.000294	0.003334	0.54
261407_at	unknown protein ;supported by full-len	---	AT1G18810	-2.41	-1.27	-6.83	0.000294	0.003334	0.54
266500_at	Expressed protein ; supported by full-l	PLA2-ALPH/	AT2G06925	-2.64	-1.40	-6.83	0.000294	0.003334	0.54
263809_at	putative GDSL-motif lipase/hydrolase s	---	AT2G04570	-3.65	-1.87	-6.83	0.000295	0.003341	0.54
258365_s_	putative diaminopimelate decarboxylas	---	AT3G14390 /	-1.81	-0.85	-6.82	0.000295	0.003347	0.54
262590_at	putative RING-H2 zinc finger protein E	RHA2A	AT1G15100	1.84	0.88	6.82	0.000296	0.003356	0.53
265471_at	putative peroxidase ATP2a ;supported	---	AT2G37130	3.84	1.94	6.82	0.000297	0.003364	0.53
255926_at	AP2 domain containing protein RAP2,	---	AT1G22190	3.23	1.69	6.82	0.000297	0.003364	0.53
260706_at	oxidase, putative similar to oxidase GI	AOX1D	AT1G32350	62.49	5.97	6.81	0.000298	0.003367	0.53
252272_at	receptor protein kinase - like protein C	BAM2	AT3G49670	-3.20	-1.68	-6.81	0.000298	0.003367	0.53
261161_at	hypothetical protein contains Pfam pro	---	AT1G34420	2.59	1.38	6.81	0.000298	0.003367	0.53
255331_at	hypothetical protein ; supported by cD	---	AT4G04330	-1.76	-0.81	-6.81	0.000298	0.003367	0.53
262914_at	auxin response factor 1 identical to aux	ARF1	AT1G59750	-1.77	-0.82	-6.81	0.000299	0.003378	0.52
245029_at	hypothetical protein predicted by gens	YAB5	AT2G26580	-3.65	-1.87	-6.80	0.000301	0.003397	0.52
262665_at	xyloglucan fucosyltransferase, putativ	FUT7	AT1G14070	4.30	2.10	6.80	0.000302	0.003404	0.51
259661_at	Expressed protein ; supported by full-l	---	AT1G55265	2.08	1.06	6.80	0.000302	0.003406	0.51
262174_at	putative GDP-mannose pyrophosphory	---	AT1G74910	-2.05	-1.03	-6.79	0.000304	0.003419	0.51
255676_at	putative beta-amylase similar to the fa	BAM2	AT4G00490	-3.61	-1.85	-6.79	0.000304	0.003419	0.51
263570_at	aldehyde oxidase identical to GP:3172	AAO3	AT2G27150	2.55	1.35	6.79	0.000303	0.003419	0.51
248127_at	transport protein particle component B	---	AT5G54750	-1.62	-0.70	-6.79	0.000305	0.00343	0.50
258415_at	putative s-adenosylmethionine synthet	MTO3	AT3G17390	-3.26	-1.70	-6.79	0.000305	0.003435	0.50

253394_at	putative protein predicted protein, Syn	VTE1	AT4G32770	-2.76	-1.46	-6.79	0.000306	0.003435	0.50
255595_at	putative chitinase similar to peanut typ	---	AT4G01700	6.72	2.75	6.78	0.000306	0.003443	0.50
259393_at	trehalose-6-phosphate synthase, puta	ATTPS7	AT1G06410	-1.77	-0.82	-6.78	0.000307	0.003443	0.50
255662_at	putative protein	GPAT8	AT4G00400	-3.03	-1.60	-6.78	0.000307	0.003443	0.50
261944_at	unknown protein	---	AT1G64650	-2.06	-1.04	-6.77	0.000309	0.003464	0.49
266608_at	hypothetical protein predicted by gene	---	AT2G35500	-2.07	-1.05	-6.77	0.000309	0.003464	0.49
253886_at	cytochrome P450 - like protein cytoch	CYP709B3	AT4G27710	-1.64	-0.72	-6.77	0.000309	0.003468	0.49
262977_at	transcription factor, putative similar to	---	AT1G75490	-1.86	-0.89	-6.77	0.00031	0.003468	0.49
260793_at	unknown protein ;supported by full-len	---	AT1G06190	-1.72	-0.78	-6.77	0.00031	0.003468	0.49
266992_at	similar to Mlo proteins from H. vulgare	MLO12	AT2G39200	9.66	3.27	6.77	0.00031	0.003471	0.48
261930_at	alcohol dehydrogenase ADH, putative	---	AT1G22440	2.19	1.13	6.77	0.00031	0.003471	0.48
248828_at	Lil3 protein	---	AT5G47110	-1.58	-0.66	-6.77	0.00031	0.003471	0.48
250727_at	putative protein similar to unknown pro	---	AT5G06430	-1.62	-0.69	-6.77	0.000311	0.003474	0.48
252116_at	putative protein ;supported by full-leng	---	AT3G51510	-1.90	-0.93	-6.76	0.000311	0.003478	0.48
250330_at	putative protein	---	AT5G11810	-1.81	-0.86	-6.76	0.000313	0.003487	0.48
250470_at	(3R)-hydroxymyristoyl-[acyl carrier pro	---	AT5G10160	-1.95	-0.96	-6.76	0.000312	0.003487	0.48
254370_at	L1 specific homeobox gene ATML1/ov	ATML1	AT4G21750	-2.02	-1.02	-6.76	0.000313	0.00349	0.47
263515_at	unknown protein	---	AT2G21640	6.46	2.69	6.76	0.000313	0.003492	0.47
262342_at	unknown protein similar to hypothetica	---	AT1G64150	-2.54	-1.35	-6.76	0.000314	0.003496	0.47
247361_at	unknown protein ;supported by full-ler	---	AT5G63480	-2.01	-1.01	-6.75	0.000314	0.003497	0.47
266292_at	putative tropinone reductase ;supporte	SAG13	AT2G29350	32.79	5.04	6.75	0.000315	0.0035	0.47
250743_at	phosphate/phosphoenolpyruvate trans	---	AT5G05820	-1.81	-0.86	-6.75	0.000315	0.0035	0.47
256569_at	hypothetical protein ; supported by ful	---	AT3G19550	4.83	2.27	6.74	0.000317	0.003516	0.46
255561_at	putative hexose transporter similar to p	---	AT4G02050	2.29	1.20	6.74	0.000317	0.003516	0.46
257093_at	hypothetical protein ;supported by full-	---	AT3G20570	-2.51	-1.33	-6.74	0.000317	0.003516	0.46
245783_s_	hypothetical protein similar to hypothet	---	AT1G35170 /	-4.53	-2.18	-6.74	0.000318	0.003516	0.46
247199_at	DNA binding protein TGA1a homolog	TGA1	AT5G65210	2.95	1.56	6.74	0.000317	0.003516	0.46
253358_at	gamma-VPE (vacuolar processing enz	GAMMA-VP	AT4G32940	1.69	0.76	6.74	0.000318	0.003516	0.46
253926_at	hnRNP-like protein ; supported by cDI	---	AT4G26650	-1.65	-0.72	-6.74	0.000318	0.003516	0.46
256808_at	unknown protein	ALY3	AT3G21430	1.57	0.65	6.74	0.000317	0.003516	0.46
259323_at	unknown protein	---	AT3G05280	-1.50	-0.58	-6.74	0.000318	0.003516	0.46
249385_at	thioredoxin ; supported by full-length c	ATTRX2	AT5G39950	1.95	0.96	6.74	0.000317	0.003516	0.46
247447_at	nitrate transporter NTL1 - like protein	---	AT5G62730	-3.75	-1.91	-6.74	0.000318	0.003516	0.46
252972_at	auxin-induced protein - like auxin-indu	---	AT4G38840	-3.69	-1.88	-6.74	0.000318	0.003516	0.46
267384_at	unknown protein highly similar to GP|2	---	AT2G44370	7.96	2.99	6.74	0.000317	0.003516	0.46

267140_at	putative GT-1-like transcription factor	---	AT2G38250	2.66	1.41	6.75	0.000316	0.003516	0.46
246957_at	unknown protein	---	AT5G24670	1.53	0.61	6.73	0.00032	0.003533	0.45
266172_at	putative aquaporin (water channel prot	PIP2E	AT2G39010	-3.22	-1.69	-6.73	0.00032	0.003538	0.45
260014_at	hydroxypyruvate reductase (HPR) iden	HPR	AT1G68010	-1.87	-0.90	-6.73	0.000321	0.003539	0.45
256456_at	unknown protein ; supported by full-ler	---	AT1G75180	-2.75	-1.46	-6.72	0.000323	0.003554	0.44
262026_at	calcium-dependent protein kinase iden	ATCDPK2	AT1G35670	-1.96	-0.97	-6.72	0.000323	0.003554	0.44
258845_at	unknown protein ; supported by full-le	---	AT3G03150	-1.83	-0.87	-6.72	0.000323	0.003554	0.44
262517_at	putative glutathione transferase Secon	ATGSTU25	AT1G17180	23.33	4.54	6.72	0.000323	0.003554	0.44
258554_at	putative DEAD/DEAH box helicase co	---	AT3G06980	-1.63	-0.70	-6.72	0.000323	0.003554	0.44
254647_at	hypothetical protein	---	AT4G18540	1.52	0.60	6.72	0.000323	0.003554	0.44
265582_at	putative RING zinc finger protein	---	AT2G20030	1.88	0.91	6.72	0.000324	0.003558	0.44
260056_at	hypothetical protein predicted by gens	---	AT1G78140	-2.30	-1.20	-6.72	0.000324	0.00356	0.44
258674_at	putative elongation factor P (EF-P) sim	---	AT3G08740	-2.37	-1.25	-6.72	0.000324	0.003562	0.43
262208_at	hypothetical protein predicted by gens	---	AT1G74800	-1.86	-0.90	-6.72	0.000324	0.003563	0.43
261317_at	cytochrome C oxidase assembly prote	---	AT1G53030	1.72	0.78	6.72	0.000325	0.003565	0.43
262003_at	unknown protein	---	AT1G64460	1.74	0.80	6.72	0.000325	0.003565	0.43
249779_at	putative protein similar to unknown pro	---	AT5G24230	1.62	0.70	6.71	0.000325	0.003565	0.43
252325_at	acetolactate synthase ; supported by	CSR1	AT3G48560	-1.54	-0.62	-6.71	0.000325	0.003565	0.43
258585_at	unknown protein C-term similar to cell	emb2458	AT3G04340	-1.68	-0.75	-6.71	0.000325	0.003565	0.43
247188_at	14-3-3 protein GF14kappa (grf8) iden	GRF8	AT5G65430	-1.80	-0.84	-6.71	0.000326	0.003568	0.43
262459_at	hypothetical protein similar to hypothet	---	AT1G50400	2.05	1.04	6.71	0.000326	0.003568	0.43
257157_at	syntaxin-like protein similar to syntaxi	SYP32	AT3G24350	-2.11	-1.08	-6.71	0.000326	0.00357	0.43
255728_at	unknown protein	---	AT1G25500	2.59	1.38	6.71	0.000327	0.003576	0.43
255537_at	protoporphyrinogen oxidase ; support	PPOX	AT4G01690	-1.95	-0.97	-6.71	0.000327	0.003578	0.42
260345_at	receptor protein kinase, putative simil	RPK1	AT1G69270	2.26	1.18	6.70	0.000328	0.003585	0.42
248404_at	trehalose-6-phosphate phosphatase ;	ATTPPA	AT5G51460	-3.16	-1.66	-6.70	0.000328	0.003585	0.42
256570_at	unknown protein ; supported by cDNA	---	AT3G19540	-1.56	-0.64	-6.70	0.00033	0.003594	0.42
251379_at	putative protein various predicted Arab	---	AT3G60680	2.50	1.32	6.70	0.000329	0.003594	0.42
248773_at	kinesin-like protein	FRA1	AT5G47820	-1.97	-0.98	-6.70	0.00033	0.003594	0.42
245830_at	hypothetical protein predicted by gene	---	AT1G57790	-1.62	-0.69	-6.70	0.00033	0.003594	0.42
267161_at	hypothetical protein predicted by gene	---	AT2G37680	-1.60	-0.68	-6.70	0.000331	0.0036	0.41
267219_at	putative transport protein ;supported b	---	AT2G02590	-2.09	-1.07	-6.69	0.000331	0.003607	0.41
250728_at	putative protein similar to unknown pro	---	AT5G06440	-1.86	-0.89	-6.69	0.000331	0.003607	0.41
251342_at	putative protein SAUR-AC1, Arabidop	---	AT3G60690	2.11	1.08	6.69	0.000332	0.003608	0.41
252853_at	hypothetical protein ; supported by cDI	---	AT4G39710	-3.43	-1.78	-6.69	0.000332	0.003608	0.41

256934_at	unknown protein contains Pfam profile	---	AT3G22530	1.86	0.90	6.69	0.000333	0.003619	0.41
254343_at	PRH26 protein ;supported by full-leng	אפר-03	AT4G21990	5.32	2.41	6.69	0.000333	0.003619	0.40
258812_at	unknown protein similar to GB:AAD10(	ECT1	AT3G03950	1.84	0.88	6.69	0.000333	0.003619	0.40
263513_at	unknown protein	---	AT2G12400	-2.48	-1.31	-6.68	0.000334	0.003627	0.40
261070_at	disease resistance protein, putative si	AtRLP1	AT1G07390	1.97	0.97	6.68	0.000335	0.003631	0.40
254892_at	putative protein other hypothetical prot	---	AT4G11800	1.86	0.90	6.68	0.000335	0.003632	0.40
266004_at	unknown protein predicted by genscan	ALS3	AT2G37330	-1.55	-0.63	-6.68	0.000336	0.003636	0.40
267511_at	unknown protein	---	AT2G45670	-1.68	-0.75	-6.68	0.000336	0.003638	0.40
245330_at	hypothetical protein ;supported by full-	---	AT4G14930	1.93	0.95	6.68	0.000336	0.003638	0.40
257463_at	phosphatidylinositol/phosphatidylcholi	---	AT1G14820	-1.96	-0.97	-6.68	0.000336	0.003638	0.40
247287_at	unknown protein ; supported by cDNA	---	AT5G64230	2.73	1.45	6.68	0.000336	0.003638	0.39
258897_at	unknown protein	---	AT3G05730	-38.25	-5.26	-6.68	0.000337	0.00364	0.39
262727_at	thaumatin, putative contains Pfam pro	---	AT1G75800	-1.63	-0.71	-6.67	0.000337	0.00364	0.39
256240_at	unknown protein ; supported by cDNA	atnudt16	AT3G12600	-1.73	-0.79	-6.67	0.000337	0.003641	0.39
265868_at	unknown protein ;supported by full-ler	PUX2	AT2G01650	2.06	1.05	6.67	0.000338	0.003644	0.39
259578_at	unknown protein	---	AT1G27990	-2.33	-1.22	-6.67	0.000338	0.003644	0.39
263543_at	putative pectinesterase	PE11	AT2G21610	1.57	0.65	6.67	0.000338	0.003644	0.39
256061_at	unknown protein ;supported by full-len	---	AT1G07040	2.41	1.27	6.67	0.000338	0.003645	0.39
263529_at	ADP-ribosylation factor 3	ARF3	AT2G24765	-1.62	-0.69	-6.67	0.000338	0.003645	0.39
259058_at	putative cytochrome P450 similar to cy	CYP89A9	AT3G03470	3.42	1.77	6.67	0.000339	0.003651	0.39
261487_at	hypothetical protein predicted by gene	---	AT1G14340	1.65	0.72	6.67	0.000339	0.003651	0.39
246230_at	SCARECROW-like protein	---	AT4G36710	1.66	0.73	6.66	0.00034	0.003658	0.38
250307_at	putative protein similar to unknown pro	---	AT5G12170	2.58	1.37	6.66	0.000341	0.003663	0.38
258357_at	putative leucine-rich repeat transmemb	SRF7	AT3G14350	-2.60	-1.38	-6.66	0.000341	0.003667	0.38
260005_at	unknown protein ;supported by full-ler	---	AT1G67920	5.95	2.57	6.65	0.000343	0.003686	0.37
251951_s_	putative protein predicted proteins, Ar	---	AT1G55710 /	1.72	0.78	6.65	0.000344	0.003686	0.37
249553_at	receptor serine/threonine protein kinas	---	AT5G38260	2.13	1.09	6.65	0.000344	0.003686	0.37
247842_at	SPP30 - like protein SPP30, Solanum	---	AT5G58030	-1.57	-0.65	-6.65	0.000344	0.003686	0.37
264435_at	putative glutathione S-transferase TSI-	ATGSTU18	AT1G10360	-2.58	-1.37	-6.65	0.000345	0.003703	0.37
254384_at	heat shock protein - like heat shock pr	---	AT4G21870	-5.01	-2.32	-6.64	0.000346	0.003711	0.36
245346_at	putative beta-amylase ;supported by fu	CT-BMY	AT4G17090	-1.91	-0.93	-6.64	0.000347	0.003715	0.36
252318_at	glutamate-1-semialdehyde aminotrans	GSA2	AT3G48730	-2.32	-1.22	-6.64	0.000347	0.003715	0.36
251676_at	hypothetical protein	---	AT3G57320	-2.19	-1.13	-6.64	0.000348	0.003723	0.36
254014_at	NPR1 like protein regulatory protein N	---	AT4G26120	3.66	1.87	6.64	0.000348	0.003724	0.36
266168_at	putative protease inhibitor ;supported	---	AT2G38870	5.21	2.38	6.64	0.000349	0.003727	0.36

266163_at	hypothetical protein predicted by gens	---	AT2G28130	-2.32	-1.21	-6.64	0.000349	0.003727	0.36
247075_at	putative protein contains similarity to A	PLP3b	AT5G66410	-1.85	-0.89	-6.64	0.000349	0.003729	0.35
248094_at	trigger factor-like protein	---	AT5G55220	-2.02	-1.01	-6.63	0.00035	0.003739	0.35
245061_at	hypothetical protein ;supported by full-	RCA	AT2G39730	-1.56	-0.64	-6.63	0.00035	0.003741	0.35
249244_at	FtsH protease, putative similar to FtsH	VAR1	AT5G42270	-1.73	-0.79	-6.63	0.000351	0.003741	0.35
245695_at	rec - like protein	---	AT5G04270	-1.73	-0.79	-6.63	0.000351	0.003745	0.35
251848_at	Expressed protein ; supported by cDN	BZIP25	AT3G54620	1.74	0.80	6.63	0.000351	0.003745	0.35
263177_at	hypothetical protein predicted by gene	---	AT1G05540	-1.66	-0.73	-6.63	0.000352	0.00375	0.35
267008_at	putative ABC transporter	---	AT2G39350	-2.34	-1.23	-6.62	0.000352	0.003752	0.34
245460_at	disease resistance RPP5 like protein (	RLM3	AT4G16990	-2.85	-1.51	-6.62	0.000353	0.003755	0.34
259033_at	putative pectinacetylesterase similar to	---	AT3G09405 /	18.86	4.24	6.62	0.000353	0.003759	0.34
255923_at	hypothetical protein contains Pfam pro	---	AT1G22180	4.22	2.08	6.62	0.000354	0.003759	0.34
254938_at	putative oligopeptide transporter simil	OPT7	AT4G10770	-1.65	-0.72	-6.62	0.000354	0.003759	0.34
263132_at	unknown protein ;supported by full-len	---	AT1G78560	-1.56	-0.64	-6.62	0.000354	0.003765	0.34
253747_at	serine threonine-specific kinase like p	---	AT4G29050	2.78	1.48	6.62	0.000355	0.003771	0.33
265220_at	histidine transport protein (PTR2-B) ;	PTR2	AT2G02040	1.57	0.65	6.62	0.000355	0.003771	0.33
252573_at	zinc finger protein zinc finger protein l	---	AT3G45260	-1.70	-0.77	-6.61	0.000356	0.003775	0.33
261254_at	Expressed protein ; supported by full-l	---	AT1G05805	-1.75	-0.81	-6.61	0.000356	0.003775	0.33
262791_at	unknown protein EST gb|F13926 come	---	AT1G10830	-1.87	-0.91	-6.61	0.000357	0.003781	0.33
262745_at	lipase, putative contains Pfam profile:	---	AT1G28600	1.96	0.97	6.61	0.000357	0.003785	0.33
250498_at	microbody NAD-dependent malate deh	PMDH2	AT5G09660	-2.34	-1.23	-6.61	0.000357	0.003785	0.33
250647_at	putative protein contains similarity to u	---	AT5G06770	-1.71	-0.78	-6.61	0.000358	0.003785	0.33
264648_at	putative luminal binding protein Similar	BIP3	AT1G09080	1.99	1.00	6.60	0.000359	0.003796	0.32
257129_at	cytochrome P450, putative contains P	CYP705A19	AT3G20100	2.45	1.29	6.60	0.00036	0.003806	0.32
263931_at	unknown protein ;supported by full-ler	---	AT2G36220	3.90	1.96	6.60	0.00036	0.003807	0.32
247726_at	telomere repeat-binding protein	TRP1	AT5G59430	1.96	0.97	6.60	0.000361	0.003813	0.32
249144_at	squamosa promoter binding protein-lik	SPL2	AT5G43270	-1.74	-0.80	-6.60	0.000362	0.003816	0.32
247266_at	beta-xylosidase	XYL4	AT5G64570	2.51	1.33	6.60	0.000361	0.003816	0.32
253272_at	putative protein ;supported by full-leng	ספט-01	AT4G34190	-2.20	-1.14	-6.60	0.000362	0.003816	0.32
260688_at	hypothetical protein similar to dehydro	---	AT1G17665	1.77	0.82	6.59	0.000362	0.003818	0.31
258375_at	hypothetical protein predicted by gene	---	AT3G17470	-1.61	-0.68	-6.59	0.000363	0.003825	0.31
265141_at	hypothetical protein predicted by gens	---	AT1G51350	1.72	0.78	6.59	0.000363	0.003827	0.31
249346_at	amino acid permease	LTH1	AT5G40780	1.94	0.95	6.59	0.000364	0.003829	0.31
259430_at	hypothetical protein similar to unknown	GPAT4	AT1G01610	-2.26	-1.18	-6.59	0.000364	0.00383	0.31
262769_at	actin-like protein strong similarity to gb	DIS1	AT1G13180	-1.86	-0.90	-6.59	0.000365	0.003832	0.31

245178_at	putative protein similarity to cDNA clon	FIS1B	AT5G12390	1.59	0.67	6.59	0.000365	0.003832	0.31
265917_at	putative disease resistance protein	AtRLP19	AT2G15080	1.99	0.99	6.59	0.000364	0.003832	0.31
251246_at	auxin-induced protein homolog auxin-	IAA30	AT3G62100	-1.54	-0.62	-6.59	0.000365	0.003835	0.31
266140_at	nodulin-like protein ; supported by cDI	---	AT2G28120	-2.07	-1.05	-6.58	0.000366	0.003837	0.30
246451_at	Inositol 1,3,4-Trisphosphate 5/6 kinas	---	AT5G16760	1.53	0.61	6.58	0.000366	0.003837	0.30
254198_at	hypothetical protein	---	AT4G24090	-1.76	-0.81	-6.58	0.000365	0.003837	0.30
251663_at	putative protein hypothetical protein A	---	AT3G57070	-1.69	-0.76	-6.58	0.000366	0.00384	0.30
259364_at	DNA-binding protein RAV1 identical to	RAV1	AT1G13260	-1.84	-0.88	-6.58	0.000368	0.003862	0.30
265120_at	3-ketoacyl-acyl carrier protein synthas	KAS III	AT1G62640	-1.90	-0.93	-6.57	0.000369	0.003863	0.29
248906_at	putative protein similar to unknown pro	---	AT5G46420	-1.66	-0.73	-6.57	0.00037	0.003871	0.29
249152_s_	inorganic phosphate transporter (dbj|B	APT1	AT5G43350 /	2.24	1.16	6.57	0.00037	0.003871	0.29
246909_at	putative protein predicted protein, Ory	---	AT5G25770	3.59	1.84	6.57	0.00037	0.003876	0.29
267034_at	unknown protein ;supported by full-ler	---	AT2G38310	-4.94	-2.30	-6.57	0.000371	0.003884	0.29
267314_at	putative myosin heavy chain	---	AT2G34730	2.04	1.03	6.56	0.000372	0.003892	0.28
265342_at	hypothetical protein predicted by gens	---	AT2G18300	-2.71	-1.44	-6.56	0.000373	0.003894	0.28
246488_at	steroid 5alpha-reductase-like protein s	---	AT5G16010	-2.64	-1.40	-6.56	0.000373	0.003899	0.28
255232_at	putative protein phosphatidylinositol-3	AGD13	AT4G05330	-2.06	-1.04	-6.56	0.000375	0.003908	0.28
261273_at	unknown protein ; supported by cDNA	---	AT1G26650	-2.24	-1.16	-6.56	0.000375	0.003908	0.28
266289_at	putative C-4 sterol methyl oxidase ;su	SMO2-2	AT2G29390	-1.65	-0.73	-6.56	0.000375	0.003908	0.28
262397_at	hypothetical protein predicted by gene	---	AT1G49380	-2.46	-1.30	-6.56	0.000375	0.003908	0.28
262366_at	disease resistance protein, putative si	---	AT1G72890	3.83	1.94	6.55	0.000375	0.003909	0.27
266400_at	methylenetetrahydrofolate dehydrogen	---	AT2G38660	1.54	0.63	6.55	0.000375	0.003909	0.27
264512_at	Expressed protein ; supported by cDN	---	AT1G09575	-1.80	-0.85	-6.55	0.000376	0.003909	0.27
245692_at	myc - like protein	BHLH101	AT5G04150	-2.10	-1.07	-6.55	0.000376	0.00391	0.27
266887_at	unknown protein ; supported by cDNA	CHL-CPN10	AT2G44650	-1.89	-0.92	-6.55	0.000376	0.00391	0.27
266503_at	unknown protein	---	AT2G47780	-2.94	-1.55	-6.55	0.000376	0.003912	0.27
246198_at	geranylgeranyl pyrophosphate synthas	GGPS1	AT4G36810	-2.02	-1.02	-6.55	0.000376	0.003912	0.27
267425_at	putative berberine bridge enzyme	---	AT2G34810	5.09	2.35	6.55	0.000377	0.003915	0.27
252969_at	putative protein vsf-1 protein, Lycoper	---	AT4G38900	-1.63	-0.70	-6.55	0.000378	0.003918	0.27
251815_at	putative protein thioredoxin-like protei	CXIP1	AT3G54900	-1.85	-0.89	-6.55	0.000377	0.003918	0.27
262920_at	2-dehydro-3-deoxyphosphooctonate a	---	AT1G79500	-3.30	-1.72	-6.55	0.000378	0.003923	0.27
247801_at	putative protein ; supported by full-leng	---	AT5G58560	-1.71	-0.77	-6.54	0.000379	0.00393	0.26
254260_at	hypothetical protein	---	AT4G23440	-2.27	-1.18	-6.54	0.000379	0.003931	0.26
258269_at	putative acetyl-CoA carboxylase biotin	---	AT3G15690	-1.64	-0.72	-6.54	0.00038	0.003937	0.26
260356_at	unknown protein ; supported by full-le	ATMINE1	AT1G69390	-1.67	-0.74	-6.54	0.00038	0.003938	0.26

245006_at	PSI P700 apoprotein A2	---	---	-1.48	-0.57	-6.54	0.000381	0.003941	0.26
258406_at	hypothetical protein similar to hypothet	ATRBL14	AT3G17611	1.50	0.58	6.54	0.000381	0.003942	0.26
262099_s_	auxin-regulated protein GH3, putative	GH3.4	AT1G59500 /	18.07	4.18	6.53	0.000383	0.003958	0.25
253224_at	invertase - like protein mRNA, Lilium l	---	AT4G34860	2.26	1.17	6.53	0.000384	0.003964	0.25
260985_at	dTDP-D-glucose 4,6-dehydratase, put	MUM4	AT1G53500	-1.78	-0.83	-6.53	0.000385	0.003973	0.25
255931_at	hypothetical protein similar to putative	AtPP2-A12	AT1G12710	-2.43	-1.28	-6.53	0.000385	0.003974	0.25
261154_at	unknown protein ;supported by full-len	---	AT1G04970	2.00	1.00	6.52	0.000387	0.00399	0.24
255061_at	putative protein disulfide isomerase	ATAPRL6	AT4G08930	-1.55	-0.63	-6.52	0.000387	0.00399	0.24
259358_at	hypothetical protein similar to putative	GATL3	AT1G13250	-4.97	-2.31	-6.52	0.000387	0.003991	0.24
266329_at	unknown protein ; supported by cDNA	CRR3	AT2G01590	-2.89	-1.53	-6.52	0.000387	0.003991	0.24
248338_at	HCF106 (gb|AAD32652.1) ; supported	HCF106	AT5G52440	-1.84	-0.88	-6.52	0.000388	0.003991	0.24
248770_at	unknown protein	---	AT5G47740	1.91	0.94	6.52	0.000387	0.003991	0.24
267526_at	photosystem II reaction center 6.1KD p	PSBW	AT2G30570	-1.49	-0.58	-6.52	0.000388	0.003991	0.24
253189_at	putative protein	---	AT4G35335	-2.25	-1.17	-6.52	0.000388	0.003995	0.24
264824_at	unknown protein similar to gb|T45484	2A6	---	-2.34	-1.23	-6.51	0.000391	0.004017	0.23
252647_at	protein-tyrosine-phosphatase-like prot	---	AT3G44620	-2.32	-1.22	-6.50	0.000393	0.004044	0.22
252859_at	putative protein AP2 domain containin	---	AT4G39780	2.39	1.26	6.50	0.000394	0.004049	0.22
247246_at	invertase inhibitor homolog (emb|CAA	C/VIF2	AT5G64620	-2.55	-1.35	-6.50	0.000395	0.004053	0.22
258787_at	hypothetical protein predicted by gens	PUB24	AT3G11840	11.23	3.49	6.50	0.000395	0.004055	0.22
251019_at	putative protein predicted proteins, Ar	---	AT5G02420	1.75	0.81	6.50	0.000396	0.004063	0.22
258282_at	unknown protein	---	AT3G26910	4.00	2.00	6.49	0.000396	0.004063	0.22
251325_s_	Lhca2 protein ;supported by full-length	LHCA2	AT3G61470 /	-1.48	-0.57	-6.49	0.000397	0.004066	0.21
256516_at	receptor protein kinase (TMK1), putati	TMK1	AT1G66150	-2.35	-1.23	-6.49	0.000397	0.004072	0.21
248639_at	anthranilate N-benzoyltransferase ;su	HCT	AT5G48930	2.32	1.21	6.49	0.000398	0.004079	0.21
252131_at	BCS1 protein-like protein Homo sapie	BCS1	AT3G50930	11.77	3.56	6.49	0.000398	0.004079	0.21
247763_at	RNA polymerase II	NRPB7	AT5G59180	1.68	0.75	6.49	0.000399	0.004084	0.21
261919_at	type 2 peroxiredoxin, putative similar t	TPX1	AT1G65980	1.82	0.87	6.49	0.0004	0.004086	0.21
267448_at	putative protein phosphatase 2C	---	AT2G33700	1.52	0.60	6.48	0.0004	0.004086	0.21
250843_at	putative RNA-binding protein astrocyti	BTR1L	AT5G04430	-1.59	-0.67	-6.48	0.0004	0.004086	0.21
253956_at	fimbrin-like protein (ATFIM1) ; support	FIM1	AT4G26700	-2.44	-1.28	-6.48	0.0004	0.004086	0.20
251930_at	putative protein several hypothetical pr	ATRBL4	AT3G53780	1.88	0.91	6.48	0.0004	0.004086	0.20
248568_at	receptor protein kinase-like	---	AT5G49760	1.85	0.88	6.48	0.0004	0.004086	0.20
262248_at	hypothetical protein predicted by gens	YSL8	AT1G48370	2.70	1.43	6.48	0.000401	0.004086	0.20
256589_at	cytochrome P450, putative contains P	CYP81D1	AT3G28740	13.98	3.80	6.48	0.000401	0.004091	0.20
266270_at	putative glutathione S-transferase ; su	ATGSTU3	AT2G29470	30.68	4.94	6.48	0.000402	0.004098	0.20

247609_at	cleavage stimulation factor 50K chain	---	AT5G60940	-1.67	-0.74	-6.48	0.000402	0.004098	0.20
251272_at	homeobox-leucine zipper protein ATHI	ATHB-12	AT3G61890	4.40	2.14	6.48	0.000403	0.004105	0.20
247545_at	putative protein rhoGAP, Homo sapie	---	AT5G61530	1.59	0.67	6.47	0.000405	0.004126	0.19
258568_at	unknown protein contains Pfam profile	---	AT3G04470	-1.67	-0.74	-6.46	0.000409	0.004155	0.18
247830_at	putative protein predicted proteins, Ar	---	AT5G58530	-2.26	-1.18	-6.46	0.000409	0.004155	0.18
259178_at	unknown protein similar to hypothetica	RGLG1	AT3G01650	1.95	0.96	6.46	0.000409	0.004155	0.18
258489_at	14-3-3 protein GF14nu (grf7) identical	GRF7	AT3G02520	1.56	0.64	6.46	0.00041	0.004156	0.18
262245_at	unknown protein	NPSN12	AT1G48240	-1.95	-0.96	-6.46	0.000409	0.004156	0.18
264766_at	receptor kinase, putative similar to rec	---	AT1G61420	3.17	1.67	6.46	0.000409	0.004156	0.18
262411_at	hypothetical protein predicted by gene	---	AT1G34640	-1.73	-0.79	-6.46	0.000409	0.004156	0.18
264568_at	putative O-GlcNAc transferase similar	---	AT1G05150	-1.92	-0.94	-6.46	0.00041	0.004156	0.18
254686_at	putative protein putative oncogene pr	---	AT4G13720	-1.78	-0.83	-6.46	0.00041	0.004156	0.18
256770_at	hypothetical protein predicted by gene	---	AT3G13700 /	-1.97	-0.98	-6.46	0.00041	0.004157	0.18
251919_at	putative protein Hsp70 binding protein	---	AT3G53800	-2.24	-1.16	-6.46	0.00041	0.004157	0.18
257674_at	translational inhibitor protein, putative	---	AT3G20390	-1.62	-0.69	-6.46	0.000411	0.004158	0.18
256451_s_	unknown protein	---	AT1G75170 /	4.20	2.07	6.45	0.000411	0.004164	0.17
252075_at	putative protein saposin precursor - H	---	AT3G51730	2.03	1.02	6.45	0.000413	0.004172	0.17
260979_at	MAP kinase ATMPK9, putative similar	ATMPK18	AT1G53510	-1.62	-0.69	-6.45	0.000412	0.004172	0.17
250354_at	putative protein predicted proteins, Dr	---	AT5G11640	-1.66	-0.73	-6.45	0.000414	0.004183	0.17
264158_at	hypothetical protein contains similarity	PTAC4	AT1G65260	-1.88	-0.91	-6.44	0.000415	0.004192	0.16
250985_at	putative protein various predicted prot	---	AT5G02830	1.58	0.66	6.44	0.000416	0.004198	0.16
248718_at	farnesyl diphosphate synthase precurs	FPS1	AT5G47770	-2.29	-1.19	-6.44	0.000416	0.004198	0.16
247601_at	zinc finger protein OBP4 - like zinc fin	OBP4	AT5G60850	-2.18	-1.12	-6.44	0.000416	0.004198	0.16
255809_at	putative protein predicted protein, Ara	---	AT4G10300	-1.81	-0.85	-6.44	0.000416	0.004198	0.16
245339_at	hypothetical protein ;supported by full-	COBL7	AT4G16120	-2.60	-1.38	-6.44	0.000417	0.004202	0.16
248152_at	DNA repair and meiosis protein Mre11	MRE11	AT5G54260	-2.05	-1.03	-6.44	0.000418	0.004208	0.16
249064_at	putative protein contains similarity to u	---	AT5G44250	-1.54	-0.62	-6.44	0.000418	0.00421	0.16
246552_at	putative protein	---	AT5G15420	-2.79	-1.48	-6.43	0.000419	0.004222	0.15
250515_at	putative protein	---	AT5G09570	1.46	0.54	6.43	0.00042	0.004228	0.15
262640_at	hypothetical protein	---	AT1G62760	55.43	5.79	6.43	0.00042	0.004229	0.15
265849_at	hypothetical protein predicted by gens	---	AT2G35736	2.09	1.06	6.43	0.000421	0.004229	0.15
254535_at	aspartate kinase-homoserine dehydro	AK-HSDH II	AT4G19710	-1.58	-0.66	-6.43	0.000421	0.004229	0.15
253066_at	1-aminocyclopropane-1-carboxylate s	ACS8	AT4G37770	-9.91	-3.31	-6.43	0.000421	0.004229	0.15
263628_at	unknown protein ;supported by full-ler	FLA7	AT2G04780	-6.62	-2.73	-6.42	0.000422	0.004241	0.14
252970_at	small auxin up RNA (SAUR-AC1) ;sup	SAUR15	AT4G38850	-2.38	-1.25	-6.42	0.000423	0.004245	0.14

246384_at	glutaredoxin, putative similar to glutar	---	AT1G77370	1.56	0.64	6.42	0.000424	0.00425	0.14
251969_at	Cytochrom P450 -like protein CYTOC	LUT1	AT3G53130	-1.94	-0.95	-6.42	0.000424	0.00425	0.14
265844_at	putative receptor-like protein kinase	FEI2	AT2G35620	-2.10	-1.07	-6.42	0.000424	0.00425	0.14
259175_at	unknown protein	---	AT3G01560	-1.84	-0.88	-6.41	0.000427	0.004273	0.13
258162_at	dehydrogenase, putative similar to dih	---	AT3G17810	2.03	1.02	6.41	0.000427	0.004273	0.13
251107_at	putative protein several hypothetical pr	---	AT5G01610	1.84	0.88	6.41	0.000428	0.00428	0.13
249322_at	protein import receptor TOM20, mitoc	TOM20-4	AT5G40930	1.54	0.63	6.41	0.000429	0.004293	0.13
249284_at	unknown protein ;supported by full-ler	---	AT5G41810	1.74	0.80	6.41	0.000429	0.004293	0.13
257253_at	unknown protein ; supported by cDNA	---	AT3G24190	-1.74	-0.80	-6.41	0.000429	0.004293	0.13
251834_at	ribosomal protein L35 -like various ribo	---	AT3G55170	-1.63	-0.71	-6.40	0.00043	0.004297	0.13
266606_at	putative AP2 domain transcription fact	CRF5	AT2G46310	2.52	1.33	6.40	0.000431	0.004301	0.12
251291_at	putative protein auxin-induced protein	---	AT3G61900	1.63	0.71	6.40	0.000432	0.004313	0.12
262309_at	phosphoglucomutase, putative similar	---	AT1G70820	-2.84	-1.51	-6.40	0.000432	0.004315	0.12
250293_s_	auxin reponsive - like protein Nt-gh3 d	---	AT5G13360 /	3.29	1.72	6.40	0.000433	0.004315	0.12
251941_at	putative protein ribosomal protein S25	---	AT3G53470	-1.67	-0.74	-6.40	0.000433	0.004315	0.12
257267_at	unknown protein similar to TCP3 GB:A	TCP4	AT3G15030	-1.76	-0.81	-6.40	0.000433	0.004315	0.12
267202_s_	putative oxysterol-binding protein	ORP1A	AT2G31020 /	2.37	1.24	6.40	0.000433	0.004315	0.12
251140_at	lectin - like protein lectin precursor LE	---	AT5G01090	-1.74	-0.80	-6.39	0.000434	0.004323	0.11
263491_at	phosphoenolpyruvate carboxylase	ATPPC2	AT2G42600	-1.76	-0.82	-6.39	0.000435	0.004328	0.11
251023_at	putative protein amino acid transport p	---	AT5G02170	-1.78	-0.83	-6.39	0.000435	0.004328	0.11
247453_at	putative protein similar to unknown pro	---	AT5G62440	1.94	0.96	6.39	0.000437	0.004344	0.11
266154_at	putative cytochrome p450	---	AT2G12190	2.14	1.10	6.39	0.000437	0.004347	0.11
246110_at	putative protein predicted proteins - Ar	---	AT5G20140	-2.26	-1.18	-6.39	0.000438	0.004347	0.11
249306_at	RING zinc finger protein-like ;supporte	---	AT5G41400	3.74	1.90	6.38	0.000439	0.004353	0.10
249703_at	putative protein strong similarity to unk	---	AT5G35560	1.55	0.64	6.38	0.000439	0.004353	0.10
262230_at	alpha-xylosidase precursor identical to	XYL1	AT1G68560	-3.29	-1.72	-6.38	0.000439	0.004353	0.10
264199_at	unknown protein contains similarity to	---	AT1G22700	-1.76	-0.82	-6.38	0.000439	0.004353	0.10
251801_at	cytosolic triosephosphatisomerase ;su	TPI	AT3G55440	-1.48	-0.57	-6.38	0.000439	0.004356	0.10
254910_at	translation initiation factor IF-1, putativ	---	AT4G11175	-1.56	-0.65	-6.38	0.00044	0.004356	0.10
246026_at	putative protein predicted protein - Ory	---	AT5G21070	-1.65	-0.72	-6.38	0.00044	0.00436	0.10
256812_at	hypothetical protein contains similarity	---	AT3G21350	-1.57	-0.65	-6.38	0.000441	0.004362	0.10
262708_at	UV-sensitive rad23, putative similar to	---	AT1G16190	-1.53	-0.61	-6.38	0.000441	0.004365	0.10
263597_at	hypothetical protein predicted by gens	---	AT2G01870	-3.60	-1.85	-6.38	0.000441	0.004365	0.10
264757_at	receptor protein kinase (IRK1), putativ	---	AT1G61360	9.00	3.17	6.37	0.000442	0.004366	0.09
258925_at	unknown protein similar to hypothetica	---	AT3G10420	1.84	0.88	6.38	0.000442	0.004366	0.10

245806_at	light-harvesting complex protein simila	LHCA5	AT1G45474	-2.40	-1.26	-6.37	0.000442	0.004366	0.09
257317_at	hypothetical protein	AT2G07743	---	1.78	0.83	6.37	0.000442	0.004366	0.09
263755_at	unknown protein ;supported by full-ler	---	AT2G21340	-1.97	-0.98	-6.38	0.000442	0.004366	0.10
253484_at	Transcription factor II homolog ;suppo	TAFII15	AT4G31720	-1.53	-0.62	-6.37	0.000443	0.004366	0.09
264698_at	unknown protein	---	AT1G70200	-1.65	-0.72	-6.37	0.000443	0.004371	0.09
266873_at	putative PREG1-like negative regulato	CYCP4;1	AT2G44740	-6.02	-2.59	-6.37	0.000444	0.004373	0.09
251144_at	anthranilate N-benzoyltransferase - lik	---	AT5G01210	2.75	1.46	6.37	0.000444	0.004374	0.09
256064_at	Expressed protein ; supported by full-l	---	AT1G07020	-1.66	-0.73	-6.37	0.000444	0.004374	0.09
249550_at	protein kinase - like protein wall-assoc	---	AT5G38210	2.77	1.47	6.37	0.000445	0.004377	0.09
266616_at	putative CDC6 protein ; supported by	CDC6	AT2G29680	-1.61	-0.68	-6.37	0.000445	0.004383	0.09
259402_at	developmental protein, putative simila	VPS46.1	AT1G17730	-1.60	-0.67	-6.36	0.000448	0.004403	0.08
259499_at	PRLI-interacting factor L, putative sim	---	AT1G15730	-1.91	-0.94	-6.36	0.000448	0.004403	0.08
245211_at	putative protein similarity to sec10, Dr	SEC10	AT5G12370	-1.49	-0.57	-6.36	0.000448	0.004407	0.08
254601_at	putative protein DNA (cytosine-5-)-me	CMT2	AT4G19020	-2.17	-1.12	-6.36	0.000449	0.004411	0.08
267430_at	unknown protein	EDA3	AT2G34860	-2.14	-1.10	-6.36	0.000449	0.004411	0.08
251819_at	phosphatidylglycerophosphate syntha	PGPS2	AT3G55030	-1.70	-0.76	-6.36	0.00045	0.004415	0.08
253373_at	lysine-ketoglutarate reductase/saccha	---	AT4G33150	4.35	2.12	6.35	0.000451	0.004422	0.07
252449_at	FtsH protease, putative contains simil	ftsh7	AT3G47060	1.50	0.58	6.35	0.000451	0.004425	0.07
257087_at	purple acid phosphatase, putative sim	PAP18	AT3G20500	1.81	0.85	6.35	0.000453	0.004438	0.07
257083_s_	non-race specific disease resistance p	---	AT3G20590 /	2.55	1.35	6.35	0.000453	0.004438	0.07
257185_at	ABC transporter, putative similar to At	ATMRP7	AT3G13100	2.43	1.28	6.35	0.000453	0.00444	0.07
259545_at	hypothetical protein ; supported by cDI	AAE1	AT1G20560	1.69	0.75	6.34	0.000457	0.00447	0.06
262910_at	unknown protein ;supported by full-len	---	AT1G59710	-2.01	-1.01	-6.34	0.000457	0.004472	0.06
262846_at	endomembrane protein, putative simil	---	AT1G14670	-1.72	-0.78	-6.34	0.000458	0.004479	0.06
253286_at	hypothetical protein	FUC95A	AT4G34260	-7.80	-2.96	-6.34	0.000458	0.004479	0.06
264298_at	hypothetical protein contains similarity	---	AT1G78690	-1.67	-0.74	-6.34	0.000459	0.004479	0.05
253966_at	fructose-bisphosphate aldolase	---	AT4G26520	-1.96	-0.97	-6.34	0.000459	0.004479	0.06
255611_at	hypothetical protein	---	AT4G01210	-1.57	-0.65	-6.33	0.000459	0.004481	0.05
251722_at	putative protein neuronal glutamine tra	---	AT3G56200	2.55	1.35	6.33	0.000459	0.004481	0.05
266824_at	homeodomain transcription factor (HA	HAT9	AT2G22800	1.60	0.67	6.33	0.00046	0.004484	0.05
267355_at	putative LIM-domain protein	---	AT2G39900	-2.02	-1.01	-6.33	0.00046	0.004484	0.05
257919_at	myb-related transcription factor, putati	MYB15	AT3G23250	15.50	3.95	6.33	0.000461	0.00449	0.05
248385_at	putative protein contains similarity to D	---	AT5G51910	-1.87	-0.90	-6.33	0.000461	0.004492	0.05
265989_at	unknown protein	---	AT2G24260	1.60	0.68	6.33	0.000461	0.004492	0.05
245877_at	unknown protein	---	AT1G26220	-2.01	-1.01	-6.33	0.000462	0.004497	0.05

246799_at	putative protein various predicted bact	---	AT5G26940	2.00	1.00	6.33	0.000462	0.004497	0.05
257045_at	dynamin-like protein similar to phragm	ARC5	AT3G19720	-2.28	-1.19	-6.33	0.000462	0.004497	0.05
263218_at	putative serine/threonine protein kinas	---	AT1G30570	-1.95	-0.97	-6.32	0.000463	0.004506	0.04
244986_at	ribosomal protein S19	---	---	-2.26	-1.17	-6.32	0.000464	0.004506	0.04
257750_at	unknown protein ;supported by full-ler	---	AT3G18800	-1.80	-0.85	-6.32	0.000465	0.004511	0.04
252827_at	cytochrome P450 - like protein cytoch	CYP79B2	AT4G39950	8.79	3.14	6.32	0.000465	0.004511	0.04
263066_at	unknown protein	---	AT2G17540	-1.50	-0.58	-6.32	0.000466	0.004521	0.04
258679_at	putative 2,3-bisphosphoglycerate-inde	---	AT3G08590	2.70	1.43	6.32	0.000467	0.004531	0.03
251141_at	Expressed protein ; supported by full-l	---	AT5G01075	-2.60	-1.38	-6.31	0.000468	0.004533	0.03
258421_at	MtN3-like protein similar to MtN3 GB:C	---	AT3G16690	-2.77	-1.47	-6.31	0.000469	0.004533	0.03
254688_at	DnaJ-like protein DnaJ-like protein, PI	J20	AT4G13830	-1.63	-0.71	-6.31	0.000468	0.004533	0.03
256856_at	Expressed protein ; supported by full-l	---	AT3G15110	-2.11	-1.08	-6.31	0.000468	0.004533	0.03
255720_at	phosphoribulokinase precursor identic	PRK	AT1G32060	-1.70	-0.76	-6.31	0.000468	0.004533	0.03
260972_at	hypothetical protein contains similarity	---	AT1G53530	-1.65	-0.72	-6.31	0.000469	0.004533	0.03
266120_at	putative C2H2-type zinc finger protein	AtIDD5	AT2G02070	-1.72	-0.79	-6.31	0.000468	0.004533	0.03
255657_at	acidic ribosomal protein p1 similar to a	---	AT4G00810	-1.78	-0.83	-6.31	0.000469	0.004538	0.03
247679_at	1-aminocyclopropane-1-carboxylate o	---	AT5G59540	2.90	1.54	6.31	0.000471	0.004541	0.03
259787_at	auxin-induced protein, putative similar	---	AT1G29460	-4.76	-2.25	-6.31	0.000471	0.004541	0.03
253096_at	cytochrome P450-like protein	CYP81D4	AT4G37330	1.75	0.81	6.31	0.00047	0.004541	0.03
267535_at	putative C2H2-type zinc finger protein	ZFP8	AT2G41940	-2.58	-1.37	-6.31	0.000471	0.004541	0.03
257178_at	hemolysin-like protein similar to hemol	---	AT3G13070	1.74	0.80	6.31	0.000471	0.004541	0.03
251082_at	chlorophyll a/b-binding protein CP29 ;	---	AT5G01530	-1.46	-0.54	-6.31	0.000471	0.004541	0.03
264381_at	putative ribonuclease large subunit sir	---	AT2G25100	-2.16	-1.11	-6.31	0.00047	0.004541	0.03
247632_at	protein transport protein subunit - like	---	AT5G60460	1.78	0.83	6.30	0.000473	0.004553	0.02
247389_at	putative protein strong similarity to unk	---	AT5G63490	2.03	1.02	6.30	0.000473	0.004553	0.02
259825_at	RNA and export factor binding protein	---	AT1G66260	-1.89	-0.92	-6.30	0.000473	0.004556	0.02
260878_at	scarecrow-like 1 identical to scarecrow	SCL1	AT1G21450	2.06	1.04	6.30	0.000473	0.004556	0.02
261653_at	subtilisin-like serine protease, putative	SBTI1.1	AT1G01900	-3.52	-1.81	-6.30	0.000474	0.004557	0.02
257556_at	hypothetical protein predicted by gene	---	AT3G28100	3.61	1.85	6.30	0.000474	0.004559	0.02
250512_at	Expressed protein ; supported by full-l	---	AT5G09995	-1.78	-0.83	-6.30	0.000475	0.004561	0.02
260580_at	unknown protein	---	AT2G47390	1.51	0.60	6.30	0.000475	0.004561	0.02
250262_at	putative protein peptidyl-prolyl cis-tran	---	AT5G13410	-2.43	-1.28	-6.30	0.000475	0.004561	0.02
247903_at	unknown protein ; supported by cDNA	---	AT5G57340	-1.92	-0.94	-6.29	0.000476	0.004571	0.01
250090_at	glutamate decarboxylase 1 (GAD 1) (s	GAD	AT5G17330	10.10	3.34	6.29	0.000476	0.004572	0.01
256803_at	cytochrome P450, putative similar to c	CYP705A33	AT3G20960	1.55	0.63	6.29	0.000479	0.004595	0.01

267368_at	citrate synthase similar to GB:X17528	ATCS	AT2G44350	1.76	0.82	6.29	0.000479	0.004597	0.01
247734_at	putative protein predicted protein, Ara	---	AT5G59400	1.72	0.78	6.28	0.000481	0.004607	0.00
244933_at	NADH dehydrogenase ND4L	---	---	-1.71	-0.77	-6.28	0.000482	0.004613	0.00
266294_at	putative small heat shock protein ;sup	---	AT2G29500	10.16	3.34	6.28	0.000484	0.004628	0.00
263231_at	putative indole-3-acetate beta-glucosy	---	AT1G05680	82.88	6.37	6.28	0.000484	0.004628	0.00
254999_at	putative protein ; supported by full-len	---	AT4G09830	1.94	0.95	6.28	0.000484	0.004628	-0.01
250314_at	putative protein contains similarity to R	---	AT5G12190	1.55	0.63	6.28	0.000485	0.004628	-0.01
248495_at	putative protein strong similarity to unk	---	AT5G50780	1.79	0.84	6.28	0.000483	0.004628	0.00
253922_at	putative protein ; supported by cDNA:	VTC2	AT4G26850	2.18	1.12	6.28	0.000485	0.004628	-0.01
253796_at	hypothetical protein	---	AT4G28460	13.94	3.80	6.28	0.000485	0.004628	-0.01
253697_at	nucleotide pyrophosphatase -like prot	---	AT4G29700	14.78	3.89	6.28	0.000484	0.004628	0.00
255068_at	Arabidopsis thaliana flavin-type blue-li	CRY1	AT4G08920	-1.49	-0.57	-6.28	0.000485	0.004628	-0.01
247575_at	RNA-binding protein - like RNA-bindin	GR-RBP3	AT5G61030	1.95	0.97	6.27	0.000485	0.00463	-0.01
267607_s_	epoxide hydrolase (ATsEH) identical to	ATSEH	AT2G26740 /	-2.49	-1.31	-6.27	0.000486	0.004631	-0.01
253569_at	receptor kinase - like protein receptor	---	AT4G31250	-1.84	-0.88	-6.27	0.000486	0.004631	-0.01
256524_at	glutamine synthetase, putative similar	ATGSR2	AT1G66200	1.71	0.77	6.27	0.000486	0.004634	-0.01
259788_at	lipase/hydrolase, putative contains Pfa	---	AT1G29670	-7.92	-2.99	-6.27	0.000487	0.004635	-0.01
264583_at	putative AVR9 elicitor response protein	---	AT1G05170	1.89	0.92	6.27	0.000487	0.004635	-0.01
267262_at	putative serine carboxypeptidase I ; su	SNG1	AT2G22990	-2.07	-1.05	-6.27	0.000487	0.004635	-0.01
244974_at	PSII low MW protein	---	---	-1.65	-0.72	-6.27	0.000487	0.004635	-0.01
247154_at	receptor protein kinase-like protein	HSL2	AT5G65710	-1.59	-0.67	-6.27	0.00049	0.004654	-0.02
249052_at	antifungal protein-like (PDF1.2)	PDF1.2	AT5G44420	8.88	3.15	6.26	0.000491	0.004661	-0.02
249016_at	putative protein contains similarity to D	REV1	AT5G44750	1.91	0.93	6.26	0.000491	0.004661	-0.02
254515_at	CLV1 receptor kinase like protein CLA	BAM3	AT4G20270	-1.61	-0.69	-6.26	0.000491	0.004661	-0.02
247278_at	fructose-bisphosphatase-like protein ;	---	AT5G64380	-1.83	-0.87	-6.26	0.000492	0.004668	-0.02
250012_x_	auxin-induced protein-like	---	AT5G18060	-14.48	-3.86	-6.26	0.000493	0.004676	-0.02
AFFX-Atha	Arabidopsis thaliana /REF=M64116 /D	GAPC1	---	2.19	1.13	6.26	0.000494	0.004685	-0.03
258072_at	unknown protein	RGS1	AT3G26090	1.54	0.62	6.25	0.000494	0.004685	-0.03
254917_at	putative protein various hypothetical pr	---	AT4G11350	2.22	1.15	6.25	0.000494	0.004685	-0.03
258917_at	unknown protein C-terminal portion sin	---	AT3G10630	-1.46	-0.55	-6.25	0.000495	0.004693	-0.03
264736_at	oligopeptide transporter, putative simi	---	AT1G62200	1.96	0.97	6.25	0.000498	0.004711	-0.03
258955_s_	unknown protein ;supported by full-ler	---	AT3G01450 /	-1.93	-0.95	-6.25	0.000498	0.004711	-0.03
254894_at	putative phospholipase D-gamma pho	PLDGAMMA	AT4G11840	2.13	1.09	6.25	0.000498	0.004713	-0.04
262489_at	unknown protein EST gb|T21171 come	---	AT1G21830	-1.99	-0.99	-6.24	0.000502	0.004745	-0.04
247563_at	putative protein various predicted prot	PDCB1	AT5G61130	-1.94	-0.96	-6.24	0.000502	0.004745	-0.04

256735_at	hypothetical protein predicted by gene	ATEXO70E1	AT3G29400	1.82	0.86	6.24	0.000502	0.004745	-0.04
261248_at	calreticulin, putative similar to GB:AAF	---	AT1G20030	-3.63	-1.86	-6.24	0.000503	0.004752	-0.05
246228_at	peroxidase like protein	---	AT4G36430	7.12	2.83	6.24	0.000503	0.004752	-0.05
263199_at	hypothetical protein Similar to hexosa	HEXO2	AT1G05590	-1.93	-0.95	-6.23	0.000505	0.004762	-0.05
258133_at	ethylene-responsive transcriptional co	MBF1C	AT3G24500	2.02	1.02	6.23	0.000505	0.004762	-0.05
249139_at	Cys2/His2-type zinc finger protein 3 (d	AZF3	AT5G43170	3.02	1.59	6.23	0.000506	0.00477	-0.05
261717_at	helix-loop-helix protein homolog, puta	BEE1	AT1G18400	-6.27	-2.65	-6.23	0.000506	0.004771	-0.05
264611_at	putative pectate lyase A11 similar to G	---	AT1G04680	-7.53	-2.91	-6.23	0.000507	0.004776	-0.06
267532_at	unknown protein ;supported by full-ler	---	AT2G42040	-2.35	-1.24	-6.23	0.000508	0.004781	-0.06
256262_at	unknown protein	---	AT3G12150	-1.87	-0.90	-6.23	0.000508	0.004781	-0.06
255587_at	putative inorganic phosphatase ; supp	AtPPa5	AT4G01480	1.95	0.97	6.23	0.000508	0.004781	-0.06
259965_at	transcriptional regulator, putative foun	MSRB1	AT1G53670	-1.85	-0.88	-6.22	0.000508	0.004782	-0.06
267136_at	putative GTP-binding protein (extra lar	XLG1	AT2G23460	-1.68	-0.75	-6.22	0.000509	0.004783	-0.06
256754_at	unknown protein	CHUP1	AT3G25690	-1.74	-0.80	-6.22	0.000511	0.004799	-0.06
258729_at	putative amino acid transporter protein	ANT1	AT3G11900	1.55	0.63	6.22	0.000511	0.004799	-0.06
259688_at	membrane protein, putative similar to	ATRBL2	AT1G63120	-2.14	-1.10	-6.22	0.000511	0.0048	-0.06
265735_at	putative aldolase ;supported by full-ler	---	AT2G01140	2.10	1.07	6.22	0.000513	0.004814	-0.07
245796_at	unknown protein similar to unknown pr	RCD1	AT1G32230	1.65	0.72	6.21	0.000513	0.004816	-0.07
257628_at	cytochrome P450, putative contains P	CYP71B26	AT3G26290	2.96	1.57	6.21	0.000515	0.004826	-0.07
265674_at	unknown protein ; supported by full-le	---	AT2G32190	4.89	2.29	6.21	0.000515	0.004829	-0.07
264000_at	putative mitochondrial dicarboxylate ca	UCP5	AT2G22500	6.49	2.70	6.21	0.000515	0.004829	-0.07
260770_at	RING-H2 finger protein RHA3a, putati	---	AT1G49200	-8.89	-3.15	-6.21	0.000516	0.004834	-0.07
258570_at	phosphoenolpyruvate carboxylase kin	PPCK2	AT3G04530	1.85	0.89	6.21	0.000517	0.004842	-0.08
257466_at	hypothetical protein predicted by gene	---	AT1G62840	3.58	1.84	6.20	0.000518	0.004851	-0.08
255946_at	glycine hydroxymethyltransferase, put	SHM6	AT1G22020	1.46	0.55	6.20	0.000519	0.004851	-0.08
253113_at	putative protein physical impedance ir	---	AT4G35985	-2.36	-1.24	-6.20	0.000519	0.004851	-0.08
254624_at	hypothetical protein ;supported by full-	---	AT4G18580	1.64	0.71	6.20	0.000519	0.004852	-0.08
259174_at	hypothetical protein similar to putative	UNE7	AT3G03690	-1.45	-0.54	-6.20	0.000519	0.004852	-0.08
255594_at	putative ABC transporter	ATABC1	AT4G01660	-1.61	-0.69	-6.20	0.000519	0.004852	-0.08
249467_at	NAM / CUC2 - like protein CUC2, Ara	ATNAC6	AT5G39610	5.12	2.36	6.20	0.00052	0.004852	-0.08
267380_at	putative thromboxane-A synthase ; su	CYP711A1	AT2G26170	2.98	1.57	6.20	0.000521	0.004867	-0.09
259980_at	unknown protein ;supported by full-ler	---	AT1G76520	2.75	1.46	6.20	0.000522	0.004871	-0.09
245290_at	hypothetical protein ; supported by cDI	---	AT4G16490	-2.03	-1.02	-6.19	0.000524	0.004874	-0.09
249121_at	aluminum-induced protein-like ; suppo	---	AT5G43830	-1.66	-0.73	-6.19	0.000523	0.004874	-0.09
254549_at	putative protein various predicted prote	---	AT4G19880	2.03	1.02	6.19	0.000523	0.004874	-0.09

245413_at	asparagine--tRNA ligase	NS1	AT4G17300	-1.62	-0.70	-6.20	0.000523	0.004874	-0.09
253861_at	putative protein MSP1 protein, Saccha	---	AT4G27680	1.62	0.69	6.19	0.000523	0.004874	-0.09
266078_at	putative two-component response regu	ARR16	AT2G40670	1.62	0.69	6.19	0.000524	0.004874	-0.09
259962_at	RNA polymerase II, putative similar to	---	AT1G53690	-1.71	-0.78	-6.19	0.000524	0.004875	-0.09
259207_at	unknown protein	---	AT3G09050	-1.86	-0.89	-6.19	0.000525	0.004878	-0.09
259591_at	unknown protein ;supported by full-len	---	AT1G28150	-1.46	-0.54	-6.19	0.000525	0.004878	-0.09
258529_at	hypothetical protein predicted by gene	---	AT3G06740	-1.97	-0.98	-6.19	0.000525	0.004882	-0.09
262986_at	unknown protein similar to hypothetica	---	AT1G23390	-2.62	-1.39	-6.19	0.000526	0.004888	-0.10
245351_at	casein kinase II beta chain CKB2 ;sup	CKB2	AT4G17640	-1.67	-0.74	-6.19	0.000527	0.004889	-0.10
259102_at	unknown protein similar to hin1 GB:CA	NHL1	AT3G11660	1.82	0.86	6.19	0.000527	0.004889	-0.10
254320_at	putative protein various predicted prot	---	AT4G22580	-1.53	-0.61	-6.19	0.000527	0.004889	-0.10
254466_at	subtilisin-like serine protease contains	---	AT4G20430	-1.96	-0.97	-6.19	0.000527	0.004889	-0.10
248044_at	putative protein similar to unknown pro	---	AT5G56020	-1.63	-0.71	-6.18	0.000529	0.004905	-0.10
258156_at	unknown protein ; supported by cDNA	---	AT3G18050	-2.67	-1.42	-6.18	0.00053	0.004911	-0.10
262678_at	hypothetical protein ;supported by full-	---	AT1G75810	1.96	0.97	6.18	0.000531	0.004913	-0.11
256050_at	leucine zipper protein, putative similar	ATEXO70B2	AT1G07000	1.66	0.73	6.18	0.000531	0.004913	-0.11
265262_at	putative chloroplast nucleoid DNA bind	---	AT2G42980	1.87	0.90	6.18	0.000531	0.004913	-0.11
267452_at	auxin response transcription factor 3 (E	ETT	AT2G33860	-1.70	-0.76	-6.18	0.000531	0.004913	-0.11
255319_at	putative disease resistance protein sim	AtRLP46	AT4G04220	2.85	1.51	6.17	0.000534	0.004941	-0.11
248950_at	ATP-dependent Clp protease proteolyt	CLPP4	AT5G45390	-1.77	-0.82	-6.17	0.000535	0.004941	-0.11
262396_at	unknown protein ;supported by full-len	---	AT1G49470	2.87	1.52	6.17	0.000536	0.004952	-0.12
251884_at	embryonic abundant protein -like emb	---	AT3G54150	10.95	3.45	6.17	0.000536	0.004952	-0.12
260775_at	14-3-3 protein GF14omega (grf2) iden	GRF2	AT1G78300	-1.88	-0.91	-6.17	0.000537	0.004952	-0.12
257970_at	putative sucrose cleavage protein simi	---	AT3G27570	1.71	0.77	6.17	0.000537	0.004952	-0.12
248282_at	unknown protein ;supported by full-ler	---	AT5G52900	-5.33	-2.41	-6.17	0.000537	0.004954	-0.12
247304_at	amino acid transporter AAP4 (pir||S51	AAP4	AT5G63850	2.13	1.09	6.16	0.000539	0.004965	-0.12
262599_at	unknown protein ESTs gb|R65145, gb	---	AT1G15350	-1.62	-0.69	-6.16	0.000539	0.00497	-0.12
258633_at	putative serine carboxypeptidase II sim	SCPL27	AT3G07990	-2.76	-1.47	-6.16	0.00054	0.004977	-0.12
262996_at	hypothetical protein predicted by gens	---	AT1G54440	1.62	0.70	6.16	0.000541	0.004979	-0.13
261412_at	L-ascorbate peroxidase identical to GI	APX1	AT1G07890	2.53	1.34	6.16	0.000541	0.004981	-0.13
264338_at	potassium transporter, putative similar	KUP6	AT1G70300	2.20	1.13	6.15	0.000543	0.004997	-0.13
261455_at	unknown protein ;supported by full-len	---	AT1G21070	-2.25	-1.17	-6.15	0.000543	0.004997	-0.13
246821_at	calmodulin-binding - like protein calm	CBP60G	AT5G26920	6.81	2.77	6.15	0.000543	0.004997	-0.13
264777_at	unknown protein similar to L-allo-thred	THA1	AT1G08630	7.40	2.89	6.15	0.000544	0.005001	-0.13
260047_at	putative UDP-N-acetylglucosamine--N	---	AT1G73740	1.62	0.69	6.15	0.000545	0.005011	-0.14

258099_at	unknown protein similar to hypothetica	---	AT3G23540	1.60	0.68	6.15	0.000546	0.005011	-0.14
247072_at	putative protein similar to unknown pro	---	AT5G66490	2.13	1.09	6.15	0.000547	0.005013	-0.14
255928_at	unknown protein	---	AT1G12640	2.14	1.10	6.15	0.000546	0.005013	-0.14
266863_at	putative ripening-associated protein ;	ATCDPMEK	AT2G26930	-1.58	-0.66	-6.15	0.000546	0.005013	-0.14
260672_at	Expressed protein ; supported by full-l	---	AT1G19480	-1.57	-0.65	-6.15	0.000547	0.005019	-0.14
262047_at	hypothetical protein predicted by gene	---	AT1G80160	7.43	2.89	6.14	0.000549	0.005032	-0.14
253234_at	Expressed protein ; supported by full-l	---	AT4G34265	-1.66	-0.73	-6.14	0.000549	0.005034	-0.14
252276_at	hypothetical protein ; supported by cD	---	AT3G49490	1.75	0.80	6.14	0.000551	0.005043	-0.15
264517_at	hypothetical protein predicted by gens	---	AT1G10120	-1.95	-0.96	-6.14	0.000551	0.005045	-0.15
266942_at	putative ATP binding protein	TXND9	AT2G18990	-2.22	-1.15	-6.14	0.000552	0.005054	-0.15
261223_at	hypothetical protein predicted by gene	HVA22H	AT1G19950	-1.46	-0.55	-6.14	0.000553	0.005056	-0.15
265150_at	unknown protein ; supported by cDNA	---	AT1G51200	1.84	0.88	6.13	0.000556	0.005087	-0.16
262954_at	rubredoxin, putative similar to rubredo	---	AT1G54500	-1.85	-0.89	-6.13	0.000557	0.00509	-0.16
261421_at	hypothetical protein similar to unknowr	IQD30	AT1G18840	-3.23	-1.69	-6.13	0.000558	0.005093	-0.16
259868_at	thioredoxin-like protein similar to thior	ATY1	AT1G76760	1.58	0.66	6.13	0.000558	0.005093	-0.16
251349_s_	putative protein several hypothetical pr	---	AT3G11030 /	-1.95	-0.96	-6.13	0.000558	0.005093	-0.16
254788_at	putative protein other predicted protein	---	AT4G12790	-1.54	-0.62	-6.13	0.000558	0.005093	-0.16
253139_at	ankyrin repeat-containing protein 2 ;su	AKR2	AT4G35450	-1.53	-0.62	-6.13	0.000558	0.005093	-0.16
252002_at	hypothetical protein YIP1 protein, Sac	---	AT3G52760	-1.59	-0.67	-6.12	0.000559	0.005095	-0.16
249801_at	calcium-dependent protein kinase (pir|	CDPK9	AT5G23580	1.64	0.72	6.12	0.000559	0.005097	-0.16
263664_at	putative auxin-induced protein, IAA17	AXR3	AT1G04250	-3.71	-1.89	-6.12	0.00056	0.005101	-0.16
253954_at	putative aconitase Pumpkin mRNA fo	---	AT4G26970	2.19	1.13	6.12	0.00056	0.005101	-0.16
252200_at	anthranilate N-hydroxycinnamoyl/ben	---	AT3G50280	4.36	2.12	6.12	0.000561	0.005103	-0.17
245682_at	Expressed protein ; supported by cDN	---	AT5G08750	1.65	0.73	6.12	0.000561	0.005107	-0.17
255011_at	cytochrome c several plant cytochrom	CYTC-2	AT4G10040	4.95	2.31	6.12	0.000562	0.005107	-0.17
264315_at	aromatic rich glycoprotein, putative sir	---	AT1G70370	-5.59	-2.48	-6.12	0.000563	0.005109	-0.17
251975_at	CDC48 - like protein transitional endo	---	AT3G53230	4.70	2.23	6.12	0.000562	0.005109	-0.17
246017_at	putative protein predicted proteins fron	---	AT5G10730	1.54	0.63	6.12	0.000563	0.005109	-0.17
247182_at	putative protein contains similarity to u	HB25	AT5G65410	-1.76	-0.81	-6.12	0.000563	0.005109	-0.17
265386_at	unknown protein ;supported by full-ler	---	AT2G20930	-1.56	-0.64	-6.12	0.000562	0.005109	-0.17
248026_at	putative protein similar to unknown pro	---	AT5G55710	-1.73	-0.79	-6.12	0.000563	0.005109	-0.17
247573_at	anthocyanin 5-aromatic acyltransferas	AACT1	AT5G61160	14.65	3.87	6.11	0.000564	0.005113	-0.17
257846_at	unknown protein	---	AT3G12910	6.77	2.76	6.11	0.000564	0.005113	-0.17
254447_at	berberine bridge enzyme - like protein	---	AT4G20860	5.74	2.52	6.11	0.000564	0.005113	-0.17
248613_at	phytoene dehydrogenase-like	---	AT5G49555	-1.98	-0.99	-6.11	0.000565	0.005113	-0.17

248855_at	NAM-like	anac096	AT5G46590	2.43	1.28	6.11	0.000565	0.005113	-0.17
264317_at	spermidine synthase, putative similar	SPDS2	AT1G70310	-1.63	-0.71	-6.11	0.000565	0.005117	-0.17
247474_at	putative protein predicted proteins, Ar	---	AT5G62280	-19.84	-4.31	-6.11	0.000566	0.005117	-0.18
247399_at	putative protein similar to unknown pro	---	AT5G62960	-2.48	-1.31	-6.11	0.000566	0.005118	-0.18
257624_at	cytochrome P450 monooxygenase (C	CYP71B3	AT3G26220	6.43	2.69	6.11	0.000566	0.005118	-0.18
262280_at	unknown protein	---	AT1G68580	-2.59	-1.37	-6.11	0.000568	0.005128	-0.18
262728_at	receptor kinase (CLV1) identical to rec	CLV1	AT1G75820	-2.45	-1.29	-6.11	0.000568	0.005128	-0.18
255151_at	putative protein oxysterol-binding prot	ORP1C	AT4G08180	1.44	0.52	6.11	0.000568	0.005128	-0.18
261743_s_	protein serine/threonine phosphatase	BSL2	AT1G08420 /	1.59	0.67	6.11	0.000569	0.005137	-0.18
252379_at	ABC-type transport protein-like protein	ATH1	AT3G47730	1.67	0.74	6.10	0.000569	0.005137	-0.18
265679_at	putative myosin heavy chain ; support	---	AT2G32235 /	1.69	0.75	6.10	0.00057	0.005137	-0.18
256813_at	unknown protein	---	AT3G21360	-1.66	-0.73	-6.10	0.00057	0.005137	-0.18
246310_at	sulfate transporter ATST1 ; supported	SULTR3;1	AT3G51895	2.28	1.19	6.10	0.000571	0.005141	-0.19
246997_at	putative protein similar to unknown pro	---	AT5G67390	-2.06	-1.04	-6.10	0.000571	0.005141	-0.18
251831_at	pectate lyase -like protein pectate lyas	---	AT3G55140	-1.47	-0.56	-6.10	0.000571	0.005145	-0.19
247347_at	putative protein similar to unknown pro	SHA1	AT5G63780	-3.26	-1.70	-6.10	0.000572	0.005147	-0.19
247960_at	N-myristoyl transferase ;supported by	NMT1	AT5G57020	-1.51	-0.59	-6.10	0.000573	0.005154	-0.19
260444_at	unknown protein ;supported by full-ler	---	AT1G68300	1.70	0.77	6.10	0.000573	0.005157	-0.19
250999_at	putative protein predicted proyeins, Ar	---	AT5G02630	1.92	0.94	6.10	0.000574	0.005157	-0.19
250796_at	putative protein similar to unknown pro	---	AT5G05300	9.53	3.25	6.10	0.000574	0.005159	-0.19
258140_at	Expressed protein ; supported by cDN	ALDH2C4	AT3G24503	3.59	1.85	6.09	0.000575	0.00517	-0.19
248158_at	unknown protein	---	AT5G54440	-1.48	-0.56	-6.09	0.000577	0.00518	-0.20
257724_at	hypothetical protein predicted by gene	---	AT3G18510	1.76	0.82	6.09	0.000578	0.005185	-0.20
251221_at	putative protein ER6 protein - Lycoper	---	AT3G62550	1.64	0.71	6.09	0.000578	0.005185	-0.20
251163_at	putative protein S1R protein - Homo s	---	AT3G63310	1.48	0.56	6.09	0.000578	0.005185	-0.20
255881_at	phosphomannose isomerase, putative	DIN9	AT1G67070	4.48	2.16	6.09	0.000578	0.005185	-0.20
256285_at	hypothetical protein predicted by gens	---	AT3G12510	2.04	1.03	6.09	0.000579	0.00519	-0.20
264575_at	putative chloroplast 50S ribosomal pro	emb2394	AT1G05190	-1.63	-0.71	-6.09	0.00058	0.005191	-0.20
254318_at	putative protein embryo-abundant pro	---	AT4G22530	6.10	2.61	6.09	0.00058	0.005191	-0.20
263939_at	hypothetical protein predicted by gene	ATTIM44-2	AT2G36070	1.61	0.69	6.09	0.00058	0.005195	-0.20
247239_at	pectin methylesterase-like protein sup	---	AT5G64640	-1.70	-0.76	-6.08	0.000581	0.005195	-0.20
250259_at	putative protein similar to unknown pro	---	AT5G13800	1.94	0.96	6.08	0.000581	0.005199	-0.21
244984_at	ribosomal protein S3	---	---	-2.09	-1.06	-6.08	0.000581	0.005199	-0.21
257623_at	cytochrome P450, putative contains P	CYP71B23	AT3G26210	4.48	2.16	6.08	0.000582	0.005202	-0.21
253322_at	putative protein ;supported by full-leng	---	AT4G33980	1.89	0.92	6.08	0.000582	0.005202	-0.21

265900_at	unknown protein	---	AT2G25730	1.44	0.52	6.08	0.000582	0.005202	-0.21
253232_at	hypothetical protein ;supported by full-	TAF8	AT4G34340	1.69	0.76	6.08	0.000584	0.005209	-0.21
257381_at	unknown protein	---	AT2G37950	-2.47	-1.30	-6.08	0.000584	0.005215	-0.21
254727_at	hypothetical protein	PTAC5	AT4G13670	-1.48	-0.57	-6.08	0.000585	0.005216	-0.21
247189_at	unknown protein ;supported by full-ler	AGP7	AT5G65390	-4.14	-2.05	-6.07	0.000586	0.005224	-0.21
266044_s_	hypothetical protein	---	AT2G07725	2.62	1.39	6.07	0.000586	0.005224	-0.21
254221_at	putative polygalacturonase polygalact	---	AT4G23820	-6.77	-2.76	-6.07	0.000586	0.005224	-0.21
265869_at	putative two-component response regu	ARR14	AT2G01760	-1.89	-0.92	-6.07	0.000586	0.005224	-0.21
256117_at	unknown protein ; supported by cDNA	---	AT1G16840	-1.53	-0.61	-6.07	0.000587	0.005224	-0.22
264638_at	flowering signals mediating protein FT	FT	AT1G65480	3.85	1.94	6.07	0.000587	0.005224	-0.22
260406_at	putative glutathione transferase similar	ATGSTU12	AT1G69920	24.32	4.60	6.07	0.000587	0.005224	-0.22
246429_at	farnesylated protein ATFP6-like protei	---	AT5G17450	3.50	1.81	6.07	0.000587	0.005224	-0.22
264525_at	unknown protein Highly Similar to bran	ATBCAT-1	AT1G10060	-6.25	-2.64	-6.07	0.000589	0.005232	-0.22
256013_at	unknown protein	DA1	AT1G19270	1.86	0.89	6.07	0.000589	0.005236	-0.22
260082_at	putative mitochondrial carrier protein c	---	AT1G78180	-1.86	-0.90	-6.07	0.00059	0.005239	-0.22
253773_s_	Expressed protein ; supported by full-le	---	AT1G52370 /	-1.78	-0.83	-6.07	0.00059	0.005239	-0.22
254416_at	receptor-like serine/threonine protein k	ARK3	AT4G21380	4.86	2.28	6.06	0.000592	0.005251	-0.22
247297_at	peroxidase ATP3a (emb|CAA67340.1)	---	AT5G64100	3.76	1.91	6.06	0.000594	0.005268	-0.23
261553_at	hypothetical protein	---	AT1G63420	-1.73	-0.79	-6.06	0.000595	0.005274	-0.23
267586_at	hypothetical protein predicted by genfi	---	AT2G41950	-1.93	-0.95	-6.06	0.000595	0.005276	-0.23
264800_at	hypothetical protein similar to IFA-bind	---	AT1G08800	1.81	0.85	6.06	0.000596	0.005284	-0.23
267374_at	putative uricase subunit similar to nod	---	AT2G26230	1.50	0.59	6.05	0.000598	0.005293	-0.24
258049_at	hypothetical protein similar to CGI-18 p	---	AT3G16220	1.51	0.59	6.05	0.000598	0.005294	-0.24
246607_at	receptor-like protein kinase - like prote	---	AT5G35370	3.08	1.62	6.05	0.000599	0.005304	-0.24
263607_at	unknown protein predicted by genscan	---	AT2G16270	-1.92	-0.94	-6.05	0.000601	0.005319	-0.24
266361_at	putative O-GlcNAc transferase	---	AT2G32450	-2.56	-1.36	-6.05	0.000602	0.005323	-0.24
250848_at	3-phosphoinositide-dependent protein	PDK1	AT5G04510	-1.67	-0.74	-6.05	0.000602	0.005323	-0.24
260589_at	hypothetical protein predicted by gene	---	AT1G53400	-1.49	-0.57	-6.05	0.000603	0.005324	-0.24
253981_at	putative protein ;supported by full-leng	---	AT4G26670	-1.56	-0.64	-6.05	0.000603	0.005324	-0.24
248149_at	Expressed protein ; supported by full-le	---	AT5G54855	-1.54	-0.62	-6.04	0.000603	0.005327	-0.25
266715_at	putative RNA-binding protein	---	AT2G46780	-1.75	-0.81	-6.04	0.000605	0.005342	-0.25
254328_at	adenine phosphoribosyltransferase (E	APT3	AT4G22570	-2.60	-1.38	-6.04	0.000607	0.005357	-0.25
267624_at	putative protein kinase	BIK1	AT2G39660	2.95	1.56	6.03	0.000609	0.005371	-0.26
253422_at	putative protein ;supported by full-leng	---	AT4G32240	1.66	0.73	6.03	0.000609	0.005374	-0.26
262119_s_	glutathione S-transferase, putative sin	ATGSTF6	AT1G02920 /	5.11	2.35	6.03	0.00061	0.005375	-0.26

248530_at	putative protein strong similarity to unk	---	AT5G49945	-1.78	-0.84	-6.03	0.000611	0.005379	-0.26
257173_at	S-adenosyl-L-homocysteinas, putative	SAHH2	AT3G23810	-6.47	-2.69	-6.03	0.000612	0.005387	-0.26
266519_at	unknown protein ; supported by cDNA	---	AT2G35155	-1.71	-0.77	-6.03	0.000612	0.005387	-0.26
262969_at	unknown protein	---	AT1G75710	-1.94	-0.96	-6.03	0.000613	0.005395	-0.26
259404_at	type 2A protein serine/threonine phosp	ATB BETA	AT1G17720	1.45	0.54	6.03	0.000613	0.005396	-0.26
254089_at	putative protein apoptosis gene MA3,	---	AT4G24800	-1.65	-0.72	-6.03	0.000614	0.005398	-0.27
246483_at	receptor protein kinase-like protein pr	NIK1	AT5G16000	-3.09	-1.63	-6.03	0.000614	0.0054	-0.27
258752_at	hypothetical protein predicted by gens	ATEXO70H4	AT3G09520	2.71	1.44	6.02	0.000616	0.005411	-0.27
251814_at	chlorophyll a/b-binding protein ; suppo	LHCA1	AT3G54890	-1.44	-0.53	-6.02	0.000616	0.005412	-0.27
258263_at	unknown protein	---	AT3G15780	-2.35	-1.23	-6.02	0.000616	0.005412	-0.27
254761_at	Expressed protein ; supported by full-l	CLE44	AT4G13195	2.01	1.01	6.02	0.000617	0.005412	-0.27
256385_at	60S ribosomal protein L10, putative c	---	AT1G66580	2.32	1.22	6.02	0.000619	0.005427	-0.27
247138_at	3-dehydroquinate synthase-like protein	---	AT5G66120	2.09	1.06	6.02	0.000619	0.005428	-0.27
245130_at	putative receptor-like protein kinase	---	AT2G45340	-1.51	-0.59	-6.02	0.00062	0.005434	-0.28
248198_at	putative protein contains similarity to W	---	AT5G54200	-2.67	-1.42	-6.01	0.000622	0.005445	-0.28
255782_at	transcription factor identical to transcri	MP	AT1G19850	2.67	1.42	6.01	0.000622	0.005445	-0.28
265008_at	Mlo protein, putative similar to Mlo pro	MLO6	AT1G61560	5.91	2.56	6.01	0.000622	0.005447	-0.28
258783_at	unknown protein	---	AT3G11760	-1.69	-0.76	-6.01	0.000624	0.005459	-0.28
267377_at	beta-ketoacyl-CoA synthase (FIDDLEH	KCS10	AT2G26250	-2.80	-1.49	-6.01	0.000626	0.00547	-0.29
255859_at	putative protein embryonic abundant p	---	AT5G34930	2.14	1.10	6.01	0.000626	0.00547	-0.29
245201_at	F12A21.3 unknown protein; similar to	CSK	AT1G67840	-1.67	-0.74	-6.01	0.000625	0.00547	-0.29
251927_at	hypothetical protein ER6 protein - Lyc	---	AT3G53990	-1.54	-0.62	-6.00	0.000629	0.005496	-0.29
265480_at	similar to cold acclimation protein WC	COR413-PM	AT2G15970	-2.27	-1.18	-6.00	0.00063	0.005503	-0.29
260494_at	putative receptor-like protein kinase	---	AT2G41820	-1.80	-0.85	-6.00	0.00063	0.005504	-0.29
263591_at	unknown protein	ATMAP65-6	AT2G01910	-5.28	-2.40	-6.00	0.000632	0.005512	-0.30
264633_at	step II splicing factor, putative similar	SMP1	AT1G65660	1.64	0.72	6.00	0.000632	0.005512	-0.30
254643_at	putative protein DNA polymerase III h	---	AT4G18820	-1.65	-0.72	-6.00	0.000632	0.005514	-0.30
263182_at	Expressed protein ; supported by full-l	---	AT1G05575	21.68	4.44	6.00	0.000633	0.005517	-0.30
257580_at	hypothetical protein	---	AT3G06210	-1.67	-0.74	-5.99	0.000634	0.005523	-0.30
247571_at	snap25a ;supported by full-length cDN	SNAP33	AT5G61210	1.51	0.59	5.99	0.000634	0.005523	-0.30
248739_at	DnaJ protein-like ;supported by full-le	GFA2	AT5G48030	1.53	0.62	5.99	0.000635	0.005528	-0.30
261409_at	zinc finger protein OBP2 identical to G	OBP2	AT1G07640	1.66	0.73	5.99	0.000635	0.005528	-0.30
253387_at	P-Protein - like protein P-Protein prec	AtGLDP1	AT4G33010	-2.80	-1.49	-5.99	0.000635	0.005528	-0.30
255328_at	putative leucyl tRNA synthetase	EMB2369	AT4G04350	-1.91	-0.94	-5.99	0.000636	0.005535	-0.30
259479_at	Expressed protein ; supported by full-l	---	AT1G19020	7.65	2.94	5.99	0.000637	0.00554	-0.31

253137_at	protein kinase - like protein protein kir	---	AT4G35500	1.86	0.89	5.99	0.000639	0.005549	-0.31
250177_at	putative protein copine I, Homo sapier	RGLG2	AT5G14420	1.74	0.80	5.99	0.000639	0.005549	-0.31
245060_at	GDP-mannose pyrophosphorylase up	CYT1	AT2G39770	-1.50	-0.59	-5.98	0.000639	0.005552	-0.31
259357_at	unknown protein ;supported by full-len	---	AT1G13380	-1.76	-0.82	-5.98	0.000639	0.005552	-0.31
262000_at	Expressed protein ; supported by full-l	---	AT1G33810	-1.74	-0.80	-5.98	0.000641	0.005562	-0.31
246260_at	amino acid permease, putative contai	---	AT1G31820	1.93	0.95	5.98	0.000642	0.00557	-0.31
266620_at	unknown protein	---	AT2G35450	-1.77	-0.82	-5.98	0.000643	0.005577	-0.32
251293_at	hypothetical protein	---	AT3G61930	20.46	4.36	5.98	0.000644	0.005587	-0.32
264223_s_	receptor kinase, putative similar to rec	---	AT1G67520 /	3.35	1.74	5.97	0.000646	0.005594	-0.32
261667_at	unknown protein similar to putative lipa	---	AT1G18460	-1.97	-0.98	-5.97	0.000646	0.005595	-0.32
253950_at	putative dihydrolipoamide succinyltran	---	AT4G26910	2.25	1.17	5.97	0.000646	0.005597	-0.32
253553_at	putative protein LipB gene, Prochlorot	---	AT4G31050	-1.69	-0.76	-5.97	0.000647	0.005597	-0.32
247063_at	unknown protein	---	AT5G66820	2.07	1.05	5.97	0.000647	0.0056	-0.32
251310_at	homeobox protein Anthocyaninless2 A	HDG1	AT3G61150	-1.86	-0.90	-5.97	0.000647	0.0056	-0.32
261338_at	hypothetical protein predicted by gene	---	AT1G44920	-1.76	-0.82	-5.97	0.000648	0.005603	-0.32
260372_at	unknown protein contains a region sim	---	AT1G73980	1.57	0.65	5.97	0.000649	0.005607	-0.33
262559_at	unknown protein similar to hypothetica	---	AT1G31300	-1.69	-0.76	-5.97	0.000651	0.005623	-0.33
246319_at	putative protein HYPOTHETICAL PR	---	AT3G56680	-1.57	-0.65	-5.97	0.000651	0.005623	-0.33
246268_at	cytochrome P450, putative contains P	CYP97A3	AT1G31800	-1.84	-0.88	-5.97	0.000651	0.005623	-0.33
AFFX-Atha	Arabidopsis thaliana /REF=M64116 /D	GAPC1	---	1.92	0.94	5.96	0.000656	0.005658	-0.34
255583_at	hypothetical protein similar to C. elega	ARV2	AT4G01510	-1.70	-0.77	-5.96	0.000656	0.005658	-0.34
246746_at	putative protein predicted proteins, Or	---	AT5G27820	-1.72	-0.78	-5.96	0.000656	0.005658	-0.34
249914_at	protease-like protein	---	AT5G22850	1.85	0.89	5.96	0.000657	0.005661	-0.34
265011_at	putative chloroplast membrane protei	ALB4	AT1G24490	1.46	0.54	5.96	0.000657	0.005665	-0.34
257024_at	CDPK-related kinase identical to GB:2	---	AT3G19100	2.00	1.00	5.96	0.000658	0.005665	-0.34
264324_at	myosin heavy chain MYA2 Strong simi	XIB	AT1G04160	-2.55	-1.35	-5.95	0.00066	0.005685	-0.34
248124_at	putative protein contains similarity to u	ATG18F	AT5G54730	1.68	0.75	5.95	0.000662	0.005695	-0.35
259211_at	unknown protein identical to GB:AAD5	---	AT3G09020	5.54	2.47	5.94	0.000665	0.005719	-0.35
259516_at	hypothetical protein ; supported by cDI	ERD10	AT1G20450	-2.66	-1.41	-5.94	0.000665	0.00572	-0.35
248970_at	urea active transporter-like protein	---	AT5G45380	3.14	1.65	5.94	0.000666	0.005723	-0.35
253559_at	1,3-beta-glucanase - like protein 1,3-b	---	AT4G31140	-1.57	-0.65	-5.94	0.000666	0.005723	-0.35
261925_at	oligopeptide transporter, putative simi	---	AT1G22540	-1.61	-0.68	-5.94	0.000667	0.005726	-0.36
251120_at	chloroplast ribosomal L1 - like protein	---	AT3G63490	-1.83	-0.87	-5.94	0.000667	0.005726	-0.36
259188_at	unknown protein ;supported by full-ler	---	AT3G01510	-1.97	-0.98	-5.94	0.000667	0.005729	-0.36
247124_at	prolyl 4-hydroxylase, alpha subunit-lik	---	AT5G66060	-1.53	-0.61	-5.94	0.000668	0.00573	-0.36

254224_at	calcium-dependent protein kinase (CD	CDPK6	AT4G23650	-1.54	-0.62	-5.94	0.000669	0.005737	-0.36
254476_at	putative protein gamma-SNAP protein	GSNAP	AT4G20410	-1.55	-0.63	-5.94	0.00067	0.005747	-0.36
251374_at	homeobox-leucine zipper protein HAT3	HAT3	AT3G60390	-2.68	-1.42	-5.93	0.000671	0.005754	-0.36
252293_at	4-coumarate-CoA ligase -like protein 4	---	AT3G48990	1.55	0.63	5.93	0.000671	0.005754	-0.36
247123_at	unknown protein	---	AT5G66050	-2.01	-1.00	-5.93	0.000672	0.005754	-0.36
263558_at	putative phosphatidylinositol/phosphat	---	AT2G16380	-1.93	-0.95	-5.93	0.000672	0.005754	-0.36
265391_at	Expressed protein ; supported by cDN	GAUT10	AT2G20810	-1.48	-0.57	-5.93	0.000673	0.005757	-0.37
249524_at	putative protein similar to unknown pro	---	AT5G38520	-2.16	-1.11	-5.93	0.000673	0.005757	-0.37
262878_at	hypothetical protein predicted by gene	NDF2	AT1G64770	-1.74	-0.80	-5.93	0.000674	0.005768	-0.37
256713_at	putative peroxidase	---	AT2G34060	-2.22	-1.15	-5.93	0.000675	0.005768	-0.37
249755_at	unknown protein ;supported by full-ler	---	AT5G24580	-4.23	-2.08	-5.93	0.000675	0.005768	-0.37
264248_at	hypothetical protein predicted by gens	---	AT1G78700	-1.92	-0.94	-5.93	0.000675	0.005768	-0.37
252924_at	putative zinc finger protein salt-toleran	---	AT4G39070	-3.41	-1.77	-5.93	0.000676	0.00577	-0.37
252481_at	putative protein DCL PROTEIN, CHL	---	AT3G46630	-1.73	-0.79	-5.93	0.000677	0.005771	-0.37
267470_at	cinnamate-4-hydroxylase molecular m	C4H	AT2G30490	3.79	1.92	5.93	0.000677	0.005771	-0.37
251475_at	putative protein other hypothetical prot	---	AT3G59660	2.23	1.15	5.93	0.000677	0.005771	-0.37
265353_at	unknown protein ;supported by full-ler	---	AT2G16800	-1.48	-0.57	-5.93	0.000677	0.005771	-0.37
249489_at	acyltransferase -like protein anthocya	---	AT5G39090	1.82	0.87	5.92	0.000677	0.005772	-0.37
247627_at	cysteine proteinase AALP identical to A	AALP	AT5G60360	1.51	0.60	5.92	0.000678	0.005774	-0.37
266351_at	unknown protein ;supported by full-ler	---	AT2G01490	1.72	0.78	5.92	0.00068	0.005791	-0.38
257788_at	unknown protein	TCP20	AT3G27010	1.84	0.88	5.92	0.000681	0.005794	-0.38
247936_at	lycopene epsilon cyclase ; supported	LUT2	AT5G57030	-1.97	-0.98	-5.92	0.000681	0.005794	-0.38
250129_at	S-adenosylmethionine:2-demethylmen	---	AT5G16450	1.69	0.75	5.91	0.000685	0.005828	-0.39
258534_at	thioredoxin, putative similar to thiored	---	AT3G06730	-1.55	-0.63	-5.91	0.000687	0.005844	-0.39
256676_at	putative protein ;supported by full-leng	SEX4	AT3G52180	-2.14	-1.10	-5.91	0.000687	0.005844	-0.39
264773_at	putative disease resistance response p	---	AT1G22900	3.78	1.92	5.91	0.000688	0.005846	-0.39
263715_at	unknown protein ; supported by cDNA	GPRI1	AT2G20570	-1.60	-0.68	-5.91	0.000688	0.005847	-0.39
266772_s_	predicted by genefinder	---	AT2G03020 /	-2.11	-1.07	-5.91	0.000689	0.005848	-0.39
250267_at	putative protein predicted proteins	---	AT5G12930	6.94	2.79	5.91	0.00069	0.00586	-0.39
258295_at	unknown protein ;supported by full-ler	---	AT3G23400	-2.04	-1.03	-5.90	0.000691	0.00586	-0.39
245545_at	UTP-glucose glucosyltransferase	UGT71B5	AT4G15280	1.82	0.86	5.90	0.000691	0.005865	-0.40
250286_at	auxin-responsive - like protein Nt-gh3	PBS3	AT5G13320	15.75	3.98	5.90	0.000692	0.005866	-0.40
264836_at	unknown protein similar to hypothetica	---	AT1G03610	-2.17	-1.12	-5.90	0.000696	0.005899	-0.40
253534_at	cytochrome P450 monooxygenase ;su	CYP83B1	AT4G31500	3.04	1.60	5.90	0.000696	0.005899	-0.40
253213_at	RNA helicase (RH16)	---	AT4G34910	1.60	0.68	5.90	0.000697	0.005904	-0.40

267494_at	TCP1-chaperonin cofactor A isolog ;s	KIS	AT2G30410	-1.61	-0.69	-5.89	0.000697	0.005905	-0.41
250323_at	putative protein hydroxyproline-rich gl	---	AT5G12880	5.74	2.52	5.89	0.000698	0.00591	-0.41
254265_s_	serine threonine kinase - like protein k	CRK6	AT4G23140 /	5.84	2.55	5.89	0.0007	0.00592	-0.41
255674_at	probable plasma membrane intrinsic p	PIP1;4	AT4G00430	-2.50	-1.32	-5.89	0.0007	0.005924	-0.41
244998_at	RNA polymerase beta' subunit-1	---	---	-1.90	-0.92	-5.89	0.000701	0.005924	-0.41
259971_at	unknown protein similar to SPL1-relat	---	AT1G76580	-2.01	-1.01	-5.89	0.000702	0.005924	-0.41
247554_at	putative protein leucine zipper-contain	ATEXO70E2	AT5G61010	3.51	1.81	5.89	0.000701	0.005924	-0.41
263773_at	putative xylulose kinase	---	AT2G21370	-1.89	-0.92	-5.89	0.000701	0.005924	-0.41
253281_at	predicted protein	UGT73B1	AT4G34138	2.81	1.49	5.89	0.000703	0.005932	-0.41
246756_at	protein phosphatase - like protein pho	---	AT5G27930	-1.82	-0.87	-5.89	0.000703	0.005932	-0.41
249988_at	putative protein predicted proteins, Dr	---	AT5G18310	1.83	0.87	5.88	0.000705	0.005946	-0.42
248459_at	putative protein similar to unknown pro	CRL	AT5G51020	-1.60	-0.68	-5.88	0.000707	0.005961	-0.42
259477_at	unknown protein ;supported by full-len	---	AT1G19120	-1.51	-0.59	-5.88	0.000707	0.005961	-0.42
266856_at	putative ABC transporter related to mu	PDR4	AT2G26910	-2.51	-1.33	-5.88	0.000709	0.005971	-0.42
258050_at	unknown protein	---	AT3G16200	-1.74	-0.80	-5.88	0.000709	0.005975	-0.42
260902_at	hypothetical protein similar to carboxy	---	AT1G21440	-2.30	-1.20	-5.88	0.00071	0.005976	-0.42
250146_at	putative protein polypeptide deformyla	PDF1B	AT5G14660	-2.18	-1.12	-5.87	0.000712	0.005991	-0.43
264261_at	putative nicotianamine synthase simila	NAS3	AT1G09240	6.37	2.67	5.87	0.000713	0.005999	-0.43
260490_at	ATP-dependent transmembrane trans	CER5	AT1G51500	-2.54	-1.34	-5.87	0.000713	0.005999	-0.43
255378_at	putative glucan synthase component s	ATGSL05	AT4G03550	-1.55	-0.63	-5.87	0.000714	0.006001	-0.43
266939_at	plasma membrane proton ATPase (PI	AHA1	AT2G18960	1.46	0.54	5.87	0.000714	0.006001	-0.43
260238_at	AtHVA22a identical to AtHVA22a GB:	ATHVA22A	AT1G74520	-1.82	-0.86	-5.87	0.000714	0.006001	-0.43
248410_at	putative protein similar to unknown pro	---	AT5G51570	1.57	0.65	5.87	0.000715	0.006006	-0.43
265385_at	putative diacylglycerol kinase ;suppor	---	AT2G20900	2.29	1.19	5.87	0.000716	0.006009	-0.43
265325_at	putative integral membrane protein	---	AT2G18240	1.83	0.87	5.87	0.000716	0.00601	-0.43
260397_at	hypothetical protein predicted by gene	---	AT1G69680	1.62	0.69	5.86	0.000718	0.006026	-0.44
259642_at	hypothetical protein predicted by gens	---	AT1G69030	-2.04	-1.03	-5.86	0.000719	0.006031	-0.44
267339_at	unknown protein ; supported by cDNA	---	AT2G39870	-2.34	-1.23	-5.86	0.000719	0.006031	-0.44
261071_at	unknown protein	---	AT1G07380	1.78	0.83	5.86	0.000721	0.006044	-0.44
253399_at	putative poly(A) polymerase polynucle	nPAP	AT4G32850	1.52	0.60	5.86	0.000722	0.006044	-0.44
263583_at	putative NAD+ dependent isocitrate d	IDH2	AT2G17130	2.03	1.02	5.86	0.000722	0.006044	-0.44
263221_at	UDP-galactose 4-epimerase-like prote	MUR4	AT1G30620	4.18	2.07	5.86	0.000722	0.006044	-0.44
252004_at	purple acid phosphatase-like protein p	PAP20	AT3G52780	2.73	1.45	5.86	0.000722	0.006044	-0.44
264501_at	putative lipase Similar to nodulins and	---	AT1G09390	-3.81	-1.93	-5.86	0.000723	0.006049	-0.44
249947_at	FVT1 - like protein follicular lymphoma	---	AT5G19200	-1.49	-0.58	-5.86	0.000725	0.006055	-0.45

254393_at	putative NADPH quinone oxidoreducta	---	AT4G21580	1.58	0.66	5.86	0.000724	0.006055	-0.45
257888_at	seed maturation protein, putative simi	---	AT3G16990	2.28	1.19	5.86	0.000725	0.006055	-0.45
261272_at	Expressed protein ; supported by cDN	---	AT1G26665	2.60	1.38	5.86	0.000725	0.006056	-0.45
247149_at	unknown protein ;supported by full-ler	---	AT5G65660	-2.73	-1.45	-5.85	0.000726	0.006058	-0.45
250420_at	HY5(bZIP transcription factor family) id	HY5	AT5G11260	1.73	0.79	5.85	0.00073	0.006089	-0.45
249070_at	cellulose synthase catalytic subunit-lik	CESA4	AT5G44030	-1.78	-0.83	-5.85	0.00073	0.006094	-0.46
249960_at	squamosa promoter binding protein-lik	SPL7	AT5G18830	1.58	0.66	5.85	0.000731	0.006096	-0.46
254122_at	CER2 ;supported by full-length cDNA:	CER2	AT4G24510	-14.79	-3.89	-5.85	0.000732	0.006098	-0.46
259231_at	protein phosphatase 2C (PP2C) identi	PP2CA	AT3G11410	2.36	1.24	5.85	0.000731	0.006098	-0.46
255933_at	membrane protein, putative similar to	ATRBL6	AT1G12750	-2.12	-1.08	-5.84	0.000734	0.006113	-0.46
267279_at	hypothetical protein predicted by gene	---	AT2G19460	-2.77	-1.47	-5.84	0.000734	0.006116	-0.46
262932_at	glutathione-s-transferase, putative sim	---	AT1G65820	1.89	0.92	5.84	0.000735	0.006116	-0.46
261429_at	hypothetical protein contains similarity	WRKY61	AT1G18860	1.58	0.66	5.84	0.000736	0.006123	-0.46
258998_at	putative adenylate kinase similar to Ad	---	AT3G01820	1.77	0.82	5.84	0.000737	0.006129	-0.47
247291_at	unknown protein	---	AT5G64480	-1.61	-0.68	-5.84	0.000737	0.00613	-0.47
264693_at	hypothetical protein predicted by gene	CLE26	AT1G69970	-1.57	-0.65	-5.84	0.000738	0.006134	-0.47
245067_at	S-like ribonuclease RNS2 identical to	RNS2	AT2G39780	1.65	0.72	5.83	0.00074	0.006146	-0.47
257036_at	hypothetical protein predicted by gene	---	AT3G19120	-1.53	-0.61	-5.83	0.00074	0.006146	-0.47
256510_at	ATP-dependent Clp protease ATP-bir	---	AT1G33360	1.67	0.74	5.83	0.000741	0.006149	-0.47
254553_at	TMV resistance protein N - like TMV r	---	AT4G19530	-2.45	-1.29	-5.83	0.000742	0.006159	-0.47
265253_at	putative peptide/amino acid transporte	---	AT2G02020	-1.50	-0.59	-5.83	0.000745	0.006185	-0.48
255686_at	putative potassium/H+ antiporter	KEA2	AT4G00630	1.78	0.83	5.82	0.000748	0.006199	-0.48
245822_at	unknown protein ; supported by cDNA:	---	AT1G26110	1.75	0.81	5.82	0.000748	0.006199	-0.48
259246_s_	hypothetical protein predicted by gens	---	AT3G07730 /	1.83	0.87	5.82	0.000748	0.006202	-0.48
262796_at	cysteine proteinase XCP2 identical to	XCP2	AT1G20850	-3.55	-1.83	-5.82	0.000749	0.006207	-0.48
246042_at	cinnamyl-alcohol dehydrogenase - like	---	AT5G19440	2.88	1.52	5.82	0.00075	0.00621	-0.48
246378_at	integral membrane protein, putative si	---	AT1G57620	-1.51	-0.59	-5.82	0.00075	0.006212	-0.49
248974_at	disease resistance protein-like	---	AT5G45060	1.55	0.63	5.82	0.000753	0.006236	-0.49
249818_at	Expressed protein ; supported by cDN	TUB8	AT5G23860	-2.36	-1.24	-5.82	0.000754	0.00624	-0.49
255910_at	unknown protein contains similarity to	---	AT1G18030	-1.59	-0.67	-5.81	0.000756	0.006252	-0.49
258424_at	hypothetical protein predicted by gene	---	AT3G16750	-1.68	-0.75	-5.81	0.000757	0.006256	-0.49
266775_at	putative SCARECROW gene regulator	---	AT2G29060	2.62	1.39	5.81	0.000759	0.006275	-0.50
266867_at	putative signal recognition particle rece	CPFTSY	AT2G45770	-1.60	-0.68	-5.81	0.00076	0.006278	-0.50
264805_at	unknown protein similar to putative DN	ATRX	AT1G08600	1.61	0.69	5.81	0.000761	0.006288	-0.50
260884_at	unknown protein similar to unknown pr	---	AT1G29240	3.05	1.61	5.81	0.000762	0.006288	-0.50

262926_s_	receptor kinase, putative similar to rec	ARK1	AT1G65790 /	3.59	1.85	5.80	0.000762	0.00629	-0.50
248528_at	putative protein similar to unknown pro	---	AT5G50760	15.94	3.99	5.80	0.000765	0.006312	-0.51
255866_at	hypothetical protein predicted by gens	---	AT2G30350	-1.64	-0.71	-5.80	0.000765	0.006312	-0.51
247025_at	zeaxanthin epoxidase precursor ; sup	ABA1	AT5G67030	-1.79	-0.84	-5.80	0.000768	0.006335	-0.51
251387_at	putative protein	---	AT3G60810	-2.14	-1.10	-5.79	0.00077	0.006342	-0.51
249928_at	CCR4-associated factor-like protein	---	AT5G22250	13.45	3.75	5.79	0.00077	0.006342	-0.51
261498_at	receptor kinase, putative similar to rec	HSL1	AT1G28440	-1.83	-0.87	-5.79	0.00077	0.006342	-0.51
246335_at	lethal leaf-spot 1 homolog Lls1	ACD1	AT3G44880	1.86	0.89	5.79	0.00077	0.006342	-0.51
251973_at	nodulin / glutamate-ammonia ligase -	---	AT3G53180	-2.31	-1.21	-5.79	0.000771	0.006346	-0.52
261033_at	unknown protein ;supported by full-len	JAZ5	AT1G17380	5.86	2.55	5.79	0.000773	0.006358	-0.52
261474_at	anionic peroxidase, putative similar to	---	AT1G14540	14.70	3.88	5.79	0.000774	0.006367	-0.52
253583_at	translation initiation factor-like protein	---	AT4G30680	-1.79	-0.84	-5.78	0.000777	0.006385	-0.52
258201_at	hypothetical protein predicted by gens	---	AT3G13910	2.46	1.30	5.78	0.000777	0.006385	-0.52
266898_at	unknown protein ; supported by cDNA	---	AT2G45990	-1.74	-0.80	-5.78	0.000779	0.006397	-0.53
246490_at	S-adenosylmethionine decarboxylase	CPuORF10	AT5G15948 /	1.89	0.92	5.78	0.000781	0.006409	-0.53
261132_at	hypothetical protein predicted by gene	TGD1	AT1G19800	-1.55	-0.63	-5.78	0.000781	0.006409	-0.53
258606_at	unknown protein ;supported by full-ler	---	AT3G02840	23.86	4.58	5.78	0.000782	0.006419	-0.53
251922_at	protein kinase -like protein protein kin	---	AT3G54030	-2.47	-1.30	-5.78	0.000784	0.00643	-0.53
245731_at	MAP kinase, putative similar to MAP k	MKK9	AT1G73500	2.60	1.38	5.77	0.000786	0.006447	-0.54
264860_at	hypothetical protein contains ATP/GTP	---	AT1G24290	-1.48	-0.57	-5.77	0.000787	0.00645	-0.54
264820_at	putative coproporphyrinogen III oxidas	LIN2	AT1G03475	-1.43	-0.52	-5.77	0.000787	0.00645	-0.54
248255_at	ATP-dependent Clp protease ATP-bin	CLPX	AT5G53350	1.68	0.75	5.77	0.000788	0.00645	-0.54
264375_at	putative protein kinase contains a prot	CIPK16	AT2G25090	3.79	1.92	5.77	0.000788	0.00645	-0.54
267499_at	hypothetical protein predicted by gens	---	AT2G45500	1.61	0.69	5.77	0.00079	0.006464	-0.54
266831_at	putative squalene epoxidase	SQE2	AT2G22830	-3.95	-1.98	-5.77	0.000792	0.006479	-0.54
253393_at	Expressed protein ; supported by cDN	GLB3	AT4G32690	1.64	0.71	5.76	0.000795	0.006502	-0.55
259089_at	hypothetical protein similar to GB:CAB	---	AT3G04960	-1.56	-0.64	-5.76	0.000796	0.00651	-0.55
258744_at	hypothetical protein similar to plant IF	---	AT3G05830	1.70	0.77	5.76	0.000798	0.006516	-0.55
245094_at	4-alpha-glucanotransferase	DPE2	AT2G40840	-1.80	-0.85	-5.76	0.000797	0.006516	-0.55
250197_at	isocitrate dehydrogenase - like protein	---	AT5G14590	1.50	0.59	5.76	0.000799	0.006521	-0.55
257530_at	unknown protein	---	AT3G03040	-1.54	-0.63	-5.76	0.000799	0.006521	-0.55
257754_at	GTP binding protein, putative similar t	ATRAB7B	AT3G18820	-1.52	-0.60	-5.76	0.000799	0.006523	-0.55
244939_at	ribosomal protein S12 (trans-splice pa	---	---	-2.14	-1.10	-5.75	0.000801	0.006532	-0.56
254679_at	putative protein Mei2-like protein, Ara	AML3	AT4G18120	1.61	0.68	5.75	0.000801	0.006534	-0.56
264222_at	hypothetical protein predicted by gene	---	AT1G60230	-1.56	-0.64	-5.75	0.000802	0.006534	-0.56

267165_at	putative receptor-like protein kinase sa	RLK	AT2G37710	3.13	1.65	5.75	0.000802	0.006535	-0.56
251770_at	leucoanthocyanidin dioxygenase -like	---	AT3G55970	8.93	3.16	5.75	0.000802	0.006537	-0.56
261814_at	unknown protein	---	AT1G08310	8.75	3.13	5.75	0.000804	0.006547	-0.56
257887_at	protein phosphatase-2c, putative simil	---	AT3G17090	-1.73	-0.79	-5.75	0.000804	0.006548	-0.56
267162_s_	putative phosphoribosylaminoimidazol	---	AT2G05140 /	2.03	1.02	5.75	0.000806	0.00656	-0.56
247944_at	putative protein similar to unknown pro	---	AT5G57100	-1.72	-0.78	-5.75	0.000807	0.006562	-0.56
256600_at	hypothetical protein predicted by gene	---	AT3G14850	4.76	2.25	5.75	0.000808	0.006572	-0.57
257868_at	unknown protein	RIN4	AT3G25070	1.83	0.87	5.74	0.000809	0.006576	-0.57
261433_s_	endoplasmic reticulum-type calcium-tra	---	AT1G07670 /	1.45	0.53	5.74	0.000809	0.006576	-0.57
257621_at	calmodulin-domain protein kinase CDP	CPK9	AT3G20410	2.35	1.23	5.74	0.00081	0.006583	-0.57
248688_at	indole-3-glycerol phosphate synthase	---	AT5G48220	-1.87	-0.90	-5.74	0.000811	0.006583	-0.57
249515_at	tryptophan synthase beta chain	---	AT5G38530	4.82	2.27	5.74	0.000813	0.006598	-0.57
261793_at	unknown protein ; supported by cDNA:	---	AT1G16080	-2.85	-1.51	-5.74	0.000813	0.006598	-0.57
261566_at	unknown protein ;supported by full-len	---	AT1G33230	-1.80	-0.85	-5.74	0.000814	0.006606	-0.58
258710_s_	putative coatomer zeta subunit (zeta-c	---	AT3G09800 /	-1.51	-0.59	-5.74	0.000815	0.006608	-0.58
250329_at	putative potassium transport protein g	KEA6	AT5G11800	-1.61	-0.69	-5.73	0.000817	0.006622	-0.58
248958_at	unknown protein ; supported by full-le	---	AT5G45590	-1.91	-0.93	-5.73	0.00082	0.006642	-0.58
248007_at	S-adenosylmethionine:2-demethylmen	---	AT5G56260	1.48	0.56	5.73	0.000821	0.006651	-0.58
248339_at	prolyl tRNA synthetase	OVA6	AT5G52520	-1.63	-0.70	-5.73	0.000823	0.006667	-0.59
252863_at	myo-inositol-1-phosphate synthase ;s	MIPS1	AT4G39800	-9.76	-3.29	-5.73	0.000824	0.006667	-0.59
259947_at	putative protein kinase similar to protei	---	AT1G71530	1.73	0.79	5.73	0.000824	0.006671	-0.59
254665_at	beta-1,3-glucanase-like protein strong	---	AT4G18340	-2.30	-1.20	-5.72	0.000827	0.00668	-0.59
254408_at	serine/threonine kinase - like protein s	B120	AT4G21390	14.62	3.87	5.72	0.000826	0.00668	-0.59
247668_at	pseudo-response regulator - like pseu	APRR3	AT5G60100	1.46	0.54	5.72	0.000827	0.00668	-0.59
250609_at	peptide methionine sulfoxide reductase	PMSR3	AT5G07470	1.50	0.59	5.72	0.000827	0.00668	-0.59
256146_at	delta-adaptin, putative similar to delta-	delta-ADR	AT1G48760	-1.52	-0.61	-5.72	0.000829	0.006694	-0.59
258782_at	putative dihydroneopterin aldolase sim	---	AT3G11750	-1.85	-0.89	-5.72	0.000832	0.006717	-0.60
257038_at	longevity factor-like protein similar to l	LOH2	AT3G19260	2.33	1.22	5.71	0.000834	0.006732	-0.60
264700_at	hypothetical protein predicted by gene	---	AT1G70100	-1.75	-0.81	-5.71	0.000835	0.006732	-0.60
253872_at	putative protein Arabidopsis thaliana r	RD26	AT4G27410	2.07	1.05	5.71	0.000835	0.006732	-0.60
249087_at	DNA binding protein EREBP-3-like pro	ERF9	AT5G44210	-2.08	-1.05	-5.71	0.000835	0.006734	-0.60
257672_at	unknown protein ;supported by full-ler	---	AT3G20300	-2.28	-1.19	-5.71	0.000836	0.006739	-0.60
258901_at	putative protein phosphatase-2C simila	---	AT3G05640	-8.23	-3.04	-5.71	0.000837	0.00674	-0.61
265572_at	putative carbonic anhydrase	ATACA2	AT2G28210	17.47	4.13	5.71	0.000837	0.00674	-0.61
250896_at	putative protein ; supported by cDNA:	---	AT5G03560	1.93	0.95	5.71	0.000838	0.00674	-0.61

245456_at	disease resistance RPP5 like protein	RPP5	AT4G16950	1.74	0.80	5.71	0.000838	0.00674	-0.61
266463_at	hypothetical protein predicted by gene	---	AT2G47840	-1.66	-0.73	-5.71	0.000837	0.00674	-0.60
247822_at	putative protein sorting nexin 2, Homo	SNX2a	AT5G58440	-1.71	-0.77	-5.71	0.000838	0.006741	-0.61
251015_at	putative protein predicted protein, Ara	---	AT5G02480	1.49	0.58	5.71	0.000839	0.006741	-0.61
265876_at	putative receptor-like protein kinase	---	AT2G42290	-1.50	-0.59	-5.71	0.000839	0.006741	-0.61
254505_at	Expressed protein ; supported by full-l	---	AT4G19985	-1.95	-0.96	-5.71	0.000841	0.006753	-0.61
245297_at	hypothetical protein ; supported by cDI	---	AT4G16510	-1.70	-0.77	-5.71	0.000841	0.006753	-0.61
249361_at	protein kinase - like protein protein kin	---	AT5G40540	-2.56	-1.35	-5.71	0.000841	0.006753	-0.61
255864_at	putative pseudouridine synthase	---	AT2G30320	-1.67	-0.74	-5.70	0.000843	0.006767	-0.61
248578_at	putative protein contains similarity to u	emb1879	AT5G49820	-1.86	-0.89	-5.70	0.000845	0.006779	-0.62
260587_at	unknown protein ; supported by cDNA	---	AT1G53210	-1.61	-0.69	-5.70	0.000846	0.006786	-0.62
245477_at	hypothetical protein	ARR2	AT4G16110	-1.60	-0.68	-5.70	0.000846	0.006786	-0.62
247207_at	putative protein similar to unknown pro	---	AT5G65000	1.43	0.51	5.70	0.000848	0.006793	-0.62
247000_at	casein kinase II alpha subunit ; suppo	CKA1	AT5G67380	1.72	0.78	5.70	0.000849	0.006803	-0.62
263044_at	spore germination protein c2 similar to	---	AT1G23360	-1.60	-0.68	-5.69	0.00085	0.006807	-0.62
261646_at	putative lipase similar to hypothetical p	---	AT1G27690	-1.60	-0.67	-5.69	0.00085	0.006807	-0.62
258563_at	putative long-chain-fatty-acid--CoA liga	LACS6	AT3G05970	1.62	0.70	5.69	0.000853	0.006817	-0.63
264984_at	unknown protein ;supported by full-len	---	AT1G27000	1.45	0.54	5.69	0.000853	0.006817	-0.63
250944_at	putative protein	---	AT5G03380	5.13	2.36	5.69	0.000852	0.006817	-0.62
257150_at	unknown protein ;supported by full-ler	---	AT3G27230	-1.76	-0.82	-5.69	0.000853	0.006817	-0.63
247326_at	peroxidase ATP3a homolog ;supporte	---	AT5G64110	6.94	2.79	5.69	0.000853	0.006817	-0.63
247641_at	imidazoleglycerol-phosphate synthase	PDX2	AT5G60540	1.60	0.68	5.69	0.000854	0.00682	-0.63
262786_at	putative lipase similar to gb|X02844 lip	---	AT1G10740	-1.89	-0.92	-5.69	0.000854	0.00682	-0.63
267602_at	unknown protein ; supported by cDNA	---	AT2G32970	-1.86	-0.90	-5.69	0.000854	0.006821	-0.63
257717_at	unknown protein	EMB1865	AT3G18390	-1.77	-0.82	-5.69	0.000855	0.006824	-0.63
255479_at	coded for by A. thaliana cDNA T4683	SAG21	AT4G02380	6.20	2.63	5.69	0.000856	0.006831	-0.63
245319_at	Expressed protein ; supported by full-l	---	AT4G16146	2.23	1.16	5.69	0.000857	0.006835	-0.63
263565_at	unknown protein	FUT4	AT2G15390	4.59	2.20	5.68	0.00086	0.006852	-0.63
261178_at	synaptobrevin 7B, putative similar to (	ATVAMP726	AT1G04760	-1.48	-0.57	-5.68	0.00086	0.006852	-0.63
263168_at	putative glutaredoxin Strong similarity	---	AT1G03020	-4.37	-2.13	-5.68	0.00086	0.006852	-0.63
253404_at	putative pyrophosphate--fructose-6-ph	PFK6	AT4G32840	-1.73	-0.79	-5.68	0.000862	0.006862	-0.64
263404_s_	hypothetical protein similar to hypothet	---	AT2G04090 /	4.44	2.15	5.68	0.000862	0.006862	-0.64
264113_at	unknown protein	APG9	AT2G31260	1.71	0.77	5.68	0.000862	0.006862	-0.64
253696_at	cytokinin oxidase - like protein cytokin	CKX4	AT4G29740	3.10	1.63	5.68	0.000863	0.006868	-0.64
263678_at	hypothetical protein Similar to Babesia	---	AT1G04420	-2.11	-1.08	-5.68	0.000865	0.006879	-0.64

245854_at	adenosine nucleotide translocator ; su	AAC2	AT5G13490	9.84	3.30	5.68	0.000866	0.006886	-0.64
259819_at	unknown protein ; supported by cDNA	ATMTK	AT1G49820	1.44	0.53	5.68	0.000866	0.006886	-0.64
259592_at	lipid transfer protein, putative contains	LTPG1	AT1G27950	-4.00	-2.00	-5.67	0.00087	0.006905	-0.65
248420_at	receptor-like protein kinase ;supported	---	AT5G51560	-3.56	-1.83	-5.67	0.000869	0.006905	-0.65
253873_at	hypothetical protein ;supported by full-	PRA1.H	AT4G27540	1.54	0.62	5.67	0.00087	0.006905	-0.65
263956_at	putative homeodomain transcription fa	BLH1	AT2G35940	2.27	1.18	5.67	0.00087	0.006905	-0.65
255035_at	putative protein	---	AT4G09550	-1.92	-0.94	-5.67	0.00087	0.006905	-0.65
250813_at	GTP-binding protein (gb|AAD09203.1)	TOC34	AT5G05000	-1.73	-0.79	-5.67	0.000873	0.006921	-0.65
247110_at	putative protein contains similarity to re	---	AT5G65830	-1.88	-0.91	-5.67	0.000873	0.006923	-0.65
247889_at	putative protein similar to unknown pro	APO2	AT5G57930	-1.59	-0.67	-5.67	0.000875	0.006932	-0.65
256114_at	unknown protein ; supported by cDNA	---	AT1G16850	-4.36	-2.12	-5.67	0.000875	0.006933	-0.65
266591_at	expressed protein supported by cDNA	ABIL1	AT2G46225	-2.09	-1.06	-5.66	0.000876	0.006941	-0.66
245281_at	DEF (CLA1) protein ; supported by cD	CLA1	AT4G15560	-1.69	-0.75	-5.66	0.000877	0.006941	-0.66
250424_at	bromodomain protein - like bromodom	GTE2	AT5G10550	-1.48	-0.56	-5.66	0.000877	0.006943	-0.66
264471_at	hypothetical protein predicted by gene	---	AT1G67120	2.27	1.18	5.66	0.000879	0.006947	-0.66
246651_at	adenylate kinase -like protein adenyla	---	AT5G35170	-1.88	-0.91	-5.66	0.000878	0.006947	-0.66
258935_at	unknown protein predicted by genscan	---	AT3G10120	-2.28	-1.19	-5.66	0.000879	0.006947	-0.66
260629_at	unknown protein	---	AT1G62330	-1.69	-0.76	-5.66	0.000881	0.006961	-0.66
251187_at	putative protein putative proteins - diffe	AtATG18a	AT3G62770	1.43	0.52	5.66	0.000882	0.006968	-0.66
262744_at	anthranilate N-hydroxycinnamoyl/ben	---	AT1G28680	2.24	1.16	5.66	0.000883	0.006972	-0.66
249383_at	putative protein putative DNA-binding	PRE1	AT5G39860	-2.24	-1.16	-5.65	0.000885	0.006984	-0.67
267356_at	putative isoamylase	ISA1	AT2G39930	-1.59	-0.67	-5.65	0.000885	0.006984	-0.67
256252_at	glucosyl transferase, putative similar t	---	AT3G11340	15.03	3.91	5.65	0.000885	0.006986	-0.67
247077_at	putative protein similar to unknown pro	---	AT5G66420	-1.70	-0.77	-5.65	0.000888	0.007005	-0.67
259875_s_	12-oxophytodienoate reductase (OPR2	OPR1	AT1G76680 /	3.77	1.92	5.65	0.000888	0.007005	-0.67
260368_at	AtHVA22c identical to AtHVA22c GB:A	ATHVA22C	AT1G69700	-4.20	-2.07	-5.65	0.000889	0.007005	-0.67
252507_at	putative protein predicted protein, Sac	aTNUDT9	AT3G46200	-1.95	-0.97	-5.65	0.000889	0.007005	-0.67
262340_at	Expressed protein ; supported by full-le	ANAC027	AT1G64100 /	-1.51	-0.60	-5.65	0.000889	0.007005	-0.67
257021_at	branched-chain amino acid aminotran	BCAT4	AT3G19710	-2.71	-1.44	-5.65	0.000893	0.007032	-0.68
265419_at	putative secretory carrier-associated m	---	AT2G20840	-1.73	-0.79	-5.64	0.000895	0.007041	-0.68
257807_at	glyceraldehyde 3-phosphate dehydrog	GAPA	AT3G26650	-1.49	-0.58	-5.64	0.000895	0.007041	-0.68
245693_at	thioredoxin - like protein	WCRKC2	AT5G04260	1.64	0.72	5.64	0.000895	0.007043	-0.68
250316_at	cystatin (emb|CAA03929.1) ; supporte	ATCYS1	AT5G12140	-1.54	-0.63	-5.64	0.000896	0.007044	-0.68
263574_at	putative tetracycline transporter protein	---	AT2G16990	-1.49	-0.58	-5.64	0.000896	0.007044	-0.68
264553_s_	putative cinnamyl alcohol dehydrogen	---	AT1G09480 /	1.71	0.77	5.64	0.000897	0.007051	-0.68

254355_at	Ribosomal protein L7Ae - like NHP2/F	---	AT4G22380	-2.04	-1.03	-5.64	0.000898	0.007051	-0.68
245101_at	putative cytochrome P450 ; supported	CYP98A3	AT2G40890	1.95	0.97	5.64	0.000898	0.007052	-0.68
259087_at	hypothetical protein, contains DnaJ m	---	AT3G04980	-1.43	-0.52	-5.64	0.0009	0.007067	-0.69
248344_at	hyaluronan mediated motility receptor-	---	AT5G52280	-2.30	-1.20	-5.64	0.000902	0.007074	-0.69
262072_at	hypothetical protein predicted by gene	ZCF37	AT1G59590	3.15	1.66	5.64	0.000902	0.007074	-0.69
262059_at	DnaJ protein, putative similar to DnaJ	---	AT1G80030	-1.90	-0.92	-5.64	0.000903	0.007074	-0.69
253708_at	gamma-glutamyltransferase-like prote	GGT4	AT4G29210	2.77	1.47	5.64	0.000902	0.007074	-0.69
257264_at	hypothetical protein contains Pfam pro	---	AT3G22060	6.44	2.69	5.63	0.000904	0.007083	-0.69
256765_at	aminotransferase, putative similar to a	POP2	AT3G22200	1.81	0.85	5.63	0.000906	0.007095	-0.69
248587_at	Expressed protein ; supported by full-l	---	AT5G49550	-1.58	-0.66	-5.63	0.000907	0.007099	-0.69
260279_at	putative DNA repair protein similar to	---	AT1G80420	-1.56	-0.64	-5.63	0.000908	0.007111	-0.70
258976_at	putative dehydrogenase contains Pfar	---	AT3G01980	-1.48	-0.56	-5.63	0.000909	0.007114	-0.70
259081_at	putative sodium proton exchanger sim	NHX2	AT3G05030	1.74	0.80	5.63	0.00091	0.007114	-0.70
255121_at	putative mitogen-activated protein kina	MAPKKK9	AT4G08480	1.99	0.99	5.63	0.00091	0.007114	-0.70
256169_at	receptor protein kinase, putative conta	---	AT1G51800	7.31	2.87	5.63	0.00091	0.007114	-0.70
259880_at	hypothetical protein similar to hypothe	---	AT1G76730	-1.97	-0.98	-5.63	0.000911	0.007115	-0.70
248789_at	putative protein strong similarity to unk	---	AT5G47440	-1.93	-0.95	-5.62	0.000912	0.007127	-0.70
259605_at	unknown protein	PUB45	AT1G27910	-2.25	-1.17	-5.62	0.000913	0.007127	-0.70
246033_at	hydroxymethylbilane synthase ;suppo	HEMC	AT5G08280	-1.88	-0.91	-5.62	0.000914	0.007133	-0.70
252134_at	putative protein ; supported by cDNA:	---	AT3G50910	3.04	1.61	5.62	0.000914	0.007133	-0.70
254050_s_	hypothetical protein ; supported by cD	---	AT4G25670 /	1.55	0.64	5.62	0.000915	0.007138	-0.70
245929_at	alcohol dehydrogenase - like protein a	---	AT5G24760	3.96	1.99	5.62	0.000916	0.007139	-0.70
260879_at	hypothetical protein predicted by gene	---	AT1G21480	-1.59	-0.67	-5.62	0.000916	0.007139	-0.70
251244_at	pectinacetylesterase precursor-like pr	---	AT3G62060	-1.63	-0.71	-5.62	0.000917	0.007145	-0.71
255622_at	putative flavonol glucosyltransferase s	GT72B1	AT4G01070	1.79	0.84	5.62	0.000917	0.007145	-0.71
248181_at	cytochrome c biogenesis protein precu	---	AT5G54290	-1.88	-0.91	-5.62	0.000918	0.007145	-0.71
258924_at	putative diadenosine 5',5'''-P1,P4-tetra	ATNUDX26	AT3G10620	-1.50	-0.59	-5.62	0.00092	0.007162	-0.71
248833_at	Bax inhibitor-1 like ;supported by full-l	ATBI1	AT5G47120	1.72	0.79	5.62	0.00092	0.007163	-0.71
259293_at	putative DNA binding protein similarity	---	AT3G11580	2.21	1.14	5.61	0.000921	0.007167	-0.71
248235_at	unknown protein ;supported by full-len	emb2737	AT5G53860	-1.44	-0.53	-5.61	0.000922	0.007171	-0.71
258678_at	E2, ubiquitin-conjugating enzyme 11 (	UBC11	AT3G08690	1.80	0.85	5.61	0.000923	0.007178	-0.71
256251_at	hypothetical protein predicted by gene	---	AT3G11330	1.80	0.85	5.61	0.000924	0.007178	-0.71
247459_at	putative protein embryo-specific prote	---	AT5G62200	1.58	0.66	5.61	0.000925	0.007187	-0.71
257573_at	putative SF16 protein {Helianthus annu	iqd9	AT2G33990	-1.93	-0.95	-5.61	0.000926	0.007192	-0.72
257880_at	AMP-binding protein, putative contain	AAE7	AT3G16910	2.27	1.18	5.61	0.000927	0.007195	-0.72

247145_at	receptor protein kinase-like protein	---	AT5G65600	11.17	3.48	5.61	0.000929	0.00721	-0.72
247008_at	ADP-ribosylation factor-like protein ;su	ATARLA1D	AT5G67560	-1.52	-0.60	-5.61	0.00093	0.007215	-0.72
262634_at	unknown protein ; supported by cDNA:	---	AT1G06690	-3.15	-1.66	-5.60	0.000931	0.007217	-0.72
259429_at	cytochrome P450, putative similar to c	CYP86A4	AT1G01600	-5.65	-2.50	-5.60	0.000931	0.007217	-0.72
258173_at	putative protein kinase similar to serin	CERK1	AT3G21630	1.57	0.65	5.60	0.000931	0.007217	-0.72
252016_at	putative protein predicted protein, Ara	---	AT3G52950	1.57	0.65	5.60	0.000932	0.007219	-0.72
244966_at	cytochrome b6-f complex, subunit V	---	---	-1.96	-0.97	-5.60	0.000932	0.00722	-0.72
257154_at	unknown protein ; supported by cDNA	---	AT3G27210	1.78	0.83	5.60	0.000934	0.007225	-0.72
256428_at	putative disease resistance protein sim	AtRLP35	AT3G11080	2.22	1.15	5.60	0.000933	0.007225	-0.72
251612_at	putative protein hypothetical protein T	---	AT3G57950	1.58	0.66	5.60	0.000934	0.007225	-0.73
248968_at	pectin acetylesterase ;supported by fu	---	AT5G45280	-2.50	-1.32	-5.60	0.000936	0.007241	-0.73
247743_at	protein kinase - like serine/threonine/t	---	AT5G59010	-1.75	-0.80	-5.60	0.000937	0.007241	-0.73
261459_at	O-methyltransferase, putative similar t	---	AT1G21100	10.11	3.34	5.60	0.000937	0.007246	-0.73
248883_at	putative protein strong similarity to unk	---	AT5G46190	-1.52	-0.60	-5.60	0.000938	0.007248	-0.73
259743_at	hypothetical protein predicted by gene	---	AT1G71140	5.80	2.54	5.60	0.000939	0.00725	-0.73
257626_s_	hypothetical protein	---	AT3G26240 /	-1.61	-0.68	-5.60	0.000939	0.00725	-0.73
259426_at	hypothetical protein contains similarity	LEA14	AT1G01470	-1.64	-0.72	-5.59	0.000943	0.007278	-0.74
264524_at	tat-binding protein, putative Highly Sin	ATBCAT-2	AT1G10070	6.57	2.72	5.59	0.000944	0.007283	-0.74
254508_at	putative protein gene F4P9.34 chromo	---	AT4G20170	-1.71	-0.77	-5.59	0.000944	0.007283	-0.74
267567_at	putative cytochrome P450	CYP71A13	AT2G30770	49.75	5.64	5.59	0.000947	0.007302	-0.74
254682_at	putative protein WERBP-1 - Nicotiana	UNE16	AT4G13640	-1.65	-0.72	-5.59	0.000948	0.007308	-0.74
246496_at	putative protein KIAA1468 - Homo sap	---	AT5G16210	-1.62	-0.70	-5.59	0.000948	0.007308	-0.74
251104_at	F-box protein family, AtFBL3 contains	---	AT5G01720	1.80	0.85	5.58	0.000955	0.007357	-0.75
262980_at	endo-beta-1,4-glucanase, putative sim	AtGH9B7	AT1G75680	-6.84	-2.77	-5.58	0.000956	0.007362	-0.75
264716_at	matrix metalloproteinase, putative sim	MMP	AT1G70170	3.41	1.77	5.58	0.000956	0.007362	-0.75
258612_at	putative replication factor A similar to r	---	AT3G02920	-1.59	-0.67	-5.58	0.000957	0.007362	-0.75
251753_at	putative protein predicted protein, Ara	---	AT3G55760	-2.97	-1.57	-5.58	0.000957	0.007362	-0.75
262143_at	unknown protein	---	AT1G52630	-1.61	-0.68	-5.58	0.000958	0.007365	-0.75
254249_at	serine /threonine kinase - like protein	---	AT4G23280	3.21	1.68	5.58	0.000958	0.007365	-0.75
245982_at	senescence-associated protein (SAG2	SAG29	AT5G13170	9.11	3.19	5.58	0.000958	0.007365	-0.75
247237_at	auxin-independent growth promoter-lik	---	AT5G64600	-1.65	-0.73	-5.58	0.000959	0.007366	-0.75
266183_at	unknown protein	ATPT2	AT2G38940	1.76	0.82	5.57	0.000959	0.007368	-0.75
267163_at	unknown protein	---	AT2G37520	1.79	0.84	5.57	0.000962	0.00738	-0.76
265659_at	putative disease resistance protein	AtRLP20	AT2G25440	2.80	1.49	5.57	0.000962	0.00738	-0.76
263914_at	unknown protein	AtGRF3	AT2G36400	-2.23	-1.16	-5.57	0.000963	0.007386	-0.76

251684_at	putative protein	---	AT3G56410	2.14	1.10	5.57	0.000963	0.007387	-0.76
256948_at	unknown protein	---	AT3G18930	1.51	0.59	5.57	0.000968	0.007415	-0.76
255992_at	unknown protein	---	AT1G29790	-1.65	-0.72	-5.57	0.000968	0.007415	-0.76
262501_at	putative replication factor Similar to gb	emb1968	AT1G21690	-1.66	-0.73	-5.57	0.000968	0.007415	-0.76
248075_at	selenium-binding protein-like	CRR21	AT5G55740	-2.00	-1.00	-5.56	0.000969	0.007421	-0.77
255681_at	predicted protein of unknown function	DGD2	AT4G00550	1.69	0.76	5.56	0.00097	0.007426	-0.77
245757_at	phosphate-induced (phi-1) protein, pu	PHI-1	AT1G35140	-10.40	-3.38	-5.56	0.000971	0.007433	-0.77
248853_at	protein kinase-like protein	BSK2	AT5G46570	-1.75	-0.80	-5.56	0.000972	0.007433	-0.77
244951_s_	cytochrome c biogenesis orf452	---	AT2G07723	2.47	1.30	5.56	0.000972	0.007433	-0.77
251679_at	putative protein strictosidine synthase	---	AT3G57030	-2.33	-1.22	-5.56	0.000974	0.007451	-0.77
248719_at	respiratory burst oxidase protein ; sup	RBOHD	AT5G47910	4.63	2.21	5.56	0.000975	0.007453	-0.77
260309_at	putative alanine aminotransferase simi	AOAT2	AT1G70580	-1.79	-0.84	-5.56	0.000977	0.007469	-0.78
262848_at	unknown protein ; supported by cDNA:	BPC2	AT1G14685	-1.58	-0.66	-5.55	0.00098	0.007489	-0.78
251249_at	putative protein 10-deacetylbaccatin I	---	AT3G62160	-1.59	-0.67	-5.55	0.000984	0.007512	-0.78
265461_at	unknown protein similarity to ubiquitin	---	AT2G46500	1.55	0.64	5.55	0.000984	0.007512	-0.78
255043_at	putative protein several hypothetical pr	---	AT4G09640	-2.18	-1.13	-5.55	0.000985	0.007513	-0.78
265338_at	putative ribosomal protein L6 ; suppor	---	AT2G18400	-1.56	-0.64	-5.55	0.000985	0.007515	-0.78
254066_at	transcriptional activator CBF1-like pro	DREB1A	AT4G25480	3.55	1.83	5.55	0.000987	0.007522	-0.79
267188_at	6,7-dimethyl-8-ribityllumazine synthas	COS1	AT2G44050 /	-1.56	-0.64	-5.55	0.000987	0.007522	-0.79
258608_at	unknown protein ;supported by full-ler	---	AT3G03020	-2.41	-1.27	-5.55	0.000987	0.007523	-0.79
249835_s_	putative protein similar to unknown pro	---	AT5G23490 /	2.43	1.28	5.55	0.000989	0.007531	-0.79
260840_at	hypothetical protein similar to hypothet	---	AT1G29050	1.73	0.79	5.54	0.00099	0.007538	-0.79
252950_at	putative protein phospholipase C (EC	---	AT4G38690	-2.71	-1.44	-5.54	0.000993	0.007554	-0.79
253562_at	putative protein ;supported by full-leng	---	AT4G31130	1.43	0.52	5.54	0.000994	0.007554	-0.79
251772_at	cyclophilin-like protein ROC7, cycloph	---	AT3G55920	-1.72	-0.78	-5.54	0.000993	0.007554	-0.79
258637_at	putative RHO GDP-dissociation inhibit	---	AT3G07880	-1.72	-0.78	-5.54	0.000993	0.007554	-0.79
260841_at	Expressed protein ; supported by full-le	---	AT1G29195	1.70	0.77	5.54	0.000993	0.007554	-0.79
267646_at	putative phosphate transporter	PHT5	AT2G32830	2.00	1.00	5.54	0.000994	0.007558	-0.79
245930_at	transcriptional co-activator-like protein	---	AT5G09240	-2.05	-1.04	-5.54	0.000995	0.007559	-0.80
252953_at	putative phosphatidylinositol synthase	PIS2	AT4G38570	-1.54	-0.62	-5.54	0.000995	0.007559	-0.80
254969_at	hypothetical protein ;supported by full-	---	AT4G10360	1.50	0.58	5.54	0.000996	0.00756	-0.80
254529_at	ATP binding protein - like nucleotide-b	INDL	AT4G19540	-1.48	-0.56	-5.54	0.000998	0.007573	-0.80
260913_at	s-adenosylmethionine synthetase iden	SAM1	AT1G02500	2.13	1.09	5.53	0.001	0.007589	-0.80
248326_at	Notchless protein homolog	---	AT5G52820	1.78	0.83	5.53	0.001002	0.007598	-0.80
257840_at	protein kinase, putative contains Pfam	AGC2-1	AT3G25250	9.19	3.20	5.53	0.001002	0.007598	-0.80

265795_at	putative serine carboxypeptidase II ;su	scpl26	AT2G35780	-1.60	-0.68	-5.53	0.001002	0.007599	-0.80
247360_at	cytochrome P450-like protein ;suppor	CYP94B1	AT5G63450	-3.68	-1.88	-5.53	0.001004	0.007608	-0.80
253889_at	forever young gene (FEY)	FEY	AT4G27760	-1.46	-0.54	-5.53	0.001004	0.007608	-0.81
265266_at	putative RNA-binding protein ; suppor	AML2	AT2G42890	1.71	0.77	5.53	0.001007	0.007629	-0.81
252995_at	hypothetical protein ;supported by full-	---	AT4G38370	-1.74	-0.80	-5.52	0.001009	0.007641	-0.81
249009_at	unknown protein ; supported by full-le	MAP18	AT5G44610	2.09	1.07	5.52	0.001011	0.007651	-0.81
260644_at	hypothetical protein contains similarity	---	AT1G53290	-1.75	-0.80	-5.52	0.001011	0.007651	-0.81
248248_at	spermidine synthase ;supported by fu	SPDS3	AT5G53120	2.18	1.12	5.52	0.001012	0.007651	-0.81
247232_at	ABC transporter-like	ATH13	AT5G64940	-1.79	-0.84	-5.52	0.001012	0.007651	-0.81
258507_at	neutral invertase, putative similar to n	---	AT3G06500	2.83	1.50	5.52	0.001012	0.007651	-0.81
263946_at	hypothetical protein ;supported by full-	---	AT2G36000	-1.63	-0.71	-5.52	0.001013	0.007653	-0.81
267577_at	unknown protein ; supported by cDNA	---	AT2G30710	-1.41	-0.50	-5.52	0.001014	0.00766	-0.82
260103_at	unknown protein	---	AT1G35430	-1.53	-0.61	-5.52	0.001015	0.00766	-0.82
263793_at	putative glucosyltransferase	ATCSLC08	AT2G24630	-2.49	-1.32	-5.52	0.001015	0.00766	-0.82
250265_at	putative protein predicted proteins, Ar	---	AT5G12900	-1.92	-0.94	-5.52	0.001015	0.00766	-0.82
245803_at	cysteine proteinase RD21A identical to	RD21	AT1G47128	1.75	0.81	5.52	0.001016	0.007662	-0.82
251367_at	SKP1 interacting partner 4 (SKIP4), p	SKIP4	AT3G61350	-1.69	-0.76	-5.52	0.001016	0.007662	-0.82
266893_at	hypothetical protein predicted by gens	RTE1	AT2G26070	-1.61	-0.69	-5.52	0.001016	0.007662	-0.82
258298_at	unknown protein ; supported by cDNA	---	AT3G23300	-1.82	-0.86	-5.52	0.001018	0.007672	-0.82
256156_at	phosphoinositide specific phospholipas	ATPLC2	AT3G08510	-1.53	-0.61	-5.52	0.001019	0.007677	-0.82
257983_at	unknown protein	---	AT3G20790	-3.21	-1.68	-5.51	0.00102	0.00768	-0.82
252652_at	putative chloroplast prephenate dehyd	ADT4	AT3G44720	5.04	2.33	5.51	0.00102	0.00768	-0.82
251282_at	putative protein transcription factor Pti	CRF6	AT3G61630	2.89	1.53	5.51	0.001022	0.007685	-0.82
249469_at	UDP-glucose dehydrogenase-like pro	---	AT5G39320	-2.88	-1.53	-5.51	0.001022	0.007685	-0.82
253200_at	vacuolar H+-transporting ATPase 16K	AVA-P1	AT4G34720	-1.70	-0.77	-5.51	0.001022	0.007685	-0.82
252470_at	protein kinase 6-like protein protein ki	---	AT3G46930	3.40	1.77	5.51	0.001022	0.007685	-0.82
250232_at	unknown protein	---	AT5G13950	-1.50	-0.58	-5.51	0.001023	0.007685	-0.82
265319_at	auxin-regulated protein (IAA8) ;suppo	IAA8	AT2G22670	-2.46	-1.30	-5.51	0.001023	0.007687	-0.83
258000_at	AIG2-like protein similar to AIG2 protei	---	AT3G28940	2.26	1.18	5.51	0.001025	0.00769	-0.83
264257_at	unknown protein	---	AT1G09230	1.68	0.75	5.51	0.001025	0.00769	-0.83
256160_at	pyruvate dehydrogenase E1 beta sub	PDH-E1 BE	AT1G30120	-1.86	-0.89	-5.51	0.001025	0.00769	-0.83
260042_at	hypothetical protein C-term similar to C	---	AT1G68820	2.09	1.07	5.51	0.001024	0.00769	-0.83
245284_at	phytoene dehydrogenase precursor (p	PDS3	AT4G14210	-1.90	-0.93	-5.51	0.001025	0.00769	-0.83
254602_at	hypothetical protein	EDR2	AT4G19040	1.53	0.62	5.51	0.001026	0.00769	-0.83
247100_at	selenium-binding protein-like	---	AT5G66520	-1.59	-0.67	-5.51	0.001028	0.007701	-0.83

263537_at	CONSTANS-like B-box zinc finger prot	COL3	AT2G24790	-1.51	-0.60	-5.51	0.001028	0.007701	-0.83
262210_at	hypothetical protein predicted by gens	IQD31	AT1G74690	-2.80	-1.48	-5.51	0.00103	0.007714	-0.83
251968_at	putative protein proline-rich protein, R	---	AT3G53100	-1.82	-0.86	-5.50	0.001032	0.007731	-0.84
249178_at	putative protein similar to unknown pro	SCP2	AT5G42890	1.51	0.59	5.50	0.001033	0.007733	-0.84
254755_at	hypothetical protein	---	AT4G13220	-1.64	-0.71	-5.50	0.001037	0.007759	-0.84
251251_at	serine/threonine protein kinase-like pr	---	AT3G62220	-1.61	-0.69	-5.50	0.001037	0.007761	-0.84
250255_at	sigma-like factor (gb|AAC97954.1) ; s	SIG4	AT5G13730	-2.45	-1.29	-5.50	0.001038	0.007764	-0.84
252383_at	ABC-type transport protein-like protein	ATH6	AT3G47780	3.45	1.78	5.50	0.001038	0.007764	-0.84
267475_at	expressed protein ; supported by full-le	---	AT2G02730	1.69	0.75	5.50	0.001039	0.007767	-0.84
249485_at	receptor protein kinase - like protein re	---	AT5G39020	3.50	1.81	5.49	0.001041	0.007773	-0.84
246644_at	putative protein	---	AT5G35100	-1.90	-0.93	-5.50	0.001041	0.007773	-0.84
262279_at	hypothetical protein predicted by gens	---	AT1G68630	2.55	1.35	5.49	0.001041	0.007773	-0.84
261795_at	unknown protein ; supported by cDNA:	---	AT1G16010	1.46	0.54	5.49	0.001042	0.007778	-0.85
246993_at	Cys2/His2-type zinc finger protein 1 (d	AZF1	AT5G67450	4.37	2.13	5.49	0.001043	0.007784	-0.85
267082_at	CPDK-related protein kinase CDPK:ca	CRK1	AT2G41140	1.48	0.56	5.49	0.001045	0.007794	-0.85
256178_s_	auxin conjugate hydrolase (ILL5) ident	ILL5	AT1G51760 /	4.44	2.15	5.49	0.001045	0.007795	-0.85
248088_at	2-oxoglutarate dehydrogenase E2 sub	---	AT5G55070	1.87	0.90	5.49	0.001046	0.0078	-0.85
260144_at	putative ABC transporter similar to bre	---	AT1G71960	1.79	0.84	5.49	0.001048	0.007806	-0.85
261057_at	hypothetical protein predicted by gene	---	AT1G01230	-1.56	-0.64	-5.49	0.001051	0.007831	-0.86
258068_at	putative DNA-binding protein, GT-1 si	---	AT3G25990	1.51	0.59	5.48	0.001053	0.007838	-0.86
258394_at	unknown protein ;supported by full-ler	---	AT3G15530	-2.35	-1.23	-5.48	0.001054	0.007849	-0.86
261601_at	ARP protein, putative similar to ARP p	NQR	AT1G49670	1.51	0.59	5.48	0.001055	0.007849	-0.86
245408_at	putative protein	---	AT4G17180	-1.69	-0.76	-5.48	0.001055	0.007851	-0.86
245736_at	Dr4(protease inhibitor) identical to Dr4	ATDR4	AT1G73330	-2.76	-1.47	-5.48	0.001059	0.007875	-0.86
247388_s_	transcription factor Hap5a-like protein	NF-YC1	AT3G48590 /	-2.44	-1.28	-5.48	0.00106	0.00788	-0.86
266366_at	unknown protein	---	AT2G41420	-1.73	-0.79	-5.48	0.001061	0.007882	-0.87
260639_at	hypothetical protein predicted by gene	---	AT1G53180	2.98	1.57	5.48	0.001061	0.007882	-0.87
255743_at	unknown protein ; supported by cDNA:	---	AT1G25375	-1.56	-0.64	-5.48	0.001062	0.007885	-0.87
267259_at	Expressed protein ; supported by full-le	---	AT2G23090 /	1.59	0.67	5.48	0.001062	0.007885	-0.87
256910_at	hypothetical protein	---	AT3G24080	1.71	0.77	5.47	0.001063	0.007893	-0.87
257477_at	unknown protein	---	AT1G10660	1.78	0.83	5.47	0.001067	0.007916	-0.87
250960_at	putative protein	---	AT5G02940	-2.28	-1.19	-5.47	0.001069	0.007927	-0.87
246593_at	putative protein predicted protein, Ara	---	AT5G14790	-1.86	-0.90	-5.47	0.001069	0.007927	-0.87
250402_at	putative protein unnamed ORF cDNA	---	AT5G10940	1.50	0.58	5.47	0.001069	0.007927	-0.87
247677_at	oxysterol-binding protein - like oyster	ORP3C	AT5G59420	1.47	0.55	5.46	0.001074	0.007956	-0.88

250858_at	I-box binding factor - like protein I-box	---	AT5G04760	1.91	0.94	5.46	0.001077	0.007979	-0.88
252549_at	protein kinase - like receptor-like prote	---	AT3G45860	-3.01	-1.59	-5.46	0.001078	0.007986	-0.88
256098_at	unknown protein similar to 6-phosphog	---	AT1G13700	-2.38	-1.25	-5.46	0.001081	0.008002	-0.89
246630_at	hypothetical protein predicted by gene	---	AT1G50730	-2.15	-1.10	-5.46	0.001081	0.008004	-0.89
247983_at	pyrophosphate-dependent phosphofru	PFK7	AT5G56630	3.19	1.68	5.46	0.001083	0.008014	-0.89
259460_at	unknown protein ; supported by cDNA:	---	AT1G44000	-2.28	-1.19	-5.46	0.001084	0.008014	-0.89
262612_at	unknown protein location of ESTs 144	---	AT1G14150	-3.04	-1.60	-5.45	0.001088	0.008047	-0.89
249951_at	S-adenosyl-L-methionine decarboxyla	BUD2	AT5G18930	-1.99	-0.99	-5.45	0.001089	0.008051	-0.89
261649_at	putative clathrin-coat assembly protein	---	AT1G27700	-1.53	-0.61	-5.45	0.001091	0.008061	-0.90
250337_at	putative protein SF21 protein, Heliantl	---	AT5G11790	-4.12	-2.04	-5.45	0.001094	0.008075	-0.90
256706_at	auxin-independent growth promoter, p	---	AT3G30300	-1.60	-0.67	-5.45	0.001094	0.008075	-0.90
246405_at	disease resistance protein RPP1-WsE	---	AT1G57630	9.56	3.26	5.45	0.001093	0.008075	-0.90
255257_at	score=526.5, E=1.9e-154, N=3 ;supp	UBQ11	AT4G05050	1.45	0.53	5.45	0.001095	0.008077	-0.90
257403_at	hypothetical protein similar to hypothet	---	AT1G62520	-1.55	-0.63	-5.45	0.001095	0.008078	-0.90
246923_at	putative multispanning membrane pro	---	AT5G25100	-1.70	-0.77	-5.44	0.001096	0.008078	-0.90
251644_at	putative protein putative DNA binding	---	AT3G57540	2.33	1.22	5.44	0.001096	0.008078	-0.90
258247_at	hypothetical protein predicted by gene	---	AT3G29130	-1.37	-0.46	-5.45	0.001096	0.008078	-0.90
253397_at	putative protein kinase protein kinase	---	AT4G32710	-1.46	-0.54	-5.44	0.001098	0.008092	-0.90
254144_at	putative protein	---	AT4G24690	1.56	0.64	5.44	0.001103	0.00812	-0.91
250575_at	putative protein	---	AT5G08240	2.17	1.12	5.44	0.001103	0.00812	-0.91
255259_at	coded for by A. thaliana cDNA W4343	NDB2	AT4G05020	6.95	2.80	5.44	0.001105	0.00813	-0.91
263073_at	unknown protein ;supported by full-ler	---	AT2G17500	29.28	4.87	5.44	0.001105	0.008131	-0.91
262200_at	unknown protein similar to membrane	---	AT2G01070	-1.72	-0.78	-5.44	0.001105	0.008131	-0.91
250582_at	transcription factor-like protein ethyler	---	AT5G07580	-2.39	-1.25	-5.43	0.001107	0.008142	-0.91
251816_at	Expressed protein ; supported by cDN	TON1B	AT3G55005	-1.81	-0.86	-5.43	0.001108	0.008146	-0.91
253579_at	SERINE CARBOXYPEPTIDASE II-lik	BRS1	AT4G30610	-2.87	-1.52	-5.43	0.001109	0.008147	-0.91
249537_at	cysteine-tRNA ligase -like protein cyst	---	AT5G38830	1.74	0.80	5.43	0.001109	0.00815	-0.91
264545_at	photosystem I subunit V precursor, pu	PSAG	AT1G55670	-1.40	-0.49	-5.43	0.00111	0.008153	-0.92
265411_at	unknown protein	---	AT2G16630	-4.62	-2.21	-5.43	0.001114	0.008178	-0.92
260163_at	putative carnitine/acylcarnitine translo	BAC2	AT1G79900	3.87	1.95	5.42	0.00112	0.008222	-0.93
249720_at	fimbrin ; supported by cDNA: gi_1502	FIM2	AT5G35700	1.51	0.59	5.42	0.001121	0.008228	-0.93
249554_at	CRS2 -like protein CRS2, Zea mays,	---	AT5G38290	-2.90	-1.53	-5.42	0.001124	0.008241	-0.93
251198_at	putative protein PGP237-11, Petunia	---	AT3G62970	-1.50	-0.58	-5.42	0.001125	0.008247	-0.93
254460_at	putative protein sigma70 operon, Stap	ATRP1	AT4G21210	-1.76	-0.81	-5.42	0.001127	0.008258	-0.93
251503_at	ABC transporter-like protein putative r	ATMRP14	AT3G59140	2.17	1.12	5.42	0.001128	0.008264	-0.93

256274_at	GTPase, putative contains Pfam profil	emb2738	AT3G12080	-1.48	-0.57	-5.42	0.001128	0.008264	-0.93
253475_at	putative protein predicted protein, Ara	---	AT4G32290	-2.32	-1.21	-5.42	0.001129	0.008266	-0.93
263516_at	AtRer1B ;supported by full-length cDN	ATRER1B	AT2G21600	-1.60	-0.68	-5.41	0.001131	0.008276	-0.94
263566_at	hypothetical protein predicted by gene	---	AT2G15340	1.63	0.70	5.41	0.001131	0.008276	-0.94
263871_at	hypothetical protein predicted by gens	RKP	AT2G22010	1.67	0.74	5.41	0.001131	0.008277	-0.94
265344_at	unknown protein predicted by genefinc	---	AT2G22660	1.87	0.90	5.41	0.001133	0.008288	-0.94
262368_at	unknown protein ;supported by full-len	---	AT1G73060 /	-2.03	-1.02	-5.41	0.001134	0.008289	-0.94
255999_at	DNA-binding protein, putative similar t	WRKY71	AT1G29860	2.92	1.55	5.41	0.001135	0.00829	-0.94
246041_at	phospholipase - like protein various pr	---	AT5G19290	-1.42	-0.51	-5.41	0.001134	0.00829	-0.94
249109_at	auxin-induced protein AUX2-11 (sp P3	ATAUX2-11	AT5G43700	-4.54	-2.18	-5.41	0.001136	0.008292	-0.94
258107_at	unknown protein ; supported by cDNA	ALF5	AT3G23560	1.53	0.61	5.41	0.001136	0.008292	-0.94
249359_at	putative protein unnamed ORF, Homo	---	AT5G40470	1.70	0.77	5.41	0.001138	0.008304	-0.94
266291_at	putative tropinone reductase ;supporte	---	AT2G29320	2.30	1.20	5.41	0.001139	0.008309	-0.94
245679_at	clathrin-associated protein, putative si	---	AT1G56590	-1.59	-0.67	-5.41	0.001139	0.008309	-0.94
256525_at	unknown protein ;supported by full-len	---	AT1G66180	-2.42	-1.27	-5.41	0.001139	0.008309	-0.94
245749_at	proline-rich protein, putative similar to	---	AT1G51090	-3.76	-1.91	-5.41	0.001141	0.008315	-0.94
258202_at	unknown protein	---	AT3G13940	2.08	1.06	5.40	0.001142	0.008323	-0.95
253826_s_	E2, ubiquitin-conjugating enzyme 9 (U	UBC9	AT4G27960 /	1.42	0.50	5.40	0.001144	0.008325	-0.95
245082_at	hypothetical protein predicted by gene	---	AT2G23270	16.11	4.01	5.40	0.001143	0.008325	-0.95
261090_at	protein kinase, putative contains Pfam	---	AT1G07560	1.65	0.72	5.40	0.001144	0.008325	-0.95
256319_at	trehalose-phosphatase, putative conta	---	AT1G35910	3.83	1.94	5.40	0.001144	0.008325	-0.95
259346_at	putative glutamate dehydrogenase sim	GDH3	AT3G03910	-1.46	-0.54	-5.40	0.001144	0.008326	-0.95
264371_at	pEARLI 1-like protein may be induced	ELP	AT1G12090	-2.36	-1.24	-5.40	0.001145	0.008331	-0.95
247913_at	unknown protein	---	AT5G57510	10.73	3.42	5.40	0.001146	0.008336	-0.95
264574_at	putative zinc transporter Similar to Ara	ZIP5	AT1G05300	2.47	1.31	5.40	0.001147	0.008339	-0.95
266052_at	putative WRKY-type DNA binding prot	WRKY55	AT2G40740	2.25	1.17	5.40	0.001148	0.008344	-0.95
259080_at	putative mitogen activated protein kina	WNK1	AT3G04910	-1.67	-0.74	-5.40	0.00115	0.00835	-0.95
267208_at	putative shaggy-like protein kinase dze	ASKdZeta	AT2G30980	-1.41	-0.50	-5.40	0.00115	0.00835	-0.95
245009_at	ribosomal protein S4	---	---	-1.42	-0.51	-5.40	0.001151	0.008359	-0.95
260986_at	glyoxalase II, putative similar to GI:16	GLY3	AT1G53580	2.06	1.05	5.40	0.001153	0.008365	-0.96
266229_at	putative RING zinc finger ankyrin prote	---	AT2G28840	1.48	0.57	5.39	0.001154	0.008373	-0.96
264580_at	unknown protein EST gb|ATTS0295 co	---	AT1G05340	2.57	1.36	5.39	0.001155	0.008376	-0.96
259232_at	unknown protein similar to hypothetica	---	AT3G11420	-2.00	-1.00	-5.39	0.001156	0.008377	-0.96
255731_at	phosphoprotein phosphatase 2A, regu	RCN1	AT1G25490	-1.41	-0.49	-5.39	0.001156	0.008377	-0.96
266821_at	putative ethylene response element bi	ERF13	AT2G44840	9.31	3.22	5.39	0.001158	0.008392	-0.96

246796_at	putative protein myosin heavy chain, c	---	AT5G26770	-1.80	-0.84	-5.39	0.001161	0.008412	-0.96
252527_at	dTDP-glucose 4-6-dehydratases-like p	UXS5	AT3G46440	1.67	0.74	5.39	0.001164	0.008427	-0.97
253575_at	putative protein TINY, Arabidopsis tha	---	AT4G31060	-1.52	-0.61	-5.38	0.001167	0.008451	-0.97
248134_at	putative protein contains similarity to ir	---	AT5G54860	2.26	1.17	5.38	0.001168	0.008456	-0.97
259881_at	Expressed protein ; supported by cDN	---	AT1G76820	1.91	0.93	5.38	0.001169	0.008458	-0.97
249333_at	GDSL-motif lipase/hydrolase-like prote	GLIP1	AT5G40990	5.38	2.43	5.38	0.00117	0.008463	-0.97
263106_at	hypothetical protein predicted by gens	---	AT2G05160	-1.70	-0.77	-5.38	0.001171	0.008469	-0.97
258992_at	unknown protein similar to unknown pr	---	AT3G08930	-1.40	-0.48	-5.38	0.001172	0.008473	-0.97
254737_at	fatty acid elongase - like protein (cer2	---	AT4G13840	-3.24	-1.70	-5.38	0.001174	0.008483	-0.98
260060_at	feebly-like protein similar to feebly prot	---	AT1G73680	1.72	0.78	5.38	0.001175	0.008486	-0.98
250617_at	Mei2-like protein Mei2-like protein - A	AML4	AT5G07290	1.65	0.72	5.38	0.001175	0.008486	-0.98
267363_at	putative peroxisomal membrane carrie	---	AT2G39970	1.51	0.60	5.38	0.001176	0.008486	-0.98
260748_at	RING-H2 finger protein RHA3a, putati	---	AT1G49210	-5.03	-2.33	-5.38	0.001178	0.008498	-0.98
255077_at	putative protein	---	AT4G09150	-1.97	-0.98	-5.37	0.001179	0.008502	-0.98
251100_at	aldose reductase-like protein aldose r	---	AT5G01670	2.20	1.14	5.37	0.001179	0.008506	-0.98
255575_at	predicted protein of unknown function	---	AT4G01430	3.34	1.74	5.37	0.00118	0.008506	-0.98
258970_at	putative serine carboxypeptidase prec	scpl49	AT3G10410	1.79	0.84	5.37	0.00118	0.008506	-0.98
261451_at	unknown protein	---	AT1G21060	-3.63	-1.86	-5.37	0.001181	0.008507	-0.98
264429_at	hypothetical protein similar to membra	---	AT1G61670	-1.45	-0.53	-5.37	0.001182	0.00851	-0.98
256411_at	ATP-dependent Clp protease proteolyt	CLPP3	AT1G66670	2.02	1.01	5.37	0.001183	0.008517	-0.98
256786_at	unknown protein ;supported by full-ler	---	AT3G13740	-1.73	-0.79	-5.37	0.001183	0.008517	-0.98
266226_at	histone H4 identical to GB:M17133 an	HIS4	AT2G28740	-2.02	-1.01	-5.37	0.001184	0.008517	-0.99
267549_at	hypothetical protein predicted by gens	---	AT2G32640	-3.32	-1.73	-5.37	0.001187	0.008531	-0.99
246280_at	hypothetical protein	---	AT4G36660	-2.51	-1.33	-5.37	0.00119	0.008531	-0.99
245821_at	hypothetical protein similar to putative	---	AT1G26270	-1.72	-0.78	-5.37	0.001188	0.008531	-0.99
250851_at	putative protein rngB protein, Dictyost	---	AT5G04420	-1.68	-0.75	-5.37	0.001188	0.008531	-0.99
260626_at	storage protein, putative similar to GB	---	AT1G08040	-1.63	-0.70	-5.37	0.00119	0.008531	-0.99
262135_at	AP2 domain containing protein, putati	RAP2.4	AT1G78080	2.34	1.23	5.37	0.001186	0.008531	-0.99
253581_at	stress responsive protein homolog lov	---	AT4G30660	-2.56	-1.36	-5.37	0.001189	0.008531	-0.99
265030_at	receptor-like kinase, putative similar t	---	AT1G61610	2.47	1.30	5.37	0.001189	0.008531	-0.99
249126_at	Expressed protein ; supported by cDN	TOPP6	AT5G43380	2.59	1.37	5.37	0.001189	0.008531	-0.99
250994_at	dnaK-type molecular chaperone hsc7	---	AT5G02490	3.36	1.75	5.37	0.001188	0.008531	-0.99
248140_at	putative protein similar to unknown pro	---	AT5G54980	-1.54	-0.63	-5.37	0.001188	0.008531	-0.99
263823_s_	AP2 domain transcription factor	---	AT2G40340 /	2.55	1.35	5.36	0.001191	0.008536	-0.99
265815_at	predicted protein	---	AT2G17975	-1.38	-0.47	-5.36	0.001192	0.008543	-0.99

265226_at	unknown protein ; supported by cDNA	---	AT2G28430	-1.43	-0.52	-5.36	0.001195	0.00856	-1.00
262483_at	putative translation initiation factor IF2	FUG1	AT1G17220	-1.48	-0.57	-5.36	0.001196	0.008562	-1.00
265076_at	Rubisco subunit binding-protein beta s	CPN60B	AT1G55490	-2.18	-1.12	-5.36	0.001197	0.008571	-1.00
249171_at	putative protein contains similarity to R	---	AT5G42940	1.72	0.78	5.36	0.001198	0.008571	-1.00
254078_at	putative protein various predicted prot	---	AT4G25710	1.60	0.68	5.36	0.0012	0.008584	-1.00
253343_at	putative protein	---	AT4G33540	3.02	1.60	5.36	0.001202	0.008585	-1.00
255879_at	receptor-like kinase, putative similar t	---	AT1G67000	2.68	1.42	5.36	0.001201	0.008585	-1.00
252066_at	receptor-protein kinase-like protein re	FER	AT3G51550	-1.92	-0.94	-5.36	0.001201	0.008585	-1.00
257950_at	putative UDP-glucose glucosyltransfer	UGT71B6	AT3G21780	4.08	2.03	5.36	0.001201	0.008585	-1.00
250383_at	putative GTP-binding protein GTP-bin	---	AT5G11480	-1.86	-0.90	-5.36	0.001201	0.008585	-1.00
249619_at	stelar K+ outward rectifying channel (	GORK	AT5G37500	-1.89	-0.92	-5.35	0.001204	0.008597	-1.00
253964_at	putative protein qkI-7, Mus musculus	---	AT4G26480	-1.53	-0.61	-5.35	0.001207	0.00861	-1.01
262837_at	dynamin, putative similar to dynamin-	ADL1C	AT1G14830	-1.57	-0.65	-5.35	0.001207	0.00861	-1.01
248948_at	putative protein strong similarity to unk	---	AT5G45560	-1.85	-0.89	-5.35	0.001206	0.00861	-1.01
252410_at	putative protein br-1 protein (NITRIC (	NOA1	AT3G47450	-1.70	-0.77	-5.35	0.001207	0.00861	-1.01
253118_at	ras-related small GTP-binding protein	ARAC6	AT4G35950	-1.72	-0.79	-5.35	0.001208	0.008612	-1.01
258452_at	alternative oxidase 1a precursor identi	AOX1A	AT3G22370	4.02	2.01	5.35	0.001209	0.008617	-1.01
254742_at	putative protein various predicted 3-iso	IIL1	AT4G13430	-1.41	-0.50	-5.35	0.001209	0.008617	-1.01
248726_at	RAS superfamily GTP-binding protein-	ATRABA4C	AT5G47960	6.87	2.78	5.35	0.00121	0.008622	-1.01
249932_at	unknown protein	---	AT5G22390	-3.28	-1.71	-5.35	0.001212	0.008633	-1.01
251689_at	putative protein motif in hypothetical p	---	AT3G56500	4.48	2.16	5.35	0.001214	0.008644	-1.01
255536_at	Expressed protein ; supported by full-l	---	AT4G01575	-2.03	-1.02	-5.34	0.001216	0.008654	-1.01
264657_at	putative 26S protease regulatory subu	RPT5B	AT1G09100	1.50	0.58	5.34	0.001217	0.008659	-1.02
246568_at	E2F transcription factor -like protein E	DEL2	AT5G14960	-1.67	-0.74	-5.34	0.001217	0.008659	-1.02
263760_at	unknown protein ; supported by cDNA	SULA	AT2G21280	-2.03	-1.02	-5.34	0.001218	0.008662	-1.02
258730_at	putative GTP-binding protein (ATFP8)	ATFP8	AT3G11730	-1.38	-0.47	-5.34	0.001219	0.008666	-1.02
250763_at	short chain alcohol dehydrogenase-lik	---	AT5G06060	-1.63	-0.70	-5.34	0.001221	0.008678	-1.02
267614_at	putative cytochrome P450	BAS1	AT2G26710	-3.79	-1.92	-5.34	0.001224	0.008694	-1.02
251630_at	putative protein unknown protein - Arb	---	AT3G57420	-1.46	-0.54	-5.34	0.001225	0.008697	-1.02
262879_at	plastid RNA polymerase sigma-subuni	SIGA	AT1G64860	-1.60	-0.68	-5.34	0.001225	0.008697	-1.02
266566_at	unknown protein	---	AT2G24040	1.61	0.69	5.34	0.001226	0.008697	-1.02
261420_at	fatty acid elongase 3-ketoacyl-CoA sy	KCS3	AT1G07720	-2.54	-1.35	-5.33	0.001229	0.008712	-1.03
251308_at	putative protein several hypothetical pr	GAUT1	AT3G61130	-1.50	-0.58	-5.33	0.001229	0.008712	-1.03
264968_at	stress related protein, putative similar	---	AT1G67360	2.77	1.47	5.34	0.001228	0.008712	-1.03
248566_s_	FRO2-like protein; NADPH oxidase-lik	ATFRO7	AT5G49730 /	-2.26	-1.17	-5.34	0.001228	0.008712	-1.03

265643_at	hypothetical protein predicted by gene	---	AT2G27390 /	2.26	1.18	5.33	0.001235	0.008752	-1.03
247478_at	DC1.2 homologue - like protein DC1.2	---	AT5G62360	-3.80	-1.93	-5.33	0.001236	0.008753	-1.03
261133_at	DYW7 protein identical to DYW7 prote	---	AT1G19715	-1.95	-0.97	-5.33	0.001236	0.008754	-1.03
259564_at	hypothetical protein	---	AT1G20540	-1.44	-0.52	-5.33	0.001237	0.008757	-1.03
266288_s_	putative pumilio/Mpt5 family RNA-bind	APUM1	AT2G29140 /	1.65	0.72	5.33	0.001238	0.00876	-1.03
259185_at	putative phosphate/phosphoenolpyruv	PPT2	AT3G01550	-5.35	-2.42	-5.33	0.001239	0.008768	-1.04
267337_at	putative anthocyanin 5-aromatic acyltra	---	AT2G39980	-1.93	-0.95	-5.33	0.00124	0.008769	-1.04
261375_at	transcription factor, putative similar to	SPL4	AT1G53160	-5.97	-2.58	-5.32	0.001241	0.008778	-1.04
259892_at	germin-like protein similar to germin pr	GER1	AT1G72610	-6.83	-2.77	-5.32	0.001244	0.008786	-1.04
251057_at	putative protein alkB protein - Escheri	---	AT5G01780	-1.39	-0.48	-5.32	0.001244	0.008786	-1.04
253806_at	putative protein Arabidopsis thaliana F	---	AT4G28270	-1.70	-0.77	-5.32	0.001243	0.008786	-1.04
262700_at	unknown protein	---	AT1G76020	-1.73	-0.79	-5.32	0.001248	0.008808	-1.04
251733_at	copper homeostasis factor ;supported	CCH	AT3G56240	1.58	0.66	5.32	0.001248	0.008808	-1.04
250549_at	N-hydroxycinnamoyl benzoyltransfera	---	AT5G07860	-1.96	-0.97	-5.32	0.001248	0.008808	-1.04
257533_at	putative alpha/beta hydrolase contains	---	AT3G10840	-2.12	-1.08	-5.32	0.001248	0.008808	-1.04
261406_at	unknown protein contains similarity to	NRP2	AT1G18800	1.96	0.97	5.32	0.001249	0.008809	-1.04
248914_at	Rab-type small GTP-binding protein-lik	AtRABA1c	AT5G45750	-2.07	-1.05	-5.32	0.00125	0.00881	-1.05
257365_x_	putative antifungal protein	PDF1.2b	AT2G26020	8.95	3.16	5.32	0.00125	0.00881	-1.04
254926_at	ACC synthase (AtACS-6) ; supported	ACS6	AT4G11280	9.33	3.22	5.32	0.00125	0.00881	-1.05
247132_at	putative protein strong similarity to unk	ARO2	AT5G66200	-1.78	-0.83	-5.32	0.001251	0.008811	-1.05
266536_at	hypothetical protein predicted by gene	---	AT2G16900	3.53	1.82	5.32	0.001252	0.008813	-1.05
256159_at	Expressed protein ; supported by full-le	JAZ8	AT1G30135	6.82	2.77	5.32	0.001252	0.008813	-1.05
252965_at	putative auxin-induced protein auxin-i	---	AT4G38860	-2.92	-1.55	-5.32	0.001253	0.008814	-1.05
247034_at	cyclin D3-like protein ;supported by ful	CYCD3;2	AT5G67260	-1.83	-0.87	-5.32	0.001253	0.008814	-1.05
252105_at	protein phosphatase 2C-like protein p	---	AT3G51470	-1.70	-0.76	-5.32	0.001254	0.008817	-1.05
256928_at	unknown protein	---	AT3G22590	-1.55	-0.63	-5.31	0.001255	0.008818	-1.05
265369_s_	putative retroelement pol polyprotein c	---	---	-1.48	-0.57	-5.32	0.001254	0.008818	-1.05
264929_at	auxin-induced protein, putative similar	---	AT1G60730	6.41	2.68	5.31	0.001255	0.008819	-1.05
247486_at	putative protein	---	AT5G62140	-1.93	-0.95	-5.31	0.001255	0.008819	-1.05
266672_at	putative Na+-dependent inorganic pho	PHT4;1	AT2G29650	-1.50	-0.59	-5.31	0.001257	0.008825	-1.05
265440_at	pEARLI 4 protein Same as GB: L4308	pEARLI4	AT2G20960	2.17	1.12	5.31	0.001258	0.008825	-1.05
262793_at	putative cytochrome P450 monooxyge	CYP71B7	AT1G13110	2.73	1.45	5.31	0.001258	0.008825	-1.05
249035_at	putative protein contains similarity to u	GLK2	AT5G44190	-1.65	-0.73	-5.31	0.001258	0.008825	-1.05
250998_at	ankyrin - like protein ankyrin G119, Ho	---	AT5G02620	1.86	0.89	5.31	0.001258	0.008827	-1.05
245347_at	ferredoxin ;supported by full-length cD	---	AT4G14890	-1.76	-0.81	-5.31	0.001262	0.008848	-1.06

260872_at	hypothetical protein predicted by gene	---	AT1G21350	-1.90	-0.93	-5.31	0.001262	0.00885	-1.06
267060_at	unknown protein ; supported by full-le	---	AT2G32580	-1.93	-0.95	-5.31	0.001265	0.008864	-1.06
258381_at	kinesin-like protein similar to mitotic ce	KINESIN-13	AT3G16630	-1.60	-0.67	-5.31	0.001267	0.008879	-1.06
257933_at	aminoalcoholphosphotransferase, put	AAPT2	AT3G25585	2.04	1.03	5.30	0.001269	0.008887	-1.06
265571_s_	unknown protein	---	AT2G28020 /	-1.47	-0.56	-5.30	0.001269	0.008887	-1.06
254301_at	predicted protein predicted protein, Ar	---	AT4G22790	1.91	0.94	5.30	0.00127	0.008889	-1.06
246305_at	putative protein protein At2g40060 - A	---	AT3G51890	1.65	0.73	5.30	0.00127	0.008889	-1.06
254965_at	putative protein other hypothetical prot	---	AT4G11090	-1.44	-0.53	-5.30	0.001272	0.008893	-1.06
266394_at	Ras-related GTP-binding protein (ARA	ARA4	AT2G43130	-1.54	-0.62	-5.30	0.001272	0.008893	-1.06
254730_at	putative protein GTPase activating pro	---	AT4G13730	-1.44	-0.53	-5.30	0.001275	0.008911	-1.07
250918_at	putative protein proline-rich protein AF	---	AT5G03610	6.44	2.69	5.30	0.001277	0.008924	-1.07
259023_at	unknown protein ; supported by cDNA	---	AT3G07510	-2.03	-1.02	-5.30	0.001277	0.008924	-1.07
252039_at	Expressed protein ; supported by cDN	---	AT3G52155	-1.64	-0.71	-5.30	0.001278	0.008924	-1.07
254280_at	Expressed protein ; supported by full-le	SMO1-2	AT4G22756	-1.90	-0.92	-5.29	0.001281	0.008946	-1.07
264142_at	hypothetical protein predicted by gens	---	AT1G78930	1.86	0.90	5.29	0.001282	0.008951	-1.07
249354_at	nuclear pore protein -like nuclear pore	EMB3012	AT5G40480	1.90	0.92	5.29	0.001284	0.008962	-1.07
267405_at	putative related to microbial divalent ca	CUTA	AT2G33740	1.46	0.54	5.29	0.00129	0.009001	-1.08
245359_at	carnitine racemase like protein ;suppor	IBR10	AT4G14430	2.18	1.13	5.29	0.001294	0.009016	-1.08
247864_s_	anthranilate synthase beta chain ;sup	---	AT1G24807 /	4.76	2.25	5.29	0.001294	0.009016	-1.08
263072_at	putative protein kinase contains a prot	---	AT2G17530	1.50	0.58	5.29	0.001294	0.009016	-1.08
267026_at	DREB-like AP2 domain transcription fa	---	AT2G38340	3.81	1.93	5.29	0.001294	0.009017	-1.08
252983_at	cinnamyl-alcohol dehydrogenase ELI3	ELI3-1	AT4G37980	2.15	1.10	5.28	0.001295	0.009017	-1.08
248219_at	unknown protein ; supported by full-le	---	AT5G53650	1.37	0.46	5.28	0.001296	0.009026	-1.09
261982_at	hypothetical protein predicted by gene	---	AT1G33780	-1.46	-0.54	-5.28	0.001298	0.009033	-1.09
258796_at	unknown protein ;supported by full-ler	WDL1	AT3G04630	-2.57	-1.36	-5.28	0.001299	0.009036	-1.09
262856_at	unknown protein contains Pfam profile	---	AT1G14910	-1.66	-0.73	-5.28	0.0013	0.009045	-1.09
254878_at	heat shock transcription factor - like p	AT-HSFB2B	AT4G11660	-2.08	-1.05	-5.28	0.001303	0.00906	-1.09
265618_at	hypothetical protein predicted by gens	---	AT2G25460	1.58	0.66	5.28	0.001304	0.00906	-1.09
260653_at	pyruvate kinase, plastid isozyme, puta	PKp3	AT1G32440	-1.56	-0.64	-5.28	0.001303	0.00906	-1.09
257113_at	cytochrome P450, putative contains P	CYP705A22	AT3G20130	-2.41	-1.27	-5.28	0.001305	0.009064	-1.09
245301_at	farnesyl-pyrophosphate synthetase FP	FPS2	AT4G17190	-2.33	-1.22	-5.28	0.001305	0.009064	-1.09
257994_at	unknown protein	---	AT3G19920	1.83	0.87	5.28	0.001306	0.009071	-1.09
251108_at	putative protein several hypothetical pr	---	AT5G01620	-1.90	-0.93	-5.28	0.001307	0.009072	-1.09
249242_at	alcohol dehydrogenase	---	AT5G42250	1.66	0.73	5.28	0.001308	0.009077	-1.09
265877_at	unknown protein ; supported by cDNA	BZIP34	AT2G42380	-2.19	-1.13	-5.27	0.001309	0.009083	-1.10

253028_at	putative protein	pde191	AT4G38160	-1.52	-0.60	-5.27	0.00131	0.009083	-1.10
245158_at	hypothetical protein predicted by gene	RALFL18	AT2G33130	1.84	0.88	5.27	0.00131	0.009083	-1.10
249475_at	putative protein CGI-108 protein, Hom	---	AT5G38890	1.75	0.81	5.27	0.001311	0.009085	-1.10
266141_at	protease inhibitor II contains a gamma	PDF2.1	AT2G02120	1.45	0.53	5.27	0.001315	0.009112	-1.10
262960_at	unknown protein ; supported by cDNA	---	AT1G54320	1.53	0.61	5.27	0.001318	0.009131	-1.10
252215_at	kinesin -like protein KINESIN-LIKE PR	KICP-02	AT3G50240	-3.35	-1.74	-5.26	0.001322	0.009157	-1.11
255702_at	subtilisin-like serine protease XSP1 ide	XSP1	AT4G00230	-1.88	-0.91	-5.26	0.001323	0.009158	-1.11
258662_at	unknown protein	---	AT3G02900	-2.45	-1.29	-5.26	0.001324	0.009163	-1.11
256296_at	hypothetical protein	---	AT1G69480	1.45	0.53	5.26	0.001325	0.009164	-1.11
254112_at	putative protein KIAA0136 gene, Hom	---	AT4G24970	1.52	0.60	5.26	0.001327	0.009176	-1.11
263345_s_	putative chlorophyll a/b binding protein	LHCB2.1	AT2G05070 /	-3.00	-1.59	-5.26	0.001327	0.009176	-1.11
254656_at	putative protein ;supported by full-leng	---	AT4G18070	-1.84	-0.88	-5.26	0.00133	0.009196	-1.11
263788_at	putative sarcosine oxidase	---	AT2G24580	1.99	0.99	5.26	0.001333	0.009213	-1.12
262711_at	hypothetical protein predicted by gens	---	AT1G16500	1.88	0.91	5.25	0.001337	0.009227	-1.12
256799_at	unknown protein ; supported by cDNA	---	AT3G18560	2.80	1.48	5.26	0.001336	0.009227	-1.12
247610_at	putative protein predicted protein, Ara	---	AT5G60630	10.26	3.36	5.25	0.001336	0.009227	-1.12
258434_at	AP2 domain containing protein RAP2.3	ATEBP	AT3G16770	1.89	0.92	5.25	0.001337	0.00923	-1.12
254687_at	cytochrome P450 monooxygenase (CY	CYP83A1	AT4G13770 /	-1.88	-0.91	-5.25	0.001339	0.009241	-1.12
266679_at	putative helicase ; supported by cDNA	---	AT2G03270	1.57	0.65	5.25	0.00134	0.009244	-1.12
260324_at	unknown protein similar to hypothetica	ISPF	AT1G63970	-1.69	-0.76	-5.25	0.001341	0.009244	-1.12
266304_at	hypothetical protein	---	AT2G27090	1.48	0.57	5.25	0.001343	0.009257	-1.12
245613_at	hypothetical protein	---	AT4G14450 /	9.35	3.22	5.25	0.001343	0.009257	-1.12
251105_at	putative protein unknown protein At2g	ATSCAR4	AT5G01730	-2.57	-1.36	-5.25	0.001344	0.009258	-1.12
253417_at	putative protein	PC-MYB1	AT4G32730	1.50	0.59	5.25	0.001344	0.009258	-1.12
245395_at	hypothetical protein ;supported by full-	---	AT4G17420	-1.66	-0.73	-5.25	0.001346	0.009267	-1.13
262944_at	phosphoglycerate kinase, putative sim	PGK	AT1G79550	1.82	0.86	5.25	0.001348	0.009279	-1.13
266142_at	unknown protein ; supported by cDNA	---	AT2G39030	9.47	3.24	5.24	0.001351	0.009293	-1.13
260133_at	ethylene-response protein, ETR1 iden	ETR1	AT1G66340	1.41	0.50	5.24	0.001351	0.009297	-1.13
252122_at	putative protein hypothetical protein -	---	AT3G51140	-1.56	-0.65	-5.24	0.001353	0.009301	-1.13
261762_at	hypothetical protein predicted by gene	---	AT1G15510	2.24	1.16	5.24	0.001357	0.00933	-1.14
259878_at	putative catechol O-methyltransferase	---	AT1G76790	-2.57	-1.36	-5.24	0.001361	0.00935	-1.14
250611_at	gibberellin 20-oxidase	GA20OX3	AT5G07200	-2.02	-1.01	-5.24	0.001361	0.00935	-1.14
263494_at	14-3-3 protein GF14mu (grf9) identica	GRF9	AT2G42590	-1.44	-0.53	-5.24	0.001361	0.00935	-1.14
254848_at	putative protein hypothetical protein F	PGRL1B	AT4G11960	1.52	0.61	5.24	0.001365	0.009367	-1.14
256837_at	hypothetical protein similar to DNA-dire	NRPD7	AT3G22900	-2.07	-1.05	-5.24	0.001365	0.009367	-1.14

260800_at	unknown protein	TSD2	AT1G78240	-1.83	-0.87	-5.23	0.001365	0.009368	-1.14
267619_at	putative receptor-like protein kinase ;	---	AT2G26730	-2.18	-1.12	-5.23	0.001367	0.00938	-1.14
247881_at	putative protein similar to unknown pro	---	AT5G57700	-2.76	-1.46	-5.23	0.001368	0.009382	-1.14
251432_at	putative protein leucine zipper-EF-har	---	AT3G59820	1.90	0.92	5.23	0.001368	0.009382	-1.14
251852_at	putative protein	---	AT3G54750	-1.84	-0.88	-5.23	0.001369	0.009384	-1.14
247415_at	unknown protein	---	AT5G63060	-2.25	-1.17	-5.23	0.001373	0.009407	-1.15
253759_at	AIM1 protein ; supported by cDNA: gi_	AIM1	AT4G29010	1.41	0.49	5.23	0.001373	0.009407	-1.15
250161_at	putative protein amino acid transport p	---	AT5G15240	2.10	1.07	5.23	0.001374	0.009408	-1.15
250094_at	2-hydroxyphytanoyl-CoA lyase-like pro	---	AT5G17380	2.86	1.52	5.23	0.001376	0.009418	-1.15
255438_at	putative oxidoreductase	AOP1	AT4G03070	-2.57	-1.36	-5.23	0.001376	0.009419	-1.15
255458_at	small nuclear riboprotein Sm-D1-like p	---	AT4G02840	-1.44	-0.53	-5.23	0.001377	0.00942	-1.15
265005_at	Expressed protein ; supported by full-l	---	AT1G61667	-2.10	-1.07	-5.22	0.001381	0.009443	-1.15
258871_at	putative 26S proteosome regulatory su	---	AT3G03060	2.64	1.40	5.22	0.001382	0.009452	-1.16
246329_at	putative protein gamma-tubulin intera	---	AT3G43610	-1.59	-0.67	-5.22	0.001386	0.009472	-1.16
255766_at	unknown protein ;supported by full-len	---	AT1G16750	-1.72	-0.78	-5.22	0.001389	0.009492	-1.16
247184_at	putative protein contains similarity to u	UBP17	AT5G65450	-1.70	-0.76	-5.22	0.001391	0.009499	-1.16
250644_at	protein phosphatase 2C-like ;supporte	---	AT5G06750	1.92	0.94	5.22	0.001391	0.009499	-1.16
253999_at	1-aminocyclopropane-1-carboxylate s	ACS7	AT4G26200	2.45	1.29	5.22	0.001393	0.009511	-1.16
266055_at	hypothetical protein predicted by gens	---	AT2G40650	1.62	0.69	5.22	0.001394	0.009514	-1.16
256529_at	protein kinase, putative contains Pfam	---	AT1G33260	-2.25	-1.17	-5.21	0.001396	0.009526	-1.17
255059_at	putative protein downy mildew resista	---	AT4G09420	-2.67	-1.42	-5.21	0.001397	0.009526	-1.17
244999_at	RNA polymerase beta subunit	---	---	-1.96	-0.97	-5.21	0.001397	0.009526	-1.17
252123_at	flavanone 3-hydroxylase (FH3) ;suppo	F3H	AT3G51240	-1.48	-0.56	-5.21	0.001398	0.009529	-1.17
246251_at	cold acclimation protein homolog	---	AT4G37220	-3.04	-1.61	-5.21	0.001399	0.00953	-1.17
250970_at	putative protein ; supported by cDNA:	---	AT5G02770	1.46	0.54	5.21	0.001399	0.00953	-1.17
252480_at	putative protein methyl-CpG-binding p	MBD5	AT3G46580	-1.40	-0.49	-5.21	0.001399	0.00953	-1.17
263797_at	putative WRKY-type DNA binding prot	WRKY17	AT2G24570	4.31	2.11	5.21	0.001404	0.009555	-1.17
258497_at	putative flowering-time gene CONSTA	COL2	AT3G02380	-1.55	-0.63	-5.21	0.001404	0.009555	-1.17
261753_at	unknown protein	---	AT1G76340	-1.61	-0.69	-5.21	0.001405	0.009561	-1.17
263750_at	unknown protein	---	AT2G21530	-1.73	-0.79	-5.21	0.001405	0.009561	-1.17
259593_at	nuclear transport factor 2, putative sim	NTF2B	AT1G27970	1.40	0.49	5.21	0.001407	0.009567	-1.18
266656_at	putative CCCH-type zinc finger protein	ATCTH	AT2G25900	-1.81	-0.85	-5.21	0.001407	0.009567	-1.17
259749_at	putative ribose 5-phosphate isomerase	RSW10	AT1G71100	2.38	1.25	5.21	0.001408	0.009567	-1.18
262126_at	disease resistance protein, putative si	CW9	AT1G59620	1.79	0.84	5.20	0.001412	0.009595	-1.18
251850_at	F-box protein family, AtFBL17 contain	FBL17	AT3G54650	-1.83	-0.87	-5.20	0.001413	0.009599	-1.18

252939_at	NAD(P)H oxidoreductase, isoflavone r	---	AT4G39230	4.24	2.08	5.20	0.001415	0.009609	-1.18
252338_at	putative progesterone-binding protein I	MAPR3	AT3G48890	3.95	1.98	5.20	0.00142	0.009641	-1.18
253362_s_	putative protein cyclopropane-fatty-ac	---	AT4G33110 /	-1.79	-0.84	-5.20	0.001422	0.009653	-1.19
257444_at	hypothetical protein predicted by gens	---	AT2G12550	1.65	0.72	5.20	0.001424	0.009662	-1.19
250993_at	putative protein HSPC172, Homo sap	---	AT5G02280	-1.57	-0.65	-5.19	0.001427	0.009676	-1.19
253398_at	putative protein retinal pigment micros	CCD8	AT4G32810	2.75	1.46	5.19	0.001429	0.009689	-1.19
252824_at	histone H3.3 ; supported by cDNA: gi_	---	AT4G40030	1.56	0.64	5.19	0.00143	0.009694	-1.19
263980_at	hypothetical protein predicted by grail;s	---	AT2G42770	-1.69	-0.76	-5.19	0.001432	0.0097	-1.19
261718_at	wall-associated kinase, putative simila	---	AT1G18390	3.55	1.83	5.19	0.001432	0.0097	-1.19
260373_at	unknown protein	---	AT1G73970	1.50	0.59	5.19	0.001433	0.009702	-1.19
249375_at	putative protein predicted proteins, Ar	AGP24	AT5G40730	-1.53	-0.61	-5.19	0.001433	0.009705	-1.20
258557_at	hypothetical protein similar to recepto	---	AT3G05990	1.49	0.57	5.19	0.001438	0.009735	-1.20
248006_at	unknown protein	HAP8	AT5G56250	-1.50	-0.58	-5.18	0.001441	0.00975	-1.20
260882_at	DNA binding protein, putative similar t	WRKY65	AT1G29280	2.25	1.17	5.18	0.001442	0.009756	-1.20
260079_s_	helix-loop-helix protein 1A, putative si	---	AT1G35460 /	-1.52	-0.60	-5.18	0.001448	0.009791	-1.21
255421_at	putative protein phosphatase regulator	---	AT4G03260	1.58	0.66	5.18	0.001451	0.00981	-1.21
246263_at	unknown protein	---	AT1G31780	-1.70	-0.77	-5.18	0.001454	0.009828	-1.21
264674_at	Expressed protein ; supported by full-l	POLD4	AT1G09815	1.57	0.65	5.17	0.001456	0.009839	-1.21
261838_at	heat shock protein hsp70, putative sin	Hsp70b	AT1G16030	1.51	0.60	5.17	0.001457	0.009839	-1.21
260491_at	hypothetical protein predicted by gene	---	AT1G51440	-1.83	-0.87	-5.17	0.001458	0.009839	-1.21
249237_at	putative protein similar to unknown pro	---	AT5G42050	1.89	0.92	5.17	0.001457	0.009839	-1.21
251334_at	putative protein several hypothetical pr	---	AT3G61390	1.68	0.75	5.17	0.001459	0.009849	-1.21
261663_at	hypothetical protein similar to hypothet	EPR1	AT1G18330 /	-3.51	-1.81	-5.17	0.001461	0.009852	-1.22
258323_at	unknown protein similar to putative pro	---	AT3G22750	1.78	0.83	5.17	0.00146	0.009852	-1.22
259550_at	hypothetical protein ;supported by full-	AGP5	AT1G35230	5.22	2.38	5.17	0.001461	0.009852	-1.22
266984_at	unknown protein ; supported by cDNA	---	AT2G39570	2.24	1.16	5.17	0.001465	0.009877	-1.22
249279_at	SCARECROW gene regulator-like pro	---	AT5G41920	-1.41	-0.49	-5.17	0.001468	0.009889	-1.22
260496_at	putative ABC transporter	---	AT2G41700	1.41	0.50	5.17	0.001468	0.00989	-1.22
248207_at	tyrosine aminotransferase	---	AT5G53970	3.37	1.75	5.17	0.001469	0.00989	-1.22
250131_at	unknown protein ; supported by cDNA	---	AT5G16550	-1.91	-0.94	-5.16	0.001472	0.009911	-1.22
264071_at	putative carboxypeptidase ; supported	SCPL51	AT2G27920	-2.10	-1.07	-5.16	0.001473	0.009912	-1.22
261935_at	phosphoribosylanthranilate transferas	---	AT1G22610	-1.43	-0.52	-5.16	0.001476	0.00993	-1.23
263260_at	putative protein-tyrosine phosphatase	OTS2	AT1G10570	-1.45	-0.53	-5.16	0.001476	0.00993	-1.23
265025_at	Expressed protein ; supported by full-l	---	AT1G24575	1.57	0.65	5.16	0.001478	0.009936	-1.23
266010_at	putative C2H2-type zinc finger protein	---	AT2G37430	17.89	4.16	5.16	0.00148	0.009952	-1.23

251915_at	putative protein peroxisomal Ca-depe	---	AT3G53940	1.70	0.76	5.16	0.001482	0.009957	-1.23
265316_at	unknown protein	---	AT2G20400	1.84	0.88	5.16	0.001483	0.009957	-1.23
260086_at	hypothetical protein predicted by gens	---	AT1G63240	-1.78	-0.83	-5.16	0.001482	0.009957	-1.23
252469_at	protein kinase - like protein Raf protei	---	AT3G46920	1.73	0.79	5.16	0.001483	0.009957	-1.23
254545_at	putative protein FKBP-type peptidyl-p	---	AT4G19830	-2.05	-1.04	-5.16	0.001485	0.009971	-1.23
260747_at	unknown protein ; supported by cDNA	---	AT1G78420	1.42	0.50	5.15	0.001488	0.009984	-1.24
261488_at	Expressed protein ; supported by full-l	---	AT1G14345	-1.66	-0.74	-5.15	0.00149	0.009998	-1.24
253207_at	putative protein small auxin up-regula	---	AT4G34770	-3.24	-1.69	-5.15	0.001491	0.009999	-1.24
260928_at	hypothetical protein similar to putative	GATL5	AT1G02720	-1.52	-0.60	-5.15	0.001491	0.009999	-1.24
261025_at	Expressed protein ; supported by full-l	---	AT1G01225	-2.13	-1.09	-5.15	0.001499	0.010031	-1.24
245742_at	aldehyde dehydrogenase, putative sir	ALDH3H1	AT1G44170	1.92	0.94	5.15	0.001499	0.010031	-1.24
246120_at	tetratricopeptide repeat protein tetratri	---	AT5G20360	1.64	0.72	5.15	0.001499	0.010031	-1.24
255602_at	Expressed protein ; supported by full-l	---	AT4G01026	-1.61	-0.68	-5.15	0.001498	0.010031	-1.24
255798_at	unknown protein predicted by genefinc	---	AT2G33255	-1.56	-0.64	-5.15	0.001497	0.010031	-1.24
257250_at	transfactor, putative similar to GB:BAA	---	AT3G24120	-1.54	-0.62	-5.15	0.001499	0.010031	-1.24
249007_at	unknown protein ;supported by full-ler	---	AT5G44650	-2.01	-1.01	-5.15	0.001498	0.010031	-1.24
264191_at	integral membrane protein, putative	---	AT1G54730	-1.90	-0.93	-5.15	0.001501	0.010043	-1.25
261116_at	sec14 cytosolic factor, putative similar	---	AT1G75370	-1.50	-0.58	-5.14	0.001503	0.010049	-1.25
260167_at	hypothetical protein predicted by gens	---	AT1G71970	-1.61	-0.69	-5.14	0.001503	0.010049	-1.25
264922_s_	U2 snRNP auxiliary factor, large subu	---	AT1G60830 /	1.42	0.50	5.14	0.001504	0.01005	-1.25
260350_at	Eukaryotic initiation factor 5A , putati	ELF5A-3	AT1G69410	1.81	0.85	5.14	0.001505	0.010052	-1.25
249574_at	putative protein embryonic abundant p	PDLP7	AT5G37660	-1.53	-0.61	-5.14	0.001505	0.010052	-1.25
254921_at	putative protein hypothetical protein F	---	AT4G11300	1.89	0.92	5.14	0.001505	0.010052	-1.25
258641_at	unknown protein ;supported by full-ler	---	AT3G08030	-4.17	-2.06	-5.14	0.001507	0.010057	-1.25
255240_at	coded for by A. thaliana cDNA Z18000	IBR1	AT4G05530	1.49	0.57	5.14	0.001508	0.010057	-1.25
254020_at	beta-carotene hydroxylase ; supporte	BETA-OHAS	AT4G25700	4.06	2.02	5.14	0.001508	0.010057	-1.25
250371_at	putative protein 23 kDa polypeptide of	---	AT5G11450	-1.62	-0.70	-5.14	0.001507	0.010057	-1.25
248146_at	translation initiation factor-like protein	---	AT5G54940	1.50	0.58	5.14	0.001509	0.010063	-1.25
254433_at	putative protein tripeptidyl-peptidase I	TPP2	AT4G20850	1.41	0.49	5.14	0.001512	0.01008	-1.25
263274_at	putative protein kinase contains a prot	CRCK3	AT2G11520	1.59	0.67	5.14	0.001513	0.010082	-1.25
253191_at	cysteine protease XCP1 identical to pa	XCP1	AT4G35350	-4.13	-2.05	-5.14	0.001513	0.010082	-1.25
246953_at	unknown protein ;supported by full-ler	VPS60.2	AT5G04850	1.49	0.57	5.14	0.001517	0.010101	-1.26
252010_at	hypothetical protein ; supported by cDI	---	AT3G52740	-1.72	-0.78	-5.14	0.001517	0.010101	-1.26
247768_at	I-box binding factor - like protein I-box	---	AT5G58900	-3.47	-1.79	-5.13	0.00152	0.010117	-1.26
262104_at	hypothetical protein predicted by gene	LPA1	AT1G02910	-1.51	-0.60	-5.13	0.001521	0.010118	-1.26

247107_at	senescence-associated protein almost	STR16	AT5G66040	1.95	0.96	5.13	0.001522	0.010126	-1.26
248708_at	putative protein contains similarity to u	---	AT5G48560	-2.47	-1.30	-5.13	0.001523	0.010126	-1.26
251425_at	putative protein chloroplast Cpn21 pro	---	AT3G60210	-1.56	-0.64	-5.13	0.001523	0.010126	-1.26
258880_at	hypothetical protein similar to symbios	ATG8H	AT3G06420	2.57	1.36	5.13	0.001525	0.010134	-1.26
250061_at	chloroplast GrpE protein ; supported b	EMB1241	AT5G17710	-1.65	-0.72	-5.13	0.001527	0.010147	-1.26
250516_at	putative protein predicted proteins, Ar	---	AT5G09620	1.50	0.59	5.13	0.001528	0.01015	-1.27
248079_at	unknown protein	---	AT5G55790	-1.77	-0.83	-5.13	0.001532	0.010176	-1.27
262407_at	hypothetical protein predicted by gene	---	AT1G34630	-2.07	-1.05	-5.13	0.001534	0.01018	-1.27
248710_at	unknown protein ;supported by full-ler	---	AT5G48480	1.71	0.78	5.13	0.001534	0.01018	-1.27
261183_at	hypothetical protein predicted by gene	EMB2756	AT1G34550	-1.65	-0.72	-5.12	0.001536	0.010191	-1.27
252904_at	putative protein crp1 protein, Zea may	EMB2453	AT4G39620	-1.57	-0.65	-5.12	0.001538	0.010203	-1.27
254190_at	Expressed protein ; supported by full-l	---	AT4G23885	1.93	0.95	5.12	0.001545	0.010245	-1.28
251492_at	putative protein CGI-136 protein - Hor	TXR1	AT3G59280	1.39	0.48	5.12	0.001546	0.010246	-1.28
267169_at	putative oxidoreductase	---	AT2G37540	-2.38	-1.25	-5.12	0.001546	0.010248	-1.28
252135_at	putative cold acclimation protein cold	COR413-PM	AT3G50830	-1.78	-0.83	-5.12	0.001547	0.010252	-1.28
253453_at	protein phosphatase 2C - like protein	---	AT4G31860	1.41	0.49	5.12	0.00155	0.010269	-1.28
255177_at	strong similarity to 1-aminocyclopropa	ACS11	AT4G08040	-3.63	-1.86	-5.12	0.001551	0.01027	-1.28
257848_at	hypothetical protein predicted by gens	---	AT3G13030	-1.66	-0.73	-5.11	0.001553	0.010277	-1.28
267129_at	curly leaf protein (polycomb-group) ide	CLF	AT2G23380	-1.45	-0.54	-5.11	0.001555	0.010289	-1.28
247740_at	receptor-like protein kinase precursor	CRCK1	AT5G58940	3.35	1.75	5.11	0.001557	0.0103	-1.29
251306_at	putative DNA-binding protein DNA-bin	---	AT3G61260	-1.69	-0.76	-5.11	0.001558	0.010304	-1.29
246250_at	cysteine proteinase similar to cysteine	CP1	AT4G36880	8.45	3.08	5.11	0.001559	0.010309	-1.29
263155_at	transcriptional activation factor TAFII3	TAFII21	AT1G54140	-1.58	-0.66	-5.11	0.00156	0.01031	-1.29
262202_at	TATC-like protein similar to GB:AAD33	APG2	AT2G01110	-1.86	-0.89	-5.11	0.00156	0.01031	-1.29
259091_at	hypothetical protein predicted by gens	---	AT3G04890	-1.56	-0.64	-5.11	0.001562	0.010321	-1.29
249650_at	Expressed protein ; supported by cDN	SEF	AT5G37055	-1.59	-0.67	-5.11	0.001563	0.010325	-1.29
246162_at	actin interacting protein ; supported by	---	AT4G36400	1.69	0.76	5.11	0.001565	0.010329	-1.29
262891_at	ent-kaurene synthase, putative similar	GA2	AT1G79460	-1.95	-0.96	-5.11	0.001566	0.010331	-1.29
263692_at	unknown protein Location of ESTs 10	---	AT1G26850	-1.50	-0.58	-5.11	0.001565	0.010331	-1.29
259727_at	ferrodoxin precursor identical to FERR	FED A	AT1G60950	-1.42	-0.51	-5.11	0.001568	0.010341	-1.29
253012_at	putative protein Caenorhabditis elega	---	AT4G37900	1.52	0.60	5.11	0.001568	0.010341	-1.29
260068_at	putative calmodulin-binding protein sim	---	AT1G73805	3.62	1.86	5.10	0.001569	0.010344	-1.29
263243_at	putative glyoxalase II	GLX2-5	AT2G31350	1.59	0.67	5.10	0.00157	0.01035	-1.30
261639_at	tubulin alpha-2/alpha-4 chain, putative	TUA2	AT1G50010	-3.47	-1.79	-5.10	0.001574	0.010361	-1.30
246880_s_	myrosinase TGG2 ; supported by cDN	TGG2	AT5G25980 /	-3.68	-1.88	-5.10	0.001573	0.010361	-1.30

261032_at	unknown protein ;supported by full-len	---	AT1G17430	-3.28	-1.71	-5.10	0.001573	0.010361	-1.30
265768_at	putative sugar transporter ;supported	---	AT2G48020	-1.45	-0.54	-5.10	0.001574	0.010361	-1.30
257984_at	putative cell differentiation protein sim	---	AT3G20800	1.73	0.79	5.10	0.001575	0.010361	-1.30
266694_at	putative clathrin assembly protein ;sup	---	AT2G19790	-1.39	-0.47	-5.10	0.001574	0.010361	-1.30
245768_at	hypothetical protein similar to putative	---	AT1G33590	2.54	1.35	5.10	0.001575	0.010361	-1.30
262051_at	putative coatomer protein complex, su	---	AT1G79990	-1.64	-0.72	-5.10	0.001576	0.010365	-1.30
256406_at	unknown protein	---	AT1G50710	-1.56	-0.64	-5.10	0.001577	0.010367	-1.30
247155_at	2-oxoglutarate dehydrogenase, E1 co	---	AT5G65750	1.82	0.86	5.10	0.001581	0.010392	-1.30
246911_at	transcription factor TINY	tny	AT5G25810	-2.72	-1.44	-5.10	0.001583	0.010394	-1.30
256863_at	CCHC-type zinc finger protein, putativ	---	AT3G24070	-1.40	-0.49	-5.10	0.001582	0.010394	-1.30
250916_at	monodehydroascorbate reductase (N/	ATMDAR2	AT5G03630	3.59	1.84	5.10	0.001584	0.010403	-1.30
261269_at	unknown protein ; supported by full-ler	---	AT1G26690	1.61	0.68	5.10	0.001585	0.010403	-1.31
254716_at	putative protein LEA protein , Cicer ar	UNE15	AT4G13560	-1.83	-0.87	-5.09	0.001587	0.010414	-1.31
262566_at	auxin response factor 1, putative simil	ARF12	AT1G34310	-1.83	-0.87	-5.09	0.001588	0.010417	-1.31
259017_at	unknown protein ; supported by full-le	---	AT3G07310	-1.54	-0.62	-5.09	0.001588	0.010418	-1.31
257122_at	RNA-binding protein, putative contain	APUM5	AT3G20250	1.89	0.92	5.09	0.00159	0.010425	-1.31
249290_at	putative protein strong similarity to unk	---	AT5G41060	-2.04	-1.03	-5.09	0.001591	0.010426	-1.31
251980_at	putative protein endopeptidase Clp AT	---	AT3G53270	1.40	0.48	5.09	0.001591	0.010428	-1.31
262661_s_	hypothetical protein	---	AT1G14230 /	-4.91	-2.30	-5.09	0.001594	0.010434	-1.31
245331_at	hypothetical protein ;supported by full-	---	AT4G14410	1.47	0.56	5.09	0.001594	0.010434	-1.31
249519_at	putative protein similar to unknown pro	APE1	AT5G38660	-1.68	-0.75	-5.09	0.001593	0.010434	-1.31
253632_at	senescence-associated protein homol	TET9	AT4G30430	1.37	0.45	5.09	0.001597	0.01045	-1.31
244945_at	cytochrome c biogenesis orf206	---	---	1.67	0.74	5.09	0.001598	0.01045	-1.31
255779_at	unknown protein similar to beta-1,3-gl	PDCB3	AT1G18650	-2.42	-1.28	-5.09	0.001597	0.01045	-1.31
253297_at	beta-xylan endohydrolase -like protein	---	AT4G33810	-1.49	-0.57	-5.09	0.001601	0.010465	-1.32
259874_at	unknown protein	---	AT1G76660	-1.78	-0.83	-5.09	0.001601	0.010465	-1.32
257248_at	hypothetical protein predicted by gens	---	AT3G24150	-1.75	-0.81	-5.09	0.001602	0.010469	-1.32
249691_at	translation releasing factor RF-2 ;supp	HCF109	AT5G36170	-1.40	-0.48	-5.08	0.001603	0.010477	-1.32
247439_at	plasma membrane proton ATPase-like	AHA11	AT5G62670	-2.31	-1.21	-5.08	0.001604	0.010478	-1.32
255451_at	putative protein similar to T5J8.17	---	AT4G02860	1.61	0.69	5.08	0.001607	0.010497	-1.32
266002_at	hypothetical protein predicted by gens	---	AT2G37310	1.51	0.60	5.08	0.001608	0.010499	-1.32
267611_at	unknown protein	SPX2	AT2G26660	2.09	1.07	5.08	0.001611	0.010512	-1.32
255913_at	kinase, putative similar to leaf rust res	---	AT1G66980	1.38	0.47	5.08	0.001614	0.01053	-1.33
249513_at	glucosyltransferase-like protein ; supp	---	AT5G38460	-1.48	-0.56	-5.08	0.001615	0.010531	-1.33
253485_at	Expressed protein ; supported by full-l	WRKY18	AT4G31800	2.45	1.29	5.08	0.00162	0.010562	-1.33

266206_at	unknown protein ; supported by full-le	---	AT2G27730	1.70	0.77	5.07	0.001621	0.010566	-1.33
257217_at	phosphoenolpyruvate carboxylase (PP	ATPPC3	AT3G14940	-1.77	-0.83	-5.07	0.001623	0.010577	-1.33
259015_at	unknown protein similar to hypothetica	---	AT3G07350	-2.85	-1.51	-5.07	0.001624	0.010577	-1.33
252862_at	putative L-ascorbate oxidase L-ascort	---	AT4G39830	2.98	1.58	5.07	0.001624	0.010577	-1.33
258399_at	early auxin-induced protein, IAA19 ide	IAA19	AT3G15540	-4.28	-2.10	-5.07	0.001624	0.010578	-1.33
249636_at	beta-glucosidase -like protein prunasi	BGLU42	AT5G36890	-1.51	-0.60	-5.07	0.001631	0.010618	-1.34
255733_at	unknown protein similar to unknown pr	---	AT1G25400	1.99	0.99	5.07	0.001634	0.010633	-1.34
250761_at	ankyrin-like protein	---	AT5G06050	-1.55	-0.63	-5.07	0.001635	0.010637	-1.34
258060_at	protein phosphatase 2A regulatory sub	ATB' DELTA	AT3G26030	-1.42	-0.50	-5.07	0.001636	0.010638	-1.34
256070_at	hypothetical protein predicted by gens	---	AT1G13730	-1.46	-0.54	-5.07	0.001637	0.010641	-1.34
257719_at	unknown protein	AtALMT9	AT3G18440	1.75	0.81	5.06	0.001641	0.010665	-1.34
260303_at	putative protein kinase similar to C-ter	---	AT1G70520	2.35	1.24	5.06	0.001642	0.01067	-1.34
267197_at	hypothetical protein predicted by gens	---	AT2G30960	-1.46	-0.55	-5.06	0.001644	0.010683	-1.35
254645_at	putative protein	---	AT4G18520	-1.56	-0.64	-5.06	0.001647	0.010696	-1.35
250017_at	unknown protein	---	AT5G18140	-1.95	-0.96	-5.06	0.001648	0.010704	-1.35
251035_at	Expressed protein ; supported by full-l	---	AT5G02220	-1.84	-0.88	-5.06	0.00165	0.010711	-1.35
264024_at	hypothetical protein predicted by gene	---	AT2G21180	2.21	1.15	5.06	0.001651	0.010711	-1.35
255305_at	putative ABC transporter similar to Gu	ATABC1	AT4G04770	1.71	0.77	5.06	0.001652	0.01072	-1.35
250986_at	putative protein	---	AT5G02850	-1.48	-0.57	-5.05	0.001656	0.010741	-1.35
245756_at	hyoscyamine 6-dioxygenase hydroxyl	---	AT1G35190	1.81	0.86	5.05	0.001657	0.010741	-1.35
260820_at	receptor protein kinase, putative simil	---	AT1G06840	2.14	1.09	5.05	0.001658	0.010744	-1.35
263488_at	hypothetical protein predicted by gens	---	AT2G31840	-1.71	-0.77	-5.05	0.001659	0.010749	-1.36
257047_at	hypothetical protein predicted by gene	---	AT3G19570	-1.78	-0.83	-5.05	0.00166	0.010754	-1.36
262050_at	unknown protein ;supported by full-len	---	AT1G80130	-5.66	-2.50	-5.05	0.001662	0.010758	-1.36
246597_at	L-aspartate oxidase -like protein L-asp	AO	AT5G14760	3.72	1.90	5.05	0.001662	0.010758	-1.36
250005_at	putative protein predicted proteins, Ar	---	AT5G18760	-1.43	-0.52	-5.05	0.001665	0.010774	-1.36
248819_at	putative protein contains similarity to S	---	AT5G47050	2.04	1.03	5.05	0.001666	0.010774	-1.36
259461_at	unknown protein	---	AT1G18900	1.93	0.95	5.05	0.001666	0.010774	-1.36
250208_at	unknown protein ;supported by full-ler	anac084	AT5G14000	3.34	1.74	5.05	0.001666	0.010774	-1.36
255171_at	hypothetical protein	---	AT4G07990	1.44	0.53	5.05	0.001668	0.010785	-1.36
262900_at	hypothetical protein contains similarity	SNL5	AT1G59890	1.60	0.68	5.05	0.00167	0.010787	-1.36
252234_at	putative protein ; supported by full-len	ATPSK4	AT3G49780	4.88	2.29	5.05	0.00167	0.010787	-1.36
267056_at	hypothetical protein predicted by gens	---	AT2G32470	1.70	0.77	5.05	0.001669	0.010787	-1.36
247493_at	copine - like protein copine I, Homo sa	BON1	AT5G61900	2.19	1.13	5.05	0.00167	0.010787	-1.36
246269_at	putative protein	---	AT4G37110	-2.34	-1.22	-5.05	0.001673	0.010796	-1.36

247078_at	unknown protein ; supported by cDNA	---	AT5G66000	-1.55	-0.64	-5.05	0.001673	0.010796	-1.36
253053_at	putative protein beta-ketoadipate enol	---	AT4G37470	-1.69	-0.75	-5.05	0.001673	0.010796	-1.36
259659_at	hypothetical protein contains similarity	---	AT1G55170	1.76	0.81	5.04	0.001674	0.0108	-1.37
252412_at	Expressed protein ; supported by full-l	---	AT3G47295	-2.04	-1.03	-5.04	0.001675	0.010803	-1.37
257925_at	unknown protein ;supported by full-ler	---	AT3G23170	6.79	2.76	5.04	0.001678	0.010816	-1.37
245882_at	mitochondrial carrier-like protein mitoc	DIC3	AT5G09470	1.58	0.66	5.04	0.00168	0.010825	-1.37
246418_at	quinone oxidoreductase -like protein p	---	AT5G16960	1.66	0.73	5.04	0.001682	0.01084	-1.37
260033_at	putative mutT protein contains Pfam p	ATNUDX1	AT1G68760	-1.59	-0.67	-5.04	0.001684	0.010846	-1.37
248064_at	unknown protein	---	AT5G55570	-2.75	-1.46	-5.04	0.001686	0.010854	-1.37
255778_at	3-phosphoserine phosphatase identica	PSP	AT1G18640	-1.39	-0.47	-5.04	0.001686	0.010854	-1.37
245251_at	calcineurin B-like protein 1 ; supported	CBL1	AT4G17615	3.28	1.71	5.04	0.001688	0.010861	-1.37
262933_at	polyamine oxidase, putative similar to	ATPAO4	AT1G65840	1.95	0.96	5.04	0.001688	0.010861	-1.37
264948_at	RNA helicase, putative similar to RNA	---	AT1G77030	1.45	0.53	5.04	0.001688	0.010861	-1.37
251496_at	putative protein crp1 protein, involved	---	AT3G59040	-1.43	-0.52	-5.04	0.001691	0.010873	-1.38
254791_at	SERINE CARBOXYPEPTIDASE I PR	scpl20	AT4G12910	1.60	0.68	5.03	0.001695	0.010896	-1.38
245506_at	glutaredoxin homolog	---	AT4G15700	-2.47	-1.31	-5.03	0.001697	0.010907	-1.38
260607_at	putative receptor protein kinase	---	AT2G43700	1.70	0.76	5.03	0.001699	0.010919	-1.38
252375_at	rac GTP binding protein Arac8 ; suppo	ROP10	AT3G48040	-1.55	-0.63	-5.03	0.0017	0.010921	-1.38
266598_at	3-methyl-2-oxobutanoate hydroxy-met	KPHMT1	AT2G46110	-1.68	-0.74	-5.03	0.001701	0.010924	-1.38
253266_s_	putative protein predicted protein, Ara	---	AT2G45260 /	-1.60	-0.68	-5.03	0.001703	0.010931	-1.38
249780_at	ubiquitin	---	AT5G24240	1.63	0.71	5.03	0.00171	0.010973	-1.39
251254_at	putative protein anion exchanger 3, ca	---	AT3G62270	1.62	0.70	5.02	0.00171	0.010974	-1.39
262195_at	allergen, putative similar to allergen (C	---	AT1G78040	-2.53	-1.34	-5.02	0.001712	0.010979	-1.39
250680_at	putative protein similar to unknown pro	---	AT5G06570	-2.44	-1.29	-5.02	0.001713	0.010979	-1.39
256528_at	C2H2-type zinc finger protein, putative	ZFP4	AT1G66140	1.85	0.88	5.02	0.001712	0.010979	-1.39
265132_at	unknown protein ; supported by cDNA	---	AT1G23830	2.13	1.09	5.02	0.001714	0.010988	-1.39
259783_at	auxin-induced protein, putative similar	SAUR68	AT1G29510	-6.70	-2.74	-5.02	0.001716	0.010997	-1.39
259173_at	beta-glucosidase identical to beta-gluc	BGLU25	AT3G03640	-2.08	-1.06	-5.02	0.001718	0.011007	-1.39
262780_at	putative cytochrome P450 monooxyge	CYP71B28	AT1G13090	1.70	0.77	5.02	0.00172	0.011014	-1.39
266719_at	MYB-related transcription factor (CCA	CCA1	AT2G46830	-1.67	-0.74	-5.02	0.001721	0.011017	-1.40
245788_at	hypothetical protein similar to hypothet	---	AT1G32120 /	2.58	1.36	5.02	0.001722	0.011018	-1.40
262871_at	hypothetical protein predicted by gene	---	AT1G65010	-3.41	-1.77	-5.02	0.001723	0.011024	-1.40
261883_at	protein kinase, putative similar to rece	---	AT1G80870	-1.53	-0.62	-5.02	0.001724	0.01103	-1.40
263550_at	Expressed protein ; supported by cDN	---	AT2G17033	-1.59	-0.67	-5.02	0.001727	0.011043	-1.40
253465_at	putative protein ATAC98, Arabidopsis	---	AT4G32120	-1.67	-0.74	-5.02	0.001728	0.011043	-1.40

261087_at	hypothetical protein similar to unknown	---	AT1G17350	-1.88	-0.91	-5.02	0.001727	0.011043	-1.40
258094_at	putative cytochrome P450 similar to G	CYP72A15	AT3G14690	1.53	0.62	5.02	0.001728	0.011043	-1.40
261613_at	abscisic acid responsive elements-bin	ABF1	AT1G49720	1.86	0.89	5.01	0.001731	0.011057	-1.40
252646_at	protein kinase-like protein protein kina	---	AT3G44610	-1.44	-0.52	-5.01	0.001732	0.011058	-1.40
259830_at	hypothetical protein predicted by gens	---	AT1G80630	-1.53	-0.61	-5.01	0.001733	0.011066	-1.40
246252_s_	patatin-like protein ;supported by full-le	PLP1	AT4G37060 /	1.39	0.47	5.01	0.001734	0.011068	-1.40
246653_at	putative protein clathrin assembly prot	---	AT5G35200	1.50	0.58	5.01	0.001736	0.011072	-1.40
257833_at	transcriptional regulator protein, putati	LWD2	AT3G26640	-1.40	-0.49	-5.01	0.001736	0.011072	-1.40
260477_at	Ser/Thr protein kinase isolog	---	AT1G11050	5.15	2.37	5.01	0.00174	0.011095	-1.41
246547_at	seed maturation -like protein seed ma	---	AT5G14970	-1.73	-0.79	-5.01	0.00174	0.011095	-1.41
251494_at	protein kinase-like protein Pto kinase	---	AT3G59350	-2.59	-1.37	-5.01	0.001744	0.011118	-1.41
247205_at	unknown protein ;supported by full-ler	PROPEP2	AT5G64890	7.11	2.83	5.01	0.001747	0.011126	-1.41
254532_at	putative protein regulatory protein NPI	NPR4	AT4G19660	1.94	0.96	5.01	0.001747	0.011126	-1.41
250511_at	putative protein similar to unknown pro	---	AT5G09960	-1.51	-0.59	-5.00	0.001749	0.011138	-1.41
264924_at	RNA polymerase subunit identical to R	ATRPAC43	AT1G60620	1.43	0.52	5.00	0.00175	0.011141	-1.41
255365_at	putative phosphofructokinase beta sub	MEE51	AT4G04040	1.45	0.53	5.00	0.001753	0.011154	-1.42
260369_at	60S ribosomal protein L34, putative si	RPL34	AT1G69620	-1.76	-0.82	-5.00	0.001755	0.011166	-1.42
251656_at	putative protein N-ACETYLGLUCOSA	---	AT3G57170	-1.51	-0.59	-5.00	0.001759	0.011192	-1.42
254919_at	RING-H2 finger protein RHA1b ;suppo	RHA1B	AT4G11360	1.93	0.95	5.00	0.001761	0.011194	-1.42
261676_at	Expressed protein ; supported by full-le	---	AT1G18480	1.64	0.71	5.00	0.00176	0.011194	-1.42
253088_at	ferulate-5-hydroxylase (FAH1) ; suppo	FAH1	AT4G36220	2.44	1.29	5.00	0.001762	0.011196	-1.42
263924_at	enolase (2-phospho-D-glycerate hydro	LOS2	AT2G36530	2.44	1.28	5.00	0.001763	0.011201	-1.42
252095_at	epoxide hydrolase-like protein epoxide	---	AT3G51000	1.64	0.71	5.00	0.001763	0.011201	-1.42
247212_at	putative protein similar to unknown pro	---	AT5G65040	1.41	0.50	4.99	0.001768	0.01123	-1.43
258588_s_	glyceraldehyde-3-phosphate dehydrog	GAPC1	AT3G04120	2.32	1.21	4.99	0.001772	0.011252	-1.43
261304_at	unknown protein ;supported by full-len	---	AT1G48440	-1.37	-0.45	-4.99	0.001774	0.011259	-1.43
254306_at	putative protein ; supported by cDNA:	ATCES1	AT4G22330	-1.39	-0.47	-4.99	0.001778	0.011269	-1.43
264255_at	putative SF2/ASF splicing modulator,	---	AT1G09140	1.73	0.79	4.99	0.001777	0.011269	-1.43
254620_at	pollen-specific protein - like 18.3K pro	---	AT4G18590	-1.51	-0.60	-4.99	0.001777	0.011269	-1.43
253620_at	receptor-like kinase homolog somatic	---	AT4G30520	-1.54	-0.63	-4.99	0.001777	0.011269	-1.43
252931_at	putative ubiquitin-dependent proteolyt	---	AT4G38930	1.49	0.57	4.99	0.001778	0.011269	-1.43
252189_at	cyclin D3-like protein Nicotiana tabacu	CYCD3;3	AT3G50070	-1.86	-0.89	-4.99	0.001779	0.011272	-1.43
263763_at	Expressed protein ; supported by cDN	---	AT2G21385	-2.08	-1.05	-4.99	0.00178	0.011272	-1.43
252430_at	CHLOROPHYLL A-B BINDING PROT	LHCA4	AT3G47470	-1.63	-0.70	-4.99	0.001782	0.011285	-1.43
253420_at	H+-transporting ATP synthase chain 9	---	AT4G32260	-1.57	-0.65	-4.99	0.001783	0.011286	-1.43

254051_at	putative protein other Arabidopsis puta	---	AT4G25270	-1.49	-0.57	-4.99	0.001784	0.011288	-1.43
267539_at	putative RING zinc finger protein ; sup	---	AT2G42030	-1.55	-0.63	-4.99	0.001784	0.011289	-1.44
252254_at	hypothetical protein ; supported by cD	DMS3	AT3G49250	-1.41	-0.49	-4.99	0.001785	0.011289	-1.44
254350_at	putative protein hypothetical protein, c	---	AT4G22280	-1.39	-0.47	-4.98	0.001788	0.011306	-1.44
263733_at	polyprotein, putative similar to polypro	---	---	-1.35	-0.44	-4.98	0.00179	0.011318	-1.44
255638_at	predicted protein of unknown function	---	AT4G00740	-1.70	-0.76	-4.98	0.001793	0.01133	-1.44
259428_at	MAP kinase, putative similar to MAP k	ATMPK11	AT1G01560	7.89	2.98	4.98	0.001793	0.011332	-1.44
245685_at	Expressed protein ; supported by cDN	E2F1	AT5G22220	-1.39	-0.48	-4.98	0.001795	0.011336	-1.44
246247_at	putative protein	---	AT4G36640	3.45	1.79	4.98	0.001796	0.011341	-1.44
261438_at	metallothionein-like protein identical to	---	AT1G07590 /	1.41	0.50	4.98	0.001799	0.01136	-1.44
258113_at	putative cytochrome P450 similar to G	CYP72A11	AT3G14650	-1.92	-0.94	-4.98	0.001801	0.011368	-1.45
261450_s_	O-methyltransferase, putative similar t	---	AT1G21110 /	18.80	4.23	4.98	0.001804	0.011384	-1.45
252421_at	endochitinase-like protein BASIC END	---	AT3G47540	9.14	3.19	4.97	0.001807	0.011396	-1.45
249783_at	calcium sensor homolog (gb|AAC2611	SOS3	AT5G24270	2.31	1.21	4.97	0.001808	0.011396	-1.45
267153_at	glutathione S-transferase identical to G	ATGSTF9	AT2G30860	1.75	0.81	4.97	0.001807	0.011396	-1.45
248091_at	putative protein strong similarity to unk	VTC5	AT5G55120	3.21	1.68	4.97	0.001808	0.011396	-1.45
262193_at	eukaryotic initiation factor 5 (eIF-5), pu	---	AT1G77840	1.76	0.82	4.97	0.001809	0.011399	-1.45
266927_at	aquaporin (plasma membrane intrinsi	PIP1B	AT2G45960	-1.65	-0.72	-4.97	0.00181	0.011403	-1.45
250339_at	NADP dependent malic enzyme - like	ATNADP-ME	AT5G11670	1.70	0.77	4.97	0.001815	0.011428	-1.45
266896_at	putative ATP-dependent RNA helicase	---	AT2G45810	-1.38	-0.47	-4.97	0.001815	0.01143	-1.45
254869_at	protein kinase - like protein KI domain	---	AT4G11890	2.52	1.33	4.97	0.001817	0.011438	-1.45
262177_at	isochorismate synthase (icsI) identica	EDS16	AT1G74710	3.34	1.74	4.97	0.001819	0.011446	-1.46
255447_at	hypothetical protein similar to A. thalia	---	AT4G02790	-2.09	-1.06	-4.97	0.001825	0.011481	-1.46
247285_at	putative protein similar to unknown pro	---	AT5G64400	1.44	0.52	4.96	0.001827	0.011491	-1.46
256147_at	hypothetical protein predicted by gene	---	AT1G55080	1.65	0.72	4.96	0.001828	0.011491	-1.46
254872_at	putative protein several hypothetical pr	---	AT4G11560	1.43	0.52	4.96	0.001828	0.011493	-1.46
266799_at	unknown protein	ATPSK2	AT2G22860	2.17	1.12	4.96	0.001839	0.011554	-1.47
262170_at	hypothetical protein predicted by gene	---	AT1G74940	-1.84	-0.88	-4.96	0.00184	0.011555	-1.47
251610_at	putative protein hypothetical protein T	---	AT3G57930	-3.40	-1.77	-4.96	0.00184	0.011555	-1.47
253462_at	synaptobrevin-like protein synaptobre	ATVAMP711	AT4G32150	1.60	0.68	4.96	0.00184	0.011555	-1.47
246398_at	auxin-induced basic helix-loop-helix tr	---	AT1G58100	-1.36	-0.44	-4.96	0.001842	0.011556	-1.47
266845_at	unknown protein	---	AT2G26110	-1.94	-0.95	-4.96	0.001841	0.011556	-1.47
247925_at	TCH4 protein (gb|AAA92363.1) ; supp	TCH4	AT5G57560	-5.37	-2.43	-4.96	0.001843	0.011559	-1.47
261265_at	hypothetical protein predicted by gens	---	AT1G26800	-2.03	-1.02	-4.96	0.001843	0.011559	-1.47
245031_at	putative mitochondrial carrier protein	---	AT2G26360	-1.40	-0.48	-4.96	0.001846	0.011573	-1.47

247835_at	putative protein similar to unknown pro	---	AT5G57910	2.20	1.14	4.95	0.001851	0.011601	-1.48
253516_at	hypothetical protein	---	AT4G31360	-1.86	-0.90	-4.95	0.001854	0.011615	-1.48
264781_at	putative plastid RNA polymerase sigm	SIG2	AT1G08540	-1.72	-0.78	-4.95	0.001855	0.011623	-1.48
257547_at	hypothetical protein predicted by gens	---	AT3G13000	-2.93	-1.55	-4.95	0.001856	0.011624	-1.48
250021_at	casein kinase-like protein	---	AT5G18190	-1.35	-0.44	-4.95	0.001857	0.011625	-1.48
245501_at	hypothetical protein	---	AT4G15620	2.48	1.31	4.95	0.001857	0.011625	-1.48
245755_at	hypothetical protein predicted by gene	---	AT1G35210	10.66	3.41	4.95	0.001858	0.011628	-1.48
260857_at	unknown protein contains Pfam profile	LYM1	AT1G21880	-2.54	-1.34	-4.95	0.00186	0.011634	-1.48
266464_at	glutathione-conjugate transporter AtMI	ATMRP4	AT2G47800	7.40	2.89	4.95	0.001861	0.011634	-1.48
261481_at	nucleoside triphosphatase, putative si	---	AT1G14260	1.67	0.74	4.95	0.00186	0.011634	-1.48
262616_at	oxidoreductase, putative contains Pfa	---	AT1G06620	2.20	1.14	4.95	0.001865	0.011654	-1.48
251302_at	RAV-like protein DNA-binding protein	NGA2	AT3G61970	-1.36	-0.44	-4.95	0.001865	0.011654	-1.48
266331_at	putative RGA1, giberellin repsonse m	RGA1	AT2G01570	-1.62	-0.70	-4.95	0.001866	0.011655	-1.48
250711_at	cell division related protein-like	---	AT5G06110	1.47	0.56	4.94	0.001867	0.011663	-1.48
245133_at	putative nucleotide sugar epimerase	GAE4	AT2G45310	-1.89	-0.92	-4.94	0.00187	0.011672	-1.49
265595_at	26S proteasome subunit 4 ;supported	---	AT2G20140	-1.61	-0.68	-4.94	0.00187	0.011672	-1.49
249726_at	unknown protein	---	AT5G35480	-2.04	-1.03	-4.94	0.00187	0.011672	-1.49
245411_at	hypothetical protein	---	AT4G17240	-2.00	-1.00	-4.94	0.001872	0.011677	-1.49
257923_at	hypothetical protein predicted by gens	---	AT3G23160	2.84	1.51	4.94	0.001874	0.01168	-1.49
267033_at	unknown protein ;supported by full-ler	---	AT2G38450	1.37	0.45	4.94	0.001874	0.01168	-1.49
245084_at	putative MYB family transcription facto	AtMYB70	AT2G23290	-2.00	-1.00	-4.94	0.001874	0.01168	-1.49
267609_at	unknown protein similar to GP|522127	---	AT2G26780	1.34	0.42	4.94	0.001875	0.01168	-1.49
265965_at	putative glutamate/ornithine acetyltran	---	AT2G37500	-1.52	-0.60	-4.94	0.001875	0.01168	-1.49
253710_at	putative protein hypothetical protein F	anac075	AT4G29230	1.62	0.70	4.94	0.001875	0.01168	-1.49
258226_at	putative phospholipase D similar to ph	PLDALPHA1	AT3G15730	-1.50	-0.58	-4.94	0.001876	0.011684	-1.49
246809_s_	SAR DNA-binding protein - like SAR D	---	AT5G27120 /	1.36	0.44	4.94	0.001883	0.011719	-1.49
245059_at	unknown protein ;supported by full-ler	RHC2A	AT2G39720	-1.41	-0.49	-4.94	0.001883	0.011719	-1.49
262176_at	3-ketoacyl-ACP synthase, putative sin	FAB1	AT1G74960	-1.60	-0.67	-4.94	0.001883	0.011719	-1.49
254847_at	putative phospholipase D-gamma pho	PLDGAMMA	AT4G11850	2.68	1.42	4.94	0.001886	0.011731	-1.50
266402_at	hypothetical protein predicted by gene	---	AT2G38780	-1.89	-0.92	-4.93	0.001888	0.011738	-1.50
251181_at	putative protein pectinesterase homol	---	AT3G62820	1.67	0.74	4.93	0.001889	0.011743	-1.50
249558_at	hypothetical protein	---	AT5G38310	4.01	2.00	4.93	0.00189	0.011744	-1.50
256920_at	hypothetical protein predicted by gene	---	AT3G18980	-1.40	-0.48	-4.93	0.001891	0.01175	-1.50
247427_at	putative protein similar to unknown pro	---	AT5G62580	-2.05	-1.03	-4.93	0.001892	0.011753	-1.50
248433_at	putative protein strong similarity to unk	---	AT5G51400	-1.43	-0.51	-4.93	0.001895	0.011767	-1.50

262394_at	unknown protein	emb1273	AT1G49510	-1.88	-0.91	-4.93	0.001895	0.011767	-1.50
265268_at	putative protein kinase contains a prot	---	AT2G42960	-1.49	-0.57	-4.93	0.001897	0.011777	-1.50
250738_at	anthranilate synthase component I-1 p	ASA1	AT5G05730	3.48	1.80	4.93	0.001899	0.011783	-1.50
253900_at	translation initiation factor ; supported	---	AT4G27130	1.47	0.55	4.93	0.001901	0.01179	-1.50
259164_at	hypothetical protein contains bromodo	ATBET10	AT3G01770	1.73	0.79	4.93	0.001901	0.01179	-1.50
244972_at	PSII 47KDa protein	---	---	-2.77	-1.47	-4.93	0.001902	0.01179	-1.50
251178_at	cytokinin oxidase -like protein cytokini	CKX6	AT3G63440	-2.43	-1.28	-4.93	0.001904	0.011799	-1.51
250034_at	apyrase (gb|AAF00612.1) ; supported	ATAPY2	AT5G18280	-1.55	-0.63	-4.93	0.001904	0.011801	-1.51
254448_at	fatty acid hydroxylase - like protein fat	FAH2	AT4G20870	-3.14	-1.65	-4.93	0.001907	0.011812	-1.51
251962_at	plasma membrane intrinsic protein 2a	PIP2A	AT3G53420	-2.03	-1.02	-4.93	0.001908	0.011812	-1.51
256112_at	guanine nucleotide regulatory protein,	ATRABA1B	AT1G16920	-3.06	-1.61	-4.93	0.001908	0.011812	-1.51
254857_at	putative protein acetylcholine regulato	SEC1B	AT4G12120	1.56	0.64	4.92	0.001908	0.011813	-1.51
252280_at	SF16 -like protein SF16 protein, poller	iqd21	AT3G49260	-2.76	-1.46	-4.92	0.001911	0.011822	-1.51
247977_at	putative protein similar to unknown pro	---	AT5G56850	-1.73	-0.79	-4.92	0.00191	0.011822	-1.51
252289_at	putative protein pre-mRNA splicing fa	---	AT3G49130	1.83	0.87	4.92	0.001911	0.011822	-1.51
251056_at	putative protein KIAA1303 protein - H	RAPTOR2	AT5G01770	1.64	0.72	4.92	0.001913	0.011829	-1.51
247996_at	putative protein contains similarity to G	---	AT5G56170	-1.99	-1.00	-4.92	0.001919	0.011863	-1.51
247368_at	putative protein contains similarity to k	---	AT5G63320	1.60	0.68	4.92	0.001923	0.011887	-1.52
262290_at	Expressed protein ; supported by full-le	---	AT1G70985	-1.79	-0.84	-4.92	0.001925	0.011893	-1.52
267490_at	putative receptor-like protein kinase	---	AT2G19130	2.17	1.12	4.92	0.001926	0.011896	-1.52
259257_at	unknown protein ;supported by full-ler	---	AT3G07760	1.56	0.64	4.91	0.001931	0.011921	-1.52
254108_at	putative protein	RIN2	AT4G25230	1.57	0.65	4.91	0.001931	0.011921	-1.52
264448_at	putative sensory transduction histidine	AHK3	AT1G27320	1.39	0.48	4.91	0.001933	0.011926	-1.52
251411_at	regulatory subunit of protein kinase CK	CKB3	AT3G60250	-1.53	-0.61	-4.91	0.001933	0.011926	-1.52
254236_at	putative protein VSG expression site-a	---	AT4G23840	-1.45	-0.53	-4.91	0.001936	0.01194	-1.52
260413_at	hypothetical protein predicted by gene	---	AT1G69800	1.72	0.78	4.91	0.001939	0.011955	-1.53
253971_at	fructose-bisphosphate aldolase - like p	---	AT4G26530	-2.32	-1.21	-4.91	0.001939	0.011955	-1.53
252834_at	putative protein RING-H2 zinc finger p	---	AT4G40070	-2.24	-1.16	-4.91	0.001943	0.011976	-1.53
263864_at	hypothetical protein predicted by gens	CPZ	AT2G04530	-1.51	-0.59	-4.91	0.001945	0.011984	-1.53
259050_at	hypothetical protein similar to GB:AAC	---	AT3G03356 /	1.35	0.43	4.91	0.001947	0.011992	-1.53
264726_at	Expressed protein ; supported by full-le	---	AT1G22985	1.67	0.74	4.91	0.001948	0.011994	-1.53
253669_at	dihydropteroate synthase-like protein	---	AT4G30000	-1.44	-0.53	-4.91	0.001949	0.011997	-1.53
259641_at	putative protease similar to protease I	---	AT1G69020	-1.61	-0.69	-4.91	0.00195	0.012	-1.53
253188_at	putative sugar transporter protein sug	TMT2	AT4G35300	-1.52	-0.61	-4.91	0.00195	0.012	-1.53
266478_at	putative cysteinyl-tRNA synthetase ; su	SYCO ARAT	AT2G31170	-1.87	-0.91	-4.90	0.001952	0.012006	-1.53

267233_s_	unknown protein	---	AT2G43910 /	-1.79	-0.84	-4.90	0.001952	0.012006	-1.53
259932_at	zinc finger protein, putative similar to (	STOP1	AT1G34370	1.51	0.59	4.90	0.001954	0.01201	-1.53
261164_at	hypothetical protein ;supported by full-	---	AT1G34470	-1.52	-0.60	-4.90	0.001954	0.01201	-1.53
251847_at	tryptophan synthase alpha chain ; sup	TSA1	AT3G54640	5.57	2.48	4.90	0.00196	0.01204	-1.54
256943_at	hypothetical protein similar to hypothet	---	AT3G18910	-1.41	-0.50	-4.90	0.00196	0.01204	-1.54
258409_at	hypothetical protein similar to GB:AAB	---	AT3G17640	-2.12	-1.09	-4.90	0.00196	0.01204	-1.54
255071_at	putative protein putative chloroplast 3	---	AT4G09040	-1.52	-0.61	-4.90	0.001961	0.01204	-1.54
264774_at	unknown protein	---	AT1G22890	2.71	1.44	4.90	0.001965	0.012062	-1.54
255786_at	unknown protein contains similarity to (	ATCLH1	AT1G19670	2.65	1.41	4.90	0.001966	0.012066	-1.54
248391_at	putative protein similar to unknown pro	---	AT5G52030	-1.51	-0.60	-4.90	0.001968	0.012071	-1.54
248063_at	RNA-binding protein-like ; supported b	---	AT5G55550	-1.44	-0.53	-4.90	0.001969	0.012074	-1.54
261354_at	unknown protein ; supported by cDNA	atnudt3	AT1G79690	1.48	0.56	4.90	0.001971	0.012087	-1.54
267481_at	putative receptor-like protein kinase	---	AT2G02780	-2.69	-1.43	-4.90	0.001972	0.012087	-1.54
251594_at	putative protein DOC4, Mus musculus	---	AT3G57630	3.35	1.74	4.89	0.001976	0.012109	-1.55
245270_at	tubulin alpha-6 chain (TUA6) ; support	TUA6	AT4G14960	-2.14	-1.10	-4.89	0.00198	0.012127	-1.55
250524_at	putative protein contains similarity to I-	---	AT5G08520	-1.44	-0.52	-4.89	0.00198	0.012127	-1.55
258398_at	thioredoxin m4 identical to GB:AAF159	TRX-M4	AT3G15360	-1.41	-0.50	-4.89	0.00198	0.012127	-1.55
246863_at	nodulin - like protein early nodulin N93	---	AT5G25940	2.30	1.20	4.89	0.001983	0.012133	-1.55
258850_at	putative cellulose synthase catalytic su	CSLD3	AT3G03050	-1.50	-0.58	-4.89	0.001983	0.012133	-1.55
265347_at	similar to mammalian MHC III region p	SUVH6	AT2G22740	-1.37	-0.45	-4.89	0.001983	0.012133	-1.55
250011_at	putative protein crp1 protein, maize, P	---	AT5G18475	-1.41	-0.50	-4.89	0.001984	0.012133	-1.55
259922_at	protein phosphatase 2C (AtP2C-HA) i	HAB1	AT1G72770	1.83	0.87	4.89	0.001984	0.012134	-1.55
256185_at	dof zinc finger protein identical to dof z	ADOF1	AT1G51700	3.23	1.69	4.89	0.001987	0.012147	-1.55
247813_at	NADP-dependent malate dehydrogena	---	AT5G58330	-1.48	-0.57	-4.89	0.00199	0.012163	-1.55
255558_at	P II nitrogen sensing protein GLB I ; s	GLB1	AT4G01900	-1.54	-0.62	-4.89	0.001993	0.01217	-1.56
249299_at	E2, ubiquitin-conjugating enzyme 4 (U	UBC4	AT5G41340	-1.60	-0.68	-4.89	0.001992	0.01217	-1.56
256129_at	calcium-binding protein, putative simil	---	AT1G18210	2.02	1.01	4.89	0.001993	0.01217	-1.56
257660_at	unknown protein ; supported by cDNA	WIP3	AT3G13360	-1.38	-0.46	-4.89	0.001993	0.01217	-1.56
266682_at	putative disease resistance protein	---	AT2G19780	-2.00	-1.00	-4.88	0.001997	0.012187	-1.56
258575_at	putative O-linked GlcNAc transferase s	SEC	AT3G04240	1.44	0.52	4.88	0.001999	0.012197	-1.56
258876_at	putative ADP-ribosylation factor simila	ATARFB1C	AT3G03120	1.39	0.48	4.88	0.001999	0.012198	-1.56
263536_at	putative WRKY-type DNA binding prot	WRKY60	AT2G25000	2.47	1.30	4.88	0.002001	0.012202	-1.56
267029_at	unknown protein	ATIREG1	AT2G38460	-1.58	-0.66	-4.88	0.002005	0.012224	-1.56
251972_at	nodulin / glutamate-ammonia ligase -	---	AT3G53170	-1.53	-0.61	-4.88	0.002007	0.012234	-1.56
265345_at	copia-like retroelement pol polyprotein	---	AT2G22680	1.45	0.54	4.88	0.002008	0.012235	-1.56

251641_at	protease-like protein INSULIN-DEGR/	---	AT3G57470	-1.75	-0.81	-4.88	0.00201	0.012243	-1.57
257180_at	sun protein (fmu protein), putative sim	---	AT3G13180	-1.63	-0.71	-4.88	0.00201	0.012243	-1.57
253140_at	RING-H2 finger protein RHA3b ;suppo	RHA3B	AT4G35480	1.63	0.70	4.88	0.002014	0.012265	-1.57
248552_at	RNA-binding protein-like ; supported b	---	AT5G50250	-1.48	-0.56	-4.87	0.00202	0.012298	-1.57
260394_at	putative transcription factor similar to G	MYB122	AT1G74080	6.98	2.80	4.87	0.002021	0.012299	-1.57
251559_at	putative protein hypothetical protein T	---	AT3G58010	-1.67	-0.74	-4.87	0.002021	0.012299	-1.57
260858_at	hypothetical protein predicted by gene	---	AT1G43770	1.48	0.57	4.87	0.002023	0.0123	-1.57
262717_s_	putative cytochrome P450 similar to gb	CYP79F2	AT1G16400 /	-1.81	-0.86	-4.87	0.002022	0.0123	-1.57
264379_at	hypothetical protein predicted by grail	---	AT2G25200	-2.12	-1.08	-4.87	0.002025	0.012314	-1.57
264653_at	unknown protein Contains similarity to	AMI1	AT1G08980	-1.75	-0.81	-4.87	0.002029	0.012326	-1.58
263846_at	putative RNA polymerase sigma-70 fa	SIGF	AT2G36990	-1.77	-0.83	-4.87	0.002029	0.012326	-1.58
261454_at	hypothetical protein predicted by gene	---	AT1G21090	-1.51	-0.59	-4.87	0.002029	0.012326	-1.58
250248_at	transporter-like protein	ZIF1	AT5G13740	-2.35	-1.23	-4.87	0.002033	0.012349	-1.58
256455_at	unknown protein ;supported by full-len	---	AT1G75190	-1.46	-0.55	-4.87	0.002035	0.012355	-1.58
262505_at	unknown protein ESTs gb|N96028, gb	---	AT1G21680	1.56	0.64	4.87	0.002038	0.012367	-1.58
254901_at	serine/threonine kinase-like protein (fr	---	AT4G11530	1.47	0.56	4.87	0.002038	0.012367	-1.58
253974_at	receptor protein kinase - like protein C	---	AT4G26540	-2.14	-1.10	-4.86	0.00204	0.012372	-1.58
247918_at	putative protein contains similarity to p	---	AT5G57610	1.64	0.71	4.86	0.00204	0.012372	-1.58
266407_at	putative elongation factor	TFIIS	AT2G38560	1.45	0.54	4.86	0.002041	0.012377	-1.58
252512_at	receptor protein kinase -like receptor-l	---	AT3G46290	-1.46	-0.55	-4.86	0.002043	0.012386	-1.58
249423_at	Expressed protein ; supported by full-le	---	AT5G39785	1.66	0.73	4.86	0.002045	0.012391	-1.58
258453_at	RNA polymerase I, II and III 24.3 kDa	NRPB5	AT3G22320	1.39	0.48	4.86	0.002046	0.012393	-1.58
251840_at	protein disulfide-isomerase-like protei	ATPDIL1-3	AT3G54960	2.16	1.11	4.86	0.002049	0.012413	-1.59
246501_at	putative protein KIAA1012 protein - H	---	AT5G16280	-1.46	-0.54	-4.86	0.002051	0.01242	-1.59
259626_at	bZIP transcription factor, putative con	ATBZIP60	AT1G42990	4.15	2.05	4.86	0.002054	0.012432	-1.59
250847_at	putative protein predicted protein, Ara	---	AT5G04480	-2.21	-1.15	-4.86	0.002057	0.01245	-1.59
257337_at	NADH dehydrogenase subunit 5 (nad5	---	---	2.33	1.22	4.86	0.002058	0.012454	-1.59
250923_at	putative protein ; supported by full-len	CDC25	AT5G03455	1.61	0.68	4.86	0.002059	0.012454	-1.59
253212_s_	xanthine dehydrogenase - like protein	XDH1	AT4G34890 /	1.67	0.74	4.86	0.002059	0.012454	-1.59
256575_at	dTDP-glucose 4,6-dehydratase, putat	RHM3	AT3G14790	-1.73	-0.79	-4.86	0.002062	0.012463	-1.59
251712_at	putative protein non-consensus TT do	---	AT3G56120	-1.38	-0.47	-4.85	0.002063	0.012472	-1.59
262772_at	puative calcium-transporting ATPase s	ACA.I	AT1G13210	2.21	1.14	4.85	0.002066	0.012481	-1.60
251810_at	putative protein predicted pectate-lyas	---	AT3G55250	-1.65	-0.72	-4.85	0.002072	0.012514	-1.60
264756_at	receptor protein kinase (IRK1), putativ	---	AT1G61370	4.21	2.07	4.85	0.002075	0.012528	-1.60
250950_at	putative protein	ATEXO70A1	AT5G03540 /	-1.61	-0.69	-4.85	0.002078	0.012545	-1.60

249049_at	tubulin beta-4 chain (sp|P24636) ; sup	TUB4	AT5G44340	-1.77	-0.83	-4.85	0.002079	0.012548	-1.60
252613_at	putative protein hypothetical protein A	---	AT3G45190	1.38	0.46	4.85	0.002085	0.012581	-1.61
251304_at	putative protein several O-methyltrans	---	AT3G61990	3.73	1.90	4.84	0.002088	0.012588	-1.61
256819_at	unknown protein contains Pfam profile	---	AT3G21390	-1.44	-0.52	-4.84	0.002087	0.012588	-1.61
251264_at	multifunctional aminoacyl-tRNA ligase	---	AT3G62120	-1.42	-0.50	-4.84	0.002087	0.012588	-1.61
253879_s_	UDP rhamnose--anthocyanidin-3-gluc	---	AT4G27560 /	-2.26	-1.18	-4.84	0.002089	0.01259	-1.61
265852_at	putative RING zinc finger protein	---	AT2G42350	2.01	1.01	4.84	0.002089	0.01259	-1.61
253238_at	putative protein (fragment)	---	AT4G34480	-1.57	-0.65	-4.84	0.00209	0.012593	-1.61
261426_at	unknown protein contains similarity to	---	AT1G18680	-1.42	-0.50	-4.84	0.002091	0.012593	-1.61
249974_at	putative protein predicted proteins, Ar	---	AT5G18780	2.18	1.13	4.84	0.002092	0.012595	-1.61
251456_at	beta-glucosidase-like protein several b	BGLU27	AT3G60120	27.32	4.77	4.84	0.002094	0.012606	-1.61
261719_at	hypothetical protein similar to hypothet	---	AT1G18390	3.29	1.72	4.84	0.002095	0.012609	-1.61
255483_at	putative glycosyltransferase similar to	XT2	AT4G02500	-1.76	-0.81	-4.84	0.002099	0.012627	-1.61
265842_at	putative AP2 domain transcription fact	ERF38	AT2G35700	-2.33	-1.22	-4.84	0.002104	0.012653	-1.62
254103_at	putative protein ;supported by full-leng	---	AT4G25030	2.68	1.42	4.83	0.002116	0.012727	-1.62
257844_at	prolyl 4-hydroxylase, putative similar t	---	AT3G28480	1.70	0.76	4.83	0.002117	0.012728	-1.62
259860_at	putative protein kinase similar to leucir	---	AT1G80640	-1.73	-0.79	-4.83	0.00212	0.012745	-1.62
245334_at	Expressed protein ; supported by full-l	RALFL33	AT4G15800	-2.24	-1.16	-4.83	0.002122	0.012752	-1.62
249459_at	peroxidase ATP24a	---	AT5G39580	8.58	3.10	4.83	0.002123	0.012752	-1.63
264926_at	cytochrome b5, putative similar to cyt	CB5LP	AT1G60660	-1.47	-0.56	-4.83	0.002125	0.01276	-1.63
262686_at	proteasome regulatory subunit S3, pu	---	AT1G75990	-1.55	-0.63	-4.83	0.002126	0.012766	-1.63
256680_at	unknown protein ; supported by full-ler	---	AT3G52230	-1.75	-0.81	-4.83	0.002131	0.012792	-1.63
259808_at	hypothetical protein contains Pfam pro	---	AT1G49790	-1.38	-0.46	-4.82	0.002134	0.012809	-1.63
253535_at	putaive DNA-binding protein DNA-bin	WRKY11	AT4G31550	4.29	2.10	4.82	0.002135	0.012809	-1.63
260448_at	hypothetical protein predicted by gens	---	AT1G72410	-1.53	-0.62	-4.82	0.002141	0.012843	-1.63
259730_at	unknown protein similar to hypothetica	---	AT1G77660	2.83	1.50	4.82	0.002147	0.012867	-1.64
266414_at	mevalonate diphosphate decarboxylas	MVD1	AT2G38700	-1.50	-0.59	-4.82	0.002147	0.012867	-1.64
262951_at	nodulin-like protein similar to MtN21 G	---	AT1G75500	-1.65	-0.72	-4.82	0.002148	0.012867	-1.64
258655_at	putative isocitrate dehydrogenase (NA	---	AT3G09810	1.72	0.79	4.82	0.002146	0.012867	-1.64
254457_at	putative protein various predicted prot	---	AT4G21170	1.66	0.73	4.82	0.002149	0.012869	-1.64
260645_at	hypothetical protein predicted by gene	TTL1	AT1G53300	-1.99	-0.99	-4.82	0.00215	0.012869	-1.64
252350_at	ataxia-telangiectasia mutated protein ,	ATM	AT3G48190	-1.39	-0.48	-4.82	0.002149	0.012869	-1.64
254289_at	putative protein predicted protein, Ara	---	AT4G22980	5.17	2.37	4.82	0.002151	0.012873	-1.64
252365_at	Expressed protein ; supported by full-l	---	AT3G48350	-2.56	-1.36	-4.82	0.002154	0.012891	-1.64
249690_at	acyl-peptide hydrolase-like	---	AT5G36210	-1.44	-0.53	-4.81	0.002156	0.0129	-1.64

248868_at	putative protein similar to unknown pro	---	AT5G46780	2.38	1.25	4.81	0.002159	0.01291	-1.64
245778_at	RNA-binding glycine-rich protein, puta	---	AT1G73530	-1.75	-0.81	-4.81	0.002162	0.012927	-1.65
260176_at	unknown protein similar to Pi starvatio	---	AT1G71950	-1.51	-0.59	-4.81	0.002167	0.012955	-1.65
252411_at	putative protein PMP31 protein - Can	PEX11B	AT3G47430	2.23	1.15	4.81	0.00217	0.012964	-1.65
248812_at	palmitoyl-protein thioesterase precurs	---	AT5G47330	-4.26	-2.09	-4.81	0.002171	0.012964	-1.65
249705_at	serine/threonine protein kinase-like	---	AT5G35580	1.80	0.85	4.81	0.002171	0.012964	-1.65
249197_at	putative protein contains similarity to c	CML37	AT5G42380	13.62	3.77	4.81	0.002171	0.012964	-1.65
261224_at	subtilisin-like serine protease similar to	ATSBT5.2	AT1G20160	-2.79	-1.48	-4.81	0.002172	0.012966	-1.65
254827_at	putative protein KIAA0255 gene, Hom	---	AT4G12650	-1.50	-0.58	-4.81	0.002177	0.012992	-1.65
263542_at	putative protein transport protein SEC2	---	AT2G21630	-1.73	-0.79	-4.81	0.002178	0.012996	-1.65
253768_at	putative protein	---	AT4G28550	1.82	0.87	4.80	0.002182	0.013013	-1.65
261913_at	flavin-containing monooxygenase FM	FMO GS-OX	AT1G65860	-2.45	-1.29	-4.80	0.002183	0.013015	-1.66
251406_at	putative protein various predicted prot	---	AT3G60260	-2.01	-1.01	-4.80	0.002185	0.013022	-1.66
252363_at	lipase - like protein lipase Arab-1, Ara	---	AT3G48460	-3.26	-1.70	-4.80	0.002185	0.013022	-1.66
266205_s_	putative dTDP-glucose 4-6-dehydratas	AXS2	AT1G08200 /	-1.56	-0.64	-4.80	0.002186	0.013023	-1.66
256781_at	dirigent protein, putative similar to diri	---	AT3G13650	16.83	4.07	4.80	0.002188	0.013036	-1.66
254592_at	heat shock transcription factor - like p	HSF A4A	AT4G18880	3.30	1.72	4.80	0.002191	0.013047	-1.66
251781_at	P-glycoprotein - like P-glycoprotein (p	PGP20	AT3G55320	1.48	0.56	4.80	0.002192	0.013049	-1.66
264177_at	hypothetical protein contains Pfam pro	---	AT1G02150	-1.45	-0.54	-4.80	0.002199	0.013088	-1.66
245781_at	S-ribonuclease binding protein SBP1,	SBP1	AT1G45976	1.58	0.66	4.80	0.0022	0.01309	-1.66
253629_at	glycine-rich protein glycine-rich cell wa	---	AT4G30450	-1.60	-0.68	-4.80	0.002201	0.013097	-1.66
253054_at	probable N-acetyltransferase hookless	HLS1	AT4G37580	-1.44	-0.53	-4.80	0.002204	0.013109	-1.67
246028_at	AKIN beta1 ; supported by full-length	---	AT5G21170	-1.84	-0.88	-4.79	0.002205	0.013112	-1.67
AFFX-r2-At	Arabidopsis thaliana /REF=U84969 /D	---	---	1.33	0.42	4.79	0.002206	0.013112	-1.67
248191_at	putative protein similar to unknown pro	---	AT5G54130	1.55	0.63	4.79	0.002207	0.013118	-1.67
247029_at	TINY-like protein	---	AT5G67190	-1.67	-0.74	-4.79	0.002209	0.013127	-1.67
266628_at	unknown protein	---	AT2G35330	1.38	0.47	4.79	0.002215	0.013156	-1.67
266599_at	unknown protein	---	AT2G46100	-1.41	-0.50	-4.79	0.002219	0.013174	-1.67
263157_at	aldehyde dehydrogenase homolog, pu	ALDH7B4	AT1G54100	1.99	1.00	4.79	0.002219	0.013174	-1.67
254238_at	putative protein probable membrane p	---	AT4G23540	1.63	0.71	4.79	0.002223	0.013193	-1.68
245567_at	germin precursor oxalate oxidase	GLP9	AT4G14630	5.00	2.32	4.79	0.002223	0.013193	-1.68
260582_at	hypothetical protein predicted by gene	---	AT2G47200	1.53	0.61	4.79	0.002226	0.013207	-1.68
253977_at	putative protein various Caenorhabditis	---	AT4G26630	1.78	0.83	4.78	0.00223	0.013224	-1.68
246288_at	unknown protein	---	AT1G31850	-1.67	-0.74	-4.78	0.00223	0.013224	-1.68
246237_at	putative protein	---	AT4G36390	-1.54	-0.63	-4.78	0.002233	0.013234	-1.68

248500_at	unknown protein	---	AT5G50410	-1.58	-0.66	-4.78	0.002235	0.013243	-1.68
261534_at	unknown protein ;supported by full-len	PEX11C	AT1G01820	1.39	0.47	4.78	0.00224	0.01327	-1.68
266595_at	hypothetical protein predicted by gens	GC4	AT2G46180	-1.52	-0.60	-4.78	0.002242	0.013278	-1.68
251230_at	beta-glucosidase-like protein several b	BGLU8	AT3G62750	-1.38	-0.47	-4.78	0.002242	0.013278	-1.68
263545_at	unknown protein	---	AT2G21560	2.53	1.34	4.78	0.002244	0.013283	-1.69
253201_at	putative ribosomal protein S16 riboso	SSR16	AT4G34620	-1.46	-0.54	-4.78	0.002244	0.013283	-1.69
258276_at	putative signal peptidase 21kDa subur	---	AT3G15710	-1.58	-0.66	-4.78	0.002245	0.013286	-1.69
257727_at	unknown protein	---	AT3G18380	-1.44	-0.53	-4.78	0.002248	0.013298	-1.69
258373_at	20S proteasome subunit PAE2 identic	PAE2	AT3G14290	-1.45	-0.53	-4.78	0.002252	0.01332	-1.69
259562_at	hypothetical protein ; supported by cDI	---	AT1G21200	1.48	0.57	4.78	0.002254	0.013323	-1.69
262490_at	hypothetical protein predicted by gens	UREF	AT1G21840	-1.60	-0.68	-4.78	0.002254	0.013323	-1.69
245363_at	hypothetical protein ;supported by full-	---	AT4G15120	3.57	1.84	4.77	0.002257	0.013335	-1.69
265272_at	unknown protein	ARF10	AT2G28350	1.73	0.79	4.77	0.002258	0.013341	-1.69
260260_at	putative reductase similar to cinnamoy	---	AT1G68540	-1.65	-0.73	-4.77	0.002262	0.013359	-1.69
257227_at	monodehydroascorbate reductase sim	MDAR4	AT3G27820	1.49	0.57	4.77	0.002264	0.013369	-1.70
250132_at	putative protein similar to unknown pro	KAN	AT5G16560	-2.12	-1.09	-4.77	0.002265	0.013371	-1.70
247166_at	unknown protein	---	AT5G65840	-2.11	-1.07	-4.77	0.002267	0.013381	-1.70
254658_at	putative protein predicted gene M02B	---	AT4G18230	-1.46	-0.54	-4.77	0.002274	0.013418	-1.70
256576_at	zinc finger protein (PMZ), putative ide	PMZ	AT3G28210	3.52	1.82	4.77	0.002277	0.013434	-1.70
253486_at	putative protein KIAA0260 gene, hum	---	AT4G31600	-1.46	-0.55	-4.77	0.002279	0.013438	-1.70
250867_at	putative protein predicted protein, Ara	---	AT5G03880	-1.77	-0.82	-4.77	0.002279	0.013438	-1.70
259431_at	plasma membrane intrinsic protein 1c	PIP1C	AT1G01620	-4.55	-2.18	-4.76	0.002281	0.013443	-1.70
259067_at	F-box protein family, AtFBL12 contain	---	AT3G07550	-1.40	-0.48	-4.76	0.002282	0.013447	-1.70
266782_at	putative ligand-gated ion channel prote	ATGLR2.7	AT2G29120	-1.43	-0.52	-4.76	0.002289	0.013483	-1.71
256424_at	unknown protein ;supported by full-len	---	AT1G33490	1.45	0.54	4.76	0.002289	0.013484	-1.71
261585_at	NAC domain protein, putative similar t	ANAC001	AT1G01010	1.90	0.92	4.76	0.002294	0.013509	-1.71
259817_at	hypothetical protein predicted by gene	---	AT1G49880	-1.46	-0.55	-4.76	0.002297	0.013522	-1.71
250627_at	putative amidase	---	AT5G07360	1.57	0.65	4.76	0.0023	0.013538	-1.71
250513_at	protein kinase ;supported by full-lengt	---	AT5G09890	-1.45	-0.54	-4.76	0.002303	0.013544	-1.71
248689_at	SCARECROW gene regulator-like ; s	PAT1	AT5G48150	1.58	0.66	4.76	0.002303	0.013544	-1.71
251330_at	putative protein putative protein At2g4	---	AT3G61550	-1.73	-0.79	-4.76	0.002303	0.013544	-1.71
266311_at	hypothetical protein predicted by gens	---	AT2G27130	-3.29	-1.72	-4.76	0.002306	0.013554	-1.72
258074_at	unknown protein	---	AT3G25890	2.81	1.49	4.75	0.00231	0.013578	-1.72
258286_at	kinesin-like protein similar to kinesin he	---	AT3G16060	-1.53	-0.61	-4.75	0.002312	0.01358	-1.72
259447_s_	ADP-ribosylation factor, putative simil	ATARFD1A	AT1G02430 /	1.45	0.53	4.75	0.002312	0.01358	-1.72

264301_at	hypothetical protein contains similarity	---	AT1G78780	2.63	1.39	4.75	0.002315	0.013594	-1.72
261011_at	cytochrome b5 similar to cytochrome b	CB5-A	AT1G26340	1.53	0.62	4.75	0.002315	0.013594	-1.72
251900_at	putative protein lateral root primordia (	SRS6	AT3G54430	-1.61	-0.69	-4.75	0.002317	0.013599	-1.72
247444_at	putative protein strong similarity to unk	HIPL2	AT5G62630	2.61	1.38	4.75	0.002321	0.013619	-1.72
249221_at	serine/threonine protein kinase-like pro	---	AT5G42440	1.61	0.69	4.75	0.002324	0.013636	-1.72
255413_at	putative alcohol dehydrogenase simila	---	AT4G03140	-1.52	-0.60	-4.75	0.002327	0.013642	-1.73
251639_at	acetylglutamate kinase-like protein ac	---	AT3G57560	-1.61	-0.68	-4.75	0.002327	0.013642	-1.73
252830_at	putative protein 70K peroxisomal mem	PXA1	AT4G39850	1.37	0.45	4.75	0.002326	0.013642	-1.73
248538_at	putative protein contains similarity to g	---	AT5G50110	-1.65	-0.72	-4.75	0.002328	0.013642	-1.73
254846_at	Expressed protein ; supported by full-le	PLDGAMMA	AT4G11830	-1.60	-0.68	-4.75	0.002329	0.013646	-1.73
258943_at	hypothetical protein predicted by gene	---	AT3G10400	1.53	0.61	4.75	0.002331	0.013649	-1.73
258037_at	putative 4-coumarate:CoA ligase 2 sim	4CL5	AT3G21230	7.57	2.92	4.75	0.00233	0.013649	-1.73
245261_at	Expressed protein ; supported by cDN	---	AT4G14385	-1.42	-0.51	-4.74	0.002338	0.013689	-1.73
258717_at	unknown protein ; supported by cDNA	SYP71	AT3G09740	-1.35	-0.43	-4.74	0.002339	0.013693	-1.73
260568_at	endochitinase isolog	---	AT2G43570	18.79	4.23	4.74	0.002343	0.013708	-1.73
266441_at	hypothetical protein predicted by gens	---	AT2G43250	1.45	0.54	4.74	0.002343	0.013708	-1.73
264086_at	unknown protein ;supported by full-ler	---	AT2G31190	1.63	0.70	4.74	0.002344	0.013708	-1.73
256593_at	hypothetical protein similar to putative	---	AT3G28510	2.85	1.51	4.74	0.002347	0.013722	-1.73
267013_at	putative protein kinase contains a prot	CCR2	AT2G39180	-1.48	-0.56	-4.74	0.002351	0.013742	-1.74
258217_at	unknown protein contains Pfam profile	XPL1	AT3G17998 /	-1.93	-0.95	-4.74	0.002353	0.013754	-1.74
258063_at	putative cytochrome P450 similar to G	CYP72A8	AT3G14620	3.22	1.69	4.74	0.002355	0.013757	-1.74
265238_s_	hypothetical protein	---	AT2G07696	1.76	0.81	4.74	0.002355	0.013757	-1.74
247418_at	glutaredoxin-like protein ; supported b	---	AT5G63030	1.64	0.72	4.74	0.002357	0.013767	-1.74
253372_at	pectinesterase - like protein pectineste	PME44	AT4G33220	-2.70	-1.43	-4.73	0.002364	0.013801	-1.74
262583_at	putative phosphatidylserine synthase S	---	AT1G15110	1.64	0.71	4.73	0.002366	0.013808	-1.74
250095_at	phytoene synthase (gb|AAB65697.1)	---	AT5G17230	-2.03	-1.02	-4.73	0.002366	0.013808	-1.74
267038_at	expressed protein supported by cDNA	---	AT2G38480	-2.57	-1.36	-4.73	0.002369	0.01382	-1.75
AFFX-r2-At	Arabidopsis thaliana /REF=M64116 /D	---	---	2.12	1.09	4.73	0.00237	0.01382	-1.75
249112_at	ATP sulfurylase precursor (gb|AAD266	APS4	AT5G43780	2.07	1.05	4.73	0.002371	0.013823	-1.75
249129_at	cyclin A-type	CYCA3;1	AT5G43080	-1.49	-0.58	-4.73	0.002374	0.013841	-1.75
246290_at	calmodulin-3 ;supported by full-length	CAM3	AT3G56800	-1.39	-0.48	-4.73	0.002378	0.013858	-1.75
265570_at	unknown protein	---	AT2G28310	-1.60	-0.68	-4.73	0.002381	0.01387	-1.75
265252_at	putative Na+/H+ antiporter	SOS1	AT2G01980	1.38	0.46	4.73	0.002383	0.013882	-1.75
258097_at	transport protein, putative similar to tra	---	AT3G23660	-1.37	-0.46	-4.72	0.002392	0.013928	-1.76
250777_at	putative protein similar to unknown pro	---	AT5G05440	-4.74	-2.24	-4.72	0.002392	0.013928	-1.76

248823_s_	unknown protein ;supported by full-ler	---	AT5G46950 /	15.91	3.99	4.72	0.002396	0.013948	-1.76
259864_at	hypothetical protein predicted by gens	---	AT1G72800	1.98	0.99	4.72	0.002397	0.013949	-1.76
252031_at	putative protein 150-kD protein cluA -	---	AT3G52140	1.42	0.51	4.72	0.0024	0.013962	-1.76
245505_at	glutaredoxin	---	AT4G15690	-2.76	-1.47	-4.72	0.002402	0.013969	-1.76
247009_at	unknown protein ;supported by full-ler	---	AT5G67600	2.15	1.10	4.72	0.002403	0.013973	-1.76
261583_at	pyruvate dehydrogenase E1 alpha sub	PDH-E1 ALF	AT1G01090	-1.44	-0.53	-4.72	0.002404	0.013973	-1.76
266752_at	putative ABC transporter related to mu	ABCB4	AT2G47000	8.34	3.06	4.72	0.00241	0.014002	-1.76
251795_at	putative protein MtN24, Medicago trur	---	AT3G55390	1.78	0.83	4.72	0.00241	0.014002	-1.76
264402_at	HSP100/ClpB, putative similar to HSP	CLPB4	AT2G25140	2.10	1.07	4.72	0.002412	0.014012	-1.76
247880_at	putative protein similar to unknown pro	---	AT5G57780	-3.96	-1.98	-4.71	0.002413	0.014015	-1.77
254331_s_	cytochrome P450 - like protein flavonc	CYP706A2	AT4G22690 /	2.93	1.55	4.71	0.002415	0.014018	-1.77
255773_at	flavonol 4'-sulfotransferase, putative s	SOT17	AT1G18590	3.05	1.61	4.71	0.002416	0.014021	-1.77
250774_at	ATP-dependent RNA helicase-like pro	---	AT5G05450	-1.69	-0.76	-4.71	0.002418	0.014031	-1.77
259316_at	unknown protein	---	AT3G01175	1.61	0.69	4.71	0.00242	0.014036	-1.77
251526_at	putative protein several serine/threonir	---	AT3G58640	-1.54	-0.63	-4.71	0.002421	0.014041	-1.77
264226_at	hypothetical protein similar to putative	---	AT1G67510	-1.47	-0.56	-4.71	0.002422	0.014044	-1.77
251984_at	phenylalanine ammonia-lyase ;suppor	PAL2	AT3G53260	4.52	2.17	4.71	0.002423	0.014044	-1.77
262244_at	serine threonine kinase, putative simil	CIPK17	AT1G48260	5.41	2.44	4.71	0.002429	0.014075	-1.77
254984_s_	putative protein Homo sapiens deubiq	UBP10	AT4G10570 /	1.33	0.41	4.71	0.002434	0.014099	-1.77
251273_at	serine/threonine-protein kinase-like pr	---	AT3G61960	1.79	0.84	4.71	0.002436	0.01411	-1.78
251599_at	adenylosuccinate synthetase ;support	ADSS	AT3G57610	-1.48	-0.57	-4.71	0.002437	0.014113	-1.78
261946_at	unknown protein	---	AT1G64560	-1.59	-0.67	-4.71	0.002439	0.014119	-1.78
265738_at	NADC homolog identical to GP|12160	QPT	AT2G01350	1.49	0.58	4.71	0.002439	0.014119	-1.78
265235_s_	hypothetical protein	---	AT2G07719	1.51	0.59	4.70	0.002454	0.014198	-1.78
259769_at	RNA-binding protein MEI2, putative si	AML5	AT1G29400	1.81	0.85	4.70	0.002456	0.014201	-1.78
260064_at	ethylene-insensitive3-like3 (EIL3) iden	EIL3	AT1G73730	1.64	0.71	4.70	0.002456	0.014201	-1.78
263478_at	putative receptor-like protein kinase ;	---	AT2G31880	3.07	1.62	4.70	0.002456	0.014201	-1.78
257615_at	unknown protein	---	AT3G26510	-1.74	-0.80	-4.70	0.002457	0.014201	-1.78
245474_at	hypothetical protein	---	AT4G16060	-1.57	-0.65	-4.70	0.002459	0.014213	-1.79
250988_at	putative protein thyroid receptor intera	UPL4	AT5G02880	1.37	0.46	4.70	0.002462	0.014224	-1.79
249895_at	male sterility 2-like protein (emb|CAA6	FAR1	AT5G22500	-3.64	-1.87	-4.70	0.002468	0.01425	-1.79
251438_s_	putative protein hypothetical protein F	---	AT3G59930 /	7.11	2.83	4.70	0.002468	0.01425	-1.79
262648_at	putative ribulose-1,5 bisphosphate ca	---	AT1G14030	-1.44	-0.52	-4.69	0.002469	0.01425	-1.79
262120_at	glutathione-S-transferase, putative sir	ATGSTF4	AT1G02950	-1.66	-0.73	-4.69	0.002468	0.01425	-1.79
256091_at	Expressed protein ; supported by full-l	HMGB2	AT1G20693	1.46	0.55	4.69	0.002471	0.014258	-1.79

265029_at	zinc finger protein 7, ZFP7 ; supporte	ZFP7	AT1G24625	1.69	0.76	4.69	0.002472	0.014258	-1.79
259664_at	unknown protein ; supported by full-ler	AGP21	AT1G55330	-9.91	-3.31	-4.69	0.002476	0.01427	-1.79
256321_at	lipoxygenase, putative similar to lipoxy	LOX1	AT1G55020	5.29	2.40	4.69	0.002475	0.01427	-1.79
249942_at	Nitrilase 4 (sp|P46011) ; supported by	GAPB	AT1G42970 /	12.27	3.62	4.69	0.002475	0.01427	-1.79
253917_at	hypothetical protein ;supported by full-	---	AT4G27380	1.76	0.81	4.69	0.002477	0.014271	-1.79
248008_at	transcription factor NtWRKY4-like ; su	WRKY2	AT5G56270	1.74	0.80	4.69	0.002477	0.014271	-1.79
253047_at	Expressed protein ; supported by full-l	---	AT4G37295	1.97	0.98	4.69	0.002488	0.014329	-1.80
249775_at	squalene monooxygenase 1,2 (squale	SQE6	AT5G24160	1.88	0.91	4.69	0.002489	0.014329	-1.80
263722_at	putative vanadate resistance protein	GONST1	AT2G13650	1.47	0.56	4.69	0.002489	0.014329	-1.80
254680_at	phytochrome E	PHYE	AT4G18130	-1.63	-0.70	-4.69	0.00249	0.014332	-1.80
258062_at	unknown protein ; supported by cDNA	---	AT3G26000	1.67	0.74	4.69	0.002494	0.01435	-1.80
245129_at	hypothetical protein predicted by gene	CRR4	AT2G45350	-1.34	-0.42	-4.69	0.002494	0.01435	-1.80
254822_at	polyubiquitin-like protein polyubiquitin	UPL5	AT4G12570	1.42	0.50	4.68	0.002497	0.014362	-1.80
260556_at	putative endochitinase	---	AT2G43620	9.28	3.21	4.68	0.002498	0.014362	-1.80
261648_at	salt-tolerance zinc finger protein identi	STZ	AT1G27730	4.78	2.26	4.68	0.0025	0.014368	-1.80
266582_at	unknown protein ; supported by cDNA	---	AT2G46090	-1.59	-0.67	-4.68	0.0025	0.014368	-1.80
260499_at	unknown protein ; supported by cDNA	---	AT2G41760	-1.40	-0.49	-4.68	0.002501	0.014372	-1.80
252394_at	heat shock protein-like protein heat-sh	---	AT3G47940	-1.67	-0.74	-4.68	0.002502	0.014372	-1.80
262206_at	putative ubiquinol-cytochrome c reduct	---	AT2G01090	-1.58	-0.66	-4.68	0.002503	0.014374	-1.81
251942_at	ABC transporter - like protein PDR5-li	PDR9	AT3G53480	2.90	1.54	4.68	0.002504	0.014374	-1.81
258114_at	putative cytochrome P450 similar to G	CYP72A13	AT3G14660	1.44	0.53	4.68	0.002505	0.014381	-1.81
247114_at	unknown protein ; supported by cDNA	---	AT5G65910	-1.54	-0.62	-4.68	0.002507	0.014387	-1.81
253203_at	arginine decarboxylase SPE2 ; suppo	ADC2	AT4G34710	2.88	1.53	4.68	0.00251	0.014402	-1.81
259083_at	putative kinase similar to NIMA-related	ATNEK2	AT3G04810	-1.42	-0.51	-4.68	0.002516	0.014428	-1.81
257280_at	9-cis-epoxycarotenoid dioxygenase, p	NCED3	AT3G14440	1.89	0.91	4.68	0.002517	0.014433	-1.81
253278_at	receptor protein kinase - like protein p	---	AT4G34220	-3.36	-1.75	-4.68	0.002518	0.014433	-1.81
257323_at	hypothetical protein	---	AT2G07698	2.75	1.46	4.68	0.002519	0.014437	-1.81
261170_at	growth regulator protein similar to GB:J	---	AT1G04910	-1.46	-0.55	-4.68	0.00252	0.01444	-1.81
250550_at	N-hydroxycinnamoyl benzoyltransfera	---	AT5G07870	-2.24	-1.17	-4.68	0.002521	0.014443	-1.81
263707_at	hypothetical protein Similar to gi|1573	---	AT1G09300	1.77	0.82	4.68	0.002522	0.014445	-1.81
255994_at	hypothetical protein predicted by gens	---	AT1G29760	1.40	0.49	4.67	0.002526	0.014465	-1.82
263911_at	hypothetical protein predicted by gene	---	AT2G36560	-1.39	-0.47	-4.67	0.002527	0.014466	-1.82
245229_at	putative protein contains EST gb:T450	---	AT4G25620	-1.98	-0.99	-4.67	0.002536	0.014515	-1.82
252437_at	putative protein pectinesterase homol	---	AT3G47380	2.87	1.52	4.67	0.002541	0.014535	-1.82
261544_at	unknown protein	---	AT1G63540	1.66	0.73	4.67	0.002548	0.014575	-1.82

253890_s_	putative protein contains similarity to s	---	AT4G27585 /	2.42	1.27	4.67	0.002552	0.014588	-1.83
248234_at	putative protein contains similarity to e	---	AT5G53850	-1.38	-0.47	-4.67	0.002552	0.014588	-1.83
250233_at	putative protein weak homology with p	IQD11	AT5G13460	-3.63	-1.86	-4.66	0.002554	0.014594	-1.83
249146_at	putative protein contains similarity to C	---	AT5G43310	-1.42	-0.51	-4.66	0.002555	0.014594	-1.83
263426_at	putative glutathione peroxidase ;supp	ATGPX2	AT2G31570	1.77	0.82	4.66	0.002554	0.014594	-1.83
263067_at	hypothetical protein predicted by gens	---	AT2G17550	-1.90	-0.93	-4.66	0.002557	0.0146	-1.83
251846_at	histone H2A.F/Z ;supported by full-len	HTA11	AT3G54560	-3.26	-1.71	-4.66	0.002556	0.0146	-1.83
254232_at	tyrosine transaminase like protein tyr	CORI3	AT4G23600	-3.69	-1.88	-4.66	0.002562	0.014625	-1.83
245142_at	putative O-sialoglycoprotein endopepti	---	AT2G45270	-1.46	-0.55	-4.66	0.002568	0.014657	-1.83
258665_at	thioredoxin-like protein similar to thiore	ATH9	AT3G08710	2.00	1.00	4.66	0.002569	0.014658	-1.83
252022_at	fructose bisphosphate aldolase - like p	---	AT3G52930	1.75	0.81	4.66	0.00257	0.014662	-1.83
251637_at	hypothetical protein	---	AT3G57570	1.50	0.58	4.66	0.002572	0.014664	-1.83
261303_at	unknown protein contains DNA-binding	HON5	AT1G48620	1.35	0.43	4.66	0.002572	0.014664	-1.83
264155_at	unknown protein	GTB1	AT1G65440	1.71	0.77	4.66	0.002577	0.014686	-1.84
259120_at	unknown protein	---	AT3G02240	10.05	3.33	4.66	0.002578	0.014688	-1.84
254610_at	putative protein predicted protein, Ara	---	AT4G18890	1.47	0.56	4.66	0.002581	0.014699	-1.84
254576_at	putative protein ;supported by full-leng	EMB3006	AT4G19350	-1.41	-0.49	-4.66	0.00258	0.014699	-1.84
262070_at	far-red impaired response protein, put	FRS8	AT1G80010	1.40	0.49	4.65	0.002584	0.014714	-1.84
260403_at	hypothetical protein predicted by gens	WRKY36	AT1G69810	1.38	0.46	4.65	0.002586	0.01472	-1.84
247729_at	1-aminocyclopropane-1-carboxylate o	---	AT5G59530	2.08	1.06	4.65	0.002587	0.014722	-1.84
257275_at	RNA-binding protein, putative contain	CID9	AT3G14450	-1.93	-0.95	-4.65	0.002588	0.014725	-1.84
252667_at	protein kinase-like protein MSTK2S ki	NEK6	AT3G44200	-1.64	-0.72	-4.65	0.002589	0.014727	-1.84
266596_at	hypothetical protein predicted by gens	---	AT2G46150	2.56	1.35	4.65	0.002592	0.014738	-1.84
255302_at	putative protein similar to transcription	ATMSRB5	AT4G04830	-1.71	-0.77	-4.65	0.002592	0.014738	-1.84
252977_at	Phospholipase like protein Arabidopsi	---	AT4G38560	2.77	1.47	4.65	0.002599	0.014771	-1.85
261150_at	floral nectary-specific protein, putative	JMT	AT1G19640	-3.76	-1.91	-4.65	0.0026	0.014772	-1.85
251261_at	putative protein polygalacturonase - L	---	AT3G62110	-2.26	-1.17	-4.65	0.002601	0.014772	-1.85
263192_at	hypothetical protein putative acetyl-Co	ACC1	AT1G36160	-1.74	-0.80	-4.65	0.002602	0.014772	-1.85
247441_at	receptor - like protein kinase - like pro	---	AT5G62710	-1.51	-0.59	-4.65	0.002601	0.014772	-1.85
250941_at	putative protein	---	AT5G03320	1.59	0.67	4.65	0.002604	0.014783	-1.85
260804_at	hypothetical protein predicted by gene	---	AT1G78410	16.01	4.00	4.65	0.002607	0.014798	-1.85
259420_at	hypothetical protein similar to putative	---	AT1G13900	-1.31	-0.39	-4.65	0.002612	0.014819	-1.85
249746_at	NAC2-like protein	TIP	AT5G24590	1.53	0.62	4.64	0.002613	0.014819	-1.85
264161_at	antigen receptor, putative similar to ar	---	AT1G65420	-1.47	-0.55	-4.65	0.002612	0.014819	-1.85
261832_at	S-ribonuclease binding protein SBP1,	---	AT1G10650	1.79	0.84	4.64	0.002614	0.014819	-1.85

245977_at	glucose-6-phosphate 1-dehydrogenas	G6PD2	AT5G13110	2.06	1.04	4.64	0.002617	0.014837	-1.85
262801_at	unknown protein ;supported by full-ler	---	AT1G21010	2.58	1.37	4.64	0.002618	0.014838	-1.85
248705_at	putative protein similar to unknown pro	---	AT5G48520	-1.63	-0.71	-4.64	0.002619	0.014839	-1.85
262839_at	PhD-finger protein, putative contains F	---	AT1G14770	-1.91	-0.93	-4.64	0.002621	0.014844	-1.86
260993_at	hypothetical protein predicted by gene	FMO GS-OX	AT1G12140	1.34	0.42	4.64	0.002621	0.014844	-1.86
252275_at	ubiquitin-specific protease 26 (UBP26	UBP26	AT3G49600	1.69	0.76	4.64	0.002626	0.01487	-1.86
264990_at	unknown protein supported by cDNA:	---	AT1G27210	-2.08	-1.06	-4.64	0.002631	0.014885	-1.86
251539_at	serine/threonine-specific protein kinas	---	AT3G58690	-1.62	-0.70	-4.64	0.00263	0.014885	-1.86
261617_s_	hypothetical protein predicted by gene	---	AT1G33090 /	1.37	0.46	4.64	0.002631	0.014885	-1.86
251484_at	putative protein putative protein At2g4	---	AT3G59640	1.37	0.46	4.64	0.002638	0.014919	-1.86
250112_at	low density lipoprotein B-like protein	---	AT5G16300	-1.40	-0.48	-4.64	0.00264	0.014927	-1.86
263629_at	hypothetical protein predicted by gens	---	AT2G04850	-1.84	-0.88	-4.64	0.002642	0.014933	-1.86
266317_at	calmodulin identical to GB:L18912; su	CAM5	AT2G27030	-1.42	-0.51	-4.63	0.002647	0.014953	-1.87
250149_at	cinnamoyl CoA reductase - like protei	---	AT5G14700	6.55	2.71	4.63	0.002647	0.014953	-1.87
250494_at	embryogenic callus protein - like embr	HAM2	AT5G09740	-1.58	-0.66	-4.63	0.002647	0.014953	-1.87
253162_at	phosphoserine aminotransferase ;sup	PSAT	AT4G35630	4.04	2.01	4.63	0.00265	0.014962	-1.87
256192_at	diadenosine 5,5-P1,P4-tetraphosphat	ATNUDX25	AT1G30110	1.49	0.58	4.63	0.00265	0.014962	-1.87
245426_at	hypothetical protein	---	AT4G17540	-1.55	-0.63	-4.63	0.002651	0.014962	-1.87
255338_at	PEROXISOMAL MEMBRANE PROTE	PMP22	AT4G04470	1.37	0.46	4.63	0.002658	0.014994	-1.87
249991_at	zinc finger -like protein zinc finger pro	---	AT5G18550	-1.44	-0.52	-4.63	0.002657	0.014994	-1.87
248034_at	serine threonine-specific protein kinase	D6PK	AT5G55910	-1.50	-0.59	-4.63	0.002658	0.014994	-1.87
255154_at	putative protein several hypothetical pr	---	---	-1.35	-0.44	-4.63	0.00266	0.015002	-1.87
257104_at	ER lumen retaining receptor (HDEL re	---	AT3G25040	-1.43	-0.52	-4.63	0.002663	0.015014	-1.87
264676_at	unknown protein EST gb|R64758 com	---	AT1G09870	1.37	0.45	4.63	0.002667	0.015034	-1.87
254346_at	symbiosis-related like protein symbios	APG8A	AT4G21980	1.91	0.94	4.63	0.002672	0.015056	-1.88
264169_at	hypothetical protein predicted by gens	---	AT1G02020	1.31	0.39	4.63	0.002673	0.015057	-1.88
250355_at	putative protein predicted protein, Ara	---	AT5G11700	-1.55	-0.63	-4.62	0.002683	0.015108	-1.88
256861_at	beta-amylase, putative similar to beta-	BAM1	AT3G23920	2.00	1.00	4.62	0.002683	0.015108	-1.88
258332_at	putative transport protein similar to tra	---	AT3G16180	-2.76	-1.46	-4.62	0.002686	0.01512	-1.88
264433_at	beta-glucosidase, putative similar to b	BGLU45	AT1G61810	5.88	2.56	4.62	0.002691	0.015144	-1.88
245626_at	unknown protein ;supported by full-len	---	AT1G56700	1.70	0.77	4.62	0.002691	0.015144	-1.88
248070_at	putative protein similar to unknown pro	---	AT5G55660	1.42	0.50	4.62	0.002694	0.015155	-1.89
261135_at	defensin AMP1, putative similar to PIF	PDF1.4	AT1G19610	5.38	2.43	4.62	0.002699	0.015163	-1.89
250252_at	transporter-like protein ;supported by f	ZIFL1	AT5G13750	3.66	1.87	4.62	0.002697	0.015163	-1.89
253898_s_	tryptophan synthase beta-subunit (TSE	TSB2	AT4G27070 /	3.04	1.61	4.62	0.002699	0.015163	-1.89

259240_at	unknown protein ; supported by cDNA	---	AT3G11590	-1.66	-0.73	-4.62	0.002697	0.015163	-1.89
260772_at	unknown protein contains similarity to	---	AT1G49050	1.56	0.64	4.62	0.002699	0.015163	-1.89
250691_at	glycolate oxidase subunit D-like; D-lac	---	AT5G06580	-1.34	-0.43	-4.62	0.0027	0.015163	-1.89
261577_at	ribonucleoprotein, putative similar to 3	---	AT1G01080	-1.70	-0.77	-4.62	0.002703	0.015181	-1.89
265725_at	putative alanine acetyl transferase	---	AT2G32030	13.75	3.78	4.61	0.002707	0.015198	-1.89
259166_at	unknown protein ; supported by cDNA	---	AT3G01670	-3.13	-1.64	-4.61	0.002709	0.015202	-1.89
252331_s_	serine palmitoyltransferase-like protein	SPT1	AT3G48780 /	1.49	0.58	4.61	0.002709	0.015202	-1.89
252015_at	putative protein growth-regulating fact	AtGRF4	AT3G52910	-1.33	-0.41	-4.61	0.00271	0.015204	-1.89
261039_at	Expressed protein ; supported by full-le	ELF4-L4	AT1G17455	-1.76	-0.81	-4.61	0.002711	0.015204	-1.89
246072_at	PISTILLATA ; supported by full-length	PI	AT5G20240	1.39	0.47	4.61	0.002713	0.015207	-1.89
256193_at	hypothetical protein similar to hypothet	---	AT1G30200	-1.41	-0.49	-4.61	0.002713	0.015207	-1.89
259521_at	ATP-dependent Clp protease proteolyt	CLP2	AT1G12410	-1.57	-0.65	-4.61	0.002714	0.01521	-1.89
255248_at	Oxygen-evolving enhancer protein 3 p	PSBQ-2	AT4G05180	-1.33	-0.41	-4.61	0.002715	0.01521	-1.89
264460_at	hypothetical protein similar to transcrip	ATNFXL1	AT1G10170	1.59	0.67	4.61	0.002717	0.015218	-1.89
263526_at	hypothetical protein predicted by gens	---	AT2G24830	1.40	0.48	4.61	0.002717	0.015219	-1.89
249103_at	N-carbamyl-L-amino acid amidohydrol	UAH	AT5G43600	-1.47	-0.56	-4.61	0.002726	0.015262	-1.90
263942_at	unknown protein	FLA16	AT2G35860	-8.03	-3.01	-4.61	0.002729	0.015278	-1.90
248292_at	putative protein similar to unknown pro	---	AT5G53030	1.76	0.81	4.61	0.002731	0.015281	-1.90
266857_at	putative Na+ dependent ileal bile acid	---	AT2G26900	-1.41	-0.50	-4.61	0.002735	0.015299	-1.90
251820_at	putative protein In2-1 protein, Zea ma	GSTL2	AT3G55040	-2.14	-1.10	-4.60	0.002741	0.015332	-1.90
258650_at	putative protein kinase similar to protei	---	AT3G09830	1.94	0.95	4.60	0.002742	0.015332	-1.90
245760_s_	receptor serine/threonine kinase PR5l	---	AT1G66910 /	2.37	1.25	4.60	0.002747	0.015352	-1.91
258281_at	putative shikimate kinase similar to shi	---	AT3G26900	-1.33	-0.41	-4.60	0.002747	0.015352	-1.91
258622_at	unknown protein contains Pfam profile	---	AT3G02720	-1.42	-0.51	-4.60	0.002746	0.015352	-1.91
248738_at	unknown protein ;supported by full-ler	---	AT5G48020	1.45	0.53	4.60	0.002751	0.015368	-1.91
265898_at	hypothetical protein predicted by gens	---	AT2G25690	1.91	0.93	4.60	0.002753	0.015375	-1.91
260284_at	unknown protein ; supported by full-le	---	AT1G80380	-1.39	-0.48	-4.60	0.002756	0.015388	-1.91
260388_at	hypothetical protein predicted by gens	---	AT1G74070	-2.12	-1.09	-4.60	0.002761	0.015414	-1.91
256244_at	sulphate transporter, putative similar t	SULTR4;2	AT3G12520	-1.40	-0.48	-4.60	0.002762	0.015416	-1.91
246523_at	CONSTANS-like 1	COL1	AT5G15850	-1.81	-0.86	-4.60	0.002765	0.01543	-1.91
251092_at	putative protein ;supported by full-leng	---	AT5G01470	-1.45	-0.54	-4.59	0.002771	0.015457	-1.92
257989_at	unknown protein ; supported by cDNA	VPS9A	AT3G19770	1.47	0.55	4.59	0.002772	0.015458	-1.92
266523_at	putative transportin	TRN1	AT2G16950	1.41	0.49	4.59	0.002773	0.015461	-1.92
259309_at	putative cyclin-dependent protein kinas	---	AT3G05050	1.64	0.71	4.59	0.002777	0.015476	-1.92
249395_at	putative protein	---	AT5G40190	-1.36	-0.45	-4.59	0.002777	0.015476	-1.92

264389_at	unknown protein similar to hypothetica	---	AT1G11960	-1.87	-0.90	-4.59	0.002786	0.015522	-1.92
254480_at	translation elongation factor EF-Tu pr	ATRABE1B	AT4G20360	-1.50	-0.59	-4.59	0.002788	0.015531	-1.92
255456_at	hypothetical protein ;supported by full-	---	AT4G02920	-1.43	-0.52	-4.59	0.002792	0.015549	-1.92
248583_at	putative protein strong similarity to unk	emb1441	AT5G49930	1.53	0.62	4.59	0.002794	0.015553	-1.93
260696_at	unknown protein	---	AT1G32520	1.48	0.57	4.59	0.002795	0.01556	-1.93
266157_at	unknown protein	ATFUC1	AT2G28100	-1.32	-0.40	-4.59	0.002796	0.015561	-1.93
266934_at	unknown protein	---	AT2G18900	1.51	0.60	4.58	0.0028	0.015575	-1.93
250868_at	malate synthase -like protein malate s	MLS	AT5G03860	-1.73	-0.79	-4.58	0.002807	0.015613	-1.93
249811_at	unknown protein ;supported by full-ler	---	AT5G23760	1.37	0.46	4.58	0.002811	0.015629	-1.93
265673_at	unknown protein ;supported by full-ler	---	AT2G32090	-1.59	-0.67	-4.58	0.002812	0.015634	-1.93
259802_at	thionin identical to GI:1181531 from [A	THI2.1	AT1G72260	9.39	3.23	4.58	0.002814	0.01564	-1.93
261547_at	protein kinase, putative contains Pfam	---	AT1G63500	-1.46	-0.55	-4.58	0.002815	0.015644	-1.93
256433_at	unknown protein	SAG20	AT3G10985	1.71	0.78	4.58	0.002817	0.015648	-1.93
264694_at	receptor serine/threonine kinase PR5,	---	AT1G70250	1.36	0.44	4.58	0.00282	0.015661	-1.94
245287_at	imidazoleglycerol-phosphate dehydrat	---	AT4G14910	-1.68	-0.75	-4.58	0.002827	0.015696	-1.94
247065_s_	disease resistance protein-like	---	AT5G66900 /	1.61	0.68	4.58	0.002828	0.015698	-1.94
249996_at	glutaredoxin -like protein glutaredoxin	---	AT5G18600	-2.12	-1.08	-4.58	0.00283	0.015706	-1.94
257058_at	Expressed protein ; supported by cDN	COX17	AT3G15352	4.02	2.01	4.57	0.002833	0.015717	-1.94
250004_at	putative protein predicted proteins - Ar	---	AT5G18750	1.64	0.71	4.57	0.002834	0.015717	-1.94
259784_at	auxin-induced protein, putative similar	---	AT1G29450	-2.18	-1.12	-4.57	0.002834	0.015717	-1.94
259507_at	unknown protein	---	AT1G43910	2.77	1.47	4.57	0.002836	0.015719	-1.94
264482_at	sugar carrier protein, putative similar t	---	AT1G77210	2.45	1.29	4.57	0.002836	0.015719	-1.94
257608_at	chaperonin, putative similar to CHAPE	HSP60-3A	AT3G13860	1.45	0.54	4.57	0.002841	0.015742	-1.94
246516_at	putative protein auxin-independent gr	---	AT5G15740	-3.50	-1.81	-4.57	0.002845	0.015758	-1.94
249372_at	glucose-6-phosphate dehydrogenase	G6PD6	AT5G40760	2.03	1.02	4.57	0.002845	0.015758	-1.94
250119_at	putative protein similar to unknown pro	---	AT5G16470	1.40	0.48	4.57	0.002847	0.015764	-1.95
262173_at	betaine aldehyde dehydrogenase, put	ALDH10A8	AT1G74920	-1.48	-0.56	-4.57	0.002848	0.015768	-1.95
248387_at	unknown protein	---	AT5G51960	-1.53	-0.61	-4.57	0.002862	0.015843	-1.95
259607_at	P-glycoprotein, putative similar to P-gl	PGP13	AT1G27940	-1.33	-0.41	-4.56	0.002864	0.015848	-1.95
262372_at	hypothetical protein predicted by gene	---	AT1G73130	1.86	0.89	4.56	0.002873	0.015896	-1.96
259513_at	hypothetical protein ; supported by cDI	ARK3	AT1G12430	1.48	0.56	4.56	0.002874	0.015896	-1.96
262085_at	hypothetical protein predicted by gene	---	AT1G56060	5.28	2.40	4.56	0.002875	0.0159	-1.96
255619_s_	putative CHP-rich zinc finger protein s	---	AT4G01350 /	-1.64	-0.71	-4.56	0.002878	0.015908	-1.96
254578_at	putative pectinacetylesterase protein	---	AT4G19400 /	-1.79	-0.84	-4.56	0.002878	0.015908	-1.96
247289_at	2-oxoglutarate/malate translocator ; s	DIT2.1	AT5G64290	-1.57	-0.65	-4.56	0.00288	0.015913	-1.96

262782_at	Expressed protein ; supported by full-l	---	AT1G13195	1.40	0.49	4.56	0.002883	0.015926	-1.96
264309_at	coatomer alpha subunit, putative simil	---	AT1G62020	-1.37	-0.45	-4.56	0.002892	0.015973	-1.96
AFFX-r2-At	Arabidopsis thaliana /REF=M64116 /D	---	---	2.52	1.33	4.56	0.002895	0.01598	-1.96
250079_at	putative protein similar to unknown pro	---	AT5G16650	-1.53	-0.61	-4.56	0.002894	0.01598	-1.96
261518_at	peroxidase ATP4a identical to GB:CAA	---	AT1G71695	-1.55	-0.64	-4.55	0.002898	0.015995	-1.97
266099_at	putative alpha-carboxyltransferase ; s	CAC3	AT2G38040	-1.68	-0.75	-4.55	0.002901	0.016004	-1.97
259280_at	putative polypyrimidine tract-binding p	PTB1	AT3G01150	-1.35	-0.43	-4.55	0.002908	0.016044	-1.97
247407_at	putative protein predicted proteins, Ar	---	AT5G62900	1.61	0.69	4.55	0.00291	0.016046	-1.97
264793_at	unknown protein similar to beta-galact	---	AT1G08660	-1.70	-0.77	-4.55	0.002911	0.016051	-1.97
252389_at	Expressed protein ; supported by full-l	---	AT3G47833	1.99	0.99	4.55	0.002921	0.0161	-1.97
251309_at	putative protein carbonyl reductase (N	---	AT3G61220	1.53	0.61	4.55	0.002924	0.016115	-1.97
262619_at	3-hydroxyisobutyryl-coenzyme A hydr	---	AT1G06550	3.08	1.62	4.55	0.002926	0.016121	-1.98
258519_at	unknown protein	---	AT3G06760	-1.58	-0.66	-4.55	0.002931	0.016143	-1.98
261661_at	lysophospholipase homolog, putative	---	AT1G18360	-1.81	-0.85	-4.54	0.002931	0.016143	-1.98
258908_at	putative dehydroquinase shikimate del	MEE32	AT3G06350	1.69	0.76	4.54	0.002933	0.016148	-1.98
264219_at	unknown protein contains similarity to	---	AT1G60420	1.72	0.78	4.54	0.002937	0.016164	-1.98
247630_at	putative protein	SIZ1	AT5G60410	1.50	0.59	4.54	0.002937	0.016164	-1.98
265479_at	hypothetical protein ;supported by full-	---	AT2G15760	5.23	2.39	4.54	0.002938	0.016166	-1.98
246469_at	putative protein predicted protein, Dro	---	AT5G17070	-1.41	-0.49	-4.54	0.00294	0.016174	-1.98
249795_at	40S ribosomal protein S11 ;supported	RPS11-BET	AT5G23740	-2.00	-1.00	-4.54	0.00295	0.016218	-1.98
256536_at	peptide chain release factor, putative	---	AT1G33330	-1.40	-0.48	-4.54	0.00295	0.016218	-1.98
251368_at	putative protein hypothetical protein A	---	AT3G61380	-1.86	-0.89	-4.54	0.002951	0.016218	-1.99
250433_at	histone H3 - like protein histone H3, A	---	AT5G10400	-1.51	-0.60	-4.54	0.002951	0.016218	-1.98
258045_at	ubiquitin-specific protease 7 (UBP7),	UBP7	AT3G21280	-1.47	-0.56	-4.54	0.002956	0.016238	-1.99
261395_at	unknown protein similar to putative AP	---	AT1G79700	-2.45	-1.29	-4.53	0.002965	0.01627	-1.99
264561_at	uracil phosphoribosyltransferase, puta	---	AT1G55810	1.69	0.76	4.53	0.002966	0.01627	-1.99
258707_at	putative histone H2B similar to histone	---	AT3G09480	1.59	0.67	4.54	0.002963	0.01627	-1.99
250991_at	metallothionein 2b ; supported by full-	MT2B	AT5G02380	1.48	0.57	4.53	0.002966	0.01627	-1.99
253401_at	putative protein hypothetical protein F	---	AT4G32870	8.69	3.12	4.54	0.002963	0.01627	-1.99
253173_at	putative protein pEARLI 4, Arabidopsi	---	AT4G35110	2.93	1.55	4.53	0.002965	0.01627	-1.99
AFFX-Atha	Arabidopsis thaliana /REF=M64116 /D	GAPC1	---	2.08	1.06	4.53	0.00297	0.016291	-1.99
265230_s_	hypothetical protein	---	AT2G07707	1.66	0.73	4.53	0.002973	0.0163	-1.99
255690_at	probable cytochrome P450	CYP86A2	AT4G00360	-5.81	-2.54	-4.53	0.002977	0.016322	-1.99
252113_at	putative protein predicted protein, Ara	---	AT3G51620	1.36	0.45	4.53	0.002983	0.016346	-2.00
260908_at	maternal embryogenesis control prote	MEA	AT1G02580	1.98	0.98	4.53	0.00299	0.016384	-2.00

246445_at	glucose 6 phosphate/phosphate trans	---	AT5G17630	-1.51	-0.60	-4.53	0.002992	0.016391	-2.00
250822_at	unknown protein	---	AT5G05230	1.37	0.46	4.53	0.002998	0.016421	-2.00
266663_at	putative receptor-like protein kinase ;	---	AT2G25790	-1.74	-0.80	-4.52	0.003	0.016426	-2.00
248222_at	GTPase activator protein of Rab-like s	---	AT5G53570	1.58	0.66	4.52	0.003001	0.01643	-2.00
250811_at	cysteine proteinase inhibitor-like protei	---	AT5G05110	1.96	0.97	4.52	0.003003	0.016437	-2.00
253080_at	hypothatical protein	---	---	-1.40	-0.49	-4.52	0.003005	0.016443	-2.00
263783_at	putative WRKY-type DNA binding prot	WRKY46	AT2G46400	4.62	2.21	4.52	0.003007	0.016451	-2.01
247755_at	subtilisin-like serine protease contains	ATSBT4.12	AT5G59090	-1.37	-0.45	-4.52	0.003009	0.016453	-2.01
264904_s_	putative thioredoxin reductase	NTRA	AT2G17420 /	1.63	0.70	4.52	0.00301	0.016456	-2.01
265056_at	mitochondrial processing peptidase al	---	AT1G51980	1.61	0.68	4.52	0.003014	0.016474	-2.01
256020_at	glutamyl-tRNA reductase, putative sim	HEMA1	AT1G58290	-1.72	-0.78	-4.52	0.003017	0.016481	-2.01
258109_at	hypothetical protein contains Pfam pro	HGL1	AT3G23640	-1.45	-0.53	-4.52	0.003016	0.016481	-2.01
250482_at	putative protein	---	AT5G10320	-1.56	-0.64	-4.52	0.003018	0.016485	-2.01
255677_at	putative calmodulin-binding heat shock	---	AT4G00500	1.74	0.80	4.52	0.003022	0.016498	-2.01
263490_at	F-box protein ORE9, AtFBL7 identical	MAX2	AT2G42620	-2.01	-1.01	-4.52	0.003021	0.016498	-2.01
254723_at	ammonium transport protein (AMT1) ;	AMT1;1	AT4G13510	1.64	0.72	4.52	0.003023	0.016499	-2.01
265475_at	ferredoxin--nitrite reductase ; supporte	NIR1	AT2G15620	1.72	0.79	4.52	0.003031	0.016526	-2.01
261168_at	unknown protein	---	AT1G04940 /	1.92	0.94	4.52	0.00303	0.016526	-2.01
257536_at	unknown protein	---	AT3G02800	5.99	2.58	4.52	0.00303	0.016526	-2.01
260384_at	putative 2-isopropylmalate synthase si	IMS1	AT1G74040	-1.43	-0.52	-4.52	0.003031	0.016526	-2.01
260267_at	very-long-chain fatty acid condensing	KCS6	AT1G68530	-2.23	-1.16	-4.52	0.003032	0.016528	-2.01
257730_at	unknown protein contains Pfam profile	---	AT3G18420	1.67	0.74	4.52	0.003034	0.016536	-2.02
259887_at	putative protein kinase similar to protei	---	AT1G76360	1.45	0.54	4.51	0.003041	0.016568	-2.02
249860_at	prolylcarboxypeptidase-like protein ;su	---	AT5G22860	7.90	2.98	4.51	0.003041	0.016568	-2.02
262955_at	unknown protein ;supported by full-len	---	AT1G54520	-1.53	-0.62	-4.51	0.003043	0.016572	-2.02
252932_at	putative proton pump vacuolar proton	VHA-A3	AT4G39080	-1.44	-0.52	-4.51	0.003047	0.016584	-2.02
254359_at	putative protein hypothetical protein Y	---	AT4G22360	-1.48	-0.57	-4.51	0.003047	0.016584	-2.02
265648_at	putative beta-1,3-glucanase ;supporte	---	AT2G27500	2.26	1.18	4.51	0.003047	0.016584	-2.02
253335_at	putative protein YHR077c (NMD2,IFS	---	AT4G33500	-1.49	-0.57	-4.51	0.003048	0.016588	-2.02
262398_at	hypothetical protein predicted by gene	---	AT1G49350	-1.34	-0.43	-4.51	0.00305	0.01659	-2.02
253263_at	abscisic acid responsive elements-bin	ABF3	AT4G34000	2.25	1.17	4.51	0.003052	0.0166	-2.02
258425_at	unknown protein	---	AT3G16760	-1.33	-0.42	-4.51	0.003054	0.016608	-2.02
253942_at	putative protein	---	AT4G27010	1.80	0.85	4.51	0.003057	0.016617	-2.02
254041_at	Expressed protein ; supported by full-l	---	AT4G25830	-3.25	-1.70	-4.51	0.003062	0.016634	-2.03
256745_at	UDP-glucose dehydrogenase, putativ	---	AT3G29360	-1.55	-0.63	-4.51	0.003063	0.016634	-2.03

252949_at	putative thaumatin-like protein thauma	---	AT4G38670	-1.99	-0.99	-4.51	0.003062	0.016634	-2.03
256654_at	ribosomal protein, putative similar to 4	---	AT3G18880	-1.70	-0.77	-4.51	0.003063	0.016634	-2.03
262381_at	virus resistance protein, putative simil	---	AT1G72900	4.37	2.13	4.51	0.003066	0.016647	-2.03
259994_at	putative C2H2-type zinc finger protein	AtIDD14	AT1G68130 /	-1.76	-0.82	-4.51	0.003067	0.016647	-2.03
251804_at	beta-1,3-glucanase - like protein prob	---	AT3G55430	1.67	0.74	4.50	0.003074	0.016677	-2.03
252241_at	putative protein CND41, chloroplast n	---	AT3G50050	-1.44	-0.53	-4.50	0.003074	0.016677	-2.03
248434_at	mitochondrial heat shock 22 kd protein	---	AT5G51440	6.90	2.79	4.50	0.003074	0.016677	-2.03
257252_at	glutathione reductase, cytosolic identi	ATGR1	AT3G24170	2.02	1.01	4.50	0.003077	0.016686	-2.03
261425_at	peptide transporter, putative similar to	---	AT1G18880	2.20	1.13	4.50	0.003083	0.016703	-2.03
262432_at	unknown protein	---	AT1G47530	1.99	0.99	4.50	0.003081	0.016703	-2.03
245439_at	hypothetical protein	---	AT4G16670	2.12	1.08	4.50	0.003082	0.016703	-2.03
260614_at	hypothetical protein contains Pfam pro	---	AT1G53390	1.35	0.44	4.50	0.003082	0.016703	-2.03
258577_at	putative disease resistance protein sim	---	AT3G04220	2.18	1.12	4.50	0.003089	0.016734	-2.03
260744_at	hypothetical protein predicted by gene	---	AT1G15010	-5.00	-2.32	-4.50	0.003094	0.016754	-2.04
256933_at	unknown protein contains Pfam profile	---	AT3G22600	14.29	3.84	4.50	0.003099	0.016768	-2.04
257137_at	P-glycoprotein, putative similar to P-gl	ABCB19	AT3G28860	-3.46	-1.79	-4.50	0.003099	0.016768	-2.04
262811_at	unknown protein ESTs gb|R65381 and	---	AT1G11700	1.47	0.55	4.50	0.003097	0.016768	-2.04
258862_at	putative mitochondrial processing pept	MPPBETA	AT3G02090	1.44	0.53	4.50	0.003099	0.016768	-2.04
263963_at	putative DNA-binding protein RAV2	---	AT2G36080	1.72	0.78	4.50	0.003103	0.01678	-2.04
251659_at	hypothetical protein ;supported by full-	BIGYIN	AT3G57090	1.45	0.54	4.50	0.003104	0.01678	-2.04
247102_at	putative protein similar to unknown pro	---	AT5G66550	-1.51	-0.59	-4.50	0.003104	0.01678	-2.04
265840_at	hypothetical protein predicted by gens	---	AT2G14530	-1.57	-0.65	-4.50	0.003104	0.01678	-2.04
262401_at	small GTP-binding protein, putative si	RABG3E	AT1G49300	-1.34	-0.42	-4.49	0.003106	0.016784	-2.04
250031_at	transfactor-like protein ; supported by	MYR1	AT5G18240	-1.67	-0.74	-4.49	0.003109	0.016797	-2.04
255502_at	contains similarity to a protein kinase	---	AT4G02410	4.21	2.07	4.49	0.003119	0.016846	-2.05
245504_at	glutaredoxin	---	AT4G15660	-1.82	-0.86	-4.49	0.003122	0.016857	-2.05
255599_at	cyclic nucleotide gated channel (CNG	ATCNGC13	AT4G01010	2.07	1.05	4.49	0.003129	0.01689	-2.05
264616_at	unknown protein	---	AT2G17740	8.18	3.03	4.49	0.003134	0.016915	-2.05
254746_at	putative protein hypothetical protein -	---	AT4G12980	-2.00	-1.00	-4.49	0.003135	0.016915	-2.05
248885_at	putative protein similar to unknown pro	---	AT5G46150	-1.40	-0.48	-4.49	0.003137	0.016919	-2.05
250016_at	Cu/Zn superoxide dismutase-like prote	CSD3	AT5G18100	-1.46	-0.54	-4.49	0.003138	0.016919	-2.05
266227_at	unknown protein ;supported by full-ler	---	AT2G28870	-1.33	-0.41	-4.49	0.003138	0.016919	-2.05
266363_at	hypothetical protein predicted by gens	---	AT2G41250	1.93	0.95	4.49	0.00314	0.016931	-2.05
252179_at	putative protein UDP-glucose:(glucosy	GATL2	AT3G50760	1.73	0.79	4.48	0.003143	0.016935	-2.05
266300_at	putative auxin transport protein ; supp	PIN4	AT2G01420	-3.47	-1.80	-4.49	0.003142	0.016935	-2.05

262622_at	hypothetical protein predicted by gene	---	AT1G06510	-1.38	-0.46	-4.48	0.003147	0.016952	-2.06
245776_at	hypothetical protein predicted by gens	---	AT1G30260	1.92	0.94	4.48	0.003161	0.017025	-2.06
264783_at	putative calcium-dependent protein ki	PPCK1	AT1G08650	2.09	1.07	4.48	0.003164	0.017037	-2.06
267000_at	Expressed protein ; supported by full-l	---	AT2G34310	-1.94	-0.96	-4.48	0.003177	0.017106	-2.07
264810_at	putative GPI-anchor transamidase (U3	---	AT1G08750	-1.50	-0.59	-4.48	0.003178	0.017106	-2.07
250060_at	chromo domain protein polycomb-like	TFL2	AT5G17690	1.53	0.61	4.47	0.003185	0.017137	-2.07
251257_at	ADP-ribosylation factor-like protein AD	ATARFA1E	AT3G62290	1.66	0.73	4.47	0.00319	0.017159	-2.07
250540_at	unknown protein ; supported by cDNA	---	AT5G08580	-1.65	-0.73	-4.47	0.00319	0.017159	-2.07
248085_at	putative protein similar to unknown pro	SVL1	AT5G55480	-2.10	-1.07	-4.47	0.003192	0.017162	-2.07
249090_at	Expressed protein ; supported by cDN	---	AT5G43745	-1.67	-0.74	-4.47	0.003192	0.017162	-2.07
266971_at	unknown protein	---	AT2G39580	-2.09	-1.07	-4.47	0.003195	0.017164	-2.07
261053_at	hypothetical protein predicted by gene	---	AT1G01320	1.62	0.70	4.47	0.003194	0.017164	-2.07
257297_at	unknown protein contains Pfam profile	---	AT3G28040	-2.41	-1.27	-4.47	0.003195	0.017164	-2.07
253396_at	putative protein RNA-binding protein L	AtLa1	AT4G32720	1.42	0.51	4.47	0.003197	0.01717	-2.07
260579_at	putative cytochrome c oxidase Vc subu	---	AT2G47380	1.46	0.54	4.47	0.003202	0.01719	-2.07
265273_at	unknown protein	---	AT2G28320	1.46	0.54	4.47	0.003202	0.01719	-2.07
256965_at	branched chain alpha-keto acid dehyd	DIN4	AT3G13450	2.20	1.13	4.47	0.003203	0.017192	-2.07
254432_at	reticuline oxidase -like protein reticulin	---	AT4G20830 /	3.26	1.70	4.47	0.003211	0.017231	-2.08
250987_at	putative protein crp1 protein, Zea may	---	AT5G02860	1.50	0.59	4.47	0.003214	0.01724	-2.08
245831_at	unknown protein	---	AT1G48840	-1.47	-0.55	-4.46	0.003222	0.017279	-2.08
249824_at	putative protein similar to unknown pro	---	AT5G23380	-1.41	-0.49	-4.46	0.003225	0.017292	-2.08
252377_at	putative peptide transporter peptide tr	---	AT3G47960	1.59	0.67	4.46	0.003237	0.017354	-2.09
252023_at	putative protein various predicted prot	---	AT3G52920	2.42	1.28	4.46	0.003239	0.017358	-2.09
262672_at	RNA pseudouridylate synthase, putati	---	AT1G76050	-1.43	-0.51	-4.46	0.003245	0.017388	-2.09
254805_at	pEARLI 1 ; supported by cDNA: gi_87	pEARLI 1	AT4G12480	8.84	3.14	4.46	0.00325	0.017411	-2.09
261149_s_	GSH-dependent dehydroascorbate re	DHAR1	AT1G19550 /	-1.84	-0.88	-4.45	0.003257	0.017442	-2.09
254859_at	putative protein Arabidopsis thaliana (	---	AT4G12060	-1.58	-0.66	-4.45	0.003262	0.017466	-2.09
252866_at	putative protein	---	AT4G39840	-2.68	-1.42	-4.45	0.003267	0.017476	-2.10
246253_at	myb-related protein	MYB73	AT4G37260	-1.64	-0.71	-4.45	0.003266	0.017476	-2.10
247013_at	putative protein strong similarity to unk	BT4	AT5G67480	-1.88	-0.91	-4.45	0.003268	0.017476	-2.10
262262_at	unknown protein identical to unknown	---	AT1G70780 /	1.82	0.86	4.45	0.003268	0.017476	-2.10
247651_at	histone H2A - like protein histone H2A	HTA6	AT5G59870	-4.23	-2.08	-4.45	0.003268	0.017476	-2.10
260618_at	flower development protein cycloidea	TCP3	AT1G53230	-1.53	-0.61	-4.45	0.003269	0.01748	-2.10
263412_at	putative histone H2B ;supported by fu	---	AT2G28720	1.42	0.50	4.45	0.00327	0.01748	-2.10
253020_at	hypothetical protein	---	AT4G38020	-1.60	-0.68	-4.45	0.003272	0.017481	-2.10

245216_at	Expressed protein non-consensus GG	IMPA-2	AT4G16143	-1.31	-0.39	-4.45	0.003271	0.017481	-2.10
249698_at	unknown protein	MIS12	AT5G35520	-1.66	-0.73	-4.45	0.003273	0.017482	-2.10
258877_at	putative expansin precursor similar to (	ATEXPA13	AT3G03220	-2.26	-1.18	-4.45	0.003278	0.017506	-2.10
245443_at	limonene cyclase like protein	---	AT4G16730	24.92	4.64	4.45	0.003282	0.017524	-2.10
265967_at	nodulin-like protein ; supported by cDI	---	AT2G37450	-1.64	-0.72	-4.45	0.003286	0.017537	-2.10
256328_at	6-phosphogluconate dehydrogenase,	---	AT3G02360	1.94	0.96	4.45	0.003286	0.017537	-2.10
257084_at	unknown protein	---	AT3G20620	1.75	0.81	4.45	0.003287	0.017539	-2.10
259423_at	unknown protein similar to putative MY	---	AT1G13880	-1.62	-0.70	-4.45	0.003291	0.017557	-2.10
248151_at	Lhcb3 chlorophyll a/b binding protein (	LHCB3	AT5G54270	-1.96	-0.97	-4.44	0.003293	0.01756	-2.10
256300_at	unknown protein similar to N-term half	NAP	AT1G69490	3.65	1.87	4.44	0.003298	0.017577	-2.11
258996_at	putative ribosome recycling factor simi	---	AT3G01800	1.59	0.67	4.44	0.003299	0.017577	-2.11
245219_at	viral resistance protein, putative simila	---	AT1G58807 /	1.40	0.49	4.44	0.003299	0.017577	-2.11
263459_at	ankyrin-like protein	---	AT2G31820	1.72	0.79	4.44	0.003297	0.017577	-2.11
246117_at	CAF-like protein CAF protein - Arabid	DCL4	AT5G20320	1.70	0.76	4.44	0.003304	0.017602	-2.11
265872_at	unknown protein ;supported by full-ler	atnudt17	AT2G01670	1.69	0.76	4.44	0.003309	0.017618	-2.11
257215_at	RING zinc finger protein, putative con	---	AT3G15070	-1.42	-0.50	-4.44	0.003309	0.017618	-2.11
257635_at	cytochrome P450 monooxygenase (C	CYP71B4	AT3G26280	1.54	0.62	4.44	0.003312	0.01763	-2.11
260794_at	unknown protein ; supported by cDNA:	---	AT1G06210	1.46	0.55	4.44	0.003316	0.017646	-2.11
248612_at	putative protein contains similarity to u	---	AT5G49530	1.74	0.80	4.44	0.003323	0.017683	-2.11
248517_at	St12p protein	---	AT5G50550 /	-1.42	-0.50	-4.44	0.00333	0.017716	-2.12
255579_at	putative bHLH DNA-binding protein	---	AT4G01460	-2.12	-1.08	-4.43	0.003333	0.017727	-2.12
256545_at	hypothetical protein predicted by gene	---	---	-1.44	-0.53	-4.43	0.003335	0.017731	-2.12
254011_at	putative protein transcription terminati	---	AT4G26370	-1.48	-0.56	-4.43	0.003339	0.017747	-2.12
248799_at	ethylene responsive element binding fa	ERF5	AT5G47230	6.61	2.72	4.43	0.00334	0.017748	-2.12
251744_at	putative protein CHLOROPLAST 30S	---	AT3G56010	-1.54	-0.63	-4.43	0.00334	0.017748	-2.12
260107_at	fructokinase, putative similar to fructol	---	AT1G66430	-3.85	-1.94	-4.43	0.003344	0.017766	-2.12
259412_at	DNA binding protein GT-1, putative si	---	AT1G13450	-1.42	-0.50	-4.43	0.003354	0.017811	-2.12
256514_at	oxidoreductase, putative contains Pfa	---	AT1G66130	-1.79	-0.84	-4.43	0.003355	0.017812	-2.12
253809_at	putative (1-4)-beta-mannan endohydr	---	AT4G28320	-1.63	-0.70	-4.43	0.003359	0.017825	-2.13
253543_at	hypothetical protein	---	AT4G31270	-1.41	-0.50	-4.43	0.003358	0.017825	-2.13
247275_at	beta-ureidopropionase	BETA-UP	AT5G64370	1.85	0.89	4.43	0.003361	0.017828	-2.13
255547_at	putative CHP-rich zinc finger protein si	---	AT4G01920	1.64	0.72	4.43	0.003361	0.017828	-2.13
256892_at	hypothetical protein contains similarity	---	AT3G19000	1.88	0.91	4.42	0.003371	0.01787	-2.13
266231_at	putative protein kinase	PSKR1	AT2G02220	3.21	1.68	4.42	0.003371	0.01787	-2.13
247522_at	putative protein ; supported by cDNA:	---	AT5G61340	-1.59	-0.67	-4.43	0.00337	0.01787	-2.13

249794_at	putative protein contains similarity to u	AtCXE18	AT5G23530	-1.34	-0.42	-4.42	0.003374	0.017879	-2.13
245327_at	hypothetical protein ; supported by full-	---	AT4G16850	-1.38	-0.47	-4.42	0.003375	0.017883	-2.13
260919_at	hypothetical protein predicted by gene	---	AT1G21520 /	3.75	1.91	4.42	0.003384	0.017919	-2.13
253274_at	Phosphoglycerate dehydrogenase - li	EDA9	AT4G34200	7.56	2.92	4.42	0.003385	0.017919	-2.13
AFFX-Atha	Arabidopsis thaliana /REF=U84969 /D	---	---	1.32	0.40	4.42	0.003385	0.017919	-2.13
261219_at	hypothetical protein predicted by gene	---	AT1G19980	1.50	0.59	4.42	0.003384	0.017919	-2.13
258002_at	AIG2-like protein similar to AIG2 protei	AIG2	AT3G28930	5.83	2.54	4.42	0.00339	0.017939	-2.14
266834_s_	putative protein phosphatase 2C	---	AT2G05050 /	5.83	2.54	4.42	0.00339	0.017939	-2.14
251399_at	putative protein	---	AT3G60590	-1.52	-0.60	-4.42	0.003401	0.017989	-2.14
260464_at	disease resistance protein RPM1 isolo	LOV1	AT1G10920	1.37	0.45	4.42	0.003401	0.017989	-2.14
264289_at	hypothetical protein similar to hypothet	---	AT1G61890	2.52	1.33	4.42	0.003406	0.018008	-2.14
266880_at	hypothetical protein predicted by gene	---	AT2G44770	-1.51	-0.59	-4.41	0.003421	0.018086	-2.15
249416_at	putative protein DNA DAMAGE-RESP	---	AT5G39570	-1.43	-0.52	-4.41	0.00343	0.01813	-2.15
266234_at	SKP1 interacting partner 3 (SKIP3), p	SKIP3	AT2G02350	1.47	0.56	4.41	0.003436	0.018155	-2.15
244988_s_	ribosomal protein L23	---	---	-1.53	-0.62	-4.41	0.003441	0.018177	-2.15
249523_at	cytochrome b-561 (gb|AAD45585.1) ;s	ACYB-1	AT5G38630	-1.42	-0.51	-4.40	0.003453	0.018235	-2.16
256503_at	myb-related protein similar to GI:7981	ATRL6	AT1G75250	-3.69	-1.88	-4.40	0.003454	0.018237	-2.16
246012_at	Pspzf zinc finger protein - like DNA bi	---	AT5G10650	1.70	0.77	4.40	0.003456	0.018243	-2.16
258661_at	unknown protein	---	AT3G02930	2.27	1.19	4.40	0.003461	0.018263	-2.16
265357_at	E2, ubiquitin-conjugating enzyme, put	UBC29	AT2G16740	1.65	0.72	4.40	0.003464	0.018277	-2.16
266303_at	putative receptor-like protein kinase	---	AT2G27060	-1.89	-0.92	-4.40	0.003466	0.018285	-2.16
257532_at	hypothetical protein similar to hypothet	---	AT3G04700	3.69	1.88	4.40	0.003471	0.018303	-2.16
250151_at	high affinity nitrate transporter - like pr	ATNRT2.7	AT5G14570	-1.93	-0.95	-4.40	0.003471	0.018303	-2.16
258389_at	hypothetical protein predicted by gens	SDE5	AT3G15390	1.55	0.63	4.40	0.003474	0.018313	-2.16
248307_at	selenium-binding protein-like	---	AT5G52850	1.49	0.57	4.40	0.003481	0.018348	-2.17
256281_at	myb-family transcription factor, putativ	TRFL9	AT3G12560	-1.54	-0.62	-4.40	0.003482	0.01835	-2.17
249201_at	putative protein similar to unknown pro	---	AT5G42370	1.59	0.67	4.40	0.003485	0.018359	-2.17
259871_at	nodulin-like protein similar to nodulin G	---	AT1G76800	-2.32	-1.21	-4.40	0.003491	0.018386	-2.17
245396_at	hypothetical protein ;supported by full-	---	AT4G14870	-1.82	-0.86	-4.39	0.003493	0.018392	-2.17
252474_at	putative protein several hypothetical pr	---	AT3G46620	2.73	1.45	4.39	0.003494	0.018392	-2.17
254269_at	putative serine/threonine kinase MAP	---	AT4G23050	1.52	0.61	4.39	0.003497	0.018403	-2.17
257654_at	DnaJ protein, putative contains Pfam	---	AT3G13310	3.06	1.62	4.39	0.003497	0.018403	-2.17
245311_at	ribosomal protein ; supported by full-le	---	AT4G14320	-1.72	-0.79	-4.39	0.003499	0.018404	-2.17
261427_at	protein kinase, putative similar to CRK	IBS1	AT1G18670	-1.94	-0.95	-4.39	0.0035	0.018408	-2.17
247625_at	zinc finger protein - like dof6 zinc finge	---	AT5G60200	-1.61	-0.69	-4.39	0.003504	0.018426	-2.17

256967_at	hypothetical protein predicted by gene	---	AT3G21060	-1.47	-0.56	-4.39	0.003508	0.01844	-2.17
265646_at	putative lipase	---	AT2G27360	1.46	0.55	4.39	0.00352	0.018502	-2.18
253803_at	putative protein hypothetical protein -	---	AT4G28200	1.40	0.48	4.39	0.003525	0.018523	-2.18
267523_at	unknown protein	---	AT2G30600	-1.46	-0.55	-4.39	0.003531	0.01854	-2.18
AFFX-r2-At	Arabidopsis thaliana /REF=U84969 /D	---	---	1.37	0.45	4.39	0.003531	0.01854	-2.18
250128_at	zinc finger protein 3 (gb|AAD27875.1)	ZFN3	AT5G16540	-1.72	-0.78	-4.39	0.00353	0.01854	-2.18
259351_at	putative sugar transporter similar to pu	---	AT3G05150	1.40	0.49	4.39	0.003533	0.018546	-2.18
257712_at	hypothetical protein predicted by gene	---	AT3G27420	-1.32	-0.40	-4.38	0.003534	0.018547	-2.18
245657_at	unknown protein similar to receptor-lik	---	AT1G56720	-2.55	-1.35	-4.38	0.003545	0.018595	-2.18
246906_at	Expressed protein ; supported by full-le	---	AT5G25475	1.40	0.49	4.38	0.003545	0.018595	-2.18
258516_at	myb-related protein, putative similar to	MYB108	AT3G06490	3.07	1.62	4.38	0.003546	0.018597	-2.19
265767_at	putative exonuclease contains zinc-fin	REF4	AT2G48110	1.48	0.56	4.38	0.003549	0.018612	-2.19
247495_at	putative protein predicted protein, Ara	IPK2BETA	AT5G61760	1.52	0.61	4.38	0.003554	0.018634	-2.19
261187_at	beta-1,3-glucanase precursor, putative	---	AT1G32860	-1.82	-0.86	-4.38	0.003561	0.018664	-2.19
253147_at	protein kinase - like protein serine/thre	CONNEXIN	AT4G35600	1.87	0.90	4.38	0.003568	0.018695	-2.19
263480_at	putative root iron transporter protein	ZIP7	AT2G04032	-1.49	-0.58	-4.38	0.003572	0.018706	-2.19
251136_at	mRNA capping enzyme - like protein r	---	AT5G01290	1.34	0.42	4.38	0.003571	0.018706	-2.19
253614_at	putative protein heat shock protein 10	---	AT4G30350	1.85	0.89	4.38	0.003571	0.018706	-2.19
246346_at	hypothetical protein	---	AT3G56810	-1.72	-0.79	-4.37	0.003582	0.018755	-2.20
253041_at	phosphoenolpyruvate carboxykinase (A	PCK1	AT4G37870	1.99	0.99	4.37	0.003583	0.018755	-2.20
247435_at	glutathione S-transferase-like protein	ATGSTU9	AT5G62480	7.44	2.90	4.37	0.003586	0.018763	-2.20
262722_at	sterol glucosyltransferase, putative sir	---	AT1G43620	-1.38	-0.46	-4.37	0.003588	0.018768	-2.20
260922_at	hypothetical protein predicted by gene	---	AT1G21560	-1.41	-0.49	-4.37	0.003588	0.018768	-2.20
259776_s_	eukaryotic translation initiation factor 4	---	AT1G29550 /	-1.41	-0.49	-4.37	0.003593	0.018788	-2.20
254356_at	hypothetical protein ;supported by full-	---	AT4G22190	-1.53	-0.62	-4.37	0.003599	0.018818	-2.20
265943_at	putative cytidine deaminase ;supporte	CDA1	AT2G19570	2.09	1.06	4.37	0.003608	0.018854	-2.20
264867_at	unknown protein	FH4	AT1G24150	2.30	1.20	4.37	0.003608	0.018854	-2.20
258649_at	putative transitional endoplasmic retic	CDC48	AT3G09840	1.32	0.40	4.37	0.00361	0.018858	-2.20
265254_at	unknown protein ; supported by cDNA	DRB2	AT2G28380	-1.43	-0.51	-4.37	0.00361	0.018858	-2.20
257008_at	myrosinase-associated protein, putativ	ESM1	AT3G14210	-5.06	-2.34	-4.37	0.003616	0.018875	-2.21
254954_at	hypothetical protein ;supported by full-	---	AT4G10910	-2.65	-1.41	-4.37	0.003615	0.018875	-2.21
261089_at	protein kinase APK1A identical to SP:(	APK1A	AT1G07570	-1.73	-0.79	-4.37	0.003616	0.018875	-2.21
255753_at	myb factor, putative similar to myb fac	MYB51	AT1G18570	6.94	2.80	4.36	0.00362	0.018888	-2.21
254270_at	gamma-glutamylcysteine synthetase ;	GSH1	AT4G23100	2.44	1.29	4.36	0.003621	0.018888	-2.21
252404_at	glycine--tRNA ligase precursor, chlorc	EDD1	AT3G48110	-1.40	-0.48	-4.36	0.00362	0.018888	-2.21

265573_at	putative zinc-finger protein similar to zi	---	AT2G28200	2.07	1.05	4.36	0.003627	0.018905	-2.21
245300_at	hypothetical protein ; supported by cDI	CBL6	AT4G16350	1.34	0.43	4.36	0.003626	0.018905	-2.21
244970_at	ribosomal protein L20	---	---	-1.88	-0.91	-4.36	0.003627	0.018905	-2.21
253035_at	glycosyltransferase like protein alpha-	CGL1	AT4G38240	1.37	0.45	4.36	0.003632	0.018908	-2.21
245825_at	protein kinase, putative similar to prot	ATSK42	AT1G57870	-1.42	-0.51	-4.36	0.003628	0.018908	-2.21
247664_at	APETALA2 protein - like APETALA2 p	TOE2	AT5G60120	-1.42	-0.50	-4.36	0.003631	0.018908	-2.21
258760_at	putative membrane protein similar to i	---	AT3G10780	1.93	0.95	4.36	0.003632	0.018908	-2.21
255884_at	hypothetical protein predicted by gene	---	AT1G20310	4.77	2.25	4.36	0.003631	0.018908	-2.21
248023_at	ADP/ATP translocase-like protein ;sup	---	AT5G56450	-1.44	-0.53	-4.36	0.003631	0.018908	-2.21
255856_at	unknown protein identical to unknown	---	AT1G66940	-4.26	-2.09	-4.36	0.003635	0.01891	-2.21
252374_at	response reactor 2 (ATRR2) ; support	ARR5	AT3G48100	1.84	0.88	4.36	0.003634	0.01891	-2.21
253360_at	aminopeptidase- like protein aminope	APM1	AT4G33090	1.48	0.56	4.36	0.003638	0.018923	-2.21
264761_at	hypothetical protein predicted by gene	---	AT1G61280	-1.37	-0.46	-4.36	0.00364	0.01893	-2.21
254072_at	putative protein ClpC protease - Spina	---	AT4G25370	-1.46	-0.54	-4.36	0.003641	0.018934	-2.21
254633_at	putative protein (fragment)	MRH1	AT4G18640	-1.73	-0.79	-4.36	0.003645	0.01895	-2.22
253468_at	putative protein predicted gene T10G3	---	AT4G32160	1.53	0.62	4.36	0.003648	0.018961	-2.22
266513_at	unknown protein	---	AT2G47700	-1.55	-0.64	-4.36	0.003651	0.018966	-2.22
261050_at	transcription factor MYC7E, putative s	---	AT1G01260	-1.76	-0.82	-4.36	0.00365	0.018966	-2.22
253061_at	putative protein SPOP, Homo sapiens	BT5	AT4G37610	-1.89	-0.92	-4.35	0.003677	0.019096	-2.22
249718_at	putative protein contains similarity to b	---	AT5G35740	-1.52	-0.60	-4.35	0.003683	0.019124	-2.23
265668_at	putative alanine acetyl transferase ;su	---	AT2G32020	3.49	1.80	4.35	0.003684	0.019126	-2.23
258615_at	putative aspartyl protease contains Pfa	---	AT3G02740	1.55	0.64	4.35	0.003685	0.019127	-2.23
248698_at	receptor-like protein kinase ; supported	---	AT5G48380	1.78	0.83	4.35	0.003689	0.01914	-2.23
258047_at	putative 4-coumarate:CoA ligase 2 alm	4CL2	AT3G21240	3.78	1.92	4.35	0.003693	0.019159	-2.23
253607_at	small nuclear ribonucleoprotein homo	---	AT4G30330	-1.60	-0.68	-4.35	0.003695	0.019163	-2.23
263534_at	putative steroid binding protein ;suppo	AtMAPR2	AT2G24940 /	1.47	0.56	4.35	0.003697	0.01917	-2.23
255047_at	AX110P -like protein AX110P -Daucus	---	AT4G09670	-1.41	-0.50	-4.35	0.003699	0.01917	-2.23
252226_at	putative protein transcribed gene of ur	---	AT3G49880	-1.37	-0.45	-4.35	0.003698	0.01917	-2.23
255176_s_	putative DNA-directed RNA polymeras	---	AT1G01210 /	1.40	0.48	4.35	0.003702	0.019185	-2.23
265390_at	unknown protein ; supported by full-le	---	AT2G20820	1.37	0.46	4.35	0.003704	0.019189	-2.23
257793_at	unknown protein ;supported by full-ler	---	AT3G26960	-4.09	-2.03	-4.34	0.003707	0.019199	-2.23
246155_at	putative protein predicted proteins, Ar	---	AT5G20030	-1.33	-0.41	-4.34	0.003708	0.019202	-2.23
259272_at	unknown protein similar to hypothetica	---	AT3G01290	1.52	0.61	4.34	0.00371	0.019208	-2.23
261319_at	phytochrome A supressor spa1, putat	SPA4	AT1G53090	1.29	0.37	4.34	0.00372	0.019244	-2.24
249544_at	anti-silencing factor 1-like protein S-lo	ASF1B	AT5G38110	-1.65	-0.72	-4.34	0.00372	0.019244	-2.24

254413_at	myb-related protein M4 ;supported by	ATMYB102	AT4G21440	1.77	0.83	4.34	0.003719	0.019244	-2.24
266051_at	rhodanese-like family protein	---	AT2G40760	-1.64	-0.71	-4.34	0.003721	0.019244	-2.24
254705_at	putative protein ; supported by cDNA:	---	AT4G17870	-1.74	-0.80	-4.34	0.003721	0.019244	-2.24
248636_at	putative protein similar to unknown pro	---	---	-1.43	-0.51	-4.34	0.003725	0.019256	-2.24
253425_at	putative protein myosin heavy chain-E	---	AT4G32190	-1.81	-0.85	-4.34	0.003726	0.019261	-2.24
248794_at	ethylene responsive element binding fa	ERF2	AT5G47220	5.37	2.42	4.34	0.003731	0.019278	-2.24
251109_at	ferritin 1 precursor ;supported by full-l	FER1	AT5G01600	2.10	1.07	4.34	0.003734	0.01929	-2.24
259660_at	unknown protein ; supported by full-ler	---	AT1G55260	-3.62	-1.85	-4.34	0.003736	0.0193	-2.24
263117_at	putative lipoamide dehydrogenase co	---	AT1G03040	1.33	0.41	4.34	0.003739	0.019307	-2.24
248021_at	RuBisCO subunit binding-protein beta	---	AT5G56500	1.92	0.94	4.34	0.003742	0.019321	-2.24
258009_at	unknown protein	---	AT3G19440	1.31	0.39	4.34	0.003745	0.019332	-2.24
266087_at	putative alcohol dehydrogenase	---	AT2G37790	-1.53	-0.61	-4.33	0.003748	0.019344	-2.25
258721_at	unknown protein similar to hypothetica	---	AT3G09560	1.68	0.75	4.33	0.003751	0.019355	-2.25
247302_at	unknown protein ;supported by full-ler	VPS20.1	AT5G63880	1.39	0.48	4.33	0.00376	0.019394	-2.25
259489_at	unknown protein	---	AT1G15790	1.88	0.91	4.33	0.003764	0.019405	-2.25
244965_at	hypothetical protein	---	---	-1.66	-0.73	-4.33	0.003763	0.019405	-2.25
263305_at	unknown protein ;supported by full-ler	BPC1	AT2G01930	-1.64	-0.71	-4.33	0.003771	0.019436	-2.25
266349_at	unknown protein predicted by genscan	---	AT2G01460	1.43	0.52	4.33	0.003774	0.019451	-2.25
249930_at	synaptobrevin-like protein	ATVAMP714	AT5G22360	-1.39	-0.47	-4.33	0.003778	0.019468	-2.25
259818_at	unknown protein ; supported by cDNA:	---	AT1G49890	-1.64	-0.71	-4.33	0.003781	0.019476	-2.26
257644_at	unknown protein ;supported by full-ler	AOC3	AT3G25780	4.01	2.00	4.33	0.003785	0.019496	-2.26
261482_at	unknown protein ;supported by full-len	THH1	AT1G14530	1.43	0.52	4.33	0.003787	0.019496	-2.26
246781_at	sugar transporter-like protein putative	SFP1	AT5G27350	2.16	1.11	4.33	0.003787	0.019496	-2.26
263126_at	hypothetical protein predicted by gene	---	AT1G78460	3.20	1.68	4.32	0.003794	0.019515	-2.26
260712_at	protein phosphatase 2C, putative simi	HAB2	AT1G17550	1.61	0.68	4.33	0.003793	0.019515	-2.26
248429_at	putative protein contains similarity to p	---	AT5G51770	2.06	1.04	4.33	0.003793	0.019515	-2.26
265959_at	unknown protein ;supported by full-ler	---	AT2G37240	-2.11	-1.08	-4.32	0.003795	0.019515	-2.26
248527_at	putative protein contains similarity to A	---	AT5G50740	-1.44	-0.52	-4.32	0.003795	0.019515	-2.26
252037_at	putative calmodulin calmodulin - Tetra	CAM9	AT3G51920	1.74	0.80	4.32	0.003798	0.019523	-2.26
259610_at	bZIP protein, putative similar to GI:60	---	AT1G52320	1.35	0.43	4.32	0.003808	0.01957	-2.26
260547_at	putative trypsin inhibitor ;supported by	---	AT2G43550	-3.39	-1.76	-4.32	0.003811	0.019583	-2.26
252948_at	putative protein NLS receptor - Oryza	KAK	AT4G38600	1.45	0.54	4.32	0.003813	0.01959	-2.26
253301_at	pathogenesis-related protein 1 precur	---	AT4G33720	2.76	1.47	4.32	0.003819	0.019615	-2.27
245940_at	putative protein predicted proteins - dif	---	AT5G19630	-1.50	-0.59	-4.32	0.003831	0.019671	-2.27
257054_at	Expressed protein ; supported by full-l	MT3	AT3G15353	1.31	0.39	4.32	0.003833	0.019678	-2.27

249216_at	serine carboxypeptidase II-like ; suppo	scpl42	AT5G42240	-1.99	-0.99	-4.32	0.003834	0.019678	-2.27
260034_at	putative DNA-binding protein Pfam HM	---	AT1G68810	-2.69	-1.43	-4.32	0.003836	0.019678	-2.27
255793_at	Expressed protein ; supported by cDN	---	AT2G33250	-1.53	-0.61	-4.32	0.003835	0.019678	-2.27
253193_at	putative protein SEC7 protein, Saccha	---	AT4G35380	1.63	0.71	4.32	0.003836	0.019678	-2.27
256442_at	hypothetical protein predicted by gene	---	AT3G10930	5.73	2.52	4.31	0.00384	0.019694	-2.27
258412_at	unknown protein similar to pop3 peptid	HS1	AT3G17210	-1.44	-0.53	-4.31	0.003843	0.019705	-2.27
260221_at	GAST1-like protein similar to GAST1	---	AT1G74670	-5.44	-2.44	-4.31	0.003849	0.019729	-2.27
257883_at	calmodulin-binding protein, putative c	---	AT3G16940	1.57	0.65	4.31	0.003851	0.019737	-2.28
254286_at	putative MADS Box / AGL protein MA	AGL19	AT4G22950	1.83	0.87	4.31	0.003858	0.019765	-2.28
249993_at	GTP-binding protein obg -like GTP-bi	---	AT5G18570	-1.31	-0.39	-4.31	0.003863	0.019783	-2.28
267520_at	putative integral membrane protein	---	AT2G30460	-1.78	-0.84	-4.31	0.003863	0.019783	-2.28
260339_at	putative serine/threonine kinase simila	SIK1	AT1G69220	-1.63	-0.71	-4.31	0.003866	0.019794	-2.28
263100_at	hypothetical protein predicted by gens	AtPOT1a	AT2G05210	-1.61	-0.68	-4.31	0.003871	0.019812	-2.28
263374_at	putative heat shock protein ;supporte	---	AT2G20560	2.03	1.02	4.31	0.003871	0.019812	-2.28
255724_at	hypothetical protein	BRCA2(IV)	AT4G00020	-1.36	-0.45	-4.31	0.003872	0.019814	-2.28
266338_at	putative ligand-gated ion channel subu	GLR5	AT2G32400	1.54	0.62	4.31	0.003874	0.019814	-2.28
258550_at	putative mudrA protein similar to mudr	---	---	1.47	0.55	4.31	0.003873	0.019814	-2.28
252225_at	ADP-RIBOSYLATION FACTOR -like	ATARLA1C	AT3G49870	-1.37	-0.45	-4.31	0.003884	0.019859	-2.28
251072_at	putative protein wound-inducible prote	---	AT5G01740	-2.05	-1.03	-4.30	0.003886	0.019865	-2.28
251097_at	receptor like protein kinase receptor li	LECRKA4.3	AT5G01560	3.87	1.95	4.30	0.003887	0.019865	-2.29
245899_at	putative protein	ALF4	AT5G11030	1.42	0.50	4.30	0.003893	0.019894	-2.29
260012_at	Expressed protein ; supported by cDN	---	AT1G67865	1.94	0.95	4.30	0.003897	0.019907	-2.29
260904_at	unknown protein	NIMIN1	AT1G02450	3.46	1.79	4.30	0.0039	0.01992	-2.29
261899_at	cinnamoyl CoA reductase, putative sir	CCR2	AT1G80820	7.18	2.84	4.30	0.003907	0.019949	-2.29
245250_at	ethylene responsive element binding fa	ATERF6	AT4G17490	6.96	2.80	4.30	0.00391	0.019956	-2.29
263674_at	hypothetical protein predicted by gene	---	AT2G04790	-1.45	-0.54	-4.30	0.003909	0.019956	-2.29
258082_at	Expressed protein ; supported by full-l	CLE27	AT3G25905	-1.95	-0.96	-4.30	0.003919	0.019996	-2.29
255010_at	lipase-like protein monoglyceride lipas	---	AT4G10050	1.37	0.45	4.30	0.003923	0.020012	-2.30
267382_at	unknown protein	---	AT2G44300	1.73	0.79	4.30	0.003924	0.020016	-2.30
254291_at	putative protein UDP-galactose transp	UTR2	AT4G23010	1.71	0.78	4.30	0.003928	0.020029	-2.30
266416_at	unknown protein ; supported by full-le	---	AT2G38710	1.64	0.71	4.30	0.00393	0.020036	-2.30
249421_at	DegP protease contains similarity to D	DEG8	AT5G39830	-1.46	-0.55	-4.29	0.003934	0.020052	-2.30
251169_at	putative protein putative protein At2g2	MARD1	AT3G63210	2.17	1.12	4.29	0.00394	0.020078	-2.30
248217_at	cytochrome b5 (dbj|BAA74839.1) ;sup	CB5-E	AT5G53560	1.51	0.60	4.29	0.003944	0.020091	-2.30
260511_at	anthranilate phosphoribosyltransferas	---	AT1G51570	-1.62	-0.70	-4.29	0.003944	0.020091	-2.30

245156_at	calcium-dependent protein kinase-like	CPK7	AT5G12480	1.42	0.51	4.29	0.003947	0.020099	-2.30
261138_at	hypothetical protein contains Pfam pro	---	AT1G19710	-1.45	-0.54	-4.29	0.003949	0.020108	-2.30
250336_at	alpha-glucosidase 1 ; supported by cD	---	AT5G11720	-1.51	-0.59	-4.29	0.003952	0.020118	-2.30
257238_at	unknown protein ; supported by cDNA	---	AT3G17430	-1.61	-0.68	-4.29	0.003959	0.020148	-2.31
248423_at	putative protein contains similarity to u	---	AT5G51670	-1.71	-0.78	-4.29	0.003963	0.020163	-2.31
264415_at	AP2 domain containing protein, putati	RAP2.6	AT1G43160	-1.54	-0.62	-4.29	0.003965	0.020172	-2.31
259757_at	putative thioredoxin similar to protein d	ATPDIL1-2	AT1G77510	3.08	1.62	4.29	0.003967	0.020176	-2.31
247974_at	putative protein contains similarity to tr	---	AT5G56780	-1.36	-0.45	-4.29	0.003968	0.020176	-2.31
254329_at	putative protein oxysterol-binding prot	ORP2A	AT4G22540	-1.45	-0.53	-4.29	0.003972	0.020186	-2.31
253700_at	threonine synthase	MTO2	AT4G29840	1.69	0.75	4.29	0.003971	0.020186	-2.31
254087_at	brefeldin A-sensitive Golgi protein - lik	---	AT4G24840	-1.33	-0.41	-4.28	0.003984	0.020238	-2.31
254613_at	ankyrin-like protein ankyrin 3, Mus mu	---	AT4G19150	-1.43	-0.51	-4.28	0.003986	0.020238	-2.31
257751_at	hypothetical protein predicted by gene	MKS1	AT3G18690	3.26	1.70	4.28	0.003985	0.020238	-2.31
249312_at	disease resistance protein-like	---	AT5G41550	1.55	0.64	4.28	0.003985	0.020238	-2.31
251376_at	scarecrow - like protein scarecrow-like	---	AT3G60630	-1.73	-0.79	-4.28	0.003997	0.020276	-2.32
248458_at	putative protein contains similarity to u	EYE	AT5G51430	-1.38	-0.46	-4.28	0.003997	0.020276	-2.32
247198_at	unknown protein	---	AT5G65290	1.37	0.45	4.28	0.003996	0.020276	-2.32
265628_at	hypothetical protein predicted by gene	---	AT2G27290	-1.80	-0.84	-4.28	0.003997	0.020276	-2.32
261241_at	subtilisin-like serine protease contains	---	AT1G32950	1.38	0.46	4.28	0.003997	0.020276	-2.32
246270_at	putative protein	---	AT4G36500	3.42	1.77	4.28	0.004003	0.020293	-2.32
251052_at	DP-2 transcription factor - like transcri	DPA	AT5G02470	-1.45	-0.54	-4.28	0.004002	0.020293	-2.32
249872_at	unknown protein	---	AT5G23130	-2.81	-1.49	-4.28	0.004004	0.020297	-2.32
251956_at	RNA-binding protein cp29 protein ;sup	CP29	AT3G53460	-1.40	-0.49	-4.28	0.00401	0.020321	-2.32
262525_at	putative cytochrome P450 41% identic	CYP72C1	AT1G17060	-1.81	-0.86	-4.28	0.00402	0.020369	-2.32
262225_at	pectinesterase, putative similar to pec	ATPME1	AT1G53840	-2.08	-1.06	-4.28	0.004025	0.020384	-2.32
265189_at	unknown protein ; supported by cDNA	---	AT1G23840	2.09	1.06	4.27	0.004027	0.020384	-2.32
251561_at	E2 ubiquitin-conjugating-like enzyme A	SCE1	AT3G57870	-1.35	-0.43	-4.27	0.004027	0.020384	-2.32
264838_at	putative AHP2 similar to GB:BAA3633	AHP5	AT1G03430	-1.30	-0.37	-4.28	0.004026	0.020384	-2.32
264063_at	unknown protein	---	AT2G27900	-1.39	-0.47	-4.27	0.004028	0.020385	-2.32
261629_at	unknown protein	---	AT1G49980	-1.36	-0.44	-4.27	0.00403	0.020389	-2.32
261815_at	leucine zipper protein, putative similar	---	AT1G08320	1.55	0.63	4.27	0.004032	0.020397	-2.33
255380_at	putative calcium channel ; supported b	ATTPC1	AT4G03560	-1.62	-0.70	-4.27	0.004034	0.020401	-2.33
263714_at	putative tyrosine aminotransferase ; s	SUR1	AT2G20610	1.93	0.95	4.27	0.004035	0.020401	-2.33
248818_at	Lon protease homolog 1 precursor ide	LON2	AT5G47040	-1.57	-0.65	-4.27	0.004038	0.020414	-2.33
247314_at	3(2),5-bisphosphate nucleotidase (em	SAL2	AT5G64000	2.52	1.33	4.27	0.00404	0.02042	-2.33

245810_at	axi 1 protein, putative similar to axi 1 p	---	AT1G38065 /	-1.44	-0.53	-4.27	0.004042	0.020427	-2.33
254970_at	chlorophyll a/b-binding protein - like cl	LHCB5	AT4G10340	-1.38	-0.47	-4.27	0.004046	0.020443	-2.33
265062_at	receptor kinase, putative similar to rec	---	AT1G61550	1.81	0.85	4.27	0.004051	0.020462	-2.33
255615_at	hypothetical protein	---	AT4G01290	1.29	0.37	4.27	0.004059	0.020496	-2.33
247834_at	cinnamoyl-CoA reductase - like protei	---	AT5G58490	1.35	0.43	4.27	0.004068	0.020538	-2.33
256256_at	unknown protein ; supported by full-ler	---	AT3G11230	1.42	0.50	4.26	0.004077	0.02058	-2.34
248186_at	unknown protein ;supported by full-ler	---	AT5G53880	-3.88	-1.95	-4.26	0.004084	0.020607	-2.34
247910_at	putative protein similar to unknown pro	---	AT5G57410	-1.55	-0.63	-4.26	0.004086	0.020617	-2.34
262939_s_	glyceraldehyde-3-phosphate dehydrog	GAPCP-2	AT1G16300 /	4.04	2.02	4.26	0.004092	0.02064	-2.34
266005_at	unknown protein	RSZ33	AT2G37340	1.57	0.65	4.26	0.004097	0.02066	-2.34
259812_at	unknown protein	---	AT1G49840	-1.67	-0.74	-4.26	0.004098	0.020663	-2.34
265283_at	unknown protein predicted by genefinc	MUR3	AT2G20370	-1.67	-0.74	-4.26	0.0041	0.020667	-2.34
253597_at	putative protein translation initiation fa	---	AT4G30690	-1.85	-0.89	-4.26	0.004103	0.020678	-2.34
266983_at	putative phospholipase ; supported by	---	AT2G39400	1.70	0.77	4.26	0.004109	0.020703	-2.35
266228_at	unknown protein ; supported by full-le	CXIP4	AT2G28910	1.50	0.58	4.26	0.00411	0.020703	-2.35
260635_at	unknown protein	---	AT1G62420 /	1.55	0.63	4.26	0.004117	0.020733	-2.35
261858_at	Expressed protein ; supported by full-le	---	AT1G50570	1.34	0.43	4.25	0.00413	0.020796	-2.35
246882_at	putative protein predicted proteins, Ho	---	AT5G26180	1.34	0.42	4.25	0.004135	0.020818	-2.35
264262_at	Expressed protein ; supported by full-le	---	AT1G09200	-4.47	-2.16	-4.25	0.004137	0.020824	-2.35
254560_at	kinase-like protein protein kinase rck,	---	AT4G19110 /	1.32	0.40	4.25	0.004143	0.020848	-2.35
248197_at	NADPH:protochlorophyllide oxidoredu	PORA	AT5G54190	-1.39	-0.48	-4.25	0.004145	0.020849	-2.36
258117_at	hypothetical protein predicted by gens	---	AT3G14700	1.38	0.46	4.25	0.004145	0.020849	-2.36
263632_at	Expressed protein ; supported by cDN	---	AT2G04795	-2.50	-1.32	-4.25	0.004148	0.020861	-2.36
262246_at	leaf development protein Argonaute id	AGO1	AT1G48410	-1.46	-0.54	-4.25	0.004154	0.020884	-2.36
266059_at	predicted protein ;supported by cDNA:	---	AT2G40765	1.97	0.98	4.25	0.004169	0.020957	-2.36
263929_at	hypothetical protein predicted by gene	URH1	AT2G36310	-1.46	-0.55	-4.24	0.004175	0.020977	-2.36
257602_at	hydrolase, putative similar to Metal De	---	AT3G13800	-1.39	-0.48	-4.24	0.004175	0.020977	-2.36
264960_at	hypothetical protein contains similarity	ATEXT4	AT1G76930	5.16	2.37	4.24	0.004178	0.020986	-2.36
247859_at	unknown protein	---	AT5G58410	1.30	0.38	4.24	0.00418	0.020991	-2.36
259531_at	hypothetical protein	---	AT1G12460	-1.67	-0.74	-4.24	0.004184	0.021008	-2.37
251805_at	putative protein RING-H2 finger protei	SDIR1	AT3G55530	1.36	0.45	4.24	0.004185	0.02101	-2.37
261222_at	anter-specific proline-rich protein APG	---	AT1G20120	1.36	0.45	4.24	0.004188	0.021018	-2.37
258183_at	unknown protein ;supported by full-ler	---	AT3G21550	-3.08	-1.62	-4.24	0.00419	0.021026	-2.37
265663_at	unknown protein predicted by genscan	---	AT2G24290	-1.47	-0.55	-4.24	0.004192	0.02103	-2.37
261522_at	RIBOSOMAL PROTEIN, putative simi	---	AT1G71710	-1.99	-0.99	-4.24	0.004197	0.021049	-2.37

254804_at	putative protein putative oxidoreducta	---	AT4G13010	-1.47	-0.55	-4.24	0.004203	0.021074	-2.37
264362_at	unknown protein ESTs gb|H36966, gb	---	AT1G03290	1.66	0.73	4.24	0.004204	0.021074	-2.37
267610_at	K+ transporter, AKT1 identical to GB:	AKT1	AT2G26650	2.45	1.30	4.24	0.00421	0.021094	-2.37
245864_at	hypothetical protein predicted by gene	---	AT1G58070	-1.79	-0.84	-4.24	0.004209	0.021094	-2.37
263127_at	hypothetical protein predicted by gene	MSL6	AT1G78610	-1.48	-0.57	-4.24	0.004213	0.021099	-2.37
261712_at	alcohol dehydrogenase, putative simil	---	AT1G32780	-1.44	-0.53	-4.24	0.004212	0.021099	-2.37
261479_at	unknown protein ;supported by full-len	IQD28	AT1G14380	-1.68	-0.75	-4.24	0.004213	0.021099	-2.37
261238_at	hypothetical protein predicted by gene	---	AT1G32810	1.42	0.50	4.24	0.00422	0.021115	-2.37
259396_at	shaggy-like kinase, putative similar to	GSK1	AT1G06390	-1.34	-0.42	-4.24	0.00422	0.021115	-2.37
259747_at	putative dehydrogenase similar to D-th	---	AT1G71170	1.47	0.56	4.24	0.004218	0.021115	-2.37
248401_at	putative protein similar to unknown pro	HCF208	AT5G52110	-1.93	-0.95	-4.24	0.00422	0.021115	-2.37
259856_at	unknown protein ;supported by full-ler	---	AT1G68440	2.27	1.19	4.23	0.004226	0.021137	-2.38
249834_at	putative protein contains similarity to fe	FTRA1	AT5G23440	-1.58	-0.66	-4.23	0.004227	0.021139	-2.38
245556_at	HSR201 like protein	---	AT4G15400	1.32	0.40	4.23	0.004235	0.021177	-2.38
259093_at	unknown protein similar to putative pro	---	AT3G04860	-1.95	-0.96	-4.23	0.004236	0.021177	-2.38
248109_at	DNA topoisomerase I	TOP1BETA	AT5G55310	1.39	0.47	4.23	0.004246	0.021222	-2.38
258249_s_	unknown protein ; supported by full-le	---	AT3G15820 /	-1.65	-0.73	-4.23	0.004248	0.021223	-2.38
250502_at	heat shock protein 70 (Hsc70-5) ; sup	MTHSC70-2	AT5G09590	2.12	1.08	4.23	0.004248	0.021223	-2.38
262211_at	AP2 domain containing protein, putati	ORA47	AT1G74930	3.54	1.82	4.23	0.00425	0.021226	-2.38
248238_at	putative protein similar to unknown pro	---	AT5G53900	-1.61	-0.69	-4.23	0.004255	0.021245	-2.38
259852_at	disulfide bond formation protein, putat	AERO1	AT1G72280	2.13	1.09	4.23	0.004261	0.021268	-2.39
260199_at	unknown protein similar to putative DN	---	AT1G67590	-1.35	-0.43	-4.23	0.004261	0.021268	-2.39
248399_at	putative protein strong similarity to unk	---	AT5G52010	-1.37	-0.45	-4.23	0.004264	0.021274	-2.39
261579_at	soluble inorganic pyrophosphatase, p	AtPPa1	AT1G01050	-1.33	-0.41	-4.23	0.004264	0.021274	-2.39
250493_at	putative protein various predicted prot	---	AT5G09800	8.82	3.14	4.23	0.00427	0.021299	-2.39
262219_at	hypothetical protein predicted by gene	---	AT1G74750	1.72	0.78	4.22	0.004277	0.021328	-2.39
256413_at	hypothetical protein predicted by gene	---	AT3G11100	1.42	0.51	4.22	0.004279	0.021334	-2.39
260590_at	phosphoenolpyruvate carboxylase 1,	ATPPC1	AT1G53310	1.55	0.63	4.22	0.004286	0.021366	-2.39
265000_at	hypothetical protein predicted by gene	---	AT1G67410	-1.43	-0.52	-4.22	0.004287	0.021366	-2.39
253627_at	low temperature and salt responsive p	---	AT4G30650	-7.13	-2.83	-4.22	0.004289	0.02137	-2.39
262149_at	hypothetical protein predicted by gene	---	AT1G52530	-1.56	-0.64	-4.22	0.00429	0.02137	-2.39
245868_at	hypothetical protein	CAT2	AT1G58030	1.50	0.58	4.22	0.004302	0.021426	-2.40
253975_at	putative protein proliferating-cell nucle	---	AT4G26600	2.19	1.13	4.22	0.004303	0.021427	-2.40
251727_at	putative protein	---	AT3G56290	-2.14	-1.10	-4.22	0.004306	0.021438	-2.40
256511_at	RNA helicase, putative similar to GI:1	---	AT1G33390	1.36	0.45	4.22	0.004308	0.021442	-2.40

261476_at	hypothetical protein contains similarity	---	AT1G14480	2.11	1.08	4.22	0.004313	0.021463	-2.40
266101_at	unknown protein ; supported by cDNA	---	AT2G37940	2.61	1.38	4.22	0.004317	0.021473	-2.40
249799_at	serine palmitoyltransferase ; supporte	LCB2	AT5G23670	-1.32	-0.40	-4.22	0.004317	0.021473	-2.40
264373_at	putative vesicle transport protein Conta	SEC22	AT1G11890	-1.57	-0.65	-4.22	0.004325	0.021504	-2.40
249452_at	Sec7/gnom -like protein GNOM, Arabi	---	AT5G39500	-1.38	-0.47	-4.22	0.004325	0.021504	-2.40
260634_at	initiation factor isozyme 4F p82 subun	---	AT1G62410	-1.41	-0.50	-4.21	0.004342	0.021582	-2.41
253271_s_	SKP1/ASK1 (At11), putative similar to	ASK12	AT4G34210 /	1.51	0.60	4.21	0.004343	0.021582	-2.41
267196_at	FtsH protease (VAR2) identical to zinc	VAR2	AT2G30950	-1.40	-0.49	-4.21	0.004344	0.021583	-2.41
260087_at	hypothetical protein predicted by gens	---	AT1G73200	-1.58	-0.66	-4.21	0.004346	0.021587	-2.41
251881_at	DIPHOSPHOMEVALONATE DECAR	---	AT3G54250	-1.93	-0.95	-4.21	0.004349	0.02159	-2.41
265043_at	Expressed protein ; supported by cDN	ATNAP4	AT1G03900	1.43	0.52	4.21	0.00435	0.02159	-2.41
255301_at	putative protein similar to transcription	ATMSRB3	AT4G04800	1.87	0.90	4.21	0.00435	0.02159	-2.41
256306_at	lipase, putative contains Pfam profile:	---	AT1G30370	11.02	3.46	4.21	0.004348	0.02159	-2.41
259248_at	putative heat-shock protein similar to h	---	AT3G07770	2.12	1.08	4.21	0.004359	0.021629	-2.41
255742_at	DNA-binding protein RAV2, putative s	TEM1	AT1G25560	-1.36	-0.45	-4.21	0.004364	0.021641	-2.41
249506_at	putative protein	---	AT5G38880	-1.46	-0.54	-4.21	0.004364	0.021641	-2.41
246772_at	putative protein unknown protein T12H	---	AT5G27490	-1.90	-0.93	-4.21	0.004364	0.021641	-2.41
247735_at	thymidylate kinase - like protein thymi	ZEU1	AT5G59440	1.99	0.99	4.21	0.004371	0.02167	-2.41
247222_at	ABC transporter protein 1-like ; suppo	ATGCN5	AT5G64840	-1.75	-0.81	-4.21	0.004372	0.02167	-2.41
265512_at	hypothetical protein predicted by gens	---	AT2G05590	-1.53	-0.62	-4.21	0.004375	0.021678	-2.41
252484_at	glucuronosyl transferase-like protein g	---	AT3G46690	1.50	0.59	4.21	0.004377	0.021684	-2.41
246864_at	cytochrome P450 GA3 ; supported by	GA3	AT5G25900	-1.91	-0.93	-4.20	0.004383	0.021711	-2.42
262911_s_	heat shock protein, putative similar to	---	AT1G07400 /	3.10	1.63	4.20	0.004384	0.021712	-2.42
266353_at	unknown protein ;supported by full-ler	MLP328	AT2G01520	1.78	0.83	4.20	0.004386	0.021716	-2.42
251925_at	hypothetical protein ;supported by full-	---	AT3G54000	1.71	0.78	4.20	0.004387	0.021717	-2.42
256161_at	unknown protein ; supported by cDNA	---	AT1G30090	1.41	0.50	4.20	0.004391	0.021729	-2.42
255546_at	putative CHP-rich zinc finger protein si	---	AT4G01910	2.23	1.16	4.20	0.004393	0.021737	-2.42
253731_at	acid phosphatase-like protein acid ph	---	AT4G29260	-1.33	-0.41	-4.20	0.004403	0.021783	-2.42
262476_at	phosphoprotein phosphatase identical	---	AT1G50370	1.37	0.45	4.20	0.004411	0.021817	-2.42
266815_at	F-box protein family, AtFBX5 contains	---	AT2G44900	-1.47	-0.56	-4.20	0.004415	0.021833	-2.42
247150_at	putative protein similar to unknown pro	---	AT5G65650	-1.51	-0.59	-4.20	0.004427	0.021884	-2.43
265634_at	hypothetical protein predicted by gens	---	AT2G25530	1.41	0.50	4.20	0.004431	0.021899	-2.43
265804_at	putative peptide methionine sulfoxide r	---	AT2G18030	-1.32	-0.40	-4.19	0.004436	0.02192	-2.43
247355_at	unknown protein ; supported by full-le	SPT42	AT5G63670	1.36	0.45	4.19	0.004439	0.021928	-2.43
266581_at	putative desiccation related protein ; s	---	AT2G46140	4.77	2.25	4.19	0.00444	0.02193	-2.43

250080_at	translocon Tic40-like protein ; support	TIC40	AT5G16620	-1.32	-0.40	-4.19	0.004452	0.021981	-2.43
248446_at	putative protein similar to unknown pro	---	AT5G51140	-1.37	-0.46	-4.19	0.004452	0.021981	-2.43
248382_at	peroxidase	---	AT5G51890	-3.38	-1.76	-4.19	0.004468	0.022055	-2.44
252313_at	RNA-binding - like protein RNA-bindin	CID10	AT3G49390	1.81	0.86	4.19	0.004475	0.022086	-2.44
260049_at	DNA-directed RNA polymerase subun	NRPA2	AT1G29940	1.92	0.94	4.19	0.00448	0.022091	-2.44
257986_at	Expressed protein ; supported by full-l	AGP40	AT3G20865	-1.69	-0.76	-4.19	0.004478	0.022091	-2.44
250343_at	putative protein density regulated prot	---	AT5G11900	1.38	0.47	4.19	0.004479	0.022091	-2.44
261379_at	unknown protein similar to YGL010w-li	---	AT1G18720	1.34	0.42	4.19	0.004479	0.022091	-2.44
257619_at	unknown protein	ICK3	AT3G24810	1.47	0.55	4.19	0.004484	0.022101	-2.44
261308_at	protein kinase, putative contains simil	RKL1	AT1G48480	-3.89	-1.96	-4.19	0.004484	0.022101	-2.44
245336_at	Expressed protein ; supported by full-l	---	AT4G16515	-4.18	-2.06	-4.18	0.004494	0.022134	-2.44
252084_at	wax synthase-like protein wax synthas	AtSAT1	AT3G51970	1.52	0.60	4.18	0.004492	0.022134	-2.44
246528_at	putative mitochondrial carrier protein I	---	AT5G15640	1.79	0.84	4.18	0.004493	0.022134	-2.44
255628_at	coded for by A. thaliana cDNA T45454	GIF3	AT4G00850	-1.40	-0.49	-4.18	0.0045	0.022159	-2.44
262884_at	membrane related protein CP5, putati	CP5	AT1G64720	-1.39	-0.48	-4.18	0.004513	0.022219	-2.45
252996_s_	geranylgeranyl pyrophosphate synthas	GGR	AT4G38460	1.46	0.54	4.18	0.004516	0.022229	-2.45
255088_at	putative protein heat shock protein dn	---	AT4G09350	-1.75	-0.81	-4.18	0.004524	0.022261	-2.45
265103_at	UDP-N-acetylglucosamine pyrophosp	---	AT1G31070	-1.52	-0.60	-4.18	0.004525	0.022262	-2.45
249736_at	unknown protein	---	AT5G24460	-1.30	-0.38	-4.18	0.004529	0.022279	-2.45
259110_at	unknown protein	---	AT3G05570	1.60	0.68	4.18	0.004536	0.022306	-2.45
246034_at	putative protein FH protein interacting	---	AT5G08350	-1.77	-0.83	-4.18	0.004541	0.022328	-2.45
262589_s_	hypothetical protein Strong similarity to	---	AT1G15150 /	-1.37	-0.46	-4.17	0.004551	0.022371	-2.46
258287_at	putative sulfate transporter similar to s	SULTR3;4	AT3G15990	2.46	1.30	4.17	0.004552	0.022371	-2.46
261322_at	hypothetical protein predicted by gene	ATPUP11	AT1G44750	1.44	0.53	4.17	0.004554	0.022375	-2.46
255309_at	hypothetical protein	SFR6	AT4G04920	1.32	0.41	4.17	0.004556	0.02238	-2.46
248744_at	putative protein contains similarity to C	---	AT5G48250	1.59	0.67	4.17	0.004559	0.022393	-2.46
263379_at	putative CCCH-type zinc finger protein	CZF1	AT2G40140	3.97	1.99	4.17	0.004566	0.022422	-2.46
252315_at	putative protein PrMC3 - Pinus radiata	CXE12	AT3G48690	1.51	0.59	4.17	0.004576	0.022467	-2.46
252487_at	glucosyltransferase-like protein UDP-g	UGT76E12	AT3G46660	4.56	2.19	4.17	0.004586	0.022509	-2.47
246553_at	putative protein hypothetical protein T	EDL1	AT5G15440	-1.43	-0.52	-4.17	0.004591	0.022527	-2.47
249633_at	sucrose synthase-like protein sucrose	SUS5	AT5G37180	-1.35	-0.44	-4.17	0.00459	0.022527	-2.47
254004_at	arginyl-tRNA synthetase	emb1027	AT4G26300	-1.29	-0.36	-4.17	0.004593	0.022529	-2.47
257907_at	hemolysin, putative similar to hemolys	---	AT3G25470	-1.29	-0.37	-4.17	0.004594	0.022529	-2.47
250485_at	Expressed protein ; supported by full-l	PROPEP5	AT5G09990	1.82	0.86	4.16	0.004605	0.02258	-2.47
258059_at	NAM-like protein (No Apical Meristem	ATNAC3	AT3G29035	1.70	0.77	4.16	0.004614	0.022621	-2.47

255959_at	phosphatidylinositol-4-phosphate 5-ki	ATPIP5K1	AT1G21980	-3.26	-1.71	-4.16	0.004618	0.022627	-2.47
262434_at	lysine and histidine specific transporte	---	AT1G47670	-1.89	-0.92	-4.16	0.004617	0.022627	-2.47
265501_at	putative glucosyltransferase	UGT73B4	AT2G15490	2.60	1.38	4.16	0.004619	0.022628	-2.47
267375_at	G protein alpha subunit 1 (GPA1) iden	GP ALPHA 1	AT2G26300	1.46	0.55	4.16	0.004622	0.022638	-2.47
263935_at	unknown protein	PUB23	AT2G35930	7.74	2.95	4.16	0.00463	0.022672	-2.48
267036_at	Expressed protein ; supported by full-l	---	AT2G38465	1.83	0.87	4.16	0.004639	0.022702	-2.48
263171_at	unknown protein	CCX4	AT1G54115	1.41	0.50	4.16	0.004638	0.022702	-2.48
251324_at	plasma membrane intrinsic protein 1a	PIP1A	AT3G61430	-1.49	-0.58	-4.16	0.004639	0.022702	-2.48
249217_at	ubiquitin-like protein ; supported by c	UBL5	AT5G42300	1.30	0.37	4.16	0.004644	0.022722	-2.48
247258_at	expressed protein similar to unknown	---	AT5G64816	-1.47	-0.55	-4.16	0.004649	0.022735	-2.48
262473_at	chloroplast FtsH protease almost iden	FTSH1	AT1G50250	-1.54	-0.62	-4.16	0.004648	0.022735	-2.48
247760_at	subtilisin-like serine protease contains	---	AT5G59130	-3.90	-1.96	-4.15	0.004671	0.022834	-2.49
263973_at	60S ribosomal protein L11B	RPL16A	AT2G42740	-1.79	-0.84	-4.15	0.00467	0.022834	-2.48
258470_at	Expressed protein ; supported by full-l	---	AT3G06035	-5.20	-2.38	-4.15	0.004674	0.022842	-2.49
249841_at	unknown protein	---	AT5G23520	1.39	0.48	4.15	0.00468	0.022868	-2.49
255997_s_	photosystem II type I chlorophyll a /b	CAB3	AT1G29910 /	-1.64	-0.71	-4.15	0.004684	0.022884	-2.49
246870_at	ferrochelatase-I	FC1	AT5G26030	2.90	1.54	4.15	0.004685	0.022884	-2.49
251429_at	dynamin-like protein 4 (ADL4) ; suppo	ADL1E	AT3G60190	1.43	0.51	4.15	0.004689	0.0229	-2.49
250436_at	RNA binding protein - like rna binding	---	AT5G10350	-1.43	-0.52	-4.15	0.004697	0.022934	-2.49
266309_at	unknown protein ;supported by full-ler	---	AT2G27140	-1.60	-0.68	-4.15	0.004703	0.022954	-2.49
261825_at	endo-xyloglucan transferase, putative	---	AT1G11545	-6.81	-2.77	-4.15	0.004703	0.022954	-2.49
248369_at	arginine/serine-rich splicing factor RSF	ATRSP41	AT5G52040	1.55	0.63	4.15	0.004708	0.022963	-2.49
262940_at	unknown protein	---	AT1G79520	1.67	0.74	4.15	0.004709	0.022963	-2.49
245706_at	putative protein	---	AT5G04310	-1.39	-0.48	-4.14	0.00471	0.022963	-2.49
258977_s_	putative aspartate kinase similar to asp	AK3	AT3G02020 /	-1.68	-0.75	-4.15	0.004709	0.022963	-2.49
254321_at	trehalose-6-phosphate phosphatase -	CPuORF27	AT4G22590 /	1.81	0.85	4.15	0.004707	0.022963	-2.49
264573_at	putative pectin methylesterase Similar	---	AT1G05310	-1.55	-0.63	-4.14	0.004712	0.022966	-2.49
255443_at	sulfate transporter protein similar to su	SULTR3;2	AT4G02700	-1.47	-0.55	-4.14	0.004713	0.022967	-2.49
254079_at	putative protein pmt2 methyltransferas	---	AT4G25730	1.88	0.91	4.14	0.004717	0.02298	-2.50
253719_at	putative protein, fragment prolidase -	---	AT4G29490	1.30	0.38	4.14	0.004719	0.022983	-2.50
256958_at	unknown protein contains Pfam profile	---	AT3G13430	1.71	0.78	4.14	0.00472	0.022983	-2.50
255902_at	transcription factor, putative similar to	---	AT1G17880	-1.38	-0.46	-4.14	0.004721	0.022983	-2.50
250602_s_	unknown protein	---	AT5G07940 /	1.38	0.47	4.14	0.004733	0.023036	-2.50
257517_at	unknown protein	---	AT3G16330	3.20	1.68	4.14	0.004733	0.023036	-2.50
262847_at	unknown protein similar to myosin hea	ATMAP70-4	AT1G14840	-2.00	-1.00	-4.14	0.004736	0.023043	-2.50

247901_at	ubiquinone/menaquinone biosynthesis	---	AT5G57300	-1.36	-0.45	-4.14	0.00474	0.023056	-2.50
260182_at	unknown protein similar to IFA-binding	---	AT1G70750	1.43	0.51	4.14	0.004741	0.02306	-2.50
259165_at	homeobox-leucine zipper protein HAT5	ATHB-1	AT3G01470 /	1.96	0.97	4.14	0.004744	0.023067	-2.50
264581_at	hypothetical protein predicted by gene	---	AT1G05210	-2.04	-1.03	-4.14	0.004745	0.023068	-2.50
264556_at	putative transcription factor contains M	MYB61	AT1G09540	-1.30	-0.38	-4.14	0.004747	0.023068	-2.50
264930_at	receptor-like kinase, putative similar to	NIK3	AT1G60800	-1.54	-0.63	-4.14	0.004747	0.023068	-2.50
264866_at	putative metalloproteinase similar to G	---	AT1G24140	6.32	2.66	4.14	0.004755	0.0231	-2.50
253049_at	putative protein ; supported by cDNA: (	MEE59	AT4G37300	-2.04	-1.03	-4.14	0.004758	0.023111	-2.51
248337_at	low-temperature-induced protein 78 (s	LTI78	AT5G52310	-5.40	-2.43	-4.14	0.004763	0.023128	-2.51
244968_at	ribosomal protein L33	---	---	-1.44	-0.53	-4.13	0.004781	0.023214	-2.51
259675_at	unknown protein similar to hypothetica	---	AT1G77710	1.36	0.45	4.13	0.004785	0.023222	-2.51
265761_at	putative stress protein	---	AT2G01330	1.37	0.45	4.13	0.004785	0.023222	-2.51
253606_at	putative protein component of aniline (	---	AT4G30530	1.99	0.99	4.13	0.004796	0.02327	-2.51
252884_at	SEC14 - like protein phosphatidylinos	---	AT4G39170	-1.46	-0.55	-4.13	0.004803	0.023298	-2.52
259397_at	hypothetical protein predicted by gene	---	AT1G17680	1.36	0.44	4.13	0.004815	0.023353	-2.52
265467_at	putative receptor-like protein kinase	---	AT2G37050	-1.63	-0.70	-4.13	0.00482	0.023373	-2.52
259548_at	hypothetical protein similar to ripening-	MLP165	AT1G35260	2.22	1.15	4.12	0.00483	0.023415	-2.52
247997_at	putative protein contains similarity to a	ATARP8	AT5G56180	1.47	0.55	4.12	0.004833	0.023426	-2.52
265075_at	hypothetical protein similar to embryo-	---	AT1G55450	3.38	1.76	4.12	0.004838	0.023443	-2.52
251203_at	putative protein putative transcription	---	AT3G63070	1.33	0.41	4.12	0.004843	0.023464	-2.52
249034_at	putative protein contains similarity to z	NUC	AT5G44160	-1.43	-0.51	-4.12	0.004853	0.02351	-2.53
263881_at	unknown protein ; supported by cDNA	---	AT2G21820	1.38	0.47	4.12	0.004858	0.023528	-2.53
247219_at	COP1-interacting protein CIP8 ; suppo	CIP8	AT5G64920	-1.40	-0.49	-4.12	0.004861	0.023535	-2.53
253819_at	receptor protein kinase like protein lec	---	AT4G28350	5.39	2.43	4.11	0.004887	0.023656	-2.53
252713_at	calmodulin 7 ; supported by full-length	CAM7	AT3G43810	-1.42	-0.50	-4.11	0.004899	0.023708	-2.54
248775_at	receptor kinase-like protein	CCR4	AT5G47850	5.50	2.46	4.11	0.0049	0.023708	-2.54
254029_at	putative protein other hypothetical prot	---	AT4G25870	-1.45	-0.53	-4.11	0.004906	0.02373	-2.54
266258_at	60S acidic ribosomal protein P2 ;supp	---	AT2G27720	-1.79	-0.84	-4.11	0.004906	0.02373	-2.54
252616_at	serine threonine-protein kinase-like pr	GRIK1	AT3G45240 /	1.50	0.59	4.11	0.004909	0.02374	-2.54
248584_at	putative protein similar to unknown pro	---	AT5G49960	-1.67	-0.74	-4.11	0.004913	0.023752	-2.54
255437_at	putative oxidoreductase similar to P. v	AOP2	AT4G03060	-2.66	-1.41	-4.11	0.004919	0.023767	-2.54
265576_at	unknown protein	CLASP	AT2G20190	-1.33	-0.41	-4.11	0.004918	0.023767	-2.54
254342_at	receptor like protein (fragment) ES43	---	AT4G22140	-1.32	-0.40	-4.11	0.004919	0.023767	-2.54
265777_at	hypothetical protein predicted by gene	---	AT2G07340	-1.34	-0.43	-4.11	0.004922	0.023776	-2.54
257938_at	cell elongation protein, Dwarf1 identic	DWF1	AT3G19820	-4.15	-2.05	-4.11	0.004923	0.023777	-2.54

245329_at	Expressed protein ; supported by full-l	---	AT4G14365	2.34	1.23	4.11	0.004931	0.023809	-2.54
249319_s_	putative protein similar to unknown pro	---	AT5G40880 /	1.46	0.55	4.11	0.004933	0.023815	-2.54
258291_at	putative protein kinase similar to protei	---	AT3G23310	-1.44	-0.53	-4.11	0.004934	0.023816	-2.54
261038_at	unknown protein ; supported by full-ler	---	AT1G17490	1.49	0.57	4.11	0.004945	0.023855	-2.55
251074_at	putative protein hypothetical protein T	---	AT5G01800	1.46	0.54	4.11	0.004944	0.023855	-2.55
258621_at	zinc finger protein 1 (zfn1) identical to	ZFN1	AT3G02830	-1.35	-0.44	-4.10	0.00495	0.023874	-2.55
245146_at	putative cis-Golgi SNARE protein ; su	GOS12	AT2G45200	-1.43	-0.52	-4.10	0.004956	0.023898	-2.55
266709_at	unknown protein ;supported by full-ler	ATSPP	AT2G03120	1.59	0.67	4.10	0.004959	0.02391	-2.55
245867_at	ATP phosphoribosyl transferase identi	ATATP-PRT	AT1G58080	-1.43	-0.52	-4.10	0.00496	0.02391	-2.55
260505_at	Cyclin, putative similar to GB:CAB772	CYCA3;4	AT1G47230	-1.35	-0.43	-4.10	0.004966	0.02393	-2.55
264662_at	putative sucrose/H+ symporter similar	SUT4	AT1G09960	1.60	0.68	4.10	0.004966	0.02393	-2.55
245579_at	hypothetical protein	---	AT4G14810	1.32	0.40	4.10	0.004969	0.023939	-2.55
250603_at	putative protein mature parasite-infect	---	AT5G07820	-1.42	-0.50	-4.10	0.004972	0.023946	-2.55
263521_at	hypothetical protein predicted by gens	---	AT2G24960	1.58	0.66	4.10	0.004975	0.023947	-2.55
261972_at	hypothetical protein predicted by gene	---	AT1G64600	1.75	0.81	4.10	0.004974	0.023947	-2.55
252242_at	F-box protein family, AtFBL16 contain	VFB2	AT3G50080	1.42	0.50	4.10	0.004974	0.023947	-2.55
247030_at	putative protein similar to unknown pro	---	AT5G67210	-1.30	-0.38	-4.10	0.004985	0.023988	-2.56
267223_at	hypothetical protein predicted by grail	AtITPK4	AT2G43980	1.41	0.50	4.10	0.004986	0.023988	-2.56
251622_at	dnaJ-like protein DNAJ protein - Schiz	---	AT3G57340	-1.32	-0.40	-4.10	0.004992	0.024015	-2.56
255025_at	putative host response protein pir7a p	MES12	AT4G09900	-1.77	-0.82	-4.09	0.005021	0.024148	-2.56
265796_at	Expressed protein ; supported by full-l	---	AT2G35730	5.90	2.56	4.09	0.005027	0.024171	-2.56
259041_at	unknown protein similar to putative glu	ATCSLC6	AT3G07330	-1.62	-0.70	-4.09	0.005029	0.024175	-2.57
264989_at	unknown protein ; supported by cDNA	---	AT1G27200	-1.60	-0.68	-4.09	0.005031	0.024179	-2.57
251026_at	hypothetical protein	FHL	AT5G02200	-3.48	-1.80	-4.09	0.005036	0.024201	-2.57
245981_at	putative protein ;supported by full-leng	---	AT5G13100	-1.45	-0.53	-4.09	0.00504	0.024212	-2.57
249983_at	putative protein S-receptor kinase PK	---	AT5G18470	8.60	3.10	4.09	0.005054	0.024275	-2.57
256118_at	hypothetical protein predicted by gene	KU70	AT1G16970	1.51	0.59	4.09	0.005061	0.024305	-2.57
251971_at	glucosyltransferase - like protein gluc	UGT73C7	AT3G53160	5.40	2.43	4.09	0.005063	0.024308	-2.57
251029_at	putative protein gene product of suAp	---	AT5G02050	1.97	0.98	4.09	0.005066	0.024318	-2.57
249986_at	putative protein predicted proteins, Ar	---	AT5G18460	-2.13	-1.09	-4.08	0.00507	0.024325	-2.57
254594_at	putative protein	---	AT4G18930	1.70	0.76	4.08	0.005069	0.024325	-2.57
267527_at	unknown protein	---	AT2G45610	-1.46	-0.54	-4.08	0.005075	0.024339	-2.58
265193_at	unknown protein ESTs gb|T144077 an	---	AT1G05070	-1.35	-0.43	-4.08	0.005075	0.024339	-2.58
252858_at	puative protein various predicted prote	---	AT4G39770	-1.45	-0.54	-4.08	0.005076	0.02434	-2.58
261370_at	cell division-related protein, putative s	---	AT1G53050	-1.35	-0.44	-4.08	0.005081	0.024359	-2.58

258400_at	unknown protein ; supported by cDNA	---	AT3G15470	-1.51	-0.60	-4.08	0.005086	0.024379	-2.58
257948_at	hypothetical protein predicted by gene	APO4	AT3G21740	1.42	0.51	4.08	0.005101	0.024444	-2.58
245925_at	bZIP transcription factor family protein	BZO2H3	AT5G28770	-1.60	-0.67	-4.08	0.005104	0.024451	-2.58
252923_at	kinesin like protein kinesin motor prote	---	AT4G39050	-1.57	-0.65	-4.08	0.005113	0.024489	-2.58
261572_at	unknown protein	---	AT1G01170	-1.46	-0.55	-4.08	0.005114	0.02449	-2.58
255962_at	glycine-rich RNA-binding protein, puta	---	AT1G22330	-3.27	-1.71	-4.08	0.005118	0.024501	-2.58
262673_at	unknown protein	EMB1793	AT1G76060	1.39	0.47	4.08	0.005118	0.024501	-2.58
261688_at	unknown protein contains similarity to	---	AT1G47380	-2.63	-1.39	-4.08	0.005121	0.024503	-2.58
259294_at	hypothetical protein predicted by gens	ATN	AT3G05330	1.63	0.70	4.08	0.005122	0.024503	-2.59
264870_at	hypothetical protein ;supported by full-	---	AT1G24210	-1.43	-0.52	-4.08	0.005122	0.024503	-2.59
262883_at	ammonium transporter, puitative simil	ATAMT1;2	AT1G64780	-1.76	-0.82	-4.08	0.005127	0.024523	-2.59
266990_at	putative ABC transporter	ATATH8	AT2G39190	-1.88	-0.91	-4.07	0.00513	0.024533	-2.59
248327_at	putative protein similar to unknown pro	---	AT5G52750	6.66	2.73	4.07	0.005134	0.024543	-2.59
262130_at	hypothetical protein predicted by gene	---	AT1G02890	1.43	0.51	4.07	0.005142	0.024576	-2.59
266448_s_	unknown protein ;supported by full-ler	---	AT2G43210	-1.36	-0.44	-4.07	0.005144	0.024583	-2.59
248895_at	receptor protein kinase	FLS2	AT5G46330	-2.09	-1.07	-4.07	0.005153	0.024615	-2.59
250928_at	putative protein	EIN2	AT5G03280	1.35	0.43	4.07	0.005152	0.024615	-2.59
259245_at	unknown protein predicted by genefin	---	AT3G07660	1.46	0.54	4.07	0.005155	0.024621	-2.59
255554_at	Expressed protein ; supported by full-l	---	AT4G01897	-1.38	-0.46	-4.07	0.005156	0.024622	-2.59
252096_at	hypothetical protein ; supported by cD	---	AT3G51180	1.76	0.82	4.07	0.005163	0.024648	-2.59
266440_at	unknown protein	---	AT2G43235 /	1.37	0.45	4.07	0.005173	0.024693	-2.60
254140_at	putative protein	---	AT4G24610	-1.62	-0.70	-4.07	0.005176	0.024699	-2.60
260741_at	hypothetical protein contains Pfam pro	---	AT1G15040	14.10	3.82	4.07	0.005177	0.024699	-2.60
262522_at	putative amino acid transporter Very si	CAT8	AT1G17120	-1.42	-0.51	-4.07	0.005191	0.024741	-2.60
256226_at	unknown protein ; supported by cDNA	ATDI19	AT1G56280	1.56	0.64	4.07	0.005192	0.024741	-2.60
257814_at	acyl-(acyl carrier protein) thioesterase	AtFaTA	AT3G25110	-2.04	-1.03	-4.07	0.005192	0.024741	-2.60
262557_at	photosystem I subunit III precursor, pu	---	AT1G31330 /	-1.39	-0.48	-4.07	0.005188	0.024741	-2.60
252053_at	syntaxin-like protein synt4 ;supported	SYP122	AT3G52400	2.84	1.51	4.07	0.005188	0.024741	-2.60
245998_at	sucrose-UDP glucosyltransferase	SUS1	AT5G20830	1.94	0.96	4.07	0.005191	0.024741	-2.60
261513_at	unknown protein contains Pfam profile	---	AT1G71840	1.44	0.52	4.06	0.005194	0.024743	-2.60
263930_at	hypothetical protein predicted by gens	---	AT2G36300	-1.39	-0.47	-4.06	0.005196	0.024745	-2.60
261748_at	hypothetical protein predicted by gene	---	AT1G76070	3.14	1.65	4.06	0.005196	0.024745	-2.60
247158_at	branched-chain amino acid aminotrans	ATBCAT-5	AT5G65780	-1.35	-0.43	-4.06	0.0052	0.024756	-2.60
264660_at	putative glutamyl-tRNA reductase 2 pr	HEMA2	AT1G09940	2.44	1.29	4.06	0.005201	0.024757	-2.60
246326_at	unknown protein ; supported by cDNA	REV7	AT1G16590	-1.34	-0.42	-4.06	0.005205	0.024772	-2.60

251094_at	putative protein ;supported by full-leng	---	AT5G01350	1.43	0.52	4.06	0.005214	0.024805	-2.60
253083_at	aldehyde dehydrogenase like protein	ALDH3F1	AT4G36250	-1.95	-0.96	-4.06	0.005214	0.024805	-2.60
253662_at	transcription factor-like protein Arabid	ARF16	AT4G30080	-1.41	-0.49	-4.06	0.005216	0.024806	-2.60
252964_at	receptor-like protein kinase - like prote	---	AT4G38830	1.37	0.46	4.06	0.005217	0.024806	-2.61
255894_at	nuclear poly(A) polymerase, putative s	---	AT1G17980	-1.39	-0.48	-4.06	0.005229	0.024858	-2.61
248448_at	putative protein contains similarity to e	---	AT5G51190	4.49	2.17	4.06	0.005231	0.024864	-2.61
262649_at	unknown protein contains similarity to	---	AT1G14040	2.41	1.27	4.06	0.005232	0.024864	-2.61
249100_at	unknown protein	---	AT5G43560	1.40	0.49	4.06	0.005235	0.024872	-2.61
251686_at	putative protein hypothetical protein - c	ATATG18D	AT3G56440	-1.34	-0.43	-4.06	0.005246	0.024913	-2.61
264869_at	hypothetical protein similar to hypothet	---	AT1G24350	1.37	0.45	4.06	0.005245	0.024913	-2.61
264963_at	hypothetical protein predicted by gene	ABC4	AT1G60600	-1.63	-0.70	-4.06	0.005247	0.024915	-2.61
253640_at	putative protein ;supported by full-leng	---	AT4G30630	1.32	0.40	4.06	0.005252	0.024929	-2.61
248611_at	putative protein contains similarity to W	WRKY48	AT5G49520	2.83	1.50	4.06	0.005252	0.024929	-2.61
262082_s_	wall-associated kinase 2, putative sim	---	AT1G56120 /	2.44	1.28	4.05	0.00529	0.025102	-2.62
254231_at	putative protein AR411 - Arabidopsis t	WRKY53	AT4G23810	6.04	2.60	4.05	0.005294	0.025112	-2.62
254794_at	putative protein	---	AT4G12970	-3.07	-1.62	-4.05	0.005294	0.025112	-2.62
257367_at	hypothetical protein predicted by gens	---	AT2G25780	-1.40	-0.48	-4.05	0.005298	0.025125	-2.62
245285_s_	selenium-binding protein like ; support	SBP1	AT4G14030 /	-1.35	-0.43	-4.05	0.005302	0.02514	-2.62
265187_at	putative ADP-ribosylation factor ; supp	---	AT1G23490 /	-1.27	-0.35	-4.05	0.005308	0.025159	-2.62
265190_at	unknown protein ; supported by cDNA	---	AT1G23780	1.31	0.39	4.05	0.005317	0.025198	-2.63
250297_at	putative protein predicted protein, Dro	---	AT5G11980	-1.44	-0.53	-4.05	0.005322	0.025216	-2.63
259544_at	hypothetical protein ; supported by full-	CAT3	AT1G20620	1.36	0.45	4.04	0.005324	0.025222	-2.63
253303_at	putative protein ; supported by full-len	---	AT4G33780	1.40	0.49	4.04	0.005325	0.025223	-2.63
248951_at	putative protein similar to unknown pro	---	AT5G45550	-1.49	-0.57	-4.04	0.005331	0.025238	-2.63
260436_at	unknown protein	---	AT1G68140	1.49	0.58	4.04	0.005332	0.025238	-2.63
254744_at	Expressed protein ; supported by cDN	MEE55	AT4G13345	1.60	0.68	4.04	0.005331	0.025238	-2.63
262899_at	ABC transporter, putative similar to AB	PEN3	AT1G59870	1.42	0.50	4.04	0.005334	0.025243	-2.63
257017_at	beta-xylosidase, putative similar to be	---	AT3G19620	-1.36	-0.44	-4.04	0.00534	0.025255	-2.63
260627_at	hypothetical protein predicted by gene	---	AT1G62310	-1.65	-0.72	-4.04	0.005339	0.025255	-2.63
253326_at	putative protein polygalacturonase(EC	---	AT4G33440	-1.40	-0.48	-4.04	0.005341	0.025255	-2.63
257865_at	protein kinase, putative contains Pfam	---	AT3G17750	-1.31	-0.39	-4.04	0.00534	0.025255	-2.63
248549_at	putative protein contains similarity to u	---	AT5G50310	1.37	0.45	4.04	0.00535	0.025289	-2.63
249148_at	unknown protein ; supported by cDNA	---	AT5G43260	1.73	0.79	4.04	0.005351	0.025289	-2.63
244931_at	hypothetical protein	---	---	1.60	0.68	4.04	0.005357	0.025316	-2.63
261434_at	receptor-like serine/threonine kinase,	---	AT1G07650	-1.63	-0.70	-4.04	0.005365	0.02534	-2.64

259288_at	putative small nuclear ribonucleoprotei	---	AT3G11500	-1.40	-0.48	-4.04	0.005365	0.02534	-2.64
259689_x_	unknown protein	---	AT1G63130	-1.77	-0.82	-4.04	0.005368	0.025353	-2.64
258225_at	unknown protein ; supported by cDNA	---	AT3G15630	-2.21	-1.15	-4.04	0.005373	0.025371	-2.64
257033_at	metalloprotease, putative similar to m	ATPREP1	AT3G19170	-1.92	-0.94	-4.04	0.005377	0.025384	-2.64
247210_at	annexin ;supported by full-length cDN	ANNAT2	AT5G65020	-1.95	-0.96	-4.04	0.005389	0.025433	-2.64
250335_at	lysophospholipase - like protein lysop	---	AT5G11650	1.73	0.79	4.03	0.005393	0.025442	-2.64
251179_at	putative protein ABP130 protein, Hom	---	AT3G63460	1.29	0.37	4.03	0.005392	0.025442	-2.64
262417_at	hypothetical protein similar to hypothet	ATSIRB	AT1G50170	1.29	0.37	4.03	0.005398	0.02546	-2.64
253464_at	putative protein ; supported by full-len	---	AT4G32030	-1.53	-0.61	-4.03	0.005399	0.02546	-2.64
260371_at	unknown protein ; supported by cDNA	---	AT1G69690	-2.32	-1.21	-4.03	0.005405	0.025483	-2.64
249987_at	putative protein predicted proteins, Ar	---	AT5G18490	1.71	0.77	4.03	0.005407	0.025486	-2.64
248923_at	putative protein similar to unknown pro	atnudt11	AT5G45940	-1.58	-0.66	-4.03	0.005411	0.025503	-2.64
262956_at	eukaryotic translation initiation factor 4	EIF4A-2	AT1G54270	1.44	0.53	4.03	0.005416	0.02552	-2.65
264586_at	putative cytochrome P450 Similar to G	CYP88A3	AT1G05160	-1.39	-0.48	-4.03	0.005419	0.025528	-2.65
248360_at	putative protein contains similarity to u	---	AT5G52430	-1.59	-0.67	-4.03	0.00542	0.025528	-2.65
259241_at	unknown protein similar to unknown pr	---	AT3G33530	-1.32	-0.40	-4.03	0.005428	0.02556	-2.65
250980_at	putative protein	---	AT5G03130	-2.08	-1.06	-4.03	0.005433	0.025579	-2.65
254258_at	hypothetical protein	TET5	AT4G23410	-1.47	-0.56	-4.03	0.005434	0.025579	-2.65
253770_at	protein kinase ADK1-like protein protei	CKL6	AT4G28540	1.33	0.41	4.03	0.005436	0.02558	-2.65
266835_at	putative NADH dehydrogenase (ubiqui	NDA2	AT2G29990	2.48	1.31	4.03	0.005439	0.02558	-2.65
265632_at	hypothetical protein predicted by gens	---	AT2G14290	6.12	2.61	4.03	0.005438	0.02558	-2.65
254200_at	putative protein predicted proteins, Ar	---	AT4G24110	4.25	2.09	4.03	0.005439	0.02558	-2.65
251533_at	putative protein several hypothetical pr	ATRBL15	AT3G58460	1.30	0.38	4.03	0.005443	0.025593	-2.65
255936_at	calcium dependent protein kinase, put	---	AT1G12680 /	-1.37	-0.45	-4.03	0.005446	0.025603	-2.65
267305_at	high affinity K+ transporter (AtKUP1/At	ATKT1	AT2G30070	-1.87	-0.90	-4.03	0.005447	0.025603	-2.65
252998_at	probable H+-transporting ATPase H+-	---	AT4G38510	-1.43	-0.51	-4.03	0.005449	0.025606	-2.65
253065_at	putative protein predicted proteins, Ar	AtGRF2	AT4G37740	-1.55	-0.64	-4.03	0.00545	0.025606	-2.65
260536_at	putative electron transfer flavoprotein u	ETFQO	AT2G43400	1.77	0.82	4.02	0.005464	0.025665	-2.66
265958_at	putative adenylate kinase ;supported l	ADK	AT2G37250	1.75	0.81	4.02	0.005467	0.025667	-2.66
260956_at	salt-tolerance protein identical to salt-t	STO	AT1G06040	-1.34	-0.42	-4.02	0.005466	0.025667	-2.66
260357_at	unknown protein ;supported by full-len	AFP1	AT1G69260	1.52	0.61	4.02	0.005472	0.025689	-2.66
258003_at	expansin At-EXP5 identical to expansi	EXPA5	AT3G29030	-3.00	-1.59	-4.02	0.005475	0.02569	-2.66
261570_at	fatty acid elongase 3-ketoacyl-CoA syr	KCS1	AT1G01120	-4.35	-2.12	-4.02	0.005474	0.02569	-2.66
267123_at	putative acetone-cyanohydrin lyase	MES7	AT2G23560	-1.81	-0.85	-4.02	0.005479	0.025701	-2.66
259304_at	putative nucleotide repair protein simila	ERCC1	AT3G05210	1.37	0.46	4.02	0.005479	0.025701	-2.66

255111_at	peroxidase C2 precursor like protein p	---	AT4G08780	10.77	3.43	4.02	0.005482	0.025708	-2.66
251483_at	putative protein hypothetical protein S	---	AT3G59650	-1.45	-0.53	-4.02	0.005486	0.02572	-2.66
267073_at	unknown protein	---	AT2G41160	1.51	0.60	4.02	0.005491	0.025741	-2.66
261279_at	class I chitinase, putative similar to GI	POM1	AT1G05850	-4.60	-2.20	-4.02	0.005498	0.025754	-2.66
251917_at	putative protein	---	AT3G53970	1.34	0.42	4.02	0.005498	0.025754	-2.66
254100_at	hypothetical protein ;supported by full-	---	AT4G25020	1.83	0.87	4.02	0.0055	0.025754	-2.66
253588_at	putative protein	---	AT4G30790	1.42	0.50	4.02	0.005498	0.025754	-2.66
251326_at	putative protein stamina pistilloidia (St	HWS	AT3G61590	-1.54	-0.63	-4.02	0.005499	0.025754	-2.66
267079_at	hypothetical protein predicted by gens	---	AT2G41200	-1.32	-0.40	-4.02	0.005514	0.025811	-2.67
247505_at	signal recognition particle - like protei	---	AT5G61970	-1.29	-0.37	-4.02	0.005514	0.025811	-2.67
265630_at	unknown protein similar to ovarian tum	---	AT2G27350	1.31	0.39	4.02	0.005523	0.025847	-2.67
267159_at	putative SCARECROW gene regulator	---	AT2G37650	1.39	0.47	4.01	0.005528	0.025866	-2.67
261888_at	ribosomal protein, putative similar to r	---	AT1G80800	-1.43	-0.51	-4.01	0.005529	0.025867	-2.67
255979_at	hypothetical protein	UPF3	AT1G33980	1.38	0.46	4.01	0.005535	0.025887	-2.67
258029_at	serine/threonine-protein kinase, PK7 i	ATPK7	AT3G27580	1.32	0.41	4.01	0.005536	0.025889	-2.67
247185_at	putative protein contains similarity to k	---	AT5G65460	-1.46	-0.55	-4.01	0.005538	0.025892	-2.67
247489_at	carbonyl reductase - like protein induc	---	AT5G61830	-1.42	-0.51	-4.01	0.005548	0.025932	-2.67
259801_at	blue copper protein, putative similar to	---	AT1G72230	-2.22	-1.15	-4.01	0.00555	0.025934	-2.67
254376_at	putative protein ; supported by cDNA:	TOM1	AT4G21790	1.29	0.36	4.01	0.005558	0.02597	-2.67
249933_at	rac GTPase activating protein	---	AT5G22400	-1.33	-0.41	-4.01	0.005562	0.025982	-2.67
264936_at	hypothetical protein predicted by gene	EDA16	AT1G61140	1.33	0.41	4.01	0.005564	0.025987	-2.68
259251_at	unknown protein identical to residues 2	---	AT3G07600	2.63	1.40	4.01	0.005568	0.025997	-2.68
263493_at	putative ATP-dependent RNA helicase	---	AT2G42520	1.59	0.67	4.01	0.005577	0.026036	-2.68
260440_at	hypothetical protein predicted by gens	---	AT1G68160	1.35	0.44	4.01	0.005581	0.026051	-2.68
264831_at	hypothetical protein predicted by gens	---	AT1G03687	-1.39	-0.48	-4.01	0.005586	0.026065	-2.68
264537_at	receptor kinase, putative similar to CL	BRL1	AT1G55610	1.62	0.70	4.01	0.005588	0.026071	-2.68
264147_at	receptor-like protein glossy1 (gl1), put	CER1	AT1G02205	-11.19	-3.48	-4.00	0.005592	0.026085	-2.68
250486_at	putative protein predicted proteins, Ar	---	AT5G09670 /	-1.39	-0.48	-4.00	0.005612	0.026169	-2.68
246303_at	putative carrier protein peroxisomal C	---	AT3G51870	1.71	0.77	4.00	0.005612	0.026169	-2.68
255280_at	score=179, E=5.7e-06, N=1)	---	AT4G04960	2.01	1.01	4.00	0.005615	0.026177	-2.68
265944_at	putative SET-domain transcriptional re	ASHR2	AT2G19640	1.46	0.55	4.00	0.005617	0.026182	-2.69
265662_at	putative C2H2-type zinc finger protein	FZF	AT2G24500	1.53	0.61	4.00	0.005619	0.026183	-2.69
250453_at	putative protein predicted protein, Bac	---	AT5G10620	-1.50	-0.59	-4.00	0.005646	0.026299	-2.69
262420_at	hypothetical protein contains similarity	TAF15	AT1G50300	-1.29	-0.36	-4.00	0.005646	0.026299	-2.69
252659_at	putative protein	---	AT3G44430	-1.43	-0.52	-4.00	0.005647	0.026299	-2.69

247875_at	putative protein similar to unknown pro	---	AT5G57720	-1.40	-0.49	-4.00	0.005654	0.026323	-2.69
258953_at	hypothetical protein predicted by gens	---	AT3G01430	-1.46	-0.55	-4.00	0.005657	0.026327	-2.69
246440_at	glycine/proline-rich protein glycine/pro	---	AT5G17650	1.95	0.97	4.00	0.005656	0.026327	-2.69
252624_at	Expressed protein ; supported by full-l	PSK1	AT3G44735	-2.03	-1.02	-3.99	0.005664	0.026355	-2.69
254256_at	serine/threonine kinase -like protein s	CRK10	AT4G23180	1.67	0.74	3.99	0.005666	0.026362	-2.69
247818_at	contains similarity to GTP-binding prot	---	AT5G58370	1.37	0.46	3.99	0.005669	0.026367	-2.70
256725_at	hypothetical protein predicted by gene	---	AT2G34070	-2.02	-1.01	-3.99	0.005675	0.026384	-2.70
246221_at	step II splicing factor - like protein ; su	SMP2	AT4G37120	1.38	0.47	3.99	0.005675	0.026384	-2.70
249542_at	putative protein transcription factor Ha	NF-YC12	AT5G38140	-1.54	-0.62	-3.99	0.005677	0.026387	-2.70
258331_at	putative coatomer complex subunit sim	---	AT3G15980	-1.45	-0.53	-3.99	0.005681	0.026403	-2.70
265711_at	unknown protein	---	AT2G03360	1.30	0.38	3.99	0.005684	0.02641	-2.70
264171_at	hypothetical protein predicted by gens	---	AT1G02100	1.47	0.55	3.99	0.0057	0.026479	-2.70
248272_at	Expressed protein ; supported by full-l	---	AT5G53480	-1.53	-0.61	-3.99	0.005707	0.026509	-2.70
262824_at	putative DNA binding protein similar t	RBP45B	AT1G11650	1.29	0.37	3.99	0.005711	0.02652	-2.70
247403_at	putative protein hypersensitive-induce	---	AT5G62740	1.37	0.45	3.99	0.005719	0.026551	-2.70
248478_at	ubiquitin-conjugating enzyme-like prot	UBC27	AT5G50870	-1.30	-0.38	-3.99	0.005728	0.026582	-2.71
247288_at	non-phototropic hypocotyl 3 (gb|AAF05	NPH3	AT5G64330	-2.77	-1.47	-3.99	0.005727	0.026582	-2.71
254704_at	putative protein predicted protein, Ara	APRR2	AT4G18020	1.41	0.50	3.99	0.00573	0.026582	-2.71
261754_at	alpha-amylase, putative similar to alp	AMY2	AT1G76130	2.34	1.22	3.99	0.005729	0.026582	-2.71
247175_at	G protein-coupled receptor-like protein	GCL1	AT5G65280	-2.41	-1.27	-3.98	0.005737	0.026607	-2.71
246069_at	zinc finger protein ;supported by full-l	---	AT5G20220	-1.72	-0.78	-3.98	0.005738	0.026607	-2.71
245957_at	putative protein predicted proteins - Ar	---	AT5G19590	1.30	0.38	3.98	0.005741	0.026616	-2.71
256972_at	unknown protein	---	AT3G21140	1.38	0.47	3.98	0.005745	0.026629	-2.71
248059_at	putative protein similar to unknown pro	TRN1	AT5G55540	-1.84	-0.88	-3.98	0.005747	0.026633	-2.71
254834_at	flavonoid 3,5-hydroxylase -like protein	CYP706A4	AT4G12300	1.51	0.60	3.98	0.005751	0.026644	-2.71
261167_at	disulfide isomerase-related protein, pu	ATPDIL2-2	AT1G04980	2.82	1.50	3.98	0.00576	0.026679	-2.71
244938_at	ribosomal protein S15	---	---	-1.77	-0.82	-3.98	0.00576	0.026679	-2.71
257373_at	hypothetical protein predicted by gene	---	AT2G43140	1.51	0.59	3.98	0.005768	0.02671	-2.71
263018_at	putative non-LTR retroelement reverse	---	---	-1.28	-0.35	-3.98	0.005773	0.026728	-2.71
265147_at	hypothetical protein	---	AT1G51380	1.60	0.68	3.98	0.005775	0.026731	-2.72
265174_s_	polygalacturonase, putative similar to	---	AT1G23460 /	-1.61	-0.69	-3.98	0.005778	0.02674	-2.72
246627_s_	5-enolpyruvylshikimate-3-phosphate (	---	AT1G48860 /	2.26	1.18	3.98	0.00578	0.026744	-2.72
266091_at	hypothetical protein predicted by gens	emb1513	AT2G37920	-1.47	-0.56	-3.98	0.005788	0.026774	-2.72
264980_at	receptor kinase, putative similar to CL	---	AT1G27190	-1.46	-0.54	-3.98	0.005798	0.026815	-2.72
259424_at	hypothetical protein contains similarity	---	AT1G13830	1.60	0.68	3.97	0.005809	0.026859	-2.72

262297_at	hypothetical protein similar to hypothet	---	AT1G27600	-1.30	-0.38	-3.97	0.005811	0.026865	-2.72
260332_at	hypothetical protein predicted by gene	---	AT1G70470	-1.28	-0.35	-3.97	0.005815	0.026876	-2.72
257051_at	squamosa promoter binding protein-lik	SPL5	AT3G15270	-2.67	-1.42	-3.97	0.005824	0.026908	-2.72
249137_at	putative protein contains similarity to 2	---	AT5G43140	-1.66	-0.73	-3.97	0.005823	0.026908	-2.72
251665_at	responce reactor 4 ; supported by cDI	ARR9	AT3G57040	-2.34	-1.22	-3.97	0.005826	0.02691	-2.72
249085_at	putative protein similar to unknown pro	---	AT5G44170	-1.41	-0.49	-3.97	0.005827	0.02691	-2.72
252982_at	Histone deacetylase ; supported by cI	HD1	AT4G38130	-1.37	-0.46	-3.97	0.005834	0.026936	-2.73
245078_at	putative AP2 domain transcription fact	---	AT2G23340	-2.42	-1.27	-3.97	0.005842	0.026963	-2.73
253206_at	putative squalene synthase non-conse	SQS1	AT4G34640	-1.41	-0.49	-3.97	0.005843	0.026963	-2.73
265658_at	putative aspartate aminotransferase ; s	ALD1	AT2G13810	3.63	1.86	3.97	0.005842	0.026963	-2.73
262959_at	protein translation factor Sui1 homolo	---	AT1G54290	1.43	0.51	3.97	0.005845	0.026969	-2.73
247306_at	ser/thr protein phosphatase catalytic s	PP7	AT5G63870	-1.47	-0.56	-3.97	0.00585	0.026982	-2.73
259018_at	unknown protein similar to unknown pr	AIR12	AT3G07390	2.85	1.51	3.97	0.005853	0.026993	-2.73
253089_at	putative protein hypothetical protein, A	---	AT4G36290	-1.32	-0.40	-3.97	0.00587	0.027065	-2.73
266860_at	putative phospholipase C	---	AT2G26870	-1.84	-0.88	-3.97	0.005873	0.027072	-2.73
263667_at	putative 40S ribosomal protein S15 St	RPS15	AT1G04270	-1.53	-0.61	-3.97	0.005874	0.027074	-2.73
261616_at	NAC domain containing protein, putat	ANAC014	AT1G33060	-1.27	-0.34	-3.96	0.005877	0.02708	-2.73
264121_at	putative GTP-binding protein Carboxy	TOC33	AT1G02280	-1.44	-0.53	-3.96	0.005889	0.027125	-2.74
253530_at	putative protein hypothetical protein -	---	AT4G31530	-1.79	-0.84	-3.96	0.00589	0.027125	-2.74
249916_at	histone H2B like protein (emb|CAA690	HTB2	AT5G22880	-1.66	-0.73	-3.96	0.005889	0.027125	-2.74
263689_at	ribonuclease, RNS3 identical to ribonu	RNS3	AT1G26820	-1.73	-0.79	-3.96	0.005893	0.027133	-2.74
246439_at	RING-H2 zinc finger protein-like RING	---	AT5G17600	-2.42	-1.27	-3.96	0.005901	0.027164	-2.74
265184_at	unknown protein ;supported by full-ler	---	AT1G23710	3.45	1.79	3.96	0.005904	0.027172	-2.74
248129_at	putative protein contains similarity to G	---	AT5G54780	1.42	0.51	3.96	0.005907	0.027179	-2.74
253249_at	GATA transcription factor 3	---	AT4G34680	1.52	0.60	3.96	0.005909	0.027187	-2.74
252927_at	cysteine proteinase RD19A identical t	RD19	AT4G39090	1.32	0.40	3.96	0.005914	0.027203	-2.74
248450_at	putative protein contains similarity to u	---	AT5G51290	1.42	0.51	3.96	0.005918	0.027218	-2.74
250071_at	putative protein similar to unknown pro	---	AT5G18000	1.30	0.38	3.96	0.005923	0.027229	-2.74
252364_at	hypothetical protein ;supported by full-	---	AT3G48450	3.14	1.65	3.96	0.005922	0.027229	-2.74
260311_at	hypothetical protein predicted by gens	---	AT1G70570	1.28	0.36	3.96	0.005926	0.027235	-2.74
253830_at	Expressed protein ; supported by full-l	---	AT4G27652	3.96	1.99	3.96	0.005932	0.027257	-2.74
255692_at	putative protein	GPAT8	AT4G00400	-2.78	-1.48	-3.96	0.005934	0.027262	-2.74
260129_at	hypothetical protein similar to vanilloid	---	AT1G36380	1.32	0.40	3.96	0.005943	0.027299	-2.75
251297_at	germin-like protein (GLP10)	GLP10	AT3G62020	-2.33	-1.22	-3.95	0.00596	0.027367	-2.75
261027_at	cyclic nucleotide and calmodulin-regu	ATCNGC10	AT1G01340	2.54	1.35	3.95	0.005961	0.027367	-2.75

250477_at	putative protein CIS,CIS-MUCONATE	---	AT5G10190	1.31	0.39	3.95	0.005965	0.027384	-2.75
246975_at	putative protein hypothetical proteins -	---	AT5G24890	-1.53	-0.62	-3.95	0.005972	0.027406	-2.75
263020_at	unknown protein	---	AT1G23880	-1.35	-0.43	-3.95	0.005976	0.027418	-2.75
253840_at	putative acyl-CoA binding protein stro	ACBP2	AT4G27780	1.49	0.58	3.95	0.005976	0.027418	-2.75
254382_at	hypothetical protein	---	AT4G21890	-1.58	-0.66	-3.95	0.005978	0.027419	-2.75
254736_at	putative disease resistance protein Cf	---	AT4G13820	1.80	0.84	3.95	0.00598	0.027425	-2.75
255094_at	putative zinc finger protein	ORTHL	AT4G08590	-1.69	-0.76	-3.95	0.005984	0.027425	-2.75
247820_at	serine/threonine protein kinase ; suppo	SIP1	AT5G58380	1.52	0.61	3.95	0.005982	0.027425	-2.75
255908_s_	unknown protein ;supported by full-len	---	AT1G18000 /	-1.38	-0.47	-3.95	0.005984	0.027425	-2.75
259540_at	nodule inception protein, putative simi	---	AT1G20640	-1.73	-0.79	-3.95	0.005988	0.027438	-2.75
263386_at	unknown protein ; supported by cDNA	---	AT2G40150	-1.91	-0.93	-3.95	0.005993	0.027454	-2.76
246425_at	cellulose synthase catalytic subunit (IR	IRX3	AT5G17420	-2.03	-1.02	-3.95	0.005999	0.027478	-2.76
257890_s_	putative protein peroxidase - Lycoper	---	AT3G17070 /	1.54	0.62	3.95	0.006006	0.027504	-2.76
247115_at	kinesin-like calmodulin-binding protein	ZWI	AT5G65930	-1.47	-0.56	-3.95	0.006015	0.02754	-2.76
251688_at	putative protein hypothetical protein A	---	AT3G56480	-2.00	-1.00	-3.95	0.00602	0.027555	-2.76
266742_at	predicted by genefinder and genscan	---	AT2G03050	-1.35	-0.44	-3.94	0.006028	0.027588	-2.76
250883_at	putative protein predicted proteins, Ar	---	AT5G03970	1.51	0.60	3.94	0.006034	0.027609	-2.76
257127_at	hypothetical protein predicted by gene	TTN9	AT3G20070	-1.46	-0.54	-3.94	0.006046	0.02766	-2.77
262503_at	hypothetical protein predicted by gens	---	AT1G21670	1.90	0.93	3.94	0.006049	0.027667	-2.77
247940_at	phosphatidylserine decarboxylase	PSD2	AT5G57190	2.51	1.33	3.94	0.006056	0.027694	-2.77
248905_at	putative protein contains similarity to R	---	AT5G46250	1.36	0.44	3.94	0.006058	0.027699	-2.77
247970_at	cytosolic malate dehydrogenase	---	AT5G56720	-1.35	-0.43	-3.94	0.006065	0.027726	-2.77
256678_at	RNA-binding protein (cp33) identical t	CP33	AT3G52380	-1.40	-0.49	-3.94	0.006075	0.027762	-2.77
261151_at	sec14 cytosolic factor, putative similar	---	AT1G19650	1.38	0.46	3.94	0.006076	0.027762	-2.77
265544_at	putative cyclic nucleotide and calmodu	ATCNGC15	AT2G28260	-1.54	-0.62	-3.94	0.006083	0.027785	-2.77
247724_at	putative protein predicted protein, Ara	MBD6	AT5G59380	-1.33	-0.42	-3.94	0.006083	0.027785	-2.77
252849_at	Histon H3 ;supported by full-length cD	---	AT4G40040	1.35	0.44	3.94	0.006088	0.0278	-2.77
264900_at	putative auxin transport protein strongl	PIN7	AT1G23080	-1.67	-0.74	-3.94	0.006092	0.027812	-2.77
262148_at	chloroplast-localized small heat shock	---	AT1G52560	1.98	0.98	3.93	0.0061	0.027846	-2.77
267187_s_	putative methylenetetrahydrofolate red	MTHFR2	AT2G44160 /	-1.58	-0.66	-3.93	0.006112	0.027893	-2.78
257791_at	unknown protein contains Pfam profile	---	AT3G27110	1.53	0.62	3.93	0.006118	0.027893	-2.78
264792_at	hypothetical protein similar to hypothet	---	AT1G08620	1.36	0.44	3.93	0.006118	0.027893	-2.78
247192_at	histone H3 (sp|P05203) ; supported b	---	AT5G65360	-5.77	-2.53	-3.93	0.006115	0.027893	-2.78
252637_at	WD repeat domain protein nuclear pro	HIRA	AT3G44530	1.43	0.51	3.93	0.006119	0.027893	-2.78
266816_at	unknown protein identical to GB:AAC3	---	AT2G44970	1.32	0.40	3.93	0.006119	0.027893	-2.78

246498_at	stearoyl-acyl carrier protein desaturas	---	AT5G16230	2.18	1.12	3.93	0.006116	0.027893	-2.78
252679_at	CCR4-associated factor 1-like protein	---	AT3G44260	5.04	2.33	3.93	0.006126	0.027917	-2.78
247642_at	putative protein various predicted prote	---	AT5G60590	1.34	0.42	3.93	0.006133	0.027944	-2.78
266156_at	hypothetical protein predicted by gens	FRA8	AT2G28110	2.81	1.49	3.93	0.006134	0.027945	-2.78
253302_at	Expressed protein ; supported by full-l	---	AT4G33660	-1.57	-0.65	-3.93	0.006141	0.027972	-2.78
251281_at	putative protein hypothetical protein A	AGP20	AT3G61640	-2.24	-1.17	-3.93	0.006165	0.028074	-2.79
267451_at	putative AP2 domain transcription fact	---	AT2G33710	5.28	2.40	3.93	0.006169	0.028088	-2.79
256518_at	hypothetical protein	---	AT1G66080	-1.45	-0.54	-3.92	0.006177	0.028119	-2.79
245906_at	putative protein ;supported by full-leng	---	AT5G11070	-2.06	-1.05	-3.92	0.006181	0.028132	-2.79
255725_at	hypothetical protein similar to putative	PFT1	AT1G25540	1.28	0.36	3.92	0.006183	0.028133	-2.79
264899_at	unknown protein similar to ripening-in	---	AT1G23130	1.89	0.91	3.92	0.006189	0.028151	-2.79
256209_at	electron transport flavoprotein, putativ	ETFALPHA	AT1G50940	1.37	0.45	3.92	0.006189	0.028151	-2.79
246779_at	putative protein peroxisomal integral m	PNC2	AT5G27520	1.80	0.85	3.92	0.006191	0.028155	-2.79
250745_at	putative protein strong similarity to unk	---	AT5G05850	1.62	0.70	3.92	0.006195	0.028166	-2.79
266114_at	hypothetical protein predicted by gens	---	AT2G02150	-1.28	-0.36	-3.92	0.006213	0.02824	-2.79
249910_at	chorismate mutase/prephenate dehydr	ADT5	AT5G22630	2.55	1.35	3.92	0.006214	0.02824	-2.79
260683_at	ribosomal protein, putative similar to C	HLL	AT1G17560	-1.39	-0.47	-3.92	0.006223	0.028274	-2.80
252335_at	putative protein putative protein - Arab	---	AT3G48860	1.42	0.50	3.92	0.006227	0.028283	-2.80
249252_at	putative protein contains similarity to u	---	AT5G42010	2.95	1.56	3.92	0.006228	0.028283	-2.80
246111_at	putative protein	---	AT5G20170	-1.39	-0.47	-3.92	0.006227	0.028283	-2.80
265337_at	putative ADP-ribosylation factor ;supp	TTN5	AT2G18390	-1.61	-0.69	-3.92	0.006233	0.028289	-2.80
251217_at	Sar1-like GTP binding protein small G	---	AT3G62560	-1.40	-0.49	-3.92	0.006231	0.028289	-2.80
253117_at	Expressed protein ; supported by full-l	---	AT4G35905	-1.48	-0.57	-3.92	0.006233	0.028289	-2.80
247806_at	ABC transporter-like protein ; supporte	STA1	AT5G58270	-1.34	-0.42	-3.92	0.006236	0.028298	-2.80
254504_at	putative protein RNPL, Homo sapiens	---	AT4G20030	-1.67	-0.74	-3.92	0.006239	0.028306	-2.80
247783_at	light harvesting pigment - like protein	---	AT5G58800	1.85	0.88	3.92	0.006244	0.028316	-2.80
265232_s_	hypothetical protein	---	AT2G07715	1.43	0.51	3.92	0.006244	0.028316	-2.80
253825_at	Expressed protein ; supported by full-l	---	AT4G28025	-1.55	-0.64	-3.91	0.006258	0.028372	-2.80
266621_at	unknown protein	---	AT2G35450	-1.66	-0.73	-3.91	0.006266	0.028406	-2.80
262376_at	unknown protein contains similarity to	HTH	AT1G72970	-1.33	-0.41	-3.91	0.006275	0.02844	-2.81
262308_at	unknown protein	---	AT1G71010	1.44	0.53	3.91	0.00628	0.028456	-2.81
252873_at	putative protein myosin heavy chain, C	---	AT4G40020	1.42	0.51	3.91	0.006284	0.02847	-2.81
249386_at	disease resistance -like protein downy	---	AT5G40060	1.36	0.45	3.91	0.006298	0.028524	-2.81
246141_at	TipD - like WD repeat protein TipD, Di	---	AT5G19920	-1.45	-0.54	-3.91	0.006299	0.028524	-2.81
247169_at	unknown protein	---	AT5G65520	-1.55	-0.63	-3.91	0.006311	0.028575	-2.81

257003_at	unknown protein ;supported by full-ler	FLU	AT3G14110	-1.56	-0.64	-3.91	0.006313	0.028579	-2.81
248896_at	putative protein contains similarity to W	WRKY8	AT5G46350	3.05	1.61	3.91	0.006329	0.028643	-2.81
248058_at	putative protein similar to unknown pro	---	AT5G55530	1.39	0.47	3.91	0.006331	0.028649	-2.81
255901_at	GDP-L-fucose synthetase, putative si	GER2	AT1G17890	-1.62	-0.70	-3.90	0.006334	0.02865	-2.82
253732_at	putative protein several hypothetical pr	---	AT4G29140	-1.36	-0.45	-3.90	0.006334	0.02865	-2.82
254380_at	putative protein	---	AT4G21865	2.78	1.48	3.90	0.006337	0.028658	-2.82
260954_at	glyoxalase II isozyme, putative similar	GLX2-4	AT1G06130	1.44	0.53	3.90	0.006345	0.028687	-2.82
252618_at	lipoxygenase AtLOX2 ; supported by c	LOX2	AT3G45140	-1.55	-0.63	-3.90	0.006348	0.028688	-2.82
247031_at	UDP-glucuronyltransferase-like protein	---	AT5G67230	-1.57	-0.65	-3.90	0.006346	0.028688	-2.82
245699_at	putative protein ;supported by full-leng	---	AT5G04250	1.77	0.82	3.90	0.006352	0.028703	-2.82
259666_at	unknown protein ; supported by cDNA	SR33	AT1G55310	1.36	0.44	3.90	0.00636	0.028733	-2.82
250978_at	putative protein contains transmembra	---	AT5G03080	-1.29	-0.37	-3.90	0.006377	0.028806	-2.82
266488_at	putative pectinesterase ; supported by	---	AT2G47670	1.63	0.70	3.90	0.006385	0.028836	-2.82
262418_at	thioredoxin, putative similar to thioredo	ATHX	AT1G50320	-1.61	-0.68	-3.90	0.006391	0.028856	-2.83
246064_at	DNA binding protein ACBF - like DNA	---	AT5G19350	1.37	0.45	3.90	0.006396	0.028868	-2.83
254418_at	glucose transporter glucose transport	---	AT4G21480	-1.37	-0.46	-3.90	0.006395	0.028868	-2.83
255560_at	hypothetical protein similar to C. elega	---	AT4G02030	-1.30	-0.38	-3.90	0.006397	0.028868	-2.83
258372_at	ubiquitin-specific protease 25 (UBP25)	UBP25	AT3G14400	1.33	0.41	3.90	0.006405	0.028897	-2.83
251442_at	putative protein multisynthetase comp	---	AT3G59980	-1.65	-0.72	-3.90	0.006411	0.028915	-2.83
254176_at	hypothetical protein hypothetical prote	---	AT4G24200	1.35	0.43	3.89	0.006414	0.028923	-2.83
248631_at	putative protein strong similarity to unk	---	AT5G49000	1.45	0.54	3.89	0.006424	0.028966	-2.83
258480_at	unknown protein ;supported by full-ler	---	AT3G02640	-1.40	-0.48	-3.89	0.006428	0.028977	-2.83
249576_at	putative protein predicted protein, Ara	---	AT5G37690	-1.30	-0.38	-3.89	0.006437	0.029011	-2.83
250829_at	disease resistance - like protein rpp8,	ADR1-L2	AT5G04720	1.44	0.53	3.89	0.006442	0.02903	-2.83
259497_at	unknown protein	---	AT1G15860	1.28	0.36	3.89	0.006448	0.029045	-2.83
256257_at	arginine-tRNA-protein transferase, pu	ATE2	AT3G11240	-1.31	-0.39	-3.89	0.006448	0.029045	-2.83
262261_at	CLE17, putative CLAVATA3/ESR-Rel	CLE17	AT1G70895	-1.45	-0.53	-3.89	0.006459	0.029083	-2.84
259119_at	transport protein SEC13, putative sim	---	AT3G01340	-1.30	-0.38	-3.89	0.00646	0.029083	-2.84
249770_at	unknown protein ;supported by full-len	WRKY30	AT5G24110	5.89	2.56	3.89	0.006459	0.029083	-2.84
246233_at	putative protein	---	AT4G36550	2.29	1.19	3.89	0.006464	0.029086	-2.84
247120_at	amino acid transporter protein-like	---	AT5G65990	1.36	0.44	3.89	0.006464	0.029086	-2.84
245264_at	Expressed protein ; supported by cDN	---	AT4G17245	-2.58	-1.37	-3.89	0.006466	0.029091	-2.84
259579_at	P-glycoprotein, putative similar to P-gl	PGP14	AT1G28010	-3.01	-1.59	-3.89	0.006468	0.029093	-2.84
263730_at	beta-glucosidase, putative similar to b	BGLU4	AT1G60090	-1.32	-0.40	-3.89	0.006472	0.029102	-2.84
251787_at	2-oxoglutarate dehydrogenase, E1 su	---	AT3G55410	1.44	0.53	3.89	0.006472	0.029102	-2.84

245065_at	unknown protein ; supported by cDNA	---	AT2G39750	-1.29	-0.37	-3.89	0.006476	0.029112	-2.84
260603_at	membrane related protein CP5, putati	---	AT1G55960	1.62	0.69	3.89	0.006481	0.029123	-2.84
265288_at	putative glutaredoxin ;supported by fu	---	AT2G20270	-1.51	-0.59	-3.89	0.00648	0.029123	-2.84
250996_at	putative protein BcDNA.LD24793, Drc	---	AT5G02530	-1.33	-0.41	-3.89	0.006486	0.029139	-2.84
256624_at	hypothetical protein predicted by gene	---	AT3G19990	1.33	0.41	3.89	0.006488	0.029143	-2.84
259406_at	hypothetical protein predicted by gene	---	AT1G17690	1.31	0.39	3.88	0.006505	0.029214	-2.84
252477_at	glucosyltransferase-like protein UDP-g	---	AT3G46680	1.52	0.61	3.88	0.006511	0.029234	-2.85
263556_at	hypothetical protein predicted by gens	---	AT2G16365	1.43	0.51	3.88	0.006514	0.029245	-2.85
245373_s_	Expressed protein ; supported by full-le	ATARD2	AT4G14710 /	1.37	0.45	3.88	0.006519	0.029258	-2.85
245040_at	hypothetical protein predicted by gene	---	AT2G26520	-1.40	-0.49	-3.88	0.00652	0.029258	-2.85
263778_at	putative cytochrome oxidase biogenes	OXA1L	AT2G46470	-1.41	-0.49	-3.88	0.006523	0.029265	-2.85
249424_s_	hypothetical protein ; supported by ful	---	AT5G39800 /	-1.42	-0.51	-3.88	0.006524	0.029266	-2.85
253798_at	predicted protein CUC2 (involved in o	ANAC073	AT4G28500	-1.40	-0.48	-3.88	0.006527	0.029273	-2.85
250056_at	putative protein predicted proteins, Sy	---	AT5G17660	-1.98	-0.98	-3.88	0.006547	0.02935	-2.85
261567_at	Expressed protein ; supported by cDN	---	AT1G33055	-2.38	-1.25	-3.88	0.006546	0.02935	-2.85
253638_at	cinnamoyl-CoA reductase - like protei	---	AT4G30470	-2.37	-1.25	-3.88	0.006553	0.029369	-2.85
266472_at	unknown protein	---	AT2G31150	-1.28	-0.36	-3.88	0.006554	0.029369	-2.85
249356_at	putative protein predicted proteins, Ar	---	AT5G40520	1.69	0.76	3.88	0.006566	0.029419	-2.85
247060_at	succinate dehydrogenase flavoprotein	SDH1-1	AT5G66760	2.58	1.37	3.88	0.006573	0.029444	-2.86
263807_at	putative indole-3-glycerol phosphate sy	---	AT2G04400	4.06	2.02	3.88	0.006576	0.029451	-2.86
253691_at	putative protein predicted proteins, Ar	EMB2752	AT4G29660	1.28	0.36	3.87	0.006586	0.029489	-2.86
252951_at	disease resistance response like prote	---	AT4G38700	-1.66	-0.73	-3.87	0.006589	0.029497	-2.86
252516_at	histidyl-tRNA synthetase ; supported b	ATHRS1	AT3G46100	-1.41	-0.50	-3.87	0.006591	0.0295	-2.86
262499_at	unknown protein EST gb|T41993 come	---	AT1G21770	1.53	0.61	3.87	0.006605	0.029554	-2.86
263700_at	unknown protein EST gb|Z33866 come	---	AT1G31150	-1.53	-0.61	-3.87	0.006605	0.029554	-2.86
267466_at	putative GDSL-motif lipase/hydrolase s	---	AT2G19010	-1.32	-0.40	-3.87	0.006613	0.029583	-2.86
253374_at	hypothetical protein ; supported by cD	---	AT4G33140	1.31	0.39	3.87	0.006619	0.029603	-2.86
265359_at	putative MYB family transcription facto	MYB7	AT2G16720	2.33	1.22	3.87	0.006625	0.029626	-2.86
265776_at	hypothetical protein predicted by gene	---	AT2G07340	-1.31	-0.39	-3.87	0.006627	0.029627	-2.86
250897_at	putative protein ; supported by cDNA:	---	AT5G03430	1.35	0.44	3.87	0.006638	0.029671	-2.87
245865_at	hypothetical protein contains similarity	---	AT1G58025	1.34	0.42	3.87	0.006641	0.02968	-2.87
246509_at	valine--tRNA ligase-like protein severa	EMB2247	AT5G16715	-1.67	-0.74	-3.87	0.006655	0.029735	-2.87
260089_at	putative ATPase contains Pfam profile	---	AT1G73170	1.29	0.37	3.86	0.00666	0.029746	-2.87
247498_at	peroxisomal Ca-dependent solute car	---	AT5G61810	-1.49	-0.58	-3.86	0.006661	0.029746	-2.87
260728_at	Pto kinase interactor 1, putative simila	---	AT1G48210	1.86	0.89	3.87	0.006659	0.029746	-2.87

264957_at	F-box protein family, AtFBL5 contains	SKP2B	AT1G77000	1.73	0.79	3.86	0.006669	0.029775	-2.87
260415_at	putative protein kinase similar to protei	---	AT1G69790	1.74	0.80	3.86	0.006676	0.029802	-2.87
248916_at	receptor protein kinase-like protein pre	---	AT5G45840	-2.11	-1.08	-3.86	0.006687	0.029836	-2.87
246234_at	putative protein	---	AT4G37280	-1.42	-0.51	-3.86	0.006686	0.029836	-2.87
267553_s_	hypothetical protein predicted by gene	---	AT2G32180 /	-1.60	-0.68	-3.86	0.006688	0.029838	-2.87
250702_at	peroxidase ;supported by full-length c	---	AT5G06730	5.32	2.41	3.86	0.006694	0.029858	-2.88
249140_at	F-box protein family, AtFBX6 contains	---	AT5G43190	-1.54	-0.62	-3.86	0.006705	0.029902	-2.88
248271_at	putative protein similar to unknown pro	---	AT5G53420	2.08	1.06	3.86	0.006709	0.029906	-2.88
252821_at	putative protein ;supported by full-leng	---	AT4G39860	-2.12	-1.09	-3.86	0.006708	0.029906	-2.88
248633_at	arginine methyltransferase-like protein	PRMT4A	AT5G49020	-1.39	-0.48	-3.86	0.006715	0.029926	-2.88
246211_at	G-box-binding factor 1 ; supported by c	GBF1	AT4G36730	-1.81	-0.86	-3.86	0.006733	0.029995	-2.88
246325_at	hypothetical protein contains similarity	ABA3	AT1G16540	2.11	1.08	3.86	0.006734	0.029995	-2.88
261828_at	unknown protein ; supported by cDNA:	---	AT1G11360	-1.34	-0.42	-3.86	0.006733	0.029995	-2.88
267628_at	unknown protein similar to GP|226214	---	AT2G42280	1.40	0.48	3.86	0.006738	0.030008	-2.88
257351_at	putative mitochondrial carrier protein	MBAC1	AT2G33820	-1.47	-0.56	-3.86	0.006743	0.030023	-2.88
266125_at	putative GATA-type zinc finger transcr	---	AT2G45050	-1.47	-0.55	-3.85	0.006746	0.030029	-2.88
252281_at	putative protein various predicted prote	---	AT3G49320	1.53	0.61	3.85	0.006749	0.030038	-2.88
261136_at	ribokinase, putative similar to GB:AAD	---	AT1G19600	1.32	0.40	3.85	0.006758	0.030069	-2.89
245397_at	auxin-responsive protein IAA1 ;suppor	IAA1	AT4G14560	-2.39	-1.26	-3.85	0.00676	0.030069	-2.89
248002_at	Expressed protein ; supported by full-le	ATARP8	AT5G56180	1.54	0.62	3.85	0.006759	0.030069	-2.89
254209_at	Expressed protein ; supported by cDN	---	AT4G23490	-1.65	-0.72	-3.85	0.006761	0.03007	-2.89
245851_at	putative protein HERC2 - Homo sapie	KEG	AT5G13530	1.36	0.44	3.85	0.006786	0.030173	-2.89
254642_at	putative protein hypothetical protein, S	---	AT4G18810	-1.73	-0.79	-3.85	0.006788	0.030174	-2.89
255281_at	contains similarity to glucan synthases	GSL1	AT4G04970	1.27	0.34	3.85	0.006794	0.030191	-2.89
248104_at	S-adenosyl-L-methionine:salicylic acid	IAMT1	AT5G55250	-2.10	-1.07	-3.85	0.006793	0.030191	-2.89
257325_at	hypothetical protein	---	AT2G07798	2.09	1.06	3.85	0.006796	0.030192	-2.89
245716_at	Expressed protein ; supported by cDN	NDC1	AT5G08740	-1.70	-0.77	-3.85	0.006802	0.030213	-2.89
251699_at	cytochrome P450-like protein cytochr	CYP94D2	AT3G56630	1.38	0.47	3.85	0.006815	0.030264	-2.89
258185_at	hypothetical protein similar to hypothet	---	AT3G21580	-1.48	-0.57	-3.85	0.006816	0.030264	-2.89
245004_at	hypothetical protein	---	---	-1.50	-0.58	-3.85	0.006822	0.030288	-2.90
264597_at	unknown protein	---	AT1G04620	1.51	0.60	3.85	0.006828	0.030302	-2.90
259219_at	hypothetical protein predicted by gens	---	AT3G03560	1.60	0.68	3.85	0.006828	0.030302	-2.90
259334_at	unknown protein similar to hect domai	---	AT3G03790	1.57	0.65	3.84	0.006834	0.030323	-2.90
248814_at	putative protein similar to unknown pro	---	AT5G46910	3.92	1.97	3.84	0.006843	0.030355	-2.90
258847_at	unknown protein ; supported by full-le	---	AT3G03100	1.30	0.38	3.84	0.006848	0.030364	-2.90

264474_s_	ribulose-bisphosphate carboxylase sm	RBCS1A	AT1G06820 /	-1.27	-0.35	-3.84	0.006847	0.030364	-2.90
253270_at	cyclin delta-3	CYCD3;1	AT4G34160	-1.59	-0.67	-3.84	0.006858	0.030401	-2.90
255639_at	putative protein	APRR8	AT4G00760	-1.47	-0.56	-3.84	0.00686	0.030401	-2.90
246027_at	homoserine dehydrogenase-like prote	---	AT5G21060	-1.63	-0.70	-3.84	0.006859	0.030401	-2.90
258210_at	Eukaryotic initiation factor 4A, putative	EIF4A1	AT3G13920	-1.34	-0.42	-3.84	0.006867	0.030427	-2.90
258139_at	heat shock transcription factor HSF1,	HSFC1	AT3G24520	1.49	0.57	3.84	0.006875	0.030457	-2.90
252974_at	putative protein ; supported by cDNA:	MTN1	AT4G38800	1.33	0.41	3.84	0.006881	0.030463	-2.90
248493_at	putative protein contains similarity to ir	FSD2	AT5G51100	-1.40	-0.49	-3.84	0.00688	0.030463	-2.90
250732_at	putative protein contains similarity to u	---	AT5G06480	-1.72	-0.78	-3.84	0.006879	0.030463	-2.90
265740_at	RING-H2 finger protein RHA2b identic	RHA2B	AT2G01150	-2.04	-1.03	-3.84	0.006906	0.030565	-2.91
262943_at	inosine-5'-monophosphate dehydroge	---	AT1G79470	1.34	0.42	3.84	0.006906	0.030565	-2.91
249337_at	putative protein contains similarity to u	---	AT5G41080	3.23	1.69	3.84	0.006916	0.030601	-2.91
260613_at	unknown protein	---	AT1G53380	-1.39	-0.47	-3.83	0.006919	0.030607	-2.91
266543_at	hypothetical protein predicted by gens	---	AT2G35075	-1.26	-0.34	-3.83	0.006925	0.03063	-2.91
258186_s_	protein kinase, putative similar to serir	---	AT1G48490 /	1.32	0.40	3.83	0.006937	0.030676	-2.91
265028_at	hypothetical protein predicted by gene	---	AT1G24530	-2.78	-1.48	-3.83	0.006939	0.030678	-2.91
245950_at	putative protein predicted protein, D. r	---	AT5G19570	-1.61	-0.69	-3.83	0.006944	0.030695	-2.91
249303_at	putative protein strong similarity to unk	---	AT5G41460	-1.62	-0.70	-3.83	0.006947	0.030705	-2.92
260454_at	RING-H2 zinc finger protein (ATL3) ide	ATL3	AT1G72310	-1.90	-0.93	-3.83	0.006961	0.030758	-2.92
254858_at	putative protein other predicted protei	---	AT4G12070	1.36	0.44	3.83	0.006963	0.030758	-2.92
264190_at	heme activated protein, putative simila	NF-YC3	AT1G54830	-1.28	-0.35	-3.83	0.006963	0.030758	-2.92
251372_at	putative protein ;supported by full-leng	---	AT3G60520	-1.48	-0.56	-3.83	0.006967	0.030762	-2.92
265680_at	putative hydrolase ; supported by cDN	---	AT2G32150	1.72	0.78	3.83	0.006967	0.030762	-2.92
251990_at	putative protein MICRONUCLEAR LIN	---	AT3G53320	-1.58	-0.66	-3.83	0.006969	0.030764	-2.92
252472_at	GTP-binding protein Rab11 ; supporte	ATRABA2C	AT3G46830	-1.41	-0.50	-3.83	0.006977	0.030788	-2.92
246915_at	malate dehydrogenase - like protein m	ATNADP-ME	AT5G25880	-1.74	-0.80	-3.83	0.006977	0.030788	-2.92
249815_at	60S ribosomal protein L13 ; supported	---	AT5G23900	-1.60	-0.68	-3.83	0.006978	0.030788	-2.92
266110_at	putative C2H2-type zinc finger protein	AtIDD4	AT2G02080	-1.39	-0.47	-3.83	0.00699	0.030834	-2.92
262565_at	hypothetical protein predicted by gens	---	AT1G34320	1.37	0.45	3.83	0.006995	0.03085	-2.92
254694_at	putative protein	---	AT4G17900	1.54	0.62	3.83	0.006998	0.030859	-2.92
261218_at	ferredoxin--NADP reductase precurso	FNR2	AT1G20020	-1.65	-0.72	-3.83	0.007001	0.030864	-2.92
262360_at	receptor protein kinase, putative simila	---	AT1G73080 /	3.59	1.84	3.82	0.007004	0.030873	-2.92
266811_at	unknown protein	---	AT2G44850	-1.33	-0.41	-3.82	0.007006	0.030875	-2.92
257962_at	hypothetical protein predicted by gens	---	AT3G19790	-1.66	-0.73	-3.82	0.007008	0.030876	-2.92
246340_s_	AtPP -like protein AtPP protein, Brass	---	AT3G44860 /	1.94	0.95	3.82	0.007012	0.030887	-2.93

253739_at	putative protein predicted protein. Arab	---	AT4G28760	-1.47	-0.55	-3.82	0.007014	0.03089	-2.93
249480_s_	protein kinase - like protein receptor-li	---	AT5G38990 /	2.11	1.08	3.82	0.007039	0.030996	-2.93
264098_at	hypothetical protein predicted by gene	---	AT1G79260	-1.69	-0.75	-3.82	0.007051	0.031042	-2.93
251916_at	transporter-like protein oligopeptide tra	---	AT3G53960	1.60	0.68	3.82	0.007052	0.031042	-2.93
245676_at	nodule-specific protein, putative simila	---	AT1G56670	-1.38	-0.47	-3.82	0.007058	0.031054	-2.93
248264_at	putative protein similar to unknown pro	---	AT5G53310	-1.40	-0.49	-3.82	0.007057	0.031054	-2.93
246822_at	putative protein predicted proteins, Ar	---	AT5G26960	-1.41	-0.49	-3.82	0.007064	0.031074	-2.93
246515_at	putative protein unusual floral organs	---	AT5G15710	-1.27	-0.34	-3.82	0.007069	0.031092	-2.93
254778_at	putative protein	---	AT4G12750	1.47	0.56	3.82	0.007072	0.031097	-2.93
250698_at	putative protein similar to unknown pro	---	AT5G06810	1.32	0.40	3.82	0.007083	0.031142	-2.94
258300_at	putative casein kinase I similar to case	ckl10	AT3G23340	1.57	0.65	3.82	0.007085	0.031146	-2.94
267373_at	unknown protein	CID7	AT2G26280	1.37	0.45	3.82	0.00709	0.03116	-2.94
245238_at	putative protein similarity to cytochrom	ACYB-2	AT4G25570	-1.46	-0.54	-3.81	0.007098	0.031192	-2.94
260867_at	hypothetical protein predicted by gene	TED6	AT1G43790	-2.76	-1.46	-3.81	0.007102	0.031199	-2.94
259774_at	plasma membrane associated protein	---	AT1G29520	-1.57	-0.65	-3.81	0.007108	0.031211	-2.94
251034_at	putative protein ;supported by full-leng	PRA1.A1	AT5G02040	1.38	0.46	3.81	0.007107	0.031211	-2.94
264563_s_	unknown protein	---	AT1G55750 /	-1.39	-0.48	-3.81	0.007108	0.031211	-2.94
257646_at	methionine aminopeptidase, putative s	MAP1B	AT3G25740	-1.81	-0.86	-3.81	0.007118	0.031248	-2.94
250529_at	RNA helicase-like protein	---	AT5G08610	1.54	0.62	3.81	0.00712	0.031249	-2.94
251177_at	cyclophylin -like protein CDC28/cdc2-	---	AT3G63400	1.45	0.53	3.81	0.007121	0.031249	-2.94
257758_at	eukaryotic translation elongation facto	---	AT3G22980	1.41	0.49	3.81	0.007132	0.031292	-2.94
251910_at	serine/threonine-specific kinase like p	---	AT3G53810	3.16	1.66	3.81	0.007134	0.031294	-2.94
256149_at	zinc finger protein, putative similar to a	AtIDD7	AT1G55110	1.54	0.62	3.81	0.007138	0.031294	-2.94
258852_at	unknown protein similar to C-terminal p	AT-P4H-2	AT3G06300	1.56	0.64	3.81	0.007136	0.031294	-2.94
254214_at	putative potassium transport protein (T	TRH1	AT4G23640	1.42	0.50	3.81	0.007138	0.031294	-2.94
249347_at	putative protein similar to unknown pro	---	AT5G40830	-1.82	-0.86	-3.81	0.007145	0.031317	-2.95
254164_at	putative protein ;supported by full-leng	TIFY1	AT4G24470	1.36	0.45	3.81	0.007146	0.031318	-2.95
251395_at	unknown protein ;supported by full-ler	FLA8	AT2G45470	-8.29	-3.05	-3.81	0.007151	0.031324	-2.95
256711_at	unknown protein contains Pfam profile	---	AT3G30390	1.65	0.72	3.81	0.00715	0.031324	-2.95
247602_at	S-receptor kinase homolog 2 precurso	RLK1	AT5G60900	2.43	1.28	3.81	0.007152	0.031324	-2.95
255490_at	putative protein lysosomal trafficking r	---	AT4G02660	-1.35	-0.43	-3.81	0.007157	0.031341	-2.95
253204_at	GTP binding protein beta subunit ; sup	AGB1	AT4G34460	1.28	0.35	3.81	0.007162	0.031357	-2.95
254153_at	putative protein hypothetical protein R	PWD	AT4G24450	1.81	0.85	3.81	0.007169	0.03138	-2.95
253573_at	putative protein BEM46 PROTEIN, Sc	---	AT4G31020	1.42	0.50	3.81	0.007178	0.031413	-2.95
261403_at	unknown protein ;supported by full-len	SYP52	AT1G79590	-1.30	-0.38	-3.80	0.007193	0.031475	-2.95

256673_at	unknown protein	FLA15	AT3G52370	-3.37	-1.75	-3.80	0.007198	0.031489	-2.95
265274_at	putative RNA methyltransferase	---	AT2G28450	-1.44	-0.52	-3.80	0.007221	0.031584	-2.96
262056_at	Expressed protein ; supported by full-l	---	AT1G80245	1.38	0.46	3.80	0.007223	0.031587	-2.96
254839_at	stress-induced protein sti1 -like protei	---	AT4G12400	2.14	1.09	3.80	0.007226	0.031593	-2.96
249400_at	putative protein MtN24 gene, Medicag	---	AT5G40300	1.47	0.56	3.80	0.007229	0.0316	-2.96
261596_at	hypothetical protein predicted by gene	---	AT1G33080	-1.38	-0.46	-3.80	0.007237	0.03163	-2.96
252188_at	putative clathrin coat assembly protei	---	AT3G50860	1.68	0.75	3.80	0.007239	0.031631	-2.96
266442_at	hypothetical protein	---	AT2G43260	-1.27	-0.34	-3.80	0.007252	0.031682	-2.96
246259_at	amino acid permease, putative contai	---	AT1G31830	1.43	0.51	3.80	0.007265	0.031732	-2.96
254854_at	putative protein hypothetical protein S	---	AT4G12130	1.52	0.60	3.79	0.007282	0.031792	-2.97
266035_at	enoyl-ACP reductase (enr-A)	MOD1	AT2G05990	-1.83	-0.87	-3.79	0.007282	0.031792	-2.97
248332_at	heat-shock protein ; supported by cDN	ATHSP90.1	AT5G52640	3.60	1.85	3.79	0.007282	0.031792	-2.97
245323_at	cysteine proteinase inhibitor like protei	---	AT4G16500	-1.47	-0.55	-3.79	0.007287	0.031804	-2.97
253033_at	putative protein aminoacylase I - Sus	---	AT4G38220	-1.34	-0.43	-3.79	0.007291	0.031813	-2.97
248852_at	unknown protein	---	AT5G46560	1.27	0.34	3.79	0.007293	0.031813	-2.97
253546_at	hypothetical protein ;supported by full-	---	AT4G31030 /	-1.45	-0.53	-3.79	0.007293	0.031813	-2.97
267288_at	similar to cold acclimation protein WC	---	AT2G23680	2.67	1.41	3.79	0.007297	0.031826	-2.97
263247_at	unknown protein	---	AT2G31440	-1.29	-0.36	-3.79	0.007304	0.031849	-2.97
264390_at	putative DNA-binding protein Contains	---	AT1G11950	-1.44	-0.53	-3.79	0.007307	0.031856	-2.97
258609_at	unknown protein ;supported by full-ler	---	AT3G02910	1.41	0.50	3.79	0.007311	0.031867	-2.97
263776_s_	putative cyclic nucleotide-regulated ion	ATCNGC3	AT2G46430 /	3.87	1.95	3.79	0.007326	0.031929	-2.97
263732_at	hypothetical protein predicted by gene	ARL2	AT1G59980	-1.38	-0.47	-3.79	0.007329	0.031935	-2.97
253414_at	putative protein	EDA39	AT4G33050	4.44	2.15	3.79	0.007333	0.031944	-2.97
247699_at	GTP-binding protein ara-3 GTP-bindir	---	AT5G59840	1.70	0.77	3.79	0.007339	0.031966	-2.97
266269_at	putative glutathione S-transferase ; su	ATGSTU2	AT2G29480	2.38	1.25	3.79	0.007342	0.031971	-2.98
247470_at	putative protein various predicted prot	---	AT5G62220	-2.59	-1.37	-3.79	0.007353	0.032012	-2.98
264729_at	putative metal-binding protein highly si	---	AT1G22990	-1.71	-0.78	-3.79	0.007357	0.032025	-2.98
260939_at	hypothetical protein contains similarity	---	AT1G45180	-2.17	-1.12	-3.79	0.007361	0.032036	-2.98
262693_at	unknown protein	---	AT1G62780	-1.89	-0.92	-3.78	0.007374	0.032087	-2.98
264873_at	putative indole-3-acetate beta-glucosy	UGT74B1	AT1G24100	2.33	1.22	3.78	0.007375	0.032087	-2.98
250249_at	putative protein similar to unknown pro	---	AT5G13760	1.41	0.50	3.78	0.007378	0.03209	-2.98
265987_at	unknown protein	---	AT2G24240	1.61	0.69	3.78	0.007382	0.032105	-2.98
265990_at	putative prolylcarboxypeptidase	---	AT2G24280	1.62	0.70	3.78	0.007386	0.032115	-2.98
260040_at	Expressed protein ; supported by full-l	IDA	AT1G68765	4.10	2.04	3.78	0.007391	0.032131	-2.98
250434_at	histone H3 - like protein histone H3, A	---	AT5G10390	-3.75	-1.91	-3.78	0.007393	0.032131	-2.98

246406_at	disease resistance protein RPP1-WsA	---	AT1G57650	1.25	0.32	3.78	0.007415	0.032225	-2.99
250163_at	putative protein various predicted prot	---	AT5G15270	-1.39	-0.48	-3.78	0.007419	0.032228	-2.99
255704_at	putative proline-rich protein ;supporte	---	AT4G00170	1.28	0.36	3.78	0.007419	0.032228	-2.99
261887_at	CCR4-associated factor, putative\0CC	---	AT1G80780	-1.28	-0.36	-3.78	0.007422	0.032233	-2.99
254845_at	hydroxymethylglutaryl-CoA synthase ;	MVA1	AT4G11820	-1.50	-0.58	-3.78	0.007432	0.032272	-2.99
267392_at	putative beta-glucosidase	PEN2	AT2G44490	1.61	0.69	3.78	0.007437	0.032282	-2.99
255566_s_	hypothetical protein	---	AT3G48670 /	-1.38	-0.46	-3.78	0.007436	0.032282	-2.99
247442_s_	tubulin beta-2/beta-3 chain (sp|P29512	TUB2	AT5G62690 /	-1.69	-0.75	-3.78	0.007447	0.03232	-2.99
262382_at	virus resistance protein, putative simil	---	AT1G72920	4.56	2.19	3.78	0.007451	0.032326	-2.99
250272_at	callose synthase catalytic subunit -like	ATGSL12	AT5G13000	-1.46	-0.54	-3.78	0.00745	0.032326	-2.99
259103_at	unknown protein ; supported by cDNA	---	AT3G11690	-2.07	-1.05	-3.78	0.007454	0.03233	-2.99
247793_at	putative protein ; supported by cDNA:	PSY1	AT5G58650	1.56	0.65	3.78	0.007459	0.032346	-2.99
251060_at	putative protein serine/threonine prote	ATSR1	AT5G01820	3.28	1.71	3.78	0.007462	0.032348	-2.99
254419_at	NADH dehydrogenase like protein NA	NDB3	AT4G21490	1.28	0.36	3.78	0.007461	0.032348	-2.99
254609_at	Expressed protein ; supported by full-l	---	AT4G18970	-2.20	-1.14	-3.77	0.007468	0.032366	-2.99
253452_at	hypothetical protein ; supported by cDI	---	AT4G31930	-1.34	-0.42	-3.77	0.00747	0.032369	-2.99
253949_at	grpE like protein ;supported by full-len	AR192	AT4G26780	2.21	1.14	3.77	0.007487	0.032417	-3.00
264511_at	putative galactinol synthase similar to (	AtGolS3	AT1G09350	-2.70	-1.43	-3.77	0.007486	0.032417	-3.00
256430_at	DREB2B transcription factor identical t	DREB2B	AT3G11020	1.34	0.42	3.77	0.007486	0.032417	-3.00
261519_at	unknown protein ; supported by cDNA:	---	AT1G71810	-1.55	-0.63	-3.77	0.007486	0.032417	-3.00
259616_at	hypothetical protein contains similarity	C/VIF1	AT1G47960	1.63	0.71	3.77	0.00749	0.032425	-3.00
245557_at	phosphatase like protein	PUX5	AT4G15410	-1.26	-0.34	-3.77	0.007495	0.032436	-3.00
251950_at	zinc finger - like protein Zat11 zinc fin	---	AT3G53600	5.37	2.42	3.77	0.007495	0.032436	-3.00
246159_at	Expressed protein ; supported by full-l	---	AT5G20935	-1.76	-0.82	-3.77	0.007504	0.032469	-3.00
256093_at	predicted protein ; supported by cDNA	---	AT1G20823	2.79	1.48	3.77	0.007508	0.032477	-3.00
262767_at	putative oxysterol-binding protein simil	ORP1D	AT1G13170	-1.90	-0.93	-3.77	0.007512	0.03248	-3.00
257263_at	unknown protein ;supported by full-ler	---	AT3G22070	-1.71	-0.77	-3.77	0.007513	0.03248	-3.00
248551_at	putative protein similar to unknown pro	WR3	AT5G50200	2.36	1.24	3.77	0.007511	0.03248	-3.00
257475_at	hypothetical protein predicted by gens	---	AT1G80880	-1.26	-0.34	-3.77	0.007529	0.032544	-3.00
260379_at	putative glucosyltransferase similar to	UGT89B1	AT1G73880 /	1.51	0.59	3.77	0.007536	0.032567	-3.00
267509_at	MADS-box protein (AGL20) ; supporte	AGL20	AT2G45660	-1.55	-0.64	-3.77	0.007547	0.032611	-3.00
261109_at	cytokinin oxidase, putative similar to C	CKX5	AT1G75450	-3.86	-1.95	-3.77	0.007557	0.032646	-3.01
257269_at	unknown protein contains Pfam profile	NPSN13	AT3G17440	-1.56	-0.64	-3.76	0.007558	0.032646	-3.01
266800_at	hypothetical protein predicted by gene	---	AT2G22880	8.10	3.02	3.76	0.00756	0.032649	-3.01
263757_at	cysteine proteinase similar to cysteine	---	AT2G21430	1.62	0.69	3.76	0.007568	0.032672	-3.01

247467_at	putative protein predicted proteins, D.	---	AT5G62130	-1.84	-0.88	-3.76	0.007569	0.032672	-3.01
261470_at	ethylene-responsive element binding f	ERF11	AT1G28370	4.13	2.05	3.76	0.007571	0.032677	-3.01
264894_at	unknown protein Location of EST gb|A	---	AT1G23040	1.43	0.52	3.76	0.007576	0.032678	-3.01
248035_at	sucrose cleavage protein-like ;support	---	AT5G55900	-1.33	-0.41	-3.76	0.007575	0.032678	-3.01
254605_at	protein kinase - like protein protein kir	---	AT4G18950	2.07	1.05	3.76	0.007576	0.032678	-3.01
252861_at	hypothetical protein	---	AT4G39820	1.63	0.70	3.76	0.007577	0.032678	-3.01
253503_at	cytochrome P450-like protein cytochr	CYP82C3	AT4G31950	1.73	0.79	3.76	0.007585	0.032705	-3.01
251624_at	hypothetical protein ;supported by full-	---	AT3G57280	1.46	0.55	3.76	0.0076	0.032763	-3.01
261106_at	homeodomain-containing protein HD1	KNAT7	AT1G62990	1.31	0.38	3.76	0.007606	0.032779	-3.01
250442_at	putative protein hypothetical bacterial p	MSL2	AT5G10490	1.34	0.42	3.76	0.007606	0.032779	-3.01
263158_at	CCAAT-binding factor B subunit, puta	NF-YA5	AT1G54160	-1.35	-0.43	-3.76	0.007608	0.03278	-3.01
256504_at	cytosolic IMP-GMP specific 5'-nucleot	---	AT1G75210	-1.35	-0.43	-3.76	0.007613	0.032797	-3.01
262657_at	ribonuclease contains similarity to RNa	---	AT1G14210	-2.06	-1.04	-3.76	0.007615	0.032799	-3.01
251902_at	uncoupling protein (ucp/PUMP) ; supp	PUMP1	AT3G54110	2.03	1.02	3.76	0.007625	0.032831	-3.02
250210_at	putative protein similar to unknown pro	---	AT5G13890	-1.40	-0.48	-3.76	0.007626	0.032831	-3.02
260730_at	lipoamide dehydrogenase precursor id	mtLPD1	AT1G48030	-1.51	-0.59	-3.76	0.007648	0.032914	-3.02
262199_at	unknown protein ; supported by cDNA	---	AT1G53800	-1.51	-0.59	-3.76	0.007646	0.032914	-3.02
255838_at	unknown protein	---	AT2G33490	1.33	0.41	3.76	0.007649	0.032914	-3.02
255267_at	putative protein LpxD gene, Brucella a	---	AT4G05210	-1.27	-0.34	-3.76	0.007654	0.032927	-3.02
248934_at	serine/threonine protein kinase-like pro	---	AT5G46080	3.29	1.72	3.75	0.007656	0.032933	-3.02
255266_at	receptor protein kinase - like protein re	---	AT4G05200	-1.35	-0.44	-3.75	0.007661	0.032947	-3.02
264372_at	lactoylglutathione lyase-like protein Si	ATGLX1	AT1G11840	-1.58	-0.66	-3.75	0.007665	0.032952	-3.02
264594_at	hypothetical protein ; supported by cDI	ATSERAT3;	AT2G17640	1.37	0.45	3.75	0.007665	0.032952	-3.02
250235_s_	ubiquinol--cytochrome-c reductase - li	---	AT5G13430 /	1.29	0.37	3.75	0.007671	0.032962	-3.02
261892_at	transcription factor, putative similar to	WRKY40	AT1G80840	6.48	2.70	3.75	0.007671	0.032962	-3.02
246485_at	putative protein cell death associated	AtCXE17	AT5G16080	3.37	1.75	3.75	0.007672	0.032962	-3.02
266193_at	unknown protein	---	AT2G39080	-1.41	-0.50	-3.75	0.007674	0.032964	-3.02
252678_s_	nitrilase 2 ;supported by full-length cD	NIT2	AT3G44300 /	1.31	0.39	3.75	0.007685	0.033008	-3.02
259775_at	hypothetical protein predicted by gene	---	AT1G29530	-1.67	-0.74	-3.75	0.007688	0.033011	-3.02
257739_at	unknown protein	---	AT3G27470	1.51	0.59	3.75	0.007703	0.033071	-3.03
251678_at	putative protein conserved hypothetic	EDA7	AT3G56990	1.31	0.39	3.75	0.007713	0.033101	-3.03
250503_at	putative protein similar to unknown pro	---	AT5G09820	-1.54	-0.62	-3.75	0.007712	0.033101	-3.03
266012_s_	predicted protein	---	AT2G07699 /	1.81	0.86	3.75	0.007715	0.033103	-3.03
247197_at	receptor-like protein kinase	---	AT5G65240	1.98	0.99	3.75	0.007722	0.033129	-3.03
245702_at	calcium lipid binding protein - like GC c	SYTC	AT5G04220	1.55	0.63	3.75	0.00775	0.03324	-3.03

261402_at	wall-associated kinase 4, putative sim	RFO1	AT1G79670	1.70	0.76	3.74	0.007753	0.03325	-3.03
251267_at	putative protein hypothetical protein B	---	AT3G62330	-1.42	-0.51	-3.74	0.007756	0.033256	-3.03
263200_at	hypothetical protein predicted by gens	---	AT1G05600	1.49	0.58	3.74	0.007764	0.033275	-3.04
262158_at	somatic embryogenesis receptor-like	---	AT1G52540	1.59	0.67	3.74	0.007762	0.033275	-3.04
266116_at	unknown protein ;supported by full-ler	TOM3	AT2G02180	-1.49	-0.57	-3.74	0.007773	0.033307	-3.04
257211_at	exonuclease, putative contains Pfam	---	AT3G15080	1.49	0.57	3.74	0.007776	0.033307	-3.04
260570_at	stearoyl-ACP desaturase ; supported	SSI2	AT2G43710	-1.56	-0.65	-3.74	0.007777	0.033307	-3.04
250245_at	alpha-N-acetylglucosaminidase	---	AT5G13690	-1.44	-0.53	-3.74	0.007776	0.033307	-3.04
256388_at	unknown protein	---	AT3G06180	-1.36	-0.45	-3.74	0.00778	0.033316	-3.04
263403_at	hypothetical protein similar to hypothet	TX1	AT2G04040	4.78	2.26	3.74	0.007796	0.033375	-3.04
245228_at	phytochelatin synthetase-like protein g	COBL2	AT3G29810	-2.03	-1.02	-3.74	0.007798	0.033378	-3.04
251729_at	alpha-galactosidase-like protein alpha	---	AT3G56310	1.73	0.79	3.74	0.007811	0.033427	-3.04
251439_at	putative protein unknown protein At2g	---	AT3G59950	1.39	0.48	3.74	0.007814	0.033432	-3.04
249889_at	putative protein strong similarity to unk	---	AT5G22540	2.54	1.35	3.74	0.007815	0.033432	-3.04
247578_at	putative protein predicted protein, Ara	---	AT5G61300	-1.42	-0.51	-3.74	0.007829	0.033472	-3.04
246441_at	putative protein ;supported by full-leng	---	AT5G17560	-1.32	-0.40	-3.74	0.007827	0.033472	-3.04
257748_at	hypothetical protein predicted by gene	PUB29	AT3G18710	6.85	2.78	3.74	0.007827	0.033472	-3.04
267469_at	unknown protein ; supported by cDNA	WRKY21	AT2G30590	-1.39	-0.47	-3.74	0.007833	0.033485	-3.04
258573_at	hypothetical protein contains Pfam pro	PTAC3	AT3G04260	-1.28	-0.36	-3.74	0.007838	0.033499	-3.05
249858_at	myb-related transcription factor-like	MYB37	AT5G23000	1.49	0.57	3.74	0.007845	0.033522	-3.05
259320_at	putative DNA-binding protein similar to	WRKY58	AT3G01080	2.41	1.27	3.74	0.007848	0.033529	-3.05
250525_at	putative protein contains similarity to u	ILP1	AT5G08550	1.33	0.41	3.73	0.007855	0.033547	-3.05
256096_at	unknown protein	---	AT1G13650	-1.95	-0.97	-3.73	0.007855	0.033547	-3.05
246778_at	mevalonate kinase supported by full-le	MK	AT5G27450	-1.40	-0.48	-3.73	0.007861	0.033566	-3.05
245107_at	putative heat shock transcription factor	AT-HSFB3	AT2G41690	2.21	1.15	3.73	0.007864	0.033574	-3.05
258773_at	hypothetical protein predicted by gens	---	AT3G10730	-1.26	-0.33	-3.73	0.007869	0.033581	-3.05
254760_at	putative protein hypothetical protein s	---	AT4G13200	-1.31	-0.39	-3.73	0.00787	0.033581	-3.05
254562_at	cytochrome P450 cytochrome P450, A	CYP707A1	AT4G19230	2.03	1.02	3.73	0.007868	0.033581	-3.05
265899_s_	SKP1/ASK1 (At3), putative similar to f	ASK4	AT1G20140 /	1.38	0.47	3.73	0.007887	0.033643	-3.05
258501_at	hypothetical protein predicted by gene	---	AT3G06780	-1.57	-0.65	-3.73	0.007894	0.033664	-3.05
247330_at	putative protein contains similarity to a	GAMMA CA	AT5G63510	-1.28	-0.35	-3.73	0.007894	0.033664	-3.05
247390_at	putative protein similar to unknown pro	---	AT5G63520	-1.30	-0.38	-3.73	0.007903	0.033695	-3.05
247855_at	similar to unknown protein (sp|P23253	---	AT5G58210	1.48	0.57	3.73	0.007914	0.033736	-3.06
263401_at	hypothetical protein similar to hypothet	---	AT2G04070	1.61	0.69	3.73	0.007918	0.033748	-3.06
265425_at	hypothetical protein	GCL2	AT2G20770	-1.45	-0.54	-3.73	0.007925	0.033769	-3.06

259180_at	unknown protein	---	AT3G01680	-2.32	-1.22	-3.73	0.007928	0.033776	-3.06
260680_s_	GATA transcription factor 3, putative s	---	AT1G08000 /	-1.28	-0.36	-3.73	0.00793	0.033777	-3.06
247348_at	beta-galactosidase (emb CAB64746.1	BGAL10	AT5G63810	-1.45	-0.54	-3.73	0.007932	0.033782	-3.06
257495_at	unknown protein	ATPDIL5-1	AT1G07960	1.40	0.48	3.73	0.00795	0.033851	-3.06
260665_at	unknown protein ;supported by full-len	---	AT1G19360	1.38	0.46	3.72	0.007956	0.033857	-3.06
256747_at	unknown protein similar to CW14 GB:E	---	AT3G29180	1.39	0.47	3.72	0.007955	0.033857	-3.06
266696_at	copia-like retroelement pol polyprotein	---	AT2G19680	-1.42	-0.51	-3.72	0.007954	0.033857	-3.06
254385_s_	putative protein CGI-131 protein, Hom	ATMSRB7	AT4G21830 /	11.58	3.53	3.72	0.007959	0.033865	-3.06
251991_at	transcription factor NF-Y, CCAAT-bind	NF-YB10	AT3G53340	-1.46	-0.55	-3.72	0.007964	0.033881	-3.06
260756_at	hypothetical protein contains similarity	---	AT1G48970	1.29	0.37	3.72	0.007977	0.033929	-3.06
253332_at	peroxidase ATP17a -like protein perox	---	AT4G33420	2.55	1.35	3.72	0.007996	0.034003	-3.07
249190_at	unknown protein ;supported by full-ler	BKI1	AT5G42750	-1.39	-0.48	-3.72	0.008018	0.034089	-3.07
261348_at	hypothetical protein contains similarity	TED3	AT1G79810	1.30	0.38	3.72	0.008026	0.034116	-3.07
260799_at	UDP-glucose glucosyltransferase, put	AtUGT85A4	AT1G78270	-1.42	-0.51	-3.72	0.008043	0.034183	-3.07
255127_at	nodulin-like protein nodulin gene MtN2	---	AT4G08300	2.91	1.54	3.72	0.008046	0.03419	-3.07
253492_at	enoyl-CoA hydratase - like protein enc	---	AT4G31810	2.08	1.06	3.72	0.008049	0.034194	-3.07
254722_at	putative protein predicted protein, Ara	---	AT4G13530	1.72	0.79	3.72	0.008055	0.034216	-3.08
252418_at	hypothetical protein	---	AT3G47490	-1.46	-0.54	-3.71	0.008059	0.034225	-3.08
264822_at	putative ribonucleoprotein	---	AT1G03457	-1.74	-0.80	-3.71	0.00806	0.034225	-3.08
266948_at	unknown protein	---	AT2G18850	-1.67	-0.74	-3.71	0.008066	0.034242	-3.08
266538_at	hypothetical protein predicted by gens	---	AT2G35230	-1.34	-0.42	-3.71	0.008069	0.034248	-3.08
266277_at	putative tropinone reductase	---	AT2G29310	-1.39	-0.47	-3.71	0.008079	0.034278	-3.08
264696_at	unknown protein	---	AT1G70230	-2.05	-1.04	-3.71	0.008079	0.034278	-3.08
246090_at	putative protein BEM46 bem1/bud5 su	WAV2	AT5G20520	1.75	0.81	3.71	0.008087	0.034305	-3.08
246073_at	ribosomal protein L36-like ribosomal p	---	AT5G20180	-1.38	-0.47	-3.71	0.008089	0.034309	-3.08
257504_at	dynein light chain, putative similar to d	ROPGEF11	AT1G52240	-1.81	-0.86	-3.71	0.008104	0.034335	-3.08
254615_at	RNase L inhibitor-like protein RNase L	RLI2	AT4G19210	1.32	0.40	3.71	0.008097	0.034335	-3.08
266642_at	putative chloroplast RNA binding prote	---	AT2G35410	-1.36	-0.44	-3.71	0.0081	0.034335	-3.08
249659_s_	putative protein similar to unknown pro	---	AT5G36710 /	-1.49	-0.57	-3.71	0.008104	0.034335	-3.08
248957_at	26S proteasome subunit-like protein	---	AT5G45620	-1.33	-0.41	-3.71	0.008099	0.034335	-3.08
266617_at	unknown protein ; supported by cDNA	---	AT2G29670	-1.96	-0.97	-3.71	0.008102	0.034335	-3.08
263216_s_	putative reticuline oxidase-like protein	---	AT1G30720 /	4.84	2.27	3.71	0.008106	0.034336	-3.08
259416_at	Expressed protein ; supported by cDN	---	AT1G02305	1.46	0.55	3.71	0.008112	0.034344	-3.08
247878_at	unknown protein	---	AT5G57760	-12.32	-3.62	-3.71	0.008113	0.034344	-3.08
250340_at	putative protein predicted proteins in S	---	AT5G11840	-1.50	-0.58	-3.71	0.008112	0.034344	-3.08

251550_at	putative protein proline-rich protein A4	---	AT3G58800	-1.37	-0.45	-3.71	0.00812	0.034359	-3.08
267030_at	unknown protein	SCAR2	AT2G38440	-1.31	-0.39	-3.71	0.008119	0.034359	-3.08
249275_at	polygalacturonase-like protein	---	AT5G41870	-1.38	-0.47	-3.71	0.00812	0.034359	-3.08
258911_at	unknown protein similar to hypothetica	---	AT3G06470	1.38	0.46	3.71	0.008127	0.034379	-3.08
262408_at	protein phosphatase type 2C, putative	---	AT1G34750	2.01	1.01	3.71	0.008129	0.034382	-3.08
263834_at	hypothetical protein	---	AT2G40316	-1.39	-0.48	-3.71	0.008133	0.034394	-3.09
246744_at	putative protein predicted protein, Ara	---	AT5G27760	2.62	1.39	3.71	0.008135	0.034395	-3.09
246803_at	tSNARE AtTLG2a ; supported by cDN	SYP41	AT5G26980	-1.32	-0.40	-3.71	0.008139	0.034405	-3.09
260953_at	transcriptional activator RF2a, putative	---	AT1G06070	-1.37	-0.46	-3.71	0.008148	0.034438	-3.09
265297_at	putative disease resistance protein cor	---	AT2G14080	1.29	0.37	3.71	0.008156	0.03446	-3.09
262454_at	bifunctional nuclease bfn1 almost iden	BFN1	AT1G11190	4.37	2.13	3.71	0.008157	0.03446	-3.09
256776_at	multispanning membrane protein, puta	---	AT3G13772	1.32	0.40	3.70	0.008164	0.034482	-3.09
257705_at	unknown protein ; supported by cDNA	---	AT3G12760	1.25	0.32	3.70	0.008165	0.034482	-3.09
261018_at	unknown protein contains similarity to	---	AT1G26550	1.25	0.32	3.70	0.008168	0.03449	-3.09
261999_at	hypothetical protein predicted by gene	---	AT1G33800	-1.43	-0.52	-3.70	0.008199	0.034612	-3.09
264094_at	unknown protein ;supported by full-len	---	AT1G79200	1.38	0.47	3.70	0.008202	0.034616	-3.09
263075_at	hypothetical protein predicted by gene	---	AT2G17570	1.55	0.63	3.70	0.008202	0.034616	-3.09
256894_at	PREG-like protein, putative similar to	CYCP2;1	AT3G21870	-1.27	-0.35	-3.70	0.008209	0.034637	-3.10
249965_at	putative protein predicted proteins, Ar	---	AT5G19020	1.25	0.32	3.70	0.008212	0.034643	-3.10
261388_at	Expressed protein ; supported by cDN	---	AT1G05385	-1.30	-0.38	-3.70	0.008222	0.034679	-3.10
266457_at	putative glyoxysomal malate dehydrog	PMDH1	AT2G22780	1.33	0.41	3.70	0.008228	0.034693	-3.10
248836_at	NBS/LRR disease resistance protein	---	AT5G47260	1.46	0.55	3.70	0.008228	0.034693	-3.10
249187_at	cysteine proteinase RD21A similar to	---	AT5G43060	2.06	1.04	3.70	0.008244	0.034751	-3.10
254048_at	putative protein various predicted prot	---	AT4G25680	-1.63	-0.70	-3.70	0.008247	0.034758	-3.10
263222_at	putative protein kinase Strong similarit	---	AT1G30640	-1.58	-0.66	-3.69	0.008267	0.034837	-3.10
263250_at	putative fructokinase ; supported by fu	---	AT2G31390	1.88	0.91	3.69	0.0083	0.034969	-3.11
264865_at	DNAJ-like heatshock protein similar to	ARL1	AT1G24120	-1.29	-0.37	-3.69	0.008304	0.03498	-3.11
266615_s_	putative monooxygenase ;supported b	CTF2A	AT2G29720 /	2.87	1.52	3.69	0.008309	0.034986	-3.11
259092_at	putative zeta-carotene desaturase pre	ZDS	AT3G04870	-1.26	-0.33	-3.69	0.008308	0.034986	-3.11
261193_at	unknown protein ; supported by cDNA	---	AT1G32920	2.39	1.25	3.69	0.008314	0.035001	-3.11
248580_at	chloride channel (emb|CAA70310.1)	CLC-C	AT5G49890	1.47	0.56	3.69	0.008315	0.035001	-3.11
256304_at	Expressed protein ; supported by cDN	---	AT1G69523	-1.69	-0.75	-3.69	0.008324	0.035031	-3.11
262094_at	SAR DNA binding protein, putative sir	NOP56	AT1G56110	1.90	0.93	3.69	0.008328	0.035043	-3.11
248347_at	putative protein contains similarity to p	---	AT5G52250	1.28	0.36	3.69	0.008347	0.035116	-3.11
250194_at	putative protein various predicted prot	---	AT5G14550	1.34	0.42	3.69	0.008355	0.035129	-3.11

261257_at	tat-binding protein, putative similar to	---	AT1G05910	1.46	0.54	3.69	0.008354	0.035129	-3.11
246190_at	hypothetical protein (fragment) ;suppo	ATBPM5	AT5G21010	-1.27	-0.34	-3.69	0.008352	0.035129	-3.11
262197_at	AP2 domain containing protein, putati	RAP2.12	AT1G53910	1.67	0.74	3.69	0.008365	0.03515	-3.12
265893_at	putative disease resistance protein	---	AT2G15040 /	2.18	1.12	3.69	0.008366	0.03515	-3.12
248395_at	putative protein contains similarity to u	AtPP2-A14	AT5G52120	1.52	0.60	3.69	0.008362	0.03515	-3.12
260771_at	serine/threonine protein kinase, putati	WNK7	AT1G49160	1.71	0.78	3.69	0.008364	0.03515	-3.12
244946_at	hypothetical protein	---	---	1.28	0.36	3.69	0.008368	0.035152	-3.12
261112_at	unknown protein	---	AT1G75420	-1.41	-0.49	-3.68	0.008374	0.035171	-3.12
260389_at	Expressed protein ; supported by full-l	---	AT1G74055	-1.56	-0.64	-3.68	0.008376	0.035171	-3.12
246633_at	hypothetical protein ; supported by cDI	---	AT1G29720	-2.40	-1.26	-3.68	0.008377	0.035172	-3.12
252632_s_	disease resistance protein -like diseas	RPP1	AT3G44480 /	1.37	0.46	3.68	0.008383	0.035187	-3.12
251054_at	receptor like protein kinase receptor li	LECRKA4.1	AT5G01540	3.97	1.99	3.68	0.008388	0.035202	-3.12
257756_at	uridylate kinase, putative similar to UM	---	AT3G18680	-1.40	-0.48	-3.68	0.00839	0.035204	-3.12
260868_at	unknown protein ;supported by full-len	---	AT1G43860	1.46	0.55	3.68	0.008391	0.035204	-3.12
255770_at	hypothetical protein predicted by gens	---	AT1G18560	-1.34	-0.42	-3.68	0.008394	0.03521	-3.12
254076_at	putative protein immunophilin FKBP46	---	AT4G25340	1.73	0.79	3.68	0.008403	0.035225	-3.12
253714_at	putative protein adaptor protein - Hom	---	AT4G29380	1.34	0.42	3.68	0.008404	0.035225	-3.12
259804_at	cytosolic factor, putative similar to GI:	---	AT1G72160	-1.72	-0.78	-3.68	0.0084	0.035225	-3.12
253785_s_	ABC transporter - like protein ABC tra	ATM2	AT4G28620 /	-1.34	-0.42	-3.68	0.008404	0.035225	-3.12
252036_at	putative protein ;supported by full-leng	---	AT3G52070	-1.46	-0.55	-3.68	0.008409	0.03524	-3.12
245832_at	chorismate synthase, putative similar	EMB1144	AT1G48850	2.43	1.28	3.68	0.008418	0.035269	-3.12
264901_at	putative sulphate transporter protein s	AST91	AT1G23090	2.54	1.34	3.68	0.008426	0.035292	-3.12
264472_at	hypothetical protein predicted by gene	SWEETIE	AT1G67140	-1.45	-0.54	-3.68	0.008425	0.035292	-3.12
262278_at	transcription factor PERIANTHIA ident	PAN	AT1G68640	-1.43	-0.52	-3.68	0.00844	0.035346	-3.13
252385_at	putative protein Vps29, Schizosaccha	MAG1	AT3G47810	1.30	0.38	3.68	0.008467	0.035446	-3.13
258706_at	unknown protein similar to putative pro	---	AT3G09570	1.34	0.43	3.68	0.008468	0.035446	-3.13
257706_at	Expressed protein ; supported by cDN	---	AT3G12685	-1.62	-0.70	-3.68	0.00847	0.035448	-3.13
263972_at	unknown protein	---	AT2G42760	2.68	1.42	3.68	0.008473	0.035456	-3.13
245318_at	Expressed protein ; supported by full-l	---	AT4G16980	-5.92	-2.57	-3.68	0.008478	0.035465	-3.13
254248_at	serine/threonine kinase serine/threoni	---	AT4G23270	1.72	0.78	3.68	0.008477	0.035465	-3.13
249239_at	MAP kinase ; supported by cDNA: gi_	CPuORF58	AT5G41990 /	1.30	0.38	3.67	0.008484	0.035482	-3.13
245096_at	putative cysteine proteinase inhibitor B	ATCYSA	AT2G40880	-1.38	-0.47	-3.67	0.008487	0.035489	-3.13
262636_at	DEIH-box RNA/DNA helicase identical	NIH	AT1G06670	1.41	0.49	3.67	0.008497	0.035517	-3.13
263873_at	unknown protein predicted by genscan	---	AT2G21860	-1.44	-0.53	-3.67	0.008497	0.035517	-3.13
248405_at	putative protein pectinesterase-like; str	SKS2	AT5G51480	-4.04	-2.02	-3.67	0.008509	0.035563	-3.13

252328_at	Expressed protein ; supported by cDN	---	AT3G48570	-1.33	-0.41	-3.67	0.008517	0.035588	-3.14
259149_at	putative phenylalanine ammonia-lyase	PAL4	AT3G10340	3.78	1.92	3.67	0.008522	0.035601	-3.14
259597_at	ATP-dependent RNA helicase, putativ	---	AT1G27900	1.39	0.48	3.67	0.008526	0.03561	-3.14
245855_at	sulfate transporter ; supported by cDN	SULTR4;1	AT5G13550	1.53	0.61	3.67	0.008531	0.03562	-3.14
252120_at	putative protein lin-10 protein - Rattus	---	AT3G51130	1.38	0.46	3.67	0.008531	0.03562	-3.14
249971_at	dermal glycoprotein - like dermal glyc	---	AT5G19110	-1.65	-0.72	-3.67	0.008539	0.035644	-3.14
250400_at	protein phosphatase 2C -like protein p	---	AT5G10740	1.61	0.69	3.67	0.00854	0.035644	-3.14
248308_at	putative protein similar to unknown pro	---	AT5G52530	1.31	0.39	3.67	0.008548	0.035664	-3.14
245594_at	acylaminoacyl-peptidase like protein	---	AT4G14570	-1.56	-0.64	-3.67	0.008548	0.035664	-3.14
260046_at	Expressed protein ; supported by cDN	---	AT1G73805	3.39	1.76	3.67	0.008555	0.035687	-3.14
260555_at	hypothetical protein predicted by gene	---	AT2G41780	2.23	1.16	3.67	0.008563	0.035702	-3.14
261791_at	unknown protein ; supported by full-ler	---	AT1G16170	-1.98	-0.98	-3.67	0.008563	0.035702	-3.14
252442_at	dUTP pyrophosphatase-like protein d	---	AT3G46940	-1.75	-0.81	-3.67	0.008562	0.035702	-3.14
254593_s_	putative protein IEF SSP 9502, Homo	---	AT4G18900 /	1.42	0.50	3.67	0.008577	0.035752	-3.14
262682_at	anter-specific proline-rich -like protein	---	AT1G75900	-2.65	-1.40	-3.67	0.008583	0.035771	-3.14
250837_at	8-amino-7-oxononanoate synthase - l	ATBIOF	AT5G04620	-1.46	-0.55	-3.67	0.008584	0.035771	-3.14
248497_at	putative protein strong similarity to unk	ATEXO70F1	AT5G50380	1.57	0.65	3.66	0.008591	0.035793	-3.14
259837_at	aquaporin, putative similar to delta tor	---	AT1G52180	-1.59	-0.67	-3.66	0.008599	0.035819	-3.15
262086_at	GTP-binding protein, putative similar t	---	AT1G56050	-1.43	-0.51	-3.66	0.008601	0.035819	-3.15
257247_at	helix-loop-helix DNA-binding protein c	FMA	AT3G24140	1.50	0.59	3.66	0.008617	0.035883	-3.15
265315_at	hypothetical protein predicted by gene	CLASP	AT2G20190	-1.33	-0.41	-3.66	0.00862	0.035888	-3.15
254015_at	putative beta-galactosidase beta-gala	BGAL12	AT4G26140	-1.57	-0.65	-3.66	0.008623	0.035891	-3.15
257965_at	unknown protein ;supported by full-ler	---	AT3G19900	1.57	0.65	3.66	0.008636	0.035942	-3.15
247037_at	putative protein similar to unknown pro	RALFL34	AT5G67070	-4.21	-2.07	-3.66	0.008656	0.036013	-3.15
255981_at	hypothetical protein ;supported by full-	---	AT1G34020	-1.41	-0.50	-3.66	0.008657	0.036013	-3.15
252104_at	putative protein KIAA0851 protein, Ho	RHD4	AT3G51460	1.43	0.52	3.66	0.008659	0.036015	-3.15
247047_at	putative protein contains similarity to u	---	AT5G66650	3.67	1.88	3.66	0.008664	0.036029	-3.15
245983_at	5-formyltetrahydrofolate cyclo-ligase-l	5-FCL	AT5G13050	1.33	0.41	3.66	0.00867	0.036049	-3.15
249791_at	amino acid transporter ; supported by	AAP7	AT5G23810	-1.61	-0.69	-3.66	0.008676	0.036066	-3.16
252553_at	putative protein	---	AT3G45910	-1.32	-0.40	-3.66	0.008679	0.036072	-3.16
259683_at	unknown protein	---	AT1G63050	-1.60	-0.68	-3.66	0.008683	0.036081	-3.16
256165_at	hypothetical protein predicted by gene	---	AT1G48780	-1.46	-0.55	-3.66	0.008694	0.036108	-3.16
266175_at	NAM (no apical meristem)-like protein	ANAC035	AT2G02450	-1.33	-0.41	-3.66	0.008694	0.036108	-3.16
249078_at	phytochelatin synthase (gb|AAD41794	CAD1	AT5G44070	2.34	1.23	3.66	0.008692	0.036108	-3.16
249900_at	unknown protein	emb1211	AT5G22640	-1.32	-0.40	-3.66	0.008696	0.03611	-3.16

260337_at	unknown protein	WRKY57	AT1G69310	1.41	0.49	3.66	0.0087	0.03612	-3.16
248101_at	chaperone GrpE-like protein ;supporte	---	AT5G55200	2.00	1.00	3.65	0.008719	0.036155	-3.16
266391_at	putative strictosidine synthase identica	---	AT2G41290	-1.46	-0.54	-3.65	0.008714	0.036155	-3.16
247331_at	putative protein contains similarity to A	FP3	AT5G63530	1.79	0.84	3.65	0.008719	0.036155	-3.16
264350_at	putative seryl-tRNA synthetase similar	SRS	AT1G11870	-1.56	-0.64	-3.65	0.008715	0.036155	-3.16
254158_at	putative protein dihydrofolate reductas	---	AT4G24380	3.46	1.79	3.65	0.008718	0.036155	-3.16
257228_at	NADPH:quinone oxidoreductase (NQR	NQR	AT3G27890	1.30	0.38	3.65	0.008715	0.036155	-3.16
247598_at	UVB-resistance protein UVR8 - like U	---	AT5G60870	-1.35	-0.43	-3.65	0.008713	0.036155	-3.16
261247_at	hypothetical protein predicted by gene	---	AT1G20070	-3.13	-1.65	-3.65	0.008729	0.036178	-3.16
264592_at	putative prolyl 4-hydroxylase, alpha su	---	AT2G17720	2.13	1.09	3.65	0.008728	0.036178	-3.16
267224_at	hypothetical protein predicted by gens	---	AT2G43990	-1.42	-0.51	-3.65	0.00873	0.036178	-3.16
259976_at	hypothetical protein ;supported by full-	CP12-3	AT1G76560	1.67	0.74	3.65	0.008747	0.036241	-3.16
256130_at	unknown protein contains Pfam profile	---	AT1G18170	-1.41	-0.49	-3.65	0.008752	0.036259	-3.16
257757_at	hypothetical protein predicted by gens	PGSIP1	AT3G18660	-1.31	-0.39	-3.65	0.008756	0.036269	-3.17
251585_at	putative protein hypothetical protein F	---	AT3G58630	-1.67	-0.74	-3.65	0.008765	0.036299	-3.17
246265_at	phosphoribosyl-ATP pyrophosphohyd	AT-IE	AT1G31860	-1.87	-0.90	-3.65	0.008779	0.036349	-3.17
249969_at	putative protein glycine-rich protein G	---	AT5G19090	-1.72	-0.78	-3.65	0.008785	0.03636	-3.17
245670_at	mitochondrial protein (AtJ1), putative	ATJ1	AT1G28210	1.77	0.82	3.65	0.008783	0.03636	-3.17
260398_at	putative RNA-binding domain contains	APUM23	AT1G72320	1.57	0.65	3.65	0.008787	0.036363	-3.17
259129_at	unknown protein predicted by genscar	PTF1	AT3G02150	1.97	0.98	3.65	0.008793	0.036379	-3.17
246919_at	putative protein hypothetical protein -	---	AT5G25460	-8.95	-3.16	-3.65	0.008805	0.036409	-3.17
259899_at	hypothetical protein predicted by gens	---	AT1G71210	1.48	0.57	3.65	0.008803	0.036409	-3.17
264560_at	hypothetical protein predicted by gene	---	AT1G55820	1.29	0.37	3.65	0.008803	0.036409	-3.17
259627_at	unknown protein ; supported by cDNA	---	AT1G42960	-1.38	-0.47	-3.65	0.008813	0.036439	-3.17
246636_at	acid phosphatase-like protein purple a	PAP26	AT5G34850	1.50	0.58	3.64	0.008819	0.036454	-3.17
245087_at	hypothetical protein predicted by gens	DAR2	AT2G39830	1.55	0.63	3.64	0.008821	0.036458	-3.17
265843_at	putative acyl-CoA oxidase possibly a p	ACX5	AT2G35690	-1.35	-0.43	-3.64	0.008827	0.036474	-3.17
261069_at	small G protein, putative similar to GB	ATRABA2B	AT1G07410	-1.27	-0.34	-3.64	0.008833	0.036495	-3.17
261576_at	unknown protein ;supported by full-len	---	AT1G01070	1.96	0.97	3.64	0.008842	0.036503	-3.18
250591_at	alpha galactosyltransferase protein	---	AT5G07720	-1.42	-0.51	-3.64	0.008838	0.036503	-3.18
245175_at	putative protein disulfide-isomerase	UNE5	AT2G47470	1.70	0.77	3.64	0.008839	0.036503	-3.18
265033_at	PSI type III chlorophyll a/b-binding pro	LHCA3	AT1G61520	-1.25	-0.32	-3.64	0.00884	0.036503	-3.18
259440_at	hypothetical protein predicted by gene	BPS1	AT1G01550	1.31	0.39	3.64	0.008853	0.036545	-3.18
253314_at	hypothetical protein	---	AT4G33890	1.29	0.36	3.64	0.008858	0.036557	-3.18
246948_at	cytochrome P450-like protein CYTOC	CYP71B12	AT5G25130	-1.28	-0.36	-3.64	0.008863	0.03657	-3.18

261839_at	unknown protein	---	AT1G16040	1.37	0.46	3.64	0.008877	0.036611	-3.18
247810_at	26S proteasome AAA-ATPase subunit	RPT3	AT5G58290	1.30	0.38	3.64	0.008877	0.036611	-3.18
260070_at	putative helix-loop-helix DNA-binding p	BEE3	AT1G73830	-3.71	-1.89	-3.64	0.008877	0.036611	-3.18
253115_at	putative protein ;supported by full-leng	---	AT4G35910	-1.31	-0.39	-3.64	0.008885	0.036635	-3.18
250500_at	periaxin - like protein periaxin, Rattus	---	AT5G09530	-17.84	-4.16	-3.64	0.008887	0.036636	-3.18
252587_at	putative protein Human (H326) transla	---	AT3G45620	1.75	0.81	3.64	0.008889	0.036637	-3.18
251317_at	putative protein polygalacturonase - Z	---	AT3G61490	-1.57	-0.65	-3.64	0.0089	0.036675	-3.18
253951_at	putative Proline synthetase associate	---	AT4G26860	-1.57	-0.65	-3.64	0.008906	0.036694	-3.18
247595_at	ring finger protein - like ring finger pro	---	AT5G60820	-1.46	-0.55	-3.64	0.008915	0.036721	-3.18
251422_at	transport protein subunit - like S61B_A	---	AT3G60540	2.03	1.02	3.64	0.008915	0.036721	-3.18
263160_at	oligouridylate binding protein, putative	UBP1A	AT1G54080	1.36	0.44	3.64	0.008918	0.036725	-3.18
258687_at	unknown protein	---	AT3G07860	1.50	0.59	3.64	0.008927	0.036755	-3.19
267556_at	putative beta-galactosidase ; supporte	BGAL9	AT2G32810	-1.40	-0.49	-3.63	0.008945	0.036825	-3.19
261471_at	hypothetical protein contains similarity	---	AT1G14460	-1.62	-0.70	-3.63	0.008949	0.03683	-3.19
247692_s_	histone H4 - like protein histone H4, Z	---	AT5G59690 /	-1.80	-0.85	-3.63	0.00895	0.03683	-3.19
252604_at	high-affinity nitrate transporter - like pr	NRT2.6	AT3G45060	-2.58	-1.37	-3.63	0.00896	0.036859	-3.19
258289_at	hypothetical protein predicted by gene	---	AT3G23450	-1.29	-0.37	-3.63	0.00896	0.036859	-3.19
251068_at	putative protein several protein kinase	STN8	AT5G01920	-1.61	-0.69	-3.63	0.008968	0.036886	-3.19
259029_at	putative oxysterol-binding protein simil	ORP3B	AT3G09300	-1.41	-0.49	-3.63	0.009021	0.037093	-3.20
254606_at	nodulin-26 - like protein major intrinsic	NLM1	AT4G19030	1.28	0.36	3.63	0.009023	0.037093	-3.20
252520_at	receptor-like protein kinase homolog I	---	AT3G46370	-1.96	-0.97	-3.63	0.009024	0.037093	-3.20
251277_at	dynamin-like protein phragmoplastin 5	ADL1B	AT3G61760	1.25	0.32	3.63	0.009026	0.037097	-3.20
264654_s_	putative sugar transport protein, ERD6	---	AT1G08890 /	-1.63	-0.70	-3.63	0.00904	0.037149	-3.20
256671_at	unknown protein	IQD3	AT3G52290	-1.55	-0.63	-3.62	0.009056	0.037194	-3.20
262804_at	putative RNA-binding protein similar t	---	AT1G20880	1.44	0.52	3.62	0.009054	0.037194	-3.20
266928_at	putative phosphomannomutase ;supp	PMM	AT2G45790	-1.50	-0.59	-3.62	0.009056	0.037194	-3.20
258027_at	hypothetical protein predicted by gene	---	AT3G19515	-1.34	-0.42	-3.62	0.009058	0.037196	-3.20
250366_at	putative protein predicted proteins in c	---	AT5G11420	-6.17	-2.63	-3.62	0.009063	0.037201	-3.20
245390_at	putative protein ;supported by full-leng	---	AT4G17650	1.78	0.83	3.62	0.009061	0.037201	-3.20
255842_at	putative serine carboxypeptidase II	scpl46	AT2G33530	-2.04	-1.03	-3.62	0.009081	0.037268	-3.20
259948_at	unknown protein similar to LIGATIN G	---	AT1G71350	1.55	0.64	3.62	0.009098	0.037323	-3.21
265464_at	putative myosin heavy chain	---	AT2G37080	-1.27	-0.34	-3.62	0.009097	0.037323	-3.21
267484_at	E2, ubiquitin-conjugating enzyme 2 (U	ATUBC2	AT2G02760	1.33	0.41	3.62	0.009105	0.037332	-3.21
256415_at	unknown protein ; supported by full-ler	---	AT3G11210	-2.35	-1.23	-3.62	0.009102	0.037332	-3.21
266050_at	putative SNF2/SWI2 family transcriptio	---	AT2G40770	-1.28	-0.36	-3.62	0.009104	0.037332	-3.21

255880_at	hypothetical protein predicted by gens	---	AT1G67060	1.30	0.38	3.62	0.009107	0.037336	-3.21
261854_at	unknown protein	---	AT1G50670	-1.26	-0.33	-3.62	0.009114	0.037359	-3.21
249586_at	putative protein predicted proteins, Ar	---	AT5G37840	2.06	1.04	3.62	0.009119	0.037372	-3.21
260142_at	unknown protein ; supported by cDNA	---	AT1G71900	-1.40	-0.49	-3.62	0.009122	0.037375	-3.21
255991_at	unknown protein	---	AT1G29820	-1.64	-0.71	-3.62	0.009126	0.037387	-3.21
264007_at	putative proline-rich protein	ATPRP2	AT2G21140	-5.52	-2.47	-3.62	0.009164	0.03753	-3.21
245432_at	putative serine protease-like protein	---	AT4G17100	-1.27	-0.35	-3.62	0.009164	0.03753	-3.21
261903_at	chromomethylase identical to GB:AAC	CMT1	AT1G80740	1.27	0.35	3.61	0.009173	0.037553	-3.22
262797_at	putative sugar transporter protein nea	TMT1	AT1G20840	1.67	0.74	3.61	0.009172	0.037553	-3.22
265940_at	putative nucleosome assembly protein	NAP1;2	AT2G19480	1.33	0.41	3.61	0.009181	0.037574	-3.22
244944_s_	ribosomal protein L16	---	---	1.52	0.61	3.61	0.009182	0.037574	-3.22
260028_at	unknown protein ; supported by cDNA	---	AT1G29980	-3.18	-1.67	-3.61	0.009195	0.037622	-3.22
249839_at	Expressed protein ; supported by cDN	---	AT5G23405	1.38	0.46	3.61	0.009204	0.037651	-3.22
250298_at	putative protein NLI-interacting factor	---	AT5G11860	1.36	0.45	3.61	0.009216	0.037694	-3.22
255891_at	hypothetical protein predicted by gens	EGY3	AT1G17870	-1.41	-0.49	-3.61	0.009222	0.037706	-3.22
257169_at	Expressed protein ; supported by full-l	AtSec20	AT3G24315	-1.39	-0.47	-3.61	0.009222	0.037706	-3.22
250199_at	putative protein contains similarity to li	MPL1	AT5G14180	2.72	1.44	3.61	0.009257	0.037834	-3.22
262088_at	unknown protein	---	AT1G56020	-1.31	-0.39	-3.61	0.009256	0.037834	-3.22
250042_at	putative protein non-consensus GC d	---	AT5G18420	1.33	0.41	3.61	0.009261	0.037845	-3.23
251095_at	putative protein hypothetical protein A	---	AT5G01510	-1.50	-0.59	-3.61	0.009265	0.037854	-3.23
267538_at	putative DNA binding protein ; support	---	AT2G41870	-1.28	-0.35	-3.61	0.009277	0.037896	-3.23
266555_at	G-box binding bZIP transcription factor	GBF3	AT2G46270	1.95	0.97	3.60	0.009294	0.037958	-3.23
248032_at	myosin heavy chain-like	---	AT5G55860	1.45	0.53	3.60	0.009319	0.038051	-3.23
261843_at	unknown protein	---	AT1G16180	1.30	0.38	3.60	0.009325	0.038073	-3.23
249325_at	urophorphyrin III methylase (gb|AAB92	UPM1	AT5G40850	1.45	0.54	3.60	0.009332	0.03808	-3.23
261605_at	CDPK-related protein kinase, putative	---	AT1G49580	-1.43	-0.52	-3.60	0.009331	0.03808	-3.23
260552_at	putative glyoxalase II ; supported by c	GLX2-1	AT2G43430	-1.27	-0.34	-3.60	0.00933	0.03808	-3.23
256877_at	unknown protein ;supported by full-ler	---	AT3G26470	2.20	1.14	3.60	0.009336	0.038091	-3.23
249767_at	acidic endochitinase (dbj|BAA21861.1)	---	AT5G24090	2.18	1.12	3.60	0.009341	0.038103	-3.23
266273_at	putative zinc transporter	MTPB1	AT2G29410	2.93	1.55	3.60	0.009344	0.038108	-3.24
264701_at	hypothetical protein similar to hypothet	---	AT1G70160	1.36	0.44	3.60	0.009348	0.038112	-3.24
259806_at	mysoin-like protein similar to GI:2351	---	AT1G47900	-1.54	-0.62	-3.60	0.009348	0.038112	-3.24
253997_at	disease resistance protein RPS2 ; sup	RPS2	AT4G26090	2.45	1.29	3.60	0.009351	0.038114	-3.24
267383_at	unknown protein	---	AT2G44360	1.26	0.33	3.60	0.009352	0.038114	-3.24
257092_at	unknown protein	DDL	AT3G20550	1.45	0.54	3.60	0.00936	0.038126	-3.24

259348_at	hypothetical protein may contain C-ter	---	AT3G03770	-1.61	-0.69	-3.60	0.00936	0.038126	-3.24
245263_at	PSII D1 protein processing enzyme ; s	---	AT4G17740	-1.30	-0.38	-3.60	0.009359	0.038126	-3.24
256805_at	unknown protein contains similarity to	---	AT3G20930	-1.84	-0.88	-3.60	0.009363	0.038133	-3.24
250318_at	dihydropyrimidinase ; supported by cD	---	AT5G12200	1.54	0.62	3.60	0.009368	0.038145	-3.24
259186_at	unknown protein similar to possible ap	---	AT3G01590	-1.37	-0.46	-3.60	0.00938	0.038186	-3.24
266192_at	unknown protein	---	AT2G39080	-1.27	-0.35	-3.60	0.009389	0.038216	-3.24
262753_at	putative 3-deoxy-D-manno-2-octulosor	ATKDSA2	AT1G16340	-1.32	-0.40	-3.60	0.009392	0.038221	-3.24
257369_at	hypothetical protein predicted by gens	BPC7	AT2G35550	1.37	0.45	3.60	0.009399	0.038243	-3.24
254608_at	major intrinsic protein (MIP)- like nodu	NIP1;2	AT4G18910	1.99	0.99	3.59	0.009422	0.038332	-3.24
262596_at	putative phosphatidic acid phosphatas	LPP2	AT1G15080	-1.38	-0.47	-3.59	0.009425	0.038335	-3.24
265366_at	putative N-acetylglucosaminyltransfera	---	AT2G13290	1.35	0.44	3.59	0.009432	0.038357	-3.25
257611_at	unknown protein	---	AT3G26580	1.47	0.56	3.59	0.009436	0.038365	-3.25
262346_at	unknown protein similar to hypothetica	---	AT1G63980	-1.47	-0.56	-3.59	0.009438	0.038367	-3.25
251058_at	putative protein	---	AT5G01790	-2.74	-1.45	-3.59	0.009453	0.038414	-3.25
251695_at	putative protein hypothetical proteins -	---	AT3G56590	-1.61	-0.69	-3.59	0.009451	0.038414	-3.25
251113_at	hypothetical protein	---	AT5G01370	-1.42	-0.50	-3.59	0.009455	0.038418	-3.25
246296_at	putative protein hypothetical protein A	---	AT3G56750	-1.30	-0.37	-3.59	0.009471	0.038475	-3.25
245913_at	predicted protein	---	AT5G19860	1.36	0.44	3.59	0.009489	0.038542	-3.25
247708_at	putative protein COP1-interacting prot	---	AT5G59550	2.97	1.57	3.59	0.009494	0.038548	-3.25
255995_at	receptor-like serine/threonine kinase,	RKF1	AT1G29750	1.44	0.52	3.59	0.009493	0.038548	-3.25
259365_at	unknown protein ; supported by cDNA	---	AT1G13300	3.15	1.66	3.59	0.009508	0.038598	-3.25
261300_at	hypothetical protein predicted by gene	---	AT1G48560	-1.38	-0.47	-3.59	0.00951	0.0386	-3.25
257213_at	mitochondrial NAD-dependent malate	---	AT3G15020	1.66	0.73	3.59	0.009517	0.038618	-3.25
257982_at	unknown protein similar to TYPE II DN	ATTOP6B	AT3G20780	-1.44	-0.52	-3.59	0.009521	0.038626	-3.26
249831_at	putative protein contains similarity to g	---	AT5G23340	1.71	0.77	3.59	0.009522	0.038626	-3.26
255017_at	hypothetical protein ;supported by full-	CNX7	AT4G10100	1.34	0.42	3.59	0.009525	0.038627	-3.26
261469_at	unknown protein	AtRLP4	AT1G28340	-1.32	-0.40	-3.59	0.009526	0.038627	-3.26
249862_at	PGPD14 protein ;supported by full-len	---	AT5G22920	-1.84	-0.88	-3.58	0.009531	0.038643	-3.26
262329_at	hypothetical protein similar to hypothet	---	AT1G64090	-1.27	-0.35	-3.58	0.009533	0.038643	-3.26
246135_at	putative protein non-consensus donor	---	AT5G20885	-1.75	-0.81	-3.58	0.009542	0.038665	-3.26
245014_at	ATPase beta subunit	---	---	-1.26	-0.33	-3.58	0.009542	0.038665	-3.26
255150_at	putative xylan endohydrolase	---	AT4G08160	-1.63	-0.70	-3.58	0.009544	0.038669	-3.26
255497_at	hypothetical protein similar to A. thalia	UNE12	AT4G02590	1.32	0.40	3.58	0.009548	0.038675	-3.26
257902_at	receptor kinase, putative similar to rec	---	AT3G28450	1.60	0.68	3.58	0.009549	0.038676	-3.26
262762_at	phosphoribosyl diphosphate synthase	---	AT1G10700	3.23	1.69	3.58	0.009551	0.038676	-3.26

245074_at	putative protein kinase contains a prot	---	AT2G23200	2.70	1.43	3.58	0.009574	0.03876	-3.26
250446_at	nucleoid DNA-binding protein cnd41 -	---	AT5G10770	1.70	0.77	3.58	0.009578	0.03877	-3.26
249885_at	putative protein strong similarity to unk	F8H	AT5G22940	-1.71	-0.78	-3.58	0.009585	0.038791	-3.26
262507_at	receptor-like protein kinase, putative s	---	AT1G11330	1.42	0.51	3.58	0.009587	0.038794	-3.26
263582_at	unknown protein similar to hypothetica	LYM2	AT2G17120	1.58	0.66	3.58	0.009592	0.038807	-3.26
248921_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G45950	-2.15	-1.10	-3.58	0.009595	0.038807	-3.26
257829_at	unknown protein	SNM1	AT3G26680	1.67	0.74	3.58	0.009595	0.038807	-3.26
253013_at	heat shock protein 70 like protein dna	mtHsc70-1	AT4G37910	1.74	0.80	3.58	0.009603	0.038817	-3.26
245248_at	Expressed protein ; supported by cDN	ATB' GAMM	AT4G15415	-1.23	-0.30	-3.58	0.0096	0.038817	-3.26
261048_at	flavonol 3-o-glucosyltransferase, puta	UGT72B3	AT1G01420	-1.39	-0.48	-3.58	0.009602	0.038817	-3.26
261897_at	hypothetical protein predicted by gene	---	AT1G80950	1.36	0.45	3.58	0.009617	0.038866	-3.27
253216_at	cyclophilin - like protein cyclophilin, Ar	---	AT4G34960	-1.41	-0.49	-3.58	0.009624	0.038879	-3.27
260172_s_	putative histidinol-phosphate aminotra	---	AT1G71920 /	-1.47	-0.56	-3.58	0.009622	0.038879	-3.27
266449_at	hypothetical protein predicted by gens	AT-P4H-1	AT2G43080	1.39	0.47	3.58	0.009635	0.038912	-3.27
258182_at	1-D-deoxyxylulose 5-phosphate synth	DXPS1	AT3G21500	2.33	1.22	3.58	0.009633	0.038912	-3.27
262534_at	unknown protein contains Pfam profile	SHA	AT1G17040	1.48	0.56	3.58	0.009651	0.038962	-3.27
249743_at	beta-glucosidase	BGLU31	AT5G24540	5.12	2.36	3.58	0.009651	0.038962	-3.27
261927_at	RING-H2 zinc finger protein ATL5, pu	---	AT1G22500	1.93	0.95	3.58	0.009653	0.038962	-3.27
265040_at	G-box binding factor, GBF4 Identical t	GBF4	AT1G03970	-1.47	-0.56	-3.57	0.009656	0.038969	-3.27
263909_at	hypothetical protein predicted by gens	DML1	AT2G36490	-1.61	-0.69	-3.57	0.009666	0.039003	-3.27
245524_at	cytochrome c oxidoreductase like prote	---	AT4G15920	-2.26	-1.17	-3.57	0.009671	0.039011	-3.27
256616_at	hypothetical protein similar to unknowr	---	AT3G22260	1.56	0.65	3.57	0.00967	0.039011	-3.27
253254_at	predicted protein	SQS2	AT4G34650	-1.78	-0.84	-3.57	0.009687	0.039066	-3.27
263037_at	conserved hypothetical protein	---	AT1G23230	1.41	0.49	3.57	0.009706	0.039135	-3.28
245167_s_	putative synaptobrevin ;supported by	ATVAMP723	AT2G33110 /	1.27	0.35	3.57	0.009713	0.039156	-3.28
252831_at	2-dehydro-3-deoxyphosphoheptonate	DHS1	AT4G39980	2.40	1.26	3.57	0.009718	0.03917	-3.28
264443_at	Expressed protein ; supported by full-l	---	AT1G27385	-1.48	-0.56	-3.57	0.009727	0.039199	-3.28
260875_at	hypothetical protein predicted by gene	SKP2A	AT1G21410	1.78	0.83	3.57	0.009732	0.039213	-3.28
266122_at	putative helicase ; supported by cDNA	ETL1	AT2G02090	1.31	0.39	3.57	0.009747	0.039268	-3.28
266042_s_	hypothetical protein	---	AT2G07734	1.56	0.64	3.57	0.009749	0.039269	-3.28
247032_at	putative protein strong similarity to unk	SDN3	AT5G67240	1.31	0.39	3.57	0.009751	0.03927	-3.28
263268_at	unknown protein	---	---	-1.34	-0.42	-3.57	0.009762	0.039305	-3.28
254982_at	putative protein ; supported by cDNA:	---	AT4G10470	-1.41	-0.49	-3.57	0.009772	0.039341	-3.28
247999_at	E2, ubiquitin-conjugating enzyme, put	UBC30	AT5G56150	1.34	0.43	3.57	0.009778	0.039357	-3.28
250929_at	putative protein ; supported by cDNA:	---	AT5G03290	1.54	0.63	3.56	0.009784	0.039374	-3.28

249050_at	cyclin-dependent protein kinase-like pr	---	AT5G44290	1.36	0.44	3.56	0.0098	0.03943	-3.29
257072_at	myrosinase-associated protein, putati	---	AT3G14220	-1.74	-0.80	-3.56	0.009809	0.039459	-3.29
267561_at	putative protein kinase contains a prot	---	AT2G45590	-1.63	-0.71	-3.56	0.009834	0.039555	-3.29
250040_at	putative protein predicted proteins, Ar	---	AT5G18390	-1.28	-0.36	-3.56	0.009847	0.039599	-3.29
248041_at	unknown protein ;supported by full-ler	emb2731	AT5G55940	-1.26	-0.34	-3.56	0.009849	0.0396	-3.29
262809_at	putative glycogen synthase strong sim	ATSS3	AT1G11720	-2.05	-1.04	-3.56	0.009856	0.039621	-3.29
260453_s_	unknown protein	---	AT1G72510 /	1.46	0.55	3.56	0.00986	0.03963	-3.29
260563_at	putative glucosyltransferase	UGT74F1	AT2G43840	1.39	0.48	3.56	0.009862	0.03963	-3.29
249211_at	putative protein similar to unknown pro	---	AT5G42680	-1.85	-0.88	-3.56	0.009864	0.039635	-3.29
261902_at	unknown protein ; supported by full-ler	PLMT	AT1G80860	-1.30	-0.38	-3.56	0.00987	0.039645	-3.29
259975_at	putative cinnamoyl-CoA reductase sim	---	AT1G76470	2.40	1.26	3.56	0.00987	0.039645	-3.29
260733_at	RNA-binding protein, putative similar t	---	AT1G17640	1.41	0.50	3.56	0.009876	0.039662	-3.29
264148_at	NAM (no apical meristem)-like protein	ANAC003	AT1G02220	10.70	3.42	3.56	0.009887	0.0397	-3.30
254922_at	RING-H2 finger protein RHA1a -like pr	RHA1A	AT4G11370	5.31	2.41	3.56	0.009892	0.039712	-3.30
260305_at	putative ADP-ribosylation factor 1 near	ARFA1D	AT1G70490	-1.40	-0.48	-3.56	0.009897	0.039723	-3.30
246204_at	putative protein ; supported by cDNA:	---	AT4G37020	-1.34	-0.42	-3.56	0.009901	0.039732	-3.30
262710_at	unknown protein ESTs gb|T04357 and	---	AT1G16210	1.28	0.36	3.56	0.009905	0.039741	-3.30
254975_at	putative Fe(II)/ascorbate oxidase SRG	---	AT4G10500	11.97	3.58	3.55	0.009911	0.03976	-3.30
245269_at	hypothetical protein ; supported by cDI	---	AT4G14500	-1.35	-0.43	-3.55	0.009919	0.039783	-3.30
250898_at	putative protein ; supported by cDNA:	ADK2	AT5G03300	-1.43	-0.52	-3.55	0.009926	0.039804	-3.30
256332_at	trihelix DNA-binding protein (GT2) ide	GT2	AT1G76890	-1.92	-0.94	-3.55	0.009936	0.039837	-3.30
254977_s_	subtilisin-like serine protease contains	---	AT4G10520 /	1.25	0.32	3.55	0.009938	0.039837	-3.30
254372_at	putative protein predicted proteins, Ar	---	AT4G21620	-1.76	-0.81	-3.55	0.009939	0.039837	-3.30
262582_at	hypothetical protein Is a member of the	---	AT1G15410	-2.19	-1.13	-3.55	0.009952	0.03988	-3.30
253470_s_	putative protein dnaK-type molecular c	SDH3-2	AT4G32210 /	1.29	0.36	3.55	0.009969	0.039943	-3.30
256007_at	allinase, putative similar to allinase GI	SAMC2	AT1G34065	-1.47	-0.56	-3.55	0.009979	0.039976	-3.31
246763_at	NHE1 Na+/H+ exchanger ; supported	NHX1	AT5G27150	1.61	0.69	3.55	0.009986	0.039997	-3.31
257311_at	phosphate transporter, putative contai	PHT2;1	AT3G26570	-1.35	-0.43	-3.55	0.009988	0.039998	-3.31
262074_at	glutathione S-transferase, putative sin	ATGSTU15	AT1G59670	1.66	0.73	3.55	0.009992	0.040005	-3.31
247468_at	ARF1-binding protein ; supported by c	ARF2	AT5G62000	-1.35	-0.44	-3.55	0.010034	0.040166	-3.31
263831_at	putative ferritin	ATFER4	AT2G40300	1.57	0.65	3.54	0.010046	0.040193	-3.31
246304_at	acyl-coA dehydrogenase Mus musculu	ACX4	AT3G51840	1.49	0.58	3.54	0.010045	0.040193	-3.31
266047_at	unknown protein	---	AT2G40800	-1.42	-0.50	-3.54	0.010045	0.040193	-3.31
246212_at	putative protein ; supported by cDNA:	SPT	AT4G36930	2.39	1.25	3.54	0.010048	0.040193	-3.31
264002_at	putative DnaJ protein ;supported by fu	---	AT2G22360	1.46	0.55	3.54	0.010049	0.040193	-3.31

265605_at	putative cellulose synthase catalytic su	CESA10	AT2G25540	-1.24	-0.31	-3.54	0.010062	0.040237	-3.31
252026_at	serine protein kinase - like serine prot	SRPK4	AT3G53030	-1.34	-0.42	-3.54	0.010075	0.040281	-3.32
258127_at	unknown protein	---	AT3G24570	-1.29	-0.36	-3.54	0.010089	0.040315	-3.32
245952_at	putative protein predicted proteins, Ar	---	AT5G28500	-1.43	-0.51	-3.54	0.01009	0.040315	-3.32
253972_at	putative protein Uvi31, Schizosacchar	CPSUFE	AT4G26500	-1.23	-0.30	-3.54	0.010089	0.040315	-3.32
245914_at	putative protein outer membrane prote	OEP80	AT5G19620	-1.35	-0.44	-3.54	0.010087	0.040315	-3.32
254668_at	neoxanthin cleavage enzyme - like pr	NCED2	AT4G18350	1.43	0.51	3.54	0.010097	0.040334	-3.32
257174_at	uracil phosphoribosyltransferase, puta	---	AT3G27190	1.45	0.54	3.54	0.010105	0.040358	-3.32
254335_at	putative protein alternative oxidase, M	IM	AT4G22260	1.29	0.37	3.54	0.010108	0.040365	-3.32
258071_s_	unknown protein	---	AT3G26070 /	-1.52	-0.61	-3.54	0.010112	0.040373	-3.32
256008_s_	allinase, putative similar to allinase GI	---	AT1G34040 /	1.33	0.41	3.54	0.01012	0.040397	-3.32
263699_at	putative potassium transporter similar	KUP10	AT1G31120	1.53	0.61	3.54	0.010139	0.040467	-3.32
266037_at	putative protein kinase contains a prot	---	AT2G05940	2.40	1.26	3.54	0.010144	0.040481	-3.32
246115_at	putative protein chloroplast outer enve	---	AT5G20300	1.39	0.47	3.54	0.01015	0.040495	-3.32
264141_at	hypothetical protein predicted by gene	---	AT1G79090	1.27	0.35	3.54	0.010152	0.040497	-3.32
258015_at	unknown protein	---	AT3G19340	-1.36	-0.45	-3.54	0.010154	0.040499	-3.32
247146_at	unknown protein	---	AT5G65610	-1.57	-0.65	-3.54	0.01017	0.040548	-3.33
245828_at	transcription factor, putative similar to	VIM1	AT1G57820	-1.39	-0.48	-3.54	0.010169	0.040548	-3.33
261640_at	permease, putative similar to permeas	---	AT1G49960	1.38	0.46	3.53	0.010188	0.040614	-3.33
253339_at	metal-transporting P-type ATPase ; su	PAA1	AT4G33520	1.55	0.63	3.53	0.010191	0.040617	-3.33
254021_at	putative protein cell death suppressor	ACD1-LIKE	AT4G25650	-1.40	-0.48	-3.53	0.010193	0.040617	-3.33
258758_at	putative RING zinc finger protein cont	---	AT3G10810	-1.54	-0.62	-3.53	0.010212	0.040689	-3.33
263593_at	hypothetical protein predicted by gens	EMB975	AT2G01860	-1.42	-0.50	-3.53	0.010221	0.040716	-3.33
247529_at	monosaccharide transporter STP3	---	AT5G61520	1.33	0.41	3.53	0.010226	0.040729	-3.33
252205_at	hypothetical protein various predicted	---	AT3G50350	-1.44	-0.53	-3.53	0.010228	0.040729	-3.33
250187_at	putative protein predicted proteins, Ar	---	AT5G14370	-1.66	-0.73	-3.53	0.01023	0.04073	-3.33
258643_at	unknown protein ;supported by full-ler	ATAB2	AT3G08010	-1.27	-0.34	-3.53	0.010241	0.040766	-3.33
246293_at	SigA binding protein ; supported by cD	SIB1	AT3G56710	3.50	1.81	3.53	0.010268	0.040869	-3.34
265718_at	putative WRKY DNA-binding protein ;	WRKY3	AT2G03340	1.36	0.44	3.53	0.010276	0.040892	-3.34
263824_at	putative WD-40 repeat protein	---	AT2G40360	1.65	0.72	3.53	0.010278	0.040893	-3.34
252079_at	MAP kinase ; supported by cDNA: gi_	CPuORF44	AT3G51630 /	1.29	0.37	3.53	0.010293	0.040939	-3.34
261280_at	hypothetical protein predicted by gene	---	AT1G05860	-1.50	-0.58	-3.53	0.010292	0.040939	-3.34
250478_at	non-phototropic hypocotyl 3-like prote	DOT3	AT5G10250	-1.42	-0.50	-3.52	0.010306	0.040982	-3.34
256042_at	hypothetical protein predicted by gene	---	AT1G07220	1.25	0.33	3.52	0.010311	0.040997	-3.34
266540_at	hypothetical protein predicted by gens	---	AT2G35310	-1.29	-0.37	-3.52	0.010332	0.041072	-3.34

264840_at	unknown protein similar to leucine-rich	---	AT1G03440	-1.30	-0.38	-3.52	0.010336	0.041082	-3.34
259060_at	hypothetical protein predicted by gens	---	AT3G07400	-1.45	-0.54	-3.52	0.010338	0.041082	-3.34
266266_at	putative enolase (2-phospho-D-glycera	---	AT2G29560	-1.40	-0.48	-3.52	0.010343	0.041094	-3.34
260862_at	unknown protein	SEU	AT1G43850	1.31	0.39	3.52	0.010348	0.041107	-3.34
261608_at	unknown protein similar to putative est	---	AT1G49650	-1.35	-0.44	-3.52	0.010354	0.041124	-3.35
259005_at	unknown protein similar to nodule-spe	---	AT3G01930	1.46	0.54	3.52	0.010357	0.041129	-3.35
262897_at	hypothetical protein predicted by gene	CCB4	AT1G59840	-1.99	-0.99	-3.52	0.010359	0.041131	-3.35
262595_at	putative ethylene responsive element S	SHN1	AT1G15360	-1.33	-0.41	-3.52	0.010371	0.041171	-3.35
255630_at	putative phosphoribosylanthranilate tra	---	AT4G00700	9.68	3.28	3.52	0.010374	0.041175	-3.35
252285_at	calmodulin-binding heat-shock - like p	---	AT3G49050	-1.32	-0.41	-3.52	0.010379	0.041187	-3.35
260062_at	hypothetical protein contains Pfam pro	---	AT1G73710	1.40	0.48	3.52	0.010383	0.041194	-3.35
262513_at	unknown protein ; supported by cDNA	---	AT1G34270	-1.34	-0.42	-3.52	0.010388	0.041209	-3.35
255542_at	hypothetical protein	---	AT4G01860	1.39	0.48	3.52	0.010392	0.041218	-3.35
262783_at	receptor-kinase isolog	---	AT1G10850	-1.81	-0.86	-3.52	0.010397	0.04123	-3.35
250028_at	putative protein similar to unknown pro	---	AT5G18130	1.32	0.40	3.52	0.010409	0.041245	-3.35
254290_at	hypothetical protein	---	AT4G23000	1.50	0.59	3.52	0.010409	0.041245	-3.35
258797_at	auxin-induced protein identical to GB:A	IAA16	AT3G04730	-1.50	-0.59	-3.52	0.010405	0.041245	-3.35
246201_at	minor allergen ;supported by full-length	---	AT4G36750	-1.26	-0.33	-3.52	0.010411	0.041245	-3.35
248176_at	putative protein contains similarity to u	Fh5	AT5G54650	1.76	0.82	3.52	0.010409	0.041245	-3.35
257422_at	hypothetical protein Contains similarity	---	AT1G11940	1.29	0.37	3.52	0.01041	0.041245	-3.35
259434_at	unknown protein	---	AT1G01490	1.30	0.37	3.52	0.01042	0.041271	-3.35
246838_at	flap endonuclease - like protein OsFE	---	AT5G26680	1.33	0.42	3.52	0.010424	0.041279	-3.35
252132_at	putative LEA protein Picea glauca late	---	AT3G50790	-1.77	-0.82	-3.52	0.01043	0.041296	-3.35
255478_at	putative protein ;supported by full-leng	EID1	AT4G02440	-1.35	-0.44	-3.52	0.010434	0.041305	-3.35
262975_at	zinc finger protein, putative similar to	STH2	AT1G75540	-1.48	-0.57	-3.52	0.010439	0.041316	-3.35
245197_at	F12A21.7 hypothetical protein;support	---	AT1G67800	1.31	0.39	3.51	0.010448	0.041347	-3.36
252282_at	6-phosphogluconolactonase - like pro	---	AT3G49360	-1.28	-0.35	-3.51	0.010454	0.041361	-3.36
266458_at	unknown protein ;supported by full-ler	---	AT2G47710	1.28	0.35	3.51	0.01046	0.04138	-3.36
261100_at	RNA polymerase IIA large subunit, pu	NRPD1A	AT1G63020	1.33	0.42	3.51	0.010467	0.041391	-3.36
251061_at	putative protein hypothetical protein A	---	AT5G01830	2.00	1.00	3.51	0.010465	0.041391	-3.36
251152_at	RAN GTPase activating protein 1 prote	RANGAP1	AT3G63130	-1.54	-0.62	-3.51	0.010481	0.041442	-3.36
267028_at	putative WRKY-type DNA binding prot	WRKY33	AT2G38470	4.35	2.12	3.51	0.010487	0.041458	-3.36
264680_at	hypothetical protein predicted by gene	---	AT1G65510	1.82	0.87	3.51	0.010493	0.041472	-3.36
266009_at	putative kinesin heavy chain	---	AT2G37420	1.32	0.40	3.51	0.01051	0.041532	-3.36
245183_at	putative protein similarity to predicted	---	AT5G12440	-1.45	-0.54	-3.51	0.010514	0.041543	-3.36

246691_at	putative protein predicted proteins - Ar	---	---	-1.26	-0.33	-3.51	0.010533	0.041602	-3.36
255341_at	putative receptor-like protein kinase	---	AT4G04500	5.34	2.42	3.51	0.010532	0.041602	-3.36
249456_at	unknown protein ;supported by full-ler	---	AT5G39410	-1.35	-0.43	-3.51	0.010543	0.041635	-3.36
266204_at	hypothetical protein predicted by gens	---	AT2G02410	-1.47	-0.55	-3.51	0.010545	0.041635	-3.36
249580_at	putative protein predicted proteins, Ar	---	AT5G37740	1.43	0.52	3.51	0.010554	0.041663	-3.37
247994_at	RNA-binding protein-like	---	AT5G56140	-1.38	-0.47	-3.51	0.01056	0.041683	-3.37
257832_at	light regulated protein, putative similar	CCL	AT3G26740	1.30	0.38	3.51	0.01057	0.041715	-3.37
246036_at	alpha-galactosidase - like protein alph	AtAGAL2	AT5G08370	-1.81	-0.85	-3.51	0.010577	0.041726	-3.37
248164_at	putative protein similar to unknown pro	PBP1	AT5G54490	5.00	2.32	3.51	0.010576	0.041726	-3.37
267304_at	putative Fe(II) transport protein	ZIP6	AT2G30080	1.43	0.52	3.50	0.010586	0.041756	-3.37
254180_at	putative protein hin1 protein homolog,	---	AT4G23930	-1.60	-0.68	-3.50	0.010595	0.041781	-3.37
266150_s_	hypothetical protein	---	AT2G12290 /	2.27	1.18	3.50	0.010601	0.0418	-3.37
245873_at	bHLH transcription factor GBOF-1, pu	CIB5	AT1G26260	-1.43	-0.51	-3.50	0.010627	0.041896	-3.37
254141_at	glucose-6-phosphate isomerase gluco	PGI1	AT4G24620	-1.31	-0.39	-3.50	0.010639	0.041934	-3.37
250088_at	APG5 (autophagy 5)-like protein	APG5	AT5G17290	1.32	0.41	3.50	0.010646	0.041955	-3.38
259608_at	unknown protein	ECT9	AT1G27960	-1.36	-0.44	-3.50	0.010652	0.041971	-3.38
256633_at	unknown protein	GATL10	AT3G28340	3.87	1.95	3.50	0.010662	0.042002	-3.38
246391_at	unknown protein ; supported by cDNA:	---	AT1G77350	-1.39	-0.48	-3.50	0.010664	0.042003	-3.38
256077_at	hypothetical protein contains similarity	---	AT1G18090	-1.41	-0.50	-3.50	0.010677	0.042046	-3.38
250038_at	disease resistance protein -like diseas	---	AT5G18360	-1.50	-0.59	-3.50	0.010691	0.042094	-3.38
249002_at	putative protein contains similarity to ri	---	AT5G44520	-1.42	-0.50	-3.50	0.010699	0.042122	-3.38
251617_at	putative protein hypothetical protein T	---	AT3G58000	-1.29	-0.37	-3.50	0.010711	0.042154	-3.38
245023_at	PSII I protein	---	---	-1.62	-0.70	-3.50	0.010712	0.042154	-3.38
255834_at	putative RNA-binding protein	---	AT2G33410	1.24	0.31	3.50	0.010713	0.042154	-3.38
264601_at	hypothetical protein similar to hypothet	---	AT1G04540	-1.33	-0.41	-3.49	0.010724	0.042188	-3.38
259258_at	putative ribulose-1,5-bisphosphate ca	---	AT3G07670	-1.63	-0.70	-3.49	0.010743	0.042258	-3.38
250404_at	CCR4-ASSOCIATED FACTOR -like	---	AT5G10960	1.26	0.33	3.49	0.010757	0.042297	-3.39
262089_s_	hypothetical protein predicted by gene	---	AT1G55980 /	-1.47	-0.56	-3.49	0.010756	0.042297	-3.39
258439_at	lipoamide dehydrogenase precursor id	mtLPD2	AT3G17240	1.53	0.62	3.49	0.010759	0.042297	-3.39
248221_at	vacuolar sorting protein-like; embryoge	VPS26A	AT5G53530	-1.26	-0.33	-3.49	0.010777	0.042361	-3.39
250518_at	Expressed protein ; supported by cDN	---	AT5G08139	1.27	0.34	3.49	0.010782	0.042367	-3.39
250561_at	glycerophosphodiester phosphodieste	---	AT5G08030	-1.41	-0.50	-3.49	0.010782	0.042367	-3.39
252391_at	putative protein ; supported by cDNA:	---	AT3G47860	-1.40	-0.49	-3.49	0.010788	0.042384	-3.39
261790_at	unknown protein ; supported by full-ler	---	AT1G16000	-1.55	-0.63	-3.49	0.010793	0.042395	-3.39
254870_at	KI domain interacting kinase 1 -like pr	---	AT4G11900	1.74	0.80	3.49	0.010798	0.042408	-3.39

264803_at	hypothetical protein predicted by gens	---	AT1G08580	1.49	0.58	3.49	0.010813	0.042457	-3.39
261355_at	putative malate oxidoreductase similar	ATNADP-ME	AT1G79750	1.38	0.47	3.49	0.010824	0.042488	-3.39
249417_at	calcium-binding protein - like cbp1 cal	---	AT5G39670	5.04	2.33	3.49	0.010823	0.042488	-3.39
250220_at	receptor protein kinase-like protein	---	AT5G14210	-1.85	-0.89	-3.49	0.010829	0.042498	-3.39
247313_at	3(2),5-bisphosphate nucleotidase ; su	SAL1	AT5G63980	1.50	0.58	3.49	0.010832	0.042503	-3.39
254208_at	Expressed protein ; supported by full-l	---	AT4G24175	-1.37	-0.45	-3.49	0.010838	0.04252	-3.39
258001_at	AIG2-like protein similar to AIG2 protei	---	AT3G28950	1.30	0.38	3.49	0.010845	0.042541	-3.40
258359_s_	putative glycolate oxidase similar to gly	---	AT3G14415 /	-1.41	-0.50	-3.49	0.010853	0.042566	-3.40
255199_at	coded for by A. thaliana cDNA N64969	---	AT4G07390	1.29	0.36	3.48	0.010866	0.04261	-3.40
250958_at	laccase precursor - like laccase precu	LAC11	AT5G03260	-2.41	-1.27	-3.48	0.010876	0.042631	-3.40
266638_at	putative fibrillin ;supported by full-leng	---	AT2G35490	-1.34	-0.42	-3.48	0.010874	0.042631	-3.40
247054_at	zinc finger protein	---	AT5G66730	1.35	0.43	3.48	0.010882	0.04265	-3.40
265352_at	cytosolic cyclophilin (ROC3) ;supporte	ROC3	AT2G16600	1.35	0.43	3.48	0.010898	0.042705	-3.40
262048_at	cytochrome c oxidase subunit, putativ	---	AT1G80230	1.36	0.44	3.48	0.010909	0.042735	-3.40
249905_at	unknown protein	---	AT5G22710	-1.32	-0.40	-3.48	0.01091	0.042735	-3.40
250509_at	cytochrome P450	CYP78A7	AT5G09970	-1.41	-0.50	-3.48	0.010912	0.042736	-3.40
267569_at	putative photosystem II oxygen-evolvir	PSBP-2	AT2G30790	-1.63	-0.70	-3.48	0.010931	0.042806	-3.40
256012_at	unknown protein similar to dimethylani	FMO1	AT1G19250	9.77	3.29	3.48	0.010935	0.042806	-3.40
260569_at	putative signal recognition particle pro	---	AT2G43640	-1.36	-0.44	-3.48	0.010937	0.042806	-3.40
261912_s_	unknown protein	---	AT1G66000 /	-1.38	-0.46	-3.48	0.010934	0.042806	-3.40
254936_at	predicted protein of unknown function	---	AT4G10790	-1.25	-0.32	-3.48	0.010947	0.042837	-3.41
250679_at	putative protein contains similarity to u	---	AT5G06550	1.53	0.61	3.48	0.010953	0.042847	-3.41
252213_at	flavonol synthase - like protein SRG1	---	AT3G50210	1.41	0.49	3.48	0.010953	0.042847	-3.41
246031_at	putative protein KIAA0731 - Homo sa	---	AT5G21160	-1.37	-0.45	-3.48	0.010959	0.042861	-3.41
255752_at	secretory carrier membrane protein, p	---	AT1G32050	-1.44	-0.53	-3.48	0.01098	0.042935	-3.41
250479_at	GTP-binding protein GTP-binding prot	AtRABH1e	AT5G10260	-1.33	-0.41	-3.48	0.010986	0.042945	-3.41
250458_s_	ACTIN 2/7 (sp|P53492) ; supported by	ACT7	AT5G09810	-1.25	-0.32	-3.48	0.010984	0.042945	-3.41
249026_at	Expressed protein ; supported by full-l	OSB3	AT5G44785	-1.43	-0.51	-3.48	0.010994	0.042949	-3.41
263978_at	unknown protein ;supported by full-len	MBF1A	AT2G42680	1.29	0.36	3.48	0.010992	0.042949	-3.41
246791_at	putative protein predicted proteins, Ar	---	AT5G27280	-1.37	-0.46	-3.48	0.010991	0.042949	-3.41
264636_at	hypothetical protein predicted by gene	---	AT1G65490	1.84	0.88	3.48	0.010994	0.042949	-3.41
259336_at	hypothetical protein C-term portion sim	SDG20	AT3G03750	-1.56	-0.64	-3.48	0.010997	0.04295	-3.41
264841_at	putative protein kinase similar to (Z71	---	AT1G03740	1.88	0.91	3.47	0.011005	0.042975	-3.41
254893_at	putative phospholipase D-gamma pho	PLDGAMMA	AT4G11830	-1.61	-0.69	-3.47	0.011034	0.043082	-3.41
266776_at	putative ubiquitin fusion-degradation p	---	AT2G29070	1.40	0.48	3.47	0.011037	0.043086	-3.41

247791_at	cyclophilin ROC7 ;supported by full-le	ROC7	AT5G58710	1.46	0.54	3.47	0.011044	0.043108	-3.41
259920_at	putative phenylalanyl-tRNA synthetase	---	AT1G72550	-1.32	-0.40	-3.47	0.011048	0.043113	-3.41
254512_at	terpene cyclase like protein vetispirad	---	AT4G20230	-1.34	-0.43	-3.47	0.011054	0.04313	-3.42
250463_at	transcription factor OBF4	TGA4	AT5G10030	1.38	0.47	3.47	0.011067	0.043175	-3.42
256853_at	hypothetical protein predicted by gene	---	AT3G18640	1.29	0.37	3.47	0.011074	0.043194	-3.42
251593_at	DNA-directed RNA polymerase I 190k	NRPA1	AT3G57660	1.59	0.67	3.47	0.011096	0.043272	-3.42
257164_at	mismatch binding protein, putative sim	MSH1	AT3G24320	1.33	0.41	3.47	0.011101	0.043283	-3.42
AFFX-Atha	Arabidopsis thaliana /REF=U84969 /D	---	---	1.35	0.44	3.47	0.01111	0.043311	-3.42
254202_at	putative protein hydroxymuconic semi	---	AT4G24140	-1.58	-0.66	-3.47	0.011119	0.043328	-3.42
262830_at	purple acid phosphatase, putative cor	PAP3	AT1G14700	-1.57	-0.65	-3.47	0.011116	0.043328	-3.42
258171_at	unknown protein	---	AT3G21610	1.32	0.40	3.47	0.01112	0.043328	-3.42
254267_at	dihydroorotase ; supported by cDNA:	PYR4	AT4G22930	-1.36	-0.44	-3.47	0.011124	0.043336	-3.42
261981_at	unknown protein	---	AT1G33811	-2.44	-1.29	-3.47	0.011126	0.043336	-3.42
249125_at	1-aminocyclopropane-1-carboxylate ox	---	AT5G43450	1.56	0.64	3.47	0.011138	0.04337	-3.42
249945_at	60S ribosomal protein L10A ; supporte	---	AT5G22440	-1.85	-0.88	-3.47	0.011137	0.04337	-3.42
245951_at	aspartate aminotransferase Asp2 ; su	ASP2	AT5G19550	1.63	0.71	3.47	0.011143	0.043381	-3.42
252901_at	putative protein various predicted prot	---	AT4G39550	1.29	0.37	3.47	0.011149	0.043389	-3.42
252990_at	putative protein	---	AT4G38440	1.77	0.82	3.47	0.011148	0.043389	-3.42
256647_at	unknown protein contains similarity to	---	AT3G13610	9.86	3.30	3.46	0.011151	0.043389	-3.42
262835_at	Na+ H+ antiporter, putative similar to	ATNHX8	AT1G14660	-1.30	-0.38	-3.46	0.011155	0.043397	-3.43
262937_at	FtsH protease, putative contains simil	FTSH12	AT1G79560	-1.27	-0.35	-3.46	0.011165	0.04343	-3.43
258110_at	putative cytochrome P450 similar to G	CYP72A7	AT3G14610	1.41	0.50	3.46	0.011176	0.043464	-3.43
256743_at	Expressed protein ; supported by full-le	---	AT3G29370	-2.19	-1.13	-3.46	0.011184	0.043489	-3.43
260438_at	putative bifunctional nuclease similar t	ENDO 2	AT1G68290	2.01	1.01	3.46	0.011186	0.043491	-3.43
258916_at	putative ABC transporter ATPase simil	ATNAP7	AT3G10670	-1.30	-0.38	-3.46	0.011228	0.043644	-3.43
262484_at	putative transcriptional regulatory prot	ATSWI3C	AT1G21700	-1.23	-0.30	-3.46	0.011239	0.04368	-3.43
252271_s_	putative protein CGI-141 protein- Hom	---	AT3G49420 /	1.26	0.34	3.46	0.011244	0.043694	-3.43
252344_s_	putative protein	---	AT3G44160 /	-1.30	-0.38	-3.46	0.011257	0.043737	-3.44
262611_at	Expressed protein ; supported by full-le	---	AT1G14060	1.59	0.67	3.46	0.011261	0.043737	-3.44
264466_at	Expressed protein ; supported by full-le	---	AT1G10380	-1.80	-0.85	-3.46	0.011261	0.043737	-3.44
248686_at	33 kDa secretory protein-like ; suppor	---	AT5G48540	2.63	1.39	3.46	0.011267	0.043753	-3.44
248977_at	putative protein strong similarity to unk	---	AT5G45020	-1.45	-0.54	-3.46	0.011278	0.043789	-3.44
262073_at	unknown protein ;supported by full-len	ZCW32	AT1G59640	1.72	0.78	3.46	0.011282	0.043794	-3.44
261772_at	hypothetical protein predicted by gene	---	AT1G76240	-1.72	-0.79	-3.46	0.01129	0.043811	-3.44
250457_at	splicing factor-like protein ; supported	---	AT5G09880	1.34	0.43	3.46	0.011289	0.043811	-3.44

257817_at	putative RNA-binding protein contains	---	AT3G25150	-1.31	-0.39	-3.46	0.011294	0.043817	-3.44
259847_at	unknown protein	---	AT1G72170	-1.38	-0.47	-3.46	0.011295	0.043817	-3.44
260949_at	F-box protein family contains similarity	SKIP16	AT1G06110	1.32	0.40	3.45	0.011304	0.043843	-3.44
264551_at	unknown protein similar to beta-1,3-gl	---	AT1G09460	-1.70	-0.76	-3.45	0.011309	0.043856	-3.44
262414_at	acyl CoA synthetase, putative similar	LACS2	AT1G49430	-2.94	-1.56	-3.45	0.011315	0.04387	-3.44
257151_at	blue copper protein, putative similar to	---	AT3G27200	-1.42	-0.50	-3.45	0.01133	0.043923	-3.44
252194_at	putative tyrosine phosphatase phosph	ATPEN3	AT3G50110	-1.36	-0.45	-3.45	0.01134	0.043953	-3.44
247221_at	Expressed protein ; supported by cDN	LIP1	AT5G64813	-1.25	-0.32	-3.45	0.011343	0.043957	-3.44
260976_at	hypothetical protein	CID8	AT1G53650	1.48	0.57	3.45	0.011347	0.043965	-3.44
248815_at	putative protein contains similarity to m	---	AT5G46920	1.50	0.59	3.45	0.011354	0.043986	-3.44
260719_at	unknown protein	---	AT1G48090	-1.41	-0.50	-3.45	0.011358	0.043995	-3.44
246030_at	Expressed protein genomic sequence	---	AT5G21105	1.32	0.40	3.45	0.011361	0.043997	-3.44
263296_at	unknown protein	---	AT2G38800	1.78	0.83	3.45	0.011367	0.044012	-3.45
253637_at	putative protein ; supported by full-len	---	AT4G30390	1.55	0.64	3.45	0.011381	0.044061	-3.45
247346_at	diacylglycerol kinase	ATDGK2	AT5G63770	1.51	0.60	3.45	0.011384	0.044066	-3.45
258039_at	unknown protein ;supported by full-ler	---	AT3G21200	-1.31	-0.39	-3.45	0.011399	0.044115	-3.45
245141_at	putative flavonol reductase	BEN1	AT2G45400	-1.37	-0.45	-3.45	0.011422	0.044198	-3.45
250111_at	acetolactate synthase-like protein	---	AT5G16290	-1.51	-0.60	-3.45	0.011439	0.044255	-3.45
247923_at	porin-like protein ;supported by full-ler	VDAC4	AT5G57490	1.36	0.45	3.44	0.011466	0.044353	-3.45
247655_at	zinc finger protein Zat12 ;supported b	RHL41	AT5G59820	2.97	1.57	3.44	0.011469	0.044357	-3.46
251904_at	Machado-Joseph disease MJD1a -like	---	AT3G54130	1.45	0.53	3.44	0.01149	0.044428	-3.46
261447_at	transcription factor, putative similar to	---	AT1G21160	1.31	0.39	3.44	0.011496	0.044446	-3.46
259054_at	putative hypersensitivity-related gene s	CHAT	AT3G03480	4.50	2.17	3.44	0.011499	0.04445	-3.46
259504_at	inorganic pyrophosphatase, putative s	AVP1	AT1G15690	-1.40	-0.48	-3.44	0.011509	0.044478	-3.46
248547_at	putative protein contains similarity to s	EMB1006	AT5G50280	-1.58	-0.66	-3.44	0.011514	0.044491	-3.46
267247_at	hypothetical protein predicted by gens	---	AT2G30170	-1.38	-0.46	-3.44	0.011519	0.044503	-3.46
266774_at	hypothetical protein predicted by gene	ATRBL1	AT2G29050	-1.42	-0.50	-3.44	0.011531	0.044534	-3.46
267388_at	putative beta-glucosidase	BGLU15	AT2G44450	1.72	0.78	3.44	0.011531	0.044534	-3.46
267106_s_	putative vacuolar sorting receptor iden	ATVSR3	AT2G14720 /	1.41	0.50	3.44	0.011551	0.044605	-3.46
261666_at	hypothetical protein contains similarity	---	AT1G18440	-1.42	-0.50	-3.44	0.011562	0.044641	-3.46
254898_at	serine/threonine kinase-like protein re	---	AT4G11480	2.98	1.58	3.44	0.01157	0.044663	-3.46
247836_at	putative protein similar to unknown pro	---	AT5G57860	1.37	0.45	3.44	0.011594	0.044749	-3.47
267518_at	unknown protein	---	AT2G30500	2.16	1.11	3.43	0.011602	0.044771	-3.47
263984_at	hypothetical protein predicted by gens	---	AT2G42670	-1.32	-0.40	-3.43	0.011608	0.044788	-3.47
258414_at	unknown protein ;supported by full-ler	---	AT3G17380	-1.33	-0.41	-3.43	0.011624	0.044842	-3.47

266865_at	omega-3 fatty acid desaturase identica	FAD3	AT2G29980	-10.13	-3.34	-3.43	0.011628	0.044847	-3.47
258366_at	DNA-binding protein contains AP2 do	RAP2.2	AT3G14230	-1.35	-0.43	-3.43	0.011654	0.04494	-3.47
264821_at	hypothetical protein predicted by gene	---	AT1G03470	1.59	0.67	3.43	0.011664	0.044964	-3.47
255740_at	wall-associated kinase, putative simila	---	AT1G25390	2.04	1.03	3.43	0.011662	0.044964	-3.47
250014_at	anthranilate phosphoribosyltransferas	TRP1	AT5G17990	2.63	1.39	3.43	0.011674	0.044994	-3.47
250443_at	Pto kinase interactor - like protein Pto	RBK1	AT5G10520	3.72	1.89	3.43	0.011681	0.045013	-3.47
262578_at	hypothetical protein Similar to gi|22113	---	---	1.32	0.40	3.43	0.011692	0.045048	-3.48
258672_at	hypothetical protein	---	AT3G08570	-1.36	-0.44	-3.43	0.0117	0.045073	-3.48
255065_s_	putative arginase similar to arginases	---	AT4G08870 /	-2.62	-1.39	-3.43	0.011721	0.045142	-3.48
249861_at	Expressed protein ; supported by full-l	---	AT5G22875	-1.36	-0.44	-3.43	0.011722	0.045142	-3.48
251416_at	putative protein various predicted prot	---	AT3G60400	-1.29	-0.37	-3.43	0.011728	0.045152	-3.48
249293_at	protein kinase-like	---	AT5G41260	-1.41	-0.49	-3.43	0.011728	0.045152	-3.48
251474_at	putative protein diphthamide synthesis	---	AT3G59630	1.32	0.40	3.43	0.011732	0.045159	-3.48
257910_at	hypothetical protein similar to hypothet	---	AT3G25580	-1.37	-0.46	-3.43	0.011743	0.045194	-3.48
260745_at	2,4-D inducible glutathione S-transfera	ATGSTU20	AT1G78370	-2.11	-1.08	-3.43	0.011751	0.045213	-3.48
255899_at	zinc-finger protein (C-terminal), putativ	---	AT1G17970	-1.53	-0.61	-3.43	0.011752	0.045213	-3.48
252712_at	glutathione transferase-like protein glu	ATGSTU27	AT3G43800	-1.63	-0.70	-3.42	0.011757	0.045225	-3.48
258660_at	hypothetical protein predicted by gens	---	AT3G09850	1.35	0.44	3.42	0.011766	0.045253	-3.48
261363_at	pectinesterase, putative similar to GB	SKS6	AT1G41830	-5.46	-2.45	-3.42	0.01178	0.045282	-3.48
252769_at	arabinose kinase - like protein putative	---	AT3G42850	-1.30	-0.38	-3.42	0.011777	0.045282	-3.48
251634_at	putative protein putative zinc finger pr	---	AT3G57480	1.33	0.41	3.42	0.01178	0.045282	-3.48
267009_at	unknown protein	---	AT2G39260	1.26	0.34	3.42	0.011788	0.045304	-3.48
260543_at	putative membrane transporter	INT1	AT2G43330	-1.53	-0.61	-3.42	0.011799	0.045334	-3.49
247890_at	cyclic nucleotide and calmodulin-regul	ATCNGC5	AT5G57940	-1.38	-0.46	-3.42	0.011799	0.045334	-3.49
263065_at	MAP kinase (ATMPK7) identical to GB	ATMPK7	AT2G18170	1.59	0.67	3.42	0.011802	0.045335	-3.49
245165_at	unknown protein predicted by genscan	---	AT2G33180	-1.85	-0.89	-3.42	0.011811	0.045363	-3.49
248097_at	protein phosphatase X isoform 2 (gb|A	PPX2	AT5G55260	1.38	0.47	3.42	0.011831	0.045431	-3.49
251976_at	disease resistance - like protein disea	AtRLP45	AT3G53240	-1.38	-0.46	-3.42	0.011833	0.045432	-3.49
247753_at	hexosyltransferase - like protein	---	AT5G59070	2.04	1.03	3.42	0.011836	0.045436	-3.49
250570_at	putative protein hypothetical bacterial p	EMB1873	AT5G08170	1.45	0.54	3.42	0.011849	0.045477	-3.49
259859_at	putative protein phosphatase similar to	---	AT1G68410	-1.98	-0.98	-3.42	0.011857	0.045493	-3.49
253333_at	2-dehydro-3-deoxyphosphoheptonate	DHS2	AT4G33510	1.32	0.40	3.42	0.011857	0.045493	-3.49
260010_at	putative trehalose-6-phosphate syntha	ATTPS6	AT1G68020	-1.55	-0.63	-3.42	0.011861	0.0455	-3.49
249595_at	putative protein SIAH1 protein, Brassi	---	AT5G37930	-1.45	-0.53	-3.42	0.011879	0.045563	-3.49
263703_at	unknown protein ;supported by full-ler	SRX	AT1G31170	-1.37	-0.46	-3.42	0.011881	0.045563	-3.49

259154_at	unknown protein similar to unknown pr	---	AT3G10260	-1.31	-0.39	-3.42	0.011883	0.045564	-3.49
264811_at	hypothetical protein predicted by gens	---	AT1G08640	1.26	0.33	3.42	0.011895	0.045601	-3.49
261129_at	tubulin alpha-2/alpha-4 chain identical	TUA4	AT1G04820	-2.04	-1.03	-3.42	0.011902	0.045621	-3.49
253289_at	putative protein F10M10_100, Arabid	---	AT4G34320	-1.31	-0.39	-3.42	0.011906	0.045621	-3.50
253364_at	F-box protein family, AtFBX13 cotains	---	AT4G33160	1.25	0.32	3.42	0.011905	0.045621	-3.50
261431_at	Myb-related transcription factor mixta,	AtMYB47	AT1G18710	2.48	1.31	3.42	0.011911	0.045633	-3.50
248911_at	tumor-related protein-like	DOG1	AT5G45830	-1.46	-0.54	-3.41	0.011916	0.045642	-3.50
250143_at	ADP-ribosylation factor - like protein A	ATARFA1B	AT5G14670	-1.32	-0.40	-3.41	0.011922	0.045657	-3.50
254259_s_	putative protein rape mRNA, Brassica	---	AT4G23420 /	-1.52	-0.60	-3.41	0.011932	0.04569	-3.50
264738_at	unknown protein contains similarity to	---	AT1G62250	-1.40	-0.48	-3.41	0.011936	0.045697	-3.50
254194_at	auxin response factor 9 (ARF9) ; supp	ARF9	AT4G23980	1.50	0.59	3.41	0.011938	0.045698	-3.50
255609_s_	hypothetical protein	---	AT4G01180 /	1.25	0.32	3.41	0.011944	0.045712	-3.50
250168_at	putative protein predicted protein, Ara	---	AT5G15320	-1.29	-0.37	-3.41	0.011953	0.045737	-3.50
258648_at	putative auxin-independent growth pro	---	AT3G07900	-1.58	-0.66	-3.41	0.011955	0.045739	-3.50
258505_at	hypothetical protein predicted by gens	---	AT3G06530	2.20	1.14	3.41	0.01197	0.045786	-3.50
248792_at	ras-related small GTP-binding protein-	ATRAB1A	AT5G47200	1.33	0.41	3.41	0.011972	0.045786	-3.50
258933_at	unknown protein similar to unknown p	---	AT3G09980	-1.32	-0.40	-3.41	0.011973	0.045786	-3.50
257088_at	unknown protein	---	AT3G20510	1.92	0.94	3.41	0.011997	0.04587	-3.50
258999_at	putative D-ribulose-5-phosphate 3-epi	---	AT3G01850	1.31	0.39	3.41	0.012004	0.045881	-3.50
247519_at	NAM, no apical meristem, - like protei	ANAC100	AT5G61430	1.40	0.48	3.41	0.012003	0.045881	-3.50
266471_at	putative GTP-binding protein	---	AT2G31060	1.57	0.65	3.41	0.012009	0.04589	-3.50
245942_at	putative protein transcription regulator	---	AT5G19490	1.24	0.31	3.41	0.01202	0.045926	-3.51
256179_at	ubiquitin-specific protease 6 (UBP6),	UBP6	AT1G51710	1.27	0.34	3.41	0.012028	0.045943	-3.51
260380_at	hypothetical protein predicted by gens	---	AT1G73870	-1.75	-0.81	-3.41	0.012028	0.045943	-3.51
262536_at	SOUL-like protein Similar to SOUL Pr	---	AT1G17100	1.76	0.82	3.41	0.012034	0.045956	-3.51
266949_s_	unknown protein ;supported by full-len	---	AT2G18840 /	-1.39	-0.48	-3.41	0.012048	0.045998	-3.51
260722_at	protein phosphatase-2C, putative simi	---	AT1G48040	1.58	0.66	3.41	0.012049	0.045998	-3.51
256458_at	integral membrane protein, putative si	---	AT1G75220	-1.58	-0.66	-3.41	0.01206	0.046007	-3.51
261266_at	expansin 10 identical to GB:AAF61712	ATEXPA10	AT1G26770	-1.47	-0.56	-3.41	0.01206	0.046007	-3.51
267101_at	putative peroxidase	---	AT2G41480	1.46	0.55	3.41	0.012064	0.046007	-3.51
254803_at	putative protein several hypothetical pr	---	AT4G13100	1.52	0.60	3.41	0.012063	0.046007	-3.51
266548_at	unknown protein ;supported by full-ler	RPA	AT2G35210	-1.50	-0.59	-3.41	0.012057	0.046007	-3.51
246999_at	photoreceptor-interacting protein-like	NPY3	AT5G67440	-1.68	-0.74	-3.41	0.012054	0.046007	-3.51
255327_at	putative malonyl-CoA decarboxylase	---	AT4G04320	1.25	0.32	3.41	0.012069	0.046019	-3.51
265309_at	putative myosin heavy chain	XIG	AT2G20290	-1.50	-0.59	-3.40	0.012074	0.04603	-3.51

251069_at	(1-4)-beta-mannan endohydrolase-like	---	AT5G01930	-1.84	-0.88	-3.40	0.012076	0.04603	-3.51
245666_at	hypothetical protein predicted by gene	---	AT1G28280	1.73	0.79	3.40	0.012083	0.046052	-3.51
266418_at	putative annexin ;supported by full-len	ANNAT4	AT2G38750	-2.26	-1.17	-3.40	0.012092	0.046053	-3.51
258436_at	putative RING zinc finger protein simila	ATL2	AT3G16720	2.15	1.10	3.40	0.012087	0.046053	-3.51
260411_at	hypothetical protein similar to GB:AAB	---	AT1G69890	1.81	0.86	3.40	0.012088	0.046053	-3.51
245690_at	phenylalanine ammonia-lyase PAL3	PAL3	AT5G04230	-1.67	-0.74	-3.40	0.012092	0.046053	-3.51
263259_at	putative zinc-binding protein similar to	PUB18	AT1G10560	-1.66	-0.73	-3.40	0.012119	0.046151	-3.51
255131_at	putative protein hypothetical protein s	---	AT4G08280	-1.30	-0.38	-3.40	0.012123	0.046156	-3.51
266019_at	putative calmodulin-binding protein ; s	---	AT2G18750	1.25	0.32	3.40	0.012128	0.04617	-3.51
266189_at	unknown protein	---	AT2G39020	-1.25	-0.32	-3.40	0.012136	0.04619	-3.52
250921_at	Expressed protein ; supported by full-l	---	AT5G03460	1.43	0.51	3.40	0.012148	0.046229	-3.52
266365_at	ferredoxin-dependent glutamate synth	GLU2	AT2G41220	1.46	0.54	3.40	0.012152	0.046236	-3.52
246070_at	ribosomal protein L7Ae-like NHP2/RS	---	AT5G20160	1.52	0.61	3.40	0.012155	0.04624	-3.52
245909_at	putative protein DNA-directed RNA po	---	AT5G09380	1.40	0.49	3.40	0.012165	0.046263	-3.52
263590_at	putative receptor-like protein kinase	---	AT2G01820	-1.28	-0.36	-3.40	0.012165	0.046263	-3.52
266760_at	putative RAV-like B3 domain DNA bind	NGA1	AT2G46870	-1.42	-0.50	-3.40	0.012177	0.046302	-3.52
251945_at	dTDP-glucose 4-6-dehydratase -like p	UXS1	AT3G53520	-1.30	-0.38	-3.40	0.012188	0.046335	-3.52
246261_at	unknown protein	---	AT1G31810	-1.33	-0.42	-3.40	0.012194	0.046344	-3.52
262378_at	CCAAT-binding factor B subunit homo	NF-YA3	AT1G72830	1.46	0.54	3.40	0.012194	0.046344	-3.52
267344_at	hypothetical protein predicted by gene	---	AT2G44230	-1.85	-0.89	-3.40	0.012203	0.046355	-3.52
252143_at	putative protein centromere protein E	---	AT3G51150	-1.30	-0.37	-3.40	0.012203	0.046355	-3.52
253357_at	Dem -like protein Dem (defective emb	---	AT4G33400	-1.30	-0.38	-3.40	0.012206	0.046355	-3.52
248666_at	cyclin C-like protein ;supported by full-	---	AT5G48630	-1.41	-0.50	-3.40	0.012205	0.046355	-3.52
245147_at	putative RAD51C-like DNA repair prote	ATRAD51C	AT2G45280	1.69	0.76	3.40	0.012224	0.046416	-3.52
254487_at	calcium-binding protein - like calcium-	---	AT4G20780	2.82	1.49	3.40	0.012228	0.046427	-3.52
256627_at	unknown protein ; supported by cDNA	---	AT3G19970	3.09	1.63	3.40	0.012232	0.046431	-3.52
263288_at	cyclophilin-like protein ;supported by f	---	AT2G36130	-1.39	-0.47	-3.39	0.012251	0.046496	-3.53
267603_at	unknown protein ; supported by cDNA	ATZW10	AT2G32900	-1.39	-0.47	-3.39	0.012262	0.046532	-3.53
257218_at	unknown protein similar to DAG protei	---	AT3G15000	1.29	0.36	3.39	0.01227	0.046554	-3.53
255509_at	hypothetical protein identical to T10M1	---	AT4G02210	-1.53	-0.62	-3.39	0.012278	0.046577	-3.53
245961_at	putative protein predicted proteins - Ar	---	AT5G19670	-1.37	-0.46	-3.39	0.012308	0.046681	-3.53
248865_at	putative protein similar to unknown pro	---	AT5G46790	1.44	0.52	3.39	0.012311	0.046685	-3.53
250892_at	putative protein beta-(1-3)-glucosyl tra	ATCSLA09	AT5G03760	-6.33	-2.66	-3.39	0.012327	0.04674	-3.53
262825_at	putative chloroplast prephenate dehyd	ADT1	AT1G11790	-1.62	-0.69	-3.39	0.012332	0.046751	-3.53
259312_at	putative RING-H2 zinc finger protein A	ATL6	AT3G05200	2.15	1.11	3.39	0.012337	0.046761	-3.53

249936_at	putative protein similar to unknown pro	---	AT5G22450	1.37	0.45	3.39	0.012356	0.046824	-3.53
253983_at	putative protein SPF1 protein -Ipomoe	WRKY20	AT4G26640	-1.37	-0.46	-3.39	0.012358	0.046824	-3.53
257954_at	putative UDP-glucose glucosyltransfer	---	AT3G21760	1.36	0.44	3.39	0.012364	0.046841	-3.54
266319_s_	putative beta-ketoacyl-CoA synthase	KCS13	AT2G46720 /	-1.53	-0.62	-3.39	0.012372	0.046863	-3.54
246958_at	putative protein similar to unknown pro	---	AT5G24690	1.45	0.54	3.39	0.01238	0.046879	-3.54
258926_s_	unknown protein N-terminus similar to	anac052	AT3G10480 /	1.43	0.52	3.39	0.01238	0.046879	-3.54
264105_x_	hypothetical protein	---	AT2G13760	1.36	0.44	3.39	0.012384	0.046885	-3.54
259318_at	unknown protein similar to HYP1 GB:C	HYP1	AT3G01100	1.41	0.50	3.39	0.012391	0.046902	-3.54
259130_at	putative ribosomal protein L39 similar t	---	AT3G02190	1.36	0.44	3.38	0.012416	0.046991	-3.54
258727_at	ethylene-responsive protein, putative :	---	AT3G11930	1.37	0.46	3.38	0.012421	0.047001	-3.54
247139_at	unknown protein ;supported by full-ler	---	AT5G66090	-1.32	-0.40	-3.38	0.012447	0.047091	-3.54
249286_at	transcription factor-like protein	---	AT5G41580	1.33	0.41	3.38	0.012456	0.047118	-3.54
255455_at	mitochondrial elongation factor Tu	---	AT4G02930	1.74	0.80	3.38	0.012471	0.047159	-3.54
250091_at	unknown protein	---	AT5G17340	-1.24	-0.31	-3.38	0.012469	0.047159	-3.54
248809_at	GTP-binding protein-like	AtRABA5a	AT5G47520	-1.36	-0.45	-3.38	0.012476	0.047165	-3.55
250020_at	putative protein contains similarity to G	---	AT5G18180	1.37	0.46	3.38	0.012477	0.047165	-3.55
245005_at	ribosomal protein S14	---	---	-1.57	-0.65	-3.38	0.01249	0.047199	-3.55
248305_at	putative protein similar to unknown pro	ATUSP	AT5G52560	-1.41	-0.50	-3.38	0.01249	0.047199	-3.55
261920_at	isocitrate dehydrogenase, putative sin	---	AT1G65930	1.33	0.41	3.38	0.012516	0.047289	-3.55
246244_at	receptor kinase-like protein	---	AT4G37250	-1.29	-0.36	-3.38	0.012528	0.047329	-3.55
254170_at	LG27/30-like gene LG27/30 gene - Ar	---	AT4G24430	-1.25	-0.32	-3.38	0.01253	0.047329	-3.55
260544_at	unknown protein predicted by genscan	---	AT2G43540	1.49	0.58	3.38	0.012538	0.047349	-3.55
263921_at	putative fructose bisphosphate aldolas	---	AT2G36460	1.42	0.50	3.38	0.012545	0.04736	-3.55
261221_at	hypothetical protein predicted by gene	---	AT1G19960	6.52	2.70	3.38	0.012544	0.04736	-3.55
248790_at	membrane channel protein-like; aquap	TIP2;3	AT5G47450	-1.49	-0.58	-3.38	0.012548	0.047362	-3.55
253838_at	putative zinc finger protein zinc finger	---	AT4G27880	-1.51	-0.60	-3.37	0.01257	0.047438	-3.55
254159_at	putative DNA-binding protein DNA-bir	WRKY7	AT4G24240	1.75	0.81	3.37	0.012576	0.047454	-3.55
246275_at	putative protein ; supported by full-leng	BEE2	AT4G36540	-3.97	-1.99	-3.37	0.01258	0.047459	-3.55
246989_at	unknown protein	---	AT5G67350	2.03	1.02	3.37	0.012582	0.047459	-3.55
263756_at	putative ubiquitin fusion-degradation p	---	AT2G21270	1.25	0.32	3.37	0.012594	0.047499	-3.56
251445_at	putative protein hypothetical protein F	---	AT3G59870	-1.25	-0.32	-3.37	0.012597	0.047501	-3.56
254867_at	hypothetical proteins	---	AT4G12240	1.47	0.56	3.37	0.012609	0.047531	-3.56
261659_at	unknown protein contains similarity to	TOR	AT1G50030	-1.28	-0.35	-3.37	0.012607	0.047531	-3.56
264510_at	putative phytochrome-associated prote	PIF3	AT1G09530	1.65	0.72	3.37	0.012617	0.047553	-3.56
246555_at	putative protein 68 kDa protein - Cicer	GAUT14	AT5G15470	-1.51	-0.60	-3.37	0.012634	0.047601	-3.56

255596_at	putative DNA-binding protein similar t	WRKY47	AT4G01720	1.91	0.93	3.37	0.012633	0.047601	-3.56
249575_at	low-molecular-weight heat shock prote	---	AT5G37670	1.51	0.59	3.37	0.012644	0.047632	-3.56
262714_s_	unknown protein similar to gb|AJ22435	---	AT1G07950 /	1.28	0.36	3.37	0.012655	0.047667	-3.56
255364_s_	putative fibrillin ; supported by full-leng	---	AT4G04020 /	1.42	0.50	3.37	0.01266	0.047676	-3.56
252694_at	nodulin -like protein nodulin-21, Glycir	---	AT3G43630	-1.31	-0.39	-3.37	0.012672	0.047713	-3.56
245051_at	putative WRKY-type DNA-binding prot	WRKY15	AT2G23320	1.89	0.91	3.37	0.012675	0.047717	-3.56
248838_at	carnitine/acylcarnitine translocase-like	BOU	AT5G46800	-1.58	-0.66	-3.37	0.012698	0.047797	-3.56
252561_at	histone H2B ;supported by full-length	HTB9	AT3G45980	-1.48	-0.57	-3.37	0.0127	0.047797	-3.56
260441_at	unknown protein ;supported by full-ler	---	AT1G68260	-1.86	-0.90	-3.37	0.012707	0.047813	-3.56
257062_at	zinc finger protein, putative contains F	EMB2454	AT3G18290	-1.82	-0.87	-3.37	0.012714	0.047822	-3.57
264339_at	trehalose-6-phosphate synthase, puta	TPS8	AT1G70290	-1.53	-0.61	-3.37	0.012713	0.047822	-3.57
251190_at	RING-H2 zinc finger protein ATL5 ; su	ATL5	AT3G62690	-1.68	-0.75	-3.37	0.012716	0.047822	-3.57
249642_at	putative protein	---	AT5G36960	-1.37	-0.46	-3.37	0.012722	0.047837	-3.57
249926_at	E1, ubiquitin-like activating enzyme E	ECR1	AT5G19180	1.38	0.47	3.36	0.012776	0.048032	-3.57
253062_at	putative protein predicted protein, Ara	NPY5	AT4G37590	-2.03	-1.02	-3.36	0.012779	0.048035	-3.57
248553_at	putative protein strong similarity to unk	---	AT5G50170	1.73	0.79	3.36	0.012798	0.048101	-3.57
258362_at	unknown protein	---	AT3G14280	2.87	1.52	3.36	0.01281	0.048139	-3.57
255263_at	4-coumarate--CoA ligase - like protein	---	AT4G05160	1.25	0.33	3.36	0.012817	0.048158	-3.57
248881_at	unknown protein ;supported by full-ler	---	AT5G46020	-1.25	-0.32	-3.36	0.012819	0.048158	-3.57
264778_at	unknown protein similar to C-1 (Homo	AIP3	AT1G08780	-1.29	-0.37	-3.36	0.012824	0.048168	-3.57
262400_at	unknown protein ; supported by cDNA	RTV1	AT1G49480	-1.24	-0.31	-3.36	0.012832	0.048183	-3.58
266013_s_	hypothetical protein	---	AT2G07702	1.28	0.36	3.36	0.012833	0.048183	-3.58
259030_at	putative alpha-hemolysin similar to alp	---	AT3G09310	-1.23	-0.29	-3.36	0.012835	0.048183	-3.58
260967_at	unknown protein contains similarity to	---	AT1G12230	-1.40	-0.49	-3.36	0.012841	0.048199	-3.58
249228_at	SKP1/ASK1 (At2) identical to UIP2 GI:	ASK2	AT5G42190	-1.44	-0.53	-3.36	0.012855	0.048245	-3.58
262049_at	unknown protein ;supported by full-len	---	AT1G80180	1.35	0.43	3.36	0.012869	0.048286	-3.58
265310_at	hypothetical protein predicted by gene	---	AT2G20280	1.29	0.36	3.36	0.012881	0.048327	-3.58
259805_at	disease resistance protein, putative si	AtRLP7	AT1G47890	1.46	0.55	3.36	0.012894	0.048366	-3.58
256143_at	40S ribosomal protein S7 homolog, pu	---	AT1G48830	-1.41	-0.50	-3.35	0.01291	0.048417	-3.58
267018_at	unknown protein	SVR1	AT2G39140	-1.54	-0.63	-3.35	0.012914	0.048425	-3.58
258855_at	unknown protein	---	AT3G02070	-1.58	-0.66	-3.35	0.012919	0.048429	-3.58
250828_at	unknown protein ; supported by cDNA	---	AT5G05250	-4.27	-2.09	-3.35	0.012918	0.048429	-3.58
267070_at	putative DnaJ protein	---	AT2G41000	1.52	0.60	3.35	0.012946	0.048523	-3.58
261105_at	unknown protein ;supported by full-len	NRS/ER	AT1G63000	-1.42	-0.50	-3.35	0.012979	0.048638	-3.59
260824_at	unknown protein	---	AT1G06720	1.70	0.77	3.35	0.012986	0.048654	-3.59

247690_at	putative protein	MBD7	AT5G59800	-1.64	-0.72	-3.35	0.012988	0.048654	-3.59
252698_at	amine oxidase -like protein amine oxi	---	AT3G43670	-1.38	-0.47	-3.35	0.013014	0.048743	-3.59
248900_at	putative protein strong similarity to unk	PRP39-2	AT5G46400	-1.47	-0.56	-3.35	0.013016	0.048744	-3.59
254045_at	pumilio-like protein abdominal segmer	APUM6	AT4G25880	1.27	0.35	3.35	0.013031	0.048792	-3.59
260352_at	Expressed protein ; supported by full-l	PDCB4	AT1G69295	1.29	0.37	3.35	0.013067	0.048911	-3.59
261147_at	unknown protein ;supported by full-len	---	AT1G19690	-1.59	-0.67	-3.35	0.013067	0.048911	-3.59
264868_at	unknown protein	---	AT1G24090	1.77	0.82	3.34	0.013076	0.048936	-3.60
254616_at	shaggy-like protein kinase etha (EC 2.	BIN2	AT4G18710	-1.28	-0.36	-3.34	0.013093	0.048993	-3.60
246594_at	pyrroline-5-carboxylate reductase ;sup	P5CR	AT5G14800	1.40	0.49	3.34	0.013098	0.049001	-3.60
257019_at	unknown protein	---	AT3G19640	1.23	0.30	3.34	0.013106	0.049023	-3.60
252445_at	beta-D-glucan exohydrolase - like pro	---	AT3G47000	-1.31	-0.39	-3.34	0.013108	0.049024	-3.60
250598_at	transcription factor-like protein ; suppo	ATMYB29	AT5G07690	-1.52	-0.60	-3.34	0.01312	0.049052	-3.60
246350_at	hypothetical protein predicted by gene	---	AT1G16650	1.37	0.45	3.34	0.013119	0.049052	-3.60
250186_at	putative protein apospory-associated	---	AT5G14500	-1.39	-0.47	-3.34	0.01314	0.049118	-3.60
245076_at	unknown protein	GH3.3	AT2G23170	4.96	2.31	3.34	0.01315	0.04915	-3.60
253919_at	putative protein ; supported by full-len	---	AT4G27350	-1.73	-0.79	-3.34	0.013166	0.049186	-3.60
267236_at	GDP dissociation inhibitor identical to	ATGDI1	AT2G44100	1.31	0.39	3.34	0.013167	0.049186	-3.60
259117_at	unknown protein similar to hypothetica	SNL1	AT3G01320	1.28	0.35	3.34	0.013166	0.049186	-3.60
250721_at	putative protein contains similarity to R	---	AT5G06210	1.28	0.35	3.34	0.013174	0.049206	-3.60
260399_at	putative lipoxygenase similar to lipoxy	---	AT1G72520	4.69	2.23	3.34	0.013179	0.049216	-3.60
260051_at	hypothetical protein	---	AT1G78210	1.80	0.85	3.34	0.013184	0.04922	-3.60
244971_at	ATP-dependent protease subunit	---	---	-1.30	-0.38	-3.34	0.013183	0.04922	-3.60
259056_at	hypothetical protein similar to Ku70-bir	---	AT3G03420	1.39	0.47	3.34	0.013217	0.049328	-3.61
249138_at	putative protein contains similarity to M	WPP1	AT5G43070	1.29	0.37	3.34	0.01322	0.049328	-3.61
258100_at	unknown protein	---	AT3G23550	3.84	1.94	3.34	0.013219	0.049328	-3.61
262075_at	hypothetical protein contains similarity	ZCF61	AT1G59560	-1.51	-0.60	-3.34	0.013222	0.049328	-3.61
255012_at	putative protein ;supported by full-leng	---	AT4G10030	-1.59	-0.67	-3.34	0.013231	0.049354	-3.61
255780_at	hypothetical protein contains Pfam pro	GAUT11	AT1G18580	-1.38	-0.46	-3.34	0.013234	0.049357	-3.61
264735_s_	hypothetical protein similar to hypothet	---	AT1G62000 /	-1.41	-0.50	-3.33	0.01328	0.04952	-3.61
261256_at	disease resistance protein RTM1 iden	RTM1	AT1G05760	-1.41	-0.49	-3.33	0.013288	0.049544	-3.61
265470_at	putative protein with C-terminal RING f	---	AT2G37150	1.38	0.46	3.33	0.013307	0.049605	-3.61
245179_at	putative protein similarity to predicted	---	AT5G12400	1.31	0.39	3.33	0.013321	0.049649	-3.62
255738_at	hypothetical protein predicted by gene	---	AT1G25570	-1.27	-0.35	-3.33	0.013351	0.049753	-3.62
255652_at	putative protein	MEE47	AT4G00950	-2.30	-1.20	-3.33	0.013361	0.049784	-3.62
263105_at	putative N-acetylglucosaminyltransfera	---	AT2G05320	1.26	0.33	3.33	0.013374	0.049821	-3.62

244969_at	ribosomal protein S18	---	---	-1.81	-0.86	-3.33	0.013395	0.049892	-3.62
247792_at	Expressed protein ; supported by full-l	---	AT5G58787	1.57	0.65	3.32	0.013443	0.050062	-3.62
259051_at	unknown protein similar to CGI-86 pro	---	AT3G03330	1.32	0.40	3.32	0.013456	0.050104	-3.63
263841_at	putative xyloglucan endo-transglycosy	---	AT2G36870	-6.29	-2.65	-3.32	0.013471	0.050152	-3.63
260675_at	unknown protein ; supported by cDNA	---	AT1G19430	-1.39	-0.48	-3.32	0.013478	0.050167	-3.63
252250_at	putative protein predicted protein, Ara	---	AT3G49790	1.52	0.61	3.32	0.013507	0.050267	-3.63
246650_at	putative protein p76, Homo sapiens, E	---	AT5G35160	-1.32	-0.40	-3.32	0.013512	0.05028	-3.63
255861_at	putative vacuolar sorting receptor	---	AT2G30290	-1.25	-0.33	-3.32	0.013523	0.050313	-3.63
246793_at	putative protein seven transmembrane	---	AT5G27210	1.29	0.37	3.32	0.013538	0.05036	-3.63
260201_at	F12A21.27 hypothetical protein;suppo	---	AT1G67600	1.74	0.80	3.32	0.013549	0.050392	-3.63
246039_at	putative protein serine-arginine-rich sp	---	AT5G19480	1.28	0.35	3.32	0.013564	0.050441	-3.63
257149_at	prohibitin, putative similar to prohibitin	ATPHB4	AT3G27280	1.74	0.80	3.32	0.013568	0.050447	-3.63
248954_at	unknown protein ; supported by cDNA	---	AT5G45420	1.26	0.33	3.32	0.013582	0.050489	-3.64
253170_at	putative protein various predicted prot	---	AT4G35130	1.25	0.32	3.32	0.013592	0.050509	-3.64
258364_at	unknown protein	GLIP4	AT3G14225	1.71	0.77	3.32	0.013592	0.050509	-3.64
256822_at	unknown protein contains PF00612 IQ	IQD5	AT3G22190	-1.35	-0.43	-3.32	0.013604	0.050546	-3.64
264752_at	unknown protein similar to Bacillus sp	LPR1	AT1G23010	1.25	0.32	3.32	0.013607	0.05055	-3.64
265702_at	putative purple acid phosphatase cont	PAP9	AT2G03450	1.34	0.42	3.31	0.013621	0.050595	-3.64
257764_at	disease resistance protein, putative si	AtRLP36	AT3G23010	1.61	0.69	3.31	0.013641	0.05066	-3.64
259672_at	DNA-directed RNA polymerase identi	---	AT1G68990	1.95	0.96	3.31	0.013646	0.050661	-3.64
262514_at	NAM(no apical meristem) protein, put	anac017	AT1G34190	1.25	0.32	3.31	0.013644	0.050661	-3.64
251961_at	inorganic pyrophosphatase -like prote	AtPPa4	AT3G53620	-1.65	-0.72	-3.31	0.01366	0.05068	-3.64
251987_at	CYTOCHROME P450 71B5 ; support	CYP71B5	AT3G53280	1.36	0.44	3.31	0.013657	0.05068	-3.64
264146_at	hypothetical protein contains similarity	CER1	AT1G02205	-12.00	-3.58	-3.31	0.013654	0.05068	-3.64
247260_at	putative protein contains similarity to u	---	AT5G64500	-1.45	-0.54	-3.31	0.01366	0.05068	-3.64
253178_at	putative protein predicted protein, Ara	---	AT4G35170	1.36	0.45	3.31	0.013677	0.050735	-3.64
257420_at	hypothetical protein predicted by gene	---	AT1G77250	-1.37	-0.45	-3.31	0.013683	0.050751	-3.64
253654_at	putative protein several hypothetical pr	---	AT4G30060	1.78	0.83	3.31	0.013703	0.050814	-3.65
254575_at	putative protein various predicted prot	---	AT4G19460	1.95	0.96	3.31	0.013707	0.050823	-3.65
261512_at	actin capping protein beta-2, putative	---	AT1G71790	-1.52	-0.60	-3.31	0.013722	0.05087	-3.65
246742_at	TOPP8 serine/threonine protein phosp	TOPP8	AT5G27840	1.23	0.29	3.31	0.013739	0.050926	-3.65
263373_at	Expressed protein ; supported by full-l	---	AT2G20515	-1.56	-0.64	-3.31	0.013744	0.050935	-3.65
251667_at	putative protein DYSKERIN (NUCLEC	NAP57	AT3G57150	1.85	0.89	3.31	0.013748	0.050942	-3.65
250557_at	putative protein ankyrin, Rattus norve	CPuORF16	AT5G07840 /	-1.27	-0.34	-3.31	0.013754	0.050956	-3.65
249253_at	putative protein similar to unknown pro	---	AT5G42060	1.34	0.43	3.31	0.013762	0.050976	-3.65

248615_at	putative protein contains similarity to p	AtPNG1	AT5G49570	1.54	0.62	3.31	0.013769	0.050993	-3.65
259902_at	disease resistance protein, putative si	AtRLP13	AT1G74170	1.80	0.85	3.31	0.013778	0.051017	-3.65
259395_at	GTP-binding protein(RAB11D), putati	ARA-2	AT1G06400	-1.29	-0.36	-3.31	0.013788	0.051049	-3.65
267623_at	unknown protein	---	AT2G39650	3.00	1.58	3.30	0.013839	0.051227	-3.66
261062_at	transcription factor scarecrow-like 14,	SCL14	AT1G07530	1.29	0.37	3.30	0.013849	0.051256	-3.66
245296_at	isp4 like protein ; supported by cDNA:	ATOPT3	AT4G16370	-1.61	-0.68	-3.30	0.013873	0.051329	-3.66
255142_at	stromal ascorbate peroxidase ; suppo	SAPX	AT4G08390	2.76	1.46	3.30	0.013873	0.051329	-3.66
262457_at	hypothetical protein similar to hypothet	---	AT1G11200	1.59	0.67	3.30	0.013884	0.051362	-3.66
254796_at	putative protein protein kinase homolo	---	AT4G13000	1.36	0.44	3.30	0.0139	0.051412	-3.66
267194_s_	putative ARP2/3 protein complex subu	ARPC1A	AT2G30910 /	-1.31	-0.39	-3.30	0.01391	0.051442	-3.66
254521_at	putative protein similar to unknown pro	---	AT5G44820	1.31	0.39	3.30	0.013917	0.051449	-3.66
250586_at	putative protein similar to unknown pro	---	AT5G07630	-1.37	-0.46	-3.30	0.013914	0.051449	-3.66
259685_at	unknown protein	AtPP2-A11	AT1G63090	-1.57	-0.65	-3.30	0.013924	0.051461	-3.66
250002_at	proline-richh protein predicted protein	AGP25	AT5G18690	-2.22	-1.15	-3.30	0.013922	0.051461	-3.66
252938_at	hypothetical protein	---	AT4G39190	2.23	1.16	3.30	0.013942	0.051511	-3.66
261552_at	receptor protein kinase, putative conta	---	AT1G63430	-1.33	-0.42	-3.30	0.013941	0.051511	-3.66
258095_at	dual-specificity protein phosphatase id	---	AT3G23610	-1.36	-0.44	-3.30	0.013949	0.051525	-3.66
253280_at	poly(A)-binding protein non-consensu	PAB2	AT4G34110	1.26	0.33	3.30	0.013955	0.051537	-3.66
254495_at	hypothetical protein	EMB1895	AT4G20060	1.49	0.58	3.30	0.013959	0.051537	-3.67
259595_at	CONSTANS family zinc finger protein	---	AT1G28050	1.49	0.58	3.30	0.013959	0.051537	-3.67
262277_at	transmembrane protein, putative simil	---	AT1G68650	1.80	0.85	3.30	0.013972	0.05157	-3.67
255710_at	predicted protein of unknown function	---	AT4G00030 /	-1.59	-0.67	-3.30	0.013971	0.05157	-3.67
259770_s_	phosphoribosylanthranilate isomerase	PAI3	AT1G07780 /	-1.52	-0.60	-3.29	0.013989	0.051626	-3.67
259756_at	unknown protein ; supported by cDNA	---	AT1G71080	-1.27	-0.35	-3.29	0.013998	0.05165	-3.67
257600_at	hypothetical protein predicted by gens	CLE41	AT3G24770	1.38	0.47	3.29	0.014042	0.051802	-3.67
249198_s_	putative protein similar to unknown pro	---	AT5G42350 /	-1.30	-0.38	-3.29	0.014068	0.05189	-3.67
266530_at	bHLH transcription factor	AMS	AT2G16910	1.23	0.29	3.29	0.01407	0.05189	-3.67
264351_at	unknown protein Contains similarity to	---	AT1G03370	1.32	0.40	3.29	0.014123	0.052077	-3.68
258857_at	putative serine carboxypeptidase II sin	scpl25	AT3G02110	-2.47	-1.30	-3.29	0.014146	0.052153	-3.68
258314_at	putative RAS-related GTP-binding pro	ATRABG3C	AT3G16100	-1.33	-0.41	-3.29	0.014153	0.052171	-3.68
254327_at	RCc3- like protein RCc3 protein, Oryz	---	AT4G22490	-1.80	-0.85	-3.29	0.014163	0.052192	-3.68
246053_at	putative protein farnesyl cysteine carb	---	AT5G08340	-1.41	-0.49	-3.29	0.014162	0.052192	-3.68
262784_at	unknown protein strong similarity to gl	SEX1	AT1G10760	-1.51	-0.60	-3.28	0.014169	0.052205	-3.68
254971_at	major intrinsic protein (MIP) - like nod	NIP5;1	AT4G10380	1.52	0.60	3.28	0.014172	0.052208	-3.68
262324_at	hypothetical protein similar to hypothet	ATCHX16	AT1G64170	3.82	1.93	3.28	0.014181	0.052232	-3.68

248529_at	protein kinase ;supported by full-length	---	AT5G50000	-1.47	-0.56	-3.28	0.014185	0.052239	-3.68
255134_at	putative protein	---	AT4G08330	-1.33	-0.41	-3.28	0.01419	0.052247	-3.68
267347_at	hypothetical protein predicted by gene	---	AT2G39950	1.27	0.35	3.28	0.014214	0.052325	-3.68
253111_at	putative protein glutamic acid-rich pro	---	AT4G35940	1.45	0.53	3.28	0.014216	0.052325	-3.68
250922_at	Expressed protein ; supported by full-l	---	AT5G03345	-1.30	-0.38	-3.28	0.01422	0.052332	-3.68
247833_at	putative protein	---	AT5G58575	1.25	0.32	3.28	0.014239	0.052396	-3.69
263430_at	unknown protein ;supported by full-ler	---	AT2G22270	-1.36	-0.44	-3.28	0.014248	0.05242	-3.69
250971_at	putative protein ABI3-interacting prote	PRR7	AT5G02810	-1.32	-0.40	-3.28	0.014264	0.05247	-3.69
258700_at	putative SF16 protein similar to SF16 p	IQD1	AT3G09710	-1.29	-0.37	-3.28	0.014273	0.052476	-3.69
257677_at	unknown protein contains Pfam profile	ATEHD1	AT3G20290	1.33	0.41	3.28	0.014271	0.052476	-3.69
257205_at	putative glucosyltransferase similar to	UGT88A1	AT3G16520	-1.29	-0.36	-3.28	0.01427	0.052476	-3.69
257578_x_	unknown protein similar to hypothetica	---	AT3G30160	1.25	0.33	3.28	0.014288	0.052514	-3.69
266789_at	unknown protein ; supported by full-le	---	AT2G29020	-1.28	-0.35	-3.28	0.014288	0.052514	-3.69
255406_at	hypothetical protein similar to hypothe	---	AT4G03450	2.07	1.05	3.28	0.014296	0.052537	-3.69
253698_at	nucleotide pyrophosphatase - like pro	---	AT4G29680	1.28	0.36	3.28	0.014302	0.052548	-3.69
250196_at	polynucleotide phosphorylase	---	AT5G14580	1.38	0.46	3.28	0.014318	0.052601	-3.69
257332_at	hypothetical protein	---	---	1.42	0.50	3.28	0.014325	0.052616	-3.69
248901_at	putative protein contains similarity to (p	---	AT5G46410	1.37	0.45	3.28	0.014331	0.052625	-3.69
255431_at	putative C-type U1 snRNP similar to U	---	AT4G03120	-1.23	-0.29	-3.28	0.014332	0.052625	-3.69
256769_at	protein kinase, putative similar to prot	---	AT3G13690	-1.62	-0.70	-3.28	0.014336	0.052633	-3.69
262921_at	transfactor, putative similar to transfac	APL	AT1G79430	1.30	0.37	3.28	0.014342	0.052647	-3.69
263406_at	subtilisin-like serine protease AIR3 alr	AIR3	AT2G04160	2.07	1.05	3.27	0.014362	0.052695	-3.70
249404_at	ankyrin repeat protein EMB506 ; supp	EMB506	AT5G40160	-1.42	-0.51	-3.27	0.014362	0.052695	-3.70
261955_at	proteasome regulatory subunit, putati	RPN12a	AT1G64520	-1.25	-0.32	-3.27	0.014361	0.052695	-3.70
251643_at	guanylate kinase-like protein guanylat	AGK2	AT3G57550	1.88	0.91	3.27	0.014373	0.052726	-3.70
261141_at	unknown protein contains Pfam profile	---	AT1G19740	-1.34	-0.42	-3.27	0.014412	0.052859	-3.70
249251_at	putative protein similar to unknown pro	---	AT5G42000	-1.40	-0.48	-3.27	0.014438	0.052946	-3.70
247048_at	photoreceptor-interacting protein-like ;	---	AT5G66560	-1.74	-0.80	-3.27	0.014458	0.053012	-3.70
253198_at	putative protein various predicted prote	---	AT4G35360	-1.31	-0.38	-3.27	0.014483	0.053092	-3.70
248619_at	amino acid permease 6 (emb CAA650	AAP6	AT5G49630	-1.43	-0.52	-3.27	0.014485	0.053092	-3.70
259546_at	unknown protein	---	AT1G35350	-1.93	-0.95	-3.27	0.014488	0.053096	-3.70
261416_at	ribosomal protein S15 identical to GB:	RPS15A	AT1G07770	-1.69	-0.76	-3.27	0.014508	0.053161	-3.71
252654_at	similar to glycyl tRNA synthetase	---	AT3G44740	-1.25	-0.32	-3.27	0.014511	0.053164	-3.71
254509_at	terpene cyclase like protein 5-epi-arist	---	AT4G20200	-1.27	-0.34	-3.27	0.014518	0.05318	-3.71
254282_at	hypothetical protein	---	AT4G22860	-1.27	-0.35	-3.27	0.014528	0.053208	-3.71

265417_at	unknown protein	---	AT2G20920	1.57	0.65	3.27	0.014536	0.053231	-3.71
249867_at	2-isopropylmalate synthase-like protei	IMS2	AT5G23020	-3.62	-1.86	-3.27	0.014551	0.053274	-3.71
260958_at	unknown protein identical to unknown	---	AT1G06060	-1.34	-0.42	-3.26	0.014562	0.053308	-3.71
245686_at	Expressed protein ; supported by cDN	J2	AT5G22060	1.71	0.78	3.26	0.014569	0.053324	-3.71
252141_at	putative protein	---	AT3G51100	1.24	0.31	3.26	0.014572	0.053327	-3.71
267423_at	putative potassium transporter	KUP11	AT2G35060	1.60	0.67	3.26	0.0146	0.05342	-3.71
254490_at	CTP synthase like protein CTP syntha	---	AT4G20320	1.52	0.60	3.26	0.014607	0.053439	-3.71
258433_at	translationally controlled tumor protein	TCTP	AT3G16640	1.36	0.44	3.26	0.014615	0.053458	-3.71
267135_at	cyclin-dependent kinase inhibitor prote	ICK1	AT2G23430	1.66	0.73	3.26	0.01462	0.053467	-3.71
248474_at	pyruvate dehydrogenase E1 compone	MAB1	AT5G50850	1.37	0.45	3.26	0.014628	0.053488	-3.72
251541_at	citrate synthase -like protein citrate sy	CSY2	AT3G58750	1.43	0.52	3.26	0.014637	0.053513	-3.72
267113_at	hypothetical protein predicted by gens	---	AT2G14850	1.25	0.32	3.26	0.014645	0.053533	-3.72
264450_s_	unknown protein similar to hypothetica	SNL6	AT1G10250 /	1.52	0.61	3.26	0.01465	0.053543	-3.72
259912_at	hypothetical protein	iqd8	AT1G72670	-1.37	-0.45	-3.26	0.014656	0.053559	-3.72
251862_at	putative protein arm repeat containing	PUB14	AT3G54850	1.27	0.35	3.26	0.014676	0.053622	-3.72
256245_at	heat shock protein 70 identical to heat	HSP70	AT3G12580	3.00	1.59	3.26	0.014686	0.053648	-3.72
253991_at	putative nucleic acid binding protein s	PEP	AT4G26000	-1.29	-0.37	-3.26	0.014701	0.053694	-3.72
245637_at	hypothetical protein similar to putative	---	AT1G25230	-2.16	-1.11	-3.26	0.014711	0.053724	-3.72
260123_at	AIG1-like protein similar to AIG1 prote	---	AT1G33890	-1.28	-0.36	-3.26	0.014716	0.053732	-3.72
261007_at	hypothetical protein similar to reticuline	---	AT1G26400	1.22	0.28	3.26	0.014742	0.053819	-3.72
249719_at	Expressed protein ; supported by full-l	---	AT5G35735	2.16	1.11	3.25	0.014771	0.053918	-3.73
263600_at	hypothetical protein predicted by gens	DRD1	AT2G16390	-1.33	-0.41	-3.25	0.014777	0.053929	-3.73
264356_at	putative DNA repair protein Strong sim	UVH6	AT1G03190	1.29	0.36	3.25	0.014783	0.053945	-3.73
260125_at	putative heat shock protein similar to G	---	AT1G36390	-1.44	-0.53	-3.25	0.014793	0.05397	-3.73
266746_s_	putative glutathione S-transferase ;su	ATGSTF3	AT2G02930 /	3.10	1.63	3.25	0.014805	0.054007	-3.73
247282_at	putative protein strong similarity to unk	AtMC3	AT5G64240	-1.33	-0.41	-3.25	0.014809	0.054012	-3.73
248148_at	putative protein similar to unknown pro	---	AT5G54930	1.52	0.60	3.25	0.014817	0.054034	-3.73
264986_at	glutathione transferase, putative simil	ATGSTU13	AT1G27130	2.80	1.49	3.25	0.014836	0.054093	-3.73
258392_at	anther development protein, ATA20 id	ATA20	AT3G15400	-1.40	-0.49	-3.25	0.014859	0.05417	-3.73
259146_at	putative glycerol-3-phosphate dehydro	SDP6	AT3G10370	1.41	0.49	3.25	0.014911	0.054346	-3.74
247105_at	putative protein similar to unknown pro	DAR5	AT5G66630	1.42	0.51	3.25	0.014913	0.054346	-3.74
250816_at	coatomer delta subunit (delta-coat prot	---	AT5G05010	-1.40	-0.49	-3.25	0.014924	0.05438	-3.74
259082_at	unknown protein similar to hypothetica	---	AT3G04820	1.55	0.63	3.25	0.014943	0.054422	-3.74
258932_at	hypothetical protein predicted by gens	PAP16	AT3G10150	1.27	0.35	3.25	0.014943	0.054422	-3.74
252045_at	putative protein arm repeat containing	PUB22	AT3G52450	4.61	2.20	3.25	0.014942	0.054422	-3.74

248646_at	unknown protein ;supported by full-ler	---	AT5G49100	-1.70	-0.76	-3.24	0.014964	0.054491	-3.74
252408_at	putative transcription factor MYB94 ; s	ATMYB94	AT3G47600	-1.24	-0.31	-3.24	0.014987	0.054562	-3.74
254086_at	putative proteasome regulatory subun	---	AT4G24820	1.23	0.30	3.24	0.014988	0.054562	-3.74
260257_at	putative dolichyl-phosphate mannosylt	---	AT1G74340	-1.27	-0.34	-3.24	0.014999	0.054582	-3.74
245875_at	hypothetical protein predicted by gene	---	AT1G26240	1.37	0.45	3.24	0.015001	0.054582	-3.74
262855_at	putative inorganic phosphate transport	---	AT1G20860	1.43	0.52	3.24	0.014998	0.054582	-3.74
251666_at	CYSTATHIONINE BETA-LYASE PRE	CBL	AT3G57050	-1.40	-0.49	-3.24	0.015014	0.05462	-3.74
260418_s_	hypothetical protein predicted by gene	COX19-1	AT1G66590 /	1.86	0.90	3.24	0.015026	0.054656	-3.74
267310_at	unknown protein	AIR9	AT2G34680	-2.02	-1.02	-3.24	0.015035	0.05467	-3.74
254243_at	serine/threonine kinase - like protein s	CRK13	AT4G23210	3.31	1.73	3.24	0.015035	0.05467	-3.74
245041_at	AR781, similar to yeast pheromone re	AR781	AT2G26530	3.43	1.78	3.24	0.01504	0.054682	-3.74
256982_at	unknown protein	ECT2	AT3G13460	1.29	0.37	3.24	0.01505	0.054701	-3.75
245458_at	kinase like protein	---	AT4G16970	-1.30	-0.37	-3.24	0.015051	0.054701	-3.75
249195_s_	disease resistance response protein-li	---	AT5G42500 /	1.49	0.57	3.24	0.015063	0.054738	-3.75
251557_at	v-ATPase subunit D (vATPD) ; suppo	---	AT3G58730	-1.29	-0.37	-3.24	0.015094	0.054841	-3.75
252128_at	transcription factor-like protein Arabid	MNP	AT3G50870	-1.26	-0.34	-3.24	0.015107	0.05487	-3.75
255512_at	Expressed protein ; supported by cDN	SYP42	AT4G02195	-1.40	-0.48	-3.24	0.015106	0.05487	-3.75
262888_at	RNA-directed RNA polymerase, putat	RDR1	AT1G14790	1.88	0.91	3.24	0.015114	0.054887	-3.75
255803_at	putative protein vesicle-associated me	---	AT4G10170	-1.27	-0.34	-3.24	0.015127	0.054926	-3.75
257937_at	hypothetical protein predicted by gens	---	AT3G19810	-1.24	-0.31	-3.24	0.015141	0.054967	-3.75
264057_at	putative AP2 domain transcription fact	RAP2.7	AT2G28550	-1.51	-0.59	-3.24	0.015145	0.054973	-3.75
265377_at	putative beta-1,3-glucanase	---	AT2G05790	-3.67	-1.87	-3.24	0.015156	0.055004	-3.75
252423_at	putative protein putative hydrolyse - A	---	AT3G47590	-1.27	-0.35	-3.23	0.01518	0.055083	-3.75
247659_at	DNA-directed RNA polymerase - like p	NRPC1	AT5G60040	1.87	0.90	3.23	0.015184	0.055089	-3.75
252268_at	kinesin-like protein several kinesin-like	---	AT3G49650	-1.43	-0.51	-3.23	0.015187	0.055091	-3.76
265019_at	putative myosin heavy chain similar to	---	AT1G24560	1.24	0.31	3.23	0.015196	0.055116	-3.76
249640_at	cationic amino acid transporter -like p	CAT3	AT5G36940	-1.51	-0.60	-3.23	0.015199	0.055116	-3.76
256266_at	unknown protein ; supported by cDNA	---	AT3G12320	-1.67	-0.74	-3.23	0.015202	0.055118	-3.76
253843_at	putative protein MLL protein, Gallus g	SDG16	AT4G27910	-1.24	-0.31	-3.23	0.015214	0.055144	-3.76
256414_at	putative nucleic acid binding protein si	AL2	AT3G11200	1.29	0.36	3.23	0.015212	0.055144	-3.76
251301_at	cytochrome p450 (CYP78A9) ;suppor	CYP78A9	AT3G61880	1.34	0.43	3.23	0.015217	0.055149	-3.76
255485_at	predicted protein of unknown function	---	AT4G02550	1.28	0.36	3.23	0.015228	0.055178	-3.76
261824_at	DAG protein, putative similar to DAG	---	AT1G11430	-1.25	-0.32	-3.23	0.015239	0.055212	-3.76
245894_at	putative protein ; supported by full-len	---	AT5G09310	-1.26	-0.33	-3.23	0.015267	0.055302	-3.76
260764_at	unknown protein	---	AT1G48950	-1.37	-0.46	-3.23	0.015274	0.055321	-3.76

253388_at	putative protein ; supported by cDNA:	---	AT4G32910	1.47	0.55	3.23	0.015279	0.055328	-3.76
265400_at	unknown protein ;supported by full-ler	---	AT2G10940	-38.13	-5.25	-3.23	0.015291	0.055363	-3.76
262571_at	hypothetical protein predicted by gens	---	AT1G15430	1.84	0.88	3.23	0.015295	0.055368	-3.76
266720_s_	hypothetical protein predicted by gene	APRR9	AT2G46670 /	-1.66	-0.73	-3.23	0.015309	0.055411	-3.76
262485_at	kinesin-like protein Similar to gb|U066	---	AT1G21730	-1.25	-0.32	-3.23	0.015318	0.055436	-3.76
260449_at	unknown protein	---	AT1G72390	1.23	0.30	3.23	0.015328	0.055461	-3.76
252083_at	putative protein hypothetical protein M	---	AT3G51960	1.87	0.90	3.23	0.015331	0.055463	-3.77
264227_at	hypothetical protein contains similarity	ATREV3	AT1G67500	-1.29	-0.37	-3.23	0.015333	0.055463	-3.77
247629_at	putative protein	SIZ1	AT5G60410	1.34	0.42	3.22	0.015377	0.055611	-3.77
244973_at	PSII T protein	---	---	-1.82	-0.86	-3.22	0.015405	0.055707	-3.77
255614_at	putative myb-related DNA-binding prot	---	AT4G01280	1.27	0.34	3.22	0.015421	0.055753	-3.77
249023_at	putative protein strong similarity to unk	---	AT5G44850	-1.75	-0.81	-3.22	0.015432	0.055787	-3.77
246937_at	phospholipase D1-like protein phosph	PLDALPHA3	AT5G25370	-1.27	-0.35	-3.22	0.015437	0.055796	-3.77
256000_at	glycyl tRNA synthetase, putative simil	---	AT1G29880	-1.33	-0.41	-3.22	0.015463	0.05588	-3.77
258078_at	unknown protein ;supported by full-ler	---	AT3G25870	1.72	0.78	3.22	0.015475	0.055912	-3.78
259822_at	myb-related transcription factor, putati	MYB20	AT1G66230	-1.65	-0.72	-3.22	0.015485	0.055943	-3.78
251640_at	putative protein ;supported by full-leng	---	AT3G57450	2.67	1.42	3.22	0.015489	0.055948	-3.78
256661_at	hypothetical protein similar to putative	---	AT3G11964	1.27	0.35	3.22	0.015509	0.056011	-3.78
257324_at	hypothetical protein	---	---	2.06	1.04	3.22	0.015519	0.056038	-3.78
251714_at	putative protein leucine-rich receptor-l	---	AT3G56370	-1.84	-0.88	-3.22	0.015526	0.056052	-3.78
255643_at	hypothetical protein	---	AT4G00840	-1.27	-0.35	-3.22	0.015572	0.056209	-3.78
263882_at	putative ribonucleoside-diphosphate re	RNR1	AT2G21790	-1.84	-0.88	-3.21	0.015575	0.056214	-3.78
249600_s_	oxidoreductase-like protein zeta-cryst	---	AT5G37940 /	1.22	0.29	3.21	0.015608	0.056321	-3.78
245993_at	putative protein predicted proteins, Ar	---	AT5G20700	1.52	0.60	3.21	0.015618	0.05635	-3.78
265996_at	putative leucine aminopeptidase identi	---	AT2G24200	1.76	0.81	3.21	0.015622	0.056357	-3.79
264211_at	putative gigantea protein strong similar	GI	AT1G22770	1.24	0.31	3.21	0.015627	0.056364	-3.79
262298_at	unknown protein Similar to gb|AF1518	---	AT1G27530	1.24	0.31	3.21	0.015634	0.056379	-3.79
264442_at	hypothetical protein similar to lecithin:c	---	AT1G27480	-1.51	-0.59	-3.21	0.015636	0.056379	-3.79
254081_at	putative protein various predicted prot	---	AT4G25660	-1.36	-0.44	-3.21	0.015642	0.056385	-3.79
266814_at	homeodomain transcription factor (ATH	ATHB4	AT2G44910	-1.22	-0.28	-3.21	0.015641	0.056385	-3.79
251719_at	putative protein PUTATIVE PROTEIN	---	AT3G56140	1.36	0.44	3.21	0.015653	0.056405	-3.79
263015_at	hypothetical protein similar to hypothet	---	AT1G23440	1.33	0.41	3.21	0.015652	0.056405	-3.79
247323_at	putative protein similar to unknown pro	---	AT5G64170	1.45	0.54	3.21	0.015674	0.056473	-3.79
253247_at	Homeodomain - like protein similaritry	BLH6	AT4G34610	-1.57	-0.65	-3.21	0.015678	0.056477	-3.79
255736_at	unknown protein contains similarity to	---	AT1G25380	1.30	0.38	3.21	0.015684	0.05649	-3.79

264025_at	AUX1-like amino acid permease ; sup	---	AT2G21050	-2.41	-1.27	-3.21	0.015693	0.056515	-3.79
261655_at	hypothetical protein predicted by gene	---	AT1G01940	1.44	0.52	3.21	0.01571	0.056567	-3.79
252570_at	isovaleryl-CoA-dehydrogenase precurs	IVD	AT3G45300	1.75	0.81	3.21	0.01572	0.056591	-3.79
248009_at	transcription factor-like; similar to CH6	CSN6A	AT5G56280	-1.29	-0.37	-3.21	0.015753	0.056694	-3.79
250419_at	RPP1 disease resistance protein - like	---	AT5G11250	1.43	0.52	3.21	0.015752	0.056694	-3.79
248679_at	unknown protein ;supported by full-ler	---	AT5G48830	-1.48	-0.56	-3.21	0.015756	0.056696	-3.79
263104_at	unknown protein	---	AT2G05120	1.33	0.41	3.20	0.015785	0.056792	-3.80
260143_at	sucrose transport protein SUC1 identic	SUC1	AT1G71880	1.85	0.89	3.20	0.015799	0.056832	-3.80
250039_at	disease resistance protein -like diseas	---	AT5G18370	1.36	0.44	3.20	0.015803	0.056836	-3.80
245817_at	hypothetical protein similar to unknowr	---	AT1G26160	-1.24	-0.31	-3.20	0.015805	0.056836	-3.80
255851_at	hypothetical protein predicted by gene	---	AT1G67040	-1.36	-0.45	-3.20	0.015836	0.056939	-3.80
245900_at	putative protein predicted proteins, Ar	---	AT5G11040	-1.34	-0.43	-3.20	0.01584	0.056942	-3.80
262523_at	ubiquitin-specific protease 15 (UBP15	UBP15	AT1G17110	-1.23	-0.30	-3.20	0.015852	0.056978	-3.80
246493_at	putative protein hypothetical proteins -	CRS1	AT5G16180	-1.34	-0.42	-3.20	0.015857	0.056987	-3.80
266921_at	putative cytochrome P450	CYP86A8	AT2G45970	-2.04	-1.03	-3.20	0.015884	0.057076	-3.80
251740_at	peptidylprolyl isomerase	ROC2	AT3G56070	1.68	0.75	3.20	0.015896	0.05709	-3.80
267579_at	metallothionein-like protein	---	AT2G42000	-1.23	-0.30	-3.20	0.015894	0.05709	-3.80
247216_at	4-alpha-glucanotransferase ; supporte	DPE1	AT5G64860	-1.42	-0.50	-3.20	0.015894	0.05709	-3.80
255442_at	predicted NADH dehydrogenase 24 k	---	AT4G02580	-1.26	-0.33	-3.20	0.015906	0.05711	-3.80
248115_at	putative protein strong similarity to unk	---	AT5G54870	1.59	0.66	3.20	0.015905	0.05711	-3.80
254125_at	putative alliin lyase alliin lyase (EC 4.4	TAR2	AT4G24670	-1.70	-0.77	-3.20	0.015913	0.057127	-3.80
249259_at	putative protein similar to unknown pro	---	AT5G41660	2.59	1.37	3.20	0.015923	0.057152	-3.81
267353_at	En/Spm-like transposon protein relatec	---	AT2G40070	-1.38	-0.47	-3.20	0.015926	0.057154	-3.81
264807_at	putative presenilin similar to presenilin	---	AT1G08700	1.41	0.49	3.20	0.015939	0.057191	-3.81
248313_at	putative protein contains similarity to G	---	AT5G52580	-1.23	-0.30	-3.20	0.015955	0.057242	-3.81
265712_s_	unknown protein	---	AT2G03330 /	1.29	0.37	3.20	0.015967	0.057273	-3.81
260152_at	putative IAA6 protein similar to IAA6 p	IAA6	AT1G52830	-1.79	-0.84	-3.20	0.015972	0.057284	-3.81
261756_at	Expressed protein ; supported by full-l	---	AT1G08315	1.73	0.79	3.20	0.015979	0.0573	-3.81
246465_at	quinone oxidoreductase - like protein	---	AT5G17000	1.55	0.63	3.20	0.015997	0.057355	-3.81
256279_at	protein phosphatase 2C, putative cont	---	AT3G12620	-1.21	-0.28	-3.19	0.016015	0.057395	-3.81
253027_at	putative protein leaf protein (PnC401)	---	AT4G38150	1.52	0.61	3.19	0.016018	0.057395	-3.81
252954_at	putative thaumatin-like protein thauma	---	AT4G38660	-2.47	-1.30	-3.19	0.016013	0.057395	-3.81
262719_at	hypothetical protein predicted by gens	---	---	1.30	0.38	3.19	0.016016	0.057395	-3.81
253539_at	putative protein RING-finger protein -	---	AT4G31450	1.32	0.40	3.19	0.016025	0.057411	-3.81
254641_at	ras-like GTP-binding protein strong ho	ATRABA1D	AT4G18800	1.49	0.58	3.19	0.016029	0.057415	-3.81

250633_at	peptide methionine sulfoxide reductas	PMSR2	AT5G07460	2.26	1.18	3.19	0.016042	0.057451	-3.81
261891_at	transcriptional regulator, putative simil	---	AT1G80790	1.23	0.30	3.19	0.01606	0.057474	-3.81
260915_at	hypothetical protein similar to hypothet	---	AT1G02660	-1.83	-0.87	-3.19	0.016059	0.057474	-3.81
257625_at	cytochrome P450, putative contains P	CYP71B24	AT3G26230	3.50	1.81	3.19	0.016057	0.057474	-3.81
263179_at	unknown protein similar to unknown pr	---	AT1G05710	1.62	0.70	3.19	0.016054	0.057474	-3.81
256254_at	hypothetical protein predicted by gens	---	AT3G11290	-1.38	-0.47	-3.19	0.01606	0.057474	-3.81
258149_at	hypothetical protein contains Pfam pro	EMB1270	AT3G18110	-1.36	-0.45	-3.19	0.016076	0.05751	-3.82
257053_at	ethylene responsive element binding fa	ERF4	AT3G15210	2.37	1.24	3.19	0.016075	0.05751	-3.82
245114_at	transcription factor IIB (TFIIB) identical	TFIIB	AT2G41630	-1.55	-0.63	-3.19	0.016082	0.057523	-3.82
247568_at	putative protein predicted proteins, Ar	---	AT5G61260	1.67	0.74	3.19	0.016085	0.057524	-3.82
263799_at	unknown protein ; supported by cDNA	---	AT2G24550	-1.48	-0.56	-3.19	0.016096	0.057557	-3.82
266915_at	hypothetical protein predicted by gens	---	AT2G45870	-1.26	-0.34	-3.19	0.016107	0.057586	-3.82
253552_at	ubiquitin-specific protease 24 (UBP24	UBP24	AT4G30890	1.27	0.34	3.19	0.016123	0.057627	-3.82
245292_at	Expressed protein ; supported by cDN	---	AT4G15093	1.38	0.47	3.19	0.016124	0.057627	-3.82
255825_at	Expressed protein ; supported by full-le	---	AT2G40475	-1.49	-0.57	-3.19	0.016134	0.057639	-3.82
245356_at	adenosylhomocysteinase ;supported b	MEE58	AT4G13940	1.46	0.54	3.19	0.016131	0.057639	-3.82
251482_s_	receptor lectin kinase 3	---	AT3G59740 /	1.33	0.41	3.19	0.016133	0.057639	-3.82
259583_at	hypothetical protein	---	AT1G28070	-1.34	-0.42	-3.19	0.016138	0.057644	-3.82
266911_at	putative protein kinase contains a prot	---	AT2G45910	1.40	0.49	3.19	0.016141	0.057645	-3.82
258861_at	putative helicase similar to C-terminal	---	AT3G02060	1.43	0.51	3.19	0.01615	0.057667	-3.82
246194_at	putative protein ;supported by full-leng	ACD2	AT4G37000	-1.41	-0.49	-3.19	0.016161	0.057697	-3.82
259405_at	Expressed protein ; supported by cDN	---	AT1G17744	1.46	0.55	3.19	0.016167	0.05771	-3.82
251886_at	putative protein various predicted prot	---	AT3G54260	-1.53	-0.61	-3.19	0.016174	0.057726	-3.82
253294_at	hypothetical protein	---	AT4G33740	1.30	0.38	3.19	0.016187	0.057763	-3.82
265657_at	unknown protein ; supported by cDNA	---	AT2G13840	-1.32	-0.40	-3.18	0.016223	0.057884	-3.83
259694_at	uridine diphosphate glucose epimeras	UGE3	AT1G63180	2.08	1.06	3.18	0.016241	0.057937	-3.83
249060_at	putative protein similar to unknown pro	VPS2.2	AT5G44560	-1.24	-0.31	-3.18	0.016253	0.057964	-3.83
252057_at	putative protein ;supported by full-leng	---	AT3G52480	1.61	0.69	3.18	0.016251	0.057964	-3.83
260789_s_	acyl-CoA oxidase ACX3 identical to ac	ACX3	AT1G06290 /	1.24	0.31	3.18	0.016257	0.05797	-3.83
258566_at	putative glutamate receptor (GLR1) ide	GLR1.1	AT3G04110	1.56	0.65	3.18	0.01627	0.058005	-3.83
249529_at	putative protein predicted proteins, Ar	---	AT5G38730	1.46	0.55	3.18	0.016279	0.058018	-3.83
263941_at	unknown protein	---	---	-1.36	-0.44	-3.18	0.016276	0.058018	-3.83
265729_at	putative glucan synthase	ATGSL03	AT2G31960	1.39	0.48	3.18	0.016293	0.058056	-3.83
259071_at	unknown protein similar to hin1 GB:CA	NHL2	AT3G11650	-1.54	-0.62	-3.18	0.016294	0.058056	-3.83
259885_at	hypothetical protein contains Pfam pro	---	AT1G76380	1.44	0.53	3.18	0.01632	0.058138	-3.83

249869_at	acetyl-CoA synthetase-like protein	AAE17	AT5G23050	1.46	0.55	3.18	0.016326	0.058147	-3.83
257321_at	hypothetical protein	---	---	1.65	0.72	3.18	0.016328	0.058147	-3.83
265993_at	putative disease resistance protein	---	AT2G24160	3.68	1.88	3.18	0.016343	0.058191	-3.83
248227_at	ABA-inducible protein-like ;supported	---	AT5G53820	1.29	0.37	3.18	0.016346	0.058196	-3.83
266889_at	hypothetical protein predicted by gens	---	AT2G44640	-1.32	-0.40	-3.18	0.016375	0.05826	-3.84
255966_at	14-3-3 protein GF14epsilon (grf10) ide	GRF10	AT1G22300	1.35	0.43	3.18	0.016374	0.05826	-3.84
253859_at	Expressed protein ; supported by full-l	---	AT4G27657	5.38	2.43	3.18	0.016372	0.05826	-3.84
253937_at	putative NPK1-related protein kinase I	MAPKKK16	AT4G26890	-1.56	-0.64	-3.18	0.016371	0.05826	-3.84
267207_at	putative dioxygenase	---	AT2G30840	1.86	0.89	3.18	0.016389	0.058303	-3.84
248462_at	nucleotide-binding protein ; supported	NBP35	AT5G50960	1.34	0.42	3.18	0.016395	0.058316	-3.84
253958_at	putative protein RING zinc finger prote	---	AT4G26400	-1.31	-0.39	-3.18	0.016401	0.058317	-3.84
255401_at	hypothetical protein ;supported by full-	---	AT4G03600	-1.36	-0.45	-3.18	0.016399	0.058317	-3.84
251879_at	putative protein hin1 protein, Nicotiana	---	AT3G54200	-1.66	-0.73	-3.18	0.016412	0.058346	-3.84
266313_at	putative protein kinase contains a prot	CIPK3	AT2G26980	-1.59	-0.67	-3.18	0.016429	0.058399	-3.84
254390_at	calcium-dependent protein kinase - lik	CPK15	AT4G21940	1.30	0.37	3.18	0.016438	0.058422	-3.84
249208_at	allene oxide synthase (emb CAA7318	AOS	AT5G42650	-2.04	-1.03	-3.17	0.016468	0.058519	-3.84
267379_at	unknown protein ; supported by cDNA	---	AT2G26340	-1.49	-0.58	-3.17	0.016478	0.058546	-3.84
266790_at	expansin AtEx6 identical to GB U3048	ATEXPA6	AT2G28950	-3.28	-1.71	-3.17	0.016499	0.05861	-3.84
258693_at	unknown protein	---	AT3G08650	1.24	0.31	3.17	0.016508	0.058633	-3.84
265308_at	putative protein kinase contains a prot	ALE2	AT2G20300	-1.22	-0.29	-3.17	0.016512	0.058639	-3.84
256715_at	hypothetical protein predicted by gene	MEE18	AT2G34090	-1.47	-0.56	-3.17	0.016529	0.058692	-3.85
249901_at	histone deacetylase-like protein non-c	HD2B	AT5G22650	1.44	0.52	3.17	0.016556	0.058759	-3.85
262800_at	putative ATP-dependent RNA helicas	emb1507	AT1G20960	1.30	0.38	3.17	0.016553	0.058759	-3.85
247839_at	eukaryotic initiation factor 4, eIF4-like	---	AT5G57870	1.47	0.56	3.17	0.016555	0.058759	-3.85
248081_at	putative protein similar to unknown pro	EDM2	AT5G55390	1.24	0.31	3.17	0.016563	0.058775	-3.85
259913_at	putative GTP-binding protein similar to	---	AT1G72660	1.22	0.29	3.17	0.016573	0.0588	-3.85
259570_at	hypothetical protein	COR47	AT1G20440	-1.63	-0.71	-3.17	0.016584	0.058829	-3.85
245770_at	hypothetical protein predicted by gene	---	AT1G30240	1.54	0.62	3.17	0.016602	0.058876	-3.85
260011_at	hypothetical protein similar to hypothe	---	AT1G68110	-1.36	-0.45	-3.17	0.0166	0.058876	-3.85
264175_at	unknown protein Similar to rice chalco	---	AT1G02050	1.36	0.45	3.17	0.01661	0.058891	-3.85
248265_at	putative protein contains similarity to z	SDG29	AT5G53430	1.42	0.50	3.17	0.016611	0.058891	-3.85
245886_at	ribosomal protein S15-like ribosomal p	---	AT5G09510	-1.23	-0.30	-3.17	0.01662	0.058913	-3.85
262249_at	root hairless 1 (RHL1) similar to root h	RHL1	AT1G48380	-1.31	-0.39	-3.17	0.016656	0.059029	-3.85
267616_at	unknown protein ;supported by full-ler	---	AT2G26680	-1.31	-0.39	-3.16	0.016667	0.059062	-3.85
257828_at	unknown protein	---	AT3G26670	1.57	0.65	3.16	0.016698	0.059163	-3.86

259873_s_	putative translation initiation factor IF-2	---	AT1G76720 /	-1.41	-0.49	-3.16	0.016714	0.059208	-3.86
255600_s_	putative protein predicted protein, Ara	---	AT4G01020 /	1.24	0.31	3.16	0.016721	0.059226	-3.86
248582_at	heat shock protein 70 (gb|AAF27639.1	CPHSC70-2	AT5G49910	1.57	0.65	3.16	0.016728	0.059239	-3.86
262984_at	hypothetical protein predicted by gene	---	AT1G54460	1.60	0.68	3.16	0.016741	0.059277	-3.86
258143_at	hypothetical protein	---	AT3G18170	-1.49	-0.58	-3.16	0.016761	0.059337	-3.86
266323_at	putative calcium-dependent protein kin	CRK3	AT2G46700	-1.31	-0.39	-3.16	0.016797	0.059458	-3.86
261196_at	unknown protein	SCRM2	AT1G12860	-1.66	-0.73	-3.16	0.01681	0.059495	-3.86
266986_at	putative dolichyl-phosphate beta-gluco	---	AT2G39630	1.24	0.31	3.16	0.016839	0.059585	-3.86
245164_at	mitochondrial chaperonin (HSP60)	HSP60-2	AT2G33210	1.85	0.89	3.16	0.016859	0.059647	-3.87
265968_at	putative protein translocase ; supporte	ATTIM17-2	AT2G37410	1.48	0.57	3.16	0.01687	0.059679	-3.87
260400_at	putative peptide transporter similar to p	---	AT1G69860	-1.23	-0.30	-3.16	0.016883	0.059715	-3.87
255480_at	Expressed protein ; supported by full-le	---	AT4G02485	-1.25	-0.32	-3.15	0.016903	0.059777	-3.87
253909_at	putative protein LEDI-3 protein, Lithos	---	AT4G27270	-1.35	-0.44	-3.15	0.016909	0.05978	-3.87
248451_at	putative protein similar to unknown pro	---	AT5G51180	-1.22	-0.29	-3.15	0.016907	0.05978	-3.87
265087_at	hypothetical protein predicted by gene	---	AT1G03760	1.57	0.65	3.15	0.016963	0.059942	-3.87
253300_at	carbonate dehydratase - like protein c	BCA5	AT4G33580	-1.49	-0.57	-3.15	0.016963	0.059942	-3.87
249046_at	berberine bridge enzyme	---	AT5G44400	1.66	0.73	3.15	0.016962	0.059942	-3.87
245681_at	alkaline/neutral invertase, putative sim	---	AT1G56560	1.24	0.31	3.15	0.016968	0.059951	-3.87
260697_at	unknown protein	---	AT1G32530	1.47	0.56	3.15	0.016973	0.059958	-3.87
266395_at	3-isopropylmalate dehydratase, small	---	AT2G43100	-1.98	-0.98	-3.15	0.016977	0.059962	-3.87
255963_at	unknown protein	MBD8	AT1G22310	-1.29	-0.36	-3.15	0.016993	0.059984	-3.87
254533_at	putative protein ARI protein - Drosoph	---	AT4G19670	1.45	0.54	3.15	0.016992	0.059984	-3.87
251369_at	putative protein ;supported by full-leng	---	AT3G60480	-1.33	-0.41	-3.15	0.016988	0.059984	-3.87
266803_at	putative protein kinase contains a prot	APK1B	AT2G28930	-1.80	-0.85	-3.15	0.016987	0.059984	-3.87
251116_at	serin carboxypeptidase - like protein c	scpl40	AT3G63470	1.36	0.44	3.15	0.017012	0.060041	-3.88
267391_at	putative beta-glucosidase	BGLU17	AT2G44480	1.46	0.54	3.15	0.017016	0.060047	-3.88
254253_at	serine/threonine kinase - like protein s	---	AT4G23320	2.16	1.11	3.15	0.017021	0.060053	-3.88
253448_at	putative protein mRNA for KIAA0079	---	AT4G32640	1.24	0.30	3.15	0.017053	0.060158	-3.88
245786_at	G-Box binding protein, putative similar	---	AT1G32150	-1.22	-0.28	-3.15	0.017056	0.060158	-3.88
261991_at	hypothetical protein predicted by gene	---	AT1G33700	-1.38	-0.47	-3.15	0.017066	0.060185	-3.88
265412_at	putative chloroplast outer membrane p	TOC132	AT2G16640	1.23	0.29	3.15	0.017074	0.060204	-3.88
267099_at	DNA-(apurinic or apyrimidinic site) lyas	ARP	AT2G41460	1.50	0.58	3.15	0.01708	0.060208	-3.88
259342_at	unknown protein ;supported by full-ler	---	AT3G03890	1.42	0.51	3.15	0.01708	0.060208	-3.88
253582_at	Expressed protein ;supported by cDNA	---	AT4G30670	-1.45	-0.53	-3.15	0.0171	0.060268	-3.88
256222_at	hypothetical protein predicted by gene	---	AT1G56210	-1.48	-0.56	-3.14	0.017131	0.060369	-3.88

258910_at	putative RNA helicase similar to RNA	---	AT3G06480	1.26	0.33	3.14	0.017135	0.060374	-3.88
247264_at	putative protein contains similarity to N	XND1	AT5G64530	1.82	0.87	3.14	0.017145	0.060399	-3.88
247931_at	putative protein similar to unknown pro	---	AT5G57040	-1.36	-0.45	-3.14	0.017154	0.060421	-3.88
256223_at	unknown protein ;supported by full-len	emb1303	AT1G56200	1.33	0.41	3.14	0.017158	0.060422	-3.88
266588_at	putative proline-rich protein ; supporte	AGP9	AT2G14890	-3.79	-1.92	-3.14	0.01716	0.060422	-3.89
260469_at	BRCA1-associated RING domain prote	AGD4	AT1G10870	-1.37	-0.45	-3.14	0.017163	0.060424	-3.89
258006_at	cysteine proteinase non-consensus A	---	AT3G19400	-1.41	-0.50	-3.14	0.01718	0.060474	-3.89
262422_at	hypothetical protein similar to hypothet	---	AT1G23440	1.35	0.43	3.14	0.017211	0.060574	-3.89
264787_at	putative senescence-associated protei	ERD7	AT2G17840	-1.56	-0.65	-3.14	0.01722	0.060596	-3.89
256534_at	unknown protein	---	AT1G33270	1.27	0.35	3.14	0.017248	0.060685	-3.89
262695_at	vacuolor sorting protein 35, putative s	VPS35B	AT1G75850	1.26	0.33	3.14	0.017265	0.060737	-3.89
251739_at	putative protein protein of unknown fu	CAN	AT3G56170	1.41	0.50	3.14	0.017282	0.060776	-3.89
266576_at	hypothetical protein predicted by gens	---	AT2G23940	-1.28	-0.35	-3.14	0.017282	0.060776	-3.89
248628_at	putative protein contains similarity to 5	---	AT5G48960	-1.30	-0.38	-3.14	0.017289	0.060792	-3.89
260484_at	putative zinc finger protein similar to zi	---	AT1G68360	1.31	0.39	3.14	0.017319	0.06089	-3.89
246603_at	copper amine oxidase, putative simila	---	AT1G31690	-1.43	-0.52	-3.14	0.017335	0.060935	-3.90
261365_at	proton pump interactor, putative simila	---	AT1G53110	1.95	0.96	3.14	0.017344	0.060958	-3.90
266763_at	unknown protein	SPL1	AT2G47070	-1.34	-0.42	-3.14	0.017355	0.060986	-3.90
267581_at	putative RING zinc finger protein	---	AT2G41980	-1.54	-0.62	-3.13	0.01737	0.061029	-3.90
265116_at	unknown protein ; supported by full-ler	---	AT1G62480	3.28	1.72	3.13	0.017381	0.061058	-3.90
261720_at	hypothetical protein similar to hypothet	HDA08	AT1G08460	1.54	0.62	3.13	0.017409	0.061134	-3.90
248279_at	putative protein similar to unknown pro	ATIM	AT5G52910	-1.75	-0.81	-3.13	0.01741	0.061134	-3.90
260726_at	signal recognition particle 19 kDa prot	---	AT1G48160	-1.41	-0.49	-3.13	0.017406	0.061134	-3.90
267629_at	putative DNA polymerase delta small s	POLD2	AT2G42120	-1.41	-0.50	-3.13	0.017423	0.06117	-3.90
AFFX-Atha	Arabidopsis thaliana /REF=U37281.1 /	---	---	-1.36	-0.44	-3.13	0.017433	0.061194	-3.90
267411_at	putative disease resistance protein	---	AT2G34930	-3.90	-1.96	-3.13	0.017439	0.061198	-3.90
255947_at	hypothetical protein contains Pfam pro	---	AT1G22040	1.28	0.35	3.13	0.017439	0.061198	-3.90
245089_at	putative transketolase precursor ; sup	---	AT2G45290	3.24	1.70	3.13	0.017444	0.061204	-3.90
258531_at	importin alpha identical to GB:AAC27	IMPA-1	AT3G06720	1.24	0.31	3.13	0.017475	0.061297	-3.90
246502_at	stearoyl-acyl carrier protein desaturas	---	AT5G16240	-1.43	-0.51	-3.13	0.017475	0.061297	-3.90
260248_at	heat shock protein 101 (HSP101) iden	ATHSP101	AT1G74310	1.66	0.73	3.13	0.017497	0.061364	-3.91
249906_at	unknown protein	---	AT5G22730	-1.24	-0.31	-3.13	0.017513	0.06141	-3.91
256183_at	MAP kinase kinase 4 (ATMKK4) identi	MKK4	AT1G51660	1.94	0.96	3.13	0.01753	0.061459	-3.91
258559_at	putative transcriptional regulator simila	ATCHR12	AT3G06010	1.36	0.45	3.13	0.017549	0.061512	-3.91
261792_at	cinnamoyl CoA reductase, puitative si	CCR1	AT1G15950	1.34	0.42	3.13	0.01755	0.061512	-3.91

258369_at	putative pectin methylesterase similar	ATPME3	AT3G14310	-1.33	-0.41	-3.12	0.017603	0.061689	-3.91
256148_at	hypothetical protein similar to putative	---	AT1G55090	-1.22	-0.29	-3.12	0.01762	0.061736	-3.91
258460_at	unknown protein	ECT6	AT3G17330	-1.36	-0.45	-3.12	0.017631	0.061768	-3.91
258868_at	putative exportin1 (XPO1) protein simi	XPO1B	AT3G03110	1.31	0.39	3.12	0.017641	0.061784	-3.91
259649_at	Serine/arginine-rich protein, putative s	TAF7	AT1G55300	-1.27	-0.34	-3.12	0.017643	0.061784	-3.91
264498_at	Expressed protein ; supported by full-l	DIS2	AT1G30825	-1.33	-0.41	-3.12	0.017647	0.061784	-3.91
250670_at	polygalacturonase inhibiting protein 1;	PGIP1	AT5G06860	2.06	1.04	3.12	0.017646	0.061784	-3.91
251605_at	receptor-like protein kinase several rec	---	AT3G57830	-1.34	-0.42	-3.12	0.017655	0.061795	-3.92
258146_at	putative WD-repeat protein (WDR1-lik	---	AT3G18060	-1.33	-0.41	-3.12	0.017654	0.061795	-3.92
255953_at	transcription factor identical to transcri	TGA3	AT1G22070	1.40	0.48	3.12	0.017663	0.061813	-3.92
265788_at	putative auxin-induced protein	IAA32	AT2G01200	-1.23	-0.30	-3.12	0.017675	0.061843	-3.92
264084_at	putative kinesin light chain	---	AT2G31240	1.29	0.36	3.12	0.017699	0.061918	-3.92
246387_at	hypothetical protein predicted by gens	---	AT1G77400	-1.40	-0.48	-3.12	0.017701	0.061918	-3.92
251931_at	putative protein glyoxal oxidase (glx2)	---	AT3G53950	-1.51	-0.59	-3.12	0.017708	0.06193	-3.92
245759_at	hypothetical protein predicted by gene	---	AT1G66900	-1.38	-0.46	-3.12	0.017718	0.061958	-3.92
265317_at	unknown protein	BRK1	AT2G22640	-1.27	-0.35	-3.12	0.017723	0.061966	-3.92
248098_at	unknown protein ; supported by cDNA	---	AT5G55290	-1.28	-0.36	-3.12	0.017728	0.061973	-3.92
267027_at	hypothetical protein	---	AT2G38330	-1.40	-0.48	-3.12	0.017748	0.062022	-3.92
257124_at	hexokinase, putative similar to hexoki	ATHXK4	AT3G20040	1.28	0.36	3.12	0.017746	0.062022	-3.92
256672_at	ABC transporter, putative contains Pfa	---	AT3G52310	-1.37	-0.46	-3.12	0.017785	0.062135	-3.92
259921_at	putative protein kinase similar to protei	---	AT1G72540	2.60	1.38	3.12	0.017785	0.062135	-3.92
258904_at	putative ATPase (ISW2-like) similar to	CHR11	AT3G06400	1.31	0.39	3.12	0.017833	0.062292	-3.93
265615_at	putative dioxygenase ; supported by c	---	AT2G25450	1.34	0.42	3.12	0.017836	0.062292	-3.93
264484_at	hypothetical protein similar to ankyrin l	---	AT1G77260	-1.26	-0.33	-3.12	0.017841	0.062302	-3.93
250193_at	putative protein proline-rich protein M1	---	AT5G14540	-1.29	-0.36	-3.11	0.017858	0.062346	-3.93
253381_at	Tic22 -like protein strong homology to	---	AT4G33350	-1.32	-0.40	-3.11	0.017862	0.062346	-3.93
248596_at	putative protein contains similarity to m	AtMYB111	AT5G49330	-1.80	-0.85	-3.11	0.01786	0.062346	-3.93
262737_at	hypothetical protein	SRD2	AT1G28560	1.33	0.41	3.11	0.017869	0.062349	-3.93
256102_at	unknown protein	---	AT1G13680	-1.24	-0.31	-3.11	0.017868	0.062349	-3.93
258984_at	putative DnaJ protein Pfam HMM hit:	ATERDJ3A	AT3G08970	1.35	0.43	3.11	0.017871	0.062349	-3.93
265510_at	putative microtubule-associated protei	ATG8D	AT2G05630	1.28	0.35	3.11	0.017881	0.062375	-3.93
255718_at	unknown protein ;supported by full-len	ATNSI	AT1G32070	-1.29	-0.37	-3.11	0.017884	0.062375	-3.93
261531_at	RB-binding protein -like similar to retin	---	AT1G63490	1.44	0.53	3.11	0.017897	0.062401	-3.93
248769_at	putative protein strong similarity to unk	---	AT5G47730	2.31	1.21	3.11	0.017897	0.062401	-3.93
253389_at	hypothetical protein ;supported by full-	---	AT4G32680	-1.24	-0.31	-3.11	0.017908	0.062429	-3.93

258731_at	unknown protein ; supported by cDNA	---	AT3G11880	1.27	0.35	3.11	0.017927	0.062486	-3.93
249585_at	5-oxoprolinase -like protein 5-oxoproli	OXP1	AT5G37830	1.27	0.35	3.11	0.01794	0.062524	-3.93
263431_at	unknown protein ;supported by full-ler	---	AT2G22170	-4.95	-2.31	-3.11	0.017958	0.062561	-3.93
257671_at	hypothetical protein predicted by gens	---	AT3G20450	-1.34	-0.42	-3.11	0.017958	0.062561	-3.93
249462_at	putative protein predicted proteins, Ar	EMB2744	AT5G39680	1.31	0.39	3.11	0.017959	0.062561	-3.93
245435_at	hypothetical protein	AT4G17140	---	-1.22	-0.29	-3.11	0.017962	0.062562	-3.93
258776_at	putative T-complex protein 1, ETA sub	---	AT3G11830	-1.33	-0.41	-3.11	0.017988	0.062644	-3.94
248388_at	putative protein contains similarity to m	---	AT5G51980	1.32	0.40	3.11	0.018012	0.062718	-3.94
250192_at	pescadillo - like protein embryonic dev	---	AT5G14520	1.48	0.57	3.11	0.018016	0.062721	-3.94
246424_at	Exportin1 (XPO1) protein ; supported	XPO1A	AT5G17020	1.33	0.41	3.11	0.018024	0.062738	-3.94
257892_at	unknown protein similar to ER6 protein	---	AT3G17020	1.28	0.36	3.11	0.018036	0.06277	-3.94
244932_at	PSI 9KDa protein	---	---	-1.33	-0.42	-3.11	0.018044	0.062789	-3.94
246127_s_	putative protein	---	---	-1.21	-0.28	-3.11	0.01805	0.062799	-3.94
251347_at	putative protein ferritin 1 precursor - A	---	AT3G61010	-1.53	-0.61	-3.11	0.018063	0.062828	-3.94
252976_s_	Phospholipase like protein Arabidopsi	---	AT4G38550	1.56	0.65	3.11	0.018063	0.062828	-3.94
257235_at	ras-related GTP-binding protein contai	AtRABA1g	AT3G15060	-2.42	-1.27	-3.11	0.018068	0.06283	-3.94
253119_at	Expressed protein ; supported by full-le	---	AT4G35980	-1.25	-0.33	-3.11	0.01807	0.06283	-3.94
262162_at	unknown protein ;supported by full-len	---	AT1G78020	1.40	0.48	3.11	0.018085	0.062866	-3.94
251649_at	Ca2+-transporting ATPase-like protein	ACA11	AT3G57330	1.53	0.61	3.11	0.018085	0.062866	-3.94
247168_at	putative protein contains similarity to p	---	AT5G65860	-1.36	-0.44	-3.10	0.01809	0.062872	-3.94
256272_at	unknown protein	---	AT3G12100	-1.27	-0.34	-3.10	0.018102	0.062906	-3.94
246850_at	Lon protease homolog 2 precursor alr	LON1	AT5G26860	1.72	0.78	3.10	0.018116	0.062944	-3.94
247136_at	senescence-associated protein contair	---	AT5G66170	2.71	1.44	3.10	0.018123	0.06295	-3.94
265093_at	unknown protein similar to NBD-like pr	---	AT1G03905	1.38	0.47	3.10	0.018123	0.06295	-3.94
263076_at	putative protein kinase/endoribonuclea	IRE1A	AT2G17520	-1.27	-0.35	-3.10	0.018143	0.062974	-3.94
252911_at	cytochrome P450 -like protein cytochr	CYP96A12	AT4G39510	-1.97	-0.98	-3.10	0.018141	0.062974	-3.94
255104_at	Expressed protein ; supported by full-le	SAH7	AT4G08685	-2.44	-1.29	-3.10	0.018143	0.062974	-3.94
252542_at	nuclear receptor binding factor-like pr	---	AT3G45770	-1.23	-0.30	-3.10	0.018144	0.062974	-3.94
250599_at	unknown protein ; supported by cDNA	---	AT5G07730	1.40	0.49	3.10	0.018143	0.062974	-3.94
246376_at	auxin regulated protein IAA18, putativ	IAA18	AT1G51950	-1.41	-0.49	-3.10	0.018157	0.063009	-3.94
257612_at	unknown protein	ARO4	AT3G26600	1.85	0.88	3.10	0.018168	0.063038	-3.95
260921_at	amp-binding protein, putative similar t	---	AT1G21540	-1.48	-0.56	-3.10	0.0182	0.06314	-3.95
255219_at	hypothetical protein	---	AT4G07720	1.24	0.32	3.10	0.018226	0.063219	-3.95
262287_at	unknown protein ;supported by full-len	---	AT1G68660	-1.31	-0.39	-3.10	0.018236	0.063234	-3.95
245188_at	F12A21.19 unknown protein; similar t	---	AT1G67660	-1.30	-0.38	-3.10	0.018234	0.063234	-3.95

247685_at	serine/threonine-specific protein kinas	---	AT5G59680	2.04	1.03	3.10	0.018253	0.063286	-3.95
262272_at	unknown protein ; supported by cDNA	---	AT1G42440	1.22	0.29	3.10	0.018257	0.063288	-3.95
258083_at	Expressed protein ; supported by full-le	---	AT3G25855	-1.32	-0.40	-3.10	0.018271	0.063328	-3.95
264992_at	integral membrane protein, putative si	---	AT1G67300	-1.36	-0.45	-3.10	0.018294	0.063399	-3.95
262584_at	hypothetical protein Strong similarity t	---	AT1G15440	1.73	0.79	3.10	0.018298	0.063401	-3.95
253227_at	protein kinase - like leucine rich repea	---	AT4G35030	-1.32	-0.40	-3.10	0.0183	0.063401	-3.95
247076_at	ferripyochelin-binding protein-like ;sup	GAMMA CA	AT5G66510	1.26	0.34	3.10	0.01831	0.063423	-3.95
256426_at	hypothetical protein predicted by gens	---	AT1G33420	1.90	0.93	3.10	0.018315	0.063432	-3.95
263847_at	putative glucosyltransferase ; support	---	AT2G36970	2.50	1.32	3.10	0.018325	0.063457	-3.95
257007_at	Expressed protein ; supported by cDN	---	AT3G14205	-1.23	-0.30	-3.09	0.018364	0.063582	-3.96
247448_at	putative protein predicted proteins, Ar	---	AT5G62770	2.31	1.21	3.09	0.018388	0.063656	-3.96
253533_at	putative protein cellulose synthase, A	ATCSLC5	AT4G31590	-2.20	-1.13	-3.09	0.018392	0.063659	-3.96
259533_at	hypothetical protein	---	AT1G12530	1.22	0.28	3.09	0.018398	0.063664	-3.96
248907_at	putative protein contains similarity to u	---	AT5G46340	1.27	0.34	3.09	0.018399	0.063664	-3.96
246794_s_	putative protein predicted proteins, Ar	---	AT5G06350 /	1.62	0.69	3.09	0.018417	0.063716	-3.96
255540_at	putative SecA-type chloroplast protein	---	AT4G01800	-1.44	-0.52	-3.09	0.018426	0.06374	-3.96
258499_at	putative RAD23 similar to RAD23 prote	RAD23-3	AT3G02540	-1.29	-0.37	-3.09	0.018434	0.063757	-3.96
266733_at	similar to axi 1 protein from Nicotiana t	---	AT2G03280	-1.28	-0.36	-3.09	0.018467	0.063861	-3.96
248331_at	putative protein contains similarity to 4	---	AT5G52650	-1.54	-0.62	-3.09	0.018483	0.063906	-3.96
252025_at	putative protein chromosome assemb	---	AT3G52900	-1.30	-0.38	-3.09	0.018515	0.063997	-3.97
263754_at	putative DnaJ protein ;supported by fu	---	AT2G21510	1.83	0.88	3.09	0.018513	0.063997	-3.97
260550_at	putative sterol dehydrogenase ; suppo	---	AT2G43420	1.43	0.51	3.09	0.018525	0.064024	-3.97
245343_at	hypothetical protein ;supported by full-	---	AT4G15830	-1.23	-0.30	-3.09	0.018528	0.064026	-3.97
247780_at	dehydrodolichyl diphosphate - like pro	---	AT5G58770	2.00	1.00	3.09	0.018535	0.064039	-3.97
265083_at	hypothetical protein predicted by gene	---	AT1G03820	-1.66	-0.73	-3.09	0.018551	0.064086	-3.97
265939_at	putative Ta11-like non-LTR retroeleme	---	AT2G19650	1.46	0.54	3.09	0.018562	0.064111	-3.97
260423_at	unknown protein	ATEXO70D1	AT1G72470	-1.78	-0.83	-3.08	0.018595	0.064218	-3.97
261581_at	serine/threonine kinase, putative simil	CIPK9	AT1G01140	1.41	0.50	3.08	0.018603	0.064225	-3.97
265194_at	1-aminocyclopropane-1-carboxylate o	EFE	AT1G05010	1.79	0.84	3.08	0.018606	0.064225	-3.97
252981_at	putative protein gene T10 protein - mo	---	AT4G38260	1.39	0.48	3.08	0.018606	0.064225	-3.97
252056_at	ubiquitin extension protein (UBQ1) ide	UBQ1	AT3G52590	-1.26	-0.34	-3.08	0.01861	0.064229	-3.97
251033_at	hypothetical protein ;supported by full-	---	AT5G01960	1.21	0.28	3.08	0.018615	0.064236	-3.97
254653_at	polygalacturonase-like protein exopoly	---	AT4G18180	-1.20	-0.27	-3.08	0.018689	0.064482	-3.98
253233_at	putative protein various predicted prote	---	AT4G34290	-1.51	-0.60	-3.08	0.018709	0.064544	-3.98
266398_at	hypothetical protein predicted by gene	---	AT2G38680	-1.72	-0.79	-3.08	0.018726	0.06459	-3.98

250655_at	transcription factor HBP-1b (gb|AAD24	OBF5	AT5G06960	1.24	0.31	3.08	0.018735	0.064613	-3.98
246854_at	mitochondrial carrier - like protein mito	---	AT5G26200	-1.31	-0.39	-3.08	0.018745	0.064638	-3.98
249013_at	receptor-like protein kinase	GSO2	AT5G44700	-1.21	-0.28	-3.08	0.018749	0.06464	-3.98
259421_at	disease resistance protein, putative si	---	AT1G13910	1.35	0.44	3.08	0.018762	0.064668	-3.98
261502_at	hypothetical protein predicted by gene	AtHB31	AT1G14440	-1.62	-0.70	-3.08	0.01876	0.064668	-3.98
260855_at	phosphatidylinositol-4-phosphate 5-ki	---	AT1G21920	1.44	0.52	3.08	0.018775	0.064702	-3.98
263906_at	plastid division protein (FtsZ) identical	FTSZ2-1	AT2G36250	-1.32	-0.40	-3.08	0.018789	0.064739	-3.98
254958_at	nucleoside diphosphate kinase 3 (ndpl	NDPK3	AT4G11010	-1.41	-0.50	-3.08	0.018795	0.064749	-3.98
251071_at	putative protein receptor protein kinase	---	AT5G01950	1.51	0.60	3.08	0.018806	0.064777	-3.98
254120_at	putative mitochondrial uncoupling pro	DIC2	AT4G24570	5.54	2.47	3.08	0.018817	0.064807	-3.98
267444_at	hypothetical protein predicted by gens	---	AT2G19180	-1.40	-0.49	-3.07	0.018847	0.064902	-3.98
265259_at	putative WD-40 repeat protein similar t	---	AT2G20330	-1.30	-0.38	-3.07	0.018856	0.064922	-3.99
262058_at	Expressed protein ; supported by full-l	---	AT1G79990	-1.21	-0.28	-3.07	0.018864	0.064941	-3.99
267311_at	hypothetical protein	---	AT2G34670	-1.22	-0.29	-3.07	0.018885	0.064993	-3.99
258348_at	unknown protein ;supported by full-ler	---	AT3G17710	1.29	0.36	3.07	0.018883	0.064993	-3.99
260387_at	putative flavonol sulfotransferase simil	SOT16	AT1G74100	1.83	0.87	3.07	0.018898	0.065026	-3.99
263986_at	putative citrate synthase ;supported b	CSY3	AT2G42790	1.39	0.48	3.07	0.018907	0.065047	-3.99
264727_at	putative cytochrome C strong similarity	CYTC-1	AT1G22840	1.71	0.77	3.07	0.018917	0.065071	-3.99
256379_at	hypothetical protein predicted by gens	---	AT1G66840	1.42	0.51	3.07	0.018944	0.065157	-3.99
256620_at	disease resistance protein, putative si	---	AT3G24480	-1.55	-0.63	-3.07	0.018959	0.065186	-3.99
247508_at	auxin response factor - like protein au	ARF2	AT5G62000	-1.43	-0.51	-3.07	0.018958	0.065186	-3.99
250407_at	chorismate mutase CM2 ; supported b	ATCM2	AT5G10870	-1.27	-0.35	-3.07	0.018961	0.065186	-3.99
259226_at	unknown protein similar to hypothetica	---	AT3G07700	1.37	0.45	3.07	0.018965	0.065187	-3.99
266924_at	unknown protein ;supported by full-ler	---	AT2G45730	-1.35	-0.43	-3.07	0.018976	0.065215	-3.99
254548_at	putative protein various predicted prot	---	AT4G19865	-1.55	-0.63	-3.07	0.018982	0.065229	-3.99
263863_at	3-oxoacyl carrier protein synthase	---	AT2G04540	-1.22	-0.28	-3.07	0.019006	0.065285	-3.99
260766_at	unknown protein similar to hypothetica	---	AT1G48960	-1.29	-0.37	-3.07	0.019007	0.065285	-3.99
253076_at	NAM like protein P.hybrida NAM gene	ANAC076	AT4G36160	-1.27	-0.34	-3.07	0.019002	0.065285	-3.99
264393_at	unknown protein Contains similarity to	---	AT1G11880	-1.28	-0.36	-3.07	0.019013	0.065295	-3.99
249551_at	putative protein predicted proteins, Ar	---	AT5G38220	1.36	0.44	3.07	0.019026	0.065328	-3.99
264032_at	unknown protein	GEK1	AT2G03800	1.30	0.38	3.07	0.019032	0.065332	-3.99
246332_at	putative protein phosphatidylcholine--	---	AT3G44830	1.36	0.45	3.07	0.019032	0.065332	-3.99
266547_at	similar to eyes absent protein ;suppor	ATEYA	AT2G35320	-1.22	-0.29	-3.07	0.01904	0.065347	-4.00
266076_at	ATP-dependent RNA helicase identica	---	AT2G40700	1.57	0.65	3.07	0.019044	0.065351	-4.00
247420_at	unknown protein	---	AT5G63100	-1.42	-0.50	-3.07	0.019058	0.065389	-4.00

259488_at	hypothetical protein preedicted by gen	---	AT1G15780	1.37	0.46	3.07	0.019062	0.065394	-4.00
256700_at	pseudouridine synthase, putative simi	---	AT3G52260	-1.25	-0.32	-3.07	0.019085	0.065462	-4.00
266542_at	unknown protein	ARAD1	AT2G35100	-1.24	-0.31	-3.07	0.019103	0.065515	-4.00
257193_at	Expressed protein ; supported by full-l	---	AT3G13160	1.24	0.31	3.06	0.019117	0.065552	-4.00
260814_at	histidine decarboxylase, putative simil	emb1075	AT1G43710	-1.26	-0.33	-3.06	0.019144	0.065635	-4.00
253124_at	putative protein unknown protein Arab	ARO3	AT4G36030	2.04	1.03	3.06	0.019158	0.065673	-4.00
264218_at	unknown protein	---	AT1G60200	1.22	0.29	3.06	0.019177	0.06573	-4.00
249433_at	putative protein hypothetical protein -	---	AT5G39940	1.41	0.49	3.06	0.019188	0.065757	-4.00
252269_at	putative protein ;supported by full-leng	LSU1	AT3G49580	-2.00	-1.00	-3.06	0.019191	0.065757	-4.00
263212_at	unknown protein similar to ribonucleas	emb2004	AT1G10510	1.28	0.35	3.06	0.019199	0.065776	-4.00
248800_at	40S ribosomal protein S19 ; supporte	RPS19	AT5G47320	-1.28	-0.36	-3.06	0.019214	0.065805	-4.00
265229_s_	hypothetical protein	---	AT2G07701	1.25	0.32	3.06	0.019213	0.065805	-4.00
253090_at	beta-galactosidase like protein ; suppo	BGAL3	AT4G36360	-2.83	-1.50	-3.06	0.019233	0.065863	-4.01
255216_s_	putative peptidase	---	AT4G07670 /	1.60	0.68	3.06	0.01924	0.06587	-4.01
262981_at	unknown protein ;supported by full-len	---	AT1G75590	-1.38	-0.47	-3.06	0.019241	0.06587	-4.01
259824_at	copper homeostasis factor, putative si	ATX1	AT1G66240	1.25	0.32	3.06	0.019267	0.065947	-4.01
261561_at	unknown protein ;supported by full-len	---	AT1G01730	1.43	0.51	3.06	0.01927	0.065947	-4.01
254925_at	beta-adaptin - like protein beta-adapti	---	AT4G11380	-1.32	-0.40	-3.06	0.019275	0.065957	-4.01
249233_at	putative protein contains similarity to g	---	AT5G42150	1.98	0.98	3.06	0.019281	0.065968	-4.01
260622_at	hypothetical protein predicted by gene	NF-YC10	AT1G07980	1.25	0.32	3.06	0.019299	0.066017	-4.01
259159_at	unknown protein contains Pfam profile	ACBP4	AT3G05420	-1.39	-0.48	-3.06	0.019319	0.066062	-4.01
257894_at	unknown protein ; supported by cDNA	---	AT3G17100	-1.61	-0.69	-3.06	0.019321	0.066062	-4.01
264547_at	unknown protein ; supported by cDNA	CLC-F	AT1G55620	-1.44	-0.52	-3.06	0.019319	0.066062	-4.01
247921_at	CONSTANS-like B-box zinc finger prot	COL5	AT5G57660	-1.42	-0.50	-3.06	0.019339	0.066115	-4.01
260538_at	60S ribosomal protein L38	---	AT2G43460	-1.45	-0.53	-3.06	0.019346	0.06613	-4.01
250532_at	putative protein similar to unknown pro	---	AT5G08540	-1.33	-0.42	-3.06	0.019356	0.066153	-4.01
265078_at	hypothetical protein contains similarity	ECT4	AT1G55500	1.59	0.67	3.06	0.019372	0.066187	-4.01
253816_at	hypothetical protein ;supported by full-	emb1923	AT4G28210	-1.34	-0.42	-3.06	0.019369	0.066187	-4.01
263003_at	protein phosphatase 2A 72 kDa regula	---	AT1G54450	1.22	0.29	3.05	0.019389	0.066238	-4.01
257336_at	hypothetical protein	---	---	1.23	0.29	3.05	0.019404	0.066238	-4.02
250288_at	auxin-responsive - like protein Nt-gh3	---	AT5G13350	1.30	0.38	3.05	0.019396	0.066238	-4.01
266444_at	putative extensin	---	AT2G43150	-1.35	-0.43	-3.05	0.019396	0.066238	-4.01
262183_at	unknown protein	---	AT1G77890	1.26	0.34	3.05	0.019399	0.066238	-4.02
248581_at	putative protein strong similarity to unk	---	AT5G49900	1.43	0.51	3.05	0.019403	0.066238	-4.02
255900_at	hypothetical protein predicted by gene	---	AT1G17830 /	2.00	1.00	3.05	0.019407	0.066239	-4.02

266908_at	putative protein kinase contains a prot	PID	AT2G34650	1.81	0.86	3.05	0.019425	0.06629	-4.02
250035_at	putative protein contains similarity to tr	---	AT5G18230	-1.23	-0.30	-3.05	0.019439	0.066328	-4.02
252921_at	putative protein DNA damage-inducib	EDS5	AT4G39030	1.72	0.79	3.05	0.01946	0.066391	-4.02
263943_at	putative mitochondrial carrier protein	---	AT2G35800	-1.33	-0.41	-3.05	0.019472	0.066419	-4.02
261225_at	unknown protein ;supported by full-len	---	AT1G20100	1.25	0.32	3.05	0.01949	0.066471	-4.02
256917_at	unknown protein contains Pfam profile	---	AT3G18930	1.24	0.31	3.05	0.019493	0.066472	-4.02
264465_at	SKP1/ASK1 (At18), putative similar to	ASK18	AT1G10230	-1.22	-0.29	-3.05	0.019506	0.066506	-4.02
262968_at	hypothetical protein predicted by gene	---	AT1G75720	-1.27	-0.35	-3.05	0.019528	0.066571	-4.02
250430_at	putative protein	---	AT5G10460	-1.23	-0.30	-3.05	0.019533	0.066578	-4.02
267092_at	unknown protein ;supported by full-ler	AUX1	AT2G38120	-1.76	-0.82	-3.05	0.019546	0.066612	-4.02
248333_at	photoassimilate-responsive protein PA	---	AT5G52390	3.03	1.60	3.05	0.019549	0.066614	-4.02
258215_at	phosphoprotein phosphatase, putative	atToc64-III	AT3G17970	1.43	0.52	3.05	0.019563	0.066653	-4.02
250948_at	putative protein	---	AT5G03490	1.49	0.58	3.05	0.019577	0.066689	-4.02
261203_at	Expressed protein ; supported by full-le	---	AT1G12845	-2.58	-1.37	-3.05	0.019584	0.066694	-4.03
262909_at	serine/threonine protein phosphatase	PP2A-1	AT1G59830	-1.29	-0.37	-3.05	0.019584	0.066694	-4.03
264802_at	putative syntaxin-related protein (U394	SYP111	AT1G08560	-1.66	-0.73	-3.05	0.019593	0.066704	-4.03
245200_at	F12A21.2 hypothetical protein; suppor	---	AT1G67850	1.61	0.68	3.05	0.019591	0.066704	-4.03
255385_at	putative hydrolase	---	AT4G03610	-1.37	-0.45	-3.05	0.0196	0.066718	-4.03
256230_at	FKBP-type peptidyl-prolyl cis-trans isc	---	AT3G12340	1.36	0.45	3.05	0.019609	0.066739	-4.03
250256_at	GTP-binding protein typA (tyrosine pho	---	AT5G13650	-1.26	-0.33	-3.05	0.019633	0.066812	-4.03
266467_at	Not56-like protein ; supported by cDN	ALG3	AT2G47760	-1.32	-0.40	-3.04	0.019641	0.066819	-4.03
261460_at	MAP kinase, putative similar to GB:CA	ATMPK13	AT1G07880	-1.21	-0.27	-3.04	0.019641	0.066819	-4.03
248681_at	pectate lyase non-consensus AG dono	---	AT5G48900	-7.22	-2.85	-3.04	0.019673	0.066917	-4.03
266388_at	hypothetical protein predicted by gens	---	AT2G32340	1.33	0.41	3.04	0.019678	0.066922	-4.03
261510_at	hypothetical protein predicted by gens	---	AT1G71760	-1.27	-0.34	-3.04	0.019692	0.06696	-4.03
250072_at	putative protein similar to unknown pro	---	AT5G17210	-1.42	-0.51	-3.04	0.019706	0.066997	-4.03
263161_at	myrosinase-associated protein, putati	---	AT1G54020	9.62	3.27	3.04	0.019709	0.066998	-4.03
252913_at	AtRer1A ; supported by full-length cDI	ATRER1A	AT4G39220	-1.27	-0.34	-3.04	0.019735	0.067077	-4.03
246865_s_	eukaryotic translation initiation factor -	TIF3B1	AT5G25780 /	1.21	0.27	3.04	0.019739	0.067077	-4.03
250469_at	pollen allergen -like protein SAH7 prot	---	AT5G10130	-1.37	-0.45	-3.04	0.019742	0.067077	-4.03
246257_at	splicing factor-like protein	ATU2AF65A	AT4G36690	-1.27	-0.34	-3.04	0.019744	0.067077	-4.03
263758_s_	putative NADPH dependent mannose	---	AT2G21250 /	-1.24	-0.31	-3.04	0.019755	0.067106	-4.03
267517_at	unknown protein	RPT2	AT2G30520	-1.32	-0.40	-3.04	0.019767	0.067135	-4.03
263046_at	unknown protein ; supported by cDNA	GRP3S	AT2G05380	1.62	0.70	3.04	0.019772	0.067136	-4.04
247686_at	receptor-like protein kinase precursor	---	AT5G59700	2.05	1.04	3.04	0.019773	0.067136	-4.04

260966_at	NBS/LRR disease resistance protein,	RPS5	AT1G12220	1.28	0.36	3.04	0.019791	0.067187	-4.04
259141_at	putative cytoskeleton-associated prote	---	AT3G10220	-1.28	-0.35	-3.04	0.019801	0.067202	-4.04
267312_at	unknown protein	---	AT2G34750	-1.38	-0.46	-3.04	0.019798	0.067202	-4.04
254496_at	hyuC-like protein 5-substituted hydant	ATAAH	AT4G20070	-1.91	-0.94	-3.04	0.019814	0.067235	-4.04
264064_at	hypothetical protein predicted by gens	---	AT2G27900	-1.26	-0.33	-3.04	0.019819	0.067243	-4.04
259862_at	hypothetical protein ;supported by full-	TRFL6	AT1G72650	1.35	0.43	3.04	0.019825	0.067252	-4.04
264131_at	unknown protein	---	AT1G79150	1.45	0.53	3.04	0.019843	0.067302	-4.04
258737_at	unknown protein similar to unknown pr	---	AT3G05940	-1.25	-0.32	-3.04	0.019846	0.067302	-4.04
245665_at	unknown protein ;supported by full-len	---	AT1G28250	-1.30	-0.38	-3.04	0.019871	0.067377	-4.04
247148_at	auxin-induced protein IAA9 (pir |T0590	IAA9	AT5G65670	-1.46	-0.55	-3.04	0.019877	0.06739	-4.04
248673_at	putative protein contains similarity to d	---	AT5G48780	-1.24	-0.31	-3.04	0.019889	0.067411	-4.04
252060_at	putative protein other hypothetical prot	PAD4	AT3G52430	2.32	1.21	3.04	0.019889	0.067411	-4.04
263042_at	conserved hypothetical protein protein	---	AT1G23340	-1.31	-0.39	-3.04	0.019895	0.067411	-4.04
254501_at	hypothetical protein	PTAC14	AT4G20130	-1.51	-0.60	-3.04	0.019894	0.067411	-4.04
259648_at	hypothetical protein predicted by gene	---	---	-1.22	-0.29	-3.04	0.019899	0.067412	-4.04
262213_at	hypothetical protein predicted by gene	---	AT1G74870	1.38	0.47	3.04	0.019906	0.067427	-4.04
255402_at	Expressed protein	hemf2	AT4G03205	-1.62	-0.70	-3.04	0.019911	0.067436	-4.04
252625_at	putative histone deacetylase similar to	HDA3	AT3G44750	1.96	0.97	3.03	0.019922	0.067461	-4.04
260429_at	unknown protein ;supported by full-ler	JAZ6	AT1G72450	1.81	0.86	3.03	0.019936	0.0675	-4.04
264039_at	putative cold-regulated protein ;suppo	---	AT2G03740	-1.25	-0.33	-3.03	0.01994	0.067503	-4.04
256444_at	hypothetical protein predicted by gene	---	AT3G11060	-1.23	-0.30	-3.03	0.01996	0.067559	-4.05
256889_at	PHD-finger protein, putative contains	ING1	AT3G24010	1.22	0.29	3.03	0.019975	0.0676	-4.05
266964_at	putative ABC transporter related to mu	PGP6	AT2G39480	1.20	0.27	3.03	0.019986	0.067629	-4.05
259877_at	unknown protein C-terminal portion sin	SDG26	AT1G76710	-1.35	-0.43	-3.03	0.019998	0.067658	-4.05
263275_at	putative methylmalonate semi-aldehyd	ALDH6B2	AT2G14170	1.42	0.50	3.03	0.020024	0.067737	-4.05
257922_at	ethylene receptor, putative (ETR2) sin	ETR2	AT3G23150	1.62	0.69	3.03	0.020047	0.067791	-4.05
250164_at	putative protein various predicted prot	---	AT5G15280	-1.37	-0.46	-3.03	0.020052	0.067791	-4.05
258930_at	unknown protein predicted by genscar	---	AT3G10040	-1.26	-0.33	-3.03	0.020048	0.067791	-4.05
262196_at	ubiquitin-fusion protein, putative simila	MUB5	AT1G77870	-1.64	-0.71	-3.03	0.020052	0.067791	-4.05
253143_at	putative protein	---	AT4G35530	1.35	0.44	3.03	0.020062	0.067815	-4.05
246703_at	mitogen activated protein kinase - like	WNK9	AT5G28080	-2.11	-1.07	-3.03	0.020078	0.06786	-4.05
246567_at	alpha-mannosidase -like protein mann	GMII	AT5G14950	1.22	0.29	3.03	0.020084	0.067866	-4.05
263949_at	E2, ubiquitin-conjugating enzyme, put	MMZ3	AT2G36060	-1.22	-0.29	-3.03	0.020086	0.067866	-4.05
261034_s_	hypothetical protein predicted by gene	---	AT1G17450 /	1.38	0.47	3.03	0.020094	0.067883	-4.05
245521_at	Expressed protein ;supported by cDNA	ESD4	AT4G15880	1.25	0.32	3.03	0.020115	0.067943	-4.05

255417_at	F-box protein GRR1-like protein 1, Atl	GRH1	AT4G03190	-2.57	-1.36	-3.03	0.020119	0.067948	-4.05
263852_at	putative mutT domain protein	ATNUDT6	AT2G04450	-3.43	-1.78	-3.03	0.020141	0.068011	-4.05
251352_at	putative protein hypothetical protein A	PEX11E	AT3G61070	1.37	0.46	3.03	0.020147	0.068023	-4.06
246240_at	nucleoporin-like protein	---	AT4G37130	-1.21	-0.28	-3.03	0.020169	0.068085	-4.06
253476_at	S-receptor kinase -like protein serine/t	SD2-5	AT4G32300	-1.64	-0.71	-3.03	0.020172	0.068087	-4.06
264925_at	hypothetical protein contains similarity	---	AT1G60670	1.32	0.40	3.03	0.020175	0.068087	-4.06
252650_at	putative protein	---	AT3G44690	1.24	0.31	3.02	0.020192	0.068123	-4.06
250925_at	putative protein ; supported by full-len	---	AT5G03370	-1.34	-0.42	-3.03	0.020189	0.068123	-4.06
247732_at	putative protein various predicted prot	---	AT5G59600	1.22	0.29	3.02	0.020237	0.068265	-4.06
266574_at	hypothetical protein predicted by gens	---	AT2G23890	1.65	0.72	3.02	0.02025	0.068296	-4.06
256246_at	betaine aldehyde dehydrogenase, put	ALDH22a1	AT3G66658	-1.37	-0.45	-3.02	0.020252	0.068296	-4.06
252013_at	putative protein	---	AT3G52860	-1.25	-0.32	-3.02	0.020259	0.068298	-4.06
250185_at	putative protein esterase HDE, Petrole	AtCXE16	AT5G14310	1.33	0.42	3.02	0.020258	0.068298	-4.06
267072_at	unknown protein	---	AT2G41170	1.35	0.43	3.02	0.020262	0.068298	-4.06
244919_at	cytochrome c biogenesis orf203 Protei	---	AT2G07768 /	1.28	0.36	3.02	0.020272	0.068321	-4.06
259977_at	unknown protein ;supported by full-ler	---	AT1G76590	1.87	0.90	3.02	0.020282	0.068335	-4.06
267229_s_	putative translation initiation factor eIF-	---	AT2G44070 /	1.64	0.71	3.02	0.020285	0.068335	-4.06
256331_at	GT-like trihelix DNA-binding protein, p	---	AT1G76880	-1.26	-0.33	-3.02	0.020285	0.068335	-4.06
257105_at	unknown protein	---	AT3G15300	1.44	0.53	3.02	0.020289	0.068338	-4.06
249778_at	Expressed protein ; supported by full-le	---	AT5G24165	1.25	0.33	3.02	0.020296	0.068345	-4.06
260395_at	homeobox gene 13 protein identical to	ATHB13	AT1G69780	-1.74	-0.80	-3.02	0.020297	0.068345	-4.06
261524_at	hypothetical protein predicted by gene	---	AT1G14300	1.31	0.39	3.02	0.020306	0.068353	-4.06
245765_at	hypothetical protein similar to putative	---	AT1G33600	2.17	1.12	3.02	0.020311	0.068353	-4.06
255967_at	protein phosphatase type 2C, putative	---	AT1G22280	1.35	0.43	3.02	0.020306	0.068353	-4.06
249343_at	succinate dehydrogenase iron-protein	SDH2-2	AT5G40650	1.38	0.46	3.02	0.020311	0.068353	-4.06
245879_at	putative subunit of TOC complex chlo	ATTOC64-V	AT5G09420	1.89	0.92	3.02	0.020314	0.068354	-4.06
250296_at	heat shock protein 17.6-II ;supported l	HSP17.6II	AT5G12020	1.74	0.80	3.02	0.020332	0.068403	-4.06
245927_at	sterol glucosyltransferase - like protei	---	AT5G24750	-1.20	-0.26	-3.02	0.020336	0.068406	-4.06
245112_at	glycerol-3-phosphate dehydrogenase	GPDHC1	AT2G41540	-2.01	-1.01	-3.02	0.020363	0.068472	-4.07
256235_at	cysteine proteinase inhibitor, putative	ATCYSB	AT3G12490	1.21	0.28	3.02	0.020365	0.068472	-4.07
251145_at	putative protein predicted protein, Ara	---	AT3G63500	1.33	0.41	3.02	0.020361	0.068472	-4.07
256286_at	unknown protein	---	AT3G12180	1.30	0.37	3.02	0.020376	0.0685	-4.07
246808_at	putative protein many predicted protei	---	AT5G27110	1.27	0.34	3.02	0.020391	0.068541	-4.07
256797_at	DEAD box helicase protein, putative s	---	AT3G18600	1.46	0.55	3.02	0.020406	0.068581	-4.07
251078_at	putative protein hypothetical proteins -	---	AT5G01990	1.47	0.55	3.02	0.020422	0.068624	-4.07

254670_at	teosinte branched1 - like protein teosi	---	AT4G18390	-1.51	-0.60	-3.02	0.020439	0.068662	-4.07
246554_at	HSP100/ClpB, putative similar to HSP	CLPB3	AT5G15450	-1.30	-0.38	-3.02	0.020438	0.068662	-4.07
255739_at	unknown protein similar to hypothetica	ANAC008	AT1G25580	1.40	0.48	3.01	0.020483	0.068794	-4.07
261517_at	unknown protein ; supported by full-ler	---	AT1G71780	1.30	0.38	3.01	0.020487	0.068794	-4.07
246533_at	putative protein	---	AT5G15880	-1.38	-0.46	-3.01	0.020488	0.068794	-4.07
261328_at	unknown protein	---	AT1G44835	-1.30	-0.38	-3.01	0.020508	0.068853	-4.07
255038_at	neutral invertase like protein Daucus c	CINV2	AT4G09510	-1.73	-0.79	-3.01	0.020532	0.068924	-4.08
253903_at	kinesin-related protein katB ; supporte	ATK2	AT4G27180	-1.20	-0.26	-3.01	0.02055	0.068953	-4.08
248589_at	von Hippel-Lindau binding protein (VH	PDF3	AT5G49510	-1.24	-0.31	-3.01	0.020546	0.068953	-4.08
258851_at	glutathione S-transferase identical to g	ATGSTF11	AT3G03190	-1.75	-0.81	-3.01	0.020549	0.068953	-4.08
254262_at	putative protein annexin VII, Dictyoste	---	AT4G23470	1.35	0.43	3.01	0.020555	0.068954	-4.08
253037_at	putative protein other predicted Arabid	GAUT3	AT4G38270	1.26	0.34	3.01	0.020559	0.068954	-4.08
257139_at	disease resistance protein, putative si	AtRLP43	AT3G28890	1.43	0.52	3.01	0.020558	0.068954	-4.08
267179_at	putative ADP ribosylation factor 1 GTP	AGD7	AT2G37550	-1.42	-0.51	-3.01	0.020599	0.069067	-4.08
263181_at	unknown protein ;supported by full-ler	---	AT1G05720	-1.24	-0.31	-3.01	0.020597	0.069067	-4.08
245092_at	putative TGACG-sequence-specific bZ	BZIP17	AT2G40950	1.33	0.41	3.01	0.02061	0.069094	-4.08
257220_at	MYB family transcription factor (Atmyt	ATMYB21	AT3G27810	1.33	0.41	3.01	0.020622	0.069124	-4.08
255500_at	NAD+ ADP-ribosyltransferase	APP	AT4G02390	-1.36	-0.45	-3.01	0.02063	0.06914	-4.08
252967_at	amidophosphoribosyltransferase - like	ATASE3	AT4G38880	-1.28	-0.35	-3.01	0.020646	0.069184	-4.08
247272_at	GTP cyclohydrolase II; 3,4-dihydroxy-	---	AT5G14040 /	1.92	0.94	3.01	0.020651	0.069192	-4.08
252851_at	putative protein CLATHRIN COAT AS	---	AT4G40080	1.85	0.89	3.01	0.020699	0.069341	-4.08
249168_at	putative protein strong similarity to unk	---	AT5G42870	1.31	0.39	3.01	0.02071	0.069368	-4.08
246082_at	receptor protein kinase - like protein k	EFR	AT5G20480	2.00	1.00	3.01	0.020721	0.069393	-4.08
260601_at	Expressed protein ; supported by cDN	ZIP11	AT1G55910	1.53	0.62	3.01	0.020725	0.069397	-4.08
256761_at	hypothetical protein predicted by gens	---	AT3G25670	-1.36	-0.44	-3.01	0.020732	0.06941	-4.09
251299_at	putative protein transcription factor MY	---	AT3G61950	-1.30	-0.37	-3.01	0.020741	0.06943	-4.09
259657_at	phospholipase D alpha, putative simila	PLDEPSILO	AT1G55180	-1.25	-0.32	-3.00	0.020795	0.069579	-4.09
265880_at	unknown protein	---	AT2G42300	-1.43	-0.51	-3.00	0.020795	0.069579	-4.09
263736_at	nucleic acid-binding protein, putative s	---	AT1G60000	-1.41	-0.50	-3.00	0.020797	0.069579	-4.09
265070_at	branched-chain alpha-keto acid decarb	BCDH BETA	AT1G55510	1.77	0.83	3.00	0.020795	0.069579	-4.09
248702_at	unknown protein	---	AT5G48420	-1.24	-0.31	-3.00	0.02081	0.069611	-4.09
257633_at	hypothetical protein	CYP86C2	AT3G26125	-1.24	-0.31	-3.00	0.02084	0.069701	-4.09
261211_at	uridine diphosphate glucose epimeras	UGE1	AT1G12780	1.53	0.61	3.00	0.020856	0.069744	-4.09
256270_at	unknown protein ; supported by cDNA	---	AT3G12300	1.27	0.35	3.00	0.02086	0.069748	-4.09
262929_at	hypothetical protein ;supported by full-	---	AT1G65720	1.40	0.48	3.00	0.020867	0.06976	-4.09

259302_at	unknown protein	GID1A	AT3G05120	-1.42	-0.50	-3.00	0.020871	0.069764	-4.09
267421_at	putative phosphoribosylaminoimidazol	---	AT2G35040	-1.36	-0.44	-3.00	0.020897	0.069839	-4.09
260275_at	hypothetical protein predicted by grail	---	AT1G80610	1.26	0.34	3.00	0.020914	0.069888	-4.09
262870_at	alcohol dehydrogenase, putative simil	---	AT1G64710	2.36	1.24	3.00	0.020933	0.069939	-4.10
259673_at	putative phorbol ester / diacylglycerol b	---	AT1G77800	1.37	0.46	3.00	0.020939	0.06995	-4.10
246538_at	40S RIBOSOMAL PROTEIN S19 - lik	---	AT5G15520	-1.49	-0.57	-3.00	0.020959	0.069989	-4.10
250768_at	signal recognition particle receptor bet	---	AT5G05670	-1.39	-0.48	-3.00	0.02096	0.069989	-4.10
253259_at	putative protein ethylene-responsive e	RRTF1	AT4G34410	2.10	1.07	3.00	0.020957	0.069989	-4.10
246312_at	G-protein, putative contains Pfam pro	XLG3	AT1G31930	1.74	0.80	3.00	0.020975	0.070028	-4.10
250326_at	putative protein strong similarity to unk	MSL10	AT5G12080	1.39	0.48	3.00	0.020986	0.070055	-4.10
262107_at	hypothetical protein predicted by gene	---	AT1G02750	1.24	0.31	3.00	0.020993	0.070068	-4.10
256363_at	unknown protein ; supported by cDNA	---	AT1G66510	-1.58	-0.66	-3.00	0.020997	0.070071	-4.10
259484_at	calcium-dependent protein kinase, pu	PEPKR1	AT1G12580	-1.35	-0.43	-3.00	0.021	0.070072	-4.10
259992_at	putative heat shock transcription facto	HSFA8	AT1G67970	1.50	0.58	3.00	0.021037	0.070184	-4.10
255325_at	putative membrane trafficking factor ;s	PUX4	AT4G04210	1.26	0.34	2.99	0.021066	0.07027	-4.10
250578_at	proanthranilate N-benzoyltransferase	---	AT5G07850	-1.23	-0.30	-2.99	0.021069	0.07027	-4.10
245350_at	nuclear antigen homolog ;supported by	---	AT4G16830	-1.31	-0.39	-2.99	0.021086	0.070318	-4.10
264189_s_	hypothetical protein similar to acyl-carr	ACP3	AT1G54580 /	-1.38	-0.47	-2.99	0.021123	0.070432	-4.11
249116_at	putative protein similar to unknown pro	---	AT5G43820 /	-1.35	-0.44	-2.99	0.021129	0.070439	-4.11
265448_at	putative DOF zinc finger protein	DAG2	AT2G46590	-1.35	-0.43	-2.99	0.021137	0.070446	-4.11
253765_at	hypothetical protein ;supported by full-	---	AT4G28740	-1.56	-0.64	-2.99	0.021135	0.070446	-4.11
264932_at	hypothetical protein similar to hypothet	---	AT1G61240	-1.39	-0.47	-2.99	0.021151	0.070484	-4.11
260258_at	putative ribosomal protein similar to rib	---	AT1G74270	1.39	0.48	2.99	0.021157	0.070492	-4.11
260819_at	b-Zip DNA binding protein, putative si	AtbZIP52	AT1G06850	-1.58	-0.66	-2.99	0.021172	0.070526	-4.11
266315_at	unknown protein ; supported by cDNA	SE	AT2G27100	1.22	0.29	2.99	0.021173	0.070526	-4.11
252952_at	putative protein cylicin II - bovine, PIR	---	AT4G38710	1.37	0.46	2.99	0.021196	0.070592	-4.11
260235_at	putative SET protein, phospatase 2A i	NRP1	AT1G74560	1.22	0.29	2.99	0.021219	0.070628	-4.11
265991_at	chloroplast single subunit DNA-depen	SCA3	AT2G24120	1.53	0.61	2.99	0.021213	0.070628	-4.11
245268_at	hypothetical protein ; supported by cDI	PRMT7	AT4G16570	-1.54	-0.62	-2.99	0.021215	0.070628	-4.11
247057_at	SCARECROW gene regulator	---	AT5G66770	-1.91	-0.93	-2.99	0.021219	0.070628	-4.11
247277_at	putative protein similar to unknown pro	---	AT5G64420	1.28	0.35	2.99	0.021223	0.070628	-4.11
246461_at	putative protein AAA family protein Bo	---	AT5G16930	1.84	0.88	2.99	0.021239	0.070672	-4.11
259734_at	unknown protein similar to GB:AAD41	---	AT1G77500	1.71	0.77	2.99	0.021248	0.070693	-4.11
259480_at	hypothetical protein predicted by gens	---	AT1G19010	1.39	0.48	2.99	0.021265	0.070724	-4.11
247479_at	NAC - like protein OsNAC7, Oryza sa	ANAC101	AT5G62380	-1.23	-0.30	-2.99	0.021267	0.070724	-4.11

251746_at	mandelonitrile lyase-like protein ADHE	---	AT3G56060	1.35	0.43	2.99	0.021266	0.070724	-4.11
251370_at	putative protein prib5, Ribes nigrum, E	---	AT3G60450	1.99	0.99	2.99	0.02127	0.070724	-4.11
256044_at	protein phosphatase 2C, putative simi	---	AT1G07160	3.70	1.89	2.99	0.021278	0.070739	-4.11
261844_at	hypothetical protein predicted by gene	---	AT1G15940	1.51	0.59	2.99	0.021293	0.070781	-4.11
248485_at	calcium-binding transporter-like protein	---	AT5G51050	1.41	0.50	2.99	0.021303	0.070802	-4.11
250324_at	putative protein nitrilase/Fhit protein, C	---	AT5G12040	-1.33	-0.41	-2.99	0.021311	0.070818	-4.11
253172_at	putative protein ;supported by full-leng	---	AT4G35060	1.94	0.95	2.99	0.021318	0.070832	-4.11
262355_at	unknown protein	---	AT1G72820	-1.38	-0.47	-2.99	0.021322	0.070834	-4.11
259138_s_	putative DNA gyrase subunit B similar	---	AT3G10270 /	-1.29	-0.36	-2.99	0.021328	0.070835	-4.12
257864_at	hypothetical protein predicted by gene	---	AT3G17740	1.40	0.49	2.99	0.021328	0.070835	-4.12
262228_at	protein kinase, putative similar to prot	---	AT1G68690	2.32	1.22	2.99	0.021331	0.070835	-4.12
247955_at	nucleosome assembly protein	NAP1;3	AT5G56950	1.34	0.42	2.98	0.021359	0.070918	-4.12
251051_at	putative zinc finger protein zinc finger	---	AT5G02460	-1.29	-0.37	-2.98	0.021363	0.07092	-4.12
264308_at	hypothetical protein similar to hypothet	---	AT1G61990	1.19	0.25	2.98	0.021367	0.070922	-4.12
253502_at	Cytochrome P450-like protein cytochr	CYP82C4	AT4G31940	1.24	0.30	2.98	0.021373	0.070931	-4.12
265907_at	unknown protein ;supported by full-ler	---	AT2G25650	1.32	0.40	2.98	0.021403	0.071001	-4.12
259823_at	beta-1,3-glucanase precursor, putativ	---	AT1G66250	1.32	0.40	2.98	0.021398	0.071001	-4.12
266257_at	putative chorismate mutase/prephenat	PD1	AT2G27820	-1.38	-0.47	-2.98	0.021406	0.071001	-4.12
263162_at	hypothetical protein predicted by gene	---	AT1G54150	-1.23	-0.29	-2.98	0.021405	0.071001	-4.12
267465_at	subtilisin-like serine protease contains	SLP3	AT2G19170	-1.79	-0.84	-2.98	0.021422	0.071042	-4.12
253827_at	Expressed protein ; supported by cDN	---	AT4G28085	2.04	1.03	2.98	0.021426	0.071046	-4.12
248663_at	putative protein strong similarity to unk	---	AT5G48590	-1.21	-0.27	-2.98	0.021442	0.071089	-4.12
262573_at	hypothetical protein Similar to gi|43774	PDF1A	AT1G15390	-1.32	-0.40	-2.98	0.021446	0.071094	-4.12
264847_at	clathrin assembly protein AP19, small	AP19	AT2G17380	-1.20	-0.27	-2.98	0.021462	0.071133	-4.12
258965_at	hypothetical protein similar to hypothe	---	AT3G10530	1.61	0.68	2.98	0.021478	0.071138	-4.12
245145_at	putative dihydrodipicolinate synthase	DHDPS2	AT2G45440	1.50	0.59	2.98	0.021473	0.071138	-4.12
248526_at	putative protein contains similarity to A	---	AT5G50740	-1.42	-0.50	-2.98	0.021482	0.071138	-4.12
245374_at	hypothetical protein	---	AT4G17620	1.29	0.37	2.98	0.02148	0.071138	-4.12
266634_at	putative G-box binding bZIP transcripti	---	AT2G35530	1.24	0.31	2.98	0.021479	0.071138	-4.12
247922_at	putative protein similar to unknown pro	---	AT5G57500	1.83	0.87	2.98	0.021468	0.071138	-4.12
263366_at	unknown protein	---	AT2G20440	1.29	0.37	2.98	0.021494	0.071168	-4.12
252080_at	putative protein polyphosphoinositide	---	AT3G51670	-1.50	-0.58	-2.98	0.021585	0.071459	-4.13
259786_at	lipase/hydrolase, putative contains Pfa	---	AT1G29660	-7.75	-2.95	-2.98	0.02159	0.071465	-4.13
248874_at	putative protein strong similarity to unk	---	AT5G46460	1.44	0.52	2.98	0.021593	0.071465	-4.13
249877_at	transcription factor-like protein (gb|AAD	HUA2	AT5G23150	1.22	0.29	2.98	0.021613	0.071519	-4.13

257949_at	putative UDP-glucose glucosyltransfer	UGT71B1	AT3G21750	1.42	0.51	2.98	0.021619	0.071532	-4.13
259478_at	germin, putative similar to germin GI:1	---	AT1G18980	4.20	2.07	2.98	0.021634	0.071566	-4.13
261622_at	hypothetical protein predicted by gene	---	AT1G01970	-1.29	-0.36	-2.97	0.021636	0.071566	-4.13
247250_at	FAS2 (dbj|BAA77766.1) ; supported b	FAS2	AT5G64630	-1.47	-0.55	-2.97	0.02168	0.0717	-4.13
253490_at	methyltransferase - like protein methy	---	AT4G31790	1.61	0.69	2.97	0.02169	0.071723	-4.13
263261_at	putative pre-mRNA splicing factor simi	---	AT1G10580	1.19	0.26	2.97	0.021698	0.07174	-4.13
255420_at	putative frataxin-like protein similar to f	FH	AT4G03240	-1.22	-0.29	-2.97	0.021705	0.071753	-4.13
249403_at	putative protein intracellular protein M	---	AT5G40270	1.36	0.44	2.97	0.02171	0.071758	-4.13
249159_at	Nicotiana lesion-inducing like ; suppor	---	AT5G43460	-1.40	-0.48	-2.97	0.021714	0.071761	-4.13
257063_s_	unknown protein ;supported by full-ler	---	AT3G18240 /	-1.22	-0.29	-2.97	0.02172	0.071772	-4.13
252127_at	putative protein ATP binding protein -	PLP3a	AT3G50960	-1.38	-0.46	-2.97	0.021728	0.071787	-4.13
245708_at	pectate lyase-like protein	---	AT5G04310	-1.33	-0.41	-2.97	0.021736	0.071803	-4.14
246514_at	DNA-directed RNA polymerase (mitocl	---	AT5G15700	1.45	0.54	2.97	0.021746	0.071807	-4.14
258222_at	putative zinc finger protein contains Pf	---	AT3G15680	-1.57	-0.65	-2.97	0.021742	0.071807	-4.14
246202_at	methionyl aminopeptidase-like protein	MAP1D	AT4G37040	-1.41	-0.50	-2.97	0.021747	0.071807	-4.14
256533_at	unknown protein	---	AT1G33250	-1.39	-0.48	-2.97	0.021776	0.071884	-4.14
252099_at	putative protein senescence-associate	---	AT3G51250	1.33	0.41	2.97	0.021775	0.071884	-4.14
249317_at	glutathione transferase	ATGSTT2	AT5G41240	-1.25	-0.33	-2.97	0.021781	0.071888	-4.14
255095_at	MEKK1/MAP kinase kinase kinase ; s	MEKK1	AT4G08500	1.43	0.52	2.97	0.021784	0.071888	-4.14
267552_at	putative purple acid phosphatase prec	PAP13	AT2G32770	-1.23	-0.30	-2.97	0.021819	0.071995	-4.14
246313_at	PPR-repeat protein, putative contains	---	AT1G31920	-1.71	-0.77	-2.97	0.021826	0.071996	-4.14
255069_s_	Met2-type cytosine DNA-methyltransf	---	AT4G08990 /	-1.46	-0.54	-2.97	0.021826	0.071996	-4.14
247436_at	dehydrogenase ; supported by cDNA:	ALDH12A1	AT5G62530	1.38	0.47	2.97	0.021842	0.072027	-4.14
265535_at	hypothetical protein predicted by gens	---	AT2G15900	1.24	0.31	2.97	0.02184	0.072027	-4.14
252528_at	E2, ubiquitin-conjugating enzyme 13 (	UBC13	AT3G46460	-1.23	-0.30	-2.97	0.021853	0.072043	-4.14
255549_at	predicted protein of unknown function	GPAT3	AT4G01950	3.15	1.65	2.97	0.021852	0.072043	-4.14
246614_at	serine/threonine protein kinase SOS2	SOS2	AT5G35410	1.25	0.33	2.97	0.021879	0.072108	-4.14
263564_s_	DNA-directed RNA polymerase II, thir	NRPB3	AT2G15400 /	-1.27	-0.35	-2.97	0.021882	0.072108	-4.14
265292_s_	hypothetical protein predicted by gens	---	---	-1.21	-0.28	-2.97	0.021881	0.072108	-4.14
261685_at	3-beta-hydroxysteroid dehydrogenase	AT3BETAHS	AT1G47290	-1.68	-0.75	-2.97	0.021896	0.072143	-4.14
245724_at	hypothetical protein predicted by gene	---	AT1G73390	1.49	0.57	2.97	0.021911	0.072182	-4.14
248491_at	unknown protein ;supported by full-ler	---	AT5G51010	-1.41	-0.49	-2.97	0.021917	0.072187	-4.14
254148_at	hsp 70-like protein heat shock 70 prot	cpHsc70-1	AT4G24280	-1.27	-0.34	-2.97	0.021919	0.072187	-4.14
251611_at	putative protein several hypothetical pr	---	AT3G57940	1.40	0.48	2.96	0.021998	0.072436	-4.15
262118_at	beta-glucosidase, putative similar to b	BGLU11	AT1G02850	2.15	1.10	2.96	0.022012	0.072459	-4.15

255895_at	12-oxophytodienoate reductase, putat	---	AT1G17990 /	-2.32	-1.22	-2.96	0.022009	0.072459	-4.15
246183_at	beta-glucosidase - like protein beta-gl	---	AT5G20940	1.31	0.39	2.96	0.022014	0.072459	-4.15
258102_at	unknown protein contains Pfam profile	---	AT3G23600	1.36	0.44	2.96	0.022057	0.072589	-4.15
267562_at	unknown protein similar to hypothetica	---	AT2G39670	-1.24	-0.31	-2.96	0.022091	0.072691	-4.15
262466_at	hypothetical protein similar to hypothet	NTMC2T5.1	AT1G50260	1.36	0.44	2.96	0.022097	0.072699	-4.15
248625_at	3-keto-acyl-CoA thiolase 2 (gb|AAC17	PKT2	AT5G48880	-1.62	-0.70	-2.96	0.02212	0.072766	-4.15
259587_at	unknown protein ;supported by full-len	---	AT1G28120	-1.28	-0.35	-2.96	0.022154	0.072866	-4.16
261757_at	hypothetical protein similar to putative	---	AT1G08210	1.44	0.52	2.96	0.022164	0.072888	-4.16
262383_at	disease resistance protein, putative si	---	AT1G72940	3.16	1.66	2.96	0.022174	0.072913	-4.16
263172_at	hypothetical protein predicted by gene	CID3	AT1G54170	1.20	0.26	2.96	0.022182	0.072928	-4.16
253775_at	putative protein T01B08.14 gene, BA	---	AT4G28440	1.22	0.29	2.96	0.022205	0.07298	-4.16
249036_at	nuclear cap-binding protein; CBP20 (g	CBP20	AT5G44200	-1.31	-0.39	-2.96	0.022207	0.07298	-4.16
258194_at	unknown protein ; supported by full-le	---	AT3G29170	-1.38	-0.46	-2.96	0.022202	0.07298	-4.16
245013_at	ATPase epsilon subunit	---	---	-1.21	-0.27	-2.96	0.022216	0.072997	-4.16
263032_at	unknown protein ;supported by full-len	---	AT1G23850	1.76	0.82	2.96	0.022224	0.073013	-4.16
258766_at	galactokinase-like protein similar to ga	---	AT3G10700	-1.24	-0.31	-2.95	0.022247	0.073077	-4.16
266866_at	putative ABC transporter	PDR3	AT2G29940	1.49	0.57	2.95	0.022259	0.073108	-4.16
265074_at	hypothetical protein ; supported by cDI	emb1011	AT1G55540	1.30	0.38	2.95	0.022278	0.073158	-4.16
258435_at	unknown protein ;supported by full-ler	---	AT3G16740	-1.29	-0.37	-2.95	0.022307	0.073244	-4.16
244962_at	NADH dehydrogenase ND4	---	---	-1.20	-0.26	-2.95	0.022324	0.073289	-4.16
250787_at	meiotic check point regulator-like prote	EMB2771	AT5G05560	-1.24	-0.31	-2.95	0.022347	0.073352	-4.16
264849_at	putative ribosomal protein S4 contains	---	AT2G17360	-1.33	-0.41	-2.95	0.022359	0.073381	-4.17
266362_at	unknown protein	---	AT2G32430	1.33	0.41	2.95	0.022374	0.073422	-4.17
257291_at	DNA-binding protein, putative similar t	---	AT3G15590	1.70	0.77	2.95	0.022393	0.073461	-4.17
253260_at	hypothetical protein	---	AT4G34420 /	-1.28	-0.36	-2.95	0.022391	0.073461	-4.17
247963_at	beta-1,3-glucanase-like protein	---	AT5G56590	-1.25	-0.32	-2.95	0.022401	0.073479	-4.17
266910_at	unknown protein	---	AT2G45920	1.75	0.81	2.95	0.022419	0.073525	-4.17
264202_at	TINY-like transcription factor Contains	---	AT1G22810	2.10	1.07	2.95	0.022426	0.07354	-4.17
251333_at	putative protein putative protein F26O	---	AT3G61690	1.20	0.26	2.95	0.022444	0.073587	-4.17
254160_at	putative protein ;supported by full-leng	SLY1	AT4G24210	-1.35	-0.43	-2.95	0.022479	0.073691	-4.17
249472_at	hypothetical protein ;supported by full-	CRR7	AT5G39210	-1.52	-0.60	-2.95	0.022529	0.073835	-4.17
247987_at	putative protein similar to unknown pro	---	AT5G56900	-1.29	-0.36	-2.95	0.022529	0.073835	-4.17
250664_at	putative protein 10-deacetylbaccatin I	---	AT5G07080	-1.70	-0.77	-2.95	0.022552	0.073889	-4.17
260932_s_	hypothetical protein contains similarity	PGP12	AT1G02520 /	2.41	1.27	2.95	0.022549	0.073889	-4.17
264949_at	unknown protein contains similarity to	MAF1	AT1G77080	-1.22	-0.28	-2.94	0.022579	0.073967	-4.18

261644_s_	hypothetical protein contains similarity	ATCSA-1	AT1G19750 /	-1.29	-0.37	-2.94	0.022617	0.074071	-4.18
254027_at	putative mitochondrial protein Homo s	---	AT4G25835	-1.46	-0.54	-2.94	0.022617	0.074071	-4.18
255389_at	putative reverse transcriptase	---	---	-1.20	-0.26	-2.94	0.022657	0.074189	-4.18
246480_at	TCP-1 chaperonin-like protein t-comp	---	AT5G16070	-1.38	-0.46	-2.94	0.022687	0.074277	-4.18
256231_at	unknown protein ; supported by full-ler	---	AT3G12630	1.25	0.32	2.94	0.022716	0.074363	-4.18
257501_at	hypothetical protein predicted by gene	---	---	-1.19	-0.26	-2.94	0.022729	0.074393	-4.18
260669_at	hypothetical protein predicted by gene	---	AT1G19340	1.27	0.34	2.94	0.022746	0.074427	-4.18
253528_s_	putative protein bcop gene product - D	---	AT4G31480 /	-1.22	-0.29	-2.94	0.022744	0.074427	-4.18
262286_at	Expressed protein ; supported by full-l	---	AT1G68585	-1.63	-0.71	-2.94	0.022751	0.074433	-4.18
262635_at	4-hydroxyphenylpyruvate dioxygenase	PDS1	AT1G06570	1.61	0.68	2.94	0.022758	0.074444	-4.18
259524_at	hypothetical protein	---	AT1G12550	-1.40	-0.49	-2.94	0.022777	0.074497	-4.18
261508_at	unknown protein	---	AT1G71730	-1.28	-0.36	-2.94	0.022785	0.074512	-4.18
245113_at	hypothetical protein predicted by gene	MIZ1	AT2G41660	1.39	0.47	2.94	0.022792	0.074524	-4.19
250791_at	nucleic acid binding protein-like ;supp	AL1	AT5G05610	-1.24	-0.31	-2.94	0.022804	0.074554	-4.19
249759_at	putative protein contains similarity to ir	YSL2	AT5G24380	1.42	0.50	2.94	0.022822	0.074602	-4.19
251769_at	receptor kinase - like protein receptor	CCR3	AT3G55950	3.47	1.80	2.94	0.022855	0.074699	-4.19
252114_at	mucin -like protein hemomucin, Droso	---	AT3G51450	-2.03	-1.02	-2.94	0.022866	0.074725	-4.19
266396_at	unknown protein	---	AT2G38790	1.41	0.50	2.93	0.022889	0.074778	-4.19
259375_at	putative APG protein similar to anter-s	---	AT3G16370	-9.09	-3.18	-2.93	0.022887	0.074778	-4.19
266802_at	Expressed protein ; supported by cDN	---	AT2G22900	-2.76	-1.47	-2.93	0.0229	0.074804	-4.19
251076_at	putative protein putative protein At2g3	---	AT5G01970	-1.45	-0.54	-2.93	0.022907	0.074817	-4.19
245095_at	putative protein kinase contains a prot	---	AT2G40860	-1.41	-0.49	-2.93	0.022919	0.074843	-4.19
249457_s_	zinc finger -like protein transcription fa	VIM4	AT1G66040 /	1.38	0.46	2.93	0.022923	0.074847	-4.19
261377_at	unknown protein ;supported by full-len	---	AT1G18850	1.64	0.72	2.93	0.022957	0.074932	-4.19
248281_at	unknown protein	---	AT5G52980	1.22	0.28	2.93	0.022958	0.074932	-4.19
247422_at	putative protein	PEX14	AT5G62810	-1.25	-0.32	-2.93	0.022959	0.074932	-4.19
255929_at	hypothetical protein predicted by gene	---	AT1G12650	1.31	0.39	2.93	0.022985	0.074996	-4.19
247745_at	copper transport protein	COPT1	AT5G59030	-1.21	-0.28	-2.93	0.022986	0.074996	-4.19
253672_at	mRNA cleavage factor subunit - like p	CFIM-25	AT4G29820	1.34	0.43	2.93	0.023025	0.075115	-4.20
258379_at	putative decarboxilase similar to 5-oxo	---	AT3G16700	-1.41	-0.49	-2.93	0.02308	0.075271	-4.20
252327_at	MTN3-like protein MtN3 gene product	---	AT3G48740	1.41	0.50	2.93	0.023079	0.075271	-4.20
265242_at	hypothetical protein	---	AT2G07705	1.51	0.60	2.93	0.023083	0.075272	-4.20
249277_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G41890	-1.89	-0.92	-2.93	0.023094	0.075298	-4.20
250188_at	putative protein COP9 complex subun	COP13	AT5G14250	1.26	0.33	2.93	0.023112	0.075331	-4.20
259450_at	hypothetical protein predicted by gene	DRL1	AT1G13870	-1.30	-0.38	-2.93	0.023115	0.075331	-4.20

258327_at	unknown protein contains similarity to	PAP85	AT3G22640	1.22	0.29	2.93	0.023109	0.075331	-4.20
256831_at	hypothetical protein	---	AT3G22870	1.26	0.34	2.93	0.023118	0.075331	-4.20
252534_at	Myb DNA binding protein -like MYB59	MYB111	AT3G46130	-1.25	-0.32	-2.93	0.023129	0.075357	-4.20
258101_at	unknown protein	RFR1	AT3G23590	-1.58	-0.66	-2.93	0.023133	0.075357	-4.20
249304_at	folylpolyglutamate synthase-like protei	GLA1	AT5G41480	-1.37	-0.45	-2.93	0.023139	0.075367	-4.20
252479_at	small zinc finger-like protein TIM9 ;su	TIM9	AT3G46560	1.41	0.49	2.93	0.023151	0.075395	-4.20
259476_at	Myb-related transcription activator, pu	---	AT1G19000	-1.36	-0.44	-2.93	0.023159	0.07541	-4.20
251646_at	putative protein	---	AT3G57780	-2.30	-1.20	-2.93	0.023178	0.075462	-4.20
261501_at	wall-associated kinase 1, putative sim	---	AT1G28390	1.40	0.49	2.92	0.023194	0.075505	-4.20
263912_at	starch branching enzyme II	SBE2.1	AT2G36390	1.36	0.44	2.92	0.023202	0.07552	-4.20
267512_at	hypothetical protein predicted by gens	SSE1	AT2G45690	-1.29	-0.37	-2.92	0.023208	0.075528	-4.20
253905_s_	putative protein retrotransposon Opie-	---	---	-1.20	-0.27	-2.92	0.023217	0.075542	-4.20
246281_at	hypothetical protein	NAPRT1	AT4G36940	-1.44	-0.53	-2.92	0.023219	0.075542	-4.20
252125_at	putative protein hypothetical protein T	RTH	AT3G51040	-1.27	-0.34	-2.92	0.023237	0.075589	-4.21
264690_at	hypothetical protein similar to hypothet	SNL4	AT1G70060	-1.34	-0.42	-2.92	0.023256	0.075629	-4.21
255284_at	5-adenylylsulfate reductase ;supporte	אפר-01	AT4G04610	2.18	1.13	2.92	0.023255	0.075629	-4.21
251797_at	putative protein AT-hook protein 1 (AH	AGF2	AT3G55560	1.37	0.45	2.92	0.023261	0.075637	-4.21
261819_at	receptor-like kinase, putative similar to	---	AT1G11410	-1.25	-0.32	-2.92	0.023274	0.075667	-4.21
260549_at	Expressed protein ; supported by full-le	---	AT2G43535	-2.04	-1.03	-2.92	0.023285	0.075692	-4.21
249918_at	putative protein predicted protein, Ara	---	AT5G19240	2.09	1.06	2.92	0.023297	0.07572	-4.21
266474_at	hypothetical protein predicted by grail	---	AT2G31110	2.03	1.02	2.92	0.02331	0.07575	-4.21
250437_at	AtAGP4 ; supported by cDNA: gi_139	AGP4	AT5G10430	-2.57	-1.36	-2.92	0.023313	0.075751	-4.21
250865_at	putative protein predicted protein, Syn	---	AT5G03900	-1.41	-0.49	-2.92	0.023336	0.075814	-4.21
255397_at	putative transposon protein	---	---	-1.35	-0.44	-2.92	0.023354	0.075862	-4.21
256686_at	non-LTR reverse transcriptase, putativ	---	---	-1.20	-0.27	-2.92	0.023367	0.075892	-4.21
247966_at	putative protein contains similarity to u	---	AT5G56610	1.27	0.34	2.92	0.023372	0.075899	-4.21
258818_at	putative ethylene receptor (EIN4) simi	EIN4	AT3G04580	1.31	0.39	2.92	0.023395	0.075964	-4.21
265212_at	putative sugar transporter protein Simi	---	AT1G05030	-1.26	-0.33	-2.92	0.023421	0.076038	-4.21
249800_at	MtN3-like protein ; supported by cDNA	MTN3	AT5G23660	1.27	0.34	2.92	0.023442	0.076094	-4.21
256425_at	disease resistance protein, putative si	ADR1	AT1G33560	1.39	0.48	2.92	0.023465	0.076158	-4.22
253518_at	hypothetical protein	---	AT4G31400	-1.32	-0.40	-2.92	0.023478	0.076188	-4.22
257966_at	unknown protein ;supported by full-ler	---	AT3G19800	-1.41	-0.49	-2.92	0.023488	0.07621	-4.22
250825_at	putative protein similar to unknown pro	---	AT5G05210	1.25	0.32	2.92	0.02351	0.07627	-4.22
259723_at	putative iron-regulated transporter sim	IRT3	AT1G60960	1.68	0.75	2.91	0.023537	0.076336	-4.22
256276_at	geranylgeranyl transferase type II beta	---	AT3G12070	1.28	0.35	2.91	0.023535	0.076336	-4.22

247965_at	putative protein similar to unknown pro	AGP14	AT5G56540	-1.46	-0.54	-2.91	0.023553	0.076379	-4.22
255040_at	putative protein hypothetical protein -	---	AT4G09580	1.28	0.35	2.91	0.023561	0.076393	-4.22
258064_at	putative cytochrome P450 similar to G	CYP72A14	AT3G14680	1.88	0.91	2.91	0.023581	0.076426	-4.22
255857_at	unknown protein ;supported by full-len	ABA4	AT1G67080	-1.21	-0.28	-2.91	0.023579	0.076426	-4.22
252724_at	putative protein hypothetical protein sl	---	AT3G43540	-1.33	-0.41	-2.91	0.023579	0.076426	-4.22
264114_at	hypothetical protein predicted by gens	CDT1A	AT2G31270	-1.71	-0.77	-2.91	0.023595	0.076462	-4.22
253421_at	putative protein predicted proteins, Ar	---	AT4G32340	1.36	0.44	2.91	0.023629	0.076548	-4.22
245898_at	ser/thr specific protein kinase-like prot	---	AT5G11020	-1.34	-0.42	-2.91	0.023627	0.076548	-4.22
247469_at	Expressed protein ; supported by cDN	AGL42	AT5G62165	-3.10	-1.63	-2.91	0.023635	0.076557	-4.22
267428_at	putative coatomer epsilon subunit	---	AT2G34840	-1.28	-0.36	-2.91	0.023651	0.076597	-4.22
258054_at	delta tonoplast integral protein (delta-	DELTA-TIP	AT3G16240	-4.41	-2.14	-2.91	0.02366	0.076615	-4.22
266473_at	unknown protein	---	AT2G31110	1.97	0.98	2.91	0.023672	0.076639	-4.23
261080_at	proliferating cellular nuclear antigen id	PCNA1	AT1G07370	-2.52	-1.33	-2.91	0.023674	0.076639	-4.23
247001_at	natural resistance-associated macroph	NRAMP4	AT5G67330	1.30	0.38	2.91	0.023686	0.076669	-4.23
254577_at	putative protein ;supported by full-leng	---	AT4G19450	1.41	0.50	2.91	0.023692	0.076672	-4.23
264184_at	early nodule-specific protein, putative	---	AT1G54790	-1.27	-0.34	-2.91	0.023694	0.076672	-4.23
256707_at	hypothetical protein predicted by gene	---	---	-1.22	-0.29	-2.91	0.023706	0.076699	-4.23
247980_at	putative protein similar to unknown pro	GNC	AT5G56860	-1.91	-0.94	-2.91	0.023729	0.076763	-4.23
246092_at	glutaredoxin ;supported by full-length	---	AT5G20500	-1.29	-0.36	-2.91	0.02375	0.076811	-4.23
247500_at	putative protein B2 protein, Daucus ca	---	AT5G61910	1.42	0.50	2.91	0.023749	0.076811	-4.23
248768_at	60S acidic ribosomal protein P1-like pr	---	AT5G47700	-1.48	-0.57	-2.91	0.023769	0.07686	-4.23
263637_at	hypothetical protein predicted by gens	---	AT2G11890	1.23	0.30	2.91	0.023802	0.076948	-4.23
262180_at	phosphoglycerate mutase, putative sir	PGM	AT1G78050	1.24	0.31	2.91	0.023804	0.076948	-4.23
262731_at	hypothetical protein similar to gb|AF09	MC8	AT1G16420	5.52	2.46	2.91	0.023806	0.076948	-4.23
252619_at	putative protein several hypothetical pr	---	AT3G45210	1.55	0.63	2.91	0.023818	0.076976	-4.23
265966_at	putative RNA-binding protein ; suppor	---	AT2G37220	-1.35	-0.43	-2.91	0.023831	0.077005	-4.23
262504_at	putative protein disulfide isomerase pr	ATPDIL1-1	AT1G21750	1.44	0.52	2.90	0.023851	0.077059	-4.23
257312_at	Expressed protein ; supported by full-l	AT3G26590	---	1.23	0.30	2.90	0.023864	0.07709	-4.23
257663_at	hypothetical protein predicted by gens	---	AT3G20260	-1.26	-0.33	-2.90	0.023869	0.077096	-4.23
245935_at	hypothetical protein	---	AT5G19840	1.23	0.30	2.90	0.023873	0.077099	-4.23
249827_at	unknown protein ;supported by full-ler	---	AT5G23330	-1.32	-0.40	-2.90	0.023886	0.077129	-4.23
261012_at	CLE9, putative CLAVATA3/ESR-Rela	CLE9	AT1G26600	-1.19	-0.26	-2.90	0.023892	0.077139	-4.23
252440_at	aquaporin-like protein aquaporin - Ver	TIP5;1	AT3G47440	-1.23	-0.30	-2.90	0.023899	0.077139	-4.24
248223_at	unknown protein ; supported by cDNA	---	AT5G53620	-1.19	-0.26	-2.90	0.023899	0.077139	-4.24
263193_at	acetyl-CoA carboxylase, putative simi	---	AT1G36050	-1.24	-0.32	-2.90	0.023905	0.077145	-4.24

254058_at	putative protein cylicin II - human, PID	---	AT4G25210	-1.31	-0.39	-2.90	0.023939	0.077244	-4.24
260652_at	putative MYB family transcription facto	---	AT1G32360	-1.23	-0.30	-2.90	0.023948	0.077263	-4.24
256225_at	unknown protein ; supported by full-ler	---	AT1G56220	1.39	0.48	2.90	0.023956	0.07728	-4.24
246417_at	quinone oxidoreductase - like protein	---	AT5G16990	-1.41	-0.49	-2.90	0.023971	0.077317	-4.24
250590_at	exonuclease-like protein	---	AT5G07710	-1.24	-0.31	-2.90	0.023982	0.07734	-4.24
266096_at	putative vacuolar protein sorting-assoc	VCL1	AT2G38020	1.24	0.31	2.90	0.02399	0.077355	-4.24
245700_at	carbonate dehydratase - like protein ;s	ACA3	AT5G04180	-1.22	-0.29	-2.90	0.024	0.077376	-4.24
267094_at	putative diphenol oxidase ; supported	IRX12	AT2G38080	-2.22	-1.15	-2.90	0.024012	0.077404	-4.24
248392_at	integral membrane protein-like	---	AT5G52050	3.35	1.74	2.90	0.024029	0.077447	-4.24
264702_at	hypothetical protein contains similarity	---	AT1G70190	-1.29	-0.37	-2.90	0.024049	0.07749	-4.24
253431_at	putative protein predicted protein, Ara	---	AT4G32440	1.28	0.35	2.90	0.024048	0.07749	-4.24
260081_at	unknown protein	---	AT1G78170	-2.90	-1.54	-2.90	0.024089	0.077609	-4.24
259835_at	unknown protein	TRZ3	AT1G52160	1.25	0.32	2.90	0.024094	0.077613	-4.24
252592_at	mitogen-activated protein kinase 3 ; s	NAXT1	AT3G45640 /	1.92	0.94	2.90	0.02411	0.077654	-4.24
261239_at	Avr9 elicitor response protein, putative	---	AT1G32930	1.23	0.29	2.90	0.024113	0.077654	-4.24
254263_at	Expressed protein ; supported by full-l	---	AT4G23493	1.24	0.31	2.90	0.02415	0.077762	-4.25
266371_at	calmodulin-like protein identical to GB:	---	AT2G41410	1.62	0.69	2.90	0.024171	0.077818	-4.25
265903_at	putative potassium transporter/channe	SPIK	AT2G25600	1.23	0.30	2.89	0.024196	0.077881	-4.25
247770_at	putative protein predicted proteins, Ar	---	AT5G58930	-1.82	-0.87	-2.89	0.024197	0.077881	-4.25
257973_at	unknown protein	---	AT3G20720	1.33	0.41	2.89	0.024203	0.077888	-4.25
261475_at	anionic peroxidase, putative similar to	---	AT1G14550	1.47	0.56	2.89	0.024225	0.077948	-4.25
251626_at	UDP-GlcNAc:dolichol phosphate N-ac	---	AT3G57220	-1.27	-0.34	-2.89	0.024229	0.07795	-4.25
255735_at	transmembrane protein, putative simil	---	AT1G25520	1.53	0.62	2.89	0.024241	0.077979	-4.25
261401_at	kinase, putative similar to Ste-20 relat	---	AT1G79640	-1.35	-0.44	-2.89	0.024249	0.077992	-4.25
266406_at	hypothetical protein predicted by gens	---	AT2G38570	-1.31	-0.39	-2.89	0.024271	0.078051	-4.25
252872_at	putative serine/threonine protein kinas	SNRK2.7	AT4G40010	1.22	0.29	2.89	0.024332	0.078236	-4.25
266469_at	myb-related protein	MYB14	AT2G31180	1.26	0.34	2.89	0.024352	0.078291	-4.25
262025_at	growth regulator, putative similar to ax	---	AT1G35510	-1.31	-0.38	-2.89	0.02436	0.078302	-4.26
259639_at	unknown protein ;supported by full-len	---	AT1G52380	-1.29	-0.37	-2.89	0.024362	0.078302	-4.26
249069_at	unknown protein	---	AT5G44010	-1.66	-0.73	-2.89	0.024424	0.078477	-4.26
252229_at	putative protein lea32, Arabidopsis tha	---	AT3G49890	1.33	0.42	2.89	0.024423	0.078477	-4.26
253095_at	putative protein ribonuclease III, Bacil	---	AT4G37510	-1.27	-0.34	-2.89	0.024472	0.078622	-4.26
264157_at	xyloglucan endotransglycosylase, put	XTH17	AT1G65310	-1.54	-0.62	-2.89	0.024512	0.078715	-4.26
249957_at	putative protein predicted proteins, Ar	---	AT5G18900	1.33	0.41	2.89	0.024505	0.078715	-4.26
255005_at	putative protein putative proteins Arabi	---	AT4G09990	-1.29	-0.37	-2.89	0.024515	0.078715	-4.26

247049_at	putative protein similar to unknown pro	---	AT5G66440	2.84	1.51	2.89	0.024509	0.078715	-4.26
257310_at	ATP-dependent RNA helicase, putativ	---	AT3G26560	1.29	0.37	2.88	0.024541	0.078778	-4.26
249487_at	ABC transporter -like protein TAP-like	TAP2	AT5G39040	1.54	0.63	2.88	0.024542	0.078778	-4.26
260407_at	putative protein kinase Pfam HMM hit:	---	AT1G69910	-1.22	-0.28	-2.88	0.024573	0.078868	-4.26
266164_at	putative salt-inducible protein	---	AT2G28050	-1.47	-0.55	-2.88	0.024611	0.078978	-4.27
259098_at	putative ribose 5-phosphate isomeras	---	AT3G04790	-1.46	-0.54	-2.88	0.024622	0.079004	-4.27
263728_at	gamma-adaptin, putative similar to ga	---	AT1G60070	-1.27	-0.34	-2.88	0.02464	0.079048	-4.27
245293_at	HSP like protein ; supported by cDNA:	---	AT4G16660	2.03	1.02	2.88	0.024672	0.079141	-4.27
258053_at	unknown protein similar to CGI-18 pro	---	AT3G16230	1.21	0.27	2.88	0.02469	0.079187	-4.27
259487_at	hypothetical protein contains similarity	TRFL5	AT1G15720	-1.19	-0.26	-2.88	0.024725	0.079288	-4.27
261979_at	nitrate reductase, putative similar to n	NIA2	AT1G37130	1.50	0.58	2.88	0.024731	0.079295	-4.27
262341_at	E2, ubiquitin-conjugating enzyme, put	UBC28	AT1G64230	1.31	0.39	2.88	0.024736	0.079301	-4.27
259537_at	hypothetical protein ; supported by cDI	PHR1	AT1G12370	-1.32	-0.40	-2.88	0.024745	0.07932	-4.27
265206_at	putative protease belongs to eukaryoti	---	AT2G36670	1.31	0.39	2.88	0.024765	0.079373	-4.27
245054_at	unknown protein	---	AT2G26460	1.31	0.39	2.88	0.024784	0.079421	-4.27
249468_at	putative protein predicted proteins, Ar	---	AT5G39650	-1.22	-0.28	-2.88	0.024798	0.079457	-4.27
246050_s_	protein phosphatase 2A regulatory su	---	AT5G28850 /	-1.20	-0.27	-2.88	0.024826	0.079523	-4.28
261766_at	auxin-induced protein IAA5, putative s	IAA5	AT1G15580	-1.96	-0.97	-2.88	0.024826	0.079523	-4.28
248820_at	putative protein similar to unknown pro	---	AT5G47060	1.37	0.45	2.88	0.024861	0.079611	-4.28
267077_at	unknown protein similar to cytoskeleta	---	AT2G40970	-1.36	-0.45	-2.88	0.024857	0.079611	-4.28
249739_at	Ttg1 protein (emb CAB45372.1)	TTG1	AT5G24520	-1.22	-0.29	-2.87	0.024892	0.079699	-4.28
267186_at	unknown protein ; supported by cDNA	---	AT2G44090	-1.25	-0.32	-2.87	0.0249	0.079712	-4.28
265423_at	unknown protein	---	AT2G20790	-1.48	-0.56	-2.87	0.024906	0.079712	-4.28
247521_at	putative protein ATP/GTP nucleotide-	---	AT5G61450	1.28	0.36	2.87	0.024903	0.079712	-4.28
259074_at	putative protein kinase contains Pfam	RPK2	AT3G02130	-1.42	-0.51	-2.87	0.024937	0.079799	-4.28
264504_at	unknown protein similar to ATP-citrate	ACLA-3	AT1G09430	1.24	0.31	2.87	0.024952	0.079825	-4.28
262393_at	hypothetical protein contains similarity	---	AT1G49490	-1.27	-0.34	-2.87	0.024949	0.079825	-4.28
262531_at	putative leucine-rich receptor protein k	---	AT1G17230 /	-1.37	-0.46	-2.87	0.024979	0.079901	-4.28
248110_at	wax synthase-like protein	---	AT5G55320	-1.20	-0.27	-2.87	0.024997	0.079937	-4.28
260269_at	putative disease resistance protein sim	---	AT1G63740	1.32	0.40	2.87	0.024996	0.079937	-4.28
246189_at	ABI3-interacting protein 2 ;supported	---	AT5G20910	1.38	0.46	2.87	0.02503	0.08003	-4.28
255860_at	putative protein heparanase, Homo sa	AtGUS3	AT5G34940	5.19	2.38	2.87	0.025038	0.080035	-4.28
248278_at	putative protein similar to unknown pro	---	AT5G52890	-1.30	-0.38	-2.87	0.025035	0.080035	-4.28
262377_at	rubisco activase, putative similar to ru	---	AT1G73110	-1.54	-0.62	-2.87	0.025049	0.080053	-4.28
260821_at	unknown protein contains Pfam profile	CRTISO	AT1G06820	-1.32	-0.40	-2.87	0.025051	0.080053	-4.28

260323_at	putative U3 small nucleolar ribonucleo	IMP4	AT1G63780	1.57	0.65	2.87	0.025071	0.080104	-4.29
262798_at	putative SPL1-related protein similar t	SPL14	AT1G20980	1.27	0.35	2.87	0.025095	0.080169	-4.29
253295_at	putative aspartate--tRNA ligase aspar	---	AT4G33760	-1.41	-0.50	-2.87	0.025102	0.080175	-4.29
267644_s_	unknown protein highly similar to T21L	---	AT2G32870 /	-1.42	-0.50	-2.87	0.025103	0.080175	-4.29
267309_at	Expressed protein ; supported by full-l	---	AT2G19385	1.40	0.49	2.87	0.025121	0.080221	-4.29
259950_at	hypothetical protein predicted by gene	---	AT1G71410	-1.28	-0.36	-2.87	0.025143	0.080278	-4.29
250564_at	putative protein sigma factor F inhibito	---	AT5G08060	1.20	0.27	2.87	0.025165	0.080337	-4.29
262993_at	hypothetical protein contains similarity	---	AT1G54230	-1.22	-0.29	-2.87	0.025181	0.080376	-4.29
265271_at	hypothetical protein predicted by gens	---	AT2G28360	-1.29	-0.37	-2.87	0.025185	0.080378	-4.29
246559_at	putative protein YTM1 - Homo sapien	---	AT5G15550	1.45	0.54	2.87	0.0252	0.080403	-4.29
264485_at	unknown protein ; supported by cDNA	---	AT1G77220	1.25	0.32	2.87	0.025198	0.080403	-4.29
261026_at	hypothetical protein predicted by gene	---	AT1G01240	-1.33	-0.41	-2.86	0.025216	0.080446	-4.29
266439_s_	hypothetical protein predicted by grail	---	AT2G43200	-1.26	-0.33	-2.86	0.025238	0.080504	-4.29
258471_at	NPK1-related protein kinase 3 identica	ANP3	AT3G06030	-1.27	-0.34	-2.86	0.025246	0.080517	-4.29
246058_at	putative protein predicted proteins, Ar	---	AT5G08430	1.28	0.35	2.86	0.025277	0.080606	-4.29
265257_at	succinyl-CoA ligase beta subunit ;sup	---	AT2G20420	1.55	0.64	2.86	0.025291	0.080638	-4.29
258187_at	HSC70-interacting protein, putative si	ATTDX	AT3G17880	1.25	0.32	2.86	0.025297	0.080647	-4.29
249798_at	putative protein contains similarity to p	---	AT5G23730	1.23	0.30	2.86	0.025314	0.08069	-4.30
264591_at	hypothetical protein contains similarity	---	AT2G17670	1.26	0.34	2.86	0.025327	0.08072	-4.30
246481_s_	cold and ABA inducible protein kin1 ;s	KIN1	AT5G15960 /	-3.42	-1.78	-2.86	0.025359	0.080799	-4.30
247174_at	unknown protein ; supported by cDNA	---	AT5G65250	-1.23	-0.30	-2.86	0.025356	0.080799	-4.30
253605_at	putative protein probable membrane p	---	AT4G30990	1.37	0.46	2.86	0.025393	0.080883	-4.30
266359_at	putative phospholipid cytidylyltransfera	CCT1	AT2G32260	1.23	0.30	2.86	0.02539	0.080883	-4.30
247086_at	GATA-binding transcription factor-like	---	AT5G66320	2.54	1.34	2.86	0.025424	0.080973	-4.30
246922_at	serine/threonine protein kinase-like pr	CIPK25	AT5G25110	-1.44	-0.53	-2.86	0.025435	0.080996	-4.30
251717_at	putative protein EXOENZYMES REG	LAF3	AT3G55850	1.35	0.43	2.86	0.025443	0.081009	-4.30
248971_at	putative protein contains similarity to d	---	AT5G45000	1.44	0.53	2.86	0.025454	0.081035	-4.30
258518_at	unknown protein ; supported by cDNA	---	AT3G06570	-1.22	-0.28	-2.86	0.025471	0.081076	-4.30
256145_at	lipid transfer protein, putative similar t	---	AT1G48750	-1.74	-0.80	-2.86	0.025482	0.081096	-4.30
262600_at	unknown protein ESTs gb|H37032, gb	MBD10	AT1G15340	-1.38	-0.47	-2.86	0.025484	0.081096	-4.30
248348_at	putative protein similar to unknown pro	---	AT5G52190	-1.25	-0.32	-2.86	0.025521	0.081201	-4.30
256373_at	hypothetical protein	SGA2	AT1G66740	1.35	0.43	2.86	0.02553	0.081218	-4.30
260295_at	putative aminopeptidase similar to ami	---	AT1G63770	1.31	0.39	2.86	0.025539	0.081226	-4.31
247904_at	putative protein contains similarity to u	AIL5	AT5G57390	-1.34	-0.42	-2.86	0.025536	0.081226	-4.30
260833_at	lipase, putative similar to lipase GB:A	---	AT1G06800	1.72	0.78	2.86	0.025555	0.081263	-4.31

251773_at	putative protein HSPC058, Homo sap	---	AT3G55960	1.45	0.54	2.86	0.025571	0.081304	-4.31
267495_at	myb-like protein isolog	ETC2	AT2G30420	-1.59	-0.67	-2.85	0.0256	0.081385	-4.31
259908_at	RNA polymerase subunit identical to G	ATRPAC42	AT1G60850	1.38	0.46	2.85	0.025609	0.081402	-4.31
267095_at	putative AMP deaminase ; supported	FAC1	AT2G38280	1.30	0.37	2.85	0.025633	0.081467	-4.31
263655_at	hypothetical protein predicted by gene	---	AT1G04500	1.25	0.32	2.85	0.025654	0.081511	-4.31
255100_at	putative MuDR-like transposon protein	---	---	-1.21	-0.28	-2.85	0.025654	0.081511	-4.31
247611_at	putative protein predicted proteins	---	AT5G60710	-1.22	-0.28	-2.85	0.02567	0.081552	-4.31
245048_at	orf within trnK intron orf within trnK intr	---	---	-1.38	-0.47	-2.85	0.025681	0.081573	-4.31
250543_at	DR1-like protein TATA-binding protein	NF-YB12	AT5G08190	-1.26	-0.33	-2.85	0.025687	0.081582	-4.31
248502_at	putative protein strong similarity to unk	---	AT5G50450	-1.36	-0.44	-2.85	0.025698	0.081607	-4.31
259216_at	hypothetical protein ; supported by cDI	---	AT3G09000	1.61	0.69	2.85	0.025702	0.081607	-4.31
253196_at	NAD+ dependent isocitrate dehydroge	IDH1	AT4G35260	1.36	0.44	2.85	0.025711	0.081624	-4.31
267342_at	putative heme A:farnesyltransferase ;	COX10	AT2G44520	1.42	0.50	2.85	0.025719	0.081637	-4.31
254734_at	methionyl-tRNA synthetase - like prote	---	AT4G13780	1.28	0.35	2.85	0.025727	0.081642	-4.31
251269_at	putative protein Pm5 protein - Homo s	---	AT3G62360	-1.33	-0.41	-2.85	0.025724	0.081642	-4.31
257081_at	RING zinc finger protein contains Pfar	---	AT3G30460	-1.24	-0.31	-2.85	0.025775	0.081781	-4.31
264464_at	putative heat-shock protein similar to C	---	AT1G10350	-1.29	-0.36	-2.85	0.025779	0.081781	-4.31
257675_at	ethylene responsive element binding f	ERF7	AT3G20310	-1.32	-0.40	-2.85	0.025782	0.081782	-4.31
256762_at	Expressed protein ; supported by full-le	IDL1	AT3G25655	3.25	1.70	2.85	0.025815	0.081873	-4.32
250165_at	putative protein many predicted protei	---	AT5G15290	-1.25	-0.32	-2.85	0.025848	0.081968	-4.32
246385_at	mitotic cyclin a2-type, putative similar	CYCA1;2	AT1G77390	-1.74	-0.80	-2.85	0.025852	0.081969	-4.32
258256_at	unknown protein ; supported by cDNA	---	AT3G26890	-1.28	-0.36	-2.85	0.025858	0.081975	-4.32
265045_s_	putative protein kinase, ADK1 dual sp	ADK1	AT1G03930 /	-1.54	-0.62	-2.85	0.02591	0.082131	-4.32
257598_at	PRT1 identical to GB:CAA11891 from	PRT1	AT3G24800	-1.34	-0.42	-2.85	0.025918	0.082144	-4.32
258859_at	Expressed protein ; supported by full-le	---	AT3G02120	-1.20	-0.26	-2.85	0.025924	0.08215	-4.32
264928_at	auxin-induced protein, putative similar	ATB2	AT1G60710	-1.26	-0.33	-2.84	0.025963	0.082262	-4.32
258189_at	unknown protein ;supported by full-ler	JAZ3	AT3G17860	-1.55	-0.64	-2.84	0.025972	0.082281	-4.32
266846_at	unknown protein	---	AT2G25970	1.22	0.29	2.84	0.02599	0.082288	-4.32
265123_at	hypothetical protein similar to putative	---	AT1G55440	-1.22	-0.28	-2.84	0.025978	0.082288	-4.32
249154_at	Nicotiana EREBP-3 like	---	AT5G43410	2.64	1.40	2.84	0.025992	0.082288	-4.32
260435_at	putative transcription factor similar to C	MYB62	AT1G68320	1.73	0.79	2.84	0.025991	0.082288	-4.32
246656_at	hypothetical protein	---	---	1.28	0.36	2.84	0.025989	0.082288	-4.32
261456_at	hypothetical protein predicted by gene	---	AT1G21050	-2.98	-1.57	-2.84	0.02602	0.082365	-4.32
264562_at	hypothetical protein predicted by gene	---	AT1G55760	1.56	0.64	2.84	0.026025	0.082369	-4.32
263400_s_	40S ribosomal protein; contains C-tern	---	AT2G31610 /	-1.31	-0.39	-2.84	0.026029	0.08237	-4.32

248155_at	putative protein 3 (2'), 5'-bisphosphate	AHL	AT5G54390	1.31	0.39	2.84	0.026049	0.082409	-4.33
251252_at	putative protein several hypothetical pr	---	AT3G62230	1.24	0.31	2.84	0.026046	0.082409	-4.33
257723_at	hypothetical protein predicted by gene	---	AT3G18500	-1.35	-0.43	-2.84	0.026079	0.082495	-4.33
255278_at	putative WD-repeat membrane protein	---	AT4G04940	1.43	0.52	2.84	0.026089	0.082503	-4.33
260173_at	NAM-like protein similar to NAM GB:C/	VND7	AT1G71930	-1.29	-0.37	-2.84	0.026089	0.082503	-4.33
252559_at	RNA binding protein -like COLD-INDU	---	AT3G46020	-1.21	-0.27	-2.84	0.026128	0.082615	-4.33
257448_s_	putative protein various predicted prote	---	AT2G11620 /	1.25	0.32	2.84	0.026174	0.08275	-4.33
262592_at	unknown protein ESTs gb|H37295 and	---	AT1G15400	1.38	0.46	2.84	0.026186	0.082763	-4.33
254937_at	putative aldolase similar to 2,4-dihydr	---	AT4G10750	-1.22	-0.29	-2.84	0.026183	0.082763	-4.33
248753_at	acyl carrier protein-like	mtACP3	AT5G47630	-1.24	-0.31	-2.84	0.026196	0.082785	-4.33
252357_at	putative protein predicted proteins, Ar	---	AT3G48410	1.40	0.49	2.84	0.026205	0.0828	-4.33
256017_at	unknown protein ;supported by full-len	JAZ1	AT1G19180	2.06	1.04	2.84	0.026212	0.082812	-4.33
245401_at	hypothetical protein ;supported by full-	---	AT4G17670	1.82	0.86	2.83	0.026318	0.083134	-4.34
266658_at	Expressed protein ; supported by full-le	---	AT2G25735	3.20	1.68	2.83	0.026342	0.0832	-4.34
265476_at	putative thioredoxin M ; supported by	ATHM3	AT2G15570	-1.21	-0.28	-2.83	0.026352	0.083218	-4.34
245143_at	unknown protein ;supported by full-ler	ZPR1	AT2G45450	1.62	0.70	2.83	0.026373	0.083272	-4.34
248764_at	putative protein contains similarity to C	NF-YB2	AT5G47640	-1.33	-0.41	-2.83	0.026387	0.083306	-4.34
257525_at	hypothetical protein predicted by gens	---	AT3G04900	1.29	0.37	2.83	0.026416	0.083387	-4.34
253622_at	cyclic nucleotide and calmodulin-regu	ATCNGC9	AT4G30560	-1.25	-0.32	-2.83	0.026423	0.083398	-4.34
265413_s_	hypothetical protein predicted by gens	---	AT2G16650 /	-1.28	-0.35	-2.83	0.026441	0.083441	-4.34
256264_at	unknown protein ; supported by full-ler	---	AT3G12210	-1.38	-0.46	-2.83	0.026455	0.083474	-4.34
254226_at	putative disease resistance response	---	AT4G23690	3.69	1.88	2.83	0.02646	0.083478	-4.34
250969_at	putative protein ;supported by full-leng	---	AT5G02740	-1.24	-0.30	-2.83	0.026475	0.083513	-4.34
245149_at	putative SWI/SNF family transcription a	ATSWI3A	AT2G47620	1.27	0.34	2.83	0.026479	0.083515	-4.34
259700_at	unknown protein	---	AT1G68980	1.19	0.25	2.83	0.026489	0.083526	-4.34
246218_at	RUB1-conjugating enzyme RCE1, put	RCE1	AT4G36800	-1.40	-0.48	-2.83	0.026487	0.083526	-4.34
258623_at	unknown protein ; supported by cDNA	---	AT3G02790	-1.60	-0.68	-2.83	0.026533	0.083652	-4.35
258090_at	putative 60S ribosomal protein L18A s	---	AT3G14600	-1.37	-0.45	-2.83	0.026556	0.083714	-4.35
249618_at	putative protein predicted proteins, Ar	---	AT5G37490	4.17	2.06	2.83	0.026564	0.083727	-4.35
257797_at	hypothetical protein contains Pfam pro	---	AT3G15940	-1.28	-0.36	-2.83	0.026587	0.083787	-4.35
256075_at	mitogen-activated protein kinase, puta	ATMPK8	AT1G18150	1.31	0.39	2.83	0.026592	0.083791	-4.35
246066_at	putative protein predicted proteins, Ho	SMG7	AT5G19400	1.28	0.35	2.83	0.026597	0.083795	-4.35
261144_s_	unknown protein ;supported by full-len	---	AT1G19660 /	1.26	0.34	2.83	0.026651	0.083954	-4.35
248766_at	putative protein strong similarity to unk	---	AT5G47580	1.61	0.68	2.83	0.026658	0.083963	-4.35
260277_at	hypothetical protein predicted by gens	---	AT1G80520	1.60	0.68	2.82	0.026683	0.084031	-4.35

263256_at	unknown protein similar to ESTs gb|H3	ATCPISCA	AT1G10500	1.34	0.43	2.82	0.026704	0.084075	-4.35
267505_at	putative cytochrome P450 ;supported	CYP76C1	AT2G45560	-1.30	-0.38	-2.82	0.026703	0.084075	-4.35
245717_at	Expressed protein ; supported by cDN	---	AT5G33390	1.27	0.34	2.82	0.026715	0.084096	-4.35
246946_at	putative protein	---	AT5G25070	-1.21	-0.27	-2.82	0.026757	0.084216	-4.35
264621_at	putative protein kinase contains a prot	---	AT2G17700	1.28	0.36	2.82	0.026764	0.084218	-4.35
247617_at	receptor like protein kinase receptor li	---	AT5G60270	1.69	0.76	2.82	0.026762	0.084218	-4.35
248144_at	glucose-6-phosphate/phosphate transl	GPT1	AT5G54800	1.31	0.39	2.82	0.026771	0.084226	-4.35
252973_s_	peptidylprolyl isomerase ROC1 ;suppo	ROC1	AT4G38740	1.40	0.48	2.82	0.026777	0.084233	-4.35
249199_at	putative protein similar to unknown pro	BPC6	AT5G42520	-1.25	-0.33	-2.82	0.0268	0.084295	-4.36
247534_at	pyrophosphate-dependent phosphofru	PFK4	AT5G61580	1.21	0.28	2.82	0.026804	0.084296	-4.36
257497_at	hypothetical protein predicted by gene	---	AT1G51430	-1.43	-0.52	-2.82	0.026833	0.084374	-4.36
253237_at	putative aldehyde dehydrogenase ald	ALDH3I1	AT4G34240	-1.44	-0.52	-2.82	0.026848	0.084411	-4.36
255624_at	MAP kinase 4 (MPK4) ;supported by f	ATMPK4	AT4G01370	1.34	0.42	2.82	0.026865	0.084454	-4.36
246733_at	serine protease-like protein serine pro	---	AT5G27660	1.28	0.36	2.82	0.026878	0.084482	-4.36
263918_at	putative proline transporter ;supported	ProT3	AT2G36590	-2.29	-1.20	-2.82	0.026889	0.084507	-4.36
259242_at	putative actin similar to actin 1 GB:P02	ATARP6	AT3G33520	-1.23	-0.30	-2.82	0.0269	0.084527	-4.36
255943_at	UDP-glucose glucosyltransferase, put	AtUGT85A5	AT1G22370	2.01	1.01	2.82	0.026908	0.084541	-4.36
262706_at	putative ATP-dependent RNA helicase	---	AT1G16280	1.35	0.44	2.82	0.026927	0.08459	-4.36
261016_at	beta-glucosidase, putative similar to b	BGLU40	AT1G26560	-2.25	-1.17	-2.82	0.026936	0.084606	-4.36
247265_at	putative protein strong similarity to unk	CPuORF22	AT5G64550 /	1.65	0.72	2.82	0.026951	0.08464	-4.36
266808_at	Expressed protein ; supported by full-l	---	AT2G29995	-1.34	-0.43	-2.82	0.02696	0.08466	-4.36
251075_at	putative protein leucine-rich receptor-l	---	AT5G01890	-1.62	-0.69	-2.82	0.026985	0.084713	-4.36
258440_at	putative protein phosphatase similar to	---	AT3G17250	1.26	0.33	2.82	0.026984	0.084713	-4.36
263560_s_	unknown protein	FUT5	AT2G15350 /	-1.28	-0.36	-2.82	0.027017	0.084804	-4.36
252354_at	betaine aldehyde dehydrogenase-like	ALDH10A9	AT3G48170	1.22	0.29	2.82	0.027033	0.084842	-4.36
256852_at	unknown protein contains Pfam profile	ATRANGAP	AT3G18610	1.38	0.46	2.81	0.027055	0.084897	-4.37
256988_s_	adenosine triphosphatase, putative si	---	AT3G28710 /	-1.20	-0.27	-2.81	0.027083	0.084974	-4.37
263786_at	putative auxin-responsive protein ; su	JAR1	AT2G46370	1.18	0.24	2.81	0.027099	0.085014	-4.37
257534_at	hypothetical protein predicted by gens	---	AT3G09670	1.23	0.30	2.81	0.027105	0.085021	-4.37
251355_at	putative protein hypothetical protein T	---	AT3G61100	-1.34	-0.42	-2.81	0.027116	0.085044	-4.37
264655_at	unknown protein Similar to Glycine SF	SRC2	AT1G09070	1.61	0.69	2.81	0.027142	0.085111	-4.37
259936_at	putative UDP-glucose:glycoprotein glu	EBS1	AT1G71220	1.22	0.29	2.81	0.027148	0.085112	-4.37
257978_at	putative serine/threonine protein kinas	ATNEK5	AT3G20860	2.08	1.05	2.81	0.027149	0.085112	-4.37
263318_at	Expressed protein ; supported by full-l	AtGDU4	AT2G24762	-2.69	-1.43	-2.81	0.027189	0.085223	-4.37
246144_at	dynein light chain - like protein dynein	---	AT5G20110	-1.45	-0.54	-2.81	0.027199	0.085243	-4.37

254835_s_	flavonoid 3,5-hydroxylase -like protein	CYP706A5	AT4G12310 /	-1.55	-0.64	-2.81	0.027221	0.085303	-4.37
251535_at	hypothetical protein ;supported by full-	---	AT3G58540	1.38	0.47	2.81	0.027246	0.085348	-4.37
249592_at	putative protein SIAH1 protein, Brassi	---	AT5G37890	-1.30	-0.38	-2.81	0.027245	0.085348	-4.37
252112_at	putative protein merozoite surface ant	---	AT3G51580	1.30	0.38	2.81	0.027247	0.085348	-4.37
245075_at	putative cytochrome P450	CYP96A1	AT2G23180	1.26	0.34	2.81	0.02727	0.085383	-4.37
245795_at	unknown protein contains similarity to	---	AT1G32160	-1.23	-0.30	-2.81	0.027266	0.085383	-4.37
249809_at	unknown protein	---	AT5G23910	1.21	0.27	2.81	0.027269	0.085383	-4.37
250776_at	monooxygenase ;supported by full-ler	---	AT5G05320	1.21	0.28	2.81	0.027286	0.085399	-4.37
265641_at	putative RNA-binding glycine rich prote	---	AT2G27330	-1.29	-0.37	-2.81	0.02728	0.085399	-4.37
250793_at	leucoanthocyanidin dioxygenase-like p	---	AT5G05600	1.80	0.85	2.81	0.027283	0.085399	-4.37
252348_at	B12D-like protein B12D protein - Hord	---	AT3G48140	1.23	0.30	2.81	0.027294	0.085414	-4.37
260637_at	ACC oxidase, putative similar to ACC	ACO2	AT1G62380	1.98	0.98	2.81	0.027325	0.085497	-4.38
254023_at	putative protein hypothetical protein T	---	AT4G25770	-1.30	-0.38	-2.81	0.027356	0.08558	-4.38
255066_at	F-box protein family, AtFBW2 contains	---	AT4G08980	-1.22	-0.28	-2.81	0.027359	0.08558	-4.38
266280_at	putative tropinone reductase	---	AT2G29260	-1.20	-0.26	-2.81	0.027369	0.085583	-4.38
264210_at	putative myb-related transcription fact	MYB3	AT1G22640	1.40	0.49	2.81	0.027365	0.085583	-4.38
257826_at	RING zinc finger protein, putative con	---	AT3G26730	1.24	0.31	2.81	0.027371	0.085583	-4.38
259492_at	hypothetical protein predicted by gene	---	AT1G15830	-1.44	-0.53	-2.81	0.027378	0.085594	-4.38
255441_at	putative cullin-like 1 protein similar to C	ATCUL1	AT4G02570	1.24	0.31	2.81	0.027394	0.085631	-4.38
262189_at	GTPase, putative similar to GTPase G	---	AT1G78010	1.26	0.33	2.81	0.027406	0.085647	-4.38
247624_at	aspartyl aminopeptidase - like protein	---	AT5G60160	1.19	0.26	2.81	0.027406	0.085647	-4.38
258902_at	putative pyruvate dehydrogenase kina	PDK	AT3G06483	-1.21	-0.28	-2.80	0.027437	0.085731	-4.38
256140_at	hypothetical protein contains similarity	---	AT1G48650	1.40	0.48	2.80	0.027468	0.085815	-4.38
253402_at	HD-zip transcription factor (athb-8)	ATHB-8	AT4G32880	-1.44	-0.53	-2.80	0.027504	0.085918	-4.38
255228_at	F-box protein family, AtFBL21 contain	---	AT4G05470	-1.22	-0.29	-2.80	0.027511	0.085927	-4.38
258145_at	integral membrane protein, putative si	---	AT3G18200	-1.31	-0.38	-2.80	0.027522	0.085949	-4.38
245283_at	Expressed protein ; supported by cDN	AT-HSFA5	AT4G13980	1.27	0.34	2.80	0.027556	0.086044	-4.38
256125_at	pathogenesis-related group 5 protein,	ATLP-1	AT1G18250	-1.38	-0.47	-2.80	0.027573	0.086074	-4.39
253704_at	X-Pro dipeptidase - like protein (fragm	---	AT4G29490	1.26	0.33	2.80	0.027572	0.086074	-4.39
265699_at	putative esterase (contains an esteras	---	AT2G03550	-1.26	-0.33	-2.80	0.027592	0.08611	-4.39
257366_s_	unknown protein	---	AT2G03040 /	1.26	0.33	2.80	0.02759	0.08611	-4.39
264625_at	hypothetical protein Contains similarity	SNF4	AT1G09020	-1.25	-0.32	-2.80	0.027606	0.086129	-4.39
250537_at	Expressed protein ; supported by full-l	---	AT5G08565	1.44	0.53	2.80	0.027605	0.086129	-4.39
252968_at	putative protein unknown mRNA, Hom	---	AT4G38890	1.40	0.48	2.80	0.02762	0.086163	-4.39
246829_at	putative protein pyruvate water dikinas	ATGWD3	AT5G26570	1.22	0.29	2.80	0.027637	0.086202	-4.39

259748_at	putative dehydrogenase similar to D-th	---	AT1G71180	-1.28	-0.35	-2.80	0.027641	0.086202	-4.39
255252_at	contains similarity to Gossypium hirsut	---	AT4G04990	-1.23	-0.30	-2.80	0.027662	0.086247	-4.39
251697_at	putative protein hypothetical protein A	---	AT3G56600	1.20	0.26	2.80	0.027662	0.086247	-4.39
258238_at	unknown protein	RST1	AT3G27670	1.20	0.27	2.80	0.027678	0.086274	-4.39
256088_at	putative FKBP-type peptidyl-prolyl cis-	---	AT1G20810	-1.40	-0.48	-2.80	0.027679	0.086274	-4.39
254171_at	PsRT17-1 like protein PsRT17-1, Pisu	---	AT4G24530	-1.21	-0.28	-2.80	0.027697	0.08632	-4.39
260076_at	putative calmodulin similar to calmodu	---	AT1G73630	1.43	0.51	2.80	0.027732	0.086417	-4.39
267454_at	putative U5 small nuclear ribonucleop	---	AT2G33730	1.24	0.30	2.80	0.027753	0.086469	-4.39
257897_at	HAL3A protein identical to GB:AAD51(	HAL3A	AT3G18030	-1.36	-0.44	-2.80	0.027762	0.086487	-4.39
257066_at	lipid transfer protein, putative similar t	---	AT3G18280	1.79	0.84	2.80	0.027773	0.086508	-4.39
248903_at	3-oxoacyl-[acyl-carrier-protein] synthas	KAS I	AT5G46290	-1.50	-0.59	-2.80	0.027779	0.086516	-4.39
245122_at	putative dimethyladenosine transferas	---	AT2G47420	1.28	0.35	2.80	0.027786	0.086526	-4.39
267376_at	putative receptor-like protein kinase, E	ER	AT2G26330	-2.44	-1.29	-2.79	0.027862	0.086749	-4.40
247635_at	serine/threonine-protein kinase - like p	GRIK2	AT5G60548 /	1.21	0.27	2.79	0.027868	0.086757	-4.40
251528_at	putative protein hypothetical protein F	---	AT3G58600	-1.31	-0.38	-2.79	0.027877	0.086773	-4.40
252186_at	putative protein	---	AT3G50810	1.30	0.38	2.79	0.027886	0.08679	-4.40
261179_at	unknown protein	---	AT1G04985	-1.29	-0.37	-2.79	0.027899	0.086817	-4.40
264406_at	putative phragmoplastin similar to dyn	ADL6	AT1G10290	1.28	0.35	2.79	0.027912	0.086848	-4.40
252064_at	putative protein various predicted prot	---	AT3G51520	-1.24	-0.31	-2.79	0.027933	0.0869	-4.40
249067_at	putative protein similar to unknown pro	---	AT5G43960	-1.25	-0.32	-2.79	0.027945	0.086913	-4.40
260274_at	putative glycerol kinase similar to GLY	NHO1	AT1G80460	1.33	0.41	2.79	0.027942	0.086913	-4.40
258658_at	putative adenosine kinase similar to ac	ADK1	AT3G09820	-1.65	-0.72	-2.79	0.027963	0.086957	-4.40
262990_at	E2, ubiquitin-conjugating enzyme, put	MMZ1	AT1G23260	-1.22	-0.29	-2.79	0.027994	0.08703	-4.40
254387_at	putative protein CGI-131 protein, Hom	ATMSRB9	AT4G21850	4.25	2.09	2.79	0.027993	0.08703	-4.40
260889_at	hypothetical protein predicted by gene	---	AT1G29120	1.22	0.29	2.79	0.028009	0.087066	-4.40
267156_at	hypothetical protein predicted by gens	---	AT2G37610	-1.26	-0.34	-2.79	0.028018	0.08708	-4.40
247464_at	putative protein various predicted prot	IQD23	AT5G62070	-1.46	-0.55	-2.79	0.028036	0.087114	-4.40
260681_at	hypothetical protein predicted by gene	AT1G08030	---	1.22	0.29	2.79	0.028034	0.087114	-4.40
249278_at	putative protein strong similarity to unk	---	AT5G41900	-4.44	-2.15	-2.79	0.028051	0.087131	-4.40
258508_at	protein kinase, putative similar to SER	---	AT3G06640	-1.19	-0.25	-2.79	0.028046	0.087131	-4.40
245083_at	putative integral membrane protein ;su	ATRER1C1	AT2G23310	-1.26	-0.33	-2.79	0.028053	0.087131	-4.40
261634_at	ATP-dependent Clp protease proteolyt	CLPR1	AT1G49970	1.34	0.42	2.79	0.028065	0.087156	-4.40
252041_at	DNA-directed RNA polymerase II 13.6	NRPB11	AT3G52090	-1.25	-0.33	-2.79	0.028069	0.087156	-4.40
245777_at	unknown protein contains similarity to	atnudt21	AT1G73540	2.71	1.44	2.79	0.028078	0.087172	-4.40
263594_at	putative purple acid phosphatase cont	PAP7	AT2G01880	1.66	0.74	2.79	0.028116	0.087278	-4.41

249355_at	hypothetical protein	---	AT5G40500	-1.23	-0.30	-2.79	0.02812	0.087279	-4.41
261558_at	unknown protein	---	AT1G01770	1.44	0.53	2.78	0.028252	0.087678	-4.41
264584_at	unknown protein Similar to Synechocy	---	AT1G05140	-1.28	-0.36	-2.78	0.028282	0.08776	-4.41
254421_at	VP1 like protein transcription activator	VAL3	AT4G21550	1.38	0.46	2.78	0.028306	0.087821	-4.41
260486_at	F-box protein ZEITLUPE/FKF/LKP/AD	---	AT1G51550	1.26	0.33	2.78	0.028329	0.08788	-4.41
253734_at	putative serine/threonine-specific rece	---	AT4G29180	-1.26	-0.33	-2.78	0.028339	0.087892	-4.41
245098_at	ethylene response sensor (ERS) ident	ERS1	AT2G40940	-1.64	-0.71	-2.78	0.02834	0.087892	-4.41
249886_at	unknown protein ; supported by cDNA	---	AT5G22320	1.41	0.49	2.78	0.028362	0.087943	-4.41
253395_at	protein kinase AME3 ; supported by c	AME3	AT4G32660	-1.20	-0.27	-2.78	0.028364	0.087943	-4.41
249113_at	putative protein similar to unknown pro	---	AT5G43790	1.36	0.44	2.78	0.028395	0.088025	-4.42
246755_at	F-box protein family contains similarity	---	AT5G27920	-1.64	-0.71	-2.78	0.028408	0.088053	-4.42
249379_at	putative protein predicted protein, Ara	---	AT5G40460	1.67	0.74	2.78	0.028456	0.08819	-4.42
256294_at	unknown protein	---	AT1G69450	1.30	0.38	2.78	0.028464	0.088204	-4.42
264152_at	Mago Nashi-like protein similar to Mag	MAGO	AT1G02140	1.26	0.33	2.78	0.028475	0.088225	-4.42
258974_at	unknown protein similar to brahma as	---	AT3G01890	1.27	0.35	2.78	0.028494	0.088273	-4.42
262826_at	putative cytochrome P450 monooxyge	CYP71B2	AT1G13080	1.63	0.71	2.78	0.028534	0.088371	-4.42
262630_at	unknown protein ;supported by full-len	GPAT1	AT1G06520	2.24	1.17	2.78	0.02853	0.088371	-4.42
254481_at	hypothetical protein ; supported by cD	---	AT4G20480	1.41	0.49	2.78	0.028582	0.088509	-4.42
247885_at	putative protein similar to unknown pro	---	AT5G57830	-1.44	-0.52	-2.78	0.02859	0.088521	-4.42
259000_at	hypothetical protein predicted by gens	---	AT3G01860	-1.61	-0.69	-2.78	0.028594	0.088523	-4.42
265442_at	hypothetical protein predicted by gene	---	AT2G20940	1.54	0.62	2.77	0.028616	0.088566	-4.42
267124_at	putative acetone-cyanohydrin lyase	MES19	AT2G23570	-1.28	-0.36	-2.77	0.028615	0.088566	-4.42
250530_at	unknown protein	---	AT5G08630	1.26	0.34	2.77	0.028634	0.088609	-4.42
246566_at	oligopeptide transporter -like protein o	---	AT5G14940	1.52	0.60	2.77	0.02866	0.088678	-4.43
251953_at	putative protein predicted protein, Ara	CPuORF51	AT3G53668 /	-1.30	-0.37	-2.77	0.028686	0.088747	-4.43
256038_at	hypothetical protein similar to polygala	---	AT1G19170	-1.30	-0.38	-2.77	0.0287	0.088777	-4.43
263112_at	unknown protein Strong similarity to gi	---	AT1G03080	1.28	0.35	2.77	0.028717	0.088818	-4.43
267180_at	unknown protein ; supported by cDNA	SLT1	AT2G37570	1.25	0.32	2.77	0.028738	0.088871	-4.43
249613_at	putative protein mDj10, Mus musculus	---	AT5G37380	1.32	0.40	2.77	0.028766	0.088941	-4.43
258212_at	unknown protein contains Pfam profile	---	AT3G17920	-1.19	-0.25	-2.77	0.028768	0.088941	-4.43
266701_at	profilin 1 ; supported by cDNA: gi_135	PRF1	AT2G19760	-1.20	-0.26	-2.77	0.028789	0.088994	-4.43
251619_at	putative protein hypothetical protein A	---	AT3G58050	-1.19	-0.25	-2.77	0.028801	0.089019	-4.43
254924_at	MAP kinase (ATMPK5) possible interr	ATMPK5	AT4G11330	1.44	0.53	2.77	0.028831	0.089097	-4.43
261233_at	hypothetical protein similar to hypothet	---	AT1G32810	1.28	0.35	2.77	0.028852	0.089153	-4.43
260776_at	zinc finger protein, putative similar to a	---	AT1G14580	-1.70	-0.77	-2.77	0.028861	0.089154	-4.43

266452_at	hypothetical protein predicted by gens	---	AT2G43320	1.41	0.49	2.77	0.028859	0.089154	-4.43
263802_at	unknown protein ;supported by full-ler	---	AT2G40430	1.48	0.57	2.77	0.028867	0.08916	-4.43
260207_at	putative phosphoglucomutase similar t	---	AT1G70730	-1.36	-0.44	-2.77	0.028878	0.089182	-4.43
262617_at	unknown protein	POR C	AT1G03630 /	-1.23	-0.30	-2.77	0.028933	0.089339	-4.44
247254_at	CLE21, putative CLAVATA3/ESR-Rel	CLE21	AT5G64800	1.52	0.60	2.77	0.028974	0.089457	-4.44
247854_at	contains similarity to phosphoesterase	---	AT5G58200	1.27	0.35	2.77	0.028981	0.089466	-4.44
262946_at	hypothetical protein predicted by gens	---	AT1G79390	1.25	0.32	2.77	0.029013	0.089553	-4.44
259422_at	unknown protein	---	AT1G13810	1.39	0.47	2.76	0.029028	0.089562	-4.44
255734_at	hypothetical protein similar to putative	---	AT1G25550	1.37	0.46	2.76	0.029024	0.089562	-4.44
266871_at	unknown protein	---	AT2G44710	1.18	0.24	2.76	0.029033	0.089562	-4.44
248031_at	unknown protein ; supported by cDNA	---	AT5G55640	1.19	0.25	2.76	0.029044	0.089562	-4.44
263644_at	hypothetical protein predicted by gens	---	AT2G04730	1.25	0.32	2.76	0.02903	0.089562	-4.44
263688_at	unknown protein Location of EST 228	---	AT1G26920	-2.07	-1.05	-2.76	0.029043	0.089562	-4.44
253038_at	homeobox protein HAT22 ;supported	HAT22	AT4G37790	1.48	0.57	2.76	0.029041	0.089562	-4.44
255737_at	unknown protein ;supported by full-len	---	AT1G25420	-1.27	-0.34	-2.76	0.029053	0.089567	-4.44
261491_at	hypothetical protein contains similarity	FLP	AT1G14350	1.83	0.87	2.76	0.029052	0.089567	-4.44
250992_at	expansin precursor - like protein expa	ATEXPA9	AT5G02260	1.74	0.80	2.76	0.029061	0.089578	-4.44
259310_s_	Expressed protein ; supported by cDN	---	AT3G05160 /	1.32	0.40	2.76	0.029071	0.089598	-4.44
245628_at	anthocyanin2, putative similar to anth	PAP1	AT1G56650	1.42	0.50	2.76	0.029084	0.089626	-4.44
265999_at	unknown protein ; supported by cDNA	---	AT2G24100	1.35	0.43	2.76	0.02909	0.089631	-4.44
260709_at	hypothetical protein predicted by gene	ATNAP6	AT1G32500	-1.28	-0.35	-2.76	0.029115	0.089687	-4.44
247153_at	receptor protein kinase-like protein	BAM1	AT5G65700	-1.58	-0.66	-2.76	0.029116	0.089687	-4.44
250719_at	putative protein contains similarity to R	---	AT5G06250	1.30	0.37	2.76	0.029139	0.089747	-4.44
263630_at	Expressed protein ; supported by full-l	---	AT2G04845	-1.22	-0.28	-2.76	0.02915	0.089767	-4.44
245459_at	hypothetical protein	---	---	-1.40	-0.48	-2.76	0.029164	0.089798	-4.44
253777_at	SOF1 protein-like protein SOF1 (involv	---	AT4G28450	1.74	0.80	2.76	0.029172	0.08981	-4.44
253709_at	pyrophosphate-dependent phosphofru	PFK1	AT4G29220	1.35	0.43	2.76	0.029182	0.089818	-4.44
252419_at	putative protein	---	AT3G47510	-1.63	-0.71	-2.76	0.029179	0.089818	-4.44
249342_at	putative protein ATP12 protein precur	---	AT5G40660	-1.28	-0.35	-2.76	0.029194	0.089844	-4.45
267367_at	unknown protein ;supported by full-ler	---	AT2G44210	-1.38	-0.47	-2.76	0.029202	0.089855	-4.45
256232_at	unknown protein ; supported by full-ler	FYD	AT3G12570	1.18	0.24	2.76	0.029234	0.08994	-4.45
254966_at	COP1 like protein photomorphogenes	SPA2	AT4G11110	1.19	0.25	2.76	0.029255	0.089995	-4.45
251631_at	putative protein several hypothetical pr	---	AT3G57430	1.28	0.36	2.76	0.029274	0.090039	-4.45
260392_at	putative enolase similar to ENOLASE (	---	AT1G74030	3.21	1.68	2.76	0.029312	0.090144	-4.45
264081_at	putative RING zinc finger transcription	---	AT2G28540	1.30	0.37	2.76	0.029319	0.090155	-4.45

262818_at	hypothetical protein predicted by gens	---	AT1G11755 /	1.24	0.31	2.76	0.029371	0.090264	-4.45
257667_at	1,4-alpha-glucan branching enzyme, p	EMB2729	AT3G20440	1.42	0.50	2.76	0.029362	0.090264	-4.45
263429_at	putative aspartate aminotransferase ;	AAT	AT2G22250	2.12	1.08	2.76	0.029366	0.090264	-4.45
261467_at	unknown protein	VOZ1	AT1G28520	1.39	0.48	2.76	0.029368	0.090264	-4.45
248173_at	putative protein contains similarity to R	---	AT5G54580	-1.23	-0.30	-2.76	0.029394	0.090324	-4.45
257799_at	protein kinase, putative similar to som	---	AT3G15890	1.26	0.33	2.76	0.029405	0.090335	-4.45
245843_at	unknown protein	---	AT1G26180	-1.28	-0.35	-2.76	0.029406	0.090335	-4.45
258181_at	nitrate transporter identical to nitrate tr	---	AT3G21670	-1.40	-0.48	-2.75	0.029441	0.090431	-4.45
257112_at	cytochrome P450, putative contains P	CYP705A21	AT3G20120	1.26	0.33	2.75	0.029446	0.090435	-4.45
259021_at	hypothetical protein predicted by gene	---	AT3G07540	-1.52	-0.60	-2.75	0.029464	0.090479	-4.45
259227_at	putative 3 exoribonuclease contains P	---	AT3G07750	1.80	0.85	2.75	0.029496	0.090564	-4.46
259111_at	alpha subunit of F-actin capping protei	---	AT3G05520	-1.33	-0.41	-2.75	0.029509	0.090591	-4.46
246891_at	putative protein various predicted prot	---	AT5G25490	-1.20	-0.26	-2.75	0.02957	0.090768	-4.46
262448_at	En/Spm-like transposon protein, putat	---	AT1G49450	1.25	0.32	2.75	0.029579	0.090784	-4.46
250734_at	putative protein similar to unknown pro	---	AT5G06270	-1.75	-0.81	-2.75	0.029609	0.090861	-4.46
258635_at	unknown protein	---	AT3G08020	1.20	0.26	2.75	0.029633	0.090911	-4.46
266828_at	putative flavonol 3-O-glucosyltransfera	---	AT2G22930	-1.20	-0.27	-2.75	0.029632	0.090911	-4.46
256191_at	unknown protein similar to hypothetica	---	AT1G30130	1.27	0.35	2.75	0.02965	0.090952	-4.46
254351_at	putative protein probable membrane p	SOBER1	AT4G22300	-1.30	-0.37	-2.75	0.029658	0.090965	-4.46
246925_at	cytochrome P450 71B1 - like protein c	CYP71B14	AT5G25180	1.23	0.30	2.75	0.029724	0.091115	-4.46
257715_at	putative zinc transporter identical to p	ZIP1	AT3G12750	1.53	0.62	2.75	0.029727	0.091115	-4.46
248801_at	homeobox-leucine zipper protein-like	HAT2	AT5G47370	-1.94	-0.96	-2.75	0.029716	0.091115	-4.46
254409_at	serine/threonine protein kinase - like p	---	AT4G21400	2.08	1.06	2.75	0.029725	0.091115	-4.46
248358_at	cytochrome P-450-like protein	CYP715A1	AT5G52400	1.67	0.74	2.75	0.029718	0.091115	-4.46
265661_at	putative protein kinase contains a prot	---	AT2G24360	1.29	0.37	2.75	0.029743	0.091152	-4.46
248511_at	Expressed protein ; supported by cDN	CPI1	AT5G50375	-1.47	-0.55	-2.75	0.029751	0.091163	-4.46
245081_at	unknown protein overlap with T20D16	---	---	-1.41	-0.50	-2.75	0.029762	0.091185	-4.47
257955_at	unknown protein ; supported by cDNA	---	AT3G21810	1.57	0.65	2.75	0.029777	0.091218	-4.47
246427_at	ADP/ATP translocase-like protein adp	ER-ANT1	AT5G17400	-1.29	-0.37	-2.75	0.029823	0.091348	-4.47
264743_at	receptor-like protein kinase, putative s	---	AT1G62090	1.21	0.27	2.75	0.02983	0.091356	-4.47
255033_at	putative protein phosphonopyruvate d	---	AT4G09520	-1.31	-0.39	-2.74	0.029859	0.091432	-4.47
266732_at	unknown protein	---	AT2G03240	-1.39	-0.47	-2.74	0.029946	0.091673	-4.47
251340_at	actin - like protein actin 3, Drosophila	ATARP7	AT3G60830	-1.24	-0.31	-2.74	0.029943	0.091673	-4.47
246884_at	putative protein cation transport protei	---	AT5G26220	-1.57	-0.65	-2.74	0.029953	0.091683	-4.47
255635_at	Shaggy related protein kinase tetha ;	ATSK32	AT4G00720	1.27	0.35	2.74	0.02996	0.091694	-4.47

259094_at	putative cysteine synthase similar to cy	CYSD1	AT3G04940	-1.39	-0.48	-2.74	0.02997	0.09171	-4.47
253758_at	Expressed protein ;supported by cDNA	emb2726	AT4G29060	-1.30	-0.38	-2.74	0.029974	0.09171	-4.47
252204_at	putative protein predicted protein, Ara	---	AT3G50340	-1.87	-0.91	-2.74	0.029993	0.091756	-4.47
266571_at	unknown protein	---	AT2G23830	1.57	0.65	2.74	0.030004	0.091777	-4.47
263090_at	hypothetical protein predicted by gens	---	AT2G16190	-1.22	-0.28	-2.74	0.030034	0.091858	-4.47
259034_at	putative pectinacetylesterase similar to	---	AT3G09410	1.41	0.50	2.74	0.030052	0.091863	-4.48
252822_at	Expressed protein ; supported by full-le	---	AT4G39955	1.29	0.37	2.74	0.030049	0.091863	-4.48
264056_at	putative DOF zinc finger protein ;supp	---	AT2G28510	1.36	0.44	2.74	0.030048	0.091863	-4.48
259171_at	hypothetical protein predicted by gene	---	AT3G03590	-1.26	-0.33	-2.74	0.030044	0.091863	-4.48
265705_at	unknown protein related to MO25 (mou	---	AT2G03410	1.81	0.86	2.74	0.030065	0.091892	-4.48
264396_at	fumarylacetoacetate hydrolase-like pr	---	AT1G12050	1.21	0.28	2.74	0.030085	0.091929	-4.48
262426_s_	cytochrome P450, putative similar to c	---	AT1G47625 /	-1.33	-0.42	-2.74	0.030085	0.091929	-4.48
259411_at	hypothetical protein contains Pfam pro	---	AT1G13410	1.24	0.31	2.74	0.030101	0.091965	-4.48
262768_at	putative beta-1,4-N-acetylglucosaminy	---	AT1G12990	-1.65	-0.73	-2.74	0.030111	0.091974	-4.48
245964_at	putative protein C-terminus of glutami	---	AT5G19720	-1.29	-0.37	-2.74	0.030112	0.091974	-4.48
266382_at	hypothetical protein predicted by gens	---	---	-1.20	-0.26	-2.74	0.030151	0.092073	-4.48
250933_at	arabinogalactan protein - like arabinog	FLA11	AT5G03170	-1.65	-0.72	-2.74	0.030153	0.092073	-4.48
259329_at	putative two-component phosphorelay	AHP4	AT3G16360	-1.74	-0.80	-2.74	0.03016	0.092082	-4.48
246225_at	putative protein ;supported by full-leng	LEJ2	AT4G36910	-1.32	-0.40	-2.74	0.030196	0.092167	-4.48
263005_at	hypothetical protein predicted by gene	---	AT1G54540	-1.45	-0.54	-2.74	0.030194	0.092167	-4.48
247193_at	putative protein strong similarity to unk	---	AT5G65380	1.35	0.44	2.74	0.030241	0.092293	-4.48
250937_at	putative protein various predicted prot	---	AT5G03230	-1.46	-0.55	-2.74	0.030251	0.092311	-4.48
253746_at	putative protein hypothetical protein -	---	AT4G29100	1.57	0.65	2.74	0.030257	0.092317	-4.48
259090_at	putative ribosomal protein s19 or s24 s	---	AT3G04920	-1.46	-0.55	-2.74	0.030268	0.092337	-4.48
262493_at	auxilin-like protein similar to GB:CAB4	---	AT1G21660	-1.23	-0.30	-2.74	0.030272	0.092338	-4.48
252649_at	putative protein histone deacetylase 1	HDA9	AT3G44680	1.20	0.26	2.73	0.030278	0.092343	-4.48
267177_at	Expressed protein ; supported by full-le	---	AT2G37580	1.44	0.53	2.73	0.030288	0.092362	-4.48
261574_at	cytochrome P450, putative similar to c	CYP78A8	AT1G01190	-1.58	-0.66	-2.73	0.030308	0.092402	-4.48
259415_at	hypothetical protein contains similarity	---	AT1G02330	-1.33	-0.41	-2.73	0.030309	0.092402	-4.48
255474_at	coded for by A. thaliana cDNA T7580	---	AT4G02480	1.24	0.32	2.73	0.030328	0.092443	-4.48
267075_at	putative bZIP transcription factor conta	EEL	AT2G41070	1.21	0.27	2.73	0.030331	0.092443	-4.49
264172_at	unknown protein	VAD1	AT1G02120	1.38	0.47	2.73	0.030335	0.092443	-4.49
252267_at	putative protein NITROGEN REGULA	---	AT3G49640	-1.37	-0.46	-2.73	0.030342	0.092452	-4.49
255955_at	hypothetical protein predicted by gens	---	AT1G22030	-1.49	-0.57	-2.73	0.030369	0.092524	-4.49
263951_at	putative harpin-induced protein ;suppo	NHL12	AT2G35960	-2.10	-1.07	-2.73	0.030384	0.092557	-4.49

245348_at	trehalose-6-phosphate synthase like p	ATTPS5	AT4G17770	-1.36	-0.45	-2.73	0.030397	0.092582	-4.49
256789_at	seven in absentia-like protein similar to	---	AT3G13672	1.59	0.67	2.73	0.030427	0.092664	-4.49
249147_at	cytosolic malate dehydrogenase ;supp	---	AT5G43330	1.33	0.41	2.73	0.03047	0.092781	-4.49
251490_at	putative protein	---	AT3G59490	-1.32	-0.40	-2.73	0.030527	0.092943	-4.49
253578_at	putative protein diacylglycerol kinase i	ATDGK7	AT4G30340	-1.39	-0.47	-2.73	0.030563	0.093039	-4.49
256959_at	methyltransferase, putative	---	AT3G13440	-1.20	-0.26	-2.73	0.030574	0.09306	-4.49
263252_at	putative CONSTANS-like B-box zinc fi	STH	AT2G31380	-1.44	-0.53	-2.73	0.030581	0.093068	-4.49
246173_s_	putative protein hypothetical protein F	---	AT3G61520 /	1.36	0.45	2.73	0.030634	0.093167	-4.50
246409_at	CRK1 protein, putative similar to CRK	---	AT1G57700	-1.36	-0.44	-2.73	0.03063	0.093167	-4.50
264376_at	putative protein phosphatase 2C ;sup	---	AT2G25070	-1.35	-0.43	-2.73	0.030625	0.093167	-4.50
267168_at	putative alcohol dehydrogenase	---	AT2G37770	3.78	1.92	2.73	0.030632	0.093167	-4.50
259637_at	protein disulfide isomerase precursor,	ATPDIL1-5	AT1G52260	-1.34	-0.43	-2.73	0.030619	0.093167	-4.49
258108_at	unknown protein contains Pfam profile	---	AT3G23570	1.88	0.91	2.73	0.030659	0.093232	-4.50
AFFX-Atha	Arabidopsis thaliana /REF=U84969 /D	---	---	1.27	0.34	2.73	0.030699	0.093341	-4.50
252417_at	putative calcium-binding protein calciu	---	AT3G47480	2.98	1.57	2.72	0.030719	0.09336	-4.50
253729_at	beta-1,3-glucanase-like protein beta-1	---	AT4G29360	-1.30	-0.38	-2.72	0.030714	0.09336	-4.50
261414_at	Expressed protein ; supported by full-l	---	AT1G07795	1.38	0.47	2.72	0.030722	0.09336	-4.50
254752_at	putative protein IFA-binding protein - A	---	AT4G13160	-1.25	-0.33	-2.72	0.030715	0.09336	-4.50
255294_at	putative sugar transporter	---	AT4G04750	-1.25	-0.32	-2.72	0.030763	0.093472	-4.50
258987_at	putative SCO1 protein similar to SCO	---	AT3G08950	1.56	0.64	2.72	0.030776	0.093501	-4.50
261313_at	hypothetical protein predicted by gens	---	AT1G52970	-1.20	-0.26	-2.72	0.030788	0.093512	-4.50
261859_at	E2, ubiquitin-conjugating enzyme, put	UBC20	AT1G50490	-1.32	-0.40	-2.72	0.030787	0.093512	-4.50
258219_at	thioredoxin, putative similar to THIOR	ATTDX	AT3G17880	1.23	0.30	2.72	0.030803	0.093544	-4.50
266897_at	remorin identical to GB:M25268, a no	---	AT2G45820	-1.45	-0.53	-2.72	0.030819	0.093582	-4.50
258485_at	putative stearoyl-acyl carrier protein de	---	AT3G02630	1.18	0.24	2.72	0.03084	0.093633	-4.50
261013_at	fatty acid elongase 3-ketoacyl-CoA syn	ATUPS5	AT1G26440	1.36	0.45	2.72	0.030846	0.093639	-4.50
259883_at	putative ribophorin I (dolichyl-diphosph	---	AT1G76400	-1.31	-0.38	-2.72	0.030906	0.093808	-4.50
248258_at	putative protein contains similarity to n	---	AT5G53400	1.54	0.62	2.72	0.030914	0.09382	-4.50
254851_at	putative disease resistance protein (T	---	AT4G12010	1.49	0.57	2.72	0.030939	0.093882	-4.51
260459_at	hypothetical protein predicted by gens	---	AT1G68240	-1.25	-0.33	-2.72	0.030943	0.093882	-4.51
255454_at	hypothetical protein	---	AT4G02910	-1.21	-0.27	-2.72	0.030948	0.093885	-4.51
261445_at	unknown protein ; supported by cDNA	NSL1	AT1G28380	1.68	0.75	2.72	0.030979	0.093968	-4.51
262865_at	cytochrome p450, putative similar to c	CYP89A7	AT1G64930	1.26	0.33	2.72	0.031003	0.094026	-4.51
253067_at	myb transcription factor - like protein	MYB87	AT4G37780	1.23	0.30	2.72	0.031017	0.094057	-4.51
259721_at	putative phosphatidylinositol-4-phosph	---	AT1G60890	1.38	0.46	2.72	0.031021	0.094057	-4.51

251597_at	protein kinase - like protein wall-assoc	---	AT3G57750	1.62	0.69	2.72	0.03103	0.094073	-4.51
265237_s_	hypothetical protein	---	AT2G07706	1.26	0.34	2.72	0.031041	0.094092	-4.51
261895_at	metal ion transporter identical to GB:A	NRAMP1	AT1G80830	1.69	0.76	2.72	0.031049	0.094105	-4.51
254530_at	small GTP-binding protein - like GTP-	ARA7	AT4G19640	1.21	0.28	2.72	0.031089	0.094212	-4.51
250565_at	putative protein various predicted prot	E13L3	AT5G08000	-1.32	-0.40	-2.72	0.03114	0.094355	-4.51
246967_at	FPF1 protein	FPF1	AT5G24860	1.44	0.52	2.71	0.031158	0.094396	-4.51
255767_at	ribosomal protein L20, putative similar	---	AT1G16740	1.24	0.31	2.71	0.031178	0.094433	-4.51
247870_at	calmodulin-binding protein ; supported	---	AT5G57580	1.22	0.28	2.71	0.031175	0.094433	-4.51
252040_at	putative protein hypothetical protein F	---	AT3G52060	1.63	0.71	2.71	0.031189	0.094452	-4.51
245627_at	water stress-induced protein, putative	AtGolS2	AT1G56600	1.60	0.68	2.71	0.031206	0.094491	-4.51
253705_at	hexokinase ; supported by cDNA: gi_8	HXK1	AT4G29130	1.39	0.48	2.71	0.031229	0.094548	-4.52
262620_at	hypothetical protein predicted by gens	---	AT1G06540	1.21	0.27	2.71	0.03125	0.094599	-4.52
264854_at	putative RING zinc finger protein ; sup	RHA3A	AT2G17450	-1.28	-0.35	-2.71	0.031271	0.094651	-4.52
262572_at	unknown protein Contains a PF|00175	---	AT1G15140	-1.31	-0.39	-2.71	0.031299	0.094723	-4.52
260322_at	unknown protein	---	AT1G63900	-1.25	-0.32	-2.71	0.03131	0.094745	-4.52
261383_at	hypothetical protein predicted by gene	---	AT1G05380	1.27	0.34	2.71	0.031331	0.094795	-4.52
266486_at	hypothetical protein predicted by gens	---	AT2G47950	2.82	1.49	2.71	0.031339	0.094808	-4.52
245151_at	putative pectinesterase ;supported by	---	AT2G47550	3.73	1.90	2.71	0.031362	0.094863	-4.52
261893_at	unknown protein ;supported by full-len	---	AT1G80690	-1.24	-0.31	-2.71	0.031393	0.094946	-4.52
247279_at	arabinogalactan-protein (gb|AAC7782	AGP1	AT5G64310	2.39	1.26	2.71	0.031398	0.094946	-4.52
264903_at	putative phosphoglucomutase similar	---	AT1G23190	1.28	0.35	2.71	0.031402	0.094946	-4.52
261621_at	hypothetical protein similar to guanine	EDA10	AT1G01960	-1.22	-0.29	-2.71	0.031413	0.094966	-4.52
260655_at	pathogenesis-related protein 5 precur	---	AT1G19320	-1.57	-0.66	-2.71	0.031436	0.095008	-4.52
248743_at	unknown protein	---	AT5G48240	1.42	0.51	2.71	0.031439	0.095008	-4.52
258378_at	hypothetical protein contains similarity	---	AT3G17490	1.21	0.28	2.71	0.031435	0.095008	-4.52
267302_at	putative unknown protein, leucine-rich	---	AT2G30100	-1.19	-0.25	-2.71	0.031464	0.095072	-4.52
245361_at	hypothetical protein ;supported by full-	---	AT4G17790	1.52	0.60	2.71	0.031475	0.095092	-4.52
265104_at	unknown protein 3'-end of protein cont	ATO2	AT1G31020	-1.24	-0.32	-2.71	0.031508	0.095179	-4.52
261751_at	chloroplast drought-induced stress pr	CDSP32	AT1G76080	1.18	0.24	2.71	0.031514	0.095185	-4.52
250693_at	ubiquitin-specific protease 12 (UBP12	UBP12	AT5G06600	1.21	0.28	2.71	0.031524	0.095203	-4.53
262270_x_	polyprotein, putative similar to polypro	---	---	1.19	0.25	2.71	0.031531	0.09521	-4.53
258048_at	FtsH protease, putative contains simil	EMB2083	AT3G16290	-1.25	-0.32	-2.71	0.031537	0.095217	-4.53
249464_at	putative protein crp1, Zea mays, PIR:	EMB2745	AT5G39710	1.70	0.77	2.71	0.031552	0.095236	-4.53
248380_at	phosphoglucomutase (emb|CAB64725	PGM	AT5G51820	-1.54	-0.62	-2.71	0.031548	0.095236	-4.53
250967_at	putative protein In2, Zea mays, EMBL	---	AT5G02790	1.35	0.44	2.70	0.031639	0.095485	-4.53

249446_at	receptor protein kinase -like protein pr	---	AT5G39390	1.22	0.29	2.70	0.031657	0.095528	-4.53
259502_at	unknown protein ; supported by cDNA	---	AT1G15670	1.58	0.66	2.70	0.031662	0.09553	-4.53
260792_at	unknown protein ;supported by full-len	---	AT1G06270	1.26	0.33	2.70	0.031697	0.095611	-4.53
262492_at	unknown protein Contains similarity to	---	AT1G21630	-1.25	-0.32	-2.70	0.031697	0.095611	-4.53
249068_at	putative protein similar to unknown pro	PDLP1	AT5G43980	1.22	0.28	2.70	0.031704	0.095618	-4.53
255459_at	polyubiquitin (UBQ14) identical to GI:1	UBQ14	AT4G02890	1.23	0.29	2.70	0.031709	0.095622	-4.53
247524_at	thioredoxin-like 3 ; supported by cDNA	ACHT5	AT5G61440	-1.96	-0.97	-2.70	0.031742	0.095707	-4.53
250239_at	ABC transporter-like protein	---	AT5G13580	-1.35	-0.43	-2.70	0.031759	0.095748	-4.53
262207_at	hypothetical protein predicted by gens	PTAC2	AT1G74850	1.32	0.40	2.70	0.031786	0.095816	-4.53
258946_at	hypothetical protein predicted by gens	---	AT3G10650	1.30	0.37	2.70	0.031808	0.095859	-4.53
258765_at	putative pectinesterase contains simila	---	AT3G10710	-1.24	-0.31	-2.70	0.031809	0.095859	-4.53
246468_at	UDP glucose:flavonoid 3-o-glucosyltra	UGT78D2	AT5G17050	1.48	0.56	2.70	0.031833	0.09592	-4.54
246886_at	CLC-d chloride channel protein	CLC-D	AT5G26240	1.25	0.33	2.70	0.031844	0.09594	-4.54
267084_at	unknown protein ; supported by cDNA	---	AT2G41180	2.27	1.18	2.70	0.031853	0.095954	-4.54
256043_at	hypothetical protein contains Pfam pro	---	AT1G07210	-1.38	-0.46	-2.70	0.031886	0.096017	-4.54
267090_at	unknown protein ; supported by full-le	CXIP2	AT2G38270	-1.19	-0.26	-2.70	0.031882	0.096017	-4.54
263838_at	putative s-adenosylmethionine synthet	MAT3	AT2G36880	1.72	0.78	2.70	0.031885	0.096017	-4.54
251710_at	putative protein several hypothetical pr	---	AT3G56930	-1.52	-0.61	-2.70	0.031906	0.09605	-4.54
266314_at	Argonaute (AGO1)-like protein ; suppo	AGO4	AT2G27040	-1.34	-0.42	-2.70	0.031906	0.09605	-4.54
265269_at	hypothetical protein predicted by gens	---	AT2G42950	1.28	0.36	2.70	0.031946	0.096158	-4.54
255807_at	probable wound-induced protein wour	---	AT4G10270	-1.18	-0.24	-2.70	0.031971	0.096221	-4.54
261881_at	nodulin-like protein similar to nodulin G	NIP6;1	AT1G80760	-1.44	-0.53	-2.70	0.031981	0.096222	-4.54
259326_at	putative mitochondrial processing pep	MPPalpha	AT3G16480	-1.21	-0.28	-2.70	0.031984	0.096222	-4.54
252446_at	beta-D-glucan exohydrolase - like pro	---	AT3G47010	-1.20	-0.27	-2.70	0.031981	0.096222	-4.54
261301_at	hypothetical protein predicted by gene	---	AT1G48570	1.67	0.74	2.70	0.032024	0.096287	-4.54
264852_at	similar to Mlo proteins from H. vulgare	MLO8	AT2G17480	-1.70	-0.77	-2.70	0.032011	0.096287	-4.54
256438_s_	ribosomal protein L41 identical to ribos	---	AT2G40205 /	-1.60	-0.68	-2.70	0.032031	0.096287	-4.54
263505_s_	hypothetical protein	---	AT2G07678	1.53	0.61	2.70	0.032016	0.096287	-4.54
264725_at	Expressed protein ; supported by full-le	---	AT1G22885	1.55	0.63	2.70	0.032018	0.096287	-4.54
260796_at	glutathione transferase, putative simila	ATGSTU21	AT1G78360	1.32	0.40	2.70	0.032029	0.096287	-4.54
258089_at	hypothetical protein predicted by gens	---	AT3G14740	-1.53	-0.61	-2.69	0.032076	0.096411	-4.54
261008_at	hypothetical protein contains similarity	---	AT1G26370	1.31	0.39	2.69	0.03211	0.0965	-4.54
245446_at	enoyl-CoA hydratase	---	AT4G16800	-1.25	-0.32	-2.69	0.032158	0.096629	-4.55
256177_at	protein kinase, putative contains Pfam	---	AT1G51620	1.90	0.93	2.69	0.032197	0.096736	-4.55
258964_at	putative 3-phosphoinositide-dependen	---	AT3G10540	-1.25	-0.32	-2.69	0.032203	0.096737	-4.55

252509_at	putative protein serine/threonine-spec	---	AT3G46240	1.18	0.24	2.69	0.032206	0.096737	-4.55
262205_at	hypothetical protein predicted by gene	---	AT2G01080	1.25	0.32	2.69	0.032226	0.096786	-4.55
251124_s_	laccase -like protein lac110 laccase, P	LAC8	AT5G01040 /	-2.81	-1.49	-2.69	0.032236	0.096801	-4.55
247445_at	putative protein similar to unknown pro	---	AT5G62640	1.25	0.32	2.69	0.032259	0.096846	-4.55
259903_at	unknown protein	---	AT1G74160	-1.43	-0.51	-2.69	0.032257	0.096846	-4.55
251536_at	ketol-acid reductoisomerase ; support	---	AT3G58610	-1.26	-0.33	-2.69	0.032284	0.096875	-4.55
258405_at	unknown protein almost identical to S	BSH	AT3G17590	-1.37	-0.45	-2.69	0.03229	0.096875	-4.55
247255_at	putative protein similar to unknown pro	---	AT5G64780	1.51	0.59	2.69	0.032273	0.096875	-4.55
253225_at	Rho1Ps homolog Rac-like protein ; su	ARAC3	AT4G35020	-1.28	-0.35	-2.69	0.032285	0.096875	-4.55
250153_at	putative protein TMV response-relate	WRKY72	AT5G15130	1.70	0.77	2.69	0.032286	0.096875	-4.55
263265_at	hypothetical protein predicted by gens	---	AT2G38820	1.42	0.51	2.69	0.032316	0.096941	-4.55
251464_at	farnesyltransferase subunit A (FTA) ;	FTA	AT3G59380	-1.29	-0.37	-2.69	0.032362	0.097065	-4.55
265633_at	F-box protein family, AtFBL6 contains	EBF1	AT2G25490	1.29	0.37	2.69	0.032378	0.0971	-4.55
251525_at	putative protein several hypothetical pr	---	AT3G59000	-1.28	-0.35	-2.69	0.032405	0.097158	-4.55
265036_at	unknown protein Contains similarity to	PRP39	AT1G04080	-1.21	-0.28	-2.69	0.03241	0.097158	-4.55
261344_at	hypothetical protein similar to hypothet	---	AT1G79710	1.23	0.30	2.69	0.032409	0.097158	-4.55
247533_at	putative protein kinase-like transmem	---	AT5G61570	-1.68	-0.75	-2.69	0.032452	0.097271	-4.56
252012_at	ubiquinol--cytochrome-c reductase-lik	---	AT3G52730	1.23	0.29	2.69	0.032479	0.097338	-4.56
258104_at	hypothetical protein predicted by gene	---	AT3G23620	1.42	0.51	2.68	0.032513	0.097428	-4.56
264651_at	putative histone H2A Strong similarity	H2AXA	AT1G08880	-1.45	-0.54	-2.68	0.032525	0.097452	-4.56
252199_at	anthranilate N-hydroxycinnamoyl/ben	---	AT3G50270	-1.28	-0.36	-2.68	0.032546	0.097502	-4.56
248196_at	putative protein similar to unknown pro	---	AT5G54150	-1.21	-0.28	-2.68	0.032564	0.097529	-4.56
249405_at	beta subunit of protein farnesyl transfe	ERA1	AT5G40280	-1.22	-0.29	-2.68	0.032564	0.097529	-4.56
252916_at	kinesin like protein kinesin-related pro	---	AT4G38950	-1.24	-0.31	-2.68	0.032569	0.097532	-4.56
248067_at	unknown protein	---	AT5G55600	1.29	0.37	2.68	0.032645	0.09773	-4.56
261882_at	GTP-binding protein, putative similar t	PDE318	AT1G80770	-1.24	-0.31	-2.68	0.032647	0.09773	-4.56
253625_at	signal recognition particle receptor-like	---	AT4G30600	1.21	0.27	2.68	0.032648	0.09773	-4.56
256989_at	hypothetical protein predicted by gene	---	AT3G28580	3.49	1.80	2.68	0.032671	0.097785	-4.56
249341_at	salt-inducible protein-like	---	AT5G41170	1.46	0.55	2.68	0.032687	0.097822	-4.56
265678_at	putative RAD50 DNA repair protein ; s	RAD50	AT2G31970	1.41	0.50	2.68	0.032697	0.097839	-4.56
258165_at	unknown protein ; supported by cDNA	---	AT3G17900	-1.25	-0.32	-2.68	0.03275	0.097984	-4.56
249398_at	RING finger -like protein RING-H2 zin	---	AT5G40250	1.27	0.34	2.68	0.032762	0.097992	-4.57
256025_at	xylan endohydrolase, putative similar	RXF12	AT1G58370	-1.42	-0.51	-2.68	0.032765	0.097992	-4.57
245355_at	60S ribosomal protein L15 homolog ;s	---	AT4G17390	-1.61	-0.69	-2.68	0.032766	0.097992	-4.57
258486_at	putative 40S ribosomal protein similar	---	AT3G02560	-1.68	-0.75	-2.68	0.032775	0.098007	-4.57

255535_at	putative RNaseP-associated protein s	---	AT4G01790	1.37	0.45	2.68	0.032797	0.098061	-4.57
263086_at	putative non-LTR retrolelement revers	---	AT2G16110	-1.23	-0.30	-2.68	0.032813	0.098096	-4.57
245645_at	F5A9.19 unknown protein; similar to E	ATMAP70-2	AT1G24764	-1.37	-0.46	-2.68	0.032856	0.09821	-4.57
262076_at	hypothetical protein identical to GB:Q3	ATMPK2	AT1G59580	-1.31	-0.39	-2.68	0.032872	0.098244	-4.57
257852_at	unknown protein	---	AT3G12950	1.30	0.38	2.68	0.032885	0.098271	-4.57
248787_at	putative protein similar to unknown pro	---	AT5G47420	-1.38	-0.46	-2.68	0.032898	0.098273	-4.57
250183_at	putative protein various predicted prot	---	AT5G14510	-1.38	-0.47	-2.68	0.032894	0.098273	-4.57
262349_at	unknown protein ;supported by full-ler	---	AT2G48130	-1.36	-0.44	-2.68	0.032902	0.098273	-4.57
253737_at	Expressed protein ; supported by full-l	---	AT4G28703	1.85	0.89	2.68	0.032903	0.098273	-4.57
257909_at	Expressed protein ; supported by full-l	---	AT3G25480	-1.31	-0.39	-2.68	0.03291	0.098281	-4.57
264335_s_	hypothetical protein contains similarity	UPL1	AT1G55860 /	1.19	0.25	2.68	0.032926	0.098303	-4.57
251531_at	putative protein hypothetical protein F	---	AT3G58550	1.27	0.34	2.68	0.032924	0.098303	-4.57
252759_at	putative protein hypothetical proteins -	---	AT3G42630	-1.18	-0.24	-2.68	0.03296	0.098392	-4.57
254861_at	putative protein zinc finger protein ZN	---	AT4G12040	1.34	0.42	2.67	0.032996	0.098477	-4.57
245696_at	phytochrome kinase substrate 1 - like	PKS4	AT5G04190	-1.91	-0.93	-2.67	0.032997	0.098477	-4.57
256009_at	AP2 domain transcription factor, putat	---	AT1G19210	2.18	1.12	2.67	0.033003	0.098482	-4.57
248498_at	selenium-binding protein-like	---	AT5G50390	-1.23	-0.30	-2.67	0.033013	0.0985	-4.57
261259_at	unknown protein	---	AT1G26660	1.25	0.32	2.67	0.03303	0.098537	-4.57
266541_at	unknown protein	GRL	AT2G35110	-1.29	-0.37	-2.67	0.033057	0.098604	-4.57
250547_at	asparaginase ; supported by cDNA: g	---	AT5G08100	-1.25	-0.32	-2.67	0.033073	0.098639	-4.58
262654_at	putative mandelonitrile lyase similar to	---	AT1G14180	-1.32	-0.41	-2.67	0.03309	0.098679	-4.58
253832_at	Expressed protein ; supported by full-l	---	AT4G27654	1.86	0.90	2.67	0.03312	0.098749	-4.58
253618_at	nodulin-like protein MtN21 gene produ	---	AT4G30420	-1.18	-0.24	-2.67	0.033123	0.098749	-4.58
263904_at	putative ABC transporter related to mu	PDR6	AT2G36380	1.88	0.91	2.67	0.033151	0.098821	-4.58
248239_at	ribosomal protein L11 methyltransferas	---	AT5G53920	1.38	0.47	2.67	0.03319	0.098925	-4.58
247170_at	putative protein contains similarity to l	---	AT5G65530	1.19	0.26	2.67	0.033209	0.098966	-4.58
262181_at	xylosidase, putative similar to xylosida	---	AT1G78060	-1.73	-0.79	-2.67	0.033219	0.098972	-4.58
255974_at	hypothetical protein	---	---	1.28	0.35	2.67	0.033216	0.098972	-4.58
246262_at	hypothetical protein	---	AT1G31790	1.36	0.44	2.67	0.033245	0.099036	-4.58
258377_at	hypothetical protein contains similarity	CNGC19	AT3G17690	1.26	0.33	2.67	0.033258	0.099062	-4.58
260336_at	putative protease IV similar to protease	SPPA	AT1G73990	-1.29	-0.37	-2.67	0.033274	0.099096	-4.58
251220_at	cytochrome c oxidase subunit 5c-like	---	AT3G62400	1.35	0.43	2.67	0.033297	0.099153	-4.58
263668_at	putative 1-aminocyclopropane-1-carbo	---	AT1G04350	1.27	0.35	2.67	0.033317	0.099182	-4.58
250127_at	putative protein similar to unknown pro	---	AT5G16380	-1.30	-0.38	-2.67	0.033316	0.099182	-4.58
263378_at	protein phosphatase 2C (AthPP2C5)	ATHPP2C5	AT2G40180	1.39	0.47	2.67	0.03332	0.099182	-4.58

245302_at	Expressed protein ; supported by cDN	KAN3	AT4G17695	1.43	0.52	2.67	0.033344	0.09924	-4.58
263798_at	putative ubiquitin carboxyl terminal hyd	UBP19	AT2G24640	1.20	0.26	2.67	0.033369	0.099303	-4.58
259569_at	hypothetical protein	---	AT1G20480	1.27	0.35	2.67	0.03342	0.099426	-4.59
252501_at	hypothetical protein	---	AT3G46880	1.23	0.29	2.67	0.033419	0.099426	-4.59
246056_at	katanin p80 subunit - like protein katar	---	AT5G08390	-1.29	-0.37	-2.66	0.033471	0.099555	-4.59
256821_at	hypothetical protein predicted by gene	---	AT3G22180	1.38	0.47	2.66	0.033472	0.099555	-4.59
246286_at	unknown protein	---	AT1G31910	1.21	0.28	2.66	0.033487	0.099588	-4.59
254204_at	putative protein CGI-58 protein - Hom	---	AT4G24160	1.59	0.67	2.66	0.033499	0.099612	-4.59
250935_at	polyubiquitin (UBQ3) identical to GI:92	UBQ3	AT5G03240	1.43	0.52	2.66	0.033511	0.099634	-4.59
261874_at	ethylene responsive element binding fa	ERF3	AT1G50640	1.29	0.37	2.66	0.033523	0.099656	-4.59
262941_at	hypothetical protein predicted by gene	EMB2217	AT1G79490	1.37	0.46	2.66	0.033598	0.099862	-4.59
249254_at	unknown protein	---	AT5G42110	-1.25	-0.32	-2.66	0.033601	0.099862	-4.59
265261_at	putative APG isolog protein	---	AT2G42990	-1.98	-0.99	-2.66	0.033613	0.099885	-4.59
267583_at	unknown protein	---	AT2G41960	-1.19	-0.25	-2.66	0.03363	0.099915	-4.59
247235_at	putative protein contains similarity to F	---	AT5G64580	-1.46	-0.55	-2.66	0.033632	0.099915	-4.59
255492_at	hypothetical protein similar to A. thalia	EOL1	AT4G02680	-1.25	-0.32	-2.66	0.033639	0.099923	-4.59
259590_at	hypothetical protein contains similarity	---	AT1G28160	-1.25	-0.33	-2.66	0.033645	0.099926	-4.59
264200_at	putative invertase Similar to LIM17 ger	---	AT1G22650	-1.42	-0.50	-2.66	0.033664	0.099958	-4.59
262667_at	amine oxidase, putative similar to ami	---	AT1G62810	-1.39	-0.48	-2.66	0.033661	0.099958	-4.59
254706_at	putative protein DNA-binding protein F	---	AT4G17950	-1.34	-0.42	-2.66	0.033727	0.100132	-4.60
253057_at	putative protein amino-acid N-acetyltra	---	AT4G37670	1.81	0.86	2.66	0.033739	0.100155	-4.60
267365_at	putative phosphoribosyl pyrophosphat	---	AT2G44530	-1.18	-0.24	-2.66	0.033749	0.100172	-4.60
258229_at	unknown protein contains Pfam profile	---	AT3G27700	1.21	0.28	2.66	0.033755	0.100177	-4.60
246981_at	unknown protein	---	AT5G04840	-1.34	-0.42	-2.66	0.033772	0.100214	-4.60
264703_at	serine threonine protein phosphatase (	PP2A	AT1G69960	1.20	0.26	2.66	0.033788	0.100244	-4.60
258301_at	hypothetical protein predicted by gene	---	---	1.18	0.24	2.66	0.033791	0.100244	-4.60
264384_at	putative chromodomain-helicase-DNA	PKL	AT2G25170	-1.19	-0.25	-2.66	0.033801	0.100261	-4.60
266278_at	putative tropinone reductase	---	AT2G29300	-1.75	-0.81	-2.66	0.033817	0.100296	-4.60
253520_at	hypothetical protein ;supported by full-	---	AT4G31410	1.20	0.26	2.66	0.033824	0.100303	-4.60
254940_at	putative protein predicted proteins, Ar	---	AT4G10820	-1.22	-0.29	-2.66	0.033857	0.100374	-4.60
245224_at	gene_id:K17E7.8~unknown protein	---	AT3G29796	-1.20	-0.26	-2.66	0.033853	0.100374	-4.60
246180_at	putative protein predicted proteins, Ar	---	AT5G20840	-1.22	-0.29	-2.66	0.033894	0.10047	-4.60
246122_at	putative protein brain specific Na+-de	PHT4;5	AT5G20380	1.27	0.35	2.65	0.033921	0.100524	-4.60
255939_at	hypothetical protein predicted by gene	---	AT1G12730	-1.36	-0.45	-2.65	0.033918	0.100524	-4.60
266490_at	unknown protein	---	AT2G07000	1.29	0.37	2.65	0.033971	0.10064	-4.60

253603_at	putative protein SP8 binding protein, (	WRKY32	AT4G30935	1.20	0.26	2.65	0.033973	0.10064	-4.60
256450_at	NADPH oxidoreductase, putative simi	---	AT1G75290	1.21	0.28	2.65	0.033968	0.10064	-4.60
257515_at	zinc finger protein, putative similar to	DOT5	AT1G13290	-1.21	-0.28	-2.65	0.034003	0.100688	-4.60
245747_at	hypothetical protein predicted by gene	---	AT1G51100	-1.35	-0.43	-2.65	0.034	0.100688	-4.60
252639_at	acyl CoA reductase -like protein acyl (	FAR5	AT3G44550	-1.19	-0.25	-2.65	0.033994	0.100688	-4.60
246738_at	replication factor C - like replication fa	EMB2775	AT5G27740	-1.23	-0.30	-2.65	0.034015	0.100713	-4.60
253085_s_	putative protein hypothetical protein, A	---	AT4G36270 /	-1.42	-0.50	-2.65	0.034035	0.100758	-4.60
248472_at	cyclin-dependent protein kinase-like	---	AT5G50860	1.26	0.34	2.65	0.03406	0.100817	-4.61
245980_at	putative protein ;supported by full-leng	---	AT5G13140	-4.21	-2.07	-2.65	0.034081	0.100853	-4.61
253168_at	putative protein various predicted prot	---	AT4G35070	1.55	0.64	2.65	0.03408	0.100853	-4.61
249486_at	receptor protein kinase - like protein re	---	AT5G39030	1.28	0.36	2.65	0.034091	0.10087	-4.61
261984_at	TINY-like protein similar to TINY GB: (	---	AT1G33760	-1.32	-0.40	-2.65	0.034102	0.100891	-4.61
257583_at	hypothetical protein	PMI2	AT1G66480	2.32	1.22	2.65	0.034123	0.100939	-4.61
258445_at	putative lipoxygenase similar to lipoxy	LOX5	AT3G22400	-1.44	-0.53	-2.65	0.034133	0.100957	-4.61
259588_at	unknown protein ;supported by full-len	---	AT1G27930	1.18	0.24	2.65	0.034155	0.101004	-4.61
257893_at	E2, ubiquitin-conjugating enzyme, put	UBC32	AT3G17000	1.42	0.51	2.65	0.034158	0.101004	-4.61
262637_at	oxidoreductase, putative contains Pfa	---	AT1G06640	-2.69	-1.43	-2.65	0.03418	0.101043	-4.61
263209_at	Expressed protein ; supported by full-l	---	AT1G10522	-1.52	-0.61	-2.65	0.034177	0.101043	-4.61
262913_at	NADPH-dependent codeinone reducta	---	AT1G59960	1.80	0.85	2.65	0.034195	0.101073	-4.61
246828_at	putative protein hypothetical protein, F	---	---	-1.23	-0.30	-2.65	0.034208	0.1011	-4.61
263885_at	unknown protein	---	AT2G36940	-1.22	-0.29	-2.65	0.034234	0.101162	-4.61
245895_at	SIR2-family protein sirtuin type 4 (SIR	SRT2	AT5G09230	-1.25	-0.32	-2.65	0.034241	0.101171	-4.61
252193_at	R2R3-MYB transcription factor ; supp	MYB77	AT3G50060	-1.78	-0.84	-2.65	0.034311	0.101354	-4.61
246590_at	cyclic nucleotide and calmodulin-regu	CNGC18	AT5G14870	-1.19	-0.25	-2.65	0.034312	0.101354	-4.61
262250_at	Expressed protein predicted by gensca	---	AT1G48280	-2.03	-1.02	-2.65	0.034331	0.101397	-4.61
260155_at	unknown protein	---	AT1G52870	-1.61	-0.69	-2.65	0.034337	0.101402	-4.61
264649_at	hypothetical protein Similar to Vicia sa	---	AT1G09060	-1.29	-0.36	-2.65	0.034369	0.101471	-4.62
245068_at	putative glucosyltransferase	UGT84B1	AT2G23260	1.24	0.31	2.65	0.034366	0.101471	-4.62
262716_at	multicatalytic endopeptidase identical	PAB1	AT1G16470	1.32	0.40	2.65	0.034378	0.101482	-4.62
259047_at	unknown protein	DegP7	AT3G03380	1.19	0.25	2.65	0.034389	0.101503	-4.62
250792_at	unknown protein ;supported by full-ler	---	AT5G05520	1.24	0.31	2.64	0.034398	0.101503	-4.62
259972_at	unknown protein N-term similar to N-t	CUC3	AT1G76420	-1.40	-0.48	-2.65	0.034395	0.101503	-4.62
261405_at	unknown protein ;supported by full-len	---	AT1G18740	1.54	0.62	2.64	0.03441	0.101526	-4.62
254013_at	putative leucine-rich-repeat protein leu	---	AT4G26050	1.37	0.46	2.64	0.034417	0.101533	-4.62
264031_at	unknown protein	---	AT2G03780	-1.29	-0.37	-2.64	0.034438	0.101581	-4.62

260321_at	putative RING zinc finger protein Pfan	---	AT1G63900	-1.23	-0.30	-2.64	0.034442	0.101581	-4.62
245344_at	F-box protein family, AtFBL4 contains	---	AT4G15475	-1.29	-0.37	-2.64	0.034474	0.101648	-4.62
254657_s_	putative protein W15DMY32F, W25DI	---	AT4G18210 /	1.53	0.61	2.64	0.034472	0.101648	-4.62
251798_at	putative RNA binding protein Serine/a	SCL30	AT3G55460	-1.22	-0.29	-2.64	0.034481	0.101656	-4.62
252422_at	putative protein PIT1 - Arabidopsis tha	---	AT3G47550	1.37	0.46	2.64	0.034517	0.101748	-4.62
249810_at	unknown protein	---	AT5G23920	1.40	0.48	2.64	0.034539	0.101788	-4.62
260293_at	unknown protein predicted by genscar	---	AT1G63670	-1.29	-0.37	-2.64	0.034537	0.101788	-4.62
246146_at	receptor-like protein kinase - like prote	---	AT5G20050	1.33	0.41	2.64	0.034546	0.101796	-4.62
249176_at	thioredoxin (clone GIF1) (pir||S58118)	ATTRX3	AT5G42980	1.20	0.26	2.64	0.034606	0.101939	-4.62
245764_s_	hypothetical protein contains similarity	ATCSA-1	AT1G19750 /	-1.21	-0.27	-2.64	0.034601	0.101939	-4.62
262461_at	myosin, putative similar to myosin GB	VIIIA	AT1G50360	1.47	0.55	2.64	0.034608	0.101939	-4.62
250375_at	putative protein L-gulono-gamma-lact	---	AT5G11540	-1.23	-0.30	-2.64	0.034655	0.102062	-4.62
260530_at	putative peptidyl-prolyl cis-trans isome	---	AT2G47320	-1.20	-0.26	-2.64	0.034678	0.102118	-4.62
249059_at	subtilisin-like serine protease contains	---	AT5G44530	-1.40	-0.49	-2.64	0.034717	0.10222	-4.63
257237_at	DNA nick sensor, putative contains Pf	---	AT3G14890	-1.74	-0.80	-2.64	0.034733	0.102253	-4.63
249917_at	putative protein strong similarity to unk	---	AT5G22460	-2.84	-1.50	-2.64	0.034801	0.10244	-4.63
254868_at	copper amine oxidase like protein (fra	---	AT4G12270	1.30	0.38	2.64	0.034831	0.102517	-4.63
253615_at	cyclic nucleotide and calmodulin-regu	CNGC17	AT4G30360	1.35	0.44	2.64	0.034867	0.102607	-4.63
262044_s_	hypothetical protein predicted by gens	---	AT1G80210 /	1.23	0.30	2.63	0.034906	0.10271	-4.63
254758_at	putative protein dimethylaniline mono	YUC2	AT4G13260	-1.52	-0.61	-2.63	0.034928	0.102762	-4.63
261530_at	unknown protein contains Pfam profile	---	AT1G63460	1.32	0.40	2.63	0.034944	0.102795	-4.63
247606_at	RNA helicase	---	AT5G61000	-1.82	-0.86	-2.63	0.034949	0.102797	-4.63
262641_at	unknown protein ;supported by full-len	---	AT1G62730	1.17	0.22	2.63	0.034956	0.102803	-4.63
258040_at	unknown protein ;supported by full-ler	---	AT3G21190	-3.07	-1.62	-2.63	0.035017	0.102965	-4.63
267145_at	putative acetyltransferase	ATMAK3	AT2G38130	-1.25	-0.32	-2.63	0.035024	0.102965	-4.63
257402_at	hypothetical protein similar to putative	---	AT1G23570	1.23	0.30	2.63	0.03502	0.102965	-4.63
265494_at	putative calmodulin-like protein	---	AT2G15680	-1.32	-0.40	-2.63	0.035033	0.102976	-4.63
257610_at	zinc finger protein, putative similar to f	AtIDD11	AT3G13810	1.64	0.71	2.63	0.035062	0.10305	-4.64
253989_at	uncharacterized protein ;supported by	---	AT4G26130	1.40	0.48	2.63	0.035137	0.103256	-4.64
253344_at	putative protein predicted protein, Ara	---	AT4G33550	-1.51	-0.60	-2.63	0.035176	0.103358	-4.64
258743_s_	shaggy related protein kinase, ASK-G	ATSK12	AT3G05840 /	1.27	0.34	2.63	0.035201	0.103416	-4.64
247230_at	putative protein similar to unknown pro	---	AT5G65170	1.20	0.27	2.63	0.035215	0.103445	-4.64
265289_at	unknown protein predicted by genscan	---	AT2G22690	1.18	0.24	2.63	0.03522	0.103448	-4.64
252329_at	putative protein several hypothetical pr	---	AT3G48760	1.20	0.27	2.63	0.035233	0.103473	-4.64
249011_at	putative protein strong similarity to unk	---	AT5G44670	-1.63	-0.71	-2.63	0.035273	0.103577	-4.64

250077_at	putative protein	---	AT5G16680	1.20	0.27	2.63	0.03528	0.103584	-4.64
256343_at	unknown protein ; supported by cDNA	---	AT1G72090	-1.28	-0.35	-2.63	0.035307	0.103648	-4.64
263024_at	hypothetical protein predicted by gene	---	AT1G23980	-1.30	-0.38	-2.63	0.035311	0.103648	-4.64
262807_at	unknown protein strong similarity to gi	---	AT1G11740	-1.32	-0.40	-2.63	0.03532	0.103659	-4.64
256626_at	hypothetical protein, 5' partial	---	AT3G20015	-1.68	-0.75	-2.63	0.035334	0.103687	-4.64
250321_at	zinc finger transcription factor -like pr	---	AT5G12850	-1.25	-0.32	-2.63	0.035342	0.103699	-4.64
260899_at	hypothetical protein predicted by gene	---	AT1G21370	1.29	0.37	2.63	0.03536	0.103725	-4.64
255513_at	PROLIFERA similar to S. cerevisiae M	PRL	AT4G02060	-2.38	-1.25	-2.63	0.035358	0.103725	-4.64
256873_at	cytochrome P450, putative contains P	CYP71B34	AT3G26300 /	-1.25	-0.33	-2.63	0.035374	0.103752	-4.65
253557_at	putative protein wall-associated kinas	---	AT4G31110 /	1.19	0.25	2.63	0.035381	0.103752	-4.65
261945_at	unknown protein	---	AT1G64530	-1.46	-0.55	-2.63	0.035383	0.103752	-4.65
261853_at	unknown protein	---	AT1G50660	-1.32	-0.40	-2.62	0.035392	0.103764	-4.65
267372_at	putative protein kinase contains a prot	ARSK1	AT2G26290	2.14	1.10	2.62	0.035402	0.103769	-4.65
261330_at	transcription factor, putative similar to	MCM2	AT1G44900	-2.12	-1.08	-2.62	0.035403	0.103769	-4.65
253817_at	hypothetical protein ;supported by full-	---	AT4G28310	-1.78	-0.83	-2.62	0.035423	0.103812	-4.65
245423_at	putative protein	---	AT4G17483	1.28	0.35	2.62	0.035426	0.103812	-4.65
258584_at	hypothetical protein predicted by gens	SIP1A	AT3G04090	-1.17	-0.23	-2.62	0.035433	0.103819	-4.65
261228_at	C-8,7 sterol isomerase identical to GB	HYD1	AT1G20050	-1.29	-0.37	-2.62	0.035443	0.103833	-4.65
262062_s_	hypothetical protein	emb1427	AT1G20570 /	-1.24	-0.31	-2.62	0.035471	0.10389	-4.65
258251_at	unknown protein ; supported by full-le	---	AT3G15810	1.24	0.31	2.62	0.035467	0.10389	-4.65
266512_at	unknown protein	---	AT2G47690	-1.19	-0.25	-2.62	0.035487	0.103922	-4.65
262367_at	hypothetical protein contains similarity	VPS46.2	AT1G73030	-1.29	-0.37	-2.62	0.035494	0.103931	-4.65
266384_at	hypothetical protein predicted by gens	---	AT2G14660	-1.26	-0.34	-2.62	0.035504	0.10394	-4.65
251315_at	putative protein protein kinase homol	---	AT3G61410	1.27	0.35	2.62	0.035506	0.10394	-4.65
247951_at	oxysterol-binding protein-like	ORP4C	AT5G57240	-1.22	-0.29	-2.62	0.03553	0.103996	-4.65
258552_at	putative pectate lyase similar to pectat	---	AT3G07010	-3.40	-1.77	-2.62	0.035564	0.104081	-4.65
263251_at	unknown protein ; supported by cDNA	---	AT2G31410	1.52	0.61	2.62	0.035571	0.10409	-4.65
265709_at	hypothetical protein predicted by gens	---	---	1.78	0.83	2.62	0.035612	0.104197	-4.65
252459_s_	1-phosphatidylinositol-4,5-bisphospha	PLC9	AT3G47220 /	1.20	0.26	2.62	0.03564	0.104265	-4.65
246404_at	hypothetical protein contains similarity	---	AT1G57600	-1.21	-0.27	-2.62	0.035647	0.104272	-4.65
265867_at	unknown protein ;supported by full-ler	MEE11	AT2G01620	-1.28	-0.36	-2.62	0.035708	0.104436	-4.65
266411_at	putative peptidyl-prolyl cis-trans isome	---	AT2G38730	-1.31	-0.39	-2.62	0.03573	0.104487	-4.66
255663_at	hypothetical protein	---	AT4G00420	-1.24	-0.31	-2.62	0.03579	0.104649	-4.66
258799_at	putative 40S ribosomal protein identica	RPSAb	AT3G04770	1.33	0.42	2.62	0.03582	0.104696	-4.66
248501_at	golgi SNARE protein	MEMB12	AT5G50440	-1.29	-0.36	-2.62	0.035824	0.104696	-4.66

260510_at	hypothetical protein predicted by gene	---	AT1G51580	-1.43	-0.52	-2.62	0.035824	0.104696	-4.66
252988_at	putative cold-regulated protein cold-re	---	AT4G38410	-1.50	-0.59	-2.62	0.035822	0.104696	-4.66
267524_at	unknown protein	---	AT2G30600	-1.37	-0.45	-2.62	0.035831	0.104701	-4.66
261541_at	unknown protein contains Pfam profile	---	AT1G63600	-1.24	-0.31	-2.62	0.035846	0.104719	-4.66
264902_at	unknown protein Location of EST gb|T	---	AT1G23060	1.55	0.63	2.62	0.035842	0.104719	-4.66
246576_at	hypothetical protein predicted by gene	ROPGEF14	AT1G31650	-1.19	-0.25	-2.62	0.035858	0.104742	-4.66
261535_at	Expressed protein ; supported by full-l	---	AT1G01725	1.29	0.37	2.62	0.035885	0.104792	-4.66
248236_at	putative protein contains similarity to p	---	AT5G53870	2.60	1.38	2.62	0.035884	0.104792	-4.66
260175_at	neutral invertase, putative similar to n	---	AT1G72000	-1.20	-0.26	-2.61	0.035916	0.104856	-4.66
249392_at	peroxidase ATP26a	---	AT5G40150	-1.27	-0.35	-2.61	0.035912	0.104856	-4.66
248294_at	RNA-binding protein-like	---	AT5G53060	1.26	0.34	2.61	0.035926	0.104873	-4.66
262664_at	hypothetical protein predicted by gene	---	AT1G13970	1.23	0.30	2.61	0.035946	0.104903	-4.66
265807_at	unknown protein	---	AT2G17990	1.24	0.32	2.61	0.035944	0.104903	-4.66
250795_at	RING zinc finger protein-like	CPuORF64	AT5G05280 /	1.26	0.34	2.61	0.035962	0.104933	-4.66
245328_at	Expressed protein ; supported by full-l	---	AT4G14465	1.22	0.29	2.61	0.035965	0.104933	-4.66
267192_at	hypothetical protein predicted by grail	---	AT2G30890	-1.29	-0.37	-2.61	0.035976	0.104951	-4.66
249276_at	DNA polymerase alpha subunit IV (prir	POLA3	AT5G41880	-2.64	-1.40	-2.61	0.036024	0.105077	-4.66
261823_at	hypothetical protein predicted by gene	PYM	AT1G11400	-1.23	-0.30	-2.61	0.036055	0.105104	-4.66
245975_at	putative protein CGI-107 protein - Hor	---	AT5G13070	1.28	0.36	2.61	0.036056	0.105104	-4.66
251443_at	putative protein unknown protein At2g	---	AT3G59940	-1.49	-0.58	-2.61	0.036054	0.105104	-4.66
252310_at	GTPase activating -like protein GTPas	---	AT3G49350	1.50	0.59	2.61	0.036061	0.105104	-4.66
264080_at	putative vacuolar proton-ATPase subu	VHA-A1	AT2G28520	-1.19	-0.25	-2.61	0.036048	0.105104	-4.66
256182_at	Expressed protein ; supported by full-l	SYP81	AT1G51740	-1.31	-0.39	-2.61	0.036059	0.105104	-4.66
252103_at	putative protein various predicted prot	---	AT3G51410	-1.20	-0.26	-2.61	0.036083	0.105155	-4.67
267397_at	hypothetical protein predicted by gens	---	AT1G76170	-1.46	-0.54	-2.61	0.036151	0.105342	-4.67
263832_at	putative polygalacturonase	---	AT2G40310	1.18	0.23	2.61	0.036164	0.105364	-4.67
245226_at	gene_id:K17E7.15~unknown protein	---	AT3G29970	2.65	1.41	2.61	0.036182	0.105376	-4.67
267630_at	unknown protein predicted by genefinc	---	AT2G42130	-1.30	-0.38	-2.61	0.036179	0.105376	-4.67
245722_at	unknown protein	---	AT1G73430	-1.33	-0.41	-2.61	0.036182	0.105376	-4.67
253377_at	putative protein NBS/LRR disease res	ADR1-L1	AT4G33300	1.26	0.33	2.61	0.036201	0.10542	-4.67
255958_at	high affinity sulphate transporter, puta	SULTR1;3	AT1G22150	-1.28	-0.36	-2.61	0.036219	0.105458	-4.67
251542_at	putative protein protein-tyrosine kinas	---	AT3G58760	-1.30	-0.38	-2.61	0.036243	0.105513	-4.67
264133_at	hypothetical protein predicted by gene	---	AT1G79080	-1.24	-0.31	-2.61	0.036305	0.105669	-4.67
262961_at	exonuclease, putative similar to 5'-3' e	XRN4	AT1G54490	1.23	0.30	2.61	0.036303	0.105669	-4.67
250290_at	putative protein ;supported by full-leng	---	AT5G13310	-1.20	-0.27	-2.61	0.036328	0.105721	-4.67

266718_at	putative zinc transporter ;supported by	ZAT	AT2G46800	-1.24	-0.31	-2.61	0.036362	0.105808	-4.67
261311_at	disease resistance protein RTM1, puta	---	AT1G05770	-1.35	-0.44	-2.61	0.036367	0.105809	-4.67
267410_at	hypothetical protein predicted by gens	EDA18	AT2G34920	-1.46	-0.54	-2.61	0.036385	0.105845	-4.67
253045_at	Expressed protein ; supported by full-l	---	AT4G37445	-1.40	-0.49	-2.60	0.036414	0.105917	-4.68
261745_at	unknown protein identical to unknown	---	AT1G08500	-1.70	-0.77	-2.60	0.03642	0.105921	-4.68
252343_at	putative protein hypothetical protein F	---	AT3G48610	-1.95	-0.97	-2.60	0.036454	0.106006	-4.68
251194_at	putative protein	---	AT3G62920	1.40	0.49	2.60	0.036472	0.106045	-4.68
250544_at	syntaxin-like protein syntaxin-related p	SYP132	AT5G08080	-1.29	-0.37	-2.60	0.036485	0.106069	-4.68
257524_at	hypothetical protein similar to putative	DEL3	AT3G01330	-1.26	-0.33	-2.60	0.03649	0.106072	-4.68
248503_at	putative protein contains similarity to tr	NF-YC7	AT5G50470	1.41	0.50	2.60	0.03651	0.106115	-4.68
245100_at	ubiquitin-specific protease 5 (UBP5), p	UBP5	AT2G40930	1.22	0.29	2.60	0.036561	0.106246	-4.68
259408_at	protein phosphatase 2A 65 kDa regula	PP2AA2	AT3G25800	1.19	0.25	2.60	0.036566	0.106246	-4.68
249163_at	glucose-6-phosphate isomerase, cyto	---	AT5G42740	1.32	0.40	2.60	0.036569	0.106246	-4.68
265333_at	hypothetical protein predicted by gens	AtHB24	AT2G18350	1.31	0.39	2.60	0.036574	0.106247	-4.68
262963_at	dihydrolipoamide S-acetyltransferase,	---	AT1G54220	-1.20	-0.27	-2.60	0.036579	0.106249	-4.68
258462_at	unknown protein	---	AT3G17350	-1.61	-0.69	-2.60	0.036619	0.106337	-4.68
259252_at	hypothetical protein similar to hypothe	IBM1	AT3G07610	1.21	0.27	2.60	0.036615	0.106337	-4.68
262579_at	hypothetical protein predicted by gens	---	AT1G15320	-1.20	-0.27	-2.60	0.036714	0.106599	-4.68
264809_at	superoxidase dismutase identical to G	CSD1	AT1G08830	1.98	0.99	2.60	0.036726	0.106622	-4.68
265988_at	hypothetical protein predicted by gene	---	AT2G24255	-1.21	-0.28	-2.60	0.036765	0.106708	-4.69
258511_at	unknown protein ;supported by full-ler	---	AT3G06590	-1.28	-0.35	-2.60	0.036764	0.106708	-4.68
262281_at	peptide transporter, putative similar to	---	AT1G68570	-1.73	-0.79	-2.60	0.03678	0.106738	-4.69
262699_at	unknown protein	---	AT1G75980	-1.24	-0.31	-2.60	0.036795	0.106767	-4.69
251832_at	putative protein tomato leucine zipper	ATEXO70H1	AT3G55150	1.77	0.83	2.60	0.036822	0.106831	-4.69
266170_at	unknown protein ;supported by full-ler	---	AT2G39050	1.47	0.55	2.60	0.036846	0.106889	-4.69
257733_at	unknown protein ; supported by cDNA	---	AT3G18350	-1.26	-0.33	-2.60	0.036904	0.107042	-4.69
250667_at	40S ribosomal protein S4 ;supported b	---	AT5G07090	-1.54	-0.63	-2.60	0.036921	0.107076	-4.69
247665_at	putative protein various predicted prot	---	AT5G60130	-1.19	-0.25	-2.60	0.036925	0.107076	-4.69
256785_at	unknown protein ;supported by full-ler	PRA8	AT3G13720	-1.34	-0.42	-2.60	0.036932	0.107083	-4.69
253451_at	putative myb-protein transforming pro	PC-MYB1	AT4G32730	1.22	0.28	2.59	0.036965	0.107157	-4.69
267440_at	putative anthranilate N-hydroxycinnam	SHT	AT2G19070	-1.23	-0.30	-2.59	0.036967	0.107157	-4.69
249998_at	putative protein unnamed ORF, Mus r	FASS	AT5G18580	-1.21	-0.28	-2.59	0.036996	0.107227	-4.69
266958_at	putative trans-prenyltransferase	GPS1	AT2G34630	1.34	0.43	2.59	0.037045	0.107357	-4.69
250358_at	putative protein gibberellin-responsive	AGP15	AT5G11740	-1.31	-0.39	-2.59	0.037054	0.107368	-4.69
266217_at	unknown protein	AT2G28830	---	1.20	0.27	2.59	0.037068	0.107396	-4.69

264380_at	unknown protein predicted by genscan	---	AT2G25190	-1.17	-0.23	-2.59	0.037076	0.107405	-4.69
253386_at	sulfolipid biosynthesis protein SQD1 ;	SQD1	AT4G33030	1.34	0.42	2.59	0.037106	0.10747	-4.69
262111_at	hypothetical protein predicted by gene	---	AT1G02960	-1.22	-0.28	-2.59	0.037108	0.10747	-4.69
266700_at	60S ribosomal protein L31 ; supported	---	AT2G19740	-1.33	-0.42	-2.59	0.037137	0.107533	-4.70
250317_at	tubulin beta-6 chain (sp|P29514) ; sup	TUB6	AT5G12250	-1.84	-0.88	-2.59	0.037142	0.107533	-4.70
249543_at	Expressed protein ; supported by full-l	---	---	-1.26	-0.33	-2.59	0.037144	0.107533	-4.70
244954_s_	hypothetical protein	---	AT2G07732	1.54	0.63	2.59	0.037156	0.107553	-4.70
247159_at	1-aminocyclopropane-1-carboxylate sy	ACS5	AT5G65800	-1.19	-0.25	-2.59	0.037206	0.107685	-4.70
264921_at	RNA binding protein, putative similar t	---	AT1G60650	1.25	0.32	2.59	0.037237	0.10773	-4.70
254660_at	receptor serine/threonine kinase-like p	---	AT4G18250	1.42	0.51	2.59	0.037237	0.10773	-4.70
255961_at	UDP-glucose glucosyltransferase, put	AtUGT85A7	AT1G22340	1.44	0.52	2.59	0.03724	0.10773	-4.70
252601_s_	40S ribsomomal protein 40S ribsomor	---	AT3G45030 /	-1.47	-0.56	-2.59	0.037228	0.10773	-4.70
259821_at	subtilisin-like serine protease contains	---	AT1G66220	-1.31	-0.39	-2.59	0.037245	0.107731	-4.70
258866_at	unknown protein	---	AT3G03180	-1.20	-0.26	-2.59	0.037275	0.107777	-4.70
254340_at	putative protein hypothetical protein H	---	AT4G22120	1.61	0.68	2.59	0.037271	0.107777	-4.70
266399_at	putative phospholipid cytidylyltransfera	PECT1	AT2G38670	-1.28	-0.36	-2.59	0.037275	0.107777	-4.70
258664_at	E2, ubiquitin-conjugating enzyme, put	UBC12	AT3G08700	1.25	0.32	2.59	0.037302	0.107827	-4.70
256034_at	unknown protein ; supported by cDNA	---	AT1G07080	-1.20	-0.27	-2.59	0.037302	0.107827	-4.70
261277_at	hypothetical protein predicted by gens	---	AT1G20230	1.28	0.35	2.59	0.037331	0.107896	-4.70
248057_at	putative protein strong similarity to unk	---	AT5G55520	-1.19	-0.26	-2.59	0.037361	0.107971	-4.70
252219_at	putative protein some putative proteins	---	AT3G50160	-1.27	-0.34	-2.59	0.037367	0.107975	-4.70
263954_at	unknown protein ; supported by cDNA	---	AT2G35840	-1.30	-0.37	-2.59	0.037401	0.108044	-4.70
261515_at	cleavage stimulation factor, putative s	---	AT1G71800	1.20	0.27	2.59	0.037397	0.108044	-4.70
246856_at	nucleic acid binding protein - like nucl	AL4	AT5G26210	1.19	0.25	2.59	0.037409	0.108055	-4.70
262231_at	putative receptor protein similar to vira	---	AT1G68740	1.64	0.71	2.59	0.037425	0.108087	-4.70
250342_at	putative protein predicted protein, Ara	---	AT5G11870	1.33	0.41	2.59	0.037455	0.108159	-4.70
255023_at	hypothetical protein	---	AT4G09850	1.24	0.31	2.58	0.037492	0.108251	-4.71
258894_at	putative disease resistance protein sim	AtRLP32	AT3G05650	-1.61	-0.69	-2.58	0.037538	0.108358	-4.71
256487_at	disease resistance gene, putative sim	---	AT1G31540	1.33	0.41	2.58	0.037534	0.108358	-4.71
256493_at	hypothetical protein predicted by gene	---	AT1G31600	-1.27	-0.35	-2.58	0.037619	0.108579	-4.71
253885_at	putative protein essential for embryog	VPS26B	AT4G27690	-1.29	-0.37	-2.58	0.037635	0.108611	-4.71
248342_at	unknown protein	MBD13	AT5G52230	1.19	0.25	2.58	0.037653	0.108649	-4.71
264438_at	putative 60S ribosomal protein L17 sim	---	AT1G27400	-1.43	-0.52	-2.58	0.03766	0.108656	-4.71
260623_at	high-affinity nitrate transporter NRT2 i	ATNRT2:1	AT1G08090	-1.27	-0.34	-2.58	0.037686	0.108691	-4.71
248371_at	gibberellin 20-oxidase (emb|CAA5829	GA20OX2	AT5G51810	-1.69	-0.75	-2.58	0.037683	0.108691	-4.71

245936_at	putative protein predicted proteins - dif	---	AT5G19850	1.30	0.38	2.58	0.037687	0.108691	-4.71
266230_at	hypothetical protein predicted by gens	---	AT2G28830	1.50	0.58	2.58	0.037728	0.108751	-4.71
253135_at	cytoplasmatic aconitate hydratase (citr	---	AT4G35830	1.35	0.43	2.58	0.037715	0.108751	-4.71
259470_at	unknown protein	---	AT1G19110	-1.18	-0.24	-2.58	0.037725	0.108751	-4.71
265267_at	hypothetical protein predicted by gens	---	AT2G42920	-1.29	-0.37	-2.58	0.037732	0.108751	-4.71
261140_at	unknown protein	---	AT1G19680	1.25	0.33	2.58	0.037718	0.108751	-4.71
247689_at	putative protein protein tyrosine phosp	---	AT5G59770	-1.33	-0.41	-2.58	0.037743	0.108771	-4.71
266751_at	putative peptide chain release factor	---	AT2G47020	-1.22	-0.28	-2.58	0.037778	0.108858	-4.71
260488_at	flowering protein CONSTANS, putativ	TIFY2A	AT1G51600	-1.29	-0.37	-2.58	0.037789	0.108875	-4.71
267048_at	hypothetical protein predicted by gene	---	AT2G34200	-1.32	-0.41	-2.58	0.037817	0.108941	-4.71
254862_at	putative transport protein Na(+) deper	---	AT4G12030	-1.45	-0.54	-2.58	0.037849	0.109022	-4.72
261765_at	cyclin, putative similar to cyclin GI:562	CYCA2;3	AT1G15570	-1.25	-0.32	-2.58	0.037863	0.109043	-4.72
253019_at	putative protein crp1-hcf111 allele,enc	---	AT4G38010	1.22	0.29	2.58	0.037866	0.109043	-4.72
246617_at	GSH-dependent dehydroascorbate rec	---	AT5G36270	-1.24	-0.31	-2.58	0.037886	0.109086	-4.72
251774_at	nematode resistance protein-like prote	---	AT3G55840	2.17	1.12	2.58	0.037894	0.109096	-4.72
260750_at	light repressible receptor protein kinas	---	AT1G49100	-1.22	-0.29	-2.58	0.037901	0.109101	-4.72
265845_at	unknown protein	---	AT2G35610	1.16	0.22	2.58	0.03793	0.109173	-4.72
259764_at	transcription factor inhibitor I kappa B,	NPR1	AT1G64280	1.38	0.46	2.58	0.037937	0.109177	-4.72
266031_at	hypothetical protein predicted by gene	---	---	1.21	0.27	2.58	0.037989	0.109312	-4.72
256961_at	transcription initiation factor TFIID-1 (T	TBP1	AT3G13445	1.24	0.31	2.57	0.038013	0.109369	-4.72
253072_at	putative protein ;supported by full-leng	---	AT4G37830	1.19	0.25	2.57	0.03803	0.109403	-4.72
258195_at	myb protein(myb26) contains myb DNA	ATMYB26	AT3G13890	-1.24	-0.31	-2.57	0.038045	0.109434	-4.72
259097_at	unknown protein similar to GB:AAD49	---	AT3G04830	-1.20	-0.26	-2.57	0.038094	0.109561	-4.72
256288_at	arginine N-methyltransferase 3, putati	PRMT3	AT3G12270	1.59	0.67	2.57	0.038131	0.109639	-4.72
258694_at	putative non-phototropic hypocotyl sim	---	AT3G08660	-1.48	-0.57	-2.57	0.038129	0.109639	-4.72
257584_at	hypothetical protein similar to putative	---	---	-1.37	-0.45	-2.57	0.038143	0.109659	-4.72
264555_at	hypothetical protein predicted by gens	---	AT1G09360	-1.22	-0.29	-2.57	0.038157	0.109686	-4.72
264675_at	putative phosphoribosylglycinamide s	---	AT1G09830	1.21	0.28	2.57	0.038185	0.109753	-4.72
263708_at	unknown protein	---	AT1G09320	1.22	0.29	2.57	0.038206	0.109801	-4.72
259296_at	putative aminopeptidase similar to X-p	---	AT3G05350	-1.28	-0.35	-2.57	0.038259	0.109939	-4.73
248703_at	dermal glycoprotein precursor, extrace	---	AT5G48430	4.63	2.21	2.57	0.038291	0.110015	-4.73
257443_at	hypothetical protein predicted by gens	---	AT2G22050	-1.21	-0.27	-2.57	0.038304	0.11004	-4.73
257011_at	predicted protein	CAX9	AT3G14070	1.55	0.63	2.57	0.038321	0.110074	-4.73
247691_at	heat shock protein 18 ;supported by fu	HSP18.2	AT5G59720	-1.24	-0.31	-2.57	0.038334	0.110085	-4.73
246125_at	Expressed protein ; supported by full-le	---	AT5G19875	1.93	0.95	2.57	0.03833	0.110085	-4.73

267545_at	unknown protein	GRP23	AT2G32690	-1.34	-0.42	-2.57	0.038407	0.11028	-4.73
251486_at	60S RIBOSOMAL PROTEIN L38-like	---	AT3G59540	-1.39	-0.48	-2.57	0.038478	0.110456	-4.73
265878_at	putative SUPERMAN-like C2H2 zinc fi	ZFP11	AT2G42410	-1.19	-0.25	-2.57	0.038478	0.110456	-4.73
262013_s_	mudrA-like protein similar to Mu transp	---	---	-1.30	-0.37	-2.57	0.038486	0.110464	-4.73
263028_at	protein kinase, putative similar to PRC	---	AT1G24030	-1.32	-0.40	-2.56	0.03856	0.110662	-4.73
264535_at	Phosphatidylinositol Transfer Protein,	---	AT1G55690	-1.70	-0.77	-2.56	0.038596	0.110754	-4.74
255833_at	unknown protein	---	AT2G33390	1.26	0.33	2.56	0.038617	0.110798	-4.74
249774_at	squalene monooxygenase	SQP1	AT5G24150	-1.44	-0.53	-2.56	0.038629	0.110819	-4.74
246623_at	nuM1 protein, putative similar to nuM1	ATNUC-L1	AT1G48920	1.32	0.40	2.56	0.038665	0.11087	-4.74
260572_at	putative molybdopterin synthase large	---	AT2G43760	-1.20	-0.27	-2.56	0.038656	0.11087	-4.74
266487_at	hypothetical protein predicted by gens	---	AT2G47660	1.17	0.23	2.56	0.038658	0.11087	-4.74
255822_at	putative expansin ;supported by full-le	ATEXPA8	AT2G40610	-5.11	-2.35	-2.56	0.038671	0.11087	-4.74
256188_at	unknown protein similar to hypothetica	---	AT1G30160	1.49	0.57	2.56	0.038666	0.11087	-4.74
265153_at	unusual floral organ (UFO), AtFBX1 a	UFO	AT1G30950	-1.25	-0.32	-2.56	0.038679	0.11088	-4.74
261202_at	flower pigmentation protein ATAN11 i	ATAN11	AT1G12910	-1.24	-0.31	-2.56	0.038782	0.111161	-4.74
254897_at	serine/threonine kinase-like protein re	---	AT4G11470	1.84	0.88	2.56	0.038817	0.111241	-4.74
247583_at	putative protein predicted protein, Syn	---	AT5G60750	1.22	0.28	2.56	0.038825	0.111241	-4.74
245956_s_	luminal binding protein ; supported by	BIP2	AT5G28540 /	1.90	0.93	2.56	0.03882	0.111241	-4.74
258335_at	unknown protein	---	AT3G16020	-1.19	-0.25	-2.56	0.038836	0.111259	-4.74
260562_at	putative protein kinase contains a prot	---	AT2G43850	-1.33	-0.41	-2.56	0.038854	0.111296	-4.74
265148_at	unknown protein	---	AT1G51160	-1.23	-0.30	-2.56	0.038873	0.111337	-4.74
245881_at	putative protein	---	AT5G09460 /	1.37	0.46	2.56	0.038913	0.111438	-4.74
258874_at	hypothetical protein similar to unknowr	---	AT3G03230	-1.29	-0.37	-2.56	0.038932	0.111478	-4.74
266221_at	putative nucleotide-sugar dehydratase	UXS6	AT2G28760	2.55	1.35	2.56	0.038938	0.111483	-4.74
250907_at	putative protein predicted proteins, Ar	---	AT5G03670	1.20	0.27	2.56	0.038968	0.111554	-4.75
266127_s_	putative mitochondrial translation elon	---	AT1G45332 /	1.33	0.42	2.56	0.038987	0.11158	-4.75
262741_at	hypothetical protein	---	AT1G28760	1.20	0.26	2.56	0.039002	0.11158	-4.75
259462_at	hypothetical protein contains similarity	---	AT1G18940	-1.33	-0.41	-2.56	0.038984	0.11158	-4.75
251757_at	Ca-dependent solute carrier - like prot	---	AT3G55640	1.36	0.45	2.56	0.038999	0.11158	-4.75
245530_at	splicing factor like protein	---	---	1.26	0.33	2.56	0.039002	0.11158	-4.75
266324_at	putative rac GTPase activating protein	---	AT2G46710	-2.07	-1.05	-2.56	0.039007	0.11158	-4.75
246176_at	putative protein DYNAMIN-LIKE PRO	---	AT5G28410	1.19	0.25	2.56	0.03902	0.111604	-4.75
248037_at	sexual differentiation process protein I	OPT1	AT5G55930	1.63	0.71	2.56	0.039069	0.111728	-4.75
247337_at	putative protein similar to unknown pro	PDF2.5	AT5G63660	-1.18	-0.24	-2.56	0.039073	0.111728	-4.75
253548_at	Expressed protein ; supported by full-l	---	AT4G30993	-1.33	-0.41	-2.55	0.039124	0.111859	-4.75

266562_at	unknown protein	---	AT2G23970	1.34	0.43	2.55	0.039152	0.111926	-4.75
250361_at	putative protein various predicted prot	---	AT5G11370	-1.19	-0.25	-2.55	0.03921	0.112079	-4.75
259160_at	unknown protein	---	AT3G05410	-1.25	-0.32	-2.55	0.039218	0.112085	-4.75
266089_at	hypothetical protein predicted by gens	---	AT2G38010	-1.50	-0.59	-2.55	0.039241	0.112124	-4.75
263111_s_	hypothetical protein contains similarity	---	AT1G65190 /	1.34	0.42	2.55	0.03924	0.112124	-4.75
263729_at	hypothetical protein predicted by gene	---	AT1G60080	1.18	0.23	2.55	0.039259	0.112149	-4.75
260738_at	hypothetical protein predicted by gene	---	AT1G14990	1.21	0.27	2.55	0.039264	0.112149	-4.75
250696_at	putative protein similar to unknown pro	---	AT5G06790	-1.16	-0.22	-2.55	0.039261	0.112149	-4.75
247106_at	WD repeat protein-like ;supported by f	---	AT5G66240	1.25	0.32	2.55	0.039275	0.112166	-4.75
254061_at	putative protein several hypothetical pr	---	AT4G25360	-1.23	-0.30	-2.55	0.03935	0.112295	-4.76
266460_at	unknown protein ; supported by cDNA	AGP26	AT2G47930	-4.01	-2.00	-2.55	0.039328	0.112295	-4.75
260017_at	hypothetical protein predicted by gene	---	---	1.39	0.48	2.55	0.039348	0.112295	-4.76
260118_s_	hypothetical protein predicted by gens	---	AT1G33940 /	-1.31	-0.38	-2.55	0.039337	0.112295	-4.75
259400_at	receptor-like protein kinase, putative s	---	AT1G17750	2.48	1.31	2.55	0.039345	0.112295	-4.76
248788_at	DNA-binding protein-like	---	AT5G47430	1.19	0.25	2.55	0.039344	0.112295	-4.76
260024_at	beta-1,3-glucanase precursor, putativ	---	AT1G30080	-1.17	-0.23	-2.55	0.039379	0.112349	-4.76
261444_at	hypothetical protein predicted by gene	SYP61	AT1G28490	-1.22	-0.28	-2.55	0.039375	0.112349	-4.76
261068_at	tropinone reductase-I, putative similar	---	AT1G07450	-1.23	-0.30	-2.55	0.039403	0.112405	-4.76
256714_at	cysteine proteinase contains similarity	---	AT2G34080	1.26	0.33	2.55	0.039416	0.112427	-4.76
251868_at	RNA polymerase 24kDa subunit -like	RPB5E	AT3G54490	1.24	0.31	2.55	0.039432	0.112458	-4.76
249753_at	putative protein similar to unknown pro	---	AT5G24610	-1.18	-0.23	-2.55	0.039542	0.112759	-4.76
252017_at	cytochrome P450 - like protein cytoch	CYP76G1	AT3G52970	1.24	0.31	2.55	0.039555	0.112766	-4.76
247362_at	putative protein strong similarity to unk	ATPAP29	AT5G63140	-1.44	-0.53	-2.55	0.039552	0.112766	-4.76
266945_at	hypothetical protein predicted by gene	VEL2	AT2G18880	1.20	0.26	2.55	0.039562	0.112773	-4.76
256111_at	unknown protein	---	AT1G16820	-1.27	-0.35	-2.55	0.03957	0.112783	-4.76
253892_at	hypothetical protein ;supported by full-	---	AT4G27620	-1.21	-0.28	-2.55	0.03961	0.11288	-4.76
250238_at	unknown protein	DCP2	AT5G13570	-1.21	-0.28	-2.55	0.039617	0.112889	-4.76
253783_at	putative protein predicted protein, Ara	NPGR2	AT4G28600	1.24	0.31	2.55	0.039637	0.112931	-4.76
266253_at	unknown protein contains non-consens	HDT4	AT2G27840	1.50	0.58	2.54	0.039673	0.113019	-4.76
247087_at	putative protein contains similarity to e	---	AT5G66330	-1.45	-0.54	-2.54	0.039689	0.113049	-4.76
255264_at	putative protein ethylene responsive E	---	AT4G05170	-1.25	-0.32	-2.54	0.039735	0.113148	-4.77
250800_at	ubiquinol-cytochrome C reductase con	HPR	AT1G68010 /	1.58	0.66	2.54	0.039738	0.113148	-4.77
262289_at	unknown protein identical to unknown	---	AT1G70770	1.20	0.26	2.54	0.039731	0.113148	-4.77
259278_at	hypothetical protein predicted by gens	---	AT3G01160	1.26	0.33	2.54	0.039745	0.113152	-4.77
259785_at	unknown protein ;supported by full-len	---	AT1G29490	-1.27	-0.35	-2.54	0.039774	0.113222	-4.77

253427_at	putative protein phosphate/phosphoer	---	AT4G32390	-1.21	-0.28	-2.54	0.039855	0.113437	-4.77
262391_at	geranyl geranyl pyrophosphate syntha	GGPS6	AT1G49530	-1.24	-0.31	-2.54	0.039872	0.113471	-4.77
257121_at	hypothetical protein similar to auxin-inc	---	AT3G20220	-1.23	-0.30	-2.54	0.039879	0.113479	-4.77
258931_at	hypothetical protein similar to hypothe	DML2	AT3G10010	1.41	0.50	2.54	0.039887	0.113485	-4.77
267289_at	putative protein kinase contains a prot	---	AT2G23770	1.19	0.25	2.54	0.039891	0.113485	-4.77
249582_at	calmodulin 1 (CAM1) ; supported by c	CAM1	AT5G37780	1.28	0.36	2.54	0.039932	0.113587	-4.77
263210_at	Expressed protein ; supported by cDN	---	AT1G10585	6.03	2.59	2.54	0.039983	0.113717	-4.77
266643_s_	putative flavonol 3-O-glucosyltransfera	---	AT2G29710 /	-1.31	-0.39	-2.54	0.039999	0.113735	-4.77
251311_at	FUSCA PROTEIN FUS6 ; supported b	FUS6	AT3G61140	1.21	0.28	2.54	0.039997	0.113735	-4.77
255277_at	putative homeotic protein ; supported	PDF2	AT4G04890	-1.32	-0.40	-2.54	0.040015	0.113766	-4.77
255258_at	contains similarity to Arabidopsis thalia	---	AT4G05060	-1.25	-0.32	-2.54	0.040037	0.113801	-4.77
265416_at	unknown protein ; supported by full-le	---	AT2G37120	-1.61	-0.69	-2.54	0.040034	0.113801	-4.77
251958_at	putative protein predicted proteins, Ar	---	AT3G53560	-1.47	-0.55	-2.54	0.040046	0.11381	-4.77
265601_at	hypothetical protein predicted by gens	---	AT2G14390	1.23	0.30	2.54	0.040057	0.113829	-4.77
264775_at	putative endo-1,4-beta-D-glucanase s	CEL5	AT1G22880	-1.28	-0.36	-2.54	0.040084	0.113892	-4.77
256876_at	hypothetical protein predicted by gene	---	AT3G26360	-1.16	-0.22	-2.54	0.040096	0.113912	-4.77
251675_at	helicase-like protein DNA helicase YG	INO80	AT3G57300	1.19	0.25	2.54	0.040143	0.11403	-4.78
258784_at	unknown protein	---	AT3G11770	-1.41	-0.50	-2.54	0.040177	0.114098	-4.78
259933_at	Expressed protein ; supported by full-le	---	AT1G34350	-1.30	-0.38	-2.54	0.040174	0.114098	-4.78
255452_at	hypothetical protein similar to A. thalia	---	AT4G02880	1.20	0.26	2.54	0.040225	0.114214	-4.78
252606_at	carboxypeptidase precursor-like prote	scpl48	AT3G45010	1.70	0.76	2.54	0.040228	0.114214	-4.78
256696_at	unknown protein	---	AT3G20650	1.21	0.27	2.53	0.040296	0.114387	-4.78
266788_at	putative receptor-like protein kinase	---	AT2G29000	-1.17	-0.23	-2.53	0.040299	0.114387	-4.78
260540_at	hypothetical protein predicted by gene	---	AT2G43500	1.19	0.25	2.53	0.040342	0.114495	-4.78
246457_at	WD40-repeat protein transducin homo	TOZ	AT5G16750	1.24	0.31	2.53	0.040355	0.114518	-4.78
247204_at	GTP binding protein-like	AtRABH1a	AT5G64990	1.24	0.32	2.53	0.040395	0.114613	-4.78
253643_at	hypothetical protein ;supported by full-	---	AT4G29780	2.07	1.05	2.53	0.040398	0.114613	-4.78
255604_at	hypothetical protein	---	AT4G01080	-1.37	-0.45	-2.53	0.040435	0.114692	-4.78
264374_at	putative two-component response reg	ARR12	AT2G25180	-1.23	-0.30	-2.53	0.040436	0.114692	-4.78
247044_at	MAP protein kinase ; supported by cD	MAPKKK5	AT5G66850	1.31	0.39	2.53	0.040503	0.114865	-4.79
265543_at	unknown protein	---	AT2G28270	-1.17	-0.22	-2.53	0.040543	0.114966	-4.79
255304_at	putative potassium transporter similar	KEA3	AT4G04850	-1.41	-0.49	-2.53	0.040556	0.114981	-4.79
247544_at	putative protein ;supported by full-leng	---	AT5G61670	1.33	0.41	2.53	0.040558	0.114981	-4.79
252076_at	LS1-like protein AT-LS1 product - Ara	---	AT3G51660	1.73	0.79	2.53	0.040579	0.115026	-4.79
266869_at	putative glucosyltransferase	---	AT2G44660	-1.37	-0.46	-2.53	0.04059	0.115042	-4.79

259273_s_	serine/threonine specific protein kinas	---	AT3G01300 /	1.22	0.29	2.53	0.040602	0.115048	-4.79
260465_at	membrane-associated salt-inducible pr	---	AT1G10910	-1.17	-0.22	-2.53	0.040601	0.115048	-4.79
257271_at	Expressed protein ; supported by full-le	---	AT3G28007	-1.90	-0.93	-2.53	0.040636	0.115129	-4.79
261424_at	unknown protein	---	AT1G18700	-1.17	-0.23	-2.53	0.040643	0.115135	-4.79
250085_at	unknown protein	---	AT5G17250	-1.30	-0.38	-2.53	0.040653	0.11515	-4.79
265482_at	hypothetical protein contains a domain	---	AT2G15780	4.75	2.25	2.53	0.040697	0.115259	-4.79
267173_at	origin recognition complex protein iden	ORC2	AT2G37560	-1.41	-0.50	-2.53	0.040795	0.115511	-4.79
258948_at	putative sulfite oxidase similar to sulfite	SOX	AT3G01910	1.19	0.26	2.53	0.040796	0.115511	-4.79
266326_at	putative cytochrome b5 ;supported by	CB5-C	AT2G46650	2.08	1.05	2.53	0.040805	0.115523	-4.79
261031_at	hypothetical protein predicted by gene	---	AT1G17360	-1.49	-0.57	-2.53	0.040821	0.115553	-4.79
252355_at	putative protein various predicted prot	---	AT3G48250	1.22	0.28	2.52	0.040858	0.115608	-4.79
263766_at	hypothetical protein predicted by gens	---	AT2G21440	1.31	0.39	2.52	0.040861	0.115608	-4.79
259714_at	putative gibberellin 20-oxidase similar	ATGA20OX4	AT1G60980	1.24	0.31	2.52	0.040849	0.115608	-4.79
250184_at	putative protein various predicted prot	---	AT5G14240	-1.20	-0.27	-2.52	0.04086	0.115608	-4.79
267486_at	putative protein kinase contains a prot	APK2B	AT2G02800	1.36	0.45	2.52	0.040873	0.11563	-4.79
254277_at	myb-like protein myb-related transcrip	MYB85	AT4G22680	1.92	0.94	2.52	0.040905	0.115706	-4.80
265850_at	putative DnaJ protein	---	AT2G35720	1.32	0.40	2.52	0.040932	0.115739	-4.80
245407_at	GTP-binding RAB2A like protein	RABB1C	AT4G17170	-1.22	-0.28	-2.52	0.040925	0.115739	-4.80
263166_at	putative protein destination factor Simi	---	AT1G03050	1.18	0.24	2.52	0.040929	0.115739	-4.80
255381_at	RMA1 RING zinc finger protein identic	RMA1	AT4G03510	-1.48	-0.56	-2.52	0.040946	0.115764	-4.80
261614_at	poly(A)-binding protein, putative simila	PAB8	AT1G49760	-1.32	-0.41	-2.52	0.04098	0.115845	-4.80
248229_at	caffeic acid 3-O-methyltransferase-like	---	AT5G53810	-1.28	-0.36	-2.52	0.040985	0.115846	-4.80
267516_at	unknown protein	RPT2	AT2G30520	-1.27	-0.34	-2.52	0.041027	0.115951	-4.80
251817_at	small GTP-binding protein - like (fragn	ARA6	AT3G54840	1.20	0.26	2.52	0.041039	0.115968	-4.80
250508_at	selenium-binding protein-like	---	AT5G09950	1.22	0.29	2.52	0.041051	0.115988	-4.80
246960_at	unknown protein	---	AT5G24710	-1.20	-0.27	-2.52	0.041072	0.116032	-4.80
246410_at	hypothetical protein predicted by gene	---	AT1G57760	-1.19	-0.25	-2.52	0.041091	0.116073	-4.80
258991_at	unknown protein contains Pfam profile	---	AT3G08820	1.23	0.30	2.52	0.041102	0.11609	-4.80
248684_at	Expressed protein ; supported by full-le	DIR1	AT5G48485	1.80	0.85	2.52	0.041116	0.116101	-4.80
251939_at	putative protein MICRONUCLEAR LIN	---	AT3G53440	-1.35	-0.44	-2.52	0.041111	0.116101	-4.80
266812_at	putative protein kinase contains a prot	---	AT2G44830	-1.31	-0.39	-2.52	0.041133	0.116111	-4.80
263833_at	hypothetical protein	---	AT2G40316	-1.19	-0.25	-2.52	0.041138	0.116111	-4.80
247111_at	unknown protein	---	AT5G65880	-1.38	-0.47	-2.52	0.04113	0.116111	-4.80
267010_at	putative AP2 domain transcription fact	SNZ	AT2G39250	-1.29	-0.36	-2.52	0.04114	0.116111	-4.80
257035_at	cytochrome P450, putative similar to c	CYP707A4	AT3G19270	1.25	0.33	2.52	0.041187	0.116227	-4.80

256334_at	oligopeptide transporter, putative simi	---	AT1G72120 /	1.34	0.42	2.52	0.041227	0.116326	-4.80
258959_at	putative amino acid transporter similar	CAT7	AT3G10600	-1.22	-0.28	-2.52	0.041274	0.116438	-4.80
257651_at	polygalacturonase, putative similar to	---	AT3G16850	-1.50	-0.58	-2.52	0.041277	0.116438	-4.80
247370_at	putative protein similar to unknown pro	---	AT5G63320	1.47	0.55	2.52	0.041283	0.116443	-4.80
259496_at	hypothetical protein predicted by gens	---	AT1G15900	-1.22	-0.29	-2.52	0.041334	0.116572	-4.81
247858_at	similar to unknown protein (pir||T34863	TTL	AT5G58220	-1.25	-0.32	-2.52	0.041374	0.116669	-4.81
258893_at	putative disease resistance protein sim	AtRLP33	AT3G05660	-2.04	-1.03	-2.52	0.041395	0.116714	-4.81
248049_at	putative protein contains similarity to c	COX15	AT5G56090	1.56	0.64	2.52	0.04141	0.116744	-4.81
257201_at	unknown protein	---	AT3G23740	-1.26	-0.33	-2.51	0.041418	0.116749	-4.81
246094_at	putative protein predicted proteins, H.	---	AT5G19300	1.39	0.47	2.51	0.041443	0.116796	-4.81
258869_at	hypothetical protein similar to xylose tr	AtVGT1	AT3G03090	-1.27	-0.34	-2.51	0.041444	0.116796	-4.81
266572_at	unknown protein	---	AT2G23840	1.35	0.43	2.51	0.041458	0.116817	-4.81
265447_at	putative laccase (diphenol oxidase)	LAC6	AT2G46570	-1.28	-0.36	-2.51	0.041462	0.116817	-4.81
251160_at	inositol-1,4,5-trisphosphate 5-Phospha	---	AT3G63240	-1.24	-0.31	-2.51	0.041481	0.116857	-4.81
267558_at	unknown protein ; supported by cDNA	LUH	AT2G32700	-1.20	-0.26	-2.51	0.041546	0.117024	-4.81
255225_at	U3 snoRNP-associated -like protein U	---	AT4G05410	1.58	0.66	2.51	0.041562	0.117056	-4.81
257208_at	hypothetical protein predicted by gens	---	AT3G14910	-1.33	-0.41	-2.51	0.04157	0.117064	-4.81
254852_at	putative disease resistance protein DI	WRKY19	AT4G12020	-1.17	-0.23	-2.51	0.041586	0.117078	-4.81
257411_s_	hypothetical protein predicted by gene	---	AT1G61320 /	1.17	0.23	2.51	0.041584	0.117078	-4.81
251506_at	putative protein ; supported by cDNA:	---	AT3G59090	-1.18	-0.23	-2.51	0.041609	0.117129	-4.81
258376_at	hypothetical protein similar to GB:AAD	---	AT3G17680	-1.19	-0.25	-2.51	0.041616	0.117135	-4.81
258216_at	unknown protein contains Pfam profile	---	AT3G17980	1.29	0.37	2.51	0.041625	0.117145	-4.81
249973_at	GPAA1 - like protein glycosylphospha	---	AT5G19130	-1.25	-0.32	-2.51	0.041662	0.117235	-4.81
263122_at	prenyltransferase, putative similar to p	SPS1	AT1G78510	1.27	0.35	2.51	0.041687	0.117281	-4.81
252635_at	putative protein predicted proteins, Ar	---	AT3G44510	1.26	0.33	2.51	0.041689	0.117281	-4.81
246295_at	calmodulin-binding protein ; supported	CIP111	AT3G56690	1.30	0.38	2.51	0.041741	0.117401	-4.82
262251_at	hypothetical protein predicted by gene	---	AT1G53760	1.43	0.52	2.51	0.041742	0.117401	-4.82
252877_at	hypothetical protein supported by full-l	---	AT4G39630	-1.24	-0.32	-2.51	0.041752	0.117403	-4.82
250910_at	heat shock transcription factor -like pr	HSFA3	AT5G03720	-1.82	-0.87	-2.51	0.041752	0.117403	-4.82
264444_at	putative squamosa-promoter binding p	---	AT1G27360	1.21	0.28	2.51	0.041758	0.117404	-4.82
252806_at	putative protein	---	AT3G42390	1.22	0.28	2.51	0.041787	0.117458	-4.82
251574_at	putative protein GLUCAN ENDO-1,3-	PDCB5	AT3G58100	-1.26	-0.33	-2.51	0.041785	0.117458	-4.82
248618_at	myb-related transcription factor	AtMYB78	AT5G49620	1.26	0.33	2.51	0.041804	0.11749	-4.82
263512_at	hypothetical protein predicted by gene	---	---	-1.20	-0.26	-2.51	0.041818	0.117514	-4.82
247268_at	putative protein contains similarity to n	---	AT5G64080	-1.29	-0.37	-2.51	0.041865	0.117633	-4.82

250312_at	unknown protein	---	AT5G12260	-1.25	-0.33	-2.51	0.041872	0.117636	-4.82
267500_s_	putative cytochrome P450	CYP704A1	AT2G44890 /	1.39	0.47	2.51	0.041884	0.117657	-4.82
253032_at	guanine nucleotide-exchange protein	---	AT4G38200	-1.20	-0.26	-2.51	0.041893	0.117667	-4.82
264069_at	putative rubisco subunit binding-protei	CPN60A	AT2G28000	-1.37	-0.45	-2.51	0.0419	0.117673	-4.82
266609_at	unknown protein ; supported by cDNA	SRO1	AT2G35510	1.32	0.40	2.51	0.041911	0.117688	-4.82
251616_at	putative protein	---	AT3G57990	-1.19	-0.25	-2.51	0.041963	0.117821	-4.82
259997_at	unknown protein similar to N-acetylglu	---	AT1G67880	1.55	0.63	2.50	0.042022	0.117971	-4.82
251723_at	putative protein speckle-type protein,	---	AT3G56230	-1.27	-0.34	-2.50	0.042033	0.117988	-4.82
253321_at	putative protein prolyl 4-hydroxylase a	---	AT4G33910	1.20	0.27	2.50	0.042062	0.118035	-4.82
253220_s_	putative protein phospholipase C, List	---	AT4G34920 /	1.32	0.40	2.50	0.042066	0.118035	-4.82
251404_at	putative protein	---	AT3G60310	-1.24	-0.31	-2.50	0.04207	0.118035	-4.82
254446_at	tubulin beta-9 chain ;supported by full	TUB9	AT4G20890	-1.19	-0.25	-2.50	0.042061	0.118035	-4.82
263033_s_	unknown protein ; supported by full-ler	---	AT1G23950 /	-1.37	-0.46	-2.50	0.042082	0.118054	-4.82
252261_at	RNA-directed RNA polymerase RNA-d	RDR6	AT3G49500	-1.25	-0.32	-2.50	0.042116	0.118133	-4.83
264349_at	putative Proline synthetase associated	---	AT1G11930	1.16	0.22	2.50	0.042124	0.118143	-4.83
246139_at	putative protein predicted protein, Dro	---	AT5G19900	1.26	0.34	2.50	0.042139	0.118168	-4.83
246311_at	high mobility group protein 2-like ; sup	HMGB1	AT3G51880	1.25	0.32	2.50	0.042159	0.118196	-4.83
267063_at	hypothetical protein predicted by gene	---	AT2G41120	1.31	0.39	2.50	0.042154	0.118196	-4.83
263119_at	hypothetical protein predicted by gene	---	AT1G03110	-1.33	-0.41	-2.50	0.042179	0.118238	-4.83
261591_at	protein kinase, putative similar to prot	---	AT1G01740	1.31	0.39	2.50	0.042193	0.118262	-4.83
253186_at	putative protein predicted proteins, Ar	---	AT4G35270	1.33	0.41	2.50	0.042203	0.118276	-4.83
266213_s_	Mutator-like transposase similar to MU	---	---	1.22	0.29	2.50	0.042258	0.118417	-4.83
247924_at	Expressed protein	---	AT5G57655	1.53	0.62	2.50	0.042273	0.118445	-4.83
259250_at	unknown protein	---	AT3G07580	1.37	0.45	2.50	0.042287	0.118468	-4.83
249979_s_	putative protein	---	AT5G18860 /	-1.62	-0.70	-2.50	0.04233	0.118568	-4.83
256817_at	F-box protein family, AtFBW1 contains	---	AT3G21410	-1.26	-0.33	-2.50	0.042333	0.118568	-4.83
254997_s_	putative protein various predicted prot	---	AT4G09920 /	-1.20	-0.26	-2.50	0.042357	0.11862	-4.83
246347_at	putative protein probable chloroplast a	---	AT3G56830	-1.22	-0.29	-2.50	0.042379	0.118668	-4.83
249994_at	putative protein cell polarity protein te	---	AT5G18590	-1.23	-0.30	-2.50	0.042402	0.118717	-4.83
264126_at	hypothetical protein predicted by gene	NUA	AT1G79280	1.18	0.24	2.50	0.042435	0.118796	-4.83
266711_at	unknown protein	---	AT2G46740	1.20	0.26	2.50	0.042446	0.11881	-4.83
266818_at	unknown protein	HUB1	AT2G44950	1.27	0.34	2.50	0.042471	0.118851	-4.83
265061_at	hypothetical protein contains similarity	---	AT1G61640	1.60	0.68	2.50	0.04247	0.118851	-4.83
261124_at	hypothetical protein predicted by gene	---	AT1G04900	1.22	0.28	2.50	0.042496	0.118864	-4.83
255487_at	tryptophan synthase alpha 1-like prote	---	AT4G02610	-1.25	-0.32	-2.50	0.042492	0.118864	-4.83

252212_at	protein kinase -like protein NTPK1 pro	MAPKKK20	AT3G50310	1.63	0.71	2.50	0.042493	0.118864	-4.83
261681_at	hypothetical protein similar to hypothet	---	AT1G47340	-1.38	-0.46	-2.50	0.042501	0.118864	-4.83
256596_at	hypothetical protein predicted by gene	---	AT3G28540	1.46	0.54	2.50	0.042501	0.118864	-4.83
255118_at	nitrilase 1 like protein nitrilase 1 - Mus	---	AT4G08790	-1.27	-0.34	-2.50	0.042509	0.11887	-4.83
258345_at	unknown protein	---	AT3G22845	1.21	0.27	2.50	0.042554	0.118983	-4.84
247328_at	unknown protein ;supported by full-ler	---	AT5G64130	-1.37	-0.45	-2.50	0.042567	0.119005	-4.84
254080_at	fibrillarin 2 (AtFib2) identical to fibrillari	FIB2	AT4G25630	1.77	0.82	2.50	0.042597	0.119058	-4.84
265580_at	putative protein phosphatase 2C	---	AT2G20050	-1.28	-0.35	-2.50	0.042592	0.119058	-4.84
265139_at	unknown protein	---	AT1G51310	1.27	0.34	2.50	0.042616	0.119098	-4.84
248767_at	putative protein contains similarity to G	---	AT5G47710	1.25	0.33	2.49	0.042627	0.119115	-4.84
264044_at	putative pyrophosphate--fructose-6-ph	PFK5	AT2G22480	1.22	0.28	2.49	0.042638	0.119119	-4.84
253863_at	putative protein D.melanogaster P ele	---	AT4G27420	1.26	0.33	2.49	0.042639	0.119119	-4.84
260654_at	hypothetical protein predicted by gene	---	AT1G19290	1.30	0.37	2.49	0.042655	0.119142	-4.84
249792_at	putative protein contains similarity to D	PHS1	AT5G23720	-1.20	-0.26	-2.49	0.042658	0.119142	-4.84
247851_at	outer membrane lipoprotein - like oute	TIL	AT5G58070	-1.52	-0.60	-2.49	0.042678	0.119184	-4.84
266957_at	unknown protein	PTAC12	AT2G34640	-1.27	-0.34	-2.49	0.042685	0.119188	-4.84
254574_at	expressed protein supported by cDNA	---	AT4G19430	2.24	1.17	2.49	0.042702	0.119221	-4.84
253624_at	putative protein 2-acylglycerophospho	ATS2	AT4G30580	-1.29	-0.37	-2.49	0.042866	0.119649	-4.84
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=gb:	---	---	-1.68	-0.75	-2.49	0.042861	0.119649	-4.84
255052_at	rab7 -like protein rab7 protein -Vigna a	ATRABG3A	AT4G09720	-1.25	-0.32	-2.49	0.042893	0.11971	-4.84
265826_at	hypothetical protein predicted by gene	---	AT2G35795	1.19	0.25	2.49	0.042974	0.119921	-4.85
257789_at	unknown protein ;supported by full-ler	YSL6	AT3G27020	1.38	0.46	2.49	0.043037	0.120068	-4.85
245573_at	hypothetical protein	---	AT4G14730	-1.18	-0.23	-2.49	0.043034	0.120068	-4.85
253156_at	putative protein mRNA for KIAA0174	---	AT4G35730	-1.25	-0.32	-2.49	0.043048	0.120071	-4.85
254860_at	putative C-4 sterol methyl oxidase C-4	SMO1-1	AT4G12110	-1.26	-0.33	-2.49	0.043049	0.120071	-4.85
260053_at	hypothetical protein similar to unknown	---	AT1G78120	-1.28	-0.36	-2.49	0.043085	0.120158	-4.85
265772_at	putative protein kinase contains a prot	RKF3	AT2G48010	1.30	0.37	2.49	0.043136	0.120286	-4.85
263877_at	hypothetical protein predicted by gene	---	AT2G21780	1.16	0.21	2.49	0.043142	0.120286	-4.85
265097_at	unknown protein	BARD1	AT1G04020	-1.36	-0.45	-2.49	0.043167	0.120343	-4.85
264945_at	MADS-box protein (MADS2), putative	MAF1	AT1G77080	-1.50	-0.59	-2.49	0.043193	0.120401	-4.85
248352_at	low-temperature-induced 65 kD protein	LTI65	AT5G52300	-1.99	-0.99	-2.48	0.043236	0.12049	-4.85
251565_at	putative protein several hypothetical pr	LBD29	AT3G58190	-1.19	-0.25	-2.49	0.043231	0.12049	-4.85
261578_at	acidic ribosomal protein, putative simi	---	AT1G01100	-1.30	-0.38	-2.48	0.043253	0.120523	-4.85
258030_at	hypothetical protein predicted by gene	---	AT3G27590	-1.26	-0.33	-2.48	0.043291	0.120614	-4.85
259331_at	putative auxin-induced protein similar t	---	AT3G03840	-1.31	-0.39	-2.48	0.043334	0.120718	-4.85

254826_at	putative protein predicted protein, Ara	---	AT4G12640	-1.27	-0.34	-2.48	0.0434	0.12089	-4.86
263064_at	putative bZIP transcription factor conta	CPuORF1	AT2G18160 /	1.32	0.41	2.48	0.043451	0.120962	-4.86
246436_at	putative protein cisplatin resistance-as	---	AT5G17440	1.18	0.24	2.48	0.043453	0.120962	-4.86
253600_at	SERINE CARBOXYPEPTIDASE II - li	scpl29	AT4G30810	-1.21	-0.28	-2.48	0.043449	0.120962	-4.86
250114_s_	AMP-binding protein	AAE5	AT5G16340 /	1.38	0.46	2.48	0.04345	0.120962	-4.86
251889_at	putative protein probable lectin 2 prec	---	AT3G54080	-1.50	-0.59	-2.48	0.043441	0.120962	-4.86
258184_at	two-component phosphorelay mediato	AHP1	AT3G21510	-1.32	-0.40	-2.48	0.043491	0.121038	-4.86
258481_at	putative phosphatidate phosphohydrol	LPP3	AT3G02600	-1.31	-0.39	-2.48	0.043487	0.121038	-4.86
258355_at	hypothetical protein predicted by gens	---	AT3G14330	-1.33	-0.42	-2.48	0.043501	0.121051	-4.86
267125_at	putative acetone-cyanohydrin lyase	MES4	AT2G23580	-1.18	-0.24	-2.48	0.043509	0.121058	-4.86
249652_at	putative protein hypothetical proteins -	---	AT5G37070	1.29	0.36	2.48	0.043533	0.121112	-4.86
254428_at	putative protein Human mRNA for KIA	ZAC	AT4G21160	1.21	0.28	2.48	0.043562	0.121176	-4.86
263470_at	putative unconventional myosin	XIF	AT2G31900	-1.20	-0.26	-2.48	0.043587	0.121231	-4.86
259745_at	unknown protein	SAG18	AT1G71190	1.24	0.31	2.48	0.043595	0.121238	-4.86
258587_at	hypothetical protein predicted by gens	---	AT3G04310	1.45	0.54	2.48	0.043616	0.121283	-4.86
264593_at	putative GTP-binding protein ; suppor	ARAC1	AT2G17800	-1.22	-0.29	-2.48	0.043635	0.121307	-4.86
254069_at	putative protein similarity to antisense	ATNUDT10	AT4G25434	1.32	0.40	2.48	0.043631	0.121307	-4.86
250755_at	DnaJ-like protein ; supported by cDNA	---	AT5G05750	-1.27	-0.35	-2.48	0.043656	0.121349	-4.86
257734_at	unknown protein contains Pfam profile	ATSYTF	AT3G18370	1.18	0.23	2.48	0.043691	0.121433	-4.86
261650_at	envelope Ca2+-ATPase identical to en	ACA1	AT1G27770	1.43	0.52	2.48	0.043699	0.121439	-4.86
245941_at	putative protein karyopherin beta 3 - H	emb2734	AT5G19820	-1.25	-0.32	-2.48	0.043719	0.12148	-4.86
245305_at	Expressed protein ; supported by full-le	---	AT4G17215	2.05	1.03	2.48	0.043732	0.121501	-4.86
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.37	-0.46	-2.48	0.043751	0.12154	-4.86
246583_at	protein kinase -like protein Ste-20 rela	---	AT5G14720	-1.27	-0.35	-2.48	0.043757	0.121541	-4.86
255629_at	stress-induced protein OZI1 precursor	ATOZI1	AT4G00860	1.36	0.44	2.48	0.043821	0.121705	-4.87
248556_at	unknown protein	---	AT5G50350	1.28	0.35	2.48	0.043827	0.121706	-4.87
253663_at	putative villin	VLN4	AT4G30160	1.23	0.30	2.48	0.043834	0.12171	-4.87
249038_at	putative protein contains similarity to u	RING1A	AT5G44280	1.24	0.31	2.48	0.043853	0.121749	-4.87
260489_at	hypothetical protein ; supported by cDI	---	AT1G51610	-1.21	-0.27	-2.47	0.043864	0.121763	-4.87
251767_at	putative protein U4/U6 small nuclear r	---	AT3G55930	1.17	0.23	2.47	0.043915	0.121892	-4.87
250076_at	putative protein; similar to unknown pr	---	AT5G16660	-1.25	-0.32	-2.47	0.043935	0.121932	-4.87
254425_at	putative membrane associated protein	---	AT4G21450	1.18	0.24	2.47	0.043978	0.122037	-4.87
267358_at	proline transporter 1 ;supported by ful	PROT1	AT2G39890	1.27	0.35	2.47	0.04403	0.122167	-4.87
251736_at	putative protein acetyl-CoA carboxyla	---	AT3G56130	-1.42	-0.51	-2.47	0.044049	0.122188	-4.87
261054_at	hypothetical protein predicted by gene	---	AT1G01320	1.46	0.55	2.47	0.044047	0.122188	-4.87

259969_at	putative pyrophosphate-dependent ph	---	AT1G76550	1.55	0.63	2.47	0.044071	0.122236	-4.87
265672_at	putative cysteine proteinase inhibitor B	---	AT2G31980	-2.15	-1.11	-2.47	0.044078	0.122239	-4.87
248505_at	putative protein similar to unknown pro	---	AT5G50360	1.27	0.34	2.47	0.044114	0.122325	-4.87
247704_at	Expressed protein ; supported by full-l	RTFL5	AT5G59510	1.71	0.78	2.47	0.044173	0.122474	-4.87
260630_at	subtilisin-like serine protease contains	ALE1	AT1G62340	-1.30	-0.38	-2.47	0.04422	0.122574	-4.88
260446_at	unknown protein	---	AT1G72420	-1.24	-0.31	-2.47	0.044218	0.122574	-4.88
265389_at	putative riboflavin synthase alpha chai	---	AT2G20690	1.25	0.33	2.47	0.044239	0.122612	-4.88
256459_at	acetyl-CoA carboxylase, putative simi	ACC2	AT1G36180	-1.28	-0.36	-2.47	0.044272	0.122687	-4.88
260847_s_	alanine aminotransferase, putative sir	AlaAT1	AT1G17290 /	1.21	0.28	2.47	0.044288	0.122718	-4.88
252358_at	putative protein cfxY protein, Alcaliger	---	AT3G48425	-1.20	-0.26	-2.47	0.044308	0.122759	-4.88
261986_s_	cytochrome P450, putative similar to C	CYP76C5	AT1G33720 /	-1.72	-0.78	-2.47	0.044328	0.122799	-4.88
251867_at	SKP1 interacting partner 5 (SKIP5)	SKIP5	AT3G54480	1.19	0.25	2.47	0.04436	0.122871	-4.88
246901_at	putative protein Leaf protein, Pharbitis	---	AT5G25630	-1.21	-0.27	-2.47	0.04439	0.122924	-4.88
263762_at	putative kinesin heavy chain ; support	---	AT2G21380	-1.37	-0.46	-2.47	0.044386	0.122924	-4.88
267420_at	hypothetical protein predicted by grail	---	AT2G35030	1.50	0.58	2.47	0.0444	0.122937	-4.88
256682_at	putative protein dihydrolipoamide S-ac	LTA3	AT3G52200	1.18	0.24	2.47	0.044408	0.122945	-4.88
255874_at	hypothetical protein predicted by gens	ETG1	AT2G40550	-1.86	-0.89	-2.47	0.044416	0.122954	-4.88
267400_at	unknown protein	---	AT2G26240	1.29	0.37	2.47	0.044452	0.123022	-4.88
256868_at	eukaryotic translation initiation factor 4	EIF4B1	AT3G26400	1.41	0.50	2.47	0.044452	0.123022	-4.88
267157_at	putative MYB family transcription facto	AS1	AT2G37630	1.37	0.45	2.47	0.044463	0.123023	-4.88
261064_at	unknown protein	ftsh10	AT1G07510	1.27	0.35	2.47	0.044459	0.123023	-4.88
257240_at	monooxygenase, putatve contains Pfa	---	AT3G24200	1.20	0.27	2.47	0.044481	0.123058	-4.88
266592_at	putative fatty acid desaturase/cytochro	---	AT2G46210	-1.21	-0.27	-2.47	0.044492	0.123075	-4.88
252829_at	homeodomain - like protein ; supporte	ATHB16	AT4G40060	-1.28	-0.35	-2.46	0.044507	0.123101	-4.88
266707_at	hypothetical protein predicted by gens	---	AT2G03310	-1.20	-0.27	-2.46	0.044514	0.123105	-4.88
260687_at	inner mitochondrial membrane protein	ATTIM23-1	AT1G17530	1.35	0.43	2.46	0.044549	0.123186	-4.88
260428_at	putative translation initiation factor EIF	---	AT1G72340	-1.31	-0.39	-2.46	0.044555	0.123187	-4.88
250448_at	putative protein lignostilbene-alpha,be	---	AT5G10820	1.41	0.49	2.46	0.044563	0.123195	-4.88
267004_at	hypothetical protein predicted by gene	---	AT2G34260	1.83	0.87	2.46	0.044664	0.123459	-4.89
246954_at	unknown protein ; supported by cDNA	---	AT5G04830	1.18	0.24	2.46	0.044672	0.123466	-4.89
263113_at	unknown protein Belongs to PF|00583	---	AT1G03150	-1.18	-0.23	-2.46	0.044722	0.12359	-4.89
248349_at	progesterone-binding protein-like ; su	MSBP1	AT5G52240	1.31	0.39	2.46	0.044734	0.123592	-4.89
256289_s_	serine carboxypeptidase, putative con	scpl14	AT3G12230 /	1.63	0.71	2.46	0.044733	0.123592	-4.89
258927_at	putative folylpolyglutamate synthetase	DFC	AT3G10160	-1.21	-0.27	-2.46	0.044766	0.123655	-4.89
260482_at	endomembrane protein EMP70 precus	---	AT1G10950	-1.21	-0.28	-2.46	0.044767	0.123655	-4.89

250073_at	unknown protein ; supported by cDNA	ENH1	AT5G17170	1.51	0.59	2.46	0.0448	0.123729	-4.89
245641_at	Expressed protein ; supported by full-le	---	AT1G25370	2.21	1.15	2.46	0.044895	0.123979	-4.89
256452_at	hypothetical protein predicted by gene	AtHB33	AT1G75240	-2.00	-1.00	-2.46	0.044904	0.123988	-4.89
250074_at	UDP-glucose pyrophosphorylase ; sup	---	AT5G17310	-1.32	-0.40	-2.46	0.044938	0.124068	-4.89
252734_at	putative protein merozoite surface pro	MEE38	AT3G43160	1.22	0.29	2.46	0.044966	0.1241	-4.89
248518_at	putative protein similar to unknown pro	---	AT5G50560 /	1.35	0.44	2.46	0.044965	0.1241	-4.89
263496_at	unknown protein ; supported by full-le	---	AT2G42570	-1.30	-0.38	-2.46	0.044957	0.1241	-4.89
251008_at	putative protein ;supported by full-leng	---	AT5G02710	-1.26	-0.34	-2.46	0.044995	0.124164	-4.89
264644_at	hypothetical protein Similar to Caenorh	CAX11	AT1G08960	-1.25	-0.33	-2.46	0.04503	0.124244	-4.89
253755_at	26S proteasome subunit 4-like protein	RPT2a	AT4G29040	1.22	0.29	2.46	0.045041	0.12426	-4.89
251581_at	putative protein CARBON CATABOLI	---	AT3G58560	1.26	0.33	2.46	0.045057	0.12429	-4.89
255836_at	putative splicing factor U2AF large cha	---	AT2G33440	1.31	0.39	2.46	0.045103	0.1244	-4.90
264045_at	putative GTP cyclohydrolase	---	AT2G22450	-1.20	-0.26	-2.46	0.045117	0.12442	-4.90
265481_at	unknown protein ; supported by cDNA	---	AT2G15960	1.23	0.30	2.46	0.045121	0.12442	-4.90
252009_at	zinc finger - like protein zinc finger pro	---	AT3G52800	1.34	0.42	2.46	0.045134	0.124441	-4.90
262751_at	hypothetical protein predicted by gens	---	AT1G16310	1.19	0.25	2.45	0.045173	0.124534	-4.90
250626_at	putative protein p100 co-activator - Mu	---	AT5G07350	1.22	0.28	2.45	0.04521	0.124622	-4.90
250236_at	delta subunit of mitochondrial F1-ATPa	---	AT5G13450	1.25	0.32	2.45	0.045222	0.124639	-4.90
260135_at	calmodulin-related protein similar to G	---	AT1G66400	1.89	0.92	2.45	0.045245	0.124688	-4.90
254255_at	serine/threonine kinase - like protein s	---	AT4G23220	1.71	0.77	2.45	0.045268	0.124736	-4.90
260433_at	MtN21-like protein similar to MtN21 GE	---	AT1G68170	-1.24	-0.31	-2.45	0.045275	0.12474	-4.90
255687_at	hypothetical protein	KEA2	AT4G00630	1.48	0.56	2.45	0.045286	0.124756	-4.90
245581_at	hypothetical protein	---	AT4G14840	-1.26	-0.33	-2.45	0.045329	0.124858	-4.90
249816_at	cleavage and polyadenylation specifici	CPSF100	AT5G23880	-1.30	-0.38	-2.45	0.045349	0.1249	-4.90
248228_at	unknown protein ;supported by full-ler	---	AT5G53800	1.30	0.38	2.45	0.04539	0.124998	-4.90
259340_at	hypothetical protein predicted using ge	PYK10	AT3G03870 /	1.25	0.32	2.45	0.04541	0.125036	-4.90
257952_at	putative peroxidase almost identical to	---	AT3G21770	-1.34	-0.42	-2.45	0.04543	0.125076	-4.90
252171_at	hypothetical protein ; supported by cD	---	AT3G50590	-1.21	-0.27	-2.45	0.04544	0.125089	-4.90
262247_at	unknown protein contains similarity to	D-CDES	AT1G48420	-1.21	-0.27	-2.45	0.045455	0.125114	-4.90
266246_at	putative cytochrome P450	CYP94C1	AT2G27690	-1.83	-0.87	-2.45	0.045497	0.125185	-4.90
264710_at	putative phytochelatin synthetase simil	COBL6	AT1G09790	-1.21	-0.27	-2.45	0.045496	0.125185	-4.90
259353_at	putative branched-chain amino acid ar	---	AT3G05190	-1.18	-0.24	-2.45	0.045488	0.125185	-4.90
264671_at	unknown protein ; supported by full-le	---	AT1G09920	1.25	0.32	2.45	0.045519	0.12523	-4.91
251807_at	methionyl-tRNA synthetase (AtcpMetR	OVA1	AT3G55400	-1.28	-0.35	-2.45	0.045524	0.125231	-4.91
246046_at	putative protein predicted proteins, Ar	---	---	-1.23	-0.30	-2.45	0.045532	0.125236	-4.91

248005_at	unknown protein	---	AT5G56240	1.28	0.35	2.45	0.04556	0.1253	-4.91
266819_at	unknown protein ;supported by full-ler	---	AT2G44870	-1.29	-0.37	-2.45	0.045591	0.125368	-4.91
255670_at	Expressed protein ; supported by full-l	RHB1A	AT4G00335	1.18	0.24	2.45	0.045603	0.125387	-4.91
256599_at	hypothetical protein predicted by gens	---	AT3G14760	-1.20	-0.26	-2.45	0.045618	0.125402	-4.91
263052_at	unknown protein	---	AT2G13430	-1.19	-0.26	-2.45	0.04562	0.125402	-4.91
252006_at	purple acid phosphatase-like protein p	PAP22	AT3G52820	2.47	1.30	2.45	0.045664	0.125509	-4.91
257251_at	type 1 membrane protein, putative ide	PMP	AT3G24160	-1.22	-0.29	-2.45	0.045672	0.125516	-4.91
245321_at	Expressed protein ; supported by full-l	---	AT4G15545	-1.18	-0.24	-2.45	0.045678	0.125517	-4.91
245015_at	large subunit of riblose-1,5-bisphosph	---	---	-1.38	-0.47	-2.45	0.045697	0.125547	-4.91
252956_at	farnesylated protein (ATFP6) ; suppor	ATFP6	AT4G38580	-1.63	-0.71	-2.45	0.0457	0.125547	-4.91
267488_at	putative cadmium-transporting ATPase	HMA4	AT2G19110	1.33	0.41	2.45	0.045725	0.125577	-4.91
254459_at	gibberellin 20-oxidase - like protein gi	GA2OX8	AT4G21200	-1.18	-0.23	-2.45	0.045727	0.125577	-4.91
260063_at	unknown protein contains Pfam profile	---	AT1G73720	-1.23	-0.30	-2.45	0.045716	0.125577	-4.91
254410_at	serine/threonine kinase - like protein	---	AT4G21410	1.69	0.76	2.45	0.045749	0.12562	-4.91
256336_at	unknown protein	---	AT1G72030	-1.29	-0.37	-2.45	0.045792	0.125702	-4.91
260137_at	unknown protein ;supported by full-len	---	AT1G66330	-1.34	-0.42	-2.44	0.045799	0.125702	-4.91
249310_at	putative protein contains similarity to 4	---	AT5G41520	-1.24	-0.31	-2.44	0.0458	0.125702	-4.91
250334_at	NADH dehydrogenase (ubiquinone) ;s	---	AT5G11770	1.22	0.28	2.45	0.045788	0.125702	-4.91
250319_at	putative protein strong similarity to unk	---	AT5G12120	-1.17	-0.22	-2.44	0.045809	0.125709	-4.91
254074_at	transcriptional activator CBF1 CRT CI	CBF1	AT4G25490	1.55	0.63	2.44	0.045819	0.125721	-4.91
253219_at	MYB-like protein myb-related protein Y	AtMYB32	AT4G34990	1.43	0.51	2.44	0.045836	0.125729	-4.91
254871_at	Srw1 -like protein WD repeat protein S	CCS52A2	AT4G11920	-1.16	-0.22	-2.44	0.045838	0.125729	-4.91
252345_at	hypothetical protein	---	AT3G48640	1.35	0.43	2.44	0.04583	0.125729	-4.91
257377_at	unknown protein	PLL4	AT2G28890	1.52	0.60	2.44	0.045847	0.125738	-4.91
266342_at	hypothetical protein predicted by grail	---	AT2G01540	1.32	0.40	2.44	0.045905	0.125882	-4.91
252629_at	cytochrome P450 - like protein cytoch	---	AT3G44970	-1.18	-0.24	-2.44	0.045916	0.125883	-4.91
253432_at	putative protein various predicted prote	---	AT4G32450	-1.18	-0.24	-2.44	0.045915	0.125883	-4.91
262498_at	8-oxoguanine DNA glycosylase-like pr	OGG1	AT1G21710	-1.23	-0.30	-2.44	0.045983	0.126052	-4.92
266553_at	unknown protein ; supported by cDNA	---	AT2G46170	1.26	0.33	2.44	0.046	0.126084	-4.92
251242_at	ARGININE/SERINE-RICH SPLICING I	RSP31	AT3G61860	1.19	0.25	2.44	0.046011	0.126098	-4.92
256547_at	receptor-like serine/threonine kinase,	---	AT3G14840	1.50	0.58	2.44	0.046032	0.12614	-4.92
249797_at	putative protein contains similarity to re	---	AT5G23750	-1.29	-0.37	-2.44	0.046069	0.126226	-4.92
260095_at	putative transcription factor BTF3 (RN	---	AT1G73230	-1.34	-0.42	-2.44	0.046092	0.126275	-4.92
255306_at	putative calcium dependent protein kin	CPK23	AT4G04740	1.33	0.42	2.44	0.046102	0.126286	-4.92
252999_at	putative protein other Arabidopsis hypo	---	AT4G38500	-1.22	-0.29	-2.44	0.046136	0.126348	-4.92

256872_at	non-phototropic hypocotyl, putative si	---	AT3G26490	-1.21	-0.27	-2.44	0.046132	0.126348	-4.92
257413_at	putative RNA-binding protein contains	---	AT1G22910	-1.35	-0.43	-2.44	0.046178	0.126449	-4.92
251869_at	putative protein	---	AT3G54500	-1.40	-0.48	-2.44	0.046216	0.126538	-4.92
248722_at	pyrophosphate-fructose-6-phosphate 1	PFK2	AT5G47810	1.16	0.22	2.44	0.046275	0.126669	-4.92
261845_at	metal ion transporter, putative similar	NRAMP6	AT1G15960	-1.33	-0.41	-2.44	0.046275	0.126669	-4.92
255727_at	hypothetical protein similar to unknowr	---	AT1G25510	-1.23	-0.30	-2.44	0.046301	0.126719	-4.92
261836_at	hypothetical protein contains similarity	WAKL7	AT1G16090	2.11	1.07	2.44	0.046305	0.126719	-4.92
258265_at	putative beta-1,3-glucanase precursor	---	AT3G15800	-1.23	-0.30	-2.44	0.046324	0.126758	-4.92
252603_at	putative protein	---	AT3G45050	-1.29	-0.36	-2.44	0.046335	0.126771	-4.92
247460_at	AtOXA1 ;supported by full-length cDN	OXA1	AT5G62050	1.16	0.21	2.43	0.046465	0.127081	-4.93
247190_at	D-type cyclin (emb|CAB41347.1) ;sup	CYCD4;1	AT5G65420	-1.23	-0.30	-2.43	0.046464	0.127081	-4.93
263865_at	putative ABC transporter related to mu	ABCB1	AT2G36910	-1.33	-0.41	-2.44	0.046456	0.127081	-4.93
252101_at	rac-like GTP binding protein Arac11 ;	ROP1	AT3G51300	-1.22	-0.28	-2.43	0.046725	0.127778	-4.93
263960_at	putative kinesin-related cytokinesis pro	---	AT2G36200	-1.22	-0.29	-2.43	0.046757	0.127834	-4.93
267381_at	unknown protein ; supported by cDNA	---	AT2G26190	2.47	1.31	2.43	0.046752	0.127834	-4.93
248964_at	cytochrome P450	CYP707A3	AT5G45340	1.75	0.81	2.43	0.046765	0.127841	-4.93
258275_at	unknown protein ;supported by full-ler	---	AT3G15760	1.41	0.49	2.43	0.046802	0.127927	-4.93
262465_at	hypothetical protein similar to hypothet	---	AT1G50270	-1.18	-0.24	-2.43	0.046815	0.127947	-4.93
264377_at	similar to early nodulins	---	AT2G25060	-1.18	-0.24	-2.43	0.046825	0.127957	-4.93
249590_at	putative protein SIAH1, Brassica napu	---	AT5G37870	-1.18	-0.24	-2.43	0.04683	0.127957	-4.93
257884_at	hypothetical protein predicted by gene	---	AT3G16960	-1.22	-0.28	-2.43	0.046849	0.127994	-4.93
254163_s_	putative protein storage protein - Popu	---	AT4G24340 /	2.25	1.17	2.43	0.046863	0.128017	-4.94
255578_at	predicted protein of unknown function	---	AT4G01450	1.54	0.62	2.43	0.046869	0.128019	-4.94
260472_at	hypothetical protein predicted by gene	---	AT1G10990	3.08	1.63	2.43	0.046889	0.128058	-4.94
251115_at	putative protein symplekin - Homo sap	ESP4	AT5G01400	1.22	0.28	2.43	0.046896	0.128061	-4.94
261258_at	unknown protein	---	AT1G26640	-1.27	-0.35	-2.43	0.046948	0.128188	-4.94
261176_at	hypothetical protein predicted by gene	---	AT1G04780	1.18	0.24	2.43	0.046955	0.128192	-4.94
267069_at	unknown protein	ATCAMBP2	AT2G41010	1.90	0.92	2.43	0.046979	0.128242	-4.94
251455_at	citrate synthase-like protein citrate syr	CSY5	AT3G60100	1.18	0.23	2.43	0.046993	0.128251	-4.94
258319_at	hypothetical protein similar to hypothet	---	AT3G22700	1.19	0.25	2.43	0.046994	0.128251	-4.94
255029_x_	hypothetical protein	---	AT4G09470	1.17	0.22	2.43	0.047064	0.128427	-4.94
249427_at	40S ribosomal protein S9-like 40S ribo	---	AT5G39850	1.68	0.75	2.43	0.047086	0.128468	-4.94
267152_at	hypothetical protein predicted by grail;	---	AT2G31040	-1.32	-0.40	-2.43	0.04709	0.128468	-4.94
264652_at	putative sugar transport protein, ERD6	---	AT1G08920	1.64	0.71	2.43	0.047125	0.128549	-4.94
247771_at	Ran binding protein 1 homolog - like F	RANBP1	AT5G58590	1.24	0.31	2.42	0.047145	0.128588	-4.94

263903_at	putative touch-induced calmodulin	---	AT2G36180	-1.18	-0.24	-2.42	0.047182	0.128672	-4.94
263471_at	hypothetical protein predicted by gens	RAP	AT2G31890	-1.24	-0.31	-2.42	0.047204	0.128719	-4.94
264914_at	clathrin adaptor medium chain protein	HAP13	AT1G60780	-1.23	-0.30	-2.42	0.047288	0.128931	-4.94
266256_at	60S acidic ribosomal protein P2 ;supp	---	AT2G27710	-1.42	-0.51	-2.42	0.047324	0.129014	-4.95
245282_at	hypothetical protein ; supported by cDI	---	AT4G14990	1.29	0.37	2.42	0.047336	0.129031	-4.95
246564_at	putative protein hypothetical protein F	---	AT5G15610	-1.17	-0.23	-2.42	0.047354	0.129042	-4.95
248506_at	adenylate kinase ;supported by full-le	---	AT5G50370	1.66	0.73	2.42	0.047357	0.129042	-4.95
253185_at	putative protein bZIP protein - Arabido	---	AT4G35240	-1.26	-0.34	-2.42	0.047357	0.129042	-4.95
261928_at	uclacyanin II, putative similar to uclacy	---	AT1G22480	1.33	0.41	2.42	0.047412	0.129177	-4.95
250536_at	Expressed protein ; supported by full-le	---	AT5G08535	-1.24	-0.31	-2.42	0.047421	0.129185	-4.95
258070_at	hypothetical protein predicted by gene	---	AT3G26040	-1.28	-0.35	-2.42	0.047474	0.129315	-4.95
254923_at	protein phosphatase type 1 PP1BG ;s	TOPP7	AT4G11240	1.28	0.35	2.42	0.047504	0.129382	-4.95
251090_at	putative protein ACR1-protein - Sacch	---	AT5G01340	1.77	0.82	2.42	0.047528	0.12943	-4.95
262427_s_	thioglucosidase, putative similar to thi	BGLU34	AT1G47600 /	-1.18	-0.24	-2.42	0.047533	0.12943	-4.95
249821_at	putative protein contains similarity to p	---	AT5G23690	1.40	0.48	2.42	0.047567	0.129461	-4.95
260001_at	putative S-adenosyl-L-methionine:tran	TSM1	AT1G67990	1.27	0.34	2.42	0.047563	0.129461	-4.95
257861_at	putative transporter similar to SV2 rela	---	AT3G13050	1.26	0.33	2.42	0.047565	0.129461	-4.95
257918_at	ethylene responsive element binding p	---	AT3G23230	4.79	2.26	2.42	0.047564	0.129461	-4.95
253457_at	putative protein C56A3.6,Caenorhabd	---	AT4G32060	-1.24	-0.32	-2.42	0.047575	0.129466	-4.95
264539_at	hypothetical protein predicted by gene	---	AT1G55590	-1.23	-0.30	-2.42	0.047588	0.129487	-4.95
249587_at	putative protein copper homeostasis f	---	AT5G37860	-1.17	-0.22	-2.42	0.04765	0.129639	-4.95
256902_s_	HAPp48,5 protein identical to HAPp48	---	AT3G23910 /	-1.35	-0.43	-2.42	0.047655	0.129639	-4.95
266072_at	putative trehalose-6-phosphate syntha	ATTPS11	AT2G18700	-1.40	-0.48	-2.42	0.047676	0.129679	-4.95
249956_at	putative protein CGI-66 protein, Homo	---	AT5G18940	1.20	0.27	2.42	0.047692	0.129704	-4.95
261152_at	hypothetical protein predicted by gene	---	AT1G04930	-1.34	-0.43	-2.42	0.047697	0.129704	-4.95
259052_at	unknown protein	PEX19-1	AT3G03490	1.20	0.27	2.42	0.047713	0.129732	-4.95
260353_at	putative nitrilase-associated protein sir	SP1L2	AT1G69230	1.25	0.33	2.42	0.047728	0.129758	-4.95
267371_at	Expressed protein ; supported by cDN	---	AT2G44510	1.36	0.44	2.42	0.047773	0.129781	-4.95
267462_at	Expressed protein ; supported by full-le	---	AT2G33735	-1.42	-0.51	-2.42	0.04777	0.129781	-4.95
266755_at	putative alcohol dehydrogenase	---	AT2G47150	-1.24	-0.31	-2.42	0.047783	0.129781	-4.95
245315_at	proteasome chain protein ; supported I	PBD2	AT4G14800	-1.19	-0.25	-2.42	0.047782	0.129781	-4.95
251351_s_	CaLB protein	NTMC2T4	AT3G60950 /	-1.22	-0.29	-2.42	0.047743	0.129781	-4.95
251708_at	Expressed protein ; supported by cDN	---	AT3G56580	-1.28	-0.35	-2.42	0.047788	0.129781	-4.96
260708_at	expressed protein ; supported by full-le	---	AT1G32310	-1.24	-0.31	-2.42	0.047761	0.129781	-4.95
251430_at	putative protein hypothetical protein A	---	AT3G60110	1.23	0.30	2.42	0.04775	0.129781	-4.95

265642_at	putative nitrilase ;supported by full-len	NLP1	AT2G27450	1.29	0.37	2.42	0.047758	0.129781	-4.95
263569_at	putative chromosome associated prote	TTN7	AT2G27170	1.35	0.43	2.42	0.047804	0.129811	-4.96
265199_s_	putative glucosyl transferase	---	AT2G36770 /	1.37	0.46	2.41	0.04782	0.129838	-4.96
254375_at	putative protein (fragment) ATP(GTP)	QQT2	AT4G21800	1.21	0.27	2.41	0.047837	0.12987	-4.96
256649_at	serine/arginine-rich protein, putative s	SCL30A	AT3G13570	-1.28	-0.36	-2.41	0.047853	0.129881	-4.96
253574_at	putative protein	---	AT4G31030	-1.32	-0.40	-2.41	0.047848	0.129881	-4.96
259062_at	unknown protein est hits to genscan m	---	AT3G07440	-1.32	-0.40	-2.41	0.047878	0.129933	-4.96
257020_at	mitotic checkpoint protein, putative sir	---	AT3G19590	-1.24	-0.31	-2.41	0.047908	0.130001	-4.96
249692_s_	putative protein strong similarity to unk	---	AT5G36670 /	1.25	0.32	2.41	0.047946	0.130087	-4.96
266094_at	Expressed protein ; supported by full-le	---	AT2G37975	-1.23	-0.30	-2.41	0.047975	0.130151	-4.96
250370_at	putative protein putative transcription	---	AT5G11430	1.17	0.22	2.41	0.048004	0.130214	-4.96
252717_at	putative protein predicted proteins, Ar	---	AT3G43930	1.43	0.52	2.41	0.048026	0.130258	-4.96
258823_at	putative RING zinc finger protein cont	---	AT3G07200	-1.29	-0.37	-2.41	0.048065	0.130349	-4.96
248558_at	permease	---	AT5G49990	-1.37	-0.45	-2.41	0.048133	0.130517	-4.96
266028_at	hypothetical protein predicted by gens	---	AT2G06000	1.31	0.39	2.41	0.048192	0.130661	-4.96
255916_at	putative protein	---	AT5G28550	-1.25	-0.33	-2.41	0.048203	0.130675	-4.96
249611_at	putative protein unnamed ORF, Homo	ATSRL1	AT5G37370	1.26	0.33	2.41	0.048243	0.130769	-4.96
258449_s_	putative RNA helicase similar to RNA h	PMH1	AT3G22310 /	1.33	0.41	2.41	0.048304	0.130897	-4.97
248346_at	GTP-binding protein-like ;supported b	ATGB1	AT5G52210	-1.39	-0.48	-2.41	0.0483	0.130897	-4.97
254783_at	hydrolase-like protein 2-hydroxy-6-oxo	---	AT4G12830	-1.55	-0.64	-2.41	0.048307	0.130897	-4.97
267625_at	putative RNA-binding protein	---	AT2G42240	-1.21	-0.28	-2.41	0.048314	0.1309	-4.97
247142_at	putative protein strong similarity to unk	---	AT5G65570	1.22	0.29	2.41	0.048339	0.130952	-4.97
245479_at	extensin like protein	---	AT4G16140	-1.22	-0.29	-2.41	0.048351	0.130954	-4.97
255791_at	plastid protein identical to GB:Z86094;	DAL1	AT2G33430	-1.30	-0.38	-2.41	0.048346	0.130954	-4.97
259361_at	glyceraldehyde-3-phosphate dehydrog	GAPC2	AT1G13440	1.24	0.31	2.41	0.048366	0.130978	-4.97
255539_at	putative actin polymerization factor sir	CRK	AT4G01710	-1.22	-0.29	-2.41	0.048386	0.131017	-4.97
265299_at	putative retroelement pol polyprotein c	---	---	1.32	0.41	2.41	0.048429	0.131101	-4.97
260045_at	putative MAP kinase similar to mitoger	ATMPK15	AT1G73670	1.16	0.22	2.41	0.048426	0.131101	-4.97
250801_at	pectinesterase	---	AT5G04960	-1.19	-0.25	-2.41	0.048464	0.13118	-4.97
249167_at	putative protein similar to unknown pro	---	AT5G42860	-1.63	-0.70	-2.40	0.048515	0.131303	-4.97
263375_s_	putative prohibitin ;supported by full-le	ATPHB6	AT2G20530 /	1.25	0.32	2.40	0.048537	0.131333	-4.97
254213_at	tyrosine transaminase like protein tyro	---	AT4G23590	-1.20	-0.26	-2.40	0.048539	0.131333	-4.97
265256_at	hypothetical protein predicted by gens	---	AT2G28390	-1.16	-0.21	-2.40	0.048545	0.131333	-4.97
252187_at	putative protein UV inducible protein U	---	AT3G50850	1.25	0.32	2.40	0.048549	0.131333	-4.97
263532_s_	putative protein RIO1 protein, Saccha	---	AT2G24990 /	1.31	0.38	2.40	0.048595	0.131443	-4.97

264076_at	unknown protein	---	AT2G28540	1.17	0.22	2.40	0.048672	0.131635	-4.97
247404_at	permease 1 - like protein permease 1	---	AT5G62890	-1.50	-0.59	-2.40	0.048683	0.13165	-4.97
256860_at	hypothetical protein similar to acetyl-C	---	AT3G23840	-1.22	-0.28	-2.40	0.048723	0.131741	-4.97
265336_at	hypothetical protein predicted by gens	APC10	AT2G18290	-1.19	-0.25	-2.40	0.04874	0.131772	-4.98
248080_at	wax synthase-like protein	---	AT5G55380	-1.28	-0.35	-2.40	0.048759	0.131806	-4.98
261295_at	unknown protein	---	AT1G48450	-1.18	-0.24	-2.40	0.048764	0.131806	-4.98
247765_at	cytochrome P450 CYP86A1	CYP86A1	AT5G58860	-1.45	-0.53	-2.40	0.048788	0.131855	-4.98
246344_at	putative protein predicted proteins - Ar	---	AT3G56730	-1.44	-0.53	-2.40	0.048795	0.131857	-4.98
259099_at	unknown protein similar to GB:AAB61(	---	AT3G05010	-1.22	-0.28	-2.40	0.048801	0.131858	-4.98
266287_at	putative tropinone reductase	---	AT2G29150	1.26	0.33	2.40	0.048836	0.131937	-4.98
266881_at	putative casein kinase II beta subunit	CKB4	AT2G44680	-1.21	-0.28	-2.40	0.048852	0.131964	-4.98
248540_at	FRO1 and FRO2-like protein	FRO8	AT5G50160	1.17	0.22	2.40	0.048891	0.132055	-4.98
259506_at	protein phosphatase type 2C, putative	---	AT1G43900	1.20	0.27	2.40	0.048907	0.132066	-4.98
249425_at	putative protein 5'-AMP-ACTIVATED	---	AT5G39790	-1.48	-0.56	-2.40	0.048903	0.132066	-4.98
266135_at	putative transcription factor IIIB 70 KD	---	AT2G45100	-1.38	-0.47	-2.40	0.04895	0.132167	-4.98
245623_s_	hypothetical protein	---	AT4G14096 /	-1.20	-0.26	-2.40	0.04897	0.132206	-4.98
259739_at	unknown protein supported by cDNA:	SEH1H	AT1G64350	1.22	0.28	2.40	0.049012	0.132299	-4.98
266056_at	hypothetical protein predicted by gens	ATATG18C	AT2G40810	-1.18	-0.24	-2.40	0.049016	0.132299	-4.98
258017_at	unknown protein	---	AT3G19370	-1.45	-0.54	-2.40	0.049055	0.132381	-4.98
250452_at	putative protein KIAA1038 protein, Ho	---	AT5G10630	-1.24	-0.31	-2.40	0.049058	0.132381	-4.98
248154_at	putative protein strong similarity to unk	---	AT5G54400	2.06	1.04	2.40	0.049072	0.132404	-4.98
262567_at	hypothetical protein contains similarity	---	AT1G34300	1.36	0.44	2.40	0.049098	0.132457	-4.98
263928_at	hypothetical protein predicted by gens	---	AT2G36330	1.32	0.41	2.40	0.049117	0.13249	-4.98
259221_s_	putative phospholipase similar to unkr	NPC5	AT3G03530 /	2.92	1.55	2.40	0.049122	0.13249	-4.98
264884_at	unknown protein ;supported by full-len	---	AT1G61170	-1.49	-0.57	-2.40	0.049152	0.132557	-4.98
260534_at	hypothetical protein predicted by grail	---	---	-1.19	-0.25	-2.40	0.049198	0.132664	-4.98
259803_at	cytosolic factor, putative similar to GI:	PATL1	AT1G72150	-1.20	-0.26	-2.40	0.049215	0.132695	-4.99
259407_at	protein phosphatase 2A regulatory su	PP2AA3	AT1G13320	-1.17	-0.23	-2.39	0.049226	0.132707	-4.99
263477_at	putative glucosyltransferase ; support	---	AT2G31790	-1.33	-0.42	-2.39	0.049241	0.132733	-4.99
248623_at	putative protein similar to unknown pro	---	AT5G49170	-1.89	-0.92	-2.39	0.049259	0.132767	-4.99
247869_at	CCHH finger protein 2-like protein (pir	ZFP2	AT5G57520	1.15	0.20	2.39	0.049305	0.132874	-4.99
246676_at	putative protein	---	---	-1.17	-0.22	-2.39	0.049356	0.132997	-4.99
264050_at	putative non-LTR retroelement reverse	---	---	-1.29	-0.37	-2.39	0.049389	0.133068	-4.99
245932_at	3'(2'),5'-bisphosphate nucleotidase-lik	---	AT5G09290	1.54	0.62	2.39	0.049529	0.133393	-4.99
262815_at	putative cytochrome P450 strong simil	CYP71A18	AT1G11610	1.45	0.54	2.39	0.049533	0.133393	-4.99

267151_at	aspartate aminotransferase (AAT1) ide	ASP1	AT2G30970	1.30	0.38	2.39	0.049528	0.133393	-4.99
250548_at	myosin heavy chain-like protein ; supp	MBP2C	AT5G08120	-1.22	-0.29	-2.39	0.049522	0.133393	-4.99
259037_at	hypothetical protein predicted by gens	---	AT3G09350	1.93	0.95	2.39	0.049566	0.133468	-4.99
253383_at	putative protein ;supported by full-leng	---	AT4G32900	1.33	0.41	2.39	0.049573	0.133469	-4.99
245934_at	putative protein NAC1 - Medicago trur	anac082	AT5G09330	1.28	0.35	2.39	0.049584	0.133474	-4.99
265285_at	hypothetical protein predicted by gens	---	AT2G20410	1.25	0.32	2.39	0.049586	0.133474	-4.99
247240_at	putative protein strong similarity to unk	CMPG2	AT5G64660	2.71	1.44	2.39	0.049599	0.133478	-4.99
252928_at	putative protein more than 30 predicte	---	AT4G38940	1.47	0.56	2.39	0.049595	0.133478	-4.99
261657_at	pathogenesis-related protein 1b precu	---	AT1G50050	-1.22	-0.29	-2.39	0.049615	0.133504	-4.99
260298_at	putative oxidoreductase contains Pfam	---	AT1G80320	1.18	0.24	2.39	0.049626	0.133519	-4.99
265432_at	hypothetical protein predicted by grail	---	AT2G20650	1.25	0.32	2.39	0.049652	0.133572	-4.99
253647_at	putative protein KIAA0210 gene, Hom	---	AT4G29950	1.25	0.33	2.39	0.04968	0.133633	-4.99
252622_at	cysteine proteinase AALP, putative sir	---	AT3G45310	1.23	0.30	2.39	0.049706	0.133685	-5.00
260560_at	putative endochitinase	---	AT2G43590	1.37	0.45	2.39	0.049733	0.133711	-5.00
259752_at	spore coat protein-like protein similar t	LPR2	AT1G71040	1.31	0.39	2.39	0.049732	0.133711	-5.00
259765_at	unknown protein ;supported by full-len	---	AT1G64370	1.32	0.40	2.39	0.049732	0.133711	-5.00
260100_at	Expressed protein ; supported by full-le	BNS	AT1G73177	-1.18	-0.23	-2.39	0.04978	0.133775	-5.00
249248_at	unknown protein	---	AT5G42320	-1.25	-0.32	-2.39	0.049774	0.133775	-5.00
245869_at	hypothetical protein predicted by gene	---	AT1G26330	-1.19	-0.25	-2.39	0.049768	0.133775	-5.00
247527_at	leucine-rich receptor-like protein kinas	---	AT5G61480	-1.34	-0.42	-2.39	0.049773	0.133775	-5.00
250527_at	serine/threonine-protein kinase	SNRK2.1	AT5G08590	-1.18	-0.24	-2.39	0.049791	0.133787	-5.00
259448_at	hypothetical protein similar to transcrip	---	AT1G13790	-1.24	-0.31	-2.39	0.049805	0.13381	-5.00
260151_at	unknown protein ;supported by full-ler	---	AT1G52910	-1.93	-0.95	-2.39	0.04982	0.133836	-5.00
256062_at	unknown protein ;supported by full-len	LSH6	AT1G07090	-1.18	-0.24	-2.39	0.049828	0.133842	-5.00
254850_at	putative protein predicted proteins Ara	---	AT4G12000	-1.31	-0.40	-2.39	0.049884	0.133975	-5.00
265707_at	unknown protein	---	AT2G03390	-1.25	-0.32	-2.39	0.049896	0.133992	-5.00
253365_at	putative protein various predicted prot	---	AT4G33170	1.21	0.27	2.38	0.049934	0.134063	-5.00
254618_at	cellulose synthase - like protein cellulo	IRX1	AT4G18780	-1.40	-0.48	-2.39	0.04993	0.134063	-5.00
266447_at	putative calcium binding protein ;suppo	MSS3	AT2G43290	1.66	0.73	2.38	0.049976	0.134159	-5.00
248430_at	putative protein similar to unknown pro	---	AT5G51800	-1.22	-0.29	-2.38	0.049987	0.134173	-5.00
261604_at	unknown protein contains similarity to	---	AT1G49590	-1.24	-0.31	-2.38	0.049997	0.134183	-5.00
245604_at	hypothetical protein	---	AT4G14290	-1.23	-0.30	-2.38	0.050113	0.134479	-5.00
253284_at	putative protein hydroxyproline-rich gl	---	AT4G34150	1.50	0.58	2.38	0.050168	0.134597	-5.00
248145_at	unknown protein ;supported by full-ler	---	AT5G54880	-1.23	-0.30	-2.38	0.050165	0.134597	-5.00
255627_at	Expressed protein ; supported by full-le	---	AT4G00955	1.18	0.24	2.38	0.050199	0.134663	-5.01

255777_at	glycine-rich RNA-binding protein, puta	GR-RBP6	AT1G18630	1.28	0.36	2.38	0.050302	0.134875	-5.01
254993_at	putative protein kinase	---	AT4G10730	1.19	0.25	2.38	0.050311	0.134875	-5.01
246035_at	succinyl-CoA-ligase alpha subunit ;su	---	AT5G08300	1.59	0.67	2.38	0.050312	0.134875	-5.01
257331_at	hypothetical protein	---	---	-1.25	-0.32	-2.38	0.050309	0.134875	-5.01
251373_at	GATA transcription factor 4 ; supporte	---	AT3G60530	-1.90	-0.93	-2.38	0.050314	0.134875	-5.01
251000_at	putative protein	---	AT5G02650	-1.22	-0.29	-2.38	0.050298	0.134875	-5.01
253131_at	homeodomain - like protein several ho	WOX13	AT4G35550	-1.26	-0.33	-2.38	0.050357	0.134943	-5.01
254314_at	extensin - like protein hybrid proline-ri	---	AT4G22470	3.72	1.89	2.38	0.050357	0.134943	-5.01
251457_s_	multi resistance protein homolog multi	ATMRP9	AT3G60160 /	1.21	0.27	2.38	0.050351	0.134943	-5.01
254957_at	putative protein ; supported by full-len	---	AT4G10970	1.24	0.30	2.38	0.050364	0.134946	-5.01
259617_at	hypothetical protein predicted by gene	---	AT1G47970	1.25	0.32	2.38	0.050376	0.13496	-5.01
264240_at	protein kinase, putative Simisimilar to	---	AT1G54820	-2.16	-1.11	-2.38	0.050381	0.13496	-5.01
246318_at	putative protein predicted protein BAA	---	AT3G56740	1.25	0.33	2.38	0.050404	0.135008	-5.01
263934_at	hypothetical protein predicted by gene	EDA12	AT2G35950	1.16	0.22	2.38	0.050421	0.135037	-5.01
257148_at	cytochrome c, putative similar to cytoc	---	AT3G27240	1.37	0.45	2.38	0.050453	0.135079	-5.01
244991_s_	NADH dehydrogenase ND2	---	---	-1.20	-0.26	-2.38	0.050461	0.135079	-5.01
251122_at	protein kinase -like protein serine/thre	---	AT5G01020	-1.31	-0.39	-2.38	0.050459	0.135079	-5.01
257095_at	unknown protein ; supported by cDNA	ATPDIL5-3	AT3G20560	-1.27	-0.35	-2.38	0.050451	0.135079	-5.01
247141_at	putative protein strong similarity to unk	---	AT5G65560	1.33	0.41	2.38	0.050493	0.135116	-5.01
253673_at	putative protein putative phosphatase	---	AT4G29530	-1.23	-0.30	-2.38	0.050504	0.135116	-5.01
256100_at	unknown protein	---	AT1G13750	1.80	0.85	2.38	0.050484	0.135116	-5.01
261724_at	Expressed protein ; supported by full-l	---	AT1G76185	-1.20	-0.26	-2.38	0.050487	0.135116	-5.01
254950_at	putative protein ;supported by full-leng	---	AT4G10810	-1.17	-0.22	-2.38	0.0505	0.135116	-5.01
248397_at	unknown protein	---	AT5G52140	-1.21	-0.27	-2.38	0.050521	0.135144	-5.01
255344_s_	putative receptor-like protein kinase	---	AT4G04540 /	-1.69	-0.76	-2.38	0.050547	0.135199	-5.01
258347_at	unknown protein identical to LEA-like p	---	AT3G17520	-1.22	-0.29	-2.38	0.050597	0.135318	-5.01
255505_at	SAR1/GTP-binding secretory factor ;s	ATSAR2	AT4G02080	1.21	0.27	2.38	0.05061	0.135335	-5.01
247324_at	putative protein strong similarity to unk	---	AT5G64190	2.05	1.03	2.38	0.050635	0.135387	-5.01
251025_at	putative protein CND41, chloroplast n	PCS1	AT5G02190	-1.28	-0.35	-2.37	0.050665	0.135419	-5.01
252636_at	putative protein triacylglycerol lipase,	---	AT3G44510	1.22	0.29	2.37	0.050662	0.135419	-5.01
262813_at	unknown protein strong similarity to gi	---	AT1G11670	1.74	0.80	2.38	0.050653	0.135419	-5.01
252361_at	hypothetical protein	---	AT3G48490	-1.48	-0.57	-2.37	0.050676	0.135432	-5.02
255802_s_	putative protein RING-H2 finger protei	---	AT4G10150 /	-1.18	-0.24	-2.37	0.050731	0.135564	-5.02
260671_at	unknown protein ;supported by full-len	---	AT1G19310	-1.25	-0.33	-2.37	0.05074	0.135572	-5.02
248933_at	putative protein contains similarity to g	---	AT5G46070	1.20	0.26	2.37	0.050784	0.135673	-5.02

245249_at	acyl-CoA oxidase like protein ; support	ACX1	AT4G16760	1.31	0.39	2.37	0.05082	0.135755	-5.02
246258_at	PPR-repeat protein, putative contains	---	AT1G31840	1.19	0.25	2.37	0.050836	0.135781	-5.02
265387_at	unknown protein ;supported by full-ler	---	AT2G20670	-1.67	-0.74	-2.37	0.050889	0.135906	-5.02
258038_at	unknown protein ;supported by full-ler	---	AT3G21260	1.40	0.48	2.37	0.050913	0.135954	-5.02
264418_at	nuclear ribonucleoprotein, putative sir	---	AT1G43190	-1.31	-0.39	-2.37	0.050942	0.136017	-5.02
255608_at	hypothetical protein	---	AT4G01140	-1.28	-0.36	-2.37	0.050957	0.13604	-5.02
264637_at	allyl alcohol dehydrogenase, putative	---	AT1G65560	1.33	0.42	2.37	0.050983	0.136094	-5.02
255580_at	putative water channel protein	TIP1;3	AT4G01470	-1.26	-0.34	-2.37	0.051006	0.136138	-5.02
266325_at	putative extensin	---	AT2G46630	-1.88	-0.91	-2.37	0.05108	0.13632	-5.02
260223_at	putative exonuclease contains Pfam pr	---	AT1G74390	-1.20	-0.27	-2.37	0.051119	0.136409	-5.02
266691_at	hypothetical protein predicted by gens	---	AT2G19890	-1.24	-0.31	-2.37	0.051157	0.136493	-5.02
245517_at	hypothetical protein	---	AT4G15840	1.15	0.20	2.37	0.051184	0.136551	-5.03
254584_at	putative protein probable membrane p	VPS54	AT4G19490	-1.18	-0.24	-2.37	0.051201	0.136581	-5.03
266111_at	unknown protein	---	AT2G02060 /	-1.21	-0.28	-2.37	0.051218	0.136608	-5.03
255026_at	hypothetical protein	MES12	AT4G09900	-1.44	-0.53	-2.37	0.05126	0.136705	-5.03
260425_at	hypothetical protein similar to CCAAT	EDA25	AT1G72440	1.57	0.65	2.37	0.051297	0.136787	-5.03
250332_at	putative protein predicted proteins, Ar	---	AT5G11680	-1.25	-0.32	-2.37	0.051353	0.136921	-5.03
256779_at	beta-fructofuranosidase, putative simi	AtcwINV5	AT3G13784	1.16	0.21	2.37	0.051373	0.136954	-5.03
251512_at	putative protein several hypothetical pr	---	AT3G59190	-1.20	-0.26	-2.37	0.051377	0.136954	-5.03
265258_at	hypothetical protein predicted by gene	---	AT2G20390	1.17	0.23	2.36	0.0514	0.136966	-5.03
260096_at	hypothetical protein predicted by gene	---	AT1G73240	1.26	0.33	2.36	0.0514	0.136966	-5.03
249339_at	putative protein similar to unknown pro	---	AT5G41100	1.83	0.87	2.36	0.051393	0.136966	-5.03
251662_at	putative protein DNA-DIRECTED RNA	NRPE5	AT3G57080	-1.27	-0.34	-2.36	0.051429	0.137027	-5.03
261905_at	hypothetical protein contains similarity	---	AT1G65070	1.20	0.27	2.36	0.051441	0.137044	-5.03
258718_at	unknown protein ; supported by cDNA	---	AT3G09760	1.21	0.28	2.36	0.05146	0.137077	-5.03
247643_at	auxin response factor 4 ; supported by	ARF4	AT5G60450	-1.35	-0.43	-2.36	0.051483	0.137124	-5.03
264527_at	putative reticuline oxidase-like protein	---	AT1G30760	1.53	0.61	2.36	0.051525	0.137187	-5.03
266241_s_	hypothetical protein predicted by gens	---	AT2G27800 /	-1.23	-0.30	-2.36	0.05152	0.137187	-5.03
245564_at	hypothetical protein	emb2739	AT4G14590	1.23	0.30	2.36	0.051513	0.137187	-5.03
265213_at	clathrin protein family Similar to clathr	---	AT1G05020	-1.31	-0.39	-2.36	0.051537	0.137202	-5.03
249711_at	putative protein contains similarity to tr	---	AT5G35680	1.26	0.34	2.36	0.051545	0.137208	-5.03
260651_at	hypothetical protein predicted by gene	---	AT1G32460	1.20	0.26	2.36	0.051575	0.137263	-5.03
252936_at	putative protein transcription initiation	---	AT4G39160	1.34	0.42	2.36	0.051577	0.137263	-5.03
263152_at	hypothetical protein predicted by gene	ASIL1	AT1G54060	-1.32	-0.40	-2.36	0.051591	0.137266	-5.03
262549_at	hypothetical protein similar to hypothet	---	AT1G31290	1.19	0.25	2.36	0.051589	0.137266	-5.03

252151_at	putative protein several hypothetical pr	---	AT3G51320	1.17	0.23	2.36	0.051606	0.137281	-5.03
266147_at	putative C-1-tetrahydrofolate synthase	---	AT2G12230	1.15	0.20	2.36	0.051608	0.137281	-5.03
256157_at	longevity assurance protein, putative s	LAG13	AT1G13580	-1.29	-0.36	-2.36	0.051754	0.137651	-5.04
250109_at	GASA4 ; supported by cDNA: gi_950(	GASA4	AT5G15230	-3.01	-1.59	-2.36	0.051787	0.137726	-5.04
264027_at	putative AAA-type ATPase similar to C	CDC48B	AT2G03670	1.29	0.37	2.36	0.05181	0.13777	-5.04
261682_at	unknown protein similar to hypothetica	---	AT1G47330	1.25	0.32	2.36	0.051826	0.137783	-5.04
264667_s_	hypothetical protein identical to hypoth	ZW18	AT1G09980 /	-1.19	-0.25	-2.36	0.051827	0.137783	-5.04
246955_at	calcium-dependent protein kinase ; su	CPK1	AT5G04870	-1.58	-0.66	-2.36	0.051841	0.137803	-5.04
264779_at	putative thioredoxin similar to ESTs gl	ACHT4	AT1G08570	-1.53	-0.62	-2.36	0.051864	0.137848	-5.04
255499_at	putative WD-repeat protein similar to (	---	AT4G02730	1.18	0.24	2.36	0.051884	0.137866	-5.04
261521_at	protein kinase, putative similar to rece	SERK1	AT1G71830	1.60	0.68	2.36	0.051888	0.137866	-5.04
254292_at	putative protein	---	AT4G23030	1.78	0.83	2.36	0.051889	0.137866	-5.04
264507_at	Expressed protein ; supported by cDN	NIMIN-3	AT1G09415	-1.28	-0.36	-2.36	0.0519	0.137881	-5.04
252110_at	disease resistance-like protein TMV re	---	AT3G51560	-1.18	-0.24	-2.36	0.051916	0.137906	-5.04
252351_at	putative protein ;supported by full-leng	---	AT3G48210	1.27	0.34	2.36	0.051922	0.137906	-5.04
267044_at	nodulin-like protein	---	AT2G34357	1.39	0.48	2.36	0.051961	0.137931	-5.04
245962_at	putative protein predicted proteins - Ar	---	AT5G19700	-1.22	-0.29	-2.36	0.05194	0.137931	-5.04
253888_at	hypothetical protein	ISI1	AT4G27750	-1.18	-0.24	-2.36	0.051954	0.137931	-5.04
246140_at	SOH1 - like protein SOH1, Saccharon	---	AT5G19910	-1.16	-0.21	-2.36	0.051967	0.137931	-5.04
249114_at	putative protein similar to unknown pro	---	---	-1.27	-0.34	-2.36	0.051962	0.137931	-5.04
263153_s_	myrosinase-associated protein, putativ	---	AT1G54000 /	1.55	0.63	2.36	0.051967	0.137931	-5.04
252991_at	protein kinase like protein protein kina	---	AT4G38470	1.85	0.89	2.36	0.051999	0.137999	-5.04
245654_at	disease resistance protein, putative si	---	AT1G56540	1.21	0.28	2.36	0.052005	0.137999	-5.04
247676_at	putative protein RNaseP protein p30,	---	AT5G59980	1.39	0.48	2.36	0.052045	0.138088	-5.04
253963_at	putative protein probable calcium-dep	---	AT4G26470	1.42	0.51	2.36	0.052069	0.138137	-5.04
256795_at	20S proteasome subunit PAC1 identic	PAC1	AT3G22110	-1.17	-0.23	-2.36	0.052087	0.138168	-5.04
247130_at	putative protein contains similarity to n	---	AT5G66180	1.44	0.53	2.36	0.052108	0.138188	-5.04
252473_s_	hypothetical protein several hypothetic	---	AT3G46610 /	1.33	0.41	2.36	0.052113	0.138188	-5.04
262819_at	putative cytochrome P450 strong simil	CYP77B1	AT1G11600	-1.18	-0.24	-2.36	0.052104	0.138188	-5.04
255527_at	putative protein	---	AT4G02360	-2.05	-1.04	-2.35	0.052147	0.138264	-5.04
255233_at	putative protein ADRENODOXIN PRE	MFDX1	AT4G05450	1.22	0.29	2.35	0.052167	0.138296	-5.04
260419_at	putative protein kinase contains Pfam	---	AT1G69730	1.63	0.70	2.35	0.052173	0.138296	-5.04
251111_at	putative protein different hypothetical p	---	AT5G01310	1.23	0.30	2.35	0.052178	0.138296	-5.04
245272_at	hypothetical protein ; supported by cDI	---	AT4G17250	1.47	0.55	2.35	0.052198	0.138332	-5.05
256263_at	5,10-methylenetetrahydrofolate dehyd	---	AT3G12290	-1.22	-0.29	-2.35	0.052216	0.138357	-5.05

251182_at	putative protein HIRA interacting prote	ATERDJ3B	AT3G62600	1.84	0.88	2.35	0.052223	0.138357	-5.05
253694_at	Expressed protein ; supported by full-le	---	AT4G29735	-1.23	-0.30	-2.35	0.052225	0.138357	-5.05
251813_at	Expressed protein ; supported by full-le	TON1A	AT3G55000	-1.27	-0.34	-2.35	0.052231	0.138357	-5.05
249763_at	receptor-protein kinase-like protein	---	AT5G24010	-1.37	-0.45	-2.35	0.052268	0.138438	-5.05
261043_at	hypothetical protein similar to unknown	---	AT1G01220	-1.26	-0.33	-2.35	0.052285	0.138459	-5.05
260409_at	Expressed protein ; supported by full-le	SHW1	AT1G69935	-1.38	-0.47	-2.35	0.052288	0.138459	-5.05
254239_at	water channel - like protein plasma m	PIP1;5	AT4G23400	-1.39	-0.47	-2.35	0.052305	0.138487	-5.05
257476_at	unknown protein	---	AT1G80960	1.17	0.22	2.35	0.052368	0.13864	-5.05
264973_at	nitrate transporter, putative nitrate tran	---	AT1G27040	-1.26	-0.33	-2.35	0.05242	0.13876	-5.05
260931_at	hypothetical protein predicted by gene	---	AT1G02550	1.26	0.33	2.35	0.052427	0.138762	-5.05
260548_at	biotin synthase (Bio B) ;supported by	BIO2	AT2G43360	-1.35	-0.43	-2.35	0.052451	0.138811	-5.05
254972_at	putative protein more than 10 putative	---	AT4G10440	1.22	0.29	2.35	0.052479	0.138868	-5.05
258493_at	Expressed protein ; supported by full-le	---	AT3G02555	-1.22	-0.29	-2.35	0.052492	0.138887	-5.05
267587_at	unknown protein	---	AT2G42080	-1.30	-0.38	-2.35	0.052552	0.139029	-5.05
253970_at	putative uracil phosphoribosyl transfer	---	AT4G26510	-1.21	-0.28	-2.35	0.052569	0.139058	-5.05
264118_at	unknown protein	---	AT1G79150	1.54	0.62	2.35	0.052591	0.139099	-5.05
257969_at	hypothetical protein predicted by gene	---	AT3G27520	-1.39	-0.47	-2.35	0.052654	0.139252	-5.05
258713_at	Expressed protein ; supported by full-le	---	AT3G09735	-1.19	-0.25	-2.35	0.052663	0.139258	-5.05
253693_at	Thioredoxin - like protein thioredoxin;L	ACHT2	AT4G29670	1.37	0.45	2.35	0.052709	0.139365	-5.06
265599_at	unknown protein	AT2G14255	---	-1.20	-0.26	-2.35	0.052761	0.139485	-5.06
260364_at	putative alliinase similar to aliinase pre	TAA1	AT1G70560	1.31	0.39	2.35	0.05279	0.139547	-5.06
254339_at	glucosidase like protein furostanol gly	BGLU3	AT4G22100	-1.20	-0.26	-2.35	0.052815	0.139596	-5.06
253728_at	putative protein unknown protein chro	---	AT4G29410	-1.35	-0.44	-2.35	0.052829	0.139617	-5.06
266756_at	putative cytochrome P450	CYP709B2	AT2G46950	2.55	1.35	2.35	0.052849	0.139653	-5.06
247815_at	ribosomal protein S4 - like ribosomal p	---	AT5G58420	-1.33	-0.41	-2.35	0.052869	0.139674	-5.06
267341_at	hypothetical protein predicted by gens	---	AT2G44200	1.29	0.37	2.35	0.052866	0.139674	-5.06
253304_at	putative protein ;supported by full-leng	---	AT4G33640	-1.23	-0.29	-2.35	0.052896	0.139729	-5.06
245416_at	putative protein	---	AT4G17350	-1.25	-0.32	-2.34	0.053057	0.140137	-5.06
257541_at	hypothetical protein predicted by gene	---	AT3G25950	1.55	0.64	2.34	0.053082	0.140189	-5.06
253880_at	Expressed protein ;supported by cDNA	---	AT4G27590	-1.25	-0.33	-2.34	0.053115	0.140257	-5.06
266852_at	hypothetical protein predicted by gens	---	AT2G26810	-1.20	-0.26	-2.34	0.053135	0.140296	-5.06
254692_at	putative protein predicted protein, Ara	---	AT4G17860	-1.20	-0.27	-2.34	0.053142	0.140296	-5.06
256969_at	unknown protein	---	AT3G21080	1.92	0.94	2.34	0.053156	0.140318	-5.06
256763_at	unknown protein	COBL8	AT3G16860	1.82	0.86	2.34	0.053169	0.14032	-5.06
254206_at	thaumatin-like protein thaumatin-like p	---	AT4G24180	-1.24	-0.31	-2.34	0.053168	0.14032	-5.06

259935_at	putative GDSL-motif lipase/acylhydrola	---	AT1G71250	1.24	0.31	2.34	0.0532	0.140371	-5.06
265378_at	putative GATA-type zinc finger transcr	---	AT2G18380	-1.20	-0.26	-2.34	0.053197	0.140371	-5.06
252150_at	vacuolar sorting protein 35 homolog v	VPS35C	AT3G51310	1.18	0.24	2.34	0.053231	0.140436	-5.07
250990_at	serine/threonine-specific protein kinas	NAK	AT5G02290	1.43	0.51	2.34	0.05324	0.140438	-5.07
257535_at	hypothetical protein predicted by gens	---	AT3G09490	1.49	0.57	2.34	0.053244	0.140438	-5.07
251647_at	protein kinase - like protein wall-assoc	---	AT3G57770	1.25	0.32	2.34	0.053271	0.140475	-5.07
266666_at	hypothetical protein predicted by gens	---	AT2G29780	-1.20	-0.26	-2.34	0.053271	0.140475	-5.07
249219_at	putative protein contains similarity to S	SDG25	AT5G42400	1.25	0.33	2.34	0.05332	0.140589	-5.07
263156_at	myrosinase-associated protein, putati	---	AT1G54030	1.46	0.54	2.34	0.05336	0.140652	-5.07
248014_at	putative protein similar to unknown pro	---	AT5G56340	-1.28	-0.35	-2.34	0.053369	0.140652	-5.07
249870_at	unknown protein	TGH	AT5G23080	1.56	0.64	2.34	0.053365	0.140652	-5.07
248108_at	molybdopterin synthase sulphurylase (	CNX5	AT5G55130	1.23	0.30	2.34	0.053361	0.140652	-5.07
252593_at	putative protein tRNA intron endonucl	ATSEN1	AT3G45590	1.26	0.33	2.34	0.053477	0.14092	-5.07
247191_at	homeobox-leucine zipper protein ATHI	ATHB5	AT5G65310	-1.38	-0.47	-2.34	0.053548	0.141091	-5.07
250504_at	putative protein similar to unknown pro	---	AT5G09840	1.26	0.33	2.34	0.05357	0.141134	-5.07
252043_at	putative protein mttC protein, Escheric	---	AT3G52390	-1.23	-0.30	-2.34	0.05365	0.141313	-5.07
246735_at	histone H2A-like protein histone H2A	HTA7	AT5G27670	-1.23	-0.30	-2.34	0.05365	0.141313	-5.07
265048_at	jasmonate inducible protein, putative	---	AT1G52050	1.25	0.32	2.33	0.05367	0.141349	-5.07
247377_at	pectate lyase ; supported by cDNA: gi	---	AT5G63180	-4.16	-2.05	-2.33	0.053681	0.141359	-5.07
262385_at	root hair defective, putative similar to	---	AT1G72960	-1.16	-0.22	-2.33	0.053772	0.141585	-5.08
267416_at	putative phosphatidylinositol-glycan sy	SETH1	AT2G34980	-1.19	-0.25	-2.33	0.05379	0.141615	-5.08
262756_at	putative transport protein may be a me	אוק-06	AT1G16370	-1.94	-0.95	-2.33	0.053832	0.141692	-5.08
267588_at	unknown protein	---	AT2G42060	1.17	0.23	2.33	0.053831	0.141692	-5.08
248647_at	sucrose synthase	SUS2	AT5G49190	-1.18	-0.23	-2.33	0.053863	0.141758	-5.08
251289_at	auxin response factor-like protein aux	ARF18	AT3G61830	-1.27	-0.35	-2.33	0.053877	0.141769	-5.08
260684_at	transcription factor, putative similar to	NF-YA8	AT1G17590	1.30	0.37	2.33	0.053896	0.141769	-5.08
264599_at	putative myosin heavy chain similar to	XIA	AT1G04600	-1.19	-0.25	-2.33	0.05388	0.141769	-5.08
262623_at	integral membrane protein, putative c	---	AT1G06470	-1.25	-0.32	-2.33	0.053891	0.141769	-5.08
262748_at	lipase, putative contains Pfam profile:	---	AT1G28610	1.40	0.48	2.33	0.053898	0.141769	-5.08
266795_at	unknown protein	---	AT2G03070	-1.24	-0.31	-2.33	0.053916	0.141798	-5.08
247007_at	porin-like protein ;supported by full-ler	VDAC2	AT5G67500	1.26	0.33	2.33	0.053959	0.141893	-5.08
253839_at	putative protein prolactin-induced T ce	---	AT4G27890	1.23	0.30	2.33	0.053969	0.141893	-5.08
267142_at	putative ammonium transporter	ATAMT2	AT2G38290	1.43	0.51	2.33	0.05397	0.141893	-5.08
257886_at	pectinesterase, putative similar to pec	---	AT3G17060	-1.21	-0.27	-2.33	0.053986	0.141919	-5.08
263402_at	hypothetical protein similar to hypothet	---	AT2G04050	2.07	1.05	2.33	0.054011	0.141967	-5.08

251782_at	beta-N-acetylhexosaminidase -like pro	HEXO1	AT3G55260	-1.31	-0.39	-2.33	0.054076	0.142123	-5.08
255175_at	putative glucosyltransferase ;supporte	ATCSLC12	AT4G07960	-1.21	-0.27	-2.33	0.054101	0.14217	-5.08
249949_at	SAE1-S9-protein - like SAE1-S9-prote	---	AT5G18880	-1.20	-0.26	-2.33	0.054178	0.142358	-5.08
253459_at	hypothetical protein	---	AT4G32080	-1.16	-0.22	-2.33	0.054185	0.142358	-5.08
256991_at	unknown protein	---	AT3G28600	-1.17	-0.23	-2.33	0.054238	0.142481	-5.08
250510_at	15.9 kDa subunit of RNA polymerase I	NRPB4	AT5G09920	1.19	0.25	2.33	0.054248	0.14249	-5.08
257145_at	esterase, putative similar to esterase	---	AT3G27320	-1.28	-0.35	-2.33	0.054258	0.142501	-5.08
262078_at	hypothetical protein predicted by gens	CW7	AT1G59520	-1.17	-0.22	-2.33	0.054304	0.142605	-5.09
246255_at	transcription initiation factor like protei	ATPBRP	AT4G36650	1.22	0.29	2.33	0.054336	0.14266	-5.09
252124_at	hypothetical protein ;supported by full-	---	AT3G51010	-1.26	-0.34	-2.33	0.054337	0.14266	-5.09
259515_at	hypothetical protein ; supported by cDI	---	AT1G20430	1.17	0.23	2.33	0.054349	0.142675	-5.09
257768_at	RING zinc finger protein, putative con	---	AT3G23060	1.27	0.34	2.33	0.054364	0.142697	-5.09
251345_at	putative protein hypothetical proteins -	---	AT3G60940	-1.20	-0.27	-2.33	0.054384	0.142718	-5.09
255616_at	hypothetical protein	---	AT4G01290	1.33	0.41	2.33	0.054381	0.142718	-5.09
261584_at	CAF protein identical to RNA helicase/	DCL1	AT1G01040	1.31	0.39	2.33	0.054401	0.142745	-5.09
262685_at	unknown protein ; supported by cDNA	---	AT1G76010	1.32	0.40	2.33	0.054438	0.142812	-5.09
259001_at	hypothetical protein predicted by gens	---	AT3G01960	-1.66	-0.73	-2.33	0.054439	0.142812	-5.09
261408_s_	histone H4 identical to GB:M36659 fro	---	AT1G07660 /	-1.29	-0.37	-2.32	0.054454	0.142836	-5.09
254000_at	galactinol synthase WSI76 protein ind	AtGolS6	AT4G26250	-1.15	-0.21	-2.32	0.054466	0.14285	-5.09
255289_at	score=11/3, E=0.23, N=1 contains F-b	---	AT4G04690	-1.21	-0.27	-2.32	0.054524	0.142987	-5.09
267468_at	unknown protein ; supported by cDNA	---	AT2G30530	1.24	0.31	2.32	0.054537	0.143003	-5.09
262079_at	unknown protein ; supported by cDNA	ZCW7	AT1G59600	-1.31	-0.39	-2.32	0.054557	0.14304	-5.09
246316_at	putative protein predicted proteins - Ar	---	AT3G56890	1.16	0.21	2.32	0.054574	0.143052	-5.09
257613_at	polygalacturonase, putative similar to	---	AT3G26610	-1.18	-0.24	-2.32	0.054573	0.143052	-5.09
246830_at	chaperonin gamma chain - like protein	---	AT5G26360	1.41	0.50	2.32	0.054652	0.143226	-5.09
254691_at	hypothetical protein ; supported by ful	---	AT4G17840	1.36	0.44	2.32	0.054653	0.143226	-5.09
253717_at	putative protein putative suppressor p	---	AT4G29440	-1.20	-0.26	-2.32	0.054668	0.143235	-5.09
258686_at	putative polygalacturonase similar to p	---	AT3G07840	-1.17	-0.23	-2.32	0.054669	0.143235	-5.09
250726_at	putative protein similar to unknown pro	---	AT5G06410	1.26	0.33	2.32	0.054678	0.143242	-5.09
248135_at	putative protein similar to unknown pro	---	AT5G54890	-1.28	-0.35	-2.32	0.054686	0.143247	-5.09
265856_at	hypothetical protein predicted by gene	LBD16	AT2G42430	-1.30	-0.38	-2.32	0.054695	0.143253	-5.09
257067_at	unknown protein contains Pfam profile	CYP77A5P	AT3G18270	1.23	0.30	2.32	0.054725	0.143315	-5.09
246317_at	putative protein unnamed ORF - Hom	---	AT3G56900	-1.32	-0.40	-2.32	0.054734	0.143323	-5.09
255133_at	putative protein (fragment) glutamine-	---	AT4G08320	1.24	0.31	2.32	0.054774	0.143377	-5.09
250104_at	unknown protein	---	AT5G16610	1.30	0.38	2.32	0.05478	0.143377	-5.09

246219_at	aminopeptidase-like protein ; supporte	APP1	AT4G36760	1.30	0.38	2.32	0.054764	0.143377	-5.09
264885_s_	NBS/LRR disease resistance protein,	---	AT1G61180 /	-1.24	-0.31	-2.32	0.054777	0.143377	-5.09
256069_at	hypothetical protein predicted by gens	AFP2	AT1G13740	1.41	0.50	2.32	0.054806	0.14343	-5.09
257806_at	hypothetical protein predicted by gens	---	AT3G18670	-1.20	-0.26	-2.32	0.054837	0.143492	-5.10
266560_at	putative LRR receptor protein kinase	---	AT2G23950	-1.25	-0.33	-2.32	0.054843	0.143492	-5.10
255508_at	putative zinc finger protein identical to	---	AT4G02220	1.24	0.31	2.32	0.054887	0.14359	-5.10
259170_at	hypothetical protein similar to putative	---	AT3G03510	-1.18	-0.24	-2.32	0.054902	0.143615	-5.10
260192_at	putative DNA polymerase alpha subun	POLA2	AT1G67630	-1.71	-0.77	-2.32	0.054918	0.143639	-5.10
258478_at	unknown protein	---	AT3G02710	1.20	0.27	2.32	0.054958	0.143728	-5.10
264150_at	unknown protein similar to FUS5 prote	FUS5	AT1G02090	1.17	0.23	2.32	0.054979	0.143767	-5.10
247853_at	non phototropic hypocotyl 1-like ; supp	PHOT2	AT5G58140	-1.23	-0.29	-2.32	0.054999	0.143802	-5.10
264754_at	receptor kinase, putative similar to rec	---	AT1G61400	1.23	0.30	2.32	0.055064	0.143955	-5.10
265964_at	putative RNA-binding protein ; suppor	---	AT2G37510	-1.21	-0.28	-2.32	0.055094	0.144017	-5.10
260290_at	hypothetical protein predicted by gens	---	AT1G80510	-1.21	-0.28	-2.32	0.055135	0.14409	-5.10
252372_at	aldehyde dehydrogenase (NAD+)-like	ALDH2B4	AT3G48000	1.30	0.38	2.32	0.055131	0.14409	-5.10
258949_at	unknown protein	ATCFM2	AT3G01370	-1.28	-0.36	-2.32	0.055189	0.1442	-5.10
246780_at	seryl-tRNA synthetase ; supported by	---	AT5G27470	-1.21	-0.28	-2.32	0.055189	0.1442	-5.10
252467_at	putative protein predicted proteins, Ar	---	AT3G47080	1.28	0.35	2.31	0.055271	0.144397	-5.10
249958_at	plasma membrane associated protein	---	AT5G18970	-1.29	-0.37	-2.31	0.055298	0.144452	-5.10
261624_at	nucleotide sugar epimerase, putative	GAE2	AT1G02000	-1.40	-0.48	-2.31	0.055312	0.144454	-5.10
267489_s_	putative DNA2-NAM7 helicase family p	---	AT2G19120 /	1.33	0.41	2.31	0.055307	0.144454	-5.10
265640_at	putative cysteine proteinase	---	AT2G27395	-1.16	-0.21	-2.31	0.055319	0.144456	-5.10
250539_at	WD-repeat protein-like ; supported by	---	AT5G08560	1.26	0.33	2.31	0.055337	0.144487	-5.10
253000_at	putative protein other predicted protein	---	AT4G38360	1.25	0.32	2.31	0.055371	0.144558	-5.11
259134_at	hypothetical protein predicted by gens	---	AT3G05390	1.78	0.83	2.31	0.055396	0.14459	-5.11
264762_at	receptor kinase, putative similar to rec	---	AT1G61460	1.24	0.31	2.31	0.055396	0.14459	-5.11
246849_at	putative protein various predicted prot	---	AT5G26850	-1.52	-0.61	-2.31	0.055435	0.144676	-5.11
255756_at	endo-beta-1,4-D-glucanase, putative s	AtGH9B5	AT1G19940	-1.21	-0.28	-2.31	0.055503	0.144838	-5.11
262872_at	hypothetical protein predicted by gene	---	AT1G64690	-1.31	-0.39	-2.31	0.055526	0.144882	-5.11
263696_at	putative aspartate kinase-homoserine	AK-HSDH I	AT1G31230	-1.35	-0.43	-2.31	0.055566	0.144969	-5.11
262165_at	putative acyl-CoA:1-acylglycerol-3-pho	LPAT4	AT1G75020	1.37	0.45	2.31	0.055579	0.144986	-5.11
249609_at	putative protein predicted proteins, Ar	---	---	-1.18	-0.24	-2.31	0.055603	0.145033	-5.11
250573_at	putative protein	---	AT5G08220 /	1.24	0.31	2.31	0.055634	0.145096	-5.11
259474_at	unknown protein ;supported by full-len	---	AT1G19130	1.56	0.64	2.31	0.055657	0.145124	-5.11
259325_at	unknown protein	---	AT3G05320	-3.08	-1.62	-2.31	0.055656	0.145124	-5.11

248084_at	sodium proton exchanger	NHX3	AT5G55470	-1.29	-0.36	-2.31	0.055682	0.145171	-5.11
263735_s_	hypothetical protein predicted by gene	AGL50	AT1G59810 /	1.17	0.23	2.31	0.055798	0.145457	-5.11
249220_at	putative protein strong similarity to unk	---	AT5G42420	-1.23	-0.30	-2.31	0.055815	0.145485	-5.11
267182_at	unknown protein	---	AT2G23360	-1.25	-0.32	-2.31	0.055825	0.145491	-5.11
257643_at	AP2 domain transcription factor conta	---	AT3G25730	1.62	0.70	2.31	0.055836	0.145491	-5.11
259298_at	putative disease resistance protein sim	AtRLP31	AT3G05370	2.16	1.11	2.31	0.055832	0.145491	-5.11
265837_at	unknown protein	LURP1	AT2G14560	3.95	1.98	2.31	0.055844	0.145494	-5.11
253778_at	heat-shock protein heat-shock protein	---	AT4G28480	-1.25	-0.32	-2.31	0.055862	0.145522	-5.11
265713_at	putative integral membrane protein	UPS2	AT2G03530	1.72	0.78	2.31	0.055868	0.145522	-5.11
247964_at	profilin-like protein ; supported by full-l	PRF3	AT5G56600	-1.32	-0.40	-2.31	0.055931	0.14567	-5.12
257510_at	unknown protein	---	AT1G55360	-1.65	-0.72	-2.31	0.055945	0.14569	-5.12
261923_at	UDP-glucose glucosyltransferase, put	AtUGT85A3	AT1G22380	1.23	0.30	2.31	0.055954	0.145697	-5.12
262198_at	pectin methylesterase (PMEU1), puta	ATPME2	AT1G53830	-1.80	-0.85	-2.31	0.055979	0.145746	-5.12
264173_at	unknown protein	---	AT1G02160	-1.19	-0.25	-2.31	0.055998	0.145778	-5.12
261041_at	hypothetical protein contains similarity	EER4	AT1G17440	1.20	0.27	2.31	0.056024	0.145829	-5.12
261871_at	similar to serine/threonine protein kina	---	AT1G11440	-1.24	-0.31	-2.31	0.056045	0.145869	-5.12
253810_at	putative NADH dehydrogenase NADH	NDB1	AT4G28220	-1.60	-0.68	-2.30	0.056132	0.146078	-5.12
252373_at	disease resistance protein EDS1 ; sup	EDS1	AT3G48090	1.78	0.83	2.30	0.056149	0.146105	-5.12
267150_at	putative anthranilate N-hydroxycinnam	SDT	AT2G23510	-1.16	-0.21	-2.30	0.056168	0.146137	-5.12
256697_at	hypothetical protein contains similarity	AtOCT4	AT3G20660	1.49	0.57	2.30	0.056216	0.146247	-5.12
256248_at	hypothetical protein	---	AT3G66652	1.31	0.39	2.30	0.056224	0.146251	-5.12
262223_at	hypothetical protein predicted by gene	---	AT1G74680	1.35	0.44	2.30	0.056257	0.14629	-5.12
245748_at	unknown protein contains similarity to	---	AT1G51140	1.43	0.52	2.30	0.056259	0.14629	-5.12
250749_at	26S proteasome regulatory subunit S1	RPN8A	AT5G05780	-1.17	-0.22	-2.30	0.056249	0.14629	-5.12
267268_at	hypothetical protein predicted by gens	---	AT2G02570	1.21	0.27	2.30	0.05629	0.146349	-5.12
264238_at	hypothetical protein predicted by gens	---	AT1G54740	-1.52	-0.61	-2.30	0.056294	0.146349	-5.12
257851_at	unknown protein	---	AT3G12940	-1.21	-0.27	-2.30	0.056335	0.146439	-5.12
247814_at	polyneuridine aldehyde esterase-like; a	MES18	AT5G58310	-2.20	-1.14	-2.30	0.056398	0.146587	-5.12
259206_at	hypothetical protein similar to putative	---	AT3G09040	1.24	0.31	2.30	0.056424	0.14662	-5.12
254111_at	putative protein acid phosphatase (EC	PAP24	AT4G24890	1.33	0.41	2.30	0.056421	0.14662	-5.12
259136_at	unknown protein	---	AT3G05470	-1.30	-0.37	-2.30	0.056465	0.146709	-5.13
253504_at	hypothetical protein	---	AT4G31960	1.14	0.19	2.30	0.056498	0.146779	-5.13
261320_at	unknown protein ; supported by cDNA	---	AT1G53120	-1.17	-0.23	-2.30	0.056516	0.14678	-5.13
266423_at	putative DNA-directed RNA polymeras	RPB5D	AT2G41340	-1.26	-0.34	-2.30	0.056507	0.14678	-5.13
264629_at	hypothetical protein similar to hypothet	---	AT1G65540	1.25	0.32	2.30	0.056518	0.14678	-5.13

258010_at	unknown protein similar to receptor-lik	---	AT3G19300	-1.18	-0.24	-2.30	0.056535	0.146809	-5.13
251412_at	RING-H2 zinc finger protein ATL4 ; su	ATL4	AT3G60220	-1.53	-0.61	-2.30	0.056604	0.146972	-5.13
256227_at	unknown protein ; supported by cDNA:	---	AT1G56290	1.17	0.23	2.30	0.056623	0.147002	-5.13
260252_at	putative mitochondrial carrier protein s	---	AT1G74240	1.29	0.37	2.30	0.056629	0.147002	-5.13
259343_s_	putative methionine synthase similar to	ATMS2	AT3G03780 /	-1.33	-0.42	-2.30	0.056659	0.147063	-5.13
258536_at	Rab escort protein, putative similar to	---	AT3G06540	1.23	0.30	2.30	0.056665	0.147063	-5.13
250198_at	expressed protein contains similarity t	NAP14	AT5G14100	-1.33	-0.41	-2.30	0.056691	0.147112	-5.13
245574_at	hypothetical protein	IQD19	AT4G14750	-1.30	-0.38	-2.30	0.056711	0.147132	-5.13
260481_at	ferredoxin precusor isolog ;supported	ATFD1	AT1G10960	-1.39	-0.47	-2.30	0.056708	0.147132	-5.13
251465_at	transporter-like protein UDP-galactose	UTR6	AT3G59360	-1.16	-0.22	-2.30	0.056722	0.147143	-5.13
257399_at	putative OBP32pep protein	---	AT1G23690	-1.15	-0.20	-2.30	0.056775	0.147257	-5.13
251887_at	FKBP12 interacting protein (FIP37) ; s	ATFIP37	AT3G54170	-1.32	-0.40	-2.30	0.056779	0.147257	-5.13
254507_at	Glu-rich protein mature-parasite-infect	---	AT4G20160	-1.18	-0.24	-2.30	0.056796	0.147284	-5.13
254276_at	predicted protein PVPR3 protein, Pha	---	AT4G22820	1.46	0.55	2.30	0.056815	0.147302	-5.13
264673_at	Expressed protein ; supported by full-l	ATATP-PRT	AT1G09795	-1.20	-0.27	-2.30	0.056812	0.147302	-5.13
248193_at	homogentisate 1,2-dioxygenase ;sup	HGO	AT5G54080	1.42	0.50	2.30	0.05684	0.14735	-5.13
253501_at	predicted protein predicted protein on	HSL1	AT4G32010	1.20	0.27	2.30	0.056854	0.147369	-5.13
263469_at	putative Na+/H+ antiporter	ATCHX21	AT2G31910	1.19	0.25	2.29	0.056899	0.147467	-5.13
260300_at	gibberellin 3 beta-hydroxylase identica	GA3OX2	AT1G80340	-1.37	-0.46	-2.29	0.056921	0.147509	-5.13
265015_at	putative Ta11-1 reverse transcriptase	---	---	-1.15	-0.21	-2.29	0.05693	0.147515	-5.13
251162_at	putative protein hypothetical proteins -	---	AT3G63300	-1.19	-0.25	-2.29	0.057029	0.147722	-5.14
249891_at	unknown protein	---	AT5G22590	-1.14	-0.19	-2.29	0.057019	0.147722	-5.14
261014_at	unknown protein ;supported by full-len	---	AT1G26460	-1.20	-0.26	-2.29	0.057028	0.147722	-5.14
257309_at	hypothetical protein predicted by gene	---	AT3G28150	-1.15	-0.20	-2.29	0.057037	0.147726	-5.14
245592_at	CCAAT-binding transcription factor sul	NF-YB3	AT4G14540	-1.29	-0.37	-2.29	0.05709	0.147846	-5.14
247253_at	beta-1,3-glucanase	---	AT5G64790	1.72	0.78	2.29	0.057104	0.147865	-5.14
264295_at	hypothetical protein predicted by gene	---	AT1G78740	-1.16	-0.21	-2.29	0.057149	0.147965	-5.14
246990_at	subtilisin-like serine protease ARA12 a	ARA12	AT5G67360	-1.36	-0.45	-2.29	0.057156	0.147966	-5.14
253498_at	putative protein various predicted prote	---	AT4G31890	-1.49	-0.57	-2.29	0.057186	0.148027	-5.14
251356_at	putative protein hypothetical proteins -	AtPP2-A13	AT3G61060	1.25	0.32	2.29	0.057218	0.148092	-5.14
263230_at	putative indole-3-acetate beta-glucosy	---	AT1G05670	1.41	0.50	2.29	0.057265	0.148197	-5.14
255882_x_	hypothetical protein contains similarity	---	AT1G20280	1.22	0.29	2.29	0.057365	0.14844	-5.14
262601_at	hypothetical protein similar to GB:P49	ATHSRP54A	AT1G15310	1.29	0.36	2.29	0.057379	0.148458	-5.14
260823_at	hypothetical protein predicted by gene	DRIP1	AT1G06770	1.19	0.25	2.29	0.057392	0.148477	-5.14
259566_at	hypothetical protein	---	AT1G20520	1.17	0.22	2.29	0.057445	0.148596	-5.14

249196_at	unknown protein supported by full-len	---	AT5G42560	1.20	0.26	2.29	0.057453	0.148601	-5.14
267399_at	hypothetical protein predicted by gens	---	AT2G44195	-1.16	-0.21	-2.29	0.057562	0.148845	-5.14
252741_at	putative protein predicted protein, Ara	---	AT3G43280	-1.18	-0.24	-2.29	0.057569	0.148845	-5.14
247119_at	ATP-dependent RNA helicase-like ; su	---	AT5G65900	-1.15	-0.20	-2.29	0.057569	0.148845	-5.14
266435_s_	hypothetical protein predicted by gens	---	AT2G07130 /	-1.20	-0.26	-2.29	0.057574	0.148845	-5.14
246716_s_	putative protein	---	AT5G28910 /	-1.16	-0.21	-2.29	0.057582	0.148849	-5.14
250055_at	NADH-cytochrome b5 reductase ;sup	ATCBR	AT5G17770	1.55	0.63	2.29	0.057623	0.148939	-5.15
265969_at	En/Spm-like transposon protein relate	---	---	1.20	0.26	2.29	0.057652	0.14897	-5.15
263897_at	putative shikimate kinase precursor	---	AT2G21940	1.36	0.44	2.29	0.057646	0.14897	-5.15
250487_at	putative protein MRS2 protein, Sacch	---	AT5G09690	-1.26	-0.33	-2.29	0.057655	0.14897	-5.15
244920_s_	NADH dehydrogenase subunit 3 Prote	---	AT2G07751	1.23	0.29	2.29	0.057674	0.149002	-5.15
252148_at	MS5-like protein	---	AT3G51280	-1.22	-0.29	-2.28	0.057703	0.149061	-5.15
254695_at	putative protein predicted protein, Sac	ATL4H	AT4G17905 /	-1.23	-0.30	-2.28	0.057735	0.149126	-5.15
267250_at	similar to hookless1 (HLS1)	---	AT2G23060	-1.17	-0.23	-2.28	0.057768	0.149194	-5.15
265888_at	putative cleavage and polyadenylation	RIE1	AT2G01735	-1.17	-0.22	-2.28	0.057781	0.149212	-5.15
265124_at	hypothetical protein similar to putative	---	AT1G55430	-1.23	-0.30	-2.28	0.057794	0.149212	-5.15
247570_at	putative protein heparanase, Homo sa	AtGUS1	AT5G61250	1.58	0.66	2.28	0.057794	0.149212	-5.15
266330_at	unknown protein ; supported by cDNA	MLP329	AT2G01530	1.33	0.41	2.28	0.057811	0.149238	-5.15
253199_at	clathrin assembly protein AP19 homol	---	AT4G35410	-1.47	-0.55	-2.28	0.057819	0.149243	-5.15
251156_at	putative protein ZCF61, Arabidopsis th	EDL3	AT3G63060	1.26	0.33	2.28	0.057849	0.149302	-5.15
251235_at	putative protein lysophospholipase ho	---	AT3G62860	-1.38	-0.46	-2.28	0.057873	0.149348	-5.15
257652_at	unknown protein contains Pfam profile	APUM24	AT3G16810	1.42	0.50	2.28	0.0579	0.149401	-5.15
249267_at	putative protein contains similarity to 2	BTI3	AT5G41600	-1.35	-0.43	-2.28	0.057956	0.149527	-5.15
252971_at	extensin - like protein proline-rich prot	PRP4	AT4G38770	-3.24	-1.69	-2.28	0.058161	0.15004	-5.16
248938_at	receptor-like protein kinase	---	AT5G45780	1.17	0.23	2.28	0.05819	0.150099	-5.16
267315_at	putative CCAAT-binding transcription f	NF-YA4	AT2G34720	1.33	0.41	2.28	0.05821	0.150108	-5.16
246852_at	putative protein various predicted bact	---	AT5G26880	1.18	0.24	2.28	0.058214	0.150108	-5.16
247744_at	putative protein various predicted prot	---	AT5G59020	-1.27	-0.35	-2.28	0.058213	0.150108	-5.16
261684_at	hypothetical protein predicted by gene	---	AT1G47400	-1.89	-0.92	-2.28	0.058279	0.150191	-5.16
259255_at	putative glycerol-3-phosphate dehydro	---	AT3G07690	1.40	0.49	2.28	0.058267	0.150191	-5.16
264528_at	hypothetical protein similar to Human X	---	AT1G30810	1.16	0.21	2.28	0.058276	0.150191	-5.16
247318_at	3(2),5-bisphosphate nucleotidase ;su	---	AT5G63990	1.61	0.68	2.28	0.058275	0.150191	-5.16
264850_at	unknown protein similar to F5J6.8 and	---	AT2G17340	-1.19	-0.25	-2.28	0.058274	0.150191	-5.16
260228_at	putative cytochrome P450 similar to cy	CYP98A8	AT1G74540	1.20	0.27	2.28	0.058286	0.150192	-5.16
253532_at	putative protein centromere protein E,	---	AT4G31570	-1.19	-0.25	-2.28	0.058304	0.150223	-5.16

255070_at	isoamylase-like protein probable isoar	ISA3	AT4G09020	-1.18	-0.24	-2.28	0.05836	0.150349	-5.16
257016_at	protein kinase, putative similar to PRC	---	AT3G28690	1.23	0.29	2.28	0.05839	0.150409	-5.16
250931_at	putative protein various predicted prot	---	AT5G03200	1.65	0.72	2.28	0.058418	0.150464	-5.16
265778_at	unknown protein	---	AT2G07360	-1.17	-0.23	-2.28	0.058439	0.150501	-5.16
260837_at	fructose 1,6-bisphosphatase, putative	---	AT1G43670	-1.40	-0.49	-2.28	0.058468	0.150558	-5.16
251737_at	40S ribosomal protein S26 homolog se	---	AT3G56340	-1.50	-0.59	-2.28	0.058475	0.150562	-5.16
250552_at	putative protein microtubule binding p	---	AT5G07890	1.18	0.24	2.27	0.058581	0.150818	-5.16
261052_at	hypothetical protein similar to hypothet	---	AT1G01440	1.26	0.33	2.27	0.058616	0.150891	-5.16
244947_at	hypothetical protein	---	---	1.25	0.33	2.27	0.058669	0.151008	-5.16
257199_at	Tic22, putative similar to Tic22 GB:AA	---	AT3G23710	-1.23	-0.30	-2.27	0.058679	0.151017	-5.16
254579_at	hypothetical protein ;supported by full-	---	AT4G19400	-1.25	-0.32	-2.27	0.058691	0.151032	-5.16
258888_at	putative pectinesterase similar to pecti	---	AT3G05620	-1.37	-0.45	-2.27	0.058719	0.151086	-5.16
250946_at	putative protein	---	AT5G03420	1.18	0.24	2.27	0.058785	0.15124	-5.17
265222_at	putative endosomal protein ; supporte	---	AT2G01970	-1.16	-0.21	-2.27	0.058813	0.151295	-5.17
248499_at	putative protein contains similarity to u	PAP27	AT5G50400	1.16	0.22	2.27	0.05883	0.151321	-5.17
250007_at	beta-amylase-like proten beta-amylas	BMY3	AT5G18670	-2.07	-1.05	-2.27	0.058861	0.151384	-5.17
265396_at	predicted protein	---	AT2G21040	-1.31	-0.39	-2.27	0.058895	0.151436	-5.17
255644_at	coded for by A. thaliana cDNA T43872	---	AT4G00870	-1.18	-0.24	-2.27	0.058894	0.151436	-5.17
254042_at	xyloglucan endo-1,4-beta-D-glucanas	XTR6	AT4G25810	-2.36	-1.24	-2.27	0.058905	0.151445	-5.17
261058_at	histone, putative similar to histone H3	HTR12	AT1G01370	-1.17	-0.22	-2.27	0.058917	0.151459	-5.17
265354_at	actin depolymerizing factor 5 ;support	ADF5	AT2G16700	1.51	0.60	2.27	0.058947	0.151518	-5.17
246550_at	putative protein predicted protein, Ara	---	AT5G14920	-2.05	-1.04	-2.27	0.058954	0.15152	-5.17
262821_at	unknown protein EST gb|F14156 come	---	AT1G11800	-1.14	-0.19	-2.27	0.058962	0.151524	-5.17
247006_at	unknown protein ;supported by full-ler	---	AT5G67490	1.14	0.19	2.27	0.059057	0.151752	-5.17
262854_at	unknown protein	---	AT1G20870	-1.20	-0.26	-2.27	0.059124	0.151891	-5.17
246007_at	Expressed protein ; supported by full-l	FTRA2	AT5G08410	-1.24	-0.31	-2.27	0.059125	0.151891	-5.17
253444_at	putative protein ring finger protein, Ho	---	AT4G32600	1.17	0.23	2.27	0.059163	0.151971	-5.17
254944_at	putative protein proliferation potential	---	AT4G10930	1.14	0.19	2.27	0.059194	0.152033	-5.17
266138_at	unknown protein ; supported by full-le	---	AT2G28060	-1.21	-0.28	-2.27	0.059213	0.152065	-5.17
260057_at	putative protein phosphatase 2C simila	---	AT1G78200	1.17	0.23	2.27	0.059289	0.152243	-5.17
260097_at	putative transporter similar to organic c	AtOCT1	AT1G73220	2.88	1.52	2.27	0.059313	0.152272	-5.17
246966_at	DNA photolyase - like protein DNA ph	CRY3	AT5G24850	1.30	0.38	2.27	0.059313	0.152272	-5.17
247779_at	putative protein damage-specific DNA	DDB2	AT5G58760	1.25	0.32	2.27	0.059322	0.152278	-5.18
247738_at	putative protein myosin heavy chain, I	---	AT5G59210	-1.22	-0.29	-2.27	0.05935	0.152333	-5.18
248510_at	Expressed protein ; supported by full-l	---	---	1.16	0.21	2.27	0.059372	0.152338	-5.18

249088_at	selenium-binding protein-like	---	AT5G44230	1.29	0.37	2.27	0.059368	0.152338	-5.18
247494_at	calnexin - like protein calnexin homolo	CNX1	AT5G61790	1.74	0.80	2.27	0.059372	0.152338	-5.18
258214_at	amidase, putative similar to amidase (	atToc64-III	AT3G17970	1.39	0.48	2.27	0.059387	0.152358	-5.18
246367_at	light repressible receptor protein kinas	---	AT1G51880	-1.19	-0.25	-2.26	0.059405	0.152387	-5.18
260707_s_	Expressed protein ; supported by full-l	---	AT1G32410	-1.26	-0.33	-2.26	0.059528	0.152686	-5.18
256242_at	actin-like protein contains Pfam profile	ATARP5	AT3G12380	1.26	0.34	2.26	0.059567	0.152767	-5.18
261019_at	unknown protein ; supported by cDNA	---	AT1G26470	1.21	0.28	2.26	0.059592	0.152815	-5.18
250301_at	putative protein predicted proteins, Ar	---	AT5G11970	1.29	0.37	2.26	0.059647	0.152929	-5.18
246996_at	putative protein similar to unknown pro	LBD37	AT5G67420	-1.35	-0.44	-2.26	0.05965	0.152929	-5.18
246153_s_	RAN1 small Ras-like GTP-binding nuc	RAN-1	AT5G20010 /	1.36	0.44	2.26	0.05969	0.152981	-5.18
262067_at	hypothetical protein predicted by gens	---	AT1G80060	-1.24	-0.32	-2.26	0.059688	0.152981	-5.18
246397_at	hypothetical protein contains similarity	AtRLP9	AT1G58190	1.17	0.23	2.26	0.059679	0.152981	-5.18
247454_at	unknown protein	---	AT5G62440	1.42	0.50	2.26	0.059712	0.153019	-5.18
247720_at	dTDP-glucose 4-6-dehydratase - like	UXS3	AT5G59290	-1.23	-0.30	-2.26	0.059768	0.15313	-5.18
264663_at	unknown protein Similar to A. thaliana	LRR XI-23	AT1G09970	1.71	0.77	2.26	0.059764	0.15313	-5.18
AFFX-r2-At	Arabidopsis thaliana /REF=U37281 /D	---	---	-1.17	-0.23	-2.26	0.059784	0.153153	-5.18
260343_at	fructokinase (Frk1), putative similar to	---	AT1G69200	-1.29	-0.37	-2.26	0.059953	0.15355	-5.19
249380_at	glutaredoxin -like protein glutaredoxin	---	AT5G40370	1.17	0.23	2.26	0.059947	0.15355	-5.19
249029_at	disease resistance protein-like	---	AT5G44870	1.20	0.26	2.26	0.060029	0.153728	-5.19
259295_at	hypothetical protein predicted by gens	---	AT3G05340	1.26	0.33	2.26	0.060079	0.153805	-5.19
260955_at	unknown protein contains similarity to	---	AT1G06000	1.50	0.59	2.26	0.060077	0.153805	-5.19
257839_at	hypothetical protein	---	AT3G25080	-1.17	-0.22	-2.26	0.060079	0.153805	-5.19
262881_at	unknown protein ; supported by cDNA	---	AT1G64890	-1.39	-0.48	-2.26	0.060126	0.153909	-5.19
253342_at	Expressed protein ; supported by cDN	PAA1	AT4G33520	-1.52	-0.61	-2.26	0.060144	0.153936	-5.19
252566_at	cytoplasmic ribosomal protein S15a -l	RPS15AD	AT3G46040	-1.27	-0.34	-2.26	0.060177	0.154004	-5.19
263535_at	hypothetical protein predicted by gens	---	AT2G24970	-1.24	-0.31	-2.26	0.060198	0.154041	-5.19
258438_at	hypothetical protein predicted by gens	---	AT3G17230	-1.15	-0.21	-2.26	0.060217	0.154073	-5.19
250277_at	putative protein DRT100 protein precu	---	AT5G12940	-2.58	-1.37	-2.26	0.060246	0.154128	-5.19
257319_at	hypothetical protein	---	---	1.29	0.37	2.25	0.060268	0.154168	-5.19
265402_at	hypothetical protein predicted by gens	---	AT2G10950	-1.19	-0.25	-2.25	0.060279	0.154178	-5.19
247334_at	cdc2-like protein kinase-like protein su	CDKE;1	AT5G63610	-1.15	-0.20	-2.25	0.060294	0.154192	-5.19
259003_at	hypothetical protein similar to hypothe	---	AT3G02010	1.31	0.39	2.25	0.060298	0.154192	-5.19
245577_at	kinase like protein	---	AT4G14780	-1.23	-0.30	-2.25	0.060419	0.154485	-5.19
249484_at	cytochrome P450 - like protein cytoch	BR6OX1	AT5G38970	-1.18	-0.24	-2.25	0.060442	0.154527	-5.19
249788_at	putative protein contains similarity to u	ATXR6	AT5G24330	-1.31	-0.39	-2.25	0.060462	0.154559	-5.19

264941_at	auxin-induced protein, putative similar	---	AT1G60680	1.37	0.46	2.25	0.060507	0.154658	-5.20
252870_at	adenosine-5-phosphosulfate-kinase	AKN2	AT4G39940	1.93	0.95	2.25	0.060516	0.154663	-5.20
266778_at	putative cytochrome P450	CYP707A2	AT2G29090	-1.24	-0.31	-2.25	0.060544	0.154718	-5.20
266034_at	Expressed protein ; supported by full-le	FIP1	AT2G06005	-1.17	-0.22	-2.25	0.060564	0.154751	-5.20
265311_at	hypothetical protein predicted by gens	---	AT2G20250	-1.35	-0.43	-2.25	0.06059	0.154784	-5.20
247171_at	unknown protein	---	AT5G65540	-1.17	-0.23	-2.25	0.060587	0.154784	-5.20
248368_at	mandelonitrile lyase-like protein ; supp	---	AT5G51950	-1.18	-0.24	-2.25	0.060598	0.154786	-5.20
258005_at	cysteine proteinase contains similarity	---	AT3G19390	2.04	1.03	2.25	0.060621	0.154827	-5.20
262438_at	hypothetical protein identical to hypoth	---	AT1G47410	-1.41	-0.49	-2.25	0.06063	0.154832	-5.20
264751_at	putative superoxide-generating NADP	FRO3	AT1G23020	-1.80	-0.85	-2.25	0.060656	0.154865	-5.20
261656_at	unknown protein similar to kinesin-like	ARK2	AT1G01950	-1.60	-0.68	-2.25	0.060652	0.154865	-5.20
258209_at	expressed protein supported by cDNA	GAPC1	AT3G04120 /	1.54	0.62	2.25	0.060726	0.155026	-5.20
267103_at	putative UDP-N-acetylglucosamine--d	GPT	AT2G41490	1.20	0.26	2.25	0.060754	0.155081	-5.20
257487_at	hypothetical protein predicted by gene	---	AT1G71850	1.41	0.49	2.25	0.060783	0.155138	-5.20
252608_at	putative protein 2-phosphoglycerate k	---	AT3G45090	1.22	0.29	2.25	0.06083	0.155239	-5.20
258597_x_	hypothetical protein predicted by gene	---	AT3G04390	1.16	0.22	2.25	0.060868	0.155319	-5.20
261155_at	unknown protein ;supported by full-len	---	AT1G04960	1.23	0.30	2.25	0.060883	0.155341	-5.20
261827_at	unknown protein contains similarity to	---	AT1G11480	1.18	0.24	2.25	0.060891	0.155343	-5.20
266346_at	putative homeodomain transcription fa	ATHB17	AT2G01430	-1.25	-0.33	-2.25	0.060942	0.155455	-5.20
250302_at	fructosidase - like protein fructosidase	AtcwINV6	AT5G11920	2.44	1.29	2.25	0.061122	0.155897	-5.21
263380_at	hypothetical protein	---	AT2G40200	1.19	0.25	2.25	0.061138	0.15592	-5.21
260349_at	mitotic checkpoint protein, putative sir	---	AT1G69400	-1.22	-0.28	-2.24	0.061201	0.156019	-5.21
257930_at	hypothetical protein	---	AT3G17010	-1.27	-0.35	-2.24	0.06119	0.156019	-5.21
254863_at	putative protein predicted protein W02	ATNUDX14	AT4G11980	-1.23	-0.30	-2.24	0.061211	0.156019	-5.21
247956_at	cytokinin oxidase ; supported by cDNA	CKX3	AT5G56970	-1.19	-0.26	-2.24	0.061207	0.156019	-5.21
261797_at	cation-chloride co-transporter, putative	---	AT1G30455	-1.21	-0.27	-2.24	0.061203	0.156019	-5.21
244903_at	hypothetical protein	---	---	1.61	0.69	2.24	0.061219	0.156023	-5.21
257300_at	unknown protein ; supported by full-le	---	AT3G28080	1.39	0.47	2.24	0.061243	0.156031	-5.21
266510_at	unknown protein	SWA1	AT2G47990	1.45	0.54	2.24	0.061237	0.156031	-5.21
260002_at	putative ABC transporter similar to AB	ATNAP3	AT1G67940	1.34	0.42	2.24	0.061233	0.156031	-5.21
265569_at	unknown protein ;supported by full-ler	PGR5	AT2G05620	-1.20	-0.26	-2.24	0.061269	0.156059	-5.21
256667_at	hypothetical protein predicted by gene	---	AT3G32180	1.15	0.20	2.24	0.061273	0.156059	-5.21
247336_at	putative protein similar to unknown pro	---	AT5G63640	-1.25	-0.33	-2.24	0.061274	0.156059	-5.21
264955_at	F-box protein family, AtFBX3 contains	---	AT1G76920	-1.26	-0.33	-2.24	0.06136	0.156261	-5.21
263009_at	hypothetical protein contains similarity	NHX5	AT1G54370	1.18	0.24	2.24	0.061418	0.156355	-5.21

245194_at	F12A21.5 similar to protein phosphata	---	AT1G67820	1.38	0.47	2.24	0.061413	0.156355	-5.21
247671_at	putative protein slow myosin heavy ch	---	AT5G60210	-1.16	-0.21	-2.24	0.061416	0.156355	-5.21
246609_at	putative receptor-like protein kinase re	---	AT5G35390	-1.16	-0.22	-2.24	0.061445	0.156406	-5.21
261392_at	hypothetical protein predicted by gene	---	AT1G79780	-1.17	-0.23	-2.24	0.061482	0.156474	-5.21
264179_at	hypothetical protein predicted by gene	---	AT1G02180	-1.33	-0.41	-2.24	0.061485	0.156474	-5.21
257393_at	unknown protein	---	AT2G20080	1.15	0.20	2.24	0.061523	0.156552	-5.21
258455_at	unknown protein ;supported by full-ler	---	AT3G22440	1.30	0.38	2.24	0.061545	0.15659	-5.21
262006_at	hypothetical protein predicted by gens	---	AT1G64570	1.19	0.25	2.24	0.061561	0.156613	-5.21
252312_at	hypothetical protein SF16 protein, Hel	iqd15	AT3G49380	-1.24	-0.30	-2.24	0.061579	0.156643	-5.21
254096_at	acid phosphatase - like protein acid pl	---	AT4G25150	-1.22	-0.28	-2.24	0.061587	0.156646	-5.21
250369_at	cyclin 3b ; supported by cDNA: gi_600	CYC3B	AT5G11300	1.25	0.33	2.24	0.061602	0.156667	-5.21
262175_at	unknown protein ; supported by cDNA	NDH-O	AT1G74880	-1.27	-0.35	-2.24	0.061706	0.156913	-5.21
244928_s_	hypothetical protein	---	AT2G07716	1.19	0.25	2.24	0.061746	0.156997	-5.22
265170_at	putative carbonic anhydrase	BCA3	AT1G23730	2.76	1.47	2.24	0.061783	0.157074	-5.22
247886_at	branched-chain amino acid aminotrans	---	AT5G57850	1.29	0.37	2.24	0.061794	0.157084	-5.22
260358_at	unknown protein ; supported by cDNA	---	AT1G69340	-1.17	-0.23	-2.24	0.061803	0.15709	-5.22
247061_at	putative protein similar to unknown pro	---	AT5G66780	1.32	0.40	2.24	0.061821	0.15712	-5.22
255613_at	putative RING zinc finger protein	---	AT4G01270	-1.23	-0.30	-2.24	0.061841	0.157153	-5.22
261397_at	hexose transporter, putative similar to	SGB1	AT1G79820	-1.37	-0.46	-2.24	0.061861	0.157185	-5.22
259543_at	hypothetical protein ; supported by full-	---	AT1G20580	-1.23	-0.29	-2.24	0.061891	0.157245	-5.22
260315_at	hypothetical protein similar to C-termi	---	AT1G63820	-1.18	-0.24	-2.24	0.061919	0.157297	-5.22
246934_at	putative protein several hypothetical pr	---	AT5G25290	-1.24	-0.31	-2.24	0.061936	0.157324	-5.22
248664_at	peptidyl-prolyl cis-trans isomerase-like	FKBP15-2	AT5G48580	-1.30	-0.38	-2.24	0.061969	0.157389	-5.22
264843_at	putative 1-aminocyclopropane-1-carbo	---	AT1G03400	-1.36	-0.44	-2.24	0.061986	0.157405	-5.22
261609_at	unknown protein similar to MAP3K-like	---	AT1G49740	1.34	0.42	2.24	0.061992	0.157405	-5.22
258630_at	putative CCHC-type zinc finger protei	---	AT3G02820	-1.31	-0.39	-2.24	0.061996	0.157405	-5.22
248637_at	DNAJ-like protein	---	AT5G49060	1.18	0.24	2.24	0.062018	0.157408	-5.22
249859_at	serine protein kinase-like protein ;sup	---	AT5G22840 /	1.39	0.48	2.24	0.062012	0.157408	-5.22
264572_at	unknown protein ESTs gb|AA042402,	---	AT1G05320	-1.21	-0.28	-2.24	0.062014	0.157408	-5.22
250714_at	sorting nexin-like protein	SNX1	AT5G06140	1.22	0.29	2.23	0.062075	0.157535	-5.22
255117_s_	putative protein various hypothetical pr	ATPUP13	AT4G08700 /	-1.15	-0.21	-2.23	0.06213	0.157644	-5.22
248030_at	transcription regulator Sir2-like protein	SRT1	AT5G55760	-1.28	-0.36	-2.23	0.062132	0.157644	-5.22
264628_at	hypothetical protein contains similarity	---	AT1G65540	1.15	0.20	2.23	0.062141	0.157649	-5.22
250742_at	putative protein similar to unknown pro	---	AT5G05800	-1.21	-0.28	-2.23	0.062172	0.157711	-5.22
247369_at	unknown protein	---	AT5G63340	-1.23	-0.30	-2.23	0.062341	0.158124	-5.23

257790_at	gda-1, putative similar to gda-1 GB:CA	---	AT3G27090	1.26	0.33	2.23	0.062379	0.158184	-5.23
247919_at	putative protein similar to unknown pro	---	AT5G57650	1.22	0.29	2.23	0.062375	0.158184	-5.23
253239_at	putative serine/threonine protein kinas	---	AT4G34500	-1.32	-0.41	-2.23	0.062476	0.158341	-5.23
259760_at	hypothetical protein similar to GB:AAD	---	AT1G77580	-1.15	-0.20	-2.23	0.062461	0.158341	-5.23
256968_at	unknown protein	NADK1	AT3G21070	2.37	1.24	2.23	0.062474	0.158341	-5.23
255311_at	putative protein	---	---	-1.17	-0.23	-2.23	0.062449	0.158341	-5.23
257375_at	unknown protein	---	AT2G38640	1.69	0.76	2.23	0.062462	0.158341	-5.23
263328_at	hypothetical protein similar to hypothet	---	AT2G15280	-1.25	-0.33	-2.23	0.062581	0.158591	-5.23
267110_at	hypothetical protein predicted by gens	---	AT2G14800	-1.25	-0.32	-2.23	0.062589	0.158593	-5.23
259200_at	unknown protein similar to hypothetica	---	AT3G09070	1.19	0.25	2.23	0.062601	0.158606	-5.23
249063_at	NBD-like protein (gb|AAD20643.1) ;su	POP1	AT5G44110	-1.28	-0.36	-2.23	0.062657	0.158713	-5.23
256216_at	calreticulin (crt1) identical to calreticuli	CRT1	AT1G56340 /	1.44	0.52	2.23	0.062652	0.158713	-5.23
248716_at	unknown protein ;supported by full-ler	---	AT5G48210	-1.25	-0.32	-2.23	0.062717	0.158846	-5.23
254422_at	putative protein hypothetical protein Y	VPS28-1	AT4G21560	-1.40	-0.49	-2.23	0.062757	0.15893	-5.23
261635_at	tubulin alpha-6 chain, putative identica	---	AT1G50020	1.26	0.33	2.23	0.062773	0.158941	-5.23
259542_at	Expressed protein ; supported by full-le	---	AT1G20575	-1.19	-0.26	-2.23	0.062775	0.158941	-5.23
247605_at	DNA binding protein - like putative bas	TCP5	AT5G60970	-1.24	-0.31	-2.23	0.062807	0.159005	-5.23
248257_at	putative protein similar to unknown pro	---	AT5G53410	-1.27	-0.34	-2.23	0.062826	0.159035	-5.23
248984_at	DNA-directed RNA polymerase subuni	NRPC2	AT5G45140	1.25	0.32	2.23	0.062849	0.159058	-5.23
254779_at	hypothetical protein	---	AT4G12760	1.17	0.23	2.23	0.062849	0.159058	-5.23
255706_at	putative ribosomal protein S13 similar	ATRPS13A	AT4G00100	-1.31	-0.39	-2.23	0.062859	0.159065	-5.23
255285_at	putative protein A. thaliana hypothetic	---	AT4G04630	-1.75	-0.81	-2.23	0.062883	0.159109	-5.23
246112_at	putative protein predicted proteins - Ar	---	AT5G20200	1.23	0.30	2.23	0.062925	0.15918	-5.23
251219_at	putative protein several hypothetical pr	---	AT3G62390	-1.42	-0.50	-2.23	0.062922	0.15918	-5.23
266011_at	unknown protein	---	AT2G37440	1.20	0.26	2.22	0.062959	0.159248	-5.24
260769_at	Expressed protein ; supported by full-le	---	AT1G49010	-1.37	-0.46	-2.22	0.062973	0.159266	-5.24
261175_at	unknown protein	---	AT1G04800	-1.20	-0.27	-2.22	0.06302	0.15936	-5.24
246109_at	hypothetical protein (fragment?)	---	AT5G20120	-1.23	-0.30	-2.22	0.063048	0.15936	-5.24
257759_at	hypothetical protein	---	AT3G23070	-1.31	-0.39	-2.22	0.063027	0.15936	-5.24
264965_at	hypothetical protein predicted by gene	---	AT1G60560	-1.24	-0.32	-2.22	0.063052	0.15936	-5.24
265091_s_	hypothetical protein similar to Anthocy	---	AT1G03495 /	1.26	0.33	2.22	0.063038	0.15936	-5.24
248891_at	MCM3 homolog (emb|CAA03887.1)	MCM3	AT5G46280	-2.01	-1.01	-2.22	0.063046	0.15936	-5.24
257714_at	histone H3, putative similar to histone	---	AT3G27360	-1.23	-0.30	-2.22	0.06308	0.159413	-5.24
248988_at	putative protein contains similarity to c	---	AT5G45190	1.21	0.27	2.22	0.063128	0.159444	-5.24
246301_at	calcium-dependent protein kinase	CPK13	AT3G51850	-1.18	-0.24	-2.22	0.063108	0.159444	-5.24

255985_at	putative protein contains similarity to p	---	AT1G34150	1.16	0.22	2.22	0.063127	0.159444	-5.24
258073_at	putative auxin-resistance protein, AXF	---	AT3G25880	-1.18	-0.24	-2.22	0.063124	0.159444	-5.24
259839_at	peptide transporter, putative similar to	---	AT1G52190	-2.66	-1.41	-2.22	0.063109	0.159444	-5.24
250824_at	putative protein contains similarity to u	---	AT5G05200	-1.27	-0.34	-2.22	0.063145	0.15947	-5.24
257780_at	hypothetical protein predicted by gene	---	AT3G27100	1.24	0.30	2.22	0.063195	0.15958	-5.24
252425_at	putative protein auxin-induced basic h	AtTCP14	AT3G47620	-1.32	-0.40	-2.22	0.063225	0.159619	-5.24
262666_at	xyloglucan fucosyltransferase, putativ	FUT6	AT1G14080	1.43	0.51	2.22	0.063222	0.159619	-5.24
251858_at	aquaporin MIP - like protein aquaporin	PIP2;5	AT3G54820	-1.34	-0.43	-2.22	0.063241	0.159641	-5.24
266108_at	putative peptide/amino acid transporte	---	AT2G37900	-1.24	-0.31	-2.22	0.063263	0.159681	-5.24
257775_at	short-chain alcohol dehydrogenase, p	---	AT3G29260	-1.21	-0.27	-2.22	0.063376	0.159913	-5.24
266238_at	phosphoprotein phosphatase, type 1 c	TOPP1	AT2G29400	1.33	0.41	2.22	0.063362	0.159913	-5.24
250022_at	Brn1-like protein	---	AT5G18210	-1.38	-0.46	-2.22	0.063371	0.159913	-5.24
250616_at	receptor-like protein kinase-like protei	EMS1	AT5G07280	1.23	0.30	2.22	0.063389	0.159927	-5.24
258329_at	putative protein disulfide isomerase sir	ATPDIL1-6	AT3G16110	-1.19	-0.25	-2.22	0.063425	0.15996	-5.24
251055_at	putative protein putative protein F4P1	---	AT5G01710 /	-1.18	-0.23	-2.22	0.063413	0.15996	-5.24
267501_at	unknown protein	---	AT2G45540	-1.25	-0.33	-2.22	0.063427	0.15996	-5.24
265064_at	hypothetical protein contains similarity	ENT7	AT1G61630	1.32	0.40	2.22	0.06343	0.15996	-5.24
256854_at	hypothetical protein predicted by gene	---	AT3G15180	1.18	0.24	2.22	0.063548	0.16024	-5.24
248357_at	putative protein similar to unknown pro	---	AT5G52380	1.42	0.51	2.22	0.063558	0.160247	-5.24
263473_at	putative glucosyltransferase ; support	UGT74D1	AT2G31750	-1.63	-0.70	-2.22	0.063578	0.16028	-5.25
265243_at	hypothetical protein predicted by gens	NPG1	AT2G43040	-1.20	-0.27	-2.22	0.063607	0.160336	-5.25
245687_at	unknown protein	DEG15	AT1G28320	1.15	0.20	2.22	0.063644	0.16034	-5.25
246300_at	putative transmembrane protein G5p	SAC8	AT3G51830	1.18	0.23	2.22	0.06363	0.16034	-5.25
257484_at	unknown protein	---	AT1G01650	-1.17	-0.23	-2.22	0.063625	0.16034	-5.25
245787_at	unknown protein	---	AT1G32130	1.21	0.27	2.22	0.063623	0.16034	-5.25
254008_at	hypothetical protein various predicted	---	AT4G26380	1.20	0.26	2.22	0.063639	0.16034	-5.25
245451_at	disease resistance RPP5 like protein	SNC1	AT4G16890	-1.16	-0.22	-2.22	0.063687	0.160431	-5.25
265859_at	hypothetical protein predicted by gens	---	---	-1.19	-0.25	-2.22	0.063707	0.160463	-5.25
246847_at	putative protein ferroportin1, Mus mus	ATIREG3	AT5G26820	-1.36	-0.45	-2.22	0.063835	0.160768	-5.25
257866_at	dihydroxyacetone kinase, putative sim	---	AT3G17770	1.52	0.60	2.21	0.063868	0.160834	-5.25
255339_at	hypothetical protein similar to A. thalia	---	AT4G04480	1.41	0.49	2.21	0.063879	0.160844	-5.25
263414_at	putative bZIP transcription factor conta	---	AT2G21230	1.18	0.24	2.21	0.06389	0.160854	-5.25
263626_at	transcription factor ZAP1 identical to G	ZAP1	AT2G04880	1.16	0.21	2.21	0.063909	0.160884	-5.25
252565_at	actin depolymerizing factor 2 (ADF2) ;	ADF2	AT3G46000	1.16	0.21	2.21	0.063969	0.161	-5.25
265157_at	putative reverse transcriptase similar t	---	---	-1.20	-0.26	-2.21	0.063964	0.161	-5.25

248821_at	protein serine threonine kinase-like	---	AT5G47070	1.49	0.57	2.21	0.063983	0.161017	-5.25
259292_at	unknown protein	---	AT3G11560	1.20	0.27	2.21	0.063992	0.161021	-5.25
259669_at	short chain alcohol dehydrogenase, p	ABA2	AT1G52340	-1.24	-0.31	-2.21	0.064052	0.161154	-5.25
265604_s_	hypothetical protein predicted by gens	---	---	-1.20	-0.26	-2.21	0.064061	0.161159	-5.25
245493_at	hypothetical protein	---	---	-1.17	-0.22	-2.21	0.064097	0.161233	-5.25
260963_at	hypothetical protein predicted by gene	---	AT1G44990	1.19	0.25	2.21	0.064136	0.161312	-5.25
255691_at	hypothetical protein	ANTR2	AT4G00370	-1.22	-0.29	-2.21	0.064151	0.161333	-5.25
255129_at	nodulin-like protein nodulin gene MtN	---	AT4G08290	1.55	0.63	2.21	0.064165	0.161349	-5.25
262322_at	hypothetical protein similar to hypothet	---	AT1G27590	1.24	0.31	2.21	0.064254	0.161557	-5.26
265909_at	unknown protein ;supported by full-ler	---	AT2G25720	1.21	0.28	2.21	0.064273	0.161586	-5.26
250484_at	asparagine synthetase ASN3 ; suppor	ASN3	AT5G10240	-1.19	-0.25	-2.21	0.064304	0.161645	-5.26
250172_at	putative protein	---	AT5G14330	-1.27	-0.35	-2.21	0.06439	0.161843	-5.26
252785_at	putative protein AND-1 protein - Hom	---	AT3G42660	-1.39	-0.47	-2.21	0.064426	0.161895	-5.26
263623_at	hypothetical protein predicted by gens	---	AT2G04860	-1.15	-0.21	-2.21	0.064438	0.161895	-5.26
263387_at	unknown protein ; supported by cDNA	---	AT2G40160	-1.21	-0.28	-2.21	0.064438	0.161895	-5.26
252326_at	putative protein ferripyochelin binding	GAMMA CA	AT3G48680	-1.21	-0.27	-2.21	0.064429	0.161895	-5.26
261835_at	hypothetical protein contains similarity	---	AT1G16040	1.21	0.27	2.21	0.064463	0.161938	-5.26
258545_at	putative GTPase contains Pfam profile	---	AT3G07050	1.35	0.43	2.21	0.064474	0.161947	-5.26
257571_at	hypothetical protein predicted by gene	---	AT3G16870	1.40	0.48	2.21	0.064503	0.162002	-5.26
250895_at	RIBOSOMAL PROTEIN S28- like ribo	---	AT5G03850	-1.32	-0.41	-2.21	0.06454	0.162079	-5.26
248560_at	putative protein contains similarity to p	ATPPOX	AT5G49970	-1.25	-0.32	-2.21	0.064574	0.162146	-5.26
245673_at	hypothetical protein similar to putative	---	AT1G56690	1.22	0.29	2.21	0.064635	0.162281	-5.26
245949_at	elongation factor 1B alpha-subunit ;su	---	AT5G19510	-1.26	-0.33	-2.21	0.064654	0.162311	-5.26
253384_at	Expressed protein ; supported by full-l	---	AT4G32915	-1.23	-0.30	-2.21	0.064728	0.162478	-5.26
266453_at	putative protein kinase contains a prot	---	AT2G43230	-1.16	-0.21	-2.21	0.06474	0.16249	-5.26
264049_at	putative GTP-binding protein	---	AT2G22390	-1.29	-0.37	-2.21	0.064768	0.162543	-5.26
251487_at	cysteine synthase	OASC	AT3G59760	-1.42	-0.51	-2.20	0.06492	0.1629	-5.27
248973_at	disease resistance protein-like	TTR1	AT5G45050	1.15	0.20	2.20	0.064924	0.1629	-5.27
258646_at	MATE efflux family protein, putative c	FRD3	AT3G08040	1.17	0.23	2.20	0.064977	0.162996	-5.27
251856_at	Peptidase - like protein ileal peptidase	AMP1	AT3G54720	-1.34	-0.43	-2.20	0.064973	0.162996	-5.27
246540_at	nitrilase associated protein-like nitrilas	SP1L4	AT5G15600	-1.29	-0.36	-2.20	0.065013	0.163069	-5.27
263894_at	putative cytochrome P450	CYP96A5	AT2G21910	-1.20	-0.27	-2.20	0.065025	0.163081	-5.27
258654_at	unknown protein	---	AT3G09860	-1.32	-0.40	-2.20	0.065046	0.163116	-5.27
264760_at	syntaxin-related protein Nt-syr1, putat	SYP124	AT1G61290	1.27	0.35	2.20	0.065075	0.16317	-5.27
266725_at	SKP1/ASK1 (At14), putative similar to	ASK14	AT2G03170	1.18	0.24	2.20	0.065083	0.163172	-5.27

264378_at	hypothetical protein predicted by gens	---	AT2G25220	-1.62	-0.70	-2.20	0.065093	0.163179	-5.27
264253_at	putative kinesin similar to GB:AAB610	---	AT1G09170	-1.31	-0.39	-2.20	0.065135	0.16325	-5.27
250810_at	putative protein contains similarity to u	---	AT5G05090	-1.35	-0.43	-2.20	0.065134	0.16325	-5.27
251134_at	hypothetical protein RNA polymerase	AtQSOX2	AT2G01270 /	1.20	0.26	2.20	0.065143	0.163251	-5.27
252299_at	putative protein various predicted prot	---	AT3G49150	1.23	0.29	2.20	0.065157	0.163267	-5.27
259084_at	putative inner mitochondrial membrane	ATTIM23-3	AT3G04800	1.19	0.25	2.20	0.065205	0.16337	-5.27
253338_at	somatic embryogenesis receptor-like	BAK1	AT4G33430	1.20	0.26	2.20	0.065268	0.163493	-5.27
266505_at	unknown protein	---	AT2G47830	1.18	0.24	2.20	0.065268	0.163493	-5.27
258980_at	putative reversibly glycosylatable polyp	RGP3	AT3G08900	-1.18	-0.24	-2.20	0.065311	0.163581	-5.27
258075_at	homocysteine S-methyltransferase AtH	HMT-1	AT3G25900	2.30	1.20	2.20	0.065347	0.163654	-5.27
255410_at	putative rac GTPase activating protein	---	AT4G03100	-1.19	-0.26	-2.20	0.065367	0.163688	-5.27
250899_at	putative protein ; supported by cDNA:	---	AT5G03340	1.29	0.36	2.20	0.065384	0.163711	-5.27
248408_at	ripening-related protein-like	---	AT5G51520	-1.16	-0.22	-2.20	0.065406	0.163749	-5.27
247303_at	histidinol dehydrogenase ;supported b	ATHDH	AT5G63890	-1.28	-0.35	-2.20	0.065423	0.163774	-5.27
265130_at	unknown protein similar to ESTs gb|T7	---	AT1G30890	-1.14	-0.19	-2.20	0.065442	0.163802	-5.27
251745_at	putative protein zinc finger transcriptio	SZF1	AT3G55980	2.62	1.39	2.20	0.065467	0.163848	-5.27
251534_at	ATP-dependent RNA helicase-like pro	---	AT3G58510	1.35	0.43	2.20	0.065503	0.16392	-5.28
251660_at	Expressed protein ; supported by full-l	---	AT3G57160	-1.28	-0.36	-2.20	0.065518	0.163923	-5.28
265942_at	putative casein kinase I ;supported by	ckl5	AT2G19470	1.19	0.25	2.20	0.065519	0.163923	-5.28
246074_at	hypothetical protein ; supported by ful	---	AT5G20130	-1.17	-0.23	-2.20	0.065582	0.164046	-5.28
267265_at	putative serine carboxypeptidase I ; su	SCPL13	AT2G22980	-1.30	-0.38	-2.20	0.065577	0.164046	-5.28
260729_at	regulatory protein, putative contains P	KU80	AT1G48050	1.16	0.21	2.20	0.065592	0.164053	-5.28
259679_at	putative protein kinase Pfam HMM hit	---	AT1G77720	-1.15	-0.21	-2.20	0.065652	0.164185	-5.28
250666_at	SPF1-like protein SPF1 protein - Ipom	WRKY26	AT5G07100	1.49	0.58	2.20	0.065712	0.164308	-5.28
255679_at	putative acetyl CoA thioesterase	---	AT4G00520	-1.27	-0.35	-2.20	0.065716	0.164308	-5.28
252027_at	Spot 3 protein and vacuolar sorting rec	VSR1	AT3G52850	1.16	0.22	2.20	0.065725	0.164312	-5.28
257000_at	hypothetical protein predicted by gene	---	AT3G14120	1.32	0.40	2.19	0.065751	0.16436	-5.28
259678_at	putative 30S ribosomal protein S13 si	---	AT1G77750	-1.30	-0.38	-2.19	0.065906	0.16473	-5.28
249108_at	steroid sulfotransferase-like	---	AT5G43690	-1.14	-0.19	-2.19	0.065932	0.164775	-5.28
264767_at	hypothetical protein similar to putative	SD1-29	AT1G61380	1.59	0.67	2.19	0.065961	0.164831	-5.28
263539_at	putative tyrosine aminotransferase ;su	TAT3	AT2G24850	3.08	1.62	2.19	0.065974	0.164845	-5.28
263219_at	putative serine proteinase Strong simil	---	AT1G30600	-1.28	-0.36	-2.19	0.066007	0.16491	-5.28
266360_at	Mutator-like transposase similar to MU	FRS2	AT2G32250	1.45	0.53	2.19	0.066045	0.164987	-5.28
248494_at	putative protein contains similarity to o	AtHSD6	AT5G50770	-1.20	-0.26	-2.19	0.0661	0.165105	-5.28
261208_at	unknown protein ; supported by cDNA	---	AT1G12930	1.26	0.34	2.19	0.066144	0.165197	-5.28

255494_at	predicted protein of unknown function	---	AT4G02710	1.17	0.23	2.19	0.066157	0.165211	-5.29
250836_at	putative protein various predicted prot	DME	AT5G04560	-1.15	-0.21	-2.19	0.066164	0.165212	-5.29
250465_at	putative protein various predicted prote	---	AT5G10070	-1.15	-0.20	-2.19	0.06624	0.165381	-5.29
265697_at	hypothetical protein predicted by gens	---	AT2G32170	-1.18	-0.23	-2.19	0.066266	0.16543	-5.29
257708_at	hypothetical protein predicted by gens	---	AT3G13330	1.19	0.25	2.19	0.066276	0.165437	-5.29
256280_at	unknown protein	---	AT3G12590	-1.22	-0.28	-2.19	0.066313	0.165493	-5.29
246702_at	putative cytidine deaminase - like puta	---	AT5G28050	1.63	0.70	2.19	0.066308	0.165493	-5.29
264491_at	hypothetical protein predicted by gens	---	AT1G27410	1.18	0.24	2.19	0.066365	0.165605	-5.29
267604_at	hypothetical protein predicted by gene	ZFN2	AT2G32930	-1.43	-0.51	-2.19	0.066422	0.165709	-5.29
246883_at	putative protein many predicted protei	---	AT5G26190	-1.16	-0.21	-2.19	0.066428	0.165709	-5.29
255250_at	MYB - like protein cM4 myb transcript	AtMYB74	AT4G05100	1.95	0.96	2.19	0.066429	0.165709	-5.29
245616_at	kinase like protein	---	AT4G14480	-1.39	-0.48	-2.19	0.066494	0.165836	-5.29
250911_at	SERINE/THREONINE-PROTEIN KINA	CTR1	AT5G03730	1.26	0.33	2.19	0.066494	0.165836	-5.29
247555_at	putative protein various predicted prote	ECT3	AT5G61020	1.35	0.43	2.19	0.066546	0.165936	-5.29
249094_at	dimethylaniline monooxygenase-like	YUC5	AT5G43890	-1.24	-0.31	-2.19	0.066556	0.165936	-5.29
253943_at	putative protein gene F19K23.12 of B	---	AT4G27030	-1.64	-0.71	-2.19	0.066554	0.165936	-5.29
245447_at	triacylglycerol lipase like protein	---	AT4G16820	1.74	0.80	2.19	0.066648	0.166148	-5.29
264021_at	putative auxin-regulated protein ;supp	---	AT2G21200	-1.50	-0.59	-2.19	0.06667	0.166184	-5.29
247636_at	putative protein predicted proteins fron	---	AT5G60570	-1.19	-0.25	-2.18	0.066752	0.166335	-5.29
266722_at	unknown protein	FUT2	AT2G03210	-1.20	-0.27	-2.18	0.06676	0.166335	-5.29
247033_at	SKP1 interacting partner 2 (SKIP2) ide	SKIP2	AT5G67250	1.22	0.28	2.18	0.06676	0.166335	-5.29
251907_at	putative protein 85p protein - Medicag	---	AT3G53760	-1.36	-0.45	-2.18	0.066752	0.166335	-5.29
260460_at	unknown protein	---	AT1G68230	-1.19	-0.26	-2.18	0.066792	0.166397	-5.29
256367_at	C-x8-C-x5-C-x3-H type Zinc finger pro	---	AT1G66810	-1.20	-0.27	-2.18	0.066842	0.166502	-5.30
259270_at	putative porin similar to outer mitochor	VDAC1	AT3G01280	1.22	0.29	2.18	0.066875	0.166567	-5.30
245187_s_	F12A21.17 similar to signal recognitior	---	AT1G67650 /	1.18	0.24	2.18	0.066999	0.166859	-5.30
250018_at	putative protein similar to unknown pro	---	AT5G18150	1.72	0.78	2.18	0.067022	0.166898	-5.30
247167_at	unknown protein	---	AT5G65850	-1.24	-0.31	-2.18	0.067073	0.167004	-5.30
262380_at	threonine synthase, putative similar to	---	AT1G72810	-1.22	-0.28	-2.18	0.067103	0.167062	-5.30
260890_at	cysteine proteinase contains similarity	---	AT1G29090	1.29	0.36	2.18	0.067147	0.167154	-5.30
245600_at	hypothetical protein	---	AT4G14230	-1.25	-0.32	-2.18	0.067247	0.167351	-5.30
260476_at	unknown protein	---	AT1G11060	1.24	0.32	2.18	0.067249	0.167351	-5.30
252847_at	putative transposase hypothetical prot	---	AT3G42170	-1.21	-0.28	-2.18	0.067247	0.167351	-5.30
250246_at	polyamine oxidase	ATPAO1	AT5G13700	-1.15	-0.21	-2.18	0.06726	0.167362	-5.30
259999_at	hypothetical protein predicted by gene	---	AT1G68080	-1.29	-0.37	-2.18	0.067325	0.167504	-5.30

250650_at	anthranilate phosphoribosyltransferase	---	AT5G06850	1.32	0.40	2.18	0.067358	0.167567	-5.30
264554_at	putative cinnamyl alcohol dehydrogen	---	AT1G09510	1.25	0.33	2.18	0.067382	0.167611	-5.30
266951_at	putative salt-inducible protein ; suppor	---	AT2G18940	1.16	0.21	2.18	0.067419	0.167669	-5.30
264978_at	unknown protein contains Pfam profile	---	AT1G27120	-1.40	-0.49	-2.18	0.06742	0.167669	-5.30
254431_at	reticuline oxidase - like protein reticuli	---	AT4G20840	-1.34	-0.42	-2.18	0.067437	0.167692	-5.30
251467_at	putative protein putative proteins - Ara	---	AT3G59470	-1.24	-0.31	-2.18	0.067517	0.167872	-5.31
252340_at	myb-like protein	AtMYB45	AT3G48920	1.31	0.39	2.18	0.067557	0.167955	-5.31
251067_at	hypothetical protein	---	AT5G01910	-1.29	-0.37	-2.18	0.067575	0.167979	-5.31
267017_at	unknown protein	SVR1	AT2G39140	-1.47	-0.55	-2.18	0.067582	0.16798	-5.31
263482_at	putative GDSL-motif lipase/hydrolase s	---	AT2G03980	-2.26	-1.18	-2.18	0.067604	0.168015	-5.31
263438_at	unknown protein	---	AT2G28660	1.25	0.32	2.18	0.067659	0.168133	-5.31
258994_at	unknown protein similar to putative gua	RAPTOR1	AT3G08850	1.17	0.22	2.17	0.067727	0.168285	-5.31
262303_at	homeobox protein, putative similar to	ATHB18	AT1G70920	1.33	0.42	2.17	0.067771	0.168376	-5.31
244927_at	hypothetical protein	---	AT2G07776	1.25	0.32	2.17	0.067835	0.168517	-5.31
245465_at	cellulose synthase like protein	ATCSLA01	AT4G16590	-1.98	-0.98	-2.17	0.067863	0.168568	-5.31
259582_at	hypothetical protein	---	AT1G28060	1.23	0.30	2.17	0.067892	0.16862	-5.31
256466_at	plastid protein, putative similar to GI:2	---	AT1G32580	-1.15	-0.21	-2.17	0.067911	0.168649	-5.31
255816_at	unknown protein ;supported by full-ler	GLTP1	AT2G33470	1.16	0.21	2.17	0.067931	0.168681	-5.31
261989_at	disease resistance protein, putative si	---	AT1G33670	1.20	0.27	2.17	0.067943	0.168692	-5.31
253456_at	putative protein norbin, Rattus norveg	---	AT4G32050	1.25	0.32	2.17	0.06797	0.168742	-5.31
253369_at	F-box protein family, AtFBL15 contain	---	AT4G33210	-1.14	-0.19	-2.17	0.068014	0.168832	-5.31
255675_at	MYC1 transcription factor	ATMYC1	AT4G00480	-1.20	-0.26	-2.17	0.068054	0.168912	-5.31
251233_at	putative protein hypothetical protein A	DRB4	AT3G62800	1.19	0.25	2.17	0.068066	0.168925	-5.31
263038_at	conserved hypothetical protein protein	---	AT1G23270	-1.18	-0.23	-2.17	0.068098	0.168967	-5.31
248268_at	importin beta	---	AT5G53480	-1.23	-0.30	-2.17	0.068098	0.168967	-5.31
252539_at	putative protein	---	AT3G45730	-1.25	-0.33	-2.17	0.068144	0.169064	-5.31
251849_at	Expressed protein ; supported by cDN	HAG1	AT3G54610	-1.21	-0.28	-2.17	0.06817	0.16909	-5.32
246841_at	nectarin - like protein nectarin I precur	---	AT5G26700	1.38	0.46	2.17	0.068166	0.16909	-5.32
267001_at	putative urease accessory protein ; su	UREG	AT2G34470	-1.27	-0.34	-2.17	0.0682	0.169148	-5.32
249842_at	putative protein contains similarity to u	---	AT5G23550	-1.17	-0.22	-2.17	0.068227	0.169196	-5.32
263711_at	putative protein phosphatase 2C ;sup	---	AT2G20630	-1.19	-0.25	-2.17	0.06827	0.169266	-5.32
245419_at	putative protein	MSH4	AT4G17380	-1.16	-0.21	-2.17	0.068267	0.169266	-5.32
249032_at	putative protein contains similarity to d	---	AT5G44910	2.07	1.05	2.17	0.068292	0.169301	-5.32
256748_x_	En/Spm transposon protein, putative s	---	---	-1.20	-0.26	-2.17	0.068345	0.169395	-5.32
252209_at	putative protein RXF26, Arabidopsis t	---	AT3G50400	-1.38	-0.46	-2.17	0.068343	0.169395	-5.32

248367_at	actin depolymerizing factor-like ;suppo	ADF10	AT5G52360	-1.23	-0.30	-2.17	0.068358	0.169409	-5.32
248396_at	unknown protein	---	AT5G52130	-1.22	-0.28	-2.17	0.068412	0.169526	-5.32
260208_s_	unknown protein similar to Ca+2-bindi	---	AT1G70670 /	-1.41	-0.49	-2.17	0.068516	0.169764	-5.32
250809_at	putative protein contains similarity to u	---	AT5G05140	1.46	0.54	2.17	0.068575	0.169893	-5.32
250497_at	putative protein predicted proteins, Ar	---	AT5G09630	1.25	0.32	2.17	0.068592	0.169915	-5.32
257348_at	hypothetical protein predicted by gene	---	AT2G42140	1.36	0.45	2.17	0.068637	0.17001	-5.32
252248_at	putative protein resistance gene Hcr2-	AtRLP44	AT3G49750	-1.36	-0.44	-2.16	0.06868	0.170097	-5.32
258811_at	unknown protein similar to putative pro	---	AT3G03990	-1.31	-0.39	-2.16	0.068698	0.170122	-5.32
254787_at	putative protein hypothetical proteins A	---	AT4G12690	-1.34	-0.42	-2.16	0.068717	0.170151	-5.32
257875_at	hypothetical protein	---	AT3G17120	-1.20	-0.26	-2.16	0.06877	0.170168	-5.32
253367_at	hypothetical protein	---	AT4G33180	-1.33	-0.41	-2.16	0.068755	0.170168	-5.32
265587_at	putative pathogenesis-related protein	---	AT2G19980	-1.19	-0.25	-2.16	0.06875	0.170168	-5.32
262894_at	disease resistance protein, putative si	---	AT1G59780	-1.21	-0.27	-2.16	0.068732	0.170168	-5.32
258745_at	unknown protein ; supported by full-ler	---	AT3G05920	-1.20	-0.26	-2.16	0.068791	0.170168	-5.32
249003_at	putative protein contains similarity to s	---	AT5G44500	-1.21	-0.27	-2.16	0.06879	0.170168	-5.32
259199_at	putative signal peptidase similar to MIT	---	AT3G08980	-1.16	-0.22	-2.16	0.068774	0.170168	-5.32
258833_at	unknown protein	---	---	-1.22	-0.28	-2.16	0.068791	0.170168	-5.32
265424_at	putative sugar transporter	---	AT2G20780	1.21	0.28	2.16	0.068786	0.170168	-5.32
264108_at	hypothetical protein predicted by gens	CALS5	AT2G13680	-1.17	-0.22	-2.16	0.068818	0.170217	-5.32
260679_at	unknown protein	---	AT1G07990	1.17	0.22	2.16	0.068877	0.170345	-5.33
249707_at	putative protein similar to unknown pro	---	AT5G35640	-1.29	-0.36	-2.16	0.068893	0.170364	-5.33
265586_at	pathogenesis-related protein (PR-1) co	PR-1-LIKE	AT2G19990	-1.24	-0.31	-2.16	0.068911	0.170391	-5.33
264589_at	hypothetical protein	---	AT2G17650	-1.25	-0.32	-2.16	0.06895	0.170469	-5.33
264138_at	beta-Amyrin Synthase, putative simila	---	AT1G78950	-1.21	-0.27	-2.16	0.068996	0.170564	-5.33
252746_at	sucrose synthase -like protein SUCRO	SUS4	AT3G43190	-1.19	-0.25	-2.16	0.069044	0.170665	-5.33
257904_at	myb transcription factor, putative simil	TDF1	AT3G28470	-1.15	-0.20	-2.16	0.069059	0.170684	-5.33
258043_at	unknown protein ; supported by cDNA	---	AT3G21290	1.15	0.20	2.16	0.069177	0.170957	-5.33
250753_at	glucuronosyl transferase-like protein ;	UGT76C2	AT5G05860	-1.25	-0.32	-2.16	0.069221	0.171045	-5.33
260608_at	putative polygalacturonase	---	AT2G43870	4.03	2.01	2.16	0.069234	0.171059	-5.33
245119_at	unknown protein ; supported by cDNA	---	AT2G41640	2.21	1.14	2.16	0.069291	0.171182	-5.33
258900_at	putative 60S ribosomal protein L18 sim	RPL18	AT3G05590	-1.36	-0.45	-2.16	0.06933	0.17126	-5.33
247127_at	putative protein similar to unknown pro	---	AT5G66100	-1.18	-0.23	-2.16	0.069354	0.1713	-5.33
260535_at	hypothetical protein predicted by gens	---	AT2G43390	1.15	0.21	2.16	0.069366	0.171312	-5.33
267566_at	unknown protein predicted by genscan	---	AT2G30760	-1.14	-0.19	-2.16	0.069378	0.171322	-5.33
255784_at	hypothetical protein predicted by gens	---	AT1G19860	1.18	0.24	2.16	0.069435	0.171394	-5.33

265609_at	hypothetical protein predicted by gens	---	AT2G25420	-1.32	-0.40	-2.16	0.069433	0.171394	-5.33
263780_at	hypothetical protein predicted by gene	SPA1	AT2G46340	1.36	0.45	2.16	0.069431	0.171394	-5.33
262822_at	putative membrane-associated salt-inc	---	AT1G11630	-1.19	-0.25	-2.16	0.069437	0.171394	-5.33
262317_at	unknown protein ;supported by full-ler	EDA4	AT2G48140	-1.40	-0.48	-2.16	0.069539	0.171628	-5.34
260806_at	RNA recognition motif-containing prote	---	AT1G78260	1.15	0.20	2.16	0.069562	0.171667	-5.34
267492_at	histone H1 ;supported by full-length cD	---	AT2G30620	1.26	0.33	2.16	0.069589	0.171696	-5.34
258709_at	putative 60S ribosomal protein L35 sim	---	AT3G09500	-1.41	-0.50	-2.16	0.069582	0.171696	-5.34
256538_x_	hypothetical protein predicted by gene	---	---	-1.17	-0.22	-2.16	0.069612	0.171733	-5.34
246621_at	putative protein strong similarity to unk	---	AT5G36230	-1.14	-0.19	-2.16	0.069622	0.171739	-5.34
257999_at	hypothetical protein similar to hypothet	---	AT3G27540	1.39	0.47	2.16	0.069637	0.171739	-5.34
256166_at	hypothetical protein	---	AT1G36920	-1.15	-0.20	-2.16	0.069633	0.171739	-5.34
254388_at	Expressed protein ; supported by full-l	MSRB2	AT4G21860	-1.19	-0.25	-2.15	0.069721	0.171929	-5.34
257152_at	Expressed protein ; supported by full-l	PUX1	AT3G27310	-1.16	-0.21	-2.15	0.069781	0.172057	-5.34
259717_at	putative cleavage and polyadenylation	CPSF73-I	AT1G61010	-1.22	-0.29	-2.15	0.069818	0.17213	-5.34
247693_at	putative protein leucine zipper-contain	ATEXO70H7	AT5G59730	1.71	0.77	2.15	0.069828	0.172132	-5.34
249149_at	casein kinase I ; supported by cDNA: g	ckl8	AT5G43320	1.15	0.20	2.15	0.069834	0.172132	-5.34
262901_at	hypothetical protein predicted by gene	---	AT1G59910	1.52	0.61	2.15	0.069929	0.172347	-5.34
260094_at	GDP-4-keto-6-deoxy-D-mannose-3,5-	GER1	AT1G73250	-1.25	-0.32	-2.15	0.069953	0.172388	-5.34
266244_at	unknown protein	---	AT2G27740	-1.59	-0.67	-2.15	0.070003	0.172492	-5.34
265343_at	unknown protein ; supported by full-ler	NIC1	AT2G22570	1.37	0.45	2.15	0.070023	0.172523	-5.34
265831_at	unknown protein	---	AT2G14460	1.47	0.56	2.15	0.070039	0.172546	-5.34
264797_at	unknown protein similar to ESTs gb|T2	---	AT1G08710	1.20	0.27	2.15	0.070087	0.172638	-5.34
248706_at	unknown protein	---	AT5G48530	-1.21	-0.28	-2.15	0.070092	0.172638	-5.34
254168_at	Mlo-like protein Mlo protein - Hordeum	MLO13	AT4G24250	-1.21	-0.28	-2.15	0.07017	0.172811	-5.34
257433_at	hypothetical protein predicted by gene	---	AT2G21990	-1.16	-0.22	-2.15	0.070188	0.172836	-5.34
255147_at	hypothetical protein	---	AT4G08460	-1.20	-0.26	-2.15	0.070246	0.172961	-5.35
260760_at	hypothetical protein predicted by gene	---	AT1G49170	1.24	0.31	2.15	0.070265	0.172988	-5.35
264672_at	hypothetical protein predicted by gens	---	AT1G09750	-4.26	-2.09	-2.15	0.070345	0.173148	-5.35
255921_at	hypothetical protein contains Pfam pro	APUM8	AT1G22240	1.19	0.25	2.15	0.070342	0.173148	-5.35
251765_at	putative protein	---	---	1.19	0.25	2.15	0.070373	0.173198	-5.35
260830_at	histone H1, putative similar to histone	---	AT1G06760	1.35	0.44	2.15	0.070435	0.173314	-5.35
254082_at	glutamine cyclotransferase precursor	QC	AT4G25720	1.43	0.52	2.15	0.070433	0.173314	-5.35
247113_at	unknown protein ;supported by full-len	---	AT5G65960	-1.19	-0.25	-2.15	0.070474	0.173392	-5.35
255020_at	isoleucine-tRNA ligase - like protein is	---	AT4G10320	1.14	0.19	2.15	0.070554	0.17357	-5.35
251750_at	glucuronosyl transferase - like protein	---	AT3G55710	-1.27	-0.34	-2.15	0.070563	0.173572	-5.35

258403_at	hypothetical protein predicted by gens	---	AT3G15380	-1.18	-0.24	-2.15	0.070654	0.173759	-5.35
266912_at	hypothetical protein predicted by gene	---	AT2G45900	-1.86	-0.90	-2.15	0.070651	0.173759	-5.35
264276_at	hypothetical protein contains similarity	---	AT1G60380	1.16	0.21	2.15	0.070665	0.173767	-5.35
251673_at	beta-1,3-glucanase	BG3	AT3G57240	-5.17	-2.37	-2.14	0.070715	0.173871	-5.35
253413_at	putative protein Fe(II) transport protei	ZIP9	AT4G33020	1.13	0.18	2.14	0.070743	0.173921	-5.35
256794_at	ribosomal protein L27, putative similar	---	AT3G22230	-1.48	-0.56	-2.14	0.070777	0.173988	-5.35
252062_at	hypothetical protein KIAA0253 protein	---	AT3G52640	-1.26	-0.33	-2.14	0.070879	0.174219	-5.35
261970_at	glutamate decarboxylase (gad), putati	GAD2	AT1G65960	-1.27	-0.34	-2.14	0.070898	0.174246	-5.35
256337_at	unknown protein	---	AT1G72060	1.65	0.73	2.14	0.070936	0.174322	-5.36
261872_s_	hypthetical protein contains similarity t	---	AT1G11520 /	1.20	0.26	2.14	0.070958	0.174343	-5.36
250962_at	putative protein various predicted prot	---	AT5G02990	-1.19	-0.25	-2.14	0.070962	0.174343	-5.36
252290_at	putative protein various predicted prot	---	AT3G49140	-1.22	-0.29	-2.14	0.070975	0.174343	-5.36
247523_at	ribulose-5-phosphate-3-epimerase ; s	RPE	AT5G61410	-1.22	-0.29	-2.14	0.070975	0.174343	-5.36
256229_at	unknown protein	MSL3	AT1G58200	-1.26	-0.33	-2.14	0.071013	0.174417	-5.36
262092_at	unknown protein	---	AT1G56150	-1.69	-0.76	-2.14	0.071025	0.174428	-5.36
265219_at	unknown protein ; supported by full-le	---	AT2G02050	1.23	0.30	2.14	0.071039	0.174444	-5.36
259984_at	putative RNA-binding protein contains	---	AT1G76460	-1.21	-0.28	-2.14	0.071078	0.174506	-5.36
254183_at	putative protein predicted protein, Ara	---	AT4G23960	1.20	0.27	2.14	0.07108	0.174506	-5.36
259191_at	unknown protein	---	AT3G01720	1.24	0.31	2.14	0.071094	0.174521	-5.36
248209_at	flavonol 3-O-glucosyltransferase-like p	---	AT5G53990	1.26	0.33	2.14	0.071166	0.174681	-5.36
256326_at	RING zinc-finger protein, putative con	---	AT3G02340	-1.24	-0.31	-2.14	0.071201	0.174746	-5.36
246767_at	putative protein CG6949 - Drosophila	---	AT5G27395	1.55	0.64	2.14	0.071267	0.174871	-5.36
254939_at	putative protein predicted proteins, Ar	---	AT4G10800	-1.30	-0.38	-2.14	0.071267	0.174871	-5.36
263765_at	putative phosphatidylinositol phophatic	SFH3	AT2G21540	-1.74	-0.80	-2.14	0.071276	0.174875	-5.36
245409_at	putative protein	---	AT4G17200	1.14	0.19	2.14	0.071359	0.175058	-5.36
246321_at	unknown protein	---	AT1G16640	1.20	0.26	2.14	0.071377	0.175084	-5.36
262770_at	hypothetical protein predicted by gens	---	AT1G13190	-1.31	-0.39	-2.14	0.071393	0.175105	-5.36
247345_at	putative protein contains similarity to A	---	AT5G63760	1.22	0.29	2.14	0.071454	0.175217	-5.36
256172_at	hypothetical protein	---	AT1G51745	1.16	0.22	2.14	0.071453	0.175217	-5.36
245124_at	small nuclear ribonucleoprotein U1A id	U1A	AT2G47580	-1.19	-0.26	-2.14	0.071469	0.175233	-5.36
266920_at	hypothetical protein predicted by gens	---	AT2G45750	-1.21	-0.28	-2.14	0.071476	0.175234	-5.36
263108_at	hypothetical protein similar to putative	---	AT1G65240	-1.75	-0.81	-2.14	0.071519	0.175301	-5.36
247576_at	putative protein predicted protein, Ara	---	AT5G61280	-1.14	-0.19	-2.14	0.071513	0.175301	-5.36
246722_at	putative protein various predicted prot	---	---	1.23	0.30	2.14	0.07154	0.175333	-5.36
246902_at	putative protein	---	AT5G25640	-1.16	-0.21	-2.14	0.071555	0.175351	-5.36

263134_at	dTDP-glucose 4,6-dehydratase, putat	RHM1	AT1G78570	1.28	0.35	2.14	0.071577	0.175372	-5.36
247492_at	putative protein AP2 domain containin	---	AT5G61890	1.61	0.69	2.14	0.071579	0.175372	-5.36
249528_at	putative protein predicted protein, Dro	---	AT5G38720	1.32	0.40	2.14	0.071708	0.175669	-5.37
251618_at	putative protein unknown protein At2g	---	AT3G58020	-1.30	-0.38	-2.13	0.071795	0.175864	-5.37
267214_at	unknown protein ; supported by cDNA	---	AT2G43970	1.26	0.33	2.13	0.071848	0.175956	-5.37
264354_s_	unknown protein similar to Lambda-PR	---	AT1G03200 /	1.19	0.26	2.13	0.071845	0.175956	-5.37
252943_at	cinnamyl-alcohol dehydrogenase CAD	CAD9	AT4G39330	-3.30	-1.72	-2.13	0.071865	0.175978	-5.37
266976_at	putative phospholipase	---	AT2G39410	1.30	0.38	2.13	0.071898	0.176042	-5.37
252591_at	putative protein senescence-associate	TET3	AT3G45600	-1.35	-0.44	-2.13	0.071921	0.176077	-5.37
249984_at	putative protein rsc43, Dictyostelium d	---	AT5G18400	1.40	0.49	2.13	0.071933	0.176089	-5.37
263115_at	Expressed protein ; supported by cDN	---	AT1G03055	-1.37	-0.46	-2.13	0.071946	0.176101	-5.37
256258_at	unknown protein	NF-YC11	AT3G12480	1.15	0.20	2.13	0.071956	0.176108	-5.37
259469_at	hypothetical protein predicted by gens	---	AT1G19100	1.17	0.23	2.13	0.071968	0.176117	-5.37
250473_at	annexin -like protein annexin (AnnAt2	ANN6	AT5G10220	-1.15	-0.20	-2.13	0.071977	0.17612	-5.37
AFFX-DapX	B. subtilis /GEN=jojG /DB_XREF=gb:L	---	---	-1.23	-0.30	-2.13	0.072026	0.176222	-5.37
260483_at	Barley Mlo protein isolog ; supported	MLO4	AT1G11000	-1.27	-0.35	-2.13	0.072054	0.176271	-5.37
264201_at	unknown protein ;supported by full-len	---	AT1G22630	-1.30	-0.38	-2.13	0.072102	0.176369	-5.37
250924_at	putative protein ;supported by full-leng	---	AT5G03440	-1.19	-0.25	-2.13	0.07211	0.176369	-5.37
255993_at	hypothetical protein contains similarity	---	AT1G29770	1.16	0.21	2.13	0.072129	0.176397	-5.37
259367_at	hypothetical protein predicted by gene	---	AT1G69070	1.31	0.39	2.13	0.072207	0.17657	-5.37
245514_at	OEP8 like protein	---	AT4G15810	-1.30	-0.38	-2.13	0.072238	0.176619	-5.37
266133_at	putative C2H2-type zinc finger protein	---	AT2G45120	1.17	0.23	2.13	0.072249	0.176619	-5.37
247308_at	receptor-like protein kinase	---	AT5G63930	1.19	0.25	2.13	0.07225	0.176619	-5.37
266364_at	unknown protein	---	AT2G41230	2.09	1.06	2.13	0.072339	0.176817	-5.37
264692_at	DNA binding protein MybSt1, putative	---	AT1G70000	1.23	0.30	2.13	0.072367	0.176866	-5.37
255236_at	score=11.7, E=0.66,N=1	ATEHD2	AT4G05520	-1.33	-0.41	-2.13	0.072376	0.17687	-5.38
266130_at	putative transcription activator	---	AT2G44980	1.31	0.39	2.13	0.072393	0.176885	-5.38
261593_at	unknown protein	---	AT1G33170	-2.68	-1.42	-2.13	0.072405	0.176885	-5.38
252893_at	hypothetical protein	---	AT4G39420	1.14	0.19	2.13	0.072413	0.176885	-5.38
266779_at	putative ligand-gated ion channel prote	ATGLR2.9	AT2G29100	1.21	0.28	2.13	0.072411	0.176885	-5.38
253674_at	UDP-N-acetylglucosamine O-acyltran	---	AT4G29540	-1.18	-0.24	-2.13	0.072441	0.176934	-5.38
266584_s_	putative steroid sulfotransferase	ST4C	AT1G13430 /	-1.14	-0.19	-2.13	0.072465	0.176972	-5.38
247577_at	putative protein flavin-containing mon	---	AT5G61290	-1.20	-0.26	-2.13	0.072485	0.177003	-5.38
253998_at	putative peroxidase peroxidase ATP1	---	AT4G26010	1.15	0.20	2.13	0.072506	0.177036	-5.38
257606_at	root hair defective 3 (RHD3) identical	RHD3	AT3G13870	-1.23	-0.30	-2.13	0.072559	0.177146	-5.38

254644_at	CLE2, putative CLAVATA3/ESR-Rela	CLE2	AT4G18510	-1.21	-0.27	-2.13	0.072621	0.177279	-5.38
248839_at	putative protein contains similarity to b	bHLH071	AT5G46690	-1.57	-0.65	-2.13	0.072663	0.177351	-5.38
252126_at	putative disease resistance protein	---	AT3G50950	1.27	0.35	2.13	0.072666	0.177351	-5.38
260829_s_	chloroplast thylakoidal processing pep	---	AT1G06870 /	1.28	0.35	2.13	0.072677	0.177358	-5.38
247299_at	putative protein contains similarity to P	---	AT5G63900	-1.16	-0.21	-2.13	0.07271	0.177407	-5.38
266826_at	putative amino acid acetyltransferase	---	AT2G22910	-1.43	-0.52	-2.13	0.072713	0.177407	-5.38
255781_at	unknown protein	---	AT1G19880	-1.17	-0.22	-2.13	0.072728	0.177425	-5.38
246827_at	copper binding - like protein mavicyan	---	AT5G26330	-1.21	-0.28	-2.13	0.072746	0.177451	-5.38
248533_at	putative protein contains similarity to u	---	AT5G50020	-1.27	-0.35	-2.12	0.072785	0.177527	-5.38
259202_at	putative mRNA capping enzyme, RNA	---	AT3G09100	1.20	0.26	2.12	0.072846	0.177657	-5.38
248508_at	histone acetyltransferase ;supported b	ELO3	AT5G50320	1.25	0.33	2.12	0.072936	0.177855	-5.38
245159_at	putative cellulose synthase	ATCSLD1	AT2G33100	-1.22	-0.29	-2.12	0.072943	0.177855	-5.38
266284_at	putative pumilio/Mpt5 family RNA-bind	APUM2	AT2G29190	1.20	0.27	2.12	0.072961	0.177879	-5.38
250589_at	transcription factor (gb|AAD53097.1) ;	MYB76	AT5G07700	-1.60	-0.68	-2.12	0.072995	0.177924	-5.38
245630_at	hypothetical protein similar to putative	---	AT1G25360	1.18	0.24	2.12	0.072988	0.177924	-5.38
265498_at	putative C2H2-type zinc finger protein	---	AT2G15740	-1.15	-0.21	-2.12	0.073026	0.177981	-5.38
258667_at	hypothetical protein	---	AT3G08750	-1.17	-0.23	-2.12	0.073092	0.178122	-5.38
262361_at	unknown protein contains similarity to	GTE3	AT1G73150	1.18	0.24	2.12	0.07317	0.178265	-5.39
251188_at	putative protein DESSICATION-RELA	---	AT3G62730	-1.19	-0.25	-2.12	0.073172	0.178265	-5.39
267453_at	putative homeodomain transcription fa	HB-3	AT2G33880	-1.27	-0.35	-2.12	0.073174	0.178265	-5.39
260975_at	receptor-like serine/threonine kinase,	---	AT1G53430	1.56	0.64	2.12	0.073265	0.178469	-5.39
253542_at	putative protein deubiquitinating enzy	UBP18	AT4G31670	1.18	0.23	2.12	0.073301	0.178525	-5.39
244960_at	ribosomal protein L32	---	---	-1.47	-0.55	-2.12	0.073304	0.178525	-5.39
260832_at	unknown protein ; supported by cDNA	GAUT6	AT1G06780	1.21	0.27	2.12	0.073341	0.178596	-5.39
251149_at	putative protein CGI-77 protein, Homo	---	AT3G62940	-1.14	-0.19	-2.12	0.073379	0.17865	-5.39
248256_at	developmental protein SINA (seven in	---	AT5G53360	1.20	0.26	2.12	0.073378	0.17865	-5.39
250788_at	putative protein similar to unknown pro	---	AT5G05570	-1.25	-0.32	-2.12	0.073431	0.178757	-5.39
251205_at	glutathione peroxidase -like protein ph	ATGPX5	AT3G63080	-1.24	-0.31	-2.12	0.073503	0.178865	-5.39
262415_at	40S ribosomal protein S17, putative s	emb1129	AT1G49400	-1.24	-0.31	-2.12	0.073507	0.178865	-5.39
264970_at	glyoxalase I, putative similar to glyoxa	---	AT1G67280	-1.17	-0.23	-2.12	0.073504	0.178865	-5.39
257364_at	hypothetical protein predicted by gens	---	AT2G45940	-1.14	-0.19	-2.12	0.073498	0.178865	-5.39
251683_at	putative protein several hypothetical p	---	AT3G57120	-1.44	-0.53	-2.12	0.073566	0.178984	-5.39
253908_at	GH3 like protein GH3 protein, Glycine	WES1	AT4G27260	2.11	1.08	2.12	0.073571	0.178984	-5.39
250556_at	diacylglycerol kinase (ATDGK1) ; supp	DGK1	AT5G07920	1.43	0.52	2.12	0.073593	0.179019	-5.39
266886_at	Expressed protein ; supported by full-l	---	AT2G44745	1.22	0.29	2.12	0.073618	0.179061	-5.39

265458_at	unknown protein ;supported by full-ler	---	AT2G46580	-1.21	-0.28	-2.12	0.073642	0.179099	-5.39
249335_at	putative protein contains similarity to m	NRPB12	AT5G41010	1.18	0.24	2.12	0.073672	0.179153	-5.39
249473_at	His-Asp Phosphotransfer Signal Trans	AHP3	AT5G39340	-1.20	-0.26	-2.12	0.073705	0.179215	-5.39
254201_at	putative protein predicted proteins	---	AT4G24130	-1.26	-0.33	-2.12	0.073722	0.179224	-5.39
265736_at	putative ribosomal protein L7 ;support	---	AT2G01250	-1.40	-0.49	-2.12	0.073725	0.179224	-5.39
251756_at	putative protein	---	AT3G55820	-1.16	-0.22	-2.12	0.073762	0.179294	-5.39
247011_at	putative protein contains similarity to N	FRO1	AT5G67590	1.33	0.41	2.12	0.073769	0.179294	-5.39
255472_at	82.09 and 30.80) similar to alternative	---	AT4G02430	-1.18	-0.24	-2.12	0.073784	0.179311	-5.39
261125_at	zinc finger protein 2, putative similar t	---	AT1G04990	1.38	0.46	2.12	0.0738	0.179331	-5.39
263413_at	unknown protein ;supported by full-ler	BPC4	AT2G21240	-1.21	-0.28	-2.12	0.073821	0.179362	-5.39
249578_at	putative protein predicted protein, Ara	---	AT5G37730	-1.14	-0.19	-2.11	0.073859	0.179437	-5.40
256530_at	unknown protein	---	AT1G33290	-1.18	-0.24	-2.11	0.073909	0.179538	-5.40
263022_s_	gamma-adaptin, putative similar to ga	---	AT1G23900 /	1.26	0.33	2.11	0.073919	0.179543	-5.40
245771_at	hypothetical protein predicted by gene	---	AT1G30250	-2.44	-1.29	-2.11	0.073977	0.179665	-5.40
256613_at	hypothetical protein predicted by gene	emb2076	AT3G29290	-1.24	-0.31	-2.11	0.073986	0.179669	-5.40
266504_at	hypothetical protein predicted by gens	---	AT2G47820	1.22	0.29	2.11	0.07407	0.179854	-5.40
265961_at	unknown protein ;supported by full-ler	---	AT2G37400	1.30	0.38	2.11	0.074143	0.18001	-5.40
252256_at	PRE-MRNA SPLICING FACTOR SF2	SRp34a	AT3G49430	1.24	0.31	2.11	0.074162	0.180018	-5.40
265806_at	putative auxin-regulated protein	---	AT2G18010	-1.68	-0.75	-2.11	0.074162	0.180018	-5.40
254813_at	putative transcription factor myb-relate	MYB42	AT4G12350	1.15	0.20	2.11	0.074227	0.180156	-5.40
252376_at	L-galactono-1,4-lactone dehydrogena	ATGLDH	AT3G47930	-1.27	-0.34	-2.11	0.074288	0.180285	-5.40
261867_at	unknown protein ; supported by cDNA	---	AT1G50575	-1.21	-0.27	-2.11	0.074381	0.180479	-5.40
252311_at	calcium dependent protein kinase - lik	---	AT3G49370	1.49	0.57	2.11	0.07439	0.180479	-5.40
254622_at	hypothetical protein contains similarity	---	AT4G18375	-1.32	-0.40	-2.11	0.074396	0.180479	-5.40
264217_at	hypothetical protein predicted by gene	---	AT1G60190	2.16	1.11	2.11	0.074406	0.180479	-5.40
263455_at	hypothetical protein predicted by gene	---	AT2G22320	1.32	0.40	2.11	0.074407	0.180479	-5.40
264697_at	cyclin, putative similar to cyclin D GI:3	CYCD1;1	AT1G70210	-2.12	-1.08	-2.11	0.074555	0.18082	-5.40
251806_at	zinc finger protein OBP3 ; supported b	OBP3	AT3G55370	1.16	0.22	2.11	0.074564	0.180821	-5.40
264558_at	putative protein kinase Similar to cdc2	---	AT1G09600	1.16	0.21	2.11	0.074653	0.181017	-5.41
261037_at	lipoxygenase identical to GB:CAB5669	LOX3	AT1G17420	2.21	1.14	2.11	0.074689	0.181086	-5.41
251562_at	putative protein hypothetical protein T	---	AT3G57890	-1.17	-0.23	-2.11	0.074699	0.18109	-5.41
255568_at	putative DNA-binding protein ; suppor	WRKY22	AT4G01250	-1.81	-0.85	-2.11	0.074731	0.18115	-5.41
262444_at	hypothetical protein similar to putative	---	AT1G47480	1.37	0.45	2.11	0.074743	0.18116	-5.41
251828_at	putative protein unnamed sequence, h	---	AT3G55070	-1.20	-0.26	-2.11	0.074795	0.181266	-5.41
251944_at	ABC transporter -like protein breast ca	---	AT3G53510	-1.26	-0.33	-2.11	0.074815	0.181295	-5.41

248967_at	unknown protein ;supported by full-len	---	AT5G45350	1.24	0.31	2.11	0.074843	0.181344	-5.41
254037_at	hypothetical protein hypothetical prote	ATGDU2	AT4G25760	-1.17	-0.23	-2.11	0.074873	0.181398	-5.41
254832_at	pEARLI 1-like protein Arabidopsis tha	---	AT4G12490	2.73	1.45	2.11	0.074916	0.18146	-5.41
262876_at	unknown protein ;supported by full-len	ATDSS1(I)	AT1G64750	1.24	0.31	2.10	0.074917	0.18146	-5.41
258242_at	hypothetical protein predicted by gene	---	AT3G27640	-1.17	-0.23	-2.10	0.074923	0.18146	-5.41
263085_at	hypothetical protein predicted by gens	ARI12	AT2G16090	-1.25	-0.32	-2.10	0.075003	0.181634	-5.41
250481_at	putative protein	---	AT5G10310	1.18	0.24	2.10	0.07503	0.181682	-5.41
260927_at	hypothetical protein predicted by gene	CAT9	AT1G05940	1.23	0.29	2.10	0.075068	0.181717	-5.41
251288_at	exonuclease RRP41 ; supported by cl	RRP41	AT3G61620	-1.26	-0.34	-2.10	0.075069	0.181717	-5.41
247993_at	putative protein similar to unknown pro	---	AT5G56130	-1.23	-0.30	-2.10	0.075055	0.181717	-5.41
250053_at	potassium-dependent sodium-calcium	---	AT5G17850	1.22	0.28	2.10	0.075077	0.181717	-5.41
259511_at	unknown protein contains similarity to	ATCCS	AT1G12520	1.68	0.75	2.10	0.075105	0.181766	-5.41
246565_at	biotin carboxyl carrier protein precurso	BCCP2	AT5G15530	-1.19	-0.25	-2.10	0.07521	0.182001	-5.41
265327_at	unknown protein	---	AT2G18210	2.37	1.25	2.10	0.075218	0.182001	-5.41
259713_at	unknown protein similar to phosphate	---	AT1G77610	1.28	0.35	2.10	0.075231	0.182013	-5.41
255919_at	putative protein	---	---	-1.18	-0.24	-2.10	0.075277	0.182086	-5.41
245491_at	hypothetical protein	LDL3	---	1.22	0.29	2.10	0.07527	0.182086	-5.41
261088_at	DNA-binding protein, putative similar t	---	AT1G07590	1.22	0.29	2.10	0.075299	0.18212	-5.41
249573_at	ubiquitin-like protein (UBQ9), putative	UBQ9	AT5G37640	1.16	0.22	2.10	0.075318	0.182146	-5.41
246089_at	ring-box protein - like ring-box protein-	RBX1	AT5G20570	-1.14	-0.19	-2.10	0.07536	0.182229	-5.42
253602_s_	leucyl aminopeptidase - like protein le	---	AT4G30910 /	-1.16	-0.22	-2.10	0.075372	0.182239	-5.42
245647_at	F5A9.22 hypothetical protein	---	AT1G24706	-1.14	-0.19	-2.10	0.075381	0.18224	-5.42
260597_at	hypothetical protein predicted by gene	---	AT1G55915	1.29	0.36	2.10	0.075399	0.182253	-5.42
248741_at	putative protein similar to unknown pro	SLY2	AT5G48170	1.29	0.37	2.10	0.075402	0.182253	-5.42
253155_at	putative protein predicted protein, Ara	---	AT4G35720	-1.20	-0.26	-2.10	0.075416	0.182267	-5.42
261494_at	homeobox transcription factor Hox7,	HB-1	AT1G28420	1.21	0.27	2.10	0.075487	0.18242	-5.42
263551_at	hypothetical protein contains NLS (PS	---	AT2G17110	1.42	0.51	2.10	0.075515	0.182469	-5.42
245047_at	PSII 32 KDa protein	---	---	-1.17	-0.23	-2.10	0.075526	0.182475	-5.42
251527_at	putative protein hypothetical protein A	---	AT3G58650	-1.17	-0.23	-2.10	0.075679	0.182825	-5.42
250130_at	amylogenin; reversibly glycosylatable p	---	AT5G16510	1.26	0.33	2.10	0.075691	0.182835	-5.42
265825_at	ubiquitin-like (UBQ7), putative similar	UBQ7	AT2G35635	1.19	0.26	2.10	0.075722	0.182891	-5.42
246447_at	putative protein SART-1 protein - Hom	DOT2	AT5G16780	1.20	0.27	2.10	0.075842	0.183161	-5.42
251959_at	putative protein KIAA0544 protein, Ho	---	AT3G53410	-1.17	-0.23	-2.10	0.075853	0.183168	-5.42
262917_at	hypothetical protein contains similarity	---	AT1G64800	-1.23	-0.29	-2.10	0.075868	0.183184	-5.42
261113_at	hypothetical protein predicted by gene	---	AT1G75400	1.25	0.32	2.10	0.075895	0.18323	-5.42

259486_at	embryo abundance protein (EMB20),	---	AT1G15710	-1.21	-0.27	-2.10	0.075957	0.183343	-5.42
251924_at	histone H4-like protein several histone	---	AT3G53730	-1.27	-0.35	-2.10	0.075952	0.183343	-5.42
247507_at	putative protein predicted protein, Ara	APO3	AT5G61930	-1.39	-0.48	-2.09	0.0761	0.183668	-5.43
256150_at	beta-fructofuranosidase identical to be	ATFRUCT5	AT1G55120	1.45	0.53	2.09	0.076163	0.183801	-5.43
259600_at	hypothetical protein predicted by gens	---	AT1G35220	1.24	0.31	2.09	0.076238	0.183962	-5.43
256816_at	unknown protein	---	AT3G21400	-1.20	-0.26	-2.09	0.07626	0.183995	-5.43
266853_at	putative salt-inducible protein	---	AT2G26790	1.16	0.22	2.09	0.076297	0.184064	-5.43
260073_at	putative protein kinase contains Pfam	---	AT1G73660	1.24	0.32	2.09	0.076343	0.184156	-5.43
258163_at	aldose 1-epimerase, putative similar t	---	AT3G17940	-1.17	-0.23	-2.09	0.076352	0.184159	-5.43
252220_at	putative protein hypothetical protein -	LBD38	AT3G49940	-1.32	-0.40	-2.09	0.07647	0.184424	-5.43
249838_at	unknown protein ;supported by full-ler	---	AT5G23460	1.25	0.33	2.09	0.076484	0.184438	-5.43
254054_at	putative protein DNA-binding protein F	---	AT4G25320	1.27	0.35	2.09	0.076516	0.184497	-5.43
261597_at	hypothetical protein predicted by gene	PUB26	AT1G49780	-1.85	-0.89	-2.09	0.076539	0.184532	-5.43
259498_at	unknown protein similar to putative cis	GOS11	AT1G15880	-1.17	-0.23	-2.09	0.076574	0.184596	-5.43
248289_at	unknown protein ; supported by cDNA	---	AT5G52880	1.17	0.22	2.09	0.076616	0.184679	-5.43
267413_at	putative amino acid transporter	CAT5	AT2G34960	1.32	0.40	2.09	0.076625	0.18468	-5.43
265800_at	similar to ch-TOG protein from Homo s	MOR1	AT2G35630	-1.20	-0.26	-2.09	0.076634	0.184683	-5.43
254233_at	98b like protein 98b - Daucus carota (	---	AT4G23800	-1.32	-0.40	-2.09	0.076671	0.184751	-5.43
253580_at	putative protein RING-H2 finger protei	---	AT4G30400	-1.46	-0.54	-2.09	0.076705	0.184814	-5.43
259687_at	unknown protein	---	AT1G63110	-1.24	-0.31	-2.09	0.076767	0.184945	-5.43
263264_at	histone H2A ; supported by full-length	HTA8	AT2G38810	-1.34	-0.42	-2.09	0.076795	0.184994	-5.43
256290_at	serine carboxypeptidase, putative con	scpl17	AT3G12203	-1.17	-0.22	-2.09	0.076824	0.185042	-5.43
262114_at	unknown protein contains similarity to	NLA	AT1G02860	1.35	0.44	2.09	0.076865	0.185121	-5.44
263205_at	Ca2+-dependent lipid-binding protein,	NTMC2T2.1	AT1G05500	-1.17	-0.22	-2.09	0.077013	0.18546	-5.44
252164_at	hypothetical protein nodH - Rhizobium	---	AT3G50620	-1.44	-0.52	-2.09	0.077042	0.185488	-5.44
263663_at	putative malate dehydrogenase similar	---	AT1G04410	1.18	0.23	2.09	0.07705	0.185488	-5.44
254211_at	phosphatase like protein phosphoprote	SGT1A	AT4G23570	-1.31	-0.39	-2.09	0.077048	0.185488	-5.44
267605_at	putative protein disulfide isomerase ; s	ATPDIL2-3	AT2G32920	1.25	0.32	2.09	0.077072	0.185524	-5.44
254063_at	receptor kinase-like protein receptor-li	---	AT4G25390	1.43	0.52	2.08	0.077139	0.185663	-5.44
261538_at	unknown protein ; supported by cDNA	---	AT1G01830	1.42	0.50	2.08	0.077275	0.185972	-5.44
255582_at	putative DNA-binding protein similar to	NGA4	AT4G01500	-1.16	-0.21	-2.08	0.077379	0.186202	-5.44
257374_at	hypothetical protein predicted by gens	---	AT2G43280	-1.26	-0.34	-2.08	0.077413	0.186258	-5.44
267463_at	Expressed protein ; supported by full-l	---	AT2G33845	1.37	0.45	2.08	0.077427	0.186258	-5.44
252370_at	putative protein	---	AT3G48600	-1.34	-0.42	-2.08	0.077425	0.186258	-5.44
256825_at	unknown protein similar to cell wall-pla	CWLP	AT3G22120	-3.74	-1.90	-2.08	0.077482	0.186373	-5.44

245184_at	F12A21.8 hypothetical protein	---	AT1G67790	-1.20	-0.26	-2.08	0.077503	0.186383	-5.44
262873_at	hypothetical protein predicted by gene	---	AT1G64700	-1.18	-0.24	-2.08	0.077496	0.186383	-5.44
249854_at	putative protein contains similarity to s	---	AT5G22960	-1.21	-0.28	-2.08	0.077531	0.186431	-5.44
251218_at	CP12 protein precursor-like protein Cl	CP12-2	AT3G62410	1.24	0.32	2.08	0.07756	0.18648	-5.44
263504_s_	hypothetical protein	---	AT2G07677	1.16	0.22	2.08	0.077613	0.186588	-5.44
257560_at	galactosyltransferase, putative contair	---	AT3G14960	1.15	0.20	2.08	0.077636	0.186624	-5.45
259706_at	unknown protein similar to GB:AAD41	---	AT1G77540	1.21	0.27	2.08	0.07767	0.186687	-5.45
262150_at	hypothetical protein contains similarity	FRS6	AT1G52520	-1.21	-0.27	-2.08	0.077704	0.186748	-5.45
257222_at	DegP protease almost identical to De	DEGP1	AT3G27925	-1.23	-0.30	-2.08	0.077725	0.18678	-5.45
248870_at	putative protein similar to unknown pr	---	AT5G46710	-1.75	-0.81	-2.08	0.077747	0.186812	-5.45
249266_at	6-phosphogluconate dehydrogenase ;	---	AT5G41670	1.26	0.33	2.08	0.077779	0.18685	-5.45
267591_at	Expressed protein ; supported by full-l	RTFL8	AT2G39705	-1.60	-0.68	-2.08	0.077775	0.18685	-5.45
247812_at	peroxidase ;supported by full-length c	---	AT5G58390	1.66	0.73	2.08	0.077804	0.18688	-5.45
248407_at	pectinesterase	---	AT5G51500	-1.16	-0.22	-2.08	0.077808	0.18688	-5.45
261281_at	hypothetical protein predicted by gene	---	AT1G35740	-1.15	-0.20	-2.08	0.077828	0.186904	-5.45
250030_at	putative protein contains similarity to p	ATAPRL7	AT5G18120	-1.17	-0.22	-2.08	0.077834	0.186904	-5.45
262593_at	putative ubiquinol--cytochrome-c reduc	---	AT1G15120	1.31	0.38	2.08	0.077872	0.186976	-5.45
254461_at	receptor kinase - like protein SRK3 re	---	AT4G21230	1.27	0.34	2.08	0.077891	0.187	-5.45
255041_at	putative protein hypothetical protein F	---	AT4G09620	-1.22	-0.29	-2.08	0.077956	0.187136	-5.45
249997_at	chromatin remodelling complex ATPa	CHR17	AT5G18620	1.20	0.27	2.08	0.07803	0.187291	-5.45
253223_at	L-ascorbate peroxidase ;supported by	APX3	AT4G35000	-1.16	-0.22	-2.08	0.078036	0.187291	-5.45
246267_at	Acyl CoA binding protein, putative cor	ACBP6	AT1G31812	-1.15	-0.20	-2.08	0.078066	0.187342	-5.45
262462_at	hypothetical protein predicted by gene	---	AT1G50350	1.16	0.21	2.08	0.078082	0.18736	-5.45
252406_at	putative protein pectinesterase - Arab	---	AT3G47670	-1.14	-0.19	-2.08	0.078133	0.187443	-5.45
263579_at	hypothetical protein similar to hypothet	---	AT2G17030	1.25	0.32	2.08	0.078129	0.187443	-5.45
261114_at	bZIP transcription factor ATB2, putativ	AtbZIP44	AT1G75388 /	2.58	1.37	2.08	0.078163	0.187496	-5.45
246377_at	low-temperature-specific protein, puta	---	AT1G57550	-1.30	-0.38	-2.08	0.078179	0.187515	-5.45
264794_at	hypothetical protein predicted by gens	---	AT1G08670	1.16	0.21	2.08	0.078196	0.187536	-5.45
265757_x_	putative PttA2-like transposon protein	---	---	-1.24	-0.31	-2.07	0.078314	0.187798	-5.45
248640_at	selenium-binding protein-like ; suppor	---	AT5G48910	-1.21	-0.27	-2.07	0.078369	0.18791	-5.45
250705_at	diadenosine 5,5-P1,P4-tetraphosphat	ATNUDX27	AT5G06340	-1.22	-0.29	-2.07	0.078381	0.187912	-5.45
266420_at	putative RNA-binding protein ; suppor	---	AT2G38610	-1.14	-0.19	-2.07	0.078386	0.187912	-5.45
252895_at	hypothetical protein	---	AT4G39450	1.16	0.22	2.07	0.078456	0.188061	-5.46
250098_at	putative protein ;supported by full-leng	---	AT5G17350	2.75	1.46	2.07	0.078469	0.188071	-5.46
249111_at	unknown protein	---	AT5G43770	-1.14	-0.19	-2.07	0.078559	0.188268	-5.46

250588_at	SMC-like protein	---	AT5G07660	-1.17	-0.22	-2.07	0.078578	0.188293	-5.46
252596_at	receptor-like protein kinase receptor li	---	AT3G45330	1.15	0.20	2.07	0.07864	0.188422	-5.46
250872_at	putative protein SF16 protein, commo	IQD12	AT5G03960	-1.17	-0.23	-2.07	0.07865	0.188427	-5.46
252055_at	putative ribosomal protein S14 riboso	---	AT3G52580	-1.23	-0.30	-2.07	0.078727	0.188553	-5.46
266864_at	putative hydroxymethylglutaryl-CoA lya	---	AT2G26800	-1.24	-0.31	-2.07	0.078715	0.188553	-5.46
253209_at	putative protein membrane-associate	---	AT4G34830	1.24	0.31	2.07	0.078728	0.188553	-5.46
AFFX-Atha	Arabidopsis thaliana /REF=U37281 /D	ACT7	---	-1.16	-0.22	-2.07	0.078744	0.188571	-5.46
264818_at	hypothetical protein similar to hypothet	NAF1	AT1G03530	1.44	0.52	2.07	0.07876	0.188591	-5.46
246499_at	putative protein Tat-SF1 - Homo sapie	---	AT5G16260	1.23	0.30	2.07	0.078897	0.188898	-5.46
247832_at	putative protein predicted proteins, Ar	EOL2	AT5G58550	-1.20	-0.26	-2.07	0.07891	0.188911	-5.46
250159_at	40S ribosomal protein - like 40S ribos	---	AT5G15200	-1.29	-0.36	-2.07	0.07894	0.188962	-5.46
262684_s_	vacuolar ATP synthase subunit B iden	---	AT1G20260 /	-1.21	-0.28	-2.07	0.078961	0.188992	-5.46
246973_at	putative protein UBIQUINONE BIOSY	---	AT5G24970	-1.29	-0.37	-2.07	0.07897	0.188995	-5.46
265312_at	unknown protein	---	AT2G20240	-1.41	-0.49	-2.07	0.078988	0.189005	-5.46
250124_at	putative protein contains similarity to ty	---	AT5G16480	-1.20	-0.26	-2.07	0.078991	0.189005	-5.46
252443_at	putative helicase helicase SKI2W - hu	---	AT3G46960	-1.20	-0.27	-2.07	0.079016	0.189044	-5.46
245428_at	putative protein	---	AT4G17570	1.18	0.24	2.07	0.079026	0.189048	-5.46
246580_at	ABC transporter, putative contains Pfa	---	AT1G31770	1.23	0.30	2.07	0.079035	0.18905	-5.46
251003_at	putative protein	---	AT5G02690	1.19	0.25	2.07	0.079057	0.189083	-5.46
261606_at	peroxidase, putative similar to peroxid	---	AT1G49570	-1.23	-0.30	-2.07	0.079077	0.1891	-5.46
262054_s_	putative heat-shock protein contains P	---	AT1G79920 /	1.25	0.32	2.07	0.07908	0.1891	-5.46
262405_at	hypothetical protein contains similarity	HDG10	AT1G34650	-1.20	-0.26	-2.07	0.07909	0.189102	-5.46
248231_at	putative protein contains similarity to to	---	AT5G53770	-1.20	-0.26	-2.07	0.079137	0.189196	-5.46
249911_at	glucosyltransferase-like protein ; supp	CSLA02	AT5G22740	-1.84	-0.88	-2.07	0.079154	0.189207	-5.46
257179_at	topoisomerase VIA (SPO11 gene 1), p	---	AT3G13160 /	1.15	0.20	2.07	0.079158	0.189207	-5.46
247807_at	similar to unknown protein (gb|AAB63	OFP3	AT5G58360	-1.20	-0.27	-2.07	0.079172	0.189221	-5.46
252586_at	dof6 zinc finger protein	---	AT3G45610	-1.19	-0.25	-2.07	0.0792	0.189247	-5.46
259122_at	unknown protein similar to putative ph	COBL1	AT3G02210	1.22	0.28	2.07	0.079192	0.189247	-5.46
258197_at	hypothetical protein predicted by gene	ATBRXL2	AT3G14000	-1.21	-0.28	-2.07	0.079209	0.189249	-5.46
247841_at	putative protein predicted proteins, Dr	ATFIP1[V]	AT5G58040	1.19	0.26	2.07	0.079229	0.189277	-5.47
259551_at	hypothetical protein	---	AT1G21190	1.17	0.23	2.07	0.079277	0.18935	-5.47
251935_at	fructokinase - like protein fructokinase	---	AT3G54090	-1.27	-0.35	-2.07	0.079287	0.18935	-5.47
258446_at	hypothetical protein predicted by genm	---	AT3G22430	1.17	0.22	2.07	0.079293	0.18935	-5.47
267471_at	putative ferrochelatase precusor ; sup	FC2	AT2G30390	-1.33	-0.41	-2.07	0.079269	0.18935	-5.47
256237_at	leucine rich repeat protein, putative co	DRT100	AT3G12610	-5.37	-2.42	-2.07	0.079303	0.189354	-5.47

249787_at	putative protein contains similarity to u	---	AT5G24320	1.15	0.21	2.07	0.079313	0.189357	-5.47
246473_at	putative protein cathepsin L-like cyste	---	AT5G17140	-1.19	-0.25	-2.07	0.079363	0.189458	-5.47
261855_at	unknown protein	---	AT1G50510	-1.23	-0.30	-2.07	0.079379	0.189477	-5.47
260138_at	calmodulin-4 identical to GB:Q03510 f	CAM4	AT1G66410	1.22	0.28	2.07	0.079388	0.189479	-5.47
256905_at	mitochondrial chaperonin hsp60 ident	HSP60	AT3G23990	1.48	0.56	2.06	0.079418	0.18953	-5.47
247896_at	26S proteasome regulatory subunit p2	---	AT5G57950	1.15	0.20	2.06	0.079435	0.189551	-5.47
255323_at	putative transposon protein	---	---	-1.15	-0.20	-2.06	0.079451	0.189568	-5.47
262544_at	hypothetical protein predicted by gens	---	AT1G15420	1.21	0.28	2.06	0.079515	0.189642	-5.47
259140_at	lycopene beta cyclase identical to lyco	LYC	AT3G10230	-1.16	-0.21	-2.06	0.079511	0.189642	-5.47
251532_at	putative protein F-box protein Fbl2 - H	---	AT3G58530	-1.17	-0.23	-2.06	0.07951	0.189642	-5.47
266173_at	unknown protein	---	AT2G02410	-1.16	-0.21	-2.06	0.079515	0.189642	-5.47
258712_s_	putative 40S ribosomal protein S23 si	---	AT3G09680 /	-1.23	-0.30	-2.06	0.079531	0.189661	-5.47
263016_at	ubiquitin extension protein, putative si	---	AT1G23410	-1.20	-0.26	-2.06	0.079571	0.189737	-5.47
262018_at	hypothetical protein predicted by gens	---	AT1G35617	-1.21	-0.27	-2.06	0.079615	0.18982	-5.47
263640_at	hypothetical protein predicted by gens	---	AT2G25270	-1.17	-0.23	-2.06	0.079664	0.189918	-5.47
259606_at	hypothetical protein predicted by gene	MAP65-8	AT1G27920	-1.15	-0.20	-2.06	0.079807	0.190238	-5.47
254251_at	serine/threonine kinase - like protein k	---	AT4G23300	-1.22	-0.29	-2.06	0.079822	0.190254	-5.47
265986_at	putative receptor-like protein kinase	---	AT2G24230	-1.27	-0.35	-2.06	0.079892	0.190402	-5.47
247978_at	60S ribosomal protein L31 ;supported	---	AT5G56710	-1.49	-0.57	-2.06	0.080013	0.190669	-5.48
262052_at	hypothetical protein identical to hypoth	---	---	1.19	0.25	2.06	0.080139	0.190951	-5.48
260008_at	putative RING zinc finger protein cont	---	AT1G68070	-1.16	-0.21	-2.06	0.080175	0.191017	-5.48
251758_at	transcription factor L2 ;supported by fu	---	AT3G55770	1.19	0.25	2.06	0.080199	0.191054	-5.48
264940_at	galactinol synthase, putative similar to	AtGolS4	AT1G60470	1.69	0.76	2.06	0.080246	0.191145	-5.48
265100_at	hypothetical protein predicted by gens	OSB4	AT1G31010	1.27	0.34	2.06	0.08032	0.191303	-5.48
261709_at	RNA-binding protein, putative similar t	CID11	AT1G32790	1.17	0.22	2.06	0.080382	0.19143	-5.48
261873_at	serine/threonine kinase, putative simil	SD1-13	AT1G11350	-1.32	-0.40	-2.06	0.08041	0.191475	-5.48
252081_at	putative heat shock transcription facto	HSFA7A	AT3G51910	1.45	0.54	2.06	0.080453	0.191539	-5.48
261992_at	unknown protein	---	AT1G33680	-1.18	-0.24	-2.06	0.080447	0.191539	-5.48
267286_at	putative seed maturation protein	---	AT2G23640	1.15	0.20	2.06	0.08047	0.191559	-5.48
253058_at	ribosomal - like protein ribosomal prot	---	AT4G37660	-1.28	-0.35	-2.06	0.08049	0.191587	-5.48
251837_s_	spliceosomal - like protein spliceosom	---	AT3G55200 /	1.22	0.28	2.06	0.080516	0.191613	-5.48
255444_at	LUMINIDEPENDENS protein ; suppor	LD	AT4G02560	1.17	0.23	2.06	0.080518	0.191613	-5.48
258228_at	unknown protein similar to unknown pr	---	AT3G27610	1.15	0.20	2.06	0.080533	0.191629	-5.48
251227_at	ABC transporter-like protein glutathior	ATMRP10	AT3G62700	-1.34	-0.42	-2.06	0.080549	0.191646	-5.48
249999_at	triacylglycerol lipase-like protein triacy	---	AT5G18640	1.36	0.45	2.05	0.080609	0.191771	-5.48

246815_at	putative protein integrin analogue, Sa	---	AT5G27220	1.15	0.20	2.05	0.080625	0.191787	-5.48
253613_at	PR-1-like protein gene PR-1 protein -	---	AT4G30320	-1.21	-0.27	-2.05	0.080672	0.191881	-5.48
255941_at	mitochondrial inner membrane translo	ATTIM17-1	AT1G20350	-1.30	-0.38	-2.05	0.080703	0.191933	-5.48
253577_at	putative protein	---	AT4G31080	1.32	0.40	2.05	0.080739	0.191959	-5.48
266749_at	putative protein kinase contains a prot	---	AT2G47060	-1.41	-0.50	-2.05	0.080733	0.191959	-5.48
245442_at	hypothetical protein	---	AT4G16710	-1.15	-0.20	-2.05	0.080724	0.191959	-5.48
259643_at	putative menaquinone biosynthesis pr	---	AT1G68890	-1.15	-0.21	-2.05	0.080771	0.192016	-5.48
248130_at	unknown protein	---	AT5G54790	-1.16	-0.22	-2.05	0.080795	0.192052	-5.48
255523_at	pectinesterase - like protein similar to t	---	AT4G02320	-1.17	-0.23	-2.05	0.080884	0.192243	-5.49
265082_at	hypothetical protein predicted by gene	---	AT1G03830	-1.17	-0.23	-2.05	0.080923	0.192316	-5.49
254099_at	protein-methionine-S-oxide reductase	---	AT4G25130	-1.28	-0.35	-2.05	0.080942	0.192342	-5.49
259539_at	axi 1 protein, putative similar to axi 1 p	---	AT1G20550	-1.20	-0.26	-2.05	0.08099	0.192436	-5.49
249084_at	unknown protein	---	AT5G44150	-1.19	-0.25	-2.05	0.081	0.192439	-5.49
266922_s_	SKP1/ASK1-related, putative similar t	ASK20	AT2G45950 /	1.33	0.41	2.05	0.081033	0.192497	-5.49
254352_at	hypothetical protein	---	AT4G22320	1.15	0.20	2.05	0.081073	0.192574	-5.49
260006_at	phosphatidylinositol synthase (PIS1) id	ATPIS1	AT1G68000	-1.14	-0.19	-2.05	0.081159	0.192757	-5.49
261612_at	fucosyltransferase c3 protein, putative	FUT12	AT1G49710	1.16	0.22	2.05	0.08119	0.192792	-5.49
263503_s_	hypothetical protein	---	AT2G07676	1.16	0.21	2.05	0.081191	0.192792	-5.49
252058_at	putative protein hin1 protein -Nicotian	---	AT3G52470	1.31	0.39	2.05	0.081243	0.192895	-5.49
260410_at	putative peptide transporter similar to p	---	AT1G69870	1.39	0.47	2.05	0.081258	0.192911	-5.49
257391_at	hypothetical protein predicted by gens	---	AT2G32050	1.14	0.19	2.05	0.08127	0.192919	-5.49
246494_at	putative protein putative cellulose syn	CSLA11	AT5G16190	1.20	0.27	2.05	0.081286	0.192938	-5.49
263415_at	hypothetical protein similar to GB:AAB	EMB2762	AT2G17250	1.26	0.33	2.05	0.081353	0.193074	-5.49
259750_at	hypothetical protein predicted by gens	---	AT1G71130	1.29	0.36	2.05	0.08136	0.193074	-5.49
264856_at	3-hydroxy-3-methylglutaryl-coenzyme	HMG2	AT2G17370	-1.25	-0.32	-2.05	0.081378	0.193097	-5.49
247638_at	arabinogalactan protein - like arabinog	FLA12	AT5G60490	-1.43	-0.52	-2.05	0.081388	0.193099	-5.49
245555_at	HSR201 like protein	---	AT4G15390	-1.17	-0.23	-2.05	0.081415	0.193143	-5.49
263820_at	hypothetical protein predicted by gens	---	---	-1.28	-0.36	-2.05	0.081431	0.193162	-5.49
252207_at	putative protein mRNA of unknown fu	---	AT3G50370	1.18	0.24	2.05	0.081448	0.193182	-5.49
259725_at	Expressed protein ; supported by full-l	---	AT1G61065	1.30	0.38	2.05	0.081512	0.193314	-5.49
249630_s_	sen1-like protein SEN1 - Saccharomy	---	AT5G37150 /	1.14	0.19	2.05	0.081553	0.19339	-5.49
257946_at	hypothetical protein predicted by gene	---	AT3G21710	1.17	0.23	2.05	0.081601	0.193463	-5.49
253893_at	putative protein hypothetical protein, S	---	AT4G27390	-1.25	-0.33	-2.05	0.081593	0.193463	-5.49
266494_at	putative receptor-like protein kinase	PRK2A	AT2G07040	-1.16	-0.22	-2.05	0.08165	0.19356	-5.50
260616_at	hypothetical protein contains Pfam pro	---	AT1G53280	1.25	0.32	2.05	0.08169	0.193634	-5.50

253474_at	hypothetical protein	---	AT4G32270	1.21	0.28	2.04	0.081745	0.193724	-5.50
247867_at	SNF1 related protein kinase-like protei	CIPK21	AT5G57630	1.32	0.40	2.04	0.081743	0.193724	-5.50
256790_at	ARR1 protein, putative similar to ARR	ARR1	AT3G16857	-1.18	-0.24	-2.04	0.081774	0.193773	-5.50
253833_at	putative calcium binding protein taipox	---	AT4G27790	-1.30	-0.38	-2.04	0.081812	0.193845	-5.50
260377_at	unknown protein	---	AT1G73930	-1.14	-0.19	-2.04	0.081889	0.194007	-5.50
253218_at	subtilisin-like serine protease similar t	SLP2	AT4G34980	-1.38	-0.47	-2.04	0.081993	0.194211	-5.50
263349_at	putative chromodomain-helicase-DNA-	CHR5	AT2G13370	1.24	0.31	2.04	0.081988	0.194211	-5.50
252322_at	putative protein putative zinc-finger pr	---	AT3G48550	-1.42	-0.51	-2.04	0.082065	0.194322	-5.50
258829_at	putative Sec24-like COPII protein simil	---	AT3G07100	1.14	0.18	2.04	0.082058	0.194322	-5.50
263883_at	hypothetical protein predicted by gens	---	AT2G21830	-1.19	-0.25	-2.04	0.082064	0.194322	-5.50
258657_at	hypothetical protein predicted by gens	---	AT3G09890	1.27	0.35	2.04	0.082094	0.194351	-5.50
245792_at	pinoresinol-lariciresinol reductase, put	PRR1	AT1G32100	-1.66	-0.73	-2.04	0.082092	0.194351	-5.50
255775_at	hypothetical protein predicted by gens	RBL12	AT1G18600	-1.17	-0.23	-2.04	0.082164	0.194495	-5.50
260013_at	putative annexin similar to annexin p33	ANN5	AT1G68090	1.15	0.20	2.04	0.082291	0.194775	-5.50
260647_at	hypothetical protein predicted by gene	---	AT1G08030	1.21	0.28	2.04	0.082319	0.194822	-5.50
253897_at	putative protein	---	AT4G27120	1.16	0.22	2.04	0.082373	0.19491	-5.50
260253_at	disease resistance protein, putative si	AtRLP15	AT1G74190	1.15	0.20	2.04	0.082369	0.19491	-5.50
250155_at	putative protein predicted proteins, Ar	---	AT5G15160	-1.51	-0.60	-2.04	0.082458	0.19507	-5.50
264302_at	ATPase 70 kDa subunit, putative simi	VHA-A	AT1G78900	-1.20	-0.26	-2.04	0.08245	0.19507	-5.50
256311_at	auxin response factor 6 (ARF6) identi	ARF6	AT1G30330	-1.33	-0.41	-2.04	0.082476	0.195092	-5.51
245789_at	hypothetical protein similar to hypothet	---	AT1G32090	1.40	0.48	2.04	0.082486	0.195097	-5.51
261437_at	hypothetical protein predicted by gens	RAD51D	AT1G07745	-1.19	-0.25	-2.04	0.082517	0.19515	-5.51
252253_at	Expressed protein ; supported by full-l	---	AT3G49300	-1.14	-0.18	-2.04	0.082586	0.195292	-5.51
253882_at	pelota (PEL1)	PEL1	AT4G27650	-1.22	-0.28	-2.04	0.082617	0.195345	-5.51
259444_at	hypothetical protein predicted by gens	---	AT1G02370	1.45	0.54	2.04	0.082682	0.195437	-5.51
253995_at	Col-0 casein kinase I-like protein ; sup	CK1	AT4G26100	-1.24	-0.31	-2.04	0.082684	0.195437	-5.51
246403_at	pectinacetylesterase precursor, putati	---	AT1G57590	1.29	0.36	2.04	0.082679	0.195437	-5.51
245258_at	lupeol synthase like protein ; supporte	ATPEN1	AT4G15340	1.19	0.25	2.04	0.08269	0.195437	-5.51
247926_at	protein carboxyl methylase-like	---	AT5G57280	1.41	0.50	2.04	0.082741	0.195512	-5.51
248185_at	flavonol 3-O-glucosyltransferase-like	UF3GT	AT5G54060	-1.17	-0.23	-2.04	0.082748	0.195512	-5.51
254172_at	clathrin coat assembly like protein clat	---	AT4G24550	-1.16	-0.21	-2.04	0.082742	0.195512	-5.51
244961_at	hypothetical protein	---	---	-1.15	-0.20	-2.04	0.082769	0.195543	-5.51
251777_s_	pyruvate kinase - like protein pyruvate	---	AT3G55650 /	-1.20	-0.26	-2.04	0.082791	0.195575	-5.51
250278_at	2-oxoglutarate/malate translocator pre	DiT1	AT5G12860	-1.33	-0.41	-2.04	0.082856	0.195686	-5.51
262663_at	hypothetical protein identical to hypoth	---	AT1G13940	-1.19	-0.26	-2.04	0.082852	0.195686	-5.51

245387_at	nuclear RNA binding protein A-like pro	---	AT4G17520	-1.24	-0.31	-2.04	0.082885	0.195734	-5.51
261668_at	2-isopropylmalate synthase, putative s	MAML-4	AT1G18500	-1.21	-0.28	-2.04	0.08291	0.195774	-5.51
263599_at	putative histidine kinase ; supported b	WOL	AT2G01830	-1.29	-0.37	-2.04	0.082926	0.195792	-5.51
248841_at	ubiquitin-specific protease 21 (UBP21)	UBP21	AT5G46740	1.28	0.36	2.03	0.082961	0.195853	-5.51
250117_at	isopentenyl pyrophosphate:dimethyllal	IPP1	AT5G16440	-1.29	-0.37	-2.03	0.083017	0.195966	-5.51
249229_at	putative protein similar to unknown pro	---	AT5G42090	1.18	0.24	2.03	0.083066	0.195982	-5.51
267213_at	60S ribosomal protein L7 ;supported b	---	AT2G44120	-1.37	-0.46	-2.03	0.083043	0.195982	-5.51
254219_at	putative protein	---	AT4G23760	-1.18	-0.23	-2.03	0.083034	0.195982	-5.51
265841_at	putative glycogenin	---	AT2G35710	2.15	1.10	2.03	0.083067	0.195982	-5.51
266624_s_	phosphoribosyl pyrophosphate synthet	---	AT1G32380 /	1.45	0.53	2.03	0.083053	0.195982	-5.51
250216_at	unknown protein	---	AT5G14090	-1.23	-0.30	-2.03	0.083089	0.196013	-5.51
249224_at	mitochondrial carrier protein-like	---	AT5G42130	-1.14	-0.19	-2.03	0.083151	0.19612	-5.51
252190_at	putative protein various predicted gen	---	AT3G50170	-1.16	-0.21	-2.03	0.083144	0.19612	-5.51
248306_at	unknown protein ; supported by cDNA	WRKY27	AT5G52830	1.30	0.38	2.03	0.083181	0.196171	-5.51
264639_at	unknown protein similar to ubiquitin C-	UCH2	AT1G65650	-1.21	-0.28	-2.03	0.083198	0.196186	-5.51
252966_at	putative protein various predicted prot	---	AT4G38870	-1.19	-0.25	-2.03	0.083205	0.196186	-5.51
254517_at	putative protein conserved hypothetic	---	AT4G20310	-1.17	-0.23	-2.03	0.083239	0.196246	-5.51
259053_at	unknown protein similar to hypothetica	---	AT3G03320	1.19	0.25	2.03	0.083254	0.196262	-5.51
253692_at	putative protein Cs protein, Drosophila	ATPAO5	AT4G29720	-1.14	-0.19	-2.03	0.083263	0.196263	-5.51
265696_at	putative molybdopterin biosynthesis C	CNX2	AT2G31955	1.34	0.43	2.03	0.083272	0.196263	-5.51
262552_at	hypothetical protein similar to hypothet	---	AT1G31350	1.31	0.39	2.03	0.083307	0.196325	-5.51
262978_at	tubulin beta-1 chain identical to GB:P1	TUB1	AT1G75780	-2.79	-1.48	-2.03	0.083322	0.19634	-5.52
261947_at	ubiquitin, putative similar to poly-ubiqu	---	AT1G64470	1.22	0.29	2.03	0.083331	0.196342	-5.52
264328_at	putative IAA1 protein Match to IAA10 p	IAA10	AT1G04100	1.27	0.34	2.03	0.083359	0.196387	-5.52
255481_at	T14P8.6 ; supported by cDNA: gi_156	PMS1	AT4G02460	1.24	0.31	2.03	0.083372	0.196398	-5.52
265896_at	unknown protein	emb2410	AT2G25660	1.18	0.24	2.03	0.0834	0.196423	-5.52
251966_at	receptor lectin kinase -like protein rec	---	AT3G53380	-1.25	-0.32	-2.03	0.083396	0.196423	-5.52
AFFX-r2-Bs	B. subtilis /GEN=pheB /DB_XREF=gb:	---	---	-1.32	-0.40	-2.03	0.083434	0.196482	-5.52
252508_at	putative protein tRNA nucleotidyltrans	---	AT3G46210	1.30	0.38	2.03	0.08353	0.196676	-5.52
266959_at	putative DNA replication licensing fact	MCM5	AT2G07690	-1.66	-0.73	-2.03	0.083533	0.196676	-5.52
255469_at	predicted OR23 protein of unknown fu	---	AT4G03030	1.19	0.25	2.03	0.08356	0.196718	-5.52
258274_at	putative cytochrome c oxidase subunit	---	AT3G15640	1.21	0.28	2.03	0.083571	0.196724	-5.52
256486_at	chloroplast nucleoid DNA binding prot	---	AT1G31450	-1.18	-0.24	-2.03	0.083595	0.196761	-5.52
253652_at	putative protein nucleoid DNA-binding	---	AT4G30040	1.14	0.18	2.03	0.08364	0.196845	-5.52
245844_at	hypothetical protein predicted by gene	---	AT1G26170	1.18	0.24	2.03	0.083665	0.196884	-5.52

250662_at	steroid sulfotransferase-like protein ;s	ST2A	AT5G07010	-1.45	-0.54	-2.03	0.0837	0.196946	-5.52
266297_at	putative proliferating cell nuclear antig	PCNA2	AT2G29570	-1.76	-0.82	-2.03	0.083729	0.196953	-5.52
258279_at	putative self-incompatibility protein sin	---	AT3G26870	-1.13	-0.17	-2.03	0.083727	0.196953	-5.52
246160_at	putative protein predicted protein, Ory	FBX2	AT5G21040	-1.16	-0.21	-2.03	0.083711	0.196953	-5.52
266783_at	putative laccase (diphenol oxidase)	LAC2	AT2G29130	-1.27	-0.34	-2.03	0.083787	0.19706	-5.52
261045_at	pathogenesis related protein, putative	---	AT1G01310	-1.14	-0.19	-2.03	0.0838	0.19706	-5.52
247430_at	putative protein contains similarity to D	---	AT5G62610	-1.21	-0.27	-2.03	0.0838	0.19706	-5.52
260231_at	putative RING zinc finger protein cont	---	AT1G74410	1.23	0.30	2.03	0.083836	0.197125	-5.52
267128_at	putative acetone-cyanohydrin lyase	MES1	AT2G23620	-1.22	-0.28	-2.03	0.083879	0.197164	-5.52
246136_at	peptide transporter - like protein pepti	---	AT5G28470	-1.19	-0.25	-2.03	0.083886	0.197164	-5.52
259983_at	3-hydroxy-3-methylglutaryl CoA reduc	HMG1	AT1G76490	-1.19	-0.25	-2.03	0.083888	0.197164	-5.52
259601_s_	CACTA-element transposase, putative	---	---	-1.16	-0.21	-2.03	0.083883	0.197164	-5.52
249591_at	putative protein predicted protein, Ara	---	---	1.15	0.20	2.03	0.083903	0.197181	-5.52
252161_at	proline-rich protein	---	AT3G50580	-1.13	-0.18	-2.03	0.083959	0.197274	-5.52
254062_at	putative protein zinc finger protein ZN	---	AT4G25380	1.76	0.82	2.03	0.08396	0.197274	-5.52
251322_at	cysteine synthase AtcysC1 ;supported	CYSC1	AT3G61440	1.49	0.58	2.03	0.083975	0.197288	-5.52
263796_at	unknown protein ;supported by full-ler	AFR	AT2G24540	-1.32	-0.40	-2.03	0.084048	0.19744	-5.52
246444_at	putative protein predicted protein T21	---	AT5G17570	-1.28	-0.36	-2.02	0.084188	0.197748	-5.53
261898_at	hypothetical protein predicted by gene	---	AT1G80720	1.40	0.48	2.02	0.084302	0.197994	-5.53
261701_at	hypothetical protein similar to hypothet	HAF01	AT1G32750	1.13	0.18	2.02	0.084379	0.198135	-5.53
267293_at	hypothetical protein	TET8	AT2G23810	1.33	0.42	2.02	0.084374	0.198135	-5.53
253601_at	hypothetical protein	---	AT4G30900	-1.14	-0.19	-2.02	0.084433	0.198242	-5.53
263434_at	putative homeodomain transcription fa	PRS	AT2G28610	-1.14	-0.19	-2.02	0.08445	0.198261	-5.53
249028_at	DNA-damage-inducible protein P ; su	POLH	AT5G44740	1.23	0.30	2.02	0.084528	0.198424	-5.53
254573_at	putative pectinacetylesterase pectinac	---	AT4G19420	1.40	0.48	2.02	0.084551	0.198458	-5.53
246282_at	ATPase-like protein	---	AT4G36580	1.31	0.39	2.02	0.084656	0.198664	-5.53
267617_at	heme oxygenase 1 (HO1) identical to (	TED4	AT2G26670	1.30	0.38	2.02	0.08465	0.198664	-5.53
248674_at	non-phototropic hypocotyl-like protein	---	AT5G48800	1.36	0.45	2.02	0.084729	0.1988	-5.53
257421_at	hypothetical protein predicted by gene	---	AT1G12030	-1.33	-0.41	-2.02	0.084732	0.1988	-5.53
259197_at	putative peroxidase similar to peroxida	---	AT3G03670	1.82	0.87	2.02	0.084778	0.198888	-5.53
260088_at	tonoplast intrinsic protein, alpha (alph	TIP3;1	AT1G73190	-1.21	-0.27	-2.02	0.084813	0.198949	-5.53
257183_at	ABC transporter contains Pfam profile:	---	AT3G13220	-1.17	-0.23	-2.02	0.084826	0.198949	-5.53
266251_s_	unknown protein	---	AT2G18320 /	-1.14	-0.19	-2.02	0.08483	0.198949	-5.53
249072_at	putative protein similar to unknown pro	---	AT5G44060	1.69	0.75	2.02	0.084933	0.19917	-5.53
250780_at	expansin At-EXP2 (gb|AAB38073.1) ;	ATEXPA2	AT5G05290	-1.25	-0.33	-2.02	0.084952	0.199194	-5.53

259718_at	unknown protein	VIP5	AT1G61040	1.14	0.19	2.02	0.085005	0.199298	-5.53
263293_x_	hypothetical protein similar to hypothet	---	---	-1.15	-0.20	-2.02	0.085043	0.199366	-5.54
262045_at	hypothetical protein predicted by gene	---	AT1G80240 /	-1.29	-0.37	-2.02	0.085174	0.199652	-5.54
246452_at	putative protein predicted proteins - Ar	BPA1	AT5G16840	-1.17	-0.22	-2.02	0.085186	0.19966	-5.54
259724_at	putative serine/threonine-protein kinas	SNRK2.10	AT1G60940	1.24	0.31	2.02	0.085195	0.199662	-5.54
254216_at	V-ATPase subunit G (vag2 gene)	VAG2	AT4G23710	1.37	0.45	2.02	0.085281	0.199827	-5.54
247799_at	subtilisin-like serine protease contains	---	AT5G58840	1.25	0.33	2.02	0.085283	0.199827	-5.54
254104_at	putative protein predicted protein, Ara	---	AT4G25040	1.21	0.27	2.02	0.085349	0.19996	-5.54
261602_at	hydrogenase protein, putative similar	ATPREP2	AT1G49630	1.15	0.20	2.02	0.085363	0.199973	-5.54
246835_at	putative protein putative APC11 anapl	---	AT5G26640	-1.21	-0.28	-2.01	0.085413	0.20005	-5.54
264688_at	hypothetical protein similar to LG27/30	---	AT1G09890	-1.26	-0.33	-2.01	0.085414	0.20005	-5.54
252077_at	putative protein several putative myosi	---	AT3G51720	1.21	0.28	2.01	0.085425	0.200055	-5.54
246002_at	ripening-related protein - like grip28 ri	---	AT5G20740	-1.42	-0.50	-2.01	0.085477	0.200158	-5.54
251131_at	laccase - like protein laccase precurso	LAC10	AT5G01190	-1.14	-0.18	-2.01	0.085489	0.200165	-5.54
249348_at	unknown protein	---	AT5G40860	1.21	0.28	2.01	0.085498	0.200166	-5.54
267216_at	hypothetical protein	---	AT2G02620	-1.17	-0.23	-2.01	0.085512	0.200177	-5.54
248534_at	putative protein contains similarity to p	---	AT5G50030	-1.16	-0.22	-2.01	0.085544	0.200211	-5.54
252260_at	putative protein several hypothetical pr	---	AT3G49480	-1.25	-0.32	-2.01	0.085539	0.200211	-5.54
260822_at	RNA polymerase, putative similar to	---	AT1G06790	-1.17	-0.22	-2.01	0.085567	0.200221	-5.54
257146_at	unknown protein contains Pfam profile	GTE8	AT3G27260	1.14	0.18	2.01	0.085563	0.200221	-5.54
249099_at	putative protein similar to unknown pro	---	AT5G43550	-1.13	-0.18	-2.01	0.085575	0.200221	-5.54
253706_at	putative protein D-threonine dehydrog	---	AT4G29120	-1.17	-0.22	-2.01	0.085695	0.200421	-5.54
246209_at	BEL1-like homeobox 2 protein (BLH2)	BLH2	AT4G36870	-1.31	-0.39	-2.01	0.085691	0.200421	-5.54
254039_at	putative protein Human GS1 (protein	GPP1	AT4G25840	-1.23	-0.30	-2.01	0.085678	0.200421	-5.54
264288_at	Expressed protein ; supported by full-l	---	AT1G62045	-1.17	-0.23	-2.01	0.085676	0.200421	-5.54
260757_at	phytocyanin, putative similar to phyto	---	AT1G48940	1.15	0.20	2.01	0.085761	0.200555	-5.54
253114_at	GTP-binding protein GB2 ;supported	ATGB2	AT4G35860	1.20	0.27	2.01	0.085794	0.20061	-5.54
252429_at	H-protein promoter binding factor-2a ;	CDF3	AT3G47500	-1.28	-0.36	-2.01	0.085817	0.200645	-5.54
259151_at	kinesin-like protein similar to carboxy-t	---	AT3G10310	-1.23	-0.30	-2.01	0.085859	0.200722	-5.54
264232_at	putative protein kinase Pfam HMM hit:	---	AT1G67470	1.73	0.79	2.01	0.085959	0.200936	-5.55
261994_at	hypothetical protein contains similarity	---	AT1G33640	-1.16	-0.21	-2.01	0.085969	0.200939	-5.55
250704_at	Expressed protein ; supported by full-l	---	AT5G06265	1.22	0.29	2.01	0.085985	0.200955	-5.55
247865_at	Expressed protein ; supported by full-l	---	AT5G57815	1.16	0.22	2.01	0.086034	0.201048	-5.55
261404_at	alpha galactosyltransferase, putative	---	AT1G18690	1.32	0.40	2.01	0.086059	0.201086	-5.55
260209_at	putative AP2 domain transcription fact	CPuORF53	AT1G68550 /	-1.20	-0.26	-2.01	0.086123	0.201216	-5.55

254913_at	putative protein beta-transducin repea	---	AT4G11270	1.16	0.22	2.01	0.086149	0.201254	-5.55
248284_at	Expressed protein ; supported by full-l	---	AT5G52975	-1.22	-0.28	-2.01	0.086328	0.201652	-5.55
258878_at	hypothetical protein predicted by gens	---	AT3G03170	1.15	0.21	2.01	0.086452	0.201922	-5.55
247274_at	putative protein similar to unknown pro	---	AT5G64360	-1.22	-0.28	-2.01	0.086476	0.201958	-5.55
245863_s_	hypothetical protein contains similarity	---	AT1G58050 /	-1.20	-0.26	-2.01	0.086487	0.201963	-5.55
253555_at	putative protein predicted proetein, Ar	---	AT4G31080	1.26	0.34	2.01	0.086515	0.202006	-5.55
262362_at	disease resistance protein, putative si	---	AT1G72840	1.16	0.22	2.01	0.086582	0.202105	-5.55
266054_at	hypothetical protein predicted by gene	---	AT2G40640	-1.23	-0.29	-2.01	0.086583	0.202105	-5.55
256869_at	nodulin, putative similar to nodulin GB	---	AT3G26420 /	1.26	0.34	2.01	0.086593	0.202105	-5.55
248695_at	putative protein similar to unknown pro	---	AT5G48350	1.26	0.33	2.01	0.086588	0.202105	-5.55
265617_at	putative phosphate/phosphoenolpyruv	---	AT2G25520	1.36	0.44	2.01	0.086611	0.202127	-5.55
246348_at	putative protein putative glycerol-3-pho	---	AT3G56840	-1.12	-0.17	-2.00	0.086657	0.202215	-5.55
257224_at	P-type ATPase, putative similar to AT	---	AT3G27870	-1.20	-0.26	-2.00	0.08669	0.202272	-5.55
261773_at	hypothetical protein predicted by gens	---	AT1G76250	1.24	0.31	2.00	0.08672	0.20232	-5.55
266259_at	unknown protein ;supported by full-ler	---	AT2G27830	1.17	0.23	2.00	0.086749	0.202367	-5.55
249115_at	PINHEAD (gb|AAD40098.1); translatio	ZLL	AT5G43810	-1.14	-0.19	-2.00	0.086781	0.202421	-5.56
247941_at	putative protein strong similarity to unk	---	AT5G57200	-1.15	-0.20	-2.00	0.086805	0.202456	-5.56
248894_at	unknown protein	---	AT5G46320	1.18	0.24	2.00	0.086839	0.202515	-5.56
265340_at	putative AAA-type ATPase similar to 2	---	AT2G18330	1.34	0.43	2.00	0.086864	0.202539	-5.56
248614_at	putative protein similar to unknown pro	---	AT5G49560	-1.17	-0.22	-2.00	0.086867	0.202539	-5.56
248796_at	VAMP (vesicle-associated membrane	---	AT5G47180	-1.30	-0.38	-2.00	0.086969	0.202755	-5.56
251270_at	putative protein	---	AT3G62370	-1.27	-0.35	-2.00	0.086994	0.202792	-5.56
263025_at	reverse transcriptase, putative similar	---	---	-1.18	-0.23	-2.00	0.087031	0.20286	-5.56
251065_at	lipid-transfer protein-like lipid-transfer	---	AT5G01870	1.21	0.28	2.00	0.087058	0.202902	-5.56
248361_at	putative protein similar to unknown pro	EDA41	AT5G52460	-1.19	-0.25	-2.00	0.087069	0.202906	-5.56
262144_at	hypothetical protein predicted by gene	---	AT1G52620	1.16	0.21	2.00	0.087091	0.202938	-5.56
259473_at	hypothetical protein predicted by gens	---	AT1G19025	-1.22	-0.28	-2.00	0.087158	0.20305	-5.56
262747_at	hypothetical protein predicted by gene	---	AT1G28540	-1.15	-0.20	-2.00	0.087154	0.20305	-5.56
264279_s_	glycoprotein(EP1), putative similar to	---	AT1G78820 /	1.25	0.32	2.00	0.087262	0.203272	-5.56
255559_at	putative NAK-like ser/thr protein kinas	---	AT4G02010	-1.22	-0.29	-2.00	0.087271	0.203273	-5.56
267190_at	putative N-myristoyltransferase ; supp	NMT2	AT2G44170	-1.17	-0.23	-2.00	0.087298	0.203314	-5.56
251125_at	putative protein - kinase protein kinas	---	AT5G01060	-1.14	-0.19	-2.00	0.087307	0.203314	-5.56
245320_at	Expressed protein ; supported by full-l	---	AT4G16444	1.16	0.21	2.00	0.087394	0.203497	-5.56
249173_at	unknown protein	---	AT5G43000	-1.22	-0.29	-2.00	0.087431	0.203563	-5.56
256422_at	unknown protein	MOS2	AT1G33520	-1.17	-0.23	-2.00	0.08755	0.20382	-5.56

251062_at	putative protein putative proteins - Ara	OFP1	AT5G01840	-1.18	-0.24	-2.00	0.087576	0.203858	-5.56
251728_at	cysteine-tRNA ligase-like protein sever	---	AT3G56300	-1.17	-0.23	-2.00	0.087591	0.203872	-5.56
250207_at	chalcone synthase (naringenin-chalcor	TT4	AT5G13930	-1.61	-0.68	-2.00	0.087662	0.204003	-5.57
AFFX-r2-Bs	B. subtilis /GEN=dapB /DB_XREF=gb:	---	---	-1.39	-0.47	-2.00	0.087665	0.204003	-5.57
251576_at	putative protein several hypothetical pr	---	AT3G58200	-1.16	-0.21	-2.00	0.087676	0.204008	-5.57
252723_at	hypothetical protein ; supported by ful	---	AT3G43520	1.14	0.19	2.00	0.087696	0.204027	-5.57
253323_at	putative protein protein phosphatase \	---	AT4G33920	1.53	0.61	2.00	0.087702	0.204027	-5.57
266021_at	unknown protein	---	AT2G05910	1.28	0.36	2.00	0.087731	0.204074	-5.57
248453_at	unknown protein	---	AT5G51340	1.17	0.22	2.00	0.087766	0.204123	-5.57
253064_at	bZIP transcription factor - like protein	AtbZIP7	AT4G37730	1.18	0.24	2.00	0.08777	0.204123	-5.57
261199_at	unknown protein	---	AT1G12950	-1.14	-0.19	-2.00	0.0878	0.20415	-5.57
257542_at	hypothetical protein predicted by gene	---	AT3G26050	-1.14	-0.19	-2.00	0.087795	0.20415	-5.57
248804_at	nodulin-like protein	---	AT5G47470	1.18	0.24	2.00	0.087842	0.204227	-5.57
264323_at	putative dimethylaniline monooxygena	---	AT1G04180	-1.77	-0.82	-1.99	0.087926	0.204394	-5.57
261677_at	unknown protein ;supported by full-len	---	AT1G18470	1.28	0.36	1.99	0.087932	0.204394	-5.57
255427_at	hypothetical protein	---	AT4G03380	-1.13	-0.18	-1.99	0.087956	0.204429	-5.57
253153_at	hypothetical protein	---	AT4G35700	-1.16	-0.22	-1.99	0.087972	0.204447	-5.57
245309_at	putative protein ; supported by cDNA:	---	AT4G15140	1.31	0.39	1.99	0.088056	0.204622	-5.57
254572_at	putative protein predicted protein MTC	---	AT4G19380	-1.17	-0.22	-1.99	0.088078	0.204651	-5.57
254009_at	pyruvate kinase like protein pyruvate k	---	AT4G26390	-1.29	-0.37	-1.99	0.08814	0.204773	-5.57
245595_at	hypothetical protein	---	AT4G14170	-1.15	-0.20	-1.99	0.0882	0.204894	-5.57
263195_at	non-specific lipid transfer protein, puta	---	AT1G36150	-1.25	-0.32	-1.99	0.08821	0.204895	-5.57
264791_at	predicted protein	---	AT2G17845	-1.14	-0.18	-1.99	0.088292	0.205064	-5.57
260402_at	putative gamma-glutamyltransferase (	GGT3	AT1G69820	-1.23	-0.30	-1.99	0.088318	0.205087	-5.57
254748_at	unknown protein	---	---	-1.16	-0.22	-1.99	0.088319	0.205087	-5.57
247356_at	beta-galactosidase (emb|CAB64742.1	MUM2	AT5G63800	1.37	0.46	1.99	0.08835	0.205138	-5.57
248875_at	disease resistance protein-like	---	AT5G46470	1.31	0.39	1.99	0.0884	0.205232	-5.57
247621_at	putative protein predicted proteins fro	---	AT5G60340	1.16	0.21	1.99	0.088418	0.205253	-5.57
247764_at	subtilisin-like serine protease contains	---	AT5G59190	-1.18	-0.23	-1.99	0.088445	0.205294	-5.57
255824_at	hypothetical protein predicted by gene	---	AT2G40530	-1.60	-0.68	-1.99	0.088462	0.205312	-5.57
261029_at	unknown protein	---	AT1G17330	1.23	0.30	1.99	0.088484	0.205343	-5.57
261339_at	protein kinase, putative similar to man	---	AT1G35710	1.33	0.42	1.99	0.088494	0.205346	-5.57
264911_at	auxin-induced protein, putative similar	---	AT1G60690	-1.24	-0.31	-1.99	0.088527	0.205402	-5.57
252845_at	vacuolar H(+)-ATPase subunit-like pro	---	AT3G42050	-1.15	-0.20	-1.99	0.088537	0.205404	-5.58
247681_at	serine/threonine-specific protein kinas	---	---	1.23	0.30	1.99	0.088549	0.20541	-5.58

251636_at	calcium-dependent protein kinase cal	CPK32	AT3G57530	1.68	0.75	1.99	0.088583	0.205469	-5.58
246373_at	receptor-like protein kinase, putative s	---	AT1G51860	1.28	0.35	1.99	0.088612	0.205515	-5.58
250674_at	laccase-like protein laccase - Populus	LAC13	AT5G07130	-1.29	-0.37	-1.99	0.088629	0.205533	-5.58
248626_at	receptor protein kinase-like protein	---	AT5G48940	-1.17	-0.22	-1.99	0.088681	0.205633	-5.58
254810_at	putative protein pectinesterase - Citru	PME1	AT4G12390	-1.45	-0.53	-1.99	0.088725	0.205712	-5.58
266210_at	60S ribosomal protein L10A ; supporte	PGY1	AT2G27530	-1.33	-0.41	-1.99	0.088736	0.205712	-5.58
263308_at	hypothetical protein predicted by gens	---	---	1.15	0.20	1.99	0.088742	0.205712	-5.58
256480_at	unknown protein	SAR1	AT1G33410	1.21	0.28	1.99	0.088764	0.20572	-5.58
256362_at	hypothetical protein	---	AT1G66450	1.18	0.23	1.99	0.088764	0.20572	-5.58
258673_at	unknown protein	---	AT3G08620	1.26	0.33	1.99	0.088908	0.206021	-5.58
260404_at	unknown protein similar to activator-lik	---	---	-1.30	-0.38	-1.99	0.088914	0.206021	-5.58
261780_at	cyclin, putative similar to B-like cyclin	CYCB2;4	AT1G76310	-1.18	-0.24	-1.99	0.08892	0.206021	-5.58
255716_at	coded for by A. thaliana cDNA R30513	CRCK2	AT4G00330	-1.13	-0.17	-1.99	0.088939	0.20604	-5.58
267083_at	calmodulin-like protein identical to GB:	TCH3	AT2G41100	1.40	0.49	1.99	0.088954	0.20604	-5.58
261290_at	hypothetical protein predicted by gene	---	AT1G36990	1.26	0.34	1.99	0.088956	0.20604	-5.58
246067_at	membrane transporter - like protein w	---	AT5G19410	-1.15	-0.20	-1.99	0.088976	0.206065	-5.58
248802_at	Expressed protein ; supported by cDN	---	AT5G47435	1.18	0.24	1.99	0.088999	0.206078	-5.58
245791_at	defender against cell death protein, pu	ATDAD1	AT1G32210	-1.19	-0.25	-1.99	0.088997	0.206078	-5.58
257382_at	hypothetical protein predicted by gens	WRKY54	AT2G40750	2.97	1.57	1.99	0.089041	0.206153	-5.58
262299_at	unknown protein Similar to gb|U04299	---	AT1G27520	1.17	0.22	1.99	0.089097	0.206228	-5.58
257293_at	unknown protein similar to symbiosis-r	APG8H	AT3G15580	1.26	0.33	1.99	0.0891	0.206228	-5.58
250001_at	tub family-like protein tubby-like protei	AtTLP11	AT5G18680	-1.29	-0.36	-1.99	0.089091	0.206228	-5.58
250859_at	cytochrom P450 - like protein cytochro	CYP77A4	AT5G04660	-1.13	-0.17	-1.99	0.089139	0.206297	-5.58
251521_at	putative protein receptor kinase homo	ACR4	AT3G59420	-1.22	-0.29	-1.99	0.08918	0.206371	-5.58
260455_at	hypothetical protein predicted by gens	---	AT1G72500	-1.49	-0.58	-1.98	0.089362	0.206772	-5.58
250023_at	beta-1,3-glucanase-like protein	---	AT5G18220	-1.20	-0.27	-1.98	0.089424	0.206872	-5.58
264434_at	hypothetical protein predicted by gens	---	AT1G10340	1.71	0.78	1.98	0.08942	0.206872	-5.58
248425_at	ACC synthase; 1-aminocyclopropane-	ACS12	AT5G51690	1.22	0.29	1.98	0.089443	0.206895	-5.59
260160_at	putative RNA-binding protein contains	---	AT1G79880	1.16	0.21	1.98	0.089484	0.206906	-5.59
259068_at	unknown protein	PEX13	AT3G07560	1.18	0.24	1.98	0.089474	0.206906	-5.59
251316_s_	putative protein putative protein BcDN	---	AT3G61480 /	1.18	0.23	1.98	0.089476	0.206906	-5.59
249846_at	cation-transporting ATPase	---	AT5G23630	1.14	0.19	1.98	0.089472	0.206906	-5.59
259436_at	hypothetical protein predicted by gene	---	AT1G01500	1.17	0.22	1.98	0.089621	0.207181	-5.59
256085_at	hypothetical protein predicted by gens	---	AT1G20760	-1.14	-0.19	-1.98	0.08962	0.207181	-5.59
251829_at	putative protein KIAA0882 protein, Ho	---	AT3G55020	-1.42	-0.50	-1.98	0.089644	0.207214	-5.59

266741_s_	putative disease resistance protein	---	AT2G03030 /	1.14	0.19	1.98	0.089663	0.207237	-5.59
249271_at	myosin heavy chain-like protein	CIP1	AT5G41790	-1.28	-0.36	-1.98	0.089752	0.20742	-5.59
266600_at	putative mitogen-activated protein kina	MPK12	AT2G46070	1.30	0.38	1.98	0.089807	0.207527	-5.59
258567_at	apyrase (Atapy1) identical to apyrase (	ATAPY1	AT3G04080	-1.22	-0.29	-1.98	0.089837	0.207575	-5.59
265802_at	predicted protein	---	AT2G35733	1.21	0.27	1.98	0.089864	0.207617	-5.59
257249_at	unknown protein	---	AT3G24180	1.26	0.33	1.98	0.089879	0.20763	-5.59
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=gb:	---	---	-1.41	-0.50	-1.98	0.089954	0.207782	-5.59
256016_at	hypothetical protein predicted by gens	---	AT1G19240	1.20	0.27	1.98	0.089971	0.207801	-5.59
255534_at	CHP-rich hypothetical protein similar to	---	AT4G02190	1.16	0.21	1.98	0.090029	0.207914	-5.59
252332_at	putative protein	---	AT3G48810	-1.24	-0.31	-1.98	0.090053	0.207949	-5.59
249075_at	putative protein similar to unknown pro	---	AT5G44000	-1.23	-0.30	-1.98	0.090075	0.207977	-5.59
259379_at	putative MYB family transcription facto	---	AT3G16350	-1.43	-0.51	-1.98	0.090144	0.208115	-5.59
254765_at	hypothetical protein	---	AT4G13270	1.19	0.25	1.98	0.090211	0.208248	-5.59
247098_at	GTP-binding protein-like	---	AT5G66470	-1.29	-0.37	-1.98	0.090264	0.20835	-5.59
257025_at	hypothetical protein predicted by gene	ATG2	AT3G19190	1.25	0.32	1.98	0.090294	0.208398	-5.59
266345_at	hypothetical protein predicted by gene	---	AT2G01410	-1.16	-0.21	-1.98	0.090342	0.208488	-5.59
255544_at	predicted protein of unknown function	---	AT4G01880	1.22	0.29	1.98	0.09045	0.208717	-5.60
250421_at	putative protein	OCP3	AT5G11270	1.22	0.29	1.98	0.090479	0.208742	-5.60
257956_at	unknown protein	---	AT3G25400	1.23	0.30	1.98	0.090473	0.208742	-5.60
262609_at	unknown protein ;supported by full-len	---	AT1G13930	1.20	0.26	1.97	0.090514	0.208801	-5.60
246266_at	30S ribosomal protein S11, putative c	NFD3	AT1G31817	-1.25	-0.32	-1.97	0.090558	0.208882	-5.60
263186_at	lectin receptor kinase, putative similar	---	---	-1.25	-0.32	-1.97	0.090576	0.208902	-5.60
265472_at	putative RING-H2 zinc finger protein ;	---	AT2G15580	1.21	0.28	1.97	0.090602	0.208907	-5.60
262997_at	disease resistance protein, putative si	RPP27	AT1G54470	-1.14	-0.19	-1.97	0.090606	0.208907	-5.60
247950_at	unknown protein	---	AT5G57230	1.16	0.22	1.97	0.09059	0.208907	-5.60
259022_at	putative asparaginyl-tRNA synthetase	NS2	AT3G07420	-1.28	-0.36	-1.97	0.09068	0.209058	-5.60
251792_at	probable serine/threonine-specific pro	---	AT3G55550	-1.17	-0.23	-1.97	0.090795	0.209301	-5.60
254992_at	putative transcriptional regulator	SPT16	AT4G10710	1.24	0.31	1.97	0.090843	0.20939	-5.60
250345_at	subtilisin-like serine protease contains	---	AT5G11940	1.18	0.24	1.97	0.090877	0.209447	-5.60
262395_at	hypothetical protein similar to hypothet	---	AT1G49540	1.36	0.44	1.97	0.090888	0.209451	-5.60
258705_at	hypothetical protein predicted by gene	---	AT3G09470	1.18	0.23	1.97	0.090916	0.209484	-5.60
254056_at	putative protein Group I Pectinesteras	---	AT4G25250	-1.18	-0.24	-1.97	0.09092	0.209484	-5.60
249358_at	sucrose cleavage protein -like sucrose	---	AT5G40510	1.19	0.25	1.97	0.090947	0.209525	-5.60
256622_at	unknown protein	AtHB34	AT3G28920	1.14	0.19	1.97	0.091013	0.209647	-5.60
265799_at	unknown protein ; supported by cDNA	---	AT2G35680	1.19	0.25	1.97	0.091019	0.209647	-5.60

251592_at	zinc finger - like protein finger protein	NTT	AT3G57670	1.15	0.20	1.97	0.091053	0.209706	-5.60
260636_at	hypothetical protein contains similarity	ATCDS1	AT1G62430	-1.34	-0.42	-1.97	0.091071	0.209724	-5.60
266060_at	unknown protein unusual splice site at	---	AT2G18630	-1.24	-0.31	-1.97	0.091114	0.209783	-5.60
246126_at	putative protein predicted protein, Ory	ATNUDX19	AT5G20070	-1.38	-0.47	-1.97	0.091111	0.209783	-5.60
250966_at	putative protein various predicted prot	---	AT5G02910	-1.21	-0.27	-1.97	0.091175	0.2099	-5.60
258995_at	putative ribosomal protein L13 similar t	---	AT3G01790	-1.26	-0.33	-1.97	0.091208	0.209955	-5.60
261672_at	unknown protein contains similarity to	ATARP4	AT1G18450	-1.24	-0.31	-1.97	0.09127	0.210068	-5.60
264243_at	hypothetical protein predicted by gene	---	AT1G54650	-1.25	-0.32	-1.97	0.091275	0.210068	-5.61
255247_at	hypothetical protein	---	---	-1.13	-0.17	-1.97	0.091286	0.210072	-5.61
245933_at	putative protein KIAA1521 - Homo sap	VPS9B	AT5G09320	-1.15	-0.20	-1.97	0.09131	0.210084	-5.61
260226_at	hypothetical protein predicted by gene	MIF1	AT1G74660	-1.21	-0.28	-1.97	0.091309	0.210084	-5.61
264229_at	unknown protein	---	AT1G67480	1.29	0.36	1.97	0.091392	0.210251	-5.61
249365_at	putative protein predicted protein, Ara	---	AT5G40600	-1.17	-0.22	-1.97	0.091414	0.210282	-5.61
256755_at	calmodulin, putative similar to GB:P07	---	AT3G25600	1.36	0.45	1.97	0.091569	0.210565	-5.61
261736_at	hypothetical protein simlar to hypotheti	---	AT1G47810	1.16	0.21	1.97	0.091571	0.210565	-5.61
248751_at	putative protein similar to unknown pro	---	AT5G47540	-1.19	-0.25	-1.97	0.091574	0.210565	-5.61
264758_at	late embryogenesis abundant protein,	---	AT1G61340	2.16	1.11	1.97	0.091569	0.210565	-5.61
267437_at	hypothetical protein predicted by gene	---	AT2G19200	-1.16	-0.22	-1.97	0.091688	0.210806	-5.61
246364_at	hypothetical protein	---	---	1.15	0.20	1.97	0.091746	0.210918	-5.61
251518_at	putative protein protein CG15643 - Dr	---	AT3G59390	-1.18	-0.24	-1.97	0.091804	0.211031	-5.61
250600_at	dimethylaniline monooxygenase-like p	---	AT5G07800	-1.16	-0.21	-1.96	0.091876	0.211173	-5.61
259249_at	hypothetical protein predicted by gene	---	AT3G07790	-1.26	-0.33	-1.96	0.091919	0.21123	-5.61
245173_at	putative AP2 domain transcription fact	---	AT2G47520	1.48	0.57	1.96	0.091918	0.21123	-5.61
247041_at	floral homeotic protein apetala2-like ;s	TOE3	AT5G67180	-1.19	-0.25	-1.96	0.091933	0.211242	-5.61
251918_at	photoassimilate-responsive protein PA	---	AT3G54040	-1.16	-0.21	-1.96	0.091943	0.211244	-5.61
245723_at	hypothetical protein predicted by gene	---	AT1G73400	1.22	0.29	1.96	0.09197	0.211284	-5.61
260375_at	unknown protein	---	AT1G73950	1.18	0.23	1.96	0.091979	0.211284	-5.61
252393_at	putative protein predicted proteins, Ar	---	AT3G47910	1.19	0.25	1.96	0.092033	0.211386	-5.61
256901_at	hypothetical protein contains similarity	---	---	1.12	0.17	1.96	0.092045	0.211393	-5.61
248675_at	putative protein similar to unknown pro	ICK6	AT5G48820	1.30	0.37	1.96	0.092065	0.211417	-5.61
249966_at	putative protein COLD-INDUCIBLE R	---	AT5G19030	-1.35	-0.43	-1.96	0.092114	0.211508	-5.61
260916_at	predicted protein ; supported by cDNA	---	AT1G02475	1.18	0.24	1.96	0.092157	0.211574	-5.61
263612_at	putative CDC21 protein	MCM4	AT2G16440	-1.68	-0.75	-1.96	0.092161	0.211574	-5.61
246264_at	hypothetical protein	FRL2	AT1G31814	1.17	0.23	1.96	0.092181	0.211598	-5.61
252003_at	hypothetical protein emm32, Streptoc	ZPR3	AT3G52770	1.16	0.22	1.96	0.092204	0.21163	-5.61

251274_at	putative protein hypothetical protein A	---	AT3G61700	-1.31	-0.39	-1.96	0.09222	0.211644	-5.62
253701_at	choline monooxygenase - like protein	---	AT4G29890	-1.23	-0.29	-1.96	0.092252	0.211676	-5.62
252896_at	cytochrome P450 - like protein cytoch	CYP96A9	AT4G39480	1.15	0.20	1.96	0.092252	0.211676	-5.62
261075_at	unknown protein	---	AT1G07280	-1.19	-0.25	-1.96	0.092277	0.211713	-5.62
249531_at	putative protein predicted protein, Ara	AtGDU7	AT5G38770	-1.16	-0.21	-1.96	0.09229	0.211719	-5.62
265362_at	putative retroelement pol polyprotein	---	---	-1.15	-0.21	-1.96	0.092304	0.21173	-5.62
258854_at	putative UDP-glucosyl transferase sim	---	AT3G02100	-1.18	-0.24	-1.96	0.092327	0.211741	-5.62
257097_at	hypothetical protein predicted by gene	---	---	1.15	0.20	1.96	0.092318	0.211741	-5.62
249896_at	unknown protein ; supported by cDNA	---	AT5G22530	1.21	0.28	1.96	0.092367	0.211811	-5.62
262351_at	beta-galactosidase (BGAL), putative s	BGAL17	AT1G72990	1.14	0.19	1.96	0.092394	0.211853	-5.62
257905_at	unknown protein	---	---	-1.19	-0.25	-1.96	0.092419	0.211888	-5.62
256996_at	unknown protein similar to unknown pr	---	AT3G25850	1.14	0.18	1.96	0.092435	0.211905	-5.62
258698_at	unknown protein	---	AT3G09690	-1.19	-0.25	-1.96	0.092491	0.212012	-5.62
266007_at	unknown protein	---	AT2G37380	-1.21	-0.27	-1.96	0.09257	0.212171	-5.62
253125_at	DnaJ-like protein DnaJ-like protein, Pl	---	AT4G36040	1.22	0.29	1.96	0.092584	0.212182	-5.62
254191_at	hypothetical protein ;supported by full	---	AT4G23900	-1.21	-0.28	-1.96	0.092658	0.212329	-5.62
257474_at	DNA-3-methyladenine glycosidase, pu	---	AT1G80850	-1.19	-0.25	-1.96	0.092709	0.212425	-5.62
245196_at	F12A21.12 similar to pectate lyase lik	---	AT1G67750	-1.44	-0.53	-1.96	0.092766	0.212535	-5.62
247874_at	101 kDa heat shock protein; HSP101-l	---	AT5G57710	-1.27	-0.35	-1.96	0.092794	0.212576	-5.62
252805_at	putative protein	---	AT3G42380	-1.14	-0.19	-1.96	0.092803	0.212576	-5.62
260281_at	unknown protein	---	AT1G80500	-1.19	-0.25	-1.96	0.092814	0.21258	-5.62
246128_at	putative protein predicted proteins, Ar	---	---	-1.18	-0.24	-1.96	0.09283	0.212596	-5.62
250282_at	putative protein predicted protein, Ara	---	AT5G13260	-1.24	-0.32	-1.96	0.092905	0.212747	-5.62
251186_at	putative protein unknown protein At2g	---	AT3G62790	-1.13	-0.18	-1.96	0.09293	0.212782	-5.62
245565_at	hypothetical protein	---	AT4G14605	-1.18	-0.24	-1.96	0.092949	0.212803	-5.62
248424_at	unknown protein	---	AT5G51680	1.64	0.71	1.96	0.093073	0.213066	-5.62
247556_at	putative protein predicted protein, Ara	---	AT5G61040	1.22	0.28	1.95	0.093159	0.213228	-5.63
251629_at	villin 3 fragment ; supported by cDNA:	VLN3	AT3G57410	1.22	0.29	1.95	0.093162	0.213228	-5.63
254353_s_	putative protein probable membrane p	---	AT4G22285 /	1.24	0.32	1.95	0.093206	0.213285	-5.63
249982_at	putative protein predicted proteins, Ar	---	AT5G18520	-1.17	-0.22	-1.95	0.093197	0.213285	-5.63
262668_at	flavin-containing amine oxidase contai	LDL1	AT1G62830	-1.17	-0.23	-1.95	0.09323	0.21331	-5.63
250496_at	inorganic pyrophosphatase - like prote	AtPPa6	AT5G09650	-1.52	-0.60	-1.95	0.093235	0.21331	-5.63
264764_at	receptor kinase, putative similar to rec	---	AT1G61440	1.14	0.19	1.95	0.093249	0.21332	-5.63
257570_at	dirigent protein, putative similar to diri	---	AT3G13662	-1.16	-0.21	-1.95	0.093259	0.213322	-5.63
252985_at	putative protein Niemann-Pick C disea	---	AT4G38350	-1.16	-0.22	-1.95	0.093314	0.213426	-5.63

245454_at	disease resistance RPP5 like protein	---	AT4G16920	1.14	0.19	1.95	0.093388	0.213574	-5.63
248746_at	NADH dehydrogenase 10.5K chain-lik	---	AT5G47890	1.29	0.37	1.95	0.093437	0.213635	-5.63
257761_at	unknown protein	---	AT3G23090	-1.34	-0.43	-1.95	0.093438	0.213635	-5.63
261732_at	hypothetical protein predicted by gene	---	AT1G47770	1.17	0.22	1.95	0.093453	0.213635	-5.63
264477_at	amp-binding protein, putative similar t	---	AT1G77240	1.24	0.32	1.95	0.09345	0.213635	-5.63
252617_at	n-acetylglucosaminyl-phosphatidylinos	SETH2	AT3G45100	-1.15	-0.20	-1.95	0.093489	0.213698	-5.63
262344_at	cytochrome b245 beta chain homolog	ATRBOH F	AT1G64060	1.55	0.64	1.95	0.093606	0.213943	-5.63
258122_at	hypothetical protein contains similarity	ATGSL04	AT3G14570	-1.31	-0.39	-1.95	0.093652	0.214027	-5.63
258011_at	putative homeobox protein, HAT3.1 si	HAT3.1	AT3G19510	1.23	0.29	1.95	0.093668	0.214043	-5.63
249360_at	putative protein KIAA0409 protein, Ho	---	AT5G40530	1.16	0.22	1.95	0.0937	0.214071	-5.63
253262_at	putative serine threonine protein kinas	---	AT4G34440	-1.16	-0.21	-1.95	0.093692	0.214071	-5.63
249238_at	GAMM1 protein-like ; supported by cD	---	AT5G41970	1.17	0.22	1.95	0.093737	0.214135	-5.63
248469_at	putative protein similar to unknown pro	anac097	AT5G50820	-1.22	-0.29	-1.95	0.093876	0.214418	-5.63
251436_at	putative protein hypothetical protein A	ARGOS	AT3G59900	-2.11	-1.07	-1.95	0.093879	0.214418	-5.63
257370_at	hypothetical protein predicted by gens	---	AT2G35080	1.17	0.23	1.95	0.093894	0.21443	-5.63
245798_at	hypothetical protein predicted by gene	---	AT1G45545	-1.13	-0.18	-1.95	0.093913	0.214452	-5.63
258429_at	putative GTP-binding protein similar to	TOC120	AT3G16620	1.17	0.23	1.95	0.093927	0.214461	-5.63
247273_at	unknown protein	CPuORF40	AT5G64340 /	-1.29	-0.36	-1.95	0.093964	0.214524	-5.63
267618_at	putative cyclin ; supported by cDNA: g	CYCB1;4	AT2G26760	-1.19	-0.26	-1.95	0.09401	0.214608	-5.63
262160_at	hypothetical protein predicted by gene	---	AT1G52590	-1.34	-0.42	-1.95	0.094024	0.214619	-5.63
255292_s_	putative calcium dependent protein kin	CPK22	AT4G04710 /	1.22	0.29	1.95	0.094051	0.214641	-5.63
249074_at	putative protein contains similarity to G	---	AT5G44080	-1.17	-0.22	-1.95	0.094053	0.214641	-5.63
255569_at	putative CAAX prenyl protease ; supp	ATSTE24	AT4G01320	-1.15	-0.20	-1.95	0.094119	0.214771	-5.64
261387_at	hypothetical protein predicted by gene	---	AT1G05410	-1.31	-0.39	-1.95	0.09426	0.215072	-5.64
260714_at	chaperonin CPN10 identical to SP:P34	CPN10	AT1G14980	1.34	0.43	1.95	0.094314	0.215151	-5.64
261276_at	v-SNARE protein AtVTI1b, putative si	VTI1B	AT1G26670	1.25	0.32	1.95	0.094323	0.215151	-5.64
257467_at	hypothetical protein similar to hypothet	LBD4	AT1G31320	-1.31	-0.39	-1.95	0.094312	0.215151	-5.64
246608_at	putative protein various predicted prot	---	AT5G35380	-1.20	-0.26	-1.95	0.094341	0.215169	-5.64
252656_at	hypothetical protein	---	AT3G44770	1.23	0.30	1.95	0.09435	0.215169	-5.64
257212_at	zinc-binding dehydrogenase, putative	---	AT3G15090	1.23	0.30	1.95	0.094379	0.215214	-5.64
263549_at	unknown protein	MEE3	AT2G21650	-1.93	-0.95	-1.95	0.094389	0.215215	-5.64
255795_at	putative calcium-binding EF-hand prot	RD20	AT2G33380	-1.47	-0.55	-1.95	0.094405	0.215229	-5.64
265717_at	unknown protein ;supported by full-ler	---	AT2G03510	1.22	0.29	1.94	0.094523	0.215446	-5.64
251022_at	putative protein Hsp70 binding protein	---	AT5G02150	-1.19	-0.25	-1.94	0.094518	0.215446	-5.64
247217_s_	MADS box transcription factors-like pr	MAF3	AT5G65050 /	1.13	0.18	1.94	0.094528	0.215446	-5.64

256900_at	pectate lyase, putative similar to pecta	---	AT3G24670	-1.20	-0.26	-1.94	0.094573	0.215491	-5.64
263080_at	hypothetical protein predicted by gens	---	---	-1.19	-0.25	-1.94	0.094588	0.215491	-5.64
256349_at	late embryogenesis protein, putative s	---	AT1G54890	3.88	1.96	1.94	0.09458	0.215491	-5.64
256381_at	lipid transfer protein, putative contains	---	AT1G66850	-1.19	-0.25	-1.94	0.094582	0.215491	-5.64
257862_s_	unknown protein similar to N-terminal p	---	AT3G17720 /	1.14	0.18	1.94	0.094595	0.215491	-5.64
254012_at	putative ribosomal protein ribosomal p	---	AT4G26230	-1.36	-0.44	-1.94	0.094622	0.215532	-5.64
250634_at	putative protein 2-oxoglutarate-depen	---	AT5G07480	1.15	0.20	1.94	0.094679	0.215596	-5.64
260506_at	Cyclin, putative similar to GB:CAB772	CYCA3;2	AT1G47210	-1.36	-0.45	-1.94	0.094672	0.215596	-5.64
262374_s_	flax rust resistance protein, putative si	TIR	AT1G72910 /	1.75	0.81	1.94	0.094661	0.215596	-5.64
249054_at	unknown protein	---	AT5G02870 /	1.20	0.26	1.94	0.094729	0.215689	-5.64
250206_at	mitochondrial phosphate translocator	---	AT5G14040	1.33	0.42	1.94	0.094893	0.216041	-5.64
256644_at	unknown protein similar to hypothetica	---	---	1.16	0.21	1.94	0.094928	0.216095	-5.64
254626_at	hypothetical protein ; supported by ful	---	AT4G18400	-1.19	-0.25	-1.94	0.094936	0.216095	-5.64
255467_at	putative leucine-rich repeat protein sir	---	AT4G03010	-1.17	-0.22	-1.94	0.094946	0.216097	-5.64
261673_at	lipid transfer protein, putative similar t	---	AT1G18280	1.86	0.89	1.94	0.095009	0.216217	-5.64
265161_at	putative vacuolar sorting receptor simil	---	AT1G30900	1.86	0.90	1.94	0.095042	0.216272	-5.64
255477_at	coded for by A. thaliana cDNA R64991	---	AT4G02370	1.22	0.29	1.94	0.095056	0.216281	-5.64
254773_at	putative protein Cyclic beta-1-3-glucar	ATCSLA15	AT4G13410	-1.50	-0.58	-1.94	0.095103	0.216334	-5.65
253010_at	ovule development protein aintegumer	ANT	AT4G37750	-1.18	-0.24	-1.94	0.095107	0.216334	-5.65
258056_at	hypothetical protein similar to GB:AAD	---	AT3G29010	-1.23	-0.30	-1.94	0.095095	0.216334	-5.65
245180_at	putative protein similarity to proteins of	---	AT5G12410	1.26	0.34	1.94	0.095201	0.216526	-5.65
259481_at	germin, putative similar to germin GI:1	GLP4	AT1G18970	1.39	0.47	1.94	0.095214	0.216534	-5.65
264019_at	cyclophilin (CYP2) Same as GB: AF02	---	AT2G21130	1.21	0.28	1.94	0.095239	0.216568	-5.65
253858_at	carbohydrate kinase - like protein pho	---	AT4G27600	-1.15	-0.20	-1.94	0.095256	0.216586	-5.65
251929_at	sigma factor SigC ; supported by cDN	SIGC	AT3G53920	-1.16	-0.22	-1.94	0.095284	0.216628	-5.65
249699_at	putative protein similar to unknown pro	---	AT5G35540	1.13	0.17	1.94	0.095302	0.216647	-5.65
254053_s_	SRG1-like protein strong homology to	---	AT4G25300 /	1.33	0.42	1.94	0.095322	0.216649	-5.65
253938_at	putative homeodomain protein homeo	---	AT4G26920	-1.18	-0.24	-1.94	0.095313	0.216649	-5.65
264432_at	hypothetical protein similar to hypothet	---	AT1G61710	-1.16	-0.21	-1.94	0.095333	0.216652	-5.65
258972_at	hypothetical protein predicted by gens	---	AT3G01920	-1.28	-0.36	-1.94	0.09535	0.21667	-5.65
265693_at	putative poly(A) binding protein	---	AT2G24350	-1.18	-0.24	-1.94	0.095445	0.216864	-5.65
259943_at	unknown protein	---	AT1G71480	-1.28	-0.36	-1.94	0.095476	0.216913	-5.65
258611_at	unknown protein ;supported by full-ler	---	AT3G02860	1.17	0.23	1.94	0.095512	0.216963	-5.65
261376_at	hypothetical protein contains similarity	---	AT1G18660	-1.18	-0.24	-1.94	0.095517	0.216963	-5.65
262495_at	unknown protein Contains similarity to	---	AT1G21780	1.25	0.32	1.94	0.095559	0.217015	-5.65

248622_at	xylosidase	---	AT5G01980 /	1.46	0.54	1.94	0.095559	0.217015	-5.65
248314_at	putative protein similar to unknown pro	---	AT5G52620	-1.14	-0.18	-1.94	0.095582	0.217046	-5.65
266955_at	mitochondrial ribosomal protein S14	RPS14	AT2G34520	-1.20	-0.26	-1.94	0.095611	0.21709	-5.65
262857_at	major latex homologue type2 identical	---	AT1G14930	-1.15	-0.20	-1.94	0.095648	0.217153	-5.65
252192_at	CASEIN KINASE II, ALPHA CHAIN 2	CKA2	AT3G50000	-1.14	-0.19	-1.94	0.095658	0.217154	-5.65
254178_at	hypothetical protein	---	AT4G23880	1.90	0.92	1.94	0.095745	0.217312	-5.65
251146_at	neoxanthin cleavage enzyme nc1	CCD1	AT3G63520	-1.24	-0.31	-1.94	0.095747	0.217312	-5.65
249096_at	putative protein similar to unknown pro	---	AT5G43910	1.34	0.42	1.94	0.095767	0.217335	-5.65
256133_at	hypothetical protein predicted by gene	---	AT1G13570	-1.31	-0.39	-1.94	0.095801	0.217391	-5.65
248372_at	putative protein similar to unknown pro	---	AT5G51850	-1.14	-0.19	-1.94	0.095851	0.217483	-5.65
254493_at	DAG-like protein DAG precursor, Anti	---	AT4G20020	1.32	0.40	1.94	0.095867	0.217494	-5.65
262124_at	nucleoporin 98-like protein similar to n	---	AT1G59660	1.14	0.19	1.94	0.095874	0.217494	-5.65
251463_at	hypothetical protein	---	AT3G59800	-1.18	-0.23	-1.93	0.095906	0.217542	-5.65
258417_at	Expressed protein ; supported by cDN	---	AT3G17365	1.22	0.29	1.93	0.095928	0.217571	-5.65
255055_at	hypothetical protein	---	AT4G09810	-1.22	-0.29	-1.93	0.09594	0.217572	-5.65
257698_at	regulatory protein of P-starvation accli	---	AT3G12730	-1.17	-0.23	-1.93	0.095947	0.217572	-5.65
266977_at	putative phospholipase	---	AT2G39420	-1.47	-0.56	-1.93	0.09599	0.217624	-5.65
245989_s_	polyubiquitin (UBQ4) identical to GI:17	UBQ4	AT5G20620	1.18	0.24	1.93	0.095999	0.217624	-5.65
255942_at	UDP-glucose glucosyltransferase iden	AtUGT85A2	AT1G22360	1.69	0.76	1.93	0.095998	0.217624	-5.65
255226_at	UV-damaged DNA binding factor - like	DDB1A	AT4G05420	1.15	0.20	1.93	0.096103	0.217838	-5.66
259220_at	expressed protein predicted by genefi	---	AT3G03550	-1.20	-0.27	-1.93	0.096176	0.21796	-5.66
256200_at	hypothetical protein predicted by gene	EMB1674	AT1G58210	-1.17	-0.23	-1.93	0.096171	0.21796	-5.66
262618_at	unknown protein	---	AT1G06560	1.14	0.18	1.93	0.096187	0.217964	-5.66
258207_at	putative GTP pyrophosphokinase simi	RSH2	AT3G14050	1.38	0.47	1.93	0.096284	0.218161	-5.66
257988_at	unknown protein ; supported by cDNA	---	AT3G20870	1.17	0.22	1.93	0.096347	0.218283	-5.66
249538_at	kanadaptin - like protein unnamed OR	---	AT5G38840	1.16	0.21	1.93	0.096474	0.218549	-5.66
267118_at	hypothetical protein	---	AT2G32590	-1.19	-0.25	-1.93	0.096488	0.218559	-5.66
253392_at	potassium channel protein AtKC potas	ATKC1	AT4G32650	1.64	0.72	1.93	0.09653	0.218633	-5.66
255574_at	putative calcium-regulated protein pho	CBL5	AT4G01420	1.17	0.23	1.93	0.096554	0.218665	-5.66
250237_at	putative protein strong similarity to unk	---	AT5G13560	-1.21	-0.27	-1.93	0.096575	0.218691	-5.66
251776_at	eukaryotic translation initiation factor 6	emb1624	AT3G55620	1.23	0.30	1.93	0.096585	0.218693	-5.66
263661_at	unknown protein EST gb|T45093 come	---	AT1G04290	-1.30	-0.38	-1.93	0.096603	0.21871	-5.66
253720_at	acid phosphatase-like protein acid ph	---	AT4G29270	-1.15	-0.20	-1.93	0.096612	0.21871	-5.66
255498_at	putative vacuolar ATPase similar to va	---	AT4G02620	-1.12	-0.16	-1.93	0.096726	0.218941	-5.66
254272_at	predicted protein hypothetical protein,	---	AT4G22850	1.13	0.18	1.93	0.096733	0.218941	-5.66

248237_at	receptor protein kinase-like protein	---	AT5G53890	1.21	0.28	1.93	0.096805	0.219083	-5.66
259872_at	putative translation initiation factor IF-2	---	AT1G76810	1.15	0.20	1.93	0.096817	0.219088	-5.66
255003_at	AIG1-like protein AIG1 - Arabidopsis t	---	AT4G09950	-1.15	-0.20	-1.93	0.096852	0.219144	-5.66
265974_at	unknown protein	---	---	-1.30	-0.38	-1.93	0.09691	0.219253	-5.66
255371_at	putative RPP1-like disease resistance	---	AT4G04110	1.15	0.20	1.93	0.096934	0.219287	-5.66
259107_at	hypothetical protein predicted by gene	---	AT3G05460	1.14	0.18	1.93	0.096955	0.219313	-5.66
256210_at	hypothetical protein	---	AT1G50950	1.57	0.65	1.93	0.096969	0.219323	-5.66
258431_at	hypothetical protein predicted by gene	---	AT3G16580	-1.15	-0.20	-1.93	0.096997	0.219364	-5.66
245057_at	En/Spm-like transposon protein relate	---	AT2G26490	1.12	0.17	1.93	0.097029	0.219414	-5.66
256046_at	unknown protein	---	AT1G07135	1.85	0.88	1.93	0.097063	0.21947	-5.67
266166_at	putative glucosyltransferase ; support	---	AT2G28080	-1.26	-0.33	-1.93	0.097132	0.219604	-5.67
248324_at	putative protein similar to unknown pro	---	AT5G52790	-1.19	-0.25	-1.93	0.097145	0.219612	-5.67
264355_at	unknown protein similar to PHZF, cata	---	AT1G03210	-1.27	-0.34	-1.93	0.097216	0.219727	-5.67
263099_at	putative non-LTR retroelement reverse	---	---	1.22	0.29	1.93	0.097211	0.219727	-5.67
262370_at	hypothetical protein predicted by gene	---	AT1G73090	-1.23	-0.30	-1.93	0.097253	0.21979	-5.67
245244_at	IAA-amino acid hydrolase, putative sir	ILL6	AT1G44350	-1.27	-0.35	-1.93	0.097271	0.219808	-5.67
254145_at	hypothetical protein	---	AT4G24700	1.39	0.48	1.93	0.097286	0.219821	-5.67
248866_s_	putative protein contains similarity to c	---	AT5G46810 /	-1.14	-0.19	-1.92	0.097308	0.219849	-5.67
264395_at	putative GDP-dissociation inhibitor Co	---	AT1G12070	-1.22	-0.29	-1.92	0.097324	0.219864	-5.67
247984_s_	IAA-amino acid hydrolase homolog 1 p	ILL1	AT5G56650 /	-1.25	-0.32	-1.92	0.097371	0.219948	-5.67
266837_x_	unknown protein	---	AT2G25990	-1.14	-0.20	-1.92	0.097454	0.220113	-5.67
247053_at	protein kinase ATN1-like protein	---	AT5G66710	-1.13	-0.18	-1.92	0.097496	0.220187	-5.67
255317_at	putative vesicle transfer ATPase	---	AT4G04180	1.32	0.40	1.92	0.097531	0.220231	-5.67
266593_at	hypothetical protein predicted by gens	---	AT2G46200	-1.17	-0.23	-1.92	0.097535	0.220231	-5.67
254427_at	putative protein predicted protein, Ara	emb1417	AT4G21190	1.31	0.38	1.92	0.097592	0.22028	-5.67
264895_at	putative 10kd chaperonin strongly simi	---	AT1G23100	1.46	0.54	1.92	0.097605	0.22028	-5.67
257039_at	tRNA isopentenyl transferase, putative	ATIPT8	AT3G19160	-1.18	-0.24	-1.92	0.097602	0.22028	-5.67
252850_at	putative protein ;supported by full-leng	---	AT4G39880	-1.22	-0.29	-1.92	0.097604	0.22028	-5.67
245872_at	hypothetical protein contains similarity	---	AT1G26300	-1.17	-0.23	-1.92	0.097596	0.22028	-5.67
251253_at	putative zinc-finger protein zinc-finger	---	AT3G62240	1.28	0.36	1.92	0.097648	0.220355	-5.67
244929_at	NADH dehydrogenase subunit 4	---	---	1.27	0.35	1.92	0.097681	0.220387	-5.67
249437_at	putative protein predicted proteins - Ar	---	AT5G39990	1.20	0.27	1.92	0.097675	0.220387	-5.67
262446_at	hypothetical protein predicted by gens	---	AT1G49310	-1.48	-0.57	-1.92	0.0977	0.220407	-5.67
247688_at	putative protein predicted proteins, Ar	---	AT5G59760	1.15	0.20	1.92	0.097726	0.220445	-5.67
260507_at	unknown protein contains similarity to	WPP2	AT1G47200	-1.23	-0.30	-1.92	0.097747	0.220469	-5.67

254743_at	potassium transporter - like protein po	HAK5	AT4G13420	2.93	1.55	1.92	0.097759	0.220474	-5.67
260755_at	hypothetical protein predicted by gene	---	AT1G48980	-1.16	-0.21	-1.92	0.097777	0.220494	-5.67
265818_at	putative peptidyl-prolyl cis-trans isome	PIN1AT	AT2G18040	1.15	0.21	1.92	0.097842	0.220574	-5.67
255473_at	putative protein similar to several prote	---	AT4G02450	1.14	0.19	1.92	0.097834	0.220574	-5.67
259630_at	peptide chain release factor 2, putativ	---	AT1G56350	-1.27	-0.34	-1.92	0.097826	0.220574	-5.67
248771_at	unknown protein	---	AT5G47790	-1.20	-0.26	-1.92	0.097878	0.220633	-5.67
265922_at	putative sugar transporter	---	AT2G18480	-1.15	-0.21	-1.92	0.097912	0.220672	-5.67
258613_at	putative myo-inositol monophosphatas	VTC4	AT3G02870	-1.33	-0.41	-1.92	0.097914	0.220672	-5.67
246675_at	putative protein	---	AT5G30420	-1.18	-0.23	-1.92	0.097998	0.220793	-5.67
262212_at	response regulator 7, putative similar	ARR15	AT1G74890	-1.23	-0.30	-1.92	0.098006	0.220793	-5.67
250890_at	3-oxoacyl-[acyl-carrier-protein] syntha	---	AT5G04520	1.15	0.20	1.92	0.097995	0.220793	-5.67
262896_at	chromaffin granule ATPase II homolog	ALA3	AT1G59820	1.19	0.26	1.92	0.097993	0.220793	-5.67
258382_at	hypothetical protein	UBC25	AT3G15355	1.22	0.29	1.92	0.098026	0.220815	-5.67
250495_at	ribsomal protein - like chloroplast ribos	---	AT5G09770	1.21	0.28	1.92	0.098049	0.220845	-5.68
245022_at	PSII L protein	---	---	-1.25	-0.32	-1.92	0.098154	0.221059	-5.68
266878_at	putative RING zinc finger protein	---	AT2G44580	1.17	0.22	1.92	0.098172	0.221079	-5.68
257073_at	hypothetical protein predicted by gens	---	AT3G19650	1.21	0.28	1.92	0.098249	0.221231	-5.68
261210_at	vacuolar ATP synthase subunit C, put	DET3	AT1G12840	-1.13	-0.18	-1.92	0.098322	0.221373	-5.68
257927_at	ethylene response factor 1 (ERF1) ide	ERF1	AT3G23240	3.24	1.70	1.92	0.098333	0.221376	-5.68
250325_s_	putative protein contains similarity to S	---	AT5G12060 /	-1.14	-0.18	-1.92	0.098352	0.221396	-5.68
249948_at	eIF-4AII - like protein EUKARYOTIC I	---	AT5G19210	-1.22	-0.29	-1.92	0.09842	0.221505	-5.68
249757_at	Expressed protein ; supported by full-l	---	AT5G24316	1.19	0.25	1.92	0.09841	0.221505	-5.68
253320_at	putative protein ThiJ protein, Escheric	---	AT4G34020	1.16	0.22	1.92	0.098453	0.221558	-5.68
245621_at	AMP-binding protein	AAE15	AT4G14070	-1.25	-0.32	-1.92	0.09847	0.221574	-5.68
256404_at	unknown protein similar to far-red impa	FRS7	AT3G06250	1.23	0.30	1.92	0.09853	0.221688	-5.68
252891_at	putative WRKY DNA-binding protein D	WRKY13	AT4G39410	-1.24	-0.31	-1.92	0.09855	0.221711	-5.68
267299_at	putative glucosyltransferase	---	AT2G30150	1.22	0.28	1.92	0.09864	0.221861	-5.68
267160_at	putative WD-40 repeat protein	---	AT2G37670	-1.14	-0.19	-1.92	0.098646	0.221861	-5.68
251529_at	ATP-dependent RNA helicase-like pro	---	AT3G58570	1.15	0.21	1.92	0.098635	0.221861	-5.68
254333_at	predicted protein predicted protein ER	SMO1-3	AT4G22753	-1.59	-0.67	-1.92	0.098711	0.221964	-5.68
262587_at	unknown protein Contains PF|00561 a	---	AT1G15490	-1.31	-0.39	-1.92	0.098707	0.221964	-5.68
255951_at	unknown protein contains similarity to	MUB6	AT1G22050	-1.20	-0.27	-1.91	0.098724	0.221971	-5.68
257959_at	somatic embryogenesis receptor-like	NIK2	AT3G25560	-1.36	-0.45	-1.91	0.098765	0.222042	-5.68
247234_at	putative protein similar to unknown pro	---	AT5G64980	-1.15	-0.20	-1.91	0.098797	0.222091	-5.68
257006_at	hypothetical protein predicted by gene	---	AT3G14075	1.15	0.21	1.91	0.098839	0.222163	-5.68

250089_at	homeobox protein	HDG9	AT5G17320	1.20	0.26	1.91	0.098862	0.222193	-5.68
262697_at	beta-glucosidase, putative similar to b	ATA27	AT1G75940	-1.15	-0.20	-1.91	0.09888	0.222212	-5.68
261489_at	hypothetical protein contains similarity	---	AT1G14450	-1.12	-0.17	-1.91	0.098935	0.222313	-5.68
250122_at	unknown protein	---	AT5G16520	-1.18	-0.23	-1.91	0.098996	0.222429	-5.68
251204_at	putative protein HMW prekininogen, M	AT3G63095	---	1.18	0.23	1.91	0.099039	0.222503	-5.68
249903_at	disease resistance protein-like	---	AT5G22690	1.62	0.69	1.91	0.099137	0.222702	-5.69
249204_at	unknown protein ;supported by full-ler	---	AT5G42570	-1.16	-0.21	-1.91	0.099207	0.222837	-5.69
251210_at	hypothetical protein ;supported by full-	---	AT3G62810	1.20	0.26	1.91	0.09922	0.222844	-5.69
259809_at	hypothetical protein predicted by gene	---	AT1G49800	1.25	0.32	1.91	0.099252	0.222895	-5.69
265430_at	hypothetical protein predicted by gene	---	AT2G20700	-1.30	-0.38	-1.91	0.099291	0.222961	-5.69
248320_at	putative protein similar to unknown pro	---	AT5G52720	1.18	0.24	1.91	0.099333	0.223013	-5.69
256582_at	unknown protein	---	AT3G28840	1.16	0.21	1.91	0.099334	0.223013	-5.69
251153_at	putative protein predicted protein, Ara	NPL41	AT3G63000	1.19	0.26	1.91	0.099367	0.223055	-5.69
AFFX-r2-Bs	B. subtilis /GEN=dapB, jojF /DB_XREF	---	---	-1.32	-0.40	-1.91	0.099373	0.223055	-5.69
267277_at	putative protein transport protein SEC1	---	AT2G30050	-1.16	-0.22	-1.91	0.099405	0.223106	-5.69
247789_at	putative protein various predicted prot	---	AT5G58680	1.19	0.25	1.91	0.099441	0.223166	-5.69
262906_at	unknown protein contains similarity to	---	AT1G59760	-1.22	-0.28	-1.91	0.099469	0.223206	-5.69
260934_at	hypothetical protein predicted by gene	---	AT1G45100	-1.13	-0.18	-1.91	0.099495	0.223243	-5.69
245996_at	putative protein predicted non-LTR rev	---	---	-1.15	-0.20	-1.91	0.09951	0.223254	-5.69
255138_at	extensin-like protein extensin class 1	---	AT4G08380	1.14	0.19	1.91	0.099544	0.223308	-5.69
255952_at	MADS-box protein (ZAP1), putative si	AGL104	AT1G22130	1.13	0.18	1.91	0.099666	0.223537	-5.69
258459_at	hypothetical protein predicted by genr	---	---	1.17	0.23	1.91	0.099661	0.223537	-5.69
249160_at	putative protein similar to unknown pro	---	AT5G42660	-1.15	-0.20	-1.91	0.09969	0.223571	-5.69
266264_at	Expressed protein ; supported by full-le	---	AT2G27775	1.15	0.20	1.91	0.099719	0.223591	-5.69
249638_at	acetyl-CoA synthetase ; supported by	---	AT5G36880	1.47	0.56	1.91	0.099715	0.223591	-5.69
253073_at	cytochrome P450 monooxygenase - li	CYP81F4	AT4G37410	1.19	0.25	1.91	0.099858	0.223881	-5.69
259116_at	putative peptide transporter similar to p	---	AT3G01350	-1.31	-0.39	-1.91	0.099879	0.223906	-5.69
261741_at	transcription factor, putative similar to	ATE2F2	AT1G47870	1.17	0.22	1.91	0.099925	0.223986	-5.69
249721_at	Expressed protein ; supported by full-le	LSU4	AT5G24655	1.13	0.18	1.91	0.099968	0.22404	-5.69
259222_at	putative phosphoribosylanthranilate tr	---	AT3G03680	1.21	0.27	1.91	0.099968	0.22404	-5.69
265216_at	putative NPK1-related MAP kinase sim	MAPKKK18	AT1G05100	1.30	0.38	1.91	0.1	0.22409	-5.69
254185_at	cellulose synthase catalytic subunit - l	CSLG3	AT4G23990	1.28	0.35	1.91	0.100029	0.224109	-5.69
265171_at	hypothetical protein	---	AT1G23790	-1.12	-0.16	-1.91	0.100027	0.224109	-5.69
261694_at	60S ribosomal protein L10A, putative	---	AT1G08360	-1.24	-0.31	-1.91	0.100075	0.224191	-5.70
254142_at	putative protein other predicted or hyp	---	AT4G24630	-1.17	-0.23	-1.90	0.100205	0.22446	-5.70

251454_at	putative protein COP1-interacting prot	---	AT3G60080	1.22	0.28	1.90	0.100248	0.22452	-5.70
258342_at	hypothetical protein similar to extensin	---	AT3G22800	1.34	0.42	1.90	0.100251	0.22452	-5.70
250397_at	histon H3 protein HISTONE H3.2, MIN	---	AT5G10980	1.12	0.16	1.90	0.100276	0.224553	-5.70
250585_at	putative protein contains similarity to re	---	AT5G07620	-1.40	-0.48	-1.90	0.100307	0.224601	-5.70
252699_at	hypothetical protein predicted proteins	---	---	-1.30	-0.37	-1.90	0.100338	0.224647	-5.70
252286_at	putative protein	---	AT3G49070	-1.12	-0.16	-1.90	0.100349	0.224649	-5.70
252011_at	carbonic anhydrase (CAH1) ; supporte	ACA1	AT3G52720	-1.25	-0.32	-1.90	0.100387	0.224713	-5.70
262787_at	putative clathrin-coat assembly protein	---	AT1G10730	1.28	0.35	1.90	0.100412	0.224747	-5.70
261092_at	unknown protein	---	AT1G62870	-1.13	-0.17	-1.90	0.100444	0.224797	-5.70
260621_at	carbonic anhydrase, putative	ACA5	AT1G08065	-1.17	-0.23	-1.90	0.100525	0.224933	-5.70
255486_at	AtMlo-h1-like protein	MLO1	AT4G02600	-1.17	-0.23	-1.90	0.100518	0.224933	-5.70
262064_at	elongation factor, putative similar to E	LOS1	AT1G56070	1.19	0.25	1.90	0.100549	0.224944	-5.70
263743_at	coatomer alpha subunit	---	AT2G21390	-1.14	-0.19	-1.90	0.100541	0.224944	-5.70
245417_at	phosphoribosylglycinamide formyltrans	---	AT4G17360	-1.28	-0.35	-1.90	0.100581	0.224993	-5.70
266033_at	putative translation initiation factor eIF-	---	AT2G05830	-1.21	-0.28	-1.90	0.100707	0.225253	-5.70
251982_at	pectate lyase -like protein pectate lyas	---	AT3G53190	-1.25	-0.32	-1.90	0.100762	0.225354	-5.70
250174_at	agp6	AGP6	AT5G14380	1.14	0.19	1.90	0.100787	0.225386	-5.70
253764_s_	protein kinase - like protein ADK1 prot	ckl4	AT4G28860 /	-1.20	-0.26	-1.90	0.100806	0.225386	-5.70
262948_at	DNA-binding protein similar to cellular	---	AT1G75560	-1.17	-0.22	-1.90	0.100799	0.225386	-5.70
245896_at	putative transcriptional co-activator (KI	KIWI	AT5G09250	-1.21	-0.28	-1.90	0.100864	0.225493	-5.70
259904_at	hypothetical protein predicted by gene	---	AT1G74150	-1.19	-0.25	-1.90	0.100912	0.225578	-5.70
250568_at	putative protein several putative ATP-d	---	AT5G08110	1.17	0.22	1.90	0.100955	0.225654	-5.70
260171_at	hypothetical protein predicted by gens	---	AT1G71910	1.46	0.54	1.90	0.100984	0.225694	-5.70
253648_at	pathogenesis related homeodomain pr	PRHA	AT4G29940	1.14	0.18	1.90	0.101012	0.225736	-5.70
253869_at	hypothetical protein	---	AT4G27510	-1.21	-0.27	-1.90	0.101028	0.225749	-5.70
248783_at	putative protein contains similarity to s	---	AT5G47360	-1.29	-0.37	-1.90	0.101125	0.225945	-5.71
244942_at	hypothetical protein	---	---	-1.15	-0.20	-1.90	0.101154	0.225965	-5.71
257960_at	S-adenosylmethionine decarboxylase	---	AT3G25570 /	1.14	0.19	1.90	0.101152	0.225965	-5.71
247752_at	putative protein	---	AT5G59060	-1.13	-0.17	-1.90	0.101214	0.226076	-5.71
256543_at	unknown protein supported by full-leng	---	AT1G42480	1.19	0.25	1.90	0.101296	0.226238	-5.71
265041_at	unknown protein Contains similarity to	TOM22-I	AT1G04070	1.28	0.35	1.90	0.101327	0.226284	-5.71
253544_at	hypothetical protein	---	AT4G31280	1.14	0.19	1.90	0.101338	0.226286	-5.71
260817_at	unknown protein	---	AT1G06900	-1.17	-0.23	-1.90	0.101462	0.226541	-5.71
258166_at	WD-repeat protein, putative contains I	---	AT3G21540	1.36	0.44	1.90	0.101497	0.226597	-5.71
267274_at	putative mitochondrial carrier protein ;	---	AT2G30160	-1.24	-0.31	-1.90	0.101525	0.22662	-5.71

249042_at	ethylene-regulated nuclear protein ER	---	AT5G44350	1.40	0.49	1.90	0.101527	0.22662	-5.71
267158_at	putative expansin	EXP3	AT2G37640	-2.19	-1.13	-1.90	0.101559	0.22667	-5.71
260474_at	lysophospholipase isolog	---	AT1G11090	-1.19	-0.25	-1.90	0.10157	0.226673	-5.71
257002_at	oligouridylate binding protein, putative	---	AT3G14100	1.21	0.28	1.90	0.101584	0.226681	-5.71
251730_at	N2,N2-dimethylguanosine tRNA meth	---	AT3G56330	1.21	0.27	1.90	0.101618	0.226735	-5.71
263709_at	unknown protein ESTs gb|T20589, gb	---	AT1G09310	-2.24	-1.16	-1.89	0.101653	0.226754	-5.71
262320_at	hypothetical protein predicted by gens	---	AT1G27550	-1.16	-0.21	-1.89	0.101657	0.226754	-5.71
258774_at	putative alpha-L-arabinofuranosidase	ASD1	AT3G10740	1.57	0.65	1.89	0.101648	0.226754	-5.71
258339_at	putative dynein light chain protein simi	---	AT3G16120	-1.13	-0.18	-1.89	0.101743	0.226925	-5.71
266567_at	putative eukaryotic initiation factor 4, e	---	AT2G24050	-1.25	-0.32	-1.89	0.101753	0.226925	-5.71
265754_x_	En/Spm transposon protein (mosaic-lik	---	---	-1.14	-0.19	-1.89	0.101783	0.226968	-5.71
250273_at	pre-mRNA splicing factor ATP-depend	EMB3011	AT5G13010	1.14	0.19	1.89	0.101801	0.226987	-5.71
267051_at	hypothetical protein predicted by gene	---	AT2G38500	-1.24	-0.31	-1.89	0.101825	0.227018	-5.71
252230_at	putative protein various predicted prot	---	AT3G49810	1.65	0.72	1.89	0.101874	0.227107	-5.71
251771_at	putative protein cellulose synthase (ce	CSLA14	AT3G56000	-1.18	-0.24	-1.89	0.101922	0.227191	-5.71
262456_at	glucose transporter almost identical to	STP1	AT1G11260	-1.34	-0.42	-1.89	0.101962	0.227214	-5.71
254956_at	putative protein various predicted prot	---	AT4G10850	-1.14	-0.19	-1.89	0.101956	0.227214	-5.71
258498_at	unknown protein similar to pollen coat	---	AT3G02480	-1.41	-0.50	-1.89	0.101956	0.227214	-5.71
255672_at	hypothetical protein ; supported by cD	EDA8	AT4G00310	-1.18	-0.24	-1.89	0.102008	0.227292	-5.71
264571_at	hypothetical protein predicted by gene	---	AT1G05330	1.13	0.18	1.89	0.102042	0.227303	-5.71
254143_at	putative protein histidine-rich calcium-	---	AT4G24680	1.13	0.17	1.89	0.102042	0.227303	-5.71
253325_at	Expressed protein ; supported by full-l	---	AT4G33925	1.35	0.43	1.89	0.102024	0.227303	-5.71
253865_at	putative RING zinc finger protein Arab	---	AT4G27470	-1.26	-0.34	-1.89	0.102078	0.227346	-5.71
261347_at	unknown protein	ELF7	AT1G79730	1.18	0.24	1.89	0.102082	0.227346	-5.71
247208_at	nodulin-like ;supported by full-length c	---	AT5G64870	1.18	0.24	1.89	0.102094	0.227351	-5.71
259172_at	O-acetylserine (thiol) lyase identical to	CS26	AT3G03630	-1.35	-0.43	-1.89	0.102126	0.2274	-5.71
260702_at	calmodulin, putative similar to calmod	---	AT1G32250	-1.15	-0.21	-1.89	0.102209	0.227563	-5.72
264784_s_	unknown protein similar to Arabidopsi	---	AT2G17830 /	-1.17	-0.23	-1.89	0.102233	0.227594	-5.72
261207_at	peroxisomal targeting signal type 2 rec	---	AT1G12830	1.26	0.34	1.89	0.102317	0.22776	-5.72
248521_s_	nodulin-like protein ; supported by cDN	---	AT5G50520 /	1.16	0.22	1.89	0.102345	0.227786	-5.72
259275_at	unknown protin ;supported by full-leng	---	AT3G01060	-1.31	-0.39	-1.89	0.102349	0.227786	-5.72
252109_at	putative protein mucin 5AC, Homo sa	---	AT3G51540	1.40	0.49	1.89	0.102377	0.227826	-5.72
249273_at	unknown protein	---	AT5G41850	1.20	0.26	1.89	0.102413	0.227885	-5.72
259224_at	putative thymidine kinase similar to thy	---	AT3G07800	-1.23	-0.30	-1.89	0.102425	0.22789	-5.72
248994_at	disease resistance protein-like	RPS4	AT5G45250	1.21	0.28	1.89	0.10248	0.227988	-5.72

249532_at	AtPP - like protein AtPP protein, Brass	---	AT5G38780	1.41	0.50	1.89	0.102505	0.228023	-5.72
257128_at	cytochrome P450, putative contains P	CYP705A15	AT3G20080	1.21	0.28	1.89	0.10254	0.228072	-5.72
246464_at	quinone oxidoreductase -like protein p	---	AT5G16980	1.16	0.21	1.89	0.102548	0.228072	-5.72
247942_at	putative protein similar to unknown pro	---	AT5G57120	1.24	0.32	1.89	0.10263	0.228228	-5.72
264385_at	unknown protein	---	AT1G12020	-1.26	-0.34	-1.89	0.102637	0.228228	-5.72
246060_at	rev interacting protein mis3 - like rev i	---	AT5G08420	-1.13	-0.18	-1.89	0.102699	0.228341	-5.72
256431_s_	putative disease resistance protein sim	AtRLP34	AT3G11010 /	1.35	0.43	1.89	0.102746	0.228425	-5.72
249702_at	axi 1 (auxin-independent growth promo	---	AT5G35570	-1.46	-0.55	-1.89	0.102756	0.228425	-5.72
266649_at	putative aquaporin (tonoplast intrinsic	TIP4;1	AT2G25810	-1.14	-0.19	-1.89	0.102834	0.228576	-5.72
258051_at	hypothetical protein predicted by gene	TRZ4	AT3G16260	-1.22	-0.29	-1.89	0.10287	0.228634	-5.72
248871_at	putative protein strong similarity to unk	---	AT5G46680	1.18	0.24	1.89	0.102907	0.22869	-5.72
262628_at	glucan synthase, putative similar to gl	ATGSL07	AT1G06490	-1.21	-0.28	-1.89	0.102916	0.22869	-5.72
245431_at	hypothetical protein	---	AT4G17080	-1.16	-0.21	-1.89	0.102926	0.22869	-5.72
249938_at	Ruv DNA-helicase-like protein ;suppo	RIN1	AT5G22330	1.15	0.20	1.89	0.103025	0.228889	-5.72
262639_at	calmodulin, putative similar to calmod	---	AT1G62820	-1.26	-0.33	-1.89	0.103076	0.228969	-5.72
248001_at	calcineurin B-like protein 2 (gb|AAC26	CBL2	AT5G55990	-1.22	-0.28	-1.89	0.103081	0.228969	-5.72
245889_at	PEE-rich protein ;supported by full-len	---	AT5G09480	-1.37	-0.45	-1.89	0.103101	0.22899	-5.72
255261_s_	putative protein equilibrative nucleosic	FUR1	AT4G05110 /	-1.53	-0.61	-1.88	0.103197	0.229183	-5.72
250805_at	unknown protein	---	AT5G05050	-1.14	-0.19	-1.88	0.103349	0.229475	-5.73
248200_at	O-methyltransferase ;supported by ful	ATOMT1	AT5G54160	1.52	0.60	1.88	0.103347	0.229475	-5.73
249483_at	Expressed protein ; supported by cDN	---	AT5G38895	1.20	0.26	1.88	0.103361	0.229478	-5.73
260479_at	hypothetical protein predicted by gene	---	AT1G11020	1.14	0.18	1.88	0.103371	0.229479	-5.73
262739_at	lipase, putative contains Pfam profile:	---	AT1G28650	1.31	0.39	1.88	0.103411	0.229513	-5.73
252500_at	proteinase inhibitor-like protein endope	---	AT3G46860	1.14	0.19	1.88	0.103417	0.229513	-5.73
246983_at	receptor protein kinase-like protein ; s	---	AT5G67200	-1.24	-0.31	-1.88	0.103412	0.229513	-5.73
253703_at	putative protein origin recognition com	ORC5	AT4G29910	-1.18	-0.23	-1.88	0.103475	0.229619	-5.73
266737_at	putative alcohol dehydrogenase ; sup	---	AT2G47140	1.18	0.24	1.88	0.103655	0.229997	-5.73
254762_at	Expressed protein ; supported by full-l	---	AT4G13230	-1.17	-0.22	-1.88	0.103684	0.23004	-5.73
248452_at	putative protein contains similarity to tr	---	AT5G51300	-1.13	-0.17	-1.88	0.103761	0.230188	-5.73
254337_at	putative protein hypothetical protein d	---	AT4G22060	1.17	0.22	1.88	0.103777	0.230201	-5.73
256113_at	unknown protein ;supported by full-len	---	AT1G16810	1.18	0.24	1.88	0.103803	0.230237	-5.73
254162_at	transcription factor IIA small subunit ;s	---	AT4G24440	1.23	0.30	1.88	0.103871	0.230343	-5.73
259549_at	unknown protein ;supported by full-len	---	AT1G35290	-1.16	-0.21	-1.88	0.103872	0.230343	-5.73
260532_at	putative ATP-dependent RNA helicase	---	AT2G47330	-1.13	-0.18	-1.88	0.103909	0.230404	-5.73
251303_at	NAM-like protein no apical meristem (	ANAC066	AT3G61910	-1.14	-0.18	-1.88	0.103961	0.230451	-5.73

254065_at	gibberellin 20-oxidase - Arabidopsis th	GA20OX1	AT4G25420	-1.47	-0.55	-1.88	0.103953	0.230451	-5.73
258155_at	protein kinase C-receptor/G-protein, p	RACK1C_A	AT3G18130	-1.59	-0.67	-1.88	0.10396	0.230451	-5.73
248226_at	putative protein strong similarity to unk	---	AT5G53750	1.60	0.67	1.88	0.103977	0.230466	-5.73
267472_at	putative basic blue protein (plantacyan	ARPN	AT2G02850	-1.18	-0.23	-1.88	0.103995	0.230482	-5.73
256302_at	Expressed protein ; supported by full-l	---	AT1G69526	-1.20	-0.26	-1.88	0.10402	0.230505	-5.73
247998_at	unknown protein	---	AT5G56200	1.30	0.37	1.88	0.104025	0.230505	-5.73
245891_at	amino acid transport protein AAP2 ;su	AAP2	AT5G09220	-1.50	-0.58	-1.88	0.104062	0.230564	-5.73
246512_at	putative phytochelatin synthetase puta	IRX6	AT5G15630	-1.21	-0.27	-1.88	0.104096	0.230617	-5.73
257841_at	nitrate transporter, putative similar to	---	AT3G25260	-1.14	-0.19	-1.88	0.104108	0.23062	-5.73
262777_at	hypothetical protein predicted by gens	---	AT1G13030	1.27	0.34	1.88	0.104138	0.230666	-5.73
246908_at	dehydration-induced protein RD22 ; s	RD22	AT5G25610	-1.94	-0.96	-1.88	0.104258	0.230908	-5.73
251598_at	AP2 transcription factor - like protein	---	AT3G57600	-1.14	-0.19	-1.88	0.104311	0.230957	-5.74
247002_at	putative protein strong similarity to unk	HOS15	AT5G67320	1.19	0.25	1.88	0.104331	0.230957	-5.74
261983_at	protein kinase, putative similar to cdc2	---	AT1G33770	-1.28	-0.36	-1.88	0.104303	0.230957	-5.74
267280_at	diacylglycerol O-acyltransferase ; supp	TAG1	AT2G19450	-1.23	-0.30	-1.88	0.104296	0.230957	-5.74
255032_at	putative protein anthocyanin rhamnos	---	AT4G09500	1.22	0.29	1.88	0.104341	0.230957	-5.74
263460_at	putative acetolactate synthase	---	AT2G31810	-1.22	-0.29	-1.88	0.10433	0.230957	-5.74
260880_at	hypothetical protein similar to unknown	---	AT1G21380	-1.17	-0.22	-1.88	0.104408	0.231015	-5.74
249122_at	putative protein similar to unknown pro	ARD4	AT5G43850	-1.25	-0.32	-1.88	0.104402	0.231015	-5.74
260935_at	hypothetical protein predicted by gene	---	AT1G45110	-1.21	-0.27	-1.88	0.104391	0.231015	-5.74
266861_at	putative choline kinase ;supported by	emb1187	AT2G26830	-1.19	-0.25	-1.88	0.104391	0.231015	-5.74
250422_at	putative protein KIAA0255 gene, Hom	---	AT5G10840	-1.28	-0.35	-1.88	0.104457	0.231102	-5.74
246689_at	putative protein predicted proteins - Ar	---	---	-1.12	-0.17	-1.88	0.104518	0.231214	-5.74
246235_at	putative protein	---	AT4G36830	-1.20	-0.26	-1.88	0.104594	0.231358	-5.74
247397_at	Dof zinc finger protein - like Dof zinc f	---	AT5G62940	-1.29	-0.36	-1.88	0.104603	0.231358	-5.74
267115_s_	putative cellulose synthase	ATCSLB04	AT2G32530 /	1.42	0.50	1.87	0.104657	0.231456	-5.74
255636_at	homeodomain protein AHDP ; suppor	ANL2	AT4G00730	-1.19	-0.26	-1.87	0.104675	0.231473	-5.74
265326_at	unknown protein predicted by genscan	---	AT2G18220	1.23	0.30	1.87	0.104735	0.231566	-5.74
AFFX-DapX	B. subtilis /GEN=dapB, jojF /DB_XREF	---	---	-1.28	-0.36	-1.87	0.104738	0.231566	-5.74
248890_at	disease resistance protein-like	---	AT5G46270	1.15	0.20	1.87	0.10477	0.231615	-5.74
250087_at	putative protein contains similarity to u	---	AT5G17270	1.30	0.38	1.87	0.104791	0.23163	-5.74
257589_at	hypothetical protein predicted by gens	---	AT1G55050	-1.21	-0.28	-1.87	0.104797	0.23163	-5.74
255797_at	putative steroid dehydrogenase ; supp	---	AT2G33630	1.25	0.32	1.87	0.104907	0.231828	-5.74
264447_at	hypothetical protein predicted by gens	---	AT1G27300	1.38	0.46	1.87	0.104905	0.231828	-5.74
265426_at	hypothetical protein predicted by gene	---	AT2G20740	-1.18	-0.24	-1.87	0.10492	0.231835	-5.74

256021_at	unknown protein contains Pfam profile	ZW9	AT1G58270	-1.26	-0.33	-1.87	0.104936	0.231848	-5.74
250214_at	endoxyloglucan transferase (dbj|BAA8	EXGT-A4	AT5G13870	-1.19	-0.26	-1.87	0.104995	0.231937	-5.74
252791_at	transposase - like protein putative trar	---	---	1.14	0.19	1.87	0.104997	0.231937	-5.74
261173_at	hypothetical protein predicted by gene	---	AT1G04830	-1.16	-0.22	-1.87	0.105023	0.231973	-5.74
255765_at	protein kinase, putative contains Pfam	---	AT1G16760	-1.12	-0.16	-1.87	0.105052	0.232012	-5.74
254349_at	hypothetical protein	---	AT4G22250	1.18	0.24	1.87	0.105062	0.232014	-5.74
249311_at	disease resistance protein-like	---	AT5G41540	1.19	0.25	1.87	0.105116	0.232106	-5.74
249281_at	GTPase activator protein of Rab-like s	---	AT2G36460 /	1.17	0.22	1.87	0.105125	0.232106	-5.74
253756_at	Cdk-activating kinase CAK1At ; suppo	CAK1AT	AT4G28980	-1.13	-0.18	-1.87	0.105176	0.232198	-5.74
253545_at	AIG2-like protein AIG2 protein, Arabid	---	AT4G31310	-1.22	-0.29	-1.87	0.105233	0.2323	-5.74
256221_at	DnaJ protein, putative contains Pfam	---	AT1G56300	1.15	0.20	1.87	0.105309	0.232447	-5.74
262109_at	hypothetical protein similar to cellulose	ATCSLD5	AT1G02730	-1.33	-0.41	-1.87	0.105453	0.232737	-5.75
260698_at	unknown protein contains similarity to	---	AT1G32300	-1.13	-0.18	-1.87	0.105461	0.232737	-5.75
263650_at	hypothetical protein predicted by gens	---	AT1G04360	1.16	0.22	1.87	0.105494	0.232787	-5.75
265854_at	hypothetical protein predicted by gens	---	AT2G42370	-1.14	-0.19	-1.87	0.105509	0.232797	-5.75
257690_at	unknown protein contains similarity to	---	AT3G12830	1.49	0.57	1.87	0.105571	0.232911	-5.75
260318_at	hypothetical protein predicted by gene	---	AT1G63960	-1.20	-0.26	-1.87	0.1056	0.232954	-5.75
264043_at	putative cyclin D	CYCD2;1	AT2G22490	-1.14	-0.19	-1.87	0.105677	0.2331	-5.75
247589_at	REVOLUTA or interfascicular fiberless	REV	AT5G60690	-1.18	-0.24	-1.87	0.105694	0.233115	-5.75
264331_at	hypothetical protein contains non-cons	---	AT1G04130	-1.16	-0.22	-1.87	0.105737	0.233187	-5.75
254471_s_	putative protein parts of other proteins	---	---	1.14	0.20	1.87	0.105761	0.233196	-5.75
267257_at	putative casein kinase II catalytic (alph	---	AT2G23080	-1.12	-0.16	-1.87	0.105758	0.233196	-5.75
259274_at	putative homeobox-leucine zipper pro	ATHB20	AT3G01220	1.15	0.20	1.87	0.105801	0.233239	-5.75
246964_at	putative protein crp1 protein - Zea ma	---	AT5G24830	-1.19	-0.25	-1.87	0.105799	0.233239	-5.75
260217_at	hypothetical protein contains Pfam pro	---	AT1G74600	1.13	0.18	1.87	0.105891	0.233391	-5.75
263170_at	putative peroxisome assembly factor-2	PEX6	AT1G03000	-1.12	-0.17	-1.87	0.105885	0.233391	-5.75
254603_at	putative protein hypothetical protein Y	---	AT4G19045 /	-1.18	-0.24	-1.87	0.105955	0.233511	-5.75
251783_at	ribosomal L23a - like protein various ri	RPL23AB	AT3G55280	-1.38	-0.46	-1.87	0.106003	0.233548	-5.75
261004_at	hypothetical protein similar to putative	---	AT1G26450	-1.27	-0.34	-1.87	0.105999	0.233548	-5.75
262677_at	unknown protein	---	AT1G75860	-1.31	-0.39	-1.87	0.105998	0.233548	-5.75
245191_at	F12A21.10 similar to terminal ear1 gb|	TEL2	AT1G67770	-1.27	-0.34	-1.87	0.106018	0.23356	-5.75
262746_at	Expressed protein ; supported by full-l	ATNUDX15	AT1G28960	1.13	0.17	1.86	0.106185	0.233903	-5.75
263538_at	hypothetical protein predicted by gene	---	AT2G25010	1.23	0.30	1.86	0.106354	0.234209	-5.75
251328_at	putative protein putative protein At2g4	ATPOB1	AT3G61600	-1.14	-0.18	-1.86	0.106353	0.234209	-5.75
254156_at	Rab geranylgeranyl transferase like p	---	AT4G24490	-1.23	-0.30	-1.86	0.106342	0.234209	-5.75

248811_at	putative protein contains similarity to E	---	AT5G47310	-1.18	-0.23	-1.86	0.106453	0.234405	-5.76
254547_at	putative protein	---	AT4G19860	1.26	0.33	1.86	0.106513	0.234513	-5.76
260903_at	polygalacturonase PG1, putative simil	---	AT1G02460	1.88	0.91	1.86	0.10659	0.234661	-5.76
263510_s_	hypothetical protein	---	AT2G07681 /	1.13	0.18	1.86	0.106611	0.234685	-5.76
252278_at	NAC2-like protein NAC2 - Arabidopsis	anac062	AT3G49530	1.46	0.55	1.86	0.106686	0.234828	-5.76
254819_at	pEARLI 1-like protein Arabidopsis tha	---	AT4G12500	2.70	1.43	1.86	0.106711	0.234858	-5.76
255814_at	unknown protein	---	AT1G19900	-1.14	-0.19	-1.86	0.106735	0.234879	-5.76
260761_at	hypothetical protein predicted by gene	---	AT1G49150	1.27	0.35	1.86	0.106741	0.234879	-5.76
249316_s_	glutathione transferase-like ;supported	ATGSTT2	AT5G41220 /	-1.16	-0.22	-1.86	0.106881	0.235166	-5.76
253946_at	putative APG protein proline-rich prote	---	AT4G26790	-1.26	-0.34	-1.86	0.10691	0.235206	-5.76
261094_at	hypothetical protein predicted by gene	---	AT1G62920	-1.24	-0.32	-1.86	0.10693	0.235228	-5.76
245372_at	ribosomal protein ;supported by full-ler	---	AT4G15000	-1.34	-0.42	-1.86	0.106968	0.235289	-5.76
248062_at	unknown protein ;supported by full-ler	---	AT5G55450	-3.53	-1.82	-1.86	0.107047	0.235439	-5.76
261686_at	unknown protein ;supported by full-len	---	AT1G47310	-1.16	-0.21	-1.86	0.107071	0.235469	-5.76
266601_at	hypothetical protein predicted by gens	---	AT2G46060	1.29	0.37	1.86	0.107118	0.235483	-5.76
261212_at	hypothetical protein predicted by gene	atnudt12	AT1G12880	1.26	0.33	1.86	0.107092	0.235483	-5.76
248924_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G45960	-1.14	-0.19	-1.86	0.107115	0.235483	-5.76
252917_at	putative zinc finger protein zinc finger	---	AT4G38960	1.22	0.29	1.86	0.107114	0.235483	-5.76
255665_at	hypothetical protein	CRP	AT4G00450	1.14	0.19	1.86	0.107155	0.23554	-5.76
264337_at	hypothetical protein predicted by gens	---	AT1G70350	-1.16	-0.21	-1.86	0.107203	0.235624	-5.76
259973_at	hypothetical protein contains Pfam pro	---	AT1G76630	-1.28	-0.35	-1.86	0.107239	0.23568	-5.76
259055_at	unknown protein ;supported by full-ler	UNE6	AT3G03340	1.15	0.21	1.86	0.107381	0.235952	-5.76
267544_at	putative cytochrome b5	CB5-B	AT2G32720	1.46	0.55	1.86	0.107394	0.235952	-5.76
266162_at	putative bHLH transcription factor	FRU	AT2G28160	1.16	0.22	1.86	0.107386	0.235952	-5.76
255717_at	coded for by A. thaliana cDNA H76622	---	AT4G00350	-1.15	-0.20	-1.86	0.107434	0.236018	-5.76
261804_at	UDP glucose:flavonoid 3-o-glucosyltra	UGT78D1	AT1G30530	1.26	0.33	1.86	0.107468	0.23607	-5.76
267064_at	calmodulin (cam2)	CAM2	AT2G41110	-1.35	-0.43	-1.86	0.107504	0.236126	-5.76
248442_at	DEAD-box protein abstrakt	---	AT5G51280	1.19	0.26	1.86	0.10758	0.23627	-5.77
266335_at	putative cytochrome P450 ; supported	KAO2	AT2G32440	-1.29	-0.37	-1.86	0.107643	0.236386	-5.77
258067_at	putative mitotic checkpoint protein sim	---	AT3G25980	-1.15	-0.21	-1.85	0.107871	0.236796	-5.77
248461_s_	fumarate hydratase ; supported by cD	FUM1	AT2G47510 /	-1.19	-0.25	-1.85	0.107867	0.236796	-5.77
258154_at	unknown protein ; supported by cDNA	---	AT3G18210	-1.20	-0.26	-1.85	0.107854	0.236796	-5.77
250211_at	unknown protein ; supported by cDNA	---	AT5G13880	-1.16	-0.21	-1.85	0.107843	0.236796	-5.77
255379_at	putative M-type thioredoxin similar to A	ATHM2	AT4G03520	-1.13	-0.17	-1.85	0.107889	0.236813	-5.77
249010_at	unknown protein ; supported by cDNA	---	AT5G44580	1.29	0.37	1.85	0.107933	0.236863	-5.77

244956_s_	hypothetical protein	---	---	1.17	0.23	1.85	0.107932	0.236863	-5.77
258647_at	unknown protein ; supported by cDNA	---	AT3G07870	1.17	0.23	1.85	0.108007	0.237002	-5.77
250289_at	putative protein ;supported by full-leng	---	AT5G13190	1.42	0.51	1.85	0.108059	0.23707	-5.77
266784_at	putative receptor-like protein kinase	---	AT2G28960	1.12	0.17	1.85	0.108051	0.23707	-5.77
262154_at	unknown protein contains similarity to	---	AT1G52700	-1.26	-0.34	-1.85	0.108124	0.237191	-5.77
265474_at	Expressed protein ; supported by cDN	---	AT2G15690	1.29	0.36	1.85	0.108181	0.237205	-5.77
261110_at	E2, ubiquitin-conjugating enzyme 16 (	UBC16	AT1G75440	-1.23	-0.29	-1.85	0.108193	0.237205	-5.77
261841_at	BTG1 binding factor 1, putative simila	---	AT1G15920	-1.15	-0.21	-1.85	0.108192	0.237205	-5.77
249442_at	putative protein ; supported by cDNA:	---	AT5G39590	1.41	0.50	1.85	0.108177	0.237205	-5.77
247438_at	unknown protein ; supported by cDNA	---	AT5G62460	1.30	0.38	1.85	0.108172	0.237205	-5.77
264608_at	putative acetyl-CoA acyltransferase St	PKT4	AT1G04710	1.16	0.21	1.85	0.108169	0.237205	-5.77
255412_at	auxin-binding protein 1 precursor ;sup	ABP1	AT4G02980	1.16	0.21	1.85	0.108215	0.23723	-5.77
258885_at	putative uridylate kinase similar to uric	---	AT3G10030	-1.14	-0.19	-1.85	0.108258	0.237302	-5.77
265376_at	hypothetical protein predicted by gene	---	AT2G05810	-1.17	-0.23	-1.85	0.108304	0.23738	-5.77
250066_at	unknown protein	---	AT5G17930	1.28	0.35	1.85	0.108474	0.237684	-5.77
248649_at	putative protein contains similarity to tv	APRR4	AT5G49240	1.18	0.24	1.85	0.108472	0.237684	-5.77
248806_at	putative protein contains similarity to u	---	AT5G47490	-1.14	-0.20	-1.85	0.108457	0.237684	-5.77
262545_at	prolin rich protein, putative similar to p	---	AT1G31250	-1.16	-0.21	-1.85	0.108537	0.2378	-5.77
256447_at	nitrate transporter NTL1, putative simi	---	AT1G33440	-1.20	-0.26	-1.85	0.108552	0.23781	-5.77
260632_at	homeobox protein, putative similar to	STM	AT1G62360	-1.17	-0.22	-1.85	0.108565	0.237816	-5.77
246009_at	Expressed protein ; supported by cDN	ATSTE14B	AT5G08335	1.22	0.29	1.85	0.108628	0.237929	-5.77
266552_at	unknown protein ; supported by cDNA	AGP16	AT2G46330	-1.24	-0.32	-1.85	0.108667	0.237994	-5.78
256409_at	hypothetical protein	---	AT1G66620	-1.18	-0.24	-1.85	0.108689	0.238019	-5.78
264042_at	putative steroid sulfotransferase ; sup	ST	AT2G03760	1.97	0.98	1.85	0.108752	0.238134	-5.78
246635_at	hypothetical protein predicted by gene	---	AT1G31720	-1.24	-0.31	-1.85	0.10887	0.238368	-5.78
256720_at	putative DOF zinc finger protein	---	AT2G34140	1.35	0.44	1.85	0.108901	0.238413	-5.78
257972_at	putative protein kinase, ATN1 almost	ATN1	AT3G27560	1.17	0.23	1.85	0.108951	0.238501	-5.78
267199_at	hypothetical protein predicted by gene	---	AT2G30990	-1.61	-0.68	-1.85	0.108968	0.238514	-5.78
257771_at	SNF1 related protein kinase (ATSRPK	CIPK7	AT3G23000	1.59	0.66	1.85	0.109006	0.238568	-5.78
249639_at	disease resistance like protein TMV re	---	AT5G36930	-1.14	-0.19	-1.85	0.109013	0.238568	-5.78
264204_at	putative sucrose transport protein, SU	SUC2	AT1G22710	-1.24	-0.31	-1.85	0.109045	0.238614	-5.78
248986_at	putative protein similar to unknown pro	---	AT5G45170	-1.20	-0.27	-1.85	0.109074	0.238654	-5.78
265706_at	unknown protein	---	AT2G03390	-1.22	-0.29	-1.85	0.109089	0.238664	-5.78
260020_at	hydrophilic protein, putative similar to	PDF6	AT1G29990	1.13	0.18	1.85	0.109173	0.238826	-5.78
262702_at	putative protein phosphatase 2C simila	---	AT1G16220	1.17	0.23	1.85	0.109199	0.238859	-5.78

261448_at	tonoplast intrinsic protein, alpha (alpha	---	AT1G21140	1.27	0.34	1.85	0.109242	0.238908	-5.78
252497_at	putative protein several putative protei	---	AT3G46800	-1.13	-0.18	-1.85	0.109234	0.238908	-5.78
246455_at	putative protein predicted protein F13I	---	AT5G16790	-1.17	-0.23	-1.84	0.10927	0.238946	-5.78
262776_at	unknown protein EST gb|T22808 come	---	AT1G13020	1.20	0.26	1.84	0.109373	0.239148	-5.78
246913_at	GATA transcription factor - like GATA	---	AT5G25830	-1.22	-0.28	-1.84	0.10942	0.239206	-5.78
250771_at	NBS/LRR disease resistance protein	---	AT5G05400	-1.15	-0.21	-1.84	0.109414	0.239206	-5.78
248290_at	Ca2+-transporting ATPase-like protein	---	AT5G53010	1.18	0.24	1.84	0.109471	0.239294	-5.78
247957_at	protein phosphatase 2C ABI2 (PP2C)	ABI2	AT5G57050	1.32	0.40	1.84	0.109548	0.23944	-5.78
255788_at	auxin regulated protein (IAA13) GB:S5	IAA13	AT2G33310	-1.22	-0.29	-1.84	0.109614	0.239492	-5.78
254001_at	putative protein PRE87 mRNA, Pinus	MIOX4	AT4G26260	1.57	0.65	1.84	0.109609	0.239492	-5.78
246873_at	putative protein	---	AT5G26100	-1.16	-0.21	-1.84	0.109608	0.239492	-5.78
266038_at	putative ABC transporter	ATMRP11	AT2G07680	-1.31	-0.39	-1.84	0.109587	0.239492	-5.78
246196_at	hypothetical protein ;supported by full-	---	AT4G37090	1.24	0.31	1.84	0.109655	0.239559	-5.78
258950_at	unknown protein contains Pfam profile	MBD9	AT3G01460	-1.12	-0.16	-1.84	0.109704	0.239643	-5.78
266220_at	putative dTDP-glucose 4-6-dehydratas	---	AT2G28755	1.20	0.27	1.84	0.109748	0.239717	-5.78
248288_at	unknown protein ; supported by cDNA	---	AT5G52840	-1.20	-0.27	-1.84	0.109782	0.239768	-5.78
267513_at	unknown protein ; supported by cDNA	---	AT2G45620	-1.16	-0.22	-1.84	0.109843	0.239877	-5.79
266830_at	1-aminocyclopropane-1-carboxylate sy	ACS4	AT2G22810	-1.77	-0.82	-1.84	0.109891	0.23996	-5.79
252457_at	zinc-finger protein-like protein DNA bi	---	AT3G47180	-1.14	-0.19	-1.84	0.109919	0.239976	-5.79
250492_at	putative protein Requiem protein, Xen	ATXR5	AT5G09790	1.17	0.22	1.84	0.10992	0.239976	-5.79
253261_at	putative protein mRNA, partial cds, Sc	CHB3	AT4G34430	-1.17	-0.23	-1.84	0.109982	0.240089	-5.79
256491_at	hypothetical protein contains similarity	---	AT1G31500	-1.17	-0.23	-1.84	0.110095	0.240312	-5.79
258312_at	putative long-chain acyl-CoA synthetas	---	AT3G16170	1.24	0.30	1.84	0.11012	0.24032	-5.79
261675_at	hypothetical protein predicted by gene	---	AT1G18290	1.16	0.21	1.84	0.11011	0.24032	-5.79
254463_at	putative protein transcription initiation	TAF11	AT4G20280	-1.19	-0.25	-1.84	0.110144	0.24035	-5.79
265810_at	unknown protein	---	AT2G18090	1.27	0.34	1.84	0.110156	0.240354	-5.79
263229_s_	putative polygalacturonase similar to G	---	AT1G05650 /	-1.13	-0.18	-1.84	0.11019	0.240397	-5.79
262950_at	transcription initiation factor, putative s	---	AT1G75510	1.13	0.18	1.84	0.110197	0.240397	-5.79
249758_at	putative protein similar to unknown pro	---	AT5G24350	1.21	0.28	1.84	0.110231	0.240425	-5.79
253074_at	putative disease resistance protein TM	---	AT4G36140	-1.13	-0.17	-1.84	0.11023	0.240425	-5.79
245234_at	myb-like protein similarity to ATMYB4	AtMYB18	AT4G25560	-1.18	-0.24	-1.84	0.110265	0.240477	-5.79
245612_at	carnitine racemase like protein	HCD1	AT4G14440	-1.60	-0.68	-1.84	0.110319	0.240572	-5.79
255922_at	trehalose-6-phosphate phosphatase, I	---	AT1G22210	1.14	0.19	1.84	0.110353	0.240621	-5.79
261496_at	ethylene responsive element binding f	ERF12	AT1G28360	1.18	0.24	1.84	0.110379	0.240633	-5.79
251307_at	putative protein ;supported by full-leng	---	AT3G61200	1.18	0.24	1.84	0.110373	0.240633	-5.79

261063_at	transcription factor scarecrow-like 14,	---	AT1G07520	1.70	0.77	1.84	0.110422	0.240704	-5.79
253982_at	calcineurin B-like protein 3 ;supported	ATCBL3	AT4G26570	-1.25	-0.32	-1.84	0.110453	0.240749	-5.79
264360_at	putative isoamylase Similar to gi|1652	DBE1	AT1G03310	-1.20	-0.26	-1.84	0.110523	0.240855	-5.79
260241_at	putative cytochrome P450 similar to cy	CYP86A7	AT1G63710	-1.23	-0.30	-1.84	0.110517	0.240855	-5.79
263355_at	putative RNA-binding protein ;support	---	AT2G22100	1.20	0.26	1.84	0.110557	0.240905	-5.79
266972_at	40S ribosomal protein S15A	---	AT2G39590	-1.14	-0.19	-1.84	0.110596	0.240968	-5.79
255275_at	putative protein various ubiquitin-like p	---	AT4G05310	-1.12	-0.16	-1.84	0.110619	0.240996	-5.79
253750_at	putative transcription factor leghemog	---	AT4G29000	1.22	0.29	1.84	0.110764	0.241288	-5.79
250812_at	putative protein similar to unknown pro	---	AT5G04900	1.14	0.19	1.84	0.110775	0.241289	-5.79
259311_at	putative SAR DNA-binding protein-1 si	---	AT3G05060	1.33	0.41	1.84	0.110811	0.241331	-5.79
265688_at	putative calmodulin-binding protein	---	AT2G24300	-1.12	-0.16	-1.84	0.110816	0.241331	-5.79
265356_at	putative TRAP protein	---	AT2G16595	1.21	0.28	1.83	0.110885	0.241444	-5.79
260944_at	beta-galactosidase, putative similar to	BGAL5	AT1G45130	-2.44	-1.29	-1.83	0.110888	0.241444	-5.79
264405_at	putative mitogen-activated protein kin	ATMPK1	AT1G10210	1.34	0.43	1.83	0.111021	0.24171	-5.80
253359_at	putative protein kinase protein kinase,	---	AT4G33080	1.20	0.26	1.83	0.111034	0.241716	-5.80
253626_at	F-box protein family, AtFBL19 contain	---	AT4G30640	1.28	0.36	1.83	0.11109	0.241813	-5.80
266470_at	putative non-LTR retroelement reverse	---	---	-1.30	-0.37	-1.83	0.111111	0.241836	-5.80
266809_at	unknown protein ; supported by cDNA	---	AT2G29970	1.32	0.40	1.83	0.111125	0.241844	-5.80
266109_at	putative mitochondrial carrier protein	---	AT2G37890	1.33	0.41	1.83	0.111185	0.241948	-5.80
266236_at	putative glutathione S-transferase	ATGSTZ2	AT2G02380	-1.15	-0.20	-1.83	0.111201	0.241948	-5.80
253716_at	hypothetical protein	---	AT4G29420	-1.18	-0.24	-1.83	0.111205	0.241948	-5.80
264977_at	unknown protein	---	AT1G27090	-1.28	-0.35	-1.83	0.111277	0.242081	-5.80
246693_at	putative protein	---	AT5G29070	-1.15	-0.20	-1.83	0.111301	0.242088	-5.80
261889_at	unknown protein	---	AT1G80810	-1.18	-0.23	-1.83	0.111296	0.242088	-5.80
247012_at	putative protein contains similarity to M	TRB2	AT5G67580	1.16	0.22	1.83	0.111316	0.242097	-5.80
255039_at	calmodulin-domain protein kinase CDP	CPK4	AT4G09570	1.18	0.24	1.83	0.111356	0.242162	-5.80
250150_at	putative protein ;supported by full-leng	---	AT5G14710	1.24	0.31	1.83	0.111381	0.242182	-5.80
262239_at	unknown protein similar to putative pho	---	AT1G48230	-1.25	-0.32	-1.83	0.111387	0.242182	-5.80
249833_at	putative protein contains similarity to u	---	AT5G23430	-1.20	-0.26	-1.83	0.111429	0.242252	-5.80
252401_at	putative protein predicted proteins, Ar	---	AT3G48030	-1.19	-0.25	-1.83	0.111446	0.242255	-5.80
245619_at	hypothetical protein	---	AT4G13990	-1.24	-0.31	-1.83	0.111452	0.242255	-5.80
245658_at	hypothetical protein predicted by gene	RALFL4	AT1G28270	-1.14	-0.19	-1.83	0.111467	0.242263	-5.80
246998_at	putative protein similar to unknown pro	---	AT5G67370	1.32	0.41	1.83	0.11149	0.242291	-5.80
245111_at	putative Ta11-like non-LTR retroeleme	---	---	-1.16	-0.22	-1.83	0.111531	0.242356	-5.80
252154_at	putative DNA-3-methyladenine glycos	---	AT3G50880	-1.23	-0.29	-1.83	0.111549	0.242372	-5.80

262832_s_	unknown protein	---	AT1G14870 /	3.62	1.86	1.83	0.111608	0.242478	-5.80
263383_at	putative protein kinase contains a prot	---	AT2G40120	1.18	0.24	1.83	0.111645	0.242536	-5.80
258533_at	hypothetical protein	---	AT3G06670	1.17	0.23	1.83	0.111687	0.242582	-5.80
267547_at	putative synaptobrevin	ATVAMP725	AT2G32670	1.21	0.27	1.83	0.111688	0.242582	-5.80
246714_at	putative protein predicted proteins, Ar	---	AT5G28220	1.13	0.18	1.83	0.111767	0.242731	-5.80
245247_at	scarecrow-like 13 (SCL13) ; supported	SCL13	AT4G17230	1.50	0.58	1.83	0.111852	0.242893	-5.80
252946_at	Expressed protein ; supported by full-l	---	AT4G39235	1.27	0.34	1.83	0.111872	0.242911	-5.80
247443_at	putative protein predicted proteins, Ar	---	AT5G62720	-1.25	-0.33	-1.83	0.111882	0.242911	-5.80
254115_at	putative protein binding protein HPV1	---	AT4G24710	-1.14	-0.20	-1.83	0.11193	0.242993	-5.80
251472_at	putative protein nodule inception prote	---	AT3G59580	1.15	0.20	1.83	0.111949	0.242996	-5.80
249873_at	ATP-dependent Clp protease proteoly	NCLPP7	AT5G23140	-1.17	-0.23	-1.83	0.111953	0.242996	-5.80
253784_at	putative protein WREBP-1, Nicotiana	PHR1	AT4G28610	1.17	0.23	1.83	0.112054	0.243193	-5.80
255541_s_	P-glycoprotein-like protein pgp3 simila	PGP5	AT4G01820 /	-1.13	-0.18	-1.83	0.112075	0.243215	-5.80
252790_at	putative protein various predicted trans	---	---	1.14	0.19	1.83	0.112153	0.243361	-5.81
264641_at	ATP-dependent Clp protease proteoly	---	AT1G09130	1.18	0.24	1.83	0.112165	0.243364	-5.81
264203_at	putative 40S ribosomal protein S18 M	PFL	AT1G22780	-1.37	-0.46	-1.83	0.112197	0.243411	-5.81
256862_at	dihydroxyacid dehydratase, putative s	---	AT3G23940	1.42	0.50	1.83	0.112215	0.243427	-5.81
246562_at	putative protein unknown protein F14F	LNG1	AT5G15580	-2.28	-1.19	-1.83	0.112258	0.243497	-5.81
256749_at	hypothetical protein similar to putative	---	---	-1.14	-0.19	-1.83	0.112302	0.243569	-5.81
258380_at	PP1/PP2A phosphatases pleiotropic re	---	AT3G16650	1.17	0.22	1.83	0.112358	0.243598	-5.81
265960_at	putative histone H2B ;supported by fu	---	AT2G37470	-1.32	-0.40	-1.83	0.112331	0.243598	-5.81
253967_at	putative protein probable membrane p	---	AT4G26550	-1.24	-0.31	-1.83	0.112369	0.243598	-5.81
251732_at	putative protein prenylated Rab accep	PRA1.B1	AT3G56110	1.14	0.19	1.83	0.112361	0.243598	-5.81
254154_at	hypothetical protein	---	AT4G24460	-1.21	-0.28	-1.83	0.11234	0.243598	-5.81
255683_at	putative malate oxidoreductase	---	AT4G00570	-1.18	-0.24	-1.83	0.112414	0.243671	-5.81
256104_at	trehalose-6-phosphate synthase, puta	ATTPS2	AT1G16980	-1.14	-0.19	-1.83	0.112428	0.24368	-5.81
245847_at	MYB DNA-binding - like protein myb-r	MYB64	AT5G11050	-1.19	-0.25	-1.82	0.112466	0.243738	-5.81
262624_at	CCR4-associated factor, putative simi	---	AT1G06450	1.17	0.23	1.82	0.112513	0.243784	-5.81
267369_at	unknown protein ;supported by full-ler	---	AT2G44420	1.18	0.24	1.82	0.112506	0.243784	-5.81
250926_at	Expressed protein ; supported by full-l	---	AT5G03555	-1.39	-0.47	-1.82	0.112519	0.243784	-5.81
255563_at	putative CHP-rich zinc finger protein s	---	AT4G01740	-1.14	-0.19	-1.82	0.112562	0.243853	-5.81
247359_at	acyltransferase-like protein ;supported	---	AT5G63560	1.20	0.26	1.82	0.112586	0.243882	-5.81
263077_at	putative mitotic control protein dis3 ; s	EMB2763	AT2G17510	-1.13	-0.17	-1.82	0.112618	0.243929	-5.81
260981_at	hypothetical protein predicted by gens	---	AT1G53460	-1.19	-0.26	-1.82	0.112719	0.244044	-5.81
251785_at	ABC transporter - like protein breast c	ATWBC19	AT3G55130	1.37	0.46	1.82	0.112725	0.244044	-5.81

259792_at	unknown protein ; supported by cDNA	CAD1	AT1G29690	1.52	0.61	1.82	0.112707	0.244044	-5.81
262538_at	Expressed protein ; supported by full-l	---	AT1G17140	-1.32	-0.40	-1.82	0.112697	0.244044	-5.81
256090_at	predicted protein	---	AT1G20816	-1.19	-0.26	-1.82	0.112683	0.244044	-5.81
255538_at	putative transcription factor ; supporte	MYB55	AT4G01680	-1.48	-0.56	-1.82	0.112774	0.244105	-5.81
255700_at	putative transcription factor similar to A	---	AT4G00200	1.30	0.38	1.82	0.112768	0.244105	-5.81
259814_at	zinc finger protein ATZF1, putative sir	---	AT1G49900	1.27	0.35	1.82	0.112832	0.244207	-5.81
262375_at	unknown protein ; supported by cDNA	SUVH3	AT1G73100	1.19	0.25	1.82	0.112945	0.244406	-5.81
252589_s_	putative protein different transporter pr	NAXT1	AT3G45650 /	1.47	0.55	1.82	0.112942	0.244406	-5.81
249015_at	Dreg-2 like protein	---	AT5G44730	-1.16	-0.21	-1.82	0.112998	0.244497	-5.81
250972_at	putative protein various Myb related p	LCL1	AT5G02840	1.27	0.34	1.82	0.113037	0.244508	-5.81
253666_at	xyloglucan endo-1,4-beta-D-glucanas	MERI5B	AT4G30270	1.14	0.19	1.82	0.113036	0.244508	-5.81
250576_at	cytochrome P450-like protein several	---	AT5G08250	1.16	0.22	1.82	0.113045	0.244508	-5.81
250203_at	alpha-mannosidase	---	AT5G13980	-1.26	-0.34	-1.82	0.113046	0.244508	-5.81
265829_at	unknown protein	---	AT2G14490	-1.13	-0.18	-1.82	0.113061	0.244516	-5.81
259198_at	hypothetical protein similar to F1N21.1	---	AT3G03610	1.16	0.22	1.82	0.11309	0.244556	-5.81
264342_at	unknown protein ; supported by full-ler	---	AT1G12080	-1.91	-0.94	-1.82	0.113135	0.24463	-5.81
248322_at	putative protein similar to unknown pro	---	AT5G52760	3.09	1.63	1.82	0.113178	0.244701	-5.81
264382_at	unknown protein similarity to stromal c	SDF2	AT2G25110	1.28	0.36	1.82	0.113208	0.244742	-5.81
264264_at	unknown protein ESTs gb|T04610, gb	---	AT1G09250	-1.38	-0.46	-1.82	0.113362	0.24502	-5.82
250853_s_	putative protein prtedicted prteins, Ara	---	AT5G04680 /	-1.13	-0.17	-1.82	0.113369	0.24502	-5.82
249458_at	putative protein predicted proteins, Ar	---	AT5G39560	1.14	0.19	1.82	0.113367	0.24502	-5.82
254003_at	hypothetical protein	---	AT4G26290	1.17	0.22	1.82	0.113396	0.245056	-5.82
257120_at	protein kinase, putative contains Pfam	---	AT3G20200	-1.16	-0.21	-1.82	0.113472	0.245198	-5.82
258396_at	unknown protein similar to unknown pr	---	AT3G15460	1.33	0.41	1.82	0.113501	0.245236	-5.82
246895_at	putative protein predicted protein, Ara	CID6	AT5G25540	1.15	0.20	1.82	0.11353	0.245251	-5.82
250064_at	disease resistance protein - like down	DAR4	AT5G17890	-1.21	-0.28	-1.82	0.113526	0.245251	-5.82
248003_at	putative protein contains similarity to u	---	AT5G56220	-1.65	-0.73	-1.82	0.113584	0.245345	-5.82
249124_at	disease resistance protein ; supported	---	AT5G43740	1.15	0.20	1.82	0.113627	0.245415	-5.82
246537_at	putative protein protochlorophyllide re	---	AT5G15940	-1.17	-0.23	-1.82	0.113746	0.24565	-5.82
260807_at	hypothetical protein predicted by gene	---	AT1G78310	1.12	0.16	1.82	0.113773	0.245684	-5.82
253769_at	putative protein (fragment) protein kin	RIC7	AT4G28560	-1.20	-0.26	-1.82	0.113801	0.245722	-5.82
246887_at	hexose transporter - like protein hexos	---	AT5G26250	-1.16	-0.21	-1.82	0.11386	0.245826	-5.82
248403_at	arginine-aspartate-rich RNA binding pr	---	AT5G51410	-1.16	-0.21	-1.82	0.113914	0.245919	-5.82
265590_at	SKP1/ASK1 (At17), putative similar to	MEO	AT2G20160	-1.15	-0.20	-1.82	0.11397	0.245992	-5.82
260905_at	hypothetical protein predicted by gene	---	AT1G02710	-1.12	-0.16	-1.82	0.113967	0.245992	-5.82

265032_at	ribosomal protein identical to ribosoma	RPL3B	AT1G61580	1.38	0.47	1.82	0.114075	0.246197	-5.82
259438_at	unknown protein similar to putative del	AN	AT1G01510	-1.24	-0.31	-1.81	0.114272	0.246598	-5.82
253952_at	ubiquitin-like protein ubiquitin-like prot	SUMO1	AT4G26840	1.15	0.20	1.81	0.114332	0.246693	-5.82
250222_at	putative protein similar to unknown pro	---	AT5G14050	1.27	0.35	1.81	0.114338	0.246693	-5.82
246893_at	PHD finger protein - like PHD finger p	---	AT5G25520	-1.12	-0.16	-1.81	0.114422	0.246851	-5.82
252233_at	AtMYB84 ;supported by full-length cD	MYB84	AT3G49690	-1.17	-0.23	-1.81	0.114566	0.247139	-5.83
263149_at	unknown protein	---	AT1G53970	1.15	0.20	1.81	0.114658	0.247314	-5.83
253161_at	senescence-associated protein sen1 ic	SEN1	AT4G35770	1.47	0.56	1.81	0.114806	0.24761	-5.83
246585_at	myb transcription factor werewolf (WE	ATMYB66	AT5G14750	-1.14	-0.18	-1.81	0.114858	0.247687	-5.83
260668_at	unknown protein ;supported by full-len	---	AT1G19530	1.90	0.93	1.81	0.114863	0.247687	-5.83
261829_at	P-glycoprotein, putative similar to P-gl	PGP10	AT1G10680	-1.19	-0.26	-1.81	0.114933	0.247814	-5.83
251089_at	heat shock protein 40-like heat shock	---	AT5G01390	-1.15	-0.20	-1.81	0.114994	0.247922	-5.83
263811_at	putative acyl-CoA synthetase ; support	---	AT2G04350	1.17	0.22	1.81	0.115045	0.248009	-5.83
262844_at	unknown protein similar to pectinestera	---	AT1G14890	1.48	0.57	1.81	0.115174	0.248263	-5.83
253094_at	putative protein DnaJ-like protein, Pha	---	AT4G37480	-1.12	-0.17	-1.81	0.115284	0.248453	-5.83
261990_at	unknown protein	---	AT1G33660	1.15	0.21	1.81	0.115276	0.248453	-5.83
257896_at	basic chitinase, putative similar to bas	---	AT3G16920	-1.68	-0.75	-1.81	0.115304	0.248473	-5.83
263621_at	putative DNA-directed RNA polymeras	NRPB6B	AT2G04630	-1.16	-0.22	-1.81	0.11535	0.248548	-5.83
255668_s_	predicted protein ; supported by full-le	---	AT4G00238 /	1.20	0.26	1.81	0.115375	0.248578	-5.83
256194_at	unknown protein	---	---	-1.21	-0.28	-1.81	0.115443	0.248702	-5.83
250974_at	meiosis specific - like protein Spo11, I	RHL2	AT5G02820	-1.37	-0.45	-1.81	0.115543	0.248893	-5.83
248483_at	putative protein contains similarity to s	---	AT5G50990	-1.22	-0.29	-1.81	0.115643	0.249085	-5.84
248283_at	pyruvate kinase ;supported by full-len	PKP-BETA1	AT5G52920	-1.29	-0.37	-1.81	0.115674	0.249109	-5.84
264687_at	cysteine protease XBCP3 identical to p	XBCP3	AT1G09850	-1.13	-0.18	-1.81	0.115676	0.249109	-5.84
AFFX-r2-At	Arabidopsis thaliana /REF=U37281 /D	---	---	-1.13	-0.17	-1.81	0.11569	0.249116	-5.84
253182_at	putative protein ctf, Mycobacterium le	---	AT4G35190	1.29	0.36	1.80	0.1158	0.249329	-5.84
256065_at	ribosomal protein, putative similar to r	---	AT1G07070	-1.34	-0.42	-1.80	0.11584	0.24937	-5.84
258208_at	putative acetyltransferase similar to dil	---	AT3G13930	1.25	0.32	1.80	0.11584	0.24937	-5.84
258161_at	hypothetical protein predicted by gene	---	AT3G17930	1.17	0.23	1.80	0.115892	0.249386	-5.84
261910_at	zinc finger protein identical to GB:AAA	ZFP1	AT1G80730	-1.13	-0.18	-1.80	0.115865	0.249386	-5.84
248161_at	unknown protein	---	AT5G54480	1.16	0.22	1.80	0.115885	0.249386	-5.84
252670_at	dnaJ protein homolog atj3 ;supported	ATJ3	AT3G44110	1.19	0.25	1.80	0.115872	0.249386	-5.84
254222_at	hypothetical protein	---	AT4G23840	-1.17	-0.23	-1.80	0.115956	0.249501	-5.84
245811_at	hypothetical protein similar to putative	---	---	1.16	0.21	1.80	0.115983	0.249536	-5.84
250083_at	glutathione S-transferase-like protein	ATGSTF12	AT5G17220	-1.18	-0.24	-1.80	0.116089	0.24974	-5.84

265492_at	hypothetical protein	AGL95	AT2G15660	1.15	0.20	1.80	0.11619	0.249926	-5.84
258490_at	hypothetical protein predicted by gene	---	AT3G02670	1.15	0.20	1.80	0.116198	0.249926	-5.84
259148_at	putative ATPase similar to ATPase GI	---	AT3G10350	-1.19	-0.25	-1.80	0.116214	0.249938	-5.84
258675_at	putative nonspecific lipid-transfer prote	LTP6	AT3G08770	1.16	0.21	1.80	0.116241	0.249966	-5.84
251822_at	centromere protein - like centromere p	---	AT3G55060	1.14	0.19	1.80	0.116249	0.249966	-5.84
247939_at	putative protein contains similarity to D	ATLIG4	AT5G57160	-1.15	-0.20	-1.80	0.116307	0.250066	-5.84
255983_at	polyneuridine aldehyde esterase, puta	MES14	AT1G33990	-1.16	-0.21	-1.80	0.11635	0.250135	-5.84
253690_at	putative protein various predicted prot	---	AT4G29550	-1.23	-0.30	-1.80	0.116368	0.250151	-5.84
260593_at	poly(A)-specific ribonuclease, putative	AHG2	AT1G55870	1.21	0.27	1.80	0.116381	0.250155	-5.84
265822_at	putative SEC1 family transport protein	ATSLY1	AT2G17980	-1.15	-0.20	-1.80	0.116411	0.250196	-5.84
248579_at	mitotic checkpoint protein-like	---	AT5G49880	1.23	0.30	1.80	0.116429	0.250211	-5.84
252663_at	putative protein several hypothetical pr	---	AT3G44070	-1.12	-0.17	-1.80	0.116462	0.250236	-5.84
259559_at	hypothetical protein	WAK3	AT1G21240	1.25	0.32	1.80	0.116456	0.250236	-5.84
250160_at	putative protein various predicted prot	ATHB30	AT5G15210	1.41	0.49	1.80	0.116505	0.250305	-5.84
267485_at	putative MYB family transcription facto	MYB88	AT2G02820	1.20	0.26	1.80	0.116559	0.250397	-5.84
245266_at	hypothetical protein ; supported by cDI	---	AT4G17070	1.28	0.36	1.80	0.116632	0.25053	-5.84
257125_at	t-complex polypeptide 1 homologue id	ATTCP-1	AT3G20050	1.19	0.25	1.80	0.116765	0.250772	-5.84
257144_at	glucose-6-phosphate 1-dehydrogenas	G6PD5	AT3G27300	1.14	0.19	1.80	0.116799	0.250772	-5.84
256664_at	DNA-3-methlyadenine glycosylase (MA	---	AT3G12040	1.21	0.27	1.80	0.116793	0.250772	-5.84
265293_at	hypothetical protein predicted by gens	---	---	1.16	0.22	1.80	0.1168	0.250772	-5.84
261988_at	single-strand nucleic acid-binding prot	---	AT1G33680	-1.22	-0.29	-1.80	0.116793	0.250772	-5.84
246450_at	Heat Shock Factor 3	HSF3	AT5G16820	-1.14	-0.19	-1.80	0.116879	0.250919	-5.85
247423_at	putative protein predicted proteins, Ar	---	AT5G62830	-1.13	-0.18	-1.80	0.116896	0.250932	-5.85
251680_at	putative protein 13S condensin XCAP	---	AT3G57060	-1.14	-0.19	-1.80	0.116985	0.251099	-5.85
248981_at	regulatory protein NPR1-like; transcrip	NPR3	AT5G45110	1.16	0.21	1.80	0.117117	0.251359	-5.85
260809_at	hypothetical protein predicted by gene	---	AT1G43730	-1.13	-0.17	-1.80	0.117197	0.251506	-5.85
259179_at	hypothetical protein similar to putative	---	AT3G01660	1.21	0.27	1.80	0.117259	0.251615	-5.85
246671_at	putative protein	---	---	-1.13	-0.17	-1.80	0.117272	0.25162	-5.85
265948_at	1-aminocyclopropane-1-carboxylate ox	ACO1	AT2G19590	1.17	0.22	1.80	0.11732	0.251695	-5.85
266762_at	putative alcohol dehydrogenase	---	AT2G47120	-1.13	-0.18	-1.80	0.117329	0.251695	-5.85
266623_at	unknown protein	---	AT2G35390	1.21	0.28	1.80	0.117347	0.25171	-5.85
247152_at	oligopeptidase A ; supported by cDNA	---	AT5G65620	-1.13	-0.18	-1.80	0.117382	0.251761	-5.85
258625_at	hypothetical protein predicted by gene	PDLP4	AT3G04370	1.15	0.20	1.80	0.117396	0.251767	-5.85
250367_s_	DEAD BOX RNA helicase RH15 ; sup	---	AT5G11170 /	-1.16	-0.21	-1.79	0.117473	0.251909	-5.85
245885_at	putative protein phi-1 - Nicotiana taba	EXL4	AT5G09440	1.31	0.39	1.79	0.11759	0.252136	-5.85

264559_at	unknown protein similar to hypothetica	---	AT1G09610	-1.12	-0.16	-1.79	0.117618	0.252173	-5.85
259554_at	hypothetical protein	---	---	1.21	0.27	1.79	0.117672	0.252242	-5.85
265107_s_	similar to glucose 1-dehydrogenase (A	---	AT1G62610 /	1.15	0.20	1.79	0.117664	0.252242	-5.85
251449_at	Rab GDP dissociation inhibitor ; supp	ATGDI2	AT3G59920	1.20	0.26	1.79	0.117696	0.25227	-5.85
256807_at	unknown protein contains Pfam profile	NFU4	AT3G20970	1.15	0.21	1.79	0.117716	0.252288	-5.85
247206_at	putative protein similar to unknown pro	---	AT5G64950	1.11	0.15	1.79	0.117735	0.252306	-5.85
246220_at	putative protein ; supported by cDNA:	---	AT4G37210	1.14	0.18	1.79	0.11784	0.252506	-5.85
259463_at	hypothetical protein predicted by gene	---	AT1G18950	1.28	0.36	1.79	0.117856	0.252518	-5.85
266369_at	hypothetical protein predicted by gens	BOP2	AT2G41370	1.23	0.30	1.79	0.117898	0.252584	-5.85
264566_at	hypothetical protein predicted by gene	---	AT1G05270	1.17	0.23	1.79	0.11797	0.252714	-5.85
245988_at	putative protein predicted protein, Pla	---	AT5G20610	1.21	0.28	1.79	0.118045	0.252851	-5.85
249019_at	unknown protein	---	AT5G44780	1.41	0.50	1.79	0.11808	0.252903	-5.86
255693_s_	putative BRCA2 homolog	BRCA2(IV)	AT4G00020 /	-1.16	-0.22	-1.79	0.118135	0.252995	-5.86
264988_at	glutathione transferase, putative simil	ATGSTU14	AT1G27140	1.22	0.29	1.79	0.118169	0.253044	-5.86
258235_at	alternative oxidase 1c precursor identi	AOX1C	AT3G27620	1.17	0.23	1.79	0.118236	0.253165	-5.86
249514_at	14-3-3 protein GF14psi (grf3/RCI1) id	GRF3	AT5G38480	-1.17	-0.23	-1.79	0.118269	0.253211	-5.86
250271_at	putative protein predicted protein, Ara	CLE40	AT5G12990	-1.14	-0.19	-1.79	0.118294	0.253241	-5.86
253596_s_	hypothetical protein ; supported by cD	---	AT4G30730 /	-1.24	-0.31	-1.79	0.118315	0.253262	-5.86
248939_at	tyrosine-specific protein phosphatase-	---	AT5G45790	1.16	0.21	1.79	0.118364	0.253323	-5.86
262215_at	hypothetical protein contains similarity	---	AT1G74790	-1.39	-0.47	-1.79	0.118376	0.253323	-5.86
264627_at	hypothetical protein similar to carnitine	ECI1	AT1G65520	1.17	0.23	1.79	0.118384	0.253323	-5.86
258527_at	branched chain alpha-keto acid dehyd	BCE2	AT3G06850	1.61	0.68	1.79	0.118388	0.253323	-5.86
257361_at	putative Ta11-like non-LTR retroeleme	---	---	-1.19	-0.25	-1.79	0.1184	0.253325	-5.86
258288_at	unknown protein	LSH4	---	1.34	0.43	1.79	0.118416	0.253336	-5.86
260870_at	GTP-binding protein(RAB1Y), putative	ATRAB18	AT1G43890	-1.18	-0.24	-1.79	0.118484	0.253457	-5.86
248632_at	unknown protein	SLD5	AT5G49010	-1.35	-0.44	-1.79	0.118526	0.253525	-5.86
246888_at	putative protein	---	AT5G26270	1.13	0.17	1.79	0.118551	0.253554	-5.86
251872_at	putative protein predicted protein Arab	---	AT3G54570	-1.14	-0.18	-1.79	0.118575	0.253556	-5.86
259656_at	protein kinase, putative contains Pfam	---	AT1G55200	-1.14	-0.19	-1.79	0.118586	0.253556	-5.86
256058_at	UDP-glucose glucosyltransferase, put	UGT71C5	AT1G07240	1.21	0.27	1.79	0.118579	0.253556	-5.86
260961_at	unknown protein similar to hypothetica	---	AT1G05960	-1.12	-0.17	-1.79	0.118631	0.253629	-5.86
246331_at	non-phototropic hypocotyl 3-like prote	---	AT3G44820	-1.18	-0.24	-1.79	0.11882	0.254009	-5.86
253025_at	hypothetical protein	---	AT4G38120	1.24	0.31	1.79	0.118842	0.254033	-5.86
248463_at	putative protein contains similarity to u	---	AT5G51130	1.40	0.49	1.79	0.118884	0.254051	-5.86
246170_at	putative protein various predicted prot	---	AT5G32450	-1.18	-0.23	-1.79	0.118884	0.254051	-5.86

253242_at	isoflavone reductase - like protein isof	CIB1	AT4G34530 /	-1.29	-0.37	-1.79	0.118874	0.254051	-5.86
256420_at	unknown protein	---	AT1G33475 /	-1.20	-0.26	-1.79	0.118948	0.254163	-5.86
259269_at	putative pectate lyase similar to pectat	---	AT3G01270	-1.16	-0.21	-1.79	0.118964	0.254175	-5.86
261770_at	prolyl endopeptidase, putative similar	---	AT1G76140	1.12	0.17	1.79	0.118978	0.25418	-5.86
250722_at	unknown protein ;supported by full-ler	---	AT5G06190	-1.26	-0.34	-1.79	0.119013	0.254232	-5.86
262703_at	putative auxin-induced protein similar t	---	AT1G16510	1.24	0.31	1.79	0.119108	0.254363	-5.86
249231_at	putative protein similar to unknown pro	ABIL4	AT5G42030	-1.17	-0.22	-1.79	0.119108	0.254363	-5.86
264871_at	pyruvate dehydrogenase E1 alpha sub	IAR4	AT1G24180	1.29	0.36	1.79	0.119101	0.254363	-5.86
248774_at	unknown protein	---	AT5G47830	-1.14	-0.19	-1.79	0.119141	0.254389	-5.86
258302_at	hypothetical protein predicted by gene	---	---	1.13	0.18	1.78	0.119148	0.254389	-5.86
265250_at	putative receptor protein kinase similar	BRL2	AT2G01950	-1.24	-0.31	-1.78	0.119153	0.254389	-5.86
248669_at	putative protein contains similarity to s	---	AT5G48730	1.24	0.31	1.78	0.119183	0.254429	-5.86
266016_at	putative RING zinc finger protein ; sup	---	AT2G18670 /	1.16	0.22	1.78	0.119217	0.254478	-5.86
245402_at	putative protein	---	AT4G17585	-1.17	-0.22	-1.78	0.119288	0.254605	-5.86
247702_at	putative protein ;supported by full-leng	---	AT5G59500	-1.16	-0.22	-1.78	0.119385	0.254788	-5.87
252550_at	putative protein MtN21, Medicago trur	---	AT3G45870	-1.18	-0.24	-1.78	0.119452	0.254858	-5.87
261267_at	unknown protein ;supported by full-len	---	AT1G26750	-1.17	-0.22	-1.78	0.119436	0.254858	-5.87
260439_at	hypothetical protein predicted by gens	---	AT1G68340	1.32	0.40	1.78	0.119451	0.254858	-5.87
258317_at	hypothetical protein predicted by gene	---	AT3G22670	-1.14	-0.19	-1.78	0.11948	0.254866	-5.87
266713_at	unknown protein	---	AT2G46760	-1.15	-0.20	-1.78	0.119489	0.254866	-5.87
259558_at	hypothetical protein	WAK5	AT1G21230	-1.16	-0.22	-1.78	0.11948	0.254866	-5.87
263995_at	putative MADS-box protein	SVP	AT2G22540	1.19	0.25	1.78	0.1195	0.254866	-5.87
245688_at	prolin-rich protein, putative similar to p	AGP31	AT1G28290	-2.14	-1.10	-1.78	0.119518	0.25488	-5.87
250182_at	putative protein predicted proteins, Ar	---	AT5G14470	1.51	0.59	1.78	0.119549	0.254924	-5.87
248824_at	putative protein contains similarity to ir	---	AT5G46940	5.02	2.33	1.78	0.119715	0.255253	-5.87
247569_at	Cf-5 disease resistance protein - like h	---	AT5G61240	-1.23	-0.30	-1.78	0.119761	0.255303	-5.87
250632_at	putative protein cyclin 2 - Trypanosom	CYCP4;3	AT5G07450	-1.18	-0.24	-1.78	0.119754	0.255303	-5.87
245660_at	unknown protein	---	AT1G28240	-1.27	-0.34	-1.78	0.11979	0.255342	-5.87
263826_at	hypothetical protein predicted by gens	---	AT2G40410	-1.21	-0.28	-1.78	0.119822	0.255385	-5.87
264709_at	putative DNA-binding protein, Myb Ide	ATCDC5	AT1G09770	1.26	0.33	1.78	0.119891	0.2555	-5.87
255139_s_	extensin-like protein hydroxyproline-ri	---	AT4G08400 /	1.12	0.17	1.78	0.119909	0.2555	-5.87
260743_at	unknown protein	---	AT1G15030	1.32	0.40	1.78	0.119903	0.2555	-5.87
255370_at	putative protein	---	---	-1.13	-0.17	-1.78	0.119929	0.255518	-5.87
252833_at	Expressed protein ; supported by cDN	AGP3	AT4G40090	-1.14	-0.19	-1.78	0.11996	0.255537	-5.87
264260_at	putative calcium-binding protein, calre	---	AT1G09210	1.43	0.51	1.78	0.119952	0.255537	-5.87

255932_at	mutator-like transposase, putative sim	---	---	1.15	0.20	1.78	0.119979	0.255554	-5.87
249225_at	TMV resistance protein-like	---	AT5G42140	1.25	0.32	1.78	0.120016	0.255608	-5.87
247465_at	RNA helicase ; supported by cDNA: gi	PRH75	AT5G62190	1.27	0.35	1.78	0.120102	0.255744	-5.87
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=gb:	---	---	-1.31	-0.39	-1.78	0.120111	0.255744	-5.87
255555_at	putative protein transport factor ; supp	---	AT4G01810	1.17	0.23	1.78	0.120113	0.255744	-5.87
249594_at	putative protein SIAH1 protein, Brassi	---	AT5G37910	1.14	0.19	1.78	0.120142	0.255782	-5.87
260206_at	putative protein kinase contains Pfam	---	AT1G70740	1.39	0.48	1.78	0.120221	0.255926	-5.87
248780_at	4-nitrophenylphosphatase-like protein	ATPGLP2	AT5G47760	1.15	0.21	1.78	0.120315	0.256101	-5.87
266046_at	hypothetical protein	---	AT2G07728	1.20	0.27	1.78	0.120419	0.256298	-5.87
253443_at	putative protein beta transducin-like p	LUG	AT4G32551	1.11	0.15	1.78	0.120438	0.256315	-5.87
251199_at	transport inhibitor response 1 (TIR1),	TIR1	AT3G62980	-1.28	-0.35	-1.78	0.120517	0.25644	-5.87
258326_at	unknown protein similar to putative DN	SOL1	AT3G22760	-1.22	-0.28	-1.78	0.120519	0.25644	-5.87
264712_at	unknown protein	ECT11	AT1G09810	1.21	0.28	1.78	0.120533	0.256447	-5.87
253619_at	glycine-rich protein glycine-rich cell wa	---	AT4G30460	-1.23	-0.30	-1.78	0.120579	0.25652	-5.88
265144_at	putative serine/threonine protein kinas	---	AT1G51170	-1.21	-0.28	-1.78	0.120638	0.256622	-5.88
260263_at	hypothetical protein predicted by gene	JAG	AT1G68480	-1.12	-0.17	-1.78	0.12069	0.256674	-5.88
250100_at	Expressed protein ; supported by cDN	GLN1;4	AT5G16570	1.48	0.56	1.78	0.120676	0.256674	-5.88
248729_at	cycloartenol synthase	THAS1	AT5G48010	1.12	0.17	1.78	0.120697	0.256674	-5.88
265895_at	unknown protein ;supported by full-ler	---	AT2G15000	1.17	0.23	1.78	0.120779	0.256826	-5.88
262084_at	hypothetical protein predicted by gene	---	AT1G56080	1.17	0.23	1.78	0.120835	0.25692	-5.88
259354_at	unknown protein	---	AT3G05220	1.26	0.33	1.77	0.120911	0.257058	-5.88
265081_at	hypothetical protein contains Zinc fing	MGP	AT1G03840	1.16	0.21	1.77	0.120941	0.257099	-5.88
260035_at	peroxidase ATP23a identical to peroxi	---	AT1G68850	-1.29	-0.36	-1.77	0.120953	0.2571	-5.88
256204_at	DNA polymerase A family protein, put	POLGAMMA	AT1G50840	1.20	0.26	1.77	0.120999	0.257171	-5.88
251648_at	protein kinase - like protein S-recepto	---	AT3G57720	-1.20	-0.27	-1.77	0.121009	0.257171	-5.88
267238_at	unknown protein ;supported by full-ler	---	AT2G44130	1.81	0.86	1.77	0.12105	0.257234	-5.88
251992_at	putative protein myosin heavy chain,	---	AT3G53350	1.22	0.28	1.77	0.121075	0.257264	-5.88
250956_at	putative protein	---	AT5G03210	1.24	0.31	1.77	0.12114	0.257377	-5.88
247497_at	Peter Pan - like protein Peter Pan, Dr	PPAN	AT5G61770	1.24	0.31	1.77	0.121193	0.257462	-5.88
262602_at	unknown protein ESTs gb|AA650895,	---	AT1G15270	1.13	0.17	1.77	0.121205	0.257462	-5.88
250854_at	aspartyl aminopeptidase -like protein	---	AT5G04710	-1.19	-0.25	-1.77	0.121214	0.257462	-5.88
264862_at	hypothetical protein predicted by gens	---	AT1G24330	1.24	0.31	1.77	0.121304	0.257631	-5.88
256190_at	9-cis-epoxycarotenoid dioxygenase, p	NCED5	AT1G30100	-1.15	-0.20	-1.77	0.121327	0.257639	-5.88
261921_at	hypothetical protein predicted by gene	---	AT1G65900	-1.30	-0.38	-1.77	0.121331	0.257639	-5.88
251137_at	putative protein several hypothetical pr	---	AT5G01300	-1.22	-0.29	-1.77	0.121411	0.257785	-5.88

264956_at	unknown protein similar to putative uri	ACR3	AT1G76990	-1.48	-0.56	-1.77	0.121486	0.25792	-5.88
263254_x_	hypothetical protein similar to hypothet	---	---	-1.22	-0.28	-1.77	0.121556	0.258045	-5.88
247972_at	histone acetyltransferase HAT B	HAG2	AT5G56740	1.22	0.29	1.77	0.121601	0.258117	-5.88
256399_at	hypothetical protein predicted by gene	---	AT3G06240	-1.15	-0.20	-1.77	0.121641	0.258178	-5.88
245733_at	hypothetical protein predicted by gene	---	AT1G73380	-1.24	-0.31	-1.77	0.121824	0.258541	-5.89
265291_at	unknown protein predicted by genscan	---	AT2G22720	-1.16	-0.21	-1.77	0.121908	0.258672	-5.89
244990_s_	hypothetical protein	---	---	-1.38	-0.46	-1.77	0.121904	0.258672	-5.89
261374_at	hypothetical protein contains thioredox	---	AT1G52990	-1.13	-0.17	-1.77	0.121931	0.258697	-5.89
253780_at	protein phosphatase 2C-like protein p	---	AT4G28400	-1.38	-0.47	-1.77	0.122028	0.258878	-5.89
246178_s_	putative protein predicted proteins - Ar	---	---	1.19	0.25	1.77	0.122081	0.258944	-5.89
264366_at	unknown protein EST gb|N96383 com	---	AT1G03250	1.20	0.26	1.77	0.122074	0.258944	-5.89
249915_at	putative protein similar to unknown pro	---	AT5G22870	-1.14	-0.18	-1.77	0.122124	0.259009	-5.89
259926_at	putative DNA-3-methyladenine glycosy	---	AT1G75090	-1.12	-0.16	-1.77	0.122137	0.259012	-5.89
251447_at	U6 snRNA-associated Sm-like protein	---	AT3G59810	-1.12	-0.17	-1.77	0.122199	0.259096	-5.89
259879_at	putative calmodulin similar to calmodu	CML38	AT1G76650	1.89	0.92	1.77	0.122187	0.259096	-5.89
252239_at	putative protein putative protein - Dros	---	AT3G49990	-1.27	-0.34	-1.77	0.122345	0.259316	-5.89
257744_at	hypothetical protein contains Pfam pro	---	AT3G29230	-1.19	-0.25	-1.77	0.122334	0.259316	-5.89
258677_at	putative ribosomal-protein S6 kinase (	PK1	AT3G08730	1.17	0.23	1.77	0.122348	0.259316	-5.89
246113_at	putative protein predicted proteins - Ar	---	---	1.13	0.18	1.77	0.122324	0.259316	-5.89
250344_at	glutaredoxin - like protein glutaredoxin	---	AT5G11930	1.31	0.39	1.77	0.122405	0.259413	-5.89
266796_at	predicted by genscan	---	AT2G02880	-1.15	-0.20	-1.77	0.122483	0.259457	-5.89
249202_at	cytochrome P450	CYP705A12	AT5G42580	-1.14	-0.18	-1.77	0.122456	0.259457	-5.89
254278_at	Expressed protein ; supported by full-l	---	AT4G22740	-1.16	-0.22	-1.77	0.122482	0.259457	-5.89
260251_at	putative heat shock protein similar to G	---	AT1G74250	1.22	0.29	1.77	0.122477	0.259457	-5.89
251687_at	quinone reductase-like protein zeta-cr	---	AT3G56460	-1.14	-0.18	-1.77	0.12246	0.259457	-5.89
266374_at	putative retroelement pol polyprotein	---	---	1.20	0.26	1.77	0.122542	0.259559	-5.89
246142_at	putative protein	---	AT5G19970	1.13	0.18	1.77	0.122559	0.259569	-5.89
246730_at	40S ribosomal protein S19 - like 40S r	---	AT5G28060	-1.29	-0.37	-1.77	0.122597	0.259578	-5.89
252008_at	hypothetical protein ; supported by cDI	---	AT3G52610	-1.16	-0.21	-1.77	0.122593	0.259578	-5.89
263241_at	arginine decarboxylase identical to GP	ADC1	AT2G16500	1.56	0.65	1.77	0.122585	0.259578	-5.89
263740_at	hypothetical protein predicted by gens	RALFL14	AT2G20660	-1.19	-0.25	-1.77	0.122619	0.259602	-5.89
262185_at	MADS box transcription factor, putativ	AGL67	AT1G77950	-1.12	-0.16	-1.76	0.122672	0.25969	-5.89
267409_at	hypothetical protein predicted by gene	---	AT2G34910	-1.12	-0.16	-1.76	0.122758	0.259822	-5.89
256359_at	protein kinase, putative contains Pfam	---	AT1G66460	1.13	0.17	1.76	0.122752	0.259822	-5.89
266105_at	putative transport protein SEC61 beta-	SEC61 BET	AT2G45070	1.22	0.28	1.76	0.122786	0.259859	-5.89

262928_at	hypothetical protein	---	AT1G65760	1.17	0.23	1.76	0.122892	0.260058	-5.89
254083_at	PROTEIN TRANSPORT PROTEIN SI	---	AT4G24920	1.23	0.30	1.76	0.122911	0.260075	-5.89
267550_at	putative protein kinase contains a prot	AP4.3A	AT2G32800	-1.40	-0.49	-1.76	0.122929	0.260087	-5.89
256866_at	unknown protein similar to alpha galac	---	AT3G26380	1.20	0.27	1.76	0.123053	0.260325	-5.89
266421_at	putative nonspecific lipid-transfer prote	LP1	AT2G38540	-1.62	-0.69	-1.76	0.123093	0.260387	-5.89
245304_at	hypothetical protein ; supported by full-	---	AT4G15630	-1.51	-0.60	-1.76	0.123185	0.260558	-5.90
259614_at	dioxygenase, putative similar to dioxy	ATGA2OX4	AT1G47990	-1.16	-0.21	-1.76	0.123224	0.260591	-5.90
247782_at	putative protein predicted RNA bindin	---	AT5G58790	-1.13	-0.17	-1.76	0.123215	0.260591	-5.90
253291_at	Expressed protein ; supported by full-l	---	AT4G33865	-1.22	-0.28	-1.76	0.123278	0.260681	-5.90
249378_at	putative protein microtubule-associate	---	AT5G40450	-1.23	-0.30	-1.76	0.123314	0.260734	-5.90
256932_at	unknown protein	---	AT3G22520	-1.14	-0.19	-1.76	0.123411	0.260915	-5.90
249968_at	putative protein predicted proteins, Ar	---	AT5G19070	-1.36	-0.44	-1.76	0.123427	0.260915	-5.90
253670_at	putative protein ; supported by full-len	---	AT4G30010	1.16	0.21	1.76	0.123434	0.260915	-5.90
264015_at	putative XAP-5 protein [Homo sapiens	XCT	AT2G21150	1.14	0.19	1.76	0.123448	0.260919	-5.90
254132_at	putative protein hypothetical protein T	ATHB22	AT4G24660	1.25	0.32	1.76	0.12352	0.261048	-5.90
256980_at	hypothetical protein contains Pfam pro	DRB3	AT3G26932	-1.21	-0.27	-1.76	0.123608	0.261209	-5.90
245910_at	putative protein ER66 - Lycopersicon	EICBP.B	AT5G09410	-1.15	-0.20	-1.76	0.123621	0.261214	-5.90
246837_at	pectin acetylesterase precursor - like	---	AT5G26670	-1.28	-0.35	-1.76	0.123735	0.261349	-5.90
258320_at	hypothetical protein predicted by gene	---	AT3G22710	-1.13	-0.18	-1.76	0.123743	0.261349	-5.90
258144_at	hypothetical protein	---	AT3G18180	-1.13	-0.17	-1.76	0.123724	0.261349	-5.90
256833_at	calmodulin-stimulated calcium-ATPas	---	AT3G22910	1.74	0.80	1.76	0.123718	0.261349	-5.90
248600_at	putative protein contains similarity to u	---	AT5G49390	-1.17	-0.23	-1.76	0.123726	0.261349	-5.90
257214_at	hypothetical protein ;supported by full-	---	AT3G15040	-1.18	-0.24	-1.76	0.123803	0.261405	-5.90
250140_at	putative protein	DRM2	AT5G14620	1.20	0.26	1.76	0.123794	0.261405	-5.90
249588_at	protein kinase - like protein Pto kinase	---	AT5G37790	-1.21	-0.28	-1.76	0.123792	0.261405	-5.90
AFFX-r2-Bs	B. subtilis /GEN=thrC /DB_XREF=gb:X	---	---	-1.37	-0.45	-1.76	0.123834	0.261446	-5.90
263337_at	hypothetical protein predicted by gens	---	---	-1.11	-0.15	-1.76	0.123881	0.261506	-5.90
252336_at	putative protein N7 protein - Medicago	---	AT3G48880	1.14	0.18	1.76	0.123886	0.261506	-5.90
256740_at	hypothetical protein predicted by gene	---	AT3G29330	-1.13	-0.17	-1.76	0.123913	0.261539	-5.90
266223_at	putative thaumatin ;supported by full-l	---	AT2G28790	-1.67	-0.74	-1.76	0.123982	0.261637	-5.90
261209_at	unknown protein ; supported by cDNA:	---	AT1G12810	1.21	0.27	1.76	0.123976	0.261637	-5.90
258487_at	unknown protein ;supported by full-ler	LBD41	AT3G02550	1.79	0.84	1.76	0.124077	0.261812	-5.90
264130_at	hypothetical protein predicted by gene	---	AT1G79160	1.19	0.25	1.76	0.124263	0.262109	-5.90
247844_at	ARR2 - like protein ARR2 protein, Ara	ARR18	AT5G58080	1.13	0.18	1.76	0.124237	0.262109	-5.90
256358_at	unknown protein	---	AT1G66470	-1.18	-0.23	-1.76	0.124263	0.262109	-5.90

253341_at	putative protein ; supported by cDNA:	---	AT4G33410	-1.16	-0.22	-1.76	0.124251	0.262109	-5.90
250429_at	putative protein TH65 protein, Arabido	---	AT5G10470	-1.15	-0.21	-1.76	0.124335	0.262225	-5.90
267473_at	hypothetical protein predicted by gene	---	AT2G02750	1.15	0.20	1.76	0.124341	0.262225	-5.90
245714_at	RNA-binding protein-like	---	AT5G04280	1.15	0.20	1.75	0.124413	0.262353	-5.91
263197_at	polyubiquitin, putative similar to polyu	---	AT1G53930	-1.17	-0.23	-1.75	0.124427	0.262358	-5.91
256834_at	cyclophilin, putative similar to cycloph	---	AT3G22920	1.13	0.18	1.75	0.124577	0.262649	-5.91
260554_at	putative zinc protease member of insu	---	AT2G41790	1.12	0.17	1.75	0.124592	0.262656	-5.91
251965_at	putative protein variety of predicted pr	---	AT3G53360	1.15	0.21	1.75	0.124618	0.262686	-5.91
248609_at	unknown protein ; supported by cDNA	---	AT5G49440	1.17	0.22	1.75	0.124651	0.262733	-5.91
264898_at	Unknown protein ; supported by full-le	---	AT1G23205	-1.25	-0.32	-1.75	0.124691	0.262792	-5.91
251042_at	eceriferum3 (CER3)	PRT6	AT5G02310	1.14	0.19	1.75	0.124722	0.262833	-5.91
246963_at	putative protein nucleoid DNA-binding	---	AT5G24820	-1.18	-0.24	-1.75	0.124818	0.263012	-5.91
250934_at	DNAJ protein - like DNAJ domain-con	---	AT5G03030	-1.25	-0.33	-1.75	0.124837	0.263027	-5.91
262687_at	PPR-repeat protein contains multiple P	---	AT1G62670	-1.12	-0.17	-1.75	0.12496	0.263262	-5.91
257086_at	hypothetical protein predicted by gene	---	AT3G20490	1.23	0.30	1.75	0.125044	0.263389	-5.91
265785_at	hypothetical protein predicted by gens	---	AT2G07290	-1.12	-0.16	-1.75	0.125035	0.263389	-5.91
250712_at	human RAN binding protein 16-like	---	AT5G06120	1.17	0.22	1.75	0.125068	0.263417	-5.91
259736_at	endo-beta-1,4-glucanase, putative sim	AtGH9C2	AT1G64390	-2.07	-1.05	-1.75	0.125085	0.263428	-5.91
246971_at	Protein phosphatase 2C-like protein p	---	AT5G24940	-1.14	-0.18	-1.75	0.125105	0.263434	-5.91
259066_at	hypothetical protein predicted by gene	---	AT3G07530	-1.21	-0.28	-1.75	0.125111	0.263434	-5.91
253766_at	putative protein ;supported by full-leng	---	AT4G28770	-1.14	-0.20	-1.75	0.125217	0.263634	-5.91
252935_at	dnaJ-like protein CAJ1 protein, Sacch	---	AT4G39150	-1.14	-0.19	-1.75	0.125244	0.263665	-5.91
266535_s_	50S ribosomal protein L27 ;supported	---	AT2G16930 /	-1.20	-0.26	-1.75	0.125321	0.263787	-5.91
249752_at	putative protein similar to unknown pro	LSU2	AT5G24660	1.19	0.25	1.75	0.125325	0.263787	-5.91
266807_at	hypothetical protein	---	AT2G29920	-1.18	-0.24	-1.75	0.125405	0.263932	-5.91
264476_at	hypothetical protein contains similarity	PGSIP2	AT1G77130	1.17	0.23	1.75	0.125565	0.264243	-5.91
256835_at	ATP sulfurylase, putative similar to AT	APS1	AT3G22890	1.32	0.41	1.75	0.125685	0.264473	-5.91
267043_at	unknown protein	---	AT2G34330	-1.17	-0.22	-1.75	0.125746	0.264576	-5.92
246740_at	putative protein	---	AT5G27810	-1.12	-0.17	-1.75	0.125808	0.264683	-5.92
245379_at	heat shock transcription factor HSF1	HSF1	AT4G17750	-1.18	-0.24	-1.75	0.125843	0.26473	-5.92
254776_at	3-hydroxyisobutyryl-coenzyme A hydr	---	AT4G13360	1.12	0.16	1.75	0.125878	0.26478	-5.92
251114_at	transcription factor GT-3a	---	AT5G01380	1.65	0.72	1.75	0.125902	0.264791	-5.92
250251_at	putative protein contains similarity to M	---	AT5G13670	-1.15	-0.20	-1.75	0.125906	0.264791	-5.92
245174_at	putative kinesin heavy chain	---	AT2G47500	-1.30	-0.38	-1.75	0.125933	0.264798	-5.92
265278_at	hypothetical protein predicted by gens	---	AT2G28330	-1.20	-0.26	-1.75	0.12593	0.264798	-5.92

250451_at	cdc2-like protein kinase cdc2-like prot	CDKC;1	AT5G10270	1.18	0.23	1.75	0.125996	0.264907	-5.92
262953_at	hypothetical protein predicted by gene	---	AT1G75670	1.28	0.35	1.75	0.126026	0.264945	-5.92
264622_at	putative vacuolar sorting protein 35	VPS35A	AT2G17790	1.17	0.22	1.75	0.126043	0.264956	-5.92
255586_at	hypothetical protein ;supported by full-	MEE49	AT4G01560	1.27	0.35	1.75	0.126064	0.264971	-5.92
252451_at	hypothetical protein	---	AT3G47100	-1.13	-0.18	-1.75	0.126085	0.264971	-5.92
264275_at	hypothetical protein predicted by gens	anac024	AT1G60350	-1.11	-0.16	-1.75	0.126074	0.264971	-5.92
245719_at	DNA gyrase subunit B - like protein	---	AT5G04110	1.14	0.19	1.74	0.126226	0.265242	-5.92
258196_at	hypothetical protein predicted by gene	---	AT3G13980	-1.53	-0.61	-1.74	0.126323	0.265422	-5.92
259702_at	putative endo-1,3-beta-glucanase sim	---	AT1G77780	-1.14	-0.18	-1.74	0.126346	0.265422	-5.92
248015_at	putative protein similar to unknown pro	---	AT5G56370	1.15	0.20	1.74	0.126341	0.265422	-5.92
249959_at	NADH:ubiquinone oxidoreductase - lik	---	AT5G18800	1.19	0.26	1.74	0.126521	0.265734	-5.92
259238_at	putative eukaryotic translation initiation	EIF3G1	AT3G11400	-1.15	-0.20	-1.74	0.126529	0.265734	-5.92
265443_at	beta-expansin ;supported by full-lengt	ATEXPB1	AT2G20750	-1.21	-0.27	-1.74	0.126507	0.265734	-5.92
263511_at	En/Spm-like transposon protein relate	---	---	1.14	0.19	1.74	0.126561	0.265775	-5.92
253531_at	putative protein tomato leucine zipper	ATEXO70G1	AT4G31540	1.14	0.19	1.74	0.126613	0.26586	-5.92
253941_at	putative protein	---	AT4G26980	-1.13	-0.18	-1.74	0.126637	0.265887	-5.92
260897_at	ER lumen protein retaining receptor id	ERD2	AT1G29330	1.15	0.20	1.74	0.126701	0.265995	-5.92
266836_at	hypothetical protein predicted by grail	---	AT2G26000	1.21	0.27	1.74	0.12685	0.266284	-5.92
258971_at	unknown protein similar to uridylyl tra	ACR6	AT3G01990	1.41	0.50	1.74	0.126909	0.266383	-5.92
251623_at	MADS transcription factor-like protein	AGL18	AT3G57390	1.12	0.17	1.74	0.126936	0.266416	-5.92
245279_at	putative protein ; supported by cDNA:	---	AT4G17270	-1.14	-0.19	-1.74	0.127033	0.266574	-5.92
252482_at	glucosyltransferase-like protein UDP-g	UGT76E11	AT3G46670	1.62	0.70	1.74	0.127034	0.266574	-5.93
258985_at	hypothetical protein similar to hypothe	---	AT3G08960	1.13	0.18	1.74	0.127174	0.266843	-5.93
264054_at	unknown protein	SVP	AT2G22540	1.17	0.23	1.74	0.127218	0.266893	-5.93
245799_at	disease resistance protein, putative si	AtRLP6	AT1G45616	-1.14	-0.19	-1.74	0.127222	0.266893	-5.93
259214_at	Expressed protein ; supported by full-l	---	AT3G09085	1.15	0.20	1.74	0.127259	0.266946	-5.93
266932_s_	putative RNA helicase	---	AT1G63250 /	1.25	0.32	1.74	0.127284	0.266975	-5.93
258838_at	unknown protein ; supported by cDNA	---	AT3G07140	-1.13	-0.18	-1.74	0.127348	0.267084	-5.93
254987_s_	hypothetical protein	---	AT4G10660 /	1.11	0.16	1.74	0.127399	0.267094	-5.93
254703_at	putative protein ; supported by full-len	---	AT4G17960	-1.22	-0.28	-1.74	0.127382	0.267094	-5.93
262233_at	hypothetical protein contains similarity	CHR18	AT1G48310	-1.14	-0.19	-1.74	0.127391	0.267094	-5.93
263116_s_	unknown protein Similar to gb|U51990	---	AT1G03140 /	-1.17	-0.23	-1.74	0.127381	0.267094	-5.93
253455_at	putative protein	---	AT4G32020	1.28	0.36	1.74	0.127418	0.267108	-5.93
254828_at	putative cell wall-plasma membrane di	AIR1	AT4G12550	1.14	0.18	1.74	0.127461	0.267173	-5.93
260600_at	hypothetical protein predicted by gene	---	AT1G55950	1.16	0.21	1.74	0.127496	0.267222	-5.93

261917_at	hypothetical protein similar to TMV res	---	AT1G65920	-1.35	-0.43	-1.74	0.127523	0.267254	-5.93
257614_at	putative non-LTR retroelement reverse	---	---	-1.17	-0.23	-1.74	0.127559	0.267306	-5.93
246916_at	disease resistance protein - like disea	AtRLP52	AT5G25910	1.12	0.17	1.74	0.127645	0.26746	-5.93
246486_at	putative protein ;supported by full-leng	---	AT5G15910	-1.15	-0.20	-1.74	0.12768	0.267509	-5.93
251713_at	putative protein several hypothetical pr	---	AT3G56080	1.20	0.26	1.74	0.127759	0.267626	-5.93
261477_at	unknown protein	---	AT1G14310	-1.19	-0.26	-1.74	0.12775	0.267626	-5.93
248859_at	putative protein contains similarity to C	---	AT5G46660	-1.17	-0.22	-1.74	0.127805	0.267698	-5.93
261386_at	unknown protein ;supported by full-len	---	AT1G05430	-1.17	-0.23	-1.74	0.127822	0.267708	-5.93
259234_at	unknown protein similar to unknown pr	---	AT3G11620	-1.16	-0.21	-1.74	0.127835	0.267711	-5.93
261856_at	hypothetical protein	---	AT1G50530	-1.17	-0.23	-1.74	0.127874	0.267769	-5.93
264835_at	unknown protein similar to unknown pr	---	AT1G03550	1.11	0.15	1.74	0.127912	0.267824	-5.93
248286_at	putative protein similar to unknown pro	---	AT5G52870	1.38	0.46	1.74	0.12797	0.267921	-5.93
259517_at	hypothetical protein ; supported by cDI	CAT1	AT1G20630	1.24	0.31	1.74	0.12804	0.268034	-5.93
266499_at	hypothetical protein predicted by gens	---	---	1.21	0.27	1.73	0.128048	0.268034	-5.93
256513_at	unknown protein similar to phospholipa	SGR2	AT1G31480	1.14	0.19	1.73	0.128121	0.268121	-5.93
250231_at	AP2/EREBP-like transcription factor LE	LEP	AT5G13910	-1.13	-0.18	-1.73	0.12812	0.268121	-5.93
253568_at	putative protein receptor-like kinase, F	---	AT4G31230	1.15	0.20	1.73	0.128124	0.268121	-5.93
264750_at	hypothetical protein predicted by gens	---	AT1G22870	1.13	0.17	1.73	0.128188	0.268229	-5.93
267357_at	putative nematode-resistance protein	HSPRO2	AT2G40000	1.42	0.51	1.73	0.128281	0.268399	-5.93
256269_at	transcription factor HBP-1B-like nearly	TGA6	AT3G12250	1.13	0.18	1.73	0.128303	0.26842	-5.93
265392_at	lipoic acid synthase (LIP1) ; supported	LIP1	AT2G20860	-1.13	-0.18	-1.73	0.128365	0.268526	-5.93
266637_at	hypothetical protein ;supported by full-	BRXL1	AT2G35600	-1.25	-0.32	-1.73	0.128562	0.268913	-5.94
257620_at	hypothetical protein predicted by gene	---	AT3G24850	-1.17	-0.22	-1.73	0.12859	0.268946	-5.94
249418_at	putative protein predicted protein, Ara	---	AT5G39785	1.12	0.17	1.73	0.128605	0.268954	-5.94
250846_at	sulphite reductase ; supported by cDN	SIR	AT5G04590	1.30	0.38	1.73	0.128664	0.269052	-5.94
266695_at	putative CCCH-type zinc finger protein	---	AT2G19810	-1.39	-0.48	-1.73	0.128676	0.269053	-5.94
258772_at	putative ubiquinol-cytochrome C reduc	---	AT3G10860	1.18	0.24	1.73	0.128704	0.269087	-5.94
266121_at	unknown protein ; supported by cDNA	---	AT2G02160	1.20	0.26	1.73	0.12877	0.269199	-5.94
266528_at	putative disease resistance protein	---	AT2G16870	1.12	0.16	1.73	0.128811	0.269261	-5.94
267011_at	unknown protein	---	AT2G39230	1.20	0.27	1.73	0.128838	0.269293	-5.94
257599_at	60S ribosomal protein, putative simila	---	AT3G24830	-1.35	-0.44	-1.73	0.12893	0.269447	-5.94
263945_at	hypothetical protein predicted by gene	---	AT2G36030	1.20	0.26	1.73	0.128935	0.269447	-5.94
256402_at	hypothetical protein ; supported by cD	---	AT3G06130	-1.34	-0.42	-1.73	0.129026	0.269611	-5.94
261305_at	glutamine synthetase, putative similar	GLN1;5	AT1G48470	-1.12	-0.16	-1.73	0.129037	0.269611	-5.94
251469_at	putative protein strictosidine synthase	---	AT3G59530	-1.13	-0.18	-1.73	0.129061	0.269611	-5.94

249764_at	septum site-determining MinD (dbj|BA/	MIND	AT5G24020	-1.19	-0.25	-1.73	0.129061	0.269611	-5.94
253887_at	putative protein isp4 protein, Schizosa	OPT6	AT4G27730	-1.39	-0.48	-1.73	0.12914	0.269752	-5.94
245476_at	hypothetical protein	---	AT4G16090	1.15	0.21	1.73	0.129172	0.269792	-5.94
253445_at	putative protein pAFD103 mRNA, Mal	---	AT4G32605 /	1.17	0.22	1.73	0.129205	0.269837	-5.94
253494_at	putative protein	---	AT4G31830	-1.15	-0.20	-1.73	0.129239	0.269883	-5.94
245596_at	hypothetical protein	AtPRD1	AT4G14180	-1.15	-0.20	-1.73	0.129305	0.269996	-5.94
260656_at	hypothetical protein predicted by gene	---	AT1G19380	-1.69	-0.76	-1.73	0.129322	0.270007	-5.94
264665_at	unknown protein ESTs gb|H37208,gb	---	AT1G09660	-1.18	-0.24	-1.73	0.129383	0.27011	-5.94
264001_at	putative peroxidase ;supported by full-	---	AT2G22420	-1.31	-0.39	-1.73	0.12944	0.270204	-5.94
267328_at	putative receptor-like protein kinase	---	AT2G19230	-1.17	-0.23	-1.73	0.129481	0.270265	-5.94
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.41	-0.50	-1.73	0.129611	0.270511	-5.94
262625_at	hypothetical protein predicted by gene	---	AT1G06440	1.12	0.17	1.73	0.129647	0.270563	-5.94
263633_at	putative SCARECROW gene regulator	SCL21	AT2G04890	-1.18	-0.24	-1.73	0.12966	0.270565	-5.94
260818_at	unknown protein	---	AT1G06890	-1.11	-0.16	-1.73	0.129704	0.270632	-5.94
262508_at	serine/threonine kinase, putative simil	---	AT1G11300	-1.38	-0.47	-1.73	0.129742	0.270687	-5.95
256333_at	Sm-like protein contains Pfam profile: I	---	AT1G76860	1.25	0.32	1.73	0.129783	0.270708	-5.95
246918_at	putative protein hypothetical protein F	---	AT5G25340	-1.19	-0.25	-1.73	0.1298	0.270708	-5.95
246287_at	unknown protein	---	AT1G31870	1.15	0.20	1.73	0.129795	0.270708	-5.95
267323_at	unknown protein	---	AT2G19340	-1.15	-0.20	-1.73	0.129766	0.270708	-5.95
262563_at	somatic embryogenesis receptor-like I	SERK2	AT1G34210	1.19	0.25	1.73	0.129821	0.270728	-5.95
260458_at	unknown protein	---	AT1G68250	-1.14	-0.19	-1.73	0.129855	0.270774	-5.95
259313_at	hypothetical protein predicted by gens	---	AT3G05090	1.17	0.23	1.73	0.129883	0.270791	-5.95
252175_at	zinc finger protein zinc finger protein I	AtIDD2	AT3G50700	-1.12	-0.16	-1.73	0.129891	0.270791	-5.95
267417_at	putative RING zinc finger protein	---	AT2G34990	1.13	0.17	1.73	0.129899	0.270791	-5.95
258832_at	putative protein kinase similar to APK1	---	AT3G07070	-1.16	-0.21	-1.72	0.12999	0.270931	-5.95
266212_at	putative retroelement pol polyprotein	---	---	-1.19	-0.25	-1.72	0.129989	0.270931	-5.95
261904_at	unknown protein contains similarity to	---	AT1G65040	1.12	0.16	1.72	0.130014	0.270931	-5.95
263837_at	unknown protein	---	AT2G04500	-1.11	-0.15	-1.72	0.130013	0.270931	-5.95
246860_at	putative protein various predicted prot	---	AT5G25840	-1.45	-0.54	-1.72	0.130114	0.271116	-5.95
251319_at	putative protein POSSIBLE APOSPO	---	AT3G61610	-1.22	-0.28	-1.72	0.130136	0.271137	-5.95
267476_at	putative pectate lyase	---	AT2G02720	1.14	0.19	1.72	0.13018	0.271203	-5.95
259341_at	unknown protein similar to hypothetica	ATBPM4	AT3G03740	1.13	0.18	1.72	0.130194	0.271207	-5.95
260907_at	hypothetical protein predicted by gens	---	AT1G02570	-1.13	-0.18	-1.72	0.130207	0.271211	-5.95
258786_at	putative syntaxin contains Pfam profile	SYP121	AT3G11820	1.36	0.45	1.72	0.130235	0.271219	-5.95
259049_at	unknown protein	---	AT3G03370	-1.19	-0.25	-1.72	0.13023	0.271219	-5.95

253400_at	putative protein unknown protein T02(	---	AT4G32860	1.13	0.17	1.72	0.130271	0.271269	-5.95
248937_at	putative protein contains similarity to u	AtRLP55	AT5G45770	1.22	0.29	1.72	0.130338	0.271384	-5.95
248147_at	putative protein contains similarity to p	ATRBP45A	AT5G54900	1.15	0.20	1.72	0.130441	0.271548	-5.95
257406_at	hypothetical protein predicted by gene	---	AT1G27060	-1.19	-0.25	-1.72	0.130431	0.271548	-5.95
254661_at	unknown protein multidrug resistance	---	AT4G18260	-1.16	-0.21	-1.72	0.130464	0.271571	-5.95
246372_at	hypothetical protein predicted by gene	---	AT1G51900	1.14	0.19	1.72	0.130496	0.271613	-5.95
253676_at	cytidine deaminase - like protein cytid	---	AT4G29570	-1.18	-0.24	-1.72	0.130556	0.271713	-5.95
256994_s_	limonene cyclase, putative similar to li	ATTPS-CIN	AT3G25820 /	-1.14	-0.19	-1.72	0.13059	0.27176	-5.95
247457_at	putative protein various predicted prot	---	AT5G62170	1.13	0.18	1.72	0.13063	0.271819	-5.95
261490_at	tumor suppressor, putative similar to t	SAC52	AT1G14320	1.21	0.27	1.72	0.130657	0.271829	-5.95
249243_s_	beta-glucosidase	BGLU13	AT5G42260 /	-1.13	-0.17	-1.72	0.130659	0.271829	-5.95
248863_at	zinc finger protein Glo3-like	AGD9	AT5G46750	-1.13	-0.17	-1.72	0.13068	0.271848	-5.95
258510_at	hypothetical protein predicted by gene	---	AT3G06600	-1.16	-0.22	-1.72	0.13072	0.271904	-5.95
250783_at	cytochrome P450 ; supported by cDN	CYP79A2	AT5G05260	1.17	0.22	1.72	0.130731	0.271904	-5.95
260363_at	unknown protein similar to hypothetica	---	AT1G70550	-1.19	-0.25	-1.72	0.130771	0.271962	-5.95
258538_at	putative tRNA pseudouridine synthase	---	AT3G06950	-1.14	-0.18	-1.72	0.130935	0.272264	-5.95
255471_at	putative oxidoreductase similar to A. t	AOP3	AT4G03050	-1.15	-0.20	-1.72	0.130952	0.272264	-5.95
264182_at	MADS-box protein, putative similar to	AGL23	AT1G65360	-1.13	-0.18	-1.72	0.130945	0.272264	-5.95
259321_at	unknown protein	GAUT13	AT3G01040	-1.20	-0.27	-1.72	0.13107	0.272471	-5.95
247220_at	cdc2-like protein kinase ; supported b	CDKC2	AT5G64960	1.15	0.20	1.72	0.131075	0.272471	-5.95
254088_at	putative protein snurportin1 m3G-cap-	---	AT4G24880	1.21	0.28	1.72	0.131105	0.272501	-5.95
262253_s_	unknown protein contains similarity to	---	AT1G53880 /	1.16	0.22	1.72	0.131113	0.272501	-5.96
250152_at	putative protein predicted proteins, Ar	---	AT5G15120	-1.13	-0.18	-1.72	0.131133	0.272516	-5.96
257059_at	unknown protein ; supported by cDNA	---	AT3G15280	-1.13	-0.18	-1.72	0.13116	0.272548	-5.96
250968_at	putative protein ;supported by full-leng	---	AT5G02890	-1.38	-0.46	-1.72	0.131207	0.272622	-5.96
257115_at	kinesin-like protein contains Pfam prof	---	AT3G20150	-1.15	-0.20	-1.72	0.131233	0.272641	-5.96
262217_at	hypothetical protein predicted by gene	---	AT1G74770	-1.11	-0.15	-1.72	0.13124	0.272641	-5.96
249318_at	uridine kinase-like protein	AtUK/UPRT	AT5G40870	-1.15	-0.20	-1.72	0.131287	0.272712	-5.96
251185_at	60S RIBOSOMAL PROTEIN L7A prot	---	AT3G62870	-1.20	-0.26	-1.72	0.131328	0.272773	-5.96
266015_at	putative carbonyl reductase	---	AT2G24190	-1.17	-0.22	-1.72	0.131408	0.272915	-5.96
250685_at	kinesin heavy chain-like protein	---	AT5G06670	-1.11	-0.15	-1.72	0.131483	0.273046	-5.96
265508_at	hypothetical protein predicted by gens	---	AT2G15930	1.12	0.16	1.72	0.131508	0.273072	-5.96
251564_at	myosin heavy chain MYA3	XIJ	AT3G58160	-1.16	-0.21	-1.72	0.131532	0.273096	-5.96
259985_at	unknown protein ; supported by cDNA	---	AT1G76620	-1.14	-0.19	-1.72	0.131554	0.273117	-5.96
259468_at	unknown protein	TTN10	AT1G19080 /	1.17	0.23	1.72	0.131588	0.273163	-5.96

259949_at	hypothetical protein predicted by gens	---	AT1G71420	1.16	0.21	1.72	0.131627	0.273195	-5.96
254324_at	putative protein various predicted prot	---	AT4G22640	-1.19	-0.25	-1.72	0.131621	0.273195	-5.96
266265_at	putative tropinone reductase ; support	---	AT2G29340	1.25	0.32	1.72	0.131661	0.273241	-5.96
247366_at	putative protein contains similarity to z	---	AT5G63260	-1.18	-0.24	-1.72	0.131708	0.273311	-5.96
264888_at	hypothetical protein	---	AT1G23070	-1.15	-0.20	-1.72	0.131731	0.273311	-5.96
248572_at	unknown protein	---	AT5G49800	-1.15	-0.20	-1.72	0.131723	0.273311	-5.96
245507_at	hypothetical protein	---	AT4G15710	-1.20	-0.26	-1.71	0.131783	0.273395	-5.96
248514_s_	unknown protein	---	AT5G50510 /	-1.13	-0.17	-1.71	0.131817	0.273423	-5.96
257957_at	wall-associated serine/threonine kinas	---	AT3G25490	1.22	0.28	1.71	0.131821	0.273423	-5.96
251332_at	putative protein putative protein At2g4	---	AT3G61670	1.22	0.29	1.71	0.131841	0.273441	-5.96
251331_s_	tubulin gamma-1 chain	TUBG1	AT3G61650 /	-1.41	-0.50	-1.71	0.131877	0.273489	-5.96
245618_at	hypothetical protein	---	AT4G14510	1.18	0.23	1.71	0.131948	0.273609	-5.96
264552_at	hypothetical protein predicted by gens	---	AT1G09470	-1.24	-0.31	-1.71	0.131959	0.273609	-5.96
262755_at	unknown protein	---	AT1G16360	-1.15	-0.20	-1.71	0.131983	0.273634	-5.96
247016_at	putative protein contains similarity to s	---	AT5G66970	1.16	0.21	1.71	0.132011	0.273668	-5.96
260525_at	putative pre-mRNA splicing factor RNA	---	AT2G47250	-1.13	-0.18	-1.71	0.132026	0.273674	-5.96
256036_at	fructose-2,6-bisphosphatase, putative	F2KP	AT1G07110	-1.15	-0.20	-1.71	0.132086	0.273775	-5.96
258883_at	unknown protein predicted by genscar	---	AT3G09970	1.16	0.22	1.71	0.132171	0.273926	-5.96
250299_at	putative esterase - like protein cinl pro	---	AT5G11910	1.15	0.20	1.71	0.132263	0.274091	-5.96
245938_at	putative protein protein phosphatase-	---	AT5G19680	1.20	0.27	1.71	0.132301	0.274142	-5.96
251897_at	RING finger - like protein DNA-binding	---	AT3G54360	1.18	0.24	1.71	0.132312	0.274142	-5.96
257681_at	hypothetical protein predicted by gene	---	AT3G13370	-1.11	-0.16	-1.71	0.132405	0.27431	-5.96
253104_at	thaumatin-like protein thaumatin-like p	---	AT4G36010	1.61	0.69	1.71	0.132424	0.274325	-5.96
247089_at	dimethyladenosine transferase-like pro	---	AT5G66360	1.17	0.22	1.71	0.132447	0.274347	-5.96
267422_at	putative protein kinase contains a prot	---	AT2G35050	-1.12	-0.17	-1.71	0.132477	0.274385	-5.96
251724_at	putative protein	---	AT3G56250	-1.15	-0.20	-1.71	0.132537	0.274484	-5.97
250381_at	putative protein various predicted prot	---	AT5G11610	1.29	0.37	1.71	0.132606	0.274603	-5.97
248816_at	prematurely terminated mRNA decay f	LBA1	AT5G47010	1.13	0.18	1.71	0.132664	0.274673	-5.97
264765_at	receptor kinase, putative similar to rec	---	AT1G61430	1.16	0.22	1.71	0.132658	0.274673	-5.97
250887_at	putative protein	---	---	-1.16	-0.21	-1.71	0.13271	0.274742	-5.97
253477_at	L-ascorbate peroxidase - like protein v	APX6	AT4G32320	1.29	0.36	1.71	0.132783	0.274845	-5.97
260240_at	putative tRNA isopentenyl transferase	ATIPT1	AT1G68460	-1.13	-0.17	-1.71	0.132781	0.274845	-5.97
265639_at	putative reverse transcriptase	---	---	1.14	0.19	1.71	0.132804	0.274862	-5.97
246382_at	hypothetical protein	---	---	-1.17	-0.23	-1.71	0.132854	0.27494	-5.97
256045_at	MAP3K gamma protein kinase, putati	MAPKKK13	AT1G07150	1.16	0.22	1.71	0.132884	0.274953	-5.97

255053_at	putative protein RNA helicase -Mus m	---	AT4G09730	-1.41	-0.49	-1.71	0.13288	0.274953	-5.97
248464_at	putative protein similar to unknown pro	---	AT5G51160	1.21	0.27	1.71	0.132977	0.27512	-5.97
246021_at	ascorbate oxidase-like protein ascorb	---	AT5G21100	1.25	0.32	1.71	0.13301	0.275125	-5.97
246038_s_	putative protein thiamin pyrophosphok	atnudt20	AT5G19460 /	-1.20	-0.27	-1.71	0.133027	0.275125	-5.97
250874_at	putative protein	---	AT5G04010	-1.16	-0.22	-1.71	0.133028	0.275125	-5.97
259335_s_	unknown protein similar to unknown pr	---	AT3G03930 /	-1.19	-0.25	-1.71	0.133013	0.275125	-5.97
264345_at	Expressed protein ; supported by cDN	---	AT1G11915	1.19	0.25	1.71	0.133142	0.275338	-5.97
246529_at	serine/threonine-specific protein kinase	---	AT5G15730	1.36	0.45	1.71	0.133179	0.275388	-5.97
265951_at	hypothetical protein predicted by gene	OFP7	AT2G18500	-1.25	-0.33	-1.71	0.133228	0.275465	-5.97
255377_at	hypothetical protein	---	AT4G03500	1.17	0.22	1.71	0.133312	0.275614	-5.97
257221_at	MYB family transcription factor (GL1)	ATMYB0	AT3G27920	-1.19	-0.26	-1.71	0.133333	0.275618	-5.97
265994_at	putative multispanning membrane prot	---	AT2G24170	-1.34	-0.43	-1.71	0.133338	0.275618	-5.97
260164_at	putative D-isomer specific 2-hydroxyac	---	AT1G79870	-1.14	-0.19	-1.71	0.133393	0.275706	-5.97
265322_at	hypothetical protein predicted by gens	---	AT2G18270	-1.12	-0.16	-1.71	0.133456	0.275812	-5.97
262292_at	hypothetical protein similar to hypothet	---	AT1G27595	1.16	0.21	1.71	0.133504	0.275886	-5.97
254123_at	Bnm1 like protein pollen-specific prote	APPB1	AT4G24640	-1.15	-0.20	-1.71	0.133561	0.275978	-5.97
249368_at	putative protein predicted proteins, Ar	---	AT5G40640	1.20	0.26	1.71	0.133604	0.276042	-5.97
254326_at	putative protein AIR1, Arabidopsis tha	---	AT4G22610	-1.15	-0.21	-1.71	0.13364	0.276067	-5.97
258454_at	putative 40S ribosomal protein S10 sin	RPS10	AT3G22300	-1.21	-0.28	-1.71	0.133639	0.276067	-5.97
265811_at	unknown protein possibly related to thy	EDA2	AT2G18080	1.14	0.19	1.70	0.133695	0.276156	-5.97
247680_s_	glycine-rich protein - like glycine-rich p	---	AT1G61210 /	-1.15	-0.20	-1.70	0.13373	0.276203	-5.97
251106_at	putative protein peroxisomal Ca-depe	---	AT5G01500	1.61	0.69	1.70	0.133764	0.276249	-5.97
250418_at	putative protein predicted proteins, Ho	---	AT5G11240	1.31	0.39	1.70	0.133821	0.276341	-5.97
252709_at	putative protein predicted proteins, Ar	---	AT3G43840	-1.11	-0.15	-1.70	0.133879	0.27641	-5.97
256213_at	protein kinase, putative contains Pfam	---	AT1G50990	1.16	0.21	1.70	0.133869	0.27641	-5.97
249482_at	putative protein ;supported by full-leng	---	AT5G38980	1.38	0.47	1.70	0.133924	0.276478	-5.98
255345_at	putative aspartic protease ; supported	---	AT4G04460	1.64	0.71	1.70	0.13395	0.276506	-5.98
249924_at	kinase associated protein phosphatase	KAPP	AT5G19280	1.18	0.24	1.70	0.134011	0.276588	-5.98
264038_at	putative ubiquinone biosynthesis prote	---	AT2G03690	-1.19	-0.25	-1.70	0.134014	0.276588	-5.98
254933_at	putative RNA-directed RNA polymera	RDR2	AT4G11130	-1.18	-0.24	-1.70	0.134133	0.276778	-5.98
246168_at	meristem protein - like reproductive m	---	AT5G32460	1.23	0.30	1.70	0.134142	0.276778	-5.98
245969_at	putative protein nuclear gene for chlor	---	AT5G19830	-1.28	-0.35	-1.70	0.134139	0.276778	-5.98
264576_at	unknown protein Similar to Arabidopsis	---	AT1G05360	1.14	0.19	1.70	0.134229	0.276932	-5.98
246169_at	putative protein predicted protein, Hae	---	AT5G32470	-1.16	-0.21	-1.70	0.134267	0.276935	-5.98
256364_at	wrky-type DNA binding protein, putati	WRKY67	AT1G66550	1.16	0.22	1.70	0.134256	0.276935	-5.98

249557_at	receptor serine/threonine kinase PR5K	PR5K	AT5G38280	1.28	0.36	1.70	0.134246	0.276935	-5.98
256063_at	Expressed protein ; supported by full-le	STN1	AT1G07130	1.16	0.21	1.70	0.134298	0.276974	-5.98
251583_at	putative protein several hypothetical pr	---	AT3G58590	1.22	0.29	1.70	0.134455	0.277188	-5.98
246632_at	hypothetical protein similar to putative	---	AT1G29710	1.15	0.21	1.70	0.134435	0.277188	-5.98
260463_at	DNA helicase isolog	RECQ4A	AT1G10930	-1.12	-0.16	-1.70	0.13444	0.277188	-5.98
260937_at	hypothetical protein contains similarity	---	AT1G45160	1.12	0.16	1.70	0.134462	0.277188	-5.98
261831_at	ADP-ribosylation factor, putative simil	ATARFA1F	AT1G10630	-1.22	-0.28	-1.70	0.134462	0.277188	-5.98
250681_at	unknown protein	---	AT5G06590	-1.12	-0.17	-1.70	0.134489	0.277217	-5.98
245508_at	hypothetical protein	---	AT4G15720	-1.12	-0.16	-1.70	0.134506	0.277228	-5.98
256987_at	hypothetical protein predicted by gene	---	AT3G28560	-1.13	-0.18	-1.70	0.134537	0.277266	-5.98
255515_at	putative pistil-specific protein similar t	---	AT4G02250	-1.13	-0.17	-1.70	0.134561	0.277292	-5.98
256054_at	unknown protein	---	AT1G07120	-1.11	-0.15	-1.70	0.134576	0.277296	-5.98
257528_at	hypothetical protein predicted by gene	---	AT3G02125	-1.13	-0.18	-1.70	0.134618	0.277358	-5.98
253419_at	putative protein predicted proteins, Ar	---	AT4G32780	-1.17	-0.22	-1.70	0.134637	0.277372	-5.98
253566_at	DNA topoisomerase like- protein Bacill	---	AT4G31210	1.46	0.54	1.70	0.134662	0.277398	-5.98
262115_at	Expressed protein ; supported by full-le	---	AT1G02813	-1.14	-0.20	-1.70	0.134912	0.277864	-5.98
251591_at	carboxyl terminal protease - like prote	---	AT3G57680	1.28	0.36	1.70	0.134909	0.277864	-5.98
256681_at	unknown protein ; supported by cDNA	SPP2	AT3G52340	-1.51	-0.59	-1.70	0.134943	0.277902	-5.98
256783_at	casein kinase, putative similar to case	---	AT3G13670	1.12	0.16	1.70	0.134965	0.277913	-5.98
260475_at	Serine carboxypeptidase isolog	scpl31	AT1G11080	1.33	0.42	1.70	0.134973	0.277913	-5.98
267396_at	hypothetical protein predicted by grail a	---	AT2G44270	1.18	0.24	1.70	0.134995	0.277934	-5.98
253005_at	hypothetical protein ;supported by full-	---	AT4G38100	1.24	0.31	1.70	0.135046	0.277989	-5.98
262136_at	auxin response factor, putative similar	ARF17	AT1G77850	-1.13	-0.18	-1.70	0.135044	0.277989	-5.98
262464_at	hypothetical protein contains similarity	---	AT1G50280	-1.28	-0.35	-1.70	0.135101	0.278077	-5.98
257843_at	hypothetical protein predicted by gene	---	---	-1.12	-0.17	-1.70	0.13512	0.278091	-5.98
259125_at	unknown protein Pfam HMM hit: Regu	---	AT3G02300	-1.12	-0.17	-1.70	0.135187	0.278203	-5.98
254824_s_	origin recognition complex subunit 1 -	ORC1B	AT4G12620 /	-1.21	-0.27	-1.70	0.135407	0.278632	-5.99
267557_at	unknown protein ; supported by cDNA	KRP4	AT2G32710	1.19	0.25	1.70	0.135441	0.278677	-5.99
254147_at	putative protein similarity Human mRN	---	AT4G24270	1.25	0.32	1.70	0.135495	0.278763	-5.99
246010_at	putative protein predicted proteins, Ar	---	AT5G08440	1.12	0.16	1.70	0.135558	0.278867	-5.99
263712_at	Expressed protein ; supported by full-le	NFD6	AT2G20585	1.22	0.29	1.70	0.135572	0.278871	-5.99
265619_at	hypothetical protein	---	AT2G27320	1.19	0.25	1.69	0.135775	0.279263	-5.99
255925_at	unknown protein ;supported by full-len	---	AT1G22200	1.19	0.25	1.69	0.135793	0.279275	-5.99
246243_at	trichohyalin like protein	---	AT4G36520	1.12	0.16	1.69	0.135869	0.279382	-5.99
257738_at	40S ribosomal subunit protein S21, pu	---	AT3G27450	-1.12	-0.16	-1.69	0.135858	0.279382	-5.99

247891_at	GTP binding protein-like	---	AT5G57960	-1.14	-0.19	-1.69	0.135884	0.279387	-5.99
250000_at	putative protein PGPD14 - Petunia x h	---	AT5G18650	-1.20	-0.27	-1.69	0.135905	0.279404	-5.99
264890_at	unknown protein	---	AT1G23180	-1.21	-0.27	-1.69	0.135953	0.279478	-5.99
258761_at	unknown protein	---	AT3G10760	-1.23	-0.30	-1.69	0.136007	0.279563	-5.99
257641_s_	hypothetical protein	AOC1	AT3G25760 /	-1.30	-0.38	-1.69	0.136023	0.279571	-5.99
245697_at	latex-abundant protein - like ;supporte	AtMC9	AT5G04200	1.85	0.89	1.69	0.136059	0.279621	-5.99
254946_at	putative protein proline-rich protein, B	---	AT4G10950	-1.14	-0.19	-1.69	0.136108	0.279684	-5.99
245829_at	hypothetical protein predicted by gene	---	AT1G57780	-1.15	-0.20	-1.69	0.136114	0.279684	-5.99
246727_at	major latex protein homolog - like maj	---	AT5G28010	-1.20	-0.26	-1.69	0.136206	0.279802	-5.99
254423_at	Lsd1 like protein zinc-finger protein Ls	LOL2	AT4G21610	1.19	0.26	1.69	0.136209	0.279802	-5.99
255905_at	tonoplast intrinsic protein, putative sim	BETA-TIP	AT1G17810	-1.27	-0.34	-1.69	0.136205	0.279802	-5.99
262715_at	putative myb-related transcription facto	MYB58	AT1G16490	-1.11	-0.15	-1.69	0.136256	0.279851	-5.99
262502_at	unknown protein similar to hypothetica	PTAC6	AT1G21600	-1.14	-0.19	-1.69	0.136257	0.279851	-5.99
266389_s_	unknown protein	---	AT2G31580 /	1.13	0.17	1.69	0.136272	0.279856	-5.99
251378_at	putative protein	---	AT3G60660	-1.14	-0.19	-1.69	0.136355	0.280002	-5.99
267627_at	putative ATP-dependent RNA helicase	---	AT2G42270	1.29	0.37	1.69	0.136421	0.280112	-5.99
254407_at	receptor kinase - like protein receptor-	---	AT4G21370	1.15	0.20	1.69	0.136474	0.280196	-5.99
252218_at	putative protein some putative proteins	---	AT3G50150	1.14	0.18	1.69	0.136595	0.280419	-5.99
260291_at	putative protein kinase similar to MAP3	YDA	AT1G63700	-1.11	-0.15	-1.69	0.136831	0.280878	-6.00
246119_at	ankyrin-repeat protein patsas protein -	TIP1	AT5G20350	1.17	0.23	1.69	0.136966	0.28113	-6.00
249967_at	putative protein	---	AT5G19050	1.15	0.20	1.69	0.136994	0.281136	-6.00
253907_at	putative protein dihydrokaempferol 4-r	---	AT4G27250	1.20	0.26	1.69	0.136985	0.281136	-6.00
251509_at	pectinesterase precursor-like protein p	---	AT3G59010	-1.46	-0.54	-1.69	0.137034	0.281192	-6.00
262282_at	hypothetical protein predicted by gens	---	AT1G68610	1.17	0.22	1.69	0.137061	0.281224	-6.00
250676_at	harpin-induced protein-like ; supporte	NHL3	AT5G06320	1.26	0.33	1.69	0.137168	0.281417	-6.00
246195_at	E2, ubiquitin-conjugating enzyme 17 (	UBC17	AT4G36410	-1.73	-0.79	-1.69	0.137224	0.281507	-6.00
252091_at	putative protein NADH dehydrogenas	---	AT3G51390	-1.12	-0.17	-1.69	0.137301	0.28164	-6.00
247975_at	putative protein similar to unknown pro	---	AT5G56800	-1.12	-0.16	-1.69	0.137321	0.281655	-6.00
262919_at	unknown protein ; supported by cDNA	---	AT1G79380	1.20	0.27	1.69	0.137381	0.28174	-6.00
263919_at	unknown protein ;supported by full-ler	---	AT2G36470	-1.55	-0.64	-1.69	0.137387	0.28174	-6.00
245625_at	transport protein	---	AT4G14160	1.14	0.19	1.69	0.137523	0.281994	-6.00
247477_at	putative protein 21K protein precursor	---	AT5G62340	-1.21	-0.27	-1.69	0.137577	0.28208	-6.00
259347_at	putative GAR1 protein similar to GB:P2	---	AT3G03920	-1.14	-0.18	-1.68	0.137683	0.282247	-6.00
258807_at	transfactor-like similar to transfactor G	---	AT3G04030	1.26	0.33	1.68	0.137683	0.282247	-6.00
264005_at	unknown protein ; supported by cDNA	AGP2	AT2G22470	2.11	1.07	1.68	0.137716	0.282288	-6.00

260126_at	putative hydroxymethyltransferase sim	SHM7	AT1G36370	-1.24	-0.31	-1.68	0.137777	0.282388	-6.00
259036_at	putative laccase similar to laccase GB	LAC7	AT3G09220	1.12	0.17	1.68	0.137804	0.282418	-6.00
247653_at	transcriptional coactivator - like protei	---	AT5G59950	1.13	0.17	1.68	0.137823	0.282432	-6.00
258052_at	putative hydrolase predicted by genem	---	AT3G16190	1.16	0.22	1.68	0.137863	0.282488	-6.00
258591_at	hypothetical protein ; supported by ful	---	AT3G04360	1.13	0.18	1.68	0.13792	0.282579	-6.00
252813_at	putative protein several hypothetical pr	---	---	1.13	0.18	1.68	0.137943	0.282586	-6.00
252814_at	putative protein several hypothetical pr	---	---	1.15	0.20	1.68	0.137948	0.282586	-6.00
246907_at	AtBgamma - like protein B' regulatory	---	AT5G25510	-1.18	-0.23	-1.68	0.137974	0.282615	-6.00
254888_at	putative protein predicted protein, Ara	---	AT4G11780	-1.14	-0.19	-1.68	0.138009	0.282646	-6.00
263474_at	hypothetical protein predicted by gens	---	AT2G31725	-1.19	-0.25	-1.68	0.138014	0.282646	-6.00
266985_at	putative geranylgeranyl transferase typ	PGGT-I	AT2G39550	1.17	0.23	1.68	0.138032	0.282656	-6.00
260873_at	hypothetical protein predicted by gens	---	AT1G21580	1.12	0.16	1.68	0.138055	0.282677	-6.00
252789_s_	hypothetical protein ; supported by ful	---	AT1G21930 /	-1.12	-0.17	-1.68	0.138082	0.282709	-6.00
263276_at	putative cytochrome P450	CYP705A13	AT2G14100	1.14	0.19	1.68	0.138097	0.282714	-6.00
267580_at	unknown protein	---	AT2G41990	-1.17	-0.23	-1.68	0.138153	0.282803	-6.00
250202_at	putative protein similar to unknown pro	---	AT5G13970	-1.16	-0.22	-1.68	0.138187	0.282848	-6.00
252533_at	putative protein predicted proteins, Ar	---	AT3G46110	1.47	0.55	1.68	0.138308	0.283069	-6.01
248784_at	putative protein similar to unknown pro	---	AT5G47380	-1.23	-0.29	-1.68	0.138419	0.283221	-6.01
264303_s_	E2, ubiquitin-conjugating enzyme, put	UBC35	AT1G16890 /	1.14	0.19	1.68	0.138397	0.283221	-6.01
264683_at	unknown protein similar to putative ino	FRA3	AT1G65580	1.12	0.16	1.68	0.138413	0.283221	-6.01
265838_at	putative spliceosome associated prote	---	AT2G14550	-1.13	-0.17	-1.68	0.138488	0.283336	-6.01
246652_at	extensin -like protein extensin, soybea	---	AT5G35190	-1.13	-0.18	-1.68	0.13852	0.283376	-6.01
265023_at	unknown protein weak similarity to C3I	---	AT1G24440	1.20	0.26	1.68	0.138599	0.283511	-6.01
248731_at	phosphoribosylanthranilate transferase	---	AT5G48060	-1.16	-0.22	-1.68	0.138685	0.283663	-6.01
245490_at	hypothetical protein	LDL3	AT4G16310	1.16	0.22	1.68	0.138734	0.283736	-6.01
251437_at	putative protein hypothetical protein A	---	AT3G59910	1.12	0.17	1.68	0.138856	0.283962	-6.01
263384_at	hypothetical protein predicted by gens	---	AT2G40130	-1.16	-0.22	-1.68	0.138908	0.284035	-6.01
266336_at	putative Fe(II) transporter identical to	ZIP3	AT2G32270	-1.18	-0.24	-1.68	0.138942	0.284035	-6.01
260988_at	MAP3K alpha protein kinase, putative	MAP3KA	AT1G53570	-1.23	-0.30	-1.68	0.138935	0.284035	-6.01
245104_at	hypothetical protein predicted by gene	---	AT2G41600	-1.13	-0.18	-1.68	0.138926	0.284035	-6.01
261336_at	unknown protein ;supported by full-len	---	AT1G44790	-1.23	-0.30	-1.68	0.138968	0.284037	-6.01
262100_s_	hypothetical protein similar to hypothet	---	AT1G59550 /	1.19	0.26	1.68	0.138963	0.284037	-6.01
245140_at	unknown protein predicted by genefind	LBD18	AT2G45420	-1.12	-0.17	-1.68	0.139007	0.284066	-6.01
264934_at	hypothetical protein predicted by gens	---	AT1G61090	-1.14	-0.18	-1.68	0.138998	0.284066	-6.01
258150_at	hypothetical protein ;supported by full-	---	AT3G18160	-1.31	-0.39	-1.68	0.139056	0.28413	-6.01

267154_at	glutathione S-transferase identical to G	GSTF10	AT2G30870	1.51	0.60	1.68	0.139063	0.28413	-6.01
248038_at	unknown protein	---	AT5G55980	-1.13	-0.18	-1.68	0.139091	0.284162	-6.01
258892_at	unknown protein	---	AT3G05670	-1.13	-0.18	-1.68	0.13916	0.284251	-6.01
249021_at	putative protein similar to unknown pro	---	AT5G44820	1.25	0.32	1.68	0.13915	0.284251	-6.01
254559_at	putative protein glycine/proline-rich pr	---	AT4G19200	-1.22	-0.29	-1.68	0.139193	0.284294	-6.01
262965_at	hypothetical protein predicted by gene	---	AT1G54310	-1.20	-0.27	-1.68	0.139249	0.284383	-6.01
248334_s_	unknown protein ; supported by cDNA	---	AT5G52370 /	-1.27	-0.34	-1.68	0.139266	0.284392	-6.01
248665_at	Expressed protein ; supported by full-l	---	AT5G48655	1.12	0.16	1.68	0.139343	0.284523	-6.01
257882_at	hypothetical protein predicted by gene	---	AT3G16930	-1.15	-0.21	-1.68	0.139376	0.284566	-6.01
255987_s_	putative protein predicted proteins, Ar	---	AT5G35050	-1.12	-0.16	-1.68	0.139416	0.284622	-6.01
257427_at	hypothetical protein predicted by gene	---	AT1G79060	-1.25	-0.32	-1.68	0.139523	0.284814	-6.01
265836_at	Mutator-like transposase similar to MU	---	---	-1.14	-0.19	-1.68	0.139565	0.284875	-6.01
250620_at	embryo-specific protein 3 (ATS3) ; su	ATS3	AT5G07190	1.13	0.18	1.67	0.139616	0.284954	-6.01
260401_at	unknown protein similar to hypothetica	---	AT1G69840	-1.18	-0.23	-1.67	0.139635	0.284963	-6.01
267037_at	hypothetical protein ; supported by cD	---	AT2G38320	-1.15	-0.21	-1.67	0.139646	0.284963	-6.01
249501_s_	expansin-like protein expansin - Prunu	ATEXP26	AT5G39270 /	-1.11	-0.15	-1.67	0.139733	0.285116	-6.02
264311_at	hypothetical protein similar to hypothet	---	AT1G70400	1.12	0.16	1.67	0.139827	0.285281	-6.02
263202_at	putative inositol 1,4,5-trisphosphate 5-	5PTASE13	AT1G05630	-1.39	-0.47	-1.67	0.139858	0.285293	-6.02
257426_at	hypothetical protein contains similarity	---	AT1G54850	1.19	0.25	1.67	0.139851	0.285293	-6.02
248867_at	bHLH transcription factor	---	AT5G46830	-1.13	-0.18	-1.67	0.140154	0.285859	-6.02
245497_at	hypothetical protein	---	AT4G16460	1.16	0.21	1.67	0.14016	0.285859	-6.02
249353_at	oleosin ; supported by cDNA: gi_7252	OLEO2	AT5G40420	-1.18	-0.24	-1.67	0.140182	0.285878	-6.02
263965_at	putative retroelement pol polyprotein	---	---	-1.14	-0.20	-1.67	0.140229	0.285949	-6.02
250176_at	putative protein cytochrome P450 CY	CYP724A1	AT5G14400	-1.20	-0.26	-1.67	0.140276	0.286019	-6.02
261232_at	unknown protein ; supported by cDNA	---	AT1G20220	-1.14	-0.18	-1.67	0.140408	0.286214	-6.02
250882_at	putative protein ;supported by full-leng	---	AT5G04000	-1.13	-0.18	-1.67	0.140409	0.286214	-6.02
254348_at	putative protein p47 - Homo sapiens,F	PUX3	AT4G22150	-1.12	-0.17	-1.67	0.140388	0.286214	-6.02
251002_at	putative protein predicted proteins, Ar	---	AT5G02680	1.12	0.16	1.67	0.140437	0.286245	-6.02
260316_at	hypothetical protein similar to hypothet	---	AT1G63810	1.18	0.24	1.67	0.140559	0.286468	-6.02
249822_at	unknown protein	---	AT5G23710	1.15	0.20	1.67	0.140654	0.286636	-6.02
263875_at	unknown protein ;supported by full-ler	050-02	AT2G21970	1.23	0.30	1.67	0.140776	0.286833	-6.02
250831_at	unknown protein	---	AT5G04920	1.13	0.18	1.67	0.140772	0.286833	-6.02
246546_at	voltage-dependent anion-selective cha	VDAC3	AT5G15090	1.21	0.28	1.67	0.140845	0.286948	-6.02
258457_at	Expressed protein ; supported by full-l	IGPD	AT3G22425	-1.19	-0.25	-1.67	0.140928	0.287093	-6.02
255924_at	unknown protein contains similarity to	---	AT1G22170	-1.17	-0.23	-1.67	0.141007	0.287227	-6.02

263223_at	coatomer-like protein, epsilon subunit	---	AT1G30630	-1.16	-0.21	-1.67	0.14118	0.287529	-6.02
248122_at	unknown protein	---	AT5G54700	-1.13	-0.18	-1.67	0.141176	0.287529	-6.02
263154_at	Expressed protein ; supported by full-l	---	AT1G54110	-1.17	-0.23	-1.67	0.141264	0.287674	-6.03
251841_at	putative protein CRP1, Zea mays, PIR	---	AT3G54980	1.25	0.32	1.67	0.141331	0.287708	-6.03
245340_at	elicitor like protein ; supported by full-l	---	AT4G14420	1.22	0.29	1.67	0.141305	0.287708	-6.03
252846_at	putative protein several pectin methyle	---	AT3G42160	-1.11	-0.16	-1.67	0.141319	0.287708	-6.03
246013_at	vacuolar calcium binding protein - like	---	AT5G10660	1.13	0.17	1.67	0.141327	0.287708	-6.03
265721_at	putative ABC1 protein identical to EG/	ATATH9	AT2G40090	1.21	0.27	1.67	0.141359	0.287738	-6.03
259239_at	putative 40S ribosomal protein s14 sim	---	AT3G11510	-1.42	-0.50	-1.67	0.141453	0.287824	-6.03
266061_at	putative translation initiation factor eIF-	---	AT2G18720	1.15	0.20	1.67	0.141436	0.287824	-6.03
248959_at	putative protein similar to unknown pro	---	AT5G45630	1.42	0.51	1.67	0.141468	0.287824	-6.03
254420_at	hypothetical protein	---	AT4G21500	-1.19	-0.25	-1.67	0.141489	0.287824	-6.03
252749_at	putative protein several hypothetical pr	---	---	1.14	0.19	1.67	0.141451	0.287824	-6.03
259907_at	GCN4-complementing protein, putativ	AGD2	AT1G60860	-1.27	-0.34	-1.67	0.141482	0.287824	-6.03
248995_at	disease resistance protein-like	RRS1	AT5G45260	1.13	0.18	1.67	0.141478	0.287824	-6.03
248076_at	unknown protein	---	AT5G55750	-1.12	-0.16	-1.67	0.141552	0.287927	-6.03
261166_s_	Expressed protein ; supported by full-l	---	AT1G34570 /	1.20	0.26	1.66	0.141586	0.28797	-6.03
258540_at	hypothetical protein predicted by gens	---	AT3G06990	-1.14	-0.18	-1.66	0.141627	0.288002	-6.03
257702_at	CTP-synthetase, putative similar to C	emb2742	AT3G12670	-1.17	-0.22	-1.66	0.141619	0.288002	-6.03
264823_at	putative serine/threonine protein phosp	BSU1	AT1G03445	-1.20	-0.27	-1.66	0.141674	0.288045	-6.03
256940_at	unknown protein	QQS	AT3G30720	-1.17	-0.23	-1.66	0.141673	0.288045	-6.03
245943_at	putative protein permease family prote	---	AT5G19500	-1.19	-0.25	-1.66	0.141713	0.2881	-6.03
263891_at	putative glucan synthase	GSL8	AT2G36850	-1.13	-0.18	-1.66	0.141726	0.2881	-6.03
259695_at	hypothetical protein predicted by gene	---	AT1G63170	-1.17	-0.22	-1.66	0.141873	0.288373	-6.03
266149_x_	En/Spm-like transposon protein relate	---	---	1.14	0.19	1.66	0.141905	0.288409	-6.03
258411_at	hypothetical protein predicted by genm	---	AT3G17280	1.13	0.18	1.66	0.141916	0.288409	-6.03
260641_at	hypothetical protein predicted by gens	---	AT1G53200	1.29	0.36	1.66	0.141945	0.288417	-6.03
261652_at	dimethyladenosine transferase, putati	PFC1	AT1G01860	-1.16	-0.21	-1.66	0.141943	0.288417	-6.03
254389_s_	putative protein various predicted prote	---	AT4G21903 /	-1.39	-0.47	-1.66	0.141989	0.288454	-6.03
258341_at	unknown protein similar to centromere	---	AT3G22790	-1.53	-0.61	-1.66	0.14198	0.288454	-6.03
262520_at	putative polygalacturonase After first 2	---	AT1G17150	1.17	0.23	1.66	0.142086	0.288627	-6.03
266243_at	hypothetical protein predicted by gens	---	AT2G27750	1.12	0.17	1.66	0.1422	0.288831	-6.03
261009_at	hypothetical protein similar to putative	MES13	AT1G26360	1.16	0.22	1.66	0.142281	0.28897	-6.03
264437_at	unknown protein EST gb|N65787 com	---	AT1G27510	-1.15	-0.20	-1.66	0.142334	0.289026	-6.03
267067_at	unknown protein	---	AT2G41020	-1.20	-0.26	-1.66	0.142321	0.289026	-6.03

258825_at	unknown protein	---	AT3G07180	-1.12	-0.17	-1.66	0.142487	0.289311	-6.03
257077_at	PR-1 protein, putative similar to PR-1a	---	AT3G19690	-1.21	-0.27	-1.66	0.142535	0.289383	-6.03
252797_at	putative protein	---	---	1.20	0.27	1.66	0.142582	0.289453	-6.03
247023_at	putative protein similar to unknown pro	HEC1	AT5G67060	-1.20	-0.26	-1.66	0.142638	0.289542	-6.03
252764_at	nucleic acid binding protein-like nuclei	AL3	AT3G42790	1.14	0.19	1.66	0.142775	0.289794	-6.04
256553_at	hypothetical protein contains similarity	---	---	1.14	0.19	1.66	0.142806	0.28983	-6.04
265911_at	unknown protein ;supported by full-ler	---	AT2G25670	1.12	0.16	1.66	0.142854	0.289902	-6.04
245728_at	steroid 22-alpha-hydroxylase, putative	---	AT1G73340	-1.17	-0.23	-1.66	0.142884	0.289938	-6.04
253385_at	putative protein predicted protein, Cae	---	AT4G32930	1.13	0.17	1.66	0.142911	0.289965	-6.04
252525_at	putative protein hypothetical proteins	---	AT3G46450	-1.14	-0.20	-1.66	0.142933	0.289984	-6.04
251245_at	putative protein phytochrome-associa	PIL2	AT3G62090	-1.49	-0.58	-1.66	0.142968	0.290005	-6.04
251606_at	hypothetical protein	---	AT3G57840	1.18	0.24	1.66	0.14296	0.290005	-6.04
246334_at	putative protein serine kinase SRPK2	---	AT3G44850	1.22	0.29	1.66	0.143037	0.290118	-6.04
266431_at	Mutator-like transposase similar to MU	---	---	-1.14	-0.19	-1.66	0.143059	0.290137	-6.04
250567_at	hypothetical protein	---	AT5G08090	-1.15	-0.21	-1.66	0.143077	0.290149	-6.04
250870_at	hypothetical protein	---	AT5G03920	-1.14	-0.19	-1.66	0.14317	0.290312	-6.04
267348_at	unknown protein	---	AT2G39960	-1.13	-0.17	-1.66	0.143342	0.290633	-6.04
256520_at	hypothetical protein	CYP96A14P	AT1G66030	1.13	0.18	1.66	0.143359	0.290642	-6.04
252906_at	putative gamma-glutamyltransferase g	GGT1	AT4G39640	1.28	0.35	1.66	0.143405	0.290685	-6.04
260468_at	transcription factor RUSH-1alpha isolo	---	AT1G11100	1.20	0.27	1.66	0.143405	0.290685	-6.04
250348_at	putative protein	---	AT5G11990	-1.17	-0.23	-1.66	0.143461	0.290773	-6.04
253511_at	putative protein Sly1 protein, rat, PIR2	---	AT4G31740	1.13	0.18	1.66	0.143531	0.290861	-6.04
246844_at	transcription factor ATMYB4 ; support	ATMYB86	AT5G26660	1.17	0.22	1.66	0.143526	0.290861	-6.04
246951_at	unknown protein	---	AT5G04880	1.32	0.40	1.65	0.143641	0.291048	-6.04
264912_at	auxin-induced protein, putative similar	---	AT1G60750	1.14	0.19	1.65	0.143648	0.291048	-6.04
256939_at	multicatalytic endopeptidase complex	PBD1	AT3G22630	1.21	0.27	1.65	0.143701	0.29113	-6.04
261282_at	hypothetical protein predicted by gens	APUM10	AT1G35750	-1.19	-0.25	-1.65	0.143725	0.291151	-6.04
267336_at	putative small heat shock protein ;sup	---	AT2G19310	1.21	0.27	1.65	0.143801	0.291253	-6.04
250328_at	putative protein	---	AT5G11780	-1.16	-0.22	-1.65	0.143791	0.291253	-6.04
258739_s_	unknown protein similar to hypothetica	---	AT1G54300 /	1.12	0.17	1.65	0.14387	0.291368	-6.04
261975_at	unknown protein	---	AT1G64640	-1.49	-0.57	-1.65	0.143906	0.291415	-6.04
252297_at	cytosolic ribosomal protein S11 ;supp	EMB1080	AT3G48930	-1.29	-0.37	-1.65	0.14396	0.291499	-6.04
249923_at	conglutin gamma - like protein conglut	---	AT5G19120	-1.29	-0.37	-1.65	0.143982	0.291504	-6.04
246664_at	putative protein predicted proteins - Ar	---	---	-1.14	-0.18	-1.65	0.143988	0.291504	-6.04
262350_at	putative glutathione peroxidase ;supp	ATGPX4	AT2G48150	1.13	0.18	1.65	0.144049	0.291576	-6.04

254494_at	putative protein C65DMY30S	QRT3	AT4G20050	1.12	0.17	1.65	0.144044	0.291576	-6.04
246433_at	glutamine-rich protein predicted protei	---	AT5G17510	1.21	0.28	1.65	0.144091	0.291633	-6.04
248861_at	senescence-associated protein 5-like p	TRN2	AT5G46700	-1.54	-0.62	-1.65	0.144147	0.291722	-6.04
248163_at	auxin-responsive-like protein ; suppor	DFL1	AT5G54510	1.87	0.91	1.65	0.144214	0.291806	-6.04
252631_s_	putative protein predicted proteins, Ar	---	---	-1.11	-0.15	-1.65	0.144214	0.291806	-6.04
264540_at	hypothetical protein predicted by gene	---	AT1G55630	1.15	0.20	1.65	0.144227	0.291807	-6.05
267061_at	unknown protein ;supported by full-ler	---	AT2G32480	-1.14	-0.19	-1.65	0.144256	0.291839	-6.05
266511_at	putative ATP-dependent RNA helicase	---	AT2G47680	1.17	0.23	1.65	0.144314	0.291849	-6.05
257881_at	putative serine carboxypeptidase II sim	scpl33	AT3G17180	-1.18	-0.24	-1.65	0.144415	0.291849	-6.05
254631_at	putative protein predicted proteins, Ar	LSH9	AT4G18610	-1.34	-0.43	-1.65	0.144379	0.291849	-6.05
251048_at	putative protein potassium channel re	---	AT5G02410	1.16	0.21	1.65	0.144355	0.291849	-6.05
258775_at	hydroxyacylglutathione hydrolase cyto	GLY2	AT3G10850	-1.14	-0.19	-1.65	0.144392	0.291849	-6.05
256864_at	topoisomerase II identical to topoisom	TOPII	AT3G23890	-1.19	-0.25	-1.65	0.144367	0.291849	-6.05
254604_at	cadmium-induced protein	---	AT4G19070	-1.16	-0.21	-1.65	0.144365	0.291849	-6.05
255358_at	hypothetical protein	---	AT4G03940	-1.12	-0.17	-1.65	0.144359	0.291849	-6.05
252979_at	Expressed protein ; supported by full-le	---	AT4G38225	-1.24	-0.31	-1.65	0.144401	0.291849	-6.05
265466_at	putative CCAAT-box binding trancriptio	NF-YB8	AT2G37060	1.19	0.25	1.65	0.144328	0.291849	-6.05
259360_at	hypothetical protein predicted by gene	---	AT1G13310	1.13	0.17	1.65	0.14441	0.291849	-6.05
266459_at	unknown protein supported by full-leng	---	AT2G47970	1.14	0.19	1.65	0.14431	0.291849	-6.05
264293_at	cell division cycle protein, putative sim	APC6	AT1G78770	-1.12	-0.16	-1.65	0.144488	0.291972	-6.05
253034_at	calcium-dependent protein kinase -like	CPK26	AT4G38230	-1.15	-0.20	-1.65	0.144743	0.29246	-6.05
264851_at	putative calmodulin-domain protein kir	CPK6	AT2G17290	1.28	0.35	1.65	0.144777	0.292504	-6.05
259866_at	putative calmodulin similar to calmodu	---	AT1G76640	1.48	0.56	1.65	0.144824	0.292572	-6.05
252173_at	scarecrow-like 7 (SCL7)	---	AT3G50650	1.28	0.35	1.65	0.144989	0.292833	-6.05
247094_at	GDP-D-mannose 4,6-dehydratase; GI	GMD1	AT5G66280	1.14	0.19	1.65	0.145015	0.292833	-6.05
265550_at	hypothetical protein predicted by gens	---	---	-1.14	-0.19	-1.65	0.14503	0.292833	-6.05
260022_at	unknown protein	---	AT1G30020	-1.14	-0.19	-1.65	0.145027	0.292833	-6.05
254188_at	UDPglucose 4-epimerase - like protei	UGE2	AT4G23920	1.33	0.42	1.65	0.144993	0.292833	-6.05
262169_at	hypothetical protein predicted by gene	---	AT1G74860	-1.16	-0.22	-1.65	0.144978	0.292833	-6.05
256324_at	MATE efflux family protein, putative c	---	AT1G66760	-1.72	-0.78	-1.65	0.145081	0.29291	-6.05
266347_at	putative ATP-dependent DNA helicase	---	AT2G01440	1.19	0.25	1.65	0.145097	0.292916	-6.05
261127_at	unknown protein ; supported by cDNA	---	AT1G04790	-1.19	-0.25	-1.65	0.145151	0.293	-6.05
252206_at	centrin	ATCEN2	AT3G50360	-1.14	-0.20	-1.65	0.145275	0.293223	-6.05
256956_at	expressed protein supported by cDNA	---	AT3G13410	-1.12	-0.17	-1.65	0.145328	0.293305	-6.05
250551_at	SNAP25 - like protein SNAP25A prote	SNAP29	AT5G07880	-1.15	-0.20	-1.65	0.145342	0.293307	-6.05

258898_at	putative DNA helicase	RECQI1	AT3G05740	-1.26	-0.33	-1.65	0.145379	0.293355	-6.05
266456_at	putative bHLH transcription factor	NAI1	AT2G22770	-1.15	-0.21	-1.65	0.14549	0.293527	-6.05
264115_at	hypothetical protein	---	AT2G31290	-1.17	-0.23	-1.65	0.145479	0.293527	-6.05
264782_at	putative transcription factor similar to (	MYB60	AT1G08810	-1.19	-0.25	-1.65	0.145517	0.293556	-6.05
245232_at	actin depolymerizing factor-like protei	ADF7	AT4G25590	-1.15	-0.20	-1.65	0.145548	0.293593	-6.05
260545_at	putative glutathione peroxidase ;supp	ATGPX3	AT2G43350	1.15	0.20	1.65	0.145581	0.293635	-6.05
257659_at	Expressed protein ; supported by full-l	---	AT3G13226	-1.12	-0.16	-1.65	0.145611	0.293668	-6.05
267401_at	unknown protein	---	AT2G26210	1.14	0.19	1.64	0.14569	0.293777	-6.05
247433_at	E2, ubiquitin-conjugating enzyme 3 (U	UBC3	AT5G62540	-1.23	-0.29	-1.65	0.145678	0.293777	-6.05
267111_s_	hypothetical protein predicted by gens	---	---	-1.18	-0.23	-1.64	0.145801	0.293922	-6.06
256277_at	omega-6 fatty acid desaturase, endop	FAD2	AT3G12120	-1.26	-0.33	-1.64	0.145796	0.293922	-6.06
261067_at	lectin, putative contains Pfam profile:	---	AT1G07460	-1.14	-0.19	-1.64	0.145791	0.293922	-6.06
248520_at	11-beta-hydroxysteroid dehydrogenas	AtHSD1	AT5G50600 /	-1.22	-0.29	-1.64	0.145872	0.294039	-6.06
244921_s_	hypothetical protein	---	AT2G07674 /	1.22	0.29	1.64	0.146111	0.294423	-6.06
253797_at	putative protein 55.11 protein homolo	RPN1B	AT4G28470	-1.11	-0.15	-1.64	0.146114	0.294423	-6.06
254128_at	ubiquitin-specific protease 16 (UBP16	UBP16	AT4G24560	1.11	0.15	1.64	0.14611	0.294423	-6.06
252700_at	hypothetical protein envelope-like, Gly	---	---	1.15	0.21	1.64	0.146107	0.294423	-6.06
249256_at	putative protein strong similarity to unk	---	AT5G41620	-1.20	-0.26	-1.64	0.146178	0.294526	-6.06
253361_at	putative protein various predicted prote	---	AT4G33100	1.26	0.33	1.64	0.146288	0.294722	-6.06
265244_at	putative amine oxidase	ATPAO2	AT2G43018 /	-1.29	-0.37	-1.64	0.146406	0.294921	-6.06
262972_at	unknown protein	---	AT1G75620	-1.15	-0.20	-1.64	0.146413	0.294921	-6.06
248436_at	putative protein contains similarity to u	---	AT5G51220	1.13	0.18	1.64	0.146449	0.294942	-6.06
245045_at	unknown protein similar to glycoprotei	---	AT2G26590	1.12	0.16	1.64	0.146439	0.294942	-6.06
252222_at	putative protein various predicted prot	---	AT3G49840 /	1.32	0.40	1.64	0.146537	0.295093	-6.06
263004_at	hypothetical protein contains similarity	ATNEK1	AT1G54510	1.16	0.21	1.64	0.146651	0.295297	-6.06
249351_at	MAP kinase kinase 3 (ATMKK3) 10.01	ATMKK3	AT5G40440	-1.15	-0.20	-1.64	0.146671	0.29531	-6.06
264028_at	putative nitrilase-associated protein Al	SPR1	AT2G03680	-1.26	-0.33	-1.64	0.14675	0.295444	-6.06
260467_at	unknown protein	---	AT1G10890	1.11	0.15	1.64	0.146907	0.295733	-6.06
249191_at	putative protein similar to unknown pro	---	AT5G42760	-1.19	-0.25	-1.64	0.14694	0.295773	-6.06
261560_at	acyl CoA thioesterase, putative simila	---	AT1G01710	-1.11	-0.16	-1.64	0.146978	0.295818	-6.06
252498_at	putative protein several hypothetical pr	---	AT3G46810	-1.11	-0.16	-1.64	0.146988	0.295818	-6.06
255888_at	hypothetical protein contains similarity	---	AT1G20300	1.43	0.52	1.64	0.147074	0.295964	-6.06
257305_at	hypothetical protein predicted by gene	---	---	-1.17	-0.22	-1.64	0.147092	0.295974	-6.06
252832_at	ubiquitin-specific protease 3 (UBP3) id	ATUBP3	AT4G39910	1.11	0.15	1.64	0.147107	0.295979	-6.06
265456_at	Expressed protein ; supported by full-l	SDH4	AT2G46505	1.13	0.17	1.64	0.14713	0.295998	-6.06

253437_at	putative protein mRNAs from Ricinus	---	AT4G32460	-1.44	-0.52	-1.64	0.147144	0.296002	-6.06
265172_at	putative spermidine synthase	SPDS1	AT1G23820	1.12	0.16	1.64	0.147215	0.2961	-6.06
263615_at	putative MYB family transcription facto	MYB100	AT2G25230	-1.11	-0.15	-1.64	0.147219	0.2961	-6.06
264399_at	postsynaptic protein CRIPT, putative s	---	AT1G61780	1.10	0.14	1.64	0.147276	0.296188	-6.06
246994_at	putative protein similar to unknown pro	---	AT5G67460	-1.38	-0.47	-1.64	0.147373	0.296331	-6.07
263125_at	hypothetical protein predicted by gene	---	AT1G78470	1.13	0.18	1.64	0.147368	0.296331	-6.07
257666_at	bactericidal permeability-increasing pr	---	AT3G20270	1.25	0.32	1.64	0.147419	0.296395	-6.07
267231_at	putative inositol polyphosphate 5'-phos	---	AT2G43900	-1.14	-0.19	-1.64	0.147431	0.296395	-6.07
245463_at	allergen like protein	ATEXLB1	AT4G17030	-1.33	-0.42	-1.64	0.14746	0.296427	-6.07
256844_s_	En/Spm transposon protein, putative s	---	---	1.13	0.18	1.64	0.147481	0.296443	-6.07
265169_x_	unknown protein	---	AT1G23720	1.14	0.19	1.64	0.147548	0.296551	-6.07
263677_at	unknown protein	PDLP2	AT1G04520	-1.15	-0.20	-1.64	0.147565	0.29656	-6.07
255400_at	hypothetical protein	---	---	-1.15	-0.21	-1.64	0.147646	0.296696	-6.07
266914_at	putative beta-amylase	BAM7	AT2G45880	-1.28	-0.36	-1.64	0.147673	0.296725	-6.07
245535_at	cell wall protein like	---	AT4G15160	-1.16	-0.21	-1.64	0.147703	0.296759	-6.07
252643_at	acidic ribosomal protein P2 -like acidi	---	AT3G44590	1.37	0.46	1.64	0.147774	0.296876	-6.07
251278_at	putative protein hypothetical protein -	emb1703	AT3G61780	1.16	0.22	1.63	0.147798	0.296881	-6.07
255823_at	unknown protein ;supported by full-ler	LBD15	AT2G40470	1.45	0.54	1.63	0.147803	0.296881	-6.07
263049_at	unknown protein ;supported by full-ler	---	AT2G05260	1.14	0.19	1.63	0.147828	0.296905	-6.07
248998_at	unknown protein	---	AT5G45320	-1.12	-0.17	-1.63	0.147981	0.297186	-6.07
262302_at	hypothetical protein predicted by gene	---	AT1G70910	-1.15	-0.20	-1.63	0.148047	0.297293	-6.07
263925_at	putative glycine-rich RNA binding prote	---	AT2G21690	-1.11	-0.15	-1.63	0.148093	0.297358	-6.07
262443_at	Expressed protein ; supported by full-l	---	AT1G47655	-1.20	-0.26	-1.63	0.148147	0.297441	-6.07
247981_at	putative protein similar to unknown pro	MIOX5	AT5G56640	-1.12	-0.17	-1.63	0.148176	0.297473	-6.07
254284_at	putative fizzy-related protein fizzy-rela	FZR2	AT4G22910	-1.21	-0.28	-1.63	0.148196	0.297488	-6.07
247644_s_	translation elongation factor eEF-1 alp	---	AT1G07920 /	1.14	0.18	1.63	0.148229	0.2975	-6.07
257991_at	unknown protein	---	AT3G19870	-1.18	-0.24	-1.63	0.148216	0.2975	-6.07
250720_at	putative protein similar to unknown pro	---	AT5G06180	1.21	0.27	1.63	0.148379	0.297777	-6.07
263422_s_	putative ubiquitin-like protein ; support	---	AT2G17190 /	1.12	0.16	1.63	0.148403	0.297798	-6.07
250033_at	eukaryotic cap-binding protein (gb|AA(	NCBP	AT5G18110	1.13	0.17	1.63	0.14842	0.297806	-6.07
253240_at	putative ketoacyl-CoA synthase fatty a	KCS17	AT4G34510	-1.12	-0.16	-1.63	0.148515	0.297868	-6.07
266780_at	putative ligand-gated ion channel prote	ATGLR2.8	AT2G29110	1.23	0.30	1.63	0.148479	0.297868	-6.07
261557_at	kinesin-like protein C-terminal region is	---	AT1G63640	1.20	0.26	1.63	0.148499	0.297868	-6.07
260166_at	homeobox protein (GLABRA2) identica	GL2	AT1G79840	-1.12	-0.16	-1.63	0.148516	0.297868	-6.07
261331_at	hypothetical protein predicted by gene	---	---	-1.16	-0.21	-1.63	0.148471	0.297868	-6.07

262874_at	hypothetical protein predicted by gene	---	AT1G65020	-1.17	-0.23	-1.63	0.148543	0.297895	-6.07
245418_at	putative protein	---	AT4G17370	-1.19	-0.25	-1.63	0.148575	0.297933	-6.07
251450_at	squamosa promoter binding protein-lik	SPL12	AT3G60030	-1.16	-0.22	-1.63	0.148702	0.298162	-6.07
251393_at	putative protein symbiosis-related pro	ATG8G	AT3G60640	1.21	0.28	1.63	0.148718	0.298168	-6.07
255279_at	putative thioredoxin ; supported by cD	---	AT4G04950	1.23	0.30	1.63	0.148837	0.29828	-6.07
263759_at	hypothetical protein predicted by gene	---	AT2G21290	1.15	0.20	1.63	0.148839	0.29828	-6.07
252180_at	putative protein cyclin-dependent kina	KRP2	AT3G50630	-1.22	-0.29	-1.63	0.148814	0.29828	-6.07
258858_at	putative 40S ribosomal protein S19 sin	---	AT3G02080	-1.27	-0.35	-1.63	0.148807	0.29828	-6.07
251952_at	histone H2B - like protein histone H2B	---	AT3G53650	-1.11	-0.15	-1.63	0.148822	0.29828	-6.07
252683_at	putative protein predicted proteins, Ar	---	AT3G44380	-1.18	-0.24	-1.63	0.14906	0.298697	-6.08
258199_at	unknown protein	---	AT3G14030	1.13	0.18	1.63	0.149142	0.298834	-6.08
265871_at	unknown protein ;supported by full-ler	---	AT2G01680	1.19	0.25	1.63	0.149301	0.299127	-6.08
250517_at	serine-type carboxypeptidase II-like pr	scpl35	AT5G08260	-1.43	-0.52	-1.63	0.149368	0.299231	-6.08
261318_at	Expressed protein ; supported by full-le	---	AT1G53035	-1.74	-0.80	-1.63	0.14938	0.299231	-6.08
254119_at	putative pectate lyase pectate lyase, M	---	AT4G24780	-1.68	-0.75	-1.63	0.149466	0.299377	-6.08
257653_at	hypothetical protein	---	AT3G13225	-1.17	-0.22	-1.63	0.149572	0.299564	-6.08
267415_at	putative translation initiation factor eIF-	---	AT2G34970	-1.12	-0.16	-1.63	0.149674	0.299743	-6.08
263392_at	putative PttA-like transposon protein re	---	---	-1.12	-0.16	-1.63	0.149691	0.299749	-6.08
267393_at	similar to axi 1 protein from Nicotiana t	---	AT2G44500	1.27	0.34	1.63	0.149741	0.299823	-6.08
257540_at	hypothetical protein	---	AT3G21520	1.15	0.21	1.63	0.149833	0.299948	-6.08
254807_at	putative protein	---	AT4G12700	-1.20	-0.26	-1.63	0.149823	0.299948	-6.08
264170_at	hypothetical protein	---	AT1G02260	1.14	0.19	1.63	0.149842	0.299948	-6.08
249110_at	disease resistance protein	---	AT5G43730	1.11	0.15	1.62	0.149911	0.300044	-6.08
261236_at	importin alpha, putative similar to impo	---	AT1G32880	1.13	0.17	1.62	0.14993	0.300044	-6.08
256370_at	MATE efflux family protein, putative co	---	AT1G66780	1.13	0.18	1.62	0.149927	0.300044	-6.08
262763_at	hypothetical protein	---	AT1G28690	-1.19	-0.25	-1.62	0.149953	0.300063	-6.08
265929_s_	putative flavonol 3-O-glucosyltransfera	---	AT2G18560 /	-1.26	-0.34	-1.62	0.150108	0.300347	-6.08
248477_at	putative protein similar to unknown pro	---	AT5G50900	-1.18	-0.23	-1.62	0.150147	0.300399	-6.08
248137_at	putative protein contains similarity to c	---	AT5G54950	-1.14	-0.19	-1.62	0.150173	0.300424	-6.08
262922_at	hypothetical protein predicted by gene	---	AT1G79420	-1.19	-0.25	-1.62	0.150223	0.300446	-6.08
250292_at	putative protein predicted proteins, Ar	JAZ10	AT5G13220	1.81	0.86	1.62	0.150212	0.300446	-6.08
261353_at	hypothetical protein contains similarity	---	AT1G79600	1.21	0.28	1.62	0.150223	0.300446	-6.08
254468_at	UDP-glucose 4-epimerase - like prote	---	AT4G20460	1.14	0.19	1.62	0.150246	0.300466	-6.08
263576_at	hypothetical protein similar to hypothet	---	AT2G17080	1.11	0.15	1.62	0.150266	0.300479	-6.08
265862_at	putative S-locus glycoprotein	---	AT2G01780	-1.15	-0.20	-1.62	0.150316	0.300552	-6.08

253824_at	putative protein protein kinase LePK7	MTM1	AT4G27940	1.54	0.62	1.62	0.150369	0.300632	-6.08
262754_at	putative inosine-5-monophosphate del	---	AT1G16350	1.16	0.22	1.62	0.150505	0.300878	-6.08
252444_at	putative protein Na+-dependent inorg	PHT4;3	AT3G46980	-1.11	-0.15	-1.62	0.15059	0.301022	-6.09
250984_at	protein kinase - like protein kinase AP	---	AT5G02800	1.11	0.16	1.62	0.15065	0.301115	-6.09
251329_at	putative protein hypothetical protein F	SYP73	AT3G61450	1.19	0.25	1.62	0.150664	0.301117	-6.09
261262_at	hypothetical protein predicted by gene	SDG35	AT1G26760	-1.12	-0.16	-1.62	0.15071	0.301127	-6.09
247471_at	putative protein receptor-like protein k	ERL1	AT5G62230	-1.15	-0.20	-1.62	0.150712	0.301127	-6.09
253408_at	putative protein phosphoprotein phosp	---	AT4G32950	-1.11	-0.15	-1.62	0.15072	0.301127	-6.09
249308_at	unknown protein ; supported by cDNA	---	AT5G41350	1.12	0.16	1.62	0.150722	0.301127	-6.09
249374_at	20S proteasome beta subunit PBB2 ;s	PBB2	AT5G40580	-1.15	-0.20	-1.62	0.150752	0.301162	-6.09
258024_at	hypothetical protein predicted by gene	---	AT3G19360	-1.28	-0.36	-1.62	0.150834	0.301298	-6.09
261111_at	homeodomain protein BELL1, putative	BLH11	AT1G75430	-1.11	-0.16	-1.62	0.150959	0.301521	-6.09
256874_at	cytochrome P450, putative contains P	CYP71B36	AT3G26320	-1.16	-0.21	-1.62	0.150991	0.301558	-6.09
256694_at	hypothetical protein predicted genscan	---	---	-1.14	-0.19	-1.62	0.151013	0.301576	-6.09
248512_at	protein translocation complex Sec61 g	SIG2	AT1G08540 /	1.30	0.38	1.62	0.151048	0.301619	-6.09
247805_at	ATGP1-like protein	ATYKT62	AT5G58180	1.22	0.28	1.62	0.151072	0.301641	-6.09
264468_at	unknown protein similar to daunorubici	---	AT1G10310	1.18	0.23	1.62	0.151118	0.30168	-6.09
249388_at	putative protein downy mildew resista	---	AT5G40090	-1.15	-0.20	-1.62	0.151107	0.30168	-6.09
264316_at	unknown protein ; supported by cDNA	ENT1,AT	AT1G70330	-1.17	-0.23	-1.62	0.151137	0.301693	-6.09
264522_at	putative xylan endohydrolase similar t	---	AT1G10050	1.17	0.22	1.62	0.151171	0.301707	-6.09
245499_at	membrane transporter like protein	INT4	AT4G16480	-1.13	-0.17	-1.62	0.151159	0.301707	-6.09
257290_at	hypothetical protein predicted by gens	---	AT3G15550	-1.12	-0.17	-1.62	0.151313	0.301965	-6.09
265382_at	putative gluconokinase ;supported by	---	AT2G16790	1.26	0.34	1.62	0.151434	0.302179	-6.09
265118_at	beta-fructosidase nearly identical to be	---	AT1G62660	1.24	0.32	1.62	0.151504	0.302293	-6.09
247398_at	putative protein predicted protein, Ara	---	AT5G62950	1.16	0.22	1.62	0.151518	0.302294	-6.09
256122_at	hypothetical protein predicted by gens	---	AT1G18180	-1.15	-0.20	-1.62	0.151698	0.30262	-6.09
267143_at	putative peptide/amino acid transporte	---	AT2G38100	-1.14	-0.19	-1.62	0.151708	0.30262	-6.09
251986_at	putative protein various predicted prot	---	AT3G53310	-1.32	-0.41	-1.62	0.151727	0.302631	-6.09
260598_at	unknown protein	---	AT1G55930	-1.21	-0.27	-1.62	0.151832	0.302802	-6.09
252147_at	putative protein several hypothetical pr	---	AT3G51270	-1.22	-0.28	-1.62	0.151839	0.302802	-6.09
257980_at	hypothetical protein predicted by gene	---	AT3G20760	-1.14	-0.19	-1.62	0.151875	0.302848	-6.09
252745_at	putative protein Sh3yl1 mRNA, Mus m	---	AT3G43230	1.15	0.20	1.62	0.151915	0.3029	-6.09
266515_at	putative tubby protein	AtTLP3	AT2G47900	-1.20	-0.26	-1.61	0.152076	0.303194	-6.09
265695_at	putative replication protein A1 ;suppor	RPA2	AT2G24490	-1.43	-0.51	-1.61	0.152135	0.303268	-6.09
AFFX-PheX	B. subtilis /GEN=pheB /DB_XREF=gb:	---	---	-1.22	-0.29	-1.61	0.152139	0.303268	-6.09

255366_x_	putative transposon protein	---	---	-1.14	-0.19	-1.61	0.152157	0.303277	-6.10
253176_at	putative protein Human (H326) mRNA	---	AT4G35140	1.22	0.29	1.61	0.152257	0.303451	-6.10
256195_at	hypothetical protein predicted by gene	---	---	-1.11	-0.15	-1.61	0.152357	0.303622	-6.10
259471_at	hypothetical protein contains similarity	---	AT1G19040	-1.11	-0.15	-1.61	0.152455	0.303737	-6.10
264661_at	hypothetical protein Similar to Nicotian	---	AT1G09950	-1.26	-0.33	-1.61	0.152451	0.303737	-6.10
260617_at	Expressed protein ; supported by full-l	---	AT1G53345	-1.16	-0.22	-1.61	0.152453	0.303737	-6.10
246156_at	putative protein predicted proteins fron	---	AT5G20090	1.15	0.21	1.61	0.152468	0.303737	-6.10
256509_at	NADPH oxidoreductase, putative simi	---	AT1G75300	1.27	0.34	1.61	0.152494	0.303762	-6.10
263267_at	putative vacuolar proton-ATPase 16 kI	---	AT2G16510	1.14	0.19	1.61	0.152565	0.303878	-6.10
259945_at	unknown protein	---	AT1G71460	-1.16	-0.21	-1.61	0.152738	0.304168	-6.10
249135_at	putative protein similar to unknown pro	---	AT5G43160	-1.29	-0.36	-1.61	0.152726	0.304168	-6.10
252671_at	putative protein dehydrogenases of ba	---	AT3G44190	1.18	0.24	1.61	0.152855	0.304372	-6.10
256128_at	laccase, putative similar to high-pI lac	LAC1	AT1G18140	-1.15	-0.20	-1.61	0.152867	0.304372	-6.10
264747_at	unknown protein	---	AT1G70150	-1.18	-0.24	-1.61	0.152912	0.304435	-6.10
256443_at	hypothetical protein similar to hypothet	---	AT3G10960	1.27	0.35	1.61	0.15308	0.304744	-6.10
266674_at	hypothetical protein predicted by gens	---	AT2G29620	1.12	0.16	1.61	0.15314	0.304836	-6.10
252496_at	putative protein several hypothetical pr	CRR2	AT3G46790	1.22	0.29	1.61	0.153249	0.30501	-6.10
251476_at	putative protein hypothetical protein F	---	AT3G59670	1.24	0.31	1.61	0.153254	0.30501	-6.10
260952_at	hypothetical protein predicted by gene	---	AT1G06140	1.20	0.26	1.61	0.153368	0.30521	-6.10
261156_s_	hypothetical protein predicted by gene	---	AT1G34490 /	-1.13	-0.17	-1.61	0.153397	0.305242	-6.10
266849_at	putative vacuolar processing enzyme i	ALPHA-VPE	AT2G25940	1.13	0.18	1.61	0.153432	0.305284	-6.10
244948_at	hypothetical protein	---	---	1.12	0.17	1.61	0.153492	0.30534	-6.10
264971_at	Expressed protein ; supported by full-l	---	AT1G67210	-1.11	-0.15	-1.61	0.1535	0.30534	-6.10
263135_at	flavanone 3-hydroxylase, putative sim	---	AT1G78550	-1.18	-0.24	-1.61	0.153484	0.30534	-6.10
248569_at	receptor protein kinase-like	---	AT5G49770	-1.16	-0.21	-1.61	0.153548	0.305409	-6.10
262163_at	ribosomal protein L30, putative similar	---	AT1G77940	-1.34	-0.42	-1.61	0.153663	0.305611	-6.10
265227_s_	hypothetical protein	---	AT2G07695	1.17	0.22	1.61	0.153705	0.305619	-6.10
249709_at	putative protein similar to unknown pro	iqd33	AT5G35670	-1.17	-0.22	-1.61	0.153706	0.305619	-6.10
AFFX-DapX	B. subtilis /GEN=dapB /DB_XREF=gb:	---	---	-1.31	-0.39	-1.61	0.153707	0.305619	-6.10
250562_at	putative protein	TOM5	AT5G08040	-1.17	-0.22	-1.61	0.153776	0.305729	-6.10
255300_at	putative phosphatidylglycerotransferas	CLS	AT4G04870	-1.20	-0.26	-1.61	0.153866	0.305881	-6.11
248862_at	unknown protein	---	AT5G46730	-1.21	-0.28	-1.61	0.15392	0.305963	-6.11
251800_at	putative protein various predicted prote	RBL	AT3G55510	1.30	0.38	1.61	0.154046	0.306182	-6.11
248983_at	ras-related GTP-binding protein RHA1	RHA1	AT5G45130	1.12	0.17	1.61	0.154058	0.306182	-6.11
266883_at	putative triacylglycerol lipase	DAD1	AT2G44810	1.13	0.18	1.61	0.154095	0.306188	-6.11

249490_s_	germin -like protein germin -like protei	---	AT5G39110 /	1.45	0.53	1.61	0.154101	0.306188	-6.11
263234_at	hypothetical protein predicted by gene	---	AT1G10417	-1.12	-0.16	-1.61	0.154097	0.306188	-6.11
258978_at	unknown protein ; supported by cDNA	---	AT3G09320	1.12	0.16	1.61	0.154151	0.30626	-6.11
253279_at	putative protein B subunit of propionyl	MCCB	AT4G34030	1.28	0.36	1.60	0.154402	0.306733	-6.11
259850_at	hypothetical protein predicted by gene	---	AT1G72240	-1.20	-0.26	-1.60	0.154419	0.30674	-6.11
260037_at	putative DNA-binding protein (RAV2-li	RAV2	AT1G68840	-1.65	-0.72	-1.60	0.154459	0.306766	-6.11
249352_at	putative transcription factor MYB22 ; s	MYB22	AT5G40430	-1.11	-0.15	-1.60	0.154451	0.306766	-6.11
265248_at	unknown protein ; supported by cDNA	PIF4	AT2G43010	-1.25	-0.32	-1.60	0.154543	0.306907	-6.11
261556_s_	unknown protein	---	AT1G62600 /	1.18	0.24	1.60	0.154579	0.306951	-6.11
245967_at	proline-rich protein extensins	---	AT5G19800	-1.13	-0.17	-1.60	0.15473	0.307225	-6.11
247134_at	putative protein similar to unknown pro	---	AT5G66230	-1.13	-0.18	-1.60	0.154781	0.307299	-6.11
249305_at	putative protein strong similarity to unk	---	AT5G41490	1.16	0.21	1.60	0.154849	0.307407	-6.11
257565_at	hypothetical protein predicted by gene	---	AT3G28620	1.12	0.16	1.60	0.154866	0.307413	-6.11
247509_at	heat shock factor 6	HSFB2A	AT5G62020	1.16	0.22	1.60	0.154895	0.307418	-6.11
262316_at	pale cress protein identical to GB:CAA	PAC	AT2G48120	-1.21	-0.27	-1.60	0.154886	0.307418	-6.11
247181_at	putative protein similar to unknown pro	---	AT5G65370	-1.13	-0.17	-1.60	0.154956	0.307512	-6.11
252402_s_	putative protein predicted proteins, Ar	---	AT3G48050 /	1.12	0.16	1.60	0.15499	0.307553	-6.11
247249_at	putative protein similar to unknown pro	---	AT5G64670	1.20	0.26	1.60	0.155057	0.307659	-6.11
253442_at	H+-transporting ATPase - like protein	---	AT4G32530	1.12	0.17	1.60	0.155074	0.307667	-6.11
266282_at	putative protein kinase contains a prot	---	AT2G29220	1.11	0.15	1.60	0.155125	0.30774	-6.11
260249_s_	unknown protein similar to unknown pr	---	AT1G74280 /	1.17	0.23	1.60	0.155206	0.307874	-6.11
248486_at	respiratory burst oxidase protein	RHD2	AT5G51060	1.11	0.15	1.60	0.155269	0.307973	-6.11
247741_at	putative protein predicted proteins, Ar	GIL1	AT5G58960	-1.28	-0.35	-1.60	0.155307	0.308007	-6.11
250583_at	zinc finger transcription factor ; suppo	PEI1	AT5G07500	-1.13	-0.17	-1.60	0.155327	0.308007	-6.11
265923_at	putative protein kinase contains a prot	---	AT2G18470	-1.11	-0.15	-1.60	0.155327	0.308007	-6.11
264252_at	putative GTP-binding protein, SAR1B	ATSARA1A	AT1G09180	1.13	0.18	1.60	0.155355	0.308037	-6.11
252156_at	BCS1 protein-like protein BCS1 protei	---	AT3G50940	1.17	0.23	1.60	0.155438	0.308134	-6.11
256317_at	hypothetical protein predicted by gene	---	AT1G35900	-1.22	-0.29	-1.60	0.155445	0.308134	-6.12
266681_at	copia-like retroelement pol polyprotein	---	---	1.10	0.14	1.60	0.155443	0.308134	-6.11
257111_x_	hypothetical protein	---	---	1.12	0.16	1.60	0.155478	0.308173	-6.12
259007_at	putative MYB family transcription facto	MYB3R-3	AT3G09370	-1.18	-0.24	-1.60	0.155594	0.308376	-6.12
263334_at	putative nonsense-mediated mRNA de	---	AT2G03820	1.14	0.18	1.60	0.15567	0.3085	-6.12
245073_at	putative glucosyltransferase	---	AT2G23210	1.14	0.19	1.60	0.155714	0.30856	-6.12
254617_s_	ribosomal protein L11, cytosolic ;supp	RPL16B	AT4G18730 /	-1.22	-0.29	-1.60	0.155738	0.30858	-6.12
249030_at	putative protein similar to unknown pro	---	---	-1.12	-0.16	-1.60	0.155782	0.308614	-6.12

256544_at	Mlo-like protein similar to Mlo [Hordeu	MLO9	AT1G42560	-1.16	-0.21	-1.60	0.155795	0.308614	-6.12
256731_at	hypothetical protein contains Pfam pro	---	AT3G30340	-1.13	-0.17	-1.60	0.155781	0.308614	-6.12
255796_at	similar to mammalian MHC III region p	SUVH2	AT2G33290	1.14	0.19	1.60	0.15582	0.308636	-6.12
255876_at	hypothetical protein	---	AT2G40480	-1.32	-0.40	-1.60	0.155845	0.308658	-6.12
247790_at	putative PRL1 associated protein ;sup	---	AT5G58720	-1.15	-0.20	-1.60	0.155879	0.3087	-6.12
265675_at	70kD heat shock protein ;supported b	HSP70T-2	AT2G32120	1.19	0.25	1.60	0.155929	0.308744	-6.12
259711_at	putative DNA-binding protein similarity	---	AT1G77570	1.34	0.43	1.60	0.155924	0.308744	-6.12
263002_at	hypothetical protein predicted by gene	---	AT1G54200	-1.35	-0.43	-1.60	0.156014	0.308886	-6.12
260759_at	hypothetical protein contains similarity	---	AT1G49180	-1.26	-0.33	-1.60	0.156028	0.308888	-6.12
247520_at	cytochrome c oxidase subunit - like cy	---	AT5G61310	1.26	0.33	1.60	0.156056	0.308915	-6.12
254135_at	putative protein MSP1 protein, Saccha	---	AT4G24860	1.14	0.19	1.60	0.156079	0.308934	-6.12
263684_at	hypothetical protein predicted by gens	---	AT1G26900	1.15	0.20	1.60	0.156145	0.309012	-6.12
250541_at	putative proline-rich protein surface pr	---	AT5G09520	-1.26	-0.33	-1.60	0.156145	0.309012	-6.12
261863_at	unknown protein ; supported by cDNA	---	AT1G50630	-1.18	-0.24	-1.60	0.156169	0.309033	-6.12
245039_at	putative beta-1,3-glucanase ;supporte	---	AT2G26600	1.14	0.19	1.60	0.156242	0.309122	-6.12
256915_at	unknown protein	---	AT3G23900	1.16	0.21	1.60	0.156237	0.309122	-6.12
250266_at	histone H3 -like protein histone H3, w	---	AT5G12910	1.15	0.20	1.60	0.156311	0.309225	-6.12
249681_s_	putative protein strong similarity to unk	---	---	1.18	0.24	1.60	0.156321	0.309225	-6.12
261516_at	hypoxanthine ribosyl transferase, puta	---	AT1G71750	-1.12	-0.17	-1.59	0.156484	0.309522	-6.12
248537_at	putative protein similar to unknown pro	---	AT5G50100	-1.18	-0.24	-1.59	0.156538	0.309601	-6.12
253902_at	NWMU4 - 2S albumin 4 precursor ; su	---	AT4G27170	1.12	0.16	1.59	0.156605	0.309707	-6.12
252177_at	protein kinase ATN1 - like protein prot	---	AT3G50730	-1.16	-0.22	-1.59	0.156639	0.30974	-6.12
252910_at	putative protein various predicted prot	---	AT4G39590	-1.11	-0.15	-1.59	0.156649	0.30974	-6.12
251556_at	putative protein predicted proteins, Me	---	AT3G58840	-1.19	-0.25	-1.59	0.156703	0.30982	-6.12
260774_at	serine-threonine protein kinase, putati	---	AT1G78290	1.42	0.50	1.59	0.15672	0.309826	-6.12
256241_at	nascent polypeptide associated comp	---	AT3G12390	-1.26	-0.34	-1.59	0.156774	0.309891	-6.12
263768_x_	putative Athila retroelement ORF1 prot	---	---	1.10	0.14	1.59	0.15678	0.309891	-6.12
258466_at	hypothetical protein contains similarity	---	AT3G06040	-1.16	-0.21	-1.59	0.156811	0.309926	-6.12
265246_at	putative pectinesterase	ATPMEPCR	AT2G43050	-1.16	-0.22	-1.59	0.156827	0.309931	-6.12
259483_at	hypothetical protein predicted by gene	---	AT1G43980	1.13	0.17	1.59	0.156871	0.309987	-6.12
262816_at	alkylation repair-like protein	---	AT1G11780	-1.20	-0.26	-1.59	0.156882	0.309987	-6.12
248310_at	putative protein similar to unknown pro	CPuORF14	AT5G52550 /	1.13	0.17	1.59	0.156898	0.30999	-6.12
254731_at	hypothetical protein	---	AT4G13750	-1.15	-0.21	-1.59	0.15695	0.310066	-6.12
253222_at	chalcone synthase - like protein chalc	---	AT4G34850	-1.11	-0.15	-1.59	0.157	0.310139	-6.12
256962_at	glucan endo-1,3-beta-glucosidase pre	---	AT3G13560	-1.41	-0.49	-1.59	0.157055	0.310166	-6.12

261707_at	unknown protein	---	AT1G32650	-1.12	-0.17	-1.59	0.157045	0.310166	-6.12
256851_at	hypothetical protein predicted by gene	---	AT3G27930	1.11	0.16	1.59	0.157033	0.310166	-6.12
257743_at	unknown protein	---	AT3G27390	1.20	0.26	1.59	0.157079	0.310171	-6.12
263029_at	unknown protein	---	AT1G24050	-1.10	-0.14	-1.59	0.157085	0.310171	-6.12
262506_at	unknown protein Similar to gb|X84260	NADK2	AT1G21640	-1.20	-0.26	-1.59	0.157116	0.310207	-6.12
252416_at	chromosome assembly protein homol	ATSMC2	AT3G47460	-1.10	-0.14	-1.59	0.157137	0.310221	-6.13
260128_at	hypothetical protein similar to Yml014v	---	AT1G36310	-1.15	-0.20	-1.59	0.157206	0.310331	-6.13
257231_at	DegP protease contains similarity to D	DEGP12	AT3G16550	1.11	0.16	1.59	0.157299	0.310486	-6.13
266106_at	putative microtubule-associated protei	ATATG8E	AT2G45170	-1.23	-0.29	-1.59	0.157391	0.310643	-6.13
261794_at	hypothetical protein contains similarity	---	AT1G16060	-1.17	-0.22	-1.59	0.157433	0.310698	-6.13
262556_at	hypothetical protein	---	AT1G31370	-1.12	-0.16	-1.59	0.157472	0.310747	-6.13
253267_at	putative protein TEB4 protein, Homo s	---	AT4G34100	-1.16	-0.21	-1.59	0.157485	0.310747	-6.13
260335_at	putative strictosidine synthase similar t	SS3	AT1G74000	1.37	0.46	1.59	0.157596	0.310938	-6.13
260451_at	putative AP2 domain transcription fact	---	AT1G72360	-1.58	-0.66	-1.59	0.157674	0.311066	-6.13
264016_at	putative auxin-regulated protein	---	AT2G21220	-1.14	-0.19	-1.59	0.157925	0.311534	-6.13
249806_at	putative protein contains similarity to u	---	AT5G23850	-1.31	-0.39	-1.59	0.158034	0.311695	-6.13
260711_at	myosin, putative similar to myosin GI:	MYA1	AT1G17580	-1.16	-0.21	-1.59	0.158034	0.311695	-6.13
247861_at	strong similarity to unknown protein (g	---	AT5G58160	-1.17	-0.22	-1.59	0.158086	0.31177	-6.13
245310_at	hypothetical protein ;supported by full-	RALFL31	AT4G13950	-1.36	-0.44	-1.59	0.158161	0.311865	-6.13
266008_at	hypothetical protein predicted by gens	---	AT2G37390	-1.16	-0.22	-1.59	0.15815	0.311865	-6.13
260839_at	unknown protein	---	AT1G43690	1.11	0.15	1.59	0.158283	0.312079	-6.13
252465_x_	putative protein several hypothetical pr	---	---	1.13	0.18	1.59	0.158339	0.312162	-6.13
248655_at	60S ribosomal protein L13a ;supporte	---	AT5G48760	-1.19	-0.25	-1.59	0.158603	0.312656	-6.13
262916_at	glutathione S-transferase, putative sin	ATGSTU16	AT1G59700	1.24	0.31	1.58	0.158829	0.313075	-6.14
245288_at	transcriptional adaptor like protein ; su	ADA2B	AT4G16420	1.13	0.18	1.58	0.158926	0.313237	-6.14
250849_at	putative protein NAC2, Arabidopsis th	NAC2	AT5G04410	1.13	0.18	1.58	0.158969	0.313295	-6.14
263704_at	unknown protein similar to unknown p	---	AT1G31130	1.16	0.22	1.58	0.158997	0.313324	-6.14
257046_at	ATPase, putative similar to spastin pr	---	AT3G19740	1.19	0.25	1.58	0.159031	0.313337	-6.14
264519_at	putative reverse transcriptase similar t	---	AT1G10000	-1.16	-0.22	-1.58	0.159026	0.313337	-6.14
246315_at	hypothetical protein	---	AT3G56870	-1.23	-0.30	-1.58	0.159056	0.313359	-6.14
265298_s_	putative retroelement pol polyprotein c	---	---	-1.12	-0.16	-1.58	0.159155	0.313526	-6.14
260366_at	putative protein kinase similar to C-ter	---	AT1G70460	-1.13	-0.17	-1.58	0.159299	0.313782	-6.14
253684_at	nucleotide pyrophosphatase - like prot	---	AT4G29690	1.15	0.20	1.58	0.159361	0.313879	-6.14
265208_at	putative giberellin beta-hydroxylase co	---	AT2G36690	1.42	0.51	1.58	0.159478	0.314081	-6.14
265435_s_	putative major intrinsic (channel) prote	---	AT1G31885 /	1.17	0.23	1.58	0.159498	0.314093	-6.14

255870_at	hypothetical protein predicted by gens	---	AT2G30280	1.13	0.17	1.58	0.159543	0.314156	-6.14
249796_at	26S proteasome, non-ATPase regulat	---	AT5G23540	1.13	0.18	1.58	0.15982	0.314674	-6.14
246711_at	putative protein	---	AT5G28190	-1.12	-0.16	-1.58	0.159906	0.314788	-6.14
261253_at	unknown protein ;supported by full-len	---	AT1G05840	-1.20	-0.26	-1.58	0.159899	0.314788	-6.14
253610_at	putative protein ; supported by cDNA:	VEL1	AT4G30200	1.16	0.21	1.58	0.15999	0.314873	-6.14
251960_at	GTPase AtRAB8 ;supported by full-le	HEMB1	AT1G69740 /	-1.13	-0.18	-1.58	0.159978	0.314873	-6.14
254274_at	putative DNA binding protein DNA-bin	---	AT4G22770	1.20	0.26	1.58	0.159963	0.314873	-6.14
246052_at	putative protein predicted proteins, Ar	---	AT5G08310	1.17	0.23	1.58	0.160015	0.314894	-6.14
258021_at	hypothetical protein predicted genema	PUB25	AT3G19380	1.47	0.56	1.58	0.160033	0.314902	-6.14
259505_at	hypothetical protein contains similarity	---	AT1G15810	1.18	0.24	1.58	0.16006	0.314928	-6.14
264436_at	putative glutathione S-transferase TSI	ERD9	AT1G10370	-1.61	-0.68	-1.58	0.160133	0.315045	-6.14
263812_at	putative replication protein A1	---	---	-1.11	-0.15	-1.58	0.160161	0.315072	-6.14
264587_at	putative ligand-gated ion channel prote	ATGLR3.4	AT1G05200	1.53	0.61	1.58	0.160176	0.315076	-6.14
254024_at	putative pathogenesis-related protein	---	AT4G25780	-1.23	-0.30	-1.58	0.160338	0.315367	-6.14
254025_at	putative pathogenesis-related protein	---	AT4G25790	1.10	0.14	1.58	0.160362	0.315386	-6.14
249141_at	putative protein similar to unknown pro	---	AT5G43200	-1.12	-0.16	-1.58	0.160391	0.315417	-6.14
262083_at	hypothetical protein predicted by gene	---	AT1G56100	-1.14	-0.19	-1.58	0.160425	0.315456	-6.14
256572_at	40S RIBOSOMAL PROTEIN S25, put	---	AT3G30740	-1.13	-0.17	-1.58	0.160452	0.315483	-6.14
254177_at	putative protein gene T22C1.1, Caenc	---	AT4G23860	1.19	0.26	1.58	0.160494	0.31551	-6.14
261393_at	NAM (no apical meristem)-like protein	SMB	AT1G79580	1.12	0.16	1.58	0.160491	0.31551	-6.14
254725_at	putative protein various predicted prot	---	AT4G13650	1.16	0.21	1.58	0.160633	0.315757	-6.15
254817_at	putative SWH1 protein SWH1 protein	ORP2B	AT4G12460	1.14	0.19	1.58	0.160724	0.315787	-6.15
257769_at	indoleacetic acid (IAA)-inducible gene	IAA7	AT3G23050	-2.23	-1.16	-1.58	0.160718	0.315787	-6.15
256202_s_	hypothetical protein	---	AT1G48150 /	-1.12	-0.16	-1.58	0.160726	0.315787	-6.15
263557_at	putative homeodomain transcription fa	BLH7	AT2G16400	-1.17	-0.23	-1.58	0.160692	0.315787	-6.15
256564_at	alpha/beta hydrolase, putative contain	MES11	AT3G29770	1.37	0.45	1.58	0.160694	0.315787	-6.15
260994_at	hypothetical protein contains similarity	---	AT1G12130	-1.15	-0.20	-1.58	0.160732	0.315787	-6.15
263868_at	hypothetical protein predicted by gene	---	AT2G36840	-1.15	-0.20	-1.58	0.160801	0.315897	-6.15
254671_at	MuDR transposable element - like pro	---	---	-1.13	-0.17	-1.58	0.160855	0.315976	-6.15
265797_at	Expressed protein ; supported by full-le	---	AT2G35710	1.68	0.75	1.58	0.160894	0.316025	-6.15
253167_at	calmodulin-domain protein kinase CDF	CPK5	AT4G35310	-1.17	-0.22	-1.58	0.160938	0.316084	-6.15
260200_at	unknown protein ; supported by full-le	---	AT1G67620	-1.14	-0.19	-1.58	0.160956	0.316091	-6.15
247396_at	putative protein predicted proteins, Or	---	AT5G62930	-1.12	-0.16	-1.57	0.16099	0.316131	-6.15
261327_at	transcription factor, putative contains /	---	AT1G44830	-2.04	-1.03	-1.57	0.161217	0.316551	-6.15
256383_at	hypothetical protein ; supported by full-	---	AT1G66820	-1.16	-0.21	-1.57	0.161264	0.316589	-6.15

250731_at	putative protein contains similarity to M	AGL96	AT5G06500	1.11	0.16	1.57	0.161256	0.316589	-6.15
256820_at	far-red impaired response protein, put	FHY3	AT3G22170	1.11	0.16	1.57	0.161336	0.316703	-6.15
247532_at	putative protein disease resistance pr	---	AT5G61560	1.45	0.53	1.57	0.161359	0.31672	-6.15
263286_at	40S ribosomal protein S14 ;supported	---	AT2G36160	-1.21	-0.28	-1.57	0.161386	0.31674	-6.15
254801_at	endoxyloglucan transferase-like prote	---	AT4G13080	-1.10	-0.14	-1.57	0.161397	0.31674	-6.15
256247_at	SRF-type transcription factor contains	AGL91	AT3G66656	1.12	0.16	1.57	0.161532	0.316951	-6.15
258600_at	putative protein kinase contains Pfam	---	AT3G02810	-1.13	-0.18	-1.57	0.16152	0.316951	-6.15
248445_at	unknown protein ;supported by full-ler	---	AT5G51170	1.17	0.23	1.57	0.161562	0.316981	-6.15
253558_at	kinase binding protein - like Skb1 prot	SKB1	AT4G31120	1.15	0.20	1.57	0.161583	0.316996	-6.15
266252_at	hypothetical protein predicted by gens	---	AT2G27520	1.14	0.18	1.57	0.161664	0.317127	-6.15
262934_s_	hypothetical protein contains similarity	---	AT1G16270 /	1.18	0.24	1.57	0.161787	0.317342	-6.15
260331_at	hypothetical protein contains Pfam pro	---	AT1G80270	1.71	0.78	1.57	0.161906	0.317546	-6.15
259674_at	thaumatin-like protein similar to thaum	---	AT1G77700	-1.15	-0.20	-1.57	0.161997	0.317698	-6.15
262334_at	hypothetical protein similar to putative	---	AT1G64010	-1.14	-0.19	-1.57	0.162026	0.317728	-6.15
256217_at	hypothetical protein predicted by gene	---	AT1G56320	-1.28	-0.35	-1.57	0.162041	0.31773	-6.15
254659_at	starch synthase-like protein bacterial a	SS4	AT4G18240	-1.23	-0.29	-1.57	0.1621	0.317819	-6.15
253024_at	putative protein	---	AT4G38080	-1.76	-0.81	-1.57	0.162114	0.317819	-6.15
250957_at	photoreceptor-interacting protein - like	---	AT5G03250	-1.11	-0.15	-1.57	0.16218	0.31792	-6.15
262694_at	unknown protein	---	AT1G62790	1.31	0.39	1.57	0.162224	0.31798	-6.15
266062_at	putative diacylglycerol kinase	---	AT2G18730	-1.10	-0.14	-1.57	0.162268	0.318038	-6.15
265732_at	predicted by genscan and genefinder	---	AT2G01300	-2.05	-1.03	-1.57	0.162289	0.318053	-6.15
267059_at	putative carboxymethylenebutenolidas	---	AT2G32520	1.13	0.18	1.57	0.162323	0.318091	-6.16
246871_at	extensin - like protein pAP8 protein, N	---	AT5G26070	-1.11	-0.15	-1.57	0.162403	0.318222	-6.16
266198_at	unknown protein predicted by genscan	---	AT2G38890	1.13	0.18	1.57	0.16242	0.318228	-6.16
261664_s_	hypothetical protein contains similarity	---	AT1G18320 /	1.20	0.26	1.57	0.162505	0.31831	-6.16
252426_at	putative protein proline transport helpe	---	AT3G47630	1.16	0.21	1.57	0.162484	0.31831	-6.16
254904_at	putative translation initiation factor IF-	---	AT4G11160	1.19	0.26	1.57	0.162508	0.31831	-6.16
257997_at	hypothetical protein similar to hypothet	---	AT3G27500	-1.11	-0.15	-1.57	0.162518	0.31831	-6.16
252136_at	calmodulin-like protein flagellar calmo	---	AT3G50770	1.98	0.98	1.57	0.162639	0.318493	-6.16
259290_at	putative cyclin similar to cyclin cyc1b G	CYCB1;3	AT3G11520	1.19	0.26	1.57	0.162633	0.318493	-6.16
255414_at	hypothetical protein	---	AT4G03156	-1.11	-0.15	-1.57	0.162719	0.318621	-6.16
257987_at	fertilization-independent endosperm pr	FIE	AT3G20740	-1.13	-0.17	-1.57	0.162812	0.318748	-6.16
246187_at	putative protein	AT5G21020	---	1.18	0.24	1.57	0.162811	0.318748	-6.16
265691_at	unknown protein predicted by genscan	---	AT2G24330	-1.21	-0.28	-1.57	0.162832	0.318761	-6.16
266817_at	hypothetical protein similar to hypothet	HUB1	AT2G44950	1.18	0.24	1.57	0.162846	0.318761	-6.16

264010_at	putative disease resistance response p	---	AT2G21100	-1.22	-0.29	-1.57	0.162866	0.318772	-6.16
252431_at	putative protein	MAG2	AT3G47700	1.22	0.28	1.57	0.162946	0.318902	-6.16
262957_s_	RNA polymerase II subunit, putative s	NRPB8A	AT1G54250 /	1.10	0.14	1.57	0.16298	0.31894	-6.16
249804_at	galactinol synthase	AtGolS5	AT5G23790	-1.12	-0.16	-1.57	0.163053	0.319003	-6.16
263772_at	Expressed protein ; supported by full-l	ELF4-L3	AT2G06255	-1.26	-0.33	-1.57	0.163041	0.319003	-6.16
259525_at	hypothetical protein	ATEXPA7	AT1G12560	-1.12	-0.17	-1.57	0.163054	0.319003	-6.16
247125_at	putative protein contains similarity to u	---	AT5G66070	1.40	0.48	1.57	0.163073	0.319013	-6.16
250949_at	putative protein	---	AT5G03510	-1.12	-0.16	-1.57	0.163204	0.319222	-6.16
253661_at	putative protein bZIP protein - Arabido	---	AT4G30130	1.14	0.19	1.57	0.163208	0.319222	-6.16
265013_at	unknown protein similar to EST gb|T76	---	AT1G24460	1.13	0.17	1.56	0.163289	0.319354	-6.16
261808_at	DNA damage repair protein, putative s	DRT111	AT1G30480	-1.12	-0.16	-1.56	0.163484	0.319707	-6.16
255783_at	hypothetical protein contains Pfam pro	iqd32	AT1G19870	-1.20	-0.27	-1.56	0.163509	0.319729	-6.16
260599_at	cytochrome P450, putative similar to S	CYP708A1	AT1G55940	-1.11	-0.15	-1.56	0.163544	0.31977	-6.16
258456_at	putative protein kinase similar to mitog	WNK2	AT3G22420	-1.41	-0.49	-1.56	0.163604	0.319846	-6.16
257001_at	Sm protein, putative similar to GB:AAI	---	AT3G14080	1.14	0.19	1.56	0.163611	0.319846	-6.16
261181_at	monosaccharide transporter, putative	---	AT1G34580	-1.17	-0.22	-1.56	0.163632	0.31986	-6.16
247499_at	predicted protein	---	AT5G61865	-1.13	-0.18	-1.56	0.163676	0.319919	-6.16
247787_at	putative protein various predicted prote	---	AT5G58640	1.11	0.16	1.56	0.163694	0.319925	-6.16
249647_at	putative protein hypothetical proteins -	---	AT5G37040	-1.17	-0.23	-1.56	0.163769	0.320045	-6.16
265328_at	unknown protein	---	AT2G18200	1.10	0.14	1.56	0.163825	0.320128	-6.16
260815_at	chloroplast inner envelope protein, pu	TIC110	AT1G06950	1.23	0.30	1.56	0.163889	0.320192	-6.16
257682_at	hypothetical protein predicted by gene	---	AT3G13240	-1.11	-0.15	-1.56	0.1639	0.320192	-6.16
260763_at	RING-H2 finger protein RHA3a, putati	---	AT1G49220	-1.10	-0.14	-1.56	0.163889	0.320192	-6.16
246393_at	phosphoglycerate kinase, putative sim	---	AT1G58150	-1.14	-0.19	-1.56	0.16396	0.320281	-6.16
253649_at	putative protein predicted protein, Ara	---	AT4G29790	1.27	0.34	1.56	0.163992	0.320317	-6.16
248025_at	NOI protein, nitrate-induced	NOI	AT5G55850	-1.16	-0.21	-1.56	0.164063	0.320429	-6.16
258576_at	putative 40S ribosomal protein S16 sin	---	AT3G04230	1.19	0.25	1.56	0.164111	0.320494	-6.17
261569_at	DNA-binding protein, putative similar t	LHY	AT1G01060	-1.15	-0.21	-1.56	0.16416	0.320562	-6.17
262690_at	PPR-repeat protein contains multiple P	---	AT1G62720	1.12	0.17	1.56	0.164288	0.320786	-6.17
266839_at	unknown protein	ELF3	AT2G25930	1.12	0.16	1.56	0.164325	0.320798	-6.17
248107_at	small Ras-like GTP-binding protein (gb	RAN3	AT5G55190	-1.11	-0.15	-1.56	0.164337	0.320798	-6.17
257804_at	protein kinase, putative similar to som	---	AT3G18810	-1.12	-0.16	-1.56	0.164323	0.320798	-6.17
252246_at	putative protein various predicted prote	---	AT3G49725 /	1.14	0.19	1.56	0.164375	0.320844	-6.17
263030_at	hypothetical protein predicted by gens	---	AT1G24060	-1.10	-0.14	-1.56	0.164399	0.320865	-6.17
260385_at	putative flavonol sulfotransferase simil	SOT18	AT1G74090	1.17	0.22	1.56	0.164529	0.32109	-6.17

248570_at	receptor protein kinase-like	---	AT5G49780	1.12	0.16	1.56	0.164625	0.32125	-6.17
247381_at	auxin-independent growth promoter-lik	---	AT5G63390	1.14	0.19	1.56	0.164659	0.32129	-6.17
261485_at	unknown protein ;supported by full-len	UTR3	AT1G14360	1.39	0.48	1.56	0.164696	0.321334	-6.17
264602_at	putative Ser/Thr protein kinase similar	---	AT1G04700	-1.13	-0.18	-1.56	0.164716	0.321346	-6.17
255357_at	putative pectinesterase	---	AT4G03930	-1.12	-0.16	-1.56	0.164827	0.321534	-6.17
258794_at	ankyrin-like protein similar to ankyrin p	---	AT3G04710	1.32	0.40	1.56	0.164845	0.321542	-6.17
263281_at	putative glycine-rich RNA-binding prote	---	AT2G14160	1.13	0.18	1.56	0.164935	0.32169	-6.17
263886_at	hypothetical protein predicted by gens	TKI1	AT2G36960	-1.11	-0.15	-1.56	0.165007	0.321776	-6.17
257492_at	hypothetical protein contains similarity	ARR19	AT1G49190	-1.10	-0.14	-1.56	0.164997	0.321776	-6.17
262227_s_	26S proteasome ATPase subunit, put	---	AT1G53750 /	1.11	0.16	1.56	0.165061	0.321799	-6.17
248991_at	putative protein contains similarity to d	---	AT5G45220	1.21	0.28	1.56	0.165053	0.321799	-6.17
258007_at	putative tyrosine phosphatase similar t	ATPEN2	AT3G19420	-1.20	-0.26	-1.56	0.165052	0.321799	-6.17
266614_at	unknown protein	---	AT2G14910	1.15	0.20	1.56	0.165223	0.322087	-6.17
267141_at	putative MYB family transcription facto	---	AT2G38090	1.18	0.24	1.56	0.165484	0.322569	-6.17
256584_at	unknown protein	---	AT3G28750	1.12	0.17	1.56	0.165504	0.322579	-6.17
254696_at	hypothetical protein	---	AT4G17930	1.11	0.15	1.55	0.165618	0.322774	-6.17
257478_at	hypothetical protein similar to putative	WAKL2	AT1G16130	1.33	0.41	1.55	0.165656	0.32282	-6.17
262354_at	H+-transporting ATPase protein, puta	VHA-E3	AT1G64200	-1.33	-0.41	-1.55	0.166102	0.323549	-6.18
250144_at	putative protein various predicted prot	---	AT5G14680	1.24	0.31	1.55	0.166108	0.323549	-6.18
264004_at	Expressed protein ; supported by full-le	---	AT2G22425	-1.16	-0.21	-1.55	0.166087	0.323549	-6.18
250106_at	putative protein strong similarity to unk	---	AT5G16640	-1.12	-0.17	-1.55	0.16612	0.323549	-6.18
251567_at	putative protein several hypothetical pr	---	AT3G58230	1.14	0.19	1.55	0.166129	0.323549	-6.18
255460_at	hypothetical protein similar to A. thalia	---	AT4G02800	-1.12	-0.16	-1.55	0.166129	0.323549	-6.18
257722_at	putative chloroplast nucleoid DNA-bin	---	AT3G18490	-1.25	-0.32	-1.55	0.16606	0.323549	-6.18
266187_at	putative retroelement pol polyprotein	---	AT2G38970	-1.23	-0.30	-1.55	0.166155	0.323572	-6.18
265121_at	similar to flavin-containing monooxyge	FMO GS-OX	AT1G62560	-1.26	-0.33	-1.55	0.166177	0.323586	-6.18
249205_at	cycloartenol synthase	MRN1	AT5G42600	-1.24	-0.31	-1.55	0.166252	0.323677	-6.18
249655_at	putative helicase PIF1 protein - Caeno	---	---	-1.12	-0.17	-1.55	0.166248	0.323677	-6.18
259177_at	hypothetical protein similar to putative	---	AT3G01630	-1.12	-0.16	-1.55	0.166279	0.323702	-6.18
259446_at	hypothetical protein contains similarity	---	AT1G02410	1.17	0.23	1.55	0.166315	0.323745	-6.18
260520_at	mannosyl-oligosaccharide alpha-1,2-m	---	AT1G51590	-1.14	-0.19	-1.55	0.166433	0.323948	-6.18
267536_at	phospholipase D ; supported by cDNA	PLDBETA1	AT2G42010	1.15	0.20	1.55	0.166602	0.324248	-6.18
261449_at	putative ATPase similar to GB:AAF283	---	AT1G21120	1.24	0.31	1.55	0.166644	0.324282	-6.18
247035_at	putative protein similar to unknown pro	ALC	AT5G67110	-1.12	-0.16	-1.55	0.166648	0.324282	-6.18
256354_at	dormancy related protein, putative sim	---	AT1G54870	-1.17	-0.23	-1.55	0.166697	0.324349	-6.18

257135_at	hypothetical protein similar to oxidored	---	AT3G12900	-1.16	-0.22	-1.55	0.166752	0.32443	-6.18
249288_at	unknown protein ;supported by full-ler	---	AT5G41050	-1.46	-0.54	-1.55	0.166787	0.324471	-6.18
258401_at	unknown protein ; supported by cDNA	---	AT3G15430	-1.16	-0.21	-1.55	0.166808	0.324483	-6.18
263094_at	hypothetical protein predicted by gens	---	AT2G16020	-1.14	-0.19	-1.55	0.166888	0.324611	-6.18
264096_at	Expressed protein ; supported by full-l	---	AT1G78995	-1.29	-0.37	-1.55	0.166903	0.324613	-6.18
246760_at	putative protein predicted proteins, Ca	---	AT5G27970	-1.12	-0.16	-1.55	0.166958	0.324691	-6.18
258200_at	putative ATPase similar to ATPase II C	---	AT3G13900	-1.16	-0.21	-1.55	0.167003	0.324724	-6.18
254676_at	putative protein Hypothetical protein Y	---	AT4G18460	-1.16	-0.22	-1.55	0.167002	0.324724	-6.18
245110_at	hypothetical protein predicted by gene	---	AT2G41550	-1.11	-0.15	-1.55	0.167038	0.324764	-6.18
265484_at	unknown protein ; supported by cDNA	OTP51	AT2G15820	1.14	0.19	1.55	0.167091	0.324818	-6.18
257981_at	ethylene-insensitive 3 (EIN3) identical	EIN3	AT3G20770	-1.13	-0.17	-1.55	0.167094	0.324818	-6.18
256526_at	disease resistance protein, putative si	---	AT1G66090	-1.14	-0.18	-1.55	0.167131	0.324863	-6.18
250881_at	putative protein	---	AT5G04080	-1.20	-0.26	-1.55	0.167186	0.324941	-6.18
263787_at	unknown protein ; supported by cDNA	---	AT2G46420	1.20	0.27	1.55	0.167209	0.324959	-6.18
261620_s_	ribosomal protein L9, putative similar t	PGY2	AT1G33120 /	-1.18	-0.24	-1.55	0.167348	0.325097	-6.18
246561_at	putative protein hypothetical protein F	---	AT5G15570	1.13	0.18	1.55	0.167323	0.325097	-6.18
265255_at	unknown protein ; supported by cDNA	---	AT2G28420	1.24	0.31	1.55	0.167351	0.325097	-6.18
263019_at	trehalose 6-phosphate synthase, puta	ATTPS9	AT1G23870	1.44	0.52	1.55	0.167348	0.325097	-6.18
254369_at	putative protein	---	AT4G21720	-1.19	-0.25	-1.55	0.167339	0.325097	-6.18
250414_at	putative protein Glr5, Arabidopsis thal	GLR2.6	AT5G11180	-1.11	-0.16	-1.55	0.167448	0.325258	-6.18
248737_at	unknown protein	---	AT5G48120	1.20	0.26	1.55	0.167516	0.325358	-6.18
258176_at	B regulatory subunit of PP2A, putative	---	AT3G21650	1.26	0.34	1.55	0.167543	0.325358	-6.18
260546_at	putative trypsin inhibitor ;supported by	ATTI2	AT2G43520	1.63	0.71	1.55	0.167534	0.325358	-6.18
248201_at	putative protein similar to unknown pro	PTAC15	AT5G54180	-1.30	-0.38	-1.55	0.16762	0.32548	-6.18
254095_at	oleosin, 18.5K	OLEO1	AT4G25140	1.13	0.18	1.55	0.167887	0.32597	-6.19
248976_at	putative protein strong similarity to unk	ARAD2	AT5G44930	1.17	0.22	1.55	0.167963	0.326091	-6.19
254411_at	hypothetical protein	---	---	1.15	0.20	1.54	0.167994	0.326123	-6.19
252352_at	Expressed protein ; supported by full-l	---	AT3G48185	1.17	0.23	1.54	0.16807	0.326243	-6.19
253668_at	snRNP Sm protein F - like Sm protein	RUXF	AT4G30220	-1.15	-0.21	-1.54	0.168118	0.326308	-6.19
260692_at	hypothetical protein predicted by gene	---	AT1G32430	-1.12	-0.17	-1.54	0.168142	0.326327	-6.19
246215_at	putative cytoskeletal protein ; supporte	---	AT4G37180	1.35	0.44	1.54	0.168176	0.326365	-6.19
256887_at	hypothetical protein predicted by gene	---	AT3G15150	1.15	0.20	1.54	0.168238	0.32643	-6.19
245834_at	transposon protein, putative similar to	---	---	-1.11	-0.15	-1.54	0.168228	0.32643	-6.19
249215_at	dihydroflavonol 4-reductase	DFR	AT5G42800	-1.21	-0.28	-1.54	0.168291	0.326505	-6.19
254739_at	putative disease resistance protein Hc	AtRLP48	AT4G13880	1.12	0.17	1.54	0.168338	0.326569	-6.19

259737_at	acyl-CoA synthetase, putative similar	---	AT1G64400	1.48	0.56	1.54	0.168403	0.326666	-6.19
264853_at	putative ligand-gated ion channel prote	GLR2	AT2G17260 /	-1.16	-0.21	-1.54	0.168464	0.326702	-6.19
246848_at	putative protein	---	AT5G26840	-1.14	-0.19	-1.54	0.168451	0.326702	-6.19
261571_at	hypothetical protein predicted by gene	---	AT1G01150	1.12	0.16	1.54	0.168462	0.326702	-6.19
267137_at	hypothetical protein predicted by gens	ACPT	AT2G23410	-1.11	-0.15	-1.54	0.168518	0.326752	-6.19
255308_at	putative component of vesicle-mediate	NSF	AT4G04910	-1.15	-0.21	-1.54	0.168508	0.326752	-6.19
255178_at	may be a pseudogene	---	---	-1.11	-0.15	-1.54	0.168587	0.326858	-6.19
254960_at	predicted protein	---	AT4G10845	-1.14	-0.19	-1.54	0.168654	0.326956	-6.19
264176_at	bZIP-like protein similar to bZIP (leuci	---	AT1G02110	-1.23	-0.30	-1.54	0.168667	0.326956	-6.19
250157_at	prx10 peroxidase - like protein prx10 p	---	AT5G15180	-1.13	-0.18	-1.54	0.1687	0.326983	-6.19
264874_at	unknown protein Location of EST gb|Z	---	AT1G24240	-1.12	-0.16	-1.54	0.16871	0.326983	-6.19
252092_at	mucin-like protein hemomucin, Droso	SSL4	AT3G51420	-1.24	-0.31	-1.54	0.168747	0.327028	-6.19
249327_at	anion channel protein (gb|AAC05742.1	ATCLC-A	AT5G40890	-1.29	-0.37	-1.54	0.168905	0.327196	-6.19
265886_at	putative protein phosphatase 2C ; sup	---	AT2G25610 /	1.28	0.36	1.54	0.168894	0.327196	-6.19
259978_at	putative cell division control protein cd	CDKB2;1	AT1G76540	-1.21	-0.28	-1.54	0.168864	0.327196	-6.19
248225_at	unknown protein	---	AT5G53740	1.12	0.17	1.54	0.168896	0.327196	-6.19
250029_at	galactose-1-phosphate uridyl transfera	---	AT5G18200	-1.16	-0.21	-1.54	0.168873	0.327196	-6.19
266944_at	unknown protein predicted by genefinc	---	AT2G18870 /	-1.14	-0.19	-1.54	0.168979	0.327311	-6.19
266337_at	putative ligand-gated ion channel subu	ATGLR3.5	AT2G32390	1.12	0.16	1.54	0.169163	0.32764	-6.19
252448_at	beta-D-glucan exohydrolase - like pro	---	AT3G47050	-1.14	-0.19	-1.54	0.169185	0.327655	-6.19
255877_at	putative PTR2 family peptide transport	---	AT2G40460	1.40	0.48	1.54	0.169237	0.327727	-6.19
251821_at	protein phosphatase 2C - like protein	---	AT3G55050	-1.29	-0.36	-1.54	0.1694	0.328014	-6.19
248249_at	protein phosphatase 2C-like ; support	---	AT5G53140	-1.13	-0.17	-1.54	0.169438	0.328061	-6.19
245257_at	calmodulin ; supported by cDNA: gi_58	CAM8	AT4G14640	1.13	0.18	1.54	0.169616	0.328374	-6.20
255517_at	putative endo-1,4-beta glucanase sim	AtGH9B13	AT4G02290	-1.17	-0.22	-1.54	0.169643	0.328374	-6.20
254150_at	putative protein storage protein - Popu	---	AT4G24350	1.90	0.92	1.54	0.169633	0.328374	-6.20
264006_at	homeodomain transcription factor (ATH	ATHB6	AT2G22430	-1.20	-0.26	-1.54	0.169659	0.328377	-6.20
262512_at	Expressed protein ; supported by full-le	---	AT1G17145	1.32	0.40	1.54	0.169703	0.328435	-6.20
256540_at	polyprotein, putative similar to polypro	---	---	-1.11	-0.15	-1.54	0.169728	0.328454	-6.20
258532_at	ribosomal protein L29, putative similar	---	AT3G06700	1.37	0.45	1.54	0.169765	0.328499	-6.20
263800_at	hypothetical protein predicted by gens	---	AT2G24600	2.10	1.07	1.54	0.1698	0.328539	-6.20
265370_s_	unknown protein related to GB:AAD15	---	AT3G30415	1.11	0.16	1.54	0.169829	0.328567	-6.20
255510_at	polycomb group - like protein similar t	SWN	AT4G02020	1.18	0.24	1.54	0.169904	0.32858	-6.20
261595_at	hypothetical protein predicted by gens	---	AT1G33070	-1.10	-0.14	-1.54	0.169866	0.32858	-6.20
253460_at	hypothetical protein	---	AT4G32130	1.16	0.21	1.54	0.169908	0.32858	-6.20

258019_at	hypothetical protein predicted by gene	---	AT3G19470	-1.12	-0.17	-1.54	0.169883	0.32858	-6.20
258792_at	hypothetical protein predicted by gene	---	AT3G04640	1.51	0.59	1.54	0.169897	0.32858	-6.20
246134_at	protein kinase tousled ; supported by	TSL	AT5G20930	1.16	0.22	1.54	0.169968	0.32864	-6.20
245516_at	hypothetical protein	---	AT4G15820	1.16	0.22	1.54	0.16996	0.32864	-6.20
259345_s_	hypothetical protein predicted by gene	---	AT3G03700 /	1.32	0.40	1.54	0.169992	0.328659	-6.20
266699_at	putative ribosomal protein L28 ; suppo	---	AT2G19730	-1.22	-0.29	-1.54	0.17007	0.328729	-6.20
266546_at	putative AT-hook DNA-binding protein	---	AT2G35270	-1.11	-0.15	-1.54	0.170074	0.328729	-6.20
266859_at	putative MADS-box protein	AGL41	AT2G26880	-1.15	-0.20	-1.54	0.170087	0.328729	-6.20
254700_at	hypothetical protein	---	AT4G18000	1.14	0.19	1.54	0.17006	0.328729	-6.20
264451_s_	putative lectin receptor kinase very sim	---	---	1.13	0.18	1.54	0.1701	0.328729	-6.20
257266_at	RNA-binding protein contains Pfam pr	---	AT3G15010	1.11	0.16	1.54	0.170137	0.328772	-6.20
253440_at	putative protein ;supported by full-leng	TIFY8	AT4G32570	-1.10	-0.14	-1.54	0.170203	0.328845	-6.20
263769_at	5S ribosomal RNA	---	---	-1.15	-0.20	-1.54	0.170199	0.328845	-6.20
255867_at	hypothetical protein predicted by gens	---	AT2G30370	1.12	0.16	1.54	0.170234	0.328876	-6.20
249192_at	brain and reproductive organ-expresse	---	AT5G42470	-1.10	-0.14	-1.54	0.170297	0.32897	-6.20
249740_at	unknown protein	---	AT5G24500	-1.20	-0.26	-1.54	0.170348	0.32904	-6.20
248136_at	RNA helicase-like protein	---	AT5G54910	1.25	0.32	1.53	0.170372	0.32906	-6.20
253102_at	Expressed protein ; supported by full-l	---	AT4G36105	-1.19	-0.25	-1.53	0.170507	0.329292	-6.20
260777_at	mitochondrial carrier protein, putative	---	AT1G14560	-1.13	-0.18	-1.53	0.170583	0.32941	-6.20
255821_at	putative initiator tRNA phosphoribosyl-	---	AT2G40570	1.13	0.18	1.53	0.170629	0.329471	-6.20
255730_at	dihydroflavonol 4-reductase, putative	---	AT1G25460	1.12	0.17	1.53	0.170655	0.329495	-6.20
248454_at	receptor protein kinase-like	---	AT5G51350	-1.21	-0.27	-1.53	0.170722	0.329596	-6.20
260585_at	unknown protein	EMB2777	AT2G43650	1.29	0.37	1.53	0.170765	0.329632	-6.20
255099_at	hypothetical protein	---	---	1.12	0.16	1.53	0.17077	0.329632	-6.20
252070_at	short-chain alcohol dehydrogenase-lik	---	AT3G51680	1.16	0.22	1.53	0.170809	0.32968	-6.20
255977_at	ribosomal protein S18, putative simila	---	AT1G34030	-1.18	-0.24	-1.53	0.170958	0.329938	-6.20
257090_at	protein kinase, putative contains Pfam	---	AT3G20530	-1.14	-0.19	-1.53	0.171041	0.330072	-6.20
266734_at	hypothetical protein predicted by gene	---	AT2G46900	-1.15	-0.21	-1.53	0.171057	0.330075	-6.20
249161_at	20S proteasome subunit PAF1 (gb|AA	PAF1	AT5G42790	1.10	0.14	1.53	0.171101	0.330128	-6.20
247196_at	putative protein similar to unknown pro	AIL7	AT5G65510	-1.11	-0.15	-1.53	0.171114	0.330128	-6.20
257891_at	hypothetical protein predicted by gene	RFC3	AT3G17170	-1.21	-0.28	-1.53	0.17119	0.330219	-6.20
248376_at	unknown protein ; supported by full-ler	---	AT5G51880	-1.13	-0.17	-1.53	0.17119	0.330219	-6.20
261362_s_	ribosomal protein identical to GB:CAB	---	AT1G41880 /	-1.24	-0.31	-1.53	0.171355	0.330481	-6.21
262907_at	hypothetical protein predicted by gene	CRR28	AT1G59720	-1.14	-0.19	-1.53	0.171343	0.330481	-6.20
264077_at	putative RAD51B-like DNA repair prote	RAD51B	AT2G28560	-1.13	-0.17	-1.53	0.171489	0.330684	-6.21

245536_at	hypothetical protein	SDG2	AT4G15180	1.12	0.17	1.53	0.171477	0.330684	-6.21
255570_at	putative carrier protein similar to mitoc	ADNT1	AT4G01100	1.14	0.19	1.53	0.171515	0.330698	-6.21
245691_at	zinc finger protein - like	ELF6	AT5G04240	1.20	0.26	1.53	0.171525	0.330698	-6.21
263284_at	unknown protein	---	AT2G36100	1.13	0.17	1.53	0.171563	0.330742	-6.21
AFFX-r2-At	Arabidopsis thaliana /REF=U37281 /D	---	---	-1.13	-0.17	-1.53	0.171712	0.331002	-6.21
253842_at	putative protein putative proteins from	---	AT4G27860	1.43	0.51	1.53	0.171945	0.331403	-6.21
254437_s_	putative protein	---	AT3G06433	-1.22	-0.29	-1.53	0.171949	0.331403	-6.21
264776_at	unknown protein location of EST gb|T4	---	AT1G22860	-1.13	-0.17	-1.53	0.172011	0.331495	-6.21
264530_at	hypothetical protein	---	AT1G30780	-1.16	-0.21	-1.53	0.172034	0.331511	-6.21
257140_at	MYB family transcription factor (hsr1),	MYB30	AT3G28910	-1.31	-0.39	-1.53	0.172053	0.33152	-6.21
267130_at	hypothetical protein predicted by gens	---	AT2G23390	1.19	0.25	1.53	0.172146	0.331638	-6.21
263899_at	hypothetical protein predicted by gens	EMB2219	AT2G21710	-1.16	-0.22	-1.53	0.172158	0.331638	-6.21
259692_at	unknown protein	---	AT1G63080	-1.13	-0.17	-1.53	0.172133	0.331638	-6.21
264459_at	putative reverse transcriptase similar t	---	---	-1.21	-0.28	-1.53	0.172174	0.331642	-6.21
261529_at	hypothetical protein contains similarity	---	AT1G14430	-1.12	-0.16	-1.53	0.172422	0.33209	-6.21
256432_at	hypothetical protein similar to hypothet	---	AT3G10990	1.11	0.15	1.53	0.172456	0.332101	-6.21
245462_at	transcription factor like protein	---	AT4G17020	1.14	0.19	1.53	0.172447	0.332101	-6.21
266764_at	putative pectinesterase ;supported by	---	AT2G47050	1.14	0.19	1.53	0.172485	0.332127	-6.21
256325_at	hypothetical protein	---	AT3G02330	1.15	0.21	1.53	0.172535	0.332195	-6.21
257781_at	spastin protein, putative similar to spa	---	AT3G27120	1.11	0.15	1.53	0.17257	0.332234	-6.21
258645_s_	exopolygalacturonase identical to exo	---	AT3G07850 /	1.13	0.18	1.53	0.172625	0.332313	-6.21
256184_at	epsilon subunit of mitochondrial F1-AT	---	AT1G51650	1.19	0.25	1.53	0.172663	0.332358	-6.21
246472_at	putative protein predicted protein, Ara	---	AT5G17130	1.10	0.14	1.53	0.172721	0.332441	-6.21
254684_at	glycine-rich RNA-binding protein AtGR	GR-RBP2	AT4G13850	1.20	0.26	1.52	0.172814	0.332593	-6.21
261847_at	hypothetical protein predicted by gene	---	AT1G11560	-1.16	-0.22	-1.52	0.172875	0.332682	-6.21
262042_at	polygalacturonase, putative similar to	---	AT1G80140	-1.13	-0.18	-1.52	0.172918	0.332736	-6.21
246769_at	hypothetical protein	---	AT5G27440	1.12	0.17	1.52	0.172933	0.332737	-6.21
255666_at	putative protein ;supported by full-leng	---	AT4G00390	-1.15	-0.20	-1.52	0.172957	0.332755	-6.21
260666_at	unknown protein ;supported by full-len	PARVUS	AT1G19300	-1.36	-0.44	-1.52	0.173023	0.332826	-6.21
257210_at	hypothetical protein	TTL2	AT3G14950	-1.10	-0.14	-1.52	0.173016	0.332826	-6.21
248575_at	ATP-dependent Clp protease ATP-bin	---	AT5G49840	1.11	0.15	1.52	0.173108	0.332961	-6.21
245358_at	PRL1 protein ;supported by full-length	PRL1	AT4G15900	-1.15	-0.20	-1.52	0.173141	0.332969	-6.21
251173_at	putative protein hypothetical protein A	---	AT3G63270	-1.11	-0.15	-1.52	0.173132	0.332969	-6.21
251346_at	putative protein hypothetical protein F	---	AT3G60980	-1.13	-0.17	-1.52	0.173243	0.333136	-6.22
253252_at	amidophosphoribosyltransferase 2 pre	ATASE2	AT4G34740	-1.21	-0.27	-1.52	0.173257	0.333136	-6.22

252044_at	outer envelope membrane protein-like	OEP7	AT3G52420	1.11	0.15	1.52	0.173358	0.33327	-6.22
264250_at	gamma glutamyl hydrolase, putative s	ATGGH2	AT1G78680	1.15	0.20	1.52	0.173363	0.33327	-6.22
245420_at	hypothetical protein	---	AT4G17410	1.14	0.19	1.52	0.17337	0.33327	-6.22
249832_at	disease resistance protein-like	---	AT5G23400	-1.16	-0.22	-1.52	0.173392	0.333283	-6.22
262224_at	hypothetical protein contains Pfam pro	OTP43	AT1G74900	1.11	0.15	1.52	0.173418	0.333301	-6.22
264455_at	hypothetical protein predicted by gens	---	AT1G10330	-1.15	-0.21	-1.52	0.17343	0.333301	-6.22
252397_at	hypothetical protein	---	AT3G47980	1.20	0.26	1.52	0.173592	0.333583	-6.22
266607_at	hypothetical protein predicted by gene	---	AT2G46300	-1.14	-0.20	-1.52	0.173663	0.333692	-6.22
255715_s_	hypothetical protein	---	AT4G00320 /	1.11	0.15	1.52	0.17369	0.333715	-6.22
256591_at	hypothetical protein	---	AT3G31910	1.10	0.13	1.52	0.173725	0.333744	-6.22
261143_at	unknown protein	ATPUP14	AT1G19770	1.25	0.32	1.52	0.173734	0.333744	-6.22
256638_at	RNA-binding protein, putative similar t	---	AT3G19090	-1.19	-0.25	-1.52	0.173798	0.333783	-6.22
252662_at	putative protein Sec24A protein, Hom	CEF	AT3G44340	-1.14	-0.18	-1.52	0.173797	0.333783	-6.22
262241_at	hypothetical protein predicted by gene	---	AT1G48390	-1.10	-0.14	-1.52	0.173785	0.333783	-6.22
251888_at	putative protein GTP-binding regulato	---	AT3G54190	1.11	0.15	1.52	0.173867	0.333887	-6.22
263385_at	ABA-regulated gene (ATEM6) ; suppo	GEA6	AT2G40170	-1.16	-0.21	-1.52	0.173917	0.333956	-6.22
256568_at	hypothetical protein ;supported by full-	---	AT3G19520	1.12	0.16	1.52	0.173994	0.334047	-6.22
250912_at	histone deacetylase -like protein histo	HD2C	AT5G03740	1.27	0.35	1.52	0.173988	0.334047	-6.22
253549_at	Expressed protein ; supported by full-l	NFD1	AT4G30930	1.22	0.29	1.52	0.174048	0.334121	-6.22
262530_at	putative receptor protein kinase Appro	AtRLP2	AT1G17240	-1.16	-0.21	-1.52	0.174117	0.334226	-6.22
264715_at	hypothetical protein contains similarity	---	AT1G70180	1.13	0.18	1.52	0.174229	0.334414	-6.22
259629_at	disease resistance protein contains do	WRR4	AT1G56510	-1.18	-0.24	-1.52	0.174406	0.334724	-6.22
255465_at	hypothetical protein similar to A. thalia	---	AT4G02990	1.16	0.21	1.52	0.174454	0.334789	-6.22
264245_at	galactinol synthase, putative similar to	AtGolS7	AT1G60450	-1.12	-0.16	-1.52	0.174586	0.335013	-6.22
260452_at	putative SRF-type transcription factor	---	AT1G72350	1.21	0.27	1.52	0.174637	0.335084	-6.22
261545_at	unknown protein	---	AT1G63530	1.13	0.18	1.52	0.174656	0.335091	-6.22
251760_at	Expressed protein ; supported by full-l	---	AT3G55605	1.25	0.32	1.52	0.174792	0.335321	-6.22
260355_at	transcription factor CRC identical to tra	CRC	AT1G69180	1.17	0.23	1.52	0.174817	0.335321	-6.22
262537_s_	putative ubiquitin-conjugating enzyme	UBC34	AT1G17280 /	-1.20	-0.27	-1.52	0.17482	0.335321	-6.22
263861_at	hypothetical protein	---	AT2G04560	-1.20	-0.26	-1.52	0.174845	0.335341	-6.22
245437_at	RNA helicase like protein	---	AT4G16630	1.20	0.26	1.52	0.174911	0.33544	-6.22
255152_at	Rab-like protein Rab11 protein - Arabi	---	AT4G08190	-1.10	-0.14	-1.52	0.175096	0.335738	-6.22
258777_at	hypothetical protein predicted by gens	---	AT3G11850	1.17	0.23	1.52	0.175094	0.335738	-6.22
265439_at	senescence-associated protein contair	---	AT2G21045	1.62	0.70	1.52	0.175151	0.33578	-6.23
245489_at	FCA gamma protein	FCA	AT4G16280	1.12	0.17	1.52	0.175162	0.33578	-6.23

247263_at	putative protein similar to unknown pro	---	AT5G64470	-1.18	-0.24	-1.52	0.175152	0.33578	-6.23
252403_at	hypothetical protein	---	AT3G48080	1.10	0.14	1.52	0.175232	0.335887	-6.23
246167_at	putative protein	---	---	-1.15	-0.21	-1.51	0.175248	0.335889	-6.23
266792_at	putative sucrose/H+ symporter	SUT2	AT2G02860	-1.33	-0.41	-1.51	0.175276	0.335914	-6.23
253808_at	predicted proline-rich protein hydroxyp	---	AT4G28300	-1.17	-0.22	-1.51	0.175342	0.335961	-6.23
264106_at	unknown protein	SERK4	AT2G13790	1.12	0.16	1.51	0.175345	0.335961	-6.23
260470_at	hypothetical protein predicted by gene	---	AT1G11120	-1.16	-0.21	-1.51	0.175324	0.335961	-6.23
248336_at	unknown protein ; supported by cDNA	---	AT5G52420	1.22	0.29	1.51	0.175577	0.336377	-6.23
252630_at	putative protein	---	AT3G44980	-1.12	-0.16	-1.51	0.175661	0.33651	-6.23
255956_at	Expressed protein ; supported by full-l	DD46	AT1G22015	1.14	0.19	1.51	0.175734	0.336621	-6.23
251978_at	CYTOCHROME P450 - like protein C	CYP71B30P	AT3G53290	1.16	0.21	1.51	0.175798	0.336716	-6.23
260286_at	putative acetylornithine transaminase s	WIN1	AT1G80600	-1.16	-0.22	-1.51	0.175856	0.336799	-6.23
250217_at	nodulin-like protein	---	AT5G14120	-1.18	-0.24	-1.51	0.175983	0.337014	-6.23
249175_at	COP8 (constitutive photomorphogenic	COP8	AT5G42970	1.12	0.16	1.51	0.176049	0.337112	-6.23
258631_at	putative polygalacturonase similar to p	QRT2	AT3G07970	1.46	0.55	1.51	0.176073	0.337129	-6.23
246839_at	putative protein	---	AT5G26720	1.13	0.18	1.51	0.176183	0.337311	-6.23
248172_at	unknown protein ;supported by full-ler	---	AT5G54660	1.25	0.32	1.51	0.176261	0.337433	-6.23
253048_at	formamidase - like protein formamidas	---	AT4G37560	-1.39	-0.48	-1.51	0.176284	0.337449	-6.23
264889_at	unknown protein	---	AT1G23050	-1.15	-0.20	-1.51	0.176329	0.337506	-6.23
263681_at	hypothetical protein predicted by gens	ORC6	AT1G26840	-1.19	-0.25	-1.51	0.17637	0.337532	-6.23
250036_at	putative protein predicted proteins, Ar	---	AT5G18340	-1.17	-0.23	-1.51	0.176374	0.337532	-6.23
265624_at	CLAVATA3 CLE family of proteins; liga	CLV3	AT2G27250	-1.14	-0.19	-1.51	0.176387	0.337532	-6.23
247580_at	putative protein traube, Mus musculus	---	AT5G61330	1.15	0.20	1.51	0.176425	0.337577	-6.23
253507_at	serine threonine protein kinase like pr	---	AT4G32000	-1.20	-0.26	-1.51	0.176465	0.337626	-6.23
256238_at	unknown protein ; supported by full-ler	ELC	AT3G12400	-1.17	-0.23	-1.51	0.176548	0.337745	-6.23
248048_at	nicotianamine synthase	NAS2	AT5G56080	-1.13	-0.18	-1.51	0.176559	0.337745	-6.23
246349_at	Expressed protein ; supported by full-l	---	AT1G51915	1.39	0.47	1.51	0.176572	0.337745	-6.23
248926_at	Ole e I (main olive allergen)-like protei	---	AT5G45880	-1.25	-0.32	-1.51	0.176766	0.338088	-6.23
258147_at	beta-glucosidase, putative similar to b	BGLU43	AT3G18070	-1.13	-0.18	-1.51	0.176807	0.338137	-6.23
266525_at	putative tetracycline transporter protei	MEE15	AT2G16970	-1.15	-0.20	-1.51	0.176842	0.338147	-6.23
257934_at	serine carboxypeptidase, putative sim	scpl21	AT3G25420	1.19	0.25	1.51	0.176838	0.338147	-6.23
248133_at	unknown protein	---	AT5G54850	-1.19	-0.25	-1.51	0.176861	0.338156	-6.23
265502_at	putative poly(A) binding protein	---	AT2G15500	-1.16	-0.21	-1.51	0.176942	0.338283	-6.23
254590_at	hypothetical protein	---	AT4G18860	-1.12	-0.16	-1.51	0.176962	0.338293	-6.23
248274_at	isp4 protein	ATOPT9	AT5G53510	-1.12	-0.16	-1.51	0.177029	0.338318	-6.23

256823_at	hypothetical protein predicted by gens	---	AT3G22220	-1.15	-0.20	-1.51	0.177035	0.338318	-6.23
246508_at	sugar transporter-like protein putative	PGLCT	AT5G16150	-1.16	-0.21	-1.51	0.177017	0.338318	-6.23
261798_at	hypothetical protein similar to hypothet	CPSF30	AT1G30460	-1.14	-0.19	-1.51	0.177009	0.338318	-6.23
250604_at	putative protein heparanase precurso	PIP1B	AT2G45960 /	1.20	0.27	1.51	0.177103	0.33842	-6.24
245643_at	myb-related transcription factor (cpm7	MYB116	AT1G25340	-1.12	-0.17	-1.51	0.177119	0.338422	-6.24
262860_at	unknown protein	APO1	AT1G64810	-1.17	-0.22	-1.51	0.177182	0.338486	-6.24
250294_at	auxin reponsive - like protein Nt-gh3 c	---	AT5G13380	1.12	0.17	1.51	0.177182	0.338486	-6.24
258716_at	unknown protein similar to a region of	---	AT3G09700	1.21	0.28	1.51	0.177223	0.338535	-6.24
263352_at	En/Spm-like transposon protein relate	---	AT2G22080	-1.20	-0.26	-1.51	0.177267	0.338592	-6.24
264883_s_	secretory carrier membrane protein ide	---	AT1G11180 /	1.12	0.17	1.51	0.177288	0.338602	-6.24
257079_at	unknown protein	---	AT3G15240	1.11	0.15	1.51	0.177439	0.338863	-6.24
246840_at	putative protein ;supported by full-leng	---	AT5G26610	-1.10	-0.14	-1.51	0.177489	0.33893	-6.24
253175_at	WD-40 repeat protein (MSI3) ; suppor	MSI3	AT4G35050	1.23	0.30	1.51	0.177651	0.33921	-6.24
257126_at	E2, ubiquitin-conjugating enzyme, put	UBC19	AT3G20060	1.17	0.22	1.51	0.177672	0.339222	-6.24
265941_s_	recA, putative similar to GB:CAA3909	---	AT2G19490 /	1.22	0.28	1.51	0.177733	0.339284	-6.24
258938_at	germin-like protein similar to germin ty	---	AT3G10080	-1.71	-0.77	-1.51	0.177734	0.339284	-6.24
252752_s_	putative protein hypothetical protein A	---	AT3G43470 /	1.11	0.15	1.50	0.177805	0.339391	-6.24
256792_at	hypothetical protein predicted by gene	---	AT3G22150	1.31	0.38	1.50	0.17783	0.339412	-6.24
246900_at	putative protein flavin-containing mon	YUC6	AT5G25620	-1.18	-0.23	-1.50	0.177889	0.339496	-6.24
259889_at	predicted protein ; supported by cDNA	---	AT1G76405	-1.19	-0.25	-1.50	0.177965	0.339611	-6.24
247882_at	Expressed protein ; supported by full-l	---	AT5G57785	-1.50	-0.59	-1.50	0.17798	0.339611	-6.24
258928_at	unknown protein similar to hypothetica	TAF12	AT3G10070	1.17	0.23	1.50	0.178098	0.339808	-6.24
247707_at	scarecrow-like 11 - like scarecrow-like	---	AT5G59450	1.66	0.73	1.50	0.178137	0.339854	-6.24
253945_at	putative protein gene F23F1.15 Arabi	---	AT4G27050	-1.10	-0.14	-1.50	0.178237	0.340018	-6.24
265612_at	hypothetical protein predicted by gens	---	AT2G25390 /	-1.12	-0.16	-1.50	0.178273	0.340057	-6.24
251174_at	putative protein latex protein allergen	PLP9	AT3G63200	-1.28	-0.36	-1.50	0.178293	0.340068	-6.24
261689_at	hypothetical protein contains similarity	---	AT1G50140	1.18	0.23	1.50	0.178418	0.340276	-6.24
253513_at	peroxidase - like protein peroxidase, S	---	AT4G31760	-1.11	-0.15	-1.50	0.178498	0.340402	-6.24
253329_at	hypothetical protein	---	AT4G33480	-1.11	-0.15	-1.50	0.178551	0.340473	-6.24
256078_at	hypothetical protein predicted by gene	---	AT1G20670	-1.13	-0.18	-1.50	0.178631	0.340578	-6.24
257947_at	putative isocitrate lyase similar to GB:I	ICL	AT3G21720	-1.17	-0.22	-1.50	0.178636	0.340578	-6.24
266797_at	unknown protein	AtGRF1	AT2G22840	-1.31	-0.39	-1.50	0.178763	0.340793	-6.24
257637_at	terpene synthase-related protein conta	---	AT3G25810	1.10	0.14	1.50	0.178793	0.340821	-6.24
246104_at	DNA-binding protein - like DNA-bindin	WRKY74	AT5G28650	1.11	0.15	1.50	0.17882	0.340844	-6.24
257143_at	cytochrome P450, putative contains P	CYP705A20	AT3G20110	1.15	0.20	1.50	0.178932	0.340986	-6.24

266925_at	unknown protein ;supported by full-ler	PEX11D	AT2G45740	1.11	0.16	1.50	0.17893	0.340986	-6.24
255812_at	potassium uptake transporter - like pr	HKT1	AT4G10310	-1.24	-0.31	-1.50	0.178939	0.340986	-6.24
251928_at	putative protein hypothetical protein A	---	AT3G53980	-1.46	-0.55	-1.50	0.178967	0.34101	-6.24
258500_at	S-adenosylmethionine decarboxylase	CPuORF9	AT3G02468 /	1.13	0.18	1.50	0.179053	0.341145	-6.25
255260_at	score=63.7, E=3.9e-15, N=8 ; suppor	---	AT4G05040	-1.16	-0.22	-1.50	0.179221	0.341437	-6.25
261619_x_	hypothetical protein	---	---	-1.12	-0.16	-1.50	0.179258	0.34148	-6.25
257270_at	unknown protein ; supported by full-le	---	AT3G28140	-1.11	-0.14	-1.50	0.179383	0.341688	-6.25
264100_at	lupeol synthase identical to lupeol synt	LUP1	AT1G78970	-1.47	-0.56	-1.50	0.179428	0.341747	-6.25
249627_at	NADH dehydrogenase (ubiquinone) (E	EMB1467	AT5G37510	1.16	0.21	1.50	0.179462	0.341783	-6.25
252392_s_	putative protein various predicted prot	---	AT3G47890 /	1.17	0.23	1.50	0.179602	0.342021	-6.25
259846_at	peptide transporter PTR2-B, putative s	---	AT1G72140	-1.14	-0.19	-1.50	0.179667	0.342087	-6.25
247902_at	plasma membrane ATPase 3 (proton p	AHA3	AT5G57350	-1.15	-0.20	-1.50	0.179662	0.342087	-6.25
249943_at	putative protein similar to unknown pro	---	AT5G22280	1.27	0.35	1.50	0.179733	0.342098	-6.25
250844_at	putative protein ;supported by full-leng	SIM	AT5G04470	-1.29	-0.37	-1.50	0.179702	0.342098	-6.25
245974_at	putative protein	---	---	1.21	0.27	1.50	0.179705	0.342098	-6.25
249097_at	putative protein strong similarity to unk	---	AT5G43520	-1.14	-0.19	-1.50	0.179731	0.342098	-6.25
253130_at	putative protein ;supported by full-leng	---	AT4G35510	-1.22	-0.29	-1.50	0.179772	0.342145	-6.25
264816_at	hypothetical protein similar to membra	---	AT1G03560	-1.34	-0.42	-1.50	0.179819	0.342205	-6.25
253906_at	putative protein disease resistance pr	---	AT4G27220	-1.18	-0.24	-1.50	0.179965	0.342454	-6.25
266823_at	hypothetical protein predicted by gens	---	AT2G44930	-1.13	-0.17	-1.50	0.180008	0.34248	-6.25
252485_at	disease resistance protein RPP13-like	RPP13	AT3G46530	1.13	0.17	1.50	0.179996	0.34248	-6.25
254812_at	nucleotide sugar epimerase -like prote	GAE5	AT4G12250	1.33	0.41	1.50	0.180201	0.342817	-6.25
265627_at	Expressed protein ; supported by full-l	---	AT2G27285	1.14	0.19	1.50	0.180222	0.342828	-6.25
258283_at	hypothetical protein predicted by gene	---	AT3G26750	-1.13	-0.18	-1.49	0.180339	0.343018	-6.25
258896_at	putative syntaxin protein, AtSNAP33 s	SYP43	AT3G05710	1.14	0.19	1.49	0.180422	0.343018	-6.25
253418_at	putative protein tom-1B protein, Gallus	---	AT4G32760	-1.11	-0.15	-1.49	0.180408	0.343018	-6.25
249409_at	putative protein KED, Nicotiana tabac	---	AT5G40340	-1.44	-0.52	-1.49	0.180391	0.343018	-6.25
257414_at	hypothetical protein similar to hypothet	---	AT1G62110	1.12	0.17	1.49	0.180407	0.343018	-6.25
258252_at	putative polygalacturonase similar to p	---	AT3G15720	1.27	0.35	1.49	0.180426	0.343018	-6.25
249186_at	CHP-rich zinc finger protein-like	---	AT5G43040	1.12	0.16	1.49	0.18037	0.343018	-6.25
249329_at	putative protein similar to unknown pro	---	AT5G40960	1.17	0.23	1.49	0.180517	0.343161	-6.25
266134_s_	putative beta-expansin	---	AT1G65680 /	-1.13	-0.17	-1.49	0.180535	0.343167	-6.25
248761_at	Expressed protein ; supported by full-l	---	AT5G47635	1.23	0.29	1.49	0.180559	0.343184	-6.25
264456_at	unknown protein similar to T cell recep	---	AT1G10390	1.13	0.17	1.49	0.180824	0.343478	-6.25
251998_at	putative protein KIAA0010 protein, Ho	UPL7	AT3G53090	1.13	0.17	1.49	0.180777	0.343478	-6.25

265086_at	hypothetical protein contains Zinc fing	RING1B	AT1G03770	1.18	0.24	1.49	0.180853	0.343478	-6.25
251477_at	putative protein	---	AT3G59680	-1.10	-0.14	-1.49	0.180815	0.343478	-6.25
249043_at	berberine bridge enzyme	---	AT5G44360	-1.09	-0.13	-1.49	0.180793	0.343478	-6.25
246788_at	putative protein hypothetical proteins -	AGL89	AT5G27580	1.11	0.15	1.49	0.180822	0.343478	-6.25
248293_at	unknown protein	---	AT5G53050	1.22	0.28	1.49	0.180856	0.343478	-6.25
255854_at	unknown protein ;supported by full-len	---	AT1G67050	-1.37	-0.46	-1.49	0.180865	0.343478	-6.25
260694_at	NAD+ dependent isocitrate dehydroge	---	AT1G32480	-1.10	-0.14	-1.49	0.180849	0.343478	-6.25
257242_at	9-cis-epoxycarotenoid dioxygenase, p	NCED6	AT3G24220	-1.12	-0.17	-1.49	0.180842	0.343478	-6.25
247248_at	putative protein contains similarity to u	---	AT5G64560	-1.24	-0.31	-1.49	0.180928	0.34357	-6.25
263084_at	hypothetical protein predicted by gens	---	AT2G27180	1.13	0.17	1.49	0.181093	0.343855	-6.26
247517_at	100 kDa coactivator - like protein 100	---	AT5G61780	-1.16	-0.21	-1.49	0.181146	0.343873	-6.26
261352_at	DNA repair protein RAD23, putative s	RAD23	AT1G79650	-1.13	-0.18	-1.49	0.181148	0.343873	-6.26
245549_at	cellulose synthase like protein	ATCSLB06	AT4G15320	-1.12	-0.17	-1.49	0.181124	0.343873	-6.26
267267_at	putative cytochrome P450	CYP71B9	AT2G02580	1.13	0.17	1.49	0.181193	0.343907	-6.26
263998_at	unknown protein	---	AT2G22510	-1.29	-0.37	-1.49	0.181195	0.343907	-6.26
264834_at	unknown protein similar to ESTs gb|AA	---	AT1G03730	1.27	0.35	1.49	0.181228	0.343939	-6.26
265596_at	hypothetical protein predicted by gens	CAF1	AT2G20020	1.28	0.36	1.49	0.181248	0.343949	-6.26
259905_s_	hypothetical protein predicted by gene	---	AT1G74130 /	-1.09	-0.13	-1.49	0.181313	0.344044	-6.26
258177_at	ubiquitin-regulatory protein, putative c	---	AT3G21660	-1.11	-0.16	-1.49	0.181342	0.34407	-6.26
254666_at	translation initiation factor eIF-2 gamm	---	AT4G18330	1.10	0.13	1.49	0.181413	0.344176	-6.26
246782_at	putative protein PrMC3 - Pinus radiata	GID1C	AT5G27320	1.27	0.34	1.49	0.181595	0.344463	-6.26
249980_at	putative protein	---	AT5G18870	-1.14	-0.19	-1.49	0.181591	0.344463	-6.26
266372_at	putative two-component response reg	ATRR3	AT2G41310	1.14	0.19	1.49	0.181614	0.344472	-6.26
266882_at	unknown protein ;supported by full-ler	---	AT2G44670	-1.36	-0.44	-1.49	0.181665	0.344539	-6.26
265115_at	rho GDP-dissociation inhibitor, putativ	---	AT1G62450	-1.12	-0.17	-1.49	0.18168	0.34454	-6.26
252427_at	hypothetical protein	---	AT3G47640	1.28	0.36	1.49	0.181697	0.344544	-6.26
258292_at	hypothetical protein predicted by gene	---	AT3G23330	-1.15	-0.20	-1.49	0.18173	0.344577	-6.26
251419_at	putative protein various predicted prot	---	AT3G60470	-1.12	-0.16	-1.49	0.181866	0.344806	-6.26
253854_at	putative protein zinc-finger protein S1	---	AT4G27900	-1.38	-0.47	-1.49	0.181924	0.344886	-6.26
253957_at	putative protein ; supported by cDNA:	AGP13	AT4G26320	-1.20	-0.26	-1.49	0.18196	0.344886	-6.26
262806_at	putative pyrophosphate-dependent ph	---	AT1G20950	-1.21	-0.27	-1.49	0.181948	0.344886	-6.26
261172_at	hypothetical protein predicted by gene	---	AT1G04840	-1.14	-0.19	-1.49	0.181969	0.344886	-6.26
261442_at	Expressed protein ; supported by full-l	---	AT1G28375	1.13	0.17	1.49	0.182034	0.344982	-6.26
256723_at	unknown protein ;supported by full-ler	---	AT2G34160	1.10	0.14	1.49	0.182055	0.344986	-6.26
245012_at	NADH dehydrogenase D3	---	---	-1.17	-0.22	-1.49	0.182067	0.344986	-6.26

266057_at	putative methionyl-tRNA synthetase ;	---	AT2G40660	1.11	0.15	1.49	0.182114	0.345046	-6.26
248297_at	protochlorophyllide reductase; oxidore	---	AT5G53100	-1.10	-0.14	-1.49	0.18217	0.345117	-6.26
255744_at	hypothetical protein predicted by gene	---	---	-1.10	-0.13	-1.49	0.182182	0.345117	-6.26
245948_at	putative protein ;supported by full-leng	---	AT5G19540	1.19	0.25	1.49	0.182211	0.345117	-6.26
257482_x_	hypothetical protein contains similarity	---	AT1G27820	1.19	0.25	1.49	0.182207	0.345117	-6.26
258383_at	hypothetical protein predicted by gens	---	AT3G15440	1.30	0.38	1.49	0.182263	0.345186	-6.26
256949_at	hypothetical protein predicted by gene	---	AT3G19070	-1.10	-0.14	-1.49	0.182429	0.345472	-6.26
259957_at	putative protein kinase C-terminal regi	---	AT1G67890	-1.25	-0.32	-1.49	0.182705	0.345966	-6.26
256573_at	hypothetical protein predicted by gene	---	AT3G14860	-1.12	-0.17	-1.48	0.182847	0.346199	-6.26
253098_at	cytochrome P450-like protein	CYP81D3	AT4G37340	-1.14	-0.19	-1.48	0.182859	0.346199	-6.26
266770_at	putative expansin Experimental eviden	ATEXPA15	AT2G03090	-1.21	-0.28	-1.48	0.182894	0.346238	-6.26
248083_at	unknown protein	---	AT5G55420	1.48	0.57	1.48	0.182926	0.346268	-6.26
AFFX-ThrX	B. subtilis /GEN=thrC /DB_XREF=gb:X	---	---	-1.26	-0.34	-1.48	0.183078	0.346527	-6.27
267114_at	Expressed protein ; supported by full-le	---	AT2G14835	-1.12	-0.17	-1.48	0.183104	0.346548	-6.27
257863_at	hypothetical protein similar to GRAB1	anac057	AT3G17730	1.10	0.14	1.48	0.183156	0.346618	-6.27
266611_at	putative auxin-regulated protein	GH3.1	AT2G14960	-1.12	-0.17	-1.48	0.18322	0.346711	-6.27
264897_at	dynein light subunit lc6, flagellar outer	---	AT1G23220	-1.14	-0.19	-1.48	0.183304	0.346841	-6.27
246004_at	germin-like protein ; supported by cDN	GER3	AT5G20630	-3.01	-1.59	-1.48	0.183335	0.34687	-6.27
253231_at	Nonclathrin coat protein gamma - like	---	AT4G34450	-1.13	-0.18	-1.48	0.183367	0.346902	-6.27
248880_at	putative protein contains similarity to c	---	AT5G46200	1.11	0.16	1.48	0.183438	0.346991	-6.27
255771_at	hypothetical protein contains similarity	---	AT1G18550	-1.13	-0.17	-1.48	0.183444	0.346991	-6.27
259019_at	hypothetical protein similar to serologic	CHIP	AT3G07370	1.13	0.18	1.48	0.183473	0.347017	-6.27
246846_at	putative protein	---	AT5G26760	1.11	0.15	1.48	0.183557	0.347147	-6.27
267593_at	similar to disease resistance protein (C	AtRLP25	AT2G33030	1.11	0.15	1.48	0.183624	0.347245	-6.27
266629_at	putative serpin	---	AT2G35590	1.12	0.17	1.48	0.183681	0.347324	-6.27
258316_at	unknown protein	---	AT3G22660	1.20	0.27	1.48	0.183724	0.347376	-6.27
246836_s_	putative protein MADS box protein AG	---	AT5G26650 /	-1.10	-0.14	-1.48	0.183818	0.347506	-6.27
257383_at	hypothetical protein predicted by gens	---	AT2G19630	-1.12	-0.16	-1.48	0.183823	0.347506	-6.27
249904_at	unknown protein	---	AT5G22700	-1.12	-0.16	-1.48	0.183856	0.347538	-6.27
261056_at	hypothetical protein similar to hypothet	---	AT1G01360	-1.18	-0.24	-1.48	0.183874	0.347545	-6.27
266647_at	hypothetical protein predicted by grail	---	AT2G25870	-1.17	-0.23	-1.48	0.183914	0.347565	-6.27
247352_at	serine/threonine-protein kinase ;suppo	SNRK2.5	AT5G63650	1.36	0.44	1.48	0.183915	0.347565	-6.27
245773_at	hypothetical protein predicted by gens	---	AT1G30290	1.13	0.17	1.48	0.183971	0.347584	-6.27
249625_at	hypothetical protein ;supported by full-	---	AT5G37480	1.12	0.16	1.48	0.183951	0.347584	-6.27
248742_at	unknown protein	---	AT5G48200	-1.14	-0.19	-1.48	0.183961	0.347584	-6.27

253479_at	ferredoxin-NADP+ reductase - like pro	---	AT4G32360	1.11	0.15	1.48	0.184017	0.347613	-6.27
254442_at	putative protein predicted protein T7N	---	AT4G21060	1.12	0.16	1.48	0.184001	0.347613	-6.27
265203_at	unknown protein	---	AT2G36630	-1.15	-0.20	-1.48	0.18404	0.347628	-6.27
255653_at	Similar to receptor kinase	---	AT4G00960	-1.10	-0.14	-1.48	0.184183	0.347869	-6.27
265270_at	putative ribose phosphate pyrophosph	---	AT2G42910	1.12	0.16	1.48	0.184279	0.348013	-6.27
245400_at	ATP-dependent Clp protease proteoly	---	AT4G17040	-1.16	-0.21	-1.48	0.18429	0.348013	-6.27
249268_at	Expressed protein ; supported by cDN	---	AT5G41685	-1.11	-0.15	-1.48	0.18434	0.34808	-6.27
265737_at	putative phosphatidic acid phosphatas	ATPAP1	AT2G01180	1.60	0.68	1.48	0.184383	0.348103	-6.27
262318_at	putative hypersensitivity-related protei	---	AT1G27620	-1.13	-0.18	-1.48	0.18438	0.348103	-6.27
251265_at	ATP-dependent RNA helicase-like pro	---	AT3G62310	1.17	0.22	1.48	0.184424	0.348128	-6.27
249136_at	putative protein similar to unknown pro	---	AT5G43180	1.24	0.31	1.48	0.184427	0.348128	-6.27
265526_x_	putative Athila retroelement ORF1 prot	---	---	-1.10	-0.13	-1.48	0.184498	0.348234	-6.27
246024_at	putative protein predicted protein - Ara	---	AT5G21130	1.15	0.20	1.48	0.184558	0.348298	-6.27
264497_at	hypothetical protein predicted by gens	ATPUP4	AT1G30840	1.19	0.25	1.48	0.184563	0.348298	-6.27
265453_at	putative cellular apoptosis susceptibilit	---	AT2G46520	-1.15	-0.21	-1.48	0.184597	0.348334	-6.27
258733_at	unknown protein	---	---	1.11	0.15	1.48	0.184672	0.348447	-6.27
255101_at	putative lipid transfer protein similar to	---	AT4G08670	-1.16	-0.22	-1.48	0.184736	0.348537	-6.27
250353_at	putative protein predicted proteins, Ar	---	AT5G11630	-1.14	-0.19	-1.48	0.184757	0.34855	-6.27
247481_at	putative protein predicted protein, Ara	---	AT5G62400	-1.11	-0.15	-1.48	0.184778	0.348559	-6.27
263988_at	floral homeodomain transcription facto	SHP2	AT2G42830	-1.12	-0.16	-1.48	0.184814	0.348599	-6.27
259602_at	disease resistance protein, putative si	---	AT1G56520	-1.11	-0.15	-1.48	0.184925	0.348751	-6.27
256460_at	60S ribosomal protein L30, putative si	---	AT1G36240	-1.14	-0.19	-1.48	0.184925	0.348751	-6.27
250942_at	putative protein	---	AT5G03350	-2.77	-1.47	-1.48	0.184999	0.348789	-6.27
267002_s_	putative photosystem II type I chloroph	LHB1B1	AT2G34420 /	-1.09	-0.13	-1.48	0.184965	0.348789	-6.27
246629_at	unknown protein similar to hypothetica	---	AT1G50750	-1.16	-0.22	-1.48	0.185006	0.348789	-6.27
262691_at	TPR-repeat protein contains multiple T	---	AT1G62740	1.17	0.23	1.48	0.185006	0.348789	-6.27
247386_at	putative protein similar to unknown pro	emb2746	AT5G63420	1.12	0.16	1.48	0.185045	0.34879	-6.28
263923_at	Expressed protein ; supported by cDN	---	AT2G36485	1.18	0.24	1.48	0.185034	0.34879	-6.28
250048_s_	BCS1 - like protein h-bcs1, Homo sap	---	AT5G17740 /	1.12	0.16	1.48	0.185053	0.34879	-6.28
256960_at	unknown protein ;supported by full-ler	---	AT3G13510	-1.17	-0.23	-1.48	0.185151	0.348945	-6.28
250394_at	putative protein ylIC, Enterococcus fae	---	AT5G10910	-1.15	-0.21	-1.48	0.185191	0.348993	-6.28
263133_at	hypothetical protein predicted by gene	---	AT1G78450	1.59	0.67	1.48	0.185213	0.349006	-6.28
257296_at	hypothetical protein predicted by gene	---	AT3G28020	-1.13	-0.17	-1.48	0.185232	0.349012	-6.28
263120_at	cytochrome P450, putative similar to c	CYP708A3	AT1G78490	-1.93	-0.95	-1.48	0.185258	0.349033	-6.28
250748_at	AtPH1-like protein ;supported by full-le	---	AT5G05710	1.15	0.20	1.48	0.185386	0.349244	-6.28

249212_at	putative protein strong similarity to unk	---	AT5G42690	-1.13	-0.18	-1.47	0.185405	0.349252	-6.28
245494_at	salt-inducible protein homolog	---	AT4G16390	-1.14	-0.19	-1.47	0.185524	0.349447	-6.28
255525_at	coded for by A. thaliana cDNA T04215	---	AT4G02340	-1.14	-0.19	-1.47	0.185557	0.349481	-6.28
250008_at	triacylglycerol lipase-like protein triacy	---	AT5G18630	1.27	0.34	1.47	0.18561	0.349493	-6.28
261965_at	athila ORF 1, putative similar to athila	---	---	1.10	0.13	1.47	0.18559	0.349493	-6.28
253499_at	putative protein zinc-finger helicase, H	---	AT4G31900	1.12	0.16	1.47	0.185601	0.349493	-6.28
255125_at	putative protein SCARECROW - Arab	---	AT4G08250	-1.14	-0.19	-1.47	0.18565	0.349541	-6.28
245871_at	hypothetical protein predicted by gene	---	AT1G26290	-1.16	-0.22	-1.47	0.185734	0.349669	-6.28
264343_at	unknown protein ; supported by full-le	---	AT1G11850	-1.21	-0.27	-1.47	0.186202	0.350522	-6.28
250123_at	putative protein contains similarity to a	PIN5	AT5G16530	1.15	0.20	1.47	0.186283	0.350645	-6.28
254511_at	hypothetical protein	---	AT4G20220	1.12	0.16	1.47	0.186309	0.350665	-6.28
250758_at	eukaryotic translation initiation factor 3	EIF3G2	AT5G06000	-1.18	-0.24	-1.47	0.186346	0.350706	-6.28
251586_at	zinc finger-like protein several zinc fing	GIS	AT3G58070	-1.17	-0.22	-1.47	0.186416	0.350779	-6.28
244955_at	hypothetical protein	---	---	1.19	0.25	1.47	0.186409	0.350779	-6.28
256777_at	hypothetical protein predicted by gene	---	AT3G13780	1.12	0.16	1.47	0.186536	0.350848	-6.28
247267_at	40S ribosomal protein S28 (sp|P34789	RPS28	AT5G64140	-1.28	-0.36	-1.47	0.186545	0.350848	-6.28
265210_at	60S ribosomal protein L24 ;supported	RPL24A	AT2G36620	-1.45	-0.54	-1.47	0.186477	0.350848	-6.28
256307_at	pectate lyase, putative contains Pfam	---	AT1G30350	-1.10	-0.14	-1.47	0.186524	0.350848	-6.28
246639_x_	adenylate kinase -like protein predicte	---	---	1.13	0.17	1.47	0.186526	0.350848	-6.28
248166_at	putative protein contains similarity to p	---	AT5G54520	-1.11	-0.15	-1.47	0.186522	0.350848	-6.28
262548_at	unknown protein contains similarity to	AGO2	AT1G31280	-1.15	-0.20	-1.47	0.186562	0.350851	-6.28
263178_at	hypothetical protein predicted by gene	---	AT1G05550	-1.14	-0.19	-1.47	0.186581	0.350858	-6.28
265677_at	putative purine-rich single-stranded DN	PUR ALPHA	AT2G32080	-1.11	-0.15	-1.47	0.186699	0.35102	-6.28
257327_at	hypothetical protein	---	---	1.23	0.30	1.47	0.186729	0.35102	-6.28
249664_at	putative protein histone stem-loop bin	---	AT5G36722 /	-1.12	-0.16	-1.47	0.186722	0.35102	-6.28
255694_at	putative transcriptional regulator	UNE10	AT4G00050	-1.16	-0.22	-1.47	0.186696	0.35102	-6.28
260434_at	hypothetical protein predicted by gens	---	AT1G68330	1.21	0.28	1.47	0.186807	0.351109	-6.28
250917_at	fructose-bisphosphate aldolase -like p	---	AT5G03690	1.15	0.21	1.47	0.186794	0.351109	-6.28
245214_at	F12A21.1 hypothetical protein	---	AT1G67855	-1.11	-0.15	-1.47	0.186914	0.351282	-6.28
245995_at	putative protein various predicted prot	---	---	1.18	0.24	1.47	0.186962	0.351313	-6.28
262035_at	polyprotein, putative similar to polypro	---	---	1.11	0.15	1.47	0.186965	0.351313	-6.28
259369_s_	hypothetical protein similar to putative	---	AT1G69150 /	1.12	0.17	1.47	0.186977	0.351313	-6.28
256298_at	DNA-binding protein contains Pfam pr	AGL94	AT1G69540	1.12	0.17	1.47	0.18704	0.351388	-6.28
254257_s_	putative protein predicted proteins, Ar	---	AT4G23350 /	-1.12	-0.16	-1.47	0.187048	0.351388	-6.28
259832_at	transfactor, putative similar to GI:4519	---	AT1G69580	-1.35	-0.43	-1.47	0.187112	0.351481	-6.29

265114_at	hypothetical protein contains similarity	LRX2	AT1G62440	-1.26	-0.33	-1.47	0.187316	0.351835	-6.29
246586_at	putative protein predicted protein, Ara	---	AT5G14770	1.17	0.23	1.47	0.187338	0.351846	-6.29
266026_at	putative non-LTR retroelement reverse	---	---	-1.14	-0.18	-1.47	0.187368	0.351874	-6.29
252902_at	putative protein various predicted prot	---	AT4G39560	-1.12	-0.17	-1.47	0.187395	0.351877	-6.29
247824_at	putative protein Na+/H+-exchanging p	CHX25	AT5G58460	-1.14	-0.19	-1.47	0.1874	0.351877	-6.29
254068_at	putative protein similarity to multidrug	NAP8	AT4G25450	1.13	0.18	1.47	0.187484	0.352005	-6.29
248190_at	unknown protein	---	AT5G54130	1.13	0.17	1.47	0.187573	0.352144	-6.29
253576_at	putative protein various predicted prot	---	AT4G31070	-1.10	-0.14	-1.47	0.187724	0.352398	-6.29
261231_at	unknown protein ; supported by cDNA	---	AT1G20110	1.10	0.14	1.47	0.187777	0.352448	-6.29
250067_at	unknown protein	---	AT5G17950	1.10	0.13	1.47	0.187781	0.352448	-6.29
258747_at	unknown protein ; supported by full-le	---	AT3G05810	-1.17	-0.23	-1.47	0.187886	0.352614	-6.29
255998_at	hypothetical protein contains similarity	---	AT1G29780	-1.11	-0.15	-1.47	0.187992	0.352786	-6.29
247039_at	putative protein contains similarity to A	ATEB1C	AT5G67270	-1.17	-0.23	-1.46	0.188043	0.352852	-6.29
248602_s_	MADS-box protein-like	---	AT5G38620 /	1.10	0.14	1.46	0.188224	0.353161	-6.29
264771_at	phosphomethylpyrimidine kinase prob	TH1	AT1G22940	-1.10	-0.14	-1.46	0.188434	0.353527	-6.29
259028_at	putative C2H2-type zinc finger protein	TAC1	AT3G09290	1.14	0.19	1.46	0.188487	0.353597	-6.29
266539_at	similar to mammalian MHC III region p	SUVH5	AT2G35160	1.14	0.19	1.46	0.188649	0.353872	-6.29
254720_at	DNA (cytosine-5-)-methyltransferase -	MEE57	AT4G13610	1.13	0.18	1.46	0.188771	0.354073	-6.29
249678_at	protein kinase-like	---	AT5G35980	1.10	0.13	1.46	0.188857	0.354205	-6.29
247202_at	GTP-binding protein ; supported by fu	AtRABA4a	AT5G65270	-1.15	-0.20	-1.46	0.188912	0.354277	-6.29
254903_at	H+-transporting ATPase chain E, vacu	TUF	AT4G11150	1.14	0.19	1.46	0.189029	0.354468	-6.29
253187_at	putative zinc-finger protein PEThy;ZP	---	AT4G35280	-1.10	-0.14	-1.46	0.18916	0.354685	-6.30
263371_at	unknown protein ;supported by full-ler	NOP10	AT2G20490	1.16	0.21	1.46	0.189225	0.354777	-6.30
248476_at	putative protein similar to unknown pro	---	AT5G50890	1.29	0.36	1.46	0.189301	0.354891	-6.30
254708_at	ubiquitin-specific protease 20 (UBP20	UBP20	AT4G17895	-1.12	-0.16	-1.46	0.189432	0.355107	-6.30
253723_at	extensin-like protein ;supported by full	---	AT4G29240	-1.13	-0.18	-1.46	0.189546	0.355292	-6.30
260271_at	unknown protein similar to unknown pr	---	AT1G63690	-1.12	-0.16	-1.46	0.18957	0.355307	-6.30
245558_at	hypothetical protein	---	AT4G15430	-1.10	-0.14	-1.46	0.189593	0.355321	-6.30
249536_at	pollen coat -like protein pollen coat pr	---	AT5G38760	1.10	0.14	1.46	0.189766	0.355617	-6.30
254266_at	protein kinase - like protein serine thre	CRK5	AT4G23130	1.44	0.53	1.46	0.189784	0.355621	-6.30
264368_at	hypothetical protein Contains similarity	---	AT1G03280	1.12	0.16	1.46	0.189827	0.355672	-6.30
255975_at	hypothetical protein	---	---	1.15	0.20	1.46	0.189866	0.355687	-6.30
252730_at	putative protein	---	AT3G43110	1.18	0.23	1.46	0.189863	0.355687	-6.30
255865_at	unknown protein	---	AT2G30330	1.10	0.14	1.46	0.189971	0.355825	-6.30
265098_at	unknown protein	---	AT1G04010	-1.27	-0.35	-1.46	0.189967	0.355825	-6.30

257459_at	unknown protein	---	AT1G24040	1.12	0.17	1.46	0.190017	0.355872	-6.30
256550_at	En/Spm-like transposon protein, putat	---	---	1.10	0.14	1.46	0.190027	0.355872	-6.30
264969_at	hypothetical protein contains similarity	---	AT1G67320	-1.31	-0.39	-1.46	0.190051	0.355886	-6.30
258451_at	alternative oxidase 1b precursor identi	AOX1B	AT3G22360	1.15	0.20	1.46	0.190069	0.355892	-6.30
267542_at	hypothetical protein predicted by gene	---	AT2G32740	1.11	0.15	1.46	0.190192	0.356093	-6.30
250374_at	putative protein	EMF1	AT5G11530	1.24	0.31	1.46	0.190278	0.356226	-6.30
AFFX-r2-Bs	B. subtilis /GEN=jojG /DB_XREF=gb:L	---	---	-1.21	-0.28	-1.46	0.190351	0.356332	-6.30
261938_at	hypothetical protein predicted by gens	---	AT1G22510	-1.26	-0.34	-1.46	0.190429	0.356449	-6.30
248077_at	putative protein contains similarity to C	---	AT5G55770	-1.11	-0.15	-1.46	0.190636	0.356806	-6.30
259349_at	unknown protein ; supported by cDNA	ATAPRL5	AT3G03860	-1.11	-0.15	-1.45	0.190678	0.356827	-6.30
255372_at	putative reverse transcriptase	---	---	1.20	0.26	1.45	0.190678	0.356827	-6.30
259254_at	putative P-protein: chorismate mutase	ADT2	AT3G07630	1.14	0.19	1.45	0.190694	0.356828	-6.30
253653_at	hypothetical protein	---	AT4G30050	-1.13	-0.17	-1.45	0.190835	0.357062	-6.30
252864_at	putative protein regulatory protein prr(	---	AT4G39740	1.24	0.31	1.45	0.190904	0.357162	-6.30
246246_at	putative protein	---	AT4G37170	-1.16	-0.21	-1.45	0.190992	0.357297	-6.30
267529_at	putative protein kinase contains a prot	AtAUR3	AT2G45490	-1.16	-0.21	-1.45	0.191023	0.357326	-6.30
246959_at	unknown protein	---	AT5G24690	1.27	0.34	1.45	0.191206	0.357633	-6.30
248233_at	F-box protein family, AtFBL13 contain	---	AT5G53840	-1.13	-0.17	-1.45	0.191219	0.357633	-6.30
266446_at	hypothetical protein predicted by gens	---	AT2G43310	-1.11	-0.15	-1.45	0.191327	0.357807	-6.31
267621_at	unknown protein	---	---	-1.15	-0.20	-1.45	0.191354	0.357815	-6.31
260576_at	putative FCA-related protein	---	AT2G47310	-1.17	-0.22	-1.45	0.191363	0.357815	-6.31
249265_at	E2, ubiquitin-conjugating enzyme 8 (U	---	AT5G41080 /	-1.10	-0.13	-1.45	0.191396	0.357835	-6.31
261226_at	expansin S2 precursor, putative simila	ATEXPA11	AT1G20190	-2.14	-1.10	-1.45	0.191405	0.357835	-6.31
261010_at	hypothetical protein predicted by gene	---	AT1G26350	-1.12	-0.16	-1.45	0.191482	0.357949	-6.31
250084_at	unknown protein	SDG40	AT5G17240	-1.19	-0.25	-1.45	0.191518	0.357987	-6.31
262497_at	putative 20S proteasome beta subunit	PBC1	AT1G21720	-1.13	-0.17	-1.45	0.191535	0.35799	-6.31
265846_at	putative serine carboxypeptidase II	scpl28	AT2G35770	-1.13	-0.18	-1.45	0.19161	0.358102	-6.31
262680_at	anter-specific proline-rich -like protein	---	AT1G75880	1.21	0.28	1.45	0.191702	0.358196	-6.31
256189_at	hypothetical protein predicted by gene	---	AT1G30140	-1.11	-0.15	-1.45	0.191699	0.358196	-6.31
252033_at	putative protein ;supported by full-leng	---	AT3G51950	-1.23	-0.30	-1.45	0.191708	0.358196	-6.31
260344_at	polyneuridine aldehyde esterase, puta	MES15	AT1G69240	-1.13	-0.17	-1.45	0.191801	0.358338	-6.31
247909_at	unknown protein ; supported by full-le	---	AT5G57370	-1.14	-0.19	-1.45	0.191815	0.358338	-6.31
246079_at	putative protein unconventional myosi	---	AT5G20450	-1.15	-0.21	-1.45	0.191838	0.358351	-6.31
258790_at	putative RNA-binding protein similar pu	FLK	AT3G04610	-1.10	-0.13	-1.45	0.191878	0.358397	-6.31
251417_at	putative protein prib5, Ribes nigrum, E	AT3G60420	---	-1.10	-0.14	-1.45	0.192014	0.358612	-6.31

247417_at	putative protein similar to unknown pro	---	AT5G63040	-1.11	-0.16	-1.45	0.192025	0.358612	-6.31
255729_at	hypothetical protein similar to putative	---	AT1G25470 /	1.12	0.17	1.45	0.192075	0.358677	-6.31
255723_at	hypothetical protein	AFP3	AT3G29575	-1.33	-0.41	-1.45	0.192103	0.3587	-6.31
252815_at	hypothetical protein	---	---	-1.15	-0.20	-1.45	0.192316	0.359068	-6.31
257486_at	unknown protein	---	AT1G63590	1.11	0.14	1.45	0.192368	0.359136	-6.31
254452_at	UV-damaged DNA-binding protein- lik	DDB1B	AT4G21100	1.16	0.21	1.45	0.192388	0.359143	-6.31
255027_at	hypothetical protein F21E10.5 Arabido	---	AT4G09880	1.13	0.17	1.45	0.192526	0.359342	-6.31
261497_x_	hypothetical protein contains similarity	AGL59	AT1G28460	-1.13	-0.18	-1.45	0.192516	0.359342	-6.31
260313_at	putative disease resistance protein sim	---	AT1G63870	-1.16	-0.21	-1.45	0.192577	0.359407	-6.31
262670_s_	transposase [Escherichia coli] must be	---	---	-1.12	-0.16	-1.45	0.192609	0.359439	-6.31
252038_at	gamma response I protein ; supported	---	AT3G52120	-1.17	-0.23	-1.45	0.192641	0.359467	-6.31
265567_at	unknown protein predicted by genefinc	---	AT2G05580	-1.15	-0.20	-1.45	0.192741	0.359517	-6.31
257718_at	organ separation protein, putative sim	anac058	AT3G18400	-1.13	-0.18	-1.45	0.19274	0.359517	-6.31
254203_at	putative protein various predicted prot	AtGRF8	AT4G24150	-1.11	-0.15	-1.45	0.192685	0.359517	-6.31
258441_at	hypothetical protein predicted by genm	AT3G17265	---	1.11	0.15	1.45	0.192762	0.359517	-6.31
257520_at	hypothetical protein	---	AT3G07710	1.14	0.19	1.45	0.192751	0.359517	-6.31
254254_at	hypothetical protein	---	AT4G23330	-1.14	-0.19	-1.45	0.192711	0.359517	-6.31
256010_at	auxin response factor, putative similar	ARF19	AT1G19220	1.14	0.19	1.45	0.192799	0.359558	-6.31
253782_at	hypothetical protein	---	AT4G28590	-1.10	-0.14	-1.45	0.192869	0.359618	-6.31
249376_at	Expressed protein ; supported by full-le	---	AT5G40645	1.09	0.13	1.45	0.192879	0.359618	-6.31
263409_at	predicted protein	---	AT2G04063	-1.12	-0.16	-1.45	0.192865	0.359618	-6.31
245471_at	probable ribosomal protein	---	AT4G16030	-1.11	-0.15	-1.45	0.192903	0.359633	-6.31
257975_at	unknown protein similar to GB:AAD30(	---	AT3G20830	1.19	0.25	1.45	0.193007	0.359798	-6.31
247548_at	putative protein various predicted prot	---	AT5G61400	1.17	0.22	1.45	0.193151	0.360038	-6.31
248398_at	sorbitol dehydrogenase-like protein ;s	---	AT5G51970	1.14	0.19	1.45	0.193198	0.360075	-6.31
245846_at	P-type transporting ATPase, putative	---	AT1G26130	1.16	0.22	1.45	0.193225	0.360075	-6.31
248296_at	protochlorophyllide reductase; oxidore	---	AT5G53090	-1.16	-0.22	-1.45	0.193235	0.360075	-6.31
256651_at	hypothetical protein predicted by gene	---	AT3G18840	1.15	0.20	1.45	0.19321	0.360075	-6.31
245578_at	RNA helicase like protein	ATSUV3	AT4G14790	1.15	0.20	1.45	0.19336	0.36028	-6.31
257519_at	unknown protein	---	AT3G01210	-1.14	-0.19	-1.44	0.193387	0.3603	-6.31
255072_at	outer envelope membrane protein OE	TOC75-IV	AT4G09080	-1.14	-0.19	-1.44	0.193404	0.360303	-6.32
256567_at	amino acid permease, putative contai	---	AT3G19553	-1.13	-0.18	-1.44	0.193566	0.360575	-6.32
246116_at	putative protein predicted proteins - Ar	---	AT5G20310	-1.14	-0.18	-1.44	0.193594	0.36059	-6.32
257586_at	hypothetical protein predicted by gene	---	AT1G50760	-1.10	-0.14	-1.44	0.193606	0.36059	-6.32
256726_at	unknown protein	---	AT3G52210	1.17	0.23	1.44	0.193642	0.360628	-6.32

251079_at	hypothetical protein	---	AT5G02000	-1.11	-0.15	-1.44	0.193667	0.360645	-6.32
259305_at	unknown protein ;supported by full-ler	---	AT3G05070	1.12	0.17	1.44	0.193754	0.360778	-6.32
264220_at	unknown protein similar to putative act	ARPC3	AT1G60430	1.11	0.15	1.44	0.193786	0.360808	-6.32
247714_at	wuschel protein - like wuschel protein	WOX2	AT5G59340	1.22	0.29	1.44	0.193886	0.360965	-6.32
260140_at	Myb-related transcription factor, putati	MYB90	AT1G66390	1.14	0.19	1.44	0.193903	0.360967	-6.32
253804_at	putative protein	---	AT4G28230	1.14	0.19	1.44	0.194008	0.361132	-6.32
250268_s_	putative protein putative secreted prot	---	AT5G12950 /	-1.17	-0.23	-1.44	0.194141	0.361351	-6.32
262478_at	hypothetical protein similar to hypothet	---	AT1G11170	1.13	0.18	1.44	0.194203	0.361437	-6.32
252681_at	NAC domain -like protein Tobacco eli	anac061	AT3G44350	1.14	0.19	1.44	0.194297	0.361582	-6.32
264391_at	pectate lyase-like protein Similar to sty	---	AT1G11920	1.12	0.17	1.44	0.194397	0.36174	-6.32
261065_at	hypothetical protein predicted by gene	---	AT1G07500	-1.17	-0.22	-1.44	0.194477	0.361859	-6.32
259894_at	hypothetical protein predicted by gens	---	AT1G71430	-1.14	-0.19	-1.44	0.19451	0.36189	-6.32
260813_at	VirE2-interacting protein VIP1 identica	VIP1	AT1G43700	1.18	0.24	1.44	0.194535	0.361897	-6.32
258262_at	hypothetical protein	---	AT3G15770	-1.15	-0.20	-1.44	0.194545	0.361897	-6.32
263129_at	unknown protein ;supported by full-len	---	AT1G78620	-1.12	-0.16	-1.44	0.194648	0.362058	-6.32
255625_at	GBF2, G-box binding factor ;supporte	GBF2	AT4G01120	-1.21	-0.27	-1.44	0.194768	0.362253	-6.32
247713_at	putative protein nonspecific lipid-trans	---	AT5G59330	-1.12	-0.16	-1.44	0.194823	0.362326	-6.32
248913_at	unknown protein ;supported by full-ler	---	AT5G45760	-1.12	-0.16	-1.44	0.194843	0.362332	-6.32
257803_at	unknown protein	---	AT3G18790	-1.11	-0.15	-1.44	0.194961	0.362514	-6.32
263987_at	putative lipase ; supported by cDNA: g	---	AT2G42690	-1.17	-0.23	-1.44	0.194973	0.362514	-6.32
246341_x_	putative protein predicted proteins, Ar	---	AT3G43150	-1.16	-0.21	-1.44	0.19507	0.362667	-6.32
247097_at	mannan endo-1,4-beta-mannosidase	---	AT5G66460	1.18	0.24	1.44	0.195119	0.362674	-6.32
253202_at	Expressed protein ; supported by full-l	---	AT4G34555	-1.27	-0.34	-1.44	0.195122	0.362674	-6.32
266630_at	putative serpin	---	AT2G35580	-1.11	-0.15	-1.44	0.195111	0.362674	-6.32
260170_at	putative sucrose transport protein simi	SUC5	AT1G71890	-1.18	-0.24	-1.44	0.195141	0.36268	-6.32
252086_at	hypothetical protein	---	AT3G52030	1.12	0.17	1.44	0.195176	0.362688	-6.32
245375_at	NAK like protein kinase	---	AT4G17660	1.13	0.18	1.44	0.195177	0.362688	-6.32
260595_at	unknown protein	---	AT1G55890	1.14	0.19	1.44	0.195283	0.362855	-6.32
264828_at	hypothetical protein predicted by gens	ATATG18G	AT1G03380	1.17	0.23	1.44	0.195347	0.362914	-6.32
265348_at	putative RNA-binding protein	---	AT2G22600	-1.13	-0.18	-1.44	0.195349	0.362914	-6.32
263619_at	putative GDP-mannose pyrophosphor	---	AT2G04650	-1.12	-0.17	-1.44	0.195362	0.362914	-6.32
266757_at	unknown protein	---	AT2G46940	1.23	0.30	1.44	0.195459	0.363064	-6.32
265119_at	flavin-containing monooxygenase, put	FMO GS-OX	AT1G62570	1.28	0.36	1.44	0.195525	0.363157	-6.32
255042_at	putative protein hypothetical protein T	---	AT4G09630	-1.12	-0.16	-1.44	0.195557	0.363186	-6.33
257390_x_	hypothetical protein predicted by gens	---	---	-1.17	-0.23	-1.44	0.195577	0.363194	-6.33

254252_at	serine/threonine kinase - like protein k	---	AT4G23310	1.18	0.23	1.44	0.195647	0.363295	-6.33
255203_at	hypothetical protein	---	---	-1.16	-0.22	-1.44	0.195701	0.363365	-6.33
262773_at	putative nuclear matrix constituent pro	LINC2	AT1G13220	-1.14	-0.18	-1.44	0.195763	0.363422	-6.33
263203_at	hypothetical protein predicted by gene	chr31	AT1G05490	1.09	0.13	1.44	0.195763	0.363422	-6.33
249830_at	dihydroorotate dehydrogenase precurs	PYRD	AT5G23300	1.25	0.32	1.44	0.195874	0.363568	-6.33
259390_at	hypothetical protein predicted by gene	---	AT1G06340	1.12	0.17	1.44	0.195864	0.363568	-6.33
246351_at	unknown protein contains similarity to	---	AT1G16570	1.11	0.15	1.44	0.195899	0.363584	-6.33
258653_at	hypothetical protein similar to auxin-in	---	AT3G09870	-1.15	-0.20	-1.44	0.195957	0.363634	-6.33
258129_at	hypothetical protein predicted by gene	ROPGEF8	AT3G24620	-1.13	-0.17	-1.44	0.195945	0.363634	-6.33
248312_at	unknown protein	---	AT5G52580	-1.13	-0.18	-1.44	0.196017	0.363686	-6.33
257967_at	hypothetical protein predicted by gene	---	AT3G19910	1.11	0.15	1.44	0.196003	0.363686	-6.33
253636_at	putative protein predicted protein, Ara	---	AT4G30500	1.63	0.70	1.44	0.196037	0.363692	-6.33
250834_at	putative protein various predicted prot	DME	AT5G04560	-1.17	-0.22	-1.44	0.196058	0.363702	-6.33
259190_at	unknown protein est hit, predicted by (	TPLATE	AT3G01780	-1.17	-0.23	-1.43	0.196095	0.363741	-6.33
262701_at	hypothetical protein predicted by gens	---	AT1G16480	1.14	0.19	1.43	0.196204	0.363914	-6.33
261654_at	hypothetical protein contains similarity	---	AT1G01920	1.17	0.22	1.43	0.196226	0.363925	-6.33
258385_at	putative jasmonic acid regulatory prote	ATNAC2	AT3G15510	1.18	0.24	1.43	0.196255	0.36395	-6.33
264917_at	unknown protein contains Pfam profile	---	AT1G60500	1.10	0.13	1.43	0.196339	0.364017	-6.33
265003_at	protein kinase, putative similar to prot	---	AT1G26970	1.09	0.13	1.43	0.196333	0.364017	-6.33
253230_at	putative protein ; supported by full-len	---	AT4G34700	-1.12	-0.17	-1.43	0.196337	0.364017	-6.33
255185_at	hypothetical protein	---	AT4G07740	-1.12	-0.17	-1.43	0.196454	0.364181	-6.33
266854_at	putative C2H2-type zinc finger protein	---	AT2G26940	-1.16	-0.22	-1.43	0.19646	0.364181	-6.33
265038_at	putative protein kinase highly similar t	---	AT1G03920	-1.12	-0.17	-1.43	0.196488	0.364203	-6.33
256788_at	cytochrome P450, putative similar to c	CYP90D1	AT3G13730	-1.59	-0.67	-1.43	0.196511	0.364216	-6.33
259373_at	hypothetical protein predicted by gene	---	AT1G69160	-1.33	-0.41	-1.43	0.196546	0.364222	-6.33
259076_at	hypothetical protein predicted by gens	TMAC2	AT3G02140	1.62	0.69	1.43	0.196534	0.364222	-6.33
266260_at	putative ATPase skd1 family; supporte	SKD1	AT2G27600	-1.10	-0.14	-1.43	0.196669	0.36442	-6.33
266822_at	60S ribosomal protein L30 ;supported	---	AT2G44860	1.18	0.24	1.43	0.196743	0.364528	-6.33
253753_at	glycine-rich protein like glycine-rich pr	---	AT4G29030	-1.13	-0.17	-1.43	0.196813	0.364628	-6.33
264723_at	putative salt-inducible protein similar to	---	AT1G22960	1.11	0.15	1.43	0.196859	0.364654	-6.33
264830_at	hypothetical protein predicted by gene	---	AT1G03710	1.14	0.19	1.43	0.19685	0.364654	-6.33
261660_at	kinesin heavy chain isolog, putative si	HIK	AT1G18370	1.10	0.14	1.43	0.196968	0.364797	-6.33
245849_at	leukotriene-A4 hydrolase-like protein l	---	AT5G13520	-1.28	-0.35	-1.43	0.196963	0.364797	-6.33
245120_at	hypothetical protein predicted by gens	HOS1	AT2G39810	1.15	0.20	1.43	0.197127	0.365004	-6.33
253664_at	NADPH-ferrihemoprotein reductase (A	ATR2	AT4G30210	1.42	0.50	1.43	0.197128	0.365004	-6.33

247727_at	putative ripening-related protein - like p	---	AT5G59490	1.16	0.22	1.43	0.197098	0.365004	-6.33
256890_at	glycine-rich RNA binding protein, puta	GRP4	AT3G23830	1.29	0.36	1.43	0.197161	0.365037	-6.33
263782_at	hypothetical protein predicted by gene	---	AT2G46380	1.13	0.18	1.43	0.197211	0.365099	-6.33
258863_at	unknown protein similar to RNA helica	DCL2	AT3G03300	-1.21	-0.28	-1.43	0.197258	0.365156	-6.33
264526_at	putative calcium ATPase very similar t	ECA3	AT1G10130	1.14	0.19	1.43	0.197293	0.365161	-6.33
264058_at	F-box protein family, AtFBX7 contains	---	AT2G03560	-1.11	-0.15	-1.43	0.197286	0.365161	-6.33
253447_at	hypothetical protein	---	AT4G32630	-1.10	-0.13	-1.43	0.197316	0.365174	-6.33
248779_at	acetoacyl-CoA-thiolase ;supported by	---	AT5G47720	1.22	0.29	1.43	0.197334	0.365178	-6.33
249579_at	ADP-ribosylation factor - like protein A	ATARLA1A	AT5G37680	-1.12	-0.16	-1.43	0.197385	0.365243	-6.33
258065_at	putative pyruvate kinase similar to PY	---	AT3G25960	1.14	0.19	1.43	0.197449	0.365332	-6.33
255155_at	hypothetical protein	---	AT4G08230	1.14	0.19	1.43	0.197536	0.365464	-6.33
264718_at	receptor-like kinase, putative similar to	---	AT1G70130	1.10	0.14	1.43	0.197559	0.365476	-6.33
265726_at	putative inositol polyphosphate 5'-phos	---	AT2G32010	-1.18	-0.23	-1.43	0.197728	0.365681	-6.33
256704_at	deacetylvindoline 4-O-acetyltransferas	---	AT3G30280	-1.11	-0.15	-1.43	0.19771	0.365681	-6.33
252879_at	putative protein predicted proteins, Ar	NST-K1	AT4G39390	-1.34	-0.42	-1.43	0.197691	0.365681	-6.33
245527_at	putative epoxide hydrolase	---	AT4G15955	1.16	0.21	1.43	0.197734	0.365681	-6.33
256199_at	unknown protein	SAB	AT1G58250	-1.16	-0.21	-1.43	0.197752	0.365685	-6.34
AFFX-Atha	Arabidopsis thaliana /REF=X52320 /D	---	---	-1.17	-0.23	-1.43	0.197909	0.365946	-6.34
249913_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G22810	-1.13	-0.18	-1.43	0.19795	0.365992	-6.34
267622_at	hypothetical protein predicted by gens	---	AT2G39690	1.12	0.16	1.43	0.197974	0.366007	-6.34
257618_at	protein kinase, putative similar to TYR	---	AT3G24715	-1.09	-0.13	-1.43	0.198035	0.366027	-6.34
251789_at	serine/threonine-specific protein kinas	---	AT3G55450	1.16	0.21	1.43	0.198014	0.366027	-6.34
261783_at	vacuolar assembly protein vps41, puta	---	AT1G08190	-1.14	-0.19	-1.43	0.19805	0.366027	-6.34
255073_at	beta-1,3-glucanase-like protein probal	---	AT4G09090	-1.10	-0.14	-1.43	0.198019	0.366027	-6.34
266104_at	putative phosphatidate cytidylyltransfe	---	AT2G45150	1.13	0.18	1.43	0.198115	0.366119	-6.34
267424_at	hypothetical protein predicted by gens	---	AT2G34800	1.09	0.12	1.43	0.198212	0.366268	-6.34
253628_at	xyloglucan endo-1,4-beta-D-glucanas	XTH18	AT4G30280	-2.25	-1.17	-1.43	0.198258	0.366324	-6.34
248854_at	putative protein contains similarity to s	---	AT5G46580	-1.14	-0.19	-1.43	0.198357	0.366474	-6.34
246383_at	hypothetical protein predicted by gene	---	AT1G77360	1.22	0.29	1.43	0.198371	0.366474	-6.34
246096_at	beta-1,3-glucanase bg4 ;supported b	BETAG4	AT5G20330	-1.13	-0.18	-1.43	0.198437	0.366566	-6.34
250640_at	putative protein protein kinase Xa21 -	---	AT5G07150	1.24	0.31	1.43	0.198587	0.366813	-6.34
267189_at	putative methionine aminopeptidase ;	MAP2A	AT2G44180	1.29	0.36	1.43	0.198659	0.366917	-6.34
248987_at	dimethylaniline monooxygenase (N-ox	---	AT5G45180	-1.11	-0.15	-1.43	0.198733	0.367023	-6.34
259560_at	hypothetical protein	WAK2	AT1G21270	-1.43	-0.52	-1.42	0.198896	0.367235	-6.34
247243_at	nodulin-like protein	---	AT5G64700	1.21	0.27	1.42	0.198887	0.367235	-6.34

266476_at	unknown protein ;supported by full-ler	---	AT2G31090	1.17	0.22	1.42	0.198864	0.367235	-6.34
263285_at	unknown protein	DOT1	AT2G36120	1.24	0.31	1.42	0.198923	0.367255	-6.34
258191_at	putative vesicle transport protein simila	VTI13	AT3G29100	-1.10	-0.14	-1.42	0.198984	0.367337	-6.34
252464_at	RNA-binding protein-like protein variou	---	AT3G47160	1.16	0.22	1.42	0.199023	0.36738	-6.34
253138_at	ribosomal protein L11 homolog severa	MRPL11	AT4G35490	-1.11	-0.14	-1.42	0.199064	0.367392	-6.34
260198_at	F12A21.23 hypothetical protein	---	AT1G67635	-1.10	-0.14	-1.42	0.199078	0.367392	-6.34
247739_at	40S ribosomal protein S8 - like 40S rit	---	AT5G59240	1.16	0.22	1.42	0.199055	0.367392	-6.34
255890_at	rhodanese-like family protein predicted	---	AT1G17850	-1.22	-0.28	-1.42	0.199106	0.367414	-6.34
252388_at	putative protein ;supported by full-leng	---	AT3G47850	-1.13	-0.17	-1.42	0.199149	0.367464	-6.34
251300_at	hypothetical protein ;supported by full-	---	AT3G61980	-1.17	-0.23	-1.42	0.199274	0.367666	-6.34
264089_at	actin depolymerizing factor 6 ;support	ADF6	AT2G31200	1.17	0.23	1.42	0.199348	0.367764	-6.34
264632_at	DegP protease contains similarity to D	DegP4	AT1G65640	-1.10	-0.14	-1.42	0.19936	0.367764	-6.34
263039_at	mak16-like protein-related similar to M	---	AT1G23280	1.18	0.24	1.42	0.199412	0.36783	-6.34
251260_at	putative protein ISOPENICILLIN N EP	---	AT3G62130	1.21	0.27	1.42	0.199507	0.367946	-6.34
250951_at	putative protein	---	AT5G03550	1.33	0.41	1.42	0.1995	0.367946	-6.34
246684_at	putative protein nucleoid DNA-binding	CDR1	AT5G33340	1.16	0.21	1.42	0.199569	0.368011	-6.34
263176_at	UDP-glucose:indole-3-acetate beta-D	UGT75B2	AT1G05530	1.11	0.15	1.42	0.199575	0.368011	-6.34
265496_at	copia-like retroelement pol polyprotein	---	---	-1.09	-0.13	-1.42	0.199659	0.368137	-6.34
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.21	-0.27	-1.42	0.199789	0.368347	-6.34
247952_at	salt-inducible protein-like	CYP71B10	AT5G57250 /	-1.13	-0.17	-1.42	0.199815	0.368364	-6.34
253001_at	Expressed protein ; supported by cDN	---	AT4G38490	-1.09	-0.13	-1.42	0.199956	0.36856	-6.34
245818_at	cytochrome b561, putative similar to c	---	AT1G26100	-1.24	-0.31	-1.42	0.199969	0.36856	-6.35
263781_at	hypothetical protein predicted by gene	---	AT2G46360	-1.09	-0.13	-1.42	0.199965	0.36856	-6.35
263690_at	putative DNA-binding protein Similar t	AtHB23	AT1G26960	-1.23	-0.29	-1.42	0.200041	0.368632	-6.35
256341_at	deoxyguanosine kinase, putative simil	---	AT1G72040	-1.24	-0.31	-1.42	0.200035	0.368632	-6.35
265694_at	hypothetical protein predicted by gens	---	AT2G24440	-1.13	-0.18	-1.42	0.200088	0.368689	-6.35
264825_at	hypothetical protein predicted by gens	---	AT1G03720	-1.13	-0.18	-1.42	0.200146	0.368737	-6.35
247382_at	adenylate kinase ;supported by full-len	ADK1	AT5G63400	-1.16	-0.21	-1.42	0.200142	0.368737	-6.35
245598_at	hypothetical protein	---	AT4G14200	1.17	0.22	1.42	0.200242	0.368883	-6.35
250224_at	putative protein similar to unknown pro	---	AT5G14150	1.16	0.22	1.42	0.200328	0.369012	-6.35
246503_at	40S ribosomal protein S7-like 40S ribo	---	AT5G16130	-1.25	-0.32	-1.42	0.200439	0.369157	-6.35
255988_at	putative protein	---	---	1.12	0.16	1.42	0.200429	0.369157	-6.35
254469_at	hypothetical protein	---	AT4G20470	1.11	0.15	1.42	0.200502	0.369243	-6.35
248535_at	putative protein contains similarity to G	---	AT5G50120	-1.15	-0.20	-1.42	0.20054	0.369283	-6.35
249066_at	WD-repeat protein-like	---	AT5G43920	1.10	0.13	1.42	0.200736	0.369572	-6.35

265012_at	putative b-keto acyl reductase similar	KCR2	AT1G24470	-1.12	-0.17	-1.42	0.200745	0.369572	-6.35
251515_at	putative protein several hypothetical pr	---	AT3G59270	-1.09	-0.12	-1.42	0.200735	0.369572	-6.35
262325_at	dirigent protein, putative similar to diri	---	AT1G64160	1.28	0.35	1.42	0.200771	0.369589	-6.35
253353_at	pathogenesis-related protein - like pat	---	AT4G33730	-1.10	-0.14	-1.42	0.200836	0.36968	-6.35
254018_at	putative mitochondrial carrier protein (	---	AT4G26180	-1.13	-0.18	-1.42	0.20089	0.369749	-6.35
255871_at	putative small nuclear ribonucleoprotei	U2B"	AT2G30260	-1.13	-0.18	-1.42	0.20094	0.369795	-6.35
247022_at	unknown protein	---	AT5G67050	-1.11	-0.15	-1.42	0.200947	0.369795	-6.35
263045_at	hypothetical protein predicted by gens	---	AT2G05370	-1.12	-0.16	-1.42	0.201011	0.369853	-6.35
264961_at	unknown protein contains similarity to	PRAF1	AT1G76950	-1.26	-0.34	-1.42	0.201001	0.369853	-6.35
264103_at	unknown protein	---	AT2G13660	1.13	0.18	1.42	0.201079	0.369947	-6.35
260947_at	fructokinase, putative similar to fructol	---	AT1G06020	1.09	0.13	1.42	0.201128	0.370009	-6.35
257004_s_	glycolate oxidase, putative similar to (	---	AT3G14130 /	-1.10	-0.14	-1.42	0.201171	0.370058	-6.35
257472_at	hypothetical protein predicted by gene	---	AT1G56040	-1.10	-0.14	-1.42	0.201226	0.370129	-6.35
255697_at	hypothetical protein	---	AT4G00130	-1.16	-0.22	-1.42	0.201313	0.370258	-6.35
265321_at	putative Tub family protein	AtTLP2	AT2G18280	-1.10	-0.14	-1.42	0.20133	0.37026	-6.35
267498_at	unknown protein	---	AT2G45720	1.17	0.22	1.42	0.201428	0.370411	-6.35
252283_at	60S ribosomal protein L13 (BBC1) - li	---	AT3G48960	-1.12	-0.16	-1.42	0.201545	0.370597	-6.35
247095_at	dehydrin RAB18-like protein (sp P3018	RAB18	AT5G66400	1.32	0.40	1.41	0.201668	0.370793	-6.35
260843_at	unknown protein similar to hypothetica	---	AT1G29060	-1.09	-0.13	-1.41	0.201702	0.370825	-6.35
248189_at	DNA mismatch repair protein MutS2-li	---	AT5G54090	1.15	0.20	1.41	0.201752	0.370886	-6.35
249734_at	putative protein strong similarity to unk	IRE1-1	AT5G24360	-1.09	-0.13	-1.41	0.20179	0.37092	-6.35
259011_s_	unknown protein similar to putative pro	---	AT3G07380 /	-1.12	-0.16	-1.41	0.201803	0.37092	-6.35
262024_at	protein disulfide isomerase, putative s	ATPDIL5-2	AT1G35620	-1.15	-0.20	-1.41	0.201861	0.370998	-6.35
255424_at	putative glycosylation enzyme similar	---	AT4G03340	-1.12	-0.16	-1.41	0.201951	0.371103	-6.35
256523_at	unknown protein ;supported by full-len	---	AT1G66070	1.13	0.18	1.41	0.201946	0.371103	-6.35
266208_at	putative tRNA isopentenylpyrophospha	ATIPT2	AT2G27760	-1.21	-0.27	-1.41	0.201968	0.371105	-6.35
265905_at	putative transcription elongation factor	---	AT2G25640	-1.10	-0.14	-1.41	0.201991	0.371107	-6.35
251348_at	putative protein hypothetical protein F	---	AT3G61010	-1.18	-0.24	-1.41	0.202002	0.371107	-6.35
250694_at	putative protein contains similarity to h	HAT14	AT5G06710	-1.16	-0.21	-1.41	0.202021	0.371112	-6.35
262849_at	unknown protein ; supported by cDNA	---	AT1G14710	-1.33	-0.41	-1.41	0.202104	0.371235	-6.35
263292_at	putative Ta11-like non-LTR retroeleme	---	---	1.12	0.16	1.41	0.202231	0.371438	-6.36
267426_at	hypothetical protein predicted by gens	---	AT2G34820	-1.11	-0.15	-1.41	0.202322	0.371575	-6.36
256322_at	unknown protein ; supported by cDNA	AXR4	AT1G54990	1.26	0.33	1.41	0.202434	0.371751	-6.36
252960_at	hypothetical protein	---	AT4G38750	1.22	0.29	1.41	0.202465	0.371778	-6.36
261297_at	hypothetical protein predicted by gene	JAZ4	AT1G48500	-1.10	-0.14	-1.41	0.202566	0.371934	-6.36

249623_at	putative protein Ariadne-2 protein (AR	---	AT5G37560	1.09	0.12	1.41	0.202584	0.371937	-6.36
266931_at	putative non-LTR retroelement reverse	---	---	-1.12	-0.16	-1.41	0.202673	0.372071	-6.36
245444_at	limonene cyclase like protein	ATTPS03	AT4G16740	-1.16	-0.21	-1.41	0.202732	0.372149	-6.36
254379_at	putative protein calmodulin-binding pr	---	AT4G21820	-1.09	-0.13	-1.41	0.202797	0.372207	-6.36
258427_at	putative DNA-binding protein similar t	---	AT3G16600	-1.10	-0.13	-1.41	0.202785	0.372207	-6.36
AFFX-BioB	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.21	0.28	1.41	0.202943	0.372447	-6.36
253214_at	putative protein karyopherin alpha 1,	ARO1	AT4G34940	-1.11	-0.15	-1.41	0.202987	0.372497	-6.36
263616_at	unknown protein	---	AT2G04680	1.13	0.18	1.41	0.203021	0.372499	-6.36
246324_at	arginine/serine-rich protein, putative s	SR45	AT1G16610	1.11	0.15	1.41	0.20302	0.372499	-6.36
254197_at	trehalase - like protein trehalase 1 GM	TRE1	AT4G24040	1.19	0.25	1.41	0.203118	0.372647	-6.36
254093_at	putative protein extensin, Catharanthu	AtMC2	AT4G25110	1.36	0.44	1.41	0.203191	0.372751	-6.36
259650_at	leucoanthocyanidin dioxygenase 2, pu	---	AT1G55290	1.12	0.16	1.41	0.203236	0.372797	-6.36
248817_at	putative protein strong similarity to unk	---	AT5G47020	-1.14	-0.19	-1.41	0.203249	0.372797	-6.36
260860_at	hypothetical protein predicted by gene	---	AT1G43810	-1.12	-0.16	-1.41	0.203287	0.37282	-6.36
265592_at	hypothetical protein predicted by gene	---	AT2G20110	-1.13	-0.17	-1.41	0.203294	0.37282	-6.36
264241_at	hypothetical protein contains similarity	---	AT1G54840	-1.09	-0.13	-1.41	0.203379	0.372947	-6.36
262802_at	putative cell division control protein, c	CDKB2;2	AT1G20930	1.10	0.13	1.41	0.203402	0.372958	-6.36
261486_at	nucleic acid binding protein (alfin-1), p	AL7	AT1G14510	-1.12	-0.17	-1.41	0.203459	0.373033	-6.36
264153_at	disease resistance protein RPS4, puta	ATPP2-A5	AT1G65390	1.30	0.38	1.41	0.203544	0.373158	-6.36
247451_at	MYB99 ; supported by cDNA: gi_1537	ATMYB99	AT5G62320	-1.13	-0.18	-1.41	0.20359	0.373213	-6.36
256371_at	hypothetical protein	---	AT1G66770	-1.11	-0.15	-1.41	0.203625	0.373242	-6.36
250333_at	membrane translocase - like protein ir	TIM17-3	AT5G11690	-1.24	-0.31	-1.41	0.203638	0.373242	-6.36
259009_at	thioglucosidase 3D precursor identical	PYK10	AT3G09260	1.21	0.27	1.41	0.203755	0.373425	-6.36
263484_at	putative presenilin	---	AT2G29900	-1.10	-0.14	-1.41	0.203788	0.373455	-6.36
255231_at	F-box protein family, AtFBL20 contain	---	AT4G05460	1.11	0.15	1.41	0.203874	0.373584	-6.36
260853_at	hypothetical protein predicted by gene	---	AT1G21950	-1.18	-0.24	-1.41	0.203907	0.373584	-6.36
256464_at	late-embryogenesis abundant protein,	---	AT1G32560	1.36	0.44	1.41	0.203899	0.373584	-6.36
260514_at	hypothetical protein predicted by gene	---	AT1G51480	1.11	0.16	1.41	0.203928	0.373592	-6.36
263217_at	putative reticuline oxidase-like protein	---	AT1G30740	1.11	0.15	1.41	0.203944	0.373592	-6.36
254581_at	putative protein membrane-associated	---	AT4G19440	1.17	0.23	1.41	0.204046	0.373749	-6.36
253126_at	putative protein probable membrane p	---	AT4G36050	1.22	0.29	1.41	0.204125	0.373863	-6.36
250661_at	nucleoid DNA-binding-like protein ;sup	---	AT5G07030	-1.97	-0.98	-1.41	0.20416	0.373897	-6.36
267482_s_	unknown protein	---	AT2G02770 /	-1.33	-0.41	-1.41	0.204198	0.373937	-6.36
249258_at	putative protein similar to unknown pro	---	AT5G41650	-1.10	-0.14	-1.41	0.204289	0.374073	-6.36
251110_at	putative protein various alpha amylase	---	AT5G01260	1.21	0.27	1.41	0.204333	0.374123	-6.36

258517_at	galactose kinase identical to GB:AAB	GALK	AT3G06580	-1.12	-0.17	-1.41	0.204374	0.374169	-6.36
255244_at	putative protein various hypothetical pr	---	AT4G05620	-1.12	-0.16	-1.41	0.204412	0.374182	-6.36
261690_at	branched-chain amino acid aminotran	---	AT1G50090	1.11	0.15	1.41	0.204414	0.374182	-6.36
266274_at	putative protein phosphatase 2C	---	AT2G29380	1.12	0.16	1.40	0.20452	0.374263	-6.37
253205_at	putative cyclase associated protein CA	ATCAP1	AT4G34490	-1.23	-0.30	-1.40	0.204485	0.374263	-6.36
254161_at	hypothetical protein ;supported by full-	---	AT4G24370	-1.12	-0.16	-1.40	0.20454	0.374263	-6.37
264812_at	putative thaumatin-like pathogenesis-r	---	AT2G17860	1.11	0.14	1.40	0.204524	0.374263	-6.37
262987_at	conserved hypothetical protein protein	---	AT1G23240	1.19	0.25	1.40	0.204497	0.374263	-6.37
253959_at	putative protein	---	AT4G26410	-1.10	-0.14	-1.40	0.204649	0.374432	-6.37
254881_at	hypothetical protein	---	AT4G11700	-1.10	-0.14	-1.40	0.204687	0.374471	-6.37
262425_at	hypothetical protein predicted by gens	---	AT1G47660	1.11	0.15	1.40	0.20486	0.374758	-6.37
249892_at	unknown protein	---	AT5G22600	-1.10	-0.14	-1.40	0.204906	0.374811	-6.37
259988_at	Athila ORF 1, putative simlar to GI:80	---	---	-1.10	-0.13	-1.40	0.205045	0.375035	-6.37
254362_at	Expressed protein ; supported by full-l	---	AT4G22160	-1.17	-0.23	-1.40	0.205096	0.375039	-6.37
263961_at	F-box protein family, AtFBL11 contain	---	AT2G36370	1.15	0.20	1.40	0.205081	0.375039	-6.37
252119_at	thioredoxin h ;supported by full-length	ATTRX1	AT3G51030	-1.23	-0.30	-1.40	0.205079	0.375039	-6.37
262662_at	hypothetical protein similar to hypothet	---	AT1G13920	-1.14	-0.19	-1.40	0.205124	0.37506	-6.37
258387_at	hypothetical protein predicted by gens	---	AT3G15550	-1.13	-0.18	-1.40	0.205188	0.375147	-6.37
264213_at	hypothetical protein contains similarity	ATPP2-A5	AT1G65390	1.78	0.83	1.40	0.205345	0.375404	-6.37
255576_at	predicted protein of unknown function	---	AT4G01440	-1.21	-0.28	-1.40	0.205375	0.375429	-6.37
247995_at	putative protein contains similarity to p	---	AT5G56160	-1.16	-0.22	-1.40	0.205442	0.375522	-6.37
253801_at	hypothetical protein	---	AT4G28170	1.12	0.16	1.40	0.205471	0.375543	-6.37
266377_at	Mutator-like transposase similar to MU	---	---	1.09	0.12	1.40	0.205535	0.375631	-6.37
249995_at	protein kinase -like protein protein kin	---	AT5G18610	-1.10	-0.14	-1.40	0.205574	0.375672	-6.37
256904_at	unknown protein	---	AT3G23980	-1.10	-0.13	-1.40	0.20559	0.375672	-6.37
266102_at	unknown protein	---	AT2G40720	-1.12	-0.17	-1.40	0.20568	0.375806	-6.37
252697_at	nodulin - like protein nodulin-21, Glyci	---	AT3G43660	-1.13	-0.18	-1.40	0.205783	0.375963	-6.37
247137_at	calcium-dependent protein kinase ;su	CPK28	AT5G66210	1.30	0.38	1.40	0.20588	0.376112	-6.37
254697_at	putative protein predicted protein, Ara	---	AT4G17970	1.10	0.14	1.40	0.205931	0.376175	-6.37
261909_at	hypothetical protein predicted by gene	SAR3	AT1G80680	1.15	0.20	1.40	0.206126	0.376391	-6.37
266199_at	putative calcium-dependent protein kin	CPK20	AT2G38910	-1.11	-0.15	-1.40	0.206131	0.376391	-6.37
259187_at	putative transcription factor similar to m	AtMYB57	AT3G01530	-1.15	-0.21	-1.40	0.206112	0.376391	-6.37
254685_at	SAUR-AC - like protein (small auxin u	---	AT4G13790	1.33	0.41	1.40	0.206086	0.376391	-6.37
256780_at	RNase L inhibitor, putative similar to R	ATRLI1	AT3G13640	-1.12	-0.16	-1.40	0.206132	0.376391	-6.37
262696_at	hypothetical protein	---	AT1G75870	-1.12	-0.16	-1.40	0.206157	0.376396	-6.37

254220_at	putative protein Arabidopsis hypothetic	---	AT4G23780	1.11	0.15	1.40	0.206168	0.376396	-6.37
251632_at	hypothetical protein	---	AT3G57440	-1.15	-0.20	-1.40	0.206211	0.376415	-6.37
263523_at	hypothetical protein predicted by gens	---	---	-1.10	-0.14	-1.40	0.206208	0.376415	-6.37
251558_at	putative protein ;supported by full-len	---	AT3G57810	-1.23	-0.30	-1.40	0.206264	0.376481	-6.37
267346_at	coronatine-insensitive 1 (COI1), AtFB	COI1	AT2G39940	1.16	0.21	1.40	0.206432	0.376697	-6.37
265478_at	unknown protein ;supported by full-ler	MEE14	AT2G15890	-1.11	-0.15	-1.40	0.206416	0.376697	-6.37
252957_at	glycine-rich protein 2 (GRP2) ; suppor	GRP2	AT4G38680	1.24	0.31	1.40	0.206425	0.376697	-6.37
264187_at	unknown protein ;supported by full-len	---	AT1G54860	1.09	0.13	1.40	0.20649	0.376761	-6.37
257579_at	hypothetical protein predicted by gene	---	AT3G11000	1.13	0.17	1.40	0.2065	0.376761	-6.37
267343_at	hypothetical protein predicted by grail;	---	AT2G44260	1.75	0.81	1.40	0.206545	0.376814	-6.37
257609_at	Expressed protein ; supported by full-l	---	AT3G13845	-1.14	-0.18	-1.40	0.20668	0.377028	-6.37
256139_at	Nt-gh3 deduced protein, putative simi	---	AT1G48660	-1.14	-0.18	-1.40	0.206842	0.377295	-6.38
267639_at	putative squamosa-promoter binding p	SPL9	AT2G42200	1.10	0.14	1.40	0.206981	0.377518	-6.38
256068_at	hypothetical protein contains similarity	ATE1	AT1G13690	1.11	0.15	1.40	0.20704	0.377595	-6.38
264036_at	hypothetical protein similar to hypothet	---	AT2G03810	-1.17	-0.23	-1.40	0.20706	0.377602	-6.38
258903_at	hypothetical protein similar to zinc fing	---	AT3G06410	-1.18	-0.24	-1.40	0.207081	0.37761	-6.38
254838_at	hypothetical protein	---	AT4G12380	-1.16	-0.21	-1.40	0.207114	0.37764	-6.38
261453_at	O-methyltransferase, putative similar t	---	AT1G21130	1.30	0.38	1.40	0.207153	0.37768	-6.38
267166_at	unknown protein	---	AT2G37720	-1.09	-0.12	-1.40	0.20717	0.377681	-6.38
255810_at	hypothetical protein ; supported by full-	---	AT4G10140	-1.12	-0.16	-1.39	0.207479	0.378214	-6.38
264826_at	putative 1-aminocyclopropane-1-carbo	2A6	AT1G03410	1.16	0.21	1.39	0.207498	0.378218	-6.38
249615_x_	contains similarity to unknown protein	AGL105	AT5G37420	-1.12	-0.17	-1.39	0.207692	0.378542	-6.38
257778_at	hypothetical protein predicted by gens	---	---	1.13	0.18	1.39	0.207709	0.378543	-6.38
251705_at	DNA-binding protein-like DNA-binding	WRKY70	AT3G56400	2.23	1.16	1.39	0.207757	0.378601	-6.38
263325_at	putative RING zinc finger protein ; sup	XERICO	AT2G04240	-1.25	-0.33	-1.39	0.207895	0.378822	-6.38
265529_at	hypothetical protein predicted by gens	---	---	1.10	0.14	1.39	0.207997	0.378977	-6.38
259493_at	unknown protein	---	AT1G15840	-1.12	-0.16	-1.39	0.208257	0.37942	-6.38
253707_at	hypothetical protein	---	AT4G29200	-1.10	-0.14	-1.39	0.208408	0.379635	-6.38
258788_at	unknown protein ;supported by full-ler	---	AT3G11780	-1.12	-0.17	-1.39	0.208407	0.379635	-6.38
257041_at	unknown protein	---	AT3G28550	1.16	0.22	1.39	0.208572	0.379872	-6.38
264091_at	hypothetical protein predicted by gens	---	AT1G79110	-1.30	-0.38	-1.39	0.208566	0.379872	-6.38
267176_at	putative zinc finger protein	---	AT2G37730	-1.12	-0.17	-1.39	0.208786	0.380233	-6.38
266748_at	putative squamosa-promoter binding p	SPL1	AT2G47070	-1.20	-0.26	-1.39	0.208893	0.380398	-6.38
247281_at	immunophilin (gb|AAB57847.1) ;suppo	FKBP12	AT5G64350	1.10	0.14	1.39	0.208938	0.380448	-6.38
251167_at	putative protein proteinase inhibitor - (	---	AT3G63360	-1.10	-0.14	-1.39	0.208978	0.380491	-6.38

248074_at	putative protein similar to unknown pro	FLA1	AT5G55730	-1.37	-0.45	-1.39	0.209216	0.380893	-6.39
246379_s_	60S ribosomal protein L21, putative si	---	AT1G57660 /	-1.19	-0.25	-1.39	0.20929	0.380999	-6.39
266994_at	MADS-box protein (AGL29)	AGL29	AT2G34440	-1.13	-0.18	-1.39	0.209312	0.381007	-6.39
259633_at	hypothetical protein	---	AT1G56500	-1.15	-0.20	-1.39	0.209343	0.381033	-6.39
251280_at	putative protein beta-1,3-glucanase pr	---	AT3G61810	-1.11	-0.15	-1.39	0.209495	0.38128	-6.39
246600_at	putative protein disease resistance pr	SAG101	AT5G14930	-1.24	-0.31	-1.39	0.209546	0.381342	-6.39
264731_at	hypothetical protein predicted by gene	---	AT1G62150	1.12	0.17	1.39	0.209571	0.381357	-6.39
264972_at	meiotic asynaptic mutant asy1, putativ	ASY1	AT1G67370	1.18	0.24	1.39	0.209587	0.381357	-6.39
258617_at	putative calmodulin similar to calmodu	---	AT3G03000	-1.10	-0.13	-1.39	0.209675	0.381485	-6.39
249344_at	prohibitin (gb AAC49691.1) ;supported	ATPHB3	AT5G40770	1.22	0.28	1.39	0.209693	0.381488	-6.39
261000_at	hypothetical protein predicted by gene	---	AT1G26540	-1.10	-0.14	-1.39	0.209815	0.38168	-6.39
252024_at	monodehydroascorbate reductase (N	ATMDAR1	AT3G52880	-1.15	-0.20	-1.39	0.209835	0.381686	-6.39
253416_at	pyruvate decarboxylase-1 (Pdc1)	---	AT4G33070	1.16	0.22	1.39	0.209857	0.381694	-6.39
248259_at	proline-rich cell wall protein-like ;supp	---	AT5G53330	1.12	0.16	1.39	0.210026	0.381972	-6.39
257576_at	hypothetical protein predicted by gene	---	AT3G28280	1.12	0.16	1.39	0.210063	0.38201	-6.39
261800_at	HD-Zip protein identical to HD-Zip prot	PHV	AT1G30490	-1.14	-0.19	-1.39	0.210099	0.382043	-6.39
246626_at	hypothetical protein contains similarity	---	AT1G48870	-1.17	-0.23	-1.39	0.210128	0.382066	-6.39
252707_at	transporter-like protein multidrug-efflu	ZIFL2	AT3G43790	-1.15	-0.20	-1.39	0.210197	0.382162	-6.39
249781_at	unknown protein	---	AT5G24250	1.14	0.19	1.38	0.210279	0.382279	-6.39
245569_at	RNA polymerase II fifth largest subunit	NRPE7	AT4G14660	-1.09	-0.13	-1.38	0.210361	0.382399	-6.39
252882_at	Expressed protein ; supported by full-l	---	AT4G39675	1.09	0.12	1.38	0.210442	0.382516	-6.39
263603_at	hypothetical protein	---	AT2G16340	1.15	0.20	1.38	0.21054	0.382662	-6.39
245062_at	hypothetical protein predicted by gens	BPM3	AT2G39760	1.10	0.14	1.38	0.21058	0.382706	-6.39
256340_at	DnaJ protein, putative contains Pfam	---	AT1G72070	1.13	0.18	1.38	0.210669	0.382805	-6.39
261423_at	homeodomain transcription factor, put	AGL65	AT1G18750	1.15	0.20	1.38	0.210657	0.382805	-6.39
256207_at	GTP-binding protein, putative similar t	---	AT1G50920	1.15	0.21	1.38	0.210719	0.382807	-6.39
260677_at	translation elongation factor EF-1 alph	RNL	AT1G07910	-1.21	-0.28	-1.38	0.21069	0.382807	-6.39
246834_at	putative protein homeotic protein boi1	---	AT5G26630	-1.12	-0.17	-1.38	0.21072	0.382807	-6.39
255081_at	MLH1 protein ; supported by cDNA: g	MLH1	AT4G09140	1.22	0.28	1.38	0.210789	0.382902	-6.39
245341_at	Expressed protein ; supported by full-l	---	AT4G16447	-1.35	-0.43	-1.38	0.210919	0.383083	-6.39
245887_at	putative protein CD2 cytoplasmic dom	---	AT5G09390	-1.09	-0.12	-1.38	0.210922	0.383083	-6.39
266152_s_	hypothetical protein predicted by gens	---	AT2G12050 /	1.10	0.14	1.38	0.210965	0.383129	-6.39
249747_at	putative protein similar to unknown pro	---	AT5G24600	1.14	0.19	1.38	0.21099	0.383138	-6.39
252428_at	putative protein rjs - Mus musculus, E	---	AT3G47660	1.13	0.18	1.38	0.211003	0.383138	-6.39
262991_at	hypothetical protein predicted by gens	BRX-LIKE3	AT1G54180	1.09	0.13	1.38	0.211082	0.3832	-6.39

250943_at	putative protein	---	AT5G03360	-1.10	-0.14	-1.38	0.211093	0.3832	-6.39
259126_at	putative NADPH-ferrihemoprotein redu	---	AT3G02280	-1.10	-0.14	-1.38	0.211099	0.3832	-6.39
254279_at	Expressed protein ; supported by full-l	---	AT4G22750	-1.12	-0.16	-1.38	0.211104	0.3832	-6.39
250852_at	putative protein BRL protein, Homo sa	---	AT5G04670	1.10	0.13	1.38	0.211122	0.383201	-6.39
260957_at	delta 9 desaturase identical to delta 9 (	ADS1	AT1G06080	-1.21	-0.27	-1.38	0.211178	0.383273	-6.39
253495_at	putative protein crp1 protein, Zea may	PGR3	AT4G31850	-1.18	-0.24	-1.38	0.211242	0.383358	-6.39
266703_at	unknown protein predicted by genscan	---	AT2G19880	1.18	0.24	1.38	0.211393	0.383602	-6.39
262069_at	hypothetical protein similar to SNF4-ki	---	AT1G80090	-1.13	-0.18	-1.38	0.211437	0.38365	-6.39
255746_at	heat shock transcription factor, putativ	---	AT1G32020	-1.10	-0.13	-1.38	0.211501	0.383736	-6.39
263238_at	putative auxin-induced protein	---	AT2G16580	-1.10	-0.13	-1.38	0.211568	0.383828	-6.40
254022_at	putative membrane transporter Bactro	---	AT4G25750	-1.13	-0.17	-1.38	0.21166	0.383965	-6.40
261174_at	26S proteasome regulatory subunit, p	---	AT1G04810	1.14	0.19	1.38	0.211827	0.384084	-6.40
250263_at	putative protein	---	AT5G13470	1.14	0.19	1.38	0.211812	0.384084	-6.40
250380_at	putative protein	---	AT5G11600	-1.11	-0.16	-1.38	0.211805	0.384084	-6.40
257483_at	hypothetical protein contains similarity	ICK5	AT1G49620	1.12	0.16	1.38	0.211775	0.384084	-6.40
245099_at	unknown protein ; supported by cDNA	RHC1A	AT2G40830	1.19	0.25	1.38	0.211745	0.384084	-6.40
259953_at	putative anion exchanger contains Pfa	BOR5	AT1G74810	-1.17	-0.23	-1.38	0.211803	0.384084	-6.40
265449_at	putative arginine/serine-rich splicing fa	---	AT2G46610	1.18	0.24	1.38	0.2119	0.384185	-6.40
245593_at	IAA7 like protein	IAA14	AT4G14550	-1.33	-0.41	-1.38	0.211963	0.384269	-6.40
259853_at	leucine-rich receptor-like protein kinas	---	AT1G72300	1.17	0.22	1.38	0.211985	0.384278	-6.40
246102_at	putative protein various predicted prot	---	AT5G32590	-1.10	-0.14	-1.38	0.21217	0.384583	-6.40
259612_at	60S ribosomal protein L37, putative si	---	AT1G52300	-1.26	-0.33	-1.38	0.212217	0.384637	-6.40
258349_at	Expressed protein ; supported by full-l	HYH	AT3G17609	1.30	0.38	1.38	0.212277	0.384687	-6.40
253471_at	hypothetical protein	---	---	1.12	0.17	1.38	0.212277	0.384687	-6.40
257207_at	hypothetical protein predicted by gene	---	AT3G14900	1.14	0.19	1.38	0.212323	0.384739	-6.40
265995_at	hypothetical protein predicted by gens	---	AT2G24140	1.11	0.15	1.38	0.212428	0.384869	-6.40
252719_at	putative protein predicted protein, Ara	---	AT3G43950	1.12	0.16	1.38	0.212429	0.384869	-6.40
259063_at	putative 5B-anther specific protein sim	---	AT3G07450	-1.09	-0.13	-1.38	0.212524	0.38501	-6.40
259158_at	hypothetical protein predicted by gens	---	AT3G05430	-1.09	-0.13	-1.38	0.212541	0.385012	-6.40
265998_at	putative NADP-dependent glyceraldeh	ALDH11A3	AT2G24270	-1.12	-0.17	-1.38	0.212562	0.385019	-6.40
251520_at	protein kinase like GCN2 - Saccharom	---	AT3G59410	1.10	0.14	1.38	0.212588	0.385035	-6.40
265205_at	putative poly(A) binding protein	PAB7	AT2G36660	-1.11	-0.15	-1.38	0.212634	0.385077	-6.40
259710_at	putative aminotransferase similar to k	---	AT1G77670	-1.34	-0.42	-1.38	0.212645	0.385077	-6.40
263248_at	putative endonuclease ;supported by	ATNTH1	AT2G31450	-1.11	-0.15	-1.38	0.212695	0.385137	-6.40
266603_at	hypothetical protein predicted by gens	---	AT2G46040	-1.11	-0.15	-1.38	0.212928	0.385529	-6.40

255028_at	putative protein Arabidopsis thaliana c	PMP	AT3G24160 /	-1.26	-0.33	-1.38	0.21308	0.385772	-6.40
260150_at	putative oxidoreductase similar to gibb	---	AT1G52820	1.13	0.17	1.37	0.213251	0.386052	-6.40
265682_at	similar to avrRpt2-induced protein 2	---	AT2G24390	1.16	0.22	1.37	0.213313	0.386082	-6.40
251721_s_	alpha-soluble NSF attachment protein	ALPHA-SNA	AT3G56190 /	1.13	0.18	1.37	0.213318	0.386082	-6.40
257273_at	hypothetical protein contains Pfam pro	UVH3	AT3G28030	1.14	0.19	1.37	0.213295	0.386082	-6.40
264140_at	proteasome alpha subunit, putative si	---	AT1G79210	-1.10	-0.14	-1.37	0.213509	0.386396	-6.40
261543_at	unknown protein contains Pfam profile	---	AT1G63550	-1.14	-0.19	-1.37	0.21355	0.38644	-6.40
249826_at	iron superoxide dismutase 3 (gb|AAC2	FSD3	AT5G23310	1.17	0.22	1.37	0.213581	0.386466	-6.40
250930_at	putative protein P58 protein, Bos prim	ATP58IPK	AT5G03160	1.28	0.35	1.37	0.213726	0.386698	-6.40
244909_at	hypothetical protein	---	---	-1.12	-0.16	-1.37	0.213793	0.386788	-6.40
264283_at	hypothetical protein contains similarity	---	AT1G61850	-1.12	-0.16	-1.37	0.21385	0.38683	-6.40
265281_at	unknown protein ; supported by full-le	---	AT2G28370	-1.14	-0.19	-1.37	0.213836	0.38683	-6.40
262841_at	aspartate-semialdehyde dehydrogena	---	AT1G14810	-1.18	-0.24	-1.37	0.213947	0.386974	-6.41
245097_at	Expressed protein ; supported by full-l	---	AT2G40935	1.09	0.13	1.37	0.214003	0.386991	-6.41
250643_at	putative protein similar to unknown pro	---	AT5G06780	-1.10	-0.14	-1.37	0.214007	0.386991	-6.41
246158_at	Expressed protein ; supported by full-l	---	AT5G19855	1.19	0.25	1.37	0.214001	0.386991	-6.41
257255_at	hypothetical protein contains Pfam pro	---	AT3G21960	-1.12	-0.16	-1.37	0.214189	0.387289	-6.41
266405_at	hypothetical protein predicted by gens	---	AT2G38580	-1.22	-0.28	-1.37	0.214249	0.387367	-6.41
255036_at	putative protein similarity RING zinc fi	---	AT4G09560	-1.21	-0.28	-1.37	0.214296	0.387421	-6.41
248925_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G45910	1.15	0.20	1.37	0.214326	0.387445	-6.41
261343_s_	putative protein hypothetical proteins -	---	---	-1.10	-0.14	-1.37	0.214376	0.387504	-6.41
256724_at	unknown protein ;supported by full-ler	---	AT2G34040	1.13	0.17	1.37	0.21441	0.387535	-6.41
251240_at	putative protein	---	AT3G62450	-1.10	-0.14	-1.37	0.214512	0.387689	-6.41
267294_at	hypothetical protein predicted by gens	YCF37	AT2G23670	-1.17	-0.22	-1.37	0.214672	0.387947	-6.41
249014_at	putative protein similar to unknown pro	---	AT5G44710	-1.15	-0.20	-1.37	0.214878	0.388289	-6.41
245878_at	hypothetical protein contains similarity	---	AT1G26190	-1.13	-0.18	-1.37	0.214938	0.388366	-6.41
266891_at	putative GTP-binding protein ; suppor	ARAC9	AT2G44690	-1.13	-0.18	-1.37	0.214982	0.388415	-6.41
258574_at	hypothetical protein	---	AT3G04250	1.11	0.16	1.37	0.215114	0.388622	-6.41
245256_at	Expressed protein ; supported by cDN	FAR1	AT4G15090	-1.13	-0.18	-1.37	0.21518	0.388683	-6.41
246535_at	putative protein several hypothetical pr	---	AT5G15900	-1.16	-0.22	-1.37	0.215182	0.388683	-6.41
244916_at	hypothetical protein	ORF187	ATMG00880	-1.10	-0.14	-1.37	0.215236	0.38872	-6.41
259167_at	putative oleosin similar to oleosin GB:A	---	AT3G01570	-1.10	-0.14	-1.37	0.215228	0.38872	-6.41
249227_at	peroxidase (emb|CAA66960.1)	---	AT5G42180	1.11	0.15	1.37	0.215265	0.388742	-6.41
246057_at	putative protein predicted proteins, Ar	---	AT5G08400	1.11	0.14	1.37	0.21536	0.388883	-6.41
254038_at	nitrogen fixation like protein nitrogen f	NFU3	AT4G25910	1.10	0.14	1.37	0.215455	0.388991	-6.41

260529_at	putative chloroplast protein CP12 ; su	CP12-1	AT2G47400	1.09	0.13	1.37	0.215453	0.388991	-6.41
257189_at	hypothetical protein	GIP1	AT3G13222	1.10	0.14	1.37	0.215612	0.389246	-6.41
264352_at	unknown protein Strong similarity to gi	---	AT1G03270	-1.19	-0.25	-1.37	0.215708	0.389356	-6.41
257094_at	hypothetical protein similar to tetraacyl	---	AT3G20480	-1.18	-0.24	-1.37	0.215706	0.389356	-6.41
266558_at	putative polygalacturonase	---	AT2G23900	-1.10	-0.14	-1.37	0.215749	0.389398	-6.41
255450_at	putative protein similar to T5J8.18	---	AT4G02850	-1.11	-0.15	-1.37	0.215765	0.389398	-6.41
247866_at	endoxyloglucan transferase (gb|AAD4	XTR3	AT5G57550	-1.43	-0.51	-1.37	0.215788	0.389408	-6.41
245835_at	hypothetical protein similar to putative	---	AT1G42190	1.11	0.14	1.37	0.215856	0.389501	-6.41
252607_at	xyloglucan endo-transglycosylase ; su	XTR8	AT3G44990	1.23	0.30	1.37	0.215937	0.389616	-6.41
256691_at	hypothetical protein predicted by gene	---	---	-1.09	-0.13	-1.37	0.215964	0.389634	-6.41
246521_at	N2,N2-dimethylguanine tRNA methylt	---	AT5G15810	1.15	0.20	1.37	0.216008	0.389683	-6.41
264605_at	putative auxin-induced protein, IAA12	IAA12	AT1G04550	1.12	0.16	1.37	0.2161	0.389796	-6.41
260461_at	membrane protein PTM1 precursor isc	---	AT1G10980	-1.12	-0.17	-1.37	0.216105	0.389796	-6.41
263734_at	permease, putative similar to permeas	NAT7	AT1G60030	1.16	0.22	1.36	0.216249	0.390025	-6.41
266084_at	hypothetical protein predicted by gens	---	AT2G37810	1.15	0.20	1.36	0.216308	0.390041	-6.41
265921_at	putative C2H2-type zinc finger protein	---	AT2G18490	-1.10	-0.14	-1.36	0.216293	0.390041	-6.41
267046_at	hypothetical protein	---	AT2G34360	1.17	0.22	1.36	0.216309	0.390041	-6.41
261665_at	beta-glucan-elicitor receptor, putative	---	AT1G18310	-1.11	-0.14	-1.36	0.216528	0.390403	-6.42
260689_at	hypothetical protein predicted by gene	---	AT1G32290	1.15	0.20	1.36	0.21657	0.390449	-6.42
264246_at	trehalose-6-phosphate synthase, puta	ATTPS10	AT1G60140	-1.38	-0.46	-1.36	0.216619	0.390506	-6.42
260325_at	putative monodehydroascorbate reduc	MDAR6	AT1G63940	1.16	0.21	1.36	0.216678	0.390574	-6.42
265113_at	hypothetical protein	---	---	-1.11	-0.15	-1.36	0.21669	0.390574	-6.42
245827_at	disease resistance protein RPS4, puta	---	AT1G57830	-1.13	-0.18	-1.36	0.216759	0.390667	-6.42
247515_at	ABC family transporter - like protein A	ATH14	AT5G61740	-1.09	-0.12	-1.36	0.216976	0.390965	-6.42
264407_at	unknown protein similar to EST gb|N9	---	AT1G10180	-1.14	-0.19	-1.36	0.216972	0.390965	-6.42
255811_at	heat shock protein 22.0 ; supported by	ATHSP22.0	AT4G10250	1.14	0.19	1.36	0.216975	0.390965	-6.42
249559_at	putative protein	---	AT5G38320	1.17	0.22	1.36	0.2172	0.391244	-6.42
245715_s_	Expressed protein ; supported by cDN	---	AT5G08670 /	1.13	0.17	1.36	0.217187	0.391244	-6.42
262019_s_	hypothetical protein predicted by gens	---	---	-1.11	-0.15	-1.36	0.217197	0.391244	-6.42
262430_s_	unknown protein	---	AT1G47550 /	-1.12	-0.16	-1.36	0.21715	0.391244	-6.42
250571_at	hypothetical protein	---	AT5G08200	-1.17	-0.22	-1.36	0.217231	0.39127	-6.42
257604_s_	hypothetical protein predicted by gene	---	AT1G11810 /	-1.11	-0.15	-1.36	0.217389	0.391524	-6.42
250533_at	flavonol synthase (FLS) (sp|Q96330)	FLS	AT5G08640	-1.10	-0.14	-1.36	0.217429	0.391565	-6.42
265751_at	putative retroelement pol polyprotein	---	---	1.10	0.14	1.36	0.217498	0.391658	-6.42
266522_at	putative ubiquitin-conjugating enzyme	UBC23	AT2G16920	1.13	0.17	1.36	0.217536	0.391695	-6.42

257102_at	endoxyloglucan transferase, putative	XTH3	AT3G25050	-1.09	-0.13	-1.36	0.217565	0.391712	-6.42
249326_at	unknown protein ; supported by cDNA	SYN2	AT5G40840	1.12	0.16	1.36	0.217597	0.391712	-6.42
251085_at	putative protein insulinase - Homo sap	---	AT5G01440	1.12	0.16	1.36	0.217585	0.391712	-6.42
248350_at	putative protein similar to unknown pro	---	AT5G52160	1.11	0.15	1.36	0.217614	0.391712	-6.42
261697_at	hypothetical protein identical to hypoth	---	AT1G32610	-1.20	-0.27	-1.36	0.217636	0.391722	-6.42
264815_at	hypothetical protein similar to hypothet	---	AT1G03620	-1.25	-0.33	-1.36	0.217733	0.391864	-6.42
265323_at	putative syntaxin	SYP112	AT2G18260	-1.15	-0.20	-1.36	0.217767	0.391894	-6.42
266263_at	putative flavonol sulfotransferase	---	AT2G27570	-1.11	-0.15	-1.36	0.217828	0.391973	-6.42
258939_at	unknown protein predicted by genefin	---	AT3G10020	-1.25	-0.32	-1.36	0.217973	0.392142	-6.42
252692_at	cysteine proteinase contains similarity	---	AT3G43960	-1.30	-0.38	-1.36	0.217969	0.392142	-6.42
262331_at	unknown protein	---	AT1G64050	1.09	0.12	1.36	0.217964	0.392142	-6.42
254043_at	putative protein ; supported by cDNA:	CIL	AT4G25990	-1.40	-0.48	-1.36	0.218114	0.392271	-6.42
255869_at	unknown protein	---	AT2G30270	-1.13	-0.17	-1.36	0.218084	0.392271	-6.42
248183_at	CHP-rich zinc finger protein-like	---	AT5G54040	1.09	0.13	1.36	0.218129	0.392271	-6.42
258680_at	adenylate translocator identical to ade	AAC1	AT3G08580	1.20	0.26	1.36	0.218131	0.392271	-6.42
258293_at	unknown protein	PHO1	AT3G23430	1.51	0.60	1.36	0.218104	0.392271	-6.42
258944_at	hypothetical protein similar to hypothet	FLD	AT3G10390	1.14	0.19	1.36	0.21822	0.3924	-6.42
259939_s_	ARE1-like protein similar to ARE1 GB	---	AT1G71270 /	-1.14	-0.19	-1.36	0.218246	0.392417	-6.42
248523_s_	ubiquitin activating enzyme ;supporte	SAE1B	AT5G50580 /	1.14	0.19	1.36	0.218366	0.392601	-6.42
259332_at	putative auxin-induced protein similar t	---	AT3G03830	-1.12	-0.16	-1.36	0.218426	0.392679	-6.42
246076_at	sucrose-phosphate synthase-like prot	ATSPS1F	AT5G20280	1.12	0.16	1.36	0.218489	0.392761	-6.42
250459_at	unknown protein ; supported by cDNA	---	AT5G09860	-1.12	-0.16	-1.36	0.218626	0.392975	-6.42
261378_at	calcium-dependent protein kinase, pu	ATCDPK1	AT1G18890	1.19	0.25	1.36	0.21871	0.393096	-6.42
261864_s_	10-formyltetrahydrofolate synthetase i	THFS	AT1G50480 /	1.12	0.17	1.36	0.218817	0.393131	-6.43
250154_at	putative aldose 1-epimerase - like pro	---	AT5G15140	-1.09	-0.13	-1.36	0.218803	0.393131	-6.42
251380_at	putative protein	---	AT3G60700	-1.10	-0.14	-1.36	0.218829	0.393131	-6.43
266322_at	putative auxin-regulated protein	---	AT2G46690	-1.24	-0.31	-1.36	0.218768	0.393131	-6.42
256927_at	unknown protein	---	AT3G22550	1.10	0.14	1.36	0.218833	0.393131	-6.43
248475_at	unknown protein	---	AT5G50880	-1.09	-0.13	-1.36	0.218754	0.393131	-6.42
248778_at	unknown protein	---	AT5G47940	-1.12	-0.17	-1.36	0.218968	0.393343	-6.43
250395_at	putative protein cylicin II, bovine, PIR:	---	AT5G10950	1.18	0.24	1.36	0.218989	0.39335	-6.43
249577_at	calmodulin-binding heat-shock protein	---	AT5G37710	-1.18	-0.24	-1.36	0.219078	0.393447	-6.43
260019_at	polyprotein, putative simlar to GI:4680	---	---	-1.10	-0.14	-1.36	0.219073	0.393447	-6.43
258860_at	putative potassium transporter similar	KUP3	AT3G02050	1.20	0.27	1.36	0.21911	0.393465	-6.43
255964_at	hypothetical protein predicted by gene	ZYP1b	AT1G22275	-1.11	-0.15	-1.36	0.219123	0.393465	-6.43

260605_at	hypothetical protein predicted by gene	---	AT2G43780	1.11	0.15	1.35	0.219315	0.393483	-6.43
264254_at	unknown protein	---	AT1G09150	-1.09	-0.13	-1.35	0.219254	0.393483	-6.43
251451_s_	putative protein several hypothetical pr	---	AT3G60040 /	-1.12	-0.16	-1.35	0.219304	0.393483	-6.43
260701_at	heat shock transcription factor HSF8,	ATHSFA1D	AT1G32330	1.14	0.19	1.35	0.219339	0.393483	-6.43
252217_at	putative protein some putative proteins	---	AT3G50140	1.17	0.23	1.35	0.219221	0.393483	-6.43
250710_at	MYB family transcription factor-like	MYB33	AT5G06100	1.11	0.15	1.35	0.219181	0.393483	-6.43
266455_at	putative bHLH transcription factor	---	AT2G22760	1.29	0.36	1.35	0.219194	0.393483	-6.43
265420_s_	hypothetical protein predicted by gens	BRX	AT1G31880 /	-1.16	-0.21	-1.35	0.219333	0.393483	-6.43
258044_at	Dof zinc finger protein identical to GB:	ADOF2	AT3G21270	-1.26	-0.34	-1.35	0.21921	0.393483	-6.43
246216_at	cytochrome P450 like protein ; support	ROT3	AT4G36380	-1.17	-0.23	-1.35	0.219291	0.393483	-6.43
264062_at	unknown protein	---	AT2G27950	1.12	0.16	1.35	0.219296	0.393483	-6.43
254046_at	hypothetical protein	---	AT4G26020	1.10	0.14	1.35	0.219308	0.393483	-6.43
256778_at	nucleosome assembly protein, putativ	NAP1;4	AT3G13782	1.10	0.14	1.35	0.219393	0.393549	-6.43
264085_at	putative glutamyl tRNA reductase	HEMA3	AT2G31250	-1.10	-0.14	-1.35	0.219513	0.393722	-6.43
253327_at	putative transcription factor	MYB69	AT4G33450	-1.15	-0.20	-1.35	0.219525	0.393722	-6.43
262409_at	hypothetical protein predicted by gene	---	---	-1.14	-0.19	-1.35	0.219571	0.393775	-6.43
267055_at	unknown protein	PRA1.B4	AT2G38360	-1.33	-0.42	-1.35	0.219708	0.393983	-6.43
249236_at	putative protein similar to unknown pro	---	AT5G41950	-1.10	-0.13	-1.35	0.219727	0.393983	-6.43
255648_at	coded for by A. thaliana cDNA T20730	---	AT4G00910	-1.10	-0.13	-1.35	0.219739	0.393983	-6.43
264713_at	hypothetical protein Similar to N. tabac	---	AT1G09820	-1.12	-0.17	-1.35	0.219819	0.394094	-6.43
265539_at	unknown protein	---	AT2G15830	1.32	0.40	1.35	0.219893	0.394197	-6.43
248650_at	putative protein similar to unknown pro	---	AT5G49250	-1.15	-0.21	-1.35	0.219977	0.394286	-6.43
256463_s_	unknown protein	---	---	1.11	0.15	1.35	0.219977	0.394286	-6.43
251066_at	putative protein RING-H2 finger protei	---	AT5G01880	-1.20	-0.26	-1.35	0.220064	0.394355	-6.43
257226_at	hypothetical protein predicted by gene	---	AT3G27880	1.33	0.41	1.35	0.220085	0.394355	-6.43
252776_at	putative protein predicted proteins, Ar	---	AT3G42940	-1.13	-0.18	-1.35	0.220069	0.394355	-6.43
261520_at	unknown protein ; supported by cDNA	SEC6	AT1G71820	-1.10	-0.14	-1.35	0.220036	0.394355	-6.43
263451_at	putative triacylglycerol lipase	---	AT2G31690	1.09	0.12	1.35	0.220116	0.394379	-6.43
259398_at	hypothetical protein predicted by gene	PRA1.F1	AT1G17700	-1.38	-0.46	-1.35	0.220226	0.394546	-6.43
267541_at	hypothetical protein predicted by gene	---	AT2G32750	-1.14	-0.19	-1.35	0.220405	0.394825	-6.43
250989_at	cytochrome P450 - like protein cytoch	CYP96A13	AT5G02900	1.09	0.12	1.35	0.220416	0.394825	-6.43
266276_at	putative tropinone reductase	TRI	AT2G29330	-1.09	-0.13	-1.35	0.22052	0.394979	-6.43
266587_at	unknown protein ; supported by full-le	---	AT2G14880	-1.13	-0.18	-1.35	0.220553	0.395008	-6.43
262039_at	adenine phosphoribosyltransferase alr	APT2	AT1G80050	1.16	0.21	1.35	0.220575	0.395016	-6.43
257052_at	putative 3-hydroxybutyryl-CoA dehydr	---	AT3G15290	-1.10	-0.14	-1.35	0.220614	0.395024	-6.43

259006_at	putative 60S acidic ribosomal protein P	---	AT3G09200	-1.20	-0.26	-1.35	0.220602	0.395024	-6.43
266437_at	unknown protein	---	AT2G43160	1.13	0.18	1.35	0.220643	0.395044	-6.43
255337_at	putative DNA-binding protein similar t	WRKY42	AT4G04450	1.15	0.20	1.35	0.220783	0.395264	-6.43
248406_at	pectinesterase	---	AT5G51490	-1.17	-0.22	-1.35	0.220858	0.395367	-6.43
252306_at	hypothetical protein	---	AT3G49270	-1.09	-0.12	-1.35	0.220876	0.395368	-6.43
261466_at	hypothetical protein predicted by gene	---	AT1G07690	-1.16	-0.21	-1.35	0.221075	0.395694	-6.43
263043_at	conserved hypothetical protein predict	---	AT1G23350	-1.13	-0.18	-1.35	0.221217	0.395885	-6.43
263658_at	unknown protein EST gb|T21788 come	---	AT1G04490	1.11	0.14	1.35	0.221212	0.395885	-6.43
245035_at	unknown protein similar to GP|224482	ATARD3	AT2G26400	1.30	0.38	1.35	0.221272	0.395891	-6.43
246022_at	putative protein predicted protein - Ara	---	AT5G21110	-1.11	-0.15	-1.35	0.221243	0.395891	-6.43
257974_at	unknown protein similar to NA-DAMAG	---	AT3G20820	1.41	0.49	1.35	0.221258	0.395891	-6.43
258443_at	unknown protein	---	AT3G22290	1.13	0.18	1.35	0.221345	0.39599	-6.44
253733_at	hypothetical protein	ATMND1	AT4G29170	1.13	0.18	1.35	0.221375	0.396013	-6.44
251674_at	hypothetical protein	---	AT3G57250	1.11	0.15	1.35	0.221421	0.396064	-6.44
263638_at	unknown protein	---	AT2G25310	-1.09	-0.13	-1.35	0.221451	0.396087	-6.44
248972_at	putative protein similar to unknown pro	ATDSS1(V)	AT5G45010	1.19	0.26	1.35	0.221521	0.396181	-6.44
258168_at	hypothetical protein predicted by gene	---	AT3G21570	1.09	0.13	1.35	0.221563	0.396224	-6.44
245997_at	putative protein saur1 protein, Zea ma	---	AT5G20810	1.18	0.24	1.35	0.221629	0.396312	-6.44
245610_at	hypothetical protein	---	AT4G14380	1.12	0.16	1.35	0.221673	0.396359	-6.44
263271_s_	hypothetical protein predicted by gens	---	---	-1.09	-0.12	-1.35	0.221796	0.396548	-6.44
267445_at	hypothetical protein predicted by gens	---	AT2G33680	1.12	0.17	1.35	0.221817	0.396556	-6.44
255084_s_	putative protein same aa sequence as	---	AT4G09220 /	-1.10	-0.14	-1.35	0.22184	0.396565	-6.44
263283_at	hypothetical protein predicted by gens	---	AT2G36090	1.11	0.15	1.35	0.221905	0.396638	-6.44
256278_at	unknown protein ; supported by full-ler	---	AT3G12130	-1.10	-0.14	-1.35	0.221916	0.396638	-6.44
250382_at	putative protein rjs protein, Mus musc	---	AT5G11580	1.09	0.12	1.35	0.222133	0.396968	-6.44
265438_at	hypothetical protein	---	AT2G20970	-1.09	-0.13	-1.34	0.222222	0.396968	-6.44
253008_at	expansin -like protein expansin (GhEX	ATEXPA20	AT4G38210	-1.17	-0.23	-1.34	0.222219	0.396968	-6.44
248365_at	putative protein strong similarity to unk	---	AT5G52500	1.12	0.16	1.34	0.222202	0.396968	-6.44
247976_at	unknown protein	---	---	1.13	0.18	1.34	0.222206	0.396968	-6.44
260139_at	Myb-related transcription factor, putati	MYB114	AT1G66380	1.10	0.14	1.34	0.222194	0.396968	-6.44
AFFX-Atha	Arabidopsis thaliana /REF=U37281.1 /	---	---	-1.10	-0.14	-1.34	0.222208	0.396968	-6.44
261615_at	unknown protein	---	AT1G33050	1.12	0.17	1.34	0.222273	0.397027	-6.44
262974_at	hypothetical protein predicted by gene	---	AT1G75550	-1.11	-0.15	-1.34	0.222433	0.397283	-6.44
263753_at	putative dehydrin ;supported by full-le	LEA	AT2G21490	-1.09	-0.12	-1.34	0.222572	0.3975	-6.44
245255_at	COP9 protein ; supported by cDNA: gi	COP9	AT4G14110	-1.12	-0.16	-1.34	0.2226	0.397519	-6.44

247118_at	uridylyl transferases-like ; supported b	ACR1	AT5G65890	-1.19	-0.26	-1.34	0.222704	0.397666	-6.44
244989_s_	hypothetical protein	---	---	-1.16	-0.21	-1.34	0.222728	0.397666	-6.44
249771_at	receptor-like protein kinase ; supporte	---	AT5G24080	-1.19	-0.25	-1.34	0.222736	0.397666	-6.44
260539_at	putative peroxidase	---	AT2G43480	1.09	0.13	1.34	0.222752	0.397666	-6.44
247160_at	putative protein contains similarity to s	---	AT5G65820	-1.10	-0.14	-1.34	0.222817	0.397751	-6.44
245571_at	light induced protein like	---	AT4G14695	-1.15	-0.20	-1.34	0.223023	0.398087	-6.44
248195_at	membrane associated protein ; suppo	ATMAMI	AT5G54110	-1.14	-0.19	-1.34	0.223065	0.398106	-6.44
252371_at	putative protein finger protein SIG1, S	---	AT3G48070	1.13	0.17	1.34	0.223068	0.398106	-6.44
264998_at	unknown protein similar to hypothetica	---	AT1G67330	1.46	0.54	1.34	0.223129	0.398182	-6.44
249292_at	repair endonuclease (gb|AAF01274.1)	UVH1	AT5G41150	-1.10	-0.14	-1.34	0.223282	0.398425	-6.44
248169_at	ankyrin-repeat-containing protein-like	ANK	AT5G54610	1.99	0.99	1.34	0.223503	0.398787	-6.44
252914_at	putative protein dehydrin, Glycine max	---	AT4G39130	-1.15	-0.20	-1.34	0.223542	0.398826	-6.44
263189_at	hypothetical protein similar to hypothet	---	AT1G36100	-1.10	-0.14	-1.34	0.223593	0.398886	-6.44
249729_at	6-phosphogluconolactonase-like prote	---	AT5G24410	1.12	0.16	1.34	0.223634	0.398897	-6.44
253100_at	cytochrome P450 monooxygenase -lik	CYP81F3	AT4G37400	1.40	0.49	1.34	0.223633	0.398897	-6.44
260136_at	hypothetical protein predicted by gene	---	AT1G66360	-1.11	-0.15	-1.34	0.223674	0.398937	-6.44
260790_at	hypothetical protein predicted by gens	---	AT1G06240	-1.19	-0.25	-1.34	0.223708	0.398967	-6.44
248759_at	putative protein similar to unknown pro	---	AT5G47610	-1.28	-0.36	-1.34	0.223784	0.39904	-6.44
246539_at	putative protein geranylgeranylated pr	MUB2	AT5G15460	-1.09	-0.12	-1.34	0.223768	0.39904	-6.44
252259_at	putative protein acidic ribosomal prote	---	AT3G49460	-1.17	-0.23	-1.34	0.22385	0.399127	-6.45
256843_at	hypothetical protein predicted by gene	---	---	1.11	0.15	1.34	0.223873	0.399135	-6.45
253151_at	putative polygalacturonase polygalact	---	AT4G35670	-1.10	-0.13	-1.34	0.223972	0.399252	-6.45
265138_at	hypothetical protein predicted by gens	---	AT1G51300	-1.16	-0.21	-1.34	0.223973	0.399252	-6.45
248522_at	predicted protein	---	AT5G50565 /	-1.10	-0.14	-1.34	0.223996	0.399261	-6.45
255637_at	hypothetical protein	---	AT4G00750	1.17	0.23	1.34	0.224024	0.39928	-6.45
263562_at	hypothetical protein predicted by gens	---	AT2G15420	-1.09	-0.13	-1.34	0.224211	0.399582	-6.45
252660_at	putative protein	---	AT3G44440	-1.10	-0.13	-1.34	0.22423	0.399585	-6.45
256040_at	hypothetical protein similar to putative	---	AT1G07270	-1.10	-0.14	-1.34	0.224284	0.399649	-6.45
261958_at	peptide transporter, putative predicted	---	AT1G64500	1.24	0.31	1.34	0.224348	0.399683	-6.45
252524_at	putative protein mitochondrial ATP SY	---	AT3G46430	1.13	0.17	1.34	0.224355	0.399683	-6.45
251540_at	citrate synthase -like protein citrate sy	CSY1	AT3G58740	1.09	0.12	1.34	0.224333	0.399683	-6.45
262859_at	hypothetical protein predicted by gene	---	AT1G64790	-1.12	-0.16	-1.34	0.224419	0.399738	-6.45
254426_at	putative protein predicted protein, Ara	---	AT4G21240	1.11	0.15	1.34	0.224421	0.399738	-6.45
258022_at	hypothetical protein predicted by gene	---	AT3G19460	-1.09	-0.12	-1.34	0.224467	0.399788	-6.45
258954_at	unknown protein contains Pfam profile	---	AT3G01400	-1.09	-0.12	-1.34	0.224507	0.399829	-6.45

265616_at	hypothetical protein predicted by gene	---	AT2G25500	1.09	0.12	1.34	0.224538	0.399853	-6.45
253699_at	putative protein patatin-like protein, S	PLP8	AT4G29800	-1.11	-0.15	-1.34	0.224564	0.399868	-6.45
267345_at	unknown protein ; supported by cDNA	---	AT2G44240	1.39	0.47	1.34	0.224615	0.399927	-6.45
260378_at	putative actin similar to actin GB:CAB5	ATARP4A	AT1G73910	-1.09	-0.13	-1.34	0.224645	0.39995	-6.45
265090_at	putative protein phosphatase 2A High	---	AT1G03960	-1.11	-0.16	-1.34	0.224683	0.399954	-6.45
258091_at	hypothetical protein predicted by genm	---	AT3G14560	1.40	0.48	1.34	0.224668	0.399954	-6.45
248118_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G55050	1.69	0.76	1.34	0.22472	0.399988	-6.45
256722_at	hypothetical protein predicted by gene	---	AT2G34050	-1.23	-0.29	-1.34	0.224737	0.399988	-6.45
264270_at	beta-glucosidase, putative similar to b	---	---	1.10	0.13	1.34	0.224829	0.40009	-6.45
259096_at	putative 40S ribosomal protein S3A (S	---	AT3G04840	-1.27	-0.35	-1.34	0.224828	0.40009	-6.45
264066_at	Argonaute (AGO1)-like protein	AGO5	AT2G27880	-1.12	-0.16	-1.34	0.224851	0.400098	-6.45
266640_at	Expressed protein ; supported by full-l	---	AT2G35585	-1.14	-0.19	-1.34	0.224934	0.400214	-6.45
262904_at	chaperone, putative similar to chaperc	---	AT1G59725	-1.14	-0.19	-1.34	0.224996	0.400262	-6.45
257429_at	putative RING zinc finger protein	---	AT2G27940	-1.17	-0.23	-1.34	0.22499	0.400262	-6.45
250439_at	14-3-3 protein GF14lambda (grf6/AFT	GRF6	AT5G10450	1.12	0.16	1.34	0.22507	0.400363	-6.45
258603_at	putative heat shock transcription factor	ATHSFA1E	AT3G02990	-1.16	-0.21	-1.34	0.225196	0.400556	-6.45
260973_at	hypothetical protein predicted by gene	---	AT1G53490	1.10	0.14	1.34	0.225259	0.400637	-6.45
259759_at	hypothetical protein similar to GB:CAE	---	AT1G77550	1.11	0.15	1.33	0.225405	0.400864	-6.45
256973_at	unknown protein similar to putative ret	---	AT3G20980	1.11	0.15	1.33	0.225641	0.401253	-6.45
262820_at	putative obtusifoliol 14-alpha demethy	CYP51G1	AT1G11680	-1.11	-0.15	-1.33	0.225763	0.401438	-6.45
255660_at	Expressed protein ; supported by full-l	---	AT4G00755	-1.13	-0.17	-1.33	0.225853	0.401568	-6.45
245870_at	hypothetical protein similar to hypothet	---	AT1G26300	-1.10	-0.14	-1.33	0.225875	0.401574	-6.45
257404_at	hypothetical protein predicted by gens	SUVR1	AT1G04050	-1.11	-0.16	-1.33	0.225979	0.401729	-6.45
258562_at	unknown protein ;supported by full-ler	---	AT3G05980	-1.10	-0.13	-1.33	0.225998	0.401732	-6.45
249025_at	putative protein contains similarity to u	---	AT5G44720	-1.22	-0.29	-1.33	0.22602	0.40174	-6.45
261761_at	hypothetical protein predicted by gene	CENP-C	AT1G15660	-1.11	-0.15	-1.33	0.226195	0.402008	-6.45
253848_at	putative protein regulator protein, Pse	---	AT4G28020	1.16	0.21	1.33	0.226206	0.402008	-6.45
249287_at	putative protein strong similarity to unk	---	AT5G41250	-1.13	-0.17	-1.33	0.226265	0.402081	-6.45
267107_at	hypothetical protein predicted by gens	---	---	1.11	0.16	1.33	0.226344	0.402158	-6.45
266765_at	putative inorganic pyrophosphatase	AtPPa3	AT2G46860	-1.10	-0.13	-1.33	0.226335	0.402158	-6.45
245278_at	syntaxin ; supported by cDNA: gi_214	SYP23	AT4G17730	1.17	0.22	1.33	0.226493	0.402391	-6.46
260737_at	receptor-like serine threonine kinase,	---	AT1G17540	-1.13	-0.18	-1.33	0.22652	0.402409	-6.46
263726_at	putative ABC transporter ;supported b	---	AT2G13610	-1.60	-0.68	-1.33	0.226613	0.402542	-6.46
264120_at	latex-abundant protein, putative simila	AtMC4	AT1G79340	-1.09	-0.13	-1.33	0.226637	0.402554	-6.46
267204_at	putative blue copper-binding protein	---	AT2G31050	-1.12	-0.16	-1.33	0.22667	0.402581	-6.46

251670_at	putative protein translation releasing f	---	AT3G57190	1.14	0.19	1.33	0.226748	0.402622	-6.46
251485_at	putative protein rad21 mitotic cohesin	SYN3	AT3G59550	1.09	0.13	1.33	0.226773	0.402622	-6.46
252346_at	hypothetical protein	---	AT3G48650	1.09	0.13	1.33	0.226741	0.402622	-6.46
260670_at	Expressed protein ; supported by full-l	NFD5	AT1G19520	-1.18	-0.24	-1.33	0.226781	0.402622	-6.46
250778_at	unknown protein ;supported by full-len	---	AT5G05500	1.11	0.15	1.33	0.22677	0.402622	-6.46
252216_at	putative protein several hypothetical pr	---	AT3G50420	1.14	0.19	1.33	0.226855	0.40272	-6.46
255089_at	nucleoside-diphosphate kinase ;suppo	NDPK1	AT4G09320	1.17	0.22	1.33	0.226962	0.40288	-6.46
244922_s_	hypothetical protein	---	AT2G07674	1.14	0.19	1.33	0.227	0.402916	-6.46
262284_at	hypothetical protein predicted by gene	---	AT1G68670	1.18	0.23	1.33	0.227065	0.40296	-6.46
251718_at	putative protein hypothetical proteins -	MRLK	AT3G56100	-1.15	-0.20	-1.33	0.227088	0.40296	-6.46
253807_at	putative GPI-anchored protein GPI-an	---	AT4G28280	-1.15	-0.20	-1.33	0.227094	0.40296	-6.46
263595_at	putative purple acid phosphatase cont	PAP8	AT2G01890	2.75	1.46	1.33	0.227095	0.40296	-6.46
256282_at	unknown protein	---	AT3G12550	-1.13	-0.18	-1.33	0.227116	0.402965	-6.46
267514_at	putative glycerate dehydrogenase ; su	---	AT2G45630	1.33	0.42	1.33	0.22724	0.403154	-6.46
245668_at	dormancy-associated protein, putative	DYL1	AT1G28330	1.15	0.20	1.33	0.227274	0.403182	-6.46
266820_at	putative AP2 domain transcription fact	---	AT2G44940	-1.33	-0.41	-1.33	0.227296	0.40319	-6.46
259897_at	putative beta-glucanase similar to beta	ATCEL3	AT1G71380	-1.11	-0.15	-1.33	0.227361	0.403266	-6.46
256882_at	RNA-binding protein, putative similar t	---	AT3G26420 /	-1.15	-0.20	-1.33	0.227374	0.403266	-6.46
267506_at	unknown protein ;supported by full-ler	---	AT2G45520	1.10	0.14	1.33	0.227416	0.403281	-6.46
246645_at	putative protein ;supported by full-leng	---	AT5G35080	-1.14	-0.18	-1.33	0.227418	0.403281	-6.46
250692_at	putative protein strong similarity to unk	---	AT5G06560	1.12	0.16	1.33	0.227503	0.403385	-6.46
261943_at	plasma membrane ATPase, putative s	AHA9	AT1G80660	1.11	0.16	1.33	0.227512	0.403385	-6.46
249751_at	putative protein similar to unknown pro	---	AT5G24650	-1.14	-0.19	-1.33	0.227607	0.403427	-6.46
262510_at	hypothetical protein similar to hypothet	---	AT1G11270	-1.13	-0.17	-1.33	0.227584	0.403427	-6.46
266160_at	hypothetical protein	ATCHX8	AT2G28180	1.14	0.19	1.33	0.227603	0.403427	-6.46
245271_at	transcription factor like protein ; suppo	---	AT4G16430	-1.09	-0.13	-1.33	0.227592	0.403427	-6.46
263424_at	putative RING zinc finger protein	---	AT2G31510	1.11	0.15	1.33	0.227697	0.403556	-6.46
252073_at	hypothetical protein	---	AT3G51750	-1.51	-0.60	-1.33	0.227736	0.403593	-6.46
266806_at	unknown protein ;supported by full-ler	---	AT2G30000	1.14	0.19	1.33	0.227817	0.403696	-6.46
253409_at	putative protein	---	AT4G32960	1.09	0.13	1.33	0.227829	0.403696	-6.46
261789_at	40S ribosomal protein S12, putative s	---	AT1G15930	-1.26	-0.33	-1.33	0.227945	0.40387	-6.46
253822_at	hypothetical protein	---	AT4G28410	-1.10	-0.14	-1.33	0.227989	0.403902	-6.46
249499_at	hypothetical protein	---	AT5G39250	1.10	0.14	1.33	0.227998	0.403902	-6.46
248860_at	putative protein contains similarity to C	---	AT5G46670	-1.11	-0.15	-1.33	0.228077	0.404011	-6.46
245562_at	OBP33pep like protein contains non_c	---	AT4G15520	-1.14	-0.20	-1.33	0.228124	0.404024	-6.46

264154_at	unknown protein	---	AT1G65430	1.11	0.15	1.33	0.228132	0.404024	-6.46
246029_at	leucine-rich repeat protein ; supported	---	AT5G21090	1.11	0.15	1.33	0.228156	0.404024	-6.46
246466_at	sugar transporter - like protein D-XYL	---	AT5G17010	1.17	0.22	1.33	0.228155	0.404024	-6.46
247914_at	xyloglucan endotransglycosylase	---	AT5G57540	-1.12	-0.17	-1.33	0.228183	0.404041	-6.46
251418_at	putative protein prib5, Ribes nigrum, E	---	AT3G60440	-1.20	-0.27	-1.33	0.228201	0.404042	-6.46
264065_at	hypothetical protein predicted by gens	---	AT2G27900	-1.12	-0.16	-1.32	0.228401	0.404363	-6.46
258106_at	ribonucleoside-diphosphate reductase	RNR2A	AT3G23580	1.14	0.19	1.32	0.228573	0.404638	-6.46
266298_at	unknown protein ;supported by full-ler	---	AT2G29590	1.13	0.18	1.32	0.228638	0.40472	-6.46
262614_at	putative pattern formation protein EMB	GN	AT1G13980	-1.19	-0.25	-1.32	0.228658	0.40472	-6.46
259196_at	putative ribosomal protein S2 similar to	RPS2	AT3G03600	-1.16	-0.21	-1.32	0.228673	0.40472	-6.46
260727_at	polygalacturonase PG1, putative simil	---	AT1G48100	-1.15	-0.20	-1.32	0.228692	0.404721	-6.46
251707_at	protein kinase C inhibitor-like protein p	---	AT3G56490	1.12	0.16	1.32	0.228796	0.404876	-6.46
254133_at	putative protein various predicted ABC	---	AT4G24810	-1.09	-0.13	-1.32	0.228885	0.405001	-6.46
249540_at	4-coumarate--CoA ligase -like protein	---	AT5G38120	-1.25	-0.32	-1.32	0.228958	0.405064	-6.46
258520_at	hypothetical protein predicted by gene	---	AT3G06710	-1.16	-0.21	-1.32	0.22894	0.405064	-6.46
252159_at	hypothetical protein	---	AT3G50540	1.10	0.14	1.32	0.228974	0.405064	-6.46
265808_at	hypothetical protein predicted by gens	---	AT2G17960	-1.10	-0.14	-1.32	0.229015	0.405102	-6.47
252240_at	putative protein several hypothetical pr	---	AT3G50010	-1.13	-0.17	-1.32	0.229031	0.405102	-6.47
246892_at	putative protein predicted protein, Ory	---	AT5G25500	1.12	0.16	1.32	0.229273	0.405373	-6.47
267132_at	unknown protein	NAPRT2	AT2G23420	1.22	0.28	1.32	0.229246	0.405373	-6.47
259356_at	unknown protein	---	AT3G05250	-1.10	-0.14	-1.32	0.229242	0.405373	-6.47
262469_s_	hypothetical protein identical to hypoth	---	AT1G50190 /	-1.10	-0.14	-1.32	0.229212	0.405373	-6.47
245566_at	disease resistance RPS2 like protein	---	AT4G14610	1.12	0.16	1.32	0.229256	0.405373	-6.47
255426_at	putative protein	---	AT4G03370	1.11	0.15	1.32	0.229371	0.40545	-6.47
258255_at	hypothetical protein predicted by gene	---	AT3G26800	1.10	0.14	1.32	0.229384	0.40545	-6.47
260835_at	protein kinase interactor, putative simi	---	AT1G06700	-1.11	-0.15	-1.32	0.229349	0.40545	-6.47
263836_at	unknown protein ;supported by full-ler	---	AT2G40330	-1.43	-0.51	-1.32	0.229388	0.40545	-6.47
250615_at	putative protein ankyrins - different spe	---	AT5G07270	-1.14	-0.18	-1.32	0.229455	0.405538	-6.47
256839_at	calmodulin, putative similar to calmod	---	AT3G22930	1.13	0.17	1.32	0.22948	0.40555	-6.47
265847_at	unknown protein	---	AT2G35750	-1.10	-0.14	-1.32	0.229585	0.405705	-6.47
255183_at	hypothetical protein	---	AT4G08140	1.13	0.18	1.32	0.229718	0.405908	-6.47
264092_at	photosystem II polypeptide, putative s	PSBR	AT1G79040 /	-1.10	-0.13	-1.32	0.229794	0.40601	-6.47
258619_at	isopentenyl diphosphate:dimethylallyl	IPP2	AT3G02780	-1.14	-0.19	-1.32	0.229866	0.406107	-6.47
257055_at	Expressed protein ; supported by full-l	---	AT3G15351	-1.11	-0.15	-1.32	0.229987	0.406262	-6.47
247868_at	Myb-related transcription factor-like pr	MYB36	AT5G57620	-1.11	-0.15	-1.32	0.22999	0.406262	-6.47

248175_at	histone H2A (gb|AAF64418.1) ; suppo	RAT5	AT5G54640	1.12	0.16	1.32	0.230245	0.406682	-6.47
248654_at	importin alpha	IMPA-5	AT5G49310	-1.11	-0.15	-1.32	0.230281	0.406714	-6.47
262218_at	hypothetical protein contains similarity	---	AT1G74770	-1.17	-0.23	-1.32	0.230366	0.406832	-6.47
263541_at	unknown protein ; supported by full-le	---	AT2G24860	-1.11	-0.15	-1.32	0.230445	0.406908	-6.47
AFFX-Atha	Arabidopsis thaliana /REF=M65137 /D	---	---	-1.10	-0.14	-1.32	0.23044	0.406908	-6.47
260642_at	plastid protein, putative similar to plas	---	AT1G53260	1.17	0.22	1.32	0.230486	0.406919	-6.47
266113_x_	hypothetical protein predicted by gens	---	---	1.13	0.18	1.32	0.230485	0.406919	-6.47
267320_at	hypothetical protein predicted by gens	---	AT2G19300	1.11	0.16	1.32	0.230542	0.406986	-6.47
251070_at	translation initiation factor eIF-2 beta	---	AT5G01940	1.20	0.26	1.32	0.230599	0.407024	-6.47
267326_at	putative RNA-binding protein	---	AT2G19380	1.12	0.17	1.32	0.230597	0.407024	-6.47
264134_at	unknown protein contains similarity to	---	AT1G79070	-1.09	-0.12	-1.32	0.230903	0.407528	-6.47
249616_s_	contains similarity to DnaJ protein	---	AT5G37440 /	-1.10	-0.14	-1.32	0.23093	0.407543	-6.47
252074_at	putative protein DNA helicase homolo	---	AT3G51700	-1.11	-0.15	-1.32	0.230947	0.407543	-6.47
262509_at	hypothetical protein similar to hypothet	CRR22	AT1G11290	1.12	0.17	1.32	0.23104	0.407675	-6.47
257302_at	hypothetical protein predicted by gene	---	AT3G30220	-1.09	-0.13	-1.32	0.231068	0.407694	-6.47
254781_at	putative protein putative protein F28j1	---	AT4G12840	1.10	0.14	1.32	0.231097	0.407713	-6.47
250359_at	putative protein predicted proteins, Ar	---	AT5G11350	-1.10	-0.14	-1.32	0.231541	0.408401	-6.47
261787_at	hypothetical protein predicted by gene	---	AT1G16020	-1.11	-0.15	-1.32	0.23154	0.408401	-6.47
266479_at	unknown protein ; supported by cDNA	LSH3	AT2G31160	1.44	0.52	1.32	0.231508	0.408401	-6.47
267439_at	putative GDSL-motif lipase/hydrolase s	---	AT2G19060	-1.12	-0.17	-1.31	0.231612	0.408493	-6.47
251655_at	hypothetical protein	AT3G57157	---	-1.15	-0.20	-1.31	0.23163	0.408493	-6.47
245633_at	unknown protein similar to putative Tu	AtTLP10	AT1G25280	1.08	0.12	1.31	0.231647	0.408493	-6.47
246129_at	putative protein predicted protein, Ara	---	---	-1.09	-0.12	-1.31	0.231707	0.408569	-6.48
261610_at	hypothetical protein predicted by gene	---	AT1G49560	1.19	0.25	1.31	0.231826	0.408683	-6.48
261097_at	protein kinase, putative contains prote	---	AT1G62950	-1.17	-0.23	-1.31	0.231804	0.408683	-6.48
253454_at	Expressed protein ; supported by cDN	---	AT4G31875	1.20	0.26	1.31	0.231821	0.408683	-6.48
264600_at	hypothetical protein predicted by gens	---	AT1G04730	-1.18	-0.23	-1.31	0.231931	0.408836	-6.48
246624_at	flavin-containing monooxygenase, put	YUC10	AT1G48910	-1.12	-0.16	-1.31	0.232051	0.409017	-6.48
252595_at	putative transporter protein peptide tra	---	AT3G45690	-1.12	-0.16	-1.31	0.232115	0.409099	-6.48
247821_at	WD-40 repeat protein MSI1 (sp|O2246	MSI1	AT5G58230	-1.12	-0.17	-1.31	0.232178	0.409178	-6.48
258671_at	putative vacuolar ATP synthase subun	VHA-E2	AT3G08560	1.14	0.19	1.31	0.232295	0.409352	-6.48
258296_at	putative ribosomal protein similar to rib	---	AT3G23390	-1.26	-0.34	-1.31	0.232439	0.409556	-6.48
252028_at	hypothetical protein	---	AT3G52640	-1.19	-0.25	-1.31	0.2325	0.409556	-6.48
265339_at	putative inorganic pyrophosphatase ;s	AtPPa2	AT2G18230	-1.20	-0.26	-1.31	0.232479	0.409556	-6.48
255312_at	putative transposon protein	---	---	-1.10	-0.14	-1.31	0.232501	0.409556	-6.48

251343_at	phosphatidate cytidylyltransferase - lik	---	AT3G60620	-1.21	-0.28	-1.31	0.2325	0.409556	-6.48
265198_at	putative glucosyl transferase	UGT73C2	AT2G36760	-1.09	-0.13	-1.31	0.232558	0.409626	-6.48
262875_at	gamma-tocopherol methyltransferase a	G-TMT	AT1G64970	1.13	0.17	1.31	0.232621	0.409674	-6.48
262958_at	water stress-induced protein, putative	---	AT1G54410	-1.13	-0.17	-1.31	0.232619	0.409674	-6.48
248343_at	putative protein contains similarity to m	AtMYB19	AT5G52260	-1.09	-0.12	-1.31	0.232647	0.409686	-6.48
265191_at	hypothetical protein Similar to Sacchar	---	AT1G05120	1.11	0.15	1.31	0.232671	0.409698	-6.48
251344_at	putative protein beige-like protein (CD	---	AT3G60920	-1.11	-0.15	-1.31	0.232714	0.409741	-6.48
250660_at	RNA-binding protein-like	---	AT5G07060	1.09	0.12	1.31	0.232765	0.409801	-6.48
250244_at	putative protein similar to unknown pro	ABO1	AT5G13680	1.19	0.26	1.31	0.232928	0.409992	-6.48
250116_at	putative protein similar to unknown pro	---	AT5G16430	-1.14	-0.20	-1.31	0.232902	0.409992	-6.48
254874_at	putative protein beta-phosphoglucomu	---	AT4G11570	-1.15	-0.20	-1.31	0.232918	0.409992	-6.48
248300_at	PP2A regulatory subunit ;supported b	TAP46	AT5G53000	-1.15	-0.20	-1.31	0.232957	0.410011	-6.48
255659_at	Expressed protein ; supported by full-le	---	AT4G00895	1.24	0.31	1.31	0.233049	0.410142	-6.48
264481_at	transcription factor TINY, putative sim	---	AT1G77200	1.13	0.17	1.31	0.233078	0.41016	-6.48
250455_at	unknown protein ; supported by full-le	PROPEP4	AT5G09980	-1.16	-0.22	-1.31	0.2331	0.410168	-6.48
259644_at	unknown protein	---	AT1G68910	-1.13	-0.18	-1.31	0.233141	0.410209	-6.48
245911_at	oligosaccharyl transferase STT3-like p	STT3A	AT5G19690	1.09	0.13	1.31	0.233273	0.41041	-6.48
247238_at	histone acetyltransferase	HAM1	AT5G64610	-1.09	-0.13	-1.31	0.233319	0.410459	-6.48
264753_at	receptor kinase, putative similar to rec	---	AT1G61490	-1.09	-0.12	-1.31	0.233345	0.410473	-6.48
261139_at	homeodomain protein, putative simila	BEL10	AT1G19700	1.10	0.13	1.31	0.233365	0.410477	-6.48
264878_at	unknown protein	---	AT2G17410	1.09	0.13	1.31	0.23339	0.410488	-6.48
257286_s_	transposase, putative similar to transp	---	AT1G19260 /	-1.12	-0.17	-1.31	0.233561	0.410747	-6.48
249503_at	expansin-like protein expansin - Prun	ATEXPA24	AT5G39310	-1.11	-0.15	-1.31	0.233573	0.410747	-6.48
255193_at	score=10.1, E=1.2, N=1 contains simi	VFB3	AT4G07400	1.12	0.16	1.31	0.233653	0.410856	-6.48
266450_s_	hypothetical protein predicted by gens	---	AT2G43190	-1.16	-0.21	-1.31	0.233688	0.410887	-6.48
263240_s_	unknown protein ; supported by cDNA	---	AT1G72590 /	1.17	0.23	1.31	0.233803	0.411025	-6.48
254366_s_	LTR retrotransposon like protein retro	---	---	-1.09	-0.13	-1.31	0.23379	0.411025	-6.48
255621_at	hypothetical protein	---	AT4G01390	-1.57	-0.65	-1.31	0.233998	0.411305	-6.48
254875_at	putative protein various predicted prot	---	AT4G11590	1.11	0.15	1.31	0.233984	0.411305	-6.48
266973_at	hypothetical protein predicted by grail	---	AT2G39620	-1.12	-0.16	-1.31	0.234034	0.411334	-6.48
254288_at	putative protein Human mRNA for KIA	AESP	AT4G22970	1.09	0.12	1.31	0.234051	0.411334	-6.48
248690_at	acetyl-CoA C-acetyltransferase ; supp	ACAT2	AT5G48230	1.09	0.13	1.31	0.234173	0.411517	-6.48
250409_at	putative protein 110K5.11, unknown p	---	AT5G10860	1.11	0.15	1.31	0.234311	0.411633	-6.48
260664_at	myb-related protein, putative similar to	ATRL5	AT1G19510	1.25	0.32	1.31	0.23431	0.411633	-6.48
261369_at	protein kinase, putative similar to man	---	AT1G53060	1.15	0.20	1.31	0.234293	0.411633	-6.48

249689_at	putative protein similar to unknown pro	---	AT5G36190	-1.09	-0.12	-1.31	0.234263	0.411633	-6.48
260787_at	Ring3-like bromodomain protein simila	GTE4	AT1G06230	1.12	0.16	1.31	0.234409	0.411773	-6.49
258164_at	surfeit 1 identical to GB:AAF19609 fro	SURF1	AT3G17910	1.18	0.24	1.31	0.234522	0.411939	-6.49
251861_at	putative protein GATA transcription fa	BME3	AT3G54810	-1.39	-0.48	-1.31	0.234623	0.412031	-6.49
254345_at	hypothetical protein ;supported by full-	---	AT4G22000	-1.18	-0.24	-1.31	0.234645	0.412031	-6.49
247252_at	unknown protein	---	AT5G64770	1.51	0.59	1.31	0.234646	0.412031	-6.49
250501_at	carboxypeptidase - like protein GC do	SCPL19	AT5G09640	-1.10	-0.14	-1.31	0.234633	0.412031	-6.49
265730_at	60S ribosomal protein L27	---	AT2G32220	1.40	0.49	1.30	0.234783	0.412239	-6.49
244924_at	hypothetical protein	---	---	1.12	0.16	1.30	0.23481	0.412241	-6.49
260515_at	ATP-dependent transmembrane trans	---	AT1G51460	-1.12	-0.17	-1.30	0.23482	0.412241	-6.49
262669_at	hypothetical protein	---	AT1G62850	-1.11	-0.15	-1.30	0.234907	0.412362	-6.49
262890_at	nucleoporin, putative similar to nuclea	NUP155	AT1G14850	1.17	0.23	1.30	0.234966	0.412433	-6.49
257012_at	RNA-binding protein, putative similar t	TEL1	AT3G26120	-1.10	-0.13	-1.30	0.234996	0.412455	-6.49
253910_at	putative receptor like kinase receptor-	---	AT4G27290	1.10	0.13	1.30	0.23505	0.412517	-6.49
251232_at	shock protein SRC2-like shock protein	---	AT3G62780	1.39	0.48	1.30	0.235144	0.412652	-6.49
254611_at	Expressed protein ; supported by full-le	---	AT4G19095	-1.10	-0.14	-1.30	0.235175	0.412673	-6.49
253537_at	putative protein ; supported by full-len	HCF153	AT4G31560	-1.12	-0.16	-1.30	0.235416	0.412962	-6.49
265445_at	60S ribosomal protein L12 ;supported	---	AT2G37190	-1.32	-0.40	-1.30	0.23543	0.412962	-6.49
252755_at	putative protein hypothetical proteins -	---	---	1.11	0.15	1.30	0.235415	0.412962	-6.49
267340_at	unknown protein	ACD11	AT2G34690	-1.10	-0.14	-1.30	0.23542	0.412962	-6.49
254780_s_	auxilin-like protein auxilin - bovine, Pir	---	AT4G12770	1.18	0.24	1.30	0.235366	0.412962	-6.49
257898_s_	hypothetical protein predicted by gens	---	---	-1.08	-0.12	-1.30	0.235524	0.413095	-6.49
265372_at	Ac-like transposase related to Ac/Ds tr	---	AT2G06500	1.12	0.17	1.30	0.235548	0.413105	-6.49
255221_at	putative protein various predicted prote	---	AT4G05150	1.12	0.17	1.30	0.235627	0.413181	-6.49
266355_at	hypothetical protein predicted by gens	---	AT2G01400	1.22	0.29	1.30	0.235626	0.413181	-6.49
253307_at	putative protein auxin-induced protein	---	AT4G33670	1.13	0.17	1.30	0.23572	0.41331	-6.49
252369_at	putative protein deoxycytidylate deam	---	AT3G48540	-1.10	-0.14	-1.30	0.235737	0.41331	-6.49
248400_at	putative protein contains similarity to A	---	AT5G52020	-1.14	-0.19	-1.30	0.235775	0.413345	-6.49
250581_at	copine-like protein copine VII protein -	BON2	AT5G07300	1.10	0.14	1.30	0.235904	0.413538	-6.49
251168_at	putative protein several hypothetical pr	---	AT3G63370	-1.13	-0.17	-1.30	0.236013	0.413671	-6.49
248414_at	50S ribosomal protein L11-like	---	AT5G51610	-1.12	-0.16	-1.30	0.236015	0.413671	-6.49
247024_at	Expressed protein ; supported by full-le	---	AT5G66985	1.13	0.18	1.30	0.236121	0.413767	-6.49
251247_at	hypothetical protein	---	AT3G62140	1.14	0.18	1.30	0.236117	0.413767	-6.49
263211_at	germin-like oxalate oxidase similar to E	GLP7	AT1G10460	-1.14	-0.19	-1.30	0.236125	0.413767	-6.49
262576_at	unknown protein ESTs gb|R90323, gb	---	AT1G15280	1.09	0.13	1.30	0.236296	0.414035	-6.49

264258_at	hypothetical protein predicted by gene	---	AT1G09220	1.12	0.16	1.30	0.236344	0.414056	-6.49
253446_at	putative protein predicted protein T10	---	AT4G32620	1.11	0.16	1.30	0.236336	0.414056	-6.49
262310_at	unknown protein contains similarity to	MLP31	AT1G70840	-1.11	-0.15	-1.30	0.236446	0.414075	-6.49
247209_at	putative protein contains similarity to u	---	AT5G64830	1.10	0.14	1.30	0.236377	0.414075	-6.49
255516_at	hypothetical protein similar to extensir	---	AT4G02270	-1.16	-0.22	-1.30	0.236431	0.414075	-6.49
265016_at	unknown protein similar to deacetylvir	---	AT1G24420	1.09	0.12	1.30	0.236422	0.414075	-6.49
255079_s_	14-3-3 protein GF14chi (grf1) identica	GF14 PHI	AT1G35160 /	1.09	0.13	1.30	0.236407	0.414075	-6.49
252183_at	UTP-glucose glucosyltransferase - like	UGT72E1	AT3G50740	1.14	0.19	1.30	0.236674	0.414443	-6.49
253686_at	putative protein predicted proteins, Ar	---	AT4G29750	-1.13	-0.17	-1.30	0.236741	0.414529	-6.49
247367_at	oxygen-independent coproporphyrinog	---	AT5G63290	1.19	0.25	1.30	0.236785	0.414573	-6.49
245429_at	Bax inhibitor-1-like protein	---	AT4G17580	-1.09	-0.12	-1.30	0.236816	0.414596	-6.49
262923_at	Dhp1-like protein similar to Dhp1 prote	XRN3	AT1G75660	1.11	0.15	1.30	0.236859	0.41464	-6.49
264265_at	unknown protein ; supported by cDNA	---	AT1G09280	-1.14	-0.19	-1.30	0.236903	0.414684	-6.49
251424_at	putative protein 04.05.01.01	---	AT3G60560	1.09	0.12	1.30	0.237269	0.415261	-6.50
245615_at	reverse transcriptase like protein	---	---	1.10	0.14	1.30	0.237255	0.415261	-6.50
264502_at	putative 12-oxophytodienoate reducta	---	AT1G09400	1.14	0.18	1.30	0.237326	0.41533	-6.50
260074_at	putative ras-related GTP-binding prote	AtRABA6a	AT1G73640	-1.10	-0.14	-1.30	0.237352	0.415343	-6.50
259123_at	unknown protein	---	AT3G02200	-1.10	-0.14	-1.30	0.237551	0.41566	-6.50
261806_at	ferrodoxin NADP oxidoreductase, puta	ATRFNR2	AT1G30510	1.22	0.29	1.30	0.237588	0.415692	-6.50
252224_at	putative protein various ADP-RIBOSYI	ATARLA1B	AT3G49860	-1.13	-0.17	-1.30	0.237734	0.415916	-6.50
252933_at	putative receptor-like protein kinase re	---	AT4G39110	-1.13	-0.17	-1.30	0.237766	0.415941	-6.50
250718_at	unknown protein	emb2735	AT5G06240	-1.11	-0.15	-1.30	0.237841	0.41604	-6.50
251431_at	protein synthesis initiation factor - like	EIF4G	AT3G60240	1.09	0.12	1.30	0.237892	0.416096	-6.50
256539_at	hypothetical protein predicted by gene	---	---	1.10	0.13	1.30	0.237929	0.416097	-6.50
262030_s_	mutator-like transposase, putative sim	---	---	1.12	0.16	1.30	0.237916	0.416097	-6.50
247682_at	serine/threonine-specific protein kinas	---	AT5G59650	-1.12	-0.16	-1.29	0.237991	0.416174	-6.50
259267_at	unknown protein ;supported by full-ler	---	AT3G01130	-1.10	-0.14	-1.29	0.23805	0.416245	-6.50
260367_at	unknown protein ;supported by full-ler	---	AT1G69760	1.34	0.42	1.29	0.238107	0.416282	-6.50
265701_at	unknown protein related to uncharacte	---	AT2G03460	1.10	0.14	1.29	0.238106	0.416282	-6.50
255087_at	putative protein proteins of this bac	---	AT4G09340	1.10	0.13	1.29	0.238246	0.416379	-6.50
253524_at	predicted protein ; supported by cDNA	---	AT4G31430	1.12	0.16	1.29	0.238254	0.416379	-6.50
252766_at	putative protein hypothetical proteins -	---	---	-1.15	-0.20	-1.29	0.238226	0.416379	-6.50
252149_at	putative protein hypothetical protein T	---	AT3G51290	-1.09	-0.12	-1.29	0.238194	0.416379	-6.50
261966_x_	hypothetical protein similar to putative	---	---	-1.10	-0.14	-1.29	0.238214	0.416379	-6.50
246935_at	leucine-rich repeats containing protein	EBF2	AT5G25350	-1.19	-0.26	-1.29	0.238321	0.416464	-6.50

250762_at	putative protein similar to unknown pro	---	AT5G05990	1.25	0.33	1.29	0.238419	0.416571	-6.50
265158_at	hypothetical protein predicted by gene	---	AT1G31040	1.09	0.12	1.29	0.238412	0.416571	-6.50
267263_at	similar to late embryogenesis abundan	---	AT2G23110	1.64	0.71	1.29	0.238525	0.416725	-6.50
262487_at	unknown protein ESTs gb|T42839 and	---	AT1G21610	1.08	0.11	1.29	0.238771	0.416828	-6.50
260785_at	hypothetical protein predicted by gens	---	AT1G06200	1.11	0.14	1.29	0.238761	0.416828	-6.50
251453_at	putative protein hypothetical protein A	---	AT3G60070	-1.11	-0.15	-1.29	0.238693	0.416828	-6.50
248831_at	putative protein contains similarity to S	---	AT5G47160	1.12	0.16	1.29	0.238785	0.416828	-6.50
263398_at	putative RAS superfamily GTP-binding	AtRABA5d	AT2G31680	-1.11	-0.16	-1.29	0.238763	0.416828	-6.50
266739_at	unknown protein predicted by genscan	---	AT2G46730	-1.11	-0.15	-1.29	0.238731	0.416828	-6.50
252744_at	putative protein hypothetical protein A	---	AT3G43310	-1.11	-0.14	-1.29	0.238705	0.416828	-6.50
246698_at	putative protein	---	---	1.10	0.13	1.29	0.238633	0.416828	-6.50
267459_at	unknown protein ;supported by full-ler	---	AT2G33850	-1.09	-0.13	-1.29	0.238687	0.416828	-6.50
248902_at	unknown protein	---	AT5G46440	1.11	0.15	1.29	0.238678	0.416828	-6.50
261244_at	subtilisin-like serine protease similar to	---	AT1G20150	1.08	0.11	1.29	0.238712	0.416828	-6.50
247778_at	wounding stress induced protein - like	---	AT5G58750	-1.09	-0.12	-1.29	0.238947	0.417078	-6.50
265947_at	putative WD-40 repeat protein ; suppo	---	AT2G19540	1.19	0.25	1.29	0.238996	0.417132	-6.50
263959_at	hypothetical protein predicted by gens	---	AT2G36210	1.10	0.14	1.29	0.239199	0.417454	-6.50
249164_at	U2 snRNP auxiliary factor, small subu	U2AF35B	AT5G42820	1.13	0.17	1.29	0.239246	0.417489	-6.50
264408_at	hypothetical protein predicted by gene	FRS11	AT1G10240	-1.10	-0.14	-1.29	0.239255	0.417489	-6.50
260888_at	hypothetical protein similar to allergen	---	AT1G29140	-1.10	-0.14	-1.29	0.239354	0.417629	-6.50
252324_at	protein translocation complex sec61 g	---	AT3G48570	-1.12	-0.16	-1.29	0.239373	0.417631	-6.50
263720_at	putative Na/H antiporter	ATCHX15	AT2G13620	1.09	0.13	1.29	0.239598	0.417991	-6.50
245725_at	sucrose synthase, putative similar to s	SUS6	AT1G73370	-1.25	-0.32	-1.29	0.239714	0.418098	-6.50
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_XRE	---	---	1.19	0.25	1.29	0.239683	0.418098	-6.50
246876_at	putative protein various predicted lysi	---	AT5G26140	-1.10	-0.14	-1.29	0.239709	0.418098	-6.50
249313_at	unknown protein	---	AT5G41560	1.09	0.13	1.29	0.239751	0.418129	-6.50
253305_at	Expressed protein ; supported by full-l	---	AT4G33666	-1.31	-0.39	-1.29	0.239775	0.418139	-6.50
265669_at	unknown protein ;supported by full-ler	---	AT2G32040	-1.19	-0.25	-1.29	0.239833	0.418208	-6.51
256675_at	putative protein DNA-binding protein F	---	AT3G52170	1.22	0.29	1.29	0.239854	0.418214	-6.51
250291_at	aspartate kinase ;supported by full-ler	AK-LYS1	AT5G13280	1.17	0.23	1.29	0.239948	0.418313	-6.51
257569_at	hypothetical protein	---	AT3G26350	-1.15	-0.21	-1.29	0.239943	0.418313	-6.51
254334_at	predicted protein	---	AT4G22760	1.13	0.17	1.29	0.240118	0.418578	-6.51
253466_at	homeodomain containing protein 1 ; s	KNAT5	AT4G32040	-1.13	-0.18	-1.29	0.24017	0.418637	-6.51
248544_at	putative protein contains similarity to L	PIMT2	AT5G50240	1.21	0.28	1.29	0.240441	0.419077	-6.51
247317_at	putative protein contains similarity to N	anac103	AT5G64060	-1.12	-0.16	-1.29	0.240487	0.419125	-6.51

248050_at	unknown protein	---	AT5G56100	1.23	0.29	1.29	0.240584	0.419262	-6.51
259944_at	hypothetical protein predicted by gens	---	AT1G71470	-1.10	-0.14	-1.29	0.240667	0.419359	-6.51
263446_at	putative SET-domain transcriptional re	ATX1	AT2G31650	-1.12	-0.17	-1.29	0.240676	0.419359	-6.51
257101_at	disease resistance protein, putative si	AtRLP42	AT3G25020	1.11	0.15	1.29	0.240848	0.4196	-6.51
261153_at	unknown protein ;supported by full-len	---	AT1G04850	1.11	0.15	1.29	0.240852	0.4196	-6.51
254503_at	hypothetical protein ;supported by full-	PTAC9	AT4G20010	-1.12	-0.16	-1.29	0.240911	0.419671	-6.51
266627_at	putative pre-mRNA splicing factor RNA	MEE29	AT2G35340	1.12	0.16	1.29	0.240946	0.4197	-6.51
260360_at	chorismate mutase, putative contains	CM3	AT1G69370	-1.15	-0.21	-1.29	0.240974	0.419717	-6.51
249871_at	putative protein similar to unknown pro	---	AT5G23110	-1.16	-0.21	-1.29	0.240996	0.419723	-6.51
251658_at	putative protein strictosidine synthase	---	AT3G57020	-1.28	-0.36	-1.29	0.241021	0.419735	-6.51
251775_s_	delta-1-pyrroline-5-carboxylate synthet	P5CS1	AT2G39800 /	1.25	0.33	1.29	0.24105	0.419754	-6.51
245243_at	hypothetical protein predicted by gene	---	AT1G44414	-1.10	-0.13	-1.29	0.241208	0.419996	-6.51
253403_at	putative serine/threonine protein kinas	AtAUR1	AT4G32830	-1.13	-0.17	-1.28	0.241438	0.420364	-6.51
248946_at	putative protein similar to unknown pro	---	AT5G45530	-1.09	-0.13	-1.28	0.241715	0.420814	-6.51
264919_at	hypothetical protein contains similarity	---	AT1G60540	1.11	0.15	1.28	0.241733	0.420815	-6.51
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_XRE	---	---	1.19	0.25	1.28	0.241783	0.42087	-6.51
263777_at	putative cyclic nucleotide-regulated ion	ATCNGC12	AT2G46450	1.50	0.59	1.28	0.241888	0.421019	-6.51
256022_at	amino acid permease I identical to ami	AAP1	AT1G58360	1.31	0.39	1.28	0.241997	0.421177	-6.51
256648_at	ribosomal protein, putative similar to 6	---	AT3G13580	-1.16	-0.21	-1.28	0.242121	0.421347	-6.51
266308_at	putative cytochrome P450	CYP705A9	AT2G27010	1.12	0.17	1.28	0.24215	0.421347	-6.51
253157_at	putative protein DNA helicase TPS1,	RecQl3	AT4G35740	-1.13	-0.17	-1.28	0.242138	0.421347	-6.51
249426_at	putative RNA helicase putative ATP-d	---	AT5G39840	1.27	0.34	1.28	0.242257	0.421453	-6.51
258397_at	Expressed protein ; supported by full-l	---	AT3G15357	1.10	0.14	1.28	0.242266	0.421453	-6.51
258261_at	putative RING zinc finger protein cont	---	AT3G15740	1.20	0.26	1.28	0.242233	0.421453	-6.51
261003_at	hypothetical protein predicted by gene	---	AT1G26500	-1.13	-0.18	-1.28	0.242321	0.421517	-6.51
253538_at	putative protein ribosomal protein Yml	---	AT4G31460	1.09	0.13	1.28	0.242366	0.421562	-6.51
258725_at	putative RNA helicase similar to RNA	---	AT3G09620	1.09	0.13	1.28	0.242389	0.421568	-6.51
247412_at	unknown protein	---	AT5G63010	-1.12	-0.16	-1.28	0.242406	0.421568	-6.51
250506_at	ABC transporter, ATP-binding protein	GCN2	AT5G09930	-1.12	-0.16	-1.28	0.242452	0.421615	-6.51
258548_at	hypothetical protein	ULP1A	AT3G06910	1.14	0.19	1.28	0.242529	0.421717	-6.51
253682_at	cytidine deaminase 5 (CDA5)	---	AT4G29640	1.14	0.18	1.28	0.242711	0.42197	-6.52
258922_at	putative 40S ribosomal protein S17 sin	---	AT3G10610	-1.30	-0.38	-1.28	0.24271	0.42197	-6.52
246086_at	beta-1,3-glucanase - like protein beta-	---	AT5G20560	1.09	0.13	1.28	0.242776	0.422018	-6.52
246163_at	putative protein predicted proteins, Ar	---	---	-1.13	-0.18	-1.28	0.242762	0.422018	-6.52
255194_at	score=37.6, E=2.9e-07, N=3	---	AT4G07410	1.17	0.22	1.28	0.242857	0.422062	-6.52

258681_at	unknown protein ; supported by full-le	---	AT3G08610	-1.11	-0.16	-1.28	0.242836	0.422062	-6.52
252800_at	putative protein	---	---	-1.10	-0.14	-1.28	0.24285	0.422062	-6.52
260148_at	putative oxidoreductase similar to gibb	---	AT1G52800	1.17	0.23	1.28	0.242918	0.422072	-6.52
254865_s_	putative protein, fragment other predic	---	AT4G05350 /	1.09	0.13	1.28	0.242903	0.422072	-6.52
261440_at	hypothetical protein predicted by gene	---	AT1G28510	-1.10	-0.14	-1.28	0.242907	0.422072	-6.52
263887_at	hypothetical protein predicted by gens	---	AT2G36980	1.14	0.19	1.28	0.242939	0.422076	-6.52
267613_at	putative second messenger-dependen	PID2	AT2G26700	-1.11	-0.15	-1.28	0.243028	0.422199	-6.52
252108_at	putative protein various predicted prot	---	AT3G51530	1.10	0.14	1.28	0.243121	0.422296	-6.52
246345_at	calcium-dependent protein kinase-like	---	AT3G56760	-1.14	-0.19	-1.28	0.243117	0.422296	-6.52
259441_at	cathepsin B-like cysteine protease, pu	---	AT1G02300	1.14	0.18	1.28	0.243143	0.422302	-6.52
259114_at	26S proteasome AAA-ATPase subunit	RPT5A	AT3G05530	-1.10	-0.14	-1.28	0.243191	0.422321	-6.52
267349_at	60S acidic ribosomal protein P0	---	AT2G40010	-1.09	-0.13	-1.28	0.243177	0.422321	-6.52
246236_at	hypothetical protein	---	AT4G36470	-1.13	-0.17	-1.28	0.243251	0.422393	-6.52
259027_at	hypothetical protein predicted by gens	---	AT3G09280	1.08	0.12	1.28	0.243285	0.42242	-6.52
257435_at	putative RSZp22 splicing factor	---	AT2G24590	1.15	0.20	1.28	0.243307	0.422426	-6.52
249937_at	putative protein seed maturation protei	---	AT5G22470	1.15	0.20	1.28	0.243352	0.422472	-6.52
253211_at	amidase - like protein amidase, Bacillu	---	AT4G34880	1.10	0.13	1.28	0.243601	0.422872	-6.52
259720_at	hypothetical protein predicted by gene	---	AT1G61080	1.12	0.16	1.28	0.243649	0.422923	-6.52
250947_at	putative protein	---	AT5G03450	1.14	0.19	1.28	0.243678	0.422941	-6.52
259192_at	unknown protein ;supported by full-ler	---	AT3G01740	1.13	0.18	1.28	0.243717	0.422976	-6.52
245944_at	putative protein various predicted prot	MSL9	AT5G19520	-1.10	-0.14	-1.28	0.243835	0.42315	-6.52
249730_at	calcium dependent protein kinase-like	---	AT5G24430	1.24	0.31	1.28	0.243958	0.42333	-6.52
254733_at	putative polygalacturonase polygalact	---	AT4G13760	1.09	0.13	1.28	0.244041	0.423443	-6.52
256261_at	ras-related GTP-binding protein contai	RABA4D	AT3G12160	-1.10	-0.14	-1.28	0.244159	0.423588	-6.52
255800_at	putative protein transposase, Ipomoea	---	AT4G10200	1.09	0.13	1.28	0.244162	0.423588	-6.52
252243_at	putative protein some putative proteins	---	AT3G50120	-1.25	-0.32	-1.28	0.244239	0.423657	-6.52
253235_at	putative protein hypothetical protein, S	HDR	AT4G34350	1.22	0.29	1.28	0.244231	0.423657	-6.52
255976_at	hypothetical protein predicted by gene	---	AT1G22010	1.10	0.13	1.28	0.24433	0.423782	-6.52
263165_at	putataive transport protein Similar to g	---	AT1G03060	1.09	0.12	1.28	0.244388	0.423851	-6.52
247413_at	NBS/LRR disease resistance protein	---	AT5G63020	-1.13	-0.18	-1.28	0.244423	0.423879	-6.52
264668_at	putative 2,3-bisphosphoglycerate-inde	---	AT1G09780	1.14	0.19	1.27	0.244567	0.423948	-6.52
257155_at	hypothetical protein predicted by gens	---	AT3G27290	-1.13	-0.18	-1.28	0.244527	0.423948	-6.52
253491_at	RNA lariat debranching enzyme - like	---	AT4G31770	-1.19	-0.26	-1.28	0.244518	0.423948	-6.52
266151_x_	En/Spm transposon protein (mosaic-lik	---	---	-1.11	-0.15	-1.27	0.244583	0.423948	-6.52
247968_at	40S ribosomal protein S30 homolog (e	---	AT5G56670	-1.26	-0.33	-1.28	0.244526	0.423948	-6.52

264347_at	putative extensin strong similarity to ex	LRX1	AT1G12040	1.08	0.11	1.27	0.244593	0.423948	-6.52
246412_at	phosphoglucomutase-like protein pho	---	AT5G17530	-1.19	-0.25	-1.28	0.244545	0.423948	-6.52
254628_at	Expressed protein ; supported by full-le	---	AT4G18593	-1.08	-0.12	-1.27	0.244674	0.424057	-6.52
259917_at	hypothetical protein predicted by gens	---	AT1G72580	-1.10	-0.14	-1.27	0.244714	0.424094	-6.52
252236_at	zinc-finger-like protein Cys2/His2-type	---	AT3G49930	-1.11	-0.15	-1.27	0.244863	0.42432	-6.52
261120_at	homeodomain protein BELL1, putative	BLH3	AT1G75410	1.17	0.22	1.27	0.244917	0.424349	-6.52
267322_at	putative leucine-rich-repeat protein	---	AT2G19330	1.09	0.13	1.27	0.244903	0.424349	-6.52
257658_at	unknown protein ; supported by full-le	---	AT3G13230	1.28	0.36	1.27	0.245064	0.424571	-6.52
265860_at	hypothetical protein predicted by gens	---	AT2G01810	1.09	0.13	1.27	0.245084	0.424574	-6.52
254821_at	hypothetical protein	---	AT4G12540	1.10	0.13	1.27	0.245166	0.424619	-6.52
253079_s_	putative protein F56F10.1, Caenorhab	---	AT4G36190 /	1.15	0.20	1.27	0.245158	0.424619	-6.52
252576_s_	clpC-like protein AtClpC - Arabidopsis	---	AT3G45450 /	1.19	0.25	1.27	0.245137	0.424619	-6.52
263888_at	unknown protein	---	AT2G37000	-1.14	-0.19	-1.27	0.245228	0.424694	-6.52
255772_at	calmodulin, putative similar to calmod	---	AT1G18530	-1.12	-0.16	-1.27	0.245379	0.424925	-6.52
264909_at	unknown protein	---	AT2G17300	-1.11	-0.15	-1.27	0.245589	0.425255	-6.53
249012_at	flavonoid 3,5-hydroxylase-like; cytoch	CYP706A3	AT5G44620	1.11	0.15	1.27	0.245655	0.425337	-6.53
257488_s_	putative RING-finger protein	---	AT1G36950 /	1.08	0.11	1.27	0.245686	0.425358	-6.53
257378_s_	hypothetical protein predicted by gens	---	AT2G02290 /	-1.12	-0.16	-1.27	0.245861	0.425596	-6.53
249051_at	berberine bridge enzyme-like protein ;	---	AT5G44390	1.13	0.18	1.27	0.245844	0.425596	-6.53
251005_at	putative protein various predicted prot	---	AT5G02590	-1.32	-0.40	-1.27	0.245967	0.425747	-6.53
250406_at	enhancer of rudimentary ; supported b	ER	AT5G10810	-1.16	-0.21	-1.27	0.246071	0.425895	-6.53
260117_at	AIG1-like protein similar to AIG1 prote	---	AT1G33950	1.08	0.11	1.27	0.246184	0.42604	-6.53
253086_at	hypothetical protein	---	AT4G36370	1.09	0.12	1.27	0.246191	0.42604	-6.53
246785_at	glutathione synthetase gsh2 non-cons	GSH2	AT5G27380	1.22	0.29	1.27	0.246238	0.426072	-6.53
264178_at	latex-abundant protein, putative simila	AMC1	AT1G02170	1.12	0.16	1.27	0.246248	0.426072	-6.53
247526_at	putative protein C2H2 zinc-finger prot	---	AT5G61470	1.10	0.14	1.27	0.246267	0.426074	-6.53
245063_at	Expressed protein ; supported by full-le	---	AT2G39795	1.27	0.35	1.27	0.246319	0.426098	-6.53
264244_at	pantothenate kinase, putative similar t	ATPANK1	AT1G60440	1.11	0.15	1.27	0.246309	0.426098	-6.53
259077_s_	reversibly glycosylated polypeptide-1 i	RGP1	AT3G02230 /	-1.22	-0.28	-1.27	0.246446	0.42625	-6.53
263486_at	AP2 domain transcription factor	---	AT2G22200	-1.10	-0.13	-1.27	0.246481	0.42625	-6.53
263144_at	unknown protein similar to putative aux	---	AT1G54070	1.13	0.17	1.27	0.246477	0.42625	-6.53
248381_at	fructokinase 1 ; supported by cDNA: g	---	AT5G51830	1.23	0.30	1.27	0.246437	0.42625	-6.53
248999_at	putative protein contains similarity to h	---	AT5G44970	-1.09	-0.13	-1.27	0.246514	0.426275	-6.53
257452_at	hypothetical protein predicted by gens	---	AT1G05740	-1.09	-0.13	-1.27	0.246545	0.426295	-6.53
258241_at	hypothetical protein similar to hypothet	LBD25	AT3G27650	1.15	0.20	1.27	0.246663	0.426467	-6.53

254891_at	putative protein Fly Fas-associated fa	SAY1	AT4G11740	1.09	0.13	1.27	0.246714	0.426516	-6.53
264353_at	hypothetical protein predicted by gens	---	AT1G03260	-1.10	-0.14	-1.27	0.246728	0.426516	-6.53
254962_at	putative glucanase endo-beta-1,4-D-g	AtGH9C3	AT4G11050	-1.11	-0.15	-1.27	0.246918	0.426811	-6.53
251459_at	putative protein hypothetical proteins /	---	AT3G60200	-1.33	-0.41	-1.27	0.246991	0.426906	-6.53
246323_at	hypothetical protein predicted by gene	---	AT1G16690	-1.13	-0.17	-1.27	0.247022	0.426926	-6.53
264188_at	histone H2A, putative similar to histon	GAMMA-H2/	AT1G54690	-1.24	-0.30	-1.27	0.247043	0.42693	-6.53
260825_at	hypothetical protein predicted by gene	---	AT1G06810	-1.10	-0.14	-1.27	0.247126	0.42701	-6.53
246164_at	putative protein predicted proteins, Ar	---	---	-1.10	-0.14	-1.27	0.247124	0.42701	-6.53
256031_at	choline kinase (GmCK2p), putative sir	---	AT1G34100	-1.10	-0.14	-1.27	0.247283	0.427248	-6.53
267461_at	putative auxin-regulated protein ;supp	---	AT2G33830	1.13	0.18	1.27	0.247332	0.4273	-6.53
261504_at	MADS-box protein identical to GB:AA	AGL12	AT1G71692	-1.14	-0.19	-1.27	0.247354	0.427306	-6.53
259514_at	hypothetical protein ; supported by cDI	OZS1	AT1G12480	-1.11	-0.15	-1.27	0.247431	0.427362	-6.53
266526_at	putative tetracycline transporter protein	---	AT2G16980	-1.12	-0.16	-1.27	0.247461	0.427362	-6.53
267352_at	hypothetical protein predicted by gens	---	AT2G40050	-1.09	-0.13	-1.27	0.247451	0.427362	-6.53
262470_at	disease resistance protein, putative si	---	AT1G50180	1.11	0.15	1.27	0.247461	0.427362	-6.53
263932_at	unknown protein	---	AT2G35990	1.09	0.13	1.27	0.247513	0.427418	-6.53
256729_at	hypothetical protein predicted by gene	---	AT3G25680	-1.11	-0.15	-1.27	0.247541	0.427434	-6.53
261361_at	hypothetical protein predicted by gens	---	---	-1.12	-0.16	-1.27	0.247567	0.427447	-6.53
248898_at	outward rectifying potassium channel I	KCO2	AT5G46370	-1.12	-0.17	-1.27	0.247596	0.427463	-6.53
259900_at	c-Jun coactivator-like protein (AJH2) ic	CSN5B	AT1G71230	-1.09	-0.12	-1.27	0.247614	0.427463	-6.53
264588_at	unknown protein contains similarity to	---	AT2G17730	1.24	0.31	1.27	0.247695	0.42757	-6.53
265690_at	hypothetical protein predicted by gens	---	AT2G24320	1.13	0.18	1.27	0.247766	0.427661	-6.53
259815_at	hypothetical protein predicted by gene	---	AT1G49870	-1.10	-0.14	-1.26	0.24796	0.427964	-6.53
260376_at	putative cytochrome P-450 similar to c	CYP78A10	AT1G74110	-1.10	-0.14	-1.26	0.24813	0.428224	-6.53
250654_at	receptor protein kinase-like protein	---	AT5G06940	-1.12	-0.16	-1.26	0.248234	0.428371	-6.53
249728_at	GTPase activator-like protein of Rab-li	---	AT5G24390	1.12	0.16	1.26	0.248279	0.428385	-6.53
246610_at	putative protein	---	AT5G35400	-1.11	-0.14	-1.26	0.248276	0.428385	-6.53
255701_at	predicted protein of unknown function	JLO	AT4G00220	1.09	0.13	1.26	0.248318	0.428419	-6.54
247066_at	DNA binding protein-like	---	AT5G66940	-1.09	-0.12	-1.26	0.248394	0.428518	-6.54
257695_at	hypothetical protein contains Pfam pro	HUA1	AT3G12680	-1.11	-0.16	-1.26	0.248425	0.428538	-6.54
262555_at	hypothetical protein	---	AT1G31400	1.09	0.12	1.26	0.248498	0.428633	-6.54
251563_at	anthranilate phosphoribosyltransferas	---	AT3G57880	-1.20	-0.27	-1.26	0.24857	0.428725	-6.54
247408_at	ZAP - like protein nuclear protein ZAP	---	AT5G62760	-1.09	-0.12	-1.26	0.248675	0.428845	-6.54
249920_at	putative protein various predicted prote	---	AT5G19260	-1.30	-0.38	-1.26	0.248677	0.428845	-6.54
250322_at	putative transcription factor (MYB46)	MYB46	AT5G12870	-1.09	-0.12	-1.26	0.24879	0.429007	-6.54

267455_at	hypothetical protein predicted by gens	---	AT2G33760	1.14	0.19	1.26	0.248863	0.4291	-6.54
264446_at	putative nuclear transport factor simila	NTF2A	AT1G27310	1.11	0.15	1.26	0.248888	0.429111	-6.54
251396_at	transketolase - like protein transketola	---	AT3G60750	-1.10	-0.13	-1.26	0.249025	0.429288	-6.54
245884_at	branched-chain alpha keto-acid dehyd	---	AT5G09300	1.16	0.21	1.26	0.249029	0.429288	-6.54
256476_at	TNP2-like transposon protein similar to	---	---	1.10	0.13	1.26	0.249204	0.429558	-6.54
264239_at	hypothetical protein predicted by gene	---	AT1G54770	-1.09	-0.13	-1.26	0.249267	0.429603	-6.54
263109_at	hypothetical protein similar to putative	---	AT1G65180	-1.13	-0.17	-1.26	0.24925	0.429603	-6.54
263840_at	Expressed protein ; supported by full-le	---	AT2G36885	-1.16	-0.21	-1.26	0.249295	0.429617	-6.54
261969_at	hypothetical protein contains similarity	---	AT1G65950	1.09	0.13	1.26	0.249376	0.429692	-6.54
258620_at	putative MYB family transcription facto	MYB107	AT3G02940	-1.08	-0.11	-1.26	0.249373	0.429692	-6.54
260301_at	hypothetical protein ;supported by full-	---	AT1G80290	1.12	0.17	1.26	0.249402	0.429698	-6.54
266833_at	hypothetical protein predicted by gens	---	---	-1.08	-0.11	-1.26	0.249417	0.429698	-6.54
264475_s_	hypothetical protein predicted by gene	---	AT1G77150 /	-1.14	-0.19	-1.26	0.249509	0.429727	-6.54
265373_at	putative replication protein A1	RPA1A	AT2G06510	1.21	0.27	1.26	0.249496	0.429727	-6.54
255592_s_	hypothetical protein	---	AT2G34280 /	-1.12	-0.17	-1.26	0.249485	0.429727	-6.54
252387_at	aldose 1-epimerase - like protein aldo	---	AT3G47800	1.15	0.21	1.26	0.249462	0.429727	-6.54
262526_at	putative prenyl transferase (prephytoe	SPS2	AT1G17050	-1.31	-0.39	-1.26	0.24953	0.429731	-6.54
245496_at	LET1 like protein	---	AT4G16440	1.10	0.14	1.26	0.249562	0.429754	-6.54
253169_at	putative protein various predicted prot	---	AT4G35120	-1.12	-0.16	-1.26	0.249585	0.429761	-6.54
267515_at	putative PCF2-like DNA binding protei	---	AT2G45680	-1.13	-0.18	-1.26	0.249778	0.429995	-6.54
264640_at	pollen allergen, putative similar to poll	ATEXPB2	AT1G65680	-1.17	-0.22	-1.26	0.249747	0.429995	-6.54
263879_at	hypothetical protein predicted by gene	---	AT2G22030	-1.09	-0.13	-1.26	0.249769	0.429995	-6.54
266318_at	Mutator-like transposase similar to MU	FRS3	AT2G27110	-1.08	-0.11	-1.26	0.249893	0.43016	-6.54
266981_at	60S ribosomal protein L23A identical t	RPL23AA	AT2G39460	-1.23	-0.30	-1.26	0.249928	0.430189	-6.54
247684_at	serine/threonine-specific protein kinas	---	AT5G59670	-1.84	-0.88	-1.26	0.250051	0.430367	-6.54
262863_at	rhamnosyltransferase, putative similar	---	AT1G64910	-1.11	-0.15	-1.26	0.250157	0.430485	-6.54
256719_at	En/Spm-like transposon protein related	---	---	1.10	0.14	1.26	0.250145	0.430485	-6.54
264370_at	hybrid proline-rich protein, putative sir	---	AT1G12100	-1.11	-0.15	-1.26	0.250279	0.43063	-6.54
254600_at	4-coumarate-CoA ligase - like 4-coum	---	AT4G19010	1.19	0.25	1.26	0.250279	0.43063	-6.54
245371_at	hypothetical protein ;supported by full-	---	AT4G15750	-1.12	-0.16	-1.26	0.250351	0.430721	-6.54
257661_at	unknown protein contains Pfam profile	---	AT3G13340	1.08	0.11	1.26	0.250462	0.430881	-6.54
264509_at	unknown protein Location of EST gb|Z	---	AT1G09520	-1.11	-0.15	-1.26	0.250522	0.430918	-6.54
250904_at	subtilisin-like serine protease contains	---	AT5G03620	1.09	0.13	1.26	0.250503	0.430918	-6.54
254205_at	putative protein kinesin heavy chain -	---	AT4G24170	-1.12	-0.17	-1.26	0.250557	0.430945	-6.54
247877_at	putative protein contains similarity to a	XBAT32	AT5G57740	1.18	0.24	1.26	0.25059	0.430971	-6.54

249849_at	putative protein similar to unknown pro	NIC2	AT5G23230	1.13	0.18	1.26	0.250697	0.431109	-6.54
264744_at	hypothetical protein predicted by gene	---	AT1G62050	1.20	0.26	1.26	0.250709	0.431109	-6.54
256772_at	galactosidase, putative similar to BET	BGAL1	AT3G13750	-1.41	-0.50	-1.26	0.250973	0.431531	-6.54
245466_at	glucosyltransferase like protein	---	AT4G16600	-1.13	-0.18	-1.26	0.25102	0.431576	-6.54
259851_at	kinesin, putative	---	AT1G72250	-1.09	-0.12	-1.26	0.251037	0.431576	-6.54
267525_at	putative glycine-rich protein	---	AT2G30560	1.08	0.11	1.26	0.251235	0.431787	-6.55
264112_at	putative 1,3-beta-D-glucan synthase	CALS5	AT2G13680	-1.12	-0.16	-1.26	0.251232	0.431787	-6.55
257703_at	unknown protein ; supported by full-ler	---	AT3G12640	1.09	0.12	1.26	0.251195	0.431787	-6.54
262831_at	cytochrome B561, putative similar to c	---	AT1G14730	1.19	0.25	1.26	0.251214	0.431787	-6.55
261083_at	unknown protein ; supported by cDNA	---	AT1G07310	-1.12	-0.17	-1.26	0.251293	0.431854	-6.55
258175_at	FKBP-type peptidyl-prolyl cis-trans isc	TWD1	AT3G21640	-1.10	-0.14	-1.25	0.251552	0.432168	-6.55
251468_at	epsin-like protein Af10-protein - Avena	---	AT3G59290	1.11	0.15	1.25	0.251514	0.432168	-6.55
266376_at	putative endoxyloglucan glycosyltranst	---	AT2G14620	-1.14	-0.18	-1.25	0.251519	0.432168	-6.55
246531_at	MADS box protein AGL2 ; supported b	טפס-01	AT5G15800	-1.13	-0.17	-1.25	0.251546	0.432168	-6.55
257928_at	hypothetical protein contains Pfam pro	PPR40	AT3G16890	1.08	0.11	1.25	0.251647	0.43229	-6.55
248519_at	11-beta-hydroxysteroid dehydrogenas	AtHSD7	AT5G50590 /	-1.11	-0.15	-1.25	0.25166	0.43229	-6.55
257935_at	unknown protein	---	AT3G25440	-1.10	-0.14	-1.25	0.251698	0.432321	-6.55
250242_at	putative protein similar to unknown pro	---	AT5G13620	-1.10	-0.13	-1.25	0.251717	0.432321	-6.55
245955_at	hypothetical protein	BGLU24	AT5G28510	1.10	0.13	1.25	0.25191	0.43262	-6.55
250092_at	putative protein	---	AT5G17360	-1.08	-0.11	-1.25	0.251983	0.432714	-6.55
251752_at	proline transporter 2	PROT2	AT3G55740	1.17	0.23	1.25	0.252101	0.43285	-6.55
245652_at	F-box protein family, putative	---	AT4G13960	1.12	0.16	1.25	0.252087	0.43285	-6.55
249766_at	peroxidase-like protein	---	AT5G24070	-1.11	-0.15	-1.25	0.252218	0.432961	-6.55
265585_at	CDC27/NUC2-like protein TPR-repeat	HBT	AT2G20000	1.13	0.18	1.25	0.252222	0.432961	-6.55
265982_at	putative retroelement pol polyprotein	---	---	1.09	0.12	1.25	0.252205	0.432961	-6.55
253915_at	putative protein centrin, Marsilea vesti	---	AT4G27280	1.59	0.67	1.25	0.252259	0.432967	-6.55
265936_at	putative potassium/proton antiporter	ATKEA4	AT2G19600	1.13	0.17	1.25	0.252263	0.432967	-6.55
250638_at	glycine-rich protein atGRP-6	GRP16	AT5G07540	-1.13	-0.18	-1.25	0.252315	0.433023	-6.55
255553_at	predicted protein of unknown function	---	AT4G01960	1.15	0.20	1.25	0.252384	0.433109	-6.55
249263_at	putative protein contains similarity to u	---	AT5G41730	1.09	0.13	1.25	0.252417	0.433132	-6.55
252799_at	putative protein various predicted Heli	---	---	-1.08	-0.11	-1.25	0.252482	0.433212	-6.55
245033_at	putative disease resistance protein	---	AT2G26380	1.10	0.14	1.25	0.252524	0.433251	-6.55
248413_at	putative protein strong similarity to unk	PLE	AT5G51600	-1.11	-0.15	-1.25	0.252588	0.433328	-6.55
263647_at	unknown protein	---	AT2G04690	1.14	0.19	1.25	0.252659	0.433418	-6.55
262323_at	6-phosphogluconate dehydrogenase,	---	AT1G64190	1.09	0.12	1.25	0.252731	0.433486	-6.55

252867_at	putative protein hypothetical protein, S	---	AT4G39870	1.12	0.17	1.25	0.252737	0.433486	-6.55
252843_at	glycine-rich protein other glycine-rich p	---	AT3G42130	1.14	0.18	1.25	0.252941	0.433803	-6.55
250412_at	putative protein synaptobrevin-like pro	ATVAMP713	AT5G11150	-1.14	-0.19	-1.25	0.252972	0.433825	-6.55
256645_at	hypothetical protein predicted by gene	---	AT3G24250	1.09	0.12	1.25	0.253291	0.434338	-6.55
250134_at	Expressed protein ; supported by cDN	---	---	1.12	0.17	1.25	0.253459	0.434594	-6.55
250760_at	unknown protein	---	AT5G06040	-1.10	-0.14	-1.25	0.253525	0.434674	-6.55
259638_at	coatomer complex subunit, putative si	---	AT1G52360	-1.12	-0.17	-1.25	0.25371	0.434959	-6.55
248010_at	peroxisomal targeting signal type 1 rec	PEX5	AT5G56290	1.09	0.12	1.25	0.25375	0.434962	-6.55
255395_at	hypothetical protein	---	---	-1.09	-0.13	-1.25	0.253745	0.434962	-6.55
257627_at	cytochrome P450, putative contains P	CYP71B25	AT3G26270	1.11	0.15	1.25	0.253798	0.435011	-6.55
267148_at	hypothetical protein predicted by gens	---	AT2G23470	1.13	0.18	1.25	0.253853	0.435073	-6.55
247933_at	putative protein non-consensus CG d	---	AT5G56980	1.30	0.38	1.25	0.254024	0.435333	-6.55
259002_at	putative glutaredoxin similar to glutare	ROXY1	AT3G02000	-1.15	-0.21	-1.25	0.254067	0.435375	-6.55
256782_at	dirigent protein, putative similar to diri	---	AT3G13660	1.08	0.12	1.25	0.254087	0.435376	-6.55
252828_at	DnaJ - like protein DnaJ-like protein, P	---	AT4G39960	1.12	0.16	1.25	0.254156	0.435419	-6.55
267504_at	unknown protein ;supported by full-ler	---	AT2G45530	-1.13	-0.18	-1.25	0.25417	0.435419	-6.56
263577_at	putative protein kinase identical to hyp	SSP	AT2G17090	-1.13	-0.17	-1.25	0.254145	0.435419	-6.55
252989_at	putative pectinesterase pectinesterase	sks9	AT4G38420	-1.50	-0.58	-1.25	0.254265	0.43555	-6.56
264769_at	hypothetical protein predicted by gene	---	AT1G61350	1.24	0.31	1.25	0.254285	0.435552	-6.56
254979_at	subtilisin-like serine protease contains	---	AT4G10550	1.10	0.14	1.25	0.254351	0.435632	-6.56
265666_at	putative rac GTPase activating protein	---	AT2G27440	-1.08	-0.11	-1.25	0.254438	0.435748	-6.56
258759_at	putative bZIP transcription factor conta	BZIP28	AT3G10800	1.09	0.13	1.25	0.254463	0.435757	-6.56
259890_at	inner mitochondrial membrane protein	ATTIM23-2	AT1G72750	1.19	0.25	1.25	0.254514	0.435813	-6.56
252106_at	putative glutamate receptor putative g	ATGLR3.6	AT3G51480	-1.14	-0.19	-1.25	0.254558	0.435822	-6.56
246749_at	putative protein ; supported by cDNA:	---	AT5G27830	1.15	0.21	1.25	0.254541	0.435822	-6.56
246182_at	beta-1,3-glucanase - like protein prob	---	AT5G20870	-1.13	-0.18	-1.25	0.254578	0.435824	-6.56
256708_at	hypothetical protein predicted by gene	---	AT3G30320	1.09	0.13	1.25	0.254651	0.435917	-6.56
246522_at	bZIP DNA-binding protein-like putative	AtbZIP3	AT5G15830	-1.30	-0.38	-1.25	0.254711	0.435987	-6.56
254955_at	putative protein RNA polymerase II tra	KELP	AT4G10920	1.10	0.13	1.24	0.254772	0.436035	-6.56
AFFX-r2-E	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.28	0.35	1.24	0.254778	0.436035	-6.56
248017_at	protein kinase-like protein	---	AT5G56460	1.18	0.24	1.24	0.254883	0.436182	-6.56
263589_at	hypothetical protein predicted by gens	---	AT2G25280	1.09	0.12	1.24	0.254935	0.436207	-6.56
247293_at	putative protein similar to unknown pro	---	AT5G64510	1.40	0.48	1.24	0.254924	0.436207	-6.56
245800_at	heat shock transcription factor, putativ	HSFB4	AT1G46264	-1.10	-0.14	-1.24	0.254956	0.436209	-6.56
252881_at	putative protein predicted proteins, Ar	---	AT4G39610	1.15	0.20	1.24	0.254992	0.436239	-6.56

256936_at	prefoldin-like protein similar to prefold	PDF2	AT3G22480	-1.10	-0.14	-1.24	0.255018	0.436251	-6.56
264075_at	envelope-like protein identical to GB:A	---	---	-1.14	-0.19	-1.24	0.255091	0.436334	-6.56
256701_at	transcription initiation factor IIF, beta s	---	AT3G52270	-1.11	-0.15	-1.24	0.255105	0.436334	-6.56
257165_at	beta-1,3-glucanase, putative similar to	---	AT3G24330	-1.15	-0.21	-1.24	0.255135	0.436351	-6.56
247194_at	putative protein similar to unknown pro	---	AT5G65480	-1.16	-0.21	-1.24	0.255159	0.43636	-6.56
256730_at	floral homeotic protein AGL8, putative	AGL79	AT3G30260	-1.08	-0.11	-1.24	0.255194	0.436388	-6.56
245561_at	indole-3-acetate beta-glucosyltransfera	UGT84A4	AT4G15500	1.13	0.18	1.24	0.255305	0.436544	-6.56
249203_at	cytochrome P450	CYP71A16	AT5G42590	1.11	0.15	1.24	0.255566	0.436957	-6.56
246226_at	thiol-disulfide interchange like protein	HCF164	AT4G37200	1.15	0.20	1.24	0.255592	0.436969	-6.56
260447_at	hypothetical protein similar to N-term c	---	AT1G72410	-1.09	-0.12	-1.24	0.255744	0.437196	-6.56
246413_at	unknown protein	---	AT1G77310	1.11	0.15	1.24	0.255862	0.437366	-6.56
249429_at	putative protein	---	AT5G39880	-1.08	-0.11	-1.24	0.255933	0.437442	-6.56
255006_at	putative protein kinase M.sativa mRN	---	AT4G10010	-1.09	-0.13	-1.24	0.255945	0.437442	-6.56
254998_at	choline kinase GmCK2p -like protein c	---	AT4G09760	-1.20	-0.27	-1.24	0.255987	0.437481	-6.56
260886_at	hypothetical protein contains similarity	---	AT1G29200	-1.09	-0.12	-1.24	0.256134	0.43757	-6.56
260619_at	glyoxalase I, putative similar to GB:Y1	---	AT1G08110	1.14	0.18	1.24	0.256135	0.43757	-6.56
266655_at	putative protein kinase contains a prot	AtAUR2	AT2G25880	-1.14	-0.19	-1.24	0.25608	0.43757	-6.56
254587_at	resistance protein RPP5 - like downy	---	AT4G19520	1.12	0.16	1.24	0.256118	0.43757	-6.56
257246_at	pectinesterase, putative contains Pfar	---	AT3G24130	1.10	0.13	1.24	0.25606	0.43757	-6.56
249972_at	tRNA isopentenyltransferase -like prot	IPT5	AT5G19040	-1.10	-0.14	-1.24	0.256256	0.437712	-6.56
266352_at	unknown protein	---	AT2G01610	1.34	0.43	1.24	0.25624	0.437712	-6.56
249790_at	putative protein similar to unknown pro	---	AT5G24290	1.50	0.58	1.24	0.256357	0.437819	-6.56
251938_at	60S RIBOSOMAL PROTEIN L12 -like	---	AT3G53430	-1.14	-0.19	-1.24	0.256346	0.437819	-6.56
258479_at	hypothetical protein predicted by gens	---	AT3G02440	1.11	0.15	1.24	0.256497	0.438016	-6.56
246750_at	putative protein predicted proteins, Dr	AT5G27860	---	1.18	0.24	1.24	0.256529	0.438016	-6.56
252153_at	putative protein several hypothetical pr	---	AT3G51360	1.14	0.18	1.24	0.25653	0.438016	-6.56
259013_at	unknown protein similar to putative pro	emb1990	AT3G07430	-1.10	-0.14	-1.24	0.256586	0.438079	-6.56
262471_at	hypothetical protein similar to hypothet	---	AT1G50140	1.12	0.17	1.24	0.256627	0.438116	-6.56
256030_at	hypothetical protein contains similarity	---	AT1G34110	-1.11	-0.15	-1.24	0.256704	0.438215	-6.56
256454_at	NADPH oxidoreductase, putative simi	---	AT1G75280	-1.31	-0.39	-1.24	0.256905	0.438525	-6.56
246877_at	putative protein various predicted prot	---	AT5G26150	-1.08	-0.11	-1.24	0.256926	0.438528	-6.56
259628_at	hypothetical protein contains Pfam pro	---	AT1G56440	1.15	0.21	1.24	0.257	0.438621	-6.56
261852_at	unknown protein ;supported by full-len	---	AT1G50440	1.09	0.12	1.24	0.257061	0.43866	-6.56
266605_at	putative SNF2 subfamily transcriptiona	BRM	AT2G46020	1.10	0.13	1.24	0.257044	0.43866	-6.56
257588_x_	En/Spm-like transposon protein, putat	---	---	1.15	0.20	1.24	0.257171	0.438814	-6.57

266773_at	hypothetical protein predicted by gens	---	AT2G29040	-1.10	-0.14	-1.24	0.257217	0.438827	-6.57
262927_at	hypothetical protein shares similarity to	---	AT1G65810	-1.10	-0.14	-1.24	0.257205	0.438827	-6.57
251842_at	extensin precursor -like protein extens	---	AT3G54580	1.28	0.35	1.24	0.257308	0.438949	-6.57
252899_at	putative protein leaf protein, Ipomoea	---	AT4G39530	1.11	0.15	1.24	0.257394	0.439063	-6.57
262450_at	hypothetical protein identical to hypoth	---	AT1G11320	-1.12	-0.17	-1.24	0.257433	0.439097	-6.57
247637_at	putative protein gcpE protein, Chlamy	HDS	AT5G60600	1.14	0.19	1.24	0.257496	0.439171	-6.57
248947_at	putative protein similar to unknown pro	---	AT5G45540	-1.14	-0.19	-1.24	0.257573	0.43927	-6.57
249436_at	putative protein crp1 protein - Zea ma	---	AT5G39980	-1.17	-0.22	-1.24	0.257592	0.43927	-6.57
256609_at	hypothetical protein predicted by gene	---	---	1.09	0.12	1.24	0.257679	0.439385	-6.57
255415_at	hypothetical protein	---	AT4G03160	1.08	0.11	1.24	0.257768	0.439504	-6.57
251627_at	glucan endo-1,3-beta-D-glucosidase-l	BG1	AT3G57270	1.11	0.15	1.24	0.257831	0.439578	-6.57
264249_at	vacuolar-type H+-translocating inorgar	AVP2	AT1G78920	1.11	0.16	1.24	0.257884	0.439636	-6.57
258817_at	hypothetical protein similar to hypothe	---	AT3G04750	1.09	0.12	1.24	0.257966	0.439645	-6.57
249955_at	sugar transporter - like protein probab	---	AT5G18840	-1.28	-0.36	-1.24	0.257937	0.439645	-6.57
256548_at	hypothetical protein contains similarity	---	AT3G14770	1.69	0.76	1.24	0.257949	0.439645	-6.57
250315_at	putative protein contains similarity to tr	PDE149	AT5G12130	-1.20	-0.26	-1.24	0.257943	0.439645	-6.57
258193_at	putative pectinesterase similar to pecti	PME31	AT3G29090	1.09	0.12	1.24	0.258015	0.439689	-6.57
265398_at	unknown protein	ATMAK10	AT2G11000	1.10	0.14	1.24	0.25803	0.439689	-6.57
261699_at	hypothetical protein identical to hypoth	---	AT1G32660	-1.11	-0.15	-1.24	0.258112	0.439761	-6.57
265949_at	putative vicilin storage protein (globulir	---	AT2G18540	-1.08	-0.11	-1.24	0.258101	0.439761	-6.57
253932_at	putative protein other Arabidopsis puta	---	AT4G26800	1.09	0.12	1.24	0.258159	0.439781	-6.57
248830_at	putative protein contains similarity to S	---	AT5G47150	1.11	0.15	1.24	0.258162	0.439781	-6.57
265545_at	putative protein kinase contains a prot	NCRK	AT2G28250	-1.12	-0.16	-1.23	0.258219	0.439845	-6.57
253687_at	putative protein ;supported by full-leng	---	AT4G29520	1.57	0.65	1.23	0.25826	0.439882	-6.57
259916_at	hypothetical protein predicted by gene	---	AT1G72600	-1.08	-0.11	-1.23	0.258348	0.439999	-6.57
253334_at	putative protein dihydrokaempferol 4-r	---	AT4G33360	1.17	0.22	1.23	0.258462	0.440161	-6.57
244976_at	cytochrome B6	---	---	1.09	0.13	1.23	0.258524	0.440234	-6.57
252279_at	1-aminocyclopropane-1-carboxylate s	ACS9	AT3G49700	-1.12	-0.16	-1.23	0.258551	0.440247	-6.57
267243_at	hypothetical protein predicted by gens	---	AT2G02660	-1.08	-0.11	-1.23	0.258588	0.440277	-6.57
258899_at	Expressed protein ; supported by full-le	---	AT3G05675	-1.13	-0.17	-1.23	0.25862	0.440293	-6.57
263694_at	putative reverse transcriptase strong s	---	---	1.08	0.12	1.23	0.258645	0.440293	-6.57
249562_at	disease resistance protein-like	---	AT5G38350	-1.10	-0.14	-1.23	0.258655	0.440293	-6.57
262204_at	unknown protein ; supported by full-le	---	AT2G01100	1.10	0.14	1.23	0.258808	0.44052	-6.57
267596_s_	putative leucine-rich repeat disease re	AtRLP26	AT2G33050 /	1.29	0.37	1.23	0.258827	0.44052	-6.57
257685_at	unknown protein	---	AT3G12770	1.12	0.17	1.23	0.258898	0.44059	-6.57

256766_at	Expressed protein ; supported by cDN	PCC1	AT3G22231	-2.67	-1.42	-1.23	0.258937	0.44059	-6.57
252701_at	hypothetical protein SPOP protein, Hc	ATBPM6	AT3G43700	-1.13	-0.18	-1.23	0.258931	0.44059	-6.57
251608_at	putative protein hypothetical protein A	UVI4-LIKE	AT3G57860	-1.12	-0.17	-1.23	0.258946	0.44059	-6.57
254948_at	putative protein various predicted prot	---	AT4G11000	1.11	0.16	1.23	0.259071	0.44077	-6.57
256004_at	retroelement pol polyprotein, putative	---	---	-1.09	-0.12	-1.23	0.259091	0.440771	-6.57
260036_at	putative protein kinase Pfam HMM hit:	STN7	AT1G68830	-1.13	-0.17	-1.23	0.259146	0.440832	-6.57
262365_at	disease resistance protein, putative si	---	AT1G72870	1.12	0.17	1.23	0.259209	0.440906	-6.57
264426_at	hypothetical protein similar to hypothet	---	AT1G61760	-1.12	-0.16	-1.23	0.259325	0.44107	-6.57
264679_s_	putative 60S ribosomal protein L21 Si	---	AT1G09590 /	-1.18	-0.24	-1.23	0.259553	0.441395	-6.57
253918_at	putative protein ; supported by full-len	PHOS34	AT4G27320	1.11	0.15	1.23	0.259594	0.441395	-6.57
265245_at	unknown protein	---	AT2G43060	-1.20	-0.27	-1.23	0.259555	0.441395	-6.57
265224_at	putative pectinesterase	---	AT2G36710	-1.10	-0.14	-1.23	0.259612	0.441395	-6.57
250592_at	putative protein contains similarity to u	---	AT5G07740	1.12	0.17	1.23	0.259611	0.441395	-6.57
258521_at	ribosomal protein L29, putative similar	---	AT3G06680	-1.28	-0.35	-1.23	0.259645	0.441418	-6.57
253645_at	putative protein G protein beta subuni	VIP3	AT4G29830	-1.10	-0.13	-1.23	0.259698	0.441474	-6.57
246357_x_	hypothetical protein	---	---	-1.11	-0.15	-1.23	0.25974	0.441513	-6.57
255827_at	unknown protein ; supported by cDNA	---	AT2G40600	1.12	0.16	1.23	0.259792	0.441568	-6.57
255707_at	predicted protein	MEE50	AT4G00231	-1.09	-0.12	-1.23	0.259818	0.44158	-6.57
262419_at	hypothetical protein identical to hypoth	---	AT1G50380	1.14	0.19	1.23	0.259867	0.44163	-6.57
246388_at	hypothetical protein predicted by gens	---	AT1G77405	1.14	0.19	1.23	0.25999	0.441807	-6.57
249975_s_	ribosomal protein L33 - like ribosomal	---	AT3G06320 /	-1.19	-0.25	-1.23	0.260048	0.441823	-6.57
249676_at	serine/threonine protein kinase-like	---	AT5G35960	1.12	0.16	1.23	0.260058	0.441823	-6.57
249260_at	Pto kinase interactor 1-like protein	---	AT5G41680	1.11	0.15	1.23	0.260044	0.441823	-6.57
250156_at	putative protein predicted proteins, Hc	---	AT5G15170	-1.09	-0.12	-1.23	0.260085	0.441837	-6.57
254751_at	hypothetical protein	---	AT4G13150	1.09	0.13	1.23	0.260357	0.442266	-6.58
261081_at	transformer-SR ribonucleoprotein, put	---	AT1G07350	-1.17	-0.23	-1.23	0.260477	0.442437	-6.58
259654_at	hypothetical protein predicted by gene	---	AT1G55220	1.11	0.15	1.23	0.260538	0.442508	-6.58
248295_at	putative protein contains similarity to ri	---	AT5G53070	-1.11	-0.15	-1.23	0.26061	0.442564	-6.58
266080_at	hypothetical protein predicted by gens	---	AT2G37840	-1.08	-0.11	-1.23	0.260606	0.442564	-6.58
253749_at	phytochrome-associated protein PAP2	PAP2	AT4G29080	-1.64	-0.71	-1.23	0.260689	0.442665	-6.58
264707_at	unknown protein	---	AT1G09730	1.10	0.13	1.23	0.260754	0.442709	-6.58
267333_at	putative WD-40 repeat protein contains	---	AT2G19430	-1.09	-0.13	-1.23	0.260738	0.442709	-6.58
258701_at	putative RNA helicase similar to RNA	---	AT3G09720	1.18	0.24	1.23	0.260924	0.442921	-6.58
262892_at	succinic semialdehyde dehydrogenas	ALDH5F1	AT1G79440	-1.09	-0.13	-1.23	0.260937	0.442921	-6.58
258644_at	putative RNA-binding protein contains	---	AT3G07810	-1.08	-0.11	-1.23	0.260933	0.442921	-6.58

255272_at	putative protein (ubiquitin like) to vario	---	AT4G05270	-1.08	-0.11	-1.23	0.260999	0.442993	-6.58
267582_at	putative protein kinase contains a prot	---	AT2G41970	-1.10	-0.13	-1.23	0.261093	0.44312	-6.58
263964_at	putative CCHC-type zinc finger protein	---	AT2G12880	-1.12	-0.16	-1.23	0.261184	0.443242	-6.58
255482_at	putative chloroplast outer envelope 86	TOC159	AT4G02510	1.10	0.13	1.23	0.261344	0.443381	-6.58
263416_at	hypothetical protein contains protein ki	---	AT2G17170	1.10	0.14	1.23	0.261326	0.443381	-6.58
260663_at	hypothetical protein predicted by gens	NFD5	AT1G19520	-1.18	-0.23	-1.23	0.261359	0.443381	-6.58
248805_at	putative protein similar to unknown pro	---	AT5G47480	1.09	0.13	1.23	0.261363	0.443381	-6.58
254735_at	putative disease resistance protein Cf	AtRLP47	AT4G13810	1.12	0.16	1.23	0.261306	0.443381	-6.58
262010_at	hypothetical protein predicted by gene	---	---	1.11	0.15	1.23	0.261487	0.443557	-6.58
266728_at	similar to late embryogenesis abundan	---	AT2G03140	1.10	0.14	1.23	0.261521	0.443583	-6.58
262867_at	hypothetical protein predicted by gens	---	AT1G64960	1.11	0.15	1.23	0.261609	0.443699	-6.58
251808_at	AP3-complex beta-3A adaptin subunit	---	AT3G55480	-1.11	-0.15	-1.23	0.261634	0.443708	-6.58
256840_x_	unknown protein similar to putative Ath	---	---	-1.08	-0.11	-1.23	0.261671	0.443738	-6.58
251553_at	DNA-binding WRKY - like protein AR4	WRKY69	AT3G58710	1.13	0.18	1.22	0.261728	0.443801	-6.58
263214_at	hypothetical protein predicted by gens	---	AT1G30660	1.12	0.16	1.22	0.261852	0.443978	-6.58
251312_at	MADS-box protein AGL13 ; supported	AGL13	AT3G61120	-1.10	-0.13	-1.22	0.261895	0.443986	-6.58
258310_at	unknown protein	ICE1	AT3G26744	-1.11	-0.15	-1.22	0.261882	0.443986	-6.58
254840_at	hypothetical protein	---	AT4G11930	-1.15	-0.20	-1.22	0.261952	0.444031	-6.58
247257_at	proteasome regulatory subunit-like ; s	RPN5B	AT5G64760	-1.23	-0.30	-1.22	0.261961	0.444031	-6.58
245342_at	ribosomal protein ;supported by full-ler	---	AT4G16720	-1.15	-0.21	-1.22	0.262002	0.444056	-6.58
254223_at	putative protein Pennisetum ciliare po	---	AT4G23730	1.08	0.12	1.22	0.262014	0.444056	-6.58
247431_at	putative protein similar to unknown pro	SRO5	AT5G62520	1.25	0.32	1.22	0.262056	0.444094	-6.58
257749_at	actin 2 identical to GB:AAB37098 from	ACT2	AT3G18780	-1.09	-0.13	-1.22	0.262217	0.444333	-6.58
250669_at	polygalacturonase inhibiting protein ;s	PGIP2	AT5G06870	-1.34	-0.42	-1.22	0.262418	0.444542	-6.58
245034_at	putative serpin	---	AT2G26390	1.13	0.18	1.22	0.262413	0.444542	-6.58
249545_at	putative transmembrane protein putat	---	AT5G38030	-1.09	-0.12	-1.22	0.262376	0.444542	-6.58
248546_at	putative protein similar to unknown pro	---	AT5G50270	-1.08	-0.11	-1.22	0.262392	0.444542	-6.58
248426_at	putative protein contains similarity to p	---	AT5G51740	1.09	0.12	1.22	0.262506	0.444625	-6.58
258476_at	hypothetical protein predicted by gene	---	AT3G02400	-1.14	-0.19	-1.22	0.262486	0.444625	-6.58
266196_at	putative protein kinase contains a prot	---	AT2G39110	-1.10	-0.14	-1.22	0.262584	0.444724	-6.58
255044_at	putative protein	---	AT4G09680	-1.11	-0.15	-1.22	0.262821	0.445091	-6.58
258240_at	oleosin isoform identical to oleosin isof	OLEO4	AT3G27660	-1.11	-0.15	-1.22	0.262874	0.445148	-6.58
260533_at	putative U1 small nuclear ribonucleopr	---	AT2G43370	1.09	0.13	1.22	0.262898	0.445157	-6.58
262999_at	NAM protein, putative similar to NAM	ANAC020	AT1G54330	-1.14	-0.20	-1.22	0.263043	0.445342	-6.58
252051_at	putative protein similarity hypothetical	---	AT3G52570	-1.09	-0.13	-1.22	0.263047	0.445342	-6.58

267620_at	putative beta-1,3-glucanase	---	AT2G39640	-1.09	-0.13	-1.22	0.263101	0.445402	-6.58
248603_at	WD-40 repeat protein-like	---	AT5G49430	1.09	0.12	1.22	0.263261	0.445625	-6.58
256410_at	hypothetical protein	---	AT1G66630	1.08	0.10	1.22	0.263273	0.445625	-6.58
256198_at	Myb-family transcription factor, putativ	---	AT1G58220	-1.15	-0.20	-1.22	0.263301	0.44564	-6.59
259527_at	hypothetical protein	---	AT1G12600	1.08	0.11	1.22	0.263346	0.445684	-6.59
257318_at	hypothetical protein	---	AT2G07777	-1.10	-0.13	-1.22	0.263404	0.445748	-6.59
254192_at	acyl-CoA synthetase - like protein acy	---	AT4G23850	-1.10	-0.14	-1.22	0.263475	0.445785	-6.59
252360_at	putative protein predicted protein, Ara	---	AT3G48480	1.13	0.17	1.22	0.263478	0.445785	-6.59
248922_at	putative protein contains similarity to h	WOX8	AT5G45980	1.09	0.12	1.22	0.263503	0.445785	-6.59
263185_at	transport protein, putative similar to tra	---	AT1G05520	1.08	0.12	1.22	0.263504	0.445785	-6.59
257322_at	hypothetical protein	AT2G07667	---	-1.11	-0.16	-1.22	0.263527	0.445792	-6.59
263420_at	unknown protein ; supported by full-le	---	AT2G17240	-1.09	-0.13	-1.22	0.263611	0.4459	-6.59
266987_at	unknown protein	---	AT2G39280	-1.08	-0.11	-1.22	0.263681	0.445986	-6.59
253725_at	profilin 3 ;supported by full-length cDN	PRF4	AT4G29340	1.10	0.14	1.22	0.263898	0.44632	-6.59
258463_at	putative protein kinase similar to Pto ki	---	AT3G17410	1.12	0.17	1.22	0.263948	0.446371	-6.59
251702_at	transcription factor-like protein motif ir	BZIP49	AT3G56660	1.14	0.19	1.22	0.26405	0.44651	-6.59
249422_at	putative protein predicted proteins, Ar	AtHB23	AT5G39760	-1.12	-0.17	-1.22	0.264222	0.446768	-6.59
264051_at	hypothetical protein predicted by gens	---	AT2G22340	-1.10	-0.13	-1.22	0.264245	0.446773	-6.59
266501_at	unknown protein ; supported by cDNA	HEN2	AT2G06990	1.12	0.16	1.22	0.264356	0.446929	-6.59
260788_at	cysteine proteinase contains similarity	---	AT1G06260	1.09	0.13	1.22	0.264616	0.447335	-6.59
246273_at	globulin-like protein	---	AT4G36700	-1.09	-0.12	-1.22	0.264708	0.447457	-6.59
257407_at	unknown protein	---	AT1G27100	1.10	0.14	1.22	0.264849	0.447563	-6.59
254007_s_	putative protein RNA-directed DNA po	---	AT1G60720	-1.09	-0.13	-1.22	0.264803	0.447563	-6.59
248341_at	unknown protein	---	AT5G52220	-1.14	-0.18	-1.22	0.264847	0.447563	-6.59
261503_at	hypothetical protein predicted by gene	---	AT1G71691	-1.11	-0.15	-1.22	0.264814	0.447563	-6.59
263636_at	unknown protein ; supported by full-le	---	AT2G11910	-1.11	-0.15	-1.22	0.2649	0.447615	-6.59
257301_at	hypothetical protein predicted by gene	---	---	-1.09	-0.12	-1.22	0.264928	0.447631	-6.59
252198_x_	putative protein predicted protein, Ara	---	AT3G50250	1.16	0.21	1.22	0.26497	0.447668	-6.59
264306_at	unknown protein predicted by genema	---	AT1G78890	1.12	0.16	1.22	0.26502	0.447699	-6.59
250901_at	putative protein ; supported by cDNA:	RABC2A	AT5G03530	-1.38	-0.47	-1.22	0.265028	0.447699	-6.59
263236_at	putative response regulator 3 similar t	ARR4	AT1G10470	-1.18	-0.24	-1.22	0.265098	0.447785	-6.59
262519_at	putative ribokinase Except for first 69	---	AT1G17160	1.17	0.22	1.22	0.265174	0.44788	-6.59
253487_at	ribosomal protein S6 - like ribosomal p	RPS6	AT4G31700	-1.29	-0.36	-1.22	0.265223	0.447929	-6.59
244964_at	PSII cytochrome b559	---	---	-1.07	-0.10	-1.22	0.265246	0.447936	-6.59
253594_at	Expressed protein ; supported by full-le	---	AT4G30820	-1.12	-0.16	-1.21	0.265445	0.448229	-6.59

262388_at	unknown protein	---	AT1G49320	-1.11	-0.15	-1.21	0.265459	0.448229	-6.59
245650_at	F5A9.20 similar to S-adenosyl-L-methi	---	AT1G24735	-1.11	-0.16	-1.21	0.265576	0.448302	-6.59
263643_at	unknown protein predicted by genefinc	---	AT2G04740	1.16	0.21	1.21	0.265581	0.448302	-6.59
264631_at	DegP protease contains similarity to D	DegP3	AT1G65630	-1.11	-0.14	-1.21	0.265558	0.448302	-6.59
246185_at	5-methyltetrahydropteroyltriglutamate-	ATMS3	AT5G20980	-1.08	-0.11	-1.21	0.265541	0.448302	-6.59
248709_at	unknown protein ;supported by full-ler	---	AT5G48470	-1.18	-0.24	-1.21	0.265705	0.448442	-6.59
259169_at	unknown protein similar to unknown pr	---	AT3G03520	1.35	0.44	1.21	0.265723	0.448442	-6.59
266219_at	putative para-aminobenzoate synthas	emb1997	AT2G28880	-1.10	-0.14	-1.21	0.265716	0.448442	-6.59
249165_at	putative protein similar to unknown pro	ATIPK1	AT5G42810	-1.15	-0.21	-1.21	0.266001	0.448844	-6.59
263508_s_	hypothetical protein	---	---	-1.13	-0.18	-1.21	0.26599	0.448844	-6.59
248728_at	cytochrome P450-like protein	CYP708A2	AT5G48000	1.11	0.15	1.21	0.266083	0.448949	-6.59
264330_at	multi-drug resistance protein Strong si	ATMRP5	AT1G04120	1.10	0.13	1.21	0.266146	0.449023	-6.59
250341_at	MAP3K delta-1 protein kinase	---	AT5G11850	1.09	0.12	1.21	0.266269	0.449198	-6.59
248440_at	acid phosphatase	---	AT5G51260	1.12	0.16	1.21	0.266323	0.449254	-6.59
263437_at	putative disease resistance response p	---	AT2G28670	1.12	0.16	1.21	0.266381	0.44932	-6.59
253850_at	pectinesterase like protein pectinester	sks10	AT4G28090	-1.13	-0.18	-1.21	0.266435	0.449378	-6.60
246137_at	putative protein predicted proteins, Ar	LSH1	AT5G28490	1.29	0.36	1.21	0.266506	0.449463	-6.60
254002_at	steroid sulfotransferase - like protein s	---	AT4G26280	-1.08	-0.11	-1.21	0.266582	0.449559	-6.60
251117_at	putative protein predicted protein, Cae	---	AT3G63390	1.13	0.17	1.21	0.266632	0.449576	-6.60
246504_at	hypothetical protein ;supported by full-	---	AT5G16160	-1.08	-0.11	-1.21	0.266613	0.449576	-6.60
245739_at	mitotic cyclin a2-type, putative similar	CYCA1;1	AT1G44110	-1.09	-0.12	-1.21	0.266664	0.449597	-6.60
254849_at	putative protein RNA splicing-related p	---	AT4G11970	-1.08	-0.11	-1.21	0.266746	0.449702	-6.60
259352_at	unknown protein	---	AT3G05170	-1.19	-0.25	-1.21	0.266802	0.449731	-6.60
254412_at	putative protein chloroplast DNA-bindi	B160	AT4G21430	-1.17	-0.23	-1.21	0.2668	0.449731	-6.60
250303_at	putative protein similar to unknown pro	---	AT5G12100	1.20	0.26	1.21	0.266849	0.449737	-6.60
255792_at	AT-hook DNA-binding protein (AHP1)	---	AT2G33620	1.13	0.17	1.21	0.266865	0.449737	-6.60
251514_at	pirin-like protein pirin - Lycopersicon e	---	AT3G59260	1.11	0.15	1.21	0.266833	0.449737	-6.60
258696_at	hypothetical protein predicted by gens	HCF152	AT3G09650	1.17	0.23	1.21	0.26697	0.449848	-6.60
266083_at	hypothetical protein predicted by gens	---	AT2G37820	1.08	0.11	1.21	0.266954	0.449848	-6.60
251389_at	putative protein	---	AT3G60850	1.09	0.13	1.21	0.267047	0.449944	-6.60
267434_at	3-beta-hydroxysteroid dehydrogenase	AT3BETAHS	AT2G26260	-1.12	-0.16	-1.21	0.267106	0.450005	-6.60
256374_at	DNA ligase I, putative similar to DNA l	---	AT1G66730	-1.12	-0.16	-1.21	0.267122	0.450005	-6.60
249018_at	CHP-rich zinc finger protein-like	---	AT5G44770	-1.16	-0.21	-1.21	0.267204	0.450076	-6.60
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=gb:	---	---	-1.24	-0.31	-1.21	0.26719	0.450076	-6.60
265727_at	putative DNA topoisomerase III beta	---	AT2G32000	-1.10	-0.14	-1.21	0.267228	0.450082	-6.60

256267_at	unknown protein ; supported by cDNA	---	AT3G12260	-1.10	-0.13	-1.21	0.267329	0.45022	-6.60
265779_at	unknown protein	---	AT2G07360	-1.16	-0.22	-1.21	0.26745	0.45039	-6.60
265689_at	hypothetical protein predicted by gens	---	AT2G24310	-1.08	-0.12	-1.21	0.267533	0.450464	-6.60
262895_at	hypothetical protein predicted by gene	---	AT1G59800	1.13	0.17	1.21	0.26752	0.450464	-6.60
267478_at	hypothetical protein predicted by gens	---	AT2G02700	1.08	0.12	1.21	0.267629	0.450592	-6.60
259924_at	putative DNA-binding protein similar to	---	AT1G72740	-1.11	-0.16	-1.21	0.267795	0.450775	-6.60
265664_at	unknown protein predicted by genscan	---	AT2G24420	-1.12	-0.16	-1.21	0.267797	0.450775	-6.60
254886_at	putative protein bp4A protein, Brassic	LCR17	AT4G11760	-1.11	-0.15	-1.21	0.267771	0.450775	-6.60
259826_at	arm repeat-containing protein, putativ	PUB17	AT1G29340	1.17	0.23	1.21	0.26792	0.450882	-6.60
247840_at	putative protein protein x 0001, Homo	---	AT5G58020	1.08	0.12	1.21	0.267919	0.450882	-6.60
263313_at	14-3-3 protein (grf15), putative contai	---	AT2G10450	1.10	0.14	1.21	0.267915	0.450882	-6.60
266461_at	glutathione S-transferase (GST6) ider	ATGSTF8	AT2G47730	-1.19	-0.25	-1.21	0.268062	0.451045	-6.60
264440_at	unknown protein similar to fim protein	---	AT1G27340	1.09	0.12	1.21	0.268087	0.451045	-6.60
259233_at	hypothetical protein	---	AT3G11380	1.08	0.11	1.21	0.268096	0.451045	-6.60
260232_at	unknown protein contains Pfam profile	---	AT1G74640	1.19	0.25	1.21	0.268089	0.451045	-6.60
256512_at	Expressed protein ; supported by full-l	---	AT1G33265	-1.12	-0.17	-1.21	0.268237	0.451246	-6.60
264732_at	serpin, putative similar to serpin GI:11	---	AT1G62160	1.08	0.11	1.21	0.268274	0.451246	-6.60
247203_at	unknown protein ; supported by cDNA	---	AT5G65180	-1.09	-0.13	-1.21	0.268256	0.451246	-6.60
250447_at	putative protein KIAA0332 gene, Hom	---	AT5G10800	-1.09	-0.12	-1.21	0.268306	0.451266	-6.60
252633_x_	putative protein HISTONE DEACETYI	hda17	AT3G44490 /	1.08	0.11	1.21	0.268412	0.45141	-6.60
247109_at	putative protein similar to unknown pro	ATPSK5	AT5G65870	1.23	0.30	1.21	0.268515	0.45155	-6.60
254741_s_	putative disease resistance protein Hc	AtRLP49	AT4G13900 /	-1.08	-0.12	-1.21	0.268552	0.45158	-6.60
253152_at	putative protein predicted proteins, Ar	---	AT4G35690	-1.12	-0.16	-1.21	0.268582	0.451596	-6.60
263585_at	60S ribosomal protein L39	---	AT2G25210	-1.24	-0.30	-1.21	0.268698	0.451743	-6.60
264445_at	unknown protein similar to ESTs gb|T	---	AT1G27290	-1.18	-0.24	-1.21	0.268729	0.451743	-6.60
261243_at	hypothetical protein predicted by gene	---	AT1G20180	1.31	0.39	1.21	0.268711	0.451743	-6.60
265197_at	putative glucosyl transferase	UGT73C1	AT2G36750	1.08	0.11	1.20	0.269036	0.452126	-6.60
267540_at	hypothetical protein predicted by gens	---	AT2G32760	-1.09	-0.12	-1.20	0.269027	0.452126	-6.60
249508_at	unknown protein	---	AT5G38380	-1.10	-0.13	-1.20	0.269013	0.452126	-6.60
250218_at	putative protein contains similarity to u	CHC1	AT5G14170	-1.14	-0.18	-1.20	0.268982	0.452126	-6.60
256653_at	hypothetical protein predicted by gene	---	AT3G18870	1.10	0.14	1.20	0.269076	0.45216	-6.60
261817_at	hypothetical protein predicted by gene	---	AT1G08180	1.23	0.30	1.20	0.26912	0.452201	-6.60
265511_at	putative glycine-rich protein ; supporte	---	AT2G05540	1.15	0.21	1.20	0.269197	0.452253	-6.60
267429_at	putative UDP-galactose-4-epimerase	MEE25	AT2G34850	-1.15	-0.21	-1.20	0.269219	0.452253	-6.60
252894_at	hypothetical protein	---	AT4G39440	-1.12	-0.16	-1.20	0.26923	0.452253	-6.60

263245_at	hypothetical protein predicted by gens	---	AT2G31470	-1.08	-0.11	-1.20	0.26923	0.452253	-6.60
262353_at	hypothetical protein similar to hypothet	---	AT1G64210	-1.08	-0.11	-1.20	0.269325	0.452286	-6.60
249447_at	PTEN -like protein PTEN/MMAC1, Ra	PTEN1	AT5G39400	-1.15	-0.21	-1.20	0.26933	0.452286	-6.60
257815_at	unknown protein	---	AT3G25130	-1.10	-0.14	-1.20	0.269328	0.452286	-6.60
244977_at	cytochrome b/f	---	---	-1.21	-0.27	-1.20	0.269317	0.452286	-6.60
259475_at	unknown protein ;supported by full-len	---	AT1G19140	1.18	0.23	1.20	0.269351	0.452289	-6.60
261586_at	hypothetical protein predicted by gene	---	AT1G01640	1.23	0.30	1.20	0.26942	0.452372	-6.60
266468_at	unknown protein ; supported by cDNA:	---	AT2G47960	-1.12	-0.16	-1.20	0.269445	0.452381	-6.60
254456_at	putative protein ribophorin II precurso	HAP6	AT4G21150	1.12	0.17	1.20	0.269514	0.452462	-6.60
259967_at	putative DNA-binding protein contains	---	AT1G76510	1.09	0.12	1.20	0.269605	0.452526	-6.61
256521_at	AMP-binding enzyme, putative contai	---	AT1G66120	1.10	0.14	1.20	0.269598	0.452526	-6.61
267098_at	hypothetical protein predicted by gens	---	AT2G41451	1.12	0.17	1.20	0.269611	0.452526	-6.61
260416_at	putative cullin similar to cullin 3 GB:45	CUL3B	AT1G69670	1.10	0.13	1.20	0.269867	0.452872	-6.61
253525_at	predicted protein ; supported by cDNA	---	AT4G31330	-1.11	-0.15	-1.20	0.269877	0.452872	-6.61
248732_at	xyloglucan endo-1,4-beta-D-glucanas	XTH20	AT5G48070	-1.13	-0.17	-1.20	0.269839	0.452872	-6.61
261359_at	hypothetical protein predicted by gens	---	---	-1.10	-0.14	-1.20	0.26997	0.452994	-6.61
252942_at	putative protein ;supported by full-leng	---	AT4G39300	1.12	0.16	1.20	0.270057	0.453108	-6.61
245680_at	hypothetical protein contains similarity	---	AT1G56570	-1.10	-0.13	-1.20	0.270184	0.453288	-6.61
247565_at	putative protein Atu, Drosophila melar	VIP4	AT5G61150	1.10	0.13	1.20	0.270323	0.453487	-6.61
245239_at	putative homeodomain-protein similar	FWA	AT4G25530	-1.11	-0.14	-1.20	0.270448	0.453664	-6.61
262486_at	putative bzip-like transcription factor s	---	AT1G21740	-1.15	-0.20	-1.20	0.27053	0.453769	-6.61
266933_at	putative Ta11-like non-LTR retroeleme	---	AT2G07760	-1.13	-0.17	-1.20	0.270561	0.453786	-6.61
258313_at	unknown protein contains RanBP1 dor	---	AT3G15970	-1.09	-0.12	-1.20	0.270588	0.453798	-6.61
245473_at	hypothetical protein	---	AT4G16050	-1.08	-0.12	-1.20	0.270647	0.453863	-6.61
252742_at	putative protein glyceraldehyde-3-pho	---	AT3G43290	-1.13	-0.17	-1.20	0.270669	0.453867	-6.61
265106_s_	putative membrane-associated salt-inc	---	AT1G62590 /	1.08	0.11	1.20	0.270733	0.453941	-6.61
255971_at	transposon related protein similar to re	---	---	1.08	0.11	1.20	0.270754	0.453944	-6.61
247703_at	putative protein predicted proteins, Ho	SRR1	AT5G59560	-1.11	-0.15	-1.20	0.270781	0.453956	-6.61
254055_at	hypothetical protein	---	AT4G25330	1.09	0.13	1.20	0.270883	0.454092	-6.61
263359_at	putative lysosomal acid lipase	ATLIP1	AT2G15230	-1.12	-0.16	-1.20	0.27096	0.454121	-6.61
266020_at	hypothetical protein	SDG11	AT2G05900	1.13	0.17	1.20	0.270937	0.454121	-6.61
245653_at	heat shock transcription factor like pro	FBD1	AT4G13985	-1.10	-0.14	-1.20	0.270948	0.454121	-6.61
256203_at	hypothetical protein	---	AT1G50800	-1.10	-0.14	-1.20	0.271093	0.454311	-6.61
249512_at	DNA repair protein RAD23 homolog ;s	---	AT5G38470	1.08	0.11	1.20	0.271317	0.454653	-6.61
245707_at	NAC2-like protein	anac077	AT5G04400	-1.11	-0.15	-1.20	0.271433	0.454781	-6.61

262627_at	hypothetical protein	---	AT1G06580	-1.11	-0.15	-1.20	0.271426	0.454781	-6.61
258137_at	Expressed protein ; supported by cDN	UBC37	AT3G24515	-1.09	-0.12	-1.20	0.271709	0.45521	-6.61
264975_at	hypothetical protein predicted by gene	---	AT1G27070	-1.10	-0.14	-1.20	0.271838	0.455392	-6.61
246497_at	putative protein hypothetical proteins -	---	AT5G16220	-1.20	-0.26	-1.20	0.271869	0.455411	-6.61
248882_at	cullin ;supported by full-length cDNA:	CUL4	AT5G46210	-1.08	-0.12	-1.20	0.271942	0.455499	-6.61
266916_at	hypothetical protein predicted by gens	---	AT2G45860	-1.16	-0.22	-1.20	0.271976	0.455523	-6.61
248699_at	putative protein similar to unknown pro	ATZIP4	AT5G48390	1.14	0.19	1.20	0.272005	0.455539	-6.61
263958_at	putative salt-inducible protein	---	AT2G36240	-1.08	-0.11	-1.20	0.272234	0.455757	-6.61
264548_at	unknown protein ; supported by cDNA	---	AT1G55680	1.10	0.14	1.20	0.272251	0.455757	-6.61
246581_at	hypothetical protein predicted by gene	---	AT1G31760	-1.10	-0.14	-1.20	0.272255	0.455757	-6.61
256492_at	hypothetical protein contains similarity	---	AT1G31490	-1.12	-0.16	-1.20	0.272159	0.455757	-6.61
251279_at	hypothetical protein	---	AT3G61800	1.17	0.23	1.20	0.27224	0.455757	-6.61
263869_at	unknown protein	PROPEP6	AT2G22000	-1.08	-0.11	-1.20	0.272244	0.455757	-6.61
250593_at	putative protein similar to unknown pro	---	AT5G07740	1.09	0.12	1.20	0.272289	0.455759	-6.61
257979_at	unknown protein	---	AT3G20730	1.10	0.14	1.20	0.272308	0.455759	-6.61
262429_at	polyprotein, putative similar to polypro	---	---	1.12	0.16	1.20	0.272316	0.455759	-6.61
265217_s_	unknown protein ESTs gb|H76594 and	---	AT1G05090 /	-1.15	-0.20	-1.20	0.272343	0.45577	-6.61
249033_at	putative protein contains similarity to d	---	AT5G44920	1.10	0.14	1.20	0.272383	0.455804	-6.61
265459_at	unknown protein ; supported by full-le	---	AT2G46540	-1.09	-0.12	-1.20	0.272404	0.455805	-6.61
262810_at	putative salt-inducible protein similar to	---	AT1G11710	1.16	0.21	1.19	0.27262	0.456133	-6.61
256171_s_	hypothetical protein similar to reverse t	---	---	-1.11	-0.15	-1.19	0.272761	0.456335	-6.61
250126_at	ubiquitin C-terminal hydrolase-like prot	UCH1	AT5G16310	-1.12	-0.16	-1.19	0.272897	0.456529	-6.62
266332_at	hypothetical protein predicted by gens	---	AT2G32415	-1.10	-0.14	-1.19	0.27295	0.456552	-6.62
254391_at	putative bifunctional nuclease bifuncti	ENDO3	AT4G21590	-1.09	-0.12	-1.19	0.272933	0.456552	-6.62
267563_at	putative protein kinase contains a prot	---	AT2G30730	-1.10	-0.13	-1.19	0.273046	0.456645	-6.62
252398_at	putative protein RING-H2 finger protei	---	AT3G47990	-1.10	-0.14	-1.19	0.273044	0.456645	-6.62
257871_at	hypothetical protein predicted by gens	---	AT3G28350	1.09	0.12	1.19	0.273079	0.456666	-6.62
254492_at	endomembrane-associated protein ; s	PCAP1	AT4G20260	1.11	0.15	1.19	0.273137	0.456671	-6.62
264617_at	unknown protein	---	AT2G17660	1.20	0.27	1.19	0.273115	0.456671	-6.62
246557_at	putative protein hypothetical protein T	---	AT5G15510	-1.09	-0.13	-1.19	0.273141	0.456671	-6.62
258016_at	hypothetical protein similar to poly(A)-b	MPC	AT3G19350	1.09	0.13	1.19	0.273164	0.456675	-6.62
249086_at	putative protein strong similarity to unk	---	AT5G44180	1.10	0.14	1.19	0.273211	0.45672	-6.62
245382_at	hypothetical protein	---	AT4G17800	1.10	0.13	1.19	0.273491	0.457154	-6.62
264939_at	receptor kinase, putative similar to rec	---	AT1G60630	-1.10	-0.14	-1.19	0.273543	0.457208	-6.62
259735_at	Expressed protein ; supported by full-le	---	AT1G64405	1.18	0.23	1.19	0.273663	0.457374	-6.62

249745_at	phloem-specific lectin-like protein	AtPP2-B12	AT5G24560	1.12	0.16	1.19	0.273736	0.457463	-6.62
259585_at	hypothetical protein contains similarity	---	AT1G28090	1.09	0.13	1.19	0.273797	0.457531	-6.62
259715_at	hypothetical protein predicted by gens	---	AT1G60990	1.12	0.17	1.19	0.273865	0.457578	-6.62
265069_at	awaiting functional assignment similar	---	AT1G55545	-1.10	-0.13	-1.19	0.273848	0.457578	-6.62
253762_at	putative protein conserved hypothetic	---	AT4G28830	-1.10	-0.14	-1.19	0.273899	0.457602	-6.62
246638_at	putative protein predicted proteins, Ar	---	---	-1.10	-0.14	-1.19	0.274028	0.457783	-6.62
264994_at	hypothetical protein contains similarity	---	AT1G67270	-1.09	-0.12	-1.19	0.274078	0.457834	-6.62
253721_at	hypothetical protein ;supported by full	---	AT4G29250	-1.13	-0.18	-1.19	0.274212	0.457848	-6.62
252129_at	putative protein hypothetical protein T	AtHB28	AT3G50890	1.11	0.15	1.19	0.274227	0.457848	-6.62
247046_at	unknown protein ; supported by cDNA	---	AT5G66540	1.10	0.14	1.19	0.274207	0.457848	-6.62
267225_at	hypothetical protein predicted by gens	---	AT2G44000	1.10	0.14	1.19	0.274171	0.457848	-6.62
267252_at	hypothetical protein predicted by gens	---	AT2G23100	-1.10	-0.14	-1.19	0.274225	0.457848	-6.62
248763_at	putative protein similar to unknown pro	---	AT5G47550	-1.98	-0.99	-1.19	0.274201	0.457848	-6.62
247557_at	putative protein	---	AT5G61050	1.08	0.11	1.19	0.274132	0.457848	-6.62
263844_at	unknown protein ; supported by cDNA	---	AT2G36930	1.24	0.31	1.19	0.27439	0.458086	-6.62
250070_at	phosphoribosylanthranilate transferase	---	AT5G17980	-1.18	-0.24	-1.19	0.274421	0.458105	-6.62
263810_at	putative translation initiation factor eIF	---	AT2G04520	1.08	0.11	1.19	0.274461	0.458137	-6.62
247140_at	putative protein similar to unknown pro	---	AT5G66250	1.09	0.13	1.19	0.274496	0.458163	-6.62
264682_at	polygalacturonase, putative similar to	---	AT1G65570	-1.08	-0.12	-1.19	0.274568	0.45821	-6.62
253148_at	cyclin 2b protein	CYCB2;2	AT4G35620	1.12	0.16	1.19	0.274584	0.45821	-6.62
264595_at	putative vesicle-associated membrane	VAMP721	AT1G04750	-1.14	-0.19	-1.19	0.274575	0.45821	-6.62
264009_at	putative disease resistance response p	---	AT2G21110	-1.09	-0.13	-1.19	0.27462	0.458236	-6.62
264274_at	disease resistance protein RPS4, puta	---	AT1G60320	1.10	0.14	1.19	0.274673	0.458291	-6.62
249082_at	legumin-like protein	CRA1	AT5G44120	-1.09	-0.13	-1.19	0.274718	0.458333	-6.62
251314_at	putative protein several hypothetical pr	---	AT3G61180	-1.07	-0.10	-1.19	0.274909	0.458617	-6.62
253379_at	putative protein glycogenin glucosyltra	PGSIP3	AT4G33330	-1.09	-0.13	-1.19	0.275081	0.458871	-6.62
252305_at	putative protein CRP1 protein, Zea ma	emb1796	AT3G49240	1.15	0.20	1.19	0.27531	0.459065	-6.62
264798_at	putative myosin MYA1, class V (Z283	XIC	AT1G08730	-1.09	-0.13	-1.19	0.27532	0.459065	-6.62
267284_at	unknown protein predicted by genscan	---	AT2G23700	1.13	0.18	1.19	0.275343	0.459065	-6.62
252407_at	chloroplast NAD-dependent malate de	MDH	AT3G47520	1.13	0.18	1.19	0.275266	0.459065	-6.62
262140_at	hypothetical protein predicted by gene	---	AT1G52470	1.09	0.12	1.19	0.275358	0.459065	-6.62
255030_at	putative protein retrovirus-related poly	---	---	-1.10	-0.13	-1.19	0.275283	0.459065	-6.62
256738_at	geranylgeranyl pyrophosphate syntha	---	AT3G29430	-1.11	-0.14	-1.19	0.275312	0.459065	-6.62
256167_at	hypothetical protein similar to putative	---	---	-1.09	-0.13	-1.19	0.275303	0.459065	-6.62
267041_at	unknown protein	---	AT2G34315	-1.08	-0.11	-1.19	0.275421	0.459102	-6.62

260122_at	AIG1-like protein similar to AIG1 prote	---	AT1G33900	-1.11	-0.16	-1.19	0.275408	0.459102	-6.62
266053_at	unknown protein	---	AT2G40730	-1.11	-0.15	-1.19	0.27555	0.459149	-6.62
254646_at	putative protein	---	AT4G18530	1.13	0.18	1.19	0.275526	0.459149	-6.62
255056_at	putative protein helix-loop-helix protei	TT8	AT4G09820	-1.08	-0.11	-1.19	0.275471	0.459149	-6.62
245850_at	ankyrin-repeat containing protein anky	KEG	AT5G13530	1.14	0.19	1.19	0.275521	0.459149	-6.62
254906_at	putative disease resistance response	---	AT4G11180	1.09	0.13	1.19	0.275538	0.459149	-6.62
266240_at	putative RNA-binding protein ; suppor	---	AT2G29580	-1.08	-0.11	-1.19	0.275681	0.459335	-6.62
260610_at	putative SF16 protein {Helianthus annu	IQD14	AT2G43680	1.17	0.22	1.19	0.275814	0.45935	-6.62
254525_at	putative protein predicted protein, Ara	---	AT4G19580	-1.11	-0.15	-1.19	0.275798	0.45935	-6.62
259857_at	hypothetical protein predicted by gene	---	AT1G68430	-1.10	-0.14	-1.19	0.275832	0.45935	-6.62
261703_at	OsNAC7 protein, putative similar to O	ANAC012	AT1G32770	1.09	0.12	1.19	0.275744	0.45935	-6.62
248438_at	putative protein contains similarity to fe	EMF2	AT5G51230	-1.15	-0.20	-1.19	0.275803	0.45935	-6.62
246381_at	hypothetical protein	---	---	1.17	0.23	1.19	0.27576	0.45935	-6.62
246328_at	putative protein hexamer-binding prot	---	AT3G43590	-1.10	-0.14	-1.19	0.275812	0.45935	-6.62
245028_at	unknown protein	---	AT2G26570	1.15	0.20	1.19	0.275939	0.459496	-6.62
254690_at	N-acetylornithine deacetylase-like pro	---	AT4G17830	1.08	0.10	1.19	0.276088	0.459709	-6.63
263789_at	putative GDSL-motif lipase/hydrolase s	---	AT2G24560	-1.15	-0.20	-1.19	0.276124	0.459736	-6.63
265277_at	unknown protein ;supported by full-ler	---	AT2G28410	-1.31	-0.39	-1.18	0.276193	0.459818	-6.63
266383_at	putative pathogenesis related-1 (PR1)	ATPRB1	AT2G14580	-1.15	-0.20	-1.18	0.27625	0.459879	-6.63
245121_at	60S ribosomal protein L7A ;supported	---	AT2G47610	-1.20	-0.27	-1.18	0.276281	0.459897	-6.63
258170_at	unknown protein similar to senescence	---	AT3G21600	1.26	0.33	1.18	0.276376	0.460021	-6.63
258890_at	putative transcription factor similar to C	NF-YA2	AT3G05690	-1.18	-0.24	-1.18	0.276413	0.460049	-6.63
254625_at	Expressed protein ; supported by full-le	SNI1	AT4G18470	1.11	0.15	1.18	0.276521	0.460195	-6.63
257313_at	gamma tonoplast intrinsic protein near	TIP2	AT3G26520	-1.13	-0.17	-1.18	0.276587	0.460259	-6.63
261364_at	dynamin-like protein similar to GB:U25	---	AT1G53140	-1.11	-0.15	-1.18	0.27661	0.460259	-6.63
257939_at	monosaccharide transport protein, ST	STP4	AT3G19930	1.18	0.24	1.18	0.276619	0.460259	-6.63
246062_at	putative protein VAC8 protein, Saccha	---	AT5G19330	1.09	0.12	1.18	0.276724	0.460399	-6.63
249495_at	germin - like protein GLP6 exon 2 inte	GLP6	AT5G39100	1.11	0.15	1.18	0.276793	0.46048	-6.63
245080_at	putative receptor-like protein kinase	---	AT2G23300	-1.14	-0.19	-1.18	0.277058	0.460888	-6.63
263263_at	putative guanylate binding protein	---	AT2G38840	1.13	0.17	1.18	0.277098	0.460921	-6.63
262428_at	hypothetical protein predicted by gene	---	AT1G47570	1.10	0.13	1.18	0.277136	0.46095	-6.63
250205_at	unknown protein	---	AT5G14020	-1.09	-0.13	-1.18	0.277158	0.460953	-6.63
255007_at	putative oxidoreductase 11beta-hydro	AtHSD5	AT4G10020	-1.09	-0.12	-1.18	0.277206	0.460979	-6.63
246940_at	expressed protein glucose-6-phospha	---	AT5G25400	-1.11	-0.15	-1.18	0.277214	0.460979	-6.63
246184_at	beta-D-glucan exohydrolase - like pro	---	AT5G20950	1.16	0.22	1.18	0.277295	0.46108	-6.63

260960_at	calcium-binding protein, putative simil	---	AT1G05990	-1.11	-0.15	-1.18	0.277555	0.461478	-6.63
249990_at	hypothetical protein	---	AT5G18540	1.09	0.13	1.18	0.277591	0.461505	-6.63
255130_at	hypothetical protein ; supported by ful	---	AT4G08240	-1.11	-0.15	-1.18	0.277641	0.461555	-6.63
247295_at	putative protein similar to unknown pro	---	AT5G64180	1.10	0.14	1.18	0.277693	0.461607	-6.63
262516_at	putative glutathione transferase One o	ATGSTU26	AT1G17190	-1.10	-0.14	-1.18	0.277727	0.461631	-6.63
255156_at	putative athila transposon protein	---	---	1.07	0.10	1.18	0.277846	0.461794	-6.63
244949_at	hypothetical protein	---	---	1.11	0.14	1.18	0.277994	0.462007	-6.63
246705_x_	putative protein predicted resistance p	---	---	1.10	0.14	1.18	0.278135	0.462208	-6.63
267235_at	unknown protein	---	AT2G43945	-1.07	-0.10	-1.18	0.278164	0.462222	-6.63
266312_at	20S proteasome subunit C8 (PAG1/PF	PAG1	AT2G27020	1.11	0.15	1.18	0.278203	0.462253	-6.63
260508_at	Unknown protein ; supported by cDNA	GAMMA CA	AT1G47260	-1.09	-0.12	-1.18	0.278305	0.462389	-6.63
265855_at	unknown protein ;supported by full-ler	---	AT2G42390	-1.09	-0.12	-1.18	0.278352	0.462433	-6.63
247906_at	putative protein similar to unknown pro	IAA33	AT5G57420	-1.13	-0.18	-1.18	0.278477	0.462608	-6.63
262829_at	auxin-independent growth promoter, p	---	AT1G14970	-1.19	-0.25	-1.18	0.278509	0.462627	-6.63
253831_at	Expressed protein ; supported by full-l	---	AT4G27580	1.10	0.14	1.18	0.278647	0.462756	-6.63
258121_s_	putative geranylgeranyl pyrophosphate	GGPS3	AT3G14530 /	1.12	0.16	1.18	0.278641	0.462756	-6.63
247200_at	unknown protein ;supported by full-ler	---	AT5G65120	1.12	0.17	1.18	0.27862	0.462756	-6.63
247496_at	putative protein predicted proteins, Ar	GUT1	AT5G61840	-1.09	-0.12	-1.18	0.278668	0.462756	-6.63
245544_at	UTP-glucose glucosyltransferase like p	---	AT4G15270	1.11	0.15	1.18	0.278796	0.462935	-6.63
265984_at	putative limonene cyclase	TPS10	AT2G24210	-1.09	-0.13	-1.18	0.278958	0.463096	-6.63
249776_at	unknown protein	---	AT5G24170	-1.13	-0.18	-1.18	0.278939	0.463096	-6.63
255862_at	hypothetical protein predicted by gene	---	AT2G30300	1.10	0.14	1.18	0.278959	0.463096	-6.63
254401_at	putative protein various predicted prot	---	AT4G21300	-1.10	-0.13	-1.18	0.278974	0.463096	-6.63
258638_at	unknown protein ;supported by full-ler	---	AT3G07950	-1.09	-0.13	-1.18	0.279094	0.463261	-6.63
258714_at	putative RING zinc finger protein cont	---	AT3G09770	1.15	0.20	1.18	0.279236	0.463379	-6.63
258889_at	putative pectinesterase similar to pecti	---	AT3G05610	-1.14	-0.19	-1.18	0.279206	0.463379	-6.63
262406_at	myb-related protein, putative similar to	AtMYB93	AT1G34670	-1.12	-0.16	-1.18	0.279215	0.463379	-6.63
251481_at	receptor lectin kinase-like protein (frag	---	AT3G59730	1.08	0.11	1.18	0.279246	0.463379	-6.63
263311_at	hypothetical protein predicted by gene	---	AT2G10340	-1.11	-0.15	-1.18	0.279287	0.463379	-6.63
252751_at	putative protein RING-H2 zinc finger p	---	AT3G43430	1.22	0.29	1.18	0.279276	0.463379	-6.63
252680_at	putative protein predicted protein, C.e	---	AT3G44330	-1.08	-0.11	-1.18	0.279462	0.463596	-6.64
257545_at	hypothetical protein predicted by gens	---	AT3G23200	1.15	0.20	1.18	0.279479	0.463596	-6.64
251547_at	putative protein predicted proteins, Ar	---	AT3G58860	-1.10	-0.14	-1.18	0.279459	0.463596	-6.64
266491_at	putative retroelement pol polyprotein	---	---	-1.09	-0.12	-1.18	0.279522	0.463601	-6.64
250377_at	putative protein predicted proteins, Ho	---	AT5G11560	1.13	0.18	1.18	0.279508	0.463601	-6.64

246207_at	RNA-binding like protein non-consensu	---	AT4G36960	-1.09	-0.13	-1.18	0.279652	0.463783	-6.64
247173_at	poly(A)-binding protein II-like ; suppor	---	AT5G65260	1.12	0.16	1.18	0.279762	0.463926	-6.64
252098_at	putative protein several hypothetical pr	---	AT3G51330	1.38	0.47	1.18	0.279793	0.463926	-6.64
258951_at	putative phosphatidylinositolglycan cla	---	AT3G01380	-1.10	-0.14	-1.18	0.279799	0.463926	-6.64
250806_at	putative protein similar to unknown pro	---	AT5G05070	-1.09	-0.13	-1.17	0.279927	0.464103	-6.64
266186_at	unknown protein	AERO2	AT2G38960	1.08	0.11	1.17	0.279952	0.464112	-6.64
249505_at	putative protein	---	---	-1.21	-0.28	-1.17	0.27999	0.464114	-6.64
248677_at	unknown protein	---	AT5G48860	1.10	0.14	1.17	0.279994	0.464114	-6.64
267354_at	putative MYB family transcription facto	MYB25	AT2G39880	-1.16	-0.21	-1.17	0.280085	0.464231	-6.64
257755_at	unknown protein ; supported by full-le	---	AT3G18760	1.18	0.24	1.17	0.280122	0.464244	-6.64
252249_at	putative protein heat shock protein 10	---	AT3G49770	-1.12	-0.16	-1.17	0.280134	0.464244	-6.64
247143_at	unknown protein	---	AT5G65580	-1.17	-0.23	-1.17	0.280212	0.46434	-6.64
257827_at	unknown protein contains Pfam profile	---	AT3G26630	-1.17	-0.23	-1.17	0.280282	0.464389	-6.64
266766_at	hypothetical protein predicted by gens	PAP14	AT2G46880	1.19	0.26	1.17	0.280278	0.464389	-6.64
246741_at	glycine rich protein - like glycine rich p	emb1644	AT5G27720	1.12	0.16	1.17	0.280306	0.464394	-6.64
250026_at	putative protein similar to unknown pro	---	AT5G18090	-1.11	-0.15	-1.17	0.280419	0.464522	-6.64
260348_at	PPR-repeat protein, putative contains	---	AT1G69350	1.14	0.19	1.17	0.280424	0.464522	-6.64
262433_s_	DNA binding protein, putative similar t	ATRBP47C'	AT1G47490 /	1.09	0.12	1.17	0.280484	0.464588	-6.64
255839_at	putative CONSTANS-like B-box zinc fi	---	AT2G33500	-1.09	-0.12	-1.17	0.280515	0.464605	-6.64
266549_at	Expressed protein ; supported by full-le	EXL1	AT2G35150	-1.11	-0.14	-1.17	0.280538	0.464609	-6.64
255000_at	S18.A ribosomal protein ;supported by	RPS18C	AT4G09800	-1.15	-0.20	-1.17	0.280604	0.464685	-6.64
252082_at	putative protein	---	AT3G51940	-1.08	-0.11	-1.17	0.280648	0.464721	-6.64
258808_at	putative pyruvate kinase similar to pyr	---	AT3G04050	-1.09	-0.13	-1.17	0.280666	0.464721	-6.64
256155_at	MYB-family transcription factor, putati	MYB83	AT3G08500	-1.08	-0.12	-1.17	0.280772	0.464857	-6.64
255768_at	Expressed protein ; supported by full-le	---	AT1G16705	-1.09	-0.13	-1.17	0.280789	0.464857	-6.64
267285_at	unknown protein	---	AT2G23690	-1.18	-0.24	-1.17	0.280849	0.464881	-6.64
259203_at	hypothetical protein predicted by gene	---	AT3G09130	-1.10	-0.14	-1.17	0.280865	0.464881	-6.64
263815_at	hypothetical protein predicted by gens	---	AT2G10020	1.15	0.21	1.17	0.280856	0.464881	-6.64
249593_at	putative protein SIAH1 protein, Brassi	---	AT5G37900	1.09	0.13	1.17	0.280904	0.464912	-6.64
250876_at	hypothetical protein	---	AT5G04030	-1.09	-0.12	-1.17	0.281017	0.465032	-6.64
260146_at	putative non-phototropic hypocotyl sim	---	AT1G52770	-1.29	-0.37	-1.17	0.280999	0.465032	-6.64
256565_at	hypothetical protein	AT3G19515	---	-1.10	-0.13	-1.17	0.281064	0.465076	-6.64
255291_at	putative calcium dependent protein kin	CPK27	AT4G04700	1.11	0.15	1.17	0.281194	0.465123	-6.64
248142_at	putative protein similar to unknown pro	---	AT5G55040	-1.09	-0.12	-1.17	0.281131	0.465123	-6.64
255848_at	hypothetical protein predicted by gens	---	AT2G33640	1.11	0.15	1.17	0.281178	0.465123	-6.64

246006_at	putative protein DIM1 protein, Homo s	YLS8	AT5G08290	-1.09	-0.13	-1.17	0.281172	0.465123	-6.64
249419_s_	putative protein MADS-box protein 2,	AGL98	AT5G39750 /	-1.08	-0.11	-1.17	0.281185	0.465123	-6.64
262533_at	hypothetical protein Pfam	---	AT1G17090	1.11	0.14	1.17	0.281376	0.465389	-6.64
263174_at	jasmonate inducible protein, putative s	ESP	AT1G54040	-1.29	-0.36	-1.17	0.281404	0.465403	-6.64
260077_at	thaumatin-like protein contains Pfam p	---	AT1G73620	-1.12	-0.17	-1.17	0.281444	0.465434	-6.64
248848_at	disease resistance protein-like	---	AT5G46520	1.07	0.10	1.17	0.281464	0.465434	-6.64
266885_at	putative small GTP-binding protein cor	RAB6A	AT2G44610	-1.11	-0.15	-1.17	0.281493	0.465448	-6.64
256919_at	hypothetical protein predicted by gene	---	AT3G18970	1.11	0.15	1.17	0.281555	0.465467	-6.64
251024_at	putative protein hypothetical proteins -	---	AT5G02180	-1.12	-0.16	-1.17	0.281586	0.465467	-6.64
252947_at	putative protein ubiquitin fusion degra	KAK	AT4G38600	1.08	0.11	1.17	0.281575	0.465467	-6.64
255533_at	putative CHP-rich zinc finger protein si	---	AT4G02180	1.09	0.12	1.17	0.281559	0.465467	-6.64
255887_at	hypothetical protein contains Pfam pro	---	AT1G20370	-1.08	-0.12	-1.17	0.281632	0.46547	-6.64
256386_at	cytochrome P450, putative contains P	---	AT1G66540	-1.08	-0.11	-1.17	0.28167	0.46547	-6.64
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.18	-0.24	-1.17	0.281641	0.46547	-6.64
265393_at	unknown protein ; supported by cDNA	---	AT2G20830	-1.18	-0.24	-1.17	0.281665	0.46547	-6.64
246277_at	hypothetical protein	---	AT4G36460	-1.11	-0.15	-1.17	0.281752	0.465573	-6.64
257838_at	hypothetical protein contains Pfam pro	---	AT3G25210	-1.09	-0.12	-1.17	0.281877	0.465746	-6.64
263950_at	hypothetical protein predicted by gene	HVA22J	AT2G36020	-1.07	-0.10	-1.17	0.281937	0.46581	-6.64
264859_at	glucose-6-phosphate 1-dehydrogenas	G6PD3	AT1G24280	1.34	0.42	1.17	0.282135	0.466104	-6.64
265621_at	NAM (no apical meristem)-like protein	NTL8	AT2G27300	-1.09	-0.13	-1.17	0.282232	0.466231	-6.64
247777_at	putative protein MNUDC protein, Hom	---	AT5G58740	-1.08	-0.12	-1.17	0.282333	0.466363	-6.64
253851_at	putative transcription factor MYB41	AtMYB41	AT4G28110	-1.11	-0.16	-1.17	0.282408	0.466454	-6.64
257684_s_	unknown protein contains Pfam profile	VCS	AT3G13290 /	1.11	0.16	1.17	0.282484	0.466546	-6.64
267432_at	putative UDP-N-acetylglucosamine py	---	AT2G35020	-1.17	-0.22	-1.17	0.282529	0.466585	-6.64
244987_s_	ribosomal protein L2	---	---	-1.08	-0.11	-1.17	0.282602	0.466673	-6.64
250756_at	putative protein strong similarity to unk	ROPGEF5	AT5G05940	-1.10	-0.14	-1.17	0.282628	0.466682	-6.64
264755_at	receptor kinase, putative similar to rec	---	AT1G61390	-1.10	-0.13	-1.17	0.282732	0.466819	-6.64
257853_at	hypothetical protein predicted by gene	---	AT3G12960	-1.10	-0.14	-1.17	0.282757	0.466827	-6.64
253650_at	EST GB:N37377 spans last intron and	---	AT4G30020	-1.69	-0.76	-1.17	0.282899	0.466858	-6.65
254767_s_	cytochrome p450 - like protein cytochr	CYP71A19	AT4G13290 /	-1.08	-0.11	-1.17	0.28287	0.466858	-6.65
253370_at	pectinesterase - like protein pectin me	---	AT4G33230	-1.13	-0.17	-1.17	0.282869	0.466858	-6.65
262481_at	unknown protein Location of ests 147	---	AT1G17080	1.10	0.14	1.17	0.282894	0.466858	-6.65
258307_x_	hypothetical protein predicted by gene	---	---	1.10	0.14	1.17	0.282893	0.466858	-6.65
252494_at	receptor-like protein kinase receptor li	---	AT3G46760	1.10	0.14	1.17	0.282878	0.466858	-6.65
258810_at	hypothetical protein similar to hypothet	---	AT3G03970	-1.11	-0.15	-1.17	0.282998	0.466888	-6.65

265126_s_	hypothetical protein similar to hypothet	---	AT1G55380 /	-1.10	-0.14	-1.17	0.282983	0.466888	-6.65
251489_at	putative protein putative proteins - Ara	---	AT3G59460	-1.11	-0.15	-1.17	0.28294	0.466888	-6.65
247564_at	RNA helicase - like protein RNA helica	---	AT5G61140	1.10	0.14	1.17	0.282963	0.466888	-6.65
251295_at	putative protein several O-methyltrans	---	AT3G62000	-1.13	-0.18	-1.17	0.283146	0.467098	-6.65
267100_at	unknown protein	---	AT2G41470	-1.09	-0.12	-1.17	0.283211	0.467171	-6.65
255841_at	putative tyrosine-specific transport pro	---	AT2G33260	1.14	0.19	1.17	0.283286	0.467262	-6.65
258496_at	putative plant adhesion molecule simil	---	AT3G02460	-1.14	-0.20	-1.17	0.283398	0.467405	-6.65
245077_at	hypothetical protein predicted by gens	---	AT2G23160	1.14	0.19	1.17	0.283414	0.467405	-6.65
253944_at	SNF8 like protein SNF8 protein - yeas	VPS22	AT4G27040	-1.10	-0.14	-1.17	0.28347	0.467463	-6.65
257741_at	hypothetical protein predicted by gene	---	AT3G27340	1.14	0.19	1.17	0.283534	0.467516	-6.65
265858_at	putative ribophorin I	---	AT2G01720	1.12	0.16	1.17	0.283543	0.467516	-6.65
244952_at	hypothetical protein	---	---	1.11	0.15	1.16	0.283679	0.467707	-6.65
258581_at	hypothetical protein predicted by gens	---	AT3G04160	-1.09	-0.12	-1.16	0.283723	0.467717	-6.65
248250_at	cyclic nucleotide-regulated ion channe	CNGC1	AT5G53130	-1.21	-0.28	-1.16	0.283726	0.467717	-6.65
259277_at	putative glycogen synthase similar to g	AtSS2	AT3G01180	-1.15	-0.21	-1.16	0.283792	0.467791	-6.65
259069_at	lysyl-tRNA synthetase identical to lysyl	ATKRS-1	AT3G11710	-1.12	-0.17	-1.16	0.283853	0.467858	-6.65
251400_at	putative protein prib5, Ribes nigrum, E	---	AT3G60420	1.47	0.56	1.16	0.283879	0.467868	-6.65
264268_at	hypothetical protein predicted by gene	ULP1D	AT1G60220	-1.09	-0.12	-1.16	0.284014	0.468056	-6.65
248717_at	Expressed protein ; supported by full-le	---	AT5G48175	-1.08	-0.11	-1.16	0.284114	0.468187	-6.65
266926_at	unknown protein predicted by genscan	---	AT2G46000	1.13	0.18	1.16	0.284238	0.468357	-6.65
257371_at	putative CCAAT-box binding trancriptio	NF-YB5	AT2G47810	-1.12	-0.16	-1.16	0.28427	0.468368	-6.65
259413_at	hypothetical protein contains similarity	---	AT1G02320	-1.09	-0.13	-1.16	0.284286	0.468368	-6.65
252961_at	putative protein KIAA0169 gene, Hom	---	AT4G38760	-1.11	-0.15	-1.16	0.284325	0.468399	-6.65
248869_at	putative protein contains similarity to R	---	AT5G46840	1.18	0.23	1.16	0.284374	0.468445	-6.65
257998_at	hypothetical protein similar to hypothet	---	AT3G27510	1.08	0.11	1.16	0.284586	0.468761	-6.65
266930_at	hypothetical protein predicted by gens	---	AT2G45930	1.12	0.16	1.16	0.28463	0.4688	-6.65
246713_at	mRNA capping enzyme - like capping	---	AT5G28210	1.12	0.16	1.16	0.284682	0.468852	-6.65
255468_at	putative WD-repeat protein similar to I	---	AT4G03020	1.09	0.13	1.16	0.284766	0.468956	-6.65
244912_at	cytochrome c biogenesis orf382 Protei	---	AT2G07783	1.14	0.19	1.16	0.28484	0.469045	-6.65
267211_at	Expressed protein ; supported by full-le	---	AT2G44065	1.08	0.11	1.16	0.284914	0.469098	-6.65
252706_at	putative protein predicted proteins, Ar	---	---	1.07	0.10	1.16	0.284905	0.469098	-6.65
267240_at	hypothetical protein predicted by gens	---	AT2G02680	-1.11	-0.15	-1.16	0.284962	0.469143	-6.65
249314_at	receptor kinase-like protein	---	AT5G41180	-1.12	-0.16	-1.16	0.285022	0.469208	-6.65
259966_at	unknown protein	SOB3	AT1G76500	1.10	0.14	1.16	0.285083	0.469274	-6.65
245314_at	Expressed protein ; supported by full-le	---	AT4G16745	-1.10	-0.14	-1.16	0.285323	0.469533	-6.65

260700_at	hypothetical protein identical to hypoth	---	AT1G32260	1.11	0.15	1.16	0.285313	0.469533	-6.65
252909_at	putative protein	---	AT4G39680	1.09	0.12	1.16	0.285263	0.469533	-6.65
260116_at	AIG1 identical to AIG1 (exhibits RPS2	AIG1	AT1G33960	-1.09	-0.12	-1.16	0.285322	0.469533	-6.65
260396_at	putative heme oxygenase similar to he	ho3	AT1G69720	1.17	0.23	1.16	0.285345	0.469533	-6.65
265892_at	hypothetical protein predicted by gens	---	AT2G15020	1.19	0.25	1.16	0.285363	0.469533	-6.65
245729_at	unknown protein	---	AT1G73490	1.12	0.16	1.16	0.285469	0.469639	-6.65
255048_at	gibberellin-regulated protein GASA3 p	GASA3	AT4G09600	-1.08	-0.11	-1.16	0.285452	0.469639	-6.65
260992_at	hypothetical protein predicted by gene	---	AT1G12150	-1.08	-0.11	-1.16	0.285535	0.469714	-6.65
253792_at	ammonium transporter - like protein a	AMT1;4	AT4G28700	-1.12	-0.16	-1.16	0.285605	0.469768	-6.65
267303_at	hookless1-like protein	---	AT2G30090	-1.07	-0.10	-1.16	0.285609	0.469768	-6.65
261810_at	ligase I, putative similar to ligase I GI:	ATLIG1	AT1G08130	-1.20	-0.26	-1.16	0.285639	0.469783	-6.65
246148_at	glycine-rich RNA-binding protein - like	---	AT5G19960	1.11	0.15	1.16	0.285733	0.469904	-6.65
248170_at	ankyrin-repeat-containing protein-like	---	AT5G54620	1.13	0.18	1.16	0.285786	0.469928	-6.65
254092_at	respiratory burst oxidase - like protein	---	AT4G25090	1.07	0.10	1.16	0.285789	0.469928	-6.65
255429_at	hypothetical protein	---	AT4G03410	1.13	0.18	1.16	0.286122	0.470358	-6.65
251908_at	putative protein late embryogenis abu	---	AT3G53770	-1.10	-0.14	-1.16	0.286119	0.470358	-6.65
261643_at	hypothetical protein similar to hypothet	TAF4B	AT1G27720	1.14	0.18	1.16	0.286111	0.470358	-6.65
257469_at	hypothetical protein predicted by gene	---	AT1G49290	-1.07	-0.10	-1.16	0.286133	0.470358	-6.65
255334_at	putative transposon protein	---	---	1.07	0.10	1.16	0.286178	0.470399	-6.65
266333_at	putative ubiquitin activating enzyme	AXL	AT2G32410	1.11	0.16	1.16	0.286232	0.470454	-6.66
246088_at	putative protein	---	AT5G20600	1.14	0.19	1.16	0.28632	0.470564	-6.66
252664_at	putative protein several hypothetical pr	---	AT3G44080	-1.08	-0.11	-1.16	0.286357	0.470591	-6.66
260278_at	hypothetical protein predicted by gens	WRKY66	AT1G80590	1.16	0.22	1.16	0.286402	0.47063	-6.66
266698_at	copia-like retroelement pol polyprotein	SNF7.2	AT2G19830	-1.10	-0.14	-1.16	0.286449	0.470674	-6.66
259465_at	hypothetical protein similar to putative	---	AT1G19025	-1.11	-0.15	-1.16	0.286513	0.470716	-6.66
263300_at	Mutator-like transposase similar to MU	---	---	1.08	0.11	1.16	0.286516	0.470716	-6.66
245572_at	hypothetical protein	PPD2	AT4G14720	1.18	0.23	1.16	0.286575	0.470779	-6.66
262436_at	En/Spm-like transposon protein, putat	---	AT1G47610	-1.20	-0.26	-1.16	0.286659	0.470883	-6.66
249977_at	chaperonin 60 alpha chain - like prote	EMB3007	AT5G18820	1.13	0.18	1.16	0.286695	0.470901	-6.66
256105_at	hypothetical protein predicted by gene	LSH8	AT1G16910	-1.11	-0.15	-1.16	0.286711	0.470901	-6.66
255355_at	hypothetical protein	---	---	-1.10	-0.14	-1.16	0.286746	0.470924	-6.66
261148_at	unknown protein ; supported by full-ler	GAMMA CA	AT1G19580	-1.08	-0.12	-1.16	0.286972	0.47123	-6.66
246726_at	putative protein predicted protein, Ara	---	AT5G29050	-1.09	-0.12	-1.16	0.286973	0.47123	-6.66
247406_at	response regulator 6 (ARR6) ; suppor	ARR6	AT5G62920	-1.27	-0.34	-1.16	0.287	0.471232	-6.66
256732_at	hypothetical protein predicted by gene	---	---	-1.08	-0.12	-1.16	0.287016	0.471232	-6.66

256888_at	hypothetical protein predicted by gene	---	AT3G15160	-1.09	-0.12	-1.16	0.287084	0.47131	-6.66
259392_at	hypothetical protein similar to hypothet	---	AT1G06380	1.09	0.12	1.16	0.287105	0.471311	-6.66
262477_at	hypothetical protein contains similarity	---	AT1G11220	1.15	0.20	1.16	0.287166	0.471372	-6.66
256086_at	hypothetical protein predicted by gene	---	AT1G20770	-1.10	-0.14	-1.16	0.287184	0.471372	-6.66
265225_at	putative PHD-type zinc finger protein	---	AT2G36720	-1.09	-0.13	-1.16	0.287238	0.471393	-6.66
265769_at	unknown protein weak similarity to pro	---	AT2G48090	1.11	0.15	1.16	0.287218	0.471393	-6.66
253644_at	putative protein predicted protein, Ara	---	AT4G29870	-1.14	-0.18	-1.16	0.287328	0.471508	-6.66
253194_s_	hypothetical protein	---	---	1.10	0.13	1.15	0.287494	0.471745	-6.66
258958_at	vacuolar membrane ATPase subunit G	VMA10	AT3G01390	-1.14	-0.19	-1.15	0.287536	0.471781	-6.66
256683_at	unknown protein ; supported by cDNA:	---	AT3G52220	-1.08	-0.11	-1.15	0.28758	0.471819	-6.66
251471_at	putative protein GTPASE-ACTIVATIN	---	AT3G59570	-1.10	-0.14	-1.15	0.287708	0.471873	-6.66
265554_at	hypothetical protein predicted by gens	---	AT2G07505	1.08	0.11	1.15	0.287698	0.471873	-6.66
263427_at	hypothetical protein predicted by gens	---	AT2G22260	-1.08	-0.12	-1.15	0.287716	0.471873	-6.66
252580_at	putative protein putative proteins - Ara	---	AT3G45490	1.09	0.12	1.15	0.287685	0.471873	-6.66
258096_at	hypothetical protein similar to putative	---	AT3G23650	-1.10	-0.14	-1.15	0.287664	0.471873	-6.66
251266_at	putative protein hypothetical protein A	---	AT3G62320	-1.12	-0.16	-1.15	0.287776	0.471904	-6.66
251363_at	putative transcription factor (MYB17)	AtMYB17	AT3G61250	1.17	0.22	1.15	0.287761	0.471904	-6.66
257878_at	hypothetical protein predicted by gene	---	AT3G17150	-1.10	-0.13	-1.15	0.287814	0.471931	-6.66
265635_at	hypothetical protein predicted by gens	---	AT2G25360	-1.08	-0.11	-1.15	0.28799	0.472186	-6.66
247700_at	RNA-binding protein - like cold-inducib	---	AT5G59860	-1.07	-0.10	-1.15	0.288052	0.472253	-6.66
250850_at	putative protein ; supported by cDNA:	---	AT5G04550	-1.12	-0.16	-1.15	0.288144	0.472371	-6.66
257889_at	S1 self-incompatibility protein, putative	---	AT3G17080	-1.12	-0.16	-1.15	0.288253	0.472516	-6.66
246654_s_	putative protein predicted protein from	EGY1	AT5G35210 /	1.07	0.10	1.15	0.2885	0.472886	-6.66
259910_at	putative P-type transporting ATPase si	---	AT1G72700	1.20	0.26	1.15	0.288585	0.472936	-6.66
247151_at	unknown protein ;supported by full-ler	bHLH093	AT5G65640	-1.17	-0.22	-1.15	0.288593	0.472936	-6.66
261704_at	hypothetical protein identical to hypoth	---	AT1G32600	-1.08	-0.11	-1.15	0.288592	0.472936	-6.66
249981_at	putative protein predicted proteins, Ar	---	AT5G18510	1.12	0.17	1.15	0.288707	0.47309	-6.66
266941_at	peroxidase (ATP22a) identical to GB:Y	---	AT2G18980	1.12	0.17	1.15	0.288754	0.473099	-6.66
267325_at	unknown protein predicted by genscan	---	AT2G19360	1.10	0.14	1.15	0.288741	0.473099	-6.66
256101_at	hypothetical protein predicted by gens	---	AT1G13760	1.09	0.13	1.15	0.28889	0.473288	-6.66
257585_at	hypothetical protein predicted by gene	---	AT3G12420	1.10	0.14	1.15	0.289098	0.473594	-6.66
262106_at	hypothetical protein similar to Wee1-lik	WEE1	AT1G02970	-1.12	-0.16	-1.15	0.289135	0.47362	-6.66
248593_at	pectin methylesterase ;supported by f	---	AT5G49180	-1.13	-0.18	-1.15	0.289311	0.473875	-6.66
256944_at	unknown protein similar to unknown pr	VRN1	AT3G18990	1.14	0.19	1.15	0.289471	0.474103	-6.66
262736_at	lipase, putative contains Pfam profile:	---	AT1G28570	-1.09	-0.12	-1.15	0.289549	0.474197	-6.66

245734_at	lysophospholipase homolog, putative	---	AT1G73480	1.18	0.23	1.15	0.289584	0.47422	-6.66
256469_at	zinc-finger protein, putative similar to (	LOL1	AT1G32540	1.17	0.22	1.15	0.289768	0.474488	-6.67
260487_at	RNA-binding protein, putative similar t	Y14	AT1G51510	-1.09	-0.13	-1.15	0.28996	0.474733	-6.67
249053_at	berberine bridge enzyme-like protein	---	AT5G44440	-1.11	-0.15	-1.15	0.289956	0.474733	-6.67
264420_at	hypothetical protein predicted by gene	---	AT1G43320	-1.08	-0.11	-1.15	0.290013	0.474787	-6.67
248309_at	putative protein contains similarity to u	---	AT5G52540	-1.30	-0.37	-1.15	0.290101	0.474897	-6.67
255303_at	predicted protein of unknown function	DER2.2	AT4G04860	1.10	0.13	1.15	0.290189	0.474985	-6.67
258353_s_	unknown protein similar to GB:AAD49	YSL5	AT3G17650 /	-1.13	-0.18	-1.15	0.290197	0.474985	-6.67
245389_at	putative protein ;supported by full-leng	---	AT4G17480	1.12	0.16	1.15	0.290292	0.475069	-6.67
251763_at	MYB transcription factor - like protein	MYB109	AT3G55730	-1.11	-0.15	-1.15	0.290332	0.475069	-6.67
250700_at	CDK5 activator-binding protein-like	---	AT5G06830	-1.10	-0.14	-1.15	0.290303	0.475069	-6.67
248218_at	unknown protein ;supported by full-len	---	AT5G53710	-1.13	-0.18	-1.15	0.290319	0.475069	-6.67
256841_x_	hypothetical protein predicted by gene	---	---	-1.15	-0.21	-1.15	0.290479	0.475277	-6.67
248056_at	unknown protein ; supported by cDNA	XYLT	AT5G55500	1.07	0.10	1.15	0.290504	0.475283	-6.67
252880_at	putative protein ;supported by full-leng	---	AT4G39730	1.17	0.22	1.15	0.290581	0.475375	-6.67
256580_s_	hypothetical protein	---	AT3G28810 /	1.08	0.12	1.15	0.290619	0.4754	-6.67
254506_at	leucine rich repeat-like protein Cf-2.2,	GSO1	AT4G20140	-1.13	-0.18	-1.15	0.290638	0.4754	-6.67
260912_at	ATP-dependent Clp protease proteolyt	CLPP5	AT1G02560	1.09	0.12	1.15	0.290717	0.475495	-6.67
248302_at	putative protein similar to unknown pro	---	AT5G53160	-1.14	-0.18	-1.15	0.290761	0.475525	-6.67
258614_at	putative S-adenosylmethionine:2-deme	---	AT3G02770	-1.17	-0.23	-1.15	0.290777	0.475525	-6.67
256485_at	unknown protein	---	AT1G31440	1.09	0.13	1.15	0.291049	0.475922	-6.67
256435_at	putative leucoanthocyanidin dioxygena	---	AT3G11180	1.10	0.14	1.15	0.291073	0.475922	-6.67
253145_at	hypothetical protein	---	AT4G35560	-1.19	-0.25	-1.15	0.291083	0.475922	-6.67
247561_at	putative protein	---	AT5G61110	1.09	0.12	1.15	0.291168	0.476027	-6.67
262311_at	homeodomain leucine zipper protein,	ATHB18	AT1G70920	1.10	0.14	1.14	0.291317	0.476203	-6.67
246665_s_	putative protein predicted proteins - Ar	---	---	1.10	0.14	1.14	0.291311	0.476203	-6.67
265129_at	putative zinc finger protein similar to z	SUF4	AT1G30970	1.10	0.14	1.14	0.291352	0.476218	-6.67
264737_at	unknown protein	---	AT1G62210	-1.13	-0.18	-1.14	0.291368	0.476218	-6.67
259662_at	Expressed protein ; supported by full-l	HUB2	AT1G55250	1.13	0.18	1.14	0.291394	0.476227	-6.67
259682_at	transcription factor DREB1A, putative	---	AT1G63040	-1.14	-0.19	-1.14	0.291467	0.476311	-6.67
266119_at	protease inhibitor II identical to GB:X6	LCR69	AT2G02100	1.39	0.48	1.14	0.291625	0.476354	-6.67
249533_at	putative protein predicted protein, Ara	---	AT5G38790	-1.10	-0.14	-1.14	0.29154	0.476354	-6.67
265638_at	similar to PIG-L	---	AT2G27340	-1.09	-0.12	-1.14	0.291559	0.476354	-6.67
251698_at	putative protein	---	AT3G56610	1.08	0.11	1.14	0.29166	0.476354	-6.67
249874_at	putative protein contains similarity to th	---	AT5G23070	-1.18	-0.24	-1.14	0.291607	0.476354	-6.67

261245_at	anter-specific proline-rich protein APG	---	AT1G20130 /	-1.08	-0.11	-1.14	0.291595	0.476354	-6.67
250772_at	putative protein contains similarity to p	---	AT5G05420	-1.15	-0.21	-1.14	0.291644	0.476354	-6.67
252381_s_	ABC-type transport protein-like protein	ABCA4	AT3G47750 /	1.11	0.15	1.14	0.291608	0.476354	-6.67
254808_at	adenine DNA glycosylase like protein	---	AT4G12740	1.08	0.11	1.14	0.291938	0.476775	-6.67
247157_at	nuclear matrix constituent protein 1 (N	LINC4	AT5G65770	1.10	0.13	1.14	0.292034	0.476897	-6.67
250390_at	separation anxiety protein - like separ	---	AT5G11340	1.07	0.10	1.14	0.292185	0.477109	-6.67
247187_at	putative protein similar to unknown pro	---	AT5G65490	1.09	0.13	1.14	0.292236	0.477158	-6.67
248375_at	potassium/proton antiporter-like protein	KEA5	AT5G51710	-1.08	-0.12	-1.14	0.292282	0.4772	-6.67
248590_at	receptor protein kinase	---	AT5G49660	1.09	0.12	1.14	0.29231	0.477211	-6.67
267021_at	hypothetical protein predicted by gene	---	AT2G39300	1.08	0.11	1.14	0.292337	0.47722	-6.67
250425_at	lectin-like protein kinase - like lectin-lik	---	AT5G10530	-1.08	-0.11	-1.14	0.292371	0.477242	-6.67
263439_at	hypothetical protein predicted by gens	ATEXO70H8	AT2G28650	-1.11	-0.14	-1.14	0.292525	0.477459	-6.67
251495_at	putative protein RanBP7/importin 7 - H	---	AT3G59020	-1.13	-0.18	-1.14	0.292591	0.477533	-6.67
249567_at	SAMT-like protein S-adenosyl-L-meth	---	AT5G38020	1.08	0.11	1.14	0.292702	0.47768	-6.67
256314_at	hypothetical protein	TOC75-I	AT1G35860	-1.10	-0.14	-1.14	0.292764	0.477747	-6.67
264470_at	cytochrome P450, putative similar to c	CYP735A2	AT1G67110	-1.13	-0.17	-1.14	0.29283	0.47782	-6.67
249602_at	porin -like protein porin, Prunus armer	---	AT5G37610	-1.09	-0.13	-1.14	0.292906	0.477911	-6.67
252072_at	putative protein protein kinase PK1, re	---	AT3G51710	1.09	0.13	1.14	0.293161	0.478293	-6.67
252323_at	putative protein probable transcription	KING1	AT3G48530	-1.15	-0.20	-1.14	0.293223	0.478308	-6.68
258081_at	Expressed protein ; supported by full-le	---	AT3G26085	-1.10	-0.13	-1.14	0.293233	0.478308	-6.68
257170_at	beta-1,3-glucanase, putative similar to	---	AT3G23770	-1.14	-0.18	-1.14	0.293212	0.478308	-6.68
262918_at	hypothetical protein predicted by gene	---	AT1G65000	1.11	0.14	1.14	0.293305	0.47839	-6.68
262570_at	unknown protein EST gb|H77143 com	---	AT1G15200	-1.10	-0.13	-1.14	0.293343	0.478419	-6.68
251350_at	cytochrome P450 monooxygenase-lik	CYP76C7	AT3G61040	-1.16	-0.21	-1.14	0.293397	0.478472	-6.68
262976_at	unknown protein	SRS5	AT1G75520	-1.12	-0.16	-1.14	0.293444	0.478515	-6.68
257349_at	unknown protein	---	AT2G30630	1.09	0.12	1.14	0.293465	0.478515	-6.68
245584_at	amine oxidase like protein	ATAO1	AT4G14940	-1.08	-0.11	-1.14	0.293554	0.478625	-6.68
261812_at	hypothetical protein contains similarity	---	AT1G08270	-1.08	-0.11	-1.14	0.293684	0.478802	-6.68
253029_at	hypothetical protein	FRS9	AT4G38170	1.21	0.28	1.14	0.293736	0.478853	-6.68
260715_at	hypothetical protein predicted by gene	---	AT1G48200	1.19	0.25	1.14	0.293759	0.478856	-6.68
262041_at	HPt phosphotransmitter, putative simi	AHP6	AT1G80100	-1.11	-0.16	-1.14	0.293842	0.478958	-6.68
255711_at	putative WD repeat membrane protein	---	AT4G00090	1.11	0.15	1.14	0.294003	0.47912	-6.68
246706_at	putative protein predicted proteins, Ar	---	---	1.16	0.21	1.14	0.293982	0.47912	-6.68
255423_at	putative calmodulin	---	AT4G03290	1.09	0.12	1.14	0.294004	0.47912	-6.68
263985_at	unknown protein ;supported by full-ler	---	AT2G42750	1.16	0.22	1.14	0.294043	0.479149	-6.68

261051_at	cytochrome P450, putative similar to c	CYP703A2	AT1G01280	-1.09	-0.12	-1.14	0.294229	0.479417	-6.68
254523_at	putative protein hypothetical protein, A	FRS1	AT4G19990	-1.14	-0.19	-1.14	0.294257	0.479429	-6.68
264711_at	hypothetical protein predicted by gens	---	AT1G09800	1.09	0.13	1.14	0.294518	0.47982	-6.68
247823_at	putative protein predicted proteins fro	---	AT5G58450	1.07	0.10	1.14	0.294622	0.479955	-6.68
255299_at	putative adenosine deaminase similar	---	AT4G04880	1.10	0.14	1.14	0.294741	0.480081	-6.68
262053_at	putative DnaJ protein contains Pfam p	ATERDJ2A	AT1G79940	1.11	0.15	1.14	0.294741	0.480081	-6.68
266847_at	hypothetical protein predicted by grail;	emb1345	AT2G26060	-1.12	-0.16	-1.14	0.294884	0.480279	-6.68
265485_at	putative Ta11-like non-LTR retroeleme	---	---	-1.14	-0.20	-1.14	0.294928	0.480317	-6.68
247092_at	putative protein contains similarity to p	ATFOLT1	AT5G66380	-1.12	-0.16	-1.14	0.295084	0.480536	-6.68
252854_at	ubiquitin-specific protease 27 (UBP27	UBP27	AT4G39370	-1.08	-0.11	-1.14	0.295127	0.480572	-6.68
266678_at	hypothetical protein predicted by grail	---	AT2G25870	-1.09	-0.12	-1.14	0.295158	0.480587	-6.68
262061_at	hypothetical protein contains similarity	ATPP2-B11	AT1G80110	1.10	0.14	1.13	0.295331	0.480835	-6.68
246718_at	putative protein various predicted prot	---	---	-1.10	-0.14	-1.13	0.295499	0.481074	-6.68
266232_at	putative phloem-specific lectin	AtPP2-B6	AT2G02310	1.08	0.11	1.13	0.29563	0.481253	-6.68
250310_at	unknown protein	---	AT5G12230	1.13	0.17	1.13	0.29567	0.481284	-6.68
257728_at	hypothetical protein predicted by gene	---	AT3G18295	1.12	0.16	1.13	0.295828	0.481508	-6.68
246612_at	putative protein ;supported by full-leng	---	AT5G35320	1.11	0.16	1.13	0.295854	0.481515	-6.68
263148_at	ubiquitin, putative similar to ubiquitin C	---	AT1G53950	1.10	0.14	1.13	0.296089	0.481807	-6.68
255920_at	putative protein	---	AT5G28590	1.12	0.16	1.13	0.296077	0.481807	-6.68
247394_at	putative protein predicted proteins, Ar	---	AT5G62860	1.21	0.27	1.13	0.296097	0.481807	-6.68
253171_at	putative protein ;supported by full-leng	---	AT4G35040	-1.11	-0.15	-1.13	0.296214	0.481908	-6.68
256335_at	hypothetical protein predicted by gene	---	AT1G72110	-1.11	-0.15	-1.13	0.296183	0.481908	-6.68
253990_at	putative thioredoxin thioredoxin - Liliu	ACHT1	AT4G26160	-1.17	-0.23	-1.13	0.296222	0.481908	-6.68
254073_at	splicing factor At-SRp40 contains EST	RSP35	AT4G25500	1.10	0.14	1.13	0.296253	0.481924	-6.68
267053_s_	peroxidase	---	AT2G38380 /	-1.21	-0.28	-1.13	0.296388	0.482109	-6.68
260157_at	unknown protein ; supported by cDNA	---	AT1G52930	1.22	0.29	1.13	0.296532	0.482308	-6.68
254047_at	hypothetical protein	---	AT4G26040	-1.12	-0.17	-1.13	0.2966	0.48235	-6.68
252888_at	glucose-1-phosphate adenylyltransfera	APL3	AT4G39210	-1.25	-0.32	-1.13	0.296581	0.48235	-6.68
249622_at	putative protein	---	AT5G37550	-1.14	-0.18	-1.13	0.296764	0.482583	-6.68
248776_at	unknown protein	---	AT5G47900	-1.09	-0.13	-1.13	0.296824	0.482646	-6.69
251513_at	pirin-like protein pirin - Lycopersicon e	PRN	AT3G59220	1.39	0.47	1.13	0.296903	0.48274	-6.69
252704_at	putative protein KIAA0161 gene, Hom	---	AT3G43750	1.09	0.13	1.13	0.296929	0.482748	-6.69
267251_at	putative casein kinase II catalytic (alph	---	AT2G23070	-1.08	-0.11	-1.13	0.296969	0.482778	-6.69
258514_at	unknown protein ; supported by full-le	---	AT3G06610	-1.08	-0.12	-1.13	0.297152	0.482973	-6.69
258669_at	hypothetical protein predicted by gens	---	AT3G08800	1.08	0.12	1.13	0.297139	0.482973	-6.69

263159_at	RSH3 (RelA/SpoT homolog) identical t	RSH3	AT1G54130	-1.13	-0.17	-1.13	0.297147	0.482973	-6.69
261915_at	amp-binding protein, putative similar t	BZO1	AT1G65880	1.07	0.10	1.13	0.297188	0.482996	-6.69
249006_at	putative protein similar to unknown pro	---	AT5G44650 /	1.14	0.19	1.13	0.297316	0.48317	-6.69
246179_at	putative protein hypothetical protein F	---	AT5G28440	-1.13	-0.17	-1.13	0.297447	0.483349	-6.69
264256_at	putative importin alpha similar to GB:A	IMPA-4	AT1G09270	-1.08	-0.11	-1.13	0.29762	0.483555	-6.69
255949_at	hypothetical protein predicted by gene	---	AT1G22080	-1.07	-0.10	-1.13	0.297638	0.483555	-6.69
253515_at	auxin induced like-protein auxin-induc	---	AT4G31320	-1.12	-0.17	-1.13	0.297618	0.483555	-6.69
262080_at	unknown protein ; supported by cDNA:	CW14	AT1G59650	1.13	0.17	1.13	0.29771	0.483638	-6.69
249214_at	beta-1,3-glucanase-like protein	---	AT5G42720	-1.19	-0.26	-1.13	0.297873	0.483868	-6.69
254983_at	putative protein other hypothetical prot	MEE53	AT4G10560	-1.08	-0.11	-1.13	0.297996	0.484034	-6.69
251143_at	putative protein SqdX protein, Synech	SQD2	AT5G01220	1.19	0.26	1.13	0.298091	0.484138	-6.69
259956_at	unknown protein ;supported by full-ler	RRA2	AT1G75110	-1.09	-0.12	-1.13	0.298102	0.484138	-6.69
250769_at	putative protein similar to unknown pro	---	AT5G05680	1.18	0.23	1.13	0.298124	0.484139	-6.69
246161_at	putative protein predicted proteins, Ar	JAZ12	AT5G20900	-1.14	-0.18	-1.13	0.298208	0.48424	-6.69
266174_at	hypothetical protein predicted by gens	---	AT2G02440	1.07	0.10	1.13	0.298312	0.484374	-6.69
266357_at	putative beta-amylase	BAM6	AT2G32290	1.30	0.38	1.13	0.298351	0.484403	-6.69
255804_at	putative protein IB1C3-1 protein, Arab	---	AT4G10220	-1.11	-0.15	-1.13	0.298374	0.484406	-6.69
255875_s_	putative protein kinase contains a prot	---	AT2G40500 /	-1.10	-0.14	-1.13	0.298395	0.484406	-6.69
246431_at	calcium-binding protein calcium bindir	APC1	AT5G17480	-1.07	-0.10	-1.13	0.29842	0.484412	-6.69
247967_at	putative protein similar to unknown pro	anac099	AT5G56620	1.07	0.10	1.13	0.298481	0.484442	-6.69
264110_at	unknown protein	---	---	-1.07	-0.10	-1.13	0.298477	0.484442	-6.69
262938_at	hypothetical protein predicted by gene	---	AT1G79540	1.10	0.14	1.13	0.298595	0.484566	-6.69
247733_at	putative protein heat shock protein 40	---	AT5G59610	-1.15	-0.20	-1.13	0.298642	0.484566	-6.69
256734_at	unknown protein	RIK	AT3G29390	1.09	0.12	1.13	0.298625	0.484566	-6.69
254772_at	extensin-like protein extensin class 1	---	AT4G13390	-1.07	-0.09	-1.13	0.298638	0.484566	-6.69
266872_at	unknown protein	---	AT2G44730	-1.11	-0.14	-1.13	0.298673	0.484582	-6.69
257451_at	hypothetical protein predicted by gene	BT3	AT1G05690	1.10	0.13	1.13	0.298759	0.484686	-6.69
246362_at	hypothetical protein	---	---	-1.07	-0.10	-1.13	0.298812	0.484739	-6.69
257899_at	P-glycoprotein, putative similar to P-gl	---	AT3G28345	-1.08	-0.11	-1.13	0.298838	0.484746	-6.69
248621_at	putative protein similar to unknown pro	---	AT5G49350	-1.09	-0.13	-1.13	0.298915	0.484837	-6.69
247892_at	putative protein contains similarity to D	---	AT5G57970	-1.16	-0.22	-1.12	0.299119	0.485133	-6.69
251754_at	beta-1,3-glucanase - like protein beta-	---	AT3G55780	-1.11	-0.15	-1.12	0.299141	0.485134	-6.69
266736_at	putative cytochrome P450 ; supported	CYP709B1	AT2G46960	-1.08	-0.11	-1.12	0.299241	0.485261	-6.69
261126_at	TATA binding protein-associated facto	TAF6	AT1G04950	-1.08	-0.12	-1.12	0.299291	0.48529	-6.69
245718_at	putative protein	---	AT5G04110	1.12	0.16	1.12	0.299301	0.48529	-6.69

263669_at	putative cryptochrome 2 apoprotein Ma	CRY2	AT1G04400	-1.08	-0.12	-1.12	0.299395	0.485408	-6.69
247502_at	putative protein predicted proteins, Ar	---	AT5G61940	-1.09	-0.12	-1.12	0.29949	0.485493	-6.69
260690_at	RING finger protein, putative similar to	NHL8	AT1G32340	-1.07	-0.10	-1.12	0.299476	0.485493	-6.69
246352_at	hypothetical protein	---	---	1.07	0.10	1.12	0.299588	0.485582	-6.69
262764_at	putative cytochrome P450 monooxyge	CYP86C3	AT1G13140	1.09	0.12	1.12	0.299568	0.485582	-6.69
253192_at	putative protein nuclear phosphoprote	---	AT4G35370	1.08	0.12	1.12	0.29963	0.485616	-6.69
AFFX-r2-Bs	B. subtilis /GEN=thrB /DB_XREF=gb:X	---	---	-1.16	-0.21	-1.12	0.299711	0.485713	-6.69
249307_s_	DNA excision repair cross-complemen	XPB1	AT5G41360 /	1.09	0.13	1.12	0.299844	0.485845	-6.69
263320_at	putative galactinol synthase ;supporte	AtGolS1	AT2G47180	1.34	0.42	1.12	0.299899	0.485845	-6.69
257423_at	hypothetical protein predicted by gene	---	AT1G62010	1.11	0.15	1.12	0.29989	0.485845	-6.69
246205_at	hypothetical protein ; supported by cDI	---	AT4G36970	-1.19	-0.25	-1.12	0.299823	0.485845	-6.69
246833_at	putative protein	---	AT5G26620	-1.07	-0.10	-1.12	0.299865	0.485845	-6.69
249732_at	6-phosphogluconolactonase-like prote	---	AT5G24420	-1.98	-0.98	-1.12	0.300226	0.486306	-6.69
256180_at	light repressible receptor protein kinas	---	AT1G51810	1.07	0.10	1.12	0.300226	0.486306	-6.69
249247_at	maize crp1 protein-like	---	AT5G42310	-1.12	-0.17	-1.12	0.300285	0.486366	-6.69
262300_at	ripening-induced protein, putative sim	---	AT1G70870	1.07	0.10	1.12	0.300407	0.48653	-6.69
262403_s_	mutator-like transposase, putative sim	---	---	1.08	0.11	1.12	0.300521	0.486648	-6.70
261587_at	hypothetical protein predicted by gene	---	AT1G01660	1.09	0.12	1.12	0.300523	0.486648	-6.70
258843_at	putative protein kinase similar to hypot	---	AT3G04690	-1.09	-0.12	-1.12	0.300785	0.487037	-6.70
254374_at	hypothetical protein ;supported by full-	---	AT4G21780	1.08	0.11	1.12	0.300839	0.487091	-6.70
263405_s_	hypothetical protein similar to hypothet	---	AT2G04066 /	1.08	0.11	1.12	0.300934	0.48721	-6.70
253017_at	cinnamyl alcohol dehydrogenase -like	CAD6	AT4G37970	-1.08	-0.11	-1.12	0.300973	0.487239	-6.70
247809_at	unknown protein	---	AT5G58280	-1.10	-0.14	-1.12	0.301037	0.487307	-6.70
245608_at	protein kinase	---	AT4G14350	-1.14	-0.19	-1.12	0.301185	0.48749	-6.70
255293_at	putative zinc finger protein	---	AT4G04730	-1.10	-0.13	-1.12	0.301193	0.48749	-6.70
259315_at	unknown protein	AtRP2	AT3G01200	1.08	0.11	1.12	0.30134	0.487694	-6.70
257075_at	unknown protein contains Pfam profile	---	AT3G19670	1.13	0.17	1.12	0.301361	0.487694	-6.70
250368_at	putative protein ; supported by cDNA:	---	AT5G11280	-1.11	-0.15	-1.12	0.301521	0.487919	-6.70
257009_at	unknown protein ; supported by cDNA	---	AT3G14160	1.08	0.11	1.12	0.301575	0.487936	-6.70
258578_at	germin-like protein contains Pfam prof	---	AT3G04200	-1.15	-0.21	-1.12	0.301571	0.487936	-6.70
248242_at	aldo/keto reductase-like protein	---	AT5G53580	-1.12	-0.17	-1.12	0.301623	0.487965	-6.70
248532_at	Expressed protein ; supported by cDN	NFU2	AT5G49940	-1.11	-0.15	-1.12	0.301635	0.487965	-6.70
263347_at	putative U4/U6 small nuclear ribonucle	---	AT2G05720	-1.12	-0.17	-1.12	0.301814	0.488188	-6.70
254749_at	putative protein various predicted prot	---	AT4G13130	-1.07	-0.10	-1.12	0.301816	0.488188	-6.70
251870_at	putative protein Various predicted pro	---	AT3G54510	1.09	0.12	1.12	0.301909	0.488297	-6.70

263175_at	hypothetical protein similar to unknown	---	AT1G05510	1.08	0.11	1.12	0.301926	0.488297	-6.70
254405_at	putative protein arm repeat containing	PUB8	AT4G21350	1.15	0.20	1.12	0.302045	0.488454	-6.70
256003_at	Ta11 non-LTR retroelement protein, p	---	AT3G31430	-1.10	-0.14	-1.12	0.302135	0.488549	-6.70
245410_at	putative protein	ATMAP70-5	AT4G17220	1.08	0.12	1.12	0.302146	0.488549	-6.70
249390_at	60S RIBOSOMAL PROTEIN L5 -like (	---	AT5G40130	-1.08	-0.11	-1.12	0.302263	0.488702	-6.70
262742_at	GTP-binding protein, putative similar t	AtRABA1i	AT1G28550	-1.09	-0.12	-1.12	0.302291	0.488713	-6.70
247590_at	putative protein predicted proteins, Ar	---	AT5G60720	1.11	0.14	1.12	0.302312	0.488713	-6.70
262348_at	unknown protein similar to transcriptior	---	AT2G48160	-1.08	-0.11	-1.12	0.302477	0.488945	-6.70
259108_at	putative translationally controlled tumo	---	AT3G05540	1.08	0.12	1.12	0.302552	0.489031	-6.70
256384_at	hypothetical protein	---	AT1G66660	-1.11	-0.14	-1.12	0.302698	0.489233	-6.70
261341_s_	putative purple acid phosphatase simil	PAP5	AT1G52940 /	1.07	0.10	1.12	0.302769	0.489272	-6.70
250782_at	SYN1 splice variant 1 (gb AAF08981.1	SYN1	AT5G05490	-1.10	-0.13	-1.12	0.302786	0.489272	-6.70
263208_at	zinc finger protein 5, ZFP5 possible tr	ZFP5	AT1G10480	-1.12	-0.16	-1.12	0.302754	0.489272	-6.70
250449_at	embryonic abundant protein -like emb	---	AT5G10830	1.22	0.28	1.12	0.302971	0.489536	-6.70
249601_at	quinone oxidoreductase -like protein p	---	AT5G37980	-1.12	-0.17	-1.12	0.303011	0.489565	-6.70
260417_at	putative chromomethylase similar to ch	CMT3	AT1G69770	-1.20	-0.26	-1.11	0.303117	0.489702	-6.70
247905_at	unknown protein	---	AT5G57400	-1.07	-0.10	-1.11	0.303159	0.48971	-6.70
260492_at	putative polygalacturonase	PGAZAT	AT2G41850	1.14	0.18	1.11	0.303165	0.48971	-6.70
253679_at	cytidine deaminase 6 (CDA6)	---	AT4G29610	-1.24	-0.31	-1.11	0.303356	0.489949	-6.70
261865_at	sterol delta7 reductase identical to GB	DWF5	AT1G50430	-1.16	-0.21	-1.11	0.303341	0.489949	-6.70
258267_at	putative delta 9 desaturase similar to d	---	AT3G15870	-1.08	-0.11	-1.11	0.303412	0.490004	-6.70
251833_at	putative protein various predicted prote	---	AT3G55160	-1.09	-0.12	-1.11	0.303489	0.490095	-6.70
250181_at	tRNA synthase - like protein tRNA pse	---	AT5G14460	-1.10	-0.13	-1.11	0.30361	0.490255	-6.70
265441_at	unknown protein ;supported by full-ler	---	AT2G20870	1.13	0.17	1.11	0.303657	0.490262	-6.70
255518_at	putative pectinesterase similar to seve	---	AT4G02300	1.10	0.14	1.11	0.303638	0.490262	-6.70
252165_at	hypothetical protein ;supported by full-	---	AT3G50550	1.11	0.15	1.11	0.303689	0.490278	-6.70
245480_at	transcription factor like protein	---	AT4G16150	1.07	0.10	1.11	0.303802	0.490426	-6.70
260998_at	CAF protein similar to C2H2 zinc finge	---	AT1G26590	-1.09	-0.13	-1.11	0.303916	0.490553	-6.70
264500_at	hypothetical protein predicted by gene	---	AT1G09370	1.07	0.10	1.11	0.303923	0.490553	-6.70
261324_at	unknown protein	---	AT1G44770	1.13	0.18	1.11	0.304043	0.490711	-6.70
260846_at	unknown protein	---	AT1G17300	1.10	0.13	1.11	0.304233	0.490983	-6.71
260762_at	I-box binding factor, putative similar to	---	AT1G49015	-1.09	-0.12	-1.11	0.304263	0.490996	-6.71
246213_at	serine C-palmitoyltransferase like prote	ATLCB1	AT4G36480	1.12	0.16	1.11	0.304298	0.491019	-6.71
260156_at	NAM-like protein similar to NAM (no ap	NAM	AT1G52880	1.17	0.22	1.11	0.304407	0.49116	-6.71
258594_at	hypothetical protein predicted by gens	---	AT3G04490	-1.09	-0.13	-1.11	0.304516	0.491301	-6.71

263751_at	putative kinesin heavy chain	---	AT2G21300	-1.17	-0.22	-1.11	0.304572	0.491356	-6.71
247962_at	protein kinase MEK1 homolog	MKK6	AT5G56580	-1.09	-0.12	-1.11	0.304689	0.491475	-6.71
256974_at	unknown protein similar to putative ret	---	---	-1.08	-0.11	-1.11	0.304688	0.491475	-6.71
245931_at	major pollen allergen-like protein polle	---	AT5G09280	-1.12	-0.17	-1.11	0.304804	0.491591	-6.71
263458_at	putative GTP-binding protein	ATRABH1D	AT2G22290	-1.10	-0.14	-1.11	0.304793	0.491591	-6.71
250862_s_	40S ribosomal protein S17 -like 40S ri	---	AT2G04390 /	-1.16	-0.22	-1.11	0.304901	0.491714	-6.71
262575_at	putative ABC transporter Similar to gb	PDR7	AT1G15210	-1.10	-0.13	-1.11	0.304965	0.491781	-6.71
259247_at	unknown protein predicted by genefin	---	AT3G07570	1.12	0.16	1.11	0.305074	0.491923	-6.71
266579_at	putative small nuclear ribonucleoprote	SNRNP-G	AT2G23930	1.12	0.16	1.11	0.305128	0.491941	-6.71
259646_at	n-calpain-1 large subunit, putative sim	DEK1	AT1G55350	-1.09	-0.12	-1.11	0.305122	0.491941	-6.71
247603_at	microtubule-associated motor - like m	---	AT5G60930	-1.12	-0.17	-1.11	0.30515	0.491941	-6.71
246577_at	MADS box transcription factor, putativ	AGL92	AT1G31640	-1.09	-0.12	-1.11	0.305259	0.492082	-6.71
256412_at	hypothetical protein predicted by gene	ELO1	AT3G11220	1.10	0.14	1.11	0.30535	0.492194	-6.71
248291_at	putative protein similar to unknown pro	---	AT5G53020	1.10	0.13	1.11	0.305503	0.492406	-6.71
252889_at	hypothetical protein	---	AT4G39380	-1.11	-0.15	-1.11	0.305564	0.492468	-6.71
261042_at	GTP-binding protein, putative similar t	ATRABA3	AT1G01200	-1.11	-0.15	-1.11	0.305844	0.492861	-6.71
254139_at	hypothetical protein	---	AT4G24600	1.11	0.15	1.11	0.30585	0.492861	-6.71
249925_at	putative protein predicted proteins, Ho	---	AT5G19150	-1.13	-0.18	-1.11	0.306046	0.492958	-6.71
248638_at	fatty acid elongase; beta-ketoacyl-CoA	KCS21	AT5G49070	-1.07	-0.10	-1.11	0.306002	0.492958	-6.71
255990_at	glycyl tRNA synthetase, putative simil	---	AT1G29870	1.10	0.13	1.11	0.306053	0.492958	-6.71
251127_at	putative protein predicted protein, Ara	---	AT5G01080	-1.10	-0.14	-1.11	0.306026	0.492958	-6.71
251874_at	putative protein (fragment) esterase, F	---	AT3G54240	1.12	0.17	1.11	0.305953	0.492958	-6.71
263088_at	putative replication protein A1	---	---	-1.08	-0.12	-1.11	0.30606	0.492958	-6.71
257688_at	Snf2-related CBP activator protein, pu	PIE1	AT3G12810	1.07	0.10	1.11	0.306062	0.492958	-6.71
251923_at	reductase-like protein abscisic acid ac	---	AT3G53880	-1.21	-0.28	-1.11	0.306162	0.493085	-6.71
251669_at	putative protein hypothetical protein -	---	AT3G57180	-1.20	-0.26	-1.11	0.306388	0.493275	-6.71
265044_at	hypothetical protein Similar to human	VPS2.3	AT1G03950	1.12	0.16	1.11	0.306357	0.493275	-6.71
267638_at	unknown protein ; supported by full-le	OEP16-3	AT2G42210	-1.07	-0.10	-1.11	0.306324	0.493275	-6.71
256687_x_	hypothetical protein predicted by gene	---	AT3G32120	1.08	0.12	1.11	0.306373	0.493275	-6.71
259317_at	hypothetical protein identical to hypoth	HYP1	AT3G01100	1.10	0.14	1.11	0.30635	0.493275	-6.71
246232_at	hypothetical protein	EMB2754	AT4G36630	1.09	0.12	1.11	0.306565	0.493455	-6.71
260244_at	putative choline kinase similar to GB:A	---	AT1G74320	-1.09	-0.13	-1.11	0.30655	0.493455	-6.71
251901_at	putative protein axi1 protein, Nicotiana	---	AT3G54100	1.12	0.16	1.11	0.306544	0.493455	-6.71
AFFX-CreX	Bacteriophage P1 /GEN=cre /DB_XRE	---	---	1.20	0.27	1.11	0.306614	0.493499	-6.71
267290_at	putative SET-domain transcriptional re	---	AT2G23740	-1.11	-0.15	-1.11	0.30664	0.493506	-6.71

253921_at	glutamine amidotransferase/cyclase ;	AT-HF	AT4G26900	-1.10	-0.14	-1.11	0.306691	0.493554	-6.71
266074_at	putative small nuclear ribonucleoprotei	---	AT2G18740	-1.16	-0.21	-1.11	0.306759	0.493627	-6.71
251851_at	structural maintenance of chromosom	TTN8	AT3G54670	1.10	0.13	1.11	0.306866	0.493764	-6.71
265762_at	hypothetical protein	---	AT2G01240	-1.13	-0.18	-1.11	0.307032	0.493962	-6.71
246414_at	hypothetical protein similar to hypothet	---	AT1G77340	-1.08	-0.12	-1.11	0.307031	0.493962	-6.71
257931_at	hypothetical protein predicted by gene	---	AT3G17030	-1.09	-0.12	-1.11	0.307072	0.493993	-6.71
264388_at	hypothetical protein contains similarity	---	AT1G11970	1.11	0.15	1.10	0.30711	0.494019	-6.71
262413_at	hypothetical protein contains similarity	ATAPRL4	AT1G34780	-1.12	-0.16	-1.10	0.307359	0.494384	-6.71
247701_at	putative protein many predicted protei	---	AT5G59900	-1.08	-0.12	-1.10	0.30749	0.494543	-6.71
261885_at	unknown protein	---	AT1G80930	-1.11	-0.15	-1.10	0.307501	0.494543	-6.71
254654_at	translation initiation factor eIF4E ;supp	EIF4E	AT4G18040	1.10	0.13	1.10	0.307581	0.494636	-6.71
264875_at	putative glucanase	AKR2B	AT2G17390	1.07	0.10	1.10	0.307801	0.494886	-6.71
258119_at	putative MAP kinase similar to GB:AAI	MPK19	AT3G14720	1.10	0.14	1.10	0.307772	0.494886	-6.71
245548_at	cytochrome P450 like protein	CYP702A3	AT4G15310	1.07	0.10	1.10	0.307801	0.494886	-6.71
250909_at	S-receptor kinase - like protein S-rece	---	AT5G03700	1.37	0.45	1.10	0.307846	0.494923	-6.71
265058_s_	myrosinase-binding protein homolog,	MBP2	AT1G52030 /	1.63	0.70	1.10	0.307993	0.495124	-6.72
254383_at	hypothetical protein	---	AT4G21950	-1.09	-0.12	-1.10	0.308093	0.495212	-6.72
266667_at	hypothetical protein predicted by gens	---	AT2G29770	1.08	0.11	1.10	0.308077	0.495212	-6.72
260504_at	Cyclin similar to GB:CAB77269 from [F	CYCA3;3	AT1G47220	1.10	0.14	1.10	0.308113	0.495212	-6.72
246453_at	syntaxin homologue ;supported by full	SYP21	AT5G16830	-1.10	-0.14	-1.10	0.308552	0.495884	-6.72
261417_at	Expressed protein ; supported by cDN	---	AT1G07700	1.09	0.12	1.10	0.308579	0.495891	-6.72
247099_at	putative protein contains similarity to s	---	AT5G66500	1.11	0.14	1.10	0.308747	0.496099	-6.72
251268_at	putative protein hypothetical proteins -	---	AT3G62350	-1.10	-0.14	-1.10	0.308751	0.496099	-6.72
264664_at	putative elongation factor similar to GB	---	AT1G09660	-1.14	-0.19	-1.10	0.308796	0.49613	-6.72
265574_at	putative replication protein A1	---	---	-1.08	-0.12	-1.10	0.308814	0.49613	-6.72
265665_at	cysteine proteinase contains similarity	---	AT2G27420	-1.08	-0.12	-1.10	0.308917	0.496259	-6.72
251700_at	putative protein exocyst complex prote	---	AT3G56640	-1.16	-0.21	-1.10	0.309029	0.496406	-6.72
261781_at	far-red impaired response protein, put	FRS4	AT1G76320	-1.11	-0.15	-1.10	0.30907	0.496436	-6.72
261185_at	cytochrome p450, putative similar to C	CYP94D1	AT1G34540	-1.08	-0.12	-1.10	0.309136	0.496448	-6.72
263822_at	hypothetical protein predicted by gens	---	AT2G40240	-1.12	-0.16	-1.10	0.309132	0.496448	-6.72
265562_at	hypothetical protein predicted by gens	---	AT2G05500	1.07	0.09	1.10	0.309143	0.496448	-6.72
245055_at	hypothetical protein predicted by gens	---	AT2G26470	-1.11	-0.15	-1.10	0.309187	0.496484	-6.72
262440_at	serpin, putative similar to serpin GB:X	---	AT1G47710	-1.14	-0.19	-1.10	0.309217	0.496498	-6.72
245467_at	hypothetical protein	---	AT4G16610	-1.15	-0.20	-1.10	0.309254	0.496522	-6.72
253092_at	putative protein various predicted prot	---	AT4G37380	1.17	0.22	1.10	0.309339	0.496562	-6.72

247385_at	putative protein similar to unknown pro	emb2746	AT5G63420	1.13	0.18	1.10	0.309331	0.496562	-6.72
259719_at	unknown protein contains gamma-thio	LCR66	AT1G61070	1.08	0.11	1.10	0.309344	0.496562	-6.72
256368_at	cinnamyl alcohol dehydrogenase, puta	---	AT1G66800	-1.08	-0.12	-1.10	0.309418	0.49661	-6.72
263892_at	putative MYB family transcription facto	RAX2	AT2G36890	1.07	0.10	1.10	0.309398	0.49661	-6.72
246936_at	putative protein hypothetical protein S	---	AT5G25360	1.09	0.12	1.10	0.309538	0.496767	-6.72
259210_at	hypothetical protein nearly identical to	HY2	AT3G09150	1.12	0.17	1.10	0.30975	0.497013	-6.72
251228_at	beta-D-glucan exohydrolase-like prote	---	AT3G62710	1.09	0.12	1.10	0.309748	0.497013	-6.72
250608_at	pectin methyl-esterase-like protein pe	---	AT5G07420	-1.08	-0.11	-1.10	0.309778	0.497013	-6.72
265536_at	unknown protein contains a domain re	---	AT2G15880	-1.22	-0.29	-1.10	0.309758	0.497013	-6.72
263040_at	conserved hypothetical protein predict	---	AT1G23300	-1.09	-0.12	-1.10	0.309825	0.497053	-6.72
251099_at	putative protein KIAA0132 - Homo sa	---	AT5G01660	-1.09	-0.12	-1.10	0.309847	0.497054	-6.72
255085_at	putative protein several hypothetical pr	---	---	-1.09	-0.13	-1.10	0.309872	0.497058	-6.72
265265_at	unknown protein	---	AT2G42900	-1.14	-0.19	-1.10	0.309983	0.497198	-6.72
245369_at	Expressed protein ; supported by full-l	---	AT4G15975	1.18	0.24	1.10	0.310002	0.497198	-6.72
252887_at	putative protein various predicted prot	---	AT4G39240	1.07	0.10	1.10	0.310093	0.497271	-6.72
258915_at	unknown protein similar to hypothetica	VPS60.1	AT3G10640	1.11	0.16	1.10	0.310113	0.497271	-6.72
261633_at	hypothetical protein predicted by gene	---	AT1G49930	-1.08	-0.12	-1.10	0.310079	0.497271	-6.72
252071_at	putative protein DNA helicase homolo	---	AT3G51690	1.07	0.10	1.10	0.310164	0.497318	-6.72
248694_at	unknown protein	---	AT5G48340	1.09	0.12	1.10	0.310377	0.497589	-6.72
265249_at	putative C2H2-type zinc finger protein	SGR5	AT2G01940	1.25	0.32	1.10	0.310366	0.497589	-6.72
265060_at	HD-Zip protein, putative similar to HD-	ATHB-15	AT1G52150	1.22	0.29	1.10	0.310439	0.497653	-6.72
265926_at	RUB1-conjugating enzyme, putative s	---	AT2G18600	1.14	0.19	1.10	0.310554	0.497803	-6.72
245134_s_	unknown protein	---	AT2G45250 /	-1.09	-0.13	-1.10	0.310597	0.497837	-6.72
265637_at	unknown protein	ATCOAE	AT2G27490	1.09	0.13	1.10	0.310685	0.497898	-6.72
249665_at	unknown protein	---	AT5G35830	-1.10	-0.14	-1.10	0.310701	0.497898	-6.72
252347_at	ribosomal protein L13 homolog riboso	---	AT3G48130	1.10	0.14	1.10	0.310687	0.497898	-6.72
262491_at	putative SecA-type chloroplast protein	---	AT1G21650	1.10	0.14	1.10	0.31084	0.498016	-6.72
246917_at	serine-rich protein ;supported by full-l	---	AT5G25280	-1.19	-0.25	-1.10	0.310801	0.498016	-6.72
248304_at	polypyrimidine tract-binding RNA trans	PTB2	AT5G53180	-1.07	-0.10	-1.10	0.310832	0.498016	-6.72
261220_at	ER lumen protein-retaining receptor si	---	AT1G19970	-1.22	-0.29	-1.10	0.310904	0.498084	-6.72
248850_at	putative protein contains similarity to k	---	AT5G46550	-1.10	-0.13	-1.10	0.310996	0.498197	-6.72
258914_at	hypothetical protein predicted by gene	AGP27	AT3G06360	-1.08	-0.11	-1.10	0.311138	0.498389	-6.72
260390_at	unknown protein ; supported by full-le	---	AT1G73940	-1.10	-0.14	-1.09	0.311243	0.498523	-6.72
267121_at	putative GDSL-motif lipase/hydrolase s	---	AT2G23540	-1.18	-0.24	-1.09	0.311644	0.499129	-6.72
253667_at	peroxidase ATP8a ;supported by full-l	---	AT4G30170	-1.09	-0.12	-1.09	0.311678	0.499148	-6.72

262752_at	putative mitotic cyclin similar to gb|D89	CYCB3;1	AT1G16330	-1.11	-0.15	-1.09	0.31192	0.499502	-6.73
251523_at	putative protein several hypothetical pr	---	AT3G58975	-1.09	-0.13	-1.09	0.31195	0.499514	-6.73
251522_at	hypothetical protein	---	AT3G59430	1.10	0.14	1.09	0.312069	0.49967	-6.73
252669_at	putative protein hypothetical protein F	---	AT3G44100	1.09	0.12	1.09	0.312295	0.499997	-6.73
260029_at	endoplasmic reticulum alpha-mannosi	---	AT1G30000	-1.08	-0.11	-1.09	0.312375	0.500081	-6.73
255018_at	hypothetical protein ; supported by ful	---	AT4G10090	-1.12	-0.16	-1.09	0.312392	0.500081	-6.73
266532_at	putative glucosyltransferase ;supporte	---	AT2G16890	1.56	0.64	1.09	0.312501	0.500185	-6.73
264844_at	putative glycosylation enzyme ; suppo	---	AT1G03520	-1.12	-0.17	-1.09	0.312498	0.500185	-6.73
259930_at	hypothetical protein predicted by gene	---	AT1G34355	-1.10	-0.13	-1.09	0.312668	0.500418	-6.73
259538_at	putative serine/threonine kinase ; supp	---	AT1G12310	-1.11	-0.15	-1.09	0.312707	0.500426	-6.73
250162_at	FtsH protease, putative similar to FtsH	FTSH6	AT5G15250	-1.08	-0.11	-1.09	0.312717	0.500426	-6.73
251371_at	putative protein CGI-94 protein, Homo	EDA14	AT3G60360	-1.16	-0.22	-1.09	0.312743	0.500433	-6.73
260969_at	beta-fructosidase identical to beta-fruc	ATBETAFRU	AT1G12240	1.22	0.29	1.09	0.312959	0.500716	-6.73
256233_at	ankyrin-like protein contains Pfam prof	ITN1	AT3G12360	1.08	0.11	1.09	0.312964	0.500716	-6.73
254121_at	putative protein putative protein F6I18	---	AT4G24760	-1.17	-0.23	-1.09	0.313016	0.50073	-6.73
262423_at	hypothetical protein predicted by gens	---	AT1G23450	1.08	0.12	1.09	0.313013	0.50073	-6.73
258057_at	unknown protein	AAR3	AT3G28970	1.08	0.11	1.09	0.313186	0.500966	-6.73
255749_at	p68 RNA helicase, putative similar to	STRS1	AT1G31970	1.09	0.12	1.09	0.313293	0.50106	-6.73
252434_s_	putative protein mudrA protein - maize	---	---	-1.10	-0.13	-1.09	0.31329	0.50106	-6.73
254920_at	putative protein 24 kDa seed maturati	BTI2	AT4G11220	1.11	0.15	1.09	0.313311	0.50106	-6.73
266239_at	unknown protein ; supported by cDNA	---	AT2G29530	1.21	0.27	1.09	0.313373	0.50107	-6.73
249898_at	alkaline/neutral invertase ; supported	---	AT5G22510	-1.13	-0.18	-1.09	0.313378	0.50107	-6.73
257657_at	Expressed protein ; supported by full-le	---	AT3G13235	1.08	0.11	1.09	0.313383	0.50107	-6.73
267640_at	photomorphogenesis repressor (COP1	COP1	AT2G32950	-1.12	-0.16	-1.09	0.313427	0.501105	-6.73
263622_at	hypothetical protein predicted by gens	---	AT2G04870	-1.09	-0.12	-1.09	0.313514	0.501209	-6.73
253752_at	putative protein ;supported by full-leng	---	AT4G28910	-1.12	-0.16	-1.09	0.31363	0.50136	-6.73
264055_at	putative protein kinase contains a prot	---	AT2G28590	-1.11	-0.14	-1.09	0.313688	0.501418	-6.73
263390_at	hypothetical protein similar to Ta1-1 re	---	---	1.08	0.11	1.09	0.31375	0.501448	-6.73
246470_at	putative protein predicted proteins, fro	---	AT5G17080	1.09	0.12	1.09	0.313751	0.501448	-6.73
266064_at	expressed protein	---	AT2G18780	1.12	0.16	1.09	0.313858	0.501464	-6.73
261122_at	ornithine carbamoyltransferase precur	OTC	AT1G75330	-1.13	-0.17	-1.09	0.313852	0.501464	-6.73
266801_at	putative nucleotide-binding protein ;su	EMB2001	AT2G22870	-1.19	-0.26	-1.09	0.313871	0.501464	-6.73
267331_at	putative salt-inducible protein	---	AT2G19280	-1.11	-0.15	-1.09	0.313841	0.501464	-6.73
249614_at	putative protein predicted proteins, Ar	WSD1	AT5G37300	1.07	0.10	1.09	0.313854	0.501464	-6.73
260926_at	unknown protein	GLTP2	AT1G21360	1.09	0.13	1.09	0.313923	0.501511	-6.73

258098_at	hypothetical protein similar to kinesin li	KINESIN-12	AT3G23670	-1.14	-0.19	-1.09	0.313994	0.50159	-6.73
247028_at	DNA polymerase alpha 1	ICU2	AT5G67100	-1.22	-0.28	-1.09	0.314126	0.501766	-6.73
252308_at	putative protein sugar transporter 2, D	---	AT3G49310	-1.09	-0.12	-1.09	0.314159	0.501784	-6.73
264650_at	putative transcription factor Similar to S	NF-YC9	AT1G08970	-1.09	-0.13	-1.09	0.31419	0.501797	-6.73
251802_at	E2, ubiquitin-conjugating enzyme 14 (	UBC14	AT3G55380	1.08	0.11	1.09	0.314219	0.501809	-6.73
267203_at	hypothetical protein predicted by gene	---	AT2G31035	1.07	0.10	1.09	0.314277	0.501832	-6.73
265241_at	hypothetical protein	---	---	1.11	0.15	1.09	0.314265	0.501832	-6.73
259075_at	putative N2,N2-dimethylguanosine tRI	---	AT3G02320	1.10	0.14	1.09	0.31431	0.501849	-6.73
250227_at	FtsJ (dbj|BAA83750.1)	---	AT5G13830	1.10	0.14	1.09	0.31447	0.502068	-6.73
255550_at	putative raffinose synthase or seed im	AtSTS	AT4G01970	1.08	0.11	1.09	0.314516	0.502108	-6.73
255211_at	may be a pseudogene	---	---	1.08	0.10	1.09	0.314549	0.502125	-6.73
266088_at	hypothetical protein predicted by gens	---	AT2G37780	-1.12	-0.16	-1.09	0.314683	0.502268	-6.73
249297_at	unknown protein	---	AT5G41320	-1.08	-0.11	-1.09	0.314667	0.502268	-6.73
260421_at	acid phosphatase, putative similar to (	SBH1	AT1G69640	-1.09	-0.13	-1.09	0.314739	0.502322	-6.73
265018_s_	hypothetical protein predicted by gens	---	AT2G13770	-1.08	-0.12	-1.09	0.314822	0.502421	-6.73
261670_at	hypothetical protein contains similarity	TET11	AT1G18520	1.07	0.10	1.09	0.314868	0.502423	-6.73
245972_at	putative protein predicted proteins, Ar	---	AT5G20680	1.12	0.16	1.09	0.314848	0.502423	-6.73
252578_at	putative protein Ariadne protein (ARI)	---	AT3G45480	1.08	0.11	1.09	0.314893	0.502427	-6.73
250346_at	lysine decarboxylase - like protein lysi	---	AT5G11950	1.27	0.34	1.09	0.314961	0.502467	-6.73
250241_at	photoreceptor-interacting protein-like;	---	AT5G13600	-1.12	-0.16	-1.09	0.314949	0.502467	-6.73
262817_at	putative reticuline oxidase strong simil	---	AT1G11770	1.10	0.14	1.09	0.315081	0.502623	-6.73
251672_at	MADS-box transcription factor-like pro	AGL16	AT3G57230	-1.08	-0.12	-1.09	0.315131	0.502667	-6.73
266653_at	hypothetical protein predicted by gens	---	AT2G25740	1.10	0.14	1.09	0.315177	0.502706	-6.73
246151_at	putative protein predicted proteins fron	---	AT5G19950	1.10	0.14	1.09	0.315227	0.50275	-6.73
257558_s_	hypothetical protein contains Pfam pro	---	AT3G22000 /	-1.08	-0.12	-1.08	0.315332	0.502883	-6.73
246800_at	glycine hydroxymethyltransferase - lik	SHM2	AT5G26780	-1.11	-0.16	-1.08	0.315568	0.503223	-6.73
258909_at	putative DnaJ protein Pfam HMM hit:	---	AT3G06340	1.07	0.10	1.08	0.315638	0.5033	-6.74
256119_at	guanine nucleotide regulatory protein,	---	AT1G18070	1.09	0.13	1.08	0.316046	0.503915	-6.74
261939_at	cytochrome c oxidase subunit, putativ	COX6B	AT1G22450	-1.12	-0.17	-1.08	0.316126	0.504007	-6.74
257801_at	mitogen activated protein kinase kinas	WNK6	AT3G18750	-1.10	-0.13	-1.08	0.31638	0.504378	-6.74
266409_at	hypothetical protein predicted by grail	---	AT2G38510	-1.11	-0.14	-1.08	0.316464	0.504476	-6.74
257396_at	predicted protein	EPF1	AT2G20875	-1.12	-0.16	-1.08	0.316615	0.504611	-6.74
263522_at	hypothetical protein	---	AT2G24950	-1.07	-0.10	-1.08	0.316602	0.504611	-6.74
265196_at	hypothetical protein predicted by gens	SWC2	AT2G36740	1.12	0.16	1.08	0.316587	0.504611	-6.74
246023_at	ethylene-insensitive3-like2 (EIL2)	EIL2	AT5G21120	-1.09	-0.12	-1.08	0.316637	0.504611	-6.74

246776_at	kinesin-like protein kinesin-like heavy	---	AT5G27550	-1.13	-0.18	-1.08	0.316692	0.504663	-6.74
257340_at	pseudogene, retroelement pol polypro	---	---	-1.10	-0.14	-1.08	0.316728	0.504685	-6.74
254793_at	hypothetical protein	---	AT4G12930	1.09	0.13	1.08	0.316758	0.504697	-6.74
263315_at	Expressed protein ; supported by full-l	---	AT2G05755	-1.08	-0.11	-1.08	0.316856	0.504819	-6.74
250559_at	putative protein condensin subunit SM	---	AT5G08010	1.10	0.14	1.08	0.316943	0.504921	-6.74
263034_at	pollen allergen-like protein similar to m	MLP423	AT1G24020	1.19	0.25	1.08	0.317024	0.504981	-6.74
258111_at	putative cytochrome P450 similar to G	CYP72A9	AT3G14630	-1.12	-0.16	-1.08	0.317046	0.504981	-6.74
256059_at	hypothetical protein contains similarity	---	AT1G06990	-1.11	-0.15	-1.08	0.317009	0.504981	-6.74
246661_at	putative protein various predicted prot	---	---	-1.08	-0.11	-1.08	0.317085	0.505008	-6.74
266306_at	hypothetical protein predicted by grail	---	AT2G26970	1.10	0.14	1.08	0.317164	0.505062	-6.74
247020_at	putative protein strong similarity to unk	---	AT5G67020	1.13	0.17	1.08	0.317164	0.505062	-6.74
253091_at	cytochrome p450 - like protein cytoch	CYP81D2	AT4G37360	1.09	0.12	1.08	0.317186	0.505062	-6.74
247014_at	RuvB DNA helicase-like protein ; supp	---	AT5G67630	1.19	0.25	1.08	0.317296	0.505167	-6.74
251620_at	putative protein hypothetical protein F	---	AT3G58060	1.11	0.15	1.08	0.317295	0.505167	-6.74
257499_at	hypothetical protein similar to hypothet	---	AT1G63850	-1.18	-0.24	-1.08	0.317346	0.505211	-6.74
256108_at	hypothetical protein predicted by gene	---	AT1G16940	-1.13	-0.17	-1.08	0.31744	0.505325	-6.74
251383_at	beta-tubulin cofactor - like protein beta	TTN1	AT3G60740	-1.15	-0.20	-1.08	0.317507	0.505396	-6.74
261857_at	hypothetical protein predicted by gens	---	AT1G50620	1.22	0.28	1.08	0.317577	0.505474	-6.74
255507_at	AtKAP alpha similar to AtKAP, GenBa	MOS6	AT4G02150	-1.07	-0.10	-1.08	0.317614	0.505496	-6.74
261575_at	hypothetical protein contains similarity	---	AT1G01130	-1.15	-0.20	-1.08	0.317693	0.505587	-6.74
248822_at	peroxidase ;supported by full-length c	---	AT5G47000	-1.08	-0.11	-1.08	0.317734	0.505617	-6.74
253522_at	predicted protein cation transport prot	---	AT4G31290	-1.28	-0.35	-1.08	0.317782	0.505657	-6.74
253002_at	phosphoinositide-specific phospholipa	ATPLC1	AT4G38530	-1.10	-0.14	-1.08	0.317913	0.505831	-6.74
251615_at	putative protein hypothetical protein T	---	AT3G57980	-1.14	-0.19	-1.08	0.317936	0.505833	-6.74
256826_at	hypothetical protein predicted by gene	---	AT3G18540	-1.07	-0.10	-1.08	0.318012	0.505883	-6.74
261627_at	arsA homolog (hASNA-I), putative sim	---	AT1G01910	-1.08	-0.11	-1.08	0.317997	0.505883	-6.74
249106_at	protein transport protein SEC23 ; supp	---	AT5G43670	-1.14	-0.19	-1.08	0.318045	0.5059	-6.74
252069_s_	putative protein putative protein T18N1	---	AT3G51640 /	1.08	0.11	1.08	0.318326	0.506312	-6.74
254806_at	putative trehalose-6-phosphate phosp	---	AT4G12430 /	1.09	0.13	1.08	0.318369	0.506345	-6.74
255776_at	60S ribosomal protein L6, putative sim	---	AT1G18540	-1.22	-0.28	-1.08	0.318432	0.50641	-6.74
255346_at	hypothetical protein	---	---	-1.07	-0.09	-1.08	0.318571	0.506561	-6.74
254836_at	flavonoid 3,5-hydroxylase like protein	CYP706A7	AT4G12330	1.07	0.10	1.08	0.318565	0.506561	-6.74
266730_at	putative RNA-binding protein	---	AT2G03110	-1.09	-0.13	-1.08	0.318641	0.50661	-6.74
257992_at	hypothetical protein similar to hypothet	---	AT3G19880	-1.12	-0.16	-1.08	0.318647	0.50661	-6.74
250338_at	putative protein ; supported by cDNA:	---	AT5G11760	-1.08	-0.11	-1.08	0.318671	0.506614	-6.74

247085_at	kinesin heavy chain DNA binding prote	---	AT5G66310	-1.09	-0.13	-1.08	0.318782	0.506755	-6.74
264109_at	unknown protein	---	AT2G13720	-1.08	-0.11	-1.08	0.318816	0.506773	-6.74
260442_at	unknown protein ; supported by full-le	---	AT1G68220	-1.12	-0.16	-1.08	0.318882	0.506842	-6.74
267023_at	putative protein transport protein SEC6	---	AT2G34250	1.11	0.15	1.08	0.318911	0.506853	-6.74
256398_at	putative major intrinsic protein contains	NIP7;1	AT3G06100	-1.07	-0.10	-1.08	0.318999	0.506932	-6.74
251161_at	putative protein hypothetical protein S	---	AT3G63290	-1.10	-0.13	-1.08	0.319005	0.506932	-6.74
254907_at	putative disease resistance response	---	AT4G11190	1.09	0.12	1.08	0.319136	0.507092	-6.74
252725_at	putative protein mudrA transposase, Z	---	---	1.08	0.12	1.08	0.319172	0.507092	-6.74
258428_at	unknown protein	---	AT3G16610	1.09	0.13	1.08	0.319163	0.507092	-6.74
246422_at	ADP-ribosylation factor -like protein A	ATARFB1B	AT5G17060	1.20	0.26	1.08	0.319306	0.507269	-6.74
246672_at	putative protein	---	---	-1.07	-0.10	-1.08	0.319344	0.507294	-6.74
255519_at	hypothetical protein	---	AT4G02310	1.07	0.10	1.08	0.319392	0.507335	-6.74
245163_at	putative flavin-containing monooxygen	---	AT2G33230	1.11	0.15	1.07	0.319574	0.507589	-6.75
263054_at	putative cation transport protein	---	AT2G04620	1.09	0.12	1.07	0.319678	0.507719	-6.75
247696_at	MYB27 protein - like MYB27 protein, A	MYB59	AT5G59780	1.22	0.29	1.07	0.319813	0.507863	-6.75
257043_at	receptor-like protein kinase, putative s	IKU2	AT3G19700	1.09	0.12	1.07	0.319796	0.507863	-6.75
258626_at	transfactor, putative similar to transfac	---	AT3G04450	1.10	0.14	1.07	0.319971	0.508077	-6.75
261261_at	putative aldehyde oxidase	---	AT1G26730	-1.37	-0.46	-1.07	0.320167	0.508319	-6.75
264180_at	hypothetical protein contains similarity	---	AT1G02190	1.08	0.12	1.07	0.320161	0.508319	-6.75
262515_at	unknown protein ; supported by cDNA	---	AT1G34200	1.14	0.19	1.07	0.32019	0.50832	-6.75
262220_at	calcium-dependent protein kinase, pu	CPK30	AT1G74740	-1.08	-0.11	-1.07	0.320417	0.508645	-6.75
258135_at	Expressed protein ; supported by full-le	---	AT3G24506	-1.09	-0.13	-1.07	0.320551	0.508822	-6.75
252145_at	putative protein several putative protei	---	AT3G51200	-1.08	-0.11	-1.07	0.320722	0.509057	-6.75
245108_at	putative cytokinin oxidase	CKX1	AT2G41510	1.08	0.12	1.07	0.320787	0.509111	-6.75
255014_at	MADS-box protein AGL11 ; supported	STK	AT4G09960	-1.08	-0.11	-1.07	0.3208	0.509111	-6.75
252602_at	putative protein KIAA1094 protein, Ho	---	AT3G45040	-1.10	-0.14	-1.07	0.320982	0.509285	-6.75
266403_at	putative acid phosphatase contains me	---	AT2G38600	-1.10	-0.14	-1.07	0.320996	0.509285	-6.75
262265_at	hypothetical protein predicted by gens	---	---	1.13	0.17	1.07	0.32099	0.509285	-6.75
262103_at	glutathione S-transferase, putative sin	GSTF5	AT1G02940	1.15	0.20	1.07	0.320999	0.509285	-6.75
252456_at	hypersensitivity-related protein-like pro	---	AT3G47170	1.09	0.13	1.07	0.321035	0.509306	-6.75
253748_at	putative protein RNA-binding protein E	---	AT4G28990	-1.11	-0.16	-1.07	0.321111	0.509392	-6.75
266067_s_	hypothetical protein predicted by gens	---	AT2G18810 /	-1.07	-0.10	-1.07	0.321208	0.50951	-6.75
264541_at	hypothetical protein predicted by gene	---	AT1G55660	-1.11	-0.15	-1.07	0.321257	0.509517	-6.75
252825_at	small GTP-binding protein - like SR1 I	AtRABH1c	AT4G39890	1.22	0.29	1.07	0.321247	0.509517	-6.75
253793_at	myosin heavy chain - like protein (frag	XIH	AT4G28710	1.08	0.10	1.07	0.321465	0.50975	-6.75

254275_at	HSP associated protein like p48, Hom	AtHip1	AT4G22670	-1.11	-0.15	-1.07	0.321454	0.50975	-6.75
256187_at	55 kDa B regulatory subunit of phosph	ATB ALPHA	AT1G51690	1.11	0.14	1.07	0.321488	0.50975	-6.75
253007_at	putative protein hypothetical protein H	---	AT4G38090	-1.11	-0.15	-1.07	0.321494	0.50975	-6.75
252716_at	putative protein CAF protein, Arabidop	DCL3	AT3G43920	-1.11	-0.15	-1.07	0.321534	0.50978	-6.75
249430_at	GTP-binding protein-like GTP-binding	---	AT5G39900	1.14	0.19	1.07	0.321577	0.509812	-6.75
247546_at	Expressed protein ; supported by full-l	---	AT5G61605	1.09	0.13	1.07	0.32162	0.509845	-6.75
247042_at	putative protein similar to unknown pro	---	AT5G67220	-1.08	-0.11	-1.07	0.321667	0.509883	-6.75
263746_at	putative retroelement pol polyprotein	---	---	-1.08	-0.11	-1.07	0.321723	0.509937	-6.75
265026_at	putative 3-oxoacyl [acyl-carrier protein	---	AT1G24360	-1.14	-0.18	-1.07	0.321835	0.510079	-6.75
250535_at	putative protein similar to unknown pro	---	AT5G08480	1.09	0.13	1.07	0.321908	0.51016	-6.75
255650_s_	hypothetical protein	CIP4.1	AT4G00930 /	1.11	0.15	1.07	0.322104	0.510435	-6.75
255813_at	hypothetical protein contains Pfam pro	---	AT1G19930	-1.09	-0.13	-1.07	0.322127	0.510436	-6.75
246541_at	ubiquitin-fusion degradation protein-lik	---	AT5G15400	1.08	0.12	1.07	0.322201	0.510518	-6.75
255944_at	putative protein	---	---	-1.10	-0.13	-1.07	0.322404	0.510803	-6.75
267105_at	hypothetical protein predicted by gens	---	AT2G14760	1.12	0.16	1.07	0.322581	0.511049	-6.75
265975_at	putative citrate synthetase	---	AT2G11270	1.11	0.16	1.07	0.322625	0.511082	-6.75
250689_at	putative protein similar to unknown pro	---	AT5G06610	-1.24	-0.32	-1.07	0.322837	0.511382	-6.75
259793_at	AP2-containing DNA-binding protein c	---	AT1G64380	1.27	0.35	1.07	0.32286	0.511383	-6.75
260190_at	putative lipoxygenase similar to 13-lipo	---	AT1G67560	-1.16	-0.21	-1.07	0.322976	0.511485	-6.75
254991_at	putative protein conserved hypothetica	---	AT4G10620	1.11	0.15	1.07	0.322991	0.511485	-6.75
256832_at	meiotic recombination protein (AtDMC	DMC1	AT3G22880	-1.15	-0.20	-1.07	0.322991	0.511485	-6.75
246851_at	putative protein various predicted prot	AGL26	AT5G26870	1.07	0.10	1.07	0.323038	0.511524	-6.75
251093_at	putative protein several hypothetical pr	---	AT5G01360	-1.15	-0.20	-1.07	0.323075	0.511546	-6.75
259291_at	unknown protein similar to unknown pr	---	AT3G11550	-1.11	-0.15	-1.07	0.323152	0.511598	-6.75
264348_at	putative NPK1-related protein kinase 2	NRT1.1	AT1G12110	-1.63	-0.71	-1.07	0.323134	0.511598	-6.75
249741_at	putative protein contains similarity to tv	APRR5	AT5G24470	1.07	0.09	1.07	0.323287	0.511754	-6.75
252238_at	peroxidase ATP21a	---	AT3G49960	-1.09	-0.13	-1.07	0.323295	0.511754	-6.75
257005_at	hypothetical protein predicted by gens	---	AT3G14190	-1.11	-0.14	-1.07	0.32335	0.511805	-6.75
263829_at	unknown protein	---	AT2G40435	-1.28	-0.35	-1.07	0.32343	0.511859	-6.75
254031_at	putative protein other hypothetical prot	---	AT4G25920	-1.08	-0.11	-1.07	0.323429	0.511859	-6.75
267185_at	unknown protein ; supported by cDNA	OEP37	AT2G43950	-1.10	-0.13	-1.07	0.323536	0.511993	-6.75
247612_at	ATPase - like protein ATPase, Solanu	---	AT5G60730	1.10	0.13	1.06	0.323663	0.512158	-6.76
252855_at	putative protein alpha-amino-epsilon-c	AGT2	AT4G39660	-1.11	-0.15	-1.06	0.323688	0.512161	-6.76
251420_at	transcription factor - like protein transc	---	AT3G60490	-1.12	-0.17	-1.06	0.323777	0.512267	-6.76
265747_s_	hypothetical protein predicted by gene	---	AT2G06570 /	-1.09	-0.13	-1.06	0.323852	0.51235	-6.76

265403_at	putative Ta11-like non-LTR retroeleme	---	---	1.10	0.14	1.06	0.324027	0.512592	-6.76
265465_at	hypothetical protein predicted by gene	---	AT2G37070	1.23	0.29	1.06	0.32414	0.512735	-6.76
267584_at	putative protein kinase contains a prot	---	AT2G41930	1.09	0.12	1.06	0.324307	0.512964	-6.76
263587_at	putative synaptobrevin	ATVAMP712	AT2G25340	1.09	0.13	1.06	0.324429	0.51312	-6.76
264609_at	unknown protein ;supported by full-ler	---	AT1G04530	-1.17	-0.23	-1.06	0.324483	0.513171	-6.76
249222_at	putative protein similar to unknown pro	---	AT5G42450	-1.07	-0.10	-1.06	0.324538	0.513186	-6.76
266998_at	hypothetical protein predicted by gens	---	AT2G34400	-1.09	-0.13	-1.06	0.324538	0.513186	-6.76
257362_at	hypothetical protein predicted by gene	---	AT2G45840	-1.07	-0.10	-1.06	0.324568	0.513199	-6.76
262799_at	hypothetical protein predicted by gens	---	AT1G20970	-1.15	-0.20	-1.06	0.324661	0.513215	-6.76
246395_at	dirigent protein, putative similar to diri	---	AT1G58170	-1.09	-0.12	-1.06	0.324659	0.513215	-6.76
245753_at	hypothetical protein similar to putative	---	---	1.07	0.10	1.06	0.324669	0.513215	-6.76
258702_at	hypothetical protein predicted by gene	---	AT3G09730	-1.12	-0.17	-1.06	0.324665	0.513215	-6.76
259195_at	hypothetical protein predicted by gens	---	AT3G01730	1.10	0.13	1.06	0.324717	0.513255	-6.76
265204_at	hypothetical protein predicted by gens	---	AT2G36650	1.07	0.10	1.06	0.324746	0.513266	-6.76
265805_s_	60S ribosomal protein L2	EMB2296	AT2G18020 /	-1.13	-0.17	-1.06	0.324818	0.513344	-6.76
258827_at	hypothetical protein predicted by gene	---	AT3G07150	1.13	0.17	1.06	0.324886	0.513414	-6.76
252462_at	putative protein various predicted gen	---	AT3G47250	-1.08	-0.11	-1.06	0.324907	0.513414	-6.76
249131_at	putative protein contains similarity to R	APUM14	AT5G43110	-1.07	-0.10	-1.06	0.325038	0.513585	-6.76
251043_s_	putative protein various predicted prot	---	AT5G02330 /	-1.09	-0.12	-1.06	0.325082	0.513619	-6.76
257163_at	DNA-binding protein, putative similar t	MYB305	AT3G24310	1.09	0.12	1.06	0.325128	0.513627	-6.76
257737_at	uridine kinase/uracil phosphoribosyl tr	---	AT3G27440	1.09	0.12	1.06	0.325132	0.513627	-6.76
266497_at	putative retroelement pol polyprotein	---	---	1.10	0.13	1.06	0.325257	0.513788	-6.76
260342_at	hypothetical protein predicted by gene	---	AT1G69280	-1.10	-0.14	-1.06	0.325328	0.513865	-6.76
246634_at	epsilon-adaptin, putative similar to eps	---	AT1G31730	-1.08	-0.11	-1.06	0.325359	0.513867	-6.76
251818_at	vacuolar protein sorting protein 33a-lik	ATVPS33	AT3G54860	-1.09	-0.12	-1.06	0.325374	0.513867	-6.76
253799_at	putative DNA-binding protein AP2 dor	---	AT4G28140	-1.65	-0.72	-1.06	0.325463	0.513972	-6.76
263890_at	putative auxin-induced protein	---	AT2G37030	-1.13	-0.17	-1.06	0.325567	0.514101	-6.76
263724_at	putative Ta11-like non-LTR retroeleme	---	AT2G13510	1.08	0.11	1.06	0.325804	0.514439	-6.76
249668_at	putative protein similar to unknown pro	---	AT5G35870	-1.11	-0.15	-1.06	0.325856	0.514485	-6.76
250595_at	unknown protein	---	AT5G07770	1.14	0.19	1.06	0.326003	0.514681	-6.76
249953_at	FAR1 - like protein far-red impaired re	FRS12	AT5G18960	1.10	0.14	1.06	0.326053	0.514725	-6.76
248542_at	putative protein similar to unknown pro	AT5G50190	---	-1.08	-0.11	-1.06	0.326134	0.514817	-6.76
249897_at	putative protein strong similarity to unk	---	AT5G22550	1.09	0.12	1.06	0.326255	0.514939	-6.76
263331_at	unknown protein ; supported by cDNA	---	AT2G15270	-1.08	-0.12	-1.06	0.326256	0.514939	-6.76
247971_at	zinc protease PQQL-like protein	---	AT5G56730	-1.08	-0.12	-1.06	0.326463	0.515194	-6.76

248246_at	putative protein contains similarity to M	TRY	AT5G53200	-1.09	-0.13	-1.06	0.32646	0.515194	-6.76
259259_at	spindly (gibberellin signal transduction	SPY	AT3G11540	1.09	0.12	1.06	0.326533	0.51527	-6.76
247776_at	phosphoinositide-specific phospholipa	PLC4	AT5G58700	-1.11	-0.15	-1.06	0.326561	0.515278	-6.76
251001_at	putative protein	---	AT5G02670	1.12	0.16	1.06	0.326742	0.515493	-6.76
264139_at	hypothetical protein contains similarity	---	AT1G78940	-1.08	-0.12	-1.06	0.326729	0.515493	-6.76
252720_at	putative protein predicted protein, Ara	---	AT3G43970	-1.10	-0.14	-1.06	0.326795	0.51554	-6.76
259831_at	hypothetical protein predicted by gene	ZFHD1	AT1G69600	1.08	0.11	1.06	0.327043	0.515896	-6.76
249607_at	putative protein RING-H2 finger protei	---	AT5G37280	1.08	0.11	1.06	0.327071	0.515904	-6.76
264267_at	hypothetical protein contains similarity	---	AT1G60200	-1.10	-0.13	-1.06	0.327135	0.515969	-6.76
256292_at	unknown protein	---	AT1G69430	-1.10	-0.14	-1.06	0.327211	0.516018	-6.76
259262_at	unknown protein similar to nifU-like pro	ISU2	AT3G01020	-1.08	-0.11	-1.06	0.327203	0.516018	-6.76
246734_at	putative protein WRN (Werner syndro	RECQSIM	AT5G27680	-1.08	-0.11	-1.06	0.327348	0.516198	-6.76
261774_at	unknown protein	---	AT1G76260	-1.16	-0.22	-1.06	0.327464	0.516346	-6.76
245824_at	hypothetical protein predicted by gene	ATPUP17	AT1G57943	-1.14	-0.19	-1.06	0.327519	0.516381	-6.76
261623_at	hypothetical protein similar to reticuline	ATSEC1A	AT1G01980	1.09	0.12	1.06	0.327532	0.516381	-6.76
260781_at	decoy identical to GB:AAB51588 GI:19	DECOY	AT1G14620	1.28	0.36	1.06	0.327571	0.516394	-6.76
249077_at	alcohol dehydrogenase (EC 1.1.1.1) cl	HOT5	AT5G43940	1.10	0.13	1.06	0.327653	0.516394	-6.77
251466_at	putative protein hypothetical protein S	---	AT3G59340	-1.11	-0.14	-1.06	0.327648	0.516394	-6.77
249476_at	germin - like protein probable germin	---	AT5G38910	-1.11	-0.15	-1.06	0.327645	0.516394	-6.77
261598_at	unknown protein contains similarity to	---	AT1G49750	-1.46	-0.54	-1.06	0.327649	0.516394	-6.77
250049_at	putative protein predicted proteins, Ar	---	AT5G17780	-1.09	-0.13	-1.06	0.327784	0.516529	-6.77
247661_at	protein kinase - like protein kinase 1,	---	AT5G60080	1.08	0.11	1.06	0.327779	0.516529	-6.77
247058_at	dolichyl-di-phosphooligosaccharide-pro	DGL1	AT5G66680	1.10	0.14	1.05	0.327955	0.516763	-6.77
251139_at	cell division - like protein JM23 protein	---	AT5G01230	-1.11	-0.15	-1.05	0.328112	0.516938	-6.77
267387_at	hypothetical protein predicted by gens	---	AT2G44440	-1.07	-0.10	-1.05	0.328104	0.516938	-6.77
250431_at	cyclin protein - like cyclin D2.1 protein	CYCD4;2	AT5G10440	-1.08	-0.12	-1.05	0.328167	0.51699	-6.77
259576_at	RING zinc finger protein, putative con	---	AT1G35330	1.12	0.17	1.05	0.328194	0.516996	-6.77
260055_at	unknown protein similar to putative pro	---	AT1G78150	-1.08	-0.11	-1.05	0.328476	0.517327	-6.77
265286_at	putative NADH-ubiquinone oxireductas	---	AT2G20360	-1.09	-0.12	-1.05	0.328436	0.517327	-6.77
263683_at	putative NAM protein similar to GB:AA	FEZ	AT1G26870	1.09	0.12	1.05	0.328495	0.517327	-6.77
260887_at	ascorbate oxidase promoter-binding p	---	AT1G29160	1.32	0.40	1.05	0.328486	0.517327	-6.77
247379_at	unknown protein	---	---	-1.12	-0.16	-1.05	0.32858	0.517426	-6.77
254990_at	RNA-binding protein ;supported by ful	CID12	AT4G10610	1.07	0.10	1.05	0.328691	0.517523	-6.77
249637_at	hypothetical protein	---	AT5G36900	-1.08	-0.11	-1.05	0.32871	0.517523	-6.77
248089_at	salt stress inducible small GTP binding	AtRAN4	AT5G55080	1.10	0.13	1.05	0.328684	0.517523	-6.77

247658_at	actin depolymerizing factor 3 - like pro	ADF3	AT5G59880	1.07	0.10	1.05	0.328768	0.517579	-6.77
264796_at	unknown protein similar to ESTs gb|T2	ZIGA4	AT1G08680	1.09	0.12	1.05	0.328818	0.517603	-6.77
254067_at	hypothetical protein	NAP8	AT4G25450	1.08	0.11	1.05	0.328829	0.517603	-6.77
249535_at	transporter -like protein N system ami	---	AT5G38820	-1.11	-0.15	-1.05	0.328876	0.517641	-6.77
255745_at	hypothetical protein predicted by gene	---	AT1G32030	-1.07	-0.09	-1.05	0.328942	0.51771	-6.77
257289_at	hypothetical protein	---	AT3G29690	-1.08	-0.11	-1.05	0.329267	0.51815	-6.77
248960_at	subtilisin-like protease	---	AT5G45640	-1.13	-0.17	-1.05	0.329264	0.51815	-6.77
246961_at	unknown protein	---	AT5G24710	-1.16	-0.22	-1.05	0.329381	0.51828	-6.77
261399_at	receptor protein kinase, putative simila	---	AT1G79620	-1.10	-0.14	-1.05	0.329395	0.51828	-6.77
245979_at	putative protein leucine zipper-contain	ATEXO70C1	AT5G13150	-1.07	-0.10	-1.05	0.329486	0.518387	-6.77
248000_at	WD-repeat protein-like ;supported by	---	AT5G56190	1.10	0.14	1.05	0.329562	0.518471	-6.77
261074_at	hypothetical protein predicted by gene	---	AT1G07290	-1.08	-0.12	-1.05	0.329693	0.51857	-6.77
252675_at	putative protein hypothetical proteins -	---	---	1.08	0.11	1.05	0.329693	0.51857	-6.77
258268_at	putative WD-repeat protein contains P	WSIP2	AT3G15880	1.14	0.19	1.05	0.329655	0.51857	-6.77
264964_at	hypothetical protein predicted by gene	---	AT1G60460	-1.11	-0.15	-1.05	0.329721	0.518578	-6.77
245324_at	lactate dehydrogenase (LDH1) ;suppo	---	AT4G17260	-1.22	-0.29	-1.05	0.329803	0.518635	-6.77
257631_at	cytochrome P450, putative similar to c	CYP71B17	AT3G26160	1.13	0.18	1.05	0.329794	0.518635	-6.77
267007_at	60S ribosomal protein L18A ; supporte	---	AT2G34480	-1.15	-0.20	-1.05	0.329902	0.518647	-6.77
251788_at	putative protein	---	AT3G55420	-1.22	-0.29	-1.05	0.329872	0.518647	-6.77
257879_at	unknown protein	---	AT3G17160	-1.15	-0.20	-1.05	0.329876	0.518647	-6.77
249132_at	putative protein contains similarity to u	---	AT5G43120	-1.09	-0.13	-1.05	0.329887	0.518647	-6.77
247879_at	unknown protein	---	AT5G57770	-1.07	-0.10	-1.05	0.329933	0.518661	-6.77
254309_s_	putative protein predicted protein, Ara	---	AT4G22390 /	-1.11	-0.14	-1.05	0.329974	0.518689	-6.77
253244_at	putative protein SEC14 protein, Sacch	COW1	AT4G34580	-1.12	-0.16	-1.05	0.330053	0.518779	-6.77
246192_at	translation initiation factor eIF-2 beta c	EIF2 BETA	AT5G20920	1.08	0.11	1.05	0.330094	0.518807	-6.77
258035_at	putative Ca2+-transporting ATPase sir	ACA9	AT3G21180	1.10	0.13	1.05	0.330206	0.518948	-6.77
257395_at	putative salt-inducible protein	---	AT2G15630	1.12	0.16	1.05	0.330286	0.519038	-6.77
251276_at	putative protein hypothetical protein T	SDG14	AT3G61740	1.08	0.11	1.05	0.330313	0.519043	-6.77
259581_at	RING zinc finger protein, putative con	---	AT1G28040	1.10	0.13	1.05	0.330412	0.519163	-6.77
250622_at	putative transcription factor AP2 doma	---	AT5G07310	-1.08	-0.11	-1.05	0.330541	0.519187	-6.77
253183_at	putative protein predicted protein, Ara	---	AT4G35220	1.07	0.10	1.05	0.330534	0.519187	-6.77
247542_at	autophagocytosis protein - like autoph	ATG3	AT5G61500	1.10	0.14	1.05	0.330469	0.519187	-6.77
262038_at	invertase, putative similar to neutral in	CINV1	AT1G35580	1.15	0.20	1.05	0.330512	0.519187	-6.77
255565_at	putative CHP-rich zinc finger protein s	---	AT4G01760	-1.08	-0.10	-1.05	0.330494	0.519187	-6.77
248782_at	palmitoyl-protein thioesterase precurso	---	AT5G47340	-1.09	-0.12	-1.05	0.330655	0.519331	-6.77

257232_at	phytochrome-associated protein 1 (PA	PAP1	AT3G16500	-1.11	-0.15	-1.05	0.330687	0.519345	-6.77
248415_at	unknown protein	---	AT5G51620	-1.08	-0.11	-1.05	0.330716	0.519355	-6.77
249384_at	putative protein hypothetical protein F	---	AT5G39890	1.07	0.10	1.05	0.33088	0.519577	-6.77
261115_at	hypothetical protein predicted by gene	---	AT1G75360	-1.07	-0.10	-1.05	0.330918	0.51959	-6.77
257037_at	nuclear acid binding protein, putative	ATRBP47B	AT3G19130	-1.18	-0.24	-1.05	0.330934	0.51959	-6.77
247414_at	unknown protein	EMB2759	AT5G63050	-1.11	-0.15	-1.05	0.331193	0.519949	-6.77
247736_at	actin 4 ;supported by full-length cDNA	ACT4	AT5G59370	-1.08	-0.11	-1.05	0.331209	0.519949	-6.77
261995_at	unknown protein similar to N-terminal I	---	AT1G33850 /	-1.07	-0.09	-1.05	0.331251	0.519981	-6.77
258224_at	LEA76 homologue type2 identical to LI	---	AT3G15670	-1.08	-0.11	-1.05	0.331378	0.520144	-6.77
262445_at	Expressed protein ; supported by full-le	---	AT1G47485	-1.08	-0.12	-1.05	0.331445	0.520213	-6.77
264982_at	hypothetical protein predicted by gens	---	AT1G27220	1.10	0.13	1.05	0.331476	0.520226	-6.77
248725_at	acetyl-CoA:benzylalcohol acetyltranfer	---	AT5G47980	-1.09	-0.12	-1.05	0.331545	0.520227	-6.77
251677_at	putative protein hypothetical protein A	BHLH039	AT3G56980	-1.31	-0.39	-1.05	0.331515	0.520227	-6.77
259547_at	gypsy/Ty3 element polyprotein, putati	---	---	1.09	0.12	1.05	0.331539	0.520227	-6.77
245445_at	apetala2 domain TINY like protein	---	AT4G16750	-1.24	-0.31	-1.05	0.331596	0.520271	-6.77
249882_at	putative protein contains similarity to C	---	AT5G22890	-1.07	-0.10	-1.05	0.331692	0.520382	-6.77
265452_at	putative bHLH transcription factor	ATAIB	AT2G46510	1.31	0.39	1.05	0.331712	0.520382	-6.77
258793_at	hypothetical protein supported by full-l	---	AT3G04780	1.08	0.12	1.05	0.331982	0.52077	-6.78
265006_at	unknown protein similar to small zinc fi	TIM13	AT1G61570	1.21	0.28	1.05	0.332028	0.520806	-6.78
247562_at	putative protein	---	AT5G61120	-1.07	-0.10	-1.04	0.332148	0.520929	-6.78
250773_at	putative protein similar to unknown pro	---	AT5G05430	-1.15	-0.20	-1.04	0.332152	0.520929	-6.78
254429_at	Expressed protein ; supported by full-le	---	AT4G21105	1.09	0.12	1.04	0.332233	0.520987	-6.78
264612_at	unknown protein similar to GB:AAC374	---	AT1G04560	-1.12	-0.16	-1.04	0.332235	0.520987	-6.78
267408_at	putative CTP synthase	---	AT2G34890	-1.08	-0.11	-1.04	0.332315	0.521078	-6.78
253120_at	putative protein phospholipase D, Ara	PLDDELTA	AT4G35790	-1.12	-0.16	-1.04	0.332423	0.52121	-6.78
260620_at	unknown protein	---	AT1G08070	1.09	0.12	1.04	0.332569	0.521404	-6.78
264946_at	hypothetical protein predicted by gene	---	AT1G77010	1.11	0.15	1.04	0.33262	0.521448	-6.78
249844_at	putative protein similar to unknown pro	---	AT5G23590	-1.10	-0.14	-1.04	0.33267	0.521452	-6.78
259697_at	putative DNA-binding protein similar to	---	AT1G68920	1.08	0.11	1.04	0.332691	0.521452	-6.78
255790_at	hypothetical protein predicted by gene	---	AT2G33560	1.09	0.12	1.04	0.332648	0.521452	-6.78
251234_s_	putative dTDP-glucose 4-6-dehydratas	UXS4	AT2G47650 /	-1.13	-0.18	-1.04	0.332743	0.521498	-6.78
261134_at	cytochrome P450, putative similar to C	CYP722A1	AT1G19630	1.08	0.11	1.04	0.332778	0.521516	-6.78
264995_at	mutator-like transposase, putative sim	---	---	1.12	0.16	1.04	0.332923	0.521707	-6.78
245240_at	polyprotein, putative similar to polypro	---	---	-1.10	-0.14	-1.04	0.333055	0.521878	-6.78
266693_at	unknown protein predicted by genscan	MIOX2	AT2G19800	-1.56	-0.64	-1.04	0.33308	0.521882	-6.78

265932_at	hypothetical protein predicted by grail	LBD8	AT2G19510	-1.07	-0.09	-1.04	0.333183	0.521936	-6.78
260850_at	glucose 6 phosphate/phosphate trans	---	AT1G21870	-1.10	-0.14	-1.04	0.333141	0.521936	-6.78
260571_at	MAP kinase (ATMPK6) identical to GB	ATMPK6	AT2G43790	-1.08	-0.11	-1.04	0.333164	0.521936	-6.78
247271_at	nuclear protein-like	---	AT5G64270	1.10	0.14	1.04	0.333211	0.521943	-6.78
260559_at	putative polygalacturonase	---	AT2G43860	-1.10	-0.14	-1.04	0.333281	0.522018	-6.78
258034_at	hypothetical protein predicted by gene	---	AT3G21300	-1.22	-0.29	-1.04	0.333322	0.522047	-6.78
255488_at	putative serine/threonine protein kinas	---	AT4G02630	-1.12	-0.16	-1.04	0.333484	0.522227	-6.78
252695_s_	hypothetical protein predicted proteins	---	---	-1.06	-0.09	-1.04	0.333461	0.522227	-6.78
246745_at	60S ribosomal protein L22 - like ribos	---	AT5G27770	-1.16	-0.21	-1.04	0.33363	0.52242	-6.78
256049_at	unknown protein	---	AT1G07010	1.11	0.16	1.04	0.333653	0.52242	-6.78
264505_at	putative nodulin protein, N21 Similar t	---	AT1G09380	1.13	0.18	1.04	0.333725	0.522498	-6.78
264023_at	Expressed protein ; supported by full-l	---	AT2G21195	-1.15	-0.21	-1.04	0.333778	0.522509	-6.78
251638_at	40S ribosomal protein S2 homolog 40	---	AT3G57490	1.18	0.24	1.04	0.333761	0.522509	-6.78
266128_at	hypothetical protein predicted by gens	EMB2766	---	-1.09	-0.12	-1.04	0.333869	0.522604	-6.78
255057_at	hypothetical protein	---	AT4G09840	-1.07	-0.10	-1.04	0.333885	0.522604	-6.78
266079_at	unknown protein	LCD1	AT2G37860	-1.11	-0.15	-1.04	0.333928	0.522636	-6.78
255318_at	hypothetical protein	---	AT4G04190	-1.10	-0.14	-1.04	0.334231	0.523075	-6.78
257498_at	hypothetical protein predicted by gene	---	AT1G69660	1.08	0.12	1.04	0.334329	0.523192	-6.78
260596_at	unknown protein	TIM50	AT1G55900	1.15	0.20	1.04	0.334417	0.523234	-6.78
262442_at	unknown protein identical to hypothetic	---	AT1G47420	1.08	0.11	1.04	0.33444	0.523234	-6.78
267291_at	putative C2H2-type zinc finger protein	---	AT2G23740	1.16	0.21	1.04	0.33443	0.523234	-6.78
248745_at	unknown protein	---	AT5G48250	1.11	0.15	1.04	0.334447	0.523234	-6.78
249440_at	protein kinase -like protein probable p	---	AT5G40030	1.08	0.11	1.04	0.334503	0.523285	-6.78
252510_at	putative protein serine/threonine-spec	---	AT3G46270	1.08	0.12	1.04	0.334553	0.523296	-6.78
266753_at	auxin-induced protein (IAA20) identica	IAA20	AT2G46990	-1.08	-0.11	-1.04	0.334556	0.523296	-6.78
250108_at	homeobox-leucine zipper protein HAT	ATHB-3	AT5G15150	1.11	0.15	1.04	0.334755	0.523536	-6.78
260909_at	hypothetical protein predicted by gene	---	AT1G02670	-1.10	-0.13	-1.04	0.334755	0.523536	-6.78
250105_at	putative protein contains similarity to D	RAD4	AT5G16630	1.17	0.22	1.04	0.334831	0.523618	-6.78
260779_at	splicing factor, putative similar to hum	---	AT1G14650	-1.09	-0.12	-1.04	0.334857	0.523623	-6.78
250625_at	calnexin homolog	---	AT5G07340	-1.13	-0.17	-1.04	0.334942	0.52372	-6.78
245597_at	salt-inducible protein homolog	---	AT4G14190	1.08	0.12	1.04	0.335049	0.523846	-6.78
266544_at	similar to late embryogenesis abundan	---	AT2G35300	1.07	0.10	1.04	0.335069	0.523846	-6.78
265933_at	putative esterase contains esterase/lip	---	AT2G19550	-1.10	-0.13	-1.04	0.335182	0.523987	-6.78
265626_at	unknown protein ;supported by full-len	---	AT2G27260	-1.09	-0.13	-1.04	0.335224	0.523994	-6.78
256774_at	hypothetical protein predicted by gene	---	AT3G13760	-1.07	-0.10	-1.04	0.335232	0.523994	-6.78

246933_at	ZFP3 zinc finger protein ; supported b	ZFP3	AT5G25160	1.06	0.09	1.04	0.335375	0.524169	-6.78
263447_s_	putative PHD-type zinc finger protein	ATX2	AT1G05830 /	1.19	0.25	1.04	0.33539	0.524169	-6.78
249496_s_	putative protein predicted proteins - Ar	---	AT5G39140 /	1.08	0.11	1.04	0.33547	0.524259	-6.78
267278_at	unknown protein ; supported by full-le	---	AT2G19350	1.06	0.09	1.04	0.335495	0.524262	-6.78
263983_at	unknown protein ;supported by full-ler	---	AT2G42780	1.07	0.10	1.04	0.335566	0.524337	-6.78
264565_at	hypothetical protein Similar to hypothe	---	AT1G05280	1.11	0.15	1.04	0.335596	0.524347	-6.78
263979_at	En/Spm-like transposon protein relatec	PDF1	AT2G42840	1.13	0.17	1.04	0.335689	0.524443	-6.78
262789_at	putative auxin-induced protein strong s	---	AT1G10810	1.08	0.11	1.04	0.335703	0.524443	-6.78
259282_at	unknown protein similar to unknown pr	GPAT5	AT3G11430	-1.12	-0.16	-1.04	0.335726	0.524443	-6.78
262988_at	putative alanine aminotransfera	GGT1	AT1G23310	-1.08	-0.11	-1.04	0.335797	0.524518	-6.78
259045_at	calmodulin-like protein similar to calm	---	AT3G03410	1.08	0.11	1.04	0.335853	0.52457	-6.78
261180_at	hypothetical protein predicted by gene	---	---	1.08	0.11	1.04	0.335913	0.524627	-6.78
246637_at	putative protein polymorphic membrar	---	AT5G34870	1.09	0.13	1.04	0.336097	0.524878	-6.79
249294_at	unknown protein	---	AT5G41270	-1.14	-0.19	-1.04	0.336194	0.524957	-6.79
267313_at	putative protein phosphatase 2C	---	AT2G34740	-1.11	-0.15	-1.04	0.336192	0.524957	-6.79
249843_at	putative protein similar to unknown pro	SGS3	AT5G23570	1.13	0.18	1.04	0.336247	0.525005	-6.79
263058_at	putative non-LTR retrolelement revers	---	---	-1.09	-0.12	-1.04	0.336374	0.525166	-6.79
247315_at	unknown protein	---	AT5G64010	1.09	0.12	1.03	0.336597	0.52545	-6.79
248652_at	putative protein contains similarity to p	SHV2	AT5G49270	-1.14	-0.19	-1.03	0.336601	0.52545	-6.79
264582_at	putative ovule-specific homeotic protei	HDG2	AT1G05230	1.09	0.12	1.03	0.336675	0.525529	-6.79
249674_at	unknown protein	---	AT5G35930	1.07	0.10	1.03	0.336823	0.525724	-6.79
256971_at	unknown protein contains Pfam profile	---	AT3G21100	1.12	0.16	1.03	0.336894	0.525799	-6.79
258940_at	putative lipase acylhydrolase contains	---	AT3G09930	-1.07	-0.09	-1.03	0.337062	0.526017	-6.79
258756_at	hypothetical protein similar to hypothet	---	AT3G11960	1.09	0.13	1.03	0.33708	0.526017	-6.79
258724_at	unknown protein	---	AT3G09600	-1.07	-0.10	-1.03	0.337103	0.526018	-6.79
253306_at	dynamin-like protein ADL2	DRP3A	AT4G33650	1.08	0.11	1.03	0.337276	0.526251	-6.79
255271_at	putative protein (ubiquitin like) to vario	---	AT4G05260	-1.09	-0.13	-1.03	0.33744	0.526472	-6.79
250391_at	putative protein predicted proteins, Ar	---	---	-1.09	-0.13	-1.03	0.337482	0.5265	-6.79
245206_at	putative protein similarity to NCA2 pro	DGS1	AT5G12290	1.10	0.13	1.03	0.33758	0.526617	-6.79
253567_at	protein kinase-like protein serine/threc	---	AT4G31230	1.12	0.16	1.03	0.337784	0.526864	-6.79
256976_at	unknown protein similar to putative ret	---	---	1.13	0.18	1.03	0.337763	0.526864	-6.79
257968_at	hypothetical protein predicted by gene	---	AT3G27550	1.13	0.18	1.03	0.337829	0.526878	-6.79
257849_at	unknown protein	ECT5	AT3G13060	-1.12	-0.16	-1.03	0.337839	0.526878	-6.79
262102_at	hypothetical protein contains similarity	CUL2	AT1G02980	1.07	0.10	1.03	0.337897	0.526931	-6.79
260189_at	putative urease similar to urease GB:2	URE	AT1G67550	-1.10	-0.14	-1.03	0.337967	0.527005	-6.79

246519_at	proline-rich protein other proline-rich p	---	AT3G23750 /	-1.57	-0.65	-1.03	0.338012	0.52704	-6.79
246532_at	putative protein beta-glucan-elicitor re	---	AT5G15870	1.39	0.48	1.03	0.338062	0.527081	-6.79
247992_at	unknown protein	---	AT5G56520	-1.08	-0.12	-1.03	0.338312	0.527435	-6.79
254586_at	TMV resistance protein N-like TMV re	---	AT4G19510	-1.10	-0.13	-1.03	0.338352	0.52746	-6.79
246506_at	putative protein hypothetical protein T	---	AT5G16110	1.11	0.15	1.03	0.338411	0.527518	-6.79
267093_at	high affinity Ca2+ antiporter identical t	CAX1	AT2G38170	-1.15	-0.20	-1.03	0.33844	0.52752	-6.79
248262_at	Avr9 elicitor response protein-like ; su	---	AT5G53340	-1.12	-0.16	-1.03	0.338459	0.52752	-6.79
258260_at	unknown protein ; supported by cDNA	---	AT3G26850	1.08	0.11	1.03	0.338562	0.527608	-6.79
256174_at	NADP-specific glutatamate dehydroge	---	AT1G51720	1.09	0.12	1.03	0.338555	0.527608	-6.79
264070_at	putative cyclin-dependent kinase regul	CKS1	AT2G27960	-1.13	-0.17	-1.03	0.33866	0.527629	-6.79
265977_at	putative retroelement pol polyprotein	---	---	-1.07	-0.10	-1.03	0.338626	0.527629	-6.79
267248_at	hypothetical protein predicted by gene	---	AT2G30120	-1.11	-0.15	-1.03	0.338602	0.527629	-6.79
258967_at	hypothetical protein predicted by gens	---	AT3G10470	-1.09	-0.13	-1.03	0.338668	0.527629	-6.79
264953_at	alcohol dehydrogenase identical to alc	ADH1	AT1G77120	-1.12	-0.16	-1.03	0.338739	0.527698	-6.79
261710_at	hypothetical protein identical to hypoth	---	AT1G32730	1.10	0.14	1.03	0.338758	0.527698	-6.79
258330_at	unknown protein	ROPGEF13	AT3G16130	-1.09	-0.12	-1.03	0.338907	0.527893	-6.79
253108_at	putative bZIP transcription factor Dc3	FD	AT4G35900	-1.17	-0.22	-1.03	0.33897	0.527955	-6.79
254568_x_	hypothtetical protein	---	---	-1.10	-0.14	-1.03	0.339019	0.527959	-6.79
245299_at	ras-related small GTP-binding protein	ATRAB1C	AT4G17530	1.12	0.16	1.03	0.339013	0.527959	-6.79
267359_at	hypothetical protein predicted by gene	---	AT2G40020	-1.12	-0.16	-1.03	0.339057	0.527962	-6.79
263312_at	putative replication protein A1	---	---	-1.08	-0.11	-1.03	0.339067	0.527962	-6.79
262257_at	hypothetical protein predicted by gene	---	AT1G53860	-1.09	-0.13	-1.03	0.339148	0.528052	-6.79
255234_at	contains similarity to Medicago truncat	---	AT4G05500	1.09	0.12	1.03	0.339174	0.528057	-6.79
254655_s_	ribosomal protein L32 -like protein ribo	---	AT4G18100 /	1.15	0.20	1.03	0.339198	0.528058	-6.79
257874_at	hypothetical protein	---	AT3G17110	1.09	0.13	1.03	0.339392	0.528288	-6.79
253844_at	hypothetical protein	---	AT4G27930	1.10	0.13	1.03	0.339383	0.528288	-6.79
259631_at	heat shock protein, putative similar to	ERD2	AT1G56410	-1.07	-0.10	-1.03	0.339437	0.528296	-6.79
246889_at	putative protein various predicted prot	---	AT5G25470	-1.10	-0.14	-1.03	0.339456	0.528296	-6.79
266030_x_	hypothetical protein predicted by gens	---	---	1.10	0.14	1.03	0.339467	0.528296	-6.79
266433_at	unknown protein	---	AT2G07110	1.07	0.10	1.03	0.339639	0.528528	-6.79
247530_at	glycosylasparaginase - like protein gly	---	AT5G61540	-1.12	-0.17	-1.03	0.339815	0.528735	-6.79
261866_at	scarecrow-like 3 identical to GB:AAD2	SCL3	AT1G50420	-1.39	-0.47	-1.03	0.339818	0.528735	-6.79
265816_s_	putative elongation factor beta-1 ;sup	---	AT1G30230 /	1.12	0.16	1.03	0.340004	0.528952	-6.79
264848_at	unknown protein ;supported by full-ler	---	AT2G17350	1.07	0.10	1.03	0.339985	0.528952	-6.79
249479_at	germin - like protein probable germin	---	AT5G38960	-1.11	-0.15	-1.03	0.340157	0.529106	-6.79

247811_at	leucine zipper-containing protein leuci	ATEXO70B1	AT5G58430	1.22	0.28	1.03	0.340173	0.529106	-6.79
259387_at	histone H3 protein, putative similar to	---	AT1G13370	-1.08	-0.11	-1.03	0.340169	0.529106	-6.79
257376_at	hypothetical protein predicted by gens	---	AT2G32350	-1.09	-0.12	-1.03	0.340282	0.529168	-6.80
250840_at	putative protein predicted protein, Ara	---	---	-1.12	-0.16	-1.03	0.340238	0.529168	-6.79
259634_at	hypothetical protein	---	AT1G56380	1.07	0.10	1.03	0.34026	0.529168	-6.79
260169_at	hypothetical protein predicted by gen	FUT13	AT1G71990	-1.16	-0.22	-1.03	0.340321	0.529193	-6.80
263999_at	hypothetical protein predicted by gene	---	AT2G22370	-1.09	-0.13	-1.03	0.340534	0.529487	-6.80
255143_at	putative protein several hypothetical pr	---	AT4G08430	1.06	0.09	1.03	0.340648	0.529629	-6.80
262613_at	putative DNA-binding protein similar to	WRKY4	AT1G13960	1.08	0.12	1.03	0.340685	0.52965	-6.80
250678_at	selenium-binding protein-like	---	AT5G06540	1.07	0.10	1.02	0.340804	0.529748	-6.80
257820_at	immunophilin (FKBP15-1) identical to	FKBP15-1	AT3G25220	1.10	0.14	1.02	0.340867	0.529748	-6.80
263167_at	unknown protein Belongs to PF|01121	---	AT1G03030	1.10	0.14	1.02	0.340853	0.529748	-6.80
245170_at	60S ribosomal protein L18, 5'partial N	---	AT2G47570	-1.09	-0.12	-1.02	0.340911	0.529748	-6.80
247639_s_	undecaprenyl diphosphate synthase u	---	AT5G60500 /	1.06	0.09	1.02	0.340905	0.529748	-6.80
261811_at	DNA polymerase epsilon catalytic sub	TIL1	AT1G08260	-1.13	-0.18	-1.02	0.340863	0.529748	-6.80
257709_at	unknown protein similar to negative re	---	AT3G27325	1.13	0.17	1.02	0.340872	0.529748	-6.80
261693_at	hypothetical protein similar to hypothet	DCP1	AT1G08370	-1.07	-0.10	-1.02	0.341037	0.529908	-6.80
257607_at	hypothetical protein predicted by gens	---	AT3G13880	1.07	0.09	1.02	0.341131	0.530018	-6.80
260980_at	hypothetical protein predicted by gene	---	AT1G53600	-1.12	-0.16	-1.02	0.341234	0.530142	-6.80
257288_at	anthocyanin 5-aromatic acyltransferas	---	AT3G29670	-1.08	-0.11	-1.02	0.341301	0.530173	-6.80
254261_at	beta adaptin - like protein beta-adaptin	---	AT4G23460	1.08	0.11	1.02	0.3413	0.530173	-6.80
265128_at	hypothetical protein predicted by gens	---	AT1G30860	-1.11	-0.15	-1.02	0.341376	0.530218	-6.80
262194_at	hypothetical protein similar to putative	---	AT1G77930	1.14	0.18	1.02	0.341365	0.530218	-6.80
264046_at	putative non-LTR retroelement reverse	---	AT2G22440	-1.09	-0.12	-1.02	0.341423	0.530219	-6.80
248536_at	ankyrin-like protein	---	AT5G50140	-1.08	-0.12	-1.02	0.341415	0.530219	-6.80
255520_at	putative ribosomal protein L19 similar t	---	AT4G02230	1.15	0.20	1.02	0.3417	0.530511	-6.80
246527_at	ribosomal protein-like 40S RIBOSOMA	---	AT5G15750	1.21	0.28	1.02	0.341712	0.530511	-6.80
249624_at	putative protein predicted proteins, Ar	---	AT5G37570	1.11	0.16	1.02	0.341728	0.530511	-6.80
254149_at	putative protein hypothetical protein -	---	AT4G24300	-1.12	-0.17	-1.02	0.341721	0.530511	-6.80
263910_at	hypothetical protein predicted by gens	---	AT2G36550	-1.08	-0.11	-1.02	0.341716	0.530511	-6.80
255667_at	phospholipase D, putative	PLDBETA2	AT4G00240	-1.08	-0.11	-1.02	0.341954	0.530791	-6.80
267522_at	hypothetical protein predicted by gens	---	AT2G30430	1.09	0.13	1.02	0.341936	0.530791	-6.80
246582_at	hypothetical protein predicted by gene	---	AT1G31750	1.21	0.27	1.02	0.342012	0.530808	-6.80
264958_at	unknown protein ; supported by cDNA	---	AT1G76960	1.14	0.19	1.02	0.342035	0.530808	-6.80
265970_at	Mutator-like transposase similar to MU	---	---	1.07	0.10	1.02	0.342018	0.530808	-6.80

260265_at	hypothetical protein similar to hypothet	LBD42	AT1G68510	-1.10	-0.14	-1.02	0.342146	0.530944	-6.80
263742_at	predicted protein	---	AT2G20625	-1.08	-0.11	-1.02	0.342182	0.530963	-6.80
245046_at	putative membrane transporter ; supp	PDE135	AT2G26510	1.09	0.13	1.02	0.342204	0.530963	-6.80
266758_at	unknown protein	POL	AT2G46920	-1.09	-0.13	-1.02	0.342285	0.531052	-6.80
264689_at	hypothetical protein predicted by gens	---	AT1G09900	1.13	0.17	1.02	0.34254	0.53141	-6.80
246054_at	putative protein predicted proteins, Ar	---	AT5G08360	-1.08	-0.11	-1.02	0.34261	0.531484	-6.80
262994_at	hypothetical protein predicted by gens	---	AT1G54420	-1.07	-0.10	-1.02	0.342642	0.531497	-6.80
253011_at	putative protein retrotransposon -like	EDA40	AT4G37890	1.18	0.24	1.02	0.342787	0.531686	-6.80
261820_at	hypothetical protein predicted by gene	---	AT1G11420	1.12	0.17	1.02	0.34291	0.53184	-6.80
254564_at	neoxanthin cleavage enzyme-like prot	NCED4	AT4G19170	-1.15	-0.20	-1.02	0.343046	0.532015	-6.80
261582_at	unknown protein ; supported by cDNA	GIF2	AT1G01160	-1.08	-0.11	-1.02	0.343118	0.532091	-6.80
264967_at	unknown protein ;supported by full-len	---	AT1G67250	-1.07	-0.10	-1.02	0.343273	0.532295	-6.80
247737_at	putative protein various predicted prot	---	AT5G59200	-1.06	-0.09	-1.02	0.343332	0.532349	-6.80
255054_s_	cellulase-like protein cellulase (EC 3.2	AtGH9B15	AT4G09740 /	-1.09	-0.12	-1.02	0.343355	0.532349	-6.80
257274_at	geranylgeranyl pyrophosphate synthe	---	AT3G14510	1.09	0.13	1.02	0.343458	0.532473	-6.80
254294_at	putative membrane protein membrane	ATRBL7	AT4G23070	-1.16	-0.22	-1.02	0.343531	0.532514	-6.80
264896_at	Hypothetical protein similar to endo-1,	AtGH9B6	AT1G23210	-1.08	-0.11	-1.02	0.343523	0.532514	-6.80
249435_at	putative protein tail-specific thyroid ho	---	AT5G39970	-1.07	-0.09	-1.02	0.343645	0.532654	-6.80
263660_at	unknown protein ESTs gb|N65789,gb	MPI7	AT1G04260	-1.08	-0.11	-1.02	0.343729	0.532749	-6.80
245836_at	hypothetical protein similar to hypothet	---	---	-1.08	-0.11	-1.02	0.343837	0.53288	-6.80
249048_at	auxin-repressed protein-like ;supporte	---	AT5G44300	1.09	0.12	1.02	0.343903	0.532945	-6.80
250789_at	putative protein contains similarity to c	---	AT5G05630	-1.09	-0.12	-1.02	0.343997	0.533046	-6.80
262458_at	serine/threonine kinase, putative simil	---	AT1G11280	-1.09	-0.12	-1.02	0.344014	0.533046	-6.80
255759_at	hypothetical protein predicted by gene	---	AT1G16790	1.09	0.12	1.02	0.34409	0.533126	-6.80
248431_at	auxin-responsive GH3-like protein	---	AT5G51470	-1.09	-0.12	-1.02	0.344224	0.533298	-6.80
245694_at	EF - hand Calcium binding protein - lik	---	AT5G04170	1.08	0.11	1.02	0.344291	0.533365	-6.80
255757_at	putative protein	ROPGEF3	AT4G00460	-1.07	-0.10	-1.02	0.344385	0.533476	-6.80
255422_at	putative D-type cyclin	CYCD6;1	AT4G03270	-1.09	-0.12	-1.02	0.34446	0.533555	-6.80
250770_at	laccase (diphenol oxidase)	LAC12	AT5G05390	-1.12	-0.16	-1.02	0.344545	0.533651	-6.80
246970_at	cytochrome P450-like protein fatty aci	CYP714A2	AT5G24900	-1.14	-0.19	-1.02	0.344819	0.534038	-6.81
257509_at	unknown protein	---	AT1G63190	1.09	0.13	1.02	0.344899	0.534112	-6.81
249683_x_	putative protein similar to unknown pro	---	---	-1.10	-0.13	-1.02	0.344913	0.534112	-6.81
263716_at	26S proteasome regulatory subunit S2	RPN1A	AT2G20580	-1.07	-0.10	-1.02	0.344942	0.53412	-6.81
265901_at	putative selenium-binding protein	---	AT2G25580	1.10	0.14	1.02	0.344978	0.53414	-6.81
256983_at	chaperonin 60 beta, putative very sim	---	AT3G13470	1.22	0.29	1.02	0.345011	0.534154	-6.81

266301_at	putative MYB family transcription facto	AtMYB81	AT2G26960	-1.12	-0.17	-1.02	0.345082	0.534229	-6.81
254116_at	hypothetical protein	---	AT4G24730	-1.08	-0.11	-1.02	0.345167	0.53426	-6.81
257078_at	putative MAP kinase very similar to Bn	---	AT3G15220	-1.08	-0.11	-1.02	0.345173	0.53426	-6.81
257230_at	DegP protease contains similarity to D	DegP11	AT3G16540	-1.07	-0.10	-1.02	0.345159	0.53426	-6.81
248216_at	unknown protein	---	AT5G53690	-1.08	-0.11	-1.01	0.345218	0.534294	-6.81
253633_at	putative protein tetratricopeptide repe	---	AT4G30480	-1.10	-0.14	-1.01	0.345324	0.534422	-6.81
261461_at	hypothetical protein predicted by gene	---	AT1G07860	-1.10	-0.13	-1.01	0.345386	0.534438	-6.81
254044_at	putative xyloglucan endo-1,4-beta-D-g	XTR9	AT4G25820	-1.08	-0.11	-1.01	0.345405	0.534438	-6.81
253899_at	putative protein protein disulfide-isom	ATPDIL5-4	AT4G27080	1.09	0.13	1.01	0.345404	0.534438	-6.81
245838_at	disease resistance protein, putative si	---	AT1G58410	1.09	0.12	1.01	0.345499	0.534547	-6.81
264745_at	5'-adenylylphosphosulfate reductase,	אפר-02	AT1G62180	1.15	0.20	1.01	0.345539	0.534558	-6.81
253450_at	putative protein MUS308 gene, Droso	---	AT4G32700	-1.07	-0.10	-1.01	0.345553	0.534558	-6.81
259040_at	putative glutathione transferase similar	ATGSTU8	AT3G09270	1.48	0.56	1.01	0.345621	0.534627	-6.81
257707_at	hypothetical protein predicted by gene	---	AT3G12650	-1.08	-0.11	-1.01	0.345647	0.534631	-6.81
262332_at	hypothetical protein similar to putative	---	AT1G64030	-1.08	-0.11	-1.01	0.345751	0.534755	-6.81
247623_at	receptor-like protein kinase receptor-li	---	AT5G60320	1.08	0.11	1.01	0.345823	0.53483	-6.81
264135_at	S-locus protein, putative similar to S-l	---	AT1G79030	-1.08	-0.11	-1.01	0.345959	0.535004	-6.81
265303_at	hypothetical protein	---	---	1.08	0.11	1.01	0.345993	0.535021	-6.81
256212_at	hypothetical protein	---	AT1G50970	1.10	0.13	1.01	0.34611	0.535167	-6.81
254136_at	putative protein various predicted prot	---	AT4G24860	1.08	0.11	1.01	0.346144	0.535183	-6.81
255588_at	hypothetical protein	---	AT4G01570	-1.13	-0.17	-1.01	0.346238	0.535291	-6.81
258026_at	abscisic acid responsive elements-bin	ABF4	AT3G19290	1.11	0.16	1.01	0.346333	0.535402	-6.81
247898_at	F-box protein ZTL/LFK1/ADO1, AtFBX	ZTL	AT5G57360	1.09	0.12	1.01	0.346433	0.535507	-6.81
263673_at	unknown protein	---	AT2G04800	-1.13	-0.18	-1.01	0.346448	0.535507	-6.81
256141_at	lysine and histidine specific transporte	---	AT1G48640	-1.07	-0.09	-1.01	0.346505	0.535559	-6.81
250101_at	putative protein contains similarity to b	BGLU2	AT5G16580	-1.16	-0.22	-1.01	0.34655	0.53556	-6.81
245735_at	myb-like transcription factor, putative s	MYB54	AT1G73410	-1.06	-0.09	-1.01	0.346552	0.53556	-6.81
264041_at	MADS-box protein (AGL3) ; supported	ספט-04	AT2G03710	-1.19	-0.25	-1.01	0.346601	0.535563	-6.81
254152_at	hypothetical protein	---	AT4G24410	1.08	0.10	1.01	0.34659	0.535563	-6.81
257141_at	60S ribosomal protein L34, putative si	---	AT3G28900	-1.16	-0.22	-1.01	0.346685	0.535579	-6.81
250730_at	C3HC4-type RING zinc finger protein-l	---	AT5G06490	-1.09	-0.12	-1.01	0.346706	0.535579	-6.81
259230_at	unknown protein ; supported by cDNA	OBE1	AT3G07780	1.11	0.15	1.01	0.346683	0.535579	-6.81
260557_at	putative endochitinase	---	AT2G43610	1.07	0.09	1.01	0.346642	0.535579	-6.81
252029_s_	putative RNA binding protein heteroge	---	AT3G52660 /	-1.07	-0.10	-1.01	0.346756	0.535621	-6.81
256301_at	unknown protein ;supported by full-len	---	AT1G69510	1.08	0.11	1.01	0.346837	0.535673	-6.81

257906_at	ribosomal protein, putative similar to 6	ATL5	AT3G25520	-1.22	-0.29	-1.01	0.346834	0.535673	-6.81
248629_at	mitochondrial carrier protein-like	---	AT5G48970	1.12	0.16	1.01	0.346875	0.535695	-6.81
257089_at	hypothetical protein	SVL3	AT3G20520	-1.09	-0.12	-1.01	0.346933	0.535749	-6.81
250908_at	GT2 -like protein GT2, Arabidopsis tha	PTL	AT5G03680	1.08	0.11	1.01	0.347083	0.535944	-6.81
246343_at	putative protein	---	AT3G56720	1.06	0.09	1.01	0.347365	0.536053	-6.81
251258_at	PECTINESTERASE-like protein PEC	VGDH2	AT3G62170	1.10	0.14	1.01	0.347252	0.536053	-6.81
251448_at	allyl alcohol dehydrogenase-like prote	---	AT3G59845	1.08	0.11	1.01	0.347353	0.536053	-6.81
267634_at	putative actin	---	AT2G42100	-1.07	-0.10	-1.01	0.347275	0.536053	-6.81
265540_at	Mutator-like transposase similar to MU	---	---	-1.07	-0.10	-1.01	0.347292	0.536053	-6.81
264880_at	hypothetical protein contains similarity	---	AT1G61210	1.10	0.14	1.01	0.347349	0.536053	-6.81
257581_s_	RAV-like DNA-binding protein, putativ	---	AT1G50680 /	-1.07	-0.09	-1.01	0.347184	0.536053	-6.81
265789_at	putative receptor-like protein kinase	---	AT2G01210	-1.08	-0.12	-1.01	0.347357	0.536053	-6.81
262138_at	NBS/LRR disease resistance protein,	---	AT1G52660	1.10	0.13	1.01	0.347297	0.536053	-6.81
253560_at	putative protein KIAA0800 protein, Ho	DCAF1	AT4G31160	1.09	0.12	1.01	0.347499	0.536193	-6.81
248490_at	putative protein similar to unknown pro	---	AT5G50940	-1.23	-0.30	-1.01	0.347503	0.536193	-6.81
253527_at	pathogenesis-related protein homolog	---	AT4G31470	-1.09	-0.12	-1.01	0.3476	0.536233	-6.81
262730_at	putative transport protein may be a me	ATOCT3	AT1G16390	-1.09	-0.13	-1.01	0.347582	0.536233	-6.81
259959_at	hypothetical protein predicted by gens	CYP59	AT1G53720	1.10	0.14	1.01	0.347565	0.536233	-6.81
252458_at	putative protein various predicted prot	---	AT3G47210	1.08	0.11	1.01	0.347738	0.536374	-6.81
254030_at	putative acidic ribosomal protein acidi	---	AT4G25890	-1.23	-0.29	-1.01	0.347728	0.536374	-6.81
257782_at	hypothetical protein predicted by gene	---	AT3G27120 /	-1.09	-0.12	-1.01	0.347881	0.536522	-6.81
249439_at	thaumatin-like protein thaumatin-like p	---	AT5G40020	-1.17	-0.23	-1.01	0.347863	0.536522	-6.81
266328_at	unknown protein ; supported by full-le	---	AT2G01600	1.07	0.09	1.01	0.347932	0.536565	-6.81
261721_at	unknown protein ; supported by cDNA	---	AT1G08480	1.08	0.11	1.01	0.348002	0.536636	-6.81
263051_s_	En/Spm-like transposon protein relate	---	---	1.08	0.11	1.01	0.348131	0.536767	-6.81
261880_at	unknown protein	HIT1	AT1G50500	-1.09	-0.13	-1.01	0.348134	0.536767	-6.81
257860_at	Expressed protein ; supported by cDN	---	AT3G13062	1.13	0.18	1.01	0.34822	0.536864	-6.81
255980_at	hypothetical protein ;supported by full-	---	AT1G33970	1.09	0.13	1.01	0.348362	0.537046	-6.81
246758_at	60S ribosomal protein - like 60S ribos	---	AT5G27850	-1.16	-0.21	-1.01	0.34858	0.537064	-6.81
262903_at	NADPH-dependent codeinone reducta	---	AT1G59950	1.40	0.49	1.01	0.348569	0.537064	-6.81
260237_at	putative MYB family transcription facto	MYB95	AT1G74430	1.22	0.29	1.01	0.348456	0.537064	-6.81
251569_at	putative protein several hypothetical pr	---	AT3G58290	-1.10	-0.14	-1.01	0.348609	0.537064	-6.81
260710_at	protein phosphatase 2C, putative simi	---	AT1G17545	-1.07	-0.10	-1.01	0.348606	0.537064	-6.81
248562_at	putative protein strong similarity to unk	---	AT5G49680	-1.20	-0.27	-1.01	0.34849	0.537064	-6.81
263653_at	putative ethylene receptor (ERS2) EST	ERS2	AT1G04310	1.11	0.15	1.01	0.34856	0.537064	-6.81

250363_at	putative protein predicted proteins, Or	---	AT5G11390	-1.15	-0.21	-1.01	0.348467	0.537064	-6.81
253461_at	cytochrome p450 - like protein cytochi	CYP96A2	AT4G32170	1.07	0.10	1.01	0.34847	0.537064	-6.81
259726_at	Expressed protein ; supported by full-l	SCRL6	AT1G60985	-1.07	-0.10	-1.01	0.348571	0.537064	-6.81
252362_at	hypothetical protein	PDE312	AT3G48500	1.15	0.20	1.01	0.348931	0.537452	-6.81
254228_at	putative protein ; supported by full-len	---	AT4G23620	-1.08	-0.11	-1.01	0.348891	0.537452	-6.81
249684_s_	cytochrome P450-like	---	AT5G36110 /	-1.07	-0.10	-1.01	0.348927	0.537452	-6.81
250553_at	putative protein PTD008, Homo sapie	---	AT5G07960	-1.10	-0.14	-1.01	0.349024	0.537559	-6.81
248620_at	putative protein similar to unknown pro	---	AT5G49320	-1.08	-0.11	-1.01	0.349177	0.537613	-6.82
252959_at	putative protein NADH dehydrogenas	---	AT4G38640	1.08	0.12	1.01	0.34909	0.537613	-6.82
256291_at	protein kinase, putative contains Pfam	AtNek7	AT3G12200	-1.10	-0.13	-1.01	0.349177	0.537613	-6.82
255906_at	hypothetical protein similar to RING3-li	---	AT1G17790	-1.08	-0.11	-1.01	0.349156	0.537613	-6.82
246696_at	putative protein predicted protein, Ara	---	---	1.08	0.11	1.01	0.349137	0.537613	-6.82
255265_at	kinesin - like protein kinesin like protei	ATK5	AT4G05190	-1.11	-0.15	-1.01	0.349217	0.537638	-6.82
256733_at	hypothetical protein predicted by gene	---	AT3G30370	1.08	0.11	1.01	0.349263	0.537672	-6.82
256957_at	hypothetical protein predicted by gens	---	AT3G13420	1.08	0.12	1.01	0.349312	0.537711	-6.82
255384_at	hypothetical protein	---	AT4G03580	1.07	0.09	1.01	0.349347	0.537729	-6.82
249296_at	kinesin-like protein	---	AT5G41310	-1.09	-0.13	-1.01	0.349392	0.537762	-6.82
267564_at	putative protein kinase contains a prot	---	AT2G30740	-1.09	-0.13	-1.01	0.349441	0.537802	-6.82
253380_at	hypothetical protein hypothetical prote	PGSIP3	AT4G33330	-1.09	-0.12	-1.01	0.349502	0.537859	-6.82
249744_at	beta-glucosidase	BGLU32	AT5G24550	1.11	0.15	1.01	0.349532	0.537869	-6.82
246152_at	IPP transferase - like protein tRNA de	IPT9	AT5G20040	1.08	0.11	1.00	0.349681	0.538025	-6.82
264326_at	unknown protein	---	AT1G04230	-1.10	-0.14	-1.00	0.349677	0.538025	-6.82
246700_at	cysteine synthase - like cysteine synth	---	AT5G28030	-1.18	-0.24	-1.00	0.349705	0.538026	-6.82
259955_s_	unknown protein ;supported by full-len	BZR1	AT1G19350 /	1.09	0.13	1.00	0.350033	0.538209	-6.82
261900_at	unknown protein ;supported by full-len	---	AT1G80940	1.08	0.11	1.00	0.349982	0.538209	-6.82
250542_at	hypothetical protein (fragment at BAC	---	AT5G08270	1.17	0.22	1.00	0.350037	0.538209	-6.82
261760_at	hypothetical protein similar to putative	---	AT1G15600	-1.12	-0.16	-1.00	0.349916	0.538209	-6.82
254166_at	HSP90-like protein HSP90 homolog -	SHD	AT4G24190	1.27	0.35	1.00	0.350035	0.538209	-6.82
249887_at	putative protein similar to unknown pro	---	AT5G22310	-1.28	-0.36	-1.00	0.34992	0.538209	-6.82
257328_s_	hypothetical protein	---	---	1.11	0.16	1.00	0.349973	0.538209	-6.82
246679_at	putative protein replication protein A1	---	---	-1.07	-0.10	-1.00	0.349877	0.538209	-6.82
245655_at	hypothetical protein predicted by gene	---	AT1G56530	1.07	0.09	1.00	0.349854	0.538209	-6.82
265830_at	putative helicase	---	---	1.10	0.14	1.00	0.350273	0.538537	-6.82
246942_at	anion exchanger-like protein chloride-	---	AT5G25430	-1.09	-0.12	-1.00	0.35041	0.538711	-6.82
250347_at	putative protein	---	AT5G11960	-1.08	-0.11	-1.00	0.350451	0.538738	-6.82

257445_x_	hypothetical protein predicted by gens	---	---	-1.07	-0.10	-1.00	0.35049	0.53876	-6.82
267642_at	unknown protein	---	AT2G32905 /	-1.07	-0.10	-1.00	0.35052	0.538772	-6.82
257050_at	putative protein phosphatase type 2C	---	AT3G15260	1.11	0.15	1.00	0.350571	0.5388	-6.82
247669_at	putative protein transcriptional repress	---	AT5G60170	1.11	0.15	1.00	0.350586	0.5388	-6.82
266520_at	cyclic nucleotide and calmodulin-regul	ATCNGC6	AT2G23980	1.10	0.13	1.00	0.350722	0.53883	-6.82
252930_at	putative endo-1,4-beta-glucanase end	AtGH9B18	AT4G39010	-1.10	-0.14	-1.00	0.350718	0.53883	-6.82
263520_at	putative protein kinase contains a prot	---	AT2G42640	-1.08	-0.11	-1.00	0.35063	0.53883	-6.82
263399_at	unknown protein ; supported by full-ler	---	AT2G31490	-1.08	-0.11	-1.00	0.350707	0.53883	-6.82
256522_at	unknown protein ;supported by full-len	CMPG1	AT1G66160	1.51	0.60	1.00	0.350724	0.53883	-6.82
265531_at	hypothetical protein predicted by gens	AtGRF6	AT2G06200	-1.08	-0.12	-1.00	0.350757	0.538844	-6.82
262337_at	hypothetical protein similar to hypothet	---	AT1G64260	-1.10	-0.13	-1.00	0.350997	0.539177	-6.82
259613_at	hypothetical protein predicted by gene	---	AT1G48010	1.07	0.10	1.00	0.351047	0.539218	-6.82
262384_at	disease resistance protein, putative si	---	AT1G72950	-1.11	-0.15	-1.00	0.351082	0.539236	-6.82
260246_at	hypothetical protein similar to GB:AAD	---	AT1G74220	-1.08	-0.11	-1.00	0.351123	0.539246	-6.82
267131_at	hypothetical protein predicted by gens	---	AT2G23400	-1.07	-0.10	-1.00	0.351136	0.539246	-6.82
254146_at	endo-1,4-beta-glucanase like protein	ATGH9A3	AT4G24260	-1.10	-0.14	-1.00	0.351218	0.539336	-6.82
264931_at	polygalacturonase, putative similar to	---	AT1G60590	-1.09	-0.12	-1.00	0.351255	0.539355	-6.82
266622_at	hypothetical protein predicted by gens	---	AT2G35430	1.10	0.14	1.00	0.351326	0.539428	-6.82
259712_at	putative 20S proteasome beta subunit	PBC2	AT1G77440	-1.07	-0.10	-1.00	0.351372	0.539462	-6.82
264985_at	unknown protein ;supported by full-len	---	AT1G27150	-1.15	-0.21	-1.00	0.351406	0.539478	-6.82
256506_at	unknown protein	---	AT1G75160	-1.10	-0.13	-1.00	0.351458	0.539486	-6.82
251948_at	diaminopimelate epimerase - like prot	---	AT3G53580	-1.10	-0.13	-1.00	0.351447	0.539486	-6.82
266589_at	hypothetical protein predicted by gens	---	AT2G46250	1.12	0.16	1.00	0.35163	0.539685	-6.82
256369_at	hypothetical protein predicted by gene	---	AT1G66790 /	-1.06	-0.09	-1.00	0.351635	0.539685	-6.82
255819_s_	40S ribosomal protein S26	---	AT2G40510 /	-1.08	-0.11	-1.00	0.351682	0.539718	-6.82
256074_at	unknown protein ; supported by cDNA	---	AT1G18260	1.09	0.13	1.00	0.351704	0.539718	-6.82
247887_at	unknown protein	---	AT5G57880	1.08	0.11	1.00	0.351829	0.539873	-6.82
246717_at	putative protein	---	AT5G28920	-1.07	-0.10	-1.00	0.351864	0.539891	-6.82
266729_at	50S ribosomal protein L7/L12	---	AT2G03130	1.08	0.11	1.00	0.352134	0.540269	-6.82
256880_at	major latex protein, putative similar to	---	AT3G26450	1.15	0.20	1.00	0.352221	0.540367	-6.82
249450_at	serine/threonine-specific protein kinas	SnRK1.3	AT5G39440	-1.08	-0.11	-1.00	0.352314	0.540435	-6.82
255105_at	putative sulfate transporter ; supporte	SULTR1;1	AT4G08620	-1.09	-0.12	-1.00	0.352291	0.540435	-6.82
249170_at	abscisic acid responsive elements-bin	---	AT5G42910	1.07	0.10	1.00	0.352371	0.540487	-6.82
266652_at	unknown protein	---	AT2G25760	-1.07	-0.10	-1.00	0.352409	0.540503	-6.82
249651_at	auxin response factor 8 (ARF8) ; supp	ARF8	AT5G37020	1.16	0.21	1.00	0.352429	0.540503	-6.82

248585_at	unknown protein	---	AT5G49640	-1.08	-0.11	-1.00	0.352489	0.540515	-6.82
252685_at	disease resistence - like protein RPP1	---	AT3G44410	-1.15	-0.21	-1.00	0.35246	0.540515	-6.82
267307_at	putative laccase	LAC3	AT2G30210	-1.11	-0.15	-1.00	0.352516	0.540515	-6.82
247719_at	Expressed protein ; supported by full-l	---	AT5G59305	1.09	0.12	1.00	0.352531	0.540515	-6.82
250476_at	MADS box protein FLOWERING LOC	FLC	AT5G10140	-1.08	-0.11	-1.00	0.352612	0.540602	-6.82
259228_at	unknown protein similar to hypothetica	---	AT3G07720	-1.10	-0.14	-1.00	0.352852	0.540934	-6.82
252535_at	hypothetical protein	---	AT3G46150	-1.16	-0.21	-1.00	0.352887	0.540951	-6.82
257292_s_	hypothetical protein contains Pfam pro	---	---	1.07	0.09	1.00	0.352976	0.541052	-6.82
255646_at	hypothetical protein	---	AT4G00890	-1.09	-0.12	-1.00	0.353039	0.541111	-6.82
247284_at	Isp4-like protein ; supported by full-ler	OPT4	AT5G64410	-1.20	-0.26	-1.00	0.353124	0.541152	-6.82
249184_at	receptor kinase-like protein	---	AT5G43020	-1.14	-0.18	-1.00	0.353102	0.541152	-6.82
264620_at	putative bZIP transcription factor	ATBZIP27	AT2G17770	1.10	0.14	1.00	0.353136	0.541152	-6.82
256028_at	poly(A)-binding protein, putative simila	PAB1	AT1G34140	-1.11	-0.15	-1.00	0.353209	0.541226	-6.82
256665_at	hypothetical protein predicted by gene	---	AT3G20700	-1.11	-0.15	-1.00	0.353374	0.541443	-6.82
254035_at	putative phosphatidylserine decarboxy	PSD3	AT4G25970 /	1.08	0.11	1.00	0.35362	0.541734	-6.83
250103_at	transcription factor (gb|AAD53095.1) ;	MYB43	AT5G16600	-1.08	-0.11	-1.00	0.353591	0.541734	-6.83
250331_at	putative protein self-incompatibility pr	---	AT5G11820	1.09	0.12	1.00	0.353636	0.541734	-6.83
264040_at	putative uridylyl transferase ; supporte	ACR5	AT2G03730	1.06	0.09	1.00	0.353843	0.542016	-6.83
259112_at	putative 60S ribosomal protein L22 sir	---	AT3G05560	-1.18	-0.23	-1.00	0.35387	0.542021	-6.83
267295_at	pregeranylgeranyl pyrophosphate syn	GGPS2	AT2G23800	1.08	0.11	1.00	0.354032	0.542233	-6.83
252160_at	proline-rich protein	---	AT3G50570	-1.11	-0.15	-0.99	0.35441	0.542776	-6.83
252588_at	putative protein potential transcription	---	AT3G45630	-1.07	-0.10	-0.99	0.354509	0.542891	-6.83
260158_at	unknown protein	---	AT1G79910	1.09	0.12	0.99	0.354814	0.543313	-6.83
261850_at	hypothetical protein predicted by gene	---	AT1G50470	-1.11	-0.16	-0.99	0.354832	0.543313	-6.83
245171_at	hypothetical protein predicted by gens	---	AT2G47560	-1.09	-0.12	-0.99	0.354861	0.54332	-6.83
263843_at	translin-like protein ; supported by cDI	---	AT2G37020	1.08	0.11	0.99	0.354903	0.543348	-6.83
265647_at	hypothetical protein predicted by gene	---	AT2G27410	-1.08	-0.11	-0.99	0.354971	0.54339	-6.83
256097_at	unknown protein	---	AT1G13670	-1.07	-0.09	-0.99	0.354978	0.54339	-6.83
254344_at	alcohol dehydrogenase like protein pr	---	AT4G22110	-1.13	-0.18	-0.99	0.355014	0.543406	-6.83
255484_at	putative protein similar to A. thaliana h	---	AT4G02540	-1.10	-0.13	-0.99	0.355036	0.543406	-6.83
249931_at	putative protein similar to unknown pro	QQT1	AT5G22370	-1.12	-0.16	-0.99	0.355083	0.543441	-6.83
265555_at	putative Mutator-like transposase relat	---	---	-1.06	-0.08	-0.99	0.355183	0.543557	-6.83
266943_at	putative reverse transcriptase	---	---	-1.12	-0.17	-0.99	0.35526	0.543638	-6.83
258668_at	hypothetical protein predicted by gens	---	AT3G08780	-1.08	-0.11	-0.99	0.355437	0.543873	-6.83
245663_at	steroid sulfotransferase, putative simil	---	AT1G28170	1.08	0.11	0.99	0.35559	0.544034	-6.83

256838_at	ADP-ribosylation factor, putative simil	ATARFC1	AT3G22950	1.10	0.13	0.99	0.355568	0.544034	-6.83
248245_at	MtN3 protein-like	---	AT5G53190	-1.10	-0.13	-0.99	0.355664	0.544111	-6.83
254763_at	ribosomal protein L13a like protein rib	---	AT4G13170	1.11	0.15	0.99	0.355827	0.544324	-6.83
261837_s_	transcriptional regulator, putative simil	---	AT1G15910 /	1.11	0.15	0.99	0.356138	0.544727	-6.83
255170_at	hypothetical protein similar to A. thalia	---	---	1.08	0.11	0.99	0.356138	0.544727	-6.83
253331_at	nucellin -like protein nucellin - Hordeu	---	AT4G33490	-1.12	-0.17	-0.99	0.356171	0.54474	-6.83
255593_at	hypothetical protein	---	AT4G01650	1.08	0.11	0.99	0.356221	0.544741	-6.83
267269_at	unknown protein	CAND1	AT2G02560	1.09	0.12	0.99	0.356243	0.544741	-6.83
256662_at	male sterility protein 2 (MS2) nearly ide	MS2	AT3G11980	-1.07	-0.10	-0.99	0.356219	0.544741	-6.83
262112_at	unknown protein ;supported by full-len	---	AT1G02870	-1.11	-0.15	-0.99	0.3563	0.544791	-6.83
256403_at	unknown protein similar to SPOP (nov	BPM2	AT3G06190	-1.07	-0.10	-0.99	0.356542	0.545126	-6.83
255082_at	putative protein polyphosphoinositide	---	AT4G09160	-1.08	-0.11	-0.99	0.356597	0.545173	-6.83
262908_at	pyruvate dehydrogenase e1 alpha sub	AT-E1 ALPH	AT1G59900	-1.08	-0.11	-0.99	0.356654	0.545223	-6.83
252483_at	scarecrow-like protein scarecrow-like	---	AT3G46600	1.21	0.27	0.99	0.356958	0.545652	-6.83
264417_at	hypothetical protein contains similarity	---	---	-1.13	-0.17	-0.99	0.35703	0.545724	-6.83
249695_at	putative protein similar to unknown pro	---	---	1.08	0.11	0.99	0.357171	0.545903	-6.83
267071_at	unknown protein	---	AT2G40980	1.08	0.11	0.99	0.357203	0.545916	-6.83
254636_at	putative protein kinase ; supported by	CIPK12	AT4G18700	1.07	0.10	0.99	0.357385	0.546109	-6.83
257550_at	hypothetical protein similar to GB:AAD	---	AT3G18460	-1.10	-0.14	-0.99	0.357425	0.546109	-6.83
264858_at	hypothetical protein	SNL3	AT1G24190	1.09	0.12	0.99	0.357424	0.546109	-6.83
246365_at	hypothetical protein	---	---	1.09	0.12	0.99	0.357409	0.546109	-6.83
261628_at	hypothetical protein predicted by gene	---	AT1G50000	1.07	0.10	0.99	0.357537	0.546243	-6.83
257258_at	hypothetical protein contains Pfam pro	---	AT3G22040	-1.12	-0.17	-0.99	0.357735	0.54651	-6.83
251091_at	pyridoxine biosynthesis protein - like p	RSR4	AT5G01410	1.20	0.26	0.99	0.358	0.546842	-6.83
267272_at	hypothetical protein predicted by gens	---	---	-1.07	-0.10	-0.99	0.357997	0.546842	-6.83
253105_at	putative protein zinc finger protein, Ar	---	AT4G35840	1.12	0.17	0.99	0.358137	0.546986	-6.83
244994_at	NADH dehydrogenase ND5	---	---	-1.10	-0.14	-0.99	0.358143	0.546986	-6.83
254789_at	blue copper-binding protein, 15K (lam	---	AT4G12880	-1.59	-0.67	-0.99	0.358268	0.54714	-6.84
263741_at	hypothetical protein predicted by gens	---	AT2G20620	1.11	0.15	0.99	0.358428	0.54733	-6.84
251165_at	putative protein different MAP kinases	---	AT3G63330	1.11	0.14	0.99	0.35844	0.54733	-6.84
251262_at	hypothetical protein ; supported by cD	---	AT3G62080	1.13	0.18	0.99	0.358508	0.547397	-6.84
249079_at	putative protein contains similarity to u	---	AT5G43930	1.12	0.16	0.99	0.35859	0.547486	-6.84
252651_at	putative protein several hypothetical pr	---	AT3G44700	1.09	0.13	0.99	0.358617	0.547491	-6.84
247372_at	unknown protein ;supported by full-ler	---	AT5G63280	-1.13	-0.17	-0.98	0.358777	0.547661	-6.84
248432_at	putative protein similar to unknown pro	---	AT5G51390	-1.20	-0.26	-0.98	0.358758	0.547661	-6.84

255352_at	putative transposon protein similar to a	---	---	-1.08	-0.11	-0.98	0.358894	0.547803	-6.84
249940_at	NAC-domain protein-like ;supported b	anac090	AT5G22380	1.09	0.12	0.98	0.359006	0.547938	-6.84
245986_at	protein kinase-like protein kinase 1 Pr	PBS1	AT5G13160	-1.07	-0.10	-0.98	0.359076	0.548007	-6.84
250178_at	putative protein various unknown or p	---	AT5G14430	1.07	0.10	0.98	0.359202	0.548163	-6.84
265516_at	putative Athila retroelement ORF1 prot	---	---	-1.08	-0.11	-0.98	0.35933	0.548322	-6.84
264768_at	hypothetical protein similar to putative	---	AT1G61410	-1.08	-0.11	-0.98	0.359371	0.548348	-6.84
258526_at	DAG protein, putative similar to DAG l	---	AT3G06790	-1.08	-0.12	-0.98	0.359412	0.54836	-6.84
252368_at	cytochrome P450-like protein cytochro	CYP94B3	AT3G48520	-1.21	-0.27	-0.98	0.359475	0.54836	-6.84
263110_at	unknown protein ;supported by full-len	---	AT1G65220	-1.11	-0.15	-0.98	0.359461	0.54836	-6.84
266690_at	malate oxidoreductase (malic enzyme)	ATNADP-ME	AT2G19900	-1.08	-0.11	-0.98	0.359436	0.54836	-6.84
253947_at	putative protein hypothetical protein, A	MAP65-2	AT4G26760	-1.09	-0.13	-0.98	0.359538	0.548411	-6.84
255989_at	putative protein	---	AT5G35069	1.10	0.14	0.98	0.359581	0.548411	-6.84
250635_at	glycine-rich protein glycine-rich protei	GRP14	AT5G07510	-1.09	-0.13	-0.98	0.359562	0.548411	-6.84
252727_s_	putative protein predicted proteins, Ar	---	---	1.07	0.09	0.98	0.359734	0.548608	-6.84
258651_at	putative phosphatidylinositol-4-phosph	PIP5K9	AT3G09920	-1.10	-0.13	-0.98	0.359843	0.548737	-6.84
246591_at	putative cation transport protein putati	---	AT5G14880	1.10	0.14	0.98	0.360152	0.549172	-6.84
253847_at	putative protein CRP1, Zea mays, AF	---	AT4G28010	1.08	0.11	0.98	0.360246	0.549279	-6.84
256110_at	Ser Thr protein kinase, putative simila	---	AT1G16900	1.12	0.16	0.98	0.360311	0.549341	-6.84
256249_at	26S proteasome regulatory subunit S	MEE34	AT3G11270	-1.08	-0.12	-0.98	0.360367	0.549389	-6.84
263068_at	putative poly(A) polymerase	---	AT2G17580	1.10	0.14	0.98	0.360441	0.549466	-6.84
249604_x_	putative protein RING-H2 finger protei	---	AT5G37230	1.09	0.12	0.98	0.360508	0.549532	-6.84
247592_at	high affinity nitrate transporter protein	NRT2.3	AT5G60780	1.07	0.10	0.98	0.36063	0.549681	-6.84
255721_at	unknown protein ;supported by full-len	---	AT1G31940	-1.07	-0.10	-0.98	0.360741	0.549813	-6.84
265215_at	hypothetical protein predicted by gens	---	AT1G05040	-1.07	-0.09	-0.98	0.360861	0.549884	-6.84
250785_at	unknown protein	---	AT5G05510	-1.11	-0.15	-0.98	0.360881	0.549884	-6.84
252835_at	putative protein several hypothetical pr	---	AT3G42060	-1.09	-0.13	-0.98	0.360814	0.549884	-6.84
245353_at	hypothetical protein ;supported by full-	---	AT4G16000	-1.16	-0.22	-0.98	0.360884	0.549884	-6.84
252211_at	putative protein predicted proteins, Ar	---	AT3G50220	-1.08	-0.11	-0.98	0.361057	0.550111	-6.84
261430_at	hypothetical protein predicted by gene	---	AT1G18830	-1.11	-0.15	-0.98	0.361092	0.550128	-6.84
263435_at	putative ATP-dependent RNA helicase	---	AT2G28600	1.15	0.21	0.98	0.361234	0.550274	-6.84
249415_at	promoter-binding protein like ascorbat	CDF2	AT5G39660	-1.15	-0.20	-0.98	0.361236	0.550274	-6.84
260883_at	hypothetical protein predicted by gene	---	AT1G29270	-1.06	-0.09	-0.98	0.361269	0.550287	-6.84
267062_at	putative spliceosome associated prote	---	AT2G32600	1.10	0.14	0.98	0.361309	0.550312	-6.84
251511_at	putative protein several hypothetical pr	---	AT3G59180	1.07	0.10	0.98	0.361368	0.550364	-6.84
255610_at	putative phosphatidylinositol kinase si	ATPIPK10	AT4G01190	1.08	0.11	0.98	0.361439	0.550378	-6.84

259906_at	unknown protein	---	AT1G74120	-1.07	-0.10	-0.98	0.36145	0.550378	-6.84
266974_at	unknown protein	---	AT2G39370	1.07	0.09	0.98	0.361427	0.550378	-6.84
262347_at	unknown protein similar to hypothetica	---	AT1G64110	1.09	0.13	0.98	0.361599	0.550568	-6.84
265506_at	putative non-LTR retroelement reverse	---	---	-1.10	-0.14	-0.98	0.361668	0.550596	-6.84
254107_at	putative protein putative glycerol-3-ph	---	AT4G25220	-1.10	-0.14	-0.98	0.361675	0.550596	-6.84
252185_at	putative protein	---	AT3G50780	1.11	0.15	0.98	0.361689	0.550596	-6.84
265477_at	hypothetical protein predicted by gens	GAUT2	AT2G46480	1.09	0.12	0.98	0.36173	0.550621	-6.84
263915_at	hypothetical protein predicted by gens	---	AT2G36430	1.26	0.33	0.98	0.362035	0.551049	-6.84
263779_at	putative photomorphogenesis repress	SPA1	AT2G46340	1.09	0.13	0.98	0.362104	0.551117	-6.84
266590_at	hypothetical protein predicted by gens	BAG6	AT2G46240	1.14	0.19	0.98	0.362168	0.551178	-6.84
257507_at	zinc finger protein, putative similar to	---	AT1G29600	-1.06	-0.09	-0.98	0.362277	0.551303	-6.84
245212_at	hypothetical protein predicted by gens	AT1G44224	---	-1.12	-0.16	-0.98	0.362299	0.551303	-6.84
251133_at	LAX1 / AUX1 -like permease	---	AT5G01240	1.12	0.17	0.98	0.362392	0.551409	-6.84
244910_s_	hypothetical protein	---	---	-1.08	-0.11	-0.98	0.362423	0.551418	-6.84
257976_at	putative transcription factor contains A	PLT1	AT3G20840	1.08	0.12	0.98	0.362541	0.551562	-6.84
247300_at	unknown protein	FCLY	AT5G63910	1.09	0.12	0.98	0.362747	0.551837	-6.84
262014_at	unknown protein	---	AT1G35660	1.16	0.21	0.98	0.362772	0.551839	-6.84
251853_at	putative protein various Arabidopsis th	---	AT3G54790	-1.07	-0.10	-0.98	0.362804	0.551851	-6.84
256798_at	uracil-DNA glycosylase, putative simil	---	AT3G18630	-1.11	-0.15	-0.98	0.362984	0.552088	-6.85
247064_at	putative protein contains similarity to d	---	AT5G66890	1.15	0.20	0.98	0.363019	0.552104	-6.85
258458_at	Expressed protein ; supported by cDN	---	AT3G22435	1.12	0.17	0.98	0.363074	0.55212	-6.85
248827_at	calcium sensor protein, calcineurin-lik	CBL9	AT5G47100	1.13	0.17	0.98	0.363102	0.55212	-6.85
246914_at	putative protein various predicted prot	---	AT5G25860	-1.11	-0.15	-0.98	0.363101	0.55212	-6.85
263625_at	F-box protein family, AtFBX9 contains	---	AT2G04920	1.07	0.10	0.98	0.363178	0.5522	-6.85
266466_at	hypothetical protein The first 3 exons i	---	AT2G47790	1.08	0.11	0.98	0.363231	0.552242	-6.85
246423_at	putative protein ribosomal protein L18	---	AT5G16950	1.11	0.15	0.97	0.363498	0.552575	-6.85
261093_at	non-LTR reverse transcriptase, putati	AT1G62880	---	-1.10	-0.14	-0.97	0.363477	0.552575	-6.85
250027_at	putative protein similar to unknown pro	---	AT5G18250	1.10	0.14	0.97	0.363688	0.552827	-6.85
266982_at	unknown protein ; supported by cDNA	---	AT2G39500	1.10	0.14	0.97	0.363719	0.552837	-6.85
258360_at	hypothetical protein predicted by gene	---	AT3G14250	1.08	0.11	0.97	0.363775	0.552886	-6.85
261428_at	isochorismate synthase, putative simil	ICS2	AT1G18870	1.14	0.18	0.97	0.364001	0.553193	-6.85
250258_at	floral homeotic protein AGL15 (sp|Q38	AGL15	AT5G13790	1.09	0.12	0.97	0.364034	0.553206	-6.85
249047_at	berberine bridge enzyme-like protein	---	AT5G44410	-1.09	-0.12	-0.97	0.36425	0.553479	-6.85
257287_at	hypothetical protein predicted by gene	---	---	1.07	0.09	0.97	0.364311	0.553479	-6.85
266123_at	unknown protein identical to GB:AAB8	---	AT2G45180	-1.06	-0.09	-0.97	0.364301	0.553479	-6.85

266177_at	putative phloem-specific lectin	ATPP2-B3	AT2G02270	1.11	0.15	0.97	0.364278	0.553479	-6.85
258778_s_	hypothetical protein predicted by gene	---	AT3G11860 /	-1.09	-0.13	-0.97	0.364401	0.553537	-6.85
260233_at	putative cytochrome P450 similar to cy	CYP98A9	AT1G74550	1.14	0.18	0.97	0.364422	0.553537	-6.85
257996_at	unknown protein	---	AT3G19950	1.07	0.09	0.97	0.364418	0.553537	-6.85
248467_at	MtN3-like protein ;supported by full-len	---	AT5G50800	1.24	0.31	0.97	0.364567	0.553721	-6.85
250735_at	putative protein similar to unknown pro	---	AT5G06280	-1.08	-0.11	-0.97	0.364661	0.553722	-6.85
246306_at	putative protein hypothetical proteins -	ATBAG4	AT3G51780	1.06	0.09	0.97	0.364665	0.553722	-6.85
257555_at	hypothetical protein predicted by gens	---	AT3G24780	1.11	0.15	0.97	0.364663	0.553722	-6.85
257342_at	pseudogene, putative polyprotein simi	---	---	1.13	0.18	0.97	0.364665	0.553722	-6.85
252359_at	putative protein predicted proteins, Ar	---	AT3G48440	-1.11	-0.15	-0.97	0.364695	0.55373	-6.85
249332_at	putative protein similar to unknown pro	---	AT5G40980	1.10	0.13	0.97	0.364777	0.553818	-6.85
260752_at	unknown protein contains similarity to	---	AT1G49030	-1.10	-0.14	-0.97	0.364941	0.554031	-6.85
254059_at	Arabidopsis mitochondrion-localized sr	ATHSP23.6-	AT4G25200	1.10	0.14	0.97	0.365051	0.55416	-6.85
248642_at	putative protein similar to unknown pro	---	AT5G49120	-1.08	-0.11	-0.97	0.365294	0.554455	-6.85
265912_at	hypothetical protein predicted by gens	---	AT2G25565 /	-1.08	-0.11	-0.97	0.365291	0.554455	-6.85
246147_s_	26S proteasome AAA-ATPase subuni	RPT6A	AT5G19990 /	1.09	0.12	0.97	0.36536	0.554518	-6.85
245335_at	pore protein homolog ;supported by fu	ATOEP16-2	AT4G16160	-1.10	-0.14	-0.97	0.36541	0.554557	-6.85
251985_at	thioredoxin -like protein cop c2, Copri	---	AT3G53220	-1.10	-0.14	-0.97	0.365527	0.554698	-6.85
262866_at	cytochrome p450, putative similar to c	CYP89A6	AT1G64940	1.07	0.09	0.97	0.365573	0.554731	-6.85
257735_at	pectate lyase, putative similar to pecta	---	AT3G27400	-1.15	-0.20	-0.97	0.365606	0.554745	-6.85
254424_at	hypothetical protein ;supported by full-	---	AT4G21510	-1.14	-0.20	-0.97	0.365733	0.5549	-6.85
257192_at	unknown protein ;supported by full-len	EMB2769	AT3G13200	-1.09	-0.12	-0.97	0.365779	0.554934	-6.85
247410_at	putative protein similar to unknown pro	emb1692	AT5G62990	1.16	0.21	0.97	0.366018	0.555259	-6.85
256595_x_	hypothetical protein	---	AT3G28530	-1.09	-0.13	-0.97	0.366068	0.555298	-6.85
263089_at	putative retroelement pol polyprotein	---	---	-1.10	-0.14	-0.97	0.366109	0.555323	-6.85
248029_at	beta-amylase ; supported by cDNA: g	BAM4	AT5G55700	1.09	0.12	0.97	0.366215	0.555447	-6.85
264569_at	unknown protein EST gb|ATTS1136 c	---	---	-1.07	-0.10	-0.97	0.366249	0.555461	-6.85
247325_at	putative protein contains similarity to s	SC35	AT5G64200	1.07	0.10	0.97	0.36636	0.555556	-6.85
247985_at	putative protein contains similarity to p	---	AT5G56790	-1.09	-0.13	-0.97	0.36636	0.555556	-6.85
258553_at	hypothetical protein ; supported by cD	PDE320	AT3G06960	1.07	0.10	0.97	0.366456	0.555564	-6.85
249330_at	putative protein similar to unknown pro	---	AT5G40970	-1.08	-0.11	-0.97	0.366476	0.555564	-6.85
259467_at	hypothetical protein predicted by gene	---	AT1G19060	-1.06	-0.08	-0.97	0.366392	0.555564	-6.85
265381_at	putative non-LTR retroelement reverse	---	---	-1.11	-0.15	-0.97	0.366487	0.555564	-6.85
257554_at	synaptobrevin, putative similar to SYN	VAMP728	AT3G24890	-1.08	-0.11	-0.97	0.366429	0.555564	-6.85
247245_at	putative protein similar to unknown pro	---	AT5G64720	-1.07	-0.10	-0.97	0.366548	0.55562	-6.85

265563_s_	hypothetical protein predicted by gens	---	---	1.06	0.08	0.97	0.366672	0.555685	-6.85
250684_at	zinc finger-like protein	GIS2	AT5G06650	-1.08	-0.11	-0.97	0.366707	0.555685	-6.85
248668_at	putative protein similar to unknown pro	XRI1	AT5G48720	-1.14	-0.19	-0.97	0.366713	0.555685	-6.85
250099_at	unknown protein ; supported by cDNA	---	AT5G17300	1.10	0.14	0.97	0.366636	0.555685	-6.85
246931_at	putative protein apoptosis-related prot	---	AT5G25170	1.27	0.34	0.97	0.366651	0.555685	-6.85
251779_at	putative protein various predicted prot	---	---	1.08	0.11	0.97	0.366766	0.555728	-6.85
256674_at	unknown protein ;supported by full-len	---	AT3G52360	-1.13	-0.17	-0.97	0.366876	0.555859	-6.85
254932_at	putative translation elongation factor t	---	AT4G11120	-1.13	-0.17	-0.97	0.367256	0.556351	-6.85
266626_at	hypothetical protein predicted by gens	---	AT2G35360	-1.11	-0.16	-0.97	0.367275	0.556351	-6.85
255476_at	hypothetical protein similar to reverse	---	---	1.09	0.12	0.97	0.367228	0.556351	-6.85
247706_at	putative ripening-related protein - like p	---	AT5G59480	-1.20	-0.26	-0.97	0.367344	0.55642	-6.85
259366_at	allene oxide cyclase, putative similar t	AOC4	AT1G13280	-1.12	-0.17	-0.97	0.367422	0.5565	-6.85
259147_at	putative RNA binding protein similar to	APUM4	AT3G10360	-1.14	-0.19	-0.97	0.367632	0.55667	-6.86
251248_at	P-glycoprotein-like proetin P-glycopro	PGP21	AT3G62150	1.40	0.49	0.97	0.367596	0.55667	-6.86
262363_at	disease resistance protein, putative si	---	AT1G72850	-1.08	-0.11	-0.97	0.367615	0.55667	-6.86
245414_at	hypothetical protein	---	AT4G17310	-1.10	-0.14	-0.97	0.367626	0.55667	-6.86
253724_at	Expressed protein ; supported by full-l	LCR24	AT4G29285	1.07	0.10	0.97	0.367863	0.556983	-6.86
251020_at	ABC transporter -like protein NBD-like	NAP9	AT5G02270	1.22	0.29	0.96	0.367979	0.557085	-6.86
251101_at	putative transporter protein Na+/H+ an	CHX26	AT5G01680	1.06	0.09	0.96	0.367956	0.557085	-6.86
256392_at	putative glycosyl transferase contains	GATL4	AT3G06260	-1.09	-0.12	-0.96	0.368006	0.557089	-6.86
254784_at	growth factor like protein antisense ba	NUDT7	AT4G12720	-1.20	-0.27	-0.96	0.36814	0.557164	-6.86
256250_at	integral membrane protein, putative c	---	AT3G11320	1.11	0.15	0.96	0.368142	0.557164	-6.86
257029_at	dem-like protein similar to dem GB:C	---	AT3G19240	1.08	0.11	0.96	0.368148	0.557164	-6.86
AFFX-ThrX	B. subtilis /GEN=thrC, thrB /DB_XREF	---	---	-1.19	-0.25	-0.96	0.368153	0.557164	-6.86
249334_at	putative protein strong similarity to unk	YSL4	AT5G41000	1.12	0.16	0.96	0.368184	0.557173	-6.86
262021_at	unknown protein	AT1G35545	---	-1.09	-0.12	-0.96	0.368343	0.557341	-6.86
246203_at	putative protein ; supported by full-leng	---	AT4G36610	-1.16	-0.21	-0.96	0.368319	0.557341	-6.86
251460_at	hypothetical protein	SAC9	AT3G59770	1.07	0.10	0.96	0.36839	0.557375	-6.86
262827_at	putative cytochrome P450 monooxyge	CYP71B29	AT1G13100	1.17	0.22	0.96	0.368423	0.557388	-6.86
259456_s_	unknown protein similar to putative no	---	---	-1.08	-0.12	-0.96	0.368728	0.557811	-6.86
267456_at	E2, ubiquitin-conjugating enzyme, put	PHO2	AT2G33770	1.19	0.25	0.96	0.368785	0.557861	-6.86
265284_at	unknown protein ;supported by full-ler	---	AT2G20230	1.09	0.12	0.96	0.36893	0.558003	-6.86
266909_at	hypothetical protein predicted by gens	BRM	AT2G46020	1.10	0.13	0.96	0.368936	0.558003	-6.86
248188_at	putative protein contains similarity to h	HSFA9	AT5G54070	-1.06	-0.09	-0.96	0.368952	0.558003	-6.86
267431_at	unknown protein ;supported by full-ler	MEE26	AT2G34870	-1.09	-0.12	-0.96	0.369067	0.55814	-6.86

265930_at	putative spliceosome associated prote	emb2444	AT2G18510	-1.09	-0.12	-0.96	0.369115	0.558175	-6.86
265096_at	unknown protein Location of ESTs 40	---	AT1G04030	-1.09	-0.13	-0.96	0.369147	0.558186	-6.86
263907_at	abscisic acid insensitive 5 (ABI5) conta	ABI5	AT2G36270	1.10	0.14	0.96	0.369196	0.558223	-6.86
260929_at	transcription factor TFIID, putative sim	TAF13	AT1G02680	-1.12	-0.16	-0.96	0.369257	0.558278	-6.86
250223_at	glutaredoxin-like protein ;supported by	ROXY2	AT5G14070	-1.07	-0.10	-0.96	0.369284	0.558283	-6.86
257795_at	hypothetical protein predicted by gens	---	AT3G15910	1.10	0.14	0.96	0.369445	0.558453	-6.86
247579_at	cytochrome P450 - like protein cytoch	CYP89A3	AT5G61320	-1.07	-0.10	-0.96	0.369424	0.558453	-6.86
246924_at	putative protein KIAA0332 - Homo sa	---	AT5G25060	1.06	0.09	0.96	0.369583	0.558538	-6.86
248061_at	putative protein contains similarity to w	---	AT5G55340	1.06	0.09	0.96	0.369592	0.558538	-6.86
264136_at	leucine-rich repeat transmembrane pr	SRF5	AT1G78980	-1.12	-0.16	-0.96	0.369556	0.558538	-6.86
259284_at	putative cell division related protein sir	---	AT3G11450	1.09	0.13	0.96	0.3696	0.558538	-6.86
255310_at	Expressed protein ; supported by full-l	ATALN	AT4G04955	-1.21	-0.28	-0.96	0.3697	0.558616	-6.86
251409_at	Expressed protein ; supported by full-l	---	AT3G60245	-1.21	-0.28	-0.96	0.369685	0.558616	-6.86
259536_s_	putative protein hypothetical proteins -	ATCOAB	AT1G12350 /	-1.06	-0.09	-0.96	0.36984	0.558679	-6.86
253592_at	hypothetical protein ;supported by full-	---	AT4G30840	1.07	0.10	0.96	0.369788	0.558679	-6.86
254963_at	putative protein single strand DNA-bir	MTSSB	AT4G11060	-1.09	-0.12	-0.96	0.369816	0.558679	-6.86
255912_at	2,3-oxidosqualene-triterpenoid cyclas	---	AT1G66960	-1.10	-0.14	-0.96	0.369814	0.558679	-6.86
260426_at	putative 40S ribosomal protein SA (lan	P40	AT1G72370	-1.15	-0.21	-0.96	0.369882	0.558705	-6.86
254988_at	putative protein Ran GTPase activato	GTC2	AT4G10670	1.08	0.11	0.96	0.369936	0.55875	-6.86
263336_x_	hypothetical protein predicted by gens	---	---	-1.07	-0.10	-0.96	0.369998	0.558797	-6.86
260333_at	putative polygalacturonase similar to p	---	AT1G70500	1.13	0.17	0.96	0.370016	0.558797	-6.86
264017_s_	putative ER lumen protein retaining re	---	AT2G21190 /	1.07	0.10	0.96	0.370043	0.558801	-6.86
253103_at	putative auxin-induced protein high sir	---	AT4G36110	-1.45	-0.54	-0.96	0.3703	0.559023	-6.86
256679_at	putative protein similar to ATP synthas	ATPQ	AT3G52300	1.08	0.12	0.96	0.370302	0.559023	-6.86
265133_s_	unknown protein similar to hypothetica	---	AT1G51240 /	-1.07	-0.09	-0.96	0.370225	0.559023	-6.86
260831_at	glutaredoxin, putative similar to glutar	---	AT1G06830	-1.52	-0.60	-0.96	0.370337	0.559023	-6.86
263874_at	putative ATP synthase ;supported by	---	AT2G21870	1.11	0.15	0.96	0.370307	0.559023	-6.86
267395_at	unknown protein	---	AT2G44250	1.07	0.09	0.96	0.370325	0.559023	-6.86
267442_at	unknown protein ;supported by full-ler	---	AT2G19080	-1.07	-0.10	-0.96	0.370501	0.559151	-6.86
255009_at	putative DNA-directed RNA polymera	---	AT4G10070	1.12	0.16	0.96	0.370456	0.559151	-6.86
250357_at	putative protein various predicted prot	---	AT5G11730	1.08	0.12	0.96	0.37052	0.559151	-6.86
263057_at	hypothetical protein predicted by gene	---	AT2G09840	1.11	0.15	0.96	0.370491	0.559151	-6.86
264724_at	putative JUN kinase activator protein	CSN5A	AT1G22920	-1.07	-0.10	-0.96	0.370589	0.559181	-6.86
253656_at	putative protein hypothetical protein -	emb1353	AT4G30090	-1.07	-0.10	-0.96	0.370586	0.559181	-6.86
246662_at	putative protein	---	AT5G35290	1.08	0.11	0.96	0.370731	0.559358	-6.86

246302_at	Ca2+/H+-exchanging protein-like Arab	CAX3	AT3G51860	1.28	0.35	0.96	0.370856	0.559495	-6.86
254242_at	serine /threonine kinase - like protein	---	AT4G23200	-1.29	-0.36	-0.96	0.370871	0.559495	-6.86
250472_at	putative protein	---	AT5G10210	1.11	0.14	0.96	0.3712	0.559955	-6.86
246526_at	putative protein RXF26 - Arabidopsis	GLIP7	AT5G15720	-1.07	-0.10	-0.96	0.37124	0.559978	-6.86
261565_at	beta-1,3-glucanase, putative similar to	---	AT1G33220	-1.06	-0.09	-0.96	0.371281	0.559995	-6.86
265334_at	putative lipid transfer protein ; support	---	AT2G18370	-1.18	-0.24	-0.96	0.371311	0.559995	-6.86
249667_at	unknown protein	---	---	1.06	0.09	0.96	0.371325	0.559995	-6.86
254106_at	geranylgeranylated protein ATGP4 ; s	ATGP4	AT4G24990	1.10	0.13	0.96	0.371502	0.560225	-6.86
262333_at	hypothetical protein similar to putative	---	AT1G64020	-1.08	-0.12	-0.96	0.371721	0.560518	-6.86
260673_at	unknown protein ; supported by full-ler	---	AT1G19330	-1.15	-0.21	-0.96	0.371765	0.560547	-6.86
264104_at	En/Spm-like transposon protein relate	---	---	-1.08	-0.12	-0.96	0.371902	0.560717	-6.86
245030_at	putative polygalacturonase	---	AT2G26620	1.06	0.08	0.96	0.37197	0.560782	-6.86
262236_at	hypothetical protein similar to hypothet	---	AT1G48330	-1.17	-0.23	-0.96	0.372128	0.560947	-6.86
255315_at	hypothetical protein	---	---	-1.07	-0.10	-0.96	0.372121	0.560947	-6.86
247419_at	unknown protein	---	AT5G63080	-1.10	-0.14	-0.96	0.372189	0.561001	-6.86
256099_at	cytochrome P450, putative similar to	CYP78A5	AT1G13710	-1.12	-0.17	-0.96	0.372298	0.561128	-6.86
248997_at	beta-amylase-like	BMY2	AT5G45300	-1.12	-0.16	-0.96	0.372351	0.561171	-6.86
248992_at	disease resistance protein RPS4	---	AT5G45230	1.08	0.11	0.96	0.3724	0.561208	-6.86
265375_at	unknown protein ;supported by full-ler	VPS2.1	AT2G06530	-1.10	-0.14	-0.96	0.372475	0.561253	-6.87
257091_at	DNA polymerase, putative C-term sim	POLGAMMA	AT3G20540	-1.11	-0.15	-0.96	0.372479	0.561253	-6.87
256494_at	hypothetical protein predicted by gene	---	AT1G31520	1.07	0.10	0.96	0.372565	0.561345	-6.87
259229_at	unknown protein similar to transcriptio	ADA2A	AT3G07740	1.10	0.14	0.95	0.372677	0.561476	-6.87
266953_at	hypothetical protein predicted by gens	---	AT2G34540	-1.08	-0.11	-0.95	0.372789	0.561609	-6.87
250893_at	putative protein predicted proteins - Ar	EMB175	AT5G03795 /	1.07	0.10	0.95	0.372912	0.561649	-6.87
245529_at	SEN1 like protein	MAA3	AT4G15570	1.14	0.19	0.95	0.37289	0.561649	-6.87
258352_at	putative auxin-induced protein similar t	IAA31	AT3G17600	-1.10	-0.13	-0.95	0.372853	0.561649	-6.87
254497_at	Phosphoribosylanthranilate transferas	---	AT4G20080	-1.13	-0.17	-0.95	0.372914	0.561649	-6.87
250766_at	putative protein similar to unknown pro	---	AT5G05550	-1.09	-0.13	-0.95	0.373165	0.561953	-6.87
247294_at	putative protein similar to unknown pro	XRCC2	AT5G64520	1.07	0.10	0.95	0.373162	0.561953	-6.87
250606_s_	pectin methyl-esterase-like protein pe	PPME1	AT1G69940 /	1.07	0.10	0.95	0.373195	0.561961	-6.87
245842_at	proline-rich protein, putative similar to	RXF26	AT1G58430	1.07	0.09	0.95	0.373247	0.562002	-6.87
254360_at	CDP-diacylglycerol synthetase-like pr	---	AT4G22340	-1.08	-0.11	-0.95	0.373279	0.562013	-6.87
257563_at	hypothetical protein predicted by gene	---	AT3G19610	-1.06	-0.09	-0.95	0.373305	0.562015	-6.87
252163_at	hypothetical protein	---	AT3G50610	1.08	0.11	0.95	0.373388	0.562102	-6.87
248616_at	putative protein contains similarity to u	---	AT5G49580	1.11	0.15	0.95	0.373523	0.562195	-6.87

251337_at	proteasome component C5 ;supporte	PBF1	AT3G60820	-1.06	-0.09	-0.95	0.373514	0.562195	-6.87
247228_at	trehalose-6-phosphate phosphatase	---	AT5G65140	1.28	0.36	0.95	0.373519	0.562195	-6.87
254650_at	hypothetical protein	---	---	-1.07	-0.09	-0.95	0.373649	0.562311	-6.87
258640_at	hypothetical protein predicted by gens	---	AT3G07930	-1.10	-0.14	-0.95	0.373636	0.562311	-6.87
266129_at	hypothetical protein predicted by gens	CCD7	AT2G44990	1.28	0.35	0.95	0.373831	0.56251	-6.87
258558_at	hypothetical protein predicted by gene	---	AT3G06000	-1.06	-0.08	-0.95	0.373816	0.56251	-6.87
253378_at	hypothetical protein	---	AT4G33310	1.07	0.10	0.95	0.373877	0.562542	-6.87
259307_at	unknown protein similar to MICROSOM	---	AT3G05230	-1.10	-0.14	-0.95	0.374063	0.562722	-6.87
250830_at	putative protein similar to unknown pro	---	AT5G04910	1.11	0.15	0.95	0.374083	0.562722	-6.87
252262_at	putative protein several hypothetical pr	---	AT3G49510	1.07	0.09	0.95	0.374095	0.562722	-6.87
247672_at	senescence-associated protein - like s	TET4	AT5G60220	-1.06	-0.08	-0.95	0.37408	0.562722	-6.87
250491_at	putative protein predicted proteins, Ar	---	AT5G09780	-1.12	-0.16	-0.95	0.374185	0.56282	-6.87
253572_at	hypothetical protein	---	AT4G31010	-1.08	-0.12	-0.95	0.37421	0.56282	-6.87
252567_at	zinc finger -like protein zinc finger pro	---	AT3G46070	-1.07	-0.10	-0.95	0.374387	0.563049	-6.87
256997_at	subtilisin-like serine protease, putative	---	AT3G14067	1.13	0.17	0.95	0.374474	0.563142	-6.87
249397_at	putative protein MtN21, Medicago trur	---	AT5G40230	1.11	0.15	0.95	0.374501	0.563145	-6.87
248318_at	unknown protein	---	AT5G52690	-1.07	-0.10	-0.95	0.374525	0.563145	-6.87
252415_at	glutamine-dependent asparagine synth	ASN1	AT3G47340	1.67	0.74	0.95	0.374622	0.563254	-6.87
258084_at	putative B regulatory subunit of protein	---	AT3G26020	1.13	0.17	0.95	0.37473	0.563379	-6.87
257408_at	unknown protein similar to A. thaliana	SON1	AT2G17310	-1.09	-0.12	-0.95	0.374819	0.563476	-6.87
248956_at	unknown protein	---	AT5G45610	1.08	0.11	0.95	0.374855	0.563494	-6.87
265564_s_	hypothetical protein predicted by gens	---	---	-1.08	-0.11	-0.95	0.37489	0.563509	-6.87
257726_at	hypothetical protein predicted by gene	---	AT3G18360	1.07	0.10	0.95	0.374954	0.563515	-6.87
264684_at	unknown protein	HEXO3	AT1G65590	-1.16	-0.22	-0.95	0.374967	0.563515	-6.87
257455_s_	hypothetical protein	---	AT1G27870 /	-1.06	-0.09	-0.95	0.374993	0.563515	-6.87
255418_at	predicted protein of unknown function	---	AT4G03200	1.10	0.14	0.95	0.37498	0.563515	-6.87
264404_at	putative cytochrome P450	CYP82F1	AT2G25160	1.10	0.14	0.95	0.375047	0.563522	-6.87
252837_at	putative protein hypothetical proteins -	---	---	1.07	0.09	0.95	0.375027	0.563522	-6.87
260283_at	hypothetical protein predicted by gens	PTAC17	AT1G80480	-1.06	-0.09	-0.95	0.37511	0.56358	-6.87
249890_at	putative protein contains similarity to D	WRKY38	AT5G22570	1.63	0.70	0.95	0.375149	0.563601	-6.87
251505_at	putative protein polyamine oxidase (E(	CPuORF18	AT3G59050 /	-1.13	-0.18	-0.95	0.375251	0.563682	-6.87
254561_at	putative protein ; supported by cDNA:	---	AT4G19160	-1.13	-0.18	-0.95	0.375277	0.563682	-6.87
263443_at	putative fatty acid elongase ;supporte	KCS12	AT2G28630	-1.34	-0.43	-0.95	0.375267	0.563682	-6.87
257917_at	ethylene responsive element binding p	---	AT3G23220	-1.06	-0.09	-0.95	0.375353	0.563759	-6.87
247959_at	unknown protein	---	AT5G57080	-1.11	-0.15	-0.95	0.375536	0.563993	-6.87

257926_at	unknown protein contains Pfam profile	---	AT3G23280	-1.06	-0.09	-0.95	0.375583	0.563993	-6.87
261499_at	cytochrome P450 (CYP93A1), putativ	CYP705A24	AT1G28430	-1.09	-0.12	-0.95	0.375562	0.563993	-6.87
252552_at	putative protein	---	AT3G45900	-1.11	-0.15	-0.95	0.37564	0.564004	-6.87
251838_at	cysteine proteinase non-consensus AC	---	AT3G54940	1.09	0.13	0.95	0.375636	0.564004	-6.87
261803_at	transcription factor, putative similar to	NF-YA7	AT1G30500	1.11	0.15	0.95	0.375704	0.564026	-6.87
265351_at	putative MADS-box protein AGL17	AGL17	AT2G22630	1.08	0.12	0.95	0.375702	0.564026	-6.87
265002_at	putative lysine/histidine-specific perme	LHT2	AT1G24400	1.12	0.16	0.95	0.37575	0.564057	-6.87
248832_at	putative protein similar to unknown pro	---	AT5G47170	-1.07	-0.09	-0.95	0.375857	0.564182	-6.87
260990_at	hypothetical protein predicted by gene	---	AT1G12180	-1.10	-0.14	-0.95	0.375885	0.564187	-6.87
266688_at	hypothetical protein	---	AT2G19660	-1.06	-0.09	-0.95	0.375946	0.564241	-6.87
248509_at	Expressed protein ; supported by full-le	---	AT5G50335	-2.08	-1.05	-0.95	0.376131	0.564482	-6.87
253593_at	putative protein hypothetical protein F	---	AT4G30760	-1.09	-0.12	-0.95	0.376205	0.564555	-6.87
262295_at	putative U2 snRNP auxiliary factor Str	ATU2AF35A	AT1G27650	1.10	0.14	0.95	0.376312	0.564666	-6.87
253043_at	putative protein predicted protein, Ara	LBD39	AT4G37540	-1.16	-0.21	-0.95	0.376339	0.564666	-6.87
257834_at	alpha-mannosidase, putative similar to	---	AT3G26720	-1.06	-0.09	-0.95	0.376353	0.564666	-6.87
251480_at	putative protein inducible carbonyl red	---	AT3G59710	-1.10	-0.14	-0.95	0.376687	0.56513	-6.87
259974_at	putative phosphate transporter similar	---	AT1G76430	1.10	0.13	0.95	0.376993	0.565551	-6.87
257522_at	Yippee-like protein similar to Yippee pu	---	AT3G08990	1.07	0.09	0.95	0.377023	0.56556	-6.87
245186_at	F12A21.15 hypothetical protein	ARR11	AT1G67710	-1.19	-0.25	-0.95	0.377059	0.565576	-6.87
253864_at	hypothetical protein	---	AT4G27460	-1.10	-0.13	-0.95	0.377205	0.565684	-6.87
259865_at	putative casein kinase I similar to case	CKL2	AT1G72710	1.11	0.14	0.95	0.377197	0.565684	-6.87
255122_at	putative athila-like protein	---	---	-1.11	-0.14	-0.95	0.377201	0.565684	-6.87
255019_at	putative protein IB1C3-1 protein, Arab	---	AT4G10210	1.07	0.10	0.95	0.377236	0.565692	-6.87
248548_at	transmembrane transport protein-like	---	AT5G50300	1.07	0.09	0.94	0.377357	0.565806	-6.87
266613_at	similar to gibberellin-regulated proteins	---	AT2G14900	2.02	1.01	0.94	0.377361	0.565806	-6.87
248672_at	disease resistance protein	---	AT5G48770	-1.09	-0.12	-0.94	0.377417	0.565853	-6.88
263739_at	putative CONSTANS-like B-box zinc fi	---	AT2G21320	1.16	0.21	0.94	0.37746	0.56588	-6.88
258213_at	hypothetical protein predicted by gene	---	AT3G17950	-1.12	-0.17	-0.94	0.377541	0.565964	-6.88
267174_at	60S ribosomal protein L36 ;supported	---	AT2G37600	-1.15	-0.20	-0.94	0.377622	0.566048	-6.88
255136_s_	putative protein chromatin structural p	---	AT4G08350 /	-1.09	-0.12	-0.94	0.377687	0.566108	-6.88
264336_at	hypothetical protein contains similarity	---	AT1G70360	-1.09	-0.13	-0.94	0.377741	0.566153	-6.88
263697_at	hypothetical protein contains similarity	---	AT1G31080	-1.10	-0.13	-0.94	0.377795	0.566197	-6.88
259777_at	zinc finger protein, putative similar to	---	AT1G29570	1.08	0.10	0.94	0.377843	0.56623	-6.88
260132_s_	hypothetical protein	---	AT1G66320 /	1.06	0.09	0.94	0.377901	0.56628	-6.88
258604_at	putative N-acetlytransferase contains F	---	AT3G02980	-1.09	-0.13	-0.94	0.377939	0.566301	-6.88

252382_at	ABC-type transport protein-like protein	ATH5	AT3G47770	-1.06	-0.09	-0.94	0.377978	0.566322	-6.88
245893_at	hypothetical protein ;supported by full-	---	AT5G09270	1.08	0.11	0.94	0.378098	0.566427	-6.88
249520_at	putative protein similar to unknown pro	---	AT5G38670	1.06	0.09	0.94	0.378087	0.566427	-6.88
251582_at	putative protein CARBON CATABOLI	---	AT3G58580	-1.08	-0.10	-0.94	0.37822	0.566572	-6.88
258012_at	unknown protein similar to GB:CAB16	---	AT3G19310	1.06	0.09	0.94	0.378283	0.56663	-6.88
255806_at	fructokinase - like protein fructokinase	---	AT4G10260	1.06	0.08	0.94	0.378321	0.566649	-6.88
247344_at	ARI-like RING zinc finger protein-like	---	AT5G63750	-1.09	-0.12	-0.94	0.378351	0.566657	-6.88
245470_at	retrotransposon like protein	---	---	1.10	0.13	0.94	0.378493	0.566833	-6.88
261929_at	hypothetical protein similar to axi 1-like	---	AT1G22460	-1.09	-0.12	-0.94	0.378522	0.566839	-6.88
266412_at	hypothetical protein predicted by gens	MAP65-5	AT2G38720	1.07	0.10	0.94	0.378617	0.566943	-6.88
262546_at	iron-regulated transporter protein, put	ZIP10	AT1G31260	-1.17	-0.23	-0.94	0.378673	0.566991	-6.88
257108_x_	hypothetical protein	---	---	1.07	0.09	0.94	0.378925	0.567299	-6.88
264606_at	unknown protein ;supported by full-ler	---	AT1G04660	-1.11	-0.15	-0.94	0.378929	0.567299	-6.88
250097_at	putative protein similar to unknown pro	---	AT5G17280	1.09	0.13	0.94	0.379161	0.5676	-6.88
251764_at	putative protein exostose-related prote	EPC1	AT3G55830	1.10	0.13	0.94	0.37918	0.5676	-6.88
246206_at	Expressed protein ; supported by cDN	ATPBRP	---	1.07	0.10	0.94	0.379336	0.567797	-6.88
261809_at	rac GTPase activating protein, putativ	---	AT1G08340	-1.12	-0.16	-0.94	0.379365	0.567802	-6.88
258864_at	unknown protein	---	AT3G03210	-1.10	-0.14	-0.94	0.379453	0.567898	-6.88
246289_at	putative protein predicted protein At2g	---	AT3G56880	1.15	0.20	0.94	0.379649	0.568079	-6.88
245820_at	allyl alcohol dehydrogenase, putative	---	AT1G26320	1.07	0.10	0.94	0.37963	0.568079	-6.88
254677_at	chloroplast protein cs/ch-42	---	AT4G18490	-1.09	-0.13	-0.94	0.379645	0.568079	-6.88
246752_at	putative protein predicted proteins, Ar	---	AT5G27890	1.08	0.11	0.94	0.379698	0.568115	-6.88
252420_at	putative protein several hypothetical pr	---	AT3G47530	1.12	0.16	0.94	0.379751	0.56812	-6.88
256552_at	hypothetical protein predicted by gene	---	AT3G31350	1.09	0.12	0.94	0.379733	0.56812	-6.88
257372_at	hypothetical protein predicted by gens	---	AT2G43220	-1.07	-0.10	-0.94	0.379831	0.568146	-6.88
245421_at	hypothetical protein	---	AT4G17430	-1.06	-0.09	-0.94	0.379843	0.568146	-6.88
262179_at	hypothetical protein predicted by gene	AGL66	AT1G77980	-1.09	-0.13	-0.94	0.379811	0.568146	-6.88
263418_at	putative selenium-binding protein	---	AT2G17210	1.07	0.10	0.94	0.379876	0.568157	-6.88
259781_at	reverse transcriptase, putative similar	---	---	-1.09	-0.12	-0.94	0.379905	0.568164	-6.88
259466_at	response regulator 5, putative similar	ARR7	AT1G19050	1.32	0.40	0.94	0.379972	0.5682	-6.88
248645_at	unknown protein	GEX2	AT5G49150	-1.09	-0.12	-0.94	0.380013	0.5682	-6.88
261755_at	histone H2B, putative similar to GB:AA	---	AT1G08170	1.10	0.14	0.94	0.380029	0.5682	-6.88
257048_at	hypothetical protein predicted by gene	---	AT3G19740	1.07	0.09	0.94	0.380026	0.5682	-6.88
265820_at	hypothetical protein predicted by gens	---	AT2G17940	-1.10	-0.14	-0.94	0.380064	0.568215	-6.88
250648_at	late embryogenesis abundant protein l	---	AT5G06760	-1.08	-0.12	-0.94	0.38035	0.568606	-6.88

262724_s_	PC-MYB2, putative similar to PC-MYB	---	AT1G43330 /	1.07	0.09	0.94	0.380409	0.568657	-6.88
254802_at	endoxyloglucan transferase-like prote	---	AT4G13090	-1.10	-0.14	-0.94	0.380456	0.568689	-6.88
258230_s_	hypothetical protein similar to hypothe	ARI13	AT3G27710 /	-1.07	-0.09	-0.94	0.380554	0.568761	-6.88
263060_s_	hypothetical protein	---	AT2G07679 /	1.11	0.16	0.94	0.380539	0.568761	-6.88
252087_at	putative protein putative Na+/H+-exch	chx28	AT3G52080	-1.07	-0.10	-0.94	0.380628	0.56877	-6.88
250520_at	putative protein contains similarity to A	PEX1	AT5G08470	1.06	0.09	0.94	0.380707	0.56877	-6.88
262698_at	AMP-binding protein, putative contain	---	AT1G75960	-1.20	-0.26	-0.94	0.380666	0.56877	-6.88
251604_at	putative protein 60S RIBOSOMAL PR	---	AT3G57820	1.07	0.09	0.94	0.3807	0.56877	-6.88
255160_at	putative pathogenesis-related protein	---	AT4G07820	-1.06	-0.09	-0.94	0.380693	0.56877	-6.88
247286_at	2-oxoglutarate/malate translocator ; su	DiT2.2	AT5G64280	1.08	0.11	0.94	0.380709	0.56877	-6.88
262805_at	putative DNA-binding protein similar t	ESC	AT1G20900	1.07	0.10	0.94	0.38082	0.568898	-6.88
253164_at	Expressed protein ; supported by full-le	---	AT4G35725	1.07	0.10	0.94	0.380883	0.568955	-6.88
255356_x_	putative transposon protein	---	---	1.08	0.11	0.94	0.38106	0.569153	-6.88
264294_at	hypothetical protein similar to heat sho	---	AT1G78750	-1.08	-0.11	-0.94	0.381139	0.569153	-6.88
263858_at	hypothetical protein predicted by gens	---	AT2G04370	1.07	0.10	0.94	0.3811	0.569153	-6.88
267191_at	similar to Mlo proteins from H. vulgare	MLO15	AT2G44110	-1.12	-0.16	-0.94	0.38114	0.569153	-6.88
257329_at	hypothetical protein	---	---	1.13	0.17	0.94	0.381076	0.569153	-6.88
263748_at	putative protein kinase contains a prot	---	AT2G21480	1.08	0.11	0.94	0.381203	0.56921	-6.88
265071_at	transcription initiation factor TFIID-2 id	TBP2	AT1G55520	-1.08	-0.11	-0.94	0.38124	0.569228	-6.88
253312_s_	putative protein (1,4)-beta-xylan endo	---	AT4G33850 /	1.07	0.10	0.94	0.381325	0.569314	-6.88
255153_at	putative protein several hypothetical pr	---	AT4G08210	-1.10	-0.13	-0.94	0.381348	0.569314	-6.88
252235_at	60S RIBOSOMAL PROTEIN - like 60	---	AT3G49910	-1.16	-0.21	-0.94	0.381438	0.569399	-6.88
255868_at	putative MYB family transcription facto	---	AT2G30380	1.09	0.13	0.94	0.381455	0.569399	-6.88
248982_at	chloroplast nucleoid DNA-binding prote	---	AT5G45120	-1.08	-0.11	-0.94	0.381573	0.569471	-6.88
253149_at	NAD+ dependent isocitrate dehydroge	---	AT4G35650	-1.08	-0.11	-0.94	0.381558	0.569471	-6.88
255004_at	putative protein	---	AT4G09970	-1.10	-0.14	-0.94	0.381628	0.569471	-6.88
259767_s_	unknown protein	---	AT1G29350 /	1.07	0.10	0.94	0.381579	0.569471	-6.88
248471_at	unknown protein	---	AT5G50840	-1.10	-0.14	-0.94	0.381616	0.569471	-6.88
245199_at	Expressed protein ; supported by full-le	KCR1	AT1G67730	-1.09	-0.13	-0.94	0.381924	0.569876	-6.88
248220_at	26S proteasome regulatory particle ch	---	AT5G53540	1.08	0.11	0.94	0.381983	0.569913	-6.88
265827_at	hypothetical protein predicted by gene	VOZ2	AT2G42400	1.06	0.08	0.94	0.381999	0.569913	-6.88
253087_at	purple acid phosphatase like protein	PAP25	AT4G36350	1.08	0.12	0.94	0.382035	0.569929	-6.88
259306_at	unknown protein ;supported by full-ler	PNC1	AT3G05290	-1.08	-0.10	-0.94	0.38209	0.569974	-6.88
258172_at	unknown protein similar to HYP1 GB:C	---	AT3G21620	-1.07	-0.09	-0.93	0.382237	0.570157	-6.88
257440_at	unknown protein	---	AT2G24880	-1.07	-0.09	-0.93	0.382548	0.570583	-6.89

252780_at	alcohol dehydrogenase (ATA1) ;suppo	ATA1	AT3G42960	-1.12	-0.17	-0.93	0.382656	0.570614	-6.89
247711_at	receptor-like protein kinase receptor-li	---	AT5G59270	-1.08	-0.11	-0.93	0.382691	0.570614	-6.89
245984_at	putative protein predicted proteins - Ar	---	AT5G13090	-1.08	-0.11	-0.93	0.38267	0.570614	-6.89
256080_at	high mobility group protein (HMG1), p	---	AT1G20690	-1.07	-0.09	-0.93	0.382713	0.570614	-6.89
265047_at	hypothetical protein similar to unknowr	IQD27	AT1G51960	-1.08	-0.12	-0.93	0.382656	0.570614	-6.89
257711_at	20S proteasome beta subunit (PBB1)	PBB1	AT3G27430	1.08	0.11	0.93	0.382719	0.570614	-6.89
246020_at	putative protein ; supported by cDNA:	---	AT5G10710	1.08	0.11	0.93	0.382896	0.570688	-6.89
247259_at	CPR5 protein, putative Constitutive ex	CPR5	AT5G64930	1.11	0.15	0.93	0.382838	0.570688	-6.89
253896_at	putative protein NBS/LRR disease res	---	AT4G27190	-1.08	-0.11	-0.93	0.382847	0.570688	-6.89
262705_at	putative wall-associated kinase similar	---	AT1G16260	1.31	0.39	0.93	0.382908	0.570688	-6.89
247674_at	putative protein large number of predi	---	AT5G59930	1.11	0.15	0.93	0.38284	0.570688	-6.89
245448_at	disease resistance RPP5 like protein	RPP4	AT4G16860	-1.09	-0.12	-0.93	0.382919	0.570688	-6.89
250399_at	putative protein predicted proteins, Ar	---	AT5G10750	-1.10	-0.14	-0.93	0.38295	0.570697	-6.89
258504_at	putative sterol-C5-desaturase identical	---	AT3G02590	-1.06	-0.09	-0.93	0.383107	0.570894	-6.89
249970_at	dermal glycoprotein precursor -like pr	---	AT5G19100	-1.15	-0.20	-0.93	0.383458	0.571224	-6.89
249845_at	putative protein similar to unknown pro	---	AT5G23610	1.07	0.10	0.93	0.383508	0.571224	-6.89
249510_at	putative protein similar to unknown pro	---	AT5G38510	-1.08	-0.11	-0.93	0.383504	0.571224	-6.89
248045_at	HEAT SHOCK PROTEIN 81-2 (HSP81	HSP81-2	AT5G56030	1.21	0.28	0.93	0.383369	0.571224	-6.89
263021_at	hypothetical protein predicted by gene	---	AT1G23910	-1.06	-0.08	-0.93	0.383529	0.571224	-6.89
249402_at	Expressed protein ; supported by full-le	---	AT5G40155	1.08	0.11	0.93	0.383409	0.571224	-6.89
251044_at	putative protein various predicted prot	---	AT5G02350	-1.07	-0.10	-0.93	0.383507	0.571224	-6.89
259322_at	unknown protein	---	AT3G05270	1.10	0.14	0.93	0.383519	0.571224	-6.89
251715_at	putative protein putative WRKY-type D	---	AT3G56390	-1.07	-0.09	-0.93	0.383582	0.571265	-6.89
254569_s_	hypothetical protein	---	---	-1.07	-0.09	-0.93	0.383632	0.571302	-6.89
265652_x_	hypothetical protein predicted by gens	---	---	-1.09	-0.12	-0.93	0.383716	0.571391	-6.89
262542_at	hypothetical protein similar to NAM-like	anac016	AT1G34180	1.14	0.18	0.93	0.383782	0.571452	-6.89
258188_at	unknown protein ;supported by full-ler	---	AT3G17800	-1.10	-0.13	-0.93	0.383824	0.571477	-6.89
250808_at	putative protein contains similarity to u	ATG18E	AT5G05150	-1.09	-0.13	-0.93	0.383933	0.571601	-6.89
256986_at	unknown protein	---	AT3G28700	-1.11	-0.15	-0.93	0.384003	0.571669	-6.89
254130_at	MADS-box protein AGL24 ; supported	AGL24	AT4G24540	1.14	0.19	0.93	0.384163	0.571869	-6.89
250507_at	putative protein similar to unknown pro	---	AT5G09940	1.07	0.10	0.93	0.384564	0.57243	-6.89
254438_at	translation initiation factor eIF3 - like p	---	AT4G20980	-1.10	-0.13	-0.93	0.384694	0.572586	-6.89
265101_at	unknown protein similar to ESTs gb|R3	---	AT1G30880	1.13	0.18	0.93	0.384797	0.572663	-6.89
256532_at	PPR-repeat protein, putative contains	---	AT1G33350	1.12	0.16	0.93	0.384788	0.572663	-6.89
247626_at	receptor like protein kinase receptor li	---	AT5G60300 /	1.26	0.33	0.93	0.384895	0.572735	-6.89

250063_at	disease resistance protein - like disea	CSA1	AT5G17880	1.10	0.14	0.93	0.38487	0.572735	-6.89
249626_at	putative protein nucleoid DNA-binding	---	AT5G37540	1.16	0.21	0.93	0.384929	0.572748	-6.89
264234_at	hypothetical protein contains similarity	---	AT1G54720	-1.06	-0.09	-0.93	0.3851	0.572965	-6.89
259621_at	unknown protein	---	AT1G42710	-1.06	-0.09	-0.93	0.385302	0.573191	-6.89
251734_at	putative protein Centrosome- and Gol	---	AT3G56270	-1.18	-0.23	-0.93	0.385296	0.573191	-6.89
248755_at	putative protein strong similarity to unk	---	AT5G47690	1.11	0.16	0.93	0.385333	0.5732	-6.89
252623_at	hypothetical protein	---	AT3G45320	-1.08	-0.11	-0.93	0.385359	0.573201	-6.89
258404_at	ribosomal protein L3	RPL3P	AT3G17465	1.09	0.13	0.93	0.385437	0.573279	-6.89
260307_at	unknown protein similar to unknown pr	---	AT1G70620	1.06	0.08	0.93	0.385501	0.573338	-6.89
246660_at	putative protein predicted protein, Ara	---	AT5G35180	1.08	0.11	0.93	0.385664	0.573374	-6.89
255503_at	contains similarity to a protein kinase	---	AT4G02420	1.30	0.38	0.93	0.385677	0.573374	-6.89
259401_at	hypothetical protein contains similarity	CSTF77	AT1G17760	-1.14	-0.18	-0.93	0.385628	0.573374	-6.89
262709_at	unknown protein ESTs gb|F15498, gb	SYP51	AT1G16240	1.09	0.12	0.93	0.385665	0.573374	-6.89
262845_at	unknown protein ; supported by cDNA	---	AT1G14740	1.15	0.21	0.93	0.385671	0.573374	-6.89
252551_at	phospholipase - like protein cytosolic	---	AT3G45880	-1.11	-0.14	-0.93	0.385583	0.573374	-6.89
249716_at	sterile apetala (emb|CAA11128.1)	SAP	AT5G35770	-1.08	-0.11	-0.93	0.385705	0.573379	-6.89
257729_at	histone deacetylase, putative contains	HDA15	AT3G18520	1.11	0.15	0.93	0.385784	0.57346	-6.89
258437_at	unknown protein contains protein phos	---	AT3G16560	1.12	0.17	0.93	0.385948	0.573591	-6.89
253481_at	aspartate aminotransferase ;supporte	ASP5	AT4G31990	-1.08	-0.11	-0.93	0.385939	0.573591	-6.89
258666_at	hypothetical protein	KOB1	AT3G08550	-1.07	-0.10	-0.93	0.385913	0.573591	-6.89
262524_at	tuftelin-interacting-like protein Similar t	---	AT1G17070	-1.06	-0.09	-0.93	0.3862	0.573928	-6.89
257103_at	hypothetical protein contains Pfam pro	---	AT3G25060	1.09	0.12	0.93	0.386272	0.573998	-6.89
251290_at	transcription factor BBFa	DAG1	AT3G61850	1.09	0.12	0.93	0.386383	0.574126	-6.89
249041_at	male sterility MS5; pollenless3	---	AT5G44330	-1.08	-0.11	-0.93	0.386452	0.574191	-6.89
261869_at	hypothetical protein predicted by gene	---	AT1G11470	-1.08	-0.12	-0.93	0.386516	0.574248	-6.89
256352_at	proline-rich protein, putative similar to	ATPRP1	AT1G54970	-1.10	-0.13	-0.93	0.386553	0.574265	-6.89
263842_at	Expressed protein ; supported by full-l	---	AT2G36835	1.12	0.16	0.93	0.386605	0.574306	-6.89
259986_at	thaumatin-like protein similar to thaum	---	AT1G75050	-1.08	-0.12	-0.93	0.386649	0.574334	-6.89
263527_at	putative thaumatin-like pathogenesis-r	---	AT2G24810	-1.13	-0.18	-0.93	0.386693	0.574361	-6.89
250240_at	unknown protein	---	AT5G13590	1.12	0.16	0.93	0.386869	0.574586	-6.89
264421_at	ribosomal protein identical to ribosoma	ARP1	AT1G43170	-1.11	-0.16	-0.93	0.386896	0.574587	-6.89
252609_at	putative protein	---	AT3G45110	-1.08	-0.11	-0.92	0.387007	0.574715	-6.89
260721_at	hypothetical protein predicted by gene	---	AT1G48060	-1.07	-0.10	-0.92	0.38708	0.574786	-6.89
264483_at	unknown protein	---	AT1G77230	-1.10	-0.14	-0.92	0.387172	0.574886	-6.89
263164_at	putative glutamate/aspartate-binding p	---	AT1G03070	-1.08	-0.11	-0.92	0.387422	0.575181	-6.89

264643_at	unknown protein	PGSIP5	AT1G08990	-1.07	-0.09	-0.92	0.387406	0.575181	-6.89
257731_at	unknown protein similar to CALCINEU	---	AT3G18430	1.07	0.10	0.92	0.387519	0.575288	-6.90
262785_at	putative carboxyl-terminal peptidase si	---	AT1G10750	-1.12	-0.17	-0.92	0.387767	0.575614	-6.90
253877_at	Expressed protein ; supported by cDN	---	AT4G27435	-1.17	-0.22	-0.92	0.38779	0.575614	-6.90
267045_at	putative protein kinase contains a prot	CIPK13	AT2G34180	-1.07	-0.10	-0.92	0.387814	0.575614	-6.90
260854_at	CCAAT-box binding factor HAP3 hom	LEC1	AT1G21970	-1.11	-0.15	-0.92	0.387874	0.575666	-6.90
253585_at	putative protein hypothetical protein -	---	AT4G30720	1.07	0.10	0.92	0.388009	0.575687	-6.90
247586_at	mipC protein - like (aquaporin) mipC p	PIP2;4	AT5G60660	1.08	0.11	0.92	0.388001	0.575687	-6.90
247558_at	histone deacetylase - like histone dea	HDA05	AT5G61060	1.08	0.11	0.92	0.388042	0.575687	-6.90
264999_at	hypothetical protein contains similarity	---	AT1G67310	-1.07	-0.10	-0.92	0.387999	0.575687	-6.90
252978_at	galactosidase like protein ss-1,4-exog	BGAL14	AT4G38590	-1.10	-0.14	-0.92	0.38809	0.575687	-6.90
249644_at	putative serine-rich protein hypothetic	---	AT5G37010	1.09	0.13	0.92	0.388055	0.575687	-6.90
261452_s_	hypothetical protein predicted by gene	---	---	1.08	0.10	0.92	0.387969	0.575687	-6.90
263450_at	putative calcium-dependent protein kin	CPK24	AT2G31500	-1.07	-0.09	-0.92	0.388088	0.575687	-6.90
247512_at	putative protein predicted protein, Ara	---	AT5G61720	1.07	0.09	0.92	0.388164	0.575722	-6.90
264119_at	myb-related protein, putative similar to	MYB63	AT1G79180	1.06	0.09	0.92	0.38816	0.575722	-6.90
252826_at	hypothetical protein ; supported by cD	---	AT4G40050	-1.08	-0.11	-0.92	0.388192	0.575726	-6.90
255080_at	arabinogalactan-protein homolog arab	AGP10	AT4G09030	1.14	0.19	0.92	0.388241	0.57576	-6.90
257885_at	S1 self-incompatibility protein, putative	---	AT3G16970	-1.07	-0.10	-0.92	0.388293	0.575778	-6.90
264093_at	hypothetical protein predicted by gene	---	AT1G79220	-1.07	-0.10	-0.92	0.388303	0.575778	-6.90
264518_at	unknown protein	---	AT1G09980	-1.11	-0.15	-0.92	0.388363	0.57583	-6.90
261750_at	hypothetical protein contains similarity	---	AT1G76120	1.09	0.13	0.92	0.388556	0.576041	-6.90
258734_at	putative DNA-binding protein similar to	---	AT3G05860	1.07	0.09	0.92	0.388555	0.576041	-6.90
261082_at	unknown protein ; supported by cDNA	---	AT1G07360	-1.06	-0.08	-0.92	0.388681	0.576189	-6.90
251007_at	ribosomal protein L35 - like ribosomal	---	AT5G02610	1.09	0.13	0.92	0.388914	0.576494	-6.90
262971_at	receptor-like protein kinase, putative r	---	AT1G75640	1.11	0.15	0.92	0.388938	0.576494	-6.90
246342_at	putative protein male sterility protein 2	FAR6	AT3G56700	1.06	0.09	0.92	0.389037	0.576604	-6.90
250587_at	putative protein contains similarity to R	---	AT5G07640	1.07	0.10	0.92	0.38937	0.57706	-6.90
262274_at	deaminase, putative similar to cytidine	TADA	AT1G68720	-1.06	-0.09	-0.92	0.389409	0.57708	-6.90
266036_s_	20S proteasome subunit (PAA2) identi	PAA2	AT2G05840 /	1.07	0.10	0.92	0.389473	0.577137	-6.90
249525_at	putative protein similar to unknown pro	---	AT5G38650	1.07	0.10	0.92	0.38953	0.577184	-6.90
253730_at	putative protein hypothetical protein T	---	AT4G29480	1.14	0.18	0.92	0.389562	0.577194	-6.90
255847_at	putative thioredoxin	ACHT3	AT2G33270	-1.06	-0.08	-0.92	0.389678	0.577328	-6.90
266484_at	putative putative sister-chromatide coh	SCC3	AT2G47980	-1.08	-0.11	-0.92	0.389817	0.577469	-6.90
251546_at	putative protein predicted proteins, ye	---	AT3G58830	-1.12	-0.17	-0.92	0.389823	0.577469	-6.90

263118_at	putative 3-methylcrotonyl-CoA carbox	MCCA	AT1G03090	1.20	0.27	0.92	0.389967	0.577645	-6.90
251999_at	hypothetical protein teichoic acid biosy	---	AT3G52700	1.07	0.09	0.92	0.390024	0.577692	-6.90
249432_at	putative ATP/GTP-binding protein put	CLPS5	AT5G39930	1.07	0.10	0.92	0.39014	0.577788	-6.90
249723_at	putative protein similar to unknown pro	---	AT5G35430	1.06	0.09	0.92	0.390122	0.577788	-6.90
254678_at	hypothetical protein	---	AT4G18500	1.07	0.10	0.92	0.390309	0.578	-6.90
260026_at	60S ribosomal protein L18A, putative	RPL18AA	AT1G29970	1.08	0.11	0.92	0.390417	0.578124	-6.90
259101_at	hypothetical protein predicted by gens	---	AT3G11640	-1.06	-0.09	-0.92	0.390668	0.578395	-6.90
265177_at	OBP32pep protein, putative identical t	---	AT1G23640	1.07	0.09	0.92	0.390634	0.578395	-6.90
249209_at	major surface glycoprotein-like ; suppo	---	AT5G42620	1.08	0.11	0.92	0.390677	0.578395	-6.90
245812_at	hypothetical protein predicted by gene	---	---	-1.07	-0.10	-0.92	0.390706	0.578401	-6.90
264422_at	unknown protein similar to unknown pr	LCV2	AT1G43130	-1.08	-0.11	-0.92	0.390768	0.578455	-6.90
247358_at	flavonol synthase	FLS2	AT5G63580	-1.10	-0.13	-0.92	0.390885	0.578591	-6.90
265883_at	unknown protein	---	AT2G42310	1.07	0.10	0.92	0.39093	0.57862	-6.90
251335_at	1-aminocyclopropane-1-carboxylate o	---	AT3G61400	-1.12	-0.16	-0.92	0.391016	0.578705	-6.90
249978_at	putative protein	---	AT5G18850	-1.08	-0.11	-0.92	0.391038	0.578705	-6.90
251696_at	putative protein	---	---	1.09	0.13	0.92	0.391093	0.578749	-6.90
255893_at	threonyl-tRNA synthetase, putative sir	---	AT1G17960	1.14	0.19	0.92	0.39114	0.57878	-6.90
247917_at	putative protein similar to unknown pro	BIO1	AT5G57590	-1.07	-0.10	-0.92	0.391206	0.578803	-6.90
257521_at	hypothetical protein predicted by gene	---	AT3G09140	1.06	0.09	0.92	0.391182	0.578803	-6.90
245916_at	putative protein	---	AT5G28720	-1.08	-0.12	-0.92	0.39128	0.578875	-6.90
250269_at	anthranilate phosphoribosyltransferas	---	AT5G12970	-1.08	-0.11	-0.92	0.391475	0.579127	-6.90
246694_at	putative protein	---	---	1.07	0.10	0.92	0.391564	0.57922	-6.90
253745_at	putative protein the C-terminus of the	---	AT4G29090	1.07	0.10	0.92	0.391593	0.579225	-6.90
250052_at	putative protein predicted proteins, Ar	---	AT5G17830	-1.09	-0.12	-0.92	0.391706	0.579355	-6.90
260724_at	unknown protein ;supported by full-len	---	AT1G48140	1.07	0.10	0.91	0.391865	0.579552	-6.90
248877_at	putative protein similar to unknown pro	---	AT5G46140	-1.07	-0.10	-0.91	0.391988	0.579607	-6.90
246458_at	putative protein various predicted prot	---	AT5G16860	1.09	0.12	0.91	0.391978	0.579607	-6.90
246309_at	putative transmembrane protein G1p E	ATG1	AT3G51790	1.19	0.25	0.91	0.391975	0.579607	-6.90
256109_at	hypothetical protein predicted by gene	---	AT1G16950	1.14	0.19	0.91	0.392003	0.579607	-6.90
248036_at	nucleolar protein-like	OLI2	AT5G55920	1.11	0.15	0.91	0.392188	0.579843	-6.90
248567_at	putative protein contains similarity to e	---	AT5G49750	1.07	0.10	0.91	0.392269	0.579924	-6.90
246174_s_	putative protein hypothetical protein T	---	AT5G28340 /	-1.06	-0.09	-0.91	0.392385	0.580058	-6.90
256586_at	hypothetical protein	---	AT3G28770	-1.06	-0.09	-0.91	0.392492	0.58018	-6.90
245235_at	putative protein similarity to predicted	---	AT4G25550	-1.08	-0.11	-0.91	0.392581	0.580272	-6.90
260984_at	Expressed protein ; supported by full-le	---	AT1G53645	1.15	0.20	0.91	0.392643	0.580326	-6.90

262898_at	hypothetical protein predicted by gene	---	AT1G59850	-1.08	-0.12	-0.91	0.392828	0.580563	-6.91
245515_at	hypothetical protein	---	AT4G15810	1.14	0.19	0.91	0.392964	0.580726	-6.91
245675_at	hypothetical protein similar to putative	---	---	-1.11	-0.15	-0.91	0.39302	0.580742	-6.91
262404_at	transposon-like ORF, putative similar	---	---	1.07	0.10	0.91	0.393026	0.580742	-6.91
257279_at	unknown protein ;supported by full-ler	---	AT3G14430	-1.08	-0.10	-0.91	0.393218	0.58098	-6.91
260892_at	cysteine proteinase contains similarity	---	AT1G29110	1.08	0.12	0.91	0.393238	0.58098	-6.91
247705_at	putative protein ;supported by full-leng	---	AT5G59460	-1.07	-0.10	-0.91	0.393277	0.581	-6.91
251552_at	ribosomal protein L11 -like ribosomal	---	AT3G58700	-1.14	-0.19	-0.91	0.393391	0.581127	-6.91
245585_at	hypothetical	---	AT4G14970	-1.07	-0.10	-0.91	0.393413	0.581127	-6.91
260723_at	unknown protein	---	AT1G48070	-1.07	-0.09	-0.91	0.393445	0.581136	-6.91
251040_at	ribonuclease II-like protein ribonuclea	EMB2730	AT5G02250	-1.13	-0.17	-0.91	0.393537	0.581233	-6.91
252919_at	putative endo-1,4-beta-glucanase end	AtGH9B16	AT4G38990	-1.10	-0.14	-0.91	0.393576	0.581255	-6.91
256220_at	unknown protein	---	AT1G56230	1.10	0.13	0.91	0.393857	0.58153	-6.91
251921_at	40S ribosomal protein S21 homolog ri	---	AT3G53890	-1.19	-0.25	-0.91	0.393851	0.58153	-6.91
250560_at	replication factor A - like protein replic	RPA70B	AT5G08020	-1.15	-0.20	-0.91	0.393859	0.58153	-6.91
262551_at	putative heat shock transcription factor	RUB1	AT1G31340	-1.10	-0.14	-0.91	0.393865	0.58153	-6.91
246677_at	putative protein predicted proteins - Ar	---	---	1.08	0.12	0.91	0.393927	0.581584	-6.91
246471_s_	putative protein predicted proteins, Ar	---	AT5G17100 /	-1.07	-0.09	-0.91	0.394033	0.581702	-6.91
252546_at	DNA-binding protein - like DNA-bindi	---	AT3G45830	1.07	0.10	0.91	0.394113	0.581775	-6.91
251671_at	putative protein hypothetical protein T	---	AT3G57210	1.08	0.11	0.91	0.394133	0.581775	-6.91
254555_at	putative protein curved DNA-binding p	---	AT4G19570	-1.07	-0.10	-0.91	0.394242	0.581899	-6.91
260942_s_	hypothetical protein contains similarity	---	AT1G45190 /	-1.08	-0.11	-0.91	0.394304	0.581953	-6.91
265622_at	unknown protein	---	AT2G27280	1.06	0.09	0.91	0.394408	0.582069	-6.91
260808_at	polyprotein, putative similar to polypro	---	---	-1.06	-0.09	-0.91	0.39448	0.5821	-6.91
251086_at	putative protein hypothetical protein A	---	AT5G01450	1.10	0.14	0.91	0.394481	0.5821	-6.91
254927_at	putative protein hypothetical protein -	---	AT4G11400	-1.09	-0.12	-0.91	0.394538	0.582147	-6.91
263303_at	unknown protein ;supported by full-ler	---	AT2G15240	-1.09	-0.12	-0.91	0.394719	0.582376	-6.91
251963_at	protein kinase (AME2/AFC1) ; suppor	AFC1	AT3G53570	-1.07	-0.10	-0.91	0.394943	0.582669	-6.91
247432_at	microtubule-associated protein EB1-lik	ATEB1B	AT5G62500	-1.08	-0.11	-0.91	0.39502	0.582732	-6.91
257511_at	hypothetical protein	---	AT1G43000	1.08	0.11	0.91	0.395037	0.582732	-6.91
255045_at	putative protein hypothetical protein T	---	AT4G09690	1.08	0.11	0.91	0.395076	0.582752	-6.91
263969_at	putative VSF-1-like b-ZIP transcription	UNE4	AT2G12940	-1.08	-0.11	-0.91	0.395455	0.583273	-6.91
266970_at	hypothetical protein predicted by gene	---	AT2G39560	-1.08	-0.11	-0.91	0.395574	0.583412	-6.91
262998_at	hypothetical protein predicted by gene	---	AT1G54280	-1.06	-0.08	-0.91	0.3956	0.583412	-6.91
247280_at	phi-1-like protein ;supported by full-ler	EXL2	AT5G64260	-1.17	-0.22	-0.91	0.395854	0.583598	-6.91

256858_at	hypothetical protein predicted by gene	---	AT3G15140	1.11	0.15	0.91	0.395787	0.583598	-6.91
250764_at	putative protein similar to unknown pro	---	AT5G05960	-1.73	-0.79	-0.91	0.39584	0.583598	-6.91
266082_at	hypothetical protein predicted by gens	---	AT2G37830	-1.11	-0.15	-0.91	0.395801	0.583598	-6.91
248887_at	Expressed protein ; supported by full-l	---	AT5G46115	1.08	0.11	0.91	0.39583	0.583598	-6.91
249413_at	ras - related GTP binding protein - like	AtRABG1	AT5G39620	1.07	0.09	0.91	0.395897	0.583624	-6.91
262834_at	hypothetical protein predicted by gens	MAP65-7	AT1G14690	1.07	0.10	0.91	0.395952	0.583644	-6.91
AFFX-CreX	Bacteriophage P1 /GEN=cre /DB_XRE	---	---	1.17	0.22	0.91	0.395962	0.583644	-6.91
266410_at	unknown protein	EMB2765	AT2G38770	1.07	0.09	0.91	0.396339	0.584087	-6.91
250135_at	putative protein	---	AT5G15360	1.08	0.10	0.91	0.396299	0.584087	-6.91
255545_at	putative polygalacturonidase similar to	---	AT4G01890	-1.07	-0.10	-0.91	0.396319	0.584087	-6.91
265188_at	putative aldehyde dehydrogenase ; su	ALDH2B7	AT1G23800	-1.10	-0.14	-0.91	0.3964	0.584111	-6.91
265864_at	putative myosin heavy chain-like prote	ATMAP70-3	AT2G01750	-1.11	-0.15	-0.91	0.396407	0.584111	-6.91
253129_at	glycine-rich protein glycine-rich protei	CSDP1	AT4G36020	1.11	0.15	0.91	0.39651	0.584225	-6.91
249879_at	serine/threonine protein kinase-like pro	---	AT5G23170	1.07	0.10	0.91	0.396645	0.584386	-6.91
266907_at	Expressed protein ; supported by full-l	ATGA2OX3	---	1.09	0.12	0.90	0.396709	0.584443	-6.91
264496_at	putative polyprotein similar to GB:AAC	---	---	-1.09	-0.12	-0.90	0.396761	0.584444	-6.91
263827_at	unknown protein	---	AT2G40420	1.13	0.17	0.90	0.396748	0.584444	-6.91
250086_at	NAM (no apical meristem)-like protein	anac086	AT5G17260	-1.08	-0.11	-0.90	0.396792	0.584452	-6.91
255858_at	zinc finger protein (ZFP6) identical to z	ZFP6	AT1G67030	-1.11	-0.15	-0.90	0.396825	0.584462	-6.91
262532_at	hypothetical protein predicted by gens	---	AT1G17210	-1.08	-0.10	-0.90	0.39696	0.584623	-6.91
251577_at	putative protein several hypothetical pr	---	AT3G58350	-1.09	-0.13	-0.90	0.397034	0.584695	-6.91
261786_at	cyclic nucleotide and calmodulin-regu	ATCNGC7	AT1G15990	-1.07	-0.10	-0.90	0.397065	0.584703	-6.91
248985_at	GTP-binding protein-like; root hair defe	---	AT5G45160	1.07	0.09	0.90	0.397199	0.584863	-6.91
255207_at	Expressed protein ; supported by full-l	---	AT4G07515	1.06	0.08	0.90	0.397267	0.584925	-6.91
255491_at	putative zinc finger protein similar to p	AtIDD12	AT4G02670	1.06	0.08	0.90	0.397418	0.585103	-6.91
252775_s_	putative protein various predicted prot	---	---	-1.07	-0.10	-0.90	0.397439	0.585103	-6.91
245554_at	cytochrome P450 like protein	CYP705A4	AT4G15380	1.06	0.08	0.90	0.397555	0.585236	-6.91
265611_at	unknown protein ;supported by full-ler	---	AT2G25510	-1.14	-0.19	-0.90	0.397647	0.585334	-6.91
257136_at	hypothetical protein predicted by gens	ASML2	AT3G12890	1.08	0.11	0.90	0.397717	0.585399	-6.91
249399_at	putative protein intracellular protein M	---	AT5G40290	1.06	0.08	0.90	0.397815	0.585506	-6.91
264872_at	putative floral homeotic protein, AGL9	סמס-03	AT1G24260	-1.11	-0.15	-0.90	0.397949	0.585665	-6.91
245651_s_	F5A9.18 unknown protein; similar to E	---	AT1G24793 /	1.10	0.14	0.90	0.398097	0.585845	-6.92
263444_at	putative MADS-box protein	AGL46	AT2G28700	-1.09	-0.12	-0.90	0.39821	0.585973	-6.92
251504_at	putative protein putative multidrug effl	TT12	AT3G59030	-1.08	-0.11	-0.90	0.398296	0.586062	-6.92
250468_at	transcription factor TEIL/ethylene-inse	---	AT5G10120	1.06	0.08	0.90	0.398326	0.586068	-6.92

252905_at	putative protein predicted protein, Ara	---	AT4G39720	1.10	0.13	0.90	0.398444	0.586204	-6.92
247416_at	40S ribosomal protein S15-like protein	---	AT5G63070	-1.08	-0.12	-0.90	0.398522	0.58628	-6.92
257819_at	Expressed protein ; supported by full-l	RALFL25	AT3G25165	1.07	0.10	0.90	0.398549	0.586283	-6.92
246175_s_	putative protein hypothetical protein F	---	AT5G28320 /	-1.07	-0.10	-0.90	0.398591	0.586307	-6.92
260288_at	nodulin-like protein similar to nodule-s	---	AT1G80530	-1.12	-0.16	-0.90	0.398779	0.586546	-6.92
264022_at	Expressed protein ; supported by full-l	---	AT2G21185	-1.10	-0.14	-0.90	0.398904	0.586622	-6.92
267297_at	putative RING zinc finger protein ;sup	---	AT2G23780	-1.08	-0.11	-0.90	0.398931	0.586622	-6.92
263425_at	putative preprotein translocase SECY	EMB2289	AT2G31530	-1.09	-0.12	-0.90	0.398981	0.586622	-6.92
249603_at	putative protein predicted proteins, Ar	---	AT5G37210	-1.07	-0.10	-0.90	0.39892	0.586622	-6.92
257334_at	hypothetical protein	---	---	1.19	0.25	0.90	0.398964	0.586622	-6.92
244958_at	hypothetical protein	---	---	1.07	0.09	0.90	0.398985	0.586622	-6.92
260205_at	hypothetical protein predicted by gene	TIFY7	AT1G70700	1.19	0.25	0.90	0.399025	0.586642	-6.92
251890_at	SCARECROW1 ; supported by cDNA	SCR	AT3G54220	-1.08	-0.10	-0.90	0.399073	0.586675	-6.92
256703_at	MADS-box transcription factor similar	AGL79	AT3G30260	1.06	0.08	0.90	0.399155	0.586759	-6.92
256628_at	membrane import protein, putative sin	TOM40	AT3G20000	1.12	0.17	0.90	0.399231	0.586832	-6.92
250765_at	unknown protein ;supported by full-ler	---	AT5G05930	-1.11	-0.15	-0.90	0.39942	0.587072	-6.92
246392_at	hypothetical protein predicted by gene	---	AT1G58120 /	1.06	0.09	0.90	0.399594	0.58729	-6.92
261419_at	hypothetical protein predicted by gene	---	AT1G07840	-1.06	-0.08	-0.90	0.399718	0.587435	-6.92
246045_at	putative protein predicted proteins, Dr	---	AT5G19430	1.10	0.14	0.90	0.399749	0.587442	-6.92
245807_at	AP2 domain containing protein RAP2.	RAP2.1	AT1G46768	-1.17	-0.22	-0.90	0.39988	0.587565	-6.92
252489_at	disease resistance protein RPP8-like	---	AT3G46710	1.09	0.13	0.90	0.399884	0.587565	-6.92
252611_at	oxidosqualene cyclase - like protein o	LAS1	AT3G45130	1.20	0.26	0.90	0.399971	0.587655	-6.92
245970_at	beta-galactosidase ; supported by cDI	BGAL7	AT5G20710	-1.09	-0.13	-0.90	0.400034	0.58771	-6.92
251894_at	putative protein predicted proteins, Ar	---	AT3G54380	-1.09	-0.12	-0.90	0.400076	0.587733	-6.92
250995_at	dnaK-type molecular chaperone hsc70	HSC70-1	AT5G02500	-1.11	-0.15	-0.90	0.400191	0.587864	-6.92
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=gb:J04	---	---	1.17	0.22	0.90	0.400229	0.587882	-6.92
258828_at	putative purple acid phosphatase simil	PAP15	AT3G07130	1.08	0.11	0.90	0.400308	0.587961	-6.92
259283_at	putative transcription factor similar to C	MYB65	AT3G11440	-1.08	-0.11	-0.90	0.400594	0.588342	-6.92
247458_at	putative protein PrMC3, Pinus radiata	AtCXE20	AT5G62180	1.14	0.19	0.90	0.400747	0.58853	-6.92
267324_at	hypothetical protein predicted by gens	---	AT2G19360	1.06	0.08	0.90	0.400886	0.588658	-6.92
260242_at	putative transcription factor similar to b	EGL3	AT1G63650	1.07	0.10	0.90	0.400883	0.588658	-6.92
262276_at	hypothetical protein predicted by gene	---	AT1G68700	1.08	0.11	0.90	0.400934	0.58869	-6.92
248157_at	putative protein similar to unknown pro	---	AT5G54420	-1.07	-0.10	-0.90	0.400995	0.58873	-6.92
260197_at	F12A21.25 hypothetical protein	---	AT1G67623	1.07	0.10	0.90	0.401012	0.58873	-6.92
263095_at	Ac-like transposase related to Ac/Ds tr	---	AT2G16040	-1.07	-0.09	-0.90	0.401139	0.588802	-6.92

259931_at	hypothetical protein predicted by gens	---	AT1G34400	1.08	0.11	0.90	0.401135	0.588802	-6.92
249863_at	putative protein contains similarity to u	VPS24.1	AT5G22950	1.06	0.08	0.90	0.40109	0.588802	-6.92
256517_at	PHD-finger protein, putative contains	MMD1	AT1G66170	-1.06	-0.08	-0.90	0.401269	0.588917	-6.92
253179_at	putative protein various predicted prot	---	AT4G35200	-1.06	-0.08	-0.90	0.401267	0.588917	-6.92
259843_at	hypothetical protein predicted by gene	---	AT1G73570	-1.10	-0.14	-0.90	0.40147	0.589175	-6.92
246943_at	putative protein kinase serine/threonir	---	AT5G25440	1.12	0.17	0.89	0.401694	0.589465	-6.92
266070_at	hypothetical protein predicted by gens	EXLB3	AT2G18660	2.16	1.11	0.89	0.401724	0.589471	-6.92
255140_x_	extensin-like protein hydroxyproline-ri	---	AT4G08410	1.12	0.16	0.89	0.401778	0.589512	-6.92
259362_s_	serin threonin-kinase, putative similar	---	AT1G13350 /	-1.08	-0.12	-0.89	0.401886	0.589632	-6.92
261085_at	hypothetical protein similar to hypothet	IQD7	AT1G17480	1.07	0.09	0.89	0.40199	0.589748	-6.92
247581_at	receptor-like protein kinase precursor	---	AT5G61350	-1.07	-0.09	-0.89	0.402025	0.589761	-6.92
248617_at	putative protein similar to unknown pro	---	AT5G49590	1.07	0.09	0.89	0.402106	0.589841	-6.92
263079_at	putative retroelement pol polyprotein	---	---	-1.07	-0.09	-0.89	0.402257	0.590026	-6.92
266554_s_	eukaryotic translation initiation factor 3	---	AT2G46280 /	-1.09	-0.13	-0.89	0.402373	0.590119	-6.92
250737_at	putative protein similar to unknown pro	---	AT5G06370	-1.10	-0.14	-0.89	0.402365	0.590119	-6.92
248319_at	unknown protein	---	AT5G52710	-1.06	-0.09	-0.89	0.402432	0.590131	-6.92
250417_at	putative protein predicted proteins, Ar	---	AT5G11230	-1.09	-0.13	-0.89	0.402415	0.590131	-6.92
251229_at	beta-glucosidase-like protein several b	BGLU7	AT3G62740	-1.06	-0.09	-0.89	0.402481	0.590164	-6.92
264473_at	hypothetical protein predicted by gene	---	AT1G67180	-1.15	-0.20	-0.89	0.402521	0.590175	-6.92
245190_at	F12A21.16 hypothetical protein	---	AT1G67690	-1.10	-0.14	-0.89	0.40254	0.590175	-6.92
260739_at	serine carboxypeptidase precursor, pu	scpl50	AT1G15000	-1.16	-0.21	-0.89	0.402663	0.590318	-6.92
253878_at	trehalose-6-phosphate synthase - like	TPS4	AT4G27550	1.07	0.09	0.89	0.402775	0.590406	-6.92
265156_at	hypothetical protein predicted by gens	---	AT1G31000	-1.08	-0.11	-0.89	0.402771	0.590406	-6.92
248204_at	myosin heavy chain	ATM2	AT5G54280	1.10	0.13	0.89	0.40305	0.590771	-6.92
264033_at	hypothetical protein predicted by gens	---	AT2G03580	-1.09	-0.12	-0.89	0.403348	0.59117	-6.92
262046_at	hypothetical protein predicted by gene	OFP14	AT1G79960	1.09	0.13	0.89	0.403426	0.591208	-6.92
260577_at	hypothetical protein predicted by gene	---	AT2G47340	-1.07	-0.10	-0.89	0.403425	0.591208	-6.92
256685_at	hypothetical protein predicted by gene	---	AT3G32100	1.08	0.11	0.89	0.403536	0.59133	-6.93
256347_at	unknown protein similar to putative dis	---	---	1.08	0.10	0.89	0.403656	0.591468	-6.93
254311_at	hypothetical protein	---	AT4G22440	1.08	0.11	0.89	0.40371	0.591484	-6.93
265821_at	putative homeodomain transcription fa	WUS	AT2G17950	-1.11	-0.15	-0.89	0.403718	0.591484	-6.93
261896_at	mRNA export protein, putative similar	---	AT1G80670	1.09	0.12	0.89	0.403844	0.591527	-6.93
252937_at	SEC14 - like protein phosphatidylinos	SEC14	AT4G39180	-1.07	-0.10	-0.89	0.403929	0.591527	-6.93
258354_at	putative zinc finger protein similar to R	---	AT3G14320	-1.06	-0.09	-0.89	0.403899	0.591527	-6.93
266710_at	putative Ser/Thr protein kinase	---	AT2G46850	1.07	0.10	0.89	0.403853	0.591527	-6.93

266697_at	profilin 4 ; supported by full-length cDI	PRF5	AT2G19770	-1.10	-0.13	-0.89	0.403876	0.591527	-6.93
251366_at	putative protein several hypothetical pr	---	AT3G61340	1.08	0.10	0.89	0.403913	0.591527	-6.93
254373_at	hypothetical protein ;supported by full-	---	AT4G21730	1.07	0.09	0.89	0.403922	0.591527	-6.93
260678_at	hypothetical protein predicted by gene	---	AT1G07970	1.06	0.08	0.89	0.403995	0.591585	-6.93
256885_at	chaperone-like ATPase contains Pfam	---	AT3G15120	1.09	0.12	0.89	0.404211	0.591864	-6.93
256695_at	unknown protein	---	AT3G32090	1.08	0.11	0.89	0.404266	0.591906	-6.93
260312_at	putative disease resistance protein sim	---	AT1G63880	-1.10	-0.13	-0.89	0.40433	0.591962	-6.93
251588_at	putative protein several putative protei	---	AT3G58090	-1.09	-0.12	-0.89	0.404373	0.591986	-6.93
263744_at	Mutator-like transposase similar to MU	---	AT2G21420	1.08	0.11	0.89	0.404446	0.592056	-6.93
249362_at	putative protein predicted protein, Ara	---	AT5G40550	-1.19	-0.26	-0.89	0.404568	0.592196	-6.93
256896_at	hypothetical protein predicted by gene	---	AT3G24630	-1.15	-0.20	-0.89	0.404648	0.592275	-6.93
262071_at	unknown protein ;supported by full-len	CF9	AT1G59510	1.08	0.12	0.89	0.404724	0.592348	-6.93
259048_at	DegP protease contains similarity to de	DegP7	AT3G03380	1.07	0.10	0.89	0.404771	0.59238	-6.93
266425_at	putative strictosidine synthase	---	AT2G41300	-1.08	-0.11	-0.89	0.404891	0.59248	-6.93
265525_at	putative Ty3-gypsy-like retroelement p	---	---	-1.08	-0.11	-0.89	0.404875	0.59248	-6.93
256560_s_	vetispiradiene synthase, putative, 5' p	---	AT3G31415 /	-1.07	-0.09	-0.89	0.405085	0.592725	-6.93
255564_s_	hypothetical protein T15B16.8	RGXT2	AT4G01750 /	1.08	0.11	0.89	0.405155	0.592789	-6.93
246894_at	heat-shock protein - like heat-shock p	---	AT5G25530	-1.12	-0.16	-0.89	0.405213	0.592836	-6.93
264082_at	unknown protein ;supported by full-ler	---	AT2G28570	-1.07	-0.10	-0.89	0.405323	0.592959	-6.93
260631_at	hypothetical protein predicted by gene	---	AT1G62350	-1.08	-0.12	-0.89	0.405406	0.593042	-6.93
245902_at	putative protein Scythe protein, Xenop	---	AT5G11080	1.11	0.15	0.89	0.405434	0.593045	-6.93
253319_at	putative protein various predicted prot	EMB2758	AT4G33990	1.12	0.16	0.89	0.405627	0.593165	-6.93
249406_at	putative protein MtN21, Medicago trur	---	AT5G40210	1.09	0.12	0.89	0.405717	0.593165	-6.93
257513_s_	hypothetical protein	---	AT1G12340 /	-1.08	-0.11	-0.89	0.405674	0.593165	-6.93
261146_at	hypothetical protein predicted by gene	---	AT1G19620	-1.10	-0.14	-0.89	0.405724	0.593165	-6.93
258746_at	germin-like protein similar to germin pr	---	AT3G05950	-1.08	-0.11	-0.89	0.405611	0.593165	-6.93
253210_at	putative protein predicted protein, Ara	MTN2	AT4G34840	-1.08	-0.10	-0.89	0.405707	0.593165	-6.93
266619_at	similar to harpin-induced protein hin1 f	---	AT2G35460	-1.10	-0.13	-0.89	0.405614	0.593165	-6.93
248671_at	putative protein strong similarity to unk	---	AT5G48750	1.06	0.09	0.89	0.405635	0.593165	-6.93
245161_at	putative myrosinase binding protein	NSP2	AT2G33070	-1.09	-0.13	-0.89	0.405775	0.593202	-6.93
267406_at	unknown protein	MEE22	AT2G34780	1.09	0.12	0.89	0.405859	0.593286	-6.93
263602_at	40S ribosomal protein S25	---	AT2G16360	-1.07	-0.10	-0.89	0.405955	0.593389	-6.93
254674_at	EREBP - like protein EREBP-1 (Ethyle	---	AT4G18450	-1.06	-0.08	-0.89	0.406117	0.593587	-6.93
245386_at	hypothetical protein ;supported by full-	RALFL32	AT4G14010	-1.18	-0.24	-0.89	0.406193	0.593602	-6.93
255102_s_	putative MuDR-A-like transposon prote	---	---	-1.08	-0.11	-0.89	0.40618	0.593602	-6.93

262480_at	receptor kinase, putative similar to rec	---	AT1G11340	-1.14	-0.19	-0.89	0.406205	0.593602	-6.93
258983_at	putative aminotransferase similar to b	---	AT3G08860	1.25	0.33	0.89	0.406358	0.593711	-6.93
253933_at	hypothetical protein	---	AT4G26820	-1.08	-0.12	-0.89	0.406343	0.593711	-6.93
257944_at	SKP1/ASK1 (At9), putative similar to S	ASK9	AT3G21850	1.07	0.09	0.89	0.406346	0.593711	-6.93
259494_at	mitotic checkpoint protein, putative sir	---	AT1G15850	-1.09	-0.12	-0.89	0.406454	0.593813	-6.93
246669_at	galactinol synthase, putative	---	AT5G30500	-1.10	-0.13	-0.89	0.406598	0.593987	-6.93
266585_at	putative retroelement pol polyprotein	---	---	-1.09	-0.12	-0.88	0.406785	0.594221	-6.93
264386_at	putative pyrophosphate-fructose-6-ph	---	AT1G12000	1.16	0.21	0.88	0.406813	0.594224	-6.93
250350_at	putative protein predicted proteins, Ar	---	AT5G12010	1.16	0.21	0.88	0.40706	0.594548	-6.93
261555_s_	hypothetical protein predicted by gens	---	AT1G63230 /	1.06	0.08	0.88	0.407389	0.594957	-6.93
246569_at	lysophospholipase -like protein lysoph	---	AT5G14980	-1.06	-0.09	-0.88	0.407393	0.594957	-6.93
259162_at	unknown protein similar to unknown pr	---	AT3G01640	-1.09	-0.12	-0.88	0.407741	0.59541	-6.93
254729_at	putative protein purple acid phosphata	PAP23	AT4G13700	1.08	0.11	0.88	0.407755	0.59541	-6.93
267446_s_	putative tyrosyl-tRNA synthetase	---	AT1G28350 /	-1.06	-0.09	-0.88	0.407854	0.595477	-6.93
264074_at	putative retroelement pol polyprotein re	---	---	-1.07	-0.10	-0.88	0.407836	0.595477	-6.93
267530_at	putative receptor-like protein kinase	---	AT2G41890	1.18	0.24	0.88	0.40795	0.595542	-6.93
251693_at	putative protein several hypothetical pr	---	AT3G56550	1.08	0.11	0.88	0.407924	0.595542	-6.93
260503_at	proteasome, 30 kda subunit (ec 3.4.99	PAF2	AT1G47250	-1.07	-0.10	-0.88	0.407988	0.59556	-6.93
263592_at	putative non-LTR retroelement reverse	---	---	-1.12	-0.16	-0.88	0.408035	0.59559	-6.93
250019_at	putative protein similar to unknown pro	---	AT5G18160	1.09	0.12	0.88	0.408248	0.595859	-6.93
250888_at	putative protein trichohyalin, Oryctolag	---	AT5G04460	1.12	0.16	0.88	0.408272	0.595859	-6.93
253695_at	arginine methyltransferase (pam1) ; s	PRMT11	AT4G29510	-1.11	-0.15	-0.88	0.408329	0.595904	-6.93
253508_at	putative protein various predicted prot	---	AT4G31680	-1.07	-0.10	-0.88	0.408388	0.595953	-6.93
263659_at	unknown protein EST gb|ATTS5672 co	---	AT1G04470	-1.07	-0.10	-0.88	0.408483	0.596037	-6.93
249477_s_	germin - like protein probable germin f	---	AT5G38930 /	1.06	0.08	0.88	0.408498	0.596037	-6.93
253828_at	putative protein predicted protein, Ara	SLAH2	AT4G27970	1.10	0.13	0.88	0.408553	0.596078	-6.93
261283_s_	hypothetical protein predicted by gens	---	---	-1.06	-0.08	-0.88	0.408616	0.596132	-6.93
245286_at	cytosolic O-acetylserine(thiol)lyase (EC	OASA1	AT4G14880	-1.07	-0.10	-0.88	0.408674	0.596168	-6.93
247594_at	putative protein farnesylated protein G	---	AT5G60800	1.10	0.13	0.88	0.408693	0.596168	-6.93
252574_at	receptor like protein kinase receptor li	---	AT3G45430	-1.08	-0.11	-0.88	0.408871	0.5962	-6.93
251650_at	hypothetical protein	---	AT3G57360	1.11	0.14	0.88	0.408799	0.5962	-6.93
249340_at	putative protein contains similarity to m	---	AT5G41140	-1.09	-0.12	-0.88	0.408868	0.5962	-6.93
252519_at	hypothetical protein	---	AT3G46360	-1.07	-0.10	-0.88	0.408849	0.5962	-6.93
247163_at	Expressed protein ; supported by cDN	---	AT5G65685	-1.09	-0.12	-0.88	0.408777	0.5962	-6.93
256342_at	unknown protein ; supported by full-ler	---	AT1G72020	-1.07	-0.10	-0.88	0.408751	0.5962	-6.93

267631_at	hypothetical protein predicted by gene	---	AT2G42150	-1.07	-0.09	-0.88	0.408901	0.596205	-6.93
255699_at	putative pectinesterase	PME38	AT4G00190	1.06	0.09	0.88	0.408946	0.596233	-6.93
252820_at	plasma membrane H+-ATPase-like pr	AHA8	AT3G42640	-1.12	-0.17	-0.88	0.409118	0.596445	-6.94
266209_at	similar to terminal flower ; supported b	ATC	AT2G27550	-1.12	-0.17	-0.88	0.409199	0.596526	-6.94
249250_at	arm repeat containing protein	---	AT5G42340	1.06	0.09	0.88	0.409232	0.596535	-6.94
265454_at	putative ARF1 family auxin responsive	ARF11	AT2G46530	-1.25	-0.32	-0.88	0.409281	0.596568	-6.94
256018_at	plastid heme oxygenase, putative sim	ho4	AT1G58300	-1.12	-0.16	-0.88	0.409359	0.596644	-6.94
261060_at	unknown protein	---	AT1G17340	1.09	0.12	0.88	0.409489	0.596768	-6.94
259555_at	hypothetical protein	---	---	1.07	0.09	0.88	0.409497	0.596768	-6.94
254341_at	serine/threonine protein kinase like pr	SRF8	AT4G22130	-1.21	-0.27	-0.88	0.409658	0.596965	-6.94
251098_at	light-inducible protein ATLS1	---	AT5G01650	1.06	0.08	0.88	0.409785	0.597075	-6.94
248919_at	putative protein contains similarity to is	---	AT5G45920	-1.08	-0.11	-0.88	0.409779	0.597075	-6.94
253317_at	putative protein	---	AT4G33960	-1.18	-0.23	-0.88	0.409823	0.597091	-6.94
249000_at	putative protein contains similarity to h	---	AT5G44980	-1.08	-0.11	-0.88	0.409921	0.597196	-6.94
258691_at	unknown protein	---	AT3G08630	-1.21	-0.27	-0.88	0.409992	0.597221	-6.94
244905_at	hypothetical protein	---	---	-1.07	-0.10	-0.88	0.410005	0.597221	-6.94
250411_at	putative protein	---	AT5G11120	-1.07	-0.09	-0.88	0.410017	0.597221	-6.94
245457_s_	disease resistance RPP5 like protein	---	AT4G16940 /	1.07	0.10	0.88	0.410107	0.597315	-6.94
253683_at	cytidine deaminase 4 (CDA4)	---	AT4G29650	-1.07	-0.10	-0.88	0.410307	0.597462	-6.94
249944_at	NAM (no apical meristem)-like protein	anac089	AT5G22290	1.19	0.25	0.88	0.410315	0.597462	-6.94
258735_at	low temperature and salt responsive p	RCI2A	AT3G05880	-1.12	-0.17	-0.88	0.410314	0.597462	-6.94
258388_at	putative expansin S2 precursor similar	ATEXPA12	AT3G15370	-1.06	-0.09	-0.88	0.410345	0.597462	-6.94
245440_at	RNA helicase	---	AT4G16680	1.06	0.08	0.88	0.410366	0.597462	-6.94
255361_at	hypothetical protein	---	---	1.06	0.08	0.88	0.410239	0.597462	-6.94
259640_at	beta-glucosidase, putative identical to	BGLU18	AT1G52400	1.17	0.23	0.88	0.410442	0.597536	-6.94
248693_at	regulator of chromosome condensation	---	AT5G48330	1.11	0.15	0.88	0.410483	0.597557	-6.94
255210_at	may be a pseudogene	---	---	-1.06	-0.08	-0.88	0.410585	0.597668	-6.94
256954_at	E2, ubiquitin-conjugating enzyme, put	FUS9	AT3G13550	-1.08	-0.12	-0.88	0.410653	0.597727	-6.94
263573_at	unknown protein similar to A. thaliana	---	AT2G17150	1.10	0.14	0.88	0.411024	0.598021	-6.94
250050_at	putative protein predicted protein, Ara	VAR3	AT5G17790	1.08	0.11	0.88	0.411038	0.598021	-6.94
260320_at	hypothetical protein similar to putative	---	AT1G63930	-1.11	-0.14	-0.88	0.410996	0.598021	-6.94
257254_at	salicylic acid carboxyl methyltransfera	---	AT3G21950	1.07	0.10	0.88	0.41098	0.598021	-6.94
248206_at	unknown protein	---	AT5G54350	1.09	0.12	0.88	0.411036	0.598021	-6.94
246663_at	putative protein	---	AT5G35300	1.07	0.10	0.88	0.411035	0.598021	-6.94
267316_at	homeodomain transcription factor (ATH	PHB	AT2G34710	-1.13	-0.18	-0.88	0.41097	0.598021	-6.94

245897_at	potassium transport protein-like severa	KUP7	AT5G09400	1.10	0.14	0.88	0.411285	0.598343	-6.94
250522_at	cleft lip and palate associated transme	---	AT5G08500	1.07	0.09	0.88	0.411539	0.598533	-6.94
249687_at	putative protein oxidosqualene cyclas	ATPEN3	AT5G36150	1.07	0.10	0.88	0.411547	0.598533	-6.94
260765_at	actin 8 almost identical to actin 8 GI:16	ACT8	AT1G49240	1.17	0.22	0.88	0.411518	0.598533	-6.94
245923_at	putative protein predicted proteins, Ar	---	AT5G28820	-1.08	-0.11	-0.88	0.411542	0.598533	-6.94
253026_at	hypothetical protein	---	AT4G38120	1.10	0.14	0.88	0.411477	0.598533	-6.94
256380_at	pheromone receptor, putative (AR401	AR401	AT1G66680	1.09	0.12	0.88	0.411588	0.598554	-6.94
248102_at	putative protein contains similarity to 5	---	AT5G55140	1.10	0.14	0.88	0.411646	0.5986	-6.94
256579_at	hypothetical protein	---	AT3G28720	1.06	0.09	0.87	0.411912	0.598912	-6.94
254225_at	putative major latex protein major late	---	AT4G23670	-1.36	-0.45	-0.87	0.411908	0.598912	-6.94
251826_at	ABC transporter - like protein ATP-bin	---	AT3G55110	-1.08	-0.11	-0.87	0.412003	0.598967	-6.94
267483_at	unknown protein ;supported by full-ler	UTR1	AT2G02810	1.28	0.35	0.87	0.411988	0.598967	-6.94
254943_at	putative protein predicted proteins, Ar	---	AT4G10890	-1.07	-0.10	-0.87	0.412034	0.598974	-6.94
264829_at	hypothetical protein predicted by gens	ANAC006	AT1G03490	-1.06	-0.08	-0.87	0.412066	0.598982	-6.94
260188_at	Mutator-like transposase similar to mu	---	---	1.06	0.08	0.87	0.412133	0.599042	-6.94
245538_at	p140mDia like protein	---	AT4G15200	-1.07	-0.10	-0.87	0.412201	0.599102	-6.94
253529_at	putative protein hypothetical protein -	---	AT4G31520	1.06	0.08	0.87	0.412282	0.599181	-6.94
255872_at	putative protein kinase contains a prot	SIP4	AT2G30360	1.20	0.26	0.87	0.412343	0.599183	-6.94
261953_at	UDP-galactose 4-epimerase, putative	RHD1	AT1G64440	1.14	0.19	0.87	0.412362	0.599183	-6.94
261345_at	hypothetical protein predicted by gene	DTA4	AT1G79760	-1.09	-0.12	-0.87	0.412322	0.599183	-6.94
253814_at	putative protein ;supported by full-leng	---	AT4G28290	-1.12	-0.16	-0.87	0.412394	0.599191	-6.94
257432_at	unknown protein	---	AT2G21850	-1.09	-0.12	-0.87	0.412489	0.599291	-6.94
258234_at	hypothetical protein similar to myb-rela	MYB118	AT3G27785	-1.07	-0.09	-0.87	0.412537	0.599323	-6.94
251590_at	pollen-specific protein BAN102-like pr	AGP23	AT3G57690	1.10	0.14	0.87	0.412608	0.599389	-6.94
254639_at	putative protein various predicted prot	DOT4	AT4G18750	-1.08	-0.11	-0.87	0.412654	0.599405	-6.94
248128_at	thiazole biosynthetic enzyme precurso	THI1	AT5G54770	-1.09	-0.13	-0.87	0.412701	0.599405	-6.94
252600_at	putative protein unknown protein CGI-	VPS24.2	AT3G45000	-1.09	-0.12	-0.87	0.412725	0.599405	-6.94
261807_at	Expressed protein ; supported by full-l	---	AT1G30515	-1.07	-0.09	-0.87	0.412673	0.599405	-6.94
246588_at	putative protein predicted protein, Ara	---	AT3G06433 /	1.05	0.08	0.87	0.412755	0.599411	-6.94
249961_at	putative protein predicted proteins, Ar	---	AT5G18770	1.08	0.11	0.87	0.412904	0.599589	-6.94
255695_at	putative protein	UNE11	AT4G00080	1.06	0.09	0.87	0.413035	0.599741	-6.94
253639_at	putative protein component of aniline	---	AT4G30550	1.11	0.15	0.87	0.413101	0.599798	-6.94
244904_at	hypothetical protein	---	---	1.12	0.17	0.87	0.413211	0.59992	-6.94
251214_at	putative protein hypothetical proteins -	---	AT3G62500	-1.07	-0.10	-0.87	0.413266	0.599928	-6.94
262328_at	hypothetical protein similar to hypothet	---	AT1G64100	-1.05	-0.08	-0.87	0.413269	0.599928	-6.94

247559_at	histone deacetylase - like GR AF-1 sp	HDA18	AT5G61070	-1.06	-0.09	-0.87	0.413373	0.600041	-6.94
250658_at	C3HC4-type RING zinc finger protein-l	---	AT5G07040	-1.08	-0.11	-0.87	0.413491	0.600136	-6.94
253256_at	putative protein endothelin converting	---	AT4G34360	1.09	0.13	0.87	0.413488	0.600136	-6.94
255698_at	scarecrow-like 6 (SCL6)	---	AT4G00150	-1.10	-0.13	-0.87	0.413526	0.600147	-6.94
251809_at	putative protein predicted proteins, Ar	---	AT3G55600	-1.08	-0.11	-0.87	0.413563	0.600164	-6.94
257597_at	protein kinase, putative similar to prot	---	AT3G24790	-1.06	-0.09	-0.87	0.413631	0.600187	-6.94
267414_at	putative berberine bridge enzyme	MEE23	AT2G34790	1.13	0.18	0.87	0.413609	0.600187	-6.94
247180_at	histone H3	---	AT5G65350 /	1.06	0.08	0.87	0.413716	0.600271	-6.94
258340_at	hypothetical protein predicted by gens	---	AT3G22770	1.06	0.08	0.87	0.41381	0.600369	-6.94
267167_at	putative C2H2-type zinc finger protein	ZFP10	AT2G37740	1.07	0.10	0.87	0.414075	0.600716	-6.94
260950_s_	delta 9 desaturase, putative similar to	---	AT1G06090 /	-1.08	-0.12	-0.87	0.41412	0.600723	-6.94
246810_at	putative protein many predicted protei	---	---	1.06	0.09	0.87	0.414133	0.600723	-6.94
257489_at	hypothetical protein predicted by gene	---	AT1G07330	-1.07	-0.10	-0.87	0.414213	0.600801	-6.94
258846_at	unknown protein ; supported by full-le	---	AT3G03070	1.06	0.09	0.87	0.41448	0.601151	-6.94
248012_at	putative protein strong similarity to unk	---	AT5G56310	1.09	0.13	0.87	0.414512	0.601158	-6.94
252661_at	putative protein	---	AT3G44450	-1.24	-0.31	-0.87	0.414538	0.601158	-6.94
258785_at	unknown protein	---	---	-1.09	-0.12	-0.87	0.414597	0.601205	-6.94
257233_at	hypothetical protein similar to SF16 pr	IQD10	AT3G15050	-1.07	-0.09	-0.87	0.414681	0.601289	-6.95
261580_at	unknown protein ;supported by full-len	IQD18	AT1G01110	1.11	0.16	0.87	0.414925	0.601604	-6.95
255022_at	NAM/NAP like protein nap gene, Arab	ANAC070	AT4G10350	1.06	0.09	0.87	0.414976	0.601639	-6.95
249407_at	putative protein predicted proteins, Ar	---	AT5G40320	1.06	0.09	0.87	0.415018	0.601662	-6.95
264983_at	hypothetical protein predicted by gens	---	AT1G27240	-1.07	-0.09	-0.87	0.415291	0.601957	-6.95
265861_at	hypothetical protein predicted by gens	---	AT2G01790	-1.07	-0.10	-0.87	0.415321	0.601957	-6.95
257929_at	RNA Polymerase II subunit 14.5 kD, p	NRPB9A	AT3G16980	1.08	0.11	0.87	0.415319	0.601957	-6.95
247678_at	putative zinc transporter ZIP2 - like Z2	ZIP2	AT5G59520	1.14	0.18	0.87	0.415327	0.601957	-6.95
261195_at	transport inhibitor response 1 (TIR1),	AFB3	AT1G12820	-1.07	-0.10	-0.87	0.415448	0.602095	-6.95
262474_at	hypothetical protein identical to hypoth	FU	AT1G50240	-1.08	-0.11	-0.87	0.415483	0.602107	-6.95
245486_x_	glycine-rich protein homolog	---	AT4G16240	1.07	0.10	0.87	0.415842	0.602589	-6.95
255453_at	hypothetical protein similar to A. thalia	---	AT4G02900	-1.10	-0.13	-0.87	0.415948	0.602705	-6.95
260032_at	putative phosphoenolpyruvate carboxy	ATPPC4	AT1G68750	1.07	0.10	0.87	0.415999	0.60274	-6.95
256176_at	hypothetical protein predicted by gene	ATEXO70G2	AT1G51640	-1.07	-0.09	-0.87	0.416059	0.602789	-6.95
250250_at	putative protein similar to unknown pro	---	AT5G13610	1.08	0.11	0.87	0.416537	0.603443	-6.95
261478_at	unknown protein	MIOX1	AT1G14520	-1.11	-0.15	-0.87	0.416605	0.603464	-6.95
251933_at	putative protein mucin MUC3, Homo s	---	AT3G54060	-1.09	-0.12	-0.87	0.416605	0.603464	-6.95
246047_at	putative protein predicted proteins, Ar	---	---	-1.07	-0.10	-0.87	0.41667	0.603482	-6.95

249653_at	putative protein REPLICATION PROT	---	---	-1.06	-0.09	-0.87	0.416644	0.603482	-6.95
245541_at	hypothetical protein	---	AT4G15240	1.11	0.15	0.87	0.416726	0.603525	-6.95
257080_at	unknown protein	---	AT3G15240	-1.06	-0.08	-0.86	0.416927	0.603701	-6.95
263130_at	hypothetical protein predicted by gens	POLD3	AT1G78650	1.14	0.19	0.86	0.416923	0.603701	-6.95
250566_at	putative helix-loop-helix DNA binding	TCP17	AT5G08070	1.10	0.14	0.86	0.416908	0.603701	-6.95
255808_at	putative protein predicted protein, Ara	---	AT4G10280	1.08	0.10	0.86	0.416958	0.603707	-6.95
245103_at	putative Ta11-like non-LTR retroeleme	---	AT2G41590	-1.06	-0.09	-0.86	0.417173	0.603981	-6.95
255114_at	putative protein various putative revers	---	---	-1.10	-0.14	-0.86	0.417276	0.604054	-6.95
252521_at	hypothetical protein	---	AT3G46380	-1.11	-0.15	-0.86	0.417273	0.604054	-6.95
261868_s_	hypothetical protein contains similarity	---	AT1G11450 /	1.05	0.07	0.86	0.417422	0.604226	-6.95
246551_at	putative protein predicted proteins, Ar	---	AT5G15070	-1.08	-0.11	-0.86	0.417493	0.604289	-6.95
250790_at	putative protein similar to unknown pro	---	AT5G05640	-1.11	-0.15	-0.86	0.417572	0.604289	-6.95
258741_at	Lon protease, putative similar to Lon p	LON4	AT3G05790	-1.06	-0.08	-0.86	0.41757	0.604289	-6.95
259385_at	hypothetical protein predicted by gens	---	AT1G13470	1.64	0.71	0.86	0.417519	0.604289	-6.95
252839_at	putative protein PIF1 protein - Caenor	---	---	1.10	0.14	0.86	0.417645	0.604357	-6.95
253953_at	putative protein extensin precursor - t	---	AT4G26750	-1.12	-0.16	-0.86	0.417784	0.604443	-6.95
250886_at	putative protein	---	AT5G04440	-1.08	-0.11	-0.86	0.41774	0.604443	-6.95
260574_at	hypothetical protein predicted by gene	---	AT2G47300	-1.08	-0.11	-0.86	0.417777	0.604443	-6.95
246292_at	putative protein hnRNP A/B related pr	UBA2A	AT3G56860	-1.08	-0.12	-0.86	0.417993	0.60463	-6.95
257191_at	Expressed protein ; supported by full-l	---	AT3G13175	-1.08	-0.11	-0.86	0.417952	0.60463	-6.95
259333_at	putative auxin-independent growth pro	EDA30	AT3G03810	-1.08	-0.11	-0.86	0.417967	0.60463	-6.95
256828_at	unknown protein	---	AT3G22968 /	-1.15	-0.21	-0.86	0.418047	0.60467	-6.95
265828_at	hypothetical protein predicted by gens	---	AT2G14520	1.06	0.09	0.86	0.418131	0.604754	-6.95
255353_at	putative transposon protein similar to M	---	---	-1.06	-0.08	-0.86	0.41823	0.604858	-6.95
257368_at	hypothetical protein predicted by gens	---	AT2G29860	-1.06	-0.09	-0.86	0.418276	0.604887	-6.95
255173_at	putative transposon protein similar to	---	---	-1.08	-0.11	-0.86	0.418304	0.604889	-6.95
248184_at	CHP-rich zinc finger protein-like	---	AT5G54050	-1.06	-0.08	-0.86	0.418381	0.604962	-6.95
264322_at	unknown protein Contains similarity to	---	AT1G04190	1.08	0.11	0.86	0.418729	0.605426	-6.95
263423_at	hypothetical protein predicted by gens	---	AT2G31700	1.07	0.09	0.86	0.418795	0.605445	-6.95
252807_at	putative replication protein various pre	---	---	-1.05	-0.07	-0.86	0.418785	0.605445	-6.95
259653_at	unknown protein	---	AT1G55240	-1.06	-0.08	-0.86	0.418921	0.605512	-6.95
250820_at	receptor-like protein kinase	---	AT5G05160	-1.08	-0.12	-0.86	0.418892	0.605512	-6.95
252761_at	putative protein several hypothetical pr	---	AT3G42770	-1.12	-0.16	-0.86	0.418913	0.605512	-6.95
258704_at	putative protein kinase similar to Pto ki	CCR1	AT3G09780	-1.10	-0.14	-0.86	0.418958	0.605528	-6.95
258937_at	putative ribosomal protein S28 similar	---	AT3G10090	1.12	0.16	0.86	0.418992	0.605538	-6.95

256611_at	unknown protein similar to putative RI	---	AT3G29270	1.08	0.12	0.86	0.419124	0.605653	-6.95
250464_at	hypothetical protein	---	AT5G10040	1.05	0.08	0.86	0.419101	0.605653	-6.95
245937_at	putative protein 22kDa peroxisomal m	---	AT5G19750	-1.13	-0.18	-0.86	0.419156	0.60566	-6.95
261022_at	unknown protein similar to NAM like pr	ANAC007	AT1G12260	1.07	0.10	0.86	0.419221	0.605691	-6.95
250675_at	putative protein contains similarity to u	---	AT5G06260	1.06	0.09	0.86	0.41923	0.605691	-6.95
250623_at	peroxisomal Ca-dependent solute car	---	AT5G07320	-1.07	-0.10	-0.86	0.419262	0.605698	-6.95
263304_at	hypothetical protein predicted by gens	---	AT2G01920	1.07	0.10	0.86	0.419396	0.605853	-6.95
252203_at	hypothetical protein	---	AT3G50320	-1.06	-0.09	-0.86	0.419486	0.605907	-6.95
249556_at	Expressed protein ; supported by full-l	---	AT5G38195	-1.06	-0.09	-0.86	0.419472	0.605907	-6.95
260039_at	CLE12 CLAVATA3/ESR-Related 12; s	CLE12	AT1G68795	1.09	0.12	0.86	0.419526	0.605926	-6.95
AFFX-Trpn	B. subtilis /GEN=trpD, trpC /DB_XREF	---	---	1.06	0.09	0.86	0.419633	0.606042	-6.95
256615_at	hypothetical protein predicted by gene	---	AT3G22250	1.09	0.13	0.86	0.419664	0.606048	-6.95
253586_s_	putative protein hypothetical protein T	---	AT4G30710 /	-1.12	-0.17	-0.86	0.419827	0.606245	-6.95
255255_at	coded for by A. thaliana cDNA T44741	---	AT4G05070	-1.12	-0.17	-0.86	0.419937	0.606352	-6.95
263970_at	putative cytochrome P450	CYP718	AT2G42850	-1.07	-0.10	-0.86	0.419954	0.606352	-6.95
265280_at	Expressed protein ; supported by full-l	LCR5	AT2G28355	1.07	0.09	0.86	0.419985	0.606359	-6.95
254809_at	putative protein auxin-induced protein	---	AT4G12410	-1.11	-0.15	-0.86	0.420195	0.606623	-6.95
252708_at	putative protein amine oxidase, Canav	---	AT3G43820	1.09	0.12	0.86	0.420354	0.606814	-6.95
256505_at	unknown protein	---	AT1G75200	1.10	0.14	0.86	0.420431	0.606849	-6.96
245472_at	hypothetical protein	---	AT4G16040	1.09	0.12	0.86	0.420409	0.606849	-6.95
263657_at	putative casein kinase I similar to GB:(	CKL13	AT1G04440	1.14	0.19	0.86	0.420571	0.607013	-6.96
256992_at	hypothetical protein predicted by gene	---	AT3G28630	-1.07	-0.10	-0.86	0.420629	0.607058	-6.96
246575_at	bystin, putative similar to bystin GI:11	---	AT1G31660	1.12	0.16	0.86	0.42066	0.607063	-6.96
245656_at	hypothetical protein predicted by gene	---	AT1G56620	-1.07	-0.10	-0.86	0.420697	0.60708	-6.96
247374_at	topoisomerase-like protein ;supported	---	AT5G63190	1.11	0.15	0.86	0.420852	0.607098	-6.96
259218_at	hypothetical protein similar to putative	---	AT3G03580	1.08	0.11	0.86	0.420781	0.607098	-6.96
250175_at	putative protein CGI-67, Homo sapien	---	AT5G14390	1.13	0.18	0.86	0.420799	0.607098	-6.96
263642_at	putative fimbrin	---	AT2G04750	-1.06	-0.09	-0.86	0.42087	0.607098	-6.96
256351_at	NPK1-related protein kinase, putative	ANP2	AT1G54960	-1.06	-0.09	-0.86	0.420841	0.607098	-6.96
261813_at	hypothetical protein contains similarity	---	AT1G08280	1.10	0.14	0.86	0.420854	0.607098	-6.96
247364_at	putative protein similar to unknown pro	---	AT5G63200	-1.06	-0.09	-0.86	0.42093	0.607137	-6.96
244930_at	hypothetical protein	---	AT2G07809	1.06	0.09	0.86	0.42095	0.607137	-6.96
253857_at	putative protein hypothetical chloropla	---	AT4G27990	-1.07	-0.10	-0.86	0.421139	0.607332	-6.96
264291_at	hypothetical protein contains similarity	---	AT1G78800	1.08	0.11	0.86	0.421134	0.607332	-6.96
258180_at	unknown protein	---	AT3G21480	1.12	0.17	0.86	0.421335	0.607385	-6.96

254019_at	putative protein mature-parasite-infect	---	AT4G26190	1.05	0.07	0.86	0.421237	0.607385	-6.96
257753_at	60S ribosomal protein, putative simila	---	AT3G18740	-1.11	-0.15	-0.86	0.421297	0.607385	-6.96
251159_at	hypothetical protein	---	AT3G63230	-1.10	-0.13	-0.86	0.421324	0.607385	-6.96
267480_at	putative retroelement pol polyprotein	---	---	-1.06	-0.08	-0.86	0.421308	0.607385	-6.96
264577_at	putative peroxidase Strong similarity to	RCI3	AT1G05260	1.06	0.08	0.86	0.421239	0.607385	-6.96
247849_at	putative protein fibrinogen-binding pro	---	AT5G58130	1.09	0.12	0.86	0.421387	0.607421	-6.96
260541_at	putative trypsin inhibitor	---	AT2G43530	-1.25	-0.32	-0.86	0.421464	0.607495	-6.96
249453_at	v-SNARE AtVTI1a	SGR4	AT5G39510	1.06	0.08	0.86	0.421755	0.607861	-6.96
264827_at	hypothetical protein similar to anthranil	---	AT1G03390	-1.06	-0.09	-0.86	0.421772	0.607861	-6.96
248605_at	putative protein similar to unknown pro	---	AT5G49410	1.12	0.16	0.86	0.421803	0.607867	-6.96
265530_at	12-oxophytodienoate-10,11-reductase	OPR3	AT2G06050	-1.21	-0.27	-0.86	0.421882	0.607943	-6.96
251726_at	protein kinase NPK1-related protein k	---	AT3G56280	-1.05	-0.07	-0.86	0.421928	0.607971	-6.96
261924_at	peptide transporter, putative similar to	---	AT1G22550	-1.19	-0.25	-0.85	0.421979	0.608006	-6.96
255688_at	putative RNA helicase similar to ATP-d	---	AT4G00660	1.07	0.10	0.85	0.422064	0.608091	-6.96
264087_at	hypothetical protein predicted by genso	emb1381	AT2G31340	1.07	0.09	0.85	0.422138	0.608158	-6.96
255696_at	putative nucleotide sugar epimerase	GAE3	AT4G00110	-1.08	-0.11	-0.85	0.422355	0.608393	-6.96
256637_at	unknown protein similar to membrane	---	AT3G12030	1.10	0.14	0.85	0.422353	0.608393	-6.96
257566_x_	hypothetical protein predicted by gene	---	---	1.06	0.09	0.85	0.422493	0.608554	-6.96
265495_at	unknown protein predicted by genscan	---	AT2G15695	1.07	0.10	0.85	0.42255	0.608599	-6.96
259733_at	nucellin-like protein similar to nucellin (	---	AT1G77480	-1.12	-0.17	-0.85	0.422626	0.608651	-6.96
266988_at	putative myrosinase-binding protein ;s	JAL22	AT2G39310	-1.11	-0.16	-0.85	0.42264	0.608651	-6.96
262190_at	unknown protein	---	AT1G78030	-1.09	-0.13	-0.85	0.422963	0.609078	-6.96
245441_at	decarboxylase like protein	PSD1	AT4G16700	1.09	0.13	0.85	0.423062	0.609182	-6.96
246710_at	putative protein predicted proteins, Ar	---	---	-1.06	-0.08	-0.85	0.423137	0.609251	-6.96
266272_at	hypothetical protein predicted by genso	---	AT2G29600	1.07	0.10	0.85	0.423243	0.609273	-6.96
257182_s_	crn-like protein similar to crn GB:CAA4	---	AT3G13210 /	1.10	0.13	0.85	0.423259	0.609273	-6.96
248053_at	putative protein similar to unknown pro	AtNMNAT	AT5G55810	-1.08	-0.11	-0.85	0.423224	0.609273	-6.96
258969_at	hypothetical protein predicted by gens	---	AT3G10680	-1.06	-0.08	-0.85	0.423242	0.609273	-6.96
260183_at	hypothetical protein similar to DNA sec	---	---	-1.05	-0.08	-0.85	0.423399	0.609398	-6.96
248714_at	polygalacturonase ;supported by full-l	---	AT5G48140	-1.06	-0.08	-0.85	0.423393	0.609398	-6.96
264231_at	hypothetical protein similar to hypothet	---	AT1G67450	1.06	0.08	0.85	0.423437	0.609414	-6.96
252677_at	nitrilase 3 ;supported by full-length cD	NIT3	AT3G44320	-1.13	-0.17	-0.85	0.423466	0.609417	-6.96
247147_at	putative protein contains similarity to R	GTE7	AT5G65630	-1.10	-0.14	-0.85	0.423606	0.609478	-6.96
260578_at	unknown protein predicted by genscan	---	AT2G47350	-1.07	-0.09	-0.85	0.42359	0.609478	-6.96
263395_at	putative mitochondrial inner membrane	ATTIM44-1	AT2G20500 /	1.07	0.09	0.85	0.423615	0.609478	-6.96

262527_at	SRG1-like protein Strong homology to	---	AT1G17010	-1.07	-0.10	-0.85	0.423552	0.609478	-6.96
250362_at	1-D-deoxyxylulose 5-phosphate synth	DXPS3	AT5G11380	-1.06	-0.09	-0.85	0.423706	0.609569	-6.96
247584_at	60S ribosomal protein L12 - like 60S R	---	AT5G60670	-1.18	-0.24	-0.85	0.423797	0.609663	-6.96
267264_at	putative serine carboxypeptidase II ; s	SCPL11	AT2G22970	1.21	0.27	0.85	0.42383	0.609672	-6.96
262389_at	hypothetical protein contains similarity	---	AT1G49270	1.07	0.09	0.85	0.424003	0.609883	-6.96
263635_at	hypothetical protein predicted by gens	---	---	1.05	0.08	0.85	0.424074	0.609946	-6.96
259253_at	hypothetical protein predicted by gens	---	AT3G07640	-1.06	-0.08	-0.85	0.424132	0.609952	-6.96
258748_at	germin-like protein similar to germin pr	GLP8	AT3G05930	1.08	0.11	0.85	0.424121	0.609952	-6.96
257798_at	unknown protein	NAI2	AT3G15950	-1.10	-0.14	-0.85	0.424256	0.610074	-6.96
246992_at	N-acetyltransferase hookless1-like pro	---	AT5G67430	-1.07	-0.10	-0.85	0.42427	0.610074	-6.96
248261_at	putative protein similar to unknown pro	PDV1	AT5G53280	-1.07	-0.09	-0.85	0.424339	0.610135	-6.96
245246_at	hypothetical protein predicted by gene	---	AT1G44224	1.06	0.09	0.85	0.424534	0.610377	-6.96
260849_at	pectinesterase, putative similar to pec	sks7	AT1G21860	1.06	0.08	0.85	0.424561	0.610377	-6.96
259708_at	lysophospholipase isolog, putative sim	---	AT1G77420	-1.09	-0.13	-0.85	0.424663	0.610484	-6.96
256082_at	hypothetical protein predicted by gens	---	AT1G20720	-1.13	-0.17	-0.85	0.424718	0.610525	-6.96
254464_at	putative protein retinoblastoma bindin	---	AT4G20400	-1.10	-0.14	-0.85	0.42479	0.610555	-6.96
266118_at	protease inhibitor II ; supported by cD	LCR68	AT2G02130	-1.19	-0.26	-0.85	0.424792	0.610555	-6.96
252871_at	proliferating-cell nucleolar antigen - lik	---	AT4G40000	-1.07	-0.09	-0.85	0.424848	0.610597	-6.96
246224_at	putative MADS-box protein ;supported	---	AT4G36590	1.10	0.13	0.85	0.424983	0.610752	-6.96
253744_s_	putative protein hypothetical protein F	---	---	-1.06	-0.09	-0.85	0.425072	0.610842	-6.96
255945_at	putative protein	---	AT5G28610	1.09	0.12	0.85	0.425138	0.610898	-6.96
254235_at	putative Ap2 domain protein DNA-bin	CRF2	AT4G23750	-1.07	-0.09	-0.85	0.425187	0.610931	-6.96
256344_at	C2H2-type zinc finger protein, putative	TFIIIA	AT1G72050	-1.08	-0.11	-0.85	0.425228	0.61095	-6.96
247932_at	putative protein similar to unknown pro	---	AT5G56920	1.06	0.08	0.85	0.425306	0.610989	-6.96
246855_at	putative protein various predicted prot	---	AT5G26280	1.20	0.27	0.85	0.425308	0.610989	-6.96
254774_at	hypothetical protein	---	AT4G13440	-1.13	-0.17	-0.85	0.425392	0.611071	-6.96
258495_at	unknown protein ;supported by full-ler	---	AT3G02690	-1.06	-0.09	-0.85	0.42547	0.611105	-6.96
251121_at	putative protein ; supported by cDNA:	AGG1	AT3G63420	-1.10	-0.14	-0.85	0.425458	0.611105	-6.96
266299_at	glutathione S-transferase identical to G	ATGSTU5	AT2G29450	1.16	0.21	0.85	0.425552	0.611184	-6.96
251893_at	putative protein	---	AT3G54380	1.07	0.09	0.85	0.425616	0.611201	-6.96
265904_at	putative beta-glucosidase	BGLU14	AT2G25630	-1.07	-0.10	-0.85	0.425596	0.611201	-6.96
265557_at	unknown protein	---	---	-1.08	-0.11	-0.85	0.425828	0.611427	-6.96
265851_at	hypothetical protein predicted by gens	---	AT2G42340	-1.07	-0.10	-0.85	0.42582	0.611427	-6.96
253948_at	Avr9 elicitor response like protein Avr	---	AT4G26940	-1.07	-0.10	-0.85	0.426041	0.611514	-6.96
261264_at	hypothetical protein predicted by gene	---	AT1G26710	1.08	0.12	0.85	0.426005	0.611514	-6.96

255209_at	see GB:AF077408	---	---	-1.08	-0.11	-0.85	0.426018	0.611514	-6.96
254246_at	protein kinase - like protein receptor k	EMB1290	AT4G23250	-1.06	-0.09	-0.85	0.425952	0.611514	-6.96
259886_at	putative protein kinase similar to protei	---	AT1G76370	1.06	0.09	0.85	0.426049	0.611514	-6.96
258913_at	unknown protein similar to putative Ar	---	AT3G06450	-1.10	-0.14	-0.85	0.426036	0.611514	-6.96
267193_at	hypothetical protein predicted by grail	---	AT2G30900	1.07	0.10	0.85	0.426212	0.611709	-6.96
253536_at	RSZp22 splicing factor ;supported by f	SRZ-22	AT4G31580	1.05	0.08	0.85	0.426288	0.611741	-6.96
256911_at	glutamine:fructose-6-phosphate amid	---	AT3G24090	1.27	0.34	0.85	0.426269	0.611741	-6.96
259518_at	hypothetical protein ; supported by cDI	OPCL1	AT1G20510	1.21	0.27	0.85	0.42637	0.61182	-6.97
263936_at	putative ATP-dependent RNA helicase	---	AT2G35920	1.09	0.12	0.85	0.426419	0.611852	-6.97
266180_at	putative PHD-type zinc finger protein ;	AL6	AT2G02470	1.09	0.13	0.85	0.426475	0.611894	-6.97
245453_at	disease resistance RPP5 like protein	---	AT4G16900	1.07	0.10	0.85	0.426634	0.612084	-6.97
247321_s_	phosphatidylinositol 4-kinase (emb|CA	PI-4KBETA2	AT5G09350 /	1.09	0.13	0.85	0.426777	0.612227	-6.97
266462_at	unknown protein ; supported by cDNA	---	AT2G47770	-1.22	-0.29	-0.85	0.426796	0.612227	-6.97
258233_at	hypothetical protein contains similarity	MYB118	AT3G27785	1.07	0.10	0.85	0.426815	0.612227	-6.97
246764_s_	putative protein At2g27780 and At2g1	---	AT2G13640 /	1.06	0.08	0.85	0.42686	0.612251	-6.97
266785_at	putative receptor-like protein kinase	---	AT2G28970	-1.07	-0.10	-0.85	0.426885	0.612251	-6.97
260573_at	putative pectinesterase	---	AT2G47280	1.08	0.11	0.85	0.426941	0.612293	-6.97
258088_at	hypothetical protein predicted by genm	---	AT3G14580	1.07	0.09	0.85	0.427064	0.612393	-6.97
248758_at	RNA-binding protein-like ;supported b	---	AT5G47620	-1.08	-0.12	-0.85	0.42704	0.612393	-6.97
256173_at	unknown protein	---	AT1G51730	1.06	0.08	0.84	0.427159	0.612452	-6.97
257470_at	hypothetical protein predicted by gene	---	AT1G53770	-1.08	-0.12	-0.84	0.427158	0.612452	-6.97
267572_at	3-hydroxyisobutyryl-coenzyme A hydrc	---	AT2G30660	-1.07	-0.10	-0.84	0.427303	0.612465	-6.97
263317_s_	similar to mammalian MHC III region p	SUVH7	AT1G17770 /	1.10	0.14	0.84	0.427299	0.612465	-6.97
248416_at	putative protein disease resistance pro	---	AT5G51630	-1.08	-0.11	-0.84	0.427272	0.612465	-6.97
255222_at	putative protein Mitochondrial ATPase	---	AT4G05340	1.05	0.07	0.84	0.427197	0.612465	-6.97
267066_at	hypothetical protein predicted by gene	---	AT2G41040	-1.10	-0.14	-0.84	0.427232	0.612465	-6.97
245208_at	lateral root primordia (LRP1)	LRP1	AT5G12330	-1.09	-0.12	-0.84	0.427534	0.612759	-6.97
252172_at	putative protein predicted proteins, Ar	---	AT3G50640	1.07	0.10	0.84	0.427879	0.613214	-6.97
264669_at	putative RAS-related protein, RAB11C	ATRAB11C	AT1G09630	-1.11	-0.15	-0.84	0.427995	0.613343	-6.97
252760_x_	putative protein several hypothetical pr	---	---	1.06	0.09	0.84	0.428065	0.613366	-6.97
258464_at	kinesin-like protein similar to KLP2 pro	POK1	AT3G17360	-1.05	-0.07	-0.84	0.428046	0.613366	-6.97
247270_at	ER66 protein-like	---	AT5G64220	1.06	0.09	0.84	0.428336	0.613715	-6.97
258906_at	unknown protein similar to C-terminal	ATTLP9	AT3G06380	1.08	0.11	0.84	0.428549	0.613942	-6.97
247231_at	transcription factor-like protein	AtMYB53	AT5G65230	-1.07	-0.10	-0.84	0.428531	0.613942	-6.97
265954_at	putative WRKY-type DNA binding prot	TTG2	AT2G37260	-1.06	-0.09	-0.84	0.428575	0.613942	-6.97

263806_at	hypothetical protein predicted by gene	---	AT2G04305	-1.16	-0.22	-0.84	0.428623	0.613973	-6.97
266874_at	unknown protein	---	AT2G44760	1.06	0.08	0.84	0.428713	0.614062	-6.97
251603_at	putative protein wall-associated kinas	---	AT3G57760	1.19	0.25	0.84	0.428926	0.614328	-6.97
260069_at	unknown protein	---	AT1G73820	1.07	0.09	0.84	0.428985	0.614349	-6.97
261830_at	protein kinase, putative similar to prot	---	AT1G10620	-1.07	-0.10	-0.84	0.428994	0.614349	-6.97
245992_at	receptor protein kinase - like receptor-	---	AT5G20690	-1.06	-0.08	-0.84	0.429243	0.614666	-6.97
244913_at	hypothetical protein	---	---	1.07	0.10	0.84	0.429302	0.614714	-6.97
248711_at	putative protein similar to unknown pro	---	AT5G48270	1.08	0.11	0.84	0.429605	0.615108	-6.97
251937_at	putative protein predicted protein, Ara	CPuORF46	AT3G53400 /	-1.24	-0.31	-0.84	0.429731	0.61525	-6.97
256401_at	putative guanylate kinase similar to gu	---	AT3G06200	-1.05	-0.07	-0.84	0.429786	0.615269	-6.97
260751_at	unknown protein	SCD1	AT1G49040	1.11	0.15	0.84	0.429811	0.615269	-6.97
250628_at	hypothetical protein	---	AT5G07380	-1.09	-0.13	-0.84	0.429825	0.615269	-6.97
265050_at	jasmonate inducible protein, putative s	---	AT1G52070	-1.06	-0.09	-0.84	0.429954	0.615376	-6.97
247945_at	putative protein contains similarity to u	---	AT5G57150	1.22	0.29	0.84	0.429948	0.615376	-6.97
259998_at	hypothetical protein similar to unknowr	BPC3	AT1G68120	-1.10	-0.14	-0.84	0.430095	0.61554	-6.97
250819_at	putative protein strong similarity to unk	---	AT5G05100	1.08	0.11	0.84	0.430187	0.615632	-6.97
261098_at	unknown protein	---	AT1G62970	-1.07	-0.09	-0.84	0.430425	0.615839	-6.97
245037_at	putative phosphatidylinositol-4-phosph	PIP5K3	AT2G26420	1.06	0.08	0.84	0.43036	0.615839	-6.97
245126_at	putative MYB family transcription facto	MYB12	AT2G47460	1.06	0.09	0.84	0.430439	0.615839	-6.97
260098_at	tumor-related protein, putative similar	---	AT1G73320	1.13	0.17	0.84	0.430432	0.615839	-6.97
246283_at	putative protein	---	AT4G36860	-1.08	-0.12	-0.84	0.430743	0.616209	-6.97
248470_at	unknown protein	---	AT5G50830	1.07	0.10	0.84	0.430752	0.616209	-6.97
261293_at	unknown protein ; supported by cDNA	---	AT1G36980	-1.06	-0.08	-0.84	0.430907	0.616391	-6.97
266417_at	putative non-green plastid inner envelo	---	AT2G38550	-1.08	-0.12	-0.84	0.430934	0.616392	-6.97
254980_at	putative ribosomal protein L9, cytosoli	---	AT4G10450	-1.15	-0.20	-0.84	0.431058	0.616453	-6.97
258795_at	hypothetical protein similar to putative	---	AT3G04570	-1.08	-0.12	-0.84	0.43105	0.616453	-6.97
245381_at	MYB transcription factor like protein	MYB39	AT4G17785	1.06	0.09	0.84	0.431031	0.616453	-6.97
259113_at	hypothetical protein predicted by gene	---	AT3G05510	-1.08	-0.11	-0.84	0.431136	0.616527	-6.97
265010_at	T-complex chaperonin protein , epsilo	---	AT1G24510	-1.11	-0.15	-0.84	0.431184	0.616556	-6.97
266283_at	putative proline-rich protein	---	AT2G29210	-1.07	-0.10	-0.84	0.431363	0.616774	-6.97
257792_at	TOM20, putative similar to TOM20 GE	TOM20-3	AT3G27080	1.08	0.12	0.84	0.431428	0.616827	-6.97
266305_at	putative DNA polymerase epsilon cata	TIL2	AT2G27120	1.07	0.10	0.84	0.431533	0.616939	-6.97
245326_at	Expressed protein ; supported by full-le	---	AT4G14100	-1.09	-0.13	-0.84	0.431615	0.617018	-6.97
264927_at	phosphatidylinositol 3-kinase, putative	VPS34	AT1G60490	-1.05	-0.07	-0.84	0.431742	0.61716	-6.97
265001_at	hypothetical protein contains similarity	---	AT1G67350	1.07	0.09	0.84	0.431808	0.617217	-6.97

261911_at	ribosomal protein L7, putative similar t	---	AT1G80750	1.14	0.19	0.84	0.431931	0.617353	-6.97
253469_at	putative protein gene C42D8.3, Caenc	ATPANK2	AT4G32180	1.07	0.10	0.84	0.432111	0.617529	-6.97
245412_at	hypothetical protein	---	AT4G17280	-1.11	-0.15	-0.84	0.432104	0.617529	-6.97
252523_at	putative protein light repressible recep	---	AT3G46400	-1.08	-0.11	-0.84	0.432135	0.617529	-6.97
257100_at	disease resistance protein, putative si	AtRLP41	AT3G25010	1.09	0.12	0.84	0.432215	0.617605	-6.97
245425_at	carboxyl-terminal proteinase like prote	UCH3	AT4G17510	-1.05	-0.07	-0.83	0.432379	0.617722	-6.98
249855_at	unknown protein	---	AT5G22970	-1.07	-0.10	-0.84	0.432331	0.617722	-6.98
252301_at	putative protein various predicted prot	EMB2261	---	-1.08	-0.12	-0.83	0.432371	0.617722	-6.98
261725_at	small nuclear ribonucleoprotein, putat	SmD3	AT1G76300	1.10	0.13	0.83	0.432519	0.617846	-6.98
252564_at	actin depolymerizing factor 1 (ADF1) ;	ADF1	AT3G46010	1.07	0.10	0.83	0.432502	0.617846	-6.98
246456_at	telomerase reverse transcriptase ; sup	ATTERT	AT5G16850	-1.06	-0.09	-0.83	0.432598	0.617881	-6.98
245683_at	ubiquitin-specific protease 8 (UBP8), p	UBP8	AT5G22030	-1.06	-0.08	-0.83	0.432592	0.617881	-6.98
262238_at	hypothetical protein predicted by gene	---	AT1G48300	-1.12	-0.16	-0.83	0.432646	0.617911	-6.98
255591_at	putative expansin	ATEXPA17	AT4G01630	-1.07	-0.10	-0.83	0.432722	0.617948	-6.98
254283_s_	anthocyanidin synthase - like protein p	---	AT4G22870 /	-1.09	-0.12	-0.83	0.432726	0.617948	-6.98
262761_at	unknown protein ESTs gb|AA395702,	---	AT1G10720	-1.10	-0.14	-0.83	0.432941	0.618071	-6.98
257398_at	hypothetical protein predicted by gene	---	AT2G01990	-1.06	-0.08	-0.83	0.432921	0.618071	-6.98
251433_at	putative protein SERINE/THREONINE	---	AT3G59830	1.05	0.08	0.83	0.43291	0.618071	-6.98
266245_at	putative translation initiation factor IF2	---	AT2G27700	1.07	0.10	0.83	0.432843	0.618071	-6.98
252798_at	putative protein	---	AT3G42310	-1.06	-0.08	-0.83	0.432948	0.618071	-6.98
266604_at	E2, ubiquitin-conjugating enzyme 6 (U	UBC6	AT2G46030	1.13	0.18	0.83	0.433125	0.618247	-6.98
252577_at	putative protein putative proteins - Ara	---	AT3G45460	-1.05	-0.08	-0.83	0.433104	0.618247	-6.98
248586_at	putative protein similar to unknown pro	---	AT5G49610	1.07	0.10	0.83	0.43325	0.618382	-6.98
265017_at	unknown protein similar to EST emb|Z	---	AT1G24390	1.07	0.10	0.83	0.433274	0.618382	-6.98
248351_at	unknown protein ; supported by cDNA	---	AT5G52200	1.11	0.16	0.83	0.433307	0.61839	-6.98
251936_at	putative protein crp1 protein, Zea may	MEE40	AT3G53700	-1.09	-0.12	-0.83	0.433502	0.618552	-6.98
256935_at	unknown protein ;supported by full-ler	---	AT3G22570	1.06	0.08	0.83	0.433458	0.618552	-6.98
247091_at	peroxidase (emb CAA66964.1)	---	AT5G66390	1.08	0.11	0.83	0.433489	0.618552	-6.98
256955_at	L-ascorbate oxidase precursor, putati	sks11	AT3G13390	-1.10	-0.14	-0.83	0.43358	0.618586	-6.98
252195_at	putative protein various predicted prot	---	AT3G50190	1.08	0.11	0.83	0.433566	0.618586	-6.98
260361_at	unknown protein ; supported by cDNA	---	AT1G69360	-1.10	-0.13	-0.83	0.43385	0.618855	-6.98
246016_at	histidine kinase - like protein sensory	AHK5	AT5G10720	-1.08	-0.11	-0.83	0.433843	0.618855	-6.98
257119_at	receptor kinase protein, putative simila	---	AT3G20190	1.06	0.09	0.83	0.433819	0.618855	-6.98
246495_at	putative protein hypothetical protein T	---	AT5G16200	-1.26	-0.33	-0.83	0.433948	0.618957	-6.98
251572_at	pelota-like protein pelota PEL1 - Arab	---	AT3G58390	-1.06	-0.09	-0.83	0.433988	0.618974	-6.98

262451_at	receptor-associated kinase isolog	SUB	AT1G11130	-1.12	-0.17	-0.83	0.434075	0.61906	-6.98
254873_at	putative protein a 162 kDa componen	EIF3A	AT4G11420	1.06	0.09	0.83	0.434203	0.619204	-6.98
252182_at	U1 snRNP 70K protein ; supported by	U1-70K	AT3G50670	-1.07	-0.09	-0.83	0.434281	0.619276	-6.98
246602_at	copper amine oxidase, putative simila	---	AT1G31710	-1.14	-0.19	-0.83	0.434386	0.619349	-6.98
264905_at	putative Mlo protein	MLO7	AT2G17430	1.06	0.09	0.83	0.434377	0.619349	-6.98
249207_at	C2H2-type zinc finger protein-like	---	AT5G42640	-1.07	-0.09	-0.83	0.434498	0.61947	-6.98
259281_at	putative Myb-related transcription facto	MYB106	AT3G01140	-1.08	-0.11	-0.83	0.434633	0.619584	-6.98
255531_at	hypothetical protein similar to orf on M	---	AT4G02160	1.07	0.10	0.83	0.434616	0.619584	-6.98
262779_at	putative cytochrome P450 monooxyge	---	AT1G13070	-1.05	-0.08	-0.83	0.435006	0.620078	-6.98
255713_s_	predicted protein	---	AT4G00234 /	-1.06	-0.08	-0.83	0.435092	0.620162	-6.98
264933_at	hypothetical protein predicted by gene	---	AT1G61160	1.08	0.10	0.83	0.435447	0.62059	-6.98
249598_at	putative protein AtPP protein, Brassica	---	AT5G37970	-1.06	-0.09	-0.83	0.435435	0.62059	-6.98
262007_at	hypothetical protein predicted by gens	---	AT1G64580	-1.07	-0.10	-0.83	0.43552	0.620656	-6.98
248194_at	Expressed protein ; supported by full-le	---	AT5G54095	1.05	0.08	0.83	0.435586	0.620671	-6.98
259181_at	unknown protein similar to putative pro	---	AT3G01690	-1.10	-0.13	-0.83	0.435576	0.620671	-6.98
250614_at	putative protein homeodomain protein	---	AT5G07260	-1.05	-0.07	-0.83	0.435769	0.620894	-6.98
266341_at	hypothetical protein predicted by gens	---	AT2G01510	1.07	0.09	0.83	0.435892	0.62103	-6.98
249134_at	unknown protein	---	AT5G43150	1.12	0.17	0.83	0.435975	0.621082	-6.98
250740_at	t-SNARE SED5 (gb|AAC06291.1) ; su	SYP31	AT5G05760	-1.06	-0.08	-0.83	0.435982	0.621082	-6.98
263344_at	unknown protein ;supported by full-ler	---	AT2G04940	-1.09	-0.12	-0.83	0.436155	0.621289	-6.98
253180_at	putative protein various predicted prot	---	AT4G35210	-1.06	-0.08	-0.83	0.436251	0.621386	-6.98
264327_at	putative translation initiation factor eIF	EIF2 GAMM	AT1G04170	1.06	0.09	0.83	0.43636	0.621413	-6.98
254406_at	putative transposable element reverse	---	---	1.06	0.08	0.83	0.436379	0.621413	-6.98
249880_at	putative protein similar to unknown pro	---	AT5G23180	-1.07	-0.09	-0.83	0.436368	0.621413	-6.98
261636_at	branched-chain amino acid aminotran	---	AT1G50110	-1.08	-0.11	-0.83	0.43634	0.621413	-6.98
262142_at	hypothetical protein predicted by gene	---	AT1G52640	1.08	0.11	0.83	0.436461	0.621491	-6.98
260893_at	hypothetical protein similar to hypothet	---	AT1G29180	1.06	0.09	0.83	0.436534	0.621557	-6.98
259755_at	unknown protein similar to glucosamin	---	AT1G71070	-1.08	-0.11	-0.83	0.436764	0.621844	-6.98
251403_at	putative protein RING finger protein A	---	AT3G60300	1.10	0.13	0.83	0.43679	0.621844	-6.98
256348_at	hypothetical protein predicted by gene	---	AT1G54880	-1.07	-0.09	-0.83	0.436892	0.621951	-6.98
259073_at	unknown protein contains zinc finger r	---	AT3G02290	1.13	0.18	0.83	0.437077	0.622145	-6.98
259425_at	4,5 PIP kinase, putative similar to 4,5	PIPK11	AT1G01460	-1.06	-0.09	-0.83	0.437084	0.622145	-6.98
259798_at	hypothetical protein predicted by gene	---	AT1G64310	1.09	0.13	0.83	0.437237	0.622325	-6.98
249364_at	putative protein predicted protein, Ara	---	AT5G40590	1.06	0.09	0.83	0.437317	0.6224	-6.98
253702_at	Ca2+-transporting ATPase - like prote	ACA10	AT4G29900	-1.09	-0.13	-0.83	0.437351	0.62241	-6.98

265363_at	hypothetical protein predicted by gens	---	---	-1.06	-0.08	-0.83	0.437431	0.622485	-6.98
265914_at	En/Spm-like transposon protein relate	---	---	-1.06	-0.08	-0.83	0.437523	0.622538	-6.98
265803_at	hypothetical protein predicted by gens	---	AT2G18115	1.09	0.12	0.83	0.437503	0.622538	-6.98
253415_at	putative protein peptidyl-prolyl cis-tran	---	AT4G33060	-1.11	-0.14	-0.83	0.437594	0.6226	-6.98
254728_at	hypothetical protein	---	AT4G13690	-1.06	-0.09	-0.82	0.437634	0.622606	-6.98
249935_at	acyl CoA reductase-like protein	FAR7	AT5G22420	1.06	0.08	0.82	0.437653	0.622606	-6.98
261323_at	hypothetical protein predicted by gene	---	AT1G44760	-1.11	-0.16	-0.82	0.437684	0.622607	-6.98
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.13	-0.18	-0.82	0.437708	0.622607	-6.98
255051_at	RNA-directed DNA polymerase -like p	---	---	1.11	0.15	0.82	0.43779	0.622685	-6.98
247929_at	apospory-associated protein C	---	AT5G57330	-1.08	-0.12	-0.82	0.437869	0.622758	-6.98
250285_at	putative protein GCN4-complementing	SFC	AT5G13300	-1.11	-0.15	-0.82	0.437942	0.622822	-6.98
255511_at	Expressed protein ; supported by cDN	PIT1	AT4G02075	1.15	0.20	0.82	0.438325	0.623329	-6.98
252018_at	putative protein various predicted prot	AtPP2-A15	AT3G53000	-1.10	-0.13	-0.82	0.438458	0.62344	-6.99
247798_at	subtilisin-like serine protease contains	---	AT5G58830	-1.06	-0.08	-0.82	0.438456	0.62344	-6.99
258762_at	hypothetical protein	---	AT3G10750	1.09	0.12	0.82	0.438574	0.623566	-6.99
246426_at	ovule development protein aintegume	BBM	AT5G17430	-1.06	-0.08	-0.82	0.43864	0.623584	-6.99
249185_at	CHP-rich zinc finger protein-like	---	AT5G43030	1.07	0.10	0.82	0.438641	0.623584	-6.99
264122_at	GTP-binding protein, ara-5 ras homol	ARA-5	AT1G02130	1.05	0.07	0.82	0.438985	0.624034	-6.99
247670_at	putative protein predicted proteins, C.	---	AT5G60190	1.09	0.12	0.82	0.439242	0.624361	-6.99
249020_at	helicase-like protein	CHR4	AT5G44800	-1.08	-0.11	-0.82	0.439338	0.624459	-6.99
253340_s_	WD-repeat protein -like protein WD-re	CDC20.2	AT4G33260 /	-1.07	-0.09	-0.82	0.439373	0.624468	-6.99
251154_at	tRNA isopentenyl transferase -like pro	ATIPT3	AT3G63110	1.19	0.25	0.82	0.439532	0.624626	-6.99
264369_at	Ste-20 related kinase SPAK, putative	---	AT1G70430	1.07	0.10	0.82	0.439539	0.624626	-6.99
260272_at	F-box protein family, AtFBL14 contain	---	AT1G80570	-1.10	-0.13	-0.82	0.43964	0.624731	-6.99
245892_at	putative lipid transfer protein lipid tran	---	AT5G09370	-1.10	-0.14	-0.82	0.439745	0.624811	-6.99
255106_at	putative protein hypothetical proteins c	---	---	1.06	0.08	0.82	0.439751	0.624811	-6.99
246157_at	cytochrome-b5 reductase - like protein	---	AT5G20080	-1.09	-0.12	-0.82	0.439904	0.62495	-6.99
262184_at	hypothetical protein contains similarity	---	AT1G77910	1.05	0.08	0.82	0.439887	0.62495	-6.99
251209_at	putative protein several hypothetical pr	---	AT3G62890	1.08	0.12	0.82	0.439989	0.625033	-6.99
253245_at	bZIP transcription factor ATB2	GBF6	AT4G34588 /	-1.19	-0.25	-0.82	0.440044	0.625073	-6.99
253913_at	myosin heavy chain - like protein myo	VIIIB	AT4G27370	-1.06	-0.09	-0.82	0.44027	0.625354	-6.99
262345_at	hypothetical protein similar to hypothet	---	AT1G64180	1.07	0.10	0.82	0.440298	0.625355	-6.99
265734_at	predicted by genscan and genefinder	---	AT2G01260	1.07	0.09	0.82	0.440388	0.625443	-6.99
263850_at	hypothetical protein predicted by gene	---	AT2G04480	-1.11	-0.16	-0.82	0.440451	0.625494	-6.99
259509_at	mutator-like transposase, putative sim	---	---	1.06	0.08	0.82	0.440481	0.625497	-6.99

263324_at	hypothetical protein predicted by gens	---	AT2G04220	-1.06	-0.09	-0.82	0.440714	0.625788	-6.99
266906_at	Expressed protein ; supported by full-l	---	AT2G34585	1.10	0.13	0.82	0.44074	0.625788	-6.99
249391_at	putative protein predicted proteins, Ar	---	AT5G40140	1.10	0.13	0.82	0.440846	0.625861	-6.99
260633_at	protein kinase, putative similar to prot	HT1	AT1G62400	-1.06	-0.09	-0.82	0.440828	0.625861	-6.99
264236_at	hypothetical protein predicted by gene	---	AT1G54680	1.07	0.10	0.82	0.440961	0.625984	-6.99
248125_at	2S storage protein-like	---	AT5G54740	-1.07	-0.10	-0.82	0.441094	0.626	-6.99
255163_at	putative polyprotein	---	---	1.06	0.09	0.82	0.441153	0.626	-6.99
250037_at	disease resistance protein -like diseas	---	AT5G18350	-1.09	-0.12	-0.82	0.441152	0.626	-6.99
254702_at	putative protein predicted protein, Ara	---	AT4G17940	1.07	0.10	0.82	0.441164	0.626	-6.99
247599_at	putative protein	---	AT5G60880	-1.13	-0.18	-0.82	0.441118	0.626	-6.99
256931_at	LEA protein, putative similar to LEA p	---	AT3G22490	1.06	0.08	0.82	0.441098	0.626	-6.99
249373_at	putative protein vanilloid receptor gen	---	AT5G40670	1.07	0.10	0.82	0.441011	0.626	-6.99
250440_at	40S ribsomal protein S6 ; supported b	EMB3010	AT5G10360	1.10	0.13	0.82	0.441205	0.626019	-6.99
245587_at	putative protein	---	AT4G15020	1.12	0.17	0.82	0.441575	0.626446	-6.99
262655_s_	putative mandelonitrile lyase similar to	---	AT1G14185 /	1.06	0.08	0.82	0.441588	0.626446	-6.99
246448_at	putative protein putative N-acetlytrans	---	AT5G16800	-1.07	-0.10	-0.82	0.441547	0.626446	-6.99
261435_at	GTP-binding protein, putative similar t	---	AT1G07615 /	-1.12	-0.16	-0.82	0.441646	0.626451	-6.99
260740_at	thioredoxin, putative contains Pfam pr	ATQSOX1	AT1G15020	-1.06	-0.08	-0.82	0.44162	0.626451	-6.99
259501_at	unknown protein ; supported by cDNA	TPL	AT1G15750	1.08	0.11	0.82	0.441704	0.626468	-6.99
247687_at	protein serine /threonine kinase - like	---	AT5G59740	-1.07	-0.10	-0.82	0.441721	0.626468	-6.99
250352_at	beta-adaptin-like protein A ; supported	---	AT5G11490	-1.06	-0.08	-0.82	0.441741	0.626468	-6.99
253671_at	serine threonine-specific receptor prote	---	AT4G29990	1.09	0.12	0.82	0.441812	0.626505	-6.99
AFFX-ThrX	B. subtilis /GEN=thrB /DB_XREF=gb:X	---	---	-1.12	-0.16	-0.82	0.441849	0.626505	-6.99
248455_at	unknown protein	---	AT5G51360	1.06	0.08	0.82	0.441839	0.626505	-6.99
247773_at	putative protein	---	AT5G58630	1.07	0.09	0.82	0.442126	0.62682	-6.99
255245_at	hypothetical protein	---	AT4G05630	-1.06	-0.09	-0.82	0.4421	0.62682	-6.99
251202_at	putative protein predicted protein, C.e	---	AT3G63040	1.06	0.08	0.82	0.442226	0.626922	-6.99
259519_at	hypothetical protein	---	AT1G12270	1.09	0.12	0.82	0.442281	0.626962	-6.99
253336_at	putative protein Caenorhabditis elega	EIF3K	AT4G33250	-1.07	-0.10	-0.82	0.442346	0.627007	-6.99
252034_at	putative protein ;supported by full-leng	---	AT3G52040	1.14	0.18	0.82	0.442396	0.627007	-6.99
266032_x_	putative replication protein A1	---	---	-1.07	-0.10	-0.82	0.442377	0.627007	-6.99
256625_at	uteroglobin promoter-binding protein,	---	AT3G20010	1.12	0.16	0.82	0.442431	0.627018	-6.99
258699_at	unknown protein	---	AT3G09470	1.08	0.11	0.82	0.442528	0.627116	-6.99
248571_at	putative protein similar to unknown pro	---	---	1.06	0.08	0.82	0.442557	0.627119	-6.99
265561_s_	putative glycine-rich protein	---	AT1G47480 /	1.10	0.13	0.82	0.442588	0.627123	-6.99

250869_at	Terminal flower1 (TFL1) ; supported by	TFL1	AT5G03840	1.07	0.09	0.82	0.442643	0.627162	-6.99
253226_at	beta-galactosidase - like protein beta-	BGAL11	AT4G35010	-1.06	-0.09	-0.82	0.442704	0.62721	-6.99
246298_at	putative protein sequence in GenBank	ETO1	AT3G51770	-1.06	-0.08	-0.82	0.442872	0.627409	-6.99
248444_at	putative protein similar to unknown pro	---	---	1.06	0.08	0.81	0.443225	0.62787	-6.99
256429_at	unknown protein	---	AT3G11040	-1.09	-0.12	-0.81	0.443257	0.627877	-6.99
249181_at	putative protein contains similarity to u	---	AT5G42920	1.07	0.10	0.81	0.443409	0.628014	-6.99
250814_at	E2, ubiquitin-conjugating enzyme, put	UBC22	AT5G05080	-1.08	-0.11	-0.81	0.443408	0.628014	-6.99
256929_at	unknown protein	---	---	-1.08	-0.11	-0.81	0.443605	0.628252	-6.99
258886_at	putative importin alpha similar to GB:A	IMPA-7	AT3G05720	-1.07	-0.09	-0.81	0.443632	0.628252	-6.99
246805_at	putative protein various predicted tran	AGL101	AT5G27050	-1.06	-0.09	-0.81	0.443771	0.628371	-6.99
245918_at	putative protein various predicted prot	---	---	-1.05	-0.08	-0.81	0.443772	0.628371	-6.99
258321_at	early light-induced protein identical to e	ELIP1	AT3G22840	1.07	0.10	0.81	0.444033	0.628702	-6.99
254909_at	putative disease resistance response	---	AT4G11210	-1.07	-0.10	-0.81	0.444117	0.628783	-6.99
254403_at	subtilisin-like serine protease contains	---	AT4G21323	1.05	0.07	0.81	0.444162	0.628806	-6.99
248150_at	kinesin-like protein ; supported by cDN	ATK3	AT5G54670	-1.17	-0.22	-0.81	0.444273	0.628925	-6.99
245727_at	hypothetical protein contains similarity	---	AT1G73350	-1.08	-0.11	-0.81	0.444403	0.62907	-6.99
257085_at	ubiquitin-specific protease 14 (UBP14	UBP14	AT3G20630	-1.11	-0.15	-0.81	0.444619	0.629337	-6.99
259652_at	unknown protein	HUB2	AT1G55250	1.10	0.13	0.81	0.44478	0.629498	-7.00
258779_at	putative protein kinase contains Pfam	---	AT3G11870	-1.05	-0.08	-0.81	0.444788	0.629498	-7.00
265839_at	putative serpin	---	AT2G14540	-1.07	-0.10	-0.81	0.444842	0.629535	-7.00
253351_at	putative protein hemolysin, 38K, Syne	---	AT4G33700	1.07	0.10	0.81	0.444964	0.629591	-7.00
259704_at	putative 3'-5' exoribonuclease similar t	---	AT1G77680	1.08	0.11	0.81	0.444963	0.629591	-7.00
259722_at	putative DNA helicase similar to ATP-D	ATRECQ4B	AT1G60930	1.05	0.07	0.81	0.444962	0.629591	-7.00
263102_at	unknown protein	---	AT2G05270	1.05	0.07	0.81	0.44509	0.62973	-7.00
251703_at	putative protein hypothetical proteins -	---	AT3G56670	1.09	0.12	0.81	0.445142	0.629764	-7.00
265758_at	hypothetical protein similar to myosin-l	---	---	1.05	0.08	0.81	0.445255	0.629885	-7.00
255373_s_	putative protein	---	---	-1.07	-0.10	-0.81	0.445373	0.629968	-7.00
263146_at	lipase, putative similar to lipase GI:11	GLIP2	AT1G53940	1.08	0.11	0.81	0.44536	0.629968	-7.00
259561_at	hypothetical protein ; supported by cDI	WAK1	AT1G21250	1.43	0.51	0.81	0.445396	0.629968	-7.00
263695_at	putative phosphoribosylglycinamide fo	---	AT1G31220	1.06	0.09	0.81	0.445433	0.62998	-7.00
256445_at	hypothetical protein predicted by gene	---	AT3G11160	1.07	0.10	0.81	0.445492	0.630025	-7.00
247712_at	E2, ubiquitin-conjugating enzyme 7 (U	UBC7	AT5G59300	-1.07	-0.10	-0.81	0.445547	0.630064	-7.00
254637_at	putative protein KIAA0244 gene, Hom	---	AT4G18720	-1.07	-0.09	-0.81	0.445841	0.63044	-7.00
265848_at	putative sugar transporter	INT3	AT2G35740	1.10	0.14	0.81	0.445998	0.630624	-7.00
259982_at	putative RING zinc finger protein cont	ATL8	AT1G76410	1.20	0.26	0.81	0.446036	0.630638	-7.00

250051_at	MYB56 R2R3-MYB factor family meml	AtMYB56	AT5G17800	-1.09	-0.12	-0.81	0.446139	0.630745	-7.00
255475_at	contains a short region of similarity to a	---	AT4G02480	1.08	0.11	0.81	0.446201	0.630793	-7.00
266103_at	putative VAMP-associated protein ;su	PVA12	AT2G45140	1.07	0.10	0.81	0.446298	0.630852	-7.00
264020_at	putative signal sequence receptor, alp	---	AT2G21160	-1.09	-0.12	-0.81	0.446288	0.630852	-7.00
253221_at	peptidylprolyl isomerase (cyclophilin) ;	ROC5	AT4G34870	1.09	0.12	0.81	0.446473	0.630982	-7.00
263857_at	unknown protein	---	AT2G04380	1.05	0.07	0.81	0.446451	0.630982	-7.00
255758_at	hypothetical protein predicted by gene	---	AT1G16800	1.06	0.09	0.81	0.446472	0.630982	-7.00
264488_s_	unknown protein similar to EST gb|AA	---	AT1G27330 /	1.12	0.16	0.81	0.446507	0.630991	-7.00
265910_at	putative vacuolar ATP synthase protec	---	AT2G25610	1.07	0.09	0.81	0.446645	0.631147	-7.00
245966_at	AP2 domain containing protein RAP2.	RAP2.11	AT5G19790	1.07	0.10	0.81	0.446763	0.631236	-7.00
267597_at	putative leucine-rich repeat disease re	AtRLP24	AT2G33020	1.13	0.17	0.81	0.446751	0.631236	-7.00
252264_at	putative protein hypothetical protein -	---	AT3G49590	-1.06	-0.09	-0.81	0.446842	0.631281	-7.00
260432_at	putative DNA binding protein similar to	WRKY9	AT1G68150	1.09	0.12	0.81	0.446851	0.631281	-7.00
262386_at	hypothetical protein predicted by gens	---	AT1G49370	-1.09	-0.12	-0.81	0.447011	0.631459	-7.00
261299_at	unknown protein	---	AT1G48550	-1.09	-0.12	-0.81	0.447032	0.631459	-7.00
255911_at	receptor-like kinase, putative similar t	---	AT1G66930	-1.05	-0.08	-0.81	0.447233	0.631704	-7.00
256909_at	hypothetical protein predicted by gene	---	AT3G24060	1.08	0.11	0.81	0.447535	0.632052	-7.00
262296_at	putative cyclin similar to cyclin GB:450	CYCT1;3	AT1G27630	-1.06	-0.09	-0.81	0.447515	0.632052	-7.00
245144_at	putative methionine aminopeptidase ;	MAP1A	AT2G45240	1.07	0.10	0.81	0.447672	0.632159	-7.00
253116_at	putative protein CRP1, Zea mays, gb:	---	AT4G35850	1.13	0.17	0.81	0.447657	0.632159	-7.00
247804_at	strong similarity to unknown protein (pi	SVL5	AT5G58170	1.07	0.09	0.81	0.447694	0.632159	-7.00
266610_at	Ac-like transposase related to Ac/Ds tr	---	---	-1.05	-0.08	-0.81	0.447793	0.63226	-7.00
249396_at	DegP protease contains similarity to D	DegP9	AT5G40200	-1.06	-0.08	-0.81	0.447843	0.632292	-7.00
250284_at	protein kinase precursor - like recepto	CRN	AT5G13290	-1.10	-0.14	-0.81	0.447901	0.632321	-7.00
263138_at	hypothetical protein predicted by gene	---	AT1G65090	1.06	0.08	0.81	0.447919	0.632321	-7.00
249754_at	flavanone 3-hydroxylase-like protein ;	DMR6	AT5G24530	1.36	0.44	0.81	0.447971	0.632355	-7.00
267474_at	hypothetical protein predicted by gens	WHY3	AT2G02740	-1.07	-0.10	-0.81	0.448075	0.632423	-7.00
254662_at	putative protein phospho-N-acetylmur	TRANS11	AT4G18270	-1.11	-0.14	-0.81	0.448059	0.632423	-7.00
264123_at	unknown protein ; supported by cDNA	---	AT1G02270	1.08	0.11	0.81	0.448162	0.632467	-7.00
245721_s_	hypothetical protein similar to Ser-Thr	---	AT1G73450 /	1.09	0.13	0.81	0.448139	0.632467	-7.00
259810_at	Na+/H+ antiporter, putative similar to	ATNHD2	AT1G49810	-1.06	-0.08	-0.81	0.448236	0.632532	-7.00
247504_at	putative protein various predicted prot	---	AT5G61990	1.10	0.13	0.80	0.448359	0.632667	-7.00
264014_at	putative auxin-regulated protein	---	AT2G21210	1.23	0.30	0.80	0.448534	0.632752	-7.00
258551_at	hypothetical protein predicted by gens	---	AT3G06890	-1.05	-0.07	-0.80	0.448497	0.632752	-7.00
259898_at	hypothetical protein predicted by gene	---	AT1G71200	-1.06	-0.09	-0.80	0.448447	0.632752	-7.00

257389_at	hypothetical protein predicted by gens	---	AT2G17970	-1.06	-0.08	-0.80	0.448558	0.632752	-7.00
263262_at	unknown protein	---	AT2G38830	1.07	0.09	0.80	0.448517	0.632752	-7.00
266731_at	unknown protein	---	AT2G03260	-1.06	-0.08	-0.80	0.448637	0.632798	-7.00
263794_at	similar to S-locus glycoproteins	---	AT2G24620	1.06	0.08	0.80	0.448667	0.632798	-7.00
264974_at	unknown protein contains Pfam proifle	ATHB54	AT1G27050	-1.07	-0.10	-0.80	0.448674	0.632798	-7.00
266989_at	putative myrosinase-binding protein ;s	JAL23	AT2G39330	1.44	0.53	0.80	0.448714	0.632816	-7.00
245804_at	hypothetical protein predicted by gene	---	AT1G46696	1.06	0.08	0.80	0.448882	0.633013	-7.00
265546_at	putative proline/hydroxyproline-rich gly	---	AT2G28240	-1.07	-0.10	-0.80	0.448931	0.633043	-7.00
264215_at	cytochrome P450, putative similar to c	CYP96A3	AT1G65340	1.06	0.08	0.80	0.449021	0.633132	-7.00
261446_at	unknown protein	SEC5B	AT1G21170	-1.09	-0.12	-0.80	0.449072	0.633164	-7.00
250025_at	putative protein similar to unknown pro	SIP1;2	AT5G18290	1.09	0.13	0.80	0.449166	0.633257	-7.00
265031_at	serine/threonine protein kinase, putati	---	AT1G61590	-1.05	-0.08	-0.80	0.449227	0.633304	-7.00
246511_at	UDP-glucose dehydrogenase-like pro	---	AT5G15490	-1.16	-0.22	-0.80	0.44928	0.633341	-7.00
250519_at	GDSL-motif lipase/acylhydrolase-like p	---	AT5G08460	-1.07	-0.10	-0.80	0.449363	0.63338	-7.00
248851_s_	disease resistance protein-like ; suppo	---	AT5G46260 /	-1.07	-0.10	-0.80	0.449354	0.63338	-7.00
257680_at	aspartate carbamoyltransferase precu	---	AT3G20330	1.09	0.12	0.80	0.449427	0.63343	-7.00
254308_at	putative protein snRNP assembly fact	---	AT4G22410	-1.06	-0.09	-0.80	0.449765	0.633867	-7.00
249320_at	disease resistance protein-like non-co	---	AT5G40910	1.10	0.14	0.80	0.449961	0.634051	-7.00
254880_at	putative protein Crp1, Zea mays, AF0	---	AT4G11690	1.08	0.11	0.80	0.449953	0.634051	-7.00
246783_at	sugar transporter-like protein putative	SFP2	AT5G27360	1.22	0.29	0.80	0.449979	0.634051	-7.00
264892_at	GH3-like auxin-regulated protein high	---	AT1G23160	-1.06	-0.09	-0.80	0.450049	0.634111	-7.00
266502_at	hypothetical protein predicted by gens	---	AT2G47720 /	-1.06	-0.09	-0.80	0.450136	0.634155	-7.00
258740_at	Lon protease, putative similar to Lon p	LON3	AT3G05780	1.09	0.13	0.80	0.450132	0.634155	-7.00
261894_at	unknown protein ;supported by full-len	MGT1	AT1G80900	1.06	0.09	0.80	0.450464	0.634577	-7.00
266136_at	unknown protein ;supported by full-ler	---	AT2G45060	-1.05	-0.07	-0.80	0.45076	0.634955	-7.00
248096_at	embryo-specific protein 1; Ca2+-bindir	---	AT5G55240	1.06	0.09	0.80	0.450819	0.634961	-7.00
248131_at	unknown protein	---	AT5G54830	1.14	0.19	0.80	0.450792	0.634961	-7.00
245904_at	sucrose-phosphate synthase -like pro	ATSPS2F	AT5G11110	1.08	0.11	0.80	0.451149	0.635386	-7.01
253541_at	putative protein various predicted prot	---	AT4G31630	1.06	0.08	0.80	0.451339	0.635614	-7.01
267361_at	hypothetical protein predicted by gens	---	AT2G39920	1.11	0.16	0.80	0.451453	0.635697	-7.01
245876_at	chaperonin precursor, putative similar	---	AT1G26230	-1.12	-0.17	-0.80	0.451441	0.635697	-7.01
263672_at	putative retroelement pol polyprotein	---	---	-1.06	-0.08	-0.80	0.451514	0.635743	-7.01
257356_s_	hypothetical protein predicted by gens	---	AT2G32490 /	1.07	0.10	0.80	0.451581	0.635759	-7.01
257473_at	unknown protein	---	AT1G33840	1.09	0.12	0.80	0.451577	0.635759	-7.01
258004_at	unknown protein similar to putative tra	MYB110	AT3G29020	-1.07	-0.09	-0.80	0.45165	0.635816	-7.01

AFFX-BioB	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.14	0.19	0.80	0.451735	0.635858	-7.01
261391_at	hypothetical protein similar to hypothet	---	AT1G35030	1.07	0.10	0.80	0.451717	0.635858	-7.01
245289_at	Expressed protein ; supported by cDN	---	AT4G15470	-1.05	-0.07	-0.80	0.451864	0.635961	-7.01
250961_at	putative protein various predicted prot	---	AT5G02980	1.07	0.09	0.80	0.451846	0.635961	-7.01
245430_at	hypothetical protein	FIP2	AT4G17060	-1.05	-0.07	-0.80	0.451925	0.636008	-7.01
254430_at	reticuline oxidase - like protein reticuli	---	AT4G20820	1.16	0.22	0.80	0.452028	0.636035	-7.01
254237_at	cysteine proteinase contains similarity	---	AT4G23520	1.06	0.08	0.80	0.451992	0.636035	-7.01
249805_at	putative protein similar to unknown pro	---	AT5G23800	1.06	0.09	0.80	0.452013	0.636035	-7.01
264367_at	unknown protein ESTs gb|T21276, gb	---	AT1G03350	-1.06	-0.09	-0.80	0.452238	0.636195	-7.01
249104_at	sucrose transporter protein	ATSUC6	AT5G43610	1.06	0.09	0.80	0.452207	0.636195	-7.01
256339_at	hypothetical protein	---	AT1G72080	1.06	0.09	0.80	0.452253	0.636195	-7.01
249156_s_	putative protein similar to unknown pro	---	AT5G43490 /	1.05	0.08	0.80	0.452242	0.636195	-7.01
254516_at	putative protein	---	AT4G20290	-1.07	-0.10	-0.80	0.452289	0.636206	-7.01
261759_at	hypothetical protein similar to putative	---	AT1G15590	-1.07	-0.09	-0.80	0.452318	0.636207	-7.01
260424_at	putative receptor-like protein kinase c	---	AT1G72460	-1.06	-0.09	-0.80	0.452458	0.636365	-7.01
263808_at	hypothetical protein predicted by gens	---	AT2G04340	-1.06	-0.09	-0.80	0.452505	0.636391	-7.01
246333_at	proteinkinase AtPP -like protein AtPP	---	AT3G44840	1.07	0.09	0.80	0.452552	0.636418	-7.01
246956_at	unknown protein ; supported by cDNA	RTM2	AT5G04890	1.07	0.09	0.80	0.452588	0.636431	-7.01
256950_at	hypothetical protein similar to hypothet	---	AT3G19080	-1.14	-0.18	-0.80	0.45265	0.636479	-7.01
252556_at	putative protein step II splicing factor l	---	AT3G45950	-1.05	-0.07	-0.80	0.452803	0.636654	-7.01
246238_at	sugar transporter like protein	---	AT4G36670	1.18	0.23	0.80	0.452896	0.636746	-7.01
261044_at	molybdopterin biosynthesis CNX3 pro	CNX3	AT1G01290	-1.07	-0.10	-0.80	0.453276	0.636802	-7.01
250426_at	ovule development protein - like ovule	AIL6	AT5G10510	1.06	0.08	0.80	0.453133	0.636802	-7.01
263237_at	hypothetical protein contains similarity	---	AT1G10610	1.11	0.16	0.80	0.453088	0.636802	-7.01
255968_at	Expressed protein ; supported by full-l	---	AT1G22270	1.08	0.11	0.80	0.453229	0.636802	-7.01
258981_at	hypothetical protein predicted by gens	---	AT3G08880	-1.05	-0.08	-0.80	0.453257	0.636802	-7.01
246640_x_	putative protein predicted proteins, Ar	---	---	-1.07	-0.09	-0.80	0.453102	0.636802	-7.01
250877_at	putative protein predicted protein, Ara	SDP1	AT5G04040	-1.09	-0.13	-0.80	0.453318	0.636802	-7.01
248651_at	unknown protein	---	AT5G49260	1.06	0.08	0.80	0.45326	0.636802	-7.01
254976_at	subtilisin-like serine protease contains	---	AT4G10510	1.06	0.09	0.80	0.453047	0.636802	-7.01
244941_at	hypothetical protein	---	---	1.08	0.11	0.80	0.453186	0.636802	-7.01
249814_at	putative protein similar to unknown pro	---	AT5G23840	-1.06	-0.08	-0.80	0.453327	0.636802	-7.01
254297_at	hypothetical protein	---	AT4G23110	-1.05	-0.08	-0.80	0.452987	0.636802	-7.01
245322_at	Expressed protein ; supported by full-l	---	AT4G14815	1.14	0.18	0.80	0.453065	0.636802	-7.01
252962_at	splicing factor - like protein splicing fa	---	AT4G38780	1.07	0.10	0.80	0.453129	0.636802	-7.01

247043_at	protein kinase, 41K (EC 2.7.1.-) (pir||S	SNRK2.3	AT5G66880	1.11	0.15	0.80	0.453373	0.636827	-7.01
248042_at	putative protein similar to unknown pro	---	AT5G55960	-1.08	-0.12	-0.80	0.453447	0.636892	-7.01
247800_at	Expressed protein ; supported by full-le	---	AT5G58570	1.29	0.37	0.80	0.453599	0.636897	-7.01
258350_at	unknown protein similar to serine/threo	CIPK1	AT3G17510	1.15	0.20	0.80	0.453618	0.636897	-7.01
250715_at	splicing factor 3a ; supported by cDNA	ATO	AT5G06160	-1.09	-0.13	-0.80	0.453505	0.636897	-7.01
263588_s_	unknown protein	---	AT2G25320 /	-1.06	-0.09	-0.80	0.453577	0.636897	-7.01
247224_at	MADS box transcription factor-like prot	MAF5	AT5G65080	-1.11	-0.15	-0.80	0.453616	0.636897	-7.01
252627_at	putative protein	---	AT3G44950	-1.08	-0.11	-0.80	0.453558	0.636897	-7.01
264048_at	unknown protein	---	AT2G22400	1.10	0.13	0.80	0.453647	0.636898	-7.01
261879_at	cytochrome P450, putative similar to C	CYP705A27	AT1G50520	1.06	0.08	0.79	0.453806	0.637082	-7.01
262574_at	unknown protein ESTs gb|R30529, gb	---	AT1G15230	1.12	0.16	0.79	0.453925	0.637093	-7.01
246149_at	peroxidase ATP N ;supported by full-le	---	AT5G19890	1.40	0.49	0.79	0.453919	0.637093	-7.01
249183_at	E2, ubiquitin-conjugating enzyme 18 (	UBC18	AT5G42990	-1.06	-0.08	-0.79	0.453873	0.637093	-7.01
252696_at	hypothetical protein predicted transpo	---	---	1.05	0.07	0.79	0.453882	0.637093	-7.01
255585_at	putative NAM-like protein	anac069	AT4G01550	-1.10	-0.14	-0.79	0.454298	0.637459	-7.01
262399_at	unknown protein ;supported by full-len	---	AT1G49500	-1.10	-0.14	-0.79	0.454253	0.637459	-7.01
249232_at	dynamin-like protein (pir||S59558) ;su	ADL1	AT5G42080	1.09	0.13	0.79	0.454226	0.637459	-7.01
252447_at	beta-D-glucan exohydrolase - like pro	---	AT3G47040	1.06	0.09	0.79	0.454278	0.637459	-7.01
264952_at	Tub family protein, putative contains P	AtTLP1	AT1G76900	-1.06	-0.08	-0.79	0.454386	0.637543	-7.01
255548_at	putative CHP-rich zinc finger protein si	---	AT4G01930	1.05	0.07	0.79	0.454419	0.637551	-7.01
253680_at	cytidine deaminase 2 (CDA2)	---	AT4G29620	-1.06	-0.08	-0.79	0.454564	0.637715	-7.01
257592_at	leucine-rich repeat disease resistance	---	AT3G24982	1.06	0.09	0.79	0.454735	0.637916	-7.01
255577_at	putative hypoersensitive response pro	---	AT4G01410	1.25	0.32	0.79	0.454771	0.637926	-7.01
258391_at	hypothetical protein predicted by gens	---	AT3G15420	1.10	0.14	0.79	0.454844	0.637991	-7.01
259568_at	hypothetical protein	---	AT1G20490	-1.06	-0.08	-0.79	0.45488	0.638002	-7.01
259845_at	auxin transporter splice variant b, puta	PIN1	AT1G73590	-1.10	-0.14	-0.79	0.454923	0.638023	-7.01
245954_at	far-red impaired response protein (FA	FRS10	AT5G28530	-1.07	-0.10	-0.79	0.455064	0.638181	-7.01
255789_at	60S ribosomal protein L23 ;supported	---	AT2G33370	-1.18	-0.23	-0.79	0.455159	0.638202	-7.01
247634_at	late embryonic abundant protein - like	---	AT5G60520	1.05	0.07	0.79	0.455107	0.638202	-7.01
249270_at	putative protein similar to unknown pro	---	AT5G41780	1.05	0.07	0.79	0.455163	0.638202	-7.01
254929_at	putative protein mitochondrial carrier p	---	AT4G11440	-1.07	-0.09	-0.79	0.455197	0.638211	-7.01
255200_at	hypothetical protein	---	---	-1.07	-0.10	-0.79	0.455382	0.638431	-7.01
256666_at	histone H2A, putative similar to histon	HTA13	AT3G20670	-1.15	-0.20	-0.79	0.455412	0.638433	-7.01
260119_at	AIG1-like protein similar to AIG1 prote	---	AT1G33930	-1.06	-0.09	-0.79	0.455584	0.638545	-7.01
257308_at	unknown protein	---	AT3G28120	1.05	0.07	0.79	0.455575	0.638545	-7.01

262240_at	Pto kinase interactor 1, putative simila	---	AT1G48220	-1.07	-0.09	-0.79	0.4556	0.638545	-7.01
255386_at	hypothetical protein	---	AT4G03620	-1.06	-0.08	-0.79	0.455604	0.638545	-7.01
247383_at	putative protein contains similarity to re	---	AT5G63410	1.13	0.17	0.79	0.455876	0.638887	-7.01
245502_at	hypothetical protein	---	AT4G15640	1.08	0.11	0.79	0.455921	0.638912	-7.01
258018_at	hypothetical protein predicted by gens	---	AT3G19500	-1.09	-0.12	-0.79	0.456018	0.639008	-7.01
264607_at	putative K+ channel, beta subunit sim	KAB1	AT1G04690	-1.05	-0.07	-0.79	0.456056	0.639022	-7.01
264325_at	putative phosphoribosylanthranilate tra	---	AT1G04150	-1.08	-0.12	-0.79	0.456122	0.639036	-7.01
249338_at	putative protein similar to unknown pro	anac095	AT5G41090	1.05	0.07	0.79	0.456118	0.639036	-7.01
265236_s_	hypothetical protein	---	AT2G07714	1.07	0.09	0.79	0.456172	0.639067	-7.01
255336_at	putative transposon protein	---	---	-1.05	-0.07	-0.79	0.456255	0.639121	-7.01
248872_at	Expressed protein ; supported by full-l	MSP2	AT5G46795	1.07	0.10	0.79	0.456267	0.639121	-7.01
254540_s_	putative protein chitinase / lysozyme F	---	AT4G19770 /	-1.05	-0.08	-0.79	0.456384	0.639246	-7.01
255551_at	putative potassium channel ;supporte	KCO5	AT4G01840	1.05	0.08	0.79	0.456511	0.639384	-7.01
248069_at	unknown protein	---	AT5G55650	1.07	0.10	0.79	0.456878	0.639685	-7.01
255805_at	zinc-finger - like protein zinc-finger pro	---	AT4G10240	1.07	0.09	0.79	0.456847	0.639685	-7.01
264659_at	unknown protein Similar to S. pombe I	ATOPT2	AT1G09930	1.06	0.08	0.79	0.456821	0.639685	-7.01
254472_at	putative protein predicted proteins, Ar	---	---	1.05	0.07	0.79	0.456897	0.639685	-7.01
266726_at	SKP1/ASK1 (At19), putative similar to	ASK19	AT2G03160	-1.09	-0.12	-0.79	0.456922	0.639685	-7.01
267479_at	hypothetical protein	---	AT2G02690	-1.05	-0.07	-0.79	0.456825	0.639685	-7.01
262032_at	biotin holocarboxylase synthetase, pu	HCS2	AT1G37150	1.06	0.08	0.79	0.4569	0.639685	-7.01
259827_at	hypothetical protein	---	AT1G72270	-1.06	-0.08	-0.79	0.456951	0.639686	-7.01
246505_at	putative protein hypothetical protein F	---	AT5G16250	-1.12	-0.16	-0.79	0.457032	0.639761	-7.01
251875_at	putative protein various predicted prot	---	AT3G54270	1.08	0.11	0.79	0.457092	0.639805	-7.01
254227_at	putative protein chS-Rex-b - Gallus ga	BTI1	AT4G23630	-1.10	-0.13	-0.79	0.457173	0.639879	-7.01
246068_at	putative protein ribosomal protein S8 -	---	AT5G20290	-1.13	-0.18	-0.79	0.457237	0.63993	-7.01
261514_at	hypothetical protein predicted by gene	---	AT1G71870	-1.09	-0.13	-0.79	0.457318	0.640004	-7.01
259647_at	acetyl-CoA synthetase, putative simila	---	AT1G55325	1.07	0.10	0.79	0.457539	0.640169	-7.01
245294_at	casein kinase I ; supported by cDNA: g	CKI1	AT4G14340	-1.06	-0.09	-0.79	0.457497	0.640169	-7.01
257523_at	hypothetical protein similar to putative	---	AT3G01620	1.06	0.09	0.79	0.457548	0.640169	-7.01
261061_at	DNA-binding protein, putative contain	TRFL2	AT1G07540	1.07	0.09	0.79	0.457473	0.640169	-7.01
260861_at	hypothetical protein predicted by gene	---	---	1.07	0.09	0.79	0.457588	0.640186	-7.01
247319_at	glutamate-tRNA ligase ; supported by	ERS	AT5G64050	-1.07	-0.09	-0.79	0.457642	0.640221	-7.01
249518_at	putative protein similar to unknown pro	---	AT5G38610	-1.06	-0.09	-0.79	0.457735	0.640312	-7.02
261599_at	hypothetical protein similar to hypothet	---	AT1G49700	-1.07	-0.10	-0.79	0.457763	0.640313	-7.02
261607_at	unknown protein similar to putative est	AtCXE5	AT1G49660	1.18	0.24	0.79	0.457798	0.640322	-7.02

266381_at	putative sucrose-proton symporter	ATSUC8	AT2G14670	1.06	0.08	0.79	0.457876	0.640391	-7.02
261015_at	14-3-3 protein GF14iota (grf12) identic	GRF12	AT1G26480	-1.06	-0.09	-0.79	0.458012	0.640544	-7.02
256115_at	unknown protein ; supported by cDNA:	---	AT1G16880	1.10	0.14	0.79	0.458043	0.640548	-7.02
250528_at	putative protein strong similarity to unk	---	AT5G08600	-1.05	-0.07	-0.79	0.458134	0.640616	-7.02
253874_at	putative protein stem-specific protein -	---	AT4G27450	-1.17	-0.23	-0.79	0.458149	0.640616	-7.02
265279_at	hypothetical protein predicted by gens	---	AT2G28460	-1.10	-0.14	-0.79	0.45818	0.640621	-7.02
267227_at	hypothetical protein predicted by gens	---	AT2G44030	1.08	0.12	0.79	0.45826	0.640693	-7.02
266524_at	putative importin, beta subunit	---	AT2G16960	1.07	0.09	0.79	0.458346	0.640774	-7.02
262676_at	SKP1/ASK1 (At1) identical to Skp1a C	SKP1	AT1G75950	1.05	0.07	0.79	0.458375	0.640775	-7.02
254028_s_	putative protein N.crassa mRNA for p	ORP4B	AT4G25850 /	-1.06	-0.08	-0.79	0.458504	0.640916	-7.02
254614_at	putatative protein various predicted pr	---	AT4G19191	1.09	0.12	0.79	0.458547	0.640937	-7.02
250274_at	putative protein predicted protein, Ara	---	AT5G13020	1.07	0.10	0.79	0.458652	0.641046	-7.02
256303_at	disease resistance protein, putative si	---	AT1G69550	1.08	0.11	0.79	0.458789	0.641157	-7.02
266975_at	hypothetical protein predicted by grail	ATEXO70H2	AT2G39380	1.16	0.21	0.79	0.458766	0.641157	-7.02
245857_at	putative protein various predicted prot	---	---	-1.08	-0.12	-0.79	0.45892	0.641301	-7.02
259100_at	DNA-damage-repair/toleration protein	DRT102	AT3G04880	-1.07	-0.09	-0.79	0.458949	0.641303	-7.02
265547_at	hypothetical protein similar to hypothet	---	AT2G28305	1.14	0.19	0.79	0.459051	0.641406	-7.02
259987_at	thaumatin-like protein (PR-5) similar to	ATLP-3	AT1G75030	-1.09	-0.12	-0.79	0.459092	0.641424	-7.02
266024_at	En/Spm-like transposon protein relate	---	---	-1.06	-0.08	-0.78	0.459194	0.641527	-7.02
266115_at	protease inhibitor II ;supported by full-	LCR72	AT2G02140	-1.11	-0.15	-0.78	0.459241	0.641554	-7.02
266250_at	putative reverse transcriptase	---	---	1.06	0.09	0.78	0.459361	0.641658	-7.02
255195_at	may be a pseudogene	---	---	1.06	0.08	0.78	0.459372	0.641658	-7.02
263329_at	hypothetical protein contains C3HC4 z	---	AT2G15260	-1.06	-0.08	-0.78	0.459458	0.641739	-7.02
256284_at	unknown protein	PSF2	AT3G12530	1.10	0.14	0.78	0.459568	0.641814	-7.02
257326_s_	hypothetical protein	---	---	-1.08	-0.11	-0.78	0.45954	0.641814	-7.02
248630_at	putative protein strong similarity to unk	---	AT5G48990	-1.06	-0.09	-0.78	0.459658	0.6419	-7.02
248504_at	transcription factor Hap5a-like	NF-YC6	AT5G50480	-1.10	-0.13	-0.78	0.45978	0.642031	-7.02
257229_at	putative calmodulin-binding protein cor	IQD26	AT3G16490	-1.08	-0.12	-0.78	0.459818	0.642045	-7.02
252912_at	ribosomal protein S25 ribosomal prote	---	AT4G39200	-1.10	-0.14	-0.78	0.459943	0.64207	-7.02
247378_at	ATP-dependent RNA helicase-like pro	---	AT5G63120	1.09	0.12	0.78	0.459878	0.64207	-7.02
251731_at	manganese superoxide dismutase-like	---	AT3G56350	-1.08	-0.11	-0.78	0.459946	0.64207	-7.02
255182_at	hypothetical protein	---	---	1.06	0.08	0.78	0.459966	0.64207	-7.02
254941_s_	putative protein various reverse transc	---	---	1.07	0.10	0.78	0.459976	0.64207	-7.02
267120_at	hypothetical protein predicted by gene	---	AT2G23530	-1.08	-0.11	-0.78	0.460048	0.64213	-7.02
256041_at	unknown protein	---	AT1G07230	1.08	0.12	0.78	0.460166	0.642143	-7.02

245758_at	unknown protein contains similarity to	KAN2	AT1G32240	1.10	0.14	0.78	0.460161	0.642143	-7.02
263685_at	unknown protein similar to cell differen	ATCUL3	AT1G26830	1.05	0.07	0.78	0.460198	0.642143	-7.02
266901_at	hypothetical protein predicted by gens	JAZ7	AT2G34600	-1.21	-0.27	-0.78	0.46018	0.642143	-7.02
259308_at	putative nodulin similar to nodulin GB:A	---	AT3G05180	-1.12	-0.16	-0.78	0.46016	0.642143	-7.02
255760_at	vacuolar-type H+-translocating inorga	---	AT1G16780	-1.07	-0.09	-0.78	0.460338	0.642181	-7.02
266980_at	60S ribosomal protein L35 ;supported	---	AT2G39390	1.12	0.17	0.78	0.460314	0.642181	-7.02
250779_at	eukaryotic translation initiation factor 2	EIF2 ALPHA	AT5G05470	1.10	0.14	0.78	0.460336	0.642181	-7.02
263926_at	hypothetical protein predicted by gens	ATEME1A	AT2G21800	1.07	0.10	0.78	0.4603	0.642181	-7.02
265350_at	unknown protein predicted by genscan	---	AT2G22620	-1.06	-0.09	-0.78	0.460379	0.642199	-7.02
266625_at	putative peroxidase	---	AT2G35380	1.07	0.09	0.78	0.460475	0.642255	-7.02
258840_at	unknown protein similar to unknown pr	---	AT3G04620	-1.05	-0.07	-0.78	0.46046	0.642255	-7.02
266086_at	putative Na+-dependent inorganic pho	PHT4;2	AT2G38060	-1.07	-0.09	-0.78	0.460565	0.642302	-7.02
259532_at	hypothetical protein	---	AT1G12470	-1.05	-0.07	-0.78	0.460539	0.642302	-7.02
257822_at	rotamase FKBP (ROF1) identical to ro	ROF1	AT3G25230	1.17	0.23	0.78	0.460602	0.642314	-7.02
257278_at	hypothetical protein predicted by gene	---	AT3G14480	-1.09	-0.12	-0.78	0.460637	0.642323	-7.02
254798_at	oleoyl-[acyl-carrier-protein] hydrolase-	---	AT4G13050	-1.12	-0.16	-0.78	0.460678	0.642342	-7.02
246375_at	light repressible receptor protein kinas	---	AT1G51830	-1.09	-0.13	-0.78	0.460831	0.642476	-7.02
249571_at	putative protein predicted proteins, Ar	---	AT5G37620	-1.06	-0.08	-0.78	0.460803	0.642476	-7.02
254732_at	hypothetical protein	---	AT4G13750	1.10	0.13	0.78	0.460934	0.64258	-7.02
265588_at	putative pathogenesis-related protein	---	AT2G19970	1.26	0.34	0.78	0.461058	0.642714	-7.02
255581_at	putative transposon protein similar to	---	---	1.08	0.11	0.78	0.461193	0.642863	-7.02
250744_at	putative protein strong similarity to unk	---	AT5G05840	-1.08	-0.11	-0.78	0.461241	0.642875	-7.02
252836_at	putative protein predicted polyproteins	---	---	1.06	0.08	0.78	0.461258	0.642875	-7.02
257260_at	hypothetical protein predicted by gene	---	AT3G22104	-1.09	-0.13	-0.78	0.461379	0.643004	-7.02
259368_at	aspartic protease, putative similar to a	---	AT1G69100	-1.06	-0.08	-0.78	0.461508	0.643106	-7.02
259383_at	putative lectin contains Pfam profile: F	JR1	AT3G16470	1.34	0.42	0.78	0.461487	0.643106	-7.02
253287_at	putative protein dJ69E11.3, Homo sap	---	AT4G34270	-1.05	-0.08	-0.78	0.46169	0.643319	-7.02
245079_at	putative retroelement pol polyprotein	---	---	-1.05	-0.08	-0.78	0.461893	0.643476	-7.02
250707_at	putative protein similar to unknown pro	MEE60	AT5G05950	-1.09	-0.13	-0.78	0.461905	0.643476	-7.02
246399_at	bZIP transcription factor similar to bZIP	---	AT1G58110	1.07	0.10	0.78	0.461915	0.643476	-7.02
248670_at	receptor protein kinase-like protein	---	AT5G48740	-1.08	-0.11	-0.78	0.461856	0.643476	-7.02
258447_at	hypothetical protein predicted by gene	---	AT3G22450	-1.06	-0.08	-0.78	0.462178	0.643779	-7.02
256011_at	respiratory burst oxidase protein, puta	---	AT1G19230	1.06	0.09	0.78	0.462188	0.643779	-7.02
252934_at	Inositol monophosphatase - like prote	IMPL2	AT4G39120	-1.09	-0.12	-0.78	0.462341	0.643874	-7.02
262128_at	late embryogenesis-abundant protein,	---	AT1G52690	-1.47	-0.56	-0.78	0.462296	0.643874	-7.02

266124_at	putative PREG1-like negative regulato	cycp3;1	AT2G45080	-1.07	-0.10	-0.78	0.462329	0.643874	-7.02
258715_at	putative 60S ribosomal protein L1 stro	---	AT3G09630	-1.09	-0.13	-0.78	0.462377	0.643884	-7.02
266675_s_	hypothetical protein predicted by gens	---	AT2G29610 /	1.05	0.07	0.78	0.462584	0.644133	-7.02
247335_at	RNA helicase	---	AT5G63630	1.07	0.09	0.78	0.463043	0.644732	-7.02
250454_at	unknown protein ; supported by full-le	---	AT5G09830	1.05	0.07	0.78	0.463309	0.644954	-7.02
261678_at	disease resistance protein, putative si	---	AT1G47370	-1.07	-0.10	-0.78	0.463328	0.644954	-7.02
247656_at	actin depolymerizing factor 4 - like pro	ADF4	AT5G59890	-1.08	-0.11	-0.78	0.463315	0.644954	-7.02
245135_at	putative non-LTR retroelement reverse	---	---	1.07	0.10	0.78	0.463343	0.644954	-7.02
255205_at	putative transposon protein	---	---	-1.05	-0.07	-0.78	0.463236	0.644954	-7.02
259153_at	unknown protein ;supported by full-ler	---	AT3G10250	1.07	0.10	0.78	0.463443	0.645053	-7.02
258804_at	hypothetical protein similar to hypothet	---	AT3G04760	1.09	0.12	0.78	0.463596	0.645187	-7.02
263244_at	hypothetical protein predicted by gens	---	AT2G31480	1.07	0.09	0.78	0.463575	0.645187	-7.02
253006_at	putative amino acid transport protein a	---	AT4G38250	1.07	0.10	0.78	0.463642	0.645213	-7.02
265866_at	unknown protein ;supported by full-ler	---	AT2G01710	-1.07	-0.10	-0.78	0.463682	0.645228	-7.02
258547_at	unknown protein	---	AT3G06895	-1.05	-0.07	-0.78	0.463846	0.645378	-7.02
260588_at	unknown protein contains similarity to	AtTLP7	AT1G53320	-1.08	-0.11	-0.78	0.463825	0.645378	-7.02
263290_at	unknown protein	---	AT2G10930	-1.05	-0.07	-0.78	0.46388	0.645386	-7.02
251271_at	hypothetical protein ; supported by full-	---	AT3G62050	-1.09	-0.12	-0.78	0.463975	0.645479	-7.02
262712_at	mercaptopyruvate sulfurtransferase (M	ATRDH2	AT1G16460	1.07	0.10	0.78	0.464204	0.645758	-7.02
264072_at	hypothetical protein	---	---	1.06	0.08	0.78	0.464409	0.646003	-7.03
246707_at	putative protein	---	---	-1.06	-0.09	-0.78	0.464437	0.646003	-7.03
250594_at	putative protein contains similarity to u	---	AT5G07760	1.07	0.09	0.78	0.464498	0.646048	-7.03
258848_at	Expressed protein ; supported by full-l	DCL2	AT3G03300 /	-1.06	-0.09	-0.78	0.464681	0.646264	-7.03
251844_at	putative protein retinoblastoma-assoc	---	AT3G54630	1.07	0.10	0.77	0.464746	0.646315	-7.03
249761_at	acetyl-CoA:benzylalcohol acetyltranfer	---	AT5G23970	-1.08	-0.11	-0.77	0.464822	0.646381	-7.03
248211_at	flavonol 3-O-glucosyltransferase-like p	---	AT5G54010	1.05	0.07	0.77	0.465163	0.646815	-7.03
248329_at	putative protein similar to unknown pro	---	AT5G52780	-1.09	-0.13	-0.77	0.465215	0.646849	-7.03
260134_at	Myb-related transcription factor, putati	MYB113	AT1G66370	-1.08	-0.11	-0.77	0.465258	0.646869	-7.03
263356_at	putative RNA-binding protein ; suppor	UBA1A	AT2G22090	1.05	0.08	0.77	0.465348	0.646955	-7.03
264251_at	hypothetical protein identical to GB:AA	---	AT1G09190	-1.09	-0.12	-0.77	0.465409	0.647001	-7.03
248884_at	putative protein similar to unknown pro	---	AT5G46030	1.05	0.07	0.77	0.465627	0.647223	-7.03
249401_at	putative protein LIM7, Lily, EMBL:LLO	---	AT5G40260	1.05	0.08	0.77	0.465711	0.647223	-7.03
255202_at	putative polyprotein	---	---	-1.06	-0.08	-0.77	0.465673	0.647223	-7.03
248953_at	serine/threonine-protein kinase Mak (n	---	AT5G45428 /	1.06	0.08	0.77	0.465684	0.647223	-7.03
253712_at	putative protein putative NADH oxidor	DER1	AT4G29330	-1.07	-0.09	-0.77	0.465655	0.647223	-7.03

264749_at	hypothetical protein Contains similarity	---	AT1G22830	1.11	0.15	0.77	0.466015	0.647592	-7.03
266508_at	hypothetical protein predicted by gene	---	AT2G47920	-1.08	-0.11	-0.77	0.466034	0.647592	-7.03
261974_at	protein kinase, putative similar to mito	CPuORF57	AT1G64628 /	1.06	0.09	0.77	0.466161	0.64773	-7.03
250716_at	sucrose transporter protein	ATSUC9	AT5G06170	1.06	0.08	0.77	0.466343	0.647943	-7.03
250688_at	transcription factor-like protein ;suppo	NF-YA10	AT5G06510	-1.06	-0.08	-0.77	0.466427	0.647961	-7.03
263913_at	putative receptor-like protein kinase	---	AT2G36570	-1.11	-0.15	-0.77	0.466441	0.647961	-7.03
257166_at	hypothetical protein similar to putative	---	AT3G24710	1.06	0.09	0.77	0.466421	0.647961	-7.03
245802_at	hypothetical protein similar to hypothet	---	AT1G46840	-1.05	-0.07	-0.77	0.466558	0.648084	-7.03
261091_at	protein kinase, putative contains Pfam	---	AT1G07550	-1.06	-0.09	-0.77	0.466614	0.648122	-7.03
263752_at	putative retroelement pol polyprotein	---	---	-1.08	-0.11	-0.77	0.46669	0.648188	-7.03
248428_at	protein phosphatase-2C; PP2C-like pr	AHG1	AT5G51760	-1.06	-0.08	-0.77	0.466805	0.648269	-7.03
260658_at	hypothetical protein predicted by gene	---	AT1G19410	1.07	0.10	0.77	0.466804	0.648269	-7.03
251354_at	putative protein hypothetical protein T	---	AT3G61090	1.05	0.08	0.77	0.46693	0.648403	-7.03
245590_at	hypothetical protein	---	AT4G15060	1.06	0.08	0.77	0.466998	0.648419	-7.03
259459_at	En/Spm-like transposon protein, putat	---	---	1.06	0.08	0.77	0.466975	0.648419	-7.03
257350_x_	hypothetical protein predicted by gens	RALFL12	AT2G19040	1.06	0.09	0.77	0.467054	0.648458	-7.03
259031_at	putative transcription factor similar to g	---	AT3G09360	1.09	0.12	0.77	0.467161	0.648527	-7.03
262688_at	PPR-repeat protein contains multiple P	---	AT1G62680	-1.06	-0.08	-0.77	0.467155	0.648527	-7.03
252157_at	hypothetical protein	---	AT3G50430	-1.06	-0.09	-0.77	0.467217	0.648564	-7.03
257056_at	unknown protein similar to hypothetica	---	AT3G15350	-1.07	-0.09	-0.77	0.467296	0.648619	-7.03
255062_at	hypothetical protein	---	AT4G08940	-1.08	-0.11	-0.77	0.467313	0.648619	-7.03
265700_at	putative MYB family transcription facto	---	AT2G03470	1.05	0.07	0.77	0.467411	0.648715	-7.03
254896_at	MADS-box protein AGL14	AGL14	AT4G11880	-1.06	-0.08	-0.77	0.467485	0.648779	-7.03
248418_at	cleavage and polyadenylation specifici	CPSF160	AT5G51660	1.07	0.09	0.77	0.467624	0.648856	-7.03
245127_at	putative Na+/Ca2+ antiporter ; suppor	ATMHX	AT2G47600	1.12	0.16	0.77	0.467627	0.648856	-7.03
253646_at	MAP kinase kinase 2 ; supported by c	ATMKK2	AT4G29810	1.11	0.15	0.77	0.467654	0.648856	-7.03
256474_at	unknown protein	---	---	-1.08	-0.11	-0.77	0.467623	0.648856	-7.03
245540_at	ABC transporter like protein	PDR2	AT4G15230	-1.21	-0.28	-0.77	0.467712	0.648891	-7.03
266902_at	hypothetical protein predicted by gens	---	AT2G34580	1.05	0.08	0.77	0.467736	0.648891	-7.03
263101_s_	hypothetical protein predicted by gens	---	AT2G05230 /	-1.06	-0.09	-0.77	0.467863	0.648998	-7.03
252628_at	putative protein	---	AT3G44960	-1.05	-0.07	-0.77	0.46787	0.648998	-7.03
262638_at	oxidoreductase, putative contains Pfa	---	AT1G06650	1.06	0.08	0.77	0.467916	0.649021	-7.03
258444_at	expressed protein supported by cDNA	TIC	AT3G22380	1.06	0.09	0.77	0.46798	0.649071	-7.03
252869_at	putative protein	---	AT4G39930	-1.06	-0.09	-0.77	0.46817	0.649256	-7.03
255986_x_	putative protein predicted proteins, Ar	---	---	1.05	0.07	0.77	0.468145	0.649256	-7.03

254245_at	serine/threonine kinase - like protein s	---	AT4G23240	1.06	0.08	0.77	0.46834	0.649451	-7.03
249829_at	c-myc binding protein MM-1-like protei	PDF5	AT5G23290	-1.06	-0.09	-0.77	0.468459	0.649578	-7.03
246641_s_	Expressed protein ; supported by full-l	---	AT5G34883 /	1.06	0.09	0.77	0.468489	0.649579	-7.03
262152_s_	hypothetical protein predicted by gene	---	AT1G52430 /	1.06	0.08	0.77	0.468618	0.649718	-7.03
257479_at	hypothetical protein contains similarity	WAKL4	AT1G16150	1.11	0.14	0.77	0.468645	0.649718	-7.03
245117_at	putative Ca2+-ATPase ; supported by	ACA4	AT2G41560	-1.09	-0.13	-0.77	0.468696	0.649726	-7.03
259079_at	unknown protein	---	AT3G04950	-1.09	-0.12	-0.77	0.46872	0.649726	-7.03
258842_at	unknown protein similar to putative AT	CLPS3	AT3G04680	1.08	0.12	0.77	0.468776	0.649726	-7.03
248810_at	disease resistance protein-like	ADR1-L3	AT5G47280	1.05	0.08	0.77	0.468759	0.649726	-7.03
247051_at	At14a protein-like	---	AT5G66670	-1.07	-0.10	-0.77	0.468794	0.649726	-7.03
245726_at	homeobox protein, putative similar to	HDG11	AT1G73360	-1.06	-0.08	-0.77	0.468932	0.649877	-7.03
258325_at	putative heat shock protein similar to p	HSFA6B	AT3G22830	-1.06	-0.09	-0.77	0.468982	0.649907	-7.03
264714_at	receptor-like protein kinase, putative s	---	AT1G69990	1.07	0.10	0.77	0.469022	0.649922	-7.03
267441_at	putative receptor-like protein kinase	---	AT2G19210	1.05	0.08	0.77	0.46905	0.649922	-7.03
250082_at	polygalacturonase-like protein	---	AT5G17200	1.08	0.11	0.77	0.469157	0.649961	-7.03
249261_at	putative protein similar to unknown pro	---	---	1.08	0.12	0.77	0.469163	0.649961	-7.03
265358_at	putative HesB-like protein ; supported	---	AT2G16710	-1.09	-0.12	-0.77	0.469131	0.649961	-7.03
262155_at	glycosyl transferase, putative similar t	---	AT1G52420	-1.07	-0.10	-0.77	0.469258	0.650014	-7.03
265275_at	En/Spm-like transposon protein relate	---	AT2G28440	-1.11	-0.16	-0.77	0.469258	0.650014	-7.03
252121_at	GDP-D-mannose-4,6-dehydratase (M	MUR1	AT3G51160	1.13	0.18	0.77	0.469295	0.650026	-7.03
248480_at	ATP-dependent Clp protease ATP-bin	CLPC1	AT5G50920	1.06	0.08	0.77	0.469541	0.650327	-7.03
256710_at	hypothetical protein predicted by gene	---	AT3G30350	-1.11	-0.15	-0.77	0.469678	0.650464	-7.03
257465_at	hypothetical protein predicted by gens	---	AT1G13040	-1.05	-0.07	-0.77	0.469697	0.650464	-7.03
251704_at	putative protein unknown protein 110k	---	AT3G56360	-1.16	-0.22	-0.77	0.469736	0.650479	-7.03
256315_at	hypothetical protein predicted by gene	---	AT1G35880	1.06	0.08	0.77	0.469778	0.650496	-7.03
251148_at	hypothetical protein	TKL	AT3G63180	-1.06	-0.09	-0.77	0.470181	0.651016	-7.03
258781_at	hypothetical protein predicted by gens	---	AT3G11740	-1.05	-0.07	-0.77	0.470234	0.651049	-7.03
260466_at	phosphatidylinositol-4-phosphate 5-kin	---	AT1G10900	-1.14	-0.19	-0.76	0.470359	0.651183	-7.03
261901_at	J8-like protein similar to DnaJ homolog	J8	AT1G80920	1.07	0.09	0.76	0.470504	0.651344	-7.03
263547_at	hypothetical protein predicted by gene	---	AT2G21680	-1.07	-0.10	-0.76	0.470653	0.65151	-7.03
264647_at	putative respiratory burst oxidase prote	ATRBOHB	AT1G09090	-1.07	-0.10	-0.76	0.47075	0.651564	-7.03
261441_at	NAM protein, putative similar to NAM	ANAC010	AT1G28470	-1.11	-0.15	-0.76	0.470762	0.651564	-7.03
258058_at	unknown protein	---	AT3G28980	1.06	0.09	0.76	0.470777	0.651564	-7.03
249255_at	Na+/H+ antiporter-like protein	CHX18	AT5G41610	1.07	0.10	0.76	0.47081	0.651569	-7.03
254127_at	NADPH-ferrihemoprotein reductase A	ATR1	AT4G24520	1.08	0.10	0.76	0.470974	0.651757	-7.03

256912_at	hypothetical protein predicted by gene	---	AT3G23850	-1.06	-0.09	-0.76	0.471045	0.651777	-7.03
254895_at	hypothetical protein	---	AT4G11870	1.08	0.11	0.76	0.471032	0.651777	-7.03
253488_at	putative protein reproductive meristem	REM1	AT4G31610	1.08	0.11	0.76	0.471227	0.651988	-7.03
262644_at	beta-VPE nearly identical to beta-VPE	BETA-VPE	AT1G62710	-1.07	-0.09	-0.76	0.47126	0.651995	-7.04
246118_at	beta-1,3-glucanase bg5	BG5	AT5G20340	-1.07	-0.10	-0.76	0.471338	0.65201	-7.04
251129_at	putative protein predicted protein, Ara	---	AT5G01150	1.06	0.09	0.76	0.471385	0.65201	-7.04
263646_at	Ac-like transposase related to Ac/Ds tr	---	---	-1.05	-0.07	-0.76	0.471327	0.65201	-7.04
263278_at	dynamin-like protein	DRP3B	AT2G14120	1.07	0.10	0.76	0.471362	0.65201	-7.04
257752_at	hypothetical protein predicted by gens	---	AT3G18720	-1.07	-0.09	-0.76	0.471425	0.652025	-7.04
265468_at	hypothetical protein predicted by gene	---	AT2G37210	-1.06	-0.09	-0.76	0.471489	0.652075	-7.04
247384_at	protein kinase ; supported by cDNA: g	---	AT5G63370	-1.11	-0.15	-0.76	0.471622	0.652215	-7.04
248412_at	putative protein contains similarity to D	---	AT5G51590	1.07	0.09	0.76	0.471648	0.652215	-7.04
266918_at	putative LIM-domain protein	---	AT2G45800	1.05	0.08	0.76	0.471731	0.65229	-7.04
260326_at	putative MYB family transcription facto	AtMYB103	AT1G63910	1.07	0.10	0.76	0.471765	0.652298	-7.04
250068_at	CHP-rich zinc finger protein-like	---	AT5G17960	-1.08	-0.11	-0.76	0.471803	0.652311	-7.04
260811_s_	hypothetical protein predicted by gene	---	---	-1.05	-0.07	-0.76	0.471865	0.652357	-7.04
251391_at	putative protein weak homology with p	---	AT3G60910	1.08	0.10	0.76	0.471939	0.652421	-7.04
265473_at	Expressed protein ; supported by full-l	LCR10	AT2G15535	-1.06	-0.09	-0.76	0.471987	0.652447	-7.04
263408_at	predicted protein	---	AT2G04060	-1.06	-0.08	-0.76	0.472091	0.652552	-7.04
253660_at	putative protein proline-rich protein AF	---	AT4G30140	-1.06	-0.08	-0.76	0.472165	0.652614	-7.04
252522_at	hypothetical protein	---	AT1G32337 /	1.06	0.08	0.76	0.472295	0.652753	-7.04
253845_at	putative protein myosin heavy chain c	---	AT4G27980	-1.05	-0.07	-0.76	0.472392	0.652785	-7.04
262095_at	hypothetical protein predicted by gene	---	AT1G56090	-1.09	-0.12	-0.76	0.472404	0.652785	-7.04
258891_at	unknown protein	EMB2016	AT3G05680	-1.06	-0.08	-0.76	0.472377	0.652785	-7.04
266565_at	putative serine carboxypeptidase II	scpl23	AT2G24010	-1.07	-0.10	-0.76	0.472599	0.653016	-7.04
251812_at	hypothetical protein ;supported by full-	---	AT3G54970	-1.09	-0.12	-0.76	0.472637	0.653029	-7.04
256484_at	PPR-repeat protein contains multiple P	---	AT1G31430	1.07	0.10	0.76	0.472695	0.653045	-7.04
266203_at	putative phloem-specific lectin	AtPP2-B1	AT2G02230	-1.17	-0.22	-0.76	0.472706	0.653045	-7.04
252581_at	hypothetical protein	---	AT3G45500	-1.07	-0.10	-0.76	0.472866	0.653226	-7.04
265307_at	hypothetical protein predicted by gens	RIN13	AT2G20310	1.07	0.10	0.76	0.472972	0.653316	-7.04
263967_at	En/Spm-like transposon protein	---	---	1.06	0.08	0.76	0.472988	0.653316	-7.04
257549_at	hypothetical protein predicted by gene	agl103	AT3G18650	1.08	0.11	0.76	0.473086	0.653411	-7.04
248055_at	serine/threonine-specific kinase like pr	---	AT5G55830	-1.06	-0.09	-0.76	0.473141	0.653447	-7.04
247276_at	putative protein contains similarity to R	HEN4	AT5G64390	1.11	0.15	0.76	0.473216	0.653512	-7.04
252557_at	putative protein cim1 induced allergen	ATEXLA3	AT3G45960	-1.06	-0.08	-0.76	0.473296	0.653555	-7.04

251012_at	putative protein ;supported by full-leng	---	AT5G02580	-1.38	-0.46	-0.76	0.473304	0.653555	-7.04
266344_at	hypothetical protein predicted by gens	---	AT2G01580	-1.06	-0.08	-0.76	0.473398	0.653565	-7.04
265874_at	hypothetical protein predicted by gene	---	AT2G01640	-1.07	-0.10	-0.76	0.473382	0.653565	-7.04
255204_at	putative myosin-like protein	---	---	1.08	0.12	0.76	0.473348	0.653565	-7.04
257394_at	hypothetical protein predicted by gens	---	---	-1.07	-0.10	-0.76	0.473486	0.653647	-7.04
250166_at	putative protein many predicted protei	---	AT5G15300	1.06	0.08	0.76	0.47353	0.653669	-7.04
262431_at	trypsin inhibitor 2, putative similar to tr	---	AT1G47540	1.06	0.08	0.76	0.473645	0.653717	-7.04
266687_at	putative arginine N-methyltransferase	PRMT1A	AT2G19670	-1.12	-0.16	-0.76	0.473626	0.653717	-7.04
263818_at	putative retroelement pol polyprotein a	---	---	-1.05	-0.07	-0.76	0.473651	0.653717	-7.04
264167_at	unknown protein Location of EST gb|N	---	AT1G02060	1.09	0.12	0.76	0.473691	0.653733	-7.04
252273_at	putative WD-40 repeat - protein beta-t	---	AT3G49660	-1.07	-0.09	-0.76	0.473738	0.653758	-7.04
245622_at	A6 anther-specific protein	MEE48	AT4G14080	-1.07	-0.09	-0.76	0.473816	0.653826	-7.04
246558_at	putative protein IDN3-B - Homo sapie	EMB2773	AT5G15540	1.07	0.10	0.76	0.473863	0.653851	-7.04
256632_at	hypothetical protein	---	AT3G28330	1.07	0.10	0.76	0.473903	0.653867	-7.04
256557_at	hypothetical protein similar to hypothet	---	---	1.06	0.08	0.76	0.473971	0.653921	-7.04
263362_at	putative selenium-binding protein	---	AT2G03880	-1.05	-0.07	-0.76	0.474072	0.65402	-7.04
260127_at	hypothetical protein similar to hypothe	---	AT1G36320	-1.09	-0.12	-0.76	0.474118	0.654045	-7.04
247350_at	unknown protein	---	AT5G63830	1.07	0.09	0.76	0.474168	0.654074	-7.04
249737_at	putative protein similar to unknown pro	---	AT5G24480	1.07	0.09	0.76	0.474238	0.654131	-7.04
262343_at	phosphoprotein phosphatase 1 identic	TOPP3	AT1G64040	1.06	0.08	0.76	0.474374	0.65421	-7.04
258280_at	putative self-incompatibility protein sin	---	AT3G26880	1.05	0.07	0.76	0.474367	0.65421	-7.04
252432_at	hypothetical protein	---	AT3G47675 /	1.05	0.07	0.76	0.474381	0.65421	-7.04
262033_at	terminal ear1, putative similar to termi	MCT1	AT1G37140	1.07	0.09	0.76	0.47447	0.654254	-7.04
248892_at	unknown protein	---	AT5G46300	1.05	0.08	0.76	0.474454	0.654254	-7.04
261462_at	hypothetical protein predicted by gens	---	AT1G07850	-1.07	-0.10	-0.76	0.474573	0.654284	-7.04
263580_at	hypothetical protein similar to hypothet	---	AT2G17140	1.07	0.09	0.76	0.474524	0.654284	-7.04
258422_at	hypothetical protein predicted by gens	---	AT3G16710	1.06	0.08	0.76	0.474578	0.654284	-7.04
253993_at	mitogen activated protein kinase kinas	MEK1	AT4G26070	1.12	0.16	0.76	0.474883	0.654663	-7.04
251635_at	endo-polygalacturonase	ADPG1	AT3G57510	1.08	0.11	0.76	0.474912	0.654663	-7.04
263346_at	En/Spm-like transposon protein relate	---	---	1.06	0.08	0.76	0.474939	0.654663	-7.04
245741_at	hypothetical protein similar to unknowr	---	AT1G44120	-1.06	-0.09	-0.76	0.475	0.654707	-7.04
249321_at	disease resistance protein-like	---	AT5G40920	1.09	0.12	0.76	0.475064	0.654756	-7.04
251508_at	putative protein mitochondrial RNA sp	---	AT3G58970	1.08	0.11	0.76	0.475162	0.654811	-7.04
260213_at	putative protein kinase similar to protei	---	AT1G74490	-1.05	-0.07	-0.76	0.475146	0.654811	-7.04
249934_at	peroxidase ATP14a homolog	---	AT5G22410	1.05	0.07	0.76	0.475228	0.654863	-7.04

257461_at	hypothetical protein predicted by gens	ATPUP15	AT1G75470	1.05	0.07	0.76	0.475345	0.654985	-7.04
253293_at	Expressed protein ; supported by cDN	---	AT4G33905	-1.10	-0.14	-0.76	0.475442	0.655079	-7.04
258190_at	hypothetical protein predicted by gene	---	AT3G29080	-1.06	-0.08	-0.76	0.475546	0.655183	-7.04
251940_at	putative protein lysine decarboxylase	---	AT3G53450	1.06	0.08	0.76	0.475671	0.655277	-7.04
248791_at	palmitoyl-protein thioesterase precurs	---	AT5G47350	1.05	0.07	0.76	0.475672	0.655277	-7.04
256142_at	hypothetical protein predicted by gene	---	AT1G48790	-1.07	-0.09	-0.76	0.475792	0.65537	-7.04
262864_at	anthocyanidin-3-glucoside rhamnosylt	---	AT1G64920	-1.07	-0.09	-0.76	0.475797	0.65537	-7.04
264457_at	puative glucosyl transferase similar to	---	AT1G10400	-1.06	-0.09	-0.75	0.475868	0.655428	-7.04
245308_at	putative protein ; supported by cDNA:	---	AT4G17486	-1.05	-0.07	-0.75	0.475927	0.65547	-7.04
253836_at	putative protein hypothetical protein F	---	AT4G27840	-1.06	-0.09	-0.75	0.475988	0.655515	-7.04
257590_s_	hypothetical protein predicted by gens	---	AT3G24870 /	1.08	0.11	0.75	0.476343	0.655964	-7.04
251357_at	ribosomal protein S27 ; supported by	ARS27A	AT3G61110	-1.12	-0.16	-0.75	0.476545	0.656203	-7.04
246867_at	putative protein various predicted prot	---	AT5G25990	-1.05	-0.07	-0.75	0.476831	0.656517	-7.04
262359_at	disease resistance protein, putative si	---	AT1G73060 /	1.06	0.09	0.75	0.476827	0.656517	-7.04
255673_at	Similar to receptor-like protein kinase	RLK4	AT4G00340	1.06	0.08	0.75	0.476948	0.656599	-7.04
260778_at	splicing factor, putative similar to hum	---	AT1G14640	-1.08	-0.11	-0.75	0.476929	0.656599	-7.04
252424_at	putative protein activating signal coint	---	AT3G47610	1.08	0.11	0.75	0.477143	0.656787	-7.04
255369_at	putative NifU-like metallocluster assem	ISU3	AT4G04080	-1.07	-0.09	-0.75	0.477174	0.656787	-7.04
256313_s_	RNA-binding protein, putative contain	APUM17	AT1G35850 /	-1.05	-0.07	-0.75	0.477137	0.656787	-7.04
248011_at	S-adenosyl-L-methionine:salicylic acid	GAMT2	AT5G56300	1.05	0.07	0.75	0.4772	0.656787	-7.04
266563_at	nodulin-like protein	---	AT2G23990	-1.06	-0.08	-0.75	0.477265	0.656831	-7.04
256721_at	hypothetical protein predicted by gene	WAVE1	AT2G34150	-1.07	-0.10	-0.75	0.47729	0.656831	-7.04
262016_at	unknown protein	---	---	-1.05	-0.07	-0.75	0.477357	0.656884	-7.04
249856_at	serine carboxypeptidase	scpl47	AT5G22980	1.10	0.13	0.75	0.477452	0.656976	-7.04
267102_at	putative small nuclear ribonucleoprote	LIS	AT2G41500	-1.07	-0.09	-0.75	0.477512	0.657018	-7.04
261145_at	thioredoxin identical to GB:CAA84610	ATTRX4	AT1G19730	-1.06	-0.09	-0.75	0.477648	0.657166	-7.04
263639_at	unknown protein	---	AT2G25300	-1.07	-0.10	-0.75	0.477778	0.657305	-7.04
256727_at	hypothetical protein	---	AT3G52240	-1.07	-0.10	-0.75	0.477835	0.657338	-7.04
265294_at	Mutator-like transposase similar to MU	---	---	-1.07	-0.10	-0.75	0.47786	0.657338	-7.04
264658_at	hypothetical protein similar to LG27/30	---	AT1G09910	-1.06	-0.09	-0.75	0.477928	0.657392	-7.04
249509_at	strong similarity to unknown protein (g	---	AT5G38390	-1.05	-0.07	-0.75	0.478043	0.657471	-7.04
253741_at	putative protein various hypothetical a	---	AT4G28890	1.05	0.07	0.75	0.478019	0.657471	-7.04
254478_at	putative protein TRANSCRIPTION IN	---	AT4G20330	1.08	0.11	0.75	0.478664	0.658286	-7.05
262586_at	hypothetical protein predicted by gens	---	AT1G15480	-1.11	-0.15	-0.75	0.47884	0.658363	-7.05
267230_at	unknown protein	ARL	AT2G44080	1.37	0.45	0.75	0.478864	0.658363	-7.05

255034_at	putative protein Phaseolus vulgaris cD	---	---	1.06	0.08	0.75	0.478834	0.658363	-7.05
246905_at	putative protein ;supported by full-leng	---	AT5G25570	1.13	0.18	0.75	0.478813	0.658363	-7.05
265882_at	putative copper amine oxidase	---	AT2G42490	-1.09	-0.13	-0.75	0.478785	0.658363	-7.05
267595_at	putative glucanse	AtGH9B8	AT2G32990	-1.50	-0.59	-0.75	0.47893	0.658374	-7.05
264877_at	putative obtusifoliol 14-alpha demethyl	CYP51G2	AT2G17330	1.05	0.07	0.75	0.478913	0.658374	-7.05
254596_at	putative protein proline-rich protein AF	---	AT4G18975	1.06	0.09	0.75	0.479113	0.658586	-7.05
255148_at	putative mitogen-activated protein kina	MAPKKK10	AT4G08470	1.16	0.21	0.75	0.479211	0.65868	-7.05
263196_at	hypothetical protein predicted by gene	---	AT1G36070	-1.10	-0.14	-0.75	0.479247	0.65869	-7.05
263917_at	putative AP2 domain transcription fact	HRD	AT2G36450	-1.09	-0.13	-0.75	0.479295	0.658716	-7.05
256602_at	unknown protein	---	AT3G28310	1.08	0.12	0.75	0.479388	0.658804	-7.05
266006_at	putative ABC transporter	---	AT2G37360	-1.08	-0.11	-0.75	0.479418	0.658806	-7.05
252842_at	putative protein hypothetical proteins -	---	---	-1.07	-0.10	-0.75	0.479654	0.659091	-7.05
267632_at	hypothetical protein predicted by gens	---	AT2G42160	-1.09	-0.13	-0.75	0.479899	0.659388	-7.05
248213_at	putative protein similar to unknown pro	AtGRF7	AT5G53660	-1.06	-0.09	-0.75	0.479979	0.659458	-7.05
258757_at	putative RING zinc finger protein cont	---	AT3G10910 /	1.11	0.15	0.75	0.48011	0.659599	-7.05
254212_at	putative protein many putative protein	---	AT4G23580	-1.06	-0.08	-0.75	0.480238	0.659734	-7.05
263498_at	unknown protein ; supported by cDNA	LSH10	AT2G42610	1.33	0.41	0.75	0.480272	0.659742	-7.05
257915_at	superman protein identical to superma	SUP	AT3G23130	-1.07	-0.10	-0.75	0.480474	0.659979	-7.05
248266_at	putative protein similar to unknown pro	---	AT5G53440	1.05	0.07	0.75	0.480665	0.660161	-7.05
262626_at	FtsH protease, putative similar to zinc	FTSH8	AT1G06430	-1.08	-0.11	-0.75	0.480637	0.660161	-7.05
247694_at	GTP cyclohydrolase II / 3,4-dihydroxy	---	AT5G59750	-1.07	-0.09	-0.75	0.48073	0.660211	-7.05
265346_at	hypothetical protein	---	---	-1.06	-0.08	-0.75	0.48105	0.660611	-7.05
257134_at	hypothetical protein similar to oxidored	---	AT3G12870	-1.07	-0.10	-0.75	0.481397	0.661048	-7.05
260185_at	hypothetical protein similar to hypothet	---	AT1G36030	1.05	0.07	0.75	0.481439	0.661066	-7.05
264346_at	putative amino-cyclopropane-carboxyli	---	AT1G12010	-1.06	-0.09	-0.74	0.481583	0.661223	-7.05
264197_at	unknown protein Similar to hypothetica	ATSAC1	AT1G22620	-1.05	-0.07	-0.74	0.481621	0.661236	-7.05
248720_at	protein kinase (EC 2.7.1.37) 5 (pir||JN	D6PKL2	AT5G47750	-1.06	-0.08	-0.74	0.482085	0.661754	-7.05
248178_at	root cap protein 2-like protein	---	AT5G54370	-1.08	-0.11	-0.74	0.482033	0.661754	-7.05
263194_at	AP2 domain transcription factor, putat	---	AT1G36060	-1.09	-0.13	-0.74	0.482085	0.661754	-7.05
247428_at	unknown protein	---	AT5G62600	1.05	0.07	0.74	0.482127	0.661769	-7.05
259813_at	glutathione S-transferase, putative sin	ATGSTF14	AT1G49860	-1.06	-0.09	-0.74	0.482212	0.661769	-7.05
258826_at	putative glucan synthase similar to glu	ATGSL10	AT3G07160	1.05	0.07	0.74	0.482201	0.661769	-7.05
263489_at	putative inositol polyphosphate 5'-phos	---	AT2G31830	1.07	0.09	0.74	0.482209	0.661769	-7.05
266428_at	putative protein kinase contains a prot	---	AT2G07180	1.08	0.11	0.74	0.482293	0.661836	-7.05
257161_at	hypothetical protein predicted by gens	SMAP2	AT3G24280	-1.05	-0.08	-0.74	0.482348	0.661836	-7.05

267643_at	hypothetical protein predicted by gene	RALFL17	AT2G32890	-1.05	-0.07	-0.74	0.482344	0.661836	-7.05
247591_at	high-affinity nitrate transporter ACH1 -	NRT2.4	AT5G60770	-1.06	-0.08	-0.74	0.482399	0.661847	-7.05
260168_at	unknown protein contains zinc finger,	---	AT1G71980	-1.08	-0.11	-0.74	0.48249	0.661847	-7.05
253940_at	putative protein other Arabidopsis hyp	---	AT4G26950	1.07	0.10	0.74	0.482415	0.661847	-7.05
253269_at	hypothetical protein	---	AT4G34140	1.06	0.08	0.74	0.482457	0.661847	-7.05
246105_at	putative protein predicted helicase pr	---	---	1.05	0.06	0.74	0.482501	0.661847	-7.05
247290_at	putative protein similar to unknown pr	---	AT5G64450	1.12	0.17	0.74	0.482568	0.661898	-7.05
250276_at	putative protein mRNA, Moritella mari	---	AT5G13030	1.06	0.09	0.74	0.482744	0.661947	-7.05
255930_at	hypothetical protein predicted by gens	---	AT1G12660	-1.06	-0.08	-0.74	0.482748	0.661947	-7.05
261600_x_	hypothetical protein similar to hypothet	---	AT1G49680 /	-1.05	-0.07	-0.74	0.482721	0.661947	-7.05
245469_at	reverse transcriptase like protein	---	---	1.05	0.07	0.74	0.482748	0.661947	-7.05
264414_s_	putative protein several hypothetical pr	---	---	-1.11	-0.15	-0.74	0.48267	0.661947	-7.05
266702_at	hexokinase (ATHXK2) ; supported by	HXK2	AT2G19860	1.06	0.08	0.74	0.482833	0.662024	-7.05
259690_at	replication factor, putative similar to G	---	AT1G63160	1.10	0.14	0.74	0.482901	0.662077	-7.05
259622_at	hypothetical protein predicted by gens	---	AT1G43010	-1.05	-0.08	-0.74	0.483042	0.66223	-7.05
244963_at	PSII cytochrome b559	---	---	1.05	0.07	0.74	0.483263	0.662493	-7.05
246358_x_	hypothetical protein	---	AT2G06570	-1.06	-0.09	-0.74	0.48354	0.662834	-7.05
255495_at	predicted protein of unknown function	---	AT4G02720	1.06	0.09	0.74	0.483694	0.663005	-7.05
263341_at	hypothetical protein predicted by gens	---	---	-1.07	-0.09	-0.74	0.483893	0.663118	-7.05
263361_at	putative senescence-associated protei	TET13	AT2G03840	-1.06	-0.09	-0.74	0.483877	0.663118	-7.05
258420_at	putative RNA polymerase similar to R	---	AT3G16680	-1.05	-0.07	-0.74	0.483872	0.663118	-7.05
257552_at	cellulase, putative contains Pfam prof	---	AT3G26130	1.05	0.07	0.74	0.483808	0.663118	-7.05
263035_at	splicing factor, putative similar to RSZ	RSZP21	AT1G23860	1.08	0.11	0.74	0.484126	0.663145	-7.05
263013_at	knotted-like homeobox protein, putativ	KNAT6	AT1G23380	1.07	0.10	0.74	0.484024	0.663145	-7.05
256689_at	hypothetical protein predicted by gene	---	AT3G32150	-1.05	-0.08	-0.74	0.484175	0.663145	-7.05
253677_at	cytidine deaminase - like protein cytid	---	AT4G29580	1.07	0.10	0.74	0.484167	0.663145	-7.05
262057_at	unknown protein ;supported by full-len	---	AT1G80040	1.06	0.08	0.74	0.484072	0.663145	-7.05
251748_at	putative protein predicted protein, Ara	---	AT3G55680	1.08	0.11	0.74	0.48408	0.663145	-7.05
254747_at	serine/threonine-specific protein kinas	MHK	AT4G13020	-1.06	-0.09	-0.74	0.484167	0.663145	-7.05
254124_at	hypothetical protein ; supported by cD	---	AT4G24500	-1.06	-0.09	-0.74	0.483951	0.663145	-7.05
265683_at	putative auxin-regulated protein	---	AT2G24400	-1.07	-0.09	-0.74	0.483997	0.663145	-7.05
245085_at	putative poly(A) binding protein ; supp	PAB4	AT2G23350	1.08	0.11	0.74	0.484254	0.663215	-7.05
256107_at	hypothetical protein predicted by gens	---	AT1G16830	1.05	0.07	0.74	0.484359	0.663217	-7.05
258844_at	hypothetical protein predicted by gens	SWP	AT3G04740	1.05	0.07	0.74	0.484401	0.663217	-7.05
249449_at	unknown protein	---	AT5G39430	1.05	0.07	0.74	0.4844	0.663217	-7.05

264159_at	unknown protein ;supported by full-len	---	AT1G65270	-1.05	-0.07	-0.74	0.484305	0.663217	-7.05
261371_at	ubiquitin-conjugating enzyme, putative	UBC26	AT1G53020	-1.05	-0.07	-0.74	0.484343	0.663217	-7.05
248270_at	putative protein similar to unknown pro	ORG1	AT5G53450	-1.14	-0.19	-0.74	0.484436	0.663225	-7.05
248515_at	putative protein strong similarity to unk	---	AT5G50530 /	-1.07	-0.10	-0.74	0.484604	0.663414	-7.05
256019_at	cytochrome P-450, putative similar to	---	AT1G58260 /	-1.06	-0.08	-0.74	0.484743	0.663566	-7.05
263407_at	bZIP protein (AtbZIP48) to be publishe	AtbZIP48	AT2G04038	1.06	0.08	0.74	0.484959	0.663783	-7.05
252005_at	purple acid phosphatase-like protein p	PAP21	AT3G52810	1.08	0.11	0.74	0.48496	0.663783	-7.05
267146_at	hypothetical protein predicted by gens	---	AT2G38160	1.06	0.08	0.74	0.485073	0.663897	-7.05
246818_at	putative protein crp1, Zea mays, PIR:	EMB976	AT5G27270	-1.13	-0.18	-0.74	0.485156	0.663932	-7.05
265973_at	putative non-LTR retroelement reverse	---	---	-1.05	-0.07	-0.74	0.485133	0.663932	-7.05
255161_at	putative reverse transcriptase	---	---	-1.06	-0.08	-0.74	0.485325	0.664123	-7.05
262254_at	unknown protein similar to GDSL-moti	GLIP5	AT1G53920	-1.13	-0.18	-0.74	0.485452	0.664257	-7.05
248734_at	putative protein similar to unknown pro	ELP1	AT5G48090	-1.08	-0.12	-0.74	0.485524	0.664315	-7.06
246601_at	copper amine oxidase, putative simila	---	AT1G31710	-1.51	-0.59	-0.74	0.485576	0.664347	-7.06
247553_at	MAD box containing protein NAP1-1 -	AGL8	AT5G60910	1.12	0.17	0.74	0.485875	0.664715	-7.06
251654_at	putative protein several hypothetical pr	SDP1-LIKE	AT3G57140	1.05	0.07	0.74	0.486032	0.664891	-7.06
254883_at	putative protein histidine-rich glycopro	HAP2	AT4G11720	-1.08	-0.11	-0.74	0.486117	0.664928	-7.06
249107_at	unknown protein	---	AT5G43680	-1.06	-0.08	-0.74	0.486104	0.664928	-7.06
246674_at	bcnt-like protein ; supported by full-len	---	AT5G30490	1.06	0.08	0.74	0.486223	0.665031	-7.06
266171_at	putative CCAAT-binding transcription f	NF-YB1	AT2G38880	1.08	0.11	0.74	0.48628	0.665031	-7.06
257106_at	unknown protein	---	AT3G29060	1.05	0.07	0.74	0.486272	0.665031	-7.06
264997_at	hypothetical protein contains similarity	HAC2	AT1G67220	-1.07	-0.10	-0.74	0.486322	0.665048	-7.06
267389_at	putative beta-glucosidase	BGLU28	AT2G44460	1.70	0.76	0.74	0.486547	0.665237	-7.06
245519_at	retrotransposon like protein	---	---	-1.05	-0.07	-0.74	0.486497	0.665237	-7.06
257354_x_	hypothetical protein predicted by gene	---	---	-1.07	-0.09	-0.74	0.486541	0.665237	-7.06
256318_s_	hypothetical protein	---	---	1.05	0.07	0.74	0.486596	0.665263	-7.06
259855_at	putative asparaginyl-tRNA synthetase	---	AT1G68420	-1.06	-0.08	-0.74	0.486798	0.6655	-7.06
253928_at	phosphoprotein phosphatase (PPX-1)	PPX1	AT4G26720	1.06	0.08	0.74	0.486946	0.665622	-7.06
263996_at	unknown protein	---	AT2G22530	-1.07	-0.10	-0.74	0.486936	0.665622	-7.06
254131_at	protein kinase (AFC2) ; supported by	AFC2	AT4G24740	1.07	0.10	0.74	0.487054	0.665723	-7.06
264935_at	hypothetical protein predicted by gene	---	AT1G61150	1.09	0.13	0.74	0.487078	0.665723	-7.06
245890_at	ribosomal protein S15-like ribosomal p	---	AT5G09490	-1.04	-0.06	-0.73	0.487227	0.665886	-7.06
257855_at	hypothetical protein predicted by gene	---	AT3G13040	-1.06	-0.08	-0.73	0.487451	0.666113	-7.06
266143_at	Expressed protein ; supported by cDN	---	AT2G38905	-1.08	-0.11	-0.73	0.487439	0.666113	-7.06
254451_at	adrenodoxin - like protein adrenodoxi	---	AT4G21090	1.05	0.07	0.73	0.487525	0.666133	-7.06

254217_at	putative protein other hypothetical pro	---	AT4G23720	1.05	0.07	0.73	0.487553	0.666133	-7.06
253805_at	putative protein	---	AT4G28260	-1.07	-0.10	-0.73	0.4875	0.666133	-7.06
256218_at	hypothetical protein predicted by gene	---	AT1G56270	1.07	0.10	0.73	0.487778	0.6664	-7.06
266665_at	unknown protein	---	AT2G29790	1.06	0.09	0.73	0.487901	0.666528	-7.06
263584_at	NAM (no apical meristem)-like protein	anac036	AT2G17040	1.20	0.27	0.73	0.488253	0.66695	-7.06
256736_at	terpene synthase, putative similar to t	---	AT3G29410	-1.06	-0.08	-0.73	0.488268	0.66695	-7.06
246928_at	putative protein Scythe protein - Xeno	---	AT5G25270	1.05	0.08	0.73	0.488484	0.667205	-7.06
256621_at	unknown protein ; supported by full-le	---	AT3G24450	1.06	0.09	0.73	0.488521	0.667216	-7.06
248979_at	putative protein contains similarity to d	AtPP2-A6	AT5G45080	-1.06	-0.09	-0.73	0.488619	0.66731	-7.06
255128_at	putative protein glutamic acid-rich pro	---	AT4G08310	-1.08	-0.11	-0.73	0.488842	0.667535	-7.06
253599_at	putative protein ash1 protein, Drosoph	SDG4	AT4G30860	-1.09	-0.13	-0.73	0.488821	0.667535	-7.06
267228_at	putative polygalacturonase	---	AT2G43890	-1.05	-0.07	-0.73	0.488918	0.667557	-7.06
261367_at	protein kinase, putative similar to man	---	AT1G53080	1.37	0.45	0.73	0.488902	0.667557	-7.06
255137_at	extensin-like protein extensin precurs	---	AT4G08370	-1.07	-0.09	-0.73	0.489079	0.667738	-7.06
256963_at	lysyl-tRNA synthetase, putative simila	OVA5	AT3G13490	-1.09	-0.12	-0.73	0.489224	0.667896	-7.06
261818_at	similar to hypethetical 62.8 KD protein	---	AT1G11390	-1.07	-0.09	-0.73	0.489322	0.667989	-7.06
265077_at	hypothetical protein similar to RING-H2	---	AT1G55530	1.09	0.12	0.73	0.489433	0.668101	-7.06
264733_at	phloem serpin-1, putative similar to ph	---	AT1G62170	1.05	0.07	0.73	0.489526	0.668188	-7.06
267636_at	hypothetical protein predicted by gens	---	AT2G42110	-1.05	-0.07	-0.73	0.489732	0.668429	-7.06
AFFX-BioC	E. coli /GEN=bioC /DB_XREF=gb:J04	---	---	1.15	0.20	0.73	0.489935	0.668667	-7.06
251256_at	putative protein hypothetical proteins -	---	AT3G62300	-1.08	-0.11	-0.73	0.489969	0.668673	-7.06
255075_at	putative protein RING-H2 zinc finger p	---	AT4G09110	-1.04	-0.06	-0.73	0.490135	0.66886	-7.06
260351_at	hypothetical protein predicated by gen	---	AT1G69380	1.13	0.18	0.73	0.490212	0.668923	-7.06
265625_at	hypothetical protein predicted by gens	---	AT2G27240	1.07	0.10	0.73	0.4905	0.669278	-7.06
247164_at	NifS-like aminotranfserase ; supporte	NFS1	AT5G65720	1.06	0.09	0.73	0.490591	0.669282	-7.06
259961_at	auxin-induced protein kinase, putative	WAG1	AT1G53700	1.07	0.09	0.73	0.490543	0.669282	-7.06
246795_at	putative protein	---	AT5G27020	1.06	0.08	0.73	0.490591	0.669282	-7.06
258426_at	hypothetical protein predicted by gene	PLDP1	AT3G16785	1.06	0.08	0.73	0.490688	0.669334	-7.06
250360_at	putative protein probable serine/threo	---	AT5G11360	-1.06	-0.08	-0.73	0.49067	0.669334	-7.06
245370_at	Expressed protein ; supported by full-l	---	AT4G16840	1.12	0.16	0.73	0.490781	0.66942	-7.06
250713_at	putative protein similar to unknown pro	---	AT5G06130	1.07	0.09	0.73	0.49092	0.669529	-7.06
264237_at	hypothetical protein predicted by gene	---	AT1G54700	-1.05	-0.07	-0.73	0.490891	0.669529	-7.06
250148_at	putative protein various predicted prot	---	AT5G14530	1.07	0.09	0.73	0.491211	0.669861	-7.06
264480_at	hypothetical protein predicted by gene	EFS	AT1G77300	1.06	0.09	0.73	0.491233	0.669861	-7.06
253821_at	extensin-like protein extensin-like prot	---	AT4G28380	1.06	0.09	0.73	0.491251	0.669861	-7.06

258770_at	hypothetical protein	---	AT3G10830	-1.05	-0.08	-0.73	0.491296	0.669883	-7.06
257449_at	hypothetical protein predicted by gens	---	AT2G31420	1.06	0.09	0.73	0.491338	0.6699	-7.06
252645_at	bZIP transcription factor -like protein [	DPBF2	AT3G44460	1.06	0.09	0.73	0.49138	0.669917	-7.06
249599_at	putative protein AtPP protein, Brassica	---	AT5G37990	-1.07	-0.09	-0.73	0.49154	0.670095	-7.06
257283_at	hypothetical protein predicted by gene	---	AT3G29750	-1.05	-0.07	-0.73	0.491624	0.670129	-7.06
258867_at	hypothetical protein predicted by gene	---	AT3G03130	-1.06	-0.08	-0.73	0.491594	0.670129	-7.06
260330_at	putative RING zinc finger protein cont	---	AT1G80400	-1.06	-0.08	-0.73	0.491674	0.670158	-7.06
255321_at	putative ES43-like protein	---	AT4G04260	-1.06	-0.09	-0.73	0.491727	0.67019	-7.06
254070_at	hypothetical protein	---	AT4G25430	-1.09	-0.12	-0.73	0.491924	0.670377	-7.06
254397_at	gibberellin 3 beta-hydroxylase - like pr	GA3OX3	AT4G21690	1.11	0.15	0.73	0.491898	0.670377	-7.06
247311_at	DNA polymerase III catalytic subunit	EMB2780	AT5G63960	1.06	0.09	0.73	0.491962	0.67039	-7.06
267571_at	3-hydroxyisobutyryl-coenzyme A hydro	---	AT2G30650	-1.05	-0.07	-0.73	0.492029	0.670441	-7.06
262040_at	receptor protein kinase, putative simila	TMM	AT1G80080	-1.06	-0.09	-0.73	0.492082	0.670472	-7.06
262164_at	unknown protein ; supported by cDNA	---	AT1G78070	1.08	0.11	0.73	0.492161	0.670501	-7.06
250475_at	sulfate transporter ; supported by cDN	SULTR2;1	AT5G10180	1.16	0.21	0.73	0.492144	0.670501	-7.06
249516_s_	myrosinase binding protein-like; simila	---	AT5G38540 /	1.06	0.09	0.73	0.492423	0.670778	-7.06
261340_at	hypothetical protein predicted by gene	APUM9	AT1G35730	-1.07	-0.10	-0.73	0.492406	0.670778	-7.06
247657_at	Expressed protein ; supported by full-le	---	AT5G59845	-1.07	-0.10	-0.73	0.492485	0.670822	-7.06
267528_at	MADS-box protein (AGL6) ; supported	AGL6	AT2G45650	1.06	0.08	0.73	0.492635	0.670987	-7.06
259960_at	cell division control protein, putative si	---	AT1G53710	1.08	0.11	0.73	0.492707	0.671005	-7.06
266827_at	putative serine carboxypeptidase I	SCPL12	AT2G22920	1.05	0.07	0.73	0.492679	0.671005	-7.06
258482_at	putative chaperonin similar to chapero	---	AT3G02530	-1.07	-0.10	-0.73	0.4928	0.671085	-7.06
246978_at	cytochrome P450-like protein fatty aci	CYP714A1	AT5G24910	1.10	0.14	0.73	0.492826	0.671085	-7.06
263940_at	putative calcium-dependent protein kin	CPK25	AT2G35890	-1.05	-0.07	-0.72	0.492919	0.671132	-7.07
256551_at	unknown protein	---	---	-1.06	-0.09	-0.72	0.492895	0.671132	-7.07
250526_at	pyruvate kinase	---	AT5G08570	-1.06	-0.08	-0.72	0.493159	0.671419	-7.07
249836_at	unknown protein ;supported by full-ler	HMGB6	AT5G23420	-1.13	-0.18	-0.72	0.493223	0.671466	-7.07
246657_at	putative protein predicted proteins, Ar	---	---	1.05	0.06	0.72	0.493317	0.671538	-7.07
250032_at	glutamate dehydrogenase (EC 1.4.1.-)	GDH1	AT5G18170	-1.20	-0.26	-0.72	0.493335	0.671538	-7.07
262285_at	hypothetical protein predicted by gene	---	AT1G68680	-1.06	-0.08	-0.72	0.493497	0.671719	-7.07
263143_at	hypothetical protein Contains PF|0063	---	AT1G03100	1.07	0.09	0.72	0.493769	0.672012	-7.07
261458_at	unknown protein contains DNA-J dom	---	AT1G21080	1.07	0.10	0.72	0.493801	0.672012	-7.07
260147_at	putative oxidoreductase similar to adv	---	AT1G52790	-1.06	-0.08	-0.72	0.493785	0.672012	-7.07
252762_at	putative protein hypothetical protein M	---	AT3G42780	-1.08	-0.11	-0.72	0.494048	0.672308	-7.07
258771_at	unknown protein ;supported by full-ler	---	AT3G10770	1.06	0.09	0.72	0.494139	0.672392	-7.07

AFFX-r2-E	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.17	0.22	0.72	0.494233	0.672435	-7.07
265560_at	putative glycine-rich protein	GRP-3	AT2G05520	1.05	0.08	0.72	0.49423	0.672435	-7.07
249848_at	putative protein similar to unknown pro	NIC3	AT5G23220	-1.06	-0.09	-0.72	0.494259	0.672435	-7.07
254719_at	putative protein beta 1,3-glucanase, T	---	AT4G13600	1.06	0.09	0.72	0.494308	0.672462	-7.07
261415_at	globulin-like protein similar to GB:7595	---	AT1G07750	1.12	0.16	0.72	0.494545	0.672681	-7.07
245639_at	unknown protein contains similarity to	---	AT1G25260	1.11	0.15	0.72	0.494499	0.672681	-7.07
251238_at	putative protein several hypothetical pr	---	AT3G62430	1.07	0.09	0.72	0.494558	0.672681	-7.07
262017_at	elongation factor, putative similar to E	---	AT1G35550	-1.09	-0.12	-0.72	0.494662	0.672743	-7.07
256048_at	hypothetical protein contains similarity	---	AT1G07025	1.05	0.08	0.72	0.494657	0.672743	-7.07
266804_at	cyclophilin identical to GB:AF020433;	CYP5	AT2G29960	1.06	0.09	0.72	0.494745	0.672815	-7.07
257184_at	ABC transporter, putative similar to At	ATMRP8	AT3G13090	-1.05	-0.07	-0.72	0.494802	0.672853	-7.07
255632_at	putative actin-depolymerizing factor ;s	ADF8	AT4G00680	-1.05	-0.07	-0.72	0.494955	0.673021	-7.07
255898_at	hypothetical protein similar to hypothet	---	AT1G17930	1.06	0.08	0.72	0.495035	0.67309	-7.07
250013_at	putative protein similar to unknown pro	---	AT5G18040	1.05	0.08	0.72	0.495164	0.673164	-7.07
252295_at	signal recognition particle subunit 9 - l	---	AT3G49100	1.08	0.12	0.72	0.495208	0.673164	-7.07
252541_at	putative protein hypothetical protein A	---	AT3G45750	-1.06	-0.08	-0.72	0.495139	0.673164	-7.07
247619_at	putative protein	---	AT5G60290	-1.08	-0.11	-0.72	0.495205	0.673164	-7.07
262468_at	alanine--tRNA ligase, putative similar	ALATS	AT1G50200	1.08	0.11	0.72	0.495268	0.673205	-7.07
245166_at	putative receptor-like protein kinase	---	AT2G33170	1.07	0.09	0.72	0.495305	0.673216	-7.07
255747_s_	hypothetical protein predicted by gene	---	AT1G32010 /	1.05	0.07	0.72	0.495497	0.673437	-7.07
246571_at	putative protein	---	AT5G15000	-1.04	-0.06	-0.72	0.495589	0.673521	-7.07
261288_at	hypothetical protein predicted by gene	---	AT1G37010	-1.06	-0.09	-0.72	0.495678	0.673602	-7.07
247490_at	LFY floral meristem identity control pro	LFY	AT5G61850	-1.05	-0.08	-0.72	0.495785	0.673708	-7.07
246489_at	14-3-3 protein GF14upsilon (grf5) iden	GRF5	AT5G16050	1.06	0.09	0.72	0.495845	0.673718	-7.07
246987_at	myb-related protein, 33.3K (pir |S712	MYBR1	AT5G67300	1.12	0.16	0.72	0.495911	0.673718	-7.07
249963_at	putative protein SPECKLE-TYPE PO	ATBPM1	AT5G19000	-1.07	-0.10	-0.72	0.495871	0.673718	-7.07
256120_at	hypothetical protein contains similarity	---	AT1G18130	1.05	0.07	0.72	0.495889	0.673718	-7.07
253159_at	HMG delta protein ;supported by full-l	HMGB5	AT4G35570	1.05	0.07	0.72	0.496313	0.674224	-7.07
250905_at	protein kinase -like protein protein kin	---	AT5G03640	-1.05	-0.07	-0.72	0.496585	0.67452	-7.07
254169_at	putative protein ; supported by cDNA:	---	AT4G24290	1.08	0.11	0.72	0.49659	0.67452	-7.07
252648_at	disease resistance protein homolog di	---	AT3G44630	1.06	0.08	0.72	0.49674	0.674684	-7.07
262912_at	oligopeptide transporter, putative simi	---	AT1G59740	-1.23	-0.30	-0.72	0.496776	0.674692	-7.07
249441_at	avirulence induced gene (AIG) - like p	---	AT5G39730	1.08	0.11	0.72	0.496863	0.674697	-7.07
257648_at	RNA helicase, putative similar to RNA	---	AT3G16840	1.11	0.15	0.72	0.496868	0.674697	-7.07
257577_at	hypothetical protein predicted by gene	---	---	1.06	0.09	0.72	0.496843	0.674697	-7.07

246401_at	DNA-binding protein, putative similar t	AtMYB50	AT1G57560	-1.10	-0.14	-0.72	0.496948	0.674766	-7.07
258968_at	hypothetical protein similar to hypothet	---	AT3G10460	-1.06	-0.08	-0.72	0.497135	0.674979	-7.07
260194_at	hypothetical protein similar to hypothet	---	AT1G67530	-1.11	-0.15	-0.72	0.497434	0.675344	-7.07
253912_at	putative protein met-10+ protein, Neu	---	AT4G27340	1.07	0.10	0.72	0.497471	0.675355	-7.07
254357_at	nifU-like protein nifU protein homolog	ISU1	AT4G22220	1.04	0.06	0.72	0.497599	0.675488	-7.07
245953_at	myrosinase - binding protein - like pro	---	AT5G28520	1.09	0.12	0.72	0.497678	0.675555	-7.07
252504_at	telomere repeat-binding protein homo	TRFL1	AT3G46590	-1.06	-0.08	-0.72	0.497725	0.675571	-7.07
246061_at	RAN GTPase activating protein 2 ; su	RANGAP2	AT5G19320	-1.04	-0.06	-0.72	0.497749	0.675571	-7.07
255612_at	hypothetical protein	---	AT4G01240	-1.08	-0.11	-0.72	0.497918	0.675738	-7.07
265046_s_	mutator-like transposase, putative sim	---	---	-1.06	-0.08	-0.72	0.497931	0.675738	-7.07
246177_at	putative protein predicted proteins - Ar	---	AT5G28420	-1.05	-0.07	-0.72	0.498052	0.675862	-7.07
257847_at	hypothetical protein predicted by gene	---	AT3G13020	1.06	0.08	0.72	0.498175	0.675948	-7.07
250078_at	putative protein	ORC3	AT5G16690	-1.07	-0.09	-0.72	0.498156	0.675948	-7.07
254546_at	lectin like protein lectin 2, phloem-spe	PP2-A2	AT4G19850	1.17	0.23	0.72	0.498343	0.675976	-7.07
258402_at	unknown protein very similar to unknov	---	AT3G15450	-1.15	-0.20	-0.72	0.498264	0.675976	-7.07
261998_at	putative gag-pol polyprotein similar to	---	---	1.06	0.08	0.72	0.498316	0.675976	-7.07
249884_at	Na+/H+ antiporter-like protein	CHX9	AT5G22910	-1.06	-0.09	-0.72	0.498294	0.675976	-7.07
260612_at	hypothetical protein similar to hypothet	---	AT1G53360	-1.05	-0.07	-0.72	0.498249	0.675976	-7.07
249629_at	kinesin -like protein Krm protein, L.jap	---	AT5G37590	1.08	0.12	0.72	0.498507	0.676158	-7.07
256072_at	WD-40 repeat protein identical to WD-	ATARCA	AT1G18080	-1.13	-0.17	-0.72	0.498623	0.676234	-7.07
257531_at	putative RNA-binding protein contains	---	AT3G07250	-1.05	-0.07	-0.72	0.498605	0.676234	-7.07
253497_at	putative protein microtubule-associate	---	AT4G31880	1.07	0.09	0.71	0.498682	0.676275	-7.07
262718_at	hypothetical protein similar to putative	---	---	1.06	0.08	0.71	0.498848	0.676459	-7.07
252747_at	putative protein retrotransposon finge	---	---	1.07	0.09	0.71	0.498993	0.676525	-7.07
260061_at	cell division protein kinase similar to ce	CDKD1;1	AT1G73690	-1.09	-0.12	-0.71	0.498996	0.676525	-7.07
250754_at	arginine-tRNA-protein transferase 1 ho	ATE1	AT5G05700	-1.05	-0.08	-0.71	0.499044	0.676525	-7.07
248641_at	unknown protein	---	AT5G49110	1.06	0.08	0.71	0.499014	0.676525	-7.07
245523_at	drought-induced protein like	ATDI21	AT4G15910	1.08	0.12	0.71	0.499025	0.676525	-7.07
260965_s_	hypothetical protein predicted by gene	---	---	1.05	0.07	0.71	0.499169	0.676573	-7.07
247683_at	serine/threonine-specific protein kinas	---	AT5G59660	1.07	0.10	0.71	0.49914	0.676573	-7.07
261360_at	hypothetical protein predicted by gens	---	---	1.06	0.09	0.71	0.499163	0.676573	-7.07
254570_s_	puatative protein various predicted pr	---	AT4G19250 /	-1.06	-0.09	-0.71	0.4993	0.676711	-7.07
257770_at	unknown protein ;supported by full-ler	LFR	AT3G22990	1.06	0.09	0.71	0.499453	0.67685	-7.07
259680_at	putative AUX1-like permease similar t	LAX3	AT1G77690	-1.29	-0.37	-0.71	0.499462	0.67685	-7.07
260946_at	hypothetical protein predicted by gene	---	AT1G06010	-1.07	-0.09	-0.71	0.499975	0.677424	-7.07

266689_at	hypothetical protein predicted by gens	---	AT2G19930	-1.10	-0.14	-0.71	0.499963	0.677424	-7.07
264564_at	hypothetical protein predicted by gens	---	AT1G05290	-1.04	-0.06	-0.71	0.499935	0.677424	-7.07
246165_at	putative protein	---	---	-1.05	-0.07	-0.71	0.500032	0.677461	-7.07
264221_s_	unknown protein contains similarity to	emb1220	AT1G60170 /	1.06	0.09	0.71	0.500087	0.677495	-7.07
252838_at	hypothetical protein	---	---	1.04	0.06	0.71	0.500142	0.677529	-7.07
254544_at	putative chitinase chitinase (EC 3.2.1.	---	AT4G19820	-1.07	-0.10	-0.71	0.500412	0.677855	-7.07
261539_at	hypothetical protein predicted by gene	---	AT1G01840	-1.07	-0.09	-0.71	0.500527	0.677971	-7.08
263596_at	putative inositol polyphosphate-5-phos	---	AT2G01900	-1.05	-0.07	-0.71	0.500616	0.678051	-7.08
261326_s_	aminoacylase, putative similar to amir	---	AT1G44180 /	1.09	0.13	0.71	0.500781	0.678117	-7.08
249245_at	putative protein contains similarity to C	---	AT5G42280	-1.08	-0.12	-0.71	0.500784	0.678117	-7.08
265781_at	putative Athila retroelement ORF1 prot	---	---	1.05	0.07	0.71	0.500781	0.678117	-7.08
261096_at	4-coumarate:coenzyme A ligase, puta	ACOS5	AT1G62940	1.06	0.08	0.71	0.500721	0.678117	-7.08
266003_at	hypothetical protein predicted by gens	---	AT2G37320	-1.08	-0.11	-0.71	0.500926	0.678268	-7.08
261842_at	hypothetical protein contains similarity	WAKL5	AT1G16160	1.08	0.11	0.71	0.500972	0.678291	-7.08
247715_at	putative protein predicted protein, Ara	---	AT5G59360	-1.09	-0.13	-0.71	0.501157	0.678502	-7.08
256094_at	hypothetical protein predicted by gene	SAUL1	AT1G20780	1.06	0.08	0.71	0.501399	0.678659	-7.08
263289_at	ubiquitin extension protein (UBQ2) ide	---	AT2G36170	-1.11	-0.15	-0.71	0.501326	0.678659	-7.08
255093_s_	putative microfibril-associated protein	---	AT4G08580 /	-1.05	-0.07	-0.71	0.501412	0.678659	-7.08
246100_at	putative protein predicted protein, Ara	---	---	-1.06	-0.08	-0.71	0.501452	0.678659	-7.08
255295_at	putative sugar transporter	---	AT4G04760	-1.05	-0.08	-0.71	0.501351	0.678659	-7.08
254113_at	hypothetical protein	---	AT4G24900	1.06	0.08	0.71	0.501441	0.678659	-7.08
248111_at	wax synthase-like protein	---	AT5G55330	-1.05	-0.07	-0.71	0.501484	0.678662	-7.08
248119_at	serine/threonine-specific protein kinase	---	AT5G54590	1.08	0.11	0.71	0.501533	0.678688	-7.08
246589_at	glucosyltransferase -like protein gluco	---	AT5G14860	-1.06	-0.08	-0.71	0.501619	0.678724	-7.08
266940_at	unknown protein	---	AT2G18970	-1.06	-0.09	-0.71	0.501613	0.678724	-7.08
265054_x_	mutator-like transposase, putative sim	---	---	1.08	0.10	0.71	0.501662	0.678742	-7.08
250010_at	AP2-domain DNA-binding protein -like	---	AT5G18450	-1.08	-0.11	-0.71	0.501759	0.678788	-7.08
251720_at	putative protein	---	AT3G56160	-1.12	-0.16	-0.71	0.501743	0.678788	-7.08
244908_at	hypothetical protein	---	---	1.10	0.13	0.71	0.501786	0.678788	-7.08
256546_at	hypothetical protein contains similarity	---	AT3G14820	-1.05	-0.08	-0.71	0.501836	0.678817	-7.08
264906_at	putative mitochondrial phosphate trans	---	AT2G17270	1.08	0.11	0.71	0.501992	0.678955	-7.08
251362_at	DEAD box RNA helicase RH12	---	AT3G61240	1.06	0.08	0.71	0.502026	0.678955	-7.08
260083_at	putative elicitor-responsive gene simila	---	AT1G63220	1.22	0.28	0.71	0.502028	0.678955	-7.08
258979_at	heat-shock protein (At-hsc70-3) identic	---	AT3G09440	1.12	0.16	0.71	0.502281	0.679118	-7.08
257188_at	hypothetical protein contains Pfam pro	---	AT3G13150	1.07	0.09	0.71	0.502223	0.679118	-7.08

248171_at	putative protein similar to unknown pro	ILR3	AT5G54680	1.05	0.07	0.71	0.502261	0.679118	-7.08
258627_at	unknown protein similar to peroxisoma	PEX12	AT3G04460	1.07	0.10	0.71	0.502292	0.679118	-7.08
247662_at	protein kinase - like protein kinase 1, I	---	AT5G60090	1.08	0.12	0.71	0.502297	0.679118	-7.08
255393_at	hypothetical protein	---	---	-1.04	-0.06	-0.71	0.502332	0.679125	-7.08
266714_at	NAM (no apical meristem)-like protein	EMB2301	AT2G46770	-1.06	-0.09	-0.71	0.502375	0.679143	-7.08
258358_at	unknown protein similar to unknown pr	---	AT3G14380	-1.06	-0.09	-0.71	0.502437	0.679186	-7.08
253110_at	hypothetical protein	---	AT4G35930	-1.09	-0.12	-0.71	0.502631	0.679409	-7.08
259261_at	unknown protein similar to unknown pr	---	AT3G11390	1.07	0.10	0.71	0.502731	0.679464	-7.08
260018_at	hypothetical protein predicted by gene	---	AT1G41820	-1.06	-0.08	-0.71	0.502732	0.679464	-7.08
257638_at	terpene synthase-related protein conta	ATTPS-CIN	AT3G25820 /	-1.05	-0.08	-0.71	0.502847	0.679532	-7.08
265380_at	putative retroelement pol polyprotein	---	---	1.06	0.08	0.71	0.502871	0.679532	-7.08
267052_at	unknown protein	---	AT2G38410	1.06	0.09	0.71	0.502816	0.679532	-7.08
252380_at	ABC-type transport protein-like protein	ATH2	AT3G47740	1.06	0.08	0.71	0.503186	0.679917	-7.08
264996_at	nuclear matrix constituent protein 1, p	LINC1	AT1G67230	-1.07	-0.10	-0.71	0.503242	0.679947	-7.08
246659_at	putative protein predicted proteins Ara	---	---	-1.06	-0.08	-0.71	0.503268	0.679947	-7.08
246299_at	embryonic abundant protein AtEm1	EM1	AT3G51810	-1.05	-0.06	-0.71	0.50333	0.67999	-7.08
256970_at	ABC transporter, putative similar to AT	---	AT3G21090	-1.06	-0.09	-0.71	0.503396	0.679999	-7.08
254541_at	putative LTR retrotransposon Brassica	---	---	1.05	0.07	0.71	0.50337	0.679999	-7.08
267574_at	hypothetical protein predicted by gens	---	AT2G30680	1.08	0.11	0.71	0.503556	0.680135	-7.08
248345_at	unknown protein	SHOC1	AT5G52290	1.05	0.07	0.71	0.503556	0.680135	-7.08
257057_at	hypothetical protein predicted by gens	---	---	-1.04	-0.06	-0.71	0.503587	0.680135	-7.08
262269_at	hypothetical protein predicted by gene	---	---	1.05	0.07	0.71	0.503806	0.680361	-7.08
248384_at	mandelonitrile lyase-like protein	---	AT5G51930	1.05	0.07	0.71	0.503813	0.680361	-7.08
266894_at	hypothetical protein predicted by gens	---	AT2G26050	-1.05	-0.06	-0.71	0.503846	0.680365	-7.08
262681_at	anter-specific proline-rich -like protein	---	AT1G75890	-1.05	-0.07	-0.71	0.503996	0.680527	-7.08
245468_at	pectinesterase like protein	---	AT4G15980	-1.05	-0.07	-0.71	0.504062	0.680577	-7.08
258151_at	beta-glucosidase, putative similar to b	BGLU44	AT3G18080	1.12	0.16	0.71	0.504128	0.680585	-7.08
254591_at	heat shock transcription factor - like pr	---	AT4G18870	1.04	0.06	0.71	0.50411	0.680585	-7.08
264590_at	unknown protein ;supported by full-ler	---	AT2G17710	1.29	0.37	0.71	0.504268	0.680612	-7.08
258028_at	hypothetical protein	---	AT3G27473	1.04	0.06	0.71	0.504251	0.680612	-7.08
245603_at	hypothetical protein	---	AT4G14280	1.07	0.09	0.71	0.50425	0.680612	-7.08
260906_at	hypothetical protein predicted by gene	---	AT1G02540	-1.05	-0.08	-0.71	0.50418	0.680612	-7.08
246826_at	UTP-glucose glucosyltransferase - like	UGT72E3	AT5G26310	1.06	0.08	0.70	0.504558	0.680862	-7.08
251716_at	anthranilate synthase alpha-1 chain -	---	AT3G55870	1.05	0.08	0.70	0.504572	0.680862	-7.08
261976_at	hypothetical protein predicted by gene	---	---	-1.06	-0.09	-0.70	0.504497	0.680862	-7.08

263481_at	predicted protein	---	AT2G04025	1.05	0.07	0.70	0.504515	0.680862	-7.08
250953_at	putative protein ;supported by full-leng	DPB	AT5G03415	-1.09	-0.12	-0.70	0.504795	0.681083	-7.08
248325_at	unknown protein	---	AT5G52800	-1.05	-0.07	-0.70	0.504774	0.681083	-7.08
247640_at	putative protein various predicted prot	---	AT5G60610	1.06	0.08	0.70	0.504919	0.68121	-7.08
262321_at	hypothetical protein predicted by gens	---	AT1G27570	1.06	0.08	0.70	0.504957	0.68122	-7.08
258819_at	unknown protein similar to putative DN	---	AT3G04590	-1.07	-0.10	-0.70	0.505152	0.681443	-7.08
258801_at	unknown protein predicted by genscan	---	AT3G04560	1.05	0.06	0.70	0.505185	0.681446	-7.08
258211_at	hypothetical protein predicted by gene	---	AT3G17890	-1.08	-0.11	-0.70	0.505244	0.681487	-7.08
251398_at	zinc finger protein - like ZPT3-3, Petu	---	AT3G60580	1.07	0.10	0.70	0.505443	0.681715	-7.08
251580_at	putative protein ethylene-responsive p	---	AT3G58450	-1.09	-0.12	-0.70	0.505562	0.681835	-7.08
249150_at	inorganic phosphate transporter (dbj|B	PHT6	AT5G43340	1.05	0.07	0.70	0.505653	0.681918	-7.08
252333_at	putative protein N-terminus: several p	---	AT3G48830	1.05	0.07	0.70	0.505697	0.681936	-7.08
252665_at	valine-rich protein	---	AT3G44140	1.06	0.09	0.70	0.505767	0.68199	-7.08
254310_at	putative protein predicted protein, Ara	---	AT4G22430	-1.04	-0.06	-0.70	0.505811	0.682009	-7.08
265600_at	hypothetical protein predicted by gens	---	---	-1.05	-0.07	-0.70	0.505876	0.682056	-7.08
265296_at	hypothetical protein predicted by gene	---	AT2G14060	-1.05	-0.07	-0.70	0.505978	0.682086	-7.08
250558_at	flavonoid 3-hydroxylase - like protein f	TT7	AT5G07990	-1.07	-0.09	-0.70	0.506012	0.682086	-7.08
253376_at	hypothetical protein Arabidopsis thalia	---	AT4G33290	-1.04	-0.06	-0.70	0.505981	0.682086	-7.08
246979_s_	putative protein hypothetical proteins -	---	AT5G24990 /	1.07	0.10	0.70	0.506017	0.682086	-7.08
256699_at	hypothetical protein predicted by gene	---	AT3G20690	-1.07	-0.09	-0.70	0.506079	0.682088	-7.08
251913_at	putative protein several malat dehydro	---	AT3G53910	1.05	0.07	0.70	0.506054	0.682088	-7.08
245704_at	glycine-rich protein	KTF1	AT5G04290	1.05	0.07	0.70	0.506147	0.682137	-7.08
246330_at	aldehyde oxidase ; supported by cDN	AAO2	AT3G43600	-1.14	-0.19	-0.70	0.506175	0.682137	-7.08
256137_at	auxin-regulated protein, putative simil	---	AT1G48690	-1.05	-0.07	-0.70	0.506313	0.682282	-7.08
256084_at	hypothetical protein predicted by gens	---	AT1G20750	1.07	0.09	0.70	0.506671	0.682725	-7.08
253868_at	proton pump interactor non-consensus	PPI1	AT4G27500	-1.06	-0.09	-0.70	0.506764	0.682754	-7.08
255896_at	basic blue protein, putative similar to t	---	AT1G17800	1.05	0.07	0.70	0.506767	0.682754	-7.08
249883_at	Na+/H+ antiporter-like protein	CHX3	AT5G22900	-1.05	-0.07	-0.70	0.506812	0.682754	-7.08
251377_at	putative protein	---	AT3G60650	-1.05	-0.08	-0.70	0.506806	0.682754	-7.08
260920_at	amp-binding protein, putative similar t	---	AT1G21530	1.05	0.07	0.70	0.506938	0.682883	-7.08
256234_at	50S ribosomal protein L10, putative si	---	AT3G12370	-1.06	-0.08	-0.70	0.50702	0.682925	-7.08
260084_at	chromatin structure regulator, putative	---	AT1G63210	1.06	0.09	0.70	0.507029	0.682925	-7.08
247511_at	Fdr1 Cen - like protein Fdr1, Oryza sa	---	AT5G62040	1.07	0.09	0.70	0.507181	0.683089	-7.08
263713_at	Expressed protein ; supported by full-l	---	AT2G20595	-1.07	-0.09	-0.70	0.50728	0.683142	-7.08
247631_at	putative MADS box protein various pr	AGL62	AT5G60440	-1.04	-0.06	-0.70	0.507265	0.683142	-7.08

250534_at	NADH dehydrogenase ;supported by	CI51	AT5G08530	-1.05	-0.08	-0.70	0.507441	0.683318	-7.08
254527_at	putative protein KIAA0682 protein, Ho	---	AT4G19610	1.05	0.06	0.70	0.507471	0.683318	-7.08
253127_at	putative Myc-type transcription factor	---	AT4G36060	-1.05	-0.07	-0.70	0.507521	0.683345	-7.08
265088_at	hypothetical protein similar to DNA He	SWI2	AT1G03750	1.05	0.06	0.70	0.507636	0.68346	-7.08
263257_at	putative DNA polymerase Beta similar	---	AT1G10520	-1.08	-0.11	-0.70	0.507712	0.683522	-7.08
260695_at	RNA helicase, putative similar to GB:	ESP3	AT1G32490	1.04	0.06	0.70	0.507775	0.683567	-7.08
264413_s_	hypothetical protein similar to hypothet	---	---	-1.07	-0.10	-0.70	0.507937	0.683744	-7.08
250320_at	CCAAT box binding factor/ transcriptio	NF-YA1	AT5G12840	-1.06	-0.08	-0.70	0.508079	0.683886	-7.08
261182_at	hypothetical protein predicted by gene	---	AT1G34575	-1.05	-0.07	-0.70	0.508103	0.683886	-7.08
246592_at	putative protein predicted protein, Ara	---	AT5G14890	1.07	0.10	0.70	0.508161	0.683924	-7.08
249878_at	TATA-binding protein-associated phos	NF-YB13	AT5G23090	-1.07	-0.10	-0.70	0.508198	0.683933	-7.08
262108_at	unknown protein similar to unknown pr	---	AT1G02740	1.07	0.09	0.70	0.508298	0.684028	-7.09
265314_at	hypothetical protein predicted by gens	---	AT2G20210	1.06	0.09	0.70	0.50869	0.684298	-7.09
262156_at	hypothetical protein contains similarity	---	AT1G52680	-1.06	-0.09	-0.70	0.508679	0.684298	-7.09
265507_s_	Ac-like transposase related to Ac/Ds tr	---	---	-1.05	-0.08	-0.70	0.508594	0.684298	-7.09
248829_at	putative protein contains similarity to B	---	AT5G47130	-1.09	-0.13	-0.70	0.508663	0.684298	-7.09
251571_at	putative protein several hypothetical pr	---	AT3G58330	1.05	0.07	0.70	0.508642	0.684298	-7.09
258768_at	hypothetical protein predicted by gens	---	AT3G10880	-1.05	-0.07	-0.70	0.508679	0.684298	-7.09
248354_at	putative protein contains similarity to u	---	AT5G52330	-1.05	-0.08	-0.70	0.508708	0.684298	-7.09
261977_at	hypothetical protein contains similarity	---	---	-1.05	-0.07	-0.70	0.508865	0.684468	-7.09
261533_at	hypothetical protein predicted by gene	---	AT1G71690	-1.07	-0.10	-0.70	0.508899	0.684473	-7.09
267024_s_	putative aquaporin (plasma membrane	NIP2;1	AT2G29870 /	-1.07	-0.10	-0.70	0.509072	0.684666	-7.09
265931_at	unknown protein ;supported by full-ler	---	AT2G18520	1.08	0.10	0.70	0.509105	0.684669	-7.09
265770_at	Expressed protein ; supported by full-l	---	AT2G48100	1.07	0.10	0.70	0.509166	0.684712	-7.09
253929_s_	putative protein H+-transporting ATP s	---	AT2G16030 /	-1.06	-0.09	-0.70	0.509284	0.68483	-7.09
254196_at	putative protein	---	AT4G24030	-1.08	-0.10	-0.70	0.509383	0.684923	-7.09
247920_at	putative protein contains similarity to u	---	AT5G57670	-1.07	-0.10	-0.70	0.509476	0.685008	-7.09
258315_at	Expressed protein ; supported by full-l	---	AT3G16175	-1.06	-0.09	-0.70	0.509543	0.685017	-7.09
256079_at	hypothetical protein predicted by gens	---	AT1G20680	-1.05	-0.06	-0.70	0.509525	0.685017	-7.09
251018_at	60S ribosomal protein - like 60S ribos	---	AT5G02450	-1.08	-0.12	-0.70	0.509639	0.685024	-7.09
251501_at	putative protein several hypothetical pr	---	AT3G59120	1.06	0.08	0.70	0.509616	0.685024	-7.09
AFFX-r2-E	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.11	0.16	0.70	0.509612	0.685024	-7.09
252765_at	putative protein hypothetical proteins -	---	AT3G42800	-1.11	-0.15	-0.70	0.509818	0.685148	-7.09
262605_at	hypothetical protein Strong similarity to	---	AT1G15170	1.20	0.26	0.70	0.509855	0.685148	-7.09
267633_at	hypothetical protein predicted by gene	---	AT2G42180	1.05	0.07	0.70	0.509881	0.685148	-7.09

263233_at	hypothetical protein similar to Na/H an	---	AT1G05577	1.05	0.07	0.70	0.509778	0.685148	-7.09
256287_at	hypothetical protein	---	AT3G12190	1.05	0.08	0.70	0.509833	0.685148	-7.09
245684_at	Expressed protein ; supported by cDN	RHF2A	AT5G22000	1.05	0.07	0.70	0.510001	0.685269	-7.09
249280_at	unknown protein	---	AT5G41940	1.07	0.10	0.70	0.510051	0.685295	-7.09
250386_at	MYB like protein MYB like protein, Dic	MYB3R-4	AT5G11510	-1.07	-0.10	-0.70	0.510193	0.685385	-7.09
251283_at	seven in absentia-like protein SINAH1	---	AT3G61790	-1.05	-0.08	-0.70	0.510261	0.685385	-7.09
256259_at	hypothetical protein predicted by gene	---	AT3G12460	-1.08	-0.11	-0.70	0.510267	0.685385	-7.09
248390_at	importin alpha subunit	IMPA-8	AT5G52000	1.04	0.06	0.70	0.510209	0.685385	-7.09
245901_at	HOMEOBOX PROTEIN KNOTTED-1 I	KNAT4	AT5G11060	1.09	0.12	0.70	0.510216	0.685385	-7.09
257800_at	unknown protein ;supported by full-ler	---	AT3G15900	1.07	0.10	0.69	0.510342	0.685445	-7.09
254151_at	F-box protein family, AtFBX14 similar	---	AT4G24390	1.05	0.07	0.69	0.510523	0.685647	-7.09
262327_at	hypothetical protein similar to hypothet	---	AT1G64130	1.06	0.08	0.69	0.51067	0.685804	-7.09
252634_x_	putative protein predicted proteins, Ar	---	---	-1.06	-0.09	-0.69	0.510762	0.685847	-7.09
247857_at	peroxidase	---	AT5G58400	-1.06	-0.09	-0.69	0.510747	0.685847	-7.09
257696_at	protein kinase, putative similar to prot	AGC1.5	AT3G12690	-1.09	-0.12	-0.69	0.510865	0.685945	-7.09
263938_at	hypothetical protein predicted by gene	---	AT2G35900	-1.06	-0.08	-0.69	0.511173	0.686248	-7.09
248897_at	KCO-like protein 3 (emb|CAB40380.1)	KCO3	AT5G46360	-1.06	-0.09	-0.69	0.511195	0.686248	-7.09
248457_at	putative protein contains similarity to w	---	AT5G51420	1.08	0.11	0.69	0.511189	0.686248	-7.09
245366_at	Expressed protein ; supported by full-l	AtMAPR4	AT4G14965	-1.05	-0.07	-0.69	0.511211	0.686248	-7.09
267370_at	unknown protein ;supported by full-ler	---	AT2G44525	1.04	0.06	0.69	0.511334	0.686332	-7.09
263627_at	Expressed protein ; supported by full-l	---	AT2G04675	1.06	0.09	0.69	0.51133	0.686332	-7.09
262758_at	hypothetical protein predicted by gene	---	AT1G10780	-1.06	-0.08	-0.69	0.511554	0.686587	-7.09
249570_at	hypothetical protein	---	AT5G38080	1.07	0.09	0.69	0.511619	0.686634	-7.09
258884_at	threonine dehydratase/deaminase (OI	OMR1	AT3G10050	1.11	0.15	0.69	0.511889	0.686835	-7.09
264011_at	unknown protein	---	AT2G21090	1.06	0.09	0.69	0.511851	0.686835	-7.09
265577_at	unknown protein	---	AT2G20100	-1.05	-0.07	-0.69	0.511862	0.686835	-7.09
265559_at	putative glycine-rich protein	---	AT2G05530	1.07	0.09	0.69	0.511839	0.686835	-7.09
251088_at	putative protein several hypothetical pr	---	AT5G01480	-1.09	-0.12	-0.69	0.512218	0.687219	-7.09
254968_at	putative protein various predicted prot	---	AT4G10420	1.05	0.07	0.69	0.512236	0.687219	-7.09
254935_at	putative disease resistance protein sir	---	AT4G10780	1.07	0.09	0.69	0.512303	0.687269	-7.09
259876_at	putative DnaJ protein similar to dnaJ-l	---	AT1G76700	-1.11	-0.15	-0.69	0.512484	0.687472	-7.09
248435_at	oleosin-like	OLEO3	AT5G51210	1.07	0.09	0.69	0.512617	0.687609	-7.09
262027_at	DNA-binding protein, putative similar t	HOS10	AT1G35515	-1.11	-0.15	-0.69	0.512679	0.687652	-7.09
248724_at	putative protein strong similarity to unk	---	AT5G47970	1.10	0.14	0.69	0.51277	0.687733	-7.09
252438_at	putative protein riboflavin biosynthesis	---	AT3G47390	-1.05	-0.07	-0.69	0.512937	0.687836	-7.09

253931_at	putative CDP-diacylglycerol synthetas	---	AT4G26770	-1.06	-0.08	-0.69	0.512909	0.687836	-7.09
256604_at	hypothetical protein predicted by gene	---	---	1.05	0.07	0.69	0.512917	0.687836	-7.09
249808_at	unknown protein	---	AT5G23890	1.11	0.15	0.69	0.513001	0.687881	-7.09
252714_x_	putative protein p97 homologous prote	---	AT3G43880	1.04	0.06	0.69	0.513033	0.687883	-7.09
256154_at	hypothetical protein predicted by gene	---	AT3G08490	1.07	0.09	0.69	0.513117	0.687916	-7.09
252061_at	hypothetical protein phosphate actyltra	---	AT3G52620	1.05	0.07	0.69	0.513091	0.687916	-7.09
254566_at	hypothetical protein	---	AT4G19240	-1.07	-0.10	-0.69	0.513193	0.68794	-7.09
247829_at	protein kinase - like protein kinase AT	---	AT5G58520	-1.08	-0.11	-0.69	0.513195	0.68794	-7.09
246363_at	hypothetical protein	---	AT1G40390	-1.06	-0.09	-0.69	0.513282	0.688016	-7.09
257656_at	Expressed protein ; supported by full-le	---	AT3G13228	1.05	0.07	0.69	0.51333	0.688039	-7.09
253356_at	putative protein myosin II heavy chain	---	AT4G33390	1.05	0.08	0.69	0.513561	0.688308	-7.09
257023_at	RNA helicase, putative similar to RNA	---	AT3G19760	1.06	0.08	0.69	0.513803	0.68845	-7.09
248657_at	peptidylprolyl isomerase	ROF2	AT5G48570	-1.43	-0.51	-0.69	0.513731	0.68845	-7.09
256660_at	hypothetical protein similar to hypothet	---	AT3G12060	-1.06	-0.09	-0.69	0.5137	0.68845	-7.09
251009_at	putative protein predicted proteins, Ar	---	AT5G02640	1.12	0.17	0.69	0.513846	0.68845	-7.09
260609_at	putative receptor protein kinase	---	AT2G43690	1.05	0.08	0.69	0.513848	0.68845	-7.09
264469_at	hypothetical protein similar to hypothet	LBD40	AT1G67100	-1.05	-0.07	-0.69	0.513777	0.68845	-7.09
245720_at	RNA binding protein - like	---	AT5G04210	1.05	0.07	0.69	0.513979	0.688586	-7.09
257344_s_	pseudogene, putative mutator-like tra	---	---	1.08	0.11	0.69	0.514074	0.688632	-7.09
266385_at	pathogenesis-related PR-1-like protein	PR1	AT2G14610	-2.12	-1.08	-0.69	0.514074	0.688632	-7.09
247742_at	random slug protein - like random slug	---	AT5G58980	1.07	0.09	0.69	0.514137	0.688677	-7.09
261270_at	initiation factor 5A-4, putative similar t	FBR12	AT1G26630	-1.05	-0.07	-0.69	0.514234	0.688685	-7.09
257109_s_	hypothetical protein	---	---	1.05	0.07	0.69	0.514184	0.688685	-7.09
250979_at	putative protein	---	AT5G03090	1.08	0.11	0.69	0.514234	0.688685	-7.09
255320_at	putative transposon protein	---	---	1.04	0.06	0.69	0.514363	0.688812	-7.09
261473_at	hypothetical protein similar to putative	---	AT1G14490	-1.10	-0.14	-0.69	0.51439	0.688812	-7.09
258273_at	unknown protein ;supported by full-ler	GRX4	AT3G15660	1.04	0.06	0.69	0.514497	0.688888	-7.09
256537_at	unknown protein	---	AT1G33340	-1.15	-0.21	-0.69	0.514507	0.688888	-7.09
249666_at	phytochrome C (sp|P14714)	PHYC	AT5G35840	1.07	0.10	0.69	0.514786	0.689222	-7.09
264247_at	potassium transporter, putative simila	---	AT1G60160	-1.12	-0.17	-0.69	0.514869	0.689293	-7.09
267576_at	putative Mutator-like transposase	---	---	1.07	0.10	0.69	0.515029	0.689466	-7.09
254837_at	putative protein	---	AT4G12360	1.07	0.09	0.69	0.515232	0.689697	-7.09
256629_at	serine/threonine protein phosphatase,	ATFYPP3	AT3G19980	1.05	0.08	0.69	0.515283	0.689725	-7.09
252221_at	RuvB DNA helicase - like protein DNA	---	AT3G49830	-1.06	-0.08	-0.69	0.5157	0.690081	-7.09
252860_at	putative protein bZIP protein, Arabido	---	AT4G39790	1.05	0.06	0.69	0.515624	0.690081	-7.09

249909_s_	alpha-adaptin	---	AT5G22770 /	-1.07	-0.09	-0.69	0.515657	0.690081	-7.09
254317_at	hypothetical protein	---	AT4G22510	1.05	0.06	0.69	0.515682	0.690081	-7.09
259968_at	unknown protein	---	AT1G76530	1.06	0.08	0.69	0.515649	0.690081	-7.09
262759_at	unknown protein	---	AT1G10800	-1.05	-0.07	-0.69	0.515774	0.69014	-7.09
257543_at	hypothetical protein predicted by gene	---	AT3G28960	-1.06	-0.09	-0.69	0.515917	0.690291	-7.09
258820_at	putative tryptophanyl-tRNA synthetase	---	AT3G04600	1.05	0.07	0.69	0.515951	0.690295	-7.09
258605_at	phi-1-like protein similar to phi-1 (phos	EXL6	AT3G02970	-1.06	-0.09	-0.69	0.516032	0.690364	-7.09
258602_at	putative protein phosphatase-2C (PP2	---	AT3G02750	1.05	0.06	0.69	0.516195	0.690541	-7.09
266743_at	ribonuclease, RNS1 identical to ribonu	RNS1	AT2G02990 /	-1.32	-0.40	-0.68	0.516273	0.690605	-7.10
267418_at	putative RING zinc finger protein	---	AT2G35000	1.07	0.09	0.68	0.516343	0.690657	-7.10
245160_at	putative leucine-rich repeat disease re	AtRLP28	AT2G33080	-1.05	-0.07	-0.68	0.516426	0.690729	-7.10
249095_at	myosin heavy chain MYA2 (pir||S5182	MYA2	AT5G43900	1.09	0.13	0.68	0.516612	0.690936	-7.10
264452_at	unknown protein similar to salt-inducib	GRP23	AT1G10270	1.18	0.23	0.68	0.516679	0.690986	-7.10
245794_at	endoxyloglucan transferase, putative	XTR4	AT1G32170	-1.07	-0.10	-0.68	0.516787	0.691089	-7.10
259567_at	hypothetical protein	---	AT1G20500	-1.06	-0.09	-0.68	0.51683	0.691107	-7.10
256847_at	early nodule-specific protein, putative	---	AT3G27950	-1.06	-0.08	-0.68	0.516977	0.691262	-7.10
254554_at	hypothetical protein	---	AT4G19550	1.06	0.08	0.68	0.517022	0.691283	-7.10
265462_at	putative vetispiradiene synthase	---	AT2G37140	1.06	0.08	0.68	0.517167	0.691394	-7.10
260067_at	putative lipid transfer protein similar to	---	AT1G73780	-1.06	-0.08	-0.68	0.517145	0.691394	-7.10
248421_at	unknown protein ;supported by full-ler	---	AT5G51510	1.06	0.08	0.68	0.517199	0.691397	-7.10
249092_at	putative protein similar to unknown pro	---	AT5G43710	-1.06	-0.09	-0.68	0.51744	0.691659	-7.10
266185_at	unknown protein	---	AT2G38950	-1.05	-0.07	-0.68	0.517455	0.691659	-7.10
253349_at	putative protein	---	---	-1.05	-0.07	-0.68	0.517916	0.692234	-7.10
251032_at	putative homeodomain protein several	RPL	AT5G02030	1.14	0.19	0.68	0.518042	0.692362	-7.10
245841_s_	ribosomal protein S2, putative similar	XW6	AT1G58380 /	1.09	0.13	0.68	0.518155	0.692471	-7.10
266514_at	putative zinc-finger protein (B-box zinc	---	AT2G47890	1.08	0.11	0.68	0.518186	0.692471	-7.10
261302_at	hypothetical protein predicted by gene	---	AT1G48580	-1.06	-0.08	-0.68	0.518215	0.692471	-7.10
249240_at	putative protein similar to unknown pro	---	AT5G42220	1.07	0.09	0.68	0.518331	0.692586	-7.10
257018_at	unknown protein	---	AT3G19630	-1.06	-0.08	-0.68	0.518441	0.692693	-7.10
264942_at	unknown protein ; supported by cDNA	---	AT1G67340	1.08	0.11	0.68	0.518479	0.692703	-7.10
253509_at	putative protein kainate receptor, Ratt	GLR2.4	AT4G31710	1.06	0.08	0.68	0.518632	0.692785	-7.10
262765_at	putative cytochrome P450 monooxyge	CYP86C4	AT1G13150	-1.06	-0.08	-0.68	0.518603	0.692785	-7.10
264198_at	unknown protein ESTs gb|Z34075, gb	---	AT1G22800	-1.08	-0.11	-0.68	0.518613	0.692785	-7.10
258134_at	rubisco expression protein, putative si	---	AT3G24530	-1.08	-0.11	-0.68	0.518861	0.69305	-7.10
259799_at	drought induced protein, putative simi	---	AT1G72290	-1.04	-0.06	-0.68	0.518994	0.693146	-7.10

245222_at	contains similarity to En/Spm transpos	---	---	-1.05	-0.06	-0.68	0.518965	0.693146	-7.10
249696_at	copia-like retrotransposable element	---	---	-1.05	-0.07	-0.68	0.519173	0.693345	-7.10
255439_at	putative phospho-ser/thr phosphatase	BSL1	AT4G03080	-1.05	-0.07	-0.68	0.51923	0.693381	-7.10
256811_at	serine/threonine-specific protein kinas	---	AT3G21340	1.05	0.07	0.68	0.519347	0.693497	-7.10
254664_at	initiation factor-2Bepsilon-like protein	---	AT4G18300	1.06	0.09	0.68	0.519432	0.693529	-7.10
247310_at	putative protein contains similarity to S	CHR24	AT5G63950	-1.08	-0.11	-0.68	0.51941	0.693529	-7.10
264312_at	putative protein kinase similar to prote	---	AT1G70450	1.05	0.07	0.68	0.519498	0.693576	-7.10
258370_at	Expressed protein ; supported by full-le	---	AT3G14395	-1.06	-0.09	-0.68	0.519557	0.693614	-7.10
262631_at	hypothetical protein predicted by gene	---	AT1G06500	-1.05	-0.07	-0.68	0.519636	0.69368	-7.10
245785_at	cellulose synthase catalytic subunit, p	ATCSLD6	AT1G32180	1.06	0.08	0.68	0.519682	0.6937	-7.10
245713_at	S-adenosyl-L-methionine:salicylic acid	NAMT1	AT5G04370	1.08	0.11	0.68	0.519822	0.693765	-7.10
256053_at	UDP-glucose glucosyltransferase, put	UGT71C3	AT1G07260	-1.18	-0.24	-0.68	0.519814	0.693765	-7.10
262147_at	phospholipase D1, putative similar to	PLDALPHA2	AT1G52570	-1.05	-0.07	-0.68	0.519814	0.693765	-7.10
248840_at	unknown protein ; supported by cDNA	---	AT5G46770	1.07	0.09	0.68	0.519864	0.69378	-7.10
260027_at	unknown protein	CPuORF34	AT1G29950 /	-1.08	-0.11	-0.68	0.519988	0.693865	-7.10
265955_at	putative ABC transporter	PDR5	AT2G37280	1.06	0.08	0.68	0.51998	0.693865	-7.10
266286_at	putative tropinone reductase	---	AT2G29160 /	-1.06	-0.08	-0.68	0.52026	0.694177	-7.10
248212_at	CHP-rich zinc finger protein-like	---	AT5G54020	-1.06	-0.09	-0.68	0.520283	0.694177	-7.10
263465_at	hypothetical protein predicted by gens	---	AT2G31940	-1.07	-0.10	-0.68	0.520493	0.694416	-7.10
267065_at	hypothetical protein predicted by gene	---	AT2G41080	1.06	0.09	0.68	0.520648	0.69457	-7.10
262500_at	unknown protein Contains PF|00646 F	FBP7	AT1G21760	1.05	0.07	0.68	0.520668	0.69457	-7.10
252046_at	putative protein extensin -Nicotiana ta	---	AT3G52460	-1.06	-0.09	-0.68	0.520751	0.694639	-7.10
265962_at	nodulin-like protein ;supported by full-	---	AT2G37460	1.16	0.21	0.68	0.520782	0.694641	-7.10
257526_s_	hypothetical protein similar to putative	---	AT3G09330 /	-1.05	-0.07	-0.68	0.520887	0.69474	-7.10
247915_at	putative protein similar to unknown pro	---	AT5G57570	1.05	0.07	0.68	0.521091	0.694971	-7.10
257649_at	predicted protein	ARR1	AT3G16857	1.05	0.07	0.68	0.521265	0.695162	-7.10
252688_at	putative protein	---	AT3G44020	-1.06	-0.09	-0.68	0.52151	0.695326	-7.10
261952_at	unknown protein	---	AT1G64430	1.04	0.06	0.68	0.521474	0.695326	-7.10
250047_at	BCS1 - like protein h-bcs1, Homo sap	---	AT5G17730	1.06	0.09	0.68	0.521489	0.695326	-7.10
245752_at	hypothetical protein similar to Ac-like t	---	AT1G35150	-1.05	-0.06	-0.68	0.521455	0.695326	-7.10
251298_at	hypothetical protein contains non-cons	---	AT3G62040	1.12	0.17	0.68	0.521711	0.695554	-7.10
261249_at	hypothetical protein predicted by gene	---	AT1G05880	-1.06	-0.08	-0.68	0.521809	0.69563	-7.10
245965_at	pectin methylesterase-like protein pec	---	AT5G19730	-1.10	-0.14	-0.68	0.521829	0.69563	-7.10
255830_at	putative PRP19-like spliceosomal prot	---	AT2G33340	1.11	0.15	0.68	0.521872	0.695646	-7.10
264478_at	hypothetical protein predicted by gens	---	AT1G77270	-1.05	-0.07	-0.68	0.521981	0.695711	-7.10

249992_at	AP2 domain -like protein AP2/EREBP	PUCHI	AT5G18560	-1.06	-0.09	-0.68	0.521979	0.695711	-7.10
247349_at	putative protein similar to unknown pro	---	AT5G63820	-1.05	-0.07	-0.68	0.522025	0.695729	-7.10
248594_at	unknown protein ; supported by full-le	---	AT5G49210	1.09	0.12	0.68	0.522113	0.695745	-7.10
266188_at	unknown protein	---	AT2G39000	-1.06	-0.09	-0.68	0.522129	0.695745	-7.10
259377_at	putative poly(A) binding protein simila	PAB6	AT3G16380	1.07	0.10	0.68	0.522087	0.695745	-7.10
254325_at	putative protein various predicted prot	---	AT4G22650	-1.08	-0.11	-0.67	0.522256	0.695834	-7.10
248004_at	putative protein similar to unknown pro	PRA1.G2	AT5G56230	1.12	0.16	0.67	0.522236	0.695834	-7.10
264008_at	unknown protein	---	AT2G21120	-1.07	-0.10	-0.67	0.522378	0.695889	-7.10
266750_s_	putative pectinesterase	VGDH1	AT2G47030 /	1.05	0.07	0.67	0.52242	0.695889	-7.10
263187_at	athila ORF 1, putative similar to Athila	---	---	-1.04	-0.06	-0.67	0.522368	0.695889	-7.10
250629_at	respiratory burst oxidase protein A	ATRBOHA	AT5G07390	1.06	0.08	0.67	0.522411	0.695889	-7.10
254184_at	hypothetical protein	---	AT4G23970	1.05	0.08	0.67	0.522529	0.695993	-7.10
260030_at	putative bZIP transcription factor simila	AtbZIP	AT1G68880	-1.05	-0.07	-0.67	0.522628	0.696043	-7.10
249738_at	60s acidic ribosomal protein P1	---	AT5G24510	-1.05	-0.06	-0.67	0.522619	0.696043	-7.10
264165_at	hypothetical protein contains similarity	ATNAP11	AT1G65410	-1.05	-0.07	-0.67	0.522664	0.696051	-7.10
263342_at	putative helicase	---	---	-1.04	-0.06	-0.67	0.52272	0.696086	-7.10
246868_at	protein phosphatase - like protein pho	---	AT5G26010	1.05	0.07	0.67	0.522765	0.696102	-7.10
252452_at	receptor protein kinase - like protein p	---	AT3G47110	1.04	0.06	0.67	0.522793	0.696102	-7.10
251446_at	Expressed protein ; supported by full-le	---	AT3G59840	-1.05	-0.07	-0.67	0.52323	0.696191	-7.10
255296_at	hypothetical protein	---	AT4G04790	1.11	0.15	0.67	0.523286	0.696191	-7.10
246921_at	putative protein small unique nuclear r	---	AT5G25080	1.08	0.12	0.67	0.5232	0.696191	-7.10
260999_at	hypothetical protein similar to putative	---	AT1G26580	1.05	0.07	0.67	0.523163	0.696191	-7.10
248253_at	putative protein contains similarity to p	CRF3	AT5G53290	1.05	0.07	0.67	0.523125	0.696191	-7.10
260297_at	unknown protein contains Pfam profile	---	AT1G80280	1.06	0.08	0.67	0.523071	0.696191	-7.10
251386_at	putative protein rec, Homo sapiens, E	---	AT3G60800	1.04	0.06	0.67	0.523306	0.696191	-7.10
254264_at	putative protein various predicted prot	---	AT4G23510	1.05	0.07	0.67	0.52297	0.696191	-7.10
264981_at	valyl- tRNA synthetase, putative simila	---	AT1G27160	1.06	0.09	0.67	0.523318	0.696191	-7.10
264263_at	Expressed protein ; supported by full-le	AtPP2-B15	AT1G09155	-1.05	-0.08	-0.67	0.523306	0.696191	-7.10
249840_at	unknown protein ; supported by cDNA	ATLCBK1	AT5G23450	-1.04	-0.06	-0.67	0.523084	0.696191	-7.10
261729_s_	hexokinase, putative similar to hexoki	HXK3	AT1G47840	1.04	0.06	0.67	0.523287	0.696191	-7.10
264618_at	hypothetical protein predicted by gene	---	AT2G17680	-1.05	-0.07	-0.67	0.523096	0.696191	-7.10
263855_at	putative non-LTR retrolelement revers	---	AT2G04420	1.06	0.08	0.67	0.523125	0.696191	-7.10
259355_at	hypothetical protein predicted by gene	---	AT3G05240	-1.05	-0.08	-0.67	0.523023	0.696191	-7.10
252743_at	guanine nucleotide-exchange - like pr	ATMIN7	AT3G43300	-1.05	-0.07	-0.67	0.523436	0.696306	-7.10
257034_at	hypothetical protein predicted by gens	---	AT3G19184	1.05	0.07	0.67	0.523487	0.696335	-7.10

260048_at	unknown protein contains Pfam profile	---	AT1G73750	1.21	0.27	0.67	0.523518	0.696335	-7.10
264269_at	hypothetical protein predicted by gene	---	AT1G60240	1.07	0.09	0.67	0.523675	0.696504	-7.10
256658_at	unknown protein	---	AT3G12010 /	-1.05	-0.07	-0.67	0.523769	0.696588	-7.10
250797_at	unknown protein	---	AT5G05310	1.06	0.09	0.67	0.523912	0.696737	-7.10
246759_at	putative protein kinesin heavy chain-li	---	AT5G27950	1.08	0.11	0.67	0.524154	0.696932	-7.10
255333_at	putative polyprotein	---	---	1.05	0.07	0.67	0.524178	0.696932	-7.10
259758_s_	putative caffeic acid 3-O-methyltransfe	---	AT1G77520 /	-1.05	-0.07	-0.67	0.524091	0.696932	-7.10
250171_at	prohibitin - like protein prohibitin, Arab	ATPHB5	AT5G14300	-1.05	-0.08	-0.67	0.524181	0.696932	-7.10
254583_at	hypothetical protein	---	AT4G19480	-1.05	-0.08	-0.67	0.52427	0.69701	-7.10
264439_at	adenine phosphoribosyltransferase 1,	APT1	AT1G27450	-1.06	-0.08	-0.67	0.524671	0.697462	-7.11
257241_at	hypothetical protein contains Pfam pro	---	AT3G24210	-1.07	-0.09	-0.67	0.524669	0.697462	-7.11
249210_at	unknown protein	---	AT5G42670	-1.05	-0.07	-0.67	0.524756	0.697534	-7.11
266786_at	putative non-LTR retroelement reverse	---	---	1.05	0.07	0.67	0.52488	0.697658	-7.11
245090_at	putative integral membrane protein no	---	AT2G40900	1.08	0.12	0.67	0.524958	0.697722	-7.11
252841_at	putative protein replication protein A 5	---	---	-1.07	-0.09	-0.67	0.525045	0.697796	-7.11
249762_at	putative protein contains similarity to u	---	AT5G24000	-1.05	-0.07	-0.67	0.52513	0.697869	-7.11
247080_at	20S proteasome subunit PAD2 (gb|AA	PAD2	AT5G66140	1.06	0.08	0.67	0.525266	0.697968	-7.11
246525_at	CONSTANS ;supported by full-length	CO	AT5G15840	1.06	0.08	0.67	0.525237	0.697968	-7.11
252042_at	putative serine/threonine protein kinas	---	AT3G51990	1.07	0.09	0.67	0.525367	0.697979	-7.11
257720_at	hypothetical protein similar to GB:AAD	---	AT3G18450	-1.06	-0.09	-0.67	0.525397	0.697979	-7.11
252170_at	hypothetical protein ; supported by cD	HR4	AT3G26560 /	1.07	0.09	0.67	0.525334	0.697979	-7.11
245779_at	hypothetical protein predicted by gene	---	AT1G73510	-1.05	-0.07	-0.67	0.525372	0.697979	-7.11
265457_at	unknown protein ; supported by full-le	---	AT2G46550	-1.07	-0.10	-0.67	0.525497	0.698032	-7.11
251799_at	putative protein P59 PROTEIN (HSP I	---	AT3G55520	-1.07	-0.10	-0.67	0.525492	0.698032	-7.11
254640_at	ion transporter - like protein integral m	NRAMP5	AT4G18790	-1.05	-0.08	-0.67	0.525796	0.698184	-7.11
251502_at	putative protein several hypothetical pr	---	AT3G59130	1.05	0.07	0.67	0.525675	0.698184	-7.11
245404_at	putative protein	---	AT4G17610	-1.07	-0.10	-0.67	0.525654	0.698184	-7.11
254599_at	putative protein hypothetical protein Y	---	AT4G19000	1.06	0.08	0.67	0.525774	0.698184	-7.11
249812_at	putative protein similar to unknown pro	---	AT5G23830	1.07	0.10	0.67	0.525734	0.698184	-7.11
254392_at	endonuclease, putative ; supported by	ENDO5	AT4G21600	-1.05	-0.08	-0.67	0.525754	0.698184	-7.11
266680_s_	hypothetical protein predicted by gene	---	AT2G19850 /	-1.04	-0.06	-0.67	0.525967	0.69837	-7.11
263376_at	putative surface protein ; supported by	FLA6	AT2G20520	-1.04	-0.06	-0.67	0.526161	0.698575	-7.11
259135_at	hypothetical protein predicted by gene	RAD9	AT3G05480	1.08	0.11	0.67	0.526182	0.698575	-7.11
259779_s_	hypothetical protein predicted by gene	---	AT1G29620 /	1.06	0.08	0.67	0.526288	0.698581	-7.11
260090_at	putative serine carboxypeptidase simi	scpl4	AT1G73310	-1.04	-0.06	-0.67	0.52631	0.698581	-7.11

254465_at	tapetum-specific A3 like protein Arabi	---	AT4G20420	-1.06	-0.09	-0.67	0.52626	0.698581	-7.11
245526_at	putative protein	NRPD4	AT4G15950	-1.04	-0.06	-0.67	0.526239	0.698581	-7.11
265355_at	hypothetical protein predicted by gene	---	AT2G16760	-1.09	-0.13	-0.67	0.526394	0.698653	-7.11
257818_at	hypothetical protein predicted by gens	---	AT3G25120	1.06	0.09	0.67	0.52649	0.698682	-7.11
263519_at	40S ribosomal protein S25 ; supporte	---	AT2G21580	-1.11	-0.15	-0.67	0.526486	0.698682	-7.11
267019_at	hypothetical protein predicted by gens	---	AT2G39130	-1.06	-0.09	-0.67	0.526508	0.698682	-7.11
261350_at	hypothetical protein predicted by gene	---	AT1G79770	-1.09	-0.12	-0.67	0.52655	0.698697	-7.11
253757_at	rac GTP binding protein Arac7 ; supp	ROP9	AT4G28950	-1.06	-0.09	-0.67	0.526673	0.69882	-7.11
265654_s_	En/Spm-like transposon protein relate	---	---	1.05	0.07	0.67	0.526819	0.698972	-7.11
264879_at	cotton fiber expressed protein, putativ	---	AT1G61260	-1.13	-0.18	-0.67	0.526871	0.699001	-7.11
263900_at	unknown protein ;supported by full-ler	---	AT2G36290	1.07	0.10	0.67	0.52696	0.699079	-7.11
255201_at	putative transposon protein	---	---	1.04	0.06	0.67	0.527084	0.699203	-7.11
252191_at	putative protein various predicted gen	---	AT3G50180	-1.06	-0.09	-0.67	0.527181	0.69929	-7.11
246678_at	putative protein predicted replication A	---	---	-1.06	-0.08	-0.67	0.527212	0.699292	-7.11
257277_at	disease resistance protein, putative si	---	AT3G14470	-1.06	-0.09	-0.67	0.527255	0.699307	-7.11
256597_at	acidic ribosomal protein P2b (rpp2b),	---	AT3G28500	-1.14	-0.19	-0.67	0.527501	0.699526	-7.11
257480_at	hypothetical protein similar to putative	---	AT1G15640	1.11	0.15	0.67	0.527486	0.699526	-7.11
248667_at	putative protein contains similarity to s	---	AT5G48710	1.04	0.06	0.67	0.527512	0.699526	-7.11
265946_s_	putative WD-40 repeat protein, MSI4 a	FVE	AT2G19520 /	1.05	0.07	0.67	0.527606	0.699593	-7.11
262862_at	hypothetical protein predicted by gene	---	AT1G64830	1.08	0.12	0.67	0.527623	0.699593	-7.11
253296_at	putative protein inositol 1,3,4-trisphos	---	AT4G33770	1.05	0.07	0.67	0.527707	0.699601	-7.11
263321_at	ADP-ribosylation factor 1 ;supported b	ARF1A1C	AT2G47170	-1.05	-0.07	-0.67	0.527715	0.699601	-7.11
267626_at	putative cytochrome P450	CYP712A1	AT2G42250	1.09	0.12	0.67	0.527722	0.699601	-7.11
265469_at	unknown protein predicted by genscan	---	AT2G37160	1.04	0.06	0.67	0.527793	0.699654	-7.11
260864_at	hypothetical protein predicted by gens	---	---	-1.06	-0.08	-0.67	0.527929	0.699794	-7.11
265165_at	putative OBP32pep protein	---	AT1G23610	-1.05	-0.07	-0.67	0.528024	0.699838	-7.11
261298_at	cytochrome c oxidase assembly prote	---	AT1G48510	1.05	0.07	0.67	0.52801	0.699838	-7.11
247108_at	ReMembR-H2 protein JR700 (gb|AAF	RMR1	AT5G66160	1.06	0.09	0.66	0.528289	0.700149	-7.11
247233_at	mitochondrial carrier protein-like	---	AT5G64970	1.06	0.09	0.66	0.528332	0.700153	-7.11
258639_at	polygalacturonase (PGA3) identical to	---	AT3G07820	-1.04	-0.06	-0.66	0.528353	0.700153	-7.11
247305_at	Expressed protein ; supported by full-l	---	AT5G63905	-1.16	-0.21	-0.66	0.528583	0.700383	-7.11
267573_at	putative tropinone reductase	---	AT2G30670	1.04	0.06	0.66	0.528588	0.700383	-7.11
265491_s_	putative retroelement pol polyprotein	---	---	1.04	0.06	0.66	0.528705	0.700497	-7.11
249301_at	putative protein similar to unknown pro	---	AT5G41440	1.06	0.09	0.66	0.528779	0.700555	-7.11
246467_at	UDP glucose:flavonoid 3-o-glucosyltra	---	AT5G17040	-1.08	-0.11	-0.66	0.528861	0.700622	-7.11

265251_at	unknown protein predicted by genscan	TET14	AT2G01960	1.05	0.08	0.66	0.528935	0.70068	-7.11
252168_at	putative protein pir7a protein - Oryza s	MES10	AT3G50440	1.18	0.24	0.66	0.529065	0.700811	-7.11
247122_at	putative protein non-consensus AT dc	ATSAC1B	AT5G66020	1.08	0.11	0.66	0.52915	0.700884	-7.11
265509_at	putative retroelement pol polyprotein c	---	---	-1.07	-0.10	-0.66	0.529435	0.70122	-7.11
255501_at	hypothetical protein	---	AT4G02400	1.08	0.12	0.66	0.529548	0.701288	-7.11
261495_at	hypothetical protein predicted by gene	---	AT1G28410	-1.06	-0.08	-0.66	0.529545	0.701288	-7.11
255654_at	Similar to receptor kinase	---	AT4G00970	1.18	0.24	0.66	0.529593	0.701307	-7.11
260827_at	mudrA-like protein similar to Mu transp	AT1G06750	---	-1.08	-0.11	-0.66	0.529653	0.701345	-7.11
249697_at	unknown protein	---	AT5G35510	-1.05	-0.07	-0.66	0.529702	0.70137	-7.11
250786_at	putative protein strong similarity to unk	SDN2	AT5G05540	1.08	0.10	0.66	0.529892	0.701449	-7.11
267467_at	putative C3HC4 zinc finger protein ; s	DRIP2	AT2G30580	-1.06	-0.08	-0.66	0.529976	0.701449	-7.11
261960_at	hypothetical protein similar to putative	---	---	1.04	0.06	0.66	0.529931	0.701449	-7.11
262889_at	hypothetical protein	---	AT1G14800	-1.08	-0.11	-0.66	0.529886	0.701449	-7.11
254551_at	lectin like protein lectin phloem protei	ATPP2-A1	AT4G19840	1.07	0.09	0.66	0.5298	0.701449	-7.11
252111_at	propable disease resistance protein d	---	AT3G51570	-1.08	-0.11	-0.66	0.529968	0.701449	-7.11
267217_at	hypothetical protein	---	AT2G02610	1.04	0.06	0.66	0.529842	0.701449	-7.11
251555_at	shatterproof 1 (SHP1)/ agamous -like 1	SHP1	AT3G58780	-1.05	-0.07	-0.66	0.530391	0.701956	-7.11
246108_at	putative protein retinal glutamic acid-r	---	AT5G28630	1.13	0.18	0.66	0.530519	0.702085	-7.11
257341_at	pseudogene, Mutator-like transposase	---	---	-1.05	-0.07	-0.66	0.530617	0.702174	-7.11
261537_at	carbonyl reductase, putative similar to	---	AT1G01800	1.04	0.06	0.66	0.530748	0.702306	-7.11
261432_at	hypothetical protein predicted by gene	---	AT1G07680	1.05	0.07	0.66	0.530778	0.702306	-7.11
250619_at	A9 ;supported by full-length cDNA: Ce	---	AT5G07230	1.04	0.06	0.66	0.531026	0.702593	-7.11
245606_at	hypothetical protein	---	AT4G14310	1.06	0.08	0.66	0.531112	0.702666	-7.11
258192_at	putative terpene synthase-related prot	---	AT3G29110	1.04	0.06	0.66	0.531219	0.702728	-7.11
259319_at	Snf1-related protein kinase KIN10 (AK	AKIN10	AT3G01090	1.04	0.06	0.66	0.53122	0.702728	-7.11
250280_at	putative protein many predicted protei	---	AT5G13230	-1.07	-0.09	-0.66	0.53131	0.702805	-7.11
256037_at	hypothetical protein predicted by gene	---	AT1G19160	-1.06	-0.08	-0.66	0.531377	0.702853	-7.11
253248_at	Putative S-phase-specific ribosomal pr	---	AT4G34670	1.14	0.19	0.66	0.531571	0.702974	-7.11
252676_at	putative protein	---	AT3G44280	-1.04	-0.06	-0.66	0.531596	0.702974	-7.11
252258_at	putative protein several hypothetical pr	---	AT3G49450	-1.07	-0.09	-0.66	0.53162	0.702974	-7.11
250304_at	elongation factor 1B alpha-subunit (em	---	AT5G12110	-1.18	-0.24	-0.66	0.531622	0.702974	-7.11
246628_at	signal recognition particle 54 kDa prot	---	AT1G48900	1.04	0.06	0.66	0.531558	0.702974	-7.11
265863_at	putative membrane protein	VIT1	AT2G01770	1.07	0.10	0.66	0.531761	0.703082	-7.11
263188_at	hypothetical protein predicted by gens	---	AT1G36095	-1.06	-0.08	-0.66	0.531766	0.703082	-7.11
254354_at	hypothetical protein	---	AT4G22370	-1.04	-0.06	-0.66	0.532006	0.703359	-7.11

263896_at	hypothetical protein predicted by gens	---	AT2G21930	-1.06	-0.09	-0.66	0.532037	0.703359	-7.11
257765_at	hypothetical protein contains Pfam pro	---	AT3G23020	-1.05	-0.07	-0.66	0.532371	0.703456	-7.11
251073_at	putative protein hypothetical proteins -	---	AT5G01750	-1.04	-0.06	-0.66	0.532388	0.703456	-7.11
246625_at	hypothetical protein predicted by gens	---	AT1G48880	1.05	0.08	0.66	0.532277	0.703456	-7.11
258738_at	hypothetical protein similar to hypothet	---	AT3G05750	-1.07	-0.09	-0.66	0.532349	0.703456	-7.11
264127_at	serine/threonine protein kinase, putati	AGC1.7	AT1G79250	1.04	0.06	0.66	0.532309	0.703456	-7.11
258685_at	putative polygalacturonase similar to p	---	AT3G07830	1.07	0.10	0.66	0.532241	0.703456	-7.11
253436_at	ubiquinol-cytochrome c reductase - lik	---	AT4G32470	1.05	0.08	0.66	0.532146	0.703456	-7.11
256515_at	terpene synthase, putative contains P	---	AT1G66020	1.05	0.08	0.66	0.532307	0.703456	-7.11
264780_at	putative protein kinase similar to MAP3	EDR1	AT1G08720	1.07	0.09	0.66	0.532374	0.703456	-7.11
263204_at	hypothetical protein contains similarity	chr31	AT1G05490	1.04	0.06	0.66	0.532799	0.703958	-7.11
261735_at	hypothetical protein similar to hypothet	---	AT1G47765	-1.06	-0.08	-0.66	0.53284	0.703972	-7.12
247476_at	putative protein	---	AT5G62330	-1.05	-0.07	-0.66	0.532983	0.70412	-7.12
257835_at	cytochrome P450 monooxygenase, pu	CYP82G1	AT3G25180	-1.18	-0.23	-0.66	0.533023	0.704133	-7.12
248020_at	putative protein strong similarity to unk	---	AT5G56490	1.05	0.06	0.66	0.533204	0.70425	-7.12
266043_at	hypothetical protein	---	AT2G07724	1.07	0.10	0.66	0.533162	0.70425	-7.12
261260_at	hypothetical protein predicted by gene	---	AT1G26680	-1.05	-0.07	-0.66	0.533187	0.70425	-7.12
262843_at	Expressed protein ; supported by full-le	AtHB32	AT1G14687	-1.08	-0.12	-0.66	0.533454	0.704539	-7.12
246479_at	hypothetical protein	---	AT5G16060	1.05	0.08	0.66	0.533494	0.704551	-7.12
251595_at	putative protein galactose oxidase pre	---	AT3G57620	-1.06	-0.08	-0.66	0.533775	0.704841	-7.12
251857_at	RNA binding protein - like SEB4 prote	---	AT3G54770	1.05	0.08	0.66	0.533771	0.704841	-7.12
263466_at	hypothetical protein predicted by gens	---	AT2G31740	1.05	0.07	0.66	0.533931	0.704979	-7.12
263314_at	putative membrane transporter	---	AT2G05760	-1.04	-0.06	-0.66	0.533996	0.704979	-7.12
257347_at	pseudogene, gene_id:K17E7.6	---	---	-1.05	-0.06	-0.66	0.534009	0.704979	-7.12
249367_at	putative protein predicted protein, Ara	---	AT5G40630	-1.06	-0.08	-0.66	0.534066	0.704979	-7.12
258865_at	NAM-like protein (no apical meristem)	anac045	AT3G03200	-1.04	-0.06	-0.66	0.534065	0.704979	-7.12
265361_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.66	0.533953	0.704979	-7.12
265486_at	unknown protein predicted by genscan	---	AT2G15560	1.07	0.09	0.66	0.534184	0.705094	-7.12
266936_at	hypothetical protein predicted by gene	---	AT2G18920	1.04	0.06	0.65	0.534403	0.705343	-7.12
258410_at	putative ribosomal protein similar to rib	---	AT3G16780	1.14	0.19	0.65	0.534542	0.705486	-7.12
262313_at	unknown protein ;supported by full-len	---	AT1G70900	1.08	0.11	0.65	0.534739	0.705684	-7.12
263468_at	hypothetical protein predicted by gens	---	AT2G31930	-1.06	-0.09	-0.65	0.534754	0.705684	-7.12
264003_at	Expressed protein ; supported by full-le	GEM	AT2G22475	-1.07	-0.10	-0.65	0.534907	0.705757	-7.12
262352_at	hypothetical protein similar to hypothet	---	---	1.09	0.13	0.65	0.534928	0.705757	-7.12
260003_at	unknown protein ;supported by full-ler	IAR1	AT1G68100	1.04	0.06	0.65	0.534895	0.705757	-7.12

258629_at	stelar K+ outward rectifying channel (S	SKOR	AT3G02850	1.04	0.06	0.65	0.534934	0.705757	-7.12
260526_at	putative WD-40 repeat protein	---	AT2G47410	-1.05	-0.07	-0.65	0.535037	0.705813	-7.12
257901_at	hypothetical protein predicted by gens	---	---	1.05	0.07	0.65	0.5351	0.705813	-7.12
265418_at	AP2 domain transcription factor	---	AT2G20880	-1.21	-0.28	-0.65	0.535075	0.705813	-7.12
249498_at	putative protein motif in transcription in	---	AT5G39230	1.05	0.07	0.65	0.535094	0.705813	-7.12
252396_at	hypothetical protein	---	AT3G47980	1.05	0.07	0.65	0.5352	0.705864	-7.12
262122_at	polygalacturonase, putative similar to	PGA4	AT1G02790	1.06	0.08	0.65	0.535173	0.705864	-7.12
266438_at	putative carboxyphosphonoenolpyruva	---	AT2G43180	1.07	0.09	0.65	0.535305	0.70588	-7.12
256614_at	hypothetical protein predicted by gene	---	AT3G29300	-1.05	-0.07	-0.65	0.535258	0.70588	-7.12
250636_at	glycine-rich protein atGRP	GRP18	AT5G07520	1.05	0.08	0.65	0.535282	0.70588	-7.12
259574_at	hypothetical protein	MLP168	AT1G35310	1.04	0.06	0.65	0.535383	0.705942	-7.12
259435_at	hypothetical protein similar to putative	---	AT1G01450	1.05	0.06	0.65	0.53547	0.706016	-7.12
263137_at	gamma glutamyl hydrolase, putative s	ATGGH1	AT1G78660	-1.12	-0.16	-0.65	0.535505	0.706021	-7.12
259445_at	dioxygenase, putative similar to dioxy	GA2OX6	AT1G02400	-1.36	-0.44	-0.65	0.535562	0.706055	-7.12
258821_at	putative wound-induced basic protein	---	AT3G07230	-1.07	-0.09	-0.65	0.535638	0.7061	-7.12
257284_at	TNP1-like protein similar to TNP1 prot	---	---	-1.04	-0.06	-0.65	0.535658	0.7061	-7.12
253288_at	hypothetical protein	---	AT4G34310	1.06	0.08	0.65	0.535768	0.706204	-7.12
266968_at	putative protein kinase contains a prot	---	AT2G39360	-1.13	-0.18	-0.65	0.535817	0.706229	-7.12
260359_at	hypothetical protein predicted by gene	---	AT1G69210	1.07	0.10	0.65	0.53611	0.706574	-7.12
265731_at	putative RNA helicase A 3' end of this	---	AT2G01130	1.04	0.06	0.65	0.536261	0.706731	-7.12
263552_x_	unknown protein proline, tyrosine, and	---	AT2G24980	1.08	0.11	0.65	0.536326	0.706736	-7.12
264536_at	hypothetical protein predicted by gene	PRA1.G1	AT1G55640	-1.08	-0.12	-0.65	0.536323	0.706736	-7.12
253146_at	putative protein predicted protein, Ara	---	AT4G35590	1.05	0.07	0.65	0.536406	0.7068	-7.12
252897_at	cytochrome P450 - like protein cytoch	CYP96A9	AT4G39480 /	-1.05	-0.07	-0.65	0.536507	0.706892	-7.12
256127_at	small GTP-binding protein (RAB11F),	AtRABA6b	AT1G18200	-1.06	-0.09	-0.65	0.536579	0.706947	-7.12
265915_at	En/Spm-like transposon protein relate	---	---	1.05	0.06	0.65	0.536613	0.706951	-7.12
256051_at	hypothetical protein similar to putative	CHX14	AT1G06970	-1.07	-0.09	-0.65	0.536646	0.706954	-7.12
257697_at	hypothetical protein predicted by gene	---	AT3G12700	-1.08	-0.12	-0.65	0.536685	0.706955	-7.12
261040_at	oligouridylate binding protein, putative	UBP1B	AT1G17370	-1.05	-0.07	-0.65	0.53671	0.706955	-7.12
263225_at	putative DNA-binding protein similar t	WRKY14	AT1G30650	1.06	0.08	0.65	0.536992	0.70728	-7.12
255313_at	putative transposon protein	---	---	-1.06	-0.08	-0.65	0.537018	0.70728	-7.12
265263_at	putative DNA binding protein	---	AT2G42940	-1.05	-0.07	-0.65	0.53708	0.707321	-7.12
249241_at	serine carboxypeptidase-II like	scpl41	AT5G42230	1.05	0.07	0.65	0.537201	0.707398	-7.12
266651_at	putative casein kinase I	---	AT2G25760	-1.06	-0.08	-0.65	0.537195	0.707398	-7.12
246478_at	putative protein several hypothetical pr	---	AT5G15980	1.05	0.07	0.65	0.537259	0.707405	-7.12

247616_at	putative protein various predicted prot	---	AT5G60260	-1.05	-0.07	-0.65	0.537268	0.707405	-7.12
258986_at	putative heat shock protein similar to h	---	AT3G08910	-1.06	-0.08	-0.65	0.53737	0.707416	-7.12
263814_at	putative TNP2-like transposon protein	---	---	-1.05	-0.07	-0.65	0.537319	0.707416	-7.12
260216_at	hypothetical protein contains Pfam pro	---	AT1G74580	-1.05	-0.07	-0.65	0.537366	0.707416	-7.12
254323_at	putative protein auxin-induced protein	---	AT4G22620	-1.13	-0.17	-0.65	0.537447	0.707477	-7.12
261001_at	hypothetical protein similar to hypothet	---	AT1G26530	-1.06	-0.09	-0.65	0.537578	0.707537	-7.12
266233_at	putative phloem-specific lectin	AtPP2-B8	AT2G02340	1.04	0.06	0.65	0.53763	0.707537	-7.12
248054_at	unknown protein	---	AT5G55820	-1.07	-0.10	-0.65	0.537648	0.707537	-7.12
252819_at	putative protein several hypothetical pr	---	---	1.04	0.06	0.65	0.537642	0.707537	-7.12
250398_at	putative protein predicted proteins, Ar	---	AT5G11000	1.11	0.15	0.65	0.537575	0.707537	-7.12
266507_at	unknown protein EST matches on the	---	AT2G47860	1.05	0.07	0.65	0.537685	0.707546	-7.12
248682_at	cytochrome b5 (dbj|BAA74840.1) ; su	CB5-D	AT5G48810	1.05	0.07	0.65	0.537806	0.707634	-7.12
267282_at	unknown protein ; supported by cDNA	---	AT2G19390	1.06	0.08	0.65	0.537814	0.707634	-7.12
253591_at	putative protein hypothetical protein, S	MUS81	AT4G30870	1.08	0.11	0.65	0.537856	0.707648	-7.12
255597_at	hypothetical protein	---	AT4G01730	1.06	0.08	0.65	0.537999	0.707795	-7.12
267283_at	Mutator-like transposase similar to MU	---	---	-1.04	-0.06	-0.65	0.538051	0.707823	-7.12
258539_at	putative RNA-binding protein contains	---	AT3G06970	1.05	0.07	0.65	0.538208	0.707958	-7.12
246857_at	putative protein	---	AT5G25920	1.06	0.08	0.65	0.538216	0.707958	-7.12
264419_s_	hypothetical protein contains similarity	---	AT1G43310 /	1.14	0.19	0.65	0.538248	0.707959	-7.12
266029_at	putative serine carboxypeptidase II	scpl38	AT2G05850	-1.05	-0.08	-0.65	0.538312	0.707966	-7.12
263506_s_	hypothetical protein	---	---	1.07	0.09	0.65	0.538351	0.707966	-7.12
265140_at	F-box protein family, AtFBX11 contain	---	AT1G51320	-1.05	-0.07	-0.65	0.538365	0.707966	-7.12
248662_at	unknown protein	---	AT5G48690	-1.05	-0.07	-0.65	0.538408	0.707966	-7.12
257745_at	unknown protein ;supported by full-ler	---	AT3G29240	1.16	0.21	0.65	0.538408	0.707966	-7.12
245044_at	unknown protein Alternative splice forr	---	AT2G26500	1.04	0.06	0.65	0.538471	0.708008	-7.12
252146_at	putative protein steroid sulfotransferas	---	AT3G51210	1.04	0.06	0.65	0.53855	0.708071	-7.12
260564_at	putative small nuclear ribonucleoprotei	---	AT2G43810	-1.06	-0.09	-0.65	0.538639	0.708147	-7.12
257679_at	glycine-rich protein, putative identical	GRP5	AT3G20470	-1.18	-0.24	-0.65	0.53898	0.708513	-7.12
246081_s_	myosin-like protein unconventional my	---	AT5G20470 /	1.08	0.11	0.65	0.538966	0.708513	-7.12
256836_at	pyruvate kinase, putative similar to py	PKP-ALPHA	AT3G22960	-1.07	-0.09	-0.65	0.539292	0.708869	-7.12
266408_at	putative retroelement pol polyprotein	---	---	-1.06	-0.09	-0.65	0.539312	0.708869	-7.12
248065_at	putative protein similar to unknown pro	---	AT5G55580	1.07	0.10	0.65	0.539517	0.708974	-7.12
246680_at	putative protein predicted proteins - Ar	---	---	-1.06	-0.08	-0.65	0.539465	0.708974	-7.12
257068_at	non-LTR reverse transcriptase, putativ	---	---	1.04	0.06	0.65	0.539511	0.708974	-7.12
259716_at	unknown protein	---	AT1G60995 /	-1.07	-0.10	-0.65	0.539461	0.708974	-7.12

260802_at	exopolygalacturonase, putative simila	---	AT1G78400	-1.04	-0.06	-0.65	0.539697	0.70917	-7.12
265741_at	putative membrane transporter ; supp	---	AT2G01320	-1.10	-0.14	-0.65	0.539739	0.709185	-7.12
260521_at	putative villin 2	VLN2	AT2G41740	-1.08	-0.12	-0.65	0.540067	0.709493	-7.12
261799_at	unknown protein contains similarity to	---	AT1G30473	1.07	0.10	0.65	0.540053	0.709493	-7.12
256907_at	hydoxyethylthiazole kinase, putative s	---	AT3G24030	-1.08	-0.11	-0.65	0.540044	0.709493	-7.12
259344_at	putative polynucleotide phosphorylase	RIF10	AT3G03710	1.06	0.09	0.65	0.540151	0.709562	-7.12
263282_at	Expressed protein ; supported by full-l	---	AT2G14095	-1.05	-0.07	-0.65	0.540259	0.709637	-7.12
252638_at	acyl CoA reductase - protein acyl CoA	FAR4	AT3G44540	-1.06	-0.09	-0.65	0.54027	0.709637	-7.12
252093_at	putative protein predicted protein, Ory	---	AT3G51500	1.06	0.08	0.64	0.540438	0.709653	-7.12
247144_at	DOF zinc finger protein-like	---	AT5G65590	1.08	0.11	0.64	0.540397	0.709653	-7.12
256688_at	non-LTR reverse transcriptase, putati	---	AT3G32130	-1.05	-0.06	-0.64	0.540407	0.709653	-7.12
256138_at	Nt-gh3 deduced protein, putative simi	---	AT1G48670	1.07	0.10	0.64	0.540405	0.709653	-7.12
246530_at	Expressed protein ; supported by full-l	---	AT5G15725	1.05	0.07	0.64	0.54043	0.709653	-7.12
248277_at	ABC transporter-like protein	---	AT5G52860	1.07	0.09	0.64	0.540476	0.709663	-7.12
258618_at	Expressed protein ; supported by cDN	GASA5	AT3G02885	-1.07	-0.09	-0.64	0.540523	0.709683	-7.12
249888_s_	zinc finger protein-like ; supported by	---	AT5G22480 /	1.05	0.08	0.64	0.540596	0.709697	-7.12
263944_at	hypothetical protein predicted by gene	---	---	1.04	0.06	0.64	0.540592	0.709697	-7.12
265160_at	unknown protein similar to EST gb|AA	---	AT1G31050	-1.07	-0.09	-0.64	0.540801	0.709925	-7.12
262936_at	hypothetical protein similar to putative	ATCHX2	AT1G79400	1.07	0.10	0.64	0.540904	0.71002	-7.12
254240_at	Expressed protein ; supported by full-l	SP1L5	AT4G23496	-1.05	-0.07	-0.64	0.540937	0.710023	-7.12
265497_at	putative non-LTR retroelement reverse	---	---	1.13	0.17	0.64	0.540973	0.710029	-7.12
263791_at	putative plasma membrane proton ATF	AHA5	AT2G24520	1.09	0.12	0.64	0.541019	0.710049	-7.12
260660_at	hypothetical protein contains Pfam pro	---	AT1G19485	1.07	0.09	0.64	0.541235	0.710099	-7.12
261059_at	transcription factor TINY, putative sim	---	AT1G01250	1.07	0.10	0.64	0.541123	0.710099	-7.12
251171_at	putative protein several hypothetical pr	---	AT3G63220	1.04	0.06	0.64	0.541201	0.710099	-7.12
261870_at	nuclear transport factor 2, putative sim	NTL	AT1G11570	-1.06	-0.08	-0.64	0.541244	0.710099	-7.12
259796_at	hypothetical protein predicted by gene	---	---	-1.06	-0.09	-0.64	0.541194	0.710099	-7.12
245542_at	CONSTANS like protein	---	AT4G15250	1.05	0.08	0.64	0.541214	0.710099	-7.12
253517_at	predicted protein hypothetical protein	---	AT4G31390	1.07	0.10	0.64	0.541497	0.710389	-7.12
262186_at	hypothetical protein	---	AT1G77960	1.12	0.16	0.64	0.541997	0.711005	-7.13
263975_at	hypothetical protein predicted by gene	---	AT2G42710	1.06	0.08	0.64	0.542129	0.711022	-7.13
252883_at	GTP-binding - like protein GTP-bindin	---	AT4G39520	1.07	0.10	0.64	0.542135	0.711022	-7.13
261542_at	unknown protein contains Pfam profile	---	AT1G63560	1.06	0.08	0.64	0.542127	0.711022	-7.13
249117_at	heat shock transcription factor-like pro	AT-HSFA6A	AT5G43840	-1.05	-0.07	-0.64	0.542087	0.711022	-7.13
249773_at	squalene monooxygenase 2 (squalene	SQP2	AT5G24140	-1.05	-0.07	-0.64	0.542179	0.711027	-7.13

263198_at	lipase, putative similar to lipase GI:11	GLIP3	AT1G53990	1.07	0.10	0.64	0.542224	0.711027	-7.13
266454_at	putative bHLH transcription factor	---	AT2G22750	1.05	0.08	0.64	0.542232	0.711027	-7.13
250523_at	putative protein strong similarity to unk	---	AT5G08510	-1.04	-0.06	-0.64	0.542477	0.711266	-7.13
261314_at	putative GTP-binding protein similar to	---	AT1G52980	-1.08	-0.11	-0.64	0.542449	0.711266	-7.13
247211_at	unknown protein ; supported by full-le	---	AT5G64880	-1.10	-0.14	-0.64	0.542554	0.711327	-7.13
245498_at	hypothetical protein	---	AT4G16470	-1.05	-0.06	-0.64	0.542595	0.711333	-7.13
260021_at	unknown protein	---	AT1G30010	1.09	0.13	0.64	0.542621	0.711333	-7.13
250871_at	putative protein	---	AT5G03930	1.06	0.08	0.64	0.542823	0.711516	-7.13
266966_at	hypothetical protein predicted by gens	---	AT2G39520	1.04	0.05	0.64	0.542817	0.711516	-7.13
248260_at	putative protein similar to unknown pro	---	AT5G53240	1.05	0.07	0.64	0.542881	0.711551	-7.13
265655_at	unknown protein contains weak PHD z	---	AT2G13920	-1.05	-0.07	-0.64	0.543025	0.711699	-7.13
259993_at	unknown protein	---	AT1G67960	1.06	0.08	0.64	0.543146	0.711816	-7.13
247463_at	embryo-specific protein - like embryo-	---	AT5G62210	-1.06	-0.08	-0.64	0.543302	0.711951	-7.13
257015_at	hypothetical protein predicted by gene	---	AT3G28680	-1.06	-0.08	-0.64	0.543311	0.711951	-7.13
266586_s_	putative protein	---	---	1.04	0.06	0.64	0.543606	0.712296	-7.13
256462_at	hypothetical protein predicted by gene	---	AT1G36230	-1.06	-0.08	-0.64	0.543776	0.712479	-7.13
257958_at	unknown protein similar to disease res	---	AT3G25510	1.06	0.08	0.64	0.54394	0.712652	-7.13
246291_at	hypothetical protein ; supported by ful	---	AT3G56820	1.06	0.08	0.64	0.544019	0.712714	-7.13
265493_at	unknown protein predicted by genscan	---	AT2G15670	-1.05	-0.07	-0.64	0.544053	0.712718	-7.13
259732_at	putative replication factor C similar to r	---	AT1G77470	1.06	0.08	0.64	0.544145	0.712749	-7.13
250579_at	putative protein terminal ear1, Zea ma	MCT2	AT5G07930	-1.05	-0.07	-0.64	0.544147	0.712749	-7.13
264030_at	putative steroid sulfotransferase	---	AT2G03770	1.06	0.09	0.64	0.544194	0.712749	-7.13
267531_at	putative calcium-dependent protein kin	CPK14	AT2G41860	1.05	0.07	0.64	0.544202	0.712749	-7.13
245512_at	hypothetical protein	---	AT4G15770	1.08	0.12	0.64	0.544287	0.71282	-7.13
252142_at	putative protein hypothetical protein F	---	AT3G51120	1.06	0.09	0.64	0.544384	0.712906	-7.13
266618_at	unknown protein	---	AT2G35480	-1.13	-0.17	-0.64	0.544452	0.712955	-7.13
250009_at	putative protein nuclear FMRP interac	---	AT5G18440	1.11	0.16	0.64	0.544844	0.713304	-7.13
260624_at	high-affinity nitrate transporter ACH2 i	NRT2.2	AT1G08100	-1.08	-0.11	-0.64	0.544781	0.713304	-7.13
253584_at	putative protein several hypothetical pr	---	AT4G30700	-1.05	-0.07	-0.64	0.544809	0.713304	-7.13
250572_at	putative protein	MIR834A	---	1.07	0.10	0.64	0.544814	0.713304	-7.13
253506_at	putative protein EREBP-4 homolog, A	---	AT4G31980	1.09	0.12	0.64	0.544926	0.713337	-7.13
258803_at	unknown protein similar to elicitor resp	WRKY39	AT3G04670	1.05	0.08	0.64	0.544932	0.713337	-7.13
248826_at	casein kinase II beta chain ; supported	CKB1	AT5G47080	1.07	0.09	0.64	0.544993	0.713376	-7.13
248087_at	unknown protein	---	AT5G55060	-1.04	-0.06	-0.64	0.545109	0.713487	-7.13
252094_at	multicatalytic endopeptidase complex	PAD1	AT3G51260	-1.08	-0.11	-0.64	0.54522	0.713555	-7.13

248539_at	ribitol dehydrogenase-like ; supported	---	AT5G50130	-1.06	-0.09	-0.64	0.545295	0.713555	-7.13
255049_at	gibberellin-regulated protein GASA2 p	GASA2	AT4G09610	-1.04	-0.06	-0.64	0.545302	0.713555	-7.13
263463_at	putative ARI-like RING zinc finger prot	---	AT2G31770	-1.04	-0.06	-0.64	0.545225	0.713555	-7.13
251385_at	putative protein various predicted prot	---	AT3G60790	-1.05	-0.08	-0.64	0.545318	0.713555	-7.13
254715_at	putative protein hypothetical protein, S	---	AT4G13550	-1.08	-0.11	-0.64	0.545532	0.713785	-7.13
252316_at	putative protein PrMC3 - Pinus radiata	ATCXE13	AT3G48700	1.05	0.07	0.64	0.545556	0.713785	-7.13
256211_at	gibberellin 20-oxidase, putative simila	GA2OX7	AT1G50960	-1.04	-0.06	-0.64	0.54563	0.713841	-7.13
267003_at	hypothetical protein predicted by gene	---	AT2G34340	-1.05	-0.07	-0.64	0.54584	0.714034	-7.13
249102_at	patatin-like protein	---	AT5G43590	1.04	0.06	0.64	0.545839	0.714034	-7.13
258041_at	Expressed protein ; supported by full-l	ZML1	AT3G21175	1.05	0.08	0.64	0.546042	0.714249	-7.13
263872_at	putative cellulose synthase catalytic su	CESA9	AT2G21770	-1.06	-0.08	-0.64	0.546128	0.714249	-7.13
259744_at	putative ketoacyl-CoA synthase simila	KCS7	AT1G71160	-1.05	-0.07	-0.64	0.54615	0.714249	-7.13
248740_at	putative protein contains similarity to b	---	AT5G48130	1.07	0.10	0.64	0.546132	0.714249	-7.13
263357_s_	Mutator-like transposase similar to MU	---	---	-1.05	-0.06	-0.64	0.546161	0.714249	-7.13
252035_at	beta-ketoacyl-CoA synthase like prote	KCS15	AT3G52160	1.06	0.09	0.64	0.546391	0.714509	-7.13
245378_at	GLABRA2 like protein	HDG4	AT4G17710	-1.05	-0.06	-0.63	0.546457	0.714554	-7.13
267271_at	hypothetical protein predicted by gens	ATHB21	AT2G02540	-1.05	-0.07	-0.63	0.546639	0.714719	-7.13
247353_at	alcohol dehydrogenase-like protein ;s	---	AT5G63620	1.06	0.09	0.63	0.546646	0.714719	-7.13
259263_at	putative UDP-glucose 6-dehydrogenas	---	AT3G01010	-1.05	-0.07	-0.63	0.54678	0.714813	-7.13
254974_at	putative flavanone 3-beta-hydroxylase	---	AT4G10490	-1.05	-0.06	-0.63	0.546769	0.714813	-7.13
262561_at	late embryogenesis abundant protein	---	AT1G34340	-1.05	-0.07	-0.63	0.546828	0.714834	-7.13
259580_at	oxidoreductase, putative contains Pfa	---	AT1G28030	-1.07	-0.09	-0.63	0.546894	0.71488	-7.13
265099_at	unknown protein Location of EST 248	---	AT1G03990	-1.14	-0.19	-0.63	0.546941	0.7149	-7.13
259842_at	phosphoethanolamine N-methyltransf	CPuORF32	AT1G73600 /	1.45	0.53	0.63	0.547066	0.715022	-7.13
262293_at	heat-shock protein 90, putative identic	---	AT1G27640	-1.08	-0.11	-0.63	0.547126	0.71506	-7.13
267329_at	hypothetical protein	---	AT2G19250	1.05	0.07	0.63	0.547178	0.715088	-7.13
247969_at	putative protein similar to unknown pro	---	AT5G56700	-1.09	-0.12	-0.63	0.547454	0.715406	-7.13
256764_at	hypothetical protein predicted by gens	---	AT3G29310	-1.07	-0.09	-0.63	0.547497	0.715421	-7.13
254386_at	peroxidase prxr1 ;supported by full-le	PRXR1	AT4G21960	1.11	0.14	0.63	0.547569	0.715476	-7.13
267091_at	Expressed protein ; supported by full-l	---	AT2G38185	1.08	0.11	0.63	0.547603	0.715478	-7.13
254855_s_	putative protein other predicted protei	---	AT4G12140 /	1.06	0.09	0.63	0.547709	0.715577	-7.13
245946_at	putative protein glyoxal oxidase precu	---	AT5G19580	1.07	0.09	0.63	0.547755	0.715595	-7.13
248915_at	putative protein strong similarity to unk	---	AT5G45690	1.06	0.08	0.63	0.547891	0.715731	-7.13
245091_at	unknown protein	---	AT2G40910	1.05	0.08	0.63	0.547925	0.715735	-7.13
256467_at	copia-type polyprotein, putative simila	---	---	-1.05	-0.07	-0.63	0.548109	0.715926	-7.13

255149_at	KNAT1 homeobox-like protein	KNAT1	AT4G08150	1.06	0.08	0.63	0.548133	0.715926	-7.13
251830_at	phosphoribosylformylglycinamidine cy	PUR5	AT3G55010	1.10	0.13	0.63	0.548231	0.715929	-7.13
257787_at	actin related protein, putative similar t	ARP2	AT3G27000	-1.04	-0.06	-0.63	0.548193	0.715929	-7.13
254648_at	lipase-like protein Pn47p, Ipomoea nil	---	AT4G18550	-1.05	-0.07	-0.63	0.548217	0.715929	-7.13
248039_at	putative protein similar to unknown pro	---	AT5G55950	-1.04	-0.06	-0.63	0.548271	0.715941	-7.13
260586_at	unknown protein predicted by genefind	---	AT2G43630	-1.06	-0.08	-0.63	0.54836	0.716016	-7.13
265035_at	hypothetical protein contains Pfam pro	---	AT1G61620	1.06	0.08	0.63	0.548631	0.716329	-7.13
252817_at	putative protein hypothetical proteins -	---	---	1.06	0.09	0.63	0.548804	0.716499	-7.13
254005_at	subtilisin-like serine protease contains	UNE17	AT4G26330	-1.07	-0.10	-0.63	0.548824	0.716499	-7.13
260480_at	Ser/Thr kinase ;supported by full-leng	SNRK2.4	AT1G10940	1.04	0.06	0.63	0.548946	0.716535	-7.13
254075_at	DRE CRT-binding protein DREB1C in	CBF2	AT4G25470	-1.09	-0.13	-0.63	0.548886	0.716535	-7.13
257491_at	hypothetical protein predicted by gene	---	AT1G06170	-1.04	-0.06	-0.63	0.548933	0.716535	-7.13
252505_at	dehydrogenase -like protein alcohol d	---	AT3G46170	1.06	0.08	0.63	0.549108	0.716706	-7.13
266903_at	hypothetical protein predicted by gens	MEE21	AT2G34570	1.05	0.06	0.63	0.549153	0.716723	-7.13
265792_at	predicted by genscan and genefinder	---	AT2G01390	-1.06	-0.08	-0.63	0.549269	0.716751	-7.13
264143_at	latex-abundant protein, putative simila	ATMC5	AT1G79330	-1.05	-0.07	-0.63	0.549262	0.716751	-7.13
261726_at	putative auxin-independent growth pro	---	AT1G76270	-1.09	-0.13	-0.63	0.549226	0.716751	-7.13
252754_at	putative protein hypothetical protein re	---	---	1.09	0.13	0.63	0.549555	0.716877	-7.13
245672_at	polygalacturonase, putative similar to	---	AT1G56710	1.07	0.10	0.63	0.549584	0.716877	-7.13
257544_at	putative DNA-binding protein similar to	---	AT3G20880	1.06	0.09	0.63	0.549556	0.716877	-7.13
255524_at	hypothetical protein similar to pectines	ATPMEPCR	AT4G02330	1.27	0.34	0.63	0.549486	0.716877	-7.13
263830_at	hypothetical protein predicted by gene	---	AT2G40260	-1.05	-0.07	-0.63	0.549428	0.716877	-7.13
254175_at	putative protein CGI-82 protein - Hom	---	AT4G24050	-1.05	-0.07	-0.63	0.549529	0.716877	-7.13
257616_at	hypothetical protein contains Pfam pro	---	AT3G26540	-1.07	-0.09	-0.63	0.549561	0.716877	-7.13
265834_at	hypothetical protein predicted by gens	---	AT2G14410	-1.04	-0.06	-0.63	0.549874	0.717214	-7.13
247847_at	putative protein predicted proteins, Ho	---	AT5G58110	1.08	0.11	0.63	0.550182	0.717574	-7.13
248456_at	putative protein similar to unknown pro	---	AT5G51380	-1.04	-0.06	-0.63	0.550446	0.717877	-7.13
258556_at	UDP-glucose:sterol glucosyltransferas	---	AT3G07020	1.06	0.08	0.63	0.550502	0.717909	-7.14
253154_at	putative protein predicted protein, Ara	---	AT4G35710	1.06	0.08	0.63	0.550546	0.717925	-7.14
255126_at	putative protein hypothetical protein s	---	AT4G08270	-1.04	-0.06	-0.63	0.550597	0.717951	-7.14
258881_at	unknown protein ; supported by full-le	---	AT3G06310	1.05	0.08	0.63	0.55093	0.718026	-7.14
246103_at	putative protein	AN3	AT5G28640	1.04	0.06	0.63	0.55079	0.718026	-7.14
245306_at	Expressed protein ; supported by full-l	ELIP2	AT4G14690	1.06	0.09	0.63	0.550932	0.718026	-7.14
265774_at	hypothetical protein predicted by gens	---	AT2G07240	-1.07	-0.10	-0.63	0.551053	0.718026	-7.14
257380_at	hypothetical protein predicted by gene	---	AT2G28090	-1.06	-0.08	-0.63	0.550721	0.718026	-7.14

265782_at	putative two-component response regu	---	AT2G07440	-1.05	-0.08	-0.63	0.550854	0.718026	-7.14
255642_at	hypothetical protein	iqd17	AT4G00820	1.09	0.12	0.63	0.550822	0.718026	-7.14
258543_at	unknown protein	---	AT3G06870	-1.06	-0.08	-0.63	0.550775	0.718026	-7.14
253554_at	putative protein predicted protein, Cae	---	AT4G30940	-1.08	-0.11	-0.63	0.550857	0.718026	-7.14
246121_at	putative protein motif in PGPS/D10 - P	---	AT5G20370	1.06	0.08	0.63	0.55103	0.718026	-7.14
266890_at	acyl carrier protein identical to GB:L23	MTACP-1	AT2G44620	-1.06	-0.09	-0.63	0.551064	0.718026	-7.14
253056_at	SHORT-ROOT (SHR)	SHR	AT4G37650	-1.09	-0.13	-0.63	0.550988	0.718026	-7.14
262597_at	unknown protein Strong similarity to g	---	AT1G15470	-1.07	-0.10	-0.63	0.550976	0.718026	-7.14
250826_at	unknown protein ; supported by cDNA	---	AT5G05220	-1.05	-0.08	-0.63	0.551355	0.718077	-7.14
264567_s_	putative peroxidase ATP12a Strong sir	---	AT1G05240 /	-1.06	-0.08	-0.63	0.551331	0.718077	-7.14
250373_at	putative protein	---	AT5G11470	-1.04	-0.06	-0.63	0.551285	0.718077	-7.14
265631_at	putative helicase	---	---	-1.04	-0.06	-0.63	0.551257	0.718077	-7.14
266659_at	putative poly(A) polymerase ; support	---	AT2G25850	-1.05	-0.07	-0.63	0.551234	0.718077	-7.14
264842_at	hypothetical protein predicted by gens	---	AT1G03700	1.04	0.06	0.63	0.55117	0.718077	-7.14
252684_at	disease resistence - like protein RPP1	---	AT3G44400	1.05	0.07	0.63	0.551247	0.718077	-7.14
262869_s_	putative protein predicted protein, Cae	GTG1	AT1G64990 /	-1.06	-0.09	-0.63	0.551309	0.718077	-7.14
263071_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.63	0.551421	0.718081	-7.14
256035_at	Ran-binding protein (atranbp1a) identi	SIRANBP	AT1G07140	1.06	0.08	0.63	0.551396	0.718081	-7.14
263479_x_	hypothetical protein predicted by gens	---	---	1.05	0.07	0.63	0.551494	0.718136	-7.14
256926_at	hypothetical protein predicted by gene	---	AT3G22540	-1.07	-0.10	-0.63	0.55177	0.718454	-7.14
258013_at	unknown protein	---	AT3G19320	-1.07	-0.09	-0.63	0.551813	0.718469	-7.14
257320_at	hypothetical protein	---	AT2G07749	1.06	0.08	0.63	0.551892	0.71853	-7.14
260527_at	unknown protein ;supported by full-ler	---	AT2G47270	1.20	0.26	0.63	0.551989	0.718535	-7.14
257742_at	hypothetical protein predicted by gene	SDH2-1	AT3G27380	1.05	0.07	0.63	0.55198	0.718535	-7.14
254782_at	putative calmodulin calmodulin - Chla	UNE14	AT4G12860	1.06	0.08	0.63	0.551931	0.718535	-7.14
246415_at	putative protein (fragment) predicted p	---	AT5G17160	1.08	0.11	0.63	0.552219	0.718793	-7.14
266075_s_	unknown protein	---	AT2G40710 /	1.06	0.09	0.63	0.552259	0.718804	-7.14
261380_at	hypothetical protein predicted by gene	---	AT1G05400	-1.07	-0.10	-0.63	0.552356	0.718889	-7.14
262439_at	hypothetical protein identical to hypoth	---	AT1G47730	-1.04	-0.06	-0.63	0.552394	0.718897	-7.14
251011_at	putative protein histone H2A, garden p	HTA12	AT5G02560	-1.05	-0.06	-0.63	0.552436	0.71891	-7.14
247649_at	KED - like protein KED, Nicotiana taba	---	AT5G60030	-1.06	-0.08	-0.63	0.552478	0.718924	-7.14
247112_at	unknown protein	---	AT5G65950	1.05	0.08	0.62	0.552584	0.718925	-7.14
245782_at	60S ribosomal protein (fragment), puta	---	AT1G35200	-1.07	-0.10	-0.63	0.552532	0.718925	-7.14
263901_at	unknown protein ;supported by full-ler	---	AT2G36320	-1.07	-0.10	-0.62	0.552604	0.718925	-7.14
254165_at	putative protein hypothetical protein -	---	AT4G24330	-1.07	-0.10	-0.63	0.552559	0.718925	-7.14

258322_at	putative selenocysteine methyltransfer	HMT3	AT3G22740	1.17	0.23	0.62	0.552675	0.718943	-7.14
248210_at	ethylene-forming-enzyme-like dioxyge	---	AT5G54000	1.05	0.07	0.62	0.552682	0.718943	-7.14
246804_at	putative protein	---	---	-1.04	-0.06	-0.62	0.552784	0.719035	-7.14
263050_at	unknown protein ; supported by cDNA	ATVPS11	AT2G05170	-1.05	-0.07	-0.62	0.552853	0.719084	-7.14
251932_at	pasticcino 1 ; supported by cDNA: gi_	PAS1	AT3G54010	-1.05	-0.07	-0.62	0.552937	0.719091	-7.14
265925_at	hypothetical protein predicted by gens	---	AT2G18610	1.05	0.07	0.62	0.55295	0.719091	-7.14
250260_at	putative protein contains similarity to u	---	AT5G13810	-1.06	-0.08	-0.62	0.552953	0.719091	-7.14
251694_s_	putative protein NAM (no apical meris	anac063	AT3G55210 /	-1.04	-0.06	-0.62	0.553034	0.719115	-7.14
249180_at	26S proteasome AAA-ATPase subunit	RPT4A	AT5G43010	-1.07	-0.10	-0.62	0.553013	0.719115	-7.14
248757_at	putative protein contains similarity to u	---	AT5G47680	1.04	0.06	0.62	0.553067	0.719116	-7.14
263916_at	hypothetical protein predicted by gens	---	AT2G36440	-1.05	-0.08	-0.62	0.553114	0.719136	-7.14
265613_at	putative DnaJ protein ; supported by c	---	AT2G25560	-1.06	-0.09	-0.62	0.553257	0.719241	-7.14
245070_at	metallothionein-like protein identical to	---	AT2G23240	-1.07	-0.09	-0.62	0.553258	0.719241	-7.14
265489_at	hypothetical protein predicted by gens	---	AT2G15640	1.07	0.10	0.62	0.553307	0.719243	-7.14
247426_at	putative protein contains similarity to c	---	AT5G62570	1.10	0.14	0.62	0.553322	0.719243	-7.14
250717_at	putative protein similar to unknown pro	---	AT5G06200	-1.07	-0.09	-0.62	0.553358	0.719249	-7.14
263173_at	hypothetical protein predicted by gene	BRX-LIKE3	AT1G54180	-1.04	-0.06	-0.62	0.553395	0.719256	-7.14
256056_at	hypothetical protein contains similarity	---	AT1G07190	1.04	0.06	0.62	0.553722	0.719572	-7.14
267394_s_	putative cellulase	AtGH9B9	AT2G44540 /	-1.05	-0.08	-0.62	0.553764	0.719572	-7.14
245452_at	retrotransposon like protein	---	---	-1.04	-0.06	-0.62	0.553737	0.719572	-7.14
245021_at	PSII component	---	---	-1.07	-0.09	-0.62	0.553691	0.719572	-7.14
252958_at	putative transcription factor (MYB4) ; s	MYB4	AT4G38620	1.14	0.19	0.62	0.554204	0.719917	-7.14
263462_at	similar to Ariadne protein from Drosop	ARI11	AT2G31780	-1.05	-0.07	-0.62	0.554195	0.719917	-7.14
265891_at	putative thionin	---	AT2G15010	1.05	0.07	0.62	0.554219	0.719917	-7.14
259183_at	hypothetical protein similar to putative	---	AT3G01580	1.07	0.10	0.62	0.554207	0.719917	-7.14
264666_at	hypothetical protein Similar to N. tabac	---	AT1G09680	-1.07	-0.09	-0.62	0.554157	0.719917	-7.14
252782_at	putative protein predicted proteins, Ar	---	---	1.04	0.06	0.62	0.55419	0.719917	-7.14
258231_at	hypothetical protein contains Pfam pro	RCK	AT3G27730	-1.04	-0.06	-0.62	0.554329	0.719977	-7.14
250781_at	DREB2A (dbj|BAA33794.1) ; supporte	DREB2A	AT5G05410	1.10	0.14	0.62	0.554323	0.719977	-7.14
265209_at	putative DNA binding protein with hom	ATHB22	AT2G36610	1.04	0.06	0.62	0.554508	0.720169	-7.14
264430_at	cineole synthase, putative similar to 1	TPS14	AT1G61680	-1.05	-0.07	-0.62	0.554636	0.720294	-7.14
257601_at	hypothetical protein predicted by gene	---	AT3G24820	1.05	0.06	0.62	0.554763	0.720336	-7.14
257691_at	hypothetical protein predicted by gene	FLA14	AT3G12660	1.07	0.10	0.62	0.554703	0.720336	-7.14
257921_at	hypothetical protein contains Pfam pro	---	AT3G23270	1.04	0.06	0.62	0.554743	0.720336	-7.14
260780_at	valyl-tRNA synthetase, putative simila	TWN2	AT1G14610	-1.04	-0.06	-0.62	0.55491	0.720486	-7.14

256389_at	hypothetical protein predicted by gene	---	AT3G06220	1.05	0.07	0.62	0.555103	0.720683	-7.14
255769_at	hypothetical protein predicted by gene	---	AT1G18610	-1.05	-0.07	-0.62	0.555125	0.720683	-7.14
263620_at	hypothetical protein predicted by gens	---	---	-1.05	-0.07	-0.62	0.555452	0.721066	-7.14
247916_at	adenosylmethionine-8-amino-7-oxonor	BIO1	AT5G57590	-1.05	-0.07	-0.62	0.55553	0.721085	-7.14
256208_at	hypothetical protein predicted by gene	---	AT1G50930	1.04	0.05	0.62	0.555514	0.721085	-7.14
245312_at	Expressed protein ; supported by full-l	---	AT4G14600	-1.07	-0.09	-0.62	0.555603	0.721139	-7.14
263372_at	60S ribosomal protein L14 ;supported	---	AT2G20450	-1.12	-0.16	-0.62	0.555726	0.721217	-7.14
257049_at	hypothetical protein predicted by gens	---	AT3G15250	1.07	0.09	0.62	0.555713	0.721217	-7.14
263631_at	unknown protein ; supported by full-le	---	AT2G04900	1.04	0.06	0.62	0.555765	0.721226	-7.14
252063_at	lipid transfer protein-like protein lipid t	LTP12	AT3G51590	-1.05	-0.07	-0.62	0.555917	0.721383	-7.14
264863_at	putative peroxidase similar to peroxida	---	AT1G24110	-1.06	-0.08	-0.62	0.556058	0.721525	-7.14
254455_at	hypothetical protein	---	AT4G21140	1.08	0.11	0.62	0.556173	0.721592	-7.14
249656_at	putative protein hypothetical proteins -	---	AT5G37130	1.04	0.06	0.62	0.556154	0.721592	-7.14
264145_at	latex-abundant protein, putative simila	AtMC7	AT1G79310	1.04	0.06	0.62	0.556278	0.721688	-7.14
250682_x_	putative protein similar to unknown pro	---	AT5G06630	-1.12	-0.17	-0.62	0.556337	0.721722	-7.14
250147_at	putative protein predicted proteins, Dr	---	AT5G14600	-1.08	-0.11	-0.62	0.556515	0.721871	-7.14
261968_at	disease resistance protein RPP1-WsE	---	AT1G65850	1.04	0.06	0.62	0.556499	0.721871	-7.14
261321_at	hypothetical protein predicted by gene	---	AT1G44740	-1.05	-0.07	-0.62	0.556629	0.721897	-7.14
254138_at	hypothetical protein	---	AT4G24950	-1.05	-0.07	-0.62	0.556617	0.721897	-7.14
250630_at	hypothetical protein	---	AT5G07400	1.06	0.09	0.62	0.556569	0.721897	-7.14
263908_at	hypothetical protein predicted by gene	---	AT2G36480	-1.05	-0.07	-0.62	0.556697	0.721943	-7.14
261914_at	dirigent protein, putative similar to diri	---	AT1G65870	-1.07	-0.10	-0.62	0.556827	0.72203	-7.14
258749_at	hypothetical protein predicted by gens	---	AT3G05760	-1.06	-0.08	-0.62	0.556814	0.72203	-7.14
266724_at	hypothetical protein predicted by gens	---	AT2G03180	1.04	0.06	0.62	0.556925	0.722115	-7.14
258849_at	putative UDP-glucose pyrophosphoryla	UGP	AT3G03250	-1.07	-0.09	-0.62	0.557085	0.7222	-7.14
265887_at	biotin holocarboxylase synthetase ider	HCS1	AT2G25710	-1.06	-0.09	-0.62	0.55706	0.7222	-7.14
264359_at	hypothetical protein predicted by gene	---	AT1G03320	1.06	0.08	0.62	0.557075	0.7222	-7.14
262540_at	hypothetical protein predicted by gene	---	AT1G34260	-1.08	-0.12	-0.62	0.557135	0.722224	-7.14
259339_at	putative adenylylsulfate kinase similar	---	AT3G03900	1.07	0.09	0.62	0.557322	0.722425	-7.14
262358_at	mandelonitrile lyase, putative similar t	---	AT1G73050	1.06	0.08	0.62	0.557411	0.7225	-7.14
260523_at	putative salt-inducible protein	EMB2654	AT2G41720	1.07	0.10	0.62	0.557632	0.722744	-7.14
248301_at	DnaJ protein-like	---	AT5G53150	1.05	0.06	0.62	0.557752	0.722859	-7.14
260177_at	hypothetical protein predicted by gens	---	AT1G70650	-1.08	-0.11	-0.62	0.558	0.723139	-7.14
251735_at	putative protein ferritin 2 precursor - V	ATFER3	AT3G56090	1.12	0.17	0.62	0.558124	0.723259	-7.14
265952_at	unknown protein supported by cDNA:	---	AT2G37478 /	-1.05	-0.07	-0.62	0.558213	0.723333	-7.14

252705_at	putative protein predicted proteins, Ar	---	---	1.07	0.09	0.62	0.558272	0.723369	-7.14
261876_at	pirin-like protein similar to pirin GB:AA	---	AT1G50590	1.14	0.18	0.62	0.558357	0.723438	-7.14
257845_at	unknown protein GC donor splice site	---	AT3G28430	1.05	0.07	0.62	0.558404	0.723457	-7.14
255664_at	putative protein	---	AT4G00440	-1.04	-0.06	-0.62	0.558455	0.723483	-7.14
257069_at	hypothetical protein predicted by gens	---	AT3G28170	-1.05	-0.06	-0.62	0.558516	0.72352	-7.14
259754_at	hypothetical protein predicted by gens	---	AT1G71090	1.05	0.08	0.62	0.558625	0.723614	-7.14
258492_at	unknown protein	---	AT3G02390	-1.05	-0.06	-0.62	0.558683	0.723614	-7.14
245601_at	hypothetical protein	---	AT4G14240	-1.06	-0.08	-0.62	0.558673	0.723614	-7.14
263063_s_	putative peroxidase	---	AT2G18140 /	1.08	0.11	0.62	0.558765	0.723638	-7.14
262723_at	hypothetical protein predicted by gene	---	AT1G43630	-1.07	-0.09	-0.62	0.558758	0.723638	-7.14
247056_at	SWI2/SNF2-like protein (gb|AAD28303	CHR1	AT5G66750	-1.05	-0.07	-0.61	0.558981	0.723877	-7.14
264579_at	Expressed protein ; supported by full-l	---	AT1G05205	1.07	0.10	0.61	0.559103	0.723993	-7.14
265027_at	putative ribonuclease III similar to EST	NFD2	AT1G24450	-1.07	-0.09	-0.61	0.559349	0.724024	-7.14
256705_at	cytochrome P450, putative similar to (	CYP702A8	AT3G30290	-1.06	-0.08	-0.61	0.559348	0.724024	-7.14
251358_at	shaggy-like kinase beta	---	AT3G61160	-1.12	-0.16	-0.61	0.559271	0.724024	-7.14
247501_at	putative protein predicted proteins, Ar	---	AT5G61920	1.04	0.06	0.61	0.559286	0.724024	-7.14
266517_at	glycine decarboxylase complex H-prot	---	AT2G35120	1.12	0.16	0.61	0.55928	0.724024	-7.14
249813_at	acyltransferase ; supported by full-len	EMB3009	AT5G23940	-1.04	-0.06	-0.61	0.559283	0.724024	-7.14
245703_at	S-adenosyl-L-methionine:salicylic acid	---	AT5G04380	1.05	0.06	0.61	0.559288	0.724024	-7.14
260178_at	hypothetical protein similar to unknowr	---	AT1G70720	-1.05	-0.07	-0.61	0.559557	0.724252	-7.14
265201_at	unknown protein	---	AT2G36810	1.04	0.06	0.61	0.559633	0.724306	-7.14
255354_at	putative transposon protein	---	---	-1.04	-0.06	-0.61	0.559662	0.724306	-7.14
245056_at	putative glucosyltransferase	UGT76D1	AT2G26480	1.07	0.10	0.61	0.559743	0.724329	-7.15
257116_at	arginine methyltransferase, putative s	PRMT6	AT3G20020	-1.06	-0.08	-0.61	0.559716	0.724329	-7.15
247225_at	inositol-1, 4, 5-trisphosphate 5-phosph	BST1	AT5G65090	-1.06	-0.08	-0.61	0.559804	0.724367	-7.15
258069_at	hypothetical protein predicted by gene	---	AT3G26010	1.07	0.10	0.61	0.559843	0.724375	-7.15
250965_at	putative protein various predicted prot	---	AT5G03020	1.04	0.06	0.61	0.559881	0.724383	-7.15
253132_at	NAM / CUC2 -like protein nap gene, A	NTL9	AT4G35580	1.06	0.08	0.61	0.559992	0.724445	-7.15
247852_at	ATGP1 ; supported by cDNA: gi_1335	YKT61	AT5G58060	1.05	0.07	0.61	0.55998	0.724445	-7.15
254934_at	putative Ap2 domain protein DNA-bin	CRF1	AT4G11140	1.06	0.08	0.61	0.560043	0.72447	-7.15
266787_at	putative receptor-like protein kinase	---	AT2G28990	1.04	0.06	0.61	0.560168	0.724591	-7.15
259454_at	unknown protein similar to hypothetica	---	AT1G44050	-1.06	-0.08	-0.61	0.560371	0.724812	-7.15
264882_at	NAM protein, putative similar to NAM	anac025	AT1G61110	1.05	0.06	0.61	0.560499	0.724896	-7.15
246084_at	putative protein predicted proteins, Ar	ATBRXL4	AT5G20540	-1.05	-0.07	-0.61	0.56048	0.724896	-7.15
246239_at	putative protein	---	AT4G36790	-1.05	-0.07	-0.61	0.560577	0.724914	-7.15

266844_at	hypothetical protein predicted by gene	---	AT2G26120	-1.05	-0.08	-0.61	0.560547	0.724914	-7.15
256224_at	GTP-binding protein (SAR1B) identica	ATSAR1B	AT1G56330	-1.07	-0.10	-0.61	0.560745	0.725091	-7.15
261509_at	hypothetical protein predicted by gene	---	AT1G71740	-1.07	-0.10	-0.61	0.560963	0.72533	-7.15
252689_at	putative protein predicted proteins, Ar	---	AT3G44030	-1.05	-0.07	-0.61	0.561047	0.725399	-7.15
263295_at	putative MADS-box protein ANR1	AGL44	AT2G14210	1.04	0.06	0.61	0.561119	0.725451	-7.15
254811_at	putative protein 2-hydroxy-6-oxohepta	---	AT4G12230	1.05	0.08	0.61	0.56121	0.725526	-7.15
264183_at	unknown protein	CLV2	AT1G65380	1.06	0.08	0.61	0.561314	0.72562	-7.15
257561_at	hypothetical protein predicted by gene	APUM25	AT3G24270	1.05	0.07	0.61	0.56167	0.72604	-7.15
257683_at	hypothetical protein predicted by gene	---	AT3G13280	-1.05	-0.07	-0.61	0.561895	0.726281	-7.15
263485_at	putative villin ; supported by cDNA: gi	VLN1	AT2G29890	-1.05	-0.07	-0.61	0.561921	0.726281	-7.15
257244_at	receptor kinase, putative similar to CL	---	AT3G24240	-1.10	-0.13	-0.61	0.562093	0.726462	-7.15
264205_at	hypothetical protein identical to hypoth	---	AT1G22790	-1.04	-0.06	-0.61	0.562303	0.726692	-7.15
255831_at	hypothetical protein predicted by gens	---	AT2G33350	1.05	0.07	0.61	0.562337	0.726696	-7.15
247895_at	putative protein bHLH transcription fa	---	AT5G58010	-1.05	-0.07	-0.61	0.562395	0.726729	-7.15
259024_at	hypothetical protein predicted by gene	---	---	1.07	0.09	0.61	0.562491	0.726812	-7.15
246390_at	1-aminocyclopropane-1-carboxylate o	---	AT1G77330	-1.07	-0.10	-0.61	0.562813	0.727119	-7.15
AFFX-r2-E	E. coli /GEN=bioC /DB_XREF=gb:J04	---	---	1.12	0.16	0.61	0.562824	0.727119	-7.15
248692_s_	hypothetical protein	---	AT4G15070 /	1.05	0.07	0.61	0.562814	0.727119	-7.15
247156_at	lysosomal Pro-X carboxypeptidase	---	AT5G65760	-1.05	-0.07	-0.61	0.562876	0.727145	-7.15
254510_at	cadinene synthase like protein (+)-del	---	AT4G20210	1.06	0.09	0.61	0.562969	0.727225	-7.15
254514_at	hypothetical protein	---	AT4G20250	-1.06	-0.09	-0.61	0.563026	0.727257	-7.15
258257_at	putative short chain alcohol dehydroge	---	AT3G26770	1.04	0.06	0.61	0.563152	0.727378	-7.15
261157_at	peroxidase ATP13a, putative similar t	---	AT1G34510	-1.04	-0.06	-0.61	0.563245	0.727457	-7.15
254394_at	subtilisin-like serine protease contains	---	AT4G21630	-1.04	-0.06	-0.61	0.563347	0.727548	-7.15
260085_at	putative D-ribulose-5-phosphate simila	---	AT1G63290	1.04	0.06	0.61	0.563556	0.727739	-7.15
255532_at	hypothetical protein similar to orf at er	---	AT4G02170	-1.07	-0.10	-0.61	0.563559	0.727739	-7.15
263686_at	putative 60s ribosomal protein L10 Ne	---	AT1G26910	1.08	0.11	0.61	0.563652	0.727769	-7.15
249673_at	cytochrome P450-like	CYP79A4P	AT5G35920	-1.04	-0.05	-0.61	0.56365	0.727769	-7.15
251112_s_	pyruvate decarboxylase-like protein p	PDC3	AT5G01320 /	-1.07	-0.10	-0.61	0.563678	0.727769	-7.15
253988_at	putative protein elongation factor P (e	---	AT4G26310	-1.05	-0.06	-0.61	0.563869	0.727975	-7.15
249954_at	putative protein ;supported by full-leng	---	AT5G18920	-1.04	-0.05	-0.61	0.564138	0.728198	-7.15
259452_at	En/Spm-like transposon protein, putat	---	---	1.05	0.07	0.61	0.56413	0.728198	-7.15
263091_at	unknown protein	---	AT2G16200	1.05	0.07	0.61	0.564111	0.728198	-7.15
253350_at	hypothetical protein	---	AT4G33690	-1.05	-0.06	-0.61	0.564183	0.728215	-7.15
263641_at	putative non-LTR retroelement reverse	---	---	-1.04	-0.06	-0.61	0.564262	0.728275	-7.15

261778_at	hypothetical protein predicted by gene	---	AT1G76220	-1.04	-0.06	-0.61	0.564303	0.728287	-7.15
261163_x_	auxin response factor, putative similar	ARF21	AT1G34410	1.04	0.06	0.61	0.564401	0.728332	-7.15
257617_at	hypothetical protein	---	AT3G26550	-1.05	-0.06	-0.61	0.564433	0.728332	-7.15
264235_at	myosin, putative similar to myosin GI:	XIE	AT1G54560	-1.06	-0.08	-0.61	0.564415	0.728332	-7.15
250376_at	putative protein	---	AT5G11550	1.09	0.12	0.61	0.56447	0.728338	-7.15
265111_at	similar to 14KD proline-rich protein DC	---	AT1G62510	1.29	0.36	0.61	0.564684	0.728573	-7.15
262113_at	late embryogenis abundant protein, pu	---	AT1G02820	-1.11	-0.15	-0.61	0.564813	0.728699	-7.15
250456_at	26S proteasome p55 protein-like ; sup	EMB2107	AT5G09900	-1.07	-0.10	-0.61	0.564943	0.728798	-7.15
255671_at	Expressed protein ; supported by full-l	---	AT4G00355	1.06	0.08	0.61	0.564954	0.728798	-7.15
257572_at	hypothetical protein predicted by gene	---	AT3G16880	-1.06	-0.08	-0.60	0.565022	0.728844	-7.15
264691_s_	putative reverse transcriptase	---	---	-1.05	-0.07	-0.60	0.565071	0.728867	-7.15
265185_at	OBP32pep protein, putative identical t	---	AT1G23670	1.06	0.08	0.60	0.56536	0.729198	-7.15
250349_at	putative receptor - like kinase recepto	---	AT5G12000	-1.05	-0.07	-0.60	0.565445	0.729225	-7.15
252781_at	polygalacturonase -like protein polyga	---	AT3G42950	1.05	0.07	0.60	0.565424	0.729225	-7.15
253077_at	hypothetical protein	---	AT4G36170	1.04	0.06	0.60	0.565613	0.7294	-7.15
255903_at	myb-like protein, putative similar to my	MYB52	AT1G17950	1.04	0.06	0.60	0.565694	0.729463	-7.15
251954_at	putative protein predicted protein, Ara	CPuORF51	AT3G53668 /	-1.12	-0.16	-0.60	0.565838	0.729607	-7.15
249336_at	putative protein similar to unknown pro	DRB5	AT5G41070	-1.09	-0.12	-0.60	0.566031	0.729816	-7.15
265295_at	putative DNA replication licensing fact	MCM9	AT2G14050	1.06	0.08	0.60	0.566167	0.729949	-7.15
252777_at	hypothetical protein	---	AT3G42970	1.05	0.07	0.60	0.566285	0.730061	-7.15
263235_at	serine/threonine protein phosphatase,	PP2A-2	AT1G10430	1.05	0.07	0.60	0.566328	0.730075	-7.15
255432_at	SYR1-like syntaxin ;supported by full-	SYP123	AT4G03330	1.05	0.07	0.60	0.566368	0.730085	-7.15
258157_at	putative MYB family transcription facto	MYB4R1	AT3G18100	1.08	0.11	0.60	0.566573	0.730225	-7.15
262424_at	hypothetical protein predicted by gene	---	AT1G47680	-1.04	-0.06	-0.60	0.566544	0.730225	-7.15
254534_at	putative Fe(II) transport protein Fe(II)	IRT2	AT4G19680	1.04	0.05	0.60	0.566514	0.730225	-7.15
247357_at	receptor-like protein kinase ; supporte	---	AT5G63710	1.05	0.07	0.60	0.566716	0.730324	-7.15
263396_at	unknown protein ;supported by full-ler	---	AT2G31710	1.05	0.07	0.60	0.566841	0.730324	-7.15
265963_s_	40S ribosomal protein S5 identical to C	ATRPS5B	AT2G37270 /	-1.10	-0.14	-0.60	0.56682	0.730324	-7.15
246534_at	putative protein several hypothetical pr	---	AT5G15890	-1.06	-0.09	-0.60	0.566711	0.730324	-7.15
261382_at	hypothetical protein contains similarity	CVP2	AT1G05470	1.06	0.09	0.60	0.566778	0.730324	-7.15
261878_at	cytochrome P450, putative similar to C	CYP705A25	AT1G50560	-1.05	-0.07	-0.60	0.566756	0.730324	-7.15
249569_at	putative protein Pit1 - Arabidopsis tha	---	AT5G38070	-1.06	-0.09	-0.60	0.567004	0.730492	-7.15
256951_at	hypothetical protein predicted by gene	---	AT3G19085	1.04	0.05	0.60	0.567127	0.730592	-7.15
258066_at	hypothetical protein predicted by gene	---	AT3G25970	1.04	0.05	0.60	0.567146	0.730592	-7.15
260528_at	putative WRKY-type DNA binding prot	WRKY23	AT2G47260	-1.12	-0.17	-0.60	0.567204	0.730625	-7.15

261603_at	DNA binding protein ACBF, putative s	ATRBP47A	AT1G49600	1.10	0.14	0.60	0.567309	0.73072	-7.15
265538_at	unknown protein predicted by genscan	---	AT2G15860	-1.07	-0.09	-0.60	0.567435	0.7308	-7.15
252530_at	putative protein several oxidases, mai	---	AT3G46500	1.05	0.07	0.60	0.56742	0.7308	-7.15
262838_at	major latex protein, putative similar to	---	AT1G14960	1.05	0.07	0.60	0.56756	0.730919	-7.15
257908_at	unknown protein contains Pfam profile	---	AT3G25410	1.05	0.08	0.60	0.56776	0.731135	-7.15
253208_at	putative protein	---	AT4G34830	1.05	0.06	0.60	0.567927	0.731302	-7.15
260080_at	putative RNA-binding protein contains	APUM7	AT1G78160	-1.04	-0.06	-0.60	0.567954	0.731302	-7.15
259609_at	myosin-like protein contains Pfam pro	TSA1	AT1G52410	-1.24	-0.31	-0.60	0.568065	0.731405	-7.15
250703_at	putative protein similar to unknown pro	---	AT5G06360	-1.06	-0.09	-0.60	0.568163	0.731489	-7.15
247843_at	aluminium tolerance associated - like p	SVL4	AT5G58050	-1.06	-0.08	-0.60	0.568302	0.731627	-7.15
249670_at	unknown protein	---	AT5G35890	-1.05	-0.07	-0.60	0.568439	0.731762	-7.15
261523_at	protein tyrosine phosphatase identical	PTP1	AT1G71860	1.05	0.07	0.60	0.568598	0.731925	-7.15
263693_at	hypothetical protein predicted by gene	ATPP2-A9	AT1G31200	1.13	0.17	0.60	0.568845	0.732045	-7.15
251711_at	phosphatidylinositol-4-phosphate 5-ki	PIP5K4	AT3G56960	1.06	0.09	0.60	0.568883	0.732045	-7.15
260247_at	putative disease resistance protein sim	AtRLP16	AT1G74200	-1.04	-0.06	-0.60	0.568793	0.732045	-7.15
267450_at	hypothetical protein predicted by gens	---	AT2G33720	-1.07	-0.10	-0.60	0.568765	0.732045	-7.15
246732_at	putative protein hypothetical protein F	---	AT5G27650	-1.06	-0.09	-0.60	0.568879	0.732045	-7.15
265520_at	hypothetical protein predicted by gens	---	AT2G06020	-1.06	-0.09	-0.60	0.568803	0.732045	-7.15
246991_at	peroxidase (emb|CAA66967.1)	---	AT5G67400	-1.05	-0.07	-0.60	0.569183	0.732389	-7.15
263927_s_	putative cinnamyl-alcohol dehydrogena	CAD2	AT2G21730 /	1.06	0.09	0.60	0.569291	0.732487	-7.16
249731_at	RNA-binding protein-like	CID13	AT5G24440	1.06	0.09	0.60	0.569328	0.732493	-7.16
264918_at	interferon-induced GTP-binding protei	---	AT1G60530	1.05	0.07	0.60	0.569507	0.732558	-7.16
258294_at	hypothetical protein predicted by gene	---	AT3G23350	-1.05	-0.07	-0.60	0.569474	0.732558	-7.16
246896_at	extensin - like protein Pex1 extensin-li	---	AT5G25550	-1.06	-0.08	-0.60	0.569481	0.732558	-7.16
265719_at	unknown protein related to putative tw	---	AT2G03500	-1.04	-0.06	-0.60	0.569449	0.732558	-7.16
256123_at	hypothetical protein predicted by gens	GC2	AT1G18190	-1.04	-0.05	-0.60	0.569584	0.732615	-7.16
250860_at	amino acid transport - like protein ami	CAT6	AT5G04770	-1.11	-0.15	-0.60	0.569769	0.732813	-7.16
247572_at	putative protein ; supported by full-len	---	AT5G61220	1.04	0.06	0.60	0.569915	0.732959	-7.16
264090_at	cytochrome P-450, putative similar to	CYP79C1	AT1G79370	-1.05	-0.07	-0.60	0.570038	0.733077	-7.16
258593_at	unknown protein	---	AT3G04480	1.07	0.10	0.60	0.570236	0.733289	-7.16
255238_at	see GB:AL022580)	---	---	1.04	0.05	0.60	0.570289	0.733316	-7.16
261784_at	hypothetical protein predicted by gene	---	AT1G08220	1.05	0.06	0.60	0.570343	0.733344	-7.16
247071_at	putative protein similar to unknown pro	DAR3	AT5G66640	-1.17	-0.22	-0.60	0.570511	0.733518	-7.16
261102_at	unknown protein	---	AT1G62880	1.04	0.06	0.60	0.570594	0.733585	-7.16
245177_at	annexin-like protein genmodel suppor	---	AT5G12380	1.05	0.07	0.60	0.570794	0.733799	-7.16

259327_at	putative lectin contains Pfam profile: F	---	AT3G16460	-1.23	-0.30	-0.60	0.571004	0.734028	-7.16
262256_at	hypothetical protein similar to putative	---	---	1.05	0.08	0.60	0.571083	0.734089	-7.16
265589_at	hypothetical protein predicted by gens	---	AT2G20170	1.05	0.07	0.60	0.571164	0.734124	-7.16
254882_s_	putative protein various predicted reve	---	---	-1.04	-0.06	-0.60	0.571175	0.734124	-7.16
248251_at	unknown protein	---	AT5G53220	-1.04	-0.06	-0.59	0.571302	0.734204	-7.16
249853_at	farnesyl cysteine carboxyl methyltrans	ATSTE14A	AT5G23320	-1.05	-0.07	-0.60	0.571287	0.734204	-7.16
265527_at	putative Athila retroelement ORF1 prot	---	---	-1.04	-0.06	-0.59	0.571338	0.73421	-7.16
260575_at	hypothetical protein predicted by gene	---	AT2G47300	1.05	0.07	0.59	0.571374	0.734215	-7.16
258616_at	putative protein kinase contains Pfam	---	AT3G02880	1.06	0.09	0.59	0.571483	0.734313	-7.16
250577_at	putative protein densin-180, Rattus no	---	AT5G07910	-1.04	-0.06	-0.59	0.571571	0.734384	-7.16
247566_at	40S ribsomal protein S19 - like 40S rib	---	AT5G61170	-1.11	-0.15	-0.59	0.571709	0.734515	-7.16
256558_at	hypothetical protein predicted by gene	---	---	1.04	0.06	0.59	0.571736	0.734515	-7.16
257503_at	DAG-like protein similar to DAG prote	---	AT1G72530	1.06	0.09	0.59	0.571848	0.734617	-7.16
255021_at	hypothetical protein	---	AT4G10330	-1.05	-0.07	-0.59	0.572014	0.734706	-7.16
260845_at	transcription factor, putative similar to	---	AT1G17310	-1.05	-0.07	-0.59	0.571978	0.734706	-7.16
256571_at	hypothetical protein predicted by gens	---	AT3G30730	-1.04	-0.06	-0.59	0.572008	0.734706	-7.16
245754_at	hypothetical protein predicted by gene	---	AT1G35183	-1.04	-0.06	-0.59	0.572084	0.73472	-7.16
253870_at	putative protein	---	AT4G27530	-1.05	-0.07	-0.59	0.57209	0.73472	-7.16
247762_at	cell wall protein	---	AT5G59170	-1.12	-0.16	-0.59	0.57222	0.734773	-7.16
259388_at	steroid sulfotransferase, putative simil	ST4B	AT1G13420	1.05	0.07	0.59	0.572342	0.734773	-7.16
255350_at	putative transposon protein similar to c	---	---	1.04	0.06	0.59	0.572339	0.734773	-7.16
257453_at	hypothetical protein predicted by gens	---	AT1G65130	1.06	0.08	0.59	0.572248	0.734773	-7.16
255396_at	hypothetical protein	---	---	-1.04	-0.06	-0.59	0.572237	0.734773	-7.16
265629_at	unknown protein ; supported by cDNA	LHW	AT2G27228 /	1.08	0.11	0.59	0.572308	0.734773	-7.16
263528_at	putative peroxidase	---	AT2G24800	-1.05	-0.07	-0.59	0.572356	0.734773	-7.16
265978_at	putative retroelement pol polyprotein	---	---	1.04	0.05	0.59	0.572518	0.734939	-7.16
265428_at	hypothetical protein predicted by grail	---	AT2G20720	1.11	0.15	0.59	0.572565	0.734958	-7.16
261275_at	Mlo protein, putative similar to GB:Z83	MLO14	AT1G26700	1.04	0.06	0.59	0.572726	0.735124	-7.16
264181_at	ubiquitin, putative similar to ubiquitin C	UBQ13	AT1G65350	1.04	0.05	0.59	0.573146	0.73558	-7.16
250499_at	beta-xylosidase - like protein beta-xyl	BXL3	AT5G09730	-1.05	-0.07	-0.59	0.573135	0.73558	-7.16
265410_at	putative protein kinase contains a prot	---	AT2G16620	-1.04	-0.06	-0.59	0.573232	0.735649	-7.16
264401_at	dihydroflavonol 4-reductase, putative	BAN	AT1G61720	1.04	0.05	0.59	0.573316	0.735674	-7.16
255661_at	hypothetical protein	ULP1B	AT4G00690	1.04	0.06	0.59	0.573292	0.735674	-7.16
245559_at	glycine-rich protein like	---	AT4G15460	-1.04	-0.06	-0.59	0.573477	0.735798	-7.16
246048_at	putative protein	---	---	-1.05	-0.07	-0.59	0.573447	0.735798	-7.16

262307_at	heat shock protein DnaJ, putative sim	---	AT1G71000	-1.07	-0.09	-0.59	0.573652	0.735954	-7.16
254415_at	subtilisin-like serine protease contains	ATSBT3.12	AT4G21326	1.04	0.06	0.59	0.573671	0.735954	-7.16
255187_s_	putative transposon protein	---	---	1.05	0.06	0.59	0.573696	0.735954	-7.16
263792_at	putative retroelement pol polyprotein	---	---	1.06	0.09	0.59	0.57387	0.736137	-7.16
254816_at	putative adenine phosphoribosyltransf	APT4	AT4G12440	-1.04	-0.05	-0.59	0.574007	0.736271	-7.16
264490_at	putative protein import receptor simila	TOM20-2	AT1G27390	1.08	0.11	0.59	0.574194	0.736386	-7.16
262647_at	putative growth regulator protein simil	---	AT1G14020	-1.07	-0.10	-0.59	0.574133	0.736386	-7.16
247484_at	putative protein predicted proteins, Pla	---	AT5G62110	-1.05	-0.06	-0.59	0.574186	0.736386	-7.16
252176_at	protein kinase ATN1 -like protein prote	---	AT3G50720	1.06	0.08	0.59	0.574322	0.736509	-7.16
263605_at	hypothetical protein predicted by gens	---	AT2G16485	-1.06	-0.08	-0.59	0.57449	0.736684	-7.16
247876_at	unknown protein	---	AT5G57730	-1.04	-0.06	-0.59	0.574541	0.736688	-7.16
264129_at	hypothetical protein predicted by gene	---	AT1G79170	1.05	0.08	0.59	0.574559	0.736688	-7.16
266657_at	unknown protein ;supported by full-ler	---	AT2G25910	-1.04	-0.05	-0.59	0.574612	0.736716	-7.16
264789_at	putative glycine-rich, zinc-finger DNA-	---	AT2G17870	-1.04	-0.06	-0.59	0.574738	0.736835	-7.16
266997_at	hypothetical protein predicted by gene	---	AT2G34410	-1.08	-0.11	-0.59	0.574794	0.736866	-7.16
261826_at	pectin methylesterase, putative simila	PMEPCRA	AT1G11580	-1.11	-0.15	-0.59	0.575087	0.737095	-7.16
248797_at	putative protein similar to unknown pro	---	AT5G47210	-1.06	-0.08	-0.59	0.57512	0.737095	-7.16
255269_at	putative protein various predicted prot	---	AT4G05240	-1.05	-0.07	-0.59	0.575051	0.737095	-7.16
264817_at	hypothetical protein similar to membra	---	AT1G03540	1.04	0.06	0.59	0.575134	0.737095	-7.16
249022_s_	polygalacturonase-like protein	---	AT5G44830 /	1.05	0.06	0.59	0.575037	0.737095	-7.16
247710_at	receptor-like protein kinase receptor-li	---	AT5G59260	1.04	0.05	0.59	0.575246	0.737197	-7.16
262757_at	putative Na/H antiporter similar to gi|48	ATCHX1	AT1G16380	-1.05	-0.07	-0.59	0.575317	0.737205	-7.16
254799_at	putative protein various predicted prote	---	AT4G13060	-1.05	-0.07	-0.59	0.575309	0.737205	-7.16
246723_at	putative protein various predicted prot	---	AT5G29030	-1.05	-0.07	-0.59	0.575381	0.737245	-7.16
253927_at	putative protein	---	AT4G26710	-1.06	-0.08	-0.59	0.575483	0.737333	-7.16
252536_at	putative transporter protein peptide tra	---	AT3G45700	1.06	0.08	0.59	0.575514	0.737333	-7.16
247721_at	elongin - like protein elongin C, Droso	---	AT5G59140	1.04	0.05	0.59	0.575743	0.737437	-7.16
267362_at	hypothetical protein predicted by gene	---	AT2G39910	1.04	0.06	0.59	0.575724	0.737437	-7.16
257494_at	hypothetical protein predicted by gene	---	AT1G32375	1.04	0.05	0.59	0.575757	0.737437	-7.16
262828_at	major latex protein type1 identical to m	---	AT1G14950	1.08	0.11	0.59	0.5757	0.737437	-7.16
257493_at	unknown protein	---	AT1G48180	1.08	0.11	0.59	0.575718	0.737437	-7.16
246428_at	spindle pole body protein-like spindle	---	AT5G17410	-1.06	-0.08	-0.59	0.576097	0.737832	-7.16
265202_at	unknown protein	AT2G36810	---	-1.05	-0.07	-0.59	0.576226	0.737955	-7.16
263856_at	unknown protein	---	AT2G04410	1.07	0.09	0.59	0.576555	0.738318	-7.16
261511_at	polyadenylate-binding protein 5 identic	PAB5	AT1G71770	-1.05	-0.07	-0.59	0.576607	0.738318	-7.16

264207_at	unknown protein strong similarity to hy	---	AT1G22750	1.06	0.09	0.59	0.576593	0.738318	-7.16
259636_at	RNA pseudouridylate synthase, putati	---	AT1G56345	-1.10	-0.14	-0.59	0.576761	0.738474	-7.16
258023_at	cinnamyl alcohol dehydrogenase ident	ATCAD4	AT3G19450	1.12	0.17	0.59	0.576856	0.738503	-7.16
263805_at	unknown protein ; supported by cDNA	---	AT2G40400	-1.04	-0.06	-0.59	0.576861	0.738503	-7.16
247767_at	putative protein various predicted prot	AGL82	AT5G58890	1.04	0.06	0.59	0.576913	0.738503	-7.16
266095_at	3-oxo-5-alpha-steroid 4-dehydrogenas	DET2	AT2G38050	1.07	0.10	0.59	0.576902	0.738503	-7.16
247543_at	DNA binding protein - like DNA bindin	---	AT5G61600	1.16	0.21	0.59	0.577017	0.738595	-7.16
263047_at	putative phosphoserine aminotransfera	---	AT2G17630	-1.10	-0.14	-0.59	0.577179	0.73876	-7.16
247796_at	Expressed protein ;supported by cDNA	---	AT5G58782	-1.05	-0.07	-0.59	0.577253	0.738814	-7.16
251138_at	putative protein various predicted prote	---	AT5G01160	-1.05	-0.07	-0.59	0.577291	0.738822	-7.16
247766_at	FtsH protease, putative contains simil	ftsh9	AT5G58870	1.05	0.07	0.59	0.577381	0.738895	-7.16
246737_at	putative protein	---	AT5G27710	1.09	0.13	0.59	0.577509	0.738975	-7.16
266810_at	hypothetical protein predicted by gens	---	AT2G44880	1.04	0.06	0.59	0.577489	0.738975	-7.16
257450_at	unknown protein similar to gb|AAD144	---	AT1G10530	1.06	0.08	0.59	0.577547	0.738982	-7.16
252337_at	CELL DIVISION CONTROL PROTEIN	CDC2	AT3G48750	-1.08	-0.11	-0.59	0.577603	0.739013	-7.16
252554_s_	protein kinase - like receptor-like prote	MEE39	AT3G45920 /	1.04	0.06	0.58	0.577775	0.739191	-7.16
247549_at	putative transcription factor MYB28 ; s	MYB28	AT5G61420	-1.08	-0.11	-0.58	0.577981	0.739289	-7.16
265037_at	putative prohibitin 2 B-cell receptor ass	ATPHB2	AT1G03860	1.06	0.08	0.58	0.577901	0.739289	-7.16
255297_x_	hypothetical protein	---	---	-1.06	-0.08	-0.58	0.577949	0.739289	-7.16
249438_at	putative protein BCS1 nuclear gene e	AATP1	AT5G40010	1.06	0.08	0.58	0.577972	0.739289	-7.16
254483_at	putative protein CRP1, Zea mays, PID	---	AT4G20740	-1.07	-0.09	-0.58	0.57808	0.739333	-7.16
266851_at	similar to avrRpt2-induced protein 1	ATPP2-A3	AT2G26820	-1.04	-0.05	-0.58	0.578069	0.739333	-7.16
266255_at	putative selenium-binding protein	---	AT2G27610	-1.04	-0.06	-0.58	0.578149	0.739379	-7.16
259394_at	hypothetical protein predicted by gene	---	AT1G06420	1.04	0.06	0.58	0.578244	0.739419	-7.16
252898_at	cytochrome P450 -like protein simialri	CYP96A11	AT4G39500	1.04	0.06	0.58	0.578238	0.739419	-7.16
267139_s_	hypothetical protein predicted by gene	---	AT2G38195 /	-1.04	-0.06	-0.58	0.578364	0.739531	-7.16
260842_at	19S proteosome subunit 9, putative si	ATS9	AT1G29150	1.05	0.07	0.58	0.578499	0.739661	-7.16
251983_at	putative protein MtN21, Medicago trur	---	AT3G53210	-1.07	-0.10	-0.58	0.578582	0.739718	-7.16
247256_at	putative protein contains similarity to u	---	AT5G64730	-1.04	-0.06	-0.58	0.578608	0.739718	-7.16
256984_at	hypothetical protein predicted by gens	---	AT3G13480	-1.05	-0.08	-0.58	0.578844	0.739979	-7.16
248073_at	pectate lyase	---	AT5G55720	1.05	0.07	0.58	0.578942	0.740062	-7.16
259433_at	hypothetical protein predicted by gens	---	AT1G01570	-1.05	-0.08	-0.58	0.579305	0.740443	-7.17
255835_at	unknown protein	---	AT2G33420	-1.05	-0.07	-0.58	0.579294	0.740443	-7.17
263971_at	hypothetical protein predicted by gene	AtRLP29	AT2G42800	-1.06	-0.08	-0.58	0.579413	0.740539	-7.17
259391_s_	delta 9 desaturase, putative similar to	---	AT1G06350 /	1.05	0.07	0.58	0.579445	0.740539	-7.17

257117_at	geranyl geranyl pyrophosphate syntha	---	AT3G20160	-1.04	-0.06	-0.58	0.57954	0.740618	-7.17
266686_at	hypothetical protein	---	AT2G19700	-1.05	-0.07	-0.58	0.579613	0.74063	-7.17
253678_at	cytidine deaminase 7	---	AT4G29600	-1.04	-0.06	-0.58	0.579589	0.74063	-7.17
247607_at	putative protein various predicted prot	---	AT5G60960	1.09	0.13	0.58	0.579746	0.740674	-7.17
246611_at	putative protein predicted proteins, Ar	MBD02	AT5G35330	-1.09	-0.12	-0.58	0.579778	0.740674	-7.17
254155_at	putative protein kinase putative protei	---	AT4G24480	-1.05	-0.08	-0.58	0.57971	0.740674	-7.17
263476_at	putative poly(ADP-ribose) glycohydrola	TEJ	AT2G31870	1.04	0.06	0.58	0.579723	0.740674	-7.17
263483_at	putative heat shock protein ; supporte	CR88	AT2G04030	1.05	0.07	0.58	0.579826	0.740694	-7.17
253290_at	putative protein predicted protein F10	---	AT4G34330	-1.04	-0.06	-0.58	0.580168	0.741089	-7.17
248762_at	Expressed protein ; supported by full-l	---	AT5G47455	1.08	0.11	0.58	0.580572	0.741398	-7.17
255601_at	putative protein (fragment) various hy	---	AT4G01030	-1.05	-0.07	-0.58	0.580523	0.741398	-7.17
260848_at	pectinesterase, putative similar to pec	sks8	AT1G21850	-1.07	-0.09	-0.58	0.5805	0.741398	-7.17
261072_at	hexose transporter, putative similar to	ATSTP2	AT1G07340	-1.06	-0.08	-0.58	0.580446	0.741398	-7.17
256378_at	receptor protein kinase, putative conta	---	AT1G66830	1.04	0.06	0.58	0.580565	0.741398	-7.17
249155_at	unknown protein	---	AT5G43480	1.04	0.05	0.58	0.58073	0.741558	-7.17
266159_at	putative chloroplast nucleoid DNA bind	---	AT2G28030	1.04	0.06	0.58	0.580961	0.741811	-7.17
264806_at	hypothetical protein predicted by gens	---	AT1G08610	1.10	0.13	0.58	0.581044	0.741834	-7.17
256581_at	hypothetical protein	---	AT3G28830	1.04	0.05	0.58	0.581033	0.741834	-7.17
249249_at	unknown protein	---	AT5G42330	1.05	0.07	0.58	0.581092	0.741853	-7.17
262090_at	CREB-binding protein, putative simila	HAC4	AT1G55970	1.05	0.07	0.58	0.581124	0.741853	-7.17
253818_at	hypothetical protein	---	AT4G28330	-1.06	-0.09	-0.58	0.581339	0.741882	-7.17
247409_at	dihydroneopterin aldolase-like protein	---	AT5G62980	1.08	0.10	0.58	0.581246	0.741882	-7.17
251668_at	putative protein strictosidine synthase	---	AT3G57010	1.11	0.15	0.58	0.581303	0.741882	-7.17
258870_at	putative NADP-dependent oxidoreduct	---	AT3G03080	1.05	0.07	0.58	0.581342	0.741882	-7.17
259829_at	oligopeptide transporter, putative simi	---	---	-1.06	-0.08	-0.58	0.581263	0.741882	-7.17
248873_at	disease resistance protein-like	---	AT5G46450	1.16	0.21	0.58	0.581197	0.741882	-7.17
254899_at	serine/threonine kinase-like protein re	---	AT4G11490	1.06	0.09	0.58	0.581406	0.741888	-7.17
265290_at	putative anthocyanidin-3-glucoside rha	---	AT2G22590	1.04	0.06	0.58	0.581411	0.741888	-7.17
246107_at	putative protein various predicted prot	---	---	-1.04	-0.06	-0.58	0.581605	0.742093	-7.17
247503_at	GCN4-complementing protein - like G	AGD1	AT5G61980	-1.05	-0.08	-0.58	0.581649	0.742108	-7.17
247021_at	putative protein similar to unknown pro	---	AT5G67040	1.05	0.07	0.58	0.581699	0.74213	-7.17
AFFX-r2-At	/FEATURE=cds-2 /GENE= /LABEL= /F	---	---	1.05	0.07	0.58	0.581873	0.742269	-7.17
257920_at	hypothetical protein predicted by gene	---	AT3G23260	1.04	0.06	0.58	0.581857	0.742269	-7.17
255849_at	hypothetical protein predicted by gene	---	AT2G33320	-1.04	-0.06	-0.58	0.582142	0.742529	-7.17
260256_at	putative type II intron maturase contair	---	AT1G74350	1.05	0.08	0.58	0.582141	0.742529	-7.17

248735_at	laccase (diphenol oxidase)	TT10	AT5G48100	1.04	0.06	0.58	0.582225	0.742594	-7.17
266153_at	hypothetical protein	---	---	-1.04	-0.06	-0.58	0.582293	0.742639	-7.17
256897_at	hypothetical protein predicted by gens	---	AT3G24640	-1.04	-0.06	-0.58	0.582424	0.742723	-7.17
259449_at	hypothetical protein similar to putative	---	AT1G13800	-1.06	-0.08	-0.58	0.58241	0.742723	-7.17
256757_at	membrane transporter, putative simila	---	AT3G25620	1.05	0.07	0.58	0.582718	0.743056	-7.17
261287_at	hypothetical protein predicted by gene	---	AT1G37020	1.04	0.05	0.58	0.582845	0.743178	-7.17
260075_at	putative integral membrane protein co	---	AT1G73700	-1.06	-0.09	-0.58	0.582911	0.743219	-7.17
249349_at	putative transcription factor MYB24 ; s	MYB24	AT5G40350	1.05	0.06	0.58	0.582953	0.743232	-7.17
264813_at	putative Ca2+-dependent ser/thr prote	CPK16	AT2G17890	-1.06	-0.09	-0.58	0.583017	0.743271	-7.17
266850_at	unknown protein	---	AT2G26850	-1.04	-0.06	-0.58	0.58315	0.7434	-7.17
267519_at	putative VP1/ABI3 family regulatory pr	HSI2	AT2G30470	-1.07	-0.09	-0.58	0.583335	0.743511	-7.17
252386_at	putative protein various predicted proe	---	AT3G47840	1.06	0.08	0.58	0.583304	0.743511	-7.17
250432_at	putative protein various predicted prot	---	AT5G10420	-1.04	-0.06	-0.58	0.583293	0.743511	-7.17
247068_at	putative protein similar to unknown pro	---	AT5G66800	1.05	0.08	0.58	0.583411	0.743525	-7.17
256162_at	hypothetical protein similar to hypothet	---	AT1G55390	-1.04	-0.06	-0.58	0.583387	0.743525	-7.17
251381_at	secretory protein - like 33 kDa secreto	PDLP8	AT3G60720 /	-1.09	-0.12	-0.58	0.583515	0.743616	-7.17
260104_x_	hypothetical protein predicted by gene	---	AT1G35410	1.05	0.07	0.58	0.583635	0.743727	-7.17
250757_at	tetrahydrofolylpolyglutamate synthase-	ATDFB	AT5G05980	1.05	0.07	0.57	0.584045	0.743923	-7.17
266320_at	hypothetical protein predicted by gens	---	AT2G46640	-1.08	-0.11	-0.57	0.584082	0.743923	-7.17
255846_at	putative SWI/SNF complex subunit SW	ATSWI3B	AT2G33610	-1.06	-0.09	-0.58	0.583902	0.743923	-7.17
257873_at	P-glycoprotein, putative similar to P-gl	PGP17	AT3G28380	1.06	0.08	0.58	0.583948	0.743923	-7.17
253016_at	putative protein partial LG127/30 gene	---	AT4G37950	-1.03	-0.05	-0.58	0.583963	0.743923	-7.17
267022_at	hypothetical protein predicted by gens	---	AT2G34230	1.04	0.05	0.57	0.584081	0.743923	-7.17
261158_at	hypothetical protein predicted by gene	---	AT1G34500	-1.04	-0.06	-0.58	0.583913	0.743923	-7.17
259276_at	putative peroxidase very similar to per	---	AT3G01190	-1.04	-0.06	-0.58	0.583956	0.743923	-7.17
262081_at	kinesin motor protein (kin2), putative s	ZCF125	AT1G59540	-1.05	-0.08	-0.57	0.584046	0.743923	-7.17
251979_at	caffeic acid O-methyltransferase - like	LUT1	AT3G53130 /	1.05	0.07	0.57	0.584146	0.743962	-7.17
250873_at	lipase -like protein lipase Arab-1, Arab	---	AT5G03980	-1.05	-0.07	-0.57	0.584274	0.744043	-7.17
259731_at	unknown protein similar to unknown pr	---	AT1G77460	1.11	0.15	0.57	0.584264	0.744043	-7.17
259314_at	putative glucose and ribitol dehydroge	---	AT3G05260	-1.07	-0.10	-0.57	0.584309	0.744046	-7.17
262312_at	hypothetical protein similar to putative	MLP28	AT1G70830	1.48	0.56	0.57	0.584665	0.744249	-7.17
257261_s_	hypothetical protein contains Pfam pro	---	AT3G21920 /	-1.04	-0.05	-0.57	0.584653	0.744249	-7.17
256606_at	hypothetical protein	---	AT3G32960	-1.04	-0.06	-0.57	0.584639	0.744249	-7.17
247946_at	putative protein similar to unknown pro	CIA2	AT5G57180	-1.13	-0.18	-0.57	0.584624	0.744249	-7.17
265349_at	putative kinesin heavy chain	---	AT2G22610	-1.05	-0.07	-0.57	0.584635	0.744249	-7.17

260382_at	unknown protein	---	AT1G73850	1.06	0.08	0.57	0.58465	0.744249	-7.17
262562_at	hypothetical protein predicted by gene	---	AT1G34220	-1.04	-0.06	-0.57	0.584724	0.744283	-7.17
250959_at	F-box protein family, AtFBL25 contain	---	AT5G02920	1.05	0.07	0.57	0.584769	0.744299	-7.17
260509_at	natural resistance-associated macroph	NRAMP2	AT1G47240	-1.04	-0.05	-0.57	0.584887	0.744408	-7.17
262182_at	hypothetical protein predicted by gene	---	AT1G77890	1.04	0.06	0.57	0.584981	0.744475	-7.17
247695_at	putative protein Not2p, Homo sapiens	VIP2	AT5G59710	-1.04	-0.06	-0.57	0.585006	0.744475	-7.17
262646_at	aspartate aminotransferase nearly ide	ASP4	AT1G62800	-1.10	-0.13	-0.57	0.585123	0.744584	-7.17
257133_at	hypothetical protein predicted by gene	---	AT3G17190	-1.03	-0.05	-0.57	0.585183	0.744618	-7.17
266443_at	putative myb-related transcription facto	---	AT2G43270	-1.04	-0.05	-0.57	0.585407	0.744862	-7.17
258430_at	phospholipase D, putative similar to p	PLDP1	AT3G16785	-1.04	-0.06	-0.57	0.585573	0.744906	-7.17
259698_at	hypothetical protein similar to hypothe	---	AT1G68930	1.06	0.08	0.57	0.58554	0.744906	-7.17
255218_at	putative athila transposon protein	---	---	1.04	0.05	0.57	0.585561	0.744906	-7.17
247244_at	putative protein similar to unknown pro	---	AT5G64710	1.04	0.06	0.57	0.585488	0.744906	-7.17
245710_at	ferulate-5-hydroxylase	---	AT5G04330	1.07	0.09	0.57	0.585737	0.744908	-7.17
245833_at	transposon protein, putative similar to	---	---	1.05	0.07	0.57	0.585736	0.744908	-7.17
251338_at	putative protein VAP27, Nicotiana plu	VAP	AT3G60600 /	1.04	0.06	0.57	0.585732	0.744908	-7.17
266632_at	putative serpin	---	AT2G35570	1.05	0.07	0.57	0.585708	0.744908	-7.17
267334_at	hypothetical protein predicted by gens	---	AT2G19420	1.05	0.07	0.57	0.585705	0.744908	-7.17
259070_at	digalactosyldiacylglycerol synthase ide	DGD1	AT3G11670	1.10	0.13	0.57	0.585772	0.74491	-7.17
262577_at	unknown protein ESTs gb|F20110 and	---	AT1G15290	1.06	0.09	0.57	0.585829	0.744941	-7.17
252818_at	putative protein several hypothetical pr	---	---	1.05	0.07	0.57	0.58594	0.74501	-7.17
265341_at	hypothetical protein predicted by gens	---	AT2G18360	1.06	0.09	0.57	0.585949	0.74501	-7.17
260749_at	hypothetical protein predicted by gene	---	AT1G49110	-1.05	-0.07	-0.57	0.586108	0.745171	-7.17
254900_at	hypothetical protein	RALFL28	AT4G11510	1.04	0.06	0.57	0.586283	0.745352	-7.17
246402_at	jasmonate inducible protein, putative s	---	AT1G57570	1.04	0.06	0.57	0.586347	0.745392	-7.17
247195_at	putative protein contains similarity to re	---	AT5G65500	-1.06	-0.08	-0.57	0.586446	0.745477	-7.17
247873_at	diacylglycerol kinase-like protein	---	AT5G57690	1.04	0.06	0.57	0.586524	0.745492	-7.17
255840_at	unknown protein	---	AT2G33520	-1.07	-0.10	-0.57	0.586498	0.745492	-7.17
263563_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.57	0.586572	0.745513	-7.17
264101_at	unknown protein similar to putative CR	HAC1	AT1G79000	-1.06	-0.08	-0.57	0.586798	0.745758	-7.17
266794_at	hypothetical protein	---	AT2G02980	-1.04	-0.06	-0.57	0.586988	0.745833	-7.17
265379_at	similar to late embryogenesis abundan	---	AT2G18340	1.04	0.06	0.57	0.586932	0.745833	-7.17
245280_at	Expressed protein ; supported by cDN	VRN2	AT4G16845	-1.05	-0.07	-0.57	0.586902	0.745833	-7.17
266937_at	hypothetical protein predicted by gene	---	AT2G18930	-1.05	-0.07	-0.57	0.586962	0.745833	-7.17
263369_at	unknown protein	---	AT2G20480	-1.04	-0.06	-0.57	0.587042	0.74586	-7.17

251275_at	putative protein anthranilate phosphor	---	AT3G61720	1.07	0.10	0.57	0.587191	0.745925	-7.17
261349_at	Expressed protein ; supported by full-l	AT1G79610	---	-1.04	-0.06	-0.57	0.587174	0.745925	-7.17
257842_at	P-glycoprotein, putative similar to P-gl	PGP18	AT3G28390	-1.04	-0.06	-0.57	0.587138	0.745925	-7.17
253482_at	Expressed protein ; supported by cDN	---	AT4G31985	1.12	0.17	0.57	0.587275	0.745989	-7.17
264487_at	vacuolar protein sorting homolog almo	VPS45	AT1G77140	1.04	0.06	0.57	0.587542	0.746181	-7.17
252223_at	MYB -like protein DNA-binding protein	TRB3	AT3G49850	1.07	0.10	0.57	0.587574	0.746181	-7.17
255419_at	putative receptor kinase	---	AT4G03230	-1.05	-0.07	-0.57	0.587589	0.746181	-7.17
260803_at	glutathione transferase, putative simil	ATGSTU22	AT1G78340	-1.04	-0.06	-0.57	0.587555	0.746181	-7.17
245202_at	F12A21.14 similar to receptor protein k	---	AT1G67720	-1.06	-0.08	-0.57	0.587516	0.746181	-7.17
266805_at	hypothetical protein ;supported by full-	---	AT2G30010	-1.32	-0.40	-0.57	0.587758	0.746213	-7.17
262028_at	DNA binding protein, putative similar t	---	AT1G35560	1.04	0.06	0.57	0.587778	0.746213	-7.17
248723_at	acetyl-CoA:benzylalcohol acetyltranfer	---	AT5G47950	1.05	0.07	0.57	0.587722	0.746213	-7.17
245819_at	cauliflower identical to CAULIFLOWER	CAL	AT1G26310	-1.05	-0.06	-0.57	0.587732	0.746213	-7.17
257359_x_	putative protein kinase contains a prot	---	AT2G34290	-1.04	-0.06	-0.57	0.587759	0.746213	-7.17
252270_at	putative protein ;supported by full-leng	---	AT3G49560	-1.05	-0.08	-0.57	0.587895	0.746301	-7.17
259925_at	thaumatin-like protein similar to thaum	PR5	AT1G75040	1.66	0.73	0.57	0.587913	0.746301	-7.17
251039_at	putative protein hypothetical protein T	---	AT5G02020	1.12	0.16	0.57	0.588081	0.746372	-7.17
256501_at	hypothetical protein predicted by gene	---	AT1G36756	-1.04	-0.06	-0.57	0.588001	0.746372	-7.17
267074_s_	hypothetical protein predicted by gens	---	AT2G40955 /	-1.04	-0.06	-0.57	0.588086	0.746372	-7.17
251873_at	putative protein KIAA0122 gene , Hon	---	AT3G54230	-1.04	-0.05	-0.57	0.588099	0.746372	-7.17
249612_at	putative protein CG14881, Drosophila	---	AT5G37290	1.09	0.13	0.57	0.588304	0.746585	-7.17
265578_at	unknown protein	---	AT2G20100	-1.06	-0.08	-0.57	0.588398	0.746585	-7.17
251216_at	putative protein hypothetical protein a	---	---	1.04	0.06	0.57	0.588333	0.746585	-7.17
263461_at	putative protein kinase contains a prot	---	AT2G31800	-1.06	-0.08	-0.57	0.588395	0.746585	-7.17
247395_at	putative protein predicted proteins, Ar	---	AT5G62910	-1.05	-0.07	-0.57	0.588465	0.746628	-7.17
253438_at	glycine hydroxymethyltransferase (EC	SHM3	AT4G32520	-1.06	-0.09	-0.57	0.588556	0.746702	-7.17
259157_at	hypothetical protein predicted by gene	---	AT3G05440	-1.04	-0.05	-0.57	0.588633	0.746758	-7.17
256316_at	hypothetical protein	---	AT1G35890	1.04	0.05	0.57	0.588724	0.746832	-7.17
251926_at	60S RIBOSOMAL PROTEIN L36 hom	---	AT3G53740	-1.09	-0.12	-0.57	0.588763	0.74684	-7.17
257821_at	Expressed protein ; supported by full-l	RALFL26	AT3G25170	-1.04	-0.05	-0.57	0.588869	0.746933	-7.17
255522_at	putative GTP pyrophosphokinase sim	RSH1	AT4G02260	1.05	0.07	0.57	0.58916	0.747261	-7.17
266191_at	putative peroxidase	---	AT2G39040	1.05	0.07	0.57	0.589215	0.747289	-7.17
252067_at	protein phosphatase 2C -like protein p	---	AT3G51370	-1.05	-0.07	-0.57	0.589444	0.747505	-7.18
252585_s_	putative protein UbcH 7-binding protei	---	AT3G45570 /	1.03	0.05	0.57	0.589483	0.747505	-7.18
258236_at	hypothetical protein predicted by gene	---	AT3G27800	1.04	0.06	0.57	0.589459	0.747505	-7.18

265953_at	unknown protein	---	AT2G37478 /	1.04	0.06	0.57	0.589553	0.747516	-7.18
263854_at	putative mutT domain protein	atnudt5	AT2G04430	-1.04	-0.06	-0.57	0.589558	0.747516	-7.18
247514_at	peptide methionine sulfoxide reductas	PMSR1	AT5G61640	1.06	0.08	0.57	0.589882	0.747885	-7.18
267568_at	hypothetical protein predicted by gens	---	AT2G30780	1.05	0.07	0.57	0.589993	0.747985	-7.18
265602_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.57	0.590147	0.748127	-7.18
266401_s_	putative cell division control protein kin	CDKB1;2	AT2G38620 /	-1.04	-0.05	-0.57	0.590171	0.748127	-7.18
266798_at	putative embryo-abundant protein con	AtbZIP6	AT2G22850	1.09	0.13	0.57	0.59026	0.748199	-7.18
258962_at	putative cytochrome P450 similar to cy	CYP77A6	AT3G10570	-1.26	-0.34	-0.57	0.590363	0.748287	-7.18
259615_at	dessication-related protein, putative s	---	AT1G47980	-1.05	-0.08	-0.56	0.590456	0.748323	-7.18
254918_at	putative protein phosphatase like prot	SGT1B	AT4G11260	1.05	0.07	0.56	0.590455	0.748323	-7.18
261588_at	hypothetical protein predicted by gene	---	AT1G01670	1.04	0.05	0.56	0.590685	0.748405	-7.18
248299_at	unknown protein ;supported by full-ler	---	AT5G53080	1.05	0.07	0.56	0.590604	0.748405	-7.18
259209_at	putative RNA-binding protein identical	---	AT3G09160	1.04	0.05	0.56	0.590564	0.748405	-7.18
266397_at	unknown protein	---	AT2G38690	-1.04	-0.06	-0.56	0.590676	0.748405	-7.18
246605_at	putative protein predicted proteins, Ar	---	---	1.05	0.07	0.56	0.590633	0.748405	-7.18
257859_at	Expressed protein ; supported by full-l	---	AT3G12955	-1.05	-0.07	-0.56	0.590817	0.74853	-7.18
259861_at	unknown protein similar to ribosomal p	---	AT1G80620	1.06	0.08	0.56	0.59087	0.748555	-7.18
265211_at	late embryogenesis abundant protein (	ATECP63	AT2G36640	-1.04	-0.05	-0.56	0.591033	0.748721	-7.18
263819_x_	putative TNP2-like transposon protein	---	---	-1.04	-0.05	-0.56	0.591127	0.748798	-7.18
245640_at	helix-loop-helix protein homolog, puta	---	AT1G25330	-1.04	-0.06	-0.56	0.591287	0.74896	-7.18
266237_at	DNA-directed RNA polymerase 14 kD	ATRPC14	AT2G29540	1.08	0.10	0.56	0.591394	0.749011	-7.18
257562_at	hypothetical protein	---	---	-1.05	-0.08	-0.56	0.591383	0.749011	-7.18
265505_at	putative RING zinc finger protein	---	AT2G15530	1.04	0.06	0.56	0.591536	0.749149	-7.18
265532_at	hypothetical protein predicted by gens	---	---	-1.05	-0.07	-0.56	0.591693	0.749265	-7.18
259772_at	hypothetical protein predicted by gene	---	AT1G29480	1.04	0.05	0.56	0.591691	0.749265	-7.18
265752_at	putative Athila retroelement ORF1 prot	---	---	1.04	0.06	0.56	0.591908	0.749424	-7.18
265152_s_	hypothetical protein predicted by gens	---	AT1G30935 /	1.04	0.06	0.56	0.5919	0.749424	-7.18
255181_at	predicted protein of unknown function	---	---	1.05	0.07	0.56	0.591917	0.749424	-7.18
259374_at	putative AP2 domain transcription fact	---	AT3G16280	1.06	0.09	0.56	0.592132	0.749655	-7.18
262629_at	heat shock protein, putative contains I	ACD32.1	AT1G06460	1.04	0.06	0.56	0.592209	0.749711	-7.18
249017_at	C2 domain-containing protein-like	---	AT5G44760	-1.06	-0.08	-0.56	0.592247	0.749717	-7.18
257010_at	Expressed protein ; supported by cDN	ATEXO70D3	AT3G14090	-1.07	-0.10	-0.56	0.592324	0.749731	-7.18
252399_at	putative cyclic nucleotide-gated chanr	CNGC16	AT3G48010	-1.04	-0.06	-0.56	0.59232	0.749731	-7.18
259535_at	hypothetical protein	---	AT1G12280	1.07	0.10	0.56	0.592381	0.749763	-7.18
265935_at	putative senescence-associated protei	TET2	AT2G19580	-1.08	-0.11	-0.56	0.592497	0.749784	-7.18

255528_at	hypothetical protein	---	AT4G02090	1.04	0.06	0.56	0.592477	0.749784	-7.18
247466_at	putative protein predicted proteins, Ar	---	AT5G62090	-1.07	-0.10	-0.56	0.592485	0.749784	-7.18
250480_at	protein serine/threonine kinase-like pr	---	AT5G10290	1.12	0.17	0.56	0.59262	0.749898	-7.18
253761_at	putative protein thyroid receptor intera	---	AT4G28820	1.05	0.07	0.56	0.592743	0.750012	-7.18
252655_at	hypothetical protein with predicted hen	---	AT3G44760	-1.04	-0.06	-0.56	0.593069	0.750352	-7.18
267133_at	unknown protein	---	AT2G23440	1.05	0.07	0.56	0.593083	0.750352	-7.18
247728_at	putative protein	---	---	-1.05	-0.07	-0.56	0.59311	0.750352	-7.18
266996_at	putative cytochrome P450 ;supported	CYP710A2	AT2G34490	-1.29	-0.37	-0.56	0.593168	0.750383	-7.18
255092_s_	putative protein various predicted prote	---	---	1.04	0.06	0.56	0.593291	0.750446	-7.18
252054_at	hypothetical protein ;supported by full-	OFP18	AT3G52540	-1.05	-0.07	-0.56	0.593316	0.750446	-7.18
261312_at	putative NPK1-related protein kinase 2	---	AT1G05790	1.05	0.07	0.56	0.593295	0.750446	-7.18
258963_at	putative myotubularin similar to myotul	---	AT3G10550	-1.05	-0.07	-0.56	0.593586	0.750562	-7.18
246245_at	putative protein	---	AT4G36440	-1.04	-0.06	-0.56	0.593526	0.750562	-7.18
263727_at	putative cap-binding protein ; supporte	ABH1	AT2G13540	-1.06	-0.08	-0.56	0.593638	0.750562	-7.18
266492_at	putative protein kinase contains a prot	---	AT2G07020	-1.05	-0.07	-0.56	0.593594	0.750562	-7.18
262447_at	hypothetical protein contains similarity	---	AT1G49250	1.04	0.06	0.56	0.593502	0.750562	-7.18
250393_at	serine/threonine protein phosphatase	---	AT5G10900	1.05	0.07	0.56	0.59363	0.750562	-7.18
245583_at	hypothetical protein	---	AT4G14920	-1.05	-0.07	-0.56	0.593589	0.750562	-7.18
250221_at	protoporphyrinogen oxidase - like prot	HEMG2	AT5G14220	-1.07	-0.10	-0.56	0.593728	0.750634	-7.18
245162_at	putative myosin heavy chain	XID	AT2G33240	-1.08	-0.11	-0.56	0.593812	0.750698	-7.18
249946_at	putative protein predicted proteins, Ar	---	AT5G19170	1.10	0.13	0.56	0.593845	0.750699	-7.18
249632_at	caffeic acid O-methyltransferase-like p	---	AT5G37170	-1.04	-0.06	-0.56	0.59403	0.750891	-7.18
254129_at	putative tRNA isopentenyltransferase	IPT4	AT4G24650	-1.04	-0.06	-0.56	0.594295	0.751101	-7.18
262392_at	hypothetical protein predicted by gens	---	AT1G49520	1.07	0.09	0.56	0.594322	0.751101	-7.18
253371_at	putative protein FAB1 protein, Saccha	---	AT4G33240	-1.05	-0.07	-0.56	0.594328	0.751101	-7.18
267433_at	putative peroxisome assembly protein	PEX10	AT2G26350	-1.05	-0.07	-0.56	0.59425	0.751101	-7.18
252874_at	putative protein ipiB1 gene, Phytopht	---	---	-1.05	-0.06	-0.56	0.594432	0.751149	-7.18
253106_at	putative protein predicted proteins, Ar	---	AT4G35870	-1.04	-0.06	-0.56	0.594428	0.751149	-7.18
245241_at	hypothetical protein contains similarity	---	AT1G44478	-1.04	-0.06	-0.56	0.594548	0.751254	-7.18
257153_at	unknown protein ; supported by cDNA	---	AT3G27220	1.07	0.09	0.56	0.594624	0.751271	-7.18
259681_at	nitrate reductase 1 (NR1) identical to n	NIA1	AT1G77760	1.38	0.46	0.56	0.594627	0.751271	-7.18
251570_at	putative protein several hypothetical pr	---	AT3G58300	1.05	0.07	0.56	0.595032	0.751491	-7.18
259168_at	unknown protein similar to hypothetica	---	AT3G03570	-1.05	-0.07	-0.56	0.594988	0.751491	-7.18
265409_at	unknown protein	PIP2;8	AT2G16830 /	-1.05	-0.07	-0.56	0.594984	0.751491	-7.18
258841_at	hypothetical protein similar to hypothet	---	AT3G04660	-1.04	-0.06	-0.56	0.594928	0.751491	-7.18

249772_at	unknown protein	---	AT5G24130	1.08	0.11	0.56	0.595026	0.751491	-7.18
258839_at	unknown protein ; supported by cDNA	---	AT3G07170	-1.04	-0.06	-0.56	0.594873	0.751491	-7.18
259223_at	hypothetical protein	WOX11	AT3G03660	1.04	0.06	0.56	0.594901	0.751491	-7.18
253241_at	fatty acid elongase 1	KCS18	AT4G34520	-1.06	-0.09	-0.56	0.595246	0.751678	-7.18
260478_at	DnaJ isolog	---	AT1G11040	1.04	0.06	0.56	0.595228	0.751678	-7.18
261846_at	hypothetical protein similar to hypothet	---	AT1G11540	1.05	0.07	0.56	0.595292	0.751682	-7.18
257913_at	unknown protein ; supported by cDNA	LAG1	AT3G25540	-1.05	-0.07	-0.56	0.595332	0.751682	-7.18
246186_at	PINHEAD - like protein PINHEAD, Ara	---	AT5G21030	-1.07	-0.09	-0.56	0.595357	0.751682	-7.18
265365_at	En/Spm-like transposon protein relate	---	---	1.04	0.06	0.56	0.595381	0.751682	-7.18
246806_at	putative cdc20 protein	---	AT5G27080	-1.04	-0.06	-0.56	0.595658	0.75199	-7.18
257418_at	hypothetical protein predicted by gene	---	AT1G30850	-1.06	-0.09	-0.56	0.595788	0.752113	-7.18
259121_at	unknown protein	---	AT3G02220	-1.06	-0.08	-0.56	0.595999	0.752337	-7.18
265455_at	hypothetical protein predicted by gens	---	AT2G46560	1.04	0.06	0.56	0.596048	0.752337	-7.18
257823_at	integral membrane protein, putative c	---	AT3G25190	1.05	0.07	0.56	0.596129	0.752337	-7.18
262096_at	NAC1 identical to NAC1 GB:AAF2143	NAC1	AT1G56010	-1.10	-0.14	-0.56	0.59613	0.752337	-7.18
257582_at	hypothetical protein	---	AT1G50720	-1.04	-0.05	-0.56	0.596131	0.752337	-7.18
253285_at	fatty acid elongase - like protein fatty a	KCS16	AT4G34250	-1.09	-0.12	-0.56	0.596456	0.752665	-7.18
254856_at	putative ribosomal protein (fragment)	---	AT4G12160	1.05	0.06	0.56	0.59643	0.752665	-7.18
250209_at	putative protein similar to unknown pro	---	AT5G14030	-1.06	-0.08	-0.56	0.596504	0.752683	-7.18
256308_s_	ABC transporter, putative contains Pfa	ATMRP13	AT1G30410 /	1.08	0.11	0.56	0.596714	0.752865	-7.18
249507_at	similar to unknown protein (pir||T02618	---	AT5G38370	-1.04	-0.05	-0.56	0.596697	0.752865	-7.18
261472_at	hypothetical protein predicted by gene	---	AT1G14470	-1.03	-0.05	-0.55	0.596867	0.752974	-7.18
252733_at	putative protein INDOLE-3-ACETIC A	---	AT3G43120	-1.04	-0.06	-0.56	0.596845	0.752974	-7.18
253881_at	putative protein Ran_GTP binding pro	---	AT4G27640	-1.04	-0.06	-0.55	0.596984	0.753081	-7.18
263525_at	putative MADS-box protein	AGL61	AT2G24840	-1.06	-0.08	-0.55	0.597032	0.7531	-7.18
264149_at	NAM (no apical meristem)-like protein	anac005	AT1G02250	1.04	0.06	0.55	0.59721	0.753283	-7.18
247539_at	putative protein predicted protein, Ara	---	AT5G61710	-1.04	-0.05	-0.55	0.597416	0.753501	-7.18
261205_at	hypothetical protein predicted by gene	---	AT1G12790	-1.08	-0.11	-0.55	0.597505	0.753572	-7.18
258423_at	hypothetical protein predicted by gene	---	AT3G16730	-1.04	-0.05	-0.55	0.59755	0.753587	-7.18
265039_at	unknown protein Location of ESTs 20	---	AT1G04000	1.04	0.06	0.55	0.597744	0.753789	-7.18
255123_at	putative lipid transfer protein	---	AT4G08530	-1.04	-0.06	-0.55	0.597793	0.753809	-7.18
264132_at	hypothetical protein predicted by gene	---	AT1G79100	-1.05	-0.08	-0.55	0.597849	0.753838	-7.18
252330_at	hypothetical protein	---	AT3G48770	1.06	0.09	0.55	0.597884	0.753841	-7.18
249466_at	ribosomal protein L5 - like ribosomal p	RPL5B	AT5G39740	-1.07	-0.10	-0.55	0.598013	0.753878	-7.18
251517_at	putative protein hypothetical protein F	---	AT3G59370	1.03	0.05	0.55	0.597976	0.753878	-7.18

248893_at	unknown protein	---	AT5G46310	-1.05	-0.07	-0.55	0.59799	0.753878	-7.18
257160_at	hypothetical protein predicted by gene	---	---	-1.07	-0.10	-0.55	0.598343	0.754227	-7.18
253774_at	NAM / CUC2 -like protein No apical m	anac074	AT4G28530	1.08	0.11	0.55	0.598356	0.754227	-7.18
261358_s_	hypothetical protein predicted by gens	---	AT1G41920 /	1.04	0.06	0.55	0.598672	0.754584	-7.18
267641_at	Argonaute (AGO1)-like protein	AGO6	AT2G32940	-1.04	-0.05	-0.55	0.598716	0.754598	-7.18
255024_at	hypothetical protein	---	AT4G09860	1.04	0.05	0.55	0.598803	0.754666	-7.18
266211_at	putative retroelement pol polyprotein	---	---	-1.04	-0.06	-0.55	0.598915	0.754766	-7.18
253556_at	serine/threonine-specific protein kinas	---	AT4G31100	1.04	0.05	0.55	0.598959	0.754779	-7.18
248955_at	putative protein contains similarity to u	GAS41	AT5G45600	-1.04	-0.06	-0.55	0.599062	0.754799	-7.18
255398_at	hypothetical protein	---	AT4G03740	1.04	0.06	0.55	0.599074	0.754799	-7.18
255167_at	putative protein hypothetical protein T	---	---	-1.03	-0.05	-0.55	0.599062	0.754799	-7.18
245750_at	histone H2A, putative similar to histon	HTA10	AT1G51060	1.10	0.13	0.55	0.599176	0.754886	-7.18
265908_at	contains similarity to S. cerevisiae ADF	---	AT4G00270	1.07	0.09	0.55	0.599266	0.754957	-7.18
262161_at	signal peptidase subunit, putative sim	---	AT1G52600	1.04	0.06	0.55	0.599362	0.755037	-7.18
258561_at	putative hexose transporter similar to H	STP6	AT3G05960	-1.06	-0.09	-0.55	0.599445	0.7551	-7.18
256881_at	hypothetical protein ; supported by cD	---	AT3G26410	1.04	0.06	0.55	0.599574	0.755221	-7.18
263307_at	hypothetical protein similar to myosin-l	---	---	1.05	0.07	0.55	0.599611	0.755225	-7.18
267032_at	putative protein kinase contains a prot	CIPK22	AT2G38490	1.07	0.10	0.55	0.599762	0.75529	-7.18
262023_at	hypothetical protein predicted by gene	---	AT1G35500	1.05	0.06	0.55	0.599752	0.75529	-7.18
257605_at	hypothetical protein predicted by gene	---	AT3G13840	1.04	0.05	0.55	0.599738	0.75529	-7.18
257551_at	hypothetical protein contains similarity	---	---	-1.05	-0.07	-0.55	0.599814	0.755313	-7.18
258270_at	putative lysophospholipase similar to l	---	AT3G15650	-1.11	-0.15	-0.55	0.600001	0.755508	-7.19
256268_at	retinoblastoma-related protein, putativ	RBR1	AT3G12280	1.06	0.08	0.55	0.6001	0.75556	-7.19
245823_at	hypothetical protein predicted by gene	---	AT1G57906	-1.05	-0.07	-0.55	0.600109	0.75556	-7.19
247036_at	putative protein contains similarity to M	---	AT5G67130	-1.06	-0.09	-0.55	0.600145	0.755564	-7.19
249076_at	putative protein similar to unknown pro	TOM22-V	AT5G43970	-1.06	-0.09	-0.55	0.600284	0.755668	-7.19
247935_at	30S ribosomal protein S16 ; supporte	---	AT5G56940	1.06	0.09	0.55	0.600294	0.755668	-7.19
252739_at	putative protein mRNA, Homo sapiens	---	AT3G43250	1.05	0.06	0.55	0.60044	0.755769	-7.19
249289_at	N-hydroxycinnamoyl/benzoyltransferas	---	AT5G41040	-1.19	-0.26	-0.55	0.600419	0.755769	-7.19
246816_at	putative protein	---	AT5G27230	-1.04	-0.06	-0.55	0.600481	0.755779	-7.19
258494_at	cell division protein FtsH-like protein si	---	AT3G02450	1.06	0.08	0.55	0.600531	0.755785	-7.19
267016_at	hypothetical protein predicted by gens	---	AT2G39160 /	1.04	0.06	0.55	0.600586	0.755785	-7.19
261342_at	putative replication protein similar to re	---	AT1G52950	1.04	0.05	0.55	0.600567	0.755785	-7.19
247456_at	iron-regulated transporter - like protei	AtZIP12	AT5G62160	1.04	0.06	0.55	0.60072	0.755912	-7.19
260214_at	hypothetical protein contains Pfam pro	---	AT1G74510	1.04	0.06	0.55	0.600884	0.756077	-7.19

245109_at	hypothetical protein predicted by gene	---	AT2G41520	1.05	0.07	0.55	0.600939	0.756105	-7.19
262221_at	hypothetical protein predicted by gene	ARC3	AT1G75010	-1.06	-0.08	-0.55	0.6011	0.756266	-7.19
254830_at	putative protein predicted protein, Sac	---	AT4G12590	-1.03	-0.05	-0.55	0.601173	0.756315	-7.19
255434_at	predicted protein of unknown function	---	AT4G03180	-1.05	-0.06	-0.55	0.601286	0.756416	-7.19
262063_at	unknown protein identical to unknown	---	AT1G80000	-1.05	-0.08	-0.55	0.601477	0.756614	-7.19
247247_at	50S ribosomal protein L17 ;supported	---	AT5G64650	-1.04	-0.06	-0.55	0.601616	0.756716	-7.19
255950_at	hypothetical protein predicted by gene	---	AT1G22110	1.06	0.08	0.55	0.601624	0.756716	-7.19
264976_at	peptide transporter, putative similar to	NRT1.6	AT1G27080	-1.05	-0.07	-0.55	0.601743	0.756824	-7.19
245406_at	GTP-binding RAB2A like protein	ATRABB1A	AT4G17160	-1.04	-0.05	-0.55	0.601831	0.756851	-7.19
254381_at	putative protein membrane-associated	---	AT4G21880	1.05	0.07	0.55	0.601808	0.756851	-7.19
256924_at	Anthocyanin 5-aromatic acyltransferas	AT5MAT	AT3G29590	-1.05	-0.07	-0.55	0.601894	0.756888	-7.19
257358_at	unknown protein predicted by genscan	---	AT2G40990	-1.07	-0.10	-0.55	0.602424	0.757514	-7.19
266214_at	putative retroelement integrase	---	---	1.04	0.05	0.55	0.602524	0.757597	-7.19
251909_at	putative protein initiator-binding protei	TRFL4	AT3G53790	-1.05	-0.07	-0.55	0.602712	0.757792	-7.19
266583_at	Expressed protein ; supported by cDN	---	AT2G46220	1.06	0.09	0.55	0.602796	0.757855	-7.19
246874_at	arabinosidase - like protein arabinosid	ASD2	AT5G26120	-1.05	-0.07	-0.55	0.602884	0.757925	-7.19
265145_at	unknown protein similar to GB:CAA87	PLT2	AT1G51190	-1.05	-0.07	-0.55	0.602971	0.757951	-7.19
AFFX-BioB	E. coli /GEN=bioB /DB_XREF=gb:J04	---	---	1.14	0.19	0.55	0.602971	0.757951	-7.19
260553_at	unknown protein similar to T11A07.9	---	AT2G41800	-1.04	-0.06	-0.55	0.60301	0.757958	-7.19
245813_at	hypothetical protein contains similarity	---	AT1G49920	1.06	0.09	0.55	0.603096	0.758024	-7.19
248858_at	AP47 50p (gb|AAB88283.1) ; supporte	---	AT5G46630	-1.05	-0.07	-0.55	0.603246	0.758141	-7.19
261316_at	MAP kinase BnMAP4K alpha1, putati	ATMAP4K A	AT1G53165	-1.04	-0.06	-0.55	0.603256	0.758141	-7.19
251943_at	splicing factor - like protein splicing fa	RSZ32	AT3G53500	1.04	0.05	0.54	0.603349	0.758217	-7.19
255253_at	contains similarity to S. cerevisiae vac	VPS28-2	AT4G05000	-1.04	-0.06	-0.54	0.603417	0.75826	-7.19
247614_at	putative protein	---	AT5G60240	1.04	0.06	0.54	0.603571	0.758412	-7.19
262979_s_	unknown protein similar to histone H3.	---	AT1G13370 /	-1.05	-0.06	-0.54	0.603759	0.758607	-7.19
253084_at	putative protein lateral root primordia	STY2	AT4G36260	-1.07	-0.09	-0.54	0.603851	0.758632	-7.19
255970_s_	hypothetical protein predicted by gene	---	---	1.04	0.05	0.54	0.603826	0.758632	-7.19
248989_at	disease resistance protein RPS4	---	AT5G45200	-1.05	-0.07	-0.54	0.603879	0.758632	-7.19
250938_at	putative protein various predicted prot	---	AT5G03180	-1.06	-0.09	-0.54	0.604136	0.758871	-7.19
265463_at	unknown protein	IRX9	AT2G37090	-1.07	-0.10	-0.54	0.604117	0.758871	-7.19
265553_at	putative retroelement pol polyprotein	---	---	-1.04	-0.06	-0.54	0.604452	0.759226	-7.19
265173_at	unknown protein	---	AT1G23530	1.04	0.06	0.54	0.604541	0.759296	-7.19
257701_at	unknown protein contains similarity to	---	AT3G12710	-1.20	-0.26	-0.54	0.604668	0.759372	-7.19
259807_at	hypothetical protein predicted by gens	---	AT1G47920	1.04	0.05	0.54	0.604638	0.759372	-7.19

259795_at	hypothetical protein predicted by gene	---	AT1G64290	1.05	0.07	0.54	0.60482	0.759456	-7.19
263862_at	putative protein phosphatase	IBR5	AT2G04550	1.04	0.06	0.54	0.604833	0.759456	-7.19
263682_at	hypothetical protein similar to reverse t	AT5G49590	---	-1.04	-0.05	-0.54	0.604844	0.759456	-7.19
252078_at	putative protein brassinosteroid-insen	IMK2	AT3G51740	-1.03	-0.05	-0.54	0.604868	0.759456	-7.19
258895_at	putative epoxide hydrolase similar to e	---	AT3G05600	1.04	0.05	0.54	0.60494	0.759504	-7.19
257027_at	DNA repair protein, putative similar to	ATRAD54	AT3G19210	1.04	0.06	0.54	0.60512	0.759689	-7.19
267458_at	similar to Mlo proteins from H. vulgare	MLO5	AT2G33670	1.06	0.08	0.54	0.605212	0.759763	-7.19
265146_at	putative glucosyl transferase	---	AT1G51210	1.09	0.12	0.54	0.605397	0.759883	-7.19
257767_at	hypothetical protein predicted by gene	---	AT3G23040	-1.06	-0.08	-0.54	0.605441	0.759883	-7.19
252545_at	putative protein	---	AT3G45820	-1.05	-0.07	-0.54	0.605434	0.759883	-7.19
261274_at	myb-related protein, putative similar to	MYB117	AT1G26780	-1.04	-0.05	-0.54	0.605389	0.759883	-7.19
265636_at	putative calcium binding protein	---	AT2G27480	1.05	0.07	0.54	0.605691	0.760154	-7.19
248604_at	protein kinase	---	AT5G49470	-1.08	-0.11	-0.54	0.605766	0.760207	-7.19
266862_at	putative MYB family transcription facto	AtMYB104	AT2G26950	-1.04	-0.05	-0.54	0.605943	0.760305	-7.19
254316_at	putative protein glycine-rich cell wall p	---	---	1.05	0.07	0.54	0.605944	0.760305	-7.19
265686_at	hypothetical protein predicted by gens	---	AT2G24460	1.04	0.05	0.54	0.605885	0.760305	-7.19
260287_at	unknown protein contains two Kelch m	---	AT1G80440	-1.07	-0.10	-0.54	0.606082	0.760311	-7.19
247096_at	S-adenosyl-L-methionine:salicylic acid	---	AT5G66430	-1.03	-0.05	-0.54	0.606021	0.760311	-7.19
260674_at	unknown protein ; supported by cDNA	---	AT1G19370	1.04	0.06	0.54	0.606055	0.760311	-7.19
246729_at	putative protein	---	AT5G28070	-1.04	-0.06	-0.54	0.606025	0.760311	-7.19
267317_at	putative proline-rich glycoprotein	---	AT2G34700	-1.04	-0.06	-0.54	0.606228	0.76041	-7.19
260918_at	hypothetical protein predicted by gene	---	AT1G21510	1.04	0.06	0.54	0.606203	0.76041	-7.19
261625_at	hypothetical protein predicted by gene	---	AT1G01930	-1.04	-0.05	-0.54	0.606263	0.760412	-7.19
256087_at	hypothetical protein predicted by gens	---	AT1G20800	-1.04	-0.06	-0.54	0.606481	0.760518	-7.19
249389_at	disease resistence like - protein down	---	AT5G40100	1.06	0.08	0.54	0.606435	0.760518	-7.19
249534_at	bZIP transcription factor - like protein	AtbZIP43	AT5G38800	-1.04	-0.05	-0.54	0.606456	0.760518	-7.19
256966_at	pollen specific protein, putative similar	sks13	AT3G13400	-1.04	-0.05	-0.54	0.606428	0.760518	-7.19
246051_at	epimerase/dehydratase - like protein c	GME	AT5G28840	-1.06	-0.08	-0.54	0.606564	0.76058	-7.19
251997_at	60S ribosomal protein - like 60S ribos	STV1	AT3G53020	-1.06	-0.09	-0.54	0.606631	0.760622	-7.19
245052_at	putative pectinesterase	---	AT2G26440	1.06	0.08	0.54	0.606807	0.760802	-7.19
258789_at	Mutator-like transposase similar to MU	---	---	1.04	0.06	0.54	0.606944	0.760932	-7.19
265384_at	unknown protein ;supported by full-ler	---	AT2G20760	-1.04	-0.05	-0.54	0.607083	0.76098	-7.19
264748_at	hypothetical protein predicted by gene	EMB25	AT1G70070	-1.04	-0.05	-0.54	0.607032	0.76098	-7.19
246032_s_	putative protein	---	---	1.05	0.07	0.54	0.607054	0.76098	-7.19
252059_at	E2, ubiquitin-conjugating enzyme, put	UEV1D-4	AT3G52560	1.04	0.06	0.54	0.607242	0.761115	-7.19

267012_at	similar to latex allergen from Hevea br	PLP6	AT2G39220	1.12	0.16	0.54	0.607257	0.761115	-7.19
251318_at	putative protein putative protein At2g4	GDAP1	AT3G61570	-1.04	-0.06	-0.54	0.607357	0.761115	-7.19
246715_at	putative protein glucose-6-phosphate/	---	AT5G28230	1.06	0.08	0.54	0.607315	0.761115	-7.19
248643_at	putative protein strong similarity to unk	---	AT5G49130	-1.04	-0.06	-0.54	0.607343	0.761115	-7.19
252612_at	hypothetical protein	---	AT3G45160	-1.25	-0.32	-0.54	0.607402	0.761129	-7.19
265429_at	hypothetical protein predicted by gens	---	AT2G20710	1.05	0.08	0.54	0.607483	0.76119	-7.19
246043_at	putative protein predicted protein, Ara	---	AT5G19380	1.08	0.12	0.54	0.60768	0.761388	-7.19
257392_at	hypothetical protein	FLA3	AT2G24450	1.04	0.06	0.54	0.607742	0.761388	-7.19
248543_at	putative protein similar to unknown pro	---	AT5G50230	-1.04	-0.05	-0.54	0.607734	0.761388	-7.19
AFFX-r2-Bs	B. subtilis /GEN=thrC, thrB /DB_XREF	---	---	-1.09	-0.12	-0.54	0.607869	0.761506	-7.19
260108_at	hypothetical protein similar to putative	---	AT1G63280	-1.05	-0.07	-0.54	0.607993	0.761578	-7.19
255409_at	NDX1 homeobox protein homolog	---	AT4G03090	-1.03	-0.05	-0.54	0.607964	0.761578	-7.19
263518_at	Expressed protein ; supported by full-l	---	AT2G21655	-1.04	-0.06	-0.54	0.608136	0.761715	-7.19
255251_at	see GB:U95973 similar to a family of A	---	AT4G04980	-1.04	-0.05	-0.54	0.608183	0.761732	-7.19
248928_at	Rac-like gtp binding protein ARAC2 (s	ARAC2	AT5G45970	-1.03	-0.05	-0.54	0.608481	0.76196	-7.19
263581_at	hypothetical protein identical to hypoth	---	AT2G17160	1.05	0.07	0.54	0.608489	0.76196	-7.19
250652_at	putative protein similar to unknown pro	FLA21	AT5G06920	1.04	0.06	0.54	0.608499	0.76196	-7.19
263338_at	hypothetical protein predicted by gens	---	---	-1.05	-0.07	-0.54	0.608498	0.76196	-7.19
259285_at	hypothetical protein similar to putative	---	AT3G11460	1.04	0.06	0.54	0.608825	0.762082	-7.19
246681_at	chloride channel-like protein chloride	---	AT5G33280	1.04	0.05	0.54	0.60883	0.762082	-7.19
255883_at	unknown protein similar to putative pr	---	AT1G20270	1.05	0.08	0.54	0.608736	0.762082	-7.19
264886_at	S-linalool synthase, putative similar to	TPS04	AT1G61120	1.38	0.46	0.54	0.608646	0.762082	-7.19
267412_at	putative vacuolar sorting receptor	---	AT2G34940	1.14	0.19	0.54	0.60874	0.762082	-7.19
250624_at	putative protein	---	AT5G07330	1.05	0.07	0.54	0.608821	0.762082	-7.19
249561_at	disease resistance - like protein disea	---	AT5G38340	1.04	0.06	0.54	0.608717	0.762082	-7.19
256913_at	unknown protein	---	AT3G23870	-1.08	-0.10	-0.54	0.608934	0.76217	-7.19
259109_at	putative serine threonine protein phosp	---	AT3G05580	-1.07	-0.10	-0.54	0.609267	0.762544	-7.19
252468_at	starch phosphorylase H (cytosolic forr	PHS2	AT3G46970	1.06	0.08	0.54	0.60931	0.762557	-7.19
263747_at	putative ubiquitin activating enzyme	SAE2	AT2G21470	1.04	0.05	0.54	0.609487	0.762737	-7.19
247391_at	unknown protein	---	AT5G63540	-1.04	-0.05	-0.54	0.609648	0.762819	-7.19
254330_at	predicted protein predicted gene F5I1	LBD32	AT4G22700	1.04	0.06	0.54	0.609598	0.762819	-7.19
261716_at	kinesin-related protein, putative simila	---	AT1G18410	1.04	0.05	0.54	0.609653	0.762819	-7.19
263335_x_	hypothetical protein	---	---	1.04	0.05	0.54	0.609726	0.762868	-7.19
266387_at	hypothetical protein predicted by gens	---	AT2G32360	-1.04	-0.06	-0.54	0.609844	0.762974	-7.19
260259_at	unknown protein similar to unknown pr	---	AT1G74300	1.04	0.06	0.53	0.609915	0.76298	-7.19

255972_at	hypothetical protein similar to hypothet	---	---	-1.03	-0.05	-0.53	0.609903	0.76298	-7.19
263087_s_	putative sugar transporter	---	AT2G16120 /	-1.04	-0.06	-0.53	0.609951	0.762982	-7.19
257914_at	Expressed protein ; supported by cDN	---	AT3G25545	-1.05	-0.07	-0.53	0.61006	0.763047	-7.19
256693_at	hypothetical protein predicted by gene	---	---	1.04	0.05	0.53	0.610069	0.763047	-7.19
259381_s_	putative lectin contains Pfam profile: F	NSP1	AT3G16390 /	1.20	0.26	0.53	0.610178	0.763141	-7.19
264284_at	protein kinase, putative similar to prot	---	AT1G61860	1.04	0.06	0.53	0.610263	0.763164	-7.19
261702_at	unknown protein similar to hypothetica	---	AT1G32760	-1.05	-0.06	-0.53	0.610258	0.763164	-7.19
248843_at	homeobox protein	HB-7	AT5G46880	1.05	0.07	0.53	0.610314	0.763186	-7.19
261592_at	double-stranded RNA-specific editase	---	AT1G01760	1.05	0.07	0.53	0.610392	0.763241	-7.19
251223_at	putative transcription factor MYB11	ATMYB11	AT3G62610	-1.04	-0.05	-0.53	0.610425	0.763241	-7.19
261997_at	hypothetical protein similar C-term of g	---	---	-1.04	-0.05	-0.53	0.610562	0.76337	-7.19
249733_at	6-phosphogluconolactonase-like prote	emb2024	AT5G24400	-1.04	-0.06	-0.53	0.610653	0.7634	-7.19
259623_at	hypothetical protein predicted by gene	---	AT1G42700	1.05	0.08	0.53	0.610651	0.7634	-7.19
245919_at	putative protein various predicted prot	---	AT5G28780	1.04	0.05	0.53	0.610708	0.763427	-7.19
250894_s_	putative protein proline-rich protein AF	---	AT5G03810 /	-1.05	-0.07	-0.53	0.610973	0.763716	-7.20
266842_at	FtsH protease, putative contains simil	ftsh4	AT2G26140	1.05	0.07	0.53	0.611033	0.763749	-7.20
254118_at	DNA polymerase III like protein DNA p	---	AT4G24790	1.04	0.05	0.53	0.61111	0.763769	-7.20
265105_s_	unknown protein contains similarity to	---	AT1G62580 /	-1.03	-0.05	-0.53	0.611115	0.763769	-7.20
254721_at	hypothetical protein ;supported by full-	SMAP1	AT4G13520	-1.05	-0.06	-0.53	0.611164	0.763788	-7.20
260102_at	unknown protein	---	AT1G35470	-1.05	-0.07	-0.53	0.611285	0.763896	-7.20
255526_at	hypothetical protein	---	AT4G02350	1.05	0.07	0.53	0.611408	0.763966	-7.20
260091_at	putative serine carboxypeptidase simi	scpl5	AT1G73290	-1.04	-0.06	-0.53	0.611389	0.763966	-7.20
262812_at	hypothetical protein predicted by gens	---	AT1G11690	-1.03	-0.05	-0.53	0.611447	0.763974	-7.20
264486_at	hypothetical protein contains similarity	---	AT1G77180	1.05	0.07	0.53	0.611674	0.764195	-7.20
266058_at	glycerol-3-phosphate dehydrogenase	GLY1	AT2G40690	-1.06	-0.08	-0.53	0.611691	0.764195	-7.20
245189_at	F12A21.18 hypothetical protein	---	AT1G67670	1.03	0.05	0.53	0.611833	0.764331	-7.20
255529_at	CTP synthase - like protein	---	AT4G02120	1.05	0.07	0.53	0.611885	0.764354	-7.20
258408_at	unknown protein similar to putative Na	ATCHX19	AT3G17630	1.04	0.05	0.53	0.612018	0.764478	-7.20
252792_at	hypothetical protein	---	---	-1.05	-0.07	-0.53	0.61219	0.764651	-7.20
256875_at	cytochrome P450, putative contains P	CYP71B37	AT3G26330	-1.05	-0.07	-0.53	0.612237	0.764655	-7.20
254589_at	hypothetical protein	---	AT4G18850	-1.05	-0.07	-0.53	0.61226	0.764655	-7.20
264128_at	unknown protein	---	AT1G79190	-1.04	-0.06	-0.53	0.612464	0.764741	-7.20
251725_at	putative protein	---	AT3G56260	-1.07	-0.10	-0.53	0.612564	0.764741	-7.20
266848_at	unknown protein ;supported by full-ler	---	AT2G25950	1.06	0.09	0.53	0.612532	0.764741	-7.20
248945_at	putative protein strong similarity to unk	---	AT5G45510	1.05	0.07	0.53	0.612474	0.764741	-7.20

260716_at	peroxiredoxin identical to SP:O04005 f	ATPER1	AT1G48130	-1.05	-0.08	-0.53	0.612428	0.764741	-7.20
260561_at	putative endochitinase	---	AT2G43580	1.05	0.08	0.53	0.61255	0.764741	-7.20
253069_at	hexokinase - like protein hexokinase,	HKL3	AT4G37840	1.04	0.06	0.53	0.612368	0.764741	-7.20
266664_at	hypothetical protein predicted by grail	---	AT2G29800	-1.04	-0.06	-0.53	0.612725	0.764859	-7.20
252795_at	putative protein predicted proteins, Ar	---	---	1.04	0.06	0.53	0.612708	0.764859	-7.20
251434_at	polygalacturonase-like protein polygal	---	AT3G59850	1.04	0.06	0.53	0.612895	0.765028	-7.20
261747_at	unknown protein similar to putative en	---	AT1G08350	-1.06	-0.08	-0.53	0.612959	0.76505	-7.20
259571_at	hypothetical protein	---	AT1G20410	-1.06	-0.08	-0.53	0.612997	0.76505	-7.20
262129_at	mutM homologue-1 identical to mutM h	ATMMH-1	AT1G52500	1.05	0.08	0.53	0.613013	0.76505	-7.20
251538_at	putative protein PBK1 protein, Homo s	---	AT3G58660	1.07	0.10	0.53	0.61313	0.765151	-7.20
253229_at	putative protein ;supported by full-leng	---	AT4G34660	1.03	0.04	0.53	0.613194	0.765151	-7.20
254090_at	MtN3 - like protein MtN3 (induced dur	---	AT4G25010	-1.05	-0.07	-0.53	0.613171	0.765151	-7.20
253141_at	putative protein hypothetical protein F	---	AT4G35430 /	-1.05	-0.07	-0.53	0.613236	0.765161	-7.20
260159_at	putative helicase similar to helicase GI	---	AT1G79890	1.04	0.06	0.53	0.613301	0.7652	-7.20
260365_at	hypothetical protein predicted by gene	---	AT1G70630	1.04	0.06	0.53	0.613418	0.765276	-7.20
255852_at	unknown protein	SVL2	AT1G66970	-1.13	-0.17	-0.53	0.613429	0.765276	-7.20
257060_at	unknown protein	---	AT3G18230	1.05	0.06	0.53	0.613577	0.765377	-7.20
246797_at	putative protein ;supported by full-leng	---	AT5G26790	1.04	0.05	0.53	0.613571	0.765377	-7.20
251824_at	ABC transporter - like protein ATP-bin	---	AT3G55090	1.05	0.06	0.53	0.613662	0.765442	-7.20
254436_at	putative protein receptor kinase-like p	---	AT4G20940	-1.04	-0.05	-0.53	0.61387	0.765636	-7.20
262043_at	unknown protein	PSF1	AT1G80190	-1.06	-0.08	-0.53	0.613885	0.765636	-7.20
253023_at	hypothetical protein	---	AT4G38070	1.06	0.08	0.53	0.61401	0.765751	-7.20
264387_at	putative growth regulator protein conta	---	AT1G11990	-1.04	-0.06	-0.53	0.614061	0.765772	-7.20
256899_at	putative kinase-like protein TMKL1 pr	TMKL1	AT3G24660	1.05	0.06	0.53	0.614212	0.765919	-7.20
248942_at	putative protein similar to unknown pro	---	AT5G45480	-1.05	-0.07	-0.53	0.614326	0.765976	-7.20
250136_at	putative protein de novo DNA methylt	DRM1	AT5G15380	-1.08	-0.11	-0.53	0.614317	0.765976	-7.20
248199_at	membrane related protein-like ;suppo	---	AT5G54170	1.10	0.13	0.53	0.614508	0.766078	-7.20
249782_at	dipeptidyl peptidase IV-like protein	---	AT5G24260	-1.04	-0.06	-0.53	0.614452	0.766078	-7.20
254361_at	Expressed protein ; supported by full-l	---	AT4G22212	-1.06	-0.08	-0.53	0.614495	0.766078	-7.20
259217_at	unknown protein similar to F16N3.20 (	---	AT3G03620	-1.04	-0.06	-0.53	0.614557	0.766097	-7.20
255086_at	putative protein chromosome I BAC F	---	AT4G09300	-1.05	-0.07	-0.53	0.614649	0.76617	-7.20
260174_at	unknown protein ;supported by full-ler	---	AT1G71940	1.04	0.06	0.53	0.614839	0.766365	-7.20
259833_at	MYB-family transcription factor, putati	MYB105	AT1G69560	-1.04	-0.05	-0.53	0.614877	0.766371	-7.20
258311_at	transport inhibitor response 1 (TIR1),	AFB2	AT3G26810	-1.04	-0.06	-0.53	0.615166	0.766688	-7.20
257995_at	putative monosaccharide transport pr	---	AT3G19940	-1.05	-0.07	-0.53	0.615237	0.766736	-7.20

245659_at	hypothetical protein predicted by gene	---	AT1G28260	1.08	0.11	0.53	0.615343	0.766781	-7.20
259740_at	phytochrome, putative similar to GI:29	---	AT1G64300	1.06	0.09	0.53	0.615375	0.766781	-7.20
246687_at	putative protein proline-rich protein AF	---	AT5G33370	1.06	0.08	0.53	0.61531	0.766781	-7.20
252342_at	endo-polygalacturonase - like protein	---	AT3G48950	1.03	0.04	0.53	0.615505	0.76686	-7.20
246721_at	putative protein glycine-rich protein, P	---	---	-1.04	-0.05	-0.53	0.615505	0.76686	-7.20
252569_at	receptor-like protein kinase receptor li	---	AT3G45420	-1.05	-0.06	-0.53	0.615714	0.767079	-7.20
266569_at	unknown protein	---	AT2G24080	-1.04	-0.05	-0.53	0.615794	0.767136	-7.20
262643_at	unknown protein ;supported by full-len	---	AT1G62770	-1.08	-0.11	-0.53	0.61588	0.767201	-7.20
266465_at	putative auxin-responsive protein ; su	GH3.9	AT2G47750	-1.05	-0.07	-0.53	0.61597	0.767272	-7.20
246885_at	putative protein predicted protein, Ara	---	AT5G26230	1.12	0.16	0.53	0.61611	0.767372	-7.20
252892_at	hypothetical protein	---	AT4G39420	1.04	0.05	0.53	0.616118	0.767372	-7.20
257594_at	unknown protein	---	AT3G24740	1.05	0.07	0.53	0.616184	0.767413	-7.20
249040_at	eukaryotic translation initiation factor 3	---	AT5G44320	-1.04	-0.06	-0.53	0.616232	0.76743	-7.20
262652_at	hypothetical protein One of a cluster o	FUT9	AT1G14110	-1.04	-0.05	-0.53	0.616283	0.767451	-7.20
267493_at	unknown protein	OFP2	AT2G30400	1.07	0.10	0.53	0.616404	0.767517	-7.20
265780_at	Mutator-like transposase similar to MU	---	---	1.04	0.06	0.53	0.61642	0.767517	-7.20
267287_at	putative pectinesterase	sks16	AT2G23630	1.04	0.05	0.52	0.616437	0.767517	-7.20
260031_at	putative nuclear matrix constituent pro	LINC3	AT1G68790	-1.05	-0.06	-0.52	0.616613	0.767673	-7.20
257776_at	terpene synthase-related protein conta	---	AT3G29190	-1.05	-0.07	-0.52	0.616629	0.767673	-7.20
253311_s_	putative protein xylan endohydrolase i	---	AT4G33830 /	-1.03	-0.05	-0.52	0.617039	0.768099	-7.20
260838_at	hypothetical protein predicted by gene	---	AT1G43680	1.04	0.05	0.52	0.617011	0.768099	-7.20
259124_at	floral homeotic protein AGL4 identical	סקס-02	AT3G02310	-1.03	-0.05	-0.52	0.617107	0.768142	-7.20
266952_at	putative gibberellin 2-oxidase	ATGA2OX3	AT2G34555	1.05	0.07	0.52	0.617246	0.768273	-7.20
248685_at	putative protein similar to unknown pro	---	AT5G48500	1.07	0.09	0.52	0.617322	0.768284	-7.20
257784_at	geranylgeranylated protein, putative s	MUB4	AT3G26980	-1.14	-0.19	-0.52	0.617318	0.768284	-7.20
246784_at	signal peptidase ; supported by cDNA	---	AT5G27430	1.04	0.05	0.52	0.617412	0.768355	-7.20
255960_at	unknown protein ; supported by cDNA	---	AT1G22140	1.06	0.08	0.52	0.617567	0.768505	-7.20
247103_at	putative protein similar to unknown pro	DAR7	AT5G66610	-1.04	-0.06	-0.52	0.617645	0.76856	-7.20
253472_at	hypothetical protein	---	AT4G32230	1.04	0.06	0.52	0.617806	0.768719	-7.20
249381_at	acidic ribosomal protein P2 -like acidi	---	AT5G40040	1.05	0.07	0.52	0.617864	0.768749	-7.20
262528_at	H+-transporting ATPase AHA10 Identi	AHA10	AT1G17260	1.05	0.07	0.52	0.617993	0.768867	-7.20
251296_at	putative protein paladin - Mus muscul	---	AT3G62010	1.05	0.06	0.52	0.618132	0.768999	-7.20
256541_at	ligand-gated ion channel, putative cor	GLR3.3	AT1G42540	1.06	0.08	0.52	0.618243	0.769095	-7.20
253955_at	putative DNA binding protein DNA bin	ATRBP45C	AT4G27000	1.07	0.09	0.52	0.61837	0.769197	-7.20
256827_at	hypothetical protein contains similarity	---	AT3G18570	1.03	0.05	0.52	0.618393	0.769197	-7.20

258418_at	unknown protein	---	AT3G16660	1.16	0.22	0.52	0.618509	0.7693	-7.20
259144_at	putative kinesin-like centromere protei	---	AT3G10180	1.04	0.06	0.52	0.618546	0.769304	-7.20
250605_at	glycine/proline-rich protein flagelliform	---	AT5G07570	1.05	0.07	0.52	0.618589	0.769316	-7.20
253969_at	putative protein hypothetical protein Y	CSN6B	AT4G26430	-1.08	-0.11	-0.52	0.618704	0.769392	-7.20
245751_s_	hypothetical protein contains similarity	---	AT1G25682 /	-1.08	-0.11	-0.52	0.618718	0.769392	-7.20
249621_at	putative protein predicted proteins, Ar	---	AT5G37530	1.04	0.06	0.52	0.618779	0.769426	-7.20
247990_at	unknown protein ;supported by full-ler	---	AT5G56360	-1.04	-0.05	-0.52	0.618851	0.769474	-7.20
249572_at	chromosome condensation protein -lik	EMB2656	AT5G37630	-1.05	-0.07	-0.52	0.61914	0.769665	-7.20
251977_at	putative protein auxin-induced protein	---	AT3G53250	-1.04	-0.05	-0.52	0.619046	0.769665	-7.20
257353_at	hypothetical protein predicted by gens	NPY4	AT2G23050	-1.04	-0.06	-0.52	0.619085	0.769665	-7.20
256646_at	hypothetical protein predicted by gene	---	AT3G13590	-1.05	-0.07	-0.52	0.619127	0.769665	-7.20
249142_at	putative protein similar to unknown pro	---	AT5G43230	1.05	0.07	0.52	0.619398	0.769902	-7.20
267351_at	unknown protein	NRPD1B	AT2G40030	-1.04	-0.06	-0.52	0.619366	0.769902	-7.20
246579_at	hypothetical protein predicted by gene	---	AT1G31620	-1.05	-0.07	-0.52	0.61944	0.769912	-7.20
259286_at	hypothetical protein similar to hypothet	BSMT1	AT3G11480	1.42	0.50	0.52	0.619823	0.770312	-7.20
250467_at	trehalose-6-phosphate phosphatase -	---	AT5G10100	1.04	0.06	0.52	0.619829	0.770312	-7.20
258918_at	putative cytochrome P450 similar to cy	UNE9	AT3G10560	1.06	0.09	0.52	0.620229	0.770725	-7.20
262209_at	hypothetical protein contains similarity	---	AT1G74720	-1.05	-0.07	-0.52	0.620199	0.770725	-7.20
267097_at	unknown protein predicted by genscan	---	AT2G41440	1.04	0.05	0.52	0.62029	0.770759	-7.20
254689_at	putative pectate lyase A11 ; supporte	---	AT4G13710	-1.06	-0.08	-0.52	0.620379	0.770801	-7.20
260066_at	putative lipase/acylhydrolase contains	---	AT1G73610	1.10	0.14	0.52	0.620392	0.770801	-7.20
263991_at	putative retroelement pol polyprotein	---	---	1.06	0.08	0.52	0.620454	0.770836	-7.20
247759_at	copper transport protein - like ;support	COPT3	AT5G59040	1.04	0.05	0.52	0.620655	0.770918	-7.20
245254_at	ATP-sulfurylase ; supported by cDNA:	APS3	AT4G14680	-1.18	-0.24	-0.52	0.620649	0.770918	-7.20
250697_at	putative protein contains similarity to tr	---	AT5G06800	1.05	0.07	0.52	0.620595	0.770918	-7.20
251682_s_	hypothetical protein	---	AT3G57110 /	-1.05	-0.07	-0.52	0.620561	0.770918	-7.20
257941_at	putative UDP-glucose glucosyltransfer	UGT71B8	AT3G21800	-1.04	-0.06	-0.52	0.620772	0.771004	-7.20
247371_at	histone deacetylase ;supported by full	HDA6	AT5G63110	-1.04	-0.06	-0.52	0.620792	0.771004	-7.20
247531_at	putative protein protein kinase 1, PnP	---	AT5G61550	1.05	0.07	0.52	0.620955	0.771165	-7.20
259836_at	unknown protein	ROPGEF11	AT1G52240	-1.03	-0.05	-0.52	0.621045	0.771235	-7.20
245999_at	putative protein predicted protein, Ara	COPT5	AT5G20650	1.04	0.05	0.52	0.621325	0.771373	-7.20
251905_at	putative protein zinc finger protein GC	GAPB	AT1G42970 /	-1.05	-0.07	-0.52	0.621317	0.771373	-7.20
254378_at	putative protein NADH oxidoreductase	DER2.1	AT4G21810	-1.08	-0.11	-0.52	0.621252	0.771373	-7.20
256718_at	hypothetical protein predicted by gens	---	AT2G34120	1.04	0.06	0.52	0.621308	0.771373	-7.20
263775_at	putative MYB family transcription facto	CPC	AT2G46410	1.04	0.06	0.52	0.621299	0.771373	-7.20

252770_at	putative protein cellular nucleic acid b	---	AT3G42860	1.05	0.07	0.52	0.621425	0.771454	-7.20
250139_at	putative protein de novo DNA methylt	DRM2	AT5G14620	-1.03	-0.05	-0.52	0.62172	0.771779	-7.20
252435_at	putative protein several hypothetical pr	---	---	1.05	0.07	0.52	0.621814	0.771854	-7.20
263853_at	putative mutT domain protein	---	AT2G04440	-1.06	-0.09	-0.52	0.621911	0.771931	-7.20
262808_at	Avr9 elicitor response-like protein stror	---	AT1G11730	-1.04	-0.06	-0.52	0.622025	0.772031	-7.20
254634_at	putative protein transcription factor OE	---	AT4G18650	1.05	0.06	0.52	0.622101	0.772084	-7.20
265051_at	jasmonate inducible protein, putative s	---	AT1G52100	1.06	0.08	0.52	0.622199	0.772122	-7.20
255741_at	tRNA isopentenyl transferase, putative	ATIPT6	AT1G25410	-1.04	-0.06	-0.52	0.622189	0.772122	-7.20
252088_at	putative protein	---	AT3G52100 /	-1.05	-0.07	-0.52	0.622247	0.772139	-7.21
250631_at	pectin methyl-esterase-like protein pe	---	AT5G07430	1.04	0.05	0.52	0.622427	0.77232	-7.21
248165_at	putative protein similar to unknown pro	PHOS32	AT5G54430	1.05	0.07	0.52	0.622615	0.772511	-7.21
253781_at	putative protein predicted protein, Ara	---	AT4G28580	-1.04	-0.05	-0.52	0.622927	0.772856	-7.21
255973_at	hypothetical protein predicted by gens	---	AT3G32400	-1.03	-0.05	-0.52	0.62298	0.772881	-7.21
251579_at	putative protein Bet1 homolog - Rattus	BS14A	AT3G58170	-1.04	-0.06	-0.51	0.623148	0.773046	-7.21
257553_at	unknown protein contains Pfam profile	TPR2	AT3G16830	-1.07	-0.09	-0.51	0.623292	0.773183	-7.21
267085_at	putative cellulose synthase	ATCSLB02	AT2G32620	-1.03	-0.05	-0.51	0.623576	0.773406	-7.21
265591_at	hypothetical protein predicted by gens	---	AT2G20150	-1.06	-0.08	-0.51	0.623549	0.773406	-7.21
251946_at	putative protein predicted proteins, Ar	---	AT3G53540	1.16	0.22	0.51	0.623608	0.773406	-7.21
256437_s_	putative clathrin heavy chain similar to	---	AT3G08530 /	1.04	0.05	0.51	0.623538	0.773406	-7.21
263367_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.51	0.623771	0.773525	-7.21
253195_at	putative protein dihydroflavonol-4-redu	---	AT4G35420	-1.05	-0.06	-0.51	0.623738	0.773525	-7.21
252367_at	putative protein MEL-26, Caenorhabd	BT2	AT3G48360	1.14	0.19	0.51	0.623867	0.773602	-7.21
247698_at	putative protein predicted proteins, Ar	---	AT5G59830	1.05	0.07	0.51	0.623926	0.773621	-7.21
267560_at	putative cytochrome P450	CYP76C3	AT2G45580	1.05	0.06	0.51	0.623984	0.773621	-7.21
266855_at	unknown protein	---	AT2G26920	1.05	0.07	0.51	0.62397	0.773621	-7.21
255050_at	putative protein hypothetical protein F	---	---	-1.05	-0.07	-0.51	0.624114	0.77374	-7.21
249643_at	putative transposase putative transpo	---	---	-1.05	-0.07	-0.51	0.624339	0.773914	-7.21
246091_at	putative protein various predicted prot	---	AT5G20590	-1.05	-0.07	-0.51	0.624386	0.773914	-7.21
252232_at	bZIP transcription factor - like protein	AtbZIP5	AT3G49760	1.03	0.05	0.51	0.62439	0.773914	-7.21
261035_at	hypothetical protein contains Pfam pro	---	---	1.03	0.05	0.51	0.624326	0.773914	-7.21
253726_at	ribosomal protein S15a homolog ribos	rps15ae	AT4G29430	-1.09	-0.13	-0.51	0.624485	0.77399	-7.21
261084_at	tropinone reductase-I, putative similar	---	AT1G07440	-1.07	-0.10	-0.51	0.624597	0.774026	-7.21
264542_at	hypothetical protein predicted by gene	---	AT1G55830	-1.03	-0.05	-0.51	0.624566	0.774026	-7.21
262304_at	major latex protein (MLP149), putative	MLP43	AT1G70890	1.23	0.30	0.51	0.62465	0.774026	-7.21
262191_at	hypothetical protein contains similarity	---	---	1.04	0.06	0.51	0.624617	0.774026	-7.21

246879_at	endopeptidase - like protein O-sialogly	---	AT5G26110	-1.04	-0.06	-0.51	0.624727	0.774079	-7.21
251600_at	protein kinase - like protein wall-assoc	---	AT3G57710	1.03	0.05	0.51	0.624775	0.774097	-7.21
261177_at	hypothetical protein predicted by gene	---	AT1G04770	-1.07	-0.10	-0.51	0.624836	0.77413	-7.21
252560_at	histone H2B -like protein histone H2B	HTB11	AT3G46030	-1.04	-0.05	-0.51	0.625084	0.774395	-7.21
248857_at	putative protein contains similarity to A	---	AT5G46640	1.08	0.12	0.51	0.625198	0.774452	-7.21
260270_at	putative disease resistance protein sim	---	AT1G63730	-1.04	-0.06	-0.51	0.625193	0.774452	-7.21
266597_at	putative WRKY-type DNA binding prot	WRKY43	AT2G46130	-1.03	-0.05	-0.51	0.62524	0.774462	-7.21
251543_at	putative protein	---	AT3G58770	-1.04	-0.06	-0.51	0.625435	0.774662	-7.21
245053_at	putative pectinesterase	---	AT2G26450	-1.06	-0.08	-0.51	0.625688	0.774792	-7.21
249597_at	putative protein probable quinone oxic	---	AT5G37960	1.03	0.05	0.51	0.62571	0.774792	-7.21
267330_at	unknown protein	---	AT2G19270	-1.03	-0.04	-0.51	0.625654	0.774792	-7.21
256903_at	hypothetical protein	---	AT3G23960	1.04	0.06	0.51	0.625679	0.774792	-7.21
254621_at	gene 11-1 protein - like gene 11-1 pro	WAVE5	AT4G18600	1.04	0.06	0.51	0.62568	0.774792	-7.21
245422_at	putative protein	---	AT4G17470	-1.15	-0.20	-0.51	0.625792	0.774806	-7.21
261683_at	hypothetical protein similar to hypothet	---	AT1G47300	-1.04	-0.05	-0.51	0.625784	0.774806	-7.21
266027_at	En/Spm-like transposon protein relate	---	---	1.03	0.05	0.51	0.625823	0.774806	-7.21
255169_x_	hypothetical protein	---	AT4G07940	-1.04	-0.06	-0.51	0.625953	0.774925	-7.21
252478_at	putative protein mitotic phosphoprotei	---	AT3G46540	-1.07	-0.10	-0.51	0.626036	0.774986	-7.21
245602_at	Expressed protein ;supported by cDNA	---	AT4G14270	-1.06	-0.09	-0.51	0.626201	0.775105	-7.21
259371_at	unknown protein ;supported by full-len	---	AT1G69080	-1.13	-0.18	-0.51	0.62619	0.775105	-7.21
251530_at	putative protein several hypothetical pr	---	AT3G58520	-1.06	-0.08	-0.51	0.626401	0.775311	-7.21
246686_at	putative protein predicted proteins - Ar	---	---	-1.06	-0.08	-0.51	0.62649	0.775337	-7.21
265223_at	putative pectinesterase	---	AT2G36700	1.03	0.05	0.51	0.626476	0.775337	-7.21
260795_at	CLE3, putative CLAVATA3/ESR-Rela	CLE3	AT1G06225	-1.04	-0.06	-0.51	0.626665	0.775471	-7.21
247986_at	unknown protein	---	AT5G56880	1.05	0.07	0.51	0.626666	0.775471	-7.21
256357_at	hypothetical protein	---	AT1G66490	-1.03	-0.04	-0.51	0.62684	0.775644	-7.21
255015_at	putative protein m6A methyltransferas	EMB1691	AT4G09980	1.07	0.09	0.51	0.626948	0.775735	-7.21
257559_at	hypothetical protein contains Pfam pro	---	AT3G22050	1.04	0.06	0.51	0.626995	0.775752	-7.21
264282_at	hypothetical protein similar to hypothet	---	AT1G61840	1.04	0.06	0.51	0.627237	0.776009	-7.21
256066_at	hypothetical protein similar to hypothet	---	AT1G06980	-1.12	-0.17	-0.51	0.627357	0.776116	-7.21
258990_at	unknown protein ;supported by full-ler	---	AT3G08840	1.07	0.10	0.51	0.627414	0.776131	-7.21
255589_s_	hypothetical protein	---	AT4G01590 /	-1.06	-0.09	-0.51	0.627438	0.776131	-7.21
259834_at	H-protein promoter binding factor-2b n	---	AT1G69570	-1.08	-0.11	-0.51	0.627793	0.776528	-7.21
249130_at	putative protein contains similarity to c	---	AT5G43100	1.04	0.05	0.51	0.627941	0.77667	-7.21
264790_at	putative histidine kinase histidine kinas	ATHK1	AT2G17820	1.05	0.07	0.51	0.628008	0.776677	-7.21

247600_at	Myb transcription factor homolog (ATR	MYB34	AT5G60890	-1.11	-0.15	-0.51	0.628151	0.776677	-7.21
250145_at	putative protein predicted protein, Ara	---	AT5G14690	-1.06	-0.08	-0.51	0.628131	0.776677	-7.21
253800_at	putative protein probable cell wall prot	---	AT4G28160	-1.05	-0.07	-0.51	0.628137	0.776677	-7.21
247547_at	putative protein	---	AT5G61360	-1.07	-0.09	-0.51	0.628109	0.776677	-7.21
265320_at	unknown protein predicted by genscan	---	AT2G18320	1.04	0.06	0.51	0.628115	0.776677	-7.21
254914_at	peroxidase ATP19a	---	AT4G11290	1.20	0.27	0.51	0.628243	0.776748	-7.21
250736_s_	putative protein contains similarity to z	---	AT1G01350 /	1.06	0.08	0.51	0.628408	0.776906	-7.21
251949_at	receptor protein kinase -like protein C	---	AT3G53590	-1.05	-0.07	-0.51	0.628439	0.776906	-7.21
254961_at	putative acyl-CoA synthetase acyl-Co	---	AT4G11030	-1.04	-0.06	-0.51	0.628813	0.777326	-7.21
256640_at	hypothetical protein predicted by gene	---	AT3G32260	-1.05	-0.07	-0.51	0.62898	0.77749	-7.21
250226_at	putative protein contains similarity to N	---	AT5G13780	-1.05	-0.07	-0.51	0.629065	0.777554	-7.21
260851_at	nodulin-like protein similar to MtN21 G	---	AT1G21890	-1.04	-0.06	-0.51	0.629149	0.777576	-7.21
254629_at	Expressed protein ; supported by full-l	---	AT4G18425	1.05	0.08	0.51	0.629151	0.777576	-7.21
249865_at	unknown protein ; supported by cDNA	---	AT5G22820	1.05	0.07	0.51	0.629245	0.77765	-7.21
266092_at	hypothetical protein predicted by gens	---	AT2G37880	1.04	0.06	0.51	0.629283	0.777654	-7.21
246080_at	putative protein	---	AT5G20460	1.04	0.06	0.51	0.629363	0.777711	-7.21
248051_at	Atmyb103 (gb|AAD40692.1)	ATMYB103	AT5G56110	1.04	0.06	0.51	0.629482	0.777816	-7.21
251123_at	putative protein predicted proteins, Ar	---	AT5G01030	-1.04	-0.05	-0.50	0.629723	0.778071	-7.21
255801_at	putative protein heat shock protein dn	---	AT4G10130	-1.04	-0.05	-0.50	0.629775	0.778084	-7.21
258223_at	unknown protein ; supported by cDNA	PIFI	AT3G15840	-1.05	-0.07	-0.50	0.629843	0.778084	-7.21
255618_at	hypothetical protein	---	AT4G01340	1.03	0.04	0.50	0.629869	0.778084	-7.21
265650_at	hypothetical protein predicted by gens	---	AT2G27460	-1.04	-0.06	-0.50	0.629856	0.778084	-7.21
264273_s_	hypothetical protein contains similarity	---	AT1G60300 /	-1.06	-0.08	-0.50	0.629923	0.778107	-7.21
258132_at	protein kinase, putative similar to GB:	ATPERK1	AT3G24550	1.06	0.09	0.50	0.629976	0.778117	-7.21
254825_at	putative protein Pad-1, Neurospora cr	---	AT4G12640	-1.06	-0.08	-0.50	0.629998	0.778117	-7.21
246962_s_	transcription factor-like protein light-in	BZIP9	AT5G24800	-1.08	-0.11	-0.50	0.630075	0.778169	-7.21
254307_at	putative protein various predicted prot	---	AT4G22400	1.07	0.09	0.50	0.630111	0.778171	-7.21
248965_at	nodulin-like protein	---	AT5G45370	1.05	0.07	0.50	0.630175	0.778208	-7.21
261996_at	AIG1-like protein similar to AIG1 prote	---	AT1G33830	-1.03	-0.05	-0.50	0.630285	0.778302	-7.21
259778_at	hypothetical protein predicted by gene	---	AT1G29610	-1.04	-0.05	-0.50	0.63039	0.77839	-7.21
258907_at	putative sodium proton exchanger sim	NHX4	AT3G06370	-1.05	-0.06	-0.50	0.630512	0.778409	-7.21
253068_at	putative protein Kaposi's sarcoma-ass	---	AT4G37820	-1.04	-0.06	-0.50	0.63053	0.778409	-7.21
264305_at	Expressed protein ; supported by full-l	LSH7	AT1G78815	-1.04	-0.05	-0.50	0.630499	0.778409	-7.21
265159_at	unknown protein similar to EST gb|T43	---	AT1G31060	-1.05	-0.07	-0.50	0.630542	0.778409	-7.21
262750_at	unknown protein ; supported by cDNA	---	AT1G28710	-1.05	-0.07	-0.50	0.630579	0.778413	-7.21

265397_at	hypothetical protein predicted by gens	---	---	-1.04	-0.05	-0.50	0.630711	0.778533	-7.21
267464_at	putative pectinesterase	---	AT2G19150	1.04	0.06	0.50	0.630814	0.778534	-7.21
251994_at	protein kinase - like protein kinase, Ar	KIPK	AT3G52890	-1.08	-0.11	-0.50	0.630749	0.778534	-7.21
256562_at	Ty1/Copia-type retroelement polyprote	---	---	1.04	0.05	0.50	0.63078	0.778534	-7.21
264913_at	hypothetical protein predicted by gene	---	AT1G60770	-1.07	-0.10	-0.50	0.630914	0.778594	-7.21
261368_at	protein kinase, putative similar to man	---	AT1G53070	1.05	0.08	0.50	0.63093	0.778594	-7.21
263364_at	unknown protein predicted by genscan	---	AT2G20540	1.03	0.05	0.50	0.631199	0.778883	-7.21
255001_at	AIG1-like protein AIG1 - Arabidopsis t	---	AT4G09930	1.05	0.07	0.50	0.631338	0.779013	-7.21
256365_at	arginyl-tRNA synthetase nearly identic	---	AT1G66530	1.07	0.09	0.50	0.631491	0.779136	-7.21
261987_at	hypothetical protein predicted by gene	---	AT1G33710	1.03	0.04	0.50	0.631506	0.779136	-7.21
267338_at	26S proteasome regulatory subunit ; s	EIF2	AT2G39990	-1.05	-0.07	-0.50	0.631623	0.779237	-7.21
245814_at	mitotic checkpoint protein, putative sir	---	AT1G49910	1.05	0.07	0.50	0.631696	0.779286	-7.21
259457_at	auxin response factor 1, putative simil	ARF23	AT1G43950	-1.04	-0.05	-0.50	0.631774	0.779339	-7.21
259184_at	unknown protein ;supported by full-ler	---	AT3G01520	-1.04	-0.06	-0.50	0.631845	0.779385	-7.21
267378_at	hypothetical protein	---	AT2G26200	-1.03	-0.05	-0.50	0.631913	0.779393	-7.21
265332_at	hypothetical protein predicted by gene	---	AT2G18410	1.05	0.07	0.50	0.632089	0.779393	-7.21
252925_at	ES43 like protein ES43 protein - barle	SHL1	AT4G39100	1.05	0.07	0.50	0.632108	0.779393	-7.21
262390_at	hypothetical protein predicted by gens	---	AT1G49260	-1.05	-0.06	-0.50	0.632022	0.779393	-7.21
245568_at	hypothetical protein	---	AT4G14650	-1.05	-0.08	-0.50	0.632044	0.779393	-7.21
255179_at	putative transposon protein	---	---	-1.03	-0.04	-0.50	0.632094	0.779393	-7.21
248068_at	unknown protein	---	AT5G55610	-1.06	-0.08	-0.50	0.631946	0.779393	-7.21
249526_at	putative protein contains similarity to p	---	AT5G38560	1.05	0.07	0.50	0.632125	0.779393	-7.21
259042_at	RGA1-like protein similar to RGA1 pro	RGL2	AT3G03450	-1.06	-0.09	-0.50	0.632159	0.779393	-7.21
245058_at	hypothetical protein predicted by gene	---	AT2G39790	1.04	0.05	0.50	0.632261	0.779476	-7.21
264915_at	hypothetical protein predicted by gene	---	AT1G60790	-1.03	-0.05	-0.50	0.632334	0.779524	-7.21
247730_at	glucuronosyl transferase - like protein	UGT76E1	AT5G59580	1.07	0.10	0.50	0.632486	0.77967	-7.21
261198_at	nitrate transporter, putative similar to (	ATNRT2.5	AT1G12940	-1.03	-0.05	-0.50	0.632533	0.779685	-7.21
259409_at	hypothetical protein contains similarity	---	AT1G13330	1.04	0.05	0.50	0.632703	0.779853	-7.21
246254_at	MAP kinase like protein	ATMPK14	AT4G36450	-1.07	-0.10	-0.50	0.632871	0.780018	-7.21
259963_at	phosphate/phosphoenolpyruvate trans	---	AT1G53660	-1.04	-0.06	-0.50	0.63298	0.78011	-7.21
245205_at	putative protein similarity to splicing fa	---	AT5G12280	-1.06	-0.08	-0.50	0.633077	0.780145	-7.21
248606_at	putative protein contains similarity to b	CPuORF4	AT5G49448 /	-1.07	-0.10	-0.50	0.633061	0.780145	-7.21
267350_at	putative DNA-directed RNA polymeras	NRPD1B	AT2G40030	-1.05	-0.07	-0.50	0.633252	0.780302	-7.21
251625_at	beta-1,3-glucanase 2 (BG2) (PR-2) ;s	BGL2	AT3G57260	1.65	0.72	0.50	0.633273	0.780302	-7.21
265671_at	40S ribosomal protein S12 ;supported	---	AT2G32060	1.09	0.13	0.50	0.633346	0.780308	-7.21

254841_at	putative protein predicted proteins Ara	---	AT4G11940	-1.05	-0.06	-0.50	0.633323	0.780308	-7.21
259026_at	putative protein kinase similar to hypo	---	AT3G09240	1.04	0.06	0.50	0.633416	0.78031	-7.21
256475_s_	myosin heavy chain ATM2, putative si	---	AT1G42680 /	1.04	0.06	0.50	0.633412	0.78031	-7.21
246699_at	putative protein predicted proteins, Sa	---	AT5G27990	1.06	0.08	0.50	0.633712	0.780575	-7.21
265743_s_	En/Spm-like transposon protein relate	---	---	1.04	0.05	0.50	0.633678	0.780575	-7.21
254942_at	putative protein predicted proteins, Ar	---	AT4G10880	1.03	0.04	0.50	0.633734	0.780575	-7.21
259419_at	acyl-CoA oxidase ACX3, putative simi	ACX6	AT1G06310	1.04	0.05	0.50	0.634017	0.780882	-7.21
266518_at	hypothetical protein predicted by gens	---	AT2G35170	1.04	0.06	0.50	0.634135	0.780901	-7.21
252247_at	putative protein various predicted prote	---	AT3G49740	1.04	0.05	0.50	0.634119	0.780901	-7.21
257732_at	unknown protein contains Pfam profile	AtCASP	AT3G18480	1.04	0.06	0.50	0.63411	0.780901	-7.21
261137_at	auxin-induced protein, putative similar	---	AT1G19830	1.03	0.05	0.50	0.634208	0.780949	-7.22
265885_at	hypothetical protein predicted by gene	---	AT2G42330	-1.06	-0.08	-0.50	0.634294	0.781012	-7.22
247930_at	putative protein similar to unknown pro	---	AT5G57060	1.06	0.09	0.50	0.634417	0.781122	-7.22
247761_at	phosphoprotein phosphatase 1 catalyt	TOPP2	AT5G59160	-1.04	-0.06	-0.50	0.634454	0.781125	-7.22
262234_at	putative G protein coupled receptor ide	GCR1	AT1G48270	-1.06	-0.08	-0.50	0.634528	0.781173	-7.22
248078_at	putative protein contains similarity to C	---	AT5G55780	-1.04	-0.05	-0.50	0.63459	0.781208	-7.22
254820_s_	pEARLI 1-like protein Arabidopsis tha	---	AT4G12510 /	1.09	0.13	0.50	0.634795	0.781418	-7.22
264297_at	hypothetical protein similar to hypothet	---	AT1G78710	-1.03	-0.04	-0.50	0.634993	0.78162	-7.22
264117_at	hypothetical protein predicted by gene	---	AT2G31210	1.04	0.05	0.50	0.635188	0.781817	-7.22
256132_at	hypothetical protein similar to hypothet	---	AT1G13610	-1.04	-0.05	-0.50	0.635366	0.781995	-7.22
247608_at	replication protein A1 - like probable r	---	AT5G60990	1.05	0.07	0.50	0.635546	0.782047	-7.22
251843_x_	extensin precursor -like protein extens	ATHRGP1	AT3G54590	1.08	0.11	0.50	0.635483	0.782047	-7.22
245848_at	putative protein predicted proteins - dif	FY	AT5G13480	-1.04	-0.06	-0.50	0.635528	0.782047	-7.22
253961_at	putative protein SPF1 protein, Ipomoe	WRKY34	AT4G26440	1.04	0.05	0.50	0.635523	0.782047	-7.22
259964_at	glutathione transferase, putative simil	ATGSTU28	AT1G53680	1.04	0.05	0.50	0.635677	0.782166	-7.22
261632_at	hypothetical protein predicted by gene	---	AT1G50120	1.05	0.06	0.50	0.635747	0.782209	-7.22
254474_at	putative protein predicted proteins, Ar	---	AT4G20390	1.06	0.08	0.50	0.635929	0.782392	-7.22
266825_at	unknown protein	---	AT2G22890	-1.08	-0.12	-0.50	0.636013	0.782453	-7.22
262387_s_	hypothetical protein contains similarity	---	AT1G49340 /	1.04	0.06	0.50	0.636235	0.782458	-7.22
260876_at	hypothetical protein contains similarity	---	AT1G21460	1.06	0.09	0.50	0.636188	0.782458	-7.22
251211_s_	putative protein several hypothetical pr	---	AT3G62470 /	-1.09	-0.12	-0.50	0.636257	0.782458	-7.22
263544_at	putative ADP-glucose pyrophosphoryla	APL4	AT2G21590	-1.05	-0.07	-0.50	0.636253	0.782458	-7.22
263301_x_	hypothetical protein predicted by gene	---	---	1.04	0.05	0.50	0.636169	0.782458	-7.22
257548_s_	hypothetical protein	LBD23	AT3G26620 /	1.03	0.05	0.50	0.636228	0.782458	-7.22
255220_at	polyubiquitin (UBQ10) identical to GI:8	UBQ10	AT4G05320	1.05	0.07	0.50	0.636157	0.782458	-7.22

253834_at	protein phosphatase homolog (PPH1)	---	AT4G27800	-1.05	-0.06	-0.49	0.636412	0.782563	-7.22
267042_at	putative non-LTR retroelement reverse	---	AT2G34320	1.04	0.05	0.49	0.636386	0.782563	-7.22
265703_at	putative ankyrin	---	AT2G03430	1.05	0.07	0.49	0.636493	0.782579	-7.22
250686_at	gamma-tubulin interacting protein-like	SPC98	AT5G06680	1.06	0.08	0.49	0.63647	0.782579	-7.22
254698_at	NAM (no apical meristem) - like protei	anac071	AT4G17980	-1.03	-0.04	-0.49	0.63664	0.782718	-7.22
262232_at	unknown protein ; supported by cDNA	---	AT1G68600	1.06	0.09	0.49	0.636691	0.782738	-7.22
248374_at	MADS box transcription factor-like	AGL71	AT5G51870	1.03	0.04	0.49	0.636833	0.782871	-7.22
266900_at	hypothetical protein predicted by gens	---	AT2G34610	1.03	0.05	0.49	0.636944	0.782965	-7.22
261235_x_	hypothetical protein predicted by gene	---	---	1.03	0.05	0.49	0.636986	0.782974	-7.22
249817_at	putative protein similar to unknown pro	---	AT5G23820	-1.23	-0.30	-0.49	0.637056	0.783018	-7.22
248849_at	multidrug resistance p-glycoprotein	PGP7	AT5G46540	1.03	0.05	0.49	0.637133	0.78307	-7.22
256387_at	hypothetical protein	---	AT3G06170	1.05	0.07	0.49	0.637479	0.783453	-7.22
263358_x_	hypothetical protein similar to hypothet	---	---	-1.04	-0.06	-0.49	0.637659	0.783506	-7.22
258105_at	Expressed protein ; supported by full-l	---	AT3G23605	1.08	0.11	0.49	0.637609	0.783506	-7.22
266740_at	hypothetical protein predicted by gene	---	AT2G46840	1.04	0.06	0.49	0.637657	0.783506	-7.22
262201_at	unknown protein	ORC4	AT2G01120	-1.04	-0.05	-0.49	0.637627	0.783506	-7.22
260997_at	zinc-finger protein (ZPT4-4), putative	---	AT1G26610	-1.03	-0.05	-0.49	0.637723	0.783542	-7.22
250212_at	putative protein contains similarity to S	SUVH4	AT5G13960	-1.04	-0.06	-0.49	0.637932	0.783702	-7.22
258232_at	unknown protein	---	AT3G27750	-1.06	-0.08	-0.49	0.637912	0.783702	-7.22
258530_at	hypothetical protein predicted by gene	---	AT3G06840	-1.05	-0.06	-0.49	0.637956	0.783702	-7.22
258407_at	unknown protein similar to unknown pr	---	AT3G17620	-1.06	-0.08	-0.49	0.638146	0.783894	-7.22
264397_at	hypothetical protein	---	AT1G11820	-1.06	-0.08	-0.49	0.638274	0.783966	-7.22
246825_at	putative protein various predicted prot	---	AT5G26260	1.03	0.05	0.49	0.638246	0.783966	-7.22
252089_at	putative protein	---	AT3G52110	-1.06	-0.08	-0.49	0.638411	0.784092	-7.22
265195_at	hypothetical protein	---	AT2G36730	1.03	0.05	0.49	0.638554	0.784107	-7.22
250118_at	putative protein similar to unknown pro	---	AT5G16460	-1.04	-0.06	-0.49	0.638561	0.784107	-7.22
261862_at	DNA-binding protein, putative similar t	---	AT1G50410	1.05	0.07	0.49	0.638541	0.784107	-7.22
246337_at	putative protein putative integral mem	CHX12	AT3G44910	-1.05	-0.08	-0.49	0.638497	0.784107	-7.22
256768_at	hypothetical protein predicted by gene	LDL2	AT3G13682	1.03	0.05	0.49	0.638632	0.784152	-7.22
263933_s_	putative harpin-induced protein	---	AT2G35970 /	1.04	0.06	0.49	0.6389	0.784439	-7.22
260989_at	unknown protein ; supported by cDNA	---	AT1G53450	-1.05	-0.07	-0.49	0.639071	0.784534	-7.22
247538_at	ABC family transporter - like protein A	ATH16	AT5G61700	1.03	0.04	0.49	0.639028	0.784534	-7.22
262851_at	putative RNA helicase Contains DEAD	---	AT1G20920	1.05	0.07	0.49	0.63908	0.784534	-7.22
264079_at	putative seed storage protein (vicilin-li	---	AT2G28490	-1.04	-0.05	-0.49	0.639146	0.784572	-7.22
250759_at	unknown protein	---	AT5G06020	-1.03	-0.05	-0.49	0.639334	0.78476	-7.22

259901_at	disease resistance protein, putative si	AtRLP14	AT1G74180	-1.05	-0.07	-0.49	0.639478	0.784895	-7.22
245253_at	hydroperoxide lyase (HPOL) like prote	HPL1	AT4G15440	-1.22	-0.29	-0.49	0.639541	0.784904	-7.22
252100_at	crooked neck-like protein crooked nec	---	AT3G51110	1.07	0.10	0.49	0.639589	0.784904	-7.22
253771_at	hypothetical protein ;supported by full	---	AT4G28430	-1.04	-0.06	-0.49	0.639568	0.784904	-7.22
250046_at	putative protein predicted proteins, Ar	---	AT5G17720	-1.04	-0.06	-0.49	0.639646	0.784933	-7.22
249488_at	putative protein putative transposase	---	---	-1.04	-0.05	-0.49	0.639734	0.784998	-7.22
248777_at	putative protein similar to unknown pro	---	AT5G47920	1.04	0.06	0.49	0.640178	0.785306	-7.22
262949_at	pectinesterase, putative similar to pec	sks18	AT1G75790	-1.04	-0.06	-0.49	0.640113	0.785306	-7.22
264208_at	putative polyA-binding protein, PAB3 s	PAB3	AT1G22760	1.06	0.09	0.49	0.64026	0.785306	-7.22
259455_x_	unknown protein	---	AT1G44030	1.05	0.07	0.49	0.640226	0.785306	-7.22
262097_at	hypothetical protein predicted by gene	---	AT1G55990	1.04	0.05	0.49	0.640212	0.785306	-7.22
261590_at	hypothetical protein predicted by gene	ROPGEF2	AT1G01700	-1.04	-0.05	-0.49	0.640065	0.785306	-7.22
249517_at	putative protein similar to unknown pro	---	AT5G38580	1.03	0.05	0.49	0.640149	0.785306	-7.22
249654_at	putative protein hypothetical proteins -	---	---	1.04	0.05	0.49	0.640089	0.785306	-7.22
258284_at	putative ribosomal protein similar to rib	---	AT3G16080	-1.09	-0.12	-0.49	0.640357	0.785358	-7.22
258278_at	putative self-incompatibility protein sin	---	AT3G26860	-1.04	-0.05	-0.49	0.64044	0.785358	-7.22
255855_at	ABC transporter, putative similar to AB	PDR11	AT1G66950	1.05	0.07	0.49	0.640413	0.785358	-7.22
252812_at	putative protein hypothetical proteins -	---	---	-1.03	-0.05	-0.49	0.640406	0.785358	-7.22
248577_at	myrosinase binding protein-like ; suppo	---	AT5G49870	-1.03	-0.05	-0.49	0.640945	0.78585	-7.22
264742_at	hypothetical protein similar to hypothet	---	AT1G62130	-1.05	-0.07	-0.49	0.64093	0.78585	-7.22
246616_at	aspartyl protease-like	---	AT5G36260	1.06	0.09	0.49	0.640884	0.78585	-7.22
255060_at	putative protein TMV resistance prote	---	AT4G09430	-1.05	-0.06	-0.49	0.641074	0.785966	-7.22
247883_at	unknown protein	---	AT5G57790	1.06	0.08	0.49	0.641135	0.785998	-7.22
246690_at	hypothetical protein	---	---	-1.04	-0.06	-0.49	0.64118	0.786012	-7.22
247040_at	anthranilate N-hydroxycinnamoyl/benz	---	AT5G67150	1.05	0.07	0.49	0.64131	0.786129	-7.22
255076_at	putative protein RING-H2 zinc finger p	---	AT4G09130	-1.03	-0.05	-0.49	0.641481	0.786296	-7.22
258695_at	putative ascorbate peroxidase strong s	APX2	AT3G09640	1.05	0.07	0.49	0.641521	0.786303	-7.22
258692_at	unknown protein	---	AT3G08640	-1.07	-0.10	-0.49	0.641699	0.786332	-7.22
255256_at	see GB:AC003952 similar to a family c	---	AT4G05080	-1.05	-0.07	-0.49	0.641717	0.786332	-7.22
255316_at	putative protein	---	---	1.03	0.05	0.49	0.6417	0.786332	-7.22
250976_at	putative protein various predicted prot	---	AT5G03060	-1.04	-0.05	-0.49	0.641664	0.786332	-7.22
265240_s_	hypothetical protein	---	AT2G07691	-1.05	-0.07	-0.49	0.641643	0.786332	-7.22
256297_at	cytochrome P450, putative contains P	---	AT1G69500	1.05	0.07	0.49	0.641895	0.786508	-7.22
247446_at	unknown protein ; supported by cDNA	---	AT5G62650	-1.03	-0.05	-0.49	0.642434	0.786979	-7.22
259742_at	putative proline-rich APG protein simila	GLIP6	AT1G71120	-1.06	-0.08	-0.49	0.642452	0.786979	-7.22

265835_at	putative retroelement pol polyprotein	---	---	1.05	0.07	0.49	0.64236	0.786979	-7.22
248825_at	ATP synthase delta chain, mitochondr	---	AT5G47030	-1.04	-0.05	-0.49	0.64245	0.786979	-7.22
260310_at	hypothetical protein predicted by gens	---	AT1G70590	-1.05	-0.07	-0.49	0.642395	0.786979	-7.22
256320_at	DnaJ protein, putative contains Pfam	---	AT3G12170	-1.05	-0.06	-0.49	0.642845	0.787347	-7.22
250807_at	helicase-like transcription factor-like pr	---	AT5G05130	1.05	0.07	0.49	0.642856	0.787347	-7.22
249502_s_	expansin-like protein expansin - Prun	ATEXPA23	AT5G39280 /	1.05	0.07	0.49	0.642823	0.787347	-7.22
249434_at	putative protein GTP-binding proteins	---	AT5G39960	1.06	0.08	0.49	0.642928	0.787366	-7.22
255274_at	putative protein various predicted prot	---	---	-1.05	-0.07	-0.49	0.642941	0.787366	-7.22
265733_at	unknown protein ;supported by full-ler	---	AT2G01190	1.04	0.06	0.48	0.6431	0.787519	-7.22
267112_at	putative adenosine phosphosulfate kin	APK	AT2G14750	1.09	0.12	0.48	0.643232	0.787638	-7.22
263718_at	putative CCAAT-box binding trancriptio	NF-YB7	AT2G13570	1.05	0.07	0.48	0.643371	0.787639	-7.22
253711_at	hypothetical protein	DER1	---	-1.04	-0.05	-0.48	0.643337	0.787639	-7.22
262153_at	unknown protein	---	AT1G52710	1.03	0.05	0.48	0.643284	0.787639	-7.22
252517_at	receptor-like protein kinase homolog I	---	AT3G46340	-1.04	-0.06	-0.48	0.643335	0.787639	-7.22
250701_at	bZIP transcription factor-like protein	---	AT5G06839	1.04	0.06	0.48	0.643441	0.787683	-7.22
251751_at	putative protein predicted proteins, Ar	---	AT3G55720	-1.03	-0.04	-0.48	0.643586	0.787775	-7.22
249568_at	glucosyltransferase-like protein UDP-g	---	AT5G38040	1.05	0.07	0.48	0.643569	0.787775	-7.22
251892_at	putative protein	WRI1	AT3G54320	-1.06	-0.08	-0.48	0.644077	0.78825	-7.22
262771_at	hypothetical protein predicted by gens	---	AT1G13200	-1.05	-0.07	-0.48	0.644078	0.78825	-7.22
248321_at	putative protein similar to unknown pro	---	AT5G52740	1.04	0.05	0.48	0.644032	0.78825	-7.22
249387_at	putative protein predicted proteins, Ar	---	AT5G40070	-1.05	-0.08	-0.48	0.644285	0.788461	-7.22
263500_s_	hypothetical protein	---	AT2G07672	1.04	0.06	0.48	0.644448	0.788619	-7.22
257622_at	hypothetical protein contains Pfam pro	---	AT3G20280	1.06	0.08	0.48	0.64455	0.788701	-7.22
266085_at	hypothetical protein	---	AT2G37800	-1.05	-0.07	-0.48	0.644617	0.788741	-7.22
259485_at	ATP synthase gamma-subunit, putativ	ATPC2	AT1G15700	1.09	0.12	0.48	0.644694	0.788786	-7.22
266146_at	En/Spm-like transposon protein relate	---	---	1.03	0.05	0.48	0.644899	0.788786	-7.22
262271_x_	hypothetical protein predicted by gene	---	---	-1.07	-0.09	-0.48	0.644872	0.788786	-7.22
260828_at	unknown protein	---	AT1G06750	-1.04	-0.05	-0.48	0.64476	0.788786	-7.22
267104_at	ERD15 protein identical to GB D30719	ERD15	AT2G41430	-1.05	-0.07	-0.48	0.644904	0.788786	-7.22
250940_at	putative protein	---	AT5G03310	1.03	0.05	0.48	0.644819	0.788786	-7.22
263280_x_	hypothetical protein predicted by gens	---	---	1.04	0.06	0.48	0.64493	0.788786	-7.22
259451_at	synaptosomal associated protein (SN	SNAP30	AT1G13890	1.03	0.05	0.48	0.644884	0.788786	-7.22
247455_at	MYB96 transcription factor-like protein	MYB96	AT5G62470	1.07	0.10	0.48	0.645279	0.78917	-7.22
255562_at	G/T DNA mismatch repair enzyme sim	MSH6	AT4G02070	1.05	0.07	0.48	0.645448	0.789335	-7.22
263273_x_	En/Spm-like transposon protein relate	---	---	1.04	0.05	0.48	0.645591	0.789425	-7.22

244967_at	PSI J protein	---	---	1.08	0.11	0.48	0.645563	0.789425	-7.22
256005_at	hypothetical protein similar to putative	---	---	-1.04	-0.05	-0.48	0.645683	0.789495	-7.22
265155_at	putative major latex protein type 1 sim	---	AT1G30990	1.04	0.06	0.48	0.64576	0.789546	-7.22
252466_x_	putative protein several hypothetical pr	---	---	1.04	0.05	0.48	0.645802	0.789556	-7.22
262781_s_	proteasome epsilon chain precursor id	PBE1	AT1G13060 /	1.05	0.07	0.48	0.646105	0.789681	-7.22
259686_at	transcription factor SCARECROW, pu	---	AT1G63100	-1.06	-0.08	-0.48	0.645941	0.789681	-7.22
249062_at	putative protein contains similarity to u	---	AT5G44270	-1.04	-0.06	-0.48	0.646112	0.789681	-7.22
246812_at	putative protein predicted proteins, Ar	---	---	-1.03	-0.05	-0.48	0.646085	0.789681	-7.22
248844_s_	extA (emb CAA47807.1)	---	AT5G46890 /	1.04	0.06	0.48	0.646063	0.789681	-7.22
266380_at	unknown protein	MEE13	AT2G14680	-1.04	-0.06	-0.48	0.645991	0.789681	-7.22
247748_at	putative protein ;supported by full-leng	---	AT5G58920	-1.04	-0.06	-0.48	0.646289	0.789855	-7.22
251825_at	ABC transporter - like protein ATP-bin	---	AT3G55100	1.04	0.06	0.48	0.646415	0.789966	-7.22
258227_at	6-4 photolyase (UVR3) identical to 6-4	UVR3	AT3G15620	1.15	0.21	0.48	0.646487	0.789996	-7.22
254795_at	putative protein	---	AT4G12990	1.03	0.05	0.48	0.646508	0.789996	-7.22
263227_at	Expressed protein ; supported by cDN	---	AT1G30750	1.05	0.06	0.48	0.64658	0.790041	-7.23
261493_at	DNA-binding protein p24, putative sim	WHY1	AT1G14410	1.06	0.08	0.48	0.646618	0.790045	-7.23
247227_at	putative protein contains similarity to A	---	AT5G65130	1.04	0.05	0.48	0.646689	0.790089	-7.23
260606_at	putative splicing factor	---	AT2G43770	-1.06	-0.08	-0.48	0.647139	0.790598	-7.23
255787_at	putative cinnamoyl-CoA reductase hig	---	AT2G33590	1.05	0.07	0.48	0.647224	0.790659	-7.23
258374_at	hypothetical protein predicted by gens	---	AT3G14360	-1.08	-0.11	-0.48	0.647294	0.79066	-7.23
247536_at	PREG-like - like protein PREG-like pr	CYCP4;2	AT5G61650	1.05	0.07	0.48	0.647264	0.79066	-7.23
246354_at	hypothetical protein	---	AT1G38950	-1.04	-0.06	-0.48	0.647525	0.7909	-7.23
267147_at	putative anthocyanidin synthase ;supp	---	AT2G38240	1.18	0.23	0.48	0.647638	0.790969	-7.23
253735_at	putative protein SNF7 protein - Sacch	SNF7.1	AT4G29160	1.04	0.05	0.48	0.647651	0.790969	-7.23
267253_at	putative serine carboxypeptidase I	---	AT2G22960	-1.03	-0.05	-0.48	0.647773	0.791076	-7.23
254060_at	putative protein polytropic murine leuk	SHB1	AT4G25350	1.07	0.10	0.48	0.647892	0.791178	-7.23
259699_at	hypothetical protein predicted by gene	---	AT1G68940	1.03	0.05	0.48	0.648059	0.791339	-7.23
252491_at	disease resistance protein RPP8-like	---	AT3G46730	1.03	0.04	0.48	0.648174	0.791438	-7.23
260195_at	hypothetical protein predicted by gens	---	AT1G67540	-1.04	-0.06	-0.48	0.648255	0.791495	-7.23
260105_at	hypothetical protein predicted by gens	---	---	-1.03	-0.05	-0.48	0.648304	0.791511	-7.23
263608_at	putative glycine-rich RNA-binding prot	---	---	1.05	0.07	0.48	0.648406	0.791593	-7.23
246753_at	putative protein	---	---	-1.04	-0.06	-0.48	0.648837	0.792078	-7.23
261626_at	unknown protein ; supported by cDNA	---	AT1G01990	-1.05	-0.07	-0.48	0.648907	0.792083	-7.23
244917_at	hypothetical protein	---	---	1.04	0.05	0.48	0.648941	0.792083	-7.23
260767_s_	unknown protein ; supported by full-ler	---	AT1G49140 /	-1.04	-0.05	-0.48	0.648945	0.792083	-7.23

261764_at	receptor lectin kinase, putative similar	---	AT1G15530	-1.04	-0.06	-0.48	0.649106	0.792237	-7.23
252672_at	hypothetical protein	---	AT3G44230	-1.03	-0.05	-0.48	0.649186	0.792292	-7.23
257379_x_	Mutator-like transposase similar to MU	---	---	1.04	0.05	0.48	0.649288	0.792373	-7.23
264494_at	hypothetical protein predicted by gene	---	AT1G27461	1.06	0.08	0.48	0.64934	0.792394	-7.23
252803_at	putative protein various predicted prot	---	---	-1.04	-0.06	-0.48	0.649382	0.792403	-7.23
258344_at	hypothetical protein similar to hypothet	CEG	AT3G22650	-1.04	-0.05	-0.48	0.649489	0.792412	-7.23
254305_at	potassium channel protein AKT3 ; sup	AKT2/3	AT4G22200	-1.03	-0.04	-0.48	0.649493	0.792412	-7.23
254296_at	hypothetical protein	---	AT4G23090	-1.05	-0.07	-0.48	0.64949	0.792412	-7.23
248846_at	putative protein similar to unknown pro	---	AT5G46500	1.03	0.05	0.48	0.64953	0.792415	-7.23
250191_at	kinase - like protein RING3 protein, H	ATBET9	AT5G14270	1.04	0.06	0.48	0.649678	0.792518	-7.23
257736_at	hypothetical protein predicted by gene	---	AT3G27410	-1.04	-0.06	-0.48	0.649684	0.792518	-7.23
261296_at	unknown protein	---	AT1G48460	1.07	0.10	0.48	0.64972	0.79252	-7.23
265154_at	putative GTP-binding protein, ERG sir	---	AT1G30960	1.08	0.11	0.47	0.649851	0.792637	-7.23
252319_at	putative protein putative protein - Arab	---	AT3G48710	1.05	0.08	0.47	0.650077	0.792744	-7.23
259453_at	gibberelin 20-oxidase, putative, 5' par	ATGA20OX5	AT1G44090	-1.05	-0.07	-0.47	0.65022	0.792744	-7.23
260381_at	putative kinesin similar to kinesin-C GE	---	AT1G73860	1.04	0.06	0.47	0.650007	0.792744	-7.23
257574_at	hypothetical protein predicted by gene	---	AT3G20710	-1.04	-0.06	-0.47	0.650251	0.792744	-7.23
255103_at	putative phosphoglyceride transfer pro	---	AT4G08690	1.04	0.05	0.47	0.650222	0.792744	-7.23
265142_at	unknown protein	DABB1	AT1G51360	-1.03	-0.05	-0.47	0.650184	0.792744	-7.23
251912_at	protein kinase-like protein wall-associa	---	AT3G53840	-1.04	-0.06	-0.47	0.65018	0.792744	-7.23
248736_at	terpene synthase	---	AT5G48110	1.04	0.05	0.47	0.650018	0.792744	-7.23
256395_at	putative helix-loop-helix DNA-binding p	MUTE	AT3G06120	1.04	0.06	0.47	0.650111	0.792744	-7.23
251064_at	putative zinc finger protein several zinc	---	AT5G01860	1.04	0.06	0.47	0.650465	0.792962	-7.23
256496_at	hypothetical protein similar to hypothet	---	AT1G31510	1.04	0.06	0.47	0.650549	0.793021	-7.23
251692_s_	serine carboxypeptidase-like protein c	---	AT3G52020 /	1.04	0.05	0.47	0.650679	0.793138	-7.23
265881_at	hypothetical protein predicted by gens	---	AT2G42480	1.04	0.06	0.47	0.650745	0.793175	-7.23
264979_s_	disease resistance protein, putative si	---	AT1G27170 /	1.05	0.07	0.47	0.650875	0.793292	-7.23
267332_at	hypothetical protein predicted by gens	---	AT2G19290	1.03	0.04	0.47	0.650986	0.793385	-7.23
250817_at	SET-domain protein-like ; supported b	SUVH1	AT5G04940	-1.04	-0.05	-0.47	0.65108	0.793445	-7.23
254651_at	potassium channel - like protein kco1,	KCO6	AT4G18160	1.05	0.07	0.47	0.651105	0.793445	-7.23
253144_at	putative protein transcription factor IIE	---	AT4G35540	1.04	0.05	0.47	0.651433	0.793718	-7.23
265542_at	putative SNF2 subfamily transcription	SYD	AT2G28290	1.03	0.05	0.47	0.651413	0.793718	-7.23
250281_at	putative protein prdeicted proteins, So	---	AT5G13240	-1.05	-0.07	-0.47	0.651372	0.793718	-7.23
245220_at	hypothetical protein contains similarity	---	AT1G59171	-1.03	-0.05	-0.47	0.651563	0.793834	-7.23
254157_at	putative protein protein induced upon	VEP1	AT4G24220	1.04	0.06	0.47	0.651757	0.794027	-7.23

265109_s_	NBS/LRR disease resistance protein,	---	AT1G62630 /	-1.06	-0.09	-0.47	0.651852	0.794101	-7.23
263397_s_	putative GDSL-motif lipase/hydrolase s	---	AT2G31540 /	-1.03	-0.04	-0.47	0.651918	0.794138	-7.23
250270_at	putative protein FL10, EGF responsiv	---	AT5G12980	-1.05	-0.06	-0.47	0.652209	0.794451	-7.23
259495_at	NBS/LRR disease resistance protein,	---	AT1G15890	1.04	0.06	0.47	0.652317	0.794498	-7.23
259243_at	unknown protein similar to unknown p	---	AT3G07565	1.03	0.05	0.47	0.652312	0.794498	-7.23
246242_at	putative protein	---	AT4G36600	-1.06	-0.08	-0.47	0.652405	0.794562	-7.23
247392_at	glutamate-1-semialdehyde 2,1-aminor	GSA1	AT5G63570	1.06	0.08	0.47	0.652449	0.794573	-7.23
261733_at	clathrin coat assembly protein AP17, p	---	AT1G47830	-1.03	-0.05	-0.47	0.652514	0.794611	-7.23
257042_s_	hypothetical protein predicted by gene	---	AT3G28640 /	-1.03	-0.05	-0.47	0.652604	0.79465	-7.23
265528_at	hypothetical protein predicted by gens	---	---	1.03	0.04	0.47	0.652617	0.79465	-7.23
267398_at	putative glucanase	AtGH9B11	AT2G44560	-1.04	-0.06	-0.47	0.652654	0.794653	-7.23
256709_at	hypothetical protein predicted by gene	---	---	-1.03	-0.05	-0.47	0.652768	0.79475	-7.23
250195_at	putative protein	---	AT5G14560	-1.03	-0.04	-0.47	0.652889	0.794855	-7.23
254714_at	myb-like protein snapdragon myb prot	AtMYB79	AT4G13480	1.03	0.05	0.47	0.652955	0.794893	-7.23
256421_at	hypothetical protein predicted by gene	---	AT1G33500	-1.03	-0.05	-0.47	0.653116	0.795013	-7.23
251231_at	Glutathione transferase III-like protein	ATGSTF13	AT3G62760	1.04	0.05	0.47	0.653124	0.795013	-7.23
265302_at	Mutator-like transposase similar to MU	---	---	1.03	0.04	0.47	0.653347	0.795242	-7.23
255927_at	transcriptional activator CBF1, putativ	---	AT1G12630	1.07	0.10	0.47	0.653384	0.795245	-7.23
250230_at	putative protein similar to unknown pro	---	AT5G13900	-1.06	-0.09	-0.47	0.653491	0.795248	-7.23
247296_at	unknown protein ;supported by full-ler	---	AT5G64160	1.05	0.07	0.47	0.653458	0.795248	-7.23
265623_at	hypothetical protein predicted by gene	---	AT2G27270	-1.04	-0.06	-0.47	0.653458	0.795248	-7.23
247341_at	unknown protein	---	AT5G63720	-1.03	-0.05	-0.47	0.653594	0.795331	-7.23
259046_at	calmodulin-like protein similar to calm	---	AT3G03400	1.04	0.05	0.47	0.653672	0.795383	-7.23
256360_at	hypothetical protein	---	AT1G66440	-1.05	-0.07	-0.47	0.653778	0.795429	-7.23
257760_s_	putative AC-like transposase similar to	---	---	1.04	0.05	0.47	0.653779	0.795429	-7.23
250945_at	putative protein	---	AT5G03400	-1.04	-0.05	-0.47	0.653883	0.795513	-7.23
251184_at	small nuclear ribonucleoprotein-like pr	---	AT3G62840	1.03	0.04	0.47	0.654127	0.795597	-7.23
260805_at	glutathione transferase, putative simila	ATGSTU23	AT1G78320	1.03	0.05	0.47	0.654084	0.795597	-7.23
254454_at	hypothetical protein	EMB2271	AT4G21130	-1.04	-0.05	-0.47	0.654026	0.795597	-7.23
247462_at	A9 protein precursor - like A9 protein	---	AT5G62080	-1.04	-0.06	-0.47	0.65412	0.795597	-7.23
255658_at	hypothetical protein ;supported by full-	---	AT4G00770	-1.04	-0.06	-0.47	0.654053	0.795597	-7.23
246802_at	kinesin-like heavy chain non-consensu	ATK4	AT5G27000	-1.05	-0.07	-0.47	0.654223	0.795671	-7.23
265383_at	putative WD-40 repeat protein, MSI2	MSI2	AT2G16780	1.05	0.08	0.47	0.65434	0.795695	-7.23
248052_at	putative protein contains similarity to C	---	AT5G55800	-1.04	-0.06	-0.47	0.654382	0.795695	-7.23
257837_at	hypothetical protein predicted by gene	---	AT3G25200	-1.04	-0.06	-0.47	0.654354	0.795695	-7.23

262416_at	flavonol synthase, putative similar to f	---	AT1G49390	-1.03	-0.05	-0.47	0.654315	0.795695	-7.23
252486_at	arm repeat containing protein homolo	PUB13	AT3G46510	1.04	0.06	0.47	0.654441	0.795696	-7.23
246881_at	putative protein histone deacetylase/A	HDA2	AT5G26040	-1.06	-0.09	-0.47	0.654452	0.795696	-7.23
252531_at	actin 12	ACT12	AT3G46520	-1.04	-0.05	-0.47	0.654667	0.795915	-7.23
256588_at	unknown protein	---	AT3G28790	-1.04	-0.06	-0.47	0.654854	0.796015	-7.23
266639_at	defender against cell death protein ide	DAD2	AT2G35520	1.04	0.05	0.47	0.654827	0.796015	-7.23
256977_at	hypothetical protein predicted by gene	---	---	1.04	0.05	0.47	0.654812	0.796015	-7.23
261777_at	hypothetical protein predicted by gene	---	AT1G76210	1.04	0.05	0.47	0.654912	0.796037	-7.23
252702_at	putative protein predicted proteins, Ar	---	---	-1.03	-0.05	-0.47	0.654942	0.796037	-7.23
254818_at	pEARLI 1-like protein Arabidopsis tha	---	AT4G12470	1.17	0.23	0.47	0.65499	0.796052	-7.23
258198_at	putative transcription factor similar to t	NF-YA6	AT3G14020	1.04	0.06	0.47	0.655223	0.796251	-7.23
251226_at	proline-rich protein proline-rich protein	PRP3	AT3G62680	1.04	0.06	0.47	0.655214	0.796251	-7.23
252492_at	chloroplast import-associated channel	TOC75-III	AT3G46740	1.04	0.06	0.47	0.655361	0.796345	-7.23
254627_at	Expressed protein ; supported by full-le	---	AT4G18395	-1.03	-0.05	-0.47	0.65537	0.796345	-7.23
258178_at	hypothetical protein predicted by gene	---	AT3G21680	-1.03	-0.04	-0.47	0.655423	0.796363	-7.23
264278_at	myrosinase binding protein, putative s	---	AT1G60130	-1.03	-0.05	-0.47	0.655455	0.796363	-7.23
259472_at	hypothetical protein contains similarity	---	AT1G18910	1.04	0.05	0.47	0.655524	0.796405	-7.23
258477_at	hypothetical protein predicted by gene	NBS1	AT3G02680	-1.03	-0.05	-0.47	0.655722	0.796572	-7.23
260186_at	hypothetical protein predicted by gene	---	AT1G36020	-1.05	-0.07	-0.47	0.655732	0.796572	-7.23
248807_at	pectin methylesterase-like	---	AT5G47500	-1.03	-0.04	-0.47	0.655978	0.796701	-7.23
256073_at	terminal Flower 1 (TFL1), putative sim	E12A11	AT1G18100	-1.04	-0.06	-0.47	0.655949	0.796701	-7.23
264427_at	hypothetical protein predicted by gene	---	AT1G61770	1.04	0.06	0.47	0.655905	0.796701	-7.23
263816_at	putative CCHC-type zinc finger protein	---	---	1.05	0.06	0.47	0.655926	0.796701	-7.23
260782_at	unknown protein ; supported by cDNA:	---	AT1G14570	-1.03	-0.05	-0.47	0.656099	0.796807	-7.23
245478_at	galactokinase like protein	ARA1	AT4G16130	-1.09	-0.12	-0.47	0.65621	0.796884	-7.23
264786_at	putative Ta11-like non-LTR retroeleme	---	AT2G17920	-1.04	-0.05	-0.47	0.656233	0.796884	-7.23
250065_at	putative protein predicted proteins, Ar	---	AT5G17910	1.05	0.08	0.47	0.656301	0.796906	-7.23
260699_at	MAP kinase, putative similar to MAP k	ATMKK10	AT1G32320	-1.03	-0.05	-0.47	0.656321	0.796906	-7.23
260329_at	putative cyclin similar to cyclin GB:S53	CYCA2;4	AT1G80370	1.04	0.06	0.47	0.656444	0.797014	-7.23
262840_at	linker histone protein, putative contain	HMGA	AT1G14900	1.04	0.06	0.47	0.65649	0.797027	-7.23
259382_s_	jasmonate inducible protein isolog ;su	JAL31	AT3G16420 /	-1.20	-0.27	-0.47	0.656593	0.797109	-7.23
256405_at	calcium-dependent protein kinase simi	CPK33	AT1G50700	-1.03	-0.05	-0.46	0.656638	0.797122	-7.23
264224_at	hypothetical protein predicted by gene	emb1688	AT1G67440	-1.04	-0.06	-0.46	0.65678	0.797198	-7.23
253570_at	hypothetical protein	---	AT4G31260	-1.05	-0.06	-0.46	0.65684	0.797198	-7.23
258912_at	unknown protein similar to hypothetica	---	AT3G06460	-1.06	-0.08	-0.46	0.656837	0.797198	-7.23

246222_at	TINY-like protein ; supported by cDNA	RAP2.10	AT4G36900	-1.08	-0.11	-0.46	0.656817	0.797198	-7.23
259268_at	putative lamin similar to blue copper-bi	---	AT3G01070	-1.03	-0.04	-0.46	0.657056	0.797417	-7.23
251047_at	putative protein mature-parasite-infect	---	AT5G02390	-1.04	-0.06	-0.46	0.657136	0.797452	-7.23
253449_at	putative protein hypothetical protein y	---	AT4G32700	1.04	0.05	0.46	0.657155	0.797452	-7.23
257262_at	zinc finger protein, putative contains F	---	AT3G21890	-1.07	-0.10	-0.46	0.657424	0.797685	-7.23
266413_at	unknown protein ;supported by full-ler	---	AT2G38740	-1.04	-0.06	-0.46	0.657452	0.797685	-7.23
255954_at	hypothetical protein predicted by gene	emb2204	AT1G22090	-1.04	-0.05	-0.46	0.657411	0.797685	-7.23
248899_at	carboxy-terminal proteinase D1-like pr	---	AT5G46390	-1.04	-0.06	-0.46	0.657627	0.797855	-7.23
256006_at	hypothetical protein	---	AT1G34070	1.03	0.05	0.46	0.657898	0.798141	-7.23
264012_at	hypothetical protein predicted by gens	---	AT2G21080	1.05	0.07	0.46	0.657969	0.798185	-7.23
245223_at	gene_id:K17E7.5~unknown protein	---	AT3G29791	-1.04	-0.05	-0.46	0.658007	0.798188	-7.23
256457_at	3-methyladenine DNA glycosylase, pu	---	AT1G75230	1.08	0.11	0.46	0.658139	0.798306	-7.23
257537_at	hypothetical protein predicted by genm	---	AT3G22350	1.05	0.07	0.46	0.658337	0.798442	-7.23
253352_at	pathogenesis-related protein 1 precur	---	AT4G33710	-1.04	-0.06	-0.46	0.658356	0.798442	-7.23
261186_at	hypothetical protein predicted by gene	---	---	1.03	0.04	0.46	0.658309	0.798442	-7.23
267402_at	putative SF16 protein {Helianthus annu	IQD6	AT2G26180	-1.05	-0.07	-0.46	0.658439	0.7985	-7.23
258523_at	pectin methylesterase, putative simila	---	AT3G06830	-1.03	-0.04	-0.46	0.658786	0.798624	-7.23
253934_at	putative beta-1,3-glucanase beta-1,3-	---	AT4G26830	-1.03	-0.05	-0.46	0.658705	0.798624	-7.23
264891_at	putative pectinesterase similar to GB:A	---	AT1G23200	1.06	0.09	0.46	0.658772	0.798624	-7.23
256047_at	hypothetical protein predicted by gene	---	AT1G07060	1.04	0.06	0.46	0.658748	0.798624	-7.23
246475_at	putative protein IFA-binding protein - A	---	AT5G16720	-1.05	-0.07	-0.46	0.658625	0.798624	-7.23
255347_at	putative retrotransposon protein	---	---	-1.03	-0.05	-0.46	0.658688	0.798624	-7.23
258769_at	putative alpha-hydroxynitrile lyase sim	MES17	AT3G10870	1.07	0.09	0.46	0.658592	0.798624	-7.23
247424_at	LIM7 - like protein LIM7, Lilium longifl	AtVEX1	AT5G62850	1.04	0.05	0.46	0.659118	0.798984	-7.23
247675_at	putative protein large number of predi	---	AT5G59940	1.05	0.07	0.46	0.659165	0.798998	-7.23
263428_at	ubiquitin-specific protease 4 (UBP4) id	ATUBP4	AT2G22310	-1.04	-0.06	-0.46	0.659343	0.799091	-7.23
260184_s_	putative protein predicted proteins, Ar	---	---	-1.03	-0.04	-0.46	0.659348	0.799091	-7.23
258875_at	unknown protein ;supported by full-ler	---	AT3G03160	1.05	0.07	0.46	0.659406	0.799091	-7.23
247551_at	ras-GTPase-activating protein SH3-do	---	AT5G60980	-1.03	-0.04	-0.46	0.659417	0.799091	-7.23
261637_at	DNA-binding protein PcMYB1, putativ	TRB1	AT1G49950	-1.05	-0.07	-0.46	0.659297	0.799091	-7.23
256002_at	carbamoylphosphate synthetase, puta	CARB	AT1G29900	-1.04	-0.06	-0.46	0.659697	0.799388	-7.24
255828_at	hypothetical protein predicted by gene	---	AT2G40630	-1.03	-0.05	-0.46	0.659802	0.799473	-7.24
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J04	---	---	1.10	0.14	0.46	0.659845	0.799482	-7.24
265681_at	putative protein kinase contains a prot	---	AT2G24370	1.03	0.05	0.46	0.660308	0.799959	-7.24
248113_at	wax synthase-like protein	---	AT5G55360	-1.04	-0.06	-0.46	0.660303	0.799959	-7.24

251294_at	zinc transporter-like protein zinc trans	MTPA1	AT3G61940	-1.04	-0.05	-0.46	0.660569	0.800232	-7.24
260124_at	E2, ubiquitin-conjugating enzyme, put	UBC31	AT1G36340	1.04	0.05	0.46	0.660682	0.800327	-7.24
260497_at	40S ribosomal protein S2 ;supported b	---	AT2G41840	-1.08	-0.12	-0.46	0.660806	0.800434	-7.24
251749_at	putative protein predicted proteins, Ar	---	AT3G55690	-1.03	-0.05	-0.46	0.660932	0.800459	-7.24
257527_at	hypothetical protein similar to hypothe	---	AT3G01880	-1.04	-0.05	-0.46	0.660866	0.800459	-7.24
263026_at	hypothetical protein predicted by gene	---	AT1G24000	-1.03	-0.05	-0.46	0.6609	0.800459	-7.24
262833_at	cyclin, putative contains Pfam profile:	SDS	AT1G14750	-1.03	-0.04	-0.46	0.661019	0.800509	-7.24
259205_at	hypothetical protein similar to putative	---	AT3G09030	-1.04	-0.06	-0.46	0.661043	0.800509	-7.24
267215_at	hypothetical protein	---	AT2G02630	-1.03	-0.04	-0.46	0.661083	0.800516	-7.24
261906_at	hypothetical protein predicted by gens	---	AT1G65080	-1.07	-0.09	-0.46	0.661211	0.800625	-7.24
257282_at	TNP2-like transposon protein, putative	---	---	-1.04	-0.06	-0.46	0.661244	0.800625	-7.24
260987_at	hypothetical protein predicted by gene	NTMC2T6.1	AT1G53590	-1.05	-0.07	-0.46	0.661364	0.800728	-7.24
254498_at	membrane-associated salt-inducible-li	EMB1025	AT4G20090	1.06	0.08	0.46	0.661501	0.800851	-7.24
258141_at	hypothetical protein	HON4	AT3G18035	-1.05	-0.07	-0.46	0.661726	0.801077	-7.24
258541_at	hypothetical protein	---	AT3G07000	1.03	0.04	0.46	0.661757	0.801077	-7.24
248362_at	fibrillarin 1 (AtFib1) identical to fibrillari	FIB1	AT5G52470	-1.04	-0.05	-0.46	0.661841	0.801093	-7.24
252865_at	Expressed protein ; supported by full-le	---	AT4G39753	-1.05	-0.07	-0.46	0.661816	0.801093	-7.24
255461_at	ent-kaurene synthetase A - like protein	GA1	AT4G02780	-1.04	-0.06	-0.46	0.662078	0.801191	-7.24
257518_at	hypothetical protein	---	AT3G03880	-1.03	-0.04	-0.46	0.662098	0.801191	-7.24
261573_at	hypothetical protein identical to hyothe	---	AT1G01180	-1.03	-0.05	-0.46	0.662086	0.801191	-7.24
255188_at	contains similarity to Xenopus laevis re	---	---	1.03	0.04	0.46	0.662058	0.801191	-7.24
266339_s_	hypothetical protein predicted by gens	---	AT2G01360 /	1.04	0.06	0.46	0.662091	0.801191	-7.24
245295_at	hypothetical protein ; supported by cDI	---	AT4G16100	-1.04	-0.06	-0.46	0.662233	0.801269	-7.24
247567_at	putative protein various predicted prot	---	AT5G61190	-1.05	-0.07	-0.46	0.662198	0.801269	-7.24
256619_at	hypothetical protein predicted by gens	---	AT3G24460	-1.03	-0.05	-0.46	0.6623	0.801308	-7.24
265748_at	putative Athila retroelement ORF1 prot	---	---	-1.04	-0.05	-0.46	0.662377	0.801359	-7.24
253315_at	putative protein various predicted prot	---	AT4G33900	1.04	0.05	0.46	0.662489	0.801451	-7.24
253718_at	serine/threonine-specific receptor prot	---	AT4G29450	1.04	0.06	0.46	0.6626	0.801504	-7.24
256800_at	hypothetical protein predicted by gene	---	AT3G20900	1.04	0.06	0.46	0.662602	0.801504	-7.24
249688_at	putative protein tyrosine aminotransfer	---	AT5G36160	-1.05	-0.07	-0.46	0.662835	0.801743	-7.24
248066_at	putative protein contains similarity to p	QRT1	AT5G55590	-1.04	-0.05	-0.46	0.662875	0.801749	-7.24
254740_s_	glycine hydroxymethyltransferase - lik	---	AT2G42450 /	-1.12	-0.16	-0.46	0.662997	0.801853	-7.24
267555_at	Expressed protein ; supported by full-le	SUMO5	AT2G32765	1.04	0.06	0.46	0.663113	0.801951	-7.24
264428_at	hypothetical protein predicted by gene	---	AT1G61790	-1.06	-0.08	-0.46	0.66331	0.802105	-7.24
251361_at	LIM domain protein LIM domain prote	---	AT3G61230	-1.05	-0.07	-0.46	0.663288	0.802105	-7.24

246513_at	hypothetical protein	---	AT5G15680	1.03	0.05	0.45	0.663426	0.802203	-7.24
261289_at	hypothetical protein predicted by gene	---	AT1G37000	-1.03	-0.05	-0.45	0.663497	0.802246	-7.24
257869_at	ER lumen protein retaining receptor, p	---	AT3G25160	1.03	0.04	0.45	0.663848	0.802553	-7.24
246762_at	cyclin H-like protein cycH (CAK assoc	CYCH;1	AT5G27620	-1.06	-0.08	-0.45	0.663787	0.802553	-7.24
249922_at	aluminium-induced protein - like alumi	AILP1	AT5G19140	1.04	0.05	0.45	0.663857	0.802553	-7.24
245552_at	cytochrome P450 like protein	CYP705A3	AT4G15360	1.04	0.05	0.45	0.663913	0.802579	-7.24
250914_at	myb -like protein telomeric DNA bindi	TRFL10	AT5G03780	1.04	0.06	0.45	0.663953	0.802585	-7.24
252903_at	putative protein various predicted prot	---	AT4G39570	1.06	0.09	0.45	0.664036	0.8026	-7.24
255367_at	putative transposon protein	---	---	1.04	0.05	0.45	0.664022	0.8026	-7.24
261821_at	thioredoxin h, putative similar to thiore	ATCXXS1	AT1G11530	-1.04	-0.05	-0.45	0.664092	0.802625	-7.24
253003_s_	putative protein tapetum specific prote	---	AT4G38300 /	1.04	0.06	0.45	0.664131	0.802627	-7.24
261215_at	subtilase, putative similar to subtilase	---	AT1G32970	1.03	0.05	0.45	0.664164	0.802627	-7.24
245761_at	hypothetical protein predicted by gene	---	AT1G66890	1.04	0.05	0.45	0.664236	0.802665	-7.24
247411_at	putative protein contains similarity to u	---	AT5G63000	1.05	0.06	0.45	0.664293	0.802665	-7.24
256941_at	hypothetical protein	---	---	1.04	0.06	0.45	0.664301	0.802665	-7.24
266580_at	unknown protein ;supported by full-ler	---	AT2G46260	1.04	0.06	0.45	0.664375	0.802711	-7.24
261642_at	ADP-glucose pyrophosphorylase, puta	APL2	AT1G27680	1.06	0.08	0.45	0.664491	0.80281	-7.24
251392_at	dihydrodipicolinate synthase precursor	DHDPS1	AT3G60880	-1.03	-0.05	-0.45	0.664556	0.802835	-7.24
256393_at	hypothetical protein	---	AT3G06280	-1.03	-0.05	-0.45	0.664583	0.802835	-7.24
265575_at	proline iminopeptidase identical to GP	PIP	AT2G14260	1.03	0.05	0.45	0.664685	0.802903	-7.24
245880_at	putative hydrolase EtbD1 - Rhodococ	---	AT5G09430	-1.05	-0.07	-0.45	0.664744	0.802903	-7.24
254536_at	putative protein chitinase / lysozyme F	---	AT4G19720	-1.04	-0.05	-0.45	0.664715	0.802903	-7.24
265597_at	Expressed protein ; supported by cDN	---	AT2G20142	1.12	0.17	0.45	0.664847	0.802984	-7.24
258580_at	germin-like protein contains Pfam profi	---	AT3G04170	-1.04	-0.05	-0.45	0.664923	0.803034	-7.24
249166_at	CHP-rich zinc finger protein-like	---	AT5G42840	-1.04	-0.06	-0.45	0.665017	0.803062	-7.24
246049_at	putative protein predicted proteins, Ar	---	---	1.04	0.06	0.45	0.665007	0.803062	-7.24
247339_at	unknown protein	---	AT5G63690	1.04	0.06	0.45	0.665187	0.803225	-7.24
264578_at	hypothetical protein predicted by gene	---	AT1G05370	1.03	0.04	0.45	0.665476	0.803488	-7.24
245978_at	putative protein MORC microrchidia -	---	AT5G13130	1.04	0.06	0.45	0.66547	0.803488	-7.24
249179_at	Expressed protein ; supported by full-le	---	AT5G42955	-1.04	-0.06	-0.45	0.665548	0.803533	-7.24
245866_s_	unknown protein	---	AT1G57980 /	1.16	0.21	0.45	0.665717	0.803578	-7.24
266040_at	hypothetical protein	---	AT2G07738	-1.03	-0.04	-0.45	0.665653	0.803578	-7.24
249671_at	putative protein similar to unknown pro	LBD35	AT5G35900	-1.04	-0.05	-0.45	0.665726	0.803578	-7.24
256845_x_	hypothetical protein similar to putative	---	---	1.04	0.05	0.45	0.665669	0.803578	-7.24
266708_at	putative chloroplast nucleoid DNA bind	---	AT2G03200	-1.05	-0.07	-0.45	0.665874	0.803672	-7.24

246643_s_	putative protein various predicted prot	---	---	-1.03	-0.05	-0.45	0.66584	0.803672	-7.24
264416_at	hypothetical protein similar to putative	---	AT1G43140	-1.04	-0.05	-0.45	0.666184	0.804003	-7.24
256488_at	hypothetical protein	NFD4	AT1G31470	1.04	0.05	0.45	0.666286	0.804084	-7.24
263093_at	putative replication protein A1	---	---	-1.03	-0.05	-0.45	0.666337	0.804091	-7.24
266717_at	Expressed protein ; supported by full-l	---	AT2G46735	1.04	0.05	0.45	0.666363	0.804091	-7.24
246898_at	putative protein	---	AT5G25580	-1.03	-0.04	-0.45	0.666566	0.804294	-7.24
267089_at	unknown protein	---	AT2G38300	-1.05	-0.07	-0.45	0.666626	0.804311	-7.24
250746_at	glucuronosyl transferase-like protein	---	AT5G05880	-1.03	-0.05	-0.45	0.666651	0.804311	-7.24
265924_at	putative geranylgeranyl pyrophosphate	---	AT2G18620	1.03	0.04	0.45	0.666804	0.80441	-7.24
266919_at	hypothetical protein predicted by gens	AT2G45780	---	1.03	0.05	0.45	0.666773	0.80441	-7.24
267080_at	unknown protein ; supported by cDNA	---	AT2G41190	-1.10	-0.13	-0.45	0.666884	0.804465	-7.24
250880_at	putative protein Ube-1a, Mus musculu	---	AT5G04070	-1.03	-0.04	-0.45	0.66701	0.80454	-7.24
264532_at	seed imbibition protein, putative simila	AtSIP1	AT1G55740	-1.03	-0.05	-0.45	0.667017	0.80454	-7.24
253059_s_	putative protein other predicted protein	HHP5	AT4G37680 /	1.06	0.09	0.45	0.667081	0.804575	-7.24
247888_at	phytocyanin/early nodulin-like protein	---	AT5G57920	1.04	0.05	0.45	0.667161	0.804629	-7.24
255090_at	putative protein disease resistance pr	---	AT4G09360	1.04	0.05	0.45	0.667214	0.80465	-7.24
265928_at	Ac-like transposase related to Ac/Ds tr	---	---	-1.04	-0.06	-0.45	0.667259	0.804662	-7.24
261805_at	hypothetical protein almost identical to	---	AT1G30540	-1.04	-0.05	-0.45	0.667365	0.804747	-7.24
252614_at	serpin-like protein serpin - Hordeum v	---	AT3G45220	1.03	0.04	0.45	0.667474	0.804836	-7.24
246775_at	putative protein GTP-binding proteins a	MIRO1	AT5G27540	1.03	0.04	0.45	0.667608	0.80487	-7.24
250215_at	putative protein similar to unknown pro	---	AT5G14080	-1.04	-0.05	-0.45	0.667598	0.80487	-7.24
260227_at	unknown protein similar to hypothetica	---	AT1G74450	1.10	0.14	0.45	0.667599	0.80487	-7.24
256500_at	Ty1/copia-element polyprotein	---	---	-1.04	-0.05	-0.45	0.667648	0.804876	-7.24
246897_at	putative protein predicted proteins, Ar	---	AT5G25560	-1.04	-0.06	-0.45	0.667746	0.804909	-7.24
264296_at	protein transport protein sec61 alpha s	---	AT1G78720	1.06	0.08	0.45	0.667739	0.804909	-7.24
245088_at	subtilisin-like serine protease contains	---	AT2G39850	-1.09	-0.12	-0.45	0.667863	0.804955	-7.24
249414_at	putative transcription factor MYB89 ; s	MYB89	AT5G39700	1.04	0.05	0.45	0.66789	0.804955	-7.24
259328_at	putative lectin contains Pfam profile: F	ATMLP-300	AT3G16440	1.04	0.06	0.45	0.667851	0.804955	-7.24
267241_at	hypothetical protein predicted by gens	---	AT2G02490 /	1.03	0.04	0.45	0.667998	0.804988	-7.24
253483_at	putative protein anthranilate N-hydrox	---	AT4G31910	-1.07	-0.09	-0.45	0.668059	0.804988	-7.24
257026_at	hypothetical protein predicted by gene	---	AT3G19200	1.04	0.05	0.45	0.668047	0.804988	-7.24
254473_s_	putative protein kinase like proteins, A	---	AT4G20520 /	1.03	0.05	0.45	0.667979	0.804988	-7.24
266661_at	TINY-like AP2 domain transcription fac	---	AT2G25820	1.04	0.06	0.45	0.668154	0.805032	-7.24
259870_at	putative heat shock protein predicted b	---	AT1G76780	-1.03	-0.04	-0.45	0.668166	0.805032	-7.24
256946_at	hypothetical protein contains Pfam pro	HAF2	AT3G19040	-1.06	-0.08	-0.45	0.668403	0.805191	-7.24

263201_at	putative ADP-glucose pyrophosphoryl	APS2	AT1G05610	1.04	0.05	0.45	0.668365	0.805191	-7.24
259575_at	unknown protein	---	AT1G35320	1.03	0.05	0.45	0.66837	0.805191	-7.24
264944_at	hypothetical protein similar to hypothet	---	AT1G76940	-1.05	-0.07	-0.45	0.668511	0.805235	-7.24
262541_at	hypothetical protein contains similarity	---	---	-1.03	-0.04	-0.45	0.668479	0.805235	-7.24
257245_at	hypothetical protein contains Pfam pro	---	AT3G24110	-1.04	-0.06	-0.45	0.668725	0.80545	-7.24
252529_at	putative protein several oxidases, mai	---	AT3G46490	-1.11	-0.15	-0.45	0.668853	0.805538	-7.24
265488_at	hypothetical protein predicted by gens	---	AT2G15610	1.04	0.05	0.45	0.668869	0.805538	-7.24
253587_at	hypothetical protein	---	AT4G30770	-1.04	-0.06	-0.45	0.668916	0.805547	-7.24
262995_s_	hypothetical protein predicted by gene	---	---	-1.03	-0.04	-0.45	0.668946	0.805547	-7.24
257468_at	hypothetical protein contains similarity	---	AT1G47470	1.03	0.04	0.45	0.669009	0.80558	-7.24
267138_s_	similar to SOR1 from the fungus Cercc	PDX1.1	AT2G38210 /	-1.09	-0.12	-0.45	0.669132	0.805685	-7.24
252356_at	putative protein various predicted prote	---	---	1.05	0.07	0.45	0.669207	0.805693	-7.24
246618_at	putative protein similar to unknown pro	---	AT5G36280	1.03	0.04	0.45	0.669209	0.805693	-7.24
245839_at	disease resistance protein, putative si	---	AT1G58390	1.03	0.04	0.45	0.669336	0.805803	-7.24
250396_at	zinc finger -like protein CCHH finger p	---	AT5G10970	1.09	0.12	0.45	0.669479	0.80589	-7.24
251215_at	putative protein region within disulfide	---	AT3G62510	-1.04	-0.05	-0.45	0.669473	0.80589	-7.24
266375_at	En/Spm-like transposon protein related	---	---	1.04	0.05	0.45	0.669517	0.805894	-7.24
264358_at	hypothetical protein predicted by gene	---	AT1G03180	-1.05	-0.07	-0.45	0.669633	0.80599	-7.24
245908_at	laccase-like protein laccase - Acer pse	LAC14	AT5G09360	-1.06	-0.08	-0.45	0.669683	0.806008	-7.24
261357_at	hypothetical protein predicted by gene	---	---	1.03	0.04	0.45	0.669722	0.806013	-7.24
265143_at	unknown protein	NFU5	AT1G51390	1.04	0.06	0.45	0.669763	0.80602	-7.24
258690_at	putative phosphatidylinositol-4-phosph	---	AT3G07960	1.03	0.05	0.45	0.669839	0.806069	-7.24
254831_at	Ribosomal protein L7Ae -like various L	---	AT4G12600	1.08	0.11	0.45	0.670044	0.806273	-7.24
246044_at	calcium-dependent protein kinase ; su	CDPK19	AT5G19450	1.05	0.07	0.45	0.670162	0.806372	-7.24
257138_at	hypothetical protein predicted by gene	---	AT3G28870	-1.03	-0.04	-0.45	0.670226	0.806407	-7.24
261714_at	hypothetical protein similar to hypothet	TET16	AT1G18510	1.05	0.07	0.44	0.670344	0.806506	-7.24
260513_at	cyanogenic beta-glucosidase, putative	BGLU36	AT1G51490	1.03	0.05	0.44	0.670467	0.806612	-7.24
256507_at	hypothetical protein predicted by gene	---	AT1G75150	1.04	0.06	0.44	0.670549	0.806668	-7.24
245518_at	ATP-dependent RNA helicase like prot	ATRH1	AT4G15850	1.06	0.09	0.44	0.670602	0.806689	-7.24
247937_at	Ca2+-transporting ATPase-like protein	ACA8	AT5G57110	-1.07	-0.10	-0.44	0.67068	0.80674	-7.24
251339_at	putative protein various predicted prot	---	AT3G60780	-1.05	-0.07	-0.44	0.670757	0.80679	-7.24
254985_x_	putative reverse-transcriptase -like pro	---	---	1.05	0.07	0.44	0.670897	0.806916	-7.24
267533_at	unknown protein ;supported by full-ler	ATNUDX23	AT2G42070	-1.04	-0.05	-0.44	0.671574	0.807645	-7.24
252907_at	putative gamma-glutamyltransferase g	GGT2	AT4G39650	1.03	0.05	0.44	0.671558	0.807645	-7.24
256299_at	expansin (At-EXP1) identical to expans	ATEXPA1	AT1G69530	1.17	0.22	0.44	0.671906	0.807935	-7.24

248550_at	putative protein similar to unknown pro	QS	AT5G50210	1.06	0.08	0.44	0.671921	0.807935	-7.24
258590_at	putative response regulator protein (re	ARR22	AT3G04280	1.03	0.05	0.44	0.671857	0.807935	-7.24
255213_at	putative athila transposon protein	---	---	1.03	0.04	0.44	0.672112	0.808122	-7.24
257098_at	hypothetical protein	---	---	-1.03	-0.05	-0.44	0.67219	0.808173	-7.24
260115_at	AIG1-like protein similar to AIG1 prote	---	AT1G33870	1.04	0.06	0.44	0.672324	0.808291	-7.24
256039_at	hypothetical protein contains similarity	---	AT1G19190	-1.05	-0.06	-0.44	0.672418	0.808361	-7.24
251738_at	PROBABLE EUKARYOTIC TRANSLA	EIF3C	AT3G56150	1.03	0.05	0.44	0.672623	0.808548	-7.24
265997_at	Expressed protein ; supported by cDN	---	AT2G24250	-1.03	-0.05	-0.44	0.6727	0.808548	-7.24
263036_at	hypothetical protein predicted by gene	---	AT1G23890	1.04	0.06	0.44	0.672687	0.808548	-7.24
250081_at	unknown protein	---	AT5G17180	1.03	0.05	0.44	0.672715	0.808548	-7.24
256804_at	hypothetical protein predicted by gene	---	AT3G20920	1.03	0.04	0.44	0.672981	0.808826	-7.24
266999_at	putative HMG protein ; supported by fu	---	AT2G34450	-1.05	-0.07	-0.44	0.673113	0.808941	-7.24
261951_at	hypothetical protein predicted by gene	---	AT1G64490	1.04	0.05	0.44	0.6732	0.808972	-7.24
245298_at	hypothetical protein ; supported by cDI	---	AT4G15010	1.03	0.05	0.44	0.67321	0.808972	-7.24
263370_at	hypothetical protein predicted by gens	---	AT2G20500	-1.07	-0.10	-0.44	0.673327	0.809056	-7.25
246845_at	glutamyl-tRNA synthetase ; supported	---	AT5G26710	-1.03	-0.04	-0.44	0.673386	0.809056	-7.25
265167_at	putative OBP32pep protein	---	AT1G23680	-1.03	-0.05	-0.44	0.673359	0.809056	-7.25
245217_at	retroelement pol polyprotein, putative	---	---	-1.05	-0.07	-0.44	0.673535	0.809193	-7.25
267292_at	hypothetical protein predicted by gene	---	AT2G23740	-1.04	-0.05	-0.44	0.673739	0.809305	-7.25
260092_at	putative serine carboxypeptidase simi	scpl3	AT1G73280	-1.03	-0.04	-0.44	0.6738	0.809305	-7.25
261436_at	protein kinase, putative (fragment) sim	---	AT1G07870	1.05	0.07	0.44	0.673837	0.809305	-7.25
253177_s_	O-methyltransferase - like protein caff	---	AT4G35150 /	-1.06	-0.08	-0.44	0.673863	0.809305	-7.25
258258_at	transcriptional regulator (FUSCA3) ide	FUS3	AT3G26790	-1.03	-0.05	-0.44	0.67388	0.809305	-7.25
245487_at	phytochrome D	PHYD	AT4G16250	1.04	0.06	0.44	0.673912	0.809305	-7.25
248481_at	putative protein similar to unknown pro	---	AT5G50930	1.04	0.06	0.44	0.673754	0.809305	-7.25
254539_s_	chitinase - like protein chitinase / lyso	---	AT4G19750 /	-1.03	-0.04	-0.44	0.673895	0.809305	-7.25
266602_at	hypothetical protein predicted by gens	---	AT2G46050	-1.03	-0.04	-0.44	0.674089	0.809475	-7.25
245638_s_	F5A9.10 unknown protein; similar to E	---	AT1G24822 /	-1.04	-0.05	-0.44	0.674281	0.809585	-7.25
256372_at	cell division protein kinase, putative si	CAK4	AT1G66750	-1.05	-0.07	-0.44	0.67427	0.809585	-7.25
254064_at	putative protein hypothetical protein -	---	AT4G25410	-1.03	-0.04	-0.44	0.674288	0.809585	-7.25
257096_at	hypothetical protein	---	AT3G30820	-1.03	-0.05	-0.44	0.674576	0.809837	-7.25
262105_at	pectin esterase, putative similar to pe	---	AT1G02810	1.05	0.07	0.44	0.674604	0.809837	-7.25
264453_at	putative GTP-binding protein similar to	---	AT1G10300	-1.03	-0.04	-0.44	0.67454	0.809837	-7.25
250891_at	fatty acid elongase - like protein KCS1	KCS19	AT5G04530	1.04	0.06	0.44	0.674712	0.809925	-7.25
258115_at	hypothetical protein predicted by gesc	---	AT3G14670	-1.04	-0.05	-0.44	0.674866	0.810067	-7.25

266870_at	putative heterogeneous nuclear ribonu	---	AT2G44710	1.05	0.08	0.44	0.67493	0.81007	-7.25
265095_at	putative cruciferin 12S seed storage p	CRU2	AT1G03880	1.04	0.05	0.44	0.67494	0.81007	-7.25
249443_at	putative protein ; supported by cDNA:	---	AT5G39600	1.05	0.07	0.44	0.674984	0.81008	-7.25
252658_at	hypothetical protein	---	AT3G44800	1.05	0.06	0.44	0.675411	0.810549	-7.25
267608_at	hypothetical protein predicted by gens	---	AT2G26770	1.04	0.05	0.44	0.675478	0.810549	-7.25
267254_at	putative protein kinase contains a prot	SNRK2.9	AT2G23030	1.12	0.16	0.44	0.675484	0.810549	-7.25
249412_at	putative protein predicted proteins, Ar	---	AT5G40410	1.04	0.06	0.44	0.675516	0.810549	-7.25
263310_s_	hypothetical protein	---	---	-1.03	-0.04	-0.44	0.67557	0.810557	-7.25
263648_at	hypothetical protein predicted by gens	---	AT1G04390	-1.04	-0.06	-0.44	0.675594	0.810557	-7.25
263992_at	putative retroelement pol polyprotein	---	---	1.03	0.05	0.44	0.675846	0.810773	-7.25
255404_at	predicted protein	---	AT4G03153	1.04	0.05	0.44	0.675835	0.810773	-7.25
254885_at	putative protein various predicted prot	---	AT4G11745	1.05	0.06	0.44	0.675886	0.810779	-7.25
250672_at	DnaJ homologue (gb|AAB91418.1|) ;	ATJ6	AT5G06910	1.03	0.04	0.44	0.67598	0.810849	-7.25
249828_at	succinyl-CoA synthetase, alpha subur	---	AT5G23250	1.04	0.06	0.44	0.676226	0.811101	-7.25
248116_at	putative protein contains similarity to M	MYB120	AT5G55020	-1.04	-0.06	-0.44	0.676286	0.811124	-7.25
247897_at	unknown protein ;supported by full-ler	TET15	AT5G57810	1.03	0.05	0.44	0.676316	0.811124	-7.25
257762_at	hypothetical protein	XRCC4	AT3G23100	-1.03	-0.05	-0.44	0.676492	0.811293	-7.25
262792_at	hypothetical protein predicted by gene	---	AT1G10710	1.04	0.05	0.44	0.676603	0.811383	-7.25
245537_at	hypothetical protein	---	AT4G15200	-1.03	-0.04	-0.44	0.676733	0.811496	-7.25
266430_at	unknown protein	---	AT2G07200	-1.03	-0.04	-0.44	0.676826	0.811542	-7.25
254565_at	replication A protein-like replication pr	---	AT4G19130	-1.03	-0.04	-0.44	0.676843	0.811542	-7.25
251016_at	pathogenesis related protein - like pat	---	AT5G02730	1.06	0.08	0.44	0.676967	0.811649	-7.25
262123_at	hypothetical protein predicted by gens	---	AT1G59630	-1.04	-0.06	-0.44	0.677038	0.811683	-7.25
254947_at	putative retrotransposon polyprotein v	---	---	1.06	0.08	0.44	0.677066	0.811683	-7.25
256717_at	hypothetical protein predicted by gens	---	AT2G34110	1.04	0.06	0.44	0.677122	0.811707	-7.25
246380_at	cytochrome P450, putative similar to c	CYP96A15	AT1G57750	1.05	0.07	0.43	0.677174	0.811726	-7.25
251845_at	Expressed protein ; supported by full-l	ATGCN4	AT3G54540	-1.05	-0.07	-0.43	0.67729	0.811788	-7.25
251871_at	hypothetical protein	---	AT3G54520	1.03	0.04	0.43	0.677297	0.811788	-7.25
266112_x_	hypothetical protein predicted by gens	---	---	1.04	0.06	0.43	0.677573	0.812077	-7.25
254588_at	putative protein hypothetical proteins -	---	AT4G18840	1.03	0.05	0.43	0.6777	0.812101	-7.25
260791_at	lipase-like protein similar to lipase GB:	---	AT1G06250	1.03	0.05	0.43	0.677665	0.812101	-7.25
261562_at	actin depolymerizing factor, putative s	ADF11	AT1G01750	-1.05	-0.07	-0.43	0.677679	0.812101	-7.25
249491_at	germin - like protein germin-like protei	---	AT5G39130	1.03	0.05	0.43	0.677737	0.812103	-7.25
249708_at	unknown protein	---	AT5G35660	-1.07	-0.10	-0.43	0.678102	0.812426	-7.25
258659_at	B' regulatory subunit of PP2A (AtB'bet	ATB' BETA	AT3G09880	1.04	0.05	0.43	0.678142	0.812426	-7.25

254556_at	putative protein various predicted prot	---	AT4G19220	-1.05	-0.07	-0.43	0.678127	0.812426	-7.25
255235_at	contains similarity to transposases	---	---	1.04	0.06	0.43	0.678149	0.812426	-7.25
258670_at	unknown protein	---	AT3G08810	-1.04	-0.06	-0.43	0.678258	0.812513	-7.25
257158_at	3-hydroxyisobutyryl-coenzyme A hydr	---	AT3G24360	-1.04	-0.06	-0.43	0.678365	0.812599	-7.25
267491_at	unknown protein predicted by genscan	---	---	1.05	0.06	0.43	0.678551	0.812779	-7.25
267218_at	Expressed protein ; supported by full-l	---	AT2G02515	-1.03	-0.05	-0.43	0.678917	0.813174	-7.25
264950_at	peroxidase, putative similar to peroxid	---	AT1G77100	-1.04	-0.05	-0.43	0.678993	0.813223	-7.25
263279_x_	hypothetical protein predicted by gens	---	---	1.04	0.05	0.43	0.67934	0.813442	-7.25
257234_at	hypothetical protein predicted by gene	---	AT3G14880	-1.05	-0.07	-0.43	0.679473	0.813442	-7.25
246217_at	APETALA2 protein ; supported by cDN	AP2	AT4G36920	-1.07	-0.09	-0.43	0.679439	0.813442	-7.25
265794_at	unknown protein	---	AT2G01310	-1.03	-0.04	-0.43	0.67926	0.813442	-7.25
252599_at	receptor-like protein kinase receptor li	---	AT3G45390	1.05	0.07	0.43	0.679533	0.813442	-7.25
259867_at	hypothetical protein predicted by gene	---	AT1G76740	-1.03	-0.04	-0.43	0.679509	0.813442	-7.25
245860_at	putative protein predicted proteins, Ar	---	AT5G28310	1.04	0.05	0.43	0.679437	0.813442	-7.25
266594_at	hypothetical protein	---	AT2G46190	-1.03	-0.04	-0.43	0.67941	0.813442	-7.25
250200_at	peroxidase ATP20a (emb|CAA67338.1	---	AT5G14130	-1.04	-0.06	-0.43	0.679417	0.813442	-7.25
246314_at	promoter-binding factor-like protein D	AREB3	AT3G56850	-1.04	-0.06	-0.43	0.6794	0.813442	-7.25
264855_at	3-hydroxy-3-methylglutaryl-coenzyme	HSK	AT2G17265	1.03	0.05	0.43	0.679751	0.813602	-7.25
261554_at	PPR-repeat protein contains multiple P	---	AT1G63400	-1.03	-0.04	-0.43	0.679764	0.813602	-7.25
252155_at	putative protein	---	AT3G50920	1.05	0.06	0.43	0.679773	0.813602	-7.25
262674_at	anter-specific proline-rich -like protein	EXL4	AT1G75910	1.04	0.06	0.43	0.67982	0.813615	-7.25
247784_at	subtilisin-like serine protease contains	---	AT5G58810	-1.03	-0.05	-0.43	0.680002	0.81379	-7.25
265394_at	predicted protein ; supported by cDNA	---	AT2G20725	-1.04	-0.06	-0.43	0.680225	0.814014	-7.25
261099_at	expansin At-EXP6, putative similar to	ATEXPA18	AT1G62980	1.04	0.06	0.43	0.680316	0.814081	-7.25
252321_at	hypothetical protein ;supported by full-	---	AT3G48510	1.04	0.05	0.43	0.680494	0.814251	-7.25
247615_at	putative protein various predicted prot	---	AT5G60250	-1.03	-0.04	-0.43	0.680621	0.814361	-7.25
265318_at	putative D-amino acid dehydrogenase	---	AT2G22650	1.05	0.07	0.43	0.680714	0.814402	-7.25
252251_at	hypothetical protein	---	AT3G49820	1.03	0.04	0.43	0.680727	0.814402	-7.25
245837_at	peptidylprolyl isomerase, putative sim	---	AT1G58450	1.03	0.04	0.43	0.680956	0.814633	-7.25
251545_at	zinc transporter -like protein zinc trans	MTPA2	AT3G58810	1.05	0.07	0.43	0.681131	0.814757	-7.25
245520_at	delta-cadinene synthase like protein	ATTS1	AT4G15870	-1.03	-0.05	-0.43	0.681156	0.814757	-7.25
261877_at	putative indole-3-acetate beta-glucosy	---	AT1G50580	-1.03	-0.05	-0.43	0.681167	0.814757	-7.25
258502_at	unknown protein	---	AT3G02490	-1.06	-0.09	-0.43	0.68125	0.814771	-7.25
261079_s_	transcription factor IIA large subunit sir	---	AT1G07470 /	1.03	0.05	0.43	0.681225	0.814771	-7.25
266367_s_	unknown protein	---	AT2G41390 /	-1.03	-0.04	-0.43	0.681415	0.814925	-7.25

261671_at	hypothetical protein similar to hypothet	---	AT1G18340	-1.06	-0.08	-0.43	0.68147	0.814948	-7.25
261024_at	hypothetical protein predicted by gene	---	AT1G12190	-1.03	-0.04	-0.43	0.681543	0.814951	-7.25
252857_at	putative protein various predicted prot	---	AT4G39756	1.03	0.05	0.43	0.681509	0.814951	-7.25
248120_at	putative protein similar to unknown pro	---	AT5G54540	-1.04	-0.05	-0.43	0.681598	0.814973	-7.25
252738_at	putative protein predicted protein, Dro	---	AT3G43240	1.03	0.05	0.43	0.681656	0.815	-7.25
260894_at	hypothetical protein contains similarity	---	AT1G29220	-1.03	-0.04	-0.43	0.681778	0.815033	-7.25
252314_at	hypothetical protein	---	AT3G49400	-1.04	-0.05	-0.43	0.681772	0.815033	-7.25
250747_at	glucuronosyl transferase-like protein	---	AT5G05900	-1.03	-0.04	-0.43	0.68179	0.815033	-7.25
257593_at	phosphatidylinositol transfer protein, p	---	AT3G24840	-1.03	-0.04	-0.43	0.681859	0.815057	-7.25
257330_at	hypothetical protein	---	---	1.03	0.05	0.43	0.681882	0.815057	-7.25
267612_at	putative nitrate transporter	---	AT2G26690	1.10	0.14	0.43	0.682158	0.815132	-7.25
265786_at	putative replication protein A1	---	---	-1.03	-0.04	-0.43	0.682097	0.815132	-7.25
246647_at	putative protein predicted proteins fron	---	---	-1.03	-0.04	-0.43	0.682184	0.815132	-7.25
255162_at	putative transposon protein	---	---	1.03	0.04	0.43	0.682148	0.815132	-7.25
249605_at	putative protein predicted protein, Ara	---	AT5G37240	1.04	0.05	0.43	0.682203	0.815132	-7.25
260285_at	putative 3-isopropylmalate dehydroger	---	AT1G80560	-1.04	-0.06	-0.43	0.681982	0.815132	-7.25
250997_at	putative protein histone H2B-2, tomat	---	AT5G02570	-1.04	-0.05	-0.43	0.68214	0.815132	-7.25
255853_at	hypothetical protein predicted by gens	---	AT1G67020	-1.03	-0.04	-0.43	0.682231	0.815132	-7.25
266393_at	late embryogenesis abundant M17 pro	M17	AT2G41260	-1.03	-0.04	-0.43	0.682342	0.815222	-7.25
252287_at	30S ribosomal protein S9 -like similar t	---	AT3G49080	-1.06	-0.08	-0.43	0.682468	0.815288	-7.25
254876_at	putative phosphoribosylanthranilate tr	---	AT4G11610	1.04	0.06	0.43	0.68244	0.815288	-7.25
265136_at	hypothetical protein similar to disease	---	AT1G51270	1.03	0.04	0.43	0.682728	0.815549	-7.25
254443_at	putative protein (fragment) BRCA1-as	BRCA1	AT4G21070	-1.03	-0.05	-0.43	0.682759	0.815549	-7.25
251263_at	putative protein DNAJ PROTEIN - Sy	---	AT3G62190	-1.03	-0.05	-0.43	0.682804	0.81556	-7.25
249803_at	putative protein similar to unknown pro	---	AT5G23780	1.03	0.05	0.43	0.682927	0.815664	-7.25
250392_at	putative protein multifunctional aminoa	---	AT5G10880	-1.03	-0.04	-0.43	0.68303	0.815696	-7.25
253985_at	caffeoyl-CoA O-methyltransferase - lik	---	AT4G26220	1.04	0.06	0.43	0.683018	0.815696	-7.25
256814_at	beta-glucosidase, putative similar to b	BGLU19	AT3G21370	-1.05	-0.07	-0.43	0.683061	0.815696	-7.25
247633_at	putative zinc finger protein finger prote	---	AT5G60470	1.06	0.08	0.43	0.683183	0.815738	-7.25
255112_at	casein kinase I - Arabidopsis thaliana,	---	AT4G08800	-1.03	-0.05	-0.43	0.683195	0.815738	-7.25
259854_at	RING-H2 zinc finger protein ATL3, pu	---	AT1G72200	1.05	0.07	0.43	0.683203	0.815738	-7.25
256635_at	hypothetical protein predicted by gens	---	AT3G28260	-1.03	-0.04	-0.43	0.683388	0.815917	-7.25
258343_at	unknown protein similar to hypothetica	---	AT3G22810	1.04	0.05	0.43	0.683458	0.815957	-7.25
257014_at	hypothetical protein predicted by gens	---	AT3G26930	1.05	0.06	0.43	0.683545	0.816018	-7.25
251405_at	plasma membrane H+-ATPase - like p	AHA7	AT3G60330	1.03	0.04	0.43	0.68395	0.816459	-7.25

258800_at	unknown protein predicted by genscar	---	AT3G04550	1.04	0.06	0.42	0.684108	0.81652	-7.25
253500_at	predicted protein RegA gene, Dictyost	ARR10	AT4G31920	-1.05	-0.08	-0.43	0.684082	0.81652	-7.25
265180_at	putative OBP32pep protein ;supported	---	AT1G23590	1.03	0.04	0.43	0.684082	0.81652	-7.25
267171_at	putative DOF zinc finger protein	DOF2.4	AT2G37590	-1.04	-0.06	-0.42	0.684194	0.816579	-7.25
265710_at	unknown protein	---	AT2G03370	1.03	0.04	0.42	0.684246	0.816599	-7.25
266048_at	putative thioredoxin H contains a thiore	ATCXXS2	AT2G40790	1.04	0.05	0.42	0.684516	0.816837	-7.25
245237_at	putative protein similarity to ALR - Hon	SLK1	AT4G25520	-1.03	-0.04	-0.42	0.684517	0.816837	-7.25
260518_at	cinnamyl alcohol dehydrogenase, puta	---	AT1G51410	1.03	0.04	0.42	0.684708	0.816984	-7.25
253658_at	cadmium-transporting ATPase-like pro	HMA3	AT4G30120	-1.03	-0.04	-0.42	0.684712	0.816984	-7.25
245415_at	G2484-1 protein	ATG2484-1	AT4G17330	-1.03	-0.04	-0.42	0.684786	0.816988	-7.25
254800_at	putative protein several hypothetical pr	---	AT4G13070	-1.05	-0.08	-0.42	0.684787	0.816988	-7.25
249500_at	expansin-like protein expansin - Prunu	ATEXPA21	AT5G39260	1.05	0.07	0.42	0.684866	0.81704	-7.25
258798_at	hypothetical protein predicted by gene	---	AT3G04540	-1.04	-0.05	-0.42	0.684928	0.817071	-7.25
246188_at	putative protein	---	AT5G21050	-1.03	-0.04	-0.42	0.685025	0.81713	-7.25
251964_at	hypothetical protein ; supported by cD	---	AT3G53370	1.06	0.08	0.42	0.685049	0.81713	-7.25
246083_at	zinc finger protein - like probable zinc	AL5	AT5G20510	1.03	0.04	0.42	0.685145	0.817201	-7.25
248936_at	heat shock transcription factor	RHA1	AT5G45710	1.05	0.07	0.42	0.685193	0.817216	-7.25
249583_at	CALMODULIN-RELATED PROTEIN 2	TCH2	AT5G37770	-1.13	-0.18	-0.42	0.685325	0.817303	-7.25
263330_at	putative leucine-rich repeat disease re	---	AT2G15320	-1.07	-0.10	-0.42	0.685338	0.817303	-7.25
251237_at	bZIP transcription factor-like protein D	CPuORF3	AT3G62420 /	1.03	0.05	0.42	0.685486	0.817437	-7.25
262167_at	putative RING zinc finger protein cont	---	AT1G74990	-1.04	-0.06	-0.42	0.685533	0.817441	-7.25
261848_at	pectin methylesterase, putative simila	---	AT1G11590	-1.04	-0.05	-0.42	0.685561	0.817441	-7.25
257678_at	RNA helicase, putative contains Pfam	RTL2	AT3G20420	1.04	0.06	0.42	0.685653	0.817508	-7.25
250045_at	putative protein mRNA (orf04), Arabid	---	AT5G17700	-1.05	-0.08	-0.42	0.685914	0.817649	-7.25
251038_at	putative protein unknown protein At2g	---	AT5G02240	-1.03	-0.04	-0.42	0.685865	0.817649	-7.25
255606_at	hypothetical protein similar to T3F17.5	---	AT4G01110	-1.05	-0.07	-0.42	0.685893	0.817649	-7.25
245245_at	delta-aminolevulinic acid dehydratase	hemb2	AT1G44318	-1.04	-0.05	-0.42	0.685845	0.817649	-7.25
248363_at	nodulin-like protein	---	AT5G52480	-1.03	-0.04	-0.42	0.68601	0.81772	-7.25
246725_at	putative protein various predicted prot	---	AT5G29040	-1.05	-0.07	-0.42	0.686283	0.818003	-7.25
248182_at	putative protein contains similarity to C	---	AT5G54030	-1.03	-0.04	-0.42	0.686666	0.818416	-7.25
249714_at	unknown protein	---	---	1.05	0.06	0.42	0.686857	0.818601	-7.25
246369_at	light repressible receptor protein kinas	---	AT1G51910	1.04	0.06	0.42	0.686915	0.818627	-7.25
263322_at	putative ribonuclease E	RNEE/G	AT2G04270	-1.06	-0.08	-0.42	0.687016	0.818691	-7.25
249223_at	receptor lectin kinase-like protein	---	AT5G42120	-1.04	-0.05	-0.42	0.68704	0.818691	-7.25
263731_at	metalloproteinase, putative similar to r	---	AT1G59970	1.11	0.15	0.42	0.687211	0.818851	-7.25

251988_at	CYTOCHROME P450-like protein CY	CYP71B31	AT3G53300	-1.03	-0.04	-0.42	0.68732	0.818939	-7.25
251375_at	putative protein various predicted prot	---	AT3G60410	-1.05	-0.07	-0.42	0.68746	0.818987	-7.25
255262_at	putative protein equilibrative nucleosid	---	AT4G05140	-1.03	-0.05	-0.42	0.687468	0.818987	-7.25
258246_s_	hypothetical protein similar to putative	---	---	-1.03	-0.04	-0.42	0.687429	0.818987	-7.25
246692_at	putative protein predicted protein, Ara	---	---	1.04	0.06	0.42	0.687525	0.819012	-7.25
255013_at	putative protein ;supported by full-leng	---	AT4G10000	-1.04	-0.06	-0.42	0.687717	0.819198	-7.25
259584_at	hypothetical protein predicted by gene	---	AT1G28080	1.03	0.04	0.42	0.687768	0.819216	-7.26
261738_s_	hypothetical protein identical to hypoth	---	AT1G47813 /	-1.05	-0.08	-0.42	0.687922	0.819357	-7.26
263561_at	unknown protein	---	AT2G15360	1.03	0.04	0.42	0.688062	0.819481	-7.26
262022_at	hypothetical protein predicted by gene	---	AT1G35490	1.04	0.06	0.42	0.688103	0.819487	-7.26
266386_at	putative homeodomain transcription fa	HDG3	AT2G32370	1.04	0.05	0.42	0.688161	0.819512	-7.26
266049_at	putative translation initiation factor	---	AT2G40780	1.03	0.05	0.42	0.688271	0.819601	-7.26
249820_at	putative protein contains similarity to I-	---	AT5G23650	-1.06	-0.08	-0.42	0.68834	0.819641	-7.26
265395_at	putative LRR receptor protein kinase ;	SRF1	AT2G20850	1.05	0.07	0.42	0.688388	0.819655	-7.26
256470_at	hypothetical protein predicted by gene	---	AT1G42570	1.03	0.04	0.42	0.688427	0.819658	-7.26
255820_at	putative protein kinase contains a prot	---	AT2G40580	-1.04	-0.05	-0.42	0.688464	0.81966	-7.26
251549_at	putative protein predicted proteins, Ar	---	AT3G58890	-1.03	-0.04	-0.42	0.688602	0.819728	-7.26
246972_s_	cytochrome P-450-like protein cytochr	CYP71A14	AT5G24950 /	1.08	0.10	0.42	0.68859	0.819728	-7.26
266343_at	putative non-LTR retroelement reverse	---	---	-1.04	-0.05	-0.42	0.688629	0.819728	-7.26
248373_at	MADS box transcription factor-like prot	---	AT5G51860	-1.04	-0.06	-0.42	0.688734	0.81981	-7.26
265957_at	hypothetical protein predicted by gens	---	AT2G37300	1.03	0.04	0.42	0.689245	0.820349	-7.26
267006_at	putative membrane transporter ; supp	---	AT2G34190	-1.04	-0.05	-0.42	0.689258	0.820349	-7.26
251292_at	putative protein hypothetical protein F	---	AT3G61920	-1.05	-0.07	-0.42	0.689671	0.820663	-7.26
262338_at	Expressed protein ; supported by full-le	---	AT1G64185	-1.05	-0.07	-0.42	0.689621	0.820663	-7.26
266434_s_	unknown protein	---	AT2G07120 /	-1.03	-0.04	-0.42	0.689748	0.820663	-7.26
246210_at	ribosomal protein ; supported by cDNA	---	AT4G36420	-1.05	-0.07	-0.42	0.689727	0.820663	-7.26
266683_at	hypothetical protein predicted by gens	GC1	AT2G19950	1.03	0.05	0.42	0.689657	0.820663	-7.26
265487_at	hypothetical protein	---	---	1.03	0.04	0.42	0.689722	0.820663	-7.26
253324_at	Expressed protein ; supported by full-le	---	AT4G33940	1.04	0.05	0.42	0.689774	0.820663	-7.26
255934_at	cytochrome P450, putative similar to c	CYP87A2	AT1G12740	-1.03	-0.04	-0.42	0.689888	0.820756	-7.26
262707_at	hypothetical protein	---	AT1G16290	-1.04	-0.06	-0.42	0.690146	0.821019	-7.26
256168_at	receptor protein kinase, putative conta	---	AT1G51805	1.08	0.11	0.42	0.690229	0.821076	-7.26
257197_at	selenium binding protein, putative sim	SBP3	AT3G23800	-1.03	-0.04	-0.42	0.690421	0.821262	-7.26
259182_at	hypothetical protein predicted by gene	---	AT3G01750	-1.06	-0.08	-0.42	0.690469	0.821275	-7.26
257410_at	hypothetical protein similar to polyketic	emb2421	AT1G24340	-1.05	-0.07	-0.42	0.69051	0.821282	-7.26

265422_at	putative NADH-ubiquinone oxireductas	NDB4	AT2G20800	1.04	0.05	0.42	0.690586	0.821329	-7.26
254179_at	putative protein various predicted prot	---	AT4G23910	1.05	0.07	0.42	0.690699	0.821378	-7.26
267598_at	hypothetical protein predicted by gene	---	AT2G33010	-1.04	-0.06	-0.42	0.69067	0.821378	-7.26
257945_at	SKP1/ASK1 (At10), putative similar to	ASK10	AT3G21860	1.03	0.05	0.42	0.690775	0.821383	-7.26
250179_at	putative protein	---	AT5G14440	-1.04	-0.06	-0.42	0.690762	0.821383	-7.26
252686_at	putative protein predicted protein, Ara	---	---	-1.03	-0.04	-0.42	0.690811	0.821383	-7.26
258363_at	putative pectin methylesterase similar	ATPMEPCR	AT3G14300	1.04	0.05	0.42	0.690864	0.821402	-7.26
247837_at	N-hydroxycinnamoyl/benzoyltransferas	---	AT5G57840	1.05	0.07	0.41	0.691169	0.821722	-7.26
261103_s_	O-methyltransferase 1, putative simila	---	AT1G62900 /	1.04	0.05	0.41	0.691344	0.821845	-7.26
259260_at	unknown protein similar to unknown pr	---	AT3G11370	1.04	0.05	0.41	0.691324	0.821845	-7.26
247775_at	phosphoinositide-specific phospholipa	PLC5	AT5G58690	-1.06	-0.08	-0.41	0.691384	0.821849	-7.26
266723_at	SKP1/ASK1 (At16), putative similar to	ASK16	AT2G03190	1.03	0.04	0.41	0.691576	0.821949	-7.26
252309_at	cysteine protease contains similarity to	---	AT3G49340	1.03	0.05	0.41	0.691535	0.821949	-7.26
257167_at	hypothetical protein predicted by gene	chr40	AT3G24340	1.03	0.04	0.41	0.691561	0.821949	-7.26
263895_at	hypothetical protein predicted by gens	---	AT2G21920	-1.03	-0.04	-0.41	0.691751	0.822071	-7.26
257942_at	SKP1/ASK1 (At8), putative similar to	ASK8	AT3G21830	1.04	0.06	0.41	0.691734	0.822071	-7.26
246025_at	zwille/pinhead-like protein GERp95 - F	---	AT5G21150	1.04	0.06	0.41	0.691945	0.82226	-7.26
248364_at	fibrillarin 3 (AtFib3) similar to fibrillarin	---	AT5G52490	-1.03	-0.04	-0.41	0.691994	0.822264	-7.26
257870_at	prolyl 4-hydroxylase, putative similar t	---	AT3G28490	1.03	0.04	0.41	0.692021	0.822264	-7.26
258138_at	Expressed protein GC donor splice site	MSH7	AT3G24495	-1.03	-0.04	-0.41	0.692204	0.822367	-7.26
261737_at	hypothetical protein similar to putative	---	AT1G47885	-1.04	-0.05	-0.41	0.692288	0.822367	-7.26
252579_at	putative protein hypothetical protein A	---	AT3G45510	-1.03	-0.04	-0.41	0.692227	0.822367	-7.26
255726_at	lysine and histidine specific transporte	---	AT1G25530	1.12	0.16	0.41	0.692279	0.822367	-7.26
263884_at	hypothetical protein predicted by gens	---	AT2G36920	-1.03	-0.04	-0.41	0.692222	0.822367	-7.26
255937_at	transcriptional activator CBF1, putativ	DDF1	AT1G12610	-1.07	-0.10	-0.41	0.692356	0.822405	-7.26
260346_at	hypothetical protein predicted by gene	CLE10	AT1G69320 /	-1.04	-0.06	-0.41	0.692612	0.822666	-7.26
246813_at	putative protein various predicted prot	---	---	1.03	0.04	0.41	0.692767	0.822808	-7.26
256716_at	hypothetical protein predicted by gene	---	AT2G34100	1.04	0.05	0.41	0.692818	0.822825	-7.26
260558_at	putative endochitinase	---	AT2G43600	1.04	0.06	0.41	0.692895	0.822874	-7.26
246985_at	putative protein contains similarity to u	---	AT5G67290	-1.04	-0.05	-0.41	0.693124	0.822966	-7.26
256657_at	unknown protein contains similarity to	---	AT3G18860	-1.03	-0.05	-0.41	0.693382	0.822966	-7.26
263253_at	bZIP transcription factor (POSF21) ide	---	AT2G31370	-1.04	-0.06	-0.41	0.693164	0.822966	-7.26
262463_at	hexose transporter, putative similar to	STP9	AT1G50310	1.06	0.09	0.41	0.693405	0.822966	-7.26
245620_at	hypothetical protein	---	AT4G14050	1.04	0.05	0.41	0.693022	0.822966	-7.26
255669_at	predicted protein	MBD3	AT4G00416	1.03	0.04	0.41	0.693339	0.822966	-7.26

265537_at	putative retroelement pol polyprotein c	---	---	1.04	0.05	0.41	0.693195	0.822966	-7.26
256739_s_	hypothetical protein similar to putative	---	---	-1.03	-0.04	-0.41	0.693247	0.822966	-7.26
247758_at	subtilisin-like serine protease contains	ATSBT4.13	AT5G59120	-1.04	-0.06	-0.41	0.693187	0.822966	-7.26
250677_at	putative protein similar to unknown pro	---	AT5G06520	1.03	0.05	0.41	0.693392	0.822966	-7.26
265558_at	putative non-LTR retroelement reverse	---	---	-1.03	-0.04	-0.41	0.69336	0.822966	-7.26
248525_s_	unknown protein	---	AT5G50610 /	-1.03	-0.05	-0.41	0.693236	0.822966	-7.26
262301_at	ripening-induced protein, putative sim	---	AT1G70880	-1.04	-0.05	-0.41	0.6935	0.822992	-7.26
252757_at	putative protein several hypothetical pr	---	---	-1.04	-0.05	-0.41	0.693495	0.822992	-7.26
247948_at	putative protein strong similarity to unk	---	AT5G57130	1.04	0.06	0.41	0.693601	0.82307	-7.26
251440_at	SKP1/ASK1 (At13), putative similar to	ASK13	AT3G60010	-1.05	-0.08	-0.41	0.693662	0.823099	-7.26
265603_at	hypothetical protein predicted by gens	---	---	-1.04	-0.05	-0.41	0.693738	0.823147	-7.26
256423_at	serine carboxypeptidase, putative sim	scpl18	AT1G33540	1.03	0.04	0.41	0.693901	0.823297	-7.26
267327_at	putative protein kinase contains a prot	---	AT2G19410	-1.03	-0.04	-0.41	0.693974	0.82334	-7.26
258152_at	chaperonin subunit, putative similar to	---	AT3G18190	-1.04	-0.05	-0.41	0.69407	0.823344	-7.26
247825_at	RNA/ssDNA-binding protein - like RN	TAF15b	AT5G58470	1.04	0.05	0.41	0.694085	0.823344	-7.26
246869_at	putative protein various predicted prot	---	---	1.03	0.04	0.41	0.694031	0.823344	-7.26
254916_at	putative protein hypothetical protein F	---	AT4G11340	-1.03	-0.05	-0.41	0.694274	0.823525	-7.26
264634_at	cytochrome P450, putative	CYP702A1	AT1G65670	1.02	0.04	0.41	0.694406	0.823639	-7.26
250952_at	putative protein	ATIREG2	AT5G03570	-1.04	-0.06	-0.41	0.694476	0.823679	-7.26
248114_at	wax synthase-like protein	---	AT5G55370	-1.03	-0.05	-0.41	0.69452	0.823689	-7.26
260294_at	GMP synthase similar to GMP synthas	---	AT1G63660	1.03	0.04	0.41	0.694602	0.8237	-7.26
262608_at	dioxygenase-like protein very similar t	---	AT1G14120	1.04	0.05	0.41	0.69459	0.8237	-7.26
265927_at	hypothetical protein	---	AT2G18590	-1.04	-0.06	-0.41	0.694729	0.823808	-7.26
251441_at	SKP1/ASK1 (At5), putative similar to	ASK5	AT3G60020	-1.03	-0.04	-0.41	0.694836	0.823893	-7.26
249530_at	putative protein asparaginyl-tRNA syn	---	AT5G38750	1.03	0.04	0.41	0.694957	0.823931	-7.26
249394_at	putative protein predicted protein, Ara	---	AT5G40180	-1.03	-0.04	-0.41	0.694977	0.823931	-7.26
246150_at	putative protein predicted proteins fron	---	AT5G19930	-1.06	-0.08	-0.41	0.694956	0.823931	-7.26
263572_at	putative disease resistance protein sim	---	AT2G17060	1.03	0.04	0.41	0.695138	0.824079	-7.26
248468_at	UDP-glucose:protein transglucosylase	RGP4	AT5G50750	1.04	0.06	0.41	0.69521	0.824106	-7.26
263056_at	Mutator-like transposase similar to MU	---	---	-1.03	-0.04	-0.41	0.695233	0.824106	-7.26
262116_at	Expressed protein ; supported by full-l	---	AT1G02816	-1.07	-0.10	-0.41	0.695279	0.824118	-7.26
245265_at	hypothetical protein ; supported by cDI	ACD6	AT4G14400	-1.23	-0.30	-0.41	0.695426	0.824249	-7.26
247518_at	putative protein many predicted protei	---	AT5G61800	-1.04	-0.05	-0.41	0.695571	0.824377	-7.26
267054_at	hypothetical protein	---	AT2G38370	1.06	0.08	0.41	0.695682	0.824423	-7.26
265809_at	unknown protein	---	AT2G18100	1.04	0.05	0.41	0.695657	0.824423	-7.26

257031_at	fucosyltransferase, putative similar to	FUT11	AT3G19280	1.03	0.05	0.41	0.695858	0.824546	-7.26
267050_at	putative RNA-binding protein ; suppor	---	AT2G41060	-1.04	-0.05	-0.41	0.695854	0.824546	-7.26
249768_at	receptor-like protein kinase	---	AT5G24100	1.04	0.06	0.41	0.696031	0.824708	-7.26
259696_at	unknown protein ; supported by cDNA	---	AT1G63150	1.03	0.05	0.41	0.696399	0.825037	-7.26
257557_at	terpene synthase-related protein, puta	---	AT3G14490	1.04	0.06	0.41	0.696417	0.825037	-7.26
249471_at	putative protein predicted proteins, Ar	EDL2	AT5G39360	1.05	0.07	0.41	0.696402	0.825037	-7.26
256106_at	unknown protein	---	AT1G16870	-1.03	-0.04	-0.41	0.696467	0.825042	-7.26
256806_at	CCAAT-binding factor B chain, putativ	NF-YA9	AT3G20910	-1.04	-0.05	-0.41	0.696493	0.825042	-7.26
253246_at	putative protein	---	AT4G34600	-1.04	-0.06	-0.41	0.696682	0.825223	-7.26
267508_at	hypothetical protein predicted by gens	---	AT2G45700	-1.03	-0.04	-0.41	0.696756	0.825268	-7.26
246093_at	ethylene-forming-enzyme-like dioxyge	---	AT5G20550	1.03	0.05	0.41	0.69692	0.825419	-7.26
254996_at	putative protein kinase CLV1 receptor	---	AT4G10390	1.04	0.06	0.41	0.696981	0.825426	-7.26
264795_at	unknown protein similar to ESTs emb	ZIGA4	AT1G08680	-1.07	-0.09	-0.41	0.697035	0.825426	-7.26
254435_at	putative protein	MS5	AT4G20900	-1.03	-0.05	-0.41	0.697022	0.825426	-7.26
250574_at	putative protein putative transcription	---	AT5G08230	1.03	0.04	0.41	0.697124	0.825489	-7.26
265667_at	putative CCAAT-binding transcription f	NF-YB11	AT2G27470	1.03	0.04	0.41	0.697465	0.82585	-7.26
256081_at	hypothetical protein contains Pfam pro	WOX14	AT1G20700	-1.04	-0.05	-0.41	0.697668	0.825962	-7.26
248980_at	putative protein similar to unknown pro	AtPP2-A7	AT5G45090	1.04	0.06	0.41	0.697637	0.825962	-7.26
245550_at	cytochrome P450 like protein	CYP705A1	AT4G15330	-1.03	-0.05	-0.41	0.697629	0.825962	-7.26
264493_at	unknown protein similar to multiple ex	GUT2	AT1G27440	1.06	0.09	0.41	0.697787	0.82606	-7.26
249119_at	unknown protein ;supported by full-ler	---	AT5G43720	1.03	0.04	0.41	0.697834	0.826073	-7.26
263993_at	hypothetical protein predicted by gens	---	---	-1.04	-0.05	-0.41	0.697879	0.826083	-7.26
255496_at	putative protein similar to plant nucleic	BZO2H1	AT4G02640	-1.05	-0.06	-0.40	0.698117	0.826193	-7.26
259088_at	unknown protein, contains TNFR/NGF	---	AT3G04970	-1.05	-0.07	-0.40	0.698047	0.826193	-7.26
254094_at	putative protein ATP-dependent DNA	---	AT4G25120	-1.04	-0.06	-0.40	0.698112	0.826193	-7.26
261332_s_	hypothetical protein contains similarity	---	---	-1.03	-0.04	-0.40	0.698084	0.826193	-7.26
265446_at	unknown protein ;supported by full-ler	---	AT2G37110	1.03	0.05	0.40	0.698459	0.826459	-7.26
266568_at	unknown protein	---	AT2G24070	-1.03	-0.04	-0.40	0.698447	0.826459	-7.26
250639_at	oleosin-like protein oleosin - Brassica	GRP20	AT5G07560	-1.04	-0.05	-0.40	0.698487	0.826459	-7.26
266769_s_	putative reverse transcriptase	---	---	1.04	0.05	0.40	0.698414	0.826459	-7.26
245797_at	defective chloroplasts and leaves (DC	---	AT1G45230	-1.02	-0.03	-0.40	0.698729	0.826703	-7.26
262887_at	hypothetical protein	---	AT1G14780	-1.11	-0.15	-0.40	0.698815	0.826716	-7.26
247307_at	UVB-resistance protein UVR8 (gb|AAD	---	AT5G21326 /	-1.03	-0.04	-0.40	0.698865	0.826716	-7.26
252774_at	putative protein predicted proteins, Ar	---	---	1.04	0.06	0.40	0.698792	0.826716	-7.26
251554_at	putative protein predicted protein, Ara	---	AT3G58670	-1.04	-0.05	-0.40	0.698885	0.826716	-7.26

254866_at	putative protein other predicted protei	---	AT4G12220	-1.03	-0.04	-0.40	0.699029	0.826844	-7.26
259512_at	hypothetical protein ; supported by cDI	KEU	AT1G12360	-1.03	-0.04	-0.40	0.699286	0.826977	-7.26
250855_at	putative protein predicted proteins, Ar	---	AT5G04730	-1.03	-0.05	-0.40	0.69923	0.826977	-7.26
255192_at	hypothetical protein	---	AT4G07380	-1.03	-0.04	-0.40	0.699255	0.826977	-7.26
259324_at	unknown protein	MIRO3	AT3G05310	-1.04	-0.06	-0.40	0.699227	0.826977	-7.26
252703_at	leucine-rich repeat protein LRP -like le	---	AT3G43740	1.03	0.04	0.40	0.699698	0.82742	-7.26
256083_at	hypothetical protein predicted by gens	---	AT1G20730	-1.03	-0.04	-0.40	0.699799	0.827497	-7.26
259155_at	transcription initiation factor IIB (TFIIB)	---	AT3G10330	-1.04	-0.06	-0.40	0.699866	0.827533	-7.26
255957_at	unknown protein ;supported by full-len	---	AT1G22160	1.09	0.12	0.40	0.699972	0.827615	-7.26
256775_at	hypothetical protein predicted by gene	---	AT3G13770	-1.05	-0.08	-0.40	0.700071	0.827689	-7.26
247242_at	unknown protein	---	AT5G64690	1.03	0.04	0.40	0.700155	0.827746	-7.26
254718_at	putative protein disease resistance re	---	AT4G13580	1.03	0.05	0.40	0.700256	0.82778	-7.26
256375_at	unknown protein	---	AT1G66720	-1.02	-0.03	-0.40	0.700254	0.82778	-7.26
265976_at	putative Athila retroelement ORF1 prot	---	---	1.03	0.05	0.40	0.700294	0.827781	-7.26
256630_at	unknown protein	---	AT3G28230	1.03	0.05	0.40	0.700674	0.828189	-7.26
249157_at	unknown protein	---	AT5G43510 /	1.03	0.04	0.40	0.700961	0.828485	-7.26
264864_at	hypothetical protein predicted by gens	---	AT1G24310	-1.05	-0.08	-0.40	0.701217	0.8285	-7.26
254486_at	putative protein crp1 protein, Zea may	---	AT4G20770	1.04	0.05	0.40	0.701065	0.8285	-7.26
256857_at	NAM-like protein similar to NAM (no ap	CUC1	AT3G15170	1.03	0.04	0.40	0.701301	0.8285	-7.26
260234_at	putative lipase/acylhydrolase contains	---	AT1G74460	-1.04	-0.06	-0.40	0.701015	0.8285	-7.26
259941_s_	putative DEAD/DEAH box helicase cor	---	AT1G71280 /	1.03	0.04	0.40	0.701255	0.8285	-7.26
257304_at	hypothetical protein predicted by gens	---	---	1.03	0.04	0.40	0.701089	0.8285	-7.26
254717_at	histone H2A.F/Z - like protein histone	HTA4	AT4G13570	1.04	0.06	0.40	0.701301	0.8285	-7.26
249912_at	putative protein similar to unknown pro	RER1	AT5G22790	1.07	0.10	0.40	0.701257	0.8285	-7.26
261723_at	unknown protein ; supported by full-ler	---	AT1G76200	-1.03	-0.04	-0.40	0.701168	0.8285	-7.26
249851_at	MADS-box transcription factor-like pro	TT16	AT5G23260	1.02	0.04	0.40	0.701397	0.828571	-7.26
253081_at	putative protein F35D11.3, Caenorhat	---	AT4G36210	1.04	0.06	0.40	0.701472	0.828617	-7.26
260430_at	putative zinc finger protein similar to C	---	AT1G68200	1.03	0.04	0.40	0.701812	0.828854	-7.26
265971_at	putative retroelement pol polyprotein	---	---	1.03	0.04	0.40	0.70182	0.828854	-7.26
245808_at	RNA binding protein identical to RNA b	ATRBP1	AT1G58470	-1.04	-0.06	-0.40	0.70186	0.828854	-7.26
247848_at	resistance protein - like disease resist	---	AT5G58120	1.04	0.06	0.40	0.701892	0.828854	-7.26
246646_at	putative protein ;supported by full-leng	---	AT5G35090	1.03	0.05	0.40	0.701876	0.828854	-7.26
249939_at	unknown protein ;supported by full-ler	---	AT5G22430	1.04	0.06	0.40	0.701792	0.828854	-7.26
260940_at	26S proteasome regulatory particle tri	---	AT1G45000	1.04	0.05	0.40	0.701954	0.828884	-7.26
248730_at	putative protein similar to unknown pro	---	AT5G48050	-1.04	-0.06	-0.40	0.702049	0.828912	-7.26

257575_at	hypothetical protein similar to hypothet	---	---	-1.03	-0.05	-0.40	0.702027	0.828912	-7.26
265790_at	putative amino acid or GABA permeas	BAT1	AT2G01170	-1.04	-0.06	-0.40	0.702203	0.829051	-7.26
267407_at	unknown protein	MEE27	AT2G34880	-1.03	-0.05	-0.40	0.702263	0.829078	-7.26
257030_at	unknown protein	---	---	1.03	0.04	0.40	0.702368	0.82916	-7.26
250378_at	putative oligopeptide transporter prote	---	AT5G11570	1.04	0.05	0.40	0.702597	0.829387	-7.26
252735_at	putative protein predicted proteins, Ar	---	AT3G43170	1.03	0.04	0.40	0.702655	0.829412	-7.26
262117_at	ribosomal protein L19, putative similar	emb2386	AT1G02780	1.04	0.06	0.40	0.702733	0.829461	-7.26
262243_at	hypothetical protein predicted by gene	---	---	-1.04	-0.06	-0.40	0.702803	0.8295	-7.26
263128_at	zinc finger protein, putative similar to	LZF1	AT1G78600	1.06	0.08	0.40	0.702888	0.829528	-7.26
253936_at	STIG1 like protein STIG1 protein - cor	---	AT4G26880	-1.03	-0.04	-0.40	0.702898	0.829528	-7.26
251213_at	putative protein hypothetical proteins -	---	---	-1.03	-0.04	-0.40	0.702959	0.829556	-7.26
263849_at	putative retroelement pol polyprotein	---	---	-1.04	-0.06	-0.40	0.703061	0.829634	-7.26
261484_at	E2, ubiquitin-conjugating enzyme 1 (U	UBC1	AT1G14400	1.03	0.04	0.40	0.703205	0.829674	-7.27
263327_at	putative receptor-like protein kinase	---	AT2G15300	1.03	0.04	0.40	0.70322	0.829674	-7.27
261464_at	disease resistance response protein,	---	AT1G07730 /	1.04	0.05	0.40	0.703173	0.829674	-7.27
264706_at	hypothetical protein predicted by gens	---	AT1G09720	1.02	0.03	0.40	0.703241	0.829674	-7.27
266179_at	putative phloem-specific lectin	AtPP2-B5	AT2G02300	1.03	0.04	0.40	0.703305	0.829707	-7.27
260162_at	unknown protein	GC5	AT1G79830	1.03	0.04	0.40	0.703496	0.829854	-7.27
248488_at	putative protein contains similarity to R	---	AT5G51080	1.03	0.05	0.40	0.703502	0.829854	-7.27
247808_at	contains similarity to unknown protein	ECT10	AT5G58190	1.03	0.04	0.40	0.703572	0.829893	-7.27
259265_at	hypothetical protein predicted by gens	---	AT3G01250	1.03	0.04	0.40	0.703668	0.829964	-7.27
262260_at	major latex protein (MLP149), putative	MLP34	AT1G70850	-1.05	-0.07	-0.40	0.703794	0.830049	-7.27
259753_at	putative isoprenylated protein similar t	---	AT1G71050	-1.05	-0.07	-0.40	0.703814	0.830049	-7.27
256702_at	unknown protein contains Pfam profile	---	AT3G30380	1.05	0.07	0.40	0.703937	0.830152	-7.27
251313_at	putative protein several hypothetical pr	---	AT3G61360	1.03	0.05	0.40	0.704176	0.830391	-7.27
261410_at	metallothionein-like protein identical to	MT1C	AT1G07610	1.10	0.14	0.40	0.704383	0.830592	-7.27
247027_at	subtilisin-like serine protease contains	---	AT5G67090	-1.03	-0.04	-0.40	0.704486	0.830671	-7.27
264534_at	hypothetical protein predicted by gene	---	AT1G55700	-1.04	-0.06	-0.40	0.704652	0.830756	-7.27
259844_at	lipid transfer protein, putative similar t	---	AT1G73560	-1.03	-0.04	-0.40	0.704667	0.830756	-7.27
257603_at	unknown protein	---	AT3G13820	1.02	0.04	0.40	0.704596	0.830756	-7.27
253965_at	hypothetical protein	---	AT4G26490	-1.04	-0.06	-0.40	0.70484	0.830916	-7.27
253634_at	putative protein ENOD20 gene produc	---	AT4G30590	-1.02	-0.04	-0.40	0.704901	0.830946	-7.27
255909_at	cdc2+/CDC28-related protein kinase,	CDKD1;3	AT1G18040	1.05	0.07	0.39	0.705123	0.831139	-7.27
254585_at	resistence protein - like downy mildew	---	AT4G19500	1.03	0.04	0.39	0.705139	0.831139	-7.27
260517_at	unknown protein	SPP1	AT1G51420	-1.03	-0.04	-0.39	0.705204	0.831173	-7.27

257400_s_	hypothetical protein	---	AT1G23810 /	-1.03	-0.04	-0.39	0.705339	0.83129	-7.27
257456_at	unknown protein predicted by genscan	SRS4	AT2G18120	-1.03	-0.05	-0.39	0.705535	0.831322	-7.27
253390_at	hypothetical protein ;supported by full-	---	AT4G32750	-1.04	-0.06	-0.39	0.705536	0.831322	-7.27
264489_at	putative squamosa-promoter binding p	---	AT1G27370	-1.07	-0.09	-0.39	0.705549	0.831322	-7.27
260758_at	endo-beta-1,4-glucanase, putative sin	AtGH9C1	AT1G48930	1.04	0.06	0.39	0.705532	0.831322	-7.27
255144_at	putative protein predicted proteins - Ar	---	---	-1.02	-0.04	-0.39	0.705456	0.831322	-7.27
254032_at	predicted protein destination factor sy	---	AT4G25940	1.04	0.06	0.39	0.705647	0.831396	-7.27
252644_at	putative protein KIAA0073, Homo sap	CYP71	AT3G44600	-1.04	-0.05	-0.39	0.705768	0.831495	-7.27
265084_at	hypothetical protein contains Cys3His	SOM	AT1G03790	-1.03	-0.04	-0.39	0.705864	0.831565	-7.27
247172_at	anthocyanidin-3-glucoside rhamnosyltr	---	AT5G65550	-1.03	-0.04	-0.39	0.705952	0.831625	-7.27
246484_at	UVB-resistance protein-like UVB-resis	---	AT5G16040	-1.03	-0.05	-0.39	0.706015	0.831657	-7.27
257546_s_	hypothetical protein predicted by gene	---	AT3G28410 /	-1.03	-0.04	-0.39	0.706074	0.831683	-7.27
265162_at	hypothetical protein predicted by gens	---	AT1G30910	-1.04	-0.05	-0.39	0.706279	0.831822	-7.27
246859_at	putative protein various predicted prot	---	AT5G25950	1.03	0.04	0.39	0.706296	0.831822	-7.27
252687_at	putative protein predicted protein, Ara	---	---	-1.04	-0.05	-0.39	0.706337	0.831822	-7.27
249369_at	putative protein Kelch motif containing	---	AT5G40680	1.03	0.04	0.39	0.706314	0.831822	-7.27
253904_at	NWMU1 - 2S albumin 1 precursor ; su	---	AT4G27140	-1.03	-0.04	-0.39	0.706516	0.83199	-7.27
259032_at	hypothetical protein similar to hypothe	---	AT3G09380	1.03	0.04	0.39	0.706574	0.832011	-7.27
261142_at	cyclic nucleotide and calmodulin-regu	ATCNGC8	AT1G19780	-1.02	-0.03	-0.39	0.706607	0.832011	-7.27
248996_at	unknown protein	RRS1	AT5G45260	1.05	0.07	0.39	0.706689	0.832063	-7.27
248978_at	putative protein contains similarity to d	AtPP2-A8	AT5G45070	1.04	0.06	0.39	0.706945	0.832287	-7.27
256531_at	cystathionine gamma-synthase, putati	---	AT1G33320	1.03	0.04	0.39	0.706951	0.832287	-7.27
248969_at	unknown protein ; supported by cDNA	---	AT5G45310	1.07	0.10	0.39	0.707151	0.832351	-7.27
261169_at	sucrose-phosphate synthase, putative	ATSPS3F	AT1G04920	1.03	0.05	0.39	0.707143	0.832351	-7.27
246570_at	putative protein nonmuscle myosin he	---	AT5G14990	-1.03	-0.04	-0.39	0.707093	0.832351	-7.27
262008_s_	CACTA-element, putative similar to TI	---	---	-1.04	-0.06	-0.39	0.707071	0.832351	-7.27
267443_at	hypothetical protein predicted by gene	---	AT2G19000	-1.03	-0.04	-0.39	0.707221	0.83239	-7.27
262268_at	hypothetical protein predicted by gene	---	---	-1.03	-0.04	-0.39	0.707293	0.832432	-7.27
260093_at	putative serine carboxypeptidase simi	scpl6	AT1G73270	1.03	0.04	0.39	0.707426	0.832545	-7.27
257857_s_	unknown protein contains an RNase_R	RRP45a	AT3G12990 /	1.05	0.07	0.39	0.707701	0.83274	-7.27
245231_at	hypothetical protein	---	AT4G25600	1.04	0.05	0.39	0.707659	0.83274	-7.27
261940_at	hypothetical protein predicted by gene	---	AT1G22520	1.04	0.06	0.39	0.70767	0.83274	-7.27
253823_at	putative protein ;supported by full-leng	---	AT4G28030	-1.03	-0.04	-0.39	0.707744	0.832748	-7.27
254595_at	floral homeotic protein agamous (AGA	AG	AT4G18960	1.03	0.04	0.39	0.708093	0.833072	-7.27
249549_at	lipid transfer - like protein lipid transfe	---	AT5G38180	-1.03	-0.05	-0.39	0.70806	0.833072	-7.27

254745_at	putative protein G9A protein, Mus mu	SUVH9	AT4G13460	-1.02	-0.03	-0.39	0.708281	0.83325	-7.27
261890_at	hypothetical protein predicted by gene	---	AT1G80970	1.06	0.08	0.39	0.708398	0.833345	-7.27
247449_at	putative protein swelling-induced chlo	---	AT5G62290	1.06	0.08	0.39	0.7086	0.833497	-7.27
267249_at	hypothetical protein predicted by gens	---	AT2G23040	1.03	0.04	0.39	0.70857	0.833497	-7.27
248557_at	transport inhibitor response 1 (TIR1),	AFB5	AT5G49980	1.04	0.05	0.39	0.708719	0.833594	-7.27
261985_at	terpene synthase, putative similar to D	---	AT1G33750	-1.03	-0.04	-0.39	0.708821	0.833671	-7.27
247437_at	AtHVA22b-like protein ; supported by	HVA22B	AT5G62490	-1.04	-0.05	-0.39	0.709062	0.833911	-7.27
263679_at	RNA helicase, putative similar to RNA	---	AT1G59990	1.04	0.05	0.39	0.709177	0.834001	-7.27
263453_at	hypothetical protein predicted by gene	---	AT2G22180	-1.03	-0.04	-0.39	0.709212	0.834001	-7.27
245539_at	ABC transporter homolog	PDR2	AT4G15230	-1.04	-0.06	-0.39	0.70938	0.834156	-7.27
264334_at	calcium-dependent protein kinase, pu	CPK19	AT1G61950	-1.02	-0.04	-0.39	0.709669	0.83441	-7.27
257040_at	unknown protein ; supported by cDNA	SCO2	AT3G19220	-1.05	-0.07	-0.39	0.709651	0.83441	-7.27
254114_at	putative protein (fragment) MtN21 ger	---	AT4G24980	-1.04	-0.06	-0.39	0.709706	0.834411	-7.27
261237_at	hypothetical protein contains similarity	---	AT1G32980	1.03	0.04	0.39	0.709782	0.834457	-7.27
251014_at	putative protein fimbriae-associated p	---	AT5G02520	-1.03	-0.04	-0.39	0.710241	0.834954	-7.27
246101_at	putative protein	---	---	1.03	0.05	0.39	0.710422	0.834994	-7.27
264423_at	hypothetical protein predicted by gene	---	AT1G61690	-1.04	-0.05	-0.39	0.71039	0.834994	-7.27
254823_at	putative protein predicted protein	---	AT4G12580	-1.03	-0.04	-0.39	0.710376	0.834994	-7.27
252768_at	putative protein hypothetical proteins -	---	---	-1.03	-0.04	-0.39	0.710412	0.834994	-7.27
246285_at	putative protein	---	AT4G36980	-1.03	-0.04	-0.39	0.710687	0.835243	-7.27
257268_at	unknown protein	---	AT3G17450	1.04	0.06	0.39	0.710707	0.835243	-7.27
245433_at	hypothetical protein	---	AT4G17140	-1.03	-0.04	-0.39	0.710773	0.835277	-7.27
249151_at	inorganic phosphate transporter (dbj|B	PHT3	AT5G43360	1.03	0.04	0.39	0.710933	0.835422	-7.27
255270_at	putative protein (ubiquitin like) to vario	---	AT4G05250	-1.03	-0.04	-0.39	0.710998	0.835456	-7.27
254884_at	H+-transporting ATPase - like protein	---	AT4G11730	1.02	0.04	0.39	0.711067	0.83546	-7.27
245801_at	hypothetical protein similar to hypothet	---	AT1G46912	1.03	0.04	0.39	0.711075	0.83546	-7.27
256942_at	hypothetical protein similar to unknowr	LSH4	AT3G23290	1.09	0.13	0.39	0.711205	0.83557	-7.27
252558_at	actin depolymerising like protein Actin	---	AT3G45990	-1.03	-0.04	-0.39	0.711266	0.835598	-7.27
255620_at	putative copper-containing glycoprote	---	AT4G01380	-1.03	-0.04	-0.39	0.711389	0.835672	-7.27
248389_at	AP2 domain transcription factor-like pr	CBF4	AT5G51990	-1.03	-0.04	-0.39	0.711402	0.835672	-7.27
267149_s_	Mutator-like transposase similar to MU	---	---	1.04	0.06	0.39	0.711493	0.835736	-7.27
249825_at	putative protein similar to unknown pro	---	AT5G23390	-1.03	-0.04	-0.39	0.711539	0.835747	-7.27
248555_at	DNA repair protein-like	---	AT5G50340	1.03	0.05	0.39	0.711899	0.836041	-7.27
256323_at	unknown protein ; supported by cDNA	---	AT1G54920	-1.04	-0.06	-0.39	0.711844	0.836041	-7.27
260881_at	unknown protein contains similarity to	---	AT1G21550	1.15	0.21	0.39	0.711882	0.836041	-7.27

265568_s_	hypothetical protein predicted by gens	---	---	-1.04	-0.06	-0.39	0.711974	0.836085	-7.27
264292_at	hypothetical protein predicted by gene	---	AT1G78790	-1.04	-0.05	-0.39	0.712035	0.836114	-7.27
250651_at	cytochrome P450	CYP93D1	AT5G06900	-1.02	-0.04	-0.38	0.712354	0.836402	-7.27
263610_at	putative beta-1,3-glucanase	---	AT2G16230	1.04	0.05	0.38	0.712327	0.836402	-7.27
254458_at	putative protein heat shock protein dn	ATERDJ2B	AT4G21180	1.05	0.07	0.38	0.712442	0.836463	-7.27
253410_at	putative protein various predicted prot	---	AT4G32970	1.04	0.06	0.38	0.712603	0.836465	-7.27
245316_at	hypothetical protein ;supported by full-	---	AT4G14000	-1.03	-0.05	-0.38	0.712582	0.836465	-7.27
248931_at	peptide transporter	---	AT5G46040	1.02	0.04	0.38	0.712535	0.836465	-7.27
247893_at	RNA polymerase I, II and III 24.3 kDa	RPB5C	AT5G57980	1.04	0.06	0.38	0.712627	0.836465	-7.27
259266_at	hypothetical protein predicted by gens	---	AT3G01240	-1.03	-0.04	-0.38	0.712616	0.836465	-7.27
247365_at	putative protein similar to unknown pro	---	AT5G63220	-1.04	-0.05	-0.38	0.712785	0.836607	-7.27
255273_at	putative protein various predicted prot	---	---	-1.03	-0.04	-0.38	0.712869	0.836663	-7.27
261160_at	hypothetical protein	---	AT1G34480	1.03	0.04	0.38	0.712991	0.836759	-7.27
263645_at	putative GTP-binding protein	---	AT2G04720	1.02	0.03	0.38	0.713098	0.836759	-7.27
265176_at	OBP32pep protein, putative identical t	---	AT1G23520	1.03	0.04	0.38	0.713053	0.836759	-7.27
249492_at	germin-like protein (GLP2a) copy1	GER2	AT5G39130 /	-1.03	-0.04	-0.38	0.713068	0.836759	-7.27
247991_at	expansin ;supported by full-length cDN	ATEXPA14	AT5G56320	1.02	0.04	0.38	0.713193	0.836791	-7.27
267390_at	putative beta-glucosidase	BGLU29	AT2G44470	-1.03	-0.04	-0.38	0.713198	0.836791	-7.27
255268_at	putative protein ubiquitin, Tetrahymen	---	AT4G05230	1.03	0.05	0.38	0.7133	0.83686	-7.27
248139_at	putative protein similar to unknown pro	---	AT5G54970	-1.23	-0.30	-0.38	0.713368	0.83686	-7.27
265079_at	hypothetical protein contains similarity	---	AT1G55460	-1.03	-0.04	-0.38	0.713339	0.83686	-7.27
253228_at	putative protein ;supported by full-leng	---	AT4G34630	-1.09	-0.13	-0.38	0.713406	0.836862	-7.27
247722_at	GTP-binding protein rab11 - like GTP-	ATRABA2D	AT5G59150	1.03	0.05	0.38	0.713771	0.837248	-7.27
256656_at	hypothetical protein similar to hypothet	---	AT3G18900	1.03	0.04	0.38	0.713818	0.83726	-7.27
266875_at	putative flavonol synthase	---	AT2G44800	-1.04	-0.05	-0.38	0.713961	0.837385	-7.27
263649_at	putative 1-aminocyclopropane-1-carbo	---	AT1G04380	-1.03	-0.04	-0.38	0.714012	0.837401	-7.27
245500_at	reverse transcriptase like protein	---	---	1.03	0.04	0.38	0.714112	0.837475	-7.27
263206_at	unknown protein similar to ESTs gb|T	---	AT1G10590	1.02	0.03	0.38	0.714249	0.837593	-7.27
254887_at	putative protein various predicted prot	---	AT4G11770	-1.03	-0.05	-0.38	0.714358	0.837678	-7.27
265131_at	putative polygalacuronase isoenzyme	JP630	AT1G23760	-1.07	-0.10	-0.38	0.714454	0.837747	-7.27
263340_at	hypothetical protein predicted by gens	---	---	1.03	0.04	0.38	0.714494	0.837751	-7.27
265832_at	putative replication protein A1	---	---	-1.03	-0.04	-0.38	0.714555	0.83778	-7.27
248280_at	putative protein similar to unknown pro	---	AT5G52950	-1.03	-0.04	-0.38	0.714611	0.837802	-7.27
250835_at	putative protein various predicted prot	DME	AT5G04560	-1.04	-0.05	-0.38	0.714664	0.837821	-7.27
246683_at	putative protein chromokinesin KIF4 -	---	AT5G33300	-1.03	-0.05	-0.38	0.714822	0.837964	-7.27

256850_at	hypothetical protein similar to hypothet	---	---	-1.02	-0.03	-0.38	0.714868	0.837975	-7.27
247802_at	putative protein RING-H2 zinc finger p	ATL63	AT5G58580	1.03	0.05	0.38	0.714949	0.838026	-7.27
258125_s_	hypothetical protein contains Pfam pro	---	AT3G23510 /	1.08	0.11	0.38	0.715137	0.838203	-7.27
249463_s_	putative protein predicted proteins, Ar	anac064	AT3G56530 /	1.03	0.04	0.38	0.715267	0.838313	-7.27
262242_at	hypothetical protein predicted by gene	---	AT1G48360	-1.04	-0.05	-0.38	0.715327	0.838339	-7.27
245533_at	putative phosphocholine cytidylyltransf	CCT2	AT4G15130	-1.08	-0.11	-0.38	0.715452	0.838378	-7.27
265524_at	hypothetical protein	---	---	1.03	0.04	0.38	0.715426	0.838378	-7.27
264088_at	unknown protein	emb1381	AT2G31340	-1.03	-0.05	-0.38	0.71547	0.838378	-7.27
265007_s_	Expressed protein ; supported by full-le	RALFL8	AT1G61563 /	1.02	0.03	0.38	0.715523	0.838398	-7.27
252597_at	putative protein several hypothetical pr	---	---	-1.04	-0.05	-0.38	0.715692	0.838466	-7.27
256692_at	hypothetical protein predicted by gene	---	AT3G32050	-1.02	-0.03	-0.38	0.715653	0.838466	-7.27
258720_at	putative ankyrin similar to ankyrin GB:A	---	AT3G09550	-1.04	-0.05	-0.38	0.71569	0.838466	-7.27
251882_at	peptide transport - like protein peptide	PTR1	AT3G54140	1.04	0.05	0.38	0.715887	0.838651	-7.27
252378_at	receptor kinase-like protein protein kir	---	AT3G47570	-1.05	-0.07	-0.38	0.716161	0.838886	-7.27
262066_at	hypothetical protein contains similarity	---	AT1G79950	1.06	0.08	0.38	0.716155	0.838886	-7.27
251444_at	putative protein ETHIONINE AMINOP	MAP2B	AT3G59990	1.03	0.04	0.38	0.716261	0.838937	-7.27
252736_at	kinesin -like protein kinesin-like protei	TES	AT3G43210	1.03	0.04	0.38	0.716278	0.838937	-7.27
262734_at	lipase, putative similar to lipase GB:A/	---	AT1G28640	-1.03	-0.04	-0.38	0.716361	0.838991	-7.27
262101_at	hypothetical protein identical to hypoth	---	AT1G59535	1.03	0.04	0.38	0.716481	0.839046	-7.27
258564_at	poly(A) polymerase, putative similar to	---	AT3G06560	-1.03	-0.04	-0.38	0.716447	0.839046	-7.27
252848_at	putative protein several hypothetical pr	---	---	-1.03	-0.05	-0.38	0.716651	0.839147	-7.27
260218_at	putative RING zinc finger protein cont	---	AT1G74620	1.02	0.03	0.38	0.716678	0.839147	-7.27
267360_at	unknown protein ;supported by full-ler	---	AT2G40060	-1.04	-0.05	-0.38	0.716606	0.839147	-7.27
263306_at	putative serine carboxypeptidase II	SCPL43	AT2G12480	-1.03	-0.04	-0.38	0.716946	0.839231	-7.27
252210_at	DNA binding protein	OBP1	AT3G50410	1.05	0.07	0.38	0.716858	0.839231	-7.27
267244_at	putative reverse transcriptase	---	AT2G02650	-1.03	-0.04	-0.38	0.716935	0.839231	-7.27
263893_at	putative WRKY-type DNA binding prot	WRKY59	AT2G21900	1.04	0.06	0.38	0.717081	0.839231	-7.27
265234_at	hypothetical protein	---	AT2G07721	1.03	0.05	0.38	0.717072	0.839231	-7.27
254864_at	putative reverse transcriptase other pu	---	---	-1.02	-0.03	-0.38	0.717029	0.839231	-7.27
257412_at	unknown protein	---	AT1G22980	-1.03	-0.04	-0.38	0.716872	0.839231	-7.27
256631_at	At14a-like protein similar to At14a prot	---	AT3G28320	-1.06	-0.08	-0.38	0.71691	0.839231	-7.27
263966_s_	putative TNP2-like transposon protein	---	---	-1.03	-0.04	-0.38	0.717054	0.839231	-7.27
257796_at	hypothetical protein predicted by gene	---	AT3G15930	-1.03	-0.05	-0.38	0.717186	0.839311	-7.27
249083_at	prohibitin non-consensus TT acceptor	ATPHB7	AT5G44140	-1.03	-0.04	-0.38	0.717324	0.839429	-7.27
265072_at	hypothetical protein predicted by gene	LAS	AT1G55580	1.04	0.06	0.38	0.717401	0.839477	-7.27

265746_at	hypothetical protein predicted by gens	---	---	-1.03	-0.04	-0.38	0.717444	0.839484	-7.27
246536_at	putative protein KIAA0594 - Homo sa	---	AT5G15920	1.08	0.11	0.38	0.717574	0.839593	-7.27
245917_at	putative protein HCNP, Homo sapiens	---	AT5G28740	-1.03	-0.05	-0.38	0.717658	0.839648	-7.27
251955_at	putative protein predicted proteins, Ar	---	AT3G53680	1.03	0.04	0.38	0.717797	0.839768	-7.27
265760_at	unknown protein	---	AT2G01220	-1.03	-0.04	-0.38	0.71792	0.8398	-7.27
245649_at	F5A9.21 unknown protein; similar to E	---	AT1G24706	1.04	0.05	0.38	0.717972	0.8398	-7.27
250311_at	unknown protein	---	AT5G12240	-1.02	-0.04	-0.38	0.717931	0.8398	-7.27
255363_x_	hypothetical protein	---	---	-1.04	-0.06	-0.38	0.717955	0.8398	-7.27
257977_at	hypothetical protein predicted by gene	---	AT3G20850	1.03	0.04	0.38	0.718052	0.83985	-7.27
247988_at	putative protein similar to unknown pro	---	AT5G56910	1.05	0.07	0.38	0.718094	0.839857	-7.27
263801_at	putative Athila retroelement ORF1 prot	---	---	1.03	0.04	0.38	0.71818	0.839914	-7.27
245427_at	putative protein	---	AT4G17550	-1.04	-0.06	-0.38	0.718233	0.839928	-7.27
248876_at	putative protein similar to unknown pro	---	---	-1.02	-0.03	-0.38	0.718266	0.839928	-7.27
261159_s_	cyclin, putative similar to GB:AAB020	CYCB1;5	AT1G34460 /	-1.04	-0.05	-0.38	0.7184	0.840042	-7.27
249133_at	putative protein strong similarity to unk	TAF4	AT5G43130	-1.02	-0.04	-0.38	0.718514	0.840116	-7.27
266727_at	putative calmodulin	emb1579	AT2G03150	-1.04	-0.05	-0.38	0.718537	0.840116	-7.27
249283_at	amino acid permease-like protein; prol	---	AT5G41800	-1.04	-0.06	-0.38	0.718605	0.840143	-7.27
256669_s_	hypothetical protein similar to hypothet	---	AT3G32200 /	-1.04	-0.05	-0.38	0.718695	0.840143	-7.27
246279_at	homeodomain protein	ATHB40	AT4G36740	1.04	0.06	0.38	0.718837	0.840143	-7.27
255223_at	putative protein predicted proteins, Ar	---	AT4G05370	-1.02	-0.04	-0.38	0.718854	0.840143	-7.27
250113_at	putative protein similar to unknown pro	FRL1	AT5G16320	1.03	0.04	0.38	0.718744	0.840143	-7.27
253128_at	Calcium-dependent serine/threonine p	CPK18	AT4G36070	1.03	0.04	0.38	0.718839	0.840143	-7.27
255108_at	hypothetical protein	---	AT4G08740	1.04	0.06	0.38	0.718643	0.840143	-7.27
254632_at	putative protein predicted protein, Ara	---	AT4G18630	1.03	0.04	0.38	0.718716	0.840143	-7.27
257442_at	legumin-like protein contains a 11-S pl	---	AT2G28680	1.04	0.06	0.38	0.71908	0.840257	-7.27
252405_at	putative protein RNA helicase HEL11	---	AT3G48120	1.04	0.05	0.38	0.719105	0.840257	-7.27
258831_at	putative integral membrane protein co	---	AT3G07080	-1.02	-0.03	-0.38	0.719054	0.840257	-7.27
264073_at	putative replication protein A1	---	---	-1.03	-0.05	-0.38	0.719136	0.840257	-7.27
251284_at	hypothetical protein	---	AT3G61840	-1.04	-0.06	-0.38	0.719116	0.840257	-7.27
251981_at	putative protein BETA-GALACTOSID	---	AT3G53080	1.03	0.04	0.37	0.719331	0.840442	-7.27
256871_at	WD-repeat protein, putative contains I	---	AT3G26480	1.06	0.08	0.37	0.719426	0.84051	-7.27
261875_at	receptor-like protein kinase, putative s	---	AT1G50610	1.03	0.04	0.37	0.719599	0.840669	-7.28
250461_at	hypothetical protein	---	AT5G10010	1.04	0.05	0.37	0.71978	0.840762	-7.28
265112_at	hypothetical protein predicted by gens	---	AT1G62530	-1.02	-0.03	-0.37	0.719937	0.840762	-7.28
247475_at	IRE (root hair elongation)	IRE	AT5G62310	-1.03	-0.04	-0.37	0.719837	0.840762	-7.28

263790_at	hypothetical protein predicted by gene	---	AT2G24530	-1.04	-0.06	-0.37	0.719931	0.840762	-7.28
250445_at	nucleoid DNA-binding protein cnd41 -	---	AT5G10760	1.23	0.30	0.37	0.719831	0.840762	-7.28
264596_at	unknown protein similar to polygalactu	---	AT1G04625	1.04	0.05	0.37	0.719922	0.840762	-7.28
251747_at	putative protein various predicted prot	---	AT3G55670	1.02	0.04	0.37	0.719906	0.840762	-7.28
266392_at	late embryogenesis abundant M10 pro	M10	AT2G41280	1.03	0.04	0.37	0.720017	0.840813	-7.28
246442_at	hypothetical protein ;supported by full-	---	AT5G17610	-1.03	-0.04	-0.37	0.720125	0.840896	-7.28
259762_at	hypothetical protein predicted by gens	---	AT1G77600	1.03	0.05	0.37	0.720312	0.841071	-7.28
254797_at	putative protein	---	AT4G13030	-1.05	-0.07	-0.37	0.720413	0.841146	-7.28
258153_at	Expressed protein ; supported by full-l	MOS4	AT3G18165	-1.04	-0.05	-0.37	0.720515	0.841179	-7.28
254477_at	zinc-finger protein Lsd1 ;supported by	---	AT4G20380	-1.04	-0.06	-0.37	0.720514	0.841179	-7.28
246307_at	putative nuclear DNA-binding protein C	ATG2	AT3G51800	-1.05	-0.07	-0.37	0.720579	0.841183	-7.28
256810_at	adenyl cyclase, putative similar to ade	---	AT3G21465	1.03	0.05	0.37	0.720592	0.841183	-7.28
259556_at	hypothetical protein	---	---	-1.02	-0.03	-0.37	0.720743	0.841316	-7.28
247958_at	putative protein similar to unknown pro	---	AT5G57070	-1.03	-0.05	-0.37	0.72083	0.841374	-7.28
261705_at	hypothetical protein predicted by gene	---	AT1G32670	-1.03	-0.04	-0.37	0.720905	0.841419	-7.28
247652_at	histone H2B - like protein histone H2B	HTB4	AT5G59910	-1.04	-0.05	-0.37	0.721023	0.841513	-7.28
251498_at	putative protein hypothetical proteins -	---	AT3G59070	-1.03	-0.05	-0.37	0.721101	0.841561	-7.28
257811_at	nitrate transporter, putative similar to r	---	AT3G25280	1.02	0.04	0.37	0.721208	0.841643	-7.28
245971_at	putative protein ; supported by cDNA:	NPH4	AT5G20730	-1.03	-0.04	-0.37	0.721269	0.841672	-7.28
261213_at	unknown protein ; supported by cDNA:	---	AT1G12970	-1.03	-0.04	-0.37	0.721476	0.841742	-7.28
260334_at	homeotic protein (ATK1) identical to ho	KNAT2	AT1G70510	-1.03	-0.04	-0.37	0.721478	0.841742	-7.28
256473_at	unknown protein	---	---	1.03	0.04	0.37	0.721406	0.841742	-7.28
259201_at	hypothetical protein predicted using ge	---	AT3G09080	1.04	0.06	0.37	0.721477	0.841742	-7.28
266068_at	putative geranylgeranyl pyrophosphate	GGPS4	AT2G18640	-1.04	-0.05	-0.37	0.721529	0.841759	-7.28
259620_s_	Tam3-like transposon protein similar t	---	---	1.04	0.06	0.37	0.721757	0.841982	-7.28
266641_at	Expressed protein ; supported by full-l	---	AT2G35605	-1.03	-0.04	-0.37	0.722018	0.842162	-7.28
266475_at	putative lipase	---	AT2G31100	1.03	0.04	0.37	0.722022	0.842162	-7.28
265094_at	putative cruciferin 12S seed storage p	---	AT1G03890	1.03	0.04	0.37	0.721973	0.842162	-7.28
265503_at	putative non-LTR retroelement reverse	---	---	1.04	0.05	0.37	0.722288	0.84243	-7.28
247373_at	unknown protein ;supported by full-ler	---	AT5G63150	-1.04	-0.05	-0.37	0.72234	0.842447	-7.28
267108_at	hypothetical protein predicted by gens	---	AT2G14830	-1.03	-0.04	-0.37	0.72238	0.842451	-7.28
257830_at	MutT-like protein contains Pfam profile	ATNUDX13	AT3G26690	-1.06	-0.08	-0.37	0.722576	0.842636	-7.28
263725_at	unknown protein	---	AT2G13550	-1.02	-0.03	-0.37	0.722922	0.842996	-7.28
256990_at	hypothetical protein predicted by gene	---	AT3G28590	1.04	0.06	0.37	0.72303	0.843072	-7.28
262252_at	RING-H2 zinc finger protein ATL3, pu	---	AT1G53820	1.03	0.04	0.37	0.723061	0.843072	-7.28

265514_s_	Mutator-like transposase similar to MU	---	---	-1.03	-0.04	-0.37	0.723114	0.843091	-7.28
266771_s_	unknown protein	---	AT2G03010 /	-1.03	-0.04	-0.37	0.723255	0.843212	-7.28
248208_at	unknown protein	ATHB52	AT5G53980	-1.04	-0.06	-0.37	0.723402	0.843341	-7.28
266954_at	hypothetical protein predicted by gene	---	AT2G34530	1.03	0.04	0.37	0.723463	0.843368	-7.28
249366_at	dihydroxyacetone 3-phosphate reducta	---	AT5G40610	-1.09	-0.12	-0.37	0.72354	0.843415	-7.28
265766_at	unknown protein	---	AT2G48080	-1.04	-0.06	-0.37	0.723743	0.84351	-7.28
256947_at	hypothetical protein contains Pfam pro	POK2	AT3G19050	-1.02	-0.03	-0.37	0.723728	0.84351	-7.28
261937_at	peptide transporter, putative similar to	---	AT1G22570	-1.07	-0.10	-0.37	0.723761	0.84351	-7.28
245959_at	peptide transport protein-like peptide t	---	AT5G19640	1.03	0.04	0.37	0.723769	0.84351	-7.28
261749_at	dehydrin, putative similar to dehydrin (	ERD14	AT1G76180	-1.03	-0.04	-0.37	0.72396	0.843689	-7.28
265798_at	unknown protein ; supported by cDNA	---	AT2G35790	1.05	0.06	0.37	0.724037	0.843693	-7.28
248559_at	unknown protein	---	AT5G50010 /	1.03	0.04	0.37	0.724014	0.843693	-7.28
255146_at	putative protein disease resistance pr	---	AT4G08450	-1.02	-0.03	-0.37	0.72417	0.843804	-7.28
253435_at	adenylate translocator (brittle-1) - like	SHS1	AT4G32400	1.05	0.06	0.37	0.72423	0.843831	-7.28
263339_at	Mutator-like transposase similar to MU	---	---	-1.02	-0.03	-0.37	0.724283	0.84385	-7.28
251761_at	glucuronosyl transferase - like protein	---	AT3G55700	1.04	0.06	0.37	0.724384	0.843925	-7.28
247292_at	unknown protein	---	AT5G64490	-1.03	-0.05	-0.37	0.72464	0.84418	-7.28
265368_at	hypothetical protein identical to hypoth	---	AT2G13350	-1.04	-0.06	-0.37	0.72474	0.844253	-7.28
255649_at	contains region of similarity to mouse r	---	AT4G00920	1.03	0.04	0.37	0.724977	0.844486	-7.28
265523_at	putative Ty3-gypsy-like retroelement p	---	---	-1.03	-0.04	-0.37	0.725061	0.844511	-7.28
265218_at	putative transcription factor	GTF2H2	AT1G05055	-1.02	-0.04	-0.37	0.725073	0.844511	-7.28
257462_at	hypothetical protein	---	AT1G65740	-1.03	-0.04	-0.37	0.725179	0.844592	-7.28
257539_at	hypothetical protein predicted by gene	---	AT3G29150	-1.03	-0.04	-0.37	0.725303	0.84465	-7.28
255376_x_	putative athila-like protein	---	---	1.04	0.06	0.37	0.725272	0.84465	-7.28
248465_at	putative protein contains similarity to u	---	AT5G51200	1.04	0.06	0.37	0.725437	0.844736	-7.28
245434_at	hypothetical protein	---	AT4G17140	1.03	0.04	0.37	0.725451	0.844736	-7.28
251006_at	putative protein predicted proteins, Ar	---	AT5G02600	1.03	0.05	0.37	0.725499	0.844749	-7.28
266249_at	hypothetical protein predicted by gens	---	AT2G27630	-1.02	-0.04	-0.37	0.72558	0.8448	-7.28
256587_at	histone-H4-like protein similar to H41 g	---	AT3G28780	1.03	0.04	0.37	0.725666	0.844813	-7.28
251614_at	hypothetical protein	---	AT3G57970	1.04	0.05	0.37	0.725634	0.844813	-7.28
245137_at	unknown protein	---	AT2G45460	-1.04	-0.06	-0.37	0.72585	0.844959	-7.28
254199_at	putative protein Ste-20 related kinase	---	AT4G24100	-1.03	-0.04	-0.37	0.725895	0.844959	-7.28
247088_at	unknown protein	---	AT5G66340	-1.03	-0.04	-0.37	0.725901	0.844959	-7.28
254285_at	putative cdc2 kinase homolog cdc2 ki	---	AT4G22940	-1.04	-0.05	-0.37	0.725942	0.844963	-7.28
251407_at	Arm repeat containing protein - like ar	---	AT3G60350	-1.03	-0.04	-0.37	0.726198	0.845143	-7.28

263078_at	hypothetical protein predicted by gene	---	AT2G05350	1.03	0.05	0.37	0.726195	0.845143	-7.28
246037_at	putative protein predicted chromosom	---	AT5G19420	1.03	0.04	0.37	0.726208	0.845143	-7.28
256089_at	hypothetical protein predicted by gens	---	AT1G20830	-1.05	-0.06	-0.37	0.726253	0.845152	-7.28
264285_at	symbiosis-related protein, putative sim	ATG8C	AT1G62040	-1.03	-0.05	-0.36	0.726319	0.845186	-7.28
262774_at	chloroplast nucleoid DNA binding prot	---	AT1G13230	1.02	0.03	0.36	0.726381	0.845215	-7.28
253112_at	putative ascorbate peroxidase ascorb	APX5	AT4G35970	-1.05	-0.06	-0.36	0.72647	0.845276	-7.28
260193_at	putative amino acid permease similar t	---	AT1G67640	-1.04	-0.06	-0.36	0.726584	0.845313	-7.28
260317_at	E2, ubiquitin-conjugating enzyme 5 (U	UBC5	AT1G63800	1.05	0.07	0.36	0.726611	0.845313	-7.28
247827_at	putative protein various predicted prot	LSH5	AT5G58500	-1.04	-0.05	-0.36	0.726631	0.845313	-7.28
263501_s_	hypothetical protein	---	AT2G07673	1.03	0.04	0.36	0.726687	0.845313	-7.28
252810_at	putative protein several hypothetical pr	---	---	1.03	0.05	0.36	0.726667	0.845313	-7.28
252245_at	putative protein various predicted prot	---	AT3G49710	1.05	0.07	0.36	0.72682	0.845424	-7.28
252918_at	putative protein	---	AT4G38980	-1.02	-0.03	-0.36	0.726862	0.84543	-7.28
264403_at	unknown protein similarity to HSR201	---	AT2G25150	-1.03	-0.04	-0.36	0.72707	0.845628	-7.28
249713_at	putative protein contains similarity to z	---	AT5G35690	-1.04	-0.05	-0.36	0.72711	0.845632	-7.28
255132_at	inositol 1,3,4-trisphosphate 5/6-kinase	---	AT4G08170	-1.04	-0.05	-0.36	0.727244	0.845745	-7.28
260498_at	putative AP2 domain transcription fact	---	AT2G41710	-1.04	-0.05	-0.36	0.727404	0.845888	-7.28
262402_at	unknown protein ; supported by cDNA:	TOM6	AT1G49410	1.04	0.05	0.36	0.727501	0.845957	-7.28
245624_at	glucosyltransferase like protein	---	AT4G14090	1.04	0.05	0.36	0.727832	0.846256	-7.28
252296_at	putative protein GMFP7 isoprenylated	---	AT3G48970	-1.05	-0.07	-0.36	0.727795	0.846256	-7.28
258579_s_	germin-like protein contains Pfam profi	---	AT3G04180 /	-1.02	-0.03	-0.36	0.727879	0.846267	-7.28
256152_at	ethylene-responsive RNA helicase, pu	---	AT1G55150	-1.02	-0.03	-0.36	0.728077	0.846415	-7.28
255351_x_	putative transposon protein similar to a	---	---	-1.03	-0.04	-0.36	0.72808	0.846415	-7.28
255254_at	hypothetical protein	---	AT4G05030	1.04	0.05	0.36	0.728162	0.846467	-7.28
248591_at	xylulose kinase ; supported by cDNA:	---	AT5G49650	-1.03	-0.05	-0.36	0.728274	0.846467	-7.28
246386_at	beta-galactosidase, putative similar to	BGAL16	AT1G77410	1.04	0.05	0.36	0.728267	0.846467	-7.28
264067_x_	putative chloroplast nucleoid DNA bind	---	AT2G28010	-1.04	-0.05	-0.36	0.728221	0.846467	-7.28
256253_at	60S acidic ribosomal protein, putative	---	AT3G11250	-1.03	-0.05	-0.36	0.728484	0.846669	-7.28
260650_at	Expressed protein ; supported by full-le	TOM2B	AT1G32370	-1.03	-0.04	-0.36	0.72853	0.846679	-7.28
262543_at	Expressed protein ; supported by full-le	---	AT1G34245	-1.03	-0.05	-0.36	0.728878	0.84704	-7.28
257630_at	cytochrome P450, putative similar to c	CYP71B16	AT3G26150	-1.03	-0.04	-0.36	0.729086	0.847238	-7.28
258636_at	putative GTPase activator protein cont	---	AT3G07890	-1.03	-0.04	-0.36	0.729179	0.847262	-7.28
257424_at	hypothetical protein predicted by gene	---	AT1G78840	-1.04	-0.06	-0.36	0.72918	0.847262	-7.28
251049_at	putative protein rab11 binding protein,	---	AT5G02430	1.03	0.04	0.36	0.729226	0.847272	-7.28
250683_x_	putative protein similar to unknown pro	---	AT5G06640	1.04	0.06	0.36	0.729352	0.847332	-7.28

248627_at	putative protein similar to unknown pro	---	AT5G48950	-1.04	-0.05	-0.36	0.729319	0.847332	-7.28
261956_at	oxidoreductase, putative similar to PR	---	AT1G64590	-1.05	-0.07	-0.36	0.729549	0.847431	-7.28
257357_at	hypothetical protein predicted by gens	---	AT2G41050	1.03	0.04	0.36	0.729504	0.847431	-7.28
247332_at	unknown protein ; supported by cDNA	---	AT5G63440	-1.04	-0.05	-0.36	0.729528	0.847431	-7.28
246059_at	putative protein KED, Nicotiana tabac	---	AT5G08450	1.03	0.04	0.36	0.729604	0.847452	-7.28
253978_at	putative protein probable kinesin - Ara	---	AT4G26660	-1.04	-0.05	-0.36	0.72967	0.847486	-7.28
249182_at	putative protein similar to unknown pro	---	AT5G42960	1.03	0.04	0.36	0.729774	0.847564	-7.28
257936_at	hypothetical protein contains similarity	---	---	-1.04	-0.05	-0.36	0.729819	0.847573	-7.28
249672_at	nucleolar protein-like	---	AT5G35910	1.04	0.05	0.36	0.729927	0.847632	-7.28
248599_at	putative protein contains similarity to u	---	AT5G49380	1.05	0.07	0.36	0.729945	0.847632	-7.28
251224_at	hypothetical protein	---	AT3G62620	-1.03	-0.05	-0.36	0.730081	0.847704	-7.28
263604_s_	putative replication protein A1	---	---	-1.02	-0.03	-0.36	0.730077	0.847704	-7.28
251793_at	regulator of chromosome condensatio	---	AT3G55580	-1.02	-0.03	-0.36	0.730211	0.847792	-7.28
245815_at	unknown protein	---	AT1G26090	-1.03	-0.05	-0.36	0.730231	0.847792	-7.28
260262_at	hypothetical protein similar to hypothe	---	AT1G68470	-1.07	-0.10	-0.36	0.730302	0.847832	-7.28
251394_at	endosperm specific protein - like endo	FLA10	AT3G60900	-1.04	-0.05	-0.36	0.730486	0.847872	-7.28
256898_at	abscisic acid-insensitive protein 3 ider	ABI3	AT3G24650	1.03	0.04	0.36	0.730458	0.847872	-7.28
246720_at	putative protein predicted proteins, Ar	---	AT5G28950	-1.02	-0.03	-0.36	0.730395	0.847872	-7.28
266144_at	hypothetical protein	---	AT2G12170	-1.03	-0.04	-0.36	0.730464	0.847872	-7.28
249566_at	cytochrome P450-like protein	CYP735A1	AT5G38450	-1.03	-0.04	-0.36	0.730535	0.847886	-7.28
261963_at	hypothetical protein predicted by gene	---	---	1.03	0.05	0.36	0.730844	0.84818	-7.28
249634_at	putative protein several hypothetical pr	---	---	1.03	0.05	0.36	0.730862	0.84818	-7.28
254302_at	hypothetical protein	---	AT4G22800	-1.02	-0.03	-0.36	0.731037	0.848296	-7.28
247472_at	cytokinesis regulating protein - like PR	MAP65-9	AT5G62250	1.03	0.04	0.36	0.731029	0.848296	-7.28
261046_at	flavonol 3-o-glucosyltransferase, puta	---	AT1G01390	1.05	0.06	0.36	0.731082	0.848305	-7.28
250653_at	putative protein strong similarity to unk	---	AT5G06930	-1.07	-0.10	-0.36	0.731288	0.848372	-7.28
259350_at	putative serine/threonine protein kinas	RBK2	AT3G05140	-1.03	-0.05	-0.36	0.731252	0.848372	-7.28
256849_at	hypothetical protein similar to hypothet	---	---	-1.03	-0.04	-0.36	0.731235	0.848372	-7.28
264287_at	hypothetical protein similar to hypothet	---	AT1G61930	-1.03	-0.05	-0.36	0.731192	0.848372	-7.28
253996_at	nucleosome assembly protein I-like pro	NAP1;1	AT4G26110	1.03	0.05	0.36	0.731492	0.848431	-7.28
252065_at	putative protein ;supported by full-leng	---	AT3G51610	1.04	0.05	0.36	0.731444	0.848431	-7.28
251657_at	putative protein MULTICOPY SUPPR	---	AT3G57000	1.05	0.07	0.36	0.731661	0.848431	-7.28
245991_at	24 kDa vacuolar protein - like 24 kDa	---	AT5G20660	1.03	0.04	0.36	0.73174	0.848431	-7.28
246572_at	putative protein predicted proteins, Ar	---	AT5G15010	-1.03	-0.04	-0.36	0.73154	0.848431	-7.28
256938_at	LEA protein, putative similar to LEA pr	ATECP31	AT3G22500	-1.03	-0.04	-0.36	0.731677	0.848431	-7.28

253786_at	receptor protein kinase-like protein re	---	AT4G28650	-1.03	-0.04	-0.36	0.731748	0.848431	-7.28
246078_s_	putative protein probable mitosis and	---	AT5G20430 /	1.05	0.07	0.36	0.731494	0.848431	-7.28
266858_at	unknown protein	GRV2	AT2G26890	-1.03	-0.04	-0.36	0.731568	0.848431	-7.28
265607_at	hypothetical protein predicted by gens	---	AT2G25370	1.03	0.04	0.36	0.731699	0.848431	-7.28
263191_at	polyprotein, putative similar to polypro	---	---	-1.03	-0.05	-0.36	0.731564	0.848431	-7.28
256416_at	ferritin subunit, putative similar to ferri	ATFER2	AT3G11050	-1.03	-0.05	-0.36	0.731855	0.848464	-7.28
247329_at	putative protein similar to unknown pro	---	AT5G64150	-1.05	-0.07	-0.36	0.731888	0.848464	-7.28
247354_at	flavonol synthase ;supported by full-le	FLS3	AT5G63590	-1.02	-0.03	-0.36	0.731862	0.848464	-7.28
262315_at	unknown protein ;supported by full-len	---	AT1G70990	-1.06	-0.09	-0.36	0.731963	0.848507	-7.28
249539_at	putative protein AtPP - Brassica napu	---	AT5G38100	-1.03	-0.05	-0.36	0.732284	0.848836	-7.28
261108_at	1-aminocyclopropane-1-carboxylate s	ACS10	AT1G62960	-1.04	-0.05	-0.36	0.732344	0.848863	-7.28
258560_at	hypothetical protein predicted by gene	---	AT3G06020	1.04	0.06	0.36	0.73257	0.848992	-7.28
254513_at	cytochrome p450 like protein cytochro	CYP71A27	AT4G20240	1.02	0.03	0.36	0.732608	0.848992	-7.28
250138_at	DRH1 DEAD box protein - like DRH1	---	AT5G14610	-1.03	-0.04	-0.36	0.732591	0.848992	-7.28
252758_at	putative protein several hypothetical pr	---	---	1.03	0.04	0.36	0.732641	0.848992	-7.28
260393_at	putative lipase similar to lipase GB:CA	---	AT1G73920	1.04	0.06	0.36	0.732502	0.848992	-7.28
247667_at	putative protein predicted protein, Ara	---	AT5G60150	1.03	0.05	0.36	0.732742	0.849065	-7.28
262585_at	hypothetical protein Is a member of the	BOR4	AT1G15460	-1.04	-0.06	-0.36	0.732825	0.849118	-7.28
252840_at	putative protein various predicted heli	---	---	-1.03	-0.04	-0.36	0.732871	0.849128	-7.28
253467_at	putative protein hypothetical protein Y	---	AT4G32140	1.03	0.05	0.36	0.733049	0.849279	-7.28
253433_s_	nodulin - like protein nodulin (clone Gr	---	AT4G28365 /	-1.03	-0.05	-0.36	0.733135	0.849279	-7.28
255157_at	hypothetical protein	---	---	1.02	0.03	0.36	0.733143	0.849279	-7.28
258754_at	hypothetical protein similar to hypothet	---	AT3G11920	1.03	0.04	0.36	0.73315	0.849279	-7.28
263654_at	unknown protein	---	AT1G04300	-1.03	-0.04	-0.36	0.733267	0.849371	-7.28
263889_at	putative ABC transporter	ATNAP12	AT2G37010	1.03	0.05	0.36	0.733404	0.849487	-7.28
246563_at	putative protein	---	AT5G15581	-1.03	-0.05	-0.35	0.733542	0.84956	-7.28
259279_at	putative cystathionine gamma-synthas	MTO1	AT3G01120	1.03	0.04	0.35	0.733533	0.84956	-7.28
246400_at	hypothetical protein contains similarity	---	AT1G57540	1.02	0.04	0.35	0.73378	0.849666	-7.28
249474_s_	germin-like protein (GLP2a) copy2 ; s	GER2	AT5G39130 /	1.03	0.05	0.35	0.733725	0.849666	-7.28
248328_at	putative protein contains similarity to M	---	AT5G52660	1.02	0.03	0.35	0.733692	0.849666	-7.28
267276_at	hypothetical protein predicted by gens	ASL5	AT2G30130	-1.03	-0.04	-0.35	0.733782	0.849666	-7.28
248033_s_	putative protein similar to unknown pro	---	AT5G54330 /	1.03	0.04	0.35	0.733836	0.849685	-7.28
262132_at	ribosomal protein L22, putative similar	---	AT1G02830	1.03	0.04	0.35	0.733896	0.849711	-7.28
262529_at	putative receptor protein kinase Appro	AtRLP3	AT1G17250	-1.04	-0.05	-0.35	0.733933	0.849712	-7.28
262159_at	hypothetical protein predicted by gene	---	AT1G52720	1.07	0.10	0.35	0.734041	0.849793	-7.28

261389_s_	hypothetical protein identical to hypoth	---	---	-1.02	-0.03	-0.35	0.734114	0.849834	-7.28
248834_at	unknown protein ;supported by full-ler	---	AT5G47090	-1.03	-0.04	-0.35	0.734199	0.84989	-7.28
263123_at	beta-Amyrin Synthase, putative simila	---	AT1G78500	1.03	0.04	0.35	0.734337	0.850006	-7.28
266537_at	Expressed protein ; supported by full-l	---	AT2G16860	-1.03	-0.04	-0.35	0.734583	0.850248	-7.28
255282_at	putative polyprotein	---	---	1.02	0.04	0.35	0.7347	0.850341	-7.28
258077_at	unknown protein ;supported by full-ler	---	AT3G26110	1.03	0.05	0.35	0.734752	0.850358	-7.28
263666_at	putative pre-mRNA splicing factor PRF	---	AT1G04510	1.04	0.06	0.35	0.735001	0.850517	-7.28
246544_at	auxin transport protein - like auxin tran	PIN8	AT5G15100	-1.02	-0.04	-0.35	0.734962	0.850517	-7.28
253685_at	putative protein nucleotide pyrophosp	---	AT4G29710	-1.03	-0.04	-0.35	0.735002	0.850517	-7.28
257850_at	putative protein kinase leucine-rich rep	SRF4	AT3G13065	-1.03	-0.04	-0.35	0.73521	0.850715	-7.28
261104_at	unknown protein	---	AT1G62910	1.03	0.04	0.35	0.735326	0.850805	-7.28
245424_at	putative protein	---	AT4G17505	-1.03	-0.04	-0.35	0.735497	0.850923	-7.28
266321_at	putative cytochrome P450	CYP78A6	AT2G46660	-1.04	-0.05	-0.35	0.735502	0.850923	-7.28
261776_at	hypothetical protein similar to putative	---	AT1G76190	-1.04	-0.05	-0.35	0.735549	0.850935	-7.28
255449_at	hypothetical protein	---	AT4G02820	-1.04	-0.06	-0.35	0.73593	0.851197	-7.28
262790_at	putative translation initiation factor sim	TIF3H1	AT1G10840	-1.02	-0.03	-0.35	0.735855	0.851197	-7.28
245495_at	hypothetical protein	---	AT4G16400	-1.02	-0.03	-0.35	0.735959	0.851197	-7.28
260911_at	hypothetical protein predicted by gene	---	AT1G02490	-1.03	-0.04	-0.35	0.735963	0.851197	-7.28
258872_at	hypothetical protein similar to L1 spec	HDG8	AT3G03260	-1.04	-0.06	-0.35	0.735955	0.851197	-7.28
255448_at	hypothetical protein	---	AT4G02810	-1.04	-0.05	-0.35	0.736055	0.851218	-7.28
250096_at	putative protein similar to unknown pro	---	AT5G17190	-1.03	-0.04	-0.35	0.736051	0.851218	-7.28
257405_at	putative calmodulin similar to EST gb|A	---	AT1G24620	-1.02	-0.03	-0.35	0.736114	0.851242	-7.28
258973_at	putative cytochrome P450 similar to cy	CYP94B2	AT3G01900	1.03	0.04	0.35	0.736261	0.85127	-7.28
259378_at	unknown protein supported by full-len	---	AT3G16310	-1.06	-0.08	-0.35	0.736288	0.85127	-7.28
265360_s_	putative Athila retroelement ORF1 prot	---	---	1.03	0.04	0.35	0.736325	0.85127	-7.28
258723_at	putative MYB-related protein similar to	---	AT3G09600	1.03	0.04	0.35	0.736259	0.85127	-7.28
260917_at	unknown protein similar to hypothetica	---	AT1G02700	1.03	0.05	0.35	0.736292	0.85127	-7.28
256478_at	unknown protein	---	---	1.03	0.04	0.35	0.736555	0.851494	-7.28
263990_at	putative phosphoprotein phosphatase	PP5.2	AT2G42810	1.03	0.04	0.35	0.736644	0.851553	-7.28
266316_at	unknown protein ; supported by cDNA	---	AT2G27080	1.15	0.20	0.35	0.736696	0.851571	-7.28
265053_at	myrosinase binding protein, putative s	---	AT1G52000	-1.06	-0.08	-0.35	0.736742	0.851581	-7.28
266496_at	putative zinc finger protein	---	---	1.03	0.04	0.35	0.736882	0.851699	-7.28
251222_at	putative membrane protein clone:2-72	---	AT3G62580	1.05	0.07	0.35	0.737005	0.851755	-7.29
248383_at	putative protein contains similarity to c	---	AT5G51900	-1.03	-0.04	-0.35	0.73697	0.851755	-7.28
262704_at	hypothetical protein predicted by gens	ASL9	AT1G16530	1.07	0.09	0.35	0.737054	0.851768	-7.29

261271_at	Expressed protein ; supported by full-l	---	AT1G26795	1.03	0.04	0.35	0.737211	0.851907	-7.29
263350_at	alanine-glyoxylate aminotransferase ;	AGT	AT2G13360	-1.04	-0.06	-0.35	0.737405	0.851958	-7.29
260212_at	hypothetical protein predicted by gens	---	AT1G74480	1.02	0.03	0.35	0.737378	0.851958	-7.29
256345_at	hypothetical protein similar to hypothet	---	AT1G55030	1.03	0.04	0.35	0.737324	0.851958	-7.29
255514_s_	hypothetical protein similar to MNA5.4	AGL78	AT5G65330	-1.03	-0.04	-0.35	0.737372	0.851958	-7.29
247731_at	glucuronosyl transferase - like protein	UGT76E2	AT5G59590	1.03	0.04	0.35	0.737568	0.852069	-7.29
255096_at	hypothetical protein similar to T21B4.5	---	---	-1.03	-0.04	-0.35	0.737576	0.852069	-7.29
257384_at	unknown protein	---	AT2G15110	-1.03	-0.04	-0.35	0.737616	0.852072	-7.29
259909_at	unknown protein ; supported by full-ler	MEE9	AT1G60870	-1.03	-0.04	-0.35	0.737772	0.852123	-7.29
264947_at	heat shock protein DnaJ, putative sim	---	AT1G77020	1.04	0.05	0.35	0.737752	0.852123	-7.29
261246_at	unknown protein	SYTB	AT1G20080	-1.03	-0.04	-0.35	0.737742	0.852123	-7.29
261950_at	zinc finger protein, putative similar to I	---	AT1G64620	1.04	0.06	0.35	0.737886	0.852211	-7.29
254930_at	putative protein hypothetical protein -	---	AT4G11450	-1.05	-0.07	-0.35	0.738231	0.852523	-7.29
263719_at	hypothetical protein predicted by gens	---	AT2G13600	-1.02	-0.04	-0.35	0.738227	0.852523	-7.29
248072_at	unknown protein	---	AT5G55680	1.03	0.04	0.35	0.738372	0.852561	-7.29
248316_at	putative protein similar to unknown pro	---	AT5G52670	1.04	0.05	0.35	0.738375	0.852561	-7.29
258763_s_	putative beta-mannan endohydrolase s	---	AT3G10900 /	-1.02	-0.03	-0.35	0.738333	0.852561	-7.29
261589_at	hypothetical protein predicted by gens	---	AT1G01690	-1.03	-0.05	-0.35	0.738593	0.852769	-7.29
251691_at	putative protein hypothetical protein S	---	AT3G56520	1.03	0.05	0.35	0.738775	0.852915	-7.29
256508_at	unknown protein	---	AT1G75140	-1.03	-0.04	-0.35	0.738794	0.852915	-7.29
258941_at	putative monodehydroascorbate reduc	MDHAR	AT3G09940	1.23	0.30	0.35	0.738835	0.852918	-7.29
256542_at	unknown protein	PMI1	AT1G42550	1.04	0.05	0.35	0.739312	0.852994	-7.29
254844_at	hypothetical protein supported by full-l	---	AT4G11790	-1.05	-0.06	-0.35	0.739054	0.852994	-7.29
251491_at	fructokinase-like protein fructokinase -	---	AT3G59480	-1.04	-0.06	-0.35	0.739386	0.852994	-7.29
251473_at	putative protein myrosinase-binding p	---	AT3G59610	-1.04	-0.06	-0.35	0.739372	0.852994	-7.29
260131_at	unknown protein contains Pfam profile	---	AT1G66310	-1.03	-0.04	-0.35	0.739202	0.852994	-7.29
245609_at	disease resistance N like protein	---	AT4G14368 /	1.03	0.05	0.35	0.739306	0.852994	-7.29
262222_at	unknown protein	TRZ1	AT1G74700	-1.03	-0.04	-0.35	0.739117	0.852994	-7.29
249461_at	putative protein predicted proteins, Ar	---	AT5G39640	-1.03	-0.04	-0.35	0.739077	0.852994	-7.29
248598_at	putative protein contains similarity to u	---	AT5G49370	-1.03	-0.04	-0.35	0.739359	0.852994	-7.29
263835_at	putative eukaryotic translation initiatio	---	AT2G40290	1.03	0.04	0.35	0.739026	0.852994	-7.29
266404_at	hypothetical protein predicted by gene	---	AT2G38590	1.03	0.04	0.35	0.739185	0.852994	-7.29
263454_at	putative cysteine proteinase	---	AT2G22160	1.03	0.04	0.35	0.739319	0.852994	-7.29
263041_at	putative alliinase similar to alliinase GE	TAR1	AT1G23320	-1.03	-0.04	-0.35	0.739107	0.852994	-7.29
246114_at	seed imbitition protein-like seed imbiti	DIN10	AT5G20250	-1.05	-0.07	-0.35	0.739637	0.853197	-7.29

249455_s_	putative protein predicted proteins, Ar	---	AT1G50870 /	1.02	0.03	0.35	0.739622	0.853197	-7.29
251388_at	putative protein protein regulating cyto	MAP65-4	AT3G60840	-1.03	-0.04	-0.35	0.739733	0.853221	-7.29
260191_at	putative protein kinase Pfam HMM hit:	---	AT1G67580	1.02	0.03	0.35	0.739715	0.853221	-7.29
267599_at	putative serine/threonine protein kinas	---	AT2G32850	1.02	0.04	0.35	0.739816	0.853274	-7.29
262853_at	unknown protein Location of ESTs OA	---	AT1G20890	1.03	0.04	0.35	0.739875	0.853281	-7.29
258509_at	protein kinase, putative similar to SER	---	AT3G06620	1.05	0.07	0.35	0.73991	0.853281	-7.29
256519_at	hypothetical protein predicted by gens	---	AT1G66110	1.04	0.06	0.35	0.739934	0.853281	-7.29
265014_at	hypothetical protein similar to deacety	---	AT1G24430	1.04	0.06	0.35	0.740128	0.853418	-7.29
248660_at	RNA-binding protein-like	---	AT5G48650	1.04	0.05	0.35	0.740125	0.853418	-7.29
258571_at	hypothetical protein predicted by gene	anac048	AT3G04420	1.03	0.04	0.35	0.740216	0.853476	-7.29
266917_at	unknown protein	DTA2	AT2G45830	-1.03	-0.04	-0.34	0.74085	0.854018	-7.29
250466_at	putative protein TETRATRICOPEPTID	---	AT5G10090	-1.02	-0.03	-0.34	0.740723	0.854018	-7.29
248733_at	unknown protein	ELP1	---	-1.03	-0.05	-0.34	0.740881	0.854018	-7.29
253134_at	putative protein procollagen-proline di	---	AT4G35820	1.02	0.04	0.34	0.740901	0.854018	-7.29
253015_at	hypothetical protein	---	AT4G37950	-1.03	-0.04	-0.34	0.740869	0.854018	-7.29
250069_at	disease resistance protein-like	---	AT5G17970	1.03	0.04	0.34	0.74091	0.854018	-7.29
256574_at	hypothetical protein similar to callose s	---	AT3G14780	-1.05	-0.07	-0.34	0.741036	0.85412	-7.29
245509_at	hypothetical protein	---	AT4G15730	1.03	0.05	0.34	0.741222	0.85429	-7.29
248093_at	putative protein similar to unknown pro	---	AT5G55210	-1.03	-0.05	-0.34	0.741265	0.854297	-7.29
266838_at	similar to jasmonate-inducible proteins	---	AT2G25980	-1.03	-0.04	-0.34	0.74141	0.854359	-7.29
261381_at	hypothetical protein predicted by gene	SDE3	AT1G05460	-1.02	-0.03	-0.34	0.741392	0.854359	-7.29
257665_at	unknown protein	---	AT3G20430	-1.03	-0.04	-0.34	0.741431	0.854359	-7.29
255708_at	predicted protein	---	AT4G00232	1.03	0.04	0.34	0.741483	0.854375	-7.29
250932_s_	putative protein MED7, Homo sapiens	---	AT5G03220 /	-1.03	-0.04	-0.34	0.741719	0.854605	-7.29
257437_s_	hypothetical protein predicted by gens	---	AT2G16290 /	-1.03	-0.04	-0.34	0.74202	0.854909	-7.29
250015_at	N-acetylglucosamine-phosphate mutas	DRT101	AT5G18070	1.05	0.08	0.34	0.742238	0.855117	-7.29
263878_s_	unknown protein	---	AT2G22040 /	-1.03	-0.05	-0.34	0.742293	0.855136	-7.29
258174_at	hypothetical protein contains Pfam pro	---	AT3G21470	-1.03	-0.04	-0.34	0.742358	0.855168	-7.29
262226_at	Expressed protein ; supported by full-le	---	AT1G53885 /	1.08	0.11	0.34	0.742525	0.855318	-7.29
261980_at	hypothetical protein predicted by gene	---	AT1G33820	-1.02	-0.03	-0.34	0.742596	0.855356	-7.29
263860_at	hypothetical protein predicted by gens	---	---	1.02	0.04	0.34	0.742704	0.855437	-7.29
251470_at	putative protein hypothetical protein A	---	AT3G59570	1.03	0.05	0.34	0.742786	0.855468	-7.29
258416_at	hypothetical protein predicted by gene	---	AT3G17310	-1.03	-0.04	-0.34	0.742832	0.855468	-7.29
258513_at	protein kinase, putative contains Pfam	---	AT3G06630	-1.02	-0.03	-0.34	0.742843	0.855468	-7.29
263333_at	unknown protein ; supported by cDNA	---	AT2G03890	-1.04	-0.05	-0.34	0.743105	0.855683	-7.29

247082_at	putative protein contains similarity to m	ATGRIP	AT5G66030	-1.03	-0.04	-0.34	0.743101	0.855683	-7.29
245582_at	hypothetical protein	LOI1	AT4G14850	-1.04	-0.06	-0.34	0.74324	0.855795	-7.29
252252_at	putative protein GTP-binding protein b	RID3	AT3G49180	-1.05	-0.08	-0.34	0.743524	0.856079	-7.29
249127_at	actin-like protein ; supported by cDNA	ATARP9	AT5G43500	-1.03	-0.05	-0.34	0.743688	0.856205	-7.29
260816_at	hypothetical protein predicted by gens	---	AT1G06930	1.04	0.05	0.34	0.743708	0.856205	-7.29
253434_at	potassium channel - protein	AKT5	AT4G32500	-1.03	-0.04	-0.34	0.743815	0.856241	-7.29
256592_at	hypothetical protein predicted by gene	---	---	-1.02	-0.03	-0.34	0.743808	0.856241	-7.29
254084_at	ubiquitin activating enzyme - like prote	SAE1A	AT4G24940	1.05	0.07	0.34	0.744044	0.8563	-7.29
255214_at	hypothetical protein	---	---	-1.02	-0.03	-0.34	0.743974	0.8563	-7.29
265759_at	putative membrane transporter	---	AT2G13100	1.02	0.03	0.34	0.744089	0.8563	-7.29
249802_at	putative protein similar to unknown pro	---	AT5G23770	-1.02	-0.03	-0.34	0.744091	0.8563	-7.29
267427_at	putative WRKY-type DNA binding prot	WRKY35	AT2G34830	-1.02	-0.03	-0.34	0.744073	0.8563	-7.29
248904_at	Expressed protein ; supported by full-le	---	AT5G46295	1.03	0.04	0.34	0.743969	0.8563	-7.29
250915_at	homeodomain -like protein homeodon	HB51	AT5G03790	1.05	0.06	0.34	0.744183	0.856363	-7.29
251877_at	synaptobrevin -like protein vesicle-ass	ATVAMP727	AT3G54300	-1.03	-0.05	-0.34	0.744288	0.856397	-7.29
251863_at	kinesin-like protein kinesin, Syncepha	MRH2	AT3G54870	-1.02	-0.03	-0.34	0.74426	0.856397	-7.29
252339_at	hypothetical protein	---	AT3G48900	1.02	0.03	0.34	0.744732	0.856865	-7.29
245203_at	hypothetical protein similar to protein p	---	---	1.02	0.03	0.34	0.744834	0.856939	-7.29
260078_at	hypothetical protein predicted by gene	---	AT1G73790	-1.03	-0.04	-0.34	0.744924	0.856999	-7.29
266427_at	hypothetical protein predicted by gens	---	AT2G07170	-1.03	-0.05	-0.34	0.745048	0.857098	-7.29
254619_at	myb - like protein transforming protein	MYB98	AT4G18770	-1.03	-0.04	-0.34	0.745141	0.857162	-7.29
264801_at	hypothetical protein gene overlaps Sp	emb2411	AT1G08840	-1.03	-0.04	-0.34	0.745406	0.8573	-7.29
254959_at	predicted protein	UGE5	AT4G10955 /	1.04	0.06	0.34	0.745397	0.8573	-7.29
263825_at	putative laccase (diphenol oxidase)	LAC5	AT2G40370	-1.06	-0.09	-0.34	0.745379	0.8573	-7.29
250142_at	polygalacturonase - like protein polyga	---	AT5G14650	1.06	0.08	0.34	0.745411	0.8573	-7.29
254552_at	putative protein several hypothetical pr	---	AT4G19900	1.03	0.04	0.34	0.745471	0.857326	-7.29
251197_at	glutaredoxin -like protein glutaredoxin	---	AT3G62960	1.06	0.08	0.34	0.745575	0.857402	-7.29
261333_at	hypothetical protein predicted by gene	---	AT1G44910	-1.04	-0.06	-0.34	0.745642	0.857435	-7.29
257689_at	myb-related protein, putative myb-rela	AtMYB10	AT3G12820	1.03	0.04	0.34	0.745744	0.85751	-7.29
256549_at	hypothetical protein predicted by gene	---	---	-1.03	-0.04	-0.34	0.745919	0.857667	-7.29
257876_at	hypothetical protein predicted by gene	---	AT3G17130	-1.05	-0.07	-0.34	0.746066	0.85771	-7.29
264570_at	unknown protein Similar to Caenorhab	---	AT1G05350	-1.03	-0.05	-0.34	0.746053	0.85771	-7.29
253030_at	hypothetical protein	FRS5	AT4G38180	-1.02	-0.03	-0.34	0.746068	0.85771	-7.29
266310_at	putative PCI domain protein proteasor	FUS12	AT2G26990	1.03	0.04	0.34	0.746142	0.857751	-7.29
262015_at	hypothetical protein predicted by gene	---	---	-1.02	-0.03	-0.34	0.746259	0.857842	-7.29

260591_at	predicted protein	---	AT1G53325	1.02	0.03	0.34	0.746342	0.857895	-7.29
260991_at	hypothetical protein predicted by gene	---	AT1G12160	-1.02	-0.03	-0.34	0.746569	0.858085	-7.29
266090_at	unknown protein	---	AT2G38000	1.03	0.05	0.34	0.746583	0.858085	-7.29
255387_at	putative nodulin similar to M. truncatu	---	AT4G03630	1.04	0.05	0.34	0.746677	0.85815	-7.29
253611_at	RNase L inhibitor-like protein ribonucl	NAP15	AT4G30300	1.03	0.04	0.34	0.746769	0.858212	-7.29
254986_at	putative protein SF16 protein -Heliant	IQD16	AT4G10640	-1.02	-0.03	-0.34	0.747149	0.858566	-7.29
260445_at	ARG1 protein (Altered Response to G	ARG1	AT1G68370	1.03	0.05	0.34	0.747186	0.858566	-7.29
257961_at	unknown protein	---	AT3G19780	-1.03	-0.04	-0.34	0.747189	0.858566	-7.29
262886_at	hypothetical protein	KNATM	AT1G14760	-1.04	-0.05	-0.34	0.747296	0.858645	-7.29
252304_at	hypothetical protein	---	AT3G49230	-1.02	-0.03	-0.34	0.747418	0.858674	-7.29
255164_at	hypothetical protein	---	---	-1.02	-0.03	-0.34	0.747435	0.858674	-7.29
252007_at	hypothetical protein MobA, Pseudomo	---	AT3G52830	-1.03	-0.05	-0.34	0.747398	0.858674	-7.29
245116_at	unknown protein ; supported by cDNA	---	AT2G41620	1.06	0.08	0.34	0.747501	0.858707	-7.29
255206_at	putative transposon protein	---	---	1.02	0.03	0.34	0.747593	0.85877	-7.29
256029_at	integral membrane protein, putative si	STT3B	AT1G34130	1.06	0.08	0.34	0.747716	0.858868	-7.29
249218_at	pitrilysin	---	AT5G42390	-1.04	-0.05	-0.34	0.747821	0.858946	-7.29
249324_at	cytochrome c1 precursor ; supported	---	AT5G40810	-1.02	-0.03	-0.33	0.748085	0.859164	-7.29
246974_at	putative protein	---	AT5G24980	1.03	0.05	0.33	0.748087	0.859164	-7.29
264341_at	hypothetical protein predicted by gens	---	AT1G70270	-1.02	-0.03	-0.33	0.748309	0.859376	-7.29
265894_at	putative lipid transfer protein	LTP	AT2G15050	-1.08	-0.11	-0.33	0.748382	0.859395	-7.29
249760_at	(+)-delta-cadinene synthase (d-cadine	TPS21	AT5G23960	1.02	0.03	0.33	0.748425	0.859395	-7.29
249005_at	terpene cyclase/synthase	---	AT5G44630	-1.02	-0.03	-0.33	0.748438	0.859395	-7.29
266201_at	similar to MtN3 protein ;supported by	---	AT2G39060	1.03	0.04	0.33	0.748522	0.859441	-7.29
250024_at	NAM (no apical meristem)-like protein	ANAC087	AT5G18270	1.05	0.06	0.33	0.748554	0.859441	-7.29
248411_at	unknown protein	---	AT5G51580	1.02	0.03	0.33	0.74863	0.859485	-7.29
246939_at	AP2 domain containing protein AP2 d	SHN2	AT5G25390	-1.03	-0.04	-0.33	0.748799	0.859636	-7.29
258031_s_	hypothetical protein similar to hypothet	---	AT3G27480 /	-1.03	-0.05	-0.33	0.748933	0.859746	-7.29
259271_at	Expressed protein ; supported by full-l	---	AT3G01170	1.03	0.04	0.33	0.749306	0.860131	-7.29
267438_at	putative GDSL-motif lipase/hydrolase s	---	AT2G19050	-1.04	-0.06	-0.33	0.749573	0.860394	-7.29
254713_at	hypothetical protein	---	AT4G18090	-1.04	-0.05	-0.33	0.749848	0.860667	-7.29
261268_at	unknown protein similar to 50S ribosor	---	AT1G26740	1.03	0.04	0.33	0.749895	0.860677	-7.29
255391_at	hypothetical protein similar to T6P5.7,	---	---	-1.02	-0.03	-0.33	0.75014	0.860916	-7.29
256993_at	unknown protein ; supported by cDNA	---	AT3G28670	1.02	0.03	0.33	0.750423	0.861197	-7.29
254693_at	bHLH protein - like bHLH protein, Ara	---	AT4G17880	1.09	0.12	0.33	0.750585	0.86134	-7.29
265102_at	putative peroxidase similar to cationic	---	AT1G30870	-1.03	-0.04	-0.33	0.7507	0.861406	-7.29

252208_at	putative protein hypothetical protein K	---	AT3G50380	-1.04	-0.06	-0.33	0.750718	0.861406	-7.29
255098_at	hypothetical protein	---	AT4G08640	1.02	0.03	0.33	0.750848	0.861511	-7.29
250709_at	putative protein similar to unknown pro	LBD33	AT5G06080	1.03	0.04	0.33	0.751137	0.8618	-7.29
257272_at	unknown protein ; supported by cDNA	---	AT3G28130	1.03	0.04	0.33	0.751201	0.861829	-7.29
246223_at	UDP-glucuronyltransferase-like protein	IRX14	AT4G36890	-1.02	-0.03	-0.33	0.751334	0.861895	-7.29
257177_at	cyanate lyase (CYN) identical to cyana	CYN	AT3G23490	1.04	0.06	0.33	0.75133	0.861895	-7.29
256742_at	transcription initiation factor IIB, putati	---	AT3G29380	1.03	0.04	0.33	0.751545	0.862094	-7.29
265122_at	similar to flavin-binding monooxygenas	FMO GS-OX	AT1G62540	-1.02	-0.03	-0.33	0.75163	0.862115	-7.29
259095_at	acyl carrier protein 1 precursor (ACP) i	ACP1	AT3G05020	-1.07	-0.09	-0.33	0.751639	0.862115	-7.29
262760_at	hypothetical protein contains similarity	---	AT1G10770	1.09	0.13	0.33	0.751724	0.86217	-7.29
250309_at	putative protein similar to unknown pro	---	AT5G12220	-1.04	-0.05	-0.33	0.75191	0.862296	-7.29
267502_at	putative cytochrome P450	CYP76C4	AT2G45550	1.02	0.03	0.33	0.75191	0.862296	-7.29
255584_at	putative reverse transcriptase-like prot	---	---	-1.02	-0.03	-0.33	0.751982	0.862335	-7.29
265857_s_	serine threonine protein phosphatase I	PP2A-4	AT2G42500 /	-1.03	-0.04	-0.33	0.752033	0.86235	-7.29
245481_at	hypothetical protein	---	AT4G16170	1.02	0.04	0.33	0.752307	0.862546	-7.29
254295_at	putative protein predicted protein, Ara	---	AT4G23080	1.02	0.03	0.33	0.752341	0.862546	-7.29
250043_at	putative protein proline-rich protein AF	---	AT5G18430	-1.03	-0.05	-0.33	0.752292	0.862546	-7.29
266195_at	putative RING zinc finger protein	---	AT2G39100	-1.02	-0.03	-0.33	0.752355	0.862546	-7.29
252804_at	putative protein	---	---	-1.02	-0.03	-0.33	0.752408	0.862563	-7.29
265301_s_	putative MYB family transcription facto	---	AT2G13960 /	-1.03	-0.04	-0.33	0.752671	0.862657	-7.29
247516_at	germin-like protein - like germin-like p	---	AT5G61750	-1.03	-0.04	-0.33	0.752717	0.862657	-7.29
266633_at	putative DnaJ protein	---	AT2G35540	1.03	0.04	0.33	0.752673	0.862657	-7.29
263803_at	hypothetical protein predicted by gens	---	AT2G40440	1.02	0.03	0.33	0.752695	0.862657	-7.29
263898_at	SKP1 interacting partner 6 (SKIP6), p	SKIP6	AT2G21950	1.03	0.04	0.33	0.752687	0.862657	-7.29
255374_at	hypothetical protein	---	---	1.02	0.03	0.33	0.752651	0.862657	-7.29
260211_at	hypothetical protein similar to YGL010	---	AT1G74440	1.09	0.12	0.33	0.75291	0.862835	-7.29
263974_at	hypothetical protein predicted by grail	---	AT2G42720	-1.03	-0.04	-0.33	0.752964	0.862854	-7.29
252537_at	putative transporter protein peptide tra	---	AT3G45710	-1.03	-0.04	-0.33	0.753042	0.862856	-7.29
258873_at	hypothetical protein similar to unknowr	---	AT3G03240	-1.03	-0.05	-0.33	0.753041	0.862856	-7.29
265783_at	putative Athila retroelement ORF1 prot	---	---	1.03	0.04	0.33	0.753122	0.862905	-7.29
249748_at	thaumatin-like protein	---	AT5G24620	-1.03	-0.04	-0.33	0.753248	0.862997	-7.29
248781_at	putative protein similar to unknown pro	---	AT5G47870	-1.06	-0.08	-0.33	0.753321	0.862997	-7.29
260113_at	hypothetical protein predicted by gens	---	AT1G63300	-1.02	-0.03	-0.33	0.753354	0.862997	-7.29
259432_at	myb-related protein, putative similar to	---	AT1G01520	-1.03	-0.05	-0.33	0.753299	0.862997	-7.29
260810_s_	retroelement protein, putative similar t	---	---	-1.03	-0.04	-0.33	0.753626	0.863266	-7.29

253429_at	putative protein CDC28/cdc2-like kina	---	AT4G32420	-1.03	-0.04	-0.33	0.753703	0.86331	-7.29
254195_at	putative protein various predicted prot	NLP7	AT4G24020	1.03	0.04	0.33	0.753806	0.863385	-7.29
249206_at	putative protein similar to unknown pro	ATS	AT5G42630	-1.03	-0.05	-0.33	0.753895	0.863401	-7.29
256801_at	cytochrome P450, putative similar to c	CYP705A30	AT3G20940	-1.02	-0.03	-0.33	0.753867	0.863401	-7.29
258952_at	putative RNase H contains Pfam profil	---	AT3G01410	1.03	0.04	0.33	0.753958	0.863429	-7.29
249657_at	sen1-like protein SEN1 - Saccharomy	---	AT5G37140	-1.02	-0.03	-0.33	0.75404	0.86348	-7.29
248715_at	ATFP4, putative	---	AT5G48290	1.04	0.05	0.33	0.754139	0.86355	-7.29
247090_at	putative protein similar to unknown pro	---	AT5G66370	-1.03	-0.04	-0.33	0.754223	0.86358	-7.29
266378_at	hypothetical protein predicted by gene	---	AT2G14700	1.03	0.05	0.33	0.754241	0.86358	-7.29
261204_s_	Eukaryotic peptide chain release facto	ERF1-2	AT1G12920 /	1.02	0.03	0.33	0.754303	0.863607	-7.29
265723_at	putative disease resistance protein	---	AT2G32140	-1.02	-0.03	-0.33	0.754382	0.863647	-7.29
252021_at	putative protein predicted protein, Ara	---	AT3G53070	-1.03	-0.04	-0.33	0.754413	0.863647	-7.29
263323_at	putative receptor-like protein kinase	---	AT2G04300	1.03	0.04	0.33	0.75452	0.863682	-7.29
249675_at	putative protein myrosinase-binding pr	---	AT5G35940	1.02	0.03	0.33	0.754515	0.863682	-7.29
266759_at	unknown protein predicted by genefinc	---	AT2G46915	-1.03	-0.04	-0.33	0.754576	0.863704	-7.29
261278_at	hypothetical protein predicted by gene	DGL	AT1G05800	-1.02	-0.03	-0.33	0.754629	0.863721	-7.29
248441_at	putative protein contains similarity to re	---	AT5G51270	-1.02	-0.03	-0.33	0.754919	0.86401	-7.29
250204_at	leucine zipper protein-like	ATEXO70C2	AT5G13990	-1.03	-0.04	-0.33	0.755007	0.864066	-7.29
263145_at	hypothetical protein predicted by gene	ATEXO70D2	AT1G54090	-1.04	-0.05	-0.32	0.755087	0.864114	-7.29
257028_at	hypothetical protein predicted by gene	---	AT3G19230	-1.05	-0.07	-0.32	0.75526	0.864126	-7.29
248561_at	unknown protein	---	AT5G49680	-1.04	-0.05	-0.32	0.755323	0.864126	-7.29
249852_at	monosaccharide transporter	STP11	AT5G23270	1.03	0.04	0.32	0.755183	0.864126	-7.29
249323_at	unknown protein	FLA20	AT5G40940	1.03	0.04	0.32	0.755324	0.864126	-7.29
250699_at	receptor-like protein kinase	SRF2	AT5G06820	-1.03	-0.04	-0.32	0.755287	0.864126	-7.29
260130_s_	beta-glucosidase, putative similar to G	BGLU21	AT1G66270 /	1.02	0.03	0.32	0.755206	0.864126	-7.29
256921_at	unknown protein ;supported by full-ler	---	AT3G18940	-1.03	-0.04	-0.32	0.755403	0.864143	-7.29
251364_at	anthranilate phosphoribosyltransferas	---	AT3G61300	-1.03	-0.04	-0.32	0.755453	0.864143	-7.29
256135_at	hypothetical protein predicted by gene	---	AT1G48730	-1.03	-0.04	-0.32	0.755415	0.864143	-7.29
267507_at	putative ribosomal protein S27 ;suppo	---	AT2G45710	1.04	0.06	0.32	0.755519	0.864176	-7.29
248993_at	putative protein contains similarity to d	---	AT5G45240	1.03	0.04	0.32	0.755568	0.864189	-7.29
255703_at	putative chalcone synthase similar to p	---	AT4G00040	-1.04	-0.06	-0.32	0.755662	0.864191	-7.29
248588_at	unknown protein ; supported by cDNA	---	AT5G49540	-1.02	-0.03	-0.32	0.755671	0.864191	-7.29
245461_at	hypothetical protein	---	AT4G17000	-1.03	-0.04	-0.32	0.755684	0.864191	-7.29
260768_at	Expressed protein ; supported by full-le	---	AT1G49245	-1.03	-0.04	-0.32	0.755751	0.864219	-7.29
257438_at	hypothetical protein similarity to plant l	---	AT2G15325	-1.02	-0.03	-0.32	0.755784	0.864219	-7.29

263691_at	60s ribosomal protein L34 identical to	---	AT1G26880	1.05	0.07	0.32	0.755827	0.864225	-7.29
257360_at	unknown protein	---	AT2G39240	-1.02	-0.03	-0.32	0.755944	0.864242	-7.29
249098_at	DNA repair protein-like	---	AT5G43530	-1.02	-0.03	-0.32	0.755888	0.864242	-7.29
263441_at	putative kinesin-like spindle protein	---	AT2G28620	-1.02	-0.03	-0.32	0.755956	0.864242	-7.29
253894_at	NWMU2 - 2S albumin 2 precursor	---	AT4G27150	-1.02	-0.03	-0.32	0.756004	0.864254	-7.30
257777_x_	hypothetical protein	---	---	1.03	0.04	0.32	0.75629	0.864537	-7.30
245438_at	growth regulator like protein	---	AT4G16650	1.03	0.04	0.32	0.756468	0.864654	-7.30
254319_at	putative protein predicted proteins, Ar	---	AT4G22560	-1.04	-0.05	-0.32	0.756462	0.864654	-7.30
246507_at	lipase-like protein monoglyceride lipas	---	AT5G16120	1.04	0.06	0.32	0.756559	0.864714	-7.30
250295_at	putative protein	NEF1	AT5G13390	1.03	0.04	0.32	0.756659	0.864786	-7.30
255425_s_	putative protein	---	AT4G02950 /	1.03	0.04	0.32	0.757012	0.865145	-7.30
253689_at	hypothetical protein ;supported by full-	---	AT4G29770	-1.03	-0.04	-0.32	0.757216	0.865336	-7.30
264538_at	hypothetical protein predicted by gene	WRKY10	AT1G55600	-1.03	-0.04	-0.32	0.75744	0.865462	-7.30
264116_at	putative poly (ADP-ribose) polymerase	PARP2	AT2G31320	-1.05	-0.07	-0.32	0.757427	0.865462	-7.30
246578_at	MADS-box protein, putative similar to	AGL86	AT1G31630	1.02	0.03	0.32	0.757435	0.865462	-7.30
246432_at	RGA-like protein putative member of t	RGL3	AT5G17490	-1.05	-0.07	-0.32	0.757565	0.865517	-7.30
AFFX-BioD	E. coli /GEN=bioD /DB_XREF=gb:J04	---	---	-1.06	-0.09	-0.32	0.757626	0.865517	-7.30
267551_at	ubiquitin-specific protease 1 (UBP1),	UBP1	AT2G32780	-1.03	-0.04	-0.32	0.757549	0.865517	-7.30
252598_at	putative protein putative proteins AT4	---	---	-1.02	-0.03	-0.32	0.757641	0.865517	-7.30
266644_at	unknown protein ;supported by full-ler	---	AT2G29660	1.03	0.05	0.32	0.757686	0.865526	-7.30
247749_at	myb-related protein - like myb-related	MYB119	AT5G58850	-1.03	-0.05	-0.32	0.757749	0.865553	-7.30
262192_at	hypothetical protein predicted by gene	---	AT1G77830	1.02	0.03	0.32	0.757786	0.865553	-7.30
250982_at	putative protein zinc finger protein, Ar	JKD	AT5G03150	1.05	0.06	0.32	0.757915	0.865657	-7.30
253426_at	putative protein polygalacturonase (E	---	AT4G32375	1.02	0.03	0.32	0.758308	0.866063	-7.30
266348_at	putative MAP kinase	ATMPK17	AT2G01450	-1.03	-0.05	-0.32	0.758672	0.866069	-7.30
255394_at	hypothetical protein similar to A. thalia	---	---	-1.03	-0.04	-0.32	0.758604	0.866069	-7.30
258136_at	hypothetical protein predicted by gene	RSY3	AT3G24560	1.03	0.04	0.32	0.758731	0.866069	-7.30
258642_at	unknown protein ;supported by full-ler	---	AT3G07910	1.02	0.03	0.32	0.758679	0.866069	-7.30
265614_at	Expressed protein ; supported by cDN	---	AT2G25355	1.03	0.05	0.32	0.758447	0.866069	-7.30
256273_at	senescence-assocated protein, putati	TET6	AT3G12090	1.03	0.04	0.32	0.758711	0.866069	-7.30
252514_at	GTP-binding protein ara-3 ; supported	ATRAB8A	AT3G46060	1.02	0.03	0.32	0.75846	0.866069	-7.30
254336_at	aspartic proteinase like protein oryzas	---	AT4G22050	-1.03	-0.05	-0.32	0.758495	0.866069	-7.30
257710_at	unknown protein ;supported by full-ler	---	AT3G27350	-1.03	-0.04	-0.32	0.758691	0.866069	-7.30
257285_at	unknown protein	---	AT3G29760	-1.04	-0.05	-0.32	0.758679	0.866069	-7.30
248661_at	putative protein contains similarity to M	AGL80	AT5G48670	1.04	0.06	0.32	0.758426	0.866069	-7.30

265313_at	unknown protein	---	AT2G20210	1.03	0.04	0.32	0.758873	0.866101	-7.30
254558_at	Expressed protein ; supported by full-l	---	AT4G19185	-1.02	-0.03	-0.32	0.758835	0.866101	-7.30
250601_at	putative protein contains similarity to H	---	AT5G07810	1.02	0.03	0.32	0.758859	0.866101	-7.30
267031_at	hypothetical protein predicted by gens	---	AT2G38420	-1.02	-0.03	-0.32	0.75899	0.866148	-7.30
251081_at	putative protein kinase wall-associate	---	AT5G02070	1.03	0.05	0.32	0.758985	0.866148	-7.30
260280_at	unknown protein contains AP2 DNA-bi	---	AT1G80580	1.04	0.06	0.32	0.75918	0.866321	-7.30
260866_at	polyprotein, putative similar to polypro	---	---	-1.03	-0.04	-0.32	0.759264	0.866374	-7.30
248232_at	putative protein contains similarity to s	MLO11	AT5G53760	-1.03	-0.05	-0.32	0.759364	0.866444	-7.30
245732_at	unknown protein contains similarity to	---	AT1G73440	-1.02	-0.04	-0.32	0.759461	0.866454	-7.30
261687_at	hypothetical protein predicted by gene	---	AT1G47280	-1.02	-0.03	-0.32	0.759421	0.866454	-7.30
258014_at	hypothetical protein predicted by gene	---	AT3G19330	-1.04	-0.05	-0.32	0.759486	0.866454	-7.30
266577_at	predicted protein	---	AT2G23945	-1.03	-0.04	-0.32	0.759719	0.866669	-7.30
254489_at	putative protein berberine bridge enzy	---	AT4G20800	1.02	0.03	0.32	0.75975	0.866669	-7.30
247828_at	putative protein KIAA0066, Homo sap	---	AT5G58510	-1.02	-0.03	-0.32	0.759843	0.86673	-7.30
250388_at	putative protein various predicted prot	---	AT5G11310	1.06	0.08	0.32	0.759997	0.866774	-7.30
263124_at	beta-Amyrin Synthase, putative simila	---	AT1G78480	1.03	0.05	0.32	0.760042	0.866774	-7.30
248592_at	unknown protein ;supported by full-ler	---	AT5G49280	-1.07	-0.09	-0.32	0.759931	0.866774	-7.30
255335_at	putative transposon protein	---	---	-1.03	-0.04	-0.32	0.760071	0.866774	-7.30
249902_at	unknown protein	---	AT5G22680	-1.04	-0.05	-0.32	0.759985	0.866774	-7.30
247343_at	unknown protein	---	AT5G63740	1.02	0.03	0.32	0.760178	0.866853	-7.30
256998_at	hypothetical protein predicted by gene	---	AT3G14180	-1.03	-0.05	-0.32	0.760402	0.866875	-7.30
264557_at	putative pectinacetylesterase precurs	---	AT1G09550	-1.04	-0.05	-0.32	0.760487	0.866875	-7.30
251681_at	putative protein hypothetical protein F	---	AT3G57100	-1.03	-0.04	-0.32	0.760429	0.866875	-7.30
254786_at	putative protein gamma-interferon-ind	---	AT4G12890	-1.03	-0.04	-0.32	0.760335	0.866875	-7.30
267198_at	putative gibberellin-regulated protein	---	AT2G30810	-1.02	-0.03	-0.32	0.760265	0.866875	-7.30
254450_at	putative protein prolamin box binding	---	AT4G21080	1.03	0.04	0.32	0.760395	0.866875	-7.30
259565_at	hypothetical protein	---	AT1G20530	-1.02	-0.03	-0.32	0.760497	0.866875	-7.30
251390_at	guanine nucleotide exchange factor -	---	AT3G60860	-1.03	-0.04	-0.32	0.760501	0.866875	-7.30
262964_at	hypothetical protein predicted by gene	---	AT1G54380	1.04	0.06	0.32	0.760705	0.866977	-7.30
248949_at	putative protein strong similarity to unk	---	AT5G45570	1.02	0.03	0.32	0.760633	0.866977	-7.30
251709_at	response regulator-like protein respon	ARR17	AT3G56380	-1.02	-0.03	-0.32	0.76068	0.866977	-7.30
247772_at	putative protein various predicted prot	---	AT5G58610	1.03	0.04	0.32	0.760783	0.867022	-7.30
251911_at	putative C2H2-type zinc finger protein	---	AT3G53820	1.03	0.04	0.32	0.760867	0.867075	-7.30
246087_at	putative protein predicted protein, Ara	---	AT5G20580	-1.04	-0.06	-0.32	0.760917	0.867089	-7.30
263698_at	hypothetical protein similar to a multitu	---	---	1.03	0.05	0.32	0.761011	0.867109	-7.30

246986_at	receptor-like protein kinase ;supporte	RLK	AT5G67280	1.08	0.11	0.32	0.760997	0.867109	-7.30
253589_at	puative protein membrane-associated	---	AT4G30825	-1.04	-0.05	-0.32	0.761126	0.86711	-7.30
246853_at	putative protein	---	AT5G26890	-1.02	-0.03	-0.32	0.761114	0.86711	-7.30
248772_at	photoreceptor-interacting protein-like	---	AT5G47800	-1.06	-0.08	-0.32	0.76111	0.86711	-7.30
261337_at	unknown protein ; supported by cDNA	---	AT1G44810	-1.05	-0.07	-0.32	0.761262	0.867207	-7.30
246477_at	putative transcription factor (MYB9)	AtMYB9	AT5G16770	-1.05	-0.06	-0.32	0.761287	0.867207	-7.30
253160_at	putative protein predicted protein, Syn	---	AT4G35760	-1.04	-0.06	-0.32	0.761478	0.867338	-7.30
253298_at	putative protein ;supported by full-leng	---	AT4G33560	-1.03	-0.04	-0.32	0.761472	0.867338	-7.30
246063_at	putative protein predicted proteins, Ar	---	AT5G19340	1.02	0.03	0.32	0.76152	0.867343	-7.30
249564_at	unknown protein	---	AT5G38400	-1.03	-0.04	-0.32	0.761717	0.867481	-7.30
264034_s_	unknown protein	ATUPS1	AT2G03590 /	-1.02	-0.03	-0.32	0.761687	0.867481	-7.30
245106_at	unknown protein	---	AT2G41650	-1.03	-0.04	-0.32	0.761786	0.867516	-7.30
263269_at	En/Spm-like transposon protein relate	---	---	-1.02	-0.03	-0.32	0.761906	0.867609	-7.30
261816_at	unknown protein	CHX6B	AT1G08135	-1.02	-0.03	-0.32	0.761997	0.867626	-7.30
257877_at	hypothetical protein	---	AT3G17140	-1.03	-0.04	-0.32	0.761984	0.867626	-7.30
247528_at	MIM protein ; supported by cDNA: gi_	MIM	AT5G61460	-1.03	-0.04	-0.32	0.762059	0.867653	-7.30
259632_at	nicotianamine synathase, putative sim	NAS4	AT1G56430	-1.07	-0.09	-0.32	0.762148	0.867711	-7.30
256577_at	unknown protein	---	AT3G28220	-1.10	-0.14	-0.32	0.762222	0.867715	-7.30
266738_at	unknown protein predicted by genefinc	---	AT2G47010	-1.04	-0.05	-0.32	0.762231	0.867715	-7.30
265919_at	putative retroelement pol polyprotein	---	---	-1.03	-0.04	-0.32	0.762265	0.867715	-7.30
265579_at	hypothetical protein predicted by gens	---	AT2G20070	1.02	0.03	0.31	0.76251	0.86795	-7.30
247953_at	cytochrome P450	CYP71B10	AT5G57260	-1.02	-0.03	-0.31	0.762596	0.868004	-7.30
264499_at	Expressed protein ; supported by full-l	---	AT1G30795	-1.03	-0.04	-0.31	0.762638	0.868009	-7.30
254358_at	putative protein light induced protein h	---	AT4G22310	-1.02	-0.03	-0.31	0.76273	0.868071	-7.30
257564_at	unknown protein	---	AT3G28610	-1.04	-0.05	-0.31	0.762963	0.868292	-7.30
247309_at	putative protein contains similarity to p	---	AT5G63940	1.04	0.05	0.31	0.763092	0.868396	-7.30
247894_at	putative protein similar to unknown pro	CPL4	AT5G58000 /	1.04	0.06	0.31	0.76329	0.868535	-7.30
249661_x_	putative protein similar to unknown pro	---	---	-1.03	-0.04	-0.31	0.763287	0.868535	-7.30
254441_at	prolamin box binding protein - like PB	---	AT4G21050	-1.02	-0.03	-0.31	0.76333	0.868537	-7.30
261775_at	hypothetical protein predicted by gene	---	AT1G76280	1.03	0.04	0.31	0.76346	0.868641	-7.30
259176_at	putative cell division control protein si	CDC48C	AT3G01610	1.03	0.04	0.31	0.763642	0.868805	-7.30
265745_at	hypothetical protein predicted by gens	---	---	-1.02	-0.03	-0.31	0.763706	0.868835	-7.30
260354_at	unknown protein ;supported by full-ler	---	AT1G69330	-1.04	-0.05	-0.31	0.764349	0.869522	-7.30
264492_at	unknown protein similar to unknown p	---	AT1G27430	-1.02	-0.03	-0.31	0.764495	0.869645	-7.30
265651_at	hypothetical protein predicted by gens	---	AT2G13900	-1.02	-0.03	-0.31	0.764696	0.869776	-7.30

252642_at	putative protein predicted protein, Ara	---	AT3G44580	1.02	0.03	0.31	0.764695	0.869776	-7.30
265406_at	En/Spm-like transposon protein relatec	---	---	1.02	0.03	0.31	0.764724	0.869776	-7.30
253004_at	putative protein	---	AT4G38280 /	1.04	0.05	0.31	0.764901	0.869783	-7.30
253788_at	aromatic amino-acid decarboxylase -	---	AT4G28680	1.03	0.04	0.31	0.764789	0.869783	-7.30
255329_at	hypothetical protein	---	AT4G04370	1.02	0.03	0.31	0.764921	0.869783	-7.30
250612_s_	putative protein ARR2 protein - Arabic	ARR13	AT2G27070 /	-1.03	-0.05	-0.31	0.764824	0.869783	-7.30
259869_at	putative heat shock protein predicted b	---	AT1G76770	1.03	0.04	0.31	0.764852	0.869783	-7.30
264722_at	unknown protein location of EST emb|	---	AT1G22970	1.03	0.05	0.31	0.765207	0.87002	-7.30
251426_at	URIDYLATE KINASE-like protein URI	---	AT3G60180	-1.03	-0.04	-0.31	0.765244	0.87002	-7.30
254449_at	putative protein predicted protein, Cae	HEN1	AT4G20910	-1.03	-0.05	-0.31	0.765225	0.87002	-7.30
259728_at	putative coatomer zeta subunit similar	---	AT1G60970	1.02	0.03	0.31	0.765331	0.870076	-7.30
256752_at	hypothetical protein predicted by gene	---	AT3G27180	1.04	0.06	0.31	0.765437	0.87011	-7.30
254681_at	putative protein HYA22 protein, Homo	---	AT4G18140	1.04	0.06	0.31	0.765422	0.87011	-7.30
258367_at	putative protein kinase similar to protei	WAG2	AT3G14370	1.03	0.04	0.31	0.765523	0.870164	-7.30
251126_at	putative protein various predicted prot	---	AT5G01070	-1.02	-0.03	-0.31	0.765609	0.870219	-7.30
262880_at	hypothetical protein contains similarity	---	AT1G64880	1.06	0.09	0.31	0.765704	0.87024	-7.30
251401_at	stellacyanin (uclacyanin 3) - like prote	---	AT3G60270	-1.03	-0.05	-0.31	0.765697	0.87024	-7.30
258780_at	putative ubiquitin carboxyl-terminal hyc	UBP13	AT3G11910	1.02	0.03	0.31	0.765798	0.870303	-7.30
258936_s_	hypothetical protein similar to hypothe	---	---	-1.02	-0.03	-0.31	0.765947	0.870349	-7.30
254182_at	putative protein various npredicted pro	---	AT4G23950	1.03	0.04	0.31	0.765988	0.870349	-7.30
255463_at	putative polyprotein of LTR transposo	---	---	-1.03	-0.04	-0.31	0.766025	0.870349	-7.30
256260_at	hypothetical protein	---	AT3G12440	-1.02	-0.03	-0.31	0.765949	0.870349	-7.30
264759_at	receptor protein kinase (IRK1), putativ	---	AT1G61480	-1.03	-0.04	-0.31	0.766037	0.870349	-7.30
258337_at	hypothetical protein predicted by gene	---	AT3G16040	-1.04	-0.05	-0.31	0.766068	0.870349	-7.30
261932_at	hypothetical protein predicted by gene	---	AT1G22420	1.02	0.03	0.31	0.766306	0.870533	-7.30
247135_at	auxin-induced protein-like	---	AT5G66260	1.02	0.03	0.31	0.766285	0.870533	-7.30
263586_at	unknown protein predicted by genscan	---	AT2G25350	-1.03	-0.05	-0.31	0.766419	0.870618	-7.30
258905_at	unknown protein similar to hypothetica	---	AT3G06390	-1.04	-0.06	-0.31	0.766537	0.87068	-7.30
266334_at	hypothetical protein predicted by gene	---	AT2G32380	-1.04	-0.06	-0.31	0.76655	0.87068	-7.30
259919_at	putative exportin, tRNA (nuclear expo	PSD	AT1G72560	1.03	0.05	0.31	0.766659	0.870761	-7.30
253265_at	putative protein RING-finger protein, L	---	AT4G34040	-1.02	-0.03	-0.31	0.766714	0.87078	-7.30
261227_at	proteasome regulatory subunit S3, pu	EMB2719	AT1G20200	1.02	0.03	0.31	0.766769	0.870799	-7.30
255557_at	hypothetical protein ; supported by cD	---	AT4G01990	1.04	0.06	0.31	0.766886	0.870841	-7.30
264174_s_	hypothetical protein	ANAC004	AT1G02230	1.04	0.05	0.31	0.76692	0.870841	-7.30
252992_at	putative protein phosphatase-2c prote	---	AT4G38520	-1.04	-0.05	-0.31	0.766873	0.870841	-7.30

251053_at	Ca2+/H+ exchanger-like protein Ca2+	CAX4	AT5G01490	-1.05	-0.07	-0.31	0.766961	0.870844	-7.30
246904_at	DNA methyltransferase PMT1 - like pr	DNMT2	AT5G25480	-1.03	-0.04	-0.31	0.767199	0.87095	-7.30
253366_at	putative protein predicted protein, Ara	---	AT4G33180	1.03	0.05	0.31	0.767331	0.87095	-7.30
260450_at	hypothetical protein predicted by gens	---	AT1G72390	-1.04	-0.05	-0.31	0.767222	0.87095	-7.30
266107_at	hypothetical protein predicted by gens	---	AT2G37910	-1.04	-0.05	-0.31	0.76727	0.87095	-7.30
245883_at	ribosomal protein S15-like ribosomal p	---	AT5G09500	-1.02	-0.03	-0.31	0.767358	0.87095	-7.30
257971_at	unknown protein similar to hypothetica	GC6	AT3G27530	-1.04	-0.06	-0.31	0.76736	0.87095	-7.30
247750_at	protein kinase 6 - like protein kinase 6	---	AT5G58950	1.03	0.04	0.31	0.767246	0.87095	-7.30
266063_at	putative SNF2/RAD54 family DNA rep	CHR8	AT2G18760	1.03	0.04	0.31	0.767216	0.87095	-7.30
253675_at	hypothetical protein	---	AT4G29560	1.02	0.03	0.31	0.767476	0.871039	-7.30
263487_at	hypothetical protein predicted by gene	---	AT2G31850	1.02	0.03	0.31	0.767565	0.871096	-7.30
249669_at	putative protein similar to unknown pro	---	---	-1.02	-0.03	-0.31	0.767605	0.871098	-7.30
248697_at	putative protein contains similarity to a	---	AT5G48370	-1.05	-0.07	-0.31	0.767679	0.871138	-7.30
260725_at	Expressed protein ; supported by full-l	---	AT1G48170	-1.03	-0.04	-0.31	0.767765	0.871193	-7.30
248786_at	unknown protein	---	AT5G47410	-1.04	-0.06	-0.31	0.767827	0.87122	-7.30
246765_at	glutamic acid-rich protein hypothetical	---	AT5G27330	1.03	0.04	0.31	0.768041	0.871419	-7.30
258598_at	hypothetical protein predicted by gens	---	AT3G04410	1.03	0.05	0.31	0.768165	0.871517	-7.30
245181_at	putative protein similarity to various pr	---	AT5G12420	1.07	0.10	0.31	0.768283	0.871607	-7.30
247650_at	putative protein ;supported by full-leng	---	AT5G59960	1.04	0.06	0.31	0.768418	0.871717	-7.30
250607_at	putative protein mammalian inositol h	IPK2a	AT5G07370	-1.02	-0.03	-0.31	0.768573	0.871769	-7.30
260735_at	disease resistance protein, putative si	---	AT1G17610	1.05	0.07	0.31	0.768553	0.871769	-7.30
263141_at	hypothetical protein similar to unknow	---	AT1G65210	1.02	0.03	0.31	0.768578	0.871769	-7.30
257538_at	hypothetical protein predicted by gene	---	AT3G16160	1.02	0.03	0.31	0.768649	0.871805	-7.30
249786_at	putative protein strong similarity to unk	ABIL3	AT5G24310	-1.05	-0.07	-0.31	0.768772	0.871859	-7.30
261711_at	unknown protein similar to hypothetica	---	AT1G32700	1.03	0.04	0.31	0.76877	0.871859	-7.30
246655_at	hypothetical protein	---	AT5G35230	-1.02	-0.03	-0.31	0.768864	0.87192	-7.30
247846_at	putative protein	---	AT5G58100	-1.02	-0.04	-0.31	0.769061	0.872099	-7.30
260836_at	hypothetical protein predicted by gens	---	---	-1.02	-0.03	-0.31	0.769129	0.872133	-7.30
258592_at	hypothetical protein contains Pfam pro	---	AT3G04130	-1.03	-0.04	-0.30	0.769585	0.872607	-7.30
266242_at	hypothetical protein predicted by gens	---	AT2G27790	-1.02	-0.03	-0.30	0.769671	0.872651	-7.30
252801_at	putative protein various predicted Heli	---	---	1.02	0.03	0.30	0.769735	0.872651	-7.30
246648_at	putative protein predicted proteins fron	---	---	1.02	0.03	0.30	0.769739	0.872651	-7.30
258237_at	myb protein identical to ATMYB3 GB:E	ATMYB21	AT3G27810	1.02	0.03	0.30	0.769855	0.87274	-7.30
249976_at	Serine/arginine rich protein - like Serir	SCL28	AT5G18810	1.03	0.04	0.30	0.770027	0.872891	-7.30
252526_at	putative protein ethylene-forming enzy	---	AT3G46480	1.03	0.04	0.30	0.770267	0.87312	-7.30

267068_at	unknown protein	---	AT2G41020	-1.03	-0.04	-0.30	0.770415	0.873177	-7.30
266531_at	putative plasma membrane intrinsic p	---	AT2G16835	1.02	0.03	0.30	0.770534	0.873177	-7.30
262621_at	hypothetical protein	---	AT1G06530	-1.02	-0.03	-0.30	0.770434	0.873177	-7.30
263103_at	putative Ta11-like non-LTR retroeleme	---	---	1.02	0.04	0.30	0.770498	0.873177	-7.30
260524_at	unknown protein	---	AT2G47230	1.02	0.03	0.30	0.770413	0.873177	-7.30
261662_at	MAP kinase kinase 5, putative similar	ATMKK7	AT1G18350	-1.02	-0.03	-0.30	0.770547	0.873177	-7.30
256440_at	unknown protein ;supported by full-ler	---	AT3G10970	1.02	0.03	0.30	0.770687	0.873292	-7.30
251286_at	putative protein Bcl-2-interacting prote	---	AT3G61710	-1.02	-0.03	-0.30	0.770834	0.873408	-7.30
256610_at	hypothetical protein predicted by gene	---	AT3G30845	-1.02	-0.03	-0.30	0.770866	0.873408	-7.30
259490_at	hypothetical protein preedicted by gen	---	AT1G15800	1.02	0.03	0.30	0.771016	0.873491	-7.30
264993_at	glyoxal oxidase (glx1), putative similar	---	AT1G67290	1.04	0.06	0.30	0.770982	0.873491	-7.30
257779_at	protein kinase, putative similar to PRC	CDG1	AT3G26940	1.02	0.03	0.30	0.771157	0.873494	-7.30
267447_at	putative GTP-binding protein	ArRABA1h	AT2G33870	-1.02	-0.03	-0.30	0.771171	0.873494	-7.30
255645_at	coded for by A. thaliana cDNA T43845	---	AT4G00880	-1.04	-0.06	-0.30	0.771129	0.873494	-7.30
246658_at	putative protein predicted proteins, Ar	---	---	1.02	0.03	0.30	0.771114	0.873494	-7.30
255215_at	putative athila transposon protein	---	---	-1.02	-0.03	-0.30	0.77126	0.873551	-7.30
265276_at	hypothetical protein predicted by gens	---	AT2G28400	-1.04	-0.06	-0.30	0.771448	0.873673	-7.30
264681_s_	permease 1-like protein permease 1 -	---	AT1G65550 /	1.03	0.04	0.30	0.771459	0.873673	-7.30
252049_at	putative protein putative and hypotheti	---	AT3G52510	-1.02	-0.03	-0.30	0.771482	0.873673	-7.30
263555_at	unknown protein ;supported by full-ler	---	AT2G16460	1.02	0.03	0.30	0.771587	0.873748	-7.30
267096_at	unknown protein ; supported by cDNA	---	AT2G38180	-1.05	-0.07	-0.30	0.771683	0.873813	-7.30
267543_at	26S proteasome regulatory subunit	---	AT2G32730	1.02	0.03	0.30	0.771866	0.873934	-7.30
247510_at	putative protein predicted proteins, D.	---	AT5G62030	-1.03	-0.04	-0.30	0.771842	0.873934	-7.30
256608_at	hypothetical protein predicted by gene	---	AT3G30840	-1.02	-0.03	-0.30	0.77219	0.874257	-7.30
267477_at	putative receptor-like protein kinase	PLPB	AT2G02710	1.05	0.07	0.30	0.772511	0.874558	-7.30
250597_at	NAM (no apical meristem)-like protein	ANAC080	AT5G07680	1.05	0.07	0.30	0.772533	0.874558	-7.30
258488_at	unknown protein ;supported by full-ler	---	AT3G02420	-1.03	-0.04	-0.30	0.772685	0.874688	-7.30
252793_at	hypothetical protein	---	---	1.02	0.03	0.30	0.772728	0.874692	-7.30
254395_at	subtilisin-like protease subtilisin-like p	---	AT4G21640	-1.02	-0.03	-0.30	0.773039	0.875001	-7.30
246491_at	hypothetical protein	---	AT5G16100	-1.02	-0.03	-0.30	0.773373	0.875336	-7.30
254750_at	putative protein	---	AT4G13150	-1.03	-0.04	-0.30	0.77352	0.875419	-7.30
251327_at	prolyl aminopeptidase-like protein pro	---	AT3G61540	1.02	0.03	0.30	0.773523	0.875419	-7.30
257447_at	hypothetical protein predicted by gens	---	AT2G04230	1.02	0.03	0.30	0.77368	0.875553	-7.30
248024_at	putative protein contains similarity to s	---	AT5G55840	-1.03	-0.04	-0.30	0.773769	0.875566	-7.30
260114_at	AIG1-like protein similar to AIG1 prote	---	AT1G33880	1.02	0.03	0.30	0.773745	0.875566	-7.30

246980_at	peptidylprolyl isomerase (cyclophilin)-li	---	AT5G67530	-1.02	-0.03	-0.30	0.773872	0.875621	-7.30
267183_at	hypothetical protein predicted by gens	---	AT2G44020	1.02	0.03	0.30	0.773946	0.875621	-7.30
251027_at	putative protein hypothetical protein F	---	AT5G02210	-1.02	-0.03	-0.30	0.773971	0.875621	-7.30
263316_s_	putative ligand-gated ion channel prote	ATGLR2.3	AT2G24710 /	1.02	0.03	0.30	0.773899	0.875621	-7.30
260250_at	putative phosphoribosylformylglycinam	PUR4	AT1G74260	1.03	0.04	0.30	0.774034	0.875649	-7.30
262031_x_	hypothetical protein similar to putative	---	---	1.02	0.03	0.30	0.774087	0.875665	-7.30
256151_at	multispanning membrane protein, puta	---	AT1G55130	-1.03	-0.05	-0.30	0.774211	0.875676	-7.30
247045_at	putative protein similar to unknown pro	---	AT5G66930	1.03	0.04	0.30	0.774183	0.875676	-7.30
246728_at	putative protein various predicted prot	---	AT5G28040	-1.02	-0.03	-0.30	0.774144	0.875676	-7.30
260383_s_	putative 60S ribosomal protein L6 simi	---	AT1G74050 /	-1.03	-0.05	-0.30	0.774374	0.875817	-7.30
255227_at	D123 -like protein protein D123, Rattu	EDA35	AT4G05440	1.03	0.04	0.30	0.774543	0.875906	-7.30
262778_at	hypothetical protein predicted by gene	---	AT1G13050	-1.02	-0.03	-0.30	0.774498	0.875906	-7.30
253292_at	Expressed protein ; supported by full-le	---	AT4G33985	1.04	0.05	0.30	0.774568	0.875906	-7.30
250389_at	putative protein probable flavin-contai	YUC4	AT5G11320	1.02	0.03	0.30	0.774622	0.875924	-7.30
259668_at	hypothetical protein predicted by gene	---	AT1G52390	1.02	0.03	0.30	0.774664	0.875927	-7.30
252856_at	putative protein ; supported by cDNA:	---	AT4G39690	-1.02	-0.03	-0.30	0.77487	0.876117	-7.30
257386_at	hypothetical protein predicted by gens	---	AT2G42440	1.02	0.03	0.30	0.774993	0.876212	-7.30
261698_at	unknown protein identical to hypothetic	---	AT1G32630	1.03	0.04	0.30	0.775088	0.876256	-7.30
254371_at	beta-glucosidase -like protein beta-glu	BGLU47	AT4G21760	1.02	0.03	0.30	0.775147	0.876256	-7.30
253243_at	putative protein	---	AT4G34560	-1.10	-0.13	-0.30	0.775125	0.876256	-7.30
246361_s_	hypothetical protein	---	---	1.02	0.03	0.30	0.775218	0.876294	-7.30
257587_at	3'-5' exonuclease, putative contains P	---	AT1G56310	-1.02	-0.03	-0.30	0.775317	0.876361	-7.30
262339_at	WRKY DNA binding protein, putative	WRKY56	AT1G64000	-1.02	-0.03	-0.30	0.775362	0.87637	-7.30
259016_at	unknown protein HMM hit: 2Fe-2S iron	---	AT3G07480	1.03	0.04	0.30	0.775624	0.876622	-7.30
245105_at	hypothetical protein predicted by gens	---	AT2G41610	-1.04	-0.06	-0.30	0.77573	0.876699	-7.30
250247_at	unknown protein	---	AT5G13720	-1.02	-0.03	-0.30	0.775989	0.876934	-7.30
254488_at	putative protein receptor-like protein k	---	AT4G20790	1.02	0.03	0.30	0.776084	0.876934	-7.30
253375_at	hypothetical protein	---	AT4G33280	1.02	0.03	0.30	0.776092	0.876934	-7.30
251903_at	putative protein 24 kDa seed maturati	---	AT3G54120	-1.06	-0.08	-0.30	0.776073	0.876934	-7.30
265164_at	putative OBP32pep protein	---	AT1G23600	-1.02	-0.03	-0.30	0.776185	0.876995	-7.30
253368_at	myosin - like protein unconventional m	XI-I	AT4G33200	-1.02	-0.03	-0.30	0.776309	0.877005	-7.30
250387_at	putative protein predicted proteins, Ar	---	AT5G11290	-1.02	-0.03	-0.30	0.776254	0.877005	-7.30
254462_at	putative protein ;supported by full-leng	---	AT4G20150	1.02	0.03	0.30	0.776304	0.877005	-7.30
260495_at	unknown protein similar to T11A07.10	---	AT2G41810	1.03	0.05	0.30	0.776415	0.877081	-7.30
262214_at	germin subunit, putative similar to ger	---	AT1G74820	-1.02	-0.03	-0.30	0.776564	0.877206	-7.30

252583_at	putative protein several hypothetical pr	---	AT3G45540	1.02	0.03	0.30	0.776662	0.877273	-7.30
263554_at	putative Ta11-like non-LTR retroeleme	---	---	-1.04	-0.06	-0.30	0.776748	0.877301	-7.30
261679_at	polyprotein, putative similar to polypro	---	---	-1.02	-0.03	-0.30	0.776763	0.877301	-7.30
266529_at	putative salt-inducible protein	---	AT2G16880	-1.03	-0.04	-0.29	0.777054	0.877586	-7.31
267510_at	unknown protein ; supported by full-le	SAP18	AT2G45640	1.03	0.05	0.29	0.777112	0.877608	-7.31
267386_at	unknown protein	---	AT2G44430	1.04	0.05	0.29	0.777163	0.877622	-7.31
263017_at	putative cyclin 2	CYCB2;1	AT2G17620	-1.02	-0.03	-0.29	0.777317	0.877752	-7.31
262650_at	lipoamide dehydrogenase, putative	---	AT1G14090	1.02	0.02	0.29	0.777614	0.878044	-7.31
250460_at	putative protein similar to unknown pro	---	AT5G09850	-1.02	-0.03	-0.29	0.777667	0.878059	-7.31
260437_at	hypothetical protein predicted by gens	---	AT1G68380	1.02	0.03	0.29	0.777725	0.878059	-7.31
246077_at	putative protein XNP-1, Caenorhabdit	CHR42	AT5G20420	-1.04	-0.05	-0.29	0.777742	0.878059	-7.31
253657_at	cadmium-transporting ATPase-like pr	HMA2	AT4G30110	1.06	0.09	0.29	0.778148	0.878225	-7.31
259039_at	unknown protein ;supported by full-ler	---	AT3G09250	-1.02	-0.03	-0.29	0.778055	0.878225	-7.31
267554_at	E2, ubiquitin-conjugating enzyme, put	---	AT2G32790	-1.03	-0.04	-0.29	0.778173	0.878225	-7.31
267058_at	putative protein kinase contains a prot	MAPKKK17	AT2G32510	1.04	0.05	0.29	0.778198	0.878225	-7.31
264544_s_	unknown protein	---	AT1G55790 /	-1.02	-0.03	-0.29	0.778162	0.878225	-7.31
266645_at	hypothetical protein	---	AT2G29880	1.02	0.03	0.29	0.778022	0.878225	-7.31
260611_at	putative beta-1,3-glucanase, C termin	---	AT2G43670	-1.03	-0.04	-0.29	0.778174	0.878225	-7.31
252493_at	hypothetical protein	---	AT3G46750	1.03	0.04	0.29	0.778122	0.878225	-7.31
254187_at	putative protein hypothetical protein, S	---	AT4G23890	1.02	0.03	0.29	0.778377	0.878384	-7.31
253523_at	putative protein myosin heavy chain, r	---	AT4G31340	1.02	0.03	0.29	0.778553	0.878496	-7.31
245475_at	hypothetical protein	---	AT4G16080	-1.02	-0.03	-0.29	0.778548	0.878496	-7.31
260308_at	putative ABC transporter contains Pfar	ATTAP1	AT1G70610	1.05	0.07	0.29	0.77867	0.878584	-7.31
256497_at	ORF1, putative similar to ORF1 GI:45	ECS1	AT1G31580	1.05	0.07	0.29	0.778785	0.878584	-7.31
260891_at	cysteine protease contains similarity to	---	AT1G29080	-1.02	-0.04	-0.29	0.778769	0.878584	-7.31
264991_s_	putative protein hypothetical proteins -	---	AT1G67400 /	-1.04	-0.05	-0.29	0.778741	0.878584	-7.31
246166_at	putative protein	---	---	-1.02	-0.03	-0.29	0.779064	0.878725	-7.31
252455_at	putative protein various predicted prot	---	AT3G47140	1.02	0.03	0.29	0.779026	0.878725	-7.31
265813_at	putative NAM (no apical meristem)-lik	VND1	AT2G18060	1.02	0.03	0.29	0.779034	0.878725	-7.31
247165_at	transcription factor-like protein ; suppo	MYB68	AT5G65790	1.02	0.03	0.29	0.77896	0.878725	-7.31
248112_at	wax synthase-like protein	---	AT5G55350	-1.03	-0.04	-0.29	0.779325	0.878925	-7.31
256684_at	geranylgeranyl pyrophosphate syntha	---	AT3G32040	1.03	0.04	0.29	0.779357	0.878925	-7.31
263012_at	homeotic protein, putative similar to h	KNAT6	AT1G23380	1.02	0.03	0.29	0.779317	0.878925	-7.31
250729_at	ubiquitin activating enzyme 2 (UBA2) i	UBA 2	AT5G06460	1.02	0.03	0.29	0.779448	0.878941	-7.31
247663_at	putative protein predicted proteins, Ar	APUM18	AT5G60110	1.02	0.03	0.29	0.779415	0.878941	-7.31

257943_at	SKP1/ASK1 (At7), putative similar to S	ASK7	AT3G21840	1.03	0.04	0.29	0.779604	0.879073	-7.31
262336_at	hypothetical protein predicted be gene	TOM7-2	AT1G64220	1.02	0.03	0.29	0.779725	0.879122	-7.31
251898_at	floral homeotic protein APETALA3 (AP	AP3	AT3G54340	1.02	0.03	0.29	0.779697	0.879122	-7.31
264332_at	hypothetical protein predicted by gene	---	AT1G61920	1.02	0.03	0.29	0.779876	0.879237	-7.31
253986_at	putative protein predicted protein, Ara	---	AT4G26210	1.04	0.06	0.29	0.779904	0.879237	-7.31
261411_at	histone H2B identical to GB:CAA7315	HTB1	AT1G07790	1.04	0.05	0.29	0.780178	0.879416	-7.31
254057_at	putative protein ;supported by full-leng	---	AT4G25170	1.04	0.06	0.29	0.780156	0.879416	-7.31
248016_at	putative protein similar to unknown pro	---	AT5G56380	1.03	0.04	0.29	0.780146	0.879416	-7.31
247298_at	glucosidase II alpha subunit	RSW3	AT5G63840	-1.02	-0.03	-0.29	0.78038	0.879437	-7.31
256842_at	hypothetical protein predicted by gene	---	---	1.02	0.03	0.29	0.780329	0.879437	-7.31
256605_at	hypothetical protein predicted by gens	---	AT3G32940	1.03	0.04	0.29	0.780319	0.879437	-7.31
267122_at	putative acetone-cyanohydrin lyase	MES6	AT2G23550	-1.02	-0.03	-0.29	0.780389	0.879437	-7.31
258118_at	unknown protein	---	AT3G14710	1.03	0.04	0.29	0.78035	0.879437	-7.31
254973_at	putative retrotransposon Oryza austra	---	---	-1.03	-0.04	-0.29	0.780442	0.879453	-7.31
253236_at	putative protein ARI protein, Drosophi	ARI1	AT4G34370	-1.02	-0.03	-0.29	0.780547	0.879528	-7.31
247756_at	subtilisin-like serine protease contains	---	AT5G59100	1.02	0.03	0.29	0.780863	0.87984	-7.31
264740_at	unknown protein	---	AT1G62070	-1.02	-0.03	-0.29	0.780918	0.879859	-7.31
248707_at	putative protein similar to unknown pro	---	AT5G48550	-1.02	-0.04	-0.29	0.781041	0.879954	-7.31
255135_at	putative protein several hypothetical pr	---	---	1.02	0.03	0.29	0.781188	0.880075	-7.31
262371_at	putative glycosyl transferase contains	---	AT1G73160	-1.02	-0.03	-0.29	0.781265	0.880076	-7.31
267537_at	putative guanylate kinase ; supported	GK-1	AT2G41880	1.07	0.10	0.29	0.781239	0.880076	-7.31
263031_at	glucosyltransferase, putative similar to	ATCSLA10	AT1G24070	-1.11	-0.15	-0.29	0.781385	0.880124	-7.31
263266_at	hypothetical protein predicted by gens	---	AT2G16520	1.02	0.03	0.29	0.78135	0.880124	-7.31
263617_at	putative retroelement pol polyprotein	---	---	1.03	0.04	0.29	0.781533	0.880247	-7.31
248156_at	unknown protein	---	AT5G54410	-1.02	-0.03	-0.29	0.781588	0.880266	-7.31
262467_at	hypothetical protein similar to hypothet	FU	AT1G50240	-1.03	-0.04	-0.29	0.781699	0.880316	-7.31
251077_at	putative protein COP1-interacting prot	---	AT5G01980	-1.02	-0.03	-0.29	0.78171	0.880316	-7.31
255785_at	sulfate adenylyltransferase identical to	APS2	AT1G19920	-1.02	-0.03	-0.29	0.781776	0.880347	-7.31
266978_at	putative disease resistance response p	---	AT2G39430	1.02	0.03	0.29	0.781927	0.880473	-7.31
248856_at	putative protein similar to unknown pro	---	AT5G46620	-1.02	-0.03	-0.29	0.781978	0.880488	-7.31
247757_at	putative protein	---	AT5G59105 /	-1.02	-0.03	-0.29	0.782049	0.880524	-7.31
262264_at	Niemann-Pick C disease protein-like p	---	AT1G42470	1.06	0.09	0.29	0.782253	0.880624	-7.31
257307_at	myb-like transcription factor, putative	MYB121	AT3G30210	1.03	0.04	0.29	0.782212	0.880624	-7.31
252732_at	putative protein predicted proteins, Ar	---	---	-1.02	-0.03	-0.29	0.78224	0.880624	-7.31
260071_at	putative proline-rich protein precursor	ESP1	AT1G73840	-1.02	-0.03	-0.29	0.782386	0.880729	-7.31

256027_at	putative protein	---	AT1G34160	1.02	0.03	0.29	0.782497	0.880768	-7.31
251566_at	putative protein several hypothetical pr	---	AT3G58210	-1.02	-0.03	-0.29	0.782478	0.880768	-7.31
254766_at	putative protein predicted protein, Ara	TPS12	AT4G13280	1.02	0.03	0.29	0.7826	0.88084	-7.31
251408_at	palmitoyl-protein thioesterase precurs	---	AT3G60340	-1.03	-0.04	-0.29	0.782718	0.88093	-7.31
252682_at	putative protein AtOXA1, Arabidopsis	---	AT3G44370	-1.03	-0.04	-0.29	0.782846	0.88103	-7.31
255843_at	unknown protein	CPL3	AT2G33540	-1.02	-0.03	-0.29	0.783041	0.881206	-7.31
263848_at	putative reverse transcriptase	---	---	1.03	0.04	0.29	0.783094	0.881222	-7.31
259780_at	exonuclease, putative similar to GI:48	---	AT1G29630	1.02	0.03	0.29	0.783134	0.881224	-7.31
262068_at	splicing factor Prp8, putative similar to	SUS2	AT1G80070	1.03	0.05	0.29	0.783186	0.881238	-7.31
249350_at	MYB -like protein MYB22, Arabidopsis	MYB115	AT5G40360	-1.02	-0.03	-0.29	0.783274	0.881268	-7.31
258290_at	hypothetical protein predicted by gene	---	AT3G23460	-1.02	-0.03	-0.29	0.783289	0.881268	-7.31
267164_at	CER1-like protein may be involved in v	---	AT2G37700	1.02	0.03	0.29	0.783348	0.88129	-7.31
259594_at	unknown protein contains similarity to	---	AT1G28140	1.02	0.03	0.29	0.783455	0.881368	-7.31
260025_at	unknown protein ;supported by full-len	---	AT1G30070	-1.04	-0.05	-0.29	0.78368	0.881429	-7.31
266222_at	hypothetical protein predicted by gens	---	AT2G28780	-1.02	-0.03	-0.29	0.783671	0.881429	-7.31
258537_at	putative disease resistance protein sim	---	AT3G04210	1.09	0.13	0.29	0.783736	0.881429	-7.31
248496_at	MtN3-like protein ;supported by full-le	---	AT5G50790	-1.03	-0.04	-0.29	0.783692	0.881429	-7.31
261645_at	hypothetical protein similar to hypothet	---	---	-1.02	-0.03	-0.29	0.783769	0.881429	-7.31
257346_at	pseudogene, putative retroelement po	---	---	-1.02	-0.03	-0.29	0.78372	0.881429	-7.31
260657_at	wall-associated kinase 2, putative sim	---	AT1G19390	-1.03	-0.04	-0.29	0.78378	0.881429	-7.31
256439_at	putative [Mn] superoxide dismutase sir	MSD1	AT3G10920	1.03	0.04	0.29	0.783902	0.881486	-7.31
261385_at	lipid-transfer protein, putative similar t	---	AT1G05450	1.02	0.03	0.29	0.783908	0.881486	-7.31
263567_at	hypothetical protein predicted by gene	---	AT2G15440	-1.03	-0.04	-0.29	0.783971	0.881502	-7.31
249371_at	hypothetical protein	---	AT5G40750	-1.02	-0.03	-0.29	0.784038	0.881502	-7.31
263652_at	unknown protein EST gb|H76414 com	---	AT1G04330	-1.02	-0.03	-0.29	0.784038	0.881502	-7.31
254775_at	hypothetical protein	---	AT4G13450	1.02	0.02	0.28	0.784289	0.88174	-7.31
255837_at	unknown protein	RIC1	AT2G33460	1.02	0.03	0.28	0.784549	0.881861	-7.31
248254_at	receptor protein kinase-like protein	---	AT5G53320	-1.03	-0.04	-0.28	0.784551	0.881861	-7.31
245153_at	putative protein similarity to predicted	---	AT5G12450	-1.02	-0.03	-0.28	0.784476	0.881861	-7.31
257813_at	Cdc45-like protein similar to Cdc45 GI	CDC45	AT3G25100	1.02	0.03	0.28	0.784485	0.881861	-7.31
259500_at	unknown protein ; supported by cDNA:	---	AT1G15740	-1.03	-0.04	-0.28	0.784611	0.881885	-7.31
259670_at	protein kinase, putative similar to GI:7	---	AT1G52310	1.03	0.04	0.28	0.784704	0.881894	-7.31
267025_at	unknown protein predicted by genscan	---	AT2G38350	-1.02	-0.03	-0.28	0.784685	0.881894	-7.31
250889_at	putative protein exostose-related prote	---	AT5G04500	1.02	0.03	0.28	0.784735	0.881894	-7.31
246542_at	transcriptional regulatory - like protein	SNL2	AT5G15020	1.03	0.04	0.28	0.784992	0.881986	-7.31

256153_at	ubiquitin-like (UBQ12), putative simila	UBQ12	AT1G55060	1.03	0.04	0.28	0.784967	0.881986	-7.31
249749_at	unknown protein	BIN4	AT5G24630	1.03	0.04	0.28	0.784889	0.881986	-7.31
252767_at	ring-box protein-like ring-box protein 1	---	AT3G42830	-1.02	-0.03	-0.28	0.78493	0.881986	-7.31
245230_at	hypothetical protein Contains Zinc fing	---	AT4G25610	-1.03	-0.04	-0.28	0.78501	0.881986	-7.31
254400_at	kinesin-related protein katA ; supporte	ATK1	AT4G21270	-1.02	-0.03	-0.28	0.785072	0.882012	-7.31
258542_at	unknown protein	---	AT3G07030	1.03	0.04	0.28	0.785164	0.882072	-7.31
254995_at	putative protein	---	AT4G10370	1.03	0.04	0.28	0.785445	0.88225	-7.31
267086_at	putative salt-inducible protein	---	AT2G32630	1.03	0.04	0.28	0.785477	0.88225	-7.31
249058_at	disease resistance protein-like	TAO1	AT5G44510	1.03	0.04	0.28	0.78545	0.88225	-7.31
253727_at	profilin 2 ; supported by full-length cDI	PFN2	AT4G29350	-1.02	-0.03	-0.28	0.785431	0.88225	-7.31
254607_at	hypothetical protein ;supported by full-	---	AT4G18920	-1.02	-0.03	-0.28	0.785642	0.882391	-7.31
246890_at	Expressed protein ; supported by cDN	---	AT5G25410	-1.02	-0.04	-0.28	0.785749	0.882425	-7.31
257419_at	hypothetical protein predicted by gens	---	AT1G30800	-1.02	-0.03	-0.28	0.785714	0.882425	-7.31
262606_at	hypothetical protein predicted by gens	---	AT1G15190	-1.03	-0.04	-0.28	0.785843	0.882471	-7.31
261285_at	Ca2+-dependent membrane-binding p	ANNAT1	AT1G35720	-1.06	-0.09	-0.28	0.785867	0.882471	-7.31
252162_at	hypothetical protein	---	AT3G50590	-1.04	-0.05	-0.28	0.78604	0.882535	-7.31
257785_at	geranylgeranylated protein, putative s	MUB4	AT3G26980	-1.08	-0.11	-0.28	0.785999	0.882535	-7.31
247301_at	DNA topoisomerase III	---	AT5G63920	1.03	0.05	0.28	0.786018	0.882535	-7.31
253355_at	putative protein	---	AT4G33380	-1.02	-0.03	-0.28	0.786223	0.882666	-7.31
259684_at	unknown protein	---	AT1G63070	-1.02	-0.03	-0.28	0.786234	0.882666	-7.31
261463_at	hypothetical protein predicted by gens	---	AT1G07730 /	1.02	0.03	0.28	0.786541	0.882966	-7.31
248315_at	selenium-binding protein-like	MEF1	AT5G52630	-1.02	-0.03	-0.28	0.786833	0.883251	-7.31
254377_at	subtilisin proteinase - like subtilisin-lik	---	AT4G21650	-1.12	-0.16	-0.28	0.786872	0.883251	-7.31
249411_at	raffinose synthase -like protein raffino	SIP1	AT5G40390	-1.06	-0.08	-0.28	0.787195	0.883513	-7.31
260974_at	receptor-like serine/threonine kinase,	---	AT1G53440	1.05	0.07	0.28	0.787172	0.883513	-7.31
263524_x_	hypothetical protein predicted by gens	---	---	1.03	0.04	0.28	0.787222	0.883513	-7.31
267594_at	hypothetical protein predicted by gene	---	AT2G33000	-1.02	-0.03	-0.28	0.787314	0.883573	-7.31
247513_at	quinone oxidoreductase - like protein	---	AT5G61510	1.03	0.05	0.28	0.787353	0.883574	-7.31
255863_s_	putative GDSL-motif lipase/hydrolase s	---	AT2G30220 /	-1.02	-0.03	-0.28	0.787405	0.883588	-7.31
AFFX-BioC	E. coli /GEN=bioC /DB_XREF=gb:J04	---	---	1.04	0.06	0.28	0.787453	0.883599	-7.31
259427_at	MADS-box transcription factor, putativ	AGL28	AT1G01530	1.02	0.03	0.28	0.787612	0.883734	-7.31
252691_at	kinesin -like protein KLP2 protein, Xer	---	AT3G44050	1.02	0.03	0.28	0.787676	0.883762	-7.31
265009_at	putative protein kinase similar to GB:A	---	AT1G24650	1.02	0.03	0.28	0.787715	0.883763	-7.31
258506_at	hypothetical protein predicted by gene	---	AT3G06520	1.03	0.05	0.28	0.787872	0.883895	-7.31
260154_at	putative histone H2A similar to histone	HTA9	AT1G52740	1.03	0.05	0.28	0.787962	0.883953	-7.31

267366_at	unknown protein ;supported by full-ler	---	AT2G44310 /	1.02	0.03	0.28	0.788005	0.883957	-7.31
262861_at	hypothetical protein similar to hypothet	---	AT1G64820	-1.02	-0.03	-0.28	0.788108	0.884004	-7.31
245464_at	hypothetical protein	UGLYAH	AT4G17050	-1.03	-0.04	-0.28	0.788123	0.884004	-7.31
246695_at	putative protein	---	---	1.03	0.04	0.28	0.788248	0.884091	-7.31
250641_at	putative bZIP protein bZIP protein HY	---	AT5G07160	1.03	0.04	0.28	0.788279	0.884091	-7.31
266271_at	putative glutathione S-transferase ; su	ATGSTU6	AT2G29440	-1.08	-0.11	-0.28	0.788466	0.884216	-7.31
265231_s_	hypothetical protein	---	AT2G07713	1.02	0.03	0.28	0.788468	0.884216	-7.31
251458_at	putative protein several retrotransposo	---	---	1.02	0.03	0.28	0.788581	0.8843	-7.31
246824_at	drought-induced protein - like non-cor	---	AT5G26990	1.02	0.03	0.28	0.788746	0.884329	-7.31
246666_at	hypothetical protein	---	AT5G34830	1.02	0.03	0.28	0.788956	0.884329	-7.31
251876_at	TATA box binding protein (TBP) asso	RGD3	AT3G54280	1.02	0.03	0.28	0.788911	0.884329	-7.31
260834_at	sugar kinase, putative similar to riboki	---	AT1G06730	-1.03	-0.04	-0.28	0.78893	0.884329	-7.31
262178_at	membrane protein, putative similar to	KOM	AT1G77860	-1.03	-0.05	-0.28	0.788942	0.884329	-7.31
254467_at	receptor protein kinase - like protein s	---	AT4G20450	-1.03	-0.04	-0.28	0.788926	0.884329	-7.31
246667_at	putative protein hypothetical proteins -	---	---	-1.02	-0.03	-0.28	0.788863	0.884329	-7.31
260052_at	14-3-3 protein (grf13), putative contair	GRF13	AT1G78220	-1.02	-0.03	-0.28	0.788844	0.884329	-7.31
254902_at	putative protein several hypothetical pr	---	AT4G11550	-1.02	-0.03	-0.28	0.788908	0.884329	-7.31
248909_at	serine threonine protein kinase ; suppo	CIPK19	AT5G45810	1.03	0.04	0.28	0.789105	0.884452	-7.31
246719_at	homology to many predicted putative	---	---	1.02	0.03	0.28	0.789253	0.884534	-7.31
245664_at	hypothetical protein predicted by gene	---	AT1G28327	1.02	0.03	0.28	0.789256	0.884534	-7.31
250794_at	putative protein contains similarity to c	---	AT5G05270	1.02	0.03	0.28	0.789413	0.884667	-7.31
249641_at	DegP protease contains similarity to D	DegP10	AT5G36950	-1.02	-0.04	-0.28	0.789467	0.884684	-7.31
260054_at	putative transporter contains Pfam pro	UNE2	AT1G78130	-1.04	-0.06	-0.28	0.789555	0.884739	-7.31
267301_at	ubiquitin activating enzyme 1 (UBA1) i	ATUBA1	AT2G30110	1.02	0.03	0.28	0.789664	0.884818	-7.31
261962_s_	hypothetical protein predicted by gene	---	---	1.02	0.03	0.28	0.790095	0.885257	-7.31
260273_at	unknown protein	---	AT1G80550	1.03	0.04	0.28	0.790251	0.885346	-7.31
258248_at	hypothetical protein predicted by gene	---	AT3G29140	1.03	0.05	0.28	0.790223	0.885346	-7.31
262255_at	hypothetical protein similar to hypothet	---	AT1G53790	-1.02	-0.03	-0.28	0.790312	0.88537	-7.31
248678_at	U6 snRNA-associated Sm-like protein-	SAD1	AT5G48870	1.02	0.03	0.28	0.790393	0.885374	-7.31
247241_at	unknown protein	---	AT5G64680	1.04	0.06	0.28	0.790358	0.885374	-7.31
260141_at	gibberellin regulatory protein, putative	RGL1	AT1G66350	-1.09	-0.12	-0.28	0.790486	0.885391	-7.31
265022_at	putative agp1 similar to GB:CAA48293	BCP1	AT1G24520	-1.03	-0.04	-0.28	0.79045	0.885391	-7.31
253346_at	hypothetical protein	---	AT4G33600	1.02	0.03	0.28	0.790607	0.885483	-7.31
248103_at	ubiquitin-like protein SMT3-like ; supp	SUMO2	AT5G55160	-1.03	-0.05	-0.28	0.790782	0.885635	-7.31
251742_at	putative protein kinase serine threonir	---	AT3G56050	1.02	0.03	0.28	0.790838	0.885654	-7.31

257441_at	putative GDSL-motif lipase/hydrolase s	---	AT2G04020	-1.03	-0.04	-0.28	0.790898	0.885678	-7.31
260948_at	delta 9 desaturase, putative similar to	---	AT1G06100	-1.02	-0.03	-0.28	0.791024	0.885776	-7.31
261396_at	hypothetical protein contains similarity	---	AT1G79800	1.02	0.03	0.28	0.791128	0.885849	-7.31
260682_at	hypothetical protein predicted by gene	---	AT1G17510	1.02	0.03	0.28	0.791229	0.885918	-7.31
252050_at	hypothetical protein	---	AT3G52550	1.03	0.04	0.28	0.791347	0.886007	-7.31
264623_at	putative NPK1-related protein kinase 2	ANP1	AT1G09000	1.02	0.03	0.28	0.79139	0.886011	-7.31
260161_at	hypothetical protein similar to putative	ROPGEF12	AT1G79860	1.02	0.03	0.28	0.791448	0.886033	-7.31
265166_at	putative OBP32pep protein	---	AT1G23640	1.02	0.03	0.28	0.791538	0.886068	-7.31
252653_at	putative kinesin-like protein similar to	---	AT3G44730	1.02	0.03	0.27	0.791595	0.886068	-7.31
260859_at	serine carboxypeptidase II, putative si	scpl44	AT1G43780	-1.03	-0.04	-0.27	0.791591	0.886068	-7.31
251551_at	transcriptional coactivator - like protei	MBF1B	AT3G58680	1.02	0.02	0.27	0.791714	0.886129	-7.31
261505_at	carboxypeptidase, putative similar to	SOL1	AT1G71696	1.03	0.04	0.27	0.791728	0.886129	-7.31
252052_at	beta-fructofuranosidase	AtcwINV2	AT3G52600	1.02	0.03	0.27	0.791776	0.88614	-7.31
256382_at	unknown protein ;supported by full-len	---	AT1G66860	1.06	0.08	0.27	0.791866	0.886197	-7.31
253763_at	xyloglucan endotransglycosylase - like	---	AT4G28850	1.02	0.03	0.27	0.792078	0.88633	-7.31
245513_at	SYBL1 like protein	ATVAMP724	AT4G15780	1.04	0.06	0.27	0.792044	0.88633	-7.31
254792_at	putative protein nucleoid DNA-binding	---	AT4G12920	1.02	0.03	0.27	0.792101	0.88633	-7.31
265401_at	hypothetical protein predicted by gens	---	AT2G10970	-1.02	-0.03	-0.27	0.792204	0.886401	-7.31
259118_at	unknown protein similar to unknown p	---	AT3G01310	1.03	0.04	0.27	0.792333	0.886458	-7.31
250839_at	MADS-box protein - like SLM3 MADS	AGL99	AT5G04640	-1.02	-0.03	-0.27	0.792331	0.886458	-7.31
261752_at	putative AMP-binding protein contains	---	AT1G76290	1.02	0.03	0.27	0.792584	0.886695	-7.31
262658_at	ribonuclease contains similarity to S-lik	---	AT1G14220	-1.02	-0.03	-0.27	0.79268	0.88676	-7.31
263224_at	putative GTP-binding protein Similar to	---	AT1G30580	-1.03	-0.04	-0.27	0.792767	0.886813	-7.31
263452_at	putative trehalose-6-phosphate phospl	---	AT2G22190	-1.04	-0.06	-0.27	0.792833	0.886844	-7.31
258297_at	Expressed protein ; supported by full-le	---	AT3G23325	-1.02	-0.03	-0.27	0.79292	0.886898	-7.31
258966_at	putative DNA gyrase subunit A similar	---	AT3G10690	-1.04	-0.06	-0.27	0.793274	0.887075	-7.31
250410_at	putative protein putative ATP/GTP-bir	---	AT5G11010	1.03	0.05	0.27	0.793129	0.887075	-7.31
262335_at	hypothetical protein predicted by gene	SPO11-2	AT1G63990	1.02	0.02	0.27	0.793163	0.887075	-7.31
257514_at	hypothetical protein similar to putative	---	---	-1.03	-0.05	-0.27	0.79334	0.887075	-7.31
249521_at	putative protein strong similarity to unk	---	AT5G38690	-1.02	-0.03	-0.27	0.79335	0.887075	-7.31
255229_at	F-box protein family, AtFBL22 contain	---	AT4G05490	1.02	0.02	0.27	0.793292	0.887075	-7.31
254173_at	putative protein Kaposi's sarcoma-ass	REN1	AT4G24580	1.02	0.03	0.27	0.793212	0.887075	-7.31
250225_at	Expressed protein ; supported by full-le	---	AT5G14105	1.03	0.04	0.27	0.793415	0.887104	-7.31
254829_at	AIR1A-like protein putative cell wall-pl	---	AT4G12530	-1.02	-0.03	-0.27	0.79346	0.88711	-7.31
258569_at	ribosomal protein L17, putative similar	emb2171	AT3G04400	-1.03	-0.05	-0.27	0.793541	0.887113	-7.31

254006_at	putative protein various predicted prot	---	AT4G26340	-1.02	-0.03	-0.27	0.793521	0.887113	-7.31
267087_at	putative MYB family transcription facto	MYB101	AT2G32460	1.03	0.05	0.27	0.793627	0.887123	-7.31
266559_at	unknown protein	---	AT2G23920	1.02	0.03	0.27	0.793598	0.887123	-7.31
262437_at	hypothetical protein	---	---	-1.03	-0.04	-0.27	0.79374	0.887205	-7.31
254582_at	putative protein TMV resistance prote	---	AT4G19470	-1.02	-0.03	-0.27	0.793833	0.887267	-7.31
265950_s_	putative protein kinase contains a prot	---	AT2G18530 /	-1.02	-0.03	-0.27	0.793929	0.88733	-7.31
247485_at	putative protein ARR1, Arabidopsis th	ARR23	AT5G62120	1.02	0.03	0.27	0.794239	0.887546	-7.31
247010_at	60S ribosomal protein L26 ;supported	---	AT5G67510	1.05	0.07	0.27	0.794171	0.887546	-7.31
259510_at	hypothetical protein predicted by gens	---	AT1G43970	1.02	0.02	0.27	0.794238	0.887546	-7.31
246018_at	Expressed protein ; supported by full-l	---	AT5G10695	-1.07	-0.10	-0.27	0.794304	0.887575	-7.31
253659_at	hypothetical protein	---	AT4G30150	1.02	0.03	0.27	0.794462	0.887621	-7.31
264678_at	putative U2 small nuclear ribonucleop	U2A'	AT1G09760	-1.02	-0.03	-0.27	0.794435	0.887621	-7.31
259236_at	unknown protein ; supported by full-le	---	AT3G11530	1.02	0.03	0.27	0.794455	0.887621	-7.31
256481_at	elicitor response protein, putative simi	---	AT1G33430	-1.02	-0.03	-0.27	0.794653	0.887792	-7.31
245449_at	retrotransposon like protein	---	---	1.04	0.05	0.27	0.794754	0.887861	-7.31
258544_at	disease resistance gene (RPM1) ident	RPM1	AT3G07040	-1.04	-0.06	-0.27	0.795057	0.888003	-7.31
267246_at	putative WRKY-type DNA binding prot	WRKY25	AT2G30250	1.04	0.06	0.27	0.794975	0.888003	-7.31
261731_s_	hypothetical protein similar to hypothet	---	AT1G47780 /	1.02	0.03	0.27	0.795046	0.888003	-7.31
246814_at	acyl carrier protein precursor - like acy	ACP5	AT5G27200	1.02	0.03	0.27	0.795026	0.888003	-7.31
264695_at	lipid transfer protein, putative similar t	---	AT1G70250	-1.03	-0.04	-0.27	0.795076	0.888003	-7.31
251587_at	hypothetical protein	---	AT3G58080	1.03	0.05	0.27	0.79525	0.888154	-7.31
249431_at	polygalacturonase-like protein polygal	---	AT5G39910	1.03	0.05	0.27	0.795426	0.888307	-7.31
257963_at	hypothetical protein predicted by gene	---	AT3G19840	1.04	0.06	0.27	0.795606	0.888312	-7.31
256121_at	MAP kinase, putative similar to MAP3	---	AT1G18160	-1.02	-0.03	-0.27	0.795597	0.888312	-7.31
248752_at	unknown protein	---	AT5G47600	-1.02	-0.03	-0.27	0.795572	0.888312	-7.31
265548_s_	putative helicase	---	---	1.02	0.02	0.27	0.795625	0.888312	-7.31
247236_at	putative protein similar to unknown pro	---	AT5G64590	1.02	0.03	0.27	0.795614	0.888312	-7.31
245345_at	proteinase like protein ;supported by fu	---	AT4G16640	-1.02	-0.03	-0.27	0.795696	0.888348	-7.31
249172_at	putative protein similar to unknown pro	---	AT5G42950	1.02	0.03	0.27	0.795844	0.888382	-7.31
248554_at	putative protein contains similarity to A	---	AT5G50330	1.03	0.04	0.27	0.795824	0.888382	-7.31
263977_at	hypothetical protein predicted by gens	---	AT2G42660	-1.03	-0.04	-0.27	0.795831	0.888382	-7.31
264333_at	hypothetical protein similar to putative	AtTLP4	AT1G61940	1.02	0.03	0.27	0.796014	0.888528	-7.31
260941_at	peroxidase, putative similar to peroxid	---	AT1G44970	-1.03	-0.05	-0.27	0.796073	0.888548	-7.31
244925_at	NADH dehydrogenase subunit 7	---	---	1.03	0.04	0.27	0.796109	0.888548	-7.31
246055_at	alpha-galactosidase - like protein alph	AtAGAL1	AT5G08380	1.05	0.07	0.27	0.796394	0.888736	-7.31

252640_at	acyl CoA reductase -like protein acyl (	FAR8	AT3G44560	-1.02	-0.03	-0.27	0.796372	0.888736	-7.31
263417_at	putative C2H2-type zinc finger protein	---	AT2G17180	1.03	0.04	0.27	0.796377	0.888736	-7.31
259359_at	B regulatory subunit of protein phosp	---	AT1G13460	1.02	0.03	0.27	0.796477	0.888741	-7.31
262319_s_	unknown protein similar to unknown pr	---	AT1G27540 /	-1.04	-0.05	-0.27	0.796459	0.888741	-7.31
259289_at	hypothetical protein predicted by gens	---	AT3G11350	1.02	0.03	0.27	0.796558	0.888787	-7.31
260187_at	hypothetical protein	LBD5	AT1G36000	1.02	0.03	0.27	0.796656	0.888853	-7.31
246709_s_	putative protein many predicted protei	---	AT5G28160 /	-1.02	-0.02	-0.27	0.796877	0.889056	-7.31
263107_at	putative cytochrome P450	CYP705A6	AT2G05180	1.02	0.03	0.27	0.797021	0.889174	-7.31
250405_at	ubiquitin-specific protease 22 (UBP22	UBP22	AT5G10790	-1.03	-0.04	-0.27	0.7972	0.88933	-7.31
248317_at	unknown protein	---	AT5G52680	1.02	0.03	0.27	0.797356	0.889461	-7.31
258601_at	putative histidyl tRNA synthetase simil	---	AT3G02760	1.02	0.04	0.27	0.797448	0.889519	-7.31
257924_at	unknown protein	---	AT3G23190	-1.03	-0.04	-0.27	0.797688	0.889744	-7.31
266023_at	copia-like retroelement pol polyprotein	---	---	1.02	0.03	0.27	0.797795	0.88982	-7.31
255237_at	hypothetical protein	---	---	1.02	0.03	0.27	0.797856	0.889845	-7.31
249145_at	enoyl CoA hydratase-like protein	ATDCI1	AT5G43280	1.02	0.03	0.27	0.798751	0.890755	-7.31
244923_s_	orf153b orf153b	---	AT2G07674	-1.04	-0.05	-0.27	0.798738	0.890755	-7.31
261188_at	hypothetical protein contains similarity	---	---	1.02	0.03	0.27	0.798836	0.890807	-7.31
257446_at	hypothetical protein predicted by gens	---	AT2G10440	-1.02	-0.02	-0.26	0.799098	0.891056	-7.31
245661_at	purine permease, putative similar to p	ATPUP3	AT1G28220	-1.02	-0.03	-0.26	0.799208	0.891135	-7.31
256652_at	hypothetical protein similar to putative	LPAT5	AT3G18850	-1.05	-0.08	-0.26	0.799318	0.891179	-7.31
259599_at	serine carboxypeptidase II, putative si	SCPL45	AT1G28110	-1.07	-0.10	-0.26	0.799326	0.891179	-7.31
247062_at	putative protein similar to unknown pro	---	AT5G66810	1.04	0.06	0.26	0.799378	0.891193	-7.31
245648_at	F5A9.12 hypothetical protein	---	---	1.02	0.03	0.26	0.799462	0.891199	-7.31
264290_at	hypothetical protein predicted by gene	---	AT1G78810	-1.03	-0.04	-0.26	0.799431	0.891199	-7.31
256067_at	unknown protein ;supported by full-len	---	AT1G07170	-1.03	-0.04	-0.26	0.799561	0.891267	-7.31
255763_at	hypothetical protein predicted by gene	---	AT1G16730	-1.03	-0.04	-0.26	0.799728	0.891409	-7.31
251397_at	putative protein cim1 protein, Glycine	ATEXPB5	AT3G60570	1.03	0.04	0.26	0.799853	0.891505	-7.31
256603_at	unknown protein similar to At14a prote	---	AT3G28270	1.05	0.07	0.26	0.80006	0.891693	-7.31
257343_s_	pseudogene, polyprotein similar to GE	---	---	1.02	0.02	0.26	0.800198	0.891802	-7.32
258266_at	hypothetical protein predicted by gene	---	AT3G15860	-1.03	-0.04	-0.26	0.800252	0.891818	-7.32
256219_at	hypothetical protein predicted by gene	---	AT1G56260	-1.02	-0.03	-0.26	0.800333	0.891827	-7.32
260255_at	putative protein kinase similar to p58 p	---	AT1G74330	1.04	0.06	0.26	0.8004	0.891827	-7.32
248888_at	potassium channel protein KAT1 (pir||S	KAT1	AT5G46240	-1.06	-0.08	-0.26	0.800354	0.891827	-7.32
260703_at	syntaxin, putative similar to syntaxin G	ATSYP24	AT1G32270	1.02	0.02	0.26	0.800415	0.891827	-7.32
256448_s_	unknown protein	MED21	AT4G04780 /	-1.02	-0.03	-0.26	0.800557	0.891941	-7.32

253852_at	putative protein diacylglycerol kinase	---	AT4G28130	-1.02	-0.03	-0.26	0.800694	0.892026	-7.32
257430_at	hypothetical protein similar to hypothet	---	AT2G28580	1.03	0.04	0.26	0.80076	0.892026	-7.32
253924_at	putative protein other hypothetical pro	COBL11	AT4G27110	1.02	0.03	0.26	0.80083	0.892026	-7.32
247838_at	ubiquitin-specific protease 23 (UBP23	UBP23	AT5G57990	1.04	0.05	0.26	0.800808	0.892026	-7.32
266432_s_	putative gag-protease polyprotein	---	---	-1.02	-0.03	-0.26	0.800868	0.892026	-7.32
262604_at	unknown protein similar to unknown p	---	AT1G15060	-1.02	-0.02	-0.26	0.800846	0.892026	-7.32
265517_at	putative S1 self-incompatibility protein	---	AT2G06090	1.02	0.03	0.26	0.800946	0.892069	-7.32
261908_at	stig1-like protein similar to Stig1 GB:A	---	AT1G50650	-1.03	-0.04	-0.26	0.801136	0.892194	-7.32
246336_at	putative protein putative integral mem	ATCHX4	AT3G44900	1.02	0.03	0.26	0.80113	0.892194	-7.32
246374_at	light repressible receptor protein kinas	---	AT1G51840	1.02	0.02	0.26	0.801279	0.89231	-7.32
254396_at	peptide transporter - like protein pepti	---	AT4G21680	1.11	0.16	0.26	0.801557	0.892503	-7.32
249213_at	unknown protein	---	AT5G42700	1.02	0.03	0.26	0.80151	0.892503	-7.32
262660_at	putative protein kinase	VIK	AT1G14000	1.02	0.03	0.26	0.80157	0.892503	-7.32
265714_at	putative integral membrane protein	ATUPS4	AT2G03520	-1.02	-0.03	-0.26	0.801712	0.892517	-7.32
265500_at	putative non-LTR retroelement reverse	---	---	-1.03	-0.05	-0.26	0.801674	0.892517	-7.32
263440_at	unknown protein predicted by genscan	ATEXO70H5	AT2G28640	1.02	0.02	0.26	0.801739	0.892517	-7.32
256937_at	hypothetical protein predicted by gene	---	AT3G22620	-1.15	-0.20	-0.26	0.801674	0.892517	-7.32
256329_at	unknown protein	SEC5A	AT1G76850	1.02	0.02	0.26	0.801844	0.892546	-7.32
252726_at	putative protein predicted proteins, Ar	---	---	-1.03	-0.04	-0.26	0.801836	0.892546	-7.32
261439_at	Expressed protein ; supported by full-l	---	AT1G28395	-1.04	-0.06	-0.26	0.801926	0.892552	-7.32
245531_at	hydroxynitrile lyase like protein	scpl30	AT4G15100	-1.03	-0.04	-0.26	0.801927	0.892552	-7.32
245677_at	hypothetical protein predicted by gene	---	AT1G56660	-1.02	-0.02	-0.26	0.802001	0.892591	-7.32
259152_at	hypothetical protein similar to putative	---	AT3G10210	-1.02	-0.02	-0.26	0.80219	0.892715	-7.32
253760_at	putative protein (fragment) predicted p	AT4G28815	---	-1.03	-0.04	-0.26	0.802207	0.892715	-7.32
256355_at	hypothetical protein predicted by gene	---	AT1G55040	-1.02	-0.04	-0.26	0.80223	0.892715	-7.32
260072_at	unknown protein supported by cDNA:	---	AT1G73650	-1.02	-0.03	-0.26	0.80247	0.892938	-7.32
263255_at	unknown protein similar to steroid rec	---	AT1G10490	1.03	0.04	0.26	0.802694	0.89304	-7.32
258652_at	putative Ras-like GTP-binding protein	ATRABC2B	AT3G09910	-1.04	-0.05	-0.26	0.802977	0.89304	-7.32
256668_at	hypothetical protein similar to hypothet	---	AT3G32190	-1.02	-0.03	-0.26	0.802943	0.89304	-7.32
246181_at	pectinesterase - like protein probable	---	AT5G20860	-1.02	-0.03	-0.26	0.802721	0.89304	-7.32
259918_at	putative AP2 domain transcription fact	---	AT1G72570	1.02	0.03	0.26	0.80274	0.89304	-7.32
252666_at	putative protein hypothetical proteins -	---	AT3G44180	-1.02	-0.03	-0.26	0.802691	0.89304	-7.32
256830_at	eukaryotic translation initiation factor 3	TIF3C2	AT3G22860	-1.02	-0.04	-0.26	0.802978	0.89304	-7.32
259619_at	hypothetical protein	---	AT1G42980	-1.02	-0.03	-0.26	0.802817	0.89304	-7.32
261730_s_	mutator-like transposase, putative sim	---	---	1.02	0.03	0.26	0.803031	0.89304	-7.32

263540_at	unknown protein	---	AT2G24780	1.02	0.03	0.26	0.803012	0.89304	-7.32
261066_at	hypothetical protein predicted by gene	---	AT1G07485	-1.02	-0.02	-0.26	0.802896	0.89304	-7.32
255388_at	hypothetical protein similar to A. thalia	---	---	-1.02	-0.02	-0.26	0.802845	0.89304	-7.32
251341_at	ribosomal protein S13 -like AtRPS13A	---	AT3G60770	-1.04	-0.06	-0.26	0.803179	0.893126	-7.32
245485_at	proline-rich, APG like protein	---	AT4G16230	-1.02	-0.03	-0.26	0.803186	0.893126	-7.32
255722_at	hypothetical protein	---	AT3G29570	-1.02	-0.03	-0.26	0.803232	0.893133	-7.32
253743_at	putative protein vegetative storage pr	---	AT4G28940	1.02	0.02	0.26	0.803295	0.893159	-7.32
250900_at	putative protein ; supported by cDNA:	ATB' ALPHA	AT5G03470	1.03	0.04	0.26	0.803562	0.893369	-7.32
266654_at	putative oleosin protein	---	AT2G25890	1.03	0.04	0.26	0.803566	0.893369	-7.32
261967_at	En/Spm-like transposon protein, putat	---	---	1.03	0.04	0.26	0.803601	0.893369	-7.32
254915_s_	cysteine proteinase contains similarity	---	AT4G11310 /	1.10	0.14	0.26	0.803658	0.893389	-7.32
249470_at	putative protein predicted proteins, Ar	---	AT5G39350	-1.03	-0.04	-0.26	0.803756	0.893453	-7.32
260583_x_	putative polyribonucleotide phosphoryl	---	AT2G47220	1.03	0.04	0.26	0.803805	0.893465	-7.32
265565_at	putative retroelement pol polyprotein	---	---	-1.02	-0.03	-0.26	0.803893	0.893519	-7.32
252728_at	putative protein various predicted prot	---	---	-1.02	-0.03	-0.26	0.8042	0.893817	-7.32
264721_at	hypothetical protein predicted by gens	---	AT1G23000	1.02	0.03	0.26	0.804256	0.893835	-7.32
264409_s_	hypothetical protein similar to hypothet	---	---	1.03	0.04	0.26	0.804422	0.893976	-7.32
257156_at	hypothetical protein predicted by gene	---	AT3G24260	-1.02	-0.03	-0.26	0.804615	0.894147	-7.32
251462_at	mitogen-activated protein kinase-like p	ATMPK10	AT3G59790	-1.03	-0.04	-0.26	0.8047	0.894155	-7.32
260742_at	putative glycerol kinase identical to SP	IAA34	AT1G15050	-1.02	-0.03	-0.26	0.804692	0.894155	-7.32
249370_at	zinc finger - like protein predicted prot	---	AT5G40710	-1.02	-0.02	-0.26	0.804794	0.894216	-7.32
248940_at	replication protein A1-like	---	AT5G45400	1.02	0.03	0.26	0.805031	0.894392	-7.32
263258_at	putative permease similar to putative p	---	AT1G10540	-1.03	-0.04	-0.26	0.805022	0.894392	-7.32
252284_at	putative protein various predicted prot	---	AT3G49020	-1.02	-0.03	-0.26	0.80511	0.894393	-7.32
249246_at	unknown protein	---	AT5G42290	-1.02	-0.03	-0.26	0.805084	0.894393	-7.32
260962_at	pectin methylesterase, putative simila	PME7	AT1G44980	-1.02	-0.03	-0.26	0.80523	0.894464	-7.32
247473_at	putative protein AT-hook protein 2, A	---	AT5G62260	1.03	0.04	0.26	0.805253	0.894464	-7.32
254814_at	hypothetical protein ; supported by cD	---	AT4G12340	-1.02	-0.02	-0.26	0.805487	0.89468	-7.32
255002_at	AIG1-like protein AIG1 - Arabidopsis t	---	AT4G09940	1.02	0.03	0.26	0.805594	0.894756	-7.32
261532_at	amino acid permease, putative similar	---	AT1G71680	-1.02	-0.03	-0.26	0.80577	0.894777	-7.32
249679_at	unknown protein	---	AT5G35980	1.02	0.02	0.26	0.805747	0.894777	-7.32
255197_x_	contains similarity to Oryza sativa repli	---	---	1.02	0.03	0.26	0.805704	0.894777	-7.32
245762_at	ATP-dependent DNA helicase RecQ,	---	AT1G27880	-1.02	-0.02	-0.26	0.805683	0.894777	-7.32
246191_at	T-complex protein 1, beta subunit T-C	---	AT5G20890	1.03	0.04	0.26	0.805982	0.894969	-7.32
260970_at	unknown protein	---	AT1G53640	-1.02	-0.03	-0.26	0.806244	0.895045	-7.32

263982_at	hypothetical protein predicted by gene	---	AT2G42860	-1.03	-0.04	-0.26	0.806117	0.895045	-7.32
265549_at	hypothetical protein predicted by gens	---	---	-1.02	-0.03	-0.26	0.806247	0.895045	-7.32
253328_at	putative protein ABC-type transport pr	ATNAP13	AT4G33460	1.02	0.03	0.26	0.80623	0.895045	-7.32
248917_at	putative protein similar to unknown pro	---	AT5G45850	1.02	0.02	0.26	0.806153	0.895045	-7.32
264520_at	putative amino acid permease GC spl	AAP8	AT1G10010	1.03	0.05	0.26	0.806286	0.895045	-7.32
261631_at	unknown protein contains similarity to	---	AT1G49940	1.02	0.03	0.25	0.806401	0.895129	-7.32
254479_at	putative protein hypothetical protein -	---	AT4G20350	1.02	0.03	0.25	0.806504	0.895156	-7.32
257397_at	hypothetical protein predicted by gens	RIC6	AT2G20430	-1.03	-0.04	-0.25	0.806495	0.895156	-7.32
265918_at	putative fatty acid elongase	KCS8	AT2G15090	-1.08	-0.11	-0.25	0.806837	0.895482	-7.32
264230_at	hypothetical protein predicted by gene	---	AT1G67460	-1.02	-0.03	-0.25	0.806981	0.895489	-7.32
254273_at	glycoprotein endopeptidase - like prot	---	AT4G22720	1.03	0.04	0.25	0.806965	0.895489	-7.32
249555_at	putative protein predicted protein, rice	---	AT5G38300	-1.02	-0.03	-0.25	0.806885	0.895489	-7.32
255115_at	putative protein probable regulatory pr	APUM11	AT4G08840	1.02	0.03	0.25	0.807	0.895489	-7.32
266534_at	putative splicing factor ;supported by t	---	AT2G16940	1.02	0.03	0.25	0.807218	0.895512	-7.32
247218_at	asparagine synthetase (gb|AAC72837	ASN2	AT5G65010	-1.08	-0.11	-0.25	0.807155	0.895512	-7.32
251189_at	putative protein putative mitochondria	---	AT3G62650	1.03	0.04	0.25	0.807109	0.895512	-7.32
259676_at	hypothetical protein similar to putative	---	AT1G77730	-1.02	-0.03	-0.25	0.807161	0.895512	-7.32
251236_at	putative protein hypothetical proteins -	---	AT3G62380	-1.02	-0.02	-0.25	0.807186	0.895512	-7.32
248443_at	gibberellin 20-oxidase-like protein	---	AT5G51310	-1.02	-0.03	-0.25	0.807352	0.895618	-7.32
249908_at	putative protein similar to unknown pro	---	AT5G22760	-1.02	-0.03	-0.25	0.807463	0.895654	-7.32
262814_at	putative heat-shock protein strong sim	---	AT1G11660	1.02	0.03	0.25	0.807445	0.895654	-7.32
246976_s_	putative protein UBIQUINONE BIOSY	---	AT5G24810	1.03	0.05	0.25	0.807624	0.895711	-7.32
250741_at	putative protein contains similarity to I	---	AT5G05790	1.04	0.06	0.25	0.807624	0.895711	-7.32
265870_at	hypothetical protein predicted by gene	PDLP6	AT2G01660	1.02	0.03	0.25	0.807632	0.895711	-7.32
256390_at	putative MAP kinase similar to MAP ki	ATMKK8	AT3G06230	-1.02	-0.03	-0.25	0.807746	0.895771	-7.32
254098_at	superoxide dismutase (EC 1.15.1.1) (F	FSD1	AT4G25100	-1.03	-0.04	-0.25	0.807765	0.895771	-7.32
249315_at	unknown protein	---	AT5G41190	-1.02	-0.03	-0.25	0.807929	0.895827	-7.32
257640_at	hypothetical protein	---	AT3G25750	-1.03	-0.04	-0.25	0.807862	0.895827	-7.32
249153_s_	putative protein strong similarity to unk	---	AT5G43390 /	1.02	0.03	0.25	0.807967	0.895827	-7.32
246500_at	putative protein HR21spA protein invo	SYN4	AT5G16270	-1.02	-0.03	-0.25	0.807972	0.895827	-7.32
245635_at	zinc finger protein ID1, putative simila	AtIDD16	AT1G25250	-1.02	-0.02	-0.25	0.808154	0.895837	-7.32
251250_at	putative protein pectin methylesterase	---	AT3G62180	1.03	0.04	0.25	0.80827	0.895837	-7.32
256566_at	hypothetical protein	---	AT3G19530	-1.02	-0.03	-0.25	0.808304	0.895837	-7.32
253071_at	putative protein various predicted prote	---	AT4G37880	-1.02	-0.03	-0.25	0.808413	0.895837	-7.32
263389_at	putative retroelement pol polyprotein	---	---	-1.02	-0.03	-0.25	0.808345	0.895837	-7.32

250841_at	putative protein CGI-01 protein, Homo	---	AT5G04610	-1.04	-0.05	-0.25	0.808281	0.895837	-7.32
264035_at	hypothetical protein predicted by gene	---	AT2G03630	-1.02	-0.03	-0.25	0.808093	0.895837	-7.32
257662_at	low affinity calcium antiporter CAX2 al	CAX2	AT3G13320	-1.02	-0.03	-0.25	0.808382	0.895837	-7.32
267306_at	Ran binding protein (AtRanBP1b) iden	---	AT2G30060	-1.02	-0.03	-0.25	0.808271	0.895837	-7.32
248754_at	putative protein contains similarity to C	NF-YB6	AT5G47670	1.02	0.03	0.25	0.808117	0.895837	-7.32
249408_at	myb-related protein	MYB23	AT5G40330	-1.02	-0.03	-0.25	0.808054	0.895837	-7.32
261310_at	hypothetical protein predicted by gene	PDE247	AT1G05750	1.03	0.04	0.25	0.808473	0.895859	-7.32
251602_at	Expressed protein ; supported by full-l	---	AT3G57785	-1.02	-0.03	-0.25	0.808575	0.89592	-7.32
249031_at	putative protein contains similarity to d	---	AT5G44900	-1.02	-0.03	-0.25	0.808763	0.89592	-7.32
255712_at	hypothetical protein similar to A. thalia	---	AT4G00280	1.02	0.03	0.25	0.808708	0.89592	-7.32
258036_at	unknown protein	---	AT3G21210	1.02	0.02	0.25	0.808739	0.89592	-7.32
252547_at	putative protein many predicted protei	---	AT3G45840	-1.02	-0.03	-0.25	0.808645	0.89592	-7.32
257306_at	hypothetical protein contains regions s	---	AT3G30200	1.02	0.02	0.25	0.808676	0.89592	-7.32
257123_at	hypothetical protein	---	AT3G20030	1.02	0.02	0.25	0.808867	0.895991	-7.32
248597_at	DNA (cytosine-5)-methyltransferase (D	MET1	AT5G49160	-1.05	-0.07	-0.25	0.808984	0.896077	-7.32
258461_at	hypothetical protein predicted by gene	---	AT3G17340	-1.02	-0.03	-0.25	0.80919	0.896263	-7.32
265606_s_	putative non-LTR retroelement reverse	---	AT3G09510	1.02	0.03	0.25	0.809281	0.89632	-7.32
258742_at	hypothetical protein predicted by gens	---	AT3G05800	1.04	0.06	0.25	0.809521	0.896383	-7.32
265304_at	putative AP2 domain transcription fact	---	AT2G20350	-1.02	-0.02	-0.25	0.809406	0.896383	-7.32
261734_at	hypothetical protein similar to hypothet	---	AT1G47790	1.02	0.03	0.25	0.809535	0.896383	-7.32
267242_at	hypothetical protein predicted by grail	---	AT2G02670	-1.02	-0.03	-0.25	0.809501	0.896383	-7.32
254033_at	V-ATPase G-subunit like protein G su	VATG3	AT4G25950	1.02	0.02	0.25	0.809452	0.896383	-7.32
251609_at	putative protein hypothetical protein T	---	AT3G57900	-1.02	-0.02	-0.25	0.809609	0.896422	-7.32
247070_at	Expressed protein ; supported by full-l	---	AT5G66815	-1.02	-0.03	-0.25	0.809771	0.896558	-7.32
261802_at	hypothetical protein similar to hypothet	---	AT1G30550	1.02	0.03	0.25	0.809976	0.896698	-7.32
259989_at	hypothetical protein predicted by gene	---	---	1.02	0.03	0.25	0.809962	0.896698	-7.32
245553_at	lupeol synthase like protein	BARS1	AT4G15370	-1.02	-0.02	-0.25	0.810127	0.896792	-7.32
262535_at	trehalose-6-phosphate synthase, puta	ATTPS3	AT1G17000	-1.02	-0.02	-0.25	0.810179	0.896792	-7.32
264363_at	hypothetical protein predicted by gene	---	AT1G03170	1.02	0.03	0.25	0.810171	0.896792	-7.32
266485_at	putative phospholipase ;supported by	---	AT2G47630	-1.05	-0.07	-0.25	0.810444	0.897041	-7.32
263702_at	hypothetical protein identical to hypoth	---	AT1G31240	-1.02	-0.03	-0.25	0.81053	0.897049	-7.32
255119_at	hypothetical protein	---	---	-1.02	-0.02	-0.25	0.810501	0.897049	-7.32
250659_at	MtN21 nodulin protein-like	---	AT5G07050	1.02	0.03	0.25	0.810647	0.897136	-7.32
249328_at	AtRAD3 (dbj|BAA92828.1) ; supporte	ATR	AT5G40820	-1.02	-0.03	-0.25	0.810697	0.897148	-7.32
248785_at	unknown protein	---	AT5G47400	-1.02	-0.02	-0.25	0.810929	0.897274	-7.32

265902_at	hypothetical protein predicted by gens	---	AT2G25590	1.02	0.03	0.25	0.810886	0.897274	-7.32
266646_at	unknown protein ;supported by full-ler	ATPH1	AT2G29700	1.02	0.03	0.25	0.8109	0.897274	-7.32
253984_at	isp4 like protein isp4 protein -Schizosa	OPT5	AT4G26590	-1.02	-0.03	-0.25	0.811151	0.897388	-7.32
259208_at	hypothetical protein similar to GB:AAD	---	AT3G09060	1.02	0.03	0.25	0.811093	0.897388	-7.32
249541_at	anthranilate N-benzoyltransferase -lik	---	AT5G38130	1.02	0.03	0.25	0.811148	0.897388	-7.32
246256_at	glucosyltransferase-like protein	---	AT4G36770	1.03	0.05	0.25	0.811202	0.897401	-7.32
253968_at	putative calcineurin B-like protein calc	CBL7	AT4G26560	-1.02	-0.03	-0.25	0.811259	0.89742	-7.32
265518_at	hypothetical protein predicted by gens	---	AT2G06040	-1.03	-0.04	-0.25	0.811636	0.897794	-7.32
254304_at	hypothetical protein ; supported by cD	---	AT4G22270	1.02	0.03	0.25	0.811737	0.897819	-7.32
258711_at	ubiquitin-like protein (UBQ8) identical	UBQ8	AT3G09790	1.02	0.03	0.25	0.811705	0.897819	-7.32
256985_at	myb-related protein 5 identical to GB:A	ATMYB5	AT3G13540	-1.03	-0.04	-0.25	0.811831	0.897879	-7.32
265055_at	hypothetical protein similar to hypothet	---	---	1.02	0.03	0.25	0.812056	0.898017	-7.32
252227_at	putative protein various predicted prot	---	AT3G49900	-1.02	-0.03	-0.25	0.812113	0.898017	-7.32
267109_at	hypothetical protein predicted by gens	---	AT2G14810	1.02	0.03	0.25	0.812039	0.898017	-7.32
252461_at	putative protein predicted protein, Ara	---	---	1.02	0.03	0.25	0.812086	0.898017	-7.32
267205_at	unknown protein	---	AT2G30820	-1.02	-0.03	-0.25	0.812159	0.898024	-7.32
248159_at	unknown protein	---	AT5G54460	-1.02	-0.02	-0.25	0.812452	0.898305	-7.32
254049_at	putative ribosomal protein S10 40S rib	---	AT4G25740	-1.04	-0.05	-0.25	0.812595	0.898334	-7.32
247560_at	putative protein predicted proteins, fro	---	AT5G61090	1.03	0.04	0.25	0.812596	0.898334	-7.32
248121_at	putative protein contains similarity to u	GAUT12	AT5G54690	-1.03	-0.04	-0.25	0.812586	0.898334	-7.32
259940_at	hypothetical protein	---	AT1G71290	-1.02	-0.02	-0.25	0.812719	0.898426	-7.32
263061_at	putative AAA-type ATPase	---	AT2G18190	-1.02	-0.03	-0.25	0.812879	0.898516	-7.32
245667_at	FH protein interacting protein FIP1 ide	FIP1	AT1G28200	-1.02	-0.03	-0.25	0.812875	0.898516	-7.32
255446_at	hypothetical protein similar to A. thalia	---	AT4G02750	-1.02	-0.03	-0.25	0.813016	0.898581	-7.32
262203_at	transfactor-like protein similar to transf	---	AT2G01060	1.02	0.03	0.25	0.812984	0.898581	-7.32
263377_at	AP2 domain transcription factor (ABI4:	ABI4	AT2G40220	1.02	0.02	0.25	0.813174	0.898639	-7.32
255180_at	putative polyprotein	---	---	1.02	0.02	0.25	0.813179	0.898639	-7.32
245617_at	hypothetical protein	---	AT4G14490	-1.02	-0.02	-0.25	0.813187	0.898639	-7.32
266673_at	putative thiamin biosynthesis protein	THIC	AT2G29630	1.03	0.05	0.25	0.813464	0.898858	-7.32
263059_at	putative non-LTR retrolelement revers	---	---	1.02	0.03	0.25	0.813453	0.898858	-7.32
266451_at	3-isopropylmalate dehydratase, small	---	AT2G43090	-1.02	-0.03	-0.25	0.813537	0.898895	-7.32
259923_at	putative protein kinase contains Pfam	---	AT1G72760	-1.02	-0.02	-0.25	0.813647	0.898973	-7.32
261123_at	hypothetical protein predicted by gens	---	AT1G62860	-1.03	-0.04	-0.25	0.81372	0.89901	-7.32
249628_at	putative protein tropomyosin gene 1, i	---	AT5G37590	-1.02	-0.03	-0.24	0.814193	0.899446	-7.32
255362_at	putative reverse transcriptase	---	---	-1.02	-0.02	-0.24	0.814154	0.899446	-7.32

263169_at	hypothetical protein similar to unknowr	---	AT1G03010	-1.03	-0.04	-0.24	0.814341	0.899564	-7.32
249302_at	putative protein similar to unknown pro	---	AT5G41450	-1.02	-0.03	-0.24	0.8145	0.899697	-7.32
251059_at	serine/threonine protein kinase ATPK1	CIPK15	AT5G01810	1.05	0.08	0.24	0.814552	0.89971	-7.32
261959_s_	polyprotein, putative similar to polypro	---	---	-1.02	-0.03	-0.24	0.814669	0.899753	-7.32
248247_at	putative protein contains similarity to h	SPCH	AT5G53210	1.02	0.03	0.24	0.814642	0.899753	-7.32
265179_at	unknown protein predicted by genema	---	AT1G23650	-1.03	-0.04	-0.24	0.814968	0.899837	-7.32
267296_at	hypothetical protein predicted by gene	LBD10	AT2G23660	-1.02	-0.03	-0.24	0.814982	0.899837	-7.32
265207_at	unknown protein	---	AT2G36680	-1.02	-0.02	-0.24	0.814963	0.899837	-7.32
253565_at	predicted protein DAN26, Homo sapie	---	AT4G31200	1.02	0.04	0.24	0.814942	0.899837	-7.32
260204_at	hypothetical protein predicted by gens	---	AT1G52900	-1.02	-0.03	-0.24	0.81495	0.899837	-7.32
265329_at	putative succinate dehydrogenase flav	SDH1-2	AT2G18450	1.02	0.03	0.24	0.814909	0.899837	-7.32
249511_at	putative protein contains similarity to u	---	AT5G38500	-1.02	-0.03	-0.24	0.815482	0.900345	-7.32
253142_at	putative protein methyl-directed mism	MLH3	AT4G35520	1.02	0.02	0.24	0.815531	0.900357	-7.32
261121_at	hypothetical protein predicted by gene	---	AT1G75340	-1.02	-0.02	-0.24	0.815571	0.900357	-7.32
250435_at	putative protein various predicted prot	RING1	AT5G10380	-1.04	-0.06	-0.24	0.815774	0.900518	-7.32
262011_at	hypothetical protein predicted by gene	---	AT1G35614	1.03	0.04	0.24	0.815796	0.900518	-7.32
260512_at	unknown protein	---	AT1G51520	-1.03	-0.04	-0.24	0.815918	0.900609	-7.32
263302_at	hypothetical protein predicted by gens	---	---	-1.02	-0.02	-0.24	0.816052	0.90067	-7.32
255399_at	hypothetical protein	---	---	-1.02	-0.03	-0.24	0.816032	0.90067	-7.32
245678_at	unknown protein	---	AT1G56610	-1.03	-0.04	-0.24	0.816109	0.90069	-7.32
263828_at	putative GDSL-motif lipase/hydrolase s	---	AT2G40250	1.02	0.04	0.24	0.81635	0.90088	-7.32
258806_at	unknown protein	---	AT3G04020	-1.03	-0.05	-0.24	0.816361	0.90088	-7.32
258061_at	unknown protein ; supported by cDNA	---	AT3G25910	1.02	0.03	0.24	0.81641	0.90089	-7.32
266482_at	putative small nuclear ribonucleoprotei	---	AT2G47640	-1.03	-0.04	-0.24	0.816523	0.900929	-7.32
250450_at	putative transcription factor MYB92 ; s	ATMYB92	AT5G10280	1.01	0.02	0.24	0.816506	0.900929	-7.32
266843_at	hypothetical protein predicted by gens	---	AT2G26135	1.02	0.03	0.24	0.816912	0.901293	-7.32
264881_s_	lysine and histidine specific transporte	---	AT1G61270 /	-1.01	-0.02	-0.24	0.816932	0.901293	-7.32
264603_at	hypothetical protein predicted by gens	---	AT1G04670	-1.02	-0.02	-0.24	0.816978	0.901299	-7.32
256472_at	unknown protein	---	---	-1.02	-0.03	-0.24	0.817026	0.901308	-7.32
261372_at	zinc finger protein, putative similar to	---	AT1G53010	-1.02	-0.03	-0.24	0.817199	0.901368	-7.32
267275_at	putative Na H antiporter	ATCHX13	AT2G30240	-1.02	-0.04	-0.24	0.817168	0.901368	-7.32
256618_at	hypothetical protein	VRN5	AT3G24440	1.04	0.06	0.24	0.817147	0.901368	-7.32
245482_at	hypothetical protein	---	AT4G16180	-1.03	-0.04	-0.24	0.817241	0.901371	-7.32
257409_at	unknown protein predicted by genscan	---	AT2G17470	-1.02	-0.03	-0.24	0.817321	0.901416	-7.32
246712_at	putative protein various predicted prot	---	---	-1.02	-0.02	-0.24	0.817567	0.901644	-7.32

AFFX-Trpn	B. subtilis /GEN=trpC, trpF /DB_XREF	---	---	-1.01	-0.02	-0.24	0.817625	0.901664	-7.32
251827_at	chalcone isomerase ;supported by full	TT5	AT3G55120	-1.03	-0.04	-0.24	0.817714	0.901675	-7.32
252196_at	putative protein predicted protein, Ara	---	AT3G50200	-1.03	-0.04	-0.24	0.817713	0.901675	-7.32
258169_at	hypothetical protein	---	AT3G21590	1.02	0.03	0.24	0.817835	0.901766	-7.32
256824_at	hypothetical protein predicted by gene	AT3G22121	---	1.03	0.05	0.24	0.818094	0.901964	-7.32
258304_at	hypothetical protein predicted by gene	---	---	1.01	0.02	0.24	0.818063	0.901964	-7.32
263163_at	fructokinase, putative predicted by ge	FZL	AT1G03160	1.04	0.06	0.24	0.818183	0.902018	-7.32
263568_at	hypothetical protein predicted by gens	---	AT2G27160	1.02	0.03	0.24	0.818247	0.902045	-7.32
257693_at	hypothetical protein predicted by gene	---	AT3G12850	1.03	0.05	0.24	0.818467	0.9022	-7.32
262087_at	hypothetical protein predicted by gene	---	AT1G56030	1.02	0.03	0.24	0.818447	0.9022	-7.32
259212_at	hypothetical protein predicted by gene	---	AT3G09180	-1.02	-0.03	-0.24	0.818522	0.902217	-7.32
250903_at	putative protein coil protein PO22, mic	---	AT5G03600	-1.03	-0.04	-0.24	0.818686	0.902354	-7.32
254364_at	glycine-rich protein glycine-rich cell wa	---	AT4G22020	-1.02	-0.03	-0.24	0.818928	0.902534	-7.32
248963_at	unknown protein	---	AT5G45700	-1.02	-0.03	-0.24	0.818905	0.902534	-7.32
250596_at	putative protein contains similarity to u	---	AT5G07780	-1.03	-0.04	-0.24	0.819125	0.902708	-7.32
263457_at	unknown protein	SR1	AT2G22300	-1.04	-0.06	-0.24	0.819265	0.902818	-7.32
254207_at	putative protein Dof zinc finger protein	---	AT4G24060	-1.02	-0.03	-0.24	0.819426	0.902909	-7.32
263670_at	hypothetical protein predicted by gens	---	AT2G04840	-1.02	-0.03	-0.24	0.819408	0.902909	-7.32
267117_at	unknown protein	---	AT2G32560	-1.02	-0.02	-0.24	0.819469	0.902912	-7.32
252610_x_	putative protein putative MuDR protein	---	---	1.01	0.02	0.24	0.819596	0.902925	-7.32
264630_at	hypothetical protein predicted by gene	FAS1	AT1G65470	-1.02	-0.03	-0.24	0.819526	0.902925	-7.32
252994_at	putative protein gene PC326 protein -	---	AT4G38480	-1.05	-0.07	-0.24	0.819599	0.902925	-7.32
261291_at	hypothetical protein predicted by gene	---	AT1G36970	-1.03	-0.04	-0.24	0.819661	0.902949	-7.32
247574_at	putative protein predicted protein, Ara	---	AT5G61228 /	-1.02	-0.03	-0.24	0.82	0.903279	-7.32
258835_at	putative RNA-binding protein contains	---	AT3G07250	1.02	0.03	0.24	0.820053	0.903293	-7.32
261128_at	ubiquitin-specific protease 2 (UBP2) id	UBP2	AT1G04860	1.02	0.03	0.24	0.820103	0.903305	-7.32
253345_at	putative protein	BCA5	AT4G33580	1.03	0.04	0.24	0.820274	0.90345	-7.32
257812_at	hypothetical protein	---	AT3G25090	-1.02	-0.03	-0.24	0.820317	0.903453	-7.32
252844_at	putative protein several hypothetical pr	---	AT3G42140	1.02	0.03	0.24	0.820459	0.903463	-7.32
250815_s_	putative protein similar to unknown pro	---	AT5G05040 /	-1.02	-0.04	-0.24	0.820495	0.903463	-7.32
264943_at	hypothetical protein predicted by gene	---	AT1G76910	-1.02	-0.03	-0.24	0.820455	0.903463	-7.32
248269_at	putative protein contains similarity to a	ACBP1	AT5G53470	-1.02	-0.03	-0.24	0.82039	0.903463	-7.32
249044_at	Na+-dependent inorganic phosphate c	PHT4;6	AT5G44370	1.03	0.04	0.24	0.820523	0.903463	-7.32
258722_at	putative pathogenesis-related protein s	---	AT3G09590	1.02	0.03	0.24	0.82057	0.903471	-7.32
262725_at	hypothetical protein predicted by gene	---	AT1G43580	-1.04	-0.05	-0.24	0.820651	0.903517	-7.32

245388_at	hypothetical protein ;supported by full-	---	AT4G16410	-1.02	-0.02	-0.24	0.82084	0.903655	-7.32
260268_at	unknown protein ;supported by full-ler	---	AT1G68490	1.02	0.03	0.24	0.820871	0.903655	-7.32
261101_at	transcription factor DREB1A, putative	ddf2	AT1G63030	-1.02	-0.03	-0.24	0.820951	0.903655	-7.32
264624_at	zinc finger protein ATZF1, putative ide	ERD6	AT1G08930	-1.03	-0.04	-0.24	0.820975	0.903655	-7.32
255892_at	hypothetical protein contains similarity	---	AT1G17910	-1.02	-0.02	-0.24	0.82096	0.903655	-7.32
256760_at	SKP1/ASK1 (At15), putative similar to	ASK15	AT3G25650	-1.01	-0.02	-0.24	0.821048	0.903692	-7.32
253051_at	cyclin cyc1 ; supported by cDNA: gi_1	CYCB1;1	AT4G37490	1.03	0.04	0.24	0.821095	0.9037	-7.32
260628_at	hypothetical protein predicted by gene	---	AT1G62320	-1.02	-0.02	-0.23	0.821217	0.903704	-7.32
253441_at	putative protein Fidipidine, Drosophila	---	AT4G32560	-1.02	-0.03	-0.23	0.821207	0.903704	-7.32
253883_at	hypothetical protein	---	AT4G27660	1.02	0.03	0.23	0.821217	0.903704	-7.32
247018_at	AP2 domain transcription factor-like	---	AT5G67000	-1.01	-0.02	-0.23	0.821261	0.903708	-7.32
252674_at	cytochrome P450-like protein CYTOC	CYP71B38	AT3G44250	-1.01	-0.02	-0.23	0.821327	0.903737	-7.32
258245_at	hypothetical protein	---	AT3G29075	1.02	0.03	0.23	0.821502	0.903784	-7.32
259204_s_	hypothetical protein predicted by gens	---	---	1.02	0.02	0.23	0.821549	0.903784	-7.32
256295_at	hypothetical protein	---	AT1G69470	-1.02	-0.03	-0.23	0.821567	0.903784	-7.32
262449_at	hypothetical protein similar to hypothet	---	AT1G11160	1.01	0.02	0.23	0.821474	0.903784	-7.32
261546_at	hypothetical protein	---	AT1G63520	-1.02	-0.03	-0.23	0.821523	0.903784	-7.32
262065_at	hypothetical protein predicted by gene	---	AT1G56180	1.03	0.05	0.23	0.821659	0.903797	-7.32
246899_at	putative protein various predicted prot	---	AT5G25590	1.02	0.03	0.23	0.821657	0.903797	-7.32
266358_at	hypothetical protein predicted by gens	---	AT2G32280	1.04	0.06	0.23	0.822048	0.904182	-7.32
266415_at	putative nonspecific lipid-transfer prote	LTP2	AT2G38530	-1.09	-0.13	-0.23	0.822233	0.904341	-7.32
247269_at	alternative oxidase 2 (sp|O22049)	AOX2	AT5G64210	1.02	0.02	0.23	0.822301	0.904373	-7.32
262134_at	sulfate transporter, putative similar to	AST56	AT1G77990	-1.04	-0.05	-0.23	0.822456	0.904499	-7.32
266527_at	hypothetical protein predicted by gens	---	---	-1.02	-0.03	-0.23	0.822524	0.90453	-7.32
247716_at	putative protein predicted protein, Ara	---	AT5G59350	1.03	0.04	0.23	0.822767	0.90466	-7.32
248484_at	carbonyl reductase-like protein	---	AT5G51030	1.01	0.02	0.23	0.822801	0.90466	-7.32
256809_at	hypothetical protein predicted by gene	ALY3	AT3G21430	-1.02	-0.03	-0.23	0.822788	0.90466	-7.32
245236_at	putative DNA mismatch repair protein	MSH3	AT4G25540	-1.02	-0.02	-0.23	0.822756	0.90466	-7.32
266777_at	putative AAA-type ATPase	ftsh3	AT2G29080	1.02	0.02	0.23	0.822893	0.904718	-7.32
250902_at	putative protein predicted proteins, Ar	---	AT5G03590	-1.02	-0.03	-0.23	0.822968	0.90475	-7.32
262036_at	ATP-dependent RNA helicase, putativ	---	AT1G35530	-1.03	-0.04	-0.23	0.823001	0.90475	-7.32
245000_at	hypothetical protein	---	---	-1.02	-0.03	-0.23	0.823208	0.904934	-7.32
259782_at	unknown protein	---	AT1G29680	-1.02	-0.02	-0.23	0.82329	0.904937	-7.32
256636_at	S-locus related protein SLR1 homolog	---	AT3G12000	-1.02	-0.02	-0.23	0.823276	0.904937	-7.32
246132_at	Rad51-like protein ; supported by cDN	ATRAD51	AT5G20850	-1.01	-0.02	-0.23	0.823614	0.905249	-7.32

264531_at	hypothetical protein predicted by gens	---	AT1G30790	-1.02	-0.03	-0.23	0.823888	0.905469	-7.32
246786_at	putative amino acid aminotransferase	---	AT5G27410	-1.02	-0.03	-0.23	0.823956	0.905469	-7.32
267020_at	hypothetical protein predicted by gens	---	AT2G39320	-1.02	-0.03	-0.23	0.823909	0.905469	-7.32
252731_at	putative protein predicted proteins, Ar	---	---	1.03	0.04	0.23	0.823973	0.905469	-7.32
249793_at	putative protein contains similarity to u	---	AT5G23680	1.03	0.04	0.23	0.824174	0.905647	-7.32
255907_at	homeobox protein, putative similar to	HDG12	AT1G17920	1.02	0.02	0.23	0.824457	0.905783	-7.32
252158_at	CDPK-related protein kinase	CRK	AT3G50530	-1.02	-0.03	-0.23	0.82444	0.905783	-7.32
256923_at	hypothetical protein	---	AT3G29635	1.02	0.03	0.23	0.824456	0.905783	-7.32
250802_at	pectinesterase	---	AT5G04970	-1.02	-0.03	-0.23	0.824441	0.905783	-7.32
255287_at	see T10M13.1 (GB:AF001308) similar	---	AT4G04660	1.02	0.03	0.23	0.824538	0.905828	-7.32
261739_at	hypothetical protein similar to hypothet	PEX11A	AT1G47750	-1.02	-0.02	-0.23	0.824703	0.905966	-7.32
247117_at	3-hydroxyisobutyryl-coenzyme A hydro	CHY1	AT5G65940	-1.03	-0.04	-0.23	0.824785	0.906013	-7.32
261568_at	DNA-binding protein, putative similar t	NGA3	AT1G01030	-1.02	-0.03	-0.23	0.824856	0.906046	-7.32
255208_at	see GB:AL022580	---	---	-1.02	-0.03	-0.23	0.824981	0.906097	-7.32
266493_at	Mutator-like transposase similar to MU	---	---	1.02	0.02	0.23	0.824956	0.906097	-7.32
250637_at	glycine-rich protein atGRP-7	GRP17	AT5G07530	1.02	0.03	0.23	0.825063	0.906143	-7.32
248013_at	putative protein contains similarity to c	ACA8	AT5G56330	1.03	0.04	0.23	0.825128	0.906148	-7.32
252816_at	putative protein several putative protei	---	AT3G42550	-1.01	-0.02	-0.23	0.825162	0.906148	-7.32
260180_at	E2, ubiquitin-conjugating enzyme, put	MMZ2	AT1G70660	-1.03	-0.04	-0.23	0.825187	0.906148	-7.32
255416_at	hypothetical protein	---	AT4G03170	-1.02	-0.02	-0.23	0.82544	0.906383	-7.32
245204_at	1-AMINOCYCLOPROPANE-1-CARB	---	AT5G12270	1.03	0.04	0.23	0.825589	0.906387	-7.32
245233_at	putative protein similarity to low-tempe	---	AT4G25580	1.02	0.03	0.23	0.825583	0.906387	-7.32
248160_at	putative protein similar to unknown pro	---	AT5G54470	1.03	0.04	0.23	0.82559	0.906387	-7.32
267281_at	putative protein kinase contains a prot	---	AT2G19400	-1.02	-0.03	-0.23	0.825603	0.906387	-7.32
250538_at	RNA helicase (emb|CAA09212.1) ; su	STRS2	AT5G08620	1.03	0.04	0.23	0.825995	0.90671	-7.32
246138_at	putative protein predicted proteins fron	---	AT5G19870	-1.01	-0.02	-0.23	0.826215	0.90671	-7.32
267239_at	unknown protein	---	AT2G02510	-1.02	-0.03	-0.23	0.826056	0.90671	-7.32
249091_at	AtCLH2 (gb|AAF27046.1) ; supported	CLH2	AT5G43860	1.02	0.03	0.23	0.826143	0.90671	-7.32
266307_at	putative cytochrome P450	CYP705A8	AT2G27000	1.02	0.03	0.23	0.826123	0.90671	-7.32
256103_at	hypothetical protein similar to hypothet	---	AT1G13540	-1.01	-0.02	-0.23	0.826105	0.90671	-7.32
261527_at	hypothetical protein similar to putative	---	AT1G14390	-1.02	-0.03	-0.23	0.826181	0.90671	-7.32
252532_at	glucosidase-like protein GLUCAN EN	---	AT3G46570	-1.03	-0.04	-0.23	0.826069	0.90671	-7.32
264656_at	unknown protein Contains similarity to	---	AT1G09010	-1.02	-0.02	-0.23	0.82645	0.906924	-7.32
263671_at	hypothetical protein predicted by gens	---	AT2G04830	1.02	0.02	0.23	0.826513	0.906949	-7.32
260516_at	unknown protein	---	AT1G51450	1.02	0.03	0.23	0.826811	0.907233	-7.32

259384_at	putative lectin contains Pfam profile: F	---	AT3G16450	1.02	0.03	0.23	0.826878	0.907263	-7.33
253980_at	sucrase-like protein sucrose cleavage	---	AT4G26620	-1.03	-0.04	-0.23	0.827131	0.907496	-7.33
263804_at	putative protein kinase contains a prot	---	AT2G40270	1.02	0.03	0.23	0.82718	0.907507	-7.33
254531_at	putative protein predicted protein, Ara	---	AT4G19650	1.03	0.04	0.23	0.827273	0.907565	-7.33
260043_at	hypothetical protein predicted by gene	---	---	-1.02	-0.03	-0.23	0.827451	0.907717	-7.33
261918_at	hypothetical protein	---	AT1G65940	1.01	0.02	0.23	0.827639	0.907879	-7.33
257114_at	cytochrome P450, putative contains P	CYP705A23	AT3G20140	1.02	0.03	0.23	0.827755	0.907919	-7.33
258361_at	unknown protein similar to hypothetica	---	AT3G14270	-1.03	-0.05	-0.23	0.82774	0.907919	-7.33
265890_s_	En/Spm-like transposon protein relate	---	---	-1.02	-0.02	-0.23	0.8279	0.908034	-7.33
257162_s_	ammonium transporter, putative simila	AMT1;3	AT3G24290 /	1.02	0.02	0.23	0.828029	0.908133	-7.33
244959_s_	hypothetical protein	---	AT2G07708	-1.02	-0.03	-0.23	0.828217	0.908295	-7.33
248842_at	unknown protein	---	AT5G46850	1.02	0.03	0.23	0.828365	0.90837	-7.33
263745_at	hypothetical protein predicted by gene	CHR34	AT2G21450	-1.02	-0.02	-0.23	0.828357	0.90837	-7.33
247725_at	putative Rab5-interacting protein - like	---	AT5G59410	-1.03	-0.04	-0.23	0.82852	0.908453	-7.33
252771_at	receptor protein kinase -like protein re	---	AT3G42880	-1.02	-0.03	-0.23	0.828501	0.908453	-7.33
262615_at	initiation factor 5A-4 identical to initiati	ELF5A-1	AT1G13950	1.02	0.03	0.23	0.828616	0.908514	-7.33
264462_at	putative transcription factor similar to	WLIM1	AT1G10200	1.03	0.04	0.22	0.828718	0.908516	-7.33
246143_at	lipophosphoglycan biosynthetic protei	---	AT5G19980	1.03	0.04	0.22	0.828737	0.908516	-7.33
259529_at	hypothetical protein	---	AT1G12400	-1.02	-0.02	-0.22	0.828664	0.908516	-7.33
266840_at	hypothetical protein predicted by gens	---	AT2G26160	1.01	0.02	0.22	0.82881	0.908552	-7.33
259139_at	hypothetical protein similar to F16N3.1	---	AT3G10240	-1.02	-0.02	-0.22	0.828913	0.908595	-7.33
246604_at	putative protein	---	---	1.02	0.03	0.22	0.828928	0.908595	-7.33
249704_at	Myb-related transcription factor LBM2-	TT2	AT5G35550	-1.02	-0.03	-0.22	0.828997	0.908626	-7.33
256925_at	hypothetical protein predicted by gene	---	---	1.02	0.02	0.22	0.829106	0.908702	-7.33
259934_at	unknown protein	---	AT1G71340	-1.03	-0.04	-0.22	0.829266	0.908834	-7.33
262554_at	hypothetical protein similar to hypothet	---	AT1G31380	1.02	0.02	0.22	0.829481	0.909026	-7.33
248386_at	DNA-directed RNA polymerase II subu	NRPB6A	AT5G51940	-1.02	-0.03	-0.22	0.829749	0.909276	-7.33
260798_at	unknown protein contains similarity to	---	AT1G78280	-1.03	-0.04	-0.22	0.829829	0.909276	-7.33
255186_at	putative transposon protein similar to A	---	---	1.03	0.04	0.22	0.829816	0.909276	-7.33
249169_at	putative protein strong similarity to unk	---	AT5G42880	1.02	0.03	0.22	0.829871	0.909278	-7.33
262675_at	anter-specific proline-rich -like protein	EXL6	AT1G75930	-1.02	-0.03	-0.22	0.830076	0.909334	-7.33
262905_at	thioredoxin, putative similar to thiored	ATH7	AT1G59730	1.01	0.02	0.22	0.830161	0.909334	-7.33
267521_at	hypothetical protein predicted by genfi	---	AT2G30480	1.02	0.03	0.22	0.829991	0.909334	-7.33
256001_at	unknown protein contains similarity to	---	AT1G29850	1.02	0.03	0.22	0.830153	0.909334	-7.33
250977_at	importin alpha - like protein importin a	IMPA-9	AT5G03070	-1.02	-0.03	-0.22	0.830094	0.909334	-7.33

262683_at	anter-specific proline-rich -like protein	---	AT1G75920	1.02	0.02	0.22	0.830036	0.909334	-7.33
262713_at	unknown protein	---	AT1G16520	-1.03	-0.05	-0.22	0.830213	0.909348	-7.33
263097_at	hypothetical protein predicted by gens	PDV2	AT2G16070	1.02	0.03	0.22	0.830294	0.909392	-7.33
264962_at	auxin transport protein EIR1, putative	PIN6	AT1G77110	-1.02	-0.03	-0.22	0.830394	0.909417	-7.33
263343_at	putative replication protein A1	---	---	1.01	0.02	0.22	0.830397	0.909417	-7.33
251166_at	heat shock transcription factor-like pro	AT-HSFA7B	AT3G63350	-1.02	-0.03	-0.22	0.830449	0.909431	-7.33
246862_at	E2, ubiquitin-conjugating enzyme, put	PEX4	AT5G25760	-1.02	-0.02	-0.22	0.830534	0.909437	-7.33
253411_at	homeobox gene ATH1	ATH1	AT4G32980	-1.04	-0.05	-0.22	0.830523	0.909437	-7.33
254754_at	pectate lyase like protein pectate lyas	---	AT4G13210	-1.02	-0.02	-0.22	0.830577	0.90944	-7.33
247116_at	Mlo protein-like ; supported by cDNA:	MLO10	AT5G65970	-1.02	-0.03	-0.22	0.830637	0.909462	-7.33
263905_at	putative beta-fructofuranosidase (inver	AtcwINV4	AT2G36190	1.03	0.04	0.22	0.830728	0.909483	-7.33
267404_at	hypothetical protein predicted by gene	atnudt22	AT2G33980	-1.02	-0.03	-0.22	0.830735	0.909483	-7.33
256867_at	hypothetical protein predicted by gene	---	AT3G26390	-1.02	-0.02	-0.22	0.830831	0.909544	-7.33
257355_at	hypothetical protein predicted by gens	---	AT2G38150	1.02	0.02	0.22	0.830949	0.909629	-7.33
262594_at	putative 60s ribosomal protein L37 alm	---	AT1G15250	1.05	0.07	0.22	0.831063	0.90971	-7.33
263723_at	putative Ta11-like non-LTR retroeleme	---	AT2G13500	1.02	0.02	0.22	0.831199	0.909773	-7.33
266200_at	hypothetical protein predicted by gens	---	AT2G38920	1.03	0.04	0.22	0.831163	0.909773	-7.33
254542_s_	putative LTR retrotransposon Brassica	---	---	-1.01	-0.02	-0.22	0.831361	0.909905	-7.33
256201_at	hypothetical protein predicted by gens	---	AT1G58230	-1.02	-0.02	-0.22	0.831569	0.91009	-7.33
251206_at	putative protein various predicted proe	---	AT3G63090	-1.03	-0.04	-0.22	0.831757	0.910203	-7.33
262794_at	unknown protein EST gb|N37870 com	emb1745	AT1G13120	-1.02	-0.03	-0.22	0.831792	0.910203	-7.33
265533_at	putative replication protein A1	---	---	1.01	0.02	0.22	0.831713	0.910203	-7.33
249420_at	NAC domain/ NAM like protein NAC d	anac094	AT5G39820	-1.02	-0.02	-0.22	0.831976	0.910318	-7.33
265775_at	Mutator-like transposase similar to MU	---	---	-1.03	-0.04	-0.22	0.831993	0.910318	-7.33
262689_at	unknown protein	ANAC026	AT1G62700	-1.02	-0.03	-0.22	0.832017	0.910318	-7.33
248141_at	unknown protein	---	AT5G55010	1.02	0.02	0.22	0.832277	0.910472	-7.33
263795_at	putative cyclic nucleotide-regulated ion	ATCNGC14	AT2G24610	-1.02	-0.02	-0.22	0.832228	0.910472	-7.33
246950_at	transcription initiation factor IID-assoc	TAF5	AT5G25150	-1.01	-0.02	-0.22	0.832269	0.910472	-7.33
248680_at	pantoate-beta-alanine ligase ;supporte	PANC	AT5G48840	1.02	0.03	0.22	0.832547	0.910679	-7.33
255633_at	Expressed protein ; supported by full-le	---	AT4G00585	-1.02	-0.03	-0.22	0.832538	0.910679	-7.33
256377_at	hypothetical protein	---	AT1G66650	-1.01	-0.02	-0.22	0.832654	0.910752	-7.33
266093_at	unknown protein ;supported by full-ler	---	AT2G37990	1.03	0.04	0.22	0.832698	0.910758	-7.33
264741_at	aspartic protease, putative similar to a	---	AT1G62290	1.06	0.08	0.22	0.833065	0.911071	-7.33
251613_at	hypothetical protein	---	AT3G57960	-1.02	-0.03	-0.22	0.833044	0.911071	-7.33
257802_at	unknown protein	---	AT3G18770	1.02	0.03	0.22	0.833287	0.911074	-7.33

246807_at	ion channel - like protein ligand gated	GLR2.1	AT5G27100	-1.03	-0.04	-0.22	0.83332	0.911074	-7.33
248126_at	protein translation factor Sui1 homolog	ROC5	AT4G34870 /	-1.01	-0.02	-0.22	0.833387	0.911074	-7.33
262547_at	hypothetical protein predicted by gene	---	AT1G31270	-1.01	-0.02	-0.22	0.83322	0.911074	-7.33
246697_at	putative protein	---	AT5G29210	-1.02	-0.03	-0.22	0.833239	0.911074	-7.33
246688_at	putative protein predicted proteins - Ar	---	---	-1.02	-0.02	-0.22	0.833187	0.911074	-7.33
250059_at	peroxidase ATP13a ; supported by ful	---	AT5G17820	-1.02	-0.03	-0.22	0.833357	0.911074	-7.33
258802_at	unknown protein predicted by genscar	---	AT3G04650	-1.02	-0.04	-0.22	0.833138	0.911074	-7.33
254981_at	putative alpha NAC stong similarity to	---	AT4G10480	1.03	0.04	0.22	0.833428	0.911075	-7.33
266868_at	hypothetical protein predicted by gens	---	AT2G44630	-1.02	-0.02	-0.22	0.833566	0.911182	-7.33
248696_at	putative protein similar to unknown pro	---	AT5G48360	1.02	0.03	0.22	0.833622	0.9112	-7.33
255166_at	putative protein putative centromeric p	---	---	-1.02	-0.02	-0.22	0.833853	0.911365	-7.33
249649_at	putative transporter protein Na+ H+-ex	CHX24	AT5G37060	1.01	0.02	0.22	0.833814	0.911365	-7.33
262692_at	hypothetical protein predicted by gene	---	---	1.02	0.03	0.22	0.833905	0.911379	-7.33
251524_at	3-isopropylmalate dehydratase-like pr	---	AT3G58980 /	-1.04	-0.06	-0.22	0.834044	0.911486	-7.33
257315_at	proline oxidase, mitochondrial precurs	ERD5	AT3G30775	1.07	0.09	0.22	0.834096	0.911487	-7.33
247483_at	aldose reductase-like protein	---	AT5G62420	1.02	0.03	0.22	0.834203	0.911487	-7.33
251382_at	pectinesterase - like protein pectineste	---	AT3G60730	1.01	0.02	0.22	0.834139	0.911487	-7.33
258634_at	putative RNA-binding protein contains	---	AT3G08000	-1.03	-0.05	-0.22	0.834204	0.911487	-7.33
249269_at	cell cycle control crn (crooked neck) pr	---	AT5G41770	1.02	0.03	0.22	0.83431	0.911515	-7.33
251170_at	ATMRK1 ;supported by full-length cDI	ATMRK1	AT3G63260	-1.01	-0.02	-0.22	0.834303	0.911515	-7.33
264060_at	hypothetical protein predicted by gens	---	AT2G27980	1.02	0.02	0.22	0.834364	0.911531	-7.33
265163_at	putative OBP32pep protein	---	AT1G23580	-1.01	-0.02	-0.22	0.834648	0.911797	-7.33
252693_s_	ribosomal protein S29 - like ribosomal	---	AT3G43980 /	1.02	0.02	0.22	0.834971	0.912029	-7.33
261418_at	mitochondrial ribosomal protein, putat	---	AT1G07830	1.03	0.04	0.22	0.83498	0.912029	-7.33
255383_at	hypothetical protein	---	AT4G03570	1.01	0.02	0.22	0.834962	0.912029	-7.33
266668_at	hypothetical protein predicted by grail	---	AT2G29760	1.04	0.05	0.22	0.835146	0.912149	-7.33
265875_at	unknown protein ; supported by cDNA	---	AT2G01690	1.02	0.03	0.22	0.835171	0.912149	-7.33
267232_at	hypothetical protein predicted by gens	EDE1	AT2G44190	-1.02	-0.03	-0.22	0.835271	0.912216	-7.33
257529_at	hypothetical protein predicted by gens	---	AT3G03290	1.02	0.02	0.22	0.835405	0.912318	-7.33
247660_at	ankyrin-like protein ankyrin 3, Mus mu	---	AT5G60070	-1.02	-0.02	-0.22	0.835477	0.912353	-7.33
262553_at	hypothetical protein similar to hypothet	RECQL2	AT1G31360	-1.02	-0.03	-0.22	0.835628	0.912474	-7.33
254026_at	putative calmodulin-binding protein ca	---	AT4G25800	1.01	0.02	0.22	0.835724	0.912506	-7.33
261834_at	polygalacturonase PG1, putative simil	---	AT1G10640	1.02	0.02	0.22	0.835771	0.912506	-7.33
254949_at	hypothetical protein	---	AT4G11020	1.02	0.02	0.22	0.835777	0.912506	-7.33
252085_s_	serine-type carboxypeptidase like prot	scpl37	AT3G52000 /	1.01	0.02	0.22	0.835853	0.912545	-7.33

257458_at	hypothetical protein predicted by gens	---	AT2G05400	-1.01	-0.02	-0.22	0.835955	0.912602	-7.33
255307_at	hypothetical protein similar to A. thalia	RIC10	AT4G04900	-1.02	-0.03	-0.22	0.836024	0.912602	-7.33
256559_at	Athila ORF 1, putative similar to Athila	---	---	1.02	0.02	0.22	0.836025	0.912602	-7.33
246875_at	pathogenesis-related protein - like pat	---	AT5G26130	1.02	0.02	0.21	0.836172	0.912695	-7.33
252266_at	putative protein ethylene-forming enzy	---	AT3G49630	1.03	0.04	0.21	0.83619	0.912695	-7.33
249700_at	40S ribosomal protein S3 ; supported	---	AT5G35530	-1.02	-0.03	-0.21	0.836234	0.912699	-7.33
264242_at	hypothetical protein predicted by gene	---	AT1G54640	-1.01	-0.02	-0.21	0.836395	0.912729	-7.33
255368_at	hypothetical protein	---	---	-1.02	-0.02	-0.21	0.836351	0.912729	-7.33
248574_at	putative protein strong similarity to unk	---	AT5G49830	1.01	0.02	0.21	0.836351	0.912729	-7.33
252384_at	ABC-type transport protein-like protein	ATH7	AT3G47790	-1.01	-0.02	-0.21	0.836421	0.912729	-7.33
263968_s_	PttA-like transposon protein no ATG i	---	---	-1.02	-0.03	-0.21	0.836498	0.912769	-7.33
244911_at	hypothetical protein	---	---	-1.02	-0.03	-0.21	0.836543	0.912774	-7.33
249194_at	kinesin heavy chain-like protein	---	AT5G42490	-1.01	-0.02	-0.21	0.836948	0.913172	-7.33
250313_at	Rab geranylgeranyltransferase, beta s	---	AT5G12210	-1.02	-0.03	-0.21	0.837127	0.913324	-7.33
263027_at	hypothetical protein predicted by gene	---	AT1G24010	1.01	0.02	0.21	0.83731	0.91348	-7.33
253563_at	putative protein predicted protein, Sch	---	AT4G31150	1.02	0.03	0.21	0.837661	0.913731	-7.33
254091_at	hypothetical protein	---	AT4G25070	-1.03	-0.04	-0.21	0.837614	0.913731	-7.33
264206_at	putative topoisomerase strong similarit	---	AT1G22730	-1.02	-0.03	-0.21	0.837636	0.913731	-7.33
266373_x_	putative retroelement pol polyprotein	---	---	1.02	0.03	0.21	0.837842	0.913819	-7.33
245221_s_	polyprotein, putative similar to polypro	---	---	1.01	0.02	0.21	0.837824	0.913819	-7.33
257070_at	hypothetical protein predicted by gene	---	AT3G28190	-1.01	-0.02	-0.21	0.837861	0.913819	-7.33
248202_at	unknown protein	---	AT5G54220	-1.02	-0.03	-0.21	0.837967	0.913847	-7.33
260643_at	hypothetical protein contains similarity	---	AT1G53270	-1.02	-0.02	-0.21	0.837933	0.913847	-7.33
245218_s_	viral resistance protein, putative, 5' pa	---	AT1G58848 /	-1.01	-0.02	-0.21	0.838125	0.913976	-7.33
252783_at	putative protein predicted proteins, Ar	---	---	1.01	0.02	0.21	0.838355	0.914183	-7.33
257694_at	nucleolar protein, putative nucleolar p	---	AT3G12860	1.02	0.02	0.21	0.83856	0.914319	-7.33
253439_at	dimethylaniline monooxygenase - like	YUC1	AT4G32540	-1.02	-0.03	-0.21	0.838534	0.914319	-7.33
265125_at	hypothetical protein similar to putative	---	AT1G55410	1.01	0.02	0.21	0.838638	0.91436	-7.33
255799_at	Deetiolated1 (DET1) light signal transd	DET1	AT4G10180	-1.02	-0.03	-0.21	0.838875	0.914444	-7.33
253604_at	hypothetical protein	---	AT4G30970	1.01	0.02	0.21	0.838838	0.914444	-7.33
248793_at	mutT domain protein-like ;supported b	atnudt8	AT5G47240	-1.04	-0.06	-0.21	0.83877	0.914444	-7.33
255392_at	hypothetical protein	---	---	1.01	0.02	0.21	0.838824	0.914444	-7.33
249648_at	putative protein hypothetical protein T	---	AT5G37050	1.02	0.03	0.21	0.839113	0.914573	-7.33
262494_at	myosin-like protein similar to myosin h	---	AT1G21810	-1.02	-0.03	-0.21	0.839053	0.914573	-7.33
250120_at	putative protein similar to unknown pro	RIC4	AT5G16490	1.03	0.04	0.21	0.839075	0.914573	-7.33

259482_at	receptor-like serine/threonine kinase,	RKF2	AT1G19090	-1.02	-0.03	-0.21	0.839335	0.914706	-7.33
264503_at	hypothetical protein Similar to Arabido	---	AT1G09410	1.02	0.02	0.21	0.839356	0.914706	-7.33
247452_at	H-protein promoter binding factor-like p	CDF1	AT5G62430	-1.03	-0.04	-0.21	0.839305	0.914706	-7.33
258126_at	hypothetical protein predicted by gene	---	AT3G24490	-1.02	-0.03	-0.21	0.839555	0.914879	-7.33
255445_at	hypothetical protein	---	AT4G02740	1.02	0.03	0.21	0.839656	0.914946	-7.33
251835_at	lipase -like protein monoglyceride lipa	---	AT3G55180	-1.02	-0.02	-0.21	0.839724	0.914975	-7.33
251690_at	putative protein TATA-binding protein-	---	AT3G56510	1.02	0.02	0.21	0.839801	0.915016	-7.33
262453_at	hypothetical protein predicted by gene	---	AT1G11240	1.01	0.02	0.21	0.839879	0.915058	-7.33
265134_at	putative acyl-CoA : 1-acylglycerol-3-ph	LPAT3	AT1G51260	-1.02	-0.03	-0.21	0.839987	0.915131	-7.33
264431_at	RNA polymerase II subunit (hsRPB10	---	AT1G61700	1.02	0.03	0.21	0.840064	0.915171	-7.33
255466_at	putative protein similar to A. thaliana p	---	AT4G03000	1.02	0.03	0.21	0.840279	0.915215	-7.33
254756_at	putative protein late embryogenesis a	EDA21	AT4G13235	-1.02	-0.02	-0.21	0.840344	0.915215	-7.33
256408_at	hypothetical protein	---	AT1G66610	-1.02	-0.03	-0.21	0.840267	0.915215	-7.33
259651_at	unknown protein	---	AT1G55280	1.04	0.06	0.21	0.840271	0.915215	-7.33
254964_at	98b like protein 98b - Daucus carota (	---	AT4G11080	1.02	0.03	0.21	0.840351	0.915215	-7.33
263436_at	hypothetical protein	---	AT2G28690	1.02	0.03	0.21	0.840385	0.915215	-7.33
263997_at	hypothetical protein predicted by gene	---	AT2G22520	-1.01	-0.02	-0.21	0.840187	0.915215	-7.33
250708_at	Expressed protein ; supported by full-l	RBE	AT5G06070	1.02	0.02	0.21	0.840593	0.915399	-7.33
262893_at	hypothetical protein contains similarity	---	AT1G59790	1.01	0.02	0.21	0.840643	0.915409	-7.33
244914_at	hypothetical protein	---	---	1.02	0.02	0.21	0.840848	0.915544	-7.33
259709_at	Expressed protein ; supported by full-l	---	AT1G77655	-1.02	-0.03	-0.21	0.840841	0.915544	-7.33
259816_at	RING-H2 finger protein RHY1a identic	---	AT1G49850	-1.02	-0.02	-0.21	0.840957	0.915619	-7.33
254017_at	putative transcription factor	---	AT4G26170	1.01	0.02	0.21	0.841053	0.915681	-7.33
257176_s_	cyclopropane-fatty-acyl-phospholipid s	---	AT3G23510 /	-1.06	-0.08	-0.21	0.841124	0.915714	-7.33
253621_at	putative protein component of aniline	---	AT4G30540	-1.02	-0.02	-0.21	0.841208	0.915762	-7.33
257810_at	TOM20, putative similar to TOM20 GE	TOM20-1	AT3G27070	1.02	0.02	0.21	0.841475	0.916009	-7.33
252748_at	putative protein putative proteins - Ara	---	---	-1.01	-0.02	-0.21	0.841589	0.916048	-7.33
248447_at	putative protein contains similarity to p	PABN1	AT5G51120	1.02	0.02	0.21	0.841592	0.916048	-7.33
254230_at	polyprenyltransferase like protein para	AtPPT1	AT4G23660	1.02	0.02	0.21	0.841703	0.916082	-7.33
252926_at	H+-transporting ATPase 16K chain P2	ATVHA-C3	AT4G38920	1.02	0.03	0.21	0.841693	0.916082	-7.33
259938_at	hypothetical protein predicted by gens	---	AT1G71310	1.02	0.02	0.21	0.842009	0.916346	-7.33
245215_at	F12A21.4 similar to iEP4 gb|AAD1146	ATFXG1	AT1G67830	1.04	0.05	0.21	0.842106	0.916346	-7.33
257457_at	hypothetical protein predicted by gene	---	AT2G05430	-1.02	-0.02	-0.21	0.842075	0.916346	-7.33
255349_at	hypothetical protein	---	AT4G03830	-1.01	-0.02	-0.21	0.842095	0.916346	-7.33
253960_at	putative protein various predicted prot	GAMT1	AT4G26420	1.02	0.03	0.21	0.842215	0.916421	-7.33

245607_at	kinesin like protein	---	AT4G14330	1.02	0.02	0.21	0.842616	0.916814	-7.33
256397_at	putative dual-specificity protein phosph	MKP2	AT3G06110	1.02	0.02	0.21	0.842993	0.917092	-7.33
253510_at	hypothetical protein	GDU1	AT4G31730	-1.04	-0.05	-0.21	0.842942	0.917092	-7.33
253018_at	putative protein Zn finger protein BBF	---	AT4G38000	1.02	0.02	0.21	0.842958	0.917092	-7.33
246338_s_	putative protein putative integral mem	ATCHX10	AT3G44920 /	-1.01	-0.02	-0.21	0.843121	0.917187	-7.33
261978_at	Athila retroelment ORF 1, putative sim	---	---	-1.01	-0.02	-0.21	0.843178	0.917206	-7.33
257993_at	hypothetical protein similar to hypothet	---	AT3G19890	1.02	0.02	0.21	0.843252	0.917243	-7.33
248961_at	subtilisin-like protease	---	AT5G45650	1.05	0.07	0.21	0.843328	0.917281	-7.33
255217_s_	hypothetical protein	---	---	-1.02	-0.03	-0.21	0.843393	0.917309	-7.33
253853_at	putative diacylglycerol kinase (fragme	---	AT4G28130	-1.02	-0.02	-0.21	0.843569	0.917394	-7.33
245069_at	putative glucosyltransferase	UGT84B2	AT2G23250	-1.02	-0.02	-0.21	0.843606	0.917394	-7.33
245826_at	disease resistance protein RPS4, puta	---	AT1G57850	-1.02	-0.03	-0.21	0.843632	0.917394	-7.33
256163_at	terpene cyclase, putative similar to ter	---	AT1G48820	-1.01	-0.02	-0.21	0.843603	0.917394	-7.33
252690_at	putative protein	---	---	-1.02	-0.03	-0.20	0.843881	0.917621	-7.33
262127_at	hypothetical protein predicted by gene	---	AT1G52550	-1.02	-0.03	-0.20	0.843962	0.917665	-7.33
261630_at	hypothetical protein predicted by gene	---	AT1G50080	-1.01	-0.02	-0.20	0.844079	0.917715	-7.33
252584_at	putative protein several hypothetical pr	---	AT3G45560	1.02	0.02	0.20	0.844089	0.917715	-7.33
259951_at	unknown protein	---	AT1G71490	1.01	0.02	0.20	0.844238	0.917833	-7.33
266218_s_	putative cytochrome P450	CYP710A4	AT2G28850 /	-1.02	-0.02	-0.20	0.844453	0.917855	-7.33
255996_s_	receptor-like serine threonine kinase,	---	AT1G29730 /	-1.02	-0.03	-0.20	0.844458	0.917855	-7.33
247785_at	subtilisin-like serine protease contains	---	AT5G58820	1.01	0.02	0.20	0.844339	0.917855	-7.33
259064_at	putative calmodulin similar to calmodu	AGD11	AT3G07490	-1.02	-0.03	-0.20	0.844416	0.917855	-7.33
245737_at	hypothetical protein similar to putative	---	AT1G44160	-1.02	-0.04	-0.20	0.84434	0.917855	-7.33
256590_at	recombination signal sequence recogn	ATHMG	AT3G28730	1.02	0.03	0.20	0.84455	0.91791	-7.33
265692_at	hypothetical protein predicted by gens	---	AT2G24340	1.01	0.02	0.20	0.844677	0.918005	-7.33
246599_at	putative protein ATP-dependent RNA	---	AT5G14900	-1.01	-0.02	-0.20	0.844803	0.918011	-7.33
246430_at	calmodulin-like protein calmodulin-rela	---	AT5G17470	-1.02	-0.02	-0.20	0.84477	0.918011	-7.33
267600_at	mitochondrial F1-ATPase, gamma sul	---	AT2G33040	1.03	0.04	0.20	0.844736	0.918011	-7.33
262931_at	small nuclear ribonucleoprotein, putat	---	AT1G65700	1.02	0.02	0.20	0.844855	0.918018	-7.33
245611_at	hypothetical protein	---	AT4G14390	-1.02	-0.03	-0.20	0.845017	0.918018	-7.33
250687_at	putative protein similar to unknown pro	---	AT5G06660	-1.01	-0.02	-0.20	0.844962	0.918018	-7.33
265371_at	putative PttA-like transposon protein re	---	---	-1.01	-0.02	-0.20	0.845052	0.918018	-7.33
256995_at	protein kinase, putative contains simil	---	AT3G25840	1.02	0.03	0.20	0.844994	0.918018	-7.33
254470_at	putative protein other hypothetical prot	---	---	-1.02	-0.03	-0.20	0.844982	0.918018	-7.33
245225_at	mitochondrial protein-like; contains sim	---	AT3G29800	1.02	0.03	0.20	0.845315	0.918065	-7.33

250379_at	transcription factor like protein transcr	TINY2	AT5G11590	-1.01	-0.02	-0.20	0.845321	0.918065	-7.33
249686_at	putative protein contains similarity to c	CYP716A2	AT5G36140	1.01	0.02	0.20	0.84527	0.918065	-7.33
257836_at	hypothetical protein	---	---	-1.02	-0.02	-0.20	0.845336	0.918065	-7.33
247622_at	putative protein	---	AT5G60350	-1.02	-0.02	-0.20	0.845152	0.918065	-7.33
261907_at	4-coumarate:CoA ligase 3 identical to	4CL3	AT1G65060	1.05	0.06	0.20	0.8452	0.918065	-7.33
252506_at	putative protein UDP-galactose transp	UTR5	AT3G46180	1.02	0.03	0.20	0.845504	0.918204	-7.33
262356_at	hypothetical protein predicted by gene	---	AT1G73000	1.01	0.02	0.20	0.845663	0.918289	-7.33
267195_at	putative protein kinase contains a prot	---	AT2G30940	-1.02	-0.03	-0.20	0.845628	0.918289	-7.33
252090_at	5B protein like protein cysteine-rich 5E	---	AT3G52130	-1.01	-0.02	-0.20	0.845707	0.918293	-7.33
245763_at	transposon protein, putative similar to	---	AT1G27850	-1.01	-0.02	-0.20	0.845825	0.918377	-7.33
260661_at	hypothetical protein predicted by gens	---	AT1G19500	1.02	0.03	0.20	0.845979	0.918501	-7.33
262992_at	hypothetical protein predicted by gene	ATG12A	AT1G54210	-1.02	-0.03	-0.20	0.846262	0.918744	-7.33
251435_at	putative protein hypothetical proteins -	---	---	-1.02	-0.02	-0.20	0.846283	0.918744	-7.33
248516_at	unknown protein	---	AT5G50540 /	1.02	0.03	0.20	0.846358	0.918781	-7.33
259389_at	hypothetical protein predicted by gene	---	AT1G06320	-1.01	-0.02	-0.20	0.846978	0.919236	-7.33
255286_at	see T14P8.10 (GB:AF069298)	---	AT4G04650	-1.02	-0.03	-0.20	0.846979	0.919236	-7.33
260717_at	serine/threonine phosphatase PP7, pu	---	AT1G48120	1.02	0.03	0.20	0.846889	0.919236	-7.33
259061_at	putative GTP-binding protein similar to	AtRABA5b	AT3G07410	-1.03	-0.05	-0.20	0.846977	0.919236	-7.33
249756_at	Expressed protein ; supported by full-le	---	AT5G24313	1.01	0.02	0.20	0.846878	0.919236	-7.33
245591_at	hypothetical protein	---	AT4G14530	1.01	0.02	0.20	0.847286	0.919482	-7.33
246649_at	putative protein predicted proteins, Ar	---	---	-1.01	-0.02	-0.20	0.847251	0.919482	-7.33
252436_x_	putative protein several hypothetical pr	---	---	-1.03	-0.04	-0.20	0.847514	0.919686	-7.33
245547_at	cytochrome P450 like protein	CYP702A2	AT4G15300	1.01	0.02	0.20	0.847613	0.91972	-7.33
264719_at	receptor-like kinase, putative similar to	---	AT1G70110	1.02	0.03	0.20	0.847747	0.91972	-7.33
246394_at	myrosinase binding protein, putative s	---	AT1G58160	1.01	0.02	0.20	0.847672	0.91972	-7.33
259145_at	hypothetical protein predicted by gens	---	AT3G10180	-1.01	-0.02	-0.20	0.847725	0.91972	-7.33
256670_at	Athila ORF 1, putative similar to Athila	---	---	1.01	0.02	0.20	0.847674	0.91972	-7.33
245689_at	phosphoglycerate mutase - like protein	---	AT5G04120	-1.02	-0.02	-0.20	0.847858	0.919753	-7.33
245001_at	PSII low MW protein	---	---	1.02	0.03	0.20	0.847832	0.919753	-7.33
245333_at	Expressed protein ; supported by full-le	---	AT4G14615	-1.01	-0.02	-0.20	0.847967	0.919784	-7.33
246271_at	photosystem II oxygen-evolving compl	---	AT4G37230	-1.02	-0.02	-0.20	0.847931	0.919784	-7.33
263270_at	putative replication protein A1	---	---	1.01	0.02	0.20	0.848076	0.919858	-7.33
246903_at	putative protein	---	AT5G25750	-1.02	-0.03	-0.20	0.848204	0.919923	-7.33
263277_at	hypothetical protein predicted by gens	---	AT2G14110	-1.01	-0.02	-0.20	0.848216	0.919923	-7.33
265020_at	putative cytochrome P450 similar to G	CYP86C1	AT1G24540	1.01	0.02	0.20	0.848524	0.920181	-7.33

254967_at	putative protein various predicted prot	---	AT4G10410	-1.02	-0.02	-0.20	0.848535	0.920181	-7.33
252590_at	putative protein kinase NPK1-related	---	AT3G45670	1.02	0.02	0.20	0.848692	0.920242	-7.33
262479_at	leucine-rich repeat transmembrane pr	SUB	AT1G11130	1.01	0.02	0.20	0.848763	0.920242	-7.33
264193_at	CRK1 protein, putative similar to CRK	---	AT1G54610	-1.01	-0.02	-0.20	0.848793	0.920242	-7.33
258220_at	DnaJ, putative similar to DnaJ GB:BA	---	AT3G17830	1.02	0.03	0.20	0.848699	0.920242	-7.33
265427_at	unknown protein	---	AT2G20740	-1.02	-0.03	-0.20	0.848791	0.920242	-7.33
261860_at	scarecrow-like protein similar to SCAR	SCL5	AT1G50600	-1.02	-0.03	-0.20	0.848898	0.920268	-7.33
254769_at	hypothetical protein	---	AT4G13330	1.03	0.05	0.20	0.848874	0.920268	-7.33
254853_at	putative DNA-binding protein AT-hook	---	AT4G12080	-1.02	-0.03	-0.20	0.849084	0.920426	-7.33
249264_s_	disease resistance protein-like	---	AT5G41740 /	-1.03	-0.04	-0.20	0.849124	0.920426	-7.33
247588_at	protein disulfide isomerase precursor	ATPDIL1-4	AT5G60640	1.02	0.02	0.20	0.849199	0.920463	-7.33
262982_at	unknown protein ;supported by full-len	ING2	AT1G54390	1.01	0.02	0.20	0.849421	0.920658	-7.33
248727_at	cytochrome P450	CYP705A5	AT5G47990	1.01	0.02	0.20	0.84946	0.920658	-7.33
247871_at	xyloglucan endotransglycosylase ; su	---	AT5G57530	-1.01	-0.02	-0.20	0.849515	0.920672	-7.33
245928_s_	vegetative storage protein Vsp1 ;supp	VSP1	AT5G24770 /	1.11	0.15	0.20	0.84956	0.920672	-7.33
265089_at	hypothetical protein similar to hypothet	SUVR1	AT1G04050	-1.02	-0.02	-0.20	0.849594	0.920672	-7.33
248267_at	NADH-dependent glutamate synthase	GLT1	AT5G53460	1.02	0.03	0.20	0.849759	0.920677	-7.33
264846_at	senescence-associated protein contair	---	AT2G17850	1.02	0.02	0.20	0.849756	0.920677	-7.33
262077_at	dynamin-like protein similar to dynamir	ADL3	AT1G59610	1.01	0.02	0.20	0.84969	0.920677	-7.33
257425_at	hypothetical protein similar to heat sho	---	AT1G60400	-1.02	-0.03	-0.20	0.849746	0.920677	-7.33
248941_s_	putative protein similar to unknown pro	---	AT5G45460 /	-1.02	-0.03	-0.20	0.849884	0.920691	-7.33
255172_x_	putative transposon protein similar to	---	---	-1.02	-0.03	-0.20	0.849889	0.920691	-7.33
245259_at	kinesin like protein ; supported by cDN	PAKRP1	AT4G14150	-1.01	-0.02	-0.20	0.849906	0.920691	-7.33
262475_at	hypothetical protein predicted by gene	---	AT1G50340	1.02	0.02	0.20	0.849934	0.920691	-7.33
264225_at	hypothetical protein predicted by gene	---	AT1G67420	1.03	0.04	0.20	0.850005	0.920724	-7.33
251778_at	putative protein various predicted prot	ROPGEF6	AT3G55660	-1.02	-0.03	-0.20	0.85018	0.920826	-7.33
247179_at	putative protein contains similarity to b	---	AT5G65320	-1.02	-0.02	-0.20	0.85015	0.920826	-7.33
246459_at	receptor protein kinase -like protein se	---	AT5G16900	-1.02	-0.02	-0.20	0.850242	0.92085	-7.33
261884_at	myrosinase precursor, putative	---	AT1G80910	1.02	0.02	0.20	0.850307	0.92085	-7.33
267615_at	putative phytocyanin	---	AT2G26720	-1.02	-0.03	-0.20	0.850323	0.92085	-7.33
252488_at	glucuronosyl transferase-like protein g	---	AT3G46700	-1.01	-0.02	-0.20	0.850367	0.920854	-7.33
248813_at	Expressed protein ; supported by full-le	VAM3	AT5G46860	-1.02	-0.03	-0.20	0.850455	0.920906	-7.33
265519_at	hypothetical protein	---	AT2G06040	-1.02	-0.02	-0.20	0.850731	0.921161	-7.33
249722_at	putative protein similar to unknown pro	---	AT5G35430	1.01	0.02	0.20	0.850865	0.921218	-7.33
245586_at	hypothetical protein	---	AT4G14980	1.02	0.02	0.20	0.850838	0.921218	-7.33

255556_at	putative NifU-like metallocluster asser	NFU1	AT4G01940	-1.02	-0.03	-0.20	0.851023	0.921343	-7.33
264804_at	putative receptor kinase, CLV1 similar	---	AT1G08590	1.02	0.03	0.20	0.85106	0.921343	-7.33
250201_at	ankyrin - like protein 270 kDa ankyrin	---	AT5G14230	-1.04	-0.06	-0.20	0.851131	0.921375	-7.33
260537_at	hypothetical protein predicted by gens	---	AT2G43450	-1.01	-0.02	-0.19	0.851309	0.921393	-7.33
263687_at	unknown protein ;supported by full-ler	---	AT1G26940	1.02	0.03	0.19	0.851225	0.921393	-7.33
255405_s_	hypothetical protein similar to A. thalia	---	AT4G03440 /	-1.02	-0.03	-0.19	0.851308	0.921393	-7.33
254518_at	downy mildew resistance-like protein	---	AT4G19910	-1.02	-0.02	-0.19	0.85124	0.921393	-7.33
250372_at	putative protein various predicted prot	---	AT5G11460	1.02	0.03	0.19	0.851523	0.921581	-7.33
251287_at	putative protein nucleoid DNA-binding	---	AT3G61820	1.03	0.04	0.19	0.851736	0.921767	-7.33
251004_at	putative protein predicted protein, Ara	---	AT5G02720	-1.02	-0.02	-0.19	0.851938	0.921808	-7.33
263601_s_	dihydrofolate reductase-thymidylate sy	THY-1	AT2G16370 /	-1.02	-0.03	-0.19	0.851896	0.921808	-7.33
248092_at	ubiquitin-like protein	SUMO3	AT5G55170	1.05	0.07	0.19	0.851965	0.921808	-7.33
253354_at	putative protein RNA helicase DBP2 -	---	AT4G33370	1.03	0.04	0.19	0.851975	0.921808	-7.33
258465_at	unknown protein	PMEI2	AT3G17220	-1.02	-0.03	-0.19	0.851846	0.921808	-7.33
260753_at	RING-H2 finger protein RHA3a, putati	---	AT1G49230	1.04	0.06	0.19	0.85219	0.921952	-7.33
251896_at	putative protein predicted proteins, Ar	---	AT3G54390	1.02	0.03	0.19	0.852181	0.921952	-7.33
262858_at	major latex protein type3 identical to m	---	AT1G14940	1.02	0.02	0.19	0.852241	0.921953	-7.33
265080_at	overlap with bases 100,099-109,160 c	sks12	AT1G55570	1.02	0.03	0.19	0.852271	0.921953	-7.33
257872_at	P-glycoprotein, putative similar to P-g	PGP16	AT3G28360	1.01	0.02	0.19	0.852315	0.921957	-7.33
259372_at	homeotic protein boi1AP1, putative si	AP1	AT1G69120	1.02	0.02	0.19	0.852439	0.922047	-7.33
260773_at	gibberellin 2- oxidase identical to gibbe	ATGA2OX1	AT1G78440	-1.02	-0.03	-0.19	0.852659	0.922156	-7.33
249819_at	unknown protein	---	AT5G23640	1.01	0.02	0.19	0.85266	0.922156	-7.33
262877_at	unknown protein ;supported by full-len	---	AT1G64850	1.02	0.03	0.19	0.852592	0.922156	-7.33
263239_at	amidophosphoribosyltransferase ident	ATASE1	AT2G16570	1.02	0.02	0.19	0.852722	0.922178	-7.33
247129_at	alpha-mannosidase	---	AT5G66150	-1.02	-0.03	-0.19	0.852808	0.922189	-7.33
253406_at	putative protein GATA transcription fa	---	AT4G32890	1.03	0.04	0.19	0.852812	0.922189	-7.33
249893_at	Expressed protein ; supported by full-l	---	AT5G22555	-1.02	-0.02	-0.19	0.853117	0.922475	-7.33
252294_at	60S ribosomal protein L13, BBC1 prot	ATBBC1	AT3G49010	-1.04	-0.05	-0.19	0.853267	0.922552	-7.33
245157_at	putative polygalacturonase	---	AT2G33160	-1.01	-0.02	-0.19	0.85327	0.922552	-7.33
247178_at	Expressed protein ; supported by cDN	---	AT5G65205	1.04	0.05	0.19	0.853459	0.922713	-7.33
257645_at	unknown protein ;supported by full-ler	---	AT3G25790	-1.02	-0.03	-0.19	0.853522	0.922737	-7.33
263150_at	heat-shock protein, putative similar to	---	AT1G54050	-1.03	-0.04	-0.19	0.853672	0.922782	-7.33
254036_at	putative peroxidase peroxidase (EC 1	---	AT4G25980	1.01	0.02	0.19	0.853638	0.922782	-7.33
252772_at	hypothetical protein	---	---	-1.01	-0.02	-0.19	0.853684	0.922782	-7.33
259376_at	unknown protein C-terminus similar to	CDC27a	AT3G16320	-1.02	-0.02	-0.19	0.853914	0.922987	-7.33

264615_at	unknown protein ; supported by cDNA	---	AT1G04590	-1.02	-0.04	-0.19	0.853957	0.922989	-7.33
255470_at	hypothetical protein	---	AT4G03040	-1.02	-0.02	-0.19	0.854049	0.923045	-7.33
258830_at	unknown protein	---	AT3G07090	1.03	0.04	0.19	0.854279	0.923118	-7.33
262659_at	putative nucleoside triphosphatase sir	---	AT1G14240	1.02	0.02	0.19	0.854298	0.923118	-7.33
258583_at	putative SRF-type transcription factor (	AGL57	AT3G04100	1.01	0.02	0.19	0.85418	0.923118	-7.33
255091_at	putative protein various predicted prote	---	---	-1.01	-0.02	-0.19	0.854319	0.923118	-7.33
259115_at	hypothetical protein predicted by gens	---	AT3G01360	-1.02	-0.03	-0.19	0.854225	0.923118	-7.33
254675_at	RNA helicase - like protein Cdc28p, S	---	AT4G18465	-1.02	-0.03	-0.19	0.85436	0.923118	-7.33
262410_at	MAGE protein, putative identical to GE	---	AT1G34770	-1.03	-0.04	-0.19	0.854498	0.92318	-7.33
262945_at	unknown protein ;supported by full-len	---	AT1G79510	1.03	0.04	0.19	0.85447	0.92318	-7.33
265708_at	unknown protein member of a large u	---	AT2G03380	-1.01	-0.02	-0.19	0.85464	0.923215	-7.33
252811_at	putative protein several hypothetical pr	---	---	-1.02	-0.02	-0.19	0.854673	0.923215	-7.33
245669_at	hypothetical protein contains similarity	LEC2	AT1G28300	-1.02	-0.03	-0.19	0.854683	0.923215	-7.33
256554_at	hypothetical protein similar to putative	---	---	-1.02	-0.03	-0.19	0.854733	0.923215	-7.33
260338_at	putative RNA-binding protein similar to	---	AT1G69250	1.01	0.02	0.19	0.854717	0.923215	-7.33
251164_s_	putative protein protein phosphatase 2	---	AT3G63320 /	-1.02	-0.02	-0.19	0.854814	0.923259	-7.33
247387_at	unknown protein	---	AT5G63460	-1.01	-0.02	-0.19	0.854934	0.923345	-7.33
257721_at	hypothetical protein predicted by gene	---	AT3G18310	-1.01	-0.02	-0.19	0.855097	0.923409	-7.33
250521_at	selenium-binding protein-like	---	AT5G08490	1.01	0.02	0.19	0.855061	0.923409	-7.33
258703_at	unknown protein	---	AT3G09750	-1.02	-0.03	-0.19	0.855115	0.923409	-7.33
260245_at	putative RNA-binding protein similar to	GR-RBP5	AT1G74230	1.01	0.02	0.19	0.85519	0.923445	-7.33
261500_at	hypothetical protein predicted by gene	---	AT1G28400	-1.04	-0.06	-0.19	0.855256	0.923445	-7.33
256330_at	hypothetical protein predicted by gene	---	AT1G76870	1.02	0.03	0.19	0.855269	0.923445	-7.33
263190_at	mutator-like transposase, putative sim	---	---	1.01	0.02	0.19	0.855322	0.923457	-7.33
251201_at	putative protein predicted protein, Ara	---	AT3G63020	-1.01	-0.02	-0.19	0.855407	0.923462	-7.33
250003_at	hypothetical protein predicted proteins	---	AT5G18710	-1.01	-0.02	-0.19	0.8554	0.923462	-7.33
256758_at	hypothetical protein similar to Athila re	---	---	1.02	0.02	0.19	0.855467	0.923483	-7.33
246249_at	salt-inducible like protein	---	AT4G36680	1.02	0.03	0.19	0.855657	0.923557	-7.33
249608_at	multispanning membrane protein - like	---	AT5G37310	-1.02	-0.02	-0.19	0.855635	0.923557	-7.33
255873_at	hypothetical protein predicted by gens	LBD13	AT2G30340	1.02	0.02	0.19	0.855653	0.923557	-7.33
264412_at	hypothetical protein similar to putative	---	AT1G43260	-1.01	-0.02	-0.19	0.855811	0.92368	-7.33
251741_at	putative protein predicted protein, Ara	UGP3	AT3G56040	1.03	0.05	0.19	0.856047	0.923803	-7.33
258243_at	carbamoyl phosphate synthetase smal	CARA	AT3G27740	1.02	0.03	0.19	0.85603	0.923803	-7.33
246739_at	putative protein predicted protein, Ara	---	AT5G27800	1.01	0.02	0.19	0.855974	0.923803	-7.33
249921_at	reverse-transcriptase - like protein pre	---	AT5G19270	-1.01	-0.02	-0.19	0.856348	0.923839	-7.33

261095_at	unknown protein	---	AT1G62930	-1.02	-0.02	-0.19	0.856315	0.923839	-7.33
247769_at	laccase precursor - like protein laccas	LAC16	AT5G58910	-1.01	-0.02	-0.19	0.856364	0.923839	-7.33
263213_at	unknown protein Strong similarity to gi	---	AT1G30560	-1.02	-0.02	-0.19	0.85621	0.923839	-7.33
246751_at	pectin methyl-esterase - like protein p	---	AT5G27870	-1.01	-0.02	-0.19	0.856195	0.923839	-7.33
254268_at	putative protein FAF1, Mus musculus,	---	AT4G23040	1.02	0.03	0.19	0.856332	0.923839	-7.33
253914_at	putative protein late embryogenesis a	---	AT4G27400	-1.02	-0.03	-0.19	0.856404	0.923839	-7.33
245066_at	putative serine/threonine protein phosp	TOPP4	AT2G39840	1.02	0.02	0.19	0.856286	0.923839	-7.33
245534_at	hypothetical protein	---	AT4G15150	-1.02	-0.02	-0.19	0.856531	0.923932	-7.33
248644_at	disease resistance protein-like	---	AT5G49140	-1.01	-0.02	-0.19	0.856766	0.924142	-7.33
264814_at	putative SET-domain transcriptional re	SDG37	AT2G17900	1.02	0.03	0.19	0.856826	0.924163	-7.33
258624_at	unknown protein ; supported by cDNA	---	AT3G02950	-1.02	-0.02	-0.19	0.856895	0.924194	-7.33
259573_at	hypothetical protein	---	---	-1.01	-0.02	-0.19	0.857035	0.924301	-7.33
266841_at	putative heat shock transcription factor	ATHSFA2	AT2G26150	-1.02	-0.04	-0.19	0.857635	0.924786	-7.33
263665_at	putative putative 60S ribosomal protein	---	AT1G04480	-1.03	-0.04	-0.19	0.857534	0.924786	-7.33
247229_at	putative protein contains similarity to te	---	AT5G65160	-1.02	-0.03	-0.19	0.857804	0.924786	-7.33
252518_at	receptor-like protein kinase homolog I	---	AT3G46350	1.01	0.02	0.19	0.857804	0.924786	-7.33
263055_at	unknown protein	---	---	1.01	0.02	0.19	0.857757	0.924786	-7.33
263464_at	putative ARI-like RING zinc finger prot	---	AT2G31760	1.02	0.02	0.19	0.857725	0.924786	-7.33
257439_at	hypothetical protein similar to hypothet	---	AT2G17000	1.01	0.02	0.19	0.857809	0.924786	-7.33
249857_at	C2H2-type zinc finger protein-like	---	AT5G22990	-1.02	-0.02	-0.19	0.857756	0.924786	-7.33
252721_at	putative protein predicted proteins, Ar	---	AT3G43990	1.02	0.03	0.19	0.857856	0.924793	-7.33
262141_s_	hypothetical protein predicted by gene	---	AT1G52440 /	-1.01	-0.02	-0.19	0.857911	0.924809	-7.33
266913_at	hypothetical protein predicted by gens	ROPGEF4	AT2G45890	1.01	0.02	0.19	0.858077	0.924926	-7.33
253767_at	12S cruciferin seed storage protein	CRU3	AT4G28520	1.01	0.02	0.19	0.858101	0.924926	-7.33
247781_at	dehydrodolichyl diphosphate synthase	---	AT5G58784	1.02	0.03	0.19	0.858144	0.924928	-7.33
262550_at	hypothetical protein similar to hypothet	---	AT1G31310	-1.01	-0.02	-0.19	0.858215	0.924962	-7.33
257655_at	unknown protein contains Pfam profile	---	AT3G13350	1.03	0.04	0.19	0.858418	0.924966	-7.33
258628_at	unknown protein	---	AT3G02890	1.03	0.04	0.19	0.85841	0.924966	-7.33
261528_at	pectate lyase, putative similar to pecta	AT59	AT1G14420	1.02	0.02	0.19	0.858388	0.924966	-7.33
249460_at	v-SNARE - like protein v-SNARE AtV	---	AT5G39630	-1.02	-0.02	-0.19	0.858387	0.924966	-7.33
254580_at	putative protein ; supported by cDNA:	---	AT4G19390	-1.01	-0.02	-0.19	0.858422	0.924966	-7.33
253837_at	putative proline-rich protein extensin -	---	AT4G27850	1.01	0.02	0.18	0.858723	0.925247	-7.33
266692_at	Ac-like transposase related to Ac Ds tr	---	AT2G19960	-1.01	-0.02	-0.18	0.858932	0.925428	-7.34
248878_at	50S ribosomal protein L14	---	AT5G46160	1.01	0.02	0.18	0.859102	0.925567	-7.34
255815_at	histone H3, putative similar to histone	MGH3	AT1G19890	1.02	0.02	0.18	0.859422	0.925869	-7.34

260594_at	hypothetical protein predicted by gens	---	AT1G55880	-1.01	-0.02	-0.18	0.859565	0.925936	-7.34
264604_at	hypothetical protein predicted by gens	---	AT1G04650	1.02	0.03	0.18	0.859561	0.925936	-7.34
248648_at	putative protein similar to unknown pro	---	AT5G49220	-1.02	-0.02	-0.18	0.859607	0.925937	-7.34
246947_at	cytochrome P450-like protein CYTOC	CYP71B11	AT5G25120	1.01	0.02	0.18	0.859945	0.926083	-7.34
257295_at	serine/threonine protein kinase, putati	GPK1	AT3G17420	-1.03	-0.04	-0.18	0.859801	0.926083	-7.34
265085_at	hypothetical protein predicted by gens	TPX2	AT1G03780	-1.02	-0.03	-0.18	0.859923	0.926083	-7.34
266879_at	putative phragmoplastin	ADL1D	AT2G44590	-1.02	-0.02	-0.18	0.859927	0.926083	-7.34
251811_at	APETALA2 - like protein APETALA2,	SMZ	AT3G54990	1.02	0.03	0.18	0.859919	0.926083	-7.34
256878_at	major latex protein, putative similar to	---	AT3G26460	1.02	0.03	0.18	0.860063	0.926166	-7.34
264068_at	putative homeodomain transcription fa	BLH8	AT2G27990	1.03	0.04	0.18	0.860112	0.926175	-7.34
263291_at	unknown protein	---	AT2G10920	1.01	0.02	0.18	0.860176	0.9262	-7.34
252439_at	pectinesterase-like protein pectinester	---	AT3G47400	-1.01	-0.02	-0.18	0.860287	0.926232	-7.34
257099_s_	disease resistance protein, putative, 3	---	AT3G24982 /	1.01	0.02	0.18	0.86026	0.926232	-7.34
255113_at	putative protein various hypothetical p	---	---	-1.01	-0.02	-0.18	0.860492	0.926279	-7.34
246969_at	glutamic acid-rich protein other glutam	---	AT5G24880	1.02	0.02	0.18	0.860575	0.926279	-7.34
250474_at	annexin -like protein annexin (AnnAt2	ANNAT7	AT5G10230	-1.01	-0.02	-0.18	0.860554	0.926279	-7.34
253014_at	MADS-box protein AGL17 -like protei	AGL21	AT4G37940	-1.01	-0.02	-0.18	0.860434	0.926279	-7.34
251158_at	rac-GTP binding protein -like RACC s	MIRO2	AT3G63150	-1.01	-0.02	-0.18	0.860522	0.926279	-7.34
265755_at	En/Spm transposon hypothetical prote	---	---	1.01	0.02	0.18	0.860453	0.926279	-7.34
259677_at	putative phosphatidylinositol-4-phosph	---	AT1G77740	-1.02	-0.03	-0.18	0.861138	0.926517	-7.34
245674_at	chitinase, putative similar to chitinase	---	AT1G56680	-1.01	-0.02	-0.18	0.861176	0.926517	-7.34
253772_at	Expressed protein ; supported by full-l	A7	AT4G28395	-1.01	-0.02	-0.18	0.861242	0.926517	-7.34
257692_at	hypothetical protein contains similarity	---	AT3G12840	1.01	0.02	0.18	0.860989	0.926517	-7.34
266904_at	putative pyruvate dehydrogenase E1 b	---	AT2G34590	1.03	0.04	0.18	0.860963	0.926517	-7.34
245380_at	hypothetical protein	---	AT4G17760	-1.02	-0.03	-0.18	0.861099	0.926517	-7.34
267589_at	hypothetical protein	---	---	1.01	0.02	0.18	0.861027	0.926517	-7.34
257808_at	unknown protein, putative contains Pf	---	AT3G26935	1.01	0.02	0.18	0.861061	0.926517	-7.34
245580_at	hypothetical protein	---	AT4G14820	-1.02	-0.03	-0.18	0.86107	0.926517	-7.34
257669_at	DNA mismatch repair protein, putative	MSH5	AT3G20475	1.01	0.02	0.18	0.861235	0.926517	-7.34
253078_at	putative receptor protein kinase Cf-2.1	---	AT4G36180	1.03	0.04	0.18	0.861012	0.926517	-7.34
261400_at	protein phosphatase-2C, putative simi	---	AT1G79630	-1.02	-0.03	-0.18	0.861327	0.926565	-7.34
261506_at	choline kinase, putative similar to CH	ATCK1	AT1G71697	-1.03	-0.04	-0.18	0.861628	0.926834	-7.34
260149_at	putative oxidoreductase similar to adve	---	AT1G52810	-1.03	-0.05	-0.18	0.861659	0.926834	-7.34
256197_at	hypothetical protein	---	---	1.02	0.03	0.18	0.861724	0.926861	-7.34
245614_at	retrovirus-related like polyprotein	---	---	1.02	0.02	0.18	0.861794	0.926892	-7.34

263817_at	hypothetical protein predicted by gens	---	---	1.02	0.02	0.18	0.861991	0.92706	-7.34
264908_at	unknown protein	---	AT2G17440	1.01	0.02	0.18	0.862034	0.927063	-7.34
265168_at	putative Ser/Thr protein kinase	---	AT1G23700	1.02	0.02	0.18	0.862075	0.927063	-7.34
252166_at	protein kinase SPK-2 ;supported by fu	SNRK2.2	AT3G50500	1.02	0.03	0.18	0.862221	0.92707	-7.34
253641_at	hypothetical protein ;supported by full-	---	AT4G29980	-1.02	-0.02	-0.18	0.862261	0.92707	-7.34
249789_at	putative protein similar to unknown pro	---	AT5G24340	1.02	0.02	0.18	0.862252	0.92707	-7.34
245570_at	heat shock protein 101 (HSP101),puta	CLPB2	AT4G14670	1.01	0.02	0.18	0.862285	0.92707	-7.34
265004_at	polyprotein, putative similar to polypro	---	---	-1.02	-0.03	-0.18	0.862227	0.92707	-7.34
262020_at	polyprotein, putative similar to gag-po	---	---	1.01	0.02	0.18	0.862428	0.927181	-7.34
250671_at	transcription factor HBP-1b homolog (s	AHBP-1B	AT5G06950	1.01	0.02	0.18	0.862593	0.927307	-7.34
259458_at	glycine-rich protein, putative similar to	---	AT1G44085	1.02	0.02	0.18	0.862627	0.927307	-7.34
245907_at	ubiquitin-like protein ubiquitins - differe	---	AT5G09340	-1.01	-0.02	-0.18	0.862735	0.927379	-7.34
263530_at	HSP100/ClpB, putative similar to HSP	---	AT2G25030 /	-1.01	-0.02	-0.18	0.862996	0.927616	-7.34
260121_at	AIG1-like protein similar to AIG1 prote	---	AT1G33910	-1.01	-0.02	-0.18	0.863051	0.927632	-7.34
246573_at	copper amine oxidase, putative simila	---	AT1G31690	-1.02	-0.03	-0.18	0.863276	0.927732	-7.34
247654_at	cytoplasmic ribosomal protein S15a -	---	AT5G59850	-1.04	-0.05	-0.18	0.863348	0.927732	-7.34
249039_at	late embryogenesis abundant protein-l	---	AT5G44310	-1.02	-0.02	-0.18	0.863237	0.927732	-7.34
259386_at	hypothetical protein contains similarity	NUB	AT1G13400	-1.02	-0.02	-0.18	0.863319	0.927732	-7.34
259142_at	unknown protein similar to ankyrin like	---	AT3G10200	-1.02	-0.02	-0.18	0.863231	0.927732	-7.34
266161_at	hypothetical protein	ATCHX7	AT2G28170	1.02	0.03	0.18	0.863439	0.927742	-7.34
265513_at	hypothetical protein	---	---	-1.01	-0.02	-0.18	0.8634	0.927742	-7.34
247081_at	AtRAD17 (dbj|BAA90479.1) ; supporte	ATRAD17	AT5G66130	1.02	0.02	0.18	0.863612	0.927841	-7.34
255464_s_	putative protein similar to T4I9.17	AT7SL-1	AT4G02970 /	-1.01	-0.02	-0.18	0.863593	0.927841	-7.34
256815_at	unknown protein contains Pfam profile	---	AT3G21380	-1.01	-0.02	-0.18	0.863684	0.927875	-7.34
266356_at	putative uclacyanin I identical to GP:U	UCC1	AT2G32300	1.01	0.02	0.18	0.863782	0.927893	-7.34
260016_at	Athila ORF 1, putative simlar to GI:80	---	---	1.01	0.02	0.18	0.863744	0.927893	-7.34
257385_at	hypothetical protein predicted by gens	---	AT2G01800	-1.02	-0.02	-0.18	0.86393	0.928008	-7.34
260691_s_	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.18	0.864042	0.928084	-7.34
246670_at	putative protein	---	AT5G30520	-1.02	-0.03	-0.18	0.86409	0.928092	-7.34
266573_at	unknown protein	---	AT2G23860	1.02	0.03	0.18	0.864193	0.928159	-7.34
245450_at	disease resistance RPP5 like protein (	---	AT4G16880	1.01	0.02	0.18	0.864245	0.928171	-7.34
260210_at	putative xyloglucan fucosyltransferase	FUT3	AT1G74420	-1.02	-0.03	-0.18	0.864498	0.928312	-7.34
258130_at	unknown protein	---	AT3G24510	-1.01	-0.02	-0.18	0.864426	0.928312	-7.34
267221_at	similar to prokaryotic DNA polymerase	STI	AT2G02480	1.01	0.02	0.18	0.864487	0.928312	-7.34
260801_at	hypothetical protein predicted by gene	---	AT1G78430	-1.01	-0.02	-0.18	0.864669	0.928408	-7.34

260983_at	hypothetical protein predicted by gene	---	AT1G53560	-1.03	-0.04	-0.18	0.864669	0.928408	-7.34
257786_at	hypothetical protein predicted by gene	---	AT3G26990	1.02	0.03	0.18	0.865124	0.928721	-7.34
249363_at	DegP protease contains similarity to D	DegP13	AT5G40560	-1.01	-0.02	-0.18	0.865054	0.928721	-7.34
254712_at	hypothetical protein	---	AT4G18080	-1.01	-0.02	-0.18	0.865111	0.928721	-7.34
245973_at	putative protein predicted proteins, Ar	---	---	-1.01	-0.02	-0.18	0.865043	0.928721	-7.34
252263_at	putative protein several hypothetical pr	---	AT3G49520	-1.02	-0.02	-0.18	0.865843	0.92945	-7.34
253754_at	glycine-rich protein like glycine-rich pr	---	AT4G29020	-1.05	-0.07	-0.18	0.865917	0.929463	-7.34
246811_at	putative protein	---	AT5G27170	1.01	0.02	0.18	0.865937	0.929463	-7.34
249128_at	1-aminocyclopropane-1-carboxylate ox	---	AT5G43440	1.01	0.02	0.18	0.866061	0.929493	-7.34
263770_at	Mutator-like transposase similar to MU	---	---	1.02	0.03	0.18	0.866087	0.929493	-7.34
249680_s_	putative protein strong similarity to unk	---	AT3G61730 /	1.01	0.01	0.18	0.866018	0.929493	-7.34
254313_at	extensin like protein extensin like prot	---	AT4G22460	1.02	0.02	0.17	0.866379	0.929763	-7.34
248658_at	chromosome condensation protein	ATSMC3	AT5G48600	-1.01	-0.02	-0.17	0.866437	0.929782	-7.34
257200_at	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.17	0.866815	0.930143	-7.34
249291_at	glutathione transferase AtGST 10 (eml	ATGSTT1	AT5G41210	-1.02	-0.02	-0.17	0.866893	0.930183	-7.34
245903_at	CLB1 - like protein CLB1 protein, Lyc	SYTD	AT5G11100	-1.01	-0.02	-0.17	0.86695	0.930201	-7.34
263070_at	unknown protein	---	AT2G17600	-1.01	-0.02	-0.17	0.867092	0.930309	-7.34
253895_at	NWMU3 - 2S albumin 3 precursor	AT2S3	AT4G27160	1.01	0.02	0.17	0.867316	0.930506	-7.34
254193_at	putative protein predicted proteins, Ar	---	AT4G23870	1.04	0.06	0.17	0.867518	0.930678	-7.34
258308_at	putative reverse transcriptase similar t	---	---	1.03	0.04	0.17	0.86757	0.930691	-7.34
246355_at	hypothetical protein	---	---	-1.03	-0.04	-0.17	0.867708	0.930794	-7.34
264357_at	hypothetical protein Similar to hypothe	ATRRP4	AT1G03360	1.04	0.06	0.17	0.867791	0.93084	-7.34
260945_at	hypothetical protein predicted by gene	---	AT1G05950	-1.02	-0.02	-0.17	0.867979	0.93091	-7.34
257316_at	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.17	0.867936	0.93091	-7.34
255640_at	hypothetical protein	---	AT4G00800	1.02	0.03	0.17	0.867975	0.93091	-7.34
254953_at	Expressed protein ; supported by full-l	---	AT4G10925	1.01	0.02	0.17	0.868035	0.930926	-7.34
263069_at	unknown protein	---	AT2G17590	-1.03	-0.04	-0.17	0.868115	0.930969	-7.34
246407_at	disease resistance protein RPS4, puta	---	AT1G57670	-1.01	-0.02	-0.17	0.868185	0.931	-7.34
260462_at	ZIP4, a putative zinc transporter per s	ZIP4	AT1G10970	1.03	0.04	0.17	0.868276	0.931054	-7.34
246359_x_	hypothetical protein	---	---	-1.02	-0.03	-0.17	0.868378	0.931075	-7.34
259691_at	hypothetical protein predicted by gene	---	AT1G63200	1.02	0.03	0.17	0.868349	0.931075	-7.34
256945_at	hypothetical protein similar to extensin	---	AT3G19020	-1.01	-0.02	-0.17	0.868446	0.931105	-7.34
245853_at	putative protein predicted protein At2g	---	AT5G13500	-1.02	-0.03	-0.17	0.868505	0.931124	-7.34
245154_at	putative protein similarity to predicted p	---	AT5G12460	-1.01	-0.02	-0.17	0.868599	0.931181	-7.34
256175_at	unknown protein	---	AT1G51670	-1.01	-0.02	-0.17	0.868643	0.931185	-7.34

246276_at	Cu2+-transporting ATPase-like protein	HMA1	AT4G37270	1.01	0.02	0.17	0.868768	0.931275	-7.34
256144_at	guanine nucleotide-binding protein, pu	RACK1B_AT	AT1G48630	-1.04	-0.06	-0.17	0.869075	0.931532	-7.34
260797_at	neoxanthin cleavage enzyme, putative	NCED9	AT1G78390	1.01	0.02	0.17	0.869089	0.931532	-7.34
245071_at	putative vetispiradiene synthase	---	AT2G23230	-1.02	-0.02	-0.17	0.869208	0.931615	-7.34
252900_at	shikimate kinase - like protein shikima	---	AT4G39540	-1.02	-0.03	-0.17	0.869256	0.931622	-7.34
265698_at	hypothetical protein predicted by gens	---	AT2G32160	-1.01	-0.02	-0.17	0.869398	0.931731	-7.34
259693_at	hypothetical protein predicted by gene	---	AT1G63060	-1.02	-0.02	-0.17	0.869542	0.931842	-7.34
263368_at	putative protein kinase contains a prot	---	AT2G20470	1.02	0.02	0.17	0.869754	0.932025	-7.34
250253_at	putative protein contains similarity to u	PDAT	AT5G13640	-1.02	-0.02	-0.17	0.869822	0.932054	-7.34
262034_at	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.17	0.869896	0.93209	-7.34
253521_at	multicatalytic endopeptidase complex	PBA1	AT4G31300	-1.02	-0.03	-0.17	0.869955	0.932109	-7.34
262110_at	SF2/ASF-like splicing modulator Srp3	SR1	AT1G02840	1.02	0.02	0.17	0.870159	0.932241	-7.34
258688_at	putative eukaryotic translation initiation	---	AT3G07920	-1.01	-0.02	-0.17	0.870122	0.932241	-7.34
254402_at	putative protein predicted protein, Ara	---	AT4G21310	1.02	0.03	0.17	0.870313	0.932318	-7.34
261706_at	hypothetical protein similar to hypothet	---	---	-1.01	-0.02	-0.17	0.870281	0.932318	-7.34
261465_at	unknown protein	---	AT1G07705	1.01	0.02	0.17	0.870366	0.932331	-7.34
255190_x_	may be a pseudogene similar to a fam	---	---	-1.01	-0.02	-0.17	0.870493	0.932422	-7.34
246819_at	WD-repeat protein - like WD-repeat pr	---	AT5G26900	-1.01	-0.02	-0.17	0.870533	0.932422	-7.34
251560_at	squamosa promoter-binding protein h	SPL15	AT3G57920	-1.02	-0.03	-0.17	0.870576	0.932424	-7.34
257107_at	transmembrane trafficking protein, put	---	AT3G29070	-1.01	-0.02	-0.17	0.870718	0.932477	-7.34
259035_at	hypothetical protein predicted by gene	---	AT3G09430	-1.01	-0.02	-0.17	0.870789	0.932477	-7.34
246545_at	pectate lyase -like protein pectate lyas	---	AT5G15110	1.01	0.02	0.17	0.870771	0.932477	-7.34
252750_at	putative protein hypothetical protein q	---	AT3G43420	-1.01	-0.02	-0.17	0.87069	0.932477	-7.34
262472_at	hypothetical protein similar to putative	---	AT1G50160	-1.01	-0.02	-0.17	0.870859	0.932508	-7.34
246817_at	putative protein various predicted prot	---	AT5G27240	1.02	0.02	0.17	0.871058	0.932546	-7.34
246798_at	putative protein various predicted prot	---	AT5G26930	1.01	0.02	0.17	0.871027	0.932546	-7.34
264196_at	putative RING zinc finger protein Cont	---	AT1G22670	-1.01	-0.02	-0.17	0.871033	0.932546	-7.34
247911_at	putative protein contains similarity to D	XRCC3	AT5G57450	1.01	0.02	0.17	0.871032	0.932546	-7.34
260319_at	hypothetical protein predicted by gene	---	AT1G63950	1.02	0.02	0.17	0.87112	0.932569	-7.34
260299_at	putative gibberellin 3 beta-hydroxylase	GA3OX4	AT1G80330	1.01	0.02	0.17	0.871262	0.932677	-7.34
260145_at	putative G protein-coupled receptor sir	GPCR	AT1G52920	1.01	0.02	0.17	0.87138	0.93276	-7.34
247425_at	unknown protein	---	AT5G62550	-1.01	-0.02	-0.17	0.871429	0.932768	-7.34
256555_at	hypothetical protein similar to putative	---	---	-1.01	-0.02	-0.17	0.871718	0.933034	-7.34
252540_at	putative protein CDP-alcohol phospha	---	AT3G45740	1.01	0.02	0.17	0.871777	0.933053	-7.34
256498_at	hypothetical protein	---	---	1.01	0.02	0.17	0.871859	0.933097	-7.34

260110_at	hypothetical protein similar to NBS/LR	---	AT1G63350	1.01	0.02	0.17	0.872276	0.933356	-7.34
259991_at	putative S-adenosyl-L-methionine:salic	---	AT1G68040	1.01	0.02	0.17	0.872305	0.933356	-7.34
256750_at	unknown protein contains Pfam profile	---	AT3G27150	-1.02	-0.02	-0.17	0.872239	0.933356	-7.34
265608_at	hypothetical protein predicted by gens	---	AT2G25380	1.01	0.02	0.17	0.872284	0.933356	-7.34
257388_at	putative non-LTR retroelement reverse	---	---	1.01	0.01	0.17	0.872266	0.933356	-7.34
261993_at	unknown protein	---	AT1G33860	1.01	0.02	0.17	0.872365	0.933376	-7.34
260896_at	flower pigmentation protein ATAN11 si	---	AT1G29310	-1.03	-0.04	-0.17	0.872463	0.933394	-7.34
244957_at	hypothetical protein	AT2G07835	---	-1.01	-0.02	-0.17	0.872545	0.933394	-7.34
247928_at	villin	---	AT5G57320	-1.02	-0.02	-0.17	0.872507	0.933394	-7.34
259929_at	transcription factor, putative similar to	---	AT1G34360	-1.01	-0.02	-0.17	0.872539	0.933394	-7.34
261390_at	hypothetical protein similar to hypothet	---	AT1G35040	1.01	0.02	0.17	0.872726	0.933544	-7.34
256206_at	hypothetical protein predicted by gene	---	AT1G50910	-1.02	-0.03	-0.17	0.873104	0.933904	-7.34
256744_at	ATHP2, putative similar to ATHP2 GB	ATHP2	AT3G29350	1.02	0.02	0.17	0.873236	0.934001	-7.34
250927_at	lysine decarboxylase - like protein lysi	---	AT5G03270	1.02	0.02	0.17	0.87329	0.934015	-7.34
249055_at	calmodulin-like protein	---	AT5G44460	1.01	0.02	0.17	0.873539	0.93422	-7.34
251452_at	putative protein male sterility protein 2	---	AT3G60060	1.01	0.01	0.17	0.873563	0.93422	-7.34
246171_at	putative protein centrosomal Nek2-as	---	AT5G32440	1.01	0.02	0.17	0.873606	0.934222	-7.34
264319_at	subtilisin-like serine protease, putative	SDD1	AT1G04110	-1.02	-0.02	-0.17	0.873653	0.934228	-7.34
253133_at	DNA-directed RNA polymerase (EC 2.	NRPB1	AT4G35800	1.01	0.02	0.17	0.873702	0.934237	-7.34
252773_at	putative protein predicted proteins, Ar	---	---	-1.01	-0.02	-0.16	0.873891	0.934317	-7.34
261251_at	hypothetical protein predicted by gene	---	AT1G05920	-1.02	-0.03	-0.16	0.8739	0.934317	-7.34
255375_at	putative athila-like protein	---	---	1.01	0.02	0.16	0.873868	0.934317	-7.34
257460_at	auxin induced protein, putative similar	---	AT1G75580	-1.01	-0.02	-0.16	0.874028	0.934358	-7.34
255037_at	DNA-binding protein ;supported by ful	ATMYB6	AT4G09460	1.03	0.04	0.16	0.874009	0.934358	-7.34
259893_at	putative disease resistance protein sim	AtRLP11	AT1G71390	1.01	0.02	0.16	0.874102	0.934358	-7.34
258336_at	putative ethylene-inducible protein sim	PDX1.2	AT3G16050	1.03	0.04	0.16	0.874074	0.934358	-7.34
260951_at	hypothetical protein similar to hypothet	---	AT1G06145 /	-1.02	-0.02	-0.16	0.874591	0.934712	-7.34
249497_at	putative protein predicted proteins - dif	---	AT5G39220	1.02	0.02	0.16	0.874541	0.934712	-7.34
264642_at	putative CCAAT-binding transcription f	NF-YB4	AT1G09030	1.01	0.02	0.16	0.87449	0.934712	-7.34
262421_at	hypothetical protein predicted by gene	---	AT1G50290	1.02	0.03	0.16	0.874597	0.934712	-7.34
245631_at	tRNA-glutamine synthetase, putative s	OVA9	AT1G25350	-1.01	-0.02	-0.16	0.874666	0.934723	-7.34
264310_at	hypothetical protein similar to hypothet	---	AT1G62030	1.01	0.02	0.16	0.874689	0.934723	-7.34
251836_at	lipase -like protein monoglyceride lipa	---	AT3G55190	-1.01	-0.01	-0.16	0.874761	0.934756	-7.34
267258_at	hypothetical protein predicted by gens	---	AT2G23140	1.01	0.02	0.16	0.87484	0.934797	-7.34
250555_at	putative protein ferredoxin (2Fe-2S), A	---	AT5G07950	-1.02	-0.03	-0.16	0.875079	0.93489	-7.34

255031_at	putative proteins various hypothetical p	---	AT4G09490	1.02	0.02	0.16	0.875077	0.93489	-7.34
253123_at	thaumatin-like protein thaumatin-like p	---	AT4G36000	1.02	0.02	0.16	0.875051	0.93489	-7.34
248712_at	unknown protein	---	AT5G48280	-1.01	-0.02	-0.16	0.875132	0.93489	-7.34
249226_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G42170	-1.01	-0.02	-0.16	0.875096	0.93489	-7.34
249952_at	putative protein predicted proteins, Ar	---	AT5G18950	1.01	0.02	0.16	0.875583	0.935312	-7.34
249262_at	putative protein similar to unknown pro	---	AT5G41720	-1.01	-0.02	-0.16	0.875609	0.935312	-7.34
256601_s_	At14a-1 protein identical to At14a prot	AT14A	AT3G28290 /	1.01	0.02	0.16	0.87573	0.935353	-7.34
262983_at	hypothetical protein similar to unknowr	---	AT1G54550	-1.01	-0.02	-0.16	0.875717	0.935353	-7.34
267457_at	putative proline-rich protein	AGP30	AT2G33790	-1.01	-0.02	-0.16	0.875932	0.935525	-7.34
245767_at	hypothetical protein similar to putative	---	AT1G33610	1.01	0.01	0.16	0.876078	0.935637	-7.34
266169_at	putative protease inhibitor ;supported	---	AT2G38900	-1.01	-0.02	-0.16	0.876121	0.93564	-7.34
261468_s_	hypothetical protein predicted by gene	---	AT1G27860 /	1.02	0.02	0.16	0.876232	0.935714	-7.34
255224_at	putative protein hypothetical protein, A	---	AT4G05400	-1.02	-0.02	-0.16	0.876515	0.935841	-7.34
259137_at	unknown protein Pfam HMM hit: EF ha	---	AT3G10300	-1.02	-0.03	-0.16	0.876416	0.935841	-7.34
258469_at	unknown protein contains Pfam profile	PRXIIF	AT3G06050	1.01	0.02	0.16	0.876499	0.935841	-7.34
267546_at	putative disease resistance protein	AtRLP23	AT2G32680	-1.07	-0.09	-0.16	0.876508	0.935841	-7.34
265645_at	unknown protein	---	AT2G27370	1.01	0.02	0.16	0.876631	0.935914	-7.34
253036_at	putative protein other predicted protein	---	AT4G38340	1.02	0.02	0.16	0.876707	0.935914	-7.34
250913_at	3-deoxy-D-manno-octulosonic acid tra	---	AT5G03770	1.01	0.02	0.16	0.876696	0.935914	-7.34
254071_at	hypothetical protein	---	AT4G25510	-1.01	-0.02	-0.16	0.876773	0.935941	-7.34
260662_at	2-hydroxyisoflavone reductase, putativ	---	AT1G19540	1.01	0.02	0.16	0.876945	0.936081	-7.34
258726_at	Expressed protein ; supported by full-le	---	AT3G11745	1.01	0.02	0.16	0.877033	0.936131	-7.34
258148_s_	DNA-directed RNA polymerase II sec	NRPD2B	AT3G18090 /	1.02	0.03	0.16	0.877334	0.936333	-7.34
250121_at	protein kinase-like protein	---	AT5G16500	1.01	0.02	0.16	0.877346	0.936333	-7.34
260604_at	polyphosphoinositide binding protein,	---	AT1G55840	1.02	0.03	0.16	0.877344	0.936333	-7.34
255680_at	hypothetical protein	---	AT4G00530	-1.02	-0.02	-0.16	0.877401	0.936348	-7.34
263011_at	conserved hypothetical protein protein	---	AT1G23250	-1.01	-0.02	-0.16	0.877572	0.936488	-7.34
260649_at	storage protein, putative similar to GB	ACA7	AT1G08080	1.01	0.02	0.16	0.877656	0.936533	-7.34
254475_at	putative snRNP protein small nuclear	smB	AT4G20440	1.02	0.03	0.16	0.877844	0.93669	-7.34
247647_at	respiratory burst oxidase protein - like	---	AT5G60010	-1.01	-0.02	-0.16	0.877935	0.936743	-7.34
267047_at	putative selenium-binding protein	---	AT2G34370	-1.01	-0.02	-0.16	0.878038	0.936809	-7.34
256773_at	hypothetical protein predicted by gene	---	AT3G13630	-1.01	-0.02	-0.16	0.878186	0.936924	-7.34
249635_at	putative glucan synthase glucan synth	ATGSL09	AT5G36870	-1.01	-0.02	-0.16	0.878301	0.937003	-7.34
265791_at	putative transcription factor	MEE65	AT2G01280	1.01	0.02	0.16	0.878381	0.937044	-7.34
248565_at	putative protein similar to unknown pro	---	AT5G49710	-1.02	-0.03	-0.16	0.878472	0.937097	-7.34

245260_at	kinase like protein ; supported by cDN	---	AT4G16360	-1.01	-0.02	-0.16	0.878612	0.937147	-7.34
252454_at	putative protein various predicted prot	---	AT3G47130	1.01	0.01	0.16	0.878795	0.937147	-7.34
246560_at	putative protein hypothetical protein F1	---	AT5G15560	-1.01	-0.02	-0.16	0.878774	0.937147	-7.34
267449_at	hypothetical protein predicted by gens	---	AT2G33690	1.01	0.01	0.16	0.878678	0.937147	-7.34
266935_at	F-box protein LKP2/ADO2, AtFBX2c i	LKP2	AT2G18915	1.01	0.02	0.16	0.878806	0.937147	-7.34
255196_x_	see GB:AF058826	---	---	1.01	0.02	0.16	0.87876	0.937147	-7.34
264495_at	hypothetical protein predicted by gens	RIC2	AT1G27380	-1.01	-0.02	-0.16	0.878785	0.937147	-7.34
260374_at	unknown protein	TAF2	AT1G73960	-1.01	-0.02	-0.16	0.878885	0.937187	-7.34
245709_at	putative protein	---	AT5G04320	-1.02	-0.02	-0.16	0.879001	0.937246	-7.34
266350_at	putative protein transport protein SEC	STL2P	AT2G01470	1.02	0.03	0.16	0.879022	0.937246	-7.34
253463_at	Expressed protein ; supported by full-l	---	AT4G32105	1.01	0.02	0.16	0.879176	0.937251	-7.34
249298_at	putative protein similar to unknown pro	---	AT5G41330	1.01	0.02	0.16	0.87918	0.937251	-7.34
248691_at	putative protein strong similarity to unk	---	AT5G48310	1.01	0.02	0.16	0.879191	0.937251	-7.34
260282_at	putative N-terminal acetyltransferase s	EMB2753	AT1G80410	-1.01	-0.02	-0.16	0.879081	0.937251	-7.34
252779_at	putative protein	---	AT3G42990	1.01	0.02	0.16	0.879263	0.937283	-7.34
249056_at	putative protein similar to unknown pro	---	AT5G44470	-1.01	-0.02	-0.16	0.879419	0.937406	-7.34
252915_at	EF-Hand containing protein -like stron	---	AT4G38810	1.02	0.02	0.16	0.87952	0.93747	-7.34
250229_at	putative protein contains similarity to n	NACA3	AT5G13850	1.02	0.03	0.16	0.87958	0.93749	-7.34
264966_at	hypothetical protein predicted by gene	---	AT1G60570	1.02	0.02	0.16	0.879905	0.937775	-7.34
255174_at	putative Athila-like protein	---	---	-1.01	-0.02	-0.16	0.87993	0.937775	-7.34
250856_at	putative protein salt-inducible protein,	---	AT5G04810	-1.02	-0.02	-0.16	0.880535	0.938114	-7.34
251794_at	mannose-1-phosphate guanylyltransfe	---	AT3G55590	-1.01	-0.02	-0.16	0.880522	0.938114	-7.34
256690_at	hypothetical protein predicted by gens	---	AT3G32160	1.01	0.02	0.16	0.880366	0.938114	-7.34
263220_at	hypothetical protein predicted by gens	emb2279	AT1G30610	-1.02	-0.02	-0.16	0.880465	0.938114	-7.34
254287_at	putative protein similaritry to hypotheti	---	AT4G22960	-1.01	-0.02	-0.16	0.88047	0.938114	-7.34
244907_at	hypothetical protein	---	---	-1.01	-0.01	-0.16	0.880503	0.938114	-7.34
263272_at	hypothetical protein predicted by gens	---	---	-1.01	-0.02	-0.16	0.880417	0.938114	-7.34
247067_at	putative protein strong similarity to unk	---	AT5G66950	-1.02	-0.03	-0.16	0.880651	0.938193	-7.34
262743_at	unknown protein similar to unknown pr	---	AT1G29020	1.01	0.02	0.16	0.880764	0.93827	-7.34
262852_at	hypothetical protein predicted by gens	---	AT1G20910	1.01	0.02	0.16	0.881198	0.938353	-7.34
253715_at	RIBOSOMAL PROTEIN S30 homolog	---	AT4G29390	1.01	0.02	0.16	0.881084	0.938353	-7.34
245303_at	hypothetical protein ; supported by full-	---	AT4G17010	-1.01	-0.02	-0.16	0.881254	0.938353	-7.34
252575_at	receptor like protein kinase receptor li	---	AT3G45440	1.02	0.03	0.16	0.881145	0.938353	-7.34
265916_at	hypothetical protein similar to En/Spm-	---	---	1.01	0.02	0.16	0.881246	0.938353	-7.34
253935_at	putative aspartate-tRNA ligase aspart	---	AT4G26870	1.03	0.04	0.16	0.881246	0.938353	-7.34

256663_at	unknown protein ;supported by full-len	---	AT3G12050	1.02	0.03	0.16	0.880948	0.938353	-7.34
256952_at	mannosidase, putative similar to mani	---	AT3G21160	-1.02	-0.02	-0.16	0.881235	0.938353	-7.34
252668_at	hypothetical protein	---	AT3G44210	1.01	0.01	0.16	0.881057	0.938353	-7.34
265552_at	putative plasma membrane proton ATF	AHA6	AT2G07560	1.01	0.02	0.16	0.88118	0.938353	-7.34
252796_at	putative protein predicted proteins, Ar	---	---	-1.02	-0.03	-0.16	0.88132	0.938379	-7.34
260059_at	trehalose-6-phosphate phosphatase (	ATTPPB	AT1G78090	-1.02	-0.03	-0.15	0.881376	0.938396	-7.34
247342_at	ARI-like RING zinc finger protein-like	---	AT5G63730	-1.01	-0.02	-0.15	0.881431	0.938411	-7.34
256906_at	hypothetical protein contains Pfam pro	---	AT3G24000	1.02	0.02	0.15	0.88149	0.93843	-7.34
256164_at	terpene cyclase, putative similar to ter	---	AT1G48800	-1.01	-0.02	-0.15	0.881619	0.938523	-7.34
265753_at	putative Athila retroelement ORF1 prot	---	---	1.01	0.01	0.15	0.881759	0.938543	-7.34
265979_at	putative replication protein A1	---	---	-1.01	-0.02	-0.15	0.881696	0.938543	-7.34
257259_at	hypothetical protein predicted by gene	---	AT3G22090	1.01	0.01	0.15	0.881761	0.938543	-7.34
264937_at	hypothetical protein contains similarity	SCPL32	AT1G61130	1.01	0.02	0.15	0.881925	0.938673	-7.34
257415_at	hypothetical protein similar to hypothet	---	AT1G70040	-1.01	-0.02	-0.15	0.882024	0.938691	-7.34
258522_at	hypothetical protein predicted by gene	---	AT3G06660	1.02	0.03	0.15	0.881994	0.938691	-7.34
260732_at	myb-related DNA-binding protein, puta	---	AT1G17520	-1.01	-0.02	-0.15	0.882075	0.938701	-7.34
265065_at	putative phytochelatin synthase	ATPCS2	AT1G03980	1.01	0.02	0.15	0.882191	0.938781	-7.34
255965_at	14-3-3 protein (grf14), putative similar	---	AT1G22290	-1.01	-0.02	-0.15	0.882299	0.938852	-7.34
265685_at	NAM (no apical meristem)-like protein	ANAC038	AT2G24430	-1.02	-0.02	-0.15	0.882352	0.938859	-7.34
262009_at	hypothetical protein predicted by gene	---	AT1G35610	-1.01	-0.02	-0.15	0.882387	0.938859	-7.34
267144_at	unknown protein	GPAT6	AT2G38110	1.03	0.04	0.15	0.882459	0.938891	-7.34
266148_x_	En/Spm-like transposon protein relate	---	---	-1.01	-0.02	-0.15	0.882707	0.939111	-7.34
247363_at	unknown protein	---	AT5G63200	1.01	0.02	0.15	0.882859	0.93923	-7.34
252302_at	putative protein hypothetical protein R	---	AT3G49190	-1.01	-0.01	-0.15	0.882915	0.939245	-7.34
260304_at	unknown protein identical to most of O	---	AT1G70480	-1.02	-0.03	-0.15	0.882981	0.939271	-7.34
252390_at	Expressed protein ; supported by cDN	---	AT3G47836	-1.01	-0.02	-0.15	0.883023	0.939272	-7.34
256214_x_	hypothetical protein predicted by gene	---	AT1G51000	1.01	0.02	0.15	0.883159	0.939373	-7.34
255097_at	predicted transposon protein similar to	---	---	1.02	0.02	0.15	0.883331	0.939512	-7.34
261294_at	dihydroxyacetone kinase, putative sim	---	AT1G48430	1.02	0.02	0.15	0.883383	0.939524	-7.34
264329_at	unknown protein Contains similarity to	---	AT1G04140	-1.01	-0.02	-0.15	0.883462	0.939564	-7.34
AFFX-BioD	E. coli /GEN=bioD /DB_XREF=gb:J04	---	---	1.03	0.04	0.15	0.883653	0.939724	-7.34
265330_at	unknown protein	GUT15	---	-1.01	-0.02	-0.15	0.883696	0.939725	-7.34
250115_at	salt-inducible protein-like	---	AT5G16420	1.02	0.03	0.15	0.883831	0.939788	-7.34
265765_at	hypothetical protein predicted by gens	---	AT2G48060	1.01	0.02	0.15	0.883872	0.939788	-7.34
252710_at	cellulase-like protein cellulase, Sambu	AtGH9A4	AT3G43860	1.01	0.02	0.15	0.883879	0.939788	-7.34

262726_at	hypothetical protein similar to putative	AtTLP5	AT1G43640	-1.01	-0.02	-0.15	0.884171	0.939866	-7.34
245994_at	putative protein various predicted prot	---	---	1.01	0.02	0.15	0.884059	0.939866	-7.34
261384_at	hypothetical protein predicted by gene	---	AT1G05440	-1.01	-0.02	-0.15	0.884127	0.939866	-7.34
267575_at	unknown protein predicted by genscan	---	AT2G30690	1.01	0.02	0.15	0.884014	0.939866	-7.34
255940_at	prolyl endopeptidase, putative similar	---	AT1G20380	1.01	0.01	0.15	0.884199	0.939866	-7.34
252047_at	putative protein heat shock protein - G	---	AT3G52490	1.01	0.02	0.15	0.884113	0.939866	-7.34
245072_s_	putative cytochrome P450	CYP81D7	AT2G23190 /	1.01	0.02	0.15	0.884255	0.939882	-7.34
245589_at	subtilisin-like serine protease contains	---	AT4G15040	-1.02	-0.03	-0.15	0.884525	0.940081	-7.34
262012_s_	integral membrane protein, putative si	---	AT1G35625 /	1.01	0.02	0.15	0.884512	0.940081	-7.34
260314_at	unknown protein similar to putative pro	---	AT1G63830	-1.02	-0.03	-0.15	0.884624	0.940142	-7.34
248240_at	CUC2 (dbj|BAA19529.1)	CUC2	AT5G53950	-1.01	-0.02	-0.15	0.884679	0.940157	-7.34
261550_at	hypothetical protein	---	AT1G63450	-1.01	-0.02	-0.15	0.884904	0.940216	-7.34
264061_at	putative cyclin-dependent kinase regul	CKS2	AT2G27970	-1.03	-0.04	-0.15	0.884941	0.940216	-7.34
252794_at	putative protein predicted proteins, Ar	---	---	1.01	0.01	0.15	0.884881	0.940216	-7.34
258092_at	Expressed protein ; supported by full-le	---	AT3G14595	1.02	0.03	0.15	0.88489	0.940216	-7.34
261691_at	branched-chain amino acid aminotran	---	AT1G50060	-1.01	-0.01	-0.15	0.884918	0.940216	-7.34
265534_at	En/Spm-like transposon protein relate	---	---	1.01	0.01	0.15	0.885038	0.940275	-7.34
253939_at	putative myb-related protein myb-relat	MYB97	AT4G26930	1.02	0.02	0.15	0.885277	0.940486	-7.34
250750_at	glucuronosyl transferase-like protein	UGT76C2	AT5G05860 /	-1.01	-0.02	-0.15	0.885397	0.940569	-7.34
253348_at	putative protein SMT4 protein - Sacch	---	AT4G33620	1.01	0.01	0.15	0.885554	0.940692	-7.34
263738_at	hypothetical protein predicted by gene	---	AT1G60060	-1.03	-0.05	-0.15	0.885595	0.940692	-7.34
263952_s_	unknown protein ;supported by full-ler	---	AT2G35810 /	1.01	0.02	0.15	0.885686	0.940745	-7.34
265594_at	50S ribosomal protein L4 ;supported b	---	AT2G20060	1.02	0.03	0.15	0.885729	0.940747	-7.34
249478_at	germin - like protein GLP6 germin - lik	---	AT5G38950	1.01	0.02	0.15	0.885842	0.940823	-7.34
250838_at	cytochrome P450 - like protein cytoch	CYP77A9	AT5G04630	-1.01	-0.01	-0.15	0.885922	0.940864	-7.34
266876_at	hypothetical protein predicted by gene	---	AT2G44820	1.01	0.02	0.15	0.886117	0.940984	-7.34
249465_at	AIG2 - like protein AIG2, Arabidopsis	AIG2L	AT5G39720	-1.01	-0.02	-0.15	0.886106	0.940984	-7.34
252349_at	cell division cycle protein 23 homolog	APC8	AT3G48150	-1.02	-0.03	-0.15	0.886227	0.941056	-7.34
249300_at	putative protein similar to unknown pro	---	AT5G41380	1.01	0.02	0.15	0.886358	0.941152	-7.34
258934_at	putative RecA protein similar to RecA	RECA3	AT3G10140	1.01	0.02	0.15	0.886694	0.941318	-7.34
248099_at	DNA topoisomerase I (sp P30181)	TOP1ALPHA	AT5G55300	-1.01	-0.01	-0.15	0.886662	0.941318	-7.34
257676_at	unknown protein ;supported by full-ler	TGD2	AT3G20320	-1.01	-0.02	-0.15	0.886658	0.941318	-7.34
255343_at	hypothetical protein	---	---	-1.01	-0.01	-0.15	0.886721	0.941318	-7.34
263006_at	hypothetical protein contains similarity	---	AT1G54240	-1.01	-0.02	-0.15	0.886619	0.941318	-7.34
260713_at	disease resistance protein RPP1-WsA	---	AT1G17615	1.01	0.01	0.15	0.886823	0.941383	-7.34

253299_at	hypothetical protein ;supported by full-	---	AT4G33800	-1.01	-0.02	-0.15	0.887118	0.941652	-7.34
265865_at	hypothetical protein predicted by gens	---	AT2G01740	-1.01	-0.01	-0.15	0.887351	0.941834	-7.34
259888_at	hypothetical protein similar to nodule in	---	AT1G76350	1.03	0.04	0.15	0.887455	0.941834	-7.34
258306_at	putative transcription factor similar to C	ATBZIP42	AT3G30530	-1.01	-0.01	-0.15	0.88743	0.941834	-7.34
245384_at	glycoprotein homolog ;supported by fu	---	AT4G16790	-1.02	-0.03	-0.15	0.887454	0.941834	-7.34
260964_at	E2, ubiquitin-conjugating enzyme 15 (	ATUBC2-1	AT1G45050	1.01	0.01	0.15	0.887743	0.942052	-7.34
250919_at	putative protein myosin heavy chain, C	---	AT5G03660	1.01	0.02	0.15	0.887723	0.942052	-7.34
247262_at	putative protein contains similarity to g	AtFAAH	AT5G64440	-1.01	-0.02	-0.15	0.887824	0.942095	-7.34
246274_at	transcription factor like protein	---	AT4G36620	1.01	0.02	0.15	0.888018	0.942257	-7.34
264646_at	hypothetical protein Similar to Homo c	BON3	AT1G08860	1.01	0.02	0.15	0.88828	0.942491	-7.34
257725_at	DNA mismatch repair protein MSH2, S	MSH2	AT3G18524	-1.02	-0.02	-0.15	0.888363	0.942535	-7.34
252499_s_	subtilisin-like serine protease contains	---	AT3G46840 /	-1.01	-0.02	-0.15	0.888459	0.942593	-7.34
257142_at	cytochrome P450, putative contains P	CYP705A18	AT3G20090	-1.02	-0.02	-0.15	0.888668	0.942771	-7.34
255109_s_	hypothetical protein	---	AT4G08760	1.01	0.01	0.15	0.888731	0.942794	-7.34
253318_at	extensin-like protein extensin-like prot	---	AT4G33970	1.01	0.01	0.15	0.888822	0.942847	-7.34
258131_at	protein kinase, putative similar to GB:I	---	AT3G24540	-1.02	-0.02	-0.15	0.888957	0.942902	-7.34
263575_at	hypothetical protein similar to hypothet	---	AT2G17070	-1.01	-0.02	-0.15	0.888938	0.942902	-7.34
263771_at	putative Athila retroelement ORF1 prot	---	---	1.01	0.01	0.14	0.889091	0.943	-7.34
258582_at	germin-like protein contains Pfam profi	---	AT3G04150	1.01	0.01	0.14	0.889191	0.943036	-7.34
255897_at	mutator-like transposase, putative sim	---	---	-1.01	-0.01	-0.14	0.889262	0.943036	-7.34
254322_at	hypothetical protein	---	AT4G22600	-1.02	-0.02	-0.14	0.889276	0.943036	-7.34
247938_at	putative protein similar to unknown pro	---	AT5G57140 /	-1.01	-0.02	-0.14	0.88929	0.943036	-7.34
249663_s_	unknown protein	---	---	-1.01	-0.02	-0.14	0.889391	0.9431	-7.34
246095_at	homeotic gene regulator - like protein	---	AT5G19310	1.02	0.03	0.14	0.889603	0.94328	-7.34
251135_at	putative protein proteophosphoglycan	---	AT5G01280	1.01	0.02	0.14	0.889733	0.943374	-7.34
265521_at	hypothetical protein predicted by gens	ORG4	AT2G06010	-1.01	-0.02	-0.14	0.889826	0.943429	-7.34
258303_at	hypothetical protein predicted by gene	---	---	1.01	0.01	0.14	0.889897	0.943461	-7.34
266705_at	40S ribosomal protein S30 ; supporte	---	AT2G19750	1.02	0.02	0.14	0.89071	0.943489	-7.34
258448_at	unknown protein	---	AT3G22290	1.01	0.01	0.14	0.89071	0.943489	-7.34
257187_at	hypothetical protein predicted by gens	---	AT3G13140	-1.01	-0.02	-0.14	0.890297	0.943489	-7.34
264277_at	polygalacturonase isoenzyme 1 beta s	---	AT1G60390	-1.01	-0.02	-0.14	0.890404	0.943489	-7.34
255598_at	putative protein similar to nucleolin pro	---	AT4G00830	1.01	0.02	0.14	0.890575	0.943489	-7.34
245874_at	unknown protein	---	AT1G26250	1.01	0.02	0.14	0.89067	0.943489	-7.34
253166_at	putative protein putative ligand-gated	GLUR2	AT4G35290	-1.02	-0.03	-0.14	0.89034	0.943489	-7.34
256502_at	Eukaryotic translation initiation factor S	---	AT1G36730 /	1.02	0.02	0.14	0.890673	0.943489	-7.34

265784_at	hypothetical protein predicted by gens	---	AT2G07280	-1.01	-0.02	-0.14	0.890443	0.943489	-7.34
262511_at	syntaxin-related protein At-SYR1, puta	SYP125	AT1G11250	1.01	0.02	0.14	0.89039	0.943489	-7.34
256712_at	unknown protein similar to T14G11.15	---	AT2G34020	1.01	0.01	0.14	0.890575	0.943489	-7.34
248071_at	unknown protein	---	AT5G55670	-1.01	-0.02	-0.14	0.890428	0.943489	-7.34
245563_at	SNF1 like protein kinase ; supported b	CIPK4	AT4G14580	1.03	0.05	0.14	0.890068	0.943489	-7.34
252139_at	putative protein hypothetical protein L	---	AT3G51050	1.01	0.02	0.14	0.890562	0.943489	-7.34
253681_at	cytidine deaminase 3 (CDA3)	---	AT4G29630	-1.01	-0.02	-0.14	0.890188	0.943489	-7.34
256271_at	unknown protein	---	AT3G12140	1.02	0.02	0.14	0.890013	0.943489	-7.34
246823_at	putative protein	---	AT5G26970	-1.01	-0.01	-0.14	0.890102	0.943489	-7.34
246227_at	hypothetical protein	---	AT4G36510	-1.01	-0.02	-0.14	0.89016	0.943489	-7.34
248123_at	putative protein similar to unknown pro	---	AT5G54720	1.01	0.01	0.14	0.890698	0.943489	-7.34
248180_at	unknown protein ;supported by full-ler	AGD5	AT5G54310	1.01	0.01	0.14	0.890799	0.94354	-7.34
267035_at	putative beta-alanine-pyruvate aminotr	AGT3	AT2G38400	-1.03	-0.05	-0.14	0.890972	0.943635	-7.34
265282_at	unknown protein	---	AT2G20380	-1.01	-0.02	-0.14	0.890964	0.943635	-7.34
246747_at	ribosomal protein S21 - like ribosomal	---	AT5G27700	1.02	0.02	0.14	0.89113	0.943759	-7.34
255761_at	hypothetical protein predicted by gens	---	AT1G16770	1.01	0.02	0.14	0.891614	0.94414	-7.34
266947_at	hypothetical protein predicted by gens	---	AT2G18830	1.01	0.02	0.14	0.89161	0.94414	-7.34
252641_at	putative protein predicted protein, Ara	---	AT3G44570	1.01	0.02	0.14	0.891584	0.94414	-7.34
249769_at	sigma-like factor (emb CAA77213.1)	SIGE	AT5G24120	1.02	0.02	0.14	0.891773	0.94417	-7.34
255242_at	putative protein putative retrotranspos	---	---	1.01	0.01	0.14	0.891691	0.94417	-7.34
248356_at	putative protein strong similarity to unk	ATEXO70A3	AT5G52350	1.01	0.01	0.14	0.891743	0.94417	-7.34
262788_at	unknown protein ESTs gb|T75618 and	---	AT1G10690	1.02	0.02	0.14	0.891808	0.94417	-7.34
252763_at	Expressed protein ; supported by cDN	---	AT3G42725	-1.01	-0.02	-0.14	0.891852	0.944173	-7.34
264052_at	putative cytochrome P450	CYP79B3	AT2G22330	1.02	0.03	0.14	0.892058	0.944257	-7.34
249662_s_	putative protein hypothetical proteins -	---	AT5G36680 /	-1.01	-0.01	-0.14	0.892139	0.944257	-7.34
259044_at	pollen allergen Bra r II identical to poll	---	AT3G03430	1.01	0.01	0.14	0.892123	0.944257	-7.34
266677_at	hypothetical protein predicted by gens	---	AT2G29820	1.01	0.02	0.14	0.892088	0.944257	-7.34
246556_at	putative protein hypothetical protein T	---	AT5G15480	1.01	0.02	0.14	0.892071	0.944257	-7.34
263507_s_	hypothetical protein	---	---	-1.02	-0.02	-0.14	0.892201	0.94428	-7.34
265812_at	hypothetical protein predicted by gens	---	AT2G18070	1.01	0.02	0.14	0.892357	0.9444	-7.34
262732_at	putative protein kinase similar to gb|J0	---	AT1G16440	1.01	0.02	0.14	0.892422	0.944425	-7.34
264166_at	unknown protein ; supported by cDNA	---	AT1G65370	-1.01	-0.02	-0.14	0.892578	0.944541	-7.34
258032_at	hypothetical protein predicted by gene	---	AT3G21170	-1.02	-0.02	-0.14	0.892614	0.944541	-7.34
259105_at	stress related protein, putative similar	---	AT3G05500	-1.02	-0.02	-0.14	0.892743	0.944546	-7.34
265117_at	putative proline-rich cell wall protein (p	---	AT1G62500	1.02	0.02	0.14	0.89274	0.944546	-7.34

245169_at	unknown protein predicted by genefinc	---	AT2G33220	-1.01	-0.01	-0.14	0.892695	0.944546	-7.34
252298_at	putative protein various predicted prot	---	AT3G49060	-1.01	-0.01	-0.14	0.892805	0.944567	-7.34
250963_at	putative protein various predicted prot	---	AT5G03000	-1.01	-0.02	-0.14	0.892903	0.944584	-7.34
256623_at	myosin identical to myosin GB:CAB61	ATM1	AT3G19960	-1.01	-0.02	-0.14	0.892887	0.944584	-7.34
262259_s_	hypothetical protein predicted by gene	---	AT1G53870 /	1.02	0.03	0.14	0.893084	0.944669	-7.34
260638_at	unknown protein similar to putative cyt	---	AT1G62390	1.02	0.03	0.14	0.893155	0.944669	-7.34
264785_at	putative non-LTR retroelement reverse	---	---	-1.01	-0.02	-0.14	0.89319	0.944669	-7.34
257417_at	hypothetical protein predicted by gens	---	AT1G10110	1.01	0.02	0.14	0.89307	0.944669	-7.34
252453_at	putative RNA-binding protein various p	---	AT3G47120	-1.01	-0.01	-0.14	0.893168	0.944669	-7.34
265981_s_	putative replication protein A1	---	---	-1.01	-0.02	-0.14	0.893592	0.945011	-7.34
259464_at	hypothetical protein predicted by gene	---	AT1G18990	-1.01	-0.02	-0.14	0.893635	0.945011	-7.34
267403_at	MADS-box protein (AGL33)	AGL33	AT2G26320	-1.01	-0.01	-0.14	0.893639	0.945011	-7.34
258328_at	putative zinc finger protein similar to a	---	AT3G16090	1.01	0.01	0.14	0.893717	0.94505	-7.34
257508_at	bZIP transcription factor, putative con	---	AT1G64320	-1.01	-0.01	-0.14	0.893807	0.945058	-7.34
263232_at	putative light repressible receptor prot	---	AT1G05700	-1.01	-0.02	-0.14	0.893777	0.945058	-7.34
254538_at	putative protein chitinase / lysozyme F	---	AT4G19740	1.01	0.01	0.14	0.894153	0.94538	-7.34
247491_at	putative protein supported by cDNA: C	---	AT5G61880	1.02	0.03	0.14	0.894345	0.945386	-7.34
262037_at	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.14	0.894237	0.945386	-7.34
250401_at	putative protein HSPC184, Homo sap	---	AT5G10780	1.01	0.01	0.14	0.894448	0.945386	-7.34
262651_at	hypothetical protein One of a cluster c	FUT9	AT1G14100 /	1.01	0.02	0.14	0.894382	0.945386	-7.34
247482_at	chromosomal protein - like chromosor	SMC2	AT5G62410	-1.01	-0.02	-0.14	0.894449	0.945386	-7.34
262740_at	lipase, putative contains Pfam profile:	---	AT1G28590	-1.01	-0.02	-0.14	0.894343	0.945386	-7.34
247697_at	subtilisin-like protease - like protein su	SBT5.4	AT5G59810	-1.01	-0.02	-0.14	0.894306	0.945386	-7.34
258450_at	hypothetical protein predicted by gens	---	---	-1.01	-0.02	-0.14	0.894504	0.945401	-7.34
245152_at	putative mitochondrial carrier protein s	---	AT2G47490	1.01	0.02	0.14	0.894639	0.945455	-7.34
245921_at	putative protein predicted protein, Ara	---	AT5G28800	-1.01	-0.01	-0.14	0.89463	0.945455	-7.34
263332_at	putative snRNP splicing factor ;suppo	---	AT2G03870	-1.01	-0.01	-0.14	0.894739	0.945473	-7.34
247017_at	putative protein similar to unknown pro	---	AT5G66980	-1.01	-0.01	-0.14	0.894762	0.945473	-7.34
249274_at	unknown protein	---	AT5G41860	-1.02	-0.02	-0.14	0.89478	0.945473	-7.34
267049_at	putative transcription elongation factor	---	AT2G34210	1.02	0.03	0.14	0.894925	0.945583	-7.34
249548_at	lipid transfer - like protein lipid transfe	---	AT5G38170	-1.01	-0.02	-0.14	0.895057	0.945679	-7.34
263613_at	unknown protein	---	AT2G25250	-1.02	-0.03	-0.14	0.89517	0.945754	-7.34
264763_at	hypothetical protein contains similarity	---	AT1G61450	1.01	0.01	0.14	0.895315	0.945863	-7.34
252786_at	putative protein putative DNA-helicase	CHR38	AT3G42670	1.02	0.03	0.14	0.89554	0.945925	-7.34
260844_at	peroxisomal targeting signal type 2 rec	PEX7	AT1G29260	-1.01	-0.01	-0.14	0.895473	0.945925	-7.34

263353_at	hypothetical protein predicted by gens	---	AT2G22070	-1.01	-0.02	-0.14	0.895505	0.945925	-7.34
245862_at	putative protein	---	AT5G01010	1.01	0.02	0.14	0.895478	0.945925	-7.34
248168_at	beta-glucosidase	BGLU41	AT5G54570	-1.01	-0.02	-0.14	0.895653	0.946001	-7.34
264095_at	mercaptopyruvate sulfurtransferase (M	MST1	AT1G79230	-1.01	-0.01	-0.14	0.895712	0.946019	-7.34
254519_at	putative protein W15DMY30S	---	AT4G19940	-1.01	-0.02	-0.14	0.895913	0.946188	-7.34
257867_at	unknown protein	---	AT3G17780	-1.01	-0.02	-0.14	0.896027	0.946265	-7.34
262915_at	response regulator 3 identical to respo	ARR3	AT1G59940	-1.01	-0.02	-0.14	0.896225	0.946295	-7.34
257639_at	hypothetical protein	---	AT3G25720	-1.01	-0.02	-0.14	0.896155	0.946295	-7.34
255189_at	hypothetical protein	---	AT4G07350	-1.01	-0.01	-0.14	0.896263	0.946295	-7.34
245086_at	putative translation initiation factor	---	AT2G39820	1.01	0.01	0.14	0.896108	0.946295	-7.34
254567_s_	hypothetical protein	---	AT4G19260 /	1.01	0.01	0.14	0.896193	0.946295	-7.34
255168_at	putative protein hypothetical protein T	---	---	-1.01	-0.02	-0.14	0.896452	0.946451	-7.34
245376_at	peroxidase like protein	---	AT4G17690	1.01	0.01	0.14	0.896559	0.94652	-7.34
258956_at	hypothetical protein predicted by gens	---	AT3G01440	1.03	0.05	0.13	0.89668	0.946594	-7.34
246416_at	putative protein predicted proteins, Ar	---	AT5G16920	1.01	0.02	0.13	0.896779	0.946594	-7.34
257436_s_	hypothetical protein predicted by gene	---	AT2G24650 /	-1.01	-0.02	-0.13	0.896795	0.946594	-7.34
245636_at	hypothetical protein similar to hypothet	---	AT1G25240	1.01	0.02	0.13	0.896775	0.946594	-7.34
255656_at	putative protein (fragment) DNA-bindi	---	AT4G00990	-1.01	-0.02	-0.13	0.897095	0.946823	-7.34
264013_at	unknown protein	FIO1	AT2G21070	-1.01	-0.01	-0.13	0.897065	0.946823	-7.34
250642_at	receptor-like protein kinase several rec	ERL2	AT5G07180	-1.01	-0.01	-0.13	0.897224	0.946915	-7.34
249189_at	putative protein similar to unknown pro	AtHB27	AT5G42780	1.02	0.02	0.13	0.897303	0.946955	-7.34
255407_at	hypothetical protein similar to A. thalia	---	AT4G03480	-1.01	-0.02	-0.13	0.89754	0.947118	-7.34
248601_at	putative protein contains similarity to u	---	AT5G49400	-1.01	-0.01	-0.13	0.897505	0.947118	-7.34
245960_at	subtilisin-like protein subtilisin/kexin is	S1P	AT5G19660	1.01	0.01	0.13	0.897609	0.947147	-7.34
259128_at	unknown protein similar to pushover G	BIG	AT3G02260	1.02	0.02	0.13	0.897934	0.94727	-7.34
246085_at	putative protein predicted proteins, Ar	ATBRXL4	AT5G20540	-1.01	-0.02	-0.13	0.897896	0.94727	-7.34
248022_at	putative protein contains similarity to R	APUM12	AT5G56510	1.01	0.01	0.13	0.897782	0.94727	-7.34
248018_at	putative protein strong similarity to unk	---	AT5G56470	1.01	0.02	0.13	0.897859	0.94727	-7.34
255684_at	putative glycosylasparaginase	---	AT4G00590	-1.02	-0.02	-0.13	0.897912	0.94727	-7.34
260731_at	P-type ATPase, putative similar to GB	---	AT1G17500	-1.01	-0.02	-0.13	0.898008	0.947304	-7.34
267570_at	putative RNA helicase A identical to G	HVT1	AT2G30800	-1.01	-0.02	-0.13	0.898054	0.947309	-7.34
255314_at	putative transposon protein	---	---	1.01	0.02	0.13	0.898123	0.947338	-7.34
251239_at	putative protein several hypothetical pr	---	AT3G62440	-1.01	-0.02	-0.13	0.898256	0.947391	-7.34
266176_at	lectin-like protein	AtPP2-B2	AT2G02250	1.01	0.02	0.13	0.898237	0.947391	-7.34
256312_x_	hypothetical protein	---	AT1G35820	1.01	0.01	0.13	0.898484	0.947587	-7.34

251537_at	putative protein several hypothetical pr	---	AT3G58470	1.02	0.03	0.13	0.898639	0.947663	-7.34
265404_at	putative beta-galactosidase	BGAL13	AT2G16730	-1.01	-0.02	-0.13	0.898621	0.947663	-7.34
247973_at	putative protein contains similarity to tr	---	AT5G56770	1.01	0.01	0.13	0.898724	0.947665	-7.34
263559_at	putative non-LTR retroelement reverse	---	---	1.01	0.01	0.13	0.898696	0.947665	-7.34
250964_at	putative protein various predicted prot	---	AT5G03010	-1.01	-0.02	-0.13	0.898928	0.947793	-7.34
252395_at	H+-transporting ATPase - like protein	AHA4	AT3G47950	1.02	0.02	0.13	0.898928	0.947793	-7.34
266261_at	putative zinc finger protein ;supported	---	AT2G27580	1.01	0.01	0.13	0.899056	0.947884	-7.34
254699_at	putative protein predicted protein, Ara	---	AT4G17990	1.01	0.02	0.13	0.899276	0.948072	-7.34
249715_at	putative protein similar to unknown pro	---	AT5G35760	1.01	0.02	0.13	0.899463	0.948225	-7.34
261002_at	hypothetical protein contains similarity	---	AT1G26520	1.01	0.02	0.13	0.899568	0.948289	-7.34
246208_at	hypothetical protein ; supported by cDI	SFH12	AT4G36490	-1.01	-0.02	-0.13	0.899648	0.948289	-7.34
257490_x_	Myb homolog (CPC), putative similar t	ETC1	AT1G01380	-1.01	-0.01	-0.13	0.899628	0.948289	-7.34
253158_at	putative protein protein kinase 6, Glyc	---	AT4G35780	1.01	0.02	0.13	0.899716	0.948316	-7.34
245588_at	putative protein	---	AT4G15030	1.02	0.02	0.13	0.899865	0.948429	-7.34
255689_at	hypothetical protein	---	AT4G00670	-1.01	-0.01	-0.13	0.899958	0.948484	-7.34
249285_at	unknown protein	---	AT5G41960	1.01	0.02	0.13	0.900153	0.948646	-7.34
252140_at	putative protein several hypothetical pr	---	AT3G51070	1.01	0.01	0.13	0.900247	0.948701	-7.34
264808_at	unknown protein similar to EST gb|H37	PRA1.E	AT1G08770	-1.01	-0.01	-0.13	0.900317	0.948731	-7.34
254994_at	putative methyltransferase	MTA	AT4G10760	1.02	0.03	0.13	0.900461	0.948839	-7.34
260734_at	disease resistance protein RPP1-WsE	---	AT1G17600	-1.01	-0.02	-0.13	0.900597	0.948894	-7.34
267273_at	putative non-LTR retroelement reverse	---	AT2G02520	1.01	0.01	0.13	0.900593	0.948894	-7.34
245511_at	hypothetical protein	---	AT4G15755	-1.01	-0.01	-0.13	0.900683	0.948941	-7.34
260050_at	hypothetical protein predicted by gene	AGL64	AT1G29960 /	1.01	0.02	0.13	0.900727	0.948944	-7.34
252201_at	putative protein anthranilate N-hydrox	---	AT3G50295	1.01	0.01	0.13	0.900902	0.948997	-7.34
263721_at	hypothetical protein predicted by gens	---	AT2G13630	-1.01	-0.01	-0.13	0.900842	0.948997	-7.34
247872_at	putative protein similar to unknown pro	---	AT5G57670	1.01	0.02	0.13	0.900877	0.948997	-7.34
250973_at	60S ribosomal protein - like 60S roibo	---	AT5G02870	1.02	0.03	0.13	0.901336	0.949147	-7.34
266960_at	putative retroelement pol polyprotein	---	---	-1.01	-0.02	-0.13	0.901273	0.949147	-7.34
265556_at	putative Athila retroelement ORF1-like	---	---	1.01	0.02	0.13	0.90132	0.949147	-7.34
256886_at	hypothetical protein contains Pfam pro	---	AT3G15130	1.01	0.01	0.13	0.901162	0.949147	-7.34
264194_at	putative wall-associated kinase contair	---	AT1G22720	1.01	0.01	0.13	0.901152	0.949147	-7.34
263614_at	putative serpin	---	AT2G25240	1.01	0.02	0.13	0.901283	0.949147	-7.34
260977_at	hypothetical protein predicted by gene	---	AT1G53420	1.01	0.01	0.13	0.901271	0.949147	-7.34
266165_at	putative copper/zinc superoxide dismu	CSD2	AT2G28190	1.05	0.08	0.13	0.90152	0.949297	-7.35
260219_at	hypothetical protein contains Pfam pro	---	AT1G74630	-1.01	-0.01	-0.13	0.901563	0.949298	-7.35

254989_at	retrotransposon like protein copia-like	---	---	-1.01	-0.02	-0.13	0.901658	0.949311	-7.35
245182_at	putative protein similarity to TETRATF	---	AT5G12430	1.02	0.02	0.13	0.901651	0.949311	-7.35
254663_at	potassium channel protein KAT2	KAT2	AT4G18290	1.01	0.02	0.13	0.901927	0.949518	-7.35
251878_at	putative protein predicted protein, Ara	---	AT3G54310	-1.01	-0.01	-0.13	0.901939	0.949518	-7.35
249894_at	unknown protein ; supported by cDNA	---	AT5G22580	1.15	0.20	0.13	0.901988	0.949527	-7.35
251130_at	oligopeptide transporter - like protein	PTR5	AT5G01180	-1.01	-0.01	-0.13	0.902101	0.949551	-7.35
249143_at	putative protein strong similarity to unk	---	AT5G43230	-1.01	-0.01	-0.13	0.902136	0.949551	-7.35
254842_at	putative protein other hypothetical prot	---	AT4G11950	-1.01	-0.02	-0.13	0.90206	0.949551	-7.35
257591_at	leucine-rich repeat disease resistance	AtRLP39	AT3G24900	-1.01	-0.01	-0.13	0.902193	0.949567	-7.35
265408_at	Mutator-like transposase similar to MU	---	---	1.01	0.01	0.13	0.902267	0.949601	-7.35
251132_at	putative protein Myb-related transcript	---	AT5G01200	-1.01	-0.02	-0.13	0.90231	0.949603	-7.35
246106_at	receptor-like protein kinase precursor	---	AT5G28680	1.01	0.01	0.13	0.902532	0.949792	-7.35
252292_at	RNA polymerase III subunit - like prot	---	AT3G49000	1.01	0.02	0.13	0.902654	0.949877	-7.35
256975_at	unknown protein similar to putative ret	---	AT3G21000	-1.01	-0.02	-0.13	0.90281	0.949997	-7.35
255288_at	coded for by A. thaliana cDNA T41604	---	AT4G04670	-1.02	-0.02	-0.13	0.902881	0.950028	-7.35
257013_at	hypothetical protein contains Pfam pro	---	AT3G26920 /	-1.01	-0.01	-0.13	0.902991	0.950101	-7.35
256916_at	GATA transcription factor 1 (AtGATA-1	---	AT3G24050	1.01	0.02	0.13	0.903131	0.950186	-7.35
249717_at	unknown protein ;supported by full-ler	---	AT5G35730	-1.01	-0.01	-0.13	0.903155	0.950186	-7.35
254312_s_	hypothetical protein	---	---	-1.01	-0.02	-0.13	0.903247	0.950238	-7.35
258093_at	unknown protein ; supported by cDNA	---	AT3G14750	-1.01	-0.02	-0.13	0.903328	0.950279	-7.35
264212_at	putative tRNA adenylyltransferase Sim	---	AT1G22660	-1.02	-0.02	-0.13	0.903517	0.950303	-7.35
252722_at	putative protein hypothetical protein F	---	---	1.01	0.01	0.13	0.903496	0.950303	-7.35
261849_at	pectin methylesterase, putative simila	---	AT1G11370	1.01	0.02	0.13	0.903411	0.950303	-7.35
261200_at	60S ribosomal protein L27a, putative	---	AT1G12960	1.01	0.01	0.13	0.903486	0.950303	-7.35
264228_at	hypothetical protein contains similarity	GCS1	AT1G67490	-1.01	-0.01	-0.13	0.903659	0.95031	-7.35
264392_at	hypothetical protein Similar to salt-indu	---	AT1G11900	-1.01	-0.02	-0.13	0.90358	0.95031	-7.35
265906_at	hypothetical protein predicted by gens	---	AT2G25565	1.01	0.02	0.13	0.903732	0.95031	-7.35
248275_at	isp4 protein	ATOPT8	AT5G53520	1.01	0.01	0.13	0.903727	0.95031	-7.35
265972_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.13	0.903673	0.95031	-7.35
247666_at	putative protein various predicted prot	---	AT5G60140	-1.01	-0.01	-0.13	0.903782	0.950319	-7.35
260646_at	hypothetical protein similar to CHP-rich	---	AT1G53340	-1.02	-0.02	-0.13	0.903894	0.950392	-7.35
250416_at	putative protein predicted proteins, Ar	---	AT5G11220	-1.01	-0.01	-0.13	0.903962	0.950402	-7.35
266477_at	CLE4 CLAVATA3/ESR-Related 4 (CLE	CLE6	AT2G31085	1.01	0.02	0.13	0.904028	0.950402	-7.35
251488_at	calmodulin-like protein calcium-bindin	---	AT3G59440	1.01	0.01	0.13	0.903991	0.950402	-7.35
259004_at	putative protein kinase C-terminal reg	---	AT3G01840	-1.01	-0.01	-0.13	0.904162	0.950455	-7.35

255191_at	may be a pseudogene	---	---	-1.01	-0.01	-0.13	0.904128	0.950455	-7.35
264314_at	unknown protein ; supported by cDNA	---	AT1G70420	-1.02	-0.02	-0.12	0.904369	0.95059	-7.35
245115_at	putative esterase D ;supported by full-	SFGH	AT2G41530	-1.02	-0.02	-0.12	0.904438	0.95059	-7.35
258042_at	hypothetical protein similar to hypothet	---	AT3G21310	1.01	0.01	0.12	0.904383	0.95059	-7.35
259667_at	unknown protein ; supported by cDNA	---	AT1G55270	1.01	0.02	0.12	0.904457	0.95059	-7.35
246754_at	transcription factor - like protein Hap5	NF-YC8	AT5G27910	-1.01	-0.02	-0.12	0.904569	0.950665	-7.35
252788_at	putative protein several hypothetical pr	---	---	-1.01	-0.01	-0.12	0.904747	0.950765	-7.35
250799_at	putative protein strong similarity to unk	---	AT5G05350	-1.01	-0.01	-0.12	0.904749	0.950765	-7.35
247620_at	receptor like protein kinase receptor li	---	AT5G60310	1.01	0.02	0.12	0.904831	0.950808	-7.35
257568_s_	hypothetical protein	---	AT3G23950 /	-1.01	-0.02	-0.12	0.904896	0.950832	-7.35
252784_at	putative protein predicted proteins, Ar	---	---	-1.01	-0.01	-0.12	0.905034	0.950845	-7.35
252963_at	putative protein	---	AT4G38820	1.01	0.01	0.12	0.905074	0.950845	-7.35
259589_at	unknown protein	---	AT1G28135	-1.01	-0.02	-0.12	0.904965	0.950845	-7.35
251947_at	putative protein various predicted prot	---	AT3G53550	-1.01	-0.01	-0.12	0.905059	0.950845	-7.35
245990_at	putative protein predicted proteins, Ar	---	AT5G20640	1.01	0.02	0.12	0.905193	0.950926	-7.35
253310_at	hypothetical protein ; supported by cD	EX1	AT4G33630	1.01	0.01	0.12	0.905254	0.950946	-7.35
251208_at	putative protein amino acid selective c	ATOEP16-4	AT3G62880	-1.01	-0.01	-0.12	0.905342	0.950994	-7.35
245926_at	VPS13 - like protein VPS13, Sacchar	---	AT5G24740	-1.01	-0.01	-0.12	0.905612	0.951234	-7.35
251759_at	tetrahydrofolylpolyglutamate synthase	ATDFD	AT3G55630	1.02	0.03	0.12	0.905835	0.951342	-7.35
264162_at	acyl carrier protein, putative similar to	mtACP2	AT1G65290	-1.01	-0.02	-0.12	0.905839	0.951342	-7.35
252341_at	remorin -like protein remorin, Solanum	---	AT3G48940	1.01	0.01	0.12	0.905773	0.951342	-7.35
262294_at	hypothetical protein identical to hypoth	---	AT1G27610	-1.01	-0.01	-0.12	0.90593	0.951352	-7.35
255390_at	hypothetical protein similar to A. thalia	---	---	-1.01	-0.01	-0.12	0.905986	0.951352	-7.35
247774_at	putative protein fruit ripening expresse	---	AT5G58660	1.01	0.01	0.12	0.905952	0.951352	-7.35
253962_at	hypothetical protein	---	AT4G26460	-1.01	-0.01	-0.12	0.906016	0.951352	-7.35
252756_s_	putative protein hypothetical proteins -	---	AT1G58520 /	1.01	0.01	0.12	0.906185	0.951398	-7.35
257181_at	hypothetical protein	---	AT3G13190	-1.01	-0.02	-0.12	0.906162	0.951398	-7.35
247860_at	bis(5'-adenosyl)-triphosphatase-like; al	---	AT5G58240	-1.01	-0.01	-0.12	0.906156	0.951398	-7.35
259635_at	purple acid phosphatase, putative sim	PAP6	AT1G56360	-1.01	-0.02	-0.12	0.90629	0.951465	-7.35
258413_at	unknown protein ;supported by full-ler	---	AT3G17300	1.01	0.02	0.12	0.906343	0.951477	-7.35
251103_at	putative protein protein phosphatase t	---	AT5G01700	-1.01	-0.02	-0.12	0.906392	0.951484	-7.35
267590_at	putative expansin ;supported by full-le	ATEXPA4	AT2G39700	-1.02	-0.03	-0.12	0.90653	0.951551	-7.35
265181_at	putative OBP32pep protein ;supporte	---	AT1G23510	-1.01	-0.02	-0.12	0.906539	0.951551	-7.35
260925_at	DNA-binding protein, putative contains	---	AT1G21340	-1.01	-0.02	-0.12	0.906659	0.951633	-7.35
250283_at	putative protein many hypothetical pro	---	AT5G13270	1.01	0.01	0.12	0.906937	0.951875	-7.35

253742_at	putative protein retrofit - Oryza longist	---	---	-1.01	-0.02	-0.12	0.906972	0.951875	-7.35
254912_at	respiratory burst oxidase homolog F -	---	AT4G11230	1.01	0.01	0.12	0.907091	0.951878	-7.35
250275_at	putative protein mRNA, Moritella mari	---	AT5G13030	1.01	0.02	0.12	0.907041	0.951878	-7.35
261194_at	unknown protein contains Pfam profile	---	AT1G12770 /	-1.01	-0.01	-0.12	0.907101	0.951878	-7.35
249357_at	ribonucleoprotein -like ribonucleoprote	---	AT5G40490	1.01	0.02	0.12	0.907178	0.951915	-7.35
245227_s_	gunknown protein contains non-conse	---	AT1G08410	1.01	0.02	0.12	0.90735	0.951964	-7.35
265983_at	putative homeodomain transcription fa	HB-2	AT2G18550	1.01	0.01	0.12	0.907329	0.951964	-7.35
264151_at	hypothetical protein predicted by ger	---	AT1G02070	-1.01	-0.01	-0.12	0.907309	0.951964	-7.35
248760_at	unknown protein ;supported by full-ler	---	AT5G47570	1.01	0.02	0.12	0.907606	0.952058	-7.35
255198_at	contains similarity to an Arabidopsis th	---	---	-1.01	-0.01	-0.12	0.907556	0.952058	-7.35
255914_at	hypothetical protein predicted by gene	---	AT1G20290	1.01	0.02	0.12	0.907567	0.952058	-7.35
262435_at	cytochrome P450, putative similar to c	CYP96A8	AT1G47620	1.01	0.01	0.12	0.907483	0.952058	-7.35
267419_at	putative thioredoxin	ATO1	AT2G35010	-1.01	-0.01	-0.12	0.907995	0.95229	-7.35
263098_at	Expressed protein ; supported by full-le	---	AT2G16005	-1.01	-0.01	-0.12	0.907972	0.95229	-7.35
256802_at	cytochrome P450, putative similar to c	CYP705A32	AT3G20950	-1.01	-0.01	-0.12	0.907915	0.95229	-7.35
249382_at	putative protein predicted proteins, Ar	---	AT5G40050	1.01	0.01	0.12	0.907878	0.95229	-7.35
245968_at	proline-rich protein extensins	---	AT5G19800 /	1.01	0.02	0.12	0.908047	0.952291	-7.35
255530_at	hypothetical protein	---	AT4G02140	-1.01	-0.01	-0.12	0.908079	0.952291	-7.35
263994_at	putative VSF-1-like b-ZIP transcription	---	AT2G12900	-1.01	-0.01	-0.12	0.908691	0.952889	-7.35
252729_at	putative protein replication protein A1,	---	---	1.01	0.01	0.12	0.908748	0.952905	-7.35
251880_at	hypothetical protein ;supported by full-	---	AT3G54290	-1.01	-0.02	-0.12	0.908914	0.952958	-7.35
253107_at	putative protein predicted proteins, Ar	---	AT4G35880	-1.01	-0.02	-0.12	0.908924	0.952958	-7.35
259797_at	unknown protein	---	---	-1.01	-0.02	-0.12	0.908903	0.952958	-7.35
256978_at	phosphoribosyamidoimidazole-succin	PUR7	AT3G21110	1.02	0.03	0.12	0.909168	0.953126	-7.35
261941_at	hypothetical protein contains similarity	---	AT1G22490	1.02	0.03	0.12	0.909149	0.953126	-7.35
260422_at	hypothetical protein predicted by gene	---	AT1G69630	1.01	0.01	0.12	0.909255	0.95313	-7.35
257747_at	hypothetical protein predicted by gene	---	AT3G18700	-1.01	-0.01	-0.12	0.909214	0.95313	-7.35
257953_at	predicted protein supported by full-leng	PEX22	AT3G21865	-1.02	-0.02	-0.12	0.909613	0.953352	-7.35
265324_at	hypothetical protein predicted by gene	ATCOAD	AT2G18250	1.01	0.02	0.12	0.909634	0.953352	-7.35
252244_at	putative protein some putative proteins	---	AT3G50130	1.01	0.02	0.12	0.909583	0.953352	-7.35
261744_at	nitrogen fixation protein (nifS), putativ	CPNIFS	AT1G08490	1.01	0.01	0.12	0.909606	0.953352	-7.35
264144_at	latex-abundant protein, putative simila	AtMC6	AT1G79320	1.01	0.01	0.12	0.90996	0.95365	-7.35
252513_at	putative protein KIAA0776 protein, Ho	---	AT3G46220	-1.01	-0.01	-0.12	0.910356	0.953987	-7.35
257195_at	hypothetical protein predicted by gene	---	AT3G23680	-1.01	-0.01	-0.12	0.910365	0.953987	-7.35
252413_at	40S ribosomal protein S20-like protein	---	AT3G47370	1.02	0.03	0.12	0.91051	0.954039	-7.35

257335_at	hypothetical protein	---	---	1.01	0.01	0.12	0.91048	0.954039	-7.35
252555_at	putative protein alpha-xylosidase, Ara	---	AT3G45940	1.01	0.01	0.12	0.910582	0.954039	-7.35
253363_at	hypothetical protein	---	AT4G33130	-1.01	-0.01	-0.12	0.91057	0.954039	-7.35
257481_at	hypothetical protein identical to hypoth	ALMT1	AT1G08430	1.01	0.01	0.12	0.910648	0.954063	-7.35
256095_at	hypothetical protein contains Pfam pro	---	AT1G13630	1.02	0.03	0.12	0.910822	0.954203	-7.35
246642_s_	putative protein predicted proteins, Ar	---	---	1.01	0.01	0.12	0.91092	0.954262	-7.35
254978_at	subtilisin-like serine protease contains	---	AT4G10540	-1.01	-0.01	-0.12	0.911033	0.954336	-7.35
254652_at	DNA binding-like protein SPF1 protein	WRKY28	AT4G18170	1.05	0.06	0.12	0.911107	0.95437	-7.35
255212_at	putative athila transposon protein	---	---	-1.01	-0.01	-0.12	0.91117	0.954392	-7.35
244915_s_	hypothetical protein	---	---	-1.01	-0.01	-0.12	0.911359	0.954545	-7.35
248576_at	methionine S-methyltransferase (gb|A/	MMT	AT5G49810	-1.01	-0.01	-0.12	0.911448	0.954595	-7.35
257118_at	hypothetical protein	---	AT3G20180	-1.01	-0.01	-0.12	0.9116	0.954711	-7.35
246748_at	putative protein predicted protein, Dro	---	AT5G27730	1.01	0.01	0.12	0.911777	0.954809	-7.35
251180_at	putative protein hypothetical protein (T	---	AT3G62640	-1.01	-0.02	-0.12	0.911742	0.954809	-7.35
248473_at	small zinc finger-like protein ;supporte	TIM8	AT5G50810	-1.01	-0.02	-0.11	0.911953	0.954868	-7.35
246460_at	cellulose synthase catalytic subunit -li	CSLD2	AT5G16910	-1.02	-0.02	-0.11	0.911959	0.954868	-7.35
253623_at	GDP-mannose pyrophosphorylase lik	---	AT4G30570	-1.01	-0.01	-0.11	0.911906	0.954868	-7.35
263246_at	hypothetical protein predicted by gens	---	AT2G31460	-1.01	-0.02	-0.11	0.912014	0.954881	-7.35
250875_at	putative protein fimbriae-associated p	---	AT5G04020	1.02	0.03	0.11	0.912258	0.954893	-7.35
250725_at	putative protein similar to unknown pro	---	AT5G06400	1.01	0.02	0.11	0.912187	0.954893	-7.35
259891_at	putative Eukaryotic initiation factor 4A	---	AT1G72730	1.01	0.02	0.11	0.912235	0.954893	-7.35
246771_at	putative protein putative replication pro	---	---	1.01	0.01	0.11	0.912084	0.954893	-7.35
256490_at	unknown protein ;supported by full-len	---	AT1G31460	1.01	0.02	0.11	0.912203	0.954893	-7.35
262842_at	xyloglucan endo-transglycosylase, pu	XTR2	AT1G14720	-1.02	-0.03	-0.11	0.912277	0.954893	-7.35
263294_at	hypothetical protein predicted by gene	---	---	-1.01	-0.02	-0.11	0.912533	0.955117	-7.35
248203_at	Myb-related transcription factor-like pr	MYB49	AT5G54230	1.01	0.01	0.11	0.912673	0.955221	-7.35
264441_at	Expressed protein ; supported by full-l	---	AT1G27435	-1.01	-0.02	-0.11	0.912956	0.955247	-7.35
259552_at	hypothetical protein	---	AT1G21320	-1.01	-0.01	-0.11	0.912833	0.955247	-7.35
257629_at	cellulase, putative contains Pfam profi	---	AT3G26140	-1.01	-0.01	-0.11	0.912899	0.955247	-7.35
257110_x_	hypothetical protein	---	---	1.01	0.02	0.11	0.912992	0.955247	-7.35
251974_at	myb protein(MYB27) contains myb DN	AtMYB27	AT3G53200	1.01	0.01	0.11	0.912974	0.955247	-7.35
248086_at	putative protein similar to unknown pro	GEX1	AT5G55490	1.01	0.01	0.11	0.912985	0.955247	-7.35
261692_at	calreticulin, putative similar to calretic	CRT3	AT1G08450	-1.02	-0.03	-0.11	0.912814	0.955247	-7.35
252941_at	phenylalanyl-trna synthetase - like pro	---	AT4G39280	1.01	0.01	0.11	0.913113	0.955299	-7.35
253430_at	putative protein	---	AT4G32430	1.01	0.01	0.11	0.913157	0.955299	-7.35

260659_s_	hypothetical protein predicted by gene	---	AT1G19460 /	1.01	0.01	0.11	0.913167	0.955299	-7.35
261162_at	hypothetical protein predicted by gens	---	AT1G34440	1.01	0.02	0.11	0.913254	0.955346	-7.35
256136_s_	lectin receptor kinase, putative similar	---	AT1G48720	-1.01	-0.01	-0.11	0.913426	0.955395	-7.35
257281_s_	hypothetical protein predicted by gens	---	AT3G29680 /	-1.01	-0.02	-0.11	0.913419	0.955395	-7.35
265992_at	putative receptor-like protein kinase	---	AT2G24130	1.01	0.01	0.11	0.913379	0.955395	-7.35
248935_at	salt-inducible protein-like	---	AT5G46100	1.01	0.01	0.11	0.913492	0.95542	-7.35
255326_at	hypothetical protein	---	---	1.01	0.01	0.11	0.913628	0.955519	-7.35
253595_at	putative protein M1 protein, Streptoco	---	AT4G30830	1.01	0.01	0.11	0.913833	0.955645	-7.35
256495_at	hypothetical protein contains similarity	---	AT1G31530	1.01	0.01	0.11	0.913799	0.955645	-7.35
251957_at	putative protein predicted proteins, Ar	---	AT3G53690	-1.01	-0.01	-0.11	0.914073	0.955802	-7.35
258572_at	hypothetical protein	---	AT3G04270	1.01	0.01	0.11	0.914109	0.955802	-7.35
265127_at	hypothetical protein similar to pollen sp	sks14	AT1G55560	-1.01	-0.01	-0.11	0.914067	0.955802	-7.35
264461_s_	hypothetical protein	---	AT1G10190 /	1.01	0.01	0.11	0.9142	0.955853	-7.35
253598_at	ribosomal protein S11 - like ribosomal	---	AT4G30800	-1.03	-0.04	-0.11	0.914345	0.955943	-7.35
259065_at	unknown protein similar to putative glu	GLR1.4	AT3G07520	1.02	0.02	0.11	0.914369	0.955943	-7.35
256846_at	pectin methylesterase, putative simila	---	AT3G27980	-1.01	-0.01	-0.11	0.914454	0.955949	-7.35
255124_at	putative self-incompatability RNA-bind	APUM15	AT4G08560	1.01	0.02	0.11	0.914459	0.955949	-7.35
258834_at	GTP cyclohydrolase I similar to GTP c	---	AT3G07270	1.01	0.02	0.11	0.914706	0.956164	-7.35
258159_at	receptor kinase, putative similar to rec	RLK902	AT3G17840	-1.02	-0.03	-0.11	0.914812	0.956199	-7.35
265744_at	putative CENP-B/ARS binding protein-	---	---	-1.01	-0.01	-0.11	0.91486	0.956199	-7.35
246123_at	beta-1,3-glucanase-like protein beta-1	---	AT5G20390	1.01	0.01	0.11	0.914866	0.956199	-7.35
259301_at	hypothetical protein predicted by gens	---	AT3G05110	-1.01	-0.02	-0.11	0.915188	0.956492	-7.35
262171_at	unknown protein ;supported by full-len	TIFY10B	AT1G74950	1.01	0.02	0.11	0.91543	0.956701	-7.35
246587_at	putative protein predicted proteins, Ar	---	---	-1.01	-0.01	-0.11	0.915585	0.956819	-7.35
263023_at	unknown protein	---	AT1G23960	-1.02	-0.03	-0.11	0.915684	0.956879	-7.35
256879_at	unknown protein similar to auxin-indep	---	AT3G26370	-1.01	-0.01	-0.11	0.915842	0.956896	-7.35
256239_at	hypothetical protein predicted by gene	---	AT3G12470	1.01	0.01	0.11	0.91577	0.956896	-7.35
266965_at	nodulin-like protein	---	AT2G39510	1.01	0.01	0.11	0.915869	0.956896	-7.35
245912_at	putative protein sulfate transporter AT	SULTR3;5	AT5G19600	1.02	0.03	0.11	0.915864	0.956896	-7.35
263571_at	putative disease resistance protein ide	---	AT2G17050	1.01	0.01	0.11	0.915923	0.95691	-7.35
245856_at	putative protein predicted proteins, Ar	---	---	1.01	0.02	0.11	0.915997	0.956943	-7.35
266139_at	Expressed protein ; supported by full-l	---	AT2G28085	1.02	0.03	0.11	0.916152	0.957061	-7.35
265264_at	hypothetical protein predicted by gens	---	AT2G42930	-1.01	-0.01	-0.11	0.916319	0.957093	-7.35
249645_at	thionin Thi2.2 ;supported by full-length	THI2.2	AT5G36910	-1.01	-0.02	-0.11	0.916277	0.957093	-7.35
259156_at	hypothetical protein predicted by gene	SEC8	AT3G10380	1.01	0.01	0.11	0.9163	0.957093	-7.35

266445_at	unknown protein	---	AT2G43070	1.01	0.02	0.11	0.91635	0.957093	-7.35
263839_at	putative cis-Golgi SNARE protein ;sup	MEMB11	AT2G36900	1.01	0.02	0.11	0.916496	0.957201	-7.35
251596_at	1-acylcerol-3-phosphate acyltransfera	LPAT2	AT3G57650	1.01	0.01	0.11	0.916542	0.957205	-7.35
245455_at	disease resistance RPP5 like protein (	---	AT4G16930	-1.01	-0.01	-0.11	0.916639	0.957263	-7.35
259414_at	hypothetical protein contains Pfam pro	---	AT1G02420	1.01	0.01	0.11	0.916775	0.957274	-7.35
255324_s_	putative reverse transcriptase	---	---	1.01	0.01	0.11	0.916769	0.957274	-7.35
266498_at	1-aminocyclopropane-1-carboxylate ox	---	AT2G06960	-1.01	-0.01	-0.11	0.916743	0.957274	-7.35
256535_at	unknown protein	ANAC015	AT1G33280	-1.01	-0.02	-0.11	0.916845	0.957303	-7.35
246241_at	patatin-like protein	PLP4	AT4G37050	-1.01	-0.02	-0.11	0.916909	0.957326	-7.35
257512_at	unknown protein	---	AT1G35250	1.01	0.01	0.11	0.91698	0.957356	-7.35
254753_at	putative protein Pto kinase interactor	---	AT4G13190	-1.01	-0.01	-0.11	0.917117	0.957456	-7.35
260473_at	hypothetical protein predicted by gene	---	AT1G10880	1.01	0.01	0.11	0.917228	0.957527	-7.35
246130_at	putative protein various predicted prot	---	---	-1.01	-0.02	-0.11	0.917433	0.957599	-7.35
252174_at	putative protein APRIL protein, Homo	---	AT3G50690	-1.01	-0.01	-0.11	0.917407	0.957599	-7.35
255832_at	hypothetical protein predicted by gene	---	AT2G33360	1.01	0.02	0.11	0.917481	0.957599	-7.35
246248_at	hypothetical protein	---	AT4G36560	-1.01	-0.01	-0.11	0.917507	0.957599	-7.35
256124_at	hypothetical protein predicted by gens	ATPUP9	AT1G18220	1.01	0.01	0.11	0.917478	0.957599	-7.35
250673_at	serine threonine protein kinase-like pr	CIPK2	AT5G07070	1.01	0.02	0.11	0.917681	0.95765	-7.35
258206_at	hypothetical protein predicted by gene	CID4	AT3G14010	1.01	0.01	0.11	0.917648	0.95765	-7.35
263215_at	putative reticuline oxidase-like protein	---	AT1G30710	1.01	0.01	0.11	0.917664	0.95765	-7.35
262305_at	hypothetical protein predicted by gene	---	AT1G70950	1.01	0.01	0.11	0.917786	0.957715	-7.35
260292_at	putative UDP-N-acetylmuramoylalany	MURE	AT1G63680	-1.01	-0.01	-0.11	0.918282	0.958145	-7.35
257485_at	hypothetical protein contains Pfam pro	---	AT1G63580	1.02	0.03	0.11	0.918408	0.958145	-7.35
256563_at	unknown protein	RALFL27	AT3G29780	1.01	0.01	0.11	0.918372	0.958145	-7.35
252476_at	glucosyltransferase-like protein UDP-	---	AT3G46650	-1.01	-0.02	-0.11	0.918301	0.958145	-7.35
266216_at	putative DOF zinc finger protein	---	AT2G28810	1.01	0.01	0.11	0.918384	0.958145	-7.35
266419_at	putative annexin ;supported by full-len	ANNAT3	AT2G38760	-1.01	-0.02	-0.11	0.918493	0.95819	-7.35
246920_at	phytocyanin-related protein-like phyto	---	AT5G25090	1.01	0.01	0.11	0.918537	0.958192	-7.35
256394_at	unknown protein contains non-consens	---	AT3G06290	-1.01	-0.01	-0.11	0.918753	0.958335	-7.35
267460_at	putative squamosa-promoter binding p	SPL3	AT2G33810	-1.03	-0.04	-0.11	0.9188	0.958335	-7.35
260869_at	stearoyl acyl carrier protein desaturas	---	AT1G43800	1.01	0.01	0.11	0.918796	0.958335	-7.35
248944_at	putative protein similar to unknown pro	---	AT5G45500	-1.01	-0.02	-0.11	0.919096	0.9586	-7.35
248930_at	unknown protein	---	AT5G46010	-1.01	-0.01	-0.11	0.919159	0.958621	-7.35
266781_at	putative protein kinase contains a prot	---	AT2G28940	-1.01	-0.02	-0.11	0.919247	0.958633	-7.35
265504_at	putative Ta11-like non-LTR retroeleme	---	---	1.01	0.01	0.11	0.919293	0.958633	-7.35

255322_at	putative protein	---	---	-1.01	-0.01	-0.11	0.919296	0.958633	-7.35
263618_at	hypothetical protein predicted by gens	APC2	AT2G04660	-1.01	-0.01	-0.11	0.919427	0.958726	-7.35
260910_at	importin alpha, putative similar to imp	IMPA-6	AT1G02690	-1.01	-0.02	-0.10	0.9195	0.958758	-7.35
260485_at	putative amp-binding protein similar to	---	AT1G68270	-1.01	-0.01	-0.10	0.919543	0.958759	-7.35
262187_at	hypothetical protein	---	AT1G77960	-1.01	-0.01	-0.10	0.919826	0.959011	-7.35
248845_at	disease resistance protein-like	---	AT5G46470	-1.01	-0.01	-0.10	0.919884	0.959027	-7.35
251010_at	putative protein ;supported by full-leng	---	AT5G02550	-1.01	-0.02	-0.10	0.920483	0.959476	-7.35
252014_at	putative protein predicted proteins, Ar	---	AT3G52870	-1.03	-0.04	-0.10	0.920476	0.959476	-7.35
246761_at	embryonic abundant protein - like emb	---	AT5G27980	1.01	0.01	0.10	0.920482	0.959476	-7.35
245488_at	peroxidase like protein	---	AT4G16270	-1.01	-0.01	-0.10	0.920442	0.959476	-7.35
258822_s_	unknown protein contains Pfam profile	---	AT3G07220 /	1.01	0.02	0.10	0.920535	0.959486	-7.35
260120_at	hypothetical protein	ATPP2-A4	AT1G33920	1.01	0.01	0.10	0.92058	0.95949	-7.35
260111_at	hypothetical protein similar to unknown	---	AT1G63320	1.01	0.01	0.10	0.920859	0.959737	-7.35
257345_s_	pseudogene	---	---	1.01	0.01	0.10	0.920986	0.959737	-7.35
245958_at	GNOM-like protein pattern-formation (	---	AT5G19610	1.01	0.01	0.10	0.920906	0.959737	-7.35
257159_at	protein kinase, putative similar to prot	---	AT3G24400	-1.01	-0.02	-0.10	0.921006	0.959737	-7.35
256556_at	mutator-like transposase, putative sim	---	---	1.01	0.01	0.10	0.921028	0.959737	-7.35
251548_at	putative protein predicted protein, Ara	---	---	1.01	0.01	0.10	0.921282	0.959958	-7.35
251685_at	putative protein unknown protein At2g	---	AT3G56430	1.02	0.03	0.10	0.921326	0.95996	-7.35
248167_at	putative protein similar to unknown pro	---	AT5G54530	-1.01	-0.02	-0.10	0.921474	0.960071	-7.35
264299_s_	hypothetical protein predicted by gene	---	AT1G78850 /	-1.02	-0.03	-0.10	0.921517	0.960071	-7.35
262568_at	hypothetical protein contains similarity	AtRLP5	AT1G34290	-1.01	-0.01	-0.10	0.921589	0.960103	-7.35
248047_at	putative protein similar to unknown pro	---	AT5G56070	-1.01	-0.01	-0.10	0.921878	0.96036	-7.35
265764_at	hypothetical protein predicted by gens	---	AT2G48060	-1.01	-0.01	-0.10	0.922425	0.960886	-7.35
266137_at	unknown protein ;supported by full-ler	---	AT2G45010	-1.01	-0.01	-0.10	0.922478	0.960897	-7.35
263976_at	unknown protein	---	AT2G42700	1.01	0.01	0.10	0.922551	0.960929	-7.35
259624_at	hypothetical protein similar to unknown	---	AT1G43020	1.01	0.01	0.10	0.922694	0.961035	-7.35
259849_at	phosphoglycerate dehydrogenase, pu	---	AT1G72190	-1.01	-0.01	-0.10	0.922743	0.961041	-7.35
247947_at	auxin transport protein EIR1 (gb|AAC3	EIR1	AT5G57090	-1.01	-0.01	-0.10	0.922843	0.961067	-7.35
261214_at	Mutator-like protein similar to many pre	---	---	1.01	0.02	0.10	0.922852	0.961067	-7.35
251142_at	Expressed protein ; supported by full-le	---	AT5G01015	1.01	0.01	0.10	0.923005	0.961182	-7.35
246790_at	putative protein unknown protein F22F	---	AT5G27610	-1.01	-0.02	-0.10	0.923072	0.961208	-7.35
259225_at	putative small nuclear ribonucleoprotei	---	AT3G07590	-1.02	-0.03	-0.10	0.923282	0.961296	-7.35
250864_at	putative protein predicted proteins, Ar	---	AT5G03870	1.01	0.01	0.10	0.923259	0.961296	-7.35
261255_at	hypothetical protein contains similarity	ATNTH2	AT1G05900	1.01	0.01	0.10	0.923213	0.961296	-7.35

249712_at	eIF4Eiso protein (emb|CAA71579.1) ;	LSP1	AT5G35620	1.01	0.02	0.10	0.923438	0.96133	-7.35
245436_at	membrane protein homolog	---	AT4G16620	1.01	0.01	0.10	0.923435	0.96133	-7.35
257740_at	hypothetical protein predicted by gene	---	AT3G27330	-1.01	-0.01	-0.10	0.923441	0.96133	-7.35
255120_x_	putative transposon protein similar to r	---	---	1.01	0.01	0.10	0.923548	0.961371	-7.35
263299_s_	hypothetical protein predicted by gens	---	AT2G11570	-1.01	-0.01	-0.10	0.923565	0.961371	-7.35
245360_at	naringenin 3-dioxygenase like protein ;	---	AT4G16330	1.01	0.01	0.10	0.923643	0.961408	-7.35
265541_at	hypothetical protein predicted by gens	SQN	---	-1.01	-0.01	-0.10	0.92382	0.961521	-7.35
260901_at	flavin-containing monooxygenases, pu	YUC11	AT1G21430	-1.01	-0.01	-0.10	0.923874	0.961521	-7.35
264029_at	unknown protein	MRH6	AT2G03720	-1.01	-0.01	-0.10	0.923878	0.961521	-7.35
247375_at	Expressed protein ; supported by full-le	---	AT5G63135	-1.01	-0.01	-0.10	0.923976	0.961579	-7.35
263784_at	Expressed protein ; supported by full-le	---	AT2G46375	-1.01	-0.01	-0.10	0.92407	0.961633	-7.35
245503_at	kinase like protein	---	AT4G15650	-1.01	-0.01	-0.10	0.924212	0.961737	-7.35
246770_at	putative protein DNA-binding protein -	---	AT5G27460	1.01	0.01	0.10	0.924297	0.961782	-7.35
255938_at	hypothetical protein contains Pfam pro	---	AT1G12620	-1.01	-0.01	-0.10	0.924445	0.961891	-7.35
245192_at	F12A21.9 hypothetical protein	---	AT1G67780	1.01	0.01	0.10	0.924785	0.962158	-7.35
250364_at	putative protein serine threonine tyros	---	AT5G11400	1.01	0.01	0.10	0.924777	0.962158	-7.35
264585_at	auxin-resistance protein AXR1 E1 ubic	AXR1	AT1G05180	-1.01	-0.01	-0.10	0.92502	0.962358	-7.35
256737_at	farnesyltranstransferase, putative (fra	---	AT3G29420	1.01	0.01	0.10	0.925161	0.962416	-7.35
254499_at	putative protein probable membrane p	---	AT4G20100	1.01	0.01	0.10	0.925244	0.962416	-7.35
250044_at	disease resistance protein RPP1-WsE	---	AT5G17680	1.01	0.02	0.10	0.925225	0.962416	-7.35
254777_at	putative protein hypothetical protein -	---	AT4G12960	-1.01	-0.01	-0.10	0.925144	0.962416	-7.35
256434_at	putative 60S ribosomal protein L37a si	---	AT3G10950	1.01	0.01	0.10	0.92534	0.962471	-7.35
246396_at	carbonic anhydrase, putative similar to	BCA6	AT1G58180	-1.01	-0.02	-0.10	0.925583	0.962622	-7.35
259338_at	s-syntaxin-like protein similar to s-synt	SYP131	AT3G03800	1.01	0.01	0.10	0.925664	0.962622	-7.35
250173_at	MYB40 - putative transcription factor	AtMYB40	AT5G14340	1.01	0.01	0.10	0.925527	0.962622	-7.35
249868_at	senescence-associated protein 5-like p	TET12	AT5G23030	-1.01	-0.01	-0.10	0.925695	0.962622	-7.35
253250_at	hypothetical protein	---	AT4G34690	-1.01	-0.01	-0.10	0.925611	0.962622	-7.35
264304_at	Expressed protein ; supported by full-le	---	AT1G78895	-1.01	-0.01	-0.10	0.925738	0.962623	-7.35
265801_at	fertilization-independent seed 2 protein	FIS2	AT2G35670	1.01	0.01	0.10	0.925878	0.962724	-7.35
246668_at	putative protein	---	---	-1.01	-0.01	-0.10	0.925993	0.962756	-7.35
254757_at	putative protein other putative or hypot	ROPGEF9	AT4G13240	1.01	0.01	0.10	0.925994	0.962756	-7.35
246075_at	monogalactosyldiacylglycerol synthase	MGD2	AT5G20410	-1.02	-0.03	-0.10	0.926067	0.962789	-7.35
259025_at	hypothetical protein predicted by gene	---	---	1.01	0.01	0.10	0.926158	0.96284	-7.35
251891_at	aintegumaenta-like protein ovule deve	WRI1	AT3G54320	-1.01	-0.01	-0.10	0.926354	0.963	-7.35
257298_at	hypothetical protein predicted by gene	---	AT3G28155	1.01	0.01	0.10	0.92666	0.963273	-7.35

258549_at	putative arginine methyltransferase sir	PRMT4B	AT3G06930	1.01	0.01	0.10	0.926862	0.96344	-7.35
267155_at	CLE7, putative CLAVATA3/ESR-relat	---	AT2G30925	-1.01	-0.01	-0.09	0.927413	0.963969	-7.35
260296_at	putative disease resistance protein sim	---	AT1G63750	-1.03	-0.04	-0.09	0.927606	0.964114	-7.35
263001_at	hypothetical protein contains similarity	TAF6B4	AT1G54360	-1.01	-0.02	-0.09	0.927637	0.964114	-7.35
247133_at	chalcone isomerase-like protein	---	AT5G66220	-1.01	-0.02	-0.09	0.927699	0.964134	-7.35
254537_at	putative protein chitinase / lysozyme F	---	AT4G19730	1.01	0.01	0.09	0.927742	0.964135	-7.35
248355_at	putative protein strong similarity to unk	ATEXO70A2	AT5G52340	-1.01	-0.01	-0.09	0.928028	0.964388	-7.35
260341_at	squamosa-promoter binding protein, p	---	AT1G69170	-1.01	-0.01	-0.09	0.928162	0.96444	-7.35
253055_at	putative protein cyclin delta-1, Arabido	CYCD5;1	AT4G37630	-1.01	-0.02	-0.09	0.928132	0.96444	-7.35
263394_at	hypothetical protein predicted by gene	---	---	1.01	0.01	0.09	0.928501	0.964748	-7.35
255634_at	hypothetical protein ; supported by cD	FRI	AT4G00650	-1.01	-0.01	-0.09	0.928883	0.9651	-7.35
247613_at	xABC transporter - like protein breast	---	AT5G60740	1.01	0.01	0.09	0.92898	0.965117	-7.35
245746_at	bHLH transcription factor, putative sim	---	AT1G51070	-1.01	-0.01	-0.09	0.928983	0.965117	-7.35
258120_at	hypothetical protein predicted by genm	---	AT3G14730	1.01	0.01	0.09	0.929137	0.965145	-7.35
248635_at	unknown protein	---	AT5G49050	-1.01	-0.01	-0.09	0.929082	0.965145	-7.35
248489_at	unknown protein	---	AT5G51090	-1.01	-0.01	-0.09	0.929101	0.965145	-7.35
248545_at	cysteine proteinase similar to cysteine	---	AT5G50260	1.01	0.01	0.09	0.929263	0.965232	-7.35
246615_at	putative protein similar to unknown pro	---	---	-1.01	-0.01	-0.09	0.929309	0.965235	-7.35
262521_at	unknown protein Location of est 278F3	---	AT1G17130	1.01	0.01	0.09	0.929402	0.965287	-7.35
247797_at	predicted protein	---	AT5G58780	-1.01	-0.01	-0.09	0.929485	0.965287	-7.35
249584_s_	Membrane integral protein (MIP) -like	NIP4;1	AT5G37810 /	-1.01	-0.01	-0.09	0.929446	0.965287	-7.35
252571_at	putative protein syntaxin 8 - Homo sa	SYP72	AT3G45280	-1.01	-0.01	-0.09	0.929763	0.965419	-7.35
258318_at	unknown protein	---	AT3G22680	1.01	0.02	0.09	0.929825	0.965419	-7.35
257276_at	disease resistance protein, putative si	---	AT3G14460	-1.01	-0.01	-0.09	0.929738	0.965419	-7.35
257065_at	diacylglycerol pyrophosphate phospha	---	AT3G18220	1.01	0.02	0.09	0.929667	0.965419	-7.35
262564_at	anionic peroxidase, putative similar to	---	AT1G34330	1.01	0.01	0.09	0.929807	0.965419	-7.35
266829_at	hypothetical protein predicted by gens	---	AT2G22940	-1.01	-0.01	-0.09	0.929912	0.965466	-7.35
261171_at	unknown protein	---	AT1G04880	-1.01	-0.01	-0.09	0.930115	0.965519	-7.35
264734_at	hypothetical protein predicted by gene	SLAH1	AT1G62280	1.01	0.01	0.09	0.930175	0.965519	-7.35
248482_at	unknown protein	---	AT5G50970	-1.01	-0.01	-0.09	0.930062	0.965519	-7.35
253082_at	putative glycine-rich cell wall protein g	---	AT4G36230	1.01	0.02	0.09	0.930044	0.965519	-7.35
260340_at	putative dihydropterin pyrophosphokin	---	AT1G69190	1.01	0.01	0.09	0.930153	0.965519	-7.35
251041_at	ubiquitin-protein ligase E3-alpha -like	PRT6	AT5G02310	-1.01	-0.01	-0.09	0.930276	0.96558	-7.35
246878_at	putative protein self-incompatibility pro	---	AT5G26060	-1.01	-0.01	-0.09	0.930441	0.965664	-7.35
252503_at	putative protein hypothetical protein F	---	AT3G46910	1.01	0.01	0.09	0.930439	0.965664	-7.35

249257_at	unknown protein	---	AT5G41640	1.01	0.01	0.09	0.930591	0.965729	-7.35
255678_at	predicted protein with unknown functio	AT4G00520	---	-1.01	-0.01	-0.09	0.930631	0.965729	-7.35
257496_s_	hypothetical protein predicted by grail	---	AT2G43730 /	1.01	0.01	0.09	0.930596	0.965729	-7.35
248747_at	ribosomal protein S27 ;supported by fu	---	AT5G47930	-1.01	-0.01	-0.09	0.930679	0.965735	-7.35
251628_at	translation initiation factor 3 -like prote	EIF3E	AT3G57290	-1.01	-0.01	-0.09	0.930747	0.965761	-7.35
249522_at	putative protein similar to unknown pro	---	AT5G38700	-1.01	-0.01	-0.09	0.930813	0.965786	-7.35
265750_x_	putative Athila retroelement ORF1 prot	---	---	-1.01	-0.02	-0.09	0.930896	0.965828	-7.35
258824_at	unknown protein	---	AT3G07190	-1.01	-0.01	-0.09	0.930983	0.965831	-7.35
254338_s_	pectate lyase like protein pectate lyas	---	AT4G22080 /	1.01	0.01	0.09	0.930951	0.965831	-7.35
253815_at	putative beta-expansin/allergen protei	ATEXPB3	AT4G28250	-1.01	-0.02	-0.09	0.931037	0.965843	-7.35
266631_at	putative serpin	---	AT2G35570	1.01	0.01	0.09	0.931225	0.965913	-7.35
254771_at	hypothetical protein	MEE56	AT4G13380	1.01	0.01	0.09	0.931217	0.965913	-7.35
252778_at	putative protein replication protein A 5	---	---	1.01	0.01	0.09	0.931252	0.965913	-7.35
250878_at	maturase -like protein gene cob intron	---	AT5G04050	1.01	0.02	0.09	0.931274	0.965913	-7.35
246965_at	methyltransferase-like protein methylt	---	AT5G24840	-1.01	-0.02	-0.09	0.931362	0.96596	-7.35
262139_at	mutator-like transposase, putative sim	AT1G52615	---	1.01	0.01	0.09	0.931511	0.966071	-7.35
247900_at	60S acidic ribosomal protein P3 ; supp	---	AT5G57290	-1.01	-0.02	-0.09	0.93169	0.966213	-7.35
262766_at	hypothetical protein predicted by gens	---	AT1G13160	-1.01	-0.02	-0.09	0.931924	0.966365	-7.35
247587_at	putative protein predicted proteins, C.	---	AT5G60620	1.01	0.01	0.09	0.931964	0.966365	-7.35
256418_at	hypothetical protein	---	AT3G06160	-1.01	-0.01	-0.09	0.931883	0.966365	-7.35
261548_at	DNA-binding protein, putative contains	---	AT1G63480	-1.01	-0.01	-0.09	0.932126	0.966489	-7.35
260720_at	hypothetical protein predicted by gens	---	AT1G48095	1.01	0.01	0.09	0.932189	0.966511	-7.35
263821_s_	40S ribosomal protein S16 Same as G	---	AT2G09990 /	1.01	0.01	0.09	0.932513	0.966796	-7.35
246421_at	TOM (target of myb1) -like protein TO	---	AT5G16880	1.01	0.01	0.09	0.932647	0.966796	-7.35
246438_at	putative protein non-phototropic hypo	---	AT5G17580	1.01	0.01	0.09	0.932634	0.966796	-7.35
250228_at	cell cycle switch protein	FZR3	AT5G13840	1.01	0.01	0.09	0.932676	0.966796	-7.35
247927_at	unknown protein	---	AT5G57310	-1.01	-0.01	-0.09	0.932649	0.966796	-7.35
267487_at	putative non-LTR retroelement reverse	---	---	-1.01	-0.01	-0.09	0.932905	0.966905	-7.35
251050_at	putative protein	---	AT5G02440	1.01	0.01	0.09	0.932908	0.966905	-7.35
257595_at	hypothetical protein predicted by gens	---	AT3G24750	-1.01	-0.01	-0.09	0.932907	0.966905	-7.35
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X1	---	---	-1.02	-0.03	-0.09	0.933007	0.966955	-7.35
265833_at	Mutator-like transposase similar to MU	---	---	-1.01	-0.01	-0.09	0.933042	0.966955	-7.35
266158_at	putative ABC transporter	---	AT2G28070	1.01	0.01	0.09	0.933377	0.966966	-7.35
246773_at	protein kinase-like protein MAP3Ka M	---	AT5G27510	1.01	0.01	0.09	0.933391	0.966966	-7.35
265068_at	hypothetical protein Similar to Kinesin	---	AT1G55550	-1.01	-0.01	-0.09	0.933276	0.966966	-7.35

253150_at	putative protein predicted protein, Ara	---	AT4G35660	1.01	0.01	0.09	0.933245	0.966966	-7.35
259337_at	putative cationic amino acid transporte	CAT4	AT3G03720	-1.01	-0.01	-0.09	0.933248	0.966966	-7.35
261549_at	DNA-binding protein, putative contains	---	AT1G63470	1.01	0.01	0.09	0.933105	0.966966	-7.35
247803_at	similar to unknown protein (gb|AAF631	---	AT5G58340	1.01	0.01	0.09	0.933217	0.966966	-7.35
255083_s_	hypothetical protein	---	---	1.01	0.01	0.09	0.933387	0.966966	-7.35
245043_at	putative cyclin ;supported by full-lengt	RCY1	AT2G26430	1.01	0.02	0.09	0.933469	0.967002	-7.35
249444_at	putative protein S-locus-specific glyco	---	AT5G39370	1.01	0.01	0.09	0.933788	0.967289	-7.35
263096_at	class 1 non-symbiotic hemoglobin (AH	AHB1	AT2G16060	-1.02	-0.03	-0.09	0.93409	0.967558	-7.35
260565_at	unknown protein predicted by genefinc	---	AT2G43800	1.01	0.02	0.09	0.934269	0.96758	-7.35
252626_at	putative protein predicted protein, Ara	---	AT3G44940	1.01	0.01	0.09	0.934256	0.96758	-7.35
263354_at	hypothetical protein predicted by grail	---	AT2G22060	1.01	0.01	0.09	0.934191	0.96758	-7.35
263578_at	F-box protein family, AtFBL10 contain	---	AT2G17020	-1.01	-0.01	-0.09	0.934281	0.96758	-7.35
263351_at	hypothetical protein predicted by grail	---	AT2G22120	1.01	0.01	0.09	0.934425	0.967602	-7.35
262121_at	endo-1,4-beta-glucanase precursor, p	ATCEL2	AT1G02800	-1.01	-0.01	-0.09	0.934438	0.967602	-7.35
265515_at	hypothetical protein predicted by gens	---	---	1.01	0.01	0.09	0.934471	0.967602	-7.35
262679_at	unknown protein ; supported by cDNA	LCR67	AT1G75830	-1.01	-0.01	-0.09	0.93444	0.967602	-7.35
247003_at	putative protein similar to unknown pro	---	AT5G67550	-1.01	-0.01	-0.09	0.934549	0.967638	-7.35
253930_at	embryo-specific protein 1 (ATS1)	ATS1	AT4G26740	-1.01	-0.01	-0.09	0.934711	0.967762	-7.35
264272_at	hypothetical protein contains similarity	ANAC023	AT1G60280	-1.01	-0.01	-0.08	0.934919	0.967933	-7.35
248837_at	putative protein similar to unknown pro	---	AT5G47260	-1.01	-0.01	-0.08	0.934975	0.967947	-7.35
256471_at	hypothetical protein predicted by gene	---	---	-1.01	-0.01	-0.08	0.935075	0.967963	-7.35
246320_at	unknown protein	---	AT1G16560	-1.01	-0.01	-0.08	0.935056	0.967963	-7.35
260938_at	hypothetical protein contains similarity	---	AT1G45170	1.01	0.01	0.08	0.935303	0.967977	-7.35
260895_at	unknown protein similar to unknown pr	---	AT1G29250	1.01	0.02	0.08	0.935267	0.967977	-7.35
257854_at	putative CREB-binding protein similar	HAC5	AT3G12980	-1.01	-0.01	-0.08	0.935192	0.967977	-7.35
258503_at	unknown protein	---	AT3G02500	-1.01	-0.01	-0.08	0.935343	0.967977	-7.35
265135_at	unknown protein similar to unknown pr	---	AT1G51270	1.01	0.01	0.08	0.935336	0.967977	-7.35
258595_at	unknown protein contains Pfam profile	---	AT3G04500	1.01	0.01	0.08	0.935335	0.967977	-7.35
252920_at	putative endo-1,4-beta-glucanase end	AtGH9B17	AT4G39000	1.01	0.01	0.08	0.935423	0.968015	-7.35
250279_at	ABA-responsive protein - like ABA-res	---	AT5G13200	-1.01	-0.02	-0.08	0.935496	0.968045	-7.35
253031_at	putative protein cellulose synthase - P	CSLD4	AT4G38190	-1.01	-0.01	-0.08	0.935537	0.968045	-7.35
256023_at	hypothetical protein predicted by gene	ZW2	AT1G58330	1.01	0.01	0.08	0.935644	0.968083	-7.35
AFFX-Trpn	B. subtilis /GEN=trpE, trpD /DB_XREF	---	---	-1.01	-0.01	-0.08	0.935658	0.968083	-7.35
255750_at	hypothetical protein predicted by gene	---	AT1G31960	-1.01	-0.01	-0.08	0.935781	0.968167	-7.35
265722_at	putative chlorophyll a/b binding protein	LHCB4.3	AT2G40100	-1.01	-0.02	-0.08	0.93585	0.968194	-7.35

253561_at	aspartate--tRNA ligase - like protein a	---	AT4G31180	-1.01	-0.01	-0.08	0.935988	0.968293	-7.35
254557_at	hypothetical protein ;supported by full-	---	AT4G19140	1.01	0.02	0.08	0.936147	0.968412	-7.35
256265_at	serine carboxypeptidase, putative con	scpl16	---	-1.01	-0.01	-0.08	0.936188	0.968412	-7.35
246704_at	putative protein	---	AT5G28090	1.01	0.01	0.08	0.936273	0.968416	-7.35
263360_at	unknown protein	---	AT2G03830	1.01	0.01	0.08	0.93632	0.968416	-7.35
262002_at	hypothetical protein predicted by gene	---	AT1G64450	-1.01	-0.01	-0.08	0.93631	0.968416	-7.35
262885_at	alpha-tubulin, putative similar to alpha	TUA1	AT1G64740	1.01	0.01	0.08	0.936545	0.968572	-7.35
244918_at	hypothetical protein	AT2G07742	---	-1.01	-0.01	-0.08	0.936556	0.968572	-7.35
258079_at	hypothetical protein predicted by gens	---	AT3G25940	1.01	0.01	0.08	0.936649	0.968626	-7.35
264259_at	hypothetical protein This gene is contir	---	AT1G09290	1.01	0.01	0.08	0.936753	0.968645	-7.35
255915_at	putative protein	---	AT5G28620	-1.01	-0.01	-0.08	0.936754	0.968645	-7.35
255685_s_	putative tetrahydrofolate synthase simi	---	AT4G00600 /	1.01	0.02	0.08	0.936807	0.968657	-7.35
255276_at	putative fatty acid desaturase similar t	DES-1-LIKE	AT4G04930	-1.01	-0.01	-0.08	0.93696	0.968714	-7.35
245132_at	hypothetical protein predicted by gene	---	AT2G45320	1.01	0.01	0.08	0.93699	0.968714	-7.35
261184_at	pol polyprotein, putative similar to mar	---	---	-1.01	-0.01	-0.08	0.936918	0.968714	-7.35
264137_at	lupeol synthase, putative similar to lup	ATLUP2	AT1G78960	1.01	0.01	0.08	0.937159	0.968845	-7.35
257895_at	dihydrolipoamide dehydrogenase, put	LPD1	AT3G16950	1.01	0.02	0.08	0.937223	0.968846	-7.35
265653_at	hypothetical protein	---	---	1.01	0.01	0.08	0.937245	0.968846	-7.35
261130_at	unknown protein ; supported by cDNA	PRMT10	AT1G04870	1.01	0.02	0.08	0.937334	0.968895	-7.35
256126_at	hypothetical protein similar to MuDR tr	---	AT1G18050	1.01	0.01	0.08	0.93743	0.96892	-7.35
264626_at	unknown protein	AS2	AT1G65620	-1.01	-0.01	-0.08	0.937444	0.96892	-7.35
255165_at	putative protein putative centromeric p	---	---	1.01	0.02	0.08	0.937575	0.968968	-7.35
257256_at	hypothetical protein contains Pfam pro	---	AT3G21970	1.00	0.01	0.08	0.937554	0.968968	-7.35
249989_at	putative protein FACTOR ASSOCIATI	---	AT5G18525	1.01	0.01	0.08	0.937799	0.96915	-7.35
245522_at	hypothetical protein	---	AT4G15890	1.01	0.01	0.08	0.937837	0.96915	-7.35
251128_at	putative protein crp1 protein, Zea may	---	AT5G01110	1.01	0.01	0.08	0.937978	0.969253	-7.35
246757_at	Expressed protein ; supported by full-le	WPP3	AT5G27940	-1.01	-0.01	-0.08	0.938077	0.969311	-7.35
252718_at	putative protein predicted proteins, Ar	---	AT3G43940	-1.01	-0.01	-0.08	0.938363	0.969318	-7.35
263955_at	putative E2F5 family transcription facto	E2F3	AT2G36010	-1.01	-0.01	-0.08	0.938509	0.969318	-7.35
265598_at	putative protein phosphatase 2C	---	AT2G14270	1.01	0.01	0.08	0.938396	0.969318	-7.35
255239_at	contains similarity to Arabidopsis thalia	---	---	-1.00	-0.01	-0.08	0.938482	0.969318	-7.35
249547_at	lipid transfer - like protein P48h-10 pro	---	AT5G38160	1.01	0.01	0.08	0.938216	0.969318	-7.35
261779_at	hypothetical protein predicted by gene	---	AT1G76230	-1.01	-0.01	-0.08	0.93822	0.969318	-7.35
265399_at	hypothetical protein predicted by gens	---	AT2G11010	1.01	0.02	0.08	0.938441	0.969318	-7.35
245207_at	RING finger-like protein similarity to pi	---	AT5G12310	1.01	0.01	0.08	0.938433	0.969318	-7.35

245185_at	F12A21.11 similar to T-Complex prote	---	AT1G67760	-1.01	-0.01	-0.08	0.938414	0.969318	-7.35
264125_at	hypothetical protein predicted by gene	EMB1135	AT1G79350	1.01	0.01	0.08	0.938308	0.969318	-7.35
251651_at	putative protein transcription initiation	---	AT3G57370	1.00	0.01	0.08	0.938604	0.969328	-7.35
266483_at	unknown protein ;supported by full-ler	CRR6	AT2G47910	-1.01	-0.01	-0.08	0.938593	0.969328	-7.35
259928_at	DNA polymerase type I, putative simil	---	AT1G34380	1.01	0.02	0.08	0.938755	0.969411	-7.35
265934_at	unknown protein	EER5	AT2G19560	1.01	0.01	0.08	0.938854	0.969411	-7.35
265407_at	F-box protein family, AtFBX8 contains	---	AT2G16810	-1.01	-0.01	-0.08	0.938842	0.969411	-7.35
263007_at	hypothetical protein contains similarity	---	AT1G54260	-1.01	-0.01	-0.08	0.938796	0.969411	-7.35
262645_at	unknown protein similar to elongation f	SCO1	AT1G62750	1.01	0.01	0.08	0.938984	0.969502	-7.35
256561_s_	hypothetical protein similar to putative	---	---	-1.01	-0.01	-0.08	0.939099	0.969576	-7.35
246543_at	putative protein	---	AT5G15060	-1.00	-0.01	-0.08	0.939327	0.969631	-7.35
245888_at	putative protein DNA-binding protein -	---	AT5G09450	1.01	0.01	0.08	0.939259	0.969631	-7.35
265889_at	hypothetical protein predicted by gene	---	AT2G15130	1.01	0.01	0.08	0.939364	0.969631	-7.35
252808_at	putative protein various predicted prot	---	---	1.01	0.01	0.08	0.939301	0.969631	-7.35
261936_at	seed maturation protein PM27, putativ	---	AT1G22600	-1.01	-0.01	-0.08	0.939345	0.969631	-7.35
261680_at	hypothetical protein similar to hypothet	---	AT1G47350	1.01	0.01	0.08	0.939424	0.969649	-7.35
257668_at	sugar transporter, putative similar to G	---	AT3G20460	-1.01	-0.01	-0.08	0.939469	0.969651	-7.35
264677_at	hypothetical protein predicted by gene	HYL1	AT1G09700	1.00	0.01	0.08	0.939728	0.969743	-7.35
262273_at	hypothetical protein predicted by gens	---	AT1G68730	-1.01	-0.01	-0.08	0.939681	0.969743	-7.35
262266_at	mudrA-like protein similar to mudrA GE	---	---	-1.01	-0.01	-0.08	0.939653	0.969743	-7.35
266069_at	putative RING zinc finger protein	MEE16	AT2G18650	-1.01	-0.02	-0.08	0.939722	0.969743	-7.35
255755_s_	polygalacturonase, putative similar to	---	AT1G43050 /	-1.01	-0.01	-0.08	0.940126	0.97011	-7.35
256791_at	hypothetical protein predicted by gens	---	---	-1.01	-0.01	-0.08	0.940491	0.970443	-7.35
256338_at	hypothetical protein similar to seed ma	---	AT1G72100	1.01	0.01	0.08	0.940544	0.970453	-7.35
264124_at	hypothetical protein predicted by gene	ATOCT2	AT1G79360	-1.01	-0.01	-0.08	0.940681	0.970484	-7.35
255754_at	auxin-induced protein, putative similar	---	AT1G43040	1.00	0.01	0.08	0.940625	0.970484	-7.35
264730_at	hypothetical protein similar to putative	---	AT1G62085	-1.01	-0.01	-0.08	0.940701	0.970484	-7.35
249962_at	pectin methyl esterase -like protein pe	---	AT5G18990	-1.01	-0.01	-0.08	0.940812	0.970555	-7.35
259059_at	hypothetical protein	---	AT3G07300	-1.01	-0.01	-0.08	0.941064	0.970726	-7.35
261030_at	unknown protein contains similarity to	---	AT1G17410	1.01	0.01	0.08	0.941051	0.970726	-7.35
248966_at	unknown protein ;supported by full-len	---	AT5G45360	1.01	0.01	0.08	0.94162	0.97104	-7.35
265239_s_	hypothetical protein	---	AT2G07692	1.01	0.01	0.08	0.941533	0.97104	-7.35
252138_at	peroxidase-like protein peroxidase AT	---	AT3G50990	-1.01	-0.01	-0.08	0.941566	0.97104	-7.35
255984_at	inositol polyphosphate 5-phosphatase	IP5PI	AT1G34120	1.01	0.01	0.08	0.941569	0.97104	-7.35
251212_at	putative protein hypothetical protein A	---	---	-1.01	-0.01	-0.08	0.941624	0.97104	-7.35

265421_s_	predicted protein	---	AT2G20616 /	1.01	0.01	0.08	0.941435	0.97104	-7.35
266612_at	22 kDa peroxisomal membrane protein	---	AT2G14860	1.01	0.01	0.08	0.941704	0.971079	-7.35
248835_at	NBS/LRR disease resistance protein	---	AT5G47250	1.01	0.02	0.08	0.941959	0.971123	-7.35
247019_at	AP2 domain transcription factor-like	---	AT5G67010	1.01	0.01	0.08	0.94185	0.971123	-7.35
261047_at	hypothetical protein predicted by gene	APUM22	AT1G01410	-1.01	-0.02	-0.08	0.941957	0.971123	-7.35
259820_at	subtilisin-like serine protease contains	---	AT1G66210	-1.01	-0.01	-0.08	0.941876	0.971123	-7.35
250169_at	putative protein many predicted protei	---	AT5G15340	1.01	0.01	0.08	0.941821	0.971123	-7.35
260007_at	unknown protein contains non-consens	---	AT1G67870	1.01	0.02	0.08	0.94216	0.971242	-7.35
251045_s_	putative protein various predicted prot	---	AT2G13910 /	1.00	0.01	0.08	0.942131	0.971242	-7.35
247646_at	putative protein various predicted prot	---	AT5G59990	1.01	0.01	0.08	0.942322	0.971365	-7.35
250955_at	putative protein various predicted prot	CPUORF47	AT5G03190	1.02	0.03	0.07	0.942614	0.971618	-7.35
251510_at	putative protein several hypothetical pr	---	AT3G59170	-1.00	-0.01	-0.07	0.942652	0.971618	-7.35
258271_at	hypothetical protein predicted by gene	---	AT3G15605	1.01	0.01	0.07	0.942735	0.971659	-7.35
254414_at	hypothetical protein	HSA32	AT4G21320	-1.01	-0.01	-0.07	0.943056	0.971858	-7.35
255845_at	putative cinnamoyl-CoA reductase hig	---	AT2G33600	-1.01	-0.01	-0.07	0.94303	0.971858	-7.35
261647_at	hypothetical protein similar to hypothet	---	AT1G27740	-1.01	-0.01	-0.07	0.943034	0.971858	-7.35
257464_at	hypothetical protein predicted by gens	---	AT1G20940	-1.01	-0.01	-0.07	0.943201	0.971964	-7.35
248323_at	unknown protein	---	AT5G52770	-1.00	-0.01	-0.07	0.94337	0.972094	-7.35
245560_at	indole-3-acetate beta-glucosyltransfera	UGT84A1	AT4G15480	1.01	0.01	0.07	0.943521	0.972118	-7.35
253093_at	putative protein SPINDLY protein, Pet	SRFR1	AT4G37460	1.01	0.01	0.07	0.943505	0.972118	-7.35
261284_at	hypothetical protein predicted by gens	---	---	1.01	0.01	0.07	0.943446	0.972118	-7.35
265092_at	hypothetical protein predicted by gens	---	AT1G03910	-1.00	-0.01	-0.07	0.943691	0.972119	-7.35
251030_at	putative protein kinesin light chain - P	NDP1	AT5G02130	-1.01	-0.01	-0.07	0.943693	0.972119	-7.35
263393_at	hypothetical protein similar to hypothet	---	---	-1.01	-0.01	-0.07	0.943642	0.972119	-7.35
245172_at	hypothetical protein predicted by gens	---	AT2G47540	-1.00	-0.01	-0.07	0.943632	0.972119	-7.35
250920_at	putative protein ;supported by full-leng	---	AT5G03390	1.01	0.02	0.07	0.943896	0.972123	-7.35
248912_at	GDSL-motif lipase/hydrolase-like prote	---	AT5G45670	1.01	0.01	0.07	0.943812	0.972123	-7.35
262091_at	Myb-family transcription factor, putativ	MYB72	AT1G56160	1.01	0.01	0.07	0.943953	0.972123	-7.35
267245_at	hypothetical protein	---	AT2G02640	-1.01	-0.01	-0.07	0.943939	0.972123	-7.35
248803_at	selenium-binding protein-like	---	AT5G47460	-1.01	-0.01	-0.07	0.943853	0.972123	-7.35
245646_x_	F5A9.9 hypothetical protein	---	AT1G24851 /	1.01	0.01	0.07	0.943798	0.972123	-7.35
252544_at	respiratory burst oxidase - like protein	---	AT3G45810	1.01	0.01	0.07	0.94404	0.972169	-7.35
246322_at	S-locus protein, putative similar to S-l	---	AT1G16680	1.01	0.01	0.07	0.944268	0.97236	-7.35
249777_at	putative protein similar to unknown pro	---	AT5G24210	-1.01	-0.01	-0.07	0.944389	0.972368	-7.35
251653_at	putative protein regulatory protein NP	BOP1	AT3G57130	-1.01	-0.01	-0.07	0.944452	0.972368	-7.35

251866_at	putative protein MSP58 - nucleolar pr	emb1967	AT3G54350	1.00	0.01	0.07	0.944476	0.972368	-7.35
264861_at	putative glucosidase similar to a-gluc	---	AT1G24320	-1.00	-0.01	-0.07	0.944531	0.972368	-7.35
249061_at	putative protein similar to unknown pr	---	AT5G44550	-1.01	-0.01	-0.07	0.944468	0.972368	-7.35
263388_at	En/Spm-like transposon protein relate	---	---	1.01	0.01	0.07	0.944506	0.972368	-7.35
257502_at	unknown protein	---	AT1G78110	1.01	0.02	0.07	0.944591	0.972386	-7.35
264598_at	putative dimethylaniline monooxygena	---	AT1G04610	1.01	0.01	0.07	0.944934	0.972695	-7.35
247645_at	late embryonic abundant protein - like	---	AT5G60530	-1.01	-0.01	-0.07	0.94509	0.972811	-7.35
264425_at	serine/threonine protein kinase, putati	---	AT1G61750	1.01	0.01	0.07	0.945203	0.972884	-7.35
255359_at	putative glucose-6-phosphate/phospha	---	AT4G03950	1.01	0.01	0.07	0.945319	0.972916	-7.35
251989_at	RNA helicase -like protein RNA helica	LOS4	AT3G53110	-1.01	-0.01	-0.07	0.945297	0.972916	-7.35
265793_at	unknown protein	---	AT2G01220	1.01	0.01	0.07	0.945579	0.973139	-7.35
252944_at	hypothetical protein ;supported by full	---	AT4G39320	-1.01	-0.01	-0.07	0.945658	0.973176	-7.35
253313_at	putative peroxidase peroxidase ATP1	---	AT4G33870	-1.01	-0.01	-0.07	0.945802	0.973259	-7.35
251102_at	putative transporter protein Na+/H+ an	CHX27	AT5G01690	-1.01	-0.01	-0.07	0.945823	0.973259	-7.35
251607_at	hypothetical protein	---	AT3G57850	-1.01	-0.01	-0.07	0.946013	0.97341	-7.35
247004_at	putative protein similar to unknown pr	DG1	AT5G67570	-1.01	-0.01	-0.07	0.946115	0.973412	-7.35
252673_at	CCR4-associated factor 1-like protein	---	AT3G44240	-1.01	-0.01	-0.07	0.946228	0.973412	-7.35
262989_at	F28C11.5 similar to INNER NO OUTE	INO	AT1G23420	1.01	0.01	0.07	0.946196	0.973412	-7.35
266066_at	putative xyloglucan endo-transglycosy	XTH21	AT2G18800	-1.01	-0.01	-0.07	0.946126	0.973412	-7.35
249724_at	disease resistance protein	---	AT5G35450	1.00	0.01	0.07	0.946208	0.973412	-7.35
262735_at	hypothetical protein	---	AT1G28630	-1.01	-0.01	-0.07	0.946536	0.973685	-7.35
265137_at	F-box protein family, AtFBX10 contain	---	AT1G51290	1.01	0.01	0.07	0.946629	0.973692	-7.35
259078_at	unknown protein predicted by genefinc	HST	AT3G05040	-1.00	-0.01	-0.07	0.946606	0.973692	-7.35
263531_s_	hypothetical protein predicted by gens	---	AT2G25020 /	-1.00	-0.01	-0.07	0.94673	0.973752	-7.35
252202_at	anthranilate N-hydroxycinnamoyl/ben	---	AT3G50300	1.01	0.01	0.07	0.946808	0.973788	-7.35
259189_at	unknown protein	AGP11	AT3G01700	-1.01	-0.01	-0.07	0.94685	0.973788	-7.35
256741_at	hypothetical protein predicted by gene	---	AT3G29375	-1.01	-0.01	-0.07	0.946943	0.973816	-7.35
255145_at	hypothetical protein	---	---	1.01	0.01	0.07	0.947005	0.973816	-7.35
252987_at	putative growth regulator protein auxi	---	AT4G38390	1.01	0.01	0.07	0.946967	0.973816	-7.35
249080_at	putative protein strong similarity to unk	SUVR2	AT5G43990	1.01	0.01	0.07	0.947061	0.97383	-7.35
260971_at	hypothetical protein predicted by gene	---	AT1G53620	1.01	0.01	0.07	0.947111	0.973838	-7.35
252169_at	putative protein several bacterial phos	---	AT3G50520	-1.01	-0.01	-0.07	0.947239	0.973925	-7.35
246360_at	hypothetical protein	---	---	1.01	0.01	0.07	0.947294	0.973938	-7.35
245772_at	hypothetical protein similar to putative	---	AT1G30300	1.01	0.01	0.07	0.947437	0.974041	-7.35
258080_at	unknown protein ;supported by full-ler	---	AT3G25930	-1.00	-0.01	-0.07	0.947638	0.974204	-7.35

246065_at	calcium-dependent protein kinase - lik	CPK34	AT5G19360	1.01	0.01	0.07	0.947949	0.974479	-7.35
254738_at	RNA-binding protein like	AT4G13860	---	1.01	0.01	0.07	0.948072	0.974512	-7.35
251499_at	putative protein putative callose synth	ATGSL11	AT3G59100	-1.01	-0.01	-0.07	0.948059	0.974512	-7.35
246866_at	putative protein various predicted prot	---	AT5G25960	-1.01	-0.01	-0.07	0.948109	0.974512	-7.35
267222_at	putative polygalacturonase	---	AT2G43880	-1.00	-0.01	-0.07	0.948164	0.974525	-7.35
246801_at	threonyl-tRNA synthetase ; supported	---	AT5G26830	1.01	0.01	0.07	0.948256	0.974531	-7.35
249617_at	receptor protein kinase-like protein	---	AT5G37450	-1.01	-0.01	-0.07	0.948223	0.974531	-7.35
264705_at	putative leucyl-tRNA synthetase Stron	---	AT1G09620	1.01	0.01	0.07	0.948402	0.97455	-7.35
245139_at	putative AT-hook DNA-binding protein	---	AT2G45430	1.01	0.01	0.07	0.948397	0.97455	-7.35
253616_at	blight-associated protein homolog blig	EXLB2	AT4G30380	-1.00	-0.01	-0.07	0.948336	0.97455	-7.35
266178_at	putative phloem-specific lectin	AtPP2-B4	AT2G02280	1.01	0.01	0.07	0.948467	0.974573	-7.35
262560_at	hypothetical protein predicted by gens	---	AT1G34280	-1.01	-0.01	-0.07	0.948526	0.974588	-7.35
247104_at	putative protein similar to unknown pro	DAR6	AT5G66620	1.01	0.01	0.07	0.948567	0.974588	-7.35
246419_at	UDP glucose:flavonoid 3-o-glucosyltra	UGT78D3	AT5G17030	1.00	0.01	0.07	0.948687	0.974666	-7.35
249560_at	putative protein	LCR80	AT5G38330	-1.01	-0.01	-0.07	0.948865	0.974762	-7.35
265300_at	unknown protein contains weak PHD z	---	AT2G13950	1.01	0.01	0.07	0.948847	0.974762	-7.35
248303_at	FtsH protease, putative similar to ATP	FTSH11	AT5G53170	-1.01	-0.01	-0.07	0.949027	0.974839	-7.35
266556_at	hypothetical protein predicted by gens	---	AT2G46230	-1.01	-0.01	-0.07	0.949068	0.974839	-7.35
252787_at	putative protein several En/Spm-like tr	---	---	-1.00	-0.01	-0.07	0.949052	0.974839	-7.35
256350_at	hypothetical protein contains similarity	PGSIP4	AT1G54940	-1.00	-0.01	-0.07	0.949334	0.975027	-7.35
258272_at	unknown protein similar to serine/thre	---	AT3G15610	1.01	0.01	0.07	0.949337	0.975027	-7.35
258596_at	unknown protein	LSH2	AT3G04510	-1.01	-0.01	-0.07	0.949434	0.975039	-7.35
245403_at	putative protein	---	AT4G17590	-1.00	-0.01	-0.07	0.949426	0.975039	-7.35
246524_at	Carboxylesterase-like protein sterol es	ATPCME	AT5G15860	1.01	0.01	0.07	0.949653	0.975189	-7.35
264533_s_	H+/Ca2+ antiporter, putative similar to	CAX5	AT1G55720 /	1.01	0.01	0.07	0.949666	0.975189	-7.35
263859_at	hypothetical protein predicted by gens	---	AT2G04360	-1.01	-0.01	-0.07	0.949979	0.975467	-7.35
259522_at	hypothetical protein	---	AT1G12490	-1.00	-0.01	-0.06	0.95018	0.975629	-7.35
249565_at	contains similarity to S1 self-incompati	---	AT5G38440	-1.01	-0.01	-0.06	0.950272	0.97568	-7.35
248263_at	pectinesterase ; supported by cDNA:	PMEPCRF	AT5G53370	1.01	0.02	0.06	0.950376	0.975699	-7.35
265110_at	hypothetical protein predicted by gens	---	AT1G62490	1.01	0.01	0.06	0.950351	0.975699	-7.35
259572_at	hypothetical protein	---	AT1G20400	1.01	0.01	0.06	0.950494	0.975776	-7.35
249881_at	cytochrome P450-like protein	CYP86B1	AT5G23190	-1.00	-0.01	-0.06	0.950604	0.975845	-7.35
258305_at	hypothetical protein predicted by gens	---	---	1.00	0.01	0.06	0.950675	0.975874	-7.35
248653_at	disease resistance protein-like	---	AT5G49290	-1.00	-0.01	-0.06	0.950826	0.975985	-7.35
266262_at	hypothetical protein predicted by gens	---	AT2G27590	-1.01	-0.01	-0.06	0.951007	0.97601	-7.35

267585_s_	putative actin	ACT9	AT2G42090	1.00	0.01	0.06	0.950904	0.97601	-7.35
264463_at	unknown protein similar to ESTs gb|T	---	AT1G10150	1.01	0.01	0.06	0.951021	0.97601	-7.35
257130_at	vacuolar processing enzyme/asparagi	DELTA-VPE	AT3G20210	-1.00	-0.01	-0.06	0.950958	0.97601	-7.35
249706_at	histone deacetylase	HDA7	AT5G35600	1.00	0.01	0.06	0.951198	0.976147	-7.35
247226_at	putative protein contains similarity to tr	---	AT5G65100	1.00	0.01	0.06	0.951244	0.97615	-7.35
257664_at	hypothetical protein predicted by gene	EMB2743	AT3G20400	1.01	0.01	0.06	0.951297	0.976161	-7.35
247402_at	putative protein predicted proteins, Ca	---	AT5G62750	1.00	0.01	0.06	0.951361	0.976177	-7.35
258112_at	putative cytochrome P450 similar to G	CYP72A10	AT3G14640	-1.01	-0.01	-0.06	0.951398	0.976177	-7.35
252475_s_	putative protein several hypothetical pr	PCL1	AT3G46640 /	-1.01	-0.01	-0.06	0.951463	0.976189	-7.35
246774_at	polygalacturonase-like protein polygal	---	AT5G27530	-1.00	-0.01	-0.06	0.951516	0.976189	-7.35
255705_at	hypothetical protein ;supported by full-	---	AT4G00160	-1.00	-0.01	-0.06	0.951581	0.976189	-7.35
252137_at	dehydrin-like protein dehydrin Xero2	XERO1	AT3G50980	1.01	0.01	0.06	0.951567	0.976189	-7.35
264286_at	unknown protein ;supported by full-len	PPR336	AT1G61870	-1.01	-0.01	-0.06	0.951792	0.976361	-7.35
246520_at	putative protein RING-H2 finger protei	---	AT5G15790	-1.00	-0.01	-0.06	0.951899	0.976422	-7.35
246606_at	putative protein	---	---	-1.00	-0.01	-0.06	0.951937	0.976422	-7.35
249272_at	geranylgeranyl transferase alpha subu	---	AT5G41820	-1.01	-0.01	-0.06	0.952042	0.976486	-7.35
250365_at	putative protein serine threonine tyros	---	AT5G11410	-1.01	-0.01	-0.06	0.952111	0.976513	-7.35
266768_s_	ubiquitin extension protein (UBQ6) ide	UBQ6	AT2G47110 /	-1.01	-0.01	-0.06	0.952234	0.976596	-7.35
255158_s_	hypothetical protein	---	---	1.00	0.01	0.06	0.952344	0.976664	-7.35
261234_x_	hypothetical protein predicted by gene	---	---	-1.01	-0.01	-0.06	0.952392	0.976669	-7.35
257916_at	unknown protein similar to hypothetica	---	AT3G23210	1.01	0.01	0.06	0.952483	0.976719	-7.35
264047_at	hypothetical protein predicted by gens	---	AT2G22410	1.00	0.01	0.06	0.95267	0.976775	-7.35
263611_at	hypothetical protein predicted by gens	---	AT2G16450	-1.00	-0.01	-0.06	0.952683	0.976775	-7.35
266390_at	hypothetical protein predicted by gens	---	AT2G32310	1.00	0.01	0.06	0.952669	0.976775	-7.35
254109_at	Pollen-specific protein precursor like F	SKS1	AT4G25240	1.00	0.01	0.06	0.952709	0.976775	-7.35
253075_at	putative disease resistance protein TN	---	AT4G36150	-1.00	-0.01	-0.06	0.952946	0.976842	-7.35
257032_at	zinc finger protein, putative similar to I	---	AT3G19140	-1.00	-0.01	-0.06	0.952919	0.976842	-7.35
252471_at	phosphoprotein phosphatase ;support	TOPP5	AT3G46820	-1.01	-0.01	-0.06	0.952903	0.976842	-7.35
249660_at	putative protein similar to unknown pro	---	AT5G36720 /	-1.01	-0.01	-0.06	0.952881	0.976842	-7.35
253920_at	histone H2A- like protein histone H2A	HTA2	AT4G27230	-1.01	-0.01	-0.06	0.953125	0.976946	-7.35
258309_at	putative transposase related protein si	---	---	-1.00	-0.01	-0.06	0.953133	0.976946	-7.35
251854_at	putative protein various predicted prot	---	AT3G54800	1.00	0.01	0.06	0.9535	0.977246	-7.35
257500_s_	putative serine carboxypeptidase simi	scpl2	AT1G73300 /	1.00	0.01	0.06	0.953511	0.977246	-7.35
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J04	---	---	-1.01	-0.02	-0.06	0.953554	0.977246	-7.35
263139_at	hypothetical protein similar to hypothet	---	AT1G65110	-1.00	-0.01	-0.06	0.953631	0.977281	-7.35

261217_at	hypothetical protein contains similarity	UBP11	AT1G32850	1.00	0.01	0.06	0.953985	0.977556	-7.35
249448_at	cdc2-like protein	cdc2cAt	AT5G39420	1.01	0.01	0.06	0.953978	0.977556	-7.35
259215_at	unknown protein largely predicted by g	DEX1	AT3G09090	1.00	0.01	0.06	0.954189	0.977721	-7.35
262258_at	20S proteasome subunit PAE1 identic	PAE1	AT1G53850	-1.01	-0.01	-0.06	0.954458	0.977736	-7.35
250438_at	putative protein predicted protein, Ara	---	AT5G10580	-1.00	-0.01	-0.06	0.954568	0.977736	-7.35
246014_at	putative protein	---	AT5G10680	-1.00	-0.01	-0.06	0.954665	0.977736	-7.35
251080_at	putative protein hypothetical proteins -	ROPGEF7	AT5G02010	1.01	0.02	0.06	0.954675	0.977736	-7.35
260885_at	protein kinase PK4, putative similar to	CIPK18	AT1G29230	1.01	0.01	0.06	0.954636	0.977736	-7.35
257387_s_	putative receptor-like protein kinase	---	AT2G14440 /	1.01	0.01	0.06	0.954494	0.977736	-7.35
263365_at	putative heat shock protein	---	AT2G20550	-1.01	-0.01	-0.06	0.954411	0.977736	-7.35
266660_at	hypothetical protein predicted by gens	---	AT2G25920	-1.01	-0.01	-0.06	0.954612	0.977736	-7.35
252605_s_	sulfotransferase-like protein FLAVON	---	AT3G45070 /	-1.00	-0.01	-0.06	0.95445	0.977736	-7.35
256895_at	zinc-finger protein, putative almost ide	---	---	-1.00	-0.01	-0.06	0.954389	0.977736	-7.35
249451_s_	hypothetical protein	---	AT5G39480 /	-1.00	-0.01	-0.06	0.954261	0.977736	-7.35
247537_s_	ABC transport protein - like ABC trans	ATH15	AT5G61690 /	1.00	0.01	0.06	0.95479	0.97781	-7.35
258474_at	hypothetical protein predicted by gens	---	AT3G02650	1.01	0.01	0.06	0.95498	0.97796	-7.35
257505_at	hypothetical protein	---	AT1G47940	1.00	0.01	0.06	0.95508	0.978019	-7.35
257704_at	myb-related transcription factor, putati	ATMYB67	AT3G12720	1.00	0.01	0.06	0.955211	0.978109	-7.35
257131_at	mitochondrial carrier protein, putative	---	AT3G20240	1.00	0.01	0.06	0.95531	0.978167	-7.35
248241_at	unknown protein	---	AT5G53960	-1.00	-0.01	-0.06	0.955413	0.978228	-7.35
246000_at	putative protein predicted proteins, Ar	---	AT5G20820	-1.01	-0.01	-0.06	0.955515	0.978288	-7.35
255159_at	putative polyprotein	---	---	1.01	0.01	0.06	0.95601	0.978665	-7.35
267039_at	hypothetical protein predicted by gene	---	AT2G34270	1.00	0.01	0.06	0.955985	0.978665	-7.35
253514_at	putative protein DNA-binding protein A	---	AT4G31805	1.00	0.01	0.06	0.956012	0.978665	-7.35
260502_at	putative Tub family protein contains P	AtTLP6	AT1G47270	1.01	0.01	0.06	0.956092	0.978704	-7.35
249784_at	putative protein similar to unknown pro	---	AT5G24280	-1.01	-0.01	-0.06	0.956179	0.978749	-7.35
256767_at	hypothetical protein predicted by gene	---	AT3G13680	1.00	0.01	0.06	0.956316	0.97878	-7.35
265052_at	caffeic acid O-methyltransferase, puta	---	AT1G51990	-1.00	-0.01	-0.06	0.956338	0.97878	-7.35
246872_at	extensin - like protein hydroxyproline-	---	AT5G26080	1.01	0.01	0.06	0.956289	0.97878	-7.35
266077_at	putative non-LTR retroelement reverse	---	---	1.00	0.01	0.06	0.956482	0.978884	-7.35
253901_at	ribosomal protein L14 -like protein rib	---	AT4G27090	1.01	0.01	0.06	0.956662	0.978892	-7.35
246910_at	exonuclease - like protein ribonucleas	---	AT5G25800	1.01	0.01	0.06	0.956649	0.978892	-7.35
254399_at	G10 - like protein Maternal G10 like p	---	AT4G21110	1.00	0.01	0.06	0.956622	0.978892	-7.35
245805_at	hypothetical protein predicted by gene	---	AT1G46336	-1.00	-0.01	-0.06	0.956538	0.978892	-7.35
250093_at	hypothetical protein	---	AT5G17370	-1.00	-0.01	-0.06	0.956706	0.978894	-7.35

256196_at	hypothetical protein predicted by gene	---	---	-1.00	-0.01	-0.06	0.956791	0.978936	-7.35
256071_at	ubiquitin, putative similar to ubiquitin C	---	AT1G13640	1.01	0.01	0.06	0.956871	0.978974	-7.35
247050_at	At14a protein-like	---	AT5G66660	1.01	0.01	0.06	0.956966	0.978983	-7.35
245546_at	cellulose synthase like protein	ATCSLB05	AT4G15290	1.01	0.01	0.06	0.956951	0.978983	-7.35
251255_at	putative protein early nodule-specific p	---	AT3G62280	-1.00	-0.01	-0.06	0.957045	0.97902	-7.35
245313_at	UFD1 like protein ; supported by full-le	---	AT4G15420	1.01	0.01	0.06	0.957127	0.979052	-7.35
265749_at	putative retroelement pol polyprotein	---	---	-1.00	-0.01	-0.06	0.957191	0.979052	-7.35
252620_at	hypothetical protein	---	---	1.00	0.00	0.06	0.957205	0.979052	-7.35
249004_at	unknown protein	---	AT5G44570	1.01	0.01	0.06	0.957325	0.979131	-7.35
257431_at	unknown protein	---	AT2G36360	-1.00	-0.01	-0.06	0.957381	0.979144	-7.35
260923_at	glycine-rich RNA-binding protein grp1	---	AT1G21570	-1.00	-0.01	-0.06	0.957447	0.979168	-7.35
245102_at	putative non-LTR retroelement reverse	---	---	-1.01	-0.01	-0.06	0.957497	0.979175	-7.35
255184_at	putative athila transposon protein	---	---	1.00	0.01	0.06	0.957616	0.979253	-7.35
263710_at	unknown protein ;supported by full-ler	---	AT1G09330	1.00	0.01	0.06	0.957662	0.979256	-7.35
247604_at	putative phytochelatin synthetase - lik	COBL5	AT5G60950	1.02	0.03	0.05	0.958075	0.979634	-7.35
259330_at	hypothetical protein gene model predic	---	AT3G16270	1.01	0.01	0.05	0.958226	0.97965	-7.35
257303_at	hypothetical protein predicted by gens	---	AT3G30230	-1.00	-0.01	-0.05	0.958305	0.97965	-7.35
245210_at	putative protein similarity to UVB-resis	---	AT5G12350	1.00	0.01	0.05	0.958167	0.97965	-7.35
257243_at	pectate lyase, putative similar to GB:A	---	AT3G24230	-1.00	0.00	-0.05	0.958183	0.97965	-7.35
258442_at	hypothetical protein predicted by gene	---	AT3G01015	-1.00	-0.01	-0.05	0.958273	0.97965	-7.35
248205_at	cotton fiber expressed protein 1-like pr	---	AT5G54300	1.01	0.02	0.05	0.958462	0.979723	-7.35
266754_at	hypothetical protein	---	AT2G46980	1.01	0.01	0.05	0.958455	0.979723	-7.35
260863_at	hypothetical protein predicted by gene	---	---	-1.01	-0.01	-0.05	0.958608	0.979804	-7.35
259557_at	hypothetical protein	WAK4	AT1G21210	-1.00	-0.01	-0.05	0.958628	0.979804	-7.35
266379_at	1,4-beta-xylan endohydrolase	---	AT2G14690	-1.00	-0.01	-0.05	0.958821	0.97987	-7.35
258473_s_	putative stearoyl-acyl carrier protein de	---	AT3G02610 /	1.01	0.01	0.05	0.958741	0.97987	-7.35
258103_at	hypothetical protein contains Pfam pro	IPT7	AT3G23630	1.01	0.01	0.05	0.95882	0.97987	-7.35
258204_at	hypothetical protein predicted by gene	AtGRF5	AT3G13960	-1.01	-0.01	-0.05	0.958876	0.979883	-7.35
265437_at	hypothetical protein predicted by gens	MCM10	AT2G20980	-1.00	-0.01	-0.05	0.958973	0.979938	-7.35
265879_at	hypothetical protein predicted by gens	---	AT2G42450	1.00	0.01	0.05	0.959066	0.979989	-7.35
258837_at	putative 60S ribosomal protein L13A s	---	AT3G07110	1.01	0.01	0.05	0.959222	0.980032	-7.35
263309_at	putative replication protein A1	---	---	1.01	0.01	0.05	0.959237	0.980032	-7.35
265436_at	putative retroelement pol polyprotein	---	---	1.00	0.00	0.05	0.959185	0.980032	-7.35
255493_at	putative glutamate-/aspartate-binding	---	AT4G02690	1.00	0.01	0.05	0.959395	0.980149	-7.35
245032_at	En/Spm-like transposon protein relate	---	---	-1.01	-0.01	-0.05	0.959652	0.980368	-7.35

248990_at	disease resistance protein-like	---	AT5G45210	1.00	0.01	0.05	0.959819	0.980495	-7.35
248437_at	putative protein similar to unknown pro	EMF2	AT5G51230	1.01	0.01	0.05	0.960308	0.980862	-7.35
264876_at	hypothetical protein	---	AT2G17410	1.00	0.01	0.05	0.96025	0.980862	-7.35
267321_at	hypothetical protein predicted by gene	---	AT2G19320	1.00	0.01	0.05	0.960273	0.980862	-7.35
254367_at	hypothetical protein	---	AT4G21700	1.00	0.01	0.05	0.960356	0.980868	-7.35
264364_at	unknown protein Similar to gb|U85207	---	AT1G03330	-1.00	-0.01	-0.05	0.960608	0.980949	-7.35
264819_at	hypothetical protein similar to membra	---	AT1G03510	1.01	0.01	0.05	0.960578	0.980949	-7.35
248117_at	FH protein interacting protein FIP2 (gb	FIP2	AT5G55000	1.01	0.01	0.05	0.960567	0.980949	-7.35
263081_at	putative homeodomain transcription fa	BLH5	AT2G27220	1.00	0.00	0.05	0.960549	0.980949	-7.35
249596_s_	glucuronosyl transferase-like protein g	---	AT5G37950 /	-1.01	-0.01	-0.05	0.960651	0.980949	-7.35
245036_at	putative SF16 protein {Helianthus annu	Iqd4	AT2G26410	-1.00	-0.01	-0.05	0.960756	0.980969	-7.35
247093_at	zinc finger protein SHI-like ; supported	SHI	AT5G66350	-1.01	-0.01	-0.05	0.960749	0.980969	-7.35
259503_at	unknown protein ; supported by cDNA:	---	AT1G15870	-1.01	-0.01	-0.05	0.96081	0.98098	-7.35
251427_at	beta-glucosidase-like protein several b	BGLU16	AT3G60130	-1.01	-0.01	-0.05	0.961226	0.981343	-7.35
260615_at	mitochondrial NAD-dependent malate	---	AT1G53240	-1.01	-0.01	-0.05	0.961252	0.981343	-7.35
260584_at	putative beta-1,3-glucanase, C termin	---	AT2G43660	-1.00	-0.01	-0.05	0.961298	0.981346	-7.35
252107_at	sugar transporter-like protein sugar tra	TMT3	AT3G51490	-1.01	-0.01	-0.05	0.961683	0.981402	-7.35
245484_at	enoyl-CoA hydratase like protein	ECHIA	AT4G16210	-1.00	-0.01	-0.05	0.961645	0.981402	-7.35
259256_at	putative coated vesicle membrane pro	---	AT3G07680	1.00	0.01	0.05	0.961777	0.981402	-7.35
250514_at	GDP dissociation inhibitor GDP disso	---	AT5G09550	1.00	0.01	0.05	0.961485	0.981402	-7.35
263749_at	putative phosphatidylinositol/phosphat	---	AT2G21520	1.00	0.01	0.05	0.961801	0.981402	-7.35
256346_s_	unknown protein	---	AT2G15040	-1.00	0.00	-0.05	0.961532	0.981402	-7.35
247121_at	putative protein contains similarity to ri	---	AT5G66010	-1.00	-0.01	-0.05	0.961473	0.981402	-7.35
263140_at	hypothetical protein predicted by gene	---	AT1G65120	1.00	0.00	0.05	0.961717	0.981402	-7.35
261028_at	hypothetical protein predicted by gene	---	AT1G26620	1.00	0.01	0.05	0.961653	0.981402	-7.35
258767_at	putative (1-4)-beta-mannan endohydro	---	AT3G10890	1.00	0.01	0.05	0.961866	0.981402	-7.35
263147_at	polyubiquitin, putative similar to polyu	---	AT1G53980	-1.00	0.00	-0.05	0.961582	0.981402	-7.35
256026_at	auxin response factor 1, putative simil	---	AT1G34170	-1.00	-0.01	-0.05	0.961869	0.981402	-7.35
257716_at	hypothetical protein predicted by gene	---	AT3G18300	-1.00	-0.01	-0.05	0.96197	0.981461	-7.35
249919_at	putative protein predicted protein, Ara	---	AT5G19250	1.00	0.01	0.05	0.962039	0.981488	-7.35
264059_at	Expressed protein ; supported by full-l	INH3	AT2G31305	1.00	0.01	0.05	0.962155	0.981518	-7.35
263445_at	unknown protein	---	AT2G31590	-1.00	0.00	-0.05	0.962119	0.981518	-7.35
265756_at	putative bZIP transcription factor simila	---	AT2G13150	1.00	0.00	0.05	0.962217	0.981538	-7.35
254707_at	putative protein inositol polyphosphate	AT5PTASE2	AT4G18010	1.01	0.01	0.05	0.962294	0.981573	-7.35
255241_at	putative protein hypothetical protein T	---	---	1.00	0.00	0.05	0.962386	0.981623	-7.35

255641_at	contains region of similarity to beta tra	---	AT4G00800	1.00	0.01	0.05	0.962439	0.981632	-7.35
266545_at	hypothetical protein predicted by gene	---	AT2G35290	-1.01	-0.01	-0.05	0.962569	0.981634	-7.35
256477_at	unknown protein	---	---	-1.00	-0.01	-0.05	0.962499	0.981634	-7.35
265980_at	hypothetical protein predicted by gene	---	---	1.00	0.01	0.05	0.962535	0.981634	-7.35
252657_at	hypothetical protein	---	AT3G44780	1.00	0.00	0.05	0.962795	0.98182	-7.35
250219_at	putative protein similar to unknown pro	MPL1	AT5G14180	-1.01	-0.01	-0.05	0.962839	0.981821	-7.35
248439_at	putative protein similar to unknown pro	---	AT5G51250	-1.00	-0.01	-0.05	0.962882	0.981821	-7.35
258732_at	putative alkaline/neutral invertase simi	---	AT3G05820	1.00	0.01	0.05	0.96306	0.981959	-7.35
247535_at	transcriptional activator - like protein [	---	AT5G61620	-1.01	-0.01	-0.05	0.963152	0.981964	-7.35
266706_at	hypothetical protein predicted by gens	---	AT2G03320	1.00	0.00	0.05	0.963126	0.981964	-7.35
246356_x_	hypothetical protein, 5' partial	---	---	-1.00	0.00	-0.05	0.963286	0.982058	-7.35
262098_at	transcription factor, putative similar to	NF-YC2	AT1G56170	1.01	0.01	0.05	0.963378	0.982108	-7.35
248019_at	putative protein similar to unknown pro	---	AT5G56480	1.00	0.01	0.05	0.963489	0.982123	-7.35
248359_at	unknown protein	---	AT5G52410	1.00	0.01	0.05	0.963598	0.982123	-7.35
259946_at	putative TINY similar to TINY GB:CAA	---	AT1G71450	1.00	0.00	0.05	0.963609	0.982123	-7.35
245576_at	hypothetical protein	TCX2	AT4G14770	1.01	0.01	0.05	0.963508	0.982123	-7.35
263492_at	putative seed maturation protein	---	AT2G42560	-1.00	-0.01	-0.05	0.963568	0.982123	-7.35
258254_at	unknown protein contains Pfam profile	---	AT3G26780 /	1.01	0.01	0.05	0.963684	0.982156	-7.35
253862_at	NOZZLE/SPOROCYTELESS ; suppo	SPL	AT4G27330	1.00	0.01	0.05	0.963728	0.982157	-7.35
258205_at	unknown protein	---	AT3G13965	-1.00	-0.01	-0.05	0.963788	0.982174	-7.35
252019_at	late embryogenesis abundant protein	---	AT3G53040	-1.00	0.00	-0.05	0.963833	0.982176	-7.35
259086_at	hypothetical protein predicted by gene	---	AT3G04990	1.00	0.00	0.05	0.96394	0.982241	-7.35
262795_at	hypothetical protein predicted by gens	---	AT1G13130	-1.01	-0.01	-0.05	0.964083	0.982271	-7.35
256427_at	hypothetical protein predicted by gens	LBD21	AT3G11090	1.01	0.01	0.05	0.964099	0.982271	-7.35
252460_at	putative protein predicted protein, Ara	---	---	-1.00	0.00	-0.05	0.964092	0.982271	-7.35
258346_at	hypothetical protein predicted by gene	---	AT3G22690	1.00	0.01	0.05	0.964243	0.982374	-7.35
248610_at	SRP54 (signal recognition particle 54 k	---	AT5G49500	-1.00	0.00	-0.05	0.964411	0.982502	-7.35
245510_at	hypothetical protein	---	AT4G15740	1.01	0.01	0.05	0.964546	0.982552	-7.35
251046_at	kinesin -like protein kinesin, Xenopus	---	AT5G02370	1.00	0.00	0.05	0.964546	0.982552	-7.35
246598_at	dolichyl-phosphate-mannose--glycolip	---	AT5G14850	1.00	0.01	0.05	0.964657	0.982621	-7.35
246787_s_	cdc20-like protein putative cdc20 prot	---	AT5G27570 /	1.00	0.00	0.05	0.964857	0.98278	-7.35
262125_at	heat shock protein, putative similar to	EDA1	AT1G59680	-1.00	-0.01	-0.05	0.964994	0.982876	-7.35
245963_at	putative protein HPt phosphotransmitt	---	AT5G19710	1.00	0.00	0.05	0.96504	0.982879	-7.35
266676_s_	hypothetical protein predicted by grail	---	AT2G29605 /	1.00	0.00	0.05	0.965128	0.982925	-7.35
256353_at	unknown protein ; supported by full-ler	---	AT1G55000	1.00	0.01	0.05	0.965335	0.983048	-7.35

251589_at	putative protein SINA2p zinc finger pr	SINAT2	AT3G58040	-1.00	-0.01	-0.05	0.965315	0.983048	-7.35
264214_s_	MADS-box transcription factor, putativ	AGL38	AT1G65300 /	-1.00	0.00	-0.04	0.965527	0.983169	-7.35
263121_at	receptor protein kinase, putative simil	---	AT1G78530	-1.00	-0.01	-0.04	0.96554	0.983169	-7.35
259604_at	20S proteasome beta subunit (PBG1)	PBG1	AT1G56450	1.00	0.00	0.04	0.965991	0.983528	-7.35
248524_s_	putative protein contains similarity to s	---	AT5G50570 /	1.01	0.02	0.04	0.966022	0.983528	-7.35
257434_at	hypothetical protein predicted by gens	---	AT2G21740	-1.00	0.00	-0.04	0.965994	0.983528	-7.35
254365_at	putative protein hypothetical protein D	---	AT4G22030	1.00	0.00	0.04	0.966123	0.983587	-7.35
256870_at	cytochrome P450, putative contains P	CYP71B34	AT3G26300	1.01	0.01	0.04	0.966176	0.983597	-7.35
245125_at	putative histidine kinase identical to GI	CKI1	AT2G47430	1.00	0.01	0.04	0.966282	0.983661	-7.35
249200_at	5-3 exoribonuclease 2 ; supported by c	XRN2	AT5G42540	-1.00	-0.01	-0.04	0.966342	0.983678	-7.35
266670_at	putative flavonol 3-O-glucosyltransfera	UGT71C2	AT2G29740	1.00	0.01	0.04	0.966665	0.983963	-7.35
252715_x_	putative protein predicted protein, Ara	---	AT3G43900	-1.00	-0.01	-0.04	0.966726	0.983981	-7.35
253070_at	putative protein symbiotic ammonium	---	AT4G37850	-1.00	-0.01	-0.04	0.966773	0.983986	-7.35
262005_at	ABC transporter protein, putative simi	ATGCN3	AT1G64550	1.00	0.01	0.04	0.967076	0.984185	-7.35
255246_at	putative protein hypothetical protein F	---	---	-1.00	-0.01	-0.04	0.967228	0.984185	-7.35
260640_at	viral resistance protein, putative simila	---	AT1G53350	-1.01	-0.01	-0.04	0.967224	0.984185	-7.35
253884_at	heat shock protein 21	HSP21	AT4G27670	-1.00	-0.01	-0.04	0.967162	0.984185	-7.35
260038_at	Expressed protein ; supported by full-l	---	AT1G68875	1.00	0.00	0.04	0.967133	0.984185	-7.35
246278_at	tubulin-like protein	---	AT4G37190	1.01	0.01	0.04	0.967065	0.984185	-7.35
267270_at	hypothetical protein predicted by gens	---	AT2G02550	1.00	0.01	0.04	0.967373	0.984288	-7.35
265522_at	putative TPR repeat nuclear phosphop	ELF8	AT2G06210	1.00	0.01	0.04	0.967443	0.984316	-7.35
253564_at	protein kinase - like protein protein kir	---	AT4G31170	-1.00	-0.01	-0.04	0.967539	0.984351	-7.35
253751_at	hypothetical protein ;supported by full-	---	AT4G29070	-1.01	-0.01	-0.04	0.967563	0.984351	-7.35
254368_at	DNA-directed RNA polymerase (EC 2.	NRPB2	AT4G21710	1.00	0.00	0.04	0.967712	0.984414	-7.35
266744_at	putative nucleoside triphosphatase ; s	---	AT2G02970	-1.00	0.00	-0.04	0.967688	0.984414	-7.35
245367_at	Expressed protein ; supported by full-l	NRPB9B	AT4G16265	1.00	0.01	0.04	0.967898	0.984425	-7.35
265460_at	putative caltractin ;supported by full-le	---	AT2G46600	1.01	0.01	0.04	0.967939	0.984425	-7.35
246945_s_	putative membrane protein hypothetic	---	AT5G25040 /	-1.00	-0.01	-0.04	0.967883	0.984425	-7.35
260306_at	hypothetical protein predicted by gens	EDA24	AT1G70540	1.00	0.01	0.04	0.967766	0.984425	-7.35
260202_at	hypothetical protein predicted by gens	---	---	1.00	0.00	0.04	0.967829	0.984425	-7.35
266197_at	hypothetical protein predicted by gens	---	AT2G39120	-1.00	0.00	-0.04	0.968329	0.984778	-7.35
263092_at	hypothetical protein predicted by gens	---	AT2G16210	-1.00	0.00	-0.04	0.968652	0.984975	-7.35
264216_at	hypothetical protein similar to hypothet	---	AT1G60180	-1.00	0.00	-0.04	0.968613	0.984975	-7.35
251633_at	putative protein metalloendopeptidase	---	AT3G57460	1.01	0.01	0.04	0.968632	0.984975	-7.35
259264_at	putative aldose 1-epimerase shows sir	---	AT3G01260	-1.00	-0.01	-0.04	0.968745	0.985025	-7.35

264398_at	unknown protein similar to hypothetica	---	AT1G61730	-1.00	0.00	-0.04	0.968802	0.98504	-7.35
258697_at	putative minichromosome maintenanc	MCM8	AT3G09660	-1.00	-0.01	-0.04	0.968915	0.985095	-7.35
258124_at	Expressed protein ; supported by cDN	---	AT3G18215	-1.01	-0.01	-0.04	0.968943	0.985095	-7.35
249295_at	putative protein contains similarity to u	---	AT5G41280	-1.00	0.00	-0.04	0.969169	0.985176	-7.35
254683_at	hypothetical protein ;supported by full-	---	AT4G13800	-1.00	0.00	-0.04	0.969115	0.985176	-7.35
259299_at	unknown protein	---	AT3G05080	1.00	0.01	0.04	0.969238	0.985176	-7.35
259563_s_	hypothetical protein	---	AT1G20590 /	-1.00	0.00	-0.04	0.969135	0.985176	-7.35
252307_at	putative protein SAE1-S9-protein, Bra	---	---	-1.00	0.00	-0.04	0.969205	0.985176	-7.35
253867_at	putative protein tRNA nucleotidyltrans	---	AT4G27490	-1.01	-0.01	-0.04	0.969398	0.985201	-7.35
262441_at	hypothetical protein similar to hypothet	OSB1	AT1G47720	-1.00	-0.01	-0.04	0.969436	0.985201	-7.35
262004_at	calcineurin B-like protein similar to CA	CBL8	AT1G64480	1.00	0.01	0.04	0.969354	0.985201	-7.35
245634_at	MtN21 nodulin protein, putative simila	---	AT1G25270	-1.00	-0.01	-0.04	0.969413	0.985201	-7.35
264099_at	replicase, putative similar to replicase	---	AT1G79050	-1.00	0.00	-0.04	0.969534	0.985213	-7.35
245377_at	hypothetical protein	---	AT4G17700	1.00	0.00	0.04	0.969525	0.985213	-7.35
248808_at	putative protein contains similarity to p	---	AT5G47510	1.00	0.00	0.04	0.969686	0.985324	-7.35
265483_at	hypothetical protein ; supported by cDI	SQN	AT2G15790	-1.00	-0.01	-0.04	0.969976	0.985541	-7.35
259363_at	methionine aminopeptidase I (MAP1),	MAP1C	AT1G13270	1.00	0.00	0.04	0.970073	0.985541	-7.35
258491_at	unknown protein ;supported by full-ler	---	AT3G02700	1.00	0.01	0.04	0.969987	0.985541	-7.35
245920_at	putative protein	---	---	-1.00	0.00	-0.04	0.970071	0.985541	-7.35
260443_at	Expressed protein ; supported by full-l	---	AT1G68185	-1.00	0.00	-0.04	0.970153	0.985579	-7.35
249024_at	putative protein strong similarity to unk	---	AT5G44860	-1.00	0.00	-0.04	0.970211	0.985593	-7.35
258882_at	unknown protein ; supported by full-le	---	AT3G06330	-1.00	0.00	-0.04	0.970535	0.985791	-7.35
248215_at	putative protein contains similarity to R	---	AT5G53680	-1.00	-0.01	-0.04	0.970513	0.985791	-7.35
257186_at	hypothetical protein predicted by gene	---	AT3G13130	1.00	0.01	0.04	0.970518	0.985791	-7.35
259811_at	hypothetical protein predicted by gene	---	AT1G49830	1.00	0.00	0.04	0.970587	0.9858	-7.35
257454_at	hypothetical protein predicted by gene	---	AT1G65170	-1.00	-0.01	-0.04	0.970692	0.985862	-7.35
261971_at	type 2 peroxiredoxin, putative similar t	---	AT1G65990	-1.00	-0.01	-0.04	0.970872	0.985907	-7.35
266248_at	hypothetical protein predicted by gens	---	AT2G27650	-1.00	0.00	-0.04	0.970909	0.985907	-7.35
262973_at	histone H3, putative similar to HISTOI	---	AT1G75600	-1.00	0.00	-0.04	0.970853	0.985907	-7.35
259703_at	putative endo-1,3-beta-glucanase sim	---	AT1G77790	-1.00	0.00	-0.04	0.970807	0.985907	-7.35
247322_at	unknown protein	---	AT5G64090	-1.00	0.00	-0.04	0.97109	0.986047	-7.35
265108_s_	similar to flavin-binding monooxygena	---	AT1G62620 /	-1.00	-0.01	-0.04	0.971231	0.986147	-7.35
248847_at	disease resistance protein-like	---	AT5G46510	-1.00	0.00	-0.04	0.971343	0.986216	-7.35
257082_at	hypothetical protein	COBL10	AT3G20580	1.00	0.00	0.04	0.971432	0.986253	-7.35
256594_at	hypothetical protein similar to putative	---	AT3G28520	1.00	0.00	0.04	0.971466	0.986253	-7.35

253512_at	putative protein protein phosphatase 2	WIN2	AT4G31750	1.00	0.00	0.04	0.971603	0.986343	-7.35
266001_at	hypothetical protein predicted by gene	HHP3	AT2G24150	1.00	0.00	0.04	0.971641	0.986343	-7.35
251507_at	putative protein CND41, chloroplast n	---	AT3G59080	-1.01	-0.02	-0.04	0.971794	0.986455	-7.35
256131_at	bZIP transcription factor, putative simi	AtbZIP58	AT1G13600	1.00	0.01	0.04	0.971895	0.986465	-7.35
247084_at	NAM (no apical meristem)-like protein	NAC105	AT5G66300	-1.00	0.00	-0.04	0.971934	0.986465	-7.35
263651_at	unknown protein Similar to Nicotiana le	---	AT1G04340	-1.00	-0.01	-0.04	0.971868	0.986465	-7.35
265814_at	hypothetical protein similar to hypothe	---	AT2G17930	1.00	0.00	0.04	0.972113	0.986603	-7.35
254550_at	Fe(II) transport protein ;supported by f	IRT1	AT4G19690	1.00	0.00	0.04	0.972368	0.986818	-7.35
266561_at	unknown protein	---	AT2G23960	-1.00	0.00	-0.04	0.972519	0.986839	-7.35
267119_at	putative cellulose synthase	ATCSLB01	AT2G32610	-1.00	0.00	-0.04	0.972501	0.986839	-7.35
252288_at	hypothetical protein	---	AT3G49080	-1.00	-0.01	-0.04	0.972451	0.986839	-7.35
254945_at	putative RING finger protein ring finge	---	AT4G10940	1.00	0.00	0.04	0.972593	0.98687	-7.35
256893_x_	unknown protein	---	---	-1.00	0.00	-0.04	0.972923	0.987161	-7.35
254439_s_	carbonic anhydrase -like protein carbo	ACA6	AT4G20990 /	-1.00	0.00	-0.04	0.972967	0.987162	-7.35
245391_at	symbiosis-related like protein ;supporte	ATG8F	AT4G16520	1.00	0.01	0.03	0.973161	0.987298	-7.35
249646_at	SEN1-like protein SEN1 - Saccharom	---	AT5G37030	-1.00	0.00	-0.03	0.973187	0.987298	-7.35
262145_at	unknown protein contains similarity to	---	AT1G52730	1.00	0.00	0.03	0.973249	0.987317	-7.35
252538_at	putative transporter protein peptide tra	---	AT3G45720	-1.00	0.00	-0.03	0.973517	0.987545	-7.35
262924_s_	vacuolar ATP synthase, putative simil	AVA-P4	AT1G19910 /	-1.00	0.00	-0.03	0.973583	0.987567	-7.35
253217_at	actin depolymerizing factor - like prote	ADF9	AT4G34970	1.01	0.01	0.03	0.973659	0.987571	-7.35
248750_at	putative protein similar to unknown pro	---	AT5G47530	-1.00	-0.01	-0.03	0.973673	0.987571	-7.35
266669_at	putative flavonol 3-O-glucosyltransfera	UGT71C1	AT2G29750	1.00	0.00	0.03	0.973717	0.987572	-7.35
255107_at	hypothetical protein	---	AT4G08730	1.00	0.00	0.03	0.973823	0.987591	-7.35
261329_at	hypothetical protein predicted by gene	---	AT1G44890	-1.00	0.00	-0.03	0.973828	0.987591	-7.35
261916_at	jasmonic acid, putative similar to jasm	anac028	AT1G65910	1.00	0.00	0.03	0.973866	0.987591	-7.35
258384_at	hypothetical protein predicted by gens	---	AT3G15490	-1.00	0.00	-0.03	0.973918	0.987597	-7.35
265956_at	hypothetical protein predicted by gens	---	AT2G37290	-1.00	0.00	-0.03	0.973959	0.987597	-7.35
266550_s_	Expressed protein ; supported by cDN	---	AT2G35070 /	-1.01	-0.01	-0.03	0.974077	0.98763	-7.35
252237_at	putative protein lateral suppressor pro	---	AT3G49950	-1.00	0.00	-0.03	0.974067	0.98763	-7.35
260786_s_	unknown protein similar to Cryptospori	MEE5	AT1G06220 /	1.00	0.00	0.03	0.97416	0.987656	-7.35
250403_at	argininosuccinate lyase (AtArgH) ; sup	---	AT5G10920	-1.01	-0.01	-0.03	0.97419	0.987656	-7.35
256642_at	hypothetical protein similar to hypothet	---	AT3G32280	-1.00	0.00	-0.03	0.974319	0.987743	-7.35
249589_at	pyridoxal kinase -like protein pyridoxa	SOS4	AT5G37850	1.00	0.00	0.03	0.974443	0.987825	-7.35
266969_at	similar to gibberellin-regulated proteins	---	AT2G39540	-1.00	0.00	-0.03	0.974525	0.987864	-7.35
264320_at	unknown protein	---	AT1G04090	1.00	0.00	0.03	0.97465	0.987903	-7.35

253846_at	putative protein MSP1, Saccharomyce	---	AT4G28000	-1.00	0.00	-0.03	0.974634	0.987903	-7.35
249631_at	sen1-like protein SEN1 - Saccharomy	---	AT5G37160	1.00	0.00	0.03	0.974759	0.98797	-7.35
266895_at	hypothetical protein predicted by gens	---	AT2G26040	1.00	0.00	0.03	0.97495	0.98806	-7.35
258816_at	putative T-complex protein 1, theta su	---	AT3G03960	-1.00	-0.01	-0.03	0.975006	0.98806	-7.35
249950_at	protein kinase - like protein Pto kinase	---	AT5G18910	1.00	0.00	0.03	0.975065	0.98806	-7.35
261840_at	hypothetical protein contains similarity	AtTLP8	AT1G16070	-1.00	0.00	-0.03	0.975036	0.98806	-7.35
251359_at	putative protein several hypothetical pr	---	AT3G61170	-1.00	0.00	-0.03	0.974892	0.98806	-7.35
251423_at	regulatory protein - like regulatory pro	CYCP3;2	AT3G60550	1.00	0.00	0.03	0.975264	0.98816	-7.35
263717_at	malate oxidoreductase (malic enzyme)	---	AT2G13560	-1.00	0.00	-0.03	0.975294	0.98816	-7.35
252144_at	ribosomal protein L8 homolog riboson	---	AT3G51190	1.00	0.00	0.03	0.975223	0.98816	-7.35
246297_at	putative protein hypothetical protein F	---	AT3G51760	-1.00	-0.01	-0.03	0.975399	0.988223	-7.35
246435_at	hypothetical protein ; supported by cD	---	AT5G17460	1.00	0.00	0.03	0.976166	0.988227	-7.35
262985_s_	60s ribosomal protein l27a. similar to 6	RPL27AB	AT1G23290 /	1.00	0.01	0.03	0.975888	0.988227	-7.35
253713_at	putative protein several hypothetical pr	---	AT4G29370	-1.00	0.00	-0.03	0.975987	0.988227	-7.35
250489_s_	putative protein predicted proteins, Ar	---	AT5G09710 /	-1.00	0.00	-0.03	0.97579	0.988227	-7.35
254768_at	hypothetical protein	---	AT4G13320	-1.00	0.00	-0.03	0.976043	0.988227	-7.35
265566_at	hypothetical protein predicted by gene	---	AT2G05600	1.00	0.00	0.03	0.976183	0.988227	-7.35
258960_at	hypothetical protein similar to myb-rel	---	AT3G10590	-1.00	0.00	-0.03	0.975629	0.988227	-7.35
249620_at	putative protein predicted proteins, Ar	---	AT5G37520	-1.00	0.00	-0.03	0.9761	0.988227	-7.35
263764_at	putative vacuolar proton-ATPase subu	VHA-A2	AT2G21410	-1.00	0.00	-0.03	0.976142	0.988227	-7.35
263008_at	unknown protein	RPP27	AT1G54470	1.00	0.00	0.03	0.975509	0.988227	-7.35
247582_at	putative protein various predicted prot	---	AT5G60760	1.00	0.00	0.03	0.975615	0.988227	-7.35
255408_at	hypothetical protein similar to A. thalia	---	AT4G03490	1.00	0.01	0.03	0.975931	0.988227	-7.35
253540_at	putative protein various predicted prot	---	AT4G31615	1.00	0.00	0.03	0.975976	0.988227	-7.35
245267_at	major latex protein like ; supported by	---	AT4G14060	-1.00	0.00	-0.03	0.975995	0.988227	-7.35
262720_s_	hypothetical protein similar to hypothet	---	AT1G43600 /	-1.00	0.00	-0.03	0.975642	0.988227	-7.35
245922_at	putative protein predicted proteins, Ar	---	AT5G28810	-1.00	0.00	-0.03	0.976011	0.988227	-7.35
255063_at	putative transposon protein similar to r	---	---	1.00	0.00	0.03	0.975889	0.988227	-7.35
258142_at	unknown protein	---	AT3G18120	1.00	0.00	0.03	0.975471	0.988227	-7.35
256465_at	hypothetical protein predicted by gens	---	AT1G32570	1.00	0.01	0.03	0.976239	0.98824	-7.35
262306_s_	asparaginyl-tRNA synthetase(SYNC1	SYNC3	AT1G70980 /	1.00	0.00	0.03	0.976409	0.988324	-7.35
246353_s_	hypothetical protein	---	---	-1.00	0.00	-0.03	0.976397	0.988324	-7.35
259746_at	hypothetical protein predicted by gens	---	AT1G71060	-1.00	0.00	-0.03	0.977388	0.988616	-7.35
257352_at	putative RING3 protein	IMB1	AT2G34900	-1.00	0.00	-0.03	0.977453	0.988616	-7.35
251578_at	putative protein contains alternative d	---	AT3G58180	1.00	0.00	0.03	0.977359	0.988616	-7.35

249682_at	putative protein similar to unknown pro	---	AT5G36080	-1.00	0.00	-0.03	0.976932	0.988616	-7.35
250706_at	deoxyhypusine synthase ;supported b	DHS	AT5G05920	-1.00	0.00	-0.03	0.977169	0.988616	-7.35
254404_at	hypothetical protein	B70	AT4G21340	1.00	0.00	0.03	0.97755	0.988616	-7.35
254281_at	predicted protein ileal sodium-depend	---	AT4G22840	1.01	0.01	0.03	0.977645	0.988616	-7.35
245766_at	En/Spm-like transposon protein, putat	---	---	-1.00	0.00	-0.03	0.977304	0.988616	-7.35
256032_at	polyprotein, putative similar to polypro	---	---	1.00	0.00	0.03	0.977554	0.988616	-7.35
246766_at	hypothetical protein	---	AT5G27340	1.00	0.01	0.03	0.97763	0.988616	-7.35
266354_at	putative homeodomain transcription fa	PFS2	AT2G01500	1.00	0.00	0.03	0.977717	0.988616	-7.35
257567_at	hypothetical protein predicted by gens	---	AT3G23930	1.00	0.00	0.03	0.976994	0.988616	-7.35
249504_at	disease resistance protein - like disea	---	AT5G38850	1.00	0.01	0.03	0.977741	0.988616	-7.35
246229_at	pectinesterase like protein	sks15	AT4G37160	1.00	0.00	0.03	0.976755	0.988616	-7.35
256953_at	flavonol 3-O-Glucosyltransferase, puta	---	AT3G29630	-1.00	0.00	-0.03	0.977526	0.988616	-7.35
258942_at	unknown protein predicted by genscar	---	AT3G09960	-1.00	0.00	-0.03	0.977765	0.988616	-7.35
261325_at	hypothetical protein predicted by gene	---	AT1G44780	-1.00	0.00	-0.03	0.977124	0.988616	-7.35
262836_at	hypothetical protein predicted by gene	---	AT1G14680	1.00	0.00	0.03	0.977125	0.988616	-7.35
257416_at	unknown protein	---	AT2G17750	1.00	0.00	0.03	0.977756	0.988616	-7.35
266190_at	unknown protein	---	AT2G38840	1.00	0.00	0.03	0.976835	0.988616	-7.35
245128_at	unknown protein similar to gi2344899|	---	AT2G45380	1.00	0.00	0.03	0.976972	0.988616	-7.35
248244_at	heat shock transcription factor HSF30-	---	AT5G53640	-1.00	0.00	-0.03	0.977315	0.988616	-7.35
260736_at	hypothetical protein predicted by gene	---	AT1G17630	-1.00	0.00	-0.03	0.977263	0.988616	-7.35
251384_at	putative protein	---	AT3G60760	1.00	0.00	0.03	0.977051	0.988616	-7.35
257471_at	G-box binding factor, putative similar t	ATBZIP4	AT1G59530	1.00	0.00	0.03	0.977781	0.988616	-7.35
246574_at	copper amine oxidase, putative simila	---	AT1G31670	-1.00	-0.01	-0.03	0.978291	0.988937	-7.35
248106_at	putative protein similar to unknown pro	---	AT5G55100	1.00	0.00	0.03	0.978315	0.988937	-7.35
253651_at	putative protein nucleoid DNA-binding	---	AT4G30030	1.00	0.00	0.03	0.978238	0.988937	-7.35
265364_at	putative retroelement pol polyprotein	---	---	-1.00	0.00	-0.03	0.978181	0.988937	-7.35
250610_at	glycine-rich protein PUTG1 ;supported	GRP19	AT5G07550	-1.00	-0.01	-0.03	0.9783	0.988937	-7.35
250845_at	rna binding protein - like rna binding p	---	AT5G04600	-1.00	0.00	-0.03	0.978505	0.988997	-7.35
252030_at	hypothetical protein predicted proteins	---	AT3G52690	1.00	0.00	0.03	0.978468	0.988997	-7.35
254672_at	hypothetical protein	---	---	1.00	0.00	0.03	0.978441	0.988997	-7.35
259954_at	cytochrome P450, putative similar to C	CYP721A1	AT1G75130	-1.00	-0.01	-0.03	0.978632	0.989082	-7.35
263813_s_	putative TNP1-like transposon protein	---	---	-1.00	0.00	-0.03	0.978792	0.9892	-7.35
267255_at	putative Ca2+-ATPase	---	AT2G22950	1.00	0.00	0.03	0.979008	0.989287	-7.35
248214_at	putative protein similar to unknown pro	---	AT5G53670	1.00	0.00	0.03	0.978986	0.989287	-7.35
259127_at	putative translation initiation factor EIF	---	AT3G02270	-1.00	0.00	-0.03	0.978931	0.989287	-7.35

267234_x_	putative protein kinase contains a prot	---	AT2G43930	-1.00	0.00	-0.03	0.979102	0.989338	-7.35
266793_at	homeotic protein AGL30	AGL30	AT2G03060	1.00	0.01	0.03	0.979177	0.98937	-7.35
254491_at	putative protein hypothetical protein Ar	---	AT4G20300	-1.00	0.00	-0.03	0.979276	0.989426	-7.35
246685_at	putative protein nucleoid DNA-binding	---	AT5G33350	-1.00	-0.01	-0.03	0.979385	0.989492	-7.35
256479_at	unknown protein	---	AT1G33400	-1.00	0.00	-0.03	0.979506	0.989501	-7.35
255058_s_	putative protein various hypothetical p	---	---	-1.00	0.00	-0.03	0.979567	0.989501	-7.35
246474_at	putative protein predicted protein, Ara	---	AT5G17150	1.00	0.00	0.03	0.979555	0.989501	-7.35
253526_at	putative zinc finger protein hypothetica	---	AT4G31420	-1.00	0.00	-0.03	0.979478	0.989501	-7.35
262588_at	unknown protein Similar to gb|AJ0050	---	AT1G15130	1.00	0.00	0.03	0.979617	0.989507	-7.35
259761_at	putative acyl-CoA synthetase similar to	LACS9	AT1G77590	1.00	0.00	0.03	0.980007	0.989522	-7.35
264670_s_	unknown protein Similar to elongation	---	AT1G09640 /	1.00	0.00	0.03	0.979965	0.989522	-7.35
264156_at	unknown protein	---	AT1G65280	-1.00	0.00	-0.03	0.979907	0.989522	-7.35
254908_at	putative protein other hypothetical prot	---	---	1.00	0.00	0.03	0.980022	0.989522	-7.35
263151_at	hypothetical protein predicted by gene	---	AT1G54120	-1.01	-0.01	-0.03	0.979934	0.989522	-7.35
250308_at	calcium-dependent protein kinase	CPK17	AT5G12180	1.00	0.00	0.03	0.979728	0.989522	-7.35
255935_at	hypothetical protein contains Pfam pro	---	AT1G12700	1.00	0.00	0.03	0.979945	0.989522	-7.35
248513_at	unknown protein	---	AT5G50500	1.00	0.00	0.03	0.979905	0.989522	-7.35
249445_at	putative protein predicted protein, Ara	---	AT5G39380	-1.00	0.00	-0.03	0.979844	0.989522	-7.35
248929_at	myrosinase-binding protein-like; jasmo	---	AT5G46000	1.00	0.00	0.03	0.980127	0.989585	-7.35
263381_at	putative MADS-box protein	AGL48	AT2G40210	-1.00	0.00	-0.03	0.980293	0.989709	-7.35
248379_at	RAR1 (gb|AAF18433.1) non-consensu	PBS2	AT5G51700	1.00	0.00	0.03	0.980347	0.989719	-7.35
261961_at	hypothetical protein predicted by gene	---	AT1G36510	1.00	0.00	0.03	0.980437	0.989723	-7.35
256650_at	hypothetical protein contains similarity	---	AT3G13620	1.00	0.00	0.03	0.98041	0.989723	-7.35
263675_x_	En/Spm-like transposon protein related	---	---	-1.00	0.00	-0.03	0.980512	0.989723	-7.35
266025_at	putative retroelement pol polyprotein	---	---	1.00	0.00	0.03	0.980525	0.989723	-7.35
256283_at	hypothetical protein	---	AT3G12540	1.00	0.00	0.03	0.98067	0.989826	-7.35
255748_at	hypothetical protein predicted by gene	---	AT1G32000	-1.00	0.00	-0.02	0.980932	0.989854	-7.35
253642_at	hypothetical protein ;supported by full-	---	AT4G29960	1.00	0.00	0.02	0.980887	0.989854	-7.35
247850_at	receptor-like protein kinase	---	AT5G58150	1.01	0.01	0.02	0.981001	0.989854	-7.35
261964_at	hypothetical protein similar to envelope	---	---	1.00	0.00	0.02	0.980933	0.989854	-7.35
256859_at	hypothetical protein	---	AT3G22940	-1.00	0.00	-0.02	0.98097	0.989854	-7.35
254528_at	hypothetical protein	---	AT4G19620	-1.00	0.00	-0.02	0.980809	0.989854	-7.35
252568_at	receptor-like protein kinase receptor li	---	AT3G45410	1.00	0.00	0.02	0.980824	0.989854	-7.35
256158_at	hypothetical protein contains similarity	ATPSK1	AT1G13590	1.00	0.00	0.02	0.981059	0.989869	-7.35
247421_at	SIAH1 - like protein SIAH1, Brassica r	---	AT5G62800	-1.00	0.00	-0.02	0.981236	0.989923	-7.35

252955_at	multiubiquitin chain binding protein (MI	RPN10	AT4G38630	-1.00	0.00	-0.02	0.981243	0.989923	-7.35
246172_s_	fragment of 1-aminocyclopropane-1-c	ACS1	AT3G61510 /	-1.00	0.00	-0.02	0.981179	0.989923	-7.35
260230_at	putative DNA-binding protein contains	---	AT1G74500	-1.00	0.00	-0.02	0.981307	0.989944	-7.35
247015_at	protease-like	---	AT5G66960	-1.00	0.00	-0.02	0.98144	0.990034	-7.35
251285_at	putative protein several hypothetical pr	---	AT3G61770	1.00	0.00	0.02	0.981516	0.990053	-7.35
256759_at	hypothetical protein predicted by gene	---	AT3G25640	1.00	0.00	0.02	0.981546	0.990053	-7.35
251410_at	uclacyanin 3 ; supported by cDNA: gi_	UCC3	AT3G60280	-1.00	0.00	-0.02	0.981648	0.990113	-7.35
262364_at	disease resistance protein, putative si	---	AT1G72860	-1.00	0.00	-0.02	0.98175	0.99013	-7.35
245394_at	hypothetical protein ;supported by full-	---	AT4G16450	-1.00	0.00	-0.02	0.981752	0.99013	-7.35
246005_at	lipoic acid synthase - like protein lipoic	---	AT5G08415	1.00	0.00	0.02	0.98194	0.990275	-7.35
263514_at	putative poly(ADP-ribose) glycohydrola	---	AT2G31860	1.00	0.00	0.02	0.982016	0.990308	-7.35
266923_at	unknown protein ;supported by full-ler	---	AT2G45980	-1.00	0.00	-0.02	0.982134	0.990347	-7.35
265049_at	jasmonate inducible protein, putative s	---	AT1G52060	-1.00	0.00	-0.02	0.982141	0.990347	-7.35
265367_at	hypothetical protein predicted by gens	---	---	1.00	0.00	0.02	0.982203	0.990365	-7.35
262267_at	hypothetical protein predicted by gens	---	---	1.00	0.00	0.02	0.982327	0.990447	-7.35
255751_at	terpene synthase family protein, putat	---	AT1G31950	-1.00	0.00	-0.02	0.982472	0.990549	-7.35
255382_at	putative pre-mRNA splicing factor simi	EMB2770	AT4G03430	-1.00	0.00	-0.02	0.982521	0.990555	-7.35
264529_at	CTP synthase-like protein similar to ct	---	AT1G30820	1.00	0.01	0.02	0.98265	0.99061	-7.35
258020_at	unknown protein ;supported by full-ler	NHD1	AT3G19490	-1.00	0.00	-0.02	0.982662	0.99061	-7.35
248090_at	putative protein contains similarity to N	MAPKKK15	AT5G55090	1.00	0.00	0.02	0.982796	0.990701	-7.35
252257_at	putative protein several hypothetical pr	---	AT3G49440	-1.00	0.00	-0.02	0.982843	0.990705	-7.35
259380_at	putative ABC transporter similar to AB	PDR1	AT3G16340	-1.00	0.00	-0.02	0.983043	0.990819	-7.35
252197_at	receptor protein kinase -like protein re	---	AT3G50230	1.00	0.00	0.02	0.983043	0.990819	-7.35
264410_s_	hypothetical protein predicted by gene	---	---	-1.00	0.00	-0.02	0.98309	0.990822	-7.35
253655_at	Expressed protein ;supported by cDNA	LCR59	AT4G30070	1.00	0.00	0.02	0.983351	0.991041	-7.35
264281_at	hypothetical protein similar to putative	---	AT1G61830	-1.00	0.00	-0.02	0.983488	0.991136	-7.35
255605_at	hypothetical protein	---	AT4G01090	-1.00	0.00	-0.02	0.983685	0.99129	-7.35
248143_at	putative protein similar to unknown pro	---	AT5G55040	-1.00	0.00	-0.02	0.983763	0.991325	-7.35
249105_at	40S ribosomal protein S15	---	AT5G43640	-1.00	0.00	-0.02	0.983853	0.991372	-7.35
254315_at	putative glycine-rich protein glycine-ric	---	---	1.00	0.00	0.02	0.984052	0.991441	-7.35
265178_at	Pto kinase interactor, putative similar t	---	AT1G23540	-1.00	0.00	-0.02	0.984031	0.991441	-7.35
244975_at	PSII 10KDa phosphoprotein	---	---	1.00	0.00	0.02	0.983973	0.991441	-7.35
262131_at	hypothetical protein predicted by gene	RALF1	AT1G02900	-1.01	-0.01	-0.02	0.98445	0.991745	-7.35
258961_at	hypothetical protein similar to myb-rel	---	AT3G10580	-1.00	0.00	-0.02	0.984484	0.991745	-7.35
256391_at	hypothetical protein predicted by gens	---	AT3G06090	-1.00	0.00	-0.02	0.98448	0.991745	-7.35

258656_at	putative Ras-like GTP-binding protein (	ATRABE1E	AT3G09900	1.00	0.00	0.02	0.984555	0.991772	-7.35
255762_at	unknown protein contains Pfam profile	HAC12	AT1G16710	-1.00	0.00	-0.02	0.984712	0.991822	-7.35
266041_s_	hypothetical protein	---	---	1.00	0.00	0.02	0.984735	0.991822	-7.35
258116_at	hypothetical protein similar to terpene s	---	AT3G14520	-1.00	0.00	-0.02	0.984661	0.991822	-7.35
257257_at	hypothetical protein contains Pfam pro	---	AT3G22020	-1.00	0.00	-0.02	0.984958	0.992003	-7.35
261263_at	H-protein promoter binding factor-2b,	---	AT1G26790	1.00	0.00	0.02	0.985101	0.992104	-7.35
256449_at	mutator transposase MUDRA, putativ	---	---	1.00	0.00	0.02	0.985265	0.992138	-7.35
266436_at	putative clathrin binding protein (epsin	---	AT2G43160	1.00	0.00	0.02	0.985238	0.992138	-7.35
256643_at	unknown protein similar to putative ret	---	---	1.00	0.00	0.02	0.985192	0.992138	-7.35
249428_at	putative protein predicted protein K5K	---	AT5G39870	1.00	0.00	0.02	0.98535	0.992147	-7.35
264739_at	hypothetical protein predicted by gene	---	AT1G62260	-1.00	0.00	-0.02	0.985361	0.992147	-7.35
250546_at	nhp2-like protein high mobility group-li	---	AT5G08180	1.00	0.00	0.02	0.985552	0.992295	-7.35
249158_at	electron transfer flavoprotein beta-sub	ETFBETA	AT5G43430	-1.00	0.00	-0.02	0.985611	0.99231	-7.35
252502_at	copper transport protein - like protein (	COPT2	AT3G46900	1.00	0.01	0.02	0.985724	0.992338	-7.35
250488_at	beta-glucosidase - like protein beta-gl	---	AT5G09700	1.00	0.00	0.02	0.985726	0.992338	-7.35
254482_at	TWIN SISTER OF FT (TSF) terminal f	TSF	AT4G20370	-1.00	0.00	-0.02	0.985954	0.992481	-7.35
257428_at	hypothetical protein predicted by gene	---	AT1G78990	-1.00	0.00	-0.02	0.985952	0.992481	-7.35
247052_at	homeodomain transcription factor-like	HB53	AT5G66700	1.00	0.00	0.02	0.98617	0.992654	-7.35
266961_at	Athila retroelement ORF1-like protein	---	---	1.00	0.00	0.02	0.986314	0.992756	-7.35
253979_at	putative protein other putative proteins	---	AT4G26680	-1.00	0.00	-0.02	0.986447	0.992759	-7.35
263074_at	putative HMG protein ;supported by fu	HMGB4	AT2G17560	-1.00	0.00	-0.02	0.986398	0.992759	-7.35
246930_at	KNAT3 homeodomain protein ;suppor	KNAT3	AT5G25220	1.00	0.00	0.02	0.986449	0.992759	-7.35
254186_at	putative protein cellulose synthase ca	CSLG1	AT4G24010	-1.00	0.00	-0.02	0.986549	0.992773	-7.35
266281_at	putative protein kinase contains a prot	---	AT2G29250	1.00	0.00	0.02	0.986536	0.992773	-7.35
264907_at	unknown protein similar to S.pombe pr	---	AT2G17280	1.00	0.01	0.02	0.986873	0.993055	-7.35
247223_at	MADS box transcription factor-like	MAF4	AT5G65070	-1.00	0.00	-0.02	0.987055	0.993194	-7.35
248043_s_	heat shock protein (emb|CAA72514.1)	---	AT5G56000 /	1.00	0.00	0.02	0.98725	0.993259	-7.35
249907_at	putative protein DNA repair protein RA	RAD5	AT5G22750	-1.00	0.00	-0.02	0.98722	0.993259	-7.35
261641_at	hypothetical protein similar to hypothet	---	AT1G27670	1.00	0.00	0.02	0.987238	0.993259	-7.35
252495_at	putative protein hypothetical proteins -	---	AT3G46770	1.00	0.00	0.02	0.987664	0.993608	-7.35
266039_s_	hypothetical protein	---	AT2G07739	-1.00	0.00	-0.02	0.987684	0.993608	-7.35
248427_at	subtilisin-like serine protease similar to	ATSBT1.3	AT5G51750	-1.00	0.00	-0.02	0.987819	0.993612	-7.35
246437_at	putative protein hypersensitivity-relate	---	AT5G17540	1.00	0.00	0.02	0.987789	0.993612	-7.35
253787_at	serine/threonine kinase-like protein re	---	AT4G28670	-1.00	0.00	-0.02	0.987759	0.993612	-7.35
252802_at	putative protein	---	---	-1.00	0.00	-0.02	0.987986	0.993737	-7.35

265551_at	putative replication protein A1	---	---	-1.00	0.00	-0.02	0.988067	0.993774	-7.35
258546_at	hypothetical protein predicted by gens	emb1974	AT3G07060	1.00	0.00	0.02	0.988171	0.993835	-7.35
261036_at	developmentally regulated GTP-bindi	ATDRG1	AT1G17470	1.00	0.00	0.02	0.988299	0.993867	-7.35
254097_at	putative Ser/Thr protein kinase serine	---	AT4G25160	1.00	0.00	0.02	0.988297	0.993867	-7.35
262642_at	hypothetical protein predicted by gene	---	AT1G62690	1.00	0.00	0.02	0.988377	0.993867	-7.35
246731_at	putative protein RING finger rngB prot	ACBP5	AT5G27630	1.00	0.00	0.02	0.988354	0.993867	-7.35
260471_at	hypothetical protein predicted by gene	---	AT1G11070	-1.00	0.00	-0.02	0.988447	0.993881	-7.35
266564_at	putative serine carboxypeptidase II	scpl22	AT2G24000	1.00	0.00	0.01	0.988478	0.993881	-7.35
266426_x_	hypothetical protein predicted by gens	---	AT2G07140	1.00	0.00	0.01	0.988543	0.993885	-7.35
251568_at	putative protein several hypothetical pr	---	AT3G58280	-1.00	0.00	-0.01	0.988613	0.993885	-7.35
264720_at	hypothetical protein similar to vetispira	---	AT1G70080	-1.00	0.00	-0.01	0.988595	0.993885	-7.35
256361_at	formyl transferase, putative contains F	pde194	AT1G66520	1.00	0.00	0.01	0.988676	0.993904	-7.35
262146_at	membrane protein, putative similar to	ATRBL5	AT1G52580	-1.00	0.00	-0.01	0.988812	0.993998	-7.35
246193_at	Expressed protein ; supported by full-l	---	---	1.00	0.00	0.01	0.989136	0.99428	-7.35
250804_at	putative protein contains similarity to c	---	AT5G05030	1.00	0.00	0.01	0.989229	0.994285	-7.35
255348_at	hypothetical protein	---	AT4G03820	-1.00	0.00	-0.01	0.989216	0.994285	-7.35
250427_at	putative protein myosin heavy chain fo	---	AT5G10500	-1.00	0.00	-0.01	0.98933	0.994343	-7.35
264699_at	unknown protein ;supported by full-len	---	AT1G69980 /	1.00	0.00	0.01	0.989408	0.994378	-7.35
252490_at	glucuronosyl transferase-like protein g	---	AT3G46720	1.00	0.00	0.01	0.989571	0.99441	-7.35
263183_at	putative glucan synthase Highly simila	CALS1	AT1G05570	1.00	0.00	0.01	0.989534	0.99441	-7.35
254843_at	putative protein TAK1 binding protein	---	AT4G11860	-1.00	0.00	-0.01	0.9895	0.99441	-7.35
256634_s_	hypothetical protein predicted by gens	---	---	1.00	0.00	0.01	0.989624	0.994419	-7.35
251175_at	homocysteine S-methyltransferase AtH	HMT2	AT3G63250	-1.00	0.00	-0.01	0.98988	0.994546	-7.35
256918_s_	hypothetical protein similar to hypothet	---	AT3G18960 /	1.00	0.00	0.01	0.989841	0.994546	-7.35
263062_at	putative phosphatidylinositol/phophatic	---	AT2G18180	1.00	0.00	0.01	0.989865	0.994546	-7.35
263767_at	putative retroelement pol polyprotein	---	---	-1.00	0.00	-0.01	0.989993	0.99458	-7.35
245945_at	putative protein various predicted prot	ROPGEF10	AT5G19560	1.00	0.00	0.01	0.990002	0.99458	-7.35
250554_at	unknown protein ;supported by full-ler	---	AT5G07900	1.00	0.00	0.01	0.990432	0.994968	-7.35
267206_at	putative dioxygenase	---	AT2G30830	-1.00	0.00	-0.01	0.990749	0.995243	-7.35
251084_at	putative protein putative proteins - Ara	---	AT5G01520	1.00	0.00	0.01	0.990861	0.995311	-7.35
245858_at	CER1-like protein CER1-like, A.thalian	---	AT5G28280	-1.00	0.00	-0.01	0.991029	0.995437	-7.35
258945_at	calmodulin-domain protein kinase CD	CPK2	AT3G10660	1.00	0.00	0.01	0.991266	0.995595	-7.35
256639_at	hypothetical protein predicted by gene	---	---	-1.00	0.00	-0.01	0.991284	0.995595	-7.35
246938_at	cyclin 3a	CYCA2;1	AT5G25380	-1.00	0.00	-0.01	0.991406	0.995595	-7.35
251147_at	kinesin heavy chain - like protein kines	---	AT3G63480	1.00	0.00	0.01	0.991384	0.995595	-7.35

265434_at	predicted protein	---	AT2G20805	-1.00	0.00	-0.01	0.991449	0.995595	-7.35
259508_at	hypothetical protein predicted by gene	---	---	-1.00	0.00	-0.01	0.991492	0.995595	-7.35
259663_at	hypothetical protein predicted by gene	PRA7	AT1G55190	1.00	0.00	0.01	0.991461	0.995595	-7.35
259828_at	RING-H2 zinc finger protein ATL3, pu	---	AT1G72220	1.00	0.00	0.01	0.991559	0.995618	-7.35
256641_at	hypothetical protein similar to putative	---	---	-1.00	0.00	-0.01	0.991648	0.99562	-7.35
257596_at	unknown protein	---	AT3G24760	1.00	0.00	0.01	0.991617	0.99562	-7.35
260625_at	storage protein, putative similar to GB	MOM	AT1G08060	-1.00	0.00	-0.01	0.992028	0.995958	-7.35
262216_at	hypothetical protein contains similarity	---	AT1G74780	1.00	0.00	0.01	0.992118	0.996004	-7.35
263546_at	putative dihydrofolate reductase-thymi	---	AT2G21550	-1.00	0.00	-0.01	0.992304	0.996103	-7.35
265331_at	similar to gibberellin-regulated proteins	---	AT2G18420	-1.00	0.00	-0.01	0.992284	0.996103	-7.35
261922_at	amp-binding protein, putative similar t	AAE12	AT1G65890	-1.00	0.00	-0.01	0.992546	0.996127	-7.35
267076_at	calcium binding protein (CaBP-22) ide	---	AT2G41090	1.00	0.01	0.01	0.992453	0.996127	-7.35
264097_s_	NADH dehydrogenase, putative simila	---	AT1G16700 /	-1.00	0.00	-0.01	0.992472	0.996127	-7.35
255141_at	putative protein several hypothetical pr	---	---	-1.00	0.00	-0.01	0.992539	0.996127	-7.35
255504_at	drought-induced-19-like 1 similar to dr	---	AT4G02200	-1.00	0.00	-0.01	0.992544	0.996127	-7.35
258221_at	Snf1-related protein kinase KIN11 (AK	AKIN11	AT3G29160	1.00	0.00	0.01	0.992673	0.996211	-7.35
253258_at	putative protein NF-180, Petromyzon	---	AT4G34400	1.00	0.00	0.01	0.992752	0.996246	-7.35
263634_at	putative retroelement gag/pol polyprote	---	---	-1.00	0.00	-0.01	0.992869	0.996275	-7.35
256884_at	hypothetical protein contains Pfam pro	---	AT3G15200	1.00	0.00	0.01	0.99284	0.996275	-7.35
265490_s_	putative polygalacturonase	---	AT2G15450 /	1.00	0.00	0.01	0.992916	0.996279	-7.35
249837_at	Expressed protein ; supported by full-l	---	AT5G23480	-1.00	0.00	-0.01	0.993125	0.996445	-7.35
255330_s_	putative polyprotein	---	---	-1.00	0.00	-0.01	0.993253	0.99653	-7.35
266145_at	putative TNP2-like transposon protein	---	---	-1.00	0.00	-0.01	0.993434	0.996667	-7.35
265063_at	receptor kinase, putative similar to rec	---	AT1G61500	-1.00	0.00	-0.01	0.993535	0.996725	-7.35
246743_at	putative protein predicted proteins, Ar	---	AT5G27750	-1.00	0.00	-0.01	0.993699	0.99673	-7.35
247055_at	putative protein similar to unknown pro	---	AT5G66740	-1.00	0.00	-0.01	0.993653	0.99673	-7.35
266429_at	hypothetical protein predicted by gens	---	AT2G07190	-1.00	0.00	-0.01	0.993715	0.99673	-7.35
252621_at	putative protein Ac-like transposases	---	---	-1.00	0.00	-0.01	0.993617	0.99673	-7.35
250832_at	nicotianamine synthase (dbj|BAA7458	NAS1	AT5G04950	1.00	0.00	0.01	0.993883	0.996832	-7.35
248187_at	zinc-binding protein-like ; supported b	---	AT5G53940	1.00	0.00	0.01	0.994038	0.996832	-7.35
264454_at	unknown protein similar to U2 small nu	---	AT1G10320	1.00	0.00	0.01	0.994064	0.996832	-7.35
255917_at	putative protein	---	AT5G28560	1.00	0.00	0.01	0.994078	0.996832	-7.35
258589_at	putative GDSL-motif lipase/acylhydrola	LTL1	AT3G04290	-1.00	0.00	-0.01	0.993948	0.996832	-7.35
252582_at	putative protein several hypothetical pr	---	AT3G45530	-1.00	0.00	-0.01	0.994075	0.996832	-7.35
252753_at	hypothetical protein	---	AT3G43500	-1.00	0.00	-0.01	0.994135	0.996845	-7.35

254134_at	argininosuccinate synthase -like prote	---	AT4G24830	1.00	0.00	0.01	0.994295	0.996852	-7.35
265687_s_	hypothetical protein predicted by gens	---	AT2G24470 /	1.00	0.00	0.01	0.994252	0.996852	-7.35
255655_at	contains similarity to gag proteins	---	AT4G00980	1.00	0.00	0.01	0.994205	0.996852	-7.35
260456_at	hypothetical protein	---	AT1G72490	-1.00	0.00	-0.01	0.994317	0.996852	-7.35
264546_at	Expressed protein ; supported by cDN	---	AT1G55805	1.00	0.00	0.01	0.994431	0.996922	-7.35
265739_at	unknown protein ; supported by cDNA	AtQSOX2	AT2G01270	1.00	0.00	0.01	0.994631	0.997079	-7.35
248479_at	unknown protein	---	AT5G50910	-1.00	0.00	-0.01	0.994683	0.997088	-7.35
249701_at	putative protein similar to unknown pro	---	AT5G35460	-1.00	0.00	-0.01	0.994854	0.997171	-7.35
250775_at	putative protein contains similarity to e	---	AT5G05460	-1.00	0.00	-0.01	0.994854	0.997171	-7.35
249546_at	putative protein chromosome segrega	PMI15	AT5G38150	-1.00	0.00	-0.01	0.99498	0.99721	-7.35
262460_s_	fructokinase, putative similar to fructol	---	AT1G06030 /	-1.00	0.00	-0.01	0.995024	0.99721	-7.35
265937_at	putative RING zinc finger protein	---	AT2G19610	-1.00	0.00	-0.01	0.995024	0.99721	-7.35
253347_at	putative protein	---	AT4G33610	1.00	0.00	0.01	0.995106	0.997248	-7.35
264233_at	ribosomal protein, putative similar to r	---	AT1G67430	-1.00	0.00	-0.01	0.995326	0.997424	-7.35
266877_at	putative glucanase	AtGH9B12	AT2G44570	1.00	0.00	0.01	0.995439	0.997494	-7.35
255918_at	putative protein	---	---	-1.00	0.00	-0.01	0.995646	0.997658	-7.35
267015_at	unknown protein	---	AT2G39340	1.00	0.00	0.01	0.995798	0.997766	-7.35
245551_at	cytochrome P450 like protein	CYP705A2	AT4G15350	1.00	0.00	0.01	0.995935	0.99786	-7.35
255489_at	predicted protein destination factor sir	---	AT4G02650 /	-1.00	0.00	0.00	0.996185	0.998066	-7.35
260099_at	unknown protein ;supported by full-ler	---	AT1G73180	1.00	0.00	0.00	0.996232	0.99807	-7.35
260224_at	hypothetical protein contains Pfam pro	---	AT1G74400	1.00	0.00	0.00	0.996382	0.998176	-7.35
249725_at	unknown protein	---	AT5G35470	-1.00	0.00	0.00	0.996565	0.998272	-7.35
247751_at	putative protein	---	AT5G59050	-1.00	0.00	0.00	0.996557	0.998272	-7.35
258753_at	hypothetical protein predicted by gens	ATEXO70H3	AT3G09530	1.00	0.00	0.00	0.996662	0.998281	-7.35
247083_at	unknown protein	---	AT5G66290	1.00	0.00	0.00	0.996629	0.998281	-7.35
252594_at	putative transporter protein peptide tra	---	AT3G45680	-1.00	0.00	0.00	0.996709	0.998284	-7.35
265787_at	Mutator-like transposase similar to MU	---	---	1.00	0.00	0.00	0.996964	0.998496	-7.35
264610_at	Expressed protein ; supported by full-l	---	AT1G04645	1.00	0.00	0.00	0.997152	0.998641	-7.35
250784_at	unknown protein ; supported by cDNA	---	AT5G05480	-1.00	0.00	0.00	0.997197	0.998642	-7.35
260826_at	hypothetical protein predicted by gene	---	AT1G06710	-1.00	0.00	0.00	0.99761	0.999012	-7.35
256527_at	thionin, putative similar to thionin [Ara	---	AT1G66100	1.00	0.00	0.00	0.997671	0.999028	-7.35
265684_at	unknown protein	---	AT2G24410	1.00	0.00	0.00	0.997895	0.999209	-7.35
260181_at	endo-1,4-beta-glucanase identical to e	ATGH9B1	AT1G70710	1.00	0.00	0.00	0.998066	0.999337	-7.35
246941_at	putative protein several hypothetical pr	---	AT5G25415	1.00	0.00	0.00	0.998142	0.999369	-7.35
247961_at	putative protein similar to unknown pro	---	AT5G56570	1.00	0.00	0.00	0.998259	0.999442	-7.35

258008_at	putative late embryogenesis abundant	---	AT3G19430	-1.00	0.00	0.00	0.99833	0.999469	-7.35
266081_at	putative protein kinase contains a prot	---	AT2G37840	1.00	0.00	0.00	0.99841	0.999482	-7.35
262330_at	disease resistance protein, putative si	RLM1	AT1G64070	-1.00	0.00	0.00	0.99843	0.999482	-7.35
265763_at	unknown protein	---	AT2G48060	1.00	0.00	0.00	0.998539	0.999506	-7.35
253316_s_	putative protein hyphally regulated pro	---	AT4G33930 /	1.00	0.00	0.00	0.998542	0.999506	-7.35
249735_at	putative protein contains similarity to g	---	AT5G24450	-1.00	0.00	0.00	0.998637	0.999557	-7.35
252152_at	putative protein several hypothetical pr	---	AT3G51350	-1.00	0.00	0.00	0.998778	0.999654	-7.35
254522_at	hypothetical protein	---	AT4G19980	1.00	0.00	0.00	0.998856	0.999672	-7.35
255067_at	putative phosphotyrosyl phosphatase a	---	AT4G08960	1.00	0.00	0.00	0.998883	0.999672	-7.35
256236_at	hypothetical protein predicted by gene	---	AT3G12350	1.00	0.00	0.00	0.998935	0.99968	-7.35
263448_at	putative importin (nuclear transport fac	SAD2	AT2G31660	-1.00	0.00	0.00	0.999136	0.999734	-7.35
264168_at	unknown protein Similar to yeast gene	---	AT1G02080	1.00	0.00	0.00	0.999119	0.999734	-7.35
262133_at	high affinity sulphate transporter, puta	SULTR1;2	AT1G78000	1.00	0.00	0.00	0.999249	0.999734	-7.35
265644_at	hypothetical protein predicted by gene	ATEPR1	AT2G27380	-1.00	0.00	0.00	0.999461	0.999734	-7.35
254440_at	putative protein desiccation-related pr	---	AT4G21020	1.00	0.00	0.00	0.999471	0.999734	-7.35
257673_at	unknown protein similar to GB:BAA87	---	AT3G20370	1.00	0.00	0.00	0.999369	0.999734	-7.35
257223_at	50S ribosomal protein L12-B identical	RPL12-B	AT3G27840	1.00	0.00	0.00	0.999407	0.999734	-7.35
245131_s_	unknown protein	emb1067	AT2G45330 /	1.00	0.00	0.00	0.999193	0.999734	-7.35
260196_at	hypothetical protein similar to hypothet	---	AT1G67570	1.00	0.00	0.00	0.999429	0.999734	-7.35
252809_at	putative protein various predicted prot	---	---	1.00	0.00	0.00	0.999233	0.999734	-7.35
260865_at	reverse transcriptase, putative similar	---	AT1G43760	-1.00	0.00	0.00	0.99927	0.999734	-7.35
264550_at	hypothetical protein predicted by gens	---	AT1G09450	1.00	0.00	0.00	0.999564	0.999783	-7.35
248370_at	homeodomain transcription factor-like	HDG7	AT5G52170	1.00	0.00	0.00	0.999694	0.99987	-7.35
264411_at	mutator-like transposase, putative sim	---	---	-1.00	0.00	0.00	0.999843	0.999975	-7.35
266506_at	unknown protein	---	AT2G47850	-1.00	0.00	0.00	0.999943	1	-7.35
248417_at	unknown protein	---	AT5G51650	1.00	0.00	0.00	1	1	-7.35
252020_at	SKP1/ASK1 (At6), putative similar to S	ASK6	AT3G53060	-1.00	0.00	0.00	0.999993	1	-7.35

	mut.0 vs wt.0								
ID	Description	Gene Symb	AGI	FC	logFC	t	P.Value	adj.P.Val	B
262595_at	putative ethylene responsive elem	SHN1	AT1G15360	217.78	7.77	66.77	9.50E-11	0.0000	9.03
264415_at	AP2 domain containing protein, pu	RAP2.6	AT1G43160	-17.79	-4.15	-28.74	2.71E-08	0.0002	7.80
256771_at	unknown protein	---	AT3G13700	8.24	3.04	29.97	2.04E-08	0.0002	7.90
267256_s_at	putative serine carboxypeptidase I	scpl10	AT2G23000	-8.25	-3.04	-20.83	2.31E-07	0.0009	6.79
251142_at	Expressed protein ; supported by f	---	AT5G01015	-5.89	-2.56	-20.85	2.30E-07	0.0009	6.79
262599_at	unknown protein ESTs gb|R6514	---	AT1G15350	5.28	2.40	21.35	1.96E-07	0.0009	6.88
255604_at	hypothetical protein	---	AT4G01080	-10.53	-3.40	-18.90	4.40E-07	0.0014	6.41
264160_at	hypothetical protein predicted by g	---	AT1G65450	5.25	2.39	17.54	7.22E-07	0.0021	6.09
265305_at	putative tyrosine decarboxylase	---	AT2G20340	-5.34	-2.42	-16.34	1.15E-06	0.0021	5.78
263475_at	Expressed protein ; supported by f	---	AT2G31945	4.39	2.13	16.04	1.30E-06	0.0021	5.69
262603_at	hypothetical protein Is a member	---	AT1G15380	23.02	4.52	16.45	1.10E-06	0.0021	5.81
263786_at	putative auxin-responsive protein	JAR1	AT2G46370	-2.71	-1.44	-16.79	9.61E-07	0.0021	5.90
259735_at	Expressed protein ; supported by f	---	AT1G64405	8.95	3.16	16.05	1.29E-06	0.0021	5.70
257890_s_at	putative protein peroxidase - Lyc	---	AT3G17070	-6.33	-2.66	-16.93	9.10E-07	0.0021	5.94
247030_at	putative protein similar to unknow	---	AT5G67210	-2.74	-1.45	-15.73	1.48E-06	0.0022	5.60
264573_at	putative pectin methylesterase Sim	---	AT1G05310	5.20	2.38	15.56	1.58E-06	0.0023	5.55
265511_at	putative glycine-rich protein ; supp	---	AT2G05540	6.16	2.62	15.20	1.85E-06	0.0023	5.44
251021_at	thaumatin-like protein thaumatin-li	---	AT5G02140	9.71	3.28	15.29	1.78E-06	0.0023	5.47
263809_at	putative GDSL-motif lipase/hydrola	---	AT2G04570	16.76	4.07	14.87	2.14E-06	0.0026	5.33
252377_at	putative peptide transporter peptic	---	AT3G47960	-4.47	-2.16	-14.38	2.67E-06	0.0029	5.17
256602_at	unknown protein	---	AT3G28310	-4.70	-2.23	-14.45	2.58E-06	0.0029	5.19
256603_at	unknown protein similar to At14a p	---	AT3G28270	-13.42	-3.75	-13.77	3.54E-06	0.0036	4.95
248353_at	cytochrome P450	CYP96A4	AT5G52320	-2.69	-1.43	-13.73	3.59E-06	0.0036	4.94
256489_at	unknown protein	---	AT1G31550	-2.29	-1.20	-13.00	5.15E-06	0.0045	4.65
247718_at	nonspecific lipid-transfer protein p	LTP4	AT5G59310	4.13	2.05	13.03	5.07E-06	0.0045	4.66
251181_at	putative protein pectinesterase ho	---	AT3G62820	-3.88	-1.96	-13.08	4.94E-06	0.0045	4.68
254305_at	potassium channel protein AKT3 ;	AKT2/3	AT4G22200	-2.26	-1.18	-12.94	5.30E-06	0.0045	4.63
255264_at	putative protein ethylene responsi	---	AT4G05170	-3.10	-1.63	-12.83	5.59E-06	0.0046	4.58
245422_at	putative protein	---	AT4G17470	-26.71	-4.74	-12.38	7.04E-06	0.0054	4.39
256631_at	At14a-like protein similar to At14a	---	AT3G28320	-6.70	-2.74	-12.40	6.99E-06	0.0054	4.40
252118_at	putative protein various predicted	---	AT3G51400	2.13	1.09	12.25	7.55E-06	0.0056	4.34
261804_at	UDP glucose:flavonoid 3-o-glucos	UGT78D1	AT1G30530	-4.50	-2.17	-12.18	7.83E-06	0.0056	4.31
249970_at	dermal glycoprotein precursor -lik	---	AT5G19100	-5.73	-2.52	-11.89	9.14E-06	0.0062	4.18

251130_at	oligopeptide transporter - like prot	PTR5	AT5G01180	-2.28	-1.19	-11.86	9.31E-06	0.0062	4.16
266419_at	putative annexin ;supported by ful	ANNAT3	AT2G38760	-3.84	-1.94	-11.58	1.09E-05	0.0071	4.03
262232_at	unknown protein ; supported by cD	---	AT1G68600	-4.25	-2.09	-11.51	1.13E-05	0.0072	3.99
245141_at	putative flavonol reductase	BEN1	AT2G45400	-2.82	-1.50	-11.36	1.23E-05	0.0076	3.92
266841_at	putative heat shock transcription fa	ATHSFA2	AT2G26150	-4.36	-2.13	-11.18	1.36E-05	0.0082	3.83
253277_at	cinnamyl alcohol dehydrogenase -	ATCAD5	AT4G34230	-3.53	-1.82	-11.00	1.51E-05	0.0088	3.74
254773_at	putative protein Cyclic beta-1-3-gl	ATCSLA15	AT4G13410	-9.11	-3.19	-10.62	1.90E-05	0.0108	3.54
264271_at	beta-glucosidase, putative similar	BGLU6	AT1G60270	-4.44	-2.15	-10.34	2.25E-05	0.0122	3.39
249540_at	4-coumarate--CoA ligase -like pro	---	AT5G38120	-5.71	-2.51	-10.37	2.20E-05	0.0122	3.41
261772_at	hypothetical protein predicted by g	---	AT1G76240	-5.04	-2.33	-10.27	2.35E-05	0.0123	3.35
259526_at	hypothetical protein	---	AT1G12570	5.56	2.48	10.26	2.37E-05	0.0123	3.34
256894_at	PREG-like protein, putative simila	CYCP2;1	AT3G21870	1.93	0.95	10.07	2.66E-05	0.0131	3.24
246122_at	putative protein brain specific Na+	PHT4;5	AT5G20380	2.49	1.32	10.01	2.76E-05	0.0131	3.20
251780_s_at	beta-ketoacyl-ACP reductase - lik	---	AT3G55290 /	-3.89	-1.96	-10.01	2.77E-05	0.0131	3.20
251934_at	putative protein delta-latroinsectot	---	AT3G54070	2.60	1.38	10.07	2.66E-05	0.0131	3.24
250598_at	transcription factor-like protein ; su	ATMYB29	AT5G07690	-3.44	-1.78	-9.86	3.03E-05	0.0141	3.12
251785_at	ABC transporter - like protein brea	ATWBC19	AT3G55130	-5.46	-2.45	-9.80	3.16E-05	0.0142	3.08
262598_at	unknown protein EST gb|N65467 c	---	AT1G15260	3.25	1.70	9.79	3.18E-05	0.0142	3.08
255132_at	inositol 1,3,4-trisphosphate 5/6-kir	---	AT4G08170	-2.62	-1.39	-9.75	3.26E-05	0.0143	3.05
266117_at	hypothetical protein ; supported by	---	AT2G02170	2.00	1.00	9.65	3.48E-05	0.0150	2.99
254889_at	osmotin precursor ;supported by f	ATOSM34	AT4G11650	3.58	1.84	9.54	3.75E-05	0.0159	2.92
258264_at	unknown protein	MBD11	AT3G15790	-2.49	-1.32	-9.33	4.31E-05	0.0178	2.79
258253_at	putative short chain alcohol dehydr	---	AT3G26760	1.97	0.98	9.31	4.37E-05	0.0178	2.78
264270_at	beta-glucosidase, putative similar	---	---	-1.89	-0.92	-9.27	4.48E-05	0.0179	2.76
263226_at	unknown protein Contains the PF	---	AT1G30690	1.81	0.86	9.15	4.87E-05	0.0192	2.68
255786_at	unknown protein contains similarity	ATCLH1	AT1G19670	-6.14	-2.62	-9.11	5.00E-05	0.0193	2.66
261768_at	gibberellin 3 beta-hydroxylase, pu	GA3OX1	AT1G15550	2.36	1.24	9.05	5.23E-05	0.0199	2.61
256880_at	major latex protein, putative simila	---	AT3G26450	-3.53	-1.82	-8.99	5.44E-05	0.0200	2.58
260531_at	putative acyl-CoA synthetase ; su	CER8	AT2G47240	2.67	1.41	9.01	5.37E-05	0.0200	2.59
249330_at	putative protein similar to unknown	---	AT5G40970	2.07	1.05	8.89	5.82E-05	0.0208	2.51
252303_at	putative protein hypothetical prote	---	AT3G49210	1.91	0.93	8.87	5.91E-05	0.0208	2.50
260220_at	putative MYB family transcription f	MYB31	AT1G74650	2.90	1.53	8.87	5.91E-05	0.0208	2.50
253879_s_at	UDP rhamnose--anthocyanidin-3-	---	AT4G27560 /	-4.41	-2.14	-8.82	6.12E-05	0.0212	2.46
260101_at	putative trypsin inhibitor similar to t	---	AT1G73260	2.79	1.48	8.76	6.40E-05	0.0213	2.42
250680_at	putative protein similar to unknown	---	AT5G06570	4.71	2.24	8.72	6.60E-05	0.0213	2.39

265453_at	putative cellular apoptosis suscept	---	AT2G46520	-2.31	-1.21	-8.71	6.63E-05	0.0213	2.39
267425_at	putative berberine bridge enzyme	---	AT2G34810	-8.72	-3.12	-8.71	6.62E-05	0.0213	2.39
251022_at	putative protein Hsp70 binding pro	---	AT5G02150	2.18	1.13	8.73	6.53E-05	0.0213	2.40
267592_at	unknown protein similar to GP 224	---	AT2G39710	1.78	0.83	8.65	6.91E-05	0.0216	2.35
254234_at	putative major latex protein major	---	AT4G23680	8.09	3.02	8.67	6.83E-05	0.0216	2.36
266275_at	putative tropinone reductase	---	AT2G29370	2.35	1.23	8.63	7.04E-05	0.0217	2.33
263405_s_at	hypothetical protein similar to hypo	---	AT2G04066	-1.77	-0.82	-8.60	7.19E-05	0.0219	2.31
249090_at	Expressed protein ; supported by c	---	AT5G43745	-2.66	-1.41	-8.54	7.50E-05	0.0222	2.27
245710_at	ferulate-5-hydroxylase	---	AT5G04330	-2.60	-1.38	-8.56	7.41E-05	0.0222	2.28
249454_at	expressed protein predicted prote	---	AT5G39520	10.07	3.33	8.48	7.86E-05	0.0230	2.23
246098_at	ethylene-forming-enzyme-like diox	---	AT5G20400	3.04	1.60	8.38	8.45E-05	0.0239	2.16
264516_at	unknown protein	---	AT1G10090	-1.87	-0.91	-8.40	8.33E-05	0.0239	2.17
246620_at	cytochrome P450 ; supported by c	CYP81D1	AT5G36220	-3.43	-1.78	-8.37	8.49E-05	0.0239	2.15
260873_at	hypothetical protein predicted by g	---	AT1G21580	-1.72	-0.78	-8.32	8.80E-05	0.0245	2.12
255360_at	putative protein ;supported by full-	---	AT4G03960	1.94	0.95	8.30	8.97E-05	0.0247	2.10
245275_at	beta-amylase ; supported by cDNA	BAM5	AT4G15210	-5.02	-2.33	-8.27	9.19E-05	0.0248	2.08
262307_at	heat shock protein DnaJ, putative	---	AT1G71000	-2.42	-1.27	-8.25	9.33E-05	0.0248	2.06
248564_at	putative protein contains similarity	---	AT5G49700	2.52	1.34	8.26	9.23E-05	0.0248	2.07
245060_at	GDP-mannose pyrophosphorylas	CYT1	AT2G39770	-1.75	-0.80	-8.17	9.91E-05	0.0260	2.00
249527_at	proline oxidase, mitochondrial pre	---	AT5G38710	-2.65	-1.41	-8.15	0.00010058	0.0261	1.99
264318_at	putative beta-ketoacyl-CoA syntha	KCS2	AT1G04220	3.64	1.86	8.12	0.00010235	0.0262	1.97
259878_at	putative catechol O-methyltransfer	---	AT1G76790	-4.30	-2.10	-8.11	0.00010355	0.0262	1.96
261317_at	cytochrome C oxidase assembly p	---	AT1G53030	1.91	0.94	8.03	0.00010968	0.0275	1.91
254931_at	serine/threonine kinase-like protei	---	AT4G11460	2.35	1.23	8.01	0.00011142	0.0276	1.89
250484_at	asparagine synthetase ASN3 ; su	ASN3	AT5G10240	1.85	0.89	7.97	0.000115	0.0282	1.86
254697_at	putative protein predicted protein,	---	AT4G17970	-1.74	-0.80	-7.94	0.00011735	0.0285	1.84
251109_at	ferritin 1 precursor ;supported by f	FER1	AT5G01600	3.81	1.93	7.81	0.00013012	0.0287	1.74
249375_at	putative protein predicted proteins	AGP24	AT5G40730	-1.90	-0.92	-7.86	0.00012542	0.0287	1.78
264953_at	alcohol dehydrogenase identical to	ADH1	AT1G77120	-2.33	-1.22	-7.80	0.0001316	0.0287	1.73
246494_at	putative protein putative cellulose	CSLA11	AT5G16190	-2.03	-1.02	-7.83	0.00012792	0.0287	1.76
255619_s_at	putative CHP-rich zinc finger prote	---	AT4G01350	-2.36	-1.24	-7.90	0.00012109	0.0287	1.81
247648_at	laccase - like protein laccase LAC	LAC17	AT5G60020	2.04	1.03	7.88	0.00012323	0.0287	1.79
251372_at	putative protein ;supported by full-	---	AT3G60520	2.21	1.14	7.79	0.000132	0.0287	1.73
263156_at	myrosinase-associated protein, pu	---	AT1G54030	-3.53	-1.82	-7.84	0.00012757	0.0287	1.76
259514_at	hypothetical protein ; supported by	OZS1	AT1G12480	-1.91	-0.93	-7.80	0.00013179	0.0287	1.73

248540_at	FRO1 and FRO2-like protein	FRO8	AT5G50160	-1.67	-0.74	-7.92	0.00011986	0.0287	1.82
245734_at	lysophospholipase homolog, putat	---	AT1G73480	-3.02	-1.59	-7.85	0.0001262	0.0287	1.77
255825_at	Expressed protein ; supported by f	---	AT2G40475	-2.62	-1.39	-7.76	0.00013512	0.0291	1.70
247040_at	anthranilate N-hydroxycinnamoyl/b	---	AT5G67150	-2.21	-1.15	-7.74	0.00013818	0.0295	1.68
246603_at	copper amine oxidase, putative si	---	AT1G31690	-2.42	-1.27	-7.70	0.00014266	0.0296	1.65
261872_s_at	hypthetical protein contains similar	---	AT1G11520	1.93	0.95	7.71	0.00014136	0.0296	1.66
262581_at	unknown protein ESTs gb|T22508	---	AT1G15370	1.64	0.71	7.71	0.00014065	0.0296	1.66
258167_at	UDP-glucose:indole-3-acetate bet	UGT84A2	AT3G21560	-3.23	-1.69	-7.68	0.00014453	0.0297	1.64
251037_at	putative protein oxysterol-binding	UNE18	AT5G02100	-2.58	-1.37	-7.64	0.00014894	0.0298	1.61
264862_at	hypothetical protein predicted by g	---	AT1G24330	-2.54	-1.34	-7.66	0.00014686	0.0298	1.62
254862_at	putative transport protein Na(+) de	---	AT4G12030	-3.02	-1.59	-7.64	0.0001486	0.0298	1.61
251108_at	putative protein several hypothetic	---	AT5G01620	2.52	1.34	7.60	0.00015356	0.0305	1.58
245349_at	cyanohydrin lyase like protein ;sup	MES16	AT4G16690	3.92	1.97	7.53	0.00016363	0.0322	1.51
245671_at	purine permease identical to purine	PUP1	AT1G28230	-1.75	-0.80	-7.50	0.000167	0.0323	1.49
251916_at	transporter-like protein oligopeptic	---	AT3G53960	-2.52	-1.33	-7.50	0.0001664	0.0323	1.50
247628_at	putative protein	---	AT5G60400	2.27	1.19	7.45	0.00017393	0.0333	1.45
251906_at	putative protein several hypothetic	ATCHX20	AT3G53720	-2.22	-1.15	-7.43	0.00017629	0.0335	1.44
255403_at	putative GH3-like protein similar to	DFL2	AT4G03400	-2.13	-1.09	-7.37	0.00018614	0.0348	1.39
256060_at	hypothetical protein contains simila	---	AT1G07050	-2.53	-1.34	-7.37	0.00018628	0.0348	1.39
264458_at	unknown protein similar to ESTs g	---	AT1G10410	-1.78	-0.83	-7.33	0.00019237	0.0357	1.35
259708_at	lysophospholipase isolog, putative	---	AT1G77420	-2.12	-1.08	-7.25	0.00020469	0.0377	1.29
261415_at	globulin-like protein similar to GB:7	---	AT1G07750	-3.02	-1.59	-7.22	0.00021044	0.0381	1.27
264163_at	Expressed protein ; supported by f	---	AT1G65445	1.95	0.96	7.23	0.00020884	0.0381	1.27
257035_at	cytochrome P450, putative similar	CYP707A4	AT3G19270	-1.91	-0.93	-7.20	0.00021428	0.0385	1.25
245161_at	putative myrosinase binding protei	NSP2	AT2G33070	-2.03	-1.02	-7.15	0.00022253	0.0390	1.21
263477_at	putative glucosyltransferase ; sup	---	AT2G31790	-2.37	-1.25	-7.17	0.0002202	0.0390	1.22
261107_at	unknown protein ; supported by cD	---	AT1G63010	-1.70	-0.77	-7.16	0.00022194	0.0390	1.21
251015_at	putative protein predicted protein,	---	AT5G02480	1.65	0.73	7.14	0.00022549	0.0393	1.20
264572_at	unknown protein ESTs gb|AA042	---	AT1G05320	1.85	0.89	7.12	0.00022927	0.0396	1.18
252123_at	flavanone 3-hydroxylase (FH3) ;su	F3H	AT3G51240	-1.70	-0.76	-7.08	0.00023701	0.0404	1.15
245367_at	Expressed protein ; supported by f	NRPB9B	AT4G16265	1.80	0.85	7.07	0.00023903	0.0404	1.14
258392_at	anther development protein, ATA2	ATA20	AT3G15400	-2.09	-1.07	-7.07	0.00023814	0.0404	1.14
267051_at	hypothetical protein predicted by g	---	AT2G38500	-2.25	-1.17	-7.06	0.00024167	0.0405	1.13
246302_at	Ca2+/H+-exchanging protein-like A	CAX3	AT3G51860	6.04	2.59	7.02	0.00024935	0.0415	1.10
266192_at	unknown protein	---	AT2G39080	1.59	0.67	7.00	0.00025344	0.0417	1.08

252924_at	putative zinc finger protein salt-tol	---	AT4G39070	4.25	2.09	7.00	0.00025412	0.0417	1.08
260385_at	putative flavonol sulfotransferase s	SOT18	AT1G74090	-1.98	-0.99	-6.97	0.00026105	0.0423	1.05
261713_at	protein kinase, putative identical t	MYC2	AT1G32640	-2.54	-1.35	-6.97	0.00026117	0.0423	1.05
266265_at	putative tropinone reductase ; sup	---	AT2G29340	-2.45	-1.29	-6.95	0.00026389	0.0424	1.04
263031_at	glucosyltransferase, putative simil	ATCSLA10	AT1G24070	-12.85	-3.68	-6.94	0.00026763	0.0427	1.03
248196_at	putative protein similar to unknown	---	AT5G54150	-1.64	-0.71	-6.91	0.00027333	0.0433	1.00
255734_at	hypothetical protein similar to puta	---	AT1G25550	2.21	1.14	6.90	0.00027539	0.0433	1.00
260937_at	hypothetical protein contains simila	---	AT1G45160	-1.56	-0.64	-6.89	0.00027815	0.0435	0.99
256672_at	ABC transporter, putative contains	---	AT3G52310	-2.01	-1.01	-6.88	0.00028109	0.0436	0.98
263180_at	unknown protein ;supported by ful	URH2	AT1G05620	-1.79	-0.84	-6.87	0.00028344	0.0437	0.97
245112_at	glycerol-3-phosphate dehydrogena	GPDHC1	AT2G41540	4.87	2.28	6.84	0.0002912	0.0440	0.94
247041_at	floral homeotic protein apetala2-lik	TOE3	AT5G67180	-1.85	-0.89	-6.84	0.00029083	0.0440	0.94
259429_at	cytochrome P450, putative similar	CYP86A4	AT1G01600	8.29	3.05	6.85	0.00028971	0.0440	0.95
251094_at	putative protein ;supported by full-	---	AT5G01350	1.82	0.87	6.82	0.00029577	0.0444	0.93
247954_at	beta-galactosidase (emb|CAB6474	BGAL4	AT5G56870	1.94	0.96	6.80	0.00030144	0.0447	0.91
266259_at	unknown protein ;supported by ful	---	AT2G27830	1.71	0.77	6.79	0.00030349	0.0447	0.90
262703_at	putative auxin-induced protein sim	---	AT1G16510	2.29	1.19	6.80	0.00030235	0.0447	0.90
261191_at	starch synthase, putative similar t	---	AT1G32900	-2.97	-1.57	-6.77	0.00030974	0.0447	0.88
261979_at	nitrate reductase, putative similar	NIA2	AT1G37130	2.58	1.37	6.77	0.00030997	0.0447	0.88
249800_at	MtN3-like protein ; supported by c	MTN3	AT5G23660	-1.73	-0.79	-6.78	0.00030617	0.0447	0.89
266682_at	putative disease resistance protein	---	AT2G19780	-2.61	-1.39	-6.76	0.00031264	0.0449	0.87
265656_at	putative nonspecific lipid-transfer p	---	AT2G13820	3.66	1.87	6.74	0.00031752	0.0449	0.85
251039_at	putative protein hypothetical prote	---	AT5G02020	3.71	1.89	6.74	0.00031907	0.0449	0.85
256757_at	membrane transporter, putative si	---	AT3G25620	-1.75	-0.80	-6.75	0.00031646	0.0449	0.86
260633_at	protein kinase, putative similar to	HT1	AT1G62400	-1.67	-0.74	-6.73	0.00032122	0.0450	0.84
252365_at	Expressed protein ; supported by f	---	AT3G48350	-3.68	-1.88	-6.67	0.00033722	0.0459	0.79
260897_at	ER lumen protein retaining recepto	ERD2	AT1G29330	-1.70	-0.76	-6.67	0.00033818	0.0459	0.79
252136_at	calmodulin-like protein flagellar ca	---	AT3G50770	18.31	4.19	6.68	0.0003344	0.0459	0.80
257949_at	putative UDP-glucose glucosyltran	UGT71B1	AT3G21750	-2.20	-1.14	-6.69	0.00033215	0.0459	0.81
254839_at	stress-induced protein sti1 -like pr	---	AT4G12400	-3.79	-1.92	-6.68	0.00033635	0.0459	0.80
247304_at	amino acid transporter AAP4 (pir||	AAP4	AT5G63850	-2.26	-1.18	-6.64	0.0003478	0.0469	0.76
252993_at	monooxygenase 2 (MO2)	---	AT4G38540	2.97	1.57	6.59	0.00036352	0.0472	0.72
259598_at	sphingosine-1-phosphate lyase, p	DPL1	AT1G27980	1.85	0.89	6.60	0.00035863	0.0472	0.73
261653_at	subtilisin-like serine protease, puta	SBTI1.1	AT1G01900	3.70	1.89	6.56	0.00037439	0.0472	0.69
260235_at	putative SET protein, phospatase	NRP1	AT1G74560	1.56	0.64	6.58	0.00036747	0.0472	0.71

247247_at	50S ribosomal protein L17 ;suppo	---	AT5G64650	1.62	0.70	6.55	0.00037594	0.0472	0.68
257174_at	uracil phosphoribosyltransferase,	---	AT3G27190	1.99	0.99	6.57	0.00036989	0.0472	0.70
252056_at	ubiquitin extension protein (UBQ1	UBQ1	AT3G52590	1.65	0.72	6.60	0.00036038	0.0472	0.73
247775_at	phosphoinositide-specific phospho	PLC5	AT5G58690	-2.53	-1.34	-6.58	0.00036652	0.0472	0.71
264130_at	hypothetical protein predicted by g	---	AT1G79160	1.93	0.95	6.55	0.0003767	0.0472	0.68
262580_at	hypothetical protein Similar to gb|U	---	AT1G15330	2.09	1.07	6.62	0.000355	0.0472	0.74
260237_at	putative MYB family transcription f	MYB95	AT1G74430	-3.67	-1.88	-6.55	0.00037691	0.0472	0.68
265121_at	similar to flavin-containing monoo	FMO GS-O	AT1G62560	-2.63	-1.40	-6.60	0.00035969	0.0472	0.73
259962_at	RNA polymerase II, putative simila	---	AT1G53690	1.77	0.82	6.55	0.0003754	0.0472	0.69
251018_at	60S ribosomal protein - like 60S ri	---	AT5G02450	2.13	1.09	6.54	0.0003799	0.0474	0.67
262592_at	unknown protein ESTs gb|H37295	---	AT1G15400	2.10	1.07	6.52	0.00038612	0.0477	0.66
254360_at	CDP-diacylglycerol synthetase-lik	---	AT4G22340	-1.65	-0.73	-6.52	0.00038684	0.0477	0.65
253163_at	putative protein E1B 19K/Bcl-2-int	---	AT4G35750	2.12	1.08	6.50	0.0003933	0.0479	0.64
253608_at	xyloglucan endo-1,4-beta-D-gluca	XTH19	AT4G30290	5.55	2.47	6.50	0.00039306	0.0479	0.64
250126_at	ubiquitin C-terminal hydrolase-like	UCH1	AT5G16310	1.85	0.89	6.50	0.00039573	0.0479	0.63
246214_at	heat shock transcription factor HSF	HSF4	AT4G36988 /	-2.04	-1.03	-6.49	0.00039648	0.0479	0.63
264239_at	hypothetical protein predicted by g	---	AT1G54770	1.56	0.64	6.45	0.00041229	0.0495	0.59
258395_at	putative jasmonic acid regulatory p	ANAC055	AT3G15500	2.57	1.36	6.43	0.00041951	0.0497	0.57
259942_at	unknown protein	ATWHY2	AT1G71260	1.48	0.57	6.44	0.00041757	0.0497	0.58
245886_at	ribosomal protein S15-like riboson	---	AT5G09510	1.53	0.61	6.42	0.00042278	0.0497	0.56
247600_at	Myb transcription factor homolog (	MYB34	AT5G60890	-3.87	-1.95	-6.43	0.00042164	0.0497	0.57
248060_at	putative protein contains similarity	---	AT5G55560	1.67	0.74	6.37	0.0004421	0.0507	0.52
265057_at	unknown protein ;supported by full	---	AT1G52140	-1.72	-0.78	-6.38	0.00044007	0.0507	0.52
248219_at	unknown protein ; supported by fu	---	AT5G53650	1.46	0.55	6.39	0.00043699	0.0507	0.53
249235_at	beta-1,3-glucanase-like protein ;s	BG_PPAP	AT5G42100	1.46	0.55	6.38	0.00044099	0.0507	0.52
254134_at	argininosuccinate synthase -like p	---	AT4G24830	-2.56	-1.36	-6.39	0.0004364	0.0507	0.53
265053_at	myrosinase binding protein, putati	---	AT1G52000	-2.74	-1.46	-6.36	0.00044646	0.0509	0.51
262616_at	oxidoreductase, putative contains	---	AT1G06620	-2.75	-1.46	-6.35	0.00045381	0.0515	0.49
262373_at	hypothetical protein predicted by g	---	AT1G73120	3.12	1.64	6.34	0.00045605	0.0515	0.49
245392_at	glutaredoxin ;supported by full-leng	---	AT4G15680	6.98	2.80	6.33	0.00045981	0.0517	0.48
249071_at	putative protein similar to unknown	---	AT5G44050	-3.54	-1.82	-6.32	0.00046627	0.0519	0.47
248625_at	3-keto-acyl-CoA thiolase 2 (gb|AA	PKT2	AT5G48880	-2.81	-1.49	-6.32	0.00046598	0.0519	0.47
249971_at	dermal glycoprotein - like dermal g	---	AT5G19110	-2.34	-1.23	-6.26	0.00049046	0.0533	0.41
258059_at	NAM-like protein (No Apical Meris	ATNAC3	AT3G29035	2.22	1.15	6.25	0.00049495	0.0533	0.41
265724_at	hypothetical protein predicted by g	OFP16	AT2G32100	-2.16	-1.11	-6.27	0.00048547	0.0533	0.42

247208_at	nodulin-like ;supported by full-leng	---	AT5G64870	-1.74	-0.80	-6.27	0.00048833	0.0533	0.42
253220_s_at	putative protein phospholipase C,	---	AT4G34920	-2.01	-1.01	-6.28	0.00048253	0.0533	0.43
257960_at	S-adenosylmethionine decarboxyl	---	AT3G25570	-1.53	-0.61	-6.26	0.00048993	0.0533	0.42
258807_at	transfactor-like similar to transfacto	---	AT3G04030	-2.35	-1.23	-6.26	0.00049391	0.0533	0.41
261112_at	unknown protein	---	AT1G75420	1.78	0.83	6.20	0.00052003	0.0547	0.35
253703_at	putative protein origin recognition	ORC5	AT4G29910	1.71	0.77	6.21	0.00051714	0.0547	0.36
267013_at	putative protein kinase contains a	CCR2	AT2G39180	-1.66	-0.74	-6.21	0.00051777	0.0547	0.36
264523_at	unknown protein Location of EST g	ERG28	AT1G10030	1.55	0.64	6.21	0.00051773	0.0547	0.36
251964_at	hypothetical protein ; supported by	---	AT3G53370	-2.23	-1.16	-6.22	0.00051208	0.0547	0.37
267177_at	Expressed protein ; supported by f	---	AT2G37580	-2.29	-1.20	-6.16	0.00053861	0.0563	0.32
251834_at	ribosomal protein L35 -like various	---	AT3G55170	1.60	0.68	6.16	0.00054032	0.0563	0.32
247776_at	phosphoinositide-specific phospho	PLC4	AT5G58700	-1.86	-0.90	-6.15	0.0005474	0.0565	0.30
266170_at	unknown protein ;supported by ful	---	AT2G39050	-2.48	-1.31	-6.15	0.00054727	0.0565	0.30
256062_at	unknown protein ;supported by full	LSH6	AT1G07090	-1.54	-0.63	-6.11	0.00056765	0.0571	0.27
267519_at	putative VP1/ABI3 family regulator	HSI2	AT2G30470	-1.99	-0.99	-6.12	0.00056017	0.0571	0.28
267079_at	hypothetical protein predicted by g	---	AT2G41200	1.52	0.61	6.11	0.00056781	0.0571	0.27
251330_at	putative protein putative protein At	---	AT3G61550	2.02	1.02	6.12	0.00056195	0.0571	0.28
246340_s_at	AtPP -like protein AtPP protein, B	---	AT3G44860	-2.89	-1.53	-6.13	0.00055762	0.0571	0.28
252983_at	cinnamyl-alcohol dehydrogenase E	ELI3-1	AT4G37980	-2.42	-1.28	-6.11	0.00056638	0.0571	0.27
263433_at	putative myo-inositol 1-phosphate	MIPS2	AT2G22240	-2.12	-1.09	-6.09	0.00057597	0.0576	0.25
265253_at	putative peptide/amino acid transp	---	AT2G02020	-1.53	-0.61	-6.08	0.00058209	0.0578	0.24
251172_at	putative protein chloroplast riboso	RRF	AT3G63190	1.57	0.65	6.08	0.00058291	0.0578	0.24
259410_at	hypothetical protein predicted by g	---	AT1G13340	3.50	1.81	6.07	0.00059024	0.0580	0.23
256337_at	unknown protein	---	AT1G72060	4.16	2.06	6.06	0.00059213	0.0580	0.22
262717_s_at	putative cytochrome P450 similar t	CYP79F2	AT1G16400	-2.10	-1.07	-6.07	0.00058818	0.0580	0.23
250603_at	putative protein mature parasite-in	---	AT5G07820	1.67	0.74	6.06	0.0005951	0.0580	0.22
265228_s_at	hypothetical protein	---	AT2G07698	-1.80	-0.85	-6.02	0.00061826	0.0582	0.18
266643_s_at	putative flavonol 3-O-glucosyltrans	---	AT2G29710	-1.88	-0.91	-6.02	0.00061999	0.0582	0.18
252921_at	putative protein DNA damage-indu	EDS5	AT4G39030	-2.94	-1.56	-6.04	0.00060678	0.0582	0.20
267344_at	hypothetical protein predicted by g	---	AT2G44230	-2.98	-1.58	-6.02	0.00061981	0.0582	0.18
263574_at	putative tetracycline transporter pr	---	AT2G16990	-1.53	-0.62	-6.02	0.00061997	0.0582	0.18
253842_at	putative protein putative proteins fr	---	AT4G27860	-4.08	-2.03	-6.03	0.00061107	0.0582	0.19
258977_s_at	putative aspartate kinase similar to	AK3	AT3G02020	-2.14	-1.10	-6.05	0.00060275	0.0582	0.20
260876_at	hypothetical protein contains simila	---	AT1G21460	-2.07	-1.05	-6.02	0.00061869	0.0582	0.18
264227_at	hypothetical protein contains simila	ATREV3	AT1G67500	1.61	0.69	6.03	0.00061158	0.0582	0.19

245325_at	xyloglucan endotransglycosylase-r	XTR7	AT4G14130	10.01	3.32	5.99	0.00063322	0.0585	0.15
247175_at	G protein-coupled receptor-like pro	GCL1	AT5G65280	-3.76	-1.91	-6.00	0.00062983	0.0585	0.16
260605_at	hypothetical protein predicted by g	---	AT2G43780	1.58	0.66	6.00	0.00062689	0.0585	0.16
261428_at	isochorismate synthase, putative s	ICS2	AT1G18870	-2.19	-1.13	-5.99	0.00063385	0.0585	0.15
251768_at	phosphoinositide-specific phospho	---	AT3G55940	-2.45	-1.29	-5.98	0.00063897	0.0587	0.14
250207_at	chalcone synthase (naringenin-cha	TT4	AT5G13930	-4.14	-2.05	-5.98	0.00064056	0.0587	0.14
247360_at	cytochrome P450-like protein ;sup	CYP94B1	AT5G63450	-4.08	-2.03	-5.97	0.00064857	0.0589	0.13
254869_at	protein kinase - like protein KI don	---	AT4G11890	3.03	1.60	5.97	0.00064817	0.0589	0.13
263863_at	3-oxoacyl carrier protein synthase	---	AT2G04540	1.47	0.55	5.95	0.00066273	0.0599	0.11
254389_s_at	putative protein various predicted p	---	AT4G21903 /	-3.22	-1.69	-5.94	0.00066611	0.0599	0.10
267308_at	putative malonyl-CoA:Acyl carrier p	---	AT2G30200	1.74	0.80	5.94	0.00066842	0.0599	0.10
256659_at	unknown protein similar to putative	---	AT3G12020	1.63	0.71	5.94	0.00066996	0.0599	0.10
251959_at	putative protein KIAA0544 protein	---	AT3G53410	1.56	0.64	5.92	0.00068026	0.0604	0.08
264908_at	unknown protein	---	AT2G17440	1.60	0.68	5.92	0.00067915	0.0604	0.08
257338_s_at	NADH dehydrogenase subunit 5 (r	---	AT2G07711 /	-1.95	-0.96	-5.91	0.00068702	0.0606	0.07
248461_s_at	fumarate hydratase ; supported by	FUM1	AT2G47510 /	-1.73	-0.79	-5.91	0.00068955	0.0606	0.07
264693_at	hypothetical protein predicted by g	CLE26	AT1G69970	-1.58	-0.66	-5.90	0.00069106	0.0606	0.06
252529_at	putative protein several oxidases,	---	AT3G46490	-4.06	-2.02	-5.89	0.00069907	0.0611	0.05
260733_at	RNA-binding protein, putative sim	---	AT1G17640	1.77	0.83	5.88	0.00070657	0.0612	0.04
245465_at	cellulose synthase like protein	ATCSLA01	AT4G16590	-6.33	-2.66	-5.88	0.00071057	0.0612	0.04
250483_at	alpha-hydroxynitrile lyase-like prot	MES5	AT5G10300	-1.93	-0.95	-5.88	0.00070852	0.0612	0.04
262745_at	lipase, putative contains Pfam pro	---	AT1G28600	-1.82	-0.86	-5.89	0.00070296	0.0612	0.05
262314_at	unknown protein contains similarity	---	AT1G70810	-1.74	-0.80	-5.85	0.000727	0.0618	0.01
257051_at	squamosa promoter binding protei	SPL5	AT3G15270	-4.25	-2.09	-5.86	0.0007247	0.0618	0.02
258245_at	hypothetical protein	---	AT3G29075	-1.60	-0.67	-5.85	0.00072588	0.0618	0.01
265476_at	putative thioredoxin M ; supported	ATHM3	AT2G15570	1.49	0.58	5.85	0.00072917	0.0618	0.01
247508_at	auxin response factor - like protein	ARF2	AT5G62000	-1.97	-0.98	-5.84	0.00073855	0.0622	0.00
249284_at	unknown protein ;supported by ful	---	AT5G41810	-1.65	-0.73	-5.84	0.00073711	0.0622	0.00
257194_at	serine acetyltransferase (Sat-1) id	ATSERAT2	AT3G13110	-1.64	-0.71	-5.83	0.00074673	0.0626	-0.01
248753_at	acyl carrier protein-like	mtACP3	AT5G47630	1.55	0.63	5.81	0.00075524	0.0631	-0.03
264928_at	auxin-induced protein, putative sir	ATB2	AT1G60710	-1.60	-0.68	-5.81	0.00075741	0.0631	-0.03
261044_at	molybdopterin biosynthesis CNX3	CNX3	AT1G01290	1.65	0.72	5.81	0.0007616	0.0632	-0.04
265722_at	putative chlorophyll a/b binding pro	LHCB4.3	AT2G40100	-2.20	-1.14	-5.79	0.00077159	0.0638	-0.05
259347_at	putative GAR1 protein similar to G	---	AT3G03920	1.55	0.63	5.78	0.00077763	0.0638	-0.06
245346_at	putative beta-amylase ;supported b	CT-BMY	AT4G17090	-1.76	-0.81	-5.78	0.00077756	0.0638	-0.06

247933_at	putative protein non-consensus C	---	AT5G56980	-3.37	-1.75	-5.77	0.0007864	0.0643	-0.07
259848_at	leucine-rich receptor-like protein k	---	AT1G72180	-1.78	-0.83	-5.75	0.00080223	0.0647	-0.09
256999_at	hypothetical protein predicted by g	---	AT3G14200	-1.56	-0.65	-5.76	0.00079838	0.0647	-0.08
266570_at	putative chloroplast ribosomal prot	---	AT2G24090	1.53	0.61	5.75	0.00080158	0.0647	-0.09
245002_at	PSII D2 protein	---	---	-1.77	-0.83	-5.76	0.00079379	0.0647	-0.08
261150_at	floral nectary-specific protein, puta	JMT	AT1G19640	-5.14	-2.36	-5.74	0.00081072	0.0649	-0.10
245730_at	unknown protein ;supported by full	---	AT1G73470	-1.53	-0.61	-5.75	0.00080788	0.0649	-0.10
266590_at	hypothetical protein predicted by g	BAG6	AT2G46240	-2.21	-1.14	-5.74	0.00081313	0.0649	-0.10
266977_at	putative phospholipase	---	AT2G39420	-3.13	-1.65	-5.73	0.00081897	0.0651	-0.11
265776_at	hypothetical protein predicted by g	---	AT2G07340	1.49	0.58	5.71	0.00083309	0.0655	-0.13
262600_at	unknown protein ESTs gb|H37032	MBD10	AT1G15340	1.92	0.94	5.72	0.00083171	0.0655	-0.13
253534_at	cytochrome P450 monooxygenase	CYP83B1	AT4G31500	-2.94	-1.55	-5.72	0.0008291	0.0655	-0.12
254269_at	putative serine/threonine kinase M	---	AT4G23050	-1.73	-0.79	-5.71	0.00083752	0.0656	-0.13
253203_at	arginine decarboxylase SPE2 ; su	ADC2	AT4G34710	-3.63	-1.86	-5.69	0.00085079	0.0658	-0.15
259846_at	peptide transporter PTR2-B, putat	---	AT1G72140	-1.66	-0.73	-5.69	0.0008511	0.0658	-0.15
266320_at	hypothetical protein predicted by g	---	AT2G46640	-2.16	-1.11	-5.70	0.00084836	0.0658	-0.15
248285_at	putative protein similar to unknown	---	AT5G52960	1.41	0.50	5.70	0.00084641	0.0658	-0.14
247447_at	nitrate transporter NTL1 - like prot	---	AT5G62730	3.05	1.61	5.68	0.00086118	0.0664	-0.16
253708_at	gamma-glutamyltransferase-like p	GGT4	AT4G29210	-2.79	-1.48	-5.68	0.00086526	0.0665	-0.17
251141_at	Expressed protein ; supported by f	---	AT5G01075	-2.36	-1.24	-5.67	0.00087262	0.0666	-0.17
254620_at	pollen-specific protein - like 18.3K	---	AT4G18590	1.60	0.68	5.67	0.00087221	0.0666	-0.17
259430_at	hypothetical protein similar to unkn	GPAT4	AT1G01610	2.02	1.01	5.66	0.00087724	0.0667	-0.18
248232_at	putative protein contains similarity	MLO11	AT5G53760	-1.77	-0.82	-5.65	0.00088735	0.0672	-0.19
253562_at	putative protein ;supported by full-	---	AT4G31130	1.44	0.53	5.63	0.00090274	0.0677	-0.21
267211_at	Expressed protein ; supported by f	---	AT2G44065	1.44	0.53	5.64	0.00090144	0.0677	-0.21
267515_at	putative PCF2-like DNA binding pr	---	AT2G45680	-1.73	-0.79	-5.64	0.00090211	0.0677	-0.21
264515_at	hypothetical protein similar to hypo	---	AT1G10090	-1.40	-0.49	-5.61	0.00092542	0.0691	-0.24
255788_at	auxin regulated protein (IAA13) GE	IAA13	AT2G33310	1.85	0.89	5.61	0.00092734	0.0691	-0.24
252680_at	putative protein predicted protein,	---	AT3G44330	1.43	0.52	5.60	0.00093047	0.0691	-0.24
264951_at	unknown protein contains similarity	---	AT1G76970	1.43	0.52	5.60	0.00093948	0.0696	-0.25
266488_at	putative pectinesterase ; supporte	---	AT2G47670	-2.01	-1.00	-5.58	0.00095088	0.0697	-0.26
253802_at	putative protein	---	AT4G28180	1.55	0.63	5.58	0.00094959	0.0697	-0.26
261957_at	methionine/cystathionine gamma	ATMGL	AT1G64660	-2.56	-1.36	-5.59	0.0009458	0.0697	-0.26
248467_at	MtN3-like protein ;supported by ful	---	AT5G50800	-3.36	-1.75	-5.58	0.00095733	0.0700	-0.27
267200_at	hypothetical protein predicted by g	---	AT2G31010	-1.68	-0.75	-5.57	0.00096061	0.0700	-0.27

249383_at	putative protein putative DNA-bind	PRE1	AT5G39860	-2.21	-1.14	-5.56	0.00097684	0.0703	-0.29
258426_at	hypothetical protein predicted by g	PLDP1	AT3G16785	-1.54	-0.63	-5.55	0.00097953	0.0703	-0.29
263502_s_at	hypothetical protein	---	AT2G07675	-2.05	-1.03	-5.56	0.00097162	0.0703	-0.29
249790_at	putative protein similar to unknown	---	AT5G24290	-6.15	-2.62	-5.56	0.00097491	0.0703	-0.29
259996_at	hypothetical protein predicted by g	---	AT1G67910	1.80	0.85	5.57	0.00096862	0.0703	-0.28
248798_at	putative protein contains similarity	---	AT5G47190	1.59	0.67	5.55	0.00098354	0.0703	-0.30
258851_at	glutathione S-transferase identical	ATGSTF11	AT3G03190	-2.81	-1.49	-5.54	0.00099247	0.0707	-0.31
266089_at	hypothetical protein predicted by g	---	AT2G38010	-2.42	-1.28	-5.53	0.001002	0.0711	-0.32
246003_at	chloroplast Cpn21 protein ; suppo	CPN20	AT5G20720	1.63	0.71	5.53	0.00100409	0.0711	-0.32
250489_s_at	putative protein predicted proteins	---	AT5G09710 /	1.67	0.74	5.52	0.00101091	0.0714	-0.33
247982_at	serine O-acetyltransferase (EC 2.3	ATSERAT1	AT5G56760	-1.59	-0.67	-5.50	0.00103872	0.0716	-0.35
248362_at	fibrillarin 1 (AtFib1) identical to fibri	FIB1	AT5G52470	1.52	0.60	5.51	0.0010225	0.0716	-0.34
245244_at	IAA-amino acid hydrolase, putativ	ILL6	AT1G44350	-1.98	-0.99	-5.50	0.00103836	0.0716	-0.35
252058_at	putative protein hin1 protein -Nico	---	AT3G52470	-2.06	-1.04	-5.50	0.00103862	0.0716	-0.35
267545_at	unknown protein	GRP23	AT2G32690	-1.88	-0.91	-5.51	0.00102958	0.0716	-0.35
247498_at	peroxisomal Ca-dependent solute	---	AT5G61810	-1.77	-0.82	-5.50	0.00103657	0.0716	-0.35
252250_at	putative protein predicted protein,	---	AT3G49790	2.01	1.01	5.51	0.00102456	0.0716	-0.34
252367_at	putative protein MEL-26, Caenorh	BT2	AT3G48360	4.26	2.09	5.51	0.00102121	0.0716	-0.34
257530_at	unknown protein	---	AT3G03040	1.51	0.60	5.49	0.00104886	0.0718	-0.36
265663_at	unknown protein predicted by gens	---	AT2G24290	1.64	0.71	5.49	0.00105129	0.0718	-0.37
253170_at	putative protein various predicted	---	AT4G35130	-1.44	-0.53	-5.49	0.00104539	0.0718	-0.36
249997_at	chromatin remodelling complex A	CHR17	AT5G18620	1.63	0.71	5.48	0.00105935	0.0719	-0.37
251859_at	putative protein proteophosphogly	---	AT3G54680	1.59	0.67	5.48	0.00105718	0.0719	-0.37
261292_at	hypothetical protein predicted by g	---	AT1G36940	-1.67	-0.74	-5.47	0.00106947	0.0724	-0.38
260360_at	chorismate mutase, putative conta	CM3	AT1G69370	-1.84	-0.88	-5.46	0.00107501	0.0724	-0.39
256509_at	NADPH oxidoreductase, putative	---	AT1G75300	-2.25	-1.17	-5.46	0.00107527	0.0724	-0.39
249727_at	putative protein similar to unknown	MRU1	AT5G35490	-1.47	-0.56	-5.46	0.00108064	0.0725	-0.39
263449_at	unknown protein	AtRABA5d	AT2G31670 /	-1.50	-0.59	-5.45	0.00109166	0.0728	-0.41
260843_at	unknown protein similar to hypothe	---	AT1G29060	1.40	0.48	5.45	0.0010943	0.0728	-0.41
247374_at	topoisomerase-like protein ;suppo	---	AT5G63190	1.96	0.97	5.45	0.00108867	0.0728	-0.40
259364_at	DNA-binding protein RAV1 identica	RAV1	AT1G13260	1.66	0.73	5.44	0.0010999	0.0729	-0.41
254126_at	RNA-binding protein RNP-T precu	RBP31	AT4G24770	1.58	0.66	5.43	0.00110712	0.0732	-0.42
249035_at	putative protein contains similarity	GLK2	AT5G44190	-1.67	-0.74	-5.43	0.00111191	0.0732	-0.42
248291_at	putative protein similar to unknown	---	AT5G53020	-1.57	-0.65	-5.43	0.00111375	0.0732	-0.43
255437_at	putative oxidoreductase similar to	AOP2	AT4G03060	-3.63	-1.86	-5.41	0.00113304	0.0735	-0.44

249839_at	Expressed protein ; supported by c	---	AT5G23405	1.62	0.69	5.41	0.00113347	0.0735	-0.44
251309_at	putative protein carbonyl reductas	---	AT3G61220	-1.66	-0.73	-5.41	0.00113682	0.0735	-0.45
251634_at	putative protein putative zinc finge	---	AT3G57480	1.57	0.65	5.41	0.00113174	0.0735	-0.44
259275_at	unknown protin ;supported by full-	---	AT3G01060	-2.15	-1.10	-5.42	0.00112711	0.0735	-0.44
253122_at	hypothetical protein	---	AT4G35987	1.58	0.66	5.41	0.001138	0.0735	-0.45
266168_at	putative protease inhibitor ;suppor	---	AT2G38870	3.80	1.93	5.36	0.00119092	0.0739	-0.50
266418_at	putative annexin ;supported by ful	ANNAT4	AT2G38750	-3.62	-1.86	-5.38	0.00117466	0.0739	-0.48
253281_at	predicted protein	UGT73B1	AT4G34138	2.56	1.36	5.36	0.0012003	0.0739	-0.50
266108_at	putative peptide/amino acid transp	---	AT2G37900	-1.67	-0.74	-5.37	0.00118785	0.0739	-0.49
264107_s_at	putative receptor-like protein kinas	SERK5	AT2G13790	-1.60	-0.68	-5.39	0.00116291	0.0739	-0.47
261826_at	pectin methylesterase, putative si	PMEPCRA	AT1G11580	-2.60	-1.38	-5.39	0.0011592	0.0739	-0.47
264052_at	putative cytochrome P450	CYP79B3	AT2G22330	-2.36	-1.24	-5.37	0.0011791	0.0739	-0.48
266661_at	TINY-like AP2 domain transcriptior	---	AT2G25820	-1.65	-0.72	-5.35	0.00120524	0.0739	-0.51
267088_at	30S ribosomal protein S31 ;suppo	PSRP4	AT2G38140	1.74	0.80	5.40	0.00115266	0.0739	-0.46
264071_at	putative carboxypeptidase ; suppo	SCPL51	AT2G27920	2.17	1.12	5.39	0.00115404	0.0739	-0.46
258796_at	unknown protein ;supported by ful	WDL1	AT3G04630	2.61	1.39	5.37	0.00118027	0.0739	-0.49
254376_at	putative protein ; supported by cD	TOM1	AT4G21790	-1.40	-0.49	-5.35	0.00120538	0.0739	-0.51
245769_at	hypothetical protein similar to puta	INT2	AT1G30220	-1.46	-0.54	-5.37	0.00118833	0.0739	-0.49
249801_at	calcium-dependent protein kinase	CDPK9	AT5G23580	-1.55	-0.63	-5.37	0.00118923	0.0739	-0.49
251524_at	3-isopropylmalate dehydratase-lik	---	AT3G58980	-2.59	-1.37	-5.35	0.00120431	0.0739	-0.51
260818_at	unknown protein	---	AT1G06890	1.40	0.48	5.35	0.00120715	0.0739	-0.51
258917_at	unknown protein C-terminal portior	---	AT3G10630	1.38	0.47	5.35	0.00120859	0.0739	-0.51
254612_at	putative protein hypothetical prote	---	AT4G19100	1.42	0.51	5.37	0.0011802	0.0739	-0.49
263780_at	hypothetical protein predicted by g	SPA1	AT2G46340	-2.17	-1.12	-5.37	0.00118717	0.0739	-0.49
255778_at	3-phosphoserine phosphatase ider	PSP	AT1G18640	1.42	0.50	5.36	0.00120127	0.0739	-0.50
252986_at	putative protein T19C21.18 Arabic	---	AT4G38380	-1.38	-0.47	-5.34	0.00122273	0.0742	-0.52
249817_at	putative protein similar to unknowr	---	AT5G23820	-9.47	-3.24	-5.34	0.00121804	0.0742	-0.52
259277_at	putative glycogen synthase similar	AtSS2	AT3G01180	-1.92	-0.94	-5.34	0.00122323	0.0742	-0.52
250960_at	putative protein	---	AT5G02940	-2.23	-1.16	-5.32	0.00125125	0.0745	-0.55
261187_at	beta-1,3-glucanase precursor, put	---	AT1G32860	-2.07	-1.05	-5.32	0.00124507	0.0745	-0.54
253629_at	glycine-rich protein glycine-rich ce	---	AT4G30450	-1.68	-0.75	-5.33	0.00123931	0.0745	-0.54
246602_at	copper amine oxidase, putative si	---	AT1G31710	-2.28	-1.19	-5.32	0.00124781	0.0745	-0.54
261305_at	glutamine synthetase, putative sin	GLN1;5	AT1G48470	1.42	0.50	5.32	0.00124961	0.0745	-0.54
253021_at	putative protein permease 1 - Mes	---	AT4G38050	1.60	0.68	5.33	0.00124071	0.0745	-0.54
253731_at	acid phosphatase-like protein aci	---	AT4G29260	1.43	0.52	5.32	0.00124654	0.0745	-0.54

245592_at	CCAAT-binding transcription factor	NF-YB3	AT4G14540	1.81	0.85	5.30	0.00126801	0.0748	-0.56
259381_s_at	putative lectin contains Pfam profi	NSP1	AT3G16390	-5.90	-2.56	-5.31	0.00126757	0.0748	-0.56
258713_at	Expressed protein ; supported by f	---	AT3G09735	1.47	0.56	5.30	0.00126865	0.0748	-0.56
261795_at	unknown protein ; supported by cD	---	AT1G16010	-1.44	-0.52	-5.31	0.00126761	0.0748	-0.56
246524_at	Carboxylesterase-like protein ster	ATPCME	AT5G15860	1.87	0.90	5.30	0.00127457	0.0749	-0.57
251850_at	F-box protein family, AtFBL17 cor	FBL17	AT3G54650	1.85	0.89	5.30	0.00127649	0.0749	-0.57
251031_at	one helix protein (OHP) ;supporte	OHP	AT5G02120	1.61	0.69	5.29	0.00128665	0.0749	-0.58
255812_at	potassium uptake transporter - like	HKT1	AT4G10310	2.13	1.09	5.29	0.00128592	0.0749	-0.57
262113_at	late embryogenis abundant protei	---	AT1G02820	-2.43	-1.28	-5.29	0.0012841	0.0749	-0.57
258299_at	unknown protein contains GMC ox	---	AT3G23410	-1.84	-0.88	-5.28	0.00129837	0.0754	-0.58
251256_at	putative protein hypothetical protei	---	AT3G62300	1.70	0.77	5.28	0.0013038	0.0754	-0.59
258259_s_at	unknown protein ; supported by cD	---	AT3G26820	-1.55	-0.63	-5.28	0.00130796	0.0754	-0.59
262400_at	unknown protein ; supported by cD	RTV1	AT1G49480	1.40	0.49	5.27	0.0013109	0.0754	-0.59
263714_at	putative tyrosine aminotransferase	SUR1	AT2G20610	-2.25	-1.17	-5.27	0.00131291	0.0754	-0.60
263320_at	putative galactinol synthase ;supp	AtGolS1	AT2G47180	-3.92	-1.97	-5.26	0.00133269	0.0763	-0.61
248597_at	DNA (cytosine-5)-methyltransferas	MET1	AT5G49160	2.61	1.38	5.26	0.0013352	0.0763	-0.61
262237_at	hypothetical protein predicted by g	---	AT1G48320	2.19	1.13	5.24	0.00135813	0.0774	-0.63
247800_at	Expressed protein ; supported by f	---	AT5G58570	5.35	2.42	5.23	0.00136633	0.0775	-0.64
248793_at	mutT domain protein-like ;support	atnudt8	AT5G47240	-2.68	-1.42	-5.24	0.00136357	0.0775	-0.64
256991_at	unknown protein	---	AT3G28600	-1.43	-0.52	-5.22	0.00137994	0.0776	-0.65
255742_at	DNA-binding protein RAV2, putati	TEM1	AT1G25560	1.47	0.55	5.22	0.00138289	0.0776	-0.65
261922_at	amp-binding protein, putative simi	AAE12	AT1G65890	-1.78	-0.83	-5.22	0.00138477	0.0776	-0.65
253619_at	glycine-rich protein glycine-rich ce	---	AT4G30460	-1.83	-0.87	-5.22	0.00138579	0.0776	-0.65
253028_at	putative protein	pde191	AT4G38160	1.51	0.60	5.23	0.0013784	0.0776	-0.65
262412_at	14-3-3 protein GF14omicron (grf11	GRF11	AT1G34760	1.64	0.71	5.22	0.00138823	0.0776	-0.65
246283_at	putative protein	---	AT4G36860	-1.64	-0.72	-5.21	0.00139571	0.0778	-0.66
262756_at	putative transport protein may be a	אוק-06	AT1G16370	-4.38	-2.13	-5.21	0.00140904	0.0782	-0.67
262273_at	hypothetical protein predicted by g	---	AT1G68730	-1.44	-0.53	-5.21	0.00140689	0.0782	-0.67
251544_at	putative protein general stress pro	GAUT15	AT3G58790	-1.86	-0.89	-5.19	0.00142733	0.0789	-0.68
264960_at	hypothetical protein contains simila	ATEXT4	AT1G76930	7.42	2.89	5.19	0.00143895	0.0789	-0.69
259154_at	unknown protein similar to unknow	---	AT3G10260	-1.50	-0.59	-5.19	0.00143196	0.0789	-0.69
250823_at	putative protein similar to unknown	---	AT5G05180	1.52	0.60	5.19	0.00143773	0.0789	-0.69
259705_at	GRAB1-like protein similar to GRA	anac032	AT1G77450	-2.03	-1.02	-5.19	0.001432	0.0789	-0.69
261151_at	sec14 cytosolic factor, putative sir	---	AT1G19650	-1.52	-0.61	-5.18	0.00144226	0.0789	-0.69
245026_at	ATPase III subunit	---	---	-1.44	-0.53	-5.17	0.00146132	0.0790	-0.71

249941_at	putative protein similar to unknown	---	AT5G22270	1.74	0.80	5.17	0.00146001	0.0790	-0.71
263679_at	RNA helicase, putative similar to F	---	AT1G59990	1.66	0.73	5.17	0.00145695	0.0790	-0.70
263371_at	unknown protein ;supported by ful	NOP10	AT2G20490	1.69	0.75	5.17	0.00145941	0.0790	-0.71
248491_at	unknown protein ;supported by ful	---	AT5G51010	1.81	0.86	5.17	0.00145999	0.0790	-0.71
266600_at	putative mitogen-activated protein	MPK12	AT2G46070	-1.98	-0.99	-5.17	0.00146809	0.0790	-0.71
261146_at	hypothetical protein predicted by g	---	AT1G19620	-1.75	-0.80	-5.17	0.00146851	0.0790	-0.71
259611_at	GTP-binding protein RAB7D, puta	AtRABG3d	AT1G52280	-1.58	-0.66	-5.16	0.00148057	0.0793	-0.72
248155_at	putative protein 3 (2'), 5'-bisphosp	AHL	AT5G54390	-1.64	-0.72	-5.16	0.00148026	0.0793	-0.72
245905_at	putative protein predicted proteins	---	AT5G11090	1.54	0.62	5.14	0.00151037	0.0800	-0.74
264372_at	lactoylglutathione lyase-like protei	ATGLX1	AT1G11840	-1.88	-0.91	-5.14	0.00150954	0.0800	-0.74
266045_s_at	hypothetical protein	---	AT2G07727	-1.76	-0.81	-5.14	0.0015032	0.0800	-0.74
256622_at	unknown protein	AtHB34	AT3G28920	-1.40	-0.48	-5.14	0.00151054	0.0800	-0.74
258557_at	hypothetical protein similar to rece	---	AT3G05990	-1.48	-0.57	-5.14	0.00151102	0.0800	-0.74
262736_at	lipase, putative contains Pfam pro	---	AT1G28570	-1.47	-0.56	-5.13	0.00152892	0.0804	-0.75
245642_at	Expressed protein ; supported by f	---	AT1G25275	1.40	0.49	5.13	0.0015223	0.0804	-0.75
250129_at	S-adenosylmethionine:2-demethyl	---	AT5G16450	-1.57	-0.65	-5.13	0.00152842	0.0804	-0.75
254415_at	subtilisin-like serine protease conta	ATSBT3.12	AT4G21326	-1.41	-0.49	-5.12	0.00153759	0.0806	-0.76
259782_at	unknown protein	---	AT1G29680	-1.41	-0.49	-5.12	0.00154674	0.0808	-0.77
265021_at	unknown protein ;supported by ful	---	AT1G24610	1.40	0.49	5.12	0.00154807	0.0808	-0.77
257196_at	AMP-binding protein, putative sim	---	AT3G23790	1.69	0.76	5.11	0.00156195	0.0810	-0.78
253480_at	putative protein ENOD16, Medica	---	AT4G31840	1.48	0.56	5.11	0.0015615	0.0810	-0.78
248036_at	nucleolar protein-like	OLI2	AT5G55920	-1.79	-0.84	-5.11	0.00156076	0.0810	-0.78
244902_at	NADH dehydrogenase subunit 4L	---	ATMG00650	-1.58	-0.66	-5.10	0.00157041	0.0812	-0.78
253268_s_at	glucosyltransferase -like protein in	UGT73B2	AT4G34131 /	2.14	1.09	5.10	0.00157869	0.0815	-0.79
267175_s_at	actin 3 identical to GB:U29480;sup	ACT1	AT2G37620 /	-1.79	-0.84	-5.09	0.00159374	0.0821	-0.80
267429_at	putative UDP-galactose-4-epimera	MEE25	AT2G34850	-1.83	-0.87	-5.07	0.00162743	0.0836	-0.82
253996_at	nucleosome assembly protein I-like	NAP1;1	AT4G26110	1.58	0.66	5.06	0.00164223	0.0836	-0.83
261479_at	unknown protein ;supported by full	IQD28	AT1G14380	1.86	0.89	5.06	0.00164072	0.0836	-0.83
267014_at	unknown protein	---	AT2G39170	1.37	0.45	5.06	0.00164046	0.0836	-0.83
264745_at	5'-adenylylphosphosulfate reducta	אפר-02	AT1G62180	-1.99	-0.99	-5.07	0.00163379	0.0836	-0.82
248050_at	unknown protein	---	AT5G56100	2.22	1.15	5.05	0.00166904	0.0844	-0.84
251241_s_at	putative protein hypothetical protei	---	AT3G62460 /	1.75	0.81	5.05	0.00166733	0.0844	-0.84
263374_at	putative heat shock protein ;suppo	---	AT2G20560	-2.29	-1.20	-5.05	0.00166586	0.0844	-0.84
267505_at	putative cytochrome P450 ;suppo	CYP76C1	AT2G45560	-1.59	-0.67	-5.04	0.00168845	0.0851	-0.86
261567_at	Expressed protein ; supported by f	---	AT1G33055	3.08	1.62	5.04	0.00169082	0.0851	-0.86

255479_at	coded for by A. thaliana cDNA T4	SAG21	AT4G02380	5.00	2.32	5.02	0.00172452	0.0864	-0.88
265118_at	beta-fructosidase nearly identical t	---	AT1G62660	-1.97	-0.98	-5.01	0.00173355	0.0864	-0.88
264849_at	putative ribosomal protein S4 cont	---	AT2G17360	1.62	0.70	5.01	0.00173954	0.0864	-0.89
249824_at	putative protein similar to unknown	---	AT5G23380	1.47	0.55	5.01	0.00172975	0.0864	-0.88
254027_at	putative mitochondrial protein Hor	---	AT4G25835	1.90	0.93	5.01	0.00173701	0.0864	-0.89
260144_at	putative ABC transporter similar to	---	AT1G71960	-1.70	-0.77	-5.01	0.00172951	0.0864	-0.88
253974_at	receptor protein kinase - like prote	---	AT4G26540	-2.19	-1.13	-5.00	0.0017617	0.0874	-0.90
258196_at	hypothetical protein predicted by g	---	AT3G13980	-3.36	-1.75	-4.99	0.00176851	0.0875	-0.90
248466_at	putative protein similar to unknown	HVA22E	AT5G50720	-2.04	-1.03	-4.99	0.00177782	0.0875	-0.91
260248_at	heat shock protein 101 (HSP101) i	ATHSP101	AT1G74310	-2.25	-1.17	-4.99	0.00178086	0.0875	-0.91
262630_at	unknown protein ;supported by full	GPAT1	AT1G06520	4.27	2.10	4.99	0.0017783	0.0875	-0.91
258483_at	putative mannose-6-phosphate iso	MEE31	AT3G02570	-1.84	-0.88	-4.97	0.00180686	0.0878	-0.93
256787_at	beta-fructofuranosidase 1 identical	ATBFRUCT	AT3G13790	2.19	1.13	4.98	0.00179134	0.0878	-0.92
251191_at	putative protein putative protein F	---	AT3G62590	2.20	1.14	4.98	0.00179954	0.0878	-0.92
245712_at	pullulanase-like protein (starch deb	ATLDA	AT5G04360	-1.45	-0.53	-4.97	0.0018095	0.0878	-0.93
250470_at	(3R)-hydroxymyristoyl-[acyl carrie	---	AT5G10160	1.64	0.71	4.98	0.001802	0.0878	-0.92
251722_at	putative protein neuronal glutamin	---	AT3G56200	-2.09	-1.06	-4.98	0.00180253	0.0878	-0.92
267337_at	putative anthocyanin 5-aromatic ac	---	AT2G39980	1.84	0.88	4.95	0.00185451	0.0898	-0.95
256860_at	hypothetical protein similar to acet	---	AT3G23840	-1.50	-0.59	-4.95	0.00185927	0.0899	-0.96
249115_at	PINHEAD (gb|AAD40098.1); trans	ZLL	AT5G43810	1.39	0.48	4.94	0.00187729	0.0900	-0.97
266271_at	putative glutathione S-transferase	ATGSTU6	AT2G29440	-3.90	-1.96	-4.94	0.00187549	0.0900	-0.97
251023_at	putative protein amino acid transp	---	AT5G02170	1.56	0.64	4.94	0.00187058	0.0900	-0.96
264007_at	putative proline-rich protein	ATPRP2	AT2G21140	10.32	3.37	4.94	0.00187881	0.0900	-0.97
252562_s_at	Histone H4 - like protein histone H	---	AT3G45930 /	1.50	0.58	4.94	0.00188301	0.0900	-0.97
256789_at	seven in absentia-like protein simil	---	AT3G13672	2.30	1.20	4.93	0.00189554	0.0904	-0.98
253237_at	putative aldehyde dehydrogenase	ALDH3I1	AT4G34240	-1.89	-0.92	-4.93	0.00189787	0.0904	-0.98
251036_at	putative protein ; supported by cD	---	AT5G02160	1.55	0.63	4.93	0.00190226	0.0904	-0.98
257203_at	xyloglucan endotransglycosylase,	---	AT3G23730	1.43	0.52	4.92	0.00192006	0.0911	-0.99
258663_at	hypothetical protein	---	AT3G08670	-1.41	-0.49	-4.91	0.00193433	0.0913	-1.00
258209_at	expressed protein supported by cD	GAPC1	AT3G04120 /	2.57	1.36	4.91	0.00193272	0.0913	-1.00
256274_at	GTPase, putative contains Pfam p	emb2738	AT3G12080	1.43	0.51	4.91	0.0019501	0.0919	-1.01
254687_at	cytochrome P450 monooxygenase	CYP83A1	AT4G13770 /	-1.80	-0.85	-4.90	0.00196306	0.0923	-1.01
259578_at	unknown protein	---	AT1G27990	1.86	0.90	4.89	0.00197574	0.0927	-1.02
266400_at	methylenetetrahydrofolate dehydro	---	AT2G38660	-1.38	-0.47	-4.88	0.00199843	0.0936	-1.03
254066_at	transcriptional activator CBF1-like	DREB1A	AT4G25480	-3.04	-1.61	-4.88	0.00201395	0.0938	-1.04

260361_at	unknown protein ; supported by cD	---	AT1G69360	-1.71	-0.78	-4.88	0.00201344	0.0938	-1.04
247835_at	putative protein similar to unknown	---	AT5G57910	2.18	1.12	4.88	0.00200651	0.0938	-1.04
253344_at	putative protein predicted protein,	---	AT4G33550	-2.15	-1.11	-4.87	0.00202616	0.0939	-1.05
260041_at	unknown protein similar to hypothe	---	AT1G68780	1.56	0.64	4.87	0.00202636	0.0939	-1.05
258275_at	unknown protein ;supported by ful	---	AT3G15760	1.98	0.98	4.87	0.00203111	0.0940	-1.05
265356_at	putative TRAP protein	---	AT2G16595	1.66	0.73	4.86	0.00204881	0.0946	-1.06
267112_at	putative adenosine phosphosulfate	APK	AT2G14750	-2.33	-1.22	-4.86	0.00205189	0.0946	-1.06
247072_at	putative protein similar to unknown	---	AT5G66490	1.82	0.86	4.84	0.00208931	0.0948	-1.08
261951_at	hypothetical protein predicted by g	---	AT1G64490	1.48	0.57	4.85	0.00208107	0.0948	-1.07
259081_at	putative sodium proton exchanger	NHX2	AT3G05030	-1.61	-0.69	-4.85	0.00208354	0.0948	-1.07
252693_s_at	ribosomal protein S29 - like riboso	---	AT3G43980 /	1.44	0.52	4.84	0.00209036	0.0948	-1.08
265984_at	putative limonene cyclase	TPS10	AT2G24210	-1.44	-0.52	-4.84	0.00209108	0.0948	-1.08
245266_at	hypothetical protein ; supported by	---	AT4G17070	1.95	0.96	4.84	0.00208671	0.0948	-1.08
255458_at	small nuclear riboprotein Sm-D1-li	---	AT4G02840	1.40	0.49	4.84	0.00208864	0.0948	-1.08
245628_at	anthocyanin2, putative similar to a	PAP1	AT1G56650	-1.85	-0.88	-4.84	0.0020884	0.0948	-1.08
260961_at	unknown protein similar to hypothe	---	AT1G05960	-1.37	-0.46	-4.84	0.00210834	0.0954	-1.09
249783_at	calcium sensor homolog (gb|AAC2	SOS3	AT5G24270	2.25	1.17	4.83	0.00212339	0.0957	-1.09
249975_s_at	ribosomal protein L33 - like riboso	---	AT3G06320 /	1.98	0.99	4.83	0.00213037	0.0957	-1.10
266371_at	calmodulin-like protein identical to	---	AT2G41410	2.23	1.16	4.83	0.00212908	0.0957	-1.10
254075_at	DRE CRT-binding protein DREB1(	CBF2	AT4G25470	-1.94	-0.96	-4.83	0.00212394	0.0957	-1.09
265067_at	hypothetical protein predicted by g	---	AT1G03850	3.48	1.80	4.82	0.00214517	0.0960	-1.11
246954_at	unknown protein ; supported by cI	---	AT5G04830	-1.39	-0.48	-4.82	0.00214663	0.0960	-1.11
263664_at	putative auxin-induced protein, IA	AXR3	AT1G04250	-2.80	-1.49	-4.81	0.00217064	0.0965	-1.12
256401_at	putative guanylate kinase similar to	---	AT3G06200	1.34	0.42	4.81	0.00217093	0.0965	-1.12
264712_at	unknown protein	ECT11	AT1G09810	1.69	0.76	4.81	0.00216574	0.0965	-1.12
252945_at	putative protein ;supported by full-	---	AT4G39140	1.55	0.63	4.79	0.00222327	0.0973	-1.14
261135_at	defensin AMP1, putative similar to	PDF1.4	AT1G19610	5.75	2.52	4.80	0.00220046	0.0973	-1.13
248878_at	50S ribosomal protein L14	---	AT5G46160	1.43	0.52	4.79	0.00222174	0.0973	-1.14
246188_at	putative protein	---	AT5G21050	-1.37	-0.45	-4.79	0.00222081	0.0973	-1.14
247210_at	annexin ;supported by full-length c	ANNAT2	AT5G65020	-2.21	-1.14	-4.79	0.00220666	0.0973	-1.13
245946_at	putative protein glyoxal oxidase pr	---	AT5G19580	-1.63	-0.70	-4.80	0.00219551	0.0973	-1.13
255277_at	putative homeotic protein ; suppor	PDF2	AT4G04890	1.68	0.75	4.79	0.0022185	0.0973	-1.14
261379_at	unknown protein similar to YGL01(	---	AT1G18720	-1.40	-0.48	-4.79	0.00221047	0.0973	-1.14
253493_at	putative protein various predicted p	ENP	AT4G31820	-1.93	-0.95	-4.76	0.00228149	0.0985	-1.17
267033_at	unknown protein ;supported by ful	---	AT2G38450	1.35	0.44	4.77	0.00227448	0.0985	-1.17

246076_at	sucrose-phosphate synthase-like	ATSPS1F	AT5G20280	1.49	0.57	4.76	0.00228699	0.0985	-1.17
260969_at	beta-fructosidase identical to beta-	ATBETAFR	AT1G12240	-2.41	-1.27	-4.77	0.00225824	0.0985	-1.16
245338_at	Expressed protein ; supported by f	---	AT4G16442	1.68	0.75	4.77	0.0022551	0.0985	-1.16
256049_at	unknown protein	---	AT1G07010	-1.64	-0.72	-4.76	0.00229254	0.0985	-1.17
266560_at	putative LRR receptor protein kina	---	AT2G23950	-1.59	-0.67	-4.76	0.00228793	0.0985	-1.17
265229_s_at	hypothetical protein	---	AT2G07701	-1.41	-0.50	-4.76	0.00228894	0.0985	-1.17
267410_at	hypothetical protein predicted by g	EDA18	AT2G34920	2.00	1.00	4.77	0.00226245	0.0985	-1.16
258107_at	unknown protein ; supported by cl	ALF5	AT3G23560	-1.46	-0.54	-4.76	0.00228556	0.0985	-1.17
248619_at	amino acid permease 6 (emb CAA	AAP6	AT5G49630	-1.68	-0.75	-4.76	0.00230228	0.0987	-1.18
257007_at	Expressed protein ; supported by c	---	AT3G14205	-1.38	-0.46	-4.75	0.00232011	0.0991	-1.19
254938_at	putative oligopeptide transporter s	OPT7	AT4G10770	-1.43	-0.52	-4.75	0.00231679	0.0991	-1.19
250735_at	putative protein similar to unknowr	---	AT5G06280	1.47	0.55	4.74	0.00233454	0.0994	-1.19
260112_at	unknown protein similar to unknow	---	AT1G63310	1.63	0.71	4.74	0.00233496	0.0994	-1.19
254110_at	putative protein pectinesterase - C	---	AT4G25260	-2.57	-1.36	-4.74	0.00235796	0.1002	-1.20
262811_at	unknown protein ESTs gb|R65381	---	AT1G11700	-1.50	-0.58	-4.73	0.00237529	0.1005	-1.21
260963_at	hypothetical protein predicted by g	---	AT1G44990	-1.45	-0.53	-4.73	0.00238025	0.1005	-1.21
263161_at	myrosinase-associated protein, pu	---	AT1G54020	-33.72	-5.08	-4.73	0.00237592	0.1005	-1.21
264257_at	unknown protein	---	AT1G09230	1.56	0.64	4.72	0.0023919	0.1007	-1.22
253606_at	putative protein component of anil	---	AT4G30530	-2.19	-1.13	-4.72	0.00239347	0.1007	-1.22
265175_at	hypothetical protein similar to puta	ATCSLA03	AT1G23480	-1.88	-0.91	-4.72	0.002402	0.1009	-1.22
247717_at	nonspecific lipid-transfer protein p	LTP3	AT5G59320	2.34	1.23	4.72	0.00240778	0.1010	-1.23
259607_at	P-glycoprotein, putative similar to	PGP13	AT1G27940	1.34	0.43	4.71	0.00242147	0.1013	-1.23
260551_at	putative trypsin inhibitor ; supporte	ATTI1	AT2G43510	2.45	1.30	4.69	0.00248447	0.1014	-1.26
263680_at	unknown protein	---	AT1G26930	1.35	0.43	4.69	0.00246966	0.1014	-1.25
266516_at	putative glutaredoxin ;supported b	---	AT2G47880	2.52	1.33	4.70	0.00244985	0.1014	-1.24
262505_at	unknown protein ESTs gb|N96028	---	AT1G21680	1.53	0.62	4.69	0.0024853	0.1014	-1.26
262618_at	unknown protein	---	AT1G06560	1.36	0.45	4.70	0.00244166	0.1014	-1.24
245486_x_at	glycine-rich protein homolog	---	AT4G16240	-1.45	-0.54	-4.71	0.0024362	0.1014	-1.24
246480_at	TCP-1 chaperonin-like protein t-co	---	AT5G16070	1.66	0.73	4.69	0.00247554	0.1014	-1.25
267435_at	30S ribosomal protein S5 ; suppor	---	AT2G33800	1.39	0.48	4.69	0.00247327	0.1014	-1.25
245003_at	PSII 43 KDa protein	---	---	-1.49	-0.57	-4.69	0.00247569	0.1014	-1.25
262489_at	unknown protein EST gb|T21171 c	---	AT1G21830	1.68	0.75	4.70	0.00246218	0.1014	-1.25
258133_at	ethylene-responsive transcriptiona	MBF1C	AT3G24500	-1.70	-0.76	-4.69	0.00247594	0.1014	-1.25
249025_at	putative protein contains similarity	---	AT5G44720	-2.01	-1.01	-4.71	0.00242885	0.1014	-1.23
265597_at	Expressed protein ; supported by c	---	AT2G20142	3.29	1.72	4.70	0.00245106	0.1014	-1.24

266337_at	putative ligand-gated ion channel s	ATGLR3.5	AT2G32390	-1.42	-0.50	-4.69	0.00248231	0.1014	-1.26
252115_at	non-specific lipid transfer protein ;	LTP5	AT3G51600	1.58	0.66	4.68	0.00250364	0.1019	-1.27
259286_at	hypothetical protein similar to hypo	BSMT1	AT3G11480	-22.81	-4.51	-4.68	0.00251257	0.1019	-1.27
263584_at	NAM (no apical meristem)-like prot	anac036	AT2G17040	3.25	1.70	4.68	0.00251593	0.1019	-1.27
250931_at	putative protein various predicted	---	AT5G03200	-2.78	-1.48	-4.68	0.00251256	0.1019	-1.27
259403_at	unknown protein ; supported by ful	PGDH	AT1G17745	-4.51	-2.17	-4.66	0.00256004	0.1022	-1.29
261931_at	alcohol dehydrogenase ADH, puta	---	AT1G22430	1.38	0.47	4.67	0.00254825	0.1022	-1.28
263482_at	putative GDSL-motif lipase/hydrola	---	AT2G03980	-5.75	-2.52	-4.67	0.00254527	0.1022	-1.28
247541_at	structural protein - like glycine-rich	---	AT5G61660	-1.54	-0.63	-4.67	0.00255116	0.1022	-1.29
251170_at	ATMRK1 ;supported by full-length	ATMRK1	AT3G63260	1.34	0.42	4.66	0.00256339	0.1022	-1.29
264289_at	hypothetical protein similar to hypo	---	AT1G61890	-2.65	-1.41	-4.66	0.00255445	0.1022	-1.29
257644_at	unknown protein ;supported by ful	AOC3	AT3G25780	-4.47	-2.16	-4.66	0.00255529	0.1022	-1.29
248953_at	serine/threonine-protein kinase Ma	---	AT5G45428 /	-1.42	-0.51	-4.67	0.00254066	0.1022	-1.28
266142_at	unknown protein ; supported by cl	---	AT2G39030	-7.38	-2.88	-4.66	0.00255759	0.1022	-1.29
245011_at	photosystem II G protein	---	---	-1.45	-0.54	-4.65	0.00258594	0.1024	-1.30
250589_at	transcription factor (gb|AAD53097.	MYB76	AT5G07700	-2.81	-1.49	-4.65	0.00259006	0.1024	-1.30
253222_at	chalcone synthase - like protein ch	---	AT4G34850	-1.34	-0.43	-4.66	0.00257857	0.1024	-1.30
260674_at	unknown protein ; supported by cD	---	AT1G19370	-1.45	-0.54	-4.65	0.00258956	0.1024	-1.30
248705_at	putative protein similar to unknown	---	AT5G48520	1.63	0.71	4.65	0.00258646	0.1024	-1.30
251072_at	putative protein wound-inducible p	---	AT5G01740	-2.17	-1.12	-4.64	0.00261731	0.1031	-1.31
262488_at	unknown protein EST gb|AA58624	---	AT1G21830	2.08	1.05	4.64	0.00261307	0.1031	-1.31
261252_at	RAS-related protein ARA-1 identic	RABA5E	AT1G05810	1.60	0.68	4.64	0.00263848	0.1033	-1.32
248683_at	putative protein similar to unknown	---	AT5G48490	3.38	1.76	4.63	0.00264414	0.1033	-1.32
266983_at	putative phospholipase ; supporte	---	AT2G39400	1.78	0.83	4.64	0.00263126	0.1033	-1.32
245255_at	COP9 protein ; supported by cDNA	COP9	AT4G14110	1.47	0.55	4.63	0.00264328	0.1033	-1.32
247408_at	ZAP - like protein nuclear protein /	---	AT5G62760	-1.35	-0.44	-4.64	0.00262738	0.1033	-1.32
255695_at	putative protein	UNE11	AT4G00080	-1.39	-0.48	-4.63	0.0026539	0.1035	-1.33
255977_at	ribosomal protein S18, putative sir	---	AT1G34030	1.65	0.72	4.63	0.0026624	0.1036	-1.33
263667_at	putative 40S ribosomal protein S1	RPS15	AT1G04270	1.64	0.71	4.63	0.00266489	0.1036	-1.33
248921_at	GDSL-motif lipase/hydrolase-like p	---	AT5G45950	-2.68	-1.42	-4.62	0.00269218	0.1041	-1.34
257835_at	cytochrome P450 monooxygenas	CYP82G1	AT3G25180	-3.14	-1.65	-4.62	0.00268927	0.1041	-1.34
258712_s_at	putative 40S ribosomal protein S2	---	AT3G09680 /	1.59	0.67	4.62	0.00268869	0.1041	-1.34
259911_at	putative cinnamyl-alcohol dehydro	CAD1	AT1G72680	1.72	0.78	4.61	0.00271127	0.1045	-1.35
253764_s_at	protein kinase - like protein ADK1	ckl4	AT4G28860 /	1.55	0.64	4.61	0.00270894	0.1045	-1.35
248340_at	putative protein similar to unknown	---	AT5G52180	1.44	0.52	4.61	0.00272052	0.1046	-1.35

266482_at	putative small nuclear ribonucleopr	---	AT2G47640	1.60	0.68	4.60	0.00273523	0.1047	-1.36
263216_s_at	putative reticuline oxidase-like pro	---	AT1G30720 /	7.09	2.82	4.61	0.00272807	0.1047	-1.36
257642_at	putative HLH DNA-binding protein	BHLH32	AT3G25710	1.58	0.66	4.60	0.00273586	0.1047	-1.36
259661_at	Expressed protein ; supported by f	---	AT1G55265	1.64	0.72	4.60	0.00276017	0.1049	-1.37
264436_at	putative glutathione S-transferase	ERD9	AT1G10370	-3.97	-1.99	-4.60	0.00275555	0.1049	-1.37
260548_at	biotin synthase (Bio B) ;supported	BIO2	AT2G43360	1.80	0.85	4.60	0.00274864	0.1049	-1.36
262622_at	hypothetical protein predicted by g	---	AT1G06510	1.39	0.47	4.60	0.00275753	0.1049	-1.37
247461_at	putative protein various predicted	ATBAG2	AT5G62100	-1.60	-0.68	-4.59	0.0027973	0.1061	-1.38
265058_s_at	myrosinase-binding protein homol	MBP2	AT1G52030 /	-7.62	-2.93	-4.58	0.00280095	0.1061	-1.38
257056_at	unknown protein similar to hypothe	---	AT3G15350	-1.47	-0.55	-4.58	0.00281147	0.1064	-1.39
262573_at	hypothetical protein Similar to gi|43	PDF1A	AT1G15390	1.53	0.62	4.58	0.00282485	0.1067	-1.39
254833_s_at	copper amine oxidase like protein	---	AT4G12280 /	-1.37	-0.45	-4.57	0.00285602	0.1068	-1.40
263706_s_at	3-methyladenine DNA glycosylase	---	AT1G31180 /	-1.85	-0.89	-4.56	0.00287797	0.1068	-1.41
253358_at	gamma-VPE (vacuolar processing	GAMMA-VP	AT4G32940	1.43	0.51	4.57	0.00285581	0.1068	-1.40
259593_at	nuclear transport factor 2, putative	NTF2B	AT1G27970	1.34	0.43	4.56	0.00288075	0.1068	-1.41
266957_at	unknown protein	PTAC12	AT2G34640	1.54	0.62	4.56	0.00286514	0.1068	-1.41
252081_at	putative heat shock transcription f	HSFA7A	AT3G51910	2.29	1.20	4.56	0.00287879	0.1068	-1.41
246432_at	RGA-like protein putative member	RGL3	AT5G17490	-1.91	-0.93	-4.57	0.00283307	0.1068	-1.39
253762_at	putative protein conserved hypoth	---	AT4G28830	1.45	0.54	4.56	0.00288777	0.1068	-1.41
248690_at	acetyl-CoA C-acetyltransferase ; s	ACAT2	AT5G48230	1.36	0.44	4.56	0.00286632	0.1068	-1.41
245505_at	glutaredoxin	---	AT4G15690	2.67	1.42	4.56	0.00288429	0.1068	-1.41
255154_at	putative protein several hypothetic	---	---	1.35	0.43	4.56	0.00288901	0.1068	-1.41
247486_at	putative protein	---	AT5G62140	-1.76	-0.81	-4.56	0.00287966	0.1068	-1.41
252189_at	cyclin D3-like protein Nicotiana tal	CYCD3;3	AT3G50070	1.76	0.82	4.57	0.0028405	0.1068	-1.40
254418_at	glucose transporter glucose transp	---	AT4G21480	-1.45	-0.54	-4.55	0.00290011	0.1070	-1.42
248387_at	unknown protein	---	AT5G51960	1.53	0.61	4.55	0.00291017	0.1072	-1.42
249467_at	NAM / CUC2 - like protein CUC2,	ATNAC6	AT5G39610	3.31	1.73	4.55	0.00292831	0.1075	-1.43
257022_at	zinc finger protein, putative similar	AZF2	AT3G19580	1.60	0.68	4.54	0.00294449	0.1075	-1.43
260420_at	unknown protein	---	AT1G69610	-1.44	-0.53	-4.54	0.00293819	0.1075	-1.43
258322_at	putative selenocysteine methyltran	HMT3	AT3G22740	-3.14	-1.65	-4.54	0.00293415	0.1075	-1.43
249298_at	putative protein similar to unknown	---	AT5G41330	-1.42	-0.51	-4.54	0.00294367	0.1075	-1.43
259808_at	hypothetical protein contains Pfam	---	AT1G49790	1.35	0.44	4.54	0.00294205	0.1075	-1.43
261852_at	unknown protein ;supported by full	---	AT1G50440	-1.35	-0.43	-4.54	0.00296335	0.1077	-1.44
245354_at	Lil3 protein ;supported by full-lengt	LIL3:1	AT4G17600	1.53	0.61	4.53	0.00296544	0.1077	-1.44
263972_at	unknown protein	---	AT2G42760	-3.38	-1.76	-4.54	0.0029603	0.1077	-1.44

248326_at	Notchless protein homolog	---	AT5G52820	1.60	0.68	4.53	0.00299571	0.1086	-1.45
259489_at	unknown protein	---	AT1G15790	1.93	0.95	4.52	0.00302597	0.1096	-1.46
267174_at	60S ribosomal protein L36 ;suppo	---	AT2G37600	1.92	0.94	4.51	0.00304354	0.1098	-1.47
247853_at	non phototropic hypocotyl 1-like ;	PHOT2	AT5G58140	-1.48	-0.57	-4.51	0.00303878	0.1098	-1.47
253684_at	nucleotide pyrophosphatase - like	---	AT4G29690	-1.50	-0.58	-4.51	0.00305181	0.1100	-1.47
262354_at	H+-transporting ATPase protein, p	VHA-E3	AT1G64200	-2.27	-1.19	-4.50	0.00307741	0.1103	-1.48
258192_at	putative terpene synthase-related	---	AT3G29110	-1.35	-0.43	-4.50	0.00307908	0.1103	-1.48
267180_at	unknown protein ; supported by cl	SLT1	AT2G37570	-1.44	-0.53	-4.50	0.00307325	0.1103	-1.48
251757_at	Ca-dependent solute carrier - like	---	AT3G55640	-1.73	-0.79	-4.51	0.00306888	0.1103	-1.48
263384_at	hypothetical protein predicted by g	---	AT2G40130	-1.50	-0.58	-4.50	0.00309136	0.1104	-1.49
258955_s_at	unknown protein ;supported by ful	---	AT3G01450	1.61	0.68	4.50	0.00309061	0.1104	-1.49
257712_at	hypothetical protein predicted by g	---	AT3G27420	-1.33	-0.41	-4.50	0.0031031	0.1106	-1.49
249933_at	rac GTPase activating protein	---	AT5G22400	-1.38	-0.46	-4.49	0.003116	0.1108	-1.49
266663_at	putative receptor-like protein kinas	---	AT2G25790	1.73	0.79	4.49	0.00311742	0.1108	-1.49
250657_at	steroid sulfotransferase-like protei	ST2B	AT5G07000	-2.14	-1.10	-4.49	0.00312912	0.1110	-1.50
267538_at	putative DNA binding protein ; sup	---	AT2G41870	-1.35	-0.44	-4.49	0.0031339	0.1110	-1.50
262285_at	hypothetical protein predicted by g	---	AT1G68680	1.41	0.49	4.48	0.00314434	0.1112	-1.50
267078_at	unknown protein ;supported by ful	---	AT2G40960	1.43	0.51	4.48	0.00315453	0.1114	-1.51
261851_at	hexokinase, putative similar to chl	HKL1	AT1G50460	-1.99	-0.99	-4.48	0.00316861	0.1117	-1.51
262637_at	oxidoreductase, putative contains	---	AT1G06640	-5.33	-2.41	-4.47	0.00318114	0.1120	-1.52
255582_at	putative DNA-binding protein simil	NGA4	AT4G01500	-1.38	-0.46	-4.47	0.00318787	0.1120	-1.52
264250_at	gamma glutamyl hydrolase, putati	ATGGH2	AT1G78680	-1.50	-0.59	-4.47	0.00319822	0.1122	-1.52
247748_at	putative protein ;supported by full-	---	AT5G58920	1.44	0.52	4.47	0.00320573	0.1123	-1.52
257247_at	helix-loop-helix DNA-binding prote	FMA	AT3G24140	-1.64	-0.71	-4.46	0.00322252	0.1127	-1.53
249850_at	putative protein similar to unknown	---	AT5G23240	-1.35	-0.43	-4.46	0.00323595	0.1129	-1.53
250194_at	putative protein various predicted	---	AT5G14550	1.42	0.51	4.46	0.00323438	0.1129	-1.53
253484_at	Transcription factor II homolog ;su	TAFII15	AT4G31720	1.35	0.43	4.46	0.00325326	0.1133	-1.54
252593_at	putative protein tRNA intron endo	ATSEN1	AT3G45590	1.55	0.63	4.45	0.00327443	0.1139	-1.55
254452_at	UV-damaged DNA-binding protei	DDB1B	AT4G21100	1.58	0.66	4.44	0.00330351	0.1143	-1.55
257288_at	anthocyanin 5-aromatic acyltransf	---	AT3G29670	-1.40	-0.49	-4.44	0.00331558	0.1143	-1.56
246193_at	Expressed protein ; supported by f	---	---	1.41	0.49	4.44	0.00331521	0.1143	-1.56
261761_at	hypothetical protein predicted by g	CENP-C	AT1G15660	1.40	0.48	4.44	0.00332337	0.1143	-1.56
250212_at	putative protein contains similarity	SUVH4	AT5G13960	1.45	0.53	4.44	0.00330646	0.1143	-1.56
262378_at	CCAAT-binding factor B subunit h	NF-YA3	AT1G72830	-1.64	-0.71	-4.44	0.00332258	0.1143	-1.56
248091_at	putative protein strong similarity to	VTC5	AT5G55120	-2.83	-1.50	-4.44	0.0033142	0.1143	-1.56

261578_at	acidic ribosomal protein, putative s	---	AT1G01100	1.59	0.67	4.43	0.00334556	0.1149	-1.57
253696_at	cytokinin oxidase - like protein cyt	CKX4	AT4G29740	-2.42	-1.27	-4.43	0.00335504	0.1151	-1.57
260592_at	cellulose synthase catalytic subun	CSLE1	AT1G55850	1.58	0.66	4.43	0.00336939	0.1152	-1.58
248785_at	unknown protein	---	AT5G47400	1.33	0.41	4.43	0.00336855	0.1152	-1.57
255243_at	putative protein hypothetical prote	---	AT4G05590	1.41	0.49	4.42	0.00337871	0.1154	-1.58
267153_at	glutathione S-transferase identical	ATGSTF9	AT2G30860	-1.64	-0.72	-4.42	0.0033963	0.1158	-1.58
248839_at	putative protein contains similarity	bHLH071	AT5G46690	-2.54	-1.34	-4.41	0.00341941	0.1164	-1.59
267123_at	putative acetone-cyanohydrin lyas	MES7	AT2G23560	-1.91	-0.94	-4.41	0.00344345	0.1171	-1.60
257805_at	sugar transport, putative similar to	ATPLT5	AT3G18830	-2.04	-1.03	-4.41	0.00345026	0.1171	-1.60
246038_s_at	putative protein thiamin pyrophosp	atnudt20	AT5G19460	-1.61	-0.69	-4.40	0.00345644	0.1171	-1.60
253837_at	putative proline-rich protein extens	---	AT4G27850	-1.38	-0.47	-4.40	0.0034815	0.1176	-1.61
264236_at	hypothetical protein predicted by g	---	AT1G54680	1.45	0.54	4.40	0.00348143	0.1176	-1.61
260745_at	2,4-D inducible glutathione S-trans	ATGSTU20	AT1G78370	-2.61	-1.38	-4.40	0.00349093	0.1177	-1.61
260460_at	unknown protein	---	AT1G68230	1.43	0.51	4.39	0.00349464	0.1177	-1.61
264788_at	putative DnaJ protein ;supported b	---	AT2G17880	2.89	1.53	4.39	0.00351106	0.1178	-1.62
247862_at	similar to unknown protein (sp|P72	---	AT5G58250	1.42	0.50	4.39	0.00351151	0.1178	-1.62
261401_at	kinase, putative similar to Ste-20 r	---	AT1G79640	1.58	0.66	4.39	0.00350905	0.1178	-1.62
256229_at	unknown protein	MSL3	AT1G58200	-1.60	-0.68	-4.39	0.00351885	0.1179	-1.62
247731_at	glucuronosyl transferase - like pro	UGT76E2	AT5G59590	-1.41	-0.50	-4.39	0.00352576	0.1179	-1.62
260955_at	unknown protein contains similarity	---	AT1G06000	-2.21	-1.14	-4.39	0.00352892	0.1179	-1.62
247183_at	putative protein strong similarity to	---	AT5G65440	1.37	0.45	4.38	0.00353488	0.1179	-1.63
245025_at	ATPase I subunit	---	---	-1.30	-0.37	-4.38	0.0035478	0.1181	-1.63
266700_at	60S ribosomal protein L31 ; suppo	---	AT2G19740	1.63	0.70	4.38	0.00356285	0.1181	-1.63
255877_at	putative PTR2 family peptide trans	---	AT2G40460	-2.60	-1.38	-4.38	0.00355347	0.1181	-1.63
247001_at	natural resistance-associated mac	NRAMP4	AT5G67330	-1.48	-0.56	-4.38	0.00356011	0.1181	-1.63
247703_at	putative protein predicted proteins	SRR1	AT5G59560	1.47	0.56	4.38	0.00356865	0.1181	-1.64
245377_at	hypothetical protein	---	AT4G17700	-1.42	-0.51	-4.37	0.00360485	0.1186	-1.65
260058_at	unknown protein ; supported by cl	---	AT1G78100	-1.46	-0.55	-4.37	0.00359295	0.1186	-1.64
255623_at	putative L5 ribosomal protein ;sup	---	AT4G01310	1.39	0.47	4.37	0.00359955	0.1186	-1.64
255551_at	putative potassium channel ;suppo	KCO5	AT4G01840	1.34	0.42	4.37	0.00360944	0.1186	-1.65
265232_s_at	hypothetical protein	---	AT2G07715	-1.49	-0.57	-4.37	0.00359831	0.1186	-1.64
260496_at	putative ABC transporter	---	AT2G41700	1.34	0.42	4.36	0.00362885	0.1191	-1.65
257863_at	hypothetical protein similar to GRA	anac057	AT3G17730	-1.32	-0.40	-4.36	0.00363921	0.1193	-1.66
256433_at	unknown protein	SAG20	AT3G10985	1.67	0.74	4.36	0.00364464	0.1193	-1.66
260410_at	putative peptide transporter similar	---	AT1G69870	-2.00	-1.00	-4.36	0.00365678	0.1195	-1.66

266156_at	hypothetical protein predicted by g	FRA8	AT2G28110	3.14	1.65	4.35	0.00366236	0.1195	-1.66
252912_at	ribosomal protein S25 ribosomal p	---	AT4G39200	1.73	0.79	4.35	0.00369902	0.1199	-1.67
245357_at	putative protein ;supported by full-l	---	AT4G17560	1.60	0.67	4.35	0.0036844	0.1199	-1.67
254155_at	putative protein kinase putative pr	---	AT4G24480	-1.49	-0.57	-4.35	0.00368712	0.1199	-1.67
247635_at	serine/threonine-protein kinase - li	GRIK2	AT5G60548 /	-1.34	-0.42	-4.35	0.00369637	0.1199	-1.67
262411_at	hypothetical protein predicted by g	---	AT1G34640	1.45	0.53	4.35	0.00369134	0.1199	-1.67
252942_at	putative protein ;supported by full-	---	AT4G39300	1.49	0.57	4.34	0.00371299	0.1199	-1.68
251066_at	putative protein RING-H2 finger pr	---	AT5G01880	1.78	0.83	4.34	0.00371549	0.1199	-1.68
264840_at	unknown protein similar to leucine-	---	AT1G03440	-1.38	-0.47	-4.34	0.00370599	0.1199	-1.67
267184_at	unknown protein ; supported by cl	ASHH3	AT2G44150	1.38	0.46	4.34	0.00372856	0.1201	-1.68
246301_at	calcium-dependent protein kinase	CPK13	AT3G51850	1.38	0.47	4.33	0.00376198	0.1210	-1.69
252293_at	4-coumarate-CoA ligase -like prot	---	AT3G48990	1.38	0.46	4.33	0.0037822	0.1213	-1.70
255819_s_at	40S ribosomal protein S26	---	AT2G40510 /	1.41	0.49	4.33	0.0037779	0.1213	-1.69
247734_at	putative protein predicted protein,	---	AT5G59400	1.45	0.54	4.32	0.00382077	0.1215	-1.71
258979_at	heat-shock protein (At-hsc70-3) ide	---	AT3G09440	-1.99	-0.99	-4.32	0.00382455	0.1215	-1.71
258776_at	putative T-complex protein 1, ETA	---	AT3G11830	1.49	0.57	4.32	0.00382802	0.1215	-1.71
260902_at	hypothetical protein similar to carb	---	AT1G21440	-1.84	-0.88	-4.32	0.00379756	0.1215	-1.70
245088_at	subtilisin-like serine protease conta	---	AT2G39850	-2.21	-1.14	-4.32	0.00380653	0.1215	-1.70
247128_at	atfp6-like protein	---	AT5G66110	1.63	0.70	4.32	0.00382923	0.1215	-1.71
251425_at	putative protein chloroplast Cpn21	---	AT3G60210	1.46	0.54	4.32	0.0037939	0.1215	-1.70
245420_at	hypothetical protein	---	AT4G17410	-1.45	-0.54	-4.32	0.00380985	0.1215	-1.70
262590_at	putative RING-H2 zinc finger prote	RHA2A	AT1G15100	1.47	0.56	4.32	0.00383716	0.1216	-1.71
244951_s_at	cytochrome c biogenesis orf452	---	AT2G07723	-2.01	-1.01	-4.31	0.00384254	0.1216	-1.71
253489_at	monogalactosyldiacylglycerol synt	MGD1	AT4G31780	-1.67	-0.74	-4.31	0.0038541	0.1216	-1.72
250428_at	putative protein phosphatase prot	PAS2	AT5G10480	1.87	0.90	4.31	0.00385421	0.1216	-1.72
256441_at	unknown protein ;supported by ful	---	AT3G10940	-1.91	-0.93	-4.31	0.00387349	0.1217	-1.72
245557_at	phosphatase like protein	PUX5	AT4G15410	-1.31	-0.39	-4.31	0.00387306	0.1217	-1.72
252015_at	putative protein growth-regulating	AtGRF4	AT3G52910	1.31	0.38	4.31	0.00387044	0.1217	-1.72
254608_at	major intrinsic protein (MIP)- like r	NIP1;2	AT4G18910	2.28	1.19	4.31	0.00388247	0.1218	-1.72
256466_at	plastid protein, putative similar to (	---	AT1G32580	1.33	0.41	4.30	0.00390179	0.1223	-1.73
248855_at	NAM-like	anac096	AT5G46590	-1.87	-0.90	-4.30	0.00391824	0.1226	-1.73
261325_at	hypothetical protein predicted by g	---	AT1G44780	-1.31	-0.39	-4.30	0.0039269	0.1227	-1.73
246518_at	acetyltransferase-like protein Gluc	AtGNA1	AT5G15770	1.39	0.47	4.29	0.0039394	0.1229	-1.74
265573_at	putative zinc-finger protein similar	---	AT2G28200	2.05	1.04	4.29	0.00394543	0.1229	-1.74
254996_at	putative protein kinase CLV1 rece	---	AT4G10390	-1.56	-0.64	-4.29	0.00395344	0.1230	-1.74

249752_at	putative protein similar to unknown	LSU2	AT5G24660	-1.53	-0.61	-4.29	0.00396574	0.1232	-1.75
267068_at	unknown protein	---	AT2G41020	1.52	0.60	4.28	0.00398473	0.1237	-1.75
256725_at	hypothetical protein predicted by g	---	AT2G34070	-2.12	-1.08	-4.28	0.00399783	0.1239	-1.75
252559_at	RNA binding protein -like COLD-I	---	AT3G46020	1.33	0.41	4.28	0.0040044	0.1239	-1.76
245311_at	ribosomal protein ; supported by fu	---	AT4G14320	1.70	0.76	4.27	0.00403787	0.1241	-1.76
255773_at	flavonol 4'-sulfotransferase, putati	SOT17	AT1G18590	-2.75	-1.46	-4.27	0.00403673	0.1241	-1.76
253602_s_at	leucyl aminopeptidase - like protei	---	AT4G30910 /	1.36	0.44	4.27	0.00403516	0.1241	-1.76
251349_s_at	putative protein several hypothetic	---	AT3G11030 /	1.59	0.67	4.28	0.00401617	0.1241	-1.76
266648_at	putative trytophanyl-tRNA syntheta	OVA4	AT2G25840	1.36	0.45	4.27	0.00402642	0.1241	-1.76
255430_at	putative chloroplast protein import	tic20-IV	AT4G03320	1.98	0.99	4.27	0.00405779	0.1242	-1.77
252036_at	putative protein ;supported by full-	---	AT3G52070	1.55	0.64	4.27	0.004054	0.1242	-1.77
262392_at	hypothetical protein predicted by g	---	AT1G49520	-1.64	-0.71	-4.27	0.0040561	0.1242	-1.77
266246_at	putative cytochrome P450	CYP94C1	AT2G27690	-2.86	-1.52	-4.26	0.00407529	0.1246	-1.77
247389_at	putative protein strong similarity to	---	AT5G63490	-1.61	-0.69	-4.26	0.00408014	0.1246	-1.77
255283_at	putative symbiosis-related protein	ATG8B	AT4G04620	1.67	0.74	4.26	0.004088	0.1247	-1.78
245616_at	kinase like protein	---	AT4G14480	-1.91	-0.93	-4.26	0.00409646	0.1248	-1.78
245106_at	unknown protein	---	AT2G41650	1.50	0.59	4.26	0.00411705	0.1252	-1.78
261913_at	flavin-containing monooxygenase	FMO GS-O	AT1G65860	-2.21	-1.14	-4.25	0.00415434	0.1253	-1.79
255000_at	S18.A ribosomal protein ;supporte	RPS18C	AT4G09800	1.67	0.74	4.25	0.00413778	0.1253	-1.79
245425_at	carboxyl-terminal proteinase like p	UCH3	AT4G17510	1.29	0.36	4.25	0.00414877	0.1253	-1.79
250975_at	putative protein	---	AT5G03050	1.52	0.60	4.25	0.00415007	0.1253	-1.79
254853_at	putative DNA-binding protein AT-h	---	AT4G12080	1.57	0.65	4.25	0.0041318	0.1253	-1.79
261417_at	Expressed protein ; supported by c	---	AT1G07700	-1.38	-0.46	-4.25	0.00414243	0.1253	-1.79
266745_at	unknown protein ; supported by cl	PKS1	AT2G02950	-2.32	-1.22	-4.24	0.00417419	0.1256	-1.80
258919_at	Expressed protein ; supported by f	---	AT3G10525	-1.56	-0.64	-4.24	0.00418414	0.1256	-1.80
264242_at	hypothetical protein predicted by g	---	AT1G54640	-1.30	-0.37	-4.24	0.0041839	0.1256	-1.80
251296_at	putative protein paladin - Mus mus	---	AT3G62010	-1.43	-0.52	-4.24	0.00417533	0.1256	-1.80
247440_at	peptide transporter	---	AT5G62680	-1.37	-0.45	-4.23	0.00423892	0.1260	-1.81
253519_at	predicted protein red-1 gene, M.m	---	AT4G31240	1.96	0.97	4.24	0.00421018	0.1260	-1.81
261954_at	plastid ribosomal protein S6, putat	---	AT1G64510	1.41	0.49	4.23	0.00422499	0.1260	-1.81
258647_at	unknown protein ; supported by cl	---	AT3G07870	1.43	0.52	4.23	0.0042436	0.1260	-1.82
245560_at	indole-3-acetate beta-glucosyltrans	UGT84A1	AT4G15480	-1.49	-0.57	-4.23	0.00423572	0.1260	-1.81
260165_at	30S ribosomal protein S17, chloro	RPS17	AT1G79850	1.60	0.68	4.23	0.00422625	0.1260	-1.81
258175_at	FKBP-type peptidyl-prolyl cis-trans	TWD1	AT3G21640	1.40	0.48	4.23	0.00424015	0.1260	-1.81
264504_at	unknown protein similar to ATP-ci	ACLA-3	AT1G09430	1.37	0.46	4.23	0.00423027	0.1260	-1.81

255298_at	putative protein similar to transcrip	ATMSRB6	AT4G04840	-3.40	-1.77	-4.22	0.00429432	0.1261	-1.83
260250_at	putative phosphoribosylformylglyci	PUR4	AT1G74260	1.50	0.59	4.23	0.00427436	0.1261	-1.82
261700_at	hypothetical protein similar to hypo	---	AT1G32690	-1.54	-0.62	-4.23	0.00425687	0.1261	-1.82
246573_at	copper amine oxidase, putative si	---	AT1G31690	-1.60	-0.68	-4.23	0.0042644	0.1261	-1.82
261037_at	lipoxygenase identical to GB:CAB5	LOX3	AT1G17420	-4.89	-2.29	-4.22	0.00428464	0.1261	-1.83
263686_at	putative 60s ribosomal protein L1	---	AT1G26910	1.71	0.78	4.22	0.00429193	0.1261	-1.83
246832_at	putative protein isopenicillin N epi	---	AT5G26600	-1.47	-0.55	-4.22	0.00427952	0.1261	-1.82
255657_at	acidic ribosomal protein p1 similar	---	AT4G00810	1.47	0.56	4.22	0.0042755	0.1261	-1.82
253101_at	cytochrome P450 monooxygenase	CYP91A2	AT4G37430	1.92	0.94	4.22	0.00429442	0.1261	-1.83
259609_at	myosin-like protein contains Pfam	TSA1	AT1G52410	-4.53	-2.18	-4.22	0.00430245	0.1261	-1.83
251658_at	putative protein strictosidine syntha	---	AT3G57020	-2.25	-1.17	-4.22	0.00432548	0.1267	-1.84
265025_at	Expressed protein ; supported by f	---	AT1G24575	1.44	0.53	4.21	0.00435181	0.1270	-1.84
249829_at	c-myc binding protein MM-1-like pr	PDF5	AT5G23290	1.39	0.47	4.21	0.00435535	0.1270	-1.84
255983_at	polyneuridine aldehyde esterase,	MES14	AT1G33990	1.40	0.49	4.21	0.00434695	0.1270	-1.84
251076_at	putative protein putative protein A	---	AT5G01970	1.71	0.77	4.20	0.00438385	0.1277	-1.85
260387_at	putative flavonol sulfotransferase s	SOT16	AT1G74100	-2.28	-1.19	-4.20	0.00438777	0.1277	-1.85
250955_at	putative protein various predicted	CPUORF47	AT5G03190	-3.62	-1.86	-4.20	0.00440499	0.1278	-1.85
261373_at	CMP-KDO synthetase, putative si	---	AT1G53000	1.37	0.46	4.20	0.00440475	0.1278	-1.85
262448_at	En/Spm-like transposon protein, p	---	AT1G49450	-1.41	-0.49	-4.20	0.00442594	0.1283	-1.86
265895_at	unknown protein ;supported by ful	---	AT2G15000	1.45	0.54	4.19	0.00444536	0.1287	-1.86
245668_at	dormancy-associated protein, puta	DYL1	AT1G28330	1.56	0.64	4.19	0.00445692	0.1288	-1.87
266856_at	putative ABC transporter related to	PDR4	AT2G26910	1.92	0.94	4.18	0.00448883	0.1294	-1.87
263503_s_at	hypothetical protein	---	AT2G07676	-1.35	-0.43	-4.19	0.00448649	0.1294	-1.87
249441_at	avirulence induced gene (AIG) - li	---	AT5G39730	-1.53	-0.62	-4.18	0.00449561	0.1295	-1.88
249046_at	berberine bridge enzyme	---	AT5G44400	-1.97	-0.97	-4.18	0.00450696	0.1296	-1.88
263831_at	putative ferritin	ATFER4	AT2G40300	1.70	0.77	4.18	0.00451424	0.1297	-1.88
259008_at	metallothionein-like protein similar	MT2A	AT3G09390	1.44	0.53	4.17	0.00455236	0.1298	-1.89
251196_at	glutaredoxin -like protein glutared	---	AT3G62950	2.80	1.48	4.18	0.00452744	0.1298	-1.88
249210_at	unknown protein	---	AT5G42670	1.34	0.42	4.17	0.00454484	0.1298	-1.89
266299_at	glutathione S-transferase identical	ATGSTU5	AT2G29450	-2.04	-1.03	-4.17	0.00455043	0.1298	-1.89
255628_at	coded for by A. thaliana cDNA T45	GIF3	AT4G00850	1.40	0.49	4.17	0.00455333	0.1298	-1.89
265583_at	unknown protein	---	AT2G20010	-1.32	-0.40	-4.17	0.00455091	0.1298	-1.89
256417_s_at	omega-3 fatty acid desaturase, ch	FAD7	AT3G11170	-1.82	-0.86	-4.17	0.00457793	0.1304	-1.89
253121_at	putative protein predicted protein,	---	AT4G35890	-1.29	-0.36	-4.17	0.00459469	0.1307	-1.90
264100_at	lupeol synthase identical to lupeol	LUP1	AT1G78970	-2.93	-1.55	-4.16	0.00461011	0.1307	-1.90

267553_s_at	hypothetical protein predicted by g	---	AT2G32180 /	1.66	0.73	4.16	0.00460971	0.1307	-1.90
249138_at	putative protein contains similarity	WPP1	AT5G43070	-1.37	-0.46	-4.16	0.00461331	0.1307	-1.90
263412_at	putative histone H2B ;supported b	---	AT2G28720	1.39	0.47	4.16	0.00461931	0.1307	-1.90
249026_at	Expressed protein ; supported by f	OSB3	AT5G44785	1.53	0.61	4.16	0.00462562	0.1307	-1.91
262310_at	unknown protein contains similarity	MLP31	AT1G70840	-1.40	-0.49	-4.16	0.00464192	0.1310	-1.91
264293_at	cell division cycle protein, putative	APC6	AT1G78770	1.33	0.41	4.16	0.00464475	0.1310	-1.91
256836_at	pyruvate kinase, putative similar t	PKP-ALPH/	AT3G22960	1.51	0.60	4.15	0.00466816	0.1313	-1.92
253002_at	phosphoinositide-specific phospho	ATPLC1	AT4G38530	-1.46	-0.55	-4.15	0.00466505	0.1313	-1.91
246915_at	malate dehydrogenase - like prote	ATNADP-M	AT5G25880	1.82	0.87	4.15	0.0046857	0.1316	-1.92
258856_at	hypothetical protein predicted by g	SRG3	AT3G02040	2.11	1.07	4.15	0.00469619	0.1318	-1.92
246490_at	S-adenosylmethionine decarboxyla	CPuORF10	AT5G15948 /	-1.58	-0.66	-4.15	0.00470952	0.1320	-1.92
262933_at	polyamine oxidase, putative simila	ATPAO4	AT1G65840	-1.73	-0.79	-4.14	0.00472128	0.1321	-1.93
251892_at	putative protein	WRI1	AT3G54320	1.59	0.67	4.14	0.00473832	0.1322	-1.93
261500_at	hypothetical protein predicted by g	---	AT1G28400	2.38	1.25	4.14	0.00474055	0.1322	-1.93
265271_at	hypothetical protein predicted by g	---	AT2G28360	1.45	0.54	4.14	0.00474093	0.1322	-1.93
245345_at	proteinase like protein ;supported l	---	AT4G16640	-1.35	-0.43	-4.14	0.00475111	0.1323	-1.93
248271_at	putative protein similar to unknown	---	AT5G53420	-2.19	-1.13	-4.14	0.00475642	0.1323	-1.93
263636_at	unknown protein ; supported by fu	---	AT2G11910	1.43	0.52	4.13	0.00477862	0.1324	-1.94
266534_at	putative splicing factor ;supported	---	AT2G16940	1.33	0.42	4.13	0.00478328	0.1324	-1.94
266554_s_at	eukaryotic translation initiation fact	---	AT2G46280 /	1.51	0.60	4.13	0.00477753	0.1324	-1.94
264485_at	unknown protein ; supported by cD	---	AT1G77220	-1.38	-0.46	-4.13	0.00478146	0.1324	-1.94
267300_at	putative glucosyltransferase	---	AT2G30140	1.35	0.44	4.13	0.00479136	0.1325	-1.94
263098_at	Expressed protein ; supported by f	---	AT2G16005	-1.34	-0.42	-4.13	0.0048037	0.1325	-1.94
263715_at	unknown protein ; supported by cl	GPRI1	AT2G20570	-1.39	-0.47	-4.13	0.00480439	0.1325	-1.95
249422_at	putative protein predicted proteins	AtHB23	AT5G39760	-1.48	-0.57	-4.13	0.00481471	0.1326	-1.95
264506_at	germin-like protein Identical to Ara	GLP5	AT1G09560	1.47	0.55	4.12	0.00482649	0.1328	-1.95
262047_at	hypothetical protein predicted by g	---	AT1G80160	3.84	1.94	4.12	0.00484567	0.1332	-1.95
266258_at	60S acidic ribosomal protein P2 ;s	---	AT2G27720	1.79	0.84	4.12	0.00486603	0.1336	-1.96
255678_at	predicted protein with unknown fur	AT4G0052(	---	-1.42	-0.50	-4.11	0.00488516	0.1339	-1.96
247094_at	GDP-D-mannose 4,6-dehydratase	GMD1	AT5G66280	-1.40	-0.49	-4.11	0.0048934	0.1340	-1.96
264774_at	unknown protein	---	AT1G22890	2.31	1.21	4.11	0.0049126	0.1344	-1.97
246148_at	glycine-rich RNA-binding protein -	---	AT5G19960	1.45	0.54	4.11	0.00493387	0.1344	-1.97
247378_at	ATP-dependent RNA helicase-like	---	AT5G63120	-1.57	-0.65	-4.11	0.00492326	0.1344	-1.97
262875_at	gamma-tocopherol methyltransfera	G-TMT	AT1G64970	-1.46	-0.55	-4.11	0.00493431	0.1344	-1.97
245501_at	hypothetical protein	---	AT4G15620	2.12	1.09	4.11	0.00493767	0.1344	-1.97

258181_at	nitrate transporter identical to nitra	---	AT3G21670	-1.65	-0.72	-4.10	0.00495045	0.1346	-1.98
254213_at	tyrosine transaminase like protein	---	AT4G23590	-1.36	-0.45	-4.10	0.004969	0.1348	-1.98
253291_at	Expressed protein ; supported by f	---	AT4G33865	1.57	0.65	4.10	0.00496601	0.1348	-1.98
267010_at	putative AP2 domain transcription	SNZ	AT2G39250	-1.51	-0.59	-4.10	0.00498569	0.1351	-1.98
250891_at	fatty acid elongase - like protein K	KCS19	AT5G04530	-1.50	-0.58	-4.09	0.00501003	0.1356	-1.99
266814_at	homeodomain transcription factor (	ATHB4	AT2G44910	-1.28	-0.36	-4.09	0.00501978	0.1357	-1.99
262733_s_at	lipase identical to lipase GB:AAA9	---	AT1G28660	1.46	0.55	4.09	0.00503395	0.1357	-1.99
252114_at	mucin -like protein hemomucin, D	---	AT3G51450	-2.68	-1.42	-4.09	0.005036	0.1357	-1.99
246235_at	putative protein	---	AT4G36830	-1.48	-0.56	-4.09	0.00504441	0.1357	-2.00
267361_at	hypothetical protein predicted by g	---	AT2G39920	-1.74	-0.80	-4.09	0.00504123	0.1357	-2.00
252198_x_at	putative protein predicted protein,	---	AT3G50250	-1.64	-0.72	-4.08	0.00508363	0.1366	-2.00
264575_at	putative chloroplast 50S ribosoma	emb2394	AT1G05190	1.39	0.48	4.08	0.00509786	0.1368	-2.01
250139_at	putative protein de novo DNA met	DRM2	AT5G14620	1.29	0.37	4.08	0.00510915	0.1369	-2.01
255789_at	60S ribosomal protein L23 ;suppo	---	AT2G33370	2.31	1.20	4.08	0.00511345	0.1369	-2.01
265580_at	putative protein phosphatase 2C	---	AT2G20050	-1.49	-0.57	-4.07	0.00513075	0.1372	-2.01
250300_at	putative protein various predicted	---	AT5G11890	1.63	0.71	4.07	0.00514823	0.1373	-2.02
251472_at	putative protein nodule inception p	---	AT3G59580	1.36	0.44	4.07	0.00514584	0.1373	-2.02
254764_at	putative protein ; supported by cD	---	AT4G13250	2.06	1.04	4.06	0.00522866	0.1376	-2.03
247155_at	2-oxoglutarate dehydrogenase, E	---	AT5G65750	1.61	0.69	4.06	0.00521806	0.1376	-2.03
250329_at	putative potassium transport prote	KEA6	AT5G11800	-1.40	-0.49	-4.07	0.00516411	0.1376	-2.02
251943_at	splicing factor - like protein splicin	RSZ32	AT3G53500	1.30	0.38	4.06	0.00519375	0.1376	-2.03
258090_at	putative 60S ribosomal protein L18	---	AT3G14600	1.57	0.65	4.06	0.00519584	0.1376	-2.03
258448_at	unknown protein	---	AT3G22290	-1.31	-0.39	-4.06	0.00520746	0.1376	-2.03
245347_at	ferredoxin ;supported by full-length	---	AT4G14890	1.54	0.62	4.06	0.00522235	0.1376	-2.03
263585_at	60S ribosomal protein L39	---	AT2G25210	2.04	1.03	4.07	0.00518497	0.1376	-2.02
255664_at	putative protein	---	AT4G00440	-1.32	-0.40	-4.06	0.00522402	0.1376	-2.03
266313_at	putative protein kinase contains a	CIPK3	AT2G26980	1.81	0.85	4.06	0.00520694	0.1376	-2.03
255069_s_at	Met2-type cytosine DNA-methyltra	---	AT4G08990	1.68	0.75	4.07	0.00518489	0.1376	-2.02
259477_at	unknown protein ;supported by full	---	AT1G19120	1.33	0.41	4.06	0.00521713	0.1376	-2.03
261048_at	flavonol 3-o-glucosyltransferase, p	UGT72B3	AT1G01420	-1.45	-0.54	-4.06	0.00524545	0.1378	-2.04
250633_at	peptide methionine sulfoxide redu	PMSR2	AT5G07460	-2.82	-1.50	-4.06	0.00525579	0.1378	-2.04
264847_at	clathrin assembly protein AP19, s	AP19	AT2G17380	1.28	0.36	4.06	0.00525367	0.1378	-2.04
266520_at	cyclic nucleotide and calmodulin-re	ATCNGC6	AT2G23980	1.45	0.54	4.05	0.00526577	0.1378	-2.04
257317_at	hypothetical protein	AT2G0774	---	-1.44	-0.53	-4.05	0.00526925	0.1378	-2.04
251100_at	aldose reductase-like protein aldo	---	AT5G01670	1.81	0.86	4.04	0.00532639	0.1380	-2.05

257021_at	branched-chain amino acid amino	BCAT4	AT3G19710	-2.04	-1.03	-4.05	0.00531764	0.1380	-2.05
253973_at	Expressed protein ; supported by c	---	AT4G26555	1.28	0.35	4.04	0.00536053	0.1380	-2.06
251997_at	60S ribosomal protein - like 60S ri	STV1	AT3G53020	1.56	0.64	4.04	0.00536349	0.1380	-2.06
266561_at	unknown protein	---	AT2G23960	-1.32	-0.40	-4.05	0.00530433	0.1380	-2.05
251078_at	putative protein hypothetical protei	---	AT5G01990	1.67	0.74	4.05	0.00532214	0.1380	-2.05
262172_at	ribosomal protein S9, putative sim	RPS9	AT1G74970	1.38	0.46	4.04	0.00535246	0.1380	-2.06
260526_at	putative WD-40 repeat protein	---	AT2G47410	-1.35	-0.43	-4.04	0.00537405	0.1380	-2.06
254738_at	RNA-binding protein like	AT4G1386(	---	-1.40	-0.49	-4.05	0.00531214	0.1380	-2.05
246730_at	40S ribosomal protein S19 - like 4	---	AT5G28060	1.80	0.84	4.04	0.005371	0.1380	-2.06
253312_s_at	putative protein (1,4)-beta-xylan e	---	AT4G33850 /	-1.36	-0.45	-4.05	0.00532058	0.1380	-2.05
250061_at	chloroplast GrpE protein ; support	EMB1241	AT5G17710	1.48	0.57	4.04	0.00532284	0.1380	-2.05
250580_at	glutamate dehydrogenase 2 ; sup	GDH2	AT5G07440	-2.10	-1.07	-4.04	0.00534535	0.1380	-2.06
265333_at	hypothetical protein predicted by g	AtHB24	AT2G18350	-1.53	-0.61	-4.04	0.00534246	0.1380	-2.06
261138_at	hypothetical protein contains Pfam	---	AT1G19710	1.42	0.50	4.04	0.00535597	0.1380	-2.06
266110_at	putative C2H2-type zinc finger prot	AtIDD4	AT2G02080	-1.41	-0.50	-4.05	0.0053025	0.1380	-2.05
256033_at	UDP-glucose glucosyltransferase,	UGT71C4	AT1G07250	-1.37	-0.45	-4.04	0.00538339	0.1381	-2.06
258365_s_at	putative diaminopimelate decarbox	---	AT3G14390 /	1.42	0.51	4.03	0.00539293	0.1382	-2.07
261547_at	protein kinase, putative contains P	---	AT1G63500	-1.39	-0.48	-4.03	0.00541528	0.1385	-2.07
258937_at	putative ribosomal protein S28 sim	---	AT3G10090	1.67	0.74	4.03	0.00541324	0.1385	-2.07
259643_at	putative menaquinone biosynthes	---	AT1G68890	-1.32	-0.41	-4.02	0.00545873	0.1392	-2.08
250672_at	DnaJ homologue (gb|AAB91418.1	ATJ6	AT5G06910	1.29	0.37	4.02	0.00546569	0.1392	-2.08
250776_at	monooxygenase ;supported by ful	---	AT5G05320	1.32	0.40	4.02	0.00546896	0.1392	-2.08
258141_at	hypothetical protein	HON4	AT3G18035	1.51	0.59	4.02	0.00546472	0.1392	-2.08
267481_at	putative receptor-like protein kinas	---	AT2G02780	-2.25	-1.17	-4.02	0.00548092	0.1394	-2.08
257674_at	translational inhibitor protein, puta	---	AT3G20390	-1.35	-0.43	-4.02	0.00551165	0.1398	-2.09
251030_at	putative protein kinesin light chain	NDP1	AT5G02130	-1.61	-0.69	-4.02	0.00550725	0.1398	-2.09
261102_at	unknown protein	---	AT1G62880	1.33	0.41	4.01	0.00553401	0.1403	-2.09
265206_at	putative protease belongs to eukar	---	AT2G36670	1.46	0.54	4.01	0.0055421	0.1403	-2.09
260205_at	hypothetical protein predicted by g	TIFY7	AT1G70700	-2.17	-1.12	-4.01	0.00557861	0.1409	-2.10
255978_at	hypothetical protein	---	AT1G34010	1.33	0.41	4.01	0.00557586	0.1409	-2.10
263158_at	CCAAT-binding factor B subunit, p	NF-YA5	AT1G54160	-1.37	-0.46	-4.01	0.00558716	0.1410	-2.10
264899_at	unknown protein similar to ripenin	---	AT1G23130	-1.91	-0.93	-4.00	0.00560294	0.1410	-2.11
260764_at	unknown protein	---	AT1G48950	1.48	0.56	4.00	0.00560759	0.1410	-2.11
258731_at	unknown protein ; supported by cl	---	AT3G11880	-1.36	-0.45	-4.00	0.0055982	0.1410	-2.10
266422_at	hypothetical protein predicted by g	GAUT7	AT2G38650	-1.36	-0.44	-4.00	0.0056254	0.1413	-2.11

257279_at	unknown protein ;supported by ful	---	AT3G14430	1.37	0.46	4.00	0.00564486	0.1416	-2.11
252549_at	protein kinase - like receptor-like p	---	AT3G45860	-2.24	-1.16	-3.99	0.00568057	0.1421	-2.12
248043_s_at	heat shock protein (emb|CAA7251	---	AT5G56000	-1.77	-0.82	-3.99	0.00568072	0.1421	-2.12
254742_at	putative protein various predicted 3	IIL1	AT4G13430	-1.29	-0.37	-3.99	0.00566869	0.1421	-2.12
245502_at	hypothetical protein	---	AT4G15640	1.49	0.57	3.99	0.00568947	0.1421	-2.12
265398_at	unknown protein	ATMAK10	AT2G11000	1.38	0.46	3.99	0.00570938	0.1422	-2.13
266699_at	putative ribosomal protein L28 ; su	---	AT2G19730	1.68	0.75	3.99	0.00570262	0.1422	-2.12
259493_at	unknown protein	---	AT1G15840	-1.38	-0.46	-3.99	0.00570517	0.1422	-2.12
251536_at	ketol-acid reductoisomerase ; sup	---	AT3G58610	1.41	0.49	3.98	0.00573443	0.1426	-2.13
265740_at	RING-H2 finger protein RHA2b ide	RHA2B	AT2G01150	-2.09	-1.07	-3.98	0.00576229	0.1432	-2.13
246339_at	RP19 gene for chloroplast ribosom	RPL9	AT3G44890	1.41	0.49	3.98	0.00576844	0.1432	-2.14
247038_at	anthranilate N-hydroxycinnamoyl/b	EPS1	AT5G67160	-1.55	-0.63	-3.98	0.00577895	0.1433	-2.14
247794_at	phosphoinositide specific phospho	PLC1	AT5G58670	-1.49	-0.57	-3.97	0.00582318	0.1434	-2.15
258421_at	MtN3-like protein similar to MtN3 G	---	AT3G16690	-1.90	-0.93	-3.97	0.00585737	0.1434	-2.15
257793_at	unknown protein ;supported by ful	---	AT3G26960	-3.62	-1.85	-3.97	0.0058535	0.1434	-2.15
262946_at	hypothetical protein predicted by g	---	AT1G79390	1.38	0.47	3.97	0.00586191	0.1434	-2.15
264676_at	unknown protein EST gb|R64758 c	---	AT1G09870	1.31	0.39	3.97	0.00582569	0.1434	-2.15
253922_at	putative protein ; supported by cD	VTC2	AT4G26850	-1.64	-0.71	-3.97	0.00583015	0.1434	-2.15
266189_at	unknown protein	---	AT2G39020	-1.29	-0.37	-3.97	0.00584588	0.1434	-2.15
AFFX-BioB-M_	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.89	-0.92	-3.97	0.00583532	0.1434	-2.15
263133_at	hypothetical protein predicted by g	---	AT1G78450	-3.50	-1.81	-3.97	0.0058116	0.1434	-2.14
251301_at	cytochrome p450 (CYP78A9) ;sup	CYP78A9	AT3G61880	-1.44	-0.52	-3.97	0.00586017	0.1434	-2.15
254502_at	hypothetical protein	PTAC14	AT4G20130	1.46	0.55	3.98	0.00580085	0.1434	-2.14
249797_at	putative protein contains similarity	---	AT5G23750	-1.52	-0.60	-3.98	0.00579014	0.1434	-2.14
258638_at	unknown protein ;supported by ful	---	AT3G07950	1.34	0.42	3.97	0.00586426	0.1434	-2.15
255575_at	predicted protein of unknown func	---	AT4G01430	2.44	1.28	3.96	0.00588251	0.1434	-2.16
250584_at	WD-repeat protein-like	---	AT5G07590	1.44	0.53	3.96	0.00587989	0.1434	-2.16
256835_at	ATP sulfurylase, putative similar t	APS1	AT3G22890	-1.89	-0.92	-3.96	0.00588534	0.1434	-2.16
260774_at	serine-threonine protein kinase, p	---	AT1G78290	2.38	1.25	3.96	0.00592244	0.1434	-2.16
260069_at	unknown protein	---	AT1G73820	1.35	0.43	3.95	0.00596087	0.1434	-2.17
262951_at	nodulin-like protein similar to MtN	---	AT1G75500	-1.51	-0.60	-3.96	0.0059134	0.1434	-2.16
258086_at	dihydrolipoamide S-acetyltransfera	LTA2	AT3G25860	1.46	0.55	3.96	0.00594023	0.1434	-2.17
245228_at	phytochelatin synthetase-like prote	COBL2	AT3G29810	2.11	1.08	3.96	0.00593817	0.1434	-2.17
255429_at	hypothetical protein	---	AT4G03410	-1.53	-0.61	-3.95	0.00596147	0.1434	-2.17
258385_at	putative jasmonic acid regulatory p	ATNAC2	AT3G15510	1.59	0.67	3.95	0.00595652	0.1434	-2.17

245506_at	glutaredoxin homolog	---	AT4G15700	2.04	1.03	3.95	0.00595975	0.1434	-2.17
247563_at	putative protein various predicted	PDCB1	AT5G61130	1.52	0.61	3.96	0.00591893	0.1434	-2.16
264121_at	putative GTP-binding protein Carb	TOC33	AT1G02280	1.44	0.53	3.96	0.0059436	0.1434	-2.17
258414_at	unknown protein ;supported by ful	---	AT3G17380	1.39	0.48	3.96	0.0059151	0.1434	-2.16
251287_at	putative protein nucleoid DNA-bin	---	AT3G61820	-1.67	-0.74	-3.96	0.00592472	0.1434	-2.16
253776_at	ADP,ATP carrier-like protein ADP	AAC3	AT4G28390	1.64	0.71	3.95	0.00599387	0.1437	-2.18
264045_at	putative GTP cyclohydrolase	---	AT2G22450	1.34	0.42	3.95	0.00599566	0.1437	-2.18
257522_at	Yippee-like protein similar to Yippe	---	AT3G08990	-1.31	-0.39	-3.95	0.00599828	0.1437	-2.18
252789_s_at	hypothetical protein ; supported by	---	AT1G21930 /	1.31	0.39	3.95	0.00598153	0.1437	-2.17
250509_at	cytochrome P450	CYP78A7	AT5G09970	1.48	0.56	3.95	0.00601252	0.1439	-2.18
247309_at	putative protein contains similarity	---	AT5G63940	-1.60	-0.68	-3.94	0.00602624	0.1439	-2.18
264353_at	hypothetical protein predicted by g	---	AT1G03260	1.36	0.44	3.95	0.00602112	0.1439	-2.18
245018_at	hypothetical protein	---	---	-1.31	-0.39	-3.94	0.00605214	0.1442	-2.19
254002_at	steroid sulfotransferase - like prote	---	AT4G26280	-1.28	-0.36	-3.94	0.00604226	0.1442	-2.18
249398_at	RING finger -like protein RING-H2	---	AT5G40250	1.42	0.50	3.94	0.00605451	0.1442	-2.19
264658_at	hypothetical protein similar to LG2	---	AT1G09910	-1.39	-0.47	-3.94	0.00606196	0.1442	-2.19
251793_at	regulator of chromosome condens	---	AT3G55580	-1.28	-0.35	-3.94	0.0060704	0.1442	-2.19
266705_at	40S ribosomal protein S30 ; suppo	---	AT2G19750	1.61	0.69	3.94	0.0060844	0.1444	-2.19
258531_at	importin alpha identical to GB:AAC	IMPA-1	AT3G06720	1.32	0.40	3.93	0.00610115	0.1447	-2.19
251355_at	putative protein hypothetical prote	---	AT3G61100	1.50	0.58	3.93	0.0061087	0.1447	-2.20
251357_at	ribosomal protein S27 ; supported	ARS27A	AT3G61110	1.77	0.83	3.93	0.00611547	0.1447	-2.20
251038_at	putative protein unknown protein /	---	AT5G02240	-1.33	-0.41	-3.93	0.00612408	0.1448	-2.20
250895_at	RIBOSOMAL PROTEIN S28- like	---	AT5G03850	1.65	0.72	3.93	0.00613092	0.1448	-2.20
245317_at	hypothetical protein ; supported by	---	AT4G15610	1.38	0.47	3.92	0.00619277	0.1449	-2.21
267497_at	putative glutaredoxin ;supported b	---	AT2G30540	-1.94	-0.96	-3.93	0.00614952	0.1449	-2.20
261839_at	unknown protein	---	AT1G16040	1.41	0.49	3.92	0.00620654	0.1449	-2.21
248039_at	putative protein similar to unknown	---	AT5G55950	-1.30	-0.37	-3.93	0.00616217	0.1449	-2.20
246747_at	ribosomal protein S21 - like ribosc	---	AT5G27700	1.59	0.67	3.92	0.00620954	0.1449	-2.21
251647_at	protein kinase - like protein wall-as	---	AT3G57770	1.45	0.53	3.92	0.0062302	0.1449	-2.22
260627_at	hypothetical protein predicted by g	---	AT1G62310	-1.62	-0.70	-3.92	0.00618257	0.1449	-2.21
248749_at	eukaryotic release factor 1 homolo	ERF1-1	AT5G47880	-1.31	-0.39	-3.92	0.00620939	0.1449	-2.21
257937_at	hypothetical protein predicted by g	---	AT3G19810	1.30	0.38	3.92	0.00621608	0.1449	-2.21
263871_at	hypothetical protein predicted by g	RKP	AT2G22010	-1.45	-0.53	-3.92	0.00622103	0.1449	-2.21
261942_at	unknown protein similar to putative	AGL87	AT1G22590	1.84	0.88	3.92	0.00619707	0.1449	-2.21
252348_at	B12D-like protein B12D protein - H	---	AT3G48140	1.34	0.42	3.93	0.00616696	0.1449	-2.21

252016_at	putative protein predicted protein,	---	AT3G52950	-1.37	-0.45	-3.92	0.00622688	0.1449	-2.22
254791_at	SERINE CARBOXYPEPTIDASE I	scpl20	AT4G12910	-1.44	-0.53	-3.93	0.00615176	0.1449	-2.20
255587_at	putative inorganic phosphatase ; s	AtPPa5	AT4G01480	-1.53	-0.61	-3.92	0.00618025	0.1449	-2.21
253285_at	fatty acid elongase - like protein fa	KCS16	AT4G34250	-1.84	-0.88	-3.92	0.00625248	0.1449	-2.22
266747_at	predicted by genefinder and gensc	---	AT2G02870	-1.45	-0.54	-3.92	0.00625193	0.1449	-2.22
247910_at	putative protein similar to unknown	---	AT5G57410	1.49	0.58	3.92	0.00624266	0.1449	-2.22
259766_at	unknown protein ;supported by full	---	AT1G64360	-1.77	-0.82	-3.91	0.00626656	0.1451	-2.22
255008_at	putative protein hypothetical prote	---	AT4G10060	-1.37	-0.46	-3.91	0.00627699	0.1451	-2.22
245296_at	isp4 like protein ; supported by cDI	ATOPT3	AT4G16370	-1.75	-0.81	-3.91	0.00627465	0.1451	-2.22
248850_at	putative protein contains similarity	---	AT5G46550	1.38	0.47	3.91	0.00628809	0.1452	-2.23
255041_at	putative protein hypothetical prote	---	AT4G09620	1.46	0.54	3.91	0.00632067	0.1456	-2.23
248548_at	transmembrane transport protein-li	---	AT5G50300	-1.31	-0.39	-3.91	0.00631822	0.1456	-2.23
251513_at	pirin-like protein pirin - Lycopersic	PRN	AT3G59220	-3.11	-1.64	-3.90	0.00633478	0.1458	-2.23
257650_at	protein phosphatase, putative sim	---	AT3G16800	-1.53	-0.61	-3.90	0.00635731	0.1461	-2.24
262162_at	unknown protein ;supported by full	---	AT1G78020	-1.52	-0.60	-3.90	0.00637621	0.1461	-2.24
263621_at	putative DNA-directed RNA polym	NRPB6B	AT2G04630	1.39	0.47	3.90	0.00637832	0.1461	-2.24
251185_at	60S RIBOSOMAL PROTEIN L7A	---	AT3G62870	1.51	0.60	3.90	0.00637042	0.1461	-2.24
254163_s_at	putative protein storage protein - F	---	AT4G24340 /	-3.69	-1.88	-3.90	0.0063758	0.1461	-2.24
246952_at	putative protein similar to unknown	OFP13	AT5G04820	-1.47	-0.56	-3.90	0.00639572	0.1462	-2.24
256910_at	hypothetical protein	---	AT3G24080	-1.46	-0.55	-3.90	0.00639029	0.1462	-2.24
266365_at	ferredoxin-dependent glutamate sy	GLU2	AT2G41220	1.54	0.62	3.89	0.0064203	0.1466	-2.25
248969_at	unknown protein ; supported by cI	---	AT5G45310	1.98	0.99	3.89	0.00644302	0.1468	-2.25
247468_at	ARF1-binding protein ; supported	ARF2	AT5G62000	-1.39	-0.48	-3.89	0.00644284	0.1468	-2.25
251457_s_at	multi resistance protein homolog r	ATMRP9	AT3G60160 /	-1.36	-0.44	-3.89	0.00645908	0.1470	-2.25
262646_at	aspartate aminotransferase nearly	ASP4	AT1G62800	-1.88	-0.91	-3.89	0.00649281	0.1477	-2.26
246294_at	ribosomal protein, chloroplast ribo	PSRP5	AT3G56910	1.33	0.41	3.88	0.00652799	0.1482	-2.26
267375_at	G protein alpha subunit 1 (GPA1) i	GP ALPHA	AT2G26300	1.43	0.51	3.88	0.00652714	0.1482	-2.26
257442_at	legumin-like protein contains a 11-	---	AT2G28680	-1.56	-0.64	-3.88	0.00654431	0.1484	-2.27
250616_at	receptor-like protein kinase-like pr	EMS1	AT5G07280	-1.44	-0.52	-3.88	0.00655999	0.1486	-2.27
261165_at	dihydrolipoamide S-acetyltransfer	EMB3003	AT1G34430	1.37	0.45	3.87	0.00657818	0.1489	-2.27
253490_at	methyltransferase - like protein me	---	AT4G31790	1.86	0.90	3.87	0.00659891	0.1492	-2.28
258297_at	Expressed protein ; supported by f	---	AT3G23325	1.39	0.48	3.87	0.00662679	0.1497	-2.28
257637_at	terpene synthase-related protein c	---	AT3G25810	-1.29	-0.37	-3.87	0.00663942	0.1498	-2.28
253538_at	putative protein ribosomal protein	---	AT4G31460	1.30	0.38	3.86	0.00666582	0.1500	-2.29
265680_at	putative hydrolase ; supported by	---	AT2G32150	-1.73	-0.79	-3.86	0.00666986	0.1500	-2.29

260429_at	unknown protein ;supported by ful	JAZ6	AT1G72450	-2.13	-1.09	-3.86	0.00666618	0.1500	-2.29
258445_at	putative lipoxygenase similar to lip	LOX5	AT3G22400	-1.71	-0.77	-3.86	0.00669811	0.1501	-2.29
252077_at	putative protein several putative m	---	AT3G51720	1.45	0.53	3.86	0.00668984	0.1501	-2.29
253213_at	RNA helicase (RH16)	---	AT4G34910	-1.36	-0.45	-3.86	0.00667986	0.1501	-2.29
246043_at	putative protein predicted protein,	---	AT5G19380	-1.79	-0.84	-3.86	0.00669719	0.1501	-2.29
266046_at	hypothetical protein	---	AT2G07728	-1.50	-0.58	-3.86	0.00671353	0.1501	-2.29
263192_at	hypothetical protein putative acety	ACC1	AT1G36160	1.58	0.66	3.86	0.00670902	0.1501	-2.29
251852_at	putative protein	---	AT3G54750	1.56	0.65	3.86	0.00672152	0.1502	-2.30
264922_s_at	U2 snRNP auxiliary factor, large s	---	AT1G60830	1.30	0.38	3.85	0.00675693	0.1505	-2.30
259172_at	O-acetylserine (thiol) lyase identica	CS26	AT3G03630	1.85	0.89	3.85	0.00675799	0.1505	-2.30
265304_at	putative AP2 domain transcription	---	AT2G20350	-1.29	-0.37	-3.85	0.00676451	0.1505	-2.30
258612_at	putative replication factor A similar	---	AT3G02920	1.38	0.46	3.85	0.00674536	0.1505	-2.30
262803_at	unknown protein Location of ESTs	---	AT1G21000	1.67	0.74	3.85	0.0068072	0.1510	-2.31
254663_at	potassium channel protein KAT2	KAT2	AT4G18290	-1.54	-0.62	-3.85	0.00680409	0.1510	-2.31
262561_at	late embryogenesis abundant prot	---	AT1G34340	-1.36	-0.45	-3.85	0.00679969	0.1510	-2.31
260065_at	putative RING zinc finger protein c	---	AT1G73760	-1.40	-0.49	-3.85	0.00682461	0.1512	-2.31
246779_at	putative protein peroxisomal integr	PNC2	AT5G27520	-1.78	-0.83	-3.85	0.00682607	0.1512	-2.31
251644_at	putative protein putative DNA binc	---	AT3G57540	-1.82	-0.86	-3.84	0.00683748	0.1513	-2.31
254919_at	RING-H2 finger protein RHA1b ;su	RHA1B	AT4G11360	1.66	0.73	3.84	0.00684668	0.1513	-2.31
251812_at	hypothetical protein ;supported by	---	AT3G54970	-1.51	-0.60	-3.84	0.00685154	0.1513	-2.32
257122_at	RNA-binding protein, putative con	APUM5	AT3G20250	1.62	0.69	3.84	0.00689746	0.1519	-2.32
263779_at	putative photomorphogenesis repr	SPA1	AT2G46340	-1.43	-0.51	-3.84	0.00690773	0.1519	-2.32
258674_at	putative elongation factor P (EF-P)	---	AT3G08740	1.64	0.71	3.84	0.00690318	0.1519	-2.32
254910_at	translation initiation factor IF-1, pu	---	AT4G11175	1.31	0.39	3.84	0.00689028	0.1519	-2.32
251411_at	regulatory subunit of protein kinase	CKB3	AT3G60250	1.39	0.48	3.84	0.0069104	0.1519	-2.32
249466_at	ribosomal protein L5 - like riboson	RPL5B	AT5G39740	1.63	0.71	3.83	0.00692605	0.1519	-2.33
261881_at	nodulin-like protein similar to nodu	NIP6;1	AT1G80760	-1.69	-0.75	-3.83	0.00692369	0.1519	-2.33
265699_at	putative esterase (contains an este	---	AT2G03550	-1.37	-0.46	-3.83	0.00696008	0.1525	-2.33
263711_at	putative protein phosphatase 2C ;	---	AT2G20630	-1.37	-0.45	-3.83	0.00697493	0.1525	-2.33
249331_at	50S ribosomal protein L27 ;suppor	RPL27	AT5G40950	1.37	0.45	3.83	0.006986	0.1525	-2.34
265637_at	unknown protein	ATCOAE	AT2G27490	1.36	0.44	3.83	0.00696763	0.1525	-2.33
249036_at	nuclear cap-binding protein; CBP2	CBP20	AT5G44200	1.42	0.50	3.83	0.00698762	0.1525	-2.34
262786_at	putative lipase similar to gb|X0284	---	AT1G10740	1.53	0.62	3.82	0.00701026	0.1529	-2.34
264873_at	putative indole-3-acetate beta-gluc	UGT74B1	AT1G24100	-2.35	-1.23	-3.82	0.00704887	0.1534	-2.34
259005_at	unknown protein similar to nodule-	---	AT3G01930	-1.50	-0.59	-3.82	0.00704529	0.1534	-2.34

247201_at	50S ribosomal protein L29 ; suppo	---	AT5G65220	1.45	0.54	3.82	0.00706109	0.1535	-2.35
258616_at	putative protein kinase contains P	---	AT3G02880	-1.47	-0.56	-3.82	0.00707455	0.1537	-2.35
AFFX-r2-At-U1	/FEATURE=cds-2 /GENE= /LABEI	---	---	-1.36	-0.45	-3.82	0.00709282	0.1538	-2.35
254872_at	putative protein several hypothetic	---	AT4G11560	-1.32	-0.40	-3.82	0.00709259	0.1538	-2.35
254763_at	ribosomal protein L13a like protei	---	AT4G13170	1.48	0.56	3.81	0.00710369	0.1539	-2.35
256751_at	CLC-b chloride channel protein id	CLC-B	AT3G27170	-1.88	-0.91	-3.81	0.00711643	0.1539	-2.35
256595_x_at	hypothetical protein	---	AT3G28530	1.43	0.51	3.81	0.00713286	0.1539	-2.36
258651_at	putative phosphatidylinositol-4-pho	PIP5K9	AT3G09920	-1.43	-0.51	-3.81	0.00712723	0.1539	-2.36
246746_at	putative protein predicted proteins	---	AT5G27820	1.42	0.50	3.81	0.00712947	0.1539	-2.36
253251_at	putative protein similarity predicte	---	AT4G34730	1.54	0.62	3.81	0.00714077	0.1540	-2.36
262107_at	hypothetical protein predicted by g	---	AT1G02750	1.31	0.39	3.81	0.00715906	0.1541	-2.36
261454_at	hypothetical protein predicted by g	---	AT1G21090	1.38	0.46	3.81	0.00716246	0.1541	-2.36
247313_at	3(2),5-bisphosphate nucleotidase	SAL1	AT5G63980	-1.55	-0.63	-3.81	0.0071822	0.1544	-2.36
255706_at	putative ribosomal protein S13 sim	ATRPS13A	AT4G00100	1.59	0.67	3.80	0.00719233	0.1545	-2.37
257746_at	chorismate mutase identical to cho	CM1	AT3G29200	1.31	0.39	3.80	0.00722273	0.1546	-2.37
251771_at	putative protein cellulose synthase	CSLA14	AT3G56000	-1.39	-0.47	-3.80	0.00721686	0.1546	-2.37
250440_at	40S ribsomal protein S6 ; support	EMB3010	AT5G10360	1.54	0.62	3.80	0.00721149	0.1546	-2.37
250716_at	sucrose transporter protein	ATSUC9	AT5G06170	-1.32	-0.40	-3.80	0.00721504	0.1546	-2.37
250083_at	glutathione S-transferase-like prote	ATGSTF12	AT5G17220	-1.41	-0.50	-3.80	0.00723162	0.1546	-2.37
256168_at	receptor protein kinase, putative c	---	AT1G51805	-2.03	-1.02	-3.80	0.00724334	0.1547	-2.37
266166_at	putative glucosyltransferase ; sup	---	AT2G28080	-1.56	-0.65	-3.79	0.00729557	0.1549	-2.38
250111_at	acetolactate synthase-like protein	---	AT5G16290	-1.58	-0.66	-3.79	0.00728363	0.1549	-2.38
264508_at	putative phytochrome A similar to (	PHYA	AT1G09570	1.69	0.76	3.79	0.00728024	0.1549	-2.38
254372_at	putative protein predicted proteins	---	AT4G21620	1.83	0.87	3.80	0.00726763	0.1549	-2.38
247095_at	dehydrin RAB18-like protein (sp P	RAB18	AT5G66400	-2.09	-1.06	-3.79	0.00729335	0.1549	-2.38
266857_at	putative Na+ dependent ileal bile a	---	AT2G26900	-1.33	-0.41	-3.79	0.00729238	0.1549	-2.38
261431_at	Myb-related transcription factor m	AtMYB47	AT1G18710	-2.75	-1.46	-3.79	0.00732047	0.1553	-2.38
257875_at	hypothetical protein	---	AT3G17120	-1.37	-0.46	-3.79	0.00733864	0.1555	-2.39
246868_at	protein phosphatase - like protein	---	AT5G26010	-1.33	-0.41	-3.79	0.0073441	0.1555	-2.39
247960_at	N-myristoyl transferase ;supporte	NMT1	AT5G57020	1.29	0.37	3.78	0.00736924	0.1559	-2.39
249866_at	2-isopropylmalate synthase-like; h	MAM1	AT5G23010	-1.86	-0.89	-3.78	0.00740901	0.1565	-2.40
256308_s_at	ABC transporter, putative contains	ATMRP13	AT1G30410 /	1.66	0.73	3.78	0.00740819	0.1565	-2.40
244937_at	NADH dehydrogenase 49KDa prot	---	---	-1.73	-0.79	-3.78	0.00742311	0.1566	-2.40
248403_at	arginine-aspartate-rich RNA bindin	---	AT5G51410	1.36	0.44	3.78	0.0074515	0.1570	-2.40
264154_at	unknown protein	---	AT1G65430	-1.33	-0.42	-3.78	0.00745286	0.1570	-2.40

266451_at	3-isopropylmalate dehydratase, sr	---	AT2G43090	1.34	0.42	3.77	0.0074853	0.1575	-2.41
265720_at	unknown protein	---	AT2G40110	1.89	0.92	3.77	0.00750072	0.1576	-2.41
266503_at	unknown protein	---	AT2G47780	1.86	0.89	3.77	0.00750321	0.1576	-2.41
250647_at	putative protein contains similarity	---	AT5G06770	-1.36	-0.44	-3.77	0.00752045	0.1578	-2.41
255419_at	putative receptor kinase	---	AT4G03230	-1.38	-0.47	-3.77	0.0075345	0.1578	-2.41
247786_at	putative protein various predicted	PMR5	AT5G58600	1.30	0.38	3.77	0.0075341	0.1578	-2.41
251242_at	ARGININE/SERINE-RICH SPLICII	RSP31	AT3G61860	1.31	0.39	3.76	0.00756162	0.1582	-2.42
261213_at	unknown protein ; supported by cD	---	AT1G12970	1.34	0.42	3.76	0.00760109	0.1587	-2.42
259631_at	heat shock protein, putative simila	ERD2	AT1G56410	-1.29	-0.37	-3.76	0.00759245	0.1587	-2.42
254752_at	putative protein IFA-binding protei	---	AT4G13160	1.36	0.45	3.76	0.00760474	0.1587	-2.42
248603_at	WD-40 repeat protein-like	---	AT5G49430	1.29	0.37	3.76	0.00763441	0.1592	-2.43
257690_at	unknown protein contains similarity	---	AT3G12830	2.23	1.15	3.75	0.00767382	0.1599	-2.43
250829_at	disease resistance - like protein rp	ADR1-L2	AT5G04720	1.42	0.51	3.75	0.00773645	0.1603	-2.44
266598_at	3-methyl-2-oxobutanoate hydroxy-	KPHMT1	AT2G46110	1.47	0.55	3.75	0.00771941	0.1603	-2.44
250502_at	heat shock protein 70 (Hsc70-5) ;	MTHSC70-	AT5G09590	-1.95	-0.96	-3.75	0.00772356	0.1603	-2.44
249650_at	Expressed protein ; supported by c	SEF	AT5G37055	1.41	0.49	3.75	0.00771904	0.1603	-2.44
263829_at	unknown protein	---	AT2G40435	-2.35	-1.24	-3.75	0.00771739	0.1603	-2.44
245261_at	Expressed protein ; supported by c	---	AT4G14385	1.32	0.40	3.75	0.00773058	0.1603	-2.44
246392_at	hypothetical protein predicted by g	---	AT1G58120 /	-1.29	-0.37	-3.74	0.00776145	0.1605	-2.45
260457_at	unknown protein	---	AT1G72480	1.35	0.43	3.74	0.00775871	0.1605	-2.44
247100_at	selenium-binding protein-like	---	AT5G66520	1.37	0.45	3.74	0.00777749	0.1607	-2.45
265122_at	similar to flavin-binding monooxyge	FMO GS-O	AT1G62540	-1.26	-0.34	-3.74	0.00780167	0.1608	-2.45
249334_at	putative protein strong similarity to	YSL4	AT5G41000	1.56	0.64	3.74	0.00779862	0.1608	-2.45
258710_s_at	putative coatomer zeta subunit (ze	---	AT3G09800 /	1.31	0.39	3.74	0.00779226	0.1608	-2.45
260438_at	putative bifunctional nuclease simi	ENDO 2	AT1G68290	-2.13	-1.09	-3.74	0.00781616	0.1609	-2.45
257772_at	unknown protein C-term similar to	---	AT3G23080	-1.41	-0.50	-3.74	0.00784973	0.1609	-2.46
264484_at	hypothetical protein similar to anky	---	AT1G77260	-1.31	-0.39	-3.74	0.00782622	0.1609	-2.45
254350_at	putative protein hypothetical prote	---	AT4G22280	1.28	0.35	3.74	0.00784877	0.1609	-2.46
248590_at	receptor protein kinase	---	AT5G49660	-1.33	-0.41	-3.73	0.00785925	0.1609	-2.46
258622_at	unknown protein contains Pfam pr	---	AT3G02720	-1.33	-0.41	-3.74	0.00783876	0.1609	-2.46
253998_at	putative peroxidase peroxidase A	---	AT4G26010	-1.28	-0.35	-3.73	0.00785513	0.1609	-2.46
260565_at	unknown protein predicted by gene	---	AT2G43800	-1.70	-0.76	-3.73	0.00786915	0.1610	-2.46
260898_at	plastid ribosomal protein L34 prec	---	AT1G29070	1.49	0.58	3.73	0.00789903	0.1614	-2.46
249530_at	putative protein asparaginyl-tRNA	---	AT5G38750	-1.28	-0.36	-3.73	0.00791188	0.1615	-2.47
263261_at	putative pre-mRNA splicing factor	---	AT1G10580	-1.25	-0.32	-3.73	0.00791511	0.1615	-2.47

265605_at	putative cellulose synthase catalyt	CESA10	AT2G25540	-1.26	-0.33	-3.73	0.00793436	0.1617	-2.47
251227_at	ABC transporter-like protein glutat	ATMRP10	AT3G62700	-1.69	-0.76	-3.72	0.00796238	0.1622	-2.47
247074_at	putative protein contains similarity	---	AT5G66590	-1.52	-0.61	-3.72	0.00801084	0.1630	-2.48
260533_at	putative U1 small nuclear ribonucle	---	AT2G43370	1.31	0.38	3.72	0.00805034	0.1633	-2.48
256706_at	auxin-independent growth promot	---	AT3G30300	1.38	0.46	3.72	0.00803621	0.1633	-2.48
253635_at	putative protein hypothetical prote	---	AT4G30620	1.30	0.38	3.72	0.00805479	0.1633	-2.48
264525_at	unknown protein Highly Similar to I	ATBCAT-1	AT1G10060	3.07	1.62	3.72	0.00804962	0.1633	-2.48
256982_at	unknown protein	ECT2	AT3G13460	1.34	0.42	3.71	0.00809016	0.1635	-2.49
260681_at	hypothetical protein predicted by g	AT1G08030	---	-1.30	-0.38	-3.71	0.00807315	0.1635	-2.49
249219_at	putative protein contains similarity	SDG25	AT5G42400	-1.43	-0.52	-3.71	0.00808819	0.1635	-2.49
252168_at	putative protein pir7a protein - Ory	MES10	AT3G50440	-2.58	-1.37	-3.71	0.00807739	0.1635	-2.49
250784_at	unknown protein ; supported by cD	---	AT5G05480	1.44	0.52	3.71	0.00812498	0.1637	-2.49
250538_at	RNA helicase (emb|CAA09212.1)	STRS2	AT5G08620	1.64	0.72	3.71	0.00812309	0.1637	-2.49
248035_at	sucrose cleavage protein-like ;sup	---	AT5G55900	1.32	0.40	3.71	0.00812304	0.1637	-2.49
251478_at	putative protein SF16 protein, poll	IQD13	AT3G59690	1.29	0.36	3.70	0.00820731	0.1652	-2.50
259253_at	hypothetical protein predicted by g	---	AT3G07640	1.26	0.34	3.70	0.00821845	0.1652	-2.50
253980_at	sucrase-like protein sucrose cleav	---	AT4G26620	1.63	0.70	3.70	0.00821959	0.1652	-2.50
263937_at	putative RING zinc finger protein	---	AT2G35910	-1.37	-0.45	-3.70	0.00823372	0.1653	-2.51
249322_at	protein import receptor TOM20, m	TOM20-4	AT5G40930	-1.29	-0.36	-3.70	0.00824721	0.1655	-2.51
251013_at	putative protein various predicted	---	AT5G02540	5.61	2.49	3.70	0.0082546	0.1655	-2.51
247668_at	pseudo-response regulator - like p	APRR3	AT5G60100	-1.27	-0.35	-3.69	0.00829692	0.1655	-2.51
258218_at	methyltransferase, putative simila	XPL1	AT3G17998	1.56	0.64	3.69	0.00826937	0.1655	-2.51
248476_at	putative protein similar to unknown	---	AT5G50890	-1.89	-0.92	-3.69	0.00828811	0.1655	-2.51
250793_at	leucoanthocyanidin dioxygenase-li	---	AT5G05600	-2.16	-1.11	-3.69	0.00829844	0.1655	-2.51
261177_at	hypothetical protein predicted by g	---	AT1G04770	-1.68	-0.75	-3.69	0.00827153	0.1655	-2.51
260986_at	glyoxalase II, putative similar to G	GLY3	AT1G53580	-1.64	-0.72	-3.69	0.00829711	0.1655	-2.51
264390_at	putative DNA-binding protein Cont	---	AT1G11950	1.43	0.52	3.69	0.00830598	0.1655	-2.52
262171_at	unknown protein ;supported by full	TIFY10B	AT1G74950	-1.61	-0.69	-3.69	0.00832585	0.1657	-2.52
259232_at	unknown protein similar to hypothe	---	AT3G11420	-1.61	-0.68	-3.69	0.00835965	0.1661	-2.52
264772_at	unknown protein location of EST g	---	AT1G22930	1.37	0.45	3.69	0.00835714	0.1661	-2.52
248205_at	cotton fiber expressed protein 1-lik	---	AT5G54300	-2.52	-1.33	-3.68	0.00837314	0.1662	-2.52
253377_at	putative protein NBS/LRR disease	ADR1-L1	AT4G33300	1.38	0.46	3.68	0.00839135	0.1662	-2.53
263557_at	putative homeodomain transcriptio	BLH7	AT2G16400	-1.45	-0.53	-3.68	0.00838225	0.1662	-2.53
256188_at	unknown protein similar to hypothe	---	AT1G30160	-1.77	-0.83	-3.68	0.00839258	0.1662	-2.53
251267_at	putative protein hypothetical prote	---	AT3G62330	-1.41	-0.50	-3.68	0.0084204	0.1664	-2.53

247841_at	putative protein predicted proteins	ATFIP1[V]	AT5G58040	-1.37	-0.45	-3.68	0.00842081	0.1664	-2.53
252102_at	dehydrin Xero2 ; supported by cD	LTI30	AT3G50970	-2.44	-1.29	-3.68	0.00847695	0.1668	-2.54
262493_at	auxilin-like protein similar to GB:C	---	AT1G21660	-1.32	-0.40	-3.68	0.00847207	0.1668	-2.54
256753_at	unknown protein contains Pfam pr	GHS1	AT3G27160	1.44	0.52	3.68	0.00846648	0.1668	-2.54
254945_at	putative RING finger protein ring f	---	AT4G10940	-1.43	-0.52	-3.67	0.0084862	0.1668	-2.54
261078_at	unknown protein identical to SP:O	RPL4	AT1G07320	1.34	0.42	3.67	0.00848907	0.1668	-2.54
262304_at	major latex protein (MLP149), put	MLP43	AT1G70890	-4.47	-2.16	-3.68	0.00845432	0.1668	-2.53
250430_at	putative protein	---	AT5G10460	1.28	0.36	3.68	0.00846688	0.1668	-2.54
259058_at	putative cytochrome P450 similar t	CYP89A9	AT3G03470	1.97	0.98	3.67	0.00849727	0.1668	-2.54
249979_s_at	putative protein	---	AT5G18860	-2.03	-1.02	-3.67	0.00851512	0.1670	-2.54
261075_at	unknown protein	---	AT1G07280	-1.38	-0.46	-3.67	0.00852289	0.1670	-2.54
249133_at	putative protein strong similarity to	TAF4	AT5G43130	1.27	0.34	3.67	0.00854811	0.1674	-2.55
252363_at	lipase - like protein lipase Arab-1,	---	AT3G48460	-2.46	-1.30	-3.67	0.00857319	0.1677	-2.55
263049_at	unknown protein ;supported by ful	---	AT2G05260	-1.35	-0.43	-3.66	0.00860336	0.1680	-2.55
245152_at	putative mitochondrial carrier prote	---	AT2G47490	-1.34	-0.43	-3.66	0.0086017	0.1680	-2.55
263127_at	hypothetical protein predicted by g	MSL6	AT1G78610	-1.41	-0.49	-3.66	0.00861247	0.1680	-2.55
260683_at	ribosomal protein, putative similar	HLL	AT1G17560	1.36	0.44	3.66	0.008623	0.1681	-2.55
264059_at	Expressed protein ; supported by f	INH3	AT2G31305	1.35	0.43	3.66	0.00863183	0.1681	-2.56
255696_at	putative nucleotide sugar epimeras	GAE3	AT4G00110	-1.37	-0.46	-3.66	0.00864443	0.1682	-2.56
247478_at	DC1.2 homologue - like protein D	---	AT5G62360	-2.50	-1.32	-3.65	0.0087178	0.1687	-2.57
264214_s_at	MADS-box transcription factor, pu	AGL38	AT1G65300	-1.30	-0.38	-3.65	0.00871096	0.1687	-2.57
266895_at	hypothetical protein predicted by g	---	AT2G26040	-1.31	-0.39	-3.65	0.00870643	0.1687	-2.56
264140_at	proteasome alpha subunit, putativ	---	AT1G79210	1.30	0.38	3.65	0.00870923	0.1687	-2.57
254953_at	Expressed protein ; supported by f	---	AT4G10925	1.34	0.43	3.66	0.00868457	0.1687	-2.56
262165_at	putative acyl-CoA:1-acylglycerol-3-	LPAT4	AT1G75020	1.64	0.71	3.65	0.00871617	0.1687	-2.57
246403_at	pectinacetylesterase precursor, pu	---	AT1G57590	-1.57	-0.65	-3.65	0.00870519	0.1687	-2.56
261927_at	RING-H2 zinc finger protein ATL5	---	AT1G22500	1.96	0.97	3.65	0.00874494	0.1687	-2.57
253585_at	putative protein hypothetical prote	---	AT4G30720	1.31	0.39	3.65	0.00874741	0.1687	-2.57
263090_at	hypothetical protein predicted by g	---	AT2G16190	-1.30	-0.37	-3.65	0.00873542	0.1687	-2.57
259802_at	thionin identical to GI:1181531 fro	THI2.1	AT1G72260	-5.96	-2.58	-3.65	0.00873753	0.1687	-2.57
247034_at	cyclin D3-like protein ;supported b	CYCD3;2	AT5G67260	1.51	0.60	3.65	0.00877921	0.1691	-2.57
265575_at	proline iminopeptidase identical to	PIP	AT2G14260	1.31	0.38	3.65	0.00879676	0.1693	-2.58
259671_at	protein kinase, putative similar to	---	AT1G52290	-2.00	-1.00	-3.65	0.0088085	0.1694	-2.58
259889_at	predicted protein ; supported by cD	---	AT1G76405	1.52	0.60	3.64	0.00882923	0.1694	-2.58
254865_s_at	putative protein, fragment other pr	---	AT4G05350	-1.29	-0.37	-3.64	0.00882972	0.1694	-2.58

262820_at	putative obtusifoliol 14-alpha dem	CYP51G1	AT1G11680	1.33	0.41	3.64	0.00881672	0.1694	-2.58
252400_at	hypothetical protein	---	AT3G48020	1.87	0.90	3.64	0.00890974	0.1697	-2.59
250424_at	bromodomain protein - like bromo	GTE2	AT5G10550	-1.28	-0.36	-3.64	0.00886787	0.1697	-2.58
267147_at	putative anthocyanidin synthase ;s	---	AT2G38240	-3.44	-1.78	-3.63	0.00893346	0.1697	-2.59
264053_at	hypothetical protein predicted by g	---	AT2G22560	-1.47	-0.56	-3.63	0.00894059	0.1697	-2.59
267101_at	putative peroxidase	---	AT2G41480	-1.50	-0.58	-3.64	0.00890988	0.1697	-2.59
245253_at	hydroperoxide lyase (HPOL) like p	HPL1	AT4G15440	-4.41	-2.14	-3.64	0.00891875	0.1697	-2.59
253216_at	cyclophilin - like protein cyclophilin	---	AT4G34960	1.41	0.50	3.64	0.00888709	0.1697	-2.59
251048_at	putative protein potassium channe	---	AT5G02410	1.39	0.47	3.64	0.00886593	0.1697	-2.58
255421_at	putative protein phosphatase regul	---	AT4G03260	-1.38	-0.46	-3.64	0.00885511	0.1697	-2.58
251846_at	histone H2A.F/Z ;supported by ful	HTA11	AT3G54560	2.51	1.33	3.64	0.00892186	0.1697	-2.59
251057_at	putative protein alkB protein - Esc	---	AT5G01780	1.25	0.32	3.63	0.00894194	0.1697	-2.59
248070_at	putative protein similar to unknown	---	AT5G55660	-1.32	-0.40	-3.64	0.00887588	0.1697	-2.58
266866_at	putative ABC transporter	PDR3	AT2G29940	-1.63	-0.70	-3.64	0.00891929	0.1697	-2.59
259660_at	unknown protein ; supported by ful	---	AT1G55260	-2.93	-1.55	-3.63	0.00895522	0.1698	-2.59
261315_at	AP2 domain containing protein, pu	ERF8	AT1G53170	1.87	0.90	3.63	0.00898687	0.1700	-2.60
261034_s_at	hypothetical protein predicted by g	---	AT1G17450	1.47	0.56	3.63	0.00898232	0.1700	-2.60
247330_at	putative protein contains similarity	GAMMA CA	AT5G63510	1.27	0.34	3.63	0.00897691	0.1700	-2.60
261989_at	disease resistance protein, putativ	---	AT1G33670	-1.36	-0.45	-3.63	0.00900775	0.1701	-2.60
265034_at	unknown protein ;supported by full	---	AT1G61660	-1.39	-0.47	-3.63	0.00900357	0.1701	-2.60
254758_at	putative protein dimethylaniline m	YUC2	AT4G13260	-1.78	-0.83	-3.63	0.00901753	0.1701	-2.60
247382_at	adenylate kinase ;supported by ful	ADK1	AT5G63400	1.45	0.54	3.63	0.00904449	0.1705	-2.60
255364_s_at	putative fibrillin ; supported by full	---	AT4G04020	-1.46	-0.54	-3.62	0.00905706	0.1706	-2.61
246660_at	putative protein predicted protein,	---	AT5G35180	-1.33	-0.42	-3.62	0.00907504	0.1708	-2.61
249678_at	protein kinase-like	---	AT5G35980	-1.26	-0.33	-3.62	0.0090891	0.1709	-2.61
258270_at	putative lysophospholipase similar	---	AT3G15650	-1.95	-0.96	-3.62	0.00913496	0.1715	-2.61
266989_at	putative myrosinase-binding protei	JAL23	AT2G39330	-5.21	-2.38	-3.62	0.00913182	0.1715	-2.61
258053_at	unknown protein similar to CGI-18	---	AT3G16230	-1.27	-0.34	-3.62	0.0091425	0.1715	-2.62
263929_at	hypothetical protein predicted by g	URH1	AT2G36310	-1.38	-0.47	-3.61	0.00917174	0.1719	-2.62
260618_at	flower development protein cycloi	TCP3	AT1G53230	-1.41	-0.50	-3.61	0.00917659	0.1719	-2.62
260807_at	hypothetical protein predicted by g	---	AT1G78310	1.25	0.32	3.61	0.00920768	0.1723	-2.62
246247_at	putative protein	---	AT4G36640	-2.45	-1.29	-3.61	0.00924181	0.1728	-2.63
245249_at	acyl-CoA oxidase like protein ; sup	ACX1	AT4G16760	-1.51	-0.59	-3.61	0.00927092	0.1729	-2.63
251486_at	60S RIBOSOMAL PROTEIN L38-	---	AT3G59540	1.59	0.67	3.61	0.00926943	0.1729	-2.63
249929_at	unknown protein	---	AT5G22340	1.42	0.50	3.61	0.00925887	0.1729	-2.63

253386_at	sulfolipid biosynthesis protein SQD	SQD1	AT4G33030	1.50	0.59	3.60	0.00929023	0.1730	-2.63
263660_at	unknown protein ESTs gb|N65789	MPI7	AT1G04260	1.32	0.40	3.60	0.00928415	0.1730	-2.63
248581_at	putative protein strong similarity to	---	AT5G49900	-1.52	-0.60	-3.60	0.00931348	0.1731	-2.63
263496_at	unknown protein ; supported by fu	---	AT2G42570	1.48	0.56	3.60	0.00930725	0.1731	-2.63
248197_at	NADPH:protochlorophyllide oxidor	PORA	AT5G54190	-1.33	-0.41	-3.60	0.00935125	0.1733	-2.64
266261_at	putative zinc finger protein ;suppo	---	AT2G27580	-1.26	-0.33	-3.60	0.00937714	0.1733	-2.64
250625_at	calnexin homolog	---	AT5G07340	1.51	0.60	3.60	0.00933222	0.1733	-2.64
245949_at	elongation factor 1B alpha-subunit	---	AT5G19510	1.45	0.54	3.60	0.00937475	0.1733	-2.64
254335_at	putative protein alternative oxidas	IM	AT4G22260	-1.30	-0.38	-3.60	0.00936458	0.1733	-2.64
250530_at	unknown protein	---	AT5G08630	1.35	0.44	3.60	0.00936638	0.1733	-2.64
258788_at	unknown protein ;supported by ful	---	AT3G11780	1.35	0.44	3.60	0.00936311	0.1733	-2.64
252952_at	putative protein cylicin II - bovine,	---	AT4G38710	-1.46	-0.55	-3.59	0.00943587	0.1743	-2.65
257876_at	hypothetical protein predicted by g	---	AT3G17130	-1.71	-0.78	-3.59	0.009462	0.1746	-2.65
261754_at	alpha-amylase, putative similar to	AMY2	AT1G76130	-2.15	-1.10	-3.59	0.0094718	0.1747	-2.65
253558_at	kinase binding protein - like Skb1	SKB1	AT4G31120	1.38	0.47	3.59	0.00952189	0.1751	-2.66
263870_at	unknown protein	RKP	AT2G22010	-1.36	-0.44	-3.58	0.00955851	0.1751	-2.66
256386_at	cytochrome P450, putative contair	---	AT1G66540	-1.28	-0.35	-3.58	0.00955379	0.1751	-2.66
256023_at	hypothetical protein predicted by g	ZW2	AT1G58330	-1.40	-0.49	-3.58	0.00954338	0.1751	-2.66
266344_at	hypothetical protein predicted by g	---	AT2G01580	-1.30	-0.38	-3.58	0.00953827	0.1751	-2.66
263150_at	heat-shock protein, putative simila	---	AT1G54050	-1.77	-0.83	-3.59	0.00952361	0.1751	-2.66
263253_at	bZIP transcription factor (POSF21)	---	AT2G31370	-1.43	-0.52	-3.58	0.00954638	0.1751	-2.66
256760_at	SKP1/ASK1 (At15), putative simila	ASK15	AT3G25650	-1.24	-0.32	-3.58	0.00952952	0.1751	-2.66
257141_at	60S ribosomal protein L34, putativ	---	AT3G28900	1.70	0.77	3.58	0.00965055	0.1762	-2.67
249993_at	GTP-binding protein obg -like GTF	---	AT5G18570	1.25	0.33	3.58	0.00963924	0.1762	-2.67
258623_at	unknown protein ; supported by cl	---	AT3G02790	1.82	0.86	3.58	0.00964737	0.1762	-2.67
258037_at	putative 4-coumarate:CoA ligase 2	4CL5	AT3G21230	-4.59	-2.20	-3.58	0.00964609	0.1762	-2.67
265214_at	unkown protein ESTs gb|H36249,	---	AT1G05000	1.95	0.96	3.57	0.00966432	0.1764	-2.67
260383_s_at	putative 60S ribosomal protein L6	---	AT1G74050	1.49	0.58	3.57	0.00968812	0.1766	-2.68
249589_at	pyridoxal kinase -like protein pyrid	SOS4	AT5G37850	1.26	0.33	3.57	0.0096914	0.1766	-2.68
263735_s_at	hypothetical protein predicted by g	AGL50	AT1G59810	-1.27	-0.35	-3.57	0.00972077	0.1767	-2.68
264870_at	hypothetical protein ;supported by	---	AT1G24210	1.37	0.45	3.57	0.00971322	0.1767	-2.68
248331_at	putative protein contains similarity	---	AT5G52650	1.64	0.72	3.57	0.00970868	0.1767	-2.68
249059_at	subtilisin-like serine protease conta	---	AT5G44530	-1.58	-0.66	-3.57	0.00973122	0.1767	-2.68
250461_at	hypothetical protein	---	AT5G10010	1.43	0.52	3.57	0.00974285	0.1768	-2.68
255036_at	putative protein similarity RING zi	---	AT4G09560	-1.65	-0.72	-3.57	0.00976083	0.1770	-2.68

263375_s_at	putative prohibitin ;supported by fu	ATPHB6	AT2G20530 /	1.39	0.47	3.56	0.00980158	0.1771	-2.69
250662_at	steroid sulfotransferase-like protein	ST2A	AT5G07010	-1.92	-0.94	-3.56	0.00981562	0.1771	-2.69
261694_at	60S ribosomal protein L10A, putat	---	AT1G08360	1.50	0.59	3.56	0.00982073	0.1771	-2.69
251012_at	putative protein ;supported by full-	---	AT5G02580	4.53	2.18	3.57	0.00977547	0.1771	-2.69
261106_at	homeodomain-containing protein I	KNAT7	AT1G62990	-1.29	-0.36	-3.56	0.00979542	0.1771	-2.69
250667_at	40S ribosomal protein S4 ;support	---	AT5G07090	1.81	0.86	3.56	0.00981398	0.1771	-2.69
256178_s_at	auxin conjugate hydrolase (ILL5) id	ILL5	AT1G51760 /	-2.63	-1.40	-3.56	0.00979144	0.1771	-2.69
248879_at	ornithine aminotransferase	DELTA-OA	AT5G46180	1.43	0.52	3.56	0.00990557	0.1776	-2.70
262235_at	ribosomal protein L18, putative sir	---	AT1G48350	1.53	0.61	3.56	0.00988477	0.1776	-2.70
251058_at	putative protein	---	AT5G01790	-2.71	-1.44	-3.55	0.00991903	0.1776	-2.70
252362_at	hypothetical protein	PDE312	AT3G48500	1.61	0.69	3.55	0.00991589	0.1776	-2.70
257059_at	unknown protein ; supported by cl	---	AT3G15280	-1.29	-0.37	-3.55	0.00993361	0.1776	-2.70
247815_at	ribosomal protein S4 - like riboson	---	AT5G58420	1.54	0.62	3.55	0.00990972	0.1776	-2.70
259721_at	putative phosphatidylinositol-4-pho	---	AT1G60890	1.52	0.60	3.56	0.00989483	0.1776	-2.70
257789_at	unknown protein ;supported by ful	YSL6	AT3G27020	1.59	0.66	3.56	0.00986662	0.1776	-2.69
252948_at	putative protein NLS receptor - Or	KAK	AT4G38600	-1.36	-0.44	-3.56	0.00987512	0.1776	-2.70
253504_at	hypothetical protein	---	AT4G31960	-1.23	-0.30	-3.55	0.00991194	0.1776	-2.70
248606_at	putative protein contains similarity	CPuORF4	AT5G49448 /	1.63	0.71	3.55	0.00993171	0.1776	-2.70
260095_at	putative transcription factor BTF3	---	AT1G73230	1.53	0.61	3.55	0.00999554	0.1784	-2.71
254108_at	putative protein	RIN2	AT4G25230	-1.38	-0.47	-3.55	0.00998941	0.1784	-2.71
251826_at	ABC transporter - like protein ATP	---	AT3G55110	-1.37	-0.45	-3.55	0.01000417	0.1784	-2.71
255891_at	hypothetical protein predicted by g	EGY3	AT1G17870	-1.40	-0.48	-3.55	0.01003255	0.1788	-2.71
259932_at	zinc finger protein, putative similar	STOP1	AT1G34370	1.34	0.43	3.54	0.01005956	0.1791	-2.71
247673_at	tRNA intron endonuclease - like p	SEN2	AT5G60230	1.25	0.32	3.54	0.01010952	0.1799	-2.72
259158_at	hypothetical protein predicted by g	---	AT3G05430	-1.26	-0.33	-3.54	0.01012656	0.1800	-2.72
261535_at	Expressed protein ; supported by f	---	AT1G01725	1.41	0.50	3.53	0.01018836	0.1810	-2.73
249192_at	brain and reproductive organ-expre	---	AT5G42470	1.25	0.33	3.53	0.01023212	0.1816	-2.73
259515_at	hypothetical protein ; supported by	---	AT1G20430	1.27	0.34	3.53	0.01024793	0.1817	-2.73
261119_at	chloroplast 50S ribosomal protein	emb2184	AT1G75350	1.23	0.30	3.53	0.01024925	0.1817	-2.73
250718_at	unknown protein	emb2735	AT5G06240	1.32	0.40	3.53	0.01026527	0.1818	-2.74
250787_at	meiotic check point regulator-like p	EMB2771	AT5G05560	1.29	0.37	3.53	0.01028326	0.1820	-2.74
259551_at	hypothetical protein	---	AT1G21190	1.31	0.39	3.53	0.01030093	0.1821	-2.74
255231_at	F-box protein family, AtFBL20 con	---	AT4G05460	1.29	0.36	3.52	0.01037803	0.1828	-2.75
251083_at	hypothetical protein ; supported by	---	AT5G01590	1.34	0.42	3.52	0.01036889	0.1828	-2.75
248845_at	disease resistance protein-like	---	AT5G46470	-1.42	-0.51	-3.52	0.01036509	0.1828	-2.75

266001_at	hypothetical protein predicted by g	HHP3	AT2G24150	-1.28	-0.36	-3.52	0.01037661	0.1828	-2.75
250014_at	anthranilate phosphoribosyltransfe	TRP1	AT5G17990	-2.70	-1.43	-3.52	0.01037104	0.1828	-2.75
248273_at	putative protein contains similarity	---	AT5G53500	-1.68	-0.74	-3.52	0.01039433	0.1829	-2.75
250045_at	putative protein mRNA (orf04), Ara	---	AT5G17700	-1.56	-0.64	-3.52	0.01041142	0.1830	-2.75
258406_at	hypothetical protein similar to hypo	ATRBL14	AT3G17611	-1.24	-0.31	-3.52	0.01040701	0.1830	-2.75
262921_at	transfactor, putative similar to tran	APL	AT1G79430	-1.32	-0.40	-3.52	0.01043546	0.1831	-2.75
260365_at	hypothetical protein predicted by g	---	AT1G70630	-1.33	-0.41	-3.52	0.01042963	0.1831	-2.75
255674_at	probable plasma membrane intrins	PIP1;4	AT4G00430	-1.73	-0.79	-3.51	0.010454	0.1832	-2.75
265672_at	putative cysteine proteinase inhibit	---	AT2G31980	2.98	1.57	3.51	0.01045647	0.1832	-2.76
266887_at	unknown protein ; supported by cD	CHL-CPN1	AT2G44650	1.41	0.49	3.51	0.01047459	0.1834	-2.76
266267_at	putative glutathione S-transferase	ATGSTU4	AT2G29460	-3.97	-1.99	-3.51	0.01054409	0.1844	-2.76
254333_at	predicted protein predicted protein	SMO1-3	AT4G22753	-2.33	-1.22	-3.51	0.01055379	0.1845	-2.76
250454_at	unknown protein ; supported by fu	---	AT5G09830	1.24	0.31	3.50	0.01059267	0.1846	-2.77
247098_at	GTP-binding protein-like	---	AT5G66470	1.57	0.65	3.50	0.01062194	0.1846	-2.77
261369_at	protein kinase, putative similar to	---	AT1G53060	-1.44	-0.53	-3.50	0.01062613	0.1846	-2.77
259871_at	nodulin-like protein similar to nodu	---	AT1G76800	1.96	0.97	3.50	0.01062223	0.1846	-2.77
260494_at	putative receptor-like protein kinas	---	AT2G41820	1.41	0.49	3.50	0.01061505	0.1846	-2.77
264155_at	unknown protein	GTB1	AT1G65440	-1.50	-0.58	-3.51	0.01057374	0.1846	-2.77
263452_at	putative trehalose-6-phosphate ph	---	AT2G22190	-1.71	-0.77	-3.50	0.01061895	0.1846	-2.77
247522_at	putative protein ; supported by cD	---	AT5G61340	1.45	0.53	3.50	0.01059643	0.1846	-2.77
256944_at	unknown protein similar to unknow	VRN1	AT3G18990	1.49	0.57	3.50	0.01064385	0.1848	-2.77
256577_at	unknown protein	---	AT3G28220	-2.89	-1.53	-3.50	0.01069329	0.1852	-2.78
257903_at	unknown protein	---	AT3G28460	1.31	0.39	3.50	0.01068929	0.1852	-2.78
260546_at	putative trypsin inhibitor ;supporte	ATTI2	AT2G43520	-3.03	-1.60	-3.50	0.01068316	0.1852	-2.78
262220_at	calcium-dependent protein kinase	CPK30	AT1G74740	1.28	0.36	3.49	0.01072191	0.1856	-2.78
266889_at	hypothetical protein predicted by g	---	AT2G44640	1.36	0.44	3.49	0.01074422	0.1857	-2.78
254686_at	putative protein putative oncogene	---	AT4G13720	1.37	0.45	3.49	0.01074126	0.1857	-2.78
261539_at	hypothetical protein predicted by g	---	AT1G01840	-1.36	-0.45	-3.49	0.01078915	0.1863	-2.79
252454_at	putative protein various predicted	---	AT3G47130	-1.25	-0.33	-3.49	0.01079636	0.1863	-2.79
263876_at	putative RAS superfamily GTP-bin	ATRAB7A	AT2G21880	-1.48	-0.56	-3.48	0.01096771	0.1867	-2.80
258813_at	NAM-like protein (no apical meriste	anac046	AT3G04060	1.49	0.57	3.48	0.0108827	0.1867	-2.80
261758_at	hypothetical protein contains simila	ADT6	AT1G08250	-1.58	-0.66	-3.48	0.01096821	0.1867	-2.80
258815_at	putative short-chain type dehydrog	---	AT3G04000	-1.66	-0.73	-3.48	0.01093678	0.1867	-2.80
262309_at	phosphoglucomutase, putative sim	---	AT1G70820	-1.76	-0.82	-3.47	0.01105347	0.1867	-2.81
247550_at	putative protein many predicted pr	---	AT5G61370	-1.26	-0.34	-3.48	0.01092044	0.1867	-2.80

252548_at	kinesin-related protein - like kinesi	---	AT3G45850	1.36	0.45	3.47	0.011059	0.1867	-2.81
245479_at	extensin like protein	---	AT4G16140	-1.33	-0.41	-3.47	0.01101479	0.1867	-2.81
256324_at	MATE efflux family protein, putativ	---	AT1G66760	-3.16	-1.66	-3.49	0.01083369	0.1867	-2.79
246041_at	phospholipase - like protein variou	---	AT5G19290	1.26	0.33	3.48	0.01092859	0.1867	-2.80
265742_at	putative ribose 5-phosphate isome	---	AT2G01290	-1.51	-0.59	-3.47	0.01103599	0.1867	-2.81
261490_at	tumor suppressor, putative similar	SAC52	AT1G14320	1.46	0.55	3.48	0.01092619	0.1867	-2.80
248797_at	putative protein similar to unknown	---	AT5G47210	1.38	0.46	3.48	0.01098434	0.1867	-2.81
262029_at	50S ribosomal protein L21 chlorop	---	AT1G35680	1.44	0.52	3.47	0.01104696	0.1867	-2.81
245117_at	putative Ca2+-ATPase ; supporte	ACA4	AT2G41560	1.49	0.58	3.48	0.01094863	0.1867	-2.80
266568_at	unknown protein	---	AT2G24070	-1.27	-0.35	-3.48	0.01099388	0.1867	-2.81
259834_at	H-protein promoter binding factor-2	---	AT1G69570	-1.68	-0.75	-3.48	0.01091938	0.1867	-2.80
246310_at	sulfate transporter ATST1 ; suppo	SULTR3;1	AT3G51895	-1.60	-0.68	-3.47	0.01106091	0.1867	-2.81
257494_at	hypothetical protein predicted by g	---	AT1G32375	-1.25	-0.33	-3.48	0.01094735	0.1867	-2.80
249722_at	putative protein similar to unknown	---	AT5G35430	-1.25	-0.32	-3.47	0.0110667	0.1867	-2.81
249310_at	putative protein contains similarity	---	AT5G41520	1.36	0.45	3.48	0.01098448	0.1867	-2.81
254636_at	putative protein kinase ; supporte	CIPK12	AT4G18700	-1.28	-0.35	-3.47	0.01103537	0.1867	-2.81
261323_at	hypothetical protein predicted by g	---	AT1G44760	-1.58	-0.66	-3.48	0.01090088	0.1867	-2.80
248037_at	sexual differentiation process prote	OPT1	AT5G55930	-1.95	-0.96	-3.48	0.01087169	0.1867	-2.80
253692_at	putative protein Cs protein, Droso	ATPAO5	AT4G29720	-1.25	-0.32	-3.47	0.01102472	0.1867	-2.81
255497_at	hypothetical protein similar to A. th	UNE12	AT4G02590	-1.31	-0.39	-3.48	0.01088764	0.1867	-2.80
251474_at	putative protein diphthamide synth	---	AT3G59630	-1.32	-0.40	-3.48	0.0108941	0.1867	-2.80
249336_at	putative protein similar to unknown	DRB5	AT5G41070	1.62	0.69	3.48	0.01095117	0.1867	-2.80
255666_at	putative protein ;supported by full-	---	AT4G00390	1.38	0.46	3.47	0.0110571	0.1867	-2.81
261751_at	chloroplast drought-induced stress	CDSP32	AT1G76080	-1.24	-0.31	-3.48	0.01094213	0.1867	-2.80
249408_at	myb-related protein	MYB23	AT5G40330	-1.39	-0.48	-3.47	0.01109033	0.1870	-2.82
250748_at	AtPH1-like protein ;supported by f	---	AT5G05710	1.38	0.46	3.47	0.01111939	0.1872	-2.82
261603_at	DNA binding protein ACBF, putati	ATRBP47A	AT1G49600	1.75	0.81	3.47	0.0111211	0.1872	-2.82
257979_at	unknown protein	---	AT3G20730	-1.32	-0.40	-3.47	0.01113103	0.1872	-2.82
247027_at	subtilisin-like serine protease conta	---	AT5G67090	-1.26	-0.33	-3.46	0.01128076	0.1877	-2.83
262351_at	beta-galactosidase (BGAL), putati	BGAL17	AT1G72990	1.26	0.33	3.45	0.01133717	0.1877	-2.84
246824_at	drought-induced protein - like non	---	AT5G26990	-1.27	-0.35	-3.46	0.01129171	0.1877	-2.83
261900_at	unknown protein ;supported by full	---	AT1G80940	1.31	0.39	3.46	0.01129412	0.1877	-2.84
254831_at	Ribosomal protein L7Ae -like vario	---	AT4G12600	1.83	0.87	3.45	0.01133205	0.1877	-2.84
264084_at	putative kinesin light chain	---	AT2G31240	-1.32	-0.40	-3.46	0.01126486	0.1877	-2.83
249900_at	unknown protein	emb1211	AT5G22640	1.30	0.38	3.46	0.0112391	0.1877	-2.83

261561_at	unknown protein ;supported by full	---	AT1G01730	1.50	0.58	3.46	0.01123009	0.1877	-2.83
260408_at	putative thioredoxin similar to thior	ATH8	AT1G69880	1.39	0.48	3.46	0.01118102	0.1877	-2.82
259583_at	hypothetical protein	---	AT1G28070	1.37	0.46	3.45	0.01133831	0.1877	-2.84
264821_at	hypothetical protein predicted by g	---	AT1G03470	1.59	0.67	3.45	0.0113248	0.1877	-2.84
264134_at	unknown protein contains similarity	---	AT1G79070	1.24	0.32	3.45	0.01132211	0.1877	-2.84
244939_at	ribosomal protein S12 (trans-splice	---	---	-1.58	-0.66	-3.46	0.01120648	0.1877	-2.83
261414_at	Expressed protein ; supported by f	---	AT1G07795	-1.51	-0.59	-3.45	0.01133967	0.1877	-2.84
247316_at	ankyrin-like protein	---	AT5G64030	1.30	0.38	3.46	0.01118268	0.1877	-2.82
259873_s_at	putative translation initiation factor	---	AT1G76720 /	-1.45	-0.54	-3.46	0.01126538	0.1877	-2.83
265386_at	unknown protein ;supported by ful	---	AT2G20930	1.28	0.36	3.46	0.01126994	0.1877	-2.83
250475_at	sulfate transporter ; supported by	SULTR2;1	AT5G10180	-2.01	-1.01	-3.45	0.01134031	0.1877	-2.84
252659_at	putative protein	---	AT3G44430	1.36	0.45	3.45	0.01133684	0.1877	-2.84
245791_at	defender against cell death protei	ATDAD1	AT1G32210	1.36	0.44	3.46	0.01128542	0.1877	-2.83
255622_at	putative flavonol glucosyltransfera	GT72B1	AT4G01070	-1.43	-0.51	-3.45	0.01129913	0.1877	-2.84
256245_at	heat shock protein 70 identical to h	HSP70	AT3G12580	-3.21	-1.68	-3.46	0.01119306	0.1877	-2.83
249750_at	unknown protein ;supported by ful	---	AT5G24570	1.61	0.69	3.45	0.01135756	0.1878	-2.84
252827_at	cytochrome P450 - like protein cyt	CYP79B2	AT4G39950	-3.28	-1.71	-3.45	0.01136201	0.1878	-2.84
249091_at	AtCLH2 (gb|AAF27046.1) ; suppo	CLH2	AT5G43860	-1.33	-0.41	-3.45	0.01141582	0.1886	-2.85
264057_at	putative AP2 domain transcription	RAP2.7	AT2G28550	-1.55	-0.63	-3.44	0.01145883	0.1890	-2.85
252098_at	putative protein several hypothetic	---	AT3G51330	2.58	1.37	3.44	0.01145323	0.1890	-2.85
245926_at	VPS13 - like protein VPS13, Sacc	---	AT5G24740	1.33	0.41	3.44	0.01146752	0.1890	-2.85
250124_at	putative protein contains similarity	---	AT5G16480	1.36	0.44	3.44	0.01150526	0.1895	-2.85
253697_at	nucleotide pyrophosphatase -like	---	AT4G29700	-4.38	-2.13	-3.44	0.0115164	0.1895	-2.86
262911_s_at	heat shock protein, putative simila	---	AT1G07400 /	-2.52	-1.34	-3.44	0.01153339	0.1897	-2.86
250322_at	putative transcription factor (MYB4	MYB46	AT5G12870	1.25	0.32	3.44	0.01155839	0.1899	-2.86
266963_at	unknown protein	MTP11	AT2G39450	-1.35	-0.43	-3.44	0.01157809	0.1901	-2.86
245306_at	Expressed protein ; supported by f	ELIP2	AT4G14690	-1.39	-0.48	-3.44	0.01159151	0.1901	-2.86
257232_at	phytochrome-associated protein 1	PAP1	AT3G16500	-1.40	-0.48	-3.44	0.01159488	0.1901	-2.86
250148_at	putative protein various predicted	---	AT5G14530	1.35	0.43	3.43	0.01161476	0.1903	-2.86
259984_at	putative RNA-binding protein cont	---	AT1G76460	1.37	0.45	3.43	0.01162272	0.1903	-2.86
250199_at	putative protein contains similarity	MPL1	AT5G14180	2.59	1.37	3.43	0.01163384	0.1904	-2.87
259955_s_at	unknown protein ;supported by ful	BZR1	AT1G19350 /	1.35	0.43	3.43	0.01166699	0.1905	-2.87
252032_at	putative protein RNA-binding prote	---	AT3G52150	1.26	0.34	3.43	0.01165161	0.1905	-2.87
265026_at	putative 3-oxoacyl [acyl-carrier pro	---	AT1G24360	1.50	0.59	3.43	0.0116622	0.1905	-2.87
253813_at	putative protein hypothetical prote	---	AT4G28150	1.34	0.43	3.43	0.01167535	0.1905	-2.87

266557_at	unknown protein ; supported by cl	---	AT2G46080	-1.23	-0.30	-3.43	0.01169712	0.1907	-2.87
262852_at	hypothetical protein predicted by g	---	AT1G20910	1.30	0.38	3.43	0.01174235	0.1911	-2.88
251882_at	peptide transport - like protein pep	PTR1	AT3G54140	-1.38	-0.47	-3.42	0.0117551	0.1911	-2.88
248395_at	putative protein contains similarity	AtPP2-A14	AT5G52120	-1.47	-0.56	-3.43	0.01175118	0.1911	-2.88
266227_at	unknown protein ;supported by ful	---	AT2G28870	-1.24	-0.32	-3.43	0.01173438	0.1911	-2.87
267162_s_at	putative phosphoribosylaminoimida	---	AT2G05140	1.52	0.61	3.42	0.01177556	0.1912	-2.88
257066_at	lipid transfer protein, putative simi	---	AT3G18280	2.03	1.02	3.42	0.01177203	0.1912	-2.88
250998_at	ankyrin - like protein ankyrin G119	---	AT5G02620	-1.49	-0.57	-3.42	0.0117866	0.1912	-2.88
250020_at	putative protein contains similarity	---	AT5G18180	-1.38	-0.46	-3.42	0.0117962	0.1912	-2.88
253617_at	hypothetical protein	---	AT4G30410	2.10	1.07	3.42	0.0118228	0.1914	-2.88
250350_at	putative protein predicted proteins	---	AT5G12010	-1.76	-0.81	-3.42	0.01183183	0.1914	-2.88
255637_at	hypothetical protein	---	AT4G00750	1.50	0.58	3.42	0.01182636	0.1914	-2.88
261684_at	hypothetical protein predicted by g	---	AT1G47400	-2.61	-1.38	-3.42	0.01185068	0.1916	-2.89
246434_at	root cap 1 (RCP1) ;supported by f	RCP1	AT5G17520	-1.45	-0.53	-3.42	0.01187699	0.1919	-2.89
260840_at	hypothetical protein similar to hypo	---	AT1G29050	-1.40	-0.49	-3.42	0.01189294	0.1920	-2.89
265570_at	unknown protein	---	AT2G28310	1.41	0.49	3.42	0.01190237	0.1920	-2.89
244943_at	NADH dehydrogenase subunit 9	---	ATMG00070	-1.45	-0.53	-3.41	0.01195515	0.1920	-2.89
245019_at	hypothetical protein	---	---	-1.24	-0.31	-3.41	0.01192836	0.1920	-2.89
250283_at	putative protein many hypothetica	---	AT5G13270	1.34	0.42	3.41	0.01195431	0.1920	-2.89
263607_at	unknown protein predicted by gens	---	AT2G16270	1.44	0.53	3.41	0.01196187	0.1920	-2.89
246517_at	ribosomal protein 3 precursor-like	---	AT5G15760	1.38	0.46	3.41	0.01194298	0.1920	-2.89
257626_s_at	hypothetical protein	---	AT3G26240	1.34	0.42	3.41	0.01196319	0.1920	-2.89
250264_at	glucosyltransferase -like protein g	---	AT5G12890	-1.23	-0.30	-3.41	0.01192404	0.1920	-2.89
259105_at	stress related protein, putative sim	---	AT3G05500	-1.46	-0.55	-3.41	0.01197295	0.1921	-2.90
251642_at	imbibition protein homolog probab	AtSIP2	AT3G57520	-1.34	-0.42	-3.41	0.01201755	0.1921	-2.90
251432_at	putative protein leucine zipper-EF	---	AT3G59820	-1.52	-0.60	-3.41	0.01202652	0.1921	-2.90
249443_at	putative protein ; supported by cD	---	AT5G39600	1.44	0.53	3.41	0.01204183	0.1921	-2.90
267628_at	unknown protein similar to GP|226	---	AT2G42280	1.34	0.43	3.41	0.01202549	0.1921	-2.90
257271_at	Expressed protein ; supported by f	---	AT3G28007	-2.38	-1.25	-3.41	0.01200295	0.1921	-2.90
254820_s_at	pEARLI 1-like protein Arabidopsis	---	AT4G12510	-1.83	-0.87	-3.41	0.01203588	0.1921	-2.90
263567_at	hypothetical protein predicted by g	---	AT2G15440	-1.36	-0.45	-3.41	0.01204149	0.1921	-2.90
256980_at	hypothetical protein contains Pfam	DRB3	AT3G26932	1.44	0.53	3.41	0.01199264	0.1921	-2.90
248163_at	auxin-responsive-like protein ; sup	DFL1	AT5G54510	-3.65	-1.87	-3.41	0.01205619	0.1922	-2.90
266456_at	putative bHLH transcription factor	NAI1	AT2G22770	-1.34	-0.43	-3.40	0.0120746	0.1923	-2.90
245924_at	Tha4 protein - like Tha4 protein, P	---	AT5G28750	1.27	0.34	3.40	0.01211015	0.1928	-2.91

247342_at	ARI-like RING zinc finger protein-li	---	AT5G63730	-1.29	-0.37	-3.40	0.01212981	0.1928	-2.91
258106_at	ribonucleoside-diphosphate reduct	RNR2A	AT3G23580	-1.39	-0.48	-3.40	0.01212556	0.1928	-2.91
247127_at	putative protein similar to unknown	---	AT5G66100	-1.29	-0.37	-3.40	0.01214756	0.1930	-2.91
255564_s_at	hypothetical protein T15B16.8	RGXT2	AT4G01750	1.34	0.42	3.40	0.01216571	0.1931	-2.91
252409_at	putative protein bundle sheath def	---	AT3G47650	1.32	0.40	3.40	0.01217225	0.1931	-2.91
254453_at	amino acid transport protein AAT1	AAT1	AT4G21120	1.53	0.61	3.40	0.01221504	0.1935	-2.92
253561_at	aspartate--tRNA ligase - like prote	---	AT4G31180	1.28	0.35	3.40	0.01221198	0.1935	-2.92
258158_at	acid phosphatase type 5 identical t	PAP17	AT3G17790	2.27	1.18	3.39	0.01227308	0.1940	-2.92
252202_at	anthranilate N-hydroxycinnamoyl/l	---	AT3G50300	-1.31	-0.38	-3.39	0.01227163	0.1940	-2.92
251883_at	ribosomal protein L17 -like protein	---	AT3G54210	1.31	0.39	3.39	0.01225856	0.1940	-2.92
250575_at	putative protein	---	AT5G08240	1.62	0.70	3.39	0.01227827	0.1940	-2.92
254328_at	adenine phosphoribosyltransferas	APT3	AT4G22570	-1.71	-0.77	-3.38	0.01240419	0.1942	-2.93
252300_at	pyruvate kinase -like protein variou	---	AT3G49160	1.66	0.73	3.38	0.01240388	0.1942	-2.93
254026_at	putative calmodulin-binding protei	---	AT4G25800	1.25	0.32	3.39	0.01232293	0.1942	-2.93
262678_at	hypothetical protein ;supported by	---	AT1G75810	1.45	0.53	3.39	0.01236784	0.1942	-2.93
248955_at	putative protein contains similarity	GAS41	AT5G45600	1.28	0.36	3.38	0.01241265	0.1942	-2.93
255485_at	predicted protein of unknown func	---	AT4G02550	1.30	0.38	3.38	0.01241616	0.1942	-2.93
245372_at	ribosomal protein ;supported by ful	---	AT4G15000	1.70	0.77	3.39	0.01234896	0.1942	-2.93
254744_at	Expressed protein ; supported by c	MEE55	AT4G13345	-1.48	-0.57	-3.39	0.01231459	0.1942	-2.92
266357_at	putative beta-amylase	BAM6	AT2G32290	-2.19	-1.13	-3.39	0.01236864	0.1942	-2.93
263019_at	trehalose 6-phosphate synthase, p	ATTPS9	AT1G23870	2.21	1.14	3.39	0.01238743	0.1942	-2.93
247629_at	putative protein	SIZ1	AT5G60410	-1.36	-0.44	-3.38	0.01241952	0.1942	-2.93
266019_at	putative calmodulin-binding protein	---	AT2G18750	-1.25	-0.32	-3.39	0.01237608	0.1942	-2.93
248582_at	heat shock protein 70 (gb|AAF276	CPHSC70-1	AT5G49910	-1.63	-0.70	-3.39	0.01231742	0.1942	-2.93
261871_at	similar to serine/threonine protein k	---	AT1G11440	-1.37	-0.45	-3.39	0.01237327	0.1942	-2.93
265629_at	unknown protein ; supported by cl	LHW	AT2G27228	-1.54	-0.62	-3.39	0.01234876	0.1942	-2.93
264891_at	putative pectinesterase similar to (	---	AT1G23200	-1.54	-0.63	-3.38	0.01244418	0.1944	-2.94
262064_at	elongation factor, putative similar t	LOS1	AT1G56070	1.36	0.44	3.38	0.01250115	0.1949	-2.94
246738_at	replication factor C - like replicatio	EMB2775	AT5G27740	1.30	0.38	3.38	0.01248605	0.1949	-2.94
245562_at	OBP33pep like protein contains no	---	AT4G15520	1.41	0.50	3.38	0.01249878	0.1949	-2.94
264332_at	hypothetical protein predicted by g	---	AT1G61920	-1.29	-0.37	-3.38	0.0125126	0.1950	-2.94
255673_at	Similar to receptor-like protein kin	RLK4	AT4G00340	-1.30	-0.38	-3.38	0.01252982	0.1951	-2.94
257060_at	unknown protein	---	AT3G18230	1.33	0.41	3.37	0.01257538	0.1955	-2.95
245027_at	heme oxygenase 2 (HO2)	HO2	AT2G26550	1.30	0.38	3.37	0.01256947	0.1955	-2.95
254029_at	putative protein other hypothetical	---	AT4G25870	1.35	0.44	3.37	0.01258406	0.1955	-2.95

255616_at	hypothetical protein	---	AT4G01290	-1.52	-0.60	-3.37	0.0125911	0.1955	-2.95
250703_at	putative protein similar to unknown	---	AT5G06360	1.41	0.50	3.37	0.01262313	0.1959	-2.95
263725_at	unknown protein	---	AT2G13550	1.24	0.31	3.37	0.01264926	0.1961	-2.95
252093_at	putative protein predicted protein,	---	AT3G51500	1.33	0.41	3.37	0.01267384	0.1964	-2.95
253190_at	UDP-galactose transporter - like p	---	AT4G35335	1.32	0.40	3.37	0.01272591	0.1968	-2.96
256311_at	auxin response factor 6 (ARF6) id	ARF6	AT1G30330	-1.60	-0.68	-3.36	0.01273075	0.1968	-2.96
259811_at	hypothetical protein predicted by g	---	AT1G49830	-1.30	-0.38	-3.36	0.01273359	0.1968	-2.96
247826_at	beta 1-3 glucanase - like protein b	---	AT5G58480	1.31	0.39	3.37	0.01272642	0.1968	-2.96
264702_at	hypothetical protein contains simila	---	AT1G70190	1.35	0.43	3.36	0.01275769	0.1970	-2.96
249879_at	serine/threonine protein kinase-like	---	AT5G23170	-1.30	-0.38	-3.36	0.01276713	0.1970	-2.96
247833_at	putative protein	---	AT5G58575	1.26	0.33	3.36	0.01280647	0.1975	-2.97
256231_at	unknown protein ; supported by ful	---	AT3G12630	1.29	0.36	3.36	0.01282671	0.1976	-2.97
252738_at	putative protein predicted protein,	---	AT3G43240	-1.28	-0.36	-3.36	0.0128257	0.1976	-2.97
263164_at	putative glutamate/aspartate-bindi	---	AT1G03070	-1.31	-0.39	-3.36	0.01285779	0.1979	-2.97
250857_at	unknown protein	---	AT5G04790	1.47	0.56	3.36	0.01287544	0.1980	-2.97
244926_s_at	maturase	---	AT2G07711 /	-1.38	-0.47	-3.35	0.01293028	0.1987	-2.98
256943_at	hypothetical protein similar to hypo	---	AT3G18910	1.27	0.34	3.35	0.01294471	0.1988	-2.98
252353_at	putative protein KIAA0226 gene p	---	AT3G48200	-1.32	-0.40	-3.35	0.01299055	0.1989	-2.98
257086_at	hypothetical protein predicted by g	---	AT3G20490	1.49	0.57	3.35	0.01297741	0.1989	-2.98
260076_at	putative calmodulin similar to calm	---	AT1G73630	-1.53	-0.62	-3.35	0.01297334	0.1989	-2.98
260047_at	putative UDP-N-acetylglucosamine	---	AT1G73740	-1.30	-0.38	-3.35	0.01299026	0.1989	-2.98
265237_s_at	hypothetical protein	---	AT2G07706	-1.33	-0.41	-3.35	0.01298228	0.1989	-2.98
262682_at	anter-specific proline-rich -like prot	---	AT1G75900	2.42	1.28	3.34	0.01321827	0.1989	-3.00
266551_at	unknown protein ; supported by cl	---	AT2G35260	-1.23	-0.29	-3.34	0.01312054	0.1989	-2.99
244906_at	hypothetical protein	---	ATMG00690	-1.29	-0.37	-3.34	0.01313311	0.1989	-2.99
253964_at	putative protein qkI-7, Mus muscu	---	AT4G26480	-1.30	-0.38	-3.35	0.01306778	0.1989	-2.99
256269_at	transcription factor HBP-1B-like ne	TGA6	AT3G12250	1.27	0.35	3.34	0.01311625	0.1989	-2.99
245178_at	putative protein similarity to cDNA	FIS1B	AT5G12390	1.27	0.34	3.35	0.01305155	0.1989	-2.99
254650_at	hypothetical protein	---	---	-1.26	-0.33	-3.34	0.01321029	0.1989	-3.00
267278_at	unknown protein ; supported by fu	---	AT2G19350	1.22	0.29	3.34	0.01319085	0.1989	-3.00
251794_at	mannose-1-phosphate guanylyltra	---	AT3G55590	-1.26	-0.34	-3.34	0.01313909	0.1989	-2.99
266599_at	unknown protein	---	AT2G46100	-1.27	-0.35	-3.34	0.01318762	0.1989	-3.00
264308_at	hypothetical protein similar to hypo	---	AT1G61990	-1.22	-0.28	-3.34	0.01317723	0.1989	-3.00
259373_at	hypothetical protein predicted by g	---	AT1G69160	-1.95	-0.96	-3.34	0.01319645	0.1989	-3.00
260055_at	unknown protein similar to putative	---	AT1G78150	1.27	0.34	3.34	0.01314288	0.1989	-2.99

260497_at	40S ribosomal protein S2 ;suppor	---	AT2G41840	1.79	0.84	3.35	0.01304747	0.1989	-2.98
252161_at	proline-rich protein	---	AT3G50580	-1.23	-0.30	-3.34	0.01308206	0.1989	-2.99
264365_s_at	unknown protein Strong similarity	---	AT1G03220	1.98	0.98	3.34	0.01316714	0.1989	-2.99
248283_at	pyruvate kinase ;supported by full	PKP-BETA	AT5G52920	1.61	0.68	3.34	0.0130935	0.1989	-2.99
247643_at	auxin response factor 4 ; supporte	ARF4	AT5G60450	1.53	0.61	3.35	0.0130336	0.1989	-2.98
261262_at	hypothetical protein predicted by g	SDG35	AT1G26760	-1.25	-0.33	-3.34	0.0131914	0.1989	-3.00
246272_at	hydroxynitrile lyase like protein	MES9	AT4G37150	-2.12	-1.08	-3.34	0.01321637	0.1989	-3.00
248248_at	spermidine synthase ;supported b	SPDS3	AT5G53120	-1.60	-0.68	-3.34	0.0131771	0.1989	-3.00
255436_at	Expressed protein ; supported by c	---	AT4G03150	1.23	0.30	3.35	0.01303821	0.1989	-2.98
247971_at	zinc protease PQQL-like protein	---	AT5G56730	1.29	0.37	3.34	0.01312609	0.1989	-2.99
246092_at	glutaredoxin ;supported by full-len	---	AT5G20500	1.34	0.42	3.35	0.01300395	0.1989	-2.98
251127_at	putative protein predicted protein,	---	AT5G01080	1.35	0.43	3.34	0.01318511	0.1989	-3.00
254150_at	putative protein storage protein - F	---	AT4G24350	-4.02	-2.01	-3.35	0.01305376	0.1989	-2.99
264790_at	putative histidine kinase histidine k	ATHK1	AT2G17820	1.39	0.47	3.34	0.01324042	0.1990	-3.00
255469_at	predicted OR23 protein of unknow	---	AT4G03030	1.32	0.40	3.34	0.01323331	0.1990	-3.00
254034_at	P-glycoprotein-2 (pgp2)	PGP2	AT4G25960	1.48	0.57	3.33	0.01328638	0.1990	-3.00
263332_at	putative snRNP splicing factor ;su	---	AT2G03870	1.28	0.35	3.33	0.01331067	0.1990	-3.01
252937_at	SEC14 - like protein phosphatidyli	SEC14	AT4G39180	-1.28	-0.36	-3.33	0.01329113	0.1990	-3.00
261362_s_at	ribosomal protein identical to GB:C	---	AT1G41880	1.59	0.67	3.33	0.01328581	0.1990	-3.00
250189_at	putative protein ;supported by full-	---	AT5G14410	1.56	0.64	3.33	0.01332499	0.1990	-3.01
252843_at	glycine-rich protein other glycine-ri	---	AT3G42130	-1.41	-0.49	-3.33	0.0132936	0.1990	-3.00
259383_at	putative lectin contains Pfam profi	JR1	AT3G16470	-3.44	-1.78	-3.33	0.01332425	0.1990	-3.01
246429_at	farnesylated protein ATFP6-like p	---	AT5G17450	-1.99	-0.99	-3.33	0.01332064	0.1990	-3.01
266035_at	enoyl-ACP reductase (enr-A)	MOD1	AT2G05990	1.70	0.76	3.33	0.01331423	0.1990	-3.01
263132_at	unknown protein ;supported by full	---	AT1G78560	-1.25	-0.32	-3.33	0.01335776	0.1992	-3.01
256681_at	unknown protein ; supported by cD	SPP2	AT3G52340	2.24	1.16	3.33	0.01335437	0.1992	-3.01
264056_at	putative DOF zinc finger protein ;s	---	AT2G28510	-1.45	-0.54	-3.33	0.01336554	0.1992	-3.01
252831_at	2-dehydro-3-deoxyphosphohepton	DHS1	AT4G39980	-2.26	-1.18	-3.33	0.01336858	0.1992	-3.01
263877_at	hypothetical protein predicted by g	---	AT2G21780	-1.22	-0.29	-3.33	0.01339117	0.1994	-3.01
265353_at	unknown protein ;supported by ful	---	AT2G16800	1.25	0.32	3.33	0.01342113	0.1997	-3.01
262970_at	unknown protein	---	AT1G75690	1.30	0.38	3.31	0.0136499	0.1998	-3.03
254805_at	pEARLI 1 ; supported by cDNA: g	pEARLI 1	AT4G12480	5.06	2.34	3.31	0.01362905	0.1998	-3.03
265029_at	zinc finger protein 7, ZFP7 ; supp	ZFP7	AT1G24625	-1.45	-0.54	-3.32	0.01358411	0.1998	-3.03
253672_at	mRNA cleavage factor subunit - li	CFIM-25	AT4G29820	1.40	0.48	3.31	0.01363763	0.1998	-3.03
250627_at	putative amidase	---	AT5G07360	1.37	0.45	3.32	0.01357582	0.1998	-3.03

246594_at	pyrroline-5-carboxylate reductase	P5CR	AT5G14800	1.40	0.48	3.32	0.01357451	0.1998	-3.03
255716_at	coded for by A. thaliana cDNA R30	CRCK2	AT4G00330	1.22	0.29	3.31	0.01367298	0.1998	-3.03
248624_at	unknown protein ; supported by cl	---	AT5G48790	-1.28	-0.36	-3.32	0.01349097	0.1998	-3.02
249318_at	uridine kinase-like protein	AtUK/UPRT	AT5G40870	1.30	0.38	3.32	0.01360825	0.1998	-3.03
254980_at	putative ribosomal protein L9, cyto	---	AT4G10450	1.75	0.81	3.32	0.01347174	0.1998	-3.02
254819_at	pEARLI 1-like protein Arabidopsis	---	AT4G12500	5.84	2.55	3.31	0.01366563	0.1998	-3.03
261108_at	1-aminocyclopropane-1-carboxyla	ACS10	AT1G62960	1.40	0.48	3.32	0.01359395	0.1998	-3.03
259102_at	unknown protein similar to hin1 GE	NHL1	AT3G11660	-1.38	-0.46	-3.32	0.01345353	0.1998	-3.02
267159_at	putative SCARECROW gene regu	---	AT2G37650	-1.31	-0.39	-3.32	0.01354618	0.1998	-3.02
262120_at	glutathione-S-transferase, putative	ATGSTF4	AT1G02950	1.43	0.52	3.31	0.01363047	0.1998	-3.03
260541_at	putative trypsin inhibitor	---	AT2G43530	-2.36	-1.24	-3.32	0.01359299	0.1998	-3.03
267213_at	60S ribosomal protein L7 ;support	---	AT2G44120	1.68	0.75	3.32	0.01356526	0.1998	-3.03
253191_at	cysteine protease XCP1 identical t	XCP1	AT4G35350	2.50	1.32	3.32	0.01351802	0.1998	-3.02
260538_at	60S ribosomal protein L38	---	AT2G43460	1.50	0.58	3.32	0.01348579	0.1998	-3.02
263529_at	ADP-ribosylation factor 3	ARF3	AT2G24765	1.27	0.34	3.31	0.01366091	0.1998	-3.03
256812_at	hypothetical protein contains simila	---	AT3G21350	1.27	0.34	3.32	0.01345349	0.1998	-3.02
262226_at	Expressed protein ; supported by f	---	AT1G53885 /	-2.05	-1.03	-3.31	0.01367919	0.1998	-3.03
255733_at	unknown protein similar to unknow	---	AT1G25400	1.57	0.65	3.32	0.0135553	0.1998	-3.02
251133_at	LAX1 / AUX1 -like permease	---	AT5G01240	-1.49	-0.57	-3.32	0.01346086	0.1998	-3.02
257225_s_at	50S ribosomal protein L12-C iden	RPL12-C	AT3G27830 /	1.27	0.35	3.31	0.01363726	0.1998	-3.03
245998_at	sucrose-UDP glucosyltransferase	SUS1	AT5G20830	-1.72	-0.78	-3.32	0.01348428	0.1998	-3.02
252646_at	protein kinase-like protein protein	---	AT3G44610	1.27	0.35	3.32	0.01355503	0.1998	-3.02
266216_at	putative DOF zinc finger protein	---	AT2G28810	-1.34	-0.42	-3.32	0.01354238	0.1998	-3.02
259357_at	unknown protein ;supported by full	---	AT1G13380	1.37	0.45	3.32	0.01360077	0.1998	-3.03
251073_at	putative protein hypothetical protei	---	AT5G01750	-1.24	-0.31	-3.31	0.01374342	0.2004	-3.04
263515_at	unknown protein	---	AT2G21640	-2.49	-1.32	-3.31	0.01374307	0.2004	-3.04
263228_at	putative reticuline oxidase-like pro	---	AT1G30700	1.68	0.75	3.31	0.01376801	0.2006	-3.04
249315_at	unknown protein	---	AT5G41190	1.26	0.33	3.31	0.013771	0.2006	-3.04
266791_at	unknown protein	---	AT2G02960	1.28	0.36	3.30	0.01382215	0.2008	-3.04
263286_at	40S ribosomal protein S14 ;suppo	---	AT2G36160	1.50	0.59	3.30	0.01382051	0.2008	-3.04
254466_at	subtilisin-like serine protease conta	---	AT4G20430	1.43	0.52	3.30	0.01381561	0.2008	-3.04
255803_at	putative protein vesicle-associated	---	AT4G10170	1.27	0.35	3.30	0.01380221	0.2008	-3.04
262563_at	somatic embryogenesis receptor-l	SERK2	AT1G34210	-1.40	-0.49	-3.30	0.01383016	0.2008	-3.05
267533_at	unknown protein ;supported by ful	ATNUDX23	AT2G42070	1.32	0.40	3.30	0.01386305	0.2012	-3.05
266319_s_at	putative beta-ketoacyl-CoA syntha	KCS13	AT2G46720 /	-1.52	-0.60	-3.30	0.01391396	0.2016	-3.05

261307_at	unknown protein similar to Glu-tRN	GATB	AT1G48520	1.28	0.36	3.30	0.01390557	0.2016	-3.05
245453_at	disease resistance RPP5 like prote	---	AT4G16900	-1.30	-0.38	-3.30	0.01392866	0.2017	-3.05
246045_at	putative protein predicted proteins	---	AT5G19430	1.41	0.50	3.29	0.01399068	0.2021	-3.06
258138_at	Expressed protein GC donor splice	MSH7	AT3G24495	1.25	0.32	3.29	0.01399589	0.2021	-3.06
259287_at	putative rac GTPase activating pro	---	AT3G11490	1.37	0.45	3.29	0.01399911	0.2021	-3.06
260502_at	putative Tub family protein contair	AtTLP6	AT1G47270	1.34	0.43	3.29	0.0139865	0.2021	-3.06
253234_at	Expressed protein ; supported by f	---	AT4G34265	1.31	0.39	3.29	0.01399057	0.2021	-3.06
244950_at	cytochrome c oxidase subunit 2	---	---	-1.53	-0.61	-3.29	0.01405547	0.2025	-3.06
247793_at	putative protein ; supported by cD	PSY1	AT5G58650	1.48	0.56	3.29	0.01404859	0.2025	-3.06
267090_at	unknown protein ; supported by fu	CXIP2	AT2G38270	1.24	0.31	3.29	0.01403893	0.2025	-3.06
267237_s_at	unknown protein ;supported by ful	---	AT2G44040	1.78	0.83	3.29	0.01408296	0.2028	-3.06
264687_at	cysteine protease XBCP3 identical	XBCP3	AT1G09850	-1.25	-0.32	-3.29	0.01409863	0.2028	-3.07
263178_at	hypothetical protein predicted by g	---	AT1G05550	-1.35	-0.43	-3.29	0.01409364	0.2028	-3.06
258988_at	unknown protein similar to unknow	---	AT3G08890	1.31	0.39	3.29	0.01414297	0.2031	-3.07
255596_at	putative DNA-binding protein simil	WRKY47	AT4G01720	1.88	0.91	3.29	0.0141488	0.2031	-3.07
260008_at	putative RING zinc finger protein c	---	AT1G68070	1.27	0.34	3.29	0.01414011	0.2031	-3.07
264202_at	TINY-like transcription factor Conta	---	AT1G22810	-2.28	-1.19	-3.29	0.01416257	0.2032	-3.07
250159_at	40S ribosomal protein - like 40S ri	---	AT5G15200	1.49	0.57	3.28	0.0142029	0.2035	-3.07
266696_at	copia-like retroelement pol polypro	---	AT2G19680	1.37	0.45	3.28	0.01419652	0.2035	-3.07
248107_at	small Ras-like GTP-binding protein	RAN3	AT5G55190	1.25	0.32	3.28	0.01422485	0.2037	-3.07
248173_at	putative protein contains similarity	---	AT5G54580	1.28	0.36	3.28	0.01424305	0.2038	-3.08
261532_at	amino acid permease, putative sir	---	AT1G71680	-1.27	-0.35	-3.28	0.01431498	0.2041	-3.08
255511_at	Expressed protein ; supported by c	PIT1	AT4G02075	1.73	0.79	3.28	0.01428699	0.2041	-3.08
255080_at	arabinogalactan-protein homolog	AGP10	AT4G09030	1.59	0.67	3.28	0.01431199	0.2041	-3.08
248045_at	HEAT SHOCK PROTEIN 81-2 (HS	HSP81-2	AT5G56030	-1.96	-0.97	-3.28	0.01430318	0.2041	-3.08
246144_at	dynein light chain - like protein dyr	---	AT5G20110	-1.55	-0.63	-3.28	0.01430956	0.2041	-3.08
248768_at	60S acidic ribosomal protein P1-lik	---	AT5G47700	1.56	0.64	3.28	0.0143141	0.2041	-3.08
250843_at	putative RNA-binding protein astro	BTR1L	AT5G04430	1.26	0.34	3.27	0.01436128	0.2046	-3.08
255645_at	coded for by A. thaliana cDNA T43	---	AT4G00880	-1.54	-0.63	-3.27	0.01437921	0.2047	-3.09
249257_at	unknown protein	---	AT5G41640	-1.22	-0.29	-3.27	0.01440616	0.2050	-3.09
265840_at	hypothetical protein predicted by g	---	AT2G14530	1.39	0.47	3.27	0.01442461	0.2051	-3.09
260343_at	fructokinase (Frk1), putative simila	---	AT1G69200	1.45	0.54	3.27	0.01444979	0.2052	-3.09
245016_at	carboxytransferase beta subunit	---	---	-1.27	-0.35	-3.27	0.01445394	0.2052	-3.09
247974_at	putative protein contains similarity	---	AT5G56780	1.27	0.34	3.27	0.01445379	0.2052	-3.09
259668_at	hypothetical protein predicted by g	---	AT1G52390	-1.29	-0.36	-3.27	0.01449779	0.2057	-3.09

261087_at	hypothetical protein similar to unkn	---	AT1G17350	1.51	0.59	3.27	0.01451635	0.2058	-3.10
267620_at	putative beta-1,3-glucanase	---	AT2G39640	-1.27	-0.34	-3.27	0.01454433	0.2059	-3.10
255961_at	UDP-glucose glucosyltransferase,	AtUGT85A1	AT1G22340	-1.58	-0.66	-3.27	0.01453629	0.2059	-3.10
255394_at	hypothetical protein similar to A. th	---	---	-1.30	-0.37	-3.26	0.01459413	0.2061	-3.10
253426_at	putative protein polygalacturonase	---	AT4G32375	-1.27	-0.34	-3.26	0.01457994	0.2061	-3.10
254985_x_at	putative reverse-transcriptase -like	---	---	-1.40	-0.48	-3.26	0.01457381	0.2061	-3.10
262282_at	hypothetical protein predicted by g	---	AT1G68610	-1.35	-0.43	-3.26	0.01459338	0.2061	-3.10
254563_at	putative protein several hypothetic	ERD3	AT4G19120	-1.43	-0.51	-3.26	0.01463845	0.2064	-3.10
264467_at	unknown protein similar to EST gb	---	AT1G10140	1.33	0.41	3.26	0.0146627	0.2064	-3.11
247418_at	glutaredoxin-like protein ; supporte	---	AT5G63030	1.41	0.49	3.26	0.01466504	0.2064	-3.11
264351_at	unknown protein Contains similarit	---	AT1G03370	-1.31	-0.39	-3.26	0.01464595	0.2064	-3.10
261354_at	unknown protein ; supported by cD	atnudt3	AT1G79690	-1.30	-0.38	-3.26	0.0146622	0.2064	-3.11
261845_at	metal ion transporter, putative sim	NRAMP6	AT1G15960	-1.46	-0.54	-3.26	0.0146703	0.2064	-3.11
258830_at	unknown protein	---	AT3G07090	-1.70	-0.77	-3.26	0.0146986	0.2067	-3.11
260689_at	hypothetical protein predicted by g	---	AT1G32290	-1.38	-0.47	-3.26	0.01470998	0.2067	-3.11
266127_s_at	putative mitochondrial translation e	---	AT1G45332 /	1.44	0.53	3.26	0.01471927	0.2067	-3.11
245426_at	hypothetical protein	---	AT4G17540	1.36	0.45	3.26	0.01473876	0.2069	-3.11
261308_at	protein kinase, putative contains s	RKL1	AT1G48480	2.87	1.52	3.25	0.0147709	0.2072	-3.11
260390_at	unknown protein ; supported by fu	---	AT1G73940	1.34	0.42	3.25	0.01480783	0.2073	-3.12
250666_at	SPF1-like protein SPF1 protein - l	WRKY26	AT5G07100	1.81	0.85	3.25	0.01479314	0.2073	-3.11
257003_at	unknown protein ;supported by ful	FLU	AT3G14110	1.45	0.54	3.25	0.01482035	0.2073	-3.12
267516_at	unknown protein	RPT2	AT2G30520	-1.36	-0.44	-3.25	0.01482274	0.2073	-3.12
249799_at	serine palmitoyltransferase ; supp	LCB2	AT5G23670	1.24	0.31	3.25	0.01480214	0.2073	-3.12
260982_at	chalcone isomerase, putative simi	---	AT1G53520	2.31	1.21	3.25	0.01485026	0.2074	-3.12
253791_at	early auxin-inducible protein 11 (IA	IAA11	AT4G28640	1.39	0.48	3.25	0.01484244	0.2074	-3.12
246200_at	putative protein ;supported by full-l	---	AT4G37240	1.65	0.72	3.25	0.01489093	0.2079	-3.12
257900_at	hypothetical protein predicted by g	---	AT3G28420	1.26	0.33	3.25	0.01490702	0.2079	-3.12
263668_at	putative 1-aminocyclopropane-1-ca	---	AT1G04350	-1.34	-0.43	-3.25	0.01491144	0.2079	-3.12
250246_at	polyamine oxidase	ATPAO1	AT5G13700	-1.24	-0.31	-3.25	0.01492088	0.2079	-3.12
252312_at	hypothetical protein SF16 protein,	iqd15	AT3G49380	-1.36	-0.44	-3.24	0.01497972	0.2083	-3.13
264364_at	unknown protein Similar to gb|U85	---	AT1G03330	1.26	0.33	3.24	0.01498369	0.2083	-3.13
247198_at	unknown protein	---	AT5G65290	-1.27	-0.34	-3.24	0.01497416	0.2083	-3.13
259170_at	hypothetical protein similar to puta	---	AT3G03510	-1.26	-0.34	-3.24	0.01497461	0.2083	-3.13
261498_at	receptor kinase, putative similar to	HSL1	AT1G28440	-1.40	-0.49	-3.24	0.01501008	0.2085	-3.13
248102_at	putative protein contains similarity	---	AT5G55140	1.44	0.53	3.24	0.01502847	0.2086	-3.13

254051_at	putative protein other Arabidopsis	---	AT4G25270	-1.29	-0.37	-3.24	0.01505414	0.2086	-3.13
264438_at	putative 60S ribosomal protein L17	---	AT1G27400	1.57	0.65	3.24	0.01505296	0.2086	-3.13
245942_at	putative protein transcription regul	---	AT5G19490	-1.23	-0.30	-3.24	0.01505444	0.2086	-3.13
246260_at	amino acid permease, putative co	---	AT1G31820	1.43	0.51	3.24	0.01509364	0.2090	-3.14
254726_at	isoflavone reductase-like protein is	PRR2	AT4G13660	1.89	0.92	3.24	0.01513483	0.2093	-3.14
260527_at	unknown protein ;supported by ful	---	AT2G47270	2.52	1.34	3.24	0.01513592	0.2093	-3.14
252829_at	homeodomain - like protein ; supp	ATHB16	AT4G40060	-1.38	-0.46	-3.24	0.01514005	0.2093	-3.14
264122_at	GTP-binding protein, ara-5 ras ho	ARA-5	AT1G02130	1.21	0.28	3.23	0.01519556	0.2097	-3.14
259738_at	predicted protein	---	AT1G64355	1.31	0.39	3.23	0.0151843	0.2097	-3.14
265719_at	unknown protein related to putative	---	AT2G03500	-1.26	-0.34	-3.23	0.0151958	0.2097	-3.14
258213_at	hypothetical protein predicted by g	---	AT3G17950	1.49	0.57	3.23	0.01522248	0.2099	-3.14
255539_at	putative actin polymerization facto	CRK	AT4G01710	1.31	0.39	3.23	0.01527258	0.2104	-3.15
249329_at	putative protein similar to unknown	---	AT5G40960	1.40	0.49	3.23	0.015271	0.2104	-3.15
256650_at	hypothetical protein contains simila	---	AT3G13620	-1.33	-0.41	-3.23	0.01528109	0.2104	-3.15
250733_at	2-cys peroxiredoxin-like protein ;s	2-Cys Prx B	AT5G06290	1.36	0.45	3.23	0.01531201	0.2107	-3.15
264335_s_at	hypothetical protein contains simila	UPL1	AT1G55860 /	1.23	0.30	3.22	0.01539379	0.2117	-3.16
262770_at	hypothetical protein predicted by g	---	AT1G13190	-1.50	-0.58	-3.22	0.01547346	0.2126	-3.16
258617_at	putative calmodulin similar to calm	---	AT3G03000	1.24	0.31	3.22	0.01548916	0.2127	-3.16
255531_at	hypothetical protein similar to orf c	---	AT4G02160	-1.30	-0.37	-3.22	0.01549483	0.2127	-3.16
252255_at	pectinesterase - like protein pectin	---	AT3G49220	-1.85	-0.88	-3.22	0.01554217	0.2128	-3.17
265817_at	histone H1 ;supported by full-leng	HIS1-3	AT2G18050	-2.00	-1.00	-3.22	0.0155271	0.2128	-3.16
245783_s_at	hypothetical protein similar to hypo	---	AT1G35170 /	2.06	1.04	3.22	0.01556965	0.2128	-3.17
246021_at	ascorbate oxidase-like protein asc	---	AT5G21100	-1.51	-0.60	-3.22	0.01556083	0.2128	-3.17
263400_s_at	40S ribosomal protein; contains C-	---	AT2G31610 /	1.36	0.44	3.22	0.01553527	0.2128	-3.17
249648_at	putative protein hypothetical prote	---	AT5G37050	-1.44	-0.53	-3.22	0.01554541	0.2128	-3.17
260613_at	unknown protein	---	AT1G53380	1.31	0.39	3.22	0.01555368	0.2128	-3.17
260892_at	cysteine proteinase contains simila	---	AT1G29110	-1.33	-0.41	-3.21	0.01558232	0.2128	-3.17
252940_at	receptor protein kinase - like prote	---	AT4G39270	1.54	0.62	3.21	0.01570189	0.2130	-3.18
252859_at	putative protein AP2 domain conta	---	AT4G39780	1.54	0.62	3.21	0.0156341	0.2130	-3.17
265521_at	hypothetical protein predicted by g	ORG4	AT2G06010	1.36	0.44	3.21	0.01570602	0.2130	-3.18
258728_at	unknown protein ; supported by cl	---	AT3G11800	1.26	0.33	3.21	0.01570097	0.2130	-3.18
253946_at	putative APG protein proline-rich p	---	AT4G26790	-1.50	-0.58	-3.21	0.01564251	0.2130	-3.17
251134_at	hypothetical protein RNA polymer	AtQSOX2	AT2G01270 /	-1.30	-0.38	-3.21	0.01570597	0.2130	-3.18
246443_at	hypothetical protein ;supported by	---	AT5G17620	1.33	0.41	3.21	0.01564319	0.2130	-3.17
245093_at	hypothetical protein predicted by g	---	AT2G40815 /	1.30	0.38	3.21	0.01565606	0.2130	-3.17

261583_at	pyruvate dehydrogenase E1 alpha	PDH-E1 AL	AT1G01090	1.28	0.36	3.21	0.0156954	0.2130	-3.18
258890_at	putative transcription factor similar	NF-YA2	AT3G05690	-1.56	-0.64	-3.21	0.01564296	0.2130	-3.17
260063_at	unknown protein contains Pfam pr	---	AT1G73720	1.31	0.39	3.21	0.01566728	0.2130	-3.17
258486_at	putative 40S ribosomal protein sim	---	AT3G02560	1.86	0.90	3.21	0.01566843	0.2130	-3.17
259816_at	RING-H2 finger protein RHY1a ide	---	AT1G49850	1.30	0.38	3.21	0.01572653	0.2131	-3.18
245984_at	putative protein predicted proteins	---	AT5G13090	1.31	0.39	3.21	0.01573992	0.2132	-3.18
259327_at	putative lectin contains Pfam profi	---	AT3G16460	-3.04	-1.60	-3.21	0.01577472	0.2134	-3.18
245606_at	hypothetical protein	---	AT4G14310	-1.31	-0.39	-3.21	0.01577551	0.2134	-3.18
266918_at	putative LIM-domain protein	---	AT2G45800	-1.25	-0.32	-3.20	0.01579244	0.2135	-3.18
257061_at	hypothetical protein predicted by g	---	AT3G18250	1.59	0.67	3.20	0.01586201	0.2140	-3.19
263131_at	ribosomal protein L13, putative sir	emb1473	AT1G78630	1.29	0.37	3.20	0.01588157	0.2140	-3.19
261335_at	nodulin protein, putative similar to	---	AT1G44800	1.22	0.29	3.20	0.01585876	0.2140	-3.19
255660_at	Expressed protein ; supported by f	---	AT4G00755	1.33	0.42	3.20	0.01587972	0.2140	-3.19
258636_at	putative GTPase activator protein	---	AT3G07890	-1.31	-0.39	-3.20	0.0158485	0.2140	-3.19
253227_at	protein kinase - like leucine rich re	---	AT4G35030	1.33	0.41	3.20	0.01586591	0.2140	-3.19
256930_at	O-acetylserine(thiol) lyase, putativ	OASA2	AT3G22460	1.36	0.45	3.20	0.01596756	0.2143	-3.19
260294_at	GMP synthase similar to GMP syn	---	AT1G63660	1.26	0.33	3.20	0.01595401	0.2143	-3.19
253507_at	serine threonine protein kinase lik	---	AT4G32000	-1.47	-0.56	-3.20	0.0159427	0.2143	-3.19
247376_at	nucleotide diphosphate kinase Ia (	NDPK2	AT5G63310	1.26	0.33	3.20	0.01594433	0.2143	-3.19
259006_at	putative 60S acidic ribosomal prote	---	AT3G09200	1.54	0.62	3.20	0.01592499	0.2143	-3.19
246860_at	putative protein various predicted	---	AT5G25840	-2.00	-1.00	-3.20	0.01598129	0.2143	-3.19
249815_at	60S ribosomal protein L13 ; suppo	---	AT5G23900	1.48	0.57	3.20	0.01593431	0.2143	-3.19
245462_at	transcription factor like protein	---	AT4G17020	-1.32	-0.40	-3.20	0.01597853	0.2143	-3.19
247154_at	receptor protein kinase-like protein	HSL2	AT5G65710	-1.27	-0.34	-3.19	0.01600962	0.2146	-3.20
266264_at	Expressed protein ; supported by f	---	AT2G27775	1.26	0.34	3.19	0.0160809	0.2149	-3.20
261406_at	unknown protein contains similarity	NRP2	AT1G18800	1.50	0.58	3.19	0.0160431	0.2149	-3.20
247845_at	beta-1,3 glucanase - like protein b	---	AT5G58090	1.28	0.36	3.19	0.01608747	0.2149	-3.20
254617_s_at	ribosomal protein L11, cytosolic ;;	RPL16B	AT4G18730 /	1.49	0.57	3.19	0.01608887	0.2149	-3.20
255832_at	hypothetical protein predicted by g	---	AT2G33360	1.42	0.50	3.19	0.01607504	0.2149	-3.20
265182_at	putative auxin-induced protein ;su	---	AT1G23740	-1.44	-0.53	-3.19	0.01605767	0.2149	-3.20
261016_at	beta-glucosidase, putative similar	BGLU40	AT1G26560	-2.50	-1.32	-3.19	0.01613806	0.2154	-3.20
253395_at	protein kinase AME3 ; supported b	AME3	AT4G32660	-1.24	-0.31	-3.19	0.01616603	0.2156	-3.21
264925_at	hypothetical protein contains simil	---	AT1G60670	-1.34	-0.42	-3.19	0.0161847	0.2158	-3.21
258932_at	hypothetical protein predicted by g	PAP16	AT3G10150	-1.27	-0.34	-3.18	0.01622512	0.2162	-3.21
247452_at	H-protein promoter binding factor-l	CDF1	AT5G62430	-1.49	-0.57	-3.18	0.01623538	0.2162	-3.21

257545_at	hypothetical protein predicted by g	---	AT3G23200	1.46	0.54	3.18	0.01626024	0.2162	-3.21
266098_at	hypothetical protein predicted by g	---	AT2G37870	-1.44	-0.52	-3.18	0.01626101	0.2162	-3.21
261886_s_at	hypothetical protein predicted by g	---	AT1G80700	1.22	0.29	3.18	0.01626456	0.2162	-3.21
264679_s_at	putative 60S ribosomal protein L2	---	AT1G09590	1.55	0.63	3.18	0.01633304	0.2169	-3.22
248427_at	subtilisin-like serine protease simil	ATSBT1.3	AT5G51750	-1.40	-0.48	-3.18	0.01633973	0.2169	-3.22
249494_at	acyltransferase - like protein Anth	---	AT5G39050	1.85	0.89	3.18	0.01639833	0.2171	-3.22
254955_at	putative protein RNA polymerase	KELP	AT4G10920	1.26	0.34	3.18	0.01638575	0.2171	-3.22
256205_at	hypothetical protein	---	AT1G50890	1.27	0.35	3.18	0.01638675	0.2171	-3.22
262017_at	elongation factor, putative similar	---	AT1G35550	1.44	0.53	3.18	0.01640374	0.2171	-3.22
264355_at	unknown protein similar to PHZF,	---	AT1G03210	1.48	0.57	3.18	0.01640551	0.2171	-3.22
266867_at	putative signal recognition particle	CPFTSY	AT2G45770	1.30	0.37	3.18	0.01639651	0.2171	-3.22
247632_at	protein transport protein subunit -	---	AT5G60460	1.34	0.42	3.17	0.01647702	0.2172	-3.23
257456_at	unknown protein predicted by gens	SRS4	AT2G18120	-1.30	-0.38	-3.17	0.01645567	0.2172	-3.23
261350_at	hypothetical protein predicted by g	---	AT1G79770	-1.48	-0.57	-3.18	0.01643544	0.2172	-3.22
253444_at	putative protein ring finger protein	---	AT4G32600	-1.25	-0.32	-3.17	0.01646366	0.2172	-3.23
256215_at	unknown protein ;supported by full	---	AT1G50900	1.31	0.39	3.17	0.01647133	0.2172	-3.23
255480_at	Expressed protein ; supported by f	---	AT4G02485	1.25	0.33	3.17	0.01644849	0.2172	-3.22
267134_at	putative protein kinase contains a	---	AT2G23450	-1.21	-0.28	-3.17	0.01650706	0.2175	-3.23
262347_at	unknown protein similar to hypothe	---	AT1G64110	-1.33	-0.41	-3.17	0.01658272	0.2184	-3.23
254655_s_at	ribosomal protein L32 -like protein	---	AT4G18100	1.53	0.61	3.17	0.01663909	0.2190	-3.24
258324_at	putative DNA binding protein ident	TSO1	AT3G22780	1.24	0.31	3.16	0.01668375	0.2195	-3.24
267562_at	unknown protein similar to hypothe	---	AT2G39670	1.26	0.33	3.16	0.01674253	0.2198	-3.24
257750_at	unknown protein ;supported by ful	---	AT3G18800	1.34	0.42	3.16	0.0167807	0.2198	-3.25
262991_at	hypothetical protein predicted by g	BRX-LIKE3	AT1G54180	-1.23	-0.30	-3.16	0.01675237	0.2198	-3.24
259795_at	hypothetical protein predicted by g	---	AT1G64290	-1.32	-0.40	-3.16	0.01679246	0.2198	-3.25
258805_at	putative beta-1,3-glucanase simila	---	AT3G04010	-1.45	-0.54	-3.16	0.01677691	0.2198	-3.24
261670_at	hypothetical protein contains simila	TET11	AT1G18520	-1.23	-0.30	-3.16	0.01675897	0.2198	-3.24
246662_at	putative protein	---	AT5G35290	-1.29	-0.36	-3.16	0.01672484	0.2198	-3.24
248160_at	putative protein similar to unknown	---	AT5G54470	-1.44	-0.52	-3.16	0.01678694	0.2198	-3.25
265892_at	hypothetical protein predicted by g	---	AT2G15020	-1.61	-0.69	-3.16	0.01678027	0.2198	-3.25
249795_at	40S ribosomal protein S11 ;suppor	RPS11-BE	AT5G23740	1.62	0.70	3.16	0.01680827	0.2198	-3.25
267218_at	Expressed protein ; supported by f	---	AT2G02515	-1.28	-0.35	-3.16	0.01683284	0.2200	-3.25
262813_at	unknown protein strong similarity t	---	AT1G11670	-2.09	-1.06	-3.16	0.01683854	0.2200	-3.25
249732_at	6-phosphogluconolactonase-like p	---	AT5G24420	-6.80	-2.76	-3.16	0.01686022	0.2201	-3.25
254966_at	COP1 like protein photomorphoge	SPA2	AT4G11110	-1.22	-0.28	-3.16	0.01686622	0.2201	-3.25

251995_at	nuclear envelope membrane prote	FK	AT3G52940	1.25	0.32	3.16	0.01688166	0.2202	-3.25
257752_at	hypothetical protein predicted by g	---	AT3G18720	-1.30	-0.38	-3.15	0.0169122	0.2203	-3.25
263593_at	hypothetical protein predicted by g	EMB975	AT2G01860	1.37	0.45	3.15	0.01690392	0.2203	-3.25
261304_at	unknown protein ;supported by full	---	AT1G48440	-1.22	-0.28	-3.15	0.01695889	0.2208	-3.26
261117_at	unknown protein	AUL1	AT1G75310	-1.51	-0.59	-3.15	0.01700422	0.2209	-3.26
262225_at	pectinesterase, putative similar to	ATPME1	AT1G53840	-1.71	-0.78	-3.15	0.01706979	0.2209	-3.26
267220_at	putative sugar nucleotide phospho	ISPD	AT2G02500	1.36	0.44	3.15	0.01703895	0.2209	-3.26
252023_at	putative protein various predicted	---	AT3G52920	1.87	0.90	3.15	0.01703177	0.2209	-3.26
266338_at	putative ligand-gated ion channel s	GLR5	AT2G32400	-1.37	-0.46	-3.15	0.01705881	0.2209	-3.26
246230_at	SCARECROW-like protein	---	AT4G36710	-1.27	-0.35	-3.15	0.01705926	0.2209	-3.26
260923_at	glycine-rich RNA-binding protein g	---	AT1G21570	-1.30	-0.38	-3.15	0.01702569	0.2209	-3.26
257132_at	hypothetical protein predicted by g	---	AT3G20230	1.28	0.35	3.15	0.01705129	0.2209	-3.26
244972_at	PSII 47KDa protein	---	---	-1.92	-0.94	-3.15	0.01702873	0.2209	-3.26
259594_at	unknown protein contains similarity	---	AT1G28140	-1.26	-0.34	-3.15	0.01700582	0.2209	-3.26
245279_at	putative protein ; supported by cDN	---	AT4G17270	1.27	0.35	3.15	0.01706923	0.2209	-3.26
259497_at	unknown protein	---	AT1G15860	1.22	0.29	3.15	0.01710955	0.2212	-3.27
253149_at	NAD+ dependent isocitrate dehyd	---	AT4G35650	-1.30	-0.38	-3.14	0.01714101	0.2215	-3.27
265985_at	hypothetical protein predicted by g	ATPUP5	AT2G24220	-1.25	-0.32	-3.14	0.01716371	0.2217	-3.27
249167_at	putative protein similar to unknown	---	AT5G42860	-1.89	-0.92	-3.14	0.01717909	0.2218	-3.27
249927_at	Glucose-1-phosphate adenylyltran	APL1	AT5G19220	-1.52	-0.60	-3.14	0.01726664	0.2226	-3.27
264894_at	unknown protein Location of EST g	---	AT1G23040	1.35	0.43	3.14	0.01727447	0.2226	-3.28
247191_at	homeobox-leucine zipper protein A	ATHB5	AT5G65310	-1.54	-0.63	-3.14	0.01729224	0.2226	-3.28
256794_at	ribosomal protein L27, putative sir	---	AT3G22230	1.77	0.82	3.14	0.01729057	0.2226	-3.28
261235_x_at	hypothetical protein predicted by g	---	---	-1.24	-0.31	-3.14	0.01725828	0.2226	-3.27
256854_at	hypothetical protein predicted by g	---	AT3G15180	-1.27	-0.34	-3.14	0.01731015	0.2227	-3.28
249145_at	enoyl CoA hydratase-like protein	ATDCI1	AT5G43280	-1.25	-0.32	-3.14	0.01732693	0.2227	-3.28
245736_at	Dr4(protease inhibitor) identical to	ATDR4	AT1G73330	-1.79	-0.84	-3.14	0.01733275	0.2227	-3.28
259348_at	hypothetical protein may contain C	---	AT3G03770	-1.52	-0.60	-3.14	0.0173505	0.2228	-3.28
251552_at	ribosomal protein L11 -like riboson	---	AT3G58700	1.59	0.67	3.14	0.01735734	0.2228	-3.28
246758_at	60S ribosomal protein - like 60S ri	---	AT5G27850	1.57	0.65	3.13	0.0174147	0.2233	-3.28
258858_at	putative 40S ribosomal protein S19	---	AT3G02080	1.59	0.66	3.13	0.01740806	0.2233	-3.28
266210_at	60S ribosomal protein L10A ; supp	PGY1	AT2G27530	1.57	0.65	3.13	0.01743017	0.2234	-3.28
246449_at	hypothetical protein	---	AT5G16810	-1.31	-0.39	-3.13	0.01744563	0.2234	-3.29
261794_at	hypothetical protein contains simila	---	AT1G16060	-1.36	-0.44	-3.13	0.01752701	0.2241	-3.29
245551_at	cytochrome P450 like protein	CYP705A2	AT4G15350	-1.23	-0.30	-3.13	0.01751245	0.2241	-3.29

267496_at	putative lipase ; supported by full-	---	AT2G30550	-1.41	-0.49	-3.13	0.01752178	0.2241	-3.29
260160_at	putative RNA-binding protein cont	---	AT1G79880	1.26	0.34	3.13	0.01758974	0.2248	-3.29
253072_at	putative protein ;supported by full-	---	AT4G37830	1.24	0.31	3.12	0.01761072	0.2249	-3.30
246935_at	leucine-rich repeats containing pro	EBF2	AT5G25350	1.54	0.62	3.12	0.01761568	0.2249	-3.30
262259_s_at	hypothetical protein predicted by g	---	AT1G53870	-1.49	-0.57	-3.12	0.01762839	0.2249	-3.30
258751_at	low temperature and salt responsiv	RCI2B	AT3G05890	2.35	1.23	3.12	0.01766385	0.2251	-3.30
246472_at	putative protein predicted protein,	---	AT5G17130	-1.22	-0.29	-3.12	0.01769315	0.2251	-3.30
246195_at	E2, ubiquitin-conjugating enzyme	UBC17	AT4G36410	2.77	1.47	3.12	0.01767656	0.2251	-3.30
245894_at	putative protein ; supported by full	---	AT5G09310	1.25	0.32	3.12	0.01768557	0.2251	-3.30
249759_at	putative protein contains similarity	YSL2	AT5G24380	-1.45	-0.53	-3.12	0.01765587	0.2251	-3.30
249129_at	cyclin A-type	CYCA3;1	AT5G43080	1.30	0.38	3.12	0.01774009	0.2256	-3.30
260820_at	receptor protein kinase, putative s	---	AT1G06840	1.60	0.68	3.12	0.01775276	0.2256	-3.30
247987_at	putative protein similar to unknown	---	AT5G56900	1.31	0.39	3.12	0.0177928	0.2260	-3.31
251663_at	putative protein hypothetical prote	---	AT3G57070	-1.28	-0.36	-3.12	0.0178155	0.2261	-3.31
254280_at	Expressed protein ; supported by f	SMO1-2	AT4G22756	1.46	0.54	3.12	0.01784078	0.2263	-3.31
254245_at	serine/threonine kinase - like prote	---	AT4G23240	-1.26	-0.33	-3.11	0.01785124	0.2263	-3.31
259800_at	Expressed protein ; supported by f	---	AT1G72175	-1.35	-0.44	-3.11	0.01788357	0.2266	-3.31
250495_at	ribsomal protein - like chloroplast	---	AT5G09770	1.37	0.45	3.11	0.01791293	0.2268	-3.31
246503_at	40S ribosomal protein S7-like 40S	---	AT5G16130	1.63	0.70	3.11	0.0179173	0.2268	-3.31
260430_at	putative zinc finger protein similar t	---	AT1G68200	-1.24	-0.31	-3.11	0.01793051	0.2268	-3.31
246830_at	chaperonin gamma chain - like pro	---	AT5G26360	1.59	0.67	3.11	0.01797219	0.2270	-3.32
254011_at	putative protein transcription termi	---	AT4G26370	1.31	0.39	3.11	0.01797636	0.2270	-3.32
262738_at	hypothetical protein	---	AT1G28530	1.36	0.44	3.11	0.01797526	0.2270	-3.32
253901_at	ribosomal protein L14 -like protein	---	AT4G27090	1.51	0.59	3.11	0.01798697	0.2271	-3.32
248552_at	RNA-binding protein-like ; support	---	AT5G50250	1.28	0.36	3.11	0.01800718	0.2271	-3.32
250904_at	subtilisin-like serine protease conta	---	AT5G03620	-1.25	-0.32	-3.11	0.01800985	0.2271	-3.32
247018_at	AP2 domain transcription factor-lik	---	AT5G67000	-1.21	-0.27	-3.11	0.01802846	0.2272	-3.32
248685_at	putative protein similar to unknown	---	AT5G48500	1.47	0.55	3.10	0.01813423	0.2283	-3.33
247258_at	expressed protein similar to unkno	---	AT5G64816	1.33	0.41	3.10	0.01812958	0.2283	-3.32
249093_at	putative protein similar to unknown	---	AT5G43880	-1.24	-0.30	-3.10	0.01821782	0.2291	-3.33
250190_at	ribosomal protein precursor - like	---	AT5G14320	1.26	0.33	3.10	0.01821353	0.2291	-3.33
266572_at	unknown protein	---	AT2G23840	-1.44	-0.53	-3.10	0.01825702	0.2292	-3.33
265983_at	putative homeodomain transcriptio	HB-2	AT2G18550	-1.25	-0.32	-3.10	0.01825282	0.2292	-3.33
261792_at	cinnamoyl CoA reductase, puitativ	CCR1	AT1G15950	-1.33	-0.42	-3.10	0.01824771	0.2292	-3.33
247511_at	Fdr1 Cen - like protein Fdr1, Oryz	---	AT5G62040	-1.33	-0.41	-3.10	0.01827896	0.2292	-3.33

263092_at	hypothetical protein predicted by g	---	AT2G16210	-1.24	-0.31	-3.10	0.01828044	0.2292	-3.33
256461_s_at	adenylosuccinate lyase - like prote	---	AT1G36280	-2.09	-1.07	-3.10	0.01831145	0.2294	-3.34
263525_at	putative MADS-box protein	AGL61	AT2G24840	-1.36	-0.45	-3.10	0.0183052	0.2294	-3.33
262937_at	FtsH protease, putative contains s	FTSH12	AT1G79560	1.24	0.31	3.09	0.01841948	0.2301	-3.34
267524_at	unknown protein	---	AT2G30600	-1.44	-0.53	-3.09	0.01842076	0.2301	-3.34
253903_at	kinesin-related protein katB ; supp	ATK2	AT4G27180	-1.21	-0.27	-3.09	0.01838636	0.2301	-3.34
261903_at	chromomethylase identical to GB:A	CMT1	AT1G80740	-1.23	-0.30	-3.09	0.01843004	0.2301	-3.34
262992_at	hypothetical protein predicted by g	ATG12A	AT1G54210	1.41	0.49	3.09	0.01844097	0.2301	-3.34
254236_at	putative protein VSG expression s	---	AT4G23840	1.26	0.33	3.09	0.01844885	0.2301	-3.34
245000_at	hypothetical protein	---	---	-1.28	-0.35	-3.09	0.01840041	0.2301	-3.34
254971_at	major intrinsic protein (MIP) - like	NIP5;1	AT4G10380	-1.48	-0.56	-3.09	0.01844131	0.2301	-3.34
262957_s_at	RNA polymerase II subunit, putati	NRPB8A	AT1G54250	1.20	0.27	3.09	0.01847577	0.2301	-3.34
253061_at	putative protein SPOP, Homo sap	BT5	AT4G37610	1.57	0.65	3.09	0.01848214	0.2301	-3.34
265953_at	unknown protein	---	AT2G37478	1.26	0.33	3.09	0.01846739	0.2301	-3.34
249636_at	beta-glucosidase -like protein prur	BGLU42	AT5G36890	-1.29	-0.36	-3.09	0.01850396	0.2302	-3.35
263432_at	putative beta-hydroxyacyl-ACP del	---	AT2G22230	1.38	0.46	3.09	0.01850733	0.2302	-3.35
252418_at	hypothetical protein	---	AT3G47490	1.37	0.45	3.09	0.01852866	0.2303	-3.35
249525_at	putative protein similar to unknowr	---	AT5G38650	1.25	0.33	3.09	0.01856115	0.2303	-3.35
262887_at	hypothetical protein	---	AT1G14780	-2.27	-1.18	-3.09	0.01854681	0.2303	-3.35
263996_at	unknown protein	---	AT2G22530	-1.32	-0.41	-3.09	0.01855446	0.2303	-3.35
261564_at	NAC domain protein, putative sim	ATAF1	AT1G01720	1.42	0.51	3.08	0.01859406	0.2306	-3.35
262653_at	dioxygenase-like protein very simi	---	AT1G14130	-1.23	-0.29	-3.08	0.01866105	0.2309	-3.35
255580_at	putative water channel protein	TIP1;3	AT4G01470	-1.35	-0.44	-3.08	0.01866377	0.2309	-3.35
260520_at	mannosyl-oligosaccharide alpha-1	---	AT1G51590	1.30	0.38	3.08	0.01864667	0.2309	-3.35
251770_at	leucoanthocyanidin dioxygenase -	---	AT3G55970	-3.23	-1.69	-3.08	0.01864726	0.2309	-3.35
261140_at	unknown protein	---	AT1G19680	-1.31	-0.39	-3.08	0.01862886	0.2309	-3.35
262607_at	unknown protein ;supported by full	---	AT1G13990	-1.36	-0.44	-3.08	0.01867707	0.2309	-3.36
246152_at	IPP transferase - like protein tRNA	IPT9	AT5G20040	1.27	0.34	3.08	0.01876347	0.2310	-3.36
249947_at	FVT1 - like protein follicular lymph	---	AT5G19200	1.23	0.30	3.08	0.01873111	0.2310	-3.36
251421_at	enoyl-CoA-hydratase - like protein	---	AT3G60510	1.28	0.35	3.08	0.0187671	0.2310	-3.36
258966_at	putative DNA gyrase subunit A sim	---	AT3G10690	1.58	0.66	3.08	0.01877582	0.2310	-3.36
254681_at	putative protein HYA22 protein, H	---	AT4G18140	-1.48	-0.57	-3.08	0.01877187	0.2310	-3.36
261651_at	unknown protein similar to unknow	SAT32	AT1G27760	-1.63	-0.70	-3.08	0.01871853	0.2310	-3.36
258692_at	unknown protein	---	AT3G08640	-1.57	-0.65	-3.08	0.01871453	0.2310	-3.36
260321_at	putative RING zinc finger protein F	---	AT1G63900	1.27	0.35	3.08	0.01872575	0.2310	-3.36

261054_at	hypothetical protein predicted by g	---	AT1G01320	-1.61	-0.69	-3.08	0.01874688	0.2310	-3.36
253336_at	putative protein Caenorhabditis el	EIF3K	AT4G33250	1.30	0.38	3.08	0.01881764	0.2310	-3.36
252823_at	Expressed protein ; supported by f	---	AT4G40045	1.29	0.37	3.08	0.01880174	0.2310	-3.36
267293_at	hypothetical protein	TET8	AT2G23810	1.55	0.63	3.08	0.01881568	0.2310	-3.36
260369_at	60S ribosomal protein L34, putativ	RPL34	AT1G69620	1.42	0.50	3.08	0.01880496	0.2310	-3.36
262996_at	hypothetical protein predicted by g	---	AT1G54440	1.27	0.35	3.07	0.01889103	0.2313	-3.37
260925_at	DNA-binding protein, putative con	---	AT1G21340	-1.31	-0.39	-3.07	0.01886045	0.2313	-3.37
254399_at	G10 - like protein Maternal G10 lik	---	AT4G21110	1.22	0.29	3.07	0.01886928	0.2313	-3.37
256676_at	putative protein ;supported by full-	SEX4	AT3G52180	-1.49	-0.57	-3.07	0.01888964	0.2313	-3.37
256010_at	auxin response factor, putative sir	ARF19	AT1G19220	-1.32	-0.40	-3.07	0.01887942	0.2313	-3.37
246829_at	putative protein pyruvate water dik	ATGWD3	AT5G26570	-1.25	-0.32	-3.07	0.01892078	0.2315	-3.37
256455_at	unknown protein ;supported by full	---	AT1G75190	-1.27	-0.35	-3.07	0.01894001	0.2316	-3.37
246975_at	putative protein hypothetical protei	---	AT5G24890	1.39	0.48	3.07	0.0189962	0.2322	-3.37
246510_at	cyclic nucleotide-gated cation char	DND1	AT5G15410	-1.32	-0.40	-3.07	0.01900823	0.2322	-3.37
253736_at	Proline-rich APG - like protein pro	---	AT4G28780	1.51	0.59	3.07	0.01909359	0.2326	-3.38
246442_at	hypothetical protein ;supported by	---	AT5G17610	1.24	0.31	3.07	0.01906166	0.2326	-3.38
262170_at	hypothetical protein predicted by g	---	AT1G74940	1.46	0.54	3.07	0.01909693	0.2326	-3.38
259655_at	unknown protein	---	AT1G55210	-2.15	-1.10	-3.07	0.01909347	0.2326	-3.38
266034_at	Expressed protein ; supported by f	FIP1	AT2G06005	-1.24	-0.31	-3.07	0.01905268	0.2326	-3.38
266530_at	bHLH transcription factor	AMS	AT2G16910	-1.21	-0.27	-3.07	0.01910014	0.2326	-3.38
261077_at	protein phosphatase 2C, putative	---	AT1G07430	-1.48	-0.56	-3.06	0.01911583	0.2327	-3.38
258809_at	NAM-like protein (no apical meriste	anac047	AT3G04070	1.87	0.90	3.06	0.01918042	0.2333	-3.38
251737_at	40S ribosomal protein S26 homolo	---	AT3G56340	1.73	0.79	3.06	0.0192244	0.2337	-3.39
260486_at	F-box protein ZEITLUPE/FKF/LKP	---	AT1G51550	1.29	0.36	3.06	0.01928307	0.2339	-3.39
250462_at	receptor protein kinase -like(fragm	---	AT5G10020	1.21	0.27	3.06	0.01929447	0.2339	-3.39
263294_at	hypothetical protein predicted by g	---	---	-1.38	-0.46	-3.06	0.01927102	0.2339	-3.39
247239_at	pectin methylesterase-like protein	---	AT5G64640	-1.30	-0.38	-3.06	0.01925986	0.2339	-3.39
249922_at	aluminium-induced protein - like a	AILP1	AT5G19140	-1.27	-0.34	-3.06	0.01929059	0.2339	-3.39
251991_at	transcription factor NF-Y, CCAAT-	NF-YB10	AT3G53340	1.36	0.45	3.06	0.01927974	0.2339	-3.39
247323_at	putative protein similar to unknown	---	AT5G64170	-1.43	-0.51	-3.05	0.01938229	0.2347	-3.39
259247_at	unknown protein predicted by gen	---	AT3G07570	1.36	0.45	3.05	0.01938638	0.2347	-3.39
259123_at	unknown protein	---	AT3G02200	1.25	0.32	3.05	0.01942246	0.2349	-3.40
249910_at	chorismate mutase/prephenate de	ADT5	AT5G22630	-2.07	-1.05	-3.05	0.01941887	0.2349	-3.40
249965_at	putative protein predicted proteins	---	AT5G19020	-1.20	-0.26	-3.05	0.01947624	0.2352	-3.40
259204_s_at	hypothetical protein predicted by g	---	---	-1.25	-0.32	-3.05	0.01948316	0.2352	-3.40

244931_at	hypothetical protein	---	---	-1.43	-0.51	-3.05	0.01945799	0.2352	-3.40
266391_at	putative strictosidine synthase ider	---	AT2G41290	-1.37	-0.45	-3.05	0.0194988	0.2352	-3.40
247930_at	putative protein similar to unknown	---	AT5G57060	1.44	0.53	3.05	0.01949364	0.2352	-3.40
264683_at	unknown protein similar to putative	FRA3	AT1G65580	-1.22	-0.29	-3.05	0.01955742	0.2358	-3.40
256397_at	putative dual-specificity protein pho	MKP2	AT3G06110	1.26	0.33	3.05	0.01959632	0.2359	-3.41
261620_s_at	ribosomal protein L9, putative sim	PGY2	AT1G33120	1.39	0.47	3.05	0.01959687	0.2359	-3.41
252500_at	proteinase inhibitor-like protein enc	---	AT3G46860	-1.24	-0.31	-3.05	0.01959902	0.2359	-3.41
265677_at	putative purine-rich single-strande	PUR ALPH	AT2G32080	-1.24	-0.31	-3.05	0.01961873	0.2360	-3.41
265805_s_at	60S ribosomal protein L2	EMB2296	AT2G18020	1.41	0.49	3.04	0.0196598	0.2364	-3.41
251639_at	acetylglutamate kinase-like protei	---	AT3G57560	1.35	0.44	3.04	0.01967091	0.2364	-3.41
254315_at	putative glycine-rich protein glycin	---	---	-1.41	-0.50	-3.04	0.01969452	0.2366	-3.41
262876_at	unknown protein ;supported by full	ATDSS1(I)	AT1G64750	1.36	0.45	3.04	0.01972021	0.2367	-3.41
258916_at	putative ABC transporter ATPase s	ATNAP7	AT3G10670	-1.26	-0.33	-3.04	0.01976799	0.2371	-3.41
251035_at	Expressed protein ; supported by f	---	AT5G02220	1.44	0.53	3.04	0.01976591	0.2371	-3.41
247089_at	dimethyladenosine transferase-like	---	AT5G66360	1.31	0.39	3.04	0.01983155	0.2373	-3.42
263181_at	unknown protein ;supported by ful	---	AT1G05720	1.24	0.31	3.04	0.01980702	0.2373	-3.42
257734_at	unknown protein contains Pfam pr	ATSYTF	AT3G18370	1.22	0.29	3.04	0.01983987	0.2373	-3.42
267015_at	unknown protein	---	AT2G39340	-1.34	-0.42	-3.04	0.0198451	0.2373	-3.42
251345_at	putative protein hypothetical protei	---	AT3G60940	1.27	0.35	3.04	0.01981676	0.2373	-3.42
253310_at	hypothetical protein ; supported by	EX1	AT4G33630	-1.25	-0.32	-3.04	0.01984752	0.2373	-3.42
259344_at	putative polynucleotide phosphory	RIF10	AT3G03710	1.34	0.42	3.03	0.0199919	0.2377	-3.43
250087_at	putative protein contains similarity	---	AT5G17270	1.52	0.61	3.03	0.01998123	0.2377	-3.43
256648_at	ribosomal protein, putative similar	---	AT3G13580	1.41	0.49	3.03	0.01991438	0.2377	-3.42
252566_at	cytoplasmic ribosomal protein S15	RPS15AD	AT3G46040	1.37	0.46	3.03	0.01999613	0.2377	-3.43
262680_at	anter-specific proline-rich -like prot	---	AT1G75880	-1.49	-0.58	-3.03	0.01999654	0.2377	-3.43
262380_at	threonine synthase, putative simila	---	AT1G72810	-1.31	-0.39	-3.03	0.01992534	0.2377	-3.42
258569_at	ribosomal protein L17, putative sir	emb2171	AT3G04400	1.43	0.51	3.03	0.01999861	0.2377	-3.43
251195_at	glutaredoxin -like protein glutared	---	AT3G62930	1.52	0.60	3.03	0.02000046	0.2377	-3.43
250563_at	putative protein predicted protein,	---	AT5G08050	1.44	0.53	3.03	0.0199846	0.2377	-3.43
259495_at	NBS/LRR disease resistance prot	---	AT1G15890	-1.32	-0.40	-3.03	0.01995342	0.2377	-3.42
267513_at	unknown protein ; supported by cl	---	AT2G45620	1.28	0.36	3.03	0.01993363	0.2377	-3.42
251914_at	putative protein serine/threonine-s	---	AT3G53930	-1.27	-0.35	-3.03	0.02001356	0.2378	-3.43
263733_at	polyprotein, putative similar to poly	---	---	1.20	0.27	3.03	0.02004501	0.2380	-3.43
249948_at	eIF-4AII - like protein EUKARYOT	---	AT5G19210	1.38	0.46	3.03	0.02009145	0.2384	-3.43
261322_at	hypothetical protein predicted by g	ATPUP11	AT1G44750	-1.30	-0.38	-3.03	0.02012002	0.2385	-3.43

265999_at	unknown protein ; supported by cl	---	AT2G24100	-1.39	-0.47	-3.03	0.02011216	0.2385	-3.43
248140_at	putative protein similar to unknown	---	AT5G54980	1.28	0.35	3.03	0.02014409	0.2387	-3.43
248153_at	cyclic nucleotide and calmodulin-re	ATCNGC4	AT5G54250	-1.30	-0.38	-3.03	0.02015817	0.2387	-3.43
253832_at	Expressed protein ; supported by f	---	AT4G27654	-2.02	-1.02	-3.03	0.02016847	0.2387	-3.43
250958_at	laccase precursor - like laccase pr	LAC11	AT5G03260	2.15	1.10	3.02	0.02019472	0.2389	-3.44
245198_at	Expressed protein ; supported by f	---	AT1G67700	1.26	0.34	3.02	0.02026186	0.2396	-3.44
248192_at	IAA-amino acid hydrolase homolog	ILL3	AT5G54140	1.26	0.33	3.02	0.02028006	0.2397	-3.44
248359_at	unknown protein	---	AT5G52410	-1.32	-0.40	-3.02	0.02029785	0.2398	-3.44
250486_at	putative protein predicted proteins	---	AT5G09670	-1.28	-0.36	-3.02	0.02031678	0.2399	-3.44
252220_at	putative protein hypothetical prote	LBD38	AT3G49940	1.50	0.58	3.02	0.02036549	0.2403	-3.44
248191_at	putative protein similar to unknown	---	AT5G54130	-1.32	-0.40	-3.02	0.02039842	0.2406	-3.45
266014_s_at	hypothetical protein	---	AT2G07722	-1.65	-0.73	-3.02	0.02041388	0.2406	-3.45
251841_at	putative protein CRP1, Zea mays,	---	AT3G54980	-1.49	-0.58	-3.02	0.02043487	0.2407	-3.45
256951_at	hypothetical protein predicted by g	---	AT3G19085	-1.21	-0.28	-3.02	0.02044088	0.2407	-3.45
261572_at	unknown protein	---	AT1G01170	1.33	0.41	3.02	0.02046286	0.2408	-3.45
245816_at	hypothetical protein similar to hypo	---	AT1G26210	-1.71	-0.78	-3.01	0.02050912	0.2411	-3.45
260020_at	hydrophilic protein, putative simila	PDF6	AT1G29990	1.22	0.29	3.01	0.02050538	0.2411	-3.45
260273_at	unknown protein	---	AT1G80550	1.33	0.41	3.01	0.02059197	0.2412	-3.46
252874_at	putative protein ipiB1 gene, Phyto	---	---	-1.27	-0.35	-3.01	0.02057408	0.2412	-3.46
254225_at	putative major latex protein major	---	AT4G23670	-2.89	-1.53	-3.01	0.02058776	0.2412	-3.46
261233_at	hypothetical protein similar to hypo	---	AT1G32810	-1.31	-0.39	-3.01	0.02057514	0.2412	-3.46
257999_at	hypothetical protein similar to hypo	---	AT3G27540	-1.58	-0.66	-3.01	0.02058332	0.2412	-3.46
261100_at	RNA polymerase IIA large subunit	NRPD1A	AT1G63020	-1.28	-0.36	-3.01	0.02053976	0.2412	-3.45
262183_at	unknown protein	---	AT1G77890	1.26	0.33	3.01	0.02058709	0.2412	-3.46
258720_at	putative ankyrin similar to ankyrin	---	AT3G09550	-1.33	-0.41	-3.01	0.02059685	0.2412	-3.46
248093_at	putative protein similar to unknown	---	AT5G55210	1.32	0.40	3.01	0.02063463	0.2414	-3.46
261530_at	unknown protein contains Pfam pr	---	AT1G63460	1.37	0.45	3.01	0.02062703	0.2414	-3.46
255994_at	hypothetical protein predicted by g	---	AT1G29760	1.24	0.31	3.01	0.02064924	0.2414	-3.46
246614_at	serine/threonine protein kinase SO	SOS2	AT5G35410	1.26	0.33	3.01	0.02073566	0.2415	-3.46
263730_at	beta-glucosidase, putative similar	BGLU4	AT1G60090	-1.24	-0.31	-3.01	0.02066448	0.2415	-3.46
247899_at	Expressed protein ; supported by f	---	AT5G57345	-1.34	-0.42	-3.01	0.02073441	0.2415	-3.46
261614_at	poly(A)-binding protein, putative s	PAB8	AT1G49760	1.40	0.48	3.01	0.02071384	0.2415	-3.46
254832_at	pEARLI 1-like protein Arabidopsis	---	AT4G12490	4.20	2.07	3.01	0.0207203	0.2415	-3.46
247780_at	dehydrodolichyl diphosphate - like	---	AT5G58770	-1.97	-0.98	-3.01	0.02073825	0.2415	-3.46
258262_at	hypothetical protein	---	AT3G15770	1.34	0.42	3.01	0.02068551	0.2415	-3.46

258440_at	putative protein phosphatase simil	---	AT3G17250	-1.28	-0.35	-3.01	0.02071782	0.2415	-3.46
266938_at	hypothetical protein predicted by g	HPT1	AT2G18950	-1.34	-0.43	-3.00	0.02081594	0.2418	-3.47
257337_at	NADH dehydrogenase subunit 5 (r	---	---	-1.69	-0.75	-3.00	0.0207751	0.2418	-3.47
245315_at	proteasome chain protein ; suppor	PBD2	AT4G14800	1.24	0.31	3.00	0.0208168	0.2418	-3.47
253266_s_at	putative protein predicted protein,	---	AT2G45260	1.32	0.40	3.00	0.02081292	0.2418	-3.47
266022_at	subtilisin-like serine protease, puta	---	AT2G05920	1.45	0.53	3.00	0.0207989	0.2418	-3.47
267132_at	unknown protein	NAPRT2	AT2G23420	1.57	0.65	3.00	0.02083723	0.2419	-3.47
266894_at	hypothetical protein predicted by g	---	AT2G26050	-1.21	-0.27	-3.00	0.02086166	0.2420	-3.47
264108_at	hypothetical protein predicted by g	CALS5	AT2G13680	-1.24	-0.31	-3.00	0.0208968	0.2423	-3.47
255702_at	subtilisin-like serine protease XSP	XSP1	AT4G00230	1.43	0.52	3.00	0.02093136	0.2426	-3.47
252483_at	scarecrow-like protein scarecrow-	---	AT3G46600	1.78	0.83	3.00	0.02096265	0.2428	-3.47
255662_at	putative protein	GPAT8	AT4G00400	1.63	0.71	3.00	0.02101953	0.2434	-3.48
267028_at	putative WRKY-type DNA binding	WRKY33	AT2G38470	3.50	1.81	2.99	0.02109276	0.2439	-3.48
264883_s_at	secretory carrier membrane protei	---	AT1G11180	1.26	0.33	2.99	0.02107979	0.2439	-3.48
248566_s_at	FRO2-like protein; NADPH oxidase	ATFRO7	AT5G49730	-1.58	-0.66	-2.99	0.02108269	0.2439	-3.48
265413_s_at	hypothetical protein predicted by g	---	AT2G16650	1.30	0.37	2.99	0.02111817	0.2440	-3.48
260345_at	receptor protein kinase, putative s	RPK1	AT1G69270	1.44	0.52	2.99	0.02116001	0.2442	-3.48
258296_at	putative ribosomal protein similar t	---	AT3G23390	1.70	0.77	2.99	0.02116813	0.2442	-3.48
260448_at	hypothetical protein predicted by g	---	AT1G72410	1.30	0.38	2.99	0.02116304	0.2442	-3.48
248058_at	putative protein similar to unknown	---	AT5G55530	1.29	0.36	2.99	0.0211873	0.2443	-3.49
254977_s_at	subtilisin-like serine protease conta	---	AT4G10520	-1.20	-0.27	-2.99	0.02119735	0.2443	-3.49
264507_at	Expressed protein ; supported by c	NIMIN-3	AT1G09415	1.37	0.45	2.99	0.02123324	0.2446	-3.49
267227_at	hypothetical protein predicted by g	---	AT2G44030	-1.35	-0.44	-2.99	0.02124314	0.2446	-3.49
253911_at	putative receptor protein kinase re	---	AT4G27300	-1.75	-0.80	-2.99	0.02129825	0.2451	-3.49
248901_at	putative protein contains similarity	---	AT5G46410	1.33	0.41	2.99	0.02132238	0.2451	-3.49
257641_s_at	hypothetical protein	AOC1	AT3G25760	-1.59	-0.67	-2.99	0.02132722	0.2451	-3.49
248109_at	DNA topoisomerase I	TOP1BETA	AT5G55310	-1.26	-0.33	-2.99	0.02132072	0.2451	-3.49
255603_at	hypothetical protein	---	AT4G01040	1.23	0.30	2.98	0.0214325	0.2462	-3.50
267008_at	putative ABC transporter	---	AT2G39350	1.47	0.55	2.98	0.02154287	0.2462	-3.50
257239_at	unknown protein	---	AT3G24100	1.28	0.36	2.97	0.02164933	0.2462	-3.51
265816_s_at	putative elongation factor beta-1	---	AT1G30230	1.37	0.46	2.98	0.02160048	0.2462	-3.51
250021_at	casein kinase-like protein	---	AT5G18190	-1.20	-0.26	-2.98	0.02160315	0.2462	-3.51
254573_at	putative pectinacetylesterase pect	---	AT4G19420	1.63	0.71	2.97	0.02164496	0.2462	-3.51
245999_at	putative protein predicted protein,	COPT5	AT5G20650	1.23	0.30	2.98	0.0215339	0.2462	-3.50
260465_at	membrane-associated salt-inducib	---	AT1G10910	1.20	0.26	2.98	0.02159676	0.2462	-3.51

265460_at	putative caltractin ;supported by fu	---	AT2G46600	1.52	0.60	2.98	0.02145245	0.2462	-3.50
260666_at	unknown protein ;supported by full	PARVUS	AT1G19300	-1.82	-0.86	-2.98	0.02150523	0.2462	-3.50
260051_at	hypothetical protein	---	AT1G78210	-1.69	-0.75	-2.98	0.02151965	0.2462	-3.50
249417_at	calcium-binding protein - like cbp1	---	AT5G39670	3.98	1.99	2.98	0.02160684	0.2462	-3.51
248029_at	beta-amylase ; supported by cDN/	BAM4	AT5G55700	1.29	0.37	2.98	0.02162907	0.2462	-3.51
262460_s_at	fructokinase, putative similar to fru	---	AT1G06030 /	1.24	0.31	2.98	0.02154597	0.2462	-3.50
245850_at	ankyrin-repeat containing protein a	KEG	AT5G13530	-1.40	-0.49	-2.98	0.02161172	0.2462	-3.51
263778_at	putative cytochrome oxidase bioge	OXA1L	AT2G46470	1.30	0.38	2.98	0.0216006	0.2462	-3.51
254794_at	putative protein	---	AT4G12970	2.28	1.19	2.98	0.02155173	0.2462	-3.50
250722_at	unknown protein ;supported by ful	---	AT5G06190	1.48	0.56	2.97	0.02164192	0.2462	-3.51
266326_at	putative cytochrome b5 ;supporte	CB5-C	AT2G46650	-2.37	-1.24	-2.98	0.02158925	0.2462	-3.50
247430_at	putative protein contains similarity	---	AT5G62610	1.32	0.40	2.97	0.02165016	0.2462	-3.51
266580_at	unknown protein ;supported by ful	---	AT2G46260	1.29	0.37	2.98	0.02153727	0.2462	-3.50
259188_at	unknown protein ;supported by ful	---	AT3G01510	-1.40	-0.49	-2.97	0.0216961	0.2463	-3.51
255284_at	5-adenylylsulfate reductase ;supp	אפר-01	AT4G04610	-2.21	-1.15	-2.97	0.02169632	0.2463	-3.51
265795_at	putative serine carboxypeptidase I	scpl26	AT2G35780	1.29	0.37	2.97	0.02168085	0.2463	-3.51
266892_at	putative glycine dehydrogenase	AtGLDP2	AT2G26080	-1.36	-0.44	-2.97	0.02171291	0.2464	-3.51
262490_at	hypothetical protein predicted by g	UREF	AT1G21840	1.34	0.42	2.97	0.0217214	0.2464	-3.51
255590_at	cathepsin B-like cysteine protease	---	AT4G01610	1.34	0.42	2.97	0.02173983	0.2465	-3.51
255794_at	putative NAM (no apical meristem)	ANAC041	AT2G33480	1.72	0.79	2.97	0.02185588	0.2472	-3.52
245761_at	hypothetical protein predicted by g	---	AT1G66890	1.27	0.35	2.97	0.02181932	0.2472	-3.52
248708_at	putative protein contains similarity	---	AT5G48560	1.68	0.75	2.97	0.02186309	0.2472	-3.52
256824_at	hypothetical protein predicted by g	AT3G2212	---	-1.51	-0.59	-2.97	0.021884	0.2472	-3.52
265641_at	putative RNA-binding glycine rich p	---	AT2G27330	1.31	0.39	2.97	0.02184355	0.2472	-3.52
259504_at	inorganic pyrophosphatase, putati	AVP1	AT1G15690	1.34	0.42	2.97	0.02188217	0.2472	-3.52
249126_at	Expressed protein ; supported by c	TOPP6	AT5G43380	-1.69	-0.76	-2.97	0.02184881	0.2472	-3.52
257451_at	hypothetical protein predicted by g	BT3	AT1G05690	1.27	0.35	2.97	0.02191178	0.2473	-3.52
261336_at	unknown protein ;supported by full	---	AT1G44790	-1.44	-0.53	-2.97	0.02190408	0.2473	-3.52
263438_at	unknown protein	---	AT2G28660	1.35	0.44	2.97	0.02193643	0.2473	-3.52
256438_s_at	ribosomal protein L41 identical to r	---	AT2G40205 /	1.68	0.75	2.97	0.02193336	0.2473	-3.52
266816_at	unknown protein identical to GB:A/	---	AT2G44970	-1.23	-0.30	-2.96	0.02195745	0.2475	-3.52
249067_at	putative protein similar to unknowr	---	AT5G43960	1.27	0.34	2.96	0.0220012	0.2478	-3.52
258479_at	hypothetical protein predicted by g	---	AT3G02440	-1.28	-0.35	-2.96	0.02201456	0.2479	-3.52
250813_at	GTP-binding protein (gb|AAD0920	TOC34	AT5G05000	1.33	0.41	2.96	0.02203069	0.2479	-3.53
267338_at	26S proteasome regulatory subuni	EIF2	AT2G39990	1.31	0.39	2.96	0.02208678	0.2484	-3.53

250306_at	putative protein similar to unknown	---	AT5G12170	-1.43	-0.52	-2.96	0.02216113	0.2490	-3.53
261416_at	ribosomal protein S15 identical to	RPS15A	AT1G07770	1.61	0.69	2.96	0.02216198	0.2490	-3.53
259640_at	beta-glucosidase, putative identica	BGLU18	AT1G52400	-1.69	-0.76	-2.96	0.02219753	0.2492	-3.53
264463_at	unknown protein similar to ESTs g	---	AT1G10150	1.35	0.43	2.96	0.02218805	0.2492	-3.53
260291_at	putative protein kinase similar to M	YDA	AT1G63700	-1.20	-0.27	-2.96	0.02222687	0.2494	-3.53
267358_at	proline transporter 1 ;supported by	PROT1	AT2G39890	-1.33	-0.41	-2.96	0.02224142	0.2494	-3.54
253908_at	GH3 like protein GH3 protein, Gly	WES1	AT4G27260	2.84	1.50	2.95	0.02224695	0.2494	-3.54
262859_at	hypothetical protein predicted by g	---	AT1G64790	1.27	0.35	2.95	0.02226105	0.2494	-3.54
254186_at	putative protein cellulose synthase	CSLG1	AT4G24010	-1.28	-0.35	-2.95	0.02227847	0.2495	-3.54
250287_at	putative protein AP2 domain conta	Rap2.6L	AT5G13330	1.44	0.52	2.95	0.02230178	0.2495	-3.54
259543_at	hypothetical protein ; supported by	---	AT1G20580	1.31	0.39	2.95	0.02230455	0.2495	-3.54
253394_at	putative protein predicted protein,	VTE1	AT4G32770	-1.55	-0.64	-2.95	0.02234079	0.2497	-3.54
257773_at	hypothetical protein predicted by g	---	AT3G29185	1.29	0.36	2.95	0.02234611	0.2497	-3.54
247529_at	monosaccharide transporter STP3	---	AT5G61520	1.27	0.34	2.95	0.0223904	0.2501	-3.54
246788_at	putative protein hypothetical prote	AGL89	AT5G27580	-1.23	-0.30	-2.95	0.02244223	0.2506	-3.54
257084_at	unknown protein	---	AT3G20620	-1.45	-0.53	-2.95	0.02247449	0.2508	-3.55
247063_at	unknown protein	---	AT5G66820	1.43	0.52	2.94	0.02256728	0.2511	-3.55
262661_s_at	hypothetical protein	---	AT1G14230	-2.51	-1.33	-2.94	0.02256355	0.2511	-3.55
249550_at	protein kinase - like protein wall-a	---	AT5G38210	1.60	0.68	2.94	0.02256832	0.2511	-3.55
264323_at	putative dimethylaniline monooxyg	---	AT1G04180	-2.32	-1.22	-2.95	0.02255325	0.2511	-3.55
263963_at	putative DNA-binding protein RAV2	---	AT2G36080	-1.42	-0.51	-2.95	0.02251649	0.2511	-3.55
257722_at	putative chloroplast nucleoid DNA	---	AT3G18490	-1.52	-0.61	-2.95	0.0225244	0.2511	-3.55
259420_at	hypothetical protein similar to puta	---	AT1G13900	-1.19	-0.25	-2.94	0.02265833	0.2519	-3.55
262070_at	far-red impaired response protein,	FRS8	AT1G80010	-1.24	-0.31	-2.94	0.02265857	0.2519	-3.55
254848_at	putative protein hypothetical prote	PGRL1B	AT4G11960	-1.27	-0.34	-2.94	0.02269507	0.2519	-3.56
251258_at	PECTINESTERASE-like protein P	VGDH2	AT3G62170	-1.31	-0.39	-2.94	0.02269457	0.2519	-3.56
260241_at	putative cytochrome P450 similar t	CYP86A7	AT1G63710	1.39	0.47	2.94	0.02269108	0.2519	-3.56
266521_at	unknown protein ; supported by cl	---	AT2G24020	1.23	0.30	2.94	0.02272743	0.2521	-3.56
250757_at	tetrahydrofolylpolyglutamate synth	ATDFB	AT5G05980	1.27	0.34	2.94	0.02275198	0.2522	-3.56
261148_at	unknown protein ; supported by ful	GAMMA CA	AT1G19580	-1.23	-0.29	-2.94	0.02276325	0.2522	-3.56
261324_at	unknown protein	---	AT1G44770	1.38	0.46	2.94	0.02276696	0.2522	-3.56
250897_at	putative protein ; supported by cD	---	AT5G03430	-1.26	-0.33	-2.94	0.02281721	0.2525	-3.56
254259_s_at	putative protein rape mRNA, Bras	---	AT4G23420	-1.43	-0.52	-2.94	0.02282325	0.2525	-3.56
252571_at	putative protein syntaxin 8 - Homo	SYP72	AT3G45280	-1.30	-0.37	-2.94	0.02280128	0.2525	-3.56
257299_at	unknown protein ;supported by ful	---	AT3G28050	1.30	0.38	2.94	0.02284328	0.2526	-3.56

253248_at	Putative S-phase-specific ribosoma	---	AT4G34670	1.81	0.86	2.93	0.02292961	0.2532	-3.57
253368_at	myosin - like protein unconventior	XI-I	AT4G33200	1.26	0.33	2.93	0.02293467	0.2532	-3.57
247741_at	putative protein predicted proteins	GIL1	AT5G58960	1.56	0.64	2.93	0.02292484	0.2532	-3.57
258386_at	hypothetical protein predicted by g	---	AT3G15520	1.41	0.49	2.93	0.02294983	0.2533	-3.57
255281_at	contains similarity to glucan syntha	GSL1	AT4G04970	-1.20	-0.26	-2.93	0.02297986	0.2534	-3.57
254609_at	Expressed protein ; supported by f	---	AT4G18970	1.84	0.88	2.93	0.02298099	0.2534	-3.57
247077_at	putative protein similar to unknown	---	AT5G66420	-1.32	-0.40	-2.93	0.02303358	0.2537	-3.57
255836_at	putative splicing factor U2AF large	---	AT2G33440	-1.39	-0.47	-2.93	0.02303665	0.2537	-3.57
256598_at	cytochrome P450 homolog, putati	BR6OX2	AT3G30180	-1.41	-0.49	-2.93	0.02310969	0.2537	-3.57
252915_at	EF-Hand containing protein -like s	---	AT4G38810	-1.34	-0.42	-2.93	0.02313879	0.2537	-3.58
264805_at	unknown protein similar to putative	ATRX	AT1G08600	-1.27	-0.35	-2.93	0.0230772	0.2537	-3.57
251926_at	60S RIBOSOMAL PROTEIN L36	---	AT3G53740	1.55	0.64	2.93	0.02313511	0.2537	-3.58
255814_at	unknown protein	---	AT1G19900	-1.23	-0.30	-2.93	0.02312202	0.2537	-3.58
265445_at	60S ribosomal protein L12 ;suppo	---	AT2G37190	1.87	0.90	2.93	0.02308836	0.2537	-3.57
266463_at	hypothetical protein predicted by g	---	AT2G47840	1.30	0.38	2.93	0.02307299	0.2537	-3.57
259050_at	hypothetical protein similar to GB:A	---	AT3G03356 /	-1.20	-0.26	-2.93	0.02309783	0.2537	-3.57
263719_at	hypothetical protein predicted by g	---	AT2G13600	-1.23	-0.29	-2.93	0.02310225	0.2537	-3.57
254238_at	putative protein probable membra	---	AT4G23540	-1.35	-0.43	-2.92	0.02319472	0.2542	-3.58
257052_at	putative 3-hydroxybutyryl-CoA deh	---	AT3G15290	-1.24	-0.31	-2.92	0.02321517	0.2543	-3.58
260915_at	hypothetical protein similar to hypo	---	AT1G02660	1.74	0.80	2.92	0.0233055	0.2547	-3.58
252759_at	putative protein hypothetical protei	---	AT3G42630	1.20	0.27	2.92	0.02326696	0.2547	-3.58
266297_at	putative proliferating cell nuclear a	PCNA2	AT2G29570	2.26	1.17	2.92	0.02329978	0.2547	-3.58
246538_at	40S RIBOSOMAL PROTEIN S19	---	AT5G15520	1.47	0.56	2.92	0.0233072	0.2547	-3.58
262975_at	zinc finger protein, putative similar	STH2	AT1G75540	1.39	0.47	2.92	0.02330681	0.2547	-3.58
248235_at	unknown protein ;supported by full	emb2737	AT5G53860	1.21	0.27	2.92	0.02332668	0.2548	-3.58
253459_at	hypothetical protein	---	AT4G32080	-1.21	-0.27	-2.92	0.02334709	0.2549	-3.59
264480_at	hypothetical protein predicted by g	EFS	AT1G77300	-1.28	-0.35	-2.92	0.02335714	0.2549	-3.59
260686_at	unknown protein ; supported by cD	---	AT1G17620	-1.67	-0.74	-2.92	0.02339198	0.2552	-3.59
257332_at	hypothetical protein	---	---	-1.36	-0.45	-2.92	0.02340751	0.2552	-3.59
250409_at	putative protein 110K5.11, unknov	---	AT5G10860	1.26	0.33	2.92	0.02343606	0.2553	-3.59
257743_at	unknown protein	---	AT3G27390	1.39	0.48	2.92	0.0234585	0.2553	-3.59
247806_at	ABC transporter-like protein ; supp	STA1	AT5G58270	1.24	0.31	2.92	0.02344081	0.2553	-3.59
265815_at	predicted protein	---	AT2G17975	1.19	0.25	2.92	0.02345953	0.2553	-3.59
263443_at	putative fatty acid elongase ;supp	KCS12	AT2G28630	2.48	1.31	2.92	0.02348868	0.2555	-3.59
266579_at	putative small nuclear ribonucleopr	SNRNP-G	AT2G23930	1.33	0.42	2.91	0.02352674	0.2556	-3.59

259885_at	hypothetical protein contains Pfam	---	AT1G76380	-1.40	-0.48	-2.91	0.02353591	0.2556	-3.59
250117_at	isopentenyl pyrophosphate:dimeth	IPP1	AT5G16440	1.45	0.53	2.91	0.0235166	0.2556	-3.59
258953_at	hypothetical protein predicted by g	---	AT3G01430	1.32	0.40	2.91	0.02356957	0.2556	-3.59
246756_at	protein phosphatase - like protein	---	AT5G27930	-1.35	-0.43	-2.91	0.02356326	0.2556	-3.59
255941_at	mitochondrial inner membrane tra	ATTIM17-1	AT1G20350	1.46	0.54	2.91	0.02356337	0.2556	-3.59
257311_at	phosphate transporter, putative co	PHT2;1	AT3G26570	-1.28	-0.35	-2.91	0.02358707	0.2557	-3.60
260882_at	DNA binding protein, putative simi	WRKY65	AT1G29280	1.58	0.66	2.91	0.02363499	0.2558	-3.60
247818_at	contains similarity to GTP-binding	---	AT5G58370	1.26	0.33	2.91	0.02366942	0.2558	-3.60
264491_at	hypothetical protein predicted by g	---	AT1G27410	-1.25	-0.32	-2.91	0.02363362	0.2558	-3.60
245127_at	putative Na+/Ca2+ antiporter ; sup	ATMHX	AT2G47600	-1.53	-0.62	-2.91	0.02362754	0.2558	-3.60
253797_at	putative protein 55.11 protein hom	RPN1B	AT4G28470	1.20	0.26	2.91	0.02365947	0.2558	-3.60
250444_at	beta-xylosidase - like protein beta	---	AT5G10560	1.28	0.36	2.91	0.02369053	0.2558	-3.60
265244_at	putative amine oxidase	ATPAO2	AT2G43018 /	-1.58	-0.66	-2.91	0.02369276	0.2558	-3.60
253624_at	putative protein 2-acylglycerophos	ATS2	AT4G30580	1.35	0.43	2.91	0.02368581	0.2558	-3.60
265731_at	putative RNA helicase A 3' end of	---	AT2G01130	-1.21	-0.27	-2.91	0.02364883	0.2558	-3.60
252010_at	hypothetical protein ; supported by	---	AT3G52740	-1.36	-0.44	-2.91	0.02373625	0.2560	-3.60
256526_at	disease resistance protein, putativ	---	AT1G66090	1.27	0.35	2.91	0.02373391	0.2560	-3.60
247553_at	MAD box containing protein NAP1	AGL8	AT5G60910	-1.57	-0.65	-2.91	0.02376307	0.2562	-3.60
251327_at	prolyl aminopeptidase-like protein	---	AT3G61540	1.20	0.26	2.91	0.02382812	0.2567	-3.61
252665_at	valine-rich protein	---	AT3G44140	-1.30	-0.37	-2.90	0.02388035	0.2569	-3.61
245627_at	water stress-induced protein, puta	AtGolS2	AT1G56600	-1.65	-0.72	-2.90	0.02388732	0.2569	-3.61
249405_at	beta subunit of protein farnesyl tra	ERA1	AT5G40280	1.24	0.31	2.90	0.02386331	0.2569	-3.61
252033_at	putative protein ;supported by full-	---	AT3G51950	-1.51	-0.59	-2.90	0.02387969	0.2569	-3.61
248253_at	putative protein contains similarity	CRF3	AT5G53290	-1.24	-0.31	-2.90	0.02393848	0.2572	-3.61
262748_at	lipase, putative contains Pfam pro	---	AT1G28610	-1.51	-0.60	-2.90	0.02393204	0.2572	-3.61
256645_at	hypothetical protein predicted by g	---	AT3G24250	-1.22	-0.29	-2.90	0.02396991	0.2574	-3.61
246176_at	putative protein DYNAMIN-LIKE P	---	AT5G28410	-1.22	-0.29	-2.90	0.02400912	0.2577	-3.61
248040_at	putative protein contains similarity	---	AT5G55970	1.66	0.73	2.90	0.02404151	0.2578	-3.62
267525_at	putative glycine-rich protein	---	AT2G30560	-1.20	-0.26	-2.90	0.02403059	0.2578	-3.61
254237_at	cysteine proteinase contains simil	---	AT4G23520	-1.22	-0.28	-2.90	0.02405667	0.2578	-3.62
260353_at	putative nitrilase-associated protei	SP1L2	AT1G69230	-1.31	-0.39	-2.90	0.02406243	0.2578	-3.62
263505_s_at	hypothetical protein	---	AT2G07678	-1.58	-0.66	-2.90	0.02410134	0.2581	-3.62
244916_at	hypothetical protein	ORF187	ATMG00880	-1.23	-0.30	-2.90	0.02412048	0.2581	-3.62
258934_at	putative RecA protein similar to Re	RECA3	AT3G10140	1.29	0.37	2.90	0.02413884	0.2581	-3.62
265922_at	putative sugar transporter	---	AT2G18480	-1.24	-0.31	-2.90	0.02414787	0.2581	-3.62

245928_s_at	vegetative storage protein Vsp1 ;s	VSP1	AT5G24770 /	-4.67	-2.22	-2.90	0.02416731	0.2581	-3.62
264717_at	hypothetical protein predicted by g	ATFH8	AT1G70140	-1.60	-0.68	-2.90	0.0241529	0.2581	-3.62
252539_at	putative protein	---	AT3G45730	1.35	0.43	2.90	0.0241699	0.2581	-3.62
251505_at	putative protein polyamine oxidase	CPuORF18	AT3G59050 /	-1.46	-0.54	-2.89	0.02418619	0.2582	-3.62
249641_at	DegP protease contains similarity t	DegP10	AT5G36950	1.29	0.37	2.89	0.02429071	0.2589	-3.63
259130_at	putative ribosomal protein L39 sim	---	AT3G02190	1.30	0.37	2.89	0.02433962	0.2589	-3.63
246976_s_at	putative protein UBIQUINONE BI	---	AT5G24810	-1.45	-0.53	-2.89	0.02433024	0.2589	-3.63
258018_at	hypothetical protein predicted by g	---	AT3G19500	-1.37	-0.45	-2.89	0.02433329	0.2589	-3.63
264274_at	disease resistance protein RPS4,	---	AT1G60320	-1.26	-0.33	-2.89	0.02434195	0.2589	-3.63
251629_at	villin 3 fragment ; supported by cD	VLN3	AT3G57410	1.35	0.43	2.89	0.02427595	0.2589	-3.63
266689_at	hypothetical protein predicted by g	---	AT2G19930	1.49	0.58	2.89	0.02431516	0.2589	-3.63
259817_at	hypothetical protein predicted by g	---	AT1G49880	1.26	0.33	2.89	0.024336	0.2589	-3.63
253662_at	transcription factor-like protein Ara	ARF16	AT4G30080	-1.27	-0.35	-2.89	0.02436415	0.2590	-3.63
259633_at	hypothetical protein	---	AT1G56500	-1.34	-0.42	-2.89	0.02441609	0.2594	-3.63
261175_at	unknown protein	---	AT1G04800	-1.27	-0.34	-2.89	0.02445261	0.2597	-3.63
247516_at	germin-like protein - like germin-lik	---	AT5G61750	-1.28	-0.35	-2.89	0.02446251	0.2597	-3.63
258719_at	putative pectate lyase simliar to pe	---	AT3G09540	-1.71	-0.77	-2.89	0.02449632	0.2599	-3.63
267638_at	unknown protein ; supported by fu	OEP16-3	AT2G42210	1.20	0.27	2.88	0.02453093	0.2601	-3.64
248933_at	putative protein contains similarity	---	AT5G46070	1.24	0.31	2.88	0.02457382	0.2602	-3.64
252677_at	nitrilase 3 ;supported by full-length	NIT3	AT3G44320	-1.51	-0.59	-2.88	0.0245903	0.2602	-3.64
250714_at	sorting nexin-like protein	SNX1	AT5G06140	1.29	0.37	2.88	0.02454637	0.2602	-3.64
248862_at	unknown protein	---	AT5G46730	-1.41	-0.50	-2.88	0.02455663	0.2602	-3.64
264238_at	hypothetical protein predicted by g	---	AT1G54740	1.69	0.76	2.88	0.02458701	0.2602	-3.64
266832_at	putative protein kinase contains a	MAPKKK14	AT2G30040	-1.44	-0.53	-2.88	0.02466114	0.2607	-3.64
263299_s_at	hypothetical protein predicted by g	---	AT2G11570	-1.25	-0.32	-2.88	0.02466823	0.2607	-3.64
249736_at	unknown protein	---	AT5G24460	1.20	0.26	2.88	0.0246863	0.2608	-3.64
253715_at	RIBOSOMAL PROTEIN S30 hom	---	AT4G29390	1.29	0.36	2.88	0.02470787	0.2609	-3.64
261255_at	hypothetical protein contains simila	ATNTH2	AT1G05900	-1.30	-0.38	-2.88	0.02473389	0.2611	-3.64
248608_at	ATP citrate lyase ; supported by c	ACLB-2	AT5G49460	1.31	0.39	2.87	0.02488325	0.2611	-3.65
255904_at	lemir (miraculin), putative similar t	---	AT1G17860	1.35	0.43	2.88	0.02481839	0.2611	-3.65
257477_at	unknown protein	---	AT1G10660	1.35	0.44	2.87	0.02493007	0.2611	-3.65
245868_at	hypothetical protein	CAT2	AT1G58030	1.32	0.40	2.88	0.02477809	0.2611	-3.65
261435_at	GTP-binding protein, putative simi	---	AT1G07615 /	1.48	0.56	2.87	0.02491038	0.2611	-3.65
254323_at	putative protein auxin-induced pro	---	AT4G22620	-1.71	-0.77	-2.88	0.02475043	0.2611	-3.64
249040_at	eukaryotic translation initiation fact	---	AT5G44320	1.27	0.34	2.88	0.02484717	0.2611	-3.65

262236_at	hypothetical protein similar to hypo	---	AT1G48330	-1.60	-0.68	-2.87	0.02492408	0.2611	-3.65
261925_at	oligopeptide transporter, putative	---	AT1G22540	-1.26	-0.33	-2.87	0.02491849	0.2611	-3.65
255310_at	Expressed protein ; supported by f	ATALN	AT4G04955	1.77	0.82	2.87	0.02487002	0.2611	-3.65
245713_at	S-adenosyl-L-methionine:salicylic	NAMT1	AT5G04370	-1.38	-0.47	-2.87	0.02487171	0.2611	-3.65
255478_at	putative protein ;supported by full-	EID1	AT4G02440	1.28	0.36	2.88	0.02484745	0.2611	-3.65
248042_at	putative protein similar to unknown	---	AT5G55960	-1.33	-0.42	-2.87	0.02494184	0.2611	-3.65
258721_at	unknown protein similar to hypothe	---	AT3G09560	-1.41	-0.50	-2.88	0.02484772	0.2611	-3.65
251716_at	anthranilate synthase alpha-1 cha	---	AT3G55870	-1.24	-0.31	-2.87	0.02487787	0.2611	-3.65
253856_at	hypothetical protein ;supported by	---	AT4G28100	1.21	0.28	2.88	0.02477819	0.2611	-3.65
267637_at	unknown protein predicted by gens	---	AT2G42190	1.42	0.51	2.87	0.02493655	0.2611	-3.65
261033_at	unknown protein ;supported by full	JAZ5	AT1G17380	-2.41	-1.27	-2.88	0.02486228	0.2611	-3.65
262491_at	putative SecA-type chloroplast pro	---	AT1G21650	-1.29	-0.37	-2.87	0.02496055	0.2612	-3.65
245987_at	NAM-like protein hypothetical prot	ANAC083	AT5G13180	-1.29	-0.36	-2.87	0.02497751	0.2612	-3.65
251414_at	hypothetical protein	---	AT3G60370	1.34	0.42	2.87	0.02507042	0.2620	-3.66
251878_at	putative protein predicted protein,	---	AT3G54310	-1.21	-0.28	-2.87	0.02507538	0.2620	-3.66
254943_at	putative protein predicted proteins	---	AT4G10890	1.25	0.32	2.87	0.02509534	0.2621	-3.66
255120_x_at	putative transposon protein similar	---	---	-1.22	-0.28	-2.87	0.02511114	0.2621	-3.66
259272_at	unknown protein similar to hypothe	---	AT3G01290	1.32	0.40	2.87	0.02516846	0.2625	-3.66
246613_at	acetyl-CoA carboxylase ;supporte	CAC2	AT5G35360	1.34	0.42	2.87	0.02519424	0.2625	-3.66
265857_s_at	serine threonine protein phosphata	PP2A-4	AT2G42500	1.28	0.36	2.87	0.02517541	0.2625	-3.66
260085_at	putative D-ribulose-5-phosphate si	---	AT1G63290	1.23	0.30	2.87	0.02521317	0.2625	-3.66
246209_at	BEL1-like homeobox 2 protein (BL	BLH2	AT4G36870	-1.46	-0.55	-2.87	0.02519348	0.2625	-3.66
254917_at	putative protein various hypothetic	---	AT4G11350	-1.44	-0.53	-2.86	0.02522111	0.2625	-3.66
256182_at	Expressed protein ; supported by f	SYP81	AT1G51740	1.35	0.43	2.86	0.02522422	0.2625	-3.66
250049_at	putative protein predicted proteins	---	AT5G17780	-1.27	-0.35	-2.86	0.02524637	0.2626	-3.67
262295_at	putative U2 snRNP auxiliary facto	ATU2AF35	AT1G27650	1.34	0.42	2.86	0.02525991	0.2626	-3.67
265768_at	putative sugar transporter ;suppor	---	AT2G48020	-1.23	-0.30	-2.86	0.02528461	0.2627	-3.67
266981_at	60S ribosomal protein L23A identic	RPL23AA	AT2G39460	1.59	0.67	2.86	0.02529006	0.2627	-3.67
250353_at	putative protein predicted proteins	---	AT5G11630	1.30	0.38	2.86	0.02532119	0.2628	-3.67
253201_at	putative ribosomal protein S16 rib	SSR16	AT4G34620	1.25	0.33	2.86	0.02531147	0.2628	-3.67
248267_at	NADH-dependent glutamate synth	GLT1	AT5G53460	1.41	0.49	2.86	0.02536168	0.2630	-3.67
250728_at	putative protein similar to unknown	---	AT5G06440	1.30	0.38	2.86	0.02535567	0.2630	-3.67
252193_at	R2R3-MYB transcription factor ; s	MYB77	AT3G50060	1.87	0.90	2.86	0.0254152	0.2634	-3.67
256829_at	unknown protein similar to aluminu	---	AT3G22850	-1.47	-0.56	-2.86	0.02542325	0.2634	-3.67
245202_at	F12A21.14 similar to receptor prot	---	AT1G67720	-1.33	-0.42	-2.86	0.02543461	0.2634	-3.67

260384_at	putative 2-isopropylmalate synthas	IMS1	AT1G74040	1.25	0.33	2.86	0.02548583	0.2638	-3.67
248628_at	putative protein contains similarity	---	AT5G48960	-1.27	-0.35	-2.86	0.02549849	0.2638	-3.68
257697_at	hypothetical protein predicted by g	---	AT3G12700	1.42	0.51	2.86	0.02554822	0.2639	-3.68
257756_at	uridylate kinase, putative similar t	---	AT3G18680	1.30	0.37	2.86	0.02555296	0.2639	-3.68
260264_at	hypothetical protein predicted by g	---	AT1G68500	1.38	0.47	2.86	0.02553455	0.2639	-3.68
250058_at	plastid-specific ribosomal protein (	PSRP6	AT5G17870	1.33	0.41	2.86	0.02554934	0.2639	-3.68
244977_at	cytochrome b/f	---	---	-1.56	-0.64	-2.85	0.02558605	0.2641	-3.68
254640_at	ion transporter - like protein integr	NRAMP5	AT4G18790	-1.25	-0.33	-2.85	0.02561561	0.2642	-3.68
262594_at	putative 60s ribosomal protein L37	---	AT1G15250	1.87	0.90	2.85	0.02565152	0.2642	-3.68
258329_at	putative protein disulfide isomeras	ATPDIL1-6	AT3G16110	1.25	0.32	2.85	0.02566255	0.2642	-3.68
AFFX-BioC-5_a	E. coli /GEN=bioC /DB_XREF=gb:	---	---	-1.53	-0.61	-2.85	0.02566935	0.2642	-3.68
267590_at	putative expansin ;supported by fu	ATEXPA4	AT2G39700	1.58	0.66	2.85	0.02564346	0.2642	-3.68
265197_at	putative glucosyl transferase	UGT73C1	AT2G36750	-1.20	-0.26	-2.85	0.02566144	0.2642	-3.68
253054_at	probable N-acetyltransferase hook	HLS1	AT4G37580	-1.24	-0.31	-2.85	0.02567444	0.2642	-3.68
262379_at	hypothetical protein predicted by g	---	AT1G73020	-1.23	-0.29	-2.85	0.02570763	0.2644	-3.68
252225_at	ADP-RIBOSYLATION FACTOR -l	ATARLA1C	AT3G49870	1.23	0.30	2.85	0.02573913	0.2646	-3.68
255226_at	UV-damaged DNA binding factor -	DDB1A	AT4G05420	1.22	0.29	2.85	0.02575524	0.2646	-3.69
251996_at	beta-galactosidase precursor - like	BGAL2	AT3G52840	-1.31	-0.39	-2.85	0.02584604	0.2654	-3.69
247544_at	putative protein ;supported by full-	---	AT5G61670	-1.37	-0.46	-2.85	0.0258578	0.2654	-3.69
247634_at	late embryonic abundant protein -	---	AT5G60520	-1.20	-0.26	-2.85	0.0259126	0.2656	-3.69
247938_at	putative protein similar to unknown	---	AT5G57140 /	-1.23	-0.30	-2.85	0.0259072	0.2656	-3.69
245414_at	hypothetical protein	---	AT4G17310	1.32	0.40	2.85	0.02590394	0.2656	-3.69
259340_at	hypothetical protein predicted usin	PYK10	AT3G03870 /	1.30	0.38	2.84	0.02597923	0.2659	-3.69
266280_at	putative tropinone reductase	---	AT2G29260	1.20	0.27	2.84	0.02598382	0.2659	-3.69
265530_at	12-oxophytodienoate-10,11-reduc	OPR3	AT2G06050	-1.86	-0.90	-2.84	0.02598583	0.2659	-3.69
261465_at	unknown protein	---	AT1G07705	-1.23	-0.29	-2.84	0.02596855	0.2659	-3.69
259346_at	putative glutamate dehydrogenase	GDH3	AT3G03910	-1.22	-0.29	-2.84	0.02603996	0.2660	-3.70
251617_at	putative protein hypothetical prote	---	AT3G58000	-1.23	-0.30	-2.84	0.02603123	0.2660	-3.70
258093_at	unknown protein ; supported by cl	---	AT3G14750	1.31	0.39	2.84	0.02605143	0.2660	-3.70
262130_at	hypothetical protein predicted by g	---	AT1G02890	-1.28	-0.36	-2.84	0.02605401	0.2660	-3.70
251264_at	multifunctional aminoacyl-tRNA lig	---	AT3G62120	1.23	0.30	2.84	0.02603288	0.2660	-3.70
247873_at	diacylglycerol kinase-like protein	---	AT5G57690	-1.23	-0.29	-2.84	0.02607161	0.2661	-3.70
264591_at	hypothetical protein contains simila	---	AT2G17670	-1.26	-0.33	-2.84	0.02609764	0.2662	-3.70
263034_at	pollen allergen-like protein similar t	MLP423	AT1G24020	-1.58	-0.66	-2.84	0.02611122	0.2662	-3.70
260274_at	putative glycerol kinase similar to (	NHO1	AT1G80460	1.34	0.42	2.84	0.0261424	0.2663	-3.70

247867_at	SNF1 related protein kinase-like pr	CIPK21	AT5G57630	-1.47	-0.56	-2.84	0.02614187	0.2663	-3.70
255510_at	polycomb group - like protein simi	SWN	AT4G02020	1.36	0.45	2.84	0.0261618	0.2664	-3.70
252069_s_at	putative protein putative protein T1	---	AT3G51640 /	-1.23	-0.30	-2.84	0.02622289	0.2669	-3.70
264120_at	latex-abundant protein, putative si	AtMC4	AT1G79340	-1.21	-0.27	-2.84	0.02623994	0.2670	-3.70
264476_at	hypothetical protein contains simila	PGSIP2	AT1G77130	1.30	0.38	2.84	0.02625172	0.2670	-3.71
248906_at	putative protein similar to unknown	---	AT5G46420	1.24	0.32	2.84	0.02626676	0.2670	-3.71
255240_at	coded for by A. thaliana cDNA Z18	IBR1	AT4G05530	-1.24	-0.31	-2.83	0.02631805	0.2672	-3.71
262538_at	Expressed protein ; supported by f	---	AT1G17140	1.55	0.63	2.84	0.02629748	0.2672	-3.71
267374_at	putative uricase subunit similar to	---	AT2G26230	-1.21	-0.27	-2.83	0.02631012	0.2672	-3.71
252167_at	putative protein steroid dehydroge	---	AT3G50560	1.29	0.37	2.83	0.02636832	0.2674	-3.71
247743_at	protein kinase - like serine/threoni	---	AT5G59010	1.33	0.41	2.83	0.02635832	0.2674	-3.71
253321_at	putative protein prolyl 4-hydroxyla	---	AT4G33910	1.23	0.30	2.83	0.02638461	0.2675	-3.71
250808_at	putative protein contains similarity	ATG18E	AT5G05150	-1.32	-0.40	-2.83	0.02640391	0.2676	-3.71
258399_at	early auxin-induced protein, IAA19	IAA19	AT3G15540	2.25	1.17	2.83	0.02649414	0.2680	-3.71
258097_at	transport protein, putative similar t	---	AT3G23660	1.21	0.27	2.83	0.02648082	0.2680	-3.71
249015_at	Dreg-2 like protein	---	AT5G44730	1.26	0.33	2.83	0.02648297	0.2680	-3.71
258046_at	MAP kinase kinase 5 identical to G	MKK5	AT3G21220	1.26	0.33	2.83	0.02648025	0.2680	-3.71
255553_at	predicted protein of unknown funct	---	AT4G01960	1.37	0.46	2.83	0.02651695	0.2680	-3.72
254454_at	hypothetical protein	EMB2271	AT4G21130	-1.26	-0.33	-2.83	0.02651053	0.2680	-3.72
253405_at	transcription factor TINY homolog	---	AT4G32800	-1.52	-0.60	-2.83	0.02660852	0.2683	-3.72
253811_at	hypothetical protein ;supported by	ULT1	AT4G28190	1.58	0.66	2.83	0.02662262	0.2683	-3.72
247053_at	protein kinase ATN1-like protein	---	AT5G66710	-1.20	-0.26	-2.83	0.02661823	0.2683	-3.72
247558_at	histone deacetylase - like histone	HDA05	AT5G61060	1.25	0.33	2.83	0.02659762	0.2683	-3.72
253539_at	putative protein RING-finger prote	---	AT4G31450	-1.28	-0.35	-2.83	0.02658349	0.2683	-3.72
265247_at	50S ribosomal protein L3 ;support	---	AT2G43030	1.23	0.30	2.83	0.02657883	0.2683	-3.72
261270_at	initiation factor 5A-4, putative simi	FBR12	AT1G26630	1.22	0.29	2.83	0.02664119	0.2684	-3.72
266457_at	putative glyoxysomal malate dehyd	PMDH1	AT2G22780	-1.24	-0.32	-2.83	0.02666195	0.2685	-3.72
246764_s_at	putative protein At2g27780 and At	---	AT2G13640 /	-1.21	-0.27	-2.82	0.0266851	0.2686	-3.72
245319_at	Expressed protein ; supported by f	---	AT4G16146	-1.49	-0.58	-2.82	0.02670453	0.2686	-3.72
253610_at	putative protein ; supported by cD	VEL1	AT4G30200	1.30	0.37	2.82	0.02670938	0.2686	-3.72
261256_at	disease resistance protein RTM1	RTM1	AT1G05760	1.34	0.42	2.82	0.02676381	0.2688	-3.72
265842_at	putative AP2 domain transcription	ERF38	AT2G35700	1.64	0.71	2.82	0.02676402	0.2688	-3.72
251137_at	putative protein several hypothetic	---	AT5G01300	-1.37	-0.46	-2.82	0.02676275	0.2688	-3.72
262340_at	Expressed protein ; supported by f	ANAC027	AT1G64100 /	1.23	0.30	2.82	0.02682205	0.2693	-3.73
245650_at	F5A9.20 similar to S-adenosyl-L-m	---	AT1G24735	-1.28	-0.36	-2.82	0.02687336	0.2697	-3.73

259210_at	hypothetical protein nearly identica	HY2	AT3G09150	1.35	0.43	2.82	0.0269036	0.2699	-3.73
266903_at	hypothetical protein predicted by g	MEE21	AT2G34570	1.22	0.29	2.82	0.02698166	0.2702	-3.73
253679_at	cytidine deaminase 6 (CDA6)	---	AT4G29610	-1.73	-0.79	-2.82	0.02696217	0.2702	-3.73
250174_at	agp6	AGP6	AT5G14380	-1.22	-0.29	-2.82	0.0269481	0.2702	-3.73
250080_at	translocon Tic40-like protein ; sup	TIC40	AT5G16620	1.20	0.27	2.82	0.02698353	0.2702	-3.73
251963_at	protein kinase (AME2/AFC1) ; sup	AFC1	AT3G53570	-1.23	-0.30	-2.82	0.02703111	0.2705	-3.74
267206_at	putative dioxygenase	---	AT2G30830	-1.25	-0.32	-2.81	0.02708648	0.2709	-3.74
255521_at	putative sucrose synthetase simila	SUS3	AT4G02280	-1.44	-0.53	-2.81	0.02709486	0.2709	-3.74
251561_at	E2 ubiquitin-conjugating-like enzyr	SCE1	AT3G57870	1.22	0.28	2.81	0.0271028	0.2709	-3.74
261896_at	mRNA export protein, putative sim	---	AT1G80670	1.31	0.39	2.81	0.02712726	0.2710	-3.74
253547_at	chloroplast omega-6 fatty acid des	FAD6	AT4G30950	1.24	0.31	2.81	0.02714535	0.2711	-3.74
265876_at	putative receptor-like protein kinas	---	AT2G42290	1.22	0.29	2.81	0.02716071	0.2711	-3.74
254164_at	putative protein ;supported by full-	TIFY1	AT4G24470	-1.26	-0.33	-2.81	0.02717652	0.2712	-3.74
264428_at	hypothetical protein predicted by g	---	AT1G61790	1.42	0.50	2.81	0.02720268	0.2713	-3.74
249700_at	40S ribosomal protein S3 ; suppor	---	AT5G35530	1.34	0.42	2.81	0.02723659	0.2714	-3.74
263821_s_at	40S ribosomal protein S16 Same a	---	AT2G09990 /	1.39	0.47	2.81	0.02723754	0.2714	-3.74
254278_at	Expressed protein ; supported by f	---	AT4G22740	-1.27	-0.35	-2.81	0.02725487	0.2715	-3.74
256435_at	putative leucoanthocyanidin dioxyg	---	AT3G11180	-1.26	-0.34	-2.81	0.02730029	0.2718	-3.75
258995_at	putative ribosomal protein L13 sim	---	AT3G01790	1.39	0.47	2.81	0.0273743	0.2718	-3.75
245378_at	GLABRA2 like protein	HDG4	AT4G17710	-1.22	-0.28	-2.81	0.0273728	0.2718	-3.75
252012_at	ubiquinol--cytochrome-c reductase	---	AT3G52730	1.24	0.31	2.81	0.02737066	0.2718	-3.75
257602_at	hydrolase, putative similar to Meta	---	AT3G13800	1.25	0.32	2.81	0.02735153	0.2718	-3.75
252640_at	acyl CoA reductase -like protein a	FAR8	AT3G44560	-1.22	-0.29	-2.81	0.02732014	0.2718	-3.75
262180_at	phosphoglycerate mutase, putativ	PGM	AT1G78050	1.23	0.30	2.81	0.02733571	0.2718	-3.75
251200_at	putative protein PrMC3, Pinus rad	GID1B	AT3G63010	1.34	0.42	2.81	0.02740796	0.2719	-3.75
264285_at	symbiosis-related protein, putative	ATG8C	AT1G62040	1.27	0.35	2.81	0.02740293	0.2719	-3.75
245343_at	hypothetical protein ;supported by	---	AT4G15830	1.21	0.27	2.81	0.02741554	0.2719	-3.75
262572_at	unknown protein Contains a PF|00	---	AT1G15140	-1.33	-0.41	-2.80	0.02745328	0.2721	-3.75
253381_at	Tic22 -like protein strong homolog	---	AT4G33350	1.29	0.36	2.80	0.02746378	0.2721	-3.75
267127_at	putative acetone-cyanohydrin lyas	MES3	AT2G23610	-1.27	-0.35	-2.80	0.02752812	0.2721	-3.75
253174_at	catalase ; supported by cDNA: gi_	CAT2	AT4G35090	-1.30	-0.38	-2.80	0.02747586	0.2721	-3.75
253668_at	snRNP Sm protein F - like Sm pr	RUXF	AT4G30220	1.30	0.37	2.80	0.02751863	0.2721	-3.75
252359_at	putative protein predicted proteins	---	AT3G48440	-1.35	-0.43	-2.80	0.02750141	0.2721	-3.75
245913_at	predicted protein	---	AT5G19860	1.27	0.35	2.80	0.02755936	0.2721	-3.75
261971_at	type 2 peroxiredoxin, putative sim	---	AT1G65990	-1.31	-0.39	-2.80	0.02754988	0.2721	-3.75

262096_at	NAC1 identical to NAC1 GB:AAF2	NAC1	AT1G56010	1.65	0.72	2.80	0.02754611	0.2721	-3.75
258373_at	20S proteasome subunit PAE2 ide	PAE2	AT3G14290	1.24	0.31	2.80	0.02753641	0.2721	-3.75
262402_at	unknown protein ; supported by cD	TOM6	AT1G49410	1.34	0.42	2.80	0.02763098	0.2722	-3.76
252055_at	putative ribosomal protein S14 rib	---	AT3G52580	1.32	0.40	2.80	0.0275885	0.2722	-3.76
267115_s_at	putative cellulose synthase	ATCSLB04	AT2G32530 /	1.68	0.75	2.80	0.02760035	0.2722	-3.76
250423_s_at	cytochrome P450 - like protein cyt	CYP81K2	AT5G10600 /	-1.22	-0.29	-2.80	0.02765879	0.2722	-3.76
266428_at	putative protein kinase contains a	---	AT2G07180	1.32	0.40	2.80	0.02765943	0.2722	-3.76
265764_at	hypothetical protein predicted by g	---	AT2G48060	-1.30	-0.38	-2.80	0.02764144	0.2722	-3.76
255798_at	unknown protein predicted by gene	---	AT2G33255	1.27	0.35	2.80	0.02761817	0.2722	-3.76
266505_at	unknown protein	---	AT2G47830	-1.23	-0.30	-2.80	0.02759736	0.2722	-3.76
251983_at	putative protein MtN21, Medicago	---	AT3G53210	1.39	0.48	2.80	0.02769682	0.2724	-3.76
250687_at	putative protein similar to unknown	---	AT5G06660	1.20	0.26	2.80	0.02771199	0.2725	-3.76
258715_at	putative 60S ribosomal protein L1	---	AT3G09630	1.38	0.47	2.80	0.02774691	0.2727	-3.76
259756_at	unknown protein ; supported by cl	---	AT1G71080	-1.23	-0.29	-2.79	0.02784997	0.2735	-3.77
256607_at	unknown protein ; supported by cD	---	AT3G32930	1.22	0.28	2.79	0.02786118	0.2735	-3.77
267171_at	putative DOF zinc finger protein	DOF2.4	AT2G37590	-1.32	-0.40	-2.79	0.02786305	0.2735	-3.77
256196_at	hypothetical protein predicted by g	---	---	-1.28	-0.36	-2.79	0.02793792	0.2741	-3.77
262487_at	unknown protein ESTs gb|T42839	---	AT1G21610	1.18	0.24	2.79	0.02795097	0.2741	-3.77
245007_at	PSI P700 apoprotein A1	---	---	-1.50	-0.59	-2.79	0.02799947	0.2742	-3.77
250969_at	putative protein ;supported by full-	---	AT5G02740	1.23	0.30	2.79	0.02802822	0.2742	-3.77
263018_at	putative non-LTR retroelement rev	---	---	-1.19	-0.25	-2.79	0.02799448	0.2742	-3.77
248063_at	RNA-binding protein-like ; support	---	AT5G55550	-1.23	-0.30	-2.79	0.02801967	0.2742	-3.77
260400_at	putative peptide transporter similar	---	AT1G69860	1.20	0.26	2.79	0.02804545	0.2742	-3.77
266809_at	unknown protein ; supported by cl	---	AT2G29970	-1.53	-0.61	-2.79	0.02799886	0.2742	-3.77
265536_at	unknown protein contains a domai	---	AT2G15880	1.67	0.74	2.79	0.02803838	0.2742	-3.77
265483_at	hypothetical protein ; supported by	SQN	AT2G15790	1.38	0.46	2.79	0.02808112	0.2743	-3.77
251447_at	U6 snRNA-associated Sm-like pro	---	AT3G59810	1.20	0.26	2.79	0.02817091	0.2743	-3.78
250426_at	ovule development protein - like o	AIL6	AT5G10510	-1.22	-0.29	-2.79	0.02814297	0.2743	-3.78
264996_at	nuclear matrix constituent protein	LINC1	AT1G67230	-1.30	-0.38	-2.79	0.02808459	0.2743	-3.77
251445_at	putative protein hypothetical prote	---	AT3G59870	-1.20	-0.27	-2.79	0.02813934	0.2743	-3.78
258613_at	putative myo-inositol monophosph	VTC4	AT3G02870	-1.51	-0.59	-2.79	0.02817244	0.2743	-3.78
252011_at	carbonic anhydrase (CAH1) ; supp	ACA1	AT3G52720	-1.38	-0.46	-2.79	0.0281068	0.2743	-3.77
258958_at	vacuolar membrane ATPase subu	VMA10	AT3G01390	1.37	0.46	2.79	0.02818133	0.2743	-3.78
264199_at	unknown protein contains similarit	---	AT1G22700	1.28	0.36	2.79	0.02817483	0.2743	-3.78
251154_at	tRNA isopentenyl transferase -like	ATIPT3	AT3G63110	-1.80	-0.84	-2.79	0.02818444	0.2743	-3.78

246171_at	putative protein centrosomal Nek2	---	AT5G32440	1.22	0.29	2.79	0.02811221	0.2743	-3.78
255636_at	homeodomain protein AHDP ; sup	ANL2	AT4G00730	1.30	0.38	2.78	0.02824174	0.2746	-3.78
251746_at	mandelonitrile lyase-like protein AI	---	AT3G56060	-1.32	-0.40	-2.78	0.02823835	0.2746	-3.78
249410_at	receptor-like protein kinase recept	---	AT5G40380	-1.55	-0.63	-2.78	0.02826385	0.2747	-3.78
248237_at	receptor protein kinase-like protein	---	AT5G53890	-1.32	-0.40	-2.78	0.02827721	0.2747	-3.78
265694_at	hypothetical protein predicted by g	---	AT2G24440	1.28	0.35	2.78	0.02830499	0.2749	-3.78
260985_at	dTDP-D-glucose 4,6-dehydratase	MUM4	AT1G53500	-1.28	-0.35	-2.78	0.02836388	0.2749	-3.78
247446_at	unknown protein ; supported by cl	---	AT5G62650	1.21	0.28	2.78	0.02834598	0.2749	-3.78
245635_at	zinc finger protein ID1, putative sir	AtIDD16	AT1G25250	-1.20	-0.26	-2.78	0.02832639	0.2749	-3.78
267239_at	unknown protein	---	AT2G02510	1.26	0.33	2.78	0.0283538	0.2749	-3.78
263144_at	unknown protein similar to putative	---	AT1G54070	-1.30	-0.37	-2.78	0.02836761	0.2749	-3.78
261006_at	unknown protein similar to reticulin	---	AT1G26410	1.73	0.79	2.78	0.02842005	0.2752	-3.79
254201_at	putative protein predicted proteins	---	AT4G24130	1.35	0.43	2.78	0.02841155	0.2752	-3.79
247855_at	similar to unknown protein (sp|P23	---	AT5G58210	-1.34	-0.42	-2.78	0.02844836	0.2752	-3.79
266789_at	unknown protein ; supported by fu	---	AT2G29020	1.23	0.30	2.78	0.0284416	0.2752	-3.79
248451_at	putative protein similar to unknown	---	AT5G51180	1.19	0.25	2.78	0.02847676	0.2754	-3.79
247972_at	histone acetyltransferase HAT B	HAG2	AT5G56740	1.37	0.45	2.78	0.02853874	0.2756	-3.79
252084_at	wax synthase-like protein wax syn	AtSAT1	AT3G51970	-1.32	-0.40	-2.78	0.02858312	0.2756	-3.79
258857_at	putative serine carboxypeptidase I	scpl25	AT3G02110	2.15	1.10	2.78	0.02857459	0.2756	-3.79
261257_at	tat-binding protein, putative simila	---	AT1G05910	-1.33	-0.41	-2.78	0.02857725	0.2756	-3.79
264340_at	unknown protein similar to hypothe	---	AT1G70280	1.30	0.37	2.78	0.02857451	0.2756	-3.79
253783_at	putative protein predicted protein,	NPGR2	AT4G28600	-1.27	-0.34	-2.78	0.028571	0.2756	-3.79
251573_at	phenylalanine-tRNA synthetase-lil	---	AT3G58140	1.26	0.34	2.78	0.02851163	0.2756	-3.79
256741_at	hypothetical protein predicted by g	---	AT3G29375	1.38	0.46	2.78	0.02860511	0.2756	-3.79
253172_at	putative protein ;supported by full-l	---	AT4G35060	-1.85	-0.89	-2.78	0.02861058	0.2756	-3.79
250441_at	oligopeptidase A - like protein olig	---	AT5G10540	1.20	0.26	2.77	0.02865252	0.2758	-3.79
259090_at	putative ribosomal protein s19 or s	---	AT3G04920	1.47	0.55	2.77	0.02868449	0.2758	-3.80
253702_at	Ca2+-transporting ATPase - like p	ACA10	AT4G29900	1.35	0.43	2.77	0.02867441	0.2758	-3.80
264203_at	putative 40S ribosomal protein S1	PFL	AT1G22780	1.62	0.70	2.77	0.02869245	0.2758	-3.80
266955_at	mitochondrial ribosomal protein S1	RPS14	AT2G34520	1.30	0.37	2.77	0.02869586	0.2758	-3.80
258621_at	zinc finger protein 1 (zfn1) identica	ZFN1	AT3G02830	-1.23	-0.29	-2.77	0.02875896	0.2763	-3.80
256275_at	actin 11 (ACT11) identical to actin	ACT11	AT3G12110	1.40	0.48	2.77	0.02879901	0.2766	-3.80
260450_at	hypothetical protein predicted by g	---	AT1G72390	-1.38	-0.46	-2.77	0.02881517	0.2766	-3.80
251796_at	synaptic glycoprotein SC2-like pro	---	AT3G55360	1.45	0.54	2.77	0.02885088	0.2768	-3.80
263836_at	unknown protein ;supported by ful	---	AT2G40330	2.10	1.07	2.77	0.02885465	0.2768	-3.80

255089_at	nucleoside-diphosphate kinase ;s	NDPK1	AT4G09320	1.38	0.46	2.77	0.02890086	0.2770	-3.80
253305_at	Expressed protein ; supported by f	---	AT4G33666	1.77	0.83	2.77	0.0289029	0.2770	-3.80
248098_at	unknown protein ; supported by c	---	AT5G55290	1.25	0.32	2.77	0.02893411	0.2772	-3.80
255694_at	putative transcriptional regulator	UNE10	AT4G00050	-1.33	-0.41	-2.77	0.0289769	0.2775	-3.81
245036_at	putative SF16 protein {Helianthus	Iqd4	AT2G26410	-1.21	-0.27	-2.77	0.02900381	0.2776	-3.81
254195_at	putative protein various predicted	NLP7	AT4G24020	1.24	0.31	2.76	0.02902626	0.2777	-3.81
259104_at	unknown protein ;supported by ful	LNG2	AT3G02170	-1.48	-0.56	-2.76	0.02916096	0.2781	-3.81
252663_at	putative protein several hypothetic	---	AT3G44070	-1.19	-0.25	-2.76	0.029185	0.2781	-3.81
255627_at	Expressed protein ; supported by f	---	AT4G00955	-1.21	-0.28	-2.76	0.02911863	0.2781	-3.81
256575_at	dTDP-glucose 4,6-dehydratase, p	RHM3	AT3G14790	1.37	0.45	2.76	0.0291622	0.2781	-3.81
256935_at	unknown protein ;supported by ful	---	AT3G22570	-1.21	-0.28	-2.76	0.02909435	0.2781	-3.81
266694_at	putative clathrin assembly protein	---	AT2G19790	1.19	0.26	2.76	0.02915685	0.2781	-3.81
262040_at	receptor protein kinase, putative s	TMM	AT1G80080	-1.26	-0.34	-2.76	0.02917441	0.2781	-3.81
261841_at	BTG1 binding factor 1, putative si	---	AT1G15920	1.24	0.31	2.76	0.02916857	0.2781	-3.81
254104_at	putative protein predicted protein,	---	AT4G25040	-1.30	-0.38	-2.76	0.02915976	0.2781	-3.81
258693_at	unknown protein	---	AT3G08650	-1.21	-0.27	-2.76	0.02914534	0.2781	-3.81
260258_at	putative ribosomal protein similar t	---	AT1G74270	1.36	0.44	2.76	0.0292088	0.2781	-3.81
260126_at	putative hydroxymethyltransferase	SHM7	AT1G36370	-1.42	-0.50	-2.76	0.02920975	0.2781	-3.81
260949_at	F-box protein family contains simil	SKIP16	AT1G06110	1.25	0.32	2.76	0.02925377	0.2783	-3.82
254207_at	putative protein Dof zinc finger pr	---	AT4G24060	-1.27	-0.35	-2.76	0.02925552	0.2783	-3.82
248335_at	putative protein strong similarity to	---	AT5G52450	-1.47	-0.55	-2.76	0.02937767	0.2792	-3.82
248394_at	unknown protein	---	AT5G52070	1.23	0.30	2.76	0.02937833	0.2792	-3.82
262496_at	unknown protein ; supported by ful	---	AT1G21790	1.52	0.60	2.75	0.02958077	0.2793	-3.83
246251_at	cold acclimation protein homolog	---	AT4G37220	1.80	0.85	2.75	0.02947892	0.2793	-3.82
256002_at	carbamoylphosphate synthetase,	CARB	AT1G29900	1.26	0.33	2.75	0.02965214	0.2793	-3.83
260815_at	chloroplast inner envelope protein	TIC110	AT1G06950	1.45	0.53	2.75	0.02964248	0.2793	-3.83
260370_at	putative aminolevulinate dehydrata	HEMB1	AT1G69740	1.24	0.31	2.76	0.02943023	0.2793	-3.82
248951_at	putative protein similar to unknown	---	AT5G45550	1.31	0.39	2.75	0.02958115	0.2793	-3.83
263599_at	putative histidine kinase ; supporte	WOL	AT2G01830	-1.42	-0.50	-2.75	0.02953387	0.2793	-3.83
266407_at	putative elongation factor	TFIIS	AT2G38560	1.23	0.30	2.75	0.02953714	0.2793	-3.83
247549_at	putative transcription factor MYB2	MYB28	AT5G61420	-1.43	-0.52	-2.75	0.0296505	0.2793	-3.83
251576_at	putative protein several hypothetic	---	AT3G58200	1.22	0.29	2.75	0.0296408	0.2793	-3.83
248027_at	outward rectifying potassium chan	ATKCO1	AT5G55630	1.30	0.38	2.75	0.02956079	0.2793	-3.83
251632_at	hypothetical protein	---	AT3G57440	-1.31	-0.39	-2.75	0.02954238	0.2793	-3.83
260564_at	putative small nuclear ribonucleop	---	AT2G43810	1.29	0.37	2.75	0.02955433	0.2793	-3.83

262033_at	terminal ear1, putative similar to te	MCT1	AT1G37140	-1.26	-0.33	-2.75	0.02954695	0.2793	-3.83
256581_at	hypothetical protein	---	AT3G28830	-1.19	-0.25	-2.75	0.02946224	0.2793	-3.82
263539_at	putative tyrosine aminotransferase	TAT3	AT2G24850	-4.10	-2.03	-2.75	0.02957038	0.2793	-3.83
263177_at	hypothetical protein predicted by g	---	AT1G05540	-1.23	-0.30	-2.76	0.02940309	0.2793	-3.82
266509_at	DegP2 protease identical to DegP2	DEGP2	AT2G47940	1.28	0.36	2.75	0.02947257	0.2793	-3.82
262826_at	putative cytochrome P450 monoo	CYP71B2	AT1G13080	-1.62	-0.70	-2.75	0.02962627	0.2793	-3.83
260251_at	putative heat shock protein similar	---	AT1G74250	-1.37	-0.46	-2.75	0.02947418	0.2793	-3.82
263460_at	putative acetolactate synthase	---	AT2G31810	1.35	0.43	2.75	0.02958496	0.2793	-3.83
252870_at	adenosine-5-phosphosulfate-kinas	AKN2	AT4G39940	-2.23	-1.16	-2.75	0.02964664	0.2793	-3.83
260493_at	hypothetical protein predicted by g	---	AT2G41830	1.48	0.57	2.75	0.02966511	0.2793	-3.83
254255_at	serine/threonine kinase - like prote	---	AT4G23220	1.82	0.87	2.75	0.02968264	0.2793	-3.83
265726_at	putative inositol polyphosphate 5'-p	---	AT2G32010	-1.37	-0.45	-2.75	0.0297534	0.2799	-3.83
266152_s_at	hypothetical protein predicted by g	---	AT2G12050 /	-1.21	-0.28	-2.75	0.02981554	0.2802	-3.84
244920_s_at	NADH dehydrogenase subunit 3 P	---	AT2G07751	-1.28	-0.35	-2.75	0.02981959	0.2802	-3.84
257967_at	hypothetical protein predicted by g	---	AT3G19910	1.22	0.29	2.75	0.02983286	0.2802	-3.84
251495_at	putative protein RanBP7/importin	---	AT3G59020	1.35	0.43	2.75	0.02983674	0.2802	-3.84
249120_at	unknown protein ;supported by ful	---	AT5G43750	-1.25	-0.32	-2.74	0.02991162	0.2805	-3.84
254734_at	methionyl-tRNA synthetase - like p	---	AT4G13780	1.27	0.34	2.74	0.02992747	0.2805	-3.84
262624_at	CCR4-associated factor, putative	---	AT1G06450	1.27	0.35	2.74	0.02988839	0.2805	-3.84
259765_at	unknown protein ;supported by full	---	AT1G64370	-1.38	-0.46	-2.74	0.02990334	0.2805	-3.84
260411_at	hypothetical protein similar to GB:A	---	AT1G69890	1.61	0.69	2.74	0.0299302	0.2805	-3.84
258709_at	putative 60S ribosomal protein L35	---	AT3G09500	1.55	0.63	2.74	0.02995253	0.2806	-3.84
261664_s_at	hypothetical protein contains simila	---	AT1G18320 /	1.38	0.46	2.74	0.02997859	0.2807	-3.84
259124_at	floral homeotic protein AGL4 ident	ספט-02	AT3G02310	-1.19	-0.25	-2.74	0.02998901	0.2807	-3.84
251893_at	putative protein	---	AT3G54380	1.23	0.30	2.74	0.03000878	0.2808	-3.84
248515_at	putative protein strong similarity to	---	AT5G50530 /	-1.28	-0.36	-2.74	0.03004759	0.2808	-3.84
249999_at	triacylglycerol lipase-like protein tr	---	AT5G18640	1.51	0.59	2.74	0.03004328	0.2808	-3.84
253482_at	Expressed protein ; supported by c	---	AT4G31985	1.75	0.81	2.74	0.03004665	0.2808	-3.84
245747_at	hypothetical protein predicted by g	---	AT1G51100	1.36	0.44	2.74	0.03009793	0.2810	-3.84
258377_at	hypothetical protein contains simila	CNGC19	AT3G17690	-1.27	-0.34	-2.74	0.03008866	0.2810	-3.84
246607_at	receptor-like protein kinase - like p	---	AT5G35370	1.66	0.73	2.74	0.03012796	0.2812	-3.85
255276_at	putative fatty acid desaturase simi	DES-1-LIKE	AT4G04930	-1.22	-0.28	-2.74	0.03016255	0.2814	-3.85
245972_at	putative protein predicted proteins	---	AT5G20680	-1.32	-0.40	-2.74	0.0302013	0.2816	-3.85
262853_at	unknown protein Location of ESTs	---	AT1G20890	1.26	0.33	2.74	0.0302273	0.2817	-3.85
253138_at	ribosomal protein L11 homolog se	MRPL11	AT4G35490	1.21	0.28	2.74	0.03022565	0.2817	-3.85

264820_at	putative coproporphyrinogen III ox	LIN2	AT1G03475	1.19	0.25	2.74	0.03024905	0.2817	-3.85
266536_at	hypothetical protein predicted by g	---	AT2G16900	1.91	0.94	2.73	0.03029585	0.2821	-3.85
251222_at	putative membrane protein clone:	---	AT3G62580	-1.45	-0.54	-2.73	0.0303233	0.2822	-3.85
257907_at	hemolysin, putative similar to hem	---	AT3G25470	1.18	0.24	2.73	0.03033288	0.2822	-3.85
265315_at	hypothetical protein predicted by g	CLASP	AT2G20190	-1.24	-0.31	-2.73	0.03038447	0.2824	-3.85
252263_at	putative protein several hypothetic	---	AT3G49520	-1.29	-0.37	-2.73	0.03038347	0.2824	-3.85
251305_at	peptidylprolyl isomerase ROC4 ;s	ROC4	AT3G62030	1.40	0.49	2.73	0.03042126	0.2827	-3.86
256065_at	ribosomal protein, putative similar	---	AT1G07070	1.55	0.63	2.73	0.03046126	0.2829	-3.86
245256_at	Expressed protein ; supported by c	FAR1	AT4G15090	1.28	0.36	2.73	0.03055972	0.2836	-3.86
254346_at	symbiosis-related like protein sym	APG8A	AT4G21980	1.47	0.55	2.73	0.03055294	0.2836	-3.86
250314_at	putative protein contains similarity	---	AT5G12190	1.21	0.27	2.73	0.03063989	0.2837	-3.86
260886_at	hypothetical protein contains simila	---	AT1G29200	-1.20	-0.26	-2.73	0.03065395	0.2837	-3.86
254956_at	putative protein various predicted	---	AT4G10850	-1.21	-0.27	-2.73	0.03063548	0.2837	-3.86
266309_at	unknown protein ;supported by ful	---	AT2G27140	1.36	0.44	2.73	0.03067246	0.2837	-3.86
253759_at	AIM1 protein ; supported by cDNA	AIM1	AT4G29010	-1.20	-0.26	-2.73	0.03067357	0.2837	-3.86
249945_at	60S ribosomal protein L10A ; supp	---	AT5G22440	1.62	0.70	2.73	0.03065515	0.2837	-3.86
246697_at	putative protein	---	AT5G29210	-1.27	-0.34	-2.73	0.03063193	0.2837	-3.86
250472_at	putative protein	---	AT5G10210	1.33	0.41	2.73	0.03059639	0.2837	-3.86
249024_at	putative protein strong similarity to	---	AT5G44860	1.23	0.30	2.73	0.03068641	0.2837	-3.86
250862_s_at	40S ribosomal protein S17 -like 4(	---	AT2G04390	1.45	0.54	2.72	0.0307099	0.2838	-3.87
265028_at	hypothetical protein predicted by g	---	AT1G24530	2.07	1.05	2.72	0.03073037	0.2839	-3.87
247613_at	xABC transporter - like protein bre	---	AT5G60740	-1.29	-0.37	-2.72	0.03076869	0.2841	-3.87
259279_at	putative cystathionine gamma-syn	MTO1	AT3G01120	-1.23	-0.30	-2.72	0.03077345	0.2841	-3.87
250403_at	argininosuccinate lyase (AtArgH) ;	---	AT5G10920	1.51	0.59	2.72	0.03081066	0.2843	-3.87
262024_at	protein disulfide isomerase, putati	ATPDIL5-2	AT1G35620	1.30	0.38	2.72	0.03082601	0.2843	-3.87
262923_at	Dhp1-like protein similar to Dhp1 p	XRN3	AT1G75660	1.24	0.31	2.72	0.03088427	0.2847	-3.87
264546_at	Expressed protein ; supported by c	---	AT1G55805	1.51	0.59	2.72	0.0308903	0.2847	-3.87
266213_s_at	Mutator-like transposase similar to	---	---	-1.25	-0.32	-2.72	0.03095113	0.2851	-3.87
265966_at	putative RNA-binding protein ; sup	---	AT2G37220	1.32	0.41	2.72	0.03098603	0.2853	-3.87
264481_at	transcription factor TINY, putative	---	AT1G77200	-1.28	-0.35	-2.72	0.03101032	0.2855	-3.88
250177_at	putative protein copine I, Homo sa	RGLG2	AT5G14420	1.29	0.36	2.72	0.03102821	0.2855	-3.88
253753_at	glycine-rich protein like glycine-ric	---	AT4G29030	-1.26	-0.33	-2.72	0.03111446	0.2859	-3.88
262504_at	putative protein disulfide isomeras	ATPDIL1-1	AT1G21750	1.40	0.49	2.72	0.03110523	0.2859	-3.88
247412_at	unknown protein	---	AT5G63010	1.27	0.34	2.72	0.03109013	0.2859	-3.88
260117_at	AIG1-like protein similar to AIG1 p	---	AT1G33950	-1.17	-0.23	-2.72	0.0311189	0.2859	-3.88

263536_at	putative WRKY-type DNA binding	WRKY60	AT2G25000	1.65	0.72	2.71	0.03121679	0.2859	-3.88
263846_at	putative RNA polymerase sigma-7	SIGF	AT2G36990	1.38	0.46	2.71	0.03115187	0.2859	-3.88
244904_at	hypothetical protein	---	---	-1.43	-0.52	-2.71	0.03115996	0.2859	-3.88
257043_at	receptor-like protein kinase, putati	IKU2	AT3G19700	-1.24	-0.32	-2.71	0.03120671	0.2859	-3.88
247174_at	unknown protein ; supported by cl	---	AT5G65250	1.22	0.29	2.71	0.03118727	0.2859	-3.88
263128_at	zinc finger protein, putative similar	LZF1	AT1G78600	-1.48	-0.56	-2.71	0.03122221	0.2859	-3.88
248044_at	putative protein similar to unknown	---	AT5G56020	1.24	0.31	2.71	0.03121727	0.2859	-3.88
264939_at	receptor kinase, putative similar to	---	AT1G60630	-1.25	-0.32	-2.71	0.03119043	0.2859	-3.88
267579_at	metallothionein-like protein	---	AT2G42000	-1.20	-0.26	-2.71	0.03124225	0.2860	-3.88
261055_at	chloroplast nucleoid DNA binding	---	AT1G01300	1.29	0.36	2.71	0.0312597	0.2860	-3.88
264923_s_at	peroxiredoxin, putative similar to t	---	AT1G60740 /	1.61	0.69	2.71	0.03133314	0.2865	-3.89
258662_at	unknown protein	---	AT3G02900	1.59	0.67	2.71	0.03134189	0.2865	-3.89
252649_at	putative protein histone deacetyla	HDA9	AT3G44680	1.19	0.26	2.71	0.03136031	0.2865	-3.89
255913_at	kinase, putative similar to leaf rust	---	AT1G66980	-1.19	-0.25	-2.71	0.03134796	0.2865	-3.89
248709_at	unknown protein ;supported by ful	---	AT5G48470	1.46	0.55	2.71	0.03141487	0.2867	-3.89
254952_at	UDP-galactose 4-epimerase - like	UGE5	AT4G10955 /	1.29	0.36	2.71	0.03140965	0.2867	-3.89
248332_at	heat-shock protein ; supported by	ATHSP90.1	AT5G52640	-2.49	-1.32	-2.71	0.0314289	0.2868	-3.89
246777_at	RING-H2 zinc finger protein-like R	---	AT5G27420	2.79	1.48	2.71	0.03152216	0.2868	-3.89
255527_at	putative protein	---	AT4G02360	-2.28	-1.19	-2.71	0.03148401	0.2868	-3.89
251598_at	AP2 transcription factor - like prote	---	AT3G57600	-1.21	-0.28	-2.71	0.03148757	0.2868	-3.89
250406_at	enhancer of rudimentary ; support	ER	AT5G10810	1.36	0.45	2.71	0.03146569	0.2868	-3.89
256663_at	unknown protein ;supported by full	---	AT3G12050	-1.41	-0.50	-2.71	0.03151475	0.2868	-3.89
249446_at	receptor protein kinase -like protei	---	AT5G39390	-1.22	-0.29	-2.71	0.03145365	0.2868	-3.89
253833_at	putative calcium binding protein ta	---	AT4G27790	1.42	0.51	2.71	0.03151551	0.2868	-3.89
247706_at	putative ripening-related protein - l	---	AT5G59480	-1.67	-0.74	-2.71	0.03155993	0.2870	-3.89
253296_at	putative protein inositol 1,3,4-trisp	---	AT4G33770	-1.22	-0.29	-2.71	0.03157201	0.2870	-3.89
260708_at	expressed protein ; supported by f	---	AT1G32310	1.27	0.35	2.70	0.03163774	0.2875	-3.90
254137_at	hypothetical protein	---	AT4G24930	1.47	0.56	2.70	0.03168733	0.2877	-3.90
266055_at	hypothetical protein predicted by g	---	AT2G40650	1.28	0.36	2.70	0.03173027	0.2877	-3.90
256723_at	unknown protein ;supported by ful	---	AT2G34160	1.19	0.25	2.70	0.03171623	0.2877	-3.90
261559_at	LIM domain protein, putative simil	---	AT1G01780	1.27	0.35	2.70	0.03173245	0.2877	-3.90
248747_at	ribosomal protein S27 ;supported b	---	AT5G47930	1.35	0.43	2.70	0.03171383	0.2877	-3.90
266672_at	putative Na+-dependent inorganic	PHT4;1	AT2G29650	-1.23	-0.30	-2.70	0.03168662	0.2877	-3.90
250651_at	cytochrome P450	CYP93D1	AT5G06900	-1.19	-0.25	-2.70	0.03177016	0.2879	-3.90
267614_at	putative cytochrome P450	BAS1	AT2G26710	1.96	0.97	2.70	0.03179029	0.2879	-3.90

246306_at	putative protein hypothetical prote	ATBAG4	AT3G51780	-1.18	-0.24	-2.70	0.03178545	0.2879	-3.90
255542_at	hypothetical protein	---	AT4G01860	1.29	0.37	2.70	0.03182683	0.2880	-3.90
257851_at	unknown protein	---	AT3G12940	-1.25	-0.32	-2.70	0.03181572	0.2880	-3.90
248819_at	putative protein contains similarity	---	AT5G47050	1.46	0.55	2.70	0.03191152	0.2884	-3.90
260979_at	MAP kinase ATMPK9, putative sir	ATMPK18	AT1G53510	-1.22	-0.29	-2.70	0.03189661	0.2884	-3.90
257266_at	RNA-binding protein contains Pfar	---	AT3G15010	-1.21	-0.28	-2.70	0.03191149	0.2884	-3.90
258068_at	putative DNA-binding protein, GT-	---	AT3G25990	-1.22	-0.29	-2.70	0.0319599	0.2886	-3.91
255071_at	putative protein putative chloropla	---	AT4G09040	1.26	0.33	2.70	0.03196037	0.2886	-3.91
256773_at	hypothetical protein predicted by g	---	AT3G13630	-1.26	-0.33	-2.70	0.03198035	0.2887	-3.91
252602_at	putative protein KIAA1094 protein	---	AT3G45040	-1.27	-0.35	-2.69	0.03210927	0.2896	-3.91
245933_at	putative protein KIAA1521 - Homo	VPS9B	AT5G09320	1.21	0.27	2.69	0.03213152	0.2896	-3.91
258321_at	early light-induced protein identica	ELIP1	AT3G22840	-1.27	-0.34	-2.69	0.03213054	0.2896	-3.91
258108_at	unknown protein contains Pfam pr	---	AT3G23570	-1.87	-0.90	-2.69	0.03212292	0.2896	-3.91
259433_at	hypothetical protein predicted by g	---	AT1G01570	-1.28	-0.36	-2.69	0.03216448	0.2898	-3.91
257820_at	immunophilin (FKBP15-1) identica	FKBP15-1	AT3G25220	1.28	0.36	2.69	0.03218391	0.2898	-3.91
249127_at	actin-like protein ; supported by cI	ATARP9	AT5G43500	1.28	0.36	2.69	0.03219528	0.2898	-3.91
261952_at	unknown protein	---	AT1G64430	1.18	0.24	2.69	0.03222781	0.2900	-3.91
254920_at	putative protein 24 kDa seed matu	BTI2	AT4G11220	-1.29	-0.37	-2.69	0.03231727	0.2907	-3.92
255267_at	putative protein LpxD gene, Bruce	---	AT4G05210	-1.18	-0.24	-2.69	0.03235404	0.2909	-3.92
265096_at	unknown protein Location of ESTs	---	AT1G04030	1.28	0.35	2.69	0.03236833	0.2909	-3.92
246094_at	putative protein predicted proteins	---	AT5G19300	-1.42	-0.51	-2.69	0.03240655	0.2910	-3.92
253156_at	putative protein mRNA for KIAA01	---	AT4G35730	1.27	0.35	2.69	0.03240097	0.2910	-3.92
261064_at	unknown protein	ftsh10	AT1G07510	-1.30	-0.38	-2.69	0.03242594	0.2911	-3.92
267400_at	unknown protein	---	AT2G26240	1.32	0.40	2.69	0.03244458	0.2911	-3.92
256296_at	hypothetical protein	---	AT1G69480	1.21	0.27	2.69	0.03245968	0.2911	-3.92
262569_at	hypothetical protein Strong similari	---	AT1G15180	1.41	0.50	2.69	0.03246992	0.2911	-3.92
253609_at	H+-transporting ATPase type 2, p	AHA2	AT4G30190	1.29	0.37	2.68	0.03254406	0.2917	-3.92
256179_at	ubiquitin-specific protease 6 (UBP	UBP6	AT1G51710	1.20	0.27	2.68	0.03255512	0.2917	-3.92
245629_at	hypothetical protein predicted by g	---	AT1G56580	-1.33	-0.41	-2.68	0.03261645	0.2917	-3.93
248492_at	putative protein similar to unknown	---	AT5G51040	-1.21	-0.27	-2.68	0.03260048	0.2917	-3.93
248547_at	putative protein contains similarity	EMB1006	AT5G50280	1.43	0.51	2.68	0.03264464	0.2917	-3.93
266542_at	unknown protein	ARAD1	AT2G35100	-1.21	-0.27	-2.68	0.0326017	0.2917	-3.93
AFFX-ThrX-5_a	B. subtilis /GEN=thrC /DB_XREF=	---	---	-1.52	-0.61	-2.68	0.03264542	0.2917	-3.93
247943_at	light-inducible protein ATLS1-like	---	AT5G57170	1.46	0.54	2.68	0.03259562	0.2917	-3.93
262216_at	hypothetical protein contains simila	---	AT1G74780	-1.29	-0.36	-2.68	0.03262401	0.2917	-3.93

261392_at	hypothetical protein predicted by g	---	AT1G79780	-1.21	-0.27	-2.68	0.03266269	0.2917	-3.93
252213_at	flavonol synthase - like protein SR	---	AT3G50210	1.30	0.38	2.68	0.03274781	0.2921	-3.93
259417_at	unknown protein contains similarity	HFR1	AT1G02340	1.43	0.52	2.68	0.03273539	0.2921	-3.93
261696_at	unknown protein similar to hypothe	---	AT1G08470	1.39	0.48	2.68	0.03273928	0.2921	-3.93
255136_s_at	putative protein chromatin structur	---	AT4G08350 /	1.28	0.35	2.68	0.03278134	0.2922	-3.93
249308_at	unknown protein ; supported by cl	---	AT5G41350	-1.20	-0.26	-2.68	0.03277518	0.2922	-3.93
251260_at	putative protein ISOPENICILLIN N	---	AT3G62130	1.42	0.51	2.68	0.03279982	0.2923	-3.93
258114_at	putative cytochrome P450 similar t	CYP72A13	AT3G14660	1.23	0.30	2.68	0.03282645	0.2923	-3.93
254316_at	putative protein glycine-rich cell w	---	---	-1.25	-0.32	-2.68	0.03283612	0.2923	-3.93
246888_at	putative protein	---	AT5G26270	-1.19	-0.26	-2.68	0.03287465	0.2925	-3.93
253511_at	putative protein Sly1 protein, rat, F	---	AT4G31740	-1.22	-0.29	-2.68	0.03288051	0.2925	-3.93
249718_at	putative protein contains similarity	---	AT5G35740	1.29	0.37	2.68	0.03294636	0.2929	-3.94
258436_at	putative RING zinc finger protein s	ATL2	AT3G16720	1.82	0.87	2.68	0.03295187	0.2929	-3.94
255094_at	putative zinc finger protein	ORTHL	AT4G08590	-1.43	-0.51	-2.67	0.03297257	0.2930	-3.94
253414_at	putative protein	EDA39	AT4G33050	2.86	1.52	2.67	0.03301315	0.2931	-3.94
260119_at	AIG1-like protein similar to AIG1 p	---	AT1G33930	-1.22	-0.29	-2.67	0.03301503	0.2931	-3.94
257771_at	SNF1 related protein kinase (ATSF	CIPK7	AT3G23000	1.95	0.96	2.67	0.03307233	0.2935	-3.94
254649_at	pherophorin - like protein pheroph	---	AT4G18570	-1.27	-0.34	-2.67	0.03309106	0.2935	-3.94
261678_at	disease resistance protein, putativ	---	AT1G47370	-1.28	-0.35	-2.67	0.03309698	0.2935	-3.94
253041_at	phosphoenolpyruvate carboxykina	PCK1	AT4G37870	-1.52	-0.60	-2.67	0.03313124	0.2937	-3.94
248579_at	mitotic checkpoint protein-like	---	AT5G49880	1.36	0.45	2.67	0.03322719	0.2944	-3.95
257686_at	unknown protein similar to unknow	SDRB	AT3G12800	1.27	0.34	2.67	0.03337058	0.2948	-3.95
259237_at	putative 2-cys peroxiredoxin BAS1	---	AT3G11630	1.35	0.43	2.67	0.0333572	0.2948	-3.95
258419_at	unknown protein	---	AT3G16670	2.55	1.35	2.67	0.03328576	0.2948	-3.95
261606_at	peroxidase, putative similar to per	---	AT1G49570	-1.31	-0.39	-2.67	0.03332459	0.2948	-3.95
247730_at	glucuronosyl transferase - like pro	UGT76E1	AT5G59580	-1.43	-0.51	-2.67	0.03334045	0.2948	-3.95
255731_at	phosphoprotein phosphatase 2A,	RCN1	AT1G25490	1.18	0.24	2.67	0.03336407	0.2948	-3.95
254351_at	putative protein probable membra	SOBER1	AT4G22300	1.29	0.36	2.67	0.03334445	0.2948	-3.95
266395_at	3-isopropylmalate dehydratase, sr	---	AT2G43100	-1.78	-0.83	-2.67	0.03335721	0.2948	-3.95
266175_at	NAM (no apical meristem)-like prot	ANAC035	AT2G02450	1.23	0.30	2.67	0.03338432	0.2948	-3.95
255762_at	unknown protein contains Pfam pr	HAC12	AT1G16710	-1.24	-0.31	-2.67	0.03339859	0.2948	-3.95
265119_at	flavin-containing monooxygenase	FMO GS-O	AT1G62570	-1.58	-0.66	-2.67	0.03341281	0.2948	-3.95
251886_at	putative protein various predicted	---	AT3G54260	1.42	0.51	2.66	0.03344971	0.2950	-3.95
253171_at	putative protein ;supported by full-	---	AT4G35040	1.28	0.35	2.66	0.03350847	0.2954	-3.95
260201_at	F12A21.27 hypothetical protein;su	---	AT1G67600	1.56	0.64	2.66	0.03354621	0.2956	-3.95

267007_at	60S ribosomal protein L18A ; supp	---	AT2G34480	1.43	0.51	2.66	0.03354216	0.2956	-3.95
247812_at	peroxidase ;supported by full-lengt	---	AT5G58390	-1.91	-0.93	-2.66	0.03356576	0.2956	-3.96
266616_at	putative CDC6 protein ; supported	CDC6	AT2G29680	1.22	0.29	2.66	0.03362171	0.2960	-3.96
258534_at	thioredoxin, putative similar to thio	---	AT3G06730	1.22	0.28	2.66	0.03373637	0.2969	-3.96
248995_at	disease resistance protein-like	RRS1	AT5G45260	-1.22	-0.29	-2.66	0.03375231	0.2969	-3.96
260948_at	delta 9 desaturase, putative simila	---	AT1G06100	-1.26	-0.34	-2.66	0.03377414	0.2970	-3.96
260581_at	MYB transcription factor (Atmyb2)	MYB2	AT2G47190	1.36	0.45	2.66	0.03381119	0.2972	-3.96
250238_at	unknown protein	DCP2	AT5G13570	1.22	0.29	2.66	0.03382755	0.2972	-3.96
264344_at	putative aspartic proteinase similar	---	AT1G11910	1.18	0.24	2.66	0.03390312	0.2978	-3.97
255279_at	putative thioredoxin ; supported by	---	AT4G04950	1.40	0.49	2.65	0.03392697	0.2978	-3.97
253361_at	putative protein various predicted p	---	AT4G33100	1.45	0.53	2.65	0.033922	0.2978	-3.97
264886_at	S-linalool synthase, putative simila	TPS04	AT1G61120	-4.89	-2.29	-2.65	0.03397568	0.2981	-3.97
248072_at	unknown protein	---	AT5G55680	-1.25	-0.32	-2.65	0.03400212	0.2981	-3.97
250974_at	meiosis specific - like protein Spo1	RHL2	AT5G02820	1.58	0.66	2.65	0.0340154	0.2981	-3.97
256666_at	histone H2A, putative similar to his	HTA13	AT3G20670	1.59	0.67	2.65	0.03400876	0.2981	-3.97
266274_at	putative protein phosphatase 2C	---	AT2G29380	-1.23	-0.30	-2.65	0.03403402	0.2981	-3.97
258284_at	putative ribosomal protein similar t	---	AT3G16080	1.59	0.67	2.65	0.03407192	0.2981	-3.97
256807_at	unknown protein contains Pfam pr	NFU4	AT3G20970	1.24	0.31	2.65	0.03407567	0.2981	-3.97
264530_at	hypothetical protein	---	AT1G30780	1.29	0.37	2.65	0.03405503	0.2981	-3.97
261611_at	hypothetical protein predicted by g	---	AT1G49730	1.50	0.58	2.65	0.03428693	0.2984	-3.98
248448_at	putative protein contains similarity	---	AT5G51190	2.66	1.41	2.65	0.03428005	0.2984	-3.98
259945_at	unknown protein	---	AT1G71460	1.28	0.35	2.65	0.03422338	0.2984	-3.98
265510_at	putative microtubule-associated pr	ATG8D	AT2G05630	1.23	0.30	2.65	0.03417801	0.2984	-3.97
266563_at	nodulin-like protein	---	AT2G23990	-1.22	-0.29	-2.65	0.03432444	0.2984	-3.98
252080_at	putative protein polyphosphoinosit	---	AT3G51670	-1.43	-0.52	-2.65	0.03431312	0.2984	-3.98
264825_at	hypothetical protein predicted by g	---	AT1G03720	-1.26	-0.33	-2.65	0.03430879	0.2984	-3.98
265960_at	putative histone H2B ;supported b	---	AT2G37470	1.49	0.58	2.65	0.03425943	0.2984	-3.98
263369_at	unknown protein	---	AT2G20480	1.19	0.26	2.65	0.0342042	0.2984	-3.97
264509_at	unknown protein Location of EST g	---	AT1G09520	1.25	0.33	2.65	0.03420527	0.2984	-3.97
246207_at	RNA-binding like protein non-cons	---	AT4G36960	-1.22	-0.29	-2.65	0.03413141	0.2984	-3.97
246839_at	putative protein	---	AT5G26720	-1.25	-0.32	-2.65	0.03432663	0.2984	-3.98
252944_at	hypothetical protein ;supported by	---	AT4G39320	1.22	0.29	2.65	0.03414041	0.2984	-3.97
263407_at	bZIP protein (AtbZIP48) to be publ	AtbZIP48	AT2G04038	-1.22	-0.29	-2.65	0.03423096	0.2984	-3.98
254127_at	NADPH-ferrihemoprotein reductas	ATR1	AT4G24520	1.29	0.36	2.65	0.03425942	0.2984	-3.98
253287_at	putative protein dJ69E11.3, Homo	---	AT4G34270	1.20	0.26	2.65	0.03433489	0.2984	-3.98

244928_s_at	hypothetical protein	---	AT2G07716	-1.23	-0.29	-2.65	0.03420182	0.2984	-3.97
264150_at	unknown protein similar to FUS5 p	FUS5	AT1G02090	-1.20	-0.27	-2.65	0.03414509	0.2984	-3.97
264512_at	Expressed protein ; supported by c	---	AT1G09575	1.27	0.34	2.65	0.03436999	0.2985	-3.98
258553_at	hypothetical protein ; supported by	PDE320	AT3G06960	1.21	0.27	2.64	0.03439617	0.2985	-3.98
250966_at	putative protein various predicted	---	AT5G02910	1.29	0.37	2.65	0.03439294	0.2985	-3.98
253818_at	hypothetical protein	---	AT4G28330	-1.32	-0.40	-2.64	0.03444602	0.2989	-3.98
246968_at	RING finger-like protein RING-H2	---	AT5G24870	1.33	0.41	2.64	0.03456443	0.2990	-3.99
259970_at	putative chlorophyll A-B binding pr	---	AT1G76570	-1.42	-0.50	-2.64	0.03448548	0.2990	-3.98
256458_at	integral membrane protein, putativ	---	AT1G75220	-1.43	-0.52	-2.64	0.03451841	0.2990	-3.98
258489_at	14-3-3 protein GF14nu (grf7) ident	GRF7	AT3G02520	1.20	0.26	2.64	0.03452285	0.2990	-3.98
260655_at	pathogenesis-related protein 5 pre	---	AT1G19320	-1.56	-0.64	-2.64	0.0345612	0.2990	-3.99
250390_at	separation anxiety protein - like se	---	AT5G11340	1.18	0.23	2.64	0.03457196	0.2990	-3.99
246244_at	receptor kinase-like protein	---	AT4G37250	-1.22	-0.28	-2.64	0.03454303	0.2990	-3.98
263366_at	unknown protein	---	AT2G20440	-1.26	-0.33	-2.64	0.03455897	0.2990	-3.99
253254_at	predicted protein	SQS2	AT4G34650	-1.53	-0.62	-2.64	0.03462503	0.2993	-3.99
260166_at	homeobox protein (GLABRA2) ide	GL2	AT1G79840	-1.20	-0.26	-2.64	0.03462753	0.2993	-3.99
260595_at	unknown protein	---	AT1G55890	1.27	0.35	2.64	0.03471422	0.2998	-3.99
256070_at	hypothetical protein predicted by g	---	AT1G13730	1.22	0.28	2.64	0.03470343	0.2998	-3.99
265191_at	hypothetical protein Similar to Sac	---	AT1G05120	-1.23	-0.30	-2.64	0.03471938	0.2998	-3.99
266951_at	putative salt-inducible protein ; su	---	AT2G18940	1.19	0.26	2.64	0.03480588	0.3004	-3.99
258699_at	unknown protein	---	AT3G09470	1.27	0.34	2.64	0.03484585	0.3004	-3.99
247266_at	beta-xylosidase	XYL4	AT5G64570	1.44	0.53	2.64	0.03485462	0.3004	-3.99
249324_at	cytochrome c1 precursor ; suppor	---	AT5G40810	1.19	0.25	2.64	0.03481574	0.3004	-3.99
260929_at	transcription factor TFIID, putative	TAF13	AT1G02680	1.37	0.45	2.64	0.03482872	0.3004	-3.99
254228_at	putative protein ; supported by full	---	AT4G23620	1.23	0.30	2.63	0.03489581	0.3005	-3.99
247182_at	putative protein contains similarity	HB25	AT5G65410	-1.28	-0.35	-2.63	0.03489133	0.3005	-3.99
250723_at	lysine decarboxylase-like protein	---	AT5G06300	1.34	0.42	2.63	0.03490922	0.3005	-4.00
262159_at	hypothetical protein predicted by g	---	AT1G52720	-1.64	-0.71	-2.63	0.03492705	0.3005	-4.00
262501_at	putative replication factor Similar t	emb1968	AT1G21690	1.27	0.35	2.63	0.03494419	0.3006	-4.00
251920_at	uracil phosphoribosyltransferase-l	---	AT3G53900	1.57	0.65	2.63	0.03497609	0.3006	-4.00
261984_at	TINY-like protein similar to TINY G	---	AT1G33760	-1.31	-0.39	-2.63	0.03496667	0.3006	-4.00
267458_at	similar to Mlo proteins from H. vulg	MLO5	AT2G33670	-1.30	-0.38	-2.63	0.03499032	0.3006	-4.00
250180_at	early nodule-specific protein - like	---	AT5G14450	1.23	0.30	2.63	0.0350333	0.3006	-4.00
245865_at	hypothetical protein contains simila	---	AT1G58025	1.22	0.29	2.63	0.03508243	0.3006	-4.00
248310_at	putative protein similar to unknown	CPuORF14	AT5G52550	-1.22	-0.28	-2.63	0.03506198	0.3006	-4.00

262529_at	putative receptor protein kinase Ap	AtRLP3	AT1G17250	1.30	0.38	2.63	0.0350463	0.3006	-4.00
252832_at	ubiquitin-specific protease 3 (UBP3	ATUBP3	AT4G39910	1.18	0.24	2.63	0.03500985	0.3006	-4.00
254420_at	hypothetical protein	---	AT4G21500	1.31	0.39	2.63	0.03508391	0.3006	-4.00
260032_at	putative phosphoenolpyruvate carb	ATPPC4	AT1G68750	-1.24	-0.31	-2.63	0.03502425	0.3006	-4.00
255829_at	putative potassium transporter ; su	KT2	AT2G40540	-1.19	-0.25	-2.63	0.03510541	0.3007	-4.00
258526_at	DAG protein, putative similar to DA	---	AT3G06790	1.24	0.31	2.63	0.03513795	0.3007	-4.00
248450_at	putative protein contains similarity	---	AT5G51290	-1.26	-0.34	-2.63	0.03513212	0.3007	-4.00
261767_s_at	adenine nucleotide translocase, p	NTT1	AT1G15500 /	1.28	0.35	2.63	0.03518272	0.3010	-4.00
258504_at	putative sterol-C5-desaturase iden	---	AT3G02590	-1.18	-0.24	-2.63	0.0351879	0.3010	-4.00
263862_at	putative protein phosphatase	IBR5	AT2G04550	1.22	0.29	2.63	0.0352178	0.3010	-4.00
252996_s_at	geranylgeranyl pyrophosphate syn	GGR	AT4G38460	-1.27	-0.34	-2.63	0.03520792	0.3010	-4.00
250721_at	putative protein contains similarity	---	AT5G06210	1.21	0.28	2.63	0.03525315	0.3012	-4.01
250062_at	BCS1 - like protein h-bcs1, Homo	---	AT5G17760	1.44	0.52	2.63	0.03531787	0.3016	-4.01
256404_at	unknown protein similar to far-red i	FRS7	AT3G06250	1.33	0.42	2.63	0.03536901	0.3018	-4.01
246987_at	myb-related protein, 33.3K (pir |S7	MYBR1	AT5G67300	-1.49	-0.58	-2.63	0.03537585	0.3018	-4.01
247078_at	unknown protein ; supported by cD	---	AT5G66000	1.26	0.33	2.63	0.03536485	0.3018	-4.01
267252_at	hypothetical protein predicted by g	---	AT2G23100	1.23	0.30	2.62	0.03540285	0.3019	-4.01
264708_at	putative ER6 protein similar to GB	---	AT1G09740	1.34	0.42	2.62	0.03551185	0.3019	-4.01
256887_at	hypothetical protein predicted by g	---	AT3G15150	1.27	0.34	2.62	0.03552791	0.3019	-4.01
264828_at	hypothetical protein predicted by g	ATATG18G	AT1G03380	1.34	0.42	2.62	0.03545207	0.3019	-4.01
254049_at	putative ribosomal protein S10 40	---	AT4G25740	1.49	0.57	2.62	0.0354415	0.3019	-4.01
264421_at	ribosomal protein identical to ribos	ARP1	AT1G43170	1.36	0.44	2.62	0.03549006	0.3019	-4.01
254482_at	TWIN SISTER OF FT (TSF) termi	TSF	AT4G20370	-1.28	-0.36	-2.62	0.03547255	0.3019	-4.01
266748_at	putative squamosa-promoter bindi	SPL1	AT2G47070	-1.40	-0.49	-2.62	0.03551825	0.3019	-4.01
263603_at	hypothetical protein	---	AT2G16340	-1.30	-0.38	-2.62	0.03550431	0.3019	-4.01
245478_at	galactokinase like protein	ARA1	AT4G16130	1.62	0.70	2.62	0.03548343	0.3019	-4.01
255988_at	putative protein	---	---	-1.23	-0.29	-2.62	0.03557105	0.3022	-4.01
246496_at	putative protein KIAA1468 - Homo	---	AT5G16210	-1.25	-0.33	-2.62	0.03566603	0.3022	-4.02
247398_at	putative protein predicted protein,	---	AT5G62950	1.28	0.35	2.62	0.03562968	0.3022	-4.02
247218_at	asparagine synthetase (gb|AAC72	ASN2	AT5G65010	2.24	1.16	2.62	0.03566395	0.3022	-4.02
253486_at	putative protein KIAA0260 gene, h	---	AT4G31600	-1.23	-0.30	-2.62	0.03563418	0.3022	-4.02
248923_at	putative protein similar to unknown	atnudt11	AT5G45940	1.35	0.43	2.62	0.03566428	0.3022	-4.02
252079_at	MAP kinase ; supported by cDNA	CPuORF44	AT3G51630 /	-1.21	-0.27	-2.62	0.03564087	0.3022	-4.02
254924_at	MAP kinase (ATMPK5) possible in	ATMPK5	AT4G11330	-1.41	-0.50	-2.62	0.03563877	0.3022	-4.02
257325_at	hypothetical protein	---	AT2G07798	-1.65	-0.72	-2.62	0.03570703	0.3023	-4.02

249010_at	unknown protein ; supported by cl	---	AT5G44580	-1.44	-0.52	-2.62	0.03569127	0.3023	-4.02
250369_at	cyclin 3b ; supported by cDNA: gi_	CYC3B	AT5G11300	-1.30	-0.38	-2.62	0.03571135	0.3023	-4.02
246112_at	putative protein predicted proteins	---	AT5G20200	1.28	0.36	2.62	0.03572941	0.3023	-4.02
266664_at	hypothetical protein predicted by g	---	AT2G29800	-1.23	-0.30	-2.62	0.03577787	0.3023	-4.02
251787_at	2-oxoglutarate dehydrogenase, E	---	AT3G55410	-1.28	-0.36	-2.62	0.03578097	0.3023	-4.02
264955_at	F-box protein family, AtFBX3 cont	---	AT1G76920	1.30	0.38	2.62	0.03578651	0.3023	-4.02
250436_at	RNA binding protein - like rna binc	---	AT5G10350	1.25	0.33	2.62	0.03577192	0.3023	-4.02
256743_at	Expressed protein ; supported by f	---	AT3G29370	1.81	0.85	2.62	0.03584478	0.3026	-4.02
261632_at	hypothetical protein predicted by g	---	AT1G50120	1.27	0.34	2.62	0.03583957	0.3026	-4.02
253005_at	hypothetical protein ;supported by	---	AT4G38100	1.39	0.48	2.61	0.03591843	0.3027	-4.02
250279_at	ABA-responsive protein - like ABA	---	AT5G13200	-1.41	-0.50	-2.61	0.0359593	0.3027	-4.03
252297_at	cytosolic ribosomal protein S11 ;s	EMB1080	AT3G48930	1.50	0.59	2.61	0.03596684	0.3027	-4.03
267265_at	putative serine carboxypeptidase I	SCPL13	AT2G22980	-1.37	-0.45	-2.61	0.03595282	0.3027	-4.03
262471_at	hypothetical protein similar to hypc	---	AT1G50140	-1.28	-0.36	-2.61	0.035932	0.3027	-4.02
255588_at	hypothetical protein	---	AT4G01570	-1.36	-0.44	-2.61	0.03596585	0.3027	-4.03
256217_at	hypothetical protein predicted by g	---	AT1G56320	1.51	0.59	2.62	0.03588089	0.3027	-4.02
250516_at	putative protein predicted proteins	---	AT5G09620	-1.23	-0.30	-2.61	0.03592642	0.3027	-4.02
255906_at	hypothetical protein similar to RING	---	AT1G17790	-1.23	-0.30	-2.61	0.03599891	0.3029	-4.03
257199_at	Tic22, putative similar to Tic22 GB	---	AT3G23710	1.27	0.35	2.61	0.03604429	0.3032	-4.03
245544_at	UTP-glucose glucosyltransferase I	---	AT4G15270	-1.26	-0.34	-2.61	0.03606316	0.3032	-4.03
252129_at	putative protein hypothetical prote	AtHB28	AT3G50890	-1.26	-0.33	-2.61	0.03609722	0.3033	-4.03
253582_at	Expressed protein ;supported by c	---	AT4G30670	1.36	0.44	2.61	0.03610476	0.3033	-4.03
259421_at	disease resistance protein, putativ	---	AT1G13910	-1.29	-0.37	-2.61	0.03613059	0.3034	-4.03
250838_at	cytochrome P450 - like protein cyt	CYP77A9	AT5G04630	-1.18	-0.24	-2.61	0.03613377	0.3034	-4.03
257333_at	cytochrome c oxidase subunit 1	---	---	-1.52	-0.60	-2.61	0.03618849	0.3036	-4.03
260624_at	high-affinity nitrate transporter AC	NRT2.2	AT1G08100	-1.35	-0.44	-2.61	0.03618424	0.3036	-4.03
267585_s_at	putative actin	ACT9	AT2G42090	-1.21	-0.28	-2.61	0.03622037	0.3037	-4.03
251803_at	putative protein predicted proteins	---	AT3G55350	-1.31	-0.39	-2.61	0.03639568	0.3040	-4.04
263637_at	hypothetical protein predicted by g	---	AT2G11890	1.21	0.27	2.61	0.03633237	0.3040	-4.04
255451_at	putative protein similar to T5J8.17	---	AT4G02860	1.28	0.35	2.61	0.03629875	0.3040	-4.03
248217_at	cytochrome b5 (dbj|BAA74839.1)	CB5-E	AT5G53560	1.29	0.36	2.61	0.0363097	0.3040	-4.04
263138_at	hypothetical protein predicted by g	---	AT1G65090	-1.19	-0.25	-2.61	0.03631362	0.3040	-4.04
264854_at	putative RING zinc finger protein ;	RHA3A	AT2G17450	1.27	0.34	2.61	0.03627351	0.3040	-4.03
255203_at	hypothetical protein	---	---	-1.31	-0.40	-2.61	0.03633178	0.3040	-4.04
255498_at	putative vacuolar ATPase similar t	---	AT4G02620	1.17	0.22	2.61	0.03635275	0.3040	-4.04

249514_at	14-3-3 protein GF14psi (grf3/RCI1	GRF3	AT5G38480	1.26	0.33	2.61	0.03638334	0.3040	-4.04
262582_at	hypothetical protein Is a member o	---	AT1G15410	1.78	0.83	2.61	0.03638252	0.3040	-4.04
258962_at	putative cytochrome P450 similar t	CYP77A6	AT3G10570	2.95	1.56	2.61	0.03637615	0.3040	-4.04
254564_at	neoxanthin cleavage enzyme-like	NCED4	AT4G19170	-1.42	-0.51	-2.60	0.03641592	0.3040	-4.04
259566_at	hypothetical protein	---	AT1G20520	-1.19	-0.25	-2.60	0.03646761	0.3044	-4.04
266487_at	hypothetical protein predicted by g	---	AT2G47660	-1.17	-0.23	-2.60	0.03651816	0.3047	-4.04
254445_at	3-hydroxyisobutyrate dehydrogena	---	AT4G20930	1.24	0.31	2.60	0.03656396	0.3047	-4.04
264689_at	hypothetical protein predicted by g	---	AT1G09900	1.35	0.44	2.60	0.03657185	0.3047	-4.04
255488_at	putative serine/threonine protein ki	---	AT4G02630	-1.31	-0.39	-2.60	0.03657112	0.3047	-4.04
263626_at	transcription factor ZAP1 identical	ZAP1	AT2G04880	-1.19	-0.25	-2.60	0.03656211	0.3047	-4.04
245342_at	ribosomal protein ;supported by ful	---	AT4G16720	1.36	0.44	2.60	0.03659841	0.3048	-4.04
263761_at	putative fructose bisphosphate ald	---	AT2G21330	-1.33	-0.41	-2.60	0.03664693	0.3049	-4.04
253778_at	heat-shock protein heat-shock pro	---	AT4G28480	-1.28	-0.36	-2.60	0.03665346	0.3049	-4.04
260943_at	thioredoxin, putative similar to thio	ATTRX5	AT1G45145	-1.36	-0.45	-2.60	0.03665623	0.3049	-4.04
262963_at	dihydrolipoamide S-acetyltransfera	---	AT1G54220	-1.20	-0.26	-2.60	0.03673847	0.3055	-4.05
260513_at	cyanogenic beta-glucosidase, puta	BGLU36	AT1G51490	-1.22	-0.29	-2.60	0.03677007	0.3057	-4.05
254147_at	putative protein similarity Human r	---	AT4G24270	1.40	0.48	2.60	0.03682043	0.3060	-4.05
246745_at	60S ribosomal protein L22 - like ri	---	AT5G27770	1.45	0.53	2.60	0.03683381	0.3060	-4.05
247232_at	ABC transporter-like	ATH13	AT5G64940	-1.31	-0.39	-2.60	0.03685756	0.3061	-4.05
250464_at	hypothetical protein	---	AT5G10040	-1.17	-0.23	-2.60	0.03687235	0.3061	-4.05
250545_at	serine/threonine protein kinase ;su	ATPK3	AT5G08160	-1.20	-0.27	-2.59	0.03700941	0.3061	-4.05
267596_s_at	putative leucine-rich repeat diseas	AtRLP26	AT2G33050 /	1.71	0.77	2.60	0.03689557	0.3061	-4.05
264670_s_at	unknown protein Similar to elonga	---	AT1G09640 /	1.28	0.36	2.60	0.03691417	0.3061	-4.05
248717_at	Expressed protein ; supported by f	---	AT5G48175	-1.18	-0.24	-2.59	0.03699191	0.3061	-4.05
252234_at	putative protein ; supported by full	ATPSK4	AT3G49780	2.26	1.18	2.59	0.0369391	0.3061	-4.05
250932_s_at	putative protein MED7, Homo sap	---	AT5G03220 /	1.21	0.28	2.59	0.03696996	0.3061	-4.05
265338_at	putative ribosomal protein L6 ; sup	---	AT2G18400	1.23	0.30	2.59	0.03699278	0.3061	-4.05
245439_at	hypothetical protein	---	AT4G16670	1.54	0.62	2.60	0.03692501	0.3061	-4.05
256380_at	pheromone receptor, putative (AR	AR401	AT1G66680	1.28	0.35	2.59	0.03698005	0.3061	-4.05
245254_at	ATP-sulfurylase ; supported by cD	APS3	AT4G14680	-2.30	-1.20	-2.59	0.03701436	0.3061	-4.05
251285_at	putative protein several hypothetic	---	AT3G61770	1.23	0.30	2.59	0.03710915	0.3066	-4.06
258853_at	unknown protein similar to GB:AAD	---	AT3G06440	1.22	0.29	2.59	0.0371143	0.3066	-4.06
245784_at	hypothetical protein similar to hypo	---	AT1G32190	1.25	0.32	2.59	0.03708867	0.3066	-4.06
246161_at	putative protein predicted proteins	JAZ12	AT5G20900	-1.34	-0.42	-2.59	0.03718391	0.3071	-4.06
254261_at	beta adaptin - like protein beta-ad	---	AT4G23460	1.20	0.27	2.59	0.03720967	0.3072	-4.06

252426_at	putative protein proline transport h	---	AT3G47630	1.27	0.35	2.59	0.03722478	0.3072	-4.06
266489_at	unknown protein ; supported by cI	NPSN11	AT2G35190	1.42	0.50	2.59	0.03733596	0.3076	-4.06
252927_at	cysteine proteinase RD19A identi	RD19	AT4G39090	1.20	0.26	2.59	0.03729716	0.3076	-4.06
249601_at	quinone oxidoreductase -like prote	---	AT5G37980	-1.31	-0.39	-2.59	0.03732934	0.3076	-4.06
258983_at	putative aminotransferase similar	---	AT3G08860	1.93	0.95	2.59	0.03732899	0.3076	-4.06
248511_at	Expressed protein ; supported by c	CPI1	AT5G50375	1.43	0.52	2.59	0.03730145	0.3076	-4.06
255799_at	Deetiolated1 (DET1) light signal tra	DET1	AT4G10180	1.25	0.32	2.59	0.03740479	0.3078	-4.07
263685_at	unknown protein similar to cell diffe	ATCUL3	AT1G26830	1.18	0.24	2.59	0.03740152	0.3078	-4.07
259372_at	homeotic protein boi1AP1, putativ	AP1	AT1G69120	-1.23	-0.30	-2.59	0.03744602	0.3078	-4.07
248852_at	unknown protein	---	AT5G46560	-1.18	-0.23	-2.59	0.03746466	0.3078	-4.07
258950_at	unknown protein contains Pfam pr	MBD9	AT3G01460	-1.17	-0.22	-2.59	0.03742549	0.3078	-4.07
247381_at	auxin-independent growth promote	---	AT5G63390	-1.24	-0.31	-2.59	0.03745063	0.3078	-4.07
250487_at	putative protein MRS2 protein, Sa	---	AT5G09690	1.30	0.38	2.59	0.03745431	0.3078	-4.07
264824_at	unknown protein similar to gb|T45	2A6	---	1.40	0.49	2.58	0.03750935	0.3080	-4.07
262163_at	ribosomal protein L30, putative sir	---	AT1G77940	1.60	0.68	2.58	0.03751584	0.3080	-4.07
245029_at	hypothetical protein predicted by g	YAB5	AT2G26580	1.64	0.71	2.58	0.03756318	0.3083	-4.07
262832_s_at	unknown protein	---	AT1G14870	6.15	2.62	2.58	0.03764409	0.3088	-4.07
256601_s_at	At14a-1 protein identical to At14a	AT14A	AT3G28290	-1.21	-0.28	-2.58	0.03764139	0.3088	-4.07
249798_at	putative protein contains similarity	---	AT5G23730	-1.20	-0.27	-2.58	0.03767949	0.3089	-4.07
246623_at	nuM1 protein, putative similar to n	ATNUC-L1	AT1G48920	1.32	0.40	2.58	0.03769749	0.3090	-4.07
255261_s_at	putative protein equilibrative nucle	FUR1	AT4G05110	-1.78	-0.83	-2.58	0.03773728	0.3090	-4.07
257677_at	unknown protein contains Pfam pr	ATEHD1	AT3G20290	-1.25	-0.33	-2.58	0.03772552	0.3090	-4.07
266277_at	putative tropinone reductase	---	AT2G29310	-1.25	-0.33	-2.58	0.0377243	0.3090	-4.07
245749_at	proline-rich protein, putative simila	---	AT1G51090	-1.88	-0.91	-2.58	0.03776625	0.3090	-4.07
265837_at	unknown protein	LURP1	AT2G14560	4.64	2.21	2.58	0.03776306	0.3090	-4.07
265987_at	unknown protein	---	AT2G24240	1.38	0.47	2.58	0.03779171	0.3091	-4.08
260634_at	initiation factor isozyme 4F p82 su	---	AT1G62410	1.23	0.30	2.58	0.03782958	0.3092	-4.08
264060_at	hypothetical protein predicted by g	---	AT2G27980	1.20	0.26	2.58	0.03781717	0.3092	-4.08
264529_at	CTP synthase-like protein similar	---	AT1G30820	1.61	0.68	2.58	0.03784154	0.3092	-4.08
251144_at	anthranilate N-benzoyltransferase	---	AT5G01210	-1.51	-0.59	-2.58	0.03789026	0.3094	-4.08
262291_at	zinc finger and C2 domain protein	---	AT1G70790	-1.21	-0.27	-2.57	0.03804015	0.3095	-4.08
248378_at	unknown protein ;supported by ful	---	AT5G51840	-1.21	-0.27	-2.57	0.03812669	0.3095	-4.08
265425_at	hypothetical protein	GCL2	AT2G20770	-1.29	-0.37	-2.57	0.03804795	0.3095	-4.08
260545_at	putative glutathione peroxidase ;s	ATGPX3	AT2G43350	1.24	0.32	2.57	0.03806079	0.3095	-4.08
259768_at	expressed protein supported by cI	COR314-TI	AT1G29390	-1.17	-0.23	-2.57	0.03812919	0.3095	-4.08

256094_at	hypothetical protein predicted by g	SAUL1	AT1G20780	-1.23	-0.30	-2.57	0.03802678	0.3095	-4.08
246815_at	putative protein integrin analogue,	---	AT5G27220	-1.19	-0.26	-2.58	0.03796766	0.3095	-4.08
246548_at	putative protein ;supported by full-	---	AT5G14910	1.25	0.32	2.57	0.03813705	0.3095	-4.08
263268_at	unknown protein	---	---	-1.23	-0.30	-2.57	0.03812451	0.3095	-4.08
258334_at	hypothetical protein predicted by g	---	AT3G16010	-1.23	-0.30	-2.57	0.03811562	0.3095	-4.08
264410_s_at	hypothetical protein predicted by g	---	---	1.18	0.24	2.58	0.0379873	0.3095	-4.08
261764_at	receptor lectin kinase, putative sin	---	AT1G15530	-1.26	-0.33	-2.58	0.03791934	0.3095	-4.08
248462_at	nucleotide-binding protein ; suppo	NBP35	AT5G50960	-1.27	-0.34	-2.57	0.03813796	0.3095	-4.08
246237_at	putative protein	---	AT4G36390	1.26	0.34	2.57	0.0381434	0.3095	-4.08
248256_at	developmental protein SINA (seve	---	AT5G53360	-1.25	-0.32	-2.58	0.03797419	0.3095	-4.08
247858_at	similar to unknown protein (pir||T3	TTL	AT5G58220	1.26	0.33	2.58	0.0379793	0.3095	-4.08
249912_at	putative protein similar to unknowr	RER1	AT5G22790	-1.58	-0.66	-2.57	0.03813974	0.3095	-4.08
258360_at	hypothetical protein predicted by g	---	AT3G14250	-1.22	-0.29	-2.57	0.03807094	0.3095	-4.08
248984_at	DNA-directed RNA polymerase su	NRPC2	AT5G45140	1.30	0.38	2.57	0.03828296	0.3101	-4.09
263674_at	hypothetical protein predicted by g	---	AT2G04790	1.25	0.32	2.57	0.03823113	0.3101	-4.09
246378_at	integral membrane protein, putativ	---	AT1G57620	1.20	0.26	2.57	0.03828301	0.3101	-4.09
265767_at	putative exonuclease contains zinc	REF4	AT2G48110	-1.26	-0.33	-2.57	0.03826628	0.3101	-4.09
248328_at	putative protein contains similarity	---	AT5G52660	-1.19	-0.25	-2.57	0.03824361	0.3101	-4.09
260284_at	unknown protein ; supported by fu	---	AT1G80380	1.20	0.27	2.57	0.03830087	0.3101	-4.09
259300_at	hypothetical protein predicted by g	---	AT3G05100	1.22	0.29	2.57	0.03835311	0.3103	-4.09
249591_at	putative protein predicted protein,	---	---	-1.19	-0.25	-2.57	0.03836102	0.3103	-4.09
255032_at	putative protein anthocyanin rham	---	AT4G09500	-1.31	-0.39	-2.57	0.03834743	0.3103	-4.09
246033_at	hydroxymethylbilane synthase ;su	HEMC	AT5G08280	1.33	0.41	2.57	0.03839188	0.3104	-4.09
258614_at	putative S-adenosylmethionine:2-d	---	AT3G02770	1.42	0.51	2.57	0.0383961	0.3104	-4.09
265963_s_at	40S ribosomal protein S5 identical	ATRPS5B	AT2G37270	1.50	0.59	2.57	0.03841306	0.3104	-4.09
249972_at	tRNA isopentenyltransferase -like	IPT5	AT5G19040	-1.23	-0.29	-2.57	0.03846809	0.3107	-4.09
261205_at	hypothetical protein predicted by g	---	AT1G12790	1.40	0.49	2.57	0.0385251	0.3111	-4.10
252925_at	ES43 like protein ES43 protein - b	SHL1	AT4G39100	1.30	0.37	2.57	0.03853982	0.3111	-4.10
261020_at	hypothetical protein similar to retic	---	AT1G26390	1.77	0.82	2.56	0.03858426	0.3111	-4.10
263483_at	putative heat shock protein ; supp	CR88	AT2G04030	1.24	0.31	2.56	0.03859703	0.3111	-4.10
262523_at	ubiquitin-specific protease 15 (UB	UBP15	AT1G17110	-1.18	-0.24	-2.56	0.03859572	0.3111	-4.10
265894_at	putative lipid transfer protein	LTP	AT2G15050	-1.76	-0.82	-2.56	0.03856388	0.3111	-4.10
245290_at	hypothetical protein ; supported by	---	AT4G16490	-1.34	-0.42	-2.56	0.03862414	0.3112	-4.10
258670_at	unknown protein	---	AT3G08810	-1.28	-0.36	-2.56	0.03868201	0.3116	-4.10
245941_at	putative protein karyopherin beta 3	emb2734	AT5G19820	-1.26	-0.33	-2.56	0.03872837	0.3117	-4.10

264482_at	sugar carrier protein, putative simi	---	AT1G77210	-1.65	-0.72	-2.56	0.03872856	0.3117	-4.10
265918_at	putative fatty acid elongase	KCS8	AT2G15090	-2.22	-1.15	-2.56	0.03873801	0.3117	-4.10
247375_at	Expressed protein ; supported by f	---	AT5G63135	1.17	0.23	2.56	0.03878718	0.3119	-4.10
260195_at	hypothetical protein predicted by g	---	AT1G67540	-1.23	-0.30	-2.56	0.03879238	0.3119	-4.10
266799_at	unknown protein	ATPSK2	AT2G22860	-1.49	-0.58	-2.56	0.03881236	0.3119	-4.10
265243_at	hypothetical protein predicted by g	NPG1	AT2G43040	1.24	0.31	2.56	0.03882224	0.3119	-4.10
265417_at	unknown protein	---	AT2G20920	1.42	0.51	2.56	0.0389486	0.3120	-4.11
260580_at	unknown protein	---	AT2G47390	-1.18	-0.24	-2.56	0.03895565	0.3120	-4.11
258797_at	auxin-induced protein identical to (	IAA16	AT3G04730	-1.34	-0.43	-2.56	0.03893357	0.3120	-4.11
253559_at	1,3-beta-glucanase - like protein 1	---	AT4G31140	1.21	0.28	2.56	0.03890378	0.3120	-4.10
258906_at	unknown protein similar to C-term	ATTLP9	AT3G06380	1.27	0.34	2.56	0.03896407	0.3120	-4.11
258388_at	putative expansin S2 precursor sin	ATEXPA12	AT3G15370	-1.19	-0.25	-2.56	0.03888006	0.3120	-4.10
261731_s_at	hypothetical protein similar to hypo	---	AT1G47780	-1.18	-0.24	-2.56	0.03898341	0.3120	-4.11
248175_at	histone H2A (gb|AAF64418.1) ; su	RAT5	AT5G54640	1.24	0.32	2.56	0.0389503	0.3120	-4.11
255031_at	putative proteins various hypotheti	---	AT4G09490	1.30	0.38	2.56	0.03898057	0.3120	-4.11
262286_at	Expressed protein ; supported by f	---	AT1G68585	1.53	0.62	2.56	0.03889161	0.3120	-4.10
253806_at	putative protein Arabidopsis thalia	---	AT4G28270	1.29	0.37	2.56	0.03888567	0.3120	-4.10
246601_at	copper amine oxidase, putative si	---	AT1G31710	-4.14	-2.05	-2.56	0.03903293	0.3123	-4.11
244901_at	hypothetical protein	---	ATMG00640	-1.26	-0.33	-2.56	0.03908746	0.3125	-4.11
255519_at	hypothetical protein	---	AT4G02310	-1.18	-0.24	-2.56	0.03908422	0.3125	-4.11
247248_at	putative protein contains similarity	---	AT5G64560	-1.44	-0.52	-2.55	0.03922482	0.3130	-4.11
248807_at	pectin methylesterase-like	---	AT5G47500	-1.16	-0.22	-2.55	0.03920566	0.3130	-4.11
247977_at	putative protein similar to unknown	---	AT5G56850	-1.33	-0.41	-2.55	0.03921143	0.3130	-4.11
245880_at	putative hydrolase EtbD1 - Rhodo	---	AT5G09430	-1.30	-0.38	-2.55	0.03925364	0.3130	-4.11
251752_at	proline transporter 2	PROT2	AT3G55740	-1.39	-0.47	-2.55	0.03921839	0.3130	-4.11
245146_at	putative cis-Golgi SNARE protein	GOS12	AT2G45200	1.25	0.32	2.55	0.03925451	0.3130	-4.11
262331_at	unknown protein	---	AT1G64050	-1.17	-0.23	-2.55	0.03925269	0.3130	-4.11
264789_at	putative glycine-rich, zinc-finger D	---	AT2G17870	-1.18	-0.24	-2.55	0.03916205	0.3130	-4.11
257905_at	unknown protein	---	---	-1.26	-0.33	-2.55	0.03930519	0.3133	-4.12
244940_at	ribosomal protein S12 (trans-splice	---	---	-1.28	-0.36	-2.55	0.03936244	0.3135	-4.12
259568_at	hypothetical protein	---	AT1G20490	-1.20	-0.27	-2.55	0.03935876	0.3135	-4.12
246457_at	WD40-repeat protein transducin h	TOZ	AT5G16750	1.24	0.31	2.55	0.03937688	0.3135	-4.12
256821_at	hypothetical protein predicted by g	---	AT3G22180	-1.36	-0.45	-2.55	0.03940432	0.3136	-4.12
255121_at	putative mitogen-activated protein	MAPKKK9	AT4G08480	-1.37	-0.45	-2.55	0.03945819	0.3139	-4.12
253773_s_at	Expressed protein ; supported by f	---	AT1G52370	1.27	0.35	2.55	0.03950811	0.3142	-4.12

262137_at	transcription factor, putative simila	---	AT1G77920	1.22	0.28	2.55	0.03955364	0.3143	-4.12
251028_at	putative protein putative hydrolase	---	AT5G02230	-1.27	-0.34	-2.55	0.03957558	0.3143	-4.12
256705_at	cytochrome P450, putative similar	CYP702A8	AT3G30290	-1.27	-0.35	-2.55	0.03953455	0.3143	-4.12
264602_at	putative Ser/Thr protein kinase sim	---	AT1G04700	-1.22	-0.29	-2.55	0.0395644	0.3143	-4.12
250510_at	15.9 kDa subunit of RNA polymera	NRPB4	AT5G09920	1.21	0.27	2.55	0.03962672	0.3144	-4.12
251570_at	putative protein several hypothetic	---	AT3G58300	-1.24	-0.31	-2.55	0.03961517	0.3144	-4.12
265227_s_at	hypothetical protein	---	AT2G07695	-1.28	-0.35	-2.55	0.03962351	0.3144	-4.12
257599_at	60S ribosomal protein, putative si	---	AT3G24830	1.56	0.64	2.55	0.03963775	0.3144	-4.12
249108_at	steroid sulfotransferase-like	---	AT5G43690	-1.17	-0.22	-2.54	0.0396872	0.3147	-4.13
265538_at	unknown protein predicted by gens	---	AT2G15860	1.32	0.40	2.54	0.03971449	0.3148	-4.13
250150_at	putative protein ;supported by full-l	---	AT5G14710	-1.35	-0.43	-2.54	0.03972677	0.3148	-4.13
258954_at	unknown protein contains Pfam pr	---	AT3G01400	-1.17	-0.23	-2.54	0.03976386	0.3149	-4.13
265444_s_at	aquaporin (plasma membrane intri	RD28	AT2G37170	-1.51	-0.59	-2.54	0.03980281	0.3150	-4.13
262667_at	amine oxidase, putative similar to	---	AT1G62810	1.37	0.46	2.54	0.03979824	0.3150	-4.13
249113_at	putative protein similar to unknown	---	AT5G43790	-1.32	-0.40	-2.54	0.03980916	0.3150	-4.13
251490_at	putative protein	---	AT3G59490	1.30	0.38	2.54	0.03982189	0.3150	-4.13
253520_at	hypothetical protein ;supported by	---	AT4G31410	1.19	0.25	2.54	0.03985949	0.3150	-4.13
260103_at	unknown protein	---	AT1G35430	1.22	0.28	2.54	0.03985303	0.3150	-4.13
256071_at	ubiquitin, putative similar to ubiqui	---	AT1G13640	1.37	0.45	2.54	0.03995887	0.3157	-4.13
254197_at	trehalase - like protein trehalase 1	TRE1	AT4G24040	-1.36	-0.45	-2.54	0.03997413	0.3157	-4.13
265469_at	unknown protein predicted by gens	---	AT2G37160	-1.18	-0.24	-2.54	0.03999551	0.3158	-4.13
260511_at	anthranilate phosphoribosyltransfe	---	AT1G51570	1.33	0.41	2.54	0.04002808	0.3159	-4.13
267116_at	unknown protein	---	AT2G32560	-1.48	-0.57	-2.54	0.04009092	0.3161	-4.14
249607_at	putative protein RING-H2 finger pr	---	AT5G37280	-1.20	-0.27	-2.54	0.04009604	0.3161	-4.14
252830_at	putative protein 70K peroxisomal r	PXA1	AT4G39850	-1.18	-0.24	-2.54	0.04008548	0.3161	-4.14
255127_at	nodulin-like protein nodulin gene M	---	AT4G08300	2.07	1.05	2.54	0.04018317	0.3165	-4.14
250826_at	unknown protein ; supported by cD	---	AT5G05220	-1.24	-0.31	-2.53	0.04024706	0.3165	-4.14
246924_at	putative protein KIAA0332 - Homo	---	AT5G25060	1.18	0.24	2.54	0.04019351	0.3165	-4.14
255989_at	putative protein	---	AT5G35069	-1.28	-0.35	-2.54	0.04020766	0.3165	-4.14
254683_at	hypothetical protein ;supported by	---	AT4G13800	-1.24	-0.31	-2.54	0.04021331	0.3165	-4.14
260518_at	cinnamyl alcohol dehydrogenase,	---	AT1G51410	-1.19	-0.25	-2.54	0.04021988	0.3165	-4.14
266068_at	putative geranylgeranyl pyrophosp	GGPS4	AT2G18640	-1.27	-0.34	-2.53	0.04026064	0.3165	-4.14
260965_s_at	hypothetical protein predicted by g	---	---	-1.18	-0.24	-2.54	0.04020831	0.3165	-4.14
264252_at	putative GTP-binding protein, SAR	ATSARA1A	AT1G09180	-1.22	-0.29	-2.53	0.04025662	0.3165	-4.14
263200_at	hypothetical protein predicted by g	---	AT1G05600	1.31	0.39	2.53	0.04028196	0.3165	-4.14

262117_at	ribosomal protein L19, putative sir	emb2386	AT1G02780	1.29	0.37	2.53	0.04029077	0.3165	-4.14
260053_at	hypothetical protein similar to unkr	---	AT1G78120	-1.29	-0.37	-2.53	0.04030253	0.3165	-4.14
246046_at	putative protein predicted proteins	---	---	1.24	0.31	2.53	0.04035793	0.3168	-4.14
255481_at	T14P8.6 ; supported by cDNA: gi_	PMS1	AT4G02460	1.30	0.38	2.53	0.04039277	0.3169	-4.14
245921_at	putative protein predicted protein,	---	AT5G28800	-1.18	-0.24	-2.53	0.04042088	0.3171	-4.14
247836_at	putative protein similar to unknowr	---	AT5G57860	1.26	0.33	2.53	0.04066068	0.3174	-4.15
251025_at	putative protein CND41, chloropla	PCS1	AT5G02190	-1.30	-0.38	-2.53	0.04061148	0.3174	-4.15
258215_at	phosphoprotein phosphatase, put	atToc64-III	AT3G17970	1.35	0.43	2.53	0.04077178	0.3174	-4.15
261012_at	CLE9, putative CLAVATA3/ESR-F	CLE9	AT1G26600	-1.17	-0.22	-2.53	0.04074176	0.3174	-4.15
266535_s_at	50S ribosomal protein L27 ;suppo	---	AT2G16930 /	1.30	0.38	2.53	0.0407898	0.3174	-4.15
257226_at	hypothetical protein predicted by g	---	AT3G27880	1.71	0.77	2.53	0.04056491	0.3174	-4.15
257954_at	putative UDP-glucose glucosyltran	---	AT3G21760	-1.26	-0.33	-2.53	0.04068002	0.3174	-4.15
251229_at	beta-glucosidase-like protein sever	BGLU7	AT3G62740	-1.19	-0.25	-2.53	0.04069667	0.3174	-4.15
260461_at	membrane protein PTM1 precurso	---	AT1G10980	-1.24	-0.31	-2.53	0.04056377	0.3174	-4.15
245778_at	RNA-binding glycine-rich protein,	---	AT1G73530	1.34	0.42	2.53	0.04080644	0.3174	-4.15
245138_at	unknown protein predicted by gens	AFO	AT2G45190	1.40	0.49	2.53	0.0407004	0.3174	-4.15
266909_at	hypothetical protein predicted by g	BRM	AT2G46020	-1.28	-0.35	-2.53	0.04078422	0.3174	-4.15
262328_at	hypothetical protein similar to hypo	---	AT1G64100	-1.17	-0.22	-2.53	0.04059048	0.3174	-4.15
261471_at	hypothetical protein contains simila	---	AT1G14460	1.40	0.49	2.53	0.04062736	0.3174	-4.15
258006_at	cysteine proteinase non-consensu	---	AT3G19400	1.32	0.40	2.53	0.04053339	0.3174	-4.15
261955_at	proteasome regulatory subunit, pu	RPN12a	AT1G64520	1.19	0.25	2.53	0.04048203	0.3174	-4.15
252601_s_at	40S ribsomomal protein 40S ribso	---	AT3G45030 /	1.46	0.55	2.53	0.04082402	0.3174	-4.15
254337_at	putative protein hypothetical prote	---	AT4G22060	-1.23	-0.30	-2.53	0.04076631	0.3174	-4.15
248004_at	putative protein similar to unknowr	PRA1.G2	AT5G56230	1.51	0.59	2.53	0.04067865	0.3174	-4.15
247937_at	Ca2+-transporting ATPase-like pro	ACA8	AT5G57110	-1.46	-0.55	-2.53	0.04055877	0.3174	-4.15
247692_s_at	histone H4 - like protein histone H	---	AT5G59690 /	1.50	0.59	2.53	0.04066199	0.3174	-4.15
254386_at	peroxidase prxr1 ;supported by fu	PRXR1	AT4G21960	-1.49	-0.58	-2.53	0.04070149	0.3174	-4.15
251112_s_at	pyruvate decarboxylase-like prote	PDC3	AT5G01320 /	-1.33	-0.41	-2.53	0.0405434	0.3174	-4.15
262090_at	CREB-binding protein, putative sir	HAC4	AT1G55970	-1.22	-0.29	-2.53	0.0408119	0.3174	-4.15
265912_at	hypothetical protein predicted by g	---	AT2G25565 /	-1.22	-0.29	-2.53	0.04072038	0.3174	-4.15
249861_at	Expressed protein ; supported by f	---	AT5G22875	1.25	0.33	2.53	0.04082005	0.3174	-4.15
266065_at	phytochrome B Identical to GB:X1	PHYB	AT2G18790	-1.26	-0.34	-2.52	0.04089418	0.3177	-4.16
247917_at	putative protein similar to unknowr	BIO1	AT5G57590	-1.20	-0.26	-2.52	0.04090301	0.3177	-4.16
265420_s_at	hypothetical protein predicted by g	BRX	AT1G31880 /	1.32	0.40	2.52	0.04088781	0.3177	-4.16
253944_at	SNF8 like protein SNF8 protein - y	VPS22	AT4G27040	1.23	0.30	2.52	0.04091788	0.3177	-4.16

258423_at	hypothetical protein predicted by g	---	AT3G16730	1.19	0.25	2.52	0.04097154	0.3178	-4.16
254807_at	putative protein	---	AT4G12700	1.32	0.40	2.52	0.04097222	0.3178	-4.16
262319_s_at	unknown protein similar to unknow	---	AT1G27540 /	1.42	0.50	2.52	0.04097583	0.3178	-4.16
260007_at	unknown protein contains non-con	---	AT1G67870	-1.49	-0.58	-2.52	0.04101243	0.3179	-4.16
259315_at	unknown protein	AtRP2	AT3G01200	-1.18	-0.24	-2.52	0.04100052	0.3179	-4.16
263811_at	putative acyl-CoA synthetase ; sup	---	AT2G04350	-1.24	-0.31	-2.52	0.04104025	0.3180	-4.16
251240_at	putative protein	---	AT3G62450	1.20	0.26	2.52	0.04115863	0.3183	-4.16
262154_at	unknown protein contains similarity	---	AT1G52700	-1.37	-0.46	-2.52	0.041162	0.3183	-4.16
251186_at	putative protein unknown protein /	---	AT3G62790	1.17	0.23	2.52	0.04124239	0.3183	-4.16
254721_at	hypothetical protein ;supported by	SMAP1	AT4G13520	1.23	0.30	2.52	0.04120445	0.3183	-4.16
257374_at	hypothetical protein predicted by g	---	AT2G43280	1.32	0.41	2.52	0.04117751	0.3183	-4.16
261052_at	hypothetical protein similar to hypo	---	AT1G01440	1.29	0.37	2.52	0.04111691	0.3183	-4.16
245985_at	peptidylprolyl isomerase-like prote	---	AT5G13120	1.29	0.37	2.52	0.04121557	0.3183	-4.16
244978_at	RNA polymerase alpha subunit	---	---	1.20	0.27	2.52	0.0412353	0.3183	-4.16
252765_at	putative protein hypothetical protei	---	AT3G42800	-1.46	-0.54	-2.52	0.04120586	0.3183	-4.16
256970_at	ABC transporter, putative similar t	---	AT3G21090	-1.24	-0.31	-2.52	0.04126215	0.3183	-4.16
266710_at	putative Ser/Thr protein kinase	---	AT2G46850	-1.22	-0.29	-2.52	0.04125206	0.3183	-4.16
256759_at	hypothetical protein predicted by g	---	AT3G25640	-1.31	-0.38	-2.52	0.04116281	0.3183	-4.16
254424_at	hypothetical protein ;supported by	---	AT4G21510	1.42	0.51	2.52	0.04112327	0.3183	-4.16
251987_at	CYTOCHROME P450 71B5 ; sup	CYP71B5	AT3G53280	1.26	0.34	2.52	0.04134597	0.3183	-4.17
256249_at	26S proteasome regulatory subun	MEE34	AT3G11270	1.23	0.30	2.52	0.04133908	0.3183	-4.17
245593_at	IAA7 like protein	IAA14	AT4G14550	-1.68	-0.75	-2.52	0.0413054	0.3183	-4.17
255275_at	putative protein various ubiquitin-li	---	AT4G05310	-1.16	-0.22	-2.52	0.04134896	0.3183	-4.17
247110_at	putative protein contains similarity	---	AT5G65830	1.32	0.41	2.52	0.04133262	0.3183	-4.17
256425_at	disease resistance protein, putativ	ADR1	AT1G33560	1.33	0.41	2.52	0.04127963	0.3183	-4.16
258233_at	hypothetical protein contains simila	MYB118	AT3G27785	-1.23	-0.30	-2.52	0.04137067	0.3184	-4.17
253947_at	putative protein hypothetical prote	MAP65-2	AT4G26760	1.26	0.33	2.52	0.04138584	0.3184	-4.17
253814_at	putative protein ;supported by full-	---	AT4G28290	-1.37	-0.45	-2.51	0.04144395	0.3187	-4.17
258049_at	hypothetical protein similar to CGI-	---	AT3G16220	1.19	0.25	2.51	0.04153794	0.3193	-4.17
260665_at	unknown protein ;supported by full	---	AT1G19360	1.24	0.31	2.51	0.04163776	0.3197	-4.17
248243_at	unknown protein	CPuORF50	AT5G53588 /	-1.18	-0.24	-2.51	0.04163569	0.3197	-4.17
246166_at	putative protein	---	---	-1.23	-0.29	-2.51	0.04159676	0.3197	-4.17
255867_at	hypothetical protein predicted by g	---	AT2G30370	-1.20	-0.27	-2.51	0.04161373	0.3197	-4.17
247572_at	putative protein ; supported by full	---	AT5G61220	1.20	0.26	2.51	0.04167688	0.3199	-4.17
261604_at	unknown protein contains similarity	---	AT1G49590	1.26	0.33	2.51	0.04169052	0.3199	-4.17

257189_at	hypothetical protein	GIP1	AT3G13222	-1.19	-0.25	-2.51	0.04171605	0.3199	-4.18
250927_at	lysine decarboxylase - like protein	---	AT5G03270	-1.29	-0.37	-2.51	0.04172469	0.3199	-4.18
256173_at	unknown protein	---	AT1G51730	1.19	0.25	2.51	0.04175333	0.3200	-4.18
257171_at	unknown protein ; supported by fu	---	AT3G23760	1.25	0.32	2.51	0.04184307	0.3202	-4.18
250399_at	putative protein predicted proteins	---	AT5G10750	-1.31	-0.39	-2.51	0.04182341	0.3202	-4.18
265219_at	unknown protein ; supported by fu	---	AT2G02050	1.28	0.35	2.51	0.04183587	0.3202	-4.18
253553_at	putative protein LipB gene, Prochl	---	AT4G31050	1.25	0.32	2.51	0.04184809	0.3202	-4.18
245855_at	sulfate transporter ; supported by	SULTR4;1	AT5G13550	-1.34	-0.42	-2.51	0.04184234	0.3202	-4.18
256587_at	histone-H4-like protein similar to H	---	AT3G28780	-1.24	-0.31	-2.51	0.04187041	0.3203	-4.18
258729_at	putative amino acid transporter pro	ANT1	AT3G11900	-1.19	-0.26	-2.51	0.0418847	0.3203	-4.18
252570_at	isovaleryl-CoA-dehydrogenase pre	IVD	AT3G45300	1.55	0.63	2.51	0.04192212	0.3205	-4.18
253458_at	putative protein predicted protein,	---	AT4G32070	1.39	0.47	2.51	0.04196039	0.3206	-4.18
267061_at	unknown protein ;supported by ful	---	AT2G32480	-1.21	-0.28	-2.51	0.04197333	0.3206	-4.18
257507_at	zinc finger protein, putative similar	---	AT1G29600	1.16	0.22	2.51	0.0419996	0.3207	-4.18
266713_at	unknown protein	---	AT2G46760	-1.22	-0.28	-2.50	0.04206362	0.3211	-4.18
266993_at	nodulin-like protein ; supported by	---	AT2G39210	1.44	0.53	2.50	0.04213377	0.3212	-4.19
265712_s_at	unknown protein	---	AT2G03330	1.22	0.29	2.50	0.04212907	0.3212	-4.19
247312_at	putative protein strong similarity to	---	AT5G63970	-1.28	-0.35	-2.50	0.04212083	0.3212	-4.19
245717_at	Expressed protein ; supported by c	---	AT5G33390	-1.23	-0.30	-2.50	0.04210841	0.3212	-4.18
264561_at	uracil phosphoribosyltransferase,	---	AT1G55810	1.34	0.42	2.50	0.04218042	0.3212	-4.19
265274_at	putative RNA methyltransferase	---	AT2G28450	1.27	0.34	2.50	0.04217276	0.3212	-4.19
250881_at	putative protein	---	AT5G04080	1.34	0.43	2.50	0.04215863	0.3212	-4.19
249101_at	unknown protein	---	AT5G43580	1.75	0.81	2.50	0.04219864	0.3213	-4.19
251518_at	putative protein protein CG15643	---	AT3G59390	1.23	0.30	2.50	0.042246	0.3213	-4.19
250833_at	myotubularin - like protein myotub	---	AT5G04540	-1.21	-0.27	-2.50	0.04227072	0.3213	-4.19
262329_at	hypothetical protein similar to hypo	---	AT1G64090	1.18	0.24	2.50	0.04226433	0.3213	-4.19
246194_at	putative protein ;supported by full-l	ACD2	AT4G37000	-1.31	-0.39	-2.50	0.04222965	0.3213	-4.19
247966_at	putative protein contains similarity	---	AT5G56610	-1.23	-0.29	-2.50	0.04221552	0.3213	-4.19
257274_at	geranylgeranyl pyrophosphate syr	---	AT3G14510	-1.25	-0.32	-2.50	0.04232107	0.3216	-4.19
249209_at	major surface glycoprotein-like ; s	---	AT5G42620	-1.23	-0.30	-2.50	0.04233949	0.3216	-4.19
264457_at	puative glucosyl transferase simila	---	AT1G10400	-1.23	-0.30	-2.50	0.04235628	0.3216	-4.19
252946_at	Expressed protein ; supported by f	---	AT4G39235	1.38	0.46	2.50	0.0425636	0.3217	-4.20
262044_s_at	hypothetical protein predicted by g	---	AT1G80210	1.22	0.29	2.50	0.04250569	0.3217	-4.19
253717_at	putative protein putative suppress	---	AT4G29440	-1.22	-0.28	-2.50	0.04245915	0.3217	-4.19
267093_at	high affinity Ca2+ antiporter identi	CAX1	AT2G38170	1.39	0.47	2.50	0.04259458	0.3217	-4.20

259121_at	unknown protein	---	AT3G02220	1.29	0.37	2.50	0.04244261	0.3217	-4.19
254671_at	MuDR transposable element - like	---	---	-1.21	-0.27	-2.50	0.04257674	0.3217	-4.20
245080_at	putative receptor-like protein kinas	---	AT2G23300	-1.32	-0.40	-2.50	0.04259453	0.3217	-4.20
262258_at	20S proteasome subunit PAE1 ide	PAE1	AT1G53850	1.27	0.34	2.50	0.04254711	0.3217	-4.20
257827_at	unknown protein contains Pfam pr	---	AT3G26630	1.40	0.49	2.50	0.04260192	0.3217	-4.20
250031_at	transfactor-like protein ; supported	MYR1	AT5G18240	-1.33	-0.41	-2.50	0.04241553	0.3217	-4.19
267509_at	MADS-box protein (AGL20) ; supp	AGL20	AT2G45660	1.34	0.42	2.50	0.04251752	0.3217	-4.19
262398_at	hypothetical protein predicted by g	---	AT1G49350	1.18	0.24	2.49	0.04262501	0.3217	-4.20
262856_at	unknown protein contains Pfam pr	---	AT1G14910	1.27	0.35	2.50	0.04259873	0.3217	-4.20
260802_at	exopolygalacturonase, putative si	---	AT1G78400	-1.17	-0.23	-2.49	0.0426201	0.3217	-4.20
254704_at	putative protein predicted protein,	APRR2	AT4G18020	-1.24	-0.31	-2.50	0.0425861	0.3217	-4.20
262181_at	xylosidase, putative similar to xylo	---	AT1G78060	-1.67	-0.74	-2.50	0.04248781	0.3217	-4.19
263060_s_at	hypothetical protein	---	AT2G07679	-1.33	-0.41	-2.50	0.04259	0.3217	-4.20
255302_at	putative protein similar to transcrip	ATMSRB5	AT4G04830	-1.33	-0.41	-2.50	0.04250815	0.3217	-4.19
261023_at	unknown protein similar to unknow	---	AT1G12200	-1.27	-0.34	-2.49	0.04278264	0.3221	-4.20
258120_at	hypothetical protein predicted by g	---	AT3G14730	1.19	0.25	2.49	0.0427041	0.3221	-4.20
260671_at	unknown protein ;supported by full	---	AT1G19310	-1.27	-0.34	-2.49	0.04269491	0.3221	-4.20
262730_at	putative transport protein may be a	ATOCT3	AT1G16390	-1.25	-0.32	-2.49	0.04276137	0.3221	-4.20
267595_at	putative glucanse	AtGH9B8	AT2G32990	-3.87	-1.95	-2.49	0.0427923	0.3221	-4.20
258318_at	unknown protein	---	AT3G22680	1.41	0.50	2.49	0.04274504	0.3221	-4.20
264792_at	hypothetical protein similar to hypo	---	AT1G08620	-1.21	-0.28	-2.49	0.04279815	0.3221	-4.20
249456_at	unknown protein ;supported by ful	---	AT5G39410	1.24	0.31	2.49	0.04279135	0.3221	-4.20
254447_at	berberine bridge enzyme - like pro	---	AT4G20860	-2.04	-1.03	-2.49	0.04277103	0.3221	-4.20
261765_at	cyclin, putative similar to cyclin GI	CYCA2;3	AT1G15570	-1.24	-0.31	-2.49	0.04283484	0.3223	-4.20
251303_at	NAM-like protein no apical meriste	ANAC066	AT3G61910	-1.19	-0.25	-2.49	0.04294353	0.3229	-4.20
262604_at	unknown protein similar to unknov	---	AT1G15060	-1.17	-0.22	-2.49	0.04295602	0.3229	-4.20
255749_at	p68 RNA helicase, putative simila	STRS1	AT1G31970	1.21	0.28	2.49	0.0430802	0.3237	-4.21
252143_at	putative protein centromere protei	---	AT3G51150	-1.21	-0.27	-2.49	0.04308476	0.3237	-4.21
245639_at	unknown protein contains similarity	---	AT1G25260	1.43	0.52	2.49	0.04309371	0.3237	-4.21
260748_at	RING-H2 finger protein RHA3a, p	---	AT1G49210	2.11	1.08	2.49	0.04313494	0.3239	-4.21
254343_at	PRH26 protein ;supported by full-l	אפר-03	AT4G21990	-1.86	-0.90	-2.49	0.0432319	0.3241	-4.21
251278_at	putative protein hypothetical prote	emb1703	AT3G61780	1.26	0.33	2.48	0.04328417	0.3241	-4.21
249864_at	putative protein similar to unknown	ATMGT10	AT5G22830	-1.18	-0.24	-2.48	0.04334762	0.3241	-4.21
261337_at	unknown protein ; supported by cD	---	AT1G44810	1.43	0.52	2.48	0.04334478	0.3241	-4.21
264152_at	Mago Nashi-like protein similar to	MAGO	AT1G02140	1.23	0.29	2.48	0.04334458	0.3241	-4.21

246907_at	AtBgamma - like protein B' regulat	---	AT5G25510	-1.27	-0.34	-2.48	0.043251	0.3241	-4.21
252087_at	putative protein putative Na+/H+-e	chx28	AT3G52080	-1.20	-0.26	-2.48	0.04332483	0.3241	-4.21
266317_at	calmodulin identical to GB:L18912	CAM5	AT2G27030	1.21	0.27	2.48	0.04333128	0.3241	-4.21
262073_at	unknown protein ;supported by full	ZCW32	AT1G59640	-1.47	-0.56	-2.48	0.04334187	0.3241	-4.21
257478_at	hypothetical protein similar to puta	WAKL2	AT1G16130	1.58	0.66	2.48	0.04324451	0.3241	-4.21
259972_at	unknown protein N-term similar to	CUC3	AT1G76420	1.37	0.45	2.48	0.04329392	0.3241	-4.21
264669_at	putative RAS-related protein, RAB	ATRAB11C	AT1G09630	1.36	0.44	2.48	0.04327009	0.3241	-4.21
250442_at	putative protein hypothetical bacte	MSL2	AT5G10490	-1.21	-0.28	-2.49	0.04323205	0.3241	-4.21
263249_at	delta 9 desaturase ALMOST identi	ADS2	AT2G31360	-1.19	-0.26	-2.48	0.04337353	0.3241	-4.21
261824_at	DAG protein, putative similar to D	---	AT1G11430	1.18	0.24	2.48	0.04342189	0.3241	-4.22
255593_at	hypothetical protein	---	AT4G01650	1.22	0.29	2.48	0.04338857	0.3241	-4.21
256348_at	hypothetical protein predicted by g	---	AT1G54880	-1.22	-0.28	-2.48	0.04341789	0.3241	-4.22
246998_at	putative protein similar to unknown	---	AT5G67370	-1.46	-0.55	-2.48	0.04339818	0.3241	-4.22
251707_at	protein kinase C inhibitor-like prot	---	AT3G56490	1.23	0.30	2.48	0.0434713	0.3244	-4.22
265594_at	50S ribosomal protein L4 ;support	---	AT2G20060	1.38	0.47	2.48	0.04351126	0.3246	-4.22
253831_at	Expressed protein ; supported by f	---	AT4G27580	-1.23	-0.30	-2.48	0.04353021	0.3246	-4.22
250550_at	N-hydroxycinnamoyl benzoyltrans	---	AT5G07870	1.54	0.62	2.48	0.04364309	0.3248	-4.22
262931_at	small nuclear ribonucleoprotein, p	---	AT1G65700	1.23	0.30	2.48	0.04358994	0.3248	-4.22
261169_at	sucrose-phosphate synthase, puta	ATSPS3F	AT1G04920	-1.24	-0.31	-2.48	0.04360515	0.3248	-4.22
250500_at	periaxin - like protein periaxin, Rat	---	AT5G09530	7.12	2.83	2.48	0.04362373	0.3248	-4.22
246844_at	transcription factor ATMYB4 ; sup	ATMYB86	AT5G26660	1.26	0.33	2.48	0.04360078	0.3248	-4.22
262783_at	receptor-kinase isolog	---	AT1G10850	1.52	0.61	2.48	0.04363155	0.3248	-4.22
260199_at	unknown protein similar to putative	---	AT1G67590	-1.19	-0.25	-2.48	0.04368075	0.3250	-4.22
249468_at	putative protein predicted proteins	---	AT5G39650	1.19	0.25	2.48	0.04370766	0.3251	-4.22
255617_at	putative protein kinase	---	AT4G01330	1.28	0.36	2.48	0.0437559	0.3251	-4.22
261558_at	unknown protein	---	AT1G01770	1.38	0.47	2.48	0.04383142	0.3251	-4.23
248127_at	transport protein particle compone	---	AT5G54750	1.19	0.26	2.48	0.04380395	0.3251	-4.22
260257_at	putative dolichyl-phosphate mannc	---	AT1G74340	1.20	0.26	2.48	0.04381262	0.3251	-4.22
266232_at	putative phloem-specific lectin	AtPP2-B6	AT2G02310	-1.17	-0.23	-2.48	0.04377419	0.3251	-4.22
246492_at	CRS2-like protein CRS2 - Zea ma	---	AT5G16140	1.33	0.42	2.48	0.04380312	0.3251	-4.22
249136_at	putative protein similar to unknown	---	AT5G43180	-1.43	-0.52	-2.48	0.04384484	0.3251	-4.23
250184_at	putative protein various predicted	---	AT5G14240	1.20	0.26	2.48	0.04381484	0.3251	-4.22
254652_at	DNA binding-like protein SPF1 pr	WRKY28	AT4G18170	2.58	1.37	2.48	0.04385314	0.3251	-4.23
251953_at	putative protein predicted protein,	CPuORF51	AT3G53668 /	1.26	0.33	2.48	0.04380648	0.3251	-4.22
262093_at	receptor protein kinase, putative c	---	AT1G56145	1.37	0.46	2.47	0.04392665	0.3254	-4.23

251214_at	putative protein hypothetical protei	---	AT3G62500	-1.21	-0.28	-2.47	0.0439141	0.3254	-4.23
258286_at	kinesin-like protein similar to kines	---	AT3G16060	1.25	0.32	2.47	0.04398688	0.3257	-4.23
261596_at	hypothetical protein predicted by g	---	AT1G33080	1.23	0.30	2.47	0.04397912	0.3257	-4.23
260632_at	homeobox protein, putative simila	STM	AT1G62360	-1.23	-0.30	-2.47	0.04400136	0.3257	-4.23
263289_at	ubiquitin extension protein (UBQ2	---	AT2G36170	1.44	0.53	2.47	0.04404952	0.3257	-4.23
245087_at	hypothetical protein predicted by g	DAR2	AT2G39830	-1.35	-0.43	-2.47	0.04402424	0.3257	-4.23
245872_at	hypothetical protein contains simila	---	AT1G26300	1.22	0.29	2.47	0.04405131	0.3257	-4.23
262974_at	hypothetical protein predicted by g	---	AT1G75550	1.22	0.28	2.47	0.0440893	0.3259	-4.23
265679_at	putative myosin heavy chain ; sup	---	AT2G32235	-1.24	-0.30	-2.47	0.04413498	0.3261	-4.23
259937_s_at	putative ABC transporter contains	ATNAP5	AT1G71330	-1.22	-0.29	-2.47	0.04417924	0.3263	-4.23
263572_at	putative disease resistance protein	---	AT2G17060	-1.19	-0.25	-2.47	0.04420405	0.3263	-4.23
260588_at	unknown protein contains similarity	AtTLP7	AT1G53320	-1.27	-0.34	-2.47	0.04420473	0.3263	-4.23
262868_at	unknown protein	---	AT1G64980	-1.37	-0.45	-2.47	0.04423266	0.3263	-4.23
258374_at	hypothetical protein predicted by g	---	AT3G14360	-1.47	-0.56	-2.47	0.04425191	0.3263	-4.23
265505_at	putative RING zinc finger protein	---	AT2G15530	-1.19	-0.25	-2.47	0.04424579	0.3263	-4.23
247434_at	Expressed protein ; supported by f	---	AT5G62575	1.19	0.25	2.47	0.04434339	0.3269	-4.24
261909_at	hypothetical protein predicted by g	SAR3	AT1G80680	1.27	0.35	2.47	0.04437375	0.3270	-4.24
245500_at	reverse transcriptase like protein	---	---	-1.20	-0.26	-2.47	0.04438612	0.3270	-4.24
263120_at	cytochrome P450, putative similar	CYP708A3	AT1G78490	-3.01	-1.59	-2.47	0.04440393	0.3270	-4.24
261930_at	alcohol dehydrogenase ADH, puta	---	AT1G22440	1.33	0.41	2.47	0.04443655	0.3271	-4.24
245565_at	hypothetical protein	---	AT4G14605	1.23	0.30	2.47	0.0444469	0.3271	-4.24
248766_at	putative protein strong similarity to	---	AT5G47580	1.51	0.60	2.46	0.04450888	0.3275	-4.24
251174_at	putative protein latex protein allerg	PLP9	AT3G63200	-1.50	-0.59	-2.46	0.04453828	0.3276	-4.24
246606_at	putative protein	---	---	1.17	0.22	2.46	0.04455959	0.3277	-4.24
257233_at	hypothetical protein similar to SF1	IQD10	AT3G15050	-1.20	-0.27	-2.46	0.04464736	0.3281	-4.24
253217_at	actin depolymerizing factor - like p	ADF9	AT4G34970	-1.58	-0.66	-2.46	0.04463487	0.3281	-4.24
264967_at	unknown protein ;supported by full	---	AT1G67250	1.19	0.25	2.46	0.04467815	0.3282	-4.24
258355_at	hypothetical protein predicted by g	---	AT3G14330	1.33	0.41	2.46	0.04471894	0.3284	-4.25
262431_at	trypsin inhibitor 2, putative similar	---	AT1G47540	-1.20	-0.27	-2.46	0.04474445	0.3285	-4.25
260036_at	putative protein kinase Pfam HMM	STN7	AT1G68830	-1.27	-0.34	-2.46	0.04476346	0.3285	-4.25
261407_at	unknown protein ;supported by full	---	AT1G18810	-1.37	-0.46	-2.46	0.04482908	0.3286	-4.25
251151_at	hypothetical protein ; supported by	---	AT3G63170	1.27	0.34	2.46	0.04484483	0.3286	-4.25
246240_at	nucleoporin-like protein	---	AT4G37130	1.17	0.23	2.46	0.04481552	0.3286	-4.25
254460_at	putative protein sigma70 operon,	ATRP1	AT4G21210	-1.29	-0.37	-2.46	0.04486512	0.3286	-4.25
263378_at	protein phosphatase 2C (AthPP2C	ATHPP2C5	AT2G40180	-1.35	-0.44	-2.46	0.04482004	0.3286	-4.25

252381_s_at	ABC-type transport protein-like pr	ABCA4	AT3G47750 /	-1.24	-0.31	-2.46	0.04486439	0.3286	-4.25
263758_s_at	putative NADPH dependent manno	---	AT2G21250 /	-1.19	-0.25	-2.46	0.04488743	0.3287	-4.25
252550_at	putative protein MtN21, Medicago	---	AT3G45870	-1.26	-0.34	-2.46	0.04493492	0.3289	-4.25
262316_at	pale cress protein identical to GB:(	PAC	AT2G48120	-1.34	-0.42	-2.46	0.0449746	0.3291	-4.25
257802_at	unknown protein	---	AT3G18770	1.30	0.37	2.46	0.04501844	0.3293	-4.25
261907_at	4-coumarate:CoA ligase 3 identica	4CL3	AT1G65060	1.72	0.78	2.46	0.04502556	0.3293	-4.25
245187_s_at	F12A21.17 similar to signal recogn	---	AT1G67650 /	1.20	0.27	2.46	0.0450679	0.3294	-4.25
255420_at	putative frataxin-like protein similar	FH	AT4G03240	1.18	0.24	2.46	0.04506353	0.3294	-4.25
251246_at	auxin-induced protein homolog au	IAA30	AT3G62100	1.18	0.23	2.46	0.04508529	0.3294	-4.25
256629_at	serine/threonine protein phosphat	ATFYPP3	AT3G19980	1.21	0.27	2.45	0.0451812	0.3298	-4.26
257263_at	unknown protein ;supported by ful	---	AT3G22070	1.42	0.50	2.45	0.04515671	0.3298	-4.25
259222_at	putative phosphoribosylanthranila	---	AT3G03680	-1.27	-0.35	-2.45	0.04517097	0.3298	-4.26
265930_at	putative spliceosome associated p	emb2444	AT2G18510	-1.23	-0.30	-2.45	0.04522598	0.3298	-4.26
256959_at	methyltransferase, putative	---	AT3G13440	1.18	0.23	2.45	0.04519721	0.3298	-4.26
261859_at	E2, ubiquitin-conjugating enzyme,	UBC20	AT1G50490	1.28	0.36	2.45	0.04521644	0.3298	-4.26
251204_at	putative protein HMW prekininoge	AT3G6309	---	-1.23	-0.30	-2.45	0.04526045	0.3299	-4.26
255816_at	unknown protein ;supported by ful	GLTP1	AT2G33470	1.18	0.24	2.45	0.04532143	0.3303	-4.26
261149_s_at	GSH-dependent dehydroascorbat	DHAR1	AT1G19550 /	-1.40	-0.48	-2.45	0.04536597	0.3303	-4.26
266238_at	phosphoprotein phosphatase, type	TOPP1	AT2G29400	1.37	0.45	2.45	0.04536126	0.3303	-4.26
247286_at	2-oxoglutarate/malate translocator	DiT2.2	AT5G64280	-1.22	-0.29	-2.45	0.04534663	0.3303	-4.26
250634_at	putative protein 2-oxoglutarate-de	---	AT5G07480	-1.19	-0.26	-2.45	0.04548816	0.3311	-4.26
266062_at	putative diacylglycerol kinase	---	AT2G18730	-1.17	-0.22	-2.45	0.04560409	0.3317	-4.26
265944_at	putative SET-domain transcriptiona	ASHR2	AT2G19640	-1.26	-0.33	-2.45	0.04559084	0.3317	-4.26
257975_at	unknown protein similar to GB:AAD	---	AT3G20830	-1.34	-0.42	-2.45	0.04563069	0.3318	-4.27
253815_at	putative beta-expansin/allergen pr	ATEXPB3	AT4G28250	-1.35	-0.43	-2.45	0.04566358	0.3319	-4.27
250513_at	protein kinase ;supported by full-le	---	AT5G09890	-1.21	-0.28	-2.45	0.04567983	0.3319	-4.27
256480_at	unknown protein	SAR1	AT1G33410	1.27	0.35	2.44	0.04583245	0.3320	-4.27
267580_at	unknown protein	---	AT2G41990	-1.26	-0.33	-2.45	0.04577912	0.3320	-4.27
249753_at	putative protein similar to unknown	---	AT5G24610	-1.17	-0.23	-2.45	0.04575143	0.3320	-4.27
253763_at	xyloglucan endotransglycosylase	---	AT4G28850	-1.18	-0.24	-2.45	0.04572224	0.3320	-4.27
263290_at	unknown protein	---	AT2G10930	-1.17	-0.22	-2.45	0.04578551	0.3320	-4.27
250795_at	RING zinc finger protein-like	CPuORF64	AT5G05280 /	-1.24	-0.31	-2.45	0.04575549	0.3320	-4.27
265889_at	hypothetical protein predicted by g	---	AT2G15130	-1.25	-0.32	-2.45	0.04572668	0.3320	-4.27
251798_at	putative RNA binding protein Seri	SCL30	AT3G55460	1.21	0.27	2.44	0.04582501	0.3320	-4.27
263020_at	unknown protein	---	AT1G23880	1.20	0.26	2.44	0.04583281	0.3320	-4.27

250292_at	putative protein predicted proteins	JAZ10	AT5G13220	-2.44	-1.29	-2.44	0.04580561	0.3320	-4.27
259389_at	hypothetical protein predicted by g	---	AT1G06320	-1.19	-0.25	-2.44	0.04587433	0.3322	-4.27
254574_at	expressed protein supported by cl	---	AT4G19430	-2.21	-1.14	-2.44	0.04592991	0.3323	-4.27
262908_at	pyruvate dehydrogenase e1 alpha	AT-E1 ALP	AT1G59900	1.20	0.26	2.44	0.04593907	0.3323	-4.27
260118_s_at	hypothetical protein predicted by g	---	AT1G33940	1.29	0.37	2.44	0.04594548	0.3323	-4.27
257660_at	unknown protein ; supported by cl	WIP3	AT3G13360	1.17	0.23	2.44	0.04593105	0.3323	-4.27
252192_at	CASEIN KINASE II, ALPHA CHAI	CKA2	AT3G50000	1.18	0.23	2.44	0.04599328	0.3325	-4.27
251952_at	histone H2B - like protein histone	---	AT3G53650	1.17	0.22	2.44	0.04607824	0.3330	-4.28
256921_at	unknown protein ;supported by ful	---	AT3G18940	1.23	0.30	2.44	0.04611029	0.3332	-4.28
264471_at	hypothetical protein predicted by g	---	AT1G67120	1.42	0.51	2.44	0.04613965	0.3333	-4.28
252624_at	Expressed protein ; supported by f	PSK1	AT3G44735	-1.54	-0.62	-2.44	0.04620301	0.3333	-4.28
250168_at	putative protein predicted protein,	---	AT5G15320	1.20	0.27	2.44	0.04616132	0.3333	-4.28
250215_at	putative protein similar to unknown	---	AT5G14080	1.21	0.27	2.44	0.04621732	0.3333	-4.28
260636_at	hypothetical protein contains simila	ATCDS1	AT1G62430	-1.43	-0.52	-2.44	0.04621554	0.3333	-4.28
262535_at	trehalose-6-phosphate synthase,	ATTPS3	AT1G17000	-1.16	-0.21	-2.44	0.04620843	0.3333	-4.28
257334_at	hypothetical protein	---	---	-1.61	-0.69	-2.44	0.04622577	0.3333	-4.28
254300_at	Translation factor EF-1 alpha - like	ACR7	AT4G22780	1.34	0.42	2.43	0.04658756	0.3336	-4.29
260933_at	hypothetical protein contains non-c	---	AT1G02470	2.09	1.06	2.43	0.04658374	0.3336	-4.29
246821_at	calmodulin-binding - like protein c	CBP60G	AT5G26920	2.14	1.09	2.43	0.04653355	0.3336	-4.29
261071_at	unknown protein	---	AT1G07380	1.27	0.34	2.43	0.04663849	0.3336	-4.29
256092_at	Expressed protein ; supported by f	HMGB3	AT1G20696	1.17	0.22	2.43	0.04663915	0.3336	-4.29
259285_at	hypothetical protein similar to puta	---	AT3G11460	1.20	0.27	2.44	0.04634734	0.3336	-4.28
261576_at	unknown protein ;supported by full	---	AT1G01070	1.57	0.65	2.44	0.04642017	0.3336	-4.28
245986_at	protein kinase-like protein kinase	PBS1	AT5G13160	-1.18	-0.24	-2.43	0.04649931	0.3336	-4.28
260190_at	putative lipoxygenase similar to 13	---	AT1G67560	-1.40	-0.48	-2.43	0.0465831	0.3336	-4.29
267612_at	putative nitrate transporter	---	AT2G26690	-1.75	-0.81	-2.43	0.04660419	0.3336	-4.29
257707_at	hypothetical protein predicted by g	---	AT3G12650	1.20	0.26	2.43	0.0464595	0.3336	-4.28
258771_at	unknown protein ;supported by ful	---	AT3G10770	1.22	0.29	2.43	0.04663417	0.3336	-4.29
264023_at	Expressed protein ; supported by f	---	AT2G21195	1.40	0.48	2.44	0.04637442	0.3336	-4.28
262495_at	unknown protein Contains similari	---	AT1G21780	1.32	0.41	2.44	0.04639538	0.3336	-4.28
263160_at	oligouridylate binding protein, puta	UBP1A	AT1G54080	-1.23	-0.29	-2.43	0.04653754	0.3336	-4.29
266340_at	similar to axi 1 protein from Nicotia	---	AT2G01480	-1.17	-0.22	-2.43	0.04660089	0.3336	-4.29
257276_at	disease resistance protein, putativ	---	AT3G14460	-1.18	-0.24	-2.44	0.04645634	0.3336	-4.28
263413_at	unknown protein ;supported by ful	BPC4	AT2G21240	1.25	0.32	2.43	0.0464985	0.3336	-4.28
255902_at	transcription factor, putative simila	---	AT1G17880	1.21	0.27	2.43	0.04653353	0.3336	-4.29

245094_at	4-alpha-glucanotransferase	DPE2	AT2G40840	-1.28	-0.36	-2.43	0.04660433	0.3336	-4.29
254723_at	ammonium transport protein (AMT	AMT1;1	AT4G13510	1.31	0.39	2.43	0.04649473	0.3336	-4.28
248314_at	putative protein similar to unknown	---	AT5G52620	1.17	0.23	2.44	0.04632875	0.3336	-4.28
262000_at	Expressed protein ; supported by f	---	AT1G33810	1.25	0.32	2.43	0.04647618	0.3336	-4.28
256927_at	unknown protein	---	AT3G22550	-1.20	-0.26	-2.43	0.04652454	0.3336	-4.28
259288_at	putative small nuclear ribonucleopr	---	AT3G11500	1.22	0.29	2.44	0.04628828	0.3336	-4.28
256572_at	40S RIBOSOMAL PROTEIN S25,	---	AT3G30740	1.20	0.26	2.43	0.04666524	0.3337	-4.29
254666_at	translation initiation factor eIF-2 ga	---	AT4G18330	-1.16	-0.22	-2.43	0.0466921	0.3338	-4.29
253788_at	aromatic amino-acid decarboxylas	---	AT4G28680	-1.24	-0.32	-2.43	0.04674668	0.3340	-4.29
263833_at	hypothetical protein	---	AT2G40316	1.18	0.24	2.43	0.04675051	0.3340	-4.29
249268_at	Expressed protein ; supported by c	---	AT5G41685	1.19	0.25	2.43	0.0468283	0.3344	-4.29
259150_at	unknown protein similar to unknow	---	AT3G10320	1.20	0.26	2.43	0.04686443	0.3345	-4.29
245774_at	hypothetical protein contains simila	TCP24	AT1G30210	1.19	0.25	2.43	0.04687585	0.3345	-4.29
251261_at	putative protein polygalacturonase	---	AT3G62110	1.53	0.61	2.43	0.04686052	0.3345	-4.29
250704_at	Expressed protein ; supported by f	---	AT5G06265	1.27	0.35	2.43	0.04691093	0.3346	-4.29
259379_at	putative MYB family transcription fa	---	AT3G16350	-1.54	-0.63	-2.43	0.04693183	0.3346	-4.29
259990_s_at	F-box protein FKF1/ADO3, AtFBX	FKF1	AT1G68050 /	1.35	0.43	2.43	0.04711087	0.3347	-4.30
263509_s_at	hypothetical protein	---	AT2G07687	-1.37	-0.45	-2.43	0.04709	0.3347	-4.30
265896_at	unknown protein	emb2410	AT2G25660	1.22	0.29	2.43	0.04702123	0.3347	-4.30
246191_at	T-complex protein 1, beta subunit	---	AT5G20890	1.27	0.34	2.43	0.04711228	0.3347	-4.30
267096_at	unknown protein ; supported by cl	---	AT2G38180	1.46	0.54	2.43	0.04702377	0.3347	-4.30
259528_at	hypothetical protein	---	AT1G12330	1.33	0.42	2.43	0.04697667	0.3347	-4.29
249742_at	putative protein contains similarity	---	AT5G24490	1.26	0.34	2.43	0.04710539	0.3347	-4.30
249269_at	cell cycle control crn (crooked neck	---	AT5G41770	1.29	0.37	2.43	0.04706475	0.3347	-4.30
266310_at	putative PCI domain protein prote	FUS12	AT2G26990	1.23	0.30	2.43	0.04705318	0.3347	-4.30
258521_at	ribosomal protein L29, putative sir	---	AT3G06680	1.62	0.70	2.43	0.04709492	0.3347	-4.30
247978_at	60S ribosomal protein L31 ;suppo	---	AT5G56710	1.60	0.67	2.43	0.04711423	0.3347	-4.30
257391_at	hypothetical protein predicted by g	---	AT2G32050	-1.17	-0.22	-2.43	0.04702254	0.3347	-4.30
267492_at	histone H1 ;supported by full-lengt	---	AT2G30620	1.30	0.38	2.42	0.04725464	0.3347	-4.30
255907_at	homeobox protein, putative simila	HDG12	AT1G17920	-1.19	-0.25	-2.42	0.04730492	0.3347	-4.30
245303_at	hypothetical protein ; supported by	---	AT4G17010	1.19	0.25	2.42	0.04729713	0.3347	-4.30
250532_at	putative protein similar to unknown	---	AT5G08540	1.26	0.33	2.42	0.04731285	0.3347	-4.30
260442_at	unknown protein ; supported by fu	---	AT1G68220	-1.28	-0.36	-2.42	0.04730835	0.3347	-4.30
253790_at	photosystem II protein W - like ph	PSB28	AT4G28660	1.39	0.48	2.42	0.04729839	0.3347	-4.30
262673_at	unknown protein	EMB1793	AT1G76060	-1.21	-0.28	-2.42	0.04719427	0.3347	-4.30

252540_at	putative protein CDP-alcohol phos	---	AT3G45740	-1.20	-0.26	-2.42	0.04726027	0.3347	-4.30
263739_at	putative CONSTANS-like B-box zi	---	AT2G21320	-1.45	-0.54	-2.42	0.04730773	0.3347	-4.30
247228_at	trehalose-6-phosphate phosphatas	---	AT5G65140	-1.87	-0.90	-2.42	0.04719197	0.3347	-4.30
254380_at	putative protein	---	AT4G21865	-1.89	-0.92	-2.42	0.04732013	0.3347	-4.30
248183_at	CHP-rich zinc finger protein-like	---	AT5G54040	-1.17	-0.23	-2.42	0.04723636	0.3347	-4.30
266346_at	putative homeodomain transcriptio	ATHB17	AT2G01430	1.28	0.35	2.42	0.0472937	0.3347	-4.30
251084_at	putative protein putative proteins -	---	AT5G01520	1.47	0.55	2.42	0.04716543	0.3347	-4.30
249913_at	GDSL-motif lipase/hydrolase-like p	---	AT5G22810	-1.24	-0.31	-2.42	0.04734122	0.3347	-4.30
251336_at	putative protein hypothetical prote	BAP1	AT3G61190	-1.53	-0.61	-2.42	0.04737702	0.3347	-4.30
249354_at	nuclear pore protein -like nuclear	EMB3012	AT5G40480	1.34	0.42	2.42	0.04738647	0.3347	-4.30
259799_at	drought induced protein, putative	---	AT1G72290	-1.17	-0.22	-2.42	0.04736823	0.3347	-4.30
260279_at	putative DNA repair protein similar	---	AT1G80420	1.21	0.28	2.42	0.04740313	0.3348	-4.30
257788_at	unknown protein	TCP20	AT3G27010	1.28	0.36	2.42	0.04744903	0.3350	-4.30
250156_at	putative protein predicted proteins	---	AT5G15170	1.18	0.24	2.42	0.04751938	0.3351	-4.31
262542_at	hypothetical protein similar to NAM	anac016	AT1G34180	1.39	0.48	2.42	0.04749505	0.3351	-4.31
248075_at	selenium-binding protein-like	CRR21	AT5G55740	1.35	0.44	2.42	0.04748928	0.3351	-4.31
248302_at	putative protein similar to unknown	---	AT5G53160	1.31	0.39	2.42	0.04751839	0.3351	-4.31
258584_at	hypothetical protein predicted by g	SIP1A	AT3G04090	1.16	0.21	2.42	0.04757291	0.3353	-4.31
254304_at	hypothetical protein ; supported by	---	AT4G22270	-1.26	-0.34	-2.42	0.04762076	0.3356	-4.31
261692_at	calreticulin, putative similar to calr	CRT3	AT1G08450	1.46	0.54	2.42	0.04768026	0.3359	-4.31
263252_at	putative CONSTANS-like B-box zi	STH	AT2G31380	-1.38	-0.47	-2.42	0.04774299	0.3362	-4.31
267110_at	hypothetical protein predicted by g	---	AT2G14800	1.27	0.35	2.42	0.04777103	0.3363	-4.31
265216_at	putative NPK1-related MAP kinase	MAPKKK18	AT1G05100	-1.39	-0.48	-2.42	0.04778807	0.3363	-4.31
247075_at	putative protein contains similarity	PLP3b	AT5G66410	1.25	0.32	2.41	0.04784823	0.3366	-4.31
246218_at	RUB1-conjugating enzyme RCE1	RCE1	AT4G36800	1.33	0.41	2.41	0.04786999	0.3367	-4.31
266298_at	unknown protein ;supported by ful	---	AT2G29590	1.26	0.33	2.41	0.04789895	0.3368	-4.31
252041_at	DNA-directed RNA polymerase II 1	NRPB11	AT3G52090	1.22	0.28	2.41	0.04791173	0.3368	-4.31
247169_at	unknown protein	---	AT5G65520	1.31	0.39	2.41	0.04797935	0.3372	-4.32
259694_at	uridine diphosphate glucose epim	UGE3	AT1G63180	1.74	0.80	2.41	0.04802509	0.3374	-4.32
253463_at	Expressed protein ; supported by f	---	AT4G32105	-1.21	-0.27	-2.41	0.04806141	0.3374	-4.32
246576_at	hypothetical protein predicted by g	ROPGEF14	AT1G31650	1.17	0.23	2.41	0.048051	0.3374	-4.32
266013_s_at	hypothetical protein	---	AT2G07702	-1.20	-0.26	-2.41	0.04810345	0.3376	-4.32
247267_at	40S ribosomal protein S28 (sp|P34	RPS28	AT5G64140	1.50	0.59	2.41	0.04815064	0.3378	-4.32
260226_at	hypothetical protein predicted by g	MIF1	AT1G74660	-1.27	-0.34	-2.41	0.04816032	0.3378	-4.32
260602_at	serine acetyltransferase identical	ATSERAT2	AT1G55920	-1.24	-0.31	-2.41	0.04820243	0.3380	-4.32

266481_at	unknown protein ; supported by cl	TCP10	AT2G31070	-1.29	-0.37	-2.41	0.04840363	0.3381	-4.32
251975_at	CDC48 - like protein transitional e	---	AT3G53230	-1.84	-0.88	-2.41	0.04822998	0.3381	-4.32
257062_at	zinc finger protein, putative contai	EMB2454	AT3G18290	-1.54	-0.62	-2.41	0.04829281	0.3381	-4.32
252468_at	starch phosphorylase H (cytosolic	PHS2	AT3G46970	-1.29	-0.37	-2.41	0.04832909	0.3381	-4.32
267584_at	putative protein kinase contains a	---	AT2G41930	-1.21	-0.27	-2.41	0.04836709	0.3381	-4.32
244999_at	RNA polymerase beta subunit	---	---	-1.36	-0.45	-2.41	0.04840483	0.3381	-4.32
252235_at	60S RIBOSOMAL PROTEIN - like	---	AT3G49910	1.45	0.53	2.41	0.04834787	0.3381	-4.32
265646_at	putative lipase	---	AT2G27360	-1.23	-0.30	-2.41	0.04838744	0.3381	-4.32
250946_at	putative protein	---	AT5G03420	-1.20	-0.26	-2.41	0.04839555	0.3381	-4.32
261405_at	unknown protein ;supported by full	---	AT1G18740	-1.48	-0.57	-2.41	0.04832308	0.3381	-4.32
265370_s_at	unknown protein related to GB:AA	---	AT3G30415	-1.18	-0.24	-2.41	0.0483299	0.3381	-4.32
255909_at	cdc2+/CDC28-related protein kina	CDKD1;3	AT1G18040	-1.37	-0.45	-2.41	0.04839921	0.3381	-4.32
245297_at	hypothetical protein ; supported by	---	AT4G16510	1.25	0.32	2.41	0.04826402	0.3381	-4.32
254112_at	putative protein KIAA0136 gene, H	---	AT4G24970	1.21	0.28	2.41	0.04848048	0.3385	-4.33
253073_at	cytochrome P450 monooxygenas	CYP81F4	AT4G37410	-1.25	-0.32	-2.41	0.04850549	0.3386	-4.33
254551_at	lectin like protein lectin phloem pr	ATPP2-A1	AT4G19840	-1.27	-0.34	-2.40	0.04852145	0.3386	-4.33
258580_at	germin-like protein contains Pfam	---	AT3G04170	1.22	0.29	2.40	0.04853793	0.3386	-4.33
258881_at	unknown protein ; supported by fu	---	AT3G06310	1.22	0.29	2.40	0.04859289	0.3389	-4.33
246820_at	putative protein predicted proteins	---	AT5G26910	1.17	0.22	2.40	0.04864062	0.3391	-4.33
262633_at	Expressed protein ; supported by f	---	AT1G06630	-1.19	-0.25	-2.40	0.04866035	0.3391	-4.33
253099_s_at	peroxidase - like protein peroxidas	---	AT4G37520	1.25	0.33	2.40	0.04874121	0.3395	-4.33
261735_at	hypothetical protein similar to hypo	---	AT1G47765	-1.22	-0.29	-2.40	0.04874217	0.3395	-4.33
257807_at	glyceraldehyde 3-phosphate dehy	GAPA	AT3G26650	1.19	0.25	2.40	0.04875351	0.3395	-4.33
259377_at	putative poly(A) binding protein si	PAB6	AT3G16380	-1.28	-0.36	-2.40	0.04883462	0.3399	-4.33
254374_at	hypothetical protein ;supported by	---	AT4G21780	-1.18	-0.24	-2.40	0.04886785	0.3400	-4.33
252941_at	phenylalanyl-trna synthetase - like	---	AT4G39280	1.18	0.24	2.40	0.04894763	0.3405	-4.34
249208_at	allene oxide synthase (emb CAA7	AOS	AT5G42650	-1.71	-0.78	-2.40	0.0489855	0.3406	-4.34
266252_at	hypothetical protein predicted by g	---	AT2G27520	-1.22	-0.28	-2.40	0.04900371	0.3406	-4.34
267058_at	putative protein kinase contains a	MAPKKK17	AT2G32510	-1.36	-0.45	-2.40	0.04901087	0.3406	-4.34
257906_at	ribosomal protein, putative similar	ATL5	AT3G25520	1.61	0.69	2.40	0.04902309	0.3406	-4.34
248820_at	putative protein similar to unknown	---	AT5G47060	1.30	0.38	2.40	0.04916174	0.3412	-4.34
259323_at	unknown protein	---	AT3G05280	1.15	0.21	2.40	0.04918259	0.3412	-4.34
263466_at	hypothetical protein predicted by g	---	AT2G31740	1.18	0.24	2.40	0.04920325	0.3412	-4.34
254728_at	hypothetical protein	---	AT4G13690	-1.19	-0.26	-2.40	0.04917463	0.3412	-4.34
254816_at	putative adenine phosphoribosyltr	APT4	AT4G12440	-1.16	-0.21	-2.40	0.04918974	0.3412	-4.34

250536_at	Expressed protein ; supported by f	---	AT5G08535	1.24	0.31	2.40	0.04918657	0.3412	-4.34
256253_at	60S acidic ribosomal protein, puta	---	AT3G11250	1.23	0.30	2.39	0.04927424	0.3415	-4.34
247825_at	RNA/ssDNA-binding protein - like	TAF15b	AT5G58470	-1.23	-0.30	-2.39	0.04931173	0.3415	-4.34
248857_at	putative protein contains similarity	---	AT5G46640	1.46	0.54	2.39	0.04927516	0.3415	-4.34
253334_at	putative protein dihydrokaempferc	---	AT4G33360	1.35	0.43	2.39	0.04931018	0.3415	-4.34
246278_at	tubulin-like protein	---	AT4G37190	-1.51	-0.59	-2.39	0.04931697	0.3415	-4.34
249039_at	late embryogenesis abundant prot	---	AT5G44310	-1.23	-0.30	-2.39	0.04947065	0.3425	-4.35
252269_at	putative protein ;supported by full-	LSU1	AT3G49580	1.72	0.78	2.39	0.04952954	0.3427	-4.35
253283_at	hypothetical protein ; supported by	---	AT4G34090	1.32	0.40	2.39	0.0495337	0.3427	-4.35
265792_at	predicted by genscan and genefinc	---	AT2G01390	-1.24	-0.31	-2.39	0.04958762	0.3430	-4.35
259812_at	unknown protein	---	AT1G49840	1.33	0.42	2.39	0.04961197	0.3430	-4.35
248382_at	peroxidase	---	AT5G51890	2.00	1.00	2.39	0.0496564	0.3432	-4.35
245993_at	putative protein predicted proteins	---	AT5G20700	-1.36	-0.45	-2.39	0.04971931	0.3436	-4.35
245852_at	ribosomal protein L10-like riboson	---	AT5G13510	1.27	0.34	2.39	0.04975817	0.3437	-4.35
248006_at	unknown protein	HAP8	AT5G56250	-1.20	-0.27	-2.39	0.04983676	0.3438	-4.35
264319_at	subtilisin-like serine protease, puta	SDD1	AT1G04110	-1.26	-0.33	-2.39	0.04985351	0.3438	-4.35
260770_at	RING-H2 finger protein RHA3a, p	---	AT1G49200	2.32	1.21	2.39	0.04983992	0.3438	-4.35
AFFX-r2-Bs-thr	B. subtilis /GEN=thrC /DB_XREF=	---	---	-1.53	-0.61	-2.39	0.04984102	0.3438	-4.35
260956_at	salt-tolerance protein identical to s	STO	AT1G06040	-1.19	-0.25	-2.39	0.04979844	0.3438	-4.35
259359_at	B regulatory subunit of protein ph	---	AT1G13460	-1.22	-0.29	-2.39	0.04985003	0.3438	-4.35
264902_at	unknown protein Location of EST g	---	AT1G23060	-1.49	-0.58	-2.39	0.04992956	0.3442	-4.36
248790_at	membrane channel protein-like; ac	TIP2;3	AT5G47450	1.33	0.41	2.38	0.04996357	0.3442	-4.36
258583_at	putative SRF-type transcription fac	AGL57	AT3G04100	-1.18	-0.24	-2.38	0.04995448	0.3442	-4.36
266884_at	phytocyanin identical to GB:U9042	UCC2	AT2G44790	1.71	0.77	2.38	0.05000357	0.3444	-4.36
246826_at	UTP-glucose glucosyltransferase	UGT72E3	AT5G26310	-1.20	-0.27	-2.38	0.05004714	0.3444	-4.36
251292_at	putative protein hypothetical prote	---	AT3G61920	-1.30	-0.38	-2.38	0.05004548	0.3444	-4.36
250393_at	serine/threonine protein phosphat	---	AT5G10900	-1.22	-0.29	-2.38	0.05003559	0.3444	-4.36
258976_at	putative dehydrogenase contains	---	AT3G01980	-1.18	-0.24	-2.38	0.05007802	0.3444	-4.36
245181_at	putative protein similarity to variou	---	AT5G12420	1.68	0.75	2.38	0.05009312	0.3444	-4.36
244923_s_at	orf153b orf153b	---	AT2G07674	-1.38	-0.46	-2.38	0.05007315	0.3444	-4.36
260853_at	hypothetical protein predicted by g	---	AT1G21950	-1.33	-0.41	-2.38	0.05012985	0.3444	-4.36
263254_x_at	hypothetical protein similar to hypc	---	---	-1.30	-0.38	-2.38	0.05011489	0.3444	-4.36
255874_at	hypothetical protein predicted by g	ETG1	AT2G40550	1.82	0.86	2.38	0.05014398	0.3444	-4.36
266042_s_at	hypothetical protein	---	AT2G07734	-1.34	-0.43	-2.38	0.05018112	0.3446	-4.36
255850_at	putative chloroplast 50S ribosomal	---	AT2G33450	1.25	0.32	2.38	0.05023269	0.3446	-4.36

249290_at	putative protein strong similarity to	---	AT5G41060	1.40	0.48	2.38	0.05024479	0.3446	-4.36
246654_s_at	putative protein predicted protein f	EGY1	AT5G35210	-1.16	-0.21	-2.38	0.05022944	0.3446	-4.36
263732_at	hypothetical protein predicted by g	ARL2	AT1G59980	1.22	0.29	2.38	0.05024634	0.3446	-4.36
248508_at	histone acetyltransferase ;support	ELO3	AT5G50320	1.29	0.37	2.38	0.05034567	0.3452	-4.36
262005_at	ABC transporter protein, putative	ATGCN3	AT1G64550	1.31	0.38	2.38	0.05045114	0.3456	-4.37
261709_at	RNA-binding protein, putative sim	CID11	AT1G32790	1.20	0.26	2.38	0.05054261	0.3456	-4.37
260044_at	Expressed protein ; supported by f	---	AT1G73655	1.21	0.28	2.38	0.05042662	0.3456	-4.37
250122_at	unknown protein	---	AT5G16520	1.22	0.29	2.38	0.05056218	0.3456	-4.37
248688_at	indole-3-glycerol phosphate syntha	---	AT5G48220	1.30	0.37	2.38	0.05048664	0.3456	-4.37
259863_at	hypothetical protein ;supported by	ELF4-L2	AT1G72630	1.20	0.26	2.38	0.05051035	0.3456	-4.37
252209_at	putative protein RXF26, Arabidops	---	AT3G50400	1.42	0.51	2.38	0.05046358	0.3456	-4.37
259737_at	acyl-CoA synthetase, putative sim	---	AT1G64400	1.82	0.87	2.38	0.05055534	0.3456	-4.37
259333_at	putative auxin-independent growth	EDA30	AT3G03810	1.23	0.30	2.38	0.05050355	0.3456	-4.37
252935_at	dnaJ-like protein CAJ1 protein, Sa	---	AT4G39150	1.19	0.25	2.38	0.05053857	0.3456	-4.37
264470_at	cytochrome P450, putative similar	CYP735A2	AT1G67110	-1.28	-0.35	-2.38	0.05061091	0.3457	-4.37
257319_at	hypothetical protein	---	---	-1.31	-0.39	-2.38	0.05060042	0.3457	-4.37
245794_at	endoxyloglucan transferase, putat	XTR4	AT1G32170	1.28	0.35	2.37	0.0506865	0.3461	-4.37
251289_at	auxin response factor-like protein	ARF18	AT3G61830	1.28	0.35	2.37	0.05070516	0.3461	-4.37
260417_at	putative chromomethylase similar t	CMT3	AT1G69770	1.48	0.56	2.37	0.05071249	0.3461	-4.37
265151_at	hypothetical protein similar to hypo	---	AT1G51340	-1.27	-0.35	-2.37	0.05097094	0.3464	-4.38
256385_at	60S ribosomal protein L10, putativ	---	AT1G66580	1.39	0.48	2.37	0.05083843	0.3464	-4.37
262381_at	virus resistance protein, putative s	---	AT1G72900	2.17	1.12	2.37	0.05092549	0.3464	-4.38
255443_at	sulfate transporter protein similar t	SULTR3;2	AT4G02700	-1.25	-0.32	-2.37	0.05105939	0.3464	-4.38
250671_at	transcription factor HBP-1b homol	AHBP-1B	AT5G06950	1.19	0.25	2.37	0.05091831	0.3464	-4.38
265739_at	unknown protein ; supported by cl	AtQSOX2	AT2G01270	1.16	0.21	2.37	0.05105811	0.3464	-4.38
267530_at	putative receptor-like protein kinas	---	AT2G41890	1.55	0.64	2.37	0.05104286	0.3464	-4.38
259718_at	unknown protein	VIP5	AT1G61040	1.17	0.22	2.37	0.05092875	0.3464	-4.38
255583_at	hypothetical protein similar to C. e	ARV2	AT4G01510	1.24	0.30	2.37	0.0509481	0.3464	-4.38
256708_at	hypothetical protein predicted by g	---	AT3G30320	-1.18	-0.24	-2.37	0.05080455	0.3464	-4.37
244915_s_at	hypothetical protein	---	---	-1.20	-0.26	-2.37	0.05105843	0.3464	-4.38
255703_at	putative chalcone synthase similar	---	AT4G00040	-1.36	-0.44	-2.37	0.05103055	0.3464	-4.38
244946_at	hypothetical protein	---	---	-1.18	-0.23	-2.37	0.0508642	0.3464	-4.37
246031_at	putative protein KIAA0731 - Homo	---	AT5G21160	1.24	0.31	2.37	0.05088411	0.3464	-4.37
257453_at	hypothetical protein predicted by g	---	AT1G65130	-1.24	-0.31	-2.37	0.05087693	0.3464	-4.37
259186_at	unknown protein similar to possible	---	AT3G01590	1.23	0.30	2.37	0.05105828	0.3464	-4.38

248293_at	unknown protein	---	AT5G53050	-1.36	-0.45	-2.37	0.05098049	0.3464	-4.38
245696_at	phytochrome kinase substrate 1 - l	PKS4	AT5G04190	1.77	0.83	2.37	0.05095253	0.3464	-4.38
256674_at	unknown protein ;supported by full	---	AT3G52360	1.34	0.42	2.37	0.05103513	0.3464	-4.38
250578_at	proanthranilate N-benzoyltransfera	---	AT5G07850	1.18	0.24	2.37	0.050902	0.3464	-4.37
248634_at	isoleucyl-tRNA synthetase	OVA2	AT5G49030	1.27	0.35	2.37	0.05107606	0.3464	-4.38
259821_at	subtilisin-like serine protease conta	---	AT1G66220	-1.28	-0.36	-2.37	0.0510955	0.3465	-4.38
255462_at	hypothetical protein similar to A. th	---	AT4G02940	-1.41	-0.49	-2.37	0.05122984	0.3466	-4.38
257398_at	hypothetical protein predicted by g	---	AT2G01990	1.17	0.22	2.37	0.05113341	0.3466	-4.38
255184_at	putative athila transposon protein	---	---	-1.17	-0.22	-2.37	0.05120579	0.3466	-4.38
266256_at	60S acidic ribosomal protein P2 ;s	---	AT2G27710	1.41	0.50	2.37	0.05117916	0.3466	-4.38
249708_at	unknown protein	---	AT5G35660	-1.44	-0.53	-2.37	0.05118232	0.3466	-4.38
245867_at	ATP phosphoribosyl transferase id	ATATP-PR	AT1G58080	1.23	0.30	2.37	0.05120856	0.3466	-4.38
267536_at	phospholipase D ; supported by c	PLDBETA1	AT2G42010	-1.24	-0.31	-2.37	0.05120162	0.3466	-4.38
265234_at	hypothetical protein	---	AT2G07721	-1.24	-0.31	-2.37	0.05123652	0.3466	-4.38
258923_at	putative glucose acyltransferase si	SCPL7	AT3G10450	1.52	0.60	2.37	0.05127301	0.3466	-4.38
249314_at	receptor kinase-like protein	---	AT5G41180	1.25	0.32	2.37	0.0512685	0.3466	-4.38
266923_at	unknown protein ;supported by ful	---	AT2G45980	1.21	0.28	2.37	0.05131873	0.3468	-4.38
250564_at	putative protein sigma factor F inh	---	AT5G08060	1.17	0.22	2.37	0.05138898	0.3468	-4.38
264267_at	hypothetical protein contains simila	---	AT1G60200	-1.23	-0.30	-2.37	0.05136611	0.3468	-4.38
249175_at	COP8 (constitutive photomorphoge	COP8	AT5G42970	-1.19	-0.25	-2.37	0.05136072	0.3468	-4.38
256058_at	UDP-glucose glucosyltransferase,	UGT71C5	AT1G07240	-1.28	-0.36	-2.36	0.05139566	0.3468	-4.38
248062_at	unknown protein ;supported by ful	---	AT5G55450	4.98	2.31	2.37	0.05138115	0.3468	-4.38
249982_at	putative protein predicted proteins	---	AT5G18520	1.20	0.27	2.36	0.05142038	0.3469	-4.39
255117_s_at	putative protein various hypothetic	ATPUP13	AT4G08700 /	1.16	0.22	2.36	0.05143615	0.3469	-4.39
263359_at	putative lysosomal acid lipase	ATLIP1	AT2G15230	1.25	0.32	2.36	0.05154152	0.3475	-4.39
253035_at	glycosyltransferase like protein alg	CGL1	AT4G38240	1.19	0.25	2.36	0.05160803	0.3478	-4.39
259256_at	putative coated vesicle membrane	---	AT3G07680	1.20	0.26	2.36	0.05161242	0.3478	-4.39
253694_at	Expressed protein ; supported by f	---	AT4G29735	1.23	0.30	2.36	0.05163171	0.3478	-4.39
266012_s_at	predicted protein	---	AT2G07699 /	-1.45	-0.54	-2.36	0.05170416	0.3482	-4.39
265199_s_at	putative glucosyl transferase	---	AT2G36770 /	1.36	0.45	2.36	0.05171362	0.3482	-4.39
249234_at	putative protein similar to unknown	---	AT5G42200	1.42	0.50	2.36	0.05173699	0.3482	-4.39
260992_at	hypothetical protein predicted by g	---	AT1G12150	-1.17	-0.23	-2.36	0.05176661	0.3483	-4.39
263137_at	gamma glutamyl hydrolase, putati	ATGGH1	AT1G78660	-1.48	-0.57	-2.36	0.05178928	0.3484	-4.39
261904_at	unknown protein contains similarity	---	AT1G65040	1.17	0.23	2.36	0.05181925	0.3485	-4.39
252756_s_at	putative protein hypothetical protei	---	AT1G58520 /	-1.20	-0.26	-2.36	0.05186582	0.3487	-4.39

251347_at	putative protein ferritin 1 precurso	---	AT3G61010	1.38	0.46	2.36	0.05191921	0.3489	-4.39
251003_at	putative protein	---	AT5G02690	1.22	0.28	2.36	0.05195357	0.3491	-4.40
254068_at	putative protein similarity to multid	NAP8	AT4G25450	1.22	0.29	2.36	0.05197133	0.3491	-4.40
263046_at	unknown protein ; supported by cl	GRP3S	AT2G05380	1.46	0.54	2.36	0.05198806	0.3491	-4.40
254480_at	translation elongation factor EF-Tu	ATRABE1B	AT4G20360	1.23	0.30	2.36	0.0520356	0.3492	-4.40
258968_at	hypothetical protein similar to hypo	---	AT3G10460	1.21	0.27	2.36	0.05202295	0.3492	-4.40
265342_at	hypothetical protein predicted by g	---	AT2G18300	-1.43	-0.52	-2.36	0.05212718	0.3496	-4.40
263486_at	AP2 domain transcription factor	---	AT2G22200	-1.19	-0.25	-2.36	0.05211418	0.3496	-4.40
264907_at	unknown protein similar to S.pomb	---	AT2G17280	-1.69	-0.75	-2.35	0.05215944	0.3497	-4.40
263882_at	putative ribonucleoside-diphospha	RNR1	AT2G21790	1.56	0.65	2.35	0.0522011	0.3499	-4.40
264605_at	putative auxin-induced protein, IA	IAA12	AT1G04550	1.22	0.28	2.35	0.05222882	0.3500	-4.40
261646_at	putative lipase similar to hypothetic	---	AT1G27690	1.21	0.28	2.35	0.05231871	0.3505	-4.40
256143_at	40S ribosomal protein S7 homolog	---	AT1G48830	1.27	0.35	2.35	0.05235269	0.3506	-4.40
260696_at	unknown protein	---	AT1G32520	-1.22	-0.29	-2.35	0.05238764	0.3507	-4.40
257468_at	hypothetical protein contains simila	---	AT1G47470	-1.17	-0.23	-2.35	0.05242518	0.3508	-4.40
266890_at	acyl carrier protein identical to GB:	MTACP-1	AT2G44620	1.26	0.34	2.35	0.05241559	0.3508	-4.40
247979_at	pollen specific protein SF21 ;supp	---	AT5G56750	1.25	0.32	2.35	0.05249362	0.3508	-4.41
253549_at	Expressed protein ; supported by f	NFD1	AT4G30930	1.37	0.45	2.35	0.0524864	0.3508	-4.41
254301_at	predicted protein predicted protein	---	AT4G22790	-1.33	-0.41	-2.35	0.05247809	0.3508	-4.41
258210_at	Eukaryotic initiation factor 4A, put	EIF4A1	AT3G13920	1.20	0.26	2.35	0.05247824	0.3508	-4.41
259754_at	hypothetical protein predicted by g	---	AT1G71090	1.23	0.29	2.35	0.05251403	0.3509	-4.41
258515_at	ATP citrate lyase, putative similar	ACLB-1	AT3G06650	1.19	0.25	2.35	0.05255128	0.3510	-4.41
262513_at	unknown protein ; supported by cD	---	AT1G34270	1.22	0.28	2.35	0.0525601	0.3510	-4.41
252714_x_at	putative protein p97 homologous p	---	AT3G43880	-1.16	-0.21	-2.35	0.05261339	0.3512	-4.41
256785_at	unknown protein ;supported by ful	PRA8	AT3G13720	1.30	0.38	2.35	0.05263975	0.3513	-4.41
253945_at	putative protein gene F23F1.15 A	---	AT4G27050	1.16	0.22	2.35	0.05267231	0.3513	-4.41
259065_at	unknown protein similar to putative	GLR1.4	AT3G07520	1.39	0.48	2.35	0.05267014	0.3513	-4.41
262127_at	hypothetical protein predicted by g	---	AT1G52550	1.29	0.37	2.35	0.05276021	0.3518	-4.41
244990_s_at	hypothetical protein	---	---	1.53	0.62	2.35	0.05277248	0.3518	-4.41
259226_at	unknown protein similar to hypoth	---	AT3G07700	-1.27	-0.35	-2.35	0.05278881	0.3518	-4.41
245572_at	hypothetical protein	PPD2	AT4G14720	1.39	0.47	2.34	0.05293084	0.3520	-4.41
253095_at	putative protein ribonuclease III, B	---	AT4G37510	1.21	0.28	2.35	0.05289126	0.3520	-4.41
266649_at	putative aquaporin (tonoplast intrin	TIP4;1	AT2G25810	-1.18	-0.24	-2.34	0.0529322	0.3520	-4.41
258981_at	hypothetical protein predicted by g	---	AT3G08880	1.17	0.22	2.34	0.05291258	0.3520	-4.41
251754_at	beta-1,3-glucanase - like protein b	---	AT3G55780	-1.24	-0.30	-2.35	0.05289054	0.3520	-4.41

260549_at	Expressed protein ; supported by f	---	AT2G43535	-1.77	-0.82	-2.34	0.05291591	0.3520	-4.41
250211_at	unknown protein ; supported by cl	---	AT5G13880	1.20	0.27	2.34	0.05293758	0.3520	-4.41
257272_at	unknown protein ; supported by cl	---	AT3G28130	-1.23	-0.29	-2.34	0.05295205	0.3520	-4.41
245785_at	cellulose synthase catalytic subun	ATCSLD6	AT1G32180	-1.21	-0.27	-2.34	0.05302822	0.3524	-4.42
263528_at	putative peroxidase	---	AT2G24800	-1.22	-0.29	-2.34	0.05305259	0.3525	-4.42
249691_at	translation releasing factor RF-2 ;s	HCF109	AT5G36170	1.17	0.22	2.34	0.05308637	0.3526	-4.42
259225_at	putative small nuclear ribonucleopr	---	AT3G07590	1.62	0.69	2.34	0.05312059	0.3527	-4.42
246961_at	unknown protein	---	AT5G24710	-1.40	-0.48	-2.34	0.0531775	0.3530	-4.42
254210_at	putative protein zinc finger protein	---	AT4G23450	1.45	0.54	2.34	0.053267	0.3534	-4.42
254923_at	protein phosphatase type 1 PP1B(	TOPP7	AT4G11240	1.27	0.34	2.34	0.0532835	0.3534	-4.42
248817_at	putative protein strong similarity to	---	AT5G47020	1.24	0.31	2.34	0.05327861	0.3534	-4.42
259896_at	unknown protein ;supported by full	---	AT1G71500	1.22	0.29	2.34	0.0533125	0.3535	-4.42
263351_at	hypothetical protein predicted by g	---	AT2G22120	1.16	0.21	2.34	0.05335043	0.3537	-4.42
262499_at	unknown protein EST gb|T41993 c	---	AT1G21770	1.29	0.37	2.34	0.05339271	0.3538	-4.42
266450_s_at	hypothetical protein predicted by g	---	AT2G43190	1.29	0.37	2.34	0.05340541	0.3538	-4.42
246426_at	ovule development protein aintegu	BBM	AT5G17430	-1.18	-0.23	-2.34	0.05345042	0.3539	-4.42
250113_at	putative protein similar to unknown	FRL1	AT5G16320	-1.20	-0.26	-2.34	0.05343938	0.3539	-4.42
258199_at	unknown protein	---	AT3G14030	-1.20	-0.26	-2.34	0.05352229	0.3543	-4.42
261893_at	unknown protein ;supported by full	---	AT1G80690	-1.20	-0.27	-2.34	0.05360126	0.3545	-4.43
254696_at	hypothetical protein	---	AT4G17930	-1.17	-0.23	-2.34	0.05358849	0.3545	-4.43
254406_at	putative transposable element rev	---	---	-1.17	-0.23	-2.34	0.05356588	0.3545	-4.43
262426_s_at	cytochrome P450, putative similar	---	AT1G47625 /	1.28	0.35	2.34	0.05361091	0.3545	-4.43
259048_at	DegP protease contains similarity t	DegP7	AT3G03380	-1.21	-0.27	-2.34	0.05362824	0.3545	-4.43
251562_at	putative protein hypothetical prote	---	AT3G57890	-1.19	-0.25	-2.34	0.05365688	0.3546	-4.43
266886_at	Expressed protein ; supported by f	---	AT2G44745	-1.25	-0.32	-2.33	0.05368572	0.3546	-4.43
259887_at	putative protein kinase similar to pr	---	AT1G76360	-1.21	-0.28	-2.33	0.05372916	0.3547	-4.43
264739_at	hypothetical protein predicted by g	---	AT1G62260	-1.24	-0.31	-2.33	0.05371684	0.3547	-4.43
260157_at	unknown protein ; supported by cl	---	AT1G52930	1.51	0.60	2.33	0.05388913	0.3550	-4.43
261607_at	unknown protein similar to putative	AtCXE5	AT1G49660	1.63	0.70	2.33	0.05385256	0.3550	-4.43
247676_at	putative protein RNaseP protein p	---	AT5G59980	-1.39	-0.47	-2.33	0.05390805	0.3550	-4.43
246644_at	putative protein	---	AT5G35100	1.31	0.39	2.33	0.05386725	0.3550	-4.43
256717_at	hypothetical protein predicted by g	---	AT2G34110	-1.24	-0.31	-2.33	0.05387271	0.3550	-4.43
263665_at	putative putative 60S ribosomal pr	---	AT1G04480	1.40	0.49	2.33	0.05380977	0.3550	-4.43
254501_at	hypothetical protein	PTAC14	AT4G20130	1.37	0.46	2.33	0.05391558	0.3550	-4.43
261467_at	unknown protein	VOZ1	AT1G28520	-1.32	-0.40	-2.33	0.05388001	0.3550	-4.43

247788_at	putative protein carbohydrate kina	---	AT5G58730	-1.35	-0.44	-2.33	0.05379401	0.3550	-4.43
250950_at	putative protein	ATEXO70A	AT5G03540	1.26	0.33	2.33	0.05396631	0.3551	-4.43
254247_at	putative protein receptor protein k	---	AT4G23260	-1.48	-0.56	-2.33	0.05397546	0.3551	-4.43
249871_at	putative protein similar to unknown	---	AT5G23110	1.30	0.38	2.33	0.05396825	0.3551	-4.43
258058_at	unknown protein	---	AT3G28980	-1.21	-0.27	-2.33	0.05401904	0.3553	-4.43
265647_at	hypothetical protein predicted by g	---	AT2G27410	-1.20	-0.26	-2.33	0.05407164	0.3555	-4.44
255131_at	putative protein hypothetical prote	---	AT4G08280	1.20	0.26	2.33	0.05408337	0.3555	-4.44
263912_at	starch branching enzyme II	SBE2.1	AT2G36390	-1.28	-0.35	-2.33	0.05415421	0.3556	-4.44
247449_at	putative protein swelling-induced	---	AT5G62290	1.38	0.47	2.33	0.05425654	0.3556	-4.44
246451_at	Inositol 1,3,4-Trisphosphate 5/6 ki	---	AT5G16760	-1.16	-0.22	-2.33	0.05414315	0.3556	-4.44
252241_at	putative protein CND41, chloropla	---	AT3G50050	1.21	0.27	2.33	0.05421394	0.3556	-4.44
245911_at	oligosaccharyl transferase STT3-l	STT3A	AT5G19690	1.17	0.23	2.33	0.05428056	0.3556	-4.44
248898_at	outward rectifying potassium chan	KCO2	AT5G46370	-1.24	-0.31	-2.33	0.05424687	0.3556	-4.44
251129_at	putative protein predicted protein,	---	AT5G01150	-1.20	-0.27	-2.33	0.05420411	0.3556	-4.44
264981_at	valyl- tRNA synthetase, putative s	---	AT1G27160	-1.23	-0.29	-2.33	0.05428498	0.3556	-4.44
267501_at	unknown protein	---	AT2G45540	1.27	0.34	2.33	0.0541424	0.3556	-4.44
250749_at	26S proteasome regulatory subuni	RPN8A	AT5G05780	1.17	0.23	2.33	0.05425708	0.3556	-4.44
253034_at	calcium-dependent protein kinase	CPK26	AT4G38230	1.22	0.28	2.33	0.05423603	0.3556	-4.44
263119_at	hypothetical protein predicted by g	---	AT1G03110	1.30	0.38	2.33	0.05426706	0.3556	-4.44
266656_at	putative CCCH-type zinc finger pro	ATCTH	AT2G25900	1.30	0.38	2.33	0.05430967	0.3557	-4.44
262231_at	putative receptor protein similar to	---	AT1G68740	1.56	0.64	2.33	0.05435798	0.3557	-4.44
257407_at	unknown protein	---	AT1G27100	1.20	0.26	2.33	0.05434688	0.3557	-4.44
265266_at	putative RNA-binding protein ; sup	AML2	AT2G42890	1.25	0.33	2.33	0.05434891	0.3557	-4.44
251257_at	ADP-ribosylation factor-like protei	ATARFA1E	AT3G62290	1.30	0.38	2.33	0.05440474	0.3558	-4.44
255027_at	hypothetical protein F21E10.5 Ara	---	AT4G09880	-1.21	-0.28	-2.33	0.05440067	0.3558	-4.44
259983_at	3-hydroxy-3-methylglutaryl CoA re	HMG1	AT1G76490	1.22	0.29	2.33	0.0544248	0.3558	-4.44
246521_at	N2,N2-dimethylguanine tRNA met	---	AT5G15810	1.27	0.35	2.32	0.05453561	0.3558	-4.44
254444_at	putative protein riboflavin biosynth	---	AT4G20960	1.40	0.49	2.32	0.05451119	0.3558	-4.44
262793_at	putative cytochrome P450 monoo	CYP71B7	AT1G13110	-1.55	-0.63	-2.32	0.05454977	0.3558	-4.44
253719_at	putative protein, fragment prolidas	---	AT4G29490	-1.16	-0.21	-2.32	0.05445884	0.3558	-4.44
260971_at	hypothetical protein predicted by g	---	AT1G53620	-1.19	-0.25	-2.32	0.05454382	0.3558	-4.44
251152_at	RAN GTPase activating protein 1 p	RANGAP1	AT3G63130	1.33	0.41	2.32	0.05448772	0.3558	-4.44
255834_at	putative RNA-binding protein	---	AT2G33410	-1.15	-0.21	-2.32	0.05448495	0.3558	-4.44
260462_at	ZIP4, a putative zinc transporter p	ZIP4	AT1G10970	-1.41	-0.49	-2.32	0.0545166	0.3558	-4.44
252294_at	60S ribosomal protein L13, BBC1	ATBBC1	AT3G49010	1.57	0.65	2.32	0.05456553	0.3558	-4.44

253119_at	Expressed protein ; supported by f	---	AT4G35980	1.18	0.24	2.32	0.05458168	0.3558	-4.44
251029_at	putative protein gene product of s	---	AT5G02050	-1.47	-0.56	-2.32	0.05461658	0.3559	-4.45
260262_at	hypothetical protein similar to hyp	---	AT1G68470	-1.60	-0.67	-2.32	0.0546609	0.3560	-4.45
245864_at	hypothetical protein predicted by g	---	AT1G58070	1.38	0.46	2.32	0.05467388	0.3560	-4.45
263791_at	putative plasma membrane proton	AHA5	AT2G24520	-1.35	-0.43	-2.32	0.0546463	0.3560	-4.45
251062_at	putative protein putative proteins -	OFP1	AT5G01840	-1.21	-0.28	-2.32	0.05475934	0.3564	-4.45
263631_at	unknown protein ; supported by fu	---	AT2G04900	1.17	0.23	2.32	0.05476923	0.3564	-4.45
248477_at	putative protein similar to unknown	---	AT5G50900	-1.26	-0.33	-2.32	0.05485716	0.3568	-4.45
262952_at	hypothetical protein predicted by g	---	AT1G75770	1.25	0.33	2.32	0.05485981	0.3568	-4.45
264064_at	hypothetical protein predicted by g	---	AT2G27900	-1.19	-0.25	-2.32	0.05489708	0.3570	-4.45
246478_at	putative protein several hypothetic	---	AT5G15980	1.19	0.25	2.32	0.05503874	0.3570	-4.45
258072_at	unknown protein	RGS1	AT3G26090	1.17	0.23	2.32	0.05503154	0.3570	-4.45
261314_at	putative GTP-binding protein simila	---	AT1G52980	1.32	0.40	2.32	0.05501078	0.3570	-4.45
256920_at	hypothetical protein predicted by g	---	AT3G18980	1.17	0.23	2.32	0.05494644	0.3570	-4.45
265959_at	unknown protein ;supported by ful	---	AT2G37240	-1.49	-0.58	-2.32	0.05491442	0.3570	-4.45
255207_at	Expressed protein ; supported by f	---	AT4G07515	-1.15	-0.20	-2.32	0.05499752	0.3570	-4.45
250379_at	transcription factor like protein tra	TINY2	AT5G11590	-1.18	-0.24	-2.32	0.05502167	0.3570	-4.45
245789_at	hypothetical protein similar to hypo	---	AT1G32090	1.46	0.55	2.32	0.05497966	0.3570	-4.45
256147_at	hypothetical protein predicted by g	---	AT1G55080	-1.26	-0.34	-2.32	0.05494965	0.3570	-4.45
265318_at	putative D-amino acid dehydrogen	---	AT2G22650	1.30	0.38	2.32	0.0550594	0.3570	-4.45
246231_at	putative protein	---	AT4G37080	1.29	0.37	2.32	0.05507301	0.3570	-4.45
246099_at	blue copper binding protein ;suppo	ATBCB	AT5G20230	1.41	0.49	2.32	0.05512189	0.3570	-4.45
249969_at	putative protein glycine-rich protei	---	AT5G19090	1.41	0.50	2.32	0.05512707	0.3570	-4.45
248313_at	putative protein contains similarity	---	AT5G52580	1.16	0.22	2.32	0.05512597	0.3570	-4.45
247768_at	I-box binding factor - like protein I-	---	AT5G58900	-1.75	-0.81	-2.32	0.05514662	0.3571	-4.45
246205_at	hypothetical protein ; supported by	---	AT4G36970	1.42	0.51	2.32	0.05519402	0.3573	-4.46
247007_at	porin-like protein ;supported by ful	VDAC2	AT5G67500	-1.26	-0.33	-2.31	0.05525582	0.3576	-4.46
248069_at	unknown protein	---	AT5G55650	-1.21	-0.28	-2.31	0.05527557	0.3576	-4.46
253413_at	putative protein Fe(II) transport pr	ZIP9	AT4G33020	1.14	0.19	2.31	0.05529704	0.3576	-4.46
259289_at	hypothetical protein predicted by g	---	AT3G11350	-1.23	-0.30	-2.31	0.05530922	0.3576	-4.46
259630_at	peptide chain release factor 2, put	---	AT1G56350	-1.33	-0.42	-2.31	0.05533661	0.3577	-4.46
255128_at	putative protein glutamic acid-rich	---	AT4G08310	1.26	0.34	2.31	0.05539263	0.3579	-4.46
254023_at	putative protein hypothetical prote	---	AT4G25770	-1.24	-0.31	-2.31	0.05545608	0.3582	-4.46
251368_at	putative protein hypothetical prote	---	AT3G61380	-1.37	-0.45	-2.31	0.05551358	0.3584	-4.46
265736_at	putative ribosomal protein L7 ;sup	---	AT2G01250	1.44	0.53	2.31	0.05550512	0.3584	-4.46

250738_at	anthranilate synthase component I	ASA1	AT5G05730	-1.80	-0.84	-2.31	0.05553042	0.3584	-4.46
264733_at	phloem serpin-1, putative similar t	---	AT1G62170	-1.17	-0.22	-2.31	0.05554874	0.3584	-4.46
267419_at	putative thioredoxin	ATO1	AT2G35010	1.21	0.27	2.31	0.05557327	0.3585	-4.46
249427_at	40S ribosomal protein S9-like 40S	---	AT5G39850	1.64	0.72	2.31	0.05565083	0.3586	-4.46
246611_at	putative protein predicted proteins	MBD02	AT5G35330	1.38	0.47	2.31	0.05566327	0.3586	-4.46
248967_at	unknown protein ;supported by full	---	AT5G45350	-1.26	-0.34	-2.31	0.05561142	0.3586	-4.46
246625_at	hypothetical protein predicted by g	---	AT1G48880	-1.20	-0.27	-2.31	0.0556567	0.3586	-4.46
260133_at	ethylene-response protein, ETR1	ETR1	AT1G66340	-1.16	-0.22	-2.31	0.05566205	0.3586	-4.46
259255_at	putative glycerol-3-phosphate dehy	---	AT3G07690	1.41	0.50	2.31	0.05575538	0.3589	-4.47
259501_at	unknown protein ; supported by cD	TPL	AT1G15750	1.24	0.32	2.31	0.05575221	0.3589	-4.47
263588_s_at	unknown protein	---	AT2G25320 /	-1.20	-0.26	-2.31	0.05572469	0.3589	-4.47
250879_at	putative protein various predicted	---	AT5G04060	1.28	0.35	2.31	0.05579129	0.3590	-4.47
253793_at	myosin heavy chain - like protein (	XIH	AT4G28710	-1.17	-0.23	-2.31	0.05584572	0.3592	-4.47
264585_at	auxin-resistance protein AXR1 E1	AXR1	AT1G05180	1.16	0.21	2.31	0.05586727	0.3592	-4.47
265950_s_at	putative protein kinase contains a	---	AT2G18530 /	-1.21	-0.27	-2.31	0.05587951	0.3592	-4.47
256114_at	unknown protein ; supported by cD	---	AT1G16850	-1.82	-0.86	-2.31	0.05602277	0.3598	-4.47
245893_at	hypothetical protein ;supported by	---	AT5G09270	1.20	0.26	2.31	0.05604752	0.3598	-4.47
253531_at	putative protein tomato leucine zip	ATEXO70G	AT4G31540	-1.19	-0.25	-2.31	0.05600838	0.3598	-4.47
246269_at	putative protein	---	AT4G37110	1.47	0.56	2.31	0.05603064	0.3598	-4.47
256837_at	hypothetical protein similar to DNA	NRPD7	AT3G22900	1.38	0.46	2.31	0.05604871	0.3598	-4.47
250398_at	putative protein predicted proteins	---	AT5G11000	1.44	0.53	2.30	0.05606862	0.3599	-4.47
265515_at	hypothetical protein predicted by g	---	---	-1.19	-0.26	-2.30	0.05609614	0.3599	-4.47
251526_at	putative protein several serine/thre	---	AT3G58640	1.24	0.31	2.30	0.05612551	0.3600	-4.47
245122_at	putative dimethyladenosine transfe	---	AT2G47420	1.22	0.29	2.30	0.05618589	0.3600	-4.47
264442_at	hypothetical protein similar to lecith	---	AT1G27480	1.34	0.42	2.30	0.05620658	0.3600	-4.47
249596_s_at	glucuronosyl transferase-like prote	---	AT5G37950 /	-1.35	-0.43	-2.30	0.05617999	0.3600	-4.47
262200_at	unknown protein similar to membra	---	AT2G01070	1.26	0.33	2.30	0.05620521	0.3600	-4.47
247510_at	putative protein predicted proteins	---	AT5G62030	-1.25	-0.33	-2.30	0.05616266	0.3600	-4.47
246778_at	mevalonate kinase supported by f	MK	AT5G27450	1.23	0.30	2.30	0.05633559	0.3607	-4.48
250291_at	aspartate kinase ;supported by ful	AK-LYS1	AT5G13280	1.33	0.41	2.30	0.05633461	0.3607	-4.48
251938_at	60S RIBOSOMAL PROTEIN L12	---	AT3G53430	1.28	0.35	2.30	0.0563772	0.3607	-4.48
265212_at	putative sugar transporter protein S	---	AT1G05030	-1.20	-0.26	-2.30	0.05636671	0.3607	-4.48
261309_at	phosphoethanolamine N-methyltra	CPuORF31	AT1G48598 /	-1.37	-0.46	-2.30	0.05639308	0.3607	-4.48
252158_at	CDPK-related protein kinase	CRK	AT3G50530	1.24	0.31	2.30	0.0564398	0.3609	-4.48
248812_at	palmitoyl-protein thioesterase prec	---	AT5G47330	-2.00	-1.00	-2.30	0.05646577	0.3610	-4.48

253407_at	putative protein	---	AT4G32920	1.22	0.28	2.29	0.05692914	0.3610	-4.49
260812_at	nodulin-like protein similar to MtN2	---	AT1G43650	-1.35	-0.44	-2.29	0.05692375	0.3610	-4.49
260371_at	unknown protein ; supported by cl	---	AT1G69690	-1.61	-0.69	-2.29	0.05687599	0.3610	-4.49
250356_at	clathrin binding protein - like Af10-	---	AT5G11710	-1.15	-0.20	-2.30	0.05661298	0.3610	-4.48
249089_at	ATPase, calcium-transporting	---	AT5G44240	1.15	0.20	2.30	0.05681618	0.3610	-4.48
259192_at	unknown protein ;supported by ful	---	AT3G01740	1.24	0.32	2.30	0.05664851	0.3610	-4.48
249786_at	putative protein strong similarity to	ABIL3	AT5G24310	1.42	0.51	2.29	0.05694157	0.3610	-4.49
262284_at	hypothetical protein predicted by g	---	AT1G68670	1.32	0.40	2.30	0.05672997	0.3610	-4.48
265998_at	putative NADP-dependent glyceral	ALDH11A3	AT2G24270	-1.22	-0.28	-2.29	0.05698035	0.3610	-4.49
247844_at	ARR2 - like protein ARR2 protein,	ARR18	AT5G58080	-1.17	-0.23	-2.30	0.05682358	0.3610	-4.48
260463_at	DNA helicase isolog	RECQ4A	AT1G10930	-1.16	-0.22	-2.30	0.05681046	0.3610	-4.48
258281_at	putative shikimate kinase similar to	---	AT3G26900	1.15	0.21	2.30	0.0565674	0.3610	-4.48
252947_at	putative protein ubiquitin fusion de	KAK	AT4G38600	1.16	0.22	2.30	0.05662262	0.3610	-4.48
245387_at	nuclear RNA binding protein A-like	---	AT4G17520	1.27	0.35	2.29	0.05698529	0.3610	-4.49
267456_at	E2, ubiquitin-conjugating enzyme,	PHO2	AT2G33770	1.50	0.59	2.29	0.05700434	0.3610	-4.49
248982_at	chloroplast nucleoid DNA-binding p	---	AT5G45120	-1.22	-0.28	-2.30	0.05681835	0.3610	-4.48
248587_at	Expressed protein ; supported by f	---	AT5G49550	1.21	0.27	2.30	0.05679652	0.3610	-4.48
259552_at	hypothetical protein	---	AT1G21320	-1.23	-0.30	-2.30	0.05677098	0.3610	-4.48
254231_at	putative protein AR411 - Arabidop	WRKY53	AT4G23810	2.77	1.47	2.29	0.05700055	0.3610	-4.49
246725_at	putative protein various predicted	---	AT5G29040	-1.32	-0.40	-2.30	0.05652961	0.3610	-4.48
258667_at	hypothetical protein	---	AT3G08750	-1.19	-0.25	-2.30	0.0568629	0.3610	-4.49
249544_at	anti-silencing factor 1-like protein	ASF1B	AT5G38110	1.30	0.38	2.29	0.05689343	0.3610	-4.49
263361_at	putative senescence-associated pr	TET13	AT2G03840	-1.20	-0.27	-2.30	0.05655807	0.3610	-4.48
254892_at	putative protein other hypothetical	---	AT4G11800	-1.24	-0.31	-2.30	0.05671613	0.3610	-4.48
245533_at	putative phosphocholine cytidylyltr	CCT2	AT4G15130	-1.59	-0.67	-2.29	0.05688829	0.3610	-4.49
245394_at	hypothetical protein ;supported by	---	AT4G16450	1.28	0.35	2.30	0.05651502	0.3610	-4.48
254313_at	extensin like protein extensin like	---	AT4G22460	-1.23	-0.30	-2.30	0.05655405	0.3610	-4.48
257913_at	unknown protein ; supported by cl	LAG1	AT3G25540	1.21	0.27	2.29	0.05693946	0.3610	-4.49
254702_at	putative protein predicted protein,	---	AT4G17940	-1.22	-0.29	-2.30	0.056698	0.3610	-4.48
257205_at	putative glucosyltransferase simila	UGT88A1	AT3G16520	-1.19	-0.25	-2.29	0.05687895	0.3610	-4.49
263264_at	histone H2A ; supported by full-ler	HTA8	AT2G38810	1.38	0.47	2.29	0.05696963	0.3610	-4.49
261081_at	transformer-SR ribonucleoprotein,	---	AT1G07350	-1.34	-0.43	-2.30	0.05652867	0.3610	-4.48
249920_at	putative protein various predicted p	---	AT5G19260	1.62	0.69	2.30	0.05672428	0.3610	-4.48
267188_at	6,7-dimethyl-8-ribityllumazine synt	COS1	AT2G44050	1.20	0.26	2.29	0.05686853	0.3610	-4.49
249100_at	unknown protein	---	AT5G43560	-1.21	-0.28	-2.29	0.0570347	0.3611	-4.49

253382_at	putative protein AT.I.24, Arabidop	---	AT4G33040	-1.27	-0.34	-2.29	0.05709822	0.3612	-4.49
264657_at	putative 26S protease regulatory s	RPT5B	AT1G09100	1.19	0.25	2.29	0.05715077	0.3612	-4.49
257495_at	unknown protein	ATPDIL5-1	AT1G07960	1.23	0.30	2.29	0.05714988	0.3612	-4.49
249630_s_at	sen1-like protein SEN1 - Sacchar	---	AT5G37150	-1.16	-0.21	-2.29	0.05712078	0.3612	-4.49
251956_at	RNA-binding protein cp29 protein	CP29	AT3G53460	1.20	0.26	2.29	0.05714543	0.3612	-4.49
256285_at	hypothetical protein predicted by g	---	AT3G12510	-1.31	-0.39	-2.29	0.05709145	0.3612	-4.49
263237_at	hypothetical protein contains simila	---	AT1G10610	1.36	0.45	2.29	0.05720427	0.3612	-4.49
246818_at	putative protein crp1, Zea mays, F	EMB976	AT5G27270	1.46	0.55	2.29	0.05718958	0.3612	-4.49
250694_at	putative protein contains similarity	HAT14	AT5G06710	-1.26	-0.34	-2.29	0.05721951	0.3612	-4.49
253231_at	Nonclathrin coat protein gamma -	---	AT4G34450	1.21	0.28	2.29	0.05721092	0.3612	-4.49
250119_at	putative protein similar to unknown	---	AT5G16470	1.18	0.24	2.29	0.05729144	0.3615	-4.49
246617_at	GSH-dependent dehydroascorbate	---	AT5G36270	-1.21	-0.27	-2.29	0.05728861	0.3615	-4.49
266587_at	unknown protein ; supported by fu	---	AT2G14880	1.23	0.30	2.29	0.05732051	0.3616	-4.49
258317_at	hypothetical protein predicted by g	---	AT3G22670	1.19	0.25	2.29	0.05733263	0.3616	-4.49
261560_at	acyl CoA thioesterase, putative si	---	AT1G01710	-1.16	-0.22	-2.29	0.05735771	0.3616	-4.49
263823_s_at	AP2 domain transcription factor	---	AT2G40340	1.49	0.58	2.29	0.05740276	0.3617	-4.49
252351_at	putative protein ;supported by full-	---	AT3G48210	1.26	0.33	2.29	0.05741564	0.3617	-4.49
245896_at	putative transcriptional co-activato	KIWI	AT5G09250	1.26	0.34	2.29	0.05740565	0.3617	-4.49
267102_at	putative small nuclear ribonucleop	LIS	AT2G41500	1.22	0.28	2.29	0.05743464	0.3617	-4.50
262560_at	hypothetical protein predicted by g	---	AT1G34280	-1.23	-0.30	-2.29	0.0574782	0.3619	-4.50
262773_at	putative nuclear matrix constituent	LINC2	AT1G13220	-1.22	-0.29	-2.29	0.05754464	0.3622	-4.50
251646_at	putative protein	---	AT3G57780	-1.92	-0.94	-2.29	0.05757961	0.3623	-4.50
248473_at	small zinc finger-like protein ;supp	TIM8	AT5G50810	1.25	0.33	2.29	0.05762704	0.3624	-4.50
265863_at	putative membrane protein	VIT1	AT2G01770	-1.26	-0.34	-2.29	0.05762702	0.3624	-4.50
248487_at	ATP-dependent Clp protease ATF	ERD1	AT5G51070	1.22	0.29	2.29	0.05768003	0.3625	-4.50
247450_at	ripening-related protein - like riper	---	AT5G62350	-1.26	-0.34	-2.29	0.05767283	0.3625	-4.50
253293_at	Expressed protein ; supported by c	---	AT4G33905	-1.33	-0.42	-2.28	0.05776883	0.3629	-4.50
252059_at	E2, ubiquitin-conjugating enzyme,	UEV1D-4	AT3G52560	1.19	0.25	2.28	0.05777332	0.3629	-4.50
255431_at	putative C-type U1 snRNP similar	---	AT4G03120	1.15	0.20	2.28	0.05784285	0.3633	-4.50
248594_at	unknown protein ; supported by fu	---	AT5G49210	1.32	0.40	2.28	0.05789598	0.3634	-4.50
253524_at	predicted protein ; supported by c	---	AT4G31430	1.22	0.28	2.28	0.05790957	0.3634	-4.50
247470_at	putative protein various predicted	---	AT5G62220	1.78	0.83	2.28	0.05788424	0.3634	-4.50
266583_at	Expressed protein ; supported by c	---	AT2G46220	1.29	0.37	2.28	0.05792867	0.3634	-4.50
253313_at	putative peroxidase peroxidase A	---	AT4G33870	-1.21	-0.28	-2.28	0.05795578	0.3635	-4.50
264037_at	putative steroid sulfotransferase ;s	---	AT2G03750	-1.25	-0.32	-2.28	0.05816494	0.3640	-4.51

264990_at	unknown protein supported by cD	---	AT1G27210	-1.43	-0.52	-2.28	0.05816373	0.3640	-4.51
263448_at	putative importin (nuclear transpor	SAD2	AT2G31660	1.24	0.31	2.28	0.05812505	0.3640	-4.51
266846_at	unknown protein	---	AT2G25970	1.18	0.23	2.28	0.05812434	0.3640	-4.51
253955_at	putative DNA binding protein DNA	ATRBP45C	AT4G27000	1.32	0.40	2.28	0.05814499	0.3640	-4.51
264858_at	hypothetical protein	SNL3	AT1G24190	-1.22	-0.28	-2.28	0.05813951	0.3640	-4.51
249391_at	putative protein predicted proteins	---	AT5G40140	-1.29	-0.37	-2.28	0.05811255	0.3640	-4.51
250367_s_at	DEAD BOX RNA helicase RH15 ;	---	AT5G11170	1.20	0.27	2.28	0.05811025	0.3640	-4.51
249818_at	Expressed protein ; supported by c	TUB8	AT5G23860	-1.40	-0.48	-2.27	0.05855168	0.3640	-4.51
255795_at	putative calcium-binding EF-hand	RD20	AT2G33380	-1.57	-0.65	-2.28	0.05827443	0.3640	-4.51
250555_at	putative protein ferredoxin (2Fe-2S	---	AT5G07950	1.30	0.38	2.28	0.05844149	0.3640	-4.51
248952_at	putative protein similar to unknown	---	AT5G45410	-1.23	-0.29	-2.28	0.0582991	0.3640	-4.51
255018_at	hypothetical protein ; supported by	---	AT4G10090	1.27	0.34	2.28	0.05834949	0.3640	-4.51
267446_s_at	putative tyrosyl-tRNA synthetase	---	AT1G28350	1.18	0.23	2.28	0.05843796	0.3640	-4.51
253633_at	putative protein tetratricopeptide r	---	AT4G30480	1.24	0.31	2.28	0.05829416	0.3640	-4.51
249473_at	His-Asp Phosphotransfer Signal Tr	AHP3	AT5G39340	1.22	0.28	2.27	0.05854552	0.3640	-4.51
254100_at	hypothetical protein ;supported by	---	AT4G25020	-1.41	-0.49	-2.28	0.05838423	0.3640	-4.51
258933_at	unknown protein similar to unknov	---	AT3G09980	-1.20	-0.27	-2.27	0.05854725	0.3640	-4.51
258900_at	putative 60S ribosomal protein L18	RPL18	AT3G05590	1.39	0.47	2.28	0.05850607	0.3640	-4.51
259024_at	hypothetical protein predicted by g	---	---	-1.27	-0.34	-2.28	0.05827895	0.3640	-4.51
258566_at	putative glutamate receptor (GLR1	GLR1.1	AT3G04110	-1.38	-0.46	-2.28	0.0583627	0.3640	-4.51
261059_at	transcription factor TINY, putative	---	AT1G01250	-1.29	-0.36	-2.28	0.05843104	0.3640	-4.51
264926_at	cytochrome b5, putative similar to	CB5LP	AT1G60660	1.20	0.26	2.28	0.05846385	0.3640	-4.51
267415_at	putative translation initiation factor	---	AT2G34970	-1.17	-0.22	-2.28	0.05840318	0.3640	-4.51
247083_at	unknown protein	---	AT5G66290	1.18	0.24	2.28	0.05849032	0.3640	-4.51
257739_at	unknown protein	---	AT3G27470	-1.28	-0.36	-2.28	0.05834207	0.3640	-4.51
261981_at	unknown protein	---	AT1G33811	-1.80	-0.84	-2.27	0.05855422	0.3640	-4.51
254914_at	peroxidase ATP19a	---	AT4G11290	-2.30	-1.20	-2.27	0.05856584	0.3640	-4.51
261320_at	unknown protein ; supported by cD	---	AT1G53120	1.17	0.23	2.28	0.0584278	0.3640	-4.51
250272_at	callose synthase catalytic subunit	ATGSL12	AT5G13000	1.25	0.33	2.28	0.0583011	0.3640	-4.51
264191_at	integral membrane protein, putativ	---	AT1G54730	1.33	0.41	2.28	0.05846056	0.3640	-4.51
265923_at	putative protein kinase contains a	---	AT2G18470	-1.16	-0.22	-2.28	0.05843745	0.3640	-4.51
259954_at	cytochrome P450, putative similar	CYP721A1	AT1G75130	1.33	0.42	2.28	0.05834524	0.3640	-4.51
253937_at	putative NPK1-related protein kina	MAPKKK16	AT4G26890	1.37	0.46	2.27	0.05858856	0.3640	-4.51
244934_at	NADH dehydrogenase ND6	---	---	-1.46	-0.55	-2.27	0.05862239	0.3640	-4.52
258726_at	Expressed protein ; supported by f	---	AT3G11745	1.18	0.24	2.27	0.05862253	0.3640	-4.52

255134_at	putative protein	---	AT4G08330	1.22	0.28	2.27	0.0586366	0.3640	-4.52
247814_at	polyneuridine aldehyde esterase-li	MES18	AT5G58310	-2.18	-1.12	-2.27	0.05877515	0.3643	-4.52
253187_at	putative zinc-finger protein PEThy	---	AT4G35280	-1.16	-0.22	-2.27	0.05877072	0.3643	-4.52
267164_at	CER1-like protein may be involved	---	AT2G37700	-1.20	-0.26	-2.27	0.0587529	0.3643	-4.52
267540_at	hypothetical protein predicted by g	---	AT2G32760	-1.17	-0.23	-2.27	0.05872636	0.3643	-4.52
264793_at	unknown protein similar to beta-ga	---	AT1G08660	1.31	0.38	2.27	0.05875904	0.3643	-4.52
257005_at	hypothetical protein predicted by g	---	AT3G14190	-1.24	-0.31	-2.27	0.05870207	0.3643	-4.52
249395_at	putative protein	---	AT5G40190	1.16	0.22	2.27	0.05879377	0.3643	-4.52
252308_at	putative protein sugar transporter	---	AT3G49310	1.19	0.25	2.27	0.05881859	0.3644	-4.52
251011_at	putative protein histone H2A, garc	HTA12	AT5G02560	1.18	0.23	2.27	0.05887413	0.3644	-4.52
257891_at	hypothetical protein predicted by g	RFC3	AT3G17170	1.33	0.41	2.27	0.05897376	0.3644	-4.52
250330_at	putative protein	---	AT5G11810	-1.22	-0.29	-2.27	0.05899918	0.3644	-4.52
261286_at	unknown protein ; supported by cD	---	AT1G35780	1.26	0.34	2.27	0.05899815	0.3644	-4.52
263416_at	hypothetical protein contains prote	---	AT2G17170	-1.20	-0.26	-2.27	0.05892278	0.3644	-4.52
256683_at	unknown protein ; supported by cD	---	AT3G52220	-1.16	-0.22	-2.27	0.05884164	0.3644	-4.52
257578_x_at	unknown protein similar to hypothe	---	AT3G30160	-1.17	-0.23	-2.27	0.05894574	0.3644	-4.52
256983_at	chaperonin 60 beta, putative very	---	AT3G13470	-1.57	-0.65	-2.27	0.05896957	0.3644	-4.52
259303_at	hypothetical protein predicted by g	---	AT3G05130	1.14	0.19	2.27	0.05899175	0.3644	-4.52
265174_s_at	polygalacturonase, putative simila	---	AT1G23460 /	1.31	0.39	2.27	0.05888855	0.3644	-4.52
266798_at	putative embryo-abundant protein	AtbZIP6	AT2G22850	-1.43	-0.51	-2.27	0.05890527	0.3644	-4.52
246809_s_at	SAR DNA-binding protein - like SA	---	AT5G27120 /	1.15	0.20	2.27	0.05912859	0.3649	-4.52
260793_at	unknown protein ;supported by full	---	AT1G06190	1.20	0.26	2.27	0.05910475	0.3649	-4.52
263681_at	hypothetical protein predicted by g	ORC6	AT1G26840	1.30	0.37	2.27	0.05912593	0.3649	-4.52
253952_at	ubiquitin-like protein ubiquitin-like	SUMO1	AT4G26840	1.19	0.26	2.27	0.05917425	0.3651	-4.52
248684_at	Expressed protein ; supported by f	DIR1	AT5G48485	-1.70	-0.77	-2.27	0.05918727	0.3651	-4.52
250830_at	putative protein similar to unknown	---	AT5G04910	1.27	0.35	2.27	0.05926564	0.3652	-4.53
247219_at	COP1-interacting protein CIP8 ; s	CIP8	AT5G64920	1.20	0.27	2.27	0.05924783	0.3652	-4.53
248009_at	transcription factor-like; similar to C	CSN6A	AT5G56280	-1.20	-0.26	-2.27	0.05926183	0.3652	-4.53
255257_at	score=526.5, E=1.9e-154, N=3 ;s	UBQ11	AT4G05050	-1.17	-0.22	-2.27	0.05927853	0.3652	-4.53
246124_at	putative protein acyl-protein thioes	---	AT5G20060	1.15	0.20	2.26	0.05944408	0.3653	-4.53
262525_at	putative cytochrome P450 41% ide	CYP72C1	AT1G17060	1.37	0.45	2.27	0.0593509	0.3653	-4.53
266671_at	anthranilate synthase, alpha subu	ASA2	AT2G29690	1.22	0.29	2.27	0.05936138	0.3653	-4.53
249386_at	disease resistance -like protein dc	---	AT5G40060	-1.20	-0.26	-2.26	0.05945196	0.3653	-4.53
254796_at	putative protein protein kinase hor	---	AT4G13000	-1.24	-0.31	-2.26	0.05942898	0.3653	-4.53
260397_at	hypothetical protein predicted by g	---	AT1G69680	-1.20	-0.27	-2.27	0.05938488	0.3653	-4.53

262605_at	hypothetical protein Strong similari	---	AT1G15170	1.80	0.85	2.27	0.05937493	0.3653	-4.53
245353_at	hypothetical protein ;supported by	---	AT4G16000	1.41	0.50	2.27	0.05931666	0.3653	-4.53
264363_at	hypothetical protein predicted by g	---	AT1G03170	1.22	0.29	2.26	0.05941308	0.3653	-4.53
250140_at	putative protein	DRM2	AT5G14620	-1.26	-0.33	-2.26	0.05939975	0.3653	-4.53
260129_at	hypothetical protein similar to vanil	---	AT1G36380	1.17	0.23	2.26	0.05961168	0.3660	-4.53
260249_s_at	unknown protein similar to unknow	---	AT1G74280	1.25	0.32	2.26	0.05961402	0.3660	-4.53
261928_at	uclacyanin II, putative similar to uc	---	AT1G22480	-1.31	-0.39	-2.26	0.05958195	0.3660	-4.53
245010_at	NADH dehydrogenase subunit	---	---	-1.23	-0.30	-2.26	0.05968482	0.3663	-4.53
261333_at	hypothetical protein predicted by g	---	AT1G44910	1.31	0.39	2.26	0.0596915	0.3663	-4.53
251041_at	ubiquitin-protein ligase E3-alpha -	PRT6	AT5G02310	-1.28	-0.36	-2.26	0.05972947	0.3664	-4.53
249836_at	unknown protein ;supported by ful	HMGB6	AT5G23420	1.47	0.56	2.26	0.05973667	0.3664	-4.53
245828_at	transcription factor, putative simila	VIM1	AT1G57820	1.24	0.31	2.26	0.05976235	0.3664	-4.53
265504_at	putative Ta11-like non-LTR retroel	---	---	-1.21	-0.27	-2.26	0.05979929	0.3665	-4.54
254012_at	putative ribosomal protein riboson	---	AT4G26230	1.42	0.51	2.26	0.05978564	0.3665	-4.53
264434_at	hypothetical protein predicted by g	---	AT1G10340	1.85	0.89	2.26	0.05981615	0.3665	-4.54
246893_at	PHD finger protein - like PHD fing	---	AT5G25520	-1.15	-0.20	-2.26	0.05988244	0.3668	-4.54
251742_at	putative protein kinase serine thre	---	AT3G56050	-1.19	-0.25	-2.26	0.05996412	0.3669	-4.54
257474_at	DNA-3-methyladenine glycosidase	---	AT1G80850	1.23	0.29	2.26	0.05996699	0.3669	-4.54
267140_at	putative GT-1-like transcription fac	---	AT2G38250	-1.39	-0.47	-2.26	0.05994866	0.3669	-4.54
254251_at	serine/threonine kinase - like prote	---	AT4G23300	-1.25	-0.32	-2.26	0.05992997	0.3669	-4.54
260214_at	hypothetical protein contains Pfam	---	AT1G74510	-1.19	-0.25	-2.26	0.05999745	0.3670	-4.54
258725_at	putative RNA helicase similar to F	---	AT3G09620	-1.17	-0.23	-2.26	0.0600344	0.3671	-4.54
261278_at	hypothetical protein predicted by g	DGL	AT1G05800	-1.18	-0.24	-2.26	0.0601489	0.3677	-4.54
260598_at	unknown protein	---	AT1G55930	1.30	0.38	2.26	0.06021791	0.3681	-4.54
257506_at	auxin-induced protein, putative sir	---	AT1G29440	1.93	0.95	2.25	0.06026688	0.3683	-4.54
265542_at	putative SNF2 subfamily transcript	SYD	AT2G28290	1.17	0.22	2.25	0.06032993	0.3685	-4.54
263544_at	putative ADP-glucose pyrophosph	APL4	AT2G21590	-1.24	-0.30	-2.25	0.06039254	0.3687	-4.54
266038_at	putative ABC transporter	ATMRP11	AT2G07680	1.39	0.48	2.25	0.06039897	0.3687	-4.55
266645_at	hypothetical protein	---	AT2G29880	-1.17	-0.23	-2.25	0.06038285	0.3687	-4.54
247654_at	cytoplasmic ribosomal protein S15	---	AT5G59850	1.57	0.65	2.25	0.0604524	0.3687	-4.55
261494_at	homeobox transcription factor Ho	HB-1	AT1G28420	-1.23	-0.29	-2.25	0.06044765	0.3687	-4.55
249275_at	polygalacturonase-like protein	---	AT5G41870	1.22	0.28	2.25	0.06044613	0.3687	-4.55
255668_s_at	predicted protein ; supported by fu	---	AT4G00238	1.26	0.33	2.25	0.06047157	0.3687	-4.55
250268_s_at	putative protein putative secreted	---	AT5G12950	1.28	0.36	2.25	0.06051568	0.3689	-4.55
258094_at	putative cytochrome P450 similar t	CYP72A15	AT3G14690	1.21	0.28	2.25	0.06068526	0.3694	-4.55

249164_at	U2 snRNP auxiliary factor, small s	U2AF35B	AT5G42820	1.23	0.30	2.25	0.06068705	0.3694	-4.55
245770_at	hypothetical protein predicted by g	---	AT1G30240	-1.36	-0.44	-2.25	0.06062927	0.3694	-4.55
262593_at	putative ubiquinol--cytochrome-c re	---	AT1G15120	1.33	0.42	2.25	0.06070422	0.3694	-4.55
266193_at	unknown protein	---	AT2G39080	1.23	0.30	2.25	0.06071371	0.3694	-4.55
265142_at	unknown protein	DABB1	AT1G51360	1.17	0.23	2.25	0.06070997	0.3694	-4.55
260726_at	signal recognition particle 19 kDa	---	AT1G48160	1.28	0.35	2.25	0.06068577	0.3694	-4.55
253977_at	putative protein various Caenorhat	---	AT4G26630	-1.31	-0.39	-2.25	0.06078436	0.3696	-4.55
258345_at	unknown protein	---	AT3G22845	1.18	0.24	2.25	0.06082159	0.3696	-4.55
249966_at	putative protein COLD-INDUCIBL	---	AT5G19030	1.41	0.50	2.25	0.06077103	0.3696	-4.55
267225_at	hypothetical protein predicted by g	---	AT2G44000	-1.20	-0.26	-2.25	0.06082103	0.3696	-4.55
250940_at	putative protein	---	AT5G03310	-1.17	-0.22	-2.25	0.06082835	0.3696	-4.55
247784_at	subtilisin-like serine protease conta	---	AT5G58810	-1.18	-0.24	-2.25	0.06088147	0.3697	-4.55
256714_at	cysteine proteinase contains simila	---	AT2G34080	-1.23	-0.29	-2.25	0.060879	0.3697	-4.55
252985_at	putative protein Niemann-Pick C d	---	AT4G38350	-1.19	-0.25	-2.25	0.06100322	0.3704	-4.55
257829_at	unknown protein	SNM1	AT3G26680	1.38	0.46	2.25	0.06103989	0.3704	-4.56
246515_at	putative protein unusual floral orga	---	AT5G15710	-1.15	-0.20	-2.25	0.06103152	0.3704	-4.56
266824_at	homeodomain transcription factor (	HAT9	AT2G22800	-1.18	-0.24	-2.25	0.0611037	0.3705	-4.56
254349_at	hypothetical protein	---	AT4G22250	1.22	0.29	2.25	0.06110259	0.3705	-4.56
266707_at	hypothetical protein predicted by g	---	AT2G03310	-1.18	-0.24	-2.25	0.06107225	0.3705	-4.56
257794_at	hypothetical protein predicted by g	---	AT3G27050	1.27	0.34	2.24	0.06119345	0.3709	-4.56
256808_at	unknown protein	ALY3	AT3G21430	1.16	0.22	2.24	0.06123767	0.3710	-4.56
250709_at	putative protein similar to unknown	LBD33	AT5G06080	-1.19	-0.26	-2.24	0.06127239	0.3710	-4.56
261014_at	unknown protein ;supported by full	---	AT1G26460	-1.20	-0.26	-2.24	0.06127195	0.3710	-4.56
258081_at	Expressed protein ; supported by f	---	AT3G26085	-1.20	-0.26	-2.24	0.06125672	0.3710	-4.56
255872_at	putative protein kinase contains a	SIP4	AT2G30360	-1.58	-0.66	-2.24	0.06134073	0.3712	-4.56
262539_at	unknown protein Location of est 13	---	AT1G17200	-1.30	-0.38	-2.24	0.0613985	0.3712	-4.56
262985_s_at	60s ribosomal protein l27a. similar	RPL27AB	AT1G23290	1.35	0.44	2.24	0.06135757	0.3712	-4.56
249988_at	putative protein predicted proteins	---	AT5G18310	1.26	0.33	2.24	0.0614307	0.3712	-4.56
258820_at	putative tryptophanyl-tRNA synthe	---	AT3G04600	1.17	0.22	2.24	0.06142473	0.3712	-4.56
266483_at	unknown protein ;supported by ful	CRR6	AT2G47910	1.23	0.30	2.24	0.06141978	0.3712	-4.56
260492_at	putative polygalacturonase	PGAZAT	AT2G41850	-1.29	-0.37	-2.24	0.06143468	0.3712	-4.56
255269_at	putative protein various predicted	---	AT4G05240	1.20	0.26	2.24	0.0614065	0.3712	-4.56
251502_at	putative protein several hypothetic	---	AT3G59130	-1.17	-0.23	-2.24	0.06153167	0.3716	-4.56
267639_at	putative squamosa-promoter bindi	SPL9	AT2G42200	-1.17	-0.23	-2.24	0.0615185	0.3716	-4.56
250884_at	signal recognition particle 54CP pr	CPSRP54	AT5G03940	1.18	0.24	2.24	0.06163297	0.3719	-4.57

264556_at	putative transcription factor contai	MYB61	AT1G09540	1.15	0.21	2.24	0.06162208	0.3719	-4.56
267323_at	unknown protein	---	AT2G19340	1.19	0.26	2.24	0.06161177	0.3719	-4.56
265443_at	beta-expansin ;supported by full-le	ATEXPB1	AT2G20750	1.27	0.35	2.24	0.06170595	0.3722	-4.57
247396_at	putative protein predicted proteins	---	AT5G62930	1.17	0.22	2.24	0.06171417	0.3722	-4.57
247459_at	putative protein embryo-specific p	---	AT5G62200	1.20	0.26	2.24	0.06175599	0.3724	-4.57
265702_at	putative purple acid phosphatase c	PAP9	AT2G03450	1.22	0.29	2.24	0.0618122	0.3724	-4.57
262867_at	hypothetical protein predicted by g	---	AT1G64960	1.21	0.27	2.24	0.06182999	0.3724	-4.57
255869_at	unknown protein	---	AT2G30270	1.22	0.29	2.24	0.061825	0.3724	-4.57
249158_at	electron transfer flavoprotein beta-	ETFBETA	AT5G43430	1.17	0.22	2.24	0.06178199	0.3724	-4.57
266934_at	unknown protein	---	AT2G18900	-1.22	-0.29	-2.24	0.06185636	0.3724	-4.57
257201_at	unknown protein	---	AT3G23740	1.23	0.29	2.24	0.06186534	0.3724	-4.57
253886_at	cytochrome P450 - like protein cyt	CYP709B3	AT4G27710	-1.18	-0.24	-2.24	0.0619194	0.3725	-4.57
252295_at	signal recognition particle subunit	---	AT3G49100	1.28	0.36	2.24	0.06190662	0.3725	-4.57
252878_at	mitochondrial carrier - like protein	SAMC1	AT4G39460	1.20	0.26	2.24	0.06193767	0.3725	-4.57
267569_at	putative photosystem II oxygen-ev	PSBP-2	AT2G30790	-1.37	-0.45	-2.24	0.06193637	0.3725	-4.57
245066_at	putative serine/threonine protein pl	TOPP4	AT2G39840	-1.21	-0.28	-2.24	0.06195175	0.3725	-4.57
261455_at	unknown protein ;supported by full	---	AT1G21070	1.34	0.42	2.24	0.0620059	0.3727	-4.57
263422_s_at	putative ubiquitin-like protein ; sup	---	AT2G17190 /	1.17	0.22	2.24	0.06203205	0.3727	-4.57
260798_at	unknown protein contains similarity	---	AT1G78280	-1.33	-0.42	-2.23	0.0620519	0.3728	-4.57
257250_at	transfactor, putative similar to GB:	---	AT3G24120	1.21	0.27	2.23	0.06210462	0.3728	-4.57
264081_at	putative RING zinc finger transcrip	---	AT2G28540	-1.23	-0.30	-2.23	0.06210232	0.3728	-4.57
264381_at	putative ribonuclease large subun	---	AT2G25100	1.31	0.39	2.23	0.06208586	0.3728	-4.57
264065_at	hypothetical protein predicted by g	---	AT2G27900	-1.21	-0.28	-2.23	0.06217026	0.3728	-4.57
266458_at	unknown protein ;supported by ful	---	AT2G47710	-1.17	-0.22	-2.23	0.06220254	0.3728	-4.57
249424_s_at	hypothetical protein ; supported by	---	AT5G39800 /	1.23	0.29	2.23	0.06219734	0.3728	-4.57
260970_at	unknown protein	---	AT1G53640	-1.22	-0.29	-2.23	0.06219944	0.3728	-4.57
251673_at	beta-1,3-glucanase	BG3	AT3G57240	5.53	2.47	2.23	0.06220444	0.3728	-4.57
248881_at	unknown protein ;supported by ful	---	AT5G46020	1.16	0.21	2.23	0.06221032	0.3728	-4.57
260489_at	hypothetical protein ; supported by	---	AT1G51610	-1.19	-0.25	-2.23	0.0622797	0.3729	-4.58
253387_at	P-Protein - like protein P-Protein p	AtGLDP1	AT4G33010	-1.47	-0.55	-2.23	0.06226709	0.3729	-4.58
246140_at	SOH1 - like protein SOH1, Saccha	---	AT5G19910	-1.15	-0.20	-2.23	0.06225032	0.3729	-4.57
252453_at	putative RNA-binding protein vario	---	AT3G47120	-1.16	-0.21	-2.23	0.06226341	0.3729	-4.58
259027_at	hypothetical protein predicted by g	---	AT3G09280	-1.15	-0.20	-2.23	0.06229824	0.3729	-4.58
248583_at	putative protein strong similarity to	emb1441	AT5G49930	-1.23	-0.30	-2.23	0.06235377	0.3731	-4.58
252905_at	putative protein predicted protein,	---	AT4G39720	-1.25	-0.33	-2.23	0.06238661	0.3732	-4.58

262947_at	unknown protein ;supported by full	GASA1	AT1G75750	1.15	0.20	2.23	0.06246293	0.3735	-4.58
253623_at	GDP-mannose pyrophosphorylase	---	AT4G30570	-1.20	-0.26	-2.23	0.06245148	0.3735	-4.58
262270_x_at	polyprotein, putative similar to poly	---	---	-1.15	-0.20	-2.23	0.06249094	0.3735	-4.58
263954_at	unknown protein ; supported by cl	---	AT2G35840	-1.25	-0.32	-2.23	0.06250864	0.3735	-4.58
259535_at	hypothetical protein	---	AT1G12280	-1.30	-0.38	-2.23	0.06256036	0.3738	-4.58
249541_at	anthranilate N-benzoyltransferase	---	AT5G38130	-1.21	-0.27	-2.23	0.06260864	0.3739	-4.58
250856_at	putative protein salt-inducible prot	---	AT5G04810	1.25	0.32	2.23	0.06268184	0.3741	-4.58
255133_at	putative protein (fragment) glutam	---	AT4G08320	1.23	0.29	2.23	0.06272968	0.3741	-4.58
245682_at	Expressed protein ; supported by c	---	AT5G08750	-1.20	-0.26	-2.23	0.0627167	0.3741	-4.58
247084_at	NAM (no apical meristem)-like prot	NAC105	AT5G66300	1.18	0.24	2.23	0.06272753	0.3741	-4.58
250370_at	putative protein putative transcript	---	AT5G11430	-1.15	-0.20	-2.23	0.06272153	0.3741	-4.58
259679_at	putative protein kinase Pfam HMM	---	AT1G77720	1.16	0.21	2.23	0.06273717	0.3741	-4.58
262484_at	putative transcriptional regulatory	ATSWI3C	AT1G21700	-1.14	-0.19	-2.23	0.06282348	0.3743	-4.58
248223_at	unknown protein ; supported by cl	---	AT5G53620	1.15	0.20	2.23	0.06279385	0.3743	-4.58
265634_at	hypothetical protein predicted by g	---	AT2G25530	-1.20	-0.26	-2.23	0.0628154	0.3743	-4.58
266044_s_at	hypothetical protein	---	AT2G07725	-1.42	-0.51	-2.22	0.06300119	0.3749	-4.59
260829_s_at	chloroplast thylakoidal processing	---	AT1G06870	1.29	0.37	2.22	0.06297666	0.3749	-4.59
266591_at	expressed protein supported by cl	ABIL1	AT2G46225	1.34	0.42	2.22	0.06300023	0.3749	-4.59
265952_at	unknown protein supported by cDN	---	AT2G37478	1.19	0.25	2.22	0.06300649	0.3749	-4.59
259612_at	60S ribosomal protein L37, putativ	---	AT1G52300	1.44	0.53	2.23	0.06293	0.3749	-4.59
250210_at	putative protein similar to unknown	---	AT5G13890	1.22	0.28	2.22	0.06296218	0.3749	-4.59
259759_at	hypothetical protein similar to GB:	---	AT1G77550	1.19	0.26	2.22	0.06314344	0.3753	-4.59
249014_at	putative protein similar to unknown	---	AT5G44710	1.25	0.32	2.22	0.06310204	0.3753	-4.59
255776_at	60S ribosomal protein L6, putative	---	AT1G18540	1.50	0.58	2.22	0.06315971	0.3753	-4.59
266203_at	putative phloem-specific lectin	AtPP2-B1	AT2G02230	1.56	0.65	2.22	0.06314162	0.3753	-4.59
257715_at	putative zinc transporter identical	ZIP1	AT3G12750	-1.41	-0.50	-2.22	0.06311052	0.3753	-4.59
245459_at	hypothetical protein	---	---	-1.31	-0.39	-2.22	0.06321204	0.3754	-4.59
255602_at	Expressed protein ; supported by f	---	AT4G01026	1.23	0.29	2.22	0.06322005	0.3754	-4.59
254986_at	putative protein SF16 protein -Hel	IQD16	AT4G10640	-1.15	-0.20	-2.22	0.06326481	0.3756	-4.59
259645_at	putative DNA-binding protein pred	BIM2	AT1G69010	-1.27	-0.34	-2.22	0.06339374	0.3760	-4.59
250477_at	putative protein CIS,CIS-MUCONA	---	AT5G10190	1.16	0.22	2.22	0.06336599	0.3760	-4.59
250429_at	putative protein TH65 protein, Ara	---	AT5G10470	-1.20	-0.26	-2.22	0.06337976	0.3760	-4.59
252833_at	Expressed protein ; supported by c	AGP3	AT4G40090	-1.17	-0.23	-2.22	0.06338523	0.3760	-4.59
257190_at	30S ribosomal protein S10, putativ	---	AT3G13120	1.32	0.40	2.22	0.06342945	0.3761	-4.59
259685_at	unknown protein	AtPP2-A11	AT1G63090	-1.36	-0.44	-2.22	0.06352504	0.3762	-4.59

258366_at	DNA-binding protein contains AP2	RAP2.2	AT3G14230	1.21	0.28	2.22	0.06347441	0.3762	-4.59
247584_at	60S ribosomal protein L12 - like 6	---	AT5G60670	1.55	0.63	2.22	0.06349861	0.3762	-4.59
245624_at	glucosyltransferase like protein	---	AT4G14090	-1.26	-0.33	-2.22	0.06348756	0.3762	-4.59
254651_at	potassium channel - like protein k	KCO6	AT4G18160	-1.25	-0.32	-2.22	0.06350898	0.3762	-4.59
245063_at	Expressed protein ; supported by f	---	AT2G39795	1.52	0.61	2.22	0.06357791	0.3763	-4.60
249571_at	putative protein predicted proteins	---	AT5G37620	1.17	0.22	2.22	0.06358699	0.3763	-4.60
260718_at	unknown protein	ECT7	AT1G48110	-1.14	-0.19	-2.22	0.06371288	0.3770	-4.60
249229_at	putative protein similar to unknown	---	AT5G42090	1.20	0.26	2.22	0.06379048	0.3772	-4.60
258405_at	unknown protein almost identical t	BSH	AT3G17590	1.30	0.37	2.22	0.06382195	0.3772	-4.60
248874_at	putative protein strong similarity to	---	AT5G46460	-1.31	-0.39	-2.22	0.06378652	0.3772	-4.60
261040_at	oligouridylate binding protein, puta	UBP1B	AT1G17370	-1.19	-0.25	-2.22	0.06381853	0.3772	-4.60
263946_at	hypothetical protein ;supported by	---	AT2G36000	1.22	0.28	2.21	0.06390538	0.3776	-4.60
249925_at	putative protein predicted proteins	---	AT5G19150	1.29	0.37	2.21	0.06396613	0.3778	-4.60
262552_at	hypothetical protein similar to hypo	---	AT1G31350	1.34	0.42	2.21	0.06397929	0.3778	-4.60
253078_at	putative receptor protein kinase C	---	AT4G36180	-1.36	-0.44	-2.21	0.0639853	0.3778	-4.60
251516_s_at	putative protein hypothetical prote	---	AT3G59310 /	-1.21	-0.28	-2.21	0.06414567	0.3779	-4.60
256655_at	hypothetical protein predicted by g	---	AT3G18890	-1.32	-0.40	-2.21	0.06413804	0.3779	-4.60
260292_at	putative UDP-N-acetylmuramoylal	MURE	AT1G63680	1.15	0.20	2.21	0.06412799	0.3779	-4.60
248021_at	RuBisCO subunit binding-protein	---	AT5G56500	-1.39	-0.48	-2.21	0.06414161	0.3779	-4.60
262977_at	transcription factor, putative simila	---	AT1G75490	1.22	0.29	2.21	0.06410425	0.3779	-4.60
246462_at	putative protein predicted protein,	---	AT5G16940	1.33	0.41	2.21	0.0640485	0.3779	-4.60
262828_at	major latex protein type1 identical	---	AT1G14950	-1.34	-0.43	-2.21	0.06407102	0.3779	-4.60
251085_at	putative protein insulinase - Homo	---	AT5G01440	-1.20	-0.27	-2.21	0.06410286	0.3779	-4.60
254599_at	putative protein hypothetical prote	---	AT4G19000	1.21	0.28	2.21	0.06402116	0.3779	-4.60
251749_at	putative protein predicted proteins	---	AT3G55690	-1.17	-0.23	-2.21	0.0641668	0.3779	-4.60
259349_at	unknown protein ; supported by cl	ATAPRL5	AT3G03860	1.17	0.23	2.21	0.0641839	0.3779	-4.61
258457_at	Expressed protein ; supported by f	IGPD	AT3G22425	1.26	0.34	2.21	0.06419539	0.3779	-4.61
263472_at	molybdopterin synthase (CNX2) ;s	CNX2	AT2G31955	1.25	0.32	2.21	0.06423018	0.3780	-4.61
259209_at	putative RNA-binding protein iden	---	AT3G09160	-1.15	-0.20	-2.21	0.06424906	0.3780	-4.61
264205_at	hypothetical protein identical to hy	---	AT1G22790	1.17	0.22	2.21	0.06434586	0.3784	-4.61
247670_at	putative protein predicted proteins	---	AT5G60190	1.26	0.33	2.21	0.0643612	0.3784	-4.61
248118_at	GDSL-motif lipase/hydrolase-like p	---	AT5G55050	-2.39	-1.26	-2.21	0.06439295	0.3784	-4.61
252442_at	dUTP pyrophosphatase-like prote	---	AT3G46940	1.40	0.49	2.21	0.06438855	0.3784	-4.61
249029_at	disease resistance protein-like	---	AT5G44870	-1.19	-0.25	-2.21	0.06438018	0.3784	-4.61
253308_at	putative protein aminotransferase	AGD2	AT4G33680	1.18	0.24	2.21	0.06441145	0.3784	-4.61

259117_at	unknown protein similar to hypoth	SNL1	AT3G01320	-1.18	-0.23	-2.21	0.06444925	0.3784	-4.61
259939_s_at	ARE1-like protein similar to ARE1	---	AT1G71270	1.25	0.32	2.21	0.06443561	0.3784	-4.61
263467_at	unknown protein	---	AT2G31730	1.47	0.56	2.21	0.06455252	0.3786	-4.61
264024_at	hypothetical protein predicted by g	---	AT2G21180	1.41	0.50	2.21	0.06456186	0.3786	-4.61
261565_at	beta-1,3-glucanase, putative simil	---	AT1G33220	-1.15	-0.20	-2.21	0.06466491	0.3786	-4.61
256510_at	ATP-dependent Clp protease ATP	---	AT1G33360	1.21	0.28	2.21	0.06461233	0.3786	-4.61
246206_at	Expressed protein ; supported by c	ATPBRP	---	-1.18	-0.23	-2.21	0.06462978	0.3786	-4.61
265689_at	hypothetical protein predicted by g	---	AT2G24310	-1.16	-0.21	-2.21	0.0646569	0.3786	-4.61
261610_at	hypothetical protein predicted by g	---	AT1G49560	-1.34	-0.43	-2.21	0.06467808	0.3786	-4.61
252322_at	putative protein putative zinc-finge	---	AT3G48550	-1.47	-0.55	-2.21	0.06467179	0.3786	-4.61
256415_at	unknown protein ; supported by ful	---	AT3G11210	1.68	0.75	2.21	0.06460997	0.3786	-4.61
258991_at	unknown protein contains Pfam pr	---	AT3G08820	-1.20	-0.26	-2.21	0.0645593	0.3786	-4.61
250582_at	transcription factor-like protein eth	---	AT5G07580	-1.42	-0.51	-2.21	0.06458365	0.3786	-4.61
257140_at	MYB family transcription factor (hs	MYB30	AT3G28910	1.48	0.56	2.21	0.06467601	0.3786	-4.61
245899_at	putative protein	ALF4	AT5G11030	1.20	0.26	2.21	0.06471667	0.3787	-4.61
251429_at	dynamin-like protein 4 (ADL4) ; su	ADL1E	AT3G60190	1.21	0.27	2.21	0.06475776	0.3787	-4.61
253218_at	subtilisin-like serine protease simi	SLP2	AT4G34980	-1.42	-0.50	-2.21	0.06474688	0.3787	-4.61
245374_at	hypothetical protein	---	AT4G17620	-1.21	-0.28	-2.20	0.06480314	0.3789	-4.61
266327_at	homeodomain transcription factor	ATHB-7	AT2G46680	1.45	0.54	2.20	0.06488552	0.3791	-4.62
251880_at	hypothetical protein ;supported by	---	AT3G54290	1.27	0.34	2.20	0.06485715	0.3791	-4.62
248557_at	transport inhibitor response 1 (TIR	AFB5	AT5G49980	-1.22	-0.28	-2.20	0.06487563	0.3791	-4.62
249873_at	ATP-dependent Clp protease prot	NCLPP7	AT5G23140	1.21	0.27	2.20	0.06493988	0.3792	-4.62
251889_at	putative protein probable lectin 2 p	---	AT3G54080	1.43	0.52	2.20	0.064942	0.3792	-4.62
264835_at	unknown protein similar to unknow	---	AT1G03550	-1.14	-0.19	-2.20	0.06519037	0.3805	-4.62
248390_at	importin alpha subunit	IMPA-8	AT5G52000	-1.15	-0.20	-2.20	0.06520568	0.3805	-4.62
263854_at	putative mutT domain protein	atnudt5	AT2G04430	-1.18	-0.24	-2.20	0.06523377	0.3805	-4.62
259233_at	hypothetical protein	---	AT3G11380	-1.14	-0.19	-2.20	0.06521731	0.3805	-4.62
245282_at	hypothetical protein ; supported by	---	AT4G14990	-1.26	-0.33	-2.20	0.06525331	0.3805	-4.62
249357_at	ribonucleoprotein -like ribonucleop	---	AT5G40490	-1.23	-0.29	-2.20	0.06527199	0.3805	-4.62
254936_at	predicted protein of unknown funct	---	AT4G10790	1.15	0.20	2.20	0.06527607	0.3805	-4.62
261668_at	2-isopropylmalate synthase, putat	MAML-4	AT1G18500	1.23	0.30	2.20	0.06530004	0.3806	-4.62
252661_at	putative protein	---	AT3G44450	-1.72	-0.78	-2.20	0.06537008	0.3809	-4.62
266804_at	cyclophilin identical to GB:AF0204	CYP5	AT2G29960	1.21	0.27	2.20	0.06540818	0.3810	-4.62
254565_at	replication A protein-like replicatio	---	AT4G19130	-1.15	-0.20	-2.20	0.06541926	0.3810	-4.62
263037_at	conserved hypothetical protein	---	AT1G23230	-1.23	-0.30	-2.20	0.06544097	0.3810	-4.62

255626_at	coded for by A. thaliana cDNA T20	---	AT4G00780	-1.23	-0.30	-2.20	0.06546407	0.3810	-4.62
248773_at	kinesin-like protein	FRA1	AT5G47820	1.25	0.32	2.20	0.06548962	0.3811	-4.62
264505_at	putative nodulin protein, N21 Simi	---	AT1G09380	-1.30	-0.38	-2.20	0.06554906	0.3811	-4.63
253858_at	carbohydrate kinase - like protein	---	AT4G27600	1.17	0.22	2.20	0.06556233	0.3811	-4.63
263172_at	hypothetical protein predicted by g	CID3	AT1G54170	-1.14	-0.19	-2.20	0.06556107	0.3811	-4.63
266468_at	unknown protein ; supported by cD	---	AT2G47960	1.22	0.29	2.20	0.06553475	0.3811	-4.63
257910_at	hypothetical protein similar to hypo	---	AT3G25580	1.23	0.29	2.20	0.06563809	0.3815	-4.63
252075_at	putative protein saposin precursor	---	AT3G51730	1.27	0.35	2.20	0.06566212	0.3815	-4.63
255475_at	contains a short region of similarity	---	AT4G02480	-1.24	-0.31	-2.20	0.06568015	0.3815	-4.63
251103_at	putative protein protein phosphata	---	AT5G01700	-1.27	-0.35	-2.20	0.06572078	0.3816	-4.63
252780_at	alcohol dehydrogenase (ATA1) ;s	ATA1	AT3G42960	-1.32	-0.40	-2.19	0.06583347	0.3822	-4.63
263853_at	putative mutT domain protein	---	AT2G04440	-1.29	-0.37	-2.19	0.06591795	0.3826	-4.63
254417_at	putative protein	ATFMN/FH	AT4G21470	1.30	0.38	2.19	0.06594605	0.3826	-4.63
245250_at	ethylene responsive element bindi	ATERF6	AT4G17490	2.69	1.43	2.19	0.06603647	0.3826	-4.63
246479_at	hypothetical protein	---	AT5G16060	1.19	0.26	2.19	0.06603862	0.3826	-4.63
256823_at	hypothetical protein predicted by g	---	AT3G22220	1.22	0.29	2.19	0.06604131	0.3826	-4.63
262312_at	hypothetical protein similar to puta	MLP28	AT1G70830	-4.42	-2.15	-2.19	0.0659996	0.3826	-4.63
261253_at	unknown protein ;supported by full	---	AT1G05840	1.28	0.36	2.19	0.06596799	0.3826	-4.63
267608_at	hypothetical protein predicted by g	---	AT2G26770	-1.20	-0.26	-2.19	0.06598047	0.3826	-4.63
263513_at	unknown protein	---	AT2G12400	-1.35	-0.43	-2.19	0.06653848	0.3827	-4.64
247327_at	peroxidase (emb|CAA67551.1) ;s	---	AT5G64120	2.18	1.12	2.19	0.06646939	0.3827	-4.64
246831_at	hexose transporter - like protein h	MSS1	AT5G26340	-1.36	-0.44	-2.19	0.06649244	0.3827	-4.64
257264_at	hypothetical protein contains Pfam	---	AT3G22060	2.06	1.04	2.19	0.06629833	0.3827	-4.64
254218_at	putative receptor kinase receptor-	---	AT4G23740	1.20	0.27	2.19	0.06612365	0.3827	-4.63
263705_at	unknown protein contains similarity	IMPL1	AT1G31190	-1.27	-0.34	-2.19	0.06636275	0.3827	-4.64
248869_at	putative protein contains similarity	---	AT5G46840	1.36	0.44	2.19	0.06634908	0.3827	-4.64
267535_at	putative C2H2-type zinc finger pro	ZFP8	AT2G41940	-1.39	-0.47	-2.19	0.06656204	0.3827	-4.64
265544_at	putative cyclic nucleotide and caln	ATCNGC15	AT2G28260	-1.27	-0.34	-2.19	0.06615501	0.3827	-4.63
258358_at	unknown protein similar to unknow	---	AT3G14380	-1.20	-0.26	-2.19	0.06650297	0.3827	-4.64
252456_at	hypersensitivity-related protein-like	---	AT3G47170	-1.20	-0.26	-2.19	0.06644181	0.3827	-4.64
246727_at	major latex protein homolog - like	---	AT5G28010	1.26	0.33	2.19	0.06644182	0.3827	-4.64
247524_at	thioredoxin-like 3 ; supported by c	ACHT5	AT5G61440	1.72	0.79	2.19	0.06647082	0.3827	-4.64
247716_at	putative protein predicted protein,	---	AT5G59350	-1.32	-0.40	-2.19	0.06658793	0.3827	-4.64
261752_at	putative AMP-binding protein conta	---	AT1G76290	-1.20	-0.26	-2.19	0.06628699	0.3827	-4.64
246261_at	unknown protein	---	AT1G31810	1.20	0.27	2.19	0.06657797	0.3827	-4.64

257753_at	60S ribosomal protein, putative si	---	AT3G18740	1.31	0.39	2.19	0.06655606	0.3827	-4.64
246063_at	putative protein predicted proteins	---	AT5G19340	-1.17	-0.23	-2.19	0.06645449	0.3827	-4.64
254235_at	putative Ap2 domain protein DNA-	CRF2	AT4G23750	-1.18	-0.24	-2.19	0.06647807	0.3827	-4.64
254227_at	putative protein chS-Rex-b - Gallu	BTI1	AT4G23630	-1.29	-0.37	-2.19	0.06626459	0.3827	-4.64
261961_at	hypothetical protein predicted by g	---	AT1G36510	-1.22	-0.28	-2.19	0.06612707	0.3827	-4.63
249376_at	Expressed protein ; supported by f	---	AT5G40645	-1.15	-0.20	-2.19	0.06623785	0.3827	-4.64
248910_at	serine threonine protein kinase ; su	CIPK20	AT5G45820	-1.38	-0.46	-2.19	0.06624026	0.3827	-4.64
267629_at	putative DNA polymerase delta sm	POLD2	AT2G42120	1.27	0.35	2.19	0.066316	0.3827	-4.64
244965_at	hypothetical protein	---	---	1.29	0.37	2.19	0.06609815	0.3827	-4.63
257849_at	unknown protein	ECT5	AT3G13060	1.27	0.34	2.19	0.06650954	0.3827	-4.64
265636_at	putative calcium binding protein	---	AT2G27480	1.21	0.28	2.19	0.06619567	0.3827	-4.64
254057_at	putative protein ;supported by full-	---	AT4G25170	1.38	0.46	2.19	0.06652247	0.3827	-4.64
253012_at	putative protein Caenorhabditis el	---	AT4G37900	-1.20	-0.26	-2.19	0.06628022	0.3827	-4.64
265459_at	unknown protein ; supported by fu	---	AT2G46540	1.17	0.22	2.19	0.06654119	0.3827	-4.64
247993_at	putative protein similar to unknown	---	AT5G56130	-1.24	-0.31	-2.19	0.06621999	0.3827	-4.64
247945_at	putative protein contains similarity	---	AT5G57150	-1.69	-0.75	-2.19	0.06615335	0.3827	-4.63
249592_at	putative protein SIAH1 protein, Br	---	AT5G37890	-1.23	-0.30	-2.19	0.06664708	0.3829	-4.64
265359_at	putative MYB family transcription f	MYB7	AT2G16720	-1.61	-0.69	-2.19	0.06667635	0.3830	-4.64
259112_at	putative 60S ribosomal protein L2	---	AT3G05560	1.43	0.51	2.18	0.06675706	0.3830	-4.64
254472_at	putative protein predicted proteins	---	---	-1.15	-0.20	-2.18	0.06671295	0.3830	-4.64
263271_s_at	hypothetical protein predicted by g	---	---	1.14	0.19	2.18	0.06674253	0.3830	-4.64
258938_at	germin-like protein similar to germi	---	AT3G10080	2.17	1.12	2.18	0.06674281	0.3830	-4.64
257745_at	unknown protein ;supported by ful	---	AT3G29240	1.65	0.72	2.19	0.06669775	0.3830	-4.64
253767_at	12S cruciferin seed storage protein	CRU3	AT4G28520	-1.19	-0.25	-2.18	0.06678469	0.3830	-4.64
258148_s_at	DNA-directed RNA polymerase II	NRPD2B	AT3G18090	-1.35	-0.43	-2.18	0.06688716	0.3835	-4.65
253769_at	putative protein (fragment) protein	RIC7	AT4G28560	-1.24	-0.31	-2.18	0.06707161	0.3838	-4.65
248364_at	fibrillarin 3 (AtFib3) similar to fibrilla	---	AT5G52490	-1.16	-0.22	-2.18	0.06711132	0.3838	-4.65
262459_at	hypothetical protein similar to hypo	---	AT1G50400	-1.26	-0.34	-2.18	0.06702797	0.3838	-4.65
266449_at	hypothetical protein predicted by g	AT-P4H-1	AT2G43080	1.22	0.29	2.18	0.06710552	0.3838	-4.65
247538_at	ABC family transporter - like prote	ATH16	AT5G61700	-1.15	-0.20	-2.18	0.06700916	0.3838	-4.65
246068_at	putative protein ribosomal protein	---	AT5G20290	1.40	0.49	2.18	0.06708838	0.3838	-4.65
262399_at	unknown protein ;supported by full	---	AT1G49500	1.30	0.38	2.18	0.06701991	0.3838	-4.65
250151_at	high affinity nitrate transporter - lik	ATNRT2.7	AT5G14570	1.39	0.47	2.18	0.06710561	0.3838	-4.65
266627_at	putative pre-mRNA splicing factor	MEE29	AT2G35340	-1.21	-0.27	-2.18	0.06694898	0.3838	-4.65
260883_at	hypothetical protein predicted by g	---	AT1G29270	1.14	0.19	2.18	0.06702267	0.3838	-4.65

252148_at	MS5-like protein	---	AT3G51280	1.21	0.28	2.18	0.06704599	0.3838	-4.65
254142_at	putative protein other predicted or	---	AT4G24630	1.20	0.26	2.18	0.06713589	0.3838	-4.65
250577_at	putative protein densin-180, Rattu	---	AT5G07910	-1.16	-0.22	-2.18	0.06716755	0.3839	-4.65
262006_at	hypothetical protein predicted by g	---	AT1G64570	-1.19	-0.25	-2.18	0.06717965	0.3839	-4.65
250623_at	peroxisomal Ca-dependent solute	---	AT5G07320	-1.19	-0.25	-2.18	0.06721094	0.3839	-4.65
254754_at	pectate lyase like protein pectate l	---	AT4G13210	-1.16	-0.21	-2.18	0.06729114	0.3843	-4.65
252615_at	serine/proline-rich protein	---	AT3G45230	1.32	0.40	2.18	0.06731644	0.3844	-4.65
248756_at	sodium-dicarboxylate cotransporte	TDT	AT5G47560	1.42	0.51	2.18	0.06740105	0.3846	-4.65
253247_at	Homeodomain - like protein simila	BLH6	AT4G34610	-1.36	-0.44	-2.18	0.06739304	0.3846	-4.65
267336_at	putative small heat shock protein ;	---	AT2G19310	-1.28	-0.36	-2.18	0.06740659	0.3846	-4.65
264761_at	hypothetical protein predicted by g	---	AT1G61280	1.17	0.23	2.18	0.06742736	0.3846	-4.65
256698_at	unknown protein	---	AT3G20680	1.23	0.30	2.18	0.06743848	0.3846	-4.65
253622_at	cyclic nucleotide and calmodulin-r	ATCNGC9	AT4G30560	-1.18	-0.24	-2.18	0.067522	0.3849	-4.66
251218_at	CP12 protein precursor-like protei	CP12-2	AT3G62410	-1.26	-0.33	-2.18	0.06753299	0.3849	-4.66
255066_at	F-box protein family, AtFBW2 con	---	AT4G08980	1.16	0.22	2.18	0.06757526	0.3851	-4.66
264487_at	vacuolar protein sorting homolog a	VPS45	AT1G77140	-1.16	-0.22	-2.18	0.06766558	0.3854	-4.66
265674_at	unknown protein ; supported by fu	---	AT2G32190	1.74	0.80	2.18	0.06767357	0.3854	-4.66
258675_at	putative nonspecific lipid-transfer p	LTP6	AT3G08770	-1.19	-0.26	-2.17	0.06770036	0.3855	-4.66
262260_at	major latex protein (MLP149), puta	MLP34	AT1G70850	-1.29	-0.37	-2.17	0.06771966	0.3855	-4.66
255019_at	putative protein IB1C3-1 protein, A	---	AT4G10210	-1.17	-0.23	-2.17	0.06777698	0.3857	-4.66
266174_at	hypothetical protein predicted by g	---	AT2G02440	-1.14	-0.19	-2.17	0.06781472	0.3858	-4.66
253309_at	male sterility 2-like protein male st	CER4	AT4G33790	1.46	0.55	2.17	0.06788888	0.3860	-4.66
258105_at	Expressed protein ; supported by f	---	AT3G23605	1.39	0.48	2.17	0.06789445	0.3860	-4.66
261502_at	hypothetical protein predicted by g	AtHB31	AT1G14440	1.41	0.49	2.17	0.06789575	0.3860	-4.66
245176_at	unknown protein similar to GP|210	---	AT2G47440	-1.54	-0.63	-2.17	0.06801824	0.3865	-4.66
249911_at	glucosyltransferase-like protein ; s	CSLA02	AT5G22740	-1.89	-0.92	-2.17	0.06802516	0.3865	-4.66
253941_at	putative protein	---	AT4G26980	-1.17	-0.22	-2.17	0.0680215	0.3865	-4.66
251957_at	putative protein predicted proteins	---	AT3G53690	-1.21	-0.27	-2.17	0.06805059	0.3865	-4.66
250665_at	unknown protein ;supported by ful	---	AT5G06980	1.25	0.32	2.17	0.06807877	0.3866	-4.66
265946_s_at	putative WD-40 repeat protein, MS	FVE	AT2G19520	1.17	0.22	2.17	0.06812588	0.3866	-4.66
254526_at	putative protein cyclin C homolog	CYCT1;4	AT4G19600	-1.17	-0.23	-2.17	0.06812172	0.3866	-4.66
256286_at	unknown protein	---	AT3G12180	1.21	0.27	2.17	0.06822818	0.3866	-4.67
263000_at	hypothetical protein similar to hypo	---	AT1G54350	-1.21	-0.28	-2.17	0.06823346	0.3866	-4.67
261101_at	transcription factor DREB1A, puta	ddf2	AT1G63030	-1.25	-0.32	-2.17	0.06819149	0.3866	-4.66
253351_at	putative protein hemolysin, 38K, S	---	AT4G33700	-1.20	-0.26	-2.17	0.06818543	0.3866	-4.66

254643_at	putative protein DNA polymerase	---	AT4G18820	-1.20	-0.26	-2.17	0.06817804	0.3866	-4.66
259579_at	P-glycoprotein, putative similar to	PGP14	AT1G28010	1.85	0.89	2.17	0.06826442	0.3866	-4.67
251123_at	putative protein predicted proteins	---	AT5G01030	1.16	0.21	2.17	0.06815994	0.3866	-4.66
257392_at	hypothetical protein	FLA3	AT2G24450	-1.19	-0.25	-2.17	0.06826603	0.3866	-4.67
263014_at	unknown protein similar to hypothe	CAF2	AT1G23400	1.19	0.25	2.17	0.06822259	0.3866	-4.67
257822_at	rotamase FKBP (ROF1) identical	ROF1	AT3G25230	-1.56	-0.64	-2.17	0.06837097	0.3871	-4.67
248213_at	putative protein similar to unknown	AtGRF7	AT5G53660	-1.20	-0.26	-2.17	0.06842073	0.3873	-4.67
255227_at	D123 -like protein protein D123, R	EDA35	AT4G05440	-1.25	-0.32	-2.17	0.06856442	0.3879	-4.67
264691_s_at	putative reverse transcriptase	---	---	-1.19	-0.25	-2.17	0.06856781	0.3879	-4.67
251055_at	putative protein putative protein F	---	AT5G01710	-1.17	-0.23	-2.17	0.0686218	0.3880	-4.67
245670_at	mitochondrial protein (AtJ1), putat	ATJ1	AT1G28210	-1.40	-0.49	-2.17	0.06862701	0.3880	-4.67
262346_at	unknown protein similar to hypothe	---	AT1G63980	1.26	0.34	2.16	0.06867975	0.3882	-4.67
254566_at	hypothetical protein	---	AT4G19240	1.25	0.32	2.16	0.06871154	0.3882	-4.67
246936_at	putative protein hypothetical prote	---	AT5G25360	-1.18	-0.24	-2.16	0.06870688	0.3882	-4.67
266743_at	ribonuclease, RNS1 identical to rib	RNS1	AT2G02990	-2.38	-1.25	-2.16	0.06876231	0.3884	-4.67
263985_at	unknown protein ;supported by ful	---	AT2G42750	-1.33	-0.41	-2.16	0.06876852	0.3884	-4.67
259507_at	unknown protein	---	AT1G43910	1.62	0.70	2.16	0.06882571	0.3884	-4.67
259793_at	AP2-containing DNA-binding prote	---	AT1G64380	-1.64	-0.71	-2.16	0.06880075	0.3884	-4.67
258559_at	putative transcriptional regulator si	ATCHR12	AT3G06010	1.24	0.31	2.16	0.06882373	0.3884	-4.67
255806_at	fructokinase - like protein fructokir	---	AT4G10260	-1.14	-0.19	-2.16	0.06887363	0.3886	-4.67
266262_at	hypothetical protein predicted by g	---	AT2G27590	1.36	0.44	2.16	0.06894741	0.3888	-4.68
249301_at	putative protein similar to unknown	---	AT5G41440	-1.23	-0.30	-2.16	0.06893531	0.3888	-4.68
263663_at	putative malate dehydrogenase sir	---	AT1G04410	1.18	0.24	2.16	0.06897106	0.3888	-4.68
264222_at	hypothetical protein predicted by g	---	AT1G60230	1.18	0.24	2.16	0.06900048	0.3889	-4.68
249659_s_at	putative protein similar to unknown	---	AT5G36710	1.26	0.33	2.16	0.06904976	0.3890	-4.68
246922_at	serine/threonine protein kinase-like	CIPK25	AT5G25110	-1.32	-0.40	-2.16	0.06904299	0.3890	-4.68
246379_s_at	60S ribosomal protein L21, putativ	---	AT1G57660	1.31	0.39	2.16	0.06910146	0.3891	-4.68
260483_at	Barley Mlo protein isolog ; suppor	MLO4	AT1G11000	1.28	0.35	2.16	0.0690853	0.3891	-4.68
254504_at	putative protein RNPL, Homo sap	---	AT4G20030	1.32	0.41	2.16	0.06921679	0.3896	-4.68
250324_at	putative protein nitrilase/Fhit prote	---	AT5G12040	1.23	0.30	2.16	0.06926189	0.3898	-4.68
247586_at	mipC protein - like (aquaporin) mi	PIP2;4	AT5G60660	1.19	0.25	2.16	0.06931193	0.3900	-4.68
264147_at	receptor-like protein glossy1 (gl1),	CER1	AT1G02205	3.67	1.88	2.16	0.0694081	0.3903	-4.68
259724_at	putative serine/threonine-protein ki	SNRK2.10	AT1G60940	1.26	0.33	2.16	0.06939544	0.3903	-4.68
266154_at	putative cytochrome p450	---	AT2G12190	-1.29	-0.37	-2.16	0.06942483	0.3903	-4.68
254008_at	hypothetical protein various predic	---	AT4G26380	-1.19	-0.25	-2.16	0.06945565	0.3904	-4.68

261743_s_at	protein serine/threonine phosphat	BSL2	AT1G08420 /	1.18	0.24	2.16	0.06955079	0.3905	-4.68
253090_at	beta-galactosidase like protein ; su	BGAL3	AT4G36360	-2.08	-1.06	-2.16	0.06952321	0.3905	-4.68
250137_at	rRNA methylase - like protein rRN	---	AT5G15390	1.19	0.25	2.16	0.06954534	0.3905	-4.68
253693_at	Thioredoxin - like protein thioredox	ACHT2	AT4G29670	-1.33	-0.42	-2.16	0.06949206	0.3905	-4.68
258895_at	putative epoxide hydrolase similar	---	AT3G05600	-1.15	-0.20	-2.16	0.06951238	0.3905	-4.68
246944_at	ubiquinol--cytochrome-c reductase	---	AT5G25450	-1.20	-0.26	-2.16	0.06957113	0.3905	-4.68
263852_at	putative mutT domain protein	ATNUDT6	AT2G04450	2.40	1.27	2.16	0.06960966	0.3905	-4.68
252429_at	H-protein promoter binding factor-2	CDF3	AT3G47500	-1.31	-0.39	-2.16	0.06960618	0.3905	-4.68
257987_at	fertilization-independent endosperr	FIE	AT3G20740	1.18	0.24	2.15	0.06968662	0.3906	-4.69
259371_at	unknown protein ;supported by full	---	AT1G69080	-1.70	-0.76	-2.15	0.06967152	0.3906	-4.69
247479_at	NAC - like protein OsNAC7, Oryza	ANAC101	AT5G62380	1.16	0.22	2.15	0.06968795	0.3906	-4.69
254498_at	membrane-associated salt-inducit	EMB1025	AT4G20090	-1.29	-0.36	-2.16	0.06963836	0.3906	-4.69
249047_at	berberine bridge enzyme-like prote	---	AT5G44410	1.21	0.27	2.15	0.06984009	0.3906	-4.69
247176_at	acyl-CoA oxidase (gb|AAC13497.1	ACX2	AT5G65110	1.31	0.39	2.15	0.06984394	0.3906	-4.69
261823_at	hypothetical protein predicted by g	PYM	AT1G11400	1.19	0.25	2.15	0.06974893	0.3906	-4.69
245121_at	60S ribosomal protein L7A ;suppo	---	AT2G47610	1.40	0.48	2.15	0.0697381	0.3906	-4.69
251948_at	diaminopimelate epimerase - like	---	AT3G53580	1.22	0.28	2.15	0.06979808	0.3906	-4.69
247226_at	putative protein contains similarity	---	AT5G65100	-1.15	-0.20	-2.15	0.0697442	0.3906	-4.69
258743_s_at	shaggy related protein kinase, AS	ATSK12	AT3G05840 /	-1.22	-0.28	-2.15	0.06984438	0.3906	-4.69
258075_at	homocysteine S-methyltransferase	HMT-1	AT3G25900	2.26	1.17	2.15	0.06984922	0.3906	-4.69
265819_at	Expressed protein ; supported by f	---	AT2G17972	1.22	0.29	2.15	0.06982664	0.3906	-4.69
255107_at	hypothetical protein	---	AT4G08730	-1.24	-0.31	-2.15	0.06990121	0.3908	-4.69
250692_at	putative protein strong similarity to	---	AT5G06560	1.20	0.27	2.15	0.06995785	0.3910	-4.69
245056_at	putative glucosyltransferase	UGT76D1	AT2G26480	-1.28	-0.36	-2.15	0.07001533	0.3912	-4.69
245042_at	hypothetical protein predicted by g	HEMD	AT2G26540	-1.36	-0.45	-2.15	0.07022406	0.3913	-4.69
245612_at	carnitine racemase like protein	HCD1	AT4G14440	1.74	0.80	2.15	0.07014729	0.3913	-4.69
247834_at	cinnamoyl-CoA reductase - like pr	---	AT5G58490	-1.16	-0.22	-2.15	0.07015697	0.3913	-4.69
265539_at	unknown protein	---	AT2G15830	1.56	0.64	2.15	0.07007803	0.3913	-4.69
252417_at	putative calcium-binding protein ca	---	AT3G47480	2.37	1.24	2.15	0.07010027	0.3913	-4.69
256250_at	integral membrane protein, putativ	---	AT3G11320	-1.26	-0.33	-2.15	0.07009228	0.3913	-4.69
257553_at	unknown protein contains Pfam pr	TPR2	AT3G16830	1.31	0.39	2.15	0.0700506	0.3913	-4.69
255333_at	putative polyprotein	---	---	-1.16	-0.22	-2.15	0.07018668	0.3913	-4.69
260287_at	unknown protein contains two Kelc	---	AT1G80440	1.33	0.41	2.15	0.0702297	0.3913	-4.69
263845_at	phenylalanine ammonia lyase (PA	pal1	AT2G37040	-1.82	-0.86	-2.15	0.07021913	0.3913	-4.69
248578_at	putative protein contains similarity	emb1879	AT5G49820	1.26	0.34	2.15	0.070226	0.3913	-4.69

254321_at	trehalose-6-phosphate phosphata	CPuORF27	AT4G22590 /	-1.36	-0.44	-2.15	0.07013937	0.3913	-4.69
258485_at	putative stearoyl-acyl carrier protei	---	AT3G02630	1.14	0.19	2.15	0.07029362	0.3913	-4.69
255601_at	putative protein (fragment) various	---	AT4G01030	1.21	0.28	2.15	0.07030171	0.3913	-4.69
267464_at	putative pectinesterase	---	AT2G19150	-1.19	-0.26	-2.15	0.0703088	0.3913	-4.69
259874_at	unknown protein	---	AT1G76660	1.28	0.35	2.15	0.07029294	0.3913	-4.69
265332_at	hypothetical protein predicted by g	---	AT2G18410	1.23	0.30	2.15	0.07037732	0.3914	-4.70
249748_at	thaumatin-like protein	---	AT5G24620	-1.20	-0.27	-2.15	0.0703818	0.3914	-4.70
258047_at	putative 4-coumarate:CoA ligase 2	4CL2	AT3G21240	-1.93	-0.95	-2.15	0.07034459	0.3914	-4.70
256134_at	aminoalcoholphosphotransferase i	AAPT1	AT1G13560	1.17	0.22	2.15	0.07036973	0.3914	-4.70
250626_at	putative protein p100 co-activator	---	AT5G07350	-1.19	-0.25	-2.15	0.07040103	0.3914	-4.70
258689_at	putative GTPase activating protein	---	AT3G07940	-1.16	-0.22	-2.15	0.07055161	0.3915	-4.70
245219_at	viral resistance protein, putative si	---	AT1G58807 /	-1.18	-0.24	-2.15	0.07049827	0.3915	-4.70
260777_at	mitochondrial carrier protein, puta	---	AT1G14560	-1.19	-0.25	-2.15	0.07053425	0.3915	-4.70
249508_at	unknown protein	---	AT5G38380	1.18	0.24	2.15	0.07047693	0.3915	-4.70
246962_s_at	transcription factor-like protein ligh	BZIP9	AT5G24800	1.36	0.45	2.15	0.07054992	0.3915	-4.70
244912_at	cytochrome c biogenesis orf382 Pr	---	AT2G07783	-1.28	-0.35	-2.15	0.07047792	0.3915	-4.70
245917_at	putative protein HCNP, Homo sap	---	AT5G28740	-1.20	-0.26	-2.15	0.07050646	0.3915	-4.70
250737_at	putative protein similar to unknown	---	AT5G06370	1.26	0.34	2.15	0.070504	0.3915	-4.70
253698_at	nucleotide pyrophosphatase - like	---	AT4G29680	-1.18	-0.24	-2.15	0.07063686	0.3917	-4.70
246921_at	putative protein small unique nucl	---	AT5G25080	1.30	0.37	2.15	0.07063963	0.3917	-4.70
263165_at	putataive transport protein Similar	---	AT1G03060	1.15	0.21	2.15	0.070651	0.3917	-4.70
262296_at	putative cyclin similar to cyclin GB	CYCT1;3	AT1G27630	-1.17	-0.23	-2.14	0.07071054	0.3920	-4.70
266916_at	hypothetical protein predicted by g	---	AT2G45860	1.31	0.39	2.14	0.07073206	0.3920	-4.70
250769_at	putative protein similar to unknown	---	AT5G05680	1.36	0.45	2.14	0.07079089	0.3922	-4.70
264435_at	putative glutathione S-transferase	ATGSTU18	AT1G10360	-1.36	-0.44	-2.14	0.07084048	0.3922	-4.70
266112_x_at	hypothetical protein predicted by g	---	---	-1.22	-0.29	-2.14	0.07084727	0.3922	-4.70
253288_at	hypothetical protein	---	AT4G34310	-1.20	-0.26	-2.14	0.0708374	0.3922	-4.70
258184_at	two-component phosphorelay me	AHP1	AT3G21510	-1.27	-0.34	-2.14	0.07096346	0.3924	-4.70
245674_at	chitinase, putative similar to chitin	---	AT1G56680	-1.16	-0.22	-2.14	0.07094925	0.3924	-4.70
257881_at	putative serine carboxypeptidase I	scpl33	AT3G17180	-1.24	-0.31	-2.14	0.07091996	0.3924	-4.70
267152_at	hypothetical protein predicted by g	---	AT2G31040	-1.28	-0.35	-2.14	0.07094308	0.3924	-4.70
247262_at	putative protein contains similarity	AtFAAH	AT5G64440	1.20	0.26	2.14	0.07093574	0.3924	-4.70
256360_at	hypothetical protein	---	AT1G66440	-1.27	-0.34	-2.14	0.07103988	0.3926	-4.70
254069_at	putative protein similarity to antise	ATNUDT10	AT4G25434	-1.27	-0.35	-2.14	0.07104524	0.3926	-4.71
264043_at	putative cyclin D	CYCD2;1	AT2G22490	1.16	0.22	2.14	0.07108923	0.3926	-4.71

253518_at	hypothetical protein	---	AT4G31400	1.23	0.29	2.14	0.0710728	0.3926	-4.71
253874_at	putative protein stem-specific prot	---	AT4G27450	1.53	0.61	2.14	0.07108044	0.3926	-4.71
264876_at	hypothetical protein	---	AT2G17410	-1.19	-0.26	-2.14	0.07112146	0.3927	-4.71
264833_at	putative protein phosphatase simil	---	AT1G03590	-1.32	-0.40	-2.14	0.0711744	0.3929	-4.71
263099_at	putative non-LTR retroelement rev	---	---	-1.25	-0.32	-2.14	0.07120434	0.3930	-4.71
256442_at	hypothetical protein predicted by g	---	AT3G10930	2.38	1.25	2.14	0.07123971	0.3931	-4.71
256649_at	serine/arginine-rich protein, putati	SCL30A	AT3G13570	1.25	0.32	2.14	0.07127175	0.3931	-4.71
258252_at	putative polygalacturonase similar	---	AT3G15720	-1.42	-0.50	-2.14	0.07126949	0.3931	-4.71
263134_at	dTDP-glucose 4,6-dehydratase, p	RHM1	AT1G78570	-1.28	-0.36	-2.14	0.07132375	0.3932	-4.71
251528_at	putative protein hypothetical prote	---	AT3G58600	1.23	0.29	2.14	0.07132336	0.3932	-4.71
247149_at	unknown protein ;supported by ful	---	AT5G65660	1.44	0.53	2.14	0.07135218	0.3932	-4.71
261524_at	hypothetical protein predicted by g	---	AT1G14300	1.21	0.28	2.14	0.07139378	0.3934	-4.71
251469_at	putative protein strictosidine synth	---	AT3G59530	-1.16	-0.22	-2.14	0.07143329	0.3934	-4.71
253000_at	putative protein other predicted pr	---	AT4G38360	-1.23	-0.30	-2.14	0.07142923	0.3934	-4.71
266760_at	putative RAV-like B3 domain DNA	NGA1	AT2G46870	-1.25	-0.32	-2.14	0.07154371	0.3939	-4.71
257628_at	cytochrome P450, putative contair	CYP71B26	AT3G26290	1.45	0.54	2.14	0.07170497	0.3940	-4.71
262890_at	nucleoporin, putative similar to nu	NUP155	AT1G14850	1.30	0.38	2.13	0.07172592	0.3940	-4.71
244944_s_at	ribosomal protein L16	---	---	-1.28	-0.36	-2.14	0.0716448	0.3940	-4.71
258430_at	phospholipase D, putative similar	PLDP1	AT3G16785	-1.16	-0.21	-2.14	0.07162674	0.3940	-4.71
247556_at	putative protein predicted protein,	---	AT5G61040	-1.24	-0.31	-2.14	0.07169092	0.3940	-4.71
259378_at	unknown protein supported by full	---	AT3G16310	1.43	0.52	2.14	0.07159067	0.3940	-4.71
262657_at	ribonuclease contains similarity to	---	AT1G14210	1.51	0.59	2.14	0.07167532	0.3940	-4.71
256834_at	cyclophilin, putative similar to cycl	---	AT3G22920	-1.16	-0.22	-2.13	0.0717481	0.3940	-4.71
253645_at	putative protein G protein beta sul	VIP3	AT4G29830	1.17	0.23	2.13	0.07174383	0.3940	-4.71
253094_at	putative protein DnaJ-like protein,	---	AT4G37480	1.15	0.20	2.14	0.07165995	0.3940	-4.71
252961_at	putative protein KIAA0169 gene, H	---	AT4G38760	-1.21	-0.28	-2.14	0.07165673	0.3940	-4.71
264210_at	putative myb-related transcription	MYB3	AT1G22640	1.29	0.37	2.13	0.0718003	0.3940	-4.72
254711_at	putative protein	---	AT4G18060	1.21	0.28	2.13	0.07179088	0.3940	-4.72
259322_at	unknown protein	---	AT3G05270	-1.24	-0.31	-2.13	0.07180311	0.3940	-4.72
258480_at	unknown protein ;supported by ful	---	AT3G02640	1.20	0.27	2.13	0.07182629	0.3940	-4.72
266948_at	unknown protein	---	AT2G18850	1.34	0.43	2.13	0.07184763	0.3940	-4.72
245044_at	unknown protein Alternative splice	---	AT2G26500	1.14	0.19	2.13	0.07190865	0.3940	-4.72
245272_at	hypothetical protein ; supported by	---	AT4G17250	1.41	0.50	2.13	0.07194643	0.3940	-4.72
251107_at	putative protein several hypothetic	---	AT5G01610	1.23	0.29	2.13	0.071941	0.3940	-4.72
260128_at	hypothetical protein similar to YmlC	---	AT1G36310	1.20	0.26	2.13	0.07192241	0.3940	-4.72

259563_s_at	hypothetical protein	---	AT1G20590 /	1.16	0.21	2.13	0.07188869	0.3940	-4.72
263044_at	spore germination protein c2 simil	---	AT1G23360	1.19	0.25	2.13	0.07195112	0.3940	-4.72
264423_at	hypothetical protein predicted by g	---	AT1G61690	1.22	0.29	2.13	0.07198608	0.3941	-4.72
248005_at	unknown protein	---	AT5G56240	-1.24	-0.31	-2.13	0.07203706	0.3943	-4.72
248944_at	putative protein similar to unknown	---	AT5G45500	1.25	0.32	2.13	0.07209199	0.3945	-4.72
245595_at	hypothetical protein	---	AT4G14170	-1.16	-0.22	-2.13	0.07213837	0.3947	-4.72
262565_at	hypothetical protein predicted by g	---	AT1G34320	1.19	0.25	2.13	0.0721772	0.3947	-4.72
267346_at	coronatine-insensitive 1 (COI1), A	COI1	AT2G39940	1.25	0.33	2.13	0.07217586	0.3947	-4.72
264918_at	interferon-induced GTP-binding pr	---	AT1G60530	-1.18	-0.24	-2.13	0.07219104	0.3947	-4.72
256625_at	uteroglobin promoter-binding prote	---	AT3G20010	-1.33	-0.41	-2.13	0.07222524	0.3948	-4.72
248941_s_at	putative protein similar to unknown	---	AT5G45460 /	1.23	0.30	2.13	0.07224666	0.3948	-4.72
251120_at	chloroplast ribosomal L1 - like pro	---	AT3G63490	1.24	0.31	2.13	0.07232818	0.3952	-4.72
259422_at	unknown protein	---	AT1G13810	1.29	0.36	2.13	0.072461	0.3957	-4.72
259920_at	putative phenylalanyl-tRNA synthe	---	AT1G72550	1.18	0.24	2.13	0.07246092	0.3957	-4.72
260540_at	hypothetical protein predicted by g	---	AT2G43500	-1.16	-0.21	-2.13	0.07253151	0.3960	-4.73
266828_at	putative flavonol 3-O-glucosyltrans	---	AT2G22930	-1.15	-0.21	-2.13	0.07255342	0.3960	-4.73
259549_at	unknown protein ;supported by full	---	AT1G35290	1.18	0.24	2.13	0.07258051	0.3961	-4.73
251686_at	putative protein hypothetical protei	ATATG18D	AT3G56440	-1.17	-0.22	-2.13	0.07266037	0.3963	-4.73
247797_at	predicted protein	---	AT5G58780	-1.22	-0.28	-2.13	0.07264614	0.3963	-4.73
247005_at	adenylylsulfate kinase-like protein	---	AT5G67520	-1.26	-0.33	-2.13	0.07272254	0.3963	-4.73
247407_at	putative protein predicted proteins	---	AT5G62900	1.25	0.32	2.13	0.07270465	0.3963	-4.73
246754_at	transcription factor - like protein H	NF-YC8	AT5G27910	-1.25	-0.33	-2.13	0.07273512	0.3963	-4.73
247243_at	nodulin-like protein	---	AT5G64700	-1.32	-0.40	-2.13	0.07274398	0.3963	-4.73
260363_at	unknown protein similar to hypothe	---	AT1G70550	-1.24	-0.31	-2.13	0.07275305	0.3963	-4.73
265116_at	unknown protein ; supported by ful	---	AT1G62480	2.24	1.16	2.12	0.07286244	0.3968	-4.73
248704_at	putative protein pectinesterase-like	sks3	AT5G48450	-1.26	-0.33	-2.12	0.07290544	0.3970	-4.73
261801_at	hypothetical protein similar to hypo	AAE14	AT1G30520	1.26	0.34	2.12	0.07297358	0.3970	-4.73
263864_at	hypothetical protein predicted by g	CPZ	AT2G04530	1.19	0.26	2.12	0.07295279	0.3970	-4.73
253921_at	glutamine amidotransferase/cyclas	AT-HF	AT4G26900	1.21	0.27	2.12	0.07300899	0.3970	-4.73
264420_at	hypothetical protein predicted by g	---	AT1G43320	-1.16	-0.21	-2.12	0.07299333	0.3970	-4.73
262315_at	unknown protein ;supported by full	---	AT1G70990	1.43	0.52	2.12	0.0729891	0.3970	-4.73
267144_at	unknown protein	GPAT6	AT2G38110	1.50	0.59	2.12	0.07299068	0.3970	-4.73
249846_at	cation-transporting ATPase	---	AT5G23630	-1.15	-0.20	-2.12	0.07307234	0.3972	-4.73
267442_at	unknown protein ;supported by ful	---	AT2G19080	1.16	0.21	2.12	0.07314411	0.3975	-4.73
258003_at	expansin At-EXP5 identical to exp	EXPA5	AT3G29030	-1.79	-0.84	-2.12	0.07321576	0.3975	-4.73

247644_s_at	translation elongation factor eEF-1	---	AT1G07920	1.18	0.24	2.12	0.07318845	0.3975	-4.73
249020_at	helicase-like protein	CHR4	AT5G44800	1.21	0.28	2.12	0.07324191	0.3975	-4.73
263979_at	En/Spm-like transposon protein rel	PDF1	AT2G42840	-1.27	-0.35	-2.12	0.07324936	0.3975	-4.73
260275_at	hypothetical protein predicted by g	---	AT1G80610	-1.18	-0.24	-2.12	0.07319362	0.3975	-4.73
250696_at	putative protein similar to unknown	---	AT5G06790	1.13	0.18	2.12	0.07320059	0.3975	-4.73
265088_at	hypothetical protein similar to DNA	SWI2	AT1G03750	1.15	0.20	2.12	0.07350133	0.3975	-4.74
257515_at	zinc finger protein, putative similar	DOT5	AT1G13290	-1.17	-0.22	-2.12	0.07351171	0.3975	-4.74
250852_at	putative protein BRL protein, Hom	---	AT5G04670	-1.15	-0.21	-2.12	0.07348417	0.3975	-4.74
263638_at	unknown protein	---	AT2G25310	1.15	0.20	2.12	0.07352867	0.3975	-4.74
262544_at	hypothetical protein predicted by g	---	AT1G15420	-1.22	-0.28	-2.12	0.07345959	0.3975	-4.74
267561_at	putative protein kinase contains a	---	AT2G45590	-1.34	-0.42	-2.12	0.07347503	0.3975	-4.74
253607_at	small nuclear ribonucleoprotein ho	---	AT4G30330	1.26	0.33	2.12	0.07336063	0.3975	-4.74
255150_at	putative xylan endohydrolase	---	AT4G08160	1.33	0.42	2.12	0.0734118	0.3975	-4.74
267253_at	putative serine carboxypeptidase I	---	AT2G22960	-1.15	-0.20	-2.12	0.0733761	0.3975	-4.74
263879_at	hypothetical protein predicted by g	---	AT2G22030	-1.16	-0.21	-2.12	0.07342279	0.3975	-4.74
264738_at	unknown protein contains similarity	---	AT1G62250	-1.23	-0.30	-2.12	0.07339669	0.3975	-4.74
256443_at	hypothetical protein similar to hypo	---	AT3G10960	-1.37	-0.46	-2.12	0.07332066	0.3975	-4.74
254937_at	putative aldolase similar to 2,4-dih	---	AT4G10750	1.16	0.22	2.12	0.07342151	0.3975	-4.74
252561_at	histone H2B ;supported by full-len	HTB9	AT3G45980	1.28	0.36	2.12	0.07327404	0.3975	-4.74
257388_at	putative non-LTR retroelement rev	---	---	-1.13	-0.18	-2.12	0.07345204	0.3975	-4.74
262719_at	hypothetical protein predicted by g	---	---	1.19	0.25	2.12	0.07345774	0.3975	-4.74
254467_at	receptor protein kinase - like prote	---	AT4G20450	-1.21	-0.28	-2.12	0.07362378	0.3980	-4.74
245936_at	putative protein predicted proteins	---	AT5G19850	-1.24	-0.31	-2.12	0.07365553	0.3980	-4.74
263532_s_at	putative protein RIO1 protein, Sac	---	AT2G24990	1.26	0.34	2.12	0.07367435	0.3980	-4.74
253496_at	glutathione peroxidase - like prote	ATGPX7	AT4G31870	-1.67	-0.74	-2.11	0.07405573	0.3982	-4.75
258538_at	putative tRNA pseudouridine synth	---	AT3G06950	1.17	0.23	2.11	0.07395697	0.3982	-4.74
262326_at	hypothetical protein similar to puta	---	AT1G64140	-1.16	-0.21	-2.11	0.07392855	0.3982	-4.74
259036_at	putative laccase similar to laccase	LAC7	AT3G09220	-1.16	-0.21	-2.11	0.07395892	0.3982	-4.74
258482_at	putative chaperonin similar to chap	---	AT3G02530	1.22	0.29	2.11	0.07402331	0.3982	-4.75
252424_at	putative protein activating signal c	---	AT3G47610	1.25	0.32	2.12	0.07374561	0.3982	-4.74
264588_at	unknown protein contains similarity	---	AT2G17730	1.43	0.52	2.12	0.07383173	0.3982	-4.74
261225_at	unknown protein ;supported by full	---	AT1G20100	1.17	0.22	2.11	0.07402911	0.3982	-4.75
254121_at	putative protein putative protein F	---	AT4G24760	1.36	0.44	2.11	0.07391437	0.3982	-4.74
252449_at	FtsH protease, putative contains s	ftsh7	AT3G47060	-1.14	-0.19	-2.12	0.073814	0.3982	-4.74
262091_at	Myb-family transcription factor, pu	MYB72	AT1G56160	-1.17	-0.23	-2.11	0.07394449	0.3982	-4.74

266634_at	putative G-box binding bZIP transc	---	AT2G35530	-1.17	-0.22	-2.12	0.07382702	0.3982	-4.74
265688_at	putative calmodulin-binding protein	---	AT2G24300	1.14	0.19	2.11	0.07391505	0.3982	-4.74
248903_at	3-oxoacyl-[acyl-carrier-protein] syn	KAS I	AT5G46290	1.36	0.45	2.11	0.07400087	0.3982	-4.74
265261_at	putative APG isolog protein	---	AT2G42990	1.72	0.78	2.12	0.07382534	0.3982	-4.74
247170_at	putative protein contains similarity	---	AT5G65530	-1.15	-0.20	-2.11	0.07405033	0.3982	-4.75
251483_at	putative protein hypothetical prote	---	AT3G59650	1.21	0.28	2.11	0.07389029	0.3982	-4.74
245073_at	putative glucosyltransferase	---	AT2G23210	-1.19	-0.25	-2.11	0.07405173	0.3982	-4.75
266691_at	hypothetical protein predicted by g	---	AT2G19890	1.21	0.27	2.11	0.07398498	0.3982	-4.74
266842_at	FtsH protease, putative contains s	ftsh4	AT2G26140	-1.21	-0.28	-2.11	0.07397488	0.3982	-4.74
251665_at	responce reactor 4 ; supported by	ARR9	AT3G57040	1.57	0.65	2.11	0.07409476	0.3983	-4.75
262754_at	putative inosine-5-monophosphate	---	AT1G16350	1.22	0.28	2.11	0.07410743	0.3983	-4.75
253537_at	putative protein ; supported by full	HCF153	AT4G31560	1.20	0.26	2.11	0.07419914	0.3983	-4.75
247612_at	ATPase - like protein ATPase, So	---	AT5G60730	1.20	0.26	2.11	0.07416319	0.3983	-4.75
250637_at	glycine-rich protein atGRP-7	GRP17	AT5G07530	-1.19	-0.25	-2.11	0.07413787	0.3983	-4.75
248649_at	putative protein contains similarity	APRR4	AT5G49240	-1.21	-0.27	-2.11	0.07420374	0.3983	-4.75
248270_at	putative protein similar to unknown	ORG1	AT5G53450	-1.46	-0.55	-2.11	0.07417912	0.3983	-4.75
259669_at	short chain alcohol dehydrogenas	ABA2	AT1G52340	1.23	0.30	2.11	0.07413451	0.3983	-4.75
267611_at	unknown protein	SPX2	AT2G26660	1.36	0.44	2.11	0.0742979	0.3986	-4.75
247065_s_at	disease resistance protein-like	---	AT5G66900 /	1.24	0.32	2.11	0.07428457	0.3986	-4.75
264261_at	putative nicotianamine synthase si	NAS3	AT1G09240	1.94	0.96	2.11	0.07433238	0.3986	-4.75
264531_at	hypothetical protein predicted by g	---	AT1G30790	-1.17	-0.23	-2.11	0.07433989	0.3986	-4.75
258630_at	putative CCHC-type zinc finger pr	---	AT3G02820	1.29	0.37	2.11	0.07437791	0.3987	-4.75
249000_at	putative protein contains similarity	---	AT5G44980	-1.19	-0.25	-2.11	0.07445385	0.3990	-4.75
245039_at	putative beta-1,3-glucanase ;supp	---	AT2G26600	-1.19	-0.25	-2.11	0.07449427	0.3991	-4.75
252060_at	putative protein other hypothetical	PAD4	AT3G52430	1.79	0.84	2.11	0.07447919	0.3991	-4.75
247424_at	LIM7 - like protein LIM7, Lilium lon	AtVEX1	AT5G62850	-1.19	-0.24	-2.11	0.07451983	0.3991	-4.75
260980_at	hypothetical protein predicted by g	---	AT1G53600	-1.26	-0.34	-2.11	0.07455915	0.3992	-4.75
263251_at	unknown protein ; supported by cl	---	AT2G31410	1.40	0.49	2.11	0.07464515	0.3995	-4.75
250421_at	putative protein	OCP3	AT5G11270	1.24	0.31	2.11	0.07464556	0.3995	-4.75
253567_at	protein kinase-like protein serine/t	---	AT4G31230	-1.25	-0.32	-2.11	0.07476343	0.3997	-4.75
264735_s_at	hypothetical protein similar to hypo	---	AT1G62000 /	-1.24	-0.31	-2.11	0.0747249	0.3997	-4.75
247724_at	putative protein predicted protein,	MBD6	AT5G59380	1.17	0.22	2.11	0.07474948	0.3997	-4.75
248105_at	cell division protein FtsZ chloroplas	FTSZ1-1	AT5G55280	1.25	0.33	2.11	0.07473922	0.3997	-4.75
262772_at	puative calcium-transporting ATPa	ACA.I	AT1G13210	-1.41	-0.50	-2.11	0.07475714	0.3997	-4.75
261421_at	hypothetical protein similar to unkn	IQD30	AT1G18840	1.50	0.58	2.11	0.074804	0.3997	-4.76

247765_at	cytochrome P450 CYP86A1	CYP86A1	AT5G58860	1.38	0.47	2.11	0.07480449	0.3997	-4.76
248327_at	putative protein similar to unknown	---	AT5G52750	2.66	1.41	2.10	0.07496739	0.4004	-4.76
254890_at	phospholipid hydroperoxide glutath	ATGPX6	AT4G11600	-1.19	-0.25	-2.10	0.07496885	0.4004	-4.76
255113_at	putative protein various hypothetic	---	---	-1.17	-0.22	-2.10	0.07500564	0.4005	-4.76
246596_at	CARBONIC ANHYDRASE 2 ; sup	CA2	AT5G14740	1.18	0.24	2.10	0.07507809	0.4008	-4.76
256017_at	unknown protein ;supported by full	JAZ1	AT1G19180	-1.71	-0.77	-2.10	0.07510173	0.4008	-4.76
262790_at	putative translation initiation factor	TIF3H1	AT1G10840	1.13	0.18	2.10	0.07515612	0.4009	-4.76
256067_at	unknown protein ;supported by full	---	AT1G07170	1.25	0.32	2.10	0.07516506	0.4009	-4.76
248692_s_at	hypothetical protein	---	AT4G15070	1.19	0.25	2.10	0.075145	0.4009	-4.76
254915_s_at	cysteine proteinase contains simil	---	AT4G11310	-2.20	-1.14	-2.10	0.07519163	0.4009	-4.76
257193_at	Expressed protein ; supported by f	---	AT3G13160	1.16	0.21	2.10	0.075267	0.4012	-4.76
262846_at	endomembrane protein, putative s	---	AT1G14670	1.20	0.26	2.10	0.07537496	0.4013	-4.76
261833_at	ATP citrate-lyase, putative similar	ACLA-1	AT1G10670	1.18	0.24	2.10	0.07539842	0.4013	-4.76
253714_at	putative protein adaptor protein - H	---	AT4G29380	1.18	0.24	2.10	0.07538321	0.4013	-4.76
263173_at	hypothetical protein predicted by g	BRX-LIKE3	AT1G54180	-1.16	-0.21	-2.10	0.07540467	0.4013	-4.76
262866_at	cytochrome p450, putative similar	CYP89A6	AT1G64940	-1.15	-0.20	-2.10	0.07538942	0.4013	-4.76
259720_at	hypothetical protein predicted by g	---	AT1G61080	-1.21	-0.27	-2.10	0.07540332	0.4013	-4.76
261424_at	unknown protein	---	AT1G18700	1.14	0.19	2.10	0.07538714	0.4013	-4.76
266072_at	putative trehalose-6-phosphate sy	ATTPS11	AT2G18700	1.34	0.42	2.10	0.07550951	0.4015	-4.76
262068_at	splicing factor Prp8, putative simil	SUS2	AT1G80070	1.27	0.34	2.10	0.07546612	0.4015	-4.76
266744_at	putative nucleoside triphosphatase	---	AT2G02970	-1.15	-0.20	-2.10	0.0755007	0.4015	-4.76
265554_at	hypothetical protein predicted by g	---	AT2G07505	-1.15	-0.20	-2.10	0.07548575	0.4015	-4.76
263379_at	putative CCCH-type zinc finger pro	CZF1	AT2G40140	2.00	1.00	2.10	0.07555209	0.4015	-4.77
254158_at	putative protein dihydrofolate redu	---	AT4G24380	-2.04	-1.03	-2.10	0.07554185	0.4015	-4.77
258717_at	unknown protein ; supported by c	SYP71	AT3G09740	1.14	0.19	2.10	0.0756537	0.4018	-4.77
258643_at	unknown protein ;supported by ful	ATAB2	AT3G08010	1.15	0.20	2.10	0.07565405	0.4018	-4.77
265031_at	serine/threonine protein kinase, pu	---	AT1G61590	1.15	0.20	2.10	0.07562941	0.4018	-4.77
262531_at	putative leucine-rich receptor prote	---	AT1G17230	-1.26	-0.33	-2.10	0.07570815	0.4019	-4.77
248322_at	putative protein similar to unknown	---	AT5G52760	3.67	1.87	2.10	0.07569308	0.4019	-4.77
257972_at	putative protein kinase, ATN1 alm	ATN1	AT3G27560	1.20	0.26	2.10	0.07578534	0.4019	-4.77
248677_at	unknown protein	---	AT5G48860	-1.19	-0.25	-2.10	0.07575475	0.4019	-4.77
259173_at	beta-glucosidase identical to beta-	BGLU25	AT3G03640	1.36	0.44	2.10	0.0757643	0.4019	-4.77
254560_at	kinase-like protein protein kinase	---	AT4G19110	-1.15	-0.20	-2.10	0.07577877	0.4019	-4.77
260327_at	putative RING zinc finger protein	---	AT1G63840	1.33	0.41	2.10	0.0758309	0.4019	-4.77
257080_at	unknown protein	---	AT3G15240	-1.14	-0.19	-2.10	0.0758399	0.4019	-4.77

247109_at	putative protein similar to unknown	ATPSK5	AT5G65870	-1.43	-0.52	-2.10	0.07583729	0.4019	-4.77
265567_at	unknown protein predicted by gene	---	AT2G05580	-1.22	-0.28	-2.10	0.07588018	0.4020	-4.77
259025_at	hypothetical protein predicted by g	---	---	-1.24	-0.32	-2.10	0.07586588	0.4020	-4.77
245621_at	AMP-binding protein	AAE15	AT4G14070	1.28	0.36	2.10	0.07592878	0.4020	-4.77
256904_at	unknown protein	---	AT3G23980	-1.15	-0.20	-2.10	0.07592405	0.4020	-4.77
251297_at	germin-like protein (GLP10)	GLP10	AT3G62020	1.57	0.65	2.10	0.07599265	0.4022	-4.77
259727_at	ferrodoxin precursor identical to FE	FED A	AT1G60950	1.15	0.21	2.10	0.07598006	0.4022	-4.77
247823_at	putative protein predicted proteins	---	AT5G58450	-1.14	-0.19	-2.09	0.07604299	0.4024	-4.77
256119_at	guanine nucleotide regulatory prot	---	AT1G18070	-1.19	-0.25	-2.09	0.07608424	0.4025	-4.77
261628_at	hypothetical protein predicted by g	---	AT1G50000	-1.16	-0.21	-2.09	0.07614459	0.4027	-4.77
259642_at	hypothetical protein predicted by g	---	AT1G69030	-1.29	-0.37	-2.09	0.07624826	0.4029	-4.77
256855_at	30S ribosomal protein S20 contain	---	AT3G15190	1.23	0.30	2.09	0.07626397	0.4029	-4.77
256225_at	unknown protein ; supported by ful	---	AT1G56220	1.27	0.35	2.09	0.07619869	0.4029	-4.77
260247_at	putative disease resistance protein	AtRLP16	AT1G74200	-1.15	-0.20	-2.09	0.07621975	0.4029	-4.77
252893_at	hypothetical protein	---	AT4G39420	-1.14	-0.18	-2.09	0.07625481	0.4029	-4.77
253889_at	forever young gene (FEY)	FEY	AT4G27760	1.15	0.21	2.09	0.0764612	0.4033	-4.78
265602_at	putative retroelement pol polyprote	---	---	-1.21	-0.27	-2.09	0.07642941	0.4033	-4.78
245719_at	DNA gyrase subunit B - like protein	---	AT5G04110	-1.17	-0.23	-2.09	0.07639872	0.4033	-4.78
265238_s_at	hypothetical protein	---	AT2G07696	-1.28	-0.36	-2.09	0.07643064	0.4033	-4.78
265378_at	putative GATA-type zinc finger tran	---	AT2G18380	1.18	0.23	2.09	0.07645487	0.4033	-4.78
251348_at	putative protein hypothetical prote	---	AT3G61010	1.28	0.36	2.09	0.07645171	0.4033	-4.78
265873_at	putative beta-1,3-glucanase ;supp	---	AT2G01630	1.22	0.29	2.09	0.07643049	0.4033	-4.78
250648_at	late embryogenesis abundant prot	---	AT5G06760	-1.20	-0.26	-2.09	0.07649369	0.4033	-4.78
246103_at	putative protein	AN3	AT5G28640	-1.14	-0.19	-2.09	0.07654676	0.4034	-4.78
261747_at	unknown protein similar to putative	---	AT1G08350	1.25	0.32	2.09	0.07652393	0.4034	-4.78
265129_at	putative zinc finger protein similar	SUF4	AT1G30970	-1.19	-0.25	-2.09	0.0765661	0.4034	-4.78
249380_at	glutaredoxin -like protein glutared	---	AT5G40370	-1.16	-0.21	-2.09	0.07657224	0.4034	-4.78
259595_at	CONSTANS family zinc finger pro	---	AT1G28050	-1.29	-0.37	-2.09	0.07663824	0.4036	-4.78
255625_at	GBF2, G-box binding factor ;supp	GBF2	AT4G01120	1.31	0.39	2.09	0.07665788	0.4036	-4.78
257623_at	cytochrome P450, putative contain	CYP71B23	AT3G26210	1.67	0.74	2.09	0.07677663	0.4038	-4.78
262882_at	cytochrome p450, putative similar	CYP89A2	AT1G64900	-1.62	-0.69	-2.09	0.07674124	0.4038	-4.78
263004_at	hypothetical protein contains simila	ATNEK1	AT1G54510	1.20	0.27	2.09	0.07674686	0.4038	-4.78
255632_at	putative actin-depolymerizing facto	ADF8	AT4G00680	-1.14	-0.19	-2.09	0.07678224	0.4038	-4.78
262401_at	small GTP-binding protein, putativ	RABG3E	AT1G49300	1.15	0.20	2.09	0.07679214	0.4038	-4.78
248077_at	putative protein contains similarity	---	AT5G55770	1.17	0.22	2.09	0.0767098	0.4038	-4.78

252672_at	hypothetical protein	---	AT3G44230	-1.15	-0.20	-2.09	0.07682896	0.4039	-4.78
261285_at	Ca2+-dependent membrane-bindir	ANNAT1	AT1G35720	-1.56	-0.64	-2.09	0.07687135	0.4040	-4.78
249484_at	cytochrome P450 - like protein cyt	BR6OX1	AT5G38970	-1.16	-0.22	-2.09	0.07699963	0.4046	-4.78
266980_at	60S ribosomal protein L35 ;suppo	---	AT2G39390	1.37	0.45	2.09	0.07705848	0.4048	-4.78
257072_at	myrosinase-associated protein, pu	---	AT3G14220	-1.38	-0.47	-2.09	0.07708419	0.4048	-4.78
AFFX-r2-Ec-bio	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.38	-0.47	-2.09	0.07709653	0.4048	-4.78
267586_at	hypothetical protein predicted by g	---	AT2G41950	1.25	0.33	2.08	0.07719369	0.4052	-4.79
252505_at	dehydrogenase -like protein alcoh	---	AT3G46170	-1.20	-0.26	-2.08	0.07717619	0.4052	-4.79
262610_at	putative mitochondrial uncoupling	---	AT1G14140	1.14	0.19	2.08	0.07730569	0.4056	-4.79
246352_at	hypothetical protein	---	---	-1.14	-0.19	-2.08	0.07733901	0.4057	-4.79
252488_at	glucuronosyl transferase-like prote	---	AT3G46700	-1.17	-0.22	-2.08	0.07736675	0.4058	-4.79
252586_at	dof6 zinc finger protein	---	AT3G45610	1.19	0.26	2.08	0.07739907	0.4059	-4.79
246855_at	putative protein various predicted	---	AT5G26280	1.58	0.66	2.08	0.07748003	0.4059	-4.79
252236_at	zinc-finger-like protein Cys2/His2-	---	AT3G49930	1.19	0.25	2.08	0.07746834	0.4059	-4.79
259194_at	RNA helicase, DRH1 identical to I	DRH1	AT3G01540	-1.14	-0.19	-2.08	0.07747519	0.4059	-4.79
247957_at	protein phosphatase 2C ABI2 (PP2	ABI2	AT5G57050	-1.37	-0.45	-2.08	0.07746147	0.4059	-4.79
260855_at	phosphatidylinositol-4-phosphate	---	AT1G21920	1.28	0.35	2.08	0.07751421	0.4060	-4.79
262714_s_at	unknown protein similar to gb|AJ22	---	AT1G07950	1.16	0.22	2.08	0.07753882	0.4060	-4.79
256064_at	Expressed protein ; supported by f	---	AT1G07020	1.18	0.24	2.08	0.07759974	0.4061	-4.79
259131_at	unknown protein similar to hypothe	SP1L3	AT3G02180	1.17	0.23	2.08	0.07765491	0.4061	-4.79
256996_at	unknown protein similar to unknow	---	AT3G25850	-1.15	-0.20	-2.08	0.07763961	0.4061	-4.79
245079_at	putative retroelement pol polyprote	---	---	-1.15	-0.20	-2.08	0.07763623	0.4061	-4.79
255669_at	predicted protein	MBD3	AT4G00416	-1.14	-0.19	-2.08	0.07763176	0.4061	-4.79
245601_at	hypothetical protein	---	AT4G14240	-1.20	-0.27	-2.08	0.07760788	0.4061	-4.79
254788_at	putative protein other predicted pr	---	AT4G12790	-1.16	-0.21	-2.08	0.07771009	0.4062	-4.79
261418_at	mitochondrial ribosomal protein, p	---	AT1G07830	1.29	0.36	2.08	0.0777092	0.4062	-4.79
265936_at	putative potassium/proton antiporte	ATKEA4	AT2G19600	-1.22	-0.28	-2.08	0.0777974	0.4064	-4.79
247860_at	bis(5'-adenosyl)-triphosphatase-lik	---	AT5G58240	1.17	0.23	2.08	0.07780561	0.4064	-4.79
254730_at	putative protein GTPase activating	---	AT4G13730	1.15	0.21	2.08	0.07780916	0.4064	-4.79
253920_at	histone H2A- like protein histone H	HTA2	AT4G27230	1.29	0.36	2.08	0.07787983	0.4066	-4.79
255491_at	putative zinc finger protein similar	AtIDD12	AT4G02670	-1.14	-0.19	-2.08	0.07788753	0.4066	-4.79
249190_at	unknown protein ;supported by ful	BKI1	AT5G42750	1.20	0.27	2.08	0.07789467	0.4066	-4.80
253004_at	putative protein	---	AT4G38280	1.26	0.33	2.08	0.07794991	0.4068	-4.80
260867_at	hypothetical protein predicted by g	TED6	AT1G43790	1.74	0.80	2.08	0.07810351	0.4069	-4.80
255546_at	putative CHP-rich zinc finger prote	---	AT4G01910	1.49	0.57	2.08	0.07803438	0.4069	-4.80

247048_at	photoreceptor-interacting protein-li	---	AT5G66560	-1.42	-0.51	-2.08	0.07811738	0.4069	-4.80
253329_at	hypothetical protein	---	AT4G33480	1.16	0.21	2.08	0.07812728	0.4069	-4.80
256072_at	WD-40 repeat protein identical to V	ATARCA	AT1G18080	1.41	0.49	2.08	0.07814941	0.4069	-4.80
253752_at	putative protein ;supported by full-	---	AT4G28910	-1.23	-0.30	-2.08	0.07799915	0.4069	-4.80
255198_at	contains similarity to an Arabidops	---	---	-1.16	-0.21	-2.08	0.07805437	0.4069	-4.80
248094_at	trigger factor-like protein	---	AT5G55220	1.25	0.32	2.08	0.07809493	0.4069	-4.80
261456_at	hypothetical protein predicted by g	---	AT1G21050	2.22	1.15	2.08	0.07814385	0.4069	-4.80
260507_at	unknown protein contains similarity	WPP2	AT1G47200	1.25	0.32	2.08	0.07805199	0.4069	-4.80
266074_at	putative small nuclear ribonucleopr	---	AT2G18740	1.31	0.39	2.08	0.07824014	0.4069	-4.80
252228_at	porin - like protein porin, Mesembr	VDAC5	AT3G49920	1.15	0.21	2.07	0.07826669	0.4069	-4.80
250108_at	homeobox-leucine zipper protein H	ATHB-3	AT5G15150	-1.23	-0.30	-2.07	0.07828777	0.4069	-4.80
267289_at	putative protein kinase contains a	---	AT2G23770	-1.15	-0.21	-2.07	0.07829942	0.4069	-4.80
245047_at	PSII 32 KDa protein	---	---	-1.17	-0.22	-2.08	0.07817844	0.4069	-4.80
247615_at	putative protein various predicted	---	AT5G60250	-1.15	-0.20	-2.08	0.07824743	0.4069	-4.80
257989_at	unknown protein ; supported by cD	VPS9A	AT3G19770	-1.19	-0.25	-2.07	0.0782836	0.4069	-4.80
266091_at	hypothetical protein predicted by g	emb1513	AT2G37920	1.22	0.29	2.07	0.07826242	0.4069	-4.80
254179_at	putative protein various predicted	---	AT4G23910	1.27	0.34	2.07	0.0784107	0.4070	-4.80
253745_at	putative protein the C-terminus of	---	AT4G29090	-1.17	-0.23	-2.07	0.07840758	0.4070	-4.80
265869_at	putative two-component response	ARR14	AT2G01760	1.24	0.31	2.07	0.07839709	0.4070	-4.80
249313_at	unknown protein	---	AT5G41560	1.16	0.21	2.07	0.07835485	0.4070	-4.80
247916_at	adenosylmethionine-8-amino-7-ox	BIO1	AT5G57590	-1.19	-0.25	-2.07	0.07837697	0.4070	-4.80
252618_at	lipoxygenase AtLOX2 ; supported	LOX2	AT3G45140	-1.26	-0.33	-2.07	0.07843553	0.4071	-4.80
248633_at	arginine methyltransferase-like pro	PRMT4A	AT5G49020	1.19	0.26	2.07	0.07845324	0.4071	-4.80
262414_at	acyl CoA synthetase, putative sim	LACS2	AT1G49430	1.91	0.93	2.07	0.07847975	0.4071	-4.80
262112_at	unknown protein ;supported by full	---	AT1G02870	1.25	0.32	2.07	0.07855062	0.4072	-4.80
255153_at	putative protein several hypothetic	---	AT4G08210	-1.23	-0.30	-2.07	0.07852881	0.4072	-4.80
262781_s_at	proteasome epsilon chain precurso	PBE1	AT1G13060	1.22	0.29	2.07	0.07854803	0.4072	-4.80
260481_at	ferredoxin precusor isolog ;suppor	ATFD1	AT1G10960	-1.34	-0.42	-2.07	0.07862875	0.4074	-4.80
256966_at	pollen specific protein, putative sir	sks13	AT3G13400	1.15	0.20	2.07	0.07861917	0.4074	-4.80
259746_at	hypothetical protein predicted by g	---	AT1G71060	1.26	0.34	2.07	0.07868855	0.4077	-4.80
250750_at	glucuronosyl transferase-like prote	UGT76C2	AT5G05860	-1.18	-0.24	-2.07	0.07870777	0.4077	-4.81
251402_at	SRG1 - like protein SRG1 protein,	---	AT3G60290	1.50	0.59	2.07	0.07874366	0.4077	-4.81
245144_at	putative methionine aminopeptidas	MAP1A	AT2G45240	1.19	0.25	2.07	0.07874505	0.4077	-4.81
257513_s_at	hypothetical protein	---	AT1G12340	1.19	0.25	2.07	0.07877429	0.4077	-4.81
250617_at	Mei2-like protein Mei2-like protein	AML4	AT5G07290	-1.21	-0.28	-2.07	0.07881448	0.4078	-4.81

253971_at	fructose-bisphosphate aldolase - l	---	AT4G26530	-1.43	-0.51	-2.07	0.07885045	0.4079	-4.81
266761_at	putative alcohol dehydrogenase	---	AT2G47130	1.50	0.58	2.07	0.07887073	0.4079	-4.81
245471_at	probable ribosomal protein	---	AT4G16030	-1.16	-0.21	-2.07	0.07893203	0.4082	-4.81
256699_at	hypothetical protein predicted by g	---	AT3G20690	-1.21	-0.28	-2.07	0.07897201	0.4083	-4.81
256050_at	leucine zipper protein, putative sir	ATEXO70B	AT1G07000	1.18	0.24	2.07	0.07900047	0.4083	-4.81
258784_at	unknown protein	---	AT3G11770	1.32	0.41	2.07	0.07900913	0.4083	-4.81
258021_at	hypothetical protein predicted gene	PUB25	AT3G19380	1.66	0.73	2.07	0.07905786	0.4084	-4.81
250433_at	histone H3 - like protein histone H	---	AT5G10400	1.21	0.27	2.07	0.07906045	0.4084	-4.81
263319_at	putative anion exchange protein id	BOR1	AT2G47160	-1.39	-0.47	-2.07	0.07908281	0.4084	-4.81
258945_at	calmodulin-domain protein kinase	CPK2	AT3G10660	-1.14	-0.19	-2.07	0.07910722	0.4084	-4.81
250986_at	putative protein	---	AT5G02850	1.17	0.23	2.07	0.07912821	0.4084	-4.81
267230_at	unknown protein	ARL	AT2G44080	2.37	1.24	2.07	0.07917095	0.4086	-4.81
265050_at	jasmonate inducible protein, putat	---	AT1G52070	-1.16	-0.21	-2.07	0.07921153	0.4087	-4.81
265148_at	unknown protein	---	AT1G51160	1.18	0.24	2.07	0.07936372	0.4094	-4.81
256279_at	protein phosphatase 2C, putative	---	AT3G12620	-1.13	-0.18	-2.06	0.07951463	0.4101	-4.82
246870_at	ferrochelatase-I	FC1	AT5G26030	-1.70	-0.76	-2.06	0.07955562	0.4102	-4.82
263945_at	hypothetical protein predicted by g	---	AT2G36030	-1.24	-0.31	-2.06	0.07960099	0.4103	-4.82
247770_at	putative protein predicted proteins	---	AT5G58930	1.53	0.62	2.06	0.07962115	0.4103	-4.82
253775_at	putative protein T01B08.14 gene,	---	AT4G28440	1.15	0.20	2.06	0.0796484	0.4104	-4.82
258183_at	unknown protein ;supported by ful	---	AT3G21550	1.73	0.79	2.06	0.07973889	0.4105	-4.82
244945_at	cytochrome c biogenesis orf206	---	---	-1.23	-0.30	-2.06	0.07974698	0.4105	-4.82
265524_at	hypothetical protein	---	---	-1.14	-0.19	-2.06	0.07976767	0.4105	-4.82
250373_at	putative protein	---	AT5G11470	-1.14	-0.19	-2.06	0.0797789	0.4105	-4.82
249337_at	putative protein contains similarity	---	AT5G41080	1.88	0.91	2.06	0.07973004	0.4105	-4.82
247340_at	unknown protein	---	AT5G63700	-1.15	-0.21	-2.06	0.07978594	0.4105	-4.82
247058_at	dolichyl-di-phosphooligosaccharide	DGL1	AT5G66680	1.21	0.27	2.06	0.07980908	0.4106	-4.82
253758_at	Expressed protein ;supported by c	emb2726	AT4G29060	1.22	0.29	2.06	0.07987892	0.4107	-4.82
245496_at	LET1 like protein	---	AT4G16440	-1.17	-0.23	-2.06	0.07986754	0.4107	-4.82
247099_at	putative protein contains similarity	---	AT5G66500	-1.21	-0.27	-2.06	0.0799293	0.4109	-4.82
245050_at	PSII K protein	---	---	-1.14	-0.18	-2.06	0.0799741	0.4110	-4.82
256845_x_at	hypothetical protein similar to puta	---	---	-1.17	-0.23	-2.06	0.08002333	0.4112	-4.82
264608_at	putative acetyl-CoA acyltransferas	PKT4	AT1G04710	-1.18	-0.24	-2.06	0.08009579	0.4114	-4.82
266547_at	similar to eyes absent protein ;sup	ATEYA	AT2G35320	1.15	0.20	2.06	0.08009467	0.4114	-4.82
250816_at	coatomer delta subunit (delta-coat	---	AT5G05010	1.24	0.31	2.06	0.08011504	0.4114	-4.82
253965_at	hypothetical protein	---	AT4G26490	1.24	0.31	2.06	0.08016397	0.4115	-4.82

252285_at	calmodulin-binding heat-shock - li	---	AT3G49050	1.18	0.24	2.06	0.0801478	0.4115	-4.82
251977_at	putative protein auxin-induced pro	---	AT3G53250	-1.15	-0.20	-2.06	0.08019616	0.4115	-4.82
251855_at	sugar-phosphate isomerase - like	---	AT3G54690	1.40	0.48	2.06	0.08030151	0.4116	-4.82
250938_at	putative protein various predicted	---	AT5G03180	1.26	0.33	2.06	0.08026941	0.4116	-4.82
255948_at	hypothetical protein predicted by g	---	AT1G22060	1.15	0.20	2.06	0.08028762	0.4116	-4.82
251353_at	putative protein hypothetical prote	---	AT3G61080	-1.24	-0.31	-2.06	0.0803262	0.4116	-4.82
246180_at	putative protein predicted proteins	---	AT5G20840	-1.17	-0.22	-2.06	0.08033783	0.4116	-4.83
257460_at	auxin induced protein, putative sir	---	AT1G75580	-1.17	-0.22	-2.06	0.0803135	0.4116	-4.82
262283_at	unknown protein ;supported by full	---	AT1G68590	1.24	0.32	2.06	0.08034195	0.4116	-4.83
256791_at	hypothetical protein predicted by g	---	---	-1.25	-0.32	-2.06	0.08035501	0.4116	-4.83
265990_at	putative prolylcarboxypeptidase	---	AT2G24280	-1.30	-0.38	-2.06	0.08039008	0.4117	-4.83
262161_at	signal peptidase subunit, putative	---	AT1G52600	1.16	0.22	2.06	0.08051608	0.4121	-4.83
265779_at	unknown protein	---	AT2G07360	-1.29	-0.37	-2.06	0.08048091	0.4121	-4.83
260223_at	putative exonuclease contains Pfa	---	AT1G74390	1.18	0.23	2.06	0.08051702	0.4121	-4.83
249610_at	putative protein	---	AT5G37360	-1.40	-0.49	-2.06	0.08055887	0.4122	-4.83
252210_at	DNA binding protein	OBP1	AT3G50410	-1.30	-0.37	-2.05	0.08057238	0.4122	-4.83
246465_at	quinone oxidoreductase - like prot	---	AT5G17000	-1.33	-0.41	-2.05	0.08059926	0.4122	-4.83
255082_at	putative protein polyphosphoinosi	---	AT4G09160	-1.17	-0.22	-2.05	0.08064215	0.4123	-4.83
252361_at	hypothetical protein	---	AT3G48490	1.41	0.49	2.05	0.08065376	0.4123	-4.83
248020_at	putative protein strong similarity to	---	AT5G56490	-1.15	-0.20	-2.05	0.08069546	0.4123	-4.83
263285_at	unknown protein	DOT1	AT2G36120	-1.36	-0.44	-2.05	0.08069462	0.4123	-4.83
256367_at	C-x8-C-x5-C-x3-H type Zinc finge	---	AT1G66810	-1.19	-0.25	-2.05	0.08073247	0.4124	-4.83
264196_at	putative RING zinc finger protein C	---	AT1G22670	1.16	0.22	2.05	0.0807438	0.4124	-4.83
248774_at	unknown protein	---	AT5G47830	-1.16	-0.21	-2.05	0.08077071	0.4124	-4.83
261802_at	hypothetical protein similar to hypo	---	AT1G30550	1.18	0.24	2.05	0.08088805	0.4129	-4.83
249510_at	putative protein similar to unknown	---	AT5G38510	-1.19	-0.25	-2.05	0.08102716	0.4130	-4.83
266036_s_at	20S proteasome subunit (PAA2) id	PAA2	AT2G05840	1.17	0.23	2.05	0.08101444	0.4130	-4.83
266453_at	putative protein kinase contains a	---	AT2G43230	-1.15	-0.20	-2.05	0.08099814	0.4130	-4.83
252163_at	hypothetical protein	---	AT3G50610	-1.18	-0.24	-2.05	0.08099293	0.4130	-4.83
262671_at	calcium-dependent protein kinase	CPK29	AT1G76040	-1.24	-0.31	-2.05	0.08101581	0.4130	-4.83
262007_at	hypothetical protein predicted by g	---	AT1G64580	-1.18	-0.24	-2.05	0.08094388	0.4130	-4.83
246142_at	putative protein	---	AT5G19970	-1.15	-0.20	-2.05	0.0810029	0.4130	-4.83
255750_at	hypothetical protein predicted by g	---	AT1G31960	-1.17	-0.23	-2.05	0.08105375	0.4131	-4.83
251207_at	putative protein ;supported by full-	---	AT3G63050	-1.36	-0.44	-2.05	0.08111745	0.4133	-4.83
250076_at	putative protein; similar to unknow	---	AT5G16660	1.20	0.27	2.05	0.08120094	0.4135	-4.84

261491_at	hypothetical protein contains simila	FLP	AT1G14350	-1.56	-0.64	-2.05	0.08119367	0.4135	-4.84
245386_at	hypothetical protein ;supported by	RALFL32	AT4G14010	-1.47	-0.56	-2.05	0.08127962	0.4136	-4.84
260356_at	unknown protein ; supported by fu	ATMINE1	AT1G69390	1.17	0.23	2.05	0.08130488	0.4136	-4.84
252344_s_at	putative protein	---	AT3G44160	-1.17	-0.23	-2.05	0.08123888	0.4136	-4.84
254355_at	Ribosomal protein L7Ae - like NHI	---	AT4G22380	1.30	0.37	2.05	0.08130681	0.4136	-4.84
266420_at	putative RNA-binding protein ; sup	---	AT2G38610	1.14	0.19	2.05	0.08125766	0.4136	-4.84
246822_at	putative protein predicted proteins	---	AT5G26960	-1.20	-0.27	-2.05	0.08134097	0.4137	-4.84
245340_at	elicitor like protein ; supported by f	---	AT4G14420	1.28	0.36	2.05	0.08137136	0.4137	-4.84
261298_at	cytochrome c oxidase assembly p	---	AT1G48510	-1.16	-0.22	-2.05	0.0814284	0.4139	-4.84
264705_at	putative leucyl-tRNA synthetase S	---	AT1G09620	1.20	0.27	2.05	0.08150293	0.4142	-4.84
262365_at	disease resistance protein, putativ	---	AT1G72870	-1.21	-0.28	-2.05	0.08152458	0.4143	-4.84
251637_at	hypothetical protein	---	AT3G57570	1.19	0.26	2.05	0.08154909	0.4143	-4.84
252223_at	MYB -like protein DNA-binding pro	TRB3	AT3G49850	1.28	0.35	2.05	0.08159928	0.4144	-4.84
255552_at	S-adenosylmethionine synthase 2	SAM-2	AT4G01850	1.19	0.25	2.05	0.08167386	0.4145	-4.84
258351_at	hypothetical protein contains simila	CNBT1	AT3G17700	1.29	0.37	2.05	0.08169144	0.4145	-4.84
260017_at	hypothetical protein predicted by g	---	---	-1.30	-0.38	-2.05	0.08168855	0.4145	-4.84
251286_at	putative protein Bcl-2-interacting p	---	AT3G61710	1.16	0.22	2.05	0.08166692	0.4145	-4.84
255679_at	putative acetyl CoA thioesterase	---	AT4G00520	-1.25	-0.32	-2.05	0.08171188	0.4146	-4.84
261533_at	hypothetical protein predicted by g	---	AT1G71690	-1.24	-0.31	-2.04	0.08177257	0.4148	-4.84
267099_at	DNA-(apurinic or apyrimidinic site)	ARP	AT2G41460	1.30	0.38	2.04	0.08180258	0.4148	-4.84
250054_at	potassium-dependent sodium-calc	CAX7	AT5G17860	1.55	0.63	2.04	0.08193867	0.4153	-4.84
256356_s_at	hypothetical protein	---	AT1G66500	-1.20	-0.26	-2.04	0.08193565	0.4153	-4.84
257663_at	hypothetical protein predicted by g	---	AT3G20260	1.18	0.23	2.04	0.08200729	0.4156	-4.85
252872_at	putative serine/threonine protein k	SNRK2.7	AT4G40010	-1.15	-0.20	-2.04	0.08202181	0.4156	-4.85
264684_at	unknown protein	HEXO3	AT1G65590	-1.38	-0.47	-2.04	0.08208036	0.4157	-4.85
254462_at	putative protein ;supported by full-	---	AT4G20150	1.14	0.19	2.04	0.08208754	0.4157	-4.85
248111_at	wax synthase-like protein	---	AT5G55330	-1.16	-0.22	-2.04	0.08212934	0.4158	-4.85
261222_at	anter-specific proline-rich protein A	---	AT1G20120	-1.16	-0.21	-2.04	0.08217652	0.4159	-4.85
264082_at	unknown protein ;supported by ful	---	AT2G28570	1.17	0.23	2.04	0.0821892	0.4159	-4.85
266130_at	putative transcription activator	---	AT2G44980	1.30	0.37	2.04	0.08217493	0.4159	-4.85
248379_at	RAR1 (gb|AAF18433.1) non-conse	PBS2	AT5G51700	1.18	0.24	2.04	0.08221153	0.4159	-4.85
258798_at	hypothetical protein predicted by g	---	AT3G04540	-1.19	-0.25	-2.04	0.08223272	0.4159	-4.85
258461_at	hypothetical protein predicted by g	---	AT3G17340	-1.15	-0.20	-2.04	0.08229202	0.4161	-4.85
264299_s_at	hypothetical protein predicted by g	---	AT1G78850	-1.47	-0.56	-2.04	0.08241455	0.4163	-4.85
250745_at	putative protein strong similarity to	---	AT5G05850	1.29	0.36	2.04	0.08242372	0.4163	-4.85

247250_at	FAS2 (dbj|BAA77766.1) ; support	FAS2	AT5G64630	1.30	0.38	2.04	0.08238942	0.4163	-4.85
262238_at	hypothetical protein predicted by g	---	AT1G48300	-1.31	-0.39	-2.04	0.0824233	0.4163	-4.85
253347_at	putative protein	---	AT4G33610	-1.16	-0.21	-2.04	0.08241446	0.4163	-4.85
263265_at	hypothetical protein predicted by g	---	AT2G38820	1.30	0.38	2.04	0.08245862	0.4164	-4.85
265969_at	En/Spm-like transposon protein rel	---	---	-1.17	-0.23	-2.04	0.08251681	0.4166	-4.85
250529_at	RNA helicase-like protein	---	AT5G08610	1.26	0.33	2.04	0.08262042	0.4167	-4.85
267523_at	unknown protein	---	AT2G30600	-1.19	-0.25	-2.04	0.08263765	0.4167	-4.85
257324_at	hypothetical protein	---	---	-1.58	-0.66	-2.04	0.08262531	0.4167	-4.85
253754_at	glycine-rich protein like glycine-ric	---	AT4G29020	-1.79	-0.84	-2.04	0.08258184	0.4167	-4.85
249150_at	inorganic phosphate transporter (d	PHT6	AT5G43340	-1.16	-0.21	-2.04	0.08259145	0.4167	-4.85
254676_at	putative protein Hypothetical prote	---	AT4G18460	1.22	0.29	2.04	0.08262009	0.4167	-4.85
263380_at	hypothetical protein	---	AT2G40200	-1.17	-0.23	-2.04	0.08265958	0.4167	-4.85
250822_at	unknown protein	---	AT5G05230	1.15	0.21	2.04	0.08273629	0.4170	-4.85
255923_at	hypothetical protein contains Pfam	---	AT1G22180	-1.56	-0.64	-2.04	0.08278481	0.4171	-4.85
264439_at	adenine phosphoribosyltransferas	APT1	AT1G27450	1.18	0.24	2.04	0.08279137	0.4171	-4.85
258323_at	unknown protein similar to putative	---	AT3G22750	1.26	0.33	2.04	0.08281207	0.4171	-4.85
256520_at	hypothetical protein	CYP96A14	AT1G66030	-1.17	-0.22	-2.04	0.08283076	0.4171	-4.85
259174_at	hypothetical protein similar to puta	UNE7	AT3G03690	-1.13	-0.18	-2.04	0.08292875	0.4172	-4.86
256792_at	hypothetical protein predicted by g	---	AT3G22150	1.43	0.52	2.03	0.08294638	0.4172	-4.86
252368_at	cytochrome P450-like protein cyto	CYP94B3	AT3G48520	-1.48	-0.57	-2.04	0.08288992	0.4172	-4.86
263633_at	putative SCARECROW gene regu	SCL21	AT2G04890	1.22	0.29	2.04	0.08291909	0.4172	-4.86
265106_s_at	putative membrane-associated sal	---	AT1G62590 /	-1.14	-0.19	-2.03	0.08294061	0.4172	-4.86
259093_at	unknown protein similar to putative	---	AT3G04860	1.38	0.46	2.03	0.08312122	0.4179	-4.86
255950_at	hypothetical protein predicted by g	---	AT1G22110	-1.24	-0.31	-2.03	0.08312703	0.4179	-4.86
247403_at	putative protein hypersensitive-ind	---	AT5G62740	1.17	0.23	2.03	0.08318677	0.4179	-4.86
260894_at	hypothetical protein contains simila	---	AT1G29220	1.16	0.21	2.03	0.08318049	0.4179	-4.86
252444_at	putative protein Na+-dependent in	PHT4;3	AT3G46980	1.14	0.19	2.03	0.0831759	0.4179	-4.86
257487_at	hypothetical protein predicted by g	---	AT1G71850	-1.36	-0.44	-2.03	0.08326949	0.4180	-4.86
246015_at	putative protein predicted proteins	---	AT5G10700	1.16	0.22	2.03	0.08324518	0.4180	-4.86
250288_at	auxin-responsive - like protein Nt-	---	AT5G13350	-1.19	-0.25	-2.03	0.08325003	0.4180	-4.86
259917_at	hypothetical protein predicted by g	---	AT1G72580	1.17	0.23	2.03	0.08325337	0.4180	-4.86
250277_at	putative protein DRT100 protein p	---	AT5G12940	2.35	1.23	2.03	0.08347738	0.4189	-4.86
246684_at	putative protein nucleoid DNA-bin	CDR1	AT5G33340	-1.24	-0.31	-2.03	0.08351127	0.4189	-4.86
245490_at	hypothetical protein	LDL3	AT4G16310	-1.20	-0.26	-2.03	0.08348564	0.4189	-4.86
257781_at	spastin protein, putative similar to	---	AT3G27120	-1.14	-0.19	-2.03	0.08351771	0.4189	-4.86

249222_at	putative protein similar to unknown	---	AT5G42450	1.14	0.19	2.03	0.08357976	0.4190	-4.86
259632_at	nicotianamine synathase, putative	NAS4	AT1G56430	-1.51	-0.60	-2.03	0.08358338	0.4190	-4.86
256083_at	hypothetical protein predicted by g	---	AT1G20730	-1.14	-0.19	-2.03	0.08361497	0.4191	-4.86
248144_at	glucose-6-phosphate/phosphate tr	GPT1	AT5G54800	-1.22	-0.28	-2.03	0.08365145	0.4192	-4.86
250198_at	expressed protein contains similar	NAP14	AT5G14100	1.29	0.36	2.03	0.08373162	0.4193	-4.87
248401_at	putative protein similar to unknown	HCF208	AT5G52110	1.37	0.45	2.03	0.08371842	0.4193	-4.87
257303_at	hypothetical protein predicted by g	---	AT3G30230	-1.17	-0.23	-2.03	0.08372434	0.4193	-4.87
256652_at	hypothetical protein similar to puta	LPAT5	AT3G18850	-1.50	-0.58	-2.03	0.08380787	0.4196	-4.87
259138_s_at	putative DNA gyrase subunit B sim	---	AT3G10270	1.19	0.25	2.03	0.08383848	0.4196	-4.87
254429_at	Expressed protein ; supported by f	---	AT4G21105	1.17	0.23	2.03	0.08384665	0.4196	-4.87
263645_at	putative GTP-binding protein	---	AT2G04720	-1.13	-0.18	-2.03	0.08386486	0.4196	-4.87
256745_at	UDP-glucose dehydrogenase, put	---	AT3G29360	-1.22	-0.28	-2.03	0.08397606	0.4199	-4.87
252984_at	cinnamyl-alcohol dehydrogenase E	ELI3-2	AT4G37990	-1.67	-0.74	-2.03	0.0839591	0.4199	-4.87
253676_at	cytidine deaminase - like protein c	---	AT4G29570	1.22	0.28	2.03	0.08398733	0.4199	-4.87
263875_at	unknown protein ;supported by ful	ogo-02	AT2G21970	1.29	0.37	2.03	0.08404653	0.4200	-4.87
253584_at	putative protein several hypothetic	---	AT4G30700	1.17	0.23	2.03	0.08401991	0.4200	-4.87
AFFX-DapX-5_	B. subtilis /GEN=dapB /DB_XREF=	---	---	-1.40	-0.49	-2.03	0.08404068	0.4200	-4.87
258109_at	hypothetical protein contains Pfam	HGL1	AT3G23640	-1.18	-0.24	-2.03	0.08413206	0.4202	-4.87
252393_at	putative protein predicted proteins	---	AT3G47910	-1.20	-0.26	-2.03	0.08414205	0.4202	-4.87
252824_at	histone H3.3 ; supported by cDNA	---	AT4G40030	1.19	0.25	2.02	0.08428187	0.4204	-4.87
259872_at	putative translation initiation factor	---	AT1G76810	1.16	0.21	2.02	0.08429617	0.4204	-4.87
255996_s_at	receptor-like serine threonine kina	---	AT1G29730	-1.21	-0.28	-2.02	0.08425747	0.4204	-4.87
260648_at	unknown protein	---	AT1G08050	1.33	0.41	2.02	0.08427195	0.4204	-4.87
257024_at	CDPK-related kinase identical to G	---	AT3G19100	-1.27	-0.34	-2.02	0.08421675	0.4204	-4.87
258547_at	unknown protein	---	AT3G06895	1.14	0.19	2.02	0.08422276	0.4204	-4.87
265273_at	unknown protein	---	AT2G28320	-1.19	-0.25	-2.02	0.08427262	0.4204	-4.87
260143_at	sucrose transport protein SUC1 ide	SUC1	AT1G71880	1.47	0.56	2.02	0.08433633	0.4205	-4.87
265678_at	putative RAD50 DNA repair protein	RAD50	AT2G31970	1.30	0.37	2.02	0.08442907	0.4205	-4.87
256424_at	unknown protein ;supported by full	---	AT1G33490	1.17	0.23	2.02	0.08441919	0.4205	-4.87
261370_at	cell division-related protein, putativ	---	AT1G53050	-1.16	-0.22	-2.02	0.08443189	0.4205	-4.87
250229_at	putative protein contains similarity	NACA3	AT5G13850	1.31	0.39	2.02	0.0843938	0.4205	-4.87
248799_at	ethylene responsive element bindi	ERF5	AT5G47230	2.37	1.24	2.02	0.08445025	0.4205	-4.87
257824_at	unknown protein ; supported by cl	---	AT3G25290	-1.37	-0.45	-2.02	0.08442875	0.4205	-4.87
253320_at	putative protein ThiJ protein, Esch	---	AT4G34020	1.17	0.23	2.02	0.08446929	0.4205	-4.87
265210_at	60S ribosomal protein L24 ;suppo	RPL24A	AT2G36620	1.67	0.74	2.02	0.08449635	0.4205	-4.87

255242_at	putative protein putative retrotrans	---	---	-1.16	-0.21	-2.02	0.08452167	0.4206	-4.87
255687_at	hypothetical protein	KEA2	AT4G00630	-1.38	-0.47	-2.02	0.08457014	0.4206	-4.87
265925_at	hypothetical protein predicted by g	---	AT2G18610	-1.17	-0.22	-2.02	0.08457655	0.4206	-4.88
258571_at	hypothetical protein predicted by g	anac048	AT3G04420	-1.20	-0.26	-2.02	0.0845544	0.4206	-4.87
250342_at	putative protein predicted protein,	---	AT5G11870	-1.25	-0.32	-2.02	0.08460494	0.4206	-4.88
255692_at	putative protein	GPAT8	AT4G00400	1.69	0.75	2.02	0.08478554	0.4209	-4.88
260332_at	hypothetical protein predicted by g	---	AT1G70470	1.13	0.18	2.02	0.08478845	0.4209	-4.88
251751_at	putative protein predicted proteins	---	AT3G55720	-1.14	-0.18	-2.02	0.0847969	0.4209	-4.88
252575_at	receptor like protein kinase recept	---	AT3G45440	-1.25	-0.33	-2.02	0.08479649	0.4209	-4.88
260553_at	unknown protein similar to T11A07	---	AT2G41800	-1.16	-0.21	-2.02	0.08476142	0.4209	-4.88
262512_at	Expressed protein ; supported by f	---	AT1G17145	1.43	0.52	2.02	0.08471567	0.4209	-4.88
264376_at	putative protein phosphatase 2C ;	---	AT2G25070	1.25	0.32	2.02	0.08478213	0.4209	-4.88
246584_at	putative protein predicted protein,	---	AT5G14730	1.80	0.84	2.02	0.08487306	0.4210	-4.88
265900_at	unknown protein	---	AT2G25730	-1.13	-0.17	-2.02	0.08486853	0.4210	-4.88
262795_at	hypothetical protein predicted by g	---	AT1G13130	-1.26	-0.33	-2.02	0.08487842	0.4210	-4.88
249537_at	cysteine-tRNA ligase -like protein	---	AT5G38830	-1.23	-0.30	-2.02	0.08484416	0.4210	-4.88
256191_at	unknown protein similar to hypothe	---	AT1G30130	-1.19	-0.25	-2.02	0.0849773	0.4213	-4.88
AFFX-BioB-3_a	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.61	-0.69	-2.02	0.08498722	0.4213	-4.88
245722_at	unknown protein	---	AT1G73430	1.25	0.32	2.02	0.08502452	0.4214	-4.88
247339_at	unknown protein	---	AT5G63690	1.21	0.28	2.02	0.08512175	0.4218	-4.88
249125_at	1-aminocyclopropane-1-carboxylat	---	AT5G43450	1.29	0.37	2.02	0.08521375	0.4221	-4.88
247307_at	UVB-resistance protein UVR8 (gb|	---	AT5G21326	1.16	0.22	2.02	0.08521317	0.4221	-4.88
260989_at	unknown protein ; supported by cD	---	AT1G53450	1.24	0.31	2.02	0.08526378	0.4222	-4.88
252676_at	putative protein	---	AT3G44280	1.14	0.19	2.02	0.08532555	0.4225	-4.88
254694_at	putative protein	---	AT4G17900	1.25	0.33	2.01	0.08551781	0.4229	-4.89
254873_at	putative protein a 162 kDa compo	EIF3A	AT4G11420	1.16	0.21	2.01	0.08550456	0.4229	-4.89
265492_at	hypothetical protein	AGL95	AT2G15660	-1.17	-0.23	-2.01	0.08545701	0.4229	-4.89
261737_at	hypothetical protein similar to puta	---	AT1G47885	1.20	0.26	2.01	0.0855113	0.4229	-4.89
265804_at	putative peptide methionine sulfoxi	---	AT2G18030	1.14	0.19	2.01	0.08550667	0.4229	-4.89
258619_at	isopentenyl diphosphate:dimethyla	IPP2	AT3G02780	1.22	0.29	2.01	0.08553589	0.4229	-4.89
266729_at	50S ribosomal protein L7/L12	---	AT2G03130	-1.17	-0.23	-2.01	0.08551085	0.4229	-4.89
262746_at	Expressed protein ; supported by f	ATNUDX15	AT1G28960	1.14	0.19	2.01	0.08558277	0.4229	-4.89
259484_at	calcium-dependent protein kinase	PEPKR1	AT1G12580	1.22	0.29	2.01	0.08558091	0.4229	-4.89
257192_at	unknown protein ;supported by ful	EMB2769	AT3G13200	1.19	0.25	2.01	0.08560055	0.4229	-4.89
248385_at	putative protein contains similarity	---	AT5G51910	1.22	0.29	2.01	0.08563502	0.4230	-4.89

260692_at	hypothetical protein predicted by g	---	AT1G32430	-1.16	-0.22	-2.01	0.08566449	0.4230	-4.89
252422_at	putative protein PIT1 - Arabidopsi	---	AT3G47550	-1.27	-0.35	-2.01	0.08568687	0.4231	-4.89
250973_at	60S ribosomal protein - like 60S r	---	AT5G02870	1.35	0.43	2.01	0.08588415	0.4231	-4.89
248651_at	unknown protein	---	AT5G49260	-1.15	-0.20	-2.01	0.08587947	0.4231	-4.89
254908_at	putative protein other hypothetical	---	---	-1.20	-0.26	-2.01	0.08574264	0.4231	-4.89
260899_at	hypothetical protein predicted by g	---	AT1G21370	1.22	0.29	2.01	0.08580801	0.4231	-4.89
248031_at	unknown protein ; supported by cl	---	AT5G55640	-1.14	-0.19	-2.01	0.0858735	0.4231	-4.89
267467_at	putative C3HC4 zinc finger protein	DRIP2	AT2G30580	1.18	0.24	2.01	0.08583086	0.4231	-4.89
253487_at	ribosomal protein S6 - like riboson	RPS6	AT4G31700	1.52	0.60	2.01	0.085888	0.4231	-4.89
258188_at	unknown protein ;supported by ful	---	AT3G17800	-1.22	-0.29	-2.01	0.08574742	0.4231	-4.89
266690_at	malate oxidoreductase (malic enzy	ATNADP-M	AT2G19900	1.17	0.22	2.01	0.08580749	0.4231	-4.89
266674_at	hypothetical protein predicted by g	---	AT2G29620	-1.15	-0.20	-2.01	0.08580068	0.4231	-4.89
250663_at	putative protein prenylated rab ac	PRA1.B6	AT5G07110	-1.17	-0.22	-2.01	0.08599936	0.4233	-4.89
245665_at	unknown protein ;supported by full	---	AT1G28250	1.19	0.25	2.01	0.08598681	0.4233	-4.89
263556_at	hypothetical protein predicted by g	---	AT2G16365	-1.20	-0.26	-2.01	0.08600854	0.4233	-4.89
258308_at	putative reverse transcriptase simi	---	---	-1.36	-0.44	-2.01	0.08597359	0.4233	-4.89
255533_at	putative CHP-rich zinc finger prote	---	AT4G02180	-1.16	-0.21	-2.01	0.08598057	0.4233	-4.89
258243_at	carbamoyl phosphate synthetase s	CARA	AT3G27740	1.27	0.35	2.01	0.08604559	0.4234	-4.89
257956_at	unknown protein	---	AT3G25400	-1.23	-0.30	-2.01	0.08609181	0.4235	-4.89
260547_at	putative trypsin inhibitor ;supporte	---	AT2G43550	-1.76	-0.82	-2.01	0.08611316	0.4235	-4.89
261439_at	Expressed protein ; supported by f	---	AT1G28395	1.37	0.45	2.01	0.08613947	0.4235	-4.89
259252_at	hypothetical protein similar to hyp	IBM1	AT3G07610	-1.16	-0.21	-2.01	0.08622407	0.4238	-4.89
248805_at	putative protein similar to unknown	---	AT5G47480	-1.16	-0.21	-2.01	0.0862135	0.4238	-4.89
248132_at	SGP1 monomeric G-protein (embl	SGP1	AT5G54840	-1.28	-0.35	-2.01	0.08627212	0.4239	-4.89
260801_at	hypothetical protein predicted by g	---	AT1G78430	-1.13	-0.18	-2.01	0.08628532	0.4239	-4.89
253647_at	putative protein KIAA0210 gene, h	---	AT4G29950	1.21	0.27	2.01	0.08638597	0.4239	-4.90
259596_at	auxin-regulated GH3 protein, puta	GH3.17	AT1G28130	-1.44	-0.52	-2.01	0.08639371	0.4239	-4.90
253713_at	putative protein several hypothetic	---	AT4G29370	-1.16	-0.21	-2.01	0.08635406	0.4239	-4.90
249733_at	6-phosphogluconolactonase-like p	emb2024	AT5G24400	1.17	0.23	2.01	0.08636338	0.4239	-4.90
249282_at	CMP-sialic acid transporter-like pr	---	AT5G41760	1.24	0.31	2.01	0.08630886	0.4239	-4.89
264663_at	unknown protein Similar to A. thal	LRR XI-23	AT1G09970	-1.61	-0.69	-2.01	0.08632977	0.4239	-4.89
245355_at	60S ribosomal protein L15 homolo	---	AT4G17390	1.43	0.51	2.01	0.08652075	0.4244	-4.90
250581_at	copine-like protein copine VII prot	BON2	AT5G07300	1.16	0.22	2.01	0.08661816	0.4248	-4.90
259293_at	putative DNA binding protein simila	---	AT3G11580	1.33	0.41	2.00	0.08667367	0.4250	-4.90
262695_at	vacuolor sorting protein 35, putati	VPS35B	AT1G75850	-1.16	-0.21	-2.00	0.08673042	0.4250	-4.90

249573_at	ubiquitin-like protein (UBQ9), puta	UBQ9	AT5G37640	-1.16	-0.21	-2.00	0.08670966	0.4250	-4.90
253298_at	putative protein ;supported by full-	---	AT4G33560	-1.18	-0.24	-2.00	0.08673764	0.4250	-4.90
247193_at	putative protein strong similarity to	---	AT5G65380	-1.25	-0.32	-2.00	0.0867795	0.4251	-4.90
254190_at	Expressed protein ; supported by f	---	AT4G23885	1.29	0.37	2.00	0.08686816	0.4254	-4.90
253083_at	aldehyde dehydrogenase like prot	ALDH3F1	AT4G36250	1.39	0.48	2.00	0.08687396	0.4254	-4.90
245427_at	putative protein	---	AT4G17550	-1.25	-0.32	-2.00	0.08691273	0.4254	-4.90
264311_at	hypothetical protein similar to hypo	---	AT1G70400	-1.14	-0.19	-2.00	0.08690041	0.4254	-4.90
267510_at	unknown protein ; supported by fu	SAP18	AT2G45640	1.24	0.31	2.00	0.08696092	0.4256	-4.90
252025_at	putative protein chromosome asse	---	AT3G52900	1.19	0.25	2.00	0.08702519	0.4258	-4.90
257154_at	unknown protein ; supported by cl	---	AT3G27210	-1.23	-0.30	-2.00	0.0870477	0.4258	-4.90
265945_at	putative cytokinin oxidase ; suppo	CKX2	AT2G19500	-1.17	-0.22	-2.00	0.08709452	0.4259	-4.90
246127_s_at	putative protein	---	---	1.13	0.18	2.00	0.08713426	0.4261	-4.90
261821_at	thioredoxin h, putative similar to th	ATCXXS1	AT1G11530	1.18	0.24	2.00	0.08729499	0.4266	-4.91
267350_at	putative DNA-directed RNA polym	NRPD1B	AT2G40030	-1.21	-0.28	-2.00	0.0872879	0.4266	-4.91
261800_at	HD-Zip protein identical to HD-Zip	PHV	AT1G30490	-1.20	-0.27	-2.00	0.08726931	0.4266	-4.91
253282_at	putative protein hypothetical prote	LEJ1	AT4G34120	-1.14	-0.19	-2.00	0.08736911	0.4267	-4.91
261419_at	hypothetical protein predicted by g	---	AT1G07840	-1.14	-0.19	-2.00	0.08738514	0.4267	-4.91
250182_at	putative protein predicted proteins	---	AT5G14470	1.58	0.66	2.00	0.08736045	0.4267	-4.91
260373_at	unknown protein	---	AT1G73970	-1.17	-0.23	-2.00	0.08750554	0.4268	-4.91
252479_at	small zinc finger-like protein TIM9	TIM9	AT3G46560	1.26	0.34	2.00	0.08744635	0.4268	-4.91
261627_at	arsA homolog (hASNA-I), putative	---	AT1G01910	1.15	0.20	2.00	0.08753608	0.4268	-4.91
249050_at	cyclin-dependent protein kinase-lik	---	AT5G44290	-1.19	-0.25	-2.00	0.08756424	0.4268	-4.91
261264_at	hypothetical protein predicted by g	---	AT1G26710	-1.21	-0.28	-2.00	0.08757051	0.4268	-4.91
264127_at	serine/threonine protein kinase, pu	AGC1.7	AT1G79250	-1.13	-0.18	-2.00	0.08748949	0.4268	-4.91
264558_at	putative protein kinase Similar to c	---	AT1G09600	-1.15	-0.20	-2.00	0.08754724	0.4268	-4.91
252966_at	putative protein various predicted	---	AT4G38870	1.19	0.25	2.00	0.08753492	0.4268	-4.91
257830_at	MutT-like protein contains Pfam pr	ATNUDX13	AT3G26690	1.37	0.45	2.00	0.08754994	0.4268	-4.91
262390_at	hypothetical protein predicted by g	---	AT1G49260	-1.20	-0.26	-2.00	0.08761261	0.4268	-4.91
257709_at	unknown protein similar to negativ	---	AT3G27325	-1.26	-0.34	-2.00	0.08759482	0.4268	-4.91
266291_at	putative tropinone reductase ;supp	---	AT2G29320	-1.36	-0.44	-2.00	0.08779131	0.4269	-4.91
257045_at	dynamin-like protein similar to phra	ARC5	AT3G19720	-1.30	-0.38	-2.00	0.08769493	0.4269	-4.91
250013_at	putative protein similar to unknown	---	AT5G18040	1.16	0.21	2.00	0.08780907	0.4269	-4.91
259672_at	DNA-directed RNA polymerase id	---	AT1G68990	-1.49	-0.58	-2.00	0.08784847	0.4269	-4.91
252044_at	outer envelope membrane protein	OEP7	AT3G52420	1.14	0.20	2.00	0.0878642	0.4269	-4.91
257368_at	hypothetical protein predicted by g	---	AT2G29860	-1.15	-0.21	-2.00	0.08772342	0.4269	-4.91

263887_at	hypothetical protein predicted by g	---	AT2G36980	-1.23	-0.30	-2.00	0.08771162	0.4269	-4.91
252973_s_at	peptidylprolyl isomerase ROC1 ;s	ROC1	AT4G38740	-1.27	-0.34	-2.00	0.08787097	0.4269	-4.91
246025_at	zwille/pinhead-like protein GERp9	---	AT5G21150	-1.22	-0.29	-2.00	0.08778182	0.4269	-4.91
246221_at	step II splicing factor - like protein	SMP2	AT4G37120	-1.18	-0.23	-2.00	0.0877041	0.4269	-4.91
256213_at	protein kinase, putative contains P	---	AT1G50990	-1.19	-0.25	-2.00	0.08775723	0.4269	-4.91
246315_at	hypothetical protein	---	AT3G56870	1.30	0.38	2.00	0.08765453	0.4269	-4.91
266855_at	unknown protein	---	AT2G26920	-1.20	-0.26	-2.00	0.08784264	0.4269	-4.91
248856_at	putative protein similar to unknown	---	AT5G46620	-1.15	-0.20	-1.99	0.08793429	0.4271	-4.91
255014_at	MADS-box protein AGL11 ; suppo	STK	AT4G09960	1.15	0.20	1.99	0.08795492	0.4271	-4.91
265593_s_at	unknown protein ;supported by ful	LCV1	AT2G20120	1.15	0.21	1.99	0.08798754	0.4272	-4.91
245556_at	HSR201 like protein	---	AT4G15400	-1.14	-0.19	-1.99	0.08805875	0.4275	-4.91
264005_at	unknown protein ; supported by cl	AGP2	AT2G22470	2.42	1.27	1.99	0.08808501	0.4275	-4.91
251320_at	3-methyl-2-oxobutanoate hydroxy	PANB2	AT3G61530	1.15	0.20	1.99	0.0881136	0.4275	-4.91
258936_s_at	hypothetical protein similar to hyp	---	---	-1.16	-0.21	-1.99	0.08812323	0.4275	-4.91
247132_at	putative protein strong similarity to	ARO2	AT5G66200	-1.24	-0.31	-1.99	0.08837224	0.4277	-4.92
262800_at	putative ATP-dependent RNA heli	emb1507	AT1G20960	1.18	0.24	1.99	0.08831911	0.4277	-4.92
255826_at	putative uroporphyrinogen decarbo	HEME2	AT2G40490	1.18	0.24	1.99	0.08831509	0.4277	-4.92
253726_at	ribosomal protein S15a homolog r	rps15ae	AT4G29430	1.41	0.50	1.99	0.08825882	0.4277	-4.92
247578_at	putative protein predicted protein,	---	AT5G61300	-1.21	-0.27	-1.99	0.08838761	0.4277	-4.92
247172_at	anthocyanidin-3-glucoside rhamno	---	AT5G65550	-1.16	-0.21	-1.99	0.08823203	0.4277	-4.92
265717_at	unknown protein ;supported by ful	---	AT2G03510	1.23	0.29	1.99	0.08825414	0.4277	-4.92
262892_at	succinic semialdehyde dehydroge	ALDH5F1	AT1G79440	1.16	0.21	1.99	0.08818652	0.4277	-4.92
252871_at	proliferating-cell nucleolar antigen	---	AT4G40000	-1.16	-0.22	-1.99	0.08837564	0.4277	-4.92
253437_at	putative protein mRNAs from Ricir	---	AT4G32460	1.55	0.63	1.99	0.08835591	0.4277	-4.92
258251_at	unknown protein ; supported by fu	---	AT3G15810	-1.18	-0.24	-1.99	0.08828141	0.4277	-4.92
250451_at	cdc2-like protein kinase cdc2-like	CDKC;1	AT5G10270	-1.20	-0.27	-1.99	0.08833336	0.4277	-4.92
246387_at	hypothetical protein predicted by g	---	AT1G77400	1.24	0.31	1.99	0.08841798	0.4277	-4.92
250455_at	unknown protein ; supported by fu	PROPEP4	AT5G09980	-1.26	-0.33	-1.99	0.08849019	0.4278	-4.92
265973_at	putative non-LTR retroelement rev	---	---	-1.14	-0.19	-1.99	0.08845181	0.4278	-4.92
250719_at	putative protein contains similarity	---	AT5G06250	-1.21	-0.27	-1.99	0.08847243	0.4278	-4.92
265748_at	putative Athila retroelement ORF1	---	---	-1.17	-0.23	-1.99	0.08849644	0.4278	-4.92
247589_at	REVOLUTA or interfascicular fiber	REV	AT5G60690	1.19	0.25	1.99	0.0886189	0.4283	-4.92
263700_at	unknown protein EST gb|Z33866 c	---	AT1G31150	1.24	0.31	1.99	0.0886569	0.4284	-4.92
260537_at	hypothetical protein predicted by g	---	AT2G43450	-1.13	-0.18	-1.99	0.08870814	0.4284	-4.92
250599_at	unknown protein ; supported by cl	---	AT5G07730	-1.24	-0.31	-1.99	0.08871562	0.4284	-4.92

251529_at	ATP-dependent RNA helicase-like	---	AT3G58570	-1.16	-0.21	-1.99	0.08870252	0.4284	-4.92
246561_at	putative protein hypothetical prote	---	AT5G15570	-1.17	-0.23	-1.99	0.08874101	0.4284	-4.92
246288_at	unknown protein	---	AT1G31850	1.24	0.31	1.99	0.08878607	0.4285	-4.92
262698_at	AMP-binding protein, putative con	---	AT1G75960	-1.47	-0.56	-1.99	0.08881252	0.4286	-4.92
255766_at	unknown protein ;supported by full	---	AT1G16750	1.23	0.30	1.99	0.08889712	0.4288	-4.92
260426_at	putative 40S ribosomal protein SA	P40	AT1G72370	1.34	0.43	1.99	0.08890244	0.4288	-4.92
257149_at	prohibitin, putative similar to prohi	ATPHB4	AT3G27280	1.39	0.48	1.99	0.08899828	0.4288	-4.92
249827_at	unknown protein ;supported by ful	---	AT5G23330	1.21	0.27	1.99	0.08893425	0.4288	-4.92
253105_at	putative protein zinc finger protein	---	AT4G35840	1.26	0.34	1.99	0.08898356	0.4288	-4.92
266519_at	unknown protein ; supported by cl	---	AT2G35155	-1.19	-0.26	-1.99	0.08896842	0.4288	-4.92
245248_at	Expressed protein ; supported by c	ATB' GAMM	AT4G15415	1.12	0.17	1.99	0.08900052	0.4288	-4.92
260100_at	Expressed protein ; supported by f	BNS	AT1G73177	1.14	0.19	1.99	0.08911714	0.4292	-4.93
245307_at	gibberellin oxidase-like protein nor	---	AT4G16770	-1.20	-0.27	-1.99	0.08909543	0.4292	-4.93
255503_at	contains similarity to a protein kina	---	AT4G02420	-1.76	-0.82	-1.99	0.08912466	0.4292	-4.93
255846_at	putative SWI/SNF complex subuni	ATSWI3B	AT2G33610	1.23	0.30	1.99	0.08915517	0.4292	-4.93
255759_at	hypothetical protein predicted by g	---	AT1G16790	1.18	0.24	1.98	0.0891965	0.4292	-4.93
247959_at	unknown protein	---	AT5G57080	1.25	0.32	1.98	0.08918482	0.4292	-4.93
257582_at	hypothetical protein	---	AT1G50720	-1.14	-0.19	-1.98	0.08923201	0.4293	-4.93
259524_at	hypothetical protein	---	AT1G12550	-1.26	-0.33	-1.98	0.08931316	0.4294	-4.93
254283_s_at	anthocyanidin synthase - like prot	---	AT4G22870 /	-1.23	-0.29	-1.98	0.08928034	0.4294	-4.93
265588_at	putative pathogenesis-related prot	---	AT2G19970	-1.82	-0.86	-1.98	0.08932918	0.4294	-4.93
255190_x_at	may be a pseudogene similar to a	---	---	-1.14	-0.19	-1.98	0.08932806	0.4294	-4.93
265935_at	putative senescence-associated pr	TET2	AT2G19580	-1.30	-0.38	-1.98	0.08935269	0.4294	-4.93
AFFX-BioB-5_a	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.31	-0.39	-1.98	0.08941738	0.4297	-4.93
249580_at	putative protein predicted proteins	---	AT5G37740	1.22	0.29	1.98	0.08949167	0.4297	-4.93
259813_at	glutathione S-transferase, putative	ATGSTF14	AT1G49860	-1.18	-0.24	-1.98	0.08948496	0.4297	-4.93
254521_at	putative protein similar to unknown	---	AT5G44820	1.17	0.23	1.98	0.08948278	0.4297	-4.93
264265_at	unknown protein ; supported by cl	---	AT1G09280	1.22	0.29	1.98	0.08949379	0.4297	-4.93
248962_at	putative protein contains similarity	FKBP13	AT5G45680	1.30	0.38	1.98	0.0895276	0.4297	-4.93
247517_at	100 kDa coactivator - like protein	---	AT5G61780	-1.21	-0.28	-1.98	0.0895337	0.4297	-4.93
246533_at	putative protein	---	AT5G15880	1.23	0.30	1.98	0.08955695	0.4297	-4.93
257831_at	unknown protein ;supported by ful	CCB1	AT3G26710	1.21	0.27	1.98	0.08957735	0.4297	-4.93
259648_at	hypothetical protein predicted by g	---	---	-1.14	-0.19	-1.98	0.08965869	0.4298	-4.93
266323_at	putative calcium-dependent protei	CRK3	AT2G46700	1.18	0.24	1.98	0.08965981	0.4298	-4.93
251590_at	pollen-specific protein BAN102-lik	AGP23	AT3G57690	-1.25	-0.32	-1.98	0.08963717	0.4298	-4.93

264775_at	putative endo-1,4-beta-D-glucana	CEL5	AT1G22880	-1.21	-0.28	-1.98	0.08971153	0.4300	-4.93
248622_at	xylosidase	---	AT5G01980	1.47	0.56	1.98	0.08975535	0.4301	-4.93
254846_at	Expressed protein ; supported by f	PLDGAMM	AT4G11830	1.22	0.28	1.98	0.08981669	0.4301	-4.93
252162_at	hypothetical protein	---	AT3G50590	-1.30	-0.38	-1.98	0.08978516	0.4301	-4.93
249214_at	beta-1,3-glucanase-like protein	---	AT5G42720	-1.37	-0.45	-1.98	0.08980432	0.4301	-4.93
250112_at	low density lipoprotein B-like prote	---	AT5G16300	-1.15	-0.21	-1.98	0.09001061	0.4309	-4.94
262639_at	calmodulin, putative similar to calr	---	AT1G62820	1.27	0.35	1.98	0.09002077	0.4309	-4.94
250985_at	putative protein various predicted	---	AT5G02830	-1.15	-0.20	-1.98	0.09021613	0.4311	-4.94
260682_at	hypothetical protein predicted by g	---	AT1G17510	1.17	0.23	1.98	0.09009654	0.4311	-4.94
246159_at	Expressed protein ; supported by f	---	AT5G20935	1.35	0.43	1.98	0.09014755	0.4311	-4.94
247566_at	40S ribsomal protein S19 - like 40	---	AT5G61170	1.43	0.51	1.98	0.09018928	0.4311	-4.94
263148_at	ubiquitin, putative similar to ubiqui	---	AT1G53950	-1.18	-0.24	-1.98	0.09021554	0.4311	-4.94
249625_at	hypothetical protein ;supported by	---	AT5G37480	1.16	0.22	1.98	0.09013098	0.4311	-4.94
247878_at	unknown protein	---	AT5G57760	3.81	1.93	1.98	0.09018991	0.4311	-4.94
245179_at	putative protein similarity to predic	---	AT5G12400	-1.18	-0.23	-1.98	0.09023379	0.4311	-4.94
257738_at	40S ribosomal subunit protein S21	---	AT3G27450	1.14	0.19	1.98	0.09009605	0.4311	-4.94
251418_at	putative protein prib5, Ribes nigru	---	AT3G60440	1.32	0.40	1.98	0.09024401	0.4311	-4.94
253446_at	putative protein predicted protein	---	AT4G32620	-1.18	-0.24	-1.98	0.09026965	0.4311	-4.94
252595_at	putative transporter protein peptid	---	AT3G45690	-1.18	-0.24	-1.98	0.09029236	0.4311	-4.94
245067_at	S-like ribonuclease RNS2 identica	RNS2	AT2G39780	1.18	0.24	1.98	0.0903667	0.4314	-4.94
267432_at	putative UDP-N-acetylglucosamine	---	AT2G35020	1.30	0.38	1.98	0.09040242	0.4315	-4.94
254999_at	putative protein ; supported by full	---	AT4G09830	1.23	0.30	1.97	0.09057794	0.4316	-4.94
249359_at	putative protein unnamed ORF, H	---	AT5G40470	1.21	0.28	1.97	0.09062362	0.4316	-4.94
265101_at	unknown protein similar to ESTs g	---	AT1G30880	1.30	0.38	1.97	0.09049139	0.4316	-4.94
266325_at	putative extensin	---	AT2G46630	-1.70	-0.76	-1.97	0.09051283	0.4316	-4.94
248032_at	myosin heavy chain-like	---	AT5G55860	-1.22	-0.29	-1.97	0.0906332	0.4316	-4.94
245466_at	glucosyltransferase like protein	---	AT4G16600	-1.21	-0.28	-1.97	0.09064015	0.4316	-4.94
262540_at	hypothetical protein predicted by g	---	AT1G34260	-1.29	-0.37	-1.98	0.09044316	0.4316	-4.94
262247_at	unknown protein contains similarity	D-CDES	AT1G48420	-1.17	-0.22	-1.97	0.0905333	0.4316	-4.94
250265_at	putative protein predicted proteins	---	AT5G12900	1.26	0.34	1.97	0.09064613	0.4316	-4.94
259239_at	putative 40S ribosomal protein s14	---	AT3G11510	1.51	0.59	1.97	0.09064428	0.4316	-4.94
256763_at	unknown protein	COBL8	AT3G16860	-1.66	-0.73	-1.97	0.09064065	0.4316	-4.94
256103_at	hypothetical protein similar to hypo	---	AT1G13540	-1.13	-0.17	-1.97	0.09049198	0.4316	-4.94
262839_at	PhD-finger protein, putative conta	---	AT1G14770	1.32	0.40	1.97	0.09067339	0.4316	-4.94
265831_at	unknown protein	---	AT2G14460	1.42	0.51	1.97	0.0907267	0.4316	-4.94

249048_at	auxin-repressed protein-like ;supp	---	AT5G44300	-1.17	-0.23	-1.97	0.09073192	0.4316	-4.94
247153_at	receptor protein kinase-like protein	BAM1	AT5G65700	1.39	0.47	1.97	0.09072622	0.4316	-4.94
257378_s_at	hypothetical protein predicted by g	---	AT2G02290	-1.18	-0.24	-1.97	0.09076028	0.4317	-4.94
253322_at	putative protein ;supported by full-	---	AT4G33980	1.23	0.30	1.97	0.09086263	0.4318	-4.94
260336_at	putative protease IV similar to prot	SPPA	AT1G73990	-1.21	-0.27	-1.97	0.09086223	0.4318	-4.94
249792_at	putative protein contains similarity	PHS1	AT5G23720	1.15	0.21	1.97	0.09086751	0.4318	-4.94
247111_at	unknown protein	---	AT5G65880	1.29	0.37	1.97	0.09085848	0.4318	-4.94
266666_at	hypothetical protein predicted by g	---	AT2G29780	-1.16	-0.22	-1.97	0.09093691	0.4319	-4.95
254161_at	hypothetical protein ;supported by	---	AT4G24370	1.17	0.23	1.97	0.09094047	0.4319	-4.95
246255_at	transcription initiation factor like pr	ATPBRP	AT4G36650	-1.18	-0.24	-1.97	0.09095805	0.4319	-4.95
261770_at	prolyl endopeptidase, putative sim	---	AT1G76140	-1.14	-0.19	-1.97	0.09097096	0.4319	-4.95
250607_at	putative protein mammalian inosit	IPK2a	AT5G07370	1.13	0.18	1.97	0.09102277	0.4320	-4.95
245889_at	PEE-rich protein ;supported by ful	---	AT5G09480	1.39	0.47	1.97	0.09100901	0.4320	-4.95
251706_at	nodulin-like protein MtN21 - Medic	---	AT3G56620	1.20	0.27	1.97	0.09104559	0.4320	-4.95
258641_at	unknown protein ;supported by ful	---	AT3G08030	1.73	0.79	1.97	0.09137406	0.4322	-4.95
259080_at	putative mitogen activated protein	WNK1	AT3G04910	-1.21	-0.27	-1.97	0.09126161	0.4322	-4.95
259534_at	hypothetical protein	---	AT1G12290	1.20	0.27	1.97	0.09136508	0.4322	-4.95
252644_at	putative protein KIAA0073, Homo	CYP71	AT3G44600	1.21	0.27	1.97	0.09115332	0.4322	-4.95
252773_at	putative protein predicted proteins	---	---	-1.15	-0.20	-1.97	0.09114451	0.4322	-4.95
245091_at	unknown protein	---	AT2G40910	-1.18	-0.24	-1.97	0.09129149	0.4322	-4.95
265670_s_at	unknown protein ;supported by ful	---	AT2G32190	1.63	0.71	1.97	0.09137972	0.4322	-4.95
264579_at	Expressed protein ; supported by f	---	AT1G05205	1.25	0.32	1.97	0.09112276	0.4322	-4.95
266361_at	putative O-GlcNAc transferase	---	AT2G32450	1.36	0.44	1.97	0.09138078	0.4322	-4.95
248657_at	peptidylprolyl isomerase	ROF2	AT5G48570	-2.76	-1.47	-1.97	0.09124517	0.4322	-4.95
262806_at	putative pyrophosphate-dependen	---	AT1G20950	1.28	0.36	1.97	0.09131245	0.4322	-4.95
261540_at	unknown protein	---	AT1G63610	1.19	0.25	1.97	0.09117244	0.4322	-4.95
260530_at	putative peptidyl-prolyl cis-trans is	---	AT2G47320	1.15	0.20	1.97	0.09131678	0.4322	-4.95
250994_at	dnaK-type molecular chaperone h	---	AT5G02490	-1.56	-0.64	-1.97	0.09126946	0.4322	-4.95
247611_at	putative protein predicted proteins	---	AT5G60710	1.14	0.20	1.97	0.09128611	0.4322	-4.95
255067_at	putative phosphotyrosyl phosphata	---	AT4G08960	-1.13	-0.18	-1.97	0.09130218	0.4322	-4.95
263136_at	trehalose-6-phosphate synthase,	ATTPS1	AT1G78580	-1.17	-0.23	-1.97	0.09141872	0.4323	-4.95
267082_at	CPDK-related protein kinase CDPI	CRK1	AT2G41140	1.15	0.20	1.97	0.0914431	0.4323	-4.95
253032_at	guanine nucleotide-exchange prot	---	AT4G38200	-1.15	-0.20	-1.97	0.09154535	0.4326	-4.95
250088_at	APG5 (autophagy 5)-like protein	APG5	AT5G17290	1.17	0.23	1.97	0.0915755	0.4326	-4.95
247626_at	receptor like protein kinase recept	---	AT5G60300	-1.62	-0.69	-1.97	0.09157093	0.4326	-4.95

261924_at	peptide transporter, putative simila	---	AT1G22550	-1.48	-0.57	-1.97	0.09158832	0.4326	-4.95
250920_at	putative protein ;supported by full-	---	AT5G03390	-1.33	-0.41	-1.97	0.09168508	0.4330	-4.95
254944_at	putative protein proliferation poter	---	AT4G10930	-1.12	-0.17	-1.97	0.09174161	0.4331	-4.95
256737_at	farnesyltranstransferase, putative	---	AT3G29420	-1.15	-0.20	-1.97	0.09175015	0.4331	-4.95
247585_at	putative protein predicted proteins	---	AT5G60680	1.23	0.30	1.96	0.09181441	0.4332	-4.95
248875_at	disease resistance protein-like	---	AT5G46470	-1.30	-0.38	-1.96	0.09182368	0.4332	-4.95
259030_at	putative alpha-hemolysin similar to	---	AT3G09310	1.13	0.17	1.96	0.09182454	0.4332	-4.95
251493_at	putative protein hypothetical prote	---	AT3G59300	-1.21	-0.28	-1.96	0.09186565	0.4333	-4.95
263480_at	putative root iron transporter protei	ZIP7	AT2G04032	-1.20	-0.26	-1.96	0.09196518	0.4336	-4.96
248889_at	unknown protein ;supported by full	---	AT5G46230	1.30	0.38	1.96	0.09197238	0.4336	-4.96
248499_at	putative protein contains similarity	PAP27	AT5G50400	-1.14	-0.19	-1.96	0.09199348	0.4336	-4.96
259761_at	putative acyl-CoA synthetase simil	LACS9	AT1G77590	1.26	0.34	1.96	0.09201621	0.4337	-4.96
250248_at	transporter-like protein	ZIF1	AT5G13740	-1.41	-0.50	-1.96	0.09217384	0.4342	-4.96
259103_at	unknown protein ; supported by cl	---	AT3G11690	-1.46	-0.55	-1.96	0.09219617	0.4342	-4.96
262492_at	unknown protein Contains similarit	---	AT1G21630	1.17	0.23	1.96	0.09223492	0.4342	-4.96
246859_at	putative protein various predicted	---	AT5G25950	-1.17	-0.22	-1.96	0.09222796	0.4342	-4.96
254781_at	putative protein putative protein F	---	AT4G12840	-1.15	-0.21	-1.96	0.09220976	0.4342	-4.96
263962_at	putative protein kinase contains a	---	AT2G36350	-1.25	-0.33	-1.96	0.09235196	0.4347	-4.96
250400_at	protein phosphatase 2C -like prote	---	AT5G10740	1.29	0.37	1.96	0.09236906	0.4347	-4.96
257401_at	hypothetical protein identical to hy	SRO2	AT1G23550	1.22	0.29	1.96	0.09240724	0.4348	-4.96
255482_at	putative chloroplast outer envelop	TOC159	AT4G02510	1.16	0.21	1.96	0.09254679	0.4353	-4.96
266960_at	putative retroelement pol polyprote	---	---	-1.20	-0.26	-1.96	0.09255741	0.4353	-4.96
245995_at	putative protein various predicted	---	---	-1.24	-0.32	-1.96	0.09260052	0.4354	-4.96
246040_at	peptidyl-prolyl cis-trans isomerase	---	AT5G19370	1.16	0.22	1.96	0.0926257	0.4354	-4.96
256599_at	hypothetical protein predicted by g	---	AT3G14760	-1.16	-0.21	-1.96	0.09264495	0.4354	-4.96
247735_at	thymidylate kinase - like protein th	ZEU1	AT5G59440	1.38	0.46	1.96	0.09276436	0.4359	-4.96
254084_at	ubiquitin activating enzyme - like p	SAE1A	AT4G24940	1.32	0.40	1.96	0.09288525	0.4364	-4.97
251614_at	hypothetical protein	---	AT3G57970	-1.21	-0.27	-1.96	0.09292828	0.4365	-4.97
259038_at	unknown protein predicted by gens	PTAC13	AT3G09210	1.18	0.23	1.96	0.09294984	0.4365	-4.97
255631_at	hypothetical protein	BSK3	AT4G00710	1.14	0.19	1.96	0.0929904	0.4365	-4.97
255118_at	nitrilase 1 like protein nitrilase 1 -	---	AT4G08790	1.20	0.27	1.96	0.09298584	0.4365	-4.97
256113_at	unknown protein ;supported by full	---	AT1G16810	1.19	0.25	1.96	0.09301406	0.4366	-4.97
253782_at	hypothetical protein	---	AT4G28590	1.14	0.19	1.96	0.09306985	0.4367	-4.97
264811_at	hypothetical protein predicted by g	---	AT1G08640	1.14	0.19	1.95	0.09317258	0.4368	-4.97
266237_at	DNA-directed RNA polymerase 14	ATRPC14	AT2G29540	1.29	0.36	1.96	0.09314323	0.4368	-4.97

248224_at	thylakoid lumenal 17.4 kD protein,	---	AT5G53490	1.25	0.32	1.95	0.09317962	0.4368	-4.97
260730_at	lipoamide dehydrogenase precurs	mtLPD1	AT1G48030	-1.24	-0.31	-1.96	0.09311779	0.4368	-4.97
AFFX-r2-Bs-thr	B. subtilis /GEN=thrC, thrB /DB_XI	---	---	-1.37	-0.45	-1.95	0.09318017	0.4368	-4.97
267063_at	hypothetical protein predicted by g	---	AT2G41120	1.24	0.30	1.95	0.09320403	0.4368	-4.97
259741_at	unknown protein	---	AT1G71020	-1.24	-0.32	-1.95	0.09337382	0.4373	-4.97
261190_at	ribosomal protein L11, putative sir	PRPL11	AT1G32990	1.18	0.24	1.95	0.09337103	0.4373	-4.97
250888_at	putative protein trichohyalin, Oryc	---	AT5G04460	-1.28	-0.35	-1.95	0.09334448	0.4373	-4.97
260725_at	Expressed protein ; supported by f	---	AT1G48170	1.17	0.23	1.95	0.09332233	0.4373	-4.97
250569_at	myc-like protein myc-like regulato	BIM1	AT5G08130	-1.36	-0.44	-1.95	0.09341521	0.4373	-4.97
247299_at	putative protein contains similarity	---	AT5G63900	-1.15	-0.20	-1.95	0.09343416	0.4373	-4.97
246111_at	putative protein	---	AT5G20170	-1.18	-0.23	-1.95	0.09341338	0.4373	-4.97
253918_at	putative protein ; supported by full	PHOS34	AT4G27320	1.17	0.23	1.95	0.09348985	0.4374	-4.97
253900_at	translation initiation factor ; suppo	---	AT4G27130	1.16	0.22	1.95	0.09357309	0.4377	-4.97
246264_at	hypothetical protein	FRL2	AT1G31814	-1.17	-0.23	-1.95	0.0935925	0.4377	-4.97
259790_s_at	auxin-induced protein, putative sir	---	AT1G29430 /	1.63	0.70	1.95	0.09369916	0.4378	-4.97
265032_at	ribosomal protein identical to ribos	RPL3B	AT1G61580	1.41	0.50	1.95	0.09367695	0.4378	-4.97
252110_at	disease resistance-like protein TM	---	AT3G51560	-1.15	-0.20	-1.95	0.09368946	0.4378	-4.97
261726_at	putative auxin-independent growth	---	AT1G76270	-1.31	-0.39	-1.95	0.09370515	0.4378	-4.97
245950_at	putative protein predicted protein,	---	AT5G19570	1.27	0.35	1.95	0.0936816	0.4378	-4.97
253550_at	putative protein kinase serine/thre	SIP3	AT4G30960	-1.32	-0.40	-1.95	0.09387334	0.4380	-4.98
265015_at	putative Ta11-1 reverse transcripta	---	---	-1.13	-0.17	-1.95	0.09381306	0.4380	-4.98
258241_at	hypothetical protein similar to hypo	LBD25	AT3G27650	-1.24	-0.31	-1.95	0.09378343	0.4380	-4.97
248644_at	disease resistance protein-like	---	AT5G49140	-1.13	-0.18	-1.95	0.09389561	0.4380	-4.98
245045_at	unknown protein similar to glycopr	---	AT2G26590	1.14	0.19	1.95	0.09386334	0.4380	-4.98
263807_at	putative indole-3-glycerol phospha	---	AT2G04400	-2.02	-1.02	-1.95	0.09390895	0.4380	-4.98
252519_at	hypothetical protein	---	AT3G46360	-1.17	-0.23	-1.95	0.09389959	0.4380	-4.98
244925_at	NADH dehydrogenase subunit 7	---	---	-1.21	-0.28	-1.95	0.09383646	0.4380	-4.98
263382_at	putative anthranilate N-hydroxycin	---	AT2G40230	-1.22	-0.29	-1.95	0.09400278	0.4382	-4.98
265464_at	putative myosin heavy chain	---	AT2G37080	1.14	0.18	1.95	0.09398196	0.4382	-4.98
266990_at	putative ABC transporter	ATATH8	AT2G39190	-1.35	-0.43	-1.95	0.09401919	0.4382	-4.98
259336_at	hypothetical protein C-term portion	SDG20	AT3G03750	1.28	0.36	1.95	0.09395344	0.4382	-4.98
263813_s_at	putative TNP1-like transposon pro	---	---	-1.16	-0.22	-1.95	0.09402822	0.4382	-4.98
250463_at	transcription factor OBF4	TGA4	AT5G10030	1.20	0.26	1.95	0.0940545	0.4382	-4.98
266898_at	unknown protein ; supported by cD	---	AT2G45990	-1.20	-0.27	-1.95	0.09409167	0.4382	-4.98
260210_at	putative xyloglucan fucosyltransfe	FUT3	AT1G74420	-1.22	-0.29	-1.95	0.09408685	0.4382	-4.98

267573_at	putative tropinone reductase	---	AT2G30670	-1.14	-0.18	-1.95	0.09413305	0.4383	-4.98
255065_s_at	putative arginase similar to argina	---	AT4G08870	-1.73	-0.79	-1.95	0.09425104	0.4383	-4.98
258963_at	putative myotubularin similar to my	---	AT3G10550	-1.18	-0.24	-1.95	0.09419796	0.4383	-4.98
264192_at	hypothetical protein predicted by g	ATATG18H	AT1G54710	-1.13	-0.18	-1.95	0.09424885	0.4383	-4.98
257855_at	hypothetical protein predicted by g	---	AT3G13040	-1.16	-0.21	-1.95	0.09425684	0.4383	-4.98
264804_at	putative receptor kinase, CLV1 sir	---	AT1G08590	-1.20	-0.27	-1.95	0.09423634	0.4383	-4.98
251955_at	putative protein predicted proteins	---	AT3G53680	-1.17	-0.23	-1.95	0.09420466	0.4383	-4.98
249464_at	putative protein crp1, Zea mays, F	EMB2745	AT5G39710	-1.47	-0.55	-1.95	0.09428388	0.4384	-4.98
250746_at	glucuronosyl transferase-like prote	---	AT5G05880	-1.15	-0.20	-1.95	0.09435228	0.4386	-4.98
256682_at	putative protein dihydrolipoamide S	LTA3	AT3G52200	1.14	0.19	1.95	0.09443494	0.4389	-4.98
264621_at	putative protein kinase contains a	---	AT2G17700	1.19	0.25	1.95	0.09446207	0.4389	-4.98
249373_at	putative protein vanilloid receptor	---	AT5G40670	-1.18	-0.23	-1.94	0.09451616	0.4391	-4.98
255926_at	AP2 domain containing protein RA	---	AT1G22190	1.40	0.48	1.94	0.09463634	0.4394	-4.98
247891_at	GTP binding protein-like	---	AT5G57960	1.16	0.22	1.94	0.09461961	0.4394	-4.98
247808_at	contains similarity to unknown prot	ECT10	AT5G58190	-1.14	-0.19	-1.94	0.09461284	0.4394	-4.98
265184_at	unknown protein ;supported by ful	---	AT1G23710	1.84	0.88	1.94	0.0946609	0.4394	-4.98
248161_at	unknown protein	---	AT5G54480	-1.18	-0.23	-1.94	0.09474139	0.4397	-4.98
266636_at	glycine decarboxylase complex H-	GDCH	AT2G35370	-1.19	-0.25	-1.94	0.0947696	0.4397	-4.98
247386_at	putative protein similar to unknown	emb2746	AT5G63420	1.16	0.21	1.94	0.09494069	0.4403	-4.99
254446_at	tubulin beta-9 chain ;supported by	TUB9	AT4G20890	1.15	0.20	1.94	0.09494056	0.4403	-4.99
251720_at	putative protein	---	AT3G56160	-1.36	-0.45	-1.94	0.09498155	0.4404	-4.99
267274_at	putative mitochondrial carrier prote	---	AT2G30160	1.24	0.31	1.94	0.09497762	0.4404	-4.99
252510_at	putative protein serine/threonine-s	---	AT3G46270	-1.16	-0.22	-1.94	0.09501109	0.4404	-4.99
252117_at	mucin -like protein hemomucin, D	YLS2	AT3G51430	1.29	0.37	1.94	0.09508948	0.4406	-4.99
252920_at	putative endo-1,4-beta-glucanase	AtGH9B17	AT4G39000	-1.19	-0.25	-1.94	0.09507912	0.4406	-4.99
249576_at	putative protein predicted protein,	---	AT5G37690	1.14	0.19	1.94	0.09518322	0.4409	-4.99
258791_at	hevein-like protein precursor (PR-	PR4	AT3G04720	1.53	0.61	1.94	0.09526811	0.4410	-4.99
261073_at	hypothetical protein predicted by g	---	AT1G07300	1.17	0.22	1.94	0.09531461	0.4410	-4.99
254306_at	putative protein ; supported by cD	ATCES1	AT4G22330	1.14	0.18	1.94	0.09530603	0.4410	-4.99
256154_at	hypothetical protein predicted by g	---	AT3G08490	-1.20	-0.26	-1.94	0.09525416	0.4410	-4.99
266136_at	unknown protein ;supported by ful	---	AT2G45060	1.12	0.17	1.94	0.09527144	0.4410	-4.99
265288_at	putative glutaredoxin ;supported b	---	AT2G20270	1.23	0.30	1.94	0.09530868	0.4410	-4.99
250407_at	chorismate mutase CM2 ; support	ATCM2	AT5G10870	1.16	0.22	1.94	0.09535791	0.4411	-4.99
248655_at	60S ribosomal protein L13a ;supp	---	AT5G48760	1.24	0.31	1.94	0.09538077	0.4411	-4.99
265016_at	unknown protein similar to deacet	---	AT1G24420	-1.13	-0.18	-1.94	0.09549563	0.4415	-4.99

260466_at	phosphatidylinositol-4-phosphate 5	---	AT1G10900	-1.40	-0.48	-1.94	0.09547991	0.4415	-4.99
264341_at	hypothetical protein predicted by g	---	AT1G70270	-1.14	-0.19	-1.94	0.09558723	0.4418	-4.99
254159_at	putative DNA-binding protein DNA	WRKY7	AT4G24240	1.38	0.46	1.94	0.09562964	0.4419	-4.99
263385_at	ABA-regulated gene (ATEM6) ; su	GEA6	AT2G40170	-1.20	-0.27	-1.94	0.0956365	0.4419	-4.99
260844_at	peroxisomal targeting signal type 2	PEX7	AT1G29260	1.15	0.20	1.94	0.09577016	0.4424	-5.00
263410_at	predicted protein ;supported by full	---	AT2G04039	-1.30	-0.38	-1.94	0.09587366	0.4426	-5.00
263045_at	hypothetical protein predicted by g	---	AT2G05370	-1.16	-0.22	-1.94	0.09587007	0.4426	-5.00
246108_at	putative protein retinal glutamic ac	---	AT5G28630	-1.43	-0.52	-1.94	0.09588167	0.4426	-5.00
258512_at	beta-glucosidase, putative similar	---	AT3G06510	-1.13	-0.17	-1.93	0.09604376	0.4432	-5.00
261352_at	DNA repair protein RAD23, putativ	RAD23	AT1G79650	-1.18	-0.23	-1.93	0.09602959	0.4432	-5.00
250727_at	putative protein similar to unknown	---	AT5G06430	1.15	0.20	1.93	0.09606163	0.4432	-5.00
254232_at	tyrosine transaminase like protein	CORI3	AT4G23600	-1.72	-0.78	-1.93	0.09621039	0.4436	-5.00
245043_at	putative cyclin ;supported by full-le	RCY1	AT2G26430	1.30	0.38	1.93	0.09624308	0.4436	-5.00
246050_s_at	protein phosphatase 2A regulatory	---	AT5G28850	1.13	0.18	1.93	0.09620973	0.4436	-5.00
251332_at	putative protein putative protein A	---	AT3G61670	1.25	0.32	1.93	0.09624851	0.4436	-5.00
245707_at	NAC2-like protein	anac077	AT5G04400	-1.19	-0.25	-1.93	0.09623039	0.4436	-5.00
261395_at	unknown protein similar to putative	---	AT1G79700	1.46	0.55	1.93	0.0962728	0.4436	-5.00
265934_at	unknown protein	EER5	AT2G19560	1.13	0.18	1.93	0.09632093	0.4437	-5.00
260964_at	E2, ubiquitin-conjugating enzyme	ATUBC2-1	AT1G45050	1.14	0.18	1.93	0.09638483	0.4437	-5.00
259521_at	ATP-dependent Clp protease prote	CLP2	AT1G12410	1.21	0.27	1.93	0.09635147	0.4437	-5.00
245937_at	putative protein 22kDa peroxisom	---	AT5G19750	1.32	0.40	1.93	0.09634776	0.4437	-5.00
250566_at	putative helix-loop-helix DNA bind	TCP17	AT5G08070	-1.24	-0.32	-1.93	0.09638617	0.4437	-5.00
251356_at	putative protein hypothetical protei	AtPP2-A13	AT3G61060	1.21	0.27	1.93	0.09644348	0.4437	-5.00
265022_at	putative agp1 similar to GB:CAA48	BCP1	AT1G24520	-1.23	-0.29	-1.93	0.09644793	0.4437	-5.00
258155_at	protein kinase C-receptor/G-prote	RACK1C_A	AT3G18130	1.61	0.69	1.93	0.09645279	0.4437	-5.00
265909_at	unknown protein ;supported by ful	---	AT2G25720	1.18	0.24	1.93	0.09656427	0.4442	-5.00
266476_at	unknown protein ;supported by ful	---	AT2G31090	1.23	0.30	1.93	0.09658574	0.4442	-5.00
262700_at	unknown protein	---	AT1G76020	-1.22	-0.29	-1.93	0.09661995	0.4442	-5.00
258503_at	unknown protein	---	AT3G02500	-1.21	-0.27	-1.93	0.09666422	0.4444	-5.00
264004_at	Expressed protein ; supported by f	---	AT2G22425	1.20	0.26	1.93	0.09672876	0.4446	-5.00
265914_at	En/Spm-like transposon protein rel	---	---	-1.13	-0.18	-1.93	0.09676581	0.4446	-5.00
267290_at	putative SET-domain transcriptiona	---	AT2G23740	-1.20	-0.27	-1.93	0.09676987	0.4446	-5.01
248722_at	pyrophosphate-fructose-6-phospha	PFK2	AT5G47810	-1.13	-0.17	-1.93	0.09687025	0.4448	-5.01
247225_at	inositol-1, 4, 5-trisphosphate 5-ph	BST1	AT5G65090	-1.19	-0.25	-1.93	0.09687324	0.4448	-5.01
245292_at	Expressed protein ; supported by c	---	AT4G15093	-1.22	-0.28	-1.93	0.09687873	0.4448	-5.01

260991_at	hypothetical protein predicted by g	---	AT1G12160	1.14	0.19	1.93	0.09698014	0.4451	-5.01
259362_s_at	serin threonin-kinase, putative sim	---	AT1G13350	1.19	0.25	1.93	0.09702317	0.4451	-5.01
257389_at	hypothetical protein predicted by g	---	AT2G17970	-1.15	-0.20	-1.93	0.09698625	0.4451	-5.01
AFFX-r2-Bs-da	B. subtilis /GEN=dapB /DB_XREF=	---	---	-1.37	-0.46	-1.93	0.09701579	0.4451	-5.01
260938_at	hypothetical protein contains simila	---	AT1G45170	1.20	0.27	1.93	0.09707029	0.4452	-5.01
250368_at	putative protein ; supported by cD	---	AT5G11280	1.20	0.26	1.93	0.0970761	0.4452	-5.01
247059_at	UTP-glucose glucosyltransferase	UGT72E2	AT5G66690	-1.16	-0.21	-1.93	0.0971223	0.4453	-5.01
254020_at	beta-carotene hydroxylase ; suppo	BETA-OHA	AT4G25700	1.69	0.76	1.93	0.09718653	0.4455	-5.01
266349_at	unknown protein predicted by gens	---	AT2G01460	-1.17	-0.23	-1.93	0.09720899	0.4455	-5.01
263981_at	unknown protein ;supported by ful	PAR1	AT2G42870	1.67	0.74	1.93	0.09725801	0.4457	-5.01
251930_at	putative protein several hypothetic	ATRBL4	AT3G53780	1.21	0.27	1.92	0.09739508	0.4459	-5.01
245365_at	hypothetical protein ;supported by	---	AT4G17720	-1.30	-0.38	-1.92	0.09738426	0.4459	-5.01
260215_at	unknown protein	---	AT1G74530	1.17	0.22	1.92	0.09739213	0.4459	-5.01
252205_at	hypothetical protein various predic	---	AT3G50350	-1.22	-0.29	-1.92	0.09739033	0.4459	-5.01
267633_at	hypothetical protein predicted by g	---	AT2G42180	-1.13	-0.18	-1.92	0.09742417	0.4460	-5.01
254894_at	putative phospholipase D-gamma	PLDGAMM	AT4G11840	1.26	0.34	1.92	0.097485	0.4462	-5.01
249199_at	putative protein similar to unknown	BPC6	AT5G42520	1.17	0.22	1.92	0.09761731	0.4467	-5.01
256957_at	hypothetical protein predicted by g	---	AT3G13420	-1.17	-0.22	-1.92	0.09764333	0.4467	-5.01
259646_at	n-calpain-1 large subunit, putative	DEK1	AT1G55350	-1.16	-0.21	-1.92	0.09771478	0.4469	-5.01
254030_at	putative acidic ribosomal protein a	---	AT4G25890	1.47	0.56	1.92	0.0977758	0.4470	-5.01
264326_at	unknown protein	---	AT1G04230	-1.20	-0.26	-1.92	0.0977617	0.4470	-5.01
261633_at	hypothetical protein predicted by g	---	AT1G49930	1.15	0.20	1.92	0.09780897	0.4471	-5.02
255001_at	AIG1-like protein AIG1 - Arabidop	---	AT4G09930	-1.22	-0.28	-1.92	0.09787747	0.4473	-5.02
256842_at	hypothetical protein predicted by g	---	---	-1.15	-0.21	-1.92	0.09804254	0.4480	-5.02
260026_at	60S ribosomal protein L18A, putat	RPL18AA	AT1G29970	1.17	0.22	1.92	0.09805721	0.4480	-5.02
265508_at	hypothetical protein predicted by g	---	AT2G15930	-1.13	-0.18	-1.92	0.09807776	0.4480	-5.02
256350_at	hypothetical protein contains simila	PGSIP4	AT1G54940	-1.14	-0.19	-1.92	0.09810683	0.4480	-5.02
251621_at	protein kinase - like protein wall-as	---	AT3G57700	1.32	0.40	1.92	0.09813025	0.4480	-5.02
247846_at	putative protein	---	AT5G58100	1.17	0.22	1.92	0.09820739	0.4483	-5.02
249421_at	DegP protease contains similarity t	DEG8	AT5G39830	-1.18	-0.24	-1.92	0.09827648	0.4485	-5.02
265498_at	putative C2H2-type zinc finger prot	---	AT2G15740	-1.14	-0.19	-1.92	0.09838597	0.4488	-5.02
253260_at	hypothetical protein	---	AT4G34420	-1.17	-0.23	-1.92	0.09838207	0.4488	-5.02
263471_at	hypothetical protein predicted by g	RAP	AT2G31890	1.19	0.25	1.92	0.09851897	0.4489	-5.02
247357_at	receptor-like protein kinase ; supp	---	AT5G63710	-1.17	-0.23	-1.92	0.09842433	0.4489	-5.02
245575_at	centromere protein homolog	---	AT4G14760	-1.16	-0.22	-1.92	0.09849939	0.4489	-5.02

266119_at	protease inhibitor II identical to GE	LCR69	AT2G02100	-1.74	-0.80	-1.92	0.09847214	0.4489	-5.02
249172_at	putative protein similar to unknown	---	AT5G42950	1.18	0.24	1.92	0.09852924	0.4489	-5.02
261258_at	unknown protein	---	AT1G26640	1.21	0.28	1.92	0.09845862	0.4489	-5.02
253185_at	putative protein bZIP protein - Ara	---	AT4G35240	1.20	0.27	1.92	0.09853458	0.4489	-5.02
256180_at	light repressible receptor protein k	---	AT1G51810	-1.12	-0.17	-1.92	0.09857407	0.4490	-5.02
255151_at	putative protein oxysterol-binding	ORP1C	AT4G08180	-1.12	-0.16	-1.92	0.0986073	0.4490	-5.02
250608_at	pectin methyl-esterase-like protein	---	AT5G07420	-1.14	-0.19	-1.92	0.09867802	0.4492	-5.02
265800_at	similar to ch-TOG protein from Hor	MOR1	AT2G35630	1.18	0.24	1.92	0.09866957	0.4492	-5.02
263087_s_at	putative sugar transporter	---	AT2G16120	-1.17	-0.22	-1.91	0.09872109	0.4493	-5.02
262455_at	Mlo protein, putative similar to Mlo	MLO2	AT1G11310	1.24	0.31	1.91	0.09875821	0.4494	-5.02
248298_at	putative protein similar to unknown	---	AT5G53110	-1.29	-0.37	-1.91	0.09879035	0.4494	-5.02
258994_at	unknown protein similar to putative	RAPTOR1	AT3G08850	1.14	0.19	1.91	0.09892938	0.4496	-5.03
255615_at	hypothetical protein	---	AT4G01290	-1.12	-0.17	-1.91	0.09893274	0.4496	-5.03
256641_at	hypothetical protein similar to puta	---	---	-1.20	-0.27	-1.91	0.09891992	0.4496	-5.03
259114_at	26S proteasome AAA-ATPase sub	RPT5A	AT3G05530	1.15	0.21	1.91	0.09891017	0.4496	-5.03
262878_at	hypothetical protein predicted by g	NDF2	AT1G64770	1.20	0.26	1.91	0.09885671	0.4496	-5.03
247207_at	putative protein similar to unknown	---	AT5G65000	1.13	0.17	1.91	0.09902722	0.4498	-5.03
253456_at	putative protein norbin, Rattus nor	---	AT4G32050	-1.21	-0.28	-1.91	0.09902101	0.4498	-5.03
248596_at	putative protein contains similarity	AtMYB111	AT5G49330	1.43	0.52	1.91	0.09899157	0.4498	-5.03
249807_at	pectinacetylesterase	---	AT5G23870	-1.25	-0.33	-1.91	0.09906809	0.4498	-5.03
257758_at	eukaryotic translation elongation f	---	AT3G22980	-1.19	-0.25	-1.91	0.09904856	0.4498	-5.03
248299_at	unknown protein ;supported by ful	---	AT5G53080	1.17	0.22	1.91	0.09918718	0.4501	-5.03
261736_at	hypothetical protein simlar to hypo	---	AT1G47810	-1.15	-0.20	-1.91	0.09920352	0.4501	-5.03
247426_at	putative protein contains similarity	---	AT5G62570	1.35	0.43	1.91	0.0991732	0.4501	-5.03
247968_at	40S ribosomal protein S30 homolo	---	AT5G56670	1.41	0.50	1.91	0.09924519	0.4502	-5.03
262508_at	serine/threonine kinase, putative s	---	AT1G11300	1.43	0.52	1.91	0.09927536	0.4503	-5.03
246155_at	putative protein predicted proteins	---	AT5G20030	1.13	0.18	1.91	0.09940657	0.4507	-5.03
245211_at	putative protein similarity to sec10	SEC10	AT5G12370	1.13	0.17	1.91	0.09938128	0.4507	-5.03
250266_at	histone H3 -like protein histone H3	---	AT5G12910	-1.18	-0.24	-1.91	0.09943697	0.4507	-5.03
247842_at	SPP30 - like protein SPP30, Solan	---	AT5G58030	1.14	0.19	1.91	0.09941989	0.4507	-5.03
260535_at	hypothetical protein predicted by g	---	AT2G43390	-1.13	-0.18	-1.91	0.09946581	0.4507	-5.03
254458_at	putative protein heat shock protein	ATERDJ2B	AT4G21180	1.29	0.37	1.91	0.09949578	0.4507	-5.03
250448_at	putative protein lignostilbene-alph	---	AT5G10820	-1.30	-0.38	-1.91	0.09954088	0.4508	-5.03
259280_at	putative polypyrimidine tract-bindi	PTB1	AT3G01150	1.13	0.18	1.91	0.09953491	0.4508	-5.03
248104_at	S-adenosyl-L-methionine:salicylic a	IAMT1	AT5G55250	1.45	0.53	1.91	0.09959864	0.4509	-5.03

255070_at	isoamylase-like protein probable is	ISA3	AT4G09020	-1.15	-0.20	-1.91	0.09967529	0.4512	-5.03
261986_s_at	cytochrome P450, putative similar	CYP76C5	AT1G33720 /	-1.52	-0.60	-1.91	0.09974789	0.4512	-5.03
258045_at	ubiquitin-specific protease 7 (UBP	UBP7	AT3G21280	1.18	0.24	1.91	0.09974507	0.4512	-5.03
253784_at	putative protein WREBP-1, Nicotia	PHR1	AT4G28610	-1.18	-0.24	-1.91	0.09974056	0.4512	-5.03
267466_at	putative GDSL-motif lipase/hydrola	---	AT2G19010	1.15	0.20	1.91	0.09975871	0.4512	-5.03
252164_at	hypothetical protein nodH - Rhizol	---	AT3G50620	-1.39	-0.48	-1.91	0.09980393	0.4512	-5.03
265988_at	hypothetical protein predicted by g	---	AT2G24255	-1.15	-0.20	-1.91	0.09980314	0.4512	-5.03
245252_at	ethylene responsive element bindi	ATERF-1	AT4G17500	1.61	0.69	1.91	0.09982936	0.4513	-5.03
261623_at	hypothetical protein similar to retic	ATSEC1A	AT1G01980	-1.17	-0.22	-1.91	0.09985985	0.4513	-5.04
248885_at	putative protein similar to unknown	---	AT5G46150	1.15	0.21	1.91	0.09989429	0.4514	-5.04
257662_at	low affinity calcium antiporter CAX	CAX2	AT3G13320	1.15	0.20	1.91	0.09990888	0.4514	-5.04
251858_at	aquaporin MIP - like protein aquap	PIP2;5	AT3G54820	-1.29	-0.37	-1.91	0.10006125	0.4515	-5.04
257726_at	hypothetical protein predicted by g	---	AT3G18360	-1.15	-0.21	-1.91	0.10002605	0.4515	-5.04
257798_at	unknown protein	NAI2	AT3G15950	-1.24	-0.31	-1.91	0.10003494	0.4515	-5.04
264138_at	beta-Amyrin Synthase, putative si	---	AT1G78950	-1.18	-0.24	-1.91	0.10001099	0.4515	-5.04
264567_s_at	putative peroxidase ATP12a Stron	---	AT1G05240 /	-1.18	-0.24	-1.91	0.10007352	0.4515	-5.04
267606_at	putative beta-ketoacyl-CoA syntha	KCS11	AT2G26640	1.14	0.19	1.91	0.09998521	0.4515	-5.04
265226_at	unknown protein ; supported by cl	---	AT2G28430	1.14	0.18	1.91	0.10002332	0.4515	-5.04
261433_s_at	endoplasmic reticulum-type calciu	---	AT1G07670 /	1.13	0.18	1.91	0.1001385	0.4517	-5.04
258755_at	hypothetical protein identical to hy	---	AT3G11945 /	1.19	0.25	1.90	0.10024353	0.4517	-5.04
245438_at	growth regulator like protein	---	AT4G16650	1.16	0.21	1.90	0.10022853	0.4517	-5.04
263980_at	hypothetical protein predicted by g	---	AT2G42770	-1.21	-0.28	-1.90	0.10018323	0.4517	-5.04
250558_at	flavonoid 3-hydroxylase - like prot	TT7	AT5G07990	-1.19	-0.25	-1.90	0.10022028	0.4517	-5.04
252880_at	putative protein ;supported by full-l	---	AT4G39730	-1.29	-0.37	-1.90	0.10021491	0.4517	-5.04
254096_at	acid phosphatase - like protein ac	---	AT4G25150	-1.18	-0.24	-1.90	0.10030459	0.4519	-5.04
265001_at	hypothetical protein contains simila	---	AT1G67350	1.16	0.21	1.90	0.10032672	0.4519	-5.04
261639_at	tubulin alpha-2/alpha-4 chain, puta	TUA2	AT1G50010	1.59	0.67	1.90	0.10036749	0.4520	-5.04
252633_x_at	putative protein HISTONE DEACE	hda17	AT3G44490 /	1.13	0.17	1.90	0.1004658	0.4523	-5.04
245768_at	hypothetical protein similar to puta	---	AT1G33590	-1.42	-0.50	-1.90	0.1004808	0.4523	-5.04
260729_at	regulatory protein, putative contai	KU80	AT1G48050	1.14	0.18	1.90	0.10052434	0.4524	-5.04
265486_at	unknown protein predicted by gens	---	AT2G15560	1.21	0.27	1.90	0.10055716	0.4524	-5.04
245754_at	hypothetical protein predicted by g	---	AT1G35183	1.14	0.19	1.90	0.10056444	0.4524	-5.04
245718_at	putative protein	---	AT5G04110	-1.21	-0.27	-1.90	0.10060059	0.4525	-5.04
248026_at	putative protein similar to unknown	---	AT5G55710	1.18	0.24	1.90	0.1006617	0.4526	-5.04
252103_at	putative protein various predicted	---	AT3G51410	1.14	0.19	1.90	0.10065435	0.4526	-5.04

258834_at	GTP cyclohydrolase I similar to GT	---	AT3G07270	1.20	0.27	1.90	0.10077058	0.4530	-5.04
254496_at	hyuC-like protein 5-substituted hy	ATAAH	AT4G20070	1.50	0.59	1.90	0.10077799	0.4530	-5.04
250794_at	putative protein contains similarity	---	AT5G05270	-1.15	-0.21	-1.90	0.10080675	0.4530	-5.04
248523_s_at	ubiquitin activating enzyme ;suppo	SAE1B	AT5G50580	-1.20	-0.27	-1.90	0.10086276	0.4532	-5.04
265884_at	unknown protein	---	AT2G42320	-1.21	-0.28	-1.90	0.10093077	0.4532	-5.05
261347_at	unknown protein	ELF7	AT1G79730	-1.18	-0.24	-1.90	0.10090055	0.4532	-5.05
254552_at	putative protein several hypothetic	---	AT4G19900	-1.16	-0.21	-1.90	0.10092823	0.4532	-5.05
263297_at	putative ADP-ribosylation factor ;	ATARFB1A	AT2G15310	-1.28	-0.35	-1.90	0.10098291	0.4533	-5.05
264625_at	hypothetical protein Contains simil	SNF4	AT1G09020	1.16	0.22	1.90	0.10099989	0.4533	-5.05
258396_at	unknown protein similar to unknow	---	AT3G15460	-1.34	-0.43	-1.90	0.10109686	0.4537	-5.05
255591_at	putative expansin	ATEXPA17	AT4G01630	-1.17	-0.22	-1.90	0.10127344	0.4541	-5.05
256614_at	hypothetical protein predicted by g	---	AT3G29300	-1.16	-0.21	-1.90	0.10123632	0.4541	-5.05
257723_at	hypothetical protein predicted by g	---	AT3G18500	-1.22	-0.29	-1.90	0.10122273	0.4541	-5.05
261619_x_at	hypothetical protein	---	---	1.15	0.20	1.90	0.10125843	0.4541	-5.05
246028_at	AKIN beta1 ; supported by full-len	---	AT5G21170	1.27	0.35	1.90	0.10134791	0.4543	-5.05
251656_at	putative protein N-ACETYLGLUC	---	AT3G57170	-1.17	-0.22	-1.90	0.1013292	0.4543	-5.05
260684_at	transcription factor, putative simila	NF-YA8	AT1G17590	1.23	0.30	1.90	0.10140936	0.4543	-5.05
245876_at	chaperonin precursor, putative sin	---	AT1G26230	-1.31	-0.39	-1.90	0.1014209	0.4543	-5.05
260011_at	hypothetical protein similar to hyp	---	AT1G68110	1.20	0.27	1.90	0.10140423	0.4543	-5.05
251584_at	putative protein At2g42580 - Arab	TTL4	AT3G58620	-1.46	-0.55	-1.90	0.10149336	0.4545	-5.05
258722_at	putative pathogenesis-related prot	---	AT3G09590	-1.16	-0.21	-1.90	0.10148684	0.4545	-5.05
264433_at	beta-glucosidase, putative similar	BGLU45	AT1G61810	2.07	1.05	1.90	0.10159742	0.4546	-5.05
252619_at	putative protein several hypothetic	---	AT3G45210	1.33	0.41	1.90	0.10159205	0.4546	-5.05
264848_at	unknown protein ;supported by ful	---	AT2G17350	1.13	0.18	1.89	0.10163013	0.4546	-5.05
247871_at	xyloglucan endotransglycosylase	---	AT5G57530	-1.13	-0.18	-1.89	0.10170648	0.4546	-5.05
262065_at	hypothetical protein predicted by g	---	AT1G56180	1.30	0.38	1.89	0.10168645	0.4546	-5.05
266084_at	hypothetical protein predicted by g	---	AT2G37810	-1.22	-0.28	-1.90	0.10157496	0.4546	-5.05
261959_s_at	polyprotein, putative similar to poly	---	---	-1.19	-0.25	-1.89	0.10165439	0.4546	-5.05
251441_at	SKP1/ASK1 (At5), putative similar	ASK5	AT3G60020	1.14	0.19	1.89	0.1016655	0.4546	-5.05
247687_at	protein serine /threonine kinase -	---	AT5G59740	-1.18	-0.24	-1.89	0.10173582	0.4546	-5.05
250691_at	glycolate oxidase subunit D-like; D	---	AT5G06580	1.13	0.17	1.89	0.1017374	0.4546	-5.05
262393_at	hypothetical protein contains simila	---	AT1G49490	1.17	0.23	1.90	0.10160975	0.4546	-5.05
264201_at	unknown protein ;supported by full	---	AT1G22630	1.26	0.34	1.89	0.10176921	0.4546	-5.05
261544_at	unknown protein	---	AT1G63540	-1.23	-0.30	-1.89	0.10182397	0.4547	-5.05
257860_at	Expressed protein ; supported by c	---	AT3G13062	1.26	0.33	1.89	0.10184357	0.4547	-5.05

260455_at	hypothetical protein predicted by g	---	AT1G72500	-1.46	-0.55	-1.89	0.10187805	0.4547	-5.05
246410_at	hypothetical protein predicted by g	---	AT1G57760	1.14	0.19	1.89	0.10185146	0.4547	-5.05
253304_at	putative protein ;supported by full-	---	AT4G33640	1.18	0.24	1.89	0.1018806	0.4547	-5.05
254801_at	endoxyloglucan transferase-like p	---	AT4G13080	-1.12	-0.17	-1.89	0.10192465	0.4547	-5.05
252894_at	hypothetical protein	---	AT4G39440	-1.19	-0.25	-1.89	0.10192859	0.4547	-5.05
265252_at	putative Na+/H+ antiporter	SOS1	AT2G01980	-1.14	-0.18	-1.89	0.10194946	0.4547	-5.05
246265_at	phosphoribosyl-ATP pyrophospho	AT-IE	AT1G31860	1.38	0.47	1.89	0.10206152	0.4551	-5.06
255689_at	hypothetical protein	---	AT4G00670	-1.13	-0.18	-1.89	0.10211247	0.4553	-5.06
248771_at	unknown protein	---	AT5G47790	1.19	0.26	1.89	0.1022368	0.4556	-5.06
251075_at	putative protein leucine-rich recep	---	AT5G01890	1.38	0.46	1.89	0.10222463	0.4556	-5.06
265806_at	putative auxin-regulated protein	---	AT2G18010	1.59	0.67	1.89	0.10221023	0.4556	-5.06
250553_at	putative protein PTD008, Homo sa	---	AT5G07960	1.20	0.26	1.89	0.10226905	0.4556	-5.06
246084_at	putative protein predicted proteins	ATBRXL4	AT5G20540	-1.17	-0.23	-1.89	0.10230463	0.4557	-5.06
263702_at	hypothetical protein identical to hy	---	AT1G31240	-1.16	-0.21	-1.89	0.10234805	0.4558	-5.06
246217_at	APETALA2 protein ; supported by	AP2	AT4G36920	-1.32	-0.40	-1.89	0.1024251	0.4558	-5.06
254874_at	putative protein beta-phosphoglud	---	AT4G11570	-1.22	-0.28	-1.89	0.10238896	0.4558	-5.06
258409_at	hypothetical protein similar to GB:A	---	AT3G17640	1.34	0.42	1.89	0.10240562	0.4558	-5.06
248836_at	NBS/LRR disease resistance prote	---	AT5G47260	-1.21	-0.28	-1.89	0.10239685	0.4558	-5.06
255960_at	unknown protein ; supported by cD	---	AT1G22140	1.21	0.28	1.89	0.10266043	0.4562	-5.06
262092_at	unknown protein	---	AT1G56150	1.59	0.67	1.89	0.10254554	0.4562	-5.06
245573_at	hypothetical protein	---	AT4G14730	-1.13	-0.18	-1.89	0.10259867	0.4562	-5.06
257098_at	hypothetical protein	---	---	-1.15	-0.20	-1.89	0.10263918	0.4562	-5.06
247115_at	kinesin-like calmodulin-binding pro	ZWI	AT5G65930	-1.20	-0.27	-1.89	0.10262929	0.4562	-5.06
258162_at	dehydrogenase, putative similar to	---	AT3G17810	-1.23	-0.30	-1.89	0.10265807	0.4562	-5.06
253430_at	putative protein	---	AT4G32430	-1.18	-0.24	-1.89	0.10259475	0.4562	-5.06
253557_at	putative protein wall-associated ki	---	AT4G31110 /	1.13	0.18	1.89	0.10271992	0.4563	-5.06
261463_at	hypothetical protein predicted by g	---	AT1G07730 /	-1.14	-0.19	-1.89	0.10275064	0.4563	-5.06
247521_at	putative protein ATP/GTP nucleot	---	AT5G61450	-1.18	-0.24	-1.89	0.10274185	0.4563	-5.06
257579_at	hypothetical protein predicted by g	---	AT3G11000	-1.18	-0.24	-1.89	0.10275984	0.4563	-5.06
252670_at	dnaJ protein homolog atj3 ;suppor	ATJ3	AT3G44110	-1.20	-0.26	-1.89	0.10280535	0.4564	-5.06
245804_at	hypothetical protein predicted by g	---	AT1G46696	-1.14	-0.19	-1.89	0.10290427	0.4568	-5.06
250326_at	putative protein strong similarity to	MSL10	AT5G12080	-1.23	-0.30	-1.89	0.10298534	0.4570	-5.06
260325_at	putative monodehydroascorbate re	MDAR6	AT1G63940	1.23	0.29	1.89	0.10299139	0.4570	-5.06
267215_at	hypothetical protein	---	AT2G02630	-1.12	-0.17	-1.89	0.10303163	0.4571	-5.07
252183_at	UTP-glucose glucosyltransferase	UGT72E1	AT3G50740	-1.21	-0.28	-1.89	0.10310184	0.4571	-5.07

257618_at	protein kinase, putative similar to 1	---	AT3G24715	-1.13	-0.17	-1.89	0.10306446	0.4571	-5.07
245540_at	ABC transporter like protein	PDR2	AT4G15230	-1.61	-0.69	-1.88	0.10316003	0.4571	-5.07
261443_at	glutaredoxin, putative similar to gl	GRX480	AT1G28480	-1.58	-0.66	-1.88	0.10314642	0.4571	-5.07
249784_at	putative protein similar to unknown	---	AT5G24280	-1.24	-0.31	-1.88	0.10313605	0.4571	-5.07
251033_at	hypothetical protein ;supported by	---	AT5G01960	-1.12	-0.17	-1.88	0.10312995	0.4571	-5.07
249462_at	putative protein predicted proteins	EMB2744	AT5G39680	-1.18	-0.24	-1.88	0.10319491	0.4572	-5.07
255017_at	hypothetical protein ;supported by	CNX7	AT4G10100	1.17	0.22	1.88	0.1032709	0.4574	-5.07
254804_at	putative protein putative oxidoredu	---	AT4G13010	-1.19	-0.25	-1.88	0.10329865	0.4574	-5.07
255670_at	Expressed protein ; supported by f	RHB1A	AT4G00335	1.13	0.18	1.88	0.10334248	0.4575	-5.07
266219_at	putative para-aminobenzoate synt	emb1997	AT2G28880	1.16	0.21	1.88	0.10336812	0.4576	-5.07
261867_at	unknown protein ; supported by cD	---	AT1G50575	-1.18	-0.24	-1.88	0.10339036	0.4576	-5.07
261487_at	hypothetical protein predicted by g	---	AT1G14340	1.15	0.20	1.88	0.10342535	0.4576	-5.07
263565_at	unknown protein	FUT4	AT2G15390	1.66	0.73	1.88	0.10345736	0.4577	-5.07
261168_at	unknown protein	---	AT1G04940	-1.31	-0.39	-1.88	0.10348919	0.4577	-5.07
245792_at	pinoresinol-lariciresinol reductase,	PRR1	AT1G32100	1.60	0.68	1.88	0.10354445	0.4577	-5.07
252995_at	hypothetical protein ;supported by	---	AT4G38370	1.21	0.27	1.88	0.103525	0.4577	-5.07
252734_at	putative protein merozoite surface	MEE38	AT3G43160	-1.17	-0.22	-1.88	0.10351352	0.4577	-5.07
252090_at	5B protein like protein cysteine-ric	---	AT3G52130	-1.15	-0.20	-1.88	0.10362995	0.4577	-5.07
247372_at	unknown protein ;supported by ful	---	AT5G63280	1.26	0.33	1.88	0.10357597	0.4577	-5.07
263240_s_at	unknown protein ; supported by cl	---	AT1G72590	1.25	0.32	1.88	0.10360156	0.4577	-5.07
253466_at	homeodomain containing protein 1	KNAT5	AT4G32040	1.19	0.26	1.88	0.10362116	0.4577	-5.07
248338_at	HCF106 (gb|AAD32652.1) ; suppo	HCF106	AT5G52440	1.19	0.25	1.88	0.10372884	0.4579	-5.07
261161_at	hypothetical protein contains Pfam	---	AT1G34420	-1.30	-0.38	-1.88	0.10372997	0.4579	-5.07
253195_at	putative protein dihydroflavonol-4-	---	AT4G35420	1.18	0.23	1.88	0.10372402	0.4579	-5.07
256486_at	chloroplast nucleoid DNA binding	---	AT1G31450	-1.17	-0.22	-1.88	0.10378327	0.4580	-5.07
247413_at	NBS/LRR disease resistance prote	---	AT5G63020	1.20	0.26	1.88	0.10377706	0.4580	-5.07
246801_at	threonyl-tRNA synthetase ; suppo	---	AT5G26830	1.15	0.20	1.88	0.10398596	0.4587	-5.07
253411_at	homeobox gene ATH1	ATH1	AT4G32980	-1.35	-0.43	-1.88	0.10395936	0.4587	-5.07
249629_at	kinesin -like protein Krm protein, L	---	AT5G37590	-1.24	-0.31	-1.88	0.10399902	0.4587	-5.07
251479_at	serine/threonine-specific kinase le	ATHLECRK	AT3G59700	1.49	0.58	1.88	0.10410429	0.4587	-5.07
257965_at	unknown protein ;supported by ful	---	AT3G19900	1.26	0.33	1.88	0.10410673	0.4587	-5.07
267380_at	putative thromboxane-A synthase	CYP711A1	AT2G26170	-1.39	-0.48	-1.88	0.10410391	0.4587	-5.07
248522_at	predicted protein	---	AT5G50565	1.15	0.20	1.88	0.10411592	0.4587	-5.08
261849_at	pectin methylesterase, putative sir	---	AT1G11370	-1.18	-0.24	-1.88	0.10404218	0.4587	-5.07
260203_at	NAM-like protein similar to NAM (n	ANAC019	AT1G52890	1.32	0.40	1.88	0.10421603	0.4591	-5.08

250008_at	triacylglycerol lipase-like protein tr	---	AT5G18630	1.36	0.44	1.88	0.10422991	0.4591	-5.08
248085_at	putative protein similar to unknown	SVL1	AT5G55480	-1.37	-0.45	-1.88	0.10425345	0.4591	-5.08
253683_at	cytidine deaminase 4 (CDA4)	---	AT4G29650	-1.15	-0.21	-1.88	0.10428287	0.4591	-5.08
257016_at	protein kinase, putative similar to I	---	AT3G28690	1.18	0.24	1.88	0.10431414	0.4592	-5.08
250846_at	sulphite reductase ; supported by	SIR	AT5G04590	-1.33	-0.41	-1.88	0.10437519	0.4593	-5.08
253410_at	putative protein various predicted	---	AT4G32970	1.22	0.28	1.88	0.10442809	0.4594	-5.08
261626_at	unknown protein ; supported by cD	---	AT1G01990	1.20	0.26	1.88	0.10443406	0.4594	-5.08
248746_at	NADH dehydrogenase 10.5K chair	---	AT5G47890	1.28	0.35	1.88	0.10449619	0.4596	-5.08
251508_at	putative protein mitochondrial RN/	---	AT3G58970	-1.20	-0.26	-1.88	0.10451894	0.4596	-5.08
256496_at	hypothetical protein similar to hypo	---	AT1G31510	-1.17	-0.22	-1.88	0.10460717	0.4597	-5.08
252545_at	putative protein	---	AT3G45820	1.18	0.24	1.88	0.10460326	0.4597	-5.08
267145_at	putative acetyltransferase	ATMAK3	AT2G38130	1.17	0.23	1.88	0.10455021	0.4597	-5.08
262317_at	unknown protein ;supported by ful	EDA4	AT2G48140	1.34	0.42	1.88	0.10459189	0.4597	-5.08
249236_at	putative protein similar to unknown	---	AT5G41950	1.14	0.19	1.87	0.10464483	0.4597	-5.08
255255_at	coded for by A. thaliana cDNA T44	---	AT4G05070	1.29	0.36	1.87	0.10470201	0.4598	-5.08
265060_at	HD-Zip protein, putative similar to	ATHB-15	AT1G52150	-1.41	-0.49	-1.87	0.10468779	0.4598	-5.08
260178_at	hypothetical protein similar to unkr	---	AT1G70720	-1.17	-0.22	-1.87	0.10491225	0.4606	-5.08
257160_at	hypothetical protein predicted by g	---	---	-1.25	-0.33	-1.87	0.10504071	0.4611	-5.08
248307_at	selenium-binding protein-like	---	AT5G52850	-1.18	-0.24	-1.87	0.1051532	0.4614	-5.08
245358_at	PRL1 protein ;supported by full-ler	PRL1	AT4G15900	1.19	0.25	1.87	0.1051372	0.4614	-5.08
266090_at	unknown protein	---	AT2G38000	-1.20	-0.26	-1.87	0.10515545	0.4614	-5.08
253579_at	SERINE CARBOXYPEPTIDASE I	BRS1	AT4G30610	1.44	0.52	1.87	0.10518099	0.4614	-5.08
246036_at	alpha-galactosidase - like protein	AtAGAL2	AT5G08370	-1.37	-0.46	-1.87	0.10527474	0.4615	-5.09
251895_at	class IV chitinase (CHIV)	ATEP3	AT3G54420	-1.49	-0.58	-1.87	0.10525091	0.4615	-5.09
259037_at	hypothetical protein predicted by g	---	AT3G09350	-1.67	-0.74	-1.87	0.10525345	0.4615	-5.09
266226_at	histone H4 identical to GB:M17133	HIS4	AT2G28740	1.28	0.35	1.87	0.1052924	0.4615	-5.09
255940_at	prolyl endopeptidase, putative sim	---	AT1G20380	-1.14	-0.18	-1.87	0.10534193	0.4616	-5.09
247345_at	putative protein contains similarity	---	AT5G63760	1.19	0.25	1.87	0.10536464	0.4617	-5.09
246017_at	putative protein predicted proteins	---	AT5G10730	-1.14	-0.19	-1.87	0.10544429	0.4618	-5.09
251480_at	putative protein inducible carbony	---	AT3G59710	-1.22	-0.28	-1.87	0.10545635	0.4618	-5.09
251556_at	putative protein predicted proteins	---	AT3G58840	-1.23	-0.30	-1.87	0.10542503	0.4618	-5.09
259019_at	hypothetical protein similar to sero	CHIP	AT3G07370	1.17	0.23	1.87	0.10551929	0.4620	-5.09
248871_at	putative protein strong similarity to	---	AT5G46680	-1.18	-0.24	-1.87	0.10561835	0.4620	-5.09
249734_at	putative protein strong similarity to	IRE1-1	AT5G24360	-1.13	-0.17	-1.87	0.10566387	0.4620	-5.09
262353_at	hypothetical protein similar to hypo	---	AT1G64210	-1.13	-0.17	-1.87	0.10558589	0.4620	-5.09

250982_at	putative protein zinc finger protein	JKD	AT5G03150	-1.30	-0.38	-1.87	0.10564658	0.4620	-5.09
247350_at	unknown protein	---	AT5G63830	-1.17	-0.23	-1.87	0.10556343	0.4620	-5.09
251187_at	putative protein putative proteins -	AtATG18a	AT3G62770	-1.13	-0.17	-1.87	0.10566956	0.4620	-5.09
266095_at	3-oxo-5-alpha-steroid 4-dehydrog	DET2	AT2G38050	-1.24	-0.31	-1.87	0.10566511	0.4620	-5.09
261550_at	hypothetical protein	---	AT1G63450	-1.15	-0.20	-1.87	0.10576381	0.4623	-5.09
257396_at	predicted protein	EPF1	AT2G20875	-1.21	-0.28	-1.87	0.10579111	0.4624	-5.09
256727_at	hypothetical protein	---	AT3G52240	1.19	0.25	1.87	0.10587364	0.4626	-5.09
264129_at	hypothetical protein predicted by g	---	AT1G79170	-1.18	-0.24	-1.87	0.10591507	0.4627	-5.09
266611_at	putative auxin-regulated protein	GH3.1	AT2G14960	-1.16	-0.21	-1.87	0.10606172	0.4632	-5.09
261789_at	40S ribosomal protein S12, putati	---	AT1G15930	1.38	0.47	1.87	0.10605138	0.4632	-5.09
250226_at	putative protein contains similarity	---	AT5G13780	1.18	0.24	1.87	0.10610716	0.4633	-5.09
256055_at	mitochondrial carrier protein, puta	---	AT1G07030	-1.15	-0.20	-1.87	0.10613013	0.4633	-5.09
247942_at	putative protein similar to unknown	---	AT5G57120	1.24	0.31	1.86	0.10636898	0.4634	-5.10
248757_at	putative protein contains similarity	---	AT5G47680	1.14	0.19	1.86	0.10637761	0.4634	-5.10
248398_at	sorbitol dehydrogenase-like protei	---	AT5G51970	1.19	0.25	1.86	0.1063323	0.4634	-5.10
246095_at	homeotic gene regulator - like pro	---	AT5G19310	1.27	0.35	1.86	0.10636089	0.4634	-5.10
258514_at	unknown protein ; supported by fu	---	AT3G06610	1.14	0.19	1.86	0.10631783	0.4634	-5.09
266315_at	unknown protein ; supported by cl	SE	AT2G27100	-1.13	-0.18	-1.86	0.10625912	0.4634	-5.09
265030_at	receptor-like kinase, putative simil	---	AT1G61610	-1.37	-0.45	-1.86	0.10635188	0.4634	-5.10
258567_at	apyrase (Atapy1) identical to apyra	ATAPY1	AT3G04080	1.21	0.28	1.86	0.10620397	0.4634	-5.09
265657_at	unknown protein ; supported by cl	---	AT2G13840	1.18	0.23	1.86	0.10638316	0.4634	-5.10
251810_at	putative protein predicted pectate	---	AT3G55250	1.21	0.28	1.86	0.10621879	0.4634	-5.09
266998_at	hypothetical protein predicted by g	---	AT2G34400	-1.17	-0.22	-1.86	0.10626259	0.4634	-5.09
259545_at	hypothetical protein ; supported by	AAE1	AT1G20560	-1.17	-0.22	-1.86	0.10645043	0.4635	-5.10
252139_at	putative protein hypothetical prote	---	AT3G51050	-1.15	-0.20	-1.86	0.10642358	0.4635	-5.10
264145_at	latex-abundant protein, putative si	AtMC7	AT1G79310	-1.12	-0.17	-1.86	0.10643347	0.4635	-5.10
262567_at	hypothetical protein contains simila	---	AT1G34300	1.27	0.34	1.86	0.1065338	0.4637	-5.10
249452_at	Sec7/gnom -like protein GNOM, A	---	AT5G39500	1.15	0.21	1.86	0.1065215	0.4637	-5.10
256870_at	cytochrome P450, putative contai	CYP71B34	AT3G26300	1.32	0.40	1.86	0.10659206	0.4638	-5.10
263694_at	putative reverse transcriptase stro	---	---	-1.13	-0.17	-1.86	0.10662067	0.4638	-5.10
265452_at	putative bHLH transcription factor	ATAIB	AT2G46510	-1.61	-0.69	-1.86	0.10661026	0.4638	-5.10
261482_at	unknown protein ;supported by full	THH1	AT1G14530	-1.17	-0.22	-1.86	0.10664509	0.4638	-5.10
259832_at	transfactor, putative similar to GI:4	---	AT1G69580	-1.46	-0.55	-1.86	0.10666263	0.4638	-5.10
251121_at	putative protein ; supported by cD	AGG1	AT3G63420	1.24	0.31	1.86	0.10670622	0.4639	-5.10
248920_at	magnesium chelatase subunit of p	CHLI2	AT5G45930	1.17	0.23	1.86	0.10677441	0.4641	-5.10

259165_at	homeobox-leucine zipper protein H	ATHB-1	AT3G01470 /	1.35	0.44	1.86	0.10684189	0.4642	-5.10
262199_at	unknown protein ; supported by cD	---	AT1G53800	-1.23	-0.29	-1.86	0.10683138	0.4642	-5.10
246879_at	endopeptidase - like protein O-sia	---	AT5G26110	1.16	0.22	1.86	0.10693389	0.4643	-5.10
256818_at	hypothetical protein contains Pfam	---	AT3G21420	-1.14	-0.19	-1.86	0.10694631	0.4643	-5.10
259366_at	allene oxide cyclase, putative simi	AOC4	AT1G13280	-1.25	-0.32	-1.86	0.10691729	0.4643	-5.10
250801_at	pectinesterase	---	AT5G04960	1.15	0.20	1.86	0.10690492	0.4643	-5.10
250107_at	ids-4 protein - like ids-4 protein, H	SPX4	AT5G15330	1.24	0.32	1.86	0.10704186	0.4646	-5.10
244953_s_at	NADH dehydrogenase subunit 6	---	AT2G07731	-1.27	-0.35	-1.86	0.1071753	0.4646	-5.10
260874_at	hypothetical protein predicted by g	emb2170	AT1G21390	-1.19	-0.25	-1.86	0.10714373	0.4646	-5.10
248521_s_at	nodulin-like protein ; supported by	---	AT5G50520 /	1.16	0.21	1.86	0.10717185	0.4646	-5.10
267617_at	heme oxygenase 1 (HO1) identica	TED4	AT2G26670	1.27	0.35	1.86	0.10714193	0.4646	-5.10
262614_at	putative pattern formation protein E	GN	AT1G13980	1.28	0.36	1.86	0.10710951	0.4646	-5.10
250204_at	leucine zipper protein-like	ATEXO70C	AT5G13990	-1.18	-0.24	-1.86	0.10709014	0.4646	-5.10
249276_at	DNA polymerase alpha subunit IV	POLA3	AT5G41880	2.00	1.00	1.86	0.10718596	0.4646	-5.10
249317_at	glutathione transferase	ATGSTT2	AT5G41240	-1.15	-0.20	-1.86	0.10725628	0.4648	-5.10
258459_at	hypothetical protein predicted by g	---	---	-1.17	-0.22	-1.86	0.1072533	0.4648	-5.10
251234_s_at	putative dTDP-glucose 4-6-dehydr	UXS4	AT2G47650 /	1.24	0.32	1.86	0.10734467	0.4651	-5.10
248664_at	peptidyl-prolyl cis-trans isomerase-	FKBP15-2	AT5G48580	1.24	0.31	1.86	0.10738239	0.4651	-5.10
253804_at	putative protein	---	AT4G28230	-1.18	-0.24	-1.86	0.10743313	0.4652	-5.10
261249_at	hypothetical protein predicted by g	---	AT1G05880	-1.16	-0.22	-1.86	0.10742138	0.4652	-5.10
260920_at	amp-binding protein, putative simi	---	AT1G21530	-1.13	-0.18	-1.86	0.10746797	0.4652	-5.11
259096_at	putative 40S ribosomal protein S3A	---	AT3G04840	1.40	0.49	1.86	0.10753628	0.4654	-5.11
253863_at	putative protein D.melanogaster P	---	AT4G27420	-1.19	-0.25	-1.86	0.10753936	0.4654	-5.11
258103_at	hypothetical protein contains Pfam	IPT7	AT3G23630	-1.21	-0.27	-1.86	0.10757498	0.4654	-5.11
261932_at	hypothetical protein predicted by g	---	AT1G22420	-1.13	-0.18	-1.86	0.107606	0.4655	-5.11
264611_at	putative pectate lyase A11 similar t	---	AT1G04680	1.82	0.87	1.85	0.1078471	0.4655	-5.11
255428_at	putative LRR receptor-like protein	SRF3	AT4G03390	-1.16	-0.21	-1.85	0.10796231	0.4655	-5.11
257452_at	hypothetical protein predicted by g	---	AT1G05740	-1.14	-0.18	-1.85	0.10772534	0.4655	-5.11
256043_at	hypothetical protein contains Pfam	---	AT1G07210	1.25	0.32	1.85	0.10779913	0.4655	-5.11
262227_s_at	26S proteasome ATPase subunit,	---	AT1G53750 /	1.14	0.19	1.85	0.10779565	0.4655	-5.11
255549_at	predicted protein of unknown funct	GPAT3	AT4G01950	-2.05	-1.03	-1.86	0.10767495	0.4655	-5.11
254106_at	geranylgeranylated protein ATGP4	ATGP4	AT4G24990	1.19	0.26	1.85	0.10776305	0.4655	-5.11
248490_at	putative protein similar to unknown	---	AT5G50940	-1.46	-0.55	-1.85	0.10793725	0.4655	-5.11
261210_at	vacuolar ATP synthase subunit C,	DET3	AT1G12840	1.13	0.18	1.86	0.10765421	0.4655	-5.11
249159_at	Nicotiana lesion-inducing like ; su	---	AT5G43460	1.23	0.30	1.85	0.1077174	0.4655	-5.11

260001_at	putative S-adenosyl-L-methionine:	TSM1	AT1G67990	-1.20	-0.26	-1.85	0.10786718	0.4655	-5.11
265416_at	unknown protein ; supported by fu	---	AT2G37120	1.42	0.50	1.85	0.10794719	0.4655	-5.11
266039_s_at	hypothetical protein	---	AT2G07739	-1.19	-0.25	-1.85	0.10785439	0.4655	-5.11
253049_at	putative protein ; supported by cDN	MEE59	AT4G37300	1.38	0.46	1.85	0.1078451	0.4655	-5.11
247371_at	histone deacetylase ;supported by	HDA6	AT5G63110	-1.16	-0.21	-1.85	0.1079542	0.4655	-5.11
263288_at	cyclophilin-like protein ;supported	---	AT2G36130	1.20	0.26	1.85	0.10788225	0.4655	-5.11
252325_at	acetolactate synthase ; supported	CSR1	AT3G48560	1.13	0.17	1.85	0.10783614	0.4655	-5.11
255365_at	putative phosphofructokinase beta	MEE51	AT4G04040	1.15	0.20	1.85	0.10810509	0.4660	-5.11
256430_at	DREB2B transcription factor identi	DREB2B	AT3G11020	-1.15	-0.21	-1.85	0.10812191	0.4660	-5.11
257932_at	unknown protein contains Pfam pr	HCF107	AT3G17040	-1.18	-0.24	-1.85	0.10835018	0.4667	-5.11
252065_at	putative protein ;supported by full-	---	AT3G51610	1.20	0.26	1.85	0.10830138	0.4667	-5.11
251774_at	nematode resistance protein-like p	---	AT3G55840	-1.74	-0.80	-1.85	0.10834573	0.4667	-5.11
254490_at	CTP synthase like protein CTP sy	---	AT4G20320	1.27	0.34	1.85	0.10832206	0.4667	-5.11
258602_at	putative protein phosphatase-2C (	---	AT3G02750	-1.13	-0.17	-1.85	0.10852589	0.4673	-5.11
245481_at	hypothetical protein	---	AT4G16170	1.15	0.20	1.85	0.10858461	0.4674	-5.12
AFFX-r2-Ec-bio	E. coli /GEN=bioC /DB_XREF=gb:	---	---	-1.38	-0.46	-1.85	0.10858469	0.4674	-5.12
247592_at	high affinity nitrate transporter pro	NRT2.3	AT5G60780	-1.14	-0.19	-1.85	0.10861686	0.4675	-5.12
257786_at	hypothetical protein predicted by g	---	AT3G26990	1.22	0.29	1.85	0.10864478	0.4675	-5.12
246436_at	putative protein cisplatin resistanc	---	AT5G17440	1.13	0.18	1.85	0.10871937	0.4676	-5.12
254078_at	putative protein various predicted	---	AT4G25710	1.18	0.23	1.85	0.10870902	0.4676	-5.12
267599_at	putative serine/threonine protein ki	---	AT2G32850	-1.14	-0.19	-1.85	0.10877401	0.4677	-5.12
247802_at	putative protein RING-H2 zinc fing	ATL63	AT5G58580	-1.18	-0.24	-1.85	0.10877884	0.4677	-5.12
250618_at	putative protein hypothetical protei	ATBAG3	AT5G07220	-1.15	-0.20	-1.85	0.10890199	0.4678	-5.12
248718_at	farnesyl diphosphate synthase pre	FPS1	AT5G47770	1.27	0.34	1.85	0.10895768	0.4678	-5.12
265671_at	40S ribosomal protein S12 ;suppo	---	AT2G32060	1.39	0.47	1.85	0.10897583	0.4678	-5.12
262204_at	unknown protein ; supported by fu	---	AT2G01100	1.15	0.21	1.85	0.10897361	0.4678	-5.12
266201_at	similar to MtN3 protein ;supported	---	AT2G39060	-1.17	-0.23	-1.85	0.1088498	0.4678	-5.12
259046_at	calmodulin-like protein similar to c	---	AT3G03400	-1.16	-0.22	-1.85	0.10890547	0.4678	-5.12
265360_s_at	putative Athila retroelement ORF1	---	---	-1.16	-0.21	-1.85	0.10887117	0.4678	-5.12
AFFX-BioC-3_a	E. coli /GEN=bioC /DB_XREF=gb:	---	---	-1.41	-0.50	-1.85	0.10881733	0.4678	-5.12
264905_at	putative Mlo protein	MLO7	AT2G17430	-1.15	-0.20	-1.85	0.10891898	0.4678	-5.12
256858_at	hypothetical protein predicted by g	---	AT3G15140	-1.24	-0.32	-1.85	0.10914129	0.4681	-5.12
266059_at	predicted protein ;supported by cD	---	AT2G40765	1.34	0.43	1.85	0.10911618	0.4681	-5.12
258144_at	hypothetical protein	---	AT3G18180	-1.13	-0.18	-1.85	0.10919273	0.4681	-5.12
254209_at	Expressed protein ; supported by c	---	AT4G23490	1.27	0.34	1.85	0.109158	0.4681	-5.12

264135_at	S-locus protein, putative similar to	---	AT1G79030	-1.15	-0.20	-1.85	0.10915903	0.4681	-5.12
251179_at	putative protein ABP130 protein, h	---	AT3G63460	1.12	0.17	1.85	0.1091787	0.4681	-5.12
245464_at	hypothetical protein	UGLYAH	AT4G17050	-1.23	-0.30	-1.85	0.10908336	0.4681	-5.12
267181_at	putative alcohol dehydrogenase ;	---	AT2G37760	-1.33	-0.41	-1.85	0.10923009	0.4681	-5.12
251549_at	putative protein predicted proteins	---	AT3G58890	-1.15	-0.20	-1.85	0.10923486	0.4681	-5.12
262153_at	unknown protein	---	AT1G52710	-1.13	-0.17	-1.84	0.10925899	0.4681	-5.12
266822_at	60S ribosomal protein L30 ;suppo	---	AT2G44860	1.24	0.31	1.84	0.1092953	0.4682	-5.12
254693_at	bHLH protein - like bHLH protein,	---	AT4G17880	-1.58	-0.66	-1.84	0.10931233	0.4682	-5.12
264178_at	latex-abundant protein, putative si	AMC1	AT1G02170	1.18	0.23	1.84	0.10940268	0.4685	-5.12
258783_at	unknown protein	---	AT3G11760	1.17	0.23	1.84	0.10946244	0.4686	-5.12
264807_at	putative presenilin similar to prese	---	AT1G08700	1.22	0.28	1.84	0.10952618	0.4688	-5.12
246417_at	quinone oxidoreductase - like prot	---	AT5G16990	-1.24	-0.31	-1.84	0.1095574	0.4689	-5.12
247343_at	unknown protein	---	AT5G63740	-1.15	-0.20	-1.84	0.10959676	0.4689	-5.12
265561_s_at	putative glycine-rich protein	---	AT1G47480	-1.23	-0.30	-1.84	0.1096552	0.4691	-5.12
255233_at	putative protein ADRENODOXIN I	MFDX1	AT4G05450	-1.17	-0.23	-1.84	0.10976129	0.4695	-5.13
256211_at	gibberellin 20-oxidase, putative si	GA2OX7	AT1G50960	-1.13	-0.17	-1.84	0.10982334	0.4695	-5.13
248565_at	putative protein similar to unknown	---	AT5G49710	1.23	0.30	1.84	0.10982102	0.4695	-5.13
256457_at	3-methyladenine DNA glycosylase	---	AT1G75230	-1.34	-0.43	-1.84	0.10983035	0.4695	-5.13
259001_at	hypothetical protein predicted by g	---	AT3G01960	1.50	0.58	1.84	0.10986246	0.4695	-5.13
255685_s_at	putative tetrahydrofolate synthase	---	AT4G00600	1.27	0.34	1.84	0.10997997	0.4697	-5.13
260805_at	glutathione transferase, putative s	ATGSTU23	AT1G78320	-1.13	-0.18	-1.84	0.10999079	0.4697	-5.13
260191_at	putative protein kinase Pfam HMM	---	AT1G67580	1.14	0.18	1.84	0.10997865	0.4697	-5.13
254972_at	putative protein more than 10 puta	---	AT4G10440	-1.17	-0.23	-1.84	0.10996484	0.4697	-5.13
252180_at	putative protein cyclin-dependent	KRP2	AT3G50630	-1.26	-0.33	-1.84	0.11005481	0.4698	-5.13
246437_at	putative protein hypersensitivity-re	---	AT5G17540	-1.14	-0.19	-1.84	0.1100462	0.4698	-5.13
245416_at	putative protein	---	AT4G17350	-1.19	-0.25	-1.84	0.11003184	0.4698	-5.13
259034_at	putative pectinacetylesterase simil	---	AT3G09410	1.26	0.34	1.84	0.11008642	0.4698	-5.13
260921_at	amp-binding protein, putative simi	---	AT1G21540	-1.26	-0.33	-1.84	0.11010416	0.4698	-5.13
245145_at	putative dihydrodipicolinate syntha	DHDPS2	AT2G45440	1.29	0.36	1.84	0.11013109	0.4698	-5.13
259564_at	hypothetical protein	---	AT1G20540	1.13	0.18	1.84	0.11014608	0.4698	-5.13
259146_at	putative glycerol-3-phosphate dehy	SDP6	AT3G10370	-1.21	-0.28	-1.84	0.110175	0.4698	-5.13
256450_at	NADPH oxidoreductase, putative	---	AT1G75290	-1.14	-0.19	-1.84	0.1101996	0.4698	-5.13
251392_at	dihydrodipicolinate synthase precu	DHDPS1	AT3G60880	1.15	0.20	1.84	0.11024415	0.4699	-5.13
261615_at	unknown protein	---	AT1G33050	1.17	0.23	1.84	0.11031738	0.4702	-5.13
263805_at	unknown protein ; supported by cl	---	AT2G40400	-1.13	-0.17	-1.84	0.11035312	0.4702	-5.13

267080_at	unknown protein ; supported by cl	---	AT2G41190	1.46	0.55	1.84	0.1104053	0.4704	-5.13
245842_at	proline-rich protein, putative simila	RXF26	AT1G58430	-1.13	-0.18	-1.84	0.11044735	0.4704	-5.13
253214_at	putative protein karyopherin alpha	ARO1	AT4G34940	1.14	0.19	1.84	0.11044809	0.4704	-5.13
247444_at	putative protein strong similarity to	HIPL2	AT5G62630	1.45	0.53	1.84	0.11052206	0.4706	-5.13
261250_at	unknown protein	---	AT1G05890	1.15	0.20	1.84	0.11054287	0.4706	-5.13
252991_at	protein kinase like protein protein	---	AT4G38470	-1.62	-0.69	-1.84	0.11061808	0.4708	-5.13
245492_at	putative protein	SPK1	AT4G16340	1.16	0.22	1.84	0.11064538	0.4709	-5.13
256145_at	lipid transfer protein, putative simi	---	AT1G48750	-1.43	-0.52	-1.84	0.11067842	0.4709	-5.13
247992_at	unknown protein	---	AT5G56520	1.15	0.21	1.84	0.11070383	0.4709	-5.13
256967_at	hypothetical protein predicted by g	---	AT3G21060	-1.18	-0.23	-1.84	0.11080091	0.4713	-5.13
260685_at	Expressed protein ; supported by f	GLYR2	AT1G17650	1.24	0.31	1.83	0.11088062	0.4713	-5.13
248635_at	unknown protein	---	AT5G49050	-1.15	-0.20	-1.83	0.11086844	0.4713	-5.13
264626_at	unknown protein	AS2	AT1G65620	-1.26	-0.33	-1.83	0.11088797	0.4713	-5.13
245263_at	PSII D1 protein processing enzym	---	AT4G17740	1.14	0.19	1.83	0.11087466	0.4713	-5.13
249860_at	prolylcarboxypeptidase-like protein	---	AT5G22860	-2.32	-1.21	-1.83	0.11100238	0.4715	-5.14
247483_at	aldose reductase-like protein	---	AT5G62420	-1.20	-0.27	-1.83	0.11098881	0.4715	-5.14
262757_at	putative Na/H antiporter similar to	ATCHX1	AT1G16380	-1.16	-0.22	-1.83	0.11097209	0.4715	-5.14
249497_at	putative protein predicted proteins	---	AT5G39220	-1.19	-0.25	-1.83	0.11102865	0.4715	-5.14
255268_at	putative protein ubiquitin, Tetrahy	---	AT4G05230	-1.18	-0.23	-1.83	0.11109801	0.4716	-5.14
262356_at	hypothetical protein predicted by g	---	AT1G73000	-1.14	-0.19	-1.83	0.11114659	0.4716	-5.14
250209_at	putative protein similar to unknown	---	AT5G14030	1.21	0.27	1.83	0.11107827	0.4716	-5.14
254036_at	putative peroxidase peroxidase (E	---	AT4G25980	-1.15	-0.20	-1.83	0.11111252	0.4716	-5.14
266698_at	copia-like retroelement pol polypro	SNF7.2	AT2G19830	1.17	0.22	1.83	0.11113441	0.4716	-5.14
251105_at	putative protein unknown protein	ATSCAR4	AT5G01730	-1.39	-0.47	-1.83	0.11135343	0.4716	-5.14
251087_at	putative protein unknown protein	---	AT5G01460	1.14	0.19	1.83	0.11137933	0.4716	-5.14
254951_at	putative protein various kinesin ligh	---	AT4G10840	1.14	0.19	1.83	0.11120506	0.4716	-5.14
264356_at	putative DNA repair protein Strong	UVH6	AT1G03190	1.15	0.20	1.83	0.1111949	0.4716	-5.14
250921_at	Expressed protein ; supported by f	---	AT5G03460	1.21	0.28	1.83	0.11135575	0.4716	-5.14
245963_at	putative protein HPt phosphotrans	---	AT5G19710	-1.13	-0.17	-1.83	0.11135145	0.4716	-5.14
265971_at	putative retroelement pol polyprote	---	---	-1.14	-0.19	-1.83	0.11133559	0.4716	-5.14
251346_at	putative protein hypothetical prote	---	AT3G60980	1.15	0.21	1.83	0.11127846	0.4716	-5.14
266959_at	putative DNA replication licensing	MCM5	AT2G07690	1.58	0.66	1.83	0.1113238	0.4716	-5.14
262851_at	putative RNA helicase Contains DI	---	AT1G20920	-1.18	-0.24	-1.83	0.11126393	0.4716	-5.14
256460_at	60S ribosomal protein L30, putativ	---	AT1G36240	1.17	0.23	1.83	0.1113732	0.4716	-5.14
256284_at	unknown protein	PSF2	AT3G12530	1.25	0.33	1.83	0.11147259	0.4719	-5.14

250664_at	putative protein 10-deacetylbacca	---	AT5G07080	1.39	0.48	1.83	0.11166626	0.4721	-5.14
261825_at	endo-xyloglucan transferase, puta	---	AT1G11545	2.33	1.22	1.83	0.11162527	0.4721	-5.14
260193_at	putative amino acid permease sim	---	AT1G67640	-1.22	-0.28	-1.83	0.11165104	0.4721	-5.14
249162_at	Expressed protein ; supported by f	---	AT5G42765	1.22	0.29	1.83	0.11163065	0.4721	-5.14
251311_at	FUSCA PROTEIN FUS6 ; support	FUS6	AT3G61140	-1.15	-0.20	-1.83	0.11159444	0.4721	-5.14
251397_at	putative protein cim1 protein, Glyc	ATEXPB5	AT3G60570	-1.21	-0.28	-1.83	0.11155802	0.4721	-5.14
263427_at	hypothetical protein predicted by g	---	AT2G22260	-1.14	-0.18	-1.83	0.11159726	0.4721	-5.14
247126_at	protein phosphatase 2C-like protei	---	AT5G66080	-1.25	-0.32	-1.83	0.11169355	0.4722	-5.14
252107_at	sugar transporter-like protein suga	TMT3	AT3G51490	-1.22	-0.29	-1.83	0.11177389	0.4722	-5.14
259384_at	putative lectin contains Pfam profi	---	AT3G16450	-1.20	-0.26	-1.83	0.11176202	0.4722	-5.14
245119_at	unknown protein ; supported by cl	---	AT2G41640	1.96	0.97	1.83	0.11176195	0.4722	-5.14
254653_at	polygalacturonase-like protein exc	---	AT4G18180	1.12	0.16	1.83	0.11177888	0.4722	-5.14
266913_at	hypothetical protein predicted by g	ROPGEF4	AT2G45890	-1.13	-0.17	-1.83	0.11187229	0.4723	-5.14
254605_at	protein kinase - like protein protei	---	AT4G18950	-1.43	-0.51	-1.83	0.1118969	0.4723	-5.14
252394_at	heat shock protein-like protein hea	---	AT3G47940	1.22	0.29	1.83	0.11194631	0.4723	-5.14
252471_at	phosphoprotein phosphatase ;sup	TOPP5	AT3G46820	-1.17	-0.23	-1.83	0.11191881	0.4723	-5.14
265153_at	unusual floral organ (UFO), AtFBX	UFO	AT1G30950	-1.17	-0.23	-1.83	0.1118915	0.4723	-5.14
255613_at	putative RING zinc finger protein	---	AT4G01270	1.18	0.24	1.83	0.11194966	0.4723	-5.14
254312_s_at	hypothetical protein	---	---	1.18	0.24	1.83	0.11191625	0.4723	-5.14
258425_at	unknown protein	---	AT3G16760	-1.12	-0.17	-1.83	0.1120412	0.4726	-5.14
262357_at	jacalin, putative similar to jacalin C	---	AT1G73040	-1.58	-0.66	-1.83	0.11242528	0.4728	-5.15
260500_at	Expressed protein ; supported by c	---	AT2G41705	1.13	0.18	1.83	0.11238075	0.4728	-5.15
259393_at	trehalose-6-phosphate synthase,	ATTPS7	AT1G06410	-1.17	-0.22	-1.83	0.11217602	0.4728	-5.15
250384_at	putative protein various predicted	---	AT5G11500	-1.15	-0.20	-1.83	0.11227462	0.4728	-5.15
249906_at	unknown protein	---	AT5G22730	1.13	0.18	1.83	0.11237933	0.4728	-5.15
252450_s_at	receptor kinase-like protein recept	---	AT3G47090	1.34	0.43	1.83	0.11241029	0.4728	-5.15
259706_at	unknown protein similar to GB:AAD	---	AT1G77540	1.18	0.24	1.83	0.1124529	0.4728	-5.15
248207_at	tyrosine aminotransferase	---	AT5G53970	1.54	0.62	1.82	0.11246089	0.4728	-5.15
261958_at	peptide transporter, putative predi	---	AT1G64500	-1.35	-0.43	-1.83	0.1122405	0.4728	-5.15
267270_at	hypothetical protein predicted by g	---	AT2G02550	-1.21	-0.27	-1.83	0.11227554	0.4728	-5.15
259883_at	putative ribophorin I (dolichyl-diph	---	AT1G76400	1.20	0.26	1.83	0.11243293	0.4728	-5.15
253966_at	fructose-bisphosphate aldolase	---	AT4G26520	-1.21	-0.28	-1.83	0.11221912	0.4728	-5.15
246330_at	aldehyde oxidase ; supported by c	AAO2	AT3G43600	1.42	0.51	1.83	0.11235657	0.4728	-5.15
267222_at	putative polygalacturonase	---	AT2G43880	-1.14	-0.19	-1.83	0.11214777	0.4728	-5.15
245830_at	hypothetical protein predicted by g	---	AT1G57790	1.14	0.19	1.83	0.11241945	0.4728	-5.15

251433_at	putative protein SERINE/THREON	---	AT3G59830	-1.12	-0.17	-1.83	0.11225837	0.4728	-5.15
247252_at	unknown protein	---	AT5G64770	-1.78	-0.83	-1.83	0.1122696	0.4728	-5.15
250375_at	putative protein L-gulono-gamma-	---	AT5G11540	1.16	0.21	1.83	0.11232025	0.4728	-5.15
257977_at	hypothetical protein predicted by g	---	AT3G20850	-1.15	-0.20	-1.82	0.11250351	0.4728	-5.15
253104_at	thaumatin-like protein thaumatin-li	---	AT4G36010	-1.66	-0.73	-1.82	0.11249304	0.4728	-5.15
252182_at	U1 snRNP 70K protein ; supporte	U1-70K	AT3G50670	1.15	0.20	1.82	0.11253116	0.4728	-5.15
249248_at	unknown protein	---	AT5G42320	-1.18	-0.24	-1.82	0.112557	0.4728	-5.15
252480_at	putative protein methyl-CpG-bindi	MBD5	AT3G46580	1.12	0.17	1.82	0.11257528	0.4728	-5.15
259077_s_at	reversibly glycosylated polypeptide	RGP1	AT3G02230	-1.33	-0.41	-1.82	0.11276369	0.4735	-5.15
263174_at	jasmonate inducible protein, putat	ESP	AT1G54040	-1.48	-0.57	-1.82	0.1127991	0.4735	-5.15
253654_at	putative protein several hypothetic	---	AT4G30060	-1.37	-0.46	-1.82	0.11278498	0.4735	-5.15
259067_at	F-box protein family, AtFBL12 cor	---	AT3G07550	-1.14	-0.18	-1.82	0.11287592	0.4736	-5.15
258779_at	putative protein kinase contains Pf	---	AT3G11870	-1.13	-0.17	-1.82	0.11286974	0.4736	-5.15
259966_at	unknown protein	SOB3	AT1G76500	-1.17	-0.23	-1.82	0.1129342	0.4737	-5.15
266996_at	putative cytochrome P450 ;suppo	CYP710A2	AT2G34490	-2.31	-1.21	-1.82	0.11294037	0.4737	-5.15
248287_at	putative protein similar to unknown	---	AT5G52970	1.24	0.31	1.82	0.11319883	0.4744	-5.15
251475_at	putative protein other hypothetical	---	AT3G59660	-1.28	-0.35	-1.82	0.11314091	0.4744	-5.15
246292_at	putative protein hnRNP A/B relate	UBA2A	AT3G56860	-1.19	-0.25	-1.82	0.11319195	0.4744	-5.15
253877_at	Expressed protein ; supported by c	---	AT4G27435	-1.36	-0.44	-1.82	0.11316267	0.4744	-5.15
264714_at	receptor-like protein kinase, putati	---	AT1G69990	-1.17	-0.23	-1.82	0.11318656	0.4744	-5.15
265188_at	putative aldehyde dehydrogenase	ALDH2B7	AT1G23800	-1.21	-0.28	-1.82	0.11324961	0.4745	-5.15
258596_at	unknown protein	LSH2	AT3G04510	-1.18	-0.24	-1.82	0.11331432	0.4745	-5.16
250661_at	nucleoid DNA-binding-like protein	---	AT5G07030	-2.41	-1.27	-1.82	0.11332156	0.4745	-5.16
263546_at	putative dihydrofolate reductase-th	---	AT2G21550	1.19	0.26	1.82	0.11328577	0.4745	-5.16
254641_at	ras-like GTP-binding protein stron	ATRABA1D	AT4G18800	1.26	0.33	1.82	0.11339356	0.4748	-5.16
267084_at	unknown protein ; supported by cl	---	AT2G41180	1.74	0.80	1.82	0.11349787	0.4750	-5.16
259682_at	transcription factor DREB1A, puta	---	AT1G63040	-1.23	-0.30	-1.82	0.11347801	0.4750	-5.16
264190_at	heme activated protein, putative s	NF-YC3	AT1G54830	-1.12	-0.17	-1.82	0.11353804	0.4751	-5.16
246071_at	ids4-like protein ids-4 protein - Ho	SPX1	AT5G20150	1.48	0.56	1.82	0.11384485	0.4752	-5.16
248409_at	putative protein contains similarity	LPA2	AT5G51540	1.19	0.26	1.82	0.11382304	0.4752	-5.16
254817_at	putative SWH1 protein SWH1 pro	ORP2B	AT4G12460	1.17	0.22	1.82	0.11368488	0.4752	-5.16
257647_at	Expressed protein ; supported by c	---	AT3G25805	1.30	0.38	1.82	0.11366332	0.4752	-5.16
260610_at	putative SF16 protein {Helianthus a	IQD14	AT2G43680	1.27	0.34	1.82	0.11381523	0.4752	-5.16
254669_at	HhoA protease precursor, putative	DEG5	AT4G18370	1.22	0.29	1.82	0.11366588	0.4752	-5.16
262819_at	putative cytochrome P450 strong s	CYP77B1	AT1G11600	-1.14	-0.19	-1.82	0.11386109	0.4752	-5.16

261065_at	hypothetical protein predicted by g	---	AT1G07500	-1.21	-0.28	-1.82	0.1137549	0.4752	-5.16
255908_s_at	unknown protein ;supported by full	---	AT1G18000	-1.16	-0.22	-1.82	0.11382894	0.4752	-5.16
250371_at	putative protein 23 kDa polypeptic	---	AT5G11450	1.19	0.25	1.82	0.11366936	0.4752	-5.16
255139_s_at	extensin-like protein hydroxyprolir	---	AT4G08400	-1.12	-0.17	-1.82	0.11384122	0.4752	-5.16
251600_at	protein kinase - like protein wall-a	---	AT3G57710	-1.12	-0.16	-1.82	0.11364408	0.4752	-5.16
262571_at	hypothetical protein predicted by g	---	AT1G15430	1.41	0.49	1.82	0.11382655	0.4752	-5.16
259525_at	hypothetical protein	ATEXPA7	AT1G12560	1.14	0.19	1.82	0.11374434	0.4752	-5.16
246958_at	putative protein similar to unknown	---	AT5G24690	1.22	0.29	1.82	0.11388631	0.4753	-5.16
253640_at	putative protein ;supported by full-	---	AT4G30630	-1.13	-0.18	-1.82	0.11405074	0.4757	-5.16
245218_s_at	viral resistance protein, putative, 5	---	AT1G58848	-1.13	-0.17	-1.82	0.11402846	0.4757	-5.16
247604_at	putative phytochelatin synthetase	COBL5	AT5G60950	2.01	1.00	1.82	0.11403005	0.4757	-5.16
249917_at	putative protein strong similarity to	---	AT5G22460	2.05	1.03	1.81	0.11414989	0.4760	-5.16
260094_at	GDP-4-keto-6-deoxy-D-mannose-	GER1	AT1G73250	1.20	0.27	1.81	0.11422273	0.4761	-5.16
257518_at	hypothetical protein	---	AT3G03880	1.13	0.17	1.81	0.11427311	0.4761	-5.16
263372_at	60S ribosomal protein L14 ;suppo	---	AT2G20450	1.38	0.46	1.81	0.11424042	0.4761	-5.16
253089_at	putative protein hypothetical prote	---	AT4G36290	1.13	0.18	1.81	0.1142646	0.4761	-5.16
264609_at	unknown protein ;supported by ful	---	AT1G04530	1.31	0.39	1.81	0.11425247	0.4761	-5.16
249574_at	putative protein embryonic abunda	PDLP7	AT5G37660	1.16	0.22	1.81	0.11429571	0.4761	-5.16
266484_at	putative putative sister-chromatide	SCC3	AT2G47980	1.16	0.22	1.81	0.1143434	0.4762	-5.16
265601_at	hypothetical protein predicted by g	---	AT2G14390	-1.16	-0.22	-1.81	0.11437007	0.4762	-5.16
267473_at	hypothetical protein predicted by g	---	AT2G02750	-1.16	-0.21	-1.81	0.11443399	0.4764	-5.16
267279_at	hypothetical protein predicted by g	---	AT2G19460	1.37	0.46	1.81	0.11450322	0.4766	-5.17
255398_at	hypothetical protein	---	AT4G03740	-1.15	-0.21	-1.81	0.11453178	0.4766	-5.17
265753_at	putative Athila retroelement ORF1	---	---	-1.11	-0.16	-1.81	0.11465015	0.4770	-5.17
246908_at	dehydration-induced protein RD22	RD22	AT5G25610	1.90	0.92	1.81	0.11473676	0.4772	-5.17
253661_at	putative protein bZIP protein - Ara	---	AT4G30130	-1.16	-0.22	-1.81	0.114726	0.4772	-5.17
264406_at	putative phragmoplastin similar to	ADL6	AT1G10290	1.17	0.23	1.81	0.11475921	0.4772	-5.17
260038_at	Expressed protein ; supported by f	---	AT1G68875	1.13	0.18	1.81	0.11479749	0.4773	-5.17
263437_at	putative disease resistance respor	---	AT2G28670	-1.18	-0.24	-1.81	0.1148596	0.4775	-5.17
253374_at	hypothetical protein ; supported by	---	AT4G33140	-1.14	-0.18	-1.81	0.11490198	0.4775	-5.17
258880_at	hypothetical protein similar to sym	ATG8H	AT3G06420	1.39	0.48	1.81	0.11489225	0.4775	-5.17
255505_at	SAR1/GTP-binding secretory facto	ATSAR2	AT4G02080	1.15	0.21	1.81	0.11497037	0.4777	-5.17
251670_at	putative protein translation releasi	---	AT3G57190	-1.20	-0.26	-1.81	0.11500942	0.4777	-5.17
267598_at	hypothetical protein predicted by g	---	AT2G33010	-1.19	-0.25	-1.81	0.1150132	0.4777	-5.17
247325_at	putative protein contains similarity	SC35	AT5G64200	1.14	0.19	1.81	0.11514415	0.4777	-5.17

257050_at	putative protein phosphatase type	---	AT3G15260	1.21	0.27	1.81	0.11512467	0.4777	-5.17
259992_at	putative heat shock transcription f	HSFA8	AT1G67970	1.28	0.35	1.81	0.1151211	0.4777	-5.17
249631_at	sen1-like protein SEN1 - Sacchar	---	AT5G37160	-1.15	-0.21	-1.81	0.11508894	0.4777	-5.17
257363_at	hypothetical protein predicted by g	BAP2	AT2G45760	-1.22	-0.28	-1.81	0.11512496	0.4777	-5.17
266594_at	hypothetical protein	---	AT2G46190	1.12	0.16	1.81	0.11507438	0.4777	-5.17
245399_at	membrane channel like protein ;su	TIP2;2	AT4G17340	1.32	0.40	1.81	0.11525185	0.4780	-5.17
266057_at	putative methionyl-tRNA synthetas	---	AT2G40660	1.14	0.18	1.81	0.1152648	0.4780	-5.17
250543_at	DR1-like protein TATA-binding pr	NF-YB12	AT5G08190	1.16	0.21	1.81	0.11531254	0.4781	-5.17
258847_at	unknown protein ; supported by fu	---	AT3G03100	1.13	0.18	1.81	0.11558783	0.4785	-5.17
255830_at	putative PRP19-like spliceosomal	---	AT2G33340	1.32	0.40	1.81	0.11563531	0.4785	-5.17
265309_at	putative myosin heavy chain	XIG	AT2G20290	-1.24	-0.31	-1.81	0.11550598	0.4785	-5.17
258837_at	putative 60S ribosomal protein L13	---	AT3G07110	1.41	0.50	1.81	0.11562514	0.4785	-5.17
256815_at	unknown protein contains Pfam pr	---	AT3G21380	-1.15	-0.20	-1.81	0.11548257	0.4785	-5.17
267472_at	putative basic blue protein (plantac	ARPN	AT2G02850	-1.17	-0.23	-1.81	0.11558935	0.4785	-5.17
251586_at	zinc finger-like protein several zinc	GIS	AT3G58070	-1.21	-0.28	-1.81	0.11550324	0.4785	-5.17
246590_at	cyclic nucleotide and calmodulin-r	CNGC18	AT5G14870	1.13	0.17	1.81	0.11561569	0.4785	-5.17
265848_at	putative sugar transporter	INT3	AT2G35740	-1.25	-0.32	-1.81	0.11556806	0.4785	-5.17
264391_at	pectate lyase-like protein Similar t	---	AT1G11920	-1.16	-0.21	-1.81	0.11560662	0.4785	-5.17
259894_at	hypothetical protein predicted by g	---	AT1G71430	1.18	0.24	1.81	0.11557132	0.4785	-5.17
266347_at	putative ATP-dependent DNA helic	---	AT2G01440	1.21	0.27	1.81	0.11566318	0.4786	-5.17
265714_at	putative integral membrane protein	ATUPS4	AT2G03520	-1.13	-0.18	-1.81	0.11570994	0.4787	-5.18
257608_at	chaperonin, putative similar to CH	HSP60-3A	AT3G13860	1.16	0.21	1.80	0.1157623	0.4787	-5.18
266073_at	putative signal recognition particle	---	AT2G18770	1.15	0.20	1.80	0.11576942	0.4787	-5.18
262074_at	glutathione S-transferase, putative	ATGSTU15	AT1G59670	1.29	0.37	1.80	0.11583462	0.4787	-5.18
264146_at	hypothetical protein contains simila	CER1	AT1G02205	3.87	1.95	1.80	0.11579433	0.4787	-5.18
251870_at	putative protein Various predicted	---	AT3G54510	-1.14	-0.19	-1.80	0.11582557	0.4787	-5.18
249204_at	unknown protein ;supported by ful	---	AT5G42570	-1.15	-0.20	-1.80	0.11588075	0.4788	-5.18
246619_at	transmembrane protein FT27/PFT	---	AT5G36290	1.13	0.17	1.80	0.11591012	0.4789	-5.18
247509_at	heat shock factor 6	HSFB2A	AT5G62020	1.19	0.25	1.80	0.11595848	0.4790	-5.18
258240_at	oleosin isoform identical to oleosin	OLEO4	AT3G27660	-1.17	-0.22	-1.80	0.11601412	0.4791	-5.18
247722_at	GTP-binding protein rab11 - like G	ATRABA2D	AT5G59150	1.16	0.21	1.80	0.11604018	0.4792	-5.18
258367_at	putative protein kinase similar to p	WAG2	AT3G14370	-1.16	-0.22	-1.80	0.11610477	0.4793	-5.18
259141_at	putative cytoskeleton-associated p	---	AT3G10220	1.16	0.21	1.80	0.11613233	0.4794	-5.18
263504_s_at	hypothetical protein	---	AT2G07677	-1.14	-0.19	-1.80	0.11624665	0.4796	-5.18
265803_at	hypothetical protein predicted by g	---	AT2G18115	-1.20	-0.26	-1.80	0.11627817	0.4796	-5.18

251448_at	allyl alcohol dehydrogenase-like p	---	AT3G59845	-1.14	-0.19	-1.80	0.1162487	0.4796	-5.18
255309_at	hypothetical protein	SFR6	AT4G04920	-1.13	-0.18	-1.80	0.11621797	0.4796	-5.18
258591_at	hypothetical protein ; supported by	---	AT3G04360	-1.14	-0.19	-1.80	0.11628692	0.4796	-5.18
251750_at	glucuronosyl transferase - like pro	---	AT3G55710	1.22	0.29	1.80	0.11635293	0.4798	-5.18
247759_at	copper transport protein - like ;sup	COPT3	AT5G59040	-1.13	-0.18	-1.80	0.11638299	0.4798	-5.18
258061_at	unknown protein ; supported by c	---	AT3G25910	1.16	0.21	1.80	0.11640505	0.4798	-5.18
263305_at	unknown protein ;supported by ful	BPC1	AT2G01930	1.23	0.30	1.80	0.11642129	0.4798	-5.18
254793_at	hypothetical protein	---	AT4G12930	-1.16	-0.21	-1.80	0.11643757	0.4798	-5.18
250490_at	pectin methylesterase - like protei	---	AT5G09760	1.38	0.46	1.80	0.11650471	0.4799	-5.18
254581_at	putative protein membrane-associ	---	AT4G19440	-1.22	-0.29	-1.80	0.11650033	0.4799	-5.18
261445_at	unknown protein ; supported by c	NSL1	AT1G28380	-1.41	-0.49	-1.80	0.11653118	0.4799	-5.18
249670_at	unknown protein	---	AT5G35890	1.15	0.20	1.80	0.11657224	0.4800	-5.18
254527_at	putative protein KIAA0682 protein	---	AT4G19610	-1.12	-0.16	-1.80	0.11661917	0.4800	-5.18
256914_at	hypothetical protein	---	AT3G23880	1.26	0.33	1.80	0.11662909	0.4800	-5.18
256912_at	hypothetical protein predicted by g	---	AT3G23850	-1.15	-0.21	-1.80	0.1167402	0.4801	-5.18
245531_at	hydroxynitrile lyase like protein	scpl30	AT4G15100	-1.23	-0.30	-1.80	0.11669284	0.4801	-5.18
265348_at	putative RNA-binding protein	---	AT2G22600	-1.16	-0.22	-1.80	0.11674751	0.4801	-5.18
261074_at	hypothetical protein predicted by g	---	AT1G07290	-1.15	-0.20	-1.80	0.11667	0.4801	-5.18
263625_at	F-box protein family, AtFBX9 cont	---	AT2G04920	-1.14	-0.19	-1.80	0.11674431	0.4801	-5.18
247276_at	putative protein contains similarity	HEN4	AT5G64390	-1.27	-0.34	-1.80	0.1167982	0.4802	-5.18
251537_at	putative protein several hypothetic	---	AT3G58470	1.30	0.37	1.80	0.1169036	0.4805	-5.18
260414_at	nitrate transporter (NTL1) identical	ATNRT1:2	AT1G69850	1.18	0.24	1.80	0.11691923	0.4805	-5.19
267624_at	putative protein kinase	BIK1	AT2G39660	1.38	0.46	1.80	0.11696608	0.4806	-5.19
246776_at	kinesin-like protein kinesin-like he	---	AT5G27550	-1.23	-0.30	-1.80	0.11698729	0.4806	-5.19
266626_at	hypothetical protein predicted by g	---	AT2G35360	1.22	0.29	1.80	0.11702014	0.4807	-5.19
267199_at	hypothetical protein predicted by g	---	AT2G30990	-1.59	-0.67	-1.80	0.11711546	0.4808	-5.19
245400_at	ATP-dependent Clp protease prot	---	AT4G17040	1.19	0.26	1.80	0.11707009	0.4808	-5.19
265529_at	hypothetical protein predicted by g	---	---	-1.13	-0.18	-1.80	0.11710728	0.4808	-5.19
245703_at	S-adenosyl-L-methionine:salicylic	---	AT5G04380	-1.14	-0.19	-1.80	0.11712907	0.4808	-5.19
265603_at	hypothetical protein predicted by g	---	---	1.17	0.22	1.80	0.11718385	0.4809	-5.19
247292_at	unknown protein	---	AT5G64490	1.17	0.23	1.80	0.1174016	0.4817	-5.19
267108_at	hypothetical protein predicted by g	---	AT2G14830	-1.13	-0.18	-1.80	0.11742383	0.4817	-5.19
262118_at	beta-glucosidase, putative similar	BGLU11	AT1G02850	1.59	0.67	1.79	0.11746442	0.4817	-5.19
265160_at	unknown protein similar to EST gb	---	AT1G31050	-1.19	-0.25	-1.79	0.11758927	0.4817	-5.19
265579_at	hypothetical protein predicted by g	---	AT2G20070	-1.15	-0.20	-1.79	0.11749322	0.4817	-5.19

261552_at	receptor protein kinase, putative c	---	AT1G63430	1.17	0.23	1.79	0.11752746	0.4817	-5.19
256477_at	unknown protein	---	---	-1.15	-0.21	-1.79	0.11762084	0.4817	-5.19
AFFX-DapX-3_	B. subtilis /GEN=jojG /DB_XREF=(	---	---	-1.19	-0.25	-1.79	0.11763363	0.4817	-5.19
258228_at	unknown protein similar to unknow	---	AT3G27610	1.13	0.18	1.79	0.11763667	0.4817	-5.19
247390_at	putative protein similar to unknown	---	AT5G63520	1.13	0.18	1.79	0.11760633	0.4817	-5.19
258411_at	hypothetical protein predicted by g	---	AT3G17280	-1.14	-0.20	-1.79	0.11747464	0.4817	-5.19
247829_at	protein kinase - like protein kinase	---	AT5G58520	-1.22	-0.29	-1.79	0.11755641	0.4817	-5.19
251993_at	peroxiredoxin - like protein peroxir	---	AT3G52960	1.18	0.24	1.79	0.11766458	0.4818	-5.19
254965_at	putative protein other hypothetical	---	AT4G11090	-1.13	-0.18	-1.79	0.11774214	0.4819	-5.19
256668_at	hypothetical protein similar to hypo	---	AT3G32190	-1.17	-0.23	-1.79	0.11776463	0.4819	-5.19
246678_at	putative protein predicted replicatio	---	---	1.17	0.23	1.79	0.11772561	0.4819	-5.19
250909_at	S-receptor kinase - like protein S-	---	AT5G03700	1.67	0.74	1.79	0.11777367	0.4819	-5.19
267370_at	unknown protein ;supported by ful	---	AT2G44525	1.12	0.16	1.79	0.11787594	0.4822	-5.19
263206_at	unknown protein similar to ESTs g	---	AT1G10590	1.12	0.16	1.79	0.11802669	0.4827	-5.19
256132_at	hypothetical protein similar to hypo	---	AT1G13610	-1.15	-0.20	-1.79	0.11812923	0.4829	-5.19
259097_at	unknown protein similar to GB:AAI	---	AT3G04830	1.14	0.18	1.79	0.1181421	0.4829	-5.19
253230_at	putative protein ; supported by full	---	AT4G34700	1.16	0.21	1.79	0.11813467	0.4829	-5.19
247025_at	zeaxanthin epoxidase precursor ;	ABA1	AT5G67030	-1.20	-0.26	-1.79	0.11820673	0.4831	-5.20
251554_at	putative protein predicted protein,	---	AT3G58670	1.17	0.23	1.79	0.11823272	0.4831	-5.20
259014_at	putative glucan endo-1-3-beta-gluc	---	AT3G07320	-1.25	-0.33	-1.79	0.11842666	0.4832	-5.20
245692_at	myc - like protein	BHLH101	AT5G04150	-1.22	-0.29	-1.79	0.11879634	0.4832	-5.20
245398_at	hydroxyproline-rich glycoprotein hc	---	AT4G14900	1.27	0.34	1.79	0.11836013	0.4832	-5.20
262744_at	anthranilate N-hydroxycinnamoyl/I	---	AT1G28680	1.29	0.37	1.79	0.11871122	0.4832	-5.20
260062_at	hypothetical protein contains Pfam	---	AT1G73710	-1.19	-0.25	-1.79	0.11864874	0.4832	-5.20
245052_at	putative pectinesterase	---	AT2G26440	-1.20	-0.26	-1.79	0.11833214	0.4832	-5.20
260823_at	hypothetical protein predicted by g	DRIP1	AT1G06770	1.15	0.20	1.79	0.11852345	0.4832	-5.20
249320_at	disease resistance protein-like nor	---	AT5G40910	1.24	0.31	1.79	0.11849204	0.4832	-5.20
251504_at	putative protein putative multidrug	TT12	AT3G59030	-1.17	-0.23	-1.79	0.118391	0.4832	-5.20
251847_at	tryptophan synthase alpha chain ;	TSA1	AT3G54640	-1.87	-0.90	-1.79	0.11862514	0.4832	-5.20
254176_at	hypothetical protein hypothetical p	---	AT4G24200	-1.15	-0.20	-1.79	0.11841594	0.4832	-5.20
250552_at	putative protein microtubule bindir	---	AT5G07890	-1.14	-0.19	-1.79	0.11845867	0.4832	-5.20
257262_at	zinc finger protein, putative contai	---	AT3G21890	-1.31	-0.39	-1.79	0.11855325	0.4832	-5.20
264184_at	early nodule-specific protein, puta	---	AT1G54790	1.16	0.21	1.79	0.11867048	0.4832	-5.20
266954_at	hypothetical protein predicted by g	---	AT2G34530	-1.14	-0.18	-1.79	0.11853505	0.4832	-5.20
246468_at	UDP glucose:flavonoid 3-o-glucos	UGT78D2	AT5G17050	-1.29	-0.37	-1.79	0.11873316	0.4832	-5.20

264427_at	hypothetical protein predicted by g	---	AT1G61770	1.17	0.23	1.79	0.11876052	0.4832	-5.20
246239_at	putative protein	---	AT4G36790	1.15	0.20	1.79	0.1187652	0.4832	-5.20
257036_at	hypothetical protein predicted by g	---	AT3G19120	1.14	0.19	1.79	0.11847813	0.4832	-5.20
262858_at	major latex protein type3 identical	---	AT1G14940	-1.15	-0.20	-1.79	0.11857613	0.4832	-5.20
251541_at	citrate synthase -like protein citrat	CSY2	AT3G58750	1.22	0.28	1.79	0.11872387	0.4832	-5.20
247387_at	unknown protein	---	AT5G63460	-1.14	-0.19	-1.79	0.11846337	0.4832	-5.20
251106_at	putative protein peroxisomal Ca-d	---	AT5G01500	-1.65	-0.72	-1.79	0.11873531	0.4832	-5.20
264331_at	hypothetical protein contains non-c	---	AT1G04130	-1.16	-0.21	-1.79	0.11867161	0.4832	-5.20
256362_at	hypothetical protein	---	AT1G66450	-1.16	-0.21	-1.79	0.11832822	0.4832	-5.20
263163_at	fructokinase, putative predicted by	FZL	AT1G03160	-1.37	-0.45	-1.79	0.11879772	0.4832	-5.20
262166_at	myb-related transcription activator	---	AT1G74840	1.20	0.27	1.79	0.11889204	0.4835	-5.20
261462_at	hypothetical protein predicted by g	---	AT1G07850	-1.18	-0.23	-1.79	0.118955	0.4837	-5.20
246887_at	hexose transporter - like protein h	---	AT5G26250	-1.15	-0.21	-1.79	0.119001	0.4837	-5.20
248912_at	GDSL-motif lipase/hydrolase-like p	---	AT5G45670	-1.20	-0.26	-1.79	0.1190089	0.4837	-5.20
260922_at	hypothetical protein predicted by g	---	AT1G21560	-1.15	-0.20	-1.79	0.11909246	0.4839	-5.20
262023_at	hypothetical protein predicted by g	---	AT1G35500	-1.16	-0.21	-1.79	0.11907239	0.4839	-5.20
263920_at	unknown protein ;supported by ful	---	AT2G36410	1.20	0.26	1.78	0.11915423	0.4840	-5.20
251184_at	small nuclear ribonucleoprotein-lik	---	AT3G62840	1.12	0.16	1.78	0.11923107	0.4841	-5.20
249704_at	Myb-related transcription factor LB	TT2	AT5G35550	-1.20	-0.27	-1.78	0.11925599	0.4841	-5.20
261432_at	hypothetical protein predicted by g	---	AT1G07680	-1.14	-0.18	-1.78	0.11927144	0.4841	-5.20
251060_at	putative protein serine/threonine p	ATSR1	AT5G01820	-1.75	-0.81	-1.78	0.11925366	0.4841	-5.20
251125_at	putative protein - kinase protein ki	---	AT5G01060	1.13	0.17	1.78	0.11926267	0.4841	-5.20
251928_at	putative protein hypothetical prote	---	AT3G53980	-1.57	-0.65	-1.78	0.11939726	0.4845	-5.20
253942_at	putative protein	---	AT4G27010	1.26	0.34	1.78	0.11946529	0.4847	-5.21
250097_at	putative protein similar to unknown	---	AT5G17280	1.18	0.24	1.78	0.11952006	0.4848	-5.21
252265_at	putative protein SRG1 protein - Ar	DIN11	AT3G49620	-1.80	-0.84	-1.78	0.11979547	0.4851	-5.21
248046_at	receptor protein kinase-like protein	---	AT5G56040	-1.22	-0.28	-1.78	0.11977216	0.4851	-5.21
266471_at	putative GTP-binding protein	---	AT2G31060	1.27	0.34	1.78	0.11979447	0.4851	-5.21
251605_at	receptor-like protein kinase severa	---	AT3G57830	-1.18	-0.24	-1.78	0.11968473	0.4851	-5.21
248108_at	molybdopterin synthase sulphuryla	CNX5	AT5G55130	1.17	0.23	1.78	0.11978153	0.4851	-5.21
266655_at	putative protein kinase contains a	AtAUR2	AT2G25880	-1.20	-0.27	-1.78	0.11962567	0.4851	-5.21
246402_at	jasmonate inducible protein, putat	---	AT1G57570	-1.13	-0.17	-1.78	0.11977491	0.4851	-5.21
251465_at	transporter-like protein UDP-galac	UTR6	AT3G59360	1.12	0.17	1.78	0.11966474	0.4851	-5.21
256476_at	TNP2-like transposon protein simil	---	---	-1.14	-0.19	-1.78	0.11971947	0.4851	-5.21
254582_at	putative protein TMV resistance p	---	AT4G19470	1.14	0.18	1.78	0.11971543	0.4851	-5.21

257861_at	putative transporter similar to SV2	---	AT3G13050	-1.18	-0.24	-1.78	0.11982622	0.4851	-5.21
249931_at	putative protein similar to unknown	QQT1	AT5G22370	1.22	0.29	1.78	0.11985017	0.4851	-5.21
261814_at	unknown protein	---	AT1G08310	1.96	0.97	1.78	0.11988551	0.4852	-5.21
251173_at	putative protein hypothetical prote	---	AT3G63270	1.12	0.17	1.78	0.11996542	0.4854	-5.21
266008_at	hypothetical protein predicted by g	---	AT2G37390	1.18	0.24	1.78	0.11997162	0.4854	-5.21
256105_at	hypothetical protein predicted by g	LSH8	AT1G16910	-1.17	-0.23	-1.78	0.12002174	0.4854	-5.21
250149_at	cinnamoyl CoA reductase - like pr	---	AT5G14700	-2.06	-1.04	-1.78	0.12000608	0.4854	-5.21
256695_at	unknown protein	---	AT3G32090	-1.17	-0.22	-1.78	0.12005267	0.4854	-5.21
256875_at	cytochrome P450, putative contai	CYP71B37	AT3G26330	-1.17	-0.23	-1.78	0.12007484	0.4854	-5.21
261585_at	NAC domain protein, putative sim	ANAC001	AT1G01010	1.27	0.34	1.78	0.12024237	0.4855	-5.21
260940_at	26S proteasome regulatory particl	---	AT1G45000	1.18	0.24	1.78	0.12012722	0.4855	-5.21
254469_at	hypothetical protein	---	AT4G20470	-1.14	-0.19	-1.78	0.12019116	0.4855	-5.21
267331_at	putative salt-inducible protein	---	AT2G19280	-1.19	-0.25	-1.78	0.12025183	0.4855	-5.21
247755_at	subtilisin-like serine protease conta	ATSBT4.12	AT5G59090	1.13	0.18	1.78	0.12023303	0.4855	-5.21
266141_at	protease inhibitor II contains a gan	PDF2.1	AT2G02120	-1.13	-0.18	-1.78	0.12020988	0.4855	-5.21
259529_at	hypothetical protein	---	AT1G12400	1.14	0.19	1.78	0.12012398	0.4855	-5.21
259639_at	unknown protein ;supported by full	---	AT1G52380	-1.17	-0.23	-1.78	0.12025082	0.4855	-5.21
253365_at	putative protein various predicted	---	AT4G33170	-1.15	-0.20	-1.78	0.12027882	0.4855	-5.21
263309_at	putative replication protein A1	---	---	-1.23	-0.30	-1.78	0.12030868	0.4855	-5.21
251341_at	ribosomal protein S13 -like AtRPS	---	AT3G60770	1.33	0.41	1.78	0.12039158	0.4858	-5.21
265081_at	hypothetical protein contains Zinc	MGP	AT1G03840	-1.16	-0.21	-1.78	0.12045472	0.4860	-5.21
259426_at	hypothetical protein contains simila	LEA14	AT1G01470	-1.17	-0.23	-1.78	0.1206323	0.4866	-5.21
255929_at	hypothetical protein predicted by g	---	AT1G12650	1.18	0.24	1.78	0.12068019	0.4866	-5.21
250571_at	hypothetical protein	---	AT5G08200	-1.22	-0.29	-1.78	0.12075844	0.4866	-5.22
254208_at	Expressed protein ; supported by f	---	AT4G24175	1.17	0.23	1.78	0.12074152	0.4866	-5.22
254324_at	putative protein various predicted	---	AT4G22640	1.19	0.25	1.78	0.12071226	0.4866	-5.22
264969_at	hypothetical protein contains simila	---	AT1G67320	1.39	0.47	1.78	0.12073362	0.4866	-5.22
249034_at	putative protein contains similarity	NUC	AT5G44160	1.17	0.22	1.78	0.12072714	0.4866	-5.22
261085_at	hypothetical protein similar to hypo	IQD7	AT1G17480	-1.14	-0.18	-1.78	0.12081682	0.4866	-5.22
262038_at	invertase, putative similar to neutr	CINV1	AT1G35580	1.27	0.34	1.78	0.12082486	0.4866	-5.22
262691_at	TPR-repeat protein contains multip	---	AT1G62740	-1.21	-0.28	-1.78	0.1207939	0.4866	-5.22
256041_at	unknown protein	---	AT1G07230	1.20	0.27	1.78	0.12085868	0.4866	-5.22
255444_at	LUMINIDEPENDENS protein ; su	LD	AT4G02560	-1.15	-0.20	-1.77	0.12092868	0.4868	-5.22
256110_at	Ser Thr protein kinase, putative si	---	AT1G16900	1.22	0.29	1.77	0.12095782	0.4868	-5.22
262108_at	unknown protein similar to unknow	---	AT1G02740	1.18	0.24	1.77	0.12097329	0.4868	-5.22

260755_at	hypothetical protein predicted by g	---	AT1G48980	1.14	0.19	1.77	0.12103418	0.4870	-5.22
265433_at	unknown protein	---	AT2G20950	1.21	0.28	1.77	0.12117179	0.4872	-5.22
244980_at	ribosomal protein L36	---	---	-1.15	-0.20	-1.77	0.12141592	0.4872	-5.22
266641_at	Expressed protein ; supported by f	---	AT2G35605	1.16	0.21	1.77	0.12136619	0.4872	-5.22
266774_at	hypothetical protein predicted by g	ATRBL1	AT2G29050	-1.20	-0.26	-1.77	0.12122594	0.4872	-5.22
250622_at	putative transcription factor AP2 d	---	AT5G07310	-1.13	-0.18	-1.77	0.12148717	0.4872	-5.22
258532_at	ribosomal protein L29, putative sir	---	AT3G06700	1.43	0.52	1.77	0.12148018	0.4872	-5.22
261846_at	hypothetical protein similar to hypo	---	AT1G11540	-1.17	-0.22	-1.77	0.12115669	0.4872	-5.22
259352_at	unknown protein	---	AT3G05170	-1.28	-0.36	-1.77	0.12123558	0.4872	-5.22
249682_at	putative protein similar to unknown	---	AT5G36080	-1.13	-0.17	-1.77	0.12150049	0.4872	-5.22
265397_at	hypothetical protein predicted by g	---	---	-1.13	-0.18	-1.77	0.12138732	0.4872	-5.22
261160_at	hypothetical protein	---	AT1G34480	-1.15	-0.20	-1.77	0.12124991	0.4872	-5.22
266978_at	putative disease resistance respon	---	AT2G39430	-1.15	-0.20	-1.77	0.12143854	0.4872	-5.22
250859_at	cytochrom P450 - like protein cyto	CYP77A4	AT5G04660	-1.11	-0.15	-1.77	0.12117927	0.4872	-5.22
256664_at	DNA-3-methlyadenine glycosylase	---	AT3G12040	1.21	0.27	1.77	0.1213267	0.4872	-5.22
248900_at	putative protein strong similarity to	PRP39-2	AT5G46400	1.23	0.30	1.77	0.12140252	0.4872	-5.22
263487_at	hypothetical protein predicted by g	---	AT2G31850	-1.14	-0.19	-1.77	0.1213035	0.4872	-5.22
251736_at	putative protein acetyl-CoA carbo	---	AT3G56130	1.29	0.36	1.77	0.12124554	0.4872	-5.22
247869_at	CCHH finger protein 2-like protein	ZFP2	AT5G57520	-1.11	-0.15	-1.77	0.12120363	0.4872	-5.22
262702_at	putative protein phosphatase 2C s	---	AT1G16220	-1.16	-0.22	-1.77	0.12130867	0.4872	-5.22
264662_at	putative sucrose/H+ symporter sim	SUT4	AT1G09960	-1.22	-0.29	-1.77	0.12139709	0.4872	-5.22
255928_at	unknown protein	---	AT1G12640	1.25	0.32	1.77	0.1215556	0.4872	-5.22
256159_at	Expressed protein ; supported by f	JAZ8	AT1G30135	-1.90	-0.92	-1.77	0.12154495	0.4872	-5.22
260087_at	hypothetical protein predicted by g	---	AT1G73200	-1.21	-0.28	-1.77	0.12157917	0.4872	-5.22
245622_at	A6 anther-specific protein	MEE48	AT4G14080	1.17	0.22	1.77	0.12162518	0.4873	-5.22
251827_at	chalcone isomerase ;supported by	TT5	AT3G55120	1.22	0.29	1.77	0.12170076	0.4875	-5.22
255059_at	putative protein downy mildew res	---	AT4G09420	1.40	0.48	1.77	0.12181091	0.4876	-5.22
264613_at	lipoyltransferase identical to GB:B/	LIP2	AT1G04640	1.16	0.22	1.77	0.12179751	0.4876	-5.22
248870_at	putative protein similar to unknown	---	AT5G46710	1.61	0.69	1.77	0.12181292	0.4876	-5.22
247922_at	putative protein similar to unknown	---	AT5G57500	-1.43	-0.52	-1.77	0.12177638	0.4876	-5.22
261238_at	hypothetical protein predicted by g	---	AT1G32810	-1.16	-0.21	-1.77	0.12189708	0.4878	-5.22
246549_at	putative protein predicted proteins	---	AT5G15050	1.32	0.40	1.77	0.1219245	0.4878	-5.22
251194_at	putative protein	---	AT3G62920	1.26	0.33	1.77	0.12195191	0.4878	-5.22
265374_at	hypothetical protein ;supported by	PSBX	AT2G06520	1.13	0.17	1.77	0.12194994	0.4878	-5.22
257969_at	hypothetical protein predicted by g	---	AT3G27520	1.28	0.35	1.77	0.12192416	0.4878	-5.22

266173_at	unknown protein	---	AT2G02410	1.13	0.18	1.77	0.12199623	0.4879	-5.23
248946_at	putative protein similar to unknown	---	AT5G45530	-1.13	-0.18	-1.77	0.12202153	0.4879	-5.23
254102_at	acyl carrier - like protein acyl carri	ACP4	AT4G25050	1.18	0.24	1.77	0.12211159	0.4880	-5.23
249774_at	squalene monooxygenase	SQP1	AT5G24150	-1.29	-0.36	-1.77	0.12208702	0.4880	-5.23
247827_at	putative protein various predicted	LSH5	AT5G58500	-1.19	-0.25	-1.77	0.12210992	0.4880	-5.23
265488_at	hypothetical protein predicted by g	---	AT2G15610	-1.16	-0.21	-1.77	0.12222871	0.4881	-5.23
267249_at	hypothetical protein predicted by g	---	AT2G23040	-1.13	-0.18	-1.77	0.12221765	0.4881	-5.23
262322_at	hypothetical protein similar to hypo	---	AT1G27590	-1.19	-0.25	-1.77	0.12222976	0.4881	-5.23
266286_at	putative tropinone reductase	---	AT2G29160	-1.16	-0.22	-1.77	0.1221922	0.4881	-5.23
251427_at	beta-glucosidase-like protein sever	BGLU16	AT3G60130	-1.23	-0.29	-1.77	0.12233533	0.4883	-5.23
257209_at	hypothetical protein	---	AT3G14920	1.12	0.16	1.77	0.12252877	0.4883	-5.23
253867_at	putative protein tRNA nucleotidyltr	---	AT4G27490	1.26	0.34	1.77	0.12239829	0.4883	-5.23
254765_at	hypothetical protein	---	AT4G13270	1.17	0.23	1.77	0.12253634	0.4883	-5.23
259113_at	hypothetical protein predicted by g	---	AT3G05510	1.17	0.23	1.77	0.12232407	0.4883	-5.23
257928_at	hypothetical protein contains Pfam	PPR40	AT3G16890	-1.12	-0.16	-1.77	0.12247608	0.4883	-5.23
256100_at	unknown protein	---	AT1G13750	1.55	0.63	1.77	0.12254182	0.4883	-5.23
245590_at	hypothetical protein	---	AT4G15060	-1.14	-0.19	-1.77	0.1223954	0.4883	-5.23
265242_at	hypothetical protein	---	AT2G07705	-1.28	-0.36	-1.77	0.12249362	0.4883	-5.23
263493_at	putative ATP-dependent RNA helic	---	AT2G42520	-1.23	-0.29	-1.77	0.12243083	0.4883	-5.23
245009_at	ribosomal protein S4	---	---	1.12	0.17	1.77	0.12247943	0.4883	-5.23
252956_at	farnesylated protein (ATFP6) ; sup	ATFP6	AT4G38580	1.43	0.51	1.77	0.12239888	0.4883	-5.23
248954_at	unknown protein ; supported by cl	---	AT5G45420	-1.13	-0.17	-1.76	0.1226786	0.4888	-5.23
254202_at	putative protein hydroxymuconic s	---	AT4G24140	1.26	0.34	1.76	0.12274801	0.4890	-5.23
263844_at	unknown protein ; supported by cl	---	AT2G36930	1.37	0.46	1.76	0.12289144	0.4895	-5.23
254732_at	hypothetical protein	---	AT4G13750	1.23	0.30	1.76	0.12292796	0.4895	-5.23
266158_at	putative ABC transporter	---	AT2G28070	1.22	0.28	1.76	0.12299193	0.4897	-5.23
266531_at	putative plasma membrane intrins	---	AT2G16835	-1.12	-0.16	-1.76	0.12300826	0.4897	-5.23
254492_at	endomembrane-associated protein	PCAP1	AT4G20260	1.17	0.22	1.76	0.12304226	0.4897	-5.23
251740_at	peptidylprolyl isomerase	ROC2	AT3G56070	1.33	0.41	1.76	0.1232167	0.4900	-5.23
246253_at	myb-related protein	MYB73	AT4G37260	-1.22	-0.28	-1.76	0.12321737	0.4900	-5.23
248103_at	ubiquitin-like protein SMT3-like ; s	SUMO2	AT5G55160	1.24	0.31	1.76	0.12323087	0.4900	-5.23
259435_at	hypothetical protein similar to puta	---	AT1G01450	-1.13	-0.17	-1.76	0.123232	0.4900	-5.23
254413_at	myb-related protein M4 ;supported	ATMYB102	AT4G21440	-1.26	-0.34	-1.76	0.12318172	0.4900	-5.23
255855_at	ABC transporter, putative similar t	PDR11	AT1G66950	-1.20	-0.27	-1.76	0.12323145	0.4900	-5.23
256190_at	9-cis-epoxycarotenoid dioxygenas	NCED5	AT1G30100	-1.15	-0.20	-1.76	0.12326005	0.4900	-5.23

254860_at	putative C-4 sterol methyl oxidase	SMO1-1	AT4G12110	-1.18	-0.24	-1.76	0.12334505	0.4902	-5.24
246567_at	alpha-mannosidase -like protein n	GMII	AT5G14950	-1.12	-0.17	-1.76	0.12342663	0.4905	-5.24
261242_at	subtilisin-like serine protease conta	SBT3.3	AT1G32960	-1.28	-0.36	-1.76	0.12350188	0.4905	-5.24
251406_at	putative protein various predicted	---	AT3G60260	-1.29	-0.37	-1.76	0.12347825	0.4905	-5.24
262801_at	unknown protein ;supported by ful	---	AT1G21010	1.43	0.52	1.76	0.12349324	0.4905	-5.24
264633_at	step II splicing factor, putative sim	SMP1	AT1G65660	-1.16	-0.21	-1.76	0.12362756	0.4907	-5.24
256230_at	FKBP-type peptidyl-prolyl cis-trans	---	AT3G12340	1.20	0.26	1.76	0.12362744	0.4907	-5.24
249524_at	putative protein similar to unknown	---	AT5G38520	-1.26	-0.33	-1.76	0.12362428	0.4907	-5.24
245798_at	hypothetical protein predicted by g	---	AT1G45545	1.12	0.16	1.76	0.12362161	0.4907	-5.24
246950_at	transcription initiation factor IID-as	TAF5	AT5G25150	-1.13	-0.17	-1.76	0.12375199	0.4911	-5.24
247745_at	copper transport protein	COPT1	AT5G59030	1.12	0.17	1.76	0.12384204	0.4914	-5.24
245907_at	ubiquitin-like protein ubiquitins - dif	---	AT5G09340	1.12	0.16	1.76	0.12386538	0.4914	-5.24
256965_at	branched chain alpha-keto acid de	DIN4	AT3G13450	1.36	0.45	1.76	0.12392214	0.4915	-5.24
255820_at	putative protein kinase contains a	---	AT2G40580	-1.17	-0.23	-1.76	0.12401998	0.4918	-5.24
260762_at	I-box binding factor, putative simil	---	AT1G49015	-1.15	-0.20	-1.76	0.12407307	0.4919	-5.24
255686_at	putative potassium/H+ antiporter	KEA2	AT4G00630	-1.19	-0.25	-1.76	0.12416136	0.4922	-5.24
256793_at	unknown protein ;supported by ful	---	AT3G22160	1.39	0.47	1.75	0.12442894	0.4922	-5.24
264616_at	unknown protein	---	AT2G17740	2.28	1.19	1.76	0.12440361	0.4922	-5.24
255817_at	unknown protein ;supported by ful	PDLP3	AT2G33330	1.33	0.42	1.75	0.1244221	0.4922	-5.24
262932_at	glutathione-s-transferase, putative	---	AT1G65820	1.21	0.28	1.76	0.12432032	0.4922	-5.24
259152_at	hypothetical protein similar to puta	---	AT3G10210	1.12	0.16	1.76	0.12431029	0.4922	-5.24
247791_at	cyclophilin ROC7 ;supported by fu	ROC7	AT5G58710	1.21	0.27	1.75	0.12452339	0.4922	-5.24
249237_at	putative protein similar to unknown	---	AT5G42050	1.24	0.31	1.75	0.12453505	0.4922	-5.24
247569_at	Cf-5 disease resistance protein - l	---	AT5G61240	-1.23	-0.30	-1.76	0.12421445	0.4922	-5.24
244997_at	RNA polymerase beta' subunit-2	---	---	1.16	0.21	1.75	0.12448175	0.4922	-5.24
252106_at	putative glutamate receptor putati	ATGLR3.6	AT3G51480	-1.21	-0.27	-1.76	0.12431192	0.4922	-5.24
261682_at	unknown protein similar to hypothe	---	AT1G47330	-1.18	-0.24	-1.76	0.12422967	0.4922	-5.24
258607_at	thioredoxin f1 identical to thioredox	TRXF1	AT3G02730	-1.20	-0.26	-1.76	0.12433893	0.4922	-5.24
265630_at	unknown protein similar to ovarian	---	AT2G27350	-1.13	-0.17	-1.75	0.12454274	0.4922	-5.24
259864_at	hypothetical protein predicted by g	---	AT1G72800	-1.29	-0.37	-1.75	0.12456231	0.4922	-5.24
246369_at	light repressible receptor protein k	---	AT1G51910	-1.19	-0.25	-1.76	0.12429664	0.4922	-5.24
257162_s_at	ammonium transporter, putative s	AMT1;3	AT3G24290 /	-1.13	-0.18	-1.75	0.12445892	0.4922	-5.24
246945_s_at	putative membrane protein hypoth	---	AT5G25040 /	1.16	0.22	1.75	0.12450153	0.4922	-5.24
260649_at	storage protein, putative similar to	ACA7	AT1G08080	1.14	0.19	1.75	0.12457163	0.4922	-5.24
255971_at	transposon related protein similar t	---	---	-1.12	-0.16	-1.76	0.1243825	0.4922	-5.24

257108_x_at	hypothetical protein	---	---	-1.13	-0.17	-1.75	0.12463172	0.4923	-5.25
252254_at	hypothetical protein ; supported by	DMS3	AT3G49250	1.13	0.17	1.75	0.12463766	0.4923	-5.25
248231_at	putative protein contains similarity	---	AT5G53770	1.17	0.22	1.75	0.12481084	0.4927	-5.25
266493_at	Mutator-like transposase similar to	---	---	-1.14	-0.19	-1.75	0.12482069	0.4927	-5.25
252071_at	putative protein DNA helicase hon	---	AT3G51690	-1.11	-0.15	-1.75	0.12481441	0.4927	-5.25
260437_at	hypothetical protein predicted by g	---	AT1G68380	-1.15	-0.20	-1.75	0.12477834	0.4927	-5.25
262960_at	unknown protein ; supported by cD	---	AT1G54320	1.15	0.20	1.75	0.12489188	0.4928	-5.25
265887_at	biotin holocarboxylase synthetase	HCS1	AT2G25710	1.18	0.24	1.75	0.12490713	0.4928	-5.25
254747_at	serine/threonine-specific protein ki	MHK	AT4G13020	-1.15	-0.21	-1.75	0.12493597	0.4929	-5.25
256096_at	unknown protein	---	AT1G13650	-1.37	-0.45	-1.75	0.12498822	0.4929	-5.25
263973_at	60S ribosomal protein L11B	RPL16A	AT2G42740	1.28	0.35	1.75	0.12497864	0.4929	-5.25
246807_at	ion channel - like protein ligand ga	GLR2.1	AT5G27100	-1.22	-0.29	-1.75	0.12507168	0.4932	-5.25
257832_at	light regulated protein, putative sir	CCL	AT3G26740	1.14	0.19	1.75	0.12521988	0.4933	-5.25
262132_at	ribosomal protein L22, putative sir	---	AT1G02830	-1.14	-0.19	-1.75	0.1251891	0.4933	-5.25
247939_at	putative protein contains similarity	ATLIG4	AT5G57160	1.14	0.19	1.75	0.12520889	0.4933	-5.25
262954_at	rubredoxin, putative similar to rubr	---	AT1G54500	1.19	0.25	1.75	0.12515566	0.4933	-5.25
245433_at	hypothetical protein	---	AT4G17140	1.14	0.19	1.75	0.12514003	0.4933	-5.25
267291_at	putative C2H2-type zinc finger prot	---	AT2G23740	-1.28	-0.36	-1.75	0.12524238	0.4933	-5.25
245139_at	putative AT-hook DNA-binding pro	---	AT2G45430	-1.15	-0.21	-1.75	0.12536039	0.4937	-5.25
258274_at	putative cytochrome c oxidase sub	---	AT3G15640	1.18	0.24	1.75	0.12541361	0.4938	-5.25
252029_s_at	putative RNA binding protein hete	---	AT3G52660 /	1.13	0.17	1.75	0.12542189	0.4938	-5.25
247568_at	putative protein predicted proteins	---	AT5G61260	1.33	0.41	1.75	0.12547793	0.4939	-5.25
248837_at	putative protein similar to unknown	---	AT5G47260	1.11	0.15	1.75	0.12549854	0.4939	-5.25
260487_at	RNA-binding protein, putative sim	Y14	AT1G51510	-1.14	-0.19	-1.75	0.12553791	0.4940	-5.25
246741_at	glycine rich protein - like glycine ri	emb1644	AT5G27720	1.18	0.23	1.75	0.12560157	0.4941	-5.25
264277_at	polygalacturonase isoenzyme 1 b	---	AT1G60390	-1.16	-0.21	-1.75	0.12572978	0.4945	-5.25
266982_at	unknown protein ; supported by cI	---	AT2G39500	1.19	0.26	1.75	0.12575122	0.4945	-5.25
248555_at	DNA repair protein-like	---	AT5G50340	1.16	0.21	1.75	0.12584171	0.4948	-5.25
263077_at	putative mitotic control protein dis3	EMB2763	AT2G17510	1.12	0.17	1.75	0.12586941	0.4948	-5.25
253388_at	putative protein ; supported by cD	---	AT4G32910	1.23	0.30	1.75	0.12602481	0.4952	-5.26
247054_at	zinc finger protein	---	AT5G66730	-1.16	-0.21	-1.75	0.12603019	0.4952	-5.26
263238_at	putative auxin-induced protein	---	AT2G16580	1.12	0.17	1.75	0.12601451	0.4952	-5.26
256637_at	unknown protein similar to membra	---	AT3G12030	1.21	0.28	1.75	0.12603849	0.4952	-5.26
260912_at	ATP-dependent Clp protease prote	CLPP5	AT1G02560	1.14	0.18	1.75	0.12611793	0.4952	-5.26
251350_at	cytochrome P450 monooxygenas	CYP76C7	AT3G61040	-1.25	-0.32	-1.75	0.12613095	0.4952	-5.26

247255_at	putative protein similar to unknown	---	AT5G64780	1.31	0.39	1.75	0.12611699	0.4952	-5.26
258258_at	transcriptional regulator (FUSCA3	FUS3	AT3G26790	-1.13	-0.18	-1.75	0.12611801	0.4952	-5.26
260895_at	unknown protein similar to unknow	---	AT1G29250	1.32	0.40	1.75	0.12619604	0.4954	-5.26
248000_at	WD-repeat protein-like ;supported	---	AT5G56190	-1.17	-0.23	-1.74	0.12624324	0.4955	-5.26
256099_at	cytochrome P450, putative similar	CYP78A5	AT1G13710	-1.24	-0.31	-1.74	0.12629346	0.4955	-5.26
263442_at	hypothetical protein	---	AT2G28605	1.13	0.17	1.74	0.12630635	0.4955	-5.26
251627_at	glucan endo-1,3-beta-D-glucosida	BG1	AT3G57270	-1.16	-0.21	-1.74	0.12635357	0.4956	-5.26
251651_at	putative protein transcription initia	---	AT3G57370	1.11	0.15	1.74	0.12633602	0.4956	-5.26
264325_at	putative phosphoribosylanthranilat	---	AT1G04150	-1.20	-0.26	-1.74	0.12640395	0.4956	-5.26
246980_at	peptidylprolyl isomerase (cyclophil	---	AT5G67530	-1.14	-0.19	-1.74	0.12638833	0.4956	-5.26
252070_at	short-chain alcohol dehydrogenas	---	AT3G51680	-1.19	-0.25	-1.74	0.12643329	0.4956	-5.26
264360_at	putative isoamylase Similar to gi|1	DBE1	AT1G03310	-1.19	-0.25	-1.74	0.12648709	0.4956	-5.26
245095_at	putative protein kinase contains a	---	AT2G40860	-1.23	-0.29	-1.74	0.1265082	0.4956	-5.26
244941_at	hypothetical protein	---	---	-1.18	-0.23	-1.74	0.12650453	0.4956	-5.26
256873_at	cytochrome P450, putative contair	CYP71B34	AT3G26300	-1.16	-0.22	-1.74	0.12654588	0.4957	-5.26
252356_at	putative protein various predicted	---	---	-1.20	-0.27	-1.74	0.12656931	0.4957	-5.26
249563_at	similar to unknown protein (pir |T0	---	AT5G38360	1.14	0.19	1.74	0.12659202	0.4957	-5.26
265729_at	putative glucan synthase	ATGSL03	AT2G31960	1.20	0.26	1.74	0.12665416	0.4958	-5.26
258611_at	unknown protein ;supported by ful	---	AT3G02860	-1.15	-0.20	-1.74	0.12665925	0.4958	-5.26
245960_at	subtilisin-like protein subtilisin/kex	S1P	AT5G19660	1.11	0.16	1.74	0.1266753	0.4958	-5.26
257782_at	hypothetical protein predicted by g	---	AT3G27120	-1.16	-0.21	-1.74	0.12671274	0.4959	-5.26
256184_at	epsilon subunit of mitochondrial F1	---	AT1G51650	1.22	0.29	1.74	0.12683991	0.4960	-5.26
258412_at	unknown protein similar to pop3 pe	HS1	AT3G17210	1.16	0.21	1.74	0.12680343	0.4960	-5.26
257142_at	cytochrome P450, putative contair	CYP705A1	AT3G20090	1.20	0.27	1.74	0.12682785	0.4960	-5.26
253199_at	clathrin assembly protein AP19 ho	---	AT4G35410	1.34	0.42	1.74	0.12680126	0.4960	-5.26
251899_at	nucleoid DNA-binding - like protei	---	AT3G54400	1.96	0.97	1.74	0.1269087	0.4960	-5.26
267411_at	putative disease resistance protein	---	AT2G34930	-2.13	-1.09	-1.74	0.1270742	0.4960	-5.26
265872_at	unknown protein ;supported by ful	atnudt17	AT2G01670	1.23	0.30	1.74	0.1270708	0.4960	-5.26
260806_at	RNA recognition motif-containing p	---	AT1G78260	-1.12	-0.16	-1.74	0.12687817	0.4960	-5.26
247259_at	CPR5 protein, putative Constitutiv	CPR5	AT5G64930	1.22	0.28	1.74	0.12700688	0.4960	-5.26
252583_at	putative protein several hypothetic	---	AT3G45540	-1.15	-0.21	-1.74	0.12698901	0.4960	-5.26
248457_at	putative protein contains similarity	---	AT5G51420	-1.21	-0.27	-1.74	0.12701107	0.4960	-5.26
260773_at	gibberellin 2- oxidase identical to g	ATGA2OX1	AT1G78440	-1.17	-0.23	-1.74	0.12690753	0.4960	-5.26
263830_at	hypothetical protein predicted by g	---	AT2G40260	-1.15	-0.20	-1.74	0.12694857	0.4960	-5.26
260219_at	hypothetical protein contains Pfam	---	AT1G74630	-1.14	-0.19	-1.74	0.12708027	0.4960	-5.26

259472_at	hypothetical protein contains simila	---	AT1G18910	1.14	0.19	1.74	0.1270667	0.4960	-5.26
254840_at	hypothetical protein	---	AT4G11930	-1.21	-0.28	-1.74	0.12711739	0.4961	-5.26
259193_at	putative thylakoid lumen rotamase	CYP38	AT3G01480	1.22	0.29	1.74	0.12716845	0.4962	-5.26
250752_at	cytochrome P450 90A1 (sp|Q4256	CPD	AT5G05690	-1.19	-0.25	-1.74	0.12725899	0.4964	-5.26
251808_at	AP3-complex beta-3A adaptin sub	---	AT3G55480	1.16	0.22	1.74	0.12726494	0.4964	-5.26
248897_at	KCO-like protein 3 (emb|CAB4038	KCO3	AT5G46360	-1.16	-0.22	-1.74	0.12737847	0.4967	-5.27
259167_at	putative oleosin similar to oleosin (	---	AT3G01570	1.13	0.18	1.74	0.12738911	0.4967	-5.27
262809_at	putative glycogen synthase strong	ATSS3	AT1G11720	-1.42	-0.51	-1.74	0.12748807	0.4970	-5.27
258868_at	putative exportin1 (XPO1) protein	XPO1B	AT3G03110	1.16	0.22	1.74	0.12753685	0.4970	-5.27
245807_at	AP2 domain containing protein RA	RAP2.1	AT1G46768	1.35	0.43	1.74	0.12753197	0.4970	-5.27
254749_at	putative protein various predicted	---	AT4G13130	1.11	0.15	1.74	0.12755706	0.4970	-5.27
251843_x_at	extensin precursor -like protein ex	ATHRGP1	AT3G54590	-1.30	-0.38	-1.74	0.12765229	0.4973	-5.27
256542_at	unknown protein	PMI1	AT1G42550	1.20	0.26	1.74	0.12779338	0.4975	-5.27
257797_at	hypothetical protein contains Pfam	---	AT3G15940	-1.17	-0.22	-1.74	0.12773622	0.4975	-5.27
262602_at	unknown protein ESTs gb|AA650	---	AT1G15270	1.13	0.17	1.74	0.12782997	0.4975	-5.27
265157_at	putative reverse transcriptase simi	---	---	-1.15	-0.20	-1.74	0.1278353	0.4975	-5.27
257172_at	hypothetical protein predicted by g	---	AT3G23700	1.19	0.26	1.74	0.12779864	0.4975	-5.27
266444_at	putative extensin	---	AT2G43150	1.19	0.25	1.74	0.12779425	0.4975	-5.27
250256_at	GTP-binding protein typA (tyrosine	---	AT5G13650	1.14	0.19	1.74	0.12791077	0.4976	-5.27
261063_at	transcription factor scarecrow-like	---	AT1G07520	1.65	0.72	1.74	0.12791294	0.4976	-5.27
266205_s_at	putative dTDP-glucose 4-6-dehydr	AXS2	AT1G08200 /	-1.17	-0.23	-1.73	0.12807402	0.4981	-5.27
251931_at	putative protein glyoxal oxidase (g	---	AT3G53950	1.26	0.33	1.73	0.1280705	0.4981	-5.27
267240_at	hypothetical protein predicted by g	---	AT2G02680	-1.17	-0.22	-1.73	0.12810768	0.4981	-5.27
253065_at	putative protein predicted proteins	AtGRF2	AT4G37740	-1.21	-0.27	-1.73	0.12810661	0.4981	-5.27
248294_at	RNA-binding protein-like	---	AT5G53060	-1.17	-0.22	-1.73	0.12814947	0.4981	-5.27
255484_at	putative protein similar to A. thalia	---	AT4G02540	1.18	0.24	1.73	0.12815138	0.4981	-5.27
249307_s_at	DNA excision repair cross-comple	XPB1	AT5G41360 /	1.15	0.20	1.73	0.12835458	0.4988	-5.27
254709_at	Expressed protein ; supported by c	AGD8	AT4G17890	-1.19	-0.25	-1.73	0.12843925	0.4990	-5.27
264444_at	putative squamosa-promoter bindi	---	AT1G27360	-1.14	-0.19	-1.73	0.12849056	0.4991	-5.27
263519_at	40S ribosomal protein S25 ; suppo	---	AT2G21580	1.31	0.39	1.73	0.12861838	0.4995	-5.27
256369_at	hypothetical protein predicted by g	---	AT1G66790 /	-1.11	-0.15	-1.73	0.12862517	0.4995	-5.27
264254_at	unknown protein	---	AT1G09150	1.12	0.16	1.73	0.12876425	0.4997	-5.28
251664_at	leucine zipper-containing protein A	CRD1	AT3G56940	1.17	0.23	1.73	0.12874257	0.4997	-5.28
258372_at	ubiquitin-specific protease 25 (UBI	UBP25	AT3G14400	-1.14	-0.18	-1.73	0.12881933	0.4997	-5.28
262214_at	germin subunit, putative similar to	---	AT1G74820	-1.14	-0.18	-1.73	0.1288333	0.4997	-5.28

256839_at	calmodulin, putative similar to calr	---	AT3G22930	1.17	0.23	1.73	0.12880347	0.4997	-5.28
246243_at	trichohyalin like protein	---	AT4G36520	-1.12	-0.17	-1.73	0.12873031	0.4997	-5.28
267613_at	putative second messenger-depen	PID2	AT2G26700	1.15	0.20	1.73	0.1288434	0.4997	-5.28
258682_at	putative ribosomal-protein S6 kina	S6K2	AT3G08720	1.42	0.51	1.73	0.12899822	0.4997	-5.28
248369_at	arginine/serine-rich splicing factor	ATRSP41	AT5G52040	1.20	0.26	1.73	0.12901303	0.4997	-5.28
262157_at	unknown protein contains similarity	---	AT1G52670	1.16	0.21	1.73	0.12903235	0.4997	-5.28
260749_at	hypothetical protein predicted by g	---	AT1G49110	-1.17	-0.23	-1.73	0.12904117	0.4997	-5.28
263209_at	Expressed protein ; supported by f	---	AT1G10522	1.32	0.40	1.73	0.12904535	0.4997	-5.28
267591_at	Expressed protein ; supported by f	RTFL8	AT2G39705	1.48	0.57	1.73	0.12894268	0.4997	-5.28
250828_at	unknown protein ; supported by cD	---	AT5G05250	-2.11	-1.08	-1.73	0.12899925	0.4997	-5.28
248675_at	putative protein similar to unknowr	ICK6	AT5G48820	-1.26	-0.33	-1.73	0.12896215	0.4997	-5.28
262833_at	cyclin, putative contains Pfam pro	SDS	AT1G14750	-1.12	-0.16	-1.73	0.12906362	0.4997	-5.28
251941_at	putative protein ribosomal protein	---	AT3G53470	1.15	0.20	1.73	0.12905541	0.4997	-5.28
249153_s_at	putative protein strong similarity to	---	AT5G43390	-1.16	-0.21	-1.73	0.12918848	0.5001	-5.28
263918_at	putative proline transporter ;suppo	ProT3	AT2G36590	-1.66	-0.73	-1.73	0.1292144	0.5001	-5.28
262824_at	putative DNA binding protein simil	RBP45B	AT1G11650	1.12	0.16	1.73	0.12933388	0.5002	-5.28
257806_at	hypothetical protein predicted by g	---	AT3G18670	-1.14	-0.19	-1.73	0.12948911	0.5002	-5.28
265387_at	unknown protein ;supported by ful	---	AT2G20670	1.45	0.54	1.73	0.12931487	0.5002	-5.28
252967_at	amidophosphoribosyltransferase -	ATASE3	AT4G38880	1.15	0.20	1.73	0.12937416	0.5002	-5.28
257255_at	hypothetical protein contains Pfam	---	AT3G21960	-1.15	-0.20	-1.73	0.12935975	0.5002	-5.28
249844_at	putative protein similar to unknowr	---	AT5G23590	1.17	0.22	1.73	0.12951777	0.5002	-5.28
267198_at	putative gibberellin-regulated prote	---	AT2G30810	1.12	0.17	1.73	0.12951896	0.5002	-5.28
247565_at	putative protein Atu, Drosophila m	VIP4	AT5G61150	-1.14	-0.19	-1.73	0.12948736	0.5002	-5.28
248135_at	putative protein similar to unknowr	---	AT5G54890	1.20	0.26	1.73	0.12949717	0.5002	-5.28
247370_at	putative protein similar to unknowr	---	AT5G63320	-1.30	-0.38	-1.73	0.12945111	0.5002	-5.28
256469_at	zinc-finger protein, putative simila	LOL1	AT1G32540	-1.26	-0.34	-1.73	0.12952199	0.5002	-5.28
262114_at	unknown protein contains similarity	NLA	AT1G02860	1.29	0.36	1.73	0.12947365	0.5002	-5.28
263409_at	predicted protein	---	AT2G04063	-1.14	-0.19	-1.73	0.12935031	0.5002	-5.28
250872_at	putative protein SF16 protein, con	IQD12	AT5G03960	1.14	0.19	1.73	0.12951975	0.5002	-5.28
260221_at	GAST1-like protein similar to GAS	---	AT1G74670	1.97	0.98	1.73	0.1296681	0.5003	-5.28
261076_at	unknown protein ;supported by full	SMO2-1	AT1G07420	1.13	0.17	1.73	0.12961625	0.5003	-5.28
263488_at	hypothetical protein predicted by g	---	AT2G31840	1.20	0.26	1.73	0.12969742	0.5003	-5.28
245524_at	cytochrome c oxidoreductase like p	---	AT4G15920	-1.48	-0.57	-1.73	0.12962304	0.5003	-5.28
266848_at	unknown protein ;supported by ful	---	AT2G25950	1.21	0.28	1.73	0.12963862	0.5003	-5.28
251400_at	putative protein prib5, Ribes nigru	---	AT3G60420	1.77	0.83	1.73	0.12969048	0.5003	-5.28

253440_at	putative protein ;supported by full-l	TIFY8	AT4G32570	1.11	0.15	1.73	0.12974436	0.5004	-5.28
257640_at	hypothetical protein	---	AT3G25750	-1.19	-0.25	-1.73	0.1297536	0.5004	-5.28
253916_at	hypothetical protein ;supported by	---	AT4G27240	1.29	0.37	1.73	0.12980661	0.5004	-5.28
248800_at	40S ribosomal protein S19 ; suppo	RPS19	AT5G47320	1.15	0.20	1.73	0.1298045	0.5004	-5.28
261616_at	NAC domain containing protein, p	ANAC014	AT1G33060	1.11	0.15	1.73	0.12985282	0.5005	-5.28
247456_at	iron-regulated transporter - like pr	AtZIP12	AT5G62160	-1.14	-0.19	-1.72	0.1299227	0.5007	-5.28
253206_at	putative squalene synthase non-c	SQS1	AT4G34640	1.16	0.21	1.72	0.12995675	0.5007	-5.28
256552_at	hypothetical protein predicted by g	---	AT3G31350	-1.17	-0.23	-1.72	0.13004304	0.5010	-5.29
265849_at	hypothetical protein predicted by g	---	AT2G35736	1.22	0.28	1.72	0.13009801	0.5010	-5.29
265221_s_at	putative glutamate decarboxylase	GAD3	AT2G02000	-1.67	-0.74	-1.72	0.13013711	0.5010	-5.29
260337_at	unknown protein	WRKY57	AT1G69310	1.17	0.23	1.72	0.13017761	0.5010	-5.29
255881_at	phosphomannose isomerase, puta	DIN9	AT1G67070	-1.53	-0.61	-1.72	0.13019021	0.5010	-5.29
260142_at	unknown protein ; supported by cl	---	AT1G71900	1.18	0.23	1.72	0.13019557	0.5010	-5.29
254988_at	putative protein Ran GTPase activ	GTC2	AT4G10670	-1.15	-0.20	-1.72	0.13007967	0.5010	-5.29
245683_at	ubiquitin-specific protease 8 (UBP	UBP8	AT5G22030	-1.13	-0.17	-1.72	0.13020019	0.5010	-5.29
263104_at	unknown protein	---	AT2G05120	1.16	0.22	1.72	0.13030257	0.5013	-5.29
249684_s_at	cytochrome P450-like	---	AT5G36110	-1.13	-0.17	-1.72	0.13031813	0.5013	-5.29
248460_at	Expressed protein ; supported by f	---	AT5G50915	1.65	0.72	1.72	0.13054878	0.5013	-5.29
256972_at	unknown protein	---	AT3G21140	1.15	0.20	1.72	0.1304245	0.5013	-5.29
263054_at	putative cation transport protein	---	AT2G04620	1.14	0.19	1.72	0.130367	0.5013	-5.29
264046_at	putative non-LTR retroelement rev	---	AT2G22440	-1.15	-0.20	-1.72	0.13035176	0.5013	-5.29
255466_at	putative protein similar to A. thalia	---	AT4G03000	1.16	0.21	1.72	0.13053389	0.5013	-5.29
261105_at	unknown protein ;supported by full	NRS/ER	AT1G63000	-1.20	-0.26	-1.72	0.13050829	0.5013	-5.29
253317_at	putative protein	---	AT4G33960	1.38	0.46	1.72	0.13056252	0.5013	-5.29
264255_at	putative SF2/ASF splicing modula	---	AT1G09140	-1.21	-0.27	-1.72	0.13046329	0.5013	-5.29
249505_at	putative protein	---	---	-1.32	-0.40	-1.72	0.13053096	0.5013	-5.29
248715_at	ATFP4, putative	---	AT5G48290	1.22	0.29	1.72	0.13043509	0.5013	-5.29
252425_at	putative protein auxin-induced bas	AtTCP14	AT3G47620	-1.24	-0.31	-1.72	0.1305133	0.5013	-5.29
249803_at	putative protein similar to unknown	---	AT5G23780	-1.15	-0.20	-1.72	0.13059604	0.5013	-5.29
258029_at	serine/threonine-protein kinase, P	ATPK7	AT3G27580	1.13	0.17	1.72	0.13063971	0.5014	-5.29
254925_at	beta-adaptin - like protein beta-ad	---	AT4G11380	1.17	0.23	1.72	0.13069843	0.5015	-5.29
250919_at	putative protein myosin heavy cha	---	AT5G03660	1.18	0.24	1.72	0.1306852	0.5015	-5.29
266496_at	putative zinc finger protein	---	---	-1.16	-0.21	-1.72	0.13074576	0.5016	-5.29
265791_at	putative transcription factor	MEE65	AT2G01280	-1.17	-0.23	-1.72	0.13076725	0.5016	-5.29
250988_at	putative protein thyroid receptor in	UPL4	AT5G02880	1.12	0.17	1.72	0.13089911	0.5020	-5.29

250990_at	serine/threonine-specific protein ki	NAK	AT5G02290	1.30	0.38	1.72	0.13094428	0.5021	-5.29
263118_at	putative 3-methylcrotonyl-CoA car	MCCA	AT1G03090	1.41	0.50	1.72	0.1309989	0.5022	-5.29
260606_at	putative splicing factor	---	AT2G43770	1.23	0.30	1.72	0.1310746	0.5024	-5.29
260930_at	GTP-binding protein Sar1, putativ	---	AT1G02620	1.32	0.40	1.72	0.13131493	0.5030	-5.29
251177_at	cyclophylin -like protein CDC28/c	---	AT3G63400	1.18	0.24	1.72	0.13127917	0.5030	-5.29
262761_at	unknown protein ESTs gb|AA395	---	AT1G10720	-1.22	-0.28	-1.72	0.1313096	0.5030	-5.29
264002_at	putative DnaJ protein ;supported b	---	AT2G22360	-1.20	-0.27	-1.72	0.13127245	0.5030	-5.29
258085_at	unknown protein ; supported by cl	---	AT3G26100	-1.17	-0.23	-1.72	0.13141413	0.5030	-5.29
258034_at	hypothetical protein predicted by g	---	AT3G21300	1.39	0.48	1.72	0.13139998	0.5030	-5.29
246599_at	putative protein ATP-dependent R	---	AT5G14900	-1.12	-0.16	-1.72	0.13137224	0.5030	-5.29
250849_at	putative protein NAC2, Arabidopsi	NAC2	AT5G04410	-1.14	-0.19	-1.72	0.13139847	0.5030	-5.29
263189_at	hypothetical protein similar to hypo	---	AT1G36100	1.13	0.18	1.72	0.13143591	0.5030	-5.29
267312_at	unknown protein	---	AT2G34750	1.20	0.26	1.72	0.13149177	0.5032	-5.30
259305_at	unknown protein ;supported by ful	---	AT3G05070	1.15	0.20	1.72	0.1315186	0.5032	-5.30
256901_at	hypothetical protein contains simila	---	---	-1.11	-0.15	-1.72	0.1315654	0.5033	-5.30
251743_at	Yippee-like protein Yippee protein	---	AT3G55890	1.36	0.44	1.72	0.13164593	0.5033	-5.30
266494_at	putative receptor-like protein kinas	PRK2A	AT2G07040	-1.14	-0.18	-1.72	0.13162091	0.5033	-5.30
264193_at	CRK1 protein, putative similar to C	---	AT1G54610	-1.12	-0.16	-1.72	0.13165564	0.5033	-5.30
248221_at	vacuolar sorting protein-like; embr	VPS26A	AT5G53530	1.12	0.16	1.72	0.13160764	0.5033	-5.30
255962_at	glycine-rich RNA-binding protein,	---	AT1G22330	-1.65	-0.72	-1.71	0.13193899	0.5035	-5.30
253674_at	UDP-N-acetylglucosamine O-acyl	---	AT4G29540	1.15	0.20	1.71	0.1318044	0.5035	-5.30
245454_at	disease resistance RPP5 like prote	---	AT4G16920	1.12	0.16	1.71	0.13186583	0.5035	-5.30
265010_at	T-complex chaperonin protein , ep	---	AT1G24510	1.23	0.30	1.72	0.13174303	0.5035	-5.30
261749_at	dehydrin, putative similar to dehyd	ERD14	AT1G76180	1.14	0.19	1.71	0.13181144	0.5035	-5.30
249509_at	strong similarity to unknown protei	---	AT5G38390	-1.11	-0.16	-1.71	0.13193592	0.5035	-5.30
255828_at	hypothetical protein predicted by g	---	AT2G40630	1.13	0.17	1.71	0.13190548	0.5035	-5.30
256153_at	ubiquitin-like (UBQ12), putative si	UBQ12	AT1G55060	-1.17	-0.23	-1.71	0.13190373	0.5035	-5.30
259842_at	phosphoethanolamine N-methyltra	CPuORF32	AT1G73600 /	-2.72	-1.44	-1.71	0.13178127	0.5035	-5.30
263153_s_at	myrosinase-associated protein, pu	---	AT1G54000 /	-1.37	-0.46	-1.71	0.13192849	0.5035	-5.30
253540_at	putative protein various predicted	---	AT4G31615	-1.14	-0.18	-1.71	0.13197305	0.5036	-5.30
258079_at	hypothetical protein predicted by g	---	AT3G25940	1.15	0.20	1.71	0.13204559	0.5036	-5.30
260374_at	unknown protein	TAF2	AT1G73960	-1.14	-0.19	-1.71	0.13201884	0.5036	-5.30
251696_at	putative protein	---	---	-1.18	-0.24	-1.71	0.13202376	0.5036	-5.30
254262_at	putative protein annexin VII, Dicty	---	AT4G23470	1.19	0.25	1.71	0.13211657	0.5038	-5.30
245748_at	unknown protein contains similarity	---	AT1G51140	-1.31	-0.39	-1.71	0.13218839	0.5040	-5.30

248095_at	putative protein strong similarity to	ATMAP65-	AT5G55230	1.20	0.27	1.71	0.13221778	0.5040	-5.30
258076_at	50S ribosomal protein L15, chloro	RPL15	AT3G25920	1.22	0.28	1.71	0.13236337	0.5044	-5.30
247513_at	quinone oxidoreductase - like prot	---	AT5G61510	1.21	0.28	1.71	0.13237167	0.5044	-5.30
249764_at	septum site-determining MinD (dbj	MIND	AT5G24020	1.19	0.25	1.71	0.13244623	0.5046	-5.30
251630_at	putative protein unknown protein -	---	AT3G57420	1.13	0.17	1.71	0.13255666	0.5048	-5.30
262722_at	sterol glucosyltransferase, putativ	---	AT1G43620	-1.13	-0.18	-1.71	0.13253595	0.5048	-5.30
265115_at	rho GDP-dissociation inhibitor, pu	---	AT1G62450	-1.14	-0.19	-1.71	0.13251386	0.5048	-5.30
258903_at	hypothetical protein similar to zinc	---	AT3G06410	1.23	0.30	1.71	0.13264133	0.5050	-5.30
257844_at	prolyl 4-hydroxylase, putative simi	---	AT3G28480	1.21	0.27	1.71	0.13273893	0.5053	-5.30
249224_at	mitochondrial carrier protein-like	---	AT5G42130	1.12	0.16	1.71	0.13275448	0.5053	-5.30
250278_at	2-oxoglutarate/malate translocato	DiT1	AT5G12860	1.27	0.35	1.71	0.1328616	0.5056	-5.31
246655_at	hypothetical protein	---	AT5G35230	-1.14	-0.19	-1.71	0.13296561	0.5059	-5.31
255513_at	PROLIFERA similar to S. cerevisia	PRL	AT4G02060	1.76	0.81	1.71	0.13299715	0.5059	-5.31
257093_at	hypothetical protein ;supported by	---	AT3G20570	1.26	0.34	1.71	0.13332493	0.5061	-5.31
264169_at	hypothetical protein predicted by g	---	AT1G02020	1.10	0.14	1.71	0.13335933	0.5061	-5.31
267044_at	nodulin-like protein	---	AT2G34357	1.27	0.35	1.71	0.13308474	0.5061	-5.31
251059_at	serine/threonine protein kinase AT	CIPK15	AT5G01810	1.45	0.54	1.71	0.13336164	0.5061	-5.31
255704_at	putative proline-rich protein ;suppo	---	AT4G00170	-1.12	-0.16	-1.71	0.13326778	0.5061	-5.31
256256_at	unknown protein ; supported by ful	---	AT3G11230	1.15	0.20	1.71	0.13328228	0.5061	-5.31
256241_at	nascent polypeptide associated co	---	AT3G12390	1.28	0.36	1.71	0.13330332	0.5061	-5.31
265202_at	unknown protein	AT2G3681(	---	-1.15	-0.21	-1.71	0.13323779	0.5061	-5.31
256257_at	arginine-tRNA-protein transferase	ATE2	AT3G11240	1.13	0.17	1.71	0.13332642	0.5061	-5.31
266247_at	hypothetical protein predicted by g	---	AT2G27660	-1.19	-0.25	-1.71	0.13309578	0.5061	-5.31
256962_at	glucan endo-1,3-beta-glucosidase	---	AT3G13560	1.44	0.53	1.71	0.13319707	0.5061	-5.31
253839_at	putative protein prolactin-induced	---	AT4G27890	-1.16	-0.22	-1.71	0.13322076	0.5061	-5.31
263418_at	putative selenium-binding protein	---	AT2G17210	-1.14	-0.19	-1.71	0.1330709	0.5061	-5.31
266821_at	putative ethylene response elemer	ERF13	AT2G44840	-2.03	-1.02	-1.71	0.13330383	0.5061	-5.31
266803_at	putative protein kinase contains a	APK1B	AT2G28930	1.37	0.46	1.71	0.13315312	0.5061	-5.31
259695_at	hypothetical protein predicted by g	---	AT1G63170	-1.17	-0.23	-1.71	0.13347216	0.5064	-5.31
250485_at	Expressed protein ; supported by f	PROPEP5	AT5G09990	-1.28	-0.35	-1.71	0.13349807	0.5064	-5.31
245498_at	hypothetical protein	---	AT4G16470	-1.13	-0.17	-1.71	0.13355148	0.5065	-5.31
261732_at	hypothetical protein predicted by g	---	AT1G47770	-1.15	-0.20	-1.71	0.13358564	0.5066	-5.31
251818_at	vacuolar protein sorting protein 33	ATVPS33	AT3G54860	1.15	0.20	1.71	0.13363732	0.5066	-5.31
252982_at	Histone deacetylase ; supported b	HD1	AT4G38130	1.15	0.20	1.71	0.13364164	0.5066	-5.31
266780_at	putative ligand-gated ion channel p	ATGLR2.8	AT2G29110	-1.24	-0.31	-1.70	0.13372757	0.5067	-5.31

260189_at	putative urease similar to urease G	URE	AT1G67550	1.17	0.23	1.70	0.1337233	0.5067	-5.31
262688_at	PPR-repeat protein contains multip	---	AT1G62680	-1.13	-0.18	-1.70	0.13371336	0.5067	-5.31
260909_at	hypothetical protein predicted by g	---	AT1G02670	1.17	0.22	1.70	0.1337394	0.5067	-5.31
256974_at	unknown protein similar to putative	---	---	-1.12	-0.17	-1.70	0.13380428	0.5068	-5.31
246039_at	putative protein serine-arginine-ric	---	AT5G19480	-1.13	-0.18	-1.70	0.13383043	0.5068	-5.31
259584_at	hypothetical protein predicted by g	---	AT1G28080	-1.12	-0.17	-1.70	0.13391884	0.5070	-5.31
251115_at	putative protein symplekin - Homo	ESP4	AT5G01400	1.15	0.20	1.70	0.13391205	0.5070	-5.31
258930_at	unknown protein predicted by gen	---	AT3G10040	-1.14	-0.19	-1.70	0.13398436	0.5072	-5.31
258065_at	putative pyruvate kinase similar to	---	AT3G25960	-1.17	-0.22	-1.70	0.13402389	0.5072	-5.31
265396_at	predicted protein	---	AT2G21040	-1.22	-0.29	-1.70	0.13409156	0.5073	-5.31
261349_at	Expressed protein ; supported by f	AT1G7961(	---	1.12	0.17	1.70	0.13407472	0.5073	-5.31
251703_at	putative protein hypothetical protei	---	AT3G56670	-1.20	-0.26	-1.70	0.13421427	0.5077	-5.31
259961_at	auxin-induced protein kinase, puta	WAG1	AT1G53700	-1.16	-0.21	-1.70	0.1342523	0.5077	-5.31
260962_at	pectin methylesterase, putative sir	PME7	AT1G44980	1.15	0.20	1.70	0.13424992	0.5077	-5.31
262648_at	putative ribulose-1,5 bisphosphate	---	AT1G14030	1.14	0.19	1.70	0.1343324	0.5078	-5.32
252321_at	hypothetical protein ;supported by	---	AT3G48510	-1.16	-0.21	-1.70	0.13433219	0.5078	-5.32
259181_at	unknown protein similar to putative	---	AT3G01690	-1.21	-0.27	-1.70	0.13441528	0.5080	-5.32
250427_at	putative protein myosin heavy cha	---	AT5G10500	-1.12	-0.17	-1.70	0.13442098	0.5080	-5.32
258226_at	putative phospholipase D similar t	PLDALPHA	AT3G15730	-1.15	-0.20	-1.70	0.13464957	0.5085	-5.32
264240_at	protein kinase, putative Simisimila	---	AT1G54820	-1.73	-0.79	-1.70	0.13461963	0.5085	-5.32
260769_at	Expressed protein ; supported by f	---	AT1G49010	1.27	0.35	1.70	0.13461329	0.5085	-5.32
252957_at	glycine-rich protein 2 (GRP2) ; sup	GRP2	AT4G38680	-1.30	-0.38	-1.70	0.13465131	0.5085	-5.32
256890_at	glycine-rich RNA binding protein,	GRP4	AT3G23830	1.35	0.43	1.70	0.13476367	0.5086	-5.32
245413_at	asparagine--tRNA ligase	NS1	AT4G17300	1.14	0.19	1.70	0.13473211	0.5086	-5.32
264651_at	putative histone H2A Strong simila	H2AXA	AT1G08880	1.27	0.34	1.70	0.13474712	0.5086	-5.32
262615_at	initiation factor 5A-4 identical to ini	ELF5A-1	AT1G13950	1.18	0.24	1.70	0.1347304	0.5086	-5.32
246509_at	valine--tRNA ligase-like protein se	EMB2247	AT5G16715	1.25	0.33	1.70	0.13478901	0.5086	-5.32
256075_at	mitogen-activated protein kinase,	ATMPK8	AT1G18150	-1.18	-0.24	-1.70	0.13488827	0.5089	-5.32
252332_at	putative protein	---	AT3G48810	-1.21	-0.27	-1.70	0.13493285	0.5090	-5.32
258625_at	hypothetical protein predicted by g	PDLP4	AT3G04370	-1.14	-0.19	-1.70	0.135052	0.5093	-5.32
258265_at	putative beta-1,3-glucanase precu	---	AT3G15800	-1.15	-0.21	-1.70	0.13511651	0.5095	-5.32
264422_at	unknown protein similar to unknow	LCV2	AT1G43130	1.15	0.20	1.70	0.13514065	0.5095	-5.32
256891_at	hypothetical protein contains simila	---	AT3G19030	1.20	0.26	1.70	0.13518385	0.5095	-5.32
266138_at	unknown protein ; supported by fu	---	AT2G28060	1.16	0.21	1.70	0.13518929	0.5095	-5.32
248999_at	putative protein contains similarity	---	AT5G44970	-1.13	-0.17	-1.70	0.13526961	0.5097	-5.32

254135_at	putative protein MSP1 protein, Sa	---	AT4G24860	-1.15	-0.20	-1.70	0.13526873	0.5097	-5.32
246358_x_at	hypothetical protein	---	AT2G06570	-1.15	-0.20	-1.70	0.13530444	0.5097	-5.32
256937_at	hypothetical protein predicted by g	---	AT3G22620	2.49	1.32	1.70	0.13532775	0.5097	-5.32
256713_at	putative peroxidase	---	AT2G34060	1.26	0.33	1.70	0.13542891	0.5098	-5.32
260413_at	hypothetical protein predicted by g	---	AT1G69800	1.21	0.27	1.70	0.13540143	0.5098	-5.32
245771_at	hypothetical protein predicted by g	---	AT1G30250	2.05	1.03	1.70	0.1354417	0.5098	-5.32
262186_at	hypothetical protein	---	AT1G77960	-1.34	-0.42	-1.70	0.13539518	0.5098	-5.32
266746_s_at	putative glutathione S-transferase	ATGSTF3	AT2G02930 /	1.80	0.85	1.70	0.13556838	0.5099	-5.32
258149_at	hypothetical protein contains Pfam	EMB1270	AT3G18110	1.18	0.24	1.70	0.13554561	0.5099	-5.32
260002_at	putative ABC transporter similar to	ATNAP3	AT1G67940	1.25	0.32	1.70	0.13549895	0.5099	-5.32
259007_at	putative MYB family transcription f	MYB3R-3	AT3G09370	-1.19	-0.25	-1.70	0.13555604	0.5099	-5.32
246642_s_at	putative protein predicted proteins	---	---	-1.11	-0.15	-1.70	0.13550977	0.5099	-5.32
252950_at	putative protein phospholipase C (	---	AT4G38690	-1.36	-0.44	-1.69	0.13563386	0.5099	-5.32
261199_at	unknown protein	---	AT1G12950	-1.12	-0.16	-1.69	0.13568045	0.5099	-5.32
259416_at	Expressed protein ; supported by c	---	AT1G02305	1.19	0.25	1.70	0.13561885	0.5099	-5.32
263956_at	putative homeodomain transcriptio	BLH1	AT2G35940	-1.28	-0.35	-1.69	0.13569923	0.5099	-5.32
256363_at	unknown protein ; supported by cD	---	AT1G66510	-1.29	-0.37	-1.69	0.13568876	0.5099	-5.32
250414_at	putative protein Glr5, Arabidopsis	GLR2.6	AT5G11180	-1.13	-0.17	-1.69	0.13576158	0.5101	-5.33
263456_at	unknown protein	---	AT2G22125	1.20	0.27	1.69	0.13580638	0.5102	-5.33
253225_at	Rho1Ps homolog Rac-like protein	ARAC3	AT4G35020	1.17	0.22	1.69	0.13593333	0.5106	-5.33
245818_at	cytochrome b561, putative similar	---	AT1G26100	-1.29	-0.37	-1.69	0.13596217	0.5106	-5.33
247441_at	receptor - like protein kinase - like	---	AT5G62710	1.16	0.22	1.69	0.13600366	0.5107	-5.33
259391_s_at	delta 9 desaturase, putative simila	---	AT1G06350 /	-1.15	-0.20	-1.69	0.13603118	0.5107	-5.33
248699_at	putative protein similar to unknown	ATZIP4	AT5G48390	-1.20	-0.26	-1.69	0.13605523	0.5107	-5.33
256445_at	hypothetical protein predicted by g	---	AT3G11160	-1.15	-0.21	-1.69	0.13614253	0.5109	-5.33
264118_at	unknown protein	---	AT1G79150	-1.36	-0.45	-1.69	0.13621345	0.5111	-5.33
265861_at	hypothetical protein predicted by g	---	AT2G01790	-1.15	-0.20	-1.69	0.13624338	0.5111	-5.33
260563_at	putative glucosyltransferase	UGT74F1	AT2G43840	-1.17	-0.23	-1.69	0.13623176	0.5111	-5.33
258466_at	hypothetical protein contains simil	---	AT3G06040	1.17	0.23	1.69	0.13638029	0.5115	-5.33
263063_s_at	putative peroxidase	---	AT2G18140 /	-1.24	-0.31	-1.69	0.1364077	0.5115	-5.33
264880_at	hypothetical protein contains simila	---	AT1G61210	-1.17	-0.23	-1.69	0.13645035	0.5116	-5.33
246165_at	putative protein	---	---	-1.12	-0.16	-1.69	0.13654031	0.5117	-5.33
264577_at	putative peroxidase Strong similari	RCI3	AT1G05260	-1.12	-0.17	-1.69	0.13653284	0.5117	-5.33
266768_s_at	ubiquitin extension protein (UBQ6)	UBQ6	AT2G47110 /	1.23	0.30	1.69	0.13660225	0.5118	-5.33
253161_at	senescence-associated protein se	SEN1	AT4G35770	1.43	0.52	1.69	0.13660948	0.5118	-5.33

256341_at	deoxyguanosine kinase, putative s	---	AT1G72040	-1.30	-0.37	-1.69	0.13658406	0.5118	-5.33
264582_at	putative ovule-specific homeotic pr	HDG2	AT1G05230	-1.14	-0.19	-1.69	0.13670068	0.5120	-5.33
258121_s_at	putative geranylgeranyl pyrophosp	GGPS3	AT3G14530	-1.17	-0.23	-1.69	0.13672373	0.5120	-5.33
265027_at	putative ribonuclease III similar to I	NFD2	AT1G24450	1.19	0.25	1.69	0.1367991	0.5122	-5.33
245156_at	calcium-dependent protein kinase	CPK7	AT5G12480	1.15	0.20	1.69	0.13688288	0.5124	-5.33
263913_at	putative receptor-like protein kinas	---	AT2G36570	-1.25	-0.33	-1.69	0.13695337	0.5126	-5.33
261174_at	26S proteasome regulatory subun	---	AT1G04810	1.17	0.23	1.69	0.13701504	0.5128	-5.33
261649_at	putative clathrin-coat assembly pro	---	AT1G27700	-1.14	-0.19	-1.69	0.13709527	0.5128	-5.33
244957_at	hypothetical protein	AT2G07835	---	-1.15	-0.20	-1.69	0.13707614	0.5128	-5.33
258369_at	putative pectin methylesterase sim	ATPME3	AT3G14310	-1.17	-0.22	-1.69	0.13705814	0.5128	-5.33
256644_at	unknown protein similar to hypothe	---	---	-1.13	-0.18	-1.69	0.13716368	0.5129	-5.33
252867_at	putative protein hypothetical prote	---	AT4G39870	-1.17	-0.22	-1.69	0.13714644	0.5129	-5.33
259178_at	unknown protein similar to hypoth	RGLG1	AT3G01650	1.19	0.25	1.69	0.13719199	0.5129	-5.33
261879_at	cytochrome P450, putative similar	CYP705A2	AT1G50520	-1.13	-0.17	-1.69	0.13726411	0.5130	-5.34
250980_at	putative protein	---	AT5G03130	1.36	0.44	1.69	0.13725795	0.5130	-5.34
256261_at	ras-related GTP-binding protein co	RABA4D	AT3G12160	-1.14	-0.19	-1.69	0.13745374	0.5132	-5.34
264593_at	putative GTP-binding protein ; sup	ARAC1	AT2G17800	-1.15	-0.20	-1.69	0.13736941	0.5132	-5.34
246279_at	homeodomain protein	ATHB40	AT4G36740	-1.20	-0.27	-1.69	0.13744018	0.5132	-5.34
254921_at	putative protein hypothetical prote	---	AT4G11300	1.23	0.30	1.69	0.13736348	0.5132	-5.34
251409_at	Expressed protein ; supported by f	---	AT3G60245	1.40	0.48	1.69	0.13743807	0.5132	-5.34
248623_at	putative protein similar to unknown	---	AT5G49170	1.56	0.65	1.69	0.13746072	0.5132	-5.34
259061_at	putative GTP-binding protein simil	AtRABA5b	AT3G07410	1.31	0.39	1.69	0.13746272	0.5132	-5.34
257234_at	hypothetical protein predicted by g	---	AT3G14880	-1.19	-0.26	-1.69	0.13753913	0.5134	-5.34
244982_at	ribosomal protein L14	---	---	-1.17	-0.23	-1.68	0.1376098	0.5134	-5.34
245362_at	homeobox-leucine zipper protein H	HAT1	AT4G17460	-1.21	-0.28	-1.68	0.13767404	0.5134	-5.34
261513_at	unknown protein contains Pfam pr	---	AT1G71840	-1.16	-0.22	-1.68	0.13768018	0.5134	-5.34
266738_at	unknown protein predicted by gene	---	AT2G47010	-1.21	-0.28	-1.68	0.13762152	0.5134	-5.34
246181_at	pectinesterase - like protein proba	---	AT5G20860	-1.12	-0.16	-1.68	0.13764993	0.5134	-5.34
248729_at	cycloartenol synthase	THAS1	AT5G48010	-1.11	-0.16	-1.68	0.13762771	0.5134	-5.34
252794_at	putative protein predicted proteins	---	---	-1.12	-0.16	-1.68	0.13776977	0.5137	-5.34
254667_at	glycine-rich cell wall protein-like gl	---	AT4G18280	-1.31	-0.39	-1.68	0.13798336	0.5137	-5.34
245323_at	cysteine proteinase inhibitor like pr	---	AT4G16500	-1.19	-0.25	-1.68	0.13794829	0.5137	-5.34
246838_at	flap endonuclease - like protein O	---	AT5G26680	1.15	0.20	1.68	0.13796786	0.5137	-5.34
253270_at	cyclin delta-3	CYCD3;1	AT4G34160	1.22	0.29	1.68	0.1378696	0.5137	-5.34
247158_at	branched-chain amino acid aminot	ATBCAT-5	AT5G65780	1.13	0.18	1.68	0.13790185	0.5137	-5.34

258012_at	unknown protein similar to GB:CAE	---	AT3G19310	-1.11	-0.15	-1.68	0.13787456	0.5137	-5.34
253967_at	putative protein probable membra	---	AT4G26550	1.22	0.29	1.68	0.13800037	0.5137	-5.34
265255_at	unknown protein ; supported by cl	---	AT2G28420	-1.26	-0.33	-1.68	0.13795781	0.5137	-5.34
256487_at	disease resistance gene, putative	---	AT1G31540	-1.20	-0.27	-1.68	0.13786732	0.5137	-5.34
252896_at	cytochrome P450 - like protein cyt	CYP96A9	AT4G39480	-1.13	-0.17	-1.68	0.13794416	0.5137	-5.34
257097_at	hypothetical protein predicted by g	---	---	-1.12	-0.17	-1.68	0.13804715	0.5137	-5.34
263395_at	putative mitochondrial inner memb	ATTIM44-1	AT2G20500 /	-1.13	-0.18	-1.68	0.13803849	0.5137	-5.34
253173_at	putative protein pEARLI 4, Arabid	---	AT4G35110	-1.49	-0.58	-1.68	0.1381354	0.5139	-5.34
253360_at	aminopeptidase- like protein amin	APM1	AT4G33090	1.16	0.22	1.68	0.13816546	0.5140	-5.34
266188_at	unknown protein	---	AT2G39000	1.17	0.22	1.68	0.13830097	0.5140	-5.34
249501_s_at	expansin-like protein expansin - P	ATEXP26	AT5G39270 /	-1.11	-0.16	-1.68	0.13827149	0.5140	-5.34
252086_at	hypothetical protein	---	AT3G52030	-1.15	-0.20	-1.68	0.13826027	0.5140	-5.34
264844_at	putative glycosylation enzyme ; su	---	AT1G03520	1.19	0.26	1.68	0.13823571	0.5140	-5.34
266196_at	putative protein kinase contains a	---	AT2G39110	-1.14	-0.19	-1.68	0.13828641	0.5140	-5.34
248678_at	U6 snRNA-associated Sm-like pro	SAD1	AT5G48870	1.16	0.21	1.68	0.13836262	0.5142	-5.34
258357_at	putative leucine-rich repeat transm	SRF7	AT3G14350	-1.27	-0.35	-1.68	0.13840839	0.5143	-5.34
250656_at	putative protein contains similarity	---	AT5G06970	1.21	0.27	1.68	0.13853601	0.5143	-5.34
251522_at	hypothetical protein	---	AT3G59430	-1.16	-0.21	-1.68	0.13844446	0.5143	-5.34
248264_at	putative protein similar to unknown	---	AT5G53310	1.16	0.21	1.68	0.13850687	0.5143	-5.34
265024_at	Expressed protein ; supported by f	---	AT1G24600	1.33	0.41	1.68	0.13851434	0.5143	-5.34
266885_at	putative small GTP-binding protein	RAB6A	AT2G44610	1.17	0.22	1.68	0.13845944	0.5143	-5.34
246137_at	putative protein predicted proteins	LSH1	AT5G28490	-1.42	-0.50	-1.68	0.13854188	0.5143	-5.34
254533_at	putative protein ARI protein - Dros	---	AT4G19670	-1.22	-0.29	-1.68	0.13860978	0.5144	-5.34
252951_at	disease resistance response like p	---	AT4G38700	-1.25	-0.32	-1.68	0.13870556	0.5144	-5.35
248928_at	Rac-like gtp binding protein ARAC	ARAC2	AT5G45970	-1.11	-0.14	-1.68	0.13874594	0.5144	-5.35
252229_at	putative protein lea32, Arabidopsi	---	AT3G49890	-1.18	-0.24	-1.68	0.13863356	0.5144	-5.34
255871_at	putative small nuclear ribonucleop	U2B"	AT2G30260	1.16	0.21	1.68	0.13874481	0.5144	-5.35
260301_at	hypothetical protein ;supported by	---	AT1G80290	1.16	0.22	1.68	0.13872813	0.5144	-5.35
260357_at	unknown protein ;supported by full	AFP1	AT1G69260	-1.19	-0.25	-1.68	0.13866512	0.5144	-5.34
250827_at	cellulose synthase catalytic subuni	CEV1	AT5G05170	1.21	0.27	1.68	0.1389264	0.5146	-5.35
261069_at	small G protein, putative similar to	ATRABA2B	AT1G07410	-1.12	-0.16	-1.68	0.13892423	0.5146	-5.35
263076_at	putative protein kinase/endoribonu	IRE1A	AT2G17520	-1.14	-0.19	-1.68	0.13888853	0.5146	-5.35
246002_at	ripening-related protein - like grip2	---	AT5G20740	1.34	0.42	1.68	0.13888587	0.5146	-5.35
262718_at	hypothetical protein similar to puta	---	---	-1.14	-0.20	-1.68	0.13887747	0.5146	-5.35
262725_at	hypothetical protein predicted by g	---	AT1G43580	1.28	0.36	1.68	0.13883681	0.5146	-5.35

246322_at	S-locus protein, putative similar to	---	AT1G16680	1.13	0.18	1.68	0.13897161	0.5147	-5.35
264099_at	replicase, putative similar to replic	---	AT1G79050	1.15	0.20	1.68	0.13910332	0.5151	-5.35
251089_at	heat shock protein 40-like heat sh	---	AT5G01390	1.13	0.18	1.68	0.13913618	0.5151	-5.35
263549_at	unknown protein	MEE3	AT2G21650	1.76	0.82	1.68	0.1391542	0.5151	-5.35
252787_at	putative protein several En/Spm-lik	---	---	-1.11	-0.14	-1.68	0.13920959	0.5152	-5.35
260150_at	putative oxidoreductase similar to	---	AT1G52820	-1.16	-0.21	-1.68	0.13928868	0.5154	-5.35
266056_at	hypothetical protein predicted by g	ATATG18C	AT2G40810	-1.12	-0.17	-1.68	0.13927841	0.5154	-5.35
254503_at	hypothetical protein ;supported by	PTAC9	AT4G20010	1.16	0.21	1.68	0.139353	0.5154	-5.35
255683_at	putative malate oxidoreductase	---	AT4G00570	-1.17	-0.22	-1.68	0.13938407	0.5154	-5.35
261408_s_at	histone H4 identical to GB:M3665	---	AT1G07660	1.20	0.27	1.68	0.139376	0.5154	-5.35
246695_at	putative protein	---	---	-1.19	-0.25	-1.68	0.13938159	0.5154	-5.35
265506_at	putative non-LTR retroelement rev	---	---	-1.17	-0.23	-1.68	0.13945288	0.5155	-5.35
259063_at	putative 5B-anther specific protein	---	AT3G07450	1.11	0.15	1.67	0.13958664	0.5156	-5.35
245568_at	hypothetical protein	---	AT4G14650	-1.20	-0.26	-1.68	0.13955705	0.5156	-5.35
250732_at	putative protein contains similarity	---	AT5G06480	1.27	0.34	1.68	0.13950508	0.5156	-5.35
262423_at	hypothetical protein predicted by g	---	AT1G23450	-1.13	-0.18	-1.67	0.1395801	0.5156	-5.35
253279_at	putative protein B subunit of propi	MCCB	AT4G34030	1.30	0.37	1.68	0.13952648	0.5156	-5.35
262173_at	betaine aldehyde dehydrogenase,	ALDH10A8	AT1G74920	-1.15	-0.21	-1.67	0.13965259	0.5157	-5.35
251726_at	protein kinase NPK1-related prote	---	AT3G56280	1.11	0.14	1.67	0.13966829	0.5157	-5.35
257749_at	actin 2 identical to GB:AAB37098	ACT2	AT3G18780	1.13	0.17	1.67	0.13965581	0.5157	-5.35
248442_at	DEAD-box protein abstrakt	---	AT5G51280	1.17	0.23	1.67	0.13985459	0.5162	-5.35
246905_at	putative protein ;supported by full-	---	AT5G25570	-1.32	-0.40	-1.67	0.13983743	0.5162	-5.35
252673_at	CCR4-associated factor 1-like pro	---	AT3G44240	-1.14	-0.19	-1.67	0.13988865	0.5162	-5.35
249579_at	ADP-ribosylation factor - like prote	ATARLA1A	AT5G37680	1.14	0.19	1.67	0.14003944	0.5165	-5.35
266942_at	putative ATP binding protein	TXND9	AT2G18990	1.24	0.31	1.67	0.14007678	0.5165	-5.35
264168_at	unknown protein Similar to yeast g	---	AT1G02080	1.15	0.21	1.67	0.14005909	0.5165	-5.35
263196_at	hypothetical protein predicted by g	---	AT1G36070	1.24	0.31	1.67	0.14005945	0.5165	-5.35
248541_at	protein kinase ATN1-like protein	---	AT5G50180	1.20	0.27	1.67	0.14007228	0.5165	-5.35
250755_at	DnaJ-like protein ; supported by c	---	AT5G05750	1.18	0.24	1.67	0.14009806	0.5165	-5.35
259770_s_at	phosphoribosylanthranilate isome	PAI3	AT1G07780	1.24	0.31	1.67	0.14015683	0.5166	-5.35
250604_at	putative protein heparanase precu	PIP1B	AT2G45960	1.23	0.30	1.67	0.14023109	0.5167	-5.36
263125_at	hypothetical protein predicted by g	---	AT1G78470	-1.14	-0.19	-1.67	0.14020364	0.5167	-5.35
259785_at	unknown protein ;supported by full	---	AT1G29490	1.17	0.23	1.67	0.14023394	0.5167	-5.36
264078_at	putative beta-galactosidase	BGAL8	AT2G28470	-1.58	-0.66	-1.67	0.14044999	0.5168	-5.36
260407_at	putative protein kinase Pfam HMM	---	AT1G69910	-1.12	-0.16	-1.67	0.14056911	0.5168	-5.36

259605_at	unknown protein	PUB45	AT1G27910	-1.27	-0.35	-1.67	0.14039968	0.5168	-5.36
258011_at	putative homeobox protein, HAT3	HAT3.1	AT3G19510	1.19	0.25	1.67	0.14058494	0.5168	-5.36
246837_at	pectin acetylesterase precursor - l	---	AT5G26670	-1.26	-0.34	-1.67	0.14054401	0.5168	-5.36
253734_at	putative serine/threonine-specific	---	AT4G29180	-1.15	-0.20	-1.67	0.14054954	0.5168	-5.36
254557_at	hypothetical protein ;supported by	---	AT4G19140	-1.30	-0.38	-1.67	0.14060508	0.5168	-5.36
263644_at	hypothetical protein predicted by g	---	AT2G04730	-1.14	-0.19	-1.67	0.14037387	0.5168	-5.36
252329_at	putative protein several hypothetic	---	AT3G48760	-1.12	-0.17	-1.67	0.14056051	0.5168	-5.36
256795_at	20S proteasome subunit PAC1 ide	PAC1	AT3G22110	1.12	0.16	1.67	0.14054114	0.5168	-5.36
251553_at	DNA-binding WRKY - like protein	WRKY69	AT3G58710	-1.18	-0.24	-1.67	0.14035769	0.5168	-5.36
253328_at	putative protein ABC-type transpo	ATNAP13	AT4G33460	-1.14	-0.19	-1.67	0.14055283	0.5168	-5.36
250948_at	putative protein	---	AT5G03490	-1.25	-0.32	-1.67	0.1402993	0.5168	-5.36
259658_at	hypothetical protein predicted by g	NDF5	AT1G55370	1.22	0.28	1.67	0.14061301	0.5168	-5.36
247332_at	unknown protein ; supported by cl	---	AT5G63440	-1.18	-0.24	-1.67	0.14048948	0.5168	-5.36
247268_at	putative protein contains similarity	---	AT5G64080	-1.19	-0.25	-1.67	0.14068827	0.5170	-5.36
246400_at	hypothetical protein contains simila	---	AT1G57540	1.12	0.17	1.67	0.1407273	0.5171	-5.36
247284_at	Isp4-like protein ; supported by ful	OPT4	AT5G64410	-1.35	-0.44	-1.67	0.14078117	0.5171	-5.36
247221_at	Expressed protein ; supported by c	LIP1	AT5G64813	1.11	0.15	1.67	0.14084147	0.5171	-5.36
250840_at	putative protein predicted protein,	---	---	-1.20	-0.26	-1.67	0.14084547	0.5171	-5.36
255467_at	putative leucine-rich repeat protei	---	AT4G03010	-1.14	-0.19	-1.67	0.14080941	0.5171	-5.36
265448_at	putative DOF zinc finger protein	DAG2	AT2G46590	1.18	0.24	1.67	0.1408038	0.5171	-5.36
256314_at	hypothetical protein	TOC75-I	AT1G35860	-1.15	-0.20	-1.67	0.14100552	0.5176	-5.36
245168_at	3-ketoacyl-CoA thiolase ;supporte	PKT3	AT2G33150	1.18	0.24	1.67	0.14121838	0.5178	-5.36
266224_at	chloroplast membrane protein (ALI	ALB3	AT2G28800	1.12	0.16	1.67	0.14123305	0.5178	-5.36
264003_at	Expressed protein ; supported by f	GEM	AT2G22475	-1.19	-0.25	-1.67	0.14118711	0.5178	-5.36
249721_at	Expressed protein ; supported by f	LSU4	AT5G24655	-1.11	-0.15	-1.67	0.14119856	0.5178	-5.36
260574_at	hypothetical protein predicted by g	---	AT2G47300	-1.16	-0.21	-1.67	0.14122155	0.5178	-5.36
255355_at	hypothetical protein	---	---	-1.15	-0.20	-1.67	0.1412458	0.5178	-5.36
261650_at	envelope Ca2+-ATPase identical t	ACA1	AT1G27770	1.27	0.35	1.67	0.14125365	0.5178	-5.36
259684_at	unknown protein	---	AT1G63070	-1.14	-0.19	-1.67	0.14111767	0.5178	-5.36
255647_at	Ca2+-transporting ATPase - like pr	ECA2	AT4G00900	1.18	0.24	1.67	0.14137907	0.5180	-5.36
267594_at	hypothetical protein predicted by g	---	AT2G33000	-1.13	-0.18	-1.67	0.14140723	0.5180	-5.36
263179_at	unknown protein similar to unknow	---	AT1G05710	1.29	0.36	1.67	0.14141309	0.5180	-5.36
263003_at	protein phosphatase 2A 72 kDa re	---	AT1G54450	-1.12	-0.16	-1.67	0.14135757	0.5180	-5.36
251921_at	40S ribosomal protein S21 homol	---	AT3G53890	1.38	0.46	1.67	0.14137726	0.5180	-5.36
257071_at	unknown protein ; supported by cl	ATCSLC04	AT3G28180	-1.23	-0.30	-1.67	0.1415563	0.5180	-5.36

261005_at	hypothetical protein similar to retic	---	AT1G26420	1.46	0.55	1.67	0.14155023	0.5180	-5.36
249403_at	putative protein intracellular protei	---	AT5G40270	1.19	0.25	1.67	0.1415426	0.5180	-5.36
263255_at	unknown protein similar to steroid	---	AT1G10490	1.20	0.27	1.67	0.14151461	0.5180	-5.36
262981_at	unknown protein ;supported by full	---	AT1G75590	1.19	0.25	1.66	0.14166344	0.5180	-5.36
264283_at	hypothetical protein contains simila	---	AT1G61850	-1.15	-0.20	-1.66	0.14161497	0.5180	-5.36
264233_at	ribosomal protein, putative similar	---	AT1G67430	1.32	0.40	1.66	0.14161217	0.5180	-5.36
245031_at	putative mitochondrial carrier prote	---	AT2G26360	-1.12	-0.16	-1.66	0.14159918	0.5180	-5.36
262182_at	hypothetical protein predicted by g	---	AT1G77890	-1.14	-0.18	-1.66	0.14166484	0.5180	-5.36
260571_at	MAP kinase (ATMPK6) identical to	ATMPK6	AT2G43790	1.12	0.17	1.67	0.14151087	0.5180	-5.36
253259_at	putative protein ethylene-responsi	RRTF1	AT4G34410	-1.51	-0.60	-1.66	0.14167252	0.5180	-5.36
261914_at	dirigent protein, putative similar to	---	AT1G65870	-1.21	-0.28	-1.66	0.14172055	0.5181	-5.36
259919_at	putative exportin, tRNA (nuclear e	PSD	AT1G72560	1.20	0.26	1.66	0.14177615	0.5182	-5.37
262721_at	thioredoxin, putative similar to thio	Aty2	AT1G43560	1.17	0.23	1.66	0.14181338	0.5182	-5.37
246957_at	unknown protein	---	AT5G24670	-1.11	-0.15	-1.66	0.14180987	0.5182	-5.37
262687_at	PPR-repeat protein contains multip	---	AT1G62670	1.12	0.16	1.66	0.14182254	0.5182	-5.37
253835_at	putative beta-glucosidase beta-glu	BGLU9	AT4G27820	-1.16	-0.22	-1.66	0.14185563	0.5182	-5.37
265357_at	E2, ubiquitin-conjugating enzyme,	UBC29	AT2G16740	-1.21	-0.27	-1.66	0.14196786	0.5185	-5.37
256690_at	hypothetical protein predicted by g	---	AT3G32160	-1.17	-0.23	-1.66	0.14197602	0.5185	-5.37
250556_at	diacylglycerol kinase (ATDGK1) ; s	DGK1	AT5G07920	-1.33	-0.41	-1.66	0.14200445	0.5185	-5.37
251735_at	putative protein ferritin 2 precurso	ATFER3	AT3G56090	1.37	0.45	1.66	0.14204496	0.5185	-5.37
262762_at	phosphoribosyl diphosphate synth	---	AT1G10700	-1.72	-0.78	-1.66	0.14206116	0.5185	-5.37
256376_s_at	unknown protein	PXMT1	AT1G66690	1.52	0.60	1.66	0.14211762	0.5186	-5.37
265596_at	hypothetical protein predicted by g	CAF1	AT2G20020	1.32	0.40	1.66	0.14214394	0.5186	-5.37
262589_s_at	hypothetical protein Strong similari	---	AT1G15150	-1.14	-0.18	-1.66	0.14215741	0.5186	-5.37
253097_at	cytochrome P450-like protein	CYP81D5	AT4G37320	-1.44	-0.52	-1.66	0.14216037	0.5186	-5.37
246853_at	putative protein	---	AT5G26890	-1.13	-0.17	-1.66	0.14233562	0.5191	-5.37
258519_at	unknown protein	---	AT3G06760	-1.18	-0.24	-1.66	0.14243227	0.5193	-5.37
260738_at	hypothetical protein predicted by g	---	AT1G14990	1.13	0.18	1.66	0.14243099	0.5193	-5.37
258565_at	unknown protein ; supported by cl	---	AT3G04350	1.23	0.29	1.66	0.14245633	0.5193	-5.37
245877_at	unknown protein	---	AT1G26220	-1.20	-0.26	-1.66	0.14249179	0.5194	-5.37
265411_at	unknown protein	---	AT2G16630	1.60	0.67	1.66	0.14274292	0.5195	-5.37
259912_at	hypothetical protein	iqd8	AT1G72670	-1.17	-0.23	-1.66	0.142642	0.5195	-5.37
258652_at	putative Ras-like GTP-binding prot	ATRABC2E	AT3G09910	-1.27	-0.35	-1.66	0.14273866	0.5195	-5.37
252396_at	hypothetical protein	---	AT3G47980	1.13	0.17	1.66	0.1425623	0.5195	-5.37
251672_at	MADS-box transcription factor-like	AGL16	AT3G57230	1.13	0.18	1.66	0.14270221	0.5195	-5.37

260075_at	putative integral membrane protein	---	AT1G73700	-1.19	-0.25	-1.66	0.1426342	0.5195	-5.37
257321_at	hypothetical protein	---	---	-1.30	-0.38	-1.66	0.14274225	0.5195	-5.37
260569_at	putative signal recognition particle	---	AT2G43640	1.16	0.21	1.66	0.14265962	0.5195	-5.37
247236_at	putative protein similar to unknown	---	AT5G64590	-1.15	-0.20	-1.66	0.14270159	0.5195	-5.37
247362_at	putative protein strong similarity to	ATPAP29	AT5G63140	1.27	0.34	1.66	0.14273434	0.5195	-5.37
249481_at	frnE protein - like frnE protein, De	---	AT5G38900	1.68	0.75	1.66	0.14286713	0.5198	-5.37
255199_at	coded for by A. thaliana cDNA N64	---	AT4G07390	-1.13	-0.17	-1.66	0.142912	0.5198	-5.37
248964_at	cytochrome P450	CYP707A3	AT5G45340	1.47	0.55	1.66	0.14290652	0.5198	-5.37
248760_at	unknown protein ;supported by ful	---	AT5G47570	1.20	0.26	1.66	0.14297234	0.5199	-5.37
265650_at	hypothetical protein predicted by g	---	AT2G27460	-1.14	-0.19	-1.66	0.14297669	0.5199	-5.37
261887_at	CCR4-associated factor, putative\	---	AT1G80780	1.11	0.16	1.66	0.14306787	0.5201	-5.37
266106_at	putative microtubule-associated pr	ATATG8E	AT2G45170	1.24	0.31	1.66	0.14312777	0.5203	-5.37
267601_at	hypothetical protein predicted by g	---	AT2G32980	1.15	0.20	1.66	0.14340063	0.5209	-5.38
246419_at	UDP glucose:flavonoid 3-o-glucos	UGT78D3	AT5G17030	-1.12	-0.17	-1.66	0.14337013	0.5209	-5.38
266751_at	putative peptide chain release fact	---	AT2G47020	-1.13	-0.18	-1.66	0.14335802	0.5209	-5.38
264161_at	antigen receptor, putative similar t	---	AT1G65420	1.15	0.20	1.66	0.14340154	0.5209	-5.38
258549_at	putative arginine methyltransferase	PRMT4B	AT3G06930	-1.11	-0.15	-1.66	0.14349643	0.5210	-5.38
257757_at	hypothetical protein predicted by g	PGSIP1	AT3G18660	1.13	0.18	1.66	0.1434661	0.5210	-5.38
260147_at	putative oxidoreductase similar to	---	AT1G52790	1.13	0.18	1.66	0.14349647	0.5210	-5.38
250977_at	importin alpha - like protein import	IMPA-9	AT5G03070	-1.16	-0.21	-1.66	0.1434946	0.5210	-5.38
260754_at	unknown protein	---	AT1G49000	1.37	0.45	1.65	0.14362224	0.5212	-5.38
253166_at	putative protein putative ligand-ga	GLUR2	AT4G35290	-1.23	-0.30	-1.66	0.14360347	0.5212	-5.38
259687_at	unknown protein	---	AT1G63110	1.18	0.24	1.65	0.14365612	0.5213	-5.38
263048_s_at	unknown protein ;supported by ful	---	AT2G05310 /	1.17	0.22	1.65	0.14371459	0.5213	-5.38
247821_at	WD-40 repeat protein MSI1 (sp|O2	MSI1	AT5G58230	1.16	0.21	1.65	0.14373607	0.5213	-5.38
253154_at	putative protein predicted protein,	---	AT4G35710	-1.15	-0.21	-1.65	0.14370574	0.5213	-5.38
257034_at	hypothetical protein predicted by g	---	AT3G19184	-1.12	-0.16	-1.65	0.14380096	0.5215	-5.38
253340_s_at	WD-repeat protein -like protein WI	CDC20.2	AT4G33260 /	1.14	0.18	1.65	0.14382714	0.5215	-5.38
251851_at	structural maintenance of chromos	TTN8	AT3G54670	1.15	0.20	1.65	0.14386597	0.5215	-5.38
265467_at	putative receptor-like protein kinas	---	AT2G37050	1.22	0.28	1.65	0.14387508	0.5215	-5.38
257655_at	unknown protein contains Pfam pr	---	AT3G13350	1.32	0.40	1.65	0.14391897	0.5216	-5.38
248251_at	unknown protein	---	AT5G53220	1.13	0.17	1.65	0.14395622	0.5216	-5.38
245288_at	transcriptional adaptor like protein	ADA2B	AT4G16420	-1.14	-0.19	-1.65	0.14414664	0.5220	-5.38
245935_at	hypothetical protein	---	AT5G19840	-1.12	-0.17	-1.65	0.14413182	0.5220	-5.38
255038_at	neutral invertase like protein Dauc	CINV2	AT4G09510	-1.35	-0.43	-1.65	0.14420022	0.5220	-5.38

262690_at	PPR-repeat protein contains multip	---	AT1G62720	-1.13	-0.18	-1.65	0.14420034	0.5220	-5.38
248408_at	ripening-related protein-like	---	AT5G51520	1.12	0.16	1.65	0.14418308	0.5220	-5.38
247964_at	profilin-like protein ; supported by f	PRF3	AT5G56600	-1.22	-0.29	-1.65	0.14413807	0.5220	-5.38
250908_at	GT2 -like protein GT2, Arabidopsi	PTL	AT5G03680	-1.13	-0.18	-1.65	0.14421764	0.5220	-5.38
251744_at	putative protein CHLOROPLAST	---	AT3G56010	1.18	0.23	1.65	0.14426714	0.5221	-5.38
249346_at	amino acid permease	LTH1	AT5G40780	1.18	0.24	1.65	0.14441387	0.5225	-5.38
250057_at	putative protein ; supported by full	---	AT5G17840	1.12	0.16	1.65	0.14445289	0.5226	-5.38
259915_at	unknown protein	---	AT1G72790	-1.39	-0.47	-1.65	0.14483071	0.5229	-5.39
259380_at	putative ABC transporter similar to	PDR1	AT3G16340	-1.17	-0.23	-1.65	0.14480276	0.5229	-5.38
245932_at	3'(2'),5'-bisphosphate nucleotidas	---	AT5G09290	-1.35	-0.43	-1.65	0.14467201	0.5229	-5.38
266040_at	hypothetical protein	---	AT2G07738	-1.12	-0.16	-1.65	0.14456848	0.5229	-5.38
253043_at	putative protein predicted protein,	LBD39	AT4G37540	1.29	0.37	1.65	0.14465103	0.5229	-5.38
257689_at	myb-related protein, putative myb-	AtMYB10	AT3G12820	-1.15	-0.20	-1.65	0.1448007	0.5229	-5.38
245874_at	unknown protein	---	AT1G26250	-1.15	-0.20	-1.65	0.14478486	0.5229	-5.38
248514_s_at	unknown protein	---	AT5G50510	-1.12	-0.17	-1.65	0.1446965	0.5229	-5.38
259615_at	dessication-related protein, putati	---	AT1G47980	-1.17	-0.22	-1.65	0.144797	0.5229	-5.38
267119_at	putative cellulose synthase	ATCSLB01	AT2G32610	-1.11	-0.15	-1.65	0.14468601	0.5229	-5.38
259390_at	hypothetical protein predicted by g	---	AT1G06340	-1.14	-0.19	-1.65	0.1448079	0.5229	-5.38
254950_at	putative protein ;supported by full-	---	AT4G10810	1.11	0.15	1.65	0.14468833	0.5229	-5.38
259385_at	hypothetical protein predicted by g	---	AT1G13470	2.56	1.36	1.65	0.1448253	0.5229	-5.38
256456_at	unknown protein ; supported by ful	---	AT1G75180	-1.28	-0.36	-1.65	0.14520923	0.5232	-5.39
253808_at	predicted proline-rich protein hydr	---	AT4G28300	-1.18	-0.24	-1.65	0.1450374	0.5232	-5.39
266064_at	expressed protein	---	AT2G18780	1.19	0.25	1.65	0.14516221	0.5232	-5.39
249161_at	20S proteasome subunit PAF1 (gb	PAF1	AT5G42790	1.11	0.15	1.65	0.14497568	0.5232	-5.39
250361_at	putative protein various predicted	---	AT5G11370	1.12	0.16	1.65	0.1452071	0.5232	-5.39
264656_at	unknown protein Contains similarit	---	AT1G09010	1.13	0.17	1.65	0.14512455	0.5232	-5.39
260154_at	putative histone H2A similar to hist	HTA9	AT1G52740	1.20	0.27	1.65	0.1451579	0.5232	-5.39
254809_at	putative protein auxin-induced pro	---	AT4G12410	-1.21	-0.28	-1.65	0.14522897	0.5232	-5.39
247588_at	protein disulfide isomerase precur	ATPDIL1-4	AT5G60640	1.14	0.19	1.65	0.14511724	0.5232	-5.39
256596_at	hypothetical protein predicted by g	---	AT3G28540	-1.28	-0.36	-1.65	0.14505059	0.5232	-5.39
267020_at	hypothetical protein predicted by g	---	AT2G39320	-1.15	-0.20	-1.65	0.14512623	0.5232	-5.39
254718_at	putative protein disease resistanc	---	AT4G13580	-1.14	-0.19	-1.65	0.14520928	0.5232	-5.39
264698_at	unknown protein	---	AT1G70200	1.14	0.19	1.65	0.14509103	0.5232	-5.39
265392_at	lipoic acid synthase (LIP1) ; suppo	LIP1	AT2G20860	1.13	0.17	1.65	0.1452641	0.5233	-5.39
265042_at	unknown protein Similar to acid ph	---	AT1G04040	1.50	0.58	1.65	0.14529702	0.5233	-5.39

261313_at	hypothetical protein predicted by g	---	AT1G52970	-1.11	-0.16	-1.65	0.14537516	0.5235	-5.39
251337_at	proteasome component C5 ;suppo	PBF1	AT3G60820	1.11	0.16	1.65	0.14544734	0.5236	-5.39
258885_at	putative uridylate kinase similar to	---	AT3G10030	1.12	0.17	1.65	0.14543288	0.5236	-5.39
252821_at	putative protein ;supported by full-	---	AT4G39860	1.38	0.46	1.65	0.14548308	0.5237	-5.39
250531_at	GTP-binding protein LepA homolo	---	AT5G08650	1.22	0.29	1.65	0.14550978	0.5237	-5.39
260626_at	storage protein, putative similar to	---	AT1G08040	-1.16	-0.21	-1.65	0.14556577	0.5237	-5.39
254707_at	putative protein inositol polyphosp	AT5PTASE	AT4G18010	1.40	0.49	1.65	0.14556857	0.5237	-5.39
259943_at	unknown protein	---	AT1G71480	-1.23	-0.30	-1.65	0.1456016	0.5238	-5.39
252739_at	putative protein mRNA, Homo sap	---	AT3G43250	-1.14	-0.19	-1.65	0.14565096	0.5239	-5.39
252536_at	putative transporter protein peptid	---	AT3G45700	1.17	0.23	1.64	0.14571822	0.5240	-5.39
261796_at	non-phototropic hypocotyl, putativ	---	AT1G30440	1.14	0.19	1.64	0.14595604	0.5242	-5.39
247506_at	Mei2-like protein Mei2-like protein	AML1	AT5G61960	-1.12	-0.16	-1.64	0.14589998	0.5242	-5.39
264389_at	unknown protein similar to hypothe	---	AT1G11960	-1.25	-0.32	-1.64	0.14593911	0.5242	-5.39
253749_at	phytochrome-associated protein P	PAP2	AT4G29080	-1.94	-0.95	-1.64	0.14580837	0.5242	-5.39
263629_at	hypothetical protein predicted by g	---	AT2G04850	-1.24	-0.31	-1.64	0.14595728	0.5242	-5.39
248911_at	tumor-related protein-like	DOG1	AT5G45830	-1.20	-0.26	-1.64	0.14583323	0.5242	-5.39
253795_at	tyrosine transaminase-like protein	---	AT4G28420	-1.15	-0.20	-1.64	0.14584534	0.5242	-5.39
249916_at	histone H2B like protein (emb|CAA	HTB2	AT5G22880	1.23	0.30	1.64	0.14586866	0.5242	-5.39
258495_at	unknown protein ;supported by ful	---	AT3G02690	-1.13	-0.17	-1.64	0.14601282	0.5243	-5.39
266239_at	unknown protein ; supported by c	---	AT2G29530	1.33	0.41	1.64	0.14614252	0.5247	-5.39
256102_at	unknown protein	---	AT1G13680	-1.12	-0.16	-1.64	0.14623668	0.5250	-5.39
247399_at	putative protein similar to unknown	---	AT5G62960	-1.28	-0.35	-1.64	0.14651947	0.5250	-5.40
253208_at	putative protein	---	AT4G34830	1.13	0.18	1.64	0.14626785	0.5250	-5.39
252766_at	putative protein hypothetical protei	---	---	-1.19	-0.26	-1.64	0.14634023	0.5250	-5.39
253701_at	choline monooxygenase - like pro	---	AT4G29890	1.19	0.25	1.64	0.14638814	0.5250	-5.39
255763_at	hypothetical protein predicted by g	---	AT1G16730	-1.17	-0.23	-1.64	0.14632085	0.5250	-5.39
259606_at	hypothetical protein predicted by g	MAP65-8	AT1G27920	-1.12	-0.16	-1.64	0.1464031	0.5250	-5.39
261960_at	hypothetical protein similar to puta	---	---	-1.11	-0.14	-1.64	0.1464855	0.5250	-5.40
248439_at	putative protein similar to unknown	---	AT5G51250	-1.13	-0.17	-1.64	0.14651866	0.5250	-5.40
256334_at	oligopeptide transporter, putative s	---	AT1G72120	-1.21	-0.27	-1.64	0.14634327	0.5250	-5.39
248371_at	gibberellin 20-oxidase (emb|CAA5	GA20OX2	AT5G51810	1.39	0.48	1.64	0.1464329	0.5250	-5.40
246096_at	beta-1,3-glucanase bg4 ;supporte	BETAG4	AT5G20330	1.15	0.21	1.64	0.14648399	0.5250	-5.40
251907_at	putative protein 85p protein - Med	---	AT3G53760	1.26	0.34	1.64	0.14647131	0.5250	-5.40
262337_at	hypothetical protein similar to hypo	---	AT1G64260	-1.16	-0.22	-1.64	0.14657634	0.5251	-5.40
258449_s_at	putative RNA helicase similar to R	PMH1	AT3G22310	-1.22	-0.28	-1.64	0.14663982	0.5251	-5.40

247414_at	unknown protein	EMB2759	AT5G63050	1.18	0.23	1.64	0.14661443	0.5251	-5.40
264461_s_at	hypothetical protein	---	AT1G10190	-1.10	-0.14	-1.64	0.14667274	0.5251	-5.40
253432_at	putative protein various predicted p	---	AT4G32450	-1.12	-0.16	-1.64	0.14665362	0.5251	-5.40
261271_at	Expressed protein ; supported by f	---	AT1G26795	-1.15	-0.20	-1.64	0.14688142	0.5257	-5.40
267431_at	unknown protein ;supported by ful	MEE26	AT2G34870	1.15	0.20	1.64	0.14688784	0.5257	-5.40
261912_s_at	unknown protein	---	AT1G66000	-1.16	-0.22	-1.64	0.146888	0.5257	-5.40
252319_at	putative protein putative protein -	---	AT3G48710	1.20	0.27	1.64	0.14695123	0.5258	-5.40
266807_at	hypothetical protein	---	AT2G29920	-1.17	-0.23	-1.64	0.14699904	0.5258	-5.40
267365_at	putative phosphoribosyl pyrophosp	---	AT2G44530	1.11	0.15	1.64	0.14698848	0.5258	-5.40
258340_at	hypothetical protein predicted by g	---	AT3G22770	-1.11	-0.16	-1.64	0.14701316	0.5258	-5.40
260871_at	hypothetical protein predicted by g	---	AT1G29040	1.11	0.15	1.64	0.14720874	0.5259	-5.40
254224_at	calcium-dependent protein kinase	CDPK6	AT4G23650	1.13	0.17	1.64	0.14716639	0.5259	-5.40
259774_at	plasma membrane associated pro	---	AT1G29520	1.21	0.28	1.64	0.14717432	0.5259	-5.40
264498_at	Expressed protein ; supported by f	DIS2	AT1G30825	1.16	0.21	1.64	0.14718135	0.5259	-5.40
256151_at	multispanning membrane protein,	---	AT1G55130	1.20	0.27	1.64	0.14713416	0.5259	-5.40
259926_at	putative DNA-3-methyladenine gly	---	AT1G75090	1.11	0.15	1.64	0.14720223	0.5259	-5.40
262925_at	hypothetical protein	YSL7	AT1G65730	-1.15	-0.20	-1.64	0.14717059	0.5259	-5.40
259023_at	unknown protein ; supported by cl	---	AT3G07510	1.25	0.32	1.64	0.14726464	0.5259	-5.40
245430_at	hypothetical protein	FIP2	AT4G17060	-1.11	-0.15	-1.64	0.1472537	0.5259	-5.40
251783_at	ribosomal L23a - like protein variou	RPL23AB	AT3G55280	1.33	0.41	1.64	0.14733841	0.5261	-5.40
261402_at	wall-associated kinase 4, putative	RFO1	AT1G79670	1.26	0.33	1.64	0.14749524	0.5264	-5.40
245966_at	AP2 domain containing protein RA	RAP2.11	AT5G19790	-1.15	-0.20	-1.64	0.14750091	0.5264	-5.40
264177_at	hypothetical protein contains Pfam	---	AT1G02150	1.14	0.18	1.64	0.1474789	0.5264	-5.40
266731_at	unknown protein	---	AT2G03260	-1.12	-0.16	-1.64	0.14760572	0.5267	-5.40
254604_at	cadmium-induced protein	---	AT4G19070	-1.16	-0.21	-1.64	0.14765983	0.5268	-5.40
255035_at	putative protein	---	AT4G09550	1.21	0.27	1.64	0.14773584	0.5270	-5.40
248138_at	pyruvate decarboxylase (gb|AAB1	PDC2	AT5G54960	-1.20	-0.26	-1.63	0.1479022	0.5274	-5.40
261409_at	zinc finger protein OBP2 identical t	OBP2	AT1G07640	1.15	0.20	1.63	0.14801213	0.5274	-5.41
248589_at	von Hippel-Lindau binding protein	PDF3	AT5G49510	1.12	0.17	1.63	0.14803202	0.5274	-5.41
257570_at	dirigent protein, putative similar to	---	AT3G13662	-1.13	-0.18	-1.63	0.14798708	0.5274	-5.40
255079_s_at	14-3-3 protein GF14chi (grf1) iden	GF14 PHI	AT1G35160	1.12	0.16	1.63	0.1479367	0.5274	-5.40
251049_at	putative protein rab11 binding pro	---	AT5G02430	-1.15	-0.20	-1.63	0.1480207	0.5274	-5.41
257197_at	selenium binding protein, putative	SBP3	AT3G23800	-1.13	-0.17	-1.63	0.14796182	0.5274	-5.40
266684_at	40S ribosomal protein S15A	rps15ab	AT2G19720	1.12	0.16	1.63	0.14794682	0.5274	-5.40
255584_at	putative reverse transcriptase-like	---	---	-1.12	-0.17	-1.63	0.14805856	0.5274	-5.41

258965_at	hypothetical protein similar to hyp	---	AT3G10530	-1.30	-0.37	-1.63	0.14813451	0.5274	-5.41
247107_at	senescence-associated protein alr	STR16	AT5G66040	-1.24	-0.31	-1.63	0.14814007	0.5274	-5.41
266794_at	hypothetical protein	---	AT2G02980	1.13	0.17	1.63	0.14817502	0.5274	-5.41
257670_at	unknown protein	---	AT3G20340	-1.35	-0.43	-1.63	0.14815494	0.5274	-5.41
266739_at	unknown protein predicted by gens	---	AT2G46730	1.14	0.19	1.63	0.1481484	0.5274	-5.41
263940_at	putative calcium-dependent protein	CPK25	AT2G35890	-1.12	-0.16	-1.63	0.14820433	0.5275	-5.41
255699_at	putative pectinesterase	PME38	AT4G00190	-1.12	-0.16	-1.63	0.14830383	0.5276	-5.41
251805_at	putative protein RING-H2 finger p	SDIR1	AT3G55530	-1.13	-0.17	-1.63	0.14830355	0.5276	-5.41
256437_s_at	putative clathrin heavy chain simila	---	AT3G08530	1.12	0.16	1.63	0.14827636	0.5276	-5.41
263334_at	putative nonsense-mediated mRN	---	AT2G03820	-1.14	-0.19	-1.63	0.14834737	0.5276	-5.41
260788_at	cysteine proteinase contains simil	---	AT1G06260	-1.13	-0.17	-1.63	0.14837058	0.5276	-5.41
260766_at	unknown protein similar to hypothe	---	AT1G48960	-1.15	-0.20	-1.63	0.14854663	0.5279	-5.41
265306_at	unknown protein	---	AT2G20320	-1.21	-0.28	-1.63	0.14864603	0.5279	-5.41
252215_at	kinesin -like protein KINESIN-LIKE	KICP-02	AT3G50240	1.45	0.54	1.63	0.14864556	0.5279	-5.41
255219_at	hypothetical protein	---	AT4G07720	-1.12	-0.17	-1.63	0.14847487	0.5279	-5.41
252218_at	putative protein some putative prot	---	AT3G50150	-1.13	-0.18	-1.63	0.14854694	0.5279	-5.41
264033_at	hypothetical protein predicted by g	---	AT2G03580	-1.16	-0.22	-1.63	0.14857806	0.5279	-5.41
257544_at	putative DNA-binding protein simila	---	AT3G20880	-1.18	-0.23	-1.63	0.14859626	0.5279	-5.41
266969_at	similar to gibberellin-regulated prot	---	AT2G39540	-1.17	-0.23	-1.63	0.14849342	0.5279	-5.41
244903_at	hypothetical protein	---	---	-1.41	-0.50	-1.63	0.14860406	0.5279	-5.41
249964_at	MAP kinase -like protein ATMPK9	MPK16	AT5G19010	-1.14	-0.18	-1.63	0.14871752	0.5279	-5.41
252546_at	DNA-binding protein - like DNA-b	---	AT3G45830	-1.13	-0.18	-1.63	0.14872092	0.5279	-5.41
247505_at	signal recognition particle - like pr	---	AT5G61970	1.11	0.15	1.63	0.14871714	0.5279	-5.41
262001_at	myrosinase binding protein, putati	---	AT1G33790	-1.16	-0.21	-1.63	0.14880265	0.5281	-5.41
247069_at	pectinesterase like protein ;suppo	sks17	AT5G66920	1.39	0.48	1.63	0.14909689	0.5282	-5.41
254041_at	Expressed protein ; supported by f	---	AT4G25830	-1.53	-0.62	-1.63	0.14906034	0.5282	-5.41
254061_at	putative protein several hypothetic	---	AT4G25360	-1.14	-0.19	-1.63	0.14915809	0.5282	-5.41
252413_at	40S ribosomal protein S20-like pr	---	AT3G47370	1.30	0.38	1.63	0.14912802	0.5282	-5.41
253592_at	hypothetical protein ;supported by	---	AT4G30840	-1.13	-0.17	-1.63	0.14885645	0.5282	-5.41
264581_at	hypothetical protein predicted by g	---	AT1G05210	1.33	0.41	1.63	0.14889222	0.5282	-5.41
265415_at	unknown protein ;supported by ful	PSB29	AT2G20890	1.15	0.20	1.63	0.14907104	0.5282	-5.41
252037_at	putative calmodulin calmodulin - T	CAM9	AT3G51920	1.23	0.30	1.63	0.14893944	0.5282	-5.41
264599_at	putative myosin heavy chain simila	XIA	AT1G04600	-1.13	-0.18	-1.63	0.14907777	0.5282	-5.41
261950_at	zinc finger protein, putative similar	---	AT1G64620	-1.22	-0.29	-1.63	0.14917844	0.5282	-5.41
259224_at	putative thymidine kinase similar to	---	AT3G07800	1.20	0.26	1.63	0.14894859	0.5282	-5.41

267485_at	putative MYB family transcription f	MYB88	AT2G02820	-1.18	-0.23	-1.63	0.14916373	0.5282	-5.41
246751_at	pectin methyl-esterase - like prote	---	AT5G27870	-1.11	-0.15	-1.63	0.14899384	0.5282	-5.41
244927_at	hypothetical protein	---	AT2G07776	-1.18	-0.24	-1.63	0.1490633	0.5282	-5.41
249384_at	putative protein hypothetical prote	---	AT5G39890	-1.12	-0.16	-1.63	0.14898847	0.5282	-5.41
261625_at	hypothetical protein predicted by g	---	AT1G01930	-1.12	-0.16	-1.63	0.14924619	0.5284	-5.41
255818_at	hypothetical protein predicted by g	---	AT2G33570	1.45	0.54	1.63	0.14929439	0.5284	-5.41
246219_at	aminopeptidase-like protein ; supp	APP1	AT4G36760	1.20	0.27	1.63	0.14931408	0.5284	-5.41
253031_at	putative protein cellulose synthase	CSLD4	AT4G38190	-1.15	-0.20	-1.63	0.14932469	0.5284	-5.41
255424_at	putative glycosylation enzyme sim	---	AT4G03340	1.14	0.18	1.63	0.14937694	0.5285	-5.41
266712_at	unknown protein	---	AT2G46750	-1.17	-0.23	-1.63	0.1494465	0.5287	-5.41
259602_at	disease resistance protein, putativ	---	AT1G56520	1.12	0.16	1.63	0.14961224	0.5291	-5.41
267387_at	hypothetical protein predicted by g	---	AT2G44440	-1.11	-0.15	-1.63	0.14960853	0.5291	-5.41
247156_at	lysosomal Pro-X carboxypeptidase	---	AT5G65760	1.14	0.19	1.63	0.14964854	0.5291	-5.42
249957_at	putative protein predicted proteins	---	AT5G18900	1.17	0.23	1.63	0.1496858	0.5291	-5.42
267461_at	putative auxin-regulated protein ;s	---	AT2G33830	1.17	0.23	1.63	0.14972893	0.5291	-5.42
247269_at	alternative oxidase 2 (sp|O22049)	AOX2	AT5G64210	-1.13	-0.17	-1.63	0.1497318	0.5291	-5.42
252645_at	bZIP transcription factor -like prote	DPBF2	AT3G44460	-1.14	-0.19	-1.63	0.1497057	0.5291	-5.42
249755_at	unknown protein ;supported by ful	---	AT5G24580	1.48	0.57	1.63	0.14984045	0.5294	-5.42
259729_at	hypothetical protein predicted by g	---	AT1G77640	1.46	0.54	1.62	0.15002907	0.5296	-5.42
254132_at	putative protein hypothetical prote	ATHB22	AT4G24660	-1.23	-0.30	-1.62	0.15001448	0.5296	-5.42
249842_at	putative protein contains similarity	---	AT5G23550	1.12	0.17	1.62	0.14991854	0.5296	-5.42
249056_at	putative protein similar to unknown	---	AT5G44470	-1.13	-0.17	-1.62	0.14997107	0.5296	-5.42
266805_at	hypothetical protein ;supported by	---	AT2G30010	2.19	1.13	1.62	0.1500328	0.5296	-5.42
266385_at	pathogenesis-related PR-1-like pro	PR1	AT2G14610	5.86	2.55	1.62	0.15001645	0.5296	-5.42
252741_at	putative protein predicted protein,	---	AT3G43280	1.12	0.17	1.62	0.15008805	0.5297	-5.42
257329_at	hypothetical protein	---	---	-1.23	-0.29	-1.62	0.1501301	0.5298	-5.42
266725_at	SKP1/ASK1 (At14), putative simila	ASK14	AT2G03170	-1.13	-0.17	-1.62	0.1501888	0.5299	-5.42
246324_at	arginine/serine-rich protein, putati	SR45	AT1G16610	-1.13	-0.18	-1.62	0.1502554	0.5301	-5.42
263905_at	putative beta-fructofuranosidase (i	AtcwINV4	AT2G36190	-1.21	-0.27	-1.62	0.15030924	0.5301	-5.42
251620_at	putative protein hypothetical prote	---	AT3G58060	-1.17	-0.23	-1.62	0.15028997	0.5301	-5.42
253107_at	putative protein predicted proteins	---	AT4G35880	-1.18	-0.24	-1.62	0.15038293	0.5302	-5.42
257449_at	hypothetical protein predicted by g	---	AT2G31420	-1.14	-0.19	-1.62	0.15041389	0.5302	-5.42
263151_at	hypothetical protein predicted by g	---	AT1G54120	-1.39	-0.48	-1.62	0.15040723	0.5302	-5.42
246682_at	putative protein EXOSTOSIN-1 (P	XGD1	AT5G33290	-1.16	-0.22	-1.62	0.15044321	0.5302	-5.42
245897_at	potassium transport protein-like se	KUP7	AT5G09400	-1.20	-0.26	-1.62	0.15047861	0.5303	-5.42

265475_at	ferredoxin--nitrite reductase ; supp	NIR1	AT2G15620	1.22	0.28	1.62	0.15056382	0.5305	-5.42
266881_at	putative casein kinase II beta subu	CKB4	AT2G44680	1.14	0.19	1.62	0.15065714	0.5306	-5.42
250882_at	putative protein ;supported by full-	---	AT5G04000	-1.13	-0.17	-1.62	0.1506395	0.5306	-5.42
248048_at	nicotianamine synthase	NAS2	AT5G56080	-1.14	-0.19	-1.62	0.15072972	0.5307	-5.42
263648_at	hypothetical protein predicted by g	---	AT1G04390	-1.17	-0.23	-1.62	0.15072188	0.5307	-5.42
258548_at	hypothetical protein	ULP1A	AT3G06910	-1.18	-0.24	-1.62	0.15083733	0.5310	-5.42
255051_at	RNA-directed DNA polymerase -li	---	---	-1.23	-0.29	-1.62	0.15088061	0.5311	-5.42
257131_at	mitochondrial carrier protein, puta	---	AT3G20240	-1.12	-0.16	-1.62	0.15095064	0.5313	-5.42
245600_at	hypothetical protein	---	AT4G14230	-1.18	-0.24	-1.62	0.15097683	0.5313	-5.42
258331_at	putative coatomer complex subuni	---	AT3G15980	1.16	0.22	1.62	0.15100376	0.5313	-5.42
264013_at	unknown protein	FIO1	AT2G21070	1.11	0.15	1.62	0.15112262	0.5316	-5.42
253705_at	hexokinase ; supported by cDNA:	HXK1	AT4G29130	-1.22	-0.28	-1.62	0.15113401	0.5316	-5.42
259438_at	unknown protein similar to putative	AN	AT1G01510	1.21	0.28	1.62	0.15121729	0.5318	-5.42
259732_at	putative replication factor C similar	---	AT1G77470	1.15	0.20	1.62	0.15124081	0.5318	-5.42
254329_at	putative protein oxysterol-binding	ORP2A	AT4G22540	-1.15	-0.20	-1.62	0.15131177	0.5318	-5.43
248386_at	DNA-directed RNA polymerase II s	NRPB6A	AT5G51940	1.15	0.20	1.62	0.15131805	0.5318	-5.43
247388_s_at	transcription factor Hap5a-like prot	NF-YC1	AT3G48590	1.30	0.38	1.62	0.15128383	0.5318	-5.43
244914_at	hypothetical protein	---	---	-1.13	-0.18	-1.62	0.15140618	0.5321	-5.43
251417_at	putative protein prib5, Ribes nigru	AT3G6042(	---	1.11	0.15	1.62	0.15147693	0.5322	-5.43
254549_at	putative protein various predicted p	---	AT4G19880	1.20	0.27	1.62	0.15163552	0.5326	-5.43
248041_at	unknown protein ;supported by ful	emb2731	AT5G55940	1.11	0.15	1.62	0.1516228	0.5326	-5.43
257556_at	hypothetical protein predicted by g	---	AT3G28100	1.39	0.47	1.62	0.15169909	0.5328	-5.43
253462_at	synaptobrevin-like protein synapto	ATVAMP71	AT4G32150	1.17	0.22	1.62	0.15182065	0.5328	-5.43
252975_s_at	putative protein other predicted pro	ROPGEF1	AT4G38430	1.13	0.17	1.62	0.15186308	0.5328	-5.43
246574_at	copper amine oxidase, putative si	---	AT1G31670	-1.28	-0.35	-1.62	0.15179584	0.5328	-5.43
250850_at	putative protein ; supported by cD	---	AT5G04550	-1.17	-0.23	-1.62	0.15175132	0.5328	-5.43
252315_at	putative protein PrMC3 - Pinus ra	CXE12	AT3G48690	-1.17	-0.23	-1.62	0.15186102	0.5328	-5.43
252538_at	putative transporter protein peptid	---	AT3G45720	-1.12	-0.16	-1.62	0.15173134	0.5328	-5.43
266999_at	putative HMG protein ; supported b	---	AT2G34450	1.19	0.25	1.62	0.15190823	0.5328	-5.43
247020_at	putative protein strong similarity to	---	AT5G67020	-1.20	-0.26	-1.62	0.15191053	0.5328	-5.43
251373_at	GATA transcription factor 4 ; supp	---	AT3G60530	1.55	0.63	1.62	0.15190079	0.5328	-5.43
258774_at	putative alpha-L-arabinofuranosida	ASD1	AT3G10740	1.47	0.56	1.62	0.15194769	0.5328	-5.43
258123_at	putative MAP kinase similar to blas	MPK9	AT3G18040	-1.29	-0.37	-1.61	0.15212524	0.5329	-5.43
245136_at	putative auxin-regulated protein	---	AT2G45210	1.38	0.47	1.61	0.15212466	0.5329	-5.43
266701_at	profilin 1 ; supported by cDNA: gi_	PRF1	AT2G19760	-1.11	-0.15	-1.61	0.15208472	0.5329	-5.43

257055_at	Expressed protein ; supported by f	---	AT3G15351	1.13	0.18	1.62	0.15202449	0.5329	-5.43
264294_at	hypothetical protein similar to heat	---	AT1G78750	1.14	0.19	1.61	0.15209984	0.5329	-5.43
262192_at	hypothetical protein predicted by g	---	AT1G77830	-1.12	-0.16	-1.62	0.15205963	0.5329	-5.43
266020_at	hypothetical protein	SDG11	AT2G05900	-1.17	-0.23	-1.61	0.15215612	0.5330	-5.43
261948_at	unknown protein ;supported by full	---	AT1G64680	-1.26	-0.33	-1.61	0.15219226	0.5330	-5.43
251915_at	putative protein peroxisomal Ca-d	---	AT3G53940	-1.18	-0.24	-1.61	0.15232442	0.5333	-5.43
266452_at	hypothetical protein predicted by g	---	AT2G43320	-1.22	-0.29	-1.61	0.15232123	0.5333	-5.43
249628_at	putative protein tropomyosin gene	---	AT5G37590	-1.17	-0.23	-1.61	0.15238657	0.5334	-5.43
262764_at	putative cytochrome P450 monoox	CYP86C3	AT1G13140	-1.13	-0.18	-1.61	0.15237762	0.5334	-5.43
252499_s_at	subtilisin-like serine protease cont	---	AT3G46840	1.14	0.19	1.61	0.15244344	0.5335	-5.43
257267_at	unknown protein similar to TCP3 G	TCP4	AT3G15030	-1.15	-0.20	-1.61	0.15254591	0.5335	-5.43
266370_at	hypothetical protein predicted by g	---	AT2G41350	1.11	0.15	1.61	0.15249167	0.5335	-5.43
257376_at	hypothetical protein predicted by g	---	AT2G32350	-1.14	-0.19	-1.61	0.15259929	0.5335	-5.43
259968_at	unknown protein	---	AT1G76530	-1.14	-0.19	-1.61	0.15259125	0.5335	-5.43
254474_at	putative protein predicted proteins	---	AT4G20390	-1.21	-0.27	-1.61	0.1526032	0.5335	-5.43
267348_at	unknown protein	---	AT2G39960	1.12	0.17	1.61	0.15262329	0.5335	-5.43
246326_at	unknown protein ; supported by cD	REV7	AT1G16590	1.12	0.17	1.61	0.15257165	0.5335	-5.43
246445_at	glucose 6 phosphate/phosphate tr	---	AT5G17630	1.16	0.21	1.61	0.15267489	0.5336	-5.43
257558_s_at	hypothetical protein contains Pfam	---	AT3G22000	-1.13	-0.17	-1.61	0.15279706	0.5340	-5.43
253055_at	putative protein cyclin delta-1, Ara	CYCD5;1	AT4G37630	-1.20	-0.26	-1.61	0.15285747	0.5341	-5.43
246743_at	putative protein predicted proteins	---	AT5G27750	1.15	0.21	1.61	0.1529221	0.5341	-5.44
255570_at	putative carrier protein similar to m	ADNT1	AT4G01100	1.15	0.20	1.61	0.15293014	0.5341	-5.44
247442_s_at	tubulin beta-2/beta-3 chain (sp|P2	TUB2	AT5G62690	1.25	0.32	1.61	0.15290914	0.5341	-5.43
256006_at	hypothetical protein	---	AT1G34070	-1.12	-0.16	-1.61	0.15298976	0.5342	-5.44
257638_at	terpene synthase-related protein c	ATTPS-CIN	AT3G25820	-1.13	-0.17	-1.61	0.15305057	0.5343	-5.44
266868_at	hypothetical protein predicted by g	---	AT2G44630	1.13	0.18	1.61	0.15305807	0.5343	-5.44
265881_at	hypothetical protein predicted by g	---	AT2G42480	-1.15	-0.20	-1.61	0.15308554	0.5343	-5.44
264039_at	putative cold-regulated protein ;su	---	AT2G03740	1.13	0.17	1.61	0.1530713	0.5343	-5.44
261784_at	hypothetical protein predicted by g	---	AT1G08220	-1.13	-0.17	-1.61	0.15311059	0.5343	-5.44
266735_at	putative pectinesterase ; supporte	---	AT2G46930	-1.18	-0.24	-1.61	0.15334983	0.5349	-5.44
258956_at	hypothetical protein predicted by g	---	AT3G01440	-1.47	-0.55	-1.61	0.15334388	0.5349	-5.44
262715_at	putative myb-related transcription f	MYB58	AT1G16490	-1.10	-0.14	-1.61	0.15341152	0.5349	-5.44
253730_at	putative protein hypothetical prote	---	AT4G29480	1.25	0.32	1.61	0.15342466	0.5349	-5.44
261147_at	unknown protein ;supported by full	---	AT1G19690	1.25	0.32	1.61	0.15339861	0.5349	-5.44
257012_at	RNA-binding protein, putative sim	TEL1	AT3G26120	-1.12	-0.17	-1.61	0.15353451	0.5351	-5.44

263224_at	putative GTP-binding protein Simil	---	AT1G30580	1.19	0.25	1.61	0.15352869	0.5351	-5.44
259088_at	unknown protein, contains TNFR/	---	AT3G04970	-1.21	-0.27	-1.61	0.15350873	0.5351	-5.44
249027_at	ATP dependent copper transporter	RAN1	AT5G44790	1.18	0.24	1.61	0.15369012	0.5352	-5.44
258160_at	glutamine synthetase, putative sin	GLN1.3	AT3G17820	-1.26	-0.33	-1.61	0.15367807	0.5352	-5.44
252626_at	putative protein predicted protein,	---	AT3G44940	-1.18	-0.24	-1.61	0.15363137	0.5352	-5.44
260451_at	putative AP2 domain transcription	---	AT1G72360	-1.59	-0.67	-1.61	0.15359584	0.5352	-5.44
265777_at	hypothetical protein predicted by g	---	AT2G07340	1.12	0.17	1.61	0.15373107	0.5352	-5.44
264469_at	hypothetical protein similar to hypo	LBD40	AT1G67100	-1.12	-0.17	-1.61	0.15372794	0.5352	-5.44
256977_at	hypothetical protein predicted by g	---	---	-1.14	-0.19	-1.61	0.15369889	0.5352	-5.44
267201_at	putative protein kinase contains a	---	AT2G31010	-1.27	-0.34	-1.61	0.15379649	0.5353	-5.44
257173_at	S-adenosyl-L-homocysteinas, put	SAHH2	AT3G23810	-1.65	-0.72	-1.61	0.15382464	0.5353	-5.44
252740_at	pectinesterase -like protein PECT	---	AT3G43270	-1.23	-0.30	-1.61	0.15387984	0.5353	-5.44
247932_at	putative protein similar to unknown	---	AT5G56920	-1.11	-0.15	-1.61	0.15385156	0.5353	-5.44
249687_at	putative protein oxidosqualene cy	ATPEN3	AT5G36150	-1.13	-0.18	-1.61	0.15395481	0.5353	-5.44
265612_at	hypothetical protein predicted by g	---	AT2G25390	1.12	0.17	1.61	0.15398436	0.5353	-5.44
262473_at	chloroplast FtsH protease almost	FTSH1	AT1G50250	-1.18	-0.24	-1.61	0.15398832	0.5353	-5.44
255447_at	hypothetical protein similar to A. th	---	AT4G02790	1.27	0.34	1.61	0.15397348	0.5353	-5.44
263282_at	Expressed protein ; supported by f	---	AT2G14095	1.14	0.18	1.61	0.1539218	0.5353	-5.44
245243_at	hypothetical protein predicted by g	---	AT1G44414	-1.12	-0.16	-1.61	0.15400833	0.5353	-5.44
248957_at	26S proteasome subunit-like prote	---	AT5G45620	1.13	0.18	1.61	0.1541736	0.5358	-5.44
262457_at	hypothetical protein similar to hypo	---	AT1G11200	1.25	0.32	1.61	0.15422328	0.5359	-5.44
257868_at	unknown protein	RIN4	AT3G25070	-1.18	-0.24	-1.60	0.1543415	0.5360	-5.44
254456_at	putative protein ribophorin II precu	HAP6	AT4G21150	1.17	0.22	1.60	0.15434774	0.5360	-5.44
253895_at	NWMU3 - 2S albumin 3 precursor	AT2S3	AT4G27160	-1.12	-0.16	-1.60	0.15430843	0.5360	-5.44
261820_at	hypothetical protein predicted by g	---	AT1G11420	-1.20	-0.26	-1.60	0.15429487	0.5360	-5.44
259199_at	putative signal peptidase similar to	---	AT3G08980	1.12	0.16	1.60	0.15426172	0.5360	-5.44
267423_at	putative potassium transporter	KUP11	AT2G35060	-1.26	-0.33	-1.60	0.15448011	0.5363	-5.44
257600_at	hypothetical protein predicted by g	CLE41	AT3G24770	-1.17	-0.23	-1.60	0.15449253	0.5363	-5.44
257951_at	putative SGP1 monomeric G-prote	SGP2	AT3G21700	-1.36	-0.44	-1.60	0.15464654	0.5367	-5.45
257736_at	hypothetical protein predicted by g	---	AT3G27410	1.14	0.19	1.60	0.1546658	0.5367	-5.45
250546_at	nhp2-like protein high mobility grou	---	AT5G08180	1.30	0.37	1.60	0.15477564	0.5368	-5.45
261381_at	hypothetical protein predicted by g	SDE3	AT1G05460	-1.11	-0.16	-1.60	0.15472055	0.5368	-5.45
261127_at	unknown protein ; supported by cD	---	AT1G04790	1.18	0.24	1.60	0.15478501	0.5368	-5.45
262138_at	NBS/LRR disease resistance prot	---	AT1G52660	-1.16	-0.21	-1.60	0.1547525	0.5368	-5.45
246986_at	receptor-like protein kinase ;suppo	RLK	AT5G67280	-1.49	-0.57	-1.60	0.15480327	0.5368	-5.45

254279_at	Expressed protein ; supported by f	---	AT4G22750	1.14	0.19	1.60	0.15487581	0.5370	-5.45
264258_at	hypothetical protein predicted by g	---	AT1G09220	-1.15	-0.20	-1.60	0.15500895	0.5373	-5.45
251615_at	putative protein hypothetical prote	---	AT3G57980	-1.22	-0.28	-1.60	0.15500918	0.5373	-5.45
257624_at	cytochrome P450 monooxygenas	CYP71B3	AT3G26220	1.63	0.70	1.60	0.15511809	0.5373	-5.45
254797_at	putative protein	---	AT4G13030	1.24	0.32	1.60	0.15512483	0.5373	-5.45
255060_at	putative protein TMV resistance p	---	AT4G09430	-1.16	-0.21	-1.60	0.15512915	0.5373	-5.45
262627_at	hypothetical protein	---	AT1G06580	-1.15	-0.20	-1.60	0.15512841	0.5373	-5.45
260452_at	putative SRF-type transcription fac	---	AT1G72350	-1.22	-0.29	-1.60	0.15507035	0.5373	-5.45
259604_at	20S proteasome beta subunit (PB(	PBG1	AT1G56450	1.13	0.18	1.60	0.155157	0.5373	-5.45
253093_at	putative protein SPINDLY protein,	SRFR1	AT4G37460	-1.13	-0.18	-1.60	0.15530532	0.5376	-5.45
251339_at	putative protein various predicted	---	AT3G60780	-1.18	-0.24	-1.60	0.15529886	0.5376	-5.45
263547_at	hypothetical protein predicted by g	---	AT2G21680	-1.16	-0.21	-1.60	0.15525982	0.5376	-5.45
246640_x_at	putative protein predicted proteins	---	---	-1.14	-0.19	-1.60	0.15542615	0.5377	-5.45
260081_at	unknown protein	---	AT1G78170	1.80	0.85	1.60	0.15537444	0.5377	-5.45
256449_at	mutator transposase MUDRA, put	---	---	-1.13	-0.18	-1.60	0.15543844	0.5377	-5.45
264393_at	unknown protein Contains similarit	---	AT1G11880	1.14	0.19	1.60	0.15543649	0.5377	-5.45
255756_at	endo-beta-1,4-D-glucanase, putat	AtGH9B5	AT1G19940	-1.14	-0.19	-1.60	0.15566508	0.5377	-5.45
266838_at	similar to jasmonate-inducible prot	---	AT2G25980	-1.13	-0.18	-1.60	0.15561383	0.5377	-5.45
256720_at	putative DOF zinc finger protein	---	AT2G34140	-1.30	-0.38	-1.60	0.15554573	0.5377	-5.45
252253_at	Expressed protein ; supported by f	---	AT3G49300	-1.10	-0.14	-1.60	0.15556116	0.5377	-5.45
255990_at	glycyl tRNA synthetase, putative s	---	AT1G29870	-1.14	-0.19	-1.60	0.15564681	0.5377	-5.45
251467_at	putative protein putative proteins -	---	AT3G59470	1.17	0.22	1.60	0.15563866	0.5377	-5.45
245920_at	putative protein	---	---	-1.10	-0.14	-1.60	0.15563576	0.5377	-5.45
254412_at	putative protein chloroplast DNA-b	B160	AT4G21430	-1.23	-0.30	-1.60	0.15564976	0.5377	-5.45
258828_at	putative purple acid phosphatase s	PAP15	AT3G07130	-1.15	-0.20	-1.60	0.15547679	0.5377	-5.45
245625_at	transport protein	---	AT4G14160	1.13	0.18	1.60	0.15568977	0.5377	-5.45
AFFX-BioDn-3_	E. coli /GEN=bioD /DB_XREF=gb:	---	---	-1.34	-0.43	-1.60	0.15577154	0.5379	-5.45
264563_s_at	unknown protein	---	AT1G55750 /	1.15	0.20	1.60	0.15575111	0.5379	-5.45
263763_at	Expressed protein ; supported by c	---	AT2G21385	1.26	0.34	1.60	0.15582272	0.5380	-5.45
251551_at	transcriptional coactivator - like pr	MBF1B	AT3G58680	1.10	0.14	1.60	0.15589899	0.5381	-5.45
258112_at	putative cytochrome P450 similar t	CYP72A10	AT3G14640	-1.14	-0.19	-1.60	0.15594615	0.5382	-5.45
262407_at	hypothetical protein predicted by g	---	AT1G34630	1.25	0.33	1.60	0.15607267	0.5383	-5.45
253353_at	pathogenesis-related protein - like	---	AT4G33730	-1.11	-0.16	-1.60	0.15605127	0.5383	-5.45
255528_at	hypothetical protein	---	AT4G02090	-1.12	-0.16	-1.60	0.15605506	0.5383	-5.45
258119_at	putative MAP kinase similar to GB	MPK19	AT3G14720	-1.15	-0.21	-1.60	0.15606271	0.5383	-5.45

250017_at	unknown protein	---	AT5G18140	1.23	0.30	1.60	0.15613246	0.5385	-5.45
257941_at	putative UDP-glucose glucosyltran	UGT71B8	AT3G21800	-1.12	-0.17	-1.60	0.15616925	0.5385	-5.45
254724_at	putative protein IFA-binding protei	---	AT4G13630	-1.16	-0.22	-1.60	0.15623539	0.5387	-5.45
260715_at	hypothetical protein predicted by g	---	AT1G48200	1.27	0.35	1.60	0.15629821	0.5388	-5.45
255440_at	predicted protein of unknown funct	---	AT4G02530	1.16	0.22	1.60	0.15633372	0.5388	-5.46
247642_at	putative protein various predicted p	---	AT5G60590	1.13	0.17	1.60	0.15637013	0.5389	-5.46
245116_at	unknown protein ; supported by cl	---	AT2G41620	1.30	0.38	1.60	0.15642106	0.5390	-5.46
246083_at	zinc finger protein - like probable z	AL5	AT5G20510	1.12	0.17	1.59	0.15652418	0.5392	-5.46
251940_at	putative protein lysine decarboxyla	---	AT3G53450	-1.13	-0.18	-1.59	0.1565026	0.5392	-5.46
248241_at	unknown protein	---	AT5G53960	-1.12	-0.17	-1.59	0.156585	0.5393	-5.46
259991_at	putative S-adenosyl-L-methionine:	---	AT1G68040	-1.14	-0.18	-1.59	0.15664572	0.5394	-5.46
262076_at	hypothetical protein identical to GE	ATMPK2	AT1G59580	1.17	0.23	1.59	0.15667135	0.5394	-5.46
245269_at	hypothetical protein ; supported by	---	AT4G14500	-1.14	-0.19	-1.59	0.15673033	0.5395	-5.46
256882_at	RNA-binding protein, putative sim	---	AT3G26420	1.18	0.24	1.59	0.15673046	0.5395	-5.46
266103_at	putative VAMP-associated protein	PVA12	AT2G45140	-1.14	-0.19	-1.59	0.15676434	0.5395	-5.46
247571_at	snap25a ;supported by full-length	SNAP33	AT5G61210	1.12	0.16	1.59	0.15677536	0.5395	-5.46
256193_at	hypothetical protein similar to hypo	---	AT1G30200	-1.13	-0.17	-1.59	0.15684818	0.5395	-5.46
255456_at	hypothetical protein ;supported by	---	AT4G02920	-1.13	-0.18	-1.59	0.15683008	0.5395	-5.46
266208_at	putative tRNA isopentenylpyrophos	ATIPT2	AT2G27760	-1.24	-0.31	-1.59	0.15682424	0.5395	-5.46
253834_at	protein phosphatase homolog (PPI	---	AT4G27800	-1.16	-0.21	-1.59	0.1569463	0.5396	-5.46
253051_at	cyclin cyc1 ; supported by cDNA:	CYCB1;1	AT4G37490	-1.19	-0.25	-1.59	0.15693333	0.5396	-5.46
253257_at	extra-large G-protein - like extra-la	XLG2	AT4G34390	1.17	0.22	1.59	0.15698222	0.5397	-5.46
262039_at	adenine phosphoribosyltransferase	APT2	AT1G80050	-1.19	-0.25	-1.59	0.15708144	0.5399	-5.46
248575_at	ATP-dependent Clp protease ATP	---	AT5G49840	-1.12	-0.16	-1.59	0.15717091	0.5400	-5.46
265885_at	hypothetical protein predicted by g	---	AT2G42330	-1.19	-0.25	-1.59	0.15715438	0.5400	-5.46
259886_at	putative protein kinase similar to p	---	AT1G76370	-1.12	-0.17	-1.59	0.15715437	0.5400	-5.46
AFFX-Athal-Ac	Arabidopsis thaliana /REF=U3728	---	---	-1.17	-0.22	-1.59	0.15724625	0.5401	-5.46
267447_at	putative GTP-binding protein	ArRABA1h	AT2G33870	-1.11	-0.15	-1.59	0.15724411	0.5401	-5.46
253401_at	putative protein hypothetical prote	---	AT4G32870	2.14	1.09	1.59	0.15730252	0.5402	-5.46
253348_at	putative protein SMT4 protein - Sa	---	AT4G33620	1.11	0.15	1.59	0.15734712	0.5402	-5.46
262835_at	Na+ H+ antiporter, putative similar	ATNHX8	AT1G14660	1.13	0.17	1.59	0.15736028	0.5402	-5.46
263324_at	hypothetical protein predicted by g	---	AT2G04220	-1.12	-0.17	-1.59	0.15741351	0.5403	-5.46
253861_at	putative protein MSP1 protein, Sa	---	AT4G27680	-1.13	-0.18	-1.59	0.15767869	0.5406	-5.46
265845_at	unknown protein	---	AT2G35610	1.10	0.14	1.59	0.15757474	0.5406	-5.46
256127_at	small GTP-binding protein (RAB1	AtRABA6b	AT1G18200	-1.16	-0.21	-1.59	0.15761741	0.5406	-5.46

253898_s_at	tryptophan synthase beta-subunit (	TSB2	AT4G27070 /	-1.47	-0.55	-1.59	0.15756216	0.5406	-5.46
254561_at	putative protein ; supported by cD	---	AT4G19160	1.23	0.29	1.59	0.15770244	0.5406	-5.46
251352_at	putative protein hypothetical prote	PEX11E	AT3G61070	1.18	0.24	1.59	0.15764742	0.5406	-5.46
260082_at	putative mitochondrial carrier prote	---	AT1G78180	1.18	0.24	1.59	0.157541	0.5406	-5.46
259401_at	hypothetical protein contains simila	CSTF77	AT1G17760	-1.24	-0.31	-1.59	0.15763891	0.5406	-5.46
252981_at	putative protein gene T10 protein	---	AT4G38260	1.19	0.25	1.59	0.15771456	0.5406	-5.46
248122_at	unknown protein	---	AT5G54700	-1.13	-0.17	-1.59	0.15775426	0.5407	-5.46
260311_at	hypothetical protein predicted by g	---	AT1G70570	1.11	0.14	1.59	0.1578492	0.5408	-5.46
261089_at	protein kinase APK1A identical to S	APK1A	AT1G07570	1.22	0.29	1.59	0.15783435	0.5408	-5.46
251249_at	putative protein 10-deacetylbacca	---	AT3G62160	1.14	0.19	1.59	0.15780636	0.5408	-5.46
257610_at	zinc finger protein, putative similar	AtIDD11	AT3G13810	1.35	0.43	1.59	0.15789124	0.5408	-5.46
245460_at	disease resistance RPP5 like prote	RLM3	AT4G16990	-1.29	-0.36	-1.59	0.15791898	0.5409	-5.46
263548_at	glycine-rich RNA binding protein 7	CCR2	AT2G21660 /	-1.14	-0.19	-1.59	0.15806012	0.5409	-5.47
261011_at	cytochrome b5 similar to cytochror	CB5-A	AT1G26340	1.15	0.21	1.59	0.1580768	0.5409	-5.47
261553_at	hypothetical protein	---	AT1G63420	-1.15	-0.21	-1.59	0.15804787	0.5409	-5.47
257597_at	protein kinase, putative similar to	---	AT3G24790	-1.12	-0.16	-1.59	0.15806265	0.5409	-5.47
245370_at	Expressed protein ; supported by f	---	AT4G16840	1.28	0.35	1.59	0.15808398	0.5409	-5.47
251496_at	putative protein crp1 protein, invol	---	AT3G59040	1.12	0.16	1.59	0.15795131	0.5409	-5.46
254591_at	heat shock transcription factor - lik	---	AT4G18870	1.10	0.13	1.59	0.15797399	0.5409	-5.46
248976_at	putative protein strong similarity to	ARAD2	AT5G44930	-1.17	-0.23	-1.59	0.15824989	0.5413	-5.47
259456_s_at	unknown protein similar to putative	---	---	-1.14	-0.19	-1.59	0.15832827	0.5415	-5.47
248890_at	disease resistance protein-like	---	AT5G46270	-1.13	-0.17	-1.59	0.15838266	0.5416	-5.47
261693_at	hypothetical protein similar to hypo	DCP1	AT1G08370	1.11	0.15	1.59	0.15840068	0.5416	-5.47
259592_at	lipid transfer protein, putative cont	LTPG1	AT1G27950	1.47	0.56	1.59	0.15852769	0.5419	-5.47
263731_at	metalloproteinase, putative similar	---	AT1G59970	-1.48	-0.57	-1.59	0.15855426	0.5419	-5.47
264769_at	hypothetical protein predicted by g	---	AT1G61350	1.32	0.40	1.59	0.15854655	0.5419	-5.47
253743_at	putative protein vegetative storage	---	AT4G28940	1.10	0.14	1.59	0.15863262	0.5421	-5.47
261032_at	unknown protein ;supported by full	---	AT1G17430	1.45	0.53	1.58	0.15875499	0.5421	-5.47
265730_at	60S ribosomal protein L27	---	AT2G32220	1.51	0.59	1.58	0.15876943	0.5421	-5.47
262175_at	unknown protein ; supported by cD	NDH-O	AT1G74880	-1.19	-0.25	-1.58	0.15874421	0.5421	-5.47
263024_at	hypothetical protein predicted by g	---	AT1G23980	-1.17	-0.23	-1.58	0.15877961	0.5421	-5.47
246720_at	putative protein predicted proteins	---	AT5G28950	-1.10	-0.14	-1.58	0.15875906	0.5421	-5.47
253389_at	hypothetical protein ;supported by	---	AT4G32680	1.12	0.16	1.59	0.1586612	0.5421	-5.47
258992_at	unknown protein similar to unknow	---	AT3G08930	1.10	0.14	1.58	0.15887439	0.5423	-5.47
251420_at	transcription factor - like protein tr	---	AT3G60490	-1.19	-0.25	-1.58	0.15897201	0.5425	-5.47

255515_at	putative pistil-specific protein simil	---	AT4G02250	-1.12	-0.16	-1.58	0.15894994	0.5425	-5.47
266005_at	unknown protein	RSZ33	AT2G37340	1.18	0.24	1.58	0.1592061	0.5428	-5.47
264884_at	unknown protein ;supported by full	---	AT1G61170	-1.30	-0.38	-1.58	0.1591307	0.5428	-5.47
248693_at	regulator of chromosome condens	---	AT5G48330	-1.21	-0.27	-1.58	0.15914996	0.5428	-5.47
252657_at	hypothetical protein	---	AT3G44780	-1.11	-0.15	-1.58	0.15924158	0.5428	-5.47
258117_at	hypothetical protein predicted by g	---	AT3G14700	-1.13	-0.17	-1.58	0.15916129	0.5428	-5.47
245294_at	casein kinase I ; supported by cDN	CKI1	AT4G14340	-1.13	-0.18	-1.58	0.15913881	0.5428	-5.47
265578_at	unknown protein	---	AT2G20100	-1.16	-0.22	-1.58	0.15924006	0.5428	-5.47
252003_at	hypothetical protein emm32, Strep	ZPR3	AT3G52770	-1.13	-0.18	-1.58	0.15924418	0.5428	-5.47
263459_at	ankyrin-like protein	---	AT2G31820	-1.21	-0.28	-1.58	0.15934312	0.5430	-5.47
AFFX-r2-Bs-ph	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.32	-0.40	-1.58	0.15933001	0.5430	-5.47
263074_at	putative HMG protein ;supported b	HMGB4	AT2G17560	1.17	0.22	1.58	0.15943068	0.5430	-5.47
250396_at	zinc finger -like protein CCHH fing	---	AT5G10970	-1.34	-0.42	-1.58	0.15940233	0.5430	-5.47
256665_at	hypothetical protein predicted by g	---	AT3G20700	1.18	0.24	1.58	0.15944192	0.5430	-5.47
245811_at	hypothetical protein similar to puta	---	---	-1.14	-0.19	-1.58	0.15939294	0.5430	-5.47
245270_at	tubulin alpha-6 chain (TUA6) ; sup	TUA6	AT4G14960	1.28	0.35	1.58	0.1595049	0.5430	-5.47
259149_at	putative phenylalanine ammonia-ly	PAL4	AT3G10340	1.77	0.83	1.58	0.15949347	0.5430	-5.47
258690_at	putative phosphatidylinositol-4-pho	---	AT3G07960	-1.12	-0.17	-1.58	0.15962674	0.5432	-5.47
256432_at	hypothetical protein similar to hypo	---	AT3G10990	-1.11	-0.16	-1.58	0.15965687	0.5432	-5.47
250659_at	MtN21 nodulin protein-like	---	AT5G07050	-1.16	-0.22	-1.58	0.15963385	0.5432	-5.47
261874_at	ethylene responsive element bindi	ERF3	AT1G50640	1.16	0.22	1.58	0.15961358	0.5432	-5.47
263236_at	putative response regulator 3 simi	ARR4	AT1G10470	-1.24	-0.31	-1.58	0.1597056	0.5433	-5.47
260529_at	putative chloroplast protein CP12	CP12-1	AT2G47400	1.11	0.15	1.58	0.15971793	0.5433	-5.47
252178_at	putative protein various predicted p	---	AT3G50750	-1.36	-0.44	-1.58	0.1597731	0.5433	-5.48
256570_at	unknown protein ; supported by cl	---	AT3G19540	-1.11	-0.15	-1.58	0.16019895	0.5433	-5.48
253792_at	ammonium transporter - like prote	AMT1;4	AT4G28700	-1.17	-0.22	-1.58	0.16017345	0.5433	-5.48
254886_at	putative protein bp4A protein, Bra	LCR17	AT4G11760	-1.14	-0.19	-1.58	0.15985038	0.5433	-5.48
258902_at	putative pyruvate dehydrogenase	PDK	AT3G06483	-1.11	-0.15	-1.58	0.16022162	0.5433	-5.48
251825_at	ABC transporter - like protein ATP	---	AT3G55100	-1.14	-0.19	-1.58	0.16018232	0.5433	-5.48
256988_s_at	adenosine triphosphatase, putativ	---	AT3G28710	1.11	0.15	1.58	0.16000332	0.5433	-5.48
248484_at	carbonyl reductase-like protein	---	AT5G51030	1.11	0.14	1.58	0.1600884	0.5433	-5.48
253853_at	putative diacylglycerol kinase (frag	---	AT4G28130	-1.13	-0.17	-1.58	0.1599486	0.5433	-5.48
245051_at	putative WRKY-type DNA-binding	WRKY15	AT2G23320	1.35	0.43	1.58	0.16012689	0.5433	-5.48
255114_at	putative protein various putative re	---	---	-1.20	-0.26	-1.58	0.15991103	0.5433	-5.48
256942_at	hypothetical protein similar to unkn	LSH4	AT3G23290	-1.44	-0.53	-1.58	0.16008819	0.5433	-5.48

247699_at	GTP-binding protein ara-3 GTP-bi	---	AT5G59840	1.25	0.32	1.58	0.15986599	0.5433	-5.48
256066_at	hypothetical protein similar to hypo	---	AT1G06980	-1.43	-0.51	-1.58	0.16007647	0.5433	-5.48
261966_x_at	hypothetical protein similar to puta	---	---	1.12	0.17	1.58	0.16019074	0.5433	-5.48
257966_at	unknown protein ;supported by ful	---	AT3G19800	-1.20	-0.27	-1.58	0.15998221	0.5433	-5.48
261888_at	ribosomal protein, putative similar	---	AT1G80800	1.15	0.20	1.58	0.15988923	0.5433	-5.48
264871_at	pyruvate dehydrogenase E1 alpha	IAR4	AT1G24180	1.25	0.32	1.58	0.16000196	0.5433	-5.48
266454_at	putative bHLH transcription factor	---	AT2G22750	1.14	0.19	1.58	0.16021148	0.5433	-5.48
247244_at	putative protein similar to unknown	---	AT5G64710	-1.12	-0.16	-1.58	0.16018	0.5433	-5.48
244970_at	ribosomal protein L20	---	---	1.26	0.33	1.58	0.16022366	0.5433	-5.48
260839_at	unknown protein	---	AT1G43690	-1.11	-0.15	-1.58	0.16025145	0.5433	-5.48
258687_at	unknown protein	---	AT3G07860	1.19	0.25	1.58	0.16038354	0.5433	-5.48
261685_at	3-beta-hydroxysteroid dehydroger	AT3BETAH	AT1G47290	1.32	0.40	1.58	0.16030375	0.5433	-5.48
258915_at	unknown protein similar to hypothe	VPS60.1	AT3G10640	1.17	0.22	1.58	0.16036876	0.5433	-5.48
254626_at	hypothetical protein ; supported by	---	AT4G18400	1.15	0.21	1.58	0.16037958	0.5433	-5.48
256913_at	unknown protein	---	AT3G23870	-1.24	-0.31	-1.58	0.16032915	0.5433	-5.48
247406_at	response regulator 6 (ARR6) ; sup	ARR6	AT5G62920	-1.38	-0.47	-1.58	0.16066254	0.5442	-5.48
248079_at	unknown protein	---	AT5G55790	1.19	0.25	1.58	0.16070419	0.5443	-5.48
264304_at	Expressed protein ; supported by f	---	AT1G78895	1.17	0.22	1.58	0.16085837	0.5447	-5.48
267368_at	citrate synthase similar to GB:X17	ATCS	AT2G44350	-1.15	-0.21	-1.58	0.16092224	0.5447	-5.48
252176_at	protein kinase ATN1 -like protein	---	AT3G50720	-1.16	-0.21	-1.58	0.16096166	0.5447	-5.48
265224_at	putative pectinesterase	---	AT2G36710	-1.13	-0.18	-1.58	0.16094628	0.5447	-5.48
245739_at	mitotic cyclin a2-type, putative sim	CYCA1;1	AT1G44110	1.12	0.16	1.58	0.16092446	0.5447	-5.48
266861_at	putative choline kinase ;supported	emb1187	AT2G26830	1.15	0.21	1.57	0.16103446	0.5449	-5.48
253506_at	putative protein EREBP-4 homolo	---	AT4G31980	-1.23	-0.30	-1.57	0.16106938	0.5449	-5.48
263117_at	putative lipoamide dehydrogenase	---	AT1G03040	-1.11	-0.15	-1.57	0.16110045	0.5450	-5.48
258585_at	unknown protein C-term similar to	emb2458	AT3G04340	1.13	0.18	1.57	0.16115244	0.5451	-5.48
266438_at	putative carboxyphosphonoenolpy	---	AT2G43180	1.17	0.23	1.57	0.16120289	0.5451	-5.48
255387_at	putative nodulin similar to M. trunc	---	AT4G03630	-1.18	-0.23	-1.57	0.16123455	0.5451	-5.48
267644_s_at	unknown protein highly similar to T	---	AT2G32870 /	-1.21	-0.28	-1.57	0.16121491	0.5451	-5.48
247847_at	putative protein predicted proteins	---	AT5G58110	1.22	0.29	1.57	0.16128359	0.5452	-5.48
246900_at	putative protein flavin-containing r	YUC6	AT5G25620	-1.18	-0.24	-1.57	0.16130389	0.5452	-5.48
266094_at	Expressed protein ; supported by f	---	AT2G37975	1.15	0.20	1.57	0.16134108	0.5452	-5.48
245446_at	enoyl-CoA hydratase	---	AT4G16800	-1.14	-0.19	-1.57	0.16143734	0.5455	-5.48
246130_at	putative protein various predicted	---	---	-1.21	-0.27	-1.57	0.1615353	0.5457	-5.49
250993_at	putative protein HSPC172, Homo	---	AT5G02280	1.15	0.20	1.57	0.1615623	0.5457	-5.49

247658_at	actin depolymerizing factor 3 - like	ADF3	AT5G59880	1.11	0.15	1.57	0.16163459	0.5459	-5.49
267024_s_at	putative aquaporin (plasma membr	NIP2;1	AT2G29870	-1.16	-0.22	-1.57	0.16166605	0.5459	-5.49
264503_at	hypothetical protein Similar to Ara	---	AT1G09410	-1.12	-0.16	-1.57	0.16171757	0.5460	-5.49
249685_at	putative protein similar to unknown	CCB3	AT5G36120	1.11	0.16	1.57	0.16186435	0.5460	-5.49
248913_at	unknown protein ;supported by ful	---	AT5G45760	1.13	0.17	1.57	0.16183883	0.5460	-5.49
258444_at	expressed protein supported by cD	TIC	AT3G22380	-1.13	-0.18	-1.57	0.16176636	0.5460	-5.49
244924_at	hypothetical protein	---	---	-1.14	-0.19	-1.57	0.16180261	0.5460	-5.49
247135_at	auxin-induced protein-like	---	AT5G66260	-1.10	-0.14	-1.57	0.16183305	0.5460	-5.49
249921_at	reverse-transcriptase - like protein	---	AT5G19270	-1.13	-0.17	-1.57	0.16189095	0.5460	-5.49
262104_at	hypothetical protein predicted by g	LPA1	AT1G02910	1.13	0.18	1.57	0.16188186	0.5460	-5.49
248782_at	palmitoyl-protein thioesterase prec	---	AT5G47340	-1.13	-0.18	-1.57	0.16193582	0.5460	-5.49
261452_s_at	hypothetical protein predicted by g	---	---	1.13	0.18	1.57	0.16198739	0.5460	-5.49
247986_at	unknown protein	---	AT5G56880	-1.16	-0.22	-1.57	0.16198556	0.5460	-5.49
245431_at	hypothetical protein	---	AT4G17080	1.13	0.18	1.57	0.16195969	0.5460	-5.49
249651_at	auxin response factor 8 (ARF8) ; s	ARF8	AT5G37020	-1.26	-0.33	-1.57	0.16203635	0.5460	-5.49
266544_at	similar to late embryogenesis abur	---	AT2G35300	-1.11	-0.15	-1.57	0.16203351	0.5460	-5.49
249604_x_at	putative protein RING-H2 finger pr	---	AT5G37230	-1.14	-0.19	-1.57	0.16208558	0.5461	-5.49
251489_at	putative protein putative proteins -	---	AT3G59460	-1.15	-0.20	-1.57	0.16212193	0.5462	-5.49
259491_at	chlorophyll binding protein, putativ	LHCB6	AT1G15820	1.15	0.20	1.57	0.1622417	0.5465	-5.49
264303_s_at	E2, ubiquitin-conjugating enzyme,	UBC35	AT1G16890	1.13	0.18	1.57	0.16227962	0.5465	-5.49
260638_at	unknown protein similar to putative	---	AT1G62390	1.24	0.31	1.57	0.16232563	0.5466	-5.49
248612_at	putative protein contains similarity	---	AT5G49530	-1.22	-0.28	-1.57	0.16234053	0.5466	-5.49
253202_at	Expressed protein ; supported by f	---	AT4G34555	1.29	0.37	1.57	0.16254088	0.5471	-5.49
253075_at	putative disease resistance protei	---	AT4G36150	1.12	0.16	1.57	0.16252961	0.5471	-5.49
263333_at	unknown protein ; supported by cD	---	AT2G03890	1.19	0.25	1.57	0.16258721	0.5471	-5.49
255258_at	contains similarity to Arabidopsis th	---	AT4G05060	1.15	0.20	1.57	0.16264193	0.5471	-5.49
261712_at	alcohol dehydrogenase, putative s	---	AT1G32780	1.14	0.19	1.57	0.16266134	0.5471	-5.49
256879_at	unknown protein similar to auxin-in	---	AT3G26370	1.10	0.14	1.57	0.1626079	0.5471	-5.49
245636_at	hypothetical protein similar to hypo	---	AT1G25240	-1.17	-0.23	-1.57	0.16264568	0.5471	-5.49
247106_at	WD repeat protein-like ;supported	---	AT5G66240	1.15	0.20	1.57	0.16268587	0.5471	-5.49
259928_at	DNA polymerase type I, putative s	---	AT1G34380	1.24	0.31	1.57	0.16283802	0.5472	-5.49
255791_at	plastid protein identical to GB:Z86(	DAL1	AT2G33430	1.19	0.25	1.57	0.16283394	0.5472	-5.49
257854_at	putative CREB-binding protein sim	HAC5	AT3G12980	-1.13	-0.18	-1.57	0.16288836	0.5472	-5.49
256525_at	unknown protein ;supported by full	---	AT1G66180	1.29	0.37	1.57	0.16287746	0.5472	-5.49
258753_at	hypothetical protein predicted by g	ATEXO70H	AT3G09530	-1.10	-0.14	-1.57	0.16277183	0.5472	-5.49

257557_at	terpene synthase-related protein,	---	AT3G14490	-1.17	-0.23	-1.57	0.16278736	0.5472	-5.49
256001_at	unknown protein contains similarity	---	AT1G29850	-1.19	-0.25	-1.57	0.16285054	0.5472	-5.49
250588_at	SMC-like protein	---	AT5G07660	-1.12	-0.17	-1.57	0.16293364	0.5473	-5.49
AFFX-r2-Ec-bio	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.40	-0.48	-1.57	0.16295973	0.5473	-5.49
246789_at	long-chain-fatty-acid--CoA ligase-	LACS7	AT5G27600	-1.12	-0.16	-1.57	0.16302067	0.5474	-5.49
249081_at	protein phosphatase 2A 62 kDa B	---	AT5G44090	1.13	0.18	1.57	0.16313397	0.5475	-5.49
251367_at	SKP1 interacting partner 4 (SKIP4	SKIP4	AT3G61350	1.16	0.21	1.57	0.16308785	0.5475	-5.49
253603_at	putative protein SP8 binding prote	WRKY32	AT4G30935	-1.11	-0.16	-1.57	0.16312862	0.5475	-5.49
251724_at	putative protein	---	AT3G56250	1.14	0.19	1.57	0.16308208	0.5475	-5.49
245321_at	Expressed protein ; supported by f	---	AT4G15545	-1.11	-0.15	-1.57	0.16321086	0.5476	-5.49
266295_at	tubulin beta-7 chain identical to GE	TUB7	AT2G29550	-1.29	-0.37	-1.56	0.16336735	0.5477	-5.50
260884_at	unknown protein similar to unknow	---	AT1G29240	1.35	0.43	1.56	0.16330367	0.5477	-5.49
245324_at	lactate dehydrogenase (LDH1) ;su	---	AT4G17260	-1.35	-0.43	-1.56	0.16329121	0.5477	-5.49
263673_at	unknown protein	---	AT2G04800	-1.22	-0.28	-1.56	0.16336494	0.5477	-5.50
256616_at	hypothetical protein similar to unkn	---	AT3G22260	1.22	0.28	1.56	0.16334435	0.5477	-5.50
263101_s_at	hypothetical protein predicted by g	---	AT2G05230 /	-1.13	-0.17	-1.56	0.16334939	0.5477	-5.50
257129_at	cytochrome P450, putative contai	CYP705A1	AT3G20100	-1.24	-0.31	-1.56	0.16354019	0.5480	-5.50
262891_at	ent-kaurene synthase, putative sir	GA2	AT1G79460	-1.23	-0.29	-1.56	0.16354935	0.5480	-5.50
265126_s_at	hypothetical protein similar to hypo	---	AT1G55380 /	-1.14	-0.19	-1.56	0.16355513	0.5480	-5.50
246714_at	putative protein predicted proteins	---	AT5G28220	-1.11	-0.15	-1.56	0.16351719	0.5480	-5.50
258829_at	putative Sec24-like COPII protein s	---	AT3G07100	1.10	0.14	1.56	0.16358044	0.5480	-5.50
259238_at	putative eukaryotic translation initia	EIF3G1	AT3G11400	1.13	0.18	1.56	0.16361975	0.5480	-5.50
259406_at	hypothetical protein predicted by g	---	AT1G17690	-1.11	-0.16	-1.56	0.16375147	0.5481	-5.50
259653_at	unknown protein	---	AT1G55240	-1.11	-0.15	-1.56	0.16380289	0.5481	-5.50
250341_at	MAP3K delta-1 protein kinase	---	AT5G11850	-1.11	-0.15	-1.56	0.16377643	0.5481	-5.50
249930_at	synaptobrevin-like protein	ATVAMP71	AT5G22360	1.13	0.17	1.56	0.16382052	0.5481	-5.50
267160_at	putative WD-40 repeat protein	---	AT2G37670	1.11	0.15	1.56	0.16383423	0.5481	-5.50
263910_at	hypothetical protein predicted by g	---	AT2G36550	1.13	0.17	1.56	0.16376019	0.5481	-5.50
264810_at	putative GPI-anchor transamidase	---	AT1G08750	1.15	0.20	1.56	0.16379825	0.5481	-5.50
259775_at	hypothetical protein predicted by g	---	AT1G29530	1.24	0.31	1.56	0.16378504	0.5481	-5.50
257730_at	unknown protein contains Pfam pr	---	AT3G18420	-1.19	-0.26	-1.56	0.1641595	0.5489	-5.50
252916_at	kinesin like protein kinesin-related	---	AT4G38950	1.13	0.18	1.56	0.16419878	0.5489	-5.50
260499_at	unknown protein ; supported by cl	---	AT2G41760	-1.12	-0.16	-1.56	0.16418648	0.5489	-5.50
247147_at	putative protein contains similarity	GTE7	AT5G65630	-1.19	-0.25	-1.56	0.16414106	0.5489	-5.50
266657_at	unknown protein ;supported by ful	---	AT2G25910	-1.10	-0.14	-1.56	0.16416751	0.5489	-5.50

246065_at	calcium-dependent protein kinase	CPK34	AT5G19360	-1.13	-0.18	-1.56	0.1641297	0.5489	-5.50
259473_at	hypothetical protein predicted by g	---	AT1G19025	1.16	0.22	1.56	0.16437892	0.5494	-5.50
246489_at	14-3-3 protein GF14upsilon (grf5) i	GRF5	AT5G16050	1.14	0.19	1.56	0.16453309	0.5496	-5.50
252653_at	putative kinesin-like protein simila	---	AT3G44730	1.14	0.19	1.56	0.16451102	0.5496	-5.50
248372_at	putative protein similar to unknown	---	AT5G51850	1.11	0.15	1.56	0.16453522	0.5496	-5.50
265695_at	putative replication protein A1 ;su	RPA2	AT2G24490	1.41	0.49	1.56	0.16453804	0.5496	-5.50
256446_at	RING zinc finger protein contains	---	AT3G11110	-1.24	-0.32	-1.56	0.16461444	0.5497	-5.50
256172_at	hypothetical protein	---	AT1G51745	-1.12	-0.16	-1.56	0.16462094	0.5497	-5.50
257073_at	hypothetical protein predicted by g	---	AT3G19650	-1.17	-0.23	-1.56	0.16468353	0.5498	-5.50
250916_at	monodehydroascorbate reductase	ATMDAR2	AT5G03630	-1.48	-0.56	-1.56	0.1648043	0.5499	-5.50
251871_at	hypothetical protein	---	AT3G54520	-1.10	-0.14	-1.56	0.16472	0.5499	-5.50
254900_at	hypothetical protein	RALFL28	AT4G11510	-1.11	-0.15	-1.56	0.16479818	0.5499	-5.50
251873_at	putative protein KIAA0122 gene ,	---	AT3G54230	-1.10	-0.14	-1.56	0.16481638	0.5499	-5.50
265279_at	hypothetical protein predicted by g	---	AT2G28460	1.20	0.27	1.56	0.16479949	0.5499	-5.50
248199_at	membrane related protein-like ;su	---	AT5G54170	-1.31	-0.39	-1.56	0.1648743	0.5499	-5.50
246710_at	putative protein predicted proteins	---	---	1.11	0.15	1.56	0.1648633	0.5499	-5.50
249826_at	iron superoxide dismutase 3 (gb|A	FSD3	AT5G23310	1.19	0.25	1.56	0.16494839	0.5500	-5.50
251540_at	citrate synthase -like protein citrat	CSY1	AT3G58740	-1.11	-0.14	-1.56	0.16494139	0.5500	-5.50
247640_at	putative protein various predicted	---	AT5G60610	1.13	0.18	1.56	0.16500688	0.5501	-5.50
260322_at	unknown protein	---	AT1G63900	1.13	0.18	1.56	0.16503115	0.5501	-5.50
257691_at	hypothetical protein predicted by g	FLA14	AT3G12660	-1.20	-0.26	-1.56	0.16509315	0.5502	-5.50
267165_at	putative receptor-like protein kinas	RLK	AT2G37710	-1.36	-0.45	-1.56	0.16513947	0.5503	-5.51
259518_at	hypothetical protein ; supported by	OPCL1	AT1G20510	-1.42	-0.50	-1.56	0.16516413	0.5503	-5.51
263965_at	putative retroelement pol polyprote	---	---	-1.13	-0.18	-1.56	0.16523659	0.5505	-5.51
265633_at	F-box protein family, AtFBL6 cont	EBF1	AT2G25490	-1.16	-0.21	-1.56	0.1653285	0.5507	-5.51
265891_at	putative thionin	---	AT2G15010	-1.12	-0.17	-1.56	0.16538623	0.5508	-5.51
262958_at	water stress-induced protein, puta	---	AT1G54410	-1.15	-0.21	-1.56	0.16539929	0.5508	-5.51
249479_at	germin - like protein probable gerr	---	AT5G38960	-1.17	-0.23	-1.56	0.16545895	0.5509	-5.51
252277_at	alpha NAC-like protein Nascent p	NACA2	AT3G49470	-1.10	-0.14	-1.55	0.16562294	0.5514	-5.51
252134_at	putative protein ; supported by cD	---	AT3G50910	-1.36	-0.44	-1.55	0.16579966	0.5518	-5.51
245648_at	F5A9.12 hypothetical protein	---	---	-1.13	-0.18	-1.55	0.16577715	0.5518	-5.51
264173_at	unknown protein	---	AT1G02160	1.12	0.17	1.55	0.16583175	0.5518	-5.51
260819_at	b-Zip DNA binding protein, putativ	AtbZIP52	AT1G06850	-1.27	-0.34	-1.55	0.16609083	0.5518	-5.51
257516_at	unknown protein	ACR4	AT1G69040	1.22	0.29	1.55	0.16599737	0.5518	-5.51
267172_at	unknown protein ;supported by ful	---	AT2G37660	1.17	0.23	1.55	0.16611398	0.5518	-5.51

258922_at	putative 40S ribosomal protein S1	---	AT3G10610	1.37	0.46	1.55	0.16603894	0.5518	-5.51
249142_at	putative protein similar to unknown	---	AT5G43230	-1.15	-0.20	-1.55	0.16598554	0.5518	-5.51
259918_at	putative AP2 domain transcription	---	AT1G72570	-1.11	-0.16	-1.55	0.16594104	0.5518	-5.51
266817_at	hypothetical protein similar to hypo	HUB1	AT2G44950	-1.18	-0.24	-1.55	0.16615632	0.5518	-5.51
257480_at	hypothetical protein similar to puta	---	AT1G15640	-1.26	-0.34	-1.55	0.16612966	0.5518	-5.51
253573_at	putative protein BEM46 PROTEIN	---	AT4G31020	-1.15	-0.21	-1.55	0.16590068	0.5518	-5.51
263897_at	putative shikimate kinase precurso	---	AT2G21940	-1.23	-0.30	-1.55	0.16614206	0.5518	-5.51
251385_at	putative protein various predicted	---	AT3G60790	1.14	0.18	1.55	0.1659463	0.5518	-5.51
256323_at	unknown protein ; supported by cD	---	AT1G54920	-1.18	-0.24	-1.55	0.16605881	0.5518	-5.51
249351_at	MAP kinase kinase 3 (ATMKK3) 1	ATMKK3	AT5G40440	-1.14	-0.19	-1.55	0.16606073	0.5518	-5.51
261043_at	hypothetical protein similar to unkn	---	AT1G01220	1.16	0.22	1.55	0.16636089	0.5520	-5.51
260039_at	CLE12 CLAVATA3/ESR-Related 1	CLE12	AT1G68795	-1.16	-0.21	-1.55	0.16621947	0.5520	-5.51
267189_at	putative methionine aminopeptidas	MAP2A	AT2G44180	1.31	0.39	1.55	0.16627276	0.5520	-5.51
250860_at	amino acid transport - like protein	CAT6	AT5G04770	1.31	0.39	1.55	0.1663601	0.5520	-5.51
258873_at	hypothetical protein similar to unkn	---	AT3G03240	1.17	0.22	1.55	0.16634751	0.5520	-5.51
251765_at	putative protein	---	---	-1.14	-0.18	-1.55	0.16630167	0.5520	-5.51
255308_at	putative component of vesicle-me	NSF	AT4G04910	1.15	0.21	1.55	0.16628753	0.5520	-5.51
263926_at	hypothetical protein predicted by g	ATEME1A	AT2G21800	-1.15	-0.20	-1.55	0.16644063	0.5521	-5.51
250688_at	transcription factor-like protein ;su	NF-YA10	AT5G06510	-1.12	-0.16	-1.55	0.16649023	0.5522	-5.51
255076_at	putative protein RING-H2 zinc fing	---	AT4G09130	1.12	0.16	1.55	0.16651055	0.5522	-5.51
264932_at	hypothetical protein similar to hypo	---	AT1G61240	1.19	0.25	1.55	0.1667538	0.5529	-5.51
251935_at	fructokinase - like protein fructokin	---	AT3G54090	1.20	0.26	1.55	0.16679057	0.5530	-5.51
252934_at	Inositol monophosphatase - like p	IMPL2	AT4G39120	1.18	0.24	1.55	0.16684793	0.5530	-5.51
263554_at	putative Ta11-like non-LTR retroel	---	---	-1.24	-0.31	-1.55	0.16688176	0.5530	-5.51
258769_at	putative alpha-hydroxynitrile lyase	MES17	AT3G10870	-1.24	-0.31	-1.55	0.16685811	0.5530	-5.51
264574_at	putative zinc transporter Similar to	ZIP5	AT1G05300	-1.30	-0.37	-1.55	0.16691336	0.5531	-5.51
246042_at	cinnamyl-alcohol dehydrogenase	---	AT5G19440	-1.32	-0.41	-1.55	0.16696968	0.5531	-5.52
263923_at	Expressed protein ; supported by c	---	AT2G36485	-1.19	-0.25	-1.55	0.16697435	0.5531	-5.52
265790_at	putative amino acid or GABA perm	BAT1	AT2G01170	-1.19	-0.25	-1.55	0.16707339	0.5534	-5.52
258871_at	putative 26S proteosome regulator	---	AT3G03060	-1.33	-0.41	-1.55	0.16724983	0.5535	-5.52
250935_at	polyubiquitin (UBQ3) identical to G	UBQ3	AT5G03240	1.23	0.30	1.55	0.16729996	0.5535	-5.52
265002_at	putative lysine/histidine-specific pe	LHT2	AT1G24400	-1.20	-0.27	-1.55	0.16725443	0.5535	-5.52
246364_at	hypothetical protein	---	---	-1.11	-0.15	-1.55	0.16716919	0.5535	-5.52
247152_at	oligopeptidase A ; supported by cl	---	AT5G65620	1.11	0.15	1.55	0.16720848	0.5535	-5.52
267449_at	hypothetical protein predicted by g	---	AT2G33690	-1.10	-0.14	-1.55	0.16730872	0.5535	-5.52

258581_at	hypothetical protein predicted by g	---	AT3G04160	1.12	0.17	1.55	0.16730208	0.5535	-5.52
266018_at	putative preprotein translocase SE	SCY1	AT2G18710	1.11	0.16	1.55	0.16723589	0.5535	-5.52
266912_at	hypothetical protein predicted by g	---	AT2G45900	1.57	0.65	1.55	0.16744239	0.5539	-5.52
249122_at	putative protein similar to unknown	ARD4	AT5G43850	-1.20	-0.26	-1.55	0.16762099	0.5544	-5.52
262338_at	Expressed protein ; supported by f	---	AT1G64185	1.19	0.25	1.55	0.1676457	0.5544	-5.52
259505_at	hypothetical protein contains simila	---	AT1G15810	1.18	0.23	1.55	0.16772513	0.5545	-5.52
266384_at	hypothetical protein predicted by g	---	AT2G14660	-1.15	-0.20	-1.55	0.16772996	0.5545	-5.52
252520_at	receptor-like protein kinase homol	---	AT3G46370	-1.33	-0.41	-1.55	0.16776763	0.5545	-5.52
252214_at	putative protein EREBP-3 homolo	CEJ1	AT3G50260	1.36	0.44	1.55	0.16787074	0.5545	-5.52
248367_at	actin depolymerizing factor-like ;su	ADF10	AT5G52360	-1.16	-0.21	-1.55	0.16782401	0.5545	-5.52
254818_at	pEARLI 1-like protein Arabidopsis	---	AT4G12470	1.69	0.75	1.55	0.16789106	0.5545	-5.52
263498_at	unknown protein ; supported by cl	LSH10	AT2G42610	-1.80	-0.85	-1.55	0.16790066	0.5545	-5.52
260035_at	peroxidase ATP23a identical to pe	---	AT1G68850	1.25	0.32	1.55	0.16791611	0.5545	-5.52
252639_at	acyl CoA reductase -like protein a	FAR5	AT3G44550	1.10	0.14	1.55	0.16787451	0.5545	-5.52
265295_at	putative DNA replication licensing	MCM9	AT2G14050	1.16	0.21	1.54	0.16800267	0.5547	-5.52
250466_at	putative protein TETRATRICOPE	---	AT5G10090	-1.11	-0.15	-1.54	0.16804595	0.5548	-5.52
263957_at	unknown protein ; supported by cl	---	AT2G35880	1.12	0.16	1.54	0.16808834	0.5549	-5.52
265382_at	putative gluconokinase ;supported	---	AT2G16790	1.25	0.32	1.54	0.168124	0.5549	-5.52
267205_at	unknown protein	---	AT2G30820	-1.14	-0.19	-1.54	0.16819746	0.5550	-5.52
253541_at	putative protein various predicted	---	AT4G31630	-1.11	-0.16	-1.54	0.16821329	0.5550	-5.52
254592_at	heat shock transcription factor - lik	HSF A4A	AT4G18880	1.47	0.55	1.54	0.1683495	0.5552	-5.52
255176_s_at	putative DNA-directed RNA polym	---	AT1G01210	1.13	0.17	1.54	0.16829814	0.5552	-5.52
259087_at	hypothetical protein, contains Dna	---	AT3G04980	1.10	0.14	1.54	0.1683498	0.5552	-5.52
260863_at	hypothetical protein predicted by g	---	---	-1.20	-0.27	-1.54	0.16832255	0.5552	-5.52
261152_at	hypothetical protein predicted by g	---	AT1G04930	-1.21	-0.27	-1.54	0.16839712	0.5552	-5.52
246469_at	putative protein predicted protein,	---	AT5G17070	-1.12	-0.17	-1.54	0.16850758	0.5554	-5.52
255837_at	unknown protein	RIC1	AT2G33460	-1.13	-0.18	-1.54	0.16849465	0.5554	-5.52
252318_at	glutamate-1-semialdehyde aminotr	GSA2	AT3G48730	1.22	0.28	1.54	0.16848131	0.5554	-5.52
248570_at	receptor protein kinase-like	---	AT5G49780	-1.12	-0.16	-1.54	0.16853913	0.5554	-5.52
264594_at	hypothetical protein ; supported by	ATSERAT3	AT2G17640	1.14	0.19	1.54	0.16875811	0.5554	-5.52
253037_at	putative protein other predicted Ara	GAUT3	AT4G38270	-1.13	-0.17	-1.54	0.16879615	0.5554	-5.52
266272_at	hypothetical protein predicted by g	---	AT2G29600	-1.13	-0.18	-1.54	0.16877798	0.5554	-5.52
251797_at	putative protein AT-hook protein 1	AGF2	AT3G55560	1.18	0.24	1.54	0.16869546	0.5554	-5.52
256669_s_at	hypothetical protein similar to hypo	---	AT3G32200	-1.15	-0.21	-1.54	0.1687036	0.5554	-5.52
264718_at	receptor-like kinase, putative simil	---	AT1G70130	-1.11	-0.15	-1.54	0.16867571	0.5554	-5.52

262759_at	unknown protein	---	AT1G10800	-1.12	-0.16	-1.54	0.16861185	0.5554	-5.52
250511_at	putative protein similar to unknown	---	AT5G09960	1.13	0.18	1.54	0.1686464	0.5554	-5.52
246999_at	photoreceptor-interacting protein-li	NPY3	AT5G67440	1.26	0.34	1.54	0.16872256	0.5554	-5.52
259231_at	protein phosphatase 2C (PP2C) id	PP2CA	AT3G11410	-1.25	-0.33	-1.54	0.1687527	0.5554	-5.52
266268_at	unknown protein predicted by gene	---	AT2G29510	1.12	0.16	1.54	0.16888445	0.5556	-5.53
247949_at	cytochrome P450	CYP81F2	AT5G57220	1.79	0.84	1.54	0.16902708	0.5556	-5.53
250339_at	NADP dependent malic enzyme -	ATNADP-M	AT5G11670	-1.18	-0.24	-1.54	0.16905511	0.5556	-5.53
260523_at	putative salt-inducible protein	EMB2654	AT2G41720	1.19	0.26	1.54	0.16908539	0.5556	-5.53
265389_at	putative riboflavin synthase alpha	---	AT2G20690	-1.15	-0.20	-1.54	0.16890958	0.5556	-5.53
263381_at	putative MADS-box protein	AGL48	AT2G40210	-1.12	-0.16	-1.54	0.1690771	0.5556	-5.53
260728_at	Pto kinase interactor 1, putative si	---	AT1G48210	1.28	0.36	1.54	0.16910428	0.5556	-5.53
253434_at	potassium channel - protein	AKT5	AT4G32500	-1.13	-0.17	-1.54	0.16907992	0.5556	-5.53
244986_at	ribosomal protein S19	---	---	1.22	0.29	1.54	0.16904152	0.5556	-5.53
248339_at	prolyl tRNA synthetase	OVA6	AT5G52520	1.14	0.19	1.54	0.16907665	0.5556	-5.53
259948_at	unknown protein similar to LIGATI	---	AT1G71350	1.21	0.27	1.54	0.16924112	0.5557	-5.53
248308_at	putative protein similar to unknown	---	AT5G52530	1.12	0.17	1.54	0.16920543	0.5557	-5.53
255518_at	putative pectinesterase similar to s	---	AT4G02300	-1.14	-0.19	-1.54	0.16920772	0.5557	-5.53
259506_at	protein phosphatase type 2C, puta	---	AT1G43900	-1.13	-0.17	-1.54	0.16915483	0.5557	-5.53
248200_at	O-methyltransferase ;supported b	ATOMT1	AT5G54160	-1.41	-0.49	-1.54	0.16923551	0.5557	-5.53
256035_at	Ran-binding protein (atranbp1a) id	SIRANBP	AT1G07140	1.15	0.20	1.54	0.1695551	0.5566	-5.53
258970_at	putative serine carboxypeptidase p	scpl49	AT3G10410	-1.18	-0.24	-1.54	0.16970812	0.5568	-5.53
252304_at	hypothetical protein	---	AT3G49230	-1.10	-0.14	-1.54	0.16970858	0.5568	-5.53
260389_at	Expressed protein ; supported by f	---	AT1G74055	1.20	0.27	1.54	0.16962643	0.5568	-5.53
256214_x_at	hypothetical protein predicted by g	---	AT1G51000	-1.13	-0.17	-1.54	0.16972173	0.5568	-5.53
253158_at	putative protein protein kinase 6,	---	AT4G35780	1.17	0.23	1.54	0.16969798	0.5568	-5.53
264446_at	putative nuclear transport factor si	NTF2A	AT1G27310	1.14	0.19	1.54	0.16983152	0.5570	-5.53
252988_at	putative cold-regulated protein col	---	AT4G38410	1.27	0.34	1.54	0.16984559	0.5570	-5.53
249053_at	berberine bridge enzyme-like prote	---	AT5G44440	1.15	0.20	1.54	0.16986566	0.5570	-5.53
262521_at	unknown protein Location of est 27	---	AT1G17130	-1.13	-0.18	-1.54	0.16995463	0.5571	-5.53
261162_at	hypothetical protein predicted by g	---	AT1G34440	-1.15	-0.21	-1.54	0.16997517	0.5571	-5.53
261134_at	cytochrome P450, putative similar	CYP722A1	AT1G19630	-1.12	-0.17	-1.54	0.17004486	0.5571	-5.53
260660_at	hypothetical protein contains Pfam	---	AT1G19485	-1.16	-0.22	-1.54	0.1699353	0.5571	-5.53
251937_at	putative protein predicted protein,	CPuORF46	AT3G53400	-1.48	-0.57	-1.54	0.16991647	0.5571	-5.53
251807_at	methionyl-tRNA synthetase (AtcpM	OVA1	AT3G55400	1.17	0.22	1.54	0.17004282	0.5571	-5.53
262360_at	receptor protein kinase, putative s	---	AT1G73080	-1.67	-0.74	-1.54	0.17004742	0.5571	-5.53

265638_at	similar to PIG-L	---	AT2G27340	1.12	0.17	1.54	0.17008687	0.5571	-5.53
252922_at	putative protein	---	AT4G39040	1.13	0.17	1.54	0.17016364	0.5573	-5.53
245361_at	hypothetical protein ;supported by	---	AT4G17790	1.27	0.34	1.54	0.17021672	0.5574	-5.53
261484_at	E2, ubiquitin-conjugating enzyme	UBC1	AT1G14400	1.12	0.16	1.54	0.17026682	0.5574	-5.53
248887_at	Expressed protein ; supported by f	---	AT5G46115	-1.14	-0.19	-1.54	0.17024929	0.5574	-5.53
263111_s_at	hypothetical protein contains simila	---	AT1G65190	-1.19	-0.25	-1.53	0.17037157	0.5576	-5.53
259471_at	hypothetical protein contains simila	---	AT1G19040	-1.10	-0.14	-1.53	0.17043133	0.5578	-5.53
254859_at	putative protein Arabidopsis thalia	---	AT4G12060	1.17	0.23	1.53	0.17051951	0.5580	-5.53
252349_at	cell division cycle protein 23 homo	APC8	AT3G48150	1.22	0.29	1.53	0.17054254	0.5580	-5.53
248795_at	Myb-related transcription activator-	---	AT5G47390	1.11	0.15	1.53	0.17077707	0.5580	-5.54
247173_at	poly(A)-binding protein II-like ; sup	---	AT5G65260	1.15	0.21	1.53	0.17065232	0.5580	-5.53
246733_at	serine protease-like protein serine	---	AT5G27660	-1.14	-0.19	-1.53	0.17077399	0.5580	-5.54
252275_at	ubiquitin-specific protease 26 (UB	UBP26	AT3G49600	-1.19	-0.25	-1.53	0.17072723	0.5580	-5.54
267577_at	unknown protein ; supported by cl	---	AT2G30710	1.10	0.14	1.53	0.17064154	0.5580	-5.53
262344_at	cytochrome b245 beta chain hom	ATRBOH F	AT1G64060	-1.41	-0.50	-1.53	0.17068101	0.5580	-5.54
244973_at	PSII T protein	---	---	-1.33	-0.41	-1.53	0.17068224	0.5580	-5.54
255272_at	putative protein (ubiquitin like) to v	---	AT4G05270	-1.10	-0.14	-1.53	0.17078218	0.5580	-5.54
254028_s_at	putative protein N.crassa mRNA f	ORP4B	AT4G25850	1.12	0.16	1.53	0.17076481	0.5580	-5.54
260712_at	protein phosphatase 2C, putative	HAB2	AT1G17550	1.18	0.24	1.53	0.17084493	0.5581	-5.54
255477_at	coded for by A. thaliana cDNA R64	---	AT4G02370	1.17	0.23	1.53	0.17090415	0.5583	-5.54
246698_at	putative protein	---	---	-1.12	-0.16	-1.53	0.17095178	0.5583	-5.54
253184_at	putative protein protein kinase AP	BSK1	AT4G35230	1.14	0.19	1.53	0.17117944	0.5587	-5.54
262533_at	hypothetical protein Pfam	---	AT1G17090	1.14	0.19	1.53	0.17116464	0.5587	-5.54
246047_at	putative protein predicted proteins	---	---	-1.13	-0.18	-1.53	0.17109419	0.5587	-5.54
254623_at	protein ch-42 precursor, chloropla	CHLI1	AT4G18480	1.18	0.24	1.53	0.17120832	0.5587	-5.54
265906_at	hypothetical protein predicted by g	---	AT2G25565	-1.14	-0.18	-1.53	0.17113758	0.5587	-5.54
AFFX-DapX-M	B. subtilis /GEN=dapB, jojF /DB_X	---	---	-1.22	-0.29	-1.53	0.17121507	0.5587	-5.54
253544_at	hypothetical protein	---	AT4G31280	-1.11	-0.15	-1.53	0.17124641	0.5587	-5.54
255969_at	Expressed protein ; supported by f	---	AT1G22330	-1.28	-0.36	-1.53	0.1713277	0.5587	-5.54
252410_at	putative protein br-1 protein (NITR	NOA1	AT3G47450	1.16	0.22	1.53	0.17134465	0.5587	-5.54
AFFX-ThrX-M_	B. subtilis /GEN=thrC, thrB /DB_XI	---	---	-1.32	-0.40	-1.53	0.17133999	0.5587	-5.54
245507_at	hypothetical protein	---	AT4G15710	1.18	0.23	1.53	0.17134527	0.5587	-5.54
261911_at	ribosomal protein L7, putative sim	---	AT1G80750	1.27	0.35	1.53	0.17140271	0.5588	-5.54
248446_at	putative protein similar to unknown	---	AT5G51140	1.12	0.17	1.53	0.17152868	0.5592	-5.54
264938_at	unknown protein contains similarity	---	AT1G60610	1.13	0.18	1.53	0.17158064	0.5593	-5.54

253419_at	putative protein predicted proteins	---	AT4G32780	-1.15	-0.20	-1.53	0.17160271	0.5593	-5.54
257901_at	hypothetical protein predicted by g	---	---	-1.13	-0.17	-1.53	0.1716365	0.5593	-5.54
258276_at	putative signal peptidase 21kDa su	---	AT3G15710	-1.16	-0.21	-1.53	0.17167606	0.5593	-5.54
257889_at	S1 self-incompatibility protein, put	---	AT3G17080	-1.16	-0.21	-1.53	0.17175488	0.5595	-5.54
262909_at	serine/threonine protein phosphat	PP2A-1	AT1G59830	1.14	0.19	1.53	0.17180997	0.5596	-5.54
267241_at	hypothetical protein predicted by g	---	AT2G02490	-1.11	-0.15	-1.53	0.17184883	0.5596	-5.54
264622_at	putative vacuolar sorting protein 35	VPS35A	AT2G17790	-1.14	-0.19	-1.53	0.17186762	0.5596	-5.54
245442_at	hypothetical protein	---	AT4G16710	1.11	0.15	1.53	0.17190742	0.5597	-5.54
252358_at	putative protein cfxY protein, Alca	---	AT3G48425	1.12	0.16	1.53	0.1719795	0.5598	-5.54
265403_at	putative Ta11-like non-LTR retroel	---	---	-1.14	-0.19	-1.53	0.17204617	0.5599	-5.54
250701_at	bZIP transcription factor-like protei	---	AT5G06839	-1.14	-0.19	-1.53	0.17207984	0.5599	-5.54
259627_at	unknown protein ; supported by cD	---	AT1G42960	1.14	0.20	1.53	0.1720773	0.5599	-5.54
261093_at	non-LTR reverse transcriptase, pu	AT1G62880	---	1.16	0.21	1.53	0.17212282	0.5600	-5.54
267304_at	putative Fe(II) transport protein	ZIP6	AT2G30080	-1.17	-0.23	-1.53	0.17219409	0.5601	-5.54
266630_at	putative serpin	---	AT2G35580	1.11	0.16	1.53	0.17223291	0.5602	-5.54
254751_at	hypothetical protein	---	AT4G13150	-1.12	-0.16	-1.53	0.17232397	0.5603	-5.54
251354_at	putative protein hypothetical prote	---	AT3G61090	-1.11	-0.15	-1.53	0.17232691	0.5603	-5.54
260109_at	hypothetical protein predicted by g	TET10	AT1G63260	-1.16	-0.22	-1.53	0.17238265	0.5604	-5.54
264209_at	RAS-related protein, RAB7 identic	RABG3B	AT1G22740	1.16	0.21	1.53	0.17241248	0.5605	-5.54
254356_at	hypothetical protein ;supported by	---	AT4G22190	-1.16	-0.21	-1.53	0.17247452	0.5606	-5.54
256016_at	hypothetical protein predicted by g	---	AT1G19240	1.15	0.21	1.53	0.17256964	0.5608	-5.54
262964_at	hypothetical protein predicted by g	---	AT1G54380	1.20	0.27	1.53	0.17266224	0.5610	-5.55
262028_at	DNA binding protein, putative simi	---	AT1G35560	-1.12	-0.16	-1.52	0.17283938	0.5615	-5.55
264770_at	unknown protein similar to unknow	---	AT1G23030	-1.30	-0.38	-1.52	0.17291503	0.5616	-5.55
251854_at	putative protein various predicted	---	AT3G54800	-1.12	-0.16	-1.52	0.17292661	0.5616	-5.55
266079_at	unknown protein	LCD1	AT2G37860	-1.16	-0.22	-1.52	0.17292303	0.5616	-5.55
267071_at	unknown protein	---	AT2G40980	-1.12	-0.16	-1.52	0.17299942	0.5617	-5.55
252281_at	putative protein various predicted p	---	AT3G49320	1.18	0.24	1.52	0.17306199	0.5618	-5.55
248972_at	putative protein similar to unknown	ATDSS1(V)	AT5G45010	1.22	0.29	1.52	0.17307245	0.5618	-5.55
256512_at	Expressed protein ; supported by f	---	AT1G33265	1.16	0.21	1.52	0.17309878	0.5618	-5.55
259553_x_at	hypothetical protein	ATEXT3	AT1G21310	1.36	0.44	1.52	0.17314241	0.5619	-5.55
264753_at	receptor kinase, putative similar to	---	AT1G61490	1.10	0.14	1.52	0.17317876	0.5619	-5.55
252291_s_at	peroxidase ;supported by full-leng	PRXCB	AT3G49110	-1.26	-0.33	-1.52	0.17322589	0.5619	-5.55
259191_at	unknown protein	---	AT3G01720	-1.16	-0.22	-1.52	0.17325904	0.5619	-5.55
252718_at	putative protein predicted proteins	---	AT3G43940	-1.14	-0.19	-1.52	0.17326299	0.5619	-5.55

248142_at	putative protein similar to unknown	---	AT5G55040	-1.12	-0.16	-1.52	0.17329585	0.5620	-5.55
254128_at	ubiquitin-specific protease 16 (UB	UBP16	AT4G24560	-1.10	-0.14	-1.52	0.17332933	0.5620	-5.55
255797_at	putative steroid dehydrogenase ; s	---	AT2G33630	1.20	0.26	1.52	0.17336851	0.5620	-5.55
260057_at	putative protein phosphatase 2C s	---	AT1G78200	1.11	0.16	1.52	0.17342689	0.5621	-5.55
245988_at	putative protein predicted protein,	---	AT5G20610	-1.18	-0.23	-1.52	0.17346078	0.5621	-5.55
253737_at	Expressed protein ; supported by f	---	AT4G28703	1.42	0.51	1.52	0.17342621	0.5621	-5.55
263135_at	flavanone 3-hydroxylase, putative	---	AT1G78550	1.17	0.22	1.52	0.1734693	0.5621	-5.55
245891_at	amino acid transport protein AAP2	AAP2	AT5G09220	-1.39	-0.47	-1.52	0.17350914	0.5621	-5.55
254258_at	hypothetical protein	TET5	AT4G23410	1.16	0.21	1.52	0.17362097	0.5624	-5.55
255956_at	Expressed protein ; supported by f	DD46	AT1G22015	-1.14	-0.19	-1.52	0.1736675	0.5625	-5.55
259483_at	hypothetical protein predicted by g	---	AT1G43980	-1.12	-0.16	-1.52	0.1737485	0.5626	-5.55
267285_at	unknown protein	---	AT2G23690	-1.24	-0.31	-1.52	0.17393088	0.5631	-5.55
263759_at	hypothetical protein predicted by g	---	AT2G21290	1.14	0.18	1.52	0.17408116	0.5634	-5.55
262071_at	unknown protein ;supported by full	CF9	AT1G59510	1.15	0.20	1.52	0.1741298	0.5634	-5.55
254674_at	EREBP - like protein EREBP-1 (E	---	AT4G18450	-1.10	-0.14	-1.52	0.17405953	0.5634	-5.55
247451_at	MYB99 ; supported by cDNA: gi_1	ATMYB99	AT5G62320	1.14	0.19	1.52	0.17404899	0.5634	-5.55
250035_at	putative protein contains similarity	---	AT5G18230	1.11	0.15	1.52	0.17412593	0.5634	-5.55
251579_at	putative protein Bet1 homolog - R	BS14A	AT3G58170	1.12	0.16	1.52	0.17430558	0.5638	-5.55
249779_at	putative protein similar to unknown	---	AT5G24230	-1.12	-0.16	-1.52	0.17429625	0.5638	-5.55
260946_at	hypothetical protein predicted by g	---	AT1G06010	1.15	0.20	1.52	0.17437166	0.5639	-5.55
246004_at	germin-like protein ; supported by	GER3	AT5G20630	3.09	1.63	1.52	0.17446112	0.5641	-5.55
251161_at	putative protein hypothetical prote	---	AT3G63290	1.14	0.19	1.52	0.1745264	0.5642	-5.56
252547_at	putative protein many predicted pr	---	AT3G45840	-1.15	-0.20	-1.52	0.17452845	0.5642	-5.56
253875_at	putative protein ENOD20 gene, M	---	AT4G27520	-1.28	-0.35	-1.52	0.17476412	0.5646	-5.56
256268_at	retinoblastoma-related protein, pu	RBR1	AT3G12280	1.17	0.23	1.52	0.17471599	0.5646	-5.56
247970_at	cytosolic malate dehydrogenase	---	AT5G56720	-1.12	-0.17	-1.52	0.17473892	0.5646	-5.56
247651_at	histone H2A - like protein histone	HTA6	AT5G59870	1.64	0.71	1.52	0.17476132	0.5646	-5.56
249240_at	putative protein similar to unknown	---	AT5G42220	-1.16	-0.21	-1.52	0.17478525	0.5646	-5.56
255822_at	putative expansin ;supported by fu	ATEXPA8	AT2G40610	2.63	1.39	1.52	0.17482944	0.5647	-5.56
256325_at	hypothetical protein	---	AT3G02330	-1.15	-0.20	-1.52	0.17491167	0.5648	-5.56
250541_at	putative proline-rich protein surfac	---	AT5G09520	1.25	0.32	1.52	0.17491944	0.5648	-5.56
257894_at	unknown protein ; supported by cD	---	AT3G17100	1.27	0.34	1.52	0.17500691	0.5649	-5.56
258741_at	Lon protease, putative similar to L	LON4	AT3G05790	-1.11	-0.15	-1.52	0.17498843	0.5649	-5.56
246943_at	putative protein kinase serine/thre	---	AT5G25440	-1.22	-0.28	-1.52	0.17513905	0.5650	-5.56
264262_at	Expressed protein ; supported by f	---	AT1G09200	1.71	0.77	1.52	0.17516166	0.5650	-5.56

249918_at	putative protein predicted protein,	---	AT5G19240	-1.47	-0.55	-1.52	0.17511106	0.5650	-5.56
254172_at	clathrin coat assembly like protein	---	AT4G24550	1.11	0.16	1.52	0.17507033	0.5650	-5.56
259021_at	hypothetical protein predicted by g	---	AT3G07540	1.26	0.33	1.52	0.17514818	0.5650	-5.56
253655_at	Expressed protein ;supported by c	LCR59	AT4G30070	1.10	0.14	1.52	0.17505633	0.5650	-5.56
247837_at	N-hydroxycinnamoyl/benzoyltransf	---	AT5G57840	-1.18	-0.24	-1.52	0.17522213	0.5651	-5.56
254299_at	hypothetical protein ;supported by	NYE1	AT4G22920	1.28	0.35	1.51	0.17543019	0.5653	-5.56
247271_at	nuclear protein-like	---	AT5G64270	1.15	0.20	1.51	0.17543409	0.5653	-5.56
253700_at	threonine synthase	MTO2	AT4G29840	-1.20	-0.27	-1.51	0.17539865	0.5653	-5.56
262128_at	late embryogenesis-abundant pro	---	AT1G52690	-2.11	-1.08	-1.51	0.17542808	0.5653	-5.56
255985_at	putative protein contains similarity	---	AT1G34150	1.11	0.15	1.51	0.17531507	0.5653	-5.56
250910_at	heat shock transcription factor -lik	HSFA3	AT5G03720	1.44	0.52	1.51	0.17541124	0.5653	-5.56
245797_at	defective chloroplasts and leaves	---	AT1G45230	1.09	0.13	1.51	0.17579734	0.5656	-5.56
248631_at	putative protein strong similarity to	---	AT5G49000	-1.16	-0.21	-1.51	0.17566861	0.5656	-5.56
265375_at	unknown protein ;supported by ful	VPS2.1	AT2G06530	-1.17	-0.22	-1.51	0.17575261	0.5656	-5.56
253079_s_at	putative protein F56F10.1, Caeno	---	AT4G36190 /	-1.18	-0.24	-1.51	0.17558402	0.5656	-5.56
250964_at	putative protein various predicted	---	AT5G03010	-1.16	-0.21	-1.51	0.17580813	0.5656	-5.56
261171_at	unknown protein	---	AT1G04880	-1.12	-0.17	-1.51	0.17573592	0.5656	-5.56
262823_at	ATP-dependent Clp protease prote	CLPP6	AT1G11750	1.12	0.17	1.51	0.17575464	0.5656	-5.56
265003_at	protein kinase, putative similar to	---	AT1G26970	1.10	0.13	1.51	0.17580272	0.5656	-5.56
250898_at	putative protein ; supported by cD	ADK2	AT5G03300	1.17	0.22	1.51	0.17576383	0.5656	-5.56
256719_at	En/Spm-like transposon protein rel	---	---	-1.12	-0.17	-1.51	0.17567766	0.5656	-5.56
251972_at	nodulin / glutamate-ammonia ligas	---	AT3G53170	1.14	0.19	1.51	0.17574552	0.5656	-5.56
252574_at	receptor like protein kinase recept	---	AT3G45430	-1.14	-0.19	-1.51	0.17591517	0.5659	-5.56
262758_at	hypothetical protein predicted by g	---	AT1G10780	1.14	0.18	1.51	0.17596144	0.5659	-5.56
249406_at	putative protein MtN21, Medicago	---	AT5G40210	-1.15	-0.21	-1.51	0.17599455	0.5660	-5.56
255569_at	putative CAAX prenyl protease ; s	ATSTE24	AT4G01320	1.12	0.16	1.51	0.17601467	0.5660	-5.56
249112_at	ATP sulfurylase precursor (gb|AAD	APS4	AT5G43780	-1.26	-0.34	-1.51	0.17608589	0.5660	-5.56
252112_at	putative protein merozoite surface	---	AT3G51580	-1.15	-0.20	-1.51	0.17607706	0.5660	-5.56
264307_at	hypothetical protein contains simila	---	AT1G61900	1.16	0.21	1.51	0.17614496	0.5661	-5.56
266839_at	unknown protein	ELF3	AT2G25930	1.11	0.16	1.51	0.17628186	0.5665	-5.56
264361_at	unknown protein Strong similarity t	---	AT1G03300	1.13	0.18	1.51	0.17636275	0.5667	-5.56
247113_at	unknown protein ;supported by full	---	AT5G65960	1.13	0.17	1.51	0.1763802	0.5667	-5.56
257017_at	beta-xylosidase, putative similar to	---	AT3G19620	-1.12	-0.17	-1.51	0.17645817	0.5668	-5.57
261284_at	hypothetical protein predicted by g	---	---	-1.14	-0.19	-1.51	0.17651422	0.5669	-5.57
259789_at	Expressed protein ; supported by f	COR414-TI	AT1G29395	1.14	0.19	1.51	0.17660316	0.5669	-5.57

246220_at	putative protein ; supported by cDN	---	AT4G37210	1.11	0.16	1.51	0.17656145	0.5669	-5.57
250654_at	receptor protein kinase-like protein	---	AT5G06940	1.14	0.19	1.51	0.17662053	0.5669	-5.57
246872_at	extensin - like protein hydroxyprol	---	AT5G26080	1.15	0.20	1.51	0.17658872	0.5669	-5.57
245528_at	pyruvate,orthophosphate dikinase	PPDK	AT4G15530	1.16	0.22	1.51	0.17669007	0.5670	-5.57
260676_at	integral membrane protein, putativ	---	AT1G19450	-1.26	-0.34	-1.51	0.17705524	0.5670	-5.57
259089_at	hypothetical protein similar to GB:(	---	AT3G04960	1.12	0.17	1.51	0.176861	0.5670	-5.57
249198_s_at	putative protein similar to unknown	---	AT5G42350	1.13	0.17	1.51	0.17697359	0.5670	-5.57
266847_at	hypothetical protein predicted by g	emb1345	AT2G26060	1.16	0.22	1.51	0.17682263	0.5670	-5.57
249635_at	putative glucan synthase glucan sy	ATGSL09	AT5G36870	-1.13	-0.18	-1.51	0.17687748	0.5670	-5.57
247317_at	putative protein contains similarity	anac103	AT5G64060	-1.14	-0.19	-1.51	0.17718362	0.5670	-5.57
262084_at	hypothetical protein predicted by g	---	AT1G56080	-1.14	-0.20	-1.51	0.1768745	0.5670	-5.57
259974_at	putative phosphate transporter sim	---	AT1G76430	-1.16	-0.22	-1.51	0.17712919	0.5670	-5.57
250380_at	putative protein	---	AT5G11600	1.13	0.17	1.51	0.17675236	0.5670	-5.57
258452_at	alternative oxidase 1a precursor id	AOX1A	AT3G22370	-1.48	-0.57	-1.51	0.17715221	0.5670	-5.57
249555_at	putative protein predicted protein,	---	AT5G38300	-1.13	-0.18	-1.51	0.17703161	0.5670	-5.57
251203_at	putative protein putative transcript	---	AT3G63070	-1.11	-0.15	-1.51	0.17694963	0.5670	-5.57
255149_at	KNAT1 homeobox-like protein	KNAT1	AT4G08150	-1.14	-0.19	-1.51	0.17672657	0.5670	-5.57
253625_at	signal recognition particle recepto	---	AT4G30600	-1.11	-0.15	-1.51	0.17698677	0.5670	-5.57
256294_at	unknown protein	---	AT1G69450	-1.15	-0.21	-1.51	0.17714998	0.5670	-5.57
259539_at	axi 1 protein, putative similar to ax	---	AT1G20550	1.14	0.19	1.51	0.17670749	0.5670	-5.57
259502_at	unknown protein ; supported by cD	---	AT1G15670	1.29	0.37	1.51	0.17709297	0.5670	-5.57
265361_at	putative retroelement pol polyprote	---	---	1.12	0.16	1.51	0.17717846	0.5670	-5.57
256156_at	phosphoinositide specific phospho	ATPLC2	AT3G08510	-1.12	-0.17	-1.51	0.17714289	0.5670	-5.57
259499_at	PRLI-interacting factor L, putative	---	AT1G15730	1.17	0.22	1.51	0.17690884	0.5670	-5.57
261774_at	unknown protein	---	AT1G76260	1.24	0.31	1.51	0.17683855	0.5670	-5.57
248895_at	receptor protein kinase	FLS2	AT5G46330	-1.31	-0.39	-1.51	0.17720967	0.5670	-5.57
248281_at	unknown protein	---	AT5G52980	-1.11	-0.15	-1.51	0.17727864	0.5671	-5.57
262788_at	unknown protein ESTs gb|T75618	---	AT1G10690	1.18	0.24	1.51	0.17735201	0.5673	-5.57
257268_at	unknown protein	---	AT3G17450	-1.19	-0.25	-1.51	0.17746302	0.5676	-5.57
247261_at	ZW10-like protein ; supported by c	---	AT5G64460	1.12	0.17	1.51	0.17748941	0.5676	-5.57
263866_at	putative farnesylated protein ;supp	---	AT2G36950	1.22	0.28	1.51	0.17756214	0.5677	-5.57
252251_at	hypothetical protein	---	AT3G49820	-1.11	-0.15	-1.51	0.17754636	0.5677	-5.57
262796_at	cysteine proteinase XCP2 identica	XCP2	AT1G20850	1.39	0.47	1.51	0.1776062	0.5677	-5.57
249327_at	anion channel protein (gb|AAC057	ATCLC-A	AT5G40890	-1.29	-0.36	-1.51	0.17765217	0.5677	-5.57
248559_at	unknown protein	---	AT5G50010	-1.13	-0.18	-1.51	0.17764382	0.5677	-5.57

265566_at	hypothetical protein predicted by g	---	AT2G05600	1.14	0.19	1.51	0.17769277	0.5678	-5.57
259796_at	hypothetical protein predicted by g	---	---	-1.15	-0.20	-1.51	0.17772157	0.5678	-5.57
255046_at	H+-transporting ATP synthase-like	ATPD	AT4G09650	1.15	0.20	1.50	0.17788616	0.5680	-5.57
253583_at	translation initiation factor-like pro	---	AT4G30680	-1.16	-0.22	-1.50	0.17794619	0.5680	-5.57
266526_at	putative tetracycline transporter pr	---	AT2G16980	-1.14	-0.19	-1.50	0.1778851	0.5680	-5.57
265814_at	hypothetical protein similar to hyp	---	AT2G17930	1.13	0.17	1.50	0.1778668	0.5680	-5.57
245410_at	putative protein	ATMAP70-5	AT4G17220	-1.12	-0.16	-1.50	0.17792733	0.5680	-5.57
AFFX-ThrX-3_a	B. subtilis /GEN=thrB /DB_XREF=	---	---	-1.23	-0.30	-1.50	0.17791216	0.5680	-5.57
249872_at	unknown protein	---	AT5G23130	1.44	0.52	1.50	0.17813253	0.5683	-5.57
264101_at	unknown protein similar to putative	HAC1	AT1G79000	1.15	0.21	1.50	0.17808066	0.5683	-5.57
246416_at	putative protein predicted proteins	---	AT5G16920	-1.13	-0.17	-1.50	0.17810016	0.5683	-5.57
252599_at	receptor-like protein kinase recept	---	AT3G45390	-1.17	-0.23	-1.50	0.17812204	0.5683	-5.57
265161_at	putative vacuolar sorting receptor s	---	AT1G30900	1.62	0.69	1.50	0.17814933	0.5683	-5.57
251265_at	ATP-dependent RNA helicase-like	---	AT3G62310	1.17	0.23	1.50	0.17824234	0.5684	-5.57
267269_at	unknown protein	CAND1	AT2G02560	1.14	0.19	1.50	0.178245	0.5684	-5.57
257216_at	4-methyl-5(b-hydroxyethyl)-thiazo	---	AT3G14990	1.30	0.38	1.50	0.17830723	0.5685	-5.57
258892_at	unknown protein	---	AT3G05670	-1.12	-0.16	-1.50	0.17834248	0.5686	-5.57
251175_at	homocysteine S-methyltransferase	HMT2	AT3G63250	1.13	0.17	1.50	0.17845182	0.5687	-5.58
267021_at	hypothetical protein predicted by g	---	AT2G39300	1.10	0.14	1.50	0.17845451	0.5687	-5.58
263745_at	hypothetical protein predicted by g	CHR34	AT2G21450	-1.11	-0.16	-1.50	0.17846875	0.5687	-5.58
260667_at	very-long-chain fatty acid condens	KCS4	AT1G19440	-1.12	-0.16	-1.50	0.17875319	0.5688	-5.58
266215_at	putative endoxyloglucan glycosyltr	EXGT-A1	AT2G06850	1.44	0.53	1.50	0.17869485	0.5688	-5.58
248942_at	putative protein similar to unknown	---	AT5G45480	-1.15	-0.20	-1.50	0.17877168	0.5688	-5.58
258910_at	putative RNA helicase similar to R	---	AT3G06480	1.12	0.16	1.50	0.17852469	0.5688	-5.58
254341_at	serine/threonine protein kinase lik	SRF8	AT4G22130	-1.38	-0.47	-1.50	0.17854634	0.5688	-5.58
249381_at	acidic ribosomal protein P2 -like a	---	AT5G40040	-1.16	-0.21	-1.50	0.17878991	0.5688	-5.58
247090_at	putative protein similar to unknown	---	AT5G66370	-1.13	-0.17	-1.50	0.17869604	0.5688	-5.58
252597_at	putative protein several hypothetic	---	---	-1.15	-0.21	-1.50	0.17875303	0.5688	-5.58
261703_at	OsNAC7 protein, putative similar t	ANAC012	AT1G32770	-1.11	-0.15	-1.50	0.17861947	0.5688	-5.58
252447_at	beta-D-glucan exohydrolase - like	---	AT3G47040	-1.12	-0.16	-1.50	0.17874216	0.5688	-5.58
253526_at	putative zinc finger protein hypoth	---	AT4G31420	1.12	0.16	1.50	0.17867774	0.5688	-5.58
247543_at	DNA binding protein - like DNA bi	---	AT5G61600	1.45	0.54	1.50	0.17864245	0.5688	-5.58
260174_at	unknown protein ;supported by ful	---	AT1G71940	-1.12	-0.16	-1.50	0.17886246	0.5689	-5.58
251360_at	putative protein embryonic abunda	---	AT3G61210	1.12	0.16	1.50	0.17892724	0.5690	-5.58
260525_at	putative pre-mRNA splicing factor	---	AT2G47250	1.11	0.15	1.50	0.1789866	0.5690	-5.58

264429_at	hypothetical protein similar to mem	---	AT1G61670	-1.11	-0.15	-1.50	0.17899451	0.5690	-5.58
251542_at	putative protein protein-tyrosine ki	---	AT3G58760	-1.16	-0.22	-1.50	0.1789669	0.5690	-5.58
245681_at	alkaline/neutral invertase, putative	---	AT1G56560	-1.11	-0.15	-1.50	0.17906513	0.5691	-5.58
261448_at	tonoplast intrinsic protein, alpha (a	---	AT1G21140	-1.21	-0.28	-1.50	0.17904121	0.5691	-5.58
265728_at	hypothetical protein predicted by g	---	AT2G31990	1.18	0.24	1.50	0.17918798	0.5693	-5.58
246650_at	putative protein p76, Homo sapien	---	AT5G35160	1.13	0.18	1.50	0.17918466	0.5693	-5.58
265651_at	hypothetical protein predicted by g	---	AT2G13900	1.11	0.16	1.50	0.17918322	0.5693	-5.58
267224_at	hypothetical protein predicted by g	---	AT2G43990	1.16	0.21	1.50	0.17921496	0.5693	-5.58
261728_at	pectinesterase, putative similar to	sks5	AT1G76160	-1.23	-0.30	-1.50	0.17932327	0.5694	-5.58
259292_at	unknown protein	---	AT3G11560	1.13	0.18	1.50	0.17932576	0.5694	-5.58
245527_at	putative epoxide hydrolase	---	AT4G15955	-1.17	-0.22	-1.50	0.17933029	0.5694	-5.58
252048_at	expressed protein supported by cD	---	AT3G52500	-1.18	-0.24	-1.50	0.17936723	0.5694	-5.58
264054_at	unknown protein	SVP	AT2G22540	1.15	0.20	1.50	0.179486	0.5694	-5.58
264549_at	putative ser/thr protein kinase simi	---	AT1G09440	1.12	0.16	1.50	0.17953395	0.5694	-5.58
260037_at	putative DNA-binding protein (RAV	RAV2	AT1G68840	1.60	0.68	1.50	0.17945798	0.5694	-5.58
250010_at	AP2-domain DNA-binding protein	---	AT5G18450	-1.17	-0.23	-1.50	0.179505	0.5694	-5.58
250593_at	putative protein similar to unknown	---	AT5G07740	-1.11	-0.15	-1.50	0.17953487	0.5694	-5.58
247257_at	proteasome regulatory subunit-like	RPN5B	AT5G64760	1.29	0.36	1.50	0.17943706	0.5694	-5.58
253548_at	Expressed protein ; supported by f	---	AT4G30993	1.18	0.24	1.50	0.17944214	0.5694	-5.58
265264_at	hypothetical protein predicted by g	---	AT2G42930	-1.11	-0.16	-1.50	0.1796323	0.5696	-5.58
245708_at	pectate lyase-like protein	---	AT5G04310	-1.15	-0.21	-1.50	0.17976618	0.5697	-5.58
249954_at	putative protein ;supported by full-	---	AT5G18920	1.09	0.13	1.50	0.17973207	0.5697	-5.58
257241_at	hypothetical protein contains Pfam	---	AT3G24210	1.16	0.21	1.50	0.17973381	0.5697	-5.58
247091_at	peroxidase (emb CAA66964.1)	---	AT5G66390	1.14	0.19	1.50	0.17975952	0.5697	-5.58
257580_at	hypothetical protein	---	AT3G06210	1.14	0.19	1.50	0.17983391	0.5699	-5.58
248238_at	putative protein similar to unknown	---	AT5G53900	1.18	0.24	1.50	0.17985362	0.5699	-5.58
265955_at	putative ABC transporter	PDR5	AT2G37280	1.13	0.17	1.50	0.17993716	0.5701	-5.58
253253_at	putative protein auxin-regulated g	---	AT4G34750	1.12	0.17	1.50	0.18002973	0.5703	-5.58
248804_at	nodulin-like protein	---	AT5G47470	-1.13	-0.18	-1.50	0.18010957	0.5704	-5.58
247324_at	putative protein strong similarity to	---	AT5G64190	-1.57	-0.65	-1.50	0.18013942	0.5705	-5.58
254863_at	putative protein predicted protein	ATNUDX14	AT4G11980	-1.15	-0.20	-1.50	0.18020811	0.5706	-5.58
267157_at	putative MYB family transcription f	AS1	AT2G37630	1.21	0.27	1.49	0.18025976	0.5706	-5.58
254627_at	Expressed protein ; supported by f	---	AT4G18395	-1.11	-0.15	-1.50	0.18024164	0.5706	-5.58
247119_at	ATP-dependent RNA helicase-like	---	AT5G65900	-1.10	-0.13	-1.49	0.18030397	0.5707	-5.58
266051_at	rhodanese-like family protein	---	AT2G40760	1.18	0.24	1.49	0.1803813	0.5708	-5.58

253438_at	glycine hydroxymethyltransferase	SHM3	AT4G32520	1.17	0.23	1.49	0.18048572	0.5709	-5.59
253162_at	phosphoserine aminotransferase ;	PSAT	AT4G35630	-1.57	-0.65	-1.49	0.18046313	0.5709	-5.59
266906_at	Expressed protein ; supported by f	---	AT2G34585	1.18	0.24	1.49	0.18046041	0.5709	-5.59
252764_at	nucleic acid binding protein-like nu	AL3	AT3G42790	1.13	0.17	1.49	0.18051239	0.5709	-5.59
260086_at	hypothetical protein predicted by g	---	AT1G63240	-1.18	-0.24	-1.49	0.18054656	0.5710	-5.59
258298_at	unknown protein ; supported by cl	---	AT3G23300	1.18	0.23	1.49	0.18064324	0.5710	-5.59
248918_at	senescence-specific cysteine prote	SAG12	AT5G45890	-1.17	-0.23	-1.49	0.18062232	0.5710	-5.59
263655_at	hypothetical protein predicted by g	---	AT1G04500	1.12	0.17	1.49	0.18064739	0.5710	-5.59
248404_at	trehalose-6-phosphate phosphatas	ATTPPA	AT5G51460	1.29	0.37	1.49	0.18067891	0.5711	-5.59
266796_at	predicted by genscan	---	AT2G02880	1.13	0.17	1.49	0.18076809	0.5712	-5.59
266159_at	putative chloroplast nucleoid DNA	---	AT2G28030	-1.11	-0.15	-1.49	0.18076898	0.5712	-5.59
261229_at	RAC-like GTP-binding protein ARA	ROP2	AT1G20090	1.10	0.14	1.49	0.1808811	0.5714	-5.59
260029_at	endoplasmic reticulum alpha-man	---	AT1G30000	-1.11	-0.15	-1.49	0.18090998	0.5714	-5.59
259207_at	unknown protein	---	AT3G09050	1.16	0.22	1.49	0.18089261	0.5714	-5.59
260386_at	putative strictosidine synthase sim	---	AT1G74010	1.52	0.61	1.49	0.181154	0.5714	-5.59
256468_at	ferredoxin, putative similar to GB:I	---	AT1G32550	1.15	0.20	1.49	0.1810613	0.5714	-5.59
259649_at	Serine/arginine-rich protein, putati	TAF7	AT1G55300	-1.12	-0.16	-1.49	0.18103854	0.5714	-5.59
266883_at	putative triacylglycerol lipase	DAD1	AT2G44810	-1.12	-0.17	-1.49	0.18115272	0.5714	-5.59
249130_at	putative protein contains similarity	---	AT5G43100	1.11	0.15	1.49	0.18106684	0.5714	-5.59
257657_at	Expressed protein ; supported by f	---	AT3G13235	1.11	0.15	1.49	0.18098503	0.5714	-5.59
261510_at	hypothetical protein predicted by g	---	AT1G71760	1.12	0.17	1.49	0.18114365	0.5714	-5.59
261739_at	hypothetical protein similar to hypo	PEX11A	AT1G47750	1.11	0.15	1.49	0.18114291	0.5714	-5.59
266603_at	hypothetical protein predicted by g	---	AT2G46040	1.12	0.17	1.49	0.18115441	0.5714	-5.59
253373_at	lysine-ketoglutarate reductase/sac	---	AT4G33150	1.41	0.50	1.49	0.18136064	0.5717	-5.59
251288_at	exonuclease RRP41 ; supported b	RRP41	AT3G61620	1.18	0.24	1.49	0.18128649	0.5717	-5.59
248682_at	cytochrome b5 (dbj|BAA74840.1)	CB5-D	AT5G48810	1.12	0.16	1.49	0.18135018	0.5717	-5.59
259475_at	unknown protein ;supported by full	---	AT1G19140	-1.22	-0.29	-1.49	0.18134044	0.5717	-5.59
264000_at	putative mitochondrial dicarboxylat	UCP5	AT2G22500	-1.57	-0.65	-1.49	0.18135262	0.5717	-5.59
245403_at	putative protein	---	AT4G17590	-1.11	-0.15	-1.49	0.18146691	0.5720	-5.59
246528_at	putative mitochondrial carrier prot	---	AT5G15640	-1.23	-0.30	-1.49	0.18151583	0.5720	-5.59
253058_at	ribosomal - like protein ribosomal	---	AT4G37660	1.19	0.26	1.49	0.18158798	0.5721	-5.59
252159_at	hypothetical protein	---	AT3G50540	-1.12	-0.16	-1.49	0.18158569	0.5721	-5.59
258250_at	putative delta 9 desaturase similar	FAD5	AT3G15850	-1.11	-0.15	-1.49	0.18168158	0.5722	-5.59
249253_at	putative protein similar to unknown	---	AT5G42060	1.14	0.19	1.49	0.18166134	0.5722	-5.59
252980_at	putative protein Human multiple e	---	AT4G38040	1.10	0.14	1.49	0.18170771	0.5722	-5.59

262676_at	SKP1/ASK1 (At1) identical to Skp	SKP1	AT1G75950	-1.10	-0.13	-1.49	0.18175245	0.5723	-5.59
253295_at	putative aspartate--tRNA ligase as	---	AT4G33760	1.20	0.26	1.49	0.18179082	0.5723	-5.59
262597_at	unknown protein Strong similarity	---	AT1G15470	-1.17	-0.23	-1.49	0.18183792	0.5724	-5.59
255982_at	hypothetical protein contains simila	OHP2	AT1G34000	1.12	0.16	1.49	0.18201545	0.5727	-5.59
248268_at	importin beta	---	AT5G53480	-1.15	-0.20	-1.49	0.18203677	0.5727	-5.59
262205_at	hypothetical protein predicted by g	---	AT2G01080	-1.13	-0.18	-1.49	0.18203662	0.5727	-5.59
262358_at	mandelonitrile lyase, putative simi	---	AT1G73050	-1.15	-0.20	-1.49	0.18196302	0.5727	-5.59
255848_at	hypothetical protein predicted by g	---	AT2G33640	-1.14	-0.18	-1.49	0.18219603	0.5729	-5.59
250171_at	prohibitin - like protein prohibitin,	ATPHB5	AT5G14300	-1.12	-0.17	-1.49	0.18217076	0.5729	-5.59
267148_at	hypothetical protein predicted by g	---	AT2G23470	-1.16	-0.21	-1.49	0.18212077	0.5729	-5.59
AFFX-PheX-5_	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.30	-0.38	-1.49	0.18217554	0.5729	-5.59
254358_at	putative protein light induced prote	---	AT4G22310	1.09	0.13	1.49	0.18223919	0.5730	-5.59
262916_at	glutathione S-transferase, putative	ATGSTU16	AT1G59700	1.22	0.29	1.49	0.18230082	0.5730	-5.59
257409_at	unknown protein predicted by gens	---	AT2G17470	-1.14	-0.19	-1.49	0.18229478	0.5730	-5.59
248410_at	putative protein similar to unknown	---	AT5G51570	1.12	0.17	1.49	0.18237303	0.5731	-5.59
247349_at	putative protein similar to unknown	---	AT5G63820	-1.11	-0.16	-1.49	0.18237113	0.5731	-5.59
265043_at	Expressed protein ; supported by c	ATNAP4	AT1G03900	1.13	0.18	1.49	0.18243029	0.5731	-5.59
252014_at	putative protein predicted proteins	---	AT3G52870	-1.43	-0.51	-1.49	0.1824253	0.5731	-5.59
266281_at	putative protein kinase contains a	---	AT2G29250	-1.14	-0.19	-1.49	0.18247189	0.5731	-5.60
259860_at	putative protein kinase similar to le	---	AT1G80640	1.18	0.24	1.49	0.18246054	0.5731	-5.60
263904_at	putative ABC transporter related to	PDR6	AT2G36380	-1.42	-0.51	-1.49	0.18250527	0.5731	-5.60
257953_at	predicted protein supported by full-	PEX22	AT3G21865	1.21	0.28	1.49	0.18253143	0.5731	-5.60
251132_at	putative protein Myb-related trans	---	AT5G01200	1.18	0.24	1.49	0.18259731	0.5731	-5.60
259452_at	En/Spm-like transposon protein, p	---	---	-1.13	-0.17	-1.49	0.18257726	0.5731	-5.60
253905_s_at	putative protein retrotransposon C	---	---	-1.10	-0.14	-1.49	0.1826343	0.5732	-5.60
265610_at	unknown protein ;supported by ful	---	AT2G25430	-1.10	-0.14	-1.49	0.18270516	0.5733	-5.60
255473_at	putative protein similar to several p	---	AT4G02450	-1.11	-0.15	-1.49	0.18276381	0.5734	-5.60
253200_at	vacuolar H+-transporting ATPase	AVA-P1	AT4G34720	1.15	0.21	1.49	0.18279964	0.5735	-5.60
252852_at	hypothetical protein ;supported by	---	AT4G39900	1.29	0.37	1.48	0.18287963	0.5736	-5.60
261360_at	hypothetical protein predicted by g	---	---	-1.13	-0.18	-1.48	0.18287963	0.5736	-5.60
264157_at	xyloglucan endotransglycosylase,	XTH17	AT1G65310	-1.25	-0.32	-1.48	0.18295926	0.5737	-5.60
248629_at	mitochondrial carrier protein-like	---	AT5G48970	-1.18	-0.23	-1.48	0.18303165	0.5737	-5.60
264305_at	Expressed protein ; supported by f	LSH7	AT1G78815	-1.11	-0.15	-1.48	0.18303208	0.5737	-5.60
250365_at	putative protein serine threonine t	---	AT5G11410	-1.22	-0.28	-1.48	0.183028	0.5737	-5.60
260731_at	P-type ATPase, putative similar to	---	AT1G17500	-1.15	-0.20	-1.48	0.18306711	0.5738	-5.60

262787_at	putative clathrin-coat assembly pro	---	AT1G10730	1.21	0.27	1.48	0.18317069	0.5738	-5.60
255894_at	nuclear poly(A) polymerase, putat	---	AT1G17980	-1.13	-0.17	-1.48	0.18315344	0.5738	-5.60
253530_at	putative protein hypothetical prote	---	AT4G31530	1.24	0.31	1.48	0.1831506	0.5738	-5.60
248924_at	GDSL-motif lipase/hydrolase-like p	---	AT5G45960	1.11	0.15	1.48	0.18328978	0.5741	-5.60
245404_at	putative protein	---	AT4G17610	-1.16	-0.21	-1.48	0.18331943	0.5741	-5.60
245473_at	hypothetical protein	---	AT4G16050	1.11	0.15	1.48	0.18336192	0.5742	-5.60
250937_at	putative protein various predicted	---	AT5G03230	1.23	0.30	1.48	0.18341585	0.5742	-5.60
264696_at	unknown protein	---	AT1G70230	-1.33	-0.41	-1.48	0.18339451	0.5742	-5.60
261390_at	hypothetical protein similar to hypo	---	AT1G35040	-1.11	-0.15	-1.48	0.18351709	0.5743	-5.60
254455_at	hypothetical protein	---	AT4G21140	-1.20	-0.27	-1.48	0.18353365	0.5743	-5.60
265044_at	hypothetical protein Similar to hun	VPS2.3	AT1G03950	-1.16	-0.21	-1.48	0.18346827	0.5743	-5.60
266863_at	putative ripening-associated protei	ATCDPME	AT2G26930	1.12	0.16	1.48	0.1834968	0.5743	-5.60
263283_at	hypothetical protein predicted by g	---	AT2G36090	-1.12	-0.16	-1.48	0.18368778	0.5746	-5.60
247168_at	putative protein contains similarity	---	AT5G65860	1.16	0.21	1.48	0.18370073	0.5746	-5.60
247122_at	putative protein non-consensus A	ATSAC1B	AT5G66020	-1.18	-0.24	-1.48	0.18379397	0.5748	-5.60
257223_at	50S ribosomal protein L12-B ident	RPL12-B	AT3G27840	-1.15	-0.20	-1.48	0.18381679	0.5748	-5.60
248334_s_at	unknown protein ; supported by cl	---	AT5G52370	1.23	0.30	1.48	0.18387224	0.5749	-5.60
267333_at	putative WD-40 repeat protein con	---	AT2G19430	1.11	0.15	1.48	0.18387669	0.5749	-5.60
251365_at	putative DNA-binding protein At2g	---	AT3G61310	1.17	0.22	1.48	0.18417238	0.5752	-5.60
264336_at	hypothetical protein contains simila	---	AT1G70360	1.15	0.20	1.48	0.18419742	0.5752	-5.60
253536_at	RSZp22 splicing factor ;supported	SRZ-22	AT4G31580	-1.10	-0.13	-1.48	0.18416434	0.5752	-5.60
266198_at	unknown protein predicted by gens	---	AT2G38890	-1.13	-0.17	-1.48	0.1841624	0.5752	-5.60
266734_at	hypothetical protein predicted by g	---	AT2G46900	1.15	0.20	1.48	0.18415718	0.5752	-5.60
258304_at	hypothetical protein predicted by g	---	---	-1.09	-0.13	-1.48	0.18415855	0.5752	-5.60
262497_at	putative 20S proteasome beta sub	PBC1	AT1G21720	1.13	0.17	1.48	0.18411557	0.5752	-5.60
253710_at	putative protein hypothetical prote	anac075	AT4G29230	-1.16	-0.21	-1.48	0.18409129	0.5752	-5.60
254624_at	hypothetical protein ;supported by	---	AT4G18580	-1.12	-0.17	-1.48	0.18428572	0.5754	-5.60
257671_at	hypothetical protein predicted by g	---	AT3G20450	1.15	0.20	1.48	0.18435067	0.5754	-5.60
246354_at	hypothetical protein	---	AT1G38950	-1.13	-0.18	-1.48	0.18444126	0.5754	-5.60
255058_s_at	putative protein various hypothetic	---	---	-1.10	-0.14	-1.48	0.18430448	0.5754	-5.60
251254_at	putative protein anion exchanger 3	---	AT3G62270	-1.15	-0.20	-1.48	0.18443054	0.5754	-5.60
256197_at	hypothetical protein	---	---	-1.18	-0.24	-1.48	0.18434263	0.5754	-5.60
253406_at	putative protein GATA transcriptio	---	AT4G32890	-1.24	-0.31	-1.48	0.18441277	0.5754	-5.60
245954_at	far-red impaired response protein	FRS10	AT5G28530	-1.14	-0.18	-1.48	0.18437789	0.5754	-5.60
258288_at	unknown protein	LSH4	---	-1.28	-0.35	-1.48	0.18455601	0.5756	-5.61

262323_at	6-phosphogluconate dehydrogena	---	AT1G64190	1.10	0.14	1.48	0.18465552	0.5759	-5.61
245952_at	putative protein predicted proteins	---	AT5G28500	1.16	0.21	1.48	0.18471323	0.5760	-5.61
251595_at	putative protein galactose oxidase	---	AT3G57620	-1.13	-0.18	-1.48	0.18475875	0.5760	-5.61
264968_at	stress related protein, putative sim	---	AT1G67360	-1.33	-0.41	-1.48	0.18478099	0.5760	-5.61
248512_at	protein translocation complex Sec6	SIG2	AT1G08540	1.27	0.35	1.48	0.18488378	0.5763	-5.61
259733_at	nucellin-like protein similar to nuce	---	AT1G77480	1.22	0.29	1.48	0.18496651	0.5763	-5.61
255186_at	putative transposon protein similar	---	---	-1.20	-0.26	-1.48	0.18493605	0.5763	-5.61
253067_at	myb transcription factor - like prote	MYB87	AT4G37780	-1.12	-0.16	-1.48	0.18496415	0.5763	-5.61
247904_at	putative protein contains similarity	AIL5	AT5G57390	1.16	0.22	1.48	0.18511674	0.5765	-5.61
247050_at	At14a protein-like	---	AT5G66660	-1.18	-0.24	-1.48	0.18511737	0.5765	-5.61
255717_at	coded for by A. thaliana cDNA H76	---	AT4G00350	-1.12	-0.16	-1.48	0.18509403	0.5765	-5.61
261330_at	transcription factor, putative simila	MCM2	AT1G44900	1.53	0.61	1.48	0.18509601	0.5765	-5.61
262879_at	plastid RNA polymerase sigma-sul	SIGA	AT1G64860	1.14	0.19	1.48	0.18521608	0.5766	-5.61
261489_at	hypothetical protein contains simila	---	AT1G14450	1.09	0.13	1.48	0.18520504	0.5766	-5.61
250798_at	peroxidase	---	AT5G05340	2.04	1.03	1.48	0.18525623	0.5767	-5.61
245148_at	putative pectinesterase ; supporte	---	AT2G45220	1.70	0.76	1.48	0.18532279	0.5767	-5.61
261027_at	cyclic nucleotide and calmodulin-r	ATCNGC10	AT1G01340	1.42	0.50	1.48	0.18530057	0.5767	-5.61
260006_at	phosphatidylinositol synthase (PIS	ATPIS1	AT1G68000	1.10	0.13	1.47	0.18539928	0.5768	-5.61
263675_x_at	En/Spm-like transposon protein rel	---	---	-1.18	-0.24	-1.47	0.18541413	0.5768	-5.61
253224_at	invertase - like protein mRNA, Lili	---	AT4G34860	-1.20	-0.27	-1.47	0.18550335	0.5769	-5.61
264367_at	unknown protein ESTs gb|T21276	---	AT1G03350	-1.12	-0.16	-1.47	0.18564422	0.5769	-5.61
255672_at	hypothetical protein ; supported by	EDA8	AT4G00310	-1.14	-0.19	-1.47	0.18554259	0.5769	-5.61
247229_at	putative protein contains similarity	---	AT5G65160	-1.20	-0.26	-1.47	0.18559352	0.5769	-5.61
264162_at	acyl carrier protein, putative simila	mtACP2	AT1G65290	1.15	0.20	1.47	0.18566255	0.5769	-5.61
246505_at	putative protein hypothetical prote	---	AT5G16250	1.23	0.30	1.47	0.18565853	0.5769	-5.61
254584_at	putative protein probable membra	VPS54	AT4G19490	1.11	0.15	1.47	0.18546854	0.5769	-5.61
262318_at	putative hypersensitivity-related pr	---	AT1G27620	1.13	0.18	1.47	0.18559215	0.5769	-5.61
258603_at	putative heat shock transcription fa	ATHSFA1E	AT3G02990	1.18	0.24	1.47	0.18554442	0.5769	-5.61
263053_at	similar to glucose inhibited division	---	AT2G13440	-1.13	-0.18	-1.47	0.18572246	0.5769	-5.61
265759_at	putative membrane transporter	---	AT2G13100	-1.11	-0.14	-1.47	0.18570555	0.5769	-5.61
261956_at	oxidoreductase, putative similar to	---	AT1G64590	-1.23	-0.30	-1.47	0.18575673	0.5769	-5.61
259654_at	hypothetical protein predicted by g	---	AT1G55220	-1.13	-0.18	-1.47	0.18578227	0.5769	-5.61
256186_at	4-coumarate:CoA ligase 1 identica	4CL1	AT1G51680	-1.35	-0.43	-1.47	0.18583398	0.5770	-5.61
259998_at	hypothetical protein similar to unkn	BPC3	AT1G68120	-1.18	-0.24	-1.47	0.18589507	0.5771	-5.61
252611_at	oxidosqualene cyclase - like prote	LAS1	AT3G45130	-1.34	-0.42	-1.47	0.18590446	0.5771	-5.61

252743_at	guanine nucleotide-exchange - lik	ATMIN7	AT3G43300	1.11	0.15	1.47	0.18594882	0.5772	-5.61
260866_at	polyprotein, putative similar to pol	---	---	-1.14	-0.18	-1.47	0.18617048	0.5778	-5.61
258254_at	unknown protein contains Pfam pr	---	AT3G26780	1.17	0.23	1.47	0.1862317	0.5779	-5.61
264327_at	putative translation initiation factor	EIF2 GAMM	AT1G04170	1.11	0.15	1.47	0.18631588	0.5780	-5.61
264114_at	hypothetical protein predicted by g	CDT1A	AT2G31270	1.31	0.39	1.47	0.18631833	0.5780	-5.61
263691_at	60s ribosomal protein L34 identica	---	AT1G26880	1.25	0.32	1.47	0.18644424	0.5782	-5.61
250308_at	calcium-dependent protein kinase	CPK17	AT5G12180	-1.16	-0.21	-1.47	0.18644818	0.5782	-5.61
257414_at	hypothetical protein similar to hypo	---	AT1G62110	-1.12	-0.16	-1.47	0.18656572	0.5785	-5.61
253742_at	putative protein retrofit - Oryza lor	---	---	1.14	0.19	1.47	0.186586	0.5785	-5.61
261464_at	disease resistance response prote	---	AT1G07730	-1.14	-0.19	-1.47	0.18665064	0.5786	-5.62
264715_at	hypothetical protein contains simila	---	AT1G70180	-1.13	-0.17	-1.47	0.18671412	0.5787	-5.62
245870_at	hypothetical protein similar to hypo	---	AT1G26300	-1.11	-0.16	-1.47	0.18681167	0.5790	-5.62
253552_at	ubiquitin-specific protease 24 (UB	UBP24	AT4G30890	-1.12	-0.16	-1.47	0.18683791	0.5790	-5.62
264681_s_at	permease 1-like protein permease	---	AT1G65550	-1.15	-0.20	-1.47	0.1869042	0.5790	-5.62
256906_at	hypothetical protein contains Pfam	---	AT3G24000	-1.16	-0.21	-1.47	0.18690976	0.5790	-5.62
246396_at	carbonic anhydrase, putative simil	BCA6	AT1G58180	-1.20	-0.26	-1.47	0.18697357	0.5791	-5.62
255958_at	high affinity sulphate transporter,	SULTR1;3	AT1G22150	1.15	0.20	1.47	0.18697199	0.5791	-5.62
260355_at	transcription factor CRC identical t	CRC	AT1G69180	1.17	0.22	1.47	0.18707464	0.5793	-5.62
261183_at	hypothetical protein predicted by g	EMB2756	AT1G34550	-1.15	-0.21	-1.47	0.18720657	0.5793	-5.62
259053_at	unknown protein similar to hypothe	---	AT3G03320	1.13	0.18	1.47	0.1871281	0.5793	-5.62
251189_at	putative protein putative mitochon	---	AT3G62650	-1.18	-0.24	-1.47	0.1872097	0.5793	-5.62
256019_at	cytochrome P-450, putative simila	---	AT1G58260	-1.12	-0.16	-1.47	0.18721433	0.5793	-5.62
260993_at	hypothetical protein predicted by g	FMO GS-O	AT1G12140	-1.10	-0.13	-1.47	0.18715039	0.5793	-5.62
264248_at	hypothetical protein predicted by g	---	AT1G78700	1.18	0.23	1.47	0.18730419	0.5794	-5.62
248591_at	xylulose kinase ; supported by cD	---	AT5G49650	-1.14	-0.19	-1.47	0.18734047	0.5794	-5.62
257848_at	hypothetical protein predicted by g	---	AT3G13030	1.16	0.21	1.47	0.18734963	0.5794	-5.62
265502_at	putative poly(A) binding protein	---	AT2G15500	-1.15	-0.20	-1.47	0.1872526	0.5794	-5.62
263210_at	Expressed protein ; supported by c	---	AT1G10585	-2.83	-1.50	-1.47	0.18733379	0.5794	-5.62
264642_at	putative CCAAT-binding transcripti	NF-YB4	AT1G09030	-1.12	-0.17	-1.47	0.18746431	0.5795	-5.62
253563_at	putative protein predicted protein,	---	AT4G31150	1.16	0.22	1.47	0.187453	0.5795	-5.62
249841_at	unknown protein	---	AT5G23520	-1.12	-0.17	-1.47	0.18743837	0.5795	-5.62
256483_at	hypothetical protein	---	AT1G31410	-1.16	-0.21	-1.47	0.18749606	0.5795	-5.62
248391_at	putative protein similar to unknown	---	AT5G52030	-1.13	-0.18	-1.47	0.18762351	0.5798	-5.62
267369_at	unknown protein ;supported by ful	---	AT2G44420	1.14	0.19	1.47	0.18762886	0.5798	-5.62
252971_at	extensin - like protein proline-rich	PRP4	AT4G38770	2.13	1.09	1.47	0.18770832	0.5798	-5.62

257741_at	hypothetical protein predicted by g	---	AT3G27340	1.18	0.24	1.47	0.18775494	0.5798	-5.62
265860_at	hypothetical protein predicted by g	---	AT2G01810	-1.11	-0.15	-1.47	0.1877576	0.5798	-5.62
258507_at	neutral invertase, putative similar	---	AT3G06500	-1.32	-0.40	-1.47	0.18769298	0.5798	-5.62
251653_at	putative protein regulatory protein	BOP1	AT3G57130	-1.15	-0.20	-1.47	0.18789061	0.5802	-5.62
265824_at	putative glucosyltransferase ;supp	ATCSLA07	AT2G35650	1.17	0.23	1.47	0.18801297	0.5802	-5.62
263799_at	unknown protein ; supported by cl	---	AT2G24550	1.20	0.26	1.46	0.18807648	0.5802	-5.62
251262_at	hypothetical protein ; supported by	---	AT3G62080	1.20	0.27	1.46	0.18820173	0.5802	-5.62
251070_at	translation initiation factor eIF-2 be	---	AT5G01940	1.23	0.29	1.47	0.1880098	0.5802	-5.62
246564_at	putative protein hypothetical prote	---	AT5G15610	1.10	0.14	1.46	0.18815316	0.5802	-5.62
249251_at	putative protein similar to unknown	---	AT5G42000	1.16	0.22	1.46	0.18802847	0.5802	-5.62
262784_at	unknown protein strong similarity t	SEX1	AT1G10760	-1.20	-0.27	-1.46	0.18805817	0.5802	-5.62
245961_at	putative protein predicted proteins	---	AT5G19670	1.15	0.20	1.46	0.18813845	0.5802	-5.62
260506_at	Cyclin, putative similar to GB:CAB	CYCA3;2	AT1G47210	1.26	0.34	1.46	0.18813999	0.5802	-5.62
260468_at	transcription factor RUSH-1alpha i	---	AT1G11100	1.18	0.23	1.46	0.1881582	0.5802	-5.62
264850_at	unknown protein similar to F5J6.8	---	AT2G17340	-1.12	-0.16	-1.46	0.1881772	0.5802	-5.62
260881_at	unknown protein contains similarity	---	AT1G21550	1.72	0.78	1.46	0.18810874	0.5802	-5.62
255809_at	putative protein predicted protein,	---	AT4G10300	-1.14	-0.19	-1.46	0.18822909	0.5802	-5.62
246929_at	putative protein ; supported by full	---	AT5G25210	1.17	0.23	1.46	0.18834612	0.5805	-5.62
251741_at	putative protein predicted protein,	UGP3	AT3G56040	1.28	0.35	1.46	0.18838813	0.5805	-5.62
248676_at	putative protein similar to unknown	ATSDI1	AT5G48850	-1.52	-0.61	-1.46	0.18844891	0.5806	-5.62
267506_at	unknown protein ;supported by ful	---	AT2G45520	-1.11	-0.15	-1.46	0.18852192	0.5806	-5.62
267037_at	hypothetical protein ; supported by	---	AT2G38320	1.13	0.18	1.46	0.18847358	0.5806	-5.62
265653_at	hypothetical protein	---	---	1.10	0.14	1.46	0.1885158	0.5806	-5.62
252380_at	ABC-type transport protein-like pr	ATH2	AT3G47740	-1.12	-0.16	-1.46	0.1886163	0.5808	-5.62
262341_at	E2, ubiquitin-conjugating enzyme,	UBC28	AT1G64230	1.15	0.20	1.46	0.18877399	0.5809	-5.63
246583_at	protein kinase -like protein Ste-20	---	AT5G14720	-1.15	-0.20	-1.46	0.18882728	0.5809	-5.63
265090_at	putative protein phosphatase 2A H	---	AT1G03960	1.13	0.17	1.46	0.18882234	0.5809	-5.63
252030_at	hypothetical protein predicted prot	---	AT3G52690	-1.10	-0.14	-1.46	0.18870011	0.5809	-5.63
252660_at	putative protein	---	AT3G44440	-1.11	-0.15	-1.46	0.18881558	0.5809	-5.63
260158_at	unknown protein	---	AT1G79910	-1.13	-0.18	-1.46	0.18869121	0.5809	-5.62
262041_at	HPt phosphotransmitter, putative s	AHP6	AT1G80100	1.15	0.20	1.46	0.18875869	0.5809	-5.63
AFFX-r2-At-Act	Arabidopsis thaliana /REF=U3728	---	---	-1.10	-0.14	-1.46	0.18894765	0.5812	-5.63
261387_at	hypothetical protein predicted by g	---	AT1G05410	1.23	0.30	1.46	0.18899001	0.5813	-5.63
264800_at	hypothetical protein similar to IFA-	---	AT1G08800	1.15	0.21	1.46	0.18904657	0.5814	-5.63
265484_at	unknown protein ; supported by cl	OTP51	AT2G15820	1.13	0.18	1.46	0.18931826	0.5815	-5.63

259295_at	hypothetical protein predicted by g	---	AT3G05340	-1.16	-0.21	-1.46	0.18929641	0.5815	-5.63
248680_at	pantoate-beta-alanine ligase ;supp	PANC	AT5G48840	-1.14	-0.19	-1.46	0.18920821	0.5815	-5.63
249810_at	unknown protein	---	AT5G23920	-1.20	-0.27	-1.46	0.18933253	0.5815	-5.63
266988_at	putative myrosinase-binding protei	JAL22	AT2G39310	-1.20	-0.27	-1.46	0.18921059	0.5815	-5.63
258013_at	unknown protein	---	AT3G19320	-1.16	-0.22	-1.46	0.1893238	0.5815	-5.63
264087_at	hypothetical protein predicted by g	emb1381	AT2G31340	-1.12	-0.16	-1.46	0.1892765	0.5815	-5.63
255653_at	Similar to receptor kinase	---	AT4G00960	1.10	0.14	1.46	0.18926117	0.5815	-5.63
247848_at	resistance protein - like disease re	---	AT5G58120	-1.16	-0.21	-1.46	0.18915204	0.5815	-5.63
252051_at	putative protein similarity hypothet	---	AT3G52570	1.11	0.16	1.46	0.18934454	0.5815	-5.63
249076_at	putative protein similar to unknown	TOM22-V	AT5G43970	1.18	0.24	1.46	0.18942801	0.5817	-5.63
257700_at	unknown protein similar to unknow	ALIS1	AT3G12740	1.15	0.20	1.46	0.18948177	0.5818	-5.63
251143_at	putative protein SqdX protein, Syn	SQD2	AT5G01220	1.26	0.33	1.46	0.18970184	0.5820	-5.63
265438_at	hypothetical protein	---	AT2G20970	-1.10	-0.14	-1.46	0.18964654	0.5820	-5.63
267128_at	putative acetone-cyanohydrin lyas	MES1	AT2G23620	-1.15	-0.20	-1.46	0.18974442	0.5820	-5.63
257609_at	Expressed protein ; supported by f	---	AT3G13845	1.14	0.19	1.46	0.18968431	0.5820	-5.63
264699_at	unknown protein ;supported by full	---	AT1G69980	1.10	0.14	1.46	0.18968014	0.5820	-5.63
248537_at	putative protein similar to unknown	---	AT5G50100	-1.17	-0.22	-1.46	0.18972075	0.5820	-5.63
265642_at	putative nitrilase ;supported by ful	NLP1	AT2G27450	-1.17	-0.22	-1.46	0.18962691	0.5820	-5.63
260901_at	flavin-containing monooxygenase	YUC11	AT1G21430	-1.16	-0.21	-1.46	0.18981833	0.5821	-5.63
258629_at	stelar K+ outward rectifying chann	SKOR	AT3G02850	-1.10	-0.13	-1.46	0.18982204	0.5821	-5.63
260209_at	putative AP2 domain transcription	CPuORF53	AT1G68550	-1.14	-0.19	-1.46	0.18985563	0.5821	-5.63
246051_at	epimerase/dehydratase - like prot	GME	AT5G28840	1.16	0.21	1.46	0.18989896	0.5821	-5.63
253620_at	receptor-like kinase homolog som	---	AT4G30520	1.14	0.18	1.46	0.18990033	0.5821	-5.63
266122_at	putative helicase ; supported by c	ETL1	AT2G02090	-1.12	-0.16	-1.46	0.19000248	0.5824	-5.63
264748_at	hypothetical protein predicted by g	EMB25	AT1G70070	1.10	0.14	1.46	0.1901092	0.5824	-5.63
262574_at	unknown protein ESTs gb|R30529	---	AT1G15230	1.22	0.29	1.46	0.19006303	0.5824	-5.63
247905_at	unknown protein	---	AT5G57400	-1.10	-0.13	-1.46	0.19014335	0.5824	-5.63
248568_at	receptor protein kinase-like	---	AT5G49760	-1.15	-0.20	-1.46	0.1900693	0.5824	-5.63
252847_at	putative transposase hypothetical	---	AT3G42170	1.14	0.19	1.46	0.19016381	0.5824	-5.63
251068_at	putative protein several protein kin	STN8	AT5G01920	1.21	0.28	1.46	0.19012042	0.5824	-5.63
257379_x_at	Mutator-like transposase similar to	---	---	-1.12	-0.16	-1.46	0.19022682	0.5825	-5.63
264170_at	hypothetical protein	---	AT1G02260	1.13	0.17	1.46	0.19038805	0.5829	-5.63
265146_at	putative glucosyl transferase	---	AT1G51210	-1.25	-0.32	-1.46	0.19050298	0.5832	-5.63
246284_at	putative protein	---	AT4G36780	1.13	0.18	1.46	0.19058269	0.5833	-5.63
267335_s_at	putative beta-1,3-glucanase	---	AT1G64760	1.21	0.27	1.46	0.19056484	0.5833	-5.63

248985_at	GTP-binding protein-like; root hair	---	AT5G45160	1.11	0.15	1.46	0.19063802	0.5834	-5.63
250690_at	ABC transporter-like protein ; supp	---	AT5G06530	1.20	0.26	1.45	0.19077729	0.5837	-5.63
254963_at	putative protein single strand DNA	MTSSB	AT4G11060	1.14	0.19	1.45	0.19079918	0.5837	-5.63
256883_at	unknown protein ; supported by cl	---	AT3G26440	1.43	0.51	1.45	0.19083918	0.5838	-5.64
255306_at	putative calcium dependent protein	CPK23	AT4G04740	-1.19	-0.25	-1.45	0.19086737	0.5838	-5.64
248731_at	phosphoribosylanthranilate transfe	---	AT5G48060	1.14	0.19	1.45	0.19090568	0.5838	-5.64
267089_at	unknown protein	---	AT2G38300	-1.17	-0.22	-1.45	0.19095144	0.5838	-5.64
247369_at	unknown protein	---	AT5G63340	1.14	0.19	1.45	0.19096508	0.5838	-5.64
246543_at	putative protein	---	AT5G15060	-1.09	-0.13	-1.45	0.19100776	0.5839	-5.64
250820_at	receptor-like protein kinase	---	AT5G05160	-1.15	-0.20	-1.45	0.19105832	0.5839	-5.64
248133_at	unknown protein	---	AT5G54850	1.18	0.24	1.45	0.1910358	0.5839	-5.64
248880_at	putative protein contains similarity	---	AT5G46200	-1.11	-0.15	-1.45	0.19112671	0.5840	-5.64
260870_at	GTP-binding protein(RAB1Y), put	ATRAB18	AT1G43890	1.14	0.20	1.45	0.19117195	0.5841	-5.64
246074_at	hypothetical protein ; supported by	---	AT5G20130	1.11	0.15	1.45	0.19125722	0.5841	-5.64
257320_at	hypothetical protein	---	AT2G07749	-1.14	-0.19	-1.45	0.19124702	0.5841	-5.64
250029_at	galactose-1-phosphate uridyl trans	---	AT5G18200	-1.15	-0.20	-1.45	0.19127465	0.5841	-5.64
245841_s_at	ribosomal protein S2, putative sim	XW6	AT1G58380	1.21	0.27	1.45	0.19148469	0.5845	-5.64
262361_at	unknown protein contains similarity	GTE3	AT1G73150	-1.12	-0.16	-1.45	0.19146615	0.5845	-5.64
245104_at	hypothetical protein predicted by g	---	AT2G41600	1.12	0.16	1.45	0.19144011	0.5845	-5.64
254716_at	putative protein LEA protein , Cice	UNE15	AT4G13560	-1.19	-0.25	-1.45	0.19146217	0.5845	-5.64
255608_at	hypothetical protein	---	AT4G01140	-1.16	-0.22	-1.45	0.19167123	0.5845	-5.64
267075_at	putative bZIP transcription factor c	EEL	AT2G41070	1.11	0.15	1.45	0.19162675	0.5845	-5.64
261357_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.45	0.19153797	0.5845	-5.64
257654_at	DnaJ protein, putative contains Pf	---	AT3G13310	1.45	0.53	1.45	0.19160112	0.5845	-5.64
261176_at	hypothetical protein predicted by g	---	AT1G04780	1.11	0.15	1.45	0.19160856	0.5845	-5.64
248320_at	putative protein similar to unknown	---	AT5G52720	1.14	0.19	1.45	0.19167671	0.5845	-5.64
249593_at	putative protein SIAH1 protein, Br	---	AT5G37900	-1.12	-0.16	-1.45	0.19155711	0.5845	-5.64
250906_at	1,4-alpha-glucan branching enzyn	SBE2.2	AT5G03650	-1.14	-0.18	-1.45	0.19170972	0.5845	-5.64
261478_at	unknown protein	MIOX1	AT1G14520	-1.19	-0.25	-1.45	0.19173891	0.5845	-5.64
264017_s_at	putative ER lumen protein retaining	---	AT2G21190	1.11	0.16	1.45	0.19183068	0.5847	-5.64
256112_at	guanine nucleotide regulatory pro	ATRABA1E	AT1G16920	1.39	0.48	1.45	0.19207078	0.5848	-5.64
AFFX-Athal-GA	Arabidopsis thaliana /REF=M6411	GAPC1	---	1.17	0.23	1.45	0.19210434	0.5848	-5.64
254353_s_at	putative protein probable membra	---	AT4G22285	1.18	0.23	1.45	0.19185798	0.5848	-5.64
258832_at	putative protein kinase similar to A	---	AT3G07070	-1.13	-0.18	-1.45	0.19212923	0.5848	-5.64
262900_at	hypothetical protein contains simila	SNL5	AT1G59890	1.15	0.20	1.45	0.19204895	0.5848	-5.64

257804_at	protein kinase, putative similar to S	---	AT3G18810	-1.11	-0.15	-1.45	0.19199418	0.5848	-5.64
250101_at	putative protein contains similarity	BGLU2	AT5G16580	-1.24	-0.31	-1.45	0.19192695	0.5848	-5.64
263889_at	putative ABC transporter	ATNAP12	AT2G37010	-1.14	-0.19	-1.45	0.19210815	0.5848	-5.64
255262_at	putative protein equilibrative nucle	---	AT4G05140	-1.12	-0.16	-1.45	0.19214339	0.5848	-5.64
261118_at	protease, putative similar to SP:P3	---	AT1G75460	-1.13	-0.17	-1.45	0.19216545	0.5848	-5.64
262233_at	hypothetical protein contains simila	CHR18	AT1G48310	1.11	0.15	1.45	0.19204634	0.5848	-5.64
264263_at	Expressed protein ; supported by f	AtPP2-B15	AT1G09155	1.12	0.16	1.45	0.19193134	0.5848	-5.64
251622_at	dnaJ-like protein DNAJ protein - S	---	AT3G57340	1.10	0.14	1.45	0.19207659	0.5848	-5.64
256994_s_at	limonene cyclase, putative similar	ATTPS-CIN	AT3G25820 /	-1.12	-0.16	-1.45	0.19219558	0.5848	-5.64
249552_s_at	receptor serine/threonine protein k	---	AT5G38240 /	-1.24	-0.31	-1.45	0.19235577	0.5850	-5.64
256262_at	unknown protein	---	AT3G12150	1.16	0.21	1.45	0.19237284	0.5850	-5.64
261973_at	hypothetical protein predicted by g	---	AT1G64610	1.19	0.25	1.45	0.19251996	0.5850	-5.64
258180_at	unknown protein	---	AT3G21480	1.22	0.28	1.45	0.19233966	0.5850	-5.64
252811_at	putative protein several hypothetic	---	---	-1.13	-0.17	-1.45	0.19240952	0.5850	-5.64
248092_at	ubiquitin-like protein	SUMO3	AT5G55170	1.43	0.52	1.45	0.19249106	0.5850	-5.64
249227_at	peroxidase (emb|CAA66960.1)	---	AT5G42180	-1.12	-0.16	-1.45	0.19241533	0.5850	-5.64
257710_at	unknown protein ;supported by ful	---	AT3G27350	1.13	0.18	1.45	0.19242959	0.5850	-5.64
258204_at	hypothetical protein predicted by g	AtGRF5	AT3G13960	-1.15	-0.20	-1.45	0.19253064	0.5850	-5.64
246780_at	seryl-tRNA synthetase ; supported	---	AT5G27470	1.13	0.17	1.45	0.19249313	0.5850	-5.64
265256_at	hypothetical protein predicted by g	---	AT2G28390	-1.09	-0.13	-1.45	0.19257361	0.5851	-5.64
260760_at	hypothetical protein predicted by g	---	AT1G49170	1.16	0.21	1.45	0.19262066	0.5851	-5.64
247335_at	RNA helicase	---	AT5G63630	1.13	0.17	1.45	0.19270233	0.5851	-5.64
256152_at	ethylene-responsive RNA helicase	---	AT1G55150	-1.10	-0.14	-1.45	0.192718	0.5851	-5.64
253682_at	cytidine deaminase 5 (CDA5)	---	AT4G29640	-1.15	-0.21	-1.45	0.19270861	0.5851	-5.64
254510_at	cadinene synthase like protein (+)	---	AT4G20210	-1.16	-0.21	-1.45	0.19266995	0.5851	-5.64
266905_at	putative katanin ;supported by full	---	AT2G34560	-1.18	-0.24	-1.45	0.19277883	0.5852	-5.64
253039_at	squalene epoxidase - like protein S	SQE3	AT4G37760	-1.27	-0.34	-1.45	0.19286178	0.5852	-5.64
265940_at	putative nucleosome assembly pro	NAP1;2	AT2G19480	1.12	0.16	1.45	0.19298772	0.5852	-5.64
251391_at	putative protein weak homology w	---	AT3G60910	1.15	0.20	1.45	0.19289061	0.5852	-5.64
255221_at	putative protein various predicted p	---	AT4G05150	1.14	0.19	1.45	0.1929448	0.5852	-5.64
245803_at	cysteine proteinase RD21A identic	RD21	AT1G47128	1.16	0.21	1.45	0.1928214	0.5852	-5.64
263570_at	aldehyde oxidase identical to GP:3	AAO3	AT2G27150	1.22	0.29	1.45	0.19301472	0.5852	-5.65
249643_at	putative transposase putative tran	---	---	-1.15	-0.20	-1.45	0.193082	0.5852	-5.65
264740_at	unknown protein	---	AT1G62070	-1.12	-0.16	-1.45	0.19292098	0.5852	-5.64
263390_at	hypothetical protein similar to Ta1-	---	---	-1.10	-0.14	-1.45	0.19294728	0.5852	-5.64

249542_at	putative protein transcription facto	NF-YC12	AT5G38140	1.17	0.23	1.45	0.19303085	0.5852	-5.65
257467_at	hypothetical protein similar to hypo	LBD4	AT1G31320	1.22	0.29	1.45	0.19303268	0.5852	-5.65
262545_at	prolin rich protein, putative similar	---	AT1G31250	1.12	0.17	1.45	0.19306297	0.5852	-5.65
255707_at	predicted protein	MEE50	AT4G00231	-1.10	-0.14	-1.45	0.19311957	0.5852	-5.65
262115_at	Expressed protein ; supported by f	---	AT1G02813	-1.12	-0.17	-1.45	0.19315579	0.5853	-5.65
258074_at	unknown protein	---	AT3G25890	-1.37	-0.45	-1.45	0.19325682	0.5854	-5.65
262941_at	hypothetical protein predicted by g	EMB2217	AT1G79490	-1.19	-0.25	-1.45	0.1932726	0.5854	-5.65
246541_at	ubiquitin-fusion degradation protei	---	AT5G15400	1.12	0.16	1.45	0.19328363	0.5854	-5.65
247087_at	putative protein contains similarity	---	AT5G66330	1.23	0.30	1.45	0.1933133	0.5854	-5.65
258327_at	unknown protein contains similarity	PAP85	AT3G22640	-1.10	-0.14	-1.45	0.19331651	0.5854	-5.65
253953_at	putative protein extensin precurso	---	AT4G26750	-1.20	-0.26	-1.44	0.19345797	0.5856	-5.65
266217_at	unknown protein	AT2G2883(	---	-1.11	-0.15	-1.44	0.19344764	0.5856	-5.65
265112_at	hypothetical protein predicted by g	---	AT1G62530	-1.10	-0.13	-1.44	0.19361091	0.5860	-5.65
267476_at	putative pectate lyase	---	AT2G02720	-1.11	-0.16	-1.44	0.1936176	0.5860	-5.65
254233_at	98b like protein 98b - Daucus carc	---	AT4G23800	1.21	0.28	1.44	0.19368516	0.5861	-5.65
248352_at	low-temperature-induced 65 kD pr	LTI65	AT5G52300	1.49	0.58	1.44	0.19377229	0.5863	-5.65
262463_at	hexose transporter, putative simila	STP9	AT1G50310	-1.23	-0.30	-1.44	0.1938336	0.5864	-5.65
260218_at	putative RING zinc finger protein c	---	AT1G74620	-1.09	-0.13	-1.44	0.19392815	0.5866	-5.65
AFFX-r2-Ec-bio	E. coli /GEN=bioC /DB_XREF=gb:	---	---	-1.30	-0.38	-1.44	0.19401562	0.5868	-5.65
255300_at	putative phosphatidylglycerotransf	CLS	AT4G04870	-1.18	-0.23	-1.44	0.19417083	0.5871	-5.65
255246_at	putative protein hypothetical prote	---	---	-1.15	-0.20	-1.44	0.19417315	0.5871	-5.65
252186_at	putative protein	---	AT3G50810	1.14	0.19	1.44	0.19429968	0.5872	-5.65
247281_at	immunophilin (gb|AAB57847.1) ;s	FKBP12	AT5G64350	1.11	0.15	1.44	0.19428771	0.5872	-5.65
245057_at	En/Spm-like transposon protein rel	---	AT2G26490	-1.09	-0.13	-1.44	0.19426433	0.5872	-5.65
248074_at	putative protein similar to unknown	FLA1	AT5G55730	-1.38	-0.47	-1.44	0.19444943	0.5875	-5.65
252683_at	putative protein predicted proteins	---	AT3G44380	-1.16	-0.21	-1.44	0.19445045	0.5875	-5.65
257665_at	unknown protein	---	AT3G20430	-1.11	-0.15	-1.44	0.19453523	0.5877	-5.65
249075_at	putative protein similar to unknown	---	AT5G44000	-1.16	-0.22	-1.44	0.19456424	0.5877	-5.65
260005_at	unknown protein ;supported by ful	---	AT1G67920	1.47	0.56	1.44	0.19461826	0.5878	-5.65
257990_at	putative myc-like DNA-binding prot	---	AT3G19860	1.17	0.23	1.44	0.19469269	0.5878	-5.65
265619_at	hypothetical protein	---	AT2G27320	-1.16	-0.22	-1.44	0.194706	0.5878	-5.65
252617_at	n-acetylglucosaminyl-phosphatidy	SETH2	AT3G45100	1.11	0.15	1.44	0.19464391	0.5878	-5.65
259683_at	unknown protein	---	AT1G63050	1.20	0.27	1.44	0.19469951	0.5878	-5.65
250621_at	membrane protein membrane pro	ATRBL3	AT5G07250	-1.13	-0.17	-1.44	0.19481673	0.5878	-5.65
246979_s_at	putative protein hypothetical protei	---	AT5G24990	-1.16	-0.21	-1.44	0.19480276	0.5878	-5.65

247919_at	putative protein similar to unknown	---	AT5G57650	1.14	0.19	1.44	0.19477632	0.5878	-5.65
260021_at	unknown protein	---	AT1G30010	-1.22	-0.29	-1.44	0.19479336	0.5878	-5.65
263839_at	putative cis-Golgi SNARE protein	MEMB11	AT2G36900	1.19	0.25	1.44	0.19484321	0.5878	-5.65
246897_at	putative protein predicted proteins	---	AT5G25560	-1.15	-0.20	-1.44	0.19491034	0.5879	-5.65
247177_at	unknown protein ; supported by cD	---	AT5G65300	-1.43	-0.52	-1.44	0.19493948	0.5879	-5.65
249814_at	putative protein similar to unknown	---	AT5G23840	-1.11	-0.15	-1.44	0.19496328	0.5879	-5.65
261129_at	tubulin alpha-2/alpha-4 chain ident	TUA4	AT1G04820	1.35	0.43	1.44	0.19506404	0.5880	-5.65
267193_at	hypothetical protein predicted by g	---	AT2G30900	-1.12	-0.16	-1.44	0.19511755	0.5880	-5.65
251126_at	putative protein various predicted	---	AT5G01070	-1.11	-0.15	-1.44	0.19510421	0.5880	-5.65
254786_at	putative protein gamma-interferon	---	AT4G12890	-1.13	-0.18	-1.44	0.19511876	0.5880	-5.65
248296_at	protochlorophyllide reductase; oxid	---	AT5G53090	1.16	0.21	1.44	0.19511414	0.5880	-5.65
251290_at	transcription factor BBFa	DAG1	AT3G61850	1.14	0.18	1.44	0.19513119	0.5880	-5.65
259358_at	hypothetical protein similar to puta	GATL3	AT1G13250	1.42	0.51	1.44	0.19519696	0.5881	-5.66
256390_at	putative MAP kinase similar to MA	ATMKK8	AT3G06230	-1.11	-0.15	-1.44	0.19521094	0.5881	-5.66
253631_at	nucleotide sugar epimerase-like p	GAE1	AT4G30440	-1.16	-0.22	-1.44	0.19535039	0.5883	-5.66
263696_at	putative aspartate kinase-homoser	AK-HSDH I	AT1G31230	-1.21	-0.27	-1.44	0.19537951	0.5883	-5.66
253269_at	hypothetical protein	---	AT4G34140	-1.11	-0.15	-1.44	0.19536132	0.5883	-5.66
253120_at	putative protein phospholipase D,	PLDDELTA	AT4G35790	1.17	0.22	1.44	0.1954542	0.5884	-5.66
263036_at	hypothetical protein predicted by g	---	AT1G23890	1.14	0.19	1.44	0.19545619	0.5884	-5.66
254309_s_at	putative protein predicted protein,	---	AT4G22390	-1.15	-0.20	-1.44	0.19548784	0.5884	-5.66
265461_at	unknown protein similarity to ubiqu	---	AT2G46500	-1.12	-0.16	-1.44	0.19550414	0.5884	-5.66
253215_at	putative protein AT.I.24-7, Arabido	---	AT4G34950	-1.36	-0.44	-1.44	0.19561092	0.5884	-5.66
253366_at	putative protein predicted protein,	---	AT4G33180	-1.16	-0.22	-1.44	0.19560851	0.5884	-5.66
265329_at	putative succinate dehydrogenase	SDH1-2	AT2G18450	-1.13	-0.18	-1.44	0.19558371	0.5884	-5.66
265213_at	clathrin protein family Similar to cl	---	AT1G05020	1.18	0.24	1.44	0.19562373	0.5884	-5.66
251729_at	alpha-galactosidase-like protein a	---	AT3G56310	1.23	0.30	1.44	0.19577036	0.5887	-5.66
247617_at	receptor like protein kinase recept	---	AT5G60270	1.31	0.39	1.44	0.19577211	0.5887	-5.66
258163_at	aldose 1-epimerase, putative simi	---	AT3G17940	1.11	0.16	1.44	0.19584823	0.5889	-5.66
257681_at	hypothetical protein predicted by g	---	AT3G13370	-1.09	-0.13	-1.44	0.19587857	0.5889	-5.66
246937_at	phospholipase D1-like protein pho	PLDALPHA	AT5G25370	1.11	0.15	1.44	0.19592585	0.5890	-5.66
254438_at	translation initiation factor eIF3 - li	---	AT4G20980	1.15	0.21	1.44	0.19598736	0.5890	-5.66
259644_at	unknown protein	---	AT1G68910	1.15	0.20	1.44	0.19599396	0.5890	-5.66
247351_at	putative protein contains similarity	ANAC102	AT5G63790	1.35	0.43	1.43	0.19610772	0.5891	-5.66
247011_at	putative protein contains similarity	FRO1	AT5G67590	1.21	0.28	1.44	0.19606467	0.5891	-5.66
255755_s_at	polygalacturonase, putative simila	---	AT1G43050	-1.13	-0.17	-1.43	0.19608801	0.5891	-5.66

251503_at	ABC transporter-like protein putati	ATMRP14	AT3G59140	-1.23	-0.30	-1.43	0.1962394	0.5891	-5.66
260775_at	14-3-3 protein GF14omega (grf2) i	GRF2	AT1G78300	1.16	0.21	1.43	0.19615416	0.5891	-5.66
251082_at	chlorophyll a/b-binding protein CP2	---	AT5G01530	1.09	0.12	1.43	0.19624419	0.5891	-5.66
264595_at	putative vesicle-associated memb	VAMP721	AT1G04750	1.17	0.22	1.43	0.19621932	0.5891	-5.66
251587_at	hypothetical protein	---	AT3G58080	-1.20	-0.26	-1.43	0.19622971	0.5891	-5.66
253732_at	putative protein several hypothetic	---	AT4G29140	-1.12	-0.16	-1.43	0.19635345	0.5893	-5.66
264288_at	Expressed protein ; supported by f	---	AT1G62045	1.12	0.16	1.43	0.19635796	0.5893	-5.66
250717_at	putative protein similar to unknown	---	AT5G06200	-1.16	-0.21	-1.43	0.19640442	0.5894	-5.66
262566_at	auxin response factor 1, putative s	ARF12	AT1G34310	1.19	0.25	1.43	0.19649852	0.5894	-5.66
247645_at	late embryonic abundant protein -	---	AT5G60530	-1.12	-0.16	-1.43	0.19650255	0.5894	-5.66
265500_at	putative non-LTR retroelement rev	---	---	-1.20	-0.26	-1.43	0.1965718	0.5894	-5.66
246151_at	putative protein predicted proteins	---	AT5G19950	1.14	0.18	1.43	0.19653624	0.5894	-5.66
253664_at	NADPH-ferrihemoprotein reductas	ATR2	AT4G30210	-1.42	-0.50	-1.43	0.1965559	0.5894	-5.66
250036_at	putative protein predicted proteins	---	AT5G18340	-1.16	-0.22	-1.43	0.19646955	0.5894	-5.66
264014_at	putative auxin-regulated protein	---	AT2G21210	-1.45	-0.53	-1.43	0.19667724	0.5896	-5.66
249372_at	glucose-6-phosphate dehydrogena	G6PD6	AT5G40760	-1.25	-0.32	-1.43	0.19670399	0.5896	-5.66
253147_at	protein kinase - like protein serine	CONNEXIN	AT4G35600	1.23	0.29	1.43	0.19668175	0.5896	-5.66
248536_at	ankyrin-like protein	---	AT5G50140	-1.12	-0.16	-1.43	0.19680301	0.5897	-5.66
265133_s_at	unknown protein similar to hypothe	---	AT1G51240 /	1.10	0.14	1.43	0.19680183	0.5897	-5.66
245451_at	disease resistance RPP5 like prote	SNC1	AT4G16890	1.10	0.14	1.43	0.196803	0.5897	-5.66
249669_at	putative protein similar to unknown	---	---	-1.11	-0.15	-1.43	0.19685356	0.5897	-5.66
247527_at	leucine-rich receptor-like protein k	---	AT5G61480	1.19	0.25	1.43	0.19699349	0.5898	-5.66
253830_at	Expressed protein ; supported by f	---	AT4G27652	-1.65	-0.72	-1.43	0.19696166	0.5898	-5.66
264273_s_at	hypothetical protein contains simila	---	AT1G60300 /	-1.17	-0.23	-1.43	0.19698368	0.5898	-5.66
246539_at	putative protein geranylgeranylate	MUB2	AT5G15460	-1.10	-0.13	-1.43	0.19694172	0.5898	-5.66
265268_at	putative protein kinase contains a	---	AT2G42960	1.12	0.17	1.43	0.19692931	0.5898	-5.66
248139_at	putative protein similar to unknown	---	AT5G54970	2.17	1.11	1.43	0.19703157	0.5898	-5.66
266994_at	MADS-box protein (AGL29)	AGL29	AT2G34440	-1.14	-0.19	-1.43	0.19720437	0.5901	-5.66
250789_at	putative protein contains similarity	---	AT5G05630	-1.13	-0.17	-1.43	0.19720654	0.5901	-5.66
250631_at	pectin methyl-esterase-like protein	---	AT5G07430	-1.10	-0.14	-1.43	0.19716432	0.5901	-5.66
254708_at	ubiquitin-specific protease 20 (UB	UBP20	AT4G17895	-1.12	-0.16	-1.43	0.1973533	0.5901	-5.66
251925_at	hypothetical protein ;supported by	---	AT3G54000	1.20	0.26	1.43	0.19734392	0.5901	-5.66
255779_at	unknown protein similar to beta-1,	PDCB3	AT1G18650	1.28	0.36	1.43	0.19731164	0.5901	-5.66
252931_at	putative ubiquitin-dependent prote	---	AT4G38930	-1.12	-0.16	-1.43	0.19732455	0.5901	-5.66
247546_at	Expressed protein ; supported by f	---	AT5G61605	-1.13	-0.17	-1.43	0.19726001	0.5901	-5.66

261579_at	soluble inorganic pyrophosphatas	AtPPa1	AT1G01050	1.10	0.14	1.43	0.19739289	0.5902	-5.66
258918_at	putative cytochrome P450 similar t	UNE9	AT3G10560	-1.19	-0.25	-1.43	0.19742894	0.5902	-5.67
247856_at	receptor-like protein kinase	---	AT5G58300	1.17	0.23	1.43	0.19753621	0.5903	-5.67
254725_at	putative protein various predicted	---	AT4G13650	1.14	0.19	1.43	0.19756322	0.5903	-5.67
262643_at	unknown protein ;supported by full	---	AT1G62770	-1.23	-0.30	-1.43	0.19752078	0.5903	-5.67
254168_at	Mlo-like protein Mlo protein - Hord	MLO13	AT4G24250	1.14	0.18	1.43	0.19756078	0.5903	-5.67
263423_at	hypothetical protein predicted by g	---	AT2G31700	-1.11	-0.15	-1.43	0.19759226	0.5903	-5.67
246816_at	putative protein	---	AT5G27230	1.11	0.15	1.43	0.19762168	0.5903	-5.67
255885_at	sterol-C-methyltransferase identica	SMT2	AT1G20330	1.12	0.16	1.43	0.19765901	0.5904	-5.67
264910_at	resistance protein, putative similar	---	AT1G61100	1.27	0.35	1.43	0.19770402	0.5904	-5.67
256932_at	unknown protein	---	AT3G22520	1.11	0.15	1.43	0.19795385	0.5905	-5.67
249121_at	aluminum-induced protein-like ; su	---	AT5G43830	1.12	0.17	1.43	0.19793366	0.5905	-5.67
261923_at	UDP-glucose glucosyltransferase,	AtUGT85A1	AT1G22380	-1.14	-0.18	-1.43	0.19788172	0.5905	-5.67
259068_at	unknown protein	PEX13	AT3G07560	1.13	0.17	1.43	0.19792649	0.5905	-5.67
250999_at	putative protein predicted proyeins	---	AT5G02630	1.17	0.22	1.43	0.19790359	0.5905	-5.67
255890_at	rhodanese-like family protein predi	---	AT1G17850	1.22	0.29	1.43	0.19796649	0.5905	-5.67
250164_at	putative protein various predicted	---	AT5G15280	-1.16	-0.22	-1.43	0.19783017	0.5905	-5.67
252778_at	putative protein replication protein	---	---	-1.11	-0.15	-1.43	0.19783477	0.5905	-5.67
252889_at	hypothetical protein	---	AT4G39380	1.15	0.20	1.43	0.19782769	0.5905	-5.67
266961_at	Athila retroelement ORF1-like prot	---	---	-1.14	-0.19	-1.43	0.19802671	0.5906	-5.67
266054_at	hypothetical protein predicted by g	---	AT2G40640	1.16	0.21	1.43	0.1981387	0.5907	-5.67
256467_at	copia-type polyprotein, putative si	---	---	-1.12	-0.16	-1.43	0.19816486	0.5907	-5.67
259386_at	hypothetical protein contains simila	NUB	AT1G13400	-1.13	-0.18	-1.43	0.19816102	0.5907	-5.67
265409_at	unknown protein	PIP2;8	AT2G16830	-1.13	-0.17	-1.43	0.19814648	0.5907	-5.67
264501_at	putative lipase Similar to nodulins	---	AT1G09390	1.39	0.47	1.43	0.19833523	0.5908	-5.67
258742_at	hypothetical protein predicted by g	---	AT3G05800	-1.25	-0.32	-1.43	0.19829877	0.5908	-5.67
262188_at	Avr9 elicitor response protein, put	---	AT1G77810	-1.14	-0.19	-1.43	0.19837977	0.5908	-5.67
248274_at	isp4 protein	ATOPT9	AT5G53510	-1.11	-0.15	-1.43	0.1984088	0.5908	-5.67
250764_at	putative protein similar to unknown	---	AT5G05960	-2.37	-1.25	-1.43	0.19828724	0.5908	-5.67
244932_at	PSI 9KDa protein	---	---	-1.14	-0.19	-1.43	0.19842682	0.5908	-5.67
262623_at	integral membrane protein, putativ	---	AT1G06470	-1.14	-0.19	-1.43	0.19853364	0.5908	-5.67
265308_at	putative protein kinase contains a	ALE2	AT2G20300	1.09	0.13	1.43	0.19847954	0.5908	-5.67
250712_at	human RAN binding protein 16-like	---	AT5G06120	-1.13	-0.18	-1.43	0.19854787	0.5908	-5.67
250517_at	serine-type carboxypeptidase II-lik	scpl35	AT5G08260	1.37	0.46	1.43	0.19848644	0.5908	-5.67
263235_at	serine/threonine protein phosphat	PP2A-2	AT1G10430	1.13	0.17	1.43	0.19856848	0.5908	-5.67

263001_at	hypothetical protein contains simila	TAF6B4	AT1G54360	1.22	0.29	1.43	0.19836127	0.5908	-5.67
254614_at	putatative protein various predicte	---	AT4G19191	-1.16	-0.21	-1.43	0.19831381	0.5908	-5.67
260146_at	putative non-phototropic hypocotyl	---	AT1G52770	1.36	0.44	1.43	0.19856018	0.5908	-5.67
260981_at	hypothetical protein predicted by g	---	AT1G53460	1.15	0.20	1.43	0.19866143	0.5910	-5.67
257984_at	putative cell differentiation protein	---	AT3G20800	1.16	0.22	1.43	0.19864177	0.5910	-5.67
265235_s_at	hypothetical protein	---	AT2G07719	-1.13	-0.18	-1.43	0.19871814	0.5910	-5.67
264159_at	unknown protein ;supported by full	---	AT1G65270	1.10	0.14	1.43	0.19877266	0.5911	-5.67
254198_at	hypothetical protein	---	AT4G24090	1.13	0.18	1.43	0.19875261	0.5911	-5.67
247918_at	putative protein contains similarity	---	AT5G57610	-1.16	-0.21	-1.42	0.19884678	0.5912	-5.67
258935_at	unknown protein predicted by gen	---	AT3G10120	-1.23	-0.30	-1.42	0.19928578	0.5924	-5.67
252364_at	hypothetical protein ;supported by	---	AT3G48450	-1.51	-0.59	-1.42	0.19935246	0.5926	-5.67
252769_at	arabinose kinase - like protein put	---	AT3G42850	-1.12	-0.16	-1.42	0.19942234	0.5927	-5.67
246595_at	formate dehydrogenase (FDH) ;su	FDH	AT5G14780	1.12	0.16	1.42	0.19964299	0.5930	-5.67
263953_at	hypothetical protein predicted by g	OFP15	AT2G36050	-1.24	-0.31	-1.42	0.19963	0.5930	-5.67
257554_at	synaptobrevin, putative similar to	VAMP728	AT3G24890	1.12	0.17	1.42	0.19956601	0.5930	-5.67
248707_at	putative protein similar to unknown	---	AT5G48550	-1.13	-0.17	-1.42	0.19960606	0.5930	-5.67
257509_at	unknown protein	---	AT1G63190	1.13	0.18	1.42	0.20014623	0.5932	-5.68
262654_at	putative mandelonitrile lyase simil	---	AT1G14180	-1.16	-0.22	-1.42	0.1997939	0.5932	-5.68
254425_at	putative membrane associated pr	---	AT4G21450	1.10	0.14	1.42	0.2001523	0.5932	-5.68
252018_at	putative protein various predicted	AtPP2-A15	AT3G53000	-1.17	-0.23	-1.42	0.2000362	0.5932	-5.68
246763_at	NHE1 Na+/H+ exchanger ; suppo	NHX1	AT5G27150	1.21	0.27	1.42	0.20020601	0.5932	-5.68
263097_at	hypothetical protein predicted by g	PDV2	AT2G16070	-1.15	-0.21	-1.42	0.20020249	0.5932	-5.68
AFFX-r2-At-Ub	Arabidopsis thaliana /REF=U8496	---	---	-1.09	-0.12	-1.42	0.20000384	0.5932	-5.68
255610_at	putative phosphatidylinositol kinas	ATPIPK10	AT4G01190	-1.11	-0.16	-1.42	0.19998311	0.5932	-5.68
261329_at	hypothetical protein predicted by g	---	AT1G44890	-1.13	-0.17	-1.42	0.19996484	0.5932	-5.68
250579_at	putative protein terminal ear1, Zea	MCT2	AT5G07930	-1.11	-0.15	-1.42	0.19989296	0.5932	-5.68
266477_at	CLE4 CLAVATA3/ESR-Related 4 (	CLE6	AT2G31085	-1.14	-0.19	-1.42	0.19977756	0.5932	-5.68
245344_at	F-box protein family, AtFBL4 cont	---	AT4G15475	1.15	0.20	1.42	0.20019845	0.5932	-5.68
264959_at	hypothetical protein predicted by g	---	AT1G77090	-1.14	-0.19	-1.42	0.20009258	0.5932	-5.68
254668_at	neoxanthin cleavage enzyme - like	NCED2	AT4G18350	-1.15	-0.21	-1.42	0.20015812	0.5932	-5.68
248365_at	putative protein strong similarity to	---	AT5G52500	-1.12	-0.17	-1.42	0.20019418	0.5932	-5.68
248002_at	Expressed protein ; supported by f	ATARP8	AT5G56180	-1.17	-0.23	-1.42	0.20004711	0.5932	-5.68
254364_at	glycine-rich protein glycine-rich ce	---	AT4G22020	-1.14	-0.19	-1.42	0.19980568	0.5932	-5.68
245209_at	putative protein similarity to predic	---	AT5G12340	-1.49	-0.58	-1.42	0.20008799	0.5932	-5.68
249007_at	unknown protein ;supported by ful	---	AT5G44650	1.21	0.28	1.42	0.20014647	0.5932	-5.68

257125_at	t-complex polypeptide 1 homologu	ATTCP-1	AT3G20050	1.14	0.19	1.42	0.20038451	0.5935	-5.68
254433_at	putative protein tripeptidyl-peptida	TPP2	AT4G20850	1.10	0.14	1.42	0.20045977	0.5935	-5.68
248730_at	putative protein similar to unknown	---	AT5G48050	-1.15	-0.21	-1.42	0.20053374	0.5935	-5.68
250033_at	eukaryotic cap-binding protein (gb	NCBP	AT5G18110	1.11	0.15	1.42	0.20054712	0.5935	-5.68
263580_at	hypothetical protein similar to hypo	---	AT2G17140	1.13	0.18	1.42	0.20053512	0.5935	-5.68
250624_at	putative protein	---	AT5G07330	-1.13	-0.17	-1.42	0.20051965	0.5935	-5.68
251708_at	Expressed protein ; supported by c	---	AT3G56580	1.16	0.21	1.42	0.20045756	0.5935	-5.68
257138_at	hypothetical protein predicted by g	---	AT3G28870	-1.10	-0.13	-1.42	0.20036086	0.5935	-5.68
254580_at	putative protein ; supported by cD	---	AT4G19390	-1.11	-0.16	-1.42	0.20042479	0.5935	-5.68
259958_at	leucine-rich repeat transmembran	SRF6	AT1G53730	1.13	0.17	1.42	0.20059942	0.5936	-5.68
247141_at	putative protein strong similarity to	---	AT5G65560	-1.19	-0.25	-1.42	0.200667	0.5937	-5.68
258111_at	putative cytochrome P450 similar t	CYP72A9	AT3G14630	-1.16	-0.21	-1.42	0.20071099	0.5938	-5.68
247614_at	putative protein	---	AT5G60240	-1.10	-0.14	-1.42	0.20076557	0.5939	-5.68
254267_at	dihydroorotase ; supported by cDI	PYR4	AT4G22930	1.13	0.18	1.42	0.20084179	0.5940	-5.68
261266_at	expansin 10 identical to GB:AAF61	ATEXPA10	AT1G26770	1.18	0.23	1.42	0.20087283	0.5941	-5.68
254500_at	vacuolar sorting receptor-like prot	---	AT4G20110	1.29	0.37	1.42	0.20104853	0.5941	-5.68
251376_at	scarecrow - like protein scarecrow	---	AT3G60630	-1.20	-0.26	-1.42	0.20103003	0.5941	-5.68
244910_s_at	hypothetical protein	---	---	-1.12	-0.16	-1.42	0.20098075	0.5941	-5.68
266941_at	peroxidase (ATP22a) identical to G	---	AT2G18980	-1.15	-0.20	-1.42	0.20098459	0.5941	-5.68
261787_at	hypothetical protein predicted by g	---	AT1G16020	-1.12	-0.16	-1.42	0.2009526	0.5941	-5.68
256600_at	hypothetical protein predicted by g	---	AT3G14850	-1.47	-0.56	-1.42	0.20105833	0.5941	-5.68
258530_at	hypothetical protein predicted by g	---	AT3G06840	1.14	0.18	1.42	0.20090573	0.5941	-5.68
249608_at	multispanning membrane protein	---	AT5G37310	1.13	0.18	1.42	0.20114834	0.5942	-5.68
267209_at	unknown protein ;supported by ful	---	AT2G30930	-1.16	-0.21	-1.42	0.20128308	0.5943	-5.68
261122_at	ornithine carbamoyltransferase pre	OTC	AT1G75330	1.17	0.23	1.42	0.20122793	0.5943	-5.68
265439_at	senescence-associated protein co	---	AT2G21045	-1.57	-0.65	-1.42	0.20126027	0.5943	-5.68
261828_at	unknown protein ; supported by cD	---	AT1G11360	1.11	0.15	1.42	0.20118689	0.5943	-5.68
260833_at	lipase, putative similar to lipase G	---	AT1G06800	-1.31	-0.39	-1.42	0.20125424	0.5943	-5.68
248929_at	myrosinase-binding protein-like; ja	---	AT5G46000	-1.13	-0.17	-1.42	0.20134445	0.5944	-5.68
261163_x_at	auxin response factor, putative sir	ARF21	AT1G34410	-1.09	-0.13	-1.42	0.20142363	0.5944	-5.68
256352_at	proline-rich protein, putative simila	ATPRP1	AT1G54970	-1.15	-0.21	-1.42	0.20142577	0.5944	-5.68
248304_at	polypyrimidine tract-binding RNA t	PTB2	AT5G53180	1.10	0.13	1.42	0.20137983	0.5944	-5.68
258140_at	Expressed protein ; supported by c	ALDH2C4	AT3G24503	-1.35	-0.43	-1.42	0.20151167	0.5946	-5.68
266416_at	unknown protein ; supported by fu	---	AT2G38710	1.18	0.24	1.42	0.20159478	0.5946	-5.68
252503_at	putative protein hypothetical prote	---	AT3G46910	-1.13	-0.17	-1.42	0.20157667	0.5946	-5.68

259235_at	hypothetical protein predicted by g	---	AT3G11600	-1.32	-0.40	-1.42	0.20160597	0.5946	-5.68
260614_at	hypothetical protein contains Pfam	---	AT1G53390	-1.10	-0.14	-1.41	0.20172135	0.5949	-5.68
265200_s_at	putative glucosyl transferase an E	UGT73C6	AT2G36790	1.35	0.43	1.41	0.20177352	0.5949	-5.68
264954_at	carboxyphosphonoenolpyruvate m	---	AT1G77060	-1.17	-0.23	-1.41	0.20190552	0.5950	-5.68
253425_at	putative protein myosin heavy cha	---	AT4G32190	-1.21	-0.28	-1.41	0.201851	0.5950	-5.68
267107_at	hypothetical protein predicted by g	---	---	-1.12	-0.17	-1.41	0.2018823	0.5950	-5.68
264721_at	hypothetical protein predicted by g	---	AT1G23000	1.12	0.17	1.41	0.20189907	0.5950	-5.68
246343_at	putative protein	---	AT3G56720	-1.09	-0.12	-1.41	0.2019321	0.5950	-5.69
251704_at	putative protein unknown protein 1	---	AT3G56360	-1.32	-0.40	-1.41	0.20195824	0.5950	-5.69
245948_at	putative protein ;supported by full-	---	AT5G19540	-1.18	-0.24	-1.41	0.20199672	0.5951	-5.69
252074_at	putative protein DNA helicase hon	---	AT3G51700	1.12	0.16	1.41	0.20206768	0.5952	-5.69
256524_at	glutamine synthetase, putative sin	ATGSR2	AT1G66200	1.13	0.17	1.41	0.20212749	0.5953	-5.69
252419_at	putative protein	---	AT3G47510	-1.28	-0.36	-1.41	0.20220011	0.5954	-5.69
256359_at	protein kinase, putative contains P	---	AT1G66460	-1.10	-0.14	-1.41	0.20221451	0.5954	-5.69
256478_at	unknown protein	---	---	-1.13	-0.18	-1.41	0.2022772	0.5955	-5.69
252544_at	respiratory burst oxidase - like pro	---	AT3G45810	-1.14	-0.19	-1.41	0.20230598	0.5955	-5.69
249083_at	prohibitin non-consensus TT accep	ATPHB7	AT5G44140	1.12	0.16	1.41	0.20234771	0.5956	-5.69
257611_at	unknown protein	---	AT3G26580	1.16	0.22	1.41	0.20240647	0.5956	-5.69
259055_at	unknown protein ;supported by ful	UNE6	AT3G03340	1.11	0.16	1.41	0.20242877	0.5956	-5.69
257916_at	unknown protein similar to hypothe	---	AT3G23210	-1.20	-0.26	-1.41	0.20242827	0.5956	-5.69
267482_s_at	unknown protein	---	AT2G02770	-1.33	-0.41	-1.41	0.20250514	0.5957	-5.69
245885_at	putative protein phi-1 - Nicotiana t	EXL4	AT5G09440	1.23	0.30	1.41	0.2025714	0.5958	-5.69
257293_at	unknown protein similar to symbios	APG8H	AT3G15580	1.18	0.23	1.41	0.20269895	0.5960	-5.69
262327_at	hypothetical protein similar to hypo	---	AT1G64130	-1.12	-0.16	-1.41	0.20265811	0.5960	-5.69
264629_at	hypothetical protein similar to hypo	---	AT1G65540	-1.15	-0.20	-1.41	0.20269513	0.5960	-5.69
247361_at	unknown protein ;supported by ful	---	AT5G63480	1.16	0.21	1.41	0.20272598	0.5960	-5.69
254170_at	LG27/30-like gene LG27/30 gene	---	AT4G24430	1.10	0.13	1.41	0.20279346	0.5960	-5.69
244919_at	cytochrome c biogenesis orf203 Pr	---	AT2G07768	-1.12	-0.17	-1.41	0.20277736	0.5960	-5.69
259867_at	hypothetical protein predicted by g	---	AT1G76740	1.09	0.13	1.41	0.2028235	0.5960	-5.69
249986_at	putative protein predicted proteins	---	AT5G18460	-1.30	-0.38	-1.41	0.20335219	0.5964	-5.69
248292_at	putative protein similar to unknown	---	AT5G53030	-1.19	-0.25	-1.41	0.20326397	0.5964	-5.69
259273_s_at	serine/threonine specific protein k	---	AT3G01300	1.12	0.16	1.41	0.20321705	0.5964	-5.69
262313_at	unknown protein ;supported by full	---	AT1G70900	1.18	0.24	1.41	0.20326165	0.5964	-5.69
266673_at	putative thiamin biosynthesis prote	THIC	AT2G29630	-1.20	-0.27	-1.41	0.20333043	0.5964	-5.69
263322_at	putative ribonuclease E	RNEE/G	AT2G04270	1.20	0.27	1.41	0.20335756	0.5964	-5.69

256494_at	hypothetical protein predicted by g	---	AT1G31520	-1.11	-0.15	-1.41	0.20337045	0.5964	-5.69
254053_s_at	SRG1-like protein strong homolog	---	AT4G25300	1.23	0.30	1.41	0.20313596	0.5964	-5.69
257406_at	hypothetical protein predicted by g	---	AT1G27060	1.15	0.20	1.41	0.20314796	0.5964	-5.69
262089_s_at	hypothetical protein predicted by g	---	AT1G55980	-1.17	-0.22	-1.41	0.20311297	0.5964	-5.69
252042_at	putative serine/threonine protein k	---	AT3G51990	-1.15	-0.20	-1.41	0.20304493	0.5964	-5.69
264668_at	putative 2,3-bisphosphoglycerate-	---	AT1G09780	1.16	0.21	1.41	0.20318319	0.5964	-5.69
251609_at	putative protein hypothetical prote	---	AT3G57900	-1.09	-0.12	-1.41	0.20310768	0.5964	-5.69
256987_at	hypothetical protein predicted by g	---	AT3G28560	1.11	0.15	1.41	0.20326293	0.5964	-5.69
245503_at	kinase like protein	---	AT4G15650	-1.10	-0.14	-1.41	0.20327798	0.5964	-5.69
246381_at	hypothetical protein	---	---	-1.21	-0.27	-1.41	0.20335957	0.5964	-5.69
258511_at	unknown protein ;supported by ful	---	AT3G06590	1.14	0.19	1.41	0.20345064	0.5966	-5.69
247980_at	putative protein similar to unknown	GNC	AT5G56860	-1.37	-0.45	-1.41	0.20347722	0.5966	-5.69
254778_at	putative protein	---	AT4G12750	-1.15	-0.21	-1.41	0.2035093	0.5966	-5.69
252755_at	putative protein hypothetical protei	---	---	-1.12	-0.16	-1.41	0.20353867	0.5966	-5.69
249587_at	putative protein copper homeosta	---	AT5G37860	1.09	0.13	1.41	0.20358406	0.5967	-5.69
258821_at	putative wound-induced basic pro	---	AT3G07230	1.15	0.20	1.41	0.20367964	0.5968	-5.69
257873_at	P-glycoprotein, putative similar to	PGP17	AT3G28380	-1.14	-0.19	-1.41	0.20369527	0.5968	-5.69
246277_at	hypothetical protein	---	AT4G36460	1.13	0.18	1.41	0.20373439	0.5969	-5.69
258939_at	unknown protein predicted by gen	---	AT3G10020	-1.26	-0.33	-1.41	0.20377738	0.5969	-5.69
261724_at	Expressed protein ; supported by f	---	AT1G76185	1.11	0.16	1.41	0.20381878	0.5970	-5.69
258563_at	putative long-chain-fatty-acid--CoA	LACS6	AT3G05970	1.13	0.17	1.41	0.20390211	0.5970	-5.69
249944_at	NAM (no apical meristem)-like prot	anac089	AT5G22290	1.32	0.40	1.41	0.20389906	0.5970	-5.69
258897_at	unknown protein	---	AT3G05730	2.16	1.11	1.41	0.20403132	0.5971	-5.69
246947_at	cytochrome P450-like protein CYT	CYP71B11	AT5G25120	1.11	0.15	1.41	0.20425996	0.5971	-5.70
253126_at	putative protein probable membra	---	AT4G36050	1.22	0.29	1.41	0.20399162	0.5971	-5.69
250562_at	putative protein	TOM5	AT5G08040	1.14	0.19	1.41	0.20393853	0.5971	-5.69
264852_at	similar to Mlo proteins from H. vulg	MLO8	AT2G17480	-1.32	-0.40	-1.41	0.20423038	0.5971	-5.69
263950_at	hypothetical protein predicted by g	HVA22J	AT2G36020	-1.09	-0.12	-1.41	0.20431549	0.5971	-5.70
250343_at	putative protein density regulated	---	AT5G11900	-1.12	-0.16	-1.41	0.20405876	0.5971	-5.69
257252_at	glutathione reductase, cytosolic id	ATGR1	AT3G24170	-1.25	-0.32	-1.41	0.20428415	0.5971	-5.70
265051_at	jasmonate inducible protein, putat	---	AT1G52100	-1.16	-0.22	-1.41	0.20412092	0.5971	-5.69
260271_at	unknown protein similar to unknow	---	AT1G63690	1.11	0.15	1.41	0.20404687	0.5971	-5.69
247144_at	DOF zinc finger protein-like	---	AT5G65590	-1.19	-0.25	-1.41	0.20419576	0.5971	-5.69
247192_at	histone H3 (sp|P05203) ; supporte	---	AT5G65360	1.87	0.90	1.41	0.20426792	0.5971	-5.70
252386_at	putative protein various predicted	---	AT3G47840	-1.15	-0.20	-1.41	0.20416529	0.5971	-5.69

247196_at	putative protein similar to unknown	AIL7	AT5G65510	1.10	0.14	1.41	0.20408896	0.5971	-5.69
257330_at	hypothetical protein	---	---	-1.11	-0.16	-1.41	0.20418264	0.5971	-5.69
249347_at	putative protein similar to unknown	---	AT5G40830	1.25	0.32	1.41	0.20432468	0.5971	-5.70
260073_at	putative protein kinase contains Pf	---	AT1G73660	-1.16	-0.21	-1.41	0.20438207	0.5972	-5.70
246701_at	cysteine synthase ;supported by f	CYSD2	AT5G28020	-1.14	-0.19	-1.41	0.20444525	0.5973	-5.70
251054_at	receptor like protein kinase recept	LECRKA4.1	AT5G01540	1.69	0.76	1.40	0.20453887	0.5975	-5.70
253148_at	cyclin 2b protein	CYCB2;2	AT4G35620	-1.14	-0.19	-1.40	0.20456584	0.5975	-5.70
253385_at	putative protein predicted protein,	---	AT4G32930	1.11	0.15	1.40	0.20474222	0.5977	-5.70
261592_at	double-stranded RNA-specific edi	---	AT1G01760	-1.13	-0.18	-1.40	0.20482696	0.5977	-5.70
258211_at	hypothetical protein predicted by g	---	AT3G17890	1.16	0.22	1.40	0.2047378	0.5977	-5.70
261202_at	flower pigmentation protein ATAN	ATAN11	AT1G12910	1.13	0.17	1.40	0.20475247	0.5977	-5.70
265607_at	hypothetical protein predicted by g	---	AT2G25370	1.10	0.14	1.40	0.20467628	0.5977	-5.70
253370_at	pectinesterase - like protein pectin	---	AT4G33230	1.15	0.21	1.40	0.20478317	0.5977	-5.70
257048_at	hypothetical protein predicted by g	---	AT3G19740	-1.10	-0.14	-1.40	0.20480448	0.5977	-5.70
265481_at	unknown protein ; supported by cl	---	AT2G15960	1.12	0.17	1.40	0.20489283	0.5978	-5.70
262962_at	NADP-isocitrate dehydrogenase,	ICDH	AT1G54340	-1.09	-0.12	-1.40	0.20491568	0.5978	-5.70
263050_at	unknown protein ; supported by cl	ATVPS11	AT2G05170	-1.12	-0.16	-1.40	0.20494147	0.5978	-5.70
247573_at	anthocyanin 5-aromatic acyltransf	AACT1	AT5G61160	1.85	0.89	1.40	0.20512184	0.5979	-5.70
258070_at	hypothetical protein predicted by g	---	AT3G26040	-1.15	-0.20	-1.40	0.20511202	0.5979	-5.70
259621_at	unknown protein	---	AT1G42710	-1.10	-0.14	-1.40	0.20510776	0.5979	-5.70
251247_at	hypothetical protein	---	AT3G62140	-1.15	-0.20	-1.40	0.20501188	0.5979	-5.70
255311_at	putative protein	---	---	1.10	0.14	1.40	0.20504417	0.5979	-5.70
254471_s_at	putative protein parts of other prot	---	---	-1.11	-0.15	-1.40	0.20511376	0.5979	-5.70
246372_at	hypothetical protein predicted by g	---	AT1G51900	-1.11	-0.15	-1.40	0.20519982	0.5980	-5.70
266155_at	cytochrome p450, putative similar	CYP89A5	AT1G64950 /	-1.30	-0.38	-1.40	0.20532976	0.5983	-5.70
250936_at	putative protein ;supported by full-	---	AT5G03120	-1.25	-0.33	-1.40	0.20546218	0.5986	-5.70
248388_at	putative protein contains similarity	---	AT5G51980	1.13	0.18	1.40	0.20548416	0.5986	-5.70
267388_at	putative beta-glucosidase	BGLU15	AT2G44450	-1.25	-0.32	-1.40	0.20556386	0.5986	-5.70
248832_at	putative protein similar to unknown	---	AT5G47170	-1.10	-0.14	-1.40	0.20555287	0.5986	-5.70
264614_s_at	putative aldehyde oxidase similar t	---	AT1G02590 /	-1.12	-0.16	-1.40	0.20551544	0.5986	-5.70
256964_at	unknown protein ;supported by ful	AGP12	AT3G13520	-1.13	-0.18	-1.40	0.20570562	0.5986	-5.70
264511_at	putative galactinol synthase simila	AtGolS3	AT1G09350	-1.45	-0.53	-1.40	0.20566459	0.5986	-5.70
250803_at	putative protein contains similarity	---	AT5G04980	-1.19	-0.26	-1.40	0.20574218	0.5986	-5.70
261116_at	sec14 cytosolic factor, putative sir	---	AT1G75370	-1.12	-0.16	-1.40	0.20577473	0.5986	-5.70
265563_s_at	hypothetical protein predicted by g	---	---	-1.09	-0.12	-1.40	0.20575982	0.5986	-5.70

247732_at	putative protein various predicted	---	AT5G59600	-1.10	-0.13	-1.40	0.20560731	0.5986	-5.70
250175_at	putative protein CGI-67, Homo sa	---	AT5G14390	1.23	0.29	1.40	0.20571252	0.5986	-5.70
247766_at	FtsH protease, putative contains s	ftsh9	AT5G58870	-1.13	-0.18	-1.40	0.20577088	0.5986	-5.70
254183_at	putative protein predicted protein,	---	AT4G23960	-1.13	-0.17	-1.40	0.20581952	0.5987	-5.70
257661_at	unknown protein contains Pfam pr	---	AT3G13340	-1.09	-0.13	-1.40	0.20584937	0.5987	-5.70
265693_at	putative poly(A) binding protein	---	AT2G24350	1.13	0.17	1.40	0.20587708	0.5987	-5.70
253359_at	putative protein kinase protein kin	---	AT4G33080	1.15	0.20	1.40	0.20594336	0.5988	-5.70
263741_at	hypothetical protein predicted by g	---	AT2G20620	-1.15	-0.21	-1.40	0.20604776	0.5990	-5.70
263093_at	putative replication protein A1	---	---	-1.10	-0.14	-1.40	0.20607726	0.5990	-5.70
246420_at	putative protein various predicted p	---	AT5G16870	1.14	0.20	1.40	0.20610877	0.5990	-5.70
245892_at	putative lipid transfer protein lipid	---	AT5G09370	-1.17	-0.23	-1.40	0.20616435	0.5991	-5.70
263998_at	unknown protein	---	AT2G22510	1.27	0.35	1.40	0.20644148	0.5999	-5.70
255676_at	putative beta-amylase similar to th	BAM2	AT4G00490	-1.30	-0.38	-1.40	0.20665917	0.6000	-5.71
261348_at	hypothetical protein contains simila	TED3	AT1G79810	-1.10	-0.14	-1.40	0.20659472	0.6000	-5.71
251717_at	putative protein EXOENZYMES R	LAF3	AT3G55850	1.16	0.21	1.40	0.20662299	0.6000	-5.71
256189_at	hypothetical protein predicted by g	---	AT1G30140	-1.11	-0.15	-1.40	0.20666162	0.6000	-5.71
261580_at	unknown protein ;supported by full	IQD18	AT1G01110	-1.19	-0.25	-1.40	0.20657935	0.6000	-5.71
253910_at	putative receptor like kinase recep	---	AT4G27290	-1.10	-0.14	-1.40	0.20655516	0.6000	-5.70
253801_at	hypothetical protein	---	AT4G28170	1.11	0.16	1.40	0.20665832	0.6000	-5.71
246139_at	putative protein predicted protein,	---	AT5G19900	-1.14	-0.19	-1.40	0.20685872	0.6001	-5.71
263842_at	Expressed protein ; supported by f	---	AT2G36835	1.18	0.24	1.40	0.20683285	0.6001	-5.71
257994_at	unknown protein	---	AT3G19920	-1.17	-0.23	-1.40	0.20680009	0.6001	-5.71
264729_at	putative metal-binding protein high	---	AT1G22990	1.22	0.29	1.40	0.20674978	0.6001	-5.71
264723_at	putative salt-inducible protein simil	---	AT1G22960	-1.11	-0.15	-1.40	0.20678562	0.6001	-5.71
262530_at	putative receptor protein kinase Ap	AtRLP2	AT1G17240	1.14	0.19	1.40	0.20687245	0.6001	-5.71
258380_at	PP1/PP2A phosphatases pleiotrop	---	AT3G16650	-1.13	-0.17	-1.40	0.20689886	0.6001	-5.71
258882_at	unknown protein ; supported by fu	---	AT3G06330	-1.13	-0.17	-1.40	0.20696093	0.6001	-5.71
266318_at	Mutator-like transposase similar to	FRS3	AT2G27110	-1.09	-0.12	-1.40	0.20693986	0.6001	-5.71
259976_at	hypothetical protein ;supported by	CP12-3	AT1G76560	1.22	0.28	1.40	0.20706075	0.6004	-5.71
254129_at	putative tRNA isopentenyltransfer	IPT4	AT4G24650	-1.11	-0.14	-1.40	0.2071148	0.6004	-5.71
256378_at	receptor protein kinase, putative c	---	AT1G66830	-1.11	-0.15	-1.40	0.20711624	0.6004	-5.71
245100_at	ubiquitin-specific protease 5 (UBP	UBP5	AT2G40930	-1.11	-0.16	-1.40	0.20720627	0.6005	-5.71
253076_at	NAM like protein P.hybrida NAM g	ANAC076	AT4G36160	1.11	0.16	1.40	0.20719543	0.6005	-5.71
258683_at	putative protein kinase contains Pf	ATSIK	AT3G08760	1.22	0.29	1.40	0.20728498	0.6006	-5.71
265276_at	hypothetical protein predicted by g	---	AT2G28400	1.20	0.26	1.40	0.20728191	0.6006	-5.71

256615_at	hypothetical protein predicted by g	---	AT3G22250	-1.15	-0.20	-1.39	0.20735637	0.6007	-5.71
249485_at	receptor protein kinase - like prote	---	AT5G39020	1.37	0.46	1.39	0.20744962	0.6007	-5.71
256986_at	unknown protein	---	AT3G28700	1.17	0.23	1.39	0.20747417	0.6007	-5.71
264279_s_at	glycoprotein(EP1), putative simila	---	AT1G78820	1.17	0.22	1.39	0.20747105	0.6007	-5.71
257483_at	hypothetical protein contains simila	ICK5	AT1G49620	1.12	0.16	1.39	0.20749245	0.6007	-5.71
245083_at	putative integral membrane protein	ATRER1C1	AT2G23310	1.12	0.17	1.39	0.20746076	0.6007	-5.71
262121_at	endo-1,4-beta-glucanase precurso	ATCEL2	AT1G02800	-1.14	-0.19	-1.39	0.20753305	0.6007	-5.71
259462_at	hypothetical protein contains simila	---	AT1G18940	-1.17	-0.23	-1.39	0.20757632	0.6007	-5.71
253923_at	hypothetical protein Arabidopsis th	TOR1	AT4G27060	1.12	0.16	1.39	0.207589	0.6007	-5.71
256779_at	beta-fructofuranosidase, putative s	AtcwINV5	AT3G13784	-1.09	-0.13	-1.39	0.20763441	0.6008	-5.71
255681_at	predicted protein of unknown funct	DGD2	AT4G00550	1.14	0.19	1.39	0.20779167	0.6011	-5.71
266162_at	putative bHLH transcription factor	FRU	AT2G28160	-1.12	-0.16	-1.39	0.20780728	0.6011	-5.71
258084_at	putative B regulatory subunit of pro	---	AT3G26020	-1.19	-0.25	-1.39	0.20776293	0.6011	-5.71
262480_at	receptor kinase, putative similar to	---	AT1G11340	-1.23	-0.30	-1.39	0.20787157	0.6012	-5.71
252441_at	putative protein ; supported by cD	PTAC16	AT3G46780	-1.19	-0.25	-1.39	0.20793742	0.6013	-5.71
253810_at	putative NADH dehydrogenase NA	NDB1	AT4G28220	1.33	0.41	1.39	0.20801389	0.6014	-5.71
255351_x_at	putative transposon protein similar	---	---	1.13	0.17	1.39	0.20802283	0.6014	-5.71
248252_at	putative protein similar to unknown	AGP22	AT5G53250	1.38	0.46	1.39	0.20811555	0.6015	-5.71
262656_at	unknown protein location of EST T	---	AT1G14200	-1.12	-0.17	-1.39	0.20809336	0.6015	-5.71
253934_at	putative beta-1,3-glucanase beta-	---	AT4G26830	-1.11	-0.15	-1.39	0.2082562	0.6018	-5.71
249991_at	zinc finger -like protein zinc finger	---	AT5G18550	-1.12	-0.16	-1.39	0.20834649	0.6020	-5.71
261036_at	developmentally regulated GTP-b	ATDRG1	AT1G17470	1.10	0.14	1.39	0.20842188	0.6020	-5.71
264986_at	glutathione transferase, putative s	ATGSTU13	AT1G27130	-1.55	-0.64	-1.39	0.20841297	0.6020	-5.71
246814_at	acyl carrier protein precursor - like	ACP5	AT5G27200	-1.10	-0.14	-1.39	0.20839571	0.6020	-5.71
254410_at	serine/threonine kinase - like prote	---	AT4G21410	1.35	0.43	1.39	0.20845823	0.6020	-5.71
258424_at	hypothetical protein predicted by g	---	AT3G16750	1.13	0.18	1.39	0.20849952	0.6021	-5.71
259908_at	RNA polymerase subunit identical	ATRPAC42	AT1G60850	-1.17	-0.23	-1.39	0.20869067	0.6024	-5.71
256078_at	hypothetical protein predicted by g	---	AT1G20670	-1.12	-0.16	-1.39	0.2086735	0.6024	-5.71
250130_at	amylogenin; reversibly glycosylata	---	AT5G16510	-1.16	-0.22	-1.39	0.20864642	0.6024	-5.71
253785_s_at	ABC transporter - like protein ABC	ATM2	AT4G28620	1.12	0.16	1.39	0.20870769	0.6024	-5.71
246941_at	putative protein several hypothetic	---	AT5G25415	-1.11	-0.15	-1.39	0.20881549	0.6026	-5.71
245871_at	hypothetical protein predicted by g	---	AT1G26290	1.15	0.21	1.39	0.20883906	0.6026	-5.71
261028_at	hypothetical protein predicted by g	---	AT1G26620	-1.12	-0.16	-1.39	0.20889544	0.6027	-5.71
255013_at	putative protein ;supported by full-	---	AT4G10000	1.14	0.18	1.39	0.20900106	0.6029	-5.72
259555_at	hypothetical protein	---	---	-1.11	-0.14	-1.39	0.20906782	0.6030	-5.72

267437_at	hypothetical protein predicted by g	---	AT2G19200	-1.11	-0.15	-1.39	0.20923317	0.6032	-5.72
260263_at	hypothetical protein predicted by g	JAG	AT1G68480	-1.09	-0.13	-1.39	0.20917199	0.6032	-5.72
245589_at	subtilisin-like serine protease conta	---	AT4G15040	-1.17	-0.23	-1.39	0.20924004	0.6032	-5.72
258024_at	hypothetical protein predicted by g	---	AT3G19360	1.24	0.31	1.39	0.20921903	0.6032	-5.72
261895_at	metal ion transporter identical to G	NRAMP1	AT1G80830	1.31	0.39	1.39	0.20928813	0.6033	-5.72
254907_at	putative disease resistance respo	---	AT4G11190	-1.11	-0.15	-1.39	0.20933945	0.6034	-5.72
267035_at	putative beta-alanine-pyruvate ami	AGT3	AT2G38400	-1.40	-0.48	-1.39	0.20949908	0.6035	-5.72
258487_at	unknown protein ;supported by ful	LBD41	AT3G02550	1.58	0.66	1.39	0.20947079	0.6035	-5.72
256838_at	ADP-ribosylation factor, putative s	ATARFC1	AT3G22950	1.14	0.19	1.39	0.20947965	0.6035	-5.72
257346_at	pseudogene, putative retroelemer	---	---	-1.12	-0.16	-1.39	0.20948691	0.6035	-5.72
256236_at	hypothetical protein predicted by g	---	AT3G12350	-1.14	-0.18	-1.39	0.20954312	0.6036	-5.72
250585_at	putative protein contains similarity	---	AT5G07620	-1.28	-0.35	-1.39	0.2096234	0.6036	-5.72
254169_at	putative protein ; supported by cD	---	AT4G24290	-1.15	-0.20	-1.39	0.20960893	0.6036	-5.72
259071_at	unknown protein similar to hin1 GE	NHL2	AT3G11650	1.21	0.27	1.39	0.20967801	0.6037	-5.72
248762_at	Expressed protein ; supported by f	---	AT5G47455	1.20	0.26	1.39	0.20965694	0.6037	-5.72
262888_at	RNA-directed RNA polymerase, p	RDR1	AT1G14790	1.31	0.39	1.39	0.20978606	0.6038	-5.72
251375_at	putative protein various predicted	---	AT3G60410	-1.18	-0.23	-1.39	0.20994829	0.6038	-5.72
250952_at	putative protein	ATIREG2	AT5G03570	-1.16	-0.21	-1.39	0.20994582	0.6038	-5.72
266096_at	putative vacuolar protein sorting-as	VCL1	AT2G38020	1.11	0.15	1.39	0.20991879	0.6038	-5.72
262742_at	GTP-binding protein, putative simi	AtRABA1i	AT1G28550	-1.11	-0.15	-1.39	0.20989518	0.6038	-5.72
246506_at	putative protein hypothetical prote	---	AT5G16110	1.15	0.21	1.39	0.20982291	0.6038	-5.72
266652_at	unknown protein	---	AT2G25760	1.10	0.14	1.39	0.2099683	0.6038	-5.72
252302_at	putative protein hypothetical prote	---	AT3G49190	1.10	0.13	1.39	0.20987377	0.6038	-5.72
259778_at	hypothetical protein predicted by g	---	AT1G29610	-1.10	-0.14	-1.39	0.20977615	0.6038	-5.72
258544_at	disease resistance gene (RPM1) i	RPM1	AT3G07040	-1.22	-0.29	-1.39	0.21007992	0.6039	-5.72
249958_at	plasma membrane associated pro	---	AT5G18970	1.17	0.22	1.39	0.21008121	0.6039	-5.72
247639_s_at	undecaprenyl diphosphate syntha	---	AT5G60500	-1.09	-0.12	-1.39	0.21005218	0.6039	-5.72
259109_at	putative serine threonine protein pl	---	AT3G05580	-1.19	-0.25	-1.39	0.21018525	0.6040	-5.72
258008_at	putative late embryogenesis abun	---	AT3G19430	-1.11	-0.15	-1.39	0.21022105	0.6040	-5.72
250979_at	putative protein	---	AT5G03090	-1.17	-0.23	-1.39	0.21017738	0.6040	-5.72
266369_at	hypothetical protein predicted by g	BOP2	AT2G41370	-1.18	-0.23	-1.39	0.2102081	0.6040	-5.72
254241_at	serine/threonine kinase - like prot	CRK11	AT4G23190	1.47	0.56	1.38	0.21038056	0.6042	-5.72
267619_at	putative receptor-like protein kinas	---	AT2G26730	-1.23	-0.30	-1.38	0.21048507	0.6042	-5.72
251669_at	putative protein hypothetical prote	---	AT3G57180	1.26	0.33	1.38	0.21046872	0.6042	-5.72
250387_at	putative protein predicted proteins	---	AT5G11290	-1.10	-0.13	-1.38	0.21054918	0.6042	-5.72

253068_at	putative protein Kaposi's sarcoma	---	AT4G37820	1.11	0.16	1.38	0.21051042	0.6042	-5.72
266099_at	putative alpha-carboxyltransferase	CAC3	AT2G38040	1.17	0.23	1.38	0.21041705	0.6042	-5.72
266061_at	putative translation initiation factor	---	AT2G18720	-1.12	-0.17	-1.38	0.2105437	0.6042	-5.72
254622_at	hypothetical protein contains simila	---	AT4G18375	1.20	0.26	1.38	0.21043751	0.6042	-5.72
255405_s_at	hypothetical protein similar to A. th	---	AT4G03440	-1.16	-0.21	-1.38	0.2103513	0.6042	-5.72
265364_at	putative retroelement pol polyprote	---	---	1.10	0.14	1.38	0.2104465	0.6042	-5.72
246578_at	MADS-box protein, putative simila	AGL86	AT1G31630	-1.10	-0.14	-1.38	0.21058615	0.6042	-5.72
265363_at	hypothetical protein predicted by g	---	---	-1.10	-0.13	-1.38	0.21069342	0.6044	-5.72
251954_at	putative protein predicted protein,	CPuORF51	AT3G53668	1.28	0.36	1.38	0.21071522	0.6044	-5.72
261680_at	hypothetical protein similar to hypo	---	AT1G47350	-1.09	-0.13	-1.38	0.21070651	0.6044	-5.72
256585_at	hypothetical protein	---	AT3G28760	-1.18	-0.24	-1.38	0.21082892	0.6045	-5.72
258673_at	unknown protein	---	AT3G08620	1.17	0.23	1.38	0.2108617	0.6045	-5.72
255987_s_at	putative protein predicted proteins	---	AT5G35050	1.10	0.13	1.38	0.21086175	0.6045	-5.72
264386_at	putative pyrophosphate-fructose-6	---	AT1G12000	1.26	0.33	1.38	0.21088574	0.6045	-5.72
251655_at	hypothetical protein	AT3G5715	---	1.16	0.21	1.38	0.21091451	0.6045	-5.72
259459_at	En/Spm-like transposon protein, p	---	---	-1.11	-0.14	-1.38	0.21098343	0.6047	-5.72
258433_at	translationally controlled tumor pro	TCTP	AT3G16640	1.14	0.19	1.38	0.21101923	0.6047	-5.72
265468_at	hypothetical protein predicted by g	---	AT2G37210	-1.12	-0.16	-1.38	0.21117764	0.6050	-5.72
256298_at	DNA-binding protein contains Pfan	AGL94	AT1G69540	-1.12	-0.16	-1.38	0.21118338	0.6050	-5.72
245659_at	hypothetical protein predicted by g	---	AT1G28260	1.23	0.30	1.38	0.21123003	0.6051	-5.72
247124_at	prolyl 4-hydroxylase, alpha subun	---	AT5G66060	1.10	0.14	1.38	0.21132028	0.6052	-5.72
266312_at	20S proteasome subunit C8 (PAG	PAG1	AT2G27020	1.13	0.18	1.38	0.21131995	0.6052	-5.72
257843_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.38	0.21145539	0.6054	-5.73
260042_at	hypothetical protein C-term similar	---	AT1G68820	1.20	0.27	1.38	0.2114576	0.6054	-5.73
249361_at	protein kinase - like protein protein	---	AT5G40540	1.25	0.33	1.38	0.21159237	0.6056	-5.73
251244_at	pectinacetylesterase precursor-lik	---	AT3G62060	1.13	0.17	1.38	0.21162368	0.6056	-5.73
255544_at	predicted protein of unknown funct	---	AT4G01880	-1.15	-0.20	-1.38	0.21166149	0.6056	-5.73
248882_at	cullin ;supported by full-length cDN	CUL4	AT5G46210	1.10	0.13	1.38	0.21167972	0.6056	-5.73
263329_at	hypothetical protein contains C3HC	---	AT2G15260	1.11	0.15	1.38	0.21163435	0.6056	-5.73
259828_at	RING-H2 zinc finger protein ATL3	---	AT1G72220	1.14	0.19	1.38	0.21156249	0.6056	-5.73
246559_at	putative protein YTM1 - Homo sap	---	AT5G15550	1.20	0.26	1.38	0.21180525	0.6057	-5.73
263356_at	putative RNA-binding protein ; sup	UBA1A	AT2G22090	-1.10	-0.14	-1.38	0.21177836	0.6057	-5.73
251092_at	putative protein ;supported by full-	---	AT5G01470	-1.12	-0.16	-1.38	0.21181125	0.6057	-5.73
251976_at	disease resistance - like protein di	AtRLP45	AT3G53240	1.14	0.19	1.38	0.21182549	0.6057	-5.73
246585_at	myb transcription factor werewolf (	ATMYB66	AT5G14750	-1.10	-0.14	-1.38	0.21194725	0.6060	-5.73

267632_at	hypothetical protein predicted by g	---	AT2G42160	1.18	0.24	1.38	0.21203786	0.6062	-5.73
248713_at	putative protein contains similarity	NSP5	AT5G48180	1.28	0.35	1.38	0.2120679	0.6062	-5.73
253244_at	putative protein SEC14 protein, S	COW1	AT4G34580	1.16	0.21	1.38	0.21216695	0.6063	-5.73
251640_at	putative protein ;supported by full-	---	AT3G57450	-1.52	-0.61	-1.38	0.21217437	0.6063	-5.73
259981_at	unknown protein ; supported by fu	---	AT1G76450	1.14	0.19	1.38	0.21225086	0.6064	-5.73
245517_at	hypothetical protein	---	AT4G15840	-1.09	-0.12	-1.38	0.2122835	0.6064	-5.73
245167_s_at	putative synaptobrevin ;supported	ATVAMP72	AT2G33110	1.10	0.13	1.38	0.21229594	0.6064	-5.73
256612_at	hypothetical protein predicted by g	---	AT3G29280	1.14	0.19	1.38	0.21235584	0.6065	-5.73
264818_at	hypothetical protein similar to hypo	NAF1	AT1G03530	1.27	0.35	1.38	0.21247975	0.6067	-5.73
263168_at	putative glutaredoxin Strong simila	---	AT1G03020	-1.43	-0.52	-1.38	0.21247986	0.6067	-5.73
261722_at	acyl-(acyl carrier protein) thioester	FATB	AT1G08510	1.10	0.14	1.38	0.21308005	0.6068	-5.73
265931_at	unknown protein ;supported by ful	---	AT2G18520	1.15	0.21	1.38	0.21272249	0.6068	-5.73
258925_at	unknown protein similar to hypoth	---	AT3G10420	1.14	0.19	1.37	0.21321207	0.6068	-5.73
266302_at	ethylene-insensitive3-like1 (EIL1) i	EIL1	AT2G27050	1.15	0.20	1.38	0.21312674	0.6068	-5.73
257982_at	unknown protein similar to TYPE I	ATTOP6B	AT3G20780	-1.15	-0.20	-1.37	0.21321142	0.6068	-5.73
258143_at	hypothetical protein	---	AT3G18170	-1.19	-0.25	-1.38	0.213135	0.6068	-5.73
247429_at	putative protein strong similarity to	---	AT5G62620	1.16	0.22	1.38	0.21263481	0.6068	-5.73
258151_at	beta-glucosidase, putative similar	BGLU44	AT3G18080	-1.24	-0.31	-1.38	0.21282205	0.6068	-5.73
254881_at	hypothetical protein	---	AT4G11700	-1.10	-0.14	-1.38	0.21281848	0.6068	-5.73
264012_at	hypothetical protein predicted by g	---	AT2G21080	-1.15	-0.20	-1.38	0.21253493	0.6068	-5.73
262095_at	hypothetical protein predicted by g	---	AT1G56090	1.16	0.21	1.38	0.21315178	0.6068	-5.73
263355_at	putative RNA-binding protein ;sup	---	AT2G22100	-1.15	-0.20	-1.38	0.21286362	0.6068	-5.73
261440_at	hypothetical protein predicted by g	---	AT1G28510	1.11	0.15	1.38	0.21305083	0.6068	-5.73
248066_at	putative protein contains similarity	QRT1	AT5G55590	-1.12	-0.17	-1.37	0.21320298	0.6068	-5.73
251782_at	beta-N-acetylhexosaminidase -like	HEXO1	AT3G55260	1.17	0.23	1.38	0.21275959	0.6068	-5.73
258255_at	hypothetical protein predicted by g	---	AT3G26800	-1.10	-0.14	-1.38	0.212963	0.6068	-5.73
252865_at	Expressed protein ; supported by f	---	AT4G39753	-1.17	-0.22	-1.38	0.21294796	0.6068	-5.73
249560_at	putative protein	LCR80	AT5G38330	-1.18	-0.24	-1.38	0.21265616	0.6068	-5.73
245366_at	Expressed protein ; supported by f	AtMAPR4	AT4G14965	1.10	0.14	1.38	0.21283659	0.6068	-5.73
265110_at	hypothetical protein predicted by g	---	AT1G62490	-1.15	-0.20	-1.38	0.21302489	0.6068	-5.73
256790_at	ARR1 protein, putative similar to A	ARR1	AT3G16857	1.12	0.16	1.37	0.21319849	0.6068	-5.73
258803_at	unknown protein similar to elicitor	WRKY39	AT3G04670	1.12	0.17	1.38	0.2126115	0.6068	-5.73
266037_at	putative protein kinase contains a	---	AT2G05940	-1.41	-0.49	-1.38	0.21284071	0.6068	-5.73
254906_at	putative disease resistance respo	---	AT4G11180	-1.11	-0.15	-1.38	0.21260646	0.6068	-5.73
245402_at	putative protein	---	AT4G17585	1.13	0.17	1.38	0.21296635	0.6068	-5.73

265758_at	hypothetical protein similar to myos	---	---	-1.10	-0.13	-1.38	0.21263941	0.6068	-5.73
266508_at	hypothetical protein predicted by g	---	AT2G47920	1.15	0.20	1.38	0.2131441	0.6068	-5.73
250136_at	putative protein de novo DNA met	DRM1	AT5G15380	-1.22	-0.29	-1.37	0.21326713	0.6068	-5.73
256244_at	sulphate transporter, putative simi	SULTR4;2	AT3G12520	-1.11	-0.14	-1.37	0.21327171	0.6068	-5.73
257755_at	unknown protein ; supported by fu	---	AT3G18760	1.21	0.28	1.37	0.21332074	0.6069	-5.73
259310_s_at	Expressed protein ; supported by c	---	AT3G05160	-1.15	-0.20	-1.37	0.21342881	0.6071	-5.73
251989_at	RNA helicase -like protein RNA he	LOS4	AT3G53110	1.13	0.17	1.37	0.21347326	0.6071	-5.73
257281_s_at	hypothetical protein predicted by g	---	AT3G29680	1.14	0.19	1.37	0.21348503	0.6071	-5.73
255056_at	putative protein helix-loop-helix pr	TT8	AT4G09820	-1.09	-0.13	-1.37	0.21355579	0.6072	-5.73
265618_at	hypothetical protein predicted by g	---	AT2G25460	-1.13	-0.17	-1.37	0.21359821	0.6073	-5.73
255433_at	putative xyloglucan endotransglyc	XTH9	AT4G03210	1.29	0.37	1.37	0.21363645	0.6073	-5.73
249309_at	homeotic protein BEL1 homolog ;	BEL1	AT5G41410	1.14	0.19	1.37	0.21374855	0.6075	-5.73
266187_at	putative retroelement pol polyprote	---	AT2G38970	1.20	0.27	1.37	0.21379744	0.6075	-5.74
253378_at	hypothetical protein	---	AT4G33310	-1.10	-0.14	-1.37	0.21373029	0.6075	-5.73
246866_at	putative protein various predicted	---	AT5G25960	1.11	0.15	1.37	0.21377307	0.6075	-5.73
255599_at	cyclic nucleotide gated channel (C	ATCNGC13	AT4G01010	1.25	0.32	1.37	0.21389964	0.6077	-5.74
261987_at	hypothetical protein predicted by g	---	AT1G33710	-1.09	-0.12	-1.37	0.21393259	0.6077	-5.74
248174_at	50S ribosomal protein L24, chloro	---	AT5G54600	1.12	0.16	1.37	0.2140197	0.6079	-5.74
254610_at	putative protein predicted protein,	---	AT4G18890	1.12	0.16	1.37	0.21421043	0.6081	-5.74
248236_at	putative protein contains similarity	---	AT5G53870	-1.65	-0.72	-1.37	0.21414457	0.6081	-5.74
247469_at	Expressed protein ; supported by c	AGL42	AT5G62165	1.70	0.77	1.37	0.21419894	0.6081	-5.74
265604_s_at	hypothetical protein predicted by g	---	---	1.12	0.16	1.37	0.21421008	0.6081	-5.74
267314_at	putative myosin heavy chain	---	AT2G34730	1.16	0.22	1.37	0.21430099	0.6083	-5.74
264223_s_at	receptor kinase, putative similar to	---	AT1G67520	1.32	0.40	1.37	0.21436962	0.6083	-5.74
249140_at	F-box protein family, AtFBX6 cont	---	AT5G43190	-1.17	-0.22	-1.37	0.21439449	0.6083	-5.74
247241_at	unknown protein	---	AT5G64680	1.22	0.29	1.37	0.21434838	0.6083	-5.74
251470_at	putative protein hypothetical prote	---	AT3G59570	-1.14	-0.20	-1.37	0.21449914	0.6085	-5.74
263110_at	unknown protein ;supported by full	---	AT1G65220	1.15	0.20	1.37	0.21452927	0.6086	-5.74
252350_at	ataxia-telangiectasia mutated prot	ATM	AT3G48190	1.10	0.14	1.37	0.2146329	0.6087	-5.74
257355_at	hypothetical protein predicted by g	---	AT2G38150	1.11	0.15	1.37	0.21462347	0.6087	-5.74
248065_at	putative protein similar to unknown	---	AT5G55580	1.16	0.21	1.37	0.21493054	0.6088	-5.74
252475_s_at	putative protein several hypothetic	PCL1	AT3G46640	-1.15	-0.20	-1.37	0.21502373	0.6088	-5.74
245359_at	carnitine racemase like protein ;su	IBR10	AT4G14430	1.22	0.29	1.37	0.21501674	0.6088	-5.74
256304_at	Expressed protein ; supported by c	---	AT1G69523	-1.21	-0.28	-1.37	0.21475665	0.6088	-5.74
248759_at	putative protein similar to unknown	---	AT5G47610	1.29	0.37	1.37	0.21475485	0.6088	-5.74

264550_at	hypothetical protein predicted by g	---	AT1G09450	-1.19	-0.26	-1.37	0.21486441	0.6088	-5.74
258756_at	hypothetical protein similar to hypo	---	AT3G11960	1.12	0.17	1.37	0.21497185	0.6088	-5.74
264486_at	hypothetical protein contains simila	---	AT1G77180	1.14	0.19	1.37	0.21493405	0.6088	-5.74
258082_at	Expressed protein ; supported by f	CLE27	AT3G25905	1.24	0.31	1.37	0.21472878	0.6088	-5.74
249061_at	putative protein similar to unknown	---	AT5G44550	-1.11	-0.15	-1.37	0.21501204	0.6088	-5.74
253614_at	putative protein heat shock protein	---	AT4G30350	1.21	0.28	1.37	0.21503177	0.6088	-5.74
252850_at	putative protein ;supported by full-	---	AT4G39880	1.15	0.20	1.37	0.21482855	0.6088	-5.74
251894_at	putative protein predicted proteins	---	AT3G54380	1.13	0.18	1.37	0.21494907	0.6088	-5.74
244958_at	hypothetical protein	---	---	-1.10	-0.14	-1.37	0.21492933	0.6088	-5.74
266818_at	unknown protein	HUB1	AT2G44950	-1.14	-0.19	-1.37	0.21508534	0.6088	-5.74
251436_at	putative protein hypothetical prote	ARGOS	AT3G59900	1.69	0.75	1.37	0.21507212	0.6088	-5.74
251802_at	E2, ubiquitin-conjugating enzyme	UBC14	AT3G55380	1.10	0.14	1.37	0.21514389	0.6089	-5.74
249983_at	putative protein S-receptor kinase	---	AT5G18470	2.06	1.04	1.37	0.21521289	0.6089	-5.74
263521_at	hypothetical protein predicted by g	---	AT2G24960	1.17	0.22	1.37	0.21518626	0.6089	-5.74
262472_at	hypothetical protein similar to puta	---	AT1G50160	-1.11	-0.15	-1.37	0.21536471	0.6093	-5.74
251487_at	cysteine synthase	OASC	AT3G59760	-1.25	-0.32	-1.37	0.21558129	0.6094	-5.74
259486_at	embryo abundance protein (EMB2	---	AT1G15710	-1.13	-0.18	-1.37	0.21564148	0.6094	-5.74
265104_at	unknown protein 3'-end of protein	ATO2	AT1G31020	1.12	0.16	1.37	0.21563861	0.6094	-5.74
264388_at	hypothetical protein contains simila	---	AT1G11970	-1.14	-0.19	-1.37	0.21558929	0.6094	-5.74
261657_at	pathogenesis-related protein 1b p	---	AT1G50050	1.12	0.16	1.37	0.21556932	0.6094	-5.74
251405_at	plasma membrane H+-ATPase - I	AHA7	AT3G60330	-1.10	-0.14	-1.37	0.21553911	0.6094	-5.74
267258_at	hypothetical protein predicted by g	---	AT2G23140	1.10	0.14	1.37	0.21546423	0.6094	-5.74
261797_at	cation-chloride co-transporter, put	---	AT1G30455	1.12	0.17	1.37	0.21560991	0.6094	-5.74
245309_at	putative protein ; supported by cDN	---	AT4G15140	1.20	0.27	1.37	0.21569131	0.6095	-5.74
262280_at	unknown protein	---	AT1G68580	1.24	0.31	1.37	0.21589002	0.6097	-5.74
251853_at	putative protein various Arabidopsi	---	AT3G54790	1.11	0.14	1.37	0.21591242	0.6097	-5.74
252713_at	calmodulin 7 ; supported by full-le	CAM7	AT3G43810	1.12	0.17	1.37	0.21589732	0.6097	-5.74
263341_at	hypothetical protein predicted by g	---	---	-1.12	-0.17	-1.37	0.21586722	0.6097	-5.74
260572_at	putative molybdopterin synthase la	---	AT2G43760	1.10	0.14	1.37	0.21584931	0.6097	-5.74
249211_at	putative protein similar to unknown	---	AT5G42680	1.27	0.34	1.37	0.21589733	0.6097	-5.74
265414_at	nodulin-like protein	---	AT2G16660	-1.34	-0.42	-1.37	0.21596057	0.6097	-5.74
266199_at	putative calcium-dependent protein	CPK20	AT2G38910	-1.10	-0.14	-1.37	0.2160569	0.6099	-5.74
246587_at	putative protein predicted proteins	---	---	-1.12	-0.17	-1.37	0.21604817	0.6099	-5.74
250609_at	peptide methionine sulfoxide reduc	PMSR3	AT5G07470	-1.10	-0.14	-1.36	0.21620867	0.6099	-5.74
265778_at	unknown protein	---	AT2G07360	1.10	0.14	1.37	0.21612742	0.6099	-5.74

255442_at	predicted NADH dehydrogenase 2	---	AT4G02580	1.10	0.14	1.36	0.21627275	0.6099	-5.75
246913_at	GATA transcription factor - like GA	---	AT5G25830	-1.16	-0.21	-1.36	0.21617125	0.6099	-5.74
262349_at	unknown protein ;supported by ful	---	AT2G48130	1.17	0.23	1.36	0.2161626	0.6099	-5.74
256292_at	unknown protein	---	AT1G69430	-1.13	-0.18	-1.36	0.21623268	0.6099	-5.74
263392_at	putative PttA-like transposon prote	---	---	-1.10	-0.13	-1.36	0.21626299	0.6099	-5.75
246728_at	putative protein various predicted	---	AT5G28040	-1.09	-0.13	-1.37	0.21610621	0.6099	-5.74
253969_at	putative protein hypothetical prote	CSN6B	AT4G26430	1.21	0.28	1.36	0.21636261	0.6099	-5.75
254423_at	Lsd1 like protein zinc-finger protei	LOL2	AT4G21610	1.15	0.21	1.36	0.21639697	0.6099	-5.75
260600_at	hypothetical protein predicted by g	---	AT1G55950	-1.12	-0.17	-1.36	0.21633815	0.6099	-5.75
246320_at	unknown protein	---	AT1G16560	1.18	0.24	1.36	0.21639237	0.6099	-5.75
245607_at	kinesin like protein	---	AT4G14330	-1.12	-0.16	-1.36	0.21643285	0.6099	-5.75
255882_x_at	hypothetical protein contains simila	---	AT1G20280	1.13	0.17	1.36	0.21657826	0.6102	-5.75
260918_at	hypothetical protein predicted by g	---	AT1G21510	-1.10	-0.14	-1.36	0.21659075	0.6102	-5.75
248961_at	subtilisin-like protease	---	AT5G45650	-1.38	-0.46	-1.36	0.21666516	0.6104	-5.75
257224_at	P-type ATPase, putative similar to	---	AT3G27870	1.13	0.18	1.36	0.21674588	0.6105	-5.75
266410_at	unknown protein	EMB2765	AT2G38770	1.10	0.14	1.36	0.21691939	0.6108	-5.75
262641_at	unknown protein ;supported by full	---	AT1G62730	1.08	0.12	1.36	0.21698453	0.6108	-5.75
247746_at	uncoupling protein AtUCP2 ;suppo	ATUCP2	AT5G58970	1.16	0.21	1.36	0.2169522	0.6108	-5.75
250158_at	putative protein	---	AT5G15190	-1.21	-0.28	-1.36	0.21698757	0.6108	-5.75
250887_at	putative protein	---	---	1.13	0.17	1.36	0.21694581	0.6108	-5.75
262769_at	actin-like protein strong similarity t	DIS1	AT1G13180	-1.14	-0.19	-1.36	0.21707798	0.6110	-5.75
265550_at	hypothetical protein predicted by g	---	---	-1.11	-0.15	-1.36	0.21722606	0.6113	-5.75
248860_at	putative protein contains similarity	---	AT5G46670	1.11	0.15	1.36	0.21723267	0.6113	-5.75
247302_at	unknown protein ;supported by ful	VPS20.1	AT5G63880	-1.11	-0.15	-1.36	0.21725073	0.6113	-5.75
266514_at	putative zinc-finger protein (B-box	---	AT2G47890	1.16	0.22	1.36	0.21740735	0.6116	-5.75
259500_at	unknown protein ; supported by cD	---	AT1G15740	1.16	0.21	1.36	0.2174463	0.6117	-5.75
254847_at	putative phospholipase D-gamma	PLDGAMM	AT4G11850	1.31	0.39	1.36	0.2174876	0.6117	-5.75
257112_at	cytochrome P450, putative contair	CYP705A2	AT3G20120	1.12	0.16	1.36	0.21753652	0.6118	-5.75
264965_at	hypothetical protein predicted by g	---	AT1G60560	1.14	0.19	1.36	0.21758166	0.6118	-5.75
266576_at	hypothetical protein predicted by g	---	AT2G23940	1.11	0.15	1.36	0.21758776	0.6118	-5.75
252606_at	carboxypeptidase precursor-like p	scpl48	AT3G45010	-1.33	-0.41	-1.36	0.21764775	0.6118	-5.75
259248_at	putative heat-shock protein similar	---	AT3G07770	-1.27	-0.35	-1.36	0.21772722	0.6119	-5.75
246850_at	Lon protease homolog 2 precurso	LON1	AT5G26860	1.27	0.34	1.36	0.21777052	0.6119	-5.75
258772_at	putative ubiquinol-cytochrome C re	---	AT3G10860	1.14	0.19	1.36	0.21774979	0.6119	-5.75
267121_at	putative GDSL-motif lipase/hydrola	---	AT2G23540	1.23	0.30	1.36	0.21770111	0.6119	-5.75

245887_at	putative protein CD2 cytoplasmic	---	AT5G09390	1.08	0.12	1.36	0.21781474	0.6119	-5.75
256817_at	F-box protein family, AtFBW1 con	---	AT3G21410	1.13	0.18	1.36	0.21786151	0.6120	-5.75
256310_at	unknown protein ; supported by cD	ERD4	AT1G30360	1.18	0.24	1.36	0.21800531	0.6121	-5.75
267000_at	Expressed protein ; supported by f	---	AT2G34310	-1.22	-0.29	-1.36	0.21806139	0.6121	-5.75
255356_x_at	putative transposon protein	---	---	-1.12	-0.16	-1.36	0.21802647	0.6121	-5.75
262838_at	major latex protein, putative simila	---	AT1G14960	-1.12	-0.17	-1.36	0.21797441	0.6121	-5.75
263141_at	hypothetical protein similar to unkr	---	AT1G65210	-1.10	-0.14	-1.36	0.2179487	0.6121	-5.75
250241_at	photoreceptor-interacting protein-li	---	AT5G13600	1.15	0.20	1.36	0.21807426	0.6121	-5.75
255980_at	hypothetical protein ;supported by	---	AT1G33970	1.13	0.17	1.36	0.21812027	0.6122	-5.75
267186_at	unknown protein ; supported by cD	---	AT2G44090	-1.11	-0.15	-1.36	0.21823313	0.6124	-5.75
246982_s_at	unknown protein	---	AT2G10560	-1.25	-0.32	-1.36	0.2182463	0.6124	-5.75
260914_at	beta-xylosidase, putative similar to	BXL2	AT1G02640	1.33	0.41	1.36	0.21833701	0.6124	-5.75
263541_at	unknown protein ; supported by fu	---	AT2G24860	-1.11	-0.15	-1.36	0.21830444	0.6124	-5.75
247994_at	RNA-binding protein-like	---	AT5G56140	1.13	0.18	1.36	0.21833118	0.6124	-5.75
258801_at	unknown protein predicted by gen	---	AT3G04560	1.09	0.12	1.36	0.21854626	0.6129	-5.75
257349_at	unknown protein	---	AT2G30630	-1.11	-0.15	-1.36	0.21853983	0.6129	-5.75
260396_at	putative heme oxygenase similar t	ho3	AT1G69720	-1.20	-0.27	-1.36	0.21864443	0.6131	-5.75
259815_at	hypothetical protein predicted by g	---	AT1G49870	-1.11	-0.15	-1.36	0.21873669	0.6132	-5.75
250402_at	putative protein unnamed ORF cD	---	AT5G10940	-1.10	-0.14	-1.36	0.21881611	0.6133	-5.76
265061_at	hypothetical protein contains simila	---	AT1G61640	-1.29	-0.37	-1.36	0.21881069	0.6133	-5.76
266376_at	putative endoxyloglucan glycosyltr	---	AT2G14620	1.15	0.20	1.36	0.21887302	0.6133	-5.76
245526_at	putative protein	NRPD4	AT4G15950	1.09	0.13	1.36	0.21885494	0.6133	-5.76
260640_at	viral resistance protein, putative si	---	AT1G53350	1.27	0.35	1.36	0.21897804	0.6135	-5.76
253492_at	enoyl-CoA hydratase - like protein	---	AT4G31810	1.31	0.39	1.35	0.21916302	0.6138	-5.76
264131_at	unknown protein	---	AT1G79150	-1.18	-0.24	-1.35	0.21917944	0.6138	-5.76
260127_at	hypothetical protein similar to hyp	---	AT1G36320	1.17	0.22	1.36	0.21913596	0.6138	-5.76
257031_at	fucosyltransferase, putative simila	FUT11	AT3G19280	-1.12	-0.16	-1.36	0.21913815	0.6138	-5.76
247820_at	serine/threonine protein kinase ; su	SIP1	AT5G58380	-1.16	-0.21	-1.35	0.21920787	0.6138	-5.76
262343_at	phosphoprotein phosphatase 1 ide	TOPP3	AT1G64040	1.10	0.14	1.35	0.21927901	0.6139	-5.76
261453_at	O-methyltransferase, putative sim	---	AT1G21130	1.29	0.37	1.35	0.21928302	0.6139	-5.76
245751_s_at	hypothetical protein contains simila	---	AT1G25682	-1.22	-0.28	-1.35	0.219372	0.6140	-5.76
259619_at	hypothetical protein	---	AT1G42980	-1.13	-0.18	-1.35	0.21935338	0.6140	-5.76
248250_at	cyclic nucleotide-regulated ion cha	CNGC1	AT5G53130	1.25	0.32	1.35	0.2194129	0.6140	-5.76
253925_at	putative protein ; supported by cDN	SHV3	AT4G26690	-1.23	-0.30	-1.35	0.21947971	0.6141	-5.76
261499_at	cytochrome P450 (CYP93A1), put	CYP705A2	AT1G28430	-1.13	-0.17	-1.35	0.21955737	0.6143	-5.76

257136_at	hypothetical protein predicted by g	ASML2	AT3G12890	-1.12	-0.16	-1.35	0.21958677	0.6143	-5.76
246020_at	putative protein ; supported by cD	---	AT5G10710	1.11	0.15	1.35	0.21970718	0.6144	-5.76
263248_at	putative endonuclease ;supported	ATNTH1	AT2G31450	-1.11	-0.15	-1.35	0.21968926	0.6144	-5.76
253892_at	hypothetical protein ;supported by	---	AT4G27620	-1.11	-0.15	-1.35	0.21965827	0.6144	-5.76
248971_at	putative protein contains similarity	---	AT5G45000	1.19	0.25	1.35	0.21979706	0.6144	-5.76
260735_at	disease resistance protein, putativ	---	AT1G17610	1.23	0.30	1.35	0.21975952	0.6144	-5.76
249496_s_at	putative protein predicted proteins	---	AT5G39140	-1.11	-0.15	-1.35	0.21977065	0.6144	-5.76
247881_at	putative protein similar to unknown	---	AT5G57700	1.30	0.38	1.35	0.21988113	0.6144	-5.76
247518_at	putative protein many predicted pr	---	AT5G61800	-1.13	-0.17	-1.35	0.21987243	0.6144	-5.76
264206_at	putative topoisomerase strong sim	---	AT1G22730	1.14	0.19	1.35	0.21986263	0.6144	-5.76
252166_at	protein kinase SPK-2 ;supported b	SNRK2.2	AT3G50500	1.14	0.19	1.35	0.21997815	0.6145	-5.76
267246_at	putative WRKY-type DNA binding	WRKY25	AT2G30250	-1.23	-0.30	-1.35	0.21995066	0.6145	-5.76
253091_at	cytochrome p450 - like protein cyt	CYP81D2	AT4G37360	-1.11	-0.15	-1.35	0.21996096	0.6145	-5.76
263035_at	splicing factor, putative similar to F	RSZP21	AT1G23860	1.15	0.20	1.35	0.22007161	0.6146	-5.76
267097_at	unknown protein predicted by gens	---	AT2G41440	-1.10	-0.13	-1.35	0.22008575	0.6146	-5.76
263207_at	putative endoxyloglucan transferas	XTH33	AT1G10550	1.56	0.64	1.35	0.2202893	0.6149	-5.76
257314_at	integral membrane protein, putativ	---	AT3G26590	-1.31	-0.39	-1.35	0.22034289	0.6149	-5.76
261742_at	hypothetical protein predicted by g	---	AT1G08390	1.10	0.14	1.35	0.22032718	0.6149	-5.76
260851_at	nodulin-like protein similar to MtN2	---	AT1G21890	-1.12	-0.16	-1.35	0.22035396	0.6149	-5.76
254783_at	hydrolase-like protein 2-hydroxy-6	---	AT4G12830	-1.28	-0.36	-1.35	0.22027799	0.6149	-5.76
248003_at	putative protein contains similarity	---	AT5G56220	1.45	0.54	1.35	0.22022773	0.6149	-5.76
250235_s_at	ubiquinol--cytochrome-c reductase	---	AT5G13430	1.10	0.13	1.35	0.22044094	0.6150	-5.76
256052_at	spliceosomal protein (U2B), putati	---	AT1G06960	1.12	0.16	1.35	0.22049019	0.6150	-5.76
257384_at	unknown protein	---	AT2G15110	-1.11	-0.15	-1.35	0.22047828	0.6150	-5.76
257897_at	HAL3A protein identical to GB:AAD	HAL3A	AT3G18030	1.16	0.21	1.35	0.22042703	0.6150	-5.76
251860_at	Gluthatione reductase, chloroplas	GR	AT3G54660	-1.09	-0.12	-1.35	0.22053845	0.6150	-5.76
253233_at	putative protein various predicted p	---	AT4G34290	1.20	0.26	1.35	0.22059381	0.6151	-5.76
261902_at	unknown protein ; supported by ful	PLMT	AT1G80860	1.11	0.14	1.35	0.22068571	0.6152	-5.76
261638_at	Expressed protein ; supported by f	---	AT1G49975	1.24	0.31	1.35	0.22067225	0.6152	-5.76
254254_at	hypothetical protein	---	AT4G23330	1.13	0.18	1.35	0.22068705	0.6152	-5.76
246287_at	unknown protein	---	AT1G31870	-1.11	-0.15	-1.35	0.2207173	0.6152	-5.76
255753_at	myb factor, putative similar to myb	MYB51	AT1G18570	1.82	0.86	1.35	0.2209597	0.6153	-5.76
261753_at	unknown protein	---	AT1G76340	1.13	0.18	1.35	0.22094319	0.6153	-5.76
258550_at	putative mudrA protein similar to m	---	---	-1.13	-0.17	-1.35	0.22096855	0.6153	-5.76
247457_at	putative protein various predicted	---	AT5G62170	-1.10	-0.14	-1.35	0.2208647	0.6153	-5.76

258477_at	hypothetical protein predicted by g	NBS1	AT3G02680	1.10	0.13	1.35	0.2208932	0.6153	-5.76
256820_at	far-red impaired response protein,	FHY3	AT3G22170	-1.10	-0.13	-1.35	0.22088772	0.6153	-5.76
251442_at	putative protein multisynthetase c	---	AT3G59980	1.19	0.25	1.35	0.22090278	0.6153	-5.76
251623_at	MADS transcription factor-like pro	AGL18	AT3G57390	1.09	0.13	1.35	0.22101157	0.6154	-5.76
263391_at	putative monogalactosyldiacylglyce	MGDC	AT2G11810	1.22	0.28	1.35	0.22108013	0.6155	-5.76
255259_at	coded for by A. thaliana cDNA W4	NDB2	AT4G05020	-1.62	-0.69	-1.35	0.22108841	0.6155	-5.76
252085_s_at	serine-type carboxypeptidase like	scpl37	AT3G52000	-1.09	-0.12	-1.35	0.2211961	0.6157	-5.76
256223_at	unknown protein ;supported by full	emb1303	AT1G56200	1.13	0.18	1.35	0.22127292	0.6158	-5.76
247260_at	putative protein contains similarity	---	AT5G64500	1.16	0.22	1.35	0.22133343	0.6158	-5.77
255304_at	putative potassium transporter sim	KEA3	AT4G04850	-1.20	-0.26	-1.35	0.22132773	0.6158	-5.77
245706_at	putative protein	---	AT5G04310	1.11	0.16	1.35	0.22140829	0.6160	-5.77
261884_at	myrosinase precursor, putative	---	AT1G80910	-1.13	-0.17	-1.35	0.22144864	0.6160	-5.77
259849_at	phosphoglycerate dehydrogenase	---	AT1G72190	1.09	0.13	1.35	0.22151845	0.6161	-5.77
257705_at	unknown protein ; supported by cl	---	AT3G12760	1.08	0.12	1.35	0.22153861	0.6161	-5.77
253747_at	serine threonine-specific kinase lik	---	AT4G29050	1.23	0.30	1.35	0.22162406	0.6161	-5.77
265225_at	putative PHD-type zinc finger prote	---	AT2G36720	1.11	0.15	1.35	0.22158835	0.6161	-5.77
258152_at	chaperonin subunit, putative simila	---	AT3G18190	1.13	0.18	1.35	0.22160243	0.6161	-5.77
245687_at	unknown protein	DEG15	AT1G28320	-1.09	-0.12	-1.35	0.22178385	0.6162	-5.77
257725_at	DNA mismatch repair protein MSH	MSH2	AT3G18524	1.16	0.22	1.35	0.2218534	0.6162	-5.77
250676_at	harpin-induced protein-like ; suppo	NHL3	AT5G06320	1.20	0.27	1.35	0.22173225	0.6162	-5.77
251155_at	putative protein outer envelope m	---	AT3G63160	1.10	0.13	1.35	0.22177316	0.6162	-5.77
257042_s_at	hypothetical protein predicted by g	---	AT3G28640	-1.10	-0.14	-1.35	0.22166891	0.6162	-5.77
259719_at	unknown protein contains gamma-	LCR66	AT1G61070	-1.10	-0.14	-1.35	0.2217551	0.6162	-5.77
253626_at	F-box protein family, AtFBL19 con	---	AT4G30640	1.20	0.26	1.35	0.22180728	0.6162	-5.77
248350_at	putative protein similar to unknown	---	AT5G52160	-1.11	-0.14	-1.35	0.2218391	0.6162	-5.77
255476_at	hypothetical protein similar to reve	---	---	-1.13	-0.17	-1.35	0.22190144	0.6162	-5.77
246323_at	hypothetical protein predicted by g	---	AT1G16690	-1.14	-0.18	-1.35	0.22194032	0.6162	-5.77
264988_at	glutathione transferase, putative s	ATGSTU14	AT1G27140	-1.16	-0.22	-1.35	0.22203937	0.6164	-5.77
265330_at	unknown protein	GUT15	---	1.13	0.17	1.35	0.22211188	0.6165	-5.77
265054_x_at	mutator-like transposase, putative	---	---	-1.15	-0.20	-1.35	0.22208768	0.6165	-5.77
253408_at	putative protein phosphoprotein p	---	AT4G32950	-1.09	-0.13	-1.34	0.22229331	0.6166	-5.77
259781_at	reverse transcriptase, putative sim	---	---	-1.13	-0.18	-1.34	0.22230875	0.6166	-5.77
246303_at	putative carrier protein peroxisom	---	AT3G51870	1.20	0.26	1.34	0.22226008	0.6166	-5.77
246466_at	sugar transporter - like protein D-X	---	AT5G17010	-1.17	-0.23	-1.34	0.22230307	0.6166	-5.77
260831_at	glutaredoxin, putative similar to gl	---	AT1G06830	1.80	0.84	1.34	0.22224818	0.6166	-5.77

246078_s_at	putative protein probable mitosis a	---	AT5G20430 /	-1.19	-0.25	-1.34	0.22221103	0.6166	-5.77
261299_at	unknown protein	---	AT1G48550	1.15	0.20	1.34	0.2223675	0.6167	-5.77
252834_at	putative protein RING-H2 zinc fing	---	AT4G40070	-1.25	-0.32	-1.34	0.22257898	0.6168	-5.77
250028_at	putative protein similar to unknown	---	AT5G18130	1.11	0.15	1.34	0.22260795	0.6168	-5.77
252249_at	putative protein heat shock protein	---	AT3G49770	-1.14	-0.18	-1.34	0.22256389	0.6168	-5.77
255579_at	putative bHLH DNA-binding protein	---	AT4G01460	1.26	0.33	1.34	0.22249324	0.6168	-5.77
262003_at	unknown protein	---	AT1G64460	-1.12	-0.16	-1.34	0.2225158	0.6168	-5.77
259032_at	hypothetical protein similar to hyp	---	AT3G09380	-1.09	-0.13	-1.34	0.22264276	0.6168	-5.77
252795_at	putative protein predicted proteins	---	---	-1.11	-0.15	-1.34	0.22263154	0.6168	-5.77
256515_at	terpene synthase, putative contain	---	AT1G66020	-1.12	-0.16	-1.34	0.22257841	0.6168	-5.77
256300_at	unknown protein similar to N-term	NAP	AT1G69490	1.48	0.56	1.34	0.22293969	0.6171	-5.77
250542_at	hypothetical protein (fragment at B	---	AT5G08270	1.23	0.30	1.34	0.222911	0.6171	-5.77
247321_s_at	phosphatidylinositol 4-kinase (emb	PI-4KBETA	AT5G09350 /	1.15	0.21	1.34	0.22285909	0.6171	-5.77
262619_at	3-hydroxyisobutyryl-coenzyme A h	---	AT1G06550	-1.39	-0.48	-1.34	0.22291358	0.6171	-5.77
263354_at	hypothetical protein predicted by g	---	AT2G22060	-1.09	-0.12	-1.34	0.22280534	0.6171	-5.77
263005_at	hypothetical protein predicted by g	---	AT1G54540	1.20	0.26	1.34	0.22293336	0.6171	-5.77
256374_at	DNA ligase I, putative similar to D	---	AT1G66730	-1.13	-0.18	-1.34	0.22290514	0.6171	-5.77
262477_at	hypothetical protein contains simila	---	AT1G11220	-1.17	-0.23	-1.34	0.223012	0.6173	-5.77
250503_at	putative protein similar to unknown	---	AT5G09820	-1.17	-0.22	-1.34	0.22308927	0.6174	-5.77
249277_at	GDSL-motif lipase/hydrolase-like p	---	AT5G41890	1.34	0.42	1.34	0.22321101	0.6177	-5.77
264397_at	hypothetical protein	---	AT1G11820	-1.17	-0.22	-1.34	0.22323857	0.6177	-5.77
260498_at	putative AP2 domain transcription	---	AT2G41710	1.14	0.19	1.34	0.2233816	0.6179	-5.77
257002_at	oligouridylate binding protein, puta	---	AT3G14100	-1.14	-0.19	-1.34	0.22358519	0.6179	-5.77
258671_at	putative vacuolar ATP synthase su	VHA-E2	AT3G08560	-1.15	-0.20	-1.34	0.22350283	0.6179	-5.77
248776_at	unknown protein	---	AT5G47900	-1.11	-0.15	-1.34	0.22351816	0.6179	-5.77
263227_at	Expressed protein ; supported by c	---	AT1G30750	-1.13	-0.18	-1.34	0.22346291	0.6179	-5.77
252021_at	putative protein predicted protein,	---	AT3G53070	-1.13	-0.18	-1.34	0.22345573	0.6179	-5.77
250724_at	harpin-induced protein-like	---	AT5G06330	-1.20	-0.26	-1.34	0.22349584	0.6179	-5.77
263116_s_at	unknown protein Similar to gb|U51	---	AT1G03140 /	1.13	0.18	1.34	0.22343028	0.6179	-5.77
248513_at	unknown protein	---	AT5G50500	-1.09	-0.13	-1.34	0.22356508	0.6179	-5.77
258427_at	putative DNA-binding protein simil	---	AT3G16600	1.09	0.13	1.34	0.2235986	0.6179	-5.77
266628_at	unknown protein	---	AT2G35330	1.09	0.13	1.34	0.22372653	0.6181	-5.77
258961_at	hypothetical protein similar to myb	---	AT3G10580	1.09	0.12	1.34	0.22372566	0.6181	-5.77
246598_at	dolichyl-phosphate-mannose--glyc	---	AT5G14850	-1.14	-0.19	-1.34	0.22382289	0.6183	-5.77
263277_at	hypothetical protein predicted by g	---	AT2G14110	-1.10	-0.14	-1.34	0.22384033	0.6183	-5.77

265241_at	hypothetical protein	---	---	-1.13	-0.18	-1.34	0.22390355	0.6183	-5.78
255377_at	hypothetical protein	---	AT4G03500	-1.13	-0.18	-1.34	0.22390068	0.6183	-5.78
262631_at	hypothetical protein predicted by g	---	AT1G06500	-1.11	-0.15	-1.34	0.2239619	0.6183	-5.78
250653_at	putative protein strong similarity to	---	AT5G06930	-1.28	-0.36	-1.34	0.22398521	0.6183	-5.78
265957_at	hypothetical protein predicted by g	---	AT2G37300	-1.08	-0.12	-1.34	0.22394591	0.6183	-5.78
255748_at	hypothetical protein predicted by g	---	AT1G32000	-1.09	-0.12	-1.34	0.22407653	0.6185	-5.78
263474_at	hypothetical protein predicted by g	---	AT2G31725	-1.14	-0.20	-1.34	0.22415499	0.6186	-5.78
251875_at	putative protein various predicted	---	AT3G54270	-1.14	-0.19	-1.34	0.22423484	0.6187	-5.78
256167_at	hypothetical protein similar to puta	---	---	1.10	0.14	1.34	0.22423853	0.6187	-5.78
260217_at	hypothetical protein contains Pfam	---	AT1G74600	-1.09	-0.13	-1.34	0.2243071	0.6188	-5.78
258972_at	hypothetical protein predicted by g	---	AT3G01920	-1.19	-0.25	-1.34	0.22437319	0.6188	-5.78
267006_at	putative membrane transporter ; s	---	AT2G34190	-1.12	-0.17	-1.34	0.22437664	0.6188	-5.78
248736_at	terpene synthase	---	AT5G48110	1.11	0.15	1.34	0.22437485	0.6188	-5.78
254851_at	putative disease resistance protei	---	AT4G12010	1.22	0.28	1.34	0.22440916	0.6188	-5.78
262427_s_at	thioglucosidase, putative similar to	BGLU34	AT1G47600	1.10	0.13	1.34	0.22462073	0.6193	-5.78
252465_x_at	putative protein several hypothetic	---	---	-1.11	-0.15	-1.34	0.22467036	0.6194	-5.78
262174_at	putative GDP-mannose pyrophosp	---	AT1G74910	1.15	0.20	1.34	0.22471292	0.6194	-5.78
265673_at	unknown protein ;supported by ful	---	AT2G32090	-1.15	-0.20	-1.34	0.22487508	0.6198	-5.78
248638_at	fatty acid elongase; beta-ketoacyl-	KCS21	AT5G49070	-1.09	-0.12	-1.34	0.2249253	0.6199	-5.78
257537_at	hypothetical protein predicted by g	---	AT3G22350	-1.15	-0.20	-1.34	0.22495643	0.6199	-5.78
250337_at	putative protein SF21 protein, Hel	---	AT5G11790	-1.42	-0.50	-1.34	0.22507884	0.6201	-5.78
263499_at	unknown protein ; supported by cl	TTL3	AT2G42580	1.19	0.26	1.34	0.22518313	0.6203	-5.78
252280_at	SF16 -like protein SF16 protein, p	iqd21	AT3G49260	1.32	0.40	1.33	0.22541725	0.6203	-5.78
266414_at	mevalonate diphosphate decarbox	MVD1	AT2G38700	1.12	0.16	1.33	0.22557929	0.6203	-5.78
260968_at	hypothetical protein predicted by g	---	AT1G12250	-1.13	-0.18	-1.33	0.22561495	0.6203	-5.78
263600_at	hypothetical protein predicted by g	DRD1	AT2G16390	-1.12	-0.17	-1.33	0.22544505	0.6203	-5.78
253469_at	putative protein gene C42D8.3, C	ATPANK2	AT4G32180	1.11	0.15	1.33	0.22554606	0.6203	-5.78
256856_at	Expressed protein ; supported by f	---	AT3G15110	1.17	0.23	1.33	0.22556909	0.6203	-5.78
265545_at	putative protein kinase contains a	NCRK	AT2G28250	1.13	0.17	1.33	0.225476	0.6203	-5.78
261072_at	hexose transporter, putative simila	ATSTP2	AT1G07340	-1.14	-0.18	-1.33	0.22538933	0.6203	-5.78
246847_at	putative protein ferroportin1, Mus	ATIREG3	AT5G26820	-1.20	-0.27	-1.33	0.22560111	0.6203	-5.78
249114_at	putative protein similar to unknown	---	---	1.14	0.19	1.33	0.22548403	0.6203	-5.78
244956_s_at	hypothetical protein	---	---	-1.12	-0.17	-1.33	0.22542173	0.6203	-5.78
260140_at	Myb-related transcription factor, p	MYB90	AT1G66390	-1.13	-0.18	-1.33	0.22552842	0.6203	-5.78
248348_at	putative protein similar to unknown	---	AT5G52190	1.11	0.15	1.33	0.22530566	0.6203	-5.78

262519_at	putative ribokinase Except for first	---	AT1G17160	-1.19	-0.25	-1.34	0.22520959	0.6203	-5.78
257974_at	unknown protein similar to NA-DAI	---	AT3G20820	-1.40	-0.49	-1.33	0.22534892	0.6203	-5.78
256847_at	early nodule-specific protein, puta	---	AT3G27950	1.11	0.15	1.33	0.22545676	0.6203	-5.78
248866_s_at	putative protein contains similarity	---	AT5G46810	1.10	0.14	1.33	0.22546426	0.6203	-5.78
266004_at	unknown protein predicted by gens	ALS3	AT2G37330	1.09	0.13	1.33	0.22570472	0.6204	-5.78
254362_at	Expressed protein ; supported by f	---	AT4G22160	-1.16	-0.21	-1.33	0.225763	0.6205	-5.78
265713_at	putative integral membrane protein	UPS2	AT2G03530	1.37	0.45	1.33	0.22582969	0.6205	-5.78
256364_at	wrky-type DNA binding protein, pu	WRKY67	AT1G66550	-1.13	-0.17	-1.33	0.22578859	0.6205	-5.78
246791_at	putative protein predicted proteins	---	AT5G27280	-1.13	-0.18	-1.33	0.22582505	0.6205	-5.78
255714_at	contains weak similarity to S. cerev	---	AT4G00300	-1.13	-0.17	-1.33	0.22587215	0.6205	-5.78
264527_at	putative reticuline oxidase-like pro	---	AT1G30760	-1.27	-0.35	-1.33	0.22600451	0.6208	-5.78
264917_at	unknown protein contains Pfam pr	---	AT1G60500	-1.09	-0.12	-1.33	0.22610562	0.6209	-5.78
257971_at	unknown protein similar to hypothe	GC6	AT3G27530	1.18	0.24	1.33	0.22607896	0.6209	-5.78
245809_at	squalene monooxygenase, putativ	XF1	AT1G58440	-1.14	-0.18	-1.33	0.2261562	0.6210	-5.78
250304_at	elongation factor 1B alpha-subunit	---	AT5G12110	-1.39	-0.48	-1.33	0.22622687	0.6211	-5.78
251984_at	phenylalanine ammonia-lyase ;su	PAL2	AT3G53260	-1.53	-0.61	-1.33	0.22627319	0.6212	-5.78
249295_at	putative protein contains similarity	---	AT5G41280	-1.09	-0.13	-1.33	0.22633755	0.6212	-5.78
264653_at	unknown protein Contains similari	AMI1	AT1G08980	1.17	0.22	1.33	0.22634303	0.6212	-5.78
255556_at	putative NifU-like metallocluster a	NFU1	AT4G01940	1.15	0.20	1.33	0.22644802	0.6213	-5.78
258376_at	hypothetical protein similar to GB:A	---	AT3G17680	1.10	0.13	1.33	0.22642263	0.6213	-5.78
264590_at	unknown protein ;supported by ful	---	AT2G17710	1.62	0.70	1.33	0.22641604	0.6213	-5.78
258982_at	putative serine/threonine protein k	---	AT3G08870	1.19	0.25	1.33	0.22677532	0.6213	-5.79
263347_at	putative U4/U6 small nuclear ribon	---	AT2G05720	-1.15	-0.20	-1.33	0.22662077	0.6213	-5.79
256221_at	DnaJ protein, putative contains Pf	---	AT1G56300	-1.10	-0.14	-1.33	0.22678146	0.6213	-5.79
262516_at	putative glutathione transferase Or	ATGSTU26	AT1G17190	-1.12	-0.16	-1.33	0.22651478	0.6213	-5.79
264623_at	putative NPK1-related protein kina	ANP1	AT1G09000	-1.10	-0.13	-1.33	0.22667767	0.6213	-5.79
265556_at	putative Athila retroelement ORF1	---	---	-1.12	-0.16	-1.33	0.22666299	0.6213	-5.79
258941_at	putative monodehydroascorbate re	MDHAR	AT3G09940	-2.24	-1.16	-1.33	0.22674912	0.6213	-5.79
247526_at	putative protein C2H2 zinc-finger	---	AT5G61470	-1.10	-0.14	-1.33	0.22674881	0.6213	-5.79
259445_at	dioxygenase, putative similar to di	GA2OX6	AT1G02400	1.87	0.90	1.33	0.2266073	0.6213	-5.79
254705_at	putative protein ; supported by cD	---	AT4G17870	1.19	0.25	1.33	0.22666714	0.6213	-5.79
257307_at	myb-like transcription factor, putat	MYB121	AT3G30210	-1.15	-0.21	-1.33	0.22657932	0.6213	-5.79
252076_at	LS1-like protein AT-LS1 product -	---	AT3G51660	-1.34	-0.42	-1.33	0.22669693	0.6213	-5.79
266513_at	unknown protein	---	AT2G47700	-1.14	-0.19	-1.33	0.22686336	0.6213	-5.79
249672_at	nucleolar protein-like	---	AT5G35910	1.14	0.19	1.33	0.22682834	0.6213	-5.79

264636_at	hypothetical protein predicted by g	---	AT1G65490	-1.26	-0.34	-1.33	0.2269195	0.6213	-5.79
259446_at	hypothetical protein contains simila	---	AT1G02410	-1.14	-0.20	-1.33	0.22691648	0.6213	-5.79
253369_at	F-box protein family, AtFBL15 cor	---	AT4G33210	-1.08	-0.12	-1.33	0.22688196	0.6213	-5.79
246563_at	putative protein	---	AT5G15581	-1.13	-0.18	-1.33	0.22700712	0.6215	-5.79
266133_at	putative C2H2-type zinc finger prot	---	AT2G45120	-1.11	-0.14	-1.33	0.22703065	0.6215	-5.79
258913_at	unknown protein similar to putativ	---	AT3G06450	1.16	0.22	1.33	0.22708479	0.6215	-5.79
259051_at	unknown protein similar to CGI-86	---	AT3G03330	1.12	0.16	1.33	0.22719238	0.6216	-5.79
261857_at	hypothetical protein predicted by g	---	AT1G50620	1.27	0.35	1.33	0.22717419	0.6216	-5.79
258194_at	unknown protein ; supported by fu	---	AT3G29170	1.15	0.21	1.33	0.2273064	0.6216	-5.79
258985_at	hypothetical protein similar to hyp	---	AT3G08960	-1.10	-0.14	-1.33	0.22731382	0.6216	-5.79
260470_at	hypothetical protein predicted by g	---	AT1G11120	-1.14	-0.19	-1.33	0.22727046	0.6216	-5.79
255095_at	MEKK1/MAP kinase kinase kinase	MEKK1	AT4G08500	-1.17	-0.23	-1.33	0.22732014	0.6216	-5.79
258005_at	cysteine proteinase contains simil	---	AT3G19390	1.52	0.61	1.33	0.22718873	0.6216	-5.79
265064_at	hypothetical protein contains simila	ENT7	AT1G61630	-1.18	-0.24	-1.33	0.22725076	0.6216	-5.79
245663_at	steroid sulfotransferase, putative s	---	AT1G28170	-1.10	-0.14	-1.33	0.22739326	0.6217	-5.79
265599_at	unknown protein	AT2G1425	---	-1.11	-0.15	-1.33	0.22757773	0.6218	-5.79
266679_at	putative helicase ; supported by cD	---	AT2G03270	-1.12	-0.17	-1.33	0.22747066	0.6218	-5.79
263935_at	unknown protein	PUB23	AT2G35930	-1.92	-0.94	-1.33	0.22756734	0.6218	-5.79
256059_at	hypothetical protein contains simila	---	AT1G06990	-1.14	-0.18	-1.33	0.2275634	0.6218	-5.79
266640_at	Expressed protein ; supported by f	---	AT2G35585	1.14	0.19	1.33	0.22749656	0.6218	-5.79
260804_at	hypothetical protein predicted by g	---	AT1G78410	2.21	1.14	1.33	0.22768524	0.6220	-5.79
248019_at	putative protein similar to unknown	---	AT5G56480	-1.11	-0.15	-1.33	0.22773284	0.6220	-5.79
257759_at	hypothetical protein	---	AT3G23070	1.18	0.24	1.33	0.22772355	0.6220	-5.79
248600_at	putative protein contains similarity	---	AT5G49390	1.13	0.17	1.33	0.22765853	0.6220	-5.79
262902_x_at	hypothetical protein similar to puta	---	AT1G59930	-1.19	-0.25	-1.33	0.2278244	0.6220	-5.79
259128_at	unknown protein similar to pushov	BIG	AT3G02260	1.18	0.24	1.33	0.22781595	0.6220	-5.79
249565_at	contains similarity to S1 self-incom	---	AT5G38440	-1.11	-0.15	-1.33	0.22781114	0.6220	-5.79
254431_at	reticuline oxidase - like protein ret	---	AT4G20840	1.19	0.25	1.33	0.22792741	0.6222	-5.79
245930_at	transcriptional co-activator-like pr	---	AT5G09240	1.19	0.25	1.33	0.22816092	0.6227	-5.79
264553_s_at	putative cinnamyl alcohol dehydro	---	AT1G09480	1.13	0.18	1.33	0.2281582	0.6227	-5.79
254219_at	putative protein	---	AT4G23760	1.11	0.15	1.33	0.22825845	0.6228	-5.79
251633_at	putative protein metalloendopepti	---	AT3G57460	1.23	0.30	1.33	0.22824258	0.6228	-5.79
265250_at	putative receptor protein kinase sir	BRL2	AT2G01950	1.17	0.23	1.33	0.22828353	0.6228	-5.79
266721_at	unknown protein	FT1	AT2G03220	1.15	0.21	1.32	0.22839784	0.6229	-5.79
256724_at	unknown protein ;supported by ful	---	AT2G34040	1.12	0.17	1.32	0.22844024	0.6229	-5.79

249757_at	Expressed protein ; supported by f	---	AT5G24316	-1.13	-0.17	-1.32	0.2284138	0.6229	-5.79
262269_at	hypothetical protein predicted by g	---	---	-1.10	-0.13	-1.33	0.22835856	0.6229	-5.79
252860_at	putative protein bZIP protein, Arat	---	AT4G39790	-1.09	-0.13	-1.32	0.22852196	0.6230	-5.79
264760_at	syntaxin-related protein Nt-syr1, p	SYP124	AT1G61290	-1.16	-0.21	-1.32	0.22850581	0.6230	-5.79
256926_at	hypothetical protein predicted by g	---	AT3G22540	-1.16	-0.21	-1.32	0.22856074	0.6230	-5.79
249575_at	low-molecular-weight heat shock p	---	AT5G37670	1.17	0.23	1.32	0.22869648	0.6231	-5.79
263428_at	ubiquitin-specific protease 4 (UBP4	ATUBP4	AT2G22310	1.12	0.16	1.32	0.22873892	0.6231	-5.79
261771_at	hypothetical protein contains simila	---	AT1G76150	-1.08	-0.12	-1.32	0.22866037	0.6231	-5.79
264412_at	hypothetical protein similar to puta	---	AT1G43260	-1.10	-0.14	-1.32	0.22869399	0.6231	-5.79
246156_at	putative protein predicted proteins	---	AT5G20090	1.13	0.17	1.32	0.22872505	0.6231	-5.79
248068_at	unknown protein	---	AT5G55610	1.17	0.22	1.32	0.22877417	0.6232	-5.79
263990_at	putative phosphoprotein phosphata	PP5.2	AT2G42810	1.11	0.15	1.32	0.22885985	0.6233	-5.79
AFFX-BioDn-5_	E. coli /GEN=bioD /DB_XREF=gb:	---	---	-1.29	-0.36	-1.32	0.22894903	0.6234	-5.79
245582_at	hypothetical protein	LOI1	AT4G14850	-1.16	-0.22	-1.32	0.2289514	0.6234	-5.79
245981_at	putative protein ;supported by full-	---	AT5G13100	1.13	0.17	1.32	0.22906999	0.6235	-5.79
250673_at	serine threonine protein kinase-lik	CIPK2	AT5G07070	-1.16	-0.21	-1.32	0.22915675	0.6235	-5.80
253264_at	protein kinase - like protein protein	OST1	AT4G33950	1.09	0.13	1.32	0.22907977	0.6235	-5.79
256973_at	unknown protein similar to putative	---	AT3G20980	-1.11	-0.15	-1.32	0.22912482	0.6235	-5.80
262111_at	hypothetical protein predicted by g	---	AT1G02960	-1.11	-0.14	-1.32	0.22915893	0.6235	-5.80
245598_at	hypothetical protein	---	AT4G14200	1.15	0.21	1.32	0.22916766	0.6235	-5.80
250971_at	putative protein ABI3-interacting p	PRR7	AT5G02810	-1.12	-0.16	-1.32	0.22913273	0.6235	-5.80
246628_at	signal recognition particle 54 kDa	---	AT1G48900	-1.08	-0.11	-1.32	0.22926853	0.6237	-5.80
247103_at	putative protein similar to unknown	DAR7	AT5G66610	-1.10	-0.14	-1.32	0.22943813	0.6241	-5.80
262568_at	hypothetical protein contains simila	AtRLP5	AT1G34290	-1.13	-0.17	-1.32	0.22950465	0.6242	-5.80
252604_at	high-affinity nitrate transporter - lik	NRT2.6	AT3G45060	1.41	0.50	1.32	0.22956396	0.6242	-5.80
260519_at	unknown protein	---	AT1G51540	1.09	0.13	1.32	0.22958395	0.6242	-5.80
257874_at	hypothetical protein	---	AT3G17110	-1.12	-0.17	-1.32	0.2296513	0.6244	-5.80
261998_at	putative gag-pol polyprotein simila	---	---	-1.11	-0.15	-1.32	0.22985921	0.6248	-5.80
245289_at	Expressed protein ; supported by c	---	AT4G15470	-1.09	-0.12	-1.32	0.22994527	0.6249	-5.80
245934_at	putative protein NAC1 - Medicago	anac082	AT5G09330	1.15	0.20	1.32	0.22992541	0.6249	-5.80
258660_at	hypothetical protein predicted by g	---	AT3G09850	-1.12	-0.17	-1.32	0.22999909	0.6249	-5.80
266077_at	putative non-LTR retroelement rev	---	---	-1.12	-0.16	-1.32	0.2299859	0.6249	-5.80
250316_at	cystatin (emb|CAA03929.1) ; supp	ATCYS1	AT5G12140	-1.11	-0.15	-1.32	0.2307803	0.6250	-5.80
266932_s_at	putative RNA helicase	---	AT1G63250	-1.19	-0.24	-1.32	0.23058891	0.6250	-5.80
263598_at	putative xyloglucan-specific glucan	EXGT-A3	AT2G01850	1.12	0.16	1.32	0.23059315	0.6250	-5.80

256419_at	RNA-binding protein similar to GI:8	---	AT1G33470	1.12	0.17	1.32	0.23008878	0.6250	-5.80
260651_at	hypothetical protein predicted by g	---	AT1G32460	-1.10	-0.14	-1.32	0.2307707	0.6250	-5.80
245260_at	kinase like protein ; supported by c	---	AT4G16360	1.09	0.13	1.32	0.23031236	0.6250	-5.80
248777_at	putative protein similar to unknown	---	AT5G47920	-1.12	-0.16	-1.32	0.23060792	0.6250	-5.80
251388_at	putative protein protein regulating	MAP65-4	AT3G60840	-1.12	-0.17	-1.32	0.23078204	0.6250	-5.80
266137_at	unknown protein ;supported by ful	---	AT2G45010	1.11	0.15	1.32	0.23016655	0.6250	-5.80
265071_at	transcription initiation factor TFIID-	TBP2	AT1G55520	1.11	0.15	1.32	0.23058646	0.6250	-5.80
256679_at	putative protein similar to ATP syn	ATPQ	AT3G52300	1.12	0.16	1.32	0.23011527	0.6250	-5.80
264137_at	lupeol synthase, putative similar to	ATLUP2	AT1G78960	-1.18	-0.24	-1.32	0.23039159	0.6250	-5.80
250456_at	26S proteasome p55 protein-like ;	EMB2107	AT5G09900	1.16	0.21	1.32	0.23043823	0.6250	-5.80
256636_at	S-locus related protein SLR1 homo	---	AT3G12000	-1.10	-0.14	-1.32	0.2305556	0.6250	-5.80
259291_at	unknown protein similar to unknow	---	AT3G11550	1.14	0.18	1.32	0.23075431	0.6250	-5.80
254720_at	DNA (cytosine-5-)-methyltransfera	MEE57	AT4G13610	-1.12	-0.16	-1.32	0.23030515	0.6250	-5.80
264975_at	hypothetical protein predicted by g	---	AT1G27070	-1.11	-0.16	-1.32	0.23033931	0.6250	-5.80
245652_at	F-box protein family, putative	---	AT4G13960	-1.12	-0.17	-1.32	0.23033836	0.6250	-5.80
246687_at	putative protein proline-rich protei	---	AT5G33370	-1.15	-0.20	-1.32	0.23044031	0.6250	-5.80
249012_at	flavonoid 3,5-hydroxylase-like; cyt	CYP706A3	AT5G44620	-1.11	-0.15	-1.32	0.23022705	0.6250	-5.80
245614_at	retrovirus-related like polyprotein	---	---	-1.12	-0.17	-1.32	0.23032315	0.6250	-5.80
266030_x_at	hypothetical protein predicted by g	---	---	-1.13	-0.17	-1.32	0.23077622	0.6250	-5.80
254272_at	predicted protein hypothetical prot	---	AT4G22850	-1.09	-0.12	-1.32	0.23042863	0.6250	-5.80
265490_s_at	putative polygalacturonase	---	AT2G15450 /	-1.11	-0.15	-1.32	0.23066574	0.6250	-5.80
255827_at	unknown protein ; supported by cl	---	AT2G40600	1.13	0.17	1.32	0.23045035	0.6250	-5.80
256382_at	unknown protein ;supported by full	---	AT1G66860	-1.32	-0.40	-1.32	0.23071605	0.6250	-5.80
256798_at	uracil-DNA glycosylase, putative s	---	AT3G18630	1.15	0.20	1.32	0.23047237	0.6250	-5.80
248546_at	putative protein similar to unknown	---	AT5G50270	1.08	0.12	1.32	0.23067985	0.6250	-5.80
258957_at	feebly-like protein contains similari	DOX1	AT3G01420	-1.16	-0.22	-1.32	0.23105735	0.6250	-5.80
260939_at	hypothetical protein contains simila	---	AT1G45180	-1.31	-0.39	-1.32	0.23088177	0.6250	-5.80
263880_at	unknown protein ;supported by ful	---	AT2G21960	-1.16	-0.21	-1.32	0.23084974	0.6250	-5.80
264952_at	Tub family protein, putative contai	AtTLP1	AT1G76900	-1.09	-0.13	-1.32	0.23088335	0.6250	-5.80
247315_at	unknown protein	---	AT5G64010	1.11	0.15	1.32	0.23110516	0.6250	-5.80
257393_at	unknown protein	---	AT2G20080	-1.09	-0.12	-1.32	0.23108114	0.6250	-5.80
248652_at	putative protein contains similarity	SHV2	AT5G49270	-1.18	-0.24	-1.32	0.23110587	0.6250	-5.80
247336_at	putative protein similar to unknown	---	AT5G63640	1.14	0.19	1.32	0.23097061	0.6250	-5.80
246044_at	calcium-dependent protein kinase	CDPK19	AT5G19450	-1.15	-0.20	-1.32	0.23092312	0.6250	-5.80
260821_at	unknown protein contains Pfam pr	CRTISO	AT1G06820	1.13	0.18	1.32	0.23103724	0.6250	-5.80

264780_at	putative protein kinase similar to M	EDR1	AT1G08720	-1.14	-0.19	-1.32	0.23102444	0.6250	-5.80
257992_at	hypothetical protein similar to hypo	---	AT3G19880	1.15	0.20	1.32	0.23111907	0.6250	-5.80
266853_at	putative salt-inducible protein	---	AT2G26790	-1.10	-0.14	-1.32	0.23134073	0.6252	-5.80
249401_at	putative protein LIM7, Lily, EMBL:	---	AT5G40260	-1.09	-0.13	-1.32	0.23131842	0.6252	-5.80
258620_at	putative MYB family transcription f	MYB107	AT3G02940	1.08	0.11	1.32	0.23131777	0.6252	-5.80
267357_at	putative nematode-resistance prot	HSPRO2	AT2G40000	1.31	0.39	1.32	0.23132701	0.6252	-5.80
250705_at	diadenosine 5,5-P1,P4-tetraphosp	ATNUDX27	AT5G06340	1.14	0.18	1.32	0.23132309	0.6252	-5.80
245554_at	cytochrome P450 like protein	CYP705A4	AT4G15380	-1.09	-0.12	-1.32	0.23138276	0.6253	-5.80
251973_at	nodulin / glutamate-ammonia ligas	---	AT3G53180	-1.21	-0.27	-1.31	0.2315717	0.6253	-5.80
257008_at	myrosinase-associated protein, pu	ESM1	AT3G14210	-1.63	-0.70	-1.31	0.2315779	0.6253	-5.80
264031_at	unknown protein	---	AT2G03780	1.13	0.18	1.32	0.23146874	0.6253	-5.80
265419_at	putative secretory carrier-associate	---	AT2G20840	1.14	0.18	1.32	0.23153689	0.6253	-5.80
265901_at	putative selenium-binding protein	---	AT2G25580	-1.13	-0.18	-1.31	0.23154675	0.6253	-5.80
254647_at	hypothetical protein	---	AT4G18540	-1.09	-0.12	-1.32	0.23148124	0.6253	-5.80
254059_at	Arabidopsis mitochondrion-localize	ATHSP23.6	AT4G25200	1.14	0.19	1.31	0.23159771	0.6253	-5.80
255415_at	hypothetical protein	---	AT4G03160	-1.09	-0.12	-1.31	0.23179543	0.6257	-5.80
256550_at	En/Spm-like transposon protein, p	---	---	-1.09	-0.13	-1.31	0.23178916	0.6257	-5.80
264673_at	Expressed protein ; supported by f	ATATP-PR1	AT1G09795	-1.11	-0.15	-1.31	0.23184046	0.6258	-5.81
250831_at	unknown protein	---	AT5G04920	-1.10	-0.14	-1.31	0.23195456	0.6260	-5.81
260176_at	unknown protein similar to Pi starv	---	AT1G71950	-1.12	-0.16	-1.31	0.23199525	0.6260	-5.81
248136_at	RNA helicase-like protein	---	AT5G54910	-1.21	-0.27	-1.31	0.23209303	0.6261	-5.81
251461_at	putative protein	---	AT3G59780	1.14	0.19	1.31	0.23210911	0.6261	-5.81
252590_at	putative protein kinase NPK1-rela	---	AT3G45670	-1.11	-0.15	-1.31	0.23206914	0.6261	-5.81
263657_at	putative casein kinase I similar to C	CKL13	AT1G04440	-1.22	-0.28	-1.31	0.23228098	0.6265	-5.81
253451_at	putative myb-protein transforming	PC-MYB1	AT4G32730	-1.10	-0.14	-1.31	0.2323532	0.6265	-5.81
257284_at	TNP1-like protein similar to TNP1	---	---	1.08	0.11	1.31	0.23235298	0.6265	-5.81
252662_at	putative protein Sec24A protein, H	CEF	AT3G44340	1.12	0.16	1.31	0.23248712	0.6268	-5.81
265564_s_at	hypothetical protein predicted by g	---	---	-1.11	-0.15	-1.31	0.23253517	0.6269	-5.81
264187_at	unknown protein ;supported by full	---	AT1G54860	-1.09	-0.12	-1.31	0.23256917	0.6269	-5.81
250006_at	putative protein 2'-hydroxyisoflavo	PCB2	AT5G18660	1.32	0.40	1.31	0.23273045	0.6270	-5.81
245477_at	hypothetical protein	ARR2	AT4G16110	1.11	0.16	1.31	0.23273792	0.6270	-5.81
247723_at	protein phosphatase 2C - like ABA	---	AT5G59220	-1.22	-0.29	-1.31	0.23269848	0.6270	-5.81
258775_at	hydroxyacylglutathione hydrolase	GLY2	AT3G10850	1.11	0.15	1.31	0.23276516	0.6270	-5.81
261882_at	GTP-binding protein, putative simi	PDE318	AT1G80770	1.11	0.15	1.31	0.23265336	0.6270	-5.81
260653_at	pyruvate kinase, plastid isozyme,	PKp3	AT1G32440	1.12	0.16	1.31	0.23277349	0.6270	-5.81

247693_at	putative protein leucine zipper-cor	ATEXO70H	AT5G59730	-1.39	-0.47	-1.31	0.2328376	0.6271	-5.81
260409_at	Expressed protein ; supported by f	SHW1	AT1G69935	-1.20	-0.26	-1.31	0.2329211	0.6273	-5.81
254436_at	putative protein receptor kinase-lik	---	AT4G20940	-1.10	-0.13	-1.31	0.23295954	0.6273	-5.81
245608_at	protein kinase	---	AT4G14350	-1.16	-0.22	-1.31	0.23309933	0.6276	-5.81
253250_at	hypothetical protein	---	AT4G34690	-1.09	-0.12	-1.31	0.23311259	0.6276	-5.81
AFFX-r2-At-Act	Arabidopsis thaliana /REF=U3728	---	---	1.11	0.15	1.31	0.23318993	0.6277	-5.81
256366_at	protein kinase, putative contains P	---	AT1G66880	1.26	0.33	1.31	0.23344909	0.6278	-5.81
245702_at	calcium lipid binding protein - like (	SYTC	AT5G04220	1.17	0.22	1.31	0.23336482	0.6278	-5.81
258811_at	unknown protein similar to putative	---	AT3G03990	-1.18	-0.24	-1.31	0.23354488	0.6278	-5.81
254073_at	splicing factor At-SRp40 contains	RSP35	AT4G25500	1.12	0.16	1.31	0.23330221	0.6278	-5.81
251759_at	tetrahydrofolylpolyglutamate synth	ATDFD	AT3G55630	-1.21	-0.28	-1.31	0.23346417	0.6278	-5.81
253768_at	putative protein	---	AT4G28550	-1.18	-0.24	-1.31	0.23343862	0.6278	-5.81
263124_at	beta-Amyrin Synthase, putative si	---	AT1G78480	1.15	0.20	1.31	0.23349441	0.6278	-5.81
258539_at	putative RNA-binding protein cont	---	AT3G06970	-1.10	-0.13	-1.31	0.23339237	0.6278	-5.81
251040_at	ribonuclease II-like protein ribonuc	EMB2730	AT5G02250	1.19	0.25	1.31	0.2333874	0.6278	-5.81
260724_at	unknown protein ;supported by full	---	AT1G48140	1.10	0.14	1.31	0.23334776	0.6278	-5.81
260659_s_at	hypothetical protein predicted by g	---	AT1G19460 /	-1.09	-0.12	-1.31	0.23353732	0.6278	-5.81
258975_at	putative WRKY-like transcriptional	WRKY45	AT3G01970	1.13	0.18	1.31	0.23402532	0.6282	-5.81
261594_at	DNA-binding factor, putative simila	AT-GTL1	AT1G33240	1.13	0.17	1.30	0.23500417	0.6282	-5.82
251951_s_at	putative protein predicted proteins	---	AT1G55710 /	1.11	0.15	1.31	0.23473523	0.6282	-5.82
247907_at	unknown protein	---	AT5G57460	1.10	0.13	1.30	0.23506012	0.6282	-5.82
257970_at	putative sucrose cleavage protein	---	AT3G27570	-1.12	-0.16	-1.30	0.23485607	0.6282	-5.82
248767_at	putative protein contains similarity	---	AT5G47710	1.13	0.17	1.31	0.23462086	0.6282	-5.82
264264_at	unknown protein ESTs gb|T04610	---	AT1G09250	-1.26	-0.33	-1.31	0.23387737	0.6282	-5.81
253909_at	putative protein LEDI-3 protein, Li	---	AT4G27270	1.13	0.18	1.31	0.2337424	0.6282	-5.81
251225_at	putative protein glycosyl transfera	GATL7	AT3G62660	-1.16	-0.21	-1.30	0.23506754	0.6282	-5.82
245084_at	putative MYB family transcription f	AtMYB70	AT2G23290	-1.20	-0.26	-1.31	0.23441718	0.6282	-5.81
265316_at	unknown protein	---	AT2G20400	-1.17	-0.22	-1.31	0.23451376	0.6282	-5.81
267484_at	E2, ubiquitin-conjugating enzyme	ATUBC2	AT2G02760	1.11	0.15	1.31	0.23401854	0.6282	-5.81
258300_at	putative casein kinase I similar to c	ckl10	AT3G23340	-1.17	-0.22	-1.30	0.23492157	0.6282	-5.82
246842_at	Expressed protein ; supported by f	---	AT5G26731	-1.20	-0.26	-1.31	0.2340986	0.6282	-5.81
259492_at	hypothetical protein predicted by g	---	AT1G15830	-1.19	-0.25	-1.30	0.23493685	0.6282	-5.82
257733_at	unknown protein ; supported by cl	---	AT3G18350	1.12	0.17	1.30	0.23484766	0.6282	-5.82
260436_at	unknown protein	---	AT1G68140	1.14	0.19	1.31	0.23399123	0.6282	-5.81
266026_at	putative non-LTR retroelement rev	---	---	-1.12	-0.16	-1.30	0.23499996	0.6282	-5.82

256506_at	unknown protein	---	AT1G75160	-1.13	-0.17	-1.31	0.23398426	0.6282	-5.81
266924_at	unknown protein ;supported by ful	---	AT2G45730	1.14	0.18	1.31	0.23470198	0.6282	-5.82
246997_at	putative protein similar to unknown	---	AT5G67390	1.17	0.22	1.31	0.23404896	0.6282	-5.81
250263_at	putative protein	---	AT5G13470	1.13	0.18	1.30	0.23493845	0.6282	-5.82
255301_at	putative protein similar to transcrip	ATMSRB3	AT4G04800	1.21	0.28	1.30	0.23478306	0.6282	-5.82
264994_at	hypothetical protein contains simila	---	AT1G67270	-1.10	-0.14	-1.31	0.23471209	0.6282	-5.82
252337_at	CELL DIVISION CONTROL PROT	CDC2	AT3G48750	1.19	0.24	1.31	0.23398905	0.6282	-5.81
251047_at	putative protein mature-parasite-in	---	AT5G02390	-1.13	-0.17	-1.31	0.23443063	0.6282	-5.81
248208_at	unknown protein	ATHB52	AT5G53980	-1.16	-0.21	-1.31	0.23417012	0.6282	-5.81
263058_at	putative non-LTR retrolelement rev	---	---	-1.11	-0.15	-1.31	0.23416677	0.6282	-5.81
266135_at	putative transcription factor IIIB 70	---	AT2G45100	-1.19	-0.25	-1.31	0.23407121	0.6282	-5.81
249716_at	sterile apetala (emb|CAA11128.1)	SAP	AT5G35770	-1.11	-0.15	-1.31	0.23462623	0.6282	-5.82
257399_at	putative OBP32pep protein	---	AT1G23690	-1.08	-0.11	-1.30	0.23474098	0.6282	-5.82
249165_at	putative protein similar to unknown	ATIPK1	AT5G42810	-1.17	-0.22	-1.31	0.23383659	0.6282	-5.81
251458_at	putative protein several retrotransp	---	---	-1.10	-0.14	-1.31	0.23391452	0.6282	-5.81
258554_at	putative DEAD/DEAH box helicase	---	AT3G06980	1.10	0.14	1.30	0.23481807	0.6282	-5.82
AFFX-r2-Ec-bio	E. coli /GEN=bioD /DB_XREF=gb:	---	---	-1.28	-0.35	-1.31	0.23409206	0.6282	-5.81
267551_at	ubiquitin-specific protease 1 (UBP	UBP1	AT2G32780	-1.13	-0.18	-1.31	0.23379291	0.6282	-5.81
266031_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.30	0.23475545	0.6282	-5.82
252987_at	putative growth regulator protein a	---	AT4G38390	-1.13	-0.18	-1.30	0.23485617	0.6282	-5.82
253999_at	1-aminocyclopropane-1-carboxyla	ACS7	AT4G26200	-1.25	-0.32	-1.31	0.23434487	0.6282	-5.81
245610_at	hypothetical protein	---	AT4G14380	-1.12	-0.16	-1.31	0.23462225	0.6282	-5.82
262281_at	peptide transporter, putative simila	---	AT1G68570	-1.32	-0.40	-1.31	0.23424827	0.6282	-5.81
248572_at	unknown protein	---	AT5G49800	1.11	0.15	1.30	0.23494038	0.6282	-5.82
261496_at	ethylene responsive element bind	ERF12	AT1G28360	-1.12	-0.17	-1.31	0.23453473	0.6282	-5.82
246274_at	transcription factor like protein	---	AT4G36620	1.13	0.18	1.31	0.23464614	0.6282	-5.82
252082_at	putative protein	---	AT3G51940	-1.09	-0.13	-1.30	0.23482854	0.6282	-5.82
247928_at	villin	---	AT5G57320	-1.13	-0.18	-1.31	0.23467731	0.6282	-5.82
247605_at	DNA binding protein - like putative	TCP5	AT5G60970	-1.13	-0.18	-1.31	0.23421562	0.6282	-5.81
254733_at	putative polygalacturonase polyga	---	AT4G13760	-1.10	-0.13	-1.31	0.23451321	0.6282	-5.81
247915_at	putative protein similar to unknown	---	AT5G57570	-1.10	-0.14	-1.30	0.23501613	0.6282	-5.82
252962_at	splicing factor - like protein splicin	---	AT4G38780	-1.12	-0.16	-1.30	0.23481699	0.6282	-5.82
265388_s_at	unknown protein ;supported by ful	---	AT2G20990	1.10	0.14	1.30	0.23520196	0.6284	-5.82
260872_at	hypothetical protein predicted by g	---	AT1G21350	1.17	0.23	1.30	0.23515167	0.6284	-5.82
263768_x_at	putative Athila retroelement ORF1	---	---	-1.08	-0.11	-1.30	0.23517842	0.6284	-5.82

266565_at	putative serine carboxypeptidase I	scpl23	AT2G24010	-1.12	-0.16	-1.30	0.23525752	0.6284	-5.82
261621_at	hypothetical protein similar to guar	EDA10	AT1G01960	1.10	0.14	1.30	0.23523322	0.6284	-5.82
253981_at	putative protein ;supported by full-l	---	AT4G26670	1.10	0.14	1.30	0.23531813	0.6285	-5.82
247500_at	putative protein B2 protein, Daucu	---	AT5G61910	-1.17	-0.23	-1.30	0.23538034	0.6285	-5.82
264188_at	histone H2A, putative similar to his	GAMMA-H2	AT1G54690	1.24	0.31	1.30	0.23546219	0.6286	-5.82
246965_at	methyltransferase-like protein met	---	AT5G24840	1.18	0.24	1.30	0.23545709	0.6286	-5.82
255501_at	hypothetical protein	---	AT4G02400	-1.17	-0.23	-1.30	0.23555506	0.6287	-5.82
265571_s_at	unknown protein	---	AT2G28020 /	1.10	0.14	1.30	0.2355196	0.6287	-5.82
262898_at	hypothetical protein predicted by g	---	AT1G59850	-1.12	-0.17	-1.30	0.23556314	0.6287	-5.82
249694_at	glucose-6-phosphate dehydrogena	G6PD1	AT5G35790	-1.09	-0.12	-1.30	0.23565414	0.6288	-5.82
265449_at	putative arginine/serine-rich splicin	---	AT2G46610	1.17	0.23	1.30	0.23563785	0.6288	-5.82
259895_at	unknown protein ;supported by full	PFI	AT1G71440	1.10	0.13	1.30	0.23580565	0.6288	-5.82
258316_at	unknown protein	---	AT3G22660	1.18	0.23	1.30	0.23593367	0.6288	-5.82
246759_at	putative protein kinesin heavy cha	---	AT5G27950	1.15	0.21	1.30	0.23583714	0.6288	-5.82
260714_at	chaperonin CPN10 identical to SP	CPN10	AT1G14980	-1.22	-0.28	-1.30	0.23592616	0.6288	-5.82
AFFX-r2-At-Ub	Arabidopsis thaliana /REF=U8496	---	---	-1.10	-0.13	-1.30	0.2358688	0.6288	-5.82
251466_at	putative protein hypothetical prote	---	AT3G59340	-1.13	-0.18	-1.30	0.23580549	0.6288	-5.82
254927_at	putative protein hypothetical prote	---	AT4G11400	-1.13	-0.17	-1.30	0.23591769	0.6288	-5.82
248978_at	putative protein contains similarity	AtPP2-A8	AT5G45070	-1.15	-0.20	-1.30	0.23593445	0.6288	-5.82
259701_at	unknown protein similar to GB:AA(	---	AT1G77770	1.14	0.19	1.30	0.23577081	0.6288	-5.82
261153_at	unknown protein ;supported by full	---	AT1G04850	1.11	0.15	1.30	0.23575165	0.6288	-5.82
265390_at	unknown protein ; supported by fu	---	AT2G20820	1.10	0.14	1.30	0.23596274	0.6288	-5.82
250505_at	cellulose synthase catalytic subuni	CESA5	AT5G09870	-1.16	-0.22	-1.30	0.23602403	0.6289	-5.82
246344_at	putative protein predicted proteins	---	AT3G56730	1.22	0.29	1.30	0.23613142	0.6290	-5.82
251618_at	putative protein unknown protein /	---	AT3G58020	1.17	0.23	1.30	0.23611467	0.6290	-5.82
249470_at	putative protein predicted proteins	---	AT5G39350	1.13	0.18	1.30	0.23623023	0.6290	-5.82
262792_at	hypothetical protein predicted by g	---	AT1G10710	-1.11	-0.15	-1.30	0.23620502	0.6290	-5.82
262663_at	hypothetical protein identical to hy	---	AT1G13940	-1.12	-0.16	-1.30	0.23618814	0.6290	-5.82
256747_at	unknown protein similar to CW14 (	---	AT3G29180	1.12	0.16	1.30	0.23642854	0.6291	-5.82
262522_at	putative amino acid transporter Ve	CAT8	AT1G17120	1.12	0.16	1.30	0.23635147	0.6291	-5.82
257362_at	hypothetical protein predicted by g	---	AT2G45840	-1.09	-0.12	-1.30	0.2364129	0.6291	-5.82
266642_at	putative chloroplast RNA binding p	---	AT2G35410	-1.11	-0.15	-1.30	0.23633688	0.6291	-5.82
254829_at	AIR1A-like protein putative cell wa	---	AT4G12530	-1.10	-0.13	-1.30	0.23637442	0.6291	-5.82
253435_at	adenylate translocator (brittle-1) -	SHS1	AT4G32400	-1.17	-0.23	-1.30	0.23637055	0.6291	-5.82
250048_s_at	BCS1 - like protein h-bcs1, Homo	---	AT5G17740 /	-1.10	-0.14	-1.30	0.23629367	0.6291	-5.82

264799_at	putative violaxanthin de-epoxidase	NPQ1	AT1G08550	-1.13	-0.18	-1.30	0.23656162	0.6292	-5.82
258863_at	unknown protein similar to RNA he	DCL2	AT3G03300	1.19	0.25	1.30	0.23655179	0.6292	-5.82
259906_at	unknown protein	---	AT1G74120	-1.09	-0.13	-1.30	0.23654821	0.6292	-5.82
246774_at	polygalacturonase-like protein pol	---	AT5G27530	-1.11	-0.15	-1.30	0.23664756	0.6293	-5.82
253362_s_at	putative protein cyclopropane-fatty	---	AT4G33110 /	1.16	0.21	1.30	0.23670199	0.6294	-5.82
263881_at	unknown protein ; supported by cl	---	AT2G21820	-1.11	-0.15	-1.30	0.23675257	0.6295	-5.82
246246_at	putative protein	---	AT4G37170	1.14	0.19	1.30	0.23683001	0.6295	-5.82
263522_at	hypothetical protein	---	AT2G24950	-1.09	-0.12	-1.30	0.23684321	0.6295	-5.82
267266_at	putative metal ion transporter (NR/	NRAMP3	AT2G23150	-1.11	-0.14	-1.30	0.23682671	0.6295	-5.82
247123_at	unknown protein	---	AT5G66050	-1.16	-0.22	-1.30	0.23692626	0.6295	-5.82
261273_at	unknown protein ; supported by cD	---	AT1G26650	1.17	0.23	1.30	0.23693665	0.6295	-5.82
264980_at	receptor kinase, putative similar to	---	AT1G27190	1.13	0.18	1.30	0.23692592	0.6295	-5.82
264183_at	unknown protein	CLV2	AT1G65380	1.12	0.16	1.30	0.2370211	0.6296	-5.82
253845_at	putative protein myosin heavy cha	---	AT4G27980	-1.08	-0.11	-1.30	0.23705364	0.6296	-5.82
248919_at	putative protein contains similarity	---	AT5G45920	-1.12	-0.16	-1.30	0.23710083	0.6296	-5.82
255751_at	terpene synthase family protein, p	---	AT1G31950	1.13	0.17	1.30	0.23711163	0.6296	-5.82
250121_at	protein kinase-like protein	---	AT5G16500	1.09	0.12	1.30	0.23708207	0.6296	-5.82
245424_at	putative protein	---	AT4G17505	-1.10	-0.14	-1.30	0.23719751	0.6298	-5.82
264589_at	hypothetical protein	---	AT2G17650	1.14	0.19	1.30	0.2373003	0.6299	-5.83
260539_at	putative peroxidase	---	AT2G43480	1.09	0.12	1.30	0.23731441	0.6299	-5.83
266294_at	putative small heat shock protein ;	---	AT2G29500	-1.61	-0.69	-1.30	0.237419	0.6300	-5.83
258822_s_at	unknown protein contains Pfam pr	---	AT3G07220 /	1.20	0.26	1.30	0.2374118	0.6300	-5.83
251443_at	putative protein unknown protein /	---	AT3G59940	1.22	0.29	1.30	0.23742319	0.6300	-5.83
252627_at	putative protein	---	AT3G44950	-1.13	-0.17	-1.30	0.23744174	0.6300	-5.83
254377_at	subtilisin proteinase - like subtilisir	---	AT4G21650	-1.69	-0.76	-1.30	0.23750542	0.6301	-5.83
254843_at	putative protein TAK1 binding prot	---	AT4G11860	-1.09	-0.12	-1.30	0.23760496	0.6303	-5.83
245246_at	hypothetical protein predicted by g	---	AT1G44224	-1.10	-0.13	-1.30	0.23778706	0.6304	-5.83
259453_at	gibberelin 20-oxidase, putative, 5'	ATGA20OX	AT1G44090	-1.15	-0.20	-1.30	0.23766372	0.6304	-5.83
265099_at	unknown protein Location of EST	---	AT1G03990	-1.31	-0.39	-1.30	0.23777734	0.6304	-5.83
255540_at	putative SecA-type chloroplast pro	---	AT4G01800	1.16	0.22	1.30	0.23771827	0.6304	-5.83
251114_at	transcription factor GT-3a	---	AT5G01380	-1.45	-0.54	-1.30	0.23779831	0.6304	-5.83
255995_at	receptor-like serine/threonine kina	RKF1	AT1G29750	-1.14	-0.19	-1.30	0.23775684	0.6304	-5.83
263928_at	hypothetical protein predicted by g	---	AT2G36330	-1.16	-0.22	-1.30	0.23785696	0.6304	-5.83
258574_at	hypothetical protein	---	AT3G04250	-1.11	-0.15	-1.30	0.23789514	0.6305	-5.83
261009_at	hypothetical protein similar to puta	MES13	AT1G26360	-1.12	-0.17	-1.30	0.23795155	0.6305	-5.83

264338_at	potassium transporter, putative sir	KUP6	AT1G70300	1.18	0.24	1.29	0.23801549	0.6306	-5.83
257065_at	diacylglycerol pyrophosphate phos	---	AT3G18220	-1.17	-0.23	-1.29	0.23805181	0.6307	-5.83
253294_at	hypothetical protein	---	AT4G33740	1.11	0.15	1.29	0.23833972	0.6308	-5.83
256240_at	unknown protein ; supported by cD	atnudt16	AT3G12600	1.11	0.15	1.29	0.23839693	0.6308	-5.83
249924_at	kinase associated protein phospha	KAPP	AT5G19280	1.14	0.19	1.29	0.2383042	0.6308	-5.83
247623_at	receptor-like protein kinase recept	---	AT5G60320	-1.10	-0.14	-1.29	0.23829739	0.6308	-5.83
246100_at	putative protein predicted protein,	---	---	-1.11	-0.15	-1.29	0.23820017	0.6308	-5.83
258216_at	unknown protein contains Pfam pr	---	AT3G17980	1.14	0.19	1.29	0.23830583	0.6308	-5.83
252717_at	putative protein predicted proteins	---	AT3G43930	-1.21	-0.28	-1.29	0.2383851	0.6308	-5.83
253364_at	F-box protein family, AtFBX13 cot	---	AT4G33160	1.09	0.12	1.29	0.23832646	0.6308	-5.83
261811_at	DNA polymerase epsilon catalytic	TIL1	AT1G08260	1.17	0.22	1.29	0.23824897	0.6308	-5.83
267382_at	unknown protein	---	AT2G44300	-1.18	-0.24	-1.29	0.23834764	0.6308	-5.83
250032_at	glutamate dehydrogenase (EC 1.4	GDH1	AT5G18170	1.38	0.47	1.29	0.23837965	0.6308	-5.83
251927_at	hypothetical protein ER6 protein -	---	AT3G53990	-1.10	-0.13	-1.29	0.23848469	0.6309	-5.83
260669_at	hypothetical protein predicted by g	---	AT1G19340	-1.11	-0.15	-1.29	0.23849232	0.6309	-5.83
246920_at	phytocyanin-related protein-like pl	---	AT5G25090	-1.09	-0.13	-1.29	0.23853328	0.6309	-5.83
260299_at	putative gibberellin 3 beta-hydroxy	GA3OX4	AT1G80330	-1.08	-0.12	-1.29	0.23865585	0.6312	-5.83
254814_at	hypothetical protein ; supported by	---	AT4G12340	1.08	0.12	1.29	0.23868177	0.6312	-5.83
264514_at	putative cinnamyl alcohol dehydro	---	AT1G09500	-1.69	-0.76	-1.29	0.23875933	0.6312	-5.83
262021_at	unknown protein	AT1G3554	---	1.12	0.16	1.29	0.23873379	0.6312	-5.83
261136_at	ribokinase, putative similar to GB:	---	AT1G19600	1.10	0.14	1.29	0.23881669	0.6313	-5.83
262299_at	unknown protein Similar to gb|U04	---	AT1G27520	1.11	0.15	1.29	0.23888377	0.6314	-5.83
263938_at	hypothetical protein predicted by g	---	AT2G35900	1.11	0.15	1.29	0.23897947	0.6315	-5.83
263627_at	Expressed protein ; supported by f	---	AT2G04675	-1.12	-0.16	-1.29	0.2389635	0.6315	-5.83
254077_at	putative protein NorM, Vibrio para	---	AT4G25640	1.14	0.18	1.29	0.23912349	0.6315	-5.83
252440_at	aquaporin-like protein aquaporin -	TIP5;1	AT3G47440	-1.10	-0.13	-1.29	0.23915816	0.6315	-5.83
254656_at	putative protein ;supported by full-	---	AT4G18070	-1.16	-0.22	-1.29	0.23915856	0.6315	-5.83
263002_at	hypothetical protein predicted by g	---	AT1G54200	-1.27	-0.35	-1.29	0.23903304	0.6315	-5.83
256566_at	hypothetical protein	---	AT3G19530	-1.10	-0.14	-1.29	0.23907981	0.6315	-5.83
266515_at	putative tubby protein	AtTLP3	AT2G47900	1.16	0.21	1.29	0.23911034	0.6315	-5.83
261344_at	hypothetical protein similar to hypo	---	AT1G79710	1.10	0.14	1.29	0.23919142	0.6315	-5.83
260736_at	hypothetical protein predicted by g	---	AT1G17630	-1.10	-0.13	-1.29	0.23930287	0.6318	-5.83
258909_at	putative DnaJ protein Pfam HMM	---	AT3G06340	-1.09	-0.12	-1.29	0.23934253	0.6318	-5.83
249349_at	putative transcription factor MYB24	MYB24	AT5G40350	-1.11	-0.14	-1.29	0.23937633	0.6318	-5.83
266543_at	hypothetical protein predicted by g	---	AT2G35075	1.08	0.11	1.29	0.23944741	0.6319	-5.83

256651_at	hypothetical protein predicted by g	---	AT3G18840	-1.13	-0.18	-1.29	0.23950986	0.6320	-5.83
257238_at	unknown protein ; supported by cl	---	AT3G17430	1.15	0.21	1.29	0.23956624	0.6321	-5.83
257517_at	unknown protein	---	AT3G16330	-1.44	-0.52	-1.29	0.23963633	0.6321	-5.83
255312_at	putative transposon protein	---	---	1.10	0.14	1.29	0.23966116	0.6321	-5.83
259678_at	putative 30S ribosomal protein S1	---	AT1G77750	1.17	0.22	1.29	0.23961156	0.6321	-5.83
263917_at	putative AP2 domain transcription	HRD	AT2G36450	-1.16	-0.22	-1.29	0.23983402	0.6323	-5.83
257336_at	hypothetical protein	---	---	-1.09	-0.12	-1.29	0.23982486	0.6323	-5.83
245812_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.29	0.23992048	0.6323	-5.83
253113_at	putative protein physical impedan	---	AT4G35985	1.20	0.26	1.29	0.23989863	0.6323	-5.83
255951_at	unknown protein contains similarity	MUB6	AT1G22050	-1.13	-0.18	-1.29	0.23982725	0.6323	-5.83
253177_s_at	O-methyltransferase - like protein	---	AT4G35150	-1.17	-0.23	-1.29	0.23988259	0.6323	-5.83
253517_at	predicted protein hypothetical prot	---	AT4G31390	-1.15	-0.20	-1.29	0.23988128	0.6323	-5.83
259184_at	unknown protein ;supported by ful	---	AT3G01520	-1.12	-0.16	-1.29	0.23993257	0.6323	-5.83
247288_at	non-phototropic hypocotyl 3 (gb|AA	NPH3	AT5G64330	-1.39	-0.47	-1.29	0.2400783	0.6326	-5.84
250243_at	cobalamin biosynthesis protein	GUN5	AT5G13630	1.15	0.21	1.29	0.24017622	0.6326	-5.84
246006_at	putative protein DIM1 protein, Hor	YLS8	AT5G08290	1.10	0.14	1.29	0.24025115	0.6326	-5.84
249564_at	unknown protein	---	AT5G38400	-1.12	-0.17	-1.29	0.24020962	0.6326	-5.84
262222_at	unknown protein	TRZ1	AT1G74700	-1.11	-0.16	-1.29	0.24025188	0.6326	-5.84
256150_at	beta-fructofuranosidase identical to	ATFRUCT5	AT1G55120	-1.25	-0.33	-1.29	0.24020982	0.6326	-5.84
260673_at	unknown protein ; supported by ful	---	AT1G19330	-1.21	-0.28	-1.29	0.24024644	0.6326	-5.84
245109_at	hypothetical protein predicted by g	---	AT2G41520	-1.12	-0.16	-1.29	0.24034039	0.6327	-5.84
249715_at	putative protein similar to unknown	---	AT5G35760	1.13	0.18	1.29	0.24036343	0.6327	-5.84
255732_at	fatty acid condensing enzyme CU	KCS5	AT1G25450	1.32	0.40	1.29	0.24046505	0.6328	-5.84
255878_at	putative bZIP transcription factor c	---	AT2G40620	1.17	0.23	1.29	0.24043074	0.6328	-5.84
246653_at	putative protein clathrin assembly	---	AT5G35200	1.11	0.15	1.29	0.24047002	0.6328	-5.84
263029_at	unknown protein	---	AT1G24050	1.08	0.11	1.29	0.24061519	0.6331	-5.84
260931_at	hypothetical protein predicted by g	---	AT1G02550	-1.13	-0.18	-1.29	0.24065601	0.6331	-5.84
252415_at	glutamine-dependent asparagine s	ASN1	AT3G47340	-1.99	-1.00	-1.29	0.24080405	0.6335	-5.84
248049_at	putative protein contains similarity	COX15	AT5G56090	1.25	0.33	1.29	0.24087181	0.6335	-5.84
260338_at	putative RNA-binding protein simila	---	AT1G69250	1.10	0.13	1.29	0.24086084	0.6335	-5.84
251756_at	putative protein	---	AT3G55820	1.10	0.13	1.29	0.24097275	0.6337	-5.84
257762_at	hypothetical protein	XRCC4	AT3G23100	1.10	0.14	1.29	0.24098866	0.6337	-5.84
265326_at	unknown protein predicted by gens	---	AT2G18220	1.15	0.21	1.29	0.24122447	0.6337	-5.84
260875_at	hypothetical protein predicted by g	SKP2A	AT1G21410	1.23	0.30	1.29	0.24115338	0.6337	-5.84
250332_at	putative protein predicted proteins	---	AT5G11680	-1.13	-0.18	-1.29	0.24117119	0.6337	-5.84

256199_at	unknown protein	SAB	AT1G58250	1.14	0.19	1.29	0.24121	0.6337	-5.84
252200_at	anthranilate N-hydroxycinnamoyl/I	---	AT3G50280	-1.36	-0.45	-1.29	0.24120291	0.6337	-5.84
253957_at	putative protein ; supported by cD	AGP13	AT4G26320	-1.17	-0.22	-1.28	0.24125695	0.6337	-5.84
254780_s_at	auxilin-like protein auxilin - bovine	---	AT4G12770	1.18	0.23	1.28	0.24128318	0.6337	-5.84
249562_at	disease resistance protein-like	---	AT5G38350	1.11	0.15	1.28	0.2412739	0.6337	-5.84
247212_at	putative protein similar to unknown	---	AT5G65040	-1.09	-0.13	-1.29	0.24106885	0.6337	-5.84
259270_at	putative porin similar to outer mitoc	VDAC1	AT3G01280	-1.12	-0.17	-1.29	0.24113784	0.6337	-5.84
266585_at	putative retroelement pol polyprote	---	---	-1.13	-0.18	-1.28	0.24133548	0.6338	-5.84
262969_at	unknown protein	---	AT1G75710	1.15	0.20	1.28	0.24146976	0.6339	-5.84
251986_at	putative protein various predicted	---	AT3G53310	1.25	0.32	1.28	0.24141713	0.6339	-5.84
251153_at	putative protein predicted protein,	NPL41	AT3G63000	1.13	0.17	1.28	0.24144458	0.6339	-5.84
262785_at	putative carboxyl-terminal peptidas	---	AT1G10750	-1.17	-0.23	-1.28	0.24155237	0.6340	-5.84
262206_at	putative ubiquinol-cytochrome c re	---	AT2G01090	1.13	0.18	1.28	0.24158382	0.6340	-5.84
262760_at	hypothetical protein contains simila	---	AT1G10770	-1.40	-0.49	-1.28	0.24164644	0.6341	-5.84
259993_at	unknown protein	---	AT1G67960	1.12	0.16	1.28	0.2416665	0.6341	-5.84
256166_at	hypothetical protein	---	AT1G36920	1.09	0.12	1.28	0.2417267	0.6342	-5.84
247819_at	MAP kinase ; supported by cDNA:	WNK4	AT5G58350	1.17	0.22	1.28	0.24195691	0.6343	-5.84
260208_s_at	unknown protein similar to Ca+2-b	---	AT1G70670	-1.22	-0.29	-1.28	0.2419764	0.6343	-5.84
250187_at	putative protein predicted proteins	---	AT5G14370	-1.20	-0.27	-1.28	0.24202419	0.6343	-5.84
251548_at	putative protein predicted protein,	---	---	-1.13	-0.18	-1.28	0.24191105	0.6343	-5.84
266088_at	hypothetical protein predicted by g	---	AT2G37780	-1.14	-0.19	-1.28	0.24192252	0.6343	-5.84
251990_at	putative protein MICRONUCLEAR	---	AT3G53320	1.17	0.22	1.28	0.24205109	0.6343	-5.84
247633_at	putative zinc finger protein finger p	---	AT5G60470	-1.18	-0.24	-1.28	0.24194027	0.6343	-5.84
249388_at	putative protein downy mildew res	---	AT5G40090	-1.12	-0.16	-1.28	0.24201535	0.6343	-5.84
267231_at	putative inositol polyphosphate 5'-p	---	AT2G43900	1.11	0.15	1.28	0.24204832	0.6343	-5.84
245280_at	Expressed protein ; supported by c	VRN2	AT4G16845	-1.11	-0.15	-1.28	0.2419849	0.6343	-5.84
264380_at	unknown protein predicted by gens	---	AT2G25190	1.08	0.11	1.28	0.2421628	0.6344	-5.84
252797_at	putative protein	---	---	-1.15	-0.21	-1.28	0.24211738	0.6344	-5.84
246610_at	putative protein	---	AT5G35400	1.11	0.15	1.28	0.24217203	0.6344	-5.84
263591_at	unknown protein	ATMAP65-(	AT2G01910	-1.43	-0.51	-1.28	0.24229126	0.6345	-5.84
261426_at	unknown protein contains similarity	---	AT1G18680	1.10	0.13	1.28	0.24225421	0.6345	-5.84
259092_at	putative zeta-carotene desaturase	ZDS	AT3G04870	1.08	0.12	1.28	0.24227532	0.6345	-5.84
260966_at	NBS/LRR disease resistance prot	RPS5	AT1G12220	1.11	0.15	1.28	0.24232159	0.6345	-5.84
262708_at	UV-sensitive rad23, putative simila	---	AT1G16190	-1.09	-0.12	-1.28	0.2423801	0.6345	-5.84
263447_s_at	putative PHD-type zinc finger prote	ATX2	AT1G05830	-1.24	-0.31	-1.28	0.24236402	0.6345	-5.84

254759_at	short-chain alcohol dehydrogenas	---	AT4G13180	-1.17	-0.23	-1.28	0.24242806	0.6346	-5.84
264866_at	putative metalloproteinase similar t	---	AT1G24140	1.77	0.82	1.28	0.24246293	0.6346	-5.84
265826_at	hypothetical protein predicted by g	---	AT2G35795	1.09	0.13	1.28	0.24261215	0.6347	-5.84
254577_at	putative protein ;supported by full-	---	AT4G19450	-1.16	-0.22	-1.28	0.24256982	0.6347	-5.84
265595_at	26S proteasome subunit 4 ;suppo	---	AT2G20140	1.13	0.18	1.28	0.24257205	0.6347	-5.84
252388_at	putative protein ;supported by full-	---	AT3G47850	1.11	0.16	1.28	0.24259798	0.6347	-5.84
265164_at	putative OBP32pep protein	---	AT1G23600	1.10	0.13	1.28	0.24270861	0.6348	-5.84
256423_at	serine carboxypeptidase, putative	scpl18	AT1G33540	-1.08	-0.12	-1.28	0.24269314	0.6348	-5.84
265956_at	hypothetical protein predicted by g	---	AT2G37290	1.08	0.11	1.28	0.24277724	0.6349	-5.84
247188_at	14-3-3 protein GF14kappa (grf8) i	GRF8	AT5G65430	1.12	0.16	1.28	0.24296961	0.6353	-5.85
265068_at	hypothetical protein Similar to Kine	---	AT1G55550	1.09	0.13	1.28	0.24294378	0.6353	-5.85
262967_at	hypothetical protein predicted by g	---	AT1G75730	1.12	0.16	1.28	0.24308619	0.6355	-5.85
245142_at	putative O-sialoglycoprotein endop	---	AT2G45270	1.11	0.15	1.28	0.2432891	0.6360	-5.85
263065_at	MAP kinase (ATMPK7) identical to	ATMPK7	AT2G18170	1.19	0.25	1.28	0.24346379	0.6360	-5.85
253020_at	hypothetical protein	---	AT4G38020	1.14	0.20	1.28	0.24343333	0.6360	-5.85
259657_at	phospholipase D alpha, putative s	PLDEPSIL(	AT1G55180	1.10	0.14	1.28	0.24335437	0.6360	-5.85
252610_x_at	putative protein putative MuDR pr	---	---	-1.08	-0.11	-1.28	0.24341483	0.6360	-5.85
265478_at	unknown protein ;supported by ful	MEE14	AT2G15890	1.10	0.14	1.28	0.2433903	0.6360	-5.85
254287_at	putative protein similaritry to hypo	---	AT4G22960	1.10	0.13	1.28	0.2434547	0.6360	-5.85
257594_at	unknown protein	---	AT3G24740	-1.13	-0.18	-1.28	0.2435007	0.6360	-5.85
266605_at	putative SNF2 subfamily transcript	BRM	AT2G46020	-1.10	-0.14	-1.28	0.24352936	0.6360	-5.85
249064_at	putative protein contains similarity	---	AT5G44250	1.09	0.12	1.28	0.24357071	0.6360	-5.85
264961_at	unknown protein contains similarity	PRAF1	AT1G76950	1.24	0.30	1.28	0.24359082	0.6360	-5.85
264930_at	receptor-like kinase, putative simil	NIK3	AT1G60800	-1.14	-0.19	-1.28	0.24378577	0.6365	-5.85
262652_at	hypothetical protein One of a clust	FUT9	AT1G14110	-1.10	-0.13	-1.28	0.24385695	0.6366	-5.85
254543_at	putative chitinase chitinase (EC 3.	---	AT4G19810	1.41	0.49	1.28	0.24403222	0.6368	-5.85
252061_at	hypothetical protein phosphate ac	---	AT3G52620	-1.10	-0.13	-1.28	0.24400792	0.6368	-5.85
252261_at	RNA-directed RNA polymerase RN	RDR6	AT3G49500	1.12	0.16	1.28	0.244027	0.6368	-5.85
260737_at	receptor-like serine threonine kina	---	AT1G17540	1.13	0.17	1.28	0.24407091	0.6368	-5.85
259858_at	putative receptor kinase similar to	---	AT1G68400	-1.21	-0.28	-1.28	0.24420015	0.6370	-5.85
245574_at	hypothetical protein	IQD19	AT4G14750	-1.16	-0.21	-1.28	0.24420645	0.6370	-5.85
255605_at	hypothetical protein	---	AT4G01090	1.18	0.24	1.28	0.24427764	0.6372	-5.85
258462_at	unknown protein	---	AT3G17350	1.26	0.34	1.28	0.24438185	0.6373	-5.85
257866_at	dihydroxyacetone kinase, putative	---	AT3G17770	1.27	0.35	1.28	0.24439242	0.6373	-5.85
258088_at	hypothetical protein predicted by g	---	AT3G14580	-1.10	-0.14	-1.28	0.24443508	0.6374	-5.85

250284_at	protein kinase precursor - like rec	CRN	AT5G13290	1.17	0.22	1.27	0.24456147	0.6375	-5.85
262110_at	SF2/ASF-like splicing modulator S	SR1	AT1G02840	1.13	0.18	1.28	0.244534	0.6375	-5.85
254293_at	putative protein SF16 protein, Hel	IQD22	AT4G23060	-1.22	-0.29	-1.27	0.24463309	0.6376	-5.85
247206_at	putative protein similar to unknown	---	AT5G64950	-1.08	-0.11	-1.27	0.2447087	0.6376	-5.85
264069_at	putative rubisco subunit binding-pr	CPN60A	AT2G28000	1.17	0.23	1.27	0.2446936	0.6376	-5.85
266067_s_at	hypothetical protein predicted by g	---	AT2G18810 /	-1.08	-0.12	-1.27	0.24466086	0.6376	-5.85
250354_at	putative protein predicted proteins	---	AT5G11640	1.11	0.14	1.27	0.24479361	0.6376	-5.85
265614_at	Expressed protein ; supported by c	---	AT2G25355	1.14	0.19	1.27	0.24478052	0.6376	-5.85
259022_at	putative asparaginyl-tRNA synthet	NS2	AT3G07420	1.17	0.23	1.27	0.24474867	0.6376	-5.85
247935_at	30S ribosomal protein S16 ; suppo	---	AT5G56940	1.15	0.20	1.27	0.24492373	0.6379	-5.85
257466_at	hypothetical protein predicted by g	---	AT1G62840	-1.30	-0.38	-1.27	0.24498397	0.6380	-5.85
265471_at	putative peroxidase ATP2a ;suppo	---	AT2G37130	1.29	0.36	1.27	0.24514792	0.6381	-5.85
258122_at	hypothetical protein contains simila	ATGSL04	AT3G14570	-1.19	-0.26	-1.27	0.24507258	0.6381	-5.85
257106_at	unknown protein	---	AT3G29060	-1.09	-0.13	-1.27	0.24512622	0.6381	-5.85
264742_at	hypothetical protein similar to hypo	---	AT1G62130	-1.13	-0.18	-1.27	0.24516765	0.6381	-5.85
263749_at	putative phosphatidylinositol/phosp	---	AT2G21520	1.12	0.16	1.27	0.24515664	0.6381	-5.85
261982_at	hypothetical protein predicted by g	---	AT1G33780	1.09	0.13	1.27	0.24518745	0.6381	-5.85
267352_at	hypothetical protein predicted by g	---	AT2G40050	1.09	0.13	1.27	0.24528916	0.6383	-5.85
261353_at	hypothetical protein contains simila	---	AT1G79600	-1.16	-0.22	-1.27	0.24532834	0.6383	-5.85
260286_at	putative acetylornithine transamina	WIN1	AT1G80600	1.13	0.18	1.27	0.24535735	0.6383	-5.85
265760_at	unknown protein	---	AT2G01220	1.11	0.15	1.27	0.24540788	0.6384	-5.85
257372_at	hypothetical protein predicted by g	---	AT2G43220	-1.10	-0.13	-1.27	0.24550489	0.6385	-5.85
246197_at	caltractin-like protein ;supported by	CEN2	AT4G37010	1.39	0.48	1.27	0.24556417	0.6386	-5.85
250805_at	unknown protein	---	AT5G05050	-1.10	-0.13	-1.27	0.24559768	0.6386	-5.85
245903_at	CLB1 - like protein CLB1 protein,	SYTD	AT5G11100	-1.11	-0.15	-1.27	0.24563737	0.6387	-5.85
251815_at	putative protein thioredoxin-like pr	CXIP1	AT3G54900	1.13	0.17	1.27	0.24567848	0.6387	-5.85
264200_at	putative invertase Similar to LIM17	---	AT1G22650	-1.18	-0.24	-1.27	0.24574828	0.6387	-5.85
261759_at	hypothetical protein similar to puta	---	AT1G15590	1.11	0.15	1.27	0.24575026	0.6387	-5.85
259236_at	unknown protein ; supported by fu	---	AT3G11530	1.10	0.13	1.27	0.24583989	0.6388	-5.86
251547_at	putative protein predicted proteins	---	AT3G58860	-1.11	-0.15	-1.27	0.24582	0.6388	-5.86
264889_at	unknown protein	---	AT1G23050	-1.12	-0.17	-1.27	0.24589918	0.6389	-5.86
264282_at	hypothetical protein similar to hypo	---	AT1G61840	-1.11	-0.16	-1.27	0.24598061	0.6390	-5.86
251398_at	zinc finger protein - like ZPT3-3, P	---	AT3G60580	1.13	0.18	1.27	0.24597519	0.6390	-5.86
255088_at	putative protein heat shock protei	---	AT4G09350	-1.19	-0.24	-1.27	0.24601494	0.6390	-5.86
263568_at	hypothetical protein predicted by g	---	AT2G27160	-1.14	-0.19	-1.27	0.246091	0.6391	-5.86

265086_at	hypothetical protein contains Zinc	RING1B	AT1G03770	1.15	0.21	1.27	0.24630115	0.6396	-5.86
248447_at	putative protein contains similarity	PABN1	AT5G51120	1.10	0.13	1.27	0.24634963	0.6396	-5.86
245302_at	Expressed protein ; supported by c	KAN3	AT4G17695	-1.19	-0.25	-1.27	0.24639609	0.6397	-5.86
255319_at	putative disease resistance protein	AtRLP46	AT4G04220	1.24	0.31	1.27	0.24655248	0.6398	-5.86
253822_at	hypothetical protein	---	AT4G28410	-1.10	-0.13	-1.27	0.24648094	0.6398	-5.86
264647_at	putative respiratory burst oxidase p	ATRBOHB	AT1G09090	-1.12	-0.16	-1.27	0.24652583	0.6398	-5.86
257079_at	unknown protein	---	AT3G15240	-1.09	-0.13	-1.27	0.24649888	0.6398	-5.86
250310_at	unknown protein	---	AT5G12230	1.14	0.19	1.27	0.24660064	0.6398	-5.86
265581_at	putative cAMP-dependent protein l	---	AT2G20050	1.10	0.13	1.27	0.24660183	0.6398	-5.86
257534_at	hypothetical protein predicted by g	---	AT3G09670	1.10	0.13	1.27	0.24664402	0.6398	-5.86
249492_at	germin-like protein (GLP2a) copy1	GER2	AT5G39130 /	-1.09	-0.13	-1.27	0.24666339	0.6398	-5.86
256877_at	unknown protein ;supported by ful	---	AT3G26470	1.32	0.40	1.27	0.2467208	0.6398	-5.86
252458_at	putative protein various predicted	---	AT3G47210	-1.10	-0.14	-1.27	0.24675855	0.6398	-5.86
252567_at	zinc finger -like protein zinc finger	---	AT3G46070	-1.10	-0.13	-1.27	0.24679076	0.6398	-5.86
257959_at	somatic embryogenesis receptor-l	NIK2	AT3G25560	-1.23	-0.30	-1.27	0.24679174	0.6398	-5.86
254654_at	translation initiation factor eIF4E ;s	EIF4E	AT4G18040	-1.11	-0.15	-1.27	0.24684547	0.6399	-5.86
250835_at	putative protein various predicted	DME	AT5G04560	-1.13	-0.17	-1.27	0.24692563	0.6399	-5.86
251250_at	putative protein pectin methyleste	---	AT3G62180	-1.14	-0.19	-1.27	0.2469323	0.6399	-5.86
248489_at	unknown protein	---	AT5G51090	-1.09	-0.13	-1.27	0.24691188	0.6399	-5.86
250660_at	RNA-binding protein-like	---	AT5G07060	-1.08	-0.12	-1.27	0.24695982	0.6399	-5.86
262428_at	hypothetical protein predicted by g	---	AT1G47570	-1.10	-0.14	-1.27	0.24702968	0.6400	-5.86
261189_at	hypothetical protein contains simila	NACA5	AT1G33040	1.11	0.15	1.27	0.24704049	0.6400	-5.86
251263_at	putative protein DNAJ PROTEIN -	---	AT3G62190	1.11	0.14	1.27	0.24712685	0.6401	-5.86
261939_at	cytochrome c oxidase subunit, put	COX6B	AT1G22450	1.15	0.20	1.27	0.24711464	0.6401	-5.86
261268_at	unknown protein similar to 50S ribo	---	AT1G26740	1.12	0.17	1.27	0.24717132	0.6401	-5.86
265258_at	hypothetical protein predicted by g	---	AT2G20390	1.09	0.12	1.27	0.24734191	0.6404	-5.86
262193_at	eukaryotic initiation factor 5 (eIF-5	---	AT1G77840	-1.16	-0.21	-1.27	0.24735799	0.6404	-5.86
245662_at	hypothetical protein predicted by g	---	AT1G28190	1.47	0.55	1.27	0.24741009	0.6405	-5.86
251459_at	putative protein hypothetical prote	---	AT3G60200	1.33	0.41	1.27	0.24750815	0.6405	-5.86
263434_at	putative homeodomain transcriptio	PRS	AT2G28610	1.09	0.12	1.27	0.24749774	0.6405	-5.86
263446_at	putative SET-domain transcriptiona	ATX1	AT2G31650	1.12	0.16	1.27	0.24747291	0.6405	-5.86
250996_at	putative protein BcDNA.LD24793,	---	AT5G02530	1.10	0.13	1.27	0.24756811	0.6406	-5.86
263218_at	putative serine/threonine protein k	---	AT1G30570	1.14	0.19	1.27	0.24760091	0.6406	-5.86
263903_at	putative touch-induced calmodulin	---	AT2G36180	1.09	0.13	1.27	0.24762983	0.6406	-5.86
267399_at	hypothetical protein predicted by g	---	AT2G44195	-1.08	-0.12	-1.27	0.24777343	0.6407	-5.86

AFFX-Athal-Ub	Arabidopsis thaliana /REF=U8496	---	---	-1.12	-0.16	-1.27	0.24774963	0.6407	-5.86
259601_s_at	CACTA-element transposase, put	---	---	-1.10	-0.13	-1.27	0.24774604	0.6407	-5.86
255782_at	transcription factor identical to tran	MP	AT1G19850	-1.23	-0.30	-1.27	0.24773113	0.6407	-5.86
245859_at	serine (threonine) protein kinase -	ATNEK3	AT5G28290	-1.18	-0.24	-1.26	0.24806182	0.6408	-5.86
255077_at	putative protein	---	AT4G09150	-1.17	-0.23	-1.26	0.24798321	0.6408	-5.86
255522_at	putative GTP pyrophosphokinase	RSH1	AT4G02260	-1.11	-0.16	-1.26	0.24811078	0.6408	-5.86
259914_at	hypothetical protein predicted by g	---	AT1G72640	1.14	0.18	1.26	0.2480255	0.6408	-5.86
249740_at	unknown protein	---	AT5G24500	-1.16	-0.21	-1.26	0.24809315	0.6408	-5.86
248435_at	oleosin-like	OLEO3	AT5G51210	-1.13	-0.17	-1.26	0.24805064	0.6408	-5.86
249013_at	receptor-like protein kinase	GSO2	AT5G44700	1.08	0.11	1.26	0.24808493	0.6408	-5.86
248960_at	subtilisin-like protease	---	AT5G45640	1.16	0.21	1.27	0.24787411	0.6408	-5.86
249460_at	v-SNARE - like protein v-SNARE	---	AT5G39630	-1.11	-0.15	-1.26	0.24806166	0.6408	-5.86
257286_s_at	transposase, putative similar to tra	---	AT1G19260	1.12	0.16	1.27	0.24788902	0.6408	-5.86
AFFX-r2-Ec-bio	E. coli /GEN=bioB /DB_XREF=gb:	---	---	-1.28	-0.36	-1.26	0.24792831	0.6408	-5.86
250900_at	putative protein ; supported by cD	ATB' ALPH	AT5G03470	1.15	0.20	1.26	0.24821083	0.6408	-5.86
259978_at	putative cell division control protein	CDKB2;1	AT1G76540	1.17	0.23	1.26	0.24828335	0.6408	-5.86
AFFX-Athal-Ub	Arabidopsis thaliana /REF=U8496	---	---	-1.12	-0.16	-1.26	0.2481836	0.6408	-5.86
265282_at	unknown protein	---	AT2G20380	-1.10	-0.14	-1.26	0.24827283	0.6408	-5.86
254152_at	hypothetical protein	---	AT4G24410	-1.09	-0.13	-1.26	0.24832078	0.6408	-5.86
250025_at	putative protein similar to unknown	SIP1;2	AT5G18290	1.15	0.20	1.26	0.24833267	0.6408	-5.86
262470_at	disease resistance protein, putativ	---	AT1G50180	-1.11	-0.15	-1.26	0.24831088	0.6408	-5.86
256936_at	prefoldin-like protein similar to pre	PDF2	AT3G22480	1.11	0.14	1.26	0.24839997	0.6410	-5.86
266378_at	hypothetical protein predicted by g	---	AT2G14700	-1.13	-0.17	-1.26	0.24847671	0.6410	-5.86
246353_s_at	hypothetical protein	---	---	-1.09	-0.13	-1.26	0.24848159	0.6410	-5.86
254081_at	putative protein various predicted	---	AT4G25660	-1.13	-0.17	-1.26	0.24861513	0.6411	-5.86
261133_at	DYW7 protein identical to DYW7 p	---	AT1G19715	-1.17	-0.23	-1.26	0.24857482	0.6411	-5.86
246319_at	putative protein HYPOTHETICAL	---	AT3G56680	1.10	0.14	1.26	0.24857501	0.6411	-5.86
253991_at	putative nucleic acid binding prote	PEP	AT4G26000	1.10	0.14	1.26	0.24859712	0.6411	-5.86
262037_at	hypothetical protein predicted by g	---	---	-1.11	-0.15	-1.26	0.24866093	0.6411	-5.86
257760_s_at	putative AC-like transposase simil	---	---	-1.10	-0.14	-1.26	0.24871323	0.6412	-5.87
245550_at	cytochrome P450 like protein	CYP705A1	AT4G15330	-1.11	-0.14	-1.26	0.24877427	0.6413	-5.87
265458_at	unknown protein ;supported by ful	---	AT2G46580	-1.12	-0.17	-1.26	0.24880864	0.6413	-5.87
250698_at	putative protein similar to unknown	---	AT5G06810	-1.09	-0.13	-1.26	0.24898201	0.6417	-5.87
259784_at	auxin-induced protein, putative sir	---	AT1G29450	1.24	0.31	1.26	0.24903789	0.6417	-5.87
251778_at	putative protein various predicted	ROPGEF6	AT3G55660	-1.13	-0.18	-1.26	0.24914438	0.6418	-5.87

251410_at	uclacyanin 3 ; supported by cDNA	UCC3	AT3G60280	-1.09	-0.13	-1.26	0.24910949	0.6418	-5.87
267233_s_at	unknown protein	---	AT2G43910	1.16	0.22	1.26	0.24916406	0.6418	-5.87
253460_at	hypothetical protein	---	AT4G32130	1.13	0.18	1.26	0.2492572	0.6419	-5.87
251019_at	putative protein predicted proteins	---	AT5G02420	-1.12	-0.16	-1.26	0.24923314	0.6419	-5.87
266139_at	Expressed protein ; supported by f	---	AT2G28085	1.24	0.30	1.26	0.24929468	0.6419	-5.87
251164_s_at	putative protein protein phosphata	---	AT3G63320	1.12	0.16	1.26	0.24931373	0.6419	-5.87
246985_at	putative protein contains similarity	---	AT5G67290	-1.11	-0.16	-1.26	0.24936116	0.6419	-5.87
267072_at	unknown protein	---	AT2G41170	-1.13	-0.18	-1.26	0.24941689	0.6419	-5.87
250000_at	putative protein PGPD14 - Petunia	---	AT5G18650	1.15	0.20	1.26	0.24938425	0.6419	-5.87
254407_at	receptor kinase - like protein recep	---	AT4G21370	-1.11	-0.15	-1.26	0.24942645	0.6419	-5.87
254852_at	putative disease resistance protei	WRKY19	AT4G12020	-1.08	-0.11	-1.26	0.24951756	0.6420	-5.87
262684_s_at	vacuolar ATP synthase subunit B i	---	AT1G20260	-1.13	-0.17	-1.26	0.24952598	0.6420	-5.87
253392_at	potassium channel protein AtKC p	ATKC1	AT4G32650	1.38	0.47	1.26	0.24963892	0.6420	-5.87
257213_at	mitochondrial NAD-dependent ma	---	AT3G15020	-1.19	-0.26	-1.26	0.24960756	0.6420	-5.87
256377_at	hypothetical protein	---	AT1G66650	-1.09	-0.12	-1.26	0.24963624	0.6420	-5.87
252530_at	putative protein several oxidases,	---	AT3G46500	-1.11	-0.15	-1.26	0.24957347	0.6420	-5.87
250201_at	ankyrin - like protein 270 kDa anky	---	AT5G14230	-1.29	-0.36	-1.26	0.24996107	0.6428	-5.87
245553_at	lupeol synthase like protein	BARS1	AT4G15370	-1.09	-0.12	-1.26	0.2499897	0.6428	-5.87
264544_s_at	unknown protein	---	AT1G55790	-1.10	-0.13	-1.26	0.25001924	0.6428	-5.87
265311_at	hypothetical protein predicted by g	---	AT2G20250	1.18	0.24	1.26	0.25012283	0.6430	-5.87
248171_at	putative protein similar to unknown	ILR3	AT5G54680	1.09	0.12	1.26	0.25040751	0.6435	-5.87
266770_at	putative expansin Experimental ev	ATEXPA15	AT2G03090	-1.18	-0.24	-1.26	0.25038643	0.6435	-5.87
264782_at	putative transcription factor similar	MYB60	AT1G08810	-1.14	-0.19	-1.26	0.25035981	0.6435	-5.87
261838_at	heat shock protein hsp70, putative	Hsp70b	AT1G16030	-1.11	-0.15	-1.26	0.25045847	0.6436	-5.87
256371_at	hypothetical protein	---	AT1G66770	-1.10	-0.14	-1.26	0.25051884	0.6436	-5.87
267143_at	putative peptide/amino acid transp	---	AT2G38100	-1.11	-0.15	-1.26	0.25053983	0.6436	-5.87
256872_at	non-phototropic hypocotyl, putativ	---	AT3G26490	1.10	0.14	1.26	0.25050811	0.6436	-5.87
265097_at	unknown protein	BARD1	AT1G04020	1.17	0.23	1.26	0.25061074	0.6437	-5.87
258996_at	putative ribosome recycling factor	---	AT3G01800	-1.14	-0.19	-1.26	0.25068521	0.6437	-5.87
258048_at	FtsH protease, putative contains s	EMB2083	AT3G16290	-1.11	-0.15	-1.26	0.25068516	0.6437	-5.87
254981_at	putative alpha NAC stong similarit	---	AT4G10480	1.19	0.25	1.26	0.2507333	0.6438	-5.87
255917_at	putative protein	---	AT5G28560	-1.08	-0.11	-1.26	0.25075518	0.6438	-5.87
257078_at	putative MAP kinase very similar to	---	AT3G15220	1.10	0.14	1.26	0.25081635	0.6438	-5.87
258126_at	hypothetical protein predicted by g	---	AT3G24490	1.12	0.16	1.26	0.25092668	0.6439	-5.87
245368_at	hypothetical protein ; supported by	---	AT4G15510	1.18	0.24	1.26	0.25090266	0.6439	-5.87

266113_x_at	hypothetical protein predicted by g	---	---	-1.12	-0.17	-1.26	0.25091023	0.6439	-5.87
248922_at	putative protein contains similarity	WOX8	AT5G45980	-1.09	-0.13	-1.26	0.25115193	0.6443	-5.87
254659_at	starch synthase-like protein bacte	SS4	AT4G18240	-1.18	-0.24	-1.26	0.25114144	0.6443	-5.87
260954_at	glyoxalase II isozyme, putative sir	GLX2-4	AT1G06130	1.13	0.17	1.26	0.25124781	0.6444	-5.87
258060_at	protein phosphatase 2A regulatory	ATB' DELT	AT3G26030	1.09	0.12	1.26	0.2512671	0.6444	-5.87
258125_s_at	hypothetical protein contains Pfam	---	AT3G23510	-1.30	-0.37	-1.26	0.25123141	0.6444	-5.87
248096_at	embryo-specific protein 1; Ca2+-bi	---	AT5G55240	-1.10	-0.14	-1.25	0.25133137	0.6444	-5.87
251745_at	putative protein zinc finger transcr	SZF1	AT3G55980	1.73	0.79	1.25	0.25132893	0.6444	-5.87
259326_at	putative mitochondrial processing	MPPalpha	AT3G16480	1.09	0.13	1.25	0.25137456	0.6445	-5.87
248815_at	putative protein contains similarity	---	AT5G46920	-1.16	-0.21	-1.25	0.25148458	0.6445	-5.87
258083_at	Expressed protein ; supported by f	---	AT3G25855	1.12	0.16	1.25	0.25147526	0.6445	-5.87
252146_at	putative protein steroid sulfotransf	---	AT3G51210	-1.08	-0.11	-1.25	0.25148803	0.6445	-5.87
252298_at	putative protein various predicted	---	AT3G49060	-1.09	-0.13	-1.25	0.25155514	0.6446	-5.87
254737_at	fatty acid elongase - like protein (c	---	AT4G13840	-1.32	-0.40	-1.25	0.25173741	0.6450	-5.88
263275_at	putative methylmalonate semi-alde	ALDH6B2	AT2G14170	1.16	0.21	1.25	0.25201989	0.6451	-5.88
252526_at	putative protein ethylene-forming	---	AT3G46480	-1.13	-0.18	-1.25	0.25196493	0.6451	-5.88
261436_at	protein kinase, putative (fragment	---	AT1G07870	-1.16	-0.21	-1.25	0.25193117	0.6451	-5.88
266714_at	NAM (no apical meristem)-like prot	EMB2301	AT2G46770	-1.11	-0.15	-1.25	0.2518876	0.6451	-5.88
246542_at	transcriptional regulatory - like pro	SNL2	AT5G15020	1.13	0.18	1.25	0.25185823	0.6451	-5.88
255548_at	putative CHP-rich zinc finger prote	---	AT4G01930	-1.08	-0.12	-1.25	0.25189226	0.6451	-5.88
250708_at	Expressed protein ; supported by f	RBE	AT5G06070	-1.10	-0.13	-1.25	0.25198386	0.6451	-5.88
260711_at	myosin, putative similar to myosin	MYA1	AT1G17580	1.12	0.17	1.25	0.25179328	0.6451	-5.88
260763_at	RING-H2 finger protein RHA3a, p	---	AT1G49220	1.08	0.11	1.25	0.25203992	0.6451	-5.88
265076_at	Rubisco subunit binding-protein be	CPN60B	AT1G55490	1.20	0.26	1.25	0.25198935	0.6451	-5.88
249392_at	peroxidase ATP26a	---	AT5G40150	1.12	0.17	1.25	0.25207158	0.6451	-5.88
257047_at	hypothetical protein predicted by g	---	AT3G19570	1.15	0.21	1.25	0.25221538	0.6452	-5.88
248282_at	unknown protein ;supported by ful	---	AT5G52900	1.40	0.49	1.25	0.25219828	0.6452	-5.88
245901_at	HOMEOBOX PROTEIN KNOTTEL	KNAT4	AT5G11060	-1.17	-0.22	-1.25	0.25221103	0.6452	-5.88
254188_at	UDPglucose 4-epimerase - like pr	UGE2	AT4G23920	-1.24	-0.32	-1.25	0.25227694	0.6453	-5.88
253178_at	putative protein predicted protein,	---	AT4G35170	-1.12	-0.17	-1.25	0.25225844	0.6453	-5.88
263193_at	acetyl-CoA carboxylase, putative	---	AT1G36050	1.10	0.14	1.25	0.25235832	0.6453	-5.88
254409_at	serine/threonine protein kinase - li	---	AT4G21400	-1.40	-0.48	-1.25	0.25236485	0.6453	-5.88
264315_at	aromatic rich glycoprotein, putativ	---	AT1G70370	-1.42	-0.51	-1.25	0.25243831	0.6454	-5.88
253805_at	putative protein	---	AT4G28260	1.13	0.17	1.25	0.25241528	0.6454	-5.88
265143_at	unknown protein	NFU5	AT1G51390	1.12	0.17	1.25	0.25259354	0.6456	-5.88

252964_at	receptor-like protein kinase - like p	---	AT4G38830	-1.10	-0.14	-1.25	0.25256908	0.6456	-5.88
261863_at	unknown protein ; supported by cD	---	AT1G50630	1.14	0.19	1.25	0.25266258	0.6457	-5.88
256097_at	unknown protein	---	AT1G13670	1.09	0.12	1.25	0.25268508	0.6457	-5.88
265325_at	putative integral membrane protein	---	AT2G18240	1.14	0.18	1.25	0.25282367	0.6460	-5.88
255062_at	hypothetical protein	---	AT4G08940	1.13	0.17	1.25	0.2528549	0.6460	-5.88
264284_at	protein kinase, putative similar to p	---	AT1G61860	-1.11	-0.15	-1.25	0.25289422	0.6460	-5.88
254083_at	PROTEIN TRANSPORT PROTEI	---	AT4G24920	1.16	0.21	1.25	0.25293757	0.6461	-5.88
256212_at	hypothetical protein	---	AT1G50970	-1.12	-0.16	-1.25	0.25305905	0.6463	-5.88
254830_at	putative protein predicted protein,	---	AT4G12590	1.08	0.11	1.25	0.25311916	0.6463	-5.88
265065_at	putative phytochelatin synthase	ATPCS2	AT1G03980	1.09	0.13	1.25	0.25309187	0.6463	-5.88
255102_s_at	putative MuDR-A-like transposon p	---	---	-1.12	-0.16	-1.25	0.25317718	0.6464	-5.88
255286_at	see T14P8.10 (GB:AF069298)	---	AT4G04650	-1.15	-0.21	-1.25	0.25329829	0.6466	-5.88
253024_at	putative protein	---	AT4G38080	1.57	0.65	1.25	0.25329328	0.6466	-5.88
255434_at	predicted protein of unknown funct	---	AT4G03180	1.11	0.15	1.25	0.25335292	0.6466	-5.88
251064_at	putative zinc finger protein several	---	AT5G01860	-1.11	-0.15	-1.25	0.25338117	0.6466	-5.88
257869_at	ER lumen protein retaining recept	---	AT3G25160	-1.09	-0.12	-1.25	0.25342164	0.6467	-5.88
259916_at	hypothetical protein predicted by g	---	AT1G72600	1.08	0.11	1.25	0.25344408	0.6467	-5.88
256569_at	hypothetical protein ; supported by	---	AT3G19550	1.34	0.42	1.25	0.25354352	0.6468	-5.88
258789_at	Mutator-like transposase similar to	---	---	1.11	0.15	1.25	0.25361009	0.6468	-5.88
249245_at	putative protein contains similarity	---	AT5G42280	-1.15	-0.20	-1.25	0.25359498	0.6468	-5.88
260709_at	hypothetical protein predicted by g	ATNAP6	AT1G32500	-1.12	-0.16	-1.25	0.25358347	0.6468	-5.88
258031_s_at	hypothetical protein similar to hypo	---	AT3G27480 /	-1.13	-0.18	-1.25	0.25369168	0.6469	-5.88
257124_at	hexokinase, putative similar to hex	ATHXK4	AT3G20040	-1.10	-0.14	-1.25	0.25370995	0.6469	-5.88
264259_at	hypothetical protein This gene is c	---	AT1G09290	1.17	0.22	1.25	0.25383478	0.6471	-5.88
247303_at	histidinol dehydrogenase ;support	ATHDH	AT5G63890	1.15	0.20	1.25	0.25387488	0.6472	-5.88
266504_at	hypothetical protein predicted by g	---	AT2G47820	1.12	0.17	1.25	0.25391037	0.6472	-5.88
267503_at	unknown protein ; supported by fu	---	AT2G45600	1.18	0.24	1.25	0.25419419	0.6473	-5.88
259513_at	hypothetical protein ; supported by	ARK3	AT1G12430	-1.11	-0.15	-1.25	0.25406066	0.6473	-5.88
251602_at	Expressed protein ; supported by f	---	AT3G57785	1.10	0.14	1.25	0.25422702	0.6473	-5.88
256299_at	expansin (At-EXP1) identical to ex	ATEXPA1	AT1G69530	1.55	0.63	1.25	0.25406266	0.6473	-5.88
261509_at	hypothetical protein predicted by g	---	AT1G71740	-1.15	-0.20	-1.25	0.25402662	0.6473	-5.88
258235_at	alternative oxidase 1c precursor id	AOX1C	AT3G27620	-1.12	-0.16	-1.25	0.25418296	0.6473	-5.88
259108_at	putative translationally controlled tu	---	AT3G05540	-1.09	-0.13	-1.25	0.25426964	0.6473	-5.88
254823_at	putative protein predicted protein	---	AT4G12580	1.08	0.12	1.25	0.2542754	0.6473	-5.88
252122_at	putative protein hypothetical prote	---	AT3G51140	1.11	0.15	1.25	0.25419361	0.6473	-5.88

251046_at	kinesin -like protein kinesin, Xeno	---	AT5G02370	1.09	0.12	1.25	0.25415272	0.6473	-5.88
263176_at	UDP-glucose:indole-3-acetate bet	UGT75B2	AT1G05530	-1.10	-0.14	-1.25	0.25429456	0.6473	-5.88
245690_at	phenylalanine ammonia-lyase PAL	PAL3	AT5G04230	1.21	0.27	1.25	0.25409269	0.6473	-5.88
246804_at	putative protein	---	---	1.09	0.12	1.25	0.25439424	0.6475	-5.88
256399_at	hypothetical protein predicted by g	---	AT3G06240	-1.10	-0.14	-1.25	0.25442409	0.6475	-5.88
264106_at	unknown protein	SERK4	AT2G13790	-1.10	-0.13	-1.25	0.25454189	0.6477	-5.88
252508_at	putative protein tRNA nucleotidylt	---	AT3G46210	1.17	0.23	1.25	0.25460356	0.6478	-5.88
266206_at	unknown protein ; supported by fu	---	AT2G27730	-1.14	-0.19	-1.25	0.25465389	0.6478	-5.88
262075_at	hypothetical protein contains simila	ZCF61	AT1G59560	1.17	0.22	1.25	0.25466369	0.6478	-5.88
251791_at	expansin-like protein expansin At-	ATEXPA16	AT3G55500	1.27	0.34	1.25	0.25469421	0.6478	-5.89
247140_at	putative protein similar to unknown	---	AT5G66250	1.10	0.14	1.25	0.2547325	0.6478	-5.89
248932_at	peptide transporter	PTR3	AT5G46050	1.45	0.53	1.24	0.25480666	0.6480	-5.89
265882_at	putative copper amine oxidase	---	AT2G42490	1.16	0.21	1.24	0.25485139	0.6480	-5.89
264838_at	putative AHP2 similar to GB:BAA3	AHP5	AT1G03430	1.08	0.11	1.24	0.25510681	0.6486	-5.89
263635_at	hypothetical protein predicted by g	---	---	-1.08	-0.11	-1.24	0.25515959	0.6486	-5.89
250141_at	protein kinase MSK-3 - like protein	SK13	AT5G14640	-1.13	-0.17	-1.24	0.25526598	0.6488	-5.89
248791_at	palmitoyl-protein thioesterase prec	---	AT5G47350	-1.08	-0.11	-1.24	0.25526092	0.6488	-5.89
260570_at	stearoyl-ACP desaturase ; suppor	SSI2	AT2G43710	1.16	0.21	1.24	0.25530056	0.6488	-5.89
259663_at	hypothetical protein predicted by g	PRA7	AT1G55190	1.13	0.17	1.24	0.25538855	0.6489	-5.89
256488_at	hypothetical protein	NFD4	AT1G31470	-1.10	-0.14	-1.24	0.25545782	0.6490	-5.89
263016_at	ubiquitin extension protein, putativ	---	AT1G23410	1.12	0.16	1.24	0.255459	0.6490	-5.89
257524_at	hypothetical protein similar to puta	DEL3	AT3G01330	1.12	0.16	1.24	0.25553916	0.6491	-5.89
246749_at	putative protein ; supported by cD	---	AT5G27830	1.15	0.20	1.24	0.2556068	0.6491	-5.89
260756_at	hypothetical protein contains simil	---	AT1G48970	-1.09	-0.12	-1.24	0.25558422	0.6491	-5.89
265905_at	putative transcription elongation fa	---	AT2G25640	-1.09	-0.12	-1.24	0.25575016	0.6493	-5.89
246361_s_at	hypothetical protein	---	---	-1.09	-0.13	-1.24	0.2557772	0.6493	-5.89
266829_at	hypothetical protein predicted by g	---	AT2G22940	1.08	0.11	1.24	0.2557402	0.6493	-5.89
261192_at	NAM protein, putative similar to N	ANAC13	AT1G32870	-1.15	-0.20	-1.24	0.25587788	0.6493	-5.89
255232_at	putative protein phosphatidylinosit	AGD13	AT4G05330	-1.15	-0.20	-1.24	0.25599739	0.6493	-5.89
249785_at	soluble starch synthase	SSI1	AT5G24300	-1.11	-0.15	-1.24	0.25590716	0.6493	-5.89
253131_at	homeodomain - like protein severa	WOX13	AT4G35550	-1.13	-0.17	-1.24	0.25596015	0.6493	-5.89
249559_at	putative protein	---	AT5G38320	1.15	0.20	1.24	0.25585803	0.6493	-5.89
246430_at	calmodulin-like protein calmodulin	---	AT5G17470	-1.10	-0.13	-1.24	0.2559912	0.6493	-5.89
245974_at	putative protein	---	---	-1.17	-0.23	-1.24	0.25600587	0.6493	-5.89
256111_at	unknown protein	---	AT1G16820	1.12	0.17	1.24	0.25582891	0.6493	-5.89

246699_at	putative protein predicted proteins	---	AT5G27990	1.15	0.21	1.24	0.25611786	0.6495	-5.89
246715_at	putative protein glucose-6-phosph	---	AT5G28230	-1.14	-0.19	-1.24	0.25612721	0.6495	-5.89
250408_at	serine/threonine protein kinase -lik	CIPK5	AT5G10930	-1.19	-0.25	-1.24	0.25619574	0.6495	-5.89
266129_at	hypothetical protein predicted by g	CCD7	AT2G44990	-1.37	-0.46	-1.24	0.25621882	0.6495	-5.89
250289_at	putative protein ;supported by full-	---	AT5G13190	-1.27	-0.34	-1.24	0.25616388	0.6495	-5.89
266613_at	similar to gibberellin-regulated prot	---	AT2G14900	-2.52	-1.33	-1.24	0.25625481	0.6495	-5.89
249985_at	Ser/Thr specific protein kinase - lik	---	AT5G18500	-1.13	-0.18	-1.24	0.2563354	0.6496	-5.89
265472_at	putative RING-H2 zinc finger prote	---	AT2G15580	1.13	0.17	1.24	0.25638057	0.6496	-5.89
258551_at	hypothetical protein predicted by g	---	AT3G06890	-1.08	-0.11	-1.24	0.25634531	0.6496	-5.89
247310_at	putative protein contains similarity	CHR24	AT5G63950	1.15	0.20	1.24	0.25638511	0.6496	-5.89
249433_at	putative protein hypothetical prote	---	AT5G39940	1.15	0.20	1.24	0.25645785	0.6496	-5.89
252609_at	putative protein	---	AT3G45110	-1.10	-0.14	-1.24	0.25644174	0.6496	-5.89
254646_at	putative protein	---	AT4G18530	-1.14	-0.19	-1.24	0.25664054	0.6498	-5.89
253023_at	hypothetical protein	---	AT4G38070	-1.14	-0.19	-1.24	0.25662718	0.6498	-5.89
260293_at	unknown protein predicted by gen	---	AT1G63670	-1.13	-0.17	-1.24	0.25663867	0.6498	-5.89
254587_at	resistance protein RPP5 - like dov	---	AT4G19520	-1.12	-0.16	-1.24	0.25662328	0.6498	-5.89
246423_at	putative protein ribosomal protein	---	AT5G16950	1.14	0.19	1.24	0.25667028	0.6498	-5.89
262675_at	anter-specific proline-rich -like prot	EXL6	AT1G75930	-1.12	-0.16	-1.24	0.25676116	0.6500	-5.89
267064_at	calmodulin (cam2)	CAM2	AT2G41110	1.22	0.29	1.24	0.25680082	0.6500	-5.89
250924_at	putative protein ;supported by full-	---	AT5G03440	-1.11	-0.15	-1.24	0.25687029	0.6501	-5.89
248891_at	MCM3 homolog (emb|CAA03887.1	MCM3	AT5G46280	1.48	0.56	1.24	0.25691199	0.6501	-5.89
250595_at	unknown protein	---	AT5G07770	1.17	0.22	1.24	0.25707528	0.6503	-5.89
266931_at	putative non-LTR retroelement rev	---	---	-1.10	-0.14	-1.24	0.25709541	0.6503	-5.89
261080_at	proliferating cellular nuclear antige	PCNA1	AT1G07370	1.48	0.57	1.24	0.25711718	0.6503	-5.89
256941_at	hypothetical protein	---	---	-1.12	-0.16	-1.24	0.25708863	0.6503	-5.89
266653_at	hypothetical protein predicted by g	---	AT2G25740	-1.11	-0.16	-1.24	0.25732302	0.6507	-5.89
250252_at	transporter-like protein ;supported	ZIFL1	AT5G13750	-1.42	-0.50	-1.24	0.25731061	0.6507	-5.89
263989_at	putative MAP kinase ; supported b	ATMPK20	AT2G42880	-1.16	-0.21	-1.24	0.25747388	0.6509	-5.89
267391_at	putative beta-glucosidase	BGLU17	AT2G44480	-1.16	-0.21	-1.24	0.25743988	0.6509	-5.89
266830_at	1-aminocyclopropane-1-carboxylat	ACS4	AT2G22810	1.47	0.55	1.24	0.2575027	0.6509	-5.89
247233_at	mitochondrial carrier protein-like	---	AT5G64970	-1.12	-0.16	-1.24	0.25757011	0.6509	-5.89
245658_at	hypothetical protein predicted by g	RALFL4	AT1G28270	1.09	0.13	1.24	0.25754213	0.6509	-5.89
246276_at	Cu2+-transporting ATPase-like pro	HMA1	AT4G37270	-1.09	-0.13	-1.24	0.25753747	0.6509	-5.89
264675_at	putative phosphoribosylglycinamid	---	AT1G09830	1.10	0.13	1.24	0.2578613	0.6510	-5.90
262558_at	Expressed protein ; supported by f	---	AT1G31335	1.11	0.16	1.24	0.25779662	0.6510	-5.90

251557_at	v-ATPase subunit D (vATPD) ; su	---	AT3G58730	-1.10	-0.14	-1.24	0.25774458	0.6510	-5.90
251662_at	putative protein DNA-DIRECTED	NRPE5	AT3G57080	1.13	0.18	1.24	0.25780872	0.6510	-5.90
254811_at	putative protein 2-hydroxy-6-oxoh	---	AT4G12230	1.11	0.15	1.24	0.25778198	0.6510	-5.90
262410_at	MAGE protein, putative identical t	---	AT1G34770	1.18	0.24	1.24	0.25791187	0.6510	-5.90
252851_at	putative protein CLATHRIN COAT	---	AT4G40080	1.29	0.36	1.24	0.25769781	0.6510	-5.89
254400_at	kinesin-related protein katA ; supp	ATK1	AT4G21270	-1.08	-0.12	-1.24	0.2576578	0.6510	-5.89
248751_at	putative protein similar to unknown	---	AT5G47540	1.11	0.15	1.24	0.25774511	0.6510	-5.90
254113_at	hypothetical protein	---	AT4G24900	-1.11	-0.15	-1.24	0.25786033	0.6510	-5.90
255399_at	hypothetical protein	---	---	-1.12	-0.17	-1.24	0.25790655	0.6510	-5.90
246049_at	putative protein predicted proteins	---	---	-1.12	-0.16	-1.24	0.25794107	0.6510	-5.90
259881_at	Expressed protein ; supported by c	---	AT1G76820	1.16	0.21	1.24	0.25800394	0.6511	-5.90
255887_at	hypothetical protein contains Pfam	---	AT1G20370	-1.09	-0.12	-1.24	0.25802785	0.6511	-5.90
256897_at	hypothetical protein predicted by g	---	AT3G24640	-1.09	-0.12	-1.24	0.25810418	0.6512	-5.90
264378_at	hypothetical protein predicted by g	---	AT2G25220	-1.31	-0.39	-1.24	0.2581608	0.6512	-5.90
264097_s_at	NADH dehydrogenase, putative si	---	AT1G16700 /	1.10	0.14	1.24	0.25815185	0.6512	-5.90
247547_at	putative protein	---	AT5G61360	1.17	0.23	1.24	0.25819837	0.6512	-5.90
246547_at	seed maturation -like protein seed	---	AT5G14970	-1.14	-0.19	-1.23	0.25823261	0.6512	-5.90
263010_at	T76725 come from this gene.	---	AT1G23330	-1.09	-0.13	-1.23	0.2582665	0.6512	-5.90
263015_at	hypothetical protein similar to hypo	---	AT1G23440	1.11	0.16	1.23	0.2584063	0.6514	-5.90
251913_at	putative protein several malat dehy	---	AT3G53910	-1.09	-0.13	-1.23	0.25840195	0.6514	-5.90
251739_at	putative protein protein of unknow	CAN	AT3G56170	1.14	0.19	1.23	0.25844252	0.6515	-5.90
249662_s_at	putative protein hypothetical protei	---	AT5G36680 /	-1.08	-0.11	-1.23	0.25852848	0.6515	-5.90
266353_at	unknown protein ;supported by ful	MLP328	AT2G01520	1.18	0.24	1.23	0.25857404	0.6515	-5.90
258191_at	putative vesicle transport protein s	VTI13	AT3G29100	-1.09	-0.12	-1.23	0.25855012	0.6515	-5.90
247631_at	putative MADS box protein variou	AGL62	AT5G60440	1.08	0.11	1.23	0.25851029	0.6515	-5.90
245356_at	adenosylhomocysteinase ;support	MEE58	AT4G13940	1.16	0.21	1.23	0.25865157	0.6516	-5.90
255563_at	putative CHP-rich zinc finger prote	---	AT4G01740	1.10	0.13	1.23	0.25870049	0.6517	-5.90
253660_at	putative protein proline-rich protei	---	AT4G30140	-1.10	-0.13	-1.23	0.25874702	0.6517	-5.90
252625_at	putative histone deacetylase simila	HDA3	AT3G44750	1.32	0.40	1.23	0.25882675	0.6518	-5.90
254240_at	Expressed protein ; supported by f	SP1L5	AT4G23496	-1.10	-0.14	-1.23	0.25881036	0.6518	-5.90
257675_at	ethylene responsive element bind	ERF7	AT3G20310	1.13	0.17	1.23	0.25885156	0.6518	-5.90
267575_at	unknown protein predicted by gens	---	AT2G30690	-1.11	-0.15	-1.23	0.25888954	0.6518	-5.90
249876_at	putative protein similar to unknown	CaS	AT5G23060	-1.13	-0.17	-1.23	0.2589477	0.6519	-5.90
245962_at	putative protein predicted proteins	---	AT5G19700	-1.11	-0.15	-1.23	0.2590724	0.6521	-5.90
255919_at	putative protein	---	---	-1.10	-0.14	-1.23	0.25917488	0.6522	-5.90

263478_at	putative receptor-like protein kinas	---	AT2G31880	1.34	0.42	1.23	0.25916377	0.6522	-5.90
251024_at	putative protein hypothetical protei	---	AT5G02180	-1.13	-0.17	-1.23	0.25920401	0.6522	-5.90
251102_at	putative transporter protein Na+/H-	CHX27	AT5G01690	-1.16	-0.22	-1.23	0.25923827	0.6522	-5.90
257130_at	vacuolar processing enzyme/aspa	DELTA-VPI	AT3G20210	1.08	0.11	1.23	0.25930106	0.6523	-5.90
259666_at	unknown protein ; supported by cD	SR33	AT1G55310	1.10	0.14	1.23	0.25938546	0.6525	-5.90
254553_at	TMV resistance protein N - like TM	---	AT4G19530	-1.21	-0.27	-1.23	0.25953676	0.6526	-5.90
261086_at	hypothetical protein predicted by g	TRFL3	AT1G17460	1.09	0.12	1.23	0.25950648	0.6526	-5.90
263632_at	Expressed protein ; supported by c	---	AT2G04795	-1.30	-0.38	-1.23	0.25952278	0.6526	-5.90
262434_at	lysine and histidine specific transp	---	AT1G47670	1.21	0.27	1.23	0.25957795	0.6527	-5.90
247275_at	beta-ureidopropionase	BETA-UP	AT5G64370	1.19	0.25	1.23	0.25964812	0.6528	-5.90
246703_at	mitogen activated protein kinase -	WNK9	AT5G28080	-1.35	-0.44	-1.23	0.25968436	0.6528	-5.90
257503_at	DAG-like protein similar to DAG p	---	AT1G72530	1.14	0.19	1.23	0.2597496	0.6528	-5.90
246187_at	putative protein	AT5G2102(	---	-1.14	-0.19	-1.23	0.25972657	0.6528	-5.90
259003_at	hypothetical protein similar to hyp	---	AT3G02010	-1.16	-0.21	-1.23	0.25978765	0.6528	-5.90
255920_at	putative protein	---	AT5G28590	-1.13	-0.18	-1.23	0.25984504	0.6529	-5.90
259140_at	lycopene beta cyclase identical to	LYC	AT3G10230	1.09	0.13	1.23	0.25990714	0.6530	-5.90
260175_at	neutral invertase, putative similar	---	AT1G72000	-1.09	-0.12	-1.23	0.25998198	0.6531	-5.90
261588_at	hypothetical protein predicted by g	---	AT1G01670	-1.08	-0.11	-1.23	0.26015935	0.6534	-5.90
246075_at	monogalactosyldiacylglycerol synth	MGD2	AT5G20410	1.34	0.43	1.23	0.26016593	0.6534	-5.90
266415_at	putative nonspecific lipid-transfer p	LTP2	AT2G38530	1.60	0.67	1.23	0.26010875	0.6534	-5.90
253397_at	putative protein kinase protein kin	---	AT4G32710	-1.09	-0.12	-1.23	0.26040106	0.6535	-5.90
258989_at	rhodanese-like family protein conta	---	AT3G08920	1.12	0.16	1.23	0.26026362	0.6535	-5.90
263885_at	unknown protein	---	AT2G36940	1.10	0.13	1.23	0.26035451	0.6535	-5.90
249031_at	putative protein contains similarity	---	AT5G44900	-1.12	-0.16	-1.23	0.26042895	0.6535	-5.90
247809_at	unknown protein	---	AT5G58280	-1.11	-0.16	-1.23	0.260332	0.6535	-5.90
245944_at	putative protein various predicted	MSL9	AT5G19520	1.10	0.14	1.23	0.26037242	0.6535	-5.90
244907_at	hypothetical protein	---	---	-1.08	-0.12	-1.23	0.26041597	0.6535	-5.90
248080_at	wax synthase-like protein	---	AT5G55380	-1.13	-0.18	-1.23	0.26052522	0.6537	-5.90
256624_at	hypothetical protein predicted by g	---	AT3G19990	1.10	0.13	1.23	0.26059528	0.6538	-5.90
265523_at	putative Ty3-gypsy-like retroeleme	---	---	-1.09	-0.12	-1.23	0.26066706	0.6539	-5.90
266754_at	hypothetical protein	---	AT2G46980	-1.14	-0.19	-1.23	0.26072037	0.6540	-5.90
245166_at	putative receptor-like protein kinas	---	AT2G33170	1.11	0.15	1.23	0.26080913	0.6541	-5.90
254822_at	polyubiquitin-like protein polyubiqu	UPL5	AT4G12570	-1.10	-0.13	-1.23	0.26088852	0.6542	-5.91
246621_at	putative protein strong similarity to	---	AT5G36230	1.08	0.11	1.23	0.26094285	0.6543	-5.91
246254_at	MAP kinase like protein	ATMPK14	AT4G36450	1.19	0.25	1.23	0.26099913	0.6544	-5.91

245037_at	putative phosphatidylinositol-4-phd	PIP5K3	AT2G26420	-1.08	-0.12	-1.23	0.26112607	0.6546	-5.91
258330_at	unknown protein	ROPGEF13	AT3G16130	-1.11	-0.15	-1.23	0.26126526	0.6547	-5.91
267114_at	Expressed protein ; supported by f	---	AT2G14835	1.10	0.14	1.23	0.26127232	0.6547	-5.91
252543_at	nonphototropic hypocotyl 1 ; supp	PHOT1	AT3G45780	1.09	0.12	1.23	0.26125154	0.6547	-5.91
247104_at	putative protein similar to unknown	DAR6	AT5G66620	1.16	0.21	1.23	0.26119589	0.6547	-5.91
266834_s_at	putative protein phosphatase 2C	---	AT2G05050	1.63	0.71	1.23	0.26141872	0.6549	-5.91
249637_at	hypothetical protein	---	AT5G36900	-1.10	-0.13	-1.23	0.26139715	0.6549	-5.91
248549_at	putative protein contains similarity	---	AT5G50310	1.10	0.14	1.23	0.26150274	0.6550	-5.91
248925_at	GDSL-motif lipase/hydrolase-like p	---	AT5G45910	-1.13	-0.18	-1.23	0.26154115	0.6551	-5.91
254962_at	putative glucanase endo-beta-1,4-	AtGH9C3	AT4G11050	-1.11	-0.15	-1.23	0.26158289	0.6551	-5.91
260913_at	s-adenosylmethionine synthetase i	SAM1	AT1G02500	1.18	0.24	1.22	0.26173044	0.6552	-5.91
247624_at	aspartyl aminopeptidase - like pro	---	AT5G60160	-1.08	-0.11	-1.23	0.26165032	0.6552	-5.91
249273_at	unknown protein	---	AT5G41850	1.12	0.17	1.23	0.26167996	0.6552	-5.91
251908_at	putative protein late embryogenis	---	AT3G53770	-1.11	-0.15	-1.23	0.26171373	0.6552	-5.91
247365_at	putative protein similar to unknown	---	AT5G63220	1.12	0.17	1.22	0.26179522	0.6553	-5.91
254398_at	photosystem II oxygen-evolving c	PSBQA	AT4G21280	1.11	0.15	1.22	0.26189526	0.6555	-5.91
261760_at	hypothetical protein similar to puta	---	AT1G15600	-1.14	-0.19	-1.22	0.26195808	0.6555	-5.91
251824_at	ABC transporter - like protein ATP	---	AT3G55090	-1.11	-0.15	-1.22	0.26198649	0.6555	-5.91
254494_at	putative protein C65DMY30S	QRT3	AT4G20050	-1.09	-0.12	-1.22	0.26198872	0.6555	-5.91
263069_at	unknown protein	---	AT2G17590	-1.21	-0.27	-1.22	0.26208241	0.6556	-5.91
264971_at	Expressed protein ; supported by f	---	AT1G67210	1.08	0.11	1.22	0.26214559	0.6557	-5.91
261803_at	transcription factor, putative simila	NF-YA7	AT1G30500	1.15	0.20	1.22	0.26218704	0.6558	-5.91
258413_at	unknown protein ;supported by ful	---	AT3G17300	1.12	0.16	1.22	0.26242402	0.6563	-5.91
265687_s_at	hypothetical protein predicted by g	---	AT2G24470	-1.09	-0.13	-1.22	0.26250592	0.6564	-5.91
255384_at	hypothetical protein	---	AT4G03580	-1.08	-0.11	-1.22	0.26256689	0.6564	-5.91
263197_at	polyubiquitin, putative similar to p	---	AT1G53930	-1.12	-0.16	-1.22	0.26256897	0.6564	-5.91
246317_at	putative protein unnamed ORF - H	---	AT3G56900	1.16	0.21	1.22	0.26259907	0.6564	-5.91
255004_at	putative protein	---	AT4G09970	1.13	0.18	1.22	0.2626408	0.6565	-5.91
249008_at	putative protein contains similarity	---	AT5G44680	-1.19	-0.25	-1.22	0.26270995	0.6565	-5.91
260542_at	putative FKBP type peptidyl-prolyl	---	AT2G43560	1.19	0.25	1.22	0.26289861	0.6565	-5.91
247166_at	unknown protein	---	AT5G65840	-1.21	-0.28	-1.22	0.26283243	0.6565	-5.91
259819_at	unknown protein ; supported by cD	ATMTK	AT1G49820	1.08	0.11	1.22	0.26289137	0.6565	-5.91
265928_at	Ac-like transposase related to Ac/D	---	---	-1.12	-0.17	-1.22	0.26289369	0.6565	-5.91
245902_at	putative protein Scythe protein, Xe	---	AT5G11080	-1.16	-0.21	-1.22	0.26286451	0.6565	-5.91
255250_at	MYB - like protein cM4 myb transc	AtMYB74	AT4G05100	-1.45	-0.54	-1.22	0.26282705	0.6565	-5.91

260742_at	putative glycerol kinase identical t	IAA34	AT1G15050	1.09	0.12	1.22	0.26275709	0.6565	-5.91
253263_at	abscisic acid responsive elements-	ABF3	AT4G34000	1.25	0.32	1.22	0.26305598	0.6567	-5.91
249942_at	Nitrilase 4 (sp|P46011) ; supporte	GAPB	AT1G42970	-1.92	-0.94	-1.22	0.26303605	0.6567	-5.91
258339_at	putative dynein light chain protein	---	AT3G16120	1.08	0.11	1.22	0.26302712	0.6567	-5.91
262672_at	RNA pseudouridylate synthase, p	---	AT1G76050	1.10	0.14	1.22	0.26310595	0.6568	-5.91
265676_at	putative CCR4-associated factor ;	---	AT2G32070	-1.09	-0.13	-1.22	0.26315521	0.6568	-5.91
246233_at	putative protein	---	AT4G36550	1.30	0.37	1.22	0.26328244	0.6571	-5.91
266305_at	putative DNA polymerase epsilon c	TIL2	AT2G27120	-1.10	-0.14	-1.22	0.2634118	0.6573	-5.91
257882_at	hypothetical protein predicted by g	---	AT3G16930	-1.11	-0.15	-1.22	0.26353816	0.6575	-5.91
247650_at	putative protein ;supported by full-	---	AT5G59960	1.18	0.24	1.22	0.26358244	0.6575	-5.91
253699_at	putative protein patatin-like protei	PLP8	AT4G29800	1.10	0.13	1.22	0.26359198	0.6575	-5.91
265825_at	ubiquitin-like (UBQ7), putative sim	UBQ7	AT2G35635	1.11	0.15	1.22	0.26368727	0.6576	-5.91
252324_at	protein translocation complex sec	---	AT3G48570	-1.11	-0.15	-1.22	0.2637062	0.6576	-5.91
262386_at	hypothetical protein predicted by g	---	AT1G49370	-1.13	-0.18	-1.22	0.26365806	0.6576	-5.91
264983_at	hypothetical protein predicted by g	---	AT1G27240	-1.09	-0.13	-1.22	0.26389906	0.6578	-5.91
252097_at	putative protein hypothetical protei	---	AT3G51090	-1.09	-0.13	-1.22	0.26390564	0.6578	-5.91
259129_at	unknown protein predicted by gen	PTF1	AT3G02150	-1.25	-0.33	-1.22	0.26389671	0.6578	-5.91
254606_at	nodulin-26 - like protein major intri	NLM1	AT4G19030	-1.09	-0.12	-1.22	0.2638908	0.6578	-5.91
266926_at	unknown protein predicted by gens	---	AT2G46000	1.14	0.19	1.22	0.26394531	0.6578	-5.91
255656_at	putative protein (fragment) DNA-b	---	AT4G00990	1.12	0.16	1.22	0.26404615	0.6580	-5.92
262176_at	3-ketoacyl-ACP synthase, putative	FAB1	AT1G74960	1.12	0.17	1.22	0.26405674	0.6580	-5.92
264744_at	hypothetical protein predicted by g	---	AT1G62050	-1.19	-0.25	-1.22	0.26410453	0.6580	-5.92
261936_at	seed maturation protein PM27, pu	---	AT1G22600	-1.15	-0.20	-1.22	0.26423255	0.6583	-5.92
259686_at	transcription factor SCARECROW	---	AT1G63100	-1.16	-0.21	-1.22	0.26426088	0.6583	-5.92
266070_at	hypothetical protein predicted by g	EXLB3	AT2G18660	2.86	1.52	1.22	0.26433046	0.6584	-5.92
245285_s_at	selenium-binding protein like ; sup	SBP1	AT4G14030	-1.09	-0.13	-1.22	0.26445082	0.6585	-5.92
257110_x_at	hypothetical protein	---	---	-1.12	-0.17	-1.22	0.26443648	0.6585	-5.92
249987_at	putative protein predicted proteins	---	AT5G18490	1.17	0.23	1.22	0.26451163	0.6585	-5.92
245434_at	hypothetical protein	---	AT4G17140	-1.09	-0.12	-1.22	0.26450115	0.6585	-5.92
264408_at	hypothetical protein predicted by g	FRS11	AT1G10240	1.10	0.13	1.22	0.26460179	0.6586	-5.92
263121_at	receptor protein kinase, putative s	---	AT1G78530	-1.12	-0.17	-1.22	0.26461287	0.6586	-5.92
265049_at	jasmonate inducible protein, putat	---	AT1G52060	-1.08	-0.12	-1.22	0.2647605	0.6589	-5.92
256133_at	hypothetical protein predicted by g	---	AT1G13570	1.19	0.25	1.22	0.26485793	0.6591	-5.92
248710_at	unknown protein ;supported by ful	---	AT5G48480	-1.14	-0.18	-1.22	0.26521681	0.6597	-5.92
251113_at	hypothetical protein	---	AT5G01370	1.13	0.17	1.21	0.26536867	0.6597	-5.92

245376_at	peroxidase like protein	---	AT4G17690	-1.09	-0.12	-1.21	0.26534346	0.6597	-5.92
252796_at	putative protein predicted proteins	---	---	-1.15	-0.20	-1.21	0.26530404	0.6597	-5.92
248449_at	putative protein similar to unknown	---	AT5G51110	1.09	0.12	1.21	0.26537456	0.6597	-5.92
260677_at	translation elongation factor EF-1	RNL	AT1G07910	1.18	0.24	1.22	0.26522379	0.6597	-5.92
259018_at	unknown protein similar to unknow	AIR12	AT3G07390	-1.38	-0.46	-1.21	0.26529941	0.6597	-5.92
246719_at	homology to many predicted putat	---	---	-1.08	-0.11	-1.21	0.26535675	0.6597	-5.92
256750_at	unknown protein contains Pfam pr	---	AT3G27150	-1.13	-0.18	-1.21	0.26529834	0.6597	-5.92
245188_at	F12A21.19 unknown protein; sim	---	AT1G67660	-1.11	-0.15	-1.22	0.26520459	0.6597	-5.92
263339_at	Mutator-like transposase similar to	---	---	1.08	0.11	1.21	0.2654781	0.6598	-5.92
252897_at	cytochrome P450 - like protein cyt	CYP96A9	AT4G39480	-1.10	-0.14	-1.21	0.26547913	0.6598	-5.92
250499_at	beta-xylosidase - like protein beta	BXL3	AT5G09730	1.10	0.14	1.21	0.26551197	0.6598	-5.92
260161_at	hypothetical protein similar to puta	ROPGEF12	AT1G79860	1.09	0.12	1.21	0.2656113	0.6600	-5.92
257729_at	histone deacetylase, putative cont	HDA15	AT3G18520	1.15	0.20	1.21	0.26570557	0.6601	-5.92
248384_at	mandelonitrile lyase-like protein	---	AT5G51930	-1.09	-0.13	-1.21	0.26572612	0.6601	-5.92
245878_at	hypothetical protein contains simila	---	AT1G26190	-1.12	-0.16	-1.21	0.26577089	0.6602	-5.92
246389_at	amino acid carrier, putative similar	AAP3	AT1G77380	1.15	0.20	1.21	0.26603634	0.6604	-5.92
259519_at	hypothetical protein	---	AT1G12270	1.13	0.18	1.21	0.26614643	0.6604	-5.92
251471_at	putative protein GTPASE-ACTIVA	---	AT3G59570	-1.11	-0.15	-1.21	0.26600204	0.6604	-5.92
248436_at	putative protein contains similarity	---	AT5G51220	-1.10	-0.13	-1.21	0.26626125	0.6604	-5.92
256939_at	multicatalytic endopeptidase comp	PBD1	AT3G22630	1.15	0.20	1.21	0.26598285	0.6604	-5.92
249094_at	dimethylaniline monooxygenase-lik	YUC5	AT5G43890	-1.13	-0.17	-1.21	0.26612475	0.6604	-5.92
251220_at	cytochrome c oxidase subunit 5c-l	---	AT3G62400	1.15	0.20	1.21	0.26604476	0.6604	-5.92
267262_at	putative serine carboxypeptidase I	SNG1	AT2G22990	1.15	0.20	1.21	0.2661769	0.6604	-5.92
251226_at	proline-rich protein proline-rich pro	PRP3	AT3G62680	-1.11	-0.15	-1.21	0.26616476	0.6604	-5.92
256027_at	putative protein	---	AT1G34160	1.08	0.11	1.21	0.26623149	0.6604	-5.92
246355_at	hypothetical protein	---	---	-1.21	-0.28	-1.21	0.2661636	0.6604	-5.92
262948_at	DNA-binding protein similar to cellu	---	AT1G75560	1.10	0.14	1.21	0.26623863	0.6604	-5.92
247240_at	putative protein strong similarity to	CMPG2	AT5G64660	1.66	0.73	1.21	0.26619352	0.6604	-5.92
265721_at	putative ABC1 protein identical to	ATATH9	AT2G40090	1.15	0.20	1.21	0.26593365	0.6604	-5.92
254370_at	L1 specific homeobox gene ATML	ATML1	AT4G21750	1.13	0.18	1.21	0.26641482	0.6604	-5.92
265275_at	En/Spm-like transposon protein rel	---	AT2G28440	-1.19	-0.25	-1.21	0.26632379	0.6604	-5.92
250223_at	glutaredoxin-like protein ;supporte	ROXY2	AT5G14070	1.09	0.13	1.21	0.26638737	0.6604	-5.92
263902_at	phosphoribosylformimino-5-aminoi	APG10	AT2G36230	1.10	0.13	1.21	0.26636779	0.6604	-5.92
246373_at	receptor-like protein kinase, putati	---	AT1G51860	-1.16	-0.22	-1.21	0.26635297	0.6604	-5.92
246978_at	cytochrome P450-like protein fatty	CYP714A1	AT5G24910	-1.18	-0.24	-1.21	0.26645744	0.6604	-5.92

258633_at	putative serine carboxypeptidase I	SCPL27	AT3G07990	1.22	0.29	1.21	0.26659848	0.6606	-5.92
262449_at	hypothetical protein similar to hypo	---	AT1G11160	1.08	0.11	1.21	0.26657217	0.6606	-5.92
260078_at	hypothetical protein predicted by g	---	AT1G73790	1.11	0.15	1.21	0.26665352	0.6607	-5.92
244917_at	hypothetical protein	---	---	-1.09	-0.13	-1.21	0.26680685	0.6610	-5.92
255738_at	hypothetical protein predicted by g	---	AT1G25570	1.09	0.13	1.21	0.26681699	0.6610	-5.92
246482_at	plant adhesion molecule 1 (PAM1)	PAM1	AT5G15930	-1.10	-0.14	-1.21	0.26699304	0.6610	-5.92
252990_at	putative protein	---	AT4G38440	1.22	0.29	1.21	0.26688362	0.6610	-5.92
267229_s_at	putative translation initiation factor	---	AT2G44070 /	1.22	0.28	1.21	0.26702106	0.6610	-5.92
253300_at	carbonate dehydratase - like prote	BCA5	AT4G33580	1.17	0.22	1.21	0.26702092	0.6610	-5.92
248076_at	unknown protein	---	AT5G55750	1.09	0.12	1.21	0.26699904	0.6610	-5.92
254712_at	hypothetical protein	---	AT4G18080	-1.08	-0.11	-1.21	0.26696219	0.6610	-5.92
262185_at	MADS box transcription factor, pu	AGL67	AT1G77950	-1.08	-0.11	-1.21	0.26711966	0.6611	-5.92
248330_at	putative protein contains similarity	---	AT5G52810	1.21	0.27	1.21	0.26712498	0.6611	-5.92
265788_at	putative auxin-induced protein	IAA32	AT2G01200	-1.08	-0.12	-1.21	0.26721986	0.6612	-5.93
261729_s_at	hexokinase, putative similar to hex	HXK3	AT1G47840	-1.08	-0.11	-1.21	0.26720879	0.6612	-5.93
250254_at	24-sterol C-methyltransferase ; su	SMT1	AT5G13710	1.15	0.20	1.21	0.2674032	0.6613	-5.93
246295_at	calmodulin-binding protein ; suppo	CIP111	AT3G56690	1.14	0.18	1.21	0.26737358	0.6613	-5.93
265871_at	unknown protein ;supported by ful	---	AT2G01680	-1.14	-0.19	-1.21	0.26740021	0.6613	-5.93
252197_at	receptor protein kinase -like protei	---	AT3G50230	-1.08	-0.12	-1.21	0.26736422	0.6613	-5.93
260885_at	protein kinase PK4, putative simila	CIPK18	AT1G29230	1.12	0.17	1.21	0.26732623	0.6613	-5.93
265196_at	hypothetical protein predicted by g	SWC2	AT2G36740	-1.13	-0.18	-1.21	0.26752767	0.6616	-5.93
254109_at	Pollen-specific protein precursor li	SKS1	AT4G25240	-1.09	-0.12	-1.21	0.26756171	0.6616	-5.93
262926_s_at	receptor kinase, putative similar to	ARK1	AT1G65790 /	-1.31	-0.38	-1.21	0.2676675	0.6616	-5.93
261194_at	unknown protein contains Pfam pr	---	AT1G12770 /	-1.07	-0.10	-1.21	0.26768356	0.6616	-5.93
256465_at	hypothetical protein predicted by g	---	AT1G32570	-1.15	-0.20	-1.21	0.26760432	0.6616	-5.93
257731_at	unknown protein similar to CALCI	---	AT3G18430	-1.09	-0.13	-1.21	0.26768882	0.6616	-5.93
246331_at	non-phototropic hypocotyl 3-like p	---	AT3G44820	-1.12	-0.16	-1.21	0.26775744	0.6617	-5.93
264798_at	putative myosin MYA1, class V (Z	XIC	AT1G08730	-1.10	-0.13	-1.21	0.26786185	0.6617	-5.93
248723_at	acetyl-CoA:benzylalcohol acetyltra	---	AT5G47950	-1.11	-0.15	-1.21	0.26783507	0.6617	-5.93
245190_at	F12A21.16 hypothetical protein	---	AT1G67690	1.14	0.19	1.21	0.26782092	0.6617	-5.93
261070_at	disease resistance protein, putativ	AtRLP1	AT1G07390	-1.13	-0.18	-1.21	0.26795762	0.6618	-5.93
245623_s_at	hypothetical protein	---	AT4G14096 /	1.09	0.13	1.21	0.26794318	0.6618	-5.93
250449_at	embryonic abundant protein -like e	---	AT5G10830	-1.23	-0.30	-1.21	0.26804061	0.6619	-5.93
266620_at	unknown protein	---	AT2G35450	-1.12	-0.17	-1.21	0.26811556	0.6619	-5.93
248193_at	homogentisate 1,2-dioxygenase ;	HGO	AT5G54080	1.20	0.26	1.21	0.26812058	0.6619	-5.93

257356_s_at	hypothetical protein predicted by g	---	AT2G32490	-1.11	-0.15	-1.21	0.26814113	0.6619	-5.93
260230_at	putative DNA-binding protein conta	---	AT1G74500	-1.10	-0.14	-1.21	0.26806238	0.6619	-5.93
266851_at	similar to avrRpt2-induced protein	ATPP2-A3	AT2G26820	-1.08	-0.11	-1.21	0.26819563	0.6620	-5.93
261577_at	ribonucleoprotein, putative similar	---	AT1G01080	1.15	0.20	1.21	0.26822843	0.6620	-5.93
256734_at	unknown protein	RIK	AT3G29390	-1.09	-0.13	-1.21	0.26836338	0.6623	-5.93
259267_at	unknown protein ;supported by ful	---	AT3G01130	1.09	0.13	1.21	0.26841582	0.6623	-5.93
265858_at	putative ribophorin I	---	AT2G01720	1.12	0.17	1.21	0.26857737	0.6624	-5.93
265373_at	putative replication protein A1	RPA1A	AT2G06510	1.20	0.26	1.21	0.26850415	0.6624	-5.93
250154_at	putative aldose 1-epimerase - like	---	AT5G15140	-1.08	-0.11	-1.21	0.26852776	0.6624	-5.93
261571_at	hypothetical protein predicted by g	---	AT1G01150	-1.09	-0.13	-1.21	0.26857626	0.6624	-5.93
263393_at	hypothetical protein similar to hypo	---	---	-1.09	-0.12	-1.21	0.26865343	0.6625	-5.93
246588_at	putative protein predicted protein,	---	AT3G06433	-1.08	-0.11	-1.21	0.26864182	0.6625	-5.93
259394_at	hypothetical protein predicted by g	---	AT1G06420	-1.09	-0.12	-1.21	0.26868757	0.6625	-5.93
246488_at	steroid 5alpha-reductase-like prot	---	AT5G16010	-1.19	-0.26	-1.21	0.26879165	0.6626	-5.93
261293_at	unknown protein ; supported by cD	---	AT1G36980	1.09	0.12	1.21	0.26878272	0.6626	-5.93
252013_at	putative protein	---	AT3G52860	1.09	0.13	1.21	0.2688334	0.6626	-5.93
264445_at	unknown protein similar to ESTs g	---	AT1G27290	1.18	0.24	1.20	0.26907019	0.6630	-5.93
245721_s_at	hypothetical protein similar to Ser-	---	AT1G73450	-1.14	-0.20	-1.20	0.26902708	0.6630	-5.93
251904_at	Machado-Joseph disease MJD1a	---	AT3G54130	1.14	0.19	1.20	0.26906043	0.6630	-5.93
250572_at	putative protein	MIR834A	---	1.14	0.19	1.20	0.26916601	0.6632	-5.93
258101_at	unknown protein	RFR1	AT3G23590	-1.21	-0.27	-1.20	0.26919683	0.6632	-5.93
256778_at	nucleosome assembly protein, pu	NAP1;4	AT3G13782	-1.09	-0.13	-1.20	0.26925108	0.6632	-5.93
250214_at	endoxyloglucan transferase (dbj|B	EXGT-A4	AT5G13870	1.12	0.17	1.20	0.26936142	0.6634	-5.93
251268_at	putative protein hypothetical protei	---	AT3G62350	-1.11	-0.15	-1.20	0.26934715	0.6634	-5.93
248728_at	cytochrome P450-like protein	CYP708A2	AT5G48000	-1.10	-0.14	-1.20	0.26943154	0.6635	-5.93
246637_at	putative protein polymorphic mem	---	AT5G34870	-1.11	-0.15	-1.20	0.26945974	0.6635	-5.93
259587_at	unknown protein ;supported by full	---	AT1G28120	1.11	0.14	1.20	0.26964612	0.6639	-5.93
259822_at	myb-related transcription factor, p	MYB20	AT1G66230	1.21	0.27	1.20	0.26978561	0.6641	-5.93
266000_at	putative cytochrome P450 identica	CYP71B6	AT2G24180	1.21	0.28	1.20	0.26991498	0.6642	-5.93
255344_s_at	putative receptor-like protein kinas	---	AT4G04540	-1.30	-0.38	-1.20	0.27005719	0.6642	-5.93
265037_at	putative prohibitin 2 B-cell recepto	ATPHB2	AT1G03860	1.12	0.16	1.20	0.26991772	0.6642	-5.93
264124_at	hypothetical protein predicted by g	ATOCT2	AT1G79360	-1.11	-0.15	-1.20	0.26999846	0.6642	-5.93
246571_at	putative protein	---	AT5G15000	-1.08	-0.11	-1.20	0.26991538	0.6642	-5.93
247577_at	putative protein flavin-containing m	---	AT5G61290	-1.11	-0.15	-1.20	0.269865	0.6642	-5.93
256749_at	hypothetical protein similar to puta	---	---	1.09	0.13	1.20	0.27003542	0.6642	-5.93

258593_at	unknown protein	---	AT3G04480	1.16	0.21	1.20	0.27006003	0.6642	-5.93
257776_at	terpene synthase-related protein c	---	AT3G29190	-1.11	-0.15	-1.20	0.27001961	0.6642	-5.93
248126_at	protein translation factor Sui1 hom	ROC5	AT4G34870	1.08	0.11	1.20	0.27010907	0.6642	-5.93
249852_at	monosaccharide transporter	STP11	AT5G23270	-1.11	-0.14	-1.20	0.27017556	0.6643	-5.93
257461_at	hypothetical protein predicted by g	ATPUP15	AT1G75470	-1.08	-0.11	-1.20	0.27027189	0.6643	-5.93
249183_at	E2, ubiquitin-conjugating enzyme	UBC18	AT5G42990	1.09	0.12	1.20	0.27023653	0.6643	-5.93
252120_at	putative protein lin-10 protein - Ra	---	AT3G51130	-1.11	-0.15	-1.20	0.27026597	0.6643	-5.93
264295_at	hypothetical protein predicted by g	---	AT1G78740	-1.08	-0.11	-1.20	0.27034469	0.6644	-5.93
245776_at	hypothetical protein predicted by g	---	AT1G30260	-1.19	-0.25	-1.20	0.27037748	0.6644	-5.93
246530_at	Expressed protein ; supported by f	---	AT5G15725	-1.09	-0.13	-1.20	0.27041367	0.6645	-5.94
258708_at	putative oxidoreductase similar to	---	AT3G09580	-1.16	-0.22	-1.20	0.27048065	0.6645	-5.94
248216_at	unknown protein	---	AT5G53690	1.09	0.13	1.20	0.27046843	0.6645	-5.94
245456_at	disease resistance RPP5 like prote	RPP5	AT4G16950	-1.12	-0.17	-1.20	0.27056607	0.6646	-5.94
255297_x_at	hypothetical protein	---	---	-1.12	-0.16	-1.20	0.27062539	0.6647	-5.94
260573_at	putative pectinesterase	---	AT2G47280	-1.11	-0.15	-1.20	0.27072533	0.6648	-5.94
264948_at	RNA helicase, putative similar to R	---	AT1G77030	-1.09	-0.13	-1.20	0.27074372	0.6648	-5.94
255195_at	may be a pseudogene	---	---	-1.09	-0.12	-1.20	0.27078589	0.6649	-5.94
265911_at	unknown protein ;supported by ful	---	AT2G25670	1.08	0.12	1.20	0.27084915	0.6649	-5.94
258496_at	putative plant adhesion molecule s	---	AT3G02460	-1.15	-0.20	-1.20	0.27089512	0.6649	-5.94
250320_at	CCAAT box binding factor/ transcr	NF-YA1	AT5G12840	-1.11	-0.15	-1.20	0.27089069	0.6649	-5.94
244918_at	hypothetical protein	AT2G07742	---	-1.10	-0.14	-1.20	0.2709575	0.6649	-5.94
244993_s_at	hypothetical protein	---	---	1.13	0.17	1.20	0.27094255	0.6649	-5.94
253384_at	Expressed protein ; supported by f	---	AT4G32915	1.12	0.16	1.20	0.2710026	0.6650	-5.94
250250_at	putative protein similar to unknown	---	AT5G13610	-1.11	-0.15	-1.20	0.27117602	0.6651	-5.94
249698_at	unknown protein	MIS12	AT5G35520	1.15	0.20	1.20	0.27115402	0.6651	-5.94
246677_at	putative protein predicted proteins	---	---	-1.11	-0.15	-1.20	0.2711659	0.6651	-5.94
263894_at	putative cytochrome P450	CYP96A5	AT2G21910	1.11	0.15	1.20	0.27116166	0.6651	-5.94
261503_at	hypothetical protein predicted by g	---	AT1G71691	1.11	0.15	1.20	0.2711844	0.6651	-5.94
257800_at	unknown protein ;supported by ful	---	AT3G15900	1.13	0.17	1.20	0.27122776	0.6651	-5.94
260950_s_at	delta 9 desaturase, putative simila	---	AT1G06090	-1.12	-0.16	-1.20	0.27141333	0.6651	-5.94
259083_at	putative kinase similar to NIMA-rel	ATNEK2	AT3G04810	-1.09	-0.13	-1.20	0.2715229	0.6651	-5.94
266566_at	unknown protein	---	AT2G24040	1.11	0.16	1.20	0.27153399	0.6651	-5.94
248263_at	pectinesterase ; supported by cDN	PMEPCRF	AT5G53370	-1.22	-0.28	-1.20	0.27151106	0.6651	-5.94
248204_at	myosin heavy chain	ATM2	AT5G54280	-1.13	-0.18	-1.20	0.27140377	0.6651	-5.94
248117_at	FH protein interacting protein FIP2	FIP2	AT5G55000	1.13	0.17	1.20	0.27150981	0.6651	-5.94

258681_at	unknown protein ; supported by fu	---	AT3G08610	1.11	0.15	1.20	0.27151258	0.6651	-5.94
246309_at	putative transmembrane protein G	ATG1	AT3G51790	-1.25	-0.32	-1.20	0.27129284	0.6651	-5.94
245158_at	hypothetical protein predicted by g	RALFL18	AT2G33130	-1.15	-0.20	-1.20	0.27156129	0.6651	-5.94
257563_at	hypothetical protein predicted by g	---	AT3G19610	1.08	0.11	1.20	0.27151103	0.6651	-5.94
245258_at	lupeol synthase like protein ; supp	ATPEN1	AT4G15340	-1.11	-0.15	-1.20	0.27143782	0.6651	-5.94
253919_at	putative protein ; supported by full	---	AT4G27350	-1.22	-0.28	-1.20	0.27159205	0.6651	-5.94
260910_at	importin alpha, putative similar to	IMPA-6	AT1G02690	1.16	0.21	1.20	0.2716491	0.6652	-5.94
261422_at	unknown protein	NDF6	AT1G18730	-1.12	-0.17	-1.20	0.27178257	0.6653	-5.94
258431_at	hypothetical protein predicted by g	---	AT3G16580	1.09	0.12	1.20	0.27180142	0.6653	-5.94
266303_at	putative receptor-like protein kinas	---	AT2G27060	1.19	0.25	1.20	0.27181557	0.6653	-5.94
253350_at	hypothetical protein	---	AT4G33690	1.09	0.13	1.20	0.27174525	0.6653	-5.94
254682_at	putative protein WERBP-1 - Nicot	UNE16	AT4G13640	1.11	0.15	1.20	0.27183013	0.6653	-5.94
250234_at	transaldolase - like protein transal	---	AT5G13420	-1.15	-0.20	-1.20	0.27193354	0.6653	-5.94
257163_at	DNA-binding protein, putative sim	MYB305	AT3G24310	-1.10	-0.14	-1.20	0.27190819	0.6653	-5.94
251424_at	putative protein 04.05.01.01	---	AT3G60560	-1.08	-0.11	-1.20	0.27189568	0.6653	-5.94
254867_at	hypothetical proteins	---	AT4G12240	-1.15	-0.20	-1.20	0.27208048	0.6653	-5.94
266421_at	putative nonspecific lipid-transfer p	LP1	AT2G38540	1.39	0.47	1.20	0.2720679	0.6653	-5.94
260074_at	putative ras-related GTP-binding p	AtRABA6a	AT1G73640	-1.09	-0.13	-1.20	0.27196486	0.6653	-5.94
267342_at	putative heme A:farnesyltransferas	COX10	AT2G44520	-1.16	-0.21	-1.20	0.27200376	0.6653	-5.94
253108_at	putative bZIP transcription factor [	FD	AT4G35900	-1.20	-0.26	-1.20	0.27205602	0.6653	-5.94
265421_s_at	predicted protein	---	AT2G20616 /	-1.10	-0.14	-1.20	0.27217238	0.6655	-5.94
261240_at	subtilisin-like serine protease conta	SBT3.5	AT1G32940	1.29	0.37	1.20	0.27221245	0.6655	-5.94
261566_at	unknown protein ;supported by full	---	AT1G33230	-1.13	-0.18	-1.20	0.27227507	0.6655	-5.94
252100_at	crooked neck-like protein crooked	---	AT3G51110	-1.19	-0.25	-1.20	0.27226013	0.6655	-5.94
260879_at	hypothetical protein predicted by g	---	AT1G21480	1.10	0.14	1.20	0.27240617	0.6658	-5.94
257165_at	beta-1,3-glucanase, putative simil	---	AT3G24330	-1.15	-0.20	-1.20	0.27249139	0.6658	-5.94
251482_s_at	receptor lectin kinase 3	---	AT3G59740 /	-1.11	-0.15	-1.19	0.2725017	0.6658	-5.94
267479_at	hypothetical protein	---	AT2G02690	1.08	0.11	1.19	0.27251437	0.6658	-5.94
256730_at	floral homeotic protein AGL8, puta	AGL79	AT3G30260	-1.08	-0.11	-1.19	0.27257944	0.6659	-5.94
266160_at	hypothetical protein	ATCHX8	AT2G28180	-1.12	-0.17	-1.19	0.27274802	0.6662	-5.94
261219_at	hypothetical protein predicted by g	---	AT1G19980	-1.12	-0.16	-1.19	0.27278386	0.6663	-5.94
248351_at	unknown protein ; supported by cl	---	AT5G52200	-1.17	-0.22	-1.19	0.27303224	0.6667	-5.94
249714_at	unknown protein	---	---	-1.14	-0.18	-1.19	0.27303234	0.6667	-5.94
251999_at	hypothetical protein teichoic acid t	---	AT3G52700	-1.09	-0.12	-1.19	0.27308025	0.6668	-5.94
261423_at	homeodomain transcription factor	AGL65	AT1G18750	-1.13	-0.17	-1.19	0.27326424	0.6671	-5.94

263494_at	14-3-3 protein GF14mu (grf9) ider	GRF9	AT2G42590	1.09	0.12	1.19	0.27331695	0.6672	-5.94
264711_at	hypothetical protein predicted by g	---	AT1G09800	-1.10	-0.14	-1.19	0.27334664	0.6672	-5.94
258044_at	Dof zinc finger protein identical to (	ADOF2	AT3G21270	-1.23	-0.30	-1.19	0.27348754	0.6675	-5.94
266202_at	putative cinnamoyl-CoA reductase	---	AT2G02400	1.09	0.12	1.19	0.27364126	0.6678	-5.94
254849_at	putative protein RNA splicing-relat	---	AT4G11970	-1.08	-0.11	-1.19	0.27375205	0.6680	-5.95
256248_at	hypothetical protein	---	AT3G66652	-1.15	-0.20	-1.19	0.27402389	0.6680	-5.95
257761_at	unknown protein	---	AT3G23090	-1.20	-0.26	-1.19	0.27406649	0.6680	-5.95
263067_at	hypothetical protein predicted by g	---	AT2G17550	1.18	0.24	1.19	0.27395505	0.6680	-5.95
263589_at	hypothetical protein predicted by g	---	AT2G25280	1.08	0.12	1.19	0.27403234	0.6680	-5.95
258273_at	unknown protein ;supported by ful	GRX4	AT3G15660	1.08	0.11	1.19	0.27401411	0.6680	-5.95
256916_at	GATA transcription factor 1 (AtGA	---	AT3G24050	1.13	0.17	1.19	0.27398681	0.6680	-5.95
262881_at	unknown protein ; supported by cD	---	AT1G64890	-1.19	-0.25	-1.19	0.27388847	0.6680	-5.95
247180_at	histone H3	---	AT5G65350 /	-1.08	-0.11	-1.19	0.27399116	0.6680	-5.95
259261_at	unknown protein similar to unknow	---	AT3G11390	-1.12	-0.16	-1.19	0.27406602	0.6680	-5.95
254657_s_at	putative protein W15DMY32F, W2	---	AT4G18210 /	-1.21	-0.27	-1.19	0.27389585	0.6680	-5.95
256767_at	hypothetical protein predicted by g	---	AT3G13680	-1.10	-0.13	-1.19	0.27417137	0.6681	-5.95
247789_at	putative protein various predicted	---	AT5G58680	-1.11	-0.16	-1.19	0.27415099	0.6681	-5.95
263927_s_at	putative cinnamyl-alcohol dehydro	CAD2	AT2G21730 /	-1.13	-0.18	-1.19	0.27417715	0.6681	-5.95
251206_at	putative protein various predicted	---	AT3G63090	1.16	0.21	1.19	0.27420929	0.6681	-5.95
261609_at	unknown protein similar to MAP3K	---	AT1G49740	-1.17	-0.22	-1.19	0.27425912	0.6681	-5.95
265108_s_at	similar to flavin-binding monooxyg	---	AT1G62620 /	-1.13	-0.17	-1.19	0.27429192	0.6682	-5.95
254922_at	RING-H2 finger protein RHA1a -lik	RHA1A	AT4G11370	1.75	0.81	1.19	0.27437307	0.6682	-5.95
265171_at	hypothetical protein	---	AT1G23790	1.07	0.10	1.19	0.27435774	0.6682	-5.95
259833_at	MYB-family transcription factor, pu	MYB105	AT1G69560	-1.09	-0.12	-1.19	0.27441051	0.6682	-5.95
251982_at	pectate lyase -like protein pectate	---	AT3G53190	1.15	0.20	1.19	0.27447248	0.6683	-5.95
250995_at	dnaK-type molecular chaperone hs	HSC70-1	AT5G02500	-1.14	-0.20	-1.19	0.27451723	0.6683	-5.95
259760_at	hypothetical protein similar to GB:A	---	AT1G77580	-1.08	-0.11	-1.19	0.27454994	0.6684	-5.95
255435_at	putative component of cytochrome	PETC	AT4G03280	1.11	0.15	1.19	0.27479454	0.6688	-5.95
257909_at	Expressed protein ; supported by f	---	AT3G25480	1.13	0.17	1.19	0.27476634	0.6688	-5.95
251228_at	beta-D-glucan exohydrolase-like p	---	AT3G62710	-1.09	-0.13	-1.19	0.27483833	0.6688	-5.95
251660_at	Expressed protein ; supported by f	---	AT3G57160	1.14	0.19	1.19	0.27488593	0.6689	-5.95
259304_at	putative nucleotide repair protein s	ERCC1	AT3G05210	-1.10	-0.13	-1.19	0.27498325	0.6689	-5.95
266736_at	putative cytochrome P450 ; suppo	CYP709B1	AT2G46960	-1.09	-0.12	-1.19	0.27502433	0.6689	-5.95
249218_at	pitrilysin	---	AT5G42390	1.14	0.19	1.19	0.27498946	0.6689	-5.95
267238_at	unknown protein ;supported by ful	---	AT2G44130	1.49	0.58	1.19	0.27502799	0.6689	-5.95

249084_at	unknown protein	---	AT5G44150	-1.11	-0.14	-1.19	0.27507071	0.6690	-5.95
246401_at	DNA-binding protein, putative sim	AtMYB50	AT1G57560	-1.17	-0.23	-1.19	0.27514834	0.6691	-5.95
253881_at	putative protein Ran_GTP binding	---	AT4G27640	1.09	0.13	1.19	0.27522393	0.6692	-5.95
264001_at	putative peroxidase ;supported by	---	AT2G22420	-1.20	-0.27	-1.19	0.27523687	0.6692	-5.95
250273_at	pre-mRNA splicing factor ATP-de	EMB3011	AT5G13010	-1.09	-0.12	-1.19	0.27530834	0.6692	-5.95
264028_at	putative nitrilase-associated protei	SPR1	AT2G03680	1.18	0.24	1.19	0.27529067	0.6692	-5.95
247344_at	ARI-like RING zinc finger protein-li	---	AT5G63750	-1.11	-0.15	-1.19	0.27538473	0.6693	-5.95
249535_at	transporter -like protein N system	---	AT5G38820	-1.12	-0.17	-1.19	0.27553192	0.6695	-5.95
264198_at	unknown protein ESTs gb|Z34075	---	AT1G22800	-1.14	-0.19	-1.19	0.27550264	0.6695	-5.95
249186_at	CHP-rich zinc finger protein-like	---	AT5G43040	-1.09	-0.13	-1.19	0.27556201	0.6695	-5.95
252330_at	hypothetical protein	---	AT3G48770	-1.14	-0.19	-1.19	0.27559253	0.6695	-5.95
257836_at	hypothetical protein	---	---	-1.09	-0.13	-1.19	0.27565111	0.6696	-5.95
263555_at	unknown protein ;supported by ful	---	AT2G16460	1.09	0.13	1.19	0.27566542	0.6696	-5.95
260399_at	putative lipoxygenase similar to lip	---	AT1G72520	-1.73	-0.79	-1.19	0.27575072	0.6697	-5.95
252357_at	putative protein predicted proteins	---	AT3G48410	-1.15	-0.20	-1.19	0.27587301	0.6699	-5.95
261850_at	hypothetical protein predicted by g	---	AT1G50470	1.14	0.19	1.19	0.27587741	0.6699	-5.95
255193_at	score=10.1, E=1.2, N=1 contains	VFB3	AT4G07400	-1.11	-0.15	-1.19	0.27596297	0.6700	-5.95
259512_at	hypothetical protein ; supported by	KEU	AT1G12360	1.08	0.11	1.19	0.27599686	0.6700	-5.95
250650_at	anthranilate phosphoribosyltransfe	---	AT5G06850	-1.16	-0.22	-1.19	0.27604907	0.6700	-5.95
262169_at	hypothetical protein predicted by g	---	AT1G74860	1.11	0.16	1.19	0.27605744	0.6700	-5.95
256330_at	hypothetical protein predicted by g	---	AT1G76870	1.13	0.18	1.19	0.2761402	0.6702	-5.95
262242_at	hypothetical protein predicted by g	---	AT1G48360	-1.12	-0.17	-1.18	0.27618565	0.6702	-5.95
256005_at	hypothetical protein similar to puta	---	---	-1.10	-0.13	-1.18	0.27623844	0.6702	-5.95
257919_at	myb-related transcription factor, p	MYB15	AT3G23250	-1.67	-0.74	-1.18	0.27631881	0.6704	-5.95
261051_at	cytochrome P450, putative similar	CYP703A2	AT1G01280	-1.09	-0.13	-1.18	0.27642152	0.6705	-5.95
250345_at	subtilisin-like serine protease conta	---	AT5G11940	-1.10	-0.14	-1.18	0.27642023	0.6705	-5.95
263810_at	putative translation initiation factor	---	AT2G04520	1.08	0.11	1.18	0.27648832	0.6706	-5.95
259469_at	hypothetical protein predicted by g	---	AT1G19100	1.09	0.13	1.18	0.27652724	0.6706	-5.95
246995_at	formin-like protein	---	AT5G67470	-1.17	-0.23	-1.18	0.2766172	0.6706	-5.95
256413_at	hypothetical protein predicted by g	---	AT3G11100	1.10	0.14	1.18	0.27664834	0.6706	-5.95
262644_at	beta-VPE nearly identical to beta-V	BETA-VPE	AT1G62710	-1.10	-0.14	-1.18	0.27659208	0.6706	-5.95
255895_at	12-oxophytodienoate reductase, p	---	AT1G17990	1.40	0.49	1.18	0.2766512	0.6706	-5.95
258091_at	hypothetical protein predicted by g	---	AT3G14560	1.34	0.43	1.18	0.2766751	0.6706	-5.95
267317_at	putative proline-rich glycoprotein	---	AT2G34700	-1.09	-0.13	-1.18	0.2767614	0.6707	-5.95
256905_at	mitochondrial chaperonin hsp60 ic	HSP60	AT3G23990	-1.25	-0.32	-1.18	0.27679878	0.6707	-5.95

253651_at	putative protein nucleoid DNA-bin	---	AT4G30030	-1.12	-0.16	-1.18	0.27681665	0.6707	-5.95
256623_at	myosin identical to myosin GB:CAI	ATM1	AT3G19960	-1.11	-0.15	-1.18	0.27675197	0.6707	-5.95
251828_at	putative protein unnamed sequen	---	AT3G55070	-1.11	-0.14	-1.18	0.27691038	0.6708	-5.95
265939_at	putative Ta11-like non-LTR retroel	---	AT2G19650	-1.16	-0.21	-1.18	0.27695661	0.6708	-5.95
256657_at	unknown protein contains similarity	---	AT3G18860	1.10	0.13	1.18	0.27697239	0.6708	-5.95
253865_at	putative RING zinc finger protein A	---	AT4G27470	-1.16	-0.21	-1.18	0.27704301	0.6709	-5.96
255879_at	receptor-like kinase, putative simil	---	AT1G67000	-1.24	-0.31	-1.18	0.27720128	0.6711	-5.96
245618_at	hypothetical protein	---	AT4G14510	-1.12	-0.16	-1.18	0.27719376	0.6711	-5.96
258051_at	hypothetical protein predicted by g	TRZ4	AT3G16260	1.13	0.18	1.18	0.27717675	0.6711	-5.96
266752_at	putative ABC transporter related to	ABCB4	AT2G47000	1.70	0.77	1.18	0.2772753	0.6711	-5.96
251719_at	putative protein PUTATIVE PROT	---	AT3G56140	1.12	0.16	1.18	0.27725403	0.6711	-5.96
247536_at	PREG-like - like protein PREG-like	CYCP4;2	AT5G61650	-1.12	-0.16	-1.18	0.27738454	0.6713	-5.96
263893_at	putative WRKY-type DNA binding	WRKY59	AT2G21900	-1.14	-0.18	-1.18	0.27749224	0.6714	-5.96
263389_at	putative retroelement pol polyprote	---	---	-1.09	-0.13	-1.18	0.27748457	0.6714	-5.96
250684_at	zinc finger-like protein	GIS2	AT5G06650	-1.10	-0.14	-1.18	0.27754459	0.6715	-5.96
259219_at	hypothetical protein predicted by g	---	AT3G03560	-1.16	-0.21	-1.18	0.27770822	0.6718	-5.96
252427_at	hypothetical protein	---	AT3G47640	-1.22	-0.28	-1.18	0.2777556	0.6719	-5.96
253689_at	hypothetical protein ;supported by	---	AT4G29770	-1.10	-0.13	-1.18	0.27779937	0.6719	-5.96
264863_at	putative peroxidase similar to perc	---	AT1G24110	-1.11	-0.15	-1.18	0.27787958	0.6720	-5.96
260701_at	heat shock transcription factor HS	ATHSFA1D	AT1G32330	1.12	0.16	1.18	0.27794136	0.6721	-5.96
257433_at	hypothetical protein predicted by g	---	AT2G21990	1.09	0.12	1.18	0.27796517	0.6721	-5.96
257588_x_at	En/Spm-like transposon protein, p	---	---	-1.14	-0.19	-1.18	0.27801148	0.6721	-5.96
263043_at	conserved hypothetical protein pre	---	AT1G23350	-1.12	-0.16	-1.18	0.27807384	0.6722	-5.96
263317_s_at	similar to mammalian MHC III regi	SUVH7	AT1G17770	-1.15	-0.20	-1.18	0.27813735	0.6723	-5.96
251767_at	putative protein U4/U6 small nucle	---	AT3G55930	-1.08	-0.11	-1.18	0.27817422	0.6723	-5.96
267547_at	putative synaptobrevin	ATVAMP72	AT2G32670	-1.13	-0.18	-1.18	0.27823367	0.6724	-5.96
246298_at	putative protein sequence in GenB	ETO1	AT3G51770	-1.09	-0.12	-1.18	0.27832369	0.6725	-5.96
267426_at	hypothetical protein predicted by g	---	AT2G34820	1.09	0.13	1.18	0.27852621	0.6728	-5.96
246157_at	cytochrome-b5 reductase - like pr	---	AT5G20080	-1.13	-0.17	-1.18	0.27854079	0.6728	-5.96
255643_at	hypothetical protein	---	AT4G00840	1.09	0.13	1.18	0.27852405	0.6728	-5.96
252954_at	putative thaumatin-like protein tha	---	AT4G38660	1.40	0.48	1.18	0.27860553	0.6729	-5.96
267105_at	hypothetical protein predicted by g	---	AT2G14760	-1.13	-0.17	-1.18	0.27865337	0.6730	-5.96
244996_at	ribosomal protein S2	---	---	1.11	0.15	1.18	0.27870409	0.6730	-5.96
258189_at	unknown protein ;supported by ful	JAZ3	AT3G17860	-1.20	-0.26	-1.18	0.27877778	0.6730	-5.96
252891_at	putative WRKY DNA-binding prote	WRKY13	AT4G39410	-1.14	-0.19	-1.18	0.27883924	0.6730	-5.96

264116_at	putative poly (ADP-ribose) polyme	PARP2	AT2G31320	1.19	0.26	1.18	0.27886292	0.6730	-5.96
262043_at	unknown protein	PSF1	AT1G80190	1.13	0.18	1.18	0.27880908	0.6730	-5.96
248662_at	unknown protein	---	AT5G48690	1.10	0.13	1.18	0.27882469	0.6730	-5.96
259179_at	hypothetical protein similar to puta	---	AT3G01660	-1.13	-0.18	-1.18	0.27892307	0.6731	-5.96
267396_at	hypothetical protein predicted by g	---	AT2G44270	1.12	0.17	1.18	0.27897485	0.6731	-5.96
264644_at	hypothetical protein Similar to Cae	CAX11	AT1G08960	-1.11	-0.16	-1.18	0.27901237	0.6731	-5.96
264234_at	hypothetical protein contains simila	---	AT1G54720	-1.08	-0.11	-1.18	0.27898958	0.6731	-5.96
253572_at	hypothetical protein	---	AT4G31010	1.11	0.14	1.18	0.27910875	0.6733	-5.96
250346_at	lysine decarboxylase - like protein	---	AT5G11950	1.29	0.37	1.18	0.27913995	0.6733	-5.96
257019_at	unknown protein	---	AT3G19640	1.08	0.10	1.18	0.27928521	0.6734	-5.96
261581_at	serine/threonine kinase, putative s	CIPK9	AT1G01140	-1.14	-0.19	-1.18	0.27930858	0.6734	-5.96
252509_at	putative protein serine/threonine-s	---	AT3G46240	-1.08	-0.11	-1.18	0.27924343	0.6734	-5.96
255973_at	hypothetical protein predicted by g	---	AT3G32400	-1.08	-0.11	-1.18	0.2793171	0.6734	-5.96
246245_at	putative protein	---	AT4G36440	1.10	0.13	1.18	0.27937196	0.6735	-5.96
259859_at	putative protein phosphatase simil	---	AT1G68410	-1.26	-0.34	-1.18	0.27948519	0.6737	-5.96
249201_at	putative protein similar to unknown	---	AT5G42370	-1.13	-0.18	-1.18	0.27950462	0.6737	-5.96
264330_at	multi-drug resistance protein Stron	ATMRP5	AT1G04120	-1.09	-0.13	-1.18	0.27955471	0.6737	-5.96
264607_at	putative K+ channel, beta subunit	KAB1	AT1G04690	1.08	0.11	1.18	0.27963636	0.6738	-5.96
259059_at	hypothetical protein	---	AT3G07300	-1.10	-0.13	-1.18	0.27966823	0.6738	-5.96
265507_s_at	Ac-like transposase related to Ac/D	---	---	1.09	0.13	1.18	0.27964025	0.6738	-5.96
260089_at	putative ATPase contains Pfam pr	---	AT1G73170	-1.08	-0.11	-1.18	0.27970479	0.6738	-5.96
256715_at	hypothetical protein predicted by g	MEE18	AT2G34090	-1.15	-0.21	-1.18	0.27979696	0.6739	-5.96
261776_at	hypothetical protein similar to puta	---	AT1G76190	-1.13	-0.18	-1.18	0.27977087	0.6739	-5.96
265169_x_at	unknown protein	---	AT1G23720	1.10	0.14	1.18	0.2798551	0.6739	-5.96
256933_at	unknown protein contains Pfam pr	---	AT3G22600	2.00	1.00	1.17	0.27997533	0.6739	-5.96
248146_at	translation initiation factor-like prot	---	AT5G54940	-1.10	-0.13	-1.17	0.27990656	0.6739	-5.96
255609_s_at	hypothetical protein	---	AT4G01180	1.08	0.11	1.17	0.27995691	0.6739	-5.96
262339_at	WRKY DNA binding protein, putat	WRKY56	AT1G64000	1.09	0.12	1.17	0.27991832	0.6739	-5.96
263311_at	hypothetical protein predicted by g	---	AT2G10340	-1.11	-0.15	-1.17	0.28001781	0.6740	-5.96
259424_at	hypothetical protein contains simil	---	AT1G13830	1.15	0.20	1.17	0.28005907	0.6740	-5.96
267178_at	unknown protein ; supported by fu	---	AT2G37750	1.45	0.54	1.17	0.28012937	0.6741	-5.96
256969_at	unknown protein	---	AT3G21080	1.39	0.47	1.17	0.28017448	0.6741	-5.96
248741_at	putative protein similar to unknown	SLY2	AT5G48170	-1.16	-0.21	-1.17	0.28024954	0.6742	-5.96
251386_at	putative protein rec, Homo sapien	---	AT3G60800	-1.08	-0.11	-1.17	0.28028448	0.6743	-5.96
262289_at	unknown protein identical to unkno	---	AT1G70770	-1.09	-0.12	-1.17	0.28041907	0.6744	-5.97

263365_at	putative heat shock protein	---	AT2G20550	-1.16	-0.21	-1.17	0.28039447	0.6744	-5.97
266541_at	unknown protein	GRL	AT2G35110	1.12	0.16	1.17	0.2804039	0.6744	-5.97
253478_at	putative protein trichohyalin - hum	---	AT4G32350	-1.17	-0.23	-1.17	0.28055836	0.6745	-5.97
263431_at	unknown protein ;supported by ful	---	AT2G22170	-1.83	-0.87	-1.17	0.28057848	0.6745	-5.97
251401_at	stellacyanin (uclacyanin 3) - like p	---	AT3G60270	-1.13	-0.17	-1.17	0.28055088	0.6745	-5.97
249768_at	receptor-like protein kinase	---	AT5G24100	-1.12	-0.17	-1.17	0.28049135	0.6745	-5.97
258490_at	hypothetical protein predicted by g	---	AT3G02670	-1.09	-0.13	-1.17	0.28067292	0.6746	-5.97
260358_at	unknown protein ; supported by cD	---	AT1G69340	1.09	0.12	1.17	0.28070839	0.6746	-5.97
248316_at	putative protein similar to unknowr	---	AT5G52670	-1.13	-0.18	-1.17	0.28083471	0.6748	-5.97
253400_at	putative protein unknown protein T	---	AT4G32860	-1.09	-0.12	-1.17	0.28085635	0.6748	-5.97
254756_at	putative protein late embryogenes	EDA21	AT4G13235	-1.10	-0.13	-1.17	0.28080015	0.6748	-5.97
259801_at	blue copper protein, putative simil	---	AT1G72230	1.26	0.34	1.17	0.28092195	0.6749	-5.97
249756_at	Expressed protein ; supported by f	---	AT5G24313	-1.09	-0.12	-1.17	0.28096533	0.6749	-5.97
246259_at	amino acid permease, putative co	---	AT1G31830	-1.12	-0.16	-1.17	0.28101511	0.6749	-5.97
262944_at	phosphoglycerate kinase, putative	PGK	AT1G79550	-1.14	-0.19	-1.17	0.28116028	0.6750	-5.97
244984_at	ribosomal protein S3	---	---	1.15	0.20	1.17	0.28116945	0.6750	-5.97
252204_at	putative protein predicted protein,	---	AT3G50340	-1.31	-0.39	-1.17	0.28110385	0.6750	-5.97
261897_at	hypothetical protein predicted by g	---	AT1G80950	-1.11	-0.15	-1.17	0.2811501	0.6750	-5.97
252467_at	putative protein predicted proteins	---	AT3G47080	-1.13	-0.18	-1.17	0.28114422	0.6750	-5.97
254770_at	extensin-like protein extensin-like	---	AT4G13340	1.26	0.33	1.17	0.28143192	0.6752	-5.97
248400_at	putative protein contains similarity	---	AT5G52020	-1.13	-0.17	-1.17	0.28145743	0.6752	-5.97
247492_at	putative protein AP2 domain conta	---	AT5G61890	-1.30	-0.38	-1.17	0.28138031	0.6752	-5.97
245070_at	metallothionein-like protein identica	---	AT2G23240	-1.13	-0.18	-1.17	0.28145411	0.6752	-5.97
251799_at	putative protein P59 PROTEIN (H	---	AT3G55520	-1.13	-0.18	-1.17	0.28140966	0.6752	-5.97
246464_at	quinone oxidoreductase -like prote	---	AT5G16980	-1.10	-0.13	-1.17	0.28146371	0.6752	-5.97
255512_at	Expressed protein ; supported by c	SYP42	AT4G02195	1.13	0.17	1.17	0.28142829	0.6752	-5.97
257421_at	hypothetical protein predicted by g	---	AT1G12030	-1.18	-0.24	-1.17	0.28149443	0.6752	-5.97
266717_at	Expressed protein ; supported by f	---	AT2G46735	1.10	0.13	1.17	0.28160829	0.6754	-5.97
246633_at	hypothetical protein ; supported by	---	AT1G29720	1.32	0.40	1.17	0.2817598	0.6756	-5.97
261400_at	protein phosphatase-2C, putative	---	AT1G79630	1.15	0.20	1.17	0.28177985	0.6756	-5.97
255739_at	unknown protein similar to hypothe	ANAC008	AT1G25580	1.14	0.19	1.17	0.28186961	0.6757	-5.97
247760_at	subtilisin-like serine protease conta	---	AT5G59130	-1.47	-0.55	-1.17	0.28187493	0.6757	-5.97
265880_at	unknown protein	---	AT2G42300	-1.15	-0.20	-1.17	0.28201474	0.6758	-5.97
257370_at	hypothetical protein predicted by g	---	AT2G35080	-1.10	-0.14	-1.17	0.28203702	0.6758	-5.97
259049_at	unknown protein	---	AT3G03370	1.12	0.17	1.17	0.28203457	0.6758	-5.97

263919_at	unknown protein ;supported by ful	---	AT2G36470	1.36	0.44	1.17	0.28195137	0.6758	-5.97
258872_at	hypothetical protein similar to L1 s	HDG8	AT3G03260	1.14	0.19	1.17	0.28201259	0.6758	-5.97
254441_at	prolamin box binding protein - like	---	AT4G21050	-1.08	-0.11	-1.17	0.28218737	0.6761	-5.97
256383_at	hypothetical protein ; supported by	---	AT1G66820	1.11	0.16	1.17	0.28222682	0.6761	-5.97
264851_at	putative calmodulin-domain protei	CPK6	AT2G17290	-1.19	-0.25	-1.17	0.28229311	0.6762	-5.97
264551_at	unknown protein similar to beta-1,	---	AT1G09460	1.20	0.26	1.17	0.28237154	0.6763	-5.97
266609_at	unknown protein ; supported by cl	SRO1	AT2G35510	-1.14	-0.19	-1.17	0.28243685	0.6764	-5.97
253789_at	putative protein predicted proteins	---	AT4G28570	-1.12	-0.17	-1.17	0.28303193	0.6766	-5.97
258747_at	unknown protein ; supported by fu	---	AT3G05810	1.14	0.18	1.17	0.28280452	0.6766	-5.97
250355_at	putative protein predicted protein,	---	AT5G11700	-1.12	-0.16	-1.17	0.28308787	0.6766	-5.97
249523_at	cytochrome b-561 (gb|AAD45585.	ACYB-1	AT5G38630	1.10	0.13	1.17	0.282718	0.6766	-5.97
247533_at	putative protein kinase-like transm	---	AT5G61570	-1.25	-0.32	-1.17	0.2827423	0.6766	-5.97
257536_at	unknown protein	---	AT3G02800	1.59	0.67	1.17	0.2829769	0.6766	-5.97
253494_at	putative protein	---	AT4G31830	-1.10	-0.14	-1.17	0.28295693	0.6766	-5.97
255471_at	putative oxidoreductase similar to	AOP3	AT4G03050	-1.10	-0.13	-1.17	0.28291582	0.6766	-5.97
264832_at	unknown unknown	---	AT1G03660	-1.13	-0.18	-1.17	0.28290891	0.6766	-5.97
259717_at	putative cleavage and polyadenyla	CPSF73-I	AT1G61010	1.11	0.16	1.17	0.28266399	0.6766	-5.97
245884_at	branched-chain alpha keto-acid de	---	AT5G09300	1.14	0.19	1.17	0.2830295	0.6766	-5.97
266006_at	putative ABC transporter	---	AT2G37360	-1.13	-0.18	-1.17	0.282925	0.6766	-5.97
265835_at	putative retroelement pol polyprote	---	---	-1.12	-0.16	-1.17	0.28283735	0.6766	-5.97
255652_at	putative protein	MEE47	AT4G00950	-1.34	-0.42	-1.17	0.28288995	0.6766	-5.97
255324_s_at	putative reverse transcriptase	---	---	-1.07	-0.10	-1.17	0.2830567	0.6766	-5.97
260159_at	putative helicase similar to helicas	---	AT1G79890	-1.10	-0.13	-1.17	0.28286692	0.6766	-5.97
258865_at	NAM-like protein (no apical meriste	anac045	AT3G03200	1.08	0.11	1.17	0.28309756	0.6766	-5.97
249382_at	putative protein predicted proteins	---	AT5G40050	1.08	0.11	1.17	0.28296087	0.6766	-5.97
AFFX-PheX-3_	B. subtilis /GEN=pheB /DB_XREF=	---	---	-1.16	-0.21	-1.17	0.2828365	0.6766	-5.97
260727_at	polygalacturonase PG1, putative s	---	AT1G48100	-1.13	-0.18	-1.17	0.2832255	0.6768	-5.97
245515_at	hypothetical protein	---	AT4G15810	-1.18	-0.24	-1.17	0.28326196	0.6768	-5.97
AFFX-LysX-M_	B. subtilis /GEN=lys /DB_XREF=gi	---	---	-1.17	-0.23	-1.17	0.28325346	0.6768	-5.97
260904_at	unknown protein	NIMIN1	AT1G02450	1.40	0.49	1.17	0.28333251	0.6769	-5.97
255073_at	beta-1,3-glucanase-like protein pr	---	AT4G09090	-1.08	-0.12	-1.17	0.28338568	0.6769	-5.97
254703_at	putative protein ; supported by full	---	AT4G17960	1.14	0.19	1.17	0.28347916	0.6771	-5.97
256583_at	hypothetical protein	---	AT3G28850	-1.24	-0.32	-1.17	0.28358854	0.6772	-5.97
262377_at	rubisco activase, putative similar t	---	AT1G73110	1.19	0.25	1.17	0.28356043	0.6772	-5.97
265422_at	putative NADH-ubiquinone oxiredu	NDB4	AT2G20800	-1.11	-0.15	-1.17	0.28362792	0.6772	-5.97

245945_at	putative protein various predicted	ROPGEF1(	AT5G19560	-1.08	-0.11	-1.16	0.28373329	0.6774	-5.97
253990_at	putative thioredoxin thioredoxin - l	ACHT1	AT4G26160	1.18	0.24	1.16	0.28374595	0.6774	-5.97
265847_at	unknown protein	---	AT2G35750	1.09	0.12	1.16	0.28381226	0.6774	-5.97
260795_at	CLE3, putative CLAVATA3/ESR-F	CLE3	AT1G06225	-1.09	-0.13	-1.16	0.28378526	0.6774	-5.97
262798_at	putative SPL1-related protein simi	SPL14	AT1G20980	-1.10	-0.14	-1.16	0.28386818	0.6774	-5.98
265655_at	unknown protein contains weak PH	---	AT2G13920	-1.10	-0.13	-1.16	0.28399212	0.6777	-5.98
250319_at	putative protein strong similarity to	---	AT5G12120	1.08	0.11	1.16	0.28402637	0.6777	-5.98
258453_at	RNA polymerase I, II and III 24.3 k	NRPB5	AT3G22320	1.08	0.11	1.16	0.2846771	0.6777	-5.98
253092_at	putative protein various predicted	---	AT4G37380	1.18	0.23	1.16	0.28460685	0.6777	-5.98
260004_at	unknown protein ;supported by ful	---	AT1G67860	-1.18	-0.24	-1.16	0.28436017	0.6777	-5.98
248646_at	unknown protein ;supported by ful	---	AT5G49100	-1.21	-0.27	-1.16	0.28428601	0.6777	-5.98
247071_at	putative protein similar to unknown	DAR3	AT5G66640	-1.35	-0.44	-1.16	0.28466453	0.6777	-5.98
264186_at	hypothetical protein predicted by g	---	AT1G54570	-1.27	-0.35	-1.16	0.28455832	0.6777	-5.98
254537_at	putative protein chitinase / lysozyn	---	AT4G19730	-1.10	-0.14	-1.16	0.28453529	0.6777	-5.98
246525_at	CONSTANS ;supported by full-len	CO	AT5G15840	1.11	0.14	1.16	0.28450651	0.6777	-5.98
250473_at	annexin -like protein annexin (Ann	ANN6	AT5G10220	1.08	0.11	1.16	0.28417431	0.6777	-5.98
261517_at	unknown protein ; supported by ful	---	AT1G71780	-1.11	-0.15	-1.16	0.28460731	0.6777	-5.98
251569_at	putative protein several hypothetic	---	AT3G58290	-1.11	-0.16	-1.16	0.28450056	0.6777	-5.98
265013_at	unknown protein similar to EST gb	---	AT1G24460	-1.09	-0.13	-1.16	0.28435422	0.6777	-5.98
264430_at	cineole synthase, putative similar	TPS14	AT1G61680	1.09	0.13	1.16	0.28442871	0.6777	-5.98
258654_at	unknown protein	---	AT3G09860	1.16	0.21	1.16	0.284229	0.6777	-5.98
256115_at	unknown protein ; supported by cD	---	AT1G16880	1.15	0.20	1.16	0.2846479	0.6777	-5.98
250096_at	putative protein similar to unknown	---	AT5G17190	1.10	0.14	1.16	0.28425932	0.6777	-5.98
245953_at	myrosinase - binding protein - like	---	AT5G28520	-1.14	-0.19	-1.16	0.28423196	0.6777	-5.98
266777_at	putative AAA-type ATPase	ftsh3	AT2G29080	-1.09	-0.12	-1.16	0.28456305	0.6777	-5.98
262100_s_at	hypothetical protein similar to hypo	---	AT1G59550 /	1.13	0.18	1.16	0.28434195	0.6777	-5.98
266800_at	hypothetical protein predicted by g	---	AT2G22880	-1.91	-0.93	-1.16	0.28431745	0.6777	-5.98
251202_at	putative protein predicted protein,	---	AT3G63040	-1.08	-0.11	-1.16	0.28424651	0.6777	-5.98
266802_at	Expressed protein ; supported by c	---	AT2G22900	-1.50	-0.58	-1.16	0.28473377	0.6778	-5.98
256998_at	hypothetical protein predicted by g	---	AT3G14180	-1.12	-0.17	-1.16	0.28477525	0.6778	-5.98
246802_at	kinesin-like heavy chain non-conse	ATK4	AT5G27000	-1.12	-0.16	-1.16	0.28479875	0.6778	-5.98
264090_at	cytochrome P-450, putative simila	CYP79C1	AT1G79370	-1.10	-0.13	-1.16	0.28487917	0.6779	-5.98
245742_at	aldehyde dehydrogenase, putative	ALDH3H1	AT1G44170	1.16	0.21	1.16	0.28496493	0.6780	-5.98
249092_at	putative protein similar to unknown	---	AT5G43710	1.11	0.15	1.16	0.28491568	0.6780	-5.98
252316_at	putative protein PrMC3 - Pinus ra	ATCXE13	AT3G48700	1.09	0.13	1.16	0.28497144	0.6780	-5.98

267234_x_at	putative protein kinase contains a	---	AT2G43930	1.10	0.14	1.16	0.28510427	0.6782	-5.98
250763_at	short chain alcohol dehydrogenase	---	AT5G06060	-1.11	-0.15	-1.16	0.28517269	0.6783	-5.98
252866_at	putative protein	---	AT4G39840	-1.29	-0.37	-1.16	0.2853797	0.6784	-5.98
266782_at	putative ligand-gated ion channel p	ATGLR2.7	AT2G29120	-1.09	-0.13	-1.16	0.28542414	0.6784	-5.98
245715_s_at	Expressed protein ; supported by c	---	AT5G08670	1.11	0.15	1.16	0.28535097	0.6784	-5.98
247097_at	mannan endo-1,4-beta-mannosida	---	AT5G66460	1.14	0.19	1.16	0.28527532	0.6784	-5.98
257486_at	unknown protein	---	AT1G63590	1.08	0.12	1.16	0.28542627	0.6784	-5.98
258293_at	unknown protein	PHO1	AT3G23430	-1.42	-0.51	-1.16	0.28537782	0.6784	-5.98
251643_at	guanylate kinase-like protein guar	AGK2	AT3G57550	1.25	0.32	1.16	0.28539181	0.6784	-5.98
256426_at	hypothetical protein predicted by g	---	AT1G33420	1.27	0.35	1.16	0.28584373	0.6784	-5.98
262912_at	oligopeptide transporter, putative	---	AT1G59740	-1.40	-0.48	-1.16	0.28568467	0.6784	-5.98
255005_at	putative protein putative proteins A	---	AT4G09990	-1.11	-0.15	-1.16	0.28585941	0.6784	-5.98
267126_s_at	putative acetone-cyanohydrin lyas	ACL	AT2G23590	-1.16	-0.22	-1.16	0.28562968	0.6784	-5.98
249788_at	putative protein contains similarity	ATXR6	AT5G24330	1.15	0.20	1.16	0.28589203	0.6784	-5.98
256501_at	hypothetical protein predicted by g	---	AT1G36756	-1.09	-0.13	-1.16	0.28584958	0.6784	-5.98
250844_at	putative protein ;supported by full-	SIM	AT5G04470	-1.22	-0.28	-1.16	0.28573608	0.6784	-5.98
251497_at	putative protein phytochrome-ass	PIL6	AT3G59060	1.11	0.15	1.16	0.28583672	0.6784	-5.98
260307_at	unknown protein similar to unknow	---	AT1G70620	-1.07	-0.10	-1.16	0.28589842	0.6784	-5.98
263479_x_at	hypothetical protein predicted by g	---	---	-1.09	-0.12	-1.16	0.28582745	0.6784	-5.98
250997_at	putative protein histone H2B-2, to	---	AT5G02570	1.10	0.14	1.16	0.28573746	0.6784	-5.98
266512_at	unknown protein	---	AT2G47690	1.08	0.11	1.16	0.28575072	0.6784	-5.98
247458_at	putative protein PrMC3, Pinus rad	AtCXE20	AT5G62180	1.19	0.25	1.16	0.28590363	0.6784	-5.98
248086_at	putative protein similar to unknown	GEX1	AT5G55490	1.08	0.11	1.16	0.28551182	0.6784	-5.98
262416_at	flavonol synthase, putative similar	---	AT1G49390	1.09	0.12	1.16	0.28552621	0.6784	-5.98
247006_at	unknown protein ;supported by ful	---	AT5G67490	1.07	0.10	1.16	0.28557861	0.6784	-5.98
254579_at	hypothetical protein ;supported by	---	AT4G19400	-1.12	-0.16	-1.16	0.28600168	0.6786	-5.98
250471_at	myo-inositol-1-phosphate synthas	MIPS3	AT5G10170	-1.16	-0.21	-1.16	0.28610811	0.6787	-5.98
250923_at	putative protein ; supported by full	CDC25	AT5G03455	1.12	0.16	1.16	0.28619477	0.6789	-5.98
246665_s_at	putative protein predicted proteins	---	---	-1.10	-0.14	-1.16	0.28621614	0.6789	-5.98
264047_at	hypothetical protein predicted by g	---	AT2G22410	1.10	0.13	1.16	0.28630758	0.6790	-5.98
260781_at	decoy identical to GB:AAB51588 C	DECOY	AT1G14620	1.31	0.39	1.16	0.2864014	0.6792	-5.98
266125_at	putative GATA-type zinc finger tra	---	AT2G45050	1.12	0.17	1.16	0.28651581	0.6794	-5.98
247028_at	DNA polymerase alpha 1	ICU2	AT5G67100	1.23	0.30	1.16	0.28654676	0.6794	-5.98
263349_at	putative chromodomain-helicase-D	CHR5	AT2G13370	-1.13	-0.17	-1.16	0.28658527	0.6794	-5.98
258169_at	hypothetical protein	---	AT3G21590	-1.10	-0.14	-1.16	0.28662056	0.6794	-5.98

263797_at	putative WRKY-type DNA binding	WRKY17	AT2G24570	1.38	0.47	1.16	0.28667543	0.6795	-5.98
247719_at	Expressed protein ; supported by f	---	AT5G59305	-1.10	-0.14	-1.16	0.2868142	0.6797	-5.98
252752_s_at	putative protein hypothetical prote	---	AT3G43470	-1.08	-0.12	-1.16	0.28693057	0.6799	-5.98
267582_at	putative protein kinase contains a	---	AT2G41970	1.09	0.12	1.16	0.2870019	0.6800	-5.98
256345_at	hypothetical protein similar to hypo	---	AT1G55030	-1.09	-0.13	-1.16	0.28708368	0.6801	-5.98
254722_at	putative protein predicted protein,	---	AT4G13530	1.18	0.24	1.16	0.28713914	0.6802	-5.98
257087_at	purple acid phosphatase, putative	PAP18	AT3G20500	-1.11	-0.16	-1.16	0.28724286	0.6804	-5.98
260609_at	putative receptor protein kinase	---	AT2G43690	-1.09	-0.13	-1.16	0.2872837	0.6804	-5.98
255412_at	auxin-binding protein 1 precursor	ABP1	AT4G02980	-1.10	-0.13	-1.16	0.28735887	0.6805	-5.99
254939_at	putative protein predicted proteins	---	AT4G10800	1.15	0.20	1.16	0.28740927	0.6806	-5.99
255893_at	threonyl-tRNA synthetase, putativ	---	AT1G17960	-1.18	-0.24	-1.15	0.28747581	0.6806	-5.99
267299_at	putative glucosyltransferase	---	AT2G30150	1.13	0.17	1.15	0.28754724	0.6807	-5.99
255371_at	putative RPP1-like disease resista	---	AT4G04110	-1.09	-0.12	-1.15	0.28752615	0.6807	-5.99
255042_at	putative protein hypothetical prote	---	AT4G09630	1.09	0.13	1.15	0.287697	0.6808	-5.99
267041_at	unknown protein	---	AT2G34315	-1.08	-0.11	-1.15	0.28766987	0.6808	-5.99
264080_at	putative vacuolar proton-ATPase s	VHA-A1	AT2G28520	1.08	0.11	1.15	0.28768135	0.6808	-5.99
251680_at	putative protein 13S condensin XC	---	AT3G57060	-1.09	-0.12	-1.15	0.28774772	0.6809	-5.99
259164_at	hypothetical protein contains brom	ATBET10	AT3G01770	-1.14	-0.18	-1.15	0.28804239	0.6809	-5.99
252147_at	putative protein several hypothetic	---	AT3G51270	1.15	0.20	1.15	0.2879033	0.6809	-5.99
258817_at	hypothetical protein similar to hyp	---	AT3G04750	-1.08	-0.11	-1.15	0.28817147	0.6809	-5.99
245383_at	SUPERMAN like protein	---	AT4G17810	1.18	0.24	1.15	0.28807428	0.6809	-5.99
265083_at	hypothetical protein predicted by g	---	AT1G03820	1.21	0.27	1.15	0.28815964	0.6809	-5.99
261734_at	hypothetical protein similar to hypo	---	AT1G47790	-1.09	-0.12	-1.15	0.28808401	0.6809	-5.99
251280_at	putative protein beta-1,3-glucanas	---	AT3G61810	-1.09	-0.13	-1.15	0.2881954	0.6809	-5.99
262591_at	hypothetical protein Similar to gb|X	CCMH	AT1G15220	1.09	0.12	1.15	0.28795012	0.6809	-5.99
245890_at	ribosomal protein S15-like riboson	---	AT5G09490	-1.07	-0.10	-1.15	0.28804412	0.6809	-5.99
266358_at	hypothetical protein predicted by g	---	AT2G32280	1.23	0.30	1.15	0.28783992	0.6809	-5.99
258740_at	Lon protease, putative similar to L	LON3	AT3G05780	-1.13	-0.18	-1.15	0.2881118	0.6809	-5.99
248137_at	putative protein contains similarity	---	AT5G54950	1.10	0.13	1.15	0.28802819	0.6809	-5.99
252556_at	putative protein step II splicing fac	---	AT3G45950	1.07	0.10	1.15	0.28819472	0.6809	-5.99
267122_at	putative acetone-cyanohydrin lyas	MES6	AT2G23550	1.09	0.12	1.15	0.28819777	0.6809	-5.99
262973_at	histone H3, putative similar to HIS	---	AT1G75600	-1.09	-0.12	-1.15	0.28810577	0.6809	-5.99
255116_at	receptor protein kinase-like protei	---	AT4G08850	1.14	0.19	1.15	0.28824894	0.6809	-5.99
261287_at	hypothetical protein predicted by g	---	AT1G37020	-1.07	-0.10	-1.15	0.2883627	0.6810	-5.99
247657_at	Expressed protein ; supported by f	---	AT5G59845	1.11	0.15	1.15	0.2883675	0.6810	-5.99

249739_at	Ttg1 protein (emb CAB45372.1)	TTG1	AT5G24520	1.08	0.11	1.15	0.2883904	0.6810	-5.99
253337_at	putative protein acetylpolyamine a	hda14	AT4G33470	-1.17	-0.23	-1.15	0.28853248	0.6813	-5.99
247338_at	pyruvate kinase	---	AT5G63680	-1.09	-0.13	-1.15	0.28858654	0.6814	-5.99
245991_at	24 kDa vacuolar protein - like 24 k	---	AT5G20660	1.09	0.12	1.15	0.28874661	0.6814	-5.99
252736_at	kinesin -like protein kinesin-like pr	TES	AT3G43210	-1.09	-0.13	-1.15	0.2887462	0.6814	-5.99
260612_at	hypothetical protein similar to hypo	---	AT1G53360	-1.08	-0.11	-1.15	0.28869993	0.6814	-5.99
258639_at	polygalacturonase (PGA3) identic	---	AT3G07820	1.07	0.10	1.15	0.28866951	0.6814	-5.99
265334_at	putative lipid transfer protein ; sup	---	AT2G18370	1.22	0.29	1.15	0.28874893	0.6814	-5.99
247234_at	putative protein similar to unknown	---	AT5G64980	1.09	0.12	1.15	0.28890949	0.6817	-5.99
262650_at	lipoamide dehydrogenase, putativ	---	AT1G14090	1.07	0.10	1.15	0.28895283	0.6817	-5.99
249457_s_at	zinc finger -like protein transcriptio	VIM4	AT1G66040	1.13	0.18	1.15	0.28899078	0.6818	-5.99
252686_at	putative protein predicted protein,	---	---	-1.08	-0.12	-1.15	0.28914391	0.6820	-5.99
260285_at	putative 3-isopropylmalate dehydro	---	AT1G80560	1.12	0.16	1.15	0.28914089	0.6820	-5.99
263256_at	unknown protein similar to ESTs g	ATCPISCA	AT1G10500	-1.13	-0.17	-1.15	0.28932167	0.6823	-5.99
256259_at	hypothetical protein predicted by g	---	AT3G12460	-1.13	-0.18	-1.15	0.28939454	0.6823	-5.99
250434_at	histone H3 - like protein histone H	---	AT5G10390	1.49	0.58	1.15	0.28945039	0.6823	-5.99
259382_s_at	jasmonate inducible protein isolog	JAL31	AT3G16420	-1.58	-0.66	-1.15	0.28936812	0.6823	-5.99
262333_at	hypothetical protein similar to puta	---	AT1G64020	1.10	0.14	1.15	0.28943791	0.6823	-5.99
246394_at	myrosinase binding protein, putati	---	AT1G58160	-1.08	-0.11	-1.15	0.28948537	0.6824	-5.99
252152_at	putative protein several hypothetic	---	AT3G51350	-1.09	-0.12	-1.15	0.28961713	0.6826	-5.99
255007_at	putative oxidoreductase 11beta-hy	AtHSD5	AT4G10020	1.09	0.12	1.15	0.2896614	0.6826	-5.99
264006_at	homeodomain transcription factor (	ATHB6	AT2G22430	-1.15	-0.20	-1.15	0.28968888	0.6826	-5.99
246928_at	putative protein Scythe protein - X	---	AT5G25270	1.09	0.12	1.15	0.28981956	0.6829	-5.99
267319_at	ABC transporter (AtMRP2) identica	ATMRP2	AT2G34660	1.14	0.19	1.15	0.29081783	0.6830	-5.99
255889_at	ABC transporter, putative similar t	WBC11	AT1G17840	-1.14	-0.19	-1.15	0.29069565	0.6830	-5.99
266254_at	putative membrane transporter	NAT12	AT2G27810	1.13	0.17	1.15	0.28991097	0.6830	-5.99
245078_at	putative AP2 domain transcription	---	AT2G23340	-1.29	-0.37	-1.15	0.29089605	0.6830	-6.00
256091_at	Expressed protein ; supported by f	HMGB2	AT1G20693	1.10	0.13	1.15	0.2910231	0.6830	-6.00
246555_at	putative protein 68 kDa protein - C	GAUT14	AT5G15470	-1.15	-0.20	-1.15	0.29053765	0.6830	-5.99
258356_at	unknown protein	---	AT3G14340	1.12	0.16	1.15	0.28994612	0.6830	-5.99
250818_at	Expressed protein ; supported by c	ALA1	AT5G04930	1.13	0.18	1.15	0.29109337	0.6830	-6.00
251683_at	putative protein several hypothetic	---	AT3G57120	-1.22	-0.29	-1.15	0.29091472	0.6830	-6.00
256803_at	cytochrome P450, putative similar	CYP705A3	AT3G20960	1.08	0.12	1.15	0.29026695	0.6830	-5.99
252464_at	RNA-binding protein-like protein va	---	AT3G47160	1.13	0.17	1.15	0.29018502	0.6830	-5.99
257679_at	glycine-rich protein, putative ident	GRP5	AT3G20470	-1.34	-0.42	-1.15	0.2903626	0.6830	-5.99

251026_at	hypothetical protein	FHL	AT5G02200	1.42	0.50	1.15	0.2903021	0.6830	-5.99
260309_at	putative alanine aminotransferase	AOAT2	AT1G70580	-1.13	-0.17	-1.15	0.29042059	0.6830	-5.99
259342_at	unknown protein ;supported by ful	---	AT3G03890	1.14	0.19	1.15	0.29061906	0.6830	-5.99
262158_at	somatic embryogenesis receptor-l	---	AT1G52540	1.15	0.21	1.15	0.2901584	0.6830	-5.99
250412_at	putative protein synaptobrevin-like	ATVAMP71	AT5G11150	-1.13	-0.17	-1.15	0.29076524	0.6830	-5.99
265774_at	hypothetical protein predicted by g	---	AT2G07240	-1.13	-0.18	-1.15	0.2902676	0.6830	-5.99
267474_at	hypothetical protein predicted by g	WHY3	AT2G02740	1.11	0.15	1.15	0.29019173	0.6830	-5.99
245755_at	hypothetical protein predicted by g	---	AT1G35210	1.73	0.79	1.15	0.290403	0.6830	-5.99
257698_at	regulatory protein of P-starvation a	---	AT3G12730	-1.10	-0.14	-1.15	0.2909666	0.6830	-6.00
265098_at	unknown protein	---	AT1G04010	-1.21	-0.28	-1.15	0.29045563	0.6830	-5.99
251275_at	putative protein anthranilate phosp	---	AT3G61720	-1.15	-0.21	-1.15	0.29045325	0.6830	-5.99
253924_at	putative protein other hypothetical	COBL11	AT4G27110	-1.11	-0.15	-1.15	0.29107949	0.6830	-6.00
261321_at	hypothetical protein predicted by g	---	AT1G44740	-1.10	-0.14	-1.15	0.29104847	0.6830	-6.00
257525_at	hypothetical protein predicted by g	---	AT3G04900	-1.11	-0.15	-1.15	0.29045202	0.6830	-5.99
267438_at	putative GDSL-motif lipase/hydrola	---	AT2G19050	-1.15	-0.20	-1.15	0.29026484	0.6830	-5.99
263425_at	putative preprotein translocase SE	EMB2289	AT2G31530	-1.11	-0.15	-1.15	0.29106106	0.6830	-6.00
254369_at	putative protein	---	AT4G21720	1.13	0.18	1.15	0.29037193	0.6830	-5.99
252815_at	hypothetical protein	---	---	-1.11	-0.16	-1.15	0.29091417	0.6830	-6.00
258594_at	hypothetical protein predicted by g	---	AT3G04490	-1.10	-0.13	-1.15	0.29070908	0.6830	-5.99
256805_at	unknown protein contains similarit	---	AT3G20930	1.21	0.28	1.15	0.2906716	0.6830	-5.99
265903_at	putative potassium transporter/cha	SPIK	AT2G25600	-1.09	-0.12	-1.15	0.29028473	0.6830	-5.99
264036_at	hypothetical protein similar to hypo	---	AT2G03810	1.14	0.19	1.15	0.29104047	0.6830	-6.00
260114_at	AIG1-like protein similar to AIG1 p	---	AT1G33880	1.09	0.12	1.15	0.2902872	0.6830	-5.99
250344_at	glutaredoxin - like protein glutared	---	AT5G11930	-1.19	-0.25	-1.15	0.29003392	0.6830	-5.99
245802_at	hypothetical protein similar to hypo	---	AT1G46840	-1.08	-0.11	-1.15	0.29111478	0.6830	-6.00
256109_at	hypothetical protein predicted by g	---	AT1G16950	1.18	0.23	1.15	0.2908456	0.6830	-5.99
252027_at	Spot 3 protein and vacuolar sorting	VSR1	AT3G52850	-1.08	-0.11	-1.15	0.29080886	0.6830	-5.99
267381_at	unknown protein ; supported by cl	---	AT2G26190	1.53	0.62	1.15	0.29052978	0.6830	-5.99
252391_at	putative protein ; supported by cD	---	AT3G47860	-1.12	-0.16	-1.15	0.29051386	0.6830	-5.99
267045_at	putative protein kinase contains a	CIPK13	AT2G34180	1.09	0.12	1.15	0.29097881	0.6830	-6.00
257780_at	hypothetical protein predicted by g	---	AT3G27100	1.11	0.16	1.15	0.29114749	0.6830	-6.00
262254_at	unknown protein similar to GDSL-r	GLIP5	AT1G53920	-1.21	-0.28	-1.15	0.29120995	0.6830	-6.00
265120_at	3-ketoacyl-acyl carrier protein synt	KAS III	AT1G62640	1.12	0.16	1.15	0.29123782	0.6830	-6.00
252404_at	glycine--tRNA ligase precursor, ch	EDD1	AT3G48110	1.09	0.13	1.14	0.29138152	0.6833	-6.00
257823_at	integral membrane protein, putativ	---	AT3G25190	-1.10	-0.14	-1.14	0.29144369	0.6834	-6.00

259487_at	hypothetical protein contains simila	TRFL5	AT1G15720	-1.07	-0.10	-1.14	0.29150879	0.6834	-6.00
253383_at	putative protein ;supported by full-	---	AT4G32900	1.14	0.19	1.14	0.29197781	0.6834	-6.00
251804_at	beta-1,3-glucanase - like protein p	---	AT3G55430	-1.14	-0.19	-1.14	0.29176666	0.6834	-6.00
248867_at	bHLH transcription factor	---	AT5G46830	-1.09	-0.12	-1.14	0.29191302	0.6834	-6.00
249030_at	putative protein similar to unknown	---	---	-1.08	-0.12	-1.14	0.29196549	0.6834	-6.00
255161_at	putative reverse transcriptase	---	---	1.09	0.12	1.14	0.29175286	0.6834	-6.00
249423_at	Expressed protein ; supported by f	---	AT5G39785	-1.13	-0.17	-1.14	0.29168274	0.6834	-6.00
257958_at	unknown protein similar to disease	---	AT3G25510	-1.11	-0.15	-1.14	0.29160467	0.6834	-6.00
253130_at	putative protein ;supported by full-	---	AT4G35510	-1.17	-0.22	-1.14	0.29167777	0.6834	-6.00
260782_at	unknown protein ; supported by cD	---	AT1G14570	1.08	0.12	1.14	0.29182508	0.6834	-6.00
255427_at	hypothetical protein	---	AT4G03380	-1.07	-0.10	-1.14	0.29189965	0.6834	-6.00
262549_at	hypothetical protein similar to hypo	---	AT1G31290	-1.09	-0.12	-1.14	0.29194853	0.6834	-6.00
265553_at	putative retroelement pol polyprote	---	---	1.09	0.13	1.14	0.29153613	0.6834	-6.00
246692_at	putative protein predicted protein,	---	---	-1.12	-0.16	-1.14	0.29160584	0.6834	-6.00
267257_at	putative casein kinase II catalytic (	---	AT2G23080	-1.07	-0.10	-1.14	0.29173575	0.6834	-6.00
255853_at	hypothetical protein predicted by g	---	AT1G67020	-1.08	-0.12	-1.14	0.29183359	0.6834	-6.00
261562_at	actin depolymerizing factor, putati	ADF11	AT1G01750	1.13	0.18	1.14	0.29196731	0.6834	-6.00
252997_at	putative pollen allergen pollen alle	ATEXLA2	AT4G38400	-1.28	-0.36	-1.14	0.29291982	0.6839	-6.00
258282_at	unknown protein	---	AT3G26910	1.28	0.35	1.14	0.29265817	0.6839	-6.00
256400_at	putative RING zinc finger protein c	---	AT3G06140	1.13	0.17	1.14	0.29299257	0.6839	-6.00
256220_at	unknown protein	---	AT1G56230	-1.12	-0.17	-1.14	0.2929087	0.6839	-6.00
265732_at	predicted by genscan and genefinc	---	AT2G01300	-1.68	-0.75	-1.14	0.29235909	0.6839	-6.00
250524_at	putative protein contains similarity	---	AT5G08520	1.09	0.12	1.14	0.29285223	0.6839	-6.00
257408_at	unknown protein similar to A. thalia	SON1	AT2G17310	-1.11	-0.15	-1.14	0.29250303	0.6839	-6.00
253467_at	putative protein hypothetical prote	---	AT4G32140	1.11	0.15	1.14	0.29294727	0.6839	-6.00
263510_s_at	hypothetical protein	---	AT2G07681 /	-1.08	-0.11	-1.14	0.29296336	0.6839	-6.00
267311_at	hypothetical protein	---	AT2G34670	1.08	0.11	1.14	0.29287785	0.6839	-6.00
255461_at	ent-kaurene synthetase A - like pro	GA1	AT4G02780	-1.10	-0.14	-1.14	0.29280076	0.6839	-6.00
248950_at	ATP-dependent Clp protease prote	CLPP4	AT5G45390	1.11	0.15	1.14	0.29224407	0.6839	-6.00
263738_at	hypothetical protein predicted by g	---	AT1G60060	-1.29	-0.37	-1.14	0.29275097	0.6839	-6.00
267450_at	hypothetical protein predicted by g	---	AT2G33720	-1.14	-0.20	-1.14	0.2928771	0.6839	-6.00
252203_at	hypothetical protein	---	AT3G50320	-1.08	-0.12	-1.14	0.29260769	0.6839	-6.00
252466_x_at	putative protein several hypothetic	---	---	-1.09	-0.13	-1.14	0.2927032	0.6839	-6.00
262727_at	thaumatin, putative contains Pfam	---	AT1G75800	-1.09	-0.12	-1.14	0.29261353	0.6839	-6.00
245788_at	hypothetical protein similar to hypo	---	AT1G32120 /	1.24	0.31	1.14	0.29264603	0.6839	-6.00

259681_at	nitrate reductase 1 (NR1) identical	NIA1	AT1G77760	1.93	0.95	1.14	0.29261503	0.6839	-6.00
261877_at	putative indole-3-acetate beta-gluc	---	AT1G50580	-1.09	-0.13	-1.14	0.29290986	0.6839	-6.00
260454_at	RING-H2 zinc finger protein (ATL3	ATL3	AT1G72310	1.21	0.28	1.14	0.2928854	0.6839	-6.00
AFFX-CreX-5_	Bacteriophage P1 /GEN=cre /DB_	---	---	-1.22	-0.28	-1.14	0.29265736	0.6839	-6.00
260567_at	putative glucosyltransferase ;supp	UGT74F2	AT2G43820	-1.15	-0.21	-1.14	0.29301653	0.6839	-6.00
250022_at	Brn1-like protein	---	AT5G18210	1.18	0.24	1.14	0.29299108	0.6839	-6.00
264466_at	Expressed protein ; supported by f	---	AT1G10380	1.21	0.28	1.14	0.29269472	0.6839	-6.00
259284_at	putative cell division related protei	---	AT3G11450	1.11	0.15	1.14	0.29266652	0.6839	-6.00
258702_at	hypothetical protein predicted by g	---	AT3G09730	1.13	0.18	1.14	0.29249242	0.6839	-6.00
245943_at	putative protein permease family p	---	AT5G19500	-1.13	-0.17	-1.14	0.29246333	0.6839	-6.00
256628_at	membrane import protein, putative	TOM40	AT3G20000	1.16	0.21	1.14	0.29305424	0.6839	-6.00
253070_at	putative protein symbiotic ammon	---	AT4G37850	-1.10	-0.14	-1.14	0.29308358	0.6839	-6.00
245775_at	serine/threonine kinase, putative s	CIPK23	AT1G30270	-1.10	-0.13	-1.14	0.2932854	0.6839	-6.00
259125_at	unknown protein Pfam HMM hit: R	---	AT3G02300	-1.08	-0.11	-1.14	0.29314495	0.6839	-6.00
255140_x_at	extensin-like protein hydroxyprolin	---	AT4G08410	-1.16	-0.21	-1.14	0.29319963	0.6839	-6.00
265211_at	late embryogenesis abundant prot	ATECP63	AT2G36640	-1.08	-0.11	-1.14	0.2932127	0.6839	-6.00
246629_at	unknown protein similar to hypothe	---	AT1G50750	1.12	0.17	1.14	0.2931887	0.6839	-6.00
256796_at	hypothetical protein predicted by g	---	AT3G22210	1.17	0.23	1.14	0.29329675	0.6839	-6.00
253194_s_at	hypothetical protein	---	---	-1.10	-0.13	-1.14	0.29326545	0.6839	-6.00
245875_at	hypothetical protein predicted by g	---	AT1G26240	1.12	0.16	1.14	0.29335042	0.6840	-6.00
252943_at	cinnamyl-alcohol dehydrogenase C	CAD9	AT4G39330	1.89	0.92	1.14	0.29343199	0.6841	-6.00
260515_at	ATP-dependent transmembrane t	---	AT1G51460	1.11	0.15	1.14	0.29347055	0.6841	-6.00
250125_at	biotin carboxyl carrier protein of ac	CAC1	AT5G16390	1.10	0.13	1.14	0.29351022	0.6841	-6.00
250222_at	putative protein similar to unknown	---	AT5G14050	1.16	0.22	1.14	0.2935826	0.6842	-6.00
249832_at	disease resistance protein-like	---	AT5G23400	1.12	0.16	1.14	0.29362072	0.6842	-6.00
248580_at	chloride channel (emb|CAA70310.	CLC-C	AT5G49890	-1.13	-0.17	-1.14	0.29363574	0.6842	-6.00
247560_at	putative protein predicted proteins	---	AT5G61090	-1.12	-0.16	-1.14	0.29373394	0.6843	-6.00
259095_at	acyl carrier protein 1 precursor (AC	ACP1	AT3G05020	1.25	0.32	1.14	0.29372609	0.6843	-6.00
250178_at	putative protein various unknown	---	AT5G14430	1.08	0.11	1.14	0.29383295	0.6843	-6.00
258952_at	putative RNase H contains Pfam p	---	AT3G01410	-1.11	-0.15	-1.14	0.29383738	0.6843	-6.00
249163_at	glucose-6-phosphate isomerase, c	---	AT5G42740	-1.13	-0.18	-1.14	0.29382115	0.6843	-6.00
253111_at	putative protein glutamic acid-rich	---	AT4G35940	-1.14	-0.18	-1.14	0.29388292	0.6844	-6.00
262335_at	hypothetical protein predicted by g	SPO11-2	AT1G63990	-1.07	-0.10	-1.14	0.29391733	0.6844	-6.00
258914_at	hypothetical protein predicted by g	AGP27	AT3G06360	-1.08	-0.11	-1.14	0.29398259	0.6845	-6.00
266767_at	Expressed protein ; supported by f	---	AT2G46910	1.13	0.17	1.14	0.29402071	0.6845	-6.00

253897_at	putative protein	---	AT4G27120	1.09	0.12	1.14	0.2940922	0.6846	-6.00
247958_at	putative protein similar to unknown	---	AT5G57070	-1.10	-0.14	-1.14	0.29411389	0.6846	-6.00
247293_at	putative protein similar to unknown	---	AT5G64510	-1.36	-0.44	-1.14	0.29426653	0.6849	-6.00
260953_at	transcriptional activator RF2a, put	---	AT1G06070	1.10	0.14	1.14	0.29432306	0.6849	-6.00
264128_at	unknown protein	---	AT1G79190	1.09	0.13	1.14	0.29436646	0.6849	-6.00
249232_at	dynamin-like protein (pir||S59558)	ADL1	AT5G42080	1.14	0.19	1.14	0.29439229	0.6849	-6.00
246926_at	putative protein	---	AT5G25240	1.18	0.23	1.14	0.29460645	0.6851	-6.01
252207_at	putative protein mRNA of unknow	---	AT3G50370	1.10	0.14	1.14	0.29457178	0.6851	-6.01
264686_at	shaggy-like protien kinase, kappa	ATSK41	AT1G09840	1.08	0.11	1.14	0.29460811	0.6851	-6.01
251163_at	putative protein S1R protein - Hon	---	AT3G63310	1.08	0.11	1.14	0.29463672	0.6851	-6.01
263279_x_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.14	0.29460697	0.6851	-6.01
247606_at	RNA helicase	---	AT5G61000	1.29	0.37	1.14	0.29457848	0.6851	-6.01
265351_at	putative MADS-box protein AGL17	AGL17	AT2G22630	-1.10	-0.14	-1.14	0.29467655	0.6851	-6.01
262528_at	H+-transporting ATPase AHA10 Id	AHA10	AT1G17260	-1.12	-0.16	-1.14	0.29473862	0.6852	-6.01
260974_at	receptor-like serine/threonine kina	---	AT1G53440	-1.21	-0.28	-1.14	0.29476906	0.6852	-6.01
256919_at	hypothetical protein predicted by g	---	AT3G18970	1.11	0.14	1.14	0.29492171	0.6854	-6.01
247496_at	putative protein predicted proteins	GUT1	AT5G61840	1.09	0.12	1.14	0.29492045	0.6854	-6.01
249377_at	putative protein predicted proteins	---	AT5G40690	1.18	0.24	1.14	0.29496066	0.6854	-6.01
257344_s_at	pseudogene, putative mutator-like	---	---	-1.14	-0.19	-1.14	0.29501836	0.6855	-6.01
258475_at	putative tyrosyl-tRNA synthetase s	emb2768	AT3G02660	1.09	0.12	1.14	0.29511861	0.6856	-6.01
263744_at	Mutator-like transposase similar to	---	AT2G21420	-1.10	-0.14	-1.14	0.29517033	0.6857	-6.01
247630_at	putative protein	SIZ1	AT5G60410	-1.11	-0.15	-1.13	0.29523979	0.6857	-6.01
248691_at	putative protein strong similarity to	---	AT5G48310	-1.09	-0.12	-1.13	0.295232	0.6857	-6.01
256670_at	Athila ORF 1, putative similar to A	---	---	-1.09	-0.12	-1.13	0.29536194	0.6859	-6.01
255680_at	hypothetical protein	---	AT4G00530	1.12	0.17	1.13	0.29552781	0.6862	-6.01
265832_at	putative replication protein A1	---	---	-1.08	-0.11	-1.13	0.2955807	0.6863	-6.01
AFFX-Athal-GA	Arabidopsis thaliana /REF=M6411	GAPC1	---	1.15	0.20	1.13	0.29584099	0.6867	-6.01
261661_at	lysophospholipase homolog, putat	---	AT1G18360	-1.16	-0.21	-1.13	0.29582319	0.6867	-6.01
258944_at	hypothetical protein similar to hypo	FLD	AT3G10390	-1.12	-0.16	-1.13	0.29578503	0.6867	-6.01
252762_at	putative protein hypothetical prote	---	AT3G42780	-1.13	-0.18	-1.13	0.29593288	0.6868	-6.01
266986_at	putative dolichyl-phosphate beta-g	---	AT2G39630	1.08	0.11	1.13	0.29597134	0.6869	-6.01
258723_at	putative MYB-related protein simila	---	AT3G09600	-1.09	-0.13	-1.13	0.29601792	0.6869	-6.01
245155_at	putative protein similarity to predic	---	AT5G12470	1.15	0.20	1.13	0.29609629	0.6869	-6.01
263772_at	Expressed protein ; supported by f	ELF4-L3	AT2G06255	-1.18	-0.24	-1.13	0.29607033	0.6869	-6.01
263934_at	hypothetical protein predicted by g	EDA12	AT2G35950	1.08	0.10	1.13	0.29625203	0.6870	-6.01

254326_at	putative protein AIR1, Arabidopsis	---	AT4G22610	-1.10	-0.14	-1.13	0.29616596	0.6870	-6.01
256388_at	unknown protein	---	AT3G06180	1.10	0.14	1.13	0.29620291	0.6870	-6.01
259869_at	putative heat shock protein predict	---	AT1G76770	-1.09	-0.13	-1.13	0.29622339	0.6870	-6.01
254013_at	putative leucine-rich-repeat protei	---	AT4G26050	-1.15	-0.20	-1.13	0.29634782	0.6872	-6.01
256207_at	GTP-binding protein, putative simi	---	AT1G50920	1.12	0.17	1.13	0.29641905	0.6872	-6.01
263708_at	unknown protein	---	AT1G09320	1.09	0.13	1.13	0.29644108	0.6872	-6.01
254644_at	CLE2, putative CLAVATA3/ESR-F	CLE2	AT4G18510	1.11	0.15	1.13	0.29643375	0.6872	-6.01
251628_at	translation initiation factor 3 -like p	EIF3E	AT3G57290	1.11	0.15	1.13	0.2965904	0.6875	-6.01
264437_at	unknown protein EST gb|N65787 c	---	AT1G27510	1.10	0.14	1.13	0.29663282	0.6875	-6.01
267151_at	aspartate aminotransferase (AAT1	ASP1	AT2G30970	-1.13	-0.18	-1.13	0.29671279	0.6876	-6.01
259980_at	unknown protein ;supported by ful	---	AT1G76520	-1.20	-0.27	-1.13	0.2968588	0.6876	-6.01
249582_at	calmodulin 1 (CAM1) ; supported	CAM1	AT5G37780	1.12	0.16	1.13	0.29704994	0.6876	-6.01
253873_at	hypothetical protein ;supported by	PRA1.H	AT4G27540	-1.09	-0.12	-1.13	0.29685485	0.6876	-6.01
255784_at	hypothetical protein predicted by g	---	AT1G19860	1.09	0.12	1.13	0.29708387	0.6876	-6.01
266776_at	putative ubiquitin fusion-degradatic	---	AT2G29070	1.11	0.16	1.13	0.29702588	0.6876	-6.01
250570_at	putative protein hypothetical bacte	EMB1873	AT5G08170	-1.13	-0.18	-1.13	0.2972032	0.6876	-6.01
259215_at	unknown protein largely predicted	DEX1	AT3G09090	1.09	0.12	1.13	0.29693998	0.6876	-6.01
265128_at	hypothetical protein predicted by g	---	AT1G30860	-1.12	-0.17	-1.13	0.29719276	0.6876	-6.01
257430_at	hypothetical protein similar to hypo	---	AT2G28580	-1.12	-0.16	-1.13	0.29714486	0.6876	-6.01
264306_at	unknown protein predicted by gene	---	AT1G78890	1.11	0.15	1.13	0.29719923	0.6876	-6.01
264468_at	unknown protein similar to daunoru	---	AT1G10310	-1.12	-0.16	-1.13	0.2968614	0.6876	-6.01
255299_at	putative adenosine deaminase sim	---	AT4G04880	1.10	0.14	1.13	0.29700093	0.6876	-6.01
263080_at	hypothetical protein predicted by g	---	---	-1.11	-0.15	-1.13	0.29717182	0.6876	-6.01
256608_at	hypothetical protein predicted by g	---	AT3G30840	-1.07	-0.10	-1.13	0.29711875	0.6876	-6.01
252477_at	glucosyltransferase-like protein UI	---	AT3G46680	-1.13	-0.18	-1.13	0.29702871	0.6876	-6.01
248671_at	putative protein strong similarity to	---	AT5G48750	-1.08	-0.11	-1.13	0.29720576	0.6876	-6.01
260403_at	hypothetical protein predicted by g	WRKY36	AT1G69810	-1.08	-0.11	-1.13	0.2973016	0.6878	-6.01
247875_at	putative protein similar to unknown	---	AT5G57720	1.10	0.14	1.13	0.29743537	0.6879	-6.01
251449_at	Rab GDP dissociation inhibitor ; s	ATGDI2	AT3G59920	1.12	0.16	1.13	0.29740995	0.6879	-6.01
263278_at	dynamin-like protein	DRP3B	AT2G14120	-1.11	-0.15	-1.13	0.29738083	0.6879	-6.01
261778_at	hypothetical protein predicted by g	---	AT1G76220	-1.07	-0.10	-1.13	0.29749674	0.6879	-6.01
255016_at	sucrose-phosphate synthase - like	ATSPS4F	AT4G10120	1.15	0.20	1.13	0.29776384	0.6880	-6.01
261591_at	protein kinase, putative similar to	---	AT1G01740	-1.13	-0.18	-1.13	0.29770459	0.6880	-6.01
257887_at	protein phosphatase-2c, putative s	---	AT3G17090	1.11	0.16	1.13	0.29762911	0.6880	-6.01
249645_at	thionin Thi2.2 ;supported by full-le	THI2.2	AT5G36910	-1.13	-0.18	-1.13	0.2976557	0.6880	-6.01

267626_at	putative cytochrome P450	CYP712A1	AT2G42250	-1.16	-0.21	-1.13	0.29758995	0.6880	-6.01
266423_at	putative DNA-directed RNA polym	RPB5D	AT2G41340	1.12	0.17	1.13	0.29769038	0.6880	-6.01
248254_at	receptor protein kinase-like protein	---	AT5G53320	1.13	0.17	1.13	0.29775865	0.6880	-6.01
263751_at	putative kinesin heavy chain	---	AT2G21300	1.17	0.22	1.13	0.2977158	0.6880	-6.01
258269_at	putative acetyl-CoA carboxylase bi	---	AT3G15690	1.09	0.12	1.13	0.29794737	0.6882	-6.01
265509_at	putative retroelement pol polyprote	---	---	-1.12	-0.17	-1.13	0.29792801	0.6882	-6.01
255566_s_at	hypothetical protein	---	AT3G48670	1.10	0.14	1.13	0.29789431	0.6882	-6.01
256522_at	unknown protein ;supported by full	CMPG1	AT1G66160	1.59	0.67	1.13	0.29789651	0.6882	-6.01
245476_at	hypothetical protein	---	AT4G16090	-1.10	-0.14	-1.13	0.29816766	0.6883	-6.02
246422_at	ADP-ribosylation factor -like prote	ATARFB1B	AT5G17060	-1.21	-0.28	-1.13	0.29818769	0.6883	-6.02
247431_at	putative protein similar to unknown	SRO5	AT5G62520	-1.22	-0.29	-1.13	0.29814525	0.6883	-6.02
257364_at	hypothetical protein predicted by g	---	AT2G45940	1.07	0.10	1.13	0.29819584	0.6883	-6.02
249820_at	putative protein contains similarity	---	AT5G23650	-1.16	-0.21	-1.13	0.29809643	0.6883	-6.01
254824_s_at	origin recognition complex subuni	ORC1B	AT4G12620	1.14	0.18	1.13	0.29815991	0.6883	-6.02
265405_at	putative protein kinase contains a	---	AT2G16750	1.18	0.24	1.13	0.29832753	0.6885	-6.02
261773_at	hypothetical protein predicted by g	---	AT1G76250	-1.13	-0.18	-1.13	0.29831778	0.6885	-6.02
262871_at	hypothetical protein predicted by g	---	AT1G65010	1.32	0.40	1.13	0.29866937	0.6885	-6.02
255474_at	coded for by A. thaliana cDNA T7	---	AT4G02480	1.09	0.13	1.13	0.29857845	0.6885	-6.02
245796_at	unknown protein similar to unknow	RCD1	AT1G32230	1.09	0.13	1.13	0.298965	0.6885	-6.02
264450_s_at	unknown protein similar to hypothe	SNL6	AT1G10250	1.16	0.21	1.13	0.29879849	0.6885	-6.02
255839_at	putative CONSTANS-like B-box zi	---	AT2G33500	1.08	0.11	1.13	0.29846648	0.6885	-6.02
261608_at	unknown protein similar to putative	---	AT1G49650	-1.10	-0.14	-1.13	0.29876319	0.6885	-6.02
254969_at	hypothetical protein ;supported by	---	AT4G10360	1.09	0.12	1.13	0.29840607	0.6885	-6.02
249633_at	sucrose synthase-like protein suc	SUS5	AT5G37180	-1.09	-0.12	-1.13	0.29847452	0.6885	-6.02
264624_at	zinc finger protein ATZF1, putative	ERD6	AT1G08930	1.13	0.18	1.13	0.29904135	0.6885	-6.02
245033_at	putative disease resistance protein	---	AT2G26380	-1.09	-0.12	-1.13	0.29881097	0.6885	-6.02
254114_at	putative protein (fragment) MtN21	---	AT4G24980	-1.12	-0.16	-1.13	0.29886444	0.6885	-6.02
257001_at	Sm protein, putative similar to GB	---	AT3G14080	1.10	0.13	1.13	0.29899069	0.6885	-6.02
257360_at	unknown protein	---	AT2G39240	-1.08	-0.11	-1.13	0.29910515	0.6885	-6.02
254050_s_at	hypothetical protein ; supported by	---	AT4G25670	1.09	0.13	1.13	0.29868169	0.6885	-6.02
250949_at	putative protein	---	AT5G03510	1.08	0.11	1.13	0.29893701	0.6885	-6.02
244966_at	cytochrome b6-f complex, subunit	---	---	-1.15	-0.20	-1.13	0.29876464	0.6885	-6.02
265810_at	unknown protein	---	AT2G18090	-1.16	-0.21	-1.13	0.29910742	0.6885	-6.02
253933_at	hypothetical protein	---	AT4G26820	1.11	0.15	1.13	0.29894253	0.6885	-6.02
257156_at	hypothetical protein predicted by g	---	AT3G24260	1.08	0.12	1.13	0.29898419	0.6885	-6.02

247121_at	putative protein contains similarity	---	AT5G66010	1.11	0.15	1.13	0.29850393	0.6885	-6.02
259656_at	protein kinase, putative contains F	---	AT1G55200	-1.09	-0.12	-1.13	0.29909481	0.6885	-6.02
254729_at	putative protein purple acid phosp	PAP23	AT4G13700	-1.11	-0.15	-1.13	0.2986239	0.6885	-6.02
266820_at	putative AP2 domain transcription	---	AT2G44940	-1.27	-0.35	-1.13	0.29855573	0.6885	-6.02
264747_at	unknown protein	---	AT1G70150	1.12	0.17	1.13	0.29870341	0.6885	-6.02
257768_at	RING zinc finger protein, putative	---	AT3G23060	-1.12	-0.17	-1.13	0.29874896	0.6885	-6.02
250267_at	putative protein predicted proteins	---	AT5G12930	1.45	0.53	1.12	0.29920921	0.6887	-6.02
260380_at	hypothetical protein predicted by g	---	AT1G73870	-1.20	-0.27	-1.12	0.29922833	0.6887	-6.02
252588_at	putative protein potential transcrip	---	AT3G45630	-1.09	-0.12	-1.12	0.29927111	0.6887	-6.02
249847_at	serine carboxypeptidase II-like pro	SCPL34	AT5G23210	1.15	0.20	1.12	0.29947895	0.6889	-6.02
259290_at	putative cyclin similar to cyclin cyc	CYCB1;3	AT3G11520	-1.14	-0.18	-1.12	0.29950324	0.6889	-6.02
256342_at	unknown protein ; supported by ful	---	AT1G72020	1.09	0.13	1.12	0.29942212	0.6889	-6.02
265856_at	hypothetical protein predicted by g	LBD16	AT2G42430	1.13	0.18	1.12	0.29948838	0.6889	-6.02
262063_at	unknown protein identical to unkno	---	AT1G80000	1.11	0.15	1.12	0.29949486	0.6889	-6.02
255460_at	hypothetical protein similar to A. th	---	AT4G02800	1.08	0.12	1.12	0.29955096	0.6889	-6.02
260791_at	lipase-like protein similar to lipase	---	AT1G06250	-1.09	-0.13	-1.12	0.29958548	0.6889	-6.02
248115_at	putative protein strong similarity to	---	AT5G54870	1.18	0.23	1.12	0.2997068	0.6891	-6.02
255305_at	putative ABC transporter similar to	ATABC1	AT4G04770	1.13	0.17	1.12	0.2998342	0.6892	-6.02
255524_at	hypothetical protein similar to pecti	ATPMEPCI	AT4G02330	1.52	0.61	1.12	0.2998146	0.6892	-6.02
253371_at	putative protein FAB1 protein, Sac	---	AT4G33240	1.11	0.14	1.12	0.29981537	0.6892	-6.02
248607_at	NaCl-inducible Ca2+-binding prote	ATCP1	AT5G49480	-1.26	-0.34	-1.12	0.30002367	0.6896	-6.02
252514_at	GTP-binding protein ara-3 ; suppo	ATRAB8A	AT3G46060	1.08	0.11	1.12	0.30009848	0.6897	-6.02
252063_at	lipid transfer protein-like protein lip	LTP12	AT3G51590	-1.10	-0.13	-1.12	0.30013509	0.6897	-6.02
249738_at	60s acidic ribosomal protein P1	---	AT5G24510	1.08	0.11	1.12	0.30018637	0.6898	-6.02
248474_at	pyruvate dehydrogenase E1 comp	MAB1	AT5G50850	1.11	0.16	1.12	0.30023498	0.6898	-6.02
252088_at	putative protein	---	AT3G52100 /	1.12	0.16	1.12	0.30025928	0.6898	-6.02
265868_at	unknown protein ;supported by ful	PUX2	AT2G01650	1.13	0.18	1.12	0.30047142	0.6898	-6.02
264906_at	putative mitochondrial phosphate t	---	AT2G17270	1.13	0.18	1.12	0.30043441	0.6898	-6.02
259967_at	putative DNA-binding protein conta	---	AT1G76510	1.08	0.11	1.12	0.30036215	0.6898	-6.02
264783_at	putative calcium-dependent protei	PPCK1	AT1G08650	-1.20	-0.27	-1.12	0.30047114	0.6898	-6.02
265045_s_at	putative protein kinase, ADK1 dua	ADK1	AT1G03930 /	-1.19	-0.25	-1.12	0.30044394	0.6898	-6.02
254086_at	putative proteasome regulatory su	---	AT4G24820	1.08	0.10	1.12	0.3003311	0.6898	-6.02
257695_at	hypothetical protein contains Pfam	HUA1	AT3G12680	1.10	0.14	1.12	0.30036001	0.6898	-6.02
256892_at	hypothetical protein contains simil	---	AT3G19000	1.17	0.23	1.12	0.30056685	0.6899	-6.02
246019_at	putative protein predicted proteins	---	AT5G10690	1.12	0.17	1.12	0.30054162	0.6899	-6.02

248665_at	Expressed protein ; supported by f	---	AT5G48655	1.08	0.11	1.12	0.30074917	0.6902	-6.02
252553_at	putative protein	---	AT3G45910	1.09	0.12	1.12	0.30087973	0.6903	-6.02
250093_at	hypothetical protein	---	AT5G17370	-1.08	-0.11	-1.12	0.30088049	0.6903	-6.02
251101_at	putative transporter protein Na+/H-	CHX26	AT5G01680	-1.07	-0.10	-1.12	0.30082489	0.6903	-6.02
261220_at	ER lumen protein-retaining recepto	---	AT1G19970	-1.23	-0.30	-1.12	0.30106762	0.6904	-6.02
248423_at	putative protein contains similarity	---	AT5G51670	1.15	0.20	1.12	0.30098701	0.6904	-6.02
260941_at	peroxidase, putative similar to per	---	AT1G44970	-1.15	-0.20	-1.12	0.30108927	0.6904	-6.02
252492_at	chloroplast import-associated cha	TOC75-III	AT3G46740	1.11	0.15	1.12	0.30108905	0.6904	-6.02
247984_s_at	IAA-amino acid hydrolase homolog	ILL1	AT5G56650	1.14	0.19	1.12	0.30106356	0.6904	-6.02
245522_at	hypothetical protein	---	AT4G15890	-1.09	-0.12	-1.12	0.30112044	0.6904	-6.02
264133_at	hypothetical protein predicted by g	---	AT1G79080	1.10	0.13	1.12	0.30131626	0.6908	-6.02
262419_at	hypothetical protein identical to hy	---	AT1G50380	1.13	0.18	1.12	0.30177295	0.6910	-6.02
252286_at	putative protein	---	AT3G49070	-1.07	-0.10	-1.12	0.30144565	0.6910	-6.02
258201_at	hypothetical protein predicted by g	---	AT3G13910	-1.19	-0.25	-1.12	0.30184137	0.6910	-6.03
247474_at	putative protein predicted proteins	---	AT5G62280	1.73	0.79	1.12	0.30172836	0.6910	-6.02
251146_at	neoxanthin cleavage enzyme nc1	CCD1	AT3G63520	1.13	0.18	1.12	0.30183616	0.6910	-6.03
265644_at	hypothetical protein predicted by g	ATEPR1	AT2G27380	-1.08	-0.12	-1.12	0.30167172	0.6910	-6.02
251223_at	putative transcription factor MYB11	ATMYB11	AT3G62610	-1.08	-0.11	-1.12	0.30185828	0.6910	-6.03
260098_at	tumor-related protein, putative sim	---	AT1G73320	-1.17	-0.23	-1.12	0.30160872	0.6910	-6.02
258287_at	putative sulfate transporter similar	SULTR3;4	AT3G15990	-1.27	-0.35	-1.12	0.3016816	0.6910	-6.02
256878_at	major latex protein, putative simila	---	AT3G26460	-1.12	-0.16	-1.12	0.30185811	0.6910	-6.03
248991_at	putative protein contains similarity	---	AT5G45220	-1.15	-0.20	-1.12	0.30158585	0.6910	-6.02
247035_at	putative protein similar to unknown	ALC	AT5G67110	1.08	0.12	1.12	0.30178536	0.6910	-6.02
254717_at	histone H2A.F/Z - like protein histo	HTA4	AT4G13570	-1.11	-0.16	-1.12	0.30156716	0.6910	-6.02
254297_at	hypothetical protein	---	AT4G23110	1.08	0.11	1.12	0.30183562	0.6910	-6.03
259276_at	putative peroxidase very similar to	---	AT3G01190	1.08	0.11	1.12	0.30149101	0.6910	-6.02
250873_at	lipase -like protein lipase Arab-1,	---	AT5G03980	-1.10	-0.13	-1.12	0.30190226	0.6911	-6.03
262990_at	E2, ubiquitin-conjugating enzyme,	MMZ1	AT1G23260	1.08	0.12	1.12	0.30200596	0.6911	-6.03
265231_s_at	hypothetical protein	---	AT2G07713	-1.09	-0.12	-1.12	0.30201995	0.6911	-6.03
255375_at	putative athila-like protein	---	---	-1.08	-0.12	-1.12	0.30204746	0.6911	-6.03
250778_at	unknown protein ;supported by full	---	AT5G05500	-1.09	-0.13	-1.12	0.30201687	0.6911	-6.03
258500_at	S-adenosylmethionine decarboxyla	CPuORF9	AT3G02468	1.10	0.13	1.12	0.30215693	0.6912	-6.03
257123_at	hypothetical protein	---	AT3G20030	-1.07	-0.10	-1.12	0.30211655	0.6912	-6.03
267138_s_at	similar to SOR1 from the fungus C	PDX1.1	AT2G38210	-1.23	-0.30	-1.12	0.30215329	0.6912	-6.03
256255_at	MYB-family transcription factor, pu	---	AT3G11280	1.07	0.10	1.12	0.30227466	0.6912	-6.03

257000_at	hypothetical protein predicted by g	---	AT3G14120	1.15	0.20	1.12	0.30224343	0.6912	-6.03
261217_at	hypothetical protein contains simila	UBP11	AT1G32850	-1.08	-0.11	-1.12	0.30224702	0.6912	-6.03
264401_at	dihydroflavonol 4-reductase, putat	BAN	AT1G61720	-1.07	-0.10	-1.12	0.30240801	0.6915	-6.03
261469_at	unknown protein	AtRLP4	AT1G28340	1.09	0.12	1.12	0.3024505	0.6915	-6.03
253862_at	NOZZLE/SPOROCYTELESS ; su	SPL	AT4G27330	-1.12	-0.17	-1.12	0.30261731	0.6917	-6.03
252835_at	putative protein several hypothetic	---	AT3G42060	1.11	0.14	1.12	0.30257142	0.6917	-6.03
251314_at	putative protein several hypothetic	---	AT3G61180	-1.07	-0.10	-1.12	0.30264891	0.6917	-6.03
248124_at	putative protein contains similarity	ATG18F	AT5G54730	1.10	0.14	1.12	0.3026237	0.6917	-6.03
265786_at	putative replication protein A1	---	---	1.07	0.10	1.12	0.30271052	0.6917	-6.03
246280_at	hypothetical protein	---	AT4G36660	-1.21	-0.28	-1.12	0.30280919	0.6919	-6.03
252890_at	brassinosteroid insensitive 1 gene	BRI1	AT4G39400	-1.09	-0.12	-1.12	0.30302415	0.6919	-6.03
264362_at	unknown protein ESTs gb|H36966	---	AT1G03290	1.14	0.19	1.12	0.30299935	0.6919	-6.03
255152_at	Rab-like protein Rab11 protein - A	---	AT4G08190	-1.07	-0.10	-1.12	0.30298803	0.6919	-6.03
255849_at	hypothetical protein predicted by g	---	AT2G33320	-1.08	-0.12	-1.12	0.30297412	0.6919	-6.03
261671_at	hypothetical protein similar to hypo	---	AT1G18340	1.16	0.22	1.12	0.30302833	0.6919	-6.03
265846_at	putative serine carboxypeptidase I	scpl28	AT2G35770	-1.10	-0.14	-1.12	0.30293761	0.6919	-6.03
262674_at	anter-specific proline-rich -like prot	EXL4	AT1G75910	-1.11	-0.15	-1.12	0.30295284	0.6919	-6.03
247311_at	DNA polymerase III catalytic subur	EMB2780	AT5G63960	1.10	0.14	1.11	0.30312607	0.6921	-6.03
262209_at	hypothetical protein contains simila	---	AT1G74720	-1.11	-0.15	-1.11	0.303194	0.6921	-6.03
263512_at	hypothetical protein predicted by g	---	---	1.08	0.12	1.11	0.30317245	0.6921	-6.03
263848_at	putative reverse transcriptase	---	---	-1.10	-0.14	-1.11	0.30323935	0.6921	-6.03
258478_at	unknown protein	---	AT3G02710	1.09	0.13	1.11	0.30328505	0.6921	-6.03
252174_at	putative protein APRIL protein, Hc	---	AT3G50690	-1.08	-0.11	-1.11	0.3033584	0.6922	-6.03
267500_s_at	putative cytochrome P450	CYP704A1	AT2G44890	1.16	0.21	1.11	0.30346615	0.6924	-6.03
264724_at	putative JUN kinase activator prot	CSN5A	AT1G22920	1.08	0.11	1.11	0.30358	0.6926	-6.03
256634_s_at	hypothetical protein predicted by g	---	---	1.08	0.11	1.11	0.30361789	0.6926	-6.03
260177_at	hypothetical protein predicted by g	---	AT1G70650	1.15	0.20	1.11	0.30369927	0.6927	-6.03
264215_at	cytochrome P450, putative similar	CYP96A3	AT1G65340	-1.08	-0.11	-1.11	0.30369448	0.6927	-6.03
251393_at	putative protein symbiosis-related	ATG8G	AT3G60640	1.14	0.19	1.11	0.30383756	0.6928	-6.03
252887_at	putative protein various predicted	---	AT4G39240	-1.07	-0.10	-1.11	0.30384404	0.6928	-6.03
252965_at	putative auxin-induced protein aux	---	AT4G38860	1.25	0.32	1.11	0.30384596	0.6928	-6.03
267053_s_at	peroxidase	---	AT2G38380	1.21	0.27	1.11	0.30387334	0.6928	-6.03
249614_at	putative protein predicted proteins	WSD1	AT5G37300	-1.07	-0.10	-1.11	0.30389507	0.6928	-6.03
250876_at	hypothetical protein	---	AT5G04030	-1.08	-0.12	-1.11	0.3039708	0.6928	-6.03
254046_at	hypothetical protein	---	AT4G26020	-1.08	-0.11	-1.11	0.30394207	0.6928	-6.03

252411_at	putative protein PMP31 protein - (	PEX11B	AT3G47430	-1.20	-0.27	-1.11	0.30418001	0.6929	-6.03
248719_at	respiratory burst oxidase protein ;	RBOHD	AT5G47910	-1.36	-0.44	-1.11	0.30417576	0.6929	-6.03
247134_at	putative protein similar to unknown	---	AT5G66230	-1.09	-0.12	-1.11	0.30409047	0.6929	-6.03
248468_at	UDP-glucose:protein transglucosyl	RGP4	AT5G50750	-1.11	-0.15	-1.11	0.30420104	0.6929	-6.03
259538_at	putative serine/threonine kinase ; s	---	AT1G12310	1.11	0.16	1.11	0.30424325	0.6929	-6.03
246964_at	putative protein crp1 protein - Zea	---	AT5G24830	-1.11	-0.15	-1.11	0.30421484	0.6929	-6.03
259797_at	unknown protein	---	---	-1.11	-0.16	-1.11	0.30422594	0.6929	-6.03
264606_at	unknown protein ;supported by ful	---	AT1G04660	-1.13	-0.18	-1.11	0.30452303	0.6932	-6.03
249907_at	putative protein DNA repair protein	RAD5	AT5G22750	1.09	0.12	1.11	0.30444867	0.6932	-6.03
249775_at	squalene monooxygenase 1,2 (sq	SQE6	AT5G24160	-1.16	-0.22	-1.11	0.30441515	0.6932	-6.03
256429_at	unknown protein	---	AT3G11040	1.12	0.16	1.11	0.30450337	0.6932	-6.03
262774_at	chloroplast nucleoid DNA binding	---	AT1G13230	-1.08	-0.11	-1.11	0.30443479	0.6932	-6.03
251359_at	putative protein several hypothetic	---	AT3G61170	-1.08	-0.11	-1.11	0.30446677	0.6932	-6.03
262949_at	pectinesterase, putative similar to	sks18	AT1G75790	-1.09	-0.13	-1.11	0.30458529	0.6932	-6.03
250479_at	GTP-binding protein GTP-binding	AtRABH1e	AT5G10260	1.10	0.13	1.11	0.30466844	0.6934	-6.03
246227_at	hypothetical protein	---	AT4G36510	-1.11	-0.14	-1.11	0.30471678	0.6934	-6.03
259820_at	subtilisin-like serine protease conta	---	AT1G66210	1.10	0.14	1.11	0.30473608	0.6934	-6.03
265091_s_at	hypothetical protein similar to Anth	---	AT1G03495 /	-1.12	-0.17	-1.11	0.30486195	0.6935	-6.03
253441_at	putative protein Fidipidine, Drosop	---	AT4G32560	-1.09	-0.13	-1.11	0.30485547	0.6935	-6.03
248854_at	putative protein contains similarity	---	AT5G46580	1.11	0.15	1.11	0.30490919	0.6936	-6.03
247453_at	putative protein similar to unknown	---	AT5G62440	1.12	0.17	1.11	0.30504447	0.6936	-6.03
245300_at	hypothetical protein ; supported by	CBL6	AT4G16350	-1.08	-0.11	-1.11	0.30500479	0.6936	-6.03
247484_at	putative protein predicted proteins	---	AT5G62110	-1.09	-0.12	-1.11	0.30506148	0.6936	-6.03
265463_at	unknown protein	IRX9	AT2G37090	1.15	0.20	1.11	0.30501939	0.6936	-6.03
256361_at	formyl transferase, putative contai	pde194	AT1G66520	1.12	0.17	1.11	0.30510917	0.6937	-6.03
257799_at	protein kinase, putative similar to	---	AT3G15890	1.10	0.13	1.11	0.30521868	0.6938	-6.03
252460_at	putative protein predicted protein,	---	---	-1.07	-0.10	-1.11	0.30524182	0.6938	-6.03
248986_at	putative protein similar to unknown	---	AT5G45170	-1.12	-0.16	-1.11	0.30527072	0.6938	-6.03
252512_at	receptor protein kinase -like recep	---	AT3G46290	-1.09	-0.12	-1.11	0.30531218	0.6938	-6.03
264172_at	unknown protein	VAD1	AT1G02120	1.14	0.19	1.11	0.30536549	0.6939	-6.03
250819_at	putative protein strong similarity to	---	AT5G05100	1.10	0.14	1.11	0.30555516	0.6942	-6.03
257166_at	hypothetical protein similar to puta	---	AT3G24710	-1.09	-0.13	-1.11	0.30555762	0.6942	-6.03
252206_at	centrin	ATCEN2	AT3G50360	-1.10	-0.13	-1.11	0.30559898	0.6942	-6.04
257127_at	hypothetical protein predicted by g	TTN9	AT3G20070	1.11	0.15	1.11	0.30567904	0.6943	-6.04
265716_at	unknown protein ;supported by ful	---	AT2G03350	1.13	0.18	1.11	0.30572869	0.6944	-6.04

258186_s_at	protein kinase, putative similar to	---	AT1G48490	-1.08	-0.12	-1.11	0.30580352	0.6944	-6.04
247512_at	putative protein predicted protein,	---	AT5G61720	-1.08	-0.11	-1.11	0.30578132	0.6944	-6.04
260034_at	putative DNA-binding protein Pfam	---	AT1G68810	1.29	0.37	1.11	0.30584493	0.6944	-6.04
259259_at	spindly (gibberellin signal transduc	SPY	AT3G11540	-1.09	-0.13	-1.11	0.30591622	0.6945	-6.04
251970_at	glucosyltransferase - like protein g	UGT73D1	AT3G53150	-1.17	-0.22	-1.11	0.30600346	0.6946	-6.04
266085_at	hypothetical protein	---	AT2G37800	1.11	0.15	1.11	0.30601194	0.6946	-6.04
256673_at	unknown protein	FLA15	AT3G52370	-1.42	-0.51	-1.11	0.30605609	0.6946	-6.04
263690_at	putative DNA-binding protein Simi	AtHB23	AT1G26960	-1.17	-0.23	-1.11	0.30611165	0.6947	-6.04
267627_at	putative ATP-dependent RNA helic	---	AT2G42270	-1.18	-0.24	-1.11	0.30614225	0.6947	-6.04
262635_at	4-hydroxyphenylpyruvate dioxyger	PDS1	AT1G06570	1.20	0.26	1.11	0.30618722	0.6947	-6.04
260690_at	RING finger protein, putative simil	NHL8	AT1G32340	1.07	0.10	1.11	0.30623265	0.6948	-6.04
254880_at	putative protein Crp1, Zea mays,	---	AT4G11690	-1.11	-0.16	-1.11	0.30628506	0.6948	-6.04
250077_at	putative protein	---	AT5G16680	-1.08	-0.11	-1.11	0.30639705	0.6950	-6.04
247728_at	putative protein	---	---	1.09	0.13	1.11	0.3064238	0.6950	-6.04
258393_at	unknown protein similar to unknow	---	AT3G15480	1.15	0.21	1.11	0.30652416	0.6951	-6.04
260524_at	unknown protein	---	AT2G47230	-1.09	-0.12	-1.11	0.30650678	0.6951	-6.04
263666_at	putative pre-mRNA splicing factor	---	AT1G04510	1.13	0.18	1.11	0.30674822	0.6955	-6.04
247963_at	beta-1,3-glucanase-like protein	---	AT5G56590	1.09	0.12	1.11	0.30679504	0.6956	-6.04
249146_at	putative protein contains similarity	---	AT5G43310	-1.09	-0.12	-1.11	0.30699207	0.6956	-6.04
253956_at	fimbrin-like protein (ATFIM1) ; sup	FIM1	AT4G26700	-1.16	-0.22	-1.11	0.30699368	0.6956	-6.04
256412_at	hypothetical protein predicted by g	ELO1	AT3G11220	1.10	0.14	1.11	0.30692925	0.6956	-6.04
266625_at	putative peroxidase	---	AT2G35380	-1.09	-0.13	-1.11	0.3069825	0.6956	-6.04
266455_at	putative bHLH transcription factor	---	AT2G22760	-1.23	-0.30	-1.11	0.30697587	0.6956	-6.04
246646_at	putative protein ;supported by full-	---	AT5G35090	-1.09	-0.13	-1.11	0.30687516	0.6956	-6.04
251684_at	putative protein	---	AT3G56410	1.16	0.22	1.11	0.30702824	0.6956	-6.04
247216_at	4-alpha-glucanotransferase ; supp	DPE1	AT5G64860	-1.13	-0.17	-1.10	0.30711881	0.6957	-6.04
246914_at	putative protein various predicted	---	AT5G25860	1.12	0.17	1.10	0.30715861	0.6958	-6.04
250600_at	dimethylaniline monooxygenase-lik	---	AT5G07800	1.09	0.12	1.10	0.30730984	0.6958	-6.04
253721_at	hypothetical protein ;supported by	---	AT4G29250	-1.12	-0.17	-1.10	0.30731439	0.6958	-6.04
262936_at	hypothetical protein similar to puta	ATCHX2	AT1G79400	-1.13	-0.17	-1.10	0.30729028	0.6958	-6.04
257604_s_at	hypothetical protein predicted by g	---	AT1G11810	1.09	0.12	1.10	0.30731589	0.6958	-6.04
260919_at	hypothetical protein predicted by g	---	AT1G21520	1.39	0.48	1.10	0.3074588	0.6959	-6.04
257651_at	polygalacturonase, putative simila	---	AT3G16850	-1.19	-0.26	-1.10	0.30747308	0.6959	-6.04
245234_at	myb-like protein similarity to ATMY	AtMYB18	AT4G25560	1.10	0.14	1.10	0.30742994	0.6959	-6.04
260200_at	unknown protein ; supported by fu	---	AT1G67620	1.10	0.13	1.10	0.30745247	0.6959	-6.04

256141_at	lysine and histidine specific transp	---	AT1G48640	-1.07	-0.10	-1.10	0.30751909	0.6960	-6.04
253688_at	putative protein ;supported by full-	---	AT4G29590	-1.14	-0.19	-1.10	0.30765555	0.6961	-6.04
261404_at	alpha galactosyltransferase, putat	---	AT1G18690	1.16	0.22	1.10	0.30765134	0.6961	-6.04
246569_at	lysophospholipase -like protein lys	---	AT5G14980	1.08	0.11	1.10	0.30767613	0.6961	-6.04
248586_at	putative protein similar to unknown	---	AT5G49610	1.10	0.13	1.10	0.30773753	0.6961	-6.04
251781_at	P-glycoprotein - like P-glycoprotei	PGP20	AT3G55320	-1.09	-0.13	-1.10	0.30773943	0.6961	-6.04
257304_at	hypothetical protein predicted by g	---	---	-1.08	-0.11	-1.10	0.30780249	0.6962	-6.04
255886_at	plastocyanin, putative similar to pl	DRT112	AT1G20340	1.08	0.12	1.10	0.30790529	0.6963	-6.04
259628_at	hypothetical protein contains Pfam	---	AT1G56440	-1.14	-0.18	-1.10	0.30801833	0.6964	-6.04
262387_s_at	hypothetical protein contains simila	---	AT1G49340	1.09	0.13	1.10	0.30803854	0.6964	-6.04
260779_at	splicing factor, putative similar to h	---	AT1G14650	1.10	0.13	1.10	0.30804829	0.6964	-6.04
259354_at	unknown protein	---	AT3G05220	-1.16	-0.21	-1.10	0.30800595	0.6964	-6.04
257985_at	hypothetical protein predicted by g	---	AT3G20810	1.12	0.16	1.10	0.30808458	0.6964	-6.04
255735_at	transmembrane protein, putative s	---	AT1G25520	1.18	0.24	1.10	0.30814434	0.6965	-6.04
251451_s_at	putative protein several hypothetic	---	AT3G60040	1.10	0.13	1.10	0.30821128	0.6966	-6.04
257775_at	short-chain alcohol dehydrogenas	---	AT3G29260	-1.10	-0.14	-1.10	0.30832995	0.6968	-6.04
267570_at	putative RNA helicase A identical	HVT1	AT2G30800	1.11	0.15	1.10	0.30837189	0.6968	-6.04
255774_at	unknown protein	---	AT1G18620	-1.22	-0.28	-1.10	0.30913779	0.6968	-6.04
261618_at	unknown protein	---	AT1G33110	-1.22	-0.28	-1.10	0.3086361	0.6968	-6.04
257587_at	3'-5' exonuclease, putative contair	---	AT1G56310	1.08	0.12	1.10	0.3092273	0.6968	-6.04
266939_at	plasma membrane proton ATPase	AHA1	AT2G18960	1.07	0.10	1.10	0.30931263	0.6968	-6.04
250811_at	cysteine proteinase inhibitor-like pr	---	AT5G05110	1.18	0.24	1.10	0.30925288	0.6968	-6.04
247885_at	putative protein similar to unknown	---	AT5G57830	-1.16	-0.21	-1.10	0.30861754	0.6968	-6.04
262741_at	hypothetical protein	---	AT1G28760	-1.08	-0.11	-1.10	0.3089361	0.6968	-6.04
250770_at	laccase (diphenol oxidase)	LAC12	AT5G05390	-1.13	-0.18	-1.10	0.30920805	0.6968	-6.04
247591_at	high-affinity nitrate transporter AC	NRT2.4	AT5G60770	-1.08	-0.12	-1.10	0.30853074	0.6968	-6.04
248502_at	putative protein strong similarity to	---	AT5G50450	-1.13	-0.17	-1.10	0.30884397	0.6968	-6.04
258402_at	unknown protein very similar to un	---	AT3G15450	1.23	0.30	1.10	0.30927712	0.6968	-6.04
253473_at	putative protein mixed-lineage pro	---	AT4G32250	1.18	0.24	1.10	0.30900924	0.6968	-6.04
251994_at	protein kinase - like protein kinase	KIPK	AT3G52890	1.19	0.25	1.10	0.30901946	0.6968	-6.04
267048_at	hypothetical protein predicted by g	---	AT2G34200	1.13	0.17	1.10	0.30878831	0.6968	-6.04
264808_at	unknown protein similar to EST gb	PRA1.E	AT1G08770	-1.09	-0.12	-1.10	0.3086929	0.6968	-6.04
254461_at	receptor kinase - like protein SRK	---	AT4G21230	1.13	0.18	1.10	0.30895146	0.6968	-6.04
253642_at	hypothetical protein ;supported by	---	AT4G29960	1.11	0.15	1.10	0.30873531	0.6968	-6.04
249891_at	unknown protein	---	AT5G22590	1.07	0.09	1.10	0.30897385	0.6968	-6.04

259843_at	hypothetical protein predicted by g	---	AT1G73570	-1.13	-0.17	-1.10	0.30912085	0.6968	-6.04
250871_at	putative protein	---	AT5G03930	1.10	0.14	1.10	0.3084533	0.6968	-6.04
261525_at	hypothetical protein predicted by g	---	AT1G14330	-1.12	-0.17	-1.10	0.30889754	0.6968	-6.04
262010_at	hypothetical protein predicted by g	---	---	-1.10	-0.14	-1.10	0.30905057	0.6968	-6.04
257416_at	unknown protein	---	AT2G17750	1.11	0.15	1.10	0.30896469	0.6968	-6.04
255326_at	hypothetical protein	---	---	-1.07	-0.10	-1.10	0.30878647	0.6968	-6.04
246672_at	putative protein	---	---	1.08	0.11	1.10	0.3087382	0.6968	-6.04
252564_at	actin depolymerizing factor 1 (ADF	ADF1	AT3G46010	1.10	0.13	1.10	0.30928631	0.6968	-6.04
264762_at	receptor kinase, putative similar to	---	AT1G61460	-1.11	-0.15	-1.10	0.30907838	0.6968	-6.04
245596_at	hypothetical protein	AtPRD1	AT4G14180	1.09	0.12	1.10	0.30898735	0.6968	-6.04
251903_at	putative protein 24 kDa seed matu	---	AT3G54120	1.24	0.30	1.10	0.30884648	0.6968	-6.04
251198_at	putative protein PGP237-11, Petu	---	AT3G62970	1.09	0.12	1.10	0.30928303	0.6968	-6.04
245916_at	putative protein	---	AT5G28720	1.10	0.14	1.10	0.30934369	0.6968	-6.04
263126_at	hypothetical protein predicted by g	---	AT1G78460	-1.34	-0.43	-1.10	0.3096314	0.6973	-6.05
256722_at	hypothetical protein predicted by g	---	AT2G34050	1.18	0.24	1.10	0.30961111	0.6973	-6.05
254116_at	hypothetical protein	---	AT4G24730	-1.08	-0.12	-1.10	0.30967654	0.6974	-6.05
259328_at	putative lectin contains Pfam profi	ATMLP-300	AT3G16440	-1.11	-0.15	-1.10	0.30970799	0.6974	-6.05
266082_at	hypothetical protein predicted by g	---	AT2G37830	-1.13	-0.18	-1.10	0.30979656	0.6975	-6.05
245183_at	putative protein similarity to predic	---	AT5G12440	1.12	0.17	1.10	0.30989707	0.6975	-6.05
244913_at	hypothetical protein	---	---	1.09	0.13	1.10	0.30989247	0.6975	-6.05
250534_at	NADH dehydrogenase ;supported	CI51	AT5G08530	-1.09	-0.12	-1.10	0.30992273	0.6975	-6.05
249261_at	putative protein similar to unknown	---	---	-1.12	-0.17	-1.10	0.30983597	0.6975	-6.05
259922_at	protein phosphatase 2C (AtP2C-H	HAB1	AT1G72770	-1.15	-0.20	-1.10	0.3099635	0.6975	-6.05
251560_at	squamosa promoter-binding prote	SPL15	AT3G57920	-1.12	-0.17	-1.10	0.31003154	0.6976	-6.05
260428_at	putative translation initiation factor	---	AT1G72340	-1.13	-0.18	-1.10	0.310053	0.6976	-6.05
259527_at	hypothetical protein	---	AT1G12600	-1.07	-0.10	-1.10	0.31009106	0.6976	-6.05
262997_at	disease resistance protein, putativ	RPP27	AT1G54470	1.08	0.11	1.10	0.31011442	0.6976	-6.05
245723_at	hypothetical protein predicted by g	---	AT1G73400	1.12	0.16	1.10	0.31022069	0.6977	-6.05
249019_at	unknown protein	---	AT5G44780	-1.24	-0.30	-1.10	0.31019806	0.6977	-6.05
248694_at	unknown protein	---	AT5G48340	-1.09	-0.12	-1.10	0.31027871	0.6977	-6.05
265189_at	unknown protein ; supported by cl	---	AT1G23840	1.21	0.27	1.10	0.31029072	0.6977	-6.05
263444_at	putative MADS-box protein	AGL46	AT2G28700	1.10	0.14	1.10	0.31033867	0.6978	-6.05
264659_at	unknown protein Similar to S. pom	ATOPT2	AT1G09930	-1.09	-0.12	-1.10	0.31041765	0.6979	-6.05
245919_at	putative protein various predicted	---	AT5G28780	-1.07	-0.10	-1.10	0.3104695	0.6979	-6.05
259862_at	hypothetical protein ;supported by	TRFL6	AT1G72650	1.11	0.15	1.10	0.31051509	0.6979	-6.05

255562_at	G/T DNA mismatch repair enzyme	MSH6	AT4G02070	-1.12	-0.16	-1.10	0.31053253	0.6979	-6.05
248112_at	wax synthase-like protein	---	AT5G55350	-1.12	-0.16	-1.10	0.31070291	0.6981	-6.05
261211_at	uridine diphosphate glucose epim	UGE1	AT1G12780	1.17	0.22	1.10	0.31068514	0.6981	-6.05
254835_s_at	flavonoid 3,5-hydroxylase -like pr	CYP706A5	AT4G12310	-1.19	-0.25	-1.10	0.31077582	0.6981	-6.05
253604_at	hypothetical protein	---	AT4G30970	-1.08	-0.11	-1.10	0.3107771	0.6981	-6.05
245846_at	P-type transporting ATPase, putat	---	AT1G26130	-1.12	-0.17	-1.10	0.31071529	0.6981	-6.05
257520_at	hypothetical protein	---	AT3G07710	-1.10	-0.14	-1.10	0.31074967	0.6981	-6.05
245530_at	splicing factor like protein	---	---	-1.10	-0.14	-1.10	0.31084024	0.6981	-6.05
250374_at	putative protein	EMF1	AT5G11530	1.17	0.23	1.10	0.31093226	0.6982	-6.05
251128_at	putative protein crp1 protein, Zea	---	AT5G01110	-1.07	-0.10	-1.10	0.31093583	0.6982	-6.05
266608_at	hypothetical protein predicted by g	---	AT2G35500	1.13	0.17	1.10	0.31093894	0.6982	-6.05
253989_at	uncharacterized protein ;supporte	---	AT4G26130	-1.15	-0.20	-1.10	0.3111242	0.6983	-6.05
265404_at	putative beta-galactosidase	BGAL13	AT2G16730	-1.13	-0.17	-1.10	0.31114324	0.6983	-6.05
248888_at	potassium channel protein KAT1 (	KAT1	AT5G46240	-1.25	-0.33	-1.09	0.3112085	0.6983	-6.05
258522_at	hypothetical protein predicted by g	---	AT3G06660	1.14	0.19	1.09	0.31121996	0.6983	-6.05
265924_at	putative geranylgeranyl pyrophosp	---	AT2G18620	-1.07	-0.10	-1.09	0.31123154	0.6983	-6.05
252555_at	putative protein alpha-xylosidase,	---	AT3G45940	1.07	0.10	1.10	0.31114158	0.6983	-6.05
253064_at	bZIP transcription factor - like prot	AtbZIP7	AT4G37730	-1.10	-0.13	-1.09	0.31116532	0.6983	-6.05
262265_at	hypothetical protein predicted by g	---	---	-1.13	-0.17	-1.09	0.3112923	0.6984	-6.05
250131_at	unknown protein ; supported by cl	---	AT5G16550	-1.15	-0.20	-1.09	0.31140342	0.6986	-6.05
261573_at	hypothetical protein identical to hy	---	AT1G01180	-1.08	-0.11	-1.09	0.31143082	0.6986	-6.05
248656_at	fimbrin 2 (gb|AAB97844.1) ; supp	---	AT5G48460	1.28	0.36	1.09	0.31153489	0.6987	-6.05
244992_s_at	ribosomal protein S7	---	---	-1.10	-0.14	-1.09	0.31151838	0.6987	-6.05
266518_at	hypothetical protein predicted by g	---	AT2G35170	-1.10	-0.14	-1.09	0.31157578	0.6987	-6.05
256471_at	hypothetical protein predicted by g	---	---	-1.08	-0.11	-1.09	0.31167302	0.6987	-6.05
252262_at	putative protein several hypothetic	---	AT3G49510	-1.08	-0.10	-1.09	0.31162169	0.6987	-6.05
260997_at	zinc-finger protein (ZPT4-4), putat	---	AT1G26610	-1.08	-0.11	-1.09	0.31164795	0.6987	-6.05
246177_at	putative protein predicted proteins	---	AT5G28420	-1.08	-0.11	-1.09	0.31180769	0.6989	-6.05
249249_at	unknown protein	---	AT5G42330	1.10	0.14	1.09	0.31183101	0.6989	-6.05
255883_at	unknown protein similar to putativ	---	AT1G20270	-1.11	-0.15	-1.09	0.31189919	0.6989	-6.05
265528_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-1.09	0.31190037	0.6989	-6.05
254162_at	transcription factor IIA small subun	---	AT4G24440	1.13	0.17	1.09	0.31198628	0.6991	-6.05
250099_at	unknown protein ; supported by cl	---	AT5G17300	-1.11	-0.16	-1.09	0.31204353	0.6991	-6.05
265204_at	hypothetical protein predicted by g	---	AT2G36650	-1.07	-0.10	-1.09	0.31204903	0.6991	-6.05
262664_at	hypothetical protein predicted by g	---	AT1G13970	-1.09	-0.12	-1.09	0.31210808	0.6991	-6.05

255968_at	Expressed protein ; supported by f	---	AT1G22270	1.11	0.15	1.09	0.31227793	0.6993	-6.05
254837_at	putative protein	---	AT4G12360	-1.11	-0.15	-1.09	0.31222104	0.6993	-6.05
267098_at	hypothetical protein predicted by g	---	AT2G41451	-1.11	-0.15	-1.09	0.31226346	0.6993	-6.05
253029_at	hypothetical protein	FRS9	AT4G38170	1.20	0.27	1.09	0.31231849	0.6993	-6.05
265773_at	unknown protein ; supported by cl	RPH1	AT2G48070	1.10	0.14	1.09	0.31235846	0.6993	-6.05
250957_at	photoreceptor-interacting protein -	---	AT5G03250	1.07	0.10	1.09	0.31248797	0.6995	-6.05
249243_s_at	beta-glucosidase	BGLU13	AT5G42260	1.08	0.11	1.09	0.31251037	0.6995	-6.05
266331_at	putative RGA1, giberellin repsons	RGA1	AT2G01570	-1.11	-0.15	-1.09	0.31248107	0.6995	-6.05
254750_at	putative protein	---	AT4G13150	1.12	0.16	1.09	0.31274948	0.6998	-6.05
257973_at	unknown protein	---	AT3G20720	1.11	0.15	1.09	0.31291048	0.6998	-6.05
246580_at	ABC transporter, putative contains	---	AT1G31770	-1.12	-0.16	-1.09	0.31291219	0.6998	-6.05
248485_at	calcium-binding transporter-like pr	---	AT5G51050	-1.13	-0.18	-1.09	0.31282003	0.6998	-6.05
251331_s_at	tubulin gamma-1 chain	TUBG1	AT3G61650	1.25	0.32	1.09	0.31281485	0.6998	-6.05
247024_at	Expressed protein ; supported by f	---	AT5G66985	-1.11	-0.15	-1.09	0.31289327	0.6998	-6.05
256721_at	hypothetical protein predicted by g	WAVE1	AT2G34150	1.11	0.15	1.09	0.31281654	0.6998	-6.05
265093_at	unknown protein similar to NBD-lik	---	AT1G03905	-1.12	-0.16	-1.09	0.31278017	0.6998	-6.05
249706_at	histone deacetylase	HDA7	AT5G35600	-1.09	-0.12	-1.09	0.31290545	0.6998	-6.05
250413_at	adenine phosphoribosyltransferas	APT5	AT5G11160	1.14	0.19	1.09	0.31295339	0.6998	-6.05
263497_at	cold-regulated protein cor15a prec	COR15A	AT2G42540	-1.61	-0.69	-1.09	0.31298817	0.6998	-6.05
259312_at	putative RING-H2 zinc finger prote	ATL6	AT3G05200	1.28	0.36	1.09	0.31300427	0.6998	-6.05
254119_at	putative pectate lyase pectate lyas	---	AT4G24780	-1.42	-0.50	-1.09	0.3131131	0.6999	-6.05
246565_at	biotin carboxyl carrier protein prec	BCCP2	AT5G15530	-1.09	-0.13	-1.09	0.31317454	0.6999	-6.05
251918_at	photoassimilate-responsive protei	---	AT3G54040	1.08	0.12	1.09	0.31323903	0.6999	-6.05
246713_at	mRNA capping enzyme - like capp	---	AT5G28210	-1.11	-0.15	-1.09	0.31321726	0.6999	-6.05
248893_at	unknown protein	---	AT5G46310	1.10	0.14	1.09	0.31321303	0.6999	-6.05
264694_at	receptor serine/threonine kinase F	---	AT1G70250	-1.08	-0.10	-1.09	0.31335538	0.7001	-6.06
253136_at	putative protein leucine-rich protei	---	AT4G35470	-1.10	-0.13	-1.09	0.31357957	0.7002	-6.06
251650_at	hypothetical protein	---	AT3G57360	1.13	0.18	1.09	0.31354786	0.7002	-6.06
255729_at	hypothetical protein similar to puta	---	AT1G25470	-1.09	-0.13	-1.09	0.31358679	0.7002	-6.06
254838_at	hypothetical protein	---	AT4G12380	-1.12	-0.17	-1.09	0.31347803	0.7002	-6.06
257847_at	hypothetical protein predicted by g	---	AT3G13020	1.09	0.13	1.09	0.3135172	0.7002	-6.06
252992_at	putative protein phosphatase-2c p	---	AT4G38520	1.14	0.19	1.09	0.31351057	0.7002	-6.06
253643_at	hypothetical protein ;supported by	---	AT4G29780	1.37	0.45	1.09	0.31352129	0.7002	-6.06
246803_at	tSNARE AtTLG2a ; supported by (	SYP41	AT5G26980	1.08	0.12	1.09	0.31366797	0.7003	-6.06
248480_at	ATP-dependent Clp protease ATP	CLPC1	AT5G50920	1.09	0.12	1.09	0.3137128	0.7003	-6.06

253779_at	receptor-like protein kinase 5 precu	HAE	AT4G28490	-1.21	-0.27	-1.09	0.31382929	0.7004	-6.06
250922_at	Expressed protein ; supported by f	---	AT5G03345	1.09	0.13	1.09	0.31381689	0.7004	-6.06
266901_at	hypothetical protein predicted by g	JAZ7	AT2G34600	-1.30	-0.38	-1.09	0.31388166	0.7005	-6.06
248975_at	unknown protein ; supported by cl	---	AT5G45040	1.09	0.13	1.09	0.31396101	0.7006	-6.06
263106_at	hypothetical protein predicted by g	---	AT2G05160	1.11	0.15	1.09	0.31405764	0.7007	-6.06
256871_at	WD-repeat protein, putative conta	---	AT3G26480	-1.18	-0.24	-1.09	0.31406232	0.7007	-6.06
245704_at	glycine-rich protein	KTF1	AT5G04290	-1.08	-0.11	-1.09	0.31410469	0.7007	-6.06
263262_at	unknown protein	---	AT2G38830	-1.09	-0.13	-1.09	0.31418203	0.7008	-6.06
257635_at	cytochrome P450 monooxygenas	CYP71B4	AT3G26280	1.11	0.15	1.09	0.31432895	0.7011	-6.06
253794_at	putative protein dimethylaniline m	---	AT4G28720	1.28	0.36	1.09	0.31445486	0.7013	-6.06
246153_s_at	RAN1 small Ras-like GTP-binding	RAN-1	AT5G20010 /	1.16	0.21	1.09	0.31452632	0.7014	-6.06
249434_at	putative protein GTP-binding prote	---	AT5G39960	1.13	0.17	1.09	0.31478591	0.7015	-6.06
250155_at	putative protein predicted proteins	---	AT5G15160	-1.25	-0.32	-1.09	0.31479585	0.7015	-6.06
261715_at	hypothetical protein similar to hypo	---	AT1G18485	1.09	0.13	1.09	0.31477106	0.7015	-6.06
263907_at	abscisic acid insensitive 5 (ABI5) c	ABI5	AT2G36270	-1.12	-0.16	-1.09	0.31467126	0.7015	-6.06
260259_at	unknown protein similar to unknow	---	AT1G74300	-1.09	-0.13	-1.09	0.31462304	0.7015	-6.06
254782_at	putative calmodulin calmodulin - C	UNE14	AT4G12860	-1.10	-0.14	-1.09	0.3147799	0.7015	-6.06
253062_at	putative protein predicted protein,	NPY5	AT4G37590	1.26	0.33	1.09	0.31472323	0.7015	-6.06
263867_at	putative aquaporin (tonoplast intrin	GAMMA-TI	AT2G36830	1.19	0.25	1.09	0.31520357	0.7015	-6.06
261480_at	phytochrome kinase substrate 1, p	PKS2	AT1G14280	-1.38	-0.46	-1.09	0.31507859	0.7015	-6.06
253917_at	hypothetical protein ;supported by	---	AT4G27380	1.14	0.19	1.09	0.31498444	0.7015	-6.06
258780_at	putative ubiquitin carboxyl-termina	UBP13	AT3G11910	1.07	0.10	1.09	0.3152171	0.7015	-6.06
246351_at	unknown protein contains similarit	---	AT1G16570	1.08	0.12	1.09	0.3150862	0.7015	-6.06
258899_at	Expressed protein ; supported by f	---	AT3G05675	1.11	0.15	1.09	0.31518664	0.7015	-6.06
263440_at	unknown protein predicted by gens	ATEXO70H	AT2G28640	-1.07	-0.10	-1.09	0.31490034	0.7015	-6.06
246686_at	putative protein predicted proteins	---	---	-1.12	-0.16	-1.09	0.31524633	0.7015	-6.06
257877_at	hypothetical protein	---	AT3G17140	-1.09	-0.13	-1.09	0.31490212	0.7015	-6.06
261865_at	sterol delta7 reductase identical to	DWF5	AT1G50430	1.15	0.20	1.09	0.31516414	0.7015	-6.06
246577_at	MADS box transcription factor, pu	AGL92	AT1G31640	-1.08	-0.12	-1.08	0.31528829	0.7015	-6.06
257476_at	unknown protein	---	AT1G80960	-1.07	-0.10	-1.09	0.31496369	0.7015	-6.06
264768_at	hypothetical protein similar to puta	---	AT1G61410	-1.09	-0.12	-1.08	0.31526202	0.7015	-6.06
261549_at	DNA-binding protein, putative con	---	AT1G63470	-1.11	-0.15	-1.09	0.31517018	0.7015	-6.06
249660_at	putative protein similar to unknown	---	AT5G36720 /	-1.12	-0.16	-1.09	0.31484931	0.7015	-6.06
258343_at	unknown protein similar to hypothe	---	AT3G22810	-1.10	-0.14	-1.09	0.31516798	0.7015	-6.06
259485_at	ATP synthase gamma-subunit, pu	ATPC2	AT1G15700	1.21	0.28	1.08	0.31533381	0.7015	-6.06

258879_at	unknown protein ; supported by fu	---	AT3G03270	-1.20	-0.26	-1.08	0.31545373	0.7017	-6.06
247908_at	GS1-like protein ;supported by full-	GS1	AT5G57440	1.22	0.28	1.08	0.31551704	0.7018	-6.06
258564_at	poly(A) polymerase, putative simil	---	AT3G06560	-1.09	-0.12	-1.08	0.31555015	0.7018	-6.06
251864_at	pectate lyase - like protein pectate	PMR6	AT3G54920	1.12	0.16	1.08	0.31571386	0.7020	-6.06
259773_at	auxin-induced protein, putative sir	---	AT1G29500	1.37	0.45	1.08	0.31592009	0.7020	-6.06
259665_at	unknown protein ; supported by cD	---	AT1G55160	1.12	0.16	1.08	0.31592714	0.7020	-6.06
255635_at	Shaggy related protein kinase teth	ATSK32	AT4G00720	-1.10	-0.14	-1.08	0.31588534	0.7020	-6.06
253657_at	cadmium-transporting ATPase-like	HMA2	AT4G30110	-1.25	-0.33	-1.08	0.31588905	0.7020	-6.06
264664_at	putative elongation factor similar to	---	AT1G09660	1.14	0.19	1.08	0.31599518	0.7020	-6.06
261289_at	hypothetical protein predicted by g	---	AT1G37000	1.08	0.11	1.08	0.31589764	0.7020	-6.06
262915_at	response regulator 3 identical to re	ARR3	AT1G59940	-1.11	-0.15	-1.08	0.3159271	0.7020	-6.06
250050_at	putative protein predicted protein,	VAR3	AT5G17790	1.10	0.13	1.08	0.31595657	0.7020	-6.06
266009_at	putative kinesin heavy chain	---	AT2G37420	1.09	0.12	1.08	0.31592648	0.7020	-6.06
252579_at	putative protein hypothetical prote	---	AT3G45510	-1.08	-0.11	-1.08	0.31596663	0.7020	-6.06
248249_at	protein phosphatase 2C-like ; sup	---	AT5G53140	1.09	0.12	1.08	0.31623006	0.7023	-6.06
249665_at	unknown protein	---	AT5G35830	-1.10	-0.14	-1.08	0.31619919	0.7023	-6.06
264105_x_at	hypothetical protein	---	AT2G13760	-1.10	-0.14	-1.08	0.31617512	0.7023	-6.06
259317_at	hypothetical protein identical to hy	HYP1	AT3G01100	-1.10	-0.13	-1.08	0.31622707	0.7023	-6.06
248290_at	Ca2+-transporting ATPase-like pro	---	AT5G53010	1.10	0.14	1.08	0.31632037	0.7024	-6.06
250176_at	putative protein cytochrome P450	CYP724A1	AT5G14400	-1.12	-0.17	-1.08	0.31634057	0.7024	-6.06
262094_at	SAR DNA binding protein, putative	NOP56	AT1G56110	1.21	0.27	1.08	0.31645046	0.7025	-6.06
261386_at	unknown protein ;supported by full	---	AT1G05430	1.10	0.14	1.08	0.31642256	0.7025	-6.06
254673_at	membrane-bound small GTP-bind	AtRABA1e	AT4G18430	1.29	0.37	1.08	0.31649177	0.7025	-6.06
254010_at	putative protein ;supported by full-	---	AT1G72125	1.08	0.12	1.08	0.31654454	0.7025	-6.06
252747_at	putative protein retrotransposon fi	---	---	-1.10	-0.14	-1.08	0.31651872	0.7025	-6.06
247720_at	dTDP-glucose 4-6-dehydratase - l	UXS3	AT5G59290	1.11	0.14	1.08	0.31664051	0.7026	-6.06
264373_at	putative vesicle transport protein C	SEC22	AT1G11890	-1.12	-0.17	-1.08	0.31676002	0.7026	-6.06
256711_at	unknown protein contains Pfam pr	---	AT3G30390	1.15	0.20	1.08	0.3167429	0.7026	-6.06
264098_at	hypothetical protein predicted by g	---	AT1G79260	1.16	0.21	1.08	0.31668678	0.7026	-6.06
250614_at	putative protein homeodomain pro	---	AT5G07260	-1.07	-0.09	-1.08	0.3167259	0.7026	-6.06
249428_at	putative protein predicted protein l	---	AT5G39870	-1.07	-0.10	-1.08	0.3167965	0.7027	-6.06
253899_at	putative protein protein disulfide-is	ATPDIL5-4	AT4G27080	1.10	0.14	1.08	0.31689376	0.7028	-6.06
265267_at	hypothetical protein predicted by g	---	AT2G42920	1.11	0.16	1.08	0.31702671	0.7030	-6.06
254688_at	DnaJ-like protein DnaJ-like protein	J20	AT4G13830	1.09	0.12	1.08	0.31717132	0.7031	-6.06
263560_s_at	unknown protein	FUT5	AT2G15350	-1.10	-0.14	-1.08	0.31712628	0.7031	-6.06

251131_at	laccase - like protein laccase pred	LAC10	AT5G01190	1.07	0.10	1.08	0.31717237	0.7031	-6.06
244947_at	hypothetical protein	---	---	-1.11	-0.15	-1.08	0.31726306	0.7033	-6.06
250213_at	H-protein promoter binding factor-1	TBP1	AT5G13820	1.13	0.18	1.08	0.31750078	0.7036	-6.07
251980_at	putative protein endopeptidase Cl	---	AT3G53270	-1.07	-0.10	-1.08	0.31752571	0.7036	-6.07
245781_at	S-ribonuclease binding protein SB	SBP1	AT1G45976	1.11	0.15	1.08	0.31747626	0.7036	-6.07
266815_at	F-box protein family, AtFBX5 cont	---	AT2G44900	-1.10	-0.14	-1.08	0.31757021	0.7036	-6.07
248831_at	putative protein contains similarity	---	AT5G47160	-1.10	-0.13	-1.08	0.31760272	0.7036	-6.07
251477_at	putative protein	---	AT3G59680	1.07	0.10	1.08	0.31757739	0.7036	-6.07
256260_at	hypothetical protein	---	AT3G12440	1.08	0.10	1.08	0.31760199	0.7036	-6.07
264025_at	AUX1-like amino acid permease ;	---	AT2G21050	1.34	0.43	1.08	0.31765563	0.7036	-6.07
248354_at	putative protein contains similarity	---	AT5G52330	1.09	0.12	1.08	0.31773726	0.7037	-6.07
265139_at	unknown protein	---	AT1G51310	1.11	0.15	1.08	0.31793863	0.7037	-6.07
250394_at	putative protein yllC, Enterococcu	---	AT5G10910	1.11	0.15	1.08	0.31778271	0.7037	-6.07
260691_s_at	hypothetical protein predicted by g	---	---	-1.09	-0.13	-1.08	0.31788045	0.7037	-6.07
251695_at	putative protein hypothetical protei	---	AT3G56590	-1.15	-0.21	-1.08	0.31793431	0.7037	-6.07
264032_at	unknown protein	GEK1	AT2G03800	-1.10	-0.13	-1.08	0.31796634	0.7037	-6.07
253110_at	hypothetical protein	---	AT4G35930	1.14	0.19	1.08	0.31792368	0.7037	-6.07
255099_at	hypothetical protein	---	---	-1.08	-0.11	-1.08	0.31784038	0.7037	-6.07
251772_at	cyclophilin-like protein ROC7, cyc	---	AT3G55920	-1.11	-0.15	-1.08	0.31804235	0.7038	-6.07
260639_at	hypothetical protein predicted by g	---	AT1G53180	1.24	0.31	1.08	0.31811394	0.7038	-6.07
257692_at	hypothetical protein contains simila	---	AT3G12840	-1.08	-0.11	-1.08	0.31807166	0.7038	-6.07
246582_at	hypothetical protein predicted by g	---	AT1G31750	-1.22	-0.29	-1.08	0.31809403	0.7038	-6.07
249686_at	putative protein contains similarity	CYP716A2	AT5G36140	-1.07	-0.10	-1.08	0.31825907	0.7041	-6.07
254180_at	putative protein hin1 protein homo	---	AT4G23930	1.16	0.21	1.08	0.31842088	0.7042	-6.07
264781_at	putative plastid RNA polymerase s	SIG2	AT1G08540	1.12	0.17	1.08	0.31842631	0.7042	-6.07
266469_at	myb-related protein	MYB14	AT2G31180	1.09	0.12	1.08	0.31837709	0.7042	-6.07
255318_at	hypothetical protein	---	AT4G04190	1.10	0.14	1.08	0.31860828	0.7046	-6.07
265281_at	unknown protein ; supported by fu	---	AT2G28370	1.11	0.15	1.08	0.31872995	0.7047	-6.07
253985_at	caffeoyl-CoA O-methyltransferase	---	AT4G26220	-1.10	-0.14	-1.08	0.31875125	0.7047	-6.07
260646_at	hypothetical protein similar to CHP	---	AT1G53340	1.14	0.19	1.08	0.31870674	0.7047	-6.07
253931_at	putative CDP-diacylglycerol synth	---	AT4G26770	1.09	0.13	1.08	0.31881939	0.7047	-6.07
250669_at	polygalacturonase inhibiting protei	PGIP2	AT5G06870	-1.29	-0.37	-1.08	0.31887804	0.7048	-6.07
260049_at	DNA-directed RNA polymerase su	NRPA2	AT1G29940	-1.18	-0.24	-1.08	0.31891433	0.7048	-6.07
267404_at	hypothetical protein predicted by g	atnudt22	AT2G33980	-1.09	-0.13	-1.08	0.31903394	0.7050	-6.07
259047_at	unknown protein	DegP7	AT3G03380	1.07	0.10	1.08	0.31933169	0.7056	-6.07

256454_at	NADPH oxidoreductase, putative	---	AT1G75280	-1.27	-0.34	-1.08	0.31939151	0.7057	-6.07
253236_at	putative protein ARI protein, Dros	ARI1	AT4G34370	1.07	0.10	1.07	0.31949406	0.7058	-6.07
261254_at	Expressed protein ; supported by f	---	AT1G05805	-1.10	-0.13	-1.07	0.31957237	0.7059	-6.07
262929_at	hypothetical protein ;supported by	---	AT1G65720	1.13	0.17	1.07	0.31968195	0.7061	-6.07
245242_at	chlorophyll a oxygenase identical t	CH1	AT1G44446	-1.12	-0.16	-1.07	0.31988649	0.7061	-6.07
247705_at	putative protein ;supported by full-	---	AT5G59460	1.09	0.12	1.07	0.31982179	0.7061	-6.07
247460_at	AtOXA1 ;supported by full-length	OXA1	AT5G62050	-1.07	-0.09	-1.07	0.31988765	0.7061	-6.07
267192_at	hypothetical protein predicted by g	---	AT2G30890	-1.11	-0.15	-1.07	0.31984221	0.7061	-6.07
264230_at	hypothetical protein predicted by g	---	AT1G67460	-1.08	-0.12	-1.07	0.31974879	0.7061	-6.07
260972_at	hypothetical protein contains simila	---	AT1G53530	1.09	0.12	1.07	0.31990443	0.7061	-6.07
265552_at	putative plasma membrane proton	AHA6	AT2G07560	1.09	0.12	1.07	0.31989459	0.7061	-6.07
261241_at	subtilisin-like serine protease conta	---	AT1G32950	-1.08	-0.12	-1.07	0.319973	0.7062	-6.07
247013_at	putative protein strong similarity to	BT4	AT5G67480	1.16	0.22	1.07	0.32039444	0.7065	-6.07
245118_at	putative thioredoxin reductase The	NTRC	AT2G41680	1.08	0.12	1.07	0.32040792	0.7065	-6.07
247810_at	26S proteasome AAA-ATPase sub	RPT3	AT5G58290	1.08	0.11	1.07	0.32025942	0.7065	-6.07
266511_at	putative ATP-dependent RNA helic	---	AT2G47680	1.11	0.15	1.07	0.32038348	0.7065	-6.07
252239_at	putative protein putative protein -	---	AT3G49990	1.16	0.21	1.07	0.32032267	0.7065	-6.07
247507_at	putative protein predicted protein,	APO3	AT5G61930	1.19	0.25	1.07	0.32043186	0.7065	-6.07
262883_at	ammonium transporter, puitative s	ATAMT1;2	AT1G64780	-1.16	-0.22	-1.07	0.32038276	0.7065	-6.07
248170_at	ankyrin-repeat-containing protein-l	---	AT5G54620	-1.12	-0.17	-1.07	0.32022335	0.7065	-6.07
258859_at	Expressed protein ; supported by f	---	AT3G02120	1.07	0.10	1.07	0.32048632	0.7065	-6.07
260534_at	hypothetical protein predicted by g	---	---	1.08	0.11	1.07	0.32027987	0.7065	-6.07
249745_at	phloem-specific lectin-like protein	AtPP2-B12	AT5G24560	-1.11	-0.14	-1.07	0.3204852	0.7065	-6.07
261587_at	hypothetical protein predicted by g	---	AT1G01660	-1.08	-0.12	-1.07	0.32033426	0.7065	-6.07
250504_at	putative protein similar to unknown	---	AT5G09840	-1.11	-0.15	-1.07	0.32058149	0.7066	-6.07
261214_at	Mutator-like protein similar to many	---	---	-1.12	-0.16	-1.07	0.32059999	0.7066	-6.07
261000_at	hypothetical protein predicted by g	---	AT1G26540	1.08	0.11	1.07	0.32060742	0.7066	-6.07
255331_at	hypothetical protein ; supported by	---	AT4G04330	-1.09	-0.13	-1.07	0.32063972	0.7066	-6.07
258587_at	hypothetical protein predicted by g	---	AT3G04310	-1.17	-0.23	-1.07	0.32086483	0.7070	-6.07
250678_at	selenium-binding protein-like	---	AT5G06540	1.08	0.11	1.07	0.32098737	0.7071	-6.07
262394_at	unknown protein	emb1273	AT1G49510	1.15	0.20	1.07	0.32103048	0.7071	-6.07
257177_at	cyanate lyase (CYN) identical to cy	CYN	AT3G23490	1.13	0.18	1.07	0.32103816	0.7071	-6.07
255381_at	RMA1 RING zinc finger protein ide	RMA1	AT4G03510	1.18	0.24	1.07	0.3210135	0.7071	-6.07
255329_at	hypothetical protein	---	AT4G04370	-1.07	-0.10	-1.07	0.32108622	0.7072	-6.07
246647_at	putative protein predicted proteins	---	---	-1.08	-0.11	-1.07	0.32123914	0.7074	-6.07

AFFX-TrpnX-3_	B. subtilis /GEN=trpC, trpF /DB_XF	---	---	-1.07	-0.09	-1.07	0.32126802	0.7074	-6.07
244987_s_at	ribosomal protein L2	---	---	1.07	0.10	1.07	0.32127829	0.7074	-6.07
260852_at	transmembrane protein, putative s	---	AT1G21900	1.08	0.11	1.07	0.32137803	0.7075	-6.08
252914_at	putative protein dehydrin, Glycine	---	AT4G39130	-1.12	-0.16	-1.07	0.32144365	0.7076	-6.08
248318_at	unknown protein	---	AT5G52690	1.08	0.11	1.07	0.32146544	0.7076	-6.08
252335_at	putative protein putative protein - A	---	AT3G48860	1.10	0.14	1.07	0.32166289	0.7077	-6.08
248926_at	Ole e I (main olive allergen)-like pr	---	AT5G45880	-1.17	-0.23	-1.07	0.32165808	0.7077	-6.08
246289_at	putative protein predicted protein A	---	AT3G56880	1.17	0.23	1.07	0.3215649	0.7077	-6.08
246215_at	putative cytoskeletal protein ; supp	---	AT4G37180	-1.23	-0.30	-1.07	0.32165998	0.7077	-6.08
253816_at	hypothetical protein ;supported by	emb1923	AT4G28210	1.11	0.15	1.07	0.32164363	0.7077	-6.08
249004_at	unknown protein	---	AT5G44570	-1.11	-0.16	-1.07	0.32169529	0.7077	-6.08
256563_at	unknown protein	RALFL27	AT3G29780	-1.09	-0.13	-1.07	0.32172759	0.7077	-6.08
253204_at	GTP binding protein beta subunit	AGB1	AT4G34460	1.07	0.10	1.07	0.32185125	0.7077	-6.08
263611_at	hypothetical protein predicted by g	---	AT2G16450	-1.07	-0.10	-1.07	0.32180199	0.7077	-6.08
247263_at	putative protein similar to unknown	---	AT5G64470	1.12	0.17	1.07	0.32184445	0.7077	-6.08
245049_at	ribosomal protein S16	---	---	1.15	0.20	1.07	0.32186574	0.7077	-6.08
254047_at	hypothetical protein	---	AT4G26040	-1.12	-0.16	-1.07	0.32191728	0.7078	-6.08
247081_at	AtRAD17 (dbj|BAA90479.1) ; supp	ATRAD17	AT5G66130	1.11	0.14	1.07	0.32216198	0.7079	-6.08
255130_at	hypothetical protein ; supported by	---	AT4G08240	-1.10	-0.14	-1.07	0.3221121	0.7079	-6.08
263408_at	predicted protein	---	AT2G04060	-1.08	-0.11	-1.07	0.32202227	0.7079	-6.08
245132_at	hypothetical protein predicted by g	---	AT2G45320	1.14	0.18	1.07	0.3222711	0.7079	-6.08
263047_at	putative phosphoserine aminotrans	---	AT2G17630	1.19	0.26	1.07	0.32231046	0.7079	-6.08
255934_at	cytochrome P450, putative similar	CYP87A2	AT1G12740	-1.08	-0.11	-1.07	0.32206264	0.7079	-6.08
261506_at	choline kinase, putative similar to	ATCK1	AT1G71697	1.18	0.24	1.07	0.32228841	0.7079	-6.08
249131_at	putative protein contains similarity	APUM14	AT5G43110	1.07	0.10	1.07	0.32222163	0.7079	-6.08
244975_at	PSII 10KDa phosphoprotein	---	---	-1.10	-0.13	-1.07	0.32221729	0.7079	-6.08
263531_s_at	hypothetical protein predicted by g	---	AT2G25020 A	1.07	0.10	1.07	0.32231345	0.7079	-6.08
263884_at	hypothetical protein predicted by g	---	AT2G36920	1.07	0.10	1.07	0.32217324	0.7079	-6.08
255725_at	hypothetical protein similar to puta	PFT1	AT1G25540	-1.07	-0.10	-1.07	0.32236631	0.7079	-6.08
249262_at	putative protein similar to unknown	---	AT5G41720	-1.09	-0.12	-1.07	0.32241276	0.7080	-6.08
257621_at	calmodulin-domain protein kinase	CPK9	AT3G20410	1.17	0.23	1.07	0.32244561	0.7080	-6.08
247495_at	putative protein predicted protein,	IPK2BETA	AT5G61760	-1.11	-0.15	-1.07	0.32266945	0.7082	-6.08
251795_at	putative protein MtN24, Medicago	---	AT3G55390	1.14	0.19	1.07	0.32265283	0.7082	-6.08
245415_at	G2484-1 protein	ATG2484-1	AT4G17330	1.08	0.11	1.07	0.32262051	0.7082	-6.08
267029_at	unknown protein	ATIREG1	AT2G38460	-1.11	-0.14	-1.07	0.32268865	0.7082	-6.08

250417_at	putative protein predicted proteins	---	AT5G11230	1.11	0.15	1.07	0.32265953	0.7082	-6.08
265996_at	putative leucine aminopeptidase id	---	AT2G24200	-1.21	-0.27	-1.07	0.32276827	0.7083	-6.08
254382_at	hypothetical protein	---	AT4G21890	-1.13	-0.18	-1.07	0.32295217	0.7084	-6.08
254217_at	putative protein other hypothetical	---	AT4G23720	-1.07	-0.10	-1.07	0.32296386	0.7084	-6.08
245583_at	hypothetical protein	---	AT4G14920	-1.09	-0.12	-1.07	0.32292521	0.7084	-6.08
258095_at	dual-specificity protein phosphatas	---	AT3G23610	1.10	0.14	1.07	0.32291663	0.7084	-6.08
248538_at	putative protein contains similarity	---	AT5G50110	1.12	0.16	1.07	0.32310167	0.7086	-6.08
261644_s_at	hypothetical protein contains simila	ATCSA-1	AT1G19750 /	1.10	0.13	1.07	0.32317493	0.7087	-6.08
263491_at	phosphoenolpyruvate carboxylase	ATPPC2	AT2G42600	1.10	0.14	1.07	0.32316781	0.7087	-6.08
255967_at	protein phosphatase type 2C, puta	---	AT1G22280	-1.11	-0.15	-1.07	0.3232278	0.7087	-6.08
264328_at	putative IAA1 protein Match to IAA	IAA10	AT1G04100	-1.13	-0.18	-1.07	0.32326749	0.7087	-6.08
267490_at	putative receptor-like protein kinas	---	AT2G19130	-1.18	-0.24	-1.07	0.3233026	0.7087	-6.08
249325_at	urophorphyrin III methylase (gb|AA	UPM1	AT5G40850	1.12	0.16	1.07	0.32334004	0.7088	-6.08
249723_at	putative protein similar to unknown	---	AT5G35430	-1.07	-0.10	-1.07	0.32337601	0.7088	-6.08
263183_at	putative glucan synthase Highly si	CALS1	AT1G05570	1.29	0.37	1.07	0.32356001	0.7091	-6.08
253186_at	putative protein predicted proteins	---	AT4G35270	1.13	0.18	1.06	0.32359592	0.7091	-6.08
259882_at	unknown protein similar to hypothe	---	AT1G76670	-1.10	-0.13	-1.06	0.32371452	0.7092	-6.08
266943_at	putative reverse transcriptase	---	---	-1.13	-0.18	-1.06	0.32372608	0.7092	-6.08
248482_at	unknown protein	---	AT5G50970	-1.08	-0.11	-1.06	0.32373623	0.7092	-6.08
260153_at	putative lipase similar to monoglyc	---	AT1G52760	-1.18	-0.24	-1.06	0.32386964	0.7094	-6.08
246104_at	DNA-binding protein - like DNA-bi	WRKY74	AT5G28650	1.08	0.10	1.06	0.32402138	0.7097	-6.08
265738_at	NADC homolog identical to GP|12	QPT	AT2G01350	-1.09	-0.13	-1.06	0.32405837	0.7097	-6.08
267139_s_at	hypothetical protein predicted by g	---	AT2G38195 /	-1.07	-0.10	-1.06	0.3240329	0.7097	-6.08
246622_at	protein phosphatase-2C PP2C-like	---	AT5G36250	-1.07	-0.10	-1.06	0.32424989	0.7097	-6.08
249181_at	putative protein contains similarity	---	AT5G42920	1.09	0.13	1.06	0.32423985	0.7097	-6.08
252242_at	F-box protein family, AtFBL16 con	VFB2	AT3G50080	-1.09	-0.13	-1.06	0.32426425	0.7097	-6.08
258156_at	unknown protein ; supported by cI	---	AT3G18050	1.18	0.24	1.06	0.32414094	0.7097	-6.08
258020_at	unknown protein ;supported by ful	NHD1	AT3G19490	-1.09	-0.12	-1.06	0.32425452	0.7097	-6.08
262617_at	unknown protein	POR C	AT1G03630 /	1.08	0.12	1.06	0.32424359	0.7097	-6.08
246034_at	putative protein FH protein interac	---	AT5G08350	-1.16	-0.21	-1.06	0.32439305	0.7098	-6.08
257519_at	unknown protein	---	AT3G01210	-1.10	-0.14	-1.06	0.32437395	0.7098	-6.08
246689_at	putative protein predicted proteins	---	---	1.07	0.09	1.06	0.32446256	0.7099	-6.08
262046_at	hypothetical protein predicted by g	OFP14	AT1G79960	-1.11	-0.15	-1.06	0.32450782	0.7100	-6.08
248311_at	beta-carotene hydroxylase	BETA-OHA	AT5G52570	1.16	0.21	1.06	0.32459721	0.7101	-6.08
266593_at	hypothetical protein predicted by g	---	AT2G46200	1.09	0.13	1.06	0.32462039	0.7101	-6.08

263088_at	putative replication protein A1	---	---	1.08	0.11	1.06	0.32466172	0.7101	-6.08
245777_at	unknown protein contains similarity	atnudt21	AT1G73540	-1.46	-0.55	-1.06	0.32471519	0.7101	-6.08
246304_at	acyl-coA dehydrogenase Mus mus	ACX4	AT3G51840	1.13	0.17	1.06	0.32476894	0.7102	-6.08
267504_at	unknown protein ;supported by ful	---	AT2G45530	1.11	0.15	1.06	0.32485825	0.7102	-6.08
257424_at	hypothetical protein predicted by g	---	AT1G78840	-1.12	-0.17	-1.06	0.32484094	0.7102	-6.08
255002_at	AIG1-like protein AIG1 - Arabidop	---	AT4G09940	-1.09	-0.13	-1.06	0.32480632	0.7102	-6.08
263186_at	lectin receptor kinase, putative sin	---	---	-1.13	-0.17	-1.06	0.32497025	0.7102	-6.08
252587_at	putative protein Human (H326) tra	---	AT3G45620	1.18	0.24	1.06	0.32493218	0.7102	-6.08
263573_at	unknown protein similar to A. thalia	---	AT2G17150	-1.12	-0.17	-1.06	0.32500871	0.7102	-6.08
266764_at	putative pectinesterase ;supporte	---	AT2G47050	-1.10	-0.13	-1.06	0.32501455	0.7102	-6.08
249594_at	putative protein SIAH1 protein, Br	---	AT5G37910	-1.08	-0.11	-1.06	0.32509807	0.7103	-6.08
249085_at	putative protein similar to unknown	---	AT5G44170	-1.10	-0.13	-1.06	0.32513885	0.7103	-6.08
260238_at	AtHVA22a identical to AtHVA22a	ATHVA22A	AT1G74520	1.11	0.16	1.06	0.32514276	0.7103	-6.08
253455_at	putative protein	---	AT4G32020	-1.16	-0.22	-1.06	0.32507764	0.7103	-6.08
254815_at	putative pollen-specific protein pol	SKU5	AT4G12420	1.17	0.22	1.06	0.32537497	0.7105	-6.08
250437_at	AtAGP4 ; supported by cDNA: gi_	AGP4	AT5G10430	-1.41	-0.50	-1.06	0.32535537	0.7105	-6.08
256697_at	hypothetical protein contains simila	AtOCT4	AT3G20660	1.20	0.26	1.06	0.32536734	0.7105	-6.08
248696_at	putative protein similar to unknown	---	AT5G48360	-1.09	-0.12	-1.06	0.3253486	0.7105	-6.08
251300_at	hypothetical protein ;supported by	---	AT3G61980	1.13	0.17	1.06	0.32548195	0.7107	-6.09
251958_at	putative protein predicted proteins	---	AT3G53560	1.17	0.23	1.06	0.3255707	0.7107	-6.09
256781_at	dirigent protein, putative similar to	---	AT3G13650	-1.87	-0.90	-1.06	0.32556019	0.7107	-6.09
264843_at	putative 1-aminocyclopropane-1-c	---	AT1G03400	1.16	0.21	1.06	0.325603	0.7107	-6.09
262369_at	hypothetical protein predicted by g	---	AT1G73010	1.44	0.52	1.06	0.32581805	0.7109	-6.09
262575_at	putative ABC transporter Similar to	PDR7	AT1G15210	-1.09	-0.13	-1.06	0.32582329	0.7109	-6.09
253527_at	pathogenesis-related protein hom	---	AT4G31470	-1.09	-0.13	-1.06	0.32588463	0.7109	-6.09
255665_at	hypothetical protein	CRP	AT4G00450	1.08	0.11	1.06	0.32584976	0.7109	-6.09
252165_at	hypothetical protein ;supported by	---	AT3G50550	1.10	0.14	1.06	0.3257078	0.7109	-6.09
249270_at	putative protein similar to unknown	---	AT5G41780	-1.07	-0.10	-1.06	0.32587431	0.7109	-6.09
246406_at	disease resistance protein RPP1-V	---	AT1G57650	-1.06	-0.09	-1.06	0.32581169	0.7109	-6.09
251326_at	putative protein stamina pistilloidia	HWS	AT3G61590	1.12	0.17	1.06	0.32592077	0.7109	-6.09
252428_at	putative protein rjs - Mus musculu	---	AT3G47660	-1.10	-0.14	-1.06	0.32598701	0.7109	-6.09
249597_at	putative protein probable quinone	---	AT5G37960	-1.07	-0.10	-1.06	0.32606416	0.7110	-6.09
260197_at	F12A21.25 hypothetical protein	---	AT1G67623	-1.08	-0.11	-1.06	0.32607149	0.7110	-6.09
245695_at	rec - like protein	---	AT5G04270	1.09	0.13	1.06	0.32619288	0.7112	-6.09
267259_at	Expressed protein ; supported by f	---	AT2G23090	1.09	0.13	1.06	0.32624647	0.7112	-6.09

249289_at	N-hydroxycinnamoyl/benzoyltransf	---	AT5G41040	1.41	0.49	1.06	0.32628182	0.7112	-6.09
265820_at	hypothetical protein predicted by g	---	AT2G17940	-1.11	-0.15	-1.06	0.32633601	0.7113	-6.09
252785_at	putative protein AND-1 protein - H	---	AT3G42660	1.17	0.23	1.06	0.32642703	0.7114	-6.09
248411_at	unknown protein	---	AT5G51580	-1.07	-0.10	-1.06	0.32644348	0.7114	-6.09
248948_at	putative protein strong similarity to	---	AT5G45560	1.13	0.18	1.06	0.32651322	0.7115	-6.09
253878_at	trehalose-6-phosphate synthase -	TPS4	AT4G27550	-1.08	-0.11	-1.06	0.32676431	0.7120	-6.09
260848_at	pectinesterase, putative similar to	sks8	AT1G21850	-1.12	-0.17	-1.06	0.32683443	0.7120	-6.09
262686_at	proteasome regulatory subunit S3	---	AT1G75990	1.10	0.14	1.06	0.32691865	0.7120	-6.09
254812_at	nucleotide sugar epimerase -like p	GAE5	AT4G12250	1.22	0.29	1.06	0.32692369	0.7120	-6.09
254995_at	putative protein	---	AT4G10370	-1.10	-0.14	-1.06	0.3269299	0.7120	-6.09
254616_at	shaggy-like protein kinase etha (E	BIN2	AT4G18710	-1.08	-0.11	-1.06	0.32707832	0.7121	-6.09
257435_at	putative RSZp22 splicing factor	---	AT2G24590	1.12	0.16	1.06	0.32708547	0.7121	-6.09
245316_at	hypothetical protein ;supported by	---	AT4G14000	-1.09	-0.13	-1.06	0.32708867	0.7121	-6.09
248735_at	laccase (diphenol oxidase)	TT10	AT5G48100	-1.08	-0.11	-1.06	0.32701199	0.7121	-6.09
255171_at	hypothetical protein	---	AT4G07990	-1.08	-0.11	-1.06	0.32720736	0.7121	-6.09
256061_at	unknown protein ;supported by full	---	AT1G07040	1.15	0.20	1.06	0.32717465	0.7121	-6.09
251594_at	putative protein DOC4, Mus musc	---	AT3G57630	-1.30	-0.38	-1.06	0.32717751	0.7121	-6.09
265033_at	PSI type III chlorophyll a/b-binding	LHCA3	AT1G61520	1.07	0.09	1.06	0.32721909	0.7121	-6.09
258632_s_at	putative MAP3K epsilon protein ki	MAPKKK7	AT3G07980 /	-1.12	-0.17	-1.06	0.32758313	0.7122	-6.09
262509_at	hypothetical protein similar to hypo	CRR22	AT1G11290	-1.10	-0.14	-1.06	0.32749578	0.7122	-6.09
261039_at	Expressed protein ; supported by f	ELF4-L4	AT1G17455	1.14	0.19	1.06	0.32764971	0.7122	-6.09
255701_at	predicted protein of unknown funct	JLO	AT4G00220	1.08	0.11	1.06	0.32746011	0.7122	-6.09
252712_at	glutathione transferase-like protei	ATGSTU27	AT3G43800	-1.16	-0.22	-1.06	0.32753652	0.7122	-6.09
247017_at	putative protein similar to unknown	---	AT5G66980	1.07	0.10	1.06	0.32742793	0.7122	-6.09
245495_at	hypothetical protein	---	AT4G16400	-1.07	-0.09	-1.06	0.3275376	0.7122	-6.09
255900_at	hypothetical protein predicted by g	---	AT1G17830 /	-1.27	-0.35	-1.06	0.32733238	0.7122	-6.09
249033_at	putative protein contains similarity	---	AT5G44920	-1.09	-0.12	-1.06	0.32765325	0.7122	-6.09
262105_at	pectin esterase, putative similar to	---	AT1G02810	-1.11	-0.16	-1.06	0.32763174	0.7122	-6.09
250629_at	respiratory burst oxidase protein A	ATRBOHA	AT5G07390	-1.09	-0.13	-1.06	0.32758605	0.7122	-6.09
253315_at	putative protein various predicted	---	AT4G33900	-1.09	-0.12	-1.06	0.32731009	0.7122	-6.09
249364_at	putative protein predicted protein,	---	AT5G40590	-1.08	-0.11	-1.06	0.3275641	0.7122	-6.09
256444_at	hypothetical protein predicted by g	---	AT3G11060	-1.08	-0.11	-1.06	0.32774744	0.7123	-6.09
266372_at	putative two-component response	ATRR3	AT2G41310	1.10	0.14	1.06	0.32776829	0.7123	-6.09
265989_at	unknown protein	---	AT2G24260	-1.08	-0.11	-1.05	0.32788283	0.7125	-6.09
256490_at	unknown protein ;supported by full	---	AT1G31460	-1.13	-0.17	-1.05	0.32796266	0.7126	-6.09

250244_at	putative protein similar to unknown	ABO1	AT5G13680	1.15	0.21	1.05	0.32808957	0.7128	-6.09
253777_at	SOF1 protein-like protein SOF1 (ir	---	AT4G28450	1.24	0.30	1.05	0.32831555	0.7129	-6.09
266836_at	hypothetical protein predicted by g	---	AT2G26000	-1.12	-0.16	-1.05	0.32828684	0.7129	-6.09
260905_at	hypothetical protein predicted by g	---	AT1G02710	-1.07	-0.09	-1.05	0.32825579	0.7129	-6.09
250047_at	BCS1 - like protein h-bcs1, Homo	---	AT5G17730	-1.10	-0.14	-1.05	0.32830302	0.7129	-6.09
261449_at	putative ATPase similar to GB:AAF	---	AT1G21120	1.16	0.21	1.05	0.32820391	0.7129	-6.09
246983_at	receptor protein kinase-like protein	---	AT5G67200	1.13	0.18	1.05	0.32822171	0.7129	-6.09
245640_at	helix-loop-helix protein homolog, p	---	AT1G25330	-1.09	-0.12	-1.05	0.32839809	0.7130	-6.09
250987_at	putative protein crp1 protein, Zea	---	AT5G02860	-1.10	-0.14	-1.05	0.32868973	0.7132	-6.09
247890_at	cyclic nucleotide and calmodulin-re	ATCNGC5	AT5G57940	-1.10	-0.14	-1.05	0.32860102	0.7132	-6.09
266465_at	putative auxin-responsive protein	GH3.9	AT2G47750	-1.09	-0.13	-1.05	0.3285628	0.7132	-6.09
252594_at	putative transporter protein peptid	---	AT3G45680	-1.15	-0.21	-1.05	0.32867267	0.7132	-6.09
263492_at	putative seed maturation protein	---	AT2G42560	-1.09	-0.13	-1.05	0.32861728	0.7132	-6.09
267066_at	hypothetical protein predicted by g	---	AT2G41040	-1.13	-0.18	-1.05	0.32863995	0.7132	-6.09
255796_at	similar to mammalian MHC III regi	SUVH2	AT2G33290	-1.09	-0.12	-1.05	0.32888881	0.7134	-6.09
252725_at	putative protein mudrA transposas	---	---	-1.08	-0.11	-1.05	0.32884731	0.7134	-6.09
260131_at	unknown protein contains Pfam pr	---	AT1G66310	1.09	0.12	1.05	0.32886143	0.7134	-6.09
255376_x_at	putative athila-like protein	---	---	-1.12	-0.17	-1.05	0.32884859	0.7134	-6.09
258578_at	germin-like protein contains Pfam	---	AT3G04200	-1.14	-0.19	-1.05	0.32899838	0.7134	-6.09
255158_s_at	hypothetical protein	---	---	1.08	0.11	1.05	0.32900415	0.7134	-6.09
257185_at	ABC transporter, putative similar t	ATMRP7	AT3G13100	-1.16	-0.21	-1.05	0.32899244	0.7134	-6.09
253137_at	protein kinase - like protein protein	---	AT4G35500	1.11	0.16	1.05	0.32908727	0.7135	-6.09
265383_at	putative WD-40 repeat protein, MS	MSI2	AT2G16780	1.13	0.17	1.05	0.32913555	0.7136	-6.09
262123_at	hypothetical protein predicted by g	---	AT1G59630	-1.10	-0.14	-1.05	0.32924523	0.7138	-6.09
260477_at	Ser/Thr protein kinase isolog	---	AT1G11050	1.41	0.50	1.05	0.32933274	0.7138	-6.09
248848_at	disease resistance protein-like	---	AT5G46520	-1.06	-0.09	-1.05	0.32935344	0.7138	-6.09
259455_x_at	unknown protein	---	AT1G44030	-1.11	-0.16	-1.05	0.32945059	0.7140	-6.09
253060_at	putative protein predicted protein,	---	AT4G37710	-1.23	-0.30	-1.05	0.32964053	0.7142	-6.10
247944_at	putative protein similar to unknown	---	AT5G57100	1.10	0.14	1.05	0.3297051	0.7142	-6.10
250893_at	putative protein predicted proteins	EMB175	AT5G03795	-1.08	-0.11	-1.05	0.32974596	0.7142	-6.10
258659_at	B' regulatory subunit of PP2A (AtB	ATB' BETA	AT3G09880	1.09	0.12	1.05	0.32979216	0.7142	-6.10
266007_at	unknown protein	---	AT2G37380	-1.11	-0.14	-1.05	0.32958576	0.7142	-6.10
257751_at	hypothetical protein predicted by g	MKS1	AT3G18690	1.34	0.42	1.05	0.32977234	0.7142	-6.10
257812_at	hypothetical protein	---	AT3G25090	1.10	0.14	1.05	0.32963759	0.7142	-6.10
249919_at	putative protein predicted protein,	---	AT5G19250	1.10	0.14	1.05	0.32975065	0.7142	-6.10

253535_at	putaive DNA-binding protein DNA	WRKY11	AT4G31550	1.37	0.46	1.05	0.32985297	0.7143	-6.10
249640_at	cationic amino acid transporter -lik	CAT3	AT5G36940	1.14	0.19	1.05	0.33015797	0.7148	-6.10
245847_at	MYB DNA-binding - like protein m	MYB64	AT5G11050	1.10	0.14	1.05	0.3301452	0.7148	-6.10
256370_at	MATE efflux family protein, putativ	---	AT1G66780	-1.08	-0.12	-1.05	0.33022042	0.7148	-6.10
254535_at	aspartate kinase-homoserine deh	AK-HSDH I	AT4G19710	1.08	0.11	1.05	0.33026031	0.7149	-6.10
257260_at	hypothetical protein predicted by g	---	AT3G22104	-1.12	-0.17	-1.05	0.33035929	0.7150	-6.10
259370_at	hypothetical protein predicted by g	---	AT1G69050	1.11	0.15	1.05	0.33036485	0.7150	-6.10
257207_at	hypothetical protein predicted by g	---	AT3G14900	1.10	0.14	1.05	0.33041344	0.7150	-6.10
244968_at	ribosomal protein L33	---	---	1.10	0.13	1.05	0.33057775	0.7153	-6.10
253209_at	putative protein membrane-associ	---	AT4G34830	-1.11	-0.15	-1.05	0.33061069	0.7153	-6.10
247884_at	lipid transfer protein; glossy1 homo	CER3	AT5G57800	-1.25	-0.32	-1.05	0.33092485	0.7154	-6.10
247627_at	cysteine proteinase AALP identica	AALP	AT5G60360	1.08	0.11	1.05	0.33080006	0.7154	-6.10
247280_at	phi-1-like protein ;supported by ful	EXL2	AT5G64260	-1.20	-0.26	-1.05	0.33078098	0.7154	-6.10
250903_at	putative protein coil protein PO22,	---	AT5G03600	-1.12	-0.16	-1.05	0.33093417	0.7154	-6.10
246735_at	histone H2A-like protein histone H	HTA7	AT5G27670	1.10	0.14	1.05	0.3308668	0.7154	-6.10
252817_at	putative protein hypothetical protei	---	---	-1.10	-0.14	-1.05	0.33084171	0.7154	-6.10
253417_at	putative protein	PC-MYB1	AT4G32730	-1.08	-0.12	-1.05	0.33092671	0.7154	-6.10
248632_at	unknown protein	SLD5	AT5G49010	1.19	0.26	1.05	0.33087409	0.7154	-6.10
263553_at	putative purple acid phosphatase p	PAP10	AT2G16430	1.11	0.15	1.05	0.33101543	0.7155	-6.10
246591_at	putative cation transport protein p	---	AT5G14880	1.11	0.15	1.05	0.33103953	0.7155	-6.10
245262_at	predicted protein ; supported by cD	---	AT4G16563	1.16	0.21	1.05	0.33155308	0.7155	-6.10
260254_at	putative glycerophosphodiester ph	---	AT1G74210	1.08	0.12	1.05	0.33121436	0.7155	-6.10
250233_at	putative protein weak homology w	IQD11	AT5G13460	-1.34	-0.42	-1.05	0.33148785	0.7155	-6.10
258656_at	putative Ras-like GTP-binding prot	ATRABE1E	AT3G09900	1.13	0.17	1.05	0.33120196	0.7155	-6.10
249822_at	unknown protein	---	AT5G23710	1.09	0.13	1.05	0.33150867	0.7155	-6.10
256440_at	unknown protein ;supported by ful	---	AT3G10970	1.08	0.11	1.05	0.33156999	0.7155	-6.10
248187_at	zinc-binding protein-like ; supporte	---	AT5G53940	1.09	0.13	1.05	0.33136348	0.7155	-6.10
266548_at	unknown protein ;supported by ful	RPA	AT2G35210	1.13	0.18	1.05	0.33114075	0.7155	-6.10
244933_at	NADH dehydrogenase ND4L	---	---	-1.09	-0.13	-1.05	0.33153445	0.7155	-6.10
246673_at	ribosomal protein S1 ;supported by	RPS1	AT5G30510	1.08	0.11	1.05	0.33128489	0.7155	-6.10
260635_at	unknown protein	---	AT1G62420	1.11	0.15	1.05	0.33131416	0.7155	-6.10
251789_at	serine/threonine-specific protein k	---	AT3G55450	-1.11	-0.15	-1.05	0.33117702	0.7155	-6.10
255911_at	receptor-like kinase, putative simil	---	AT1G66930	1.07	0.10	1.05	0.33132803	0.7155	-6.10
250084_at	unknown protein	SDG40	AT5G17240	-1.14	-0.18	-1.05	0.33157831	0.7155	-6.10
246927_s_at	nodulin - like protein nodulin, Glyc	---	AT5G25250	1.16	0.21	1.05	0.33143742	0.7155	-6.10

251748_at	putative protein predicted protein,	---	AT3G55680	-1.11	-0.15	-1.05	0.33138434	0.7155	-6.10
263388_at	En/Spm-like transposon protein rel	---	---	1.10	0.14	1.05	0.33148206	0.7155	-6.10
267378_at	hypothetical protein	---	AT2G26200	1.07	0.10	1.05	0.33185306	0.7159	-6.10
250397_at	histon H3 protein HISTONE H3.2,	---	AT5G10980	1.06	0.09	1.05	0.33182892	0.7159	-6.10
246268_at	cytochrome P450, putative contair	CYP97A3	AT1G31800	-1.11	-0.15	-1.05	0.33183444	0.7159	-6.10
260013_at	putative annexin similar to annexin	ANN5	AT1G68090	-1.07	-0.10	-1.05	0.33183418	0.7159	-6.10
260617_at	Expressed protein ; supported by f	---	AT1G53345	1.10	0.14	1.05	0.33188709	0.7159	-6.10
255870_at	hypothetical protein predicted by g	---	AT2G30280	1.08	0.11	1.05	0.3319504	0.7159	-6.10
245395_at	hypothetical protein ;supported by	---	AT4G17420	-1.11	-0.15	-1.05	0.33198772	0.7160	-6.10
265531_at	hypothetical protein predicted by g	AtGRF6	AT2G06200	-1.09	-0.12	-1.05	0.33202339	0.7160	-6.10
250041_at	putative protein p53 inducible prot	PIR121	AT5G18410	1.07	0.10	1.04	0.33212564	0.7160	-6.10
257653_at	hypothetical protein	---	AT3G13225	-1.10	-0.14	-1.04	0.33211286	0.7160	-6.10
254978_at	subtilisin-like serine protease conta	---	AT4G10540	1.07	0.10	1.05	0.33208599	0.7160	-6.10
258818_at	putative ethylene receptor (EIN4)	EIN4	AT3G04580	-1.10	-0.14	-1.04	0.33217469	0.7160	-6.10
249409_at	putative protein KED, Nicotiana ta	---	AT5G40340	-1.29	-0.36	-1.04	0.33234756	0.7163	-6.10
262135_at	AP2 domain containing protein, pu	RAP2.4	AT1G78080	1.18	0.24	1.04	0.3325362	0.7166	-6.10
259547_at	gypsy/Ty3 element polyprotein, pu	---	---	-1.09	-0.12	-1.04	0.33254788	0.7166	-6.10
262689_at	unknown protein	ANAC026	AT1G62700	1.09	0.12	1.04	0.33259063	0.7166	-6.10
258132_at	protein kinase, putative similar to (	ATPERK1	AT3G24550	-1.13	-0.18	-1.04	0.33263703	0.7167	-6.10
251678_at	putative protein conserved hypoth	EDA7	AT3G56990	1.08	0.11	1.04	0.33272734	0.7168	-6.10
250786_at	putative protein strong similarity to	SDN2	AT5G05540	1.12	0.17	1.04	0.33277246	0.7168	-6.10
250742_at	putative protein similar to unknown	---	AT5G05800	1.10	0.13	1.04	0.33285624	0.7169	-6.10
260501_at	unknown protein ; supported by cl	---	AT2G41770	1.12	0.17	1.04	0.3329368	0.7171	-6.10
245472_at	hypothetical protein	---	AT4G16040	-1.11	-0.15	-1.04	0.33312146	0.7172	-6.10
257574_at	hypothetical protein predicted by g	---	AT3G20710	-1.09	-0.13	-1.04	0.33311215	0.7172	-6.10
256764_at	hypothetical protein predicted by g	---	AT3G29310	1.11	0.15	1.04	0.33310338	0.7172	-6.10
252233_at	AtMYB84 ;supported by full-length	MYB84	AT3G49690	1.10	0.13	1.04	0.33314794	0.7172	-6.10
256984_at	hypothetical protein predicted by g	---	AT3G13480	-1.10	-0.14	-1.04	0.33320856	0.7173	-6.10
259009_at	thioglucosidase 3D precursor iden	PYK10	AT3G09260	-1.15	-0.20	-1.04	0.33331343	0.7175	-6.10
267403_at	MADS-box protein (AGL33)	AGL33	AT2G26320	-1.06	-0.09	-1.04	0.33344263	0.7176	-6.10
267383_at	unknown protein	---	AT2G44360	1.07	0.10	1.04	0.33344833	0.7176	-6.10
257821_at	Expressed protein ; supported by f	RALFL26	AT3G25170	-1.07	-0.10	-1.04	0.33354654	0.7178	-6.10
255349_at	hypothetical protein	---	AT4G03830	-1.07	-0.09	-1.04	0.33359001	0.7178	-6.10
248968_at	pectin acetylesterase ;supported b	---	AT5G45280	1.19	0.25	1.04	0.33369792	0.7179	-6.10
266833_at	hypothetical protein predicted by g	---	---	1.06	0.09	1.04	0.3336805	0.7179	-6.10

263698_at	hypothetical protein similar to a m	---	---	-1.11	-0.15	-1.04	0.33374727	0.7179	-6.10
249233_at	putative protein contains similarity	---	AT5G42150	-1.26	-0.33	-1.04	0.33389168	0.7180	-6.11
245327_at	hypothetical protein ; supported by	---	AT4G16850	1.08	0.11	1.04	0.33390417	0.7180	-6.11
252989_at	putative pectinesterase pectineste	sks9	AT4G38420	1.40	0.49	1.04	0.33388366	0.7180	-6.11
257054_at	Expressed protein ; supported by f	MT3	AT3G15353	-1.07	-0.09	-1.04	0.33405503	0.7182	-6.11
261411_at	histone H2B identical to GB:CAA7	HTB1	AT1G07790	-1.14	-0.18	-1.04	0.33405486	0.7182	-6.11
259713_at	unknown protein similar to phosph	---	AT1G77610	-1.13	-0.17	-1.04	0.33407831	0.7182	-6.11
253580_at	putative protein RING-H2 finger p	---	AT4G30400	-1.21	-0.27	-1.04	0.33428958	0.7183	-6.11
267367_at	unknown protein ;supported by ful	---	AT2G44210	-1.13	-0.18	-1.04	0.33428314	0.7183	-6.11
263203_at	hypothetical protein predicted by g	chr31	AT1G05490	-1.07	-0.09	-1.04	0.33419548	0.7183	-6.11
247036_at	putative protein contains similarity	---	AT5G67130	1.12	0.17	1.04	0.33423493	0.7183	-6.11
246739_at	putative protein predicted protein,	---	AT5G27800	-1.08	-0.11	-1.04	0.33414096	0.7183	-6.11
264247_at	potassium transporter, putative sir	---	AT1G60160	1.19	0.26	1.04	0.33418885	0.7183	-6.11
258432_at	unknown protein ;supported by ful	RALFL23	AT3G16570	1.15	0.20	1.04	0.33448024	0.7186	-6.11
251571_at	putative protein several hypothetic	---	AT3G58330	-1.08	-0.11	-1.04	0.33450631	0.7186	-6.11
262584_at	hypothetical protein Strong similar	---	AT1G15440	-1.20	-0.27	-1.04	0.33455157	0.7186	-6.11
263916_at	hypothetical protein predicted by g	---	AT2G36440	-1.09	-0.13	-1.04	0.33459443	0.7187	-6.11
257164_at	mismatch binding protein, putative	MSH1	AT3G24320	1.09	0.12	1.04	0.33478516	0.7187	-6.11
262685_at	unknown protein ; supported by cD	---	AT1G76010	1.13	0.18	1.04	0.33467573	0.7187	-6.11
253003_s_at	putative protein tapetum specific p	---	AT4G38300	-1.10	-0.13	-1.04	0.33476157	0.7187	-6.11
263336_x_at	hypothetical protein predicted by g	---	---	-1.08	-0.11	-1.04	0.33470382	0.7187	-6.11
246643_s_at	putative protein various predicted	---	---	-1.08	-0.11	-1.04	0.33476133	0.7187	-6.11
254857_at	putative protein acetylcholine regu	SEC1B	AT4G12120	-1.10	-0.13	-1.04	0.33481906	0.7187	-6.11
253979_at	putative protein other putative prot	---	AT4G26680	1.09	0.12	1.04	0.33490422	0.7188	-6.11
263115_at	Expressed protein ; supported by c	---	AT1G03055	-1.17	-0.22	-1.04	0.33489591	0.7188	-6.11
255993_at	hypothetical protein contains simila	---	AT1G29770	-1.07	-0.10	-1.04	0.33506481	0.7191	-6.11
265435_s_at	putative major intrinsic (channel) p	---	AT1G31885	-1.11	-0.15	-1.04	0.33526768	0.7194	-6.11
251328_at	putative protein putative protein A	ATPOB1	AT3G61600	1.07	0.10	1.04	0.33532626	0.7195	-6.11
265246_at	putative pectinesterase	ATPMEPCI	AT2G43050	-1.10	-0.14	-1.04	0.33540525	0.7195	-6.11
263535_at	hypothetical protein predicted by g	---	AT2G24970	1.10	0.14	1.04	0.3354044	0.7195	-6.11
251545_at	zinc transporter -like protein zinc t	MTPA2	AT3G58810	-1.12	-0.17	-1.04	0.33547457	0.7196	-6.11
266147_at	putative C-1-tetrahydrofolate synth	---	AT2G12230	-1.06	-0.09	-1.04	0.33550574	0.7196	-6.11
245579_at	hypothetical protein	---	AT4G14810	-1.07	-0.10	-1.04	0.33553826	0.7196	-6.11
255494_at	predicted protein of unknown func	---	AT4G02710	1.08	0.11	1.04	0.33559815	0.7197	-6.11
263298_at	unknown protein ; supported by cl	TIC21	AT2G15290	-1.07	-0.10	-1.04	0.3357341	0.7197	-6.11

255520_at	putative ribosomal protein L19 sim	---	AT4G02230	1.15	0.21	1.04	0.33576358	0.7197	-6.11
259933_at	Expressed protein ; supported by f	---	AT1G34350	1.11	0.16	1.04	0.33572222	0.7197	-6.11
252750_at	putative protein hypothetical prote	---	AT3G43420	-1.07	-0.09	-1.04	0.33573191	0.7197	-6.11
265865_at	hypothetical protein predicted by g	---	AT2G01740	1.07	0.10	1.04	0.33579739	0.7197	-6.11
263971_at	hypothetical protein predicted by g	AtRLP29	AT2G42800	-1.11	-0.15	-1.04	0.33584933	0.7198	-6.11
248259_at	proline-rich cell wall protein-like ;s	---	AT5G53330	1.09	0.12	1.04	0.33594823	0.7199	-6.11
260056_at	hypothetical protein predicted by g	---	AT1G78140	1.14	0.19	1.04	0.33607436	0.7201	-6.11
251866_at	putative protein MSP58 - nucleola	emb1967	AT3G54350	-1.07	-0.10	-1.04	0.33607487	0.7201	-6.11
258473_s_at	putative stearoyl-acyl carrier protei	---	AT3G02610 /	1.14	0.19	1.04	0.33614653	0.7201	-6.11
245539_at	ABC transporter homolog	PDR2	AT4G15230	-1.11	-0.15	-1.04	0.33615375	0.7201	-6.11
250565_at	putative protein various predicted	E13L3	AT5G08000	1.11	0.15	1.03	0.33646657	0.7203	-6.11
262131_at	hypothetical protein predicted by g	RALF1	AT1G02900	-1.34	-0.42	-1.04	0.3363962	0.7203	-6.11
253212_s_at	xanthine dehydrogenase - like pro	XDH1	AT4G34890 /	1.12	0.16	1.03	0.33646056	0.7203	-6.11
262364_at	disease resistance protein, putativ	---	AT1G72860	-1.08	-0.11	-1.03	0.33642672	0.7203	-6.11
266623_at	unknown protein	---	AT2G35390	-1.12	-0.16	-1.03	0.3364825	0.7203	-6.11
257099_s_at	disease resistance protein, putativ	---	AT3G24982 /	1.07	0.09	1.04	0.33631929	0.7203	-6.11
247851_at	outer membrane lipoprotein - like	TIL	AT5G58070	-1.19	-0.25	-1.03	0.33645756	0.7203	-6.11
266417_at	putative non-green plastid inner en	---	AT2G38550	1.11	0.14	1.03	0.33657765	0.7205	-6.11
251566_at	putative protein several hypothetic	---	AT3G58210	-1.07	-0.09	-1.03	0.33664174	0.7205	-6.11
257489_at	hypothetical protein predicted by g	---	AT1G07330	-1.08	-0.12	-1.03	0.33677	0.7206	-6.11
260125_at	putative heat shock protein similar	---	AT1G36390	1.12	0.17	1.03	0.33675098	0.7206	-6.11
256307_at	pectate lyase, putative contains P	---	AT1G30350	-1.07	-0.10	-1.03	0.33671539	0.7206	-6.11
256209_at	electron transport flavoprotein, pu	ETFALPHA	AT1G50940	-1.09	-0.12	-1.03	0.33685769	0.7207	-6.11
256313_s_at	RNA-binding protein, putative con	APUM17	AT1G35850 /	1.07	0.10	1.03	0.33684565	0.7207	-6.11
257634_s_at	cytochrome P450, putative similar	CYP71B19	AT3G26170 /	1.18	0.24	1.03	0.33703608	0.7207	-6.11
245760_s_at	receptor serine/threonine kinase F	---	AT1G66910 /	1.21	0.28	1.03	0.33726956	0.7207	-6.11
255081_at	MLH1 protein ; supported by cDN/	MLH1	AT4G09140	1.16	0.21	1.03	0.33711351	0.7207	-6.11
257427_at	hypothetical protein predicted by g	---	AT1G79060	-1.15	-0.20	-1.03	0.33715078	0.7207	-6.11
252064_at	putative protein various predicted	---	AT3G51520	1.08	0.11	1.03	0.33719113	0.7207	-6.11
245034_at	putative serpin	---	AT2G26390	-1.11	-0.15	-1.03	0.33720776	0.7207	-6.11
252495_at	putative protein hypothetical protei	---	AT3G46770	-1.09	-0.13	-1.03	0.33706704	0.7207	-6.11
255914_at	hypothetical protein predicted by g	---	AT1G20290	-1.10	-0.14	-1.03	0.33714337	0.7207	-6.11
249062_at	putative protein contains similarity	---	AT5G44270	1.09	0.13	1.03	0.33724037	0.7207	-6.11
261188_at	hypothetical protein contains simila	---	---	-1.09	-0.13	-1.03	0.33709546	0.7207	-6.11
266681_at	copia-like retroelement pol polypro	---	---	-1.06	-0.09	-1.03	0.33700979	0.7207	-6.11

248714_at	polygalacturonase ;supported by f	---	AT5G48140	1.07	0.10	1.03	0.3369971	0.7207	-6.11
262422_at	hypothetical protein similar to hypo	---	AT1G23440	-1.10	-0.14	-1.03	0.33749435	0.7211	-6.11
266880_at	hypothetical protein predicted by g	---	AT2G44770	-1.10	-0.14	-1.03	0.33761097	0.7213	-6.11
249996_at	glutaredoxin -like protein glutared	---	AT5G18600	1.18	0.24	1.03	0.33764881	0.7213	-6.11
252885_at	glycine-rich protein (clone AtGRP8	GR-RBP8	AT4G39260	-1.13	-0.18	-1.03	0.33772949	0.7214	-6.11
253063_at	plasma membrane-type calcium A	ACA2	AT4G37640	-1.16	-0.22	-1.03	0.33772116	0.7214	-6.11
250711_at	cell division related protein-like	---	AT5G06110	1.08	0.12	1.03	0.33776219	0.7214	-6.11
266813_at	unknown protein	---	AT2G44920	1.11	0.15	1.03	0.33782042	0.7214	-6.11
266167_at	unknown protein ;supported by ful	YLS5	AT2G38860	-1.33	-0.41	-1.03	0.33850129	0.7217	-6.12
253857_at	putative protein hypothetical chlor	---	AT4G27990	1.09	0.12	1.03	0.33830502	0.7217	-6.12
252095_at	epoxide hydrolase-like protein epo	---	AT3G51000	1.11	0.15	1.03	0.33822001	0.7217	-6.12
251492_at	putative protein CGI-136 protein -	TXR1	AT3G59280	1.07	0.10	1.03	0.33853777	0.7217	-6.12
256365_at	arginyl-tRNA synthetase nearly ide	---	AT1G66530	1.14	0.19	1.03	0.33803881	0.7217	-6.11
261816_at	unknown protein	CHX6B	AT1G08135	-1.08	-0.11	-1.03	0.3383509	0.7217	-6.12
264297_at	hypothetical protein similar to hypo	---	AT1G78710	-1.06	-0.09	-1.03	0.33840216	0.7217	-6.12
248966_at	unknown protein ;supported by full	---	AT5G45360	1.09	0.13	1.03	0.33855537	0.7217	-6.12
261656_at	unknown protein similar to kinesin-	ARK2	AT1G01950	1.24	0.31	1.03	0.33831583	0.7217	-6.12
252019_at	late embryogenesis abundant prot	---	AT3G53040	-1.07	-0.09	-1.03	0.33856355	0.7217	-6.12
267267_at	putative cytochrome P450	CYP71B9	AT2G02580	1.09	0.12	1.03	0.33836724	0.7217	-6.12
245520_at	delta-cadinene synthase like prote	ATTS1	AT4G15870	-1.09	-0.12	-1.03	0.33823848	0.7217	-6.12
246694_at	putative protein	---	---	-1.08	-0.12	-1.03	0.33847143	0.7217	-6.12
250445_at	nucleoid DNA-binding protein cnd	---	AT5G10760	1.78	0.83	1.03	0.33821404	0.7217	-6.12
251171_at	putative protein several hypothetic	---	AT3G63220	-1.07	-0.10	-1.03	0.33849607	0.7217	-6.12
253059_s_at	putative protein other predicted pr	HHP5	AT4G37680	-1.15	-0.20	-1.03	0.33818548	0.7217	-6.12
261316_at	MAP kinase BnMAP4K alpha1, pu	ATMAP4K	AT1G53165	1.08	0.11	1.03	0.33810356	0.7217	-6.11
256470_at	hypothetical protein predicted by g	---	AT1G42570	-1.07	-0.10	-1.03	0.33844827	0.7217	-6.12
261878_at	cytochrome P450, putative similar	CYP705A2	AT1G50560	1.08	0.11	1.03	0.33853353	0.7217	-6.12
248505_at	putative protein similar to unknow	---	AT5G50360	-1.10	-0.14	-1.03	0.33877128	0.7220	-6.12
263501_s_at	hypothetical protein	---	AT2G07673	-1.09	-0.12	-1.03	0.33877115	0.7220	-6.12
262102_at	hypothetical protein contains simila	CUL2	AT1G02980	-1.07	-0.10	-1.03	0.33872715	0.7220	-6.12
253001_at	Expressed protein ; supported by c	---	AT4G38490	1.07	0.09	1.03	0.33894408	0.7223	-6.12
250221_at	protoporphyrinogen oxidase - like	HEMG2	AT5G14220	1.14	0.19	1.03	0.33899832	0.7223	-6.12
245169_at	unknown protein predicted by gene	---	AT2G33220	-1.07	-0.10	-1.03	0.33905514	0.7224	-6.12
265913_at	Expressed protein ; supported by f	---	AT2G25625	1.24	0.31	1.03	0.33915486	0.7224	-6.12
247004_at	putative protein similar to unknow	DG1	AT5G67570	1.09	0.13	1.03	0.33916457	0.7224	-6.12

259837_at	aquaporin, putative similar to delta	---	AT1G52180	-1.14	-0.19	-1.03	0.33925584	0.7224	-6.12
253025_at	hypothetical protein	---	AT4G38120	1.13	0.18	1.03	0.3391213	0.7224	-6.12
247052_at	homeodomain transcription factor-	HB53	AT5G66700	-1.09	-0.13	-1.03	0.33921885	0.7224	-6.12
261855_at	unknown protein	---	AT1G50510	1.11	0.15	1.03	0.33925289	0.7224	-6.12
264513_at	putative glucose-6-phosphate deh	G6PD4	AT1G09420	1.09	0.12	1.03	0.33938444	0.7224	-6.12
251444_at	putative protein ETHIONINE AMIN	MAP2B	AT3G59990	1.07	0.10	1.03	0.33936899	0.7224	-6.12
259200_at	unknown protein similar to hypothe	---	AT3G09070	1.08	0.12	1.03	0.33940127	0.7224	-6.12
265365_at	En/Spm-like transposon protein rel	---	---	-1.07	-0.10	-1.03	0.33931634	0.7224	-6.12
257458_at	hypothetical protein predicted by g	---	AT2G05400	-1.07	-0.10	-1.03	0.3394639	0.7225	-6.12
263022_s_at	gamma-adaptin, putative similar to	---	AT1G23900 /	-1.12	-0.16	-1.03	0.33958051	0.7226	-6.12
255970_s_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-1.03	0.339564	0.7226	-6.12
250026_at	putative protein similar to unknown	---	AT5G18090	-1.10	-0.13	-1.03	0.33980438	0.7227	-6.12
266944_at	unknown protein predicted by gene	---	AT2G18870 /	1.09	0.12	1.03	0.3397189	0.7227	-6.12
260092_at	putative serine carboxypeptidase	scpl3	AT1G73280	-1.07	-0.10	-1.03	0.33981184	0.7227	-6.12
257030_at	unknown protein	---	---	-1.08	-0.11	-1.03	0.33974883	0.7227	-6.12
257328_s_at	hypothetical protein	---	---	-1.12	-0.16	-1.03	0.33982207	0.7227	-6.12
261501_at	wall-associated kinase 1, putative	---	AT1G28390	-1.13	-0.17	-1.03	0.33977027	0.7227	-6.12
248097_at	protein phosphatase X isoform 2 (g	PPX2	AT5G55260	1.10	0.14	1.03	0.33997291	0.7230	-6.12
265961_at	unknown protein ;supported by ful	---	AT2G37400	1.14	0.19	1.03	0.34006384	0.7230	-6.12
265335_at	Expressed protein ; supported by f	---	AT2G18245	1.07	0.09	1.03	0.34008882	0.7230	-6.12
251201_at	putative protein predicted protein,	---	AT3G63020	-1.07	-0.09	-1.03	0.3400852	0.7230	-6.12
249195_s_at	disease resistance response prote	---	AT5G42500 /	-1.13	-0.18	-1.03	0.34022982	0.7232	-6.12
248389_at	AP2 domain transcription factor-lik	CBF4	AT5G51990	-1.09	-0.12	-1.03	0.34022086	0.7232	-6.12
256770_at	hypothetical protein predicted by g	---	AT3G13700 /	1.11	0.16	1.03	0.34031368	0.7232	-6.12
255585_at	putative NAM-like protein	anac069	AT4G01550	1.14	0.19	1.03	0.34029054	0.7232	-6.12
250514_at	GDP dissociation inhibitor GDP di	---	AT5G09550	-1.08	-0.11	-1.03	0.34039351	0.7233	-6.12
253800_at	putative protein probable cell wall	---	AT4G28160	-1.10	-0.14	-1.03	0.34058678	0.7237	-6.12
264999_at	hypothetical protein contains simila	---	AT1G67310	1.08	0.11	1.03	0.34065425	0.7238	-6.12
262862_at	hypothetical protein predicted by g	---	AT1G64830	-1.13	-0.18	-1.03	0.34069088	0.7238	-6.12
262551_at	putative heat shock transcription fa	RUB1	AT1G31340	1.12	0.16	1.02	0.34081815	0.7240	-6.12
254016_at	putative transcription factor Arabid	CGA1	AT4G26150	-1.16	-0.22	-1.02	0.34101265	0.7240	-6.12
260453_s_at	unknown protein	---	AT1G72510 /	-1.12	-0.16	-1.02	0.34113075	0.7240	-6.12
254052_at	UMP/CMP kinase like protein UMI	---	AT4G25280	-1.10	-0.14	-1.02	0.34108379	0.7240	-6.12
258100_at	unknown protein	---	AT3G23550	-1.51	-0.60	-1.02	0.34113208	0.7240	-6.12
249676_at	serine/threonine protein kinase-like	---	AT5G35960	-1.10	-0.13	-1.02	0.34090847	0.7240	-6.12

266871_at	unknown protein	---	AT2G44710	-1.06	-0.09	-1.02	0.34117249	0.7240	-6.12
248672_at	disease resistance protein	---	AT5G48770	1.10	0.13	1.02	0.340935	0.7240	-6.12
265158_at	hypothetical protein predicted by g	---	AT1G31040	-1.07	-0.10	-1.02	0.34087531	0.7240	-6.12
258739_s_at	unknown protein similar to hypothe	---	AT1G54300	-1.07	-0.10	-1.02	0.34104121	0.7240	-6.12
266485_at	putative phospholipase ;supported	---	AT2G47630	1.20	0.27	1.02	0.34116373	0.7240	-6.12
252270_at	putative protein ;supported by full-	---	AT3G49560	-1.10	-0.14	-1.02	0.34118667	0.7240	-6.12
257980_at	hypothetical protein predicted by g	---	AT3G20760	-1.09	-0.12	-1.02	0.34135567	0.7243	-6.12
259923_at	putative protein kinase contains Pf	---	AT1G72760	1.07	0.10	1.02	0.34138557	0.7243	-6.12
254598_at	xyloglucan endo-transglycosylase	---	AT4G18990	1.19	0.26	1.02	0.34155646	0.7243	-6.12
245059_at	unknown protein ;supported by ful	RHC2A	AT2G39720	1.07	0.10	1.02	0.34149616	0.7243	-6.12
264654_s_at	putative sugar transport protein, E	---	AT1G08890	-1.15	-0.20	-1.02	0.34147167	0.7243	-6.12
261672_at	unknown protein contains similarity	ATARP4	AT1G18450	1.12	0.16	1.02	0.34154818	0.7243	-6.12
262251_at	hypothetical protein predicted by g	---	AT1G53760	1.16	0.21	1.02	0.34182645	0.7243	-6.12
255507_at	AtKAP alpha similar to AtKAP, Ge	MOS6	AT4G02150	-1.07	-0.10	-1.02	0.34186974	0.7243	-6.12
250127_at	putative protein similar to unknown	---	AT5G16380	-1.11	-0.15	-1.02	0.34188462	0.7243	-6.12
266050_at	putative SNF2/SWI2 family transcr	---	AT2G40770	-1.07	-0.10	-1.02	0.3417451	0.7243	-6.12
256416_at	ferritin subunit, putative similar to	ATFER2	AT3G11050	-1.10	-0.14	-1.02	0.34178153	0.7243	-6.12
258266_at	hypothetical protein predicted by g	---	AT3G15860	-1.11	-0.15	-1.02	0.341852	0.7243	-6.12
254884_at	H+-transporting ATPase - like pro	---	AT4G11730	-1.07	-0.09	-1.02	0.34193686	0.7243	-6.12
258102_at	unknown protein contains Pfam pr	---	AT3G23600	-1.11	-0.15	-1.02	0.34186862	0.7243	-6.12
262771_at	hypothetical protein predicted by g	---	AT1G13200	1.10	0.14	1.02	0.34174946	0.7243	-6.12
255414_at	hypothetical protein	---	AT4G03156	1.07	0.09	1.02	0.34167498	0.7243	-6.12
250450_at	putative transcription factor MYB92	ATMYB92	AT5G10280	1.06	0.09	1.02	0.34158348	0.7243	-6.12
265686_at	hypothetical protein predicted by g	---	AT2G24460	1.07	0.10	1.02	0.34194115	0.7243	-6.12
263784_at	Expressed protein ; supported by f	---	AT2G46375	1.08	0.11	1.02	0.34181316	0.7243	-6.12
249503_at	expansin-like protein expansin - P	ATEXPA24	AT5G39310	1.08	0.11	1.02	0.34202262	0.7244	-6.12
249693_at	histidine kinase-like protein ; supp	AHK2	AT5G35750	-1.15	-0.20	-1.02	0.34214909	0.7245	-6.12
266362_at	unknown protein	---	AT2G32430	-1.10	-0.14	-1.02	0.34215536	0.7245	-6.12
257555_at	hypothetical protein predicted by g	---	AT3G24780	1.12	0.16	1.02	0.34209807	0.7245	-6.12
258469_at	unknown protein contains Pfam pr	PRXIIF	AT3G06050	-1.08	-0.11	-1.02	0.34222828	0.7246	-6.12
260302_at	putative sulfate transporter contain	---	AT1G80310	-1.12	-0.16	-1.02	0.34237213	0.7246	-6.12
255463_at	putative polyprotein of LTR transp	---	---	-1.09	-0.12	-1.02	0.34238059	0.7246	-6.12
252144_at	ribosomal protein L8 homolog ribo	---	AT3G51190	1.08	0.10	1.02	0.34228111	0.7246	-6.12
259442_at	(1-4)-beta-mannan endohydrolase	---	AT1G02310	-1.15	-0.21	-1.02	0.34230575	0.7246	-6.12
256009_at	AP2 domain transcription factor, p	---	AT1G19210	-1.35	-0.43	-1.02	0.34239867	0.7246	-6.12

267163_at	unknown protein	---	AT2G37520	1.11	0.15	1.02	0.34249917	0.7248	-6.13
260366_at	putative protein kinase similar to C	---	AT1G70460	1.08	0.11	1.02	0.34252958	0.7248	-6.13
260375_at	unknown protein	---	AT1G73950	-1.09	-0.12	-1.02	0.3426166	0.7248	-6.13
259398_at	hypothetical protein predicted by g	PRA1.F1	AT1G17700	-1.28	-0.35	-1.02	0.34262357	0.7248	-6.13
265391_at	Expressed protein ; supported by c	GAUT10	AT2G20810	1.07	0.10	1.02	0.3429159	0.7250	-6.13
245611_at	hypothetical protein	---	AT4G14390	-1.13	-0.17	-1.02	0.34280079	0.7250	-6.13
262938_at	hypothetical protein predicted by g	---	AT1G79540	-1.09	-0.13	-1.02	0.34284237	0.7250	-6.13
247785_at	subtilisin-like serine protease conta	---	AT5G58820	1.07	0.09	1.02	0.34291761	0.7250	-6.13
263146_at	lipase, putative similar to lipase G	GLIP2	AT1G53940	-1.10	-0.14	-1.02	0.34292421	0.7250	-6.13
265193_at	unknown protein ESTs gb|T14407	---	AT1G05070	1.08	0.11	1.02	0.34283088	0.7250	-6.13
263640_at	hypothetical protein predicted by g	---	AT2G25270	1.08	0.11	1.02	0.34293436	0.7250	-6.13
266638_at	putative fibrillin ;supported by full-	---	AT2G35490	-1.09	-0.12	-1.02	0.34300943	0.7251	-6.13
259723_at	putative iron-regulated transporter	IRT3	AT1G60960	-1.20	-0.26	-1.02	0.34304979	0.7251	-6.13
262208_at	hypothetical protein predicted by g	---	AT1G74800	1.10	0.14	1.02	0.34314892	0.7253	-6.13
264539_at	hypothetical protein predicted by g	---	AT1G55590	-1.09	-0.13	-1.02	0.34320247	0.7253	-6.13
252542_at	nuclear receptor binding factor-like	---	AT3G45770	1.07	0.10	1.02	0.34328428	0.7254	-6.13
247157_at	nuclear matrix constituent protein 1	LINC4	AT5G65770	-1.08	-0.12	-1.02	0.34329871	0.7254	-6.13
254345_at	hypothetical protein ;supported by	---	AT4G22000	1.14	0.19	1.02	0.34350057	0.7257	-6.13
247967_at	putative protein similar to unknown	anac099	AT5G56620	-1.07	-0.09	-1.02	0.34354671	0.7257	-6.13
253728_at	putative protein unknown protein c	---	AT4G29410	1.14	0.19	1.02	0.34355057	0.7257	-6.13
254628_at	Expressed protein ; supported by f	---	AT4G18593	-1.07	-0.09	-1.02	0.34373519	0.7260	-6.13
264584_at	unknown protein Similar to Synech	---	AT1G05140	-1.10	-0.13	-1.02	0.34371721	0.7260	-6.13
246374_at	light repressible receptor protein k	---	AT1G51840	-1.07	-0.09	-1.02	0.34381152	0.7260	-6.13
259325_at	unknown protein	---	AT3G05320	1.64	0.72	1.02	0.34381911	0.7260	-6.13
251269_at	putative protein Pm5 protein - Hor	---	AT3G62360	1.11	0.15	1.02	0.34389627	0.7260	-6.13
267471_at	putative ferrochelatase precusor ;	FC2	AT2G30390	-1.15	-0.20	-1.02	0.34385543	0.7260	-6.13
262849_at	unknown protein ; supported by cD	---	AT1G14710	1.23	0.29	1.02	0.34386707	0.7260	-6.13
246448_at	putative protein putative N-acetlyt	---	AT5G16800	1.09	0.12	1.02	0.34393754	0.7260	-6.13
245199_at	Expressed protein ; supported by f	KCR1	AT1G67730	1.10	0.14	1.02	0.34407841	0.7262	-6.13
248184_at	CHP-rich zinc finger protein-like	---	AT5G54050	1.07	0.10	1.02	0.34410766	0.7262	-6.13
254215_at	putative Na+/H+-exchanging prote	ATCHX17	AT4G23700	-1.39	-0.48	-1.02	0.3443619	0.7266	-6.13
253431_at	putative protein predicted protein,	---	AT4G32440	1.09	0.12	1.02	0.34470787	0.7266	-6.13
267106_s_at	putative vacuolar sorting receptor i	ATVSR3	AT2G14720	1.11	0.15	1.02	0.34432221	0.7266	-6.13
246969_at	glutamic acid-rich protein other glu	---	AT5G24880	-1.09	-0.13	-1.02	0.34462136	0.7266	-6.13
263397_s_at	putative GDSL-motif lipase/hydrola	---	AT2G31540	-1.06	-0.09	-1.02	0.34470607	0.7266	-6.13

260740_at	thioredoxin, putative contains Pfar	ATQSOX1	AT1G15020	1.07	0.10	1.02	0.34473274	0.7266	-6.13
246129_at	putative protein predicted protein,	---	---	1.07	0.09	1.02	0.34470244	0.7266	-6.13
247950_at	unknown protein	---	AT5G57230	-1.08	-0.11	-1.02	0.34463483	0.7266	-6.13
260482_at	endomembrane protein EMP70 pre	---	AT1G10950	1.08	0.11	1.02	0.34441736	0.7266	-6.13
245653_at	heat shock transcription factor like	FBD1	AT4G13985	1.09	0.12	1.02	0.34467991	0.7266	-6.13
265018_s_at	hypothetical protein predicted by g	---	AT2G13770	1.08	0.11	1.02	0.34469924	0.7266	-6.13
259569_at	hypothetical protein	---	AT1G20480	1.10	0.13	1.02	0.34453869	0.7266	-6.13
256038_at	hypothetical protein similar to polyg	---	AT1G19170	1.10	0.14	1.02	0.34442024	0.7266	-6.13
245523_at	drought-induced protein like	ATDI21	AT4G15910	-1.12	-0.17	-1.02	0.34455374	0.7266	-6.13
260179_at	unknown protein similar to hypothe	HWI1	AT1G70690	1.20	0.26	1.02	0.34480888	0.7266	-6.13
256498_at	hypothetical protein	---	---	-1.07	-0.10	-1.02	0.34479999	0.7266	-6.13
248421_at	unknown protein ;supported by ful	---	AT5G51510	1.09	0.12	1.02	0.34493467	0.7268	-6.13
251897_at	RING finger - like protein DNA-bin	---	AT3G54360	-1.10	-0.14	-1.02	0.34494866	0.7268	-6.13
248864_at	bHLH protein-like	---	AT5G46760	-1.07	-0.10	-1.02	0.34509646	0.7270	-6.13
254439_s_at	carbonic anhydrase -like protein c	ACA6	AT4G20990 /	-1.06	-0.09	-1.02	0.34507988	0.7270	-6.13
262072_at	hypothetical protein predicted by g	ZCF37	AT1G59590	1.23	0.30	1.02	0.34514345	0.7270	-6.13
260780_at	valyl-tRNA synthetase, putative si	TWN2	AT1G14610	1.07	0.10	1.01	0.34551948	0.7277	-6.13
258227_at	6-4 photolyase (UVR3) identical to	UVR3	AT3G15620	1.35	0.44	1.01	0.34559542	0.7278	-6.13
247068_at	putative protein similar to unknown	---	AT5G66800	-1.10	-0.13	-1.01	0.34562814	0.7278	-6.13
264343_at	unknown protein ; supported by fu	---	AT1G11850	-1.14	-0.19	-1.01	0.3456948	0.7279	-6.13
266401_s_at	putative cell division control protein	CDKB1;2	AT2G38620 /	-1.07	-0.10	-1.01	0.34589514	0.7283	-6.13
267118_at	hypothetical protein	---	AT2G32590	1.10	0.13	1.01	0.34593622	0.7283	-6.13
261891_at	transcriptional regulator, putative s	---	AT1G80790	-1.07	-0.10	-1.01	0.34606869	0.7283	-6.13
246750_at	putative protein predicted proteins	AT5G27860	---	1.14	0.19	1.01	0.34611367	0.7283	-6.13
258205_at	unknown protein	---	AT3G13965	1.08	0.11	1.01	0.34603241	0.7283	-6.13
253339_at	metal-transporting P-type ATPase	PAA1	AT4G33520	-1.13	-0.18	-1.01	0.3460923	0.7283	-6.13
248965_at	nodulin-like protein	---	AT5G45370	1.11	0.15	1.01	0.34604523	0.7283	-6.13
259318_at	unknown protein similar to HYP1 C	HYP1	AT3G01100	1.11	0.15	1.01	0.34618454	0.7283	-6.13
260395_at	homeobox gene 13 protein identica	ATHB13	AT1G69780	-1.20	-0.27	-1.01	0.34621309	0.7283	-6.13
257057_at	hypothetical protein predicted by g	---	---	-1.06	-0.09	-1.01	0.34616582	0.7283	-6.13
255745_at	hypothetical protein predicted by g	---	AT1G32030	-1.06	-0.09	-1.01	0.34627063	0.7283	-6.13
248788_at	DNA-binding protein-like	---	AT5G47430	-1.07	-0.10	-1.01	0.34630862	0.7283	-6.13
248658_at	chromosome condensation protein	ATSMC3	AT5G48600	1.08	0.11	1.01	0.34628291	0.7283	-6.13
264719_at	receptor-like kinase, putative simil	---	AT1G70110	-1.12	-0.17	-1.01	0.34634689	0.7283	-6.13
259171_at	hypothetical protein predicted by g	---	AT3G03590	1.09	0.12	1.01	0.34654406	0.7287	-6.13

247277_at	putative protein similar to unknown	---	AT5G64420	1.09	0.12	1.01	0.34662406	0.7287	-6.13
266718_at	putative zinc transporter ;supporte	ZAT	AT2G46800	-1.09	-0.12	-1.01	0.34659872	0.7287	-6.13
263534_at	putative steroid binding protein ;su	AtMAPR2	AT2G24940	-1.09	-0.13	-1.01	0.34675003	0.7288	-6.13
257235_at	ras-related GTP-binding protein co	AtRABA1g	AT3G15060	1.33	0.41	1.01	0.34678593	0.7288	-6.13
248990_at	disease resistance protein-like	---	AT5G45210	-1.08	-0.11	-1.01	0.34673776	0.7288	-6.13
258694_at	putative non-phototropic hypocotyl	---	AT3G08660	-1.17	-0.22	-1.01	0.34686109	0.7288	-6.13
246836_s_at	putative protein MADS box protein	---	AT5G26650	1.07	0.10	1.01	0.34687427	0.7288	-6.13
254757_at	putative protein other putative or h	ROPGEF9	AT4G13240	1.08	0.12	1.01	0.34682289	0.7288	-6.13
261391_at	hypothetical protein similar to hypo	---	AT1G35030	-1.09	-0.13	-1.01	0.34700571	0.7290	-6.14
255325_at	putative membrane trafficking facto	PUX4	AT4G04210	-1.08	-0.11	-1.01	0.34708674	0.7291	-6.14
253071_at	putative protein various predicted p	---	AT4G37880	-1.08	-0.11	-1.01	0.34727609	0.7291	-6.14
265135_at	unknown protein similar to unknow	---	AT1G51270	-1.08	-0.12	-1.01	0.34726604	0.7291	-6.14
249831_at	putative protein contains similarity	---	AT5G23340	1.16	0.22	1.01	0.34713539	0.7291	-6.14
245669_at	hypothetical protein contains simila	LEC2	AT1G28300	-1.10	-0.14	-1.01	0.34725282	0.7291	-6.14
255254_at	hypothetical protein	---	AT4G05030	-1.11	-0.15	-1.01	0.34719572	0.7291	-6.14
251378_at	putative protein	---	AT3G60660	1.08	0.11	1.01	0.34724789	0.7291	-6.14
255924_at	unknown protein contains similarity	---	AT1G22170	-1.10	-0.14	-1.01	0.34742502	0.7294	-6.14
245688_at	prolin-rich protein, putative similar	AGP31	AT1G28290	-1.54	-0.62	-1.01	0.34745764	0.7294	-6.14
259826_at	arm repeat-containing protein, put	PUB17	AT1G29340	-1.14	-0.19	-1.01	0.34753907	0.7295	-6.14
263377_at	AP2 domain transcription factor (A	ABI4	AT2G40220	-1.07	-0.10	-1.01	0.34762454	0.7296	-6.14
245666_at	hypothetical protein predicted by g	---	AT1G28280	1.18	0.24	1.01	0.34769024	0.7296	-6.14
252568_at	receptor-like protein kinase recept	---	AT3G45410	-1.14	-0.18	-1.01	0.34767758	0.7296	-6.14
265239_s_at	hypothetical protein	---	AT2G07692	-1.09	-0.13	-1.01	0.34773846	0.7296	-6.14
255847_at	putative thioredoxin	ACHT3	AT2G33270	-1.07	-0.09	-1.01	0.34781072	0.7297	-6.14
266266_at	putative enolase (2-phospho-D-gly	---	AT2G29560	1.10	0.14	1.01	0.34789094	0.7298	-6.14
245667_at	FH protein interacting protein FIP1	FIP1	AT1G28200	1.08	0.11	1.01	0.34787522	0.7298	-6.14
257770_at	unknown protein ;supported by ful	LFR	AT3G22990	1.09	0.12	1.01	0.34800166	0.7299	-6.14
246174_s_at	putative protein hypothetical prote	---	AT5G28340	-1.07	-0.10	-1.01	0.3480609	0.7300	-6.14
259823_at	beta-1,3-glucanase precursor, put	---	AT1G66250	1.10	0.14	1.01	0.34819044	0.7300	-6.14
247118_at	uridylyl transferases-like ; support	ACR1	AT5G65890	-1.14	-0.19	-1.01	0.34828765	0.7300	-6.14
259039_at	unknown protein ;supported by ful	---	AT3G09250	-1.08	-0.11	-1.01	0.34828578	0.7300	-6.14
246522_at	bZIP DNA-binding protein-like put	AtbZIP3	AT5G15830	1.23	0.30	1.01	0.34812771	0.7300	-6.14
254912_at	respiratory burst oxidase homolog	---	AT4G11230	-1.08	-0.11	-1.01	0.34828192	0.7300	-6.14
259944_at	hypothetical protein predicted by g	---	AT1G71470	1.08	0.11	1.01	0.34823031	0.7300	-6.14
255811_at	heat shock protein 22.0 ; supporte	ATHSP22.0	AT4G10250	-1.10	-0.14	-1.01	0.34809984	0.7300	-6.14

260243_at	hypothetical protein similar to puta	---	AT1G63720	1.23	0.29	1.01	0.34843725	0.7300	-6.14
267534_at	putative CCCH-type zinc finger pro	---	AT2G41900	-1.08	-0.11	-1.01	0.3483677	0.7300	-6.14
259107_at	hypothetical protein predicted by g	---	AT3G05460	-1.07	-0.10	-1.01	0.34839963	0.7300	-6.14
260652_at	putative MYB family transcription f	---	AT1G32360	1.07	0.10	1.01	0.34841353	0.7300	-6.14
257289_at	hypothetical protein	---	AT3G29690	1.07	0.10	1.01	0.34861707	0.7303	-6.14
267187_s_at	putative methylenetetrahydrofolate	MTHFR2	AT2G44160	-1.12	-0.17	-1.01	0.34866163	0.7304	-6.14
245054_at	unknown protein	---	AT2G26460	-1.10	-0.13	-1.01	0.34895403	0.7305	-6.14
263239_at	amidophosphoribosyltransferase ic	ATASE1	AT2G16570	-1.09	-0.13	-1.01	0.34895569	0.7305	-6.14
260404_at	unknown protein similar to activato	---	---	1.14	0.19	1.01	0.34888791	0.7305	-6.14
261130_at	unknown protein ; supported by cD	PRMT10	AT1G04870	1.17	0.22	1.01	0.3489441	0.7305	-6.14
249904_at	unknown protein	---	AT5G22700	-1.08	-0.11	-1.01	0.34894782	0.7305	-6.14
249729_at	6-phosphogluconolactonase-like p	---	AT5G24410	-1.09	-0.12	-1.01	0.34897869	0.7305	-6.14
266844_at	hypothetical protein predicted by g	---	AT2G26120	-1.09	-0.13	-1.01	0.34888098	0.7305	-6.14
248770_at	unknown protein	---	AT5G47740	-1.11	-0.14	-1.01	0.34894329	0.7305	-6.14
264298_at	hypothetical protein contains simila	---	AT1G78690	1.09	0.12	1.01	0.34910578	0.7306	-6.14
259428_at	MAP kinase, putative similar to MA	TMPK11	AT1G01560	1.52	0.60	1.01	0.34908861	0.7306	-6.14
251809_at	putative protein predicted proteins	---	AT3G55600	1.09	0.12	1.01	0.34917152	0.7307	-6.14
253017_at	cinnamyl alcohol dehydrogenase -	CAD6	AT4G37970	-1.07	-0.10	-1.01	0.34941632	0.7308	-6.14
266092_at	hypothetical protein predicted by g	---	AT2G37880	-1.08	-0.12	-1.01	0.34933911	0.7308	-6.14
262383_at	disease resistance protein, putativ	---	AT1G72940	1.48	0.56	1.01	0.34926885	0.7308	-6.14
267059_at	putative carboxymethylenebutenol	---	AT2G32520	1.08	0.11	1.01	0.34942877	0.7308	-6.14
263622_at	hypothetical protein predicted by g	---	AT2G04870	-1.08	-0.11	-1.01	0.34944424	0.7308	-6.14
267616_at	unknown protein ;supported by ful	---	AT2G26680	1.09	0.12	1.01	0.34940133	0.7308	-6.14
266459_at	unknown protein supported by full-	---	AT2G47970	-1.08	-0.12	-1.01	0.34937003	0.7308	-6.14
252779_at	putative protein	---	AT3G42990	-1.08	-0.11	-1.01	0.34961657	0.7310	-6.14
250824_at	putative protein contains similarity	---	AT5G05200	-1.11	-0.15	-1.01	0.34961893	0.7310	-6.14
260171_at	hypothetical protein predicted by g	---	AT1G71910	1.22	0.29	1.00	0.3496582	0.7310	-6.14
250376_at	putative protein	---	AT5G11550	1.15	0.20	1.00	0.34966194	0.7310	-6.14
256479_at	unknown protein	---	AT1G33400	1.11	0.16	1.00	0.34979172	0.7311	-6.14
262439_at	hypothetical protein identical to hy	---	AT1G47730	-1.07	-0.09	-1.00	0.34977997	0.7311	-6.14
255237_at	hypothetical protein	---	---	-1.07	-0.10	-1.00	0.34980981	0.7311	-6.14
250056_at	putative protein predicted proteins	---	AT5G17660	1.19	0.25	1.00	0.34993358	0.7313	-6.14
253050_at	putative protein probable arabinog	AGP18	AT4G37450	-1.30	-0.37	-1.00	0.35011654	0.7315	-6.14
248198_at	putative protein contains similarity	---	AT5G54200	1.18	0.24	1.00	0.35022049	0.7315	-6.14
253485_at	Expressed protein ; supported by f	WRKY18	AT4G31800	1.19	0.26	1.00	0.35033988	0.7315	-6.14

256237_at	leucine rich repeat protein, putativ	DRT100	AT3G12610	2.26	1.18	1.00	0.35025994	0.7315	-6.14
246341_x_at	putative protein predicted proteins	---	AT3G43150	1.11	0.15	1.00	0.35036648	0.7315	-6.14
245586_at	hypothetical protein	---	AT4G14980	-1.08	-0.11	-1.00	0.35025897	0.7315	-6.14
256536_at	peptide chain release factor, putat	---	AT1G33330	1.08	0.11	1.00	0.35025044	0.7315	-6.14
264619_at	putative chloroplast nucleoid DNA-	---	AT2G17760	-1.09	-0.13	-1.00	0.35039988	0.7315	-6.14
257717_at	unknown protein	EMB1865	AT3G18390	1.11	0.15	1.00	0.35017031	0.7315	-6.14
246081_s_at	myosin-like protein unconventiona	---	AT5G20470	1.13	0.18	1.00	0.35005815	0.7315	-6.14
256592_at	hypothetical protein predicted by g	---	---	1.07	0.09	1.00	0.35036874	0.7315	-6.14
250576_at	cytochrome P450-like protein seve	---	AT5G08250	1.09	0.12	1.00	0.35031071	0.7315	-6.14
256704_at	deacetylvindoline 4-O-acetyltranst	---	AT3G30280	-1.08	-0.10	-1.00	0.35043999	0.7315	-6.14
262986_at	unknown protein similar to hypothe	---	AT1G23390	1.17	0.22	1.00	0.3505098	0.7315	-6.14
254099_at	protein-methionine-S-oxide reducta	---	AT4G25130	1.13	0.17	1.00	0.35051553	0.7315	-6.14
258760_at	putative membrane protein similar	---	AT3G10780	-1.16	-0.22	-1.00	0.35074358	0.7318	-6.14
266947_at	hypothetical protein predicted by g	---	AT2G18830	-1.10	-0.13	-1.00	0.35072395	0.7318	-6.14
246178_s_at	putative protein predicted proteins	---	---	1.10	0.14	1.00	0.3509179	0.7321	-6.14
248786_at	unknown protein	---	AT5G47410	1.15	0.20	1.00	0.35095362	0.7321	-6.14
255413_at	putative alcohol dehydrogenase si	---	AT4G03140	1.09	0.13	1.00	0.35099405	0.7322	-6.14
262234_at	putative G protein coupled recepto	GCR1	AT1G48270	-1.12	-0.17	-1.00	0.35110064	0.7322	-6.14
258463_at	putative protein kinase similar to P	---	AT3G17410	1.10	0.14	1.00	0.35109717	0.7322	-6.14
245860_at	putative protein predicted proteins	---	AT5G28310	-1.09	-0.13	-1.00	0.3510577	0.7322	-6.14
265217_s_at	unknown protein ESTs gb|H76594	---	AT1G05090	1.12	0.17	1.00	0.35128003	0.7325	-6.14
255500_at	NAD+ ADP-ribosyltransferase	APP	AT4G02390	1.11	0.15	1.00	0.35132425	0.7325	-6.14
266102_at	unknown protein	---	AT2G40720	1.09	0.12	1.00	0.35136051	0.7325	-6.14
263987_at	putative lipase ; supported by cDN	---	AT2G42690	-1.12	-0.16	-1.00	0.35139079	0.7325	-6.14
247186_at	putative protein contains similarity	---	AT5G65470	1.15	0.20	1.00	0.35146199	0.7325	-6.14
253812_at	putative wound induced protein w	---	AT4G28240	1.10	0.14	1.00	0.35156529	0.7325	-6.15
253219_at	MYB-like protein myb-related prot	AtMYB32	AT4G34990	-1.16	-0.21	-1.00	0.35162084	0.7325	-6.15
249207_at	C2H2-type zinc finger protein-like	---	AT5G42640	-1.08	-0.11	-1.00	0.3514927	0.7325	-6.15
258057_at	unknown protein	AAR3	AT3G28970	-1.07	-0.10	-1.00	0.3516307	0.7325	-6.15
262440_at	serpin, putative similar to serpin G	---	AT1G47710	-1.12	-0.17	-1.00	0.35151965	0.7325	-6.15
246297_at	putative protein hypothetical prote	---	AT3G51760	-1.12	-0.17	-1.00	0.35164233	0.7325	-6.15
259722_at	putative DNA helicase similar to A	ATRECQ4E	AT1G60930	-1.06	-0.09	-1.00	0.35165875	0.7325	-6.15
259143_at	calmodulin-like protein similar to c	---	AT3G10190	1.12	0.16	1.00	0.35303559	0.7326	-6.15
256661_at	hypothetical protein similar to puta	---	AT3G11964	1.08	0.11	1.00	0.35347981	0.7326	-6.15
250613_at	putative protein SF16 protein, poll	IQD24	AT5G07240	-1.10	-0.14	-1.00	0.35208279	0.7326	-6.15

246892_at	putative protein predicted protein,	---	AT5G25500	1.09	0.12	1.00	0.35360114	0.7326	-6.15
262737_at	hypothetical protein	SRD2	AT1G28560	-1.10	-0.13	-1.00	0.35355463	0.7326	-6.15
256379_at	hypothetical protein predicted by g	---	AT1G66840	-1.12	-0.16	-1.00	0.35265321	0.7326	-6.15
250525_at	putative protein contains similarity	ILP1	AT5G08550	-1.08	-0.11	-1.00	0.35289951	0.7326	-6.15
250875_at	putative protein fimbriae-associate	---	AT5G04020	-1.23	-0.29	-1.00	0.35256031	0.7326	-6.15
259013_at	unknown protein similar to putative	emb1990	AT3G07430	1.08	0.11	1.00	0.3531102	0.7326	-6.15
251255_at	putative protein early nodule-spec	---	AT3G62280	-1.07	-0.10	-1.00	0.35214064	0.7326	-6.15
260543_at	putative membrane transporter	INT1	AT2G43330	1.13	0.18	1.00	0.351998	0.7326	-6.15
248465_at	putative protein contains similarity	---	AT5G51200	1.12	0.17	1.00	0.35293695	0.7326	-6.15
262148_at	chloroplast-localized small heat sh	---	AT1G52560	-1.19	-0.25	-1.00	0.35291658	0.7326	-6.15
245672_at	polygalacturonase, putative simila	---	AT1G56710	1.11	0.16	1.00	0.35215326	0.7326	-6.15
255045_at	putative protein hypothetical prote	---	AT4G09690	-1.09	-0.13	-1.00	0.35260702	0.7326	-6.15
263167_at	unknown protein Belongs to PF|01	---	AT1G03030	1.10	0.13	1.00	0.35363351	0.7326	-6.15
263396_at	unknown protein ;supported by ful	---	AT2G31710	1.09	0.12	1.00	0.35223531	0.7326	-6.15
256545_at	hypothetical protein predicted by g	---	---	-1.09	-0.12	-1.00	0.35272459	0.7326	-6.15
260198_at	F12A21.23 hypothetical protein	---	AT1G67635	-1.07	-0.10	-1.00	0.35298444	0.7326	-6.15
259458_at	glycine-rich protein, putative simila	---	AT1G44085	-1.09	-0.13	-1.00	0.35244276	0.7326	-6.15
245350_at	nuclear antigen homolog ;supporte	---	AT4G16830	1.09	0.13	1.00	0.35328008	0.7326	-6.15
252751_at	putative protein RING-H2 zinc fing	---	AT3G43430	1.18	0.24	1.00	0.35306294	0.7326	-6.15
265697_at	hypothetical protein predicted by g	---	AT2G32170	1.08	0.11	1.00	0.35364342	0.7326	-6.15
250506_at	ABC transporter, ATP-binding pro	GCN2	AT5G09930	-1.09	-0.13	-1.00	0.35352274	0.7326	-6.15
251403_at	putative protein RING finger prote	---	AT3G60300	1.12	0.16	1.00	0.35206529	0.7326	-6.15
254976_at	subtilisin-like serine protease conta	---	AT4G10510	-1.08	-0.11	-1.00	0.35173954	0.7326	-6.15
253807_at	putative GPI-anchored protein GP	---	AT4G28280	-1.11	-0.15	-1.00	0.35316424	0.7326	-6.15
264061_at	putative cyclin-dependent kinase r	CKS2	AT2G27970	1.19	0.25	1.00	0.35311607	0.7326	-6.15
266958_at	putative trans-prenyltransferase	GPS1	AT2G34630	-1.12	-0.16	-1.00	0.35226104	0.7326	-6.15
264272_at	hypothetical protein contains simila	ANAC023	AT1G60280	-1.07	-0.10	-1.00	0.35215752	0.7326	-6.15
247711_at	receptor-like protein kinase recept	---	AT5G59270	-1.09	-0.12	-1.00	0.35177554	0.7326	-6.15
256684_at	geranylgeranyl pyrophosphate syr	---	AT3G32040	-1.11	-0.15	-1.00	0.35316436	0.7326	-6.15
248452_at	putative protein contains similarity	---	AT5G51300	1.07	0.09	1.00	0.35195019	0.7326	-6.15
249967_at	putative protein	---	AT5G19050	1.08	0.12	1.00	0.35290787	0.7326	-6.15
255439_at	putative phospho-ser/thr phosphat	BSL1	AT4G03080	1.08	0.11	1.00	0.35234871	0.7326	-6.15
259498_at	unknown protein similar to putative	GOS11	AT1G15880	1.08	0.11	1.00	0.35340274	0.7326	-6.15
251016_at	pathogenesis related protein - like	---	AT5G02730	-1.14	-0.19	-1.00	0.35327641	0.7326	-6.15
265537_at	putative retroelement pol polyprote	---	---	-1.10	-0.13	-1.00	0.35209655	0.7326	-6.15

252155_at	putative protein	---	AT3G50920	1.11	0.15	1.00	0.35365369	0.7326	-6.15
263736_at	nucleic acid-binding protein, putat	---	AT1G60000	-1.12	-0.17	-1.00	0.35330599	0.7326	-6.15
248343_at	putative protein contains similarity	AtMYB19	AT5G52260	1.07	0.09	1.00	0.35323663	0.7326	-6.15
265883_at	unknown protein	---	AT2G42310	1.08	0.11	1.00	0.35222412	0.7326	-6.15
245259_at	kinesin like protein ; supported by	PAKRP1	AT4G14150	-1.07	-0.10	-1.00	0.35359012	0.7326	-6.15
266550_s_at	Expressed protein ; supported by	---	AT2G35070	-1.31	-0.39	-1.00	0.35257029	0.7326	-6.15
255328_at	putative leucyl tRNA synthetase	EMB2369	AT4G04350	1.11	0.16	1.00	0.35282058	0.7326	-6.15
266523_at	putative transportin	TRN1	AT2G16950	-1.08	-0.11	-1.00	0.3526257	0.7326	-6.15
264472_at	hypothetical protein predicted by g	SWEETIE	AT1G67140	1.11	0.15	1.00	0.35350584	0.7326	-6.15
256726_at	unknown protein	---	AT3G52210	-1.12	-0.16	-1.00	0.35201858	0.7326	-6.15
252892_at	hypothetical protein	---	AT4G39420	-1.07	-0.10	-1.00	0.35194923	0.7326	-6.15
AFFX-TrpnX-M	B. subtilis /GEN=trpD, trpC /DB_X	---	---	-1.07	-0.10	-1.00	0.35261882	0.7326	-6.15
247421_at	SIAH1 - like protein SIAH1, Brass	---	AT5G62800	1.10	0.14	1.00	0.3522156	0.7326	-6.15
266115_at	protease inhibitor II ;supported by	LCR72	AT2G02140	1.15	0.20	1.00	0.35189916	0.7326	-6.15
249170_at	abscisic acid responsive elements-	---	AT5G42910	-1.07	-0.10	-1.00	0.35260286	0.7326	-6.15
253885_at	putative protein essential for embr	VPS26B	AT4G27690	1.10	0.14	1.00	0.35266009	0.7326	-6.15
257656_at	Expressed protein ; supported by f	---	AT3G13228	1.07	0.10	1.00	0.35348504	0.7326	-6.15
252719_at	putative protein predicted protein,	---	AT3G43950	-1.08	-0.11	-1.00	0.35334379	0.7326	-6.15
260861_at	hypothetical protein predicted by g	---	---	-1.08	-0.12	-1.00	0.35345919	0.7326	-6.15
251687_at	quinone reductase-like protein zet	---	AT3G56460	1.07	0.10	1.00	0.35322631	0.7326	-6.15
248917_at	putative protein similar to unknown	---	AT5G45850	-1.06	-0.09	-1.00	0.35324213	0.7326	-6.15
261675_at	hypothetical protein predicted by g	---	AT1G18290	1.08	0.12	1.00	0.35207014	0.7326	-6.15
247799_at	subtilisin-like serine protease conta	---	AT5G58840	-1.12	-0.16	-1.00	0.35316461	0.7326	-6.15
249600_s_at	oxidoreductase-like protein zeta-c	---	AT5G37940	-1.06	-0.09	-1.00	0.35313934	0.7326	-6.15
246863_at	nodulin - like protein early nodulin	---	AT5G25940	1.18	0.24	1.00	0.35375499	0.7326	-6.15
265245_at	unknown protein	---	AT2G43060	1.16	0.22	1.00	0.35373869	0.7326	-6.15
267416_at	putative phosphatidylinositol-glyca	SETH1	AT2G34980	-1.08	-0.11	-1.00	0.35380581	0.7327	-6.15
254133_at	putative protein various predicted	---	AT4G24810	1.07	0.10	1.00	0.35398686	0.7329	-6.15
259367_at	hypothetical protein predicted by g	---	AT1G69070	-1.13	-0.18	-1.00	0.35402859	0.7329	-6.15
253851_at	putative transcription factor MYB4	AtMYB41	AT4G28110	-1.10	-0.13	-1.00	0.35409586	0.7329	-6.15
257693_at	hypothetical protein predicted by g	---	AT3G12850	-1.14	-0.19	-1.00	0.35406683	0.7329	-6.15
257921_at	hypothetical protein contains Pfam	---	AT3G23270	-1.07	-0.10	-1.00	0.35404178	0.7329	-6.15
248872_at	Expressed protein ; supported by f	MSP2	AT5G46795	-1.09	-0.12	-1.00	0.35403273	0.7329	-6.15
259835_at	unknown protein	TRZ3	AT1G52160	-1.08	-0.11	-0.99	0.35419164	0.7329	-6.15
263671_at	hypothetical protein predicted by g	---	AT2G04830	-1.08	-0.11	-0.99	0.35419695	0.7329	-6.15

256548_at	hypothetical protein contains simila	---	AT3G14770	1.52	0.61	0.99	0.35416032	0.7329	-6.15
259116_at	putative peptide transporter similar	---	AT3G01350	1.15	0.20	0.99	0.3542656	0.7329	-6.15
260578_at	unknown protein predicted by gens	---	AT2G47350	-1.08	-0.11	-0.99	0.35423371	0.7329	-6.15
248531_at	putative protein contains similarity	---	AT5G49950	-1.09	-0.12	-0.99	0.35438547	0.7329	-6.15
255135_at	putative protein several hypothetic	---	---	-1.08	-0.12	-0.99	0.35442714	0.7329	-6.15
254185_at	cellulose synthase catalytic subun	CSLG3	AT4G23990	-1.14	-0.19	-0.99	0.35439516	0.7329	-6.15
259035_at	hypothetical protein predicted by g	---	AT3G09430	1.07	0.10	0.99	0.35439939	0.7329	-6.15
251978_at	CYTOCHROME P450 - like protei	CYP71B30	AT3G53290	-1.10	-0.14	-0.99	0.35441853	0.7329	-6.15
264731_at	hypothetical protein predicted by g	---	AT1G62150	1.09	0.12	0.99	0.35447105	0.7329	-6.15
249174_at	putative protein similar to unknown	---	AT5G42900	-1.16	-0.21	-0.99	0.35452061	0.7329	-6.15
266825_at	unknown protein	---	AT2G22890	-1.18	-0.23	-0.99	0.35459247	0.7330	-6.15
261699_at	hypothetical protein identical to hy	---	AT1G32660	-1.09	-0.12	-0.99	0.35462688	0.7330	-6.15
247525_at	pseudo-response regulator 1 ; sup	TOC1	AT5G61380	-1.06	-0.09	-0.99	0.35483479	0.7333	-6.15
250521_at	selenium-binding protein-like	---	AT5G08490	-1.08	-0.11	-0.99	0.3548603	0.7333	-6.15
255898_at	hypothetical protein similar to hypo	---	AT1G17930	-1.08	-0.11	-0.99	0.35482459	0.7333	-6.15
257747_at	hypothetical protein predicted by g	---	AT3G18700	1.07	0.09	0.99	0.35487784	0.7333	-6.15
250519_at	GDSL-motif lipase/acylhydrolase-li	---	AT5G08460	-1.09	-0.13	-0.99	0.35493247	0.7333	-6.15
261593_at	unknown protein	---	AT1G33170	1.58	0.66	0.99	0.35497298	0.7334	-6.15
261537_at	carbonyl reductase, putative simila	---	AT1G01800	1.06	0.09	0.99	0.35501266	0.7334	-6.15
260490_at	ATP-dependent transmembrane t	CER5	AT1G51500	1.17	0.23	0.99	0.35543117	0.7335	-6.15
263693_at	hypothetical protein predicted by g	ATPP2-A9	AT1G31200	1.22	0.29	0.99	0.35542483	0.7335	-6.15
252245_at	putative protein various predicted	---	AT3G49710	1.14	0.19	0.99	0.35546982	0.7335	-6.15
249529_at	putative protein predicted proteins	---	AT5G38730	-1.13	-0.17	-0.99	0.35536887	0.7335	-6.15
250649_at	thioredoxin-like ; supported by cDI	WCRKC1	AT5G06690	1.10	0.13	0.99	0.35525873	0.7335	-6.15
250508_at	selenium-binding protein-like	---	AT5G09950	-1.08	-0.11	-0.99	0.3555414	0.7335	-6.15
256011_at	respiratory burst oxidase protein,	---	AT1G19230	1.08	0.12	0.99	0.35556797	0.7335	-6.15
266737_at	putative alcohol dehydrogenase ;	---	AT2G47140	-1.09	-0.13	-0.99	0.35519865	0.7335	-6.15
247337_at	putative protein similar to unknown	PDF2.5	AT5G63660	1.07	0.09	0.99	0.35550122	0.7335	-6.15
253523_at	putative protein myosin heavy cha	---	AT4G31340	1.08	0.12	0.99	0.3551565	0.7335	-6.15
260433_at	MtN21-like protein similar to MtN21	---	AT1G68170	1.09	0.13	0.99	0.35517102	0.7335	-6.15
246742_at	TOPP8 serine/threonine protein ph	TOPP8	AT5G27840	-1.06	-0.09	-0.99	0.35536588	0.7335	-6.15
266517_at	glycine decarboxylase complex H-	---	AT2G35120	-1.20	-0.26	-0.99	0.35547181	0.7335	-6.15
256863_at	CCHC-type zinc finger protein, pu	---	AT3G24070	-1.07	-0.09	-0.99	0.35535922	0.7335	-6.15
260767_s_at	unknown protein ; supported by ful	---	AT1G49140	1.08	0.11	0.99	0.35554118	0.7335	-6.15
257496_s_at	hypothetical protein predicted by g	---	AT2G43730	-1.10	-0.14	-0.99	0.35536989	0.7335	-6.15

245764_s_at	hypothetical protein contains simila	ATCSA-1	AT1G19750 /	-1.07	-0.10	-0.99	0.3556341	0.7335	-6.15
258886_at	putative importin alpha similar to G	IMPA-7	AT3G05720	-1.08	-0.11	-0.99	0.35571579	0.7336	-6.15
253182_at	putative protein ctf, Mycobacteriur	---	AT4G35190	-1.15	-0.20	-0.99	0.35568793	0.7336	-6.15
266962_at	hypothetical protein predicted by g	---	AT2G39435 /	1.08	0.12	0.99	0.35579774	0.7336	-6.15
247355_at	unknown protein ; supported by fu	SPT42	AT5G63670	1.08	0.11	0.99	0.35577509	0.7336	-6.15
266185_at	unknown protein	---	AT2G38950	1.07	0.10	0.99	0.35585112	0.7336	-6.15
265965_at	putative glutamate/ornithine acetyl	---	AT2G37500	1.09	0.12	0.99	0.35609851	0.7339	-6.15
262290_at	Expressed protein ; supported by f	---	AT1G70985	1.12	0.17	0.99	0.35608443	0.7339	-6.15
266322_at	putative auxin-regulated protein	---	AT2G46690	1.17	0.23	0.99	0.35608622	0.7339	-6.15
250435_at	putative protein various predicted	RING1	AT5G10380	1.18	0.24	0.99	0.35623303	0.7342	-6.16
255074_at	putative protein RING-H2 zinc fing	---	AT4G09100	-1.09	-0.12	-0.99	0.35633702	0.7342	-6.16
267133_at	unknown protein	---	AT2G23440	-1.09	-0.12	-0.99	0.35635068	0.7342	-6.16
250005_at	putative protein predicted proteins	---	AT5G18760	-1.07	-0.10	-0.99	0.35629712	0.7342	-6.16
247178_at	Expressed protein ; supported by c	---	AT5G65205	1.20	0.26	0.99	0.35647476	0.7343	-6.16
263838_at	putative s-adenosylmethionine syn	MAT3	AT2G36880	-1.22	-0.29	-0.99	0.35645212	0.7343	-6.16
258474_at	hypothetical protein predicted by g	---	AT3G02650	1.13	0.17	0.99	0.35661365	0.7344	-6.16
255691_at	hypothetical protein	ANTR2	AT4G00370	1.09	0.13	0.99	0.35661396	0.7344	-6.16
259408_at	protein phosphatase 2A 65 kDa re	PP2AA2	AT3G25800	-1.07	-0.10	-0.99	0.35663498	0.7344	-6.16
261622_at	hypothetical protein predicted by g	---	AT1G01970	-1.09	-0.12	-0.99	0.35658099	0.7344	-6.16
255011_at	cytochrome c several plant cytoch	CYTC-2	AT4G10040	-1.29	-0.37	-0.99	0.35683324	0.7346	-6.16
264538_at	hypothetical protein predicted by g	WRKY10	AT1G55600	-1.10	-0.14	-0.99	0.35682986	0.7346	-6.16
249825_at	putative protein similar to unknown	---	AT5G23390	1.08	0.11	0.99	0.35683233	0.7346	-6.16
258113_at	putative cytochrome P450 similar t	CYP72A11	AT3G14650	-1.14	-0.19	-0.99	0.35689396	0.7347	-6.16
262101_at	hypothetical protein identical to hy	---	AT1G59535	-1.07	-0.10	-0.99	0.3570508	0.7349	-6.16
261977_at	hypothetical protein contains simila	---	---	-1.07	-0.10	-0.99	0.35710379	0.7350	-6.16
266772_s_at	predicted by genefinder	---	AT2G03020 /	1.13	0.18	0.99	0.35714222	0.7350	-6.16
249690_at	acyl-peptide hydrolase-like	---	AT5G36210	1.08	0.11	0.99	0.35717295	0.7350	-6.16
249066_at	WD-repeat protein-like	---	AT5G43920	1.07	0.09	0.99	0.35730101	0.7350	-6.16
257791_at	unknown protein contains Pfam pr	---	AT3G27110	-1.11	-0.15	-0.99	0.35747082	0.7350	-6.16
258765_at	putative pectinesterase contains si	---	AT3G10710	1.08	0.11	0.99	0.35747039	0.7350	-6.16
252792_at	hypothetical protein	---	---	-1.10	-0.13	-0.99	0.3574897	0.7350	-6.16
253677_at	cytidine deaminase - like protein c	---	AT4G29580	-1.10	-0.13	-0.99	0.35726421	0.7350	-6.16
262435_at	cytochrome P450, putative similar	CYP96A8	AT1G47620	-1.06	-0.09	-0.99	0.35736211	0.7350	-6.16
258942_at	unknown protein predicted by gen	---	AT3G09960	-1.09	-0.12	-0.99	0.35726902	0.7350	-6.16
259189_at	unknown protein	AGP11	AT3G01700	-1.10	-0.14	-0.99	0.35740626	0.7350	-6.16

244908_at	hypothetical protein	---	---	-1.14	-0.19	-0.99	0.35752091	0.7350	-6.16
258706_at	unknown protein similar to putative	---	AT3G09570	-1.08	-0.11	-0.99	0.35750323	0.7350	-6.16
247816_at	similar to unknown protein (pir||S7	---	AT5G58260	-1.20	-0.26	-0.99	0.35769177	0.7353	-6.16
260825_at	hypothetical protein predicted by g	---	AT1G06810	-1.08	-0.11	-0.99	0.35773284	0.7353	-6.16
262713_at	unknown protein	---	AT1G16520	1.16	0.21	0.99	0.35772118	0.7353	-6.16
250293_s_at	auxin reponsive - like protein Nt-g	---	AT5G13360	1.20	0.26	0.99	0.35785579	0.7354	-6.16
266183_at	unknown protein	ATPT2	AT2G38940	1.11	0.14	0.99	0.35790165	0.7355	-6.16
259763_at	unknown protein similar to GB:AAE	---	AT1G77630	1.13	0.18	0.99	0.3580802	0.7356	-6.16
255291_at	putative calcium dependent protein	CPK27	AT4G04700	-1.09	-0.13	-0.99	0.3580635	0.7356	-6.16
253048_at	formamidase - like protein forman	---	AT4G37560	1.24	0.31	0.99	0.3580405	0.7356	-6.16
266343_at	putative non-LTR retroelement rev	---	---	1.09	0.13	0.99	0.35817119	0.7356	-6.16
250294_at	auxin reponsive - like protein Nt-g	---	AT5G13380	-1.08	-0.11	-0.99	0.3581728	0.7356	-6.16
249561_at	disease resistance - like protein di	---	AT5G38340	-1.08	-0.12	-0.99	0.3581672	0.7356	-6.16
265344_at	unknown protein predicted by gene	---	AT2G22660	-1.12	-0.16	-0.99	0.35850239	0.7357	-6.16
249838_at	unknown protein ;supported by ful	---	AT5G23460	1.11	0.15	0.99	0.35852609	0.7357	-6.16
245134_s_at	unknown protein	---	AT2G45250	1.08	0.11	0.99	0.35833665	0.7357	-6.16
259395_at	GTP-binding protein(RAB11D), pu	ARA-2	AT1G06400	-1.08	-0.11	-0.99	0.35855041	0.7357	-6.16
250885_at	ABC transporter -like protein ABC	ATH12	AT5G03910	1.08	0.11	0.99	0.35831305	0.7357	-6.16
263490_at	F-box protein ORE9, AtFBL7 iden	MAX2	AT2G42620	1.16	0.22	0.99	0.35836149	0.7357	-6.16
245418_at	putative protein	---	AT4G17370	-1.11	-0.15	-0.99	0.35824619	0.7357	-6.16
258510_at	hypothetical protein predicted by g	---	AT3G06600	-1.09	-0.13	-0.99	0.35843111	0.7357	-6.16
265734_at	predicted by genscan and genefin	---	AT2G01260	-1.08	-0.11	-0.99	0.35835627	0.7357	-6.16
264532_at	seed imbibition protein, putative si	AtSIP1	AT1G55740	-1.08	-0.11	-0.99	0.35843609	0.7357	-6.16
266858_at	unknown protein	GRV2	AT2G26890	1.08	0.11	0.99	0.35853997	0.7357	-6.16
260846_at	unknown protein	---	AT1G17300	-1.08	-0.12	-0.99	0.35863905	0.7358	-6.16
260141_at	gibberellin regulatory protein, puta	RGL1	AT1G66350	-1.34	-0.42	-0.99	0.35868271	0.7358	-6.16
264286_at	unknown protein ;supported by full	PPR336	AT1G61870	1.15	0.20	0.98	0.35875554	0.7358	-6.16
266964_at	putative ABC transporter related to	PGP6	AT2G39480	-1.06	-0.09	-0.98	0.35873046	0.7358	-6.16
256848_at	hypothetical protein similar to hypo	---	AT3G27960	-1.27	-0.35	-0.98	0.35880198	0.7359	-6.16
262922_at	hypothetical protein predicted by g	---	AT1G79420	1.11	0.15	0.98	0.35887149	0.7359	-6.16
263292_at	putative Ta11-like non-LTR retroel	---	---	-1.08	-0.11	-0.98	0.35889414	0.7359	-6.16
262082_s_at	wall-associated kinase 2, putative	---	AT1G56120	-1.24	-0.31	-0.98	0.35900984	0.7360	-6.16
247190_at	D-type cyclin (emb|CAB41347.1)	CYCD4;1	AT5G65420	1.09	0.12	0.98	0.35898416	0.7360	-6.16
264857_at	putative glycosyl transferase simila	LGT9	AT1G24170	1.13	0.17	0.98	0.35960317	0.7364	-6.16
251661_at	putative protein NODULIN-26 - Gl	SIP2;1	AT3G56950	1.11	0.15	0.98	0.35928242	0.7364	-6.16

260744_at	hypothetical protein predicted by g	---	AT1G15010	-1.42	-0.51	-0.98	0.35978849	0.7364	-6.16
261919_at	type 2 peroxiredoxin, putative sim	TPX1	AT1G65980	-1.10	-0.13	-0.98	0.35938713	0.7364	-6.16
262699_at	unknown protein	---	AT1G75980	1.08	0.12	0.98	0.35953094	0.7364	-6.16
246775_at	putative protein GTP-binding prote	MIRO1	AT5G27540	-1.07	-0.09	-0.98	0.3595657	0.7364	-6.16
245164_at	mitochondrial chaperonin (HSP60)	HSP60-2	AT2G33210	-1.21	-0.28	-0.98	0.35970234	0.7364	-6.16
265254_at	unknown protein ; supported by cl	DRB2	AT2G28380	-1.08	-0.12	-0.98	0.3596832	0.7364	-6.16
250298_at	putative protein NLI-interacting fac	---	AT5G11860	-1.09	-0.12	-0.98	0.35968646	0.7364	-6.16
249606_at	putative protein DNA-binding prote	RVE2	AT5G37260	1.08	0.12	0.98	0.35939339	0.7364	-6.16
260211_at	hypothetical protein similar to YGL	---	AT1G74440	1.28	0.36	0.98	0.35984122	0.7364	-6.16
262503_at	hypothetical protein predicted by g	---	AT1G21670	1.17	0.23	0.98	0.35968363	0.7364	-6.16
266525_at	putative tetracycline transporter pr	MEE15	AT2G16970	-1.09	-0.13	-0.98	0.35920411	0.7364	-6.16
257146_at	unknown protein contains Pfam pr	GTE8	AT3G27260	-1.06	-0.09	-0.98	0.35976067	0.7364	-6.16
264291_at	hypothetical protein contains simila	---	AT1G78800	1.09	0.12	0.98	0.3592562	0.7364	-6.16
262256_at	hypothetical protein similar to puta	---	---	-1.09	-0.12	-0.98	0.35955541	0.7364	-6.16
264680_at	hypothetical protein predicted by g	---	AT1G65510	1.18	0.24	0.98	0.35959927	0.7364	-6.16
246491_at	hypothetical protein	---	AT5G16100	1.07	0.10	0.98	0.35984798	0.7364	-6.16
251390_at	guanine nucleotide exchange fact	---	AT3G60860	1.09	0.12	0.98	0.35981542	0.7364	-6.16
248780_at	4-nitrophenylphosphatase-like prot	ATPGLP2	AT5G47760	-1.08	-0.11	-0.98	0.3598468	0.7364	-6.16
245655_at	hypothetical protein predicted by g	---	AT1G56530	-1.07	-0.09	-0.98	0.35984689	0.7364	-6.16
263061_at	putative AAA-type ATPase	---	AT2G18190	-1.09	-0.13	-0.98	0.35993178	0.7364	-6.16
247377_at	pectate lyase ; supported by cDNA	---	AT5G63180	1.82	0.86	0.98	0.35998413	0.7364	-6.16
247532_at	putative protein disease resistanc	---	AT5G61560	1.26	0.33	0.98	0.35995347	0.7364	-6.16
250934_at	DNAJ protein - like DNAJ domain-	---	AT5G03030	1.14	0.18	0.98	0.35993465	0.7364	-6.16
248147_at	putative protein contains similarity	ATRBP45A	AT5G54900	1.08	0.12	0.98	0.36019833	0.7365	-6.16
257940_at	putative UDP-glucose glucosyltran	---	AT3G21790	-1.10	-0.14	-0.98	0.3603192	0.7365	-6.16
267486_at	putative protein kinase contains a	APK2B	AT2G02800	1.13	0.17	0.98	0.36026104	0.7365	-6.16
259064_at	putative calmodulin similar to calm	AGD11	AT3G07490	-1.09	-0.12	-0.98	0.36033636	0.7365	-6.16
256755_at	calmodulin, putative similar to GB	---	AT3G25600	1.17	0.22	0.98	0.36028718	0.7365	-6.16
264041_at	MADS-box protein (AGL3) ; suppo	ספט-04	AT2G03710	-1.18	-0.24	-0.98	0.36022953	0.7365	-6.16
257870_at	prolyl 4-hydroxylase, putative simi	---	AT3G28490	1.06	0.09	0.98	0.360295	0.7365	-6.16
246857_at	putative protein	---	AT5G25920	-1.09	-0.12	-0.98	0.36022943	0.7365	-6.16
263072_at	putative protein kinase contains a	---	AT2G17530	-1.08	-0.11	-0.98	0.36028471	0.7365	-6.16
267236_at	GDP dissociation inhibitor identica	ATGDI1	AT2G44100	1.08	0.12	0.98	0.36056195	0.7365	-6.16
246359_x_at	hypothetical protein	---	---	1.11	0.15	0.98	0.36047659	0.7365	-6.16
265879_at	hypothetical protein predicted by g	---	AT2G42450	-1.07	-0.10	-0.98	0.36047678	0.7365	-6.16

262734_at	lipase, putative similar to lipase G	---	AT1G28640	-1.07	-0.10	-0.98	0.36048371	0.7365	-6.16
256918_s_at	hypothetical protein similar to hypo	---	AT3G18960	-1.11	-0.15	-0.98	0.36056359	0.7365	-6.16
255654_at	Similar to receptor kinase	---	AT4G00970	-1.28	-0.35	-0.98	0.36052315	0.7365	-6.16
252002_at	hypothetical protein YIP1 protein,	---	AT3G52760	1.08	0.11	0.98	0.36052998	0.7365	-6.16
249469_at	UDP-glucose dehydrogenase-like	---	AT5G39320	1.21	0.27	0.98	0.36087455	0.7368	-6.17
253087_at	purple acid phosphatase like prote	PAP25	AT4G36350	-1.09	-0.12	-0.98	0.36073751	0.7368	-6.16
267176_at	putative zinc finger protein	---	AT2G37730	-1.09	-0.12	-0.98	0.36085156	0.7368	-6.17
259532_at	hypothetical protein	---	AT1G12470	-1.07	-0.09	-0.98	0.36081468	0.7368	-6.17
260234_at	putative lipase/acylhydrolase conta	---	AT1G74460	1.11	0.15	0.98	0.36078609	0.7368	-6.16
265113_at	hypothetical protein	---	---	1.08	0.11	0.98	0.36089446	0.7368	-6.17
249816_at	cleavage and polyadenylation spe	CPSF100	AT5G23880	1.11	0.15	0.98	0.36102795	0.7369	-6.17
249959_at	NADH:ubiquinone oxidoreductase	---	AT5G18800	1.10	0.14	0.98	0.36100681	0.7369	-6.17
250868_at	malate synthase -like protein mala	MLS	AT5G03860	1.12	0.17	0.98	0.36101065	0.7369	-6.17
261141_at	unknown protein contains Pfam pr	---	AT1G19740	1.09	0.13	0.98	0.361126	0.7370	-6.17
246889_at	putative protein various predicted	---	AT5G25470	-1.10	-0.14	-0.98	0.36116807	0.7370	-6.17
257150_at	unknown protein ;supported by ful	---	AT3G27230	1.10	0.14	0.98	0.36130858	0.7371	-6.17
254131_at	protein kinase (AFC2) ; supported	AFC2	AT4G24740	-1.09	-0.13	-0.98	0.36133129	0.7371	-6.17
250348_at	putative protein	---	AT5G11990	1.10	0.14	0.98	0.36130713	0.7371	-6.17
245983_at	5-formyltetrahydrofolate cyclo-liga	5-FCL	AT5G13050	1.08	0.11	0.98	0.36138686	0.7372	-6.17
266250_at	putative reverse transcriptase	---	---	-1.08	-0.11	-0.98	0.36152077	0.7374	-6.17
249962_at	pectin methyl esterase -like protei	---	AT5G18990	-1.13	-0.18	-0.98	0.36159086	0.7375	-6.17
255244_at	putative protein various hypothetic	---	AT4G05620	-1.08	-0.11	-0.98	0.36165906	0.7375	-6.17
255178_at	may be a pseudogene	---	---	-1.07	-0.10	-0.98	0.36172422	0.7375	-6.17
250959_at	F-box protein family, AtFBL25 con	---	AT5G02920	1.08	0.11	0.98	0.36171302	0.7375	-6.17
246904_at	DNA methyltransferase PMT1 - lik	DNMT2	AT5G25480	1.10	0.13	0.98	0.36188772	0.7377	-6.17
255385_at	putative hydrolase	---	AT4G03610	-1.11	-0.15	-0.98	0.36187626	0.7377	-6.17
259425_at	4,5 PIP kinase, putative similar to	PIPK11	AT1G01460	1.07	0.10	0.98	0.36188308	0.7377	-6.17
261875_at	receptor-like protein kinase, putati	---	AT1G50610	-1.08	-0.11	-0.98	0.36198936	0.7378	-6.17
253949_at	grpE like protein ;supported by ful	AR192	AT4G26780	-1.23	-0.30	-0.98	0.36209375	0.7379	-6.17
245147_at	putative RAD51C-like DNA repair p	ATRAD51C	AT2G45280	-1.16	-0.22	-0.98	0.36217693	0.7379	-6.17
259868_at	thioredoxin-like protein similar to t	ATY1	AT1G76760	1.08	0.11	0.98	0.36215589	0.7379	-6.17
254948_at	putative protein various predicted	---	AT4G11000	-1.09	-0.12	-0.98	0.36211663	0.7379	-6.17
265346_at	hypothetical protein	---	---	-1.08	-0.11	-0.98	0.36225562	0.7380	-6.17
263837_at	unknown protein	---	AT2G04500	1.06	0.09	0.98	0.36226362	0.7380	-6.17
249644_at	putative serine-rich protein hypoth	---	AT5G37010	-1.10	-0.13	-0.98	0.3623439	0.7380	-6.17

263508_s_at	hypothetical protein	---	---	-1.11	-0.15	-0.98	0.36233144	0.7380	-6.17
249622_at	putative protein	---	AT5G37550	-1.12	-0.16	-0.98	0.36240235	0.7381	-6.17
266827_at	putative serine carboxypeptidase I	SCPL12	AT2G22920	-1.07	-0.10	-0.98	0.36242632	0.7381	-6.17
261892_at	transcription factor, putative simila	WRKY40	AT1G80840	1.63	0.70	0.98	0.36246088	0.7381	-6.17
257251_at	type 1 membrane protein, putative	PMP	AT3G24160	-1.08	-0.11	-0.98	0.36255283	0.7381	-6.17
253153_at	hypothetical protein	---	AT4G35700	-1.08	-0.11	-0.98	0.36253767	0.7381	-6.17
267470_at	cinnamate-4-hydroxylase molecula	C4H	AT2G30490	-1.25	-0.32	-0.98	0.36267138	0.7382	-6.17
246718_at	putative protein various predicted	---	---	-1.09	-0.12	-0.98	0.36265302	0.7382	-6.17
248306_at	unknown protein ; supported by cl	WRKY27	AT5G52830	-1.13	-0.18	-0.98	0.36265377	0.7382	-6.17
259374_at	putative AP2 domain transcription	---	AT3G16280	1.11	0.15	0.98	0.36284145	0.7382	-6.17
249621_at	putative protein predicted proteins	---	AT5G37530	-1.08	-0.12	-0.98	0.3628227	0.7382	-6.17
266190_at	unknown protein	---	AT2G38840	1.08	0.11	0.98	0.36280219	0.7382	-6.17
252376_at	L-galactono-1,4-lactone dehydrog	ATGLDH	AT3G47930	-1.11	-0.16	-0.98	0.36279479	0.7382	-6.17
249149_at	casein kinase I ; supported by cDN	ckl8	AT5G43320	1.06	0.09	0.98	0.36283946	0.7382	-6.17
262297_at	hypothetical protein similar to hypo	---	AT1G27600	1.07	0.09	0.98	0.36292911	0.7383	-6.17
264628_at	hypothetical protein contains simila	---	AT1G65540	-1.06	-0.09	-0.98	0.36297977	0.7383	-6.17
267260_at	putative proline-rich protein ; supp	AGP17	AT2G23130	1.23	0.29	0.98	0.36308505	0.7384	-6.17
254798_at	oleoyl-[acyl-carrier-protein] hydrol	---	AT4G13050	1.15	0.20	0.98	0.36305919	0.7384	-6.17
246291_at	hypothetical protein ; supported by	---	AT3G56820	1.09	0.12	0.98	0.36309031	0.7384	-6.17
248674_at	non-phototropic hypocotyl-like prot	---	AT5G48800	1.16	0.22	0.98	0.3632171	0.7385	-6.17
250245_at	alpha-N-acetylglucosaminidase	---	AT5G13690	-1.10	-0.14	-0.98	0.36319978	0.7385	-6.17
258777_at	hypothetical protein predicted by g	---	AT3G11850	-1.11	-0.15	-0.98	0.36326305	0.7385	-6.17
258855_at	unknown protein	---	AT3G02070	1.14	0.19	0.97	0.3633116	0.7385	-6.17
266545_at	hypothetical protein predicted by g	---	AT2G35290	-1.16	-0.22	-0.97	0.36340039	0.7387	-6.17
256451_s_at	unknown protein	---	AT1G75170 /	1.24	0.31	0.97	0.36359612	0.7388	-6.17
244938_at	ribosomal protein S15	---	---	1.15	0.20	0.97	0.36355342	0.7388	-6.17
251558_at	putative protein ;supported by full	---	AT3G57810	-1.16	-0.21	-0.97	0.36359723	0.7388	-6.17
249438_at	putative protein BCS1 nuclear ger	AATP1	AT5G40010	-1.10	-0.14	-0.97	0.36357725	0.7388	-6.17
252395_at	H+-transporting ATPase - like pro	AHA4	AT3G47950	-1.13	-0.17	-0.97	0.3636412	0.7388	-6.17
259697_at	putative DNA-binding protein simi	---	AT1G68920	1.07	0.10	0.97	0.36368768	0.7388	-6.17
246058_at	putative protein predicted proteins	---	AT5G08430	-1.09	-0.12	-0.97	0.36385042	0.7391	-6.17
258244_at	unknown protein ; supported by cl	---	AT3G27770	1.08	0.10	0.97	0.36407995	0.7392	-6.17
263930_at	hypothetical protein predicted by g	---	AT2G36300	-1.08	-0.11	-0.97	0.36425701	0.7392	-6.17
260350_at	Eukaryotic initiation factor 5A , pu	ELF5A-3	AT1G69410	1.12	0.16	0.97	0.36420054	0.7392	-6.17
249230_at	putative protein similar to unknown	---	AT5G42070	1.10	0.14	0.97	0.36414452	0.7392	-6.17

248865_at	putative protein similar to unknown	---	AT5G46790	1.11	0.15	0.97	0.3641712	0.7392	-6.17
251816_at	Expressed protein ; supported by c	TON1B	AT3G55005	1.11	0.15	0.97	0.36396719	0.7392	-6.17
262726_at	hypothetical protein similar to puta	AtTLP5	AT1G43640	-1.10	-0.14	-0.97	0.36423462	0.7392	-6.17
250410_at	putative protein putative ATP/GTP	---	AT5G11010	1.13	0.17	0.97	0.36418829	0.7392	-6.17
252314_at	hypothetical protein	---	AT3G49400	1.09	0.12	0.97	0.36421632	0.7392	-6.17
259281_at	putative Myb-related transcription f	MYB106	AT3G01140	-1.09	-0.12	-0.97	0.36405132	0.7392	-6.17
251067_at	hypothetical protein	---	AT5G01910	1.12	0.16	0.97	0.3640855	0.7392	-6.17
253106_at	putative protein predicted proteins	---	AT4G35870	-1.08	-0.11	-0.97	0.36428798	0.7392	-6.17
259399_at	hypothetical protein similar to puta	---	AT1G17710	1.11	0.15	0.97	0.36444548	0.7393	-6.17
246885_at	putative protein predicted protein,	---	AT5G26230	-1.23	-0.30	-0.97	0.3644526	0.7393	-6.17
263815_at	hypothetical protein predicted by g	---	AT2G10020	-1.13	-0.17	-0.97	0.36439964	0.7393	-6.17
262609_at	unknown protein ;supported by full	---	AT1G13930	-1.09	-0.13	-0.97	0.36453301	0.7394	-6.17
262362_at	disease resistance protein, putativ	---	AT1G72840	1.08	0.10	0.97	0.36460446	0.7395	-6.17
250842_at	putative protein predicted proteins	VTE5	AT5G04490	-1.11	-0.15	-0.97	0.3646488	0.7395	-6.17
254548_at	putative protein various predicted	---	AT4G19865	1.15	0.20	0.97	0.36462359	0.7395	-6.17
263899_at	hypothetical protein predicted by g	EMB2219	AT2G21710	1.10	0.14	0.97	0.36480589	0.7395	-6.17
265436_at	putative retroelement pol polyprote	---	---	1.06	0.09	0.97	0.36483686	0.7395	-6.17
249471_at	putative protein predicted proteins	EDL2	AT5G39360	-1.12	-0.16	-0.97	0.36480315	0.7395	-6.17
262330_at	disease resistance protein, putativ	RLM1	AT1G64070	1.09	0.12	0.97	0.36477118	0.7395	-6.17
265534_at	En/Spm-like transposon protein rel	---	---	-1.06	-0.08	-0.97	0.36474977	0.7395	-6.17
260096_at	hypothetical protein predicted by g	---	AT1G73240	-1.10	-0.14	-0.97	0.36491614	0.7396	-6.17
255910_at	unknown protein contains similarity	---	AT1G18030	1.08	0.11	0.97	0.36488857	0.7396	-6.17
265592_at	hypothetical protein predicted by g	---	AT2G20110	1.08	0.12	0.97	0.36500608	0.7397	-6.17
255010_at	lipase-like protein monoglyceride l	---	AT4G10050	-1.07	-0.10	-0.97	0.36505417	0.7397	-6.17
260030_at	putative bZIP transcription factor s	AtbZIP	AT1G68880	-1.08	-0.11	-0.97	0.36530374	0.7401	-6.17
246940_at	expressed protein glucose-6-phos	---	AT5G25400	1.09	0.12	0.97	0.36531109	0.7401	-6.17
256828_at	unknown protein	---	AT3G22968	-1.17	-0.23	-0.97	0.36549492	0.7404	-6.17
264943_at	hypothetical protein predicted by g	---	AT1G76910	-1.10	-0.14	-0.97	0.36551412	0.7404	-6.17
251050_at	putative protein	---	AT5G02440	1.09	0.12	0.97	0.36557172	0.7404	-6.17
261334_at	unknown protein	---	AT1G44960	-1.08	-0.12	-0.97	0.36579524	0.7408	-6.18
261375_at	transcription factor, putative simila	SPL4	AT1G53160	-1.38	-0.47	-0.97	0.36610515	0.7410	-6.18
254153_at	putative protein hypothetical prote	PWD	AT4G24450	-1.16	-0.22	-0.97	0.36610357	0.7410	-6.18
261831_at	ADP-ribosylation factor, putative s	ATARFA1F	AT1G10630	1.12	0.16	0.97	0.36607815	0.7410	-6.18
253880_at	Expressed protein ;supported by c	---	AT4G27590	1.10	0.14	0.97	0.36600056	0.7410	-6.18
255693_s_at	putative BRCA2 homolog	BRCA2(IV)	AT4G00020	-1.08	-0.12	-0.97	0.36613038	0.7410	-6.18

267281_at	putative protein kinase contains a	---	AT2G19400	-1.10	-0.14	-0.97	0.36604219	0.7410	-6.18
262424_at	hypothetical protein predicted by g	---	AT1G47680	1.07	0.10	0.97	0.36600663	0.7410	-6.18
263925_at	putative glycine-rich RNA binding p	---	AT2G21690	1.06	0.09	0.97	0.3661257	0.7410	-6.18
248434_at	mitochondrial heat shock 22 kd pro	---	AT5G51440	-1.51	-0.60	-0.97	0.36633577	0.7413	-6.18
259575_at	unknown protein	---	AT1G35320	-1.07	-0.10	-0.97	0.36637586	0.7413	-6.18
251338_at	putative protein VAP27, Nicotiana	VAP	AT3G60600	1.07	0.10	0.97	0.36642011	0.7414	-6.18
251272_at	homeobox-leucine zipper protein A	ATHB-12	AT3G61890	-1.25	-0.32	-0.97	0.36681319	0.7414	-6.18
256899_at	putative kinase-like protein TMKL	TMKL1	AT3G24660	1.08	0.12	0.97	0.36667892	0.7414	-6.18
266439_s_at	hypothetical protein predicted by g	---	AT2G43200	1.08	0.11	0.97	0.36674546	0.7414	-6.18
250147_at	putative protein predicted proteins	---	AT5G14600	1.13	0.17	0.97	0.3665593	0.7414	-6.18
260582_at	hypothetical protein predicted by g	---	AT2G47200	1.09	0.12	0.97	0.36678639	0.7414	-6.18
250854_at	aspartyl aminopeptidase -like prot	---	AT5G04710	1.10	0.14	0.97	0.36666679	0.7414	-6.18
245705_at	zinc finger transcription factor-like	---	AT5G04390	-1.07	-0.10	-0.97	0.36671911	0.7414	-6.18
245546_at	cellulose synthase like protein	ATCSLB05	AT4G15290	-1.13	-0.17	-0.97	0.36661978	0.7414	-6.18
260557_at	putative endochitinase	---	AT2G43610	-1.06	-0.09	-0.97	0.36668563	0.7414	-6.18
266321_at	putative cytochrome P450	CYP78A6	AT2G46660	-1.11	-0.15	-0.97	0.36657608	0.7414	-6.18
267414_at	putative berberine bridge enzyme	MEE23	AT2G34790	1.15	0.20	0.97	0.36649235	0.7414	-6.18
245055_at	hypothetical protein predicted by g	---	AT2G26470	1.09	0.13	0.97	0.36675996	0.7414	-6.18
246972_s_at	cytochrome P-450-like protein cyt	CYP71A14	AT5G24950	1.18	0.24	0.97	0.36686933	0.7414	-6.18
263618_at	hypothetical protein predicted by g	APC2	AT2G04660	-1.10	-0.14	-0.97	0.36700613	0.7416	-6.18
249938_at	Ruv DNA-helicase-like protein ;su	RIN1	AT5G22330	1.07	0.10	0.97	0.36716095	0.7416	-6.18
255294_at	putative sugar transporter	---	AT4G04750	1.08	0.11	0.97	0.36717392	0.7416	-6.18
267349_at	60S acidic ribosomal protein P0	---	AT2G40010	-1.07	-0.09	-0.97	0.36706211	0.7416	-6.18
248089_at	salt stress inducible small GTP bin	AtRAN4	AT5G55080	-1.09	-0.12	-0.97	0.3671393	0.7416	-6.18
251764_at	putative protein exostose-related p	EPC1	AT3G55830	1.10	0.13	0.97	0.36710956	0.7416	-6.18
265352_at	cytosolic cyclophilin (ROC3) ;supp	ROC3	AT2G16600	1.09	0.12	0.97	0.36741061	0.7417	-6.18
249087_at	DNA binding protein EREBP-3-like	ERF9	AT5G44210	-1.13	-0.18	-0.97	0.36742824	0.7417	-6.18
259909_at	unknown protein ; supported by ful	MEE9	AT1G60870	1.07	0.10	0.97	0.36748978	0.7417	-6.18
254961_at	putative acyl-CoA synthetase acyl	---	AT4G11030	-1.08	-0.12	-0.97	0.36733087	0.7417	-6.18
259580_at	oxidoreductase, putative contains	---	AT1G28030	1.10	0.14	0.97	0.36750928	0.7417	-6.18
248087_at	unknown protein	---	AT5G55060	1.06	0.09	0.97	0.36730796	0.7417	-6.18
253429_at	putative protein CDC28/cdc2-like	---	AT4G32420	-1.08	-0.11	-0.97	0.36740779	0.7417	-6.18
249366_at	dihydroxyacetone 3-phosphate red	---	AT5G40610	1.24	0.31	0.97	0.36726213	0.7417	-6.18
261228_at	C-8,7 sterol isomerase identical to	HYD1	AT1G20050	1.10	0.14	0.97	0.36748279	0.7417	-6.18
245645_at	F5A9.19 unknown protein; similar	ATMAP70-1	AT1G24764	1.12	0.16	0.97	0.36746448	0.7417	-6.18

263687_at	unknown protein ;supported by ful	---	AT1G26940	1.12	0.16	0.97	0.36755042	0.7417	-6.18
255034_at	putative protein Phaseolus vulgari	---	---	-1.07	-0.10	-0.97	0.36760842	0.7417	-6.18
250915_at	homeodomain -like protein homed	HB51	AT5G03790	-1.13	-0.18	-0.97	0.36762749	0.7417	-6.18
258337_at	hypothetical protein predicted by g	---	AT3G16040	1.12	0.16	0.97	0.36768289	0.7417	-6.18
266053_at	unknown protein	---	AT2G40730	-1.09	-0.12	-0.97	0.36787377	0.7420	-6.18
262804_at	putative RNA-binding protein simil	---	AT1G20880	1.10	0.14	0.97	0.36791858	0.7420	-6.18
266686_at	hypothetical protein	---	AT2G19700	1.08	0.11	0.97	0.36791201	0.7420	-6.18
251009_at	putative protein predicted proteins	---	AT5G02640	-1.18	-0.24	-0.96	0.36800822	0.7421	-6.18
260280_at	unknown protein contains AP2 DN	---	AT1G80580	-1.13	-0.17	-0.96	0.36798369	0.7421	-6.18
261714_at	hypothetical protein similar to hypo	TET16	AT1G18510	-1.11	-0.15	-0.96	0.36808625	0.7422	-6.18
266329_at	unknown protein ; supported by cl	CRR3	AT2G01590	1.17	0.23	0.96	0.36814285	0.7422	-6.18
263242_at	unknown protein	---	AT2G31400	-1.09	-0.12	-0.96	0.36826759	0.7423	-6.18
249776_at	unknown protein	---	AT5G24170	-1.11	-0.15	-0.96	0.36823819	0.7423	-6.18
258350_at	unknown protein similar to serine/t	CIPK1	AT3G17510	-1.18	-0.24	-0.96	0.36835631	0.7424	-6.18
245393_at	beta-1,3-glucanase class I precurs	---	AT4G16260	1.18	0.24	0.96	0.36867378	0.7425	-6.18
249123_at	beta-ketoacyl-CoA synthase ; sup	KCS20	AT5G43760	1.06	0.09	0.96	0.36927198	0.7425	-6.18
250753_at	glucuronosyl transferase-like prote	UGT76C2	AT5G05860	1.11	0.14	0.96	0.36931028	0.7425	-6.18
249400_at	putative protein MtN24 gene, Med	---	AT5G40300	1.10	0.14	0.96	0.36871447	0.7425	-6.18
264803_at	hypothetical protein predicted by g	---	AT1G08580	-1.12	-0.16	-0.96	0.36872395	0.7425	-6.18
265715_s_at	expressed protein non-consensus	---	AT1G13860	1.15	0.21	0.96	0.36921145	0.7425	-6.18
246989_at	unknown protein	---	AT5G67350	1.22	0.29	0.96	0.36890453	0.7425	-6.18
248818_at	Lon protease homolog 1 precursor	LON2	AT5G47040	1.11	0.15	0.96	0.36868847	0.7425	-6.18
254854_at	putative protein hypothetical prote	---	AT4G12130	-1.11	-0.15	-0.96	0.36902819	0.7425	-6.18
256239_at	hypothetical protein predicted by g	---	AT3G12470	-1.09	-0.12	-0.96	0.36886226	0.7425	-6.18
256048_at	hypothetical protein contains simila	---	AT1G07025	-1.07	-0.10	-0.96	0.36912015	0.7425	-6.18
246266_at	30S ribosomal protein S11, putativ	NFD3	AT1G31817	1.11	0.16	0.96	0.36865366	0.7425	-6.18
258644_at	putative RNA-binding protein cont	---	AT3G07810	-1.06	-0.09	-0.96	0.36885756	0.7425	-6.18
254117_at	putative protein	---	AT4G24750	1.11	0.15	0.96	0.36893553	0.7425	-6.18
266475_at	putative lipase	---	AT2G31100	-1.08	-0.11	-0.96	0.36897441	0.7425	-6.18
247242_at	unknown protein	---	AT5G64690	-1.07	-0.09	-0.96	0.3691882	0.7425	-6.18
248052_at	putative protein contains similarity	---	AT5G55800	-1.08	-0.11	-0.96	0.36909158	0.7425	-6.18
260122_at	AIG1-like protein similar to AIG1 p	---	AT1G33900	-1.09	-0.13	-0.96	0.36904832	0.7425	-6.18
256971_at	unknown protein contains Pfam pr	---	AT3G21100	1.11	0.15	0.96	0.36930381	0.7425	-6.18
252371_at	putative protein finger protein SIG	---	AT3G48070	-1.09	-0.12	-0.96	0.36901093	0.7425	-6.18
264419_s_at	hypothetical protein contains simila	---	AT1G43310	-1.22	-0.29	-0.96	0.36882636	0.7425	-6.18

263873_at	unknown protein predicted by gens	---	AT2G21860	1.10	0.14	0.96	0.36911872	0.7425	-6.18
265402_at	hypothetical protein predicted by g	---	AT2G10950	-1.08	-0.11	-0.96	0.36869262	0.7425	-6.18
259844_at	lipid transfer protein, putative simi	---	AT1G73560	-1.08	-0.11	-0.96	0.36878436	0.7425	-6.18
265559_at	putative glycine-rich protein	---	AT2G05530	1.10	0.13	0.96	0.36878712	0.7425	-6.18
250837_at	8-amino-7-oxononanoate synthas	ATBIOF	AT5G04620	1.10	0.14	0.96	0.36869935	0.7425	-6.18
261186_at	hypothetical protein predicted by g	---	---	-1.07	-0.09	-0.96	0.36926396	0.7425	-6.18
256801_at	cytochrome P450, putative similar	CYP705A3	AT3G20940	1.07	0.10	0.96	0.36909414	0.7425	-6.18
258947_at	hypothetical protein similar to calm	---	AT3G01830	1.51	0.60	0.96	0.36958273	0.7430	-6.18
247465_at	RNA helicase ; supported by cDNA	PRH75	AT5G62190	1.14	0.19	0.96	0.36992162	0.7430	-6.18
251888_at	putative protein GTP-binding regu	---	AT3G54190	1.07	0.09	0.96	0.3696739	0.7430	-6.18
264018_at	putative triosephosphate isomeras	TIM	AT2G21170	1.08	0.11	0.96	0.36983708	0.7430	-6.18
265888_at	putative cleavage and polyadenyla	RIE1	AT2G01735	-1.07	-0.09	-0.96	0.37011513	0.7430	-6.18
258198_at	putative transcription factor similar	NF-YA6	AT3G14020	1.09	0.13	0.96	0.36982887	0.7430	-6.18
246014_at	putative protein	---	AT5G10680	-1.08	-0.11	-0.96	0.37000681	0.7430	-6.18
264682_at	polygalacturonase, putative simila	---	AT1G65570	-1.07	-0.09	-0.96	0.37004004	0.7430	-6.18
245795_at	unknown protein contains similarity	---	AT1G32160	-1.07	-0.10	-0.96	0.37011439	0.7430	-6.18
254344_at	alcohol dehydrogenase like protei	---	AT4G22110	-1.13	-0.18	-0.96	0.36990062	0.7430	-6.18
248022_at	putative protein contains similarity	APUM12	AT5G56510	-1.06	-0.09	-0.96	0.36990834	0.7430	-6.18
263764_at	putative vacuolar proton-ATPase s	VHA-A2	AT2G21410	-1.10	-0.13	-0.96	0.36987662	0.7430	-6.18
257549_at	hypothetical protein predicted by g	agl103	AT3G18650	-1.10	-0.14	-0.96	0.36963167	0.7430	-6.18
253245_at	bZIP transcription factor ATB2	GBF6	AT4G34588 /	-1.22	-0.29	-0.96	0.36981112	0.7430	-6.18
249292_at	repair endonuclease (gb|AAF0127	UVH1	AT5G41150	1.07	0.10	0.96	0.37009136	0.7430	-6.18
267254_at	putative protein kinase contains a	SNRK2.9	AT2G23030	1.28	0.35	0.96	0.3700851	0.7430	-6.18
263032_at	unknown protein ;supported by full	---	AT1G23850	-1.20	-0.27	-0.96	0.36968267	0.7430	-6.18
252928_at	putative protein more than 30 prec	---	AT4G38940	1.17	0.23	0.96	0.36978932	0.7430	-6.18
265127_at	hypothetical protein similar to polle	sks14	AT1G55560	1.07	0.10	0.96	0.37018911	0.7430	-6.18
250019_at	putative protein similar to unknown	---	AT5G18160	-1.09	-0.13	-0.96	0.37034365	0.7433	-6.18
261589_at	hypothetical protein predicted by g	---	AT1G01690	-1.10	-0.13	-0.96	0.37039971	0.7433	-6.18
265194_at	1-aminocyclopropane-1-carboxyla	EFE	AT1G05010	-1.20	-0.26	-0.96	0.37054263	0.7436	-6.19
258649_at	putative transitional endoplasmic r	CDC48	AT3G09840	1.06	0.09	0.96	0.37065858	0.7436	-6.19
248532_at	Expressed protein ; supported by c	NFU2	AT5G49940	1.10	0.13	0.96	0.37070711	0.7436	-6.19
248738_at	unknown protein ;supported by ful	---	AT5G48020	-1.08	-0.11	-0.96	0.37067282	0.7436	-6.19
252767_at	ring-box protein-like ring-box prote	---	AT3G42830	1.08	0.12	0.96	0.37068284	0.7436	-6.19
262502_at	unknown protein similar to hypothe	PTAC6	AT1G21600	1.08	0.11	0.96	0.37085017	0.7439	-6.19
247301_at	DNA topoisomerase III	---	AT5G63920	1.12	0.17	0.96	0.37095169	0.7440	-6.19

260700_at	hypothetical protein identical to hy	---	AT1G32260	1.09	0.13	0.96	0.37123517	0.7442	-6.19
AFFX-Athal-Ub	Arabidopsis thaliana /REF=U8496	---	---	-1.06	-0.09	-0.96	0.37123972	0.7442	-6.19
266447_at	putative calcium binding protein ;s	MSS3	AT2G43290	-1.23	-0.29	-0.96	0.37110645	0.7442	-6.19
247653_at	transcriptional coactivator - like pr	---	AT5G59950	-1.07	-0.10	-0.96	0.37130198	0.7442	-6.19
259274_at	putative homeobox-leucine zipper	ATHB20	AT3G01220	1.07	0.10	0.96	0.37121498	0.7442	-6.19
262743_at	unknown protein similar to unknow	---	AT1G29020	-1.08	-0.12	-0.96	0.37132844	0.7442	-6.19
255236_at	score=11.7, E=0.66,N=1	ATEHD2	AT4G05520	-1.14	-0.18	-0.96	0.37126079	0.7442	-6.19
255006_at	putative protein kinase M.sativa m	---	AT4G10010	1.07	0.10	0.96	0.37126896	0.7442	-6.19
251498_at	putative protein hypothetical protei	---	AT3G59070	1.09	0.13	0.96	0.37137086	0.7442	-6.19
264322_at	unknown protein Contains similarit	---	AT1G04190	1.09	0.12	0.96	0.37169452	0.7444	-6.19
247080_at	20S proteasome subunit PAD2 (gb	PAD2	AT5G66140	1.08	0.12	0.96	0.37170323	0.7444	-6.19
254993_at	putative protein kinase	---	AT4G10730	1.07	0.10	0.96	0.3716378	0.7444	-6.19
259241_at	unknown protein similar to unknow	---	AT3G33530	1.07	0.09	0.96	0.37163767	0.7444	-6.19
247663_at	putative protein predicted proteins	APUM18	AT5G60110	1.07	0.09	0.96	0.37169442	0.7444	-6.19
250488_at	beta-glucosidase - like protein bet	---	AT5G09700	-1.08	-0.11	-0.96	0.37166597	0.7444	-6.19
251813_at	Expressed protein ; supported by f	TON1A	AT3G55000	1.10	0.14	0.96	0.37152824	0.7444	-6.19
248615_at	putative protein contains similarity	AtPNG1	AT5G49570	1.13	0.18	0.96	0.37152083	0.7444	-6.19
248849_at	multidrug resistance p-glycoprotein	PGP7	AT5G46540	-1.07	-0.10	-0.96	0.37181609	0.7445	-6.19
260068_at	putative calmodulin-binding protein	---	AT1G73805	1.27	0.35	0.96	0.37183515	0.7445	-6.19
257265_at	PHD-finger protein, putative conta	---	AT3G14980	-1.09	-0.12	-0.96	0.3719116	0.7445	-6.19
252805_at	putative protein	---	AT3G42380	-1.07	-0.09	-0.96	0.3718875	0.7445	-6.19
246704_at	putative protein	---	AT5G28090	-1.08	-0.11	-0.96	0.37194937	0.7446	-6.19
266296_at	putative glutathione S-transferase	ATGSTU7	AT2G29420	1.10	0.13	0.96	0.37206417	0.7446	-6.19
245405_at	hypothetical protein	---	AT4G17150	1.06	0.09	0.96	0.37216488	0.7446	-6.19
266812_at	putative protein kinase contains a	---	AT2G44830	-1.11	-0.15	-0.96	0.37255756	0.7446	-6.19
251538_at	putative protein PBK1 protein, Ho	---	AT3G58660	-1.13	-0.18	-0.96	0.37231289	0.7446	-6.19
262375_at	unknown protein ; supported by cD	SUVH3	AT1G73100	1.09	0.13	0.96	0.3725785	0.7446	-6.19
265897_at	hypothetical protein predicted by g	MOT1	AT2G25680	-1.14	-0.19	-0.96	0.37234703	0.7446	-6.19
267454_at	putative U5 small nuclear ribonucl	---	AT2G33730	-1.07	-0.10	-0.96	0.37241392	0.7446	-6.19
258471_at	NPK1-related protein kinase 3 ide	ANP3	AT3G06030	-1.08	-0.11	-0.96	0.37236644	0.7446	-6.19
246959_at	unknown protein	---	AT5G24690	1.17	0.23	0.96	0.37215871	0.7446	-6.19
259875_s_at	12-oxophytodienoate reductase (O	OPR1	AT1G76680	-1.25	-0.32	-0.96	0.37233189	0.7446	-6.19
253772_at	Expressed protein ; supported by f	A7	AT4G28395	1.06	0.09	0.96	0.37207688	0.7446	-6.19
249538_at	kanadaptin - like protein unnamed	---	AT5G38840	-1.07	-0.10	-0.96	0.37213785	0.7446	-6.19
248141_at	unknown protein	---	AT5G55010	1.08	0.10	0.96	0.37238341	0.7446	-6.19

250587_at	putative protein contains similarity	---	AT5G07640	-1.07	-0.10	-0.96	0.37241583	0.7446	-6.19
266328_at	unknown protein ; supported by fu	---	AT2G01600	1.06	0.09	0.96	0.37248767	0.7446	-6.19
262160_at	hypothetical protein predicted by g	---	AT1G52590	-1.15	-0.20	-0.96	0.37251348	0.7446	-6.19
267440_at	putative anthranilate N-hydroxycin	SHT	AT2G19070	-1.08	-0.11	-0.96	0.37244481	0.7446	-6.19
251464_at	farnesyltransferase subunit A (FTA	FTA	AT3G59380	1.10	0.13	0.96	0.37257451	0.7446	-6.19
264067_x_at	putative chloroplast nucleoid DNA	---	AT2G28010	-1.10	-0.13	-0.96	0.37224542	0.7446	-6.19
248011_at	S-adenosyl-L-methionine:salicylic a	GAMT2	AT5G56300	-1.06	-0.09	-0.95	0.37264714	0.7446	-6.19
262184_at	hypothetical protein contains simila	---	AT1G77910	1.06	0.09	0.95	0.37266297	0.7446	-6.19
260334_at	homeotic protein (ATK1) identical t	KNAT2	AT1G70510	-1.07	-0.10	-0.95	0.37281177	0.7447	-6.19
264371_at	pEARLI 1-like protein may be indu	ELP	AT1G12090	-1.16	-0.22	-0.95	0.37276091	0.7447	-6.19
257500_s_at	putative serine carboxypeptidase	scpl2	AT1G73300	-1.06	-0.09	-0.95	0.37278937	0.7447	-6.19
260987_at	hypothetical protein predicted by g	NTMC2T6.	AT1G53590	1.10	0.14	0.95	0.37285542	0.7447	-6.19
258000_at	AIG2-like protein similar to AIG2 pr	---	AT3G28940	-1.15	-0.20	-0.95	0.37289164	0.7447	-6.19
266163_at	hypothetical protein predicted by g	---	AT2G28130	1.13	0.17	0.95	0.37316494	0.7448	-6.19
246572_at	putative protein predicted proteins	---	AT5G15010	-1.08	-0.12	-0.95	0.37315567	0.7448	-6.19
254222_at	hypothetical protein	---	AT4G23840	-1.09	-0.12	-0.95	0.37325017	0.7448	-6.19
265084_at	hypothetical protein contains Cys3	SOM	AT1G03790	-1.08	-0.11	-0.95	0.37326109	0.7448	-6.19
253751_at	hypothetical protein ;supported by	---	AT4G29070	-1.16	-0.21	-0.95	0.37305449	0.7448	-6.19
257542_at	hypothetical protein predicted by g	---	AT3G26050	1.07	0.09	0.95	0.37322352	0.7448	-6.19
260192_at	putative DNA polymerase alpha su	POLA2	AT1G67630	1.25	0.32	0.95	0.37300055	0.7448	-6.19
245163_at	putative flavin-containing monooxy	---	AT2G33230	-1.10	-0.14	-0.95	0.3730738	0.7448	-6.19
266539_at	similar to mammalian MHC III regi	SUVH5	AT2G35160	1.09	0.12	0.95	0.37321638	0.7448	-6.19
246332_at	putative protein phosphatidylcholi	---	AT3G44830	-1.10	-0.14	-0.95	0.37309538	0.7448	-6.19
266472_at	unknown protein	---	AT2G31150	-1.06	-0.09	-0.95	0.37336653	0.7448	-6.19
260435_at	putative transcription factor similar	MYB62	AT1G68320	-1.20	-0.26	-0.95	0.37335671	0.7448	-6.19
248506_at	adenylate kinase ;supported by fu	---	AT5G50370	-1.22	-0.29	-0.95	0.37339392	0.7448	-6.19
250157_at	prx10 peroxidase - like protein prx	---	AT5G15180	1.08	0.11	0.95	0.37338383	0.7448	-6.19
260641_at	hypothetical protein predicted by g	---	AT1G53200	1.16	0.21	0.95	0.37353301	0.7449	-6.19
263861_at	hypothetical protein	---	AT2G04560	-1.12	-0.17	-0.95	0.37349792	0.7449	-6.19
266390_at	hypothetical protein predicted by g	---	AT2G32310	-1.07	-0.10	-0.95	0.37350635	0.7449	-6.19
250439_at	14-3-3 protein GF14lambda (grf6/A	GRF6	AT5G10450	1.08	0.11	0.95	0.37356855	0.7449	-6.19
245364_at	hypothetical protein ;supported by	---	AT4G15790	1.10	0.14	0.95	0.37380422	0.7453	-6.19
253978_at	putative protein probable kinesin -	---	AT4G26660	-1.10	-0.13	-0.95	0.37379253	0.7453	-6.19
258825_at	unknown protein	---	AT3G07180	1.07	0.10	0.95	0.37390075	0.7454	-6.19
265131_at	putative polygalacuronase isoenzy	JP630	AT1G23760	-1.20	-0.26	-0.95	0.37401616	0.7454	-6.19

265589_at	hypothetical protein predicted by g	---	AT2G20170	-1.08	-0.12	-0.95	0.37404905	0.7454	-6.19
244959_s_at	hypothetical protein	---	AT2G07708	-1.11	-0.15	-0.95	0.3740841	0.7454	-6.19
260658_at	hypothetical protein predicted by g	---	AT1G19410	-1.09	-0.13	-0.95	0.37408676	0.7454	-6.19
265358_at	putative HesB-like protein ; suppo	---	AT2G16710	1.11	0.15	0.95	0.37403197	0.7454	-6.19
245971_at	putative protein ; supported by cD	NPH4	AT5G20730	-1.08	-0.11	-0.95	0.37420408	0.7455	-6.19
267560_at	putative cytochrome P450	CYP76C3	AT2G45580	-1.09	-0.12	-0.95	0.37417233	0.7455	-6.19
259195_at	hypothetical protein predicted by g	---	AT3G01730	-1.09	-0.12	-0.95	0.37414415	0.7455	-6.19
253330_at	putative potassium transporter AtK	KUP5	AT4G33530	1.07	0.10	0.95	0.37443205	0.7455	-6.19
247607_at	putative protein various predicted	---	AT5G60960	1.15	0.21	0.95	0.37444923	0.7455	-6.19
252506_at	putative protein UDP-galactose tra	UTR5	AT3G46180	1.09	0.12	0.95	0.37442211	0.7455	-6.19
256029_at	integral membrane protein, putativ	STT3B	AT1G34130	1.16	0.22	0.95	0.37426871	0.7455	-6.19
255720_at	phosphoribulokinase precursor ide	PRK	AT1G32060	1.08	0.11	0.95	0.37446481	0.7455	-6.19
262550_at	hypothetical protein similar to hypo	---	AT1G31310	-1.08	-0.10	-0.95	0.37440254	0.7455	-6.19
255030_at	putative protein retrovirus-related p	---	---	1.08	0.11	0.95	0.37431726	0.7455	-6.19
254294_at	putative membrane protein memb	ATRBL7	AT4G23070	-1.15	-0.20	-0.95	0.3745451	0.7456	-6.19
249283_at	amino acid permease-like protein;	---	AT5G41800	-1.11	-0.16	-0.95	0.37460932	0.7457	-6.19
248577_at	myrosinase binding protein-like ; s	---	AT5G49870	-1.06	-0.09	-0.95	0.37462362	0.7457	-6.19
263828_at	putative GDSL-motif lipase/hydrola	---	AT2G40250	-1.10	-0.14	-0.95	0.37466084	0.7457	-6.19
258456_at	putative protein kinase similar to m	WNK2	AT3G22420	1.23	0.30	0.95	0.37473459	0.7457	-6.19
258481_at	putative phosphatidate phosphohy	LPP3	AT3G02600	1.11	0.15	0.95	0.37475345	0.7457	-6.19
255916_at	putative protein	---	AT5G28550	-1.09	-0.13	-0.95	0.37481068	0.7458	-6.19
261058_at	histone, putative similar to histone	HTR12	AT1G01370	1.07	0.09	0.95	0.37494157	0.7460	-6.19
259139_at	hypothetical protein similar to F16N	---	AT3G10240	-1.08	-0.11	-0.95	0.37498758	0.7460	-6.19
245133_at	putative nucleotide sugar epimeras	GAE4	AT2G45310	1.13	0.18	0.95	0.37503332	0.7460	-6.19
261207_at	peroxisomal targeting signal type 2	---	AT1G12830	1.13	0.17	0.95	0.37518056	0.7462	-6.19
250192_at	pescadillo - like protein embryonic	---	AT5G14520	1.13	0.17	0.95	0.37527238	0.7462	-6.19
267310_at	unknown protein	AIR9	AT2G34680	-1.23	-0.30	-0.95	0.37530807	0.7462	-6.19
264692_at	DNA binding protein MybSt1, puta	---	AT1G70000	1.10	0.14	0.95	0.3754135	0.7462	-6.19
267356_at	putative isoamylase	ISA1	AT2G39930	-1.08	-0.11	-0.95	0.37537881	0.7462	-6.19
263406_at	subtilisin-like serine protease AIR3	AIR3	AT2G04160	-1.23	-0.30	-0.95	0.3753292	0.7462	-6.19
261164_at	hypothetical protein ;supported by	---	AT1G34470	1.08	0.12	0.95	0.37539924	0.7462	-6.19
258600_at	putative protein kinase contains Pf	---	AT3G02810	1.08	0.11	0.95	0.37530443	0.7462	-6.19
252848_at	putative protein several hypothetic	---	---	-1.09	-0.12	-0.95	0.37547113	0.7463	-6.20
265349_at	putative kinesin heavy chain	---	AT2G22610	1.09	0.12	0.95	0.37548885	0.7463	-6.20
267527_at	unknown protein	---	AT2G45610	1.09	0.13	0.95	0.37553893	0.7463	-6.20

265807_at	unknown protein	---	AT2G17990	1.08	0.11	0.95	0.37561668	0.7464	-6.20
257178_at	hemolysin-like protein similar to he	---	AT3G13070	1.09	0.12	0.95	0.37575203	0.7466	-6.20
247356_at	beta-galactosidase (emb|CAB6474	MUM2	AT5G63800	-1.16	-0.22	-0.95	0.37578668	0.7466	-6.20
245757_at	phosphate-induced (phi-1) protein	PHI-1	AT1G35140	1.49	0.58	0.95	0.37612389	0.7466	-6.20
253855_at	senescence-associated protein -li	TET7	AT4G28050	1.22	0.29	0.95	0.37631621	0.7466	-6.20
261526_at	protein kinase identical to protein k	APK2A	AT1G14370	1.15	0.20	0.95	0.37598446	0.7466	-6.20
256568_at	hypothetical protein ;supported by	---	AT3G19520	1.07	0.10	0.95	0.37611942	0.7466	-6.20
246390_at	1-aminocyclopropane-1-carboxyla	---	AT1G77330	-1.11	-0.15	-0.95	0.37633487	0.7466	-6.20
257302_at	hypothetical protein predicted by g	---	AT3G30220	-1.07	-0.09	-0.95	0.37631884	0.7466	-6.20
257135_at	hypothetical protein similar to oxid	---	AT3G12900	-1.10	-0.13	-0.95	0.37632287	0.7466	-6.20
257505_at	hypothetical protein	---	AT1G47940	-1.06	-0.08	-0.95	0.37597085	0.7466	-6.20
249710_at	glutamate-ammonia ligase (EC 6.3	GS2	AT5G35630	1.08	0.11	0.95	0.37612769	0.7466	-6.20
251093_at	putative protein several hypothetic	---	AT5G01360	-1.13	-0.18	-0.95	0.37613914	0.7466	-6.20
264578_at	hypothetical protein predicted by g	---	AT1G05370	1.06	0.09	0.95	0.3758691	0.7466	-6.20
254055_at	hypothetical protein	---	AT4G25330	-1.07	-0.10	-0.95	0.37609371	0.7466	-6.20
258790_at	putative RNA-binding protein simila	FLK	AT3G04610	1.06	0.09	0.95	0.37604087	0.7466	-6.20
247514_at	peptide methionine sulfoxide redu	PMSR1	AT5G61640	-1.10	-0.13	-0.95	0.3762201	0.7466	-6.20
263991_at	putative retroelement pol polyprote	---	---	-1.11	-0.15	-0.95	0.37626675	0.7466	-6.20
261744_at	nitrogen fixation protein (nifS), put	CPNIFS	AT1G08490	1.09	0.12	0.95	0.37600289	0.7466	-6.20
250944_at	putative protein	---	AT5G03380	-1.31	-0.39	-0.95	0.37637204	0.7467	-6.20
260303_at	putative protein kinase similar to C	---	AT1G70520	-1.17	-0.23	-0.95	0.37649843	0.7468	-6.20
263563_at	putative retroelement pol polyprote	---	---	-1.08	-0.11	-0.95	0.37658987	0.7470	-6.20
265470_at	putative protein with C-terminal RI	---	AT2G37150	1.10	0.13	0.95	0.37666699	0.7470	-6.20
256087_at	hypothetical protein predicted by g	---	AT1G20800	-1.07	-0.10	-0.95	0.37680819	0.7471	-6.20
255432_at	SYR1-like syntaxin ;supported by	SYP123	AT4G03330	-1.07	-0.10	-0.95	0.3767851	0.7471	-6.20
257511_at	hypothetical protein	---	AT1G43000	-1.08	-0.12	-0.95	0.376811	0.7471	-6.20
245548_at	cytochrome P450 like protein	CYP702A3	AT4G15310	-1.06	-0.09	-0.95	0.37679777	0.7471	-6.20
246212_at	putative protein ; supported by cDN	SPT	AT4G36930	1.26	0.33	0.95	0.37705488	0.7472	-6.20
253843_at	putative protein MLL protein, Gallu	SDG16	AT4G27910	-1.06	-0.09	-0.95	0.37701939	0.7472	-6.20
251318_at	putative protein putative protein At	GDAP1	AT3G61570	-1.07	-0.10	-0.95	0.37699317	0.7472	-6.20
264977_at	unknown protein	---	AT1G27090	-1.13	-0.18	-0.95	0.37706113	0.7472	-6.20
251383_at	beta-tubulin cofactor - like protein	TTN1	AT3G60740	1.13	0.17	0.95	0.37700852	0.7472	-6.20
263878_s_at	unknown protein	---	AT2G22040 /	1.09	0.13	0.95	0.37704573	0.7472	-6.20
255594_at	putative ABC transporter	ATABC1	AT4G01660	-1.08	-0.10	-0.95	0.37712856	0.7472	-6.20
260601_at	Expressed protein ; supported by c	ZIP11	AT1G55910	1.14	0.19	0.95	0.37719552	0.7473	-6.20

253512_at	putative protein protein phosphata	WIN2	AT4G31750	-1.08	-0.11	-0.95	0.37730889	0.7475	-6.20
264697_at	cyclin, putative similar to cyclin D	CYCD1;1	AT1G70210	1.40	0.49	0.94	0.37734645	0.7475	-6.20
249549_at	lipid transfer - like protein lipid tran	---	AT5G38180	1.08	0.11	0.94	0.37736339	0.7475	-6.20
257792_at	TOM20, putative similar to TOM20	TOM20-3	AT3G27080	1.09	0.13	0.94	0.37743168	0.7475	-6.20
261861_at	hypothetical protein predicted by g	---	AT1G50450	-1.17	-0.23	-0.94	0.37757282	0.7476	-6.20
245483_at	cysteine proteinase contains simila	---	AT4G16190	1.07	0.10	0.94	0.37769267	0.7476	-6.20
261110_at	E2, ubiquitin-conjugating enzyme	UBC16	AT1G75440	-1.11	-0.15	-0.94	0.37748765	0.7476	-6.20
267207_at	putative dioxygenase	---	AT2G30840	1.20	0.27	0.94	0.37762283	0.7476	-6.20
253984_at	isp4 like protein isp4 protein -Schi	OPT5	AT4G26590	-1.08	-0.12	-0.94	0.37759875	0.7476	-6.20
258672_at	hypothetical protein	---	AT3G08570	1.09	0.12	0.94	0.37771599	0.7476	-6.20
257327_at	hypothetical protein	---	---	-1.14	-0.19	-0.94	0.37765622	0.7476	-6.20
267276_at	hypothetical protein predicted by g	ASL5	AT2G30130	1.07	0.10	0.94	0.37768084	0.7476	-6.20
265290_at	putative anthocyanidin-3-glucoside	---	AT2G22590	-1.07	-0.10	-0.94	0.37779329	0.7477	-6.20
252704_at	putative protein KIAA0161 gene, H	---	AT3G43750	-1.08	-0.11	-0.94	0.37788414	0.7478	-6.20
263641_at	putative non-LTR retroelement rev	---	---	-1.07	-0.09	-0.94	0.37801866	0.7480	-6.20
259211_at	unknown protein identical to GB:A/	---	AT3G09020	1.31	0.39	0.94	0.37816924	0.7482	-6.20
260290_at	hypothetical protein predicted by g	---	AT1G80510	-1.08	-0.11	-0.94	0.37823988	0.7482	-6.20
245525_at	dynein light chain like protein	---	AT4G15930	1.06	0.08	0.94	0.37826519	0.7482	-6.20
245382_at	hypothetical protein	---	AT4G17800	1.08	0.11	0.94	0.37831341	0.7482	-6.20
262240_at	Pto kinase interactor 1, putative si	---	AT1G48220	1.08	0.11	0.94	0.37829597	0.7482	-6.20
249328_at	AtRAD3 (dbj|BAA92828.1) ; suppo	ATR	AT5G40820	-1.09	-0.12	-0.94	0.37838643	0.7483	-6.20
254642_at	putative protein hypothetical prote	---	AT4G18810	-1.14	-0.19	-0.94	0.37845016	0.7484	-6.20
256671_at	unknown protein	IQD3	AT3G52290	-1.12	-0.16	-0.94	0.37867284	0.7487	-6.20
248556_at	unknown protein	---	AT5G50350	1.10	0.13	0.94	0.37874756	0.7488	-6.20
257082_at	hypothetical protein	COBL10	AT3G20580	-1.07	-0.10	-0.94	0.37886637	0.7490	-6.20
264405_at	putative mitogen-activated protein	ATMPK1	AT1G10210	1.16	0.22	0.94	0.37894769	0.7491	-6.20
266995_at	putative cytochrome P450	CYP710A1	AT2G34500	1.39	0.47	0.94	0.37921555	0.7492	-6.20
252694_at	nodulin -like protein nodulin-21, G	---	AT3G43630	-1.08	-0.11	-0.94	0.37906506	0.7492	-6.20
249365_at	putative protein predicted protein,	---	AT5G40600	1.08	0.11	0.94	0.37917792	0.7492	-6.20
267216_at	hypothetical protein	---	AT2G02620	-1.08	-0.11	-0.94	0.37913974	0.7492	-6.20
255963_at	unknown protein	MBD8	AT1G22310	-1.08	-0.11	-0.94	0.3792113	0.7492	-6.20
258984_at	putative DnaJ protein Pfam HMM	ATERDJ3A	AT3G08970	-1.09	-0.13	-0.94	0.37908753	0.7492	-6.20
264962_at	auxin transport protein EIR1, puta	PIN6	AT1G77110	-1.11	-0.15	-0.94	0.3793099	0.7494	-6.20
264957_at	F-box protein family, AtFBL5 cont	SKP2B	AT1G77000	-1.14	-0.19	-0.94	0.37967223	0.7495	-6.20
246579_at	hypothetical protein predicted by g	---	AT1G31620	-1.09	-0.13	-0.94	0.37961528	0.7495	-6.20

264970_at	glyoxalase I, putative similar to gly	---	AT1G67280	1.07	0.10	0.94	0.37969604	0.7495	-6.20
257382_at	hypothetical protein predicted by g	WRKY54	AT2G40750	-1.68	-0.74	-0.94	0.37963572	0.7495	-6.20
267154_at	glutathione S-transferase identical	GSTF10	AT2G30870	-1.26	-0.33	-0.94	0.37945955	0.7495	-6.20
255050_at	putative protein hypothetical prote	---	---	-1.10	-0.14	-0.94	0.37947988	0.7495	-6.20
261995_at	unknown protein similar to N-termi	---	AT1G33850 /	-1.06	-0.08	-0.94	0.37965478	0.7495	-6.20
266555_at	G-box binding bZIP transcription fa	GBF3	AT2G46270	-1.19	-0.25	-0.94	0.37958044	0.7495	-6.20
248373_at	MADS box transcription factor-like	---	AT5G51860	-1.10	-0.14	-0.94	0.37953113	0.7495	-6.20
266383_at	putative pathogenesis related-1 (P	ATPRB1	AT2G14580	1.12	0.16	0.94	0.37952961	0.7495	-6.20
264678_at	putative U2 small nuclear ribonucl	U2A'	AT1G09760	1.08	0.11	0.94	0.37986675	0.7497	-6.20
258854_at	putative UDP-glucosyl transferase	---	AT3G02100	-1.08	-0.12	-0.94	0.3799563	0.7499	-6.20
267339_at	unknown protein ; supported by cl	---	AT2G39870	-1.15	-0.20	-0.94	0.38010433	0.7501	-6.20
257857_s_at	unknown protein contains an RNas	RRP45a	AT3G12990 /	1.12	0.17	0.94	0.38022046	0.7502	-6.20
261542_at	unknown protein contains Pfam pr	---	AT1G63560	-1.09	-0.12	-0.94	0.38031272	0.7503	-6.20
254698_at	NAM (no apical meristem) - like pr	anac071	AT4G17980	1.06	0.08	0.94	0.38029688	0.7503	-6.20
247897_at	unknown protein ;supported by ful	TET15	AT5G57810	1.07	0.10	0.94	0.38050067	0.7506	-6.21
251539_at	serine/threonine-specific protein k	---	AT3G58690	1.10	0.14	0.94	0.38054579	0.7506	-6.21
249760_at	(+)-delta-cadinene synthase (d-cad	TPS21	AT5G23960	-1.06	-0.09	-0.94	0.38076544	0.7508	-6.21
254542_s_at	putative LTR retrotransposon Bras	---	---	-1.06	-0.09	-0.94	0.38071517	0.7508	-6.21
263832_at	putative polygalacturonase	---	AT2G40310	-1.06	-0.08	-0.94	0.38067973	0.7508	-6.21
247499_at	predicted protein	---	AT5G61865	1.08	0.11	0.94	0.38077542	0.7508	-6.21
255054_s_at	cellulase-like protein cellulase (EC	AtGH9B15	AT4G09740 /	1.08	0.11	0.94	0.38072152	0.7508	-6.21
256185_at	dof zinc finger protein identical to c	ADOF1	AT1G51700	1.25	0.32	0.94	0.3809959	0.7508	-6.21
256068_at	hypothetical protein contains simila	ATE1	AT1G13690	1.07	0.10	0.94	0.38113704	0.7508	-6.21
264700_at	hypothetical protein predicted by g	---	AT1G70100	1.10	0.13	0.94	0.38089558	0.7508	-6.21
258497_at	putative flowering-time gene CONS	COL2	AT3G02380	-1.08	-0.11	-0.94	0.38097356	0.7508	-6.21
257027_at	DNA repair protein, putative simila	ATRAD54	AT3G19210	1.07	0.10	0.94	0.38099467	0.7508	-6.21
246093_at	ethylene-forming-enzyme-like diox	---	AT5G20550	1.08	0.11	0.94	0.38114061	0.7508	-6.21
255721_at	unknown protein ;supported by full	---	AT1G31940	-1.07	-0.09	-0.94	0.38113954	0.7508	-6.21
265982_at	putative retroelement pol polyprote	---	---	-1.06	-0.09	-0.94	0.38104751	0.7508	-6.21
259548_at	hypothetical protein similar to riper	MLP165	AT1G35260	-1.20	-0.26	-0.94	0.38085414	0.7508	-6.21
253325_at	Expressed protein ; supported by f	---	AT4G33925	-1.16	-0.21	-0.94	0.38105505	0.7508	-6.21
246933_at	ZFP3 zinc finger protein ; supporte	ZFP3	AT5G25160	-1.06	-0.08	-0.94	0.38110147	0.7508	-6.21
264777_at	unknown protein similar to L-allo-t	THA1	AT1G08630	1.36	0.44	0.94	0.38134085	0.7508	-6.21
251760_at	Expressed protein ; supported by f	---	AT3G55605	1.15	0.20	0.94	0.3813398	0.7508	-6.21
247130_at	putative protein contains similarity	---	AT5G66180	1.16	0.21	0.94	0.38141506	0.7508	-6.21

257248_at	hypothetical protein predicted by g	---	AT3G24150	-1.11	-0.15	-0.94	0.38132035	0.7508	-6.21
252390_at	Expressed protein ; supported by c	---	AT3G47836	1.09	0.12	0.94	0.38142961	0.7508	-6.21
262945_at	unknown protein ;supported by full	---	AT1G79510	-1.15	-0.20	-0.94	0.38136803	0.7508	-6.21
253226_at	beta-galactosidase - like protein b	BGAL11	AT4G35010	1.07	0.10	0.94	0.38127901	0.7508	-6.21
256947_at	hypothetical protein contains Pfam	POK2	AT3G19050	1.06	0.08	0.94	0.3814228	0.7508	-6.21
260418_s_at	hypothetical protein predicted by g	COX19-1	AT1G66590 /	1.20	0.26	0.94	0.38160177	0.7508	-6.21
265948_at	1-aminocyclopropane-1-carboxylat	ACO1	AT2G19590	-1.08	-0.12	-0.94	0.38154987	0.7508	-6.21
258536_at	Rab escort protein, putative simila	---	AT3G06540	1.09	0.12	0.94	0.38155193	0.7508	-6.21
256900_at	pectate lyase, putative similar to p	---	AT3G24670	1.09	0.13	0.94	0.38152343	0.7508	-6.21
247146_at	unknown protein	---	AT5G65610	1.13	0.17	0.94	0.38158087	0.7508	-6.21
257227_at	monodehydroascorbate reductase	MDAR4	AT3G27820	1.08	0.11	0.94	0.38190589	0.7509	-6.21
246865_s_at	eukaryotic translation initiation fac	TIF3B1	AT5G25780 /	1.06	0.08	0.94	0.38182248	0.7509	-6.21
247988_at	putative protein similar to unknown	---	AT5G56910	-1.12	-0.17	-0.94	0.38176423	0.7509	-6.21
245578_at	RNA helicase like protein	ATSUV3	AT4G14790	-1.10	-0.13	-0.94	0.38185399	0.7509	-6.21
250706_at	deoxyhypusine synthase ;support	DHS	AT5G05920	-1.09	-0.13	-0.94	0.38194595	0.7509	-6.21
247708_at	putative protein COP1-interacting	---	AT5G59550	1.33	0.41	0.94	0.38181111	0.7509	-6.21
249171_at	putative protein contains similarity	---	AT5G42940	1.10	0.14	0.94	0.38177583	0.7509	-6.21
255997_s_at	photosystem II type I chlorophyll a	CAB3	AT1G29910 /	1.12	0.16	0.94	0.38192445	0.7509	-6.21
265155_at	putative major latex protein type 1	---	AT1G30990	-1.08	-0.11	-0.94	0.3816985	0.7509	-6.21
259148_at	putative ATPase similar to ATPas	---	AT3G10350	-1.09	-0.13	-0.94	0.38167216	0.7509	-6.21
248081_at	putative protein similar to unknown	EDM2	AT5G55390	-1.07	-0.09	-0.93	0.38220804	0.7509	-6.21
260959_at	unknown protein ;supported by full	---	AT1G06050	-1.08	-0.11	-0.93	0.38216973	0.7509	-6.21
256521_at	AMP-binding enzyme, putative co	---	AT1G66120	-1.08	-0.11	-0.93	0.38222058	0.7509	-6.21
253481_at	aspartate aminotransferase ;supp	ASP5	AT4G31990	1.08	0.11	0.93	0.38216982	0.7509	-6.21
266602_at	hypothetical protein predicted by g	---	AT2G46050	-1.06	-0.08	-0.94	0.38207815	0.7509	-6.21
249305_at	putative protein strong similarity to	---	AT5G41490	-1.09	-0.12	-0.94	0.3820365	0.7509	-6.21
264934_at	hypothetical protein predicted by g	---	AT1G61090	1.07	0.10	0.93	0.38219466	0.7509	-6.21
267353_at	En/Spm-like transposon protein rel	---	AT2G40070	-1.10	-0.14	-0.94	0.38203531	0.7509	-6.21
258737_at	unknown protein similar to unknow	---	AT3G05940	-1.07	-0.10	-0.93	0.38228128	0.7509	-6.21
248806_at	putative protein contains similarity	---	AT5G47490	-1.07	-0.10	-0.93	0.38235328	0.7510	-6.21
264927_at	phosphatidylinositol 3-kinase, puta	VPS34	AT1G60490	1.06	0.08	0.93	0.38249974	0.7512	-6.21
265949_at	putative vicilin storage protein (glo	---	AT2G18540	1.06	0.09	0.93	0.3825457	0.7513	-6.21
249255_at	Na+/H+ antiporter-like protein	CHX18	AT5G41610	1.09	0.13	0.93	0.38269708	0.7514	-6.21
247379_at	unknown protein	---	---	-1.10	-0.14	-0.93	0.38270641	0.7514	-6.21
259780_at	exonuclease, putative similar to G	---	AT1G29630	1.07	0.10	0.93	0.38269411	0.7514	-6.21

252378_at	receptor kinase-like protein protei	---	AT3G47570	-1.13	-0.17	-0.93	0.3827809	0.7515	-6.21
251150_at	putative protein Sb34 (PREG-like	CYCP1;1	AT3G63120	1.09	0.12	0.93	0.38299776	0.7516	-6.21
267130_at	hypothetical protein predicted by g	---	AT2G23390	1.11	0.15	0.93	0.38307516	0.7516	-6.21
254508_at	putative protein gene F4P9.34 chr	---	AT4G20170	1.09	0.13	0.93	0.38306888	0.7516	-6.21
262067_at	hypothetical protein predicted by g	---	AT1G80060	-1.09	-0.13	-0.93	0.38302765	0.7516	-6.21
248392_at	integral membrane protein-like	---	AT5G52050	-1.48	-0.56	-0.93	0.38291243	0.7516	-6.21
255932_at	mutator-like transposase, putative	---	---	-1.08	-0.10	-0.93	0.38297636	0.7516	-6.21
263608_at	putative glycine-rich RNA-binding p	---	---	-1.09	-0.13	-0.93	0.38292735	0.7516	-6.21
256955_at	L-ascorbate oxidase precursor, pu	sks11	AT3G13390	-1.11	-0.16	-0.93	0.38311877	0.7516	-6.21
255525_at	coded for by A. thaliana cDNA T04	---	AT4G02340	-1.09	-0.12	-0.93	0.38333936	0.7519	-6.21
245110_at	hypothetical protein predicted by g	---	AT2G41550	1.07	0.09	0.93	0.38334497	0.7519	-6.21
262864_at	anthocyanidin-3-glucoside rhamno	---	AT1G64920	-1.08	-0.11	-0.93	0.38340176	0.7520	-6.21
264301_at	hypothetical protein contains simila	---	AT1G78780	1.21	0.27	0.93	0.38346331	0.7520	-6.21
249109_at	auxin-induced protein AUX2-11 (sp	ATAUX2-11	AT5G43700	1.30	0.38	0.93	0.38360326	0.7520	-6.21
265586_at	pathogenesis-related protein (PR-1	PR-1-LIKE	AT2G19990	1.10	0.13	0.93	0.38362432	0.7520	-6.21
267373_at	unknown protein	CID7	AT2G26280	-1.08	-0.11	-0.93	0.38355224	0.7520	-6.21
251580_at	putative protein ethylene-responsi	---	AT3G58450	-1.11	-0.16	-0.93	0.38367786	0.7520	-6.21
249378_at	putative protein microtubule-assoc	---	AT5G40450	-1.12	-0.16	-0.93	0.38367616	0.7520	-6.21
262831_at	cytochrome B561, putative similar	---	AT1G14730	-1.14	-0.19	-0.93	0.38351534	0.7520	-6.21
245959_at	peptide transport protein-like pept	---	AT5G19640	-1.08	-0.11	-0.93	0.38364317	0.7520	-6.21
267465_at	subtilisin-like serine protease conta	SLP3	AT2G19170	-1.20	-0.26	-0.93	0.38378258	0.7521	-6.21
258778_s_at	hypothetical protein predicted by g	---	AT3G11860 /	1.09	0.12	0.93	0.38380058	0.7521	-6.21
263171_at	unknown protein	CCX4	AT1G54115	1.08	0.11	0.93	0.38390598	0.7522	-6.21
250163_at	putative protein various predicted	---	AT5G15270	-1.09	-0.12	-0.93	0.38390318	0.7522	-6.21
258384_at	hypothetical protein predicted by g	---	AT3G15490	1.07	0.10	0.93	0.38399187	0.7522	-6.21
257566_x_at	hypothetical protein predicted by g	---	---	-1.07	-0.09	-0.93	0.38397295	0.7522	-6.21
252083_at	putative protein hypothetical prote	---	AT3G51960	-1.20	-0.26	-0.93	0.38393652	0.7522	-6.21
257711_at	20S proteasome beta subunit (PB	PBB1	AT3G27430	-1.08	-0.11	-0.93	0.3840507	0.7522	-6.21
263212_at	unknown protein similar to ribonuc	emb2004	AT1G10510	1.08	0.11	0.93	0.38415095	0.7523	-6.21
251291_at	putative protein auxin-induced pro	---	AT3G61900	-1.07	-0.10	-0.93	0.38427944	0.7524	-6.21
262196_at	ubiquitin-fusion protein, putative s	MUB5	AT1G77870	1.16	0.22	0.93	0.38426178	0.7524	-6.21
257981_at	ethylene-insensitive 3 (EIN3) ident	EIN3	AT3G20770	1.07	0.10	0.93	0.38422665	0.7524	-6.21
263781_at	hypothetical protein predicted by g	---	AT2G46360	1.06	0.08	0.93	0.3843397	0.7524	-6.21
246184_at	beta-D-glucan exohydrolase - like	---	AT5G20950	-1.13	-0.17	-0.93	0.38442697	0.7526	-6.21
260896_at	flower pigmentation protein ATAN1	---	AT1G29310	1.16	0.21	0.93	0.38452049	0.7526	-6.21

257888_at	seed maturation protein, putative s	---	AT3G16990	1.14	0.19	0.93	0.38449358	0.7526	-6.21
264853_at	putative ligand-gated ion channel p	GLR2	AT2G17260 /	-1.09	-0.13	-0.93	0.38452813	0.7526	-6.21
250863_at	F1F0-ATPase inhibitor - like prote	---	AT5G04750	1.06	0.09	0.93	0.3845863	0.7526	-6.21
246117_at	CAF-like protein CAF protein - Ara	DCL4	AT5G20320	-1.12	-0.16	-0.93	0.3849251	0.7528	-6.21
246951_at	unknown protein	---	AT5G04880	1.17	0.22	0.93	0.38489828	0.7528	-6.21
260768_at	Expressed protein ; supported by f	---	AT1G49245	1.08	0.11	0.93	0.38478438	0.7528	-6.21
247423_at	putative protein predicted proteins	---	AT5G62830	-1.07	-0.09	-0.93	0.38481472	0.7528	-6.21
266596_at	hypothetical protein predicted by g	---	AT2G46150	-1.21	-0.27	-0.93	0.38489576	0.7528	-6.21
259000_at	hypothetical protein predicted by g	---	AT3G01860	-1.17	-0.23	-0.93	0.38483475	0.7528	-6.21
246342_at	putative protein male sterility prote	FAR6	AT3G56700	1.07	0.09	0.93	0.38474798	0.7528	-6.21
249937_at	putative protein seed maturation pr	---	AT5G22470	-1.10	-0.14	-0.93	0.38494335	0.7528	-6.21
247701_at	putative protein many predicted pr	---	AT5G59900	1.07	0.10	0.93	0.38502064	0.7528	-6.21
258599_at	L-allo-threonine aldolase, putative	THA2	AT3G04520	-1.13	-0.17	-0.93	0.38500782	0.7528	-6.21
259133_at	sugar transporter, putative similar	---	AT3G05400	1.17	0.23	0.93	0.38511893	0.7529	-6.21
253273_at	putative protein hypothetical prote	---	AT4G34180	1.07	0.10	0.93	0.3852048	0.7530	-6.21
246010_at	putative protein predicted proteins	---	AT5G08440	-1.06	-0.09	-0.93	0.38522491	0.7530	-6.21
266120_at	putative C2H2-type zinc finger pro	AtIDD5	AT2G02070	-1.08	-0.12	-0.93	0.38520118	0.7530	-6.21
261232_at	unknown protein ; supported by cD	---	AT1G20220	-1.07	-0.10	-0.93	0.38527315	0.7530	-6.21
248829_at	putative protein contains similarity	---	AT5G47130	-1.12	-0.17	-0.93	0.38541328	0.7532	-6.21
266788_at	putative receptor-like protein kinas	---	AT2G29000	1.06	0.08	0.93	0.38545812	0.7532	-6.21
248494_at	putative protein contains similarity	AtHSD6	AT5G50770	-1.08	-0.11	-0.93	0.38553586	0.7533	-6.21
259341_at	unknown protein similar to hypothe	ATBPM4	AT3G03740	-1.07	-0.09	-0.93	0.38560919	0.7534	-6.21
245854_at	adenosine nucleotide translocator	AAC2	AT5G13490	1.45	0.54	0.93	0.38569344	0.7535	-6.22
265147_at	hypothetical protein	---	AT1G51380	1.12	0.16	0.93	0.3859276	0.7537	-6.22
253850_at	pectinesterase like protein pectine	sks10	AT4G28090	-1.10	-0.13	-0.93	0.38601571	0.7537	-6.22
250416_at	putative protein predicted proteins	---	AT5G11220	-1.08	-0.11	-0.93	0.38591568	0.7537	-6.22
264991_s_at	putative protein hypothetical protei	---	AT1G67400 /	-1.12	-0.16	-0.93	0.38591351	0.7537	-6.22
263394_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-0.93	0.38601104	0.7537	-6.22
258738_at	hypothetical protein similar to hypo	---	AT3G05750	1.09	0.13	0.93	0.38601186	0.7537	-6.22
247665_at	putative protein various predicted	---	AT5G60130	1.06	0.09	0.93	0.38610338	0.7538	-6.22
257167_at	hypothetical protein predicted by g	chr40	AT3G24340	-1.07	-0.09	-0.93	0.38618298	0.7539	-6.22
255504_at	drought-induced-19-like 1 similar t	---	AT4G02200	1.28	0.35	0.93	0.386224	0.7539	-6.22
247896_at	26S proteasome regulatory subun	---	AT5G57950	1.07	0.09	0.93	0.3862625	0.7539	-6.22
251519_at	putative protein hypothetical prote	GUN4	AT3G59400	1.10	0.14	0.93	0.38669162	0.7545	-6.22
265377_at	putative beta-1,3-glucanase	---	AT2G05790	1.45	0.54	0.93	0.38670315	0.7545	-6.22

252212_at	protein kinase -like protein NTPK1	MAPKKK20	AT3G50310	1.20	0.26	0.93	0.3866513	0.7545	-6.22
249350_at	MYB -like protein MYB22, Arabido	MYB115	AT5G40360	-1.07	-0.10	-0.93	0.38664042	0.7545	-6.22
252057_at	putative protein ;supported by full-	---	AT3G52480	1.15	0.20	0.93	0.38668536	0.7545	-6.22
249990_at	hypothetical protein	---	AT5G18540	-1.07	-0.10	-0.93	0.38677591	0.7545	-6.22
259845_at	auxin transporter splice variant b,	PIN1	AT1G73590	-1.12	-0.16	-0.93	0.38680035	0.7545	-6.22
253239_at	putative serine/threonine protein k	---	AT4G34500	1.12	0.17	0.93	0.38684557	0.7546	-6.22
264300_at	gamma glutamyl hydrolase, putati	ATGGH3	AT1G78670	1.07	0.10	0.93	0.38689161	0.7546	-6.22
264823_at	putative serine/threonine protein pl	BSU1	AT1G03445	-1.11	-0.15	-0.92	0.38703689	0.7546	-6.22
259206_at	hypothetical protein similar to puta	---	AT3G09040	1.09	0.13	0.92	0.38710613	0.7546	-6.22
254340_at	putative protein hypothetical prote	---	AT4G22120	1.18	0.24	0.92	0.38707516	0.7546	-6.22
260603_at	membrane related protein CP5, pu	---	AT1G55960	1.12	0.17	0.92	0.38708232	0.7546	-6.22
266779_at	putative ligand-gated ion channel p	ATGLR2.9	AT2G29100	-1.09	-0.12	-0.92	0.38704861	0.7546	-6.22
249281_at	GTPase activator protein of Rab-lil	---	AT2G36460 /	-1.08	-0.11	-0.92	0.38710221	0.7546	-6.22
251865_at	protein phosphatase 2A regulatory	---	AT3G54930	1.07	0.09	0.92	0.38726049	0.7548	-6.22
249021_at	putative protein similar to unknown	---	AT5G44820	1.13	0.18	0.92	0.38725228	0.7548	-6.22
254391_at	putative bifunctional nuclease bifu	ENDO3	AT4G21590	-1.07	-0.10	-0.92	0.38737409	0.7549	-6.22
266676_s_at	hypothetical protein predicted by g	---	AT2G29605 /	-1.07	-0.10	-0.92	0.38739719	0.7549	-6.22
259523_at	hypothetical protein	---	AT1G12500	-1.14	-0.19	-0.92	0.38745399	0.7550	-6.22
250333_at	membrane translocase - like prote	TIM17-3	AT5G11690	1.15	0.20	0.92	0.38761626	0.7552	-6.22
250169_at	putative protein many predicted pr	---	AT5G15340	-1.12	-0.17	-0.92	0.38762472	0.7552	-6.22
255020_at	isoleucine-tRNA ligase - like prote	---	AT4G10320	1.06	0.08	0.92	0.38766146	0.7552	-6.22
263551_at	hypothetical protein contains NLS	---	AT2G17110	1.17	0.22	0.92	0.38769898	0.7552	-6.22
254385_s_at	putative protein CGI-131 protein, I	ATMSRB7	AT4G21830 /	-1.84	-0.88	-0.92	0.38775622	0.7552	-6.22
247947_at	auxin transport protein EIR1 (gb|A/	EIR1	AT5G57090	-1.09	-0.13	-0.92	0.38784938	0.7554	-6.22
261873_at	serine/threonine kinase, putative s	SD1-13	AT1G11350	-1.13	-0.18	-0.92	0.38794387	0.7554	-6.22
257217_at	phosphoenolpyruvate carboxylase	ATPPC3	AT3G14940	1.11	0.15	0.92	0.38791836	0.7554	-6.22
260064_at	ethylene-insensitive3-like3 (EIL3)	EIL3	AT1G73730	-1.10	-0.14	-0.92	0.38804656	0.7556	-6.22
255813_at	hypothetical protein contains Pfam	---	AT1G19930	-1.08	-0.11	-0.92	0.38818989	0.7558	-6.22
251713_at	putative protein several hypothetic	---	AT3G56080	-1.10	-0.14	-0.92	0.38825558	0.7558	-6.22
256273_at	senescence-assocated protein, pu	TET6	AT3G12090	1.09	0.12	0.92	0.38831393	0.7559	-6.22
264142_at	hypothetical protein predicted by g	---	AT1G78930	-1.11	-0.16	-0.92	0.38846302	0.7561	-6.22
249741_at	putative protein contains similarity	APRR5	AT5G24470	-1.06	-0.08	-0.92	0.38862806	0.7561	-6.22
265850_at	putative DnaJ protein	---	AT2G35720	-1.11	-0.15	-0.92	0.38860923	0.7561	-6.22
263370_at	hypothetical protein predicted by g	---	AT2G20500	-1.16	-0.21	-0.92	0.38850445	0.7561	-6.22
253844_at	hypothetical protein	---	AT4G27930	-1.09	-0.12	-0.92	0.38856901	0.7561	-6.22

247061_at	putative protein similar to unknown	---	AT5G66780	-1.12	-0.17	-0.92	0.38858163	0.7561	-6.22
261412_at	L-ascorbate peroxidase identical t	APX1	AT1G07890	-1.15	-0.20	-0.92	0.38878069	0.7563	-6.22
252290_at	putative protein various predicted	---	AT3G49140	1.09	0.12	0.92	0.38887782	0.7565	-6.22
252671_at	putative protein dehydrogenases c	---	AT3G44190	-1.10	-0.14	-0.92	0.38895948	0.7565	-6.22
249353_at	oleosin ; supported by cDNA: gi_7	OLEO2	AT5G40420	-1.09	-0.13	-0.92	0.38895724	0.7565	-6.22
254141_at	glucose-6-phosphate isomerase g	PGI1	AT4G24620	-1.07	-0.10	-0.92	0.38909761	0.7566	-6.22
249488_at	putative protein putative transposa	---	---	1.07	0.10	0.92	0.38909615	0.7566	-6.22
252977_at	Phospholipase like protein Arabid	---	AT4G38560	1.22	0.29	0.92	0.38924922	0.7569	-6.22
263774_at	unknown protein ; supported by cl	---	AT2G40280	-1.07	-0.10	-0.92	0.38937944	0.7569	-6.22
258907_at	putative sodium proton exchanger	NHX4	AT3G06370	-1.08	-0.12	-0.92	0.38933415	0.7569	-6.22
257986_at	Expressed protein ; supported by f	AGP40	AT3G20865	1.12	0.17	0.92	0.38936523	0.7569	-6.22
261805_at	hypothetical protein almost identica	---	AT1G30540	-1.08	-0.11	-0.92	0.38948847	0.7570	-6.22
246009_at	Expressed protein ; supported by c	ATSTE14B	AT5G08335	1.10	0.14	0.92	0.38946526	0.7570	-6.22
246346_at	hypothetical protein	---	AT3G56810	1.12	0.17	0.92	0.38963028	0.7571	-6.22
267158_at	putative expansin	EXP3	AT2G37640	1.46	0.55	0.92	0.38964925	0.7571	-6.22
255162_at	putative transposon protein	---	---	-1.06	-0.08	-0.92	0.38961394	0.7571	-6.22
259949_at	hypothetical protein predicted by g	---	AT1G71420	-1.08	-0.11	-0.92	0.38972562	0.7572	-6.22
259570_at	hypothetical protein	COR47	AT1G20440	1.15	0.20	0.92	0.38981607	0.7573	-6.22
249746_at	NAC2-like protein	TIP	AT5G24590	-1.09	-0.12	-0.92	0.38983612	0.7573	-6.22
246290_at	calmodulin-3 ;supported by full-ler	CAM3	AT3G56800	1.07	0.09	0.92	0.38992622	0.7573	-6.22
252596_at	receptor-like protein kinase recept	---	AT3G45330	-1.06	-0.09	-0.92	0.39012909	0.7573	-6.22
254184_at	hypothetical protein	---	AT4G23970	-1.08	-0.11	-0.92	0.39007148	0.7573	-6.22
249624_at	putative protein predicted proteins	---	AT5G37570	-1.10	-0.14	-0.92	0.39000527	0.7573	-6.22
263398_at	putative RAS superfamily GTP-bin	AtRABA5d	AT2G31680	1.08	0.11	0.92	0.38997081	0.7573	-6.22
266875_at	putative flavonol synthase	---	AT2G44800	-1.09	-0.12	-0.92	0.39015241	0.7573	-6.22
265836_at	Mutator-like transposase similar to	---	---	1.08	0.11	0.92	0.39005103	0.7573	-6.22
253235_at	putative protein hypothetical prote	HDR	AT4G34350	1.16	0.21	0.92	0.39002676	0.7573	-6.22
256355_at	hypothetical protein predicted by g	---	AT1G55040	-1.09	-0.12	-0.92	0.3900891	0.7573	-6.22
249060_at	putative protein similar to unknown	VPS2.2	AT5G44560	1.06	0.09	0.92	0.39022161	0.7574	-6.22
262570_at	unknown protein EST gb|H77143 c	---	AT1G15200	1.08	0.11	0.92	0.39032718	0.7575	-6.22
255650_s_at	hypothetical protein	CIP4.1	AT4G00930 /	1.09	0.12	0.92	0.39036998	0.7576	-6.22
263114_at	putative photosystem I reaction ce	PSAD-2	AT1G03130	1.08	0.11	0.92	0.39056802	0.7577	-6.22
247859_at	unknown protein	---	AT5G58410	-1.06	-0.08	-0.92	0.39054665	0.7577	-6.22
260394_at	putative transcription factor similar	MYB122	AT1G74080	-1.44	-0.53	-0.92	0.3905295	0.7577	-6.22
248620_at	putative protein similar to unknown	---	AT5G49320	-1.07	-0.10	-0.92	0.39064187	0.7578	-6.22

259101_at	hypothetical protein predicted by g	---	AT3G11640	1.06	0.09	0.92	0.39060929	0.7578	-6.22
267204_at	putative blue copper-binding protei	---	AT2G31050	1.08	0.11	0.92	0.39068941	0.7578	-6.22
249619_at	stelar K+ outward rectifying chann	GORK	AT5G37500	-1.12	-0.16	-0.92	0.39076436	0.7579	-6.22
253412_at	putative protein (fragment) calcine	CBL10	AT4G33000	-1.09	-0.13	-0.92	0.39081215	0.7579	-6.22
256643_at	unknown protein similar to putative	---	---	-1.08	-0.11	-0.92	0.39085028	0.7579	-6.22
262886_at	hypothetical protein	KNATM	AT1G14760	-1.10	-0.14	-0.92	0.39093995	0.7580	-6.23
265136_at	hypothetical protein similar to disea	---	AT1G51270	-1.06	-0.08	-0.92	0.39093999	0.7580	-6.23
245729_at	unknown protein	---	AT1G73490	1.09	0.13	0.92	0.3911971	0.7580	-6.23
256266_at	unknown protein ; supported by cD	---	AT3G12320	1.16	0.21	0.92	0.39111876	0.7580	-6.23
260277_at	hypothetical protein predicted by g	---	AT1G80520	-1.17	-0.22	-0.92	0.39114751	0.7580	-6.23
248808_at	putative protein contains similarity	---	AT5G47510	-1.06	-0.08	-0.92	0.39124648	0.7580	-6.23
254416_at	receptor-like serine/threonine prote	ARK3	AT4G21380	-1.27	-0.34	-0.92	0.39098723	0.7580	-6.23
262808_at	Avr9 elicitor response-like protein s	---	AT1G11730	-1.07	-0.10	-0.92	0.39110783	0.7580	-6.23
257586_at	hypothetical protein predicted by g	---	AT1G50760	1.06	0.09	0.92	0.39104843	0.7580	-6.23
255181_at	predicted protein of unknown funct	---	---	-1.08	-0.12	-0.92	0.39105768	0.7580	-6.23
261158_at	hypothetical protein predicted by g	---	AT1G34500	1.07	0.10	0.92	0.3912145	0.7580	-6.23
263566_at	hypothetical protein predicted by g	---	AT2G15340	-1.09	-0.12	-0.92	0.39143093	0.7583	-6.23
257455_s_at	hypothetical protein	---	AT1G27870 /	-1.06	-0.09	-0.92	0.39149476	0.7583	-6.23
261643_at	hypothetical protein similar to hypo	TAF4B	AT1G27720	-1.11	-0.14	-0.92	0.39157467	0.7584	-6.23
256201_at	hypothetical protein predicted by g	---	AT1G58230	-1.07	-0.10	-0.92	0.3916109	0.7584	-6.23
247787_at	putative protein various predicted p	---	AT5G58640	1.07	0.09	0.91	0.3918262	0.7586	-6.23
260120_at	hypothetical protein	ATPP2-A4	AT1G33920	-1.08	-0.11	-0.91	0.39182234	0.7586	-6.23
259314_at	putative glucose and ribitol dehydr	---	AT3G05260	-1.12	-0.17	-0.91	0.39182669	0.7586	-6.23
258749_at	hypothetical protein predicted by g	---	AT3G05760	1.09	0.12	0.91	0.39185366	0.7586	-6.23
260216_at	hypothetical protein contains Pfam	---	AT1G74580	-1.07	-0.10	-0.92	0.39178338	0.7586	-6.23
245731_at	MAP kinase, putative similar to MA	MKK9	AT1G73500	1.16	0.22	0.91	0.39194438	0.7587	-6.23
260464_at	disease resistance protein RPM1 i	LOV1	AT1G10920	-1.07	-0.09	-0.91	0.39204164	0.7587	-6.23
258655_at	putative isocitrate dehydrogenase	---	AT3G09810	-1.11	-0.15	-0.91	0.39203573	0.7587	-6.23
264337_at	hypothetical protein predicted by g	---	AT1G70350	1.07	0.10	0.91	0.3921389	0.7589	-6.23
267214_at	unknown protein ; supported by cI	---	AT2G43970	1.10	0.14	0.91	0.39220784	0.7589	-6.23
256267_at	unknown protein ; supported by cD	---	AT3G12260	1.07	0.10	0.91	0.39222791	0.7589	-6.23
261864_s_at	10-formyltetrahydrofolate syntheta	THFS	AT1G50480 /	-1.08	-0.11	-0.91	0.39237761	0.7591	-6.23
264072_at	hypothetical protein	---	---	-1.07	-0.09	-0.91	0.39264072	0.7592	-6.23
263802_at	unknown protein ;supported by ful	---	AT2G40430	-1.14	-0.19	-0.91	0.39250666	0.7592	-6.23
249777_at	putative protein similar to unknowr	---	AT5G24210	1.10	0.14	0.91	0.39256581	0.7592	-6.23

251546_at	putative protein predicted proteins	---	AT3G58830	1.12	0.17	0.91	0.39262532	0.7592	-6.23
265660_at	putative disease resistance protein	AtRLP21	AT2G25470	-1.11	-0.15	-0.91	0.39255023	0.7592	-6.23
257526_s_at	hypothetical protein similar to puta	---	AT3G09330	1.07	0.09	0.91	0.39245345	0.7592	-6.23
246439_at	RING-H2 zinc finger protein-like R	---	AT5G17600	-1.23	-0.29	-0.91	0.39260838	0.7592	-6.23
249272_at	geranylgeranyl transferase alpha s	---	AT5G41820	-1.11	-0.16	-0.91	0.39272924	0.7593	-6.23
255783_at	hypothetical protein contains Pfam	iqd32	AT1G19870	1.11	0.16	0.91	0.39281972	0.7594	-6.23
248813_at	Expressed protein ; supported by f	VAM3	AT5G46860	1.11	0.15	0.91	0.39287838	0.7594	-6.23
258303_at	hypothetical protein predicted by g	---	---	-1.07	-0.09	-0.91	0.39287475	0.7594	-6.23
263414_at	putative bZIP transcription factor c	---	AT2G21230	-1.07	-0.10	-0.91	0.39297952	0.7595	-6.23
252907_at	putative gamma-glutamyltransfera	GGT2	AT4G39650	-1.07	-0.09	-0.91	0.39298339	0.7595	-6.23
251271_at	hypothetical protein ; supported by	---	AT3G62050	-1.11	-0.15	-0.91	0.3930269	0.7595	-6.23
261949_at	hypothetical protein predicted by g	BDG1	AT1G64670	1.20	0.27	0.91	0.39311228	0.7595	-6.23
259265_at	hypothetical protein predicted by g	---	AT3G01250	-1.06	-0.09	-0.91	0.39312953	0.7595	-6.23
253959_at	putative protein	---	AT4G26410	1.07	0.09	0.91	0.39310389	0.7595	-6.23
262370_at	hypothetical protein predicted by g	---	AT1G73090	1.10	0.14	0.91	0.39336205	0.7598	-6.23
264993_at	glyoxal oxidase (glx1), putative sir	---	AT1G67290	-1.14	-0.18	-0.91	0.39337811	0.7598	-6.23
250105_at	putative protein contains similarity	RAD4	AT5G16630	-1.15	-0.20	-0.91	0.39341584	0.7598	-6.23
248896_at	putative protein contains similarity	WRKY8	AT5G46350	1.30	0.38	0.91	0.39360137	0.7601	-6.23
262780_at	putative cytochrome P450 monoo	CYP71B28	AT1G13090	1.10	0.14	0.91	0.39357622	0.7601	-6.23
251688_at	putative protein hypothetical prote	---	AT3G56480	1.17	0.23	0.91	0.39364037	0.7601	-6.23
AFFX-CreX-3_	Bacteriophage P1 /GEN=cre /DB_	---	---	-1.16	-0.22	-0.91	0.39369648	0.7601	-6.23
266490_at	unknown protein	---	AT2G07000	1.09	0.13	0.91	0.39374569	0.7602	-6.23
254426_at	putative protein predicted protein,	---	AT4G21240	-1.07	-0.10	-0.91	0.39378249	0.7602	-6.23
261021_at	hypothetical protein similar to retic	---	AT1G26380	1.40	0.49	0.91	0.39386551	0.7602	-6.23
262924_s_at	vacuolar ATP synthase, putative s	AVA-P4	AT1G19910	1.09	0.12	0.91	0.39388409	0.7602	-6.23
261860_at	scarecrow-like protein similar to SC	SCL5	AT1G50600	1.09	0.13	0.91	0.39412395	0.7603	-6.23
263974_at	hypothetical protein predicted by g	---	AT2G42720	-1.08	-0.11	-0.91	0.39413862	0.7603	-6.23
262860_at	unknown protein	APO1	AT1G64810	1.10	0.14	0.91	0.39405747	0.7603	-6.23
264049_at	putative GTP-binding protein	---	AT2G22390	-1.11	-0.15	-0.91	0.39402702	0.7603	-6.23
255363_x_at	hypothetical protein	---	---	-1.11	-0.15	-0.91	0.39406557	0.7603	-6.23
254808_at	adenine DNA glycosylase like pro	---	AT4G12740	-1.06	-0.09	-0.91	0.39411956	0.7603	-6.23
247029_at	TINY-like protein	---	AT5G67190	1.10	0.14	0.91	0.39421347	0.7604	-6.23
261757_at	hypothetical protein similar to puta	---	AT1G08210	1.12	0.16	0.91	0.39426762	0.7604	-6.23
245098_at	ethylene response sensor (ERS) ic	ERS1	AT2G40940	1.18	0.23	0.91	0.39425573	0.7604	-6.23
262229_at	unknown protein ; supported by cD	---	AT1G68620	-1.22	-0.29	-0.91	0.39458503	0.7607	-6.23

249266_at	6-phosphogluconate dehydrogena	---	AT5G41670	1.11	0.15	0.91	0.39456023	0.7607	-6.23
261652_at	dimethyladenosine transferase, pu	PFC1	AT1G01860	1.08	0.12	0.91	0.39447939	0.7607	-6.23
249584_s_at	Membrane integral protein (MIP) -	NIP4;1	AT5G37810 /	-1.09	-0.12	-0.91	0.39461264	0.7607	-6.23
264734_at	hypothetical protein predicted by g	SLAH1	AT1G62280	-1.07	-0.10	-0.91	0.39454964	0.7607	-6.23
252790_at	putative protein various predicted t	---	---	-1.07	-0.09	-0.91	0.3944469	0.7607	-6.23
250100_at	Expressed protein ; supported by c	GLN1;4	AT5G16570	1.22	0.29	0.91	0.39468223	0.7607	-6.23
261813_at	hypothetical protein contains simil	---	AT1G08280	-1.11	-0.15	-0.91	0.39465625	0.7607	-6.23
258295_at	unknown protein ;supported by ful	---	AT3G23400	-1.12	-0.16	-0.91	0.39478309	0.7607	-6.23
250961_at	putative protein various predicted	---	AT5G02980	-1.07	-0.10	-0.91	0.39475141	0.7607	-6.23
262895_at	hypothetical protein predicted by g	---	AT1G59800	-1.09	-0.13	-0.91	0.3948876	0.7607	-6.23
255747_s_at	hypothetical protein predicted by g	---	AT1G32010 /	-1.07	-0.09	-0.91	0.39489996	0.7607	-6.23
259748_at	putative dehydrogenase similar to	---	AT1G71180	1.08	0.11	0.91	0.39484067	0.7607	-6.23
260043_at	hypothetical protein predicted by g	---	---	-1.09	-0.12	-0.91	0.39490414	0.7607	-6.23
255947_at	hypothetical protein contains Pfam	---	AT1G22040	1.07	0.10	0.91	0.39507881	0.7608	-6.23
245150_at	photolyase/blue-light receptor (PH	PHR2	AT2G47590	-1.09	-0.12	-0.91	0.39501195	0.7608	-6.23
255490_at	putative protein lysosomal trafficki	---	AT4G02660	1.07	0.10	0.91	0.39504945	0.7608	-6.23
249096_at	putative protein similar to unknown	---	AT5G43910	1.15	0.20	0.91	0.39497816	0.7608	-6.23
250494_at	embryogenic callus protein - like e	HAM2	AT5G09740	1.09	0.13	0.91	0.39509171	0.7608	-6.23
248399_at	putative protein strong similarity to	---	AT5G52010	1.07	0.10	0.91	0.3951312	0.7608	-6.23
247358_at	flavonol synthase	FLS2	AT5G63580	1.09	0.13	0.91	0.39531551	0.7611	-6.23
245817_at	hypothetical protein similar to unkn	---	AT1G26160	1.06	0.09	0.91	0.3953548	0.7611	-6.23
258748_at	germin-like protein similar to germi	GLP8	AT3G05930	-1.09	-0.12	-0.91	0.39538359	0.7611	-6.23
263376_at	putative surface protein ; supporte	FLA6	AT2G20520	-1.06	-0.09	-0.91	0.39544161	0.7611	-6.23
251730_at	N2,N2-dimethylguanosine tRNA m	---	AT3G56330	-1.09	-0.13	-0.91	0.39558432	0.7613	-6.23
265314_at	hypothetical protein predicted by g	---	AT2G20210	1.08	0.11	0.91	0.39569565	0.7615	-6.23
248939_at	tyrosine-specific protein phosphata	---	AT5G45790	-1.08	-0.11	-0.91	0.39573651	0.7615	-6.23
246055_at	alpha-galactosidase - like protein	AtAGAL1	AT5G08380	1.18	0.24	0.91	0.39589835	0.7615	-6.23
256609_at	hypothetical protein predicted by g	---	---	1.06	0.09	0.91	0.39589248	0.7615	-6.23
260621_at	carbonic anhydrase, putative	ACA5	AT1G08065	1.08	0.11	0.91	0.39589351	0.7615	-6.23
245265_at	hypothetical protein ; supported by	ACD6	AT4G14400	1.59	0.66	0.91	0.39584836	0.7615	-6.23
265272_at	unknown protein	ARF10	AT2G28350	-1.11	-0.15	-0.91	0.39597804	0.7616	-6.23
252613_at	putative protein hypothetical prote	---	AT3G45190	1.06	0.09	0.91	0.39608077	0.7617	-6.23
261193_at	unknown protein ; supported by cD	---	AT1G32920	1.24	0.31	0.91	0.3960675	0.7617	-6.23
249287_at	putative protein strong similarity to	---	AT5G41250	1.08	0.12	0.91	0.39614002	0.7618	-6.23
266348_at	putative MAP kinase	ATMPK17	AT2G01450	-1.10	-0.13	-0.91	0.39625933	0.7618	-6.24

256155_at	MYB-family transcription factor, pu	MYB83	AT3G08500	-1.06	-0.09	-0.91	0.39635268	0.7618	-6.24
253077_at	hypothetical protein	---	AT4G36170	1.06	0.09	0.91	0.3964078	0.7618	-6.24
249611_at	putative protein unnamed ORF, H	ATSRL1	AT5G37370	-1.09	-0.12	-0.91	0.39620758	0.7618	-6.23
260378_at	putative actin similar to actin GB:C	ATARP4A	AT1G73910	1.06	0.09	0.91	0.39630024	0.7618	-6.24
245069_at	putative glucosyltransferase	UGT84B2	AT2G23250	-1.07	-0.10	-0.91	0.39639046	0.7618	-6.24
253510_at	hypothetical protein	GDU1	AT4G31730	-1.17	-0.22	-0.91	0.39633168	0.7618	-6.24
267329_at	hypothetical protein	---	AT2G19250	-1.07	-0.10	-0.91	0.39644337	0.7618	-6.24
261057_at	hypothetical protein predicted by g	---	AT1G01230	1.08	0.11	0.91	0.39650808	0.7619	-6.24
266708_at	putative chloroplast nucleoid DNA	---	AT2G03200	-1.11	-0.15	-0.91	0.39654666	0.7619	-6.24
257296_at	hypothetical protein predicted by g	---	AT3G28020	1.08	0.11	0.91	0.39666365	0.7619	-6.24
253636_at	putative protein predicted protein,	---	AT4G30500	1.36	0.44	0.91	0.39667429	0.7619	-6.24
263011_at	conserved hypothetical protein pro	---	AT1G23250	-1.07	-0.10	-0.91	0.39662834	0.7619	-6.24
253278_at	receptor protein kinase - like prote	---	AT4G34220	-1.26	-0.34	-0.90	0.39672588	0.7620	-6.24
261536_at	K Efflux antiporter KEA1 identical t	KEA1	AT1G01790	-1.10	-0.14	-0.90	0.39685504	0.7620	-6.24
258816_at	putative T-complex protein 1, thet	---	AT3G03960	1.11	0.15	0.90	0.39686056	0.7620	-6.24
267420_at	hypothetical protein predicted by g	---	AT2G35030	-1.16	-0.21	-0.90	0.3968205	0.7620	-6.24
263613_at	unknown protein	---	AT2G25250	-1.16	-0.22	-0.90	0.39680471	0.7620	-6.24
244981_at	ribosomal protein S8	---	---	-1.09	-0.12	-0.90	0.39709062	0.7620	-6.24
246134_at	protein kinase tousled ; supported	TSL	AT5G20930	1.09	0.13	0.90	0.39704332	0.7620	-6.24
259363_at	methionine aminopeptidase I (MA	MAP1C	AT1G13270	1.08	0.11	0.90	0.39704491	0.7620	-6.24
256144_at	guanine nucleotide-binding protei	RACK1B_A	AT1G48630	1.23	0.30	0.90	0.3970792	0.7620	-6.24
254706_at	putative protein DNA-binding prote	---	AT4G17950	-1.10	-0.14	-0.90	0.39695763	0.7620	-6.24
254043_at	putative protein ; supported by cDN	CIL	AT4G25990	1.25	0.32	0.90	0.39700534	0.7620	-6.24
250775_at	putative protein contains similarity	---	AT5G05460	1.15	0.20	0.90	0.39717427	0.7621	-6.24
266149_x_at	En/Spm-like transposon protein rel	---	---	-1.07	-0.10	-0.90	0.39739262	0.7625	-6.24
253904_at	NWMU1 - 2S albumin 1 precursor	---	AT4G27140	1.07	0.09	0.90	0.39746054	0.7626	-6.24
265183_at	unknown protein ;supported by ful	---	AT1G23750	-1.13	-0.18	-0.90	0.39764745	0.7626	-6.24
253396_at	putative protein RNA-binding prote	AtLa1	AT4G32720	1.07	0.10	0.90	0.3978519	0.7626	-6.24
260268_at	unknown protein ;supported by ful	---	AT1G68490	-1.07	-0.10	-0.90	0.39792841	0.7626	-6.24
261434_at	receptor-like serine/threonine kina	---	AT1G07650	-1.11	-0.16	-0.90	0.39785766	0.7626	-6.24
264722_at	unknown protein location of EST e	---	AT1G22970	1.10	0.14	0.90	0.39778728	0.7626	-6.24
257719_at	unknown protein	AtALMT9	AT3G18440	-1.10	-0.14	-0.90	0.39772256	0.7626	-6.24
248181_at	cytochrome c biogenesis protein p	---	AT5G54290	1.11	0.15	0.90	0.39788659	0.7626	-6.24
260048_at	unknown protein contains Pfam pr	---	AT1G73750	-1.29	-0.37	-0.90	0.39796261	0.7626	-6.24
258080_at	unknown protein ;supported by ful	---	AT3G25930	-1.06	-0.08	-0.90	0.39750454	0.7626	-6.24

261630_at	hypothetical protein predicted by g	---	AT1G50080	-1.06	-0.09	-0.90	0.39795839	0.7626	-6.24
264600_at	hypothetical protein predicted by g	---	AT1G04730	1.12	0.16	0.90	0.397584	0.7626	-6.24
261834_at	polygalacturonase PG1, putative s	---	AT1G10640	1.07	0.09	0.90	0.39770084	0.7626	-6.24
247085_at	kinesin heavy chain DNA binding p	---	AT5G66310	-1.08	-0.11	-0.90	0.39787626	0.7626	-6.24
258248_at	hypothetical protein predicted by g	---	AT3G29140	-1.12	-0.16	-0.90	0.39759276	0.7626	-6.24
260796_at	glutathione transferase, putative s	ATGSTU21	AT1G78360	-1.10	-0.14	-0.90	0.39779028	0.7626	-6.24
245821_at	hypothetical protein similar to puta	---	AT1G26270	-1.10	-0.13	-0.90	0.39804936	0.7626	-6.24
263647_at	unknown protein	---	AT2G04690	1.10	0.14	0.90	0.39803853	0.7626	-6.24
256047_at	hypothetical protein predicted by g	---	AT1G07060	-1.09	-0.12	-0.90	0.39814006	0.7627	-6.24
257952_at	putative peroxidase almost identica	---	AT3G21770	1.11	0.16	0.90	0.39817574	0.7627	-6.24
258359_s_at	putative glycolate oxidase similar t	---	AT3G14415	-1.09	-0.13	-0.90	0.39823417	0.7628	-6.24
246834_at	putative protein homeotic protein l	---	AT5G26630	-1.08	-0.11	-0.90	0.39831352	0.7628	-6.24
248360_at	putative protein contains similarity	---	AT5G52430	1.11	0.15	0.90	0.39850513	0.7629	-6.24
264728_at	unknown protein location of EST g	---	AT1G22850	1.09	0.12	0.90	0.39837639	0.7629	-6.24
246512_at	putative phytochelatin synthetase	IRX6	AT5G15630	1.10	0.13	0.90	0.39847374	0.7629	-6.24
257499_at	hypothetical protein similar to hypo	---	AT1G63850	-1.15	-0.20	-0.90	0.3984414	0.7629	-6.24
252004_at	purple acid phosphatase-like prote	PAP20	AT3G52780	1.17	0.22	0.90	0.39844518	0.7629	-6.24
249202_at	cytochrome P450	CYP705A1	AT5G42580	-1.07	-0.09	-0.90	0.3986076	0.7630	-6.24
252385_at	putative protein Vps29, Schizosac	MAG1	AT3G47810	1.07	0.09	0.90	0.39867225	0.7631	-6.24
265929_s_at	putative flavonol 3-O-glucosyltrans	---	AT2G18560	-1.14	-0.19	-0.90	0.39872971	0.7631	-6.24
252876_at	putative protein ;supported by full-	---	AT4G39970	-1.12	-0.17	-0.90	0.39900089	0.7635	-6.24
250832_at	nicotianamine synthase (dbj|BAA7	NAS1	AT5G04950	-1.32	-0.40	-0.90	0.39899566	0.7635	-6.24
245914_at	putative protein outer membrane p	OEP80	AT5G19620	1.08	0.11	0.90	0.39901786	0.7635	-6.24
246949_at	cytochrome P450-like protein CYT	CYP71B13	AT5G25140	-1.25	-0.32	-0.90	0.39922648	0.7637	-6.24
246383_at	hypothetical protein predicted by g	---	AT1G77360	-1.13	-0.18	-0.90	0.39919451	0.7637	-6.24
246085_at	putative protein predicted proteins	ATBRXL4	AT5G20540	1.09	0.12	0.90	0.39918846	0.7637	-6.24
259106_at	unknown protein ;supported by ful	RALFL22	AT3G05490	1.19	0.25	0.89	0.40182057	0.7637	-6.25
266873_at	putative PREG1-like negative regu	CYCP4;1	AT2G44740	-1.29	-0.36	-0.90	0.40056815	0.7637	-6.24
250307_at	putative protein similar to unknown	---	AT5G12170	-1.14	-0.18	-0.90	0.39954704	0.7637	-6.24
259244_at	unknown protein similar to zinc fing	COL9	AT3G07650	1.17	0.23	0.90	0.40165267	0.7637	-6.24
249335_at	putative protein contains similarity	NRPB12	AT5G41010	1.07	0.10	0.90	0.40049243	0.7637	-6.24
267081_at	putative phosphatidylinositol-4-pho	PIP5K5	AT2G41210	1.07	0.10	0.90	0.39971908	0.7637	-6.24
252305_at	putative protein CRP1 protein, Ze	emb1796	AT3G49240	-1.11	-0.15	-0.89	0.4017432	0.7637	-6.25
249016_at	putative protein contains similarity	REV1	AT5G44750	-1.10	-0.13	-0.90	0.39941151	0.7637	-6.24
251008_at	putative protein ;supported by full-l	---	AT5G02710	1.09	0.12	0.89	0.40193388	0.7637	-6.25

251784_at	putative protein photosystem II ox	PPL1	AT3G55330	1.13	0.17	0.89	0.40201233	0.7637	-6.25
262098_at	transcription factor, putative simila	NF-YC2	AT1G56170	-1.10	-0.14	-0.90	0.40029365	0.7637	-6.24
263921_at	putative fructose bisphosphate ald	---	AT2G36460	1.10	0.13	0.90	0.40144996	0.7637	-6.24
266556_at	hypothetical protein predicted by g	---	AT2G46230	1.09	0.12	0.90	0.39962287	0.7637	-6.24
254327_at	RCc3- like protein RCc3 protein, C	---	AT4G22490	-1.17	-0.23	-0.90	0.39980173	0.7637	-6.24
266382_at	hypothetical protein predicted by g	---	---	-1.06	-0.09	-0.90	0.40136497	0.7637	-6.24
251520_at	protein kinase like GCN2 - Saccha	---	AT3G59410	1.07	0.09	0.90	0.40075425	0.7637	-6.24
255468_at	putative WD-repeat protein similar	---	AT4G03020	1.07	0.10	0.90	0.39977516	0.7637	-6.24
264228_at	hypothetical protein contains simila	GCS1	AT1G67490	1.08	0.10	0.90	0.40024759	0.7637	-6.24
252219_at	putative protein some putative prot	---	AT3G50160	-1.09	-0.12	-0.90	0.39961174	0.7637	-6.24
264314_at	unknown protein ; supported by cD	---	AT1G70420	-1.13	-0.17	-0.90	0.4003061	0.7637	-6.24
246760_at	putative protein predicted proteins	---	AT5G27970	-1.07	-0.09	-0.90	0.40019458	0.7637	-6.24
262203_at	transfactor-like protein similar to tra	---	AT2G01060	1.08	0.11	0.90	0.40164642	0.7637	-6.24
261007_at	hypothetical protein similar to retic	---	AT1G26400	-1.06	-0.08	-0.90	0.3996934	0.7637	-6.24
254904_at	putative translation initiation factor	---	AT4G11160	-1.11	-0.15	-0.90	0.40059027	0.7637	-6.24
263677_at	unknown protein	PDLP2	AT1G04520	-1.08	-0.11	-0.90	0.40117735	0.7637	-6.24
261326_s_at	aminoacylase, putative similar to a	---	AT1G44180	1.12	0.16	0.90	0.40036547	0.7637	-6.24
253824_at	putative protein protein kinase LeI	MTM1	AT4G27940	1.27	0.34	0.90	0.40155915	0.7637	-6.24
253129_at	glycine-rich protein glycine-rich pr	CSDP1	AT4G36020	1.11	0.15	0.90	0.3997796	0.7637	-6.24
245032_at	En/Spm-like transposon protein rel	---	---	-1.11	-0.15	-0.90	0.40070575	0.7637	-6.24
261013_at	fatty acid elongase 3-ketoacyl-CoA	ATUPS5	AT1G26440	1.11	0.15	0.90	0.39939614	0.7637	-6.24
263465_at	hypothetical protein predicted by g	---	AT2G31940	-1.09	-0.13	-0.90	0.40019234	0.7637	-6.24
266278_at	putative tropinone reductase	---	AT2G29300	-1.21	-0.27	-0.90	0.40057865	0.7637	-6.24
264070_at	putative cyclin-dependent kinase r	CKS1	AT2G27960	1.11	0.15	0.89	0.40201979	0.7637	-6.25
266212_at	putative retroelement pol polyprote	---	---	-1.09	-0.13	-0.90	0.40146235	0.7637	-6.24
267544_at	putative cytochrome b5	CB5-B	AT2G32720	1.20	0.26	0.90	0.40135707	0.7637	-6.24
254015_at	putative beta-galactosidase beta-g	BGAL12	AT4G26140	1.12	0.16	0.90	0.40125116	0.7637	-6.24
262697_at	beta-glucosidase, putative similar	ATA27	AT1G75940	1.07	0.09	0.90	0.39967172	0.7637	-6.24
248272_at	Expressed protein ; supported by f	---	AT5G53480	1.10	0.14	0.90	0.3999063	0.7637	-6.24
267197_at	hypothetical protein predicted by g	---	AT2G30960	-1.07	-0.10	-0.90	0.39963676	0.7637	-6.24
253570_at	hypothetical protein	---	AT4G31260	-1.09	-0.12	-0.89	0.4017243	0.7637	-6.25
248114_at	wax synthase-like protein	---	AT5G55370	-1.08	-0.11	-0.90	0.40136842	0.7637	-6.24
255526_at	hypothetical protein	---	AT4G02350	1.09	0.12	0.90	0.40005023	0.7637	-6.24
261267_at	unknown protein ;supported by full	---	AT1G26750	1.08	0.11	0.90	0.4013408	0.7637	-6.24
250106_at	putative protein strong similarity to	---	AT5G16640	1.07	0.10	0.90	0.39992613	0.7637	-6.24

265782_at	putative two-component response	---	AT2G07440	-1.08	-0.11	-0.90	0.3996016	0.7637	-6.24
259758_s_at	putative caffeic acid 3-O-methyltra	---	AT1G77520 /	-1.07	-0.10	-0.90	0.40037094	0.7637	-6.24
267418_at	putative RING zinc finger protein	---	AT2G35000	-1.09	-0.12	-0.90	0.40112938	0.7637	-6.24
267150_at	putative anthranilate N-hydroxycin	SDT	AT2G23510	-1.06	-0.08	-0.90	0.39985059	0.7637	-6.24
250699_at	receptor-like protein kinase	SRF2	AT5G06820	-1.08	-0.11	-0.90	0.39992394	0.7637	-6.24
253335_at	putative protein YHR077c (NMD2	---	AT4G33500	-1.08	-0.11	-0.89	0.40201696	0.7637	-6.25
262498_at	8-oxoguanine DNA glycosylase-lik	OGG1	AT1G21710	1.08	0.11	0.90	0.40159465	0.7637	-6.24
260947_at	fructokinase, putative similar to fru	---	AT1G06020	-1.06	-0.08	-0.90	0.39949827	0.7637	-6.24
247347_at	putative protein similar to unknown	SHA1	AT5G63780	-1.19	-0.25	-0.90	0.4015574	0.7637	-6.24
256832_at	meiotic recombination protein (At	DMC1	AT3G22880	1.12	0.17	0.90	0.40096976	0.7637	-6.24
249003_at	putative protein contains similarity	---	AT5G44500	1.08	0.11	0.90	0.40103207	0.7637	-6.24
258846_at	unknown protein ; supported by fu	---	AT3G03070	1.07	0.09	0.90	0.40155253	0.7637	-6.24
261600_x_at	hypothetical protein similar to hypo	---	AT1G49680 /	-1.06	-0.08	-0.90	0.40042717	0.7637	-6.24
249141_at	putative protein similar to unknown	---	AT5G43200	-1.06	-0.09	-0.90	0.40127157	0.7637	-6.24
246667_at	putative protein hypothetical protei	---	---	-1.07	-0.10	-0.90	0.40054704	0.7637	-6.24
260019_at	polyprotein, putative simlar to GI:4	---	---	-1.06	-0.09	-0.90	0.40091236	0.7637	-6.24
257514_at	hypothetical protein similar to puta	---	---	-1.11	-0.15	-0.89	0.40190975	0.7637	-6.25
266945_at	hypothetical protein predicted by g	VEL2	AT2G18880	-1.07	-0.09	-0.90	0.40022573	0.7637	-6.24
258170_at	unknown protein similar to senesc	---	AT3G21600	-1.19	-0.25	-0.90	0.40063207	0.7637	-6.24
246338_s_at	putative protein putative integral m	ATCHX10	AT3G44920 /	-1.06	-0.09	-0.90	0.39966015	0.7637	-6.24
261866_at	scarecrow-like 3 identical to GB:A	SCL3	AT1G50420	1.33	0.41	0.90	0.40030363	0.7637	-6.24
248679_at	unknown protein ;supported by ful	---	AT5G48830	1.12	0.16	0.90	0.40037249	0.7637	-6.24
257158_at	3-hydroxyisobutyryl-coenzyme A h	---	AT3G24360	-1.09	-0.12	-0.90	0.39950231	0.7637	-6.24
264839_at	putative protochlorophyllide reduc	POR C	AT1G03630	1.11	0.15	0.90	0.40089231	0.7637	-6.24
265497_at	putative non-LTR retroelement rev	---	---	-1.18	-0.24	-0.90	0.40146384	0.7637	-6.24
254575_at	putative protein various predicted	---	AT4G19460	-1.20	-0.26	-0.90	0.39996219	0.7637	-6.24
264877_at	putative obtusifoliol 14-alpha deme	CYP51G2	AT2G17330	1.06	0.08	0.90	0.40126071	0.7637	-6.24
265201_at	unknown protein	---	AT2G36810	-1.06	-0.08	-0.90	0.40031206	0.7637	-6.24
255274_at	putative protein various predicted	---	---	1.09	0.12	0.89	0.4018277	0.7637	-6.25
252531_at	actin 12	ACT12	AT3G46520	-1.07	-0.10	-0.90	0.40128995	0.7637	-6.24
257275_at	RNA-binding protein, putative con	CID9	AT3G14450	1.13	0.18	0.90	0.40100884	0.7637	-6.24
265975_at	putative citrate synthetase	---	AT2G11270	1.10	0.13	0.90	0.40082295	0.7637	-6.24
256813_at	unknown protein	---	AT3G21360	-1.08	-0.11	-0.90	0.40142075	0.7637	-6.24
264278_at	myrosinase binding protein, putati	---	AT1G60130	-1.07	-0.09	-0.90	0.40111631	0.7637	-6.24
250074_at	UDP-glucose pyrophosphorylase	---	AT5G17310	1.11	0.15	0.89	0.40173862	0.7637	-6.25

248977_at	putative protein strong similarity to	---	AT5G45020	1.10	0.14	0.89	0.4018595	0.7637	-6.25
253529_at	putative protein hypothetical prote	---	AT4G31520	-1.06	-0.09	-0.89	0.40192343	0.7637	-6.25
266797_at	unknown protein	AtGRF1	AT2G22840	-1.18	-0.23	-0.89	0.40197678	0.7637	-6.25
250069_at	disease resistance protein-like	---	AT5G17970	1.07	0.10	0.90	0.40100163	0.7637	-6.24
251830_at	phosphoribosylformylglycinamidine	PUR5	AT3G55010	1.14	0.19	0.89	0.40216078	0.7639	-6.25
245326_at	Expressed protein ; supported by f	---	AT4G14100	1.10	0.14	0.89	0.40215552	0.7639	-6.25
250847_at	putative protein predicted protein,	---	AT5G04480	-1.16	-0.21	-0.89	0.40223235	0.7639	-6.25
246932_at	ethylene-responsive element - like	---	AT5G25190	1.18	0.24	0.89	0.40259187	0.7641	-6.25
245337_at	Expressed protein ; supported by f	---	AT4G16566	-1.07	-0.09	-0.89	0.40242352	0.7641	-6.25
248152_at	DNA repair and meiosis protein Mr	MRE11	AT5G54260	1.10	0.14	0.89	0.40236636	0.7641	-6.25
262500_at	unknown protein Contains PF|006	FBP7	AT1G21760	1.07	0.10	0.89	0.40247092	0.7641	-6.25
258050_at	unknown protein	---	AT3G16200	1.09	0.12	0.89	0.40241929	0.7641	-6.25
259155_at	transcription initiation factor IIB (TF	---	AT3G10330	1.09	0.13	0.89	0.40255057	0.7641	-6.25
265434_at	predicted protein	---	AT2G20805	1.06	0.09	0.89	0.40253789	0.7641	-6.25
266169_at	putative protease inhibitor ;suppor	---	AT2G38900	-1.07	-0.09	-0.89	0.40257066	0.7641	-6.25
263489_at	putative inositol polyphosphate 5'-p	---	AT2G31830	-1.08	-0.11	-0.89	0.40247892	0.7641	-6.25
249144_at	squamosa promoter binding protei	SPL2	AT5G43270	-1.08	-0.11	-0.89	0.4027939	0.7643	-6.25
247448_at	putative protein predicted proteins	---	AT5G62770	1.27	0.35	0.89	0.40280474	0.7643	-6.25
248724_at	putative protein strong similarity to	---	AT5G47970	1.13	0.18	0.89	0.40287158	0.7644	-6.25
259712_at	putative 20S proteasome beta sub	PBC2	AT1G77440	1.06	0.09	0.89	0.40303912	0.7646	-6.25
255393_at	hypothetical protein	---	---	1.06	0.08	0.89	0.40312658	0.7647	-6.25
266936_at	hypothetical protein predicted by g	---	AT2G18920	-1.06	-0.08	-0.89	0.40324469	0.7649	-6.25
252972_at	auxin-induced protein - like auxin-	---	AT4G38840	-1.19	-0.25	-0.89	0.40329565	0.7649	-6.25
260978_at	17.6 kDa heat shock protein (AA 1	---	AT1G53540	-1.18	-0.24	-0.89	0.40342292	0.7651	-6.25
256639_at	hypothetical protein predicted by g	---	---	-1.09	-0.12	-0.89	0.40340158	0.7651	-6.25
249474_s_at	germin-like protein (GLP2a) copy2	GER2	AT5G39130 /	-1.09	-0.12	-0.89	0.40355973	0.7652	-6.25
250535_at	putative protein similar to unknown	---	AT5G08480	1.08	0.11	0.89	0.40357005	0.7652	-6.25
263062_at	putative phosphatidylinositol/phopl	---	AT2G18180	-1.08	-0.11	-0.89	0.40359776	0.7652	-6.25
247000_at	casein kinase II alpha subunit ; su	CKA1	AT5G67380	1.09	0.12	0.89	0.40368151	0.7653	-6.25
247619_at	putative protein	---	AT5G60290	-1.10	-0.14	-0.89	0.4037824	0.7654	-6.25
266386_at	putative homeodomain transcriptio	HDG3	AT2G32370	-1.08	-0.12	-0.89	0.40382908	0.7654	-6.25
265493_at	unknown protein predicted by gens	---	AT2G15670	-1.07	-0.10	-0.89	0.40395727	0.7656	-6.25
262062_s_at	hypothetical protein	emb1427	AT1G20570 /	1.08	0.11	0.89	0.40403889	0.7657	-6.25
260252_at	putative mitochondrial carrier prote	---	AT1G74240	-1.10	-0.14	-0.89	0.40416691	0.7659	-6.25
258927_at	putative folylpolyglutamate synthet	DFC	AT3G10160	-1.07	-0.10	-0.89	0.4042488	0.7659	-6.25

255321_at	putative ES43-like protein	---	AT4G04260	1.08	0.11	0.89	0.40419927	0.7659	-6.25
263872_at	putative cellulose synthase catalyti	CESA9	AT2G21770	-1.09	-0.12	-0.89	0.40426107	0.7659	-6.25
264949_at	unknown protein contains similarity	MAF1	AT1G77080	1.06	0.09	0.89	0.40428761	0.7659	-6.25
254040_at	possible apospory-associated like	---	AT4G25900	1.13	0.17	0.89	0.40487939	0.7662	-6.25
256407_at	sucrose-proton symporter, putativ	ATSUC7	AT1G66570	1.28	0.36	0.89	0.40516036	0.7662	-6.25
265150_at	unknown protein ; supported by cl	---	AT1G51200	-1.09	-0.13	-0.89	0.40481431	0.7662	-6.25
258814_at	putative short-chain type dehydrog	---	AT3G03980	1.08	0.12	0.89	0.40464185	0.7662	-6.25
262807_at	unknown protein strong similarity t	---	AT1G11740	-1.10	-0.13	-0.89	0.40454544	0.7662	-6.25
262588_at	unknown protein Similar to gb|AJ0	---	AT1G15130	-1.08	-0.11	-0.89	0.40482908	0.7662	-6.25
245532_at	cytochrome P450 like protein	CYP97B3	AT4G15110	1.06	0.08	0.89	0.40491847	0.7662	-6.25
265447_at	putative laccase (diphenol oxidase	LAC6	AT2G46570	1.09	0.13	0.89	0.40501458	0.7662	-6.25
266697_at	profilin 4 ; supported by full-length	PRF5	AT2G19770	-1.09	-0.13	-0.89	0.40509883	0.7662	-6.25
259002_at	putative glutaredoxin similar to glut	ROXY1	AT3G02000	-1.11	-0.15	-0.89	0.40452571	0.7662	-6.25
264417_at	hypothetical protein contains simila	---	---	-1.11	-0.16	-0.89	0.40507781	0.7662	-6.25
256387_at	hypothetical protein	---	AT3G06170	-1.10	-0.13	-0.89	0.40480007	0.7662	-6.25
263401_at	hypothetical protein similar to hypo	---	AT2G04070	-1.12	-0.16	-0.89	0.40473727	0.7662	-6.25
248733_at	unknown protein	ELP1	---	-1.08	-0.12	-0.89	0.40465533	0.7662	-6.25
266849_at	putative vacuolar processing enzyr	ALPHA-VP	AT2G25940	-1.07	-0.10	-0.89	0.40508041	0.7662	-6.25
264612_at	unknown protein similar to GB:AA0	---	AT1G04560	-1.10	-0.14	-0.89	0.40516811	0.7662	-6.25
252050_at	hypothetical protein	---	AT3G52550	-1.09	-0.12	-0.89	0.40480408	0.7662	-6.25
262893_at	hypothetical protein contains simila	---	AT1G59790	-1.06	-0.09	-0.89	0.40498037	0.7662	-6.25
252578_at	putative protein Ariadne protein (A	---	AT3G45480	1.06	0.09	0.89	0.40512852	0.7662	-6.25
250620_at	embryo-specific protein 3 (ATS3)	ATS3	AT5G07190	-1.07	-0.10	-0.89	0.4050287	0.7662	-6.25
257231_at	DegP protease contains similarity t	DEGP12	AT3G16550	-1.06	-0.09	-0.89	0.4048568	0.7662	-6.25
264011_at	unknown protein	---	AT2G21090	1.08	0.11	0.89	0.4052746	0.7662	-6.25
246440_at	glycine/proline-rich protein glycine	---	AT5G17650	-1.16	-0.21	-0.89	0.40524802	0.7662	-6.25
252841_at	putative protein replication protein	---	---	-1.09	-0.12	-0.89	0.40526155	0.7662	-6.25
267268_at	hypothetical protein predicted by g	---	AT2G02570	1.07	0.10	0.89	0.40535752	0.7663	-6.25
260509_at	natural resistance-associated mac	NRAMP2	AT1G47240	-1.06	-0.08	-0.89	0.40547449	0.7664	-6.25
266850_at	unknown protein	---	AT2G26850	-1.06	-0.09	-0.89	0.40553092	0.7664	-6.25
257790_at	gda-1, putative similar to gda-1 GI	---	AT3G27090	-1.10	-0.13	-0.89	0.4055293	0.7664	-6.25
248943_s_at	putative protein similar to unknowr	---	AT5G45440 /	1.17	0.23	0.89	0.4057121	0.7665	-6.25
260368_at	AtHVA22c identical to AtHVA22c C	ATHVA22C	AT1G69700	1.25	0.33	0.89	0.40570858	0.7665	-6.25
263071_at	putative retroelement pol polyprote	---	---	-1.07	-0.09	-0.89	0.40562631	0.7665	-6.25
261234_x_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-0.89	0.40565254	0.7665	-6.25

262277_at	transmembrane protein, putative s	---	AT1G68650	1.17	0.23	0.89	0.40588115	0.7667	-6.25
249151_at	inorganic phosphate transporter (d	PHT3	AT5G43360	1.07	0.10	0.89	0.40587816	0.7667	-6.25
245957_at	putative protein predicted proteins	---	AT5G19590	-1.06	-0.08	-0.89	0.40593541	0.7667	-6.25
256347_at	unknown protein similar to putative	---	---	1.07	0.10	0.89	0.40604002	0.7667	-6.25
251734_at	putative protein Centrosome- and	---	AT3G56270	1.17	0.22	0.89	0.40600308	0.7667	-6.25
250063_at	disease resistance protein - like di	CSA1	AT5G17880	-1.09	-0.13	-0.89	0.40605627	0.7667	-6.25
246696_at	putative protein predicted protein,	---	---	1.07	0.10	0.89	0.4060065	0.7667	-6.25
255771_at	hypothetical protein contains simila	---	AT1G18550	-1.07	-0.10	-0.89	0.40618207	0.7669	-6.25
259488_at	hypothetical protein preedicted by	---	AT1G15780	-1.10	-0.13	-0.89	0.40627371	0.7670	-6.25
259460_at	unknown protein ; supported by cD	---	AT1G44000	-1.14	-0.19	-0.89	0.40631736	0.7670	-6.25
250172_at	putative protein	---	AT5G14330	-1.10	-0.14	-0.89	0.40640583	0.7671	-6.25
253470_s_at	putative protein dnaK-type molecu	SDH3-2	AT4G32210 /	-1.06	-0.09	-0.89	0.40650365	0.7672	-6.25
245320_at	Expressed protein ; supported by f	---	AT4G16444	1.07	0.09	0.89	0.40658208	0.7672	-6.25
260232_at	unknown protein contains Pfam pr	---	AT1G74640	-1.14	-0.18	-0.89	0.40647264	0.7672	-6.25
248498_at	selenium-binding protein-like	---	AT5G50390	1.07	0.10	0.89	0.40659206	0.7672	-6.25
247750_at	protein kinase 6 - like protein kina	---	AT5G58950	1.07	0.10	0.89	0.40657185	0.7672	-6.25
257206_at	putative lectin similar to lectin SP:P	---	AT3G16530	1.42	0.50	0.88	0.40704981	0.7675	-6.25
254229_at	hypothetical protein ; supported by	---	AT4G23610	1.26	0.33	0.88	0.40704209	0.7675	-6.25
260402_at	putative gamma-glutamyltransfera	GGT3	AT1G69820	-1.10	-0.13	-0.88	0.40679014	0.7675	-6.25
259396_at	shaggy-like kinase, putative simila	GSK1	AT1G06390	1.06	0.09	0.88	0.40690145	0.7675	-6.25
250774_at	ATP-dependent RNA helicase-like	---	AT5G05450	1.10	0.14	0.88	0.40691097	0.7675	-6.25
262884_at	membrane related protein CP5, pu	CP5	AT1G64720	1.07	0.10	0.88	0.4069911	0.7675	-6.25
253448_at	putative protein mRNA for KIAA0(	---	AT4G32640	-1.06	-0.09	-0.88	0.40703122	0.7675	-6.25
256135_at	hypothetical protein predicted by g	---	AT1G48730	-1.08	-0.12	-0.88	0.40707737	0.7675	-6.25
255698_at	scarecrow-like 6 (SCL6)	---	AT4G00150	-1.10	-0.13	-0.88	0.40686463	0.7675	-6.25
267324_at	hypothetical protein predicted by g	---	AT2G19360	-1.06	-0.08	-0.88	0.40693099	0.7675	-6.25
249001_at	putative protein strong similarity to	---	AT5G44990	-1.26	-0.33	-0.88	0.40747995	0.7679	-6.26
247416_at	40S ribosomal protein S15-like pro	---	AT5G63070	-1.08	-0.11	-0.88	0.40741469	0.7679	-6.26
256519_at	hypothetical protein predicted by g	---	AT1G66110	-1.11	-0.15	-0.88	0.40737133	0.7679	-6.26
254772_at	extensin-like protein extensin clas	---	AT4G13390	1.05	0.07	0.88	0.4074876	0.7679	-6.26
245450_at	disease resistance RPP5 like prote	---	AT4G16880	-1.07	-0.10	-0.88	0.40745276	0.7679	-6.26
253950_at	putative dihydrolipoamide succiny	---	AT4G26910	-1.13	-0.17	-0.88	0.40757932	0.7679	-6.26
254375_at	putative protein (fragment) ATP(G	QQT2	AT4G21800	-1.07	-0.10	-0.88	0.40754777	0.7679	-6.26
263033_s_at	unknown protein ; supported by ful	---	AT1G23950 /	-1.12	-0.16	-0.88	0.4075913	0.7679	-6.26
254536_at	putative protein chitinase / lysozyr	---	AT4G19720	-1.07	-0.10	-0.88	0.40771404	0.7681	-6.26

266126_at	putative metalloproteinase ; suppo	---	AT2G45040	1.13	0.17	0.88	0.40788787	0.7681	-6.26
255454_at	hypothetical protein	---	AT4G02910	1.06	0.09	0.88	0.40779009	0.7681	-6.26
258523_at	pectin methylesterase, putative sir	---	AT3G06830	-1.05	-0.08	-0.88	0.40783596	0.7681	-6.26
253686_at	putative protein predicted proteins	---	AT4G29750	-1.08	-0.12	-0.88	0.40785159	0.7681	-6.26
246797_at	putative protein ;supported by full-	---	AT5G26790	-1.06	-0.08	-0.88	0.40790329	0.7681	-6.26
251838_at	cysteine proteinase non-consensu	---	AT3G54940	1.08	0.12	0.88	0.40805363	0.7683	-6.26
267610_at	K+ transporter, AKT1 identical to (	AKT1	AT2G26650	-1.21	-0.27	-0.88	0.40820521	0.7685	-6.26
264474_s_at	ribulose-bisphosphate carboxylas	RBCS1A	AT1G06820 /	1.06	0.08	0.88	0.40832276	0.7685	-6.26
252678_s_at	nitrilase 2 ;supported by full-length	NIT2	AT3G44300 /	-1.07	-0.09	-0.88	0.4082982	0.7685	-6.26
267630_at	unknown protein predicted by gene	---	AT2G42130	1.09	0.13	0.88	0.40832528	0.7685	-6.26
257429_at	putative RING zinc finger protein	---	AT2G27940	1.11	0.15	0.88	0.40830718	0.7685	-6.26
250425_at	lectin-like protein kinase - like lect	---	AT5G10530	1.06	0.08	0.88	0.40819082	0.7685	-6.26
266132_at	hypothetical protein predicted by g	SPX3	AT2G45130	1.17	0.23	0.88	0.40839321	0.7685	-6.26
247849_at	putative protein fibrinogen-binding	---	AT5G58130	1.09	0.13	0.88	0.40854462	0.7686	-6.26
265441_at	unknown protein ;supported by ful	---	AT2G20870	-1.10	-0.14	-0.88	0.40851481	0.7686	-6.26
263445_at	unknown protein	---	AT2G31590	-1.06	-0.09	-0.88	0.40855855	0.7686	-6.26
260342_at	hypothetical protein predicted by g	---	AT1G69280	-1.08	-0.12	-0.88	0.4084668	0.7686	-6.26
245006_at	PSI P700 apoprotein A2	---	---	-1.05	-0.08	-0.88	0.40862891	0.7687	-6.26
255986_x_at	putative protein predicted proteins	---	---	-1.05	-0.08	-0.88	0.40866858	0.7687	-6.26
260868_at	unknown protein ;supported by full	---	AT1G43860	-1.10	-0.13	-0.88	0.40883628	0.7687	-6.26
261975_at	unknown protein	---	AT1G64640	-1.24	-0.31	-0.88	0.40895707	0.7687	-6.26
251563_at	anthranilate phosphoribosyltransfe	---	AT3G57880	-1.14	-0.18	-0.88	0.40895162	0.7687	-6.26
257373_at	hypothetical protein predicted by g	---	AT2G43140	1.09	0.13	0.88	0.40888622	0.7687	-6.26
263770_at	Mutator-like transposase similar to	---	---	-1.11	-0.15	-0.88	0.40897923	0.7687	-6.26
254006_at	putative protein various predicted	---	AT4G26340	-1.07	-0.10	-0.88	0.40892504	0.7687	-6.26
259212_at	hypothetical protein predicted by g	---	AT3G09180	1.08	0.11	0.88	0.40879314	0.7687	-6.26
262321_at	hypothetical protein predicted by g	---	AT1G27570	-1.07	-0.10	-0.88	0.4088383	0.7687	-6.26
263078_at	hypothetical protein predicted by g	---	AT2G05350	-1.08	-0.11	-0.88	0.40890664	0.7687	-6.26
252462_at	putative protein various predicted	---	AT3G47250	-1.07	-0.09	-0.88	0.40903872	0.7687	-6.26
262119_s_at	glutathione S-transferase, putative	ATGSTF6	AT1G02920 /	1.27	0.34	0.88	0.4091642	0.7688	-6.26
262767_at	putative oxysterol-binding protein s	ORP1D	AT1G13170	1.16	0.22	0.88	0.40911369	0.7688	-6.26
253476_at	S-receptor kinase -like protein ser	SD2-5	AT4G32300	1.15	0.21	0.88	0.40913193	0.7688	-6.26
261889_at	unknown protein	---	AT1G80810	-1.08	-0.11	-0.88	0.40921024	0.7688	-6.26
251711_at	phosphatidylinositol-4-phosphate	PIP5K4	AT3G56960	1.09	0.13	0.88	0.40935968	0.7690	-6.26
258099_at	unknown protein similar to hypothe	---	AT3G23540	1.07	0.10	0.88	0.40944006	0.7691	-6.26

258577_at	putative disease resistance protein	---	AT3G04220	-1.16	-0.22	-0.88	0.40944845	0.7691	-6.26
254123_at	Bnm1 like protein pollen-specific p	APPB1	AT4G24640	-1.07	-0.10	-0.88	0.40957801	0.7691	-6.26
259930_at	hypothetical protein predicted by g	---	AT1G34355	-1.08	-0.11	-0.88	0.40961037	0.7691	-6.26
266356_at	putative uclacyanin I identical to G	UCC1	AT2G32300	-1.06	-0.08	-0.88	0.40951734	0.7691	-6.26
245283_at	Expressed protein ; supported by c	AT-HSFA5	AT4G13980	-1.08	-0.11	-0.88	0.40959207	0.7691	-6.26
253452_at	hypothetical protein ; supported by	---	AT4G31930	-1.07	-0.10	-0.88	0.40964429	0.7691	-6.26
249342_at	putative protein ATP12 protein pre	---	AT5G40660	1.08	0.11	0.88	0.40975423	0.7691	-6.26
263952_s_at	unknown protein ;supported by ful	---	AT2G35810 /	1.07	0.10	0.88	0.40975701	0.7691	-6.26
265878_at	putative SUPERMAN-like C2H2 zi	ZFP11	AT2G42410	1.06	0.09	0.88	0.40970116	0.7691	-6.26
254631_at	putative protein predicted proteins	LSH9	AT4G18610	-1.17	-0.23	-0.88	0.40979839	0.7692	-6.26
258362_at	unknown protein	---	AT3G14280	1.32	0.40	0.88	0.40999727	0.7695	-6.26
262732_at	putative protein kinase similar to g	---	AT1G16440	1.08	0.12	0.88	0.41004977	0.7695	-6.26
245449_at	retrotransposon like protein	---	---	-1.13	-0.17	-0.88	0.41015031	0.7696	-6.26
254359_at	putative protein hypothetical prote	---	AT4G22360	1.08	0.11	0.88	0.41023407	0.7697	-6.26
263342_at	putative helicase	---	---	1.05	0.07	0.88	0.41024011	0.7697	-6.26
256104_at	trehalose-6-phosphate synthase,	ATTPS2	AT1G16980	-1.06	-0.09	-0.88	0.41040349	0.7697	-6.26
248945_at	putative protein strong similarity to	---	AT5G45510	1.09	0.12	0.88	0.41040923	0.7697	-6.26
263720_at	putative Na/H antiporter	ATCHX15	AT2G13620	-1.06	-0.09	-0.88	0.41041559	0.7697	-6.26
256843_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-0.88	0.41031707	0.7697	-6.26
265798_at	unknown protein ; supported by cD	---	AT2G35790	1.11	0.15	0.88	0.41047621	0.7698	-6.26
249397_at	putative protein MtN21, Medicago	---	AT5G40230	-1.10	-0.14	-0.88	0.41049021	0.7698	-6.26
261201_at	unknown protein ;supported by full	---	AT1G12850	1.08	0.11	0.88	0.41057979	0.7698	-6.26
257639_at	hypothetical protein	---	AT3G25720	-1.08	-0.11	-0.88	0.41053435	0.7698	-6.26
251738_at	PROBABLE EUKARYOTIC TRAN	EIF3C	AT3G56150	-1.07	-0.09	-0.88	0.41059496	0.7698	-6.26
265450_at	hypothetical protein predicted by g	---	AT2G46620	1.12	0.16	0.88	0.41064859	0.7698	-6.26
250734_at	putative protein similar to unknown	---	AT5G06270	1.20	0.26	0.88	0.41068851	0.7698	-6.26
255044_at	putative protein	---	AT4G09680	-1.08	-0.11	-0.88	0.41099353	0.7703	-6.26
254203_at	putative protein various predicted	AtGRF8	AT4G24150	1.06	0.09	0.88	0.41105787	0.7704	-6.26
251624_at	hypothetical protein ;supported by	---	AT3G57280	1.09	0.13	0.88	0.4110996	0.7704	-6.26
264379_at	hypothetical protein predicted by g	---	AT2G25200	1.14	0.19	0.88	0.41125836	0.7706	-6.26
253428_at	cellulose synthase catalytic subuni	CESA1	AT4G32410	1.10	0.14	0.87	0.41242178	0.7706	-6.26
263545_at	unknown protein	---	AT2G21560	1.19	0.24	0.87	0.41222106	0.7706	-6.26
266363_at	hypothetical protein predicted by g	---	AT2G41250	-1.14	-0.18	-0.87	0.41221129	0.7706	-6.26
252108_at	putative protein various predicted	---	AT3G51530	1.07	0.10	0.88	0.41156948	0.7706	-6.26
261666_at	hypothetical protein contains simila	---	AT1G18440	1.09	0.13	0.88	0.41135394	0.7706	-6.26

261969_at	hypothetical protein contains simila	---	AT1G65950	-1.06	-0.09	-0.88	0.41155464	0.7706	-6.26
265074_at	hypothetical protein ; supported by	emb1011	AT1G55540	-1.08	-0.11	-0.88	0.41151919	0.7706	-6.26
246666_at	hypothetical protein	---	AT5G34830	-1.06	-0.08	-0.88	0.41140965	0.7706	-6.26
263306_at	putative serine carboxypeptidase I	SCPL43	AT2G12480	-1.07	-0.09	-0.88	0.41159081	0.7706	-6.26
262014_at	unknown protein	---	AT1G35660	-1.14	-0.19	-0.87	0.41236331	0.7706	-6.26
248396_at	unknown protein	---	AT5G52130	-1.08	-0.11	-0.88	0.41164519	0.7706	-6.26
249572_at	chromosome condensation protei	EMB2656	AT5G37630	-1.09	-0.12	-0.87	0.41200865	0.7706	-6.26
267508_at	hypothetical protein predicted by g	---	AT2G45700	1.07	0.10	0.88	0.41146673	0.7706	-6.26
266933_at	putative Ta11-like non-LTR retroel	---	AT2G07760	-1.09	-0.13	-0.87	0.41247575	0.7706	-6.26
257572_at	hypothetical protein predicted by g	---	AT3G16880	-1.08	-0.12	-0.87	0.41221796	0.7706	-6.26
265075_at	hypothetical protein similar to emb	---	AT1G55450	1.29	0.37	0.87	0.4122469	0.7706	-6.26
253896_at	putative protein NBS/LRR disease	---	AT4G27190	-1.07	-0.10	-0.88	0.41162494	0.7706	-6.26
258949_at	unknown protein	ATCFM2	AT3G01370	1.10	0.13	0.87	0.41246506	0.7706	-6.26
247045_at	putative protein similar to unknown	---	AT5G66930	1.09	0.12	0.87	0.41244083	0.7706	-6.26
260318_at	hypothetical protein predicted by g	---	AT1G63960	1.09	0.12	0.87	0.41222381	0.7706	-6.26
247900_at	60S acidic ribosomal protein P3 ;	---	AT5G57290	1.15	0.21	0.87	0.41235308	0.7706	-6.26
258131_at	protein kinase, putative similar to	---	AT3G24540	-1.10	-0.14	-0.88	0.41158085	0.7706	-6.26
266241_s_at	hypothetical protein predicted by g	---	AT2G27800	1.08	0.11	0.87	0.41205599	0.7706	-6.26
251924_at	histone H4-like protein several hist	---	AT3G53730	1.11	0.15	0.87	0.41220597	0.7706	-6.26
266214_at	putative retroelement integrase	---	---	-1.06	-0.08	-0.87	0.41241453	0.7706	-6.26
247710_at	receptor-like protein kinase recept	---	AT5G59260	-1.06	-0.08	-0.87	0.41198107	0.7706	-6.26
251438_s_at	putative protein hypothetical prote	---	AT3G59930	1.44	0.53	0.87	0.41219619	0.7706	-6.26
259153_at	unknown protein ;supported by ful	---	AT3G10250	-1.08	-0.12	-0.87	0.41243255	0.7706	-6.26
266567_at	putative eukaryotic initiation factor	---	AT2G24050	-1.11	-0.15	-0.87	0.41243764	0.7706	-6.26
262776_at	unknown protein EST gb|T22808 c	---	AT1G13020	-1.09	-0.12	-0.87	0.41222942	0.7706	-6.26
252825_at	small GTP-binding protein - like S	AtRABH1c	AT4G39890	1.18	0.23	0.87	0.41229272	0.7706	-6.26
257343_s_at	pseudogene, polyprotein similar to	---	---	1.05	0.07	0.87	0.41248568	0.7706	-6.26
265711_at	unknown protein	---	AT2G03360	-1.06	-0.08	-0.87	0.41176026	0.7706	-6.26
252397_at	hypothetical protein	---	AT3G47980	-1.11	-0.15	-0.87	0.41190651	0.7706	-6.26
251896_at	putative protein predicted proteins	---	AT3G54390	-1.09	-0.13	-0.87	0.41212969	0.7706	-6.26
257222_at	DegP protease almost identical to	DEGP1	AT3G27925	-1.09	-0.13	-0.87	0.41188015	0.7706	-6.26
251408_at	palmitoyl-protein thioesterase pre	---	AT3G60340	1.09	0.13	0.87	0.41265938	0.7707	-6.26
250338_at	putative protein ; supported by cD	---	AT5G11760	1.06	0.09	0.87	0.41263864	0.7707	-6.26
245535_at	cell wall protein like	---	AT4G15160	1.08	0.11	0.87	0.41261156	0.7707	-6.26
251074_at	putative protein hypothetical prote	---	AT5G01800	-1.08	-0.12	-0.87	0.4126854	0.7707	-6.26

247392_at	glutamate-1-semialdehyde 2,1-am	GSA1	AT5G63570	1.11	0.15	0.87	0.41262944	0.7707	-6.26
246114_at	seed imbitition protein-like seed in	DIN10	AT5G20250	1.13	0.17	0.87	0.41277241	0.7707	-6.26
256318_s_at	hypothetical protein	---	---	-1.06	-0.08	-0.87	0.41278758	0.7707	-6.26
255160_at	putative pathogenesis-related prot	---	AT4G07820	1.06	0.08	0.87	0.41276495	0.7707	-6.26
247010_at	60S ribosomal protein L26 ;suppo	---	AT5G67510	1.18	0.24	0.87	0.41291191	0.7708	-6.26
248571_at	putative protein similar to unknown	---	---	-1.06	-0.08	-0.87	0.41292023	0.7708	-6.26
259110_at	unknown protein	---	AT3G05570	-1.10	-0.14	-0.87	0.41308423	0.7711	-6.27
254468_at	UDP-glucose 4-epimerase - like p	---	AT4G20460	-1.07	-0.10	-0.87	0.41311281	0.7711	-6.27
252472_at	GTP-binding protein Rab11 ; supp	ATRABA2C	AT3G46830	-1.08	-0.11	-0.87	0.41318062	0.7711	-6.27
266584_s_at	putative steroid sulfotransferase	ST4C	AT1G13430	1.05	0.08	0.87	0.41323128	0.7712	-6.27
254357_at	nifU-like protein nifU protein homo	ISU1	AT4G22220	1.05	0.08	0.87	0.41364716	0.7712	-6.27
248981_at	regulatory protein NPR1-like; trans	NPR3	AT5G45110	1.07	0.10	0.87	0.4134264	0.7712	-6.27
253205_at	putative cyclase associated protei	ATCAP1	AT4G34490	-1.14	-0.18	-0.87	0.41376376	0.7712	-6.27
253098_at	cytochrome P450-like protein	CYP81D3	AT4G37340	-1.08	-0.11	-0.87	0.41376129	0.7712	-6.27
254789_at	blue copper-binding protein, 15K (	---	AT4G12880	-1.51	-0.59	-0.87	0.41359355	0.7712	-6.27
249780_at	ubiquitin	---	AT5G24240	-1.09	-0.12	-0.87	0.41380475	0.7712	-6.27
247725_at	putative Rab5-interacting protein -	---	AT5G59410	1.12	0.16	0.87	0.41383238	0.7712	-6.27
266244_at	unknown protein	---	AT2G27740	1.21	0.27	0.87	0.4136619	0.7712	-6.27
262693_at	unknown protein	---	AT1G62780	1.16	0.21	0.87	0.41374243	0.7712	-6.27
254319_at	putative protein predicted proteins	---	AT4G22560	-1.10	-0.14	-0.87	0.41356728	0.7712	-6.27
264109_at	unknown protein	---	AT2G13720	1.06	0.09	0.87	0.41373398	0.7712	-6.27
261236_at	importin alpha, putative similar to	---	AT1G32880	-1.07	-0.09	-0.87	0.41365767	0.7712	-6.27
250082_at	polygalacturonase-like protein	---	AT5G17200	-1.09	-0.12	-0.87	0.41358347	0.7712	-6.27
252774_at	putative protein predicted proteins	---	---	1.09	0.12	0.87	0.41332277	0.7712	-6.27
AFFX-Athal-Ac	Arabidopsis thaliana /REF=U3728	---	---	1.07	0.09	0.87	0.41385259	0.7712	-6.27
248381_at	fructokinase 1 ; supported by cDN	---	AT5G51830	1.15	0.21	0.87	0.41350815	0.7712	-6.27
245201_at	F12A21.3 unknown protein; simil	CSK	AT1G67840	-1.08	-0.11	-0.87	0.41343682	0.7712	-6.27
254004_at	arginyl-tRNA synthetase	emb1027	AT4G26300	1.05	0.08	0.87	0.41390772	0.7713	-6.27
261477_at	unknown protein	---	AT1G14310	1.09	0.13	0.87	0.41394214	0.7713	-6.27
254635_at	extensin-like protein extensin-like	---	AT4G18670	-1.08	-0.11	-0.87	0.41403864	0.7714	-6.27
246690_at	hypothetical protein	---	---	-1.08	-0.10	-0.87	0.41415364	0.7715	-6.27
266364_at	unknown protein	---	AT2G41230	1.35	0.43	0.87	0.41428254	0.7717	-6.27
255915_at	putative protein	---	AT5G28620	-1.07	-0.10	-0.87	0.4143268	0.7717	-6.27
247575_at	RNA-binding protein - like RNA-bi	GR-RBP3	AT5G61030	-1.10	-0.13	-0.87	0.41439078	0.7718	-6.27
254434_at	ethylene-regulated transcript 2 (ER	---	AT4G20880	1.07	0.09	0.87	0.41454298	0.7718	-6.27

252504_at	telomere repeat-binding protein h	TRFL1	AT3G46590	1.07	0.10	0.87	0.4145354	0.7718	-6.27
265069_at	awaiting functional assignment sim	---	AT1G55545	1.07	0.10	0.87	0.41458411	0.7718	-6.27
251366_at	putative protein several hypothetic	---	AT3G61340	1.07	0.10	0.87	0.41466716	0.7718	-6.27
250941_at	putative protein	---	AT5G03320	1.09	0.13	0.87	0.414476	0.7718	-6.27
263642_at	putative fimbrin	---	AT2G04750	-1.07	-0.09	-0.87	0.41459092	0.7718	-6.27
252140_at	putative protein several hypothetic	---	AT3G51070	-1.06	-0.08	-0.87	0.41465723	0.7718	-6.27
252137_at	dehydrin-like protein dehydrin Xe	XERO1	AT3G50980	1.09	0.12	0.87	0.41463402	0.7718	-6.27
266911_at	putative protein kinase contains a	---	AT2G45910	1.10	0.13	0.87	0.41476309	0.7719	-6.27
258657_at	hypothetical protein predicted by g	---	AT3G09890	-1.11	-0.15	-0.87	0.41489086	0.7721	-6.27
255406_at	hypothetical protein similar to hyp	---	AT4G03450	1.21	0.28	0.87	0.41490828	0.7721	-6.27
266352_at	unknown protein	---	AT2G01610	-1.23	-0.30	-0.87	0.41527197	0.7726	-6.27
252296_at	putative protein GMFP7 isoprenyl	---	AT3G48970	-1.13	-0.17	-0.87	0.41526385	0.7726	-6.27
266426_x_at	hypothetical protein predicted by g	---	AT2G07140	1.13	0.18	0.87	0.41531895	0.7726	-6.27
254741_s_at	putative disease resistance protei	AtRLP49	AT4G13900	-1.06	-0.08	-0.87	0.41538092	0.7727	-6.27
246769_at	hypothetical protein	---	AT5G27440	1.07	0.09	0.87	0.41542628	0.7727	-6.27
247540_at	ethylene responsive element bind	---	AT5G61590	1.17	0.23	0.87	0.41552204	0.7728	-6.27
262384_at	disease resistance protein, putativ	---	AT1G72950	1.10	0.13	0.87	0.41565971	0.7730	-6.27
259254_at	putative P-protein: chorismate mu	ADT2	AT3G07630	1.08	0.11	0.87	0.41576291	0.7732	-6.27
256861_at	beta-amylase, putative similar to b	BAM1	AT3G23920	-1.14	-0.19	-0.87	0.41580686	0.7732	-6.27
260236_at	geranylgeranyl reductase identica	---	AT1G74470	1.06	0.08	0.87	0.41602371	0.7735	-6.27
264559_at	unknown protein similar to hypothe	---	AT1G09610	1.05	0.08	0.87	0.41603171	0.7735	-6.27
256332_at	trihelix DNA-binding protein (GT2)	GT2	AT1G76890	1.17	0.23	0.87	0.41624957	0.7737	-6.27
247929_at	apospory-associated protein C	---	AT5G57330	-1.09	-0.12	-0.87	0.41622246	0.7737	-6.27
255663_at	hypothetical protein	---	AT4G00420	1.07	0.10	0.87	0.41637971	0.7739	-6.27
257109_s_at	hypothetical protein	---	---	1.06	0.08	0.87	0.41642971	0.7739	-6.27
264276_at	hypothetical protein contains simila	---	AT1G60380	-1.06	-0.09	-0.87	0.41644324	0.7739	-6.27
260283_at	hypothetical protein predicted by g	PTAC17	AT1G80480	-1.06	-0.08	-0.87	0.41656432	0.7741	-6.27
260115_at	AIG1-like protein similar to AIG1 p	---	AT1G33870	-1.09	-0.12	-0.87	0.41661231	0.7741	-6.27
255600_s_at	putative protein predicted protein,	---	AT4G01020	-1.06	-0.08	-0.87	0.41669845	0.7742	-6.27
252188_at	putative clathrin coat assembly pr	---	AT3G50860	-1.13	-0.17	-0.87	0.41675892	0.7742	-6.27
245023_at	PSII I protein	---	---	-1.13	-0.17	-0.87	0.41677673	0.7742	-6.27
252457_at	zinc-finger protein-like protein DN	---	AT3G47180	1.06	0.09	0.86	0.41695863	0.7745	-6.27
258055_at	putative 2Fe-2S iron-sulfur cluster	NDF4	AT3G16250	-1.22	-0.29	-0.86	0.41707382	0.7745	-6.27
260722_at	protein phosphatase-2C, putative	---	AT1G48040	-1.12	-0.17	-0.86	0.41702577	0.7745	-6.27
245724_at	hypothetical protein predicted by g	---	AT1G73390	-1.12	-0.17	-0.86	0.41706111	0.7745	-6.27

258646_at	MATE efflux family protein, putativ	FRD3	AT3G08040	-1.06	-0.09	-0.86	0.41726867	0.7748	-6.27
267131_at	hypothetical protein predicted by g	---	AT2G23400	1.06	0.08	0.86	0.41729699	0.7748	-6.27
249110_at	disease resistance protein	---	AT5G43730	-1.06	-0.08	-0.86	0.41732421	0.7748	-6.27
262870_at	alcohol dehydrogenase, putative s	---	AT1G64710	-1.28	-0.36	-0.86	0.41742626	0.7748	-6.27
265681_at	putative protein kinase contains a	---	AT2G24370	-1.06	-0.09	-0.86	0.41739661	0.7748	-6.27
254544_at	putative chitinase chitinase (EC 3.	---	AT4G19820	1.09	0.12	0.86	0.41740729	0.7748	-6.27
265270_at	putative ribose phosphate pyropho	---	AT2G42910	1.07	0.10	0.86	0.41752997	0.7748	-6.27
257484_at	unknown protein	---	AT1G01650	-1.06	-0.09	-0.86	0.41751605	0.7748	-6.27
246786_at	putative amino acid aminotransfer	---	AT5G27410	-1.08	-0.11	-0.86	0.41747059	0.7748	-6.27
253968_at	putative calcineurin B-like protein	CBL7	AT4G26560	-1.07	-0.09	-0.86	0.41756674	0.7748	-6.27
252491_at	disease resistance protein RPP8-l	---	AT3G46730	1.06	0.08	0.86	0.41764623	0.7749	-6.27
257028_at	hypothetical protein predicted by g	---	AT3G19230	-1.13	-0.17	-0.86	0.41791194	0.7753	-6.27
258348_at	unknown protein ;supported by ful	---	AT3G17710	-1.07	-0.10	-0.86	0.41796309	0.7754	-6.27
245210_at	putative protein similarity to UVB-r	---	AT5G12350	-1.06	-0.09	-0.86	0.41799963	0.7754	-6.27
262830_at	purple acid phosphatase, putative	PAP3	AT1G14700	1.12	0.16	0.86	0.41809831	0.7755	-6.27
264402_at	HSP100/ClpB, putative similar to I	CLPB4	AT2G25140	-1.15	-0.20	-0.86	0.41828361	0.7755	-6.27
260012_at	Expressed protein ; supported by c	---	AT1G67865	-1.14	-0.19	-0.86	0.41815472	0.7755	-6.27
251610_at	putative protein hypothetical prote	---	AT3G57930	1.24	0.31	0.86	0.41828319	0.7755	-6.27
261516_at	hypoxanthine ribosyl transferase,	---	AT1G71750	1.07	0.09	0.86	0.41830343	0.7755	-6.27
257366_s_at	unknown protein	---	AT2G03040	-1.07	-0.10	-0.86	0.41826807	0.7755	-6.27
266784_at	putative receptor-like protein kinas	---	AT2G28960	-1.06	-0.08	-0.86	0.41830513	0.7755	-6.27
263473_at	putative glucosyltransferase ; sup	UGT74D1	AT2G31750	1.21	0.27	0.86	0.41838483	0.7756	-6.27
258661_at	unknown protein	---	AT3G02930	1.17	0.23	0.86	0.41842151	0.7756	-6.27
247056_at	SWI2/SNF2-like protein (gb|AAD28	CHR1	AT5G66750	1.07	0.10	0.86	0.41864869	0.7757	-6.27
262320_at	hypothetical protein predicted by g	---	AT1G27550	-1.07	-0.10	-0.86	0.41854683	0.7757	-6.27
260434_at	hypothetical protein predicted by g	---	AT1G68330	1.12	0.16	0.86	0.41860357	0.7757	-6.27
245857_at	putative protein various predicted	---	---	1.09	0.13	0.86	0.41853386	0.7757	-6.27
247353_at	alcohol dehydrogenase-like protein	---	AT5G63620	1.09	0.12	0.86	0.41861714	0.7757	-6.27
260865_at	reverse transcriptase, putative sim	---	AT1G43760	-1.08	-0.11	-0.86	0.41869014	0.7757	-6.27
256171_s_at	hypothetical protein similar to reve	---	---	-1.08	-0.11	-0.86	0.41873015	0.7757	-6.27
257783_at	unknown protein	---	AT3G26950	-1.07	-0.10	-0.86	0.41897306	0.7758	-6.28
249528_at	putative protein predicted protein,	---	AT5G38720	-1.12	-0.16	-0.86	0.41895954	0.7758	-6.28
256754_at	unknown protein	CHUP1	AT3G25690	-1.08	-0.11	-0.86	0.41883822	0.7758	-6.28
261403_at	unknown protein ;supported by full	SYP52	AT1G79590	-1.06	-0.09	-0.86	0.41888344	0.7758	-6.28
247482_at	chromosomal protein - like chrom	SMC2	AT5G62410	1.08	0.11	0.86	0.41896465	0.7758	-6.28

248959_at	putative protein similar to unknown	---	AT5G45630	1.20	0.26	0.86	0.41894661	0.7758	-6.28
265624_at	CLAVATA3 CLE family of proteins	CLV3	AT2G27250	1.08	0.11	0.86	0.41899863	0.7758	-6.28
256312_x_at	hypothetical protein	---	AT1G35820	-1.06	-0.09	-0.86	0.41919787	0.7760	-6.28
264144_at	latex-abundant protein, putative si	AtMC6	AT1G79320	1.07	0.09	0.86	0.41917616	0.7760	-6.28
266549_at	Expressed protein ; supported by f	EXL1	AT2G35150	-1.08	-0.11	-0.86	0.41925988	0.7761	-6.28
261377_at	unknown protein ;supported by full	---	AT1G18850	-1.16	-0.21	-0.86	0.41933118	0.7761	-6.28
245436_at	membrane protein homolog	---	AT4G16620	-1.07	-0.10	-0.86	0.4193456	0.7761	-6.28
245195_at	F12A21.13 putative photosystem	PSBY	AT1G67740	1.07	0.10	0.86	0.41960222	0.7763	-6.28
261667_at	unknown protein similar to putative	---	AT1G18460	1.10	0.14	0.86	0.41958898	0.7763	-6.28
265522_at	putative TPR repeat nuclear phosp	ELF8	AT2G06210	-1.08	-0.11	-0.86	0.41953721	0.7763	-6.28
AFFX-r2-Bs-ph	B. subtilis /GEN=pheB /DB_XREF=	---	---	1.12	0.17	0.86	0.41955401	0.7763	-6.28
249950_at	protein kinase - like protein Pto kir	---	AT5G18910	1.06	0.08	0.86	0.419662	0.7763	-6.28
249102_at	patatin-like protein	---	AT5G43590	1.05	0.08	0.86	0.41963307	0.7763	-6.28
252507_at	putative protein predicted protein,	aTNUDT9	AT3G46200	-1.11	-0.15	-0.86	0.41973111	0.7763	-6.28
263526_at	hypothetical protein predicted by g	---	AT2G24830	1.06	0.09	0.86	0.4198585	0.7763	-6.28
260590_at	phosphoenolpyruvate carboxylase	ATPPC1	AT1G53310	1.09	0.13	0.86	0.41974608	0.7763	-6.28
255768_at	Expressed protein ; supported by f	---	AT1G16705	-1.07	-0.09	-0.86	0.41987892	0.7763	-6.28
252949_at	putative thaumatin-like protein tha	---	AT4G38670	-1.14	-0.19	-0.86	0.41983029	0.7763	-6.28
255025_at	putative host response protein pir	MES12	AT4G09900	-1.13	-0.17	-0.86	0.41978502	0.7763	-6.28
253143_at	putative protein	---	AT4G35530	1.09	0.12	0.86	0.42010517	0.7764	-6.28
246435_at	hypothetical protein ; supported by	---	AT5G17460	-1.06	-0.08	-0.86	0.42010635	0.7764	-6.28
248838_at	carnitine/acylcarnitine translocase-	BOU	AT5G46800	-1.12	-0.17	-0.86	0.42016099	0.7764	-6.28
250933_at	arabinogalactan protein - like arab	FLA11	AT5G03170	1.17	0.23	0.86	0.42010712	0.7764	-6.28
246296_at	putative protein hypothetical prote	---	AT3G56750	1.06	0.09	0.86	0.42019306	0.7764	-6.28
247489_at	carbonyl reductase - like protein ir	---	AT5G61830	-1.08	-0.11	-0.86	0.41999373	0.7764	-6.28
246032_s_at	putative protein	---	---	-1.08	-0.11	-0.86	0.4201879	0.7764	-6.28
247171_at	unknown protein	---	AT5G65540	1.06	0.09	0.86	0.42008187	0.7764	-6.28
253935_at	putative aspartate-tRNA ligase as	---	AT4G26870	1.18	0.23	0.86	0.42028364	0.7765	-6.28
258866_at	unknown protein	---	AT3G03180	1.06	0.09	0.86	0.42051614	0.7769	-6.28
250740_at	t-SNARE SED5 (gb|AAC06291.1)	SYP31	AT5G05760	-1.06	-0.08	-0.86	0.42066896	0.7770	-6.28
266680_s_at	hypothetical protein predicted by g	---	AT2G19850 /	-1.06	-0.08	-0.86	0.42060922	0.7770	-6.28
259127_at	putative translation initiation factor	---	AT3G02270	1.08	0.11	0.86	0.42065276	0.7770	-6.28
266865_at	omega-3 fatty acid desaturase ider	FAD3	AT2G29980	1.78	0.83	0.86	0.42092651	0.7771	-6.28
256398_at	putative major intrinsic protein con	NIP7;1	AT3G06100	-1.06	-0.08	-0.86	0.420911	0.7771	-6.28
251270_at	putative protein	---	AT3G62370	-1.11	-0.15	-0.86	0.42084899	0.7771	-6.28

259175_at	unknown protein	---	AT3G01560	1.09	0.12	0.86	0.42079374	0.7771	-6.28
247368_at	putative protein contains similarity	---	AT5G63320	-1.09	-0.12	-0.86	0.42091538	0.7771	-6.28
265658_at	putative aspartate aminotransferas	ALD1	AT2G13810	-1.32	-0.40	-0.86	0.42081246	0.7771	-6.28
260688_at	hypothetical protein similar to dehy	---	AT1G17665	-1.08	-0.11	-0.86	0.42096354	0.7771	-6.28
262417_at	hypothetical protein similar to hypo	ATSIRB	AT1G50170	-1.06	-0.08	-0.86	0.42139878	0.7772	-6.28
253477_at	L-ascorbate peroxidase - like prote	APX6	AT4G32320	1.14	0.18	0.86	0.42117387	0.7772	-6.28
245348_at	trehalose-6-phosphate synthase lik	ATTPS5	AT4G17770	1.10	0.14	0.86	0.42141929	0.7772	-6.28
251714_at	putative protein leucine-rich recep	---	AT3G56370	1.18	0.23	0.86	0.42120734	0.7772	-6.28
248088_at	2-oxoglutarate dehydrogenase E2	---	AT5G55070	-1.10	-0.14	-0.86	0.42124421	0.7772	-6.28
254393_at	putative NADPH quinone oxidored	---	AT4G21580	-1.07	-0.10	-0.86	0.42113237	0.7772	-6.28
267640_at	photomorphogenesis repressor (C	COP1	AT2G32950	-1.09	-0.13	-0.86	0.42134347	0.7772	-6.28
262989_at	F28C11.5 similar to INNER NO O	INO	AT1G23420	-1.08	-0.11	-0.86	0.42105512	0.7772	-6.28
252119_at	thioredoxin h ;supported by full-ler	ATTRX1	AT3G51030	1.13	0.18	0.86	0.42117809	0.7772	-6.28
252679_at	CCR4-associated factor 1-like pro	---	AT3G44260	-1.42	-0.51	-0.86	0.42129169	0.7772	-6.28
258326_at	unknown protein similar to putative	SOL1	AT3G22760	1.10	0.14	0.86	0.42137239	0.7772	-6.28
257469_at	hypothetical protein predicted by g	---	AT1G49290	1.05	0.07	0.86	0.42139684	0.7772	-6.28
262250_at	Expressed protein predicted by ge	---	AT1G48280	1.26	0.33	0.86	0.42148393	0.7772	-6.28
252173_at	scarecrow-like 7 (SCL7)	---	AT3G50650	-1.13	-0.18	-0.86	0.42158283	0.7773	-6.28
248376_at	unknown protein ; supported by ful	---	AT5G51880	1.07	0.10	0.86	0.42168677	0.7775	-6.28
264281_at	hypothetical protein similar to puta	---	AT1G61830	-1.08	-0.12	-0.86	0.42182622	0.7776	-6.28
262109_at	hypothetical protein similar to cellu	ATCSLD5	AT1G02730	1.14	0.19	0.85	0.42207147	0.7777	-6.28
265176_at	OBP32pep protein, putative identi	---	AT1G23520	-1.07	-0.09	-0.85	0.42206224	0.7777	-6.28
250162_at	FtsH protease, putative similar to	FTSH6	AT5G15250	-1.06	-0.08	-0.85	0.42201363	0.7777	-6.28
258352_at	putative auxin-induced protein sim	IAA31	AT3G17600	-1.09	-0.12	-0.85	0.42196198	0.7777	-6.28
263891_at	putative glucan synthase	GSL8	AT2G36850	-1.06	-0.09	-0.85	0.42203278	0.7777	-6.28
258319_at	hypothetical protein similar to hypo	---	AT3G22700	-1.06	-0.09	-0.85	0.4219497	0.7777	-6.28
264426_at	hypothetical protein similar to hypo	---	AT1G61760	-1.08	-0.11	-0.85	0.4221359	0.7778	-6.28
263590_at	putative receptor-like protein kinas	---	AT2G01820	-1.06	-0.09	-0.85	0.42220502	0.7778	-6.28
253663_at	putative villin	VLN4	AT4G30160	-1.07	-0.10	-0.85	0.42220748	0.7778	-6.28
247876_at	unknown protein	---	AT5G57730	1.06	0.09	0.85	0.42230476	0.7778	-6.28
254264_at	putative protein various predicted	---	AT4G23510	-1.07	-0.09	-0.85	0.42241387	0.7778	-6.28
262961_at	exonuclease, putative similar to 5'	XRN4	AT1G54490	-1.07	-0.10	-0.85	0.42240373	0.7778	-6.28
257669_at	DNA mismatch repair protein, puta	MSH5	AT3G20475	-1.06	-0.09	-0.85	0.42240998	0.7778	-6.28
250675_at	putative protein contains similarity	---	AT5G06260	-1.06	-0.08	-0.85	0.42224716	0.7778	-6.28
246150_at	putative protein predicted proteins	---	AT5G19930	1.12	0.17	0.85	0.42237101	0.7778	-6.28

258434_at	AP2 domain containing protein RA	ATEBP	AT3G16770	-1.11	-0.15	-0.85	0.42248846	0.7779	-6.28
266581_at	putative desiccation related protein	---	AT2G46140	1.37	0.46	0.85	0.4226625	0.7780	-6.28
252271_s_at	putative protein CGI-141 protein- l	---	AT3G49420	1.06	0.08	0.85	0.42287182	0.7780	-6.28
250551_at	SNAP25 - like protein SNAP25A p	SNAP29	AT5G07880	-1.07	-0.10	-0.85	0.42284051	0.7780	-6.28
261568_at	DNA-binding protein, putative sim	NGA3	AT1G01030	-1.07	-0.10	-0.85	0.42267635	0.7780	-6.28
250686_at	gamma-tubulin interacting protein-	SPC98	AT5G06680	-1.11	-0.14	-0.85	0.42282551	0.7780	-6.28
255790_at	hypothetical protein predicted by g	---	AT2G33560	-1.07	-0.10	-0.85	0.42272342	0.7780	-6.28
263457_at	unknown protein	SR1	AT2G22300	1.16	0.22	0.85	0.42273962	0.7780	-6.28
255576_at	predicted protein of unknown func	---	AT4G01440	-1.13	-0.17	-0.85	0.42283457	0.7780	-6.28
258546_at	hypothetical protein predicted by g	emb1974	AT3G07060	1.07	0.10	0.85	0.42266896	0.7780	-6.28
258588_s_at	glyceraldehyde-3-phosphate dehy	GAPC1	AT3G04120	1.15	0.21	0.85	0.42302236	0.7781	-6.28
264913_at	hypothetical protein predicted by g	---	AT1G60770	1.12	0.17	0.85	0.42303528	0.7781	-6.28
261355_at	putative malate oxidoreductase sin	ATNADP-M	AT1G79750	1.08	0.11	0.85	0.4230529	0.7781	-6.28
245411_at	hypothetical protein	---	AT4G17240	1.13	0.17	0.85	0.42313421	0.7782	-6.28
249613_at	putative protein mDj10, Mus musc	---	AT5G37380	-1.09	-0.12	-0.85	0.42314949	0.7782	-6.28
257765_at	hypothetical protein contains Pfam	---	AT3G23020	1.06	0.09	0.85	0.42319536	0.7782	-6.28
247070_at	Expressed protein ; supported by f	---	AT5G66815	-1.08	-0.11	-0.85	0.42325167	0.7782	-6.28
256074_at	unknown protein ; supported by cD	---	AT1G18260	1.08	0.11	0.85	0.42327191	0.7782	-6.28
251527_at	putative protein hypothetical prote	---	AT3G58650	-1.07	-0.09	-0.85	0.42335307	0.7783	-6.28
254097_at	putative Ser/Thr protein kinase se	---	AT4G25160	1.06	0.08	0.85	0.42339708	0.7783	-6.28
263310_s_at	hypothetical protein	---	---	-1.06	-0.08	-0.85	0.42338184	0.7783	-6.28
252276_at	hypothetical protein ; supported by	---	AT3G49490	-1.08	-0.11	-0.85	0.42349974	0.7784	-6.28
264601_at	hypothetical protein similar to hypo	---	AT1G04540	1.07	0.10	0.85	0.42355939	0.7784	-6.28
246307_at	putative nuclear DNA-binding prote	ATG2	AT3G51800	1.11	0.15	0.85	0.4235458	0.7784	-6.28
257636_at	cytochrome P450, putative contain	CYP71B22	AT3G26200	-1.18	-0.23	-0.85	0.42378158	0.7785	-6.28
250275_at	putative protein mRNA, Moritella r	---	AT5G13030	-1.10	-0.13	-0.85	0.42374162	0.7785	-6.28
265874_at	hypothetical protein predicted by g	---	AT2G01640	1.08	0.11	0.85	0.42371648	0.7785	-6.28
250383_at	putative GTP-binding protein GTP	---	AT5G11480	1.10	0.14	0.85	0.42377941	0.7785	-6.28
250004_at	putative protein predicted proteins	---	AT5G18750	1.10	0.13	0.85	0.42447866	0.7792	-6.28
247504_at	putative protein various predicted	---	AT5G61990	1.10	0.14	0.85	0.42455138	0.7792	-6.28
246008_at	putative protein predicted proteins	---	AT5G08320	1.08	0.12	0.85	0.42457798	0.7792	-6.28
265220_at	histidine transport protein (PTR2-B	PTR2	AT2G02040	1.06	0.08	0.85	0.42438952	0.7792	-6.28
255053_at	putative protein RNA helicase -Mu	---	AT4G09730	1.19	0.25	0.85	0.42431517	0.7792	-6.28
253720_at	acid phosphatase-like protein aci	---	AT4G29270	-1.06	-0.09	-0.85	0.42442196	0.7792	-6.28
264208_at	putative polyA-binding protein, PA	PAB3	AT1G22760	-1.12	-0.16	-0.85	0.4242294	0.7792	-6.28

251732_at	putative protein prenylated Rab ac	PRA1.B1	AT3G56110	1.06	0.09	0.85	0.42463407	0.7792	-6.28
256692_at	hypothetical protein predicted by g	---	AT3G32050	-1.05	-0.08	-0.85	0.42429698	0.7792	-6.28
249874_at	putative protein contains similarity	---	AT5G23070	-1.13	-0.17	-0.85	0.42465379	0.7792	-6.28
255640_at	hypothetical protein	---	AT4G00800	1.09	0.13	0.85	0.42439337	0.7792	-6.28
251849_at	Expressed protein ; supported by c	HAG1	AT3G54610	-1.08	-0.11	-0.85	0.42466885	0.7792	-6.28
263697_at	hypothetical protein contains simila	---	AT1G31080	-1.09	-0.12	-0.85	0.42460142	0.7792	-6.28
246639_x_at	adenylate kinase -like protein prec	---	---	-1.07	-0.10	-0.85	0.42434905	0.7792	-6.28
248973_at	disease resistance protein-like	TTR1	AT5G45050	-1.06	-0.08	-0.85	0.42423664	0.7792	-6.28
248483_at	putative protein contains similarity	---	AT5G50990	-1.10	-0.14	-0.85	0.42461705	0.7792	-6.28
250170_at	putative protein ribulose-1,5-bisph	---	AT5G14260	1.08	0.11	0.85	0.4249059	0.7793	-6.29
264103_at	unknown protein	---	AT2G13660	-1.08	-0.10	-0.85	0.42487674	0.7793	-6.29
249152_s_at	inorganic phosphate transporter (d	APT1	AT5G43350	1.11	0.15	0.85	0.42490438	0.7793	-6.29
258627_at	unknown protein similar to peroxis	PEX12	AT3G04460	1.09	0.12	0.85	0.42480906	0.7793	-6.29
259084_at	putative inner mitochondrial memb	ATTIM23-3	AT3G04800	-1.07	-0.10	-0.85	0.42478519	0.7793	-6.29
265801_at	fertilization-independent seed 2 pr	FIS2	AT2G35670	-1.07	-0.10	-0.85	0.42499062	0.7794	-6.29
247037_at	putative protein similar to unknown	RALFL34	AT5G67070	-1.40	-0.48	-0.85	0.42517313	0.7794	-6.29
267445_at	hypothetical protein predicted by g	---	AT2G33680	-1.08	-0.11	-0.85	0.42520427	0.7794	-6.29
254933_at	putative RNA-directed RNA polym	RDR2	AT4G11130	-1.08	-0.12	-0.85	0.42515059	0.7794	-6.29
262577_at	unknown protein ESTs gb|F20110	---	AT1G15290	-1.10	-0.13	-0.85	0.42518593	0.7794	-6.29
245992_at	receptor protein kinase - like recep	---	AT5G20690	1.06	0.08	0.85	0.42507662	0.7794	-6.29
255182_at	hypothetical protein	---	---	1.06	0.09	0.85	0.42507017	0.7794	-6.29
258280_at	putative self-incompatibility protei	---	AT3G26880	-1.06	-0.08	-0.85	0.42524826	0.7794	-6.29
253659_at	hypothetical protein	---	AT4G30150	1.07	0.10	0.85	0.42536164	0.7794	-6.29
265669_at	unknown protein ;supported by ful	---	AT2G32040	-1.12	-0.16	-0.85	0.4253414	0.7794	-6.29
253016_at	putative protein partial LG127/30 g	---	AT4G37950	-1.05	-0.07	-0.85	0.42530487	0.7794	-6.29
247805_at	ATGP1-like protein	ATYKT62	AT5G58180	-1.11	-0.15	-0.85	0.42541433	0.7795	-6.29
264382_at	unknown protein similarity to stron	SDF2	AT2G25110	1.12	0.17	0.85	0.42544173	0.7795	-6.29
264727_at	putative cytochrome C strong simil	CYTC-1	AT1G22840	1.16	0.21	0.85	0.42554984	0.7795	-6.29
253327_at	putative transcription factor	MYB69	AT4G33450	1.09	0.12	0.85	0.42554308	0.7795	-6.29
255086_at	putative protein chromosome I BA	---	AT4G09300	-1.08	-0.11	-0.85	0.42575436	0.7798	-6.29
263340_at	hypothetical protein predicted by g	---	---	-1.06	-0.09	-0.85	0.42578633	0.7798	-6.29
255179_at	putative transposon protein	---	---	-1.05	-0.07	-0.85	0.42592956	0.7800	-6.29
249889_at	putative protein strong similarity to	---	AT5G22540	-1.24	-0.30	-0.85	0.42610568	0.7803	-6.29
254475_at	putative snRNP protein small nucl	smB	AT4G20440	1.13	0.18	0.85	0.42624999	0.7803	-6.29
248843_at	homeobox protein	HB-7	AT5G46880	-1.08	-0.11	-0.85	0.42619868	0.7803	-6.29

249626_at	putative protein nucleoid DNA-bin	---	AT5G37540	1.14	0.19	0.85	0.42616025	0.7803	-6.29
252039_at	Expressed protein ; supported by c	---	AT3G52155	1.08	0.11	0.85	0.4262331	0.7803	-6.29
265185_at	OBP32pep protein, putative identi	---	AT1G23670	-1.08	-0.11	-0.85	0.42640018	0.7805	-6.29
264520_at	putative amino acid permease GC	AAP8	AT1G10010	-1.11	-0.16	-0.85	0.4264564	0.7806	-6.29
255183_at	hypothetical protein	---	AT4G08140	-1.08	-0.11	-0.85	0.42652171	0.7806	-6.29
251517_at	putative protein hypothetical prote	---	AT3G59370	-1.05	-0.07	-0.85	0.42651042	0.7806	-6.29
253615_at	cyclic nucleotide and calmodulin-r	CNGC17	AT4G30360	-1.10	-0.14	-0.85	0.42656832	0.7806	-6.29
261094_at	hypothetical protein predicted by g	---	AT1G62920	-1.10	-0.14	-0.85	0.42666311	0.7806	-6.29
245862_at	putative protein	---	AT5G01010	1.08	0.11	0.85	0.42663873	0.7806	-6.29
255411_at	putative ribonucleoprotein similarit	---	AT4G03110	-1.08	-0.11	-0.85	0.42686064	0.7807	-6.29
265823_at	hypothetical protein predicted by g	---	AT2G35760	-1.07	-0.10	-0.85	0.42681269	0.7807	-6.29
253232_at	hypothetical protein ;supported by	TAF8	AT4G34340	-1.08	-0.11	-0.85	0.42700243	0.7807	-6.29
264224_at	hypothetical protein predicted by g	emb1688	AT1G67440	1.08	0.11	0.85	0.42689749	0.7807	-6.29
267273_at	putative non-LTR retroelement rev	---	AT2G02520	-1.06	-0.08	-0.85	0.42694299	0.7807	-6.29
256277_at	omega-6 fatty acid desaturase, er	FAD2	AT3G12120	-1.12	-0.17	-0.84	0.42713328	0.7807	-6.29
251399_at	putative protein	---	AT3G60590	1.08	0.12	0.85	0.42705988	0.7807	-6.29
247852_at	ATGP1 ; supported by cDNA: gi_1	YKT61	AT5G58060	1.07	0.09	0.85	0.42701322	0.7807	-6.29
263159_at	RSH3 (RelA/SpoT homolog) identi	RSH3	AT1G54130	-1.09	-0.13	-0.85	0.42696759	0.7807	-6.29
262437_at	hypothetical protein	---	---	-1.08	-0.11	-0.85	0.42708671	0.7807	-6.29
265317_at	unknown protein	BRK1	AT2G22640	1.07	0.09	0.85	0.42706122	0.7807	-6.29
263523_at	hypothetical protein predicted by g	---	---	1.06	0.09	0.85	0.42711026	0.7807	-6.29
258182_at	1-D-deoxyxylulose 5-phosphate s	DXPS1	AT3G21500	-1.22	-0.29	-0.85	0.42690894	0.7807	-6.29
247117_at	3-hydroxyisobutyryl-coenzyme A h	CHY1	AT5G65940	-1.10	-0.13	-0.84	0.42720869	0.7808	-6.29
253423_at	Expressed protein ; supported by c	IAA29	AT4G32280	1.40	0.49	0.84	0.42732279	0.7809	-6.29
248915_at	putative protein strong similarity to	---	AT5G45690	-1.08	-0.11	-0.84	0.42734125	0.7809	-6.29
261665_at	beta-glucan-elicitor receptor, puta	---	AT1G18310	1.06	0.09	0.84	0.42738009	0.7809	-6.29
250800_at	ubiquinol-cytochrome C reductase	HPR	AT1G68010	1.16	0.22	0.84	0.42746625	0.7809	-6.29
261994_at	hypothetical protein contains simila	---	AT1G33640	1.06	0.09	0.84	0.42743453	0.7809	-6.29
246711_at	putative protein	---	AT5G28190	-1.06	-0.09	-0.84	0.42754836	0.7810	-6.29
250845_at	rna binding protein - like rna bindi	---	AT5G04600	1.11	0.14	0.84	0.42759496	0.7810	-6.29
263947_at	unknown protein ;supported by ful	---	AT2G35820	1.13	0.18	0.84	0.42785075	0.7810	-6.29
256098_at	unknown protein similar to 6-phosp	---	AT1G13700	1.14	0.19	0.84	0.42798572	0.7810	-6.29
251652_at	putative protein hypothetical prote	---	AT3G57380	1.11	0.15	0.84	0.42797383	0.7810	-6.29
257668_at	sugar transporter, putative similar	---	AT3G20460	-1.10	-0.14	-0.84	0.42774387	0.7810	-6.29
250815_s_at	putative protein similar to unknown	---	AT5G05040	-1.09	-0.13	-0.84	0.42780086	0.7810	-6.29

248931_at	peptide transporter	---	AT5G46040	1.06	0.08	0.84	0.42803272	0.7810	-6.29
252201_at	putative protein anthranilate N-hyd	---	AT3G50295	-1.06	-0.08	-0.84	0.4278359	0.7810	-6.29
267087_at	putative MYB family transcription fa	MYB101	AT2G32460	1.11	0.14	0.84	0.4278928	0.7810	-6.29
257326_s_at	hypothetical protein	---	---	-1.08	-0.11	-0.84	0.42798404	0.7810	-6.29
266654_at	putative oleosin protein	---	AT2G25890	-1.09	-0.13	-0.84	0.42800509	0.7810	-6.29
251361_at	LIM domain protein LIM domain p	---	AT3G61230	1.09	0.12	0.84	0.42791583	0.7810	-6.29
252045_at	putative protein arm repeat contai	PUB22	AT3G52450	-1.49	-0.57	-0.84	0.42776813	0.7810	-6.29
251844_at	putative protein retinoblastoma-as	---	AT3G54630	-1.08	-0.11	-0.84	0.42804623	0.7810	-6.29
252877_at	hypothetical protein supported by f	---	AT4G39630	1.08	0.11	0.84	0.4281229	0.7811	-6.29
255644_at	coded for by A. thaliana cDNA T43	---	AT4G00870	-1.06	-0.09	-0.84	0.42816674	0.7811	-6.29
258537_at	putative disease resistance protein	---	AT3G04210	-1.30	-0.37	-0.84	0.4283181	0.7813	-6.29
256004_at	retroelement pol polyprotein, puta	---	---	1.06	0.09	0.84	0.42835325	0.7813	-6.29
265320_at	unknown protein predicted by gens	---	AT2G18320	-1.07	-0.10	-0.84	0.42843892	0.7814	-6.29
260111_at	hypothetical protein similar to unkn	---	AT1G63320	1.05	0.08	0.84	0.42852309	0.7815	-6.29
264779_at	putative thioredoxin similar to EST	ACHT4	AT1G08570	1.16	0.22	0.84	0.42860608	0.7816	-6.29
249728_at	GTPase activator-like protein of Ra	---	AT5G24390	1.08	0.11	0.84	0.42864393	0.7816	-6.29
255100_at	putative MuDR-like transposon pro	---	---	1.06	0.08	0.84	0.42866394	0.7816	-6.29
246886_at	CLC-d chloride channel protein	CLC-D	AT5G26240	1.07	0.10	0.84	0.42872201	0.7816	-6.29
248481_at	putative protein similar to unknown	---	AT5G50930	1.08	0.11	0.84	0.42879016	0.7817	-6.29
255317_at	putative vesicle transfer ATPase	---	AT4G04180	1.13	0.17	0.84	0.42889534	0.7818	-6.29
245474_at	hypothetical protein	---	AT4G16060	-1.08	-0.12	-0.84	0.42901803	0.7820	-6.29
266290_at	putative glutathione S-transferase	ATGSTU1	AT2G29490	-1.44	-0.53	-0.84	0.42909052	0.7821	-6.29
263558_at	putative phosphatidylinositol/phosp	---	AT2G16380	-1.10	-0.13	-0.84	0.42916218	0.7821	-6.29
259157_at	hypothetical protein predicted by g	---	AT3G05440	1.06	0.08	0.84	0.4291375	0.7821	-6.29
258354_at	putative zinc finger protein similar t	---	AT3G14320	-1.06	-0.08	-0.84	0.42928442	0.7822	-6.29
251702_at	transcription factor-like protein mo	BZIP49	AT3G56660	-1.09	-0.13	-0.84	0.42930723	0.7822	-6.29
263628_at	unknown protein ;supported by ful	FLA7	AT2G04780	1.28	0.36	0.84	0.42943353	0.7823	-6.29
266146_at	En/Spm-like transposon protein rel	---	---	-1.06	-0.08	-0.84	0.42943781	0.7823	-6.29
263849_at	putative retroelement pol polyprote	---	---	-1.09	-0.12	-0.84	0.42950009	0.7824	-6.29
261602_at	hydrogenase protein, putative sim	ATPREP2	AT1G49630	-1.06	-0.08	-0.84	0.42959608	0.7825	-6.29
262168_at	unknown protein ;supported by full	---	AT1G74730	1.07	0.10	0.84	0.42992621	0.7826	-6.29
261569_at	DNA-binding protein, putative sim	LHY	AT1G01060	-1.08	-0.11	-0.84	0.42975046	0.7826	-6.29
253116_at	putative protein CRP1, Zea mays,	---	AT4G35850	1.13	0.18	0.84	0.42995199	0.7826	-6.29
251861_at	putative protein GATA transcriptio	BME3	AT3G54810	-1.24	-0.31	-0.84	0.43016353	0.7826	-6.29
255003_at	AIG1-like protein AIG1 - Arabidop	---	AT4G09950	1.06	0.09	0.84	0.42982073	0.7826	-6.29

262279_at	hypothetical protein predicted by g	---	AT1G68630	1.15	0.21	0.84	0.42996155	0.7826	-6.29
263982_at	hypothetical protein predicted by g	---	AT2G42860	-1.09	-0.12	-0.84	0.42987921	0.7826	-6.29
253718_at	serine/threonine-specific receptor	---	AT4G29450	-1.08	-0.11	-0.84	0.42976378	0.7826	-6.29
266222_at	hypothetical protein predicted by g	---	AT2G28780	-1.07	-0.09	-0.84	0.43001901	0.7826	-6.29
263008_at	unknown protein	RPP27	AT1G54470	-1.06	-0.08	-0.84	0.43008507	0.7826	-6.29
262389_at	hypothetical protein contains simila	---	AT1G49270	-1.07	-0.09	-0.84	0.43003302	0.7826	-6.29
245826_at	disease resistance protein RPS4,	---	AT1G57850	-1.08	-0.11	-0.84	0.43007009	0.7826	-6.29
257568_s_at	hypothetical protein	---	AT3G23950	-1.09	-0.12	-0.84	0.43009804	0.7826	-6.29
250335_at	lysophospholipase - like protein ly	---	AT5G11650	-1.12	-0.16	-0.84	0.43010164	0.7826	-6.29
248324_at	putative protein similar to unknown	---	AT5G52790	1.08	0.11	0.84	0.43015668	0.7826	-6.29
263415_at	hypothetical protein similar to GB:A	EMB2762	AT2G17250	-1.10	-0.14	-0.84	0.43044113	0.7827	-6.29
251641_at	protease-like protein INSULIN-DE	---	AT3G57470	-1.10	-0.14	-0.84	0.43043309	0.7827	-6.29
245186_at	F12A21.15 hypothetical protein	ARR11	AT1G67710	-1.17	-0.22	-0.84	0.43041676	0.7827	-6.29
261791_at	unknown protein ; supported by ful	---	AT1G16170	1.17	0.22	0.84	0.43043871	0.7827	-6.29
248356_at	putative protein strong similarity to	ATEXO70A	AT5G52350	1.06	0.08	0.84	0.43033404	0.7827	-6.29
260739_at	serine carboxypeptidase precurso	scpl50	AT1G15000	-1.15	-0.20	-0.84	0.43044634	0.7827	-6.29
264027_at	putative AAA-type ATPase similar	CDC48B	AT2G03670	1.09	0.13	0.84	0.43057517	0.7829	-6.29
250262_at	putative protein peptidyl-prolyl cis-	---	AT5G13410	1.13	0.17	0.84	0.43060061	0.7829	-6.29
248861_at	senescence-associated protein 5-l	TRN2	AT5G46700	-1.24	-0.31	-0.84	0.431076	0.7830	-6.30
253314_at	hypothetical protein	---	AT4G33890	-1.06	-0.08	-0.84	0.43090198	0.7830	-6.30
247790_at	putative PRL1 associated protein	---	AT5G58720	-1.08	-0.11	-0.84	0.43113759	0.7830	-6.30
254095_at	oleosin, 18.5K	OLEO1	AT4G25140	-1.07	-0.10	-0.84	0.4308467	0.7830	-6.30
267581_at	putative RING zinc finger protein	---	AT2G41980	-1.12	-0.17	-0.84	0.43106139	0.7830	-6.30
249673_at	cytochrome P450-like	CYP79A4P	AT5G35920	-1.05	-0.07	-0.84	0.43115763	0.7830	-6.30
248215_at	putative protein contains similarity	---	AT5G53680	-1.10	-0.14	-0.84	0.43114887	0.7830	-6.30
256686_at	non-LTR reverse transcriptase, pu	---	---	-1.05	-0.08	-0.84	0.43102176	0.7830	-6.30
264552_at	hypothetical protein predicted by g	---	AT1G09470	-1.11	-0.15	-0.84	0.43081837	0.7830	-6.30
259537_at	hypothetical protein ; supported by	PHR1	AT1G12370	1.08	0.12	0.84	0.43117146	0.7830	-6.30
259230_at	unknown protein ; supported by cl	OBE1	AT3G07780	-1.09	-0.12	-0.84	0.43120308	0.7830	-6.30
253086_at	hypothetical protein	---	AT4G36370	-1.06	-0.08	-0.84	0.43096438	0.7830	-6.30
251832_at	putative protein tomato leucine zip	ATEXO70H	AT3G55150	-1.20	-0.27	-0.84	0.43089634	0.7830	-6.30
258195_at	myb protein(myb26) contains myb	ATMYB26	AT3G13890	1.07	0.10	0.84	0.43086062	0.7830	-6.30
251156_at	putative protein ZCF61, Arabidops	EDL3	AT3G63060	-1.09	-0.12	-0.84	0.431148	0.7830	-6.30
256559_at	Athila ORF 1, putative similar to A	---	---	-1.06	-0.09	-0.84	0.43092617	0.7830	-6.30
245291_at	Expressed protein ; supported by c	---	AT4G16155	-1.07	-0.10	-0.84	0.43130811	0.7831	-6.30

245808_at	RNA binding protein identical to RI	ATRBP1	AT1G58470	-1.09	-0.12	-0.84	0.43137364	0.7831	-6.30
267235_at	unknown protein	---	AT2G43945	1.05	0.07	0.84	0.43135962	0.7831	-6.30
251266_at	putative protein hypothetical prote	---	AT3G62320	-1.08	-0.11	-0.84	0.43144859	0.7832	-6.30
253652_at	putative protein nucleoid DNA-bin	---	AT4G30040	1.05	0.08	0.84	0.43149955	0.7832	-6.30
256251_at	hypothetical protein predicted by g	---	AT3G11330	-1.09	-0.13	-0.84	0.43159989	0.7833	-6.30
267475_at	expressed protein ; supported by f	---	AT2G02730	1.08	0.11	0.84	0.4317241	0.7835	-6.30
256243_at	basic chitinase identical to basic c	ATHCHIB	AT3G12500	1.26	0.34	0.84	0.43192033	0.7836	-6.30
259057_at	unknown protein ; supported by cl	---	AT3G03310	1.09	0.13	0.84	0.43192062	0.7836	-6.30
253575_at	putative protein TINY, Arabidopsis	---	AT4G31060	-1.07	-0.09	-0.84	0.43191923	0.7836	-6.30
254056_at	putative protein Group I Pectineste	---	AT4G25250	-1.07	-0.10	-0.84	0.43184056	0.7836	-6.30
262363_at	disease resistance protein, putativ	---	AT1G72850	-1.07	-0.09	-0.84	0.43199218	0.7836	-6.30
256291_at	protein kinase, putative contains P	AtNek7	AT3G12200	1.08	0.11	0.84	0.43197862	0.7836	-6.30
260184_s_at	putative protein predicted proteins	---	---	-1.05	-0.07	-0.84	0.43212221	0.7837	-6.30
257454_at	hypothetical protein predicted by g	---	AT1G65170	-1.09	-0.12	-0.84	0.43213771	0.7837	-6.30
254767_s_at	cytochrome p450 - like protein cyt	CYP71A19	AT4G13290 /	-1.06	-0.08	-0.84	0.43207017	0.7837	-6.30
259841_at	unknown protein ; supported by ful	---	AT1G52200	-1.09	-0.13	-0.84	0.43218813	0.7837	-6.30
258718_at	unknown protein ; supported by cl	---	AT3G09760	-1.07	-0.10	-0.83	0.43244743	0.7840	-6.30
245284_at	phytoene dehydrogenase precurso	PDS3	AT4G14210	1.10	0.14	0.83	0.43242771	0.7840	-6.30
253846_at	putative protein MSP1, Saccharon	---	AT4G28000	-1.06	-0.08	-0.83	0.43249098	0.7840	-6.30
266377_at	Mutator-like transposase similar to	---	---	-1.05	-0.07	-0.83	0.4324759	0.7840	-6.30
265627_at	Expressed protein ; supported by f	---	AT2G27285	1.08	0.11	0.83	0.43265892	0.7842	-6.30
267210_at	dihydroxypolyprenylbenzoate meth	ATCOQ3	AT2G30920	1.05	0.07	0.83	0.43261645	0.7842	-6.30
253103_at	putative auxin-induced protein hig	---	AT4G36110	-1.38	-0.47	-0.83	0.43267682	0.7842	-6.30
257220_at	MYB family transcription factor (A	ATMYB21	AT3G27810	-1.08	-0.11	-0.83	0.43288892	0.7845	-6.30
256265_at	serine carboxypeptidase, putative	scpl16	---	1.09	0.12	0.83	0.43308167	0.7848	-6.30
265451_at	unknown protein	---	AT2G46490	1.06	0.08	0.83	0.43315867	0.7848	-6.30
262658_at	ribonuclease contains similarity to	---	AT1G14220	-1.06	-0.08	-0.83	0.43325867	0.7848	-6.30
251565_at	putative protein several hypothetic	LBD29	AT3G58190	1.06	0.08	0.83	0.43320565	0.7848	-6.30
250024_at	NAM (no apical meristem)-like prot	ANAC087	AT5G18270	1.12	0.16	0.83	0.43323293	0.7848	-6.30
260354_at	unknown protein ;supported by ful	---	AT1G69330	-1.10	-0.14	-0.83	0.43317558	0.7848	-6.30
249886_at	unknown protein ; supported by cl	---	AT5G22320	1.11	0.15	0.83	0.4334432	0.7848	-6.30
248605_at	putative protein similar to unknown	---	AT5G49410	1.11	0.16	0.83	0.4333989	0.7848	-6.30
266336_at	putative Fe(II) transporter identica	ZIP3	AT2G32270	-1.09	-0.12	-0.83	0.43353187	0.7848	-6.30
245844_at	hypothetical protein predicted by g	---	AT1G26170	1.07	0.10	0.83	0.43357877	0.7848	-6.30
261654_at	hypothetical protein contains simil	---	AT1G01920	-1.09	-0.13	-0.83	0.43332301	0.7848	-6.30

262336_at	hypothetical protein predicted be g	TOM7-2	AT1G64220	-1.06	-0.08	-0.83	0.43352448	0.7848	-6.30
258668_at	hypothetical protein predicted by g	---	AT3G08780	1.06	0.09	0.83	0.43365455	0.7848	-6.30
261934_at	UDP-glucose glucosyltransferase,	UGT85A1	AT1G22400	1.22	0.29	0.83	0.43362179	0.7848	-6.30
263068_at	putative poly(A) polymerase	---	AT2G17580	-1.08	-0.12	-0.83	0.43356598	0.7848	-6.30
264245_at	galactinol synthase, putative simil	AtGolS7	AT1G60450	-1.06	-0.09	-0.83	0.43365761	0.7848	-6.30
266078_at	putative two-component response	ARR16	AT2G40670	1.07	0.09	0.83	0.43347171	0.7848	-6.30
264086_at	unknown protein ;supported by ful	---	AT2G31190	-1.09	-0.12	-0.83	0.43371065	0.7848	-6.30
248801_at	homeobox-leucine zipper protein-li	HAT2	AT5G47370	1.22	0.29	0.83	0.43375686	0.7849	-6.30
260305_at	putative ADP-ribosylation factor 1	ARFA1D	AT1G70490	1.08	0.11	0.83	0.43381443	0.7849	-6.30
251020_at	ABC transporter -like protein NBD	NAP9	AT5G02270	1.19	0.25	0.83	0.43389001	0.7850	-6.30
253471_at	hypothetical protein	---	---	-1.07	-0.10	-0.83	0.43393842	0.7850	-6.30
251833_at	putative protein various predicted	---	AT3G55160	1.06	0.09	0.83	0.43418964	0.7854	-6.30
254035_at	putative phosphatidylserine decar	PSD3	AT4G25970	1.07	0.09	0.83	0.43424633	0.7854	-6.30
249238_at	GAMM1 protein-like ; supported b	---	AT5G41970	1.07	0.09	0.83	0.43425229	0.7854	-6.30
259771_at	unknown protein	---	AT1G29470	1.10	0.14	0.83	0.43434273	0.7854	-6.30
245111_at	putative Ta11-like non-LTR retroel	---	---	-1.07	-0.10	-0.83	0.43436312	0.7854	-6.30
267623_at	unknown protein	---	AT2G39650	1.32	0.40	0.83	0.43436521	0.7854	-6.30
256752_at	hypothetical protein predicted by g	---	AT3G27180	1.12	0.16	0.83	0.43446114	0.7855	-6.30
247620_at	receptor like protein kinase recept	---	AT5G60310	-1.07	-0.10	-0.83	0.43460865	0.7856	-6.30
266862_at	putative MYB family transcription f	AtMYB104	AT2G26950	-1.05	-0.08	-0.83	0.43459971	0.7856	-6.30
255048_at	gibberellin-regulated protein GASA	GASA3	AT4G09600	1.06	0.08	0.83	0.43457092	0.7856	-6.30
259392_at	hypothetical protein similar to hypo	---	AT1G06380	-1.06	-0.09	-0.83	0.43477312	0.7858	-6.30
261655_at	hypothetical protein predicted by g	---	AT1G01940	1.10	0.13	0.83	0.4349882	0.7859	-6.30
260156_at	NAM-like protein similar to NAM (n	NAM	AT1G52880	-1.12	-0.16	-0.83	0.43518366	0.7859	-6.30
249333_at	GDSL-motif lipase/hydrolase-like p	GLIP1	AT5G40990	-1.30	-0.37	-0.83	0.43516001	0.7859	-6.30
259876_at	putative DnaJ protein similar to dr	---	AT1G76700	1.13	0.18	0.83	0.43516629	0.7859	-6.30
263358_x_at	hypothetical protein similar to hypo	---	---	-1.07	-0.10	-0.83	0.4350116	0.7859	-6.30
249599_at	putative protein AtPP protein, Bras	---	AT5G37990	-1.08	-0.11	-0.83	0.43501262	0.7859	-6.30
251705_at	DNA-binding protein-like DNA-bin	WRKY70	AT3G56400	1.61	0.69	0.83	0.43487887	0.7859	-6.30
263267_at	putative vacuolar proton-ATPase 1	---	AT2G16510	1.07	0.10	0.83	0.43506088	0.7859	-6.30
245538_at	p140mDia like protein	---	AT4G15200	1.07	0.10	0.83	0.43508773	0.7859	-6.30
256000_at	glycyl tRNA synthetase, putative s	---	AT1G29880	1.08	0.10	0.83	0.43513615	0.7859	-6.30
250465_at	putative protein various predicted	---	AT5G10070	-1.05	-0.08	-0.83	0.43525958	0.7860	-6.30
252175_at	zinc finger protein zinc finger prote	AtIDD2	AT3G50700	-1.06	-0.08	-0.83	0.43535266	0.7861	-6.30
265040_at	G-box binding factor, GBF4 Identi	GBF4	AT1G03970	-1.09	-0.13	-0.83	0.43538516	0.7861	-6.30

248826_at	casein kinase II beta chain ; suppo	CKB1	AT5G47080	-1.09	-0.12	-0.83	0.43550816	0.7863	-6.30
252822_at	Expressed protein ; supported by f	---	AT4G39955	-1.08	-0.11	-0.83	0.4357167	0.7865	-6.30
255400_at	hypothetical protein	---	---	-1.08	-0.10	-0.83	0.43572379	0.7865	-6.30
257614_at	putative non-LTR retroelement rev	---	---	-1.08	-0.11	-0.83	0.43569374	0.7865	-6.30
267043_at	unknown protein	---	AT2G34330	-1.08	-0.11	-0.83	0.43573741	0.7865	-6.30
253367_at	hypothetical protein	---	AT4G33180	-1.12	-0.16	-0.83	0.43577714	0.7865	-6.30
247822_at	putative protein sorting nexin 2, H	SNX2a	AT5G58440	-1.08	-0.11	-0.83	0.43600181	0.7865	-6.30
251654_at	putative protein several hypothetic	SDP1-LIKE	AT3G57140	-1.06	-0.08	-0.83	0.43600175	0.7865	-6.30
267621_at	unknown protein	---	---	1.08	0.11	0.83	0.43597827	0.7865	-6.30
260445_at	ARG1 protein (Altered Response t	ARG1	AT1G68370	1.08	0.11	0.83	0.43599388	0.7865	-6.30
266403_at	putative acid phosphatase contain	---	AT2G38600	-1.08	-0.11	-0.83	0.43604734	0.7865	-6.30
264009_at	putative disease resistance respor	---	AT2G21110	1.06	0.09	0.83	0.43601514	0.7865	-6.30
247493_at	copine - like protein copine I, Hom	BON1	AT5G61900	-1.14	-0.19	-0.83	0.43605123	0.7865	-6.30
252715_x_at	putative protein predicted protein,	---	AT3G43900	-1.08	-0.11	-0.83	0.43615664	0.7866	-6.30
251217_at	Sar1-like GTP binding protein sma	---	AT3G62560	1.07	0.10	0.83	0.43614734	0.7866	-6.30
262016_at	unknown protein	---	---	1.05	0.07	0.83	0.436207	0.7866	-6.30
249294_at	unknown protein	---	AT5G41270	1.11	0.15	0.83	0.43626916	0.7867	-6.30
249419_s_at	putative protein MADS-box protein	AGL98	AT5G39750 /	1.06	0.08	0.83	0.43633903	0.7867	-6.30
263205_at	Ca2+-dependent lipid-binding pro	NTMC2T2.1	AT1G05500	1.06	0.09	0.83	0.43632719	0.7867	-6.30
246553_at	putative protein hypothetical prote	EDL1	AT5G15440	-1.07	-0.10	-0.83	0.43641847	0.7867	-6.30
265947_at	putative WD-40 repeat protein ; su	---	AT2G19540	1.12	0.16	0.83	0.43659305	0.7868	-6.30
267286_at	putative seed maturation protein	---	AT2G23640	-1.06	-0.08	-0.83	0.43654761	0.7868	-6.30
260348_at	PPR-repeat protein, putative conta	---	AT1G69350	-1.10	-0.14	-0.83	0.43657173	0.7868	-6.30
267359_at	hypothetical protein predicted by g	---	AT2G40020	1.09	0.13	0.83	0.43649785	0.7868	-6.30
246649_at	putative protein predicted proteins	---	---	1.06	0.09	0.83	0.4365869	0.7868	-6.30
264895_at	putative 10kd chaperonin strongly	---	AT1G23100	1.18	0.23	0.83	0.43665347	0.7868	-6.30
247105_at	putative protein similar to unknown	DAR5	AT5G66630	-1.09	-0.13	-0.83	0.43672629	0.7869	-6.30
253468_at	putative protein predicted gene T1	---	AT4G32160	1.08	0.12	0.83	0.43682388	0.7870	-6.30
262729_at	rac-like GTP binding protein (ARA	ARAC5	AT1G75840	1.09	0.13	0.83	0.43689078	0.7870	-6.30
256513_at	unknown protein similar to phosph	SGR2	AT1G31480	1.06	0.09	0.83	0.43689492	0.7870	-6.30
247298_at	glucosidase II alpha subunit	RSW3	AT5G63840	1.06	0.09	0.83	0.43696449	0.7870	-6.31
249225_at	TMV resistance protein-like	---	AT5G42140	-1.11	-0.15	-0.83	0.4369432	0.7870	-6.31
247246_at	invertase inhibitor homolog (emb|C	C/VIF2	AT5G64620	1.13	0.17	0.82	0.43778577	0.7871	-6.31
258379_at	putative decarboxilase similar to 5	---	AT3G16700	1.10	0.14	0.83	0.43708055	0.7871	-6.31
265114_at	hypothetical protein contains simila	LRX2	AT1G62440	-1.14	-0.18	-0.83	0.43757106	0.7871	-6.31

263709_at	unknown protein ESTs gb|T20589	---	AT1G09310	1.42	0.51	0.83	0.43745854	0.7871	-6.31
253272_at	putative protein ;supported by full-	סטפ-01	AT4G34190	1.10	0.14	0.82	0.43778478	0.7871	-6.31
261595_at	hypothetical protein predicted by g	---	AT1G33070	-1.05	-0.08	-0.82	0.43770205	0.7871	-6.31
266695_at	putative CCCH-type zinc finger pro	---	AT2G19810	-1.17	-0.23	-0.83	0.43726779	0.7871	-6.31
249892_at	unknown protein	---	AT5G22600	-1.06	-0.08	-0.83	0.4373481	0.7871	-6.31
249463_s_at	putative protein predicted proteins	anac064	AT3G56530	-1.07	-0.10	-0.82	0.43772256	0.7871	-6.31
264861_at	putative glucosidase similar to a-g	---	AT1G24320	-1.06	-0.08	-0.82	0.43767297	0.7871	-6.31
254154_at	hypothetical protein	---	AT4G24460	-1.09	-0.12	-0.82	0.43773706	0.7871	-6.31
262271_x_at	hypothetical protein predicted by g	---	---	-1.12	-0.16	-0.83	0.43734409	0.7871	-6.31
263620_at	hypothetical protein predicted by g	---	---	-1.06	-0.09	-0.82	0.43772202	0.7871	-6.31
266967_at	unknown protein	---	AT2G39530	-1.06	-0.08	-0.83	0.43741944	0.7871	-6.31
247062_at	putative protein similar to unknown	---	AT5G66810	1.14	0.19	0.83	0.43742368	0.7871	-6.31
257694_at	nucleolar protein, putative nucleol	---	AT3G12860	-1.06	-0.09	-0.82	0.43777263	0.7871	-6.31
261328_at	unknown protein	---	AT1G44835	1.07	0.10	0.83	0.43713173	0.7871	-6.31
248992_at	disease resistance protein RPS4	---	AT5G45230	-1.07	-0.10	-0.82	0.43778322	0.7871	-6.31
253884_at	heat shock protein 21	HSP21	AT4G27670	-1.08	-0.11	-0.83	0.43719704	0.7871	-6.31
251419_at	putative protein various predicted	---	AT3G60470	-1.06	-0.09	-0.83	0.43729523	0.7871	-6.31
252266_at	putative protein ethylene-forming	---	AT3G49630	1.10	0.14	0.82	0.43782884	0.7871	-6.31
258237_at	myb protein identical to ATMYB3 C	ATMYB21	AT3G27810	-1.06	-0.09	-0.82	0.43779718	0.7871	-6.31
257253_at	unknown protein ; supported by cl	---	AT3G24190	-1.07	-0.10	-0.83	0.43754754	0.7871	-6.31
265499_at	putative glucosyltransferase	UGT73B5	AT2G15480	1.28	0.36	0.82	0.43794306	0.7871	-6.31
257417_at	hypothetical protein predicted by g	---	AT1G10110	-1.07	-0.10	-0.82	0.43788135	0.7871	-6.31
266124_at	putative PREG1-like negative regu	cycp3;1	AT2G45080	1.08	0.11	0.82	0.4379402	0.7871	-6.31
253600_at	SERINE CARBOXYPEPTIDASE I	scpl29	AT4G30810	-1.07	-0.09	-0.82	0.438037	0.7872	-6.31
258325_at	putative heat shock protein similar	HSFA6B	AT3G22830	-1.07	-0.09	-0.82	0.43812429	0.7873	-6.31
245790_at	glycerol-3-phosphate acyltransfera	ATS1	AT1G32200	1.08	0.11	0.82	0.4381845	0.7874	-6.31
265000_at	hypothetical protein predicted by g	---	AT1G67410	1.07	0.10	0.82	0.43824833	0.7874	-6.31
247548_at	putative protein various predicted	---	AT5G61400	-1.09	-0.13	-0.82	0.43828297	0.7874	-6.31
249415_at	promoter-binding protein like asco	CDF2	AT5G39660	1.12	0.17	0.82	0.43839339	0.7876	-6.31
263517_at	unknown protein ;supported by ful	RD2	AT2G21620	-1.11	-0.15	-0.82	0.43907015	0.7876	-6.31
266874_at	unknown protein	---	AT2G44760	-1.06	-0.08	-0.82	0.4394531	0.7876	-6.31
250762_at	putative protein similar to unknown	---	AT5G05990	1.16	0.21	0.82	0.43874185	0.7876	-6.31
259397_at	hypothetical protein predicted by g	---	AT1G17680	-1.06	-0.09	-0.82	0.43941994	0.7876	-6.31
249531_at	putative protein predicted protein,	AtGDU7	AT5G38770	-1.06	-0.09	-0.82	0.43919546	0.7876	-6.31
246499_at	putative protein Tat-SF1 - Homo s	---	AT5G16260	-1.09	-0.12	-0.82	0.4389844	0.7876	-6.31

258347_at	unknown protein identical to LEA-li	---	AT3G17520	-1.07	-0.10	-0.82	0.4388469	0.7876	-6.31
261144_s_at	unknown protein ;supported by full	---	AT1G19660 /	-1.07	-0.10	-0.82	0.43890139	0.7876	-6.31
263742_at	predicted protein	---	AT2G20625	-1.06	-0.08	-0.82	0.43910193	0.7876	-6.31
267341_at	hypothetical protein predicted by g	---	AT2G44200	-1.09	-0.13	-0.82	0.4394147	0.7876	-6.31
260584_at	putative beta-1,3-glucanase, C ter	---	AT2G43660	-1.06	-0.09	-0.82	0.43942653	0.7876	-6.31
245435_at	hypothetical protein	AT4G1714(	---	1.05	0.08	0.82	0.43901877	0.7876	-6.31
246125_at	Expressed protein ; supported by f	---	AT5G19875	-1.23	-0.30	-0.82	0.43898898	0.7876	-6.31
252612_at	hypothetical protein	---	AT3G45160	-1.40	-0.49	-0.82	0.43865944	0.7876	-6.31
256056_at	hypothetical protein contains simila	---	AT1G07190	-1.06	-0.08	-0.82	0.43915469	0.7876	-6.31
260765_at	actin 8 almost identical to actin 8 G	ACT8	AT1G49240	1.16	0.21	0.82	0.43859353	0.7876	-6.31
265077_at	hypothetical protein similar to RING	---	AT1G55530	-1.10	-0.14	-0.82	0.43857806	0.7876	-6.31
247707_at	scarecrow-like 11 - like scarecrow	---	AT5G59450	1.32	0.40	0.82	0.43905981	0.7876	-6.31
248368_at	mandelonitrile lyase-like protein ; s	---	AT5G51950	1.06	0.09	0.82	0.439222	0.7876	-6.31
266904_at	putative pyruvate dehydrogenase l	---	AT2G34590	-1.14	-0.19	-0.82	0.43934116	0.7876	-6.31
249394_at	putative protein predicted protein,	---	AT5G40180	-1.05	-0.07	-0.82	0.43923833	0.7876	-6.31
267615_at	putative phytocyanin	---	AT2G26720	-1.10	-0.13	-0.82	0.43897162	0.7876	-6.31
255493_at	putative glutamate-/aspartate-bind	---	AT4G02690	-1.06	-0.08	-0.82	0.43876458	0.7876	-6.31
255097_at	predicted transposon protein simil	---	---	1.09	0.12	0.82	0.4385941	0.7876	-6.31
253015_at	hypothetical protein	---	AT4G37950	-1.07	-0.09	-0.82	0.4394704	0.7876	-6.31
254745_at	putative protein G9A protein, Mus	SUVH9	AT4G13460	-1.05	-0.07	-0.82	0.43907713	0.7876	-6.31
248617_at	putative protein similar to unknown	---	AT5G49590	-1.06	-0.08	-0.82	0.43921224	0.7876	-6.31
248017_at	protein kinase-like protein	---	AT5G56460	-1.12	-0.16	-0.82	0.43917898	0.7876	-6.31
263458_at	putative GTP-binding protein	ATRABH1D	AT2G22290	1.08	0.11	0.82	0.43926494	0.7876	-6.31
250925_at	putative protein ; supported by full	---	AT5G03370	1.08	0.11	0.82	0.43925105	0.7876	-6.31
250227_at	FtsJ (dbj|BAA83750.1)	---	AT5G13830	1.08	0.11	0.82	0.43875242	0.7876	-6.31
257100_at	disease resistance protein, putativ	AtRLP41	AT3G25010	-1.08	-0.12	-0.82	0.43952656	0.7876	-6.31
258172_at	unknown protein similar to HYP1 G	---	AT3G21620	-1.06	-0.08	-0.82	0.43963041	0.7877	-6.31
262940_at	unknown protein	---	AT1G79520	-1.11	-0.15	-0.82	0.43974154	0.7878	-6.31
260162_at	unknown protein	GC5	AT1G79830	1.05	0.07	0.82	0.43974091	0.7878	-6.31
249806_at	putative protein contains similarity	---	AT5G23850	-1.15	-0.20	-0.82	0.43982138	0.7879	-6.31
251342_at	putative protein SAUR-AC1, Arabi	---	AT3G60690	1.10	0.13	0.82	0.43999058	0.7880	-6.31
257147_at	unknown protein	---	AT3G27270	1.10	0.14	0.82	0.43995241	0.7880	-6.31
252035_at	beta-ketoacyl-CoA synthase like p	KCS15	AT3G52160	-1.08	-0.11	-0.82	0.43994255	0.7880	-6.31
262462_at	hypothetical protein predicted by g	---	AT1G50350	1.06	0.08	0.82	0.43999194	0.7880	-6.31
260401_at	unknown protein similar to hypothe	---	AT1G69840	1.08	0.11	0.82	0.44004438	0.7880	-6.31

260784_at	MYB-related protein identical to G	ATMYB13	AT1G06180	1.14	0.20	0.82	0.44025269	0.7881	-6.31
254629_at	Expressed protein ; supported by f	---	AT4G18425	1.09	0.12	0.82	0.44015938	0.7881	-6.31
247473_at	putative protein AT-hook protein 2	---	AT5G62260	-1.09	-0.13	-0.82	0.44027846	0.7881	-6.31
265063_at	receptor kinase, putative similar to	---	AT1G61500	1.09	0.12	0.82	0.4401705	0.7881	-6.31
262002_at	hypothetical protein predicted by g	---	AT1G64450	-1.05	-0.08	-0.82	0.4403026	0.7881	-6.31
252554_s_at	protein kinase - like receptor-like p	MEE39	AT3G45920 /	-1.06	-0.08	-0.82	0.44024084	0.7881	-6.31
245455_at	disease resistance RPP5 like prote	---	AT4G16930	-1.06	-0.09	-0.82	0.44051564	0.7884	-6.31
262080_at	unknown protein ; supported by cD	CW14	AT1G59650	1.09	0.13	0.82	0.44059848	0.7884	-6.31
254975_at	putative Fe(II)/ascorbate oxidase	---	AT4G10500	-1.77	-0.83	-0.82	0.44060381	0.7884	-6.31
250804_at	putative protein contains similarity	---	AT5G05030	-1.08	-0.11	-0.82	0.44065337	0.7884	-6.31
264062_at	unknown protein	---	AT2G27950	-1.07	-0.10	-0.82	0.44063273	0.7884	-6.31
245107_at	putative heat shock transcription fa	AT-HSFB3	AT2G41690	-1.19	-0.25	-0.82	0.44080806	0.7886	-6.31
259870_at	putative heat shock protein predict	---	AT1G76780	-1.05	-0.08	-0.82	0.44077783	0.7886	-6.31
260877_at	unknown protein ; supported by ful	---	AT1G21500	1.10	0.14	0.82	0.44119291	0.7887	-6.31
253175_at	WD-40 repeat protein (MSI3) ; sup	MSI3	AT4G35050	1.12	0.16	0.82	0.44102708	0.7887	-6.31
256045_at	MAP3K gamma protein kinase, pu	MAPKKK13	AT1G07150	-1.08	-0.10	-0.82	0.44100285	0.7887	-6.31
267477_at	putative receptor-like protein kinas	PLPB	AT2G02710	1.14	0.18	0.82	0.44105712	0.7887	-6.31
245630_at	hypothetical protein similar to puta	---	AT1G25360	-1.07	-0.09	-0.82	0.44120396	0.7887	-6.31
252936_at	putative protein transcription initia	---	AT4G39160	-1.11	-0.14	-0.82	0.44101352	0.7887	-6.31
256187_at	55 kDa B regulatory subunit of pho	ATB ALPHA	AT1G51690	1.08	0.11	0.82	0.44121806	0.7887	-6.31
247297_at	peroxidase ATP3a (emb|CAA6734	---	AT5G64100	-1.20	-0.26	-0.82	0.44112254	0.7887	-6.31
257706_at	Expressed protein ; supported by c	---	AT3G12685	-1.11	-0.16	-0.82	0.44096976	0.7887	-6.31
256963_at	lysyl-tRNA synthetase, putative si	OVA5	AT3G13490	-1.10	-0.14	-0.82	0.44120072	0.7887	-6.31
262187_at	hypothetical protein	---	AT1G77960	1.06	0.09	0.82	0.4413177	0.7888	-6.31
260324_at	unknown protein similar to hypothe	ISPF	AT1G63970	1.09	0.12	0.82	0.44153122	0.7891	-6.31
249762_at	putative protein contains similarity	---	AT5G24000	-1.06	-0.09	-0.82	0.44154912	0.7891	-6.31
257418_at	hypothetical protein predicted by g	---	AT1G30850	1.10	0.13	0.82	0.44158709	0.7891	-6.31
245800_at	heat shock transcription factor, pu	HSFB4	AT1G46264	-1.06	-0.09	-0.82	0.44163971	0.7891	-6.31
253578_at	putative protein diacylglycerol kina	ATDGK7	AT4G30340	1.10	0.14	0.82	0.44191216	0.7894	-6.31
248720_at	protein kinase (EC 2.7.1.37) 5 (pir|	D6PKL2	AT5G47750	1.07	0.09	0.82	0.44188028	0.7894	-6.31
248288_at	unknown protein ; supported by cl	---	AT5G52840	1.09	0.12	0.82	0.44186177	0.7894	-6.31
246357_x_at	hypothetical protein	---	---	-1.07	-0.10	-0.82	0.44188199	0.7894	-6.31
261481_at	nucleoside triphosphatase, putativ	---	AT1G14260	-1.09	-0.12	-0.82	0.44197799	0.7894	-6.31
261818_at	similar to hypethetical 62.8 KD pro	---	AT1G11390	1.07	0.10	0.82	0.44199296	0.7894	-6.31
245196_at	F12A21.12 similar to pectate lyase	---	AT1G67750	-1.17	-0.22	-0.82	0.44205725	0.7894	-6.31

261817_at	hypothetical protein predicted by g	---	AT1G08180	1.15	0.21	0.82	0.44210203	0.7894	-6.31
256516_at	receptor protein kinase (TMK1), p	TMK1	AT1G66150	-1.11	-0.15	-0.82	0.4427007	0.7895	-6.31
250321_at	zinc finger transcription factor -like	---	AT5G12850	-1.07	-0.10	-0.82	0.44258812	0.7895	-6.31
259977_at	unknown protein ;supported by ful	---	AT1G76590	1.18	0.24	0.82	0.44246016	0.7895	-6.31
266495_at	cycloartenol synthase identical to S	CAS1	AT2G07050	1.07	0.10	0.82	0.44221456	0.7895	-6.31
253632_at	senescence-associated protein ho	TET9	AT4G30430	1.05	0.07	0.81	0.44298644	0.7895	-6.31
266230_at	hypothetical protein predicted by g	---	AT2G28830	1.14	0.18	0.81	0.44312107	0.7895	-6.31
252135_at	putative cold acclimation protein c	COR413-PI	AT3G50830	1.10	0.13	0.81	0.4431086	0.7895	-6.31
264357_at	hypothetical protein Similar to hypo	ATRRP4	AT1G03360	1.20	0.27	0.82	0.44274337	0.7895	-6.31
266869_at	putative glucosyltransferase	---	AT2G44660	-1.11	-0.15	-0.81	0.44354391	0.7895	-6.32
256885_at	chaperone-like ATPase contains P	---	AT3G15120	-1.08	-0.11	-0.82	0.44284712	0.7895	-6.31
251862_at	putative protein arm repeat contai	PUB14	AT3G54850	1.06	0.09	0.82	0.44261741	0.7895	-6.31
245264_at	Expressed protein ; supported by c	---	AT4G17245	1.22	0.29	0.81	0.4434374	0.7895	-6.32
251648_at	protein kinase - like protein S-rece	---	AT3G57720	-1.09	-0.12	-0.82	0.44293309	0.7895	-6.31
245024_at	ATPase alpha subunit	---	---	-1.06	-0.08	-0.82	0.44249814	0.7895	-6.31
252369_at	putative protein deoxycytidylate de	---	AT3G48540	-1.06	-0.09	-0.81	0.44314024	0.7895	-6.31
266047_at	unknown protein	---	AT2G40800	1.08	0.12	0.82	0.44249238	0.7895	-6.31
250173_at	MYB40 - putative transcription fact	AtMYB40	AT5G14340	-1.08	-0.11	-0.82	0.44277944	0.7895	-6.31
253516_at	hypothetical protein	---	AT4G31360	1.11	0.15	0.82	0.4426803	0.7895	-6.31
254512_at	terpene cyclase like protein vetisp	---	AT4G20230	1.07	0.10	0.82	0.44242554	0.7895	-6.31
253709_at	pyrophosphate-dependent phosph	PFK1	AT4G29220	-1.09	-0.13	-0.81	0.4435251	0.7895	-6.32
257646_at	methionine aminopeptidase, putat	MAP1B	AT3G25740	-1.14	-0.18	-0.82	0.4423845	0.7895	-6.31
252918_at	putative protein	---	AT4G38980	1.05	0.08	0.81	0.44369158	0.7895	-6.32
246360_at	hypothetical protein	---	---	-1.06	-0.09	-0.81	0.44348602	0.7895	-6.32
263246_at	hypothetical protein predicted by g	---	AT2G31460	-1.08	-0.11	-0.81	0.44302742	0.7895	-6.31
251069_at	(1-4)-beta-mannan endohydrolase	---	AT5G01930	1.16	0.21	0.81	0.44364374	0.7895	-6.32
249439_at	thaumatin-like protein thaumatin-li	---	AT5G40020	1.14	0.19	0.82	0.44272271	0.7895	-6.31
251090_at	putative protein ACR1-protein - Sa	---	AT5G01340	1.21	0.28	0.81	0.44319618	0.7895	-6.31
259094_at	putative cysteine synthase similar	CYSD1	AT3G04940	1.10	0.14	0.82	0.44250556	0.7895	-6.31
255936_at	calcium dependent protein kinase	---	AT1G12680	-1.07	-0.09	-0.82	0.44221547	0.7895	-6.31
253501_at	predicted protein predicted protein	HSL1	AT4G32010	-1.07	-0.09	-0.81	0.44348038	0.7895	-6.32
265180_at	putative OBP32pep protein ;suppo	---	AT1G23590	-1.05	-0.07	-0.81	0.44297649	0.7895	-6.31
255815_at	histone H3, putative similar to hist	MGH3	AT1G19890	-1.08	-0.11	-0.81	0.44366818	0.7895	-6.32
264269_at	hypothetical protein predicted by g	---	AT1G60240	-1.08	-0.11	-0.82	0.44291671	0.7895	-6.31
249447_at	PTEN -like protein PTEN/MMAC1	PTEN1	AT5G39400	1.10	0.14	0.81	0.44336083	0.7895	-6.32

261263_at	H-protein promoter binding factor-	---	AT1G26790	-1.05	-0.08	-0.81	0.44354279	0.7895	-6.32
258364_at	unknown protein	GLIP4	AT3G14225	-1.14	-0.19	-0.81	0.44355581	0.7895	-6.32
245686_at	Expressed protein ; supported by c	J2	AT5G22060	-1.14	-0.19	-0.81	0.44346076	0.7895	-6.32
246333_at	proteinkinase AtPP -like protein A	---	AT3G44840	-1.07	-0.10	-0.81	0.4434495	0.7895	-6.32
247672_at	senescence-associated protein - l	TET4	AT5G60220	-1.05	-0.07	-0.81	0.44316284	0.7895	-6.31
247742_at	random slug protein - like random	---	AT5G58980	-1.08	-0.11	-0.81	0.44296264	0.7895	-6.31
256557_at	hypothetical protein similar to hypo	---	---	-1.06	-0.09	-0.81	0.44364856	0.7895	-6.32
258527_at	branched chain alpha-keto acid de	BCE2	AT3G06850	1.24	0.31	0.81	0.44322817	0.7895	-6.31
267149_s_at	Mutator-like transposase similar to	---	---	-1.08	-0.12	-0.82	0.4426473	0.7895	-6.31
251709_at	response regulator-like protein res	ARR17	AT3G56380	-1.05	-0.07	-0.82	0.44286998	0.7895	-6.31
256604_at	hypothetical protein predicted by g	---	---	-1.06	-0.08	-0.82	0.44279802	0.7895	-6.31
267287_at	putative pectinesterase	sks16	AT2G23630	-1.06	-0.08	-0.81	0.44380344	0.7896	-6.32
252387_at	aldose 1-epimerase - like protein a	---	AT3G47800	-1.10	-0.13	-0.81	0.44379422	0.7896	-6.32
256158_at	hypothetical protein contains simila	ATPSK1	AT1G13590	1.06	0.09	0.81	0.44390123	0.7896	-6.32
245726_at	homeobox protein, putative simila	HDG11	AT1G73360	-1.06	-0.09	-0.81	0.4438902	0.7896	-6.32
245656_at	hypothetical protein predicted by g	---	AT1G56620	-1.07	-0.09	-0.81	0.44403165	0.7897	-6.32
262274_at	deaminase, putative similar to cyti	TADA	AT1G68720	-1.06	-0.08	-0.81	0.44401627	0.7897	-6.32
263649_at	putative 1-aminocyclopropane-1-ca	---	AT1G04380	-1.06	-0.08	-0.81	0.44400507	0.7897	-6.32
248438_at	putative protein contains similarity	EMF2	AT5G51230	1.10	0.14	0.81	0.44413931	0.7898	-6.32
257914_at	Expressed protein ; supported by c	---	AT3G25545	-1.08	-0.11	-0.81	0.44419435	0.7898	-6.32
261145_at	thioredoxin identical to GB:CAA84	ATTRX4	AT1G19730	1.07	0.09	0.81	0.44424277	0.7899	-6.32
254402_at	putative protein predicted protein,	---	AT4G21310	1.11	0.14	0.81	0.44430235	0.7899	-6.32
256140_at	hypothetical protein contains simila	---	AT1G48650	1.10	0.14	0.81	0.44435291	0.7899	-6.32
257101_at	disease resistance protein, putativ	AtRLP42	AT3G25020	1.07	0.10	0.81	0.44440937	0.7900	-6.32
248980_at	putative protein similar to unknown	AtPP2-A7	AT5G45090	-1.09	-0.12	-0.81	0.44443133	0.7900	-6.32
264387_at	putative growth regulator protein c	---	AT1G11990	-1.07	-0.10	-0.81	0.44458417	0.7902	-6.32
252695_s_at	hypothetical protein predicted prot	---	---	1.05	0.07	0.81	0.44465959	0.7902	-6.32
267645_at	putative beta-glucosidase	BGLU33	AT2G32860	-1.20	-0.26	-0.81	0.44479426	0.7903	-6.32
261008_at	hypothetical protein contains simila	---	AT1G26370	-1.08	-0.12	-0.81	0.44489201	0.7903	-6.32
247012_at	putative protein contains similarity	TRB2	AT5G67580	-1.07	-0.10	-0.81	0.44476873	0.7903	-6.32
262815_at	putative cytochrome P450 strong s	CYP71A18	AT1G11610	-1.13	-0.18	-0.81	0.44493975	0.7903	-6.32
254899_at	serine/threonine kinase-like protei	---	AT4G11490	-1.09	-0.12	-0.81	0.44491941	0.7903	-6.32
256475_s_at	myosin heavy chain ATM2, putativ	---	AT1G42680 /	-1.07	-0.09	-0.81	0.44495592	0.7903	-6.32
252169_at	putative protein several bacterial p	---	AT3G50520	1.11	0.15	0.81	0.44494203	0.7903	-6.32
252230_at	putative protein various predicted	---	AT3G49810	1.24	0.31	0.81	0.44502731	0.7904	-6.32

267578_at	Expressed protein ; supported by c	---	AT2G30695	1.13	0.18	0.81	0.44508223	0.7904	-6.32
250259_at	putative protein similar to unknown	---	AT5G13800	-1.09	-0.13	-0.81	0.44518364	0.7906	-6.32
256816_at	unknown protein	---	AT3G21400	1.07	0.10	0.81	0.44530249	0.7906	-6.32
260869_at	stearoyl acyl carrier protein desatu	---	AT1G43800	-1.06	-0.08	-0.81	0.4452763	0.7906	-6.32
256869_at	nodulin, putative similar to nodulin	---	AT3G26420	-1.10	-0.14	-0.81	0.44546383	0.7909	-6.32
245332_at	isomerase like protein ;supported b	---	AT4G15940	-1.05	-0.07	-0.81	0.44574106	0.7909	-6.32
264856_at	3-hydroxy-3-methylglutaryl-coenzy	HMG2	AT2G17370	1.09	0.13	0.81	0.44554703	0.7909	-6.32
261125_at	zinc finger protein 2, putative simil	---	AT1G04990	1.13	0.18	0.81	0.44557502	0.7909	-6.32
262976_at	unknown protein	SRS5	AT1G75520	-1.08	-0.12	-0.81	0.44578794	0.7909	-6.32
266436_at	putative clathrin binding protein (ep	---	AT2G43160	-1.13	-0.17	-0.81	0.44563058	0.7909	-6.32
263767_at	putative retroelement pol polyprote	---	---	-1.05	-0.07	-0.81	0.44566097	0.7909	-6.32
246993_at	Cys2/His2-type zinc finger protein	AZF1	AT5G67450	1.24	0.31	0.81	0.4456931	0.7909	-6.32
253554_at	putative protein predicted protein,	---	AT4G30940	-1.10	-0.14	-0.81	0.44578354	0.7909	-6.32
261091_at	protein kinase, putative contains P	---	AT1G07550	1.06	0.09	0.81	0.44562435	0.7909	-6.32
252435_at	putative protein several hypothetic	---	---	-1.07	-0.10	-0.81	0.44589177	0.7909	-6.32
253346_at	hypothetical protein	---	AT4G33600	-1.06	-0.09	-0.81	0.44592153	0.7909	-6.32
247211_at	unknown protein ; supported by fu	---	AT5G64880	-1.13	-0.17	-0.81	0.44589394	0.7909	-6.32
265362_at	putative retroelement pol polyprote	---	---	1.06	0.09	0.81	0.44593035	0.7909	-6.32
248737_at	unknown protein	---	AT5G48120	1.10	0.14	0.81	0.44598609	0.7909	-6.32
265744_at	putative CENP-B/ARS binding prot	---	---	1.05	0.07	0.81	0.44600378	0.7909	-6.32
266668_at	hypothetical protein predicted by g	---	AT2G29760	1.14	0.19	0.81	0.44604453	0.7909	-6.32
263898_at	SKP1 interacting partner 6 (SKIP6	SKIP6	AT2G21950	1.07	0.10	0.81	0.44607746	0.7909	-6.32
252820_at	plasma membrane H+-ATPase-lik	AHA8	AT3G42640	1.11	0.15	0.81	0.44615658	0.7910	-6.32
266151_x_at	En/Spm transposon protein (mosa	---	---	1.07	0.09	0.81	0.44626256	0.7911	-6.32
255197_x_at	contains similarity to Oryza sativa	---	---	-1.08	-0.11	-0.81	0.44631847	0.7911	-6.32
246128_at	putative protein predicted proteins	---	---	1.07	0.10	0.81	0.44629894	0.7911	-6.32
246537_at	putative protein protochlorophyllid	---	AT5G15940	-1.07	-0.10	-0.81	0.44648307	0.7913	-6.32
251965_at	putative protein variety of predicte	---	AT3G53360	-1.07	-0.10	-0.81	0.44673135	0.7915	-6.32
254648_at	lipase-like protein Pn47p, Ipomoea	---	AT4G18550	1.06	0.09	0.81	0.44671973	0.7915	-6.32
263441_at	putative kinesin-like spindle protein	---	AT2G28620	1.05	0.08	0.81	0.44666439	0.7915	-6.32
249002_at	putative protein contains similarity	---	AT5G44520	-1.08	-0.12	-0.81	0.44663637	0.7915	-6.32
249855_at	unknown protein	---	AT5G22970	-1.07	-0.09	-0.81	0.44690582	0.7917	-6.32
246875_at	pathogenesis-related protein - like	---	AT5G26130	-1.06	-0.09	-0.81	0.44692047	0.7917	-6.32
251212_at	putative protein hypothetical prote	---	---	-1.06	-0.09	-0.81	0.44689238	0.7917	-6.32
265457_at	unknown protein ; supported by fu	---	AT2G46550	1.09	0.12	0.81	0.44698296	0.7917	-6.32

261303_at	unknown protein contains DNA-bir	HON5	AT1G48620	1.05	0.07	0.81	0.4472293	0.7920	-6.32
260849_at	pectinesterase, putative similar to	sks7	AT1G21860	-1.06	-0.08	-0.81	0.44721591	0.7920	-6.32
247840_at	putative protein protein x 0001, Hc	---	AT5G58020	-1.06	-0.08	-0.81	0.44728205	0.7921	-6.32
252707_at	transporter-like protein multidrug-e	ZIFL2	AT3G43790	1.08	0.11	0.81	0.44741604	0.7921	-6.32
264931_at	polygalacturonase, putative simila	---	AT1G60590	-1.07	-0.10	-0.81	0.44741488	0.7921	-6.32
257764_at	disease resistance protein, putativ	AtRLP36	AT3G23010	1.12	0.17	0.81	0.44738556	0.7921	-6.32
247652_at	histone H2B - like protein histone	HTB4	AT5G59910	-1.08	-0.11	-0.81	0.44747196	0.7921	-6.32
256206_at	hypothetical protein predicted by g	---	AT1G50910	-1.09	-0.13	-0.81	0.44752151	0.7922	-6.32
245714_at	RNA-binding protein-like	---	AT5G04280	-1.07	-0.09	-0.81	0.44772275	0.7922	-6.32
264942_at	unknown protein ; supported by cD	---	AT1G67340	-1.09	-0.13	-0.81	0.44761977	0.7922	-6.32
256384_at	hypothetical protein	---	AT1G66660	1.08	0.10	0.81	0.4476769	0.7922	-6.32
252522_at	hypothetical protein	---	AT1G32337 /	-1.06	-0.08	-0.81	0.4476795	0.7922	-6.32
262475_at	hypothetical protein predicted by g	---	AT1G50340	1.07	0.10	0.81	0.44770036	0.7922	-6.32
257044_at	hypothetical protein predicted by g	ARC5	AT3G19720	-1.08	-0.11	-0.81	0.44804857	0.7923	-6.32
264887_at	unknown protein similar to ripenin	---	AT1G23120	1.10	0.14	0.81	0.44789175	0.7923	-6.32
260858_at	hypothetical protein predicted by g	---	AT1G43770	-1.07	-0.09	-0.81	0.44817009	0.7923	-6.32
265958_at	putative adenylate kinase ;suppor	ADK	AT2G37250	1.12	0.16	0.81	0.44793942	0.7923	-6.32
260880_at	hypothetical protein similar to unkr	---	AT1G21380	-1.07	-0.10	-0.81	0.44809129	0.7923	-6.32
248725_at	acetyl-CoA:benzylalcohol acetyltra	---	AT5G47980	-1.07	-0.10	-0.81	0.44816055	0.7923	-6.32
246874_at	arabinosidase - like protein arabin	ASD2	AT5G26120	1.07	0.10	0.81	0.44815868	0.7923	-6.32
257622_at	hypothetical protein contains Pfam	---	AT3G20280	1.10	0.13	0.81	0.4479427	0.7923	-6.32
245970_at	beta-galactosidase ; supported by	BGAL7	AT5G20710	-1.08	-0.11	-0.81	0.44783728	0.7923	-6.32
245958_at	GNOM-like protein pattern-formati	---	AT5G19610	-1.06	-0.09	-0.81	0.44799602	0.7923	-6.32
249444_at	putative protein S-locus-specific g	---	AT5G39370	-1.06	-0.09	-0.81	0.44802631	0.7923	-6.32
267452_at	auxin response transcription factor	ETT	AT2G33860	-1.07	-0.10	-0.81	0.4482639	0.7924	-6.32
263712_at	Expressed protein ; supported by f	NFD6	AT2G20585	1.10	0.14	0.80	0.44852313	0.7927	-6.32
257904_at	myb transcription factor, putative s	TDF1	AT3G28470	1.05	0.08	0.80	0.44851197	0.7927	-6.32
245684_at	Expressed protein ; supported by c	RHF2A	AT5G22000	-1.06	-0.08	-0.80	0.44848412	0.7927	-6.32
255573_at	hypothetical protein	---	AT4G01400	1.05	0.07	0.80	0.44870983	0.7929	-6.32
266231_at	putative protein kinase	PSKR1	AT2G02220	1.24	0.31	0.80	0.44875624	0.7929	-6.32
263130_at	hypothetical protein predicted by g	POLD3	AT1G78650	1.13	0.17	0.80	0.4487369	0.7929	-6.32
246201_at	minor allergen ;supported by full-le	---	AT4G36750	1.05	0.08	0.80	0.44897832	0.7932	-6.32
248380_at	phosphoglucomutase (emb|CAB64	PGM	AT5G51820	1.14	0.19	0.80	0.44906538	0.7932	-6.32
246823_at	putative protein	---	AT5G26970	-1.05	-0.07	-0.80	0.44903438	0.7932	-6.32
258435_at	unknown protein ;supported by ful	---	AT3G16740	1.07	0.10	0.80	0.44899869	0.7932	-6.32

245064_at	Expressed protein ; supported by f	---	AT2G39725	1.12	0.16	0.80	0.44918152	0.7933	-6.32
265979_at	putative replication protein A1	---	---	-1.07	-0.10	-0.80	0.449155	0.7933	-6.32
252132_at	putative LEA protein Picea glauca	---	AT3G50790	-1.14	-0.19	-0.80	0.44937602	0.7934	-6.32
266917_at	unknown protein	DTA2	AT2G45830	1.06	0.08	0.80	0.44930128	0.7934	-6.32
258874_at	hypothetical protein similar to unkn	---	AT3G03230	1.08	0.12	0.80	0.44936495	0.7934	-6.32
261470_at	ethylene-responsive element bind	ERF11	AT1G28370	-1.35	-0.44	-0.80	0.44939316	0.7934	-6.32
245068_at	putative glucosyltransferase	UGT84B1	AT2G23260	-1.07	-0.09	-0.80	0.44939518	0.7934	-6.32
254105_at	magnesium-protoporphyrin IX met	CHLM	AT4G25080	1.07	0.10	0.80	0.44988012	0.7938	-6.33
251525_at	putative protein several hypothetic	---	AT3G59000	1.08	0.10	0.80	0.45004854	0.7938	-6.33
263112_at	unknown protein Strong similarity t	---	AT1G03080	-1.07	-0.10	-0.80	0.44976158	0.7938	-6.33
252436_x_at	putative protein several hypothetic	---	---	-1.12	-0.17	-0.80	0.44997212	0.7938	-6.33
250782_at	SYN1 splice variant 1 (gb AAF089	SYN1	AT5G05490	-1.07	-0.09	-0.80	0.45001595	0.7938	-6.33
249160_at	putative protein similar to unknown	---	AT5G42660	1.06	0.08	0.80	0.44978882	0.7938	-6.33
255418_at	predicted protein of unknown funct	---	AT4G03200	-1.08	-0.12	-0.80	0.45003614	0.7938	-6.33
267223_at	hypothetical protein predicted by g	AtITPK4	AT2G43980	-1.07	-0.10	-0.80	0.44978513	0.7938	-6.33
260233_at	putative cytochrome P450 similar t	CYP98A9	AT1G74550	-1.11	-0.15	-0.80	0.45000428	0.7938	-6.33
246186_at	PINHEAD - like protein PINHEAD	---	AT5G21030	-1.10	-0.13	-0.80	0.44981488	0.7938	-6.33
262845_at	unknown protein ; supported by cD	---	AT1G14740	1.13	0.18	0.80	0.45000964	0.7938	-6.33
258499_at	putative RAD23 similar to RAD23 p	RAD23-3	AT3G02540	1.07	0.09	0.80	0.4499458	0.7938	-6.33
249200_at	5-3 exoribonuclease 2 ; supported	XRN2	AT5G42540	1.08	0.12	0.80	0.45017648	0.7939	-6.33
255487_at	tryptophan synthase alpha 1-like p	---	AT4G02610	1.07	0.10	0.80	0.45018158	0.7939	-6.33
266987_at	unknown protein	---	AT2G39280	-1.05	-0.07	-0.80	0.45018252	0.7939	-6.33
257988_at	unknown protein ; supported by cl	---	AT3G20870	1.07	0.09	0.80	0.45029647	0.7940	-6.33
266182_at	hypothetical protein predicted by g	---	AT2G02370	-1.09	-0.12	-0.80	0.45044634	0.7942	-6.33
260589_at	hypothetical protein predicted by g	---	AT1G53400	1.05	0.08	0.80	0.45052947	0.7942	-6.33
256553_at	hypothetical protein contains simila	---	---	1.07	0.09	0.80	0.45053923	0.7942	-6.33
264677_at	hypothetical protein predicted by g	HYL1	AT1G09700	-1.05	-0.07	-0.80	0.45058341	0.7943	-6.33
253376_at	hypothetical protein Arabidopsis th	---	AT4G33290	-1.05	-0.07	-0.80	0.45062907	0.7943	-6.33
257200_at	hypothetical protein predicted by g	---	---	1.05	0.07	0.80	0.45069195	0.7943	-6.33
266971_at	unknown protein	---	AT2G39580	-1.14	-0.19	-0.80	0.45074579	0.7944	-6.33
266153_at	hypothetical protein	---	---	-1.06	-0.08	-0.80	0.45081746	0.7944	-6.33
257864_at	hypothetical protein predicted by g	---	AT3G17740	-1.09	-0.13	-0.80	0.4509491	0.7946	-6.33
247669_at	putative protein transcriptional rep	---	AT5G60170	-1.09	-0.12	-0.80	0.45107827	0.7948	-6.33
249177_at	unknown protein ;supported by ful	---	AT5G42850	1.06	0.09	0.80	0.45159651	0.7950	-6.33
247882_at	Expressed protein ; supported by f	---	AT5G57785	-1.24	-0.31	-0.80	0.45132288	0.7950	-6.33

265012_at	putative b-keto acyl reductase sim	KCR2	AT1G24470	-1.07	-0.09	-0.80	0.45130838	0.7950	-6.33
259234_at	unknown protein similar to unknow	---	AT3G11620	-1.07	-0.10	-0.80	0.45171997	0.7950	-6.33
258824_at	unknown protein	---	AT3G07190	1.09	0.12	0.80	0.4519236	0.7950	-6.33
251910_at	serine/threonine-specific kinase lik	---	AT3G53810	1.27	0.35	0.80	0.45157749	0.7950	-6.33
248835_at	NBS/LRR disease resistance prote	---	AT5G47250	1.12	0.16	0.80	0.45172153	0.7950	-6.33
259852_at	disulfide bond formation protein, p	AERO1	AT1G72280	-1.15	-0.21	-0.80	0.45183619	0.7950	-6.33
256782_at	dirigent protein, putative similar to	---	AT3G13660	-1.05	-0.07	-0.80	0.45177592	0.7950	-6.33
261554_at	PPR-repeat protein contains multip	---	AT1G63400	1.05	0.07	0.80	0.45165434	0.7950	-6.33
265367_at	hypothetical protein predicted by g	---	---	1.05	0.07	0.80	0.45169173	0.7950	-6.33
267583_at	unknown protein	---	AT2G41960	-1.05	-0.07	-0.80	0.45162889	0.7950	-6.33
265921_at	putative C2H2-type zinc finger prot	---	AT2G18490	-1.06	-0.08	-0.80	0.45191323	0.7950	-6.33
262478_at	hypothetical protein similar to hypo	---	AT1G11170	-1.07	-0.10	-0.80	0.45179918	0.7950	-6.33
265059_at	unknown protein ; supported by cD	AR791	AT1G52080	-1.09	-0.13	-0.80	0.45169823	0.7950	-6.33
246285_at	putative protein	---	AT4G36980	1.05	0.08	0.80	0.45179581	0.7950	-6.33
256740_at	hypothetical protein predicted by g	---	AT3G29330	1.06	0.08	0.80	0.45159489	0.7950	-6.33
265371_at	putative PttA-like transposon prote	---	---	-1.06	-0.08	-0.80	0.4514406	0.7950	-6.33
248653_at	disease resistance protein-like	---	AT5G49290	-1.06	-0.09	-0.80	0.45187868	0.7950	-6.33
261393_at	NAM (no apical meristem)-like pro	SMB	AT1G79580	-1.06	-0.08	-0.80	0.45161764	0.7950	-6.33
260135_at	calmodulin-related protein similar	---	AT1G66400	-1.23	-0.30	-0.80	0.45155992	0.7950	-6.33
265233_s_at	hypothetical protein	---	AT2G07718	-1.07	-0.10	-0.80	0.45210516	0.7952	-6.33
260785_at	hypothetical protein predicted by g	---	AT1G06200	-1.06	-0.09	-0.80	0.45213532	0.7952	-6.33
250953_at	putative protein ;supported by full-	DPB	AT5G03415	1.10	0.14	0.80	0.45219599	0.7953	-6.33
260799_at	UDP-glucose glucosyltransferase,	AtUGT85A4	AT1G78270	1.08	0.11	0.80	0.45228401	0.7953	-6.33
250567_at	hypothetical protein	---	AT5G08090	1.07	0.10	0.80	0.45228335	0.7953	-6.33
265582_at	putative RING zinc finger protein	---	AT2G20030	-1.08	-0.11	-0.80	0.45233157	0.7953	-6.33
262701_at	hypothetical protein predicted by g	---	AT1G16480	1.08	0.11	0.80	0.45237697	0.7953	-6.33
267012_at	similar to latex allergen from Heve	PLP6	AT2G39220	1.18	0.24	0.80	0.45241412	0.7953	-6.33
247404_at	permease 1 - like protein permeas	---	AT5G62890	1.15	0.20	0.80	0.45245034	0.7953	-6.33
245458_at	kinase like protein	---	AT4G16970	1.07	0.09	0.80	0.45252429	0.7954	-6.33
245915_s_at	tubulin alpha-5 chain-like protein t	TUA3	AT5G19770	1.07	0.09	0.80	0.45268354	0.7955	-6.33
261184_at	pol polyprotein, putative similar to	---	---	-1.08	-0.11	-0.80	0.45265737	0.7955	-6.33
265517_at	putative S1 self-incompatibility pro	---	AT2G06090	-1.06	-0.08	-0.80	0.45262395	0.7955	-6.33
260800_at	unknown protein	TSD2	AT1G78240	-1.10	-0.13	-0.80	0.45276031	0.7956	-6.33
259482_at	receptor-like serine/threonine kina	RKF2	AT1G19090	-1.07	-0.10	-0.80	0.45286391	0.7956	-6.33
258089_at	hypothetical protein predicted by g	---	AT3G14740	1.13	0.18	0.80	0.45284652	0.7956	-6.33

247726_at	telomere repeat-binding protein	TRP1	AT5G59430	-1.08	-0.12	-0.80	0.45292006	0.7957	-6.33
267549_at	hypothetical protein predicted by g	---	AT2G32640	-1.19	-0.26	-0.80	0.4530262	0.7958	-6.33
247264_at	putative protein contains similarity	XND1	AT5G64530	-1.16	-0.22	-0.80	0.45310246	0.7959	-6.33
255218_at	putative athila transposon protein	---	---	-1.05	-0.07	-0.80	0.45312492	0.7959	-6.33
257380_at	hypothetical protein predicted by g	---	AT2G28090	-1.08	-0.11	-0.80	0.45324056	0.7959	-6.33
263190_at	mutator-like transposase, putative	---	---	-1.05	-0.07	-0.80	0.45324871	0.7959	-6.33
257564_at	unknown protein	---	AT3G28610	-1.09	-0.13	-0.80	0.45321476	0.7959	-6.33
250422_at	putative protein KIAA0255 gene, h	---	AT5G10840	1.11	0.15	0.80	0.45331398	0.7959	-6.33
248472_at	cyclin-dependent protein kinase-lik	---	AT5G50860	-1.07	-0.10	-0.80	0.45335398	0.7960	-6.33
258027_at	hypothetical protein predicted by g	---	AT3G19515	1.07	0.09	0.80	0.45353619	0.7961	-6.33
246059_at	putative protein KED, Nicotiana ta	---	AT5G08450	-1.06	-0.08	-0.80	0.45352003	0.7961	-6.33
254826_at	putative protein predicted protein,	---	AT4G12640	1.08	0.11	0.80	0.45346687	0.7961	-6.33
245143_at	unknown protein ;supported by ful	ZPR1	AT2G45450	-1.15	-0.20	-0.80	0.45368676	0.7963	-6.33
260776_at	zinc finger protein, putative similar	---	AT1G14580	1.16	0.22	0.79	0.45377384	0.7964	-6.33
250889_at	putative protein exostose-related p	---	AT5G04500	-1.07	-0.09	-0.79	0.45388342	0.7965	-6.33
267521_at	hypothetical protein predicted by g	---	AT2G30480	-1.09	-0.12	-0.79	0.45388422	0.7965	-6.33
256911_at	glutamine:fructose-6-phosphate a	---	AT3G24090	1.25	0.32	0.79	0.45398564	0.7966	-6.33
253326_at	putative protein polygalacturonase	---	AT4G33440	-1.07	-0.10	-0.79	0.45410218	0.7967	-6.33
247395_at	putative protein predicted proteins	---	AT5G62910	1.07	0.10	0.79	0.45409865	0.7967	-6.33
246450_at	Heat Shock Factor 3	HSF3	AT5G16820	1.06	0.08	0.79	0.45424632	0.7967	-6.33
258576_at	putative 40S ribosomal protein S16	---	AT3G04230	1.09	0.13	0.79	0.45423397	0.7967	-6.33
267306_at	Ran binding protein (AtRanBP1b) i	---	AT2G30060	-1.07	-0.10	-0.79	0.45417947	0.7967	-6.33
258664_at	E2, ubiquitin-conjugating enzyme,	UBC12	AT3G08700	-1.07	-0.10	-0.79	0.45434539	0.7968	-6.33
255536_at	Expressed protein ; supported by f	---	AT4G01575	-1.11	-0.15	-0.79	0.45472675	0.7969	-6.33
257369_at	hypothetical protein predicted by g	BPC7	AT2G35550	1.07	0.10	0.79	0.45485007	0.7969	-6.33
257892_at	unknown protein similar to ER6 pro	---	AT3G17020	1.06	0.09	0.79	0.45471796	0.7969	-6.33
249303_at	putative protein strong similarity to	---	AT5G41460	1.11	0.14	0.79	0.45483363	0.7969	-6.33
261084_at	tropinone reductase-I, putative sin	---	AT1G07440	-1.11	-0.15	-0.79	0.45451157	0.7969	-6.33
247409_at	dihydroneopterin aldolase-like prot	---	AT5G62980	1.10	0.14	0.79	0.45478655	0.7969	-6.33
249411_at	raffinose synthase -like protein raf	SIP1	AT5G40390	1.18	0.24	0.79	0.45453207	0.7969	-6.33
256329_at	unknown protein	SEC5A	AT1G76850	-1.05	-0.07	-0.79	0.45444452	0.7969	-6.33
261783_at	vacuolar assembly protein vps41,	---	AT1G08190	-1.08	-0.10	-0.79	0.45475602	0.7969	-6.33
247579_at	cytochrome P450 - like protein cyt	CYP89A3	AT5G61320	-1.06	-0.08	-0.79	0.4547423	0.7969	-6.33
261239_at	Avr9 elicitor response protein, put	---	AT1G32930	-1.06	-0.08	-0.79	0.45481571	0.7969	-6.33
259623_at	hypothetical protein predicted by g	---	AT1G42700	-1.08	-0.11	-0.79	0.45447858	0.7969	-6.33

265769_at	unknown protein weak similarity to	---	AT2G48090	-1.07	-0.10	-0.79	0.45462833	0.7969	-6.33
246013_at	vacuolar calcium binding protein -	---	AT5G10660	-1.06	-0.08	-0.79	0.45466907	0.7969	-6.33
258696_at	hypothetical protein predicted by g	HCF152	AT3G09650	1.11	0.15	0.79	0.45490614	0.7969	-6.33
250075_at	putative protein	---	AT5G17670	1.12	0.17	0.79	0.45504685	0.7971	-6.33
264076_at	unknown protein	---	AT2G28540	1.05	0.07	0.79	0.45516718	0.7972	-6.33
256667_at	hypothetical protein predicted by g	---	AT3G32180	-1.05	-0.07	-0.79	0.45522614	0.7973	-6.33
263858_at	hypothetical protein predicted by g	---	AT2G04370	-1.06	-0.08	-0.79	0.45537171	0.7975	-6.33
247082_at	putative protein contains similarity	ATGRIP	AT5G66030	1.07	0.10	0.79	0.45549155	0.7976	-6.33
258997_at	hypothetical protein similar to unkr	---	AT3G01810	1.12	0.16	0.79	0.45576421	0.7978	-6.33
256482_at	protein kinase, putative contains P	FEI1	AT1G31420	-1.06	-0.09	-0.79	0.45581	0.7978	-6.33
245851_at	putative protein HERC2 - Homo s	KEG	AT5G13530	-1.06	-0.09	-0.79	0.45570556	0.7978	-6.33
248535_at	putative protein contains similarity	---	AT5G50120	-1.08	-0.11	-0.79	0.45585425	0.7978	-6.33
251079_at	hypothetical protein	---	AT5G02000	-1.06	-0.08	-0.79	0.45571661	0.7978	-6.33
245814_at	mitotic checkpoint protein, putativ	---	AT1G49910	-1.08	-0.11	-0.79	0.45565305	0.7978	-6.33
265379_at	similar to late embryogenesis abur	---	AT2G18340	-1.06	-0.08	-0.79	0.45583057	0.7978	-6.33
261662_at	MAP kinase kinase 5, putative sim	ATMKK7	AT1G18350	1.06	0.09	0.79	0.45568015	0.7978	-6.33
248534_at	putative protein contains similarity	---	AT5G50030	-1.06	-0.09	-0.79	0.45598664	0.7979	-6.33
259450_at	hypothetical protein predicted by g	DRL1	AT1G13870	1.07	0.10	0.79	0.45596997	0.7979	-6.33
261109_at	cytokinin oxidase, putative similar	CKX5	AT1G75450	-1.33	-0.41	-0.79	0.45608946	0.7980	-6.33
244985_at	ribosomal protein L22	---	---	1.10	0.14	0.79	0.45613824	0.7980	-6.33
246877_at	putative protein various predicted	---	AT5G26150	-1.05	-0.07	-0.79	0.45619097	0.7980	-6.33
245412_at	hypothetical protein	---	AT4G17280	-1.11	-0.14	-0.79	0.45616927	0.7980	-6.33
254662_at	putative protein phospho-N-acetyl	TRANS11	AT4G18270	-1.10	-0.14	-0.79	0.45621449	0.7980	-6.33
267305_at	high affinity K+ transporter (AtKUP	ATKT1	AT2G30070	-1.13	-0.18	-0.79	0.45630962	0.7981	-6.33
246825_at	putative protein various predicted	---	AT5G26260	1.06	0.08	0.79	0.45641284	0.7982	-6.34
265173_at	unknown protein	---	AT1G23530	-1.06	-0.09	-0.79	0.45645671	0.7982	-6.34
260678_at	hypothetical protein predicted by g	---	AT1G07970	1.05	0.07	0.79	0.45660925	0.7984	-6.34
263790_at	hypothetical protein predicted by g	---	AT2G24530	-1.08	-0.12	-0.79	0.45668184	0.7985	-6.34
261648_at	salt-tolerance zinc finger protein id	STZ	AT1G27730	1.30	0.38	0.79	0.45674582	0.7985	-6.34
260810_s_at	retroelement protein, putative simi	---	---	1.06	0.09	0.79	0.45679478	0.7986	-6.34
255452_at	hypothetical protein similar to A. th	---	AT4G02880	1.06	0.08	0.79	0.45689893	0.7986	-6.34
265964_at	putative RNA-binding protein ; sup	---	AT2G37510	-1.07	-0.10	-0.79	0.45688149	0.7986	-6.34
262518_at	putative glutathione transferase Or	ATGSTU24	AT1G17170	-1.64	-0.72	-0.79	0.45716512	0.7987	-6.34
251446_at	Expressed protein ; supported by f	---	AT3G59840	1.06	0.08	0.79	0.457139	0.7987	-6.34
252930_at	putative endo-1,4-beta-glucanase	AtGH9B18	AT4G39010	-1.08	-0.11	-0.79	0.45698357	0.7987	-6.34

246393_at	phosphoglycerate kinase, putative	---	AT1G58150	-1.07	-0.09	-0.79	0.45702956	0.7987	-6.34
264897_at	dynein light subunit lc6, flagellar o	---	AT1G23220	1.07	0.10	0.79	0.4571687	0.7987	-6.34
250814_at	E2, ubiquitin-conjugating enzyme,	UBC22	AT5G05080	1.07	0.10	0.79	0.45706185	0.7987	-6.34
247647_at	respiratory burst oxidase protein -	---	AT5G60010	-1.07	-0.09	-0.79	0.45712908	0.7987	-6.34
251431_at	protein synthesis initiation factor -	EIF4G	AT3G60240	1.05	0.08	0.79	0.45728944	0.7988	-6.34
257214_at	hypothetical protein ;supported by	---	AT3G15040	1.08	0.11	0.79	0.45739417	0.7989	-6.34
247291_at	unknown protein	---	AT5G64480	1.07	0.09	0.79	0.45752662	0.7990	-6.34
245518_at	ATP-dependent RNA helicase like	ATRH1	AT4G15850	-1.11	-0.15	-0.79	0.45753617	0.7990	-6.34
259567_at	hypothetical protein	---	AT1G20500	-1.07	-0.10	-0.79	0.45750072	0.7990	-6.34
250357_at	putative protein various predicted	---	AT5G11730	-1.07	-0.10	-0.79	0.45755208	0.7990	-6.34
266197_at	hypothetical protein predicted by g	---	AT2G39120	1.06	0.09	0.79	0.45775482	0.7990	-6.34
248397_at	unknown protein	---	AT5G52140	1.06	0.09	0.79	0.45765451	0.7990	-6.34
AFFX-r2-Ec-bio	E. coli /GEN=bioD /DB_XREF=gb:	---	---	-1.18	-0.24	-0.79	0.45773619	0.7990	-6.34
248349_at	progesterone-binding protein-like	MSBP1	AT5G52240	1.09	0.13	0.79	0.45772406	0.7990	-6.34
257592_at	leucine-rich repeat disease resista	---	AT3G24982	1.06	0.09	0.79	0.4576937	0.7990	-6.34
264749_at	hypothetical protein Contains simil	---	AT1G22830	-1.11	-0.15	-0.79	0.45792483	0.7992	-6.34
265323_at	putative syntaxin	SYP112	AT2G18260	1.09	0.12	0.79	0.45790267	0.7992	-6.34
263722_at	putative vanadate resistance prote	GONST1	AT2G13650	-1.07	-0.09	-0.79	0.45799637	0.7992	-6.34
250364_at	putative protein serine threonine t	---	AT5G11400	-1.07	-0.09	-0.79	0.45800549	0.7992	-6.34
253372_at	pectinesterase - like protein pectir	PME44	AT4G33220	1.18	0.24	0.79	0.45810579	0.7992	-6.34
248687_at	ADPG pyrophosphorylase small su	ADG1	AT5G48300	-1.14	-0.18	-0.79	0.45817958	0.7992	-6.34
256118_at	hypothetical protein predicted by g	KU70	AT1G16970	-1.08	-0.11	-0.79	0.45816685	0.7992	-6.34
254042_at	xyloglucan endo-1,4-beta-D-gluca	XTR6	AT4G25810	1.35	0.43	0.79	0.45824796	0.7992	-6.34
255129_at	nodulin-like protein nodulin gene M	---	AT4G08290	1.17	0.22	0.79	0.45808569	0.7992	-6.34
258022_at	hypothetical protein predicted by g	---	AT3G19460	-1.05	-0.07	-0.79	0.45826927	0.7992	-6.34
267245_at	hypothetical protein	---	AT2G02640	-1.06	-0.08	-0.79	0.45827388	0.7992	-6.34
260225_at	putative glutathione S-transferase	GSTU10	AT1G74590	-1.32	-0.40	-0.79	0.45848248	0.7993	-6.34
246953_at	unknown protein ;supported by ful	VPS60.2	AT5G04850	1.06	0.09	0.79	0.45836025	0.7993	-6.34
262818_at	hypothetical protein predicted by g	---	AT1G11755 /	1.06	0.09	0.79	0.45844716	0.7993	-6.34
246345_at	calcium-dependent protein kinase	---	AT3G56760	1.08	0.11	0.79	0.45856522	0.7993	-6.34
264643_at	unknown protein	PGSIP5	AT1G08990	-1.06	-0.08	-0.79	0.4583595	0.7993	-6.34
256541_at	ligand-gated ion channel, putative	GLR3.3	AT1G42540	-1.09	-0.12	-0.79	0.45856221	0.7993	-6.34
248550_at	putative protein similar to unknowr	QS	AT5G50210	-1.11	-0.15	-0.79	0.45839813	0.7993	-6.34
253927_at	putative protein	---	AT4G26710	1.08	0.11	0.79	0.45850622	0.7993	-6.34
253013_at	heat shock protein 70 like protein	mtHsc70-1	AT4G37910	-1.13	-0.18	-0.79	0.45872022	0.7993	-6.34

256611_at	unknown protein similar to putative	---	AT3G29270	1.08	0.11	0.79	0.45864287	0.7993	-6.34
258417_at	Expressed protein ; supported by c	---	AT3G17365	1.09	0.12	0.79	0.45867361	0.7993	-6.34
263152_at	hypothetical protein predicted by g	ASIL1	AT1G54060	-1.10	-0.13	-0.79	0.45872738	0.7993	-6.34
249489_at	acyltransferase -like protein antho	---	AT5G39090	-1.08	-0.11	-0.79	0.45880532	0.7994	-6.34
251000_at	putative protein	---	AT5G02650	1.07	0.10	0.79	0.45886902	0.7994	-6.34
254220_at	putative protein Arabidopsis hypot	---	AT4G23780	-1.06	-0.08	-0.79	0.45894375	0.7995	-6.34
AFFX-Athal-25	Arabidopsis thaliana /REF=X5232(	---	---	1.09	0.12	0.79	0.4590615	0.7996	-6.34
246376_at	auxin regulated protein IAA18, pu	IAA18	AT1G51950	-1.09	-0.12	-0.79	0.459099	0.7996	-6.34
249445_at	putative protein predicted protein,	---	AT5G39380	-1.08	-0.10	-0.79	0.45918607	0.7997	-6.34
263211_at	germin-like oxalate oxidase similar	GLP7	AT1G10460	1.08	0.12	0.79	0.45916376	0.7997	-6.34
244930_at	hypothetical protein	---	AT2G07809	1.06	0.08	0.78	0.4593319	0.7997	-6.34
267340_at	unknown protein	ACD11	AT2G34690	-1.06	-0.08	-0.78	0.45932023	0.7997	-6.34
255245_at	hypothetical protein	---	AT4G05630	-1.06	-0.08	-0.78	0.45932335	0.7997	-6.34
249977_at	chaperonin 60 alpha chain - like p	EMB3007	AT5G18820	1.09	0.12	0.78	0.45963951	0.8001	-6.34
260675_at	unknown protein ; supported by cD	---	AT1G19430	1.08	0.11	0.78	0.45967116	0.8001	-6.34
250419_at	RPP1 disease resistance protein -	---	AT5G11250	-1.09	-0.13	-0.78	0.45964322	0.8001	-6.34
249006_at	putative protein similar to unknown	---	AT5G44650 /	1.10	0.13	0.78	0.45977677	0.8001	-6.34
252836_at	putative protein predicted polyprot	---	---	-1.06	-0.08	-0.78	0.45975733	0.8001	-6.34
259223_at	hypothetical protein	WOX11	AT3G03660	-1.06	-0.09	-0.78	0.45971665	0.8001	-6.34
253590_at	putative protein various predicted p	HHP2	AT4G30850	-1.09	-0.12	-0.78	0.45995122	0.8003	-6.34
266109_at	putative mitochondrial carrier prote	---	AT2G37890	1.13	0.18	0.78	0.46003265	0.8003	-6.34
261974_at	protein kinase, putative similar to	CPuORF57	AT1G64628 /	-1.06	-0.09	-0.78	0.46001374	0.8003	-6.34
259880_at	hypothetical protein similar to hyp	---	AT1G76730	-1.10	-0.14	-0.78	0.45998959	0.8003	-6.34
246175_s_at	putative protein hypothetical prote	---	AT5G28320 /	-1.06	-0.09	-0.78	0.46002646	0.8003	-6.34
258468_at	unknown protein predicted by gens	---	AT3G06070	-1.17	-0.22	-0.78	0.46019194	0.8004	-6.34
255933_at	membrane protein, putative simila	ATRBL6	AT1G12750	-1.11	-0.14	-0.78	0.46020616	0.8004	-6.34
259404_at	type 2A protein serine/threonine ph	ATB BETA	AT1G17720	-1.05	-0.07	-0.78	0.46015014	0.8004	-6.34
253766_at	putative protein ;supported by full-	---	AT4G28770	-1.06	-0.09	-0.78	0.46030329	0.8004	-6.34
262789_at	putative auxin-induced protein stro	---	AT1G10810	-1.06	-0.08	-0.78	0.4603046	0.8004	-6.34
256054_at	unknown protein	---	AT1G07120	-1.05	-0.07	-0.78	0.46030305	0.8004	-6.34
AFFX-r2-Bs-thr	B. subtilis /GEN=thrB /DB_XREF=(	---	---	-1.11	-0.15	-0.78	0.4603272	0.8004	-6.34
261272_at	Expressed protein ; supported by c	---	AT1G26665	1.14	0.18	0.78	0.46072359	0.8004	-6.34
259791_at	unknown protein ; supported by cD	---	AT1G29700	-1.12	-0.16	-0.78	0.46072652	0.8004	-6.34
261098_at	unknown protein	---	AT1G62970	1.06	0.09	0.78	0.46041765	0.8004	-6.34
259546_at	unknown protein	---	AT1G35350	-1.17	-0.23	-0.78	0.4605297	0.8004	-6.34

250325_s_at	putative protein contains similarity	---	AT5G12060 /	1.05	0.08	0.78	0.46062847	0.8004	-6.34
247391_at	unknown protein	---	AT5G63540	-1.05	-0.08	-0.78	0.46042382	0.8004	-6.34
257837_at	hypothetical protein predicted by g	---	AT3G25200	-1.07	-0.10	-0.78	0.460556	0.8004	-6.34
257649_at	predicted protein	ARR1	AT3G16857	-1.06	-0.08	-0.78	0.46065712	0.8004	-6.34
249413_at	ras - related GTP binding protein -	AtRABG1	AT5G39620	-1.06	-0.08	-0.78	0.46072496	0.8004	-6.34
266937_at	hypothetical protein predicted by g	---	AT2G18930	-1.07	-0.09	-0.78	0.46045443	0.8004	-6.34
245922_at	putative protein predicted proteins	---	AT5G28810	-1.07	-0.10	-0.78	0.46059635	0.8004	-6.34
258517_at	galactose kinase identical to GB:A	GALK	AT3G06580	-1.07	-0.09	-0.78	0.46094508	0.8004	-6.34
255802_s_at	putative protein RING-H2 finger pı	---	AT4G10150 /	-1.06	-0.08	-0.78	0.46113711	0.8004	-6.34
252818_at	putative protein several hypothetic	---	---	-1.07	-0.10	-0.78	0.46118501	0.8004	-6.34
266367_s_at	unknown protein	---	AT2G41390 /	-1.06	-0.08	-0.78	0.4612478	0.8004	-6.34
248178_at	root cap protein 2-like protein	---	AT5G54370	1.09	0.12	0.78	0.46101987	0.8004	-6.34
252758_at	putative protein several hypothetic	---	---	-1.07	-0.10	-0.78	0.46081136	0.8004	-6.34
249882_at	putative protein contains similarity	---	AT5G22890	-1.05	-0.07	-0.78	0.46124652	0.8004	-6.34
246190_at	hypothetical protein (fragment) ;su	ATBPM5	AT5G21010	-1.05	-0.07	-0.78	0.4608458	0.8004	-6.34
262537_s_at	putative ubiquitin-conjugating enzy	UBC34	AT1G17280 /	-1.10	-0.14	-0.78	0.46119551	0.8004	-6.34
267345_at	unknown protein ; supported by cI	---	AT2G44240	-1.21	-0.27	-0.78	0.46107038	0.8004	-6.34
249656_at	putative protein hypothetical protei	---	AT5G37130	-1.05	-0.07	-0.78	0.46121601	0.8004	-6.34
251481_at	receptor lectin kinase-like protein	---	AT3G59730	-1.05	-0.07	-0.78	0.46121345	0.8004	-6.34
252888_at	glucose-1-phosphate adenylyltrans	APL3	AT4G39210	-1.17	-0.22	-0.78	0.46099265	0.8004	-6.34
265623_at	hypothetical protein predicted by g	---	AT2G27270	-1.07	-0.10	-0.78	0.46103849	0.8004	-6.34
247641_at	imidazoleglycerol-phosphate synth	PDX2	AT5G60540	-1.07	-0.09	-0.78	0.46130099	0.8005	-6.34
250102_at	receptor-like protein kinase	LRR1	AT5G16590	1.08	0.11	0.78	0.46146071	0.8005	-6.34
254363_at	pectinesterase like protein pectine	sks4	AT4G22010	1.11	0.15	0.78	0.4614816	0.8005	-6.34
261221_at	hypothetical protein predicted by g	---	AT1G19960	-1.54	-0.63	-0.78	0.4615205	0.8005	-6.34
259208_at	hypothetical protein similar to GB:A	---	AT3G09060	1.06	0.09	0.78	0.46152539	0.8005	-6.34
250731_at	putative protein contains similarity	AGL96	AT5G06500	-1.06	-0.08	-0.78	0.46141548	0.8005	-6.34
264815_at	hypothetical protein similar to hypo	---	AT1G03620	-1.14	-0.19	-0.78	0.46140416	0.8005	-6.34
254866_at	putative protein other predicted pr	---	AT4G12220	1.05	0.07	0.78	0.46159763	0.8006	-6.34
257809_at	ribonucleotide reductase small su	TSO2	AT3G27060	1.10	0.13	0.78	0.46183286	0.8006	-6.34
253665_at	hypothetical protein	---	AT4G30230	-1.12	-0.16	-0.78	0.46191617	0.8006	-6.34
260077_at	thaumatin-like protein contains Pfa	---	AT1G73620	-1.08	-0.11	-0.78	0.4617293	0.8006	-6.34
260213_at	putative protein kinase similar to pı	---	AT1G74490	1.05	0.07	0.78	0.46185828	0.8006	-6.34
254769_at	hypothetical protein	---	AT4G13330	1.13	0.18	0.78	0.46179641	0.8006	-6.34
262264_at	Niemann-Pick C disease protein-lil	---	AT1G42470	-1.18	-0.23	-0.78	0.46189198	0.8006	-6.34

251946_at	putative protein predicted proteins	---	AT3G53540	-1.25	-0.33	-0.78	0.46186103	0.8006	-6.34
257862_s_at	unknown protein similar to N-termi	---	AT3G17720	-1.05	-0.07	-0.78	0.46183196	0.8006	-6.34
266497_at	putative retroelement pol polyprote	---	---	1.07	0.10	0.78	0.46204994	0.8008	-6.34
255249_at	3(2),5-BISPHOSPHATE NUCLEO	---	AT4G05090	1.11	0.15	0.78	0.46217725	0.8008	-6.34
253637_at	putative protein ; supported by full	---	AT4G30390	1.10	0.14	0.78	0.46232915	0.8008	-6.34
257834_at	alpha-mannosidase, putative simil	---	AT3G26720	1.05	0.07	0.78	0.46229088	0.8008	-6.34
253543_at	hypothetical protein	---	AT4G31270	-1.06	-0.09	-0.78	0.46228272	0.8008	-6.34
247675_at	putative protein large number of p	---	AT5G59940	-1.09	-0.12	-0.78	0.46211357	0.8008	-6.34
259572_at	hypothetical protein	---	AT1G20400	-1.07	-0.10	-0.78	0.46237029	0.8008	-6.34
267232_at	hypothetical protein predicted by g	EDE1	AT2G44190	1.07	0.09	0.78	0.46235253	0.8008	-6.34
245391_at	symbiosis-related like protein ;supp	ATG8F	AT4G16520	1.10	0.13	0.78	0.46239029	0.8008	-6.34
263571_at	putative disease resistance protein	---	AT2G17050	-1.05	-0.07	-0.78	0.46228768	0.8008	-6.34
258002_at	AIG2-like protein similar to AIG2 p	AIG2	AT3G28930	-1.36	-0.45	-0.78	0.462477	0.8009	-6.34
AFFX-PheX-M	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.13	-0.17	-0.78	0.46251939	0.8009	-6.34
263890_at	putative auxin-induced protein	---	AT2G37030	1.09	0.13	0.78	0.46248956	0.8009	-6.34
250853_s_at	putative protein prtedicted prteins,	---	AT5G04680	1.05	0.07	0.78	0.4625794	0.8009	-6.34
265395_at	putative LRR receptor protein kina	SRF1	AT2G20850	1.09	0.12	0.78	0.46265184	0.8010	-6.34
256958_at	unknown protein contains Pfam pr	---	AT3G13430	1.11	0.15	0.78	0.46274592	0.8011	-6.34
255574_at	putative calcium-regulated protein	CBL5	AT4G01420	-1.07	-0.09	-0.78	0.46283983	0.8011	-6.34
254199_at	putative protein Ste-20 related kin	---	AT4G24100	-1.07	-0.09	-0.78	0.46281033	0.8011	-6.34
252724_at	putative protein hypothetical prote	---	AT3G43540	1.08	0.11	0.78	0.46290211	0.8012	-6.34
262345_at	hypothetical protein similar to hypo	---	AT1G64180	1.07	0.10	0.78	0.46301855	0.8013	-6.34
259031_at	putative transcription factor similar	---	AT3G09360	1.09	0.12	0.78	0.4629908	0.8013	-6.34
249231_at	putative protein similar to unknown	ABIL4	AT5G42030	1.07	0.10	0.78	0.46319467	0.8014	-6.35
264893_at	unknown protein similar to unknow	---	AT1G23140	-1.08	-0.11	-0.78	0.46322893	0.8014	-6.35
254173_at	putative protein Kaposi's sarcoma	REN1	AT4G24580	-1.05	-0.08	-0.78	0.46322188	0.8014	-6.35
246311_at	high mobility group protein 2-like ;	HMGB1	AT3G51880	1.07	0.10	0.78	0.46344274	0.8016	-6.35
253691_at	putative protein predicted proteins	EMB2752	AT4G29660	-1.05	-0.07	-0.78	0.46355552	0.8016	-6.35
246536_at	putative protein KIAA0594 - Homo	---	AT5G15920	1.16	0.22	0.78	0.46339658	0.8016	-6.35
249119_at	unknown protein ;supported by ful	---	AT5G43720	1.05	0.07	0.78	0.4636204	0.8016	-6.35
255303_at	predicted protein of unknown funct	DER2.2	AT4G04860	-1.06	-0.09	-0.78	0.46367631	0.8016	-6.35
246992_at	N-acetyltransferase hookless1-like	---	AT5G67430	-1.06	-0.09	-0.78	0.46360003	0.8016	-6.35
267307_at	putative laccase	LAC3	AT2G30210	-1.09	-0.12	-0.78	0.46378161	0.8016	-6.35
266877_at	putative glucanase	AtGH9B12	AT2G44570	-1.06	-0.09	-0.78	0.46351974	0.8016	-6.35
249304_at	folylpolyglutamate synthase-like pr	GLA1	AT5G41480	1.09	0.12	0.78	0.46372159	0.8016	-6.35

256500_at	Ty1/copia-element polyprotein	---	---	1.07	0.09	0.78	0.46376555	0.8016	-6.35
259744_at	putative ketoacyl-CoA synthase sir	KCS7	AT1G71160	-1.06	-0.08	-0.78	0.46361394	0.8016	-6.35
255840_at	unknown protein	---	AT2G33520	-1.10	-0.13	-0.78	0.46347818	0.8016	-6.35
248650_at	putative protein similar to unknown	---	AT5G49250	1.09	0.12	0.78	0.46367381	0.8016	-6.35
264180_at	hypothetical protein contains simila	---	AT1G02190	-1.06	-0.08	-0.78	0.46373641	0.8016	-6.35
257538_at	hypothetical protein predicted by g	---	AT3G16160	-1.05	-0.08	-0.78	0.4639589	0.8018	-6.35
265977_at	putative retroelement pol polyprote	---	---	1.05	0.08	0.78	0.46414452	0.8021	-6.35
266442_at	hypothetical protein	---	AT2G43260	1.05	0.07	0.78	0.46429485	0.8023	-6.35
256874_at	cytochrome P450, putative contair	CYP71B36	AT3G26320	-1.07	-0.10	-0.78	0.46437678	0.8023	-6.35
249674_at	unknown protein	---	AT5G35930	-1.05	-0.07	-0.78	0.4644424	0.8024	-6.35
259361_at	glyceraldehyde-3-phosphate dehy	GAPC2	AT1G13440	1.07	0.10	0.78	0.46451093	0.8024	-6.35
256271_at	unknown protein	---	AT3G12140	-1.09	-0.13	-0.78	0.46453583	0.8024	-6.35
250196_at	polynucleotide phosphorylase	---	AT5G14580	-1.08	-0.11	-0.77	0.46490623	0.8025	-6.35
259056_at	hypothetical protein similar to Ku70	---	AT3G03420	1.08	0.11	0.78	0.46469417	0.8025	-6.35
252528_at	E2, ubiquitin-conjugating enzyme	UBC13	AT3G46460	-1.06	-0.08	-0.77	0.46495477	0.8025	-6.35
245295_at	hypothetical protein ; supported by	---	AT4G16100	1.08	0.11	0.77	0.46486188	0.8025	-6.35
257438_at	hypothetical protein similarity to pla	---	AT2G15325	-1.05	-0.07	-0.77	0.46477711	0.8025	-6.35
250779_at	eukaryotic translation initiation fact	EIF2 ALPH	AT5G05470	-1.10	-0.14	-0.77	0.46479055	0.8025	-6.35
255761_at	hypothetical protein predicted by g	---	AT1G16770	-1.06	-0.09	-0.78	0.46465862	0.8025	-6.35
260379_at	putative glucosyltransferase simila	UGT89B1	AT1G73880 /	1.09	0.12	0.77	0.46493323	0.8025	-6.35
258387_at	hypothetical protein predicted by g	---	AT3G15550	1.07	0.10	0.77	0.46482742	0.8025	-6.35
266935_at	F-box protein LKP2/ADO2, AtFBX	LKP2	AT2G18915	1.06	0.08	0.77	0.46496103	0.8025	-6.35
252749_at	putative protein several hypothetic	---	---	-1.06	-0.09	-0.77	0.46480378	0.8025	-6.35
264243_at	hypothetical protein predicted by g	---	AT1G54650	1.09	0.13	0.77	0.46504262	0.8026	-6.35
251677_at	putative protein hypothetical prote	BHLH039	AT3G56980	-1.22	-0.29	-0.77	0.46514319	0.8027	-6.35
256931_at	LEA protein, putative similar to LE	---	AT3G22490	1.06	0.08	0.77	0.46519754	0.8027	-6.35
263978_at	unknown protein ;supported by full	MBF1A	AT2G42680	1.06	0.08	0.77	0.46541465	0.8030	-6.35
265007_s_at	Expressed protein ; supported by f	RALFL8	AT1G61563 /	-1.05	-0.07	-0.77	0.46566698	0.8033	-6.35
266615_s_at	putative monooxygenase ;support	CTF2A	AT2G29720 /	-1.25	-0.32	-0.77	0.46564059	0.8033	-6.35
258666_at	hypothetical protein	KOB1	AT3G08550	-1.06	-0.08	-0.77	0.46573659	0.8033	-6.35
257521_at	hypothetical protein predicted by g	---	AT3G09140	1.05	0.07	0.77	0.46573339	0.8033	-6.35
267395_at	unknown protein	---	AT2G44250	-1.05	-0.07	-0.77	0.46561788	0.8033	-6.35
260341_at	squamosa-promoter binding prote	---	AT1G69170	1.09	0.12	0.77	0.4659137	0.8034	-6.35
265328_at	unknown protein	---	AT2G18200	-1.05	-0.07	-0.77	0.46593861	0.8034	-6.35
253159_at	HMG delta protein ;supported by f	HMGB5	AT4G35570	-1.06	-0.08	-0.77	0.46592413	0.8034	-6.35

262510_at	hypothetical protein similar to hypo	---	AT1G11270	1.07	0.10	0.77	0.46596468	0.8034	-6.35
259542_at	Expressed protein ; supported by f	---	AT1G20575	1.06	0.09	0.77	0.46612712	0.8037	-6.35
263743_at	coatomer alpha subunit	---	AT2G21390	-1.05	-0.08	-0.77	0.46618366	0.8037	-6.35
267173_at	origin recognition complex protein	ORC2	AT2G37560	1.11	0.15	0.77	0.46639033	0.8040	-6.35
264280_at	beta-glucosidase, putative similar	BGLU46	AT1G61820	1.14	0.19	0.77	0.4666167	0.8040	-6.35
253761_at	putative protein thyroid receptor in	---	AT4G28820	1.07	0.10	0.77	0.46697116	0.8040	-6.35
260544_at	unknown protein predicted by gens	---	AT2G43540	1.10	0.13	0.77	0.46700507	0.8040	-6.35
250929_at	putative protein ; supported by cD	---	AT5G03290	1.10	0.14	0.77	0.466946	0.8040	-6.35
245756_at	hyoscyamine 6-dioxygenase hydr	---	AT1G35190	1.09	0.13	0.77	0.46706199	0.8040	-6.35
253497_at	putative protein microtubule-assoc	---	AT4G31880	1.07	0.10	0.77	0.4666603	0.8040	-6.35
251160_at	inositol-1,4,5-trisphosphate 5-Pho	---	AT3G63240	1.07	0.10	0.77	0.46695827	0.8040	-6.35
267494_at	TCP1-chaperonin cofactor A isolog	KIS	AT2G30410	1.06	0.09	0.77	0.46680065	0.8040	-6.35
263293_x_at	hypothetical protein similar to hypo	---	---	1.05	0.08	0.77	0.46686661	0.8040	-6.35
257673_at	unknown protein similar to GB:BA	---	AT3G20370	-1.08	-0.11	-0.77	0.46651808	0.8040	-6.35
253509_at	putative protein kainate receptor,	GLR2.4	AT4G31710	-1.07	-0.09	-0.77	0.46657708	0.8040	-6.35
250783_at	cytochrome P450 ; supported by c	CYP79A2	AT5G05260	-1.07	-0.10	-0.77	0.46681445	0.8040	-6.35
261441_at	NAM protein, putative similar to N	ANAC010	AT1G28470	1.11	0.15	0.77	0.4669753	0.8040	-6.35
248407_at	pectinesterase	---	AT5G51500	1.06	0.08	0.77	0.4670634	0.8040	-6.35
248203_at	Myb-related transcription factor-like	MYB49	AT5G54230	1.05	0.07	0.77	0.46646341	0.8040	-6.35
265533_at	putative replication protein A1	---	---	-1.05	-0.07	-0.77	0.46650804	0.8040	-6.35
246452_at	putative protein predicted proteins	BPA1	AT5G16840	1.06	0.09	0.77	0.46680574	0.8040	-6.35
262763_at	hypothetical protein	---	AT1G28690	-1.09	-0.12	-0.77	0.4666548	0.8040	-6.35
262053_at	putative DnaJ protein contains Pfa	ATERDJ2A	AT1G79940	-1.07	-0.10	-0.77	0.4670702	0.8040	-6.35
257630_at	cytochrome P450, putative similar	CYP71B16	AT3G26150	1.06	0.08	0.77	0.46714398	0.8040	-6.35
246016_at	histidine kinase - like protein sens	AHK5	AT5G10720	1.07	0.10	0.77	0.46711844	0.8040	-6.35
249191_at	putative protein similar to unknown	---	AT5G42760	-1.09	-0.12	-0.77	0.4671987	0.8040	-6.35
250039_at	disease resistance protein -like dis	---	AT5G18370	-1.08	-0.11	-0.77	0.46740761	0.8043	-6.35
252849_at	Histon H3 ;supported by full-length	---	AT4G40040	1.06	0.09	0.77	0.46756126	0.8045	-6.35
260015_at	putative S-adenosyl-L-methionine:	CCOAMT	AT1G67980	1.28	0.35	0.77	0.4677684	0.8046	-6.35
252433_at	putative protein putative hydrolyse	---	AT3G47560	-1.10	-0.14	-0.77	0.46808764	0.8046	-6.35
261663_at	hypothetical protein similar to hypo	EPR1	AT1G18330	-1.21	-0.27	-0.77	0.46841664	0.8046	-6.35
260656_at	hypothetical protein predicted by g	---	AT1G19380	-1.26	-0.34	-0.77	0.46833935	0.8046	-6.35
245351_at	casein kinase II beta chain CKB2 ;	CKB2	AT4G17640	-1.07	-0.09	-0.77	0.4679658	0.8046	-6.35
258200_at	putative ATPase similar to ATPase	---	AT3G13900	-1.08	-0.11	-0.77	0.46824165	0.8046	-6.35
257963_at	hypothetical protein predicted by g	---	AT3G19840	-1.12	-0.16	-0.77	0.46804452	0.8046	-6.35

250520_at	putative protein contains similarity	PEX1	AT5G08470	-1.05	-0.07	-0.77	0.46796053	0.8046	-6.35
263219_at	putative serine proteinase Strong s	---	AT1G30600	1.09	0.13	0.77	0.46832382	0.8046	-6.35
263577_at	putative protein kinase identical to	SSP	AT2G17090	1.08	0.11	0.77	0.46784201	0.8046	-6.35
248663_at	putative protein strong similarity to	---	AT5G48590	1.05	0.07	0.77	0.46791259	0.8046	-6.35
265691_at	unknown protein predicted by gens	---	AT2G24330	-1.10	-0.14	-0.77	0.46789507	0.8046	-6.35
247861_at	strong similarity to unknown protei	---	AT5G58160	1.08	0.11	0.77	0.46843486	0.8046	-6.35
249688_at	putative protein tyrosine aminotran	---	AT5G36160	-1.08	-0.12	-0.77	0.46832328	0.8046	-6.35
264966_at	hypothetical protein predicted by g	---	AT1G60570	-1.09	-0.12	-0.77	0.46795607	0.8046	-6.35
246281_at	hypothetical protein	NAPRT1	AT4G36940	1.10	0.14	0.77	0.46817594	0.8046	-6.35
257589_at	hypothetical protein predicted by g	---	AT1G55050	1.08	0.11	0.77	0.46814814	0.8046	-6.35
261686_at	unknown protein ;supported by full	---	AT1G47310	1.06	0.09	0.77	0.46838189	0.8046	-6.35
258891_at	unknown protein	EMB2016	AT3G05680	1.06	0.08	0.77	0.46763143	0.8046	-6.35
247618_at	receptor like protein kinase recept	---	AT5G60280	1.07	0.10	0.77	0.46830327	0.8046	-6.35
264095_at	mercaptopyruvate sulfurtransferas	MST1	AT1G79230	-1.06	-0.08	-0.77	0.46794835	0.8046	-6.35
257996_at	unknown protein	---	AT3G19950	-1.05	-0.07	-0.77	0.46828255	0.8046	-6.35
266646_at	unknown protein ;supported by ful	ATPH1	AT2G29700	1.07	0.10	0.77	0.46834844	0.8046	-6.35
247598_at	UVB-resistance protein UVR8 - lik	---	AT5G60870	-1.06	-0.09	-0.77	0.46794705	0.8046	-6.35
265203_at	unknown protein	---	AT2G36630	1.08	0.11	0.77	0.46850953	0.8047	-6.35
253840_at	putative acyl-CoA binding protein	ACBP2	AT4G27780	1.08	0.11	0.77	0.46861984	0.8048	-6.35
267462_at	Expressed protein ; supported by f	---	AT2G33735	-1.12	-0.16	-0.77	0.46876445	0.8049	-6.35
249246_at	unknown protein	---	AT5G42290	-1.06	-0.08	-0.77	0.46876003	0.8049	-6.35
256728_at	glutamyl-tRNA amidotransferase s	---	AT3G25660	1.09	0.13	0.77	0.46889609	0.8050	-6.35
259536_s_at	putative protein hypothetical protei	ATCOAB	AT1G12350	1.05	0.07	0.77	0.46932141	0.8050	-6.35
263516_at	AtRer1B ;supported by full-length	ATRER1B	AT2G21600	1.07	0.10	0.77	0.46895104	0.8050	-6.35
266033_at	putative translation initiation factor	---	AT2G05830	-1.08	-0.11	-0.77	0.46925727	0.8050	-6.35
247049_at	putative protein similar to unknown	---	AT5G66440	1.32	0.40	0.77	0.46930109	0.8050	-6.35
258153_at	Expressed protein ; supported by f	MOS4	AT3G18165	1.08	0.11	0.77	0.46919267	0.8050	-6.35
256517_at	PHD-finger protein, putative conta	MMD1	AT1G66170	-1.05	-0.07	-0.77	0.46922188	0.8050	-6.35
259638_at	coatomer complex subunit, putativ	---	AT1G52360	1.07	0.10	0.77	0.46923775	0.8050	-6.35
259353_at	putative branched-chain amino aci	---	AT3G05190	1.05	0.08	0.77	0.46899804	0.8050	-6.35
263017_at	putative cyclin 2	CYCB2;1	AT2G17620	-1.06	-0.08	-0.77	0.46906886	0.8050	-6.35
256357_at	hypothetical protein	---	AT1G66490	1.05	0.06	0.77	0.46901857	0.8050	-6.35
267589_at	hypothetical protein	---	---	1.05	0.07	0.77	0.4692454	0.8050	-6.35
256654_at	ribosomal protein, putative similar	---	AT3G18880	1.10	0.13	0.77	0.46895929	0.8050	-6.35
265372_at	Ac-like transposase related to Ac/D	---	AT2G06500	-1.07	-0.10	-0.77	0.46915314	0.8050	-6.35

257403_at	hypothetical protein similar to hypo	---	AT1G62520	-1.06	-0.09	-0.77	0.46937068	0.8050	-6.35
264817_at	hypothetical protein similar to mem	---	AT1G03540	-1.06	-0.08	-0.77	0.46941188	0.8051	-6.35
266835_at	putative NADH dehydrogenase (ub	NDA2	AT2G29990	1.19	0.25	0.77	0.46949518	0.8051	-6.35
263222_at	putative protein kinase Strong simi	---	AT1G30640	-1.10	-0.14	-0.77	0.46962395	0.8052	-6.35
256288_at	arginine N-methyltransferase 3, pu	PRMT3	AT3G12270	-1.15	-0.20	-0.77	0.46962181	0.8052	-6.35
247831_at	putative protein serine/threonine-s	---	AT5G58540	-1.12	-0.16	-0.77	0.4696887	0.8052	-6.35
262302_at	hypothetical protein predicted by g	---	AT1G70910	-1.07	-0.10	-0.77	0.4696732	0.8052	-6.35
249043_at	berberine bridge enzyme	---	AT5G44360	1.05	0.07	0.77	0.46976836	0.8053	-6.35
245906_at	putative protein ;supported by full-	---	AT5G11070	-1.15	-0.20	-0.77	0.46981222	0.8053	-6.35
250415_at	putative protein GLUR3 ligand-gat	GLR2.5	AT5G11210	-1.22	-0.28	-0.77	0.46992559	0.8054	-6.35
254547_at	putative protein	---	AT4G19860	1.10	0.14	0.77	0.46988079	0.8054	-6.35
257676_at	unknown protein ;supported by ful	TGD2	AT3G20320	1.06	0.09	0.77	0.469978	0.8054	-6.35
259704_at	putative 3'-5' exoribonuclease simi	---	AT1G77680	-1.08	-0.11	-0.77	0.46997008	0.8054	-6.35
253246_at	putative protein	---	AT4G34600	-1.07	-0.10	-0.77	0.47006331	0.8054	-6.36
247961_at	putative protein similar to unknown	---	AT5G56570	-1.05	-0.07	-0.77	0.47012947	0.8055	-6.36
256979_at	Expressed protein ; supported by f	PSBTN	AT3G09550 /	1.07	0.10	0.76	0.47026692	0.8055	-6.36
253589_at	puative protein membrane-associa	---	AT4G30825	1.09	0.13	0.77	0.47020997	0.8055	-6.36
248185_at	flavonol 3-O-glucosyltransferase-li	UF3GT	AT5G54060	-1.06	-0.09	-0.76	0.47032117	0.8055	-6.36
252283_at	60S ribosomal protein L13 (BBC1	---	AT3G48960	1.06	0.09	0.76	0.47030562	0.8055	-6.36
249293_at	protein kinase-like	---	AT5G41260	1.08	0.11	0.76	0.47024535	0.8055	-6.36
246242_at	putative protein	---	AT4G36600	-1.09	-0.13	-0.76	0.4703777	0.8056	-6.36
248346_at	GTP-binding protein-like ;supporte	ATGB1	AT5G52210	1.11	0.15	0.76	0.47047614	0.8056	-6.36
261364_at	dynamin-like protein similar to GB:	---	AT1G53140	-1.07	-0.10	-0.76	0.47045737	0.8056	-6.36
258129_at	hypothetical protein predicted by g	ROPGEF8	AT3G24620	-1.07	-0.09	-0.76	0.47058677	0.8057	-6.36
263901_at	unknown protein ;supported by ful	---	AT2G36320	-1.09	-0.12	-0.76	0.47061229	0.8057	-6.36
249345_at	putative protein ; supported by cD	---	AT5G40740	-1.07	-0.09	-0.76	0.47110841	0.8058	-6.36
258642_at	unknown protein ;supported by ful	---	AT3G07910	1.06	0.08	0.76	0.47100433	0.8058	-6.36
265394_at	predicted protein ; supported by cD	---	AT2G20725	1.07	0.10	0.76	0.47132866	0.8058	-6.36
245194_at	F12A21.5 similar to protein phosph	---	AT1G67820	-1.12	-0.16	-0.76	0.47112377	0.8058	-6.36
258669_at	hypothetical protein predicted by g	---	AT3G08800	1.06	0.08	0.76	0.47138715	0.8058	-6.36
266411_at	putative peptidyl-prolyl cis-trans is	---	AT2G38730	-1.08	-0.11	-0.76	0.4712837	0.8058	-6.36
247253_at	beta-1,3-glucanase	---	AT5G64790	1.20	0.26	0.76	0.47120407	0.8058	-6.36
246994_at	putative protein similar to unknown	---	AT5G67460	-1.16	-0.22	-0.76	0.47126189	0.8058	-6.36
260168_at	unknown protein contains zinc fing	---	AT1G71980	-1.08	-0.11	-0.76	0.47129865	0.8058	-6.36
258278_at	putative self-incompatibility protei	---	AT3G26860	-1.06	-0.08	-0.76	0.47086332	0.8058	-6.36

252310_at	GTPase activating -like protein GT	---	AT3G49350	-1.13	-0.17	-0.76	0.47100938	0.8058	-6.36
265902_at	hypothetical protein predicted by g	---	AT2G25590	-1.06	-0.09	-0.76	0.47102835	0.8058	-6.36
257714_at	histone H3, putative similar to hist	---	AT3G27360	1.07	0.10	0.76	0.47097794	0.8058	-6.36
247445_at	putative protein similar to unknown	---	AT5G62640	1.06	0.09	0.76	0.4708136	0.8058	-6.36
255049_at	gibberellin-regulated protein GASA	GASA2	AT4G09610	-1.05	-0.07	-0.76	0.47112444	0.8058	-6.36
261342_at	putative replication protein similar t	---	AT1G52950	-1.05	-0.07	-0.76	0.47095068	0.8058	-6.36
263313_at	14-3-3 protein (grf15), putative co	---	AT2G10450	-1.06	-0.09	-0.76	0.47137596	0.8058	-6.36
256030_at	hypothetical protein contains simila	---	AT1G34110	1.07	0.09	0.76	0.47139256	0.8058	-6.36
257309_at	hypothetical protein predicted by g	---	AT3G28150	1.05	0.07	0.76	0.47100264	0.8058	-6.36
266375_at	En/Spm-like transposon protein rel	---	---	-1.07	-0.09	-0.76	0.47107839	0.8058	-6.36
251284_at	hypothetical protein	---	AT3G61840	-1.09	-0.12	-0.76	0.47071728	0.8058	-6.36
261276_at	v-SNARE protein AtVTI1b, putativ	VTI1B	AT1G26670	1.09	0.12	0.76	0.47147715	0.8059	-6.36
244948_at	hypothetical protein	---	---	-1.06	-0.08	-0.76	0.47150965	0.8059	-6.36
245314_at	Expressed protein ; supported by f	---	AT4G16745	-1.06	-0.09	-0.76	0.47161389	0.8059	-6.36
258078_at	unknown protein ;supported by ful	---	AT3G25870	1.14	0.19	0.76	0.47158709	0.8059	-6.36
259700_at	unknown protein	---	AT1G68980	-1.05	-0.07	-0.76	0.47176067	0.8059	-6.36
254570_s_at	puatative protein various predicted	---	AT4G19250	-1.07	-0.09	-0.76	0.47172594	0.8059	-6.36
254731_at	hypothetical protein	---	AT4G13750	1.07	0.10	0.76	0.47173336	0.8059	-6.36
247674_at	putative protein large number of p	---	AT5G59930	-1.09	-0.12	-0.76	0.47172402	0.8059	-6.36
262197_at	AP2 domain containing protein, pu	RAP2.12	AT1G53910	1.11	0.15	0.76	0.47181024	0.8060	-6.36
261104_at	unknown protein	---	AT1G62910	-1.07	-0.10	-0.76	0.47185484	0.8060	-6.36
252516_at	histidyl-tRNA synthetase ; support	ATHRS1	AT3G46100	-1.07	-0.10	-0.76	0.4719133	0.8060	-6.36
256859_at	hypothetical protein	---	AT3G22940	-1.08	-0.11	-0.76	0.47192781	0.8060	-6.36
264746_at	unknown protein similar to putative	WRKY6	AT1G62300	1.19	0.25	0.76	0.47225011	0.8061	-6.36
266093_at	unknown protein ;supported by ful	---	AT2G37990	1.10	0.13	0.76	0.47224363	0.8061	-6.36
246552_at	putative protein	---	AT5G15420	1.13	0.18	0.76	0.47223151	0.8061	-6.36
250094_at	2-hydroxyphytanoyl-CoA lyase-like	---	AT5G17380	-1.17	-0.22	-0.76	0.47209585	0.8061	-6.36
259935_at	putative GDSL-motif lipase/acylhyd	---	AT1G71250	-1.07	-0.10	-0.76	0.47210324	0.8061	-6.36
258336_at	putative ethylene-inducible protein	PDX1.2	AT3G16050	-1.14	-0.19	-0.76	0.47225167	0.8061	-6.36
262054_s_at	putative heat-shock protein contai	---	AT1G79920	-1.09	-0.12	-0.76	0.47217542	0.8061	-6.36
260045_at	putative MAP kinase similar to mito	ATMPK15	AT1G73670	-1.05	-0.07	-0.76	0.47220185	0.8061	-6.36
264019_at	cyclophilin (CYP2) Same as GB: A	---	AT2G21130	-1.08	-0.11	-0.76	0.47236983	0.8061	-6.36
245075_at	putative cytochrome P450	CYP96A1	AT2G23180	-1.07	-0.09	-0.76	0.47237695	0.8061	-6.36
265366_at	putative N-acetylglucosaminyltrans	---	AT2G13290	1.07	0.09	0.76	0.47267351	0.8065	-6.36
253464_at	putative protein ; supported by full	---	AT4G32030	1.08	0.12	0.76	0.47265826	0.8065	-6.36

258190_at	hypothetical protein predicted by g	---	AT3G29080	-1.06	-0.08	-0.76	0.47266813	0.8065	-6.36
253457_at	putative protein C56A3.6,Caenorh	---	AT4G32060	-1.07	-0.10	-0.76	0.47292939	0.8067	-6.36
262511_at	syntaxin-related protein At-SYR1,	SYP125	AT1G11250	-1.08	-0.11	-0.76	0.47287137	0.8067	-6.36
250590_at	exonuclease-like protein	---	AT5G07710	1.06	0.08	0.76	0.47286844	0.8067	-6.36
255229_at	F-box protein family, AtFBL22 cor	---	AT4G05490	1.05	0.06	0.76	0.47296773	0.8067	-6.36
266711_at	unknown protein	---	AT2G46740	-1.06	-0.08	-0.76	0.4729463	0.8067	-6.36
261746_at	unknown protein ;supported by full	PSAO	AT1G08380	1.05	0.08	0.76	0.47308943	0.8068	-6.36
255523_at	pectinesterase - like protein similar	---	AT4G02320	1.06	0.09	0.76	0.47318314	0.8069	-6.36
250992_at	expansin precursor - like protein e	ATEXPA9	AT5G02260	-1.16	-0.22	-0.76	0.47331346	0.8070	-6.36
265867_at	unknown protein ;supported by ful	MEE11	AT2G01620	-1.07	-0.10	-0.76	0.47330941	0.8070	-6.36
266394_at	Ras-related GTP-binding protein (A	ARA4	AT2G43130	1.06	0.09	0.76	0.47346877	0.8072	-6.36
247151_at	unknown protein ;supported by ful	bHLH093	AT5G65640	-1.11	-0.15	-0.76	0.47351142	0.8072	-6.36
266928_at	putative phosphomannomutase ;s	PMM	AT2G45790	1.09	0.12	0.76	0.47349785	0.8072	-6.36
264791_at	predicted protein	---	AT2G17845	-1.05	-0.07	-0.76	0.47388921	0.8078	-6.36
253838_at	putative zinc finger protein zinc fin	---	AT4G27880	1.10	0.13	0.76	0.47405608	0.8080	-6.36
253276_at	caffeoyl-CoA O-methyltransferase	---	AT4G34050	-1.10	-0.13	-0.76	0.47422232	0.8080	-6.36
259074_at	putative protein kinase contains Pf	RPK2	AT3G02130	-1.10	-0.13	-0.76	0.47423031	0.8080	-6.36
257475_at	hypothetical protein predicted by g	---	AT1G80880	-1.05	-0.07	-0.76	0.47422499	0.8080	-6.36
245128_at	unknown protein similar to gi2344	---	AT2G45380	-1.07	-0.10	-0.76	0.47412514	0.8080	-6.36
257491_at	hypothetical protein predicted by g	---	AT1G06170	-1.05	-0.07	-0.76	0.47432873	0.8081	-6.36
258249_s_at	unknown protein ; supported by fu	---	AT3G15820 /	-1.09	-0.13	-0.76	0.47440548	0.8082	-6.36
247660_at	ankyrin-like protein ankyrin 3, Mus	---	AT5G60070	-1.06	-0.08	-0.76	0.4748255	0.8082	-6.36
252089_at	putative protein	---	AT3G52110	-1.09	-0.12	-0.76	0.47442407	0.8082	-6.36
260472_at	hypothetical protein predicted by g	---	AT1G10990	-1.42	-0.51	-0.76	0.47479991	0.8082	-6.36
261368_at	protein kinase, putative similar to	---	AT1G53070	-1.08	-0.12	-0.76	0.47477425	0.8082	-6.36
253894_at	NWMU2 - 2S albumin 2 precursor	---	AT4G27150	1.05	0.08	0.76	0.47474695	0.8082	-6.36
247599_at	putative protein	---	AT5G60880	-1.12	-0.17	-0.76	0.47469005	0.8082	-6.36
248909_at	serine threonine protein kinase ; su	CIPK19	AT5G45810	-1.09	-0.12	-0.76	0.47483391	0.8082	-6.36
265822_at	putative SEC1 family transport pro	ATSLY1	AT2G17980	1.06	0.09	0.76	0.47459111	0.8082	-6.36
247695_at	putative protein Not2p, Homo sap	VIP2	AT5G59710	-1.05	-0.08	-0.76	0.47484752	0.8082	-6.36
259299_at	unknown protein	---	AT3G05080	1.09	0.12	0.76	0.47464363	0.8082	-6.36
252698_at	amine oxidase -like protein amine	---	AT3G43670	1.08	0.11	0.76	0.47471825	0.8082	-6.36
264403_at	unknown protein similarity to HSR	---	AT2G25150	-1.06	-0.08	-0.76	0.47450799	0.8082	-6.36
254139_at	hypothetical protein	---	AT4G24600	-1.07	-0.10	-0.76	0.47451822	0.8082	-6.36
251969_at	Cytochrom P450 -like protein CYT	LUT1	AT3G53130	-1.08	-0.11	-0.76	0.47496316	0.8083	-6.36

266052_at	putative WRKY-type DNA binding	WRKY55	AT2G40740	-1.12	-0.16	-0.76	0.47495937	0.8083	-6.36
249045_at	berberine bridge enzyme-like prote	---	AT5G44380	1.23	0.30	0.76	0.47510998	0.8083	-6.36
258823_at	putative RING zinc finger protein (	---	AT3G07200	1.08	0.11	0.76	0.47505516	0.8083	-6.36
253053_at	putative protein beta-ketoadipate (	---	AT4G37470	-1.08	-0.11	-0.76	0.4750445	0.8083	-6.36
249884_at	Na+/H+ antiporter-like protein	CHX9	AT5G22910	-1.06	-0.09	-0.76	0.47512305	0.8083	-6.36
267430_at	unknown protein	EDA3	AT2G34860	1.09	0.13	0.76	0.4753795	0.8087	-6.36
259388_at	steroid sulfotransferase, putative s	ST4B	AT1G13420	1.06	0.09	0.76	0.47547031	0.8088	-6.36
258529_at	hypothetical protein predicted by g	---	AT3G06740	1.09	0.12	0.76	0.47562238	0.8090	-6.36
259311_at	putative SAR DNA-binding protein	---	AT3G05060	-1.12	-0.17	-0.76	0.47575649	0.8091	-6.36
249104_at	sucrose transporter protein	ATSUC6	AT5G43610	1.06	0.08	0.76	0.47571438	0.8091	-6.36
252274_at	branched-chain-amino-acid transa	BCAT3	AT3G49680	-1.06	-0.08	-0.76	0.4757852	0.8091	-6.36
254601_at	putative protein DNA (cytosine-5-)	CMT2	AT4G19020	-1.10	-0.13	-0.75	0.47590956	0.8091	-6.36
261528_at	pectate lyase, putative similar to p	AT59	AT1G14420	-1.06	-0.09	-0.75	0.47588336	0.8091	-6.36
254957_at	putative protein ; supported by full	---	AT4G10970	1.07	0.10	0.75	0.47597062	0.8092	-6.36
264349_at	putative Proline synthetase associa	---	AT1G11930	1.05	0.07	0.75	0.47610941	0.8094	-6.36
261132_at	hypothetical protein predicted by g	TGD1	AT1G19800	-1.06	-0.08	-0.75	0.47614623	0.8094	-6.36
252803_at	putative protein various predicted	---	---	-1.07	-0.10	-0.75	0.47621022	0.8094	-6.36
264580_at	unknown protein EST gb|ATTS029	---	AT1G05340	1.14	0.19	0.75	0.47633099	0.8095	-6.36
257335_at	hypothetical protein	---	---	-1.06	-0.08	-0.75	0.47636037	0.8095	-6.36
256076_at	unknown protein ; supported by cD	---	AT1G18060	-1.10	-0.14	-0.75	0.47647967	0.8097	-6.36
245180_at	putative protein similarity to protein	---	AT5G12410	1.10	0.13	0.75	0.47656797	0.8097	-6.36
256579_at	hypothetical protein	---	AT3G28720	1.05	0.08	0.75	0.47652923	0.8097	-6.36
266930_at	hypothetical protein predicted by g	---	AT2G45930	-1.08	-0.11	-0.75	0.47656486	0.8097	-6.36
264604_at	hypothetical protein predicted by g	---	AT1G04650	-1.08	-0.12	-0.75	0.47663976	0.8097	-6.36
253765_at	hypothetical protein ;supported by	---	AT4G28740	-1.12	-0.16	-0.75	0.47674684	0.8098	-6.36
254286_at	putative MADS Box / AGL protein	AGL19	AT4G22950	-1.11	-0.15	-0.75	0.47753617	0.8099	-6.37
258164_at	surfeit 1 identical to GB:AAF19609	SURF1	AT3G17910	1.10	0.14	0.75	0.47752119	0.8099	-6.37
255598_at	putative protein similar to nucleolin	---	AT4G00830	1.08	0.11	0.75	0.47736602	0.8099	-6.37
263624_at	putative ferredoxin-thioredoxin red	---	AT2G04700	1.08	0.11	0.75	0.47735921	0.8099	-6.37
245746_at	bHLH transcription factor, putative	---	AT1G51070	-1.08	-0.11	-0.75	0.47717667	0.8099	-6.37
261083_at	unknown protein ; supported by cD	---	AT1G07310	1.07	0.10	0.75	0.4770238	0.8099	-6.36
249963_at	putative protein SPECKLE-TYPE	ATBPM1	AT5G19000	1.07	0.10	0.75	0.47746144	0.8099	-6.37
262179_at	hypothetical protein predicted by g	AGL66	AT1G77980	-1.07	-0.10	-0.75	0.47755596	0.8099	-6.37
252171_at	hypothetical protein ; supported by	---	AT3G50590	1.06	0.08	0.75	0.47694552	0.8099	-6.36
265615_at	putative dioxygenase ; supported	---	AT2G25450	-1.07	-0.10	-0.75	0.47688126	0.8099	-6.36

254093_at	putative protein extensin, Cathara	AtMC2	AT4G25110	1.18	0.23	0.75	0.47713571	0.8099	-6.37
250236_at	delta subunit of mitochondrial F1-A	---	AT5G13450	1.07	0.10	0.75	0.47702919	0.8099	-6.36
257917_at	ethylene responsive element bind	---	AT3G23220	1.05	0.07	0.75	0.47738933	0.8099	-6.37
251613_at	hypothetical protein	---	AT3G57960	-1.07	-0.10	-0.75	0.47752036	0.8099	-6.37
249477_s_at	germin - like protein probable gerr	---	AT5G38930	-1.05	-0.07	-0.75	0.47752293	0.8099	-6.37
263594_at	putative purple acid phosphatase c	PAP7	AT2G01880	-1.15	-0.20	-0.75	0.47754274	0.8099	-6.37
261748_at	hypothetical protein predicted by g	---	AT1G76070	-1.24	-0.31	-0.75	0.47755851	0.8099	-6.37
254033_at	V-ATPase G-subunit like protein C	VATG3	AT4G25950	-1.05	-0.06	-0.75	0.47687132	0.8099	-6.36
254828_at	putative cell wall-plasma membran	AIR1	AT4G12550	-1.06	-0.08	-0.75	0.47741222	0.8099	-6.37
254934_at	putative Ap2 domain protein DNA-	CRF1	AT4G11140	-1.07	-0.10	-0.75	0.47733717	0.8099	-6.37
255422_at	putative D-type cyclin	CYCD6;1	AT4G03270	1.06	0.09	0.75	0.47739811	0.8099	-6.37
267522_at	hypothetical protein predicted by g	---	AT2G30430	-1.07	-0.10	-0.75	0.47749286	0.8099	-6.37
263295_at	putative MADS-box protein ANR1	AGL44	AT2G14210	1.05	0.07	0.75	0.47774763	0.8101	-6.37
246679_at	putative protein replication protein	---	---	1.05	0.08	0.75	0.4777643	0.8101	-6.37
252407_at	chloroplast NAD-dependent malate	MDH	AT3G47520	1.08	0.11	0.75	0.47790728	0.8102	-6.37
257114_at	cytochrome P450, putative contair	CYP705A2	AT3G20140	-1.08	-0.11	-0.75	0.47789149	0.8102	-6.37
266435_s_at	hypothetical protein predicted by g	---	AT2G07130	1.06	0.08	0.75	0.47807455	0.8105	-6.37
260550_at	putative sterol dehydrogenase ; su	---	AT2G43420	-1.09	-0.12	-0.75	0.47813287	0.8105	-6.37
257450_at	unknown protein similar to gb|AAD	---	AT1G10530	-1.08	-0.10	-0.75	0.47823907	0.8106	-6.37
267439_at	putative GDSL-motif lipase/hydrola	---	AT2G19060	1.07	0.10	0.75	0.4783624	0.8107	-6.37
249701_at	putative protein similar to unknown	---	AT5G35460	-1.06	-0.08	-0.75	0.47834467	0.8107	-6.37
261290_at	hypothetical protein predicted by g	---	AT1G36990	-1.09	-0.13	-0.75	0.47833758	0.8107	-6.37
254092_at	respiratory burst oxidase - like pro	---	AT4G25090	-1.05	-0.07	-0.75	0.47839984	0.8107	-6.37
255785_at	sulfate adenylyltransferase identica	APS2	AT1G19920	-1.06	-0.09	-0.75	0.47848632	0.8107	-6.37
264842_at	hypothetical protein predicted by g	---	AT1G03700	-1.05	-0.07	-0.75	0.47848343	0.8107	-6.37
263507_s_at	hypothetical protein	---	---	-1.09	-0.12	-0.75	0.47853642	0.8107	-6.37
249545_at	putative transmembrane protein p	---	AT5G38030	1.05	0.07	0.75	0.47860341	0.8108	-6.37
245904_at	sucrose-phosphate synthase -like	ATSPS2F	AT5G11110	1.07	0.10	0.75	0.47878606	0.8108	-6.37
253760_at	putative protein (fragment) predict	AT4G28815	---	-1.08	-0.11	-0.75	0.47877868	0.8108	-6.37
250103_at	transcription factor (gb|AAD53095.	MYB43	AT5G16600	1.06	0.09	0.75	0.47874976	0.8108	-6.37
258898_at	putative DNA helicase	RECQI1	AT3G05740	1.11	0.15	0.75	0.4786848	0.8108	-6.37
263855_at	putative non-LTR retrolelement rev	---	AT2G04420	-1.06	-0.09	-0.75	0.47877426	0.8108	-6.37
246367_at	light repressible receptor protein k	---	AT1G51880	1.06	0.08	0.75	0.47889726	0.8109	-6.37
251693_at	putative protein several hypothetic	---	AT3G56550	1.07	0.09	0.75	0.4789755	0.8110	-6.37
246840_at	putative protein ;supported by full-	---	AT5G26610	-1.05	-0.07	-0.75	0.47906156	0.8111	-6.37

266607_at	hypothetical protein predicted by g	---	AT2G46300	-1.07	-0.10	-0.75	0.47916541	0.8111	-6.37
258294_at	hypothetical protein predicted by g	---	AT3G23350	-1.06	-0.08	-0.75	0.47916304	0.8111	-6.37
247108_at	ReMembR-H2 protein JR700 (gb|A	RMR1	AT5G66160	1.07	0.10	0.75	0.47923542	0.8112	-6.37
256774_at	hypothetical protein predicted by g	---	AT3G13760	-1.05	-0.07	-0.75	0.47926029	0.8112	-6.37
261738_s_at	hypothetical protein identical to hy	---	AT1G47813	1.10	0.14	0.75	0.47929417	0.8112	-6.37
264151_at	hypothetical protein predicted by	---	AT1G02070	-1.07	-0.09	-0.75	0.47948077	0.8113	-6.37
262218_at	hypothetical protein contains simila	---	AT1G74770	1.09	0.13	0.75	0.47945807	0.8113	-6.37
264443_at	Expressed protein ; supported by f	---	AT1G27385	1.09	0.12	0.75	0.47945264	0.8113	-6.37
248456_at	putative protein similar to unknown	---	AT5G51380	-1.05	-0.07	-0.75	0.47950336	0.8113	-6.37
248495_at	putative protein strong similarity to	---	AT5G50780	-1.07	-0.10	-0.75	0.47968928	0.8113	-6.37
254212_at	putative protein many putative pro	---	AT4G23580	-1.06	-0.08	-0.75	0.47966458	0.8113	-6.37
260532_at	putative ATP-dependent RNA helic	---	AT2G47330	-1.05	-0.07	-0.75	0.47969479	0.8113	-6.37
250771_at	NBS/LRR disease resistance prote	---	AT5G05400	1.06	0.08	0.75	0.47971269	0.8113	-6.37
252691_at	kinesin -like protein KLP2 protein,	---	AT3G44050	-1.05	-0.08	-0.75	0.47963046	0.8113	-6.37
257261_s_at	hypothetical protein contains Pfam	---	AT3G21920	-1.05	-0.07	-0.75	0.47980664	0.8114	-6.37
265095_at	putative cruciferin 12S seed stora	CRU2	AT1G03880	-1.06	-0.09	-0.75	0.47993652	0.8116	-6.37
266393_at	late embryogenesis abundant M17	M17	AT2G41260	1.05	0.07	0.75	0.4800544	0.8117	-6.37
256295_at	hypothetical protein	---	AT1G69470	-1.06	-0.08	-0.75	0.48014874	0.8118	-6.37
253011_at	putative protein retrotransposon -l	EDA40	AT4G37890	-1.13	-0.17	-0.75	0.48029494	0.8120	-6.37
266801_at	putative nucleotide-binding protein	EMB2001	AT2G22870	-1.13	-0.18	-0.75	0.48043177	0.8121	-6.37
246029_at	leucine-rich repeat protein ; suppo	---	AT5G21090	1.06	0.08	0.75	0.48043463	0.8121	-6.37
266474_at	hypothetical protein predicted by g	---	AT2G31110	1.20	0.26	0.75	0.48059321	0.8123	-6.37
249399_at	putative protein intracellular protei	---	AT5G40290	-1.05	-0.07	-0.75	0.48068989	0.8124	-6.37
261447_at	transcription factor, putative simila	---	AT1G21160	1.06	0.08	0.75	0.48083963	0.8125	-6.37
263783_at	putative WRKY-type DNA binding	WRKY46	AT2G46400	1.29	0.36	0.75	0.48080979	0.8125	-6.37
245641_at	Expressed protein ; supported by f	---	AT1G25370	-1.27	-0.35	-0.75	0.4808542	0.8125	-6.37
252875_at	GTP-binding protein GB3 ;suppor	RABA4B	AT4G39990	1.06	0.08	0.75	0.48089227	0.8125	-6.37
265916_at	hypothetical protein similar to En/S	---	---	1.06	0.08	0.75	0.48095738	0.8125	-6.37
250431_at	cyclin protein - like cyclin D2.1 pro	CYCD4;2	AT5G10440	-1.06	-0.08	-0.75	0.48099495	0.8125	-6.37
245547_at	cytochrome P450 like protein	CYP702A2	AT4G15300	-1.05	-0.07	-0.75	0.48100089	0.8125	-6.37
261451_at	unknown protein	---	AT1G21060	1.20	0.26	0.75	0.48108084	0.8126	-6.37
260593_at	poly(A)-specific ribonuclease, puta	AHG2	AT1G55870	-1.08	-0.11	-0.75	0.48114333	0.8126	-6.37
257096_at	hypothetical protein	---	AT3G30820	-1.06	-0.08	-0.75	0.48117024	0.8126	-6.37
249878_at	TATA-binding protein-associated p	NF-YB13	AT5G23090	1.08	0.11	0.75	0.48111341	0.8126	-6.37
261383_at	hypothetical protein predicted by g	---	AT1G05380	-1.07	-0.09	-0.75	0.48139049	0.8129	-6.37

253399_at	putative poly(A) polymerase polyn	nPAP	AT4G32850	-1.05	-0.08	-0.75	0.48144673	0.8129	-6.37
266440_at	unknown protein	---	AT2G43235	-1.06	-0.08	-0.74	0.48148051	0.8129	-6.37
256886_at	hypothetical protein contains Pfam	---	AT3G15130	1.05	0.07	0.74	0.48164664	0.8131	-6.37
249476_at	germin - like protein probable gerr	---	AT5G38910	-1.08	-0.11	-0.74	0.48169115	0.8132	-6.37
263623_at	hypothetical protein predicted by g	---	AT2G04860	-1.05	-0.07	-0.74	0.48173964	0.8132	-6.37
253593_at	putative protein hypothetical prote	---	AT4G30760	1.07	0.10	0.74	0.48177516	0.8132	-6.37
254396_at	peptide transporter - like protein p	---	AT4G21680	1.36	0.44	0.74	0.48198622	0.8135	-6.37
253036_at	putative protein other predicted pr	---	AT4G38340	-1.08	-0.11	-0.74	0.48205631	0.8135	-6.37
251344_at	putative protein beige-like protein (	---	AT3G60920	-1.06	-0.08	-0.74	0.48233647	0.8138	-6.37
258732_at	putative alkaline/neutral invertase	---	AT3G05820	-1.06	-0.09	-0.74	0.48236151	0.8138	-6.37
251001_at	putative protein	---	AT5G02670	-1.08	-0.11	-0.74	0.48231697	0.8138	-6.37
255222_at	putative protein Mitochondrial ATF	---	AT4G05340	-1.05	-0.07	-0.74	0.48233858	0.8138	-6.37
248261_at	putative protein similar to unknown	PDV1	AT5G53280	-1.06	-0.08	-0.74	0.48246986	0.8139	-6.37
259617_at	hypothetical protein predicted by g	---	AT1G47970	-1.07	-0.10	-0.74	0.48253787	0.8140	-6.37
254174_at	putative protein various predicted	YSL1	AT4G24120	1.10	0.14	0.74	0.48260972	0.8140	-6.37
254487_at	calcium-binding protein - like calci	---	AT4G20780	-1.25	-0.33	-0.74	0.48261291	0.8140	-6.37
254348_at	putative protein p47 - Homo sapie	PUX3	AT4G22150	-1.05	-0.08	-0.74	0.48265593	0.8140	-6.37
266304_at	hypothetical protein	---	AT2G27090	-1.06	-0.08	-0.74	0.48290054	0.8141	-6.37
256165_at	hypothetical protein predicted by g	---	AT1G48780	-1.08	-0.11	-0.74	0.48297228	0.8141	-6.37
258458_at	Expressed protein ; supported by c	---	AT3G22435	1.09	0.13	0.74	0.48294638	0.8141	-6.37
263806_at	hypothetical protein predicted by g	---	AT2G04305	-1.14	-0.19	-0.74	0.48279016	0.8141	-6.37
253828_at	putative protein predicted protein,	SLAH2	AT4G27970	-1.08	-0.11	-0.74	0.48302297	0.8141	-6.37
252490_at	glucuronosyl transferase-like prote	---	AT3G46720	-1.06	-0.08	-0.74	0.48286718	0.8141	-6.37
255352_at	putative transposon protein similar	---	---	-1.06	-0.09	-0.74	0.48293868	0.8141	-6.37
263775_at	putative MYB family transcription f	CPC	AT2G46410	-1.06	-0.09	-0.74	0.48301945	0.8141	-6.37
254973_at	putative retrotransposon Oryza au	---	---	1.07	0.09	0.74	0.48289064	0.8141	-6.37
265598_at	putative protein phosphatase 2C	---	AT2G14270	-1.06	-0.09	-0.74	0.48319738	0.8143	-6.37
266063_at	putative SNF2/RAD54 family DNA	CHR8	AT2G18760	-1.06	-0.09	-0.74	0.48329705	0.8144	-6.37
259297_at	putative disease resistance protein	AtRLP30	AT3G05360	1.16	0.22	0.74	0.48369174	0.8145	-6.37
248647_at	sucrose synthase	SUS2	AT5G49190	-1.05	-0.07	-0.74	0.48370486	0.8145	-6.37
259702_at	putative endo-1,3-beta-glucanase	---	AT1G77780	-1.06	-0.08	-0.74	0.48364348	0.8145	-6.37
266781_at	putative protein kinase contains a	---	AT2G28940	1.08	0.11	0.74	0.48370394	0.8145	-6.37
257935_at	unknown protein	---	AT3G25440	1.06	0.08	0.74	0.48374218	0.8145	-6.37
253961_at	putative protein SPF1 protein, lpo	WRKY34	AT4G26440	-1.05	-0.07	-0.74	0.48352329	0.8145	-6.37
251877_at	synaptobrevin -like protein vesicle	ATVAMP72	AT3G54300	1.07	0.10	0.74	0.48342867	0.8145	-6.37

264088_at	unknown protein	emb1381	AT2G31340	-1.06	-0.09	-0.74	0.48355534	0.8145	-6.37
252157_at	hypothetical protein	---	AT3G50430	-1.06	-0.08	-0.74	0.48358111	0.8145	-6.37
248873_at	disease resistance protein-like	---	AT5G46450	-1.20	-0.27	-0.74	0.48372394	0.8145	-6.37
249548_at	lipid transfer - like protein lipid trar	---	AT5G38170	-1.06	-0.08	-0.74	0.48364769	0.8145	-6.37
258292_at	hypothetical protein predicted by g	---	AT3G23330	1.07	0.10	0.74	0.48379627	0.8145	-6.37
254664_at	initiation factor-2Bepsilon-like prot	---	AT4G18300	-1.07	-0.09	-0.74	0.48385862	0.8146	-6.37
251104_at	F-box protein family, AtFBL3 conta	---	AT5G01720	-1.08	-0.11	-0.74	0.48391727	0.8146	-6.37
249923_at	conglutin gamma - like protein cor	---	AT5G19120	1.12	0.17	0.74	0.48394169	0.8146	-6.37
262625_at	hypothetical protein predicted by g	---	AT1G06440	1.05	0.07	0.74	0.4840088	0.8147	-6.37
252317_at	putative protein hypersensitivity-re	---	AT3G48720	1.25	0.32	0.74	0.48424657	0.8148	-6.37
266500_at	Expressed protein ; supported by f	PLA2-ALPH	AT2G06925	1.11	0.15	0.74	0.48426728	0.8148	-6.37
250597_at	NAM (no apical meristem)-like prot	ANAC080	AT5G07680	1.13	0.17	0.74	0.48416315	0.8148	-6.37
260890_at	cysteine proteinase contains simila	---	AT1G29090	-1.09	-0.12	-0.74	0.48416489	0.8148	-6.37
254060_at	putative protein polytropic murine	SHB1	AT4G25350	-1.12	-0.16	-0.74	0.48420892	0.8148	-6.37
256876_at	hypothetical protein predicted by g	---	AT3G26360	-1.05	-0.06	-0.74	0.48441101	0.8149	-6.38
256898_at	abscisic acid-insensitive protein 3	ABI3	AT3G24650	1.05	0.08	0.74	0.48442439	0.8149	-6.38
254089_at	putative protein apoptosis gene M	---	AT4G24800	1.06	0.09	0.74	0.48465251	0.8153	-6.38
258267_at	putative delta 9 desaturase similar	---	AT3G15870	-1.05	-0.07	-0.74	0.48471879	0.8153	-6.38
255754_at	auxin-induced protein, putative sir	---	AT1G43040	-1.05	-0.07	-0.74	0.48478773	0.8154	-6.38
252970_at	small auxin up RNA (SAUR-AC1)	SAUR15	AT4G38850	-1.10	-0.14	-0.74	0.48489293	0.8154	-6.38
257631_at	cytochrome P450, putative similar	CYP71B17	AT3G26160	1.09	0.13	0.74	0.48488813	0.8154	-6.38
247893_at	RNA polymerase I, II and III 24.3 k	RPB5C	AT5G57980	-1.08	-0.11	-0.74	0.48499072	0.8155	-6.38
253495_at	putative protein crp1 protein, Zea	PGR3	AT4G31850	-1.09	-0.13	-0.74	0.48511982	0.8156	-6.38
264368_at	hypothetical protein Contains simi	---	AT1G03280	1.06	0.08	0.74	0.48509312	0.8156	-6.38
258187_at	HSC70-interacting protein, putativ	ATTDX	AT3G17880	-1.06	-0.08	-0.74	0.48521333	0.8157	-6.38
262116_at	Expressed protein ; supported by f	---	AT1G02816	1.13	0.18	0.74	0.48522537	0.8157	-6.38
245207_at	RING finger-like protein similarity	---	AT5G12310	-1.06	-0.09	-0.74	0.48528393	0.8157	-6.38
254354_at	hypothetical protein	---	AT4G22370	-1.05	-0.06	-0.74	0.48538745	0.8158	-6.38
249689_at	putative protein similar to unknown	---	AT5G36190	-1.05	-0.07	-0.74	0.48546364	0.8159	-6.38
261785_at	hypothetical protein contains simila	---	AT1G08230	-1.05	-0.08	-0.74	0.48566819	0.8159	-6.38
265285_at	hypothetical protein predicted by g	---	AT2G20410	-1.07	-0.10	-0.74	0.48560175	0.8159	-6.38
256306_at	lipase, putative contains Pfam pro	---	AT1G30370	1.52	0.61	0.74	0.48564745	0.8159	-6.38
256739_s_at	hypothetical protein similar to puta	---	---	1.05	0.06	0.74	0.48555693	0.8159	-6.38
263704_at	unknown protein similar to unknov	---	AT1G31130	1.07	0.10	0.74	0.4856248	0.8159	-6.38
249773_at	squalene monooxygenase 2 (squa	SQP2	AT5G24140	-1.06	-0.08	-0.74	0.48585253	0.8162	-6.38

260003_at	unknown protein ;supported by ful	IAR1	AT1G68100	1.05	0.07	0.74	0.48588431	0.8162	-6.38
251728_at	cysteine-tRNA ligase-like protein s	---	AT3G56300	-1.06	-0.08	-0.74	0.48601626	0.8163	-6.38
248802_at	Expressed protein ; supported by c	---	AT5G47435	1.06	0.09	0.74	0.4860821	0.8164	-6.38
254878_at	heat shock transcription factor - lik	AT-HSFB2I	AT4G11660	-1.11	-0.15	-0.74	0.48633884	0.8165	-6.38
263028_at	protein kinase, putative similar to I	---	AT1G24030	-1.08	-0.11	-0.74	0.48630772	0.8165	-6.38
253741_at	putative protein various hypothetic	---	AT4G28890	-1.05	-0.07	-0.74	0.48632501	0.8165	-6.38
245443_at	limonene cyclase like protein	---	AT4G16730	-1.70	-0.77	-0.74	0.48625653	0.8165	-6.38
260083_at	putative elicitor-responsive gene si	---	AT1G63220	1.22	0.29	0.74	0.48624407	0.8165	-6.38
246890_at	Expressed protein ; supported by c	---	AT5G25410	-1.07	-0.09	-0.74	0.48653907	0.8167	-6.38
246143_at	lipophosphoglycan biosynthetic pr	---	AT5G19980	1.09	0.12	0.74	0.48655453	0.8167	-6.38
249995_at	protein kinase -like protein protein	---	AT5G18610	-1.05	-0.07	-0.74	0.48650689	0.8167	-6.38
255322_at	putative protein	---	---	-1.05	-0.07	-0.74	0.48656821	0.8167	-6.38
257094_at	hypothetical protein similar to tetra	---	AT3G20480	1.09	0.13	0.74	0.48664581	0.8167	-6.38
258967_at	hypothetical protein predicted by g	---	AT3G10470	1.07	0.09	0.74	0.48666237	0.8167	-6.38
263582_at	unknown protein similar to hypothe	LYM2	AT2G17120	-1.10	-0.14	-0.74	0.48686084	0.8170	-6.38
254314_at	extensin - like protein hybrid prolir	---	AT4G22470	1.50	0.59	0.74	0.48695657	0.8171	-6.38
247983_at	pyrophosphate-dependent phosph	PFK7	AT5G56630	-1.17	-0.23	-0.73	0.48756276	0.8175	-6.38
257485_at	hypothetical protein contains Pfam	---	AT1G63580	-1.13	-0.17	-0.73	0.48733976	0.8175	-6.38
260212_at	hypothetical protein predicted by g	---	AT1G74480	-1.05	-0.07	-0.73	0.48738398	0.8175	-6.38
264947_at	heat shock protein DnaJ, putative	---	AT1G77020	1.08	0.11	0.73	0.48749103	0.8175	-6.38
252125_at	putative protein hypothetical prote	RTH	AT3G51040	1.06	0.09	0.73	0.48743653	0.8175	-6.38
250145_at	putative protein predicted protein,	---	AT5G14690	-1.08	-0.11	-0.73	0.48756076	0.8175	-6.38
263752_at	putative retroelement pol polyprote	---	---	-1.08	-0.11	-0.73	0.487563	0.8175	-6.38
266249_at	hypothetical protein predicted by g	---	AT2G27630	1.05	0.07	0.73	0.48742401	0.8175	-6.38
257089_at	hypothetical protein	SVL3	AT3G20520	1.06	0.09	0.73	0.48749665	0.8175	-6.38
262626_at	FtsH protease, putative similar to I	FTSH8	AT1G06430	-1.08	-0.11	-0.73	0.48750006	0.8175	-6.38
252844_at	putative protein several hypothetic	---	AT3G42140	-1.07	-0.10	-0.73	0.48775682	0.8177	-6.38
257666_at	bactericidal permeability-increasin	---	AT3G20270	1.10	0.14	0.73	0.48780287	0.8177	-6.38
258207_at	putative GTP pyrophosphokinase s	RSH2	AT3G14050	1.13	0.18	0.73	0.48779555	0.8177	-6.38
252958_at	putative transcription factor (MYB4	MYB4	AT4G38620	-1.17	-0.22	-0.73	0.48791543	0.8179	-6.38
249868_at	senescence-associated protein 5-I	TET12	AT5G23030	1.06	0.09	0.73	0.48796127	0.8179	-6.38
256008_s_at	allinase, putative similar to allinas	---	AT1G34040 /	-1.06	-0.09	-0.73	0.4880106	0.8179	-6.38
259449_at	hypothetical protein similar to puta	---	AT1G13800	-1.07	-0.10	-0.73	0.48804794	0.8179	-6.38
250469_at	pollen allergen -like protein SAH7	---	AT5G10130	1.08	0.11	0.73	0.48813121	0.8180	-6.38
257754_at	GTP binding protein, putative simi	ATRAB7B	AT3G18820	1.05	0.08	0.73	0.48827409	0.8181	-6.38

257023_at	RNA helicase, putative similar to F	---	AT3G19760	-1.06	-0.08	-0.73	0.48829025	0.8181	-6.38
256736_at	terpene synthase, putative similar	---	AT3G29410	1.06	0.08	0.73	0.48829238	0.8181	-6.38
252616_at	serine threonine-protein kinase-lik	GRIK1	AT3G45240	-1.08	-0.11	-0.73	0.48837518	0.8181	-6.38
248024_at	putative protein contains similarity	---	AT5G55840	-1.07	-0.10	-0.73	0.48835842	0.8181	-6.38
246329_at	putative protein gamma-tubulin int	---	AT3G43610	1.07	0.09	0.73	0.48841875	0.8181	-6.38
260705_at	unknown protein ;supported by full	TOM2A	AT1G32400	-1.05	-0.08	-0.73	0.48859885	0.8181	-6.38
252573_at	zinc finger protein zinc finger prote	---	AT3G45260	-1.06	-0.08	-0.73	0.48867939	0.8181	-6.38
252096_at	hypothetical protein ; supported by	---	AT3G51180	-1.11	-0.15	-0.73	0.48854036	0.8181	-6.38
249480_s_at	protein kinase - like protein recept	---	AT5G38990	-1.15	-0.21	-0.73	0.48868217	0.8181	-6.38
261556_s_at	unknown protein	---	AT1G62600	-1.08	-0.11	-0.73	0.48866701	0.8181	-6.38
245129_at	hypothetical protein predicted by g	CRR4	AT2G45350	1.05	0.07	0.73	0.48857165	0.8181	-6.38
249316_s_at	glutathione transferase-like ;suppo	ATGSTT2	AT5G41220	1.06	0.09	0.73	0.48849385	0.8181	-6.38
249808_at	unknown protein	---	AT5G23890	-1.12	-0.16	-0.73	0.48881308	0.8183	-6.38
249796_at	26S proteasome, non-ATPase reg	---	AT5G23540	1.06	0.08	0.73	0.48900668	0.8185	-6.38
255634_at	hypothetical protein ; supported by	FRI	AT4G00650	-1.05	-0.07	-0.73	0.48906965	0.8186	-6.38
265205_at	putative poly(A) binding protein	PAB7	AT2G36660	-1.06	-0.08	-0.73	0.48914244	0.8186	-6.38
262255_at	hypothetical protein similar to hypo	---	AT1G53790	1.05	0.07	0.73	0.48912678	0.8186	-6.38
254739_at	putative disease resistance protei	AtRLP48	AT4G13880	-1.06	-0.08	-0.73	0.48926134	0.8187	-6.38
247385_at	putative protein similar to unknown	emb2746	AT5G63420	1.09	0.12	0.73	0.48939928	0.8188	-6.38
267166_at	unknown protein	---	AT2G37720	-1.04	-0.06	-0.73	0.48945891	0.8188	-6.38
251118_at	putative chloroplast inner envelop	APG1	AT3G63410	1.08	0.11	0.73	0.48944141	0.8188	-6.38
264292_at	hypothetical protein predicted by g	---	AT1G78790	-1.07	-0.10	-0.73	0.4893989	0.8188	-6.38
263337_at	hypothetical protein predicted by g	---	---	-1.05	-0.06	-0.73	0.48943051	0.8188	-6.38
265747_s_at	hypothetical protein predicted by g	---	AT2G06570	-1.06	-0.09	-0.73	0.48956544	0.8189	-6.38
258794_at	ankyrin-like protein similar to anky	---	AT3G04710	-1.14	-0.19	-0.73	0.48985372	0.8193	-6.38
252711_at	lipid-transfer protein-like protein n	---	AT3G43720	-1.22	-0.28	-0.73	0.49014727	0.8193	-6.38
261259_at	unknown protein	---	AT1G26660	1.06	0.09	0.73	0.49029133	0.8193	-6.38
261844_at	hypothetical protein predicted by g	---	AT1G15940	-1.11	-0.14	-0.73	0.49015012	0.8193	-6.38
266460_at	unknown protein ; supported by cD	AGP26	AT2G47930	1.49	0.57	0.73	0.490122	0.8193	-6.38
259696_at	unknown protein ; supported by cD	---	AT1G63150	1.06	0.08	0.73	0.49031068	0.8193	-6.38
262178_at	membrane protein, putative simila	KOM	AT1G77860	-1.09	-0.12	-0.73	0.48998259	0.8193	-6.38
260046_at	Expressed protein ; supported by c	---	AT1G73805	1.27	0.35	0.73	0.49013969	0.8193	-6.38
259927_at	unknown protein ; supported by cD	JAC1	AT1G75100	1.10	0.14	0.73	0.49017692	0.8193	-6.38
250839_at	MADS-box protein - like SLM3 MA	AGL99	AT5G04640	-1.05	-0.07	-0.73	0.49030053	0.8193	-6.38
260828_at	unknown protein	---	AT1G06750	1.06	0.08	0.73	0.49031706	0.8193	-6.38

256849_at	hypothetical protein similar to hypo	---	---	-1.07	-0.09	-0.73	0.49022617	0.8193	-6.38
245135_at	putative non-LTR retroelement rev	---	---	-1.07	-0.09	-0.73	0.4902884	0.8193	-6.38
258543_at	unknown protein	---	AT3G06870	-1.07	-0.10	-0.73	0.49034342	0.8193	-6.38
259818_at	unknown protein ; supported by cD	---	AT1G49890	-1.09	-0.12	-0.73	0.49050876	0.8194	-6.38
245114_at	transcription factor IIB (TFIIB) iden	TFIIB	AT2G41630	1.10	0.14	0.73	0.49051927	0.8194	-6.38
252208_at	putative protein hypothetical prote	---	AT3G50380	1.09	0.13	0.73	0.49054985	0.8194	-6.38
260576_at	putative FCA-related protein	---	AT2G47310	-1.08	-0.11	-0.73	0.49044747	0.8194	-6.38
247696_at	MYB27 protein - like MYB27 prote	MYB59	AT5G59780	-1.15	-0.20	-0.73	0.49080871	0.8195	-6.38
248239_at	ribosomal protein L11 methyltransf	---	AT5G53920	-1.09	-0.13	-0.73	0.49074125	0.8195	-6.38
256543_at	unknown protein supported by full-	---	AT1G42480	1.07	0.10	0.73	0.49094445	0.8195	-6.38
245468_at	pectinesterase like protein	---	AT4G15980	-1.05	-0.08	-0.73	0.49075576	0.8195	-6.38
267543_at	26S proteasome regulatory subuni	---	AT2G32730	1.05	0.07	0.73	0.49080765	0.8195	-6.38
247857_at	peroxidase	---	AT5G58400	1.07	0.09	0.73	0.49088236	0.8195	-6.38
254540_s_at	putative protein chitinase / lysozyr	---	AT4G19770 /	-1.05	-0.07	-0.73	0.49063977	0.8195	-6.38
256434_at	putative 60S ribosomal protein L37	---	AT3G10950	-1.05	-0.07	-0.73	0.49091355	0.8195	-6.38
263750_at	unknown protein	---	AT2G21530	1.08	0.11	0.73	0.49077581	0.8195	-6.38
245634_at	MtN21 nodulin protein, putative si	---	AT1G25270	-1.07	-0.09	-0.73	0.49095111	0.8195	-6.38
261898_at	hypothetical protein predicted by g	---	AT1G80720	1.13	0.17	0.73	0.49100331	0.8195	-6.38
248255_at	ATP-dependent Clp protease ATP	CLPX	AT5G53350	-1.07	-0.09	-0.73	0.49113116	0.8196	-6.38
247796_at	Expressed protein ;supported by c	---	AT5G58782	1.06	0.09	0.73	0.49112401	0.8196	-6.38
257339_s_at	ATP synthase subunit 9	---	AT2G07671	-1.10	-0.13	-0.73	0.49152169	0.8197	-6.38
266464_at	glutathione-conjugate transporter A	ATMRP4	AT2G47800	1.34	0.42	0.73	0.49150576	0.8197	-6.38
256336_at	unknown protein	---	AT1G72030	1.08	0.11	0.73	0.49121995	0.8197	-6.38
262536_at	SOUL-like protein Similar to SOUI	---	AT1G17100	-1.13	-0.17	-0.73	0.49146411	0.8197	-6.38
248222_at	GTPase activator protein of Rab-lil	---	AT5G53570	1.08	0.11	0.73	0.49154132	0.8197	-6.38
264569_at	unknown protein EST gb|ATTS113	---	---	-1.05	-0.07	-0.73	0.49139049	0.8197	-6.38
266434_s_at	unknown protein	---	AT2G07120 /	-1.05	-0.07	-0.73	0.49130597	0.8197	-6.38
257737_at	uridine kinase/uracil phosphoribos	---	AT3G27440	-1.06	-0.08	-0.73	0.49131548	0.8197	-6.38
245214_at	F12A21.1 hypothetical protein	---	AT1G67855	1.05	0.07	0.73	0.49146551	0.8197	-6.38
264204_at	putative sucrose transport protein	SUC2	AT1G22710	-1.09	-0.12	-0.73	0.49134999	0.8197	-6.38
252009_at	zinc finger - like protein zinc finger	---	AT3G52800	-1.09	-0.13	-0.73	0.49134843	0.8197	-6.38
254054_at	putative protein DNA-binding prote	---	AT4G25320	1.09	0.12	0.73	0.49179784	0.8200	-6.38
250983_at	putative protein In2, Zea mays, EM	---	AT5G02780	-1.25	-0.32	-0.73	0.49214575	0.8203	-6.39
249553_at	receptor serine/threonine protein k	---	AT5G38260	-1.09	-0.12	-0.73	0.49218677	0.8203	-6.39
262164_at	unknown protein ; supported by cD	---	AT1G78070	1.08	0.11	0.73	0.49221403	0.8203	-6.39

267539_at	putative RING zinc finger protein ;	---	AT2G42030	1.07	0.09	0.73	0.49224541	0.8203	-6.39
248811_at	putative protein contains similarity	---	AT5G47310	-1.07	-0.09	-0.73	0.49222733	0.8203	-6.39
250258_at	floral homeotic protein AGL15 (spl	AGL15	AT5G13790	1.06	0.09	0.73	0.49227127	0.8203	-6.39
259268_at	putative lamin similar to blue coppe	---	AT3G01070	-1.05	-0.07	-0.73	0.49212169	0.8203	-6.39
265251_at	unknown protein predicted by gens	TET14	AT2G01960	-1.06	-0.08	-0.73	0.49210221	0.8203	-6.39
255063_at	putative transposon protein similar	---	---	-1.04	-0.06	-0.73	0.49215298	0.8203	-6.39
252177_at	protein kinase ATN1 - like protein	---	AT3G50730	-1.07	-0.10	-0.73	0.49233492	0.8203	-6.39
260579_at	putative cytochrome c oxidase Vc	---	AT2G47380	1.06	0.09	0.73	0.49282435	0.8203	-6.39
254282_at	hypothetical protein	---	AT4G22860	1.05	0.08	0.73	0.49265534	0.8203	-6.39
252675_at	putative protein hypothetical protei	---	---	-1.06	-0.08	-0.73	0.49266042	0.8203	-6.39
250313_at	Rab geranylgeranyltransferase, be	---	AT5G12210	1.07	0.10	0.73	0.49283883	0.8203	-6.39
247583_at	putative protein predicted protein,	---	AT5G60750	1.06	0.08	0.73	0.49257963	0.8203	-6.39
261155_at	unknown protein ;supported by full	---	AT1G04960	-1.07	-0.10	-0.73	0.49241922	0.8203	-6.39
254918_at	putative protein phosphatase like	SGT1B	AT4G11260	1.07	0.09	0.73	0.4924597	0.8203	-6.39
247420_at	unknown protein	---	AT5G63100	-1.09	-0.12	-0.73	0.49263585	0.8203	-6.39
252768_at	putative protein hypothetical protei	---	---	-1.05	-0.07	-0.73	0.49281895	0.8203	-6.39
267137_at	hypothetical protein predicted by g	ACPT	AT2G23410	1.05	0.07	0.73	0.49257029	0.8203	-6.39
247704_at	Expressed protein ; supported by f	RTFL5	AT5G59510	-1.17	-0.23	-0.73	0.49280912	0.8203	-6.39
264312_at	putative protein kinase similar to p	---	AT1G70450	-1.06	-0.08	-0.73	0.49267607	0.8203	-6.39
257394_at	hypothetical protein predicted by g	---	---	1.07	0.10	0.73	0.49243146	0.8203	-6.39
248830_at	putative protein contains similarity	---	AT5G47150	-1.06	-0.09	-0.73	0.49276617	0.8203	-6.39
245632_at	unknown protein contains similarity	ATRBL10	AT1G25290	-1.06	-0.09	-0.72	0.49295603	0.8204	-6.39
260575_at	hypothetical protein predicted by g	---	AT2G47300	1.06	0.09	0.72	0.49364768	0.8204	-6.39
251821_at	protein phosphatase 2C - like prot	---	AT3G55050	-1.13	-0.17	-0.72	0.49402904	0.8204	-6.39
249147_at	cytosolic malate dehydrogenase ;s	---	AT5G43330	-1.08	-0.11	-0.72	0.49393021	0.8204	-6.39
260927_at	hypothetical protein predicted by g	CAT9	AT1G05940	-1.07	-0.10	-0.72	0.49406522	0.8204	-6.39
253542_at	putative protein deubiquitinating e	UBP18	AT4G31670	-1.06	-0.08	-0.72	0.49391574	0.8204	-6.39
259467_at	hypothetical protein predicted by g	---	AT1G19060	-1.04	-0.06	-0.72	0.49374168	0.8204	-6.39
265852_at	putative RING zinc finger protein	---	AT2G42350	1.11	0.15	0.72	0.49380544	0.8204	-6.39
262397_at	hypothetical protein predicted by g	---	AT1G49380	-1.10	-0.14	-0.72	0.49334496	0.8204	-6.39
262611_at	Expressed protein ; supported by f	---	AT1G14060	-1.10	-0.14	-0.72	0.49387017	0.8204	-6.39
249951_at	S-adenosyl-L-methionine decarbo	BUD2	AT5G18930	1.10	0.13	0.72	0.49364378	0.8204	-6.39
246348_at	putative protein putative glycerol-3	---	AT3G56840	-1.04	-0.06	-0.72	0.49351595	0.8204	-6.39
259474_at	unknown protein ;supported by full	---	AT1G19130	1.15	0.20	0.72	0.49291112	0.8204	-6.39
251675_at	helicase-like protein DNA helicase	INO80	AT3G57300	-1.05	-0.07	-0.72	0.49380537	0.8204	-6.39

249908_at	putative protein similar to unknown	---	AT5G22760	-1.06	-0.08	-0.72	0.49350227	0.8204	-6.39
262086_at	GTP-binding protein, putative simi	---	AT1G56050	1.07	0.10	0.72	0.49410822	0.8204	-6.39
253594_at	Expressed protein ; supported by f	---	AT4G30820	1.07	0.10	0.72	0.49398487	0.8204	-6.39
266506_at	unknown protein	---	AT2G47850	-1.06	-0.08	-0.72	0.49342772	0.8204	-6.39
248128_at	thiazole biosynthetic enzyme precu	THI1	AT5G54770	-1.08	-0.11	-0.72	0.49402342	0.8204	-6.39
254256_at	serine/threonine kinase -like prote	CRK10	AT4G23180	-1.10	-0.13	-0.72	0.49311992	0.8204	-6.39
265797_at	Expressed protein ; supported by f	---	AT2G35710	-1.27	-0.34	-0.72	0.49379246	0.8204	-6.39
265628_at	hypothetical protein predicted by g	---	AT2G27290	-1.10	-0.14	-0.72	0.49371852	0.8204	-6.39
257777_x_at	hypothetical protein	---	---	1.07	0.09	0.72	0.49410592	0.8204	-6.39
248539_at	ribitol dehydrogenase-like ; suppo	---	AT5G50130	1.07	0.10	0.72	0.4939058	0.8204	-6.39
255253_at	contains similarity to S. cerevisiae	VPS28-2	AT4G05000	1.06	0.08	0.72	0.49379078	0.8204	-6.39
249980_at	putative protein	---	AT5G18870	1.07	0.09	0.72	0.49325034	0.8204	-6.39
245182_at	putative protein similarity to TETR	---	AT5G12430	-1.09	-0.12	-0.72	0.49407075	0.8204	-6.39
260625_at	storage protein, putative similar to	MOM	AT1G08060	1.05	0.07	0.72	0.49338092	0.8204	-6.39
246670_at	putative protein	---	AT5G30520	-1.08	-0.11	-0.72	0.4931958	0.8204	-6.39
261514_at	hypothetical protein predicted by g	---	AT1G71870	-1.09	-0.12	-0.72	0.49334048	0.8204	-6.39
264244_at	pantothenate kinase, putative sim	ATPANK1	AT1G60440	1.06	0.08	0.72	0.49373367	0.8204	-6.39
247051_at	At14a protein-like	---	AT5G66670	-1.06	-0.09	-0.72	0.4941222	0.8204	-6.39
252431_at	putative protein	MAG2	AT3G47700	-1.09	-0.13	-0.72	0.49404557	0.8204	-6.39
246783_at	sugar transporter-like protein puta	SFP2	AT5G27360	-1.20	-0.26	-0.72	0.49408427	0.8204	-6.39
253082_at	putative glycine-rich cell wall prote	---	AT4G36230	-1.11	-0.15	-0.72	0.49338192	0.8204	-6.39
266097_at	unknown protein ; supported by cl	SOUL-1	AT2G37970	-1.15	-0.20	-0.72	0.49419523	0.8204	-6.39
255922_at	trehalose-6-phosphate phosphata	---	AT1G22210	-1.05	-0.08	-0.72	0.49434779	0.8206	-6.39
252910_at	putative protein various predicted	---	AT4G39590	-1.05	-0.07	-0.72	0.49445936	0.8207	-6.39
249267_at	putative protein contains similarity	BTI3	AT5G41600	-1.10	-0.14	-0.72	0.494554	0.8208	-6.39
251626_at	UDP-GlcNAc:dolichol phosphate N	---	AT3G57220	1.06	0.09	0.72	0.49455341	0.8208	-6.39
262751_at	hypothetical protein predicted by g	---	AT1G16310	1.05	0.07	0.72	0.49465236	0.8208	-6.39
245120_at	hypothetical protein predicted by g	HOS1	AT2G39810	1.07	0.10	0.72	0.49468789	0.8208	-6.39
249909_s_at	alpha-adaptin	---	AT5G22770	1.07	0.10	0.72	0.49469523	0.8208	-6.39
245099_at	unknown protein ; supported by cl	RHC1A	AT2G40830	-1.09	-0.13	-0.72	0.49477649	0.8209	-6.39
247283_at	2-nitropropane dioxygenase-like pr	---	AT5G64250	-1.06	-0.09	-0.72	0.4948139	0.8209	-6.39
247306_at	ser/thr protein phosphatase catalyt	PP7	AT5G63870	-1.07	-0.10	-0.72	0.49489685	0.8209	-6.39
251251_at	serine/threonine protein kinase-lik	---	AT3G62220	1.06	0.09	0.72	0.49486813	0.8209	-6.39
256353_at	unknown protein ; supported by ful	---	AT1G55000	1.06	0.08	0.72	0.49499644	0.8210	-6.39
254378_at	putative protein NADH oxidoreduc	DER2.1	AT4G21810	1.11	0.15	0.72	0.49501571	0.8210	-6.39

246334_at	putative protein serine kinase SRF	---	AT3G44850	-1.09	-0.13	-0.72	0.49522137	0.8211	-6.39
247112_at	unknown protein	---	AT5G65950	1.06	0.09	0.72	0.49522854	0.8211	-6.39
253872_at	putative protein Arabidopsis thalia	RD26	AT4G27410	1.10	0.13	0.72	0.49525283	0.8211	-6.39
265117_at	putative proline-rich cell wall prote	---	AT1G62500	-1.09	-0.12	-0.72	0.49522084	0.8211	-6.39
261691_at	branched-chain amino acid amino	---	AT1G50060	-1.05	-0.07	-0.72	0.49522051	0.8211	-6.39
257633_at	hypothetical protein	CYP86C2	AT3G26125	1.05	0.07	0.72	0.49531847	0.8212	-6.39
263601_s_at	dihydrofolate reductase-thymidylat	THY-1	AT2G16370	1.08	0.11	0.72	0.49539626	0.8212	-6.39
255781_at	unknown protein	---	AT1G19880	1.05	0.07	0.72	0.49544487	0.8212	-6.39
267571_at	3-hydroxyisobutyryl-coenzyme A h	---	AT2G30650	-1.05	-0.07	-0.72	0.49566297	0.8215	-6.39
250315_at	putative protein contains similarity	PDE149	AT5G12130	-1.11	-0.15	-0.72	0.49567411	0.8215	-6.39
245193_at	F12A21.6 hypothetical protein	SUFE2	AT1G67810	1.23	0.30	0.72	0.49602821	0.8215	-6.39
250968_at	putative protein ;supported by full-	---	AT5G02890	1.14	0.19	0.72	0.49596814	0.8215	-6.39
254893_at	putative phospholipase D-gamma	PLDGAMM	AT4G11830	-1.10	-0.14	-0.72	0.49588949	0.8215	-6.39
255639_at	putative protein	APRR8	AT4G00760	-1.08	-0.10	-0.72	0.49604376	0.8215	-6.39
254989_at	retrotransposon like protein copia-	---	---	-1.07	-0.09	-0.72	0.4959624	0.8215	-6.39
245126_at	putative MYB family transcription f	MYB12	AT2G47460	-1.05	-0.08	-0.72	0.49585296	0.8215	-6.39
255804_at	putative protein IB1C3-1 protein, A	---	AT4G10220	1.07	0.10	0.72	0.49607474	0.8215	-6.39
256339_at	hypothetical protein	---	AT1G72080	-1.06	-0.08	-0.72	0.49604151	0.8215	-6.39
261937_at	peptide transporter, putative simila	---	AT1G22570	-1.14	-0.19	-0.72	0.49608447	0.8215	-6.39
249362_at	putative protein predicted protein,	---	AT5G40550	-1.16	-0.21	-0.72	0.49592801	0.8215	-6.39
248038_at	unknown protein	---	AT5G55980	1.05	0.08	0.72	0.49591933	0.8215	-6.39
257685_at	unknown protein	---	AT3G12770	-1.07	-0.10	-0.72	0.49612984	0.8215	-6.39
255514_s_at	hypothetical protein similar to MNA	AGL78	AT5G65330	-1.06	-0.09	-0.72	0.49619618	0.8216	-6.39
254250_at	serine/threonine kinase - like prote	---	AT4G23290	-1.12	-0.17	-0.72	0.49628772	0.8217	-6.39
260132_s_at	hypothetical protein	---	AT1G66320	1.05	0.07	0.72	0.49655237	0.8221	-6.39
244954_s_at	hypothetical protein	---	AT2G07732	-1.13	-0.17	-0.72	0.4966544	0.8222	-6.39
AFFX-r2-P1-cre	Bacteriophage P1 /GEN=cre /DB_	---	---	-1.10	-0.14	-0.72	0.49674342	0.8223	-6.39
262409_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-0.72	0.49684524	0.8223	-6.39
249132_at	putative protein contains similarity	---	AT5G43120	1.06	0.09	0.72	0.49684947	0.8223	-6.39
254558_at	Expressed protein ; supported by f	---	AT4G19185	1.05	0.08	0.72	0.49692237	0.8224	-6.39
251572_at	pelota-like protein pelota PEL1 - A	---	AT3G58390	1.05	0.08	0.72	0.49695699	0.8224	-6.39
262906_at	unknown protein contains similarity	---	AT1G59760	1.08	0.11	0.72	0.49701553	0.8224	-6.39
267003_at	hypothetical protein predicted by g	---	AT2G34340	1.06	0.08	0.72	0.49713543	0.8225	-6.39
253817_at	hypothetical protein ;supported by	---	AT4G28310	1.17	0.23	0.72	0.49725615	0.8227	-6.39
252184_at	steroid 22-alpha-hydroxylase (DW	DWF4	AT3G50660	-1.08	-0.11	-0.72	0.49731358	0.8227	-6.39

255938_at	hypothetical protein contains Pfam	---	AT1G12620	-1.08	-0.11	-0.72	0.49737309	0.8227	-6.39
257419_at	hypothetical protein predicted by g	---	AT1G30800	-1.05	-0.07	-0.72	0.49735234	0.8227	-6.39
251601_at	Expressed protein ; supported by f	---	AT3G57800	-1.10	-0.14	-0.72	0.49759131	0.8228	-6.39
256744_at	ATHP2, putative similar to ATHP2	AHP2	AT3G29350	1.07	0.10	0.72	0.49756201	0.8228	-6.39
264044_at	putative pyrophosphate--fructose-6	PFK5	AT2G22480	1.06	0.08	0.72	0.4976653	0.8228	-6.39
265337_at	putative ADP-ribosylation factor ;s	TTN5	AT2G18390	1.09	0.13	0.72	0.49769711	0.8228	-6.39
265933_at	putative esterase contains esteras	---	AT2G19550	-1.07	-0.09	-0.72	0.49744755	0.8228	-6.39
245882_at	mitochondrial carrier-like protein n	DIC3	AT5G09470	-1.07	-0.09	-0.72	0.49766548	0.8228	-6.39
246812_at	putative protein predicted proteins	---	---	-1.05	-0.07	-0.72	0.49769438	0.8228	-6.39
262608_at	dioxygenase-like protein very simi	---	AT1G14120	-1.06	-0.09	-0.72	0.49759052	0.8228	-6.39
253932_at	putative protein other Arabidopsis	---	AT4G26800	-1.05	-0.07	-0.72	0.49774431	0.8228	-6.39
251603_at	putative protein wall-associated ki	---	AT3G57760	1.16	0.21	0.72	0.49793874	0.8230	-6.39
261717_at	helix-loop-helix protein homolog, p	BEE1	AT1G18400	-1.23	-0.30	-0.72	0.49805204	0.8231	-6.39
252113_at	putative protein predicted protein,	---	AT3G51620	1.05	0.07	0.72	0.49801659	0.8231	-6.39
252434_s_at	putative protein mudrA protein - m	---	---	1.06	0.09	0.72	0.49802889	0.8231	-6.39
248983_at	ras-related GTP-binding protein RH	RHA1	AT5G45130	-1.05	-0.07	-0.72	0.49818481	0.8232	-6.39
248113_at	wax synthase-like protein	---	AT5G55360	-1.06	-0.09	-0.72	0.49825818	0.8232	-6.39
267390_at	putative beta-glucosidase	BGLU29	AT2G44470	1.05	0.08	0.72	0.49823862	0.8232	-6.39
255163_at	putative polyprotein	---	---	-1.05	-0.08	-0.72	0.49844634	0.8234	-6.39
257006_at	hypothetical protein predicted by g	---	AT3G14075	-1.06	-0.08	-0.72	0.49843903	0.8234	-6.39
256865_at	NAD dependent epimerase, putati	GAE6	AT3G23820	-1.12	-0.16	-0.72	0.49850164	0.8234	-6.39
247139_at	unknown protein ;supported by ful	---	AT5G66090	1.06	0.09	0.71	0.4988764	0.8239	-6.39
267393_at	similar to axi 1 protein from Nicotia	---	AT2G44500	-1.11	-0.15	-0.71	0.49884433	0.8239	-6.39
246636_at	acid phosphatase-like protein purp	PAP26	AT5G34850	-1.08	-0.11	-0.71	0.49889855	0.8239	-6.39
250270_at	putative protein FL10, EGF respor	---	AT5G12980	1.07	0.10	0.71	0.49895124	0.8239	-6.39
251183_at	putative protein putative protein A	---	AT3G62630	-1.20	-0.26	-0.71	0.49907901	0.8240	-6.39
257290_at	hypothetical protein predicted by g	---	AT3G15550	-1.05	-0.07	-0.71	0.49904963	0.8240	-6.39
253134_at	putative protein procollagen-prolin	---	AT4G35820	-1.05	-0.07	-0.71	0.4990547	0.8240	-6.39
260713_at	disease resistance protein RPP1-\	---	AT1G17615	1.05	0.07	0.71	0.49927055	0.8242	-6.39
250378_at	putative oligopeptide transporter p	---	AT5G11570	-1.07	-0.09	-0.71	0.49927373	0.8242	-6.39
246399_at	bZIP transcription factor similar to	---	AT1G58110	1.06	0.09	0.71	0.49942456	0.8244	-6.39
259320_at	putative DNA-binding protein simila	WRKY58	AT3G01080	-1.18	-0.24	-0.71	0.49945394	0.8244	-6.40
245858_at	CER1-like protein CER1-like, A.th	---	AT5G28280	1.06	0.09	0.71	0.49949802	0.8244	-6.40
247754_at	putative protein	---	AT5G59080	1.15	0.20	0.71	0.49954736	0.8244	-6.40
245081_at	unknown protein overlap with T20	---	---	1.09	0.13	0.71	0.49961869	0.8244	-6.40

247329_at	putative protein similar to unknown	---	AT5G64150	1.11	0.15	0.71	0.49960753	0.8244	-6.40
250497_at	putative protein predicted proteins	---	AT5G09630	1.08	0.10	0.71	0.49972421	0.8244	-6.40
257497_at	hypothetical protein predicted by g	---	AT1G51430	-1.09	-0.13	-0.71	0.4997495	0.8244	-6.40
262287_at	unknown protein ;supported by full	---	AT1G68660	-1.06	-0.09	-0.71	0.49984558	0.8244	-6.40
253770_at	protein kinase ADK1-like protein p	CKL6	AT4G28540	-1.05	-0.07	-0.71	0.49969611	0.8244	-6.40
261475_at	anionic peroxidase, putative simila	---	AT1G14550	-1.10	-0.14	-0.71	0.4998137	0.8244	-6.40
260994_at	hypothetical protein contains simila	---	AT1G12130	1.06	0.09	0.71	0.49980796	0.8244	-6.40
255147_at	hypothetical protein	---	AT4G08460	1.06	0.09	0.71	0.49990473	0.8244	-6.40
252104_at	putative protein KIAA0851 protein	RHD4	AT3G51460	1.07	0.10	0.71	0.49994766	0.8245	-6.40
253545_at	AIG2-like protein AIG2 protein, Ar	---	AT4G31310	-1.08	-0.11	-0.71	0.50028713	0.8246	-6.40
259581_at	RING zinc finger protein, putative	---	AT1G28040	1.06	0.09	0.71	0.50023067	0.8246	-6.40
262638_at	oxidoreductase, putative contains	---	AT1G06650	-1.05	-0.07	-0.71	0.50024691	0.8246	-6.40
262147_at	phospholipase D1, putative simila	PLDALPHA	AT1G52570	1.05	0.07	0.71	0.50022669	0.8246	-6.40
246183_at	beta-glucosidase - like protein bet	---	AT5G20940	-1.07	-0.09	-0.71	0.50028401	0.8246	-6.40
263303_at	unknown protein ;supported by ful	---	AT2G15240	1.07	0.10	0.71	0.50030686	0.8246	-6.40
258680_at	adenylate translocator identical to	AAC1	AT3G08580	1.10	0.14	0.71	0.50016988	0.8246	-6.40
259530_at	hypothetical protein	---	AT1G12450	1.11	0.16	0.71	0.50035116	0.8246	-6.40
260362_at	putative protein kinase similar to C	---	AT1G70530	1.14	0.19	0.71	0.5004583	0.8247	-6.40
248789_at	putative protein strong similarity to	---	AT5G47440	1.09	0.12	0.71	0.500467	0.8247	-6.40
252247_at	putative protein various predicted p	---	AT3G49740	-1.05	-0.08	-0.71	0.5005448	0.8248	-6.40
263082_at	putative nucleotide-binding protein	---	AT2G27200	-1.05	-0.07	-0.71	0.50069829	0.8249	-6.40
252909_at	putative protein	---	AT4G39680	1.05	0.07	0.71	0.50073049	0.8249	-6.40
249260_at	Pto kinase interactor 1-like protein	---	AT5G41680	-1.06	-0.08	-0.71	0.50072289	0.8249	-6.40
264460_at	hypothetical protein similar to trans	ATNFXL1	AT1G10170	1.07	0.10	0.71	0.50083671	0.8250	-6.40
259213_at	putative receptor ser/thr protein kir	---	AT3G09010	-1.23	-0.30	-0.71	0.5009549	0.8250	-6.40
259511_at	unknown protein contains similarity	ATCCS	AT1G12520	1.19	0.25	0.71	0.50093885	0.8250	-6.40
245072_s_at	putative cytochrome P450	CYP81D7	AT2G23190	1.07	0.09	0.71	0.50096512	0.8250	-6.40
265600_at	hypothetical protein predicted by g	---	---	1.05	0.08	0.71	0.50098191	0.8250	-6.40
254611_at	Expressed protein ; supported by f	---	AT4G19095	1.05	0.08	0.71	0.50113652	0.8252	-6.40
263352_at	En/Spm-like transposon protein rel	---	AT2G22080	-1.09	-0.12	-0.71	0.50120068	0.8253	-6.40
259011_s_at	unknown protein similar to putative	---	AT3G07380	1.06	0.08	0.71	0.50130827	0.8253	-6.40
247235_at	putative protein contains similarity	---	AT5G64580	1.11	0.15	0.71	0.50128662	0.8253	-6.40
249627_at	NADH dehydrogenase (ubiquinon	EMB1467	AT5G37510	-1.07	-0.10	-0.71	0.50126182	0.8253	-6.40
246395_at	dirigent protein, putative similar to	---	AT1G58170	1.06	0.08	0.71	0.50147417	0.8255	-6.40
255064_at	putative phi-1-like phosphate-indu	EXO	AT4G08950	1.25	0.32	0.71	0.50153447	0.8255	-6.40

254928_at	putative protein hypothetical prote	---	AT4G11410	1.06	0.08	0.71	0.501681	0.8257	-6.40
247895_at	putative protein bHLH transcriptio	---	AT5G58010	1.06	0.08	0.71	0.50183311	0.8258	-6.40
248516_at	unknown protein	---	AT5G50540	1.07	0.10	0.71	0.50179665	0.8258	-6.40
263140_at	hypothetical protein predicted by g	---	AT1G65120	-1.05	-0.06	-0.71	0.50186146	0.8258	-6.40
248245_at	MtN3 protein-like	---	AT5G53190	-1.07	-0.10	-0.71	0.50195254	0.8259	-6.40
250646_at	peroxidase (emb|CAA68212.1) ;su	---	AT5G06720	1.08	0.11	0.71	0.50267816	0.8260	-6.40
259690_at	replication factor, putative similar	---	AT1G63160	1.09	0.13	0.71	0.50214487	0.8260	-6.40
249794_at	putative protein contains similarity	AtCXE18	AT5G23530	-1.05	-0.07	-0.71	0.50271806	0.8260	-6.40
247545_at	putative protein rhoGAP, Homo sa	---	AT5G61530	-1.05	-0.07	-0.71	0.50237235	0.8260	-6.40
252895_at	hypothetical protein	---	AT4G39450	1.05	0.08	0.71	0.50219423	0.8260	-6.40
263911_at	hypothetical protein predicted by g	---	AT2G36560	-1.05	-0.07	-0.71	0.50239172	0.8260	-6.40
263986_at	putative citrate synthase ;supporte	CSY3	AT2G42790	1.08	0.11	0.71	0.50248114	0.8260	-6.40
246087_at	putative protein predicted protein,	---	AT5G20580	1.09	0.13	0.71	0.50219909	0.8260	-6.40
245675_at	hypothetical protein similar to puta	---	---	-1.08	-0.12	-0.71	0.50233569	0.8260	-6.40
258115_at	hypothetical protein predicted by g	---	AT3G14670	-1.06	-0.08	-0.71	0.50259379	0.8260	-6.40
262873_at	hypothetical protein predicted by g	---	AT1G64700	-1.06	-0.08	-0.71	0.50271115	0.8260	-6.40
254401_at	putative protein various predicted	---	AT4G21300	1.06	0.08	0.71	0.50271365	0.8260	-6.40
252185_at	putative protein	---	AT3G50780	1.08	0.11	0.71	0.50232822	0.8260	-6.40
259957_at	putative protein kinase C-terminal	---	AT1G67890	-1.11	-0.15	-0.71	0.502369	0.8260	-6.40
250389_at	putative protein probable flavin-co	YUC4	AT5G11320	-1.05	-0.07	-0.71	0.50265412	0.8260	-6.40
251044_at	putative protein various predicted	---	AT5G02350	1.05	0.07	0.71	0.50251356	0.8260	-6.40
257942_at	SKP1/ASK1 (At8), putative similar	ASK8	AT3G21830	-1.07	-0.10	-0.71	0.50245542	0.8260	-6.40
267480_at	putative retroelement pol polyprote	---	---	1.05	0.07	0.71	0.50265515	0.8260	-6.40
252656_at	hypothetical protein	---	AT3G44770	-1.08	-0.11	-0.71	0.5021081	0.8260	-6.40
246444_at	putative protein predicted protein	---	AT5G17570	-1.09	-0.12	-0.71	0.50237544	0.8260	-6.40
256343_at	unknown protein ; supported by cD	---	AT1G72090	1.07	0.09	0.71	0.50282518	0.8260	-6.40
265535_at	hypothetical protein predicted by g	---	AT2G15900	1.05	0.07	0.71	0.50281784	0.8260	-6.40
254813_at	putative transcription factor myb-r	MYB42	AT4G12350	-1.05	-0.07	-0.71	0.50284646	0.8260	-6.40
246026_at	putative protein predicted protein -	---	AT5G21070	-1.06	-0.08	-0.71	0.50292441	0.8261	-6.40
247593_at	ABC transporter homolog PnATH	GCN1	AT5G60790	-1.06	-0.09	-0.71	0.50318384	0.8264	-6.40
249223_at	receptor lectin kinase-like protein	---	AT5G42120	1.06	0.09	0.71	0.50317012	0.8264	-6.40
254143_at	putative protein histidine-rich calci	---	AT4G24680	-1.05	-0.06	-0.71	0.50329586	0.8265	-6.40
247137_at	calcium-dependent protein kinase	CPK28	AT5G66210	1.14	0.19	0.71	0.5035624	0.8269	-6.40
245480_at	transcription factor like protein	---	AT4G16150	1.05	0.07	0.71	0.5037515	0.8269	-6.40
251659_at	hypothetical protein ;supported by	BIGYIN	AT3G57090	-1.06	-0.08	-0.71	0.50364343	0.8269	-6.40

261799_at	unknown protein contains similarity	---	AT1G30473	-1.08	-0.11	-0.71	0.50370016	0.8269	-6.40
266826_at	putative amino acid acetyltransfera	---	AT2G22910	-1.13	-0.17	-0.71	0.50375717	0.8269	-6.40
254311_at	hypothetical protein	---	AT4G22440	-1.06	-0.09	-0.71	0.50376374	0.8269	-6.40
256549_at	hypothetical protein predicted by g	---	---	-1.05	-0.07	-0.71	0.50380803	0.8269	-6.40
259137_at	unknown protein Pfam HMM hit: E	---	AT3G10300	-1.10	-0.13	-0.71	0.5040411	0.8270	-6.40
248613_at	phytoene dehydrogenase-like	---	AT5G49555	-1.08	-0.11	-0.71	0.50402625	0.8270	-6.40
260837_at	fructose 1,6-bisphosphatase, puta	---	AT1G43670	-1.11	-0.15	-0.71	0.50403095	0.8270	-6.40
262728_at	receptor kinase (CLV1) identical to	CLV1	AT1G75820	1.11	0.15	0.71	0.50396545	0.8270	-6.40
266575_at	putative chloroplast initiation factor	---	AT2G24060	1.06	0.09	0.71	0.50395562	0.8270	-6.40
266058_at	glycerol-3-phosphate dehydrogena	GLY1	AT2G40690	-1.08	-0.11	-0.71	0.50403368	0.8270	-6.40
260419_at	putative protein kinase contains Pf	---	AT1G69730	-1.16	-0.21	-0.71	0.50423865	0.8272	-6.40
252078_at	putative protein brassinosteroid-in	IMK2	AT3G51740	-1.04	-0.06	-0.71	0.50427667	0.8272	-6.40
266589_at	hypothetical protein predicted by g	---	AT2G46250	1.08	0.11	0.71	0.50437993	0.8273	-6.40
250104_at	unknown protein	---	AT5G16610	1.08	0.11	0.71	0.50435657	0.8273	-6.40
260516_at	unknown protein	---	AT1G51450	-1.07	-0.10	-0.70	0.50454997	0.8275	-6.40
246236_at	hypothetical protein	---	AT4G36470	-1.07	-0.09	-0.70	0.50482939	0.8275	-6.40
247761_at	phosphoprotein phosphatase 1 cat	TOPP2	AT5G59160	-1.06	-0.08	-0.70	0.50485214	0.8275	-6.40
253621_at	putative protein component of anil	---	AT4G30540	-1.06	-0.08	-0.70	0.50486922	0.8275	-6.40
261660_at	kinesin heavy chain isolog, putativ	HIK	AT1G18370	-1.05	-0.07	-0.70	0.50469774	0.8275	-6.40
258912_at	unknown protein similar to hypoth	---	AT3G06460	-1.09	-0.12	-0.70	0.50485127	0.8275	-6.40
255125_at	putative protein SCARECROW - A	---	AT4G08250	1.07	0.09	0.70	0.50486715	0.8275	-6.40
259558_at	hypothetical protein	WAK5	AT1G21230	1.06	0.09	0.70	0.50486043	0.8275	-6.40
251099_at	putative protein KIAA0132 - Homo	---	AT5G01660	-1.05	-0.08	-0.70	0.50479897	0.8275	-6.40
248258_at	putative protein contains similarity	---	AT5G53400	-1.12	-0.16	-0.70	0.50527498	0.8276	-6.40
254194_at	auxin response factor 9 (ARF9) ; s	ARF9	AT4G23980	1.09	0.12	0.70	0.50509442	0.8276	-6.40
258905_at	unknown protein similar to hypothe	---	AT3G06390	-1.10	-0.14	-0.70	0.50506167	0.8276	-6.40
261269_at	unknown protein ; supported by ful	---	AT1G26690	1.07	0.09	0.70	0.50499549	0.8276	-6.40
245638_s_at	F5A9.10 unknown protein; similar	---	AT1G24822 /	1.06	0.08	0.70	0.50513584	0.8276	-6.40
255659_at	Expressed protein ; supported by f	---	AT4G00895	1.12	0.17	0.70	0.5050533	0.8276	-6.40
249274_at	unknown protein	---	AT5G41860	-1.08	-0.12	-0.70	0.50500177	0.8276	-6.40
265181_at	putative OBP32pep protein ;suppo	---	AT1G23510	-1.07	-0.10	-0.70	0.50505551	0.8276	-6.40
259197_at	putative peroxidase similar to pero	---	AT3G03670	-1.23	-0.30	-0.70	0.50518736	0.8276	-6.40
262481_at	unknown protein Location of ests	---	AT1G17080	1.06	0.08	0.70	0.505251	0.8276	-6.40
264375_at	putative protein kinase contains a	CIPK16	AT2G25090	-1.18	-0.23	-0.70	0.50521489	0.8276	-6.40
261425_at	peptide transporter, putative simila	---	AT1G18880	-1.13	-0.18	-0.70	0.50533998	0.8276	-6.40

258110_at	putative cytochrome P450 similar t	CYP72A7	AT3G14610	1.07	0.10	0.70	0.50546909	0.8276	-6.40
263157_at	aldehyde dehydrogenase homolog	ALDH7B4	AT1G54100	1.11	0.15	0.70	0.5054351	0.8276	-6.40
252710_at	cellulase-like protein cellulase, Sa	AtGH9A4	AT3G43860	1.05	0.07	0.70	0.5054363	0.8276	-6.40
255709_at	putative YABBY3 axial regulator ;	YAB3	AT4G00180	1.07	0.10	0.70	0.50553266	0.8277	-6.40
252753_at	hypothetical protein	---	AT3G43500	-1.06	-0.08	-0.70	0.50575671	0.8279	-6.40
254392_at	endonuclease, putative ; supporte	ENDO5	AT4G21600	1.06	0.08	0.70	0.50574698	0.8279	-6.40
248520_at	11-beta-hydroxysteroid dehydroge	AtHSD1	AT5G50600	-1.09	-0.12	-0.70	0.5058313	0.8280	-6.40
246808_at	putative protein many predicted pr	---	AT5G27110	-1.06	-0.08	-0.70	0.50591266	0.8280	-6.40
260104_x_at	hypothetical protein predicted by g	---	AT1G35410	1.06	0.09	0.70	0.50592799	0.8280	-6.40
245909_at	putative protein DNA-directed RN	---	AT5G09380	-1.07	-0.10	-0.70	0.50597059	0.8280	-6.40
248214_at	putative protein similar to unknown	---	AT5G53670	1.08	0.12	0.70	0.50604305	0.8281	-6.40
245542_at	CONSTANS like protein	---	AT4G15250	-1.06	-0.08	-0.70	0.50605411	0.8281	-6.40
251599_at	adenylosuccinate synthetase ;sup	ADSS	AT3G57610	1.06	0.09	0.70	0.50610547	0.8281	-6.40
246513_at	hypothetical protein	---	AT5G15680	1.05	0.07	0.70	0.50620789	0.8282	-6.40
249205_at	cycloartenol synthase	MRN1	AT5G42600	-1.10	-0.14	-0.70	0.5062924	0.8282	-6.40
246685_at	putative protein nucleoid DNA-bin	---	AT5G33350	-1.11	-0.15	-0.70	0.50633916	0.8282	-6.40
266360_at	Mutator-like transposase similar to	FRS2	AT2G32250	-1.13	-0.17	-0.70	0.50644559	0.8282	-6.40
252237_at	putative protein lateral suppressor	---	AT3G49950	1.07	0.10	0.70	0.50635983	0.8282	-6.40
261988_at	single-strand nucleic acid-binding	---	AT1G33680	-1.08	-0.11	-0.70	0.50642276	0.8282	-6.40
248772_at	photoreceptor-interacting protein-li	---	AT5G47800	-1.13	-0.17	-0.70	0.50642196	0.8282	-6.40
254779_at	hypothetical protein	---	AT4G12760	1.05	0.07	0.70	0.50649578	0.8282	-6.40
249949_at	SAE1-S9-protein - like SAE1-S9-p	---	AT5G18880	-1.06	-0.08	-0.70	0.50652259	0.8282	-6.40
266069_at	putative RING zinc finger protein	MEE16	AT2G18650	-1.11	-0.14	-0.70	0.50658086	0.8283	-6.40
248816_at	prematurely terminated mRNA dec	LBA1	AT5G47010	-1.05	-0.07	-0.70	0.50677258	0.8283	-6.40
267385_at	unknown protein highly similar to G	---	AT2G44380	-1.10	-0.14	-0.70	0.50667662	0.8283	-6.40
257152_at	Expressed protein ; supported by f	PUX1	AT3G27310	1.05	0.07	0.70	0.50677335	0.8283	-6.40
258465_at	unknown protein	PMEI2	AT3G17220	1.07	0.10	0.70	0.50670633	0.8283	-6.40
256786_at	unknown protein ;supported by ful	---	AT3G13740	-1.07	-0.10	-0.70	0.50685207	0.8284	-6.40
263825_at	putative laccase (diphenol oxidase	LAC5	AT2G40370	1.14	0.19	0.70	0.50687228	0.8284	-6.40
264040_at	putative uridylyl transferase ; supp	ACR5	AT2G03730	-1.04	-0.06	-0.70	0.50696948	0.8285	-6.40
267069_at	unknown protein	ATCAMBP2	AT2G41010	-1.20	-0.27	-0.70	0.50706288	0.8286	-6.40
258154_at	unknown protein ; supported by cl	---	AT3G18210	-1.07	-0.10	-0.70	0.5071167	0.8286	-6.40
260431_at	putative zinc finger protein similar t	---	AT1G68190	1.05	0.06	0.70	0.50844077	0.8288	-6.41
265431_at	(1-4)-beta-mannan endohydrolase	---	AT2G20680	-1.06	-0.08	-0.70	0.50737471	0.8288	-6.41
250457_at	splicing factor-like protein ; suppo	---	AT5G09880	1.06	0.09	0.70	0.50788649	0.8288	-6.41

257504_at	dynein light chain, putative similar	ROPGEF1	AT1G52240	-1.12	-0.16	-0.70	0.5085553	0.8288	-6.41
254803_at	putative protein several hypothetic	---	AT4G13100	-1.09	-0.12	-0.70	0.50816704	0.8288	-6.41
266283_at	putative proline-rich protein	---	AT2G29210	1.06	0.09	0.70	0.50779225	0.8288	-6.41
267094_at	putative diphenol oxidase ; suppo	IRX12	AT2G38080	1.21	0.28	0.70	0.5082156	0.8288	-6.41
256518_at	hypothetical protein	---	AT1G66080	-1.07	-0.10	-0.70	0.50742141	0.8288	-6.41
247534_at	pyrophosphate-dependent phosph	PFK4	AT5G61580	-1.05	-0.07	-0.70	0.50747109	0.8288	-6.41
252537_at	putative transporter protein peptid	---	AT3G45710	-1.06	-0.08	-0.70	0.50829888	0.8288	-6.41
257596_at	unknown protein	---	AT3G24760	1.06	0.09	0.70	0.50847088	0.8288	-6.41
261697_at	hypothetical protein identical to hy	---	AT1G32610	-1.10	-0.14	-0.70	0.50841373	0.8288	-6.41
254062_at	putative protein zinc finger protein	---	AT4G25380	1.22	0.28	0.70	0.50856791	0.8288	-6.41
254285_at	putative cdc2 kinase homolog cdc	---	AT4G22940	1.07	0.10	0.70	0.50770398	0.8288	-6.41
259836_at	unknown protein	ROPGEF1	AT1G52240	-1.05	-0.06	-0.70	0.50742139	0.8288	-6.41
254443_at	putative protein (fragment) BRCA	BRCA1	AT4G21070	1.05	0.07	0.70	0.50756859	0.8288	-6.41
253465_at	putative protein ATAC98, Arabido	---	AT4G32120	-1.07	-0.10	-0.70	0.50812139	0.8288	-6.41
257567_at	hypothetical protein predicted by g	---	AT3G23930	-1.04	-0.06	-0.70	0.50840391	0.8288	-6.41
255015_at	putative protein m6A methyltransf	EMB1691	AT4G09980	-1.09	-0.13	-0.70	0.50749527	0.8288	-6.41
263399_at	unknown protein ; supported by ful	---	AT2G31490	1.06	0.08	0.70	0.50823419	0.8288	-6.41
266660_at	hypothetical protein predicted by g	---	AT2G25920	-1.09	-0.13	-0.70	0.50746029	0.8288	-6.41
258770_at	hypothetical protein	---	AT3G10830	1.05	0.07	0.70	0.50836249	0.8288	-6.41
254211_at	phosphatase like protein phosphop	SGT1A	AT4G23570	1.09	0.13	0.70	0.50845687	0.8288	-6.41
249079_at	putative protein contains similarity	---	AT5G43930	-1.08	-0.11	-0.70	0.50843892	0.8288	-6.41
253597_at	putative protein translation initiatio	---	AT4G30690	1.11	0.15	0.70	0.50832643	0.8288	-6.41
267417_at	putative RING zinc finger protein	---	AT2G34990	-1.05	-0.07	-0.70	0.50791591	0.8288	-6.41
253145_at	hypothetical protein	---	AT4G35560	1.11	0.15	0.70	0.50740727	0.8288	-6.41
265574_at	putative replication protein A1	---	---	-1.05	-0.07	-0.70	0.50857894	0.8288	-6.41
255633_at	Expressed protein ; supported by f	---	AT4G00585	1.06	0.08	0.70	0.50800657	0.8288	-6.41
267478_at	hypothetical protein predicted by g	---	AT2G02700	-1.05	-0.07	-0.70	0.50801292	0.8288	-6.41
257385_at	hypothetical protein predicted by g	---	AT2G01800	-1.06	-0.09	-0.70	0.50783578	0.8288	-6.41
263096_at	class 1 non-symbiotic hemoglobin	AHB1	AT2G16060	1.15	0.21	0.70	0.5085403	0.8288	-6.41
245409_at	putative protein	---	AT4G17200	-1.04	-0.06	-0.70	0.50816771	0.8288	-6.41
264495_at	hypothetical protein predicted by g	RIC2	AT1G27380	-1.05	-0.07	-0.70	0.50842439	0.8288	-6.41
263266_at	hypothetical protein predicted by g	---	AT2G16520	1.05	0.08	0.70	0.50759708	0.8288	-6.41
245571_at	light induced protein like	---	AT4G14695	1.07	0.10	0.70	0.50791783	0.8288	-6.41
248374_at	MADS box transcription factor-like	AGL71	AT5G51870	-1.04	-0.06	-0.70	0.50764426	0.8288	-6.41
267251_at	putative casein kinase II catalytic (	---	AT2G23070	1.05	0.07	0.70	0.50868652	0.8289	-6.41

264454_at	unknown protein similar to U2 sma	---	AT1G10320	1.07	0.09	0.70	0.5088375	0.8290	-6.41
262146_at	membrane protein, putative simila	ATRBL5	AT1G52580	-1.10	-0.14	-0.70	0.50893146	0.8290	-6.41
259228_at	unknown protein similar to hypothe	---	AT3G07720	-1.07	-0.10	-0.70	0.50885747	0.8290	-6.41
255342_at	putative receptor-like protein kinas	---	AT4G04510	-1.07	-0.09	-0.70	0.50881093	0.8290	-6.41
266404_at	hypothetical protein predicted by g	---	AT2G38590	-1.05	-0.07	-0.70	0.50887586	0.8290	-6.41
250930_at	putative protein P58 protein, Bos	ATP58IPK	AT5G03160	-1.13	-0.18	-0.70	0.50894664	0.8290	-6.41
256170_at	receptor protein kinase, putative c	---	AT1G51790	-1.10	-0.14	-0.70	0.50903708	0.8290	-6.41
265070_at	branched-chain alpha-keto acid de	BCDH BET	AT1G55510	1.14	0.19	0.70	0.50904571	0.8290	-6.41
260723_at	unknown protein	---	AT1G48070	-1.05	-0.07	-0.70	0.50913761	0.8291	-6.41
265412_at	putative chloroplast outer membra	TOC132	AT2G16640	-1.05	-0.06	-0.70	0.50927272	0.8291	-6.41
262445_at	Expressed protein ; supported by f	---	AT1G47485	-1.06	-0.08	-0.70	0.50928963	0.8291	-6.41
264518_at	unknown protein	---	AT1G09980	-1.08	-0.11	-0.70	0.50921891	0.8291	-6.41
251974_at	myb protein(MYB27) contains myb	AtMYB27	AT3G53200	-1.05	-0.06	-0.70	0.50924429	0.8291	-6.41
261306_at	regulatory protein HAL3B similar to	---	AT1G48610	1.06	0.08	0.70	0.50937336	0.8292	-6.41
253109_at	putative protein predicted protein	MCA1	AT4G35920	-1.11	-0.15	-0.70	0.51007473	0.8294	-6.41
253343_at	putative protein	---	AT4G33540	1.15	0.21	0.70	0.50972021	0.8294	-6.41
245895_at	SIR2-family protein sirtuin type 4 (	SRT2	AT5G09230	-1.06	-0.08	-0.70	0.50997742	0.8294	-6.41
267362_at	hypothetical protein predicted by g	---	AT2G39910	1.05	0.07	0.70	0.50985278	0.8294	-6.41
267526_at	photosystem II reaction center 6.1	PSBW	AT2G30570	1.04	0.06	0.70	0.50966449	0.8294	-6.41
256254_at	hypothetical protein predicted by g	---	AT3G11290	-1.07	-0.10	-0.70	0.50992575	0.8294	-6.41
256588_at	unknown protein	---	AT3G28790	-1.07	-0.09	-0.70	0.51008445	0.8294	-6.41
254090_at	MtN3 - like protein MtN3 (induced	---	AT4G25010	-1.07	-0.10	-0.70	0.50996783	0.8294	-6.41
263451_at	putative triacylglycerol lipase	---	AT2G31690	-1.04	-0.06	-0.70	0.50953094	0.8294	-6.41
247887_at	unknown protein	---	AT5G57880	1.05	0.07	0.70	0.51011161	0.8294	-6.41
245313_at	UFD1 like protein ; supported by fu	---	AT4G15420	-1.07	-0.09	-0.70	0.50970112	0.8294	-6.41
252288_at	hypothetical protein	---	AT3G49080	-1.08	-0.11	-0.70	0.51006827	0.8294	-6.41
266432_s_at	putative gag-protease polyprotein	---	---	1.05	0.07	0.70	0.51001718	0.8294	-6.41
267243_at	hypothetical protein predicted by g	---	AT2G02660	1.05	0.06	0.70	0.50967444	0.8294	-6.41
245379_at	heat shock transcription factor HSF	HSF1	AT4G17750	1.07	0.10	0.70	0.51004601	0.8294	-6.41
260183_at	hypothetical protein similar to DNA	---	---	-1.04	-0.06	-0.70	0.51008319	0.8294	-6.41
252809_at	putative protein various predicted	---	---	-1.05	-0.07	-0.70	0.50962099	0.8294	-6.41
256331_at	GT-like trihelix DNA-binding prote	---	AT1G76880	-1.05	-0.08	-0.70	0.51027924	0.8296	-6.41
251178_at	cytokinin oxidase -like protein cyto	CKX6	AT3G63440	-1.13	-0.18	-0.69	0.51040397	0.8297	-6.41
245101_at	putative cytochrome P450 ; suppo	CYP98A3	AT2G40890	-1.09	-0.12	-0.69	0.51039858	0.8297	-6.41
266786_at	putative non-LTR retroelement rev	---	---	1.05	0.07	0.69	0.51042101	0.8297	-6.41

249338_at	putative protein similar to unknown	anac095	AT5G41090	-1.04	-0.06	-0.69	0.51048622	0.8297	-6.41
259620_s_at	Tam3-like transposon protein simi	---	---	-1.08	-0.12	-0.69	0.51052761	0.8297	-6.41
248989_at	disease resistance protein RPS4	---	AT5G45200	-1.07	-0.09	-0.69	0.51057144	0.8297	-6.41
258838_at	unknown protein ; supported by cl	---	AT3G07140	1.05	0.07	0.69	0.5106241	0.8298	-6.41
245388_at	hypothetical protein ;supported by	---	AT4G16410	1.05	0.07	0.69	0.51069279	0.8298	-6.41
251845_at	Expressed protein ; supported by f	ATGCN4	AT3G54540	1.08	0.11	0.69	0.51087071	0.8298	-6.41
265287_at	putative photosystem I reaction ce	PSAE-2	AT2G20260	1.04	0.06	0.69	0.51089289	0.8298	-6.41
251193_at	translation releasing factor RF-1 -	APG3	AT3G62910	1.09	0.12	0.69	0.51091847	0.8298	-6.41
245231_at	hypothetical protein	---	AT4G25600	-1.07	-0.09	-0.69	0.51083612	0.8298	-6.41
260670_at	Expressed protein ; supported by f	NFD5	AT1G19520	-1.09	-0.13	-0.69	0.51080895	0.8298	-6.41
247076_at	ferripyochelin-binding protein-like	GAMMA CA	AT5G66510	-1.05	-0.08	-0.69	0.51074875	0.8298	-6.41
252884_at	SEC14 - like protein phosphatidyli	---	AT4G39170	-1.07	-0.09	-0.69	0.5110905	0.8299	-6.41
245661_at	purine permease, putative similar	ATPUP3	AT1G28220	-1.06	-0.09	-0.69	0.51107206	0.8299	-6.41
255975_at	hypothetical protein	---	---	-1.07	-0.10	-0.69	0.51108815	0.8299	-6.41
258850_at	putative cellulose synthase catalyti	CSLD3	AT3G03050	-1.06	-0.08	-0.69	0.51125371	0.8300	-6.41
258733_at	unknown protein	---	---	1.05	0.07	0.69	0.51125594	0.8300	-6.41
246022_at	putative protein predicted protein -	---	AT5G21110	1.05	0.08	0.69	0.51120324	0.8300	-6.41
261343_s_at	putative protein hypothetical protei	---	---	-1.05	-0.07	-0.69	0.51131412	0.8301	-6.41
267537_at	putative guanylate kinase ; suppo	GK-1	AT2G41880	1.18	0.24	0.69	0.51140361	0.8301	-6.41
251216_at	putative protein hypothetical prote	---	---	-1.05	-0.07	-0.69	0.51147161	0.8302	-6.41
254290_at	hypothetical protein	---	AT4G23000	-1.08	-0.12	-0.69	0.51157486	0.8303	-6.41
250639_at	oleosin-like protein oleosin - Brass	GRP20	AT5G07560	-1.07	-0.09	-0.69	0.51162802	0.8303	-6.41
258212_at	unknown protein contains Pfam pr	---	AT3G17920	1.04	0.06	0.69	0.51171202	0.8304	-6.41
257422_at	hypothetical protein Contains simil	---	AT1G11940	-1.05	-0.07	-0.69	0.51173093	0.8304	-6.41
259494_at	mitotic checkpoint protein, putative	---	AT1G15850	-1.07	-0.10	-0.69	0.51176813	0.8304	-6.41
257708_at	hypothetical protein predicted by g	---	AT3G13330	-1.06	-0.08	-0.69	0.51185507	0.8304	-6.41
255105_at	putative sulfate transporter ; supp	SULTR1;1	AT4G08620	1.06	0.09	0.69	0.51187054	0.8304	-6.41
254571_at	hypothetical protein	---	AT4G19370	-1.24	-0.31	-0.69	0.51228275	0.8306	-6.41
253757_at	rac GTP binding protein Arac7 ; su	ROP9	AT4G28950	-1.07	-0.09	-0.69	0.51220755	0.8306	-6.41
257426_at	hypothetical protein contains simila	---	AT1G54850	1.07	0.10	0.69	0.51208651	0.8306	-6.41
255805_at	zinc-finger - like protein zinc-finge	---	AT4G10240	-1.06	-0.08	-0.69	0.51230307	0.8306	-6.41
264841_at	putative protein kinase similar to (	---	AT1G03740	-1.13	-0.18	-0.69	0.51214458	0.8306	-6.41
244905_at	hypothetical protein	---	---	-1.06	-0.08	-0.69	0.51209329	0.8306	-6.41
256956_at	expressed protein supported by cl	---	AT3G13410	1.05	0.07	0.69	0.51228199	0.8306	-6.41
265299_at	putative retroelement pol polyprote	---	---	-1.08	-0.12	-0.69	0.51228052	0.8306	-6.41

253416_at	pyruvate decarboxylase-1 (Pdc1)	---	AT4G33070	-1.08	-0.11	-0.69	0.5120951	0.8306	-6.41
256952_at	mannosidase, putative similar to r	---	AT3G21160	1.07	0.10	0.69	0.51238309	0.8306	-6.41
257397_at	hypothetical protein predicted by g	RIC6	AT2G20430	1.08	0.11	0.69	0.51240948	0.8306	-6.41
261265_at	hypothetical protein predicted by g	---	AT1G26800	-1.10	-0.14	-0.69	0.5124746	0.8307	-6.41
AFFX-r2-Bs-da	B. subtilis /GEN=dapB, jojF /DB_X	---	---	-1.11	-0.15	-0.69	0.51249515	0.8307	-6.41
256232_at	unknown protein ; supported by ful	FYD	AT3G12570	1.04	0.06	0.69	0.51280207	0.8311	-6.41
251671_at	putative protein hypothetical prote	---	AT3G57210	-1.06	-0.08	-0.69	0.5128416	0.8311	-6.41
248406_at	pectinesterase	---	AT5G51490	-1.08	-0.11	-0.69	0.51302514	0.8314	-6.41
247503_at	GCN4-complementing protein - lik	AGD1	AT5G61980	-1.07	-0.09	-0.69	0.51306161	0.8314	-6.41
255730_at	dihydroflavonol 4-reductase, putat	---	AT1G25460	-1.05	-0.08	-0.69	0.51316051	0.8314	-6.41
248201_at	putative protein similar to unknown	PTAC15	AT5G54180	-1.12	-0.17	-0.69	0.51314286	0.8314	-6.41
261750_at	hypothetical protein contains simila	---	AT1G76120	1.07	0.10	0.69	0.51320932	0.8314	-6.41
258036_at	unknown protein	---	AT3G21210	1.05	0.07	0.69	0.51336698	0.8316	-6.41
261741_at	transcription factor, putative simila	ATE2F2	AT1G47870	1.06	0.08	0.69	0.5133806	0.8316	-6.41
262385_at	root hair defective, putative similar	---	AT1G72960	-1.05	-0.06	-0.69	0.51345841	0.8316	-6.41
247792_at	Expressed protein ; supported by f	---	AT5G58787	-1.10	-0.13	-0.69	0.51352622	0.8316	-6.41
250230_at	putative protein similar to unknown	---	AT5G13900	-1.10	-0.13	-0.69	0.51347954	0.8316	-6.41
258843_at	putative protein kinase similar to hy	---	AT3G04690	1.05	0.07	0.69	0.51353821	0.8316	-6.41
259070_at	digalactosyldiacylglycerol synthase	DGD1	AT3G11670	-1.12	-0.16	-0.69	0.5136115	0.8317	-6.41
253826_s_at	E2, ubiquitin-conjugating enzyme	UBC9	AT4G27960 /	1.05	0.06	0.69	0.51389948	0.8320	-6.41
252592_at	mitogen-activated protein kinase 3	NAXT1	AT3G45640 /	1.17	0.22	0.69	0.51397184	0.8320	-6.41
264226_at	hypothetical protein similar to puta	---	AT1G67510	-1.06	-0.08	-0.69	0.51400201	0.8320	-6.41
250683_x_at	putative protein similar to unknown	---	AT5G06640	-1.09	-0.12	-0.69	0.51406641	0.8320	-6.41
246405_at	disease resistance protein RPP1-\	---	AT1G57630	1.33	0.41	0.69	0.51407205	0.8320	-6.41
245375_at	NAK like protein kinase	---	AT4G17660	-1.06	-0.09	-0.69	0.51400179	0.8320	-6.41
264094_at	unknown protein ;supported by full	---	AT1G79200	-1.06	-0.09	-0.69	0.51413592	0.8321	-6.41
253958_at	putative protein RING zinc finger p	---	AT4G26400	1.06	0.09	0.69	0.51436912	0.8323	-6.41
251484_at	putative protein putative protein A	---	AT3G59640	1.05	0.07	0.69	0.51436541	0.8323	-6.41
265972_at	putative retroelement pol polyprote	---	---	-1.05	-0.06	-0.69	0.51438686	0.8323	-6.41
245617_at	hypothetical protein	---	AT4G14490	-1.05	-0.07	-0.69	0.51429645	0.8323	-6.41
259054_at	putative hypersensitivity-related ge	CHAT	AT3G03480	-1.35	-0.43	-0.69	0.51472642	0.8325	-6.41
255373_s_at	putative protein	---	---	-1.06	-0.09	-0.69	0.51466559	0.8325	-6.41
246675_at	putative protein	---	AT5G30420	-1.06	-0.08	-0.69	0.51471495	0.8325	-6.41
264251_at	hypothetical protein identical to GE	---	AT1G09190	1.08	0.11	0.69	0.51468405	0.8325	-6.41
255927_at	transcriptional activator CBF1, put	---	AT1G12630	-1.10	-0.14	-0.69	0.51470242	0.8325	-6.41

262814_at	putative heat-shock protein strong	---	AT1G11660	1.05	0.07	0.69	0.51477387	0.8325	-6.41
250914_at	myb -like protein telomeric DNA b	TRFL10	AT5G03780	-1.06	-0.09	-0.69	0.51493948	0.8327	-6.41
248053_at	putative protein similar to unknown	AtNMNAT	AT5G55810	-1.06	-0.09	-0.69	0.51492953	0.8327	-6.41
267366_at	unknown protein ;supported by ful	---	AT2G44310	1.06	0.08	0.69	0.51501473	0.8327	-6.41
247683_at	serine/threonine-specific protein k	---	AT5G59660	-1.07	-0.09	-0.69	0.5149913	0.8327	-6.41
249649_at	putative transporter protein Na+ H	CHX24	AT5G37060	-1.04	-0.06	-0.69	0.51524076	0.8330	-6.41
261725_at	small nuclear ribonucleoprotein, p	SmD3	AT1G76300	1.08	0.11	0.69	0.51536714	0.8331	-6.42
254621_at	gene 11-1 protein - like gene 11-1	WAVE5	AT4G18600	-1.05	-0.08	-0.69	0.51553715	0.8333	-6.42
249812_at	putative protein similar to unknown	---	AT5G23830	-1.08	-0.11	-0.69	0.51550597	0.8333	-6.42
263185_at	transport protein, putative similar t	---	AT1G05520	1.05	0.07	0.69	0.51560211	0.8333	-6.42
249763_at	receptor-protein kinase-like protein	---	AT5G24010	-1.10	-0.13	-0.69	0.51561316	0.8333	-6.42
255214_at	hypothetical protein	---	---	1.05	0.07	0.69	0.51565979	0.8333	-6.42
266195_at	putative RING zinc finger protein	---	AT2G39100	1.05	0.07	0.69	0.51578386	0.8335	-6.42
261570_at	fatty acid elongase 3-ketoacyl-CoA	KCS1	AT1G01120	-1.28	-0.36	-0.69	0.51603321	0.8335	-6.42
246453_at	syntaxin homologue ;supported by	SYP21	AT5G16830	-1.06	-0.09	-0.69	0.51598623	0.8335	-6.42
255061_at	putative protein disulfide isomerase	ATAPRL6	AT4G08930	-1.05	-0.07	-0.69	0.51607878	0.8335	-6.42
260830_at	histone H1, putative similar to hist	---	AT1G06760	1.10	0.14	0.69	0.51597937	0.8335	-6.42
256765_at	aminotransferase, putative similar	POP2	AT3G22200	-1.07	-0.10	-0.69	0.51606786	0.8335	-6.42
262587_at	unknown protein Contains PF|005	---	AT1G15490	1.10	0.14	0.69	0.51604651	0.8335	-6.42
260207_at	putative phosphoglucomutase simi	---	AT1G70730	1.08	0.11	0.69	0.51599364	0.8335	-6.42
253893_at	putative protein hypothetical prote	---	AT4G27390	-1.08	-0.11	-0.69	0.51595887	0.8335	-6.42
251088_at	putative protein several hypothetic	---	AT5G01480	-1.09	-0.12	-0.69	0.51615462	0.8335	-6.42
248189_at	DNA mismatch repair protein MutS	---	AT5G54090	1.07	0.10	0.68	0.51633156	0.8336	-6.42
259560_at	hypothetical protein	WAK2	AT1G21270	-1.19	-0.25	-0.68	0.5162816	0.8336	-6.42
257808_at	unknown protein, putative contain	---	AT3G26935	1.06	0.08	0.68	0.51633374	0.8336	-6.42
253690_at	putative protein various predicted	---	AT4G29550	-1.08	-0.11	-0.68	0.51639102	0.8337	-6.42
249515_at	tryptophan synthase beta chain	---	AT5G38530	1.21	0.27	0.68	0.5164928	0.8337	-6.42
253825_at	Expressed protein ; supported by f	---	AT4G28025	-1.08	-0.11	-0.68	0.51654403	0.8337	-6.42
247690_at	putative protein	MBD7	AT5G59800	1.11	0.15	0.68	0.5165701	0.8337	-6.42
258782_at	putative dihydroneopterin aldolase	---	AT3G11750	1.08	0.11	0.68	0.51656246	0.8337	-6.42
248527_at	putative protein contains similarity	---	AT5G50740	1.06	0.08	0.68	0.5167798	0.8338	-6.42
253667_at	peroxidase ATP8a ;supported by f	---	AT4G30170	1.05	0.07	0.68	0.51682324	0.8338	-6.42
254982_at	putative protein ; supported by cD	---	AT4G10470	1.07	0.09	0.68	0.5168106	0.8338	-6.42
245065_at	unknown protein ; supported by cI	---	AT2G39750	1.05	0.07	0.68	0.51668149	0.8338	-6.42
263263_at	putative guanylate binding protein	---	AT2G38840	1.07	0.10	0.68	0.51676212	0.8338	-6.42

255209_at	see GB:AF077408	---	---	-1.06	-0.09	-0.68	0.51693475	0.8339	-6.42
249435_at	putative protein tail-specific thyroi	---	AT5G39970	-1.04	-0.06	-0.68	0.5169035	0.8339	-6.42
245735_at	myb-like transcription factor, putat	MYB54	AT1G73410	1.04	0.06	0.68	0.51705365	0.8339	-6.42
247804_at	strong similarity to unknown protei	SVL5	AT5G58170	-1.06	-0.08	-0.68	0.5170633	0.8339	-6.42
262720_s_at	hypothetical protein similar to hypo	---	AT1G43600 /	1.05	0.07	0.68	0.51707402	0.8339	-6.42
262486_at	putative bzip-like transcription fact	---	AT1G21740	-1.08	-0.12	-0.68	0.51717551	0.8340	-6.42
252020_at	SKP1/ASK1 (At6), putative similar	ASK6	AT3G53060	1.04	0.06	0.68	0.51714097	0.8340	-6.42
259220_at	expressed protein predicted by ge	---	AT3G03550	-1.07	-0.09	-0.68	0.51727297	0.8341	-6.42
254661_at	unknown protein multidrug resista	---	AT4G18260	1.06	0.09	0.68	0.51732623	0.8341	-6.42
252216_at	putative protein several hypothetic	---	AT3G50420	1.07	0.10	0.68	0.51744407	0.8342	-6.42
258257_at	putative short chain alcohol dehydr	---	AT3G26770	-1.05	-0.07	-0.68	0.51741046	0.8342	-6.42
266658_at	Expressed protein ; supported by f	---	AT2G25735	1.32	0.40	0.68	0.51754116	0.8343	-6.42
254085_at	abscisic acid-induced - like protein	HVA22D	AT4G24960	-1.12	-0.17	-0.68	0.51800686	0.8344	-6.42
265087_at	hypothetical protein predicted by g	---	AT1G03760	1.10	0.14	0.68	0.51766883	0.8344	-6.42
257151_at	blue copper protein, putative simil	---	AT3G27200	1.07	0.10	0.68	0.51800539	0.8344	-6.42
255780_at	hypothetical protein contains Pfam	GAUT11	AT1G18580	1.07	0.09	0.68	0.51770056	0.8344	-6.42
261512_at	actin capping protein beta-2, putat	---	AT1G71790	1.09	0.12	0.68	0.5179942	0.8344	-6.42
245089_at	putative transketolase precursor ;	---	AT2G45290	-1.29	-0.37	-0.68	0.51788466	0.8344	-6.42
248260_at	putative protein similar to unknown	---	AT5G53240	-1.05	-0.07	-0.68	0.5177332	0.8344	-6.42
266527_at	hypothetical protein predicted by g	---	---	1.07	0.10	0.68	0.51780505	0.8344	-6.42
250594_at	putative protein contains similarity	---	AT5G07760	-1.06	-0.08	-0.68	0.51789055	0.8344	-6.42
249973_at	GPAA1 - like protein glycosylphos	---	AT5G19130	1.06	0.09	0.68	0.51799001	0.8344	-6.42
261640_at	permease, putative similar to pern	---	AT1G49960	1.06	0.09	0.68	0.51783291	0.8344	-6.42
256175_at	unknown protein	---	AT1G51670	1.05	0.07	0.68	0.51807755	0.8344	-6.42
265066_at	unknown protein location of ESTs	FLA9	AT1G03870	-1.10	-0.13	-0.68	0.51814807	0.8344	-6.42
246229_at	pectinesterase like protein	sks15	AT4G37160	1.05	0.07	0.68	0.51815339	0.8344	-6.42
246483_at	receptor protein kinase-like protein	NIK1	AT5G16000	1.14	0.18	0.68	0.51832927	0.8346	-6.42
266233_at	putative phloem-specific lectin	AtPP2-B8	AT2G02340	-1.05	-0.07	-0.68	0.51833624	0.8346	-6.42
247721_at	elongin - like protein elongin C, Dr	---	AT5G59140	-1.04	-0.06	-0.68	0.51838824	0.8346	-6.42
261538_at	unknown protein ; supported by cD	---	AT1G01830	1.12	0.16	0.68	0.51841517	0.8346	-6.42
263612_at	putative CDC21 protein	MCM4	AT2G16440	1.20	0.26	0.68	0.51874259	0.8351	-6.42
250812_at	putative protein similar to unknown	---	AT5G04900	1.05	0.07	0.68	0.51892815	0.8352	-6.42
264333_at	hypothetical protein similar to puta	AtTLP4	AT1G61940	-1.05	-0.07	-0.68	0.51899249	0.8352	-6.42
253860_at	hypothetical protein ;supported by	---	AT4G27700	-1.05	-0.07	-0.68	0.51884659	0.8352	-6.42
265741_at	putative membrane transporter ; s	---	AT2G01320	1.11	0.15	0.68	0.51904462	0.8352	-6.42

265870_at	hypothetical protein predicted by g	PDLP6	AT2G01660	-1.05	-0.07	-0.68	0.51897414	0.8352	-6.42
260657_at	wall-associated kinase 2, putative	---	AT1G19390	1.06	0.09	0.68	0.51904464	0.8352	-6.42
245615_at	reverse transcriptase like protein	---	---	1.05	0.07	0.68	0.51891409	0.8352	-6.42
244936_at	NADH dehydrogenase ND1	---	---	-1.05	-0.08	-0.68	0.51910169	0.8352	-6.42
250261_at	peptide transporter - like protein p	---	AT5G13400	-1.12	-0.17	-0.68	0.51915267	0.8352	-6.42
260988_at	MAP3K alpha protein kinase, puta	MAP3KA	AT1G53570	-1.09	-0.12	-0.68	0.51925939	0.8353	-6.42
250573_at	putative protein	---	AT5G08220	-1.07	-0.09	-0.68	0.51928721	0.8353	-6.42
250467_at	trehalose-6-phosphate phosphata	---	AT5G10100	1.05	0.08	0.68	0.51933767	0.8353	-6.42
261473_at	hypothetical protein similar to puta	---	AT1G14490	-1.10	-0.14	-0.68	0.51945625	0.8355	-6.42
250009_at	putative protein nuclear FMRP int	---	AT5G18440	1.12	0.17	0.68	0.51958644	0.8356	-6.42
248558_at	permease	---	AT5G49990	1.09	0.13	0.68	0.51964243	0.8356	-6.42
249994_at	putative protein cell polarity protei	---	AT5G18590	1.06	0.08	0.68	0.51993617	0.8356	-6.42
251690_at	putative protein TATA-binding pro	---	AT3G56510	-1.06	-0.08	-0.68	0.51988744	0.8356	-6.42
245301_at	farnesyl-pyrophosphate synthetase	FPS2	AT4G17190	1.12	0.16	0.68	0.51996535	0.8356	-6.42
266720_s_at	hypothetical protein predicted by g	APRR9	AT2G46670	1.11	0.15	0.68	0.51988332	0.8356	-6.42
250360_at	putative protein probable serine/th	---	AT5G11360	1.05	0.08	0.68	0.51989511	0.8356	-6.42
246470_at	putative protein predicted proteins	---	AT5G17080	-1.05	-0.07	-0.68	0.519797	0.8356	-6.42
255744_at	hypothetical protein predicted by g	---	---	1.04	0.06	0.68	0.51971011	0.8356	-6.42
260604_at	polyphosphoinositide binding prot	---	AT1G55840	-1.08	-0.11	-0.68	0.51966632	0.8356	-6.42
265138_at	hypothetical protein predicted by g	---	AT1G51300	1.08	0.11	0.68	0.51977647	0.8356	-6.42
252521_at	hypothetical protein	---	AT3G46380	-1.09	-0.12	-0.68	0.51968484	0.8356	-6.42
248974_at	disease resistance protein-like	---	AT5G45060	-1.05	-0.07	-0.68	0.52000318	0.8356	-6.42
263793_at	putative glucosyltransferase	ATCSLC08	AT2G24630	1.12	0.16	0.68	0.52008603	0.8357	-6.42
266631_at	putative serpin	---	AT2G35570	-1.04	-0.06	-0.68	0.52020163	0.8358	-6.42
263789_at	putative GDSL-motif lipase/hydrola	---	AT2G24560	1.08	0.11	0.68	0.52035124	0.8360	-6.42
246350_at	hypothetical protein predicted by g	---	AT1G16650	-1.07	-0.09	-0.68	0.52045284	0.8361	-6.42
246514_at	DNA-directed RNA polymerase (m	---	AT5G15700	-1.09	-0.12	-0.68	0.52062126	0.8363	-6.42
264845_at	putative thioredoxin-m similar to th	ATHM1	AT1G03680	1.06	0.08	0.68	0.52083321	0.8364	-6.42
254882_s_at	putative protein various predicted	---	---	-1.05	-0.07	-0.68	0.52086699	0.8364	-6.42
259742_at	putative proline-rich APG protein s	GLIP6	AT1G71120	-1.08	-0.12	-0.68	0.52083359	0.8364	-6.42
260473_at	hypothetical protein predicted by g	---	AT1G10880	1.06	0.08	0.68	0.5207239	0.8364	-6.42
262821_at	unknown protein EST gb|F14156 c	---	AT1G11800	1.04	0.06	0.68	0.52077755	0.8364	-6.42
266373_x_at	putative retroelement pol polyprote	---	---	-1.06	-0.09	-0.68	0.52108937	0.8367	-6.42
258608_at	unknown protein ;supported by ful	---	AT3G03020	1.11	0.15	0.68	0.52113893	0.8367	-6.42
251635_at	endo-polygalacturonase	ADPG1	AT3G57510	-1.07	-0.10	-0.68	0.52118316	0.8367	-6.42

245352_at	indole-3-acetate beta-glucosyltrans	UGT84A3	AT4G15490	-1.10	-0.14	-0.68	0.52133074	0.8369	-6.42
246115_at	putative protein chloroplast outer e	---	AT5G20300	1.06	0.09	0.68	0.52150469	0.8370	-6.42
265041_at	unknown protein Contains similarit	TOM22-I	AT1G04070	1.09	0.13	0.68	0.52144441	0.8370	-6.42
255787_at	putative cinnamoyl-CoA reductase	---	AT2G33590	-1.08	-0.11	-0.68	0.52147365	0.8370	-6.42
255991_at	unknown protein	---	AT1G29820	1.10	0.13	0.68	0.52158367	0.8371	-6.42
254855_s_at	putative protein other predicted pr	---	AT4G12140 /	1.07	0.09	0.68	0.5216169	0.8371	-6.42
250217_at	nodulin-like protein	---	AT5G14120	1.08	0.11	0.68	0.5219501	0.8371	-6.42
256281_at	myb-family transcription factor, pu	TRFL9	AT3G12560	-1.07	-0.10	-0.68	0.52184223	0.8371	-6.42
261296_at	unknown protein	---	AT1G48460	1.11	0.15	0.68	0.52198004	0.8371	-6.42
262395_at	hypothetical protein similar to hypo	---	AT1G49540	1.11	0.15	0.68	0.52195502	0.8371	-6.42
258447_at	hypothetical protein predicted by g	---	AT3G22450	1.05	0.07	0.68	0.52188136	0.8371	-6.42
258145_at	integral membrane protein, putativ	---	AT3G18200	-1.07	-0.09	-0.68	0.52183632	0.8371	-6.42
263865_at	putative ABC transporter related to	ABCB1	AT2G36910	1.08	0.11	0.68	0.52184481	0.8371	-6.42
245328_at	Expressed protein ; supported by f	---	AT4G14465	1.05	0.08	0.68	0.52187173	0.8371	-6.42
252638_at	acyl CoA reductase - protein acyl	FAR4	AT3G44540	1.06	0.09	0.68	0.52178124	0.8371	-6.42
251387_at	putative protein	---	AT3G60810	-1.09	-0.13	-0.67	0.52265757	0.8372	-6.42
263182_at	Expressed protein ; supported by f	---	AT1G05575	1.41	0.50	0.67	0.5226672	0.8372	-6.42
254761_at	Expressed protein ; supported by f	CLE44	AT4G13195	-1.08	-0.11	-0.67	0.52268453	0.8372	-6.42
266087_at	putative alcohol dehydrogenase	---	AT2G37790	-1.07	-0.09	-0.67	0.52256382	0.8372	-6.42
251295_at	putative protein several O-methyltr	---	AT3G62000	-1.08	-0.10	-0.67	0.52225782	0.8372	-6.42
264797_at	unknown protein similar to ESTs g	---	AT1G08710	1.06	0.08	0.67	0.52234618	0.8372	-6.42
247223_at	MADS box transcription factor-like	MAF4	AT5G65070	-1.04	-0.06	-0.67	0.52267976	0.8372	-6.42
248561_at	unknown protein	---	AT5G49680	-1.08	-0.11	-0.67	0.52247129	0.8372	-6.42
261522_at	RIBOSOMAL PROTEIN, putative	---	AT1G71710	-1.12	-0.16	-0.67	0.5224064	0.8372	-6.42
259952_at	putative disease resistance protein	AtRLP12	AT1G71400	-1.11	-0.15	-0.67	0.522478	0.8372	-6.42
255357_at	putative pectinesterase	---	AT4G03930	-1.05	-0.07	-0.67	0.52242018	0.8372	-6.42
250652_at	putative protein similar to unknown	FLA21	AT5G06920	-1.05	-0.08	-0.67	0.5222119	0.8372	-6.42
259865_at	putative casein kinase I similar to c	CKL2	AT1G72710	-1.07	-0.10	-0.67	0.52268392	0.8372	-6.42
245810_at	axi 1 protein, putative similar to ax	---	AT1G38065 /	1.06	0.08	0.67	0.52264819	0.8372	-6.42
260090_at	putative serine carboxypeptidase s	scpl4	AT1G73310	1.04	0.06	0.67	0.52241138	0.8372	-6.42
252585_s_at	putative protein UbcH 7-binding pr	---	AT3G45570 /	1.04	0.06	0.67	0.52270154	0.8372	-6.42
260611_at	putative beta-1,3-glucanase, C ter	---	AT2G43670	-1.07	-0.09	-0.67	0.5225943	0.8372	-6.42
252461_at	putative protein predicted protein,	---	---	1.06	0.09	0.67	0.52257556	0.8372	-6.42
266762_at	putative alcohol dehydrogenase	---	AT2G47120	1.05	0.07	0.67	0.52274773	0.8372	-6.42
250883_at	putative protein predicted proteins	---	AT5G03970	1.07	0.10	0.67	0.52281302	0.8373	-6.42

252476_at	glucosyltransferase-like protein UI	---	AT3G46650	-1.07	-0.10	-0.67	0.52298271	0.8375	-6.42
265707_at	unknown protein	---	AT2G03390	1.07	0.09	0.67	0.52310602	0.8376	-6.42
249668_at	putative protein similar to unknown	---	AT5G35870	1.07	0.09	0.67	0.52313535	0.8376	-6.42
265300_at	unknown protein contains weak PH	---	AT2G13950	-1.07	-0.09	-0.67	0.52322965	0.8377	-6.42
257531_at	putative RNA-binding protein cont	---	AT3G07250	1.05	0.07	0.67	0.52327142	0.8377	-6.42
253141_at	putative protein hypothetical prote	---	AT4G35430 /	1.06	0.09	0.67	0.5233782	0.8378	-6.42
247535_at	transcriptional activator - like prote	---	AT5G61620	1.08	0.11	0.67	0.52339187	0.8378	-6.42
266845_at	unknown protein	---	AT2G26110	1.09	0.13	0.67	0.52363843	0.8379	-6.42
253612_at	putative protein D-ribulokinase - K	---	AT4G30310	1.05	0.07	0.67	0.52362994	0.8379	-6.42
259750_at	hypothetical protein predicted by g	---	AT1G71130	1.09	0.12	0.67	0.52393329	0.8379	-6.43
260654_at	hypothetical protein predicted by g	---	AT1G19290	-1.07	-0.10	-0.67	0.5242515	0.8379	-6.43
245401_at	hypothetical protein ;supported by	---	AT4G17670	1.15	0.20	0.67	0.52362951	0.8379	-6.42
252352_at	Expressed protein ; supported by f	---	AT3G48185	1.07	0.10	0.67	0.52349678	0.8379	-6.42
253045_at	Expressed protein ; supported by f	---	AT4G37445	1.09	0.13	0.67	0.52412435	0.8379	-6.43
247437_at	AtHVA22b-like protein ; supported	HVA22B	AT5G62490	-1.07	-0.09	-0.67	0.52422573	0.8379	-6.43
253706_at	putative protein D-threonine dehy	---	AT4G29120	1.05	0.07	0.67	0.5242405	0.8379	-6.43
250655_at	transcription factor HBP-1b (gb|AA	OBF5	AT5G06960	1.05	0.07	0.67	0.52441033	0.8379	-6.43
258628_at	unknown protein	---	AT3G02890	1.11	0.15	0.67	0.52386752	0.8379	-6.43
264296_at	protein transport protein sec61 alp	---	AT1G78720	-1.09	-0.12	-0.67	0.52377393	0.8379	-6.43
265262_at	putative chloroplast nucleoid DNA	---	AT2G42980	-1.07	-0.10	-0.67	0.52431809	0.8379	-6.43
249754_at	flavanone 3-hydroxylase-like prote	DMR6	AT5G24530	1.29	0.37	0.67	0.52396813	0.8379	-6.43
264030_at	putative steroid sulfotransferase	---	AT2G03770	1.07	0.10	0.67	0.52433699	0.8379	-6.43
255200_at	hypothetical protein	---	---	-1.06	-0.08	-0.67	0.52435729	0.8379	-6.43
265376_at	hypothetical protein predicted by g	---	AT2G05810	1.06	0.08	0.67	0.52415465	0.8379	-6.43
262019_s_at	hypothetical protein predicted by g	---	---	1.05	0.08	0.67	0.52442771	0.8379	-6.43
263653_at	putative ethylene receptor (ERS2)	ERS2	AT1G04310	1.07	0.10	0.67	0.52389807	0.8379	-6.43
246123_at	beta-1,3-glucanase-like protein be	---	AT5G20390	1.04	0.06	0.67	0.52430042	0.8379	-6.43
251692_s_at	serine carboxypeptidase-like prote	---	AT3G52020 /	-1.05	-0.07	-0.67	0.5243855	0.8379	-6.43
253680_at	cytidine deaminase 2 (CDA2)	---	AT4G29620	1.05	0.07	0.67	0.52415354	0.8379	-6.43
249103_at	N-carbamyl-L-amino acid amidohy	UAH	AT5G43600	-1.06	-0.08	-0.67	0.52439547	0.8379	-6.43
257278_at	hypothetical protein predicted by g	---	AT3G14480	1.08	0.10	0.67	0.52398666	0.8379	-6.43
252733_at	putative protein INDOLE-3-ACETI	---	AT3G43120	-1.05	-0.08	-0.67	0.5238691	0.8379	-6.43
252582_at	putative protein several hypothetic	---	AT3G45530	1.05	0.08	0.67	0.52378341	0.8379	-6.43
250628_at	hypothetical protein	---	AT5G07380	1.07	0.10	0.67	0.52359652	0.8379	-6.42
264806_at	hypothetical protein predicted by g	---	AT1G08610	1.11	0.15	0.67	0.52455542	0.8380	-6.43

256635_at	hypothetical protein predicted by g	---	AT3G28260	1.04	0.06	0.67	0.52460489	0.8380	-6.43
251259_at	putative protein phosphoprotein p	---	AT3G62260	-1.09	-0.13	-0.67	0.52490893	0.8382	-6.43
252737_at	putative protein KIAA0274 protein	---	AT3G43220	1.05	0.07	0.67	0.52516955	0.8382	-6.43
250193_at	putative protein proline-rich protei	---	AT5G14540	1.06	0.08	0.67	0.52520864	0.8382	-6.43
259160_at	unknown protein	---	AT3G05410	1.06	0.09	0.67	0.52507949	0.8382	-6.43
250359_at	putative protein predicted proteins	---	AT5G11350	1.05	0.07	0.67	0.52516986	0.8382	-6.43
252775_s_at	putative protein various predicted	---	---	1.05	0.07	0.67	0.5249459	0.8382	-6.43
260469_at	BRCA1-associated RING domain	AGD4	AT1G10870	1.07	0.10	0.67	0.52490366	0.8382	-6.43
252800_at	putative protein	---	---	-1.05	-0.07	-0.67	0.52499843	0.8382	-6.43
266502_at	hypothetical protein predicted by g	---	AT2G47720	-1.05	-0.07	-0.67	0.52521566	0.8382	-6.43
262194_at	hypothetical protein similar to puta	---	AT1G77930	-1.09	-0.12	-0.67	0.52506226	0.8382	-6.43
261215_at	subtilase, putative similar to subtil	---	AT1G32970	-1.05	-0.07	-0.67	0.52496896	0.8382	-6.43
249185_at	CHP-rich zinc finger protein-like	---	AT5G43030	1.06	0.08	0.67	0.52486815	0.8382	-6.43
254071_at	hypothetical protein	---	AT4G25510	1.05	0.07	0.67	0.52498449	0.8382	-6.43
265430_at	hypothetical protein predicted by g	---	AT2G20700	-1.10	-0.13	-0.67	0.52532019	0.8384	-6.43
260888_at	hypothetical protein similar to aller	---	AT1G29140	-1.05	-0.07	-0.67	0.52572751	0.8389	-6.43
251597_at	protein kinase - like protein wall-a	---	AT3G57750	-1.13	-0.17	-0.67	0.52571779	0.8389	-6.43
255338_at	PEROXISOMAL MEMBRANE PR	PMP22	AT4G04470	1.05	0.07	0.67	0.52578392	0.8389	-6.43
248099_at	DNA topoisomerase I (sp P30181)	TOP1ALPH	AT5G55300	1.05	0.07	0.67	0.52590316	0.8390	-6.43
247909_at	unknown protein ; supported by fu	---	AT5G57370	1.06	0.09	0.67	0.52591698	0.8390	-6.43
255974_at	hypothetical protein	---	---	-1.06	-0.09	-0.67	0.52592577	0.8390	-6.43
265723_at	putative disease resistance protein	---	AT2G32140	-1.05	-0.06	-0.67	0.52626034	0.8390	-6.43
249647_at	putative protein hypothetical protei	---	AT5G37040	-1.07	-0.10	-0.67	0.52637643	0.8390	-6.43
252151_at	putative protein several hypothetic	---	AT3G51320	-1.05	-0.06	-0.67	0.52635728	0.8390	-6.43
253756_at	Cdk-activating kinase CAK1At ; su	CAK1AT	AT4G28980	-1.04	-0.06	-0.67	0.52629755	0.8390	-6.43
254371_at	beta-glucosidase -like protein beta	BGLU47	AT4G21760	-1.05	-0.07	-0.67	0.52608927	0.8390	-6.43
260508_at	Unknown protein ; supported by c	GAMMA CA	AT1G47260	1.05	0.07	0.67	0.52617711	0.8390	-6.43
251180_at	putative protein hypothetical prote	---	AT3G62640	1.09	0.12	0.67	0.52617342	0.8390	-6.43
245463_at	allergen like protein	ATEXLB1	AT4G17030	1.12	0.17	0.67	0.52613418	0.8390	-6.43
248732_at	xyloglucan endo-1,4-beta-D-gluca	XTH20	AT5G48070	-1.07	-0.10	-0.67	0.52622798	0.8390	-6.43
260476_at	unknown protein	---	AT1G11060	-1.07	-0.10	-0.67	0.52628106	0.8390	-6.43
251077_at	putative protein COP1-interacting	---	AT5G01980	-1.04	-0.06	-0.67	0.52635251	0.8390	-6.43
262843_at	Expressed protein ; supported by f	AtHB32	AT1G14687	-1.08	-0.12	-0.67	0.52613082	0.8390	-6.43
260732_at	myb-related DNA-binding protein,	---	AT1G17520	1.05	0.07	0.67	0.52647024	0.8390	-6.43
253241_at	fatty acid elongase 1	KCS18	AT4G34520	-1.08	-0.11	-0.67	0.52644661	0.8390	-6.43

256459_at	acetyl-CoA carboxylase, putative	ACC2	AT1G36180	1.07	0.10	0.67	0.52652983	0.8390	-6.43
249865_at	unknown protein ; supported by cl	---	AT5G22820	1.07	0.10	0.67	0.52662685	0.8391	-6.43
266727_at	putative calmodulin	emb1579	AT2G03150	-1.06	-0.09	-0.67	0.52659698	0.8391	-6.43
254638_at	hypothetical protein	---	AT4G18740	1.09	0.12	0.67	0.52674419	0.8392	-6.43
258261_at	putative RING zinc finger protein	---	AT3G15740	1.10	0.14	0.67	0.52673759	0.8392	-6.43
251086_at	putative protein hypothetical prote	---	AT5G01450	1.07	0.10	0.67	0.52678878	0.8392	-6.43
258973_at	putative cytochrome P450 similar t	CYP94B2	AT3G01900	-1.06	-0.08	-0.67	0.52699385	0.8392	-6.43
248666_at	cyclin C-like protein ;supported by	---	AT5G48630	-1.07	-0.10	-0.67	0.52700537	0.8392	-6.43
246454_at	Expressed protein ; supported by f	DHAR3	AT5G16710	1.05	0.08	0.67	0.52697069	0.8392	-6.43
247991_at	expansin ;supported by full-length	ATEXPA14	AT5G56320	-1.04	-0.06	-0.67	0.52689382	0.8392	-6.43
253074_at	putative disease resistance protei	---	AT4G36140	1.04	0.06	0.67	0.52693959	0.8392	-6.43
245077_at	hypothetical protein predicted by g	---	AT2G23160	1.08	0.11	0.67	0.52707602	0.8393	-6.43
260024_at	beta-1,3-glucanase precursor, put	---	AT1G30080	-1.04	-0.06	-0.67	0.52718463	0.8394	-6.43
266604_at	E2, ubiquitin-conjugating enzyme	UBC6	AT2G46030	-1.11	-0.14	-0.67	0.52724749	0.8394	-6.43
252026_at	serine protein kinase - like serine	SRPK4	AT3G53030	-1.06	-0.08	-0.67	0.52732858	0.8395	-6.43
259866_at	putative calmodulin similar to calm	---	AT1G76640	-1.17	-0.23	-0.67	0.52740328	0.8395	-6.43
256368_at	cinnamyl alcohol dehydrogenase,	---	AT1G66800	1.05	0.07	0.67	0.52740719	0.8395	-6.43
251454_at	putative protein COP1-interacting	---	AT3G60080	1.07	0.10	0.67	0.5273792	0.8395	-6.43
250518_at	Expressed protein ; supported by c	---	AT5G08139	1.05	0.07	0.67	0.52748056	0.8395	-6.43
261374_at	hypothetical protein contains thiore	---	AT1G52990	-1.05	-0.07	-0.67	0.52759932	0.8396	-6.43
249887_at	putative protein similar to unknown	---	AT5G22310	1.18	0.24	0.67	0.52765711	0.8396	-6.43
262515_at	unknown protein ; supported by cD	---	AT1G34200	1.08	0.12	0.67	0.52758775	0.8396	-6.43
255180_at	putative polyprotein	---	---	1.05	0.06	0.67	0.52763207	0.8396	-6.43
261227_at	proteasome regulatory subunit S3	EMB2719	AT1G20200	1.05	0.07	0.67	0.52771078	0.8396	-6.43
255472_at	82.09 and 30.80) similar to alterna	---	AT4G02430	1.05	0.07	0.67	0.52773201	0.8396	-6.43
262914_at	auxin response factor 1 identical to	ARF1	AT1G59750	-1.06	-0.08	-0.67	0.52782493	0.8396	-6.43
262994_at	hypothetical protein predicted by g	---	AT1G54420	-1.04	-0.06	-0.67	0.52789291	0.8396	-6.43
262406_at	myb-related protein, putative simil	AtMYB93	AT1G34670	1.06	0.09	0.67	0.52790564	0.8396	-6.43
247757_at	putative protein	---	AT5G59105	1.04	0.06	0.67	0.52789453	0.8396	-6.43
251413_at	bZIP protein ; supported by cDNA	---	AT3G60320	-1.07	-0.09	-0.67	0.52796361	0.8396	-6.43
266228_at	unknown protein ; supported by fu	CXIP4	AT2G28910	1.07	0.09	0.67	0.52806339	0.8397	-6.43
257561_at	hypothetical protein predicted by g	APUM25	AT3G24270	-1.06	-0.08	-0.66	0.52825812	0.8399	-6.43
260224_at	hypothetical protein contains Pfam	---	AT1G74400	-1.04	-0.06	-0.66	0.52822047	0.8399	-6.43
258302_at	hypothetical protein predicted by g	---	---	-1.05	-0.07	-0.66	0.52826573	0.8399	-6.43
249992_at	AP2 domain -like protein AP2/ERE	PUCHI	AT5G18560	-1.06	-0.08	-0.66	0.52845731	0.8401	-6.43

253976_at	putative protein kinase protein kin	D6PKL1	AT4G26610	-1.04	-0.06	-0.66	0.52878499	0.8403	-6.43
255861_at	putative vacuolar sorting receptor	---	AT2G30290	1.05	0.07	0.66	0.52881438	0.8403	-6.43
250697_at	putative protein contains similarity	---	AT5G06800	-1.06	-0.09	-0.66	0.5286937	0.8403	-6.43
257457_at	hypothetical protein predicted by g	---	AT2G05430	-1.05	-0.07	-0.66	0.52874592	0.8403	-6.43
261318_at	Expressed protein ; supported by f	---	AT1G53035	1.25	0.32	0.66	0.52867777	0.8403	-6.43
256831_at	hypothetical protein	---	AT3G22870	-1.05	-0.08	-0.66	0.52874425	0.8403	-6.43
252007_at	hypothetical protein MobA, Pseud	---	AT3G52830	1.07	0.09	0.66	0.52882282	0.8403	-6.43
262368_at	unknown protein ;supported by full	---	AT1G73060 /	1.09	0.13	0.66	0.52889132	0.8403	-6.43
258077_at	unknown protein ;supported by ful	---	AT3G26110	-1.06	-0.09	-0.66	0.52893103	0.8404	-6.43
248573_at	cellulase homolog OR16pep precu	ATGH9A1	AT5G49720	1.06	0.09	0.66	0.52918105	0.8405	-6.43
261018_at	unknown protein contains similarity	---	AT1G26550	1.04	0.06	0.66	0.52913946	0.8405	-6.43
253445_at	putative protein pAFD103 mRNA,	---	AT4G32605 /	1.06	0.09	0.66	0.52919867	0.8405	-6.43
256408_at	hypothetical protein	---	AT1G66610	-1.07	-0.09	-0.66	0.52911759	0.8405	-6.43
259941_s_at	putative DEAD/DEAH box helicase	---	AT1G71280 /	-1.05	-0.07	-0.66	0.52908573	0.8405	-6.43
262874_at	hypothetical protein predicted by g	---	AT1G65020	-1.07	-0.09	-0.66	0.52942585	0.8407	-6.43
256409_at	hypothetical protein	---	AT1G66620	1.06	0.09	0.66	0.52939097	0.8407	-6.43
260444_at	unknown protein ;supported by ful	---	AT1G68300	1.06	0.08	0.66	0.52946931	0.8407	-6.43
247777_at	putative protein MNUDC protein, h	---	AT5G58740	-1.05	-0.07	-0.66	0.52969894	0.8410	-6.43
264195_at	putative gibberellin-regulated prote	---	AT1G22690	-1.10	-0.14	-0.66	0.53042979	0.8413	-6.43
254331_s_at	cytochrome P450 - like protein fla	CYP706A2	AT4G22690 /	1.16	0.22	0.66	0.53029775	0.8413	-6.43
250132_at	putative protein similar to unknown	KAN	AT5G16560	-1.11	-0.15	-0.66	0.53024148	0.8413	-6.43
259610_at	bZIP protein, putative similar to G	---	AT1G52320	1.05	0.07	0.66	0.53039659	0.8413	-6.43
267135_at	cyclin-dependent kinase inhibitor p	ICK1	AT2G23430	1.11	0.15	0.66	0.53015998	0.8413	-6.43
263765_at	putative phosphatidylinositol phopl	SFH3	AT2G21540	-1.19	-0.25	-0.66	0.53031679	0.8413	-6.43
258438_at	hypothetical protein predicted by g	---	AT3G17230	-1.04	-0.06	-0.66	0.53024118	0.8413	-6.43
267605_at	putative protein disulfide isomeras	ATPDIL2-3	AT2G32920	1.07	0.10	0.66	0.53011952	0.8413	-6.43
263771_at	putative Athila retroelement ORF1	---	---	-1.04	-0.06	-0.66	0.5301676	0.8413	-6.43
258069_at	hypothetical protein predicted by g	---	AT3G26010	-1.07	-0.10	-0.66	0.53033509	0.8413	-6.43
262418_at	thioredoxin, putative similar to thio	ATHX	AT1G50320	1.08	0.12	0.66	0.52996864	0.8413	-6.43
248504_at	transcription factor Hap5a-like	NF-YC6	AT5G50480	-1.08	-0.11	-0.66	0.53014408	0.8413	-6.43
253352_at	pathogenesis-related protein 1 pre	---	AT4G33710	-1.06	-0.09	-0.66	0.53023223	0.8413	-6.43
267397_at	hypothetical protein predicted by g	---	AT1G76170	-1.10	-0.14	-0.66	0.52994701	0.8413	-6.43
260935_at	hypothetical protein predicted by g	---	AT1G45110	-1.07	-0.10	-0.66	0.53047448	0.8413	-6.43
260751_at	unknown protein	SCD1	AT1G49040	1.09	0.12	0.66	0.53035173	0.8413	-6.43
267142_at	putative ammonium transporter	ATAMT2	AT2G38290	-1.11	-0.15	-0.66	0.5304809	0.8413	-6.43

253242_at	isoflavone reductase - like protein	CIB1	AT4G34530	1.10	0.14	0.66	0.53049579	0.8413	-6.43
251371_at	putative protein CGI-94 protein, H	EDA14	AT3G60360	1.10	0.13	0.66	0.53053536	0.8413	-6.43
267031_at	hypothetical protein predicted by g	---	AT2G38420	1.05	0.07	0.66	0.5306119	0.8413	-6.43
261840_at	hypothetical protein contains simila	AtTLP8	AT1G16070	1.05	0.07	0.66	0.53060933	0.8413	-6.43
254332_at	leucine rich repeat receptor kinase	---	AT4G22730	-1.08	-0.11	-0.66	0.53076379	0.8413	-6.43
250382_at	putative protein rjs protein, Mus m	---	AT5G11580	1.04	0.06	0.66	0.53080001	0.8413	-6.43
249134_at	unknown protein	---	AT5G43150	-1.10	-0.13	-0.66	0.53073359	0.8413	-6.43
258397_at	Expressed protein ; supported by f	---	AT3G15357	-1.05	-0.07	-0.66	0.53074602	0.8413	-6.43
252062_at	hypothetical protein KIAA0253 pro	---	AT3G52640	1.07	0.10	0.66	0.53075309	0.8413	-6.43
250836_at	putative protein various predicted	DME	AT5G04560	1.04	0.06	0.66	0.53087529	0.8413	-6.43
258707_at	putative histone H2B similar to hist	---	AT3G09480	1.07	0.10	0.66	0.53127503	0.8414	-6.43
263961_at	F-box protein family, AtFBL11 con	---	AT2G36370	-1.07	-0.09	-0.66	0.5311639	0.8414	-6.43
247989_at	pyruvate kinase ;supported by full	---	AT5G56350	-1.08	-0.11	-0.66	0.53127897	0.8414	-6.43
260231_at	putative RING zinc finger protein c	---	AT1G74410	-1.07	-0.10	-0.66	0.53116691	0.8414	-6.43
253084_at	putative protein lateral root primor	STY2	AT4G36260	-1.08	-0.12	-0.66	0.53114195	0.8414	-6.43
253711_at	hypothetical protein	DER1	---	-1.05	-0.07	-0.66	0.53126367	0.8414	-6.43
262069_at	hypothetical protein similar to SNF	---	AT1G80090	-1.06	-0.09	-0.66	0.53129378	0.8414	-6.43
245680_at	hypothetical protein contains simila	---	AT1G56570	1.05	0.07	0.66	0.5313035	0.8414	-6.43
259599_at	serine carboxypeptidase II, putativ	SCPL45	AT1G28110	1.19	0.25	0.66	0.53101002	0.8414	-6.43
258802_at	unknown protein predicted by gen	---	AT3G04650	-1.08	-0.11	-0.66	0.53110712	0.8414	-6.43
263944_at	hypothetical protein predicted by g	---	---	-1.05	-0.06	-0.66	0.53138367	0.8415	-6.43
261720_at	hypothetical protein similar to hypo	HDA08	AT1G08460	1.09	0.13	0.66	0.53161543	0.8415	-6.43
248998_at	unknown protein	---	AT5G45320	-1.05	-0.07	-0.66	0.53160308	0.8415	-6.43
258582_at	germin-like protein contains Pfam	---	AT3G04150	-1.04	-0.06	-0.66	0.53157064	0.8415	-6.43
259629_at	disease resistance protein contain	WRR4	AT1G56510	-1.07	-0.10	-0.66	0.5315831	0.8415	-6.43
247475_at	IRE (root hair elongation)	IRE	AT5G62310	1.05	0.07	0.66	0.53155248	0.8415	-6.43
248415_at	unknown protein	---	AT5G51620	1.05	0.07	0.66	0.53153227	0.8415	-6.43
256309_at	photosystem I subunit X precursor	PSAK	AT1G30380	1.05	0.07	0.66	0.53169789	0.8415	-6.43
259447_s_at	ADP-ribosylation factor, putative s	ATARFD1A	AT1G02430	-1.05	-0.07	-0.66	0.53170487	0.8415	-6.43
254065_at	gibberellin 20-oxidase - Arabidopsi	GA20OX1	AT4G25420	1.14	0.19	0.66	0.53174321	0.8415	-6.43
260976_at	hypothetical protein	CID8	AT1G53650	1.08	0.11	0.66	0.53180861	0.8416	-6.43
253513_at	peroxidase - like protein peroxidas	---	AT4G31760	1.05	0.06	0.66	0.53190867	0.8417	-6.43
246931_at	putative protein apoptosis-related	---	AT5G25170	1.18	0.23	0.66	0.53195745	0.8417	-6.43
245333_at	Expressed protein ; supported by f	---	AT4G14615	1.04	0.06	0.66	0.53215943	0.8420	-6.43
247955_at	nucleosome assembly protein	NAP1;3	AT5G56950	-1.07	-0.09	-0.66	0.53230261	0.8421	-6.44

262904_at	chaperone, putative similar to cha	---	AT1G59725	1.07	0.09	0.66	0.53247531	0.8423	-6.44
261810_at	ligase I, putative similar to ligase I	ATLIG1	AT1G08130	1.11	0.15	0.66	0.5324916	0.8423	-6.44
260121_at	AIG1-like protein similar to AIG1 p	---	AT1G33910	-1.04	-0.06	-0.66	0.5325385	0.8423	-6.44
246691_at	putative protein predicted proteins	---	---	1.04	0.06	0.66	0.53257767	0.8423	-6.44
262009_at	hypothetical protein predicted by g	---	AT1G35610	-1.06	-0.09	-0.66	0.5328982	0.8428	-6.44
267436_at	putative receptor-like protein kinas	FRK1	AT2G19190	-1.19	-0.25	-0.66	0.53321772	0.8430	-6.44
264329_at	unknown protein Contains similari	---	AT1G04140	1.05	0.07	0.66	0.53321335	0.8430	-6.44
245115_at	putative esterase D ;supported by	SFGH	AT2G41530	1.09	0.12	0.66	0.53320955	0.8430	-6.44
245197_at	F12A21.7 hypothetical protein;sup	---	AT1G67800	-1.05	-0.07	-0.66	0.53311723	0.8430	-6.44
254888_at	putative protein predicted protein,	---	AT4G11780	-1.05	-0.07	-0.66	0.53317233	0.8430	-6.44
263357_s_at	Mutator-like transposase similar to	---	---	-1.05	-0.07	-0.66	0.53329705	0.8431	-6.44
257291_at	DNA-binding protein, putative sim	---	AT3G15590	-1.13	-0.17	-0.66	0.5334347	0.8431	-6.44
254074_at	transcriptional activator CBF1 CR	CBF1	AT4G25490	-1.12	-0.17	-0.66	0.53343768	0.8431	-6.44
255641_at	contains region of similarity to beta	---	AT4G00800	-1.06	-0.08	-0.66	0.53343332	0.8431	-6.44
258498_at	unknown protein similar to pollen c	---	AT3G02480	-1.13	-0.17	-0.66	0.53348122	0.8431	-6.44
263958_at	putative salt-inducible protein	---	AT2G36240	-1.04	-0.06	-0.66	0.53362214	0.8432	-6.44
256903_at	hypothetical protein	---	AT3G23960	-1.05	-0.07	-0.66	0.53361492	0.8432	-6.44
254511_at	hypothetical protein	---	AT4G20220	-1.05	-0.07	-0.66	0.53357699	0.8432	-6.44
245908_at	laccase-like protein laccase - Ace	LAC14	AT5G09360	-1.09	-0.12	-0.66	0.53368426	0.8432	-6.44
258041_at	Expressed protein ; supported by f	ZML1	AT3G21175	-1.06	-0.08	-0.66	0.53378424	0.8433	-6.44
261515_at	cleavage stimulation factor, putati	---	AT1G71800	-1.05	-0.07	-0.66	0.53381465	0.8433	-6.44
261356_at	predicted protein	---	AT1G79660	1.08	0.11	0.66	0.5340113	0.8434	-6.44
265005_at	Expressed protein ; supported by f	---	AT1G61667	1.10	0.13	0.66	0.53402291	0.8434	-6.44
267603_at	unknown protein ; supported by cl	ATZW10	AT2G32900	1.07	0.09	0.66	0.53397449	0.8434	-6.44
267401_at	unknown protein	---	AT2G26210	1.05	0.07	0.65	0.53425249	0.8435	-6.44
253196_at	NAD+ dependent isocitrate dehydr	IDH1	AT4G35260	-1.07	-0.10	-0.65	0.5342165	0.8435	-6.44
264992_at	integral membrane protein, putativ	---	AT1G67300	1.07	0.09	0.65	0.53430508	0.8435	-6.44
258835_at	putative RNA-binding protein cont	---	AT3G07250	-1.06	-0.08	-0.65	0.53424443	0.8435	-6.44
249487_at	ABC transporter -like protein TAP	TAP2	AT5G39040	-1.10	-0.14	-0.65	0.53429158	0.8435	-6.44
255741_at	tRNA isopentenyl transferase, put	ATIPT6	AT1G25410	-1.06	-0.08	-0.66	0.53418494	0.8435	-6.44
257446_at	hypothetical protein predicted by g	---	AT2G10440	1.04	0.06	0.65	0.53429368	0.8435	-6.44
246225_at	putative protein ;supported by full-l	LEJ2	AT4G36910	1.07	0.10	0.65	0.53434657	0.8435	-6.44
257924_at	unknown protein	---	AT3G23190	-1.07	-0.10	-0.65	0.53450221	0.8437	-6.44
267141_at	putative MYB family transcription f	---	AT2G38090	1.07	0.10	0.65	0.53461774	0.8437	-6.44
250016_at	Cu/Zn superoxide dismutase-like p	CSD3	AT5G18100	1.06	0.08	0.65	0.53460545	0.8437	-6.44

249534_at	bZIP transcription factor - like prot	AtbZIP43	AT5G38800	1.05	0.07	0.65	0.53461341	0.8437	-6.44
245599_at	RING-H2 finger protein RHF1a	RHF1A	AT4G14220	1.09	0.12	0.65	0.53477049	0.8438	-6.44
254368_at	DNA-directed RNA polymerase (E	NRPB2	AT4G21710	1.05	0.07	0.65	0.53489066	0.8438	-6.44
261945_at	unknown protein	---	AT1G64530	1.10	0.14	0.65	0.53486968	0.8438	-6.44
256121_at	MAP kinase, putative similar to MA	---	AT1G18160	-1.05	-0.08	-0.65	0.53500122	0.8438	-6.44
264350_at	putative seryl-tRNA synthetase sim	SRS	AT1G11870	1.08	0.11	0.65	0.53497502	0.8438	-6.44
258685_at	putative polygalacturonase similar	---	AT3G07830	1.07	0.10	0.65	0.53488224	0.8438	-6.44
259807_at	hypothetical protein predicted by g	---	AT1G47920	-1.05	-0.07	-0.65	0.53503592	0.8438	-6.44
261856_at	hypothetical protein	---	AT1G50530	1.06	0.09	0.65	0.53494535	0.8438	-6.44
259251_at	unknown protein identical to residu	---	AT3G07600	-1.17	-0.23	-0.65	0.53484973	0.8438	-6.44
246163_at	putative protein predicted proteins	---	---	-1.06	-0.09	-0.65	0.53487826	0.8438	-6.44
254746_at	putative protein hypothetical prote	---	AT4G12980	1.11	0.15	0.65	0.53524094	0.8440	-6.44
259161_at	carbonic anhydrase, chloroplast p	CA1	AT3G01500	1.15	0.21	0.65	0.53543937	0.8440	-6.44
249821_at	putative protein contains similarity	---	AT5G23690	1.09	0.13	0.65	0.5355249	0.8440	-6.44
250730_at	C3HC4-type RING zinc finger prot	---	AT5G06490	-1.05	-0.08	-0.65	0.53546286	0.8440	-6.44
246544_at	auxin transport protein - like auxin	PIN8	AT5G15100	1.05	0.07	0.65	0.53544576	0.8440	-6.44
255390_at	hypothetical protein similar to A. th	---	---	-1.05	-0.07	-0.65	0.53554525	0.8440	-6.44
246615_at	putative protein similar to unknown	---	---	-1.06	-0.08	-0.65	0.53552789	0.8440	-6.44
266374_at	putative retroelement pol polyprote	---	---	-1.07	-0.10	-0.65	0.53535311	0.8440	-6.44
260934_at	hypothetical protein predicted by g	---	AT1G45100	1.04	0.06	0.65	0.53532788	0.8440	-6.44
261142_at	cyclic nucleotide and calmodulin-r	ATCNGC8	AT1G19780	1.04	0.06	0.65	0.53558901	0.8441	-6.44
246896_at	extensin - like protein Pex1 extens	---	AT5G25550	1.06	0.08	0.65	0.53563615	0.8441	-6.44
247023_at	putative protein similar to unknown	HEC1	AT5G67060	-1.07	-0.10	-0.65	0.53571297	0.8441	-6.44
266248_at	hypothetical protein predicted by g	---	AT2G27650	-1.04	-0.06	-0.65	0.53570403	0.8441	-6.44
249022_s_at	polygalacturonase-like protein	---	AT5G44830 /	-1.05	-0.07	-0.65	0.53574875	0.8441	-6.44
266218_s_at	putative cytochrome P450	CYP710A4	AT2G28850 /	-1.05	-0.07	-0.65	0.53594328	0.8443	-6.44
261763_at	ABC transporter, putative similar t	PDR12	AT1G15520	-1.25	-0.33	-0.65	0.53631725	0.8445	-6.44
263851_at	putative retroelement pol polyprote	---	---	1.15	0.20	0.65	0.53610047	0.8445	-6.44
246173_s_at	putative protein hypothetical prote	---	AT3G61520 /	1.08	0.11	0.65	0.53617322	0.8445	-6.44
247093_at	zinc finger protein SHI-like ; suppo	SHI	AT5G66350	-1.08	-0.10	-0.65	0.53629608	0.8445	-6.44
255530_at	hypothetical protein	---	AT4G02140	1.05	0.07	0.65	0.53616018	0.8445	-6.44
263617_at	putative retroelement pol polyprote	---	---	-1.06	-0.09	-0.65	0.53627781	0.8445	-6.44
248370_at	homeodomain transcription factor-	HDG7	AT5G52170	-1.07	-0.09	-0.65	0.53629803	0.8445	-6.44
248297_at	protochlorophyllide reductase; oxid	---	AT5G53100	-1.04	-0.06	-0.65	0.53635556	0.8445	-6.44
252932_at	putative proton pump vacuolar pro	VHA-A3	AT4G39080	-1.05	-0.08	-0.65	0.53643795	0.8445	-6.44

263215_at	putative reticuline oxidase-like pro	---	AT1G30710	1.06	0.08	0.65	0.53643957	0.8445	-6.44
267408_at	putative CTP synthase	---	AT2G34890	-1.05	-0.07	-0.65	0.53651592	0.8446	-6.44
262432_at	unknown protein	---	AT1G47530	1.10	0.14	0.65	0.53669679	0.8448	-6.44
255417_at	F-box protein GRR1-like protein 1	GRH1	AT4G03190	-1.22	-0.29	-0.65	0.53675242	0.8448	-6.44
255957_at	unknown protein ;supported by full	---	AT1G22160	-1.15	-0.20	-0.65	0.53689344	0.8449	-6.44
264555_at	hypothetical protein predicted by g	---	AT1G09360	1.05	0.07	0.65	0.53691868	0.8449	-6.44
245096_at	putative cysteine proteinase inhibit	ATCYSA	AT2G40880	1.06	0.08	0.65	0.53691687	0.8449	-6.44
247181_at	putative protein similar to unknown	---	AT5G65370	1.05	0.07	0.65	0.53681849	0.8449	-6.44
258371_at	hypothetical protein contains simila	---	AT3G14410	1.06	0.08	0.65	0.5371324	0.8451	-6.44
246737_at	putative protein	---	AT5G27710	-1.10	-0.14	-0.65	0.53714833	0.8451	-6.44
255408_at	hypothetical protein similar to A. th	---	AT4G03490	-1.09	-0.13	-0.65	0.53718886	0.8451	-6.44
250978_at	putative protein contains transmer	---	AT5G03080	-1.04	-0.06	-0.65	0.53731361	0.8452	-6.44
255104_at	Expressed protein ; supported by f	SAH7	AT4G08685	-1.21	-0.27	-0.65	0.53732084	0.8452	-6.44
260697_at	unknown protein	---	AT1G32530	1.08	0.11	0.65	0.53739371	0.8453	-6.44
256841_x_at	hypothetical protein predicted by g	---	---	-1.08	-0.12	-0.65	0.53752817	0.8454	-6.44
251237_at	bZIP transcription factor-like prote	CPuORF3	AT3G62420 /	-1.05	-0.08	-0.65	0.53770756	0.8456	-6.44
257498_at	hypothetical protein predicted by g	---	AT1G69660	1.05	0.07	0.65	0.53787167	0.8458	-6.44
254387_at	putative protein CGI-131 protein, I	ATMSRB9	AT4G21850	-1.40	-0.49	-0.65	0.53784108	0.8458	-6.44
266702_at	hexokinase (ATHXK2) ; supported	HXK2	AT2G19860	-1.05	-0.07	-0.65	0.53798423	0.8458	-6.44
256346_s_at	unknown protein	---	AT2G15040	1.04	0.06	0.65	0.53794346	0.8458	-6.44
263602_at	40S ribosomal protein S25	---	AT2G16360	1.05	0.07	0.65	0.53796486	0.8458	-6.44
251110_at	putative protein various alpha amy	---	AT5G01260	-1.09	-0.12	-0.65	0.53811347	0.8459	-6.44
254685_at	SAUR-AC - like protein (small aux	---	AT4G13790	1.14	0.19	0.65	0.53809222	0.8459	-6.44
246421_at	TOM (target of myb1) -like protein	---	AT5G16880	1.06	0.09	0.65	0.53820475	0.8459	-6.44
246974_at	putative protein	---	AT5G24980	1.06	0.09	0.65	0.53818458	0.8459	-6.44
252622_at	cysteine proteinase AALP, putativ	---	AT3G45310	1.06	0.08	0.65	0.53828305	0.8459	-6.44
251010_at	putative protein ;supported by full-	---	AT5G02550	-1.07	-0.10	-0.65	0.53827557	0.8459	-6.44
263850_at	hypothetical protein predicted by g	---	AT2G04480	1.09	0.12	0.65	0.53838443	0.8460	-6.44
254630_at	glycolate oxidase - like protein (S)	---	AT4G18360	-1.24	-0.31	-0.65	0.53924213	0.8461	-6.44
257058_at	Expressed protein ; supported by c	COX17	AT3G15352	1.22	0.28	0.65	0.53858853	0.8461	-6.44
258924_at	putative diadenosine 5',5"'-P1,P4-	ATNUDX26	AT3G10620	-1.05	-0.07	-0.65	0.53901553	0.8461	-6.44
250144_at	putative protein various predicted	---	AT5G14680	1.09	0.13	0.65	0.53913687	0.8461	-6.44
247926_at	protein carboxyl methylase-like	---	AT5G57280	-1.12	-0.16	-0.65	0.53884958	0.8461	-6.44
262532_at	hypothetical protein predicted by g	---	AT1G17210	1.05	0.07	0.65	0.5391319	0.8461	-6.44
259582_at	hypothetical protein	---	AT1G28060	-1.06	-0.09	-0.65	0.5392763	0.8461	-6.44

260951_at	hypothetical protein similar to hypo	---	AT1G06145	1.07	0.09	0.65	0.5385515	0.8461	-6.44
257345_s_at	pseudogene	---	---	1.04	0.06	0.65	0.53902545	0.8461	-6.44
258508_at	protein kinase, putative similar to	---	AT3G06640	1.04	0.06	0.65	0.53870604	0.8461	-6.44
246867_at	putative protein various predicted	---	AT5G25990	1.04	0.06	0.65	0.53883282	0.8461	-6.44
254281_at	predicted protein ileal sodium-dep	---	AT4G22840	1.18	0.23	0.65	0.53913092	0.8461	-6.44
247086_at	GATA-binding transcription factor-	---	AT5G66320	1.23	0.30	0.65	0.53874257	0.8461	-6.44
246790_at	putative protein unknown protein	---	AT5G27610	1.07	0.10	0.65	0.53917711	0.8461	-6.44
257445_x_at	hypothetical protein predicted by g	---	---	-1.05	-0.07	-0.65	0.53920105	0.8461	-6.44
252735_at	putative protein predicted proteins	---	AT3G43170	1.05	0.07	0.65	0.53917757	0.8461	-6.44
262447_at	hypothetical protein contains simila	---	AT1G49250	-1.05	-0.07	-0.65	0.53923185	0.8461	-6.44
258831_at	putative integral membrane protein	---	AT3G07080	1.04	0.06	0.65	0.53916515	0.8461	-6.44
262554_at	hypothetical protein similar to hypo	---	AT1G31380	-1.05	-0.07	-0.65	0.53877451	0.8461	-6.44
255876_at	hypothetical protein	---	AT2G40480	1.12	0.16	0.65	0.53911396	0.8461	-6.44
252511_at	putative protein serine/threonine-s	---	AT3G46280	-1.15	-0.20	-0.65	0.53855214	0.8461	-6.44
264814_at	putative SET-domain transcriptiona	SDG37	AT2G17900	-1.08	-0.11	-0.65	0.53924161	0.8461	-6.44
256584_at	unknown protein	---	AT3G28750	-1.05	-0.07	-0.65	0.53935833	0.8462	-6.44
259029_at	putative oxysterol-binding protein s	ORP3B	AT3G09300	1.06	0.09	0.65	0.53940571	0.8462	-6.44
253972_at	putative protein Uvi31, Schizosac	CPSUFE	AT4G26500	-1.04	-0.06	-0.65	0.53944356	0.8462	-6.44
246709_s_at	putative protein many predicted pr	---	AT5G28160	1.04	0.06	0.65	0.53947638	0.8462	-6.44
249135_at	putative protein similar to unknown	---	AT5G43160	-1.11	-0.15	-0.65	0.53957921	0.8463	-6.44
249518_at	putative protein similar to unknown	---	AT5G38610	1.05	0.07	0.65	0.53964386	0.8463	-6.44
262464_at	hypothetical protein contains simila	---	AT1G50280	-1.10	-0.14	-0.65	0.53974184	0.8464	-6.44
267244_at	putative reverse transcriptase	---	AT2G02650	-1.05	-0.07	-0.65	0.53970395	0.8464	-6.44
254464_at	putative protein retinoblastoma bi	---	AT4G20400	1.08	0.10	0.65	0.53983457	0.8464	-6.44
250446_at	nucleoid DNA-binding protein cnd	---	AT5G10770	1.10	0.14	0.65	0.53977206	0.8464	-6.44
264754_at	receptor kinase, putative similar to	---	AT1G61400	-1.06	-0.08	-0.65	0.53980535	0.8464	-6.44
265162_at	hypothetical protein predicted by g	---	AT1G30910	1.06	0.08	0.65	0.54004764	0.8464	-6.44
264984_at	unknown protein ;supported by full	---	AT1G27000	-1.04	-0.06	-0.65	0.54006851	0.8464	-6.44
261777_at	hypothetical protein predicted by g	---	AT1G76210	-1.05	-0.07	-0.65	0.54006999	0.8464	-6.44
254513_at	cytochrome p450 like protein cyto	CYP71A27	AT4G20240	-1.04	-0.06	-0.65	0.54000924	0.8464	-6.44
265937_at	putative RING zinc finger protein	---	AT2G19610	-1.06	-0.08	-0.65	0.53998438	0.8464	-6.44
246819_at	WD-repeat protein - like WD-repe	---	AT5G26900	-1.06	-0.08	-0.65	0.54010977	0.8464	-6.44
257113_at	cytochrome P450, putative contai	CYP705A2	AT3G20130	-1.11	-0.15	-0.65	0.54019514	0.8465	-6.44
258067_at	putative mitotic checkpoint protein	---	AT3G25980	-1.05	-0.07	-0.65	0.54020774	0.8465	-6.44
266398_at	hypothetical protein predicted by g	---	AT2G38680	-1.12	-0.16	-0.64	0.540332	0.8466	-6.44

259776_s_at	eukaryotic translation initiation fac	---	AT1G29550 /	1.05	0.07	0.64	0.54047867	0.8468	-6.44
257004_s_at	glycolate oxidase, putative similar	---	AT3G14130 /	1.05	0.06	0.64	0.54065247	0.8469	-6.44
249671_at	putative protein similar to unknown	LBD35	AT5G35900	-1.05	-0.08	-0.64	0.54061298	0.8469	-6.44
266389_s_at	unknown protein	---	AT2G31580 /	-1.05	-0.06	-0.64	0.54062477	0.8469	-6.44
249581_at	glutamate--ammonia ligase ; supp	GSR 1	AT5G37600	-1.05	-0.07	-0.64	0.54073849	0.8470	-6.44
256333_at	Sm-like protein contains Pfam prof	---	AT1G76860	1.09	0.12	0.64	0.54093071	0.8472	-6.44
247903_at	unknown protein ; supported by cl	---	AT5G57340	-1.07	-0.10	-0.64	0.54101893	0.8472	-6.45
252560_at	histone H2B -like protein histone H	HTB11	AT3G46030	1.05	0.06	0.64	0.54100665	0.8472	-6.45
254032_at	predicted protein destination facto	---	AT4G25940	-1.07	-0.10	-0.64	0.54149115	0.8474	-6.45
256263_at	5,10-methylenetetrahydrofolate de	---	AT3G12290	-1.06	-0.08	-0.64	0.54146781	0.8474	-6.45
250726_at	putative protein similar to unknown	---	AT5G06410	-1.07	-0.09	-0.64	0.54128398	0.8474	-6.45
251499_at	putative protein putative callose sy	ATGSL11	AT3G59100	1.05	0.07	0.64	0.541496	0.8474	-6.45
245541_at	hypothetical protein	---	AT4G15240	1.08	0.11	0.64	0.54143631	0.8474	-6.45
259959_at	hypothetical protein predicted by g	CYP59	AT1G53720	-1.06	-0.09	-0.64	0.54152898	0.8474	-6.45
248125_at	2S storage protein-like	---	AT5G54740	-1.05	-0.08	-0.64	0.54134176	0.8474	-6.45
246930_at	KNAT3 homeodomain protein ;su	KNAT3	AT5G25220	-1.07	-0.09	-0.64	0.54126153	0.8474	-6.45
255715_s_at	hypothetical protein	---	AT4G00320 /	-1.05	-0.07	-0.64	0.54137958	0.8474	-6.45
259637_at	protein disulfide isomerase precur	ATPDIL1-5	AT1G52260	-1.07	-0.10	-0.64	0.54132474	0.8474	-6.45
261842_at	hypothetical protein contains simila	WAKL5	AT1G16160	1.07	0.10	0.64	0.54143632	0.8474	-6.45
251905_at	putative protein zinc finger protein	GAPB	AT1G42970 /	-1.06	-0.08	-0.64	0.54165944	0.8475	-6.45
255618_at	hypothetical protein	---	AT4G01340	1.04	0.06	0.64	0.54167918	0.8475	-6.45
248030_at	transcription regulator Sir2-like pro	SRT1	AT5G55760	1.07	0.10	0.64	0.54203801	0.8480	-6.45
265725_at	putative alanine acetyl transferase	---	AT2G32030	1.44	0.53	0.64	0.54208061	0.8480	-6.45
257181_at	hypothetical protein	---	AT3G13190	-1.07	-0.09	-0.64	0.54212078	0.8480	-6.45
246757_at	Expressed protein ; supported by f	WPP3	AT5G27940	-1.04	-0.06	-0.64	0.54224177	0.8481	-6.45
264963_at	hypothetical protein predicted by g	ABC4	AT1G60600	1.08	0.11	0.64	0.54225004	0.8481	-6.45
254111_at	putative protein acid phosphatase	PAP24	AT4G24890	-1.08	-0.11	-0.64	0.54227269	0.8481	-6.45
252632_s_at	disease resistance protein -like dis	RPP1	AT3G44480 /	1.06	0.08	0.64	0.54240707	0.8482	-6.45
265384_at	unknown protein ;supported by ful	---	AT2G20760	1.04	0.06	0.64	0.54262415	0.8483	-6.45
258714_at	putative RING zinc finger protein c	---	AT3G09770	-1.08	-0.11	-0.64	0.54263657	0.8483	-6.45
248667_at	putative protein contains similarity	---	AT5G48710	-1.04	-0.06	-0.64	0.54264342	0.8483	-6.45
267457_at	putative proline-rich protein	AGP30	AT2G33790	-1.05	-0.07	-0.64	0.542582	0.8483	-6.45
254018_at	putative mitochondrial carrier prot	---	AT4G26180	-1.06	-0.08	-0.64	0.54255412	0.8483	-6.45
253820_at	hypothetical protein	---	AT4G28370	1.05	0.07	0.64	0.54298444	0.8487	-6.45
256826_at	hypothetical protein predicted by g	---	AT3G18540	-1.04	-0.06	-0.64	0.54297313	0.8487	-6.45

256953_at	flavonol 3-O-Glucosyltransferase,	---	AT3G29630	-1.07	-0.10	-0.64	0.54312144	0.8489	-6.45
265549_at	hypothetical protein predicted by g	---	---	-1.06	-0.08	-0.64	0.54328443	0.8490	-6.45
249890_at	putative protein contains similarity	WRKY38	AT5G22570	1.39	0.47	0.64	0.54326219	0.8490	-6.45
260449_at	unknown protein	---	AT1G72390	-1.04	-0.06	-0.64	0.54333785	0.8490	-6.45
247220_at	cdc2-like protein kinase ; supporte	CDKC2	AT5G64960	-1.05	-0.07	-0.64	0.54341905	0.8491	-6.45
264837_at	unknown protein similar to ESTs e	---	AT1G03600	1.10	0.13	0.64	0.54379673	0.8491	-6.45
260441_at	unknown protein ;supported by ful	---	AT1G68260	1.13	0.17	0.64	0.54361265	0.8491	-6.45
264736_at	oligopeptide transporter, putative	---	AT1G62200	1.07	0.10	0.64	0.54365019	0.8491	-6.45
265301_s_at	putative MYB family transcription f	---	AT2G13960	1.05	0.08	0.64	0.5436574	0.8491	-6.45
259588_at	unknown protein ;supported by full	---	AT1G27930	1.04	0.06	0.64	0.54385688	0.8491	-6.45
256533_at	unknown protein	---	AT1G33250	-1.07	-0.10	-0.64	0.54373291	0.8491	-6.45
257229_at	putative calmodulin-binding protein	IQD26	AT3G16490	1.07	0.10	0.64	0.54387316	0.8491	-6.45
262555_at	hypothetical protein	---	AT1G31400	-1.04	-0.06	-0.64	0.54362604	0.8491	-6.45
261870_at	nuclear transport factor 2, putative	NTL	AT1G11570	1.06	0.08	0.64	0.54387792	0.8491	-6.45
245440_at	RNA helicase	---	AT4G16680	-1.04	-0.06	-0.64	0.54370464	0.8491	-6.45
261781_at	far-red impaired response protein,	FRS4	AT1G76320	-1.06	-0.09	-0.64	0.543649	0.8491	-6.45
255119_at	hypothetical protein	---	---	1.04	0.06	0.64	0.54349542	0.8491	-6.45
265307_at	hypothetical protein predicted by g	RIN13	AT2G20310	-1.06	-0.08	-0.64	0.54397152	0.8492	-6.45
266427_at	hypothetical protein predicted by g	---	AT2G07170	1.06	0.09	0.64	0.5439976	0.8492	-6.45
265518_at	hypothetical protein predicted by g	---	AT2G06040	-1.08	-0.11	-0.64	0.54405036	0.8492	-6.45
255055_at	hypothetical protein	---	AT4G09810	-1.07	-0.10	-0.64	0.54410523	0.8493	-6.45
245697_at	latex-abundant protein - like ;suppo	AtMC9	AT5G04200	1.26	0.34	0.64	0.54422887	0.8494	-6.45
247455_at	MYB96 transcription factor-like pro	MYB96	AT5G62470	1.09	0.13	0.64	0.54430201	0.8494	-6.45
260699_at	MAP kinase, putative similar to MA	ATMKK10	AT1G32320	1.05	0.07	0.64	0.5443245	0.8494	-6.45
263021_at	hypothetical protein predicted by g	---	AT1G23910	-1.04	-0.06	-0.64	0.54444049	0.8495	-6.45
246500_at	putative protein HR21spA protein	SYN4	AT5G16270	-1.06	-0.08	-0.64	0.54445854	0.8495	-6.45
256571_at	hypothetical protein predicted by g	---	AT3G30730	1.04	0.06	0.64	0.5444317	0.8495	-6.45
251282_at	putative protein transcription facto	CRF6	AT3G61630	-1.13	-0.18	-0.64	0.54493746	0.8495	-6.45
247032_at	putative protein strong similarity to	SDN3	AT5G67240	-1.05	-0.07	-0.64	0.54474083	0.8495	-6.45
265465_at	hypothetical protein predicted by g	---	AT2G37070	-1.13	-0.18	-0.64	0.5446777	0.8495	-6.45
264989_at	unknown protein ; supported by cD	---	AT1G27200	1.08	0.11	0.64	0.54468206	0.8495	-6.45
260255_at	putative protein kinase similar to p	---	AT1G74330	-1.10	-0.14	-0.64	0.54476021	0.8495	-6.45
250271_at	putative protein predicted protein,	CLE40	AT5G12990	1.05	0.07	0.64	0.54494281	0.8495	-6.45
254091_at	hypothetical protein	---	AT4G25070	1.10	0.13	0.64	0.54488284	0.8495	-6.45
258407_at	unknown protein similar to unknow	---	AT3G17620	1.08	0.11	0.64	0.54456196	0.8495	-6.45

248554_at	putative protein contains similarity	---	AT5G50330	1.07	0.10	0.64	0.54489626	0.8495	-6.45
258757_at	putative RING zinc finger protein (	---	AT3G10910 /	-1.09	-0.12	-0.64	0.54469684	0.8495	-6.45
249654_at	putative protein hypothetical protei	---	---	-1.05	-0.07	-0.64	0.54458779	0.8495	-6.45
250810_at	putative protein contains similarity	---	AT5G05090	1.09	0.12	0.64	0.54481619	0.8495	-6.45
266759_at	unknown protein predicted by gene	---	AT2G46915	-1.05	-0.07	-0.64	0.54502495	0.8496	-6.45
255288_at	coded for by A. thaliana cDNA T41	---	AT4G04670	-1.08	-0.11	-0.64	0.54506681	0.8496	-6.45
266687_at	putative arginine N-methyltransfera	PRMT1A	AT2G19670	1.10	0.14	0.64	0.54510225	0.8496	-6.45
249049_at	tubulin beta-4 chain (sp|P24636) ;	TUB4	AT5G44340	1.08	0.11	0.64	0.54526068	0.8497	-6.45
253928_at	phosphoprotein phosphatase (PPX	PPX1	AT4G26720	-1.05	-0.07	-0.64	0.54526063	0.8497	-6.45
255611_at	hypothetical protein	---	AT4G01210	-1.05	-0.07	-0.64	0.5453049	0.8497	-6.45
260824_at	unknown protein	---	AT1G06720	1.11	0.15	0.64	0.54540758	0.8498	-6.45
250323_at	putative protein hydroxyproline-ric	---	AT5G12880	1.21	0.27	0.64	0.54551383	0.8498	-6.45
248585_at	unknown protein	---	AT5G49640	1.05	0.07	0.64	0.54548736	0.8498	-6.45
248745_at	unknown protein	---	AT5G48250	-1.07	-0.09	-0.64	0.54551515	0.8498	-6.45
252494_at	receptor-like protein kinase recept	---	AT3G46760	1.05	0.08	0.64	0.54541615	0.8498	-6.45
256529_at	protein kinase, putative contains P	---	AT1G33260	1.10	0.14	0.64	0.5456314	0.8498	-6.45
267027_at	hypothetical protein	---	AT2G38330	-1.07	-0.10	-0.64	0.54561505	0.8498	-6.45
248244_at	heat shock transcription factor HSF	---	AT5G53640	-1.06	-0.08	-0.64	0.54563316	0.8498	-6.45
250611_at	gibberellin 20-oxidase	GA20OX3	AT5G07200	-1.09	-0.12	-0.64	0.54577221	0.8498	-6.45
255864_at	putative pseudouridine synthase	---	AT2G30320	-1.06	-0.08	-0.64	0.54581151	0.8498	-6.45
266131_at	putative SCARECROW gene regu	---	AT2G45160	-1.08	-0.11	-0.64	0.54584259	0.8498	-6.45
266949_s_at	unknown protein ;supported by full	---	AT2G18840 /	1.06	0.09	0.64	0.54581967	0.8498	-6.45
252926_at	H+-transporting ATPase 16K chai	ATVHA-C3	AT4G38920	1.06	0.08	0.64	0.54582975	0.8498	-6.45
247682_at	serine/threonine-specific protein k	---	AT5G59650	-1.06	-0.08	-0.64	0.54599489	0.8498	-6.45
246963_at	putative protein nucleoid DNA-bin	---	AT5G24820	1.06	0.09	0.64	0.54596119	0.8498	-6.45
267468_at	unknown protein ; supported by cl	---	AT2G30530	-1.06	-0.08	-0.64	0.54590673	0.8498	-6.45
248188_at	putative protein contains similarity	HSFA9	AT5G54070	1.04	0.06	0.64	0.54598728	0.8498	-6.45
263676_at	putative RNA-binding protein Iden	CRB	AT1G09340	1.07	0.10	0.64	0.54626428	0.8498	-6.45
252420_at	putative protein several hypothetic	---	AT3G47530	1.08	0.11	0.64	0.54633056	0.8498	-6.45
263984_at	hypothetical protein predicted by g	---	AT2G42670	1.05	0.07	0.64	0.546224	0.8498	-6.45
248626_at	receptor protein kinase-like protein	---	AT5G48940	-1.05	-0.07	-0.64	0.54624019	0.8498	-6.45
259900_at	c-Jun coactivator-like protein (AJH	CSN5B	AT1G71230	1.04	0.06	0.64	0.54614507	0.8498	-6.45
253588_at	putative protein	---	AT4G30790	-1.06	-0.08	-0.64	0.54623043	0.8498	-6.45
248206_at	unknown protein	---	AT5G54350	-1.06	-0.09	-0.64	0.54630366	0.8498	-6.45
245508_at	hypothetical protein	---	AT4G15720	-1.04	-0.06	-0.64	0.54616481	0.8498	-6.45

252664_at	putative protein several hypothetic	---	AT3G44080	1.04	0.06	0.64	0.54609726	0.8498	-6.45
265938_at	putative SF21 protein {Helianthus	---	AT2G19620	1.15	0.20	0.63	0.54689322	0.8499	-6.45
255724_at	hypothetical protein	BRCA2(IV)	AT4G00020	-1.05	-0.07	-0.63	0.5465501	0.8499	-6.45
248636_at	putative protein similar to unknown	---	---	-1.05	-0.07	-0.63	0.54650446	0.8499	-6.45
257198_at	DNA-binding protein, putative sim	---	AT3G23690	-1.06	-0.09	-0.63	0.54649967	0.8499	-6.45
258040_at	unknown protein ;supported by ful	---	AT3G21190	-1.31	-0.39	-0.63	0.54660524	0.8499	-6.45
252282_at	6-phosphogluconolactonase - like	---	AT3G49360	1.05	0.06	0.63	0.5468773	0.8499	-6.45
265843_at	putative acyl-CoA oxidase possibly	ACX5	AT2G35690	1.05	0.08	0.63	0.5468331	0.8499	-6.45
263027_at	hypothetical protein predicted by g	---	AT1G24010	-1.04	-0.06	-0.63	0.54691243	0.8499	-6.45
252221_at	RuvB DNA helicase - like protein I	---	AT3G49830	-1.05	-0.08	-0.63	0.54672815	0.8499	-6.45
263701_at	putative protein kinase C inhibitor (	---	AT1G31160	1.04	0.06	0.63	0.54680225	0.8499	-6.45
249981_at	putative protein predicted proteins	---	AT5G18510	-1.07	-0.09	-0.63	0.54678909	0.8499	-6.45
246768_at	putative protein hypothetical protei	---	AT5G27400	1.04	0.06	0.63	0.54670148	0.8499	-6.45
245482_at	hypothetical protein	---	AT4G16180	-1.07	-0.10	-0.63	0.54685272	0.8499	-6.45
258785_at	unknown protein	---	---	-1.06	-0.09	-0.63	0.5468127	0.8499	-6.45
245491_at	hypothetical protein	LDL3	---	-1.06	-0.09	-0.63	0.54678359	0.8499	-6.45
256924_at	Anthocyanin 5-aromatic acyltransf	AT5MAT	AT3G29590	-1.05	-0.08	-0.63	0.5469535	0.8499	-6.45
252469_at	protein kinase - like protein Raf pr	---	AT3G46920	-1.07	-0.10	-0.63	0.54701513	0.8499	-6.45
267250_at	similar to hookless1 (HLS1)	---	AT2G23060	-1.05	-0.06	-0.63	0.54724795	0.8502	-6.45
253704_at	X-Pro dipeptidase - like protein (fr	---	AT4G29490	-1.05	-0.08	-0.63	0.54738359	0.8503	-6.45
266665_at	unknown protein	---	AT2G29790	-1.06	-0.08	-0.63	0.54751801	0.8503	-6.45
263123_at	beta-Amyrin Synthase, putative si	---	AT1G78500	1.05	0.07	0.63	0.54739347	0.8503	-6.45
257037_at	nuclear acid binding protein, putat	ATRBP47B	AT3G19130	1.10	0.14	0.63	0.5475329	0.8503	-6.45
250253_at	putative protein contains similarity	PDAT	AT5G13640	-1.06	-0.08	-0.63	0.54750217	0.8503	-6.45
247661_at	protein kinase - like protein kinase	---	AT5G60080	-1.05	-0.06	-0.63	0.54751681	0.8503	-6.45
258870_at	putative NADP-dependent oxidore	---	AT3G03080	1.05	0.08	0.63	0.54775325	0.8506	-6.45
264773_at	putative disease resistance respon	---	AT1G22900	-1.15	-0.21	-0.63	0.54828425	0.8506	-6.45
267406_at	unknown protein	MEE22	AT2G34780	1.06	0.09	0.63	0.54837349	0.8506	-6.45
245745_at	unknown protein contains similarity	---	AT1G51110	-1.08	-0.11	-0.63	0.54840855	0.8506	-6.45
261854_at	unknown protein	---	AT1G50670	-1.04	-0.06	-0.63	0.54825339	0.8506	-6.45
251124_s_at	laccase -like protein lac110 laccas	LAC8	AT5G01040 /	-1.27	-0.35	-0.63	0.54798665	0.8506	-6.45
262712_at	mercaptopyruvate sulfurtransferas	ATRDH2	AT1G16460	-1.06	-0.08	-0.63	0.54844869	0.8506	-6.45
264987_at	unknown protein ; supported by cD	---	AT1G27030	-1.12	-0.16	-0.63	0.54811863	0.8506	-6.45
246484_at	UVB-resistance protein-like UVB-r	---	AT5G16040	-1.06	-0.08	-0.63	0.5485127	0.8506	-6.45
253868_at	proton pump interactor non-conser	PPI1	AT4G27500	-1.06	-0.08	-0.63	0.54800931	0.8506	-6.45

261557_at	kinesin-like protein C-terminal regi	---	AT1G63640	-1.07	-0.10	-0.63	0.54848666	0.8506	-6.45
259897_at	putative beta-glucanase similar to	ATCEL3	AT1G71380	-1.05	-0.07	-0.63	0.54821019	0.8506	-6.45
249566_at	cytochrome P450-like protein	CYP735A1	AT5G38450	-1.05	-0.07	-0.63	0.54840651	0.8506	-6.45
267554_at	E2, ubiquitin-conjugating enzyme,	---	AT2G32790	-1.06	-0.09	-0.63	0.5481049	0.8506	-6.45
267384_at	unknown protein highly similar to C	---	AT2G44370	1.21	0.28	0.63	0.548218	0.8506	-6.45
267242_at	hypothetical protein predicted by g	---	AT2G02670	1.05	0.07	0.63	0.54836389	0.8506	-6.45
259301_at	hypothetical protein predicted by g	---	AT3G05110	-1.07	-0.10	-0.63	0.5481567	0.8506	-6.45
254459_at	gibberellin 20-oxidase - like protei	GA2OX8	AT4G21200	1.04	0.06	0.63	0.54818199	0.8506	-6.45
248169_at	ankyrin-repeat-containing protein-l	ANK	AT5G54610	1.38	0.47	0.63	0.54824641	0.8506	-6.45
266123_at	unknown protein identical to GB:A	---	AT2G45180	1.04	0.06	0.63	0.54848305	0.8506	-6.45
254200_at	putative protein predicted proteins	---	AT4G24110	1.26	0.33	0.63	0.54787108	0.8506	-6.45
266287_at	putative tropinone reductase	---	AT2G29150	-1.06	-0.09	-0.63	0.54873794	0.8509	-6.45
256902_s_at	HAPp48,5 protein identical to HAF	---	AT3G23910 /	1.08	0.11	0.63	0.54882699	0.8510	-6.45
261204_s_at	Eukaryotic peptide chain release fa	ERF1-2	AT1G12920 /	1.04	0.06	0.63	0.54893041	0.8510	-6.45
248560_at	putative protein contains similarity	ATPPOX	AT5G49970	1.07	0.09	0.63	0.54890367	0.8510	-6.45
263787_at	unknown protein ; supported by cl	---	AT2G46420	1.08	0.11	0.63	0.54903983	0.8511	-6.45
266225_at	putative membrane channel protei	ATOEP16-1	AT2G28900	1.13	0.18	0.63	0.54963892	0.8511	-6.45
248405_at	putative protein pectinesterase-like	SKS2	AT5G51480	-1.27	-0.35	-0.63	0.5496371	0.8511	-6.45
259411_at	hypothetical protein contains Pfam	---	AT1G13410	1.05	0.07	0.63	0.54956567	0.8511	-6.45
265141_at	hypothetical protein predicted by g	---	AT1G51350	-1.05	-0.07	-0.63	0.54943438	0.8511	-6.45
264882_at	NAM protein, putative similar to N	anac025	AT1G61110	-1.05	-0.07	-0.63	0.54912397	0.8511	-6.45
251649_at	Ca2+-transporting ATPase-like pr	ACA11	AT3G57330	1.09	0.12	0.63	0.54918891	0.8511	-6.45
255271_at	putative protein (ubiquitin like) to v	---	AT4G05260	-1.06	-0.08	-0.63	0.54928706	0.8511	-6.45
265794_at	unknown protein	---	AT2G01310	-1.04	-0.06	-0.63	0.54923197	0.8511	-6.45
247463_at	embryo-specific protein - like emb	---	AT5G62210	1.06	0.08	0.63	0.5491177	0.8511	-6.45
245964_at	putative protein C-terminus of glut	---	AT5G19720	1.06	0.08	0.63	0.54951098	0.8511	-6.45
247331_at	putative protein contains similarity	FP3	AT5G63530	-1.11	-0.14	-0.63	0.54946435	0.8511	-6.45
255589_s_at	hypothetical protein	---	AT4G01590 /	1.08	0.11	0.63	0.54963831	0.8511	-6.45
258464_at	kinesin-like protein similar to KLP2	POK1	AT3G17360	1.04	0.06	0.63	0.54947078	0.8511	-6.45
262541_at	hypothetical protein contains simila	---	---	-1.04	-0.06	-0.63	0.54961595	0.8511	-6.45
251909_at	putative protein initiator-binding pr	TRFL4	AT3G53790	-1.06	-0.08	-0.63	0.5493161	0.8511	-6.45
260977_at	hypothetical protein predicted by g	---	AT1G53420	-1.05	-0.07	-0.63	0.5495648	0.8511	-6.45
245237_at	putative protein similarity to ALR -	SLK1	AT4G25520	-1.05	-0.07	-0.63	0.54975123	0.8511	-6.45
246054_at	putative protein predicted proteins	---	AT5G08360	1.05	0.07	0.63	0.54968218	0.8511	-6.45
256174_at	NADP-specific glutatamate dehyd	---	AT1G51720	-1.05	-0.07	-0.63	0.54974234	0.8511	-6.45

264784_s_at	unknown protein similar to Arabido	---	AT2G17830 /	1.05	0.08	0.63	0.54979283	0.8511	-6.45
266878_at	putative RING zinc finger protein	---	AT2G44580	-1.05	-0.07	-0.63	0.54991467	0.8513	-6.45
246446_at	putative protein hypothetical prote	---	AT5G17640	1.07	0.09	0.63	0.55003172	0.8513	-6.46
258810_at	hypothetical protein similar to hypo	---	AT3G03970	-1.06	-0.08	-0.63	0.55001166	0.8513	-6.46
248496_at	MtN3-like protein ;supported by fu	---	AT5G50790	-1.06	-0.09	-0.63	0.55011326	0.8513	-6.46
258677_at	putative ribosomal-protein S6 kina	PK1	AT3G08730	-1.06	-0.08	-0.63	0.55018452	0.8513	-6.46
257287_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.63	0.55008521	0.8513	-6.46
257850_at	putative protein kinase leucine-rich	SRF4	AT3G13065	-1.05	-0.07	-0.63	0.55021676	0.8513	-6.46
264892_at	GH3-like auxin-regulated protein h	---	AT1G23160	1.05	0.07	0.63	0.5502032	0.8513	-6.46
248455_at	unknown protein	---	AT5G51360	1.04	0.06	0.63	0.55007688	0.8513	-6.46
256502_at	Eukaryotic translation initiation fac	---	AT1G36730 /	-1.07	-0.10	-0.63	0.55041322	0.8515	-6.46
253290_at	putative protein predicted protein l	---	AT4G34330	1.05	0.07	0.63	0.55045273	0.8515	-6.46
244921_s_at	hypothetical protein	---	AT2G07674 /	-1.08	-0.11	-0.63	0.55051477	0.8516	-6.46
252331_s_at	serine palmitoyltransferase-like pro	SPT1	AT3G48780 /	1.06	0.08	0.63	0.55072651	0.8516	-6.46
256157_at	longevity assurance protein, putat	LAG13	AT1G13580	1.07	0.10	0.63	0.55065002	0.8516	-6.46
264933_at	hypothetical protein predicted by g	---	AT1G61160	1.06	0.08	0.63	0.55069522	0.8516	-6.46
248834_at	unknown protein ;supported by ful	---	AT5G47090	-1.05	-0.07	-0.63	0.550553	0.8516	-6.46
245845_at	Pto kinase interactor, putative sim	PERK10	AT1G26150	-1.05	-0.07	-0.63	0.55071932	0.8516	-6.46
255156_at	putative athila transposon protein	---	---	-1.04	-0.05	-0.63	0.55062117	0.8516	-6.46
245227_s_at	gunknown protein contains non-co	---	AT1G08410	-1.08	-0.11	-0.63	0.55090939	0.8516	-6.46
252828_at	DnaJ - like protein DnaJ-like prote	---	AT4G39960	-1.06	-0.08	-0.63	0.55089895	0.8516	-6.46
246917_at	serine-rich protein ;supported by f	---	AT5G25280	1.10	0.14	0.63	0.55085983	0.8516	-6.46
254365_at	putative protein hypothetical prote	---	AT4G22030	-1.05	-0.07	-0.63	0.55081373	0.8516	-6.46
250767_at	putative protein contains similarity	ATNFXL2	AT5G05660	-1.04	-0.06	-0.63	0.55099462	0.8516	-6.46
249782_at	dipeptidyl peptidase IV-like protein	---	AT5G24260	1.05	0.07	0.63	0.55104932	0.8516	-6.46
254525_at	putative protein predicted protein,	---	AT4G19580	-1.06	-0.08	-0.63	0.55103919	0.8516	-6.46
247715_at	putative protein predicted protein,	---	AT5G59360	1.08	0.11	0.63	0.55116011	0.8516	-6.46
246024_at	putative protein predicted protein -	---	AT5G21130	-1.06	-0.09	-0.63	0.55112447	0.8516	-6.46
267528_at	MADS-box protein (AGL6) ; suppo	AGL6	AT2G45650	-1.05	-0.07	-0.63	0.55119849	0.8516	-6.46
251231_at	Glutathione transferase III-like pro	ATGSTF13	AT3G62760	1.05	0.07	0.63	0.55127349	0.8516	-6.46
247539_at	putative protein predicted protein,	---	AT5G61710	1.04	0.06	0.63	0.55124273	0.8516	-6.46
262694_at	unknown protein	---	AT1G62790	-1.11	-0.16	-0.63	0.55121161	0.8516	-6.46
264941_at	auxin-induced protein, putative sir	---	AT1G60680	-1.09	-0.13	-0.63	0.55132643	0.8517	-6.46
256080_at	high mobility group protein (HMG1	---	AT1G20690	1.04	0.06	0.63	0.55147057	0.8518	-6.46
248262_at	Avr9 elicitor response protein-like	---	AT5G53340	1.07	0.10	0.63	0.5515376	0.8519	-6.46

248794_at	ethylene responsive element bindi	ERF2	AT5G47220	1.27	0.35	0.63	0.55166839	0.8519	-6.46
255953_at	transcription factor identical to tran	TGA3	AT1G22070	-1.07	-0.10	-0.63	0.55173726	0.8519	-6.46
258849_at	putative UDP-glucose pyrophosph	UGP	AT3G03250	-1.07	-0.09	-0.63	0.55174086	0.8519	-6.46
266289_at	putative C-4 sterol methyl oxidase	SMO2-2	AT2G29390	-1.05	-0.07	-0.63	0.55176307	0.8519	-6.46
264489_at	putative squamosa-promoter bindi	---	AT1G27370	1.11	0.15	0.63	0.55170262	0.8519	-6.46
253975_at	putative protein proliferating-cell n	---	AT4G26600	-1.12	-0.17	-0.63	0.5520037	0.8521	-6.46
248739_at	DnaJ protein-like ;supported by fu	GFA2	AT5G48030	-1.05	-0.06	-0.63	0.55193512	0.8521	-6.46
250418_at	putative protein predicted proteins	---	AT5G11240	-1.10	-0.14	-0.63	0.55199587	0.8521	-6.46
252374_at	response reactor 2 (ATRR2) ; sup	ARR5	AT3G48100	-1.09	-0.13	-0.63	0.55252474	0.8522	-6.46
261745_at	unknown protein identical to unkno	---	AT1G08500	-1.14	-0.18	-0.63	0.5524927	0.8522	-6.46
254082_at	glutamine cyclotransferase precur	QC	AT4G25720	1.11	0.15	0.63	0.55227247	0.8522	-6.46
261946_at	unknown protein	---	AT1G64560	-1.06	-0.09	-0.63	0.55251828	0.8522	-6.46
258028_at	hypothetical protein	---	AT3G27473	-1.04	-0.05	-0.63	0.55232975	0.8522	-6.46
266145_at	putative TNP2-like transposon prot	---	---	1.04	0.06	0.63	0.55251639	0.8522	-6.46
260803_at	glutathione transferase, putative s	ATGSTU22	AT1G78340	1.05	0.07	0.63	0.55241696	0.8522	-6.46
253658_at	cadmium-transporting ATPase-like	HMA3	AT4G30120	-1.05	-0.06	-0.63	0.55212723	0.8522	-6.46
257285_at	unknown protein	---	AT3G29760	-1.07	-0.10	-0.63	0.55214325	0.8522	-6.46
261275_at	Mlo protein, putative similar to GB	MLO14	AT1G26700	1.04	0.06	0.63	0.55238571	0.8522	-6.46
248821_at	protein serine threonine kinase-like	---	AT5G47070	1.12	0.16	0.63	0.55241122	0.8522	-6.46
249187_at	cysteine proteinase RD21A simila	---	AT5G43060	1.13	0.18	0.63	0.55248473	0.8522	-6.46
245030_at	putative polygalacturonase	---	AT2G26620	-1.04	-0.05	-0.63	0.55243784	0.8522	-6.46
251423_at	regulatory protein - like regulatory	CYCP3;2	AT3G60550	-1.06	-0.09	-0.62	0.55265062	0.8523	-6.46
254858_at	putative protein other predicted pr	---	AT4G12070	1.05	0.07	0.62	0.55277237	0.8525	-6.46
262451_at	receptor-associated kinase isolog	SUB	AT1G11130	1.09	0.13	0.62	0.55281325	0.8525	-6.46
254322_at	hypothetical protein	---	AT4G22600	-1.08	-0.11	-0.62	0.55295484	0.8526	-6.46
245693_at	thioredoxin - like protein	WCRKC2	AT5G04260	1.06	0.08	0.62	0.55309933	0.8528	-6.46
254753_at	putative protein Pto kinase interac	---	AT4G13190	1.04	0.06	0.62	0.55334162	0.8528	-6.46
250070_at	phosphoribosylanthranilate transfe	---	AT5G17980	-1.09	-0.13	-0.62	0.55334883	0.8528	-6.46
261372_at	zinc finger protein, putative similar	---	AT1G53010	-1.06	-0.08	-0.62	0.55328859	0.8528	-6.46
258400_at	unknown protein ; supported by cl	---	AT3G15470	-1.07	-0.09	-0.62	0.55321631	0.8528	-6.46
261815_at	leucine zipper protein, putative sin	---	AT1G08320	-1.07	-0.09	-0.62	0.55318309	0.8528	-6.46
263796_at	unknown protein ;supported by ful	AFR	AT2G24540	-1.09	-0.12	-0.62	0.55334813	0.8528	-6.46
258116_at	hypothetical protein similar to terpe	---	AT3G14520	-1.06	-0.09	-0.62	0.55335684	0.8528	-6.46
245493_at	hypothetical protein	---	---	1.04	0.06	0.62	0.55338045	0.8528	-6.46
258904_at	putative ATPase (ISW2-like) simil	CHR11	AT3G06400	-1.06	-0.08	-0.62	0.55352407	0.8529	-6.46

260680_s_at	GATA transcription factor 3, putati	---	AT1G08000 /	1.04	0.06	0.62	0.55355952	0.8529	-6.46
250317_at	tubulin beta-6 chain (sp|P29514) ;	TUB6	AT5G12250	-1.16	-0.21	-0.62	0.55350702	0.8529	-6.46
251666_at	CYSTATHIONINE BETA-LYASE F	CBL	AT3G57050	1.07	0.09	0.62	0.55382462	0.8530	-6.46
251462_at	mitogen-activated protein kinase-l	ATMPK10	AT3G59790	-1.06	-0.09	-0.62	0.55382523	0.8530	-6.46
246946_at	putative protein	---	AT5G25070	-1.04	-0.06	-0.62	0.55377516	0.8530	-6.46
257565_at	hypothetical protein predicted by g	---	AT3G28620	-1.04	-0.06	-0.62	0.55385555	0.8530	-6.46
248828_at	Lil3 protein	---	AT5G47110	1.04	0.06	0.62	0.55376853	0.8530	-6.46
263999_at	hypothetical protein predicted by g	---	AT2G22370	-1.06	-0.08	-0.62	0.55378859	0.8530	-6.46
264479_at	hypothetical protein similar to rece	---	AT1G77280	-1.06	-0.08	-0.62	0.55449178	0.8531	-6.46
251786_at	phosphatase - like protein DUAL S	MKP1	AT3G55270	-1.05	-0.06	-0.62	0.55459261	0.8531	-6.46
246882_at	putative protein predicted proteins	---	AT5G26180	-1.04	-0.06	-0.62	0.55433146	0.8531	-6.46
258217_at	unknown protein contains Pfam pr	XPL1	AT3G17998 /	1.09	0.12	0.62	0.55455122	0.8531	-6.46
255718_at	unknown protein ;supported by full	ATNSI	AT1G32070	1.05	0.07	0.62	0.55421885	0.8531	-6.46
262710_at	unknown protein ESTs gb|T04357	---	AT1G16210	-1.04	-0.06	-0.62	0.55439695	0.8531	-6.46
246119_at	ankyrin-repeat protein patsas prot	TIP1	AT5G20350	1.06	0.08	0.62	0.55431243	0.8531	-6.46
258896_at	putative syntaxin protein, AtSNAP	SYP43	AT3G05710	-1.05	-0.08	-0.62	0.55436028	0.8531	-6.46
246956_at	unknown protein ; supported by cl	RTM2	AT5G04890	-1.05	-0.07	-0.62	0.55421468	0.8531	-6.46
249830_at	dihydroorotate dehydrogenase pre	PYRD	AT5G23300	-1.10	-0.14	-0.62	0.55445901	0.8531	-6.46
263350_at	alanine-glyoxylate aminotransferas	AGT	AT2G13360	1.08	0.11	0.62	0.55458739	0.8531	-6.46
249791_at	amino acid transporter ; supporte	AAP7	AT5G23810	1.08	0.12	0.62	0.55436682	0.8531	-6.46
245053_at	putative pectinesterase	---	AT2G26450	-1.07	-0.10	-0.62	0.55439654	0.8531	-6.46
246902_at	putative protein	---	AT5G25640	1.04	0.06	0.62	0.55400156	0.8531	-6.46
264220_at	unknown protein similar to putative	ARPC3	AT1G60430	1.05	0.07	0.62	0.55420925	0.8531	-6.46
250547_at	asparaginase ; supported by cDN	---	AT5G08100	-1.05	-0.07	-0.62	0.55436349	0.8531	-6.46
264117_at	hypothetical protein predicted by g	---	AT2G31210	1.04	0.06	0.62	0.55406078	0.8531	-6.46
246062_at	putative protein VAC8 protein, Sa	---	AT5G19330	1.05	0.07	0.62	0.55450163	0.8531	-6.46
257219_at	uroporphyrinogen decarboxylase,	HEME1	AT3G14930	1.07	0.10	0.62	0.5549492	0.8531	-6.46
258470_at	Expressed protein ; supported by f	---	AT3G06035	-1.28	-0.36	-0.62	0.55491013	0.8531	-6.46
256909_at	hypothetical protein predicted by g	---	AT3G24060	-1.06	-0.09	-0.62	0.55487083	0.8531	-6.46
264785_at	putative non-LTR retroelement rev	---	---	-1.05	-0.07	-0.62	0.55482807	0.8531	-6.46
260172_s_at	putative histidinol-phosphate amin	---	AT1G71920 /	1.07	0.10	0.62	0.55481368	0.8531	-6.46
253100_at	cytochrome P450 monooxygenas	CYP81F3	AT4G37400	-1.17	-0.23	-0.62	0.55501219	0.8531	-6.46
265668_at	putative alanine acetyl transferase	---	AT2G32020	-1.20	-0.26	-0.62	0.55501701	0.8531	-6.46
257852_at	unknown protein	---	AT3G12950	-1.06	-0.09	-0.62	0.55470556	0.8531	-6.46
255684_at	putative glycosylasparaginase	---	AT4G00590	-1.08	-0.11	-0.62	0.55487478	0.8531	-6.46

260911_at	hypothetical protein predicted by g	---	AT1G02490	1.05	0.07	0.62	0.55478941	0.8531	-6.46
255592_s_at	hypothetical protein	---	AT2G34280	-1.06	-0.08	-0.62	0.55495477	0.8531	-6.46
263056_at	Mutator-like transposase similar to	---	---	-1.04	-0.06	-0.62	0.55507412	0.8531	-6.46
248510_at	Expressed protein ; supported by f	---	---	1.04	0.06	0.62	0.55531303	0.8532	-6.46
261920_at	isocitrate dehydrogenase, putative	---	AT1G65930	1.05	0.08	0.62	0.55533022	0.8532	-6.46
246638_at	putative protein predicted proteins	---	---	-1.05	-0.07	-0.62	0.55524276	0.8532	-6.46
256523_at	unknown protein ;supported by full	---	AT1G66070	-1.06	-0.08	-0.62	0.55547189	0.8532	-6.46
250643_at	putative protein similar to unknown	---	AT5G06780	-1.04	-0.06	-0.62	0.55541322	0.8532	-6.46
255320_at	putative transposon protein	---	---	-1.04	-0.06	-0.62	0.55525371	0.8532	-6.46
267330_at	unknown protein	---	AT2G19270	-1.04	-0.05	-0.62	0.55528955	0.8532	-6.46
252150_at	vacuolar sorting protein 35 homol	VPS35C	AT3G51310	-1.04	-0.06	-0.62	0.55513687	0.8532	-6.46
261295_at	unknown protein	---	AT1G48450	1.04	0.06	0.62	0.55544653	0.8532	-6.46
248602_s_at	MADS-box protein-like	---	AT5G38620	-1.04	-0.06	-0.62	0.5554337	0.8532	-6.46
264976_at	peptide transporter, putative simila	NRT1.6	AT1G27080	1.06	0.08	0.62	0.55557978	0.8532	-6.46
252124_at	hypothetical protein ;supported by	---	AT3G51010	1.06	0.09	0.62	0.55556491	0.8532	-6.46
263025_at	reverse transcriptase, putative sim	---	---	1.05	0.07	0.62	0.55570638	0.8534	-6.46
254903_at	H+-transporting ATPase chain E,	TUF	AT4G11150	-1.06	-0.08	-0.62	0.55578603	0.8534	-6.46
254871_at	Srw1 -like protein WD repeat prote	CCS52A2	AT4G11920	1.04	0.06	0.62	0.55584042	0.8534	-6.46
263581_at	hypothetical protein identical to hy	---	AT2G17160	-1.06	-0.08	-0.62	0.55594001	0.8535	-6.46
248061_at	putative protein contains similarity	---	AT5G55340	-1.04	-0.06	-0.62	0.55610864	0.8537	-6.46
265277_at	unknown protein ;supported by ful	---	AT2G28410	-1.15	-0.20	-0.62	0.55609513	0.8537	-6.46
262060_at	polygalacturonase, putative simila	---	AT1G80170	-1.05	-0.07	-0.62	0.55623605	0.8538	-6.46
253819_at	receptor protein kinase like protein	---	AT4G28350	-1.29	-0.37	-0.62	0.55621736	0.8538	-6.46
249692_s_at	putative protein strong similarity to	---	AT5G36670	-1.06	-0.08	-0.62	0.55632653	0.8538	-6.46
246864_at	cytochrome P450 GA3 ; supported	GA3	AT5G25900	-1.10	-0.14	-0.62	0.55641321	0.8539	-6.46
253258_at	putative protein NF-180, Petromyz	---	AT4G34400	-1.06	-0.08	-0.62	0.55646854	0.8539	-6.46
263327_at	putative receptor-like protein kinas	---	AT2G15300	-1.04	-0.06	-0.62	0.55649228	0.8539	-6.46
260990_at	hypothetical protein predicted by g	---	AT1G12180	-1.07	-0.09	-0.62	0.55650613	0.8539	-6.46
259308_at	putative nodulin similar to nodulin	---	AT3G05180	-1.09	-0.13	-0.62	0.55659805	0.8540	-6.46
251961_at	inorganic pyrophosphatase -like p	AtPPa4	AT3G53620	-1.10	-0.13	-0.62	0.55694532	0.8543	-6.46
245637_at	hypothetical protein similar to puta	---	AT1G25230	-1.16	-0.21	-0.62	0.55699417	0.8543	-6.46
249220_at	putative protein strong similarity to	---	AT5G42420	1.06	0.08	0.62	0.5569637	0.8543	-6.46
267185_at	unknown protein ; supported by cl	OEP37	AT2G43950	1.06	0.08	0.62	0.55695511	0.8543	-6.46
265698_at	hypothetical protein predicted by g	---	AT2G32160	1.05	0.07	0.62	0.55692885	0.8543	-6.46
259613_at	hypothetical protein predicted by g	---	AT1G48010	-1.04	-0.06	-0.62	0.55705275	0.8543	-6.46

257948_at	hypothetical protein predicted by g	APO4	AT3G21740	1.05	0.08	0.62	0.55713948	0.8543	-6.46
245787_at	unknown protein	---	AT1G32130	1.05	0.08	0.62	0.55717756	0.8543	-6.46
254320_at	putative protein various predicted	---	AT4G22580	1.04	0.06	0.62	0.55710127	0.8543	-6.46
258572_at	hypothetical protein	---	AT3G04270	1.04	0.06	0.62	0.5572615	0.8543	-6.46
246848_at	putative protein	---	AT5G26840	-1.05	-0.07	-0.62	0.55721474	0.8543	-6.46
246540_at	nitrilase associated protein-like nit	SP1L4	AT5G15600	1.07	0.10	0.62	0.55727811	0.8543	-6.46
263404_s_at	hypothetical protein similar to hypo	---	AT2G04090	-1.18	-0.23	-0.62	0.55741875	0.8544	-6.46
254120_at	putative mitochondrial uncoupling	DIC2	AT4G24570	1.41	0.50	0.62	0.55736966	0.8544	-6.46
266966_at	hypothetical protein predicted by g	---	AT2G39520	-1.04	-0.05	-0.62	0.55738197	0.8544	-6.46
266968_at	putative protein kinase contains a	---	AT2G39360	-1.12	-0.17	-0.62	0.55751497	0.8544	-6.46
264392_at	hypothetical protein Similar to salt-	---	AT1G11900	1.06	0.09	0.62	0.55749486	0.8544	-6.46
260346_at	hypothetical protein predicted by g	CLE10	AT1G69320	-1.06	-0.08	-0.62	0.55759358	0.8545	-6.46
245815_at	unknown protein	---	AT1G26090	-1.06	-0.08	-0.62	0.55763802	0.8545	-6.46
246843_at	putative protein various predicted	---	AT5G26740	-1.05	-0.07	-0.62	0.55776084	0.8546	-6.46
260908_at	maternal embryogenesis control p	MEA	AT1G02580	-1.10	-0.13	-0.62	0.55780412	0.8546	-6.46
258691_at	unknown protein	---	AT3G08630	-1.14	-0.19	-0.62	0.55790809	0.8547	-6.46
263221_at	UDP-galactose 4-epimerase-like p	MUR4	AT1G30620	-1.16	-0.22	-0.62	0.55794275	0.8547	-6.46
251369_at	putative protein ;supported by full-	---	AT3G60480	1.06	0.08	0.62	0.55804937	0.8548	-6.46
250945_at	putative protein	---	AT5G03400	-1.05	-0.07	-0.62	0.5580697	0.8548	-6.46
254615_at	RNase L inhibitor-like protein RNa	RLI2	AT4G19210	1.05	0.07	0.62	0.55837061	0.8550	-6.46
250166_at	putative protein many predicted pr	---	AT5G15300	-1.05	-0.07	-0.62	0.55836851	0.8550	-6.46
267104_at	ERD15 protein identical to GB D30	ERD15	AT2G41430	-1.06	-0.08	-0.62	0.55822817	0.8550	-6.46
263244_at	hypothetical protein predicted by g	---	AT2G31480	-1.05	-0.07	-0.62	0.55826611	0.8550	-6.46
259262_at	unknown protein similar to nifU-like	ISU2	AT3G01020	-1.04	-0.06	-0.62	0.55835657	0.8550	-6.46
264750_at	hypothetical protein predicted by g	---	AT1G22870	-1.04	-0.06	-0.62	0.55844814	0.8550	-6.46
258277_at	putative cytochrome P450 similar t	PAD3	AT3G26830	-1.43	-0.52	-0.62	0.55851705	0.8551	-6.46
263824_at	putative WD-40 repeat protein	---	AT2G40360	1.09	0.13	0.62	0.55855309	0.8551	-6.46
264058_at	F-box protein family, AtFBX7 cont	---	AT2G03560	-1.05	-0.06	-0.62	0.5586441	0.8551	-6.46
263955_at	putative E2F5 family transcription f	E2F3	AT2G36010	-1.08	-0.11	-0.62	0.5586503	0.8551	-6.46
265844_at	putative receptor-like protein kinas	FEI2	AT2G35620	1.07	0.10	0.62	0.55875108	0.8552	-6.46
260099_at	unknown protein ;supported by ful	---	AT1G73180	-1.04	-0.06	-0.61	0.55884546	0.8553	-6.46
252605_s_at	sulfotransferase-like protein FLAV	---	AT3G45070	-1.04	-0.06	-0.61	0.5588897	0.8553	-6.46
262953_at	hypothetical protein predicted by g	---	AT1G75670	1.09	0.12	0.61	0.55920509	0.8554	-6.46
265440_at	pEARLI 4 protein Same as GB: L4	pEARLI4	AT2G20960	1.09	0.13	0.61	0.55920081	0.8554	-6.46
250886_at	putative protein	---	AT5G04440	1.06	0.08	0.61	0.5591462	0.8554	-6.46

257617_at	hypothetical protein	---	AT3G26550	1.05	0.07	0.61	0.55923997	0.8554	-6.46
251158_at	rac-GTP binding protein -like RAC	MIRO2	AT3G63150	-1.05	-0.07	-0.61	0.55918108	0.8554	-6.46
267631_at	hypothetical protein predicted by g	---	AT2G42150	-1.05	-0.06	-0.61	0.5591169	0.8554	-6.46
254022_at	putative membrane transporter Ba	---	AT4G25750	-1.06	-0.08	-0.61	0.55903051	0.8554	-6.46
259017_at	unknown protein ; supported by fu	---	AT3G07310	-1.05	-0.07	-0.61	0.55929405	0.8555	-6.46
257547_at	hypothetical protein predicted by g	---	AT3G13000	1.14	0.19	0.61	0.55953055	0.8555	-6.47
261389_s_at	hypothetical protein identical to hy	---	---	-1.04	-0.06	-0.61	0.55935841	0.8555	-6.47
251122_at	protein kinase -like protein serine/	---	AT5G01020	1.07	0.10	0.61	0.5594257	0.8555	-6.47
248595_at	drought-induced protein Di19-like p	HRB1	AT5G49230	1.05	0.07	0.61	0.55952056	0.8555	-6.47
254516_at	putative protein	---	AT4G20290	1.06	0.08	0.61	0.55953361	0.8555	-6.47
246222_at	TINY-like protein ; supported by c	RAP2.10	AT4G36900	1.11	0.15	0.61	0.55945431	0.8555	-6.47
247031_at	UDP-glucuronyltransferase-like pr	---	AT5G67230	-1.07	-0.10	-0.61	0.55958965	0.8555	-6.47
254266_at	protein kinase - like protein serine	CRK5	AT4G23130	1.17	0.22	0.61	0.55972851	0.8556	-6.47
258451_at	alternative oxidase 1b precursor id	AOX1B	AT3G22360	-1.06	-0.08	-0.61	0.5597408	0.8556	-6.47
252268_at	kinesin-like protein several kinesin	---	AT3G49650	1.07	0.10	0.61	0.55989312	0.8558	-6.47
246881_at	putative protein histone deacetyla	HDA2	AT5G26040	-1.08	-0.12	-0.61	0.55997122	0.8559	-6.47
262374_s_at	flax rust resistance protein, putativ	TIR	AT1G72910	1.19	0.25	0.61	0.56007301	0.8560	-6.47
252392_s_at	putative protein various predicted	---	AT3G47890	-1.07	-0.09	-0.61	0.56016025	0.8560	-6.47
248643_at	putative protein strong similarity to	---	AT5G49130	-1.05	-0.07	-0.61	0.56017914	0.8560	-6.47
259710_at	putative aminotransferase similar	---	AT1G77670	1.14	0.19	0.61	0.56028102	0.8561	-6.47
251205_at	glutathione peroxidase -like protei	ATGPX5	AT3G63080	1.06	0.09	0.61	0.56035261	0.8561	-6.47
245965_at	pectin methylesterase-like protein	---	AT5G19730	-1.09	-0.13	-0.61	0.56041511	0.8561	-6.47
252053_at	syntaxin-like protein synt4 ;suppor	SYP122	AT3G52400	1.17	0.23	0.61	0.56041534	0.8561	-6.47
258197_at	hypothetical protein predicted by g	ATBRXL2	AT3G14000	-1.06	-0.08	-0.61	0.56054368	0.8563	-6.47
267263_at	similar to late embryogenesis abur	---	AT2G23110	1.26	0.34	0.61	0.56070637	0.8565	-6.47
254226_at	putative disease resistance respo	---	AT4G23690	1.33	0.41	0.61	0.56078619	0.8565	-6.47
248059_at	putative protein similar to unknown	TRN1	AT5G55540	-1.10	-0.13	-0.61	0.56091945	0.8566	-6.47
265103_at	UDP-N-acetylglucosamine pyroph	---	AT1G31070	-1.06	-0.09	-0.61	0.56094706	0.8566	-6.47
246519_at	proline-rich protein other proline-ri	---	AT3G23750	-1.30	-0.38	-0.61	0.56088686	0.8566	-6.47
265062_at	receptor kinase, putative similar to	---	AT1G61550	-1.09	-0.12	-0.61	0.56095166	0.8566	-6.47
264400_at	glucose-6-phosphate/phosphate-t	GPT2	AT1G61800	1.33	0.41	0.61	0.56113245	0.8566	-6.47
266229_at	putative RING zinc finger ankyrin p	---	AT2G28840	1.05	0.06	0.61	0.56130625	0.8566	-6.47
260295_at	putative aminopeptidase similar to	---	AT1G63770	1.06	0.08	0.61	0.56129722	0.8566	-6.47
246910_at	exonuclease - like protein ribonuc	---	AT5G25800	1.08	0.11	0.61	0.56111813	0.8566	-6.47
266891_at	putative GTP-binding protein ; sup	ARAC9	AT2G44690	1.06	0.08	0.61	0.56126174	0.8566	-6.47

251869_at	putative protein	---	AT3G54500	-1.09	-0.12	-0.61	0.56123046	0.8566	-6.47
254136_at	putative protein various predicted	---	AT4G24860	1.05	0.07	0.61	0.56109426	0.8566	-6.47
256034_at	unknown protein ; supported by cD	---	AT1G07080	-1.04	-0.06	-0.61	0.56125487	0.8566	-6.47
262942_at	hypothetical protein similar to unkn	ALIS5	AT1G79450	1.13	0.18	0.61	0.56142048	0.8567	-6.47
253500_at	predicted protein RegA gene, Dict	ARR10	AT4G31920	1.08	0.11	0.61	0.56142146	0.8567	-6.47
262920_at	2-dehydro-3-deoxyphosphooctona	---	AT1G79500	-1.12	-0.16	-0.61	0.56149205	0.8567	-6.47
263713_at	Expressed protein ; supported by f	---	AT2G20595	1.06	0.08	0.61	0.56153613	0.8567	-6.47
255220_at	polyubiquitin (UBQ10) identical to (	UBQ10	AT4G05320	-1.06	-0.08	-0.61	0.5615635	0.8567	-6.47
262066_at	hypothetical protein contains simila	---	AT1G79950	1.10	0.13	0.61	0.5616781	0.8568	-6.47
246990_at	subtilisin-like serine protease ARA	ARA12	AT5G67360	-1.09	-0.12	-0.61	0.56168718	0.8568	-6.47
246368_at	light repressible receptor protein k	---	AT1G51890	-1.17	-0.22	-0.61	0.56201764	0.8570	-6.47
250109_at	GASA4 ; supported by cDNA: gi_9	GASA4	AT5G15230	1.33	0.41	0.61	0.56192113	0.8570	-6.47
250023_at	beta-1,3-glucanase-like protein	---	AT5G18220	-1.06	-0.08	-0.61	0.56188924	0.8570	-6.47
255307_at	hypothetical protein similar to A. th	RIC10	AT4G04900	-1.05	-0.08	-0.61	0.56203442	0.8570	-6.47
266685_at	hypothetical protein	---	AT2G19710	-1.05	-0.07	-0.61	0.56197779	0.8570	-6.47
265548_s_at	putative helicase	---	---	1.04	0.05	0.61	0.5618862	0.8570	-6.47
246656_at	hypothetical protein	---	---	-1.05	-0.08	-0.61	0.56195083	0.8570	-6.47
261613_at	abscisic acid responsive elements-	ABF1	AT1G49720	-1.08	-0.11	-0.61	0.56213542	0.8570	-6.47
250358_at	putative protein gibberellin-respon	AGP15	AT5G11740	-1.07	-0.09	-0.61	0.56226215	0.8571	-6.47
250134_at	Expressed protein ; supported by c	---	---	1.06	0.08	0.61	0.56226773	0.8571	-6.47
263006_at	hypothetical protein contains simila	---	AT1G54240	-1.05	-0.07	-0.61	0.56230825	0.8571	-6.47
250806_at	putative protein similar to unknown	---	AT5G05070	-1.05	-0.07	-0.61	0.56240888	0.8572	-6.47
262442_at	unknown protein identical to hypot	---	AT1G47420	1.04	0.06	0.61	0.56240646	0.8572	-6.47
265345_at	copia-like retroelement pol polypro	---	AT2G22680	-1.05	-0.07	-0.61	0.56247905	0.8572	-6.47
265710_at	unknown protein	---	AT2G03370	-1.04	-0.06	-0.61	0.56256727	0.8572	-6.47
264447_at	hypothetical protein predicted by g	---	AT1G27300	1.11	0.15	0.61	0.5625582	0.8572	-6.47
264171_at	hypothetical protein predicted by g	---	AT1G02100	-1.06	-0.08	-0.61	0.56278579	0.8574	-6.47
249430_at	GTP-binding protein-like GTP-bin	---	AT5G39900	-1.08	-0.11	-0.61	0.56277793	0.8574	-6.47
255897_at	mutator-like transposase, putative	---	---	-1.04	-0.05	-0.61	0.56271516	0.8574	-6.47
265904_at	putative beta-glucosidase	BGLU14	AT2G25630	1.05	0.07	0.61	0.5628496	0.8575	-6.47
263614_at	putative serpin	---	AT2G25240	-1.07	-0.09	-0.61	0.5629856	0.8576	-6.47
253008_at	expansin -like protein expansin (G	ATEXPA20	AT4G38210	1.07	0.10	0.61	0.56303057	0.8576	-6.47
247464_at	putative protein various predicted	IQD23	AT5G62070	-1.09	-0.12	-0.61	0.56329921	0.8577	-6.47
267055_at	unknown protein	PRA1.B4	AT2G38360	-1.14	-0.19	-0.61	0.56333704	0.8577	-6.47
266991_at	putative CDP-diacylglycerol--glyce	PGP1	AT2G39290	1.04	0.06	0.61	0.56334466	0.8577	-6.47

264452_at	unknown protein similar to salt-indu	GRP23	AT1G10270	-1.16	-0.21	-0.61	0.56320995	0.8577	-6.47
251755_at	putative protein predicted protein,	---	AT3G55790	-1.08	-0.11	-0.61	0.5632658	0.8577	-6.47
245737_at	hypothetical protein similar to putat	---	AT1G44160	1.08	0.10	0.61	0.56333094	0.8577	-6.47
253081_at	putative protein F35D11.3, Caeno	---	AT4G36210	1.06	0.09	0.61	0.56337417	0.8577	-6.47
246486_at	putative protein ;supported by full-	---	AT5G15910	-1.05	-0.07	-0.61	0.56316434	0.8577	-6.47
256499_at	unknown protein	---	AT1G36640	1.10	0.13	0.61	0.56347114	0.8578	-6.47
267469_at	unknown protein ; supported by cl	WRKY21	AT2G30590	1.05	0.08	0.61	0.56357103	0.8578	-6.47
257945_at	SKP1/ASK1 (At10), putative simila	ASK10	AT3G21860	1.05	0.07	0.61	0.56355456	0.8578	-6.47
265192_at	hypothetical protein predicted by g	---	AT1G05060	1.06	0.09	0.61	0.56365697	0.8579	-6.47
258808_at	putative pyruvate kinase similar to	---	AT3G04050	1.05	0.06	0.61	0.5637191	0.8579	-6.47
261798_at	hypothetical protein similar to hypo	CPSF30	AT1G30460	1.06	0.08	0.61	0.56382049	0.8580	-6.47
247946_at	putative protein similar to unknown	CIA2	AT5G57180	-1.14	-0.19	-0.61	0.56381417	0.8580	-6.47
264764_at	receptor kinase, putative similar to	---	AT1G61440	-1.04	-0.06	-0.61	0.56408895	0.8582	-6.47
259413_at	hypothetical protein contains simila	---	AT1G02320	1.05	0.07	0.61	0.56408272	0.8582	-6.47
263859_at	hypothetical protein predicted by g	---	AT2G04360	-1.08	-0.11	-0.61	0.56414471	0.8583	-6.47
253938_at	putative homeodomain protein hor	---	AT4G26920	-1.05	-0.08	-0.61	0.56432718	0.8584	-6.47
261341_s_at	putative purple acid phosphatase s	PAP5	AT1G52940 /	-1.04	-0.05	-0.61	0.56431499	0.8584	-6.47
249418_at	putative protein predicted protein,	---	AT5G39785	-1.04	-0.06	-0.61	0.56441847	0.8585	-6.47
253890_s_at	putative protein contains similarity	---	AT4G27585 /	-1.12	-0.17	-0.61	0.56448617	0.8586	-6.47
247043_at	protein kinase, 41K (EC 2.7.1.-) (p	SNRK2.3	AT5G66880	1.08	0.11	0.61	0.56463935	0.8586	-6.47
254568_x_at	hypothtetical protein	---	---	-1.06	-0.08	-0.61	0.56471733	0.8586	-6.47
252195_at	putative protein various predicted	---	AT3G50190	-1.06	-0.08	-0.61	0.56468794	0.8586	-6.47
266573_at	unknown protein	---	AT2G23860	-1.07	-0.09	-0.61	0.56463882	0.8586	-6.47
262971_at	receptor-like protein kinase, putati	---	AT1G75640	-1.07	-0.10	-0.61	0.56473129	0.8586	-6.47
267574_at	hypothetical protein predicted by g	---	AT2G30680	1.07	0.10	0.61	0.56461307	0.8586	-6.47
249761_at	acetyl-CoA:benzylalcohol acetyltra	---	AT5G23970	-1.06	-0.09	-0.61	0.5648054	0.8586	-6.47
249735_at	putative protein contains similarity	---	AT5G24450	1.06	0.09	0.61	0.56487043	0.8586	-6.47
249737_at	putative protein similar to unknown	---	AT5G24480	-1.05	-0.07	-0.61	0.56484894	0.8586	-6.47
246883_at	putative protein many predicted pr	---	AT5G26190	1.04	0.06	0.61	0.56499601	0.8587	-6.47
248599_at	putative protein contains similarity	---	AT5G49380	-1.08	-0.11	-0.61	0.56499326	0.8587	-6.47
265474_at	Expressed protein ; supported by c	---	AT2G15690	-1.09	-0.12	-0.60	0.56507552	0.8587	-6.47
263931_at	unknown protein ;supported by ful	---	AT2G36220	1.13	0.18	0.60	0.56506883	0.8587	-6.47
249475_at	putative protein CGI-108 protein, l	---	AT5G38890	-1.07	-0.09	-0.60	0.56514901	0.8588	-6.47
248763_at	putative protein similar to unknown	---	AT5G47550	1.42	0.50	0.60	0.56518782	0.8588	-6.47
253628_at	xyloglucan endo-1,4-beta-D-gluca	XTH18	AT4G30280	1.41	0.49	0.60	0.56524006	0.8588	-6.47

248863_at	zinc finger protein Glo3-like	AGD9	AT5G46750	-1.04	-0.06	-0.60	0.56528407	0.8588	-6.47
257961_at	unknown protein	---	AT3G19780	-1.05	-0.06	-0.60	0.5653228	0.8588	-6.47
259218_at	hypothetical protein similar to puta	---	AT3G03580	-1.05	-0.08	-0.60	0.56577933	0.8588	-6.47
246550_at	putative protein predicted protein,	---	AT5G14920	1.21	0.28	0.60	0.56568104	0.8588	-6.47
256317_at	hypothetical protein predicted by g	---	AT1G35900	-1.08	-0.11	-0.60	0.56573507	0.8588	-6.47
248129_at	putative protein contains similarity	---	AT5G54780	1.06	0.08	0.60	0.56579107	0.8588	-6.47
252238_at	peroxidase ATP21a	---	AT3G49960	1.05	0.07	0.60	0.56551497	0.8588	-6.47
262696_at	hypothetical protein	---	AT1G75870	-1.05	-0.07	-0.60	0.56577307	0.8588	-6.47
267546_at	putative disease resistance protein	AtRLP23	AT2G32680	1.27	0.34	0.60	0.56553758	0.8588	-6.47
255838_at	unknown protein	---	AT2G33490	-1.05	-0.07	-0.60	0.5656473	0.8588	-6.47
252309_at	cysteine protease contains similari	---	AT3G49340	-1.05	-0.07	-0.60	0.56566662	0.8588	-6.47
266619_at	similar to harpin-induced protein hi	---	AT2G35460	1.06	0.09	0.60	0.56546427	0.8588	-6.47
246851_at	putative protein various predicted	AGL26	AT5G26870	-1.04	-0.05	-0.60	0.56552298	0.8588	-6.47
267379_at	unknown protein ; supported by cl	---	AT2G26340	1.08	0.11	0.60	0.56567316	0.8588	-6.47
251550_at	putative protein proline-rich protei	---	AT3G58800	1.05	0.07	0.60	0.56592913	0.8590	-6.47
265177_at	OBP32pep protein, putative identi	---	AT1G23640	-1.04	-0.06	-0.60	0.56603676	0.8591	-6.47
248209_at	flavonol 3-O-glucosyltransferase-li	---	AT5G53990	-1.07	-0.09	-0.60	0.5660848	0.8591	-6.47
245678_at	unknown protein	---	AT1G56610	-1.07	-0.09	-0.60	0.56612814	0.8591	-6.47
257040_at	unknown protein ; supported by cl	SCO2	AT3G19220	-1.08	-0.11	-0.60	0.56636627	0.8594	-6.47
255648_at	coded for by A. thaliana cDNA T20	---	AT4G00910	1.04	0.06	0.60	0.56643251	0.8595	-6.47
263348_at	cytoplasmic aconitate hydratase	---	AT2G05710	1.07	0.10	0.60	0.56657211	0.8595	-6.47
AFFX-r2-At-GA	Arabidopsis thaliana /REF=M6411	---	---	1.13	0.18	0.60	0.56650231	0.8595	-6.47
258573_at	hypothetical protein contains Pfam	PTAC3	AT3G04260	1.04	0.06	0.60	0.56652518	0.8595	-6.47
264339_at	trehalose-6-phosphate synthase,	TPS8	AT1G70290	-1.08	-0.11	-0.60	0.56674743	0.8595	-6.47
258987_at	putative SCO1 protein similar to S	---	AT3G08950	-1.10	-0.14	-0.60	0.56661536	0.8595	-6.47
245514_at	OEP8 like protein	---	AT4G15810	-1.08	-0.11	-0.60	0.56673959	0.8595	-6.47
264213_at	hypothetical protein contains simila	ATPP2-A5	AT1G65390	-1.28	-0.36	-0.60	0.56665001	0.8595	-6.47
247656_at	actin depolymerizing factor 4 - like	ADF4	AT5G59890	1.06	0.09	0.60	0.56668066	0.8595	-6.47
256530_at	unknown protein	---	AT1G33290	1.05	0.07	0.60	0.56688046	0.8596	-6.47
253687_at	putative protein ;supported by full-	---	AT4G29520	1.25	0.32	0.60	0.56692973	0.8596	-6.47
248226_at	putative protein strong similarity to	---	AT5G53750	-1.16	-0.22	-0.60	0.56699692	0.8597	-6.47
247824_at	putative protein Na+/H+-exchangi	CHX25	AT5G58460	-1.06	-0.08	-0.60	0.56703691	0.8597	-6.47
266492_at	putative protein kinase contains a	---	AT2G07020	-1.05	-0.07	-0.60	0.56707502	0.8597	-6.47
255353_at	putative transposon protein similar	---	---	-1.04	-0.06	-0.60	0.56720767	0.8598	-6.47
266763_at	unknown protein	SPL1	AT2G47070	-1.06	-0.08	-0.60	0.56717987	0.8598	-6.47

250645_at	putative protein strong similarity to	---	AT5G06700	-1.09	-0.13	-0.60	0.56814955	0.8599	-6.47
253040_at	endo-xyloglucan transferase - like	---	AT4G37800	-1.18	-0.24	-0.60	0.56777563	0.8599	-6.47
262195_at	allergen, putative similar to allerge	---	AT1G78040	1.12	0.16	0.60	0.56782847	0.8599	-6.47
261247_at	hypothetical protein predicted by g	---	AT1G20070	-1.21	-0.27	-0.60	0.56784938	0.8599	-6.47
254079_at	putative protein pmt2 methyltranst	---	AT4G25730	1.10	0.13	0.60	0.56791919	0.8599	-6.47
245673_at	hypothetical protein similar to puta	---	AT1G56690	-1.06	-0.08	-0.60	0.56765809	0.8599	-6.47
251840_at	protein disulfide-isomerase-like pr	ATPDIL1-3	AT3G54960	1.10	0.14	0.60	0.56821002	0.8599	-6.47
245660_at	unknown protein	---	AT1G28240	1.08	0.11	0.60	0.56748308	0.8599	-6.47
264562_at	hypothetical protein predicted by g	---	AT1G55760	1.10	0.14	0.60	0.56782777	0.8599	-6.47
259368_at	aspartic protease, putative similar	---	AT1G69100	-1.05	-0.06	-0.60	0.56794241	0.8599	-6.47
247184_at	putative protein contains similarity	UBP17	AT5G65450	-1.06	-0.09	-0.60	0.56790372	0.8599	-6.47
248057_at	putative protein strong similarity to	---	AT5G55520	1.04	0.06	0.60	0.56750036	0.8599	-6.47
262133_at	high affinity sulphate transporter, p	SULTR1;2	AT1G78000	1.17	0.23	0.60	0.56766978	0.8599	-6.47
254967_at	putative protein various predicted	---	AT4G10410	1.05	0.07	0.60	0.56808286	0.8599	-6.47
258165_at	unknown protein ; supported by cI	---	AT3G17900	1.05	0.07	0.60	0.56811563	0.8599	-6.47
264936_at	hypothetical protein predicted by g	EDA16	AT1G61140	1.04	0.06	0.60	0.5678095	0.8599	-6.47
252637_at	WD repeat domain protein nuclea	HIRA	AT3G44530	1.06	0.08	0.60	0.56805551	0.8599	-6.47
248930_at	unknown protein	---	AT5G46010	-1.05	-0.07	-0.60	0.56812238	0.8599	-6.47
256200_at	hypothetical protein predicted by g	EMB1674	AT1G58210	-1.05	-0.07	-0.60	0.56823031	0.8599	-6.47
262332_at	hypothetical protein similar to puta	---	AT1G64030	1.05	0.07	0.60	0.56800393	0.8599	-6.47
259703_at	putative endo-1,3-beta-glucanase	---	AT1G77790	1.05	0.07	0.60	0.56787004	0.8599	-6.47
252839_at	putative protein PIF1 protein - Cae	---	---	-1.07	-0.10	-0.60	0.56752437	0.8599	-6.47
246077_at	putative protein XNP-1, Caenorha	CHR42	AT5G20420	-1.07	-0.10	-0.60	0.56808432	0.8599	-6.47
264665_at	unknown protein ESTs gb|H37208	---	AT1G09660	1.06	0.08	0.60	0.56822205	0.8599	-6.47
253316_s_at	putative protein hyphally regulated	---	AT4G33930 /	-1.08	-0.11	-0.60	0.56795864	0.8599	-6.47
247817_at	Expressed protein ; supported by f	---	AT5G58375	1.06	0.08	0.60	0.56893738	0.8599	-6.47
263656_at	putative auxin-induced protein AUX	SHY2	AT1G04240	-1.27	-0.35	-0.60	0.56881588	0.8599	-6.47
255561_at	putative hexose transporter similar	---	AT4G02050	1.08	0.11	0.60	0.56837238	0.8599	-6.47
260364_at	putative alliinase similar to aliinase	TAA1	AT1G70560	-1.07	-0.10	-0.60	0.5683238	0.8599	-6.47
254879_at	hypothetical protein	---	AT4G11670	1.05	0.07	0.60	0.56884628	0.8599	-6.47
251533_at	putative protein several hypothetic	ATRBL15	AT3G58460	1.04	0.06	0.60	0.56884804	0.8599	-6.47
265479_at	hypothetical protein ;supported by	---	AT2G15760	-1.24	-0.32	-0.60	0.56838857	0.8599	-6.47
250561_at	glycerophosphodiester phosphodi	---	AT5G08030	1.06	0.09	0.60	0.56885505	0.8599	-6.47
254618_at	cellulose synthase - like protein ce	IRX1	AT4G18780	1.09	0.12	0.60	0.56899154	0.8599	-6.48
248279_at	putative protein similar to unknown	ATIM	AT5G52910	1.11	0.15	0.60	0.56857795	0.8599	-6.47

247951_at	oxysterol-binding protein-like	ORP4C	AT5G57240	-1.05	-0.07	-0.60	0.56898621	0.8599	-6.48
257616_at	hypothetical protein contains Pfam	---	AT3G26540	-1.06	-0.09	-0.60	0.56864919	0.8599	-6.47
248383_at	putative protein contains similarity	---	AT5G51900	1.04	0.06	0.60	0.56876999	0.8599	-6.47
255024_at	hypothetical protein	---	AT4G09860	-1.04	-0.05	-0.60	0.56857788	0.8599	-6.47
256627_at	unknown protein ; supported by cl	---	AT3G19970	-1.22	-0.29	-0.60	0.5685378	0.8599	-6.47
266387_at	hypothetical protein predicted by g	---	AT2G32360	-1.05	-0.07	-0.60	0.56889931	0.8599	-6.47
262167_at	putative RING zinc finger protein c	---	AT1G74990	1.06	0.08	0.60	0.56849314	0.8599	-6.47
258263_at	unknown protein	---	AT3G15780	-1.09	-0.12	-0.60	0.56883294	0.8599	-6.47
249117_at	heat shock transcription factor-like	AT-HSFA6A	AT5G43840	1.04	0.06	0.60	0.56894866	0.8599	-6.47
254288_at	putative protein Human mRNA for	AESP	AT4G22970	-1.04	-0.06	-0.60	0.5682908	0.8599	-6.47
246785_at	glutathione synthetase gsh2 non-c	GSH2	AT5G27380	1.10	0.14	0.60	0.5691341	0.8600	-6.48
266011_at	unknown protein	---	AT2G37440	-1.05	-0.07	-0.60	0.56913345	0.8600	-6.48
261926_at	unknown protein	PATL2	AT1G22530	-1.06	-0.08	-0.60	0.56993021	0.8601	-6.48
252000_at	hypothetical protein predicted prot	---	AT3G52710	-1.06	-0.09	-0.60	0.56990452	0.8601	-6.48
260568_at	endochitinase isolog	---	AT2G43570	1.45	0.53	0.60	0.5699273	0.8601	-6.48
255572_at	hypothetical protein ; supported by	---	AT4G01050	1.04	0.05	0.60	0.56955902	0.8601	-6.48
256146_at	delta-adaptin, putative similar to d	delta-ADR	AT1G48760	-1.04	-0.06	-0.60	0.56930078	0.8601	-6.48
251322_at	cysteine synthase AtcysC1 ;suppo	CYSC1	AT3G61440	1.13	0.17	0.60	0.56987285	0.8601	-6.48
245968_at	proline-rich protein extensins	---	AT5G19800 /	-1.06	-0.08	-0.60	0.57001781	0.8601	-6.48
257104_at	ER lumen retaining receptor (HDE	---	AT3G25040	1.05	0.07	0.60	0.56998035	0.8601	-6.48
264456_at	unknown protein similar to T cell r	---	AT1G10390	1.05	0.07	0.60	0.56994875	0.8601	-6.48
259985_at	unknown protein ; supported by cl	---	AT1G76620	-1.05	-0.07	-0.60	0.5693632	0.8601	-6.48
262415_at	40S ribosomal protein S17, putativ	emb1129	AT1G49400	1.06	0.09	0.60	0.56989928	0.8601	-6.48
266388_at	hypothetical protein predicted by g	---	AT2G32340	-1.06	-0.08	-0.60	0.56937082	0.8601	-6.48
265685_at	NAM (no apical meristem)-like prot	ANAC038	AT2G24430	-1.06	-0.08	-0.60	0.56937089	0.8601	-6.48
250001_at	tub family-like protein tubby-like p	AtTLP11	AT5G18680	-1.08	-0.11	-0.60	0.57003998	0.8601	-6.48
246634_at	epsilon-adaptin, putative similar to	---	AT1G31730	1.05	0.06	0.60	0.5697664	0.8601	-6.48
247290_at	putative protein similar to unknown	---	AT5G64450	1.10	0.13	0.60	0.56946445	0.8601	-6.48
259831_at	hypothetical protein predicted by g	ZFHD1	AT1G69600	-1.04	-0.06	-0.60	0.57002061	0.8601	-6.48
263669_at	putative cryptochrome 2 apoprotei	CRY2	AT1G04400	1.04	0.06	0.60	0.56971322	0.8601	-6.48
256729_at	hypothetical protein predicted by g	---	AT3G25680	-1.05	-0.07	-0.60	0.56960136	0.8601	-6.48
259508_at	hypothetical protein predicted by g	---	---	-1.07	-0.10	-0.60	0.57007642	0.8601	-6.48
261504_at	MADS-box protein identical to GB	AGL12	AT1G71692	1.06	0.09	0.60	0.56974331	0.8601	-6.48
266974_at	unknown protein	---	AT2G39370	-1.04	-0.06	-0.60	0.56949964	0.8601	-6.48
255323_at	putative transposon protein	---	---	1.04	0.06	0.60	0.56985084	0.8601	-6.48

259884_at	hypothetical protein predicted by g	---	AT1G76390	1.04	0.06	0.60	0.57034727	0.8604	-6.48
255449_at	hypothetical protein	---	AT4G02820	-1.07	-0.09	-0.60	0.5702814	0.8604	-6.48
257842_at	P-glycoprotein, putative similar to	PGP18	AT3G28390	1.04	0.06	0.60	0.57035439	0.8604	-6.48
256511_at	RNA helicase, putative similar to (	---	AT1G33390	-1.04	-0.06	-0.60	0.57045475	0.8604	-6.48
253356_at	putative protein myosin II heavy cl	---	AT4G33390	-1.05	-0.06	-0.60	0.57044106	0.8604	-6.48
261218_at	ferredoxin--NADP reductase precu	FNR2	AT1G20020	-1.08	-0.11	-0.60	0.57050441	0.8604	-6.48
260746_at	glutathione transferase, putative s	ATGSTU19	AT1G78380	1.05	0.07	0.60	0.57089411	0.8605	-6.48
245925_at	bZIP transcription factor family pro	BZO2H3	AT5G28770	1.07	0.10	0.60	0.57067001	0.8605	-6.48
245421_at	hypothetical protein	---	AT4G17430	-1.04	-0.06	-0.60	0.5707657	0.8605	-6.48
257244_at	receptor kinase, putative similar to	---	AT3G24240	-1.09	-0.13	-0.60	0.57077209	0.8605	-6.48
249363_at	DegP protease contains similarity t	DegP13	AT5G40560	-1.04	-0.06	-0.60	0.57062136	0.8605	-6.48
258247_at	hypothetical protein predicted by g	---	AT3G29130	-1.04	-0.05	-0.60	0.57089633	0.8605	-6.48
256532_at	PPR-repeat protein, putative conta	---	AT1G33350	-1.07	-0.10	-0.60	0.57090625	0.8605	-6.48
260903_at	polygalacturonase PG1, putative s	---	AT1G02460	-1.22	-0.29	-0.60	0.57086746	0.8605	-6.48
266243_at	hypothetical protein predicted by g	---	AT2G27750	-1.04	-0.06	-0.60	0.5708561	0.8605	-6.48
253018_at	putative protein Zn finger protein E	---	AT4G38000	-1.05	-0.07	-0.60	0.57093796	0.8605	-6.48
255278_at	putative WD-repeat membrane pro	---	AT4G04940	1.08	0.11	0.60	0.57105569	0.8605	-6.48
256405_at	calcium-dependent protein kinase	CPK33	AT1G50700	-1.04	-0.06	-0.60	0.57105926	0.8605	-6.48
256491_at	hypothetical protein contains simila	---	AT1G31500	-1.05	-0.07	-0.60	0.57103346	0.8605	-6.48
260009_at	unknown protein ;supported by ful	---	AT1G67950	1.08	0.10	0.59	0.57130695	0.8606	-6.48
253391_at	hypothetical protein ; supported by	---	AT4G32590	1.07	0.10	0.60	0.57124935	0.8606	-6.48
249875_at	photosystem II stability/assembly f	HCF136	AT5G23120	1.08	0.11	0.60	0.5711552	0.8606	-6.48
251608_at	putative protein hypothetical prote	UVI4-LIKE	AT3G57860	-1.06	-0.08	-0.60	0.57115177	0.8606	-6.48
250780_at	expansin At-EXP2 (gb|AAB38073.	ATEXPA2	AT5G05290	-1.07	-0.10	-0.60	0.5712135	0.8606	-6.48
258335_at	unknown protein	---	AT3G16020	1.04	0.06	0.59	0.57133876	0.8606	-6.48
258541_at	hypothetical protein	---	AT3G07000	-1.04	-0.05	-0.60	0.57129133	0.8606	-6.48
261808_at	DNA damage repair protein, putat	DRT111	AT1G30480	1.04	0.06	0.59	0.57141669	0.8606	-6.48
250002_at	proline-richh protein predicted pro	AGP25	AT5G18690	-1.15	-0.21	-0.59	0.57146272	0.8606	-6.48
262151_at	hypothetical protein predicted by g	---	AT1G52510	-1.10	-0.14	-0.59	0.57150116	0.8606	-6.48
262749_at	lipase, putative contains Pfam pro	---	AT1G28580	1.05	0.07	0.59	0.57154582	0.8606	-6.48
261458_at	unknown protein contains DNA-J c	---	AT1G21080	1.06	0.08	0.59	0.57162464	0.8607	-6.48
261156_s_at	hypothetical protein predicted by g	---	AT1G34490 /	-1.04	-0.06	-0.59	0.57176416	0.8609	-6.48
261099_at	expansin At-EXP6, putative simila	ATEXPA18	AT1G62980	1.06	0.09	0.59	0.57189167	0.8609	-6.48
263026_at	hypothetical protein predicted by g	---	AT1G24000	1.04	0.06	0.59	0.57181963	0.8609	-6.48
247680_s_at	glycine-rich protein - like glycine-ri	---	AT1G61210 /	1.05	0.07	0.59	0.57192506	0.8609	-6.48

263194_at	AP2 domain transcription factor, p	---	AT1G36060	-1.07	-0.10	-0.59	0.57185956	0.8609	-6.48
247886_at	branched-chain amino acid aminot	---	AT5G57850	1.07	0.10	0.59	0.57203774	0.8609	-6.48
267009_at	unknown protein	---	AT2G39260	-1.04	-0.06	-0.59	0.57202307	0.8609	-6.48
258679_at	putative 2,3-bisphosphoglycerate-	---	AT3G08590	-1.10	-0.13	-0.59	0.57221385	0.8611	-6.48
246110_at	putative protein predicted proteins	---	AT5G20140	-1.08	-0.11	-0.59	0.57239084	0.8613	-6.48
267502_at	putative cytochrome P450	CYP76C4	AT2G45550	-1.04	-0.06	-0.59	0.5724897	0.8614	-6.48
251056_at	putative protein KIAA1303 protein	RAPTOR2	AT5G01770	1.06	0.09	0.59	0.57255604	0.8615	-6.48
265491_s_at	putative retroelement pol polyprote	---	---	-1.04	-0.05	-0.59	0.57266541	0.8616	-6.48
245457_s_at	disease resistance RPP5 like prote	---	AT4G16940	-1.05	-0.07	-0.59	0.57272925	0.8616	-6.48
259755_at	unknown protein similar to glucosa	---	AT1G71070	1.06	0.08	0.59	0.57278436	0.8617	-6.48
266956_at	unknown protein	---	AT2G34510	-1.13	-0.18	-0.59	0.57302545	0.8617	-6.48
267565_at	putative cytochrome P450	CYP71A12	AT2G30750	1.22	0.28	0.59	0.57342909	0.8617	-6.48
258535_at	unknown protein ; supported by cl	---	AT3G06750	-1.09	-0.13	-0.59	0.57336344	0.8617	-6.48
249703_at	putative protein strong similarity to	---	AT5G35560	-1.04	-0.06	-0.59	0.57283362	0.8617	-6.48
263785_at	unknown protein ; supported by cl	---	AT2G46390	-1.05	-0.07	-0.59	0.57321127	0.8617	-6.48
261208_at	unknown protein ; supported by cD	---	AT1G12930	1.07	0.09	0.59	0.57316304	0.8617	-6.48
258860_at	putative potassium transporter sim	KUP3	AT3G02050	-1.08	-0.12	-0.59	0.57327639	0.8617	-6.48
262768_at	putative beta-1,4-N-acetylglucosa	---	AT1G12990	1.11	0.16	0.59	0.57333572	0.8617	-6.48
259454_at	unknown protein similar to hypothe	---	AT1G44050	-1.05	-0.08	-0.59	0.57337278	0.8617	-6.48
263162_at	hypothetical protein predicted by g	---	AT1G54150	1.04	0.06	0.59	0.57310902	0.8617	-6.48
249216_at	serine carboxypeptidase II-like ; s	scpl42	AT5G42240	1.10	0.14	0.59	0.57310233	0.8617	-6.48
264132_at	hypothetical protein predicted by g	---	AT1G79100	-1.06	-0.08	-0.59	0.57342167	0.8617	-6.48
263801_at	putative Athila retroelement ORF1	---	---	-1.04	-0.06	-0.59	0.57311091	0.8617	-6.48
263959_at	hypothetical protein predicted by g	---	AT2G36210	-1.04	-0.06	-0.59	0.57310153	0.8617	-6.48
252006_at	purple acid phosphatase-like prote	PAP22	AT3G52820	1.24	0.32	0.59	0.57290961	0.8617	-6.48
265380_at	putative retroelement pol polyprote	---	---	-1.05	-0.07	-0.59	0.57329541	0.8617	-6.48
267531_at	putative calcium-dependent protein	CPK14	AT2G41860	-1.04	-0.06	-0.59	0.57315786	0.8617	-6.48
251564_at	myosin heavy chain MYA3	XIJ	AT3G58160	-1.05	-0.07	-0.59	0.57347798	0.8617	-6.48
255775_at	hypothetical protein predicted by g	RBL12	AT1G18600	1.05	0.07	0.59	0.57365873	0.8619	-6.48
267320_at	hypothetical protein predicted by g	---	AT2G19300	-1.05	-0.07	-0.59	0.57374963	0.8620	-6.48
248501_at	golgi SNARE protein	MEMB12	AT5G50440	1.06	0.08	0.59	0.57388978	0.8621	-6.48
267412_at	putative vacuolar sorting receptor	---	AT2G34940	-1.16	-0.21	-0.59	0.57400417	0.8622	-6.48
255937_at	transcriptional activator CBF1, put	DDF1	AT1G12610	-1.10	-0.14	-0.59	0.57399968	0.8622	-6.48
254491_at	putative protein hypothetical protei	---	AT4G20300	1.07	0.10	0.59	0.57404253	0.8622	-6.48
255772_at	calmodulin, putative similar to calr	---	AT1G18530	-1.05	-0.07	-0.59	0.57409959	0.8622	-6.48

266569_at	unknown protein	---	AT2G24080	-1.04	-0.06	-0.59	0.57430487	0.8624	-6.48
259850_at	hypothetical protein predicted by g	---	AT1G72240	-1.07	-0.10	-0.59	0.57431199	0.8624	-6.48
259162_at	unknown protein similar to unknow	---	AT3G01640	-1.06	-0.08	-0.59	0.57461032	0.8628	-6.48
259412_at	DNA binding protein GT-1, putativ	---	AT1G13450	1.05	0.07	0.59	0.57469232	0.8628	-6.48
257659_at	Expressed protein ; supported by f	---	AT3G13226	-1.04	-0.06	-0.59	0.5747307	0.8628	-6.48
262305_at	hypothetical protein predicted by g	---	AT1G70950	-1.05	-0.06	-0.59	0.57463044	0.8628	-6.48
261721_at	unknown protein ; supported by cD	---	AT1G08480	1.04	0.06	0.59	0.57470935	0.8628	-6.48
249009_at	unknown protein ; supported by fu	MAP18	AT5G44610	-1.08	-0.11	-0.59	0.57479696	0.8628	-6.48
265547_at	hypothetical protein similar to hypo	---	AT2G28305	1.10	0.14	0.59	0.57482049	0.8628	-6.48
256784_at	hypothetical protein predicted by g	---	AT3G13674	1.04	0.06	0.59	0.5748736	0.8628	-6.48
250765_at	unknown protein ;supported by ful	---	AT5G05930	-1.07	-0.10	-0.59	0.57503516	0.8628	-6.48
257885_at	S1 self-incompatibility protein, put	---	AT3G16970	-1.04	-0.06	-0.59	0.57503022	0.8628	-6.48
248180_at	unknown protein ;supported by ful	AGD5	AT5G54310	-1.04	-0.06	-0.59	0.57510292	0.8628	-6.48
250911_at	SERINE/THREONINE-PROTEIN K	CTR1	AT5G03730	-1.06	-0.09	-0.59	0.57491896	0.8628	-6.48
250290_at	putative protein ;supported by full-	---	AT5G13310	1.04	0.06	0.59	0.57503476	0.8628	-6.48
254470_at	putative protein other hypothetical	---	---	1.06	0.09	0.59	0.57507426	0.8628	-6.48
267576_at	putative Mutator-like transposase	---	---	1.06	0.09	0.59	0.5751986	0.8628	-6.48
247185_at	putative protein contains similarity	---	AT5G65460	1.06	0.08	0.59	0.57519313	0.8628	-6.48
259100_at	DNA-damage-repair/toleration prot	DRT102	AT3G04880	1.05	0.07	0.59	0.57523054	0.8628	-6.48
249532_at	AtPP - like protein AtPP protein, B	---	AT5G38780	1.11	0.16	0.59	0.5753155	0.8629	-6.48
257512_at	unknown protein	---	AT1G35250	1.04	0.06	0.59	0.57532691	0.8629	-6.48
256484_at	PPR-repeat protein contains multip	---	AT1G31430	1.05	0.07	0.59	0.57569616	0.8629	-6.48
259786_at	lipase/hydrolase, putative contains	---	AT1G29660	-1.50	-0.58	-0.59	0.57567212	0.8629	-6.48
252272_at	receptor protein kinase - like prote	BAM2	AT3G49670	-1.11	-0.14	-0.59	0.57572877	0.8629	-6.48
245879_at	putative subunit of TOC complex (	ATTOC64-V	AT5G09420	-1.13	-0.18	-0.59	0.57571136	0.8629	-6.48
258744_at	hypothetical protein similar to plan	---	AT3G05830	-1.06	-0.08	-0.59	0.57573541	0.8629	-6.48
254680_at	phytochrome E	PHYE	AT4G18130	1.06	0.09	0.59	0.57573749	0.8629	-6.48
253601_at	hypothetical protein	---	AT4G30900	-1.04	-0.06	-0.59	0.57544828	0.8629	-6.48
252654_at	similar to glycyl tRNA synthetase	---	AT3G44740	1.04	0.06	0.59	0.57556278	0.8629	-6.48
256646_at	hypothetical protein predicted by g	---	AT3G13590	1.05	0.08	0.59	0.57552986	0.8629	-6.48
266021_at	unknown protein	---	AT2G05910	-1.08	-0.11	-0.59	0.57567479	0.8629	-6.48
259971_at	unknown protein similar to SPL1-r	---	AT1G76580	-1.07	-0.10	-0.59	0.57577601	0.8629	-6.48
252257_at	putative protein several hypothetic	---	AT3G49440	1.04	0.06	0.59	0.57589025	0.8630	-6.48
261832_at	S-ribonuclease binding protein SB	---	AT1G10650	-1.08	-0.11	-0.59	0.57594821	0.8631	-6.48
262829_at	auxin-independent growth promot	---	AT1G14970	-1.09	-0.12	-0.59	0.57602284	0.8631	-6.48

258428_at	unknown protein	---	AT3G16610	-1.05	-0.07	-0.59	0.57600515	0.8631	-6.48
262930_at	hypothetical protein similar to hin1	---	AT1G65690	-1.10	-0.14	-0.59	0.57608602	0.8631	-6.48
262252_at	RING-H2 zinc finger protein ATL3	---	AT1G53820	-1.04	-0.06	-0.59	0.57610804	0.8631	-6.48
247925_at	TCH4 protein (gb|AAA92363.1) ; s	TCH4	AT5G57560	1.22	0.29	0.59	0.57618411	0.8631	-6.48
267511_at	unknown protein	---	AT2G45670	1.05	0.07	0.59	0.57662259	0.8632	-6.48
246249_at	salt-inducible like protein	---	AT4G36680	1.06	0.08	0.59	0.57685844	0.8632	-6.48
256106_at	unknown protein	---	AT1G16870	1.04	0.06	0.59	0.57704388	0.8632	-6.48
260152_at	putative IAA6 protein similar to IAA	IAA6	AT1G52830	-1.11	-0.15	-0.59	0.57693611	0.8632	-6.48
264901_at	putative sulphate transporter prote	AST91	AT1G23090	-1.16	-0.21	-0.59	0.57689936	0.8632	-6.48
261046_at	flavonol 3-o-glucosyltransferase, p	---	AT1G01390	-1.08	-0.10	-0.59	0.57681997	0.8632	-6.48
247554_at	putative protein leucine zipper-cor	ATEXO70E	AT5G61010	-1.13	-0.18	-0.59	0.57688828	0.8632	-6.48
249258_at	putative protein similar to unknown	---	AT5G41650	1.04	0.06	0.59	0.57719164	0.8632	-6.48
256161_at	unknown protein ; supported by cD	---	AT1G30090	-1.05	-0.07	-0.59	0.57670747	0.8632	-6.48
253522_at	predicted protein cation transport	---	AT4G31290	1.14	0.19	0.59	0.57667687	0.8632	-6.48
253943_at	putative protein gene F19K23.12	---	AT4G27030	-1.14	-0.19	-0.59	0.57713552	0.8632	-6.48
253821_at	extensin-like protein extensin-like	---	AT4G28380	-1.05	-0.07	-0.59	0.5763942	0.8632	-6.48
267441_at	putative receptor-like protein kinas	---	AT2G19210	-1.04	-0.06	-0.59	0.57688755	0.8632	-6.48
249602_at	porin -like protein porin, Prunus ar	---	AT5G37610	1.05	0.07	0.59	0.57704596	0.8632	-6.48
253618_at	nodulin-like protein MtN21 gene p	---	AT4G30420	-1.04	-0.05	-0.59	0.57718586	0.8632	-6.48
253115_at	putative protein ;supported by full-	---	AT4G35910	1.04	0.06	0.59	0.5768792	0.8632	-6.48
262404_at	transposon-like ORF, putative sim	---	---	-1.05	-0.07	-0.59	0.57655798	0.8632	-6.48
258792_at	hypothetical protein predicted by g	---	AT3G04640	1.17	0.23	0.59	0.57707049	0.8632	-6.48
252976_s_at	Phospholipase like protein Arabid	---	AT4G38550	-1.09	-0.12	-0.59	0.57639402	0.8632	-6.48
254094_at	putative protein ATP-dependent D	---	AT4G25120	1.06	0.08	0.59	0.57706894	0.8632	-6.48
259574_at	hypothetical protein	MLP168	AT1G35310	-1.04	-0.06	-0.59	0.57633054	0.8632	-6.48
253363_at	hypothetical protein	---	AT4G33130	1.05	0.07	0.59	0.57703986	0.8632	-6.48
254825_at	putative protein Pad-1, Neurospor	---	AT4G12640	-1.07	-0.09	-0.59	0.57656857	0.8632	-6.48
245157_at	putative polygalacturonase	---	AT2G33160	1.04	0.06	0.59	0.57702946	0.8632	-6.48
261848_at	pectin methylesterase, putative si	---	AT1G11590	1.05	0.07	0.59	0.57712925	0.8632	-6.48
263564_s_at	DNA-directed RNA polymerase II,	NRPB3	AT2G15400	-1.05	-0.07	-0.59	0.57725274	0.8632	-6.48
253454_at	Expressed protein ; supported by c	---	AT4G31875	-1.08	-0.12	-0.59	0.57731635	0.8633	-6.48
261505_at	carboxypeptidase, putative similar	SOL1	AT1G71696	-1.06	-0.09	-0.58	0.57765027	0.8634	-6.48
250161_at	putative protein amino acid transp	---	AT5G15240	-1.09	-0.12	-0.59	0.57754218	0.8634	-6.48
262027_at	DNA-binding protein, putative sim	HOS10	AT1G35515	-1.09	-0.13	-0.59	0.57755904	0.8634	-6.48
265324_at	hypothetical protein predicted by g	ATCOAD	AT2G18250	1.06	0.08	0.59	0.57758467	0.8634	-6.48

261705_at	hypothetical protein predicted by g	---	AT1G32670	1.05	0.07	0.59	0.57754207	0.8634	-6.48
261901_at	J8-like protein similar to DnaJ hom	J8	AT1G80920	1.05	0.07	0.59	0.57749284	0.8634	-6.48
260059_at	trehalose-6-phosphate phosphata	ATTPPB	AT1G78090	1.09	0.12	0.58	0.57764405	0.8634	-6.48
256177_at	protein kinase, putative contains F	---	AT1G51620	1.15	0.20	0.58	0.57766938	0.8634	-6.48
246501_at	putative protein KIAA1012 protein	---	AT5G16280	-1.05	-0.07	-0.58	0.57776542	0.8634	-6.48
252172_at	putative protein predicted proteins	---	AT3G50640	-1.05	-0.07	-0.58	0.57778767	0.8634	-6.48
250282_at	putative protein predicted protein,	---	AT5G13260	1.07	0.09	0.58	0.57792774	0.8635	-6.48
250092_at	putative protein	---	AT5G17360	1.04	0.05	0.58	0.57792312	0.8635	-6.48
250747_at	glucuronosyl transferase-like prote	---	AT5G05900	1.04	0.06	0.58	0.57790045	0.8635	-6.48
266478_at	putative cysteinyl-tRNA synthetase	SYCO ARA	AT2G31170	-1.08	-0.11	-0.58	0.57799199	0.8635	-6.48
266719_at	MYB-related transcription factor (C	CCA1	AT2G46830	-1.06	-0.09	-0.58	0.57804832	0.8635	-6.48
259698_at	hypothetical protein similar to hyp	---	AT1G68930	-1.06	-0.08	-0.58	0.57807273	0.8635	-6.48
245694_at	EF - hand Calcium binding protein	---	AT5G04170	-1.04	-0.06	-0.58	0.5782834	0.8637	-6.48
257186_at	hypothetical protein predicted by g	---	AT3G13130	-1.06	-0.08	-0.58	0.57826583	0.8637	-6.48
257432_at	unknown protein	---	AT2G21850	-1.06	-0.08	-0.58	0.57839921	0.8638	-6.48
257944_at	SKP1/ASK1 (At9), putative similar	ASK9	AT3G21850	1.04	0.06	0.58	0.5784156	0.8638	-6.48
264826_at	putative 1-aminocyclopropane-1-c	2A6	AT1G03410	1.06	0.09	0.58	0.57853134	0.8639	-6.48
262355_at	unknown protein	---	AT1G72820	1.07	0.09	0.58	0.57856967	0.8639	-6.48
253303_at	putative protein ; supported by full	---	AT4G33780	1.05	0.07	0.58	0.57869432	0.8640	-6.48
257803_at	unknown protein	---	AT3G18790	-1.04	-0.06	-0.58	0.5786957	0.8640	-6.48
252929_at	putative fructose-bisphosphate alc	---	AT4G38970	-1.05	-0.07	-0.58	0.57878103	0.8640	-6.48
265584_at	unknown protein	PIL5	AT2G20180	-1.04	-0.06	-0.58	0.57875487	0.8640	-6.48
255225_at	U3 snoRNP-associated -like prote	---	AT4G05410	-1.11	-0.15	-0.58	0.57889426	0.8640	-6.48
253569_at	receptor kinase - like protein recep	---	AT4G31250	1.06	0.08	0.58	0.57884754	0.8640	-6.48
260528_at	putative WRKY-type DNA binding	WRKY23	AT2G47260	1.12	0.16	0.58	0.57891669	0.8640	-6.48
267529_at	putative protein kinase contains a	AtAUR3	AT2G45490	-1.06	-0.08	-0.58	0.57900987	0.8641	-6.49
250482_at	putative protein	---	AT5G10320	1.06	0.08	0.58	0.57897827	0.8641	-6.49
256710_at	hypothetical protein predicted by g	---	AT3G30350	-1.08	-0.11	-0.58	0.57904833	0.8641	-6.49
249143_at	putative protein strong similarity to	---	AT5G43230	1.04	0.05	0.58	0.57936059	0.8642	-6.49
265291_at	unknown protein predicted by gens	---	AT2G22720	1.05	0.07	0.58	0.5792811	0.8642	-6.49
252046_at	putative protein extensin -Nicotian	---	AT3G52460	-1.05	-0.08	-0.58	0.57929356	0.8642	-6.49
261906_at	hypothetical protein predicted by g	---	AT1G65080	1.08	0.12	0.58	0.57923871	0.8642	-6.49
260741_at	hypothetical protein contains Pfam	---	AT1G15040	1.46	0.55	0.58	0.57923879	0.8642	-6.49
266965_at	nodulin-like protein	---	AT2G39510	-1.05	-0.07	-0.58	0.57932534	0.8642	-6.49
253564_at	protein kinase - like protein protein	---	AT4G31170	-1.05	-0.07	-0.58	0.57940361	0.8642	-6.49

263100_at	hypothetical protein predicted by g	AtPOT1a	AT2G05210	-1.07	-0.09	-0.58	0.57956255	0.8644	-6.49
260182_at	unknown protein similar to IFA-bin	---	AT1G70750	1.05	0.07	0.58	0.57968462	0.8644	-6.49
263040_at	conserved hypothetical protein pre	---	AT1G23300	-1.05	-0.06	-0.58	0.57965917	0.8644	-6.49
252328_at	Expressed protein ; supported by c	---	AT3G48570	-1.05	-0.06	-0.58	0.58028277	0.8647	-6.49
258166_at	WD-repeat protein, putative conta	---	AT3G21540	-1.10	-0.14	-0.58	0.58011239	0.8647	-6.49
258648_at	putative auxin-independent growth	---	AT3G07900	-1.08	-0.11	-0.58	0.58010287	0.8647	-6.49
245728_at	steroid 22-alpha-hydroxylase, puta	---	AT1G73340	-1.06	-0.08	-0.58	0.58029112	0.8647	-6.49
254405_at	putative protein arm repeat contai	PUB8	AT4G21350	-1.07	-0.10	-0.58	0.58024497	0.8647	-6.49
258842_at	unknown protein similar to putative	CLPS3	AT3G04680	1.06	0.09	0.58	0.58008441	0.8647	-6.49
252658_at	hypothetical protein	---	AT3G44800	-1.06	-0.08	-0.58	0.57996724	0.8647	-6.49
257351_at	putative mitochondrial carrier prote	MBAC1	AT2G33820	1.06	0.08	0.58	0.58026854	0.8647	-6.49
245360_at	naringenin 3-dioxygenase like prot	---	AT4G16330	1.05	0.07	0.58	0.58025104	0.8647	-6.49
255096_at	hypothetical protein similar to T21	---	---	-1.04	-0.06	-0.58	0.58023972	0.8647	-6.49
256316_at	hypothetical protein	---	AT1G35890	-1.04	-0.06	-0.58	0.58017126	0.8647	-6.49
253128_at	Calcium-dependent serine/threoni	CPK18	AT4G36070	-1.04	-0.06	-0.58	0.58014346	0.8647	-6.49
252563_at	putative protein cim1 induced alle	ATEXLA1	AT3G45970	1.16	0.21	0.58	0.58050809	0.8648	-6.49
262219_at	hypothetical protein predicted by g	---	AT1G74750	-1.08	-0.11	-0.58	0.58049981	0.8648	-6.49
266787_at	putative receptor-like protein kinas	---	AT2G28990	1.04	0.06	0.58	0.58052028	0.8648	-6.49
259243_at	unknown protein similar to unknov	---	AT3G07565	1.04	0.06	0.58	0.58046173	0.8648	-6.49
258104_at	hypothetical protein predicted by g	---	AT3G23620	1.08	0.11	0.58	0.58055949	0.8648	-6.49
249989_at	putative protein FACTOR ASSOC	---	AT5G18525	1.05	0.07	0.58	0.5806177	0.8648	-6.49
257613_at	polygalacturonase, putative simila	---	AT3G26610	1.04	0.06	0.58	0.58063623	0.8648	-6.49
247758_at	subtilisin-like serine protease conta	ATSBT4.13	AT5G59120	1.06	0.08	0.58	0.58068684	0.8648	-6.49
266466_at	hypothetical protein The first 3 exo	---	AT2G47790	1.05	0.07	0.58	0.58074162	0.8648	-6.49
255078_at	putative protein ascorbate peroxid	APX4	AT4G09010	1.07	0.09	0.58	0.58127384	0.8650	-6.49
262396_at	unknown protein ;supported by full	---	AT1G49470	1.10	0.14	0.58	0.5811098	0.8650	-6.49
264266_at	putative protein phosphatase 2C s	---	AT1G09160	1.07	0.10	0.58	0.58125123	0.8650	-6.49
245373_s_at	Expressed protein ; supported by f	ATARD2	AT4G14710 /	-1.05	-0.07	-0.58	0.58137204	0.8650	-6.49
246001_at	putative protein predicted protein,	---	AT5G20790	-1.10	-0.14	-0.58	0.58140293	0.8650	-6.49
262306_s_at	asparaginyl-tRNA synthetase(SYN	SYNC3	AT1G70980 /	1.06	0.09	0.58	0.58090806	0.8650	-6.49
246018_at	Expressed protein ; supported by f	---	AT5G10695	-1.16	-0.21	-0.58	0.58111121	0.8650	-6.49
248012_at	putative protein strong similarity to	---	AT5G56310	-1.06	-0.09	-0.58	0.58146999	0.8650	-6.49
263367_at	putative retroelement pol polyprote	---	---	-1.05	-0.07	-0.58	0.58101901	0.8650	-6.49
262144_at	hypothetical protein predicted by g	---	AT1G52620	1.04	0.06	0.58	0.58103598	0.8650	-6.49
246996_at	putative protein similar to unknown	LBD37	AT5G67420	-1.08	-0.11	-0.58	0.5809871	0.8650	-6.49

261442_at	Expressed protein ; supported by f	---	AT1G28375	-1.05	-0.07	-0.58	0.58128791	0.8650	-6.49
265864_at	putative myosin heavy chain-like p	ATMAP70-3	AT2G01750	-1.07	-0.09	-0.58	0.58134436	0.8650	-6.49
246526_at	putative protein RXF26 - Arabidop	GLIP7	AT5G15720	1.04	0.06	0.58	0.58127259	0.8650	-6.49
260439_at	hypothetical protein predicted by g	---	AT1G68340	1.10	0.13	0.58	0.58148131	0.8650	-6.49
262359_at	disease resistance protein, putativ	---	AT1G73060	-1.05	-0.07	-0.58	0.58126902	0.8650	-6.49
254411_at	hypothetical protein	---	---	-1.05	-0.07	-0.58	0.5814886	0.8650	-6.49
266342_at	hypothetical protein predicted by g	---	AT2G01540	1.07	0.09	0.58	0.58154949	0.8650	-6.49
250042_at	putative protein non-consensus G	---	AT5G18420	1.05	0.07	0.58	0.58161762	0.8651	-6.49
248172_at	unknown protein ;supported by ful	---	AT5G54660	-1.09	-0.12	-0.58	0.5817774	0.8652	-6.49
246082_at	receptor protein kinase - like prote	EFR	AT5G20480	-1.14	-0.19	-0.58	0.58179231	0.8652	-6.49
254821_at	hypothetical protein	---	AT4G12540	-1.04	-0.06	-0.58	0.58223216	0.8653	-6.49
266675_s_at	hypothetical protein predicted by g	---	AT2G29610	-1.04	-0.05	-0.58	0.58197518	0.8653	-6.49
256597_at	acidic ribosomal protein P2b (rpp2	---	AT3G28500	1.12	0.16	0.58	0.58221107	0.8653	-6.49
255138_at	extensin-like protein extensin clas	---	AT4G08380	-1.04	-0.06	-0.58	0.58217073	0.8653	-6.49
259319_at	Snf1-related protein kinase KIN10	AKIN10	AT3G01090	1.04	0.05	0.58	0.58222347	0.8653	-6.49
264950_at	peroxidase, putative similar to per	---	AT1G77100	-1.05	-0.07	-0.58	0.58217004	0.8653	-6.49
249536_at	pollen coat -like protein pollen coa	---	AT5G38760	-1.04	-0.05	-0.58	0.58212199	0.8653	-6.49
252551_at	phospholipase - like protein cytos	---	AT3G45880	1.06	0.09	0.58	0.58200243	0.8653	-6.49
254968_at	putative protein various predicted	---	AT4G10420	-1.04	-0.06	-0.58	0.58191474	0.8653	-6.49
255868_at	putative MYB family transcription f	---	AT2G30380	-1.06	-0.08	-0.58	0.58213395	0.8653	-6.49
248440_at	acid phosphatase	---	AT5G51260	1.06	0.08	0.58	0.5823041	0.8654	-6.49
259085_at	unknown protein similar to GB:CAE	---	AT3G05000	1.05	0.07	0.58	0.58258487	0.8655	-6.49
250179_at	putative protein	---	AT5G14440	-1.05	-0.08	-0.58	0.58250223	0.8655	-6.49
257473_at	unknown protein	---	AT1G33840	1.06	0.09	0.58	0.58259623	0.8655	-6.49
252799_at	putative protein various predicted	---	---	1.04	0.05	0.58	0.58255346	0.8655	-6.49
AFFX-LysX-3_	B. subtilis /GEN=lys /DB_XREF=gi	---	---	-1.08	-0.11	-0.58	0.58257014	0.8655	-6.49
264051_at	hypothetical protein predicted by g	---	AT2G22340	1.05	0.06	0.58	0.58244733	0.8655	-6.49
256218_at	hypothetical protein predicted by g	---	AT1G56270	-1.06	-0.08	-0.58	0.58277397	0.8656	-6.49
264982_at	hypothetical protein predicted by g	---	AT1G27220	-1.05	-0.07	-0.58	0.58275963	0.8656	-6.49
260794_at	unknown protein ; supported by cD	---	AT1G06210	1.05	0.07	0.58	0.58281335	0.8656	-6.49
255185_at	hypothetical protein	---	AT4G07740	-1.05	-0.07	-0.58	0.58293851	0.8656	-6.49
249106_at	protein transport protein SEC23 ; s	---	AT5G43670	1.07	0.10	0.58	0.58291115	0.8656	-6.49
248424_at	unknown protein	---	AT5G51680	-1.16	-0.21	-0.58	0.58295125	0.8656	-6.49
254983_at	putative protein other hypothetical	MEE53	AT4G10560	-1.04	-0.06	-0.58	0.5829935	0.8656	-6.49
254541_at	putative LTR retrotransposon Bras	---	---	1.04	0.05	0.58	0.58314332	0.8658	-6.49

260928_at	hypothetical protein similar to puta	GATL5	AT1G02720	1.05	0.07	0.58	0.58345749	0.8658	-6.49
251842_at	extensin precursor -like protein ex	---	AT3G54580	-1.12	-0.16	-0.58	0.58344721	0.8658	-6.49
261733_at	clathrin coat assembly protein AP	---	AT1G47830	1.04	0.06	0.58	0.58344176	0.8658	-6.49
247976_at	unknown protein	---	---	-1.06	-0.08	-0.58	0.58329929	0.8658	-6.49
259622_at	hypothetical protein predicted by g	---	AT1G43010	-1.04	-0.06	-0.58	0.58326567	0.8658	-6.49
252244_at	putative protein some putative prot	---	AT3G50130	-1.05	-0.08	-0.58	0.58324482	0.8658	-6.49
266651_at	putative casein kinase I	---	AT2G25760	-1.05	-0.07	-0.58	0.58331381	0.8658	-6.49
261941_at	hypothetical protein contains simila	---	AT1G22490	-1.11	-0.16	-0.58	0.58343738	0.8658	-6.49
250498_at	microbody NAD-dependent malate	PMDH2	AT5G09660	-1.08	-0.11	-0.58	0.5835522	0.8659	-6.49
264541_at	hypothetical protein predicted by g	---	AT1G55660	1.06	0.08	0.58	0.58362213	0.8659	-6.49
247828_at	putative protein KIAA0066, Homo	---	AT5G58510	1.04	0.06	0.58	0.58360719	0.8659	-6.49
254166_at	HSP90-like protein HSP90 homol	SHD	AT4G24190	1.15	0.20	0.58	0.58376669	0.8660	-6.49
257119_at	receptor kinase protein, putative s	---	AT3G20190	1.04	0.06	0.58	0.58378524	0.8660	-6.49
259132_at	putative auxin-independent growth	---	AT3G02250	-1.07	-0.10	-0.58	0.58390025	0.8661	-6.49
258592_at	hypothetical protein contains Pfam	---	AT3G04130	-1.05	-0.07	-0.58	0.58388719	0.8661	-6.49
262453_at	hypothetical protein predicted by g	---	AT1G11240	1.04	0.05	0.58	0.58392065	0.8661	-6.49
250874_at	putative protein	---	AT5G04010	1.05	0.07	0.57	0.58422052	0.8661	-6.49
250143_at	ADP-ribosylation factor - like prote	ATARFA1B	AT5G14670	-1.05	-0.07	-0.57	0.58408124	0.8661	-6.49
262651_at	hypothetical protein One of a clus	FUT9	AT1G14100	1.05	0.07	0.57	0.58422903	0.8661	-6.49
254876_at	putative phosphoribosylanthranila	---	AT4G11610	-1.06	-0.08	-0.57	0.58424026	0.8661	-6.49
267019_at	hypothetical protein predicted by g	---	AT2G39130	-1.05	-0.07	-0.57	0.58414499	0.8661	-6.49
247136_at	senescence-associated protein co	---	AT5G66170	-1.20	-0.27	-0.57	0.58416639	0.8661	-6.49
267183_at	hypothetical protein predicted by g	---	AT2G44020	-1.05	-0.07	-0.57	0.58411571	0.8661	-6.49
264909_at	unknown protein	---	AT2G17300	1.05	0.07	0.57	0.58412912	0.8661	-6.49
255737_at	unknown protein ;supported by full	---	AT1G25420	-1.05	-0.07	-0.57	0.58435588	0.8661	-6.49
252354_at	betaine aldehyde dehydrogenase-	ALDH10A9	AT3G48170	-1.04	-0.06	-0.57	0.58435258	0.8661	-6.49
252382_at	ABC-type transport protein-like pr	ATH5	AT3G47770	-1.04	-0.05	-0.57	0.58437717	0.8661	-6.49
256573_at	hypothetical protein predicted by g	---	AT3G14860	1.05	0.07	0.57	0.58445901	0.8662	-6.49
264864_at	hypothetical protein predicted by g	---	AT1G24310	1.08	0.11	0.57	0.58461294	0.8663	-6.49
247962_at	protein kinase MEK1 homolog	MKK6	AT5G56580	1.04	0.06	0.57	0.5847885	0.8663	-6.49
247684_at	serine/threonine-specific protein k	---	AT5G59670	-1.32	-0.40	-0.57	0.58479186	0.8663	-6.49
254715_at	putative protein hypothetical prote	---	AT4G13550	-1.07	-0.10	-0.57	0.58479535	0.8663	-6.49
267297_at	putative RING zinc finger protein ;	---	AT2G23780	-1.05	-0.07	-0.57	0.58462234	0.8663	-6.49
249044_at	Na+-dependent inorganic phospha	PHT4;6	AT5G44370	-1.07	-0.09	-0.57	0.58479233	0.8663	-6.49
258634_at	putative RNA-binding protein cont	---	AT3G08000	-1.09	-0.12	-0.57	0.58475785	0.8663	-6.49

265310_at	hypothetical protein predicted by g	---	AT2G20280	1.04	0.06	0.57	0.58485456	0.8663	-6.49
247428_at	unknown protein	---	AT5G62600	-1.04	-0.05	-0.57	0.58491883	0.8664	-6.49
250133_at	thioredoxin f2 (gb|AAD35004.1) ;	TRXF2	AT5G16400	1.09	0.12	0.57	0.58523053	0.8664	-6.49
254216_at	V-ATPase subunit G (vag2 gene)	VAG2	AT4G23710	-1.09	-0.13	-0.57	0.58523263	0.8664	-6.49
256183_at	MAP kinase kinase 4 (ATMKK4) id	MKK4	AT1G51660	1.13	0.18	0.57	0.58509885	0.8664	-6.49
257591_at	leucine-rich repeat disease resista	AtRLP39	AT3G24900	-1.04	-0.05	-0.57	0.5852073	0.8664	-6.49
258826_at	putative glucan synthase similar to	ATGSL10	AT3G07160	-1.04	-0.05	-0.57	0.5852119	0.8664	-6.49
257998_at	hypothetical protein similar to hypo	---	AT3G27510	1.04	0.05	0.57	0.58508573	0.8664	-6.49
250902_at	putative protein predicted proteins	---	AT5G03590	1.06	0.08	0.57	0.58506894	0.8664	-6.49
260145_at	putative G protein-coupled recepto	GPCR	AT1G52920	-1.04	-0.05	-0.57	0.58545791	0.8664	-6.49
245092_at	putative TGACG-sequence-specifi	BZIP17	AT2G40950	-1.06	-0.08	-0.57	0.58543765	0.8664	-6.49
253836_at	putative protein hypothetical prote	---	AT4G27840	-1.05	-0.07	-0.57	0.58543259	0.8664	-6.49
260555_at	hypothetical protein predicted by g	---	AT2G41780	1.13	0.18	0.57	0.58542184	0.8664	-6.49
263559_at	putative non-LTR retroelement rev	---	---	1.04	0.06	0.57	0.58546771	0.8664	-6.49
253587_at	hypothetical protein	---	AT4G30770	-1.05	-0.07	-0.57	0.58543208	0.8664	-6.49
253047_at	Expressed protein ; supported by f	---	AT4G37295	1.09	0.12	0.57	0.58554165	0.8665	-6.49
254448_at	fatty acid hydroxylase - like protei	FAH2	AT4G20870	1.14	0.19	0.57	0.58565268	0.8666	-6.49
260577_at	hypothetical protein predicted by g	---	AT2G47340	-1.04	-0.06	-0.57	0.58567517	0.8666	-6.49
251374_at	homeobox-leucine zipper protein H	HAT3	AT3G60390	-1.10	-0.14	-0.57	0.58610618	0.8666	-6.49
267062_at	putative spliceosome associated p	---	AT2G32600	1.06	0.08	0.57	0.58592506	0.8666	-6.49
265818_at	putative peptidyl-prolyl cis-trans is	PIN1AT	AT2G18040	-1.04	-0.06	-0.57	0.58624661	0.8666	-6.49
255052_at	rab7 -like protein rab7 protein -Vig	ATRABG3A	AT4G09720	-1.05	-0.07	-0.57	0.58572497	0.8666	-6.49
245310_at	hypothetical protein ;supported by	RALFL31	AT4G13950	-1.12	-0.16	-0.57	0.5862125	0.8666	-6.49
250116_at	putative protein similar to unknown	---	AT5G16430	-1.06	-0.09	-0.57	0.58595785	0.8666	-6.49
246909_at	putative protein predicted protein,	---	AT5G25770	1.12	0.16	0.57	0.58612278	0.8666	-6.49
248947_at	putative protein similar to unknown	---	AT5G45540	1.06	0.09	0.57	0.58589474	0.8666	-6.49
257645_at	unknown protein ;supported by ful	---	AT3G25790	-1.06	-0.08	-0.57	0.58614493	0.8666	-6.49
261466_at	hypothetical protein predicted by g	---	AT1G07690	1.06	0.09	0.57	0.58608864	0.8666	-6.49
248202_at	unknown protein	---	AT5G54220	1.07	0.09	0.57	0.58588467	0.8666	-6.49
248015_at	putative protein similar to unknown	---	AT5G56370	1.05	0.06	0.57	0.58624138	0.8666	-6.49
251165_at	putative protein different MAP kina	---	AT3G63330	-1.06	-0.08	-0.57	0.58581805	0.8666	-6.49
262450_at	hypothetical protein identical to hy	---	AT1G11320	-1.05	-0.08	-0.57	0.58614807	0.8666	-6.49
249312_at	disease resistance protein-like	---	AT5G41550	-1.06	-0.08	-0.57	0.58619678	0.8666	-6.49
245564_at	hypothetical protein	emb2739	AT4G14590	-1.05	-0.07	-0.57	0.58630309	0.8666	-6.49
258071_s_at	unknown protein	---	AT3G26070	1.07	0.10	0.57	0.58637665	0.8666	-6.49

263484_at	putative presenilin	---	AT2G29900	-1.04	-0.06	-0.57	0.58635662	0.8666	-6.49
263304_at	hypothetical protein predicted by g	---	AT2G01920	-1.04	-0.06	-0.57	0.58650378	0.8667	-6.49
266350_at	putative protein transport protein S	STL2P	AT2G01470	1.07	0.09	0.57	0.58648344	0.8667	-6.49
257074_at	unknown protein	---	AT3G19660	1.10	0.14	0.57	0.58701593	0.8668	-6.49
245038_at	similar to latex allergen from Heve	PLA2A	AT2G26560	-1.16	-0.22	-0.57	0.58690206	0.8668	-6.49
246630_at	hypothetical protein predicted by g	---	AT1G50730	1.08	0.12	0.57	0.58701486	0.8668	-6.49
250386_at	MYB like protein MYB like protein	MYB3R-4	AT5G11510	-1.06	-0.08	-0.57	0.587194	0.8668	-6.49
253852_at	putative protein diacylglycerol kina	---	AT4G28130	-1.04	-0.06	-0.57	0.58701681	0.8668	-6.49
265585_at	CDC27/NUC2-like protein TPR-rep	HBT	AT2G20000	-1.06	-0.08	-0.57	0.58695329	0.8668	-6.49
247102_at	putative protein similar to unknown	---	AT5G66550	1.05	0.08	0.57	0.58720159	0.8668	-6.49
248284_at	Expressed protein ; supported by f	---	AT5G52975	-1.06	-0.08	-0.57	0.586856	0.8668	-6.49
266766_at	hypothetical protein predicted by g	PAP14	AT2G46880	-1.09	-0.12	-0.57	0.58700186	0.8668	-6.49
248621_at	putative protein similar to unknown	---	AT5G49350	-1.05	-0.07	-0.57	0.58694226	0.8668	-6.49
254935_at	putative disease resistance protei	---	AT4G10780	-1.05	-0.08	-0.57	0.58676139	0.8668	-6.49
248569_at	receptor protein kinase-like	---	AT5G49770	-1.05	-0.07	-0.57	0.58715233	0.8668	-6.49
256018_at	plastid heme oxygenase, putative	ho4	AT1G58300	-1.08	-0.11	-0.57	0.58695896	0.8668	-6.49
248134_at	putative protein contains similarity	---	AT5G54860	1.09	0.12	0.57	0.58716603	0.8668	-6.49
254257_s_at	putative protein predicted proteins	---	AT4G23350	-1.04	-0.06	-0.57	0.58673142	0.8668	-6.49
249667_at	unknown protein	---	---	-1.04	-0.05	-0.57	0.58711951	0.8668	-6.49
249772_at	unknown protein	---	AT5G24130	-1.08	-0.11	-0.57	0.58669466	0.8668	-6.49
261531_at	RB-binding protein -like similar to r	---	AT1G63490	-1.07	-0.10	-0.57	0.58740571	0.8669	-6.49
256198_at	Myb-family transcription factor, pu	---	AT1G58220	-1.07	-0.09	-0.57	0.58734363	0.8669	-6.49
255726_at	lysine and histidine specific transp	---	AT1G25530	-1.17	-0.22	-0.57	0.58739284	0.8669	-6.49
248303_at	FtsH protease, putative similar to A	FTSH11	AT5G53170	1.05	0.07	0.57	0.58760255	0.8670	-6.49
248234_at	putative protein contains similarity	---	AT5G53850	-1.04	-0.06	-0.57	0.58752969	0.8670	-6.49
258626_at	transfactor, putative similar to tran	---	AT3G04450	-1.05	-0.07	-0.57	0.58762954	0.8670	-6.49
251274_at	putative protein hypothetical prote	---	AT3G61700	1.08	0.11	0.57	0.58761358	0.8670	-6.49
251992_at	putative protein myosin heavy cha	---	AT3G53350	1.06	0.09	0.57	0.58790066	0.8670	-6.49
249642_at	putative protein	---	AT5G36960	1.06	0.08	0.57	0.58771194	0.8670	-6.49
257025_at	hypothetical protein predicted by g	ATG2	AT3G19190	-1.07	-0.09	-0.57	0.58782233	0.8670	-6.49
247769_at	laccase precursor - like protein lac	LAC16	AT5G58910	1.04	0.06	0.57	0.58768974	0.8670	-6.49
246168_at	meristem protein - like reproductiv	---	AT5G32460	-1.07	-0.10	-0.57	0.58791645	0.8670	-6.49
257184_at	ABC transporter, putative similar t	ATMRP8	AT3G13090	-1.04	-0.06	-0.57	0.5879377	0.8670	-6.49
264732_at	serpin, putative similar to serpin G	---	AT1G62160	-1.04	-0.05	-0.57	0.5878785	0.8670	-6.49
264020_at	putative signal sequence receptor	---	AT2G21160	1.06	0.09	0.57	0.58776378	0.8670	-6.49

266161_at	hypothetical protein	ATCHX7	AT2G28170	-1.06	-0.09	-0.57	0.58804354	0.8671	-6.49
248242_at	aldo/keto reductase-like protein	---	AT5G53580	-1.06	-0.08	-0.57	0.58836982	0.8673	-6.49
260753_at	RING-H2 finger protein RHA3a, p	---	AT1G49230	-1.12	-0.16	-0.57	0.58846254	0.8673	-6.49
255483_at	putative glycosyltransferase simila	XT2	AT4G02500	1.07	0.10	0.57	0.58857585	0.8673	-6.49
258157_at	putative MYB family transcription f	MYB4R1	AT3G18100	-1.07	-0.10	-0.57	0.58852126	0.8673	-6.49
250183_at	putative protein various predicted	---	AT5G14510	1.07	0.10	0.57	0.588223	0.8673	-6.49
266083_at	hypothetical protein predicted by g	---	AT2G37820	-1.04	-0.05	-0.57	0.588398	0.8673	-6.49
255646_at	hypothetical protein	---	AT4G00890	1.05	0.07	0.57	0.58858031	0.8673	-6.49
248842_at	unknown protein	---	AT5G46850	1.06	0.08	0.57	0.5884564	0.8673	-6.49
256148_at	hypothetical protein similar to puta	---	AT1G55090	-1.04	-0.05	-0.57	0.58827033	0.8673	-6.49
263734_at	permease, putative similar to perm	NAT7	AT1G60030	1.07	0.09	0.57	0.58848941	0.8673	-6.49
258142_at	unknown protein	---	AT3G18120	1.05	0.08	0.57	0.58842025	0.8673	-6.49
255345_at	putative aspartic protease ; suppo	---	AT4G04460	-1.18	-0.24	-0.57	0.58864218	0.8673	-6.49
253379_at	putative protein glycogenin glucos	PGSIP3	AT4G33330	1.04	0.06	0.57	0.58870586	0.8674	-6.49
261968_at	disease resistance protein RPP1-V	---	AT1G65850	1.04	0.05	0.57	0.58877296	0.8674	-6.49
266104_at	putative phosphatidate cytidylyltran	---	AT2G45150	-1.05	-0.07	-0.57	0.58881387	0.8674	-6.49
248007_at	S-adenosylmethionine:2-demethyl	---	AT5G56260	-1.04	-0.06	-0.57	0.58885213	0.8674	-6.49
257867_at	unknown protein	---	AT3G17780	-1.05	-0.07	-0.57	0.58891992	0.8674	-6.49
267004_at	hypothetical protein predicted by g	---	AT2G34260	1.15	0.20	0.57	0.58900093	0.8675	-6.49
258342_at	hypothetical protein similar to exte	---	AT3G22800	-1.09	-0.13	-0.57	0.58904248	0.8675	-6.49
262308_at	unknown protein	---	AT1G71010	-1.05	-0.08	-0.57	0.58930529	0.8678	-6.50
247142_at	putative protein strong similarity to	---	AT5G65570	-1.05	-0.07	-0.57	0.58934654	0.8678	-6.50
248781_at	putative protein similar to unknown	---	AT5G47870	-1.10	-0.14	-0.57	0.58938205	0.8678	-6.50
262081_at	kinesin motor protein (kin2), putati	ZCF125	AT1G59540	1.05	0.07	0.57	0.58949778	0.8680	-6.50
264164_at	Expressed protein ; supported by f	---	AT1G65295	1.06	0.08	0.57	0.58965138	0.8680	-6.50
249961_at	putative protein predicted proteins	---	AT5G18770	1.05	0.07	0.57	0.58965493	0.8680	-6.50
253722_at	putative protein zinc finger transcr	---	AT4G29190	-1.06	-0.08	-0.57	0.58958698	0.8680	-6.50
247410_at	putative protein similar to unknown	emb1692	AT5G62990	1.09	0.12	0.57	0.58970239	0.8680	-6.50
263175_at	hypothetical protein similar to unkr	---	AT1G05510	-1.04	-0.06	-0.57	0.58975273	0.8681	-6.50
246413_at	unknown protein	---	AT1G77310	1.05	0.07	0.57	0.58986006	0.8682	-6.50
265052_at	caffeic acid O-methyltransferase,	---	AT1G51990	-1.04	-0.05	-0.57	0.58991476	0.8682	-6.50
260704_at	glycine cleavage system H protein	---	AT1G32470	1.14	0.19	0.57	0.5900121	0.8682	-6.50
267060_at	unknown protein ; supported by fu	---	AT2G32580	-1.07	-0.10	-0.57	0.59004744	0.8682	-6.50
260967_at	unknown protein contains similarity	---	AT1G12230	-1.06	-0.08	-0.57	0.59010505	0.8682	-6.50
264425_at	serine/threonine protein kinase, p	---	AT1G61750	-1.04	-0.06	-0.57	0.59006799	0.8682	-6.50

246146_at	receptor-like protein kinase - like p	---	AT5G20050	1.06	0.09	0.57	0.59014918	0.8682	-6.50
249835_s_at	putative protein similar to unknown	---	AT5G23490	-1.09	-0.13	-0.57	0.59024765	0.8683	-6.50
262634_at	unknown protein ; supported by cD	---	AT1G06690	-1.12	-0.17	-0.57	0.59038874	0.8684	-6.50
263643_at	unknown protein predicted by gene	---	AT2G04740	-1.07	-0.10	-0.57	0.59038556	0.8684	-6.50
253716_at	hypothetical protein	---	AT4G29420	1.05	0.07	0.57	0.59034484	0.8684	-6.50
252443_at	putative helicase helicase SKI2W	---	AT3G46960	1.05	0.07	0.56	0.59046861	0.8684	-6.50
262534_at	unknown protein contains Pfam pr	SHA	AT1G17040	1.06	0.09	0.56	0.59108892	0.8686	-6.50
259688_at	membrane protein, putative simila	ATRBL2	AT1G63120	-1.07	-0.10	-0.56	0.59096	0.8686	-6.50
251645_at	putative protein polygalacturonase	---	AT3G57790	-1.05	-0.07	-0.56	0.59071459	0.8686	-6.50
265785_at	hypothetical protein predicted by g	---	AT2G07290	1.04	0.05	0.56	0.59101005	0.8686	-6.50
245699_at	putative protein ;supported by full-l	---	AT5G04250	-1.09	-0.12	-0.56	0.59098364	0.8686	-6.50
256810_at	adenyl cyclase, putative similar to	---	AT3G21465	1.05	0.07	0.56	0.59096738	0.8686	-6.50
258450_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.56	0.59108078	0.8686	-6.50
264812_at	putative thaumatin-like pathogenes	---	AT2G17860	-1.04	-0.06	-0.56	0.59072785	0.8686	-6.50
248846_at	putative protein similar to unknown	---	AT5G46500	-1.04	-0.06	-0.56	0.59077741	0.8686	-6.50
249432_at	putative ATP/GTP-binding protein	CLPS5	AT5G39930	-1.05	-0.06	-0.56	0.59097776	0.8686	-6.50
254678_at	hypothetical protein	---	AT4G18500	-1.04	-0.06	-0.56	0.59073051	0.8686	-6.50
251213_at	putative protein hypothetical protei	---	---	-1.04	-0.06	-0.56	0.59103964	0.8686	-6.50
266617_at	unknown protein ; supported by cl	---	AT2G29670	-1.11	-0.15	-0.56	0.59095599	0.8686	-6.50
255204_at	putative myosin-like protein	---	---	-1.06	-0.09	-0.56	0.59105694	0.8686	-6.50
264091_at	hypothetical protein predicted by g	---	AT1G79110	-1.11	-0.15	-0.56	0.59117543	0.8686	-6.50
262372_at	hypothetical protein predicted by g	---	AT1G73130	1.08	0.11	0.56	0.59122696	0.8686	-6.50
255167_at	putative protein hypothetical prote	---	---	1.03	0.05	0.56	0.59125997	0.8686	-6.50
255370_at	putative protein	---	---	-1.04	-0.05	-0.56	0.59151066	0.8690	-6.50
264537_at	receptor kinase, putative similar to	BRL1	AT1G55610	-1.07	-0.10	-0.56	0.59155547	0.8690	-6.50
253498_at	putative protein various predicted p	---	AT4G31890	-1.10	-0.14	-0.56	0.59160258	0.8690	-6.50
250480_at	protein serine/threonine kinase-lik	---	AT5G10290	1.12	0.17	0.56	0.59172587	0.8691	-6.50
267036_at	Expressed protein ; supported by f	---	AT2G38465	1.09	0.12	0.56	0.59211687	0.8693	-6.50
265917_at	putative disease resistance protein	AtRLP19	AT2G15080	-1.06	-0.08	-0.56	0.59279254	0.8693	-6.50
247346_at	diacylglycerol kinase	ATDGK2	AT5G63770	1.07	0.10	0.56	0.59272522	0.8693	-6.50
259965_at	transcriptional regulator, putative f	MSRB1	AT1G53670	1.06	0.08	0.56	0.59233156	0.8693	-6.50
248158_at	unknown protein	---	AT5G54440	1.04	0.05	0.56	0.59247568	0.8693	-6.50
248668_at	putative protein similar to unknown	XRI1	AT5G48720	1.08	0.11	0.56	0.59261346	0.8693	-6.50
254689_at	putative pectate lyase A11 ; suppo	---	AT4G13710	1.07	0.09	0.56	0.5920671	0.8693	-6.50
264189_s_at	hypothetical protein similar to acyl-	ACP3	AT1G54580	1.06	0.09	0.56	0.59256314	0.8693	-6.50

257991_at	unknown protein	---	AT3G19870	-1.06	-0.08	-0.56	0.59243585	0.8693	-6.50
251691_at	putative protein hypothetical prote	---	AT3G56520	-1.05	-0.08	-0.56	0.5924108	0.8693	-6.50
251485_at	putative protein rad21 mitotic cohe	SYN3	AT3G59550	1.04	0.05	0.56	0.59194674	0.8693	-6.50
247940_at	phosphatidylserine decarboxylase	PSD2	AT5G57190	-1.14	-0.19	-0.56	0.59274052	0.8693	-6.50
251239_at	putative protein several hypothetic	---	AT3G62440	-1.06	-0.09	-0.56	0.59229718	0.8693	-6.50
246267_at	Acyl CoA binding protein, putative	ACBP6	AT1G31812	1.04	0.05	0.56	0.59192627	0.8693	-6.50
246753_at	putative protein	---	---	-1.05	-0.07	-0.56	0.59266794	0.8693	-6.50
258014_at	hypothetical protein predicted by g	---	AT3G19330	-1.07	-0.10	-0.56	0.59221931	0.8693	-6.50
254214_at	putative potassium transport prote	TRH1	AT4G23640	-1.05	-0.07	-0.56	0.59214388	0.8693	-6.50
253781_at	putative protein predicted protein,	---	AT4G28580	1.04	0.06	0.56	0.5926847	0.8693	-6.50
263976_at	unknown protein	---	AT2G42700	-1.05	-0.08	-0.56	0.59256888	0.8693	-6.50
257947_at	putative isocitrate lyase similar to (	ICL	AT3G21720	1.06	0.08	0.56	0.59278227	0.8693	-6.50
259369_s_at	hypothetical protein similar to puta	---	AT1G69150 /	-1.05	-0.06	-0.56	0.59215132	0.8693	-6.50
246884_at	putative protein cation transport pr	---	AT5G26220	1.10	0.13	0.56	0.59242847	0.8693	-6.50
261548_at	DNA-binding protein, putative con	---	AT1G63480	1.06	0.08	0.56	0.59247241	0.8693	-6.50
261361_at	hypothetical protein predicted by g	---	---	-1.05	-0.07	-0.56	0.59274198	0.8693	-6.50
262036_at	ATP-dependent RNA helicase, pu	---	AT1G35530	1.06	0.09	0.56	0.59234649	0.8693	-6.50
245793_at	unknown protein ;supported by full	---	AT1G32220	1.10	0.14	0.56	0.59287816	0.8693	-6.50
251325_s_at	Lhca2 protein ;supported by full-le	LHCA2	AT3G61470 /	-1.03	-0.05	-0.56	0.59310231	0.8693	-6.50
259418_at	unknown protein ; supported by cD	GPAT2	AT1G02390	1.06	0.08	0.56	0.59312277	0.8693	-6.50
252682_at	putative protein AtOXA1, Arabidop	---	AT3G44370	-1.06	-0.08	-0.56	0.59302014	0.8693	-6.50
254388_at	Expressed protein ; supported by f	MSRB2	AT4G21860	-1.05	-0.06	-0.56	0.59308248	0.8693	-6.50
250943_at	putative protein	---	AT5G03360	1.04	0.06	0.56	0.59309675	0.8693	-6.50
255499_at	putative WD-repeat protein simila	---	AT4G02730	-1.04	-0.06	-0.56	0.59296821	0.8693	-6.50
245267_at	major latex protein like ; supported	---	AT4G14060	-1.05	-0.06	-0.56	0.59295266	0.8693	-6.50
256462_at	hypothetical protein predicted by g	---	AT1G36230	-1.05	-0.07	-0.56	0.59318036	0.8693	-6.50
262215_at	hypothetical protein contains simila	---	AT1G74790	1.11	0.15	0.56	0.59336703	0.8694	-6.50
250682_x_at	putative protein similar to unknown	---	AT5G06630	-1.11	-0.15	-0.56	0.59326557	0.8694	-6.50
253646_at	MAP kinase kinase 2 ; supported	ATMKK2	AT4G29810	-1.08	-0.11	-0.56	0.59331061	0.8694	-6.50
257191_at	Expressed protein ; supported by f	---	AT3G13175	-1.05	-0.07	-0.56	0.59337216	0.8694	-6.50
257208_at	hypothetical protein predicted by g	---	AT3G14910	1.07	0.09	0.56	0.59351859	0.8696	-6.50
253798_at	predicted protein CUC2 (involved	ANAC073	AT4G28500	-1.05	-0.07	-0.56	0.59355955	0.8696	-6.50
247125_at	putative protein contains similarity	---	AT5G66070	1.13	0.17	0.56	0.59363952	0.8696	-6.50
257447_at	hypothetical protein predicted by g	---	AT2G04230	-1.03	-0.05	-0.56	0.59377996	0.8697	-6.50
257046_at	ATPase, putative similar to spasti	---	AT3G19740	1.06	0.09	0.56	0.59385656	0.8697	-6.50

259440_at	hypothetical protein predicted by g	BPS1	AT1G01550	-1.04	-0.06	-0.56	0.59384824	0.8697	-6.50
248073_at	pectate lyase	---	AT5G55720	-1.04	-0.06	-0.56	0.59375131	0.8697	-6.50
267622_at	hypothetical protein predicted by g	---	AT2G39690	1.04	0.06	0.56	0.59380899	0.8697	-6.50
259769_at	RNA-binding protein MEI2, putativ	AML5	AT1G29400	1.07	0.10	0.56	0.59392878	0.8697	-6.50
246813_at	putative protein various predicted	---	---	-1.04	-0.06	-0.56	0.59399954	0.8698	-6.50
248419_at	putative protein similar to unknown	EXL3	AT5G51550	1.08	0.12	0.56	0.59434536	0.8702	-6.50
260491_at	hypothetical protein predicted by g	---	AT1G51440	-1.07	-0.09	-0.56	0.59446296	0.8702	-6.50
266405_at	hypothetical protein predicted by g	---	AT2G38580	1.08	0.12	0.56	0.59456696	0.8702	-6.50
251245_at	putative protein phytochrome-ass	PIL2	AT3G62090	-1.14	-0.19	-0.56	0.59442207	0.8702	-6.50
252486_at	arm repeat containing protein hom	PUB13	AT3G46510	1.05	0.07	0.56	0.59454615	0.8702	-6.50
249180_at	26S proteasome AAA-ATPase sub	RPT4A	AT5G43010	1.06	0.09	0.56	0.59453006	0.8702	-6.50
245223_at	gene_id:K17E7.5~unknown protein	---	AT3G29791	-1.05	-0.06	-0.56	0.59456006	0.8702	-6.50
251721_s_at	alpha-soluble NSF attachment pro	ALPHA-SN	AT3G56190	1.05	0.07	0.56	0.59467433	0.8703	-6.50
251081_at	putative protein kinase wall-assoc	---	AT5G02070	-1.06	-0.08	-0.56	0.5946775	0.8703	-6.50
247655_at	zinc finger protein Zat12 ;supporte	RHL41	AT5G59820	1.19	0.25	0.56	0.59475453	0.8703	-6.50
260790_at	hypothetical protein predicted by g	---	AT1G06240	1.07	0.10	0.56	0.59481262	0.8703	-6.50
265789_at	putative receptor-like protein kinas	---	AT2G01210	1.05	0.06	0.56	0.59485011	0.8703	-6.50
265920_s_at	unknown protein	---	AT2G15120	-1.12	-0.16	-0.56	0.5961524	0.8704	-6.50
253841_at	putative beta-glucosidase beta-glu	BGLU10	AT4G27830	-1.07	-0.09	-0.56	0.59653605	0.8704	-6.50
255719_at	unknown protein ;supported by full	---	AT1G32080	1.10	0.14	0.56	0.59521642	0.8704	-6.50
249862_at	PGPD14 protein ;supported by ful	---	AT5G22920	1.10	0.14	0.56	0.59637602	0.8704	-6.50
258134_at	rubisco expression protein, putativ	---	AT3G24530	1.06	0.09	0.55	0.59687714	0.8704	-6.50
254181_at	FtsH protease, putative contains s	---	AT4G23940	-1.04	-0.05	-0.56	0.5952841	0.8704	-6.50
261049_at	hypothetical protein similar to hypo	---	AT1G01430	-1.07	-0.10	-0.56	0.59552151	0.8704	-6.50
266467_at	Not56-like protein ; supported by	ALG3	AT2G47760	1.05	0.07	0.56	0.59580141	0.8704	-6.50
252292_at	RNA polymerase III subunit - like	---	AT3G49000	1.05	0.07	0.56	0.59502078	0.8704	-6.50
250366_at	putative protein predicted proteins	---	AT5G11420	-1.32	-0.40	-0.55	0.59701963	0.8704	-6.50
252864_at	putative protein regulatory protein	---	AT4G39740	-1.09	-0.12	-0.56	0.59618007	0.8704	-6.50
262547_at	hypothetical protein predicted by g	---	AT1G31270	1.04	0.05	0.55	0.59688996	0.8704	-6.50
251316_s_at	putative protein putative protein B	---	AT3G61480	-1.05	-0.07	-0.56	0.59569656	0.8704	-6.50
258320_at	hypothetical protein predicted by g	---	AT3G22710	1.04	0.06	0.56	0.59630485	0.8704	-6.50
266859_at	putative MADS-box protein	AGL41	AT2G26880	1.05	0.07	0.55	0.59695775	0.8704	-6.50
252273_at	putative WD-40 repeat - protein be	---	AT3G49660	-1.05	-0.07	-0.55	0.59686887	0.8704	-6.50
258353_s_at	unknown protein similar to GB:AAD	YSL5	AT3G17650	1.06	0.09	0.56	0.59540441	0.8704	-6.50
259810_at	Na+/H+ antiporter, putative simila	ATNHD2	AT1G49810	-1.04	-0.05	-0.55	0.59699952	0.8704	-6.50

263542_at	putative protein transport protein S	---	AT2G21630	1.07	0.09	0.56	0.59529771	0.8704	-6.50
265107_s_at	similar to glucose 1-dehydrogenas	---	AT1G62610 /	1.04	0.06	0.56	0.59655075	0.8704	-6.50
254318_at	putative protein embryo-abundant	---	AT4G22530	-1.18	-0.24	-0.56	0.59625505	0.8704	-6.50
246007_at	Expressed protein ; supported by f	FTRA2	AT5G08410	-1.05	-0.08	-0.56	0.59642022	0.8704	-6.50
266379_at	1,4-beta-xylan endohydrolase	---	AT2G14690	-1.05	-0.07	-0.56	0.59543905	0.8704	-6.50
247832_at	putative protein predicted proteins	EOL2	AT5G58550	-1.05	-0.07	-0.56	0.59546728	0.8704	-6.50
261970_at	glutamate decarboxylase (gad), p	GAD2	AT1G65960	-1.06	-0.09	-0.56	0.59678073	0.8704	-6.50
248194_at	Expressed protein ; supported by f	---	AT5G54095	1.04	0.05	0.56	0.59653213	0.8704	-6.50
260643_at	hypothetical protein contains simila	---	AT1G53270	-1.04	-0.06	-0.56	0.59613017	0.8704	-6.50
264566_at	hypothetical protein predicted by g	---	AT1G05270	-1.05	-0.07	-0.56	0.59654289	0.8704	-6.50
246652_at	extensin -like protein extensin, soy	---	AT5G35190	1.04	0.06	0.56	0.59511246	0.8704	-6.50
251491_at	fructokinase-like protein fructokina	---	AT3G59480	-1.07	-0.09	-0.56	0.59637293	0.8704	-6.50
251351_s_at	CaLB protein	NTMC2T4	AT3G60950 /	1.05	0.07	0.56	0.59683102	0.8704	-6.50
246458_at	putative protein various predicted	---	AT5G16860	-1.05	-0.07	-0.56	0.59559373	0.8704	-6.50
254000_at	galactinol synthase WSI76 protein	AtGolS6	AT4G26250	1.03	0.05	0.56	0.5962983	0.8704	-6.50
267460_at	putative squamosa-promoter bindi	SPL3	AT2G33810	-1.17	-0.23	-0.56	0.59641732	0.8704	-6.50
254140_at	putative protein	---	AT4G24610	1.07	0.10	0.56	0.59615992	0.8704	-6.50
260312_at	putative disease resistance protein	---	AT1G63880	-1.06	-0.08	-0.56	0.59524857	0.8704	-6.50
252979_at	Expressed protein ; supported by f	---	AT4G38225	-1.07	-0.10	-0.56	0.59525933	0.8704	-6.50
266773_at	hypothetical protein predicted by g	---	AT2G29040	1.04	0.06	0.56	0.59545867	0.8704	-6.50
263721_at	hypothetical protein predicted by g	---	AT2G13630	-1.04	-0.06	-0.55	0.59703405	0.8704	-6.50
249902_at	unknown protein	---	AT5G22680	-1.07	-0.09	-0.56	0.59551065	0.8704	-6.50
246833_at	putative protein	---	AT5G26620	1.04	0.05	0.56	0.5957438	0.8704	-6.50
255280_at	score=179, E=5.7e-06, N=1)	---	AT4G04960	1.10	0.14	0.56	0.5965847	0.8704	-6.50
254625_at	Expressed protein ; supported by f	SNI1	AT4G18470	-1.05	-0.07	-0.55	0.59700328	0.8704	-6.50
261730_s_at	mutator-like transposase, putative	---	---	-1.05	-0.06	-0.56	0.59539625	0.8704	-6.50
265156_at	hypothetical protein predicted by g	---	AT1G31000	-1.05	-0.07	-0.56	0.59610986	0.8704	-6.50
249616_s_at	contains similarity to DnaJ protein	---	AT5G37440 /	1.04	0.06	0.56	0.59668153	0.8704	-6.50
264627_at	hypothetical protein similar to carn	ECI1	AT1G65520	-1.05	-0.07	-0.56	0.59654265	0.8704	-6.50
263860_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.56	0.59549015	0.8704	-6.50
260629_at	unknown protein	---	AT1G62330	1.05	0.07	0.56	0.5952827	0.8704	-6.50
246659_at	putative protein predicted proteins	---	---	1.04	0.06	0.56	0.59595723	0.8704	-6.50
267321_at	hypothetical protein predicted by g	---	AT2G19320	1.05	0.07	0.56	0.59556787	0.8704	-6.50
262303_at	homeobox protein, putative simila	ATHB18	AT1G70920	-1.08	-0.11	-0.56	0.59593508	0.8704	-6.50
248611_at	putative protein contains similarity	WRKY48	AT5G49520	-1.15	-0.21	-0.56	0.59675603	0.8704	-6.50

252373_at	disease resistance protein EDS1 ;	EDS1	AT3G48090	1.15	0.20	0.56	0.59655251	0.8704	-6.50
253123_at	thaumatin-like protein thaumatin-li	---	AT4G36000	-1.05	-0.07	-0.56	0.59640769	0.8704	-6.50
250540_at	unknown protein ; supported by cl	---	AT5G08580	1.06	0.09	0.56	0.59683578	0.8704	-6.50
263803_at	hypothetical protein predicted by g	---	AT2G40440	-1.04	-0.06	-0.55	0.59715338	0.8705	-6.50
252873_at	putative protein myosin heavy cha	---	AT4G40020	-1.05	-0.07	-0.55	0.5972088	0.8705	-6.50
260276_at	unknown protein	---	AT1G80450	1.11	0.15	0.55	0.59725517	0.8706	-6.50
248025_at	NOI protein, nitrate-induced	NOI	AT5G55850	1.05	0.08	0.55	0.59735114	0.8706	-6.50
255087_at	putative protein proteins of this bac	---	AT4G09340	-1.04	-0.06	-0.55	0.59742801	0.8707	-6.50
255550_at	putative raffinose synthase or see	AtSTS	AT4G01970	-1.04	-0.06	-0.55	0.5974444	0.8707	-6.50
249116_at	putative protein similar to unknown	---	AT5G43820 /	1.06	0.08	0.55	0.59756959	0.8708	-6.50
247251_at	cellulose synthase catalytic subuni	CESA6	AT5G64740	-1.07	-0.09	-0.55	0.59790493	0.8708	-6.50
258001_at	AIG2-like protein similar to AIG2 p	---	AT3G28950	1.04	0.06	0.55	0.59795303	0.8708	-6.50
258827_at	hypothetical protein predicted by g	---	AT3G07150	-1.06	-0.09	-0.55	0.59782753	0.8708	-6.50
262556_at	hypothetical protein	---	AT1G31370	-1.04	-0.06	-0.55	0.59778408	0.8708	-6.50
262140_at	hypothetical protein predicted by g	---	AT1G52470	1.04	0.06	0.55	0.59796764	0.8708	-6.50
261921_at	hypothetical protein predicted by g	---	AT1G65900	1.08	0.12	0.55	0.59791822	0.8708	-6.50
258488_at	unknown protein ;supported by ful	---	AT3G02420	1.05	0.07	0.55	0.59778118	0.8708	-6.50
245287_at	imidazoleglycerol-phosphate dehy	---	AT4G14910	1.06	0.09	0.55	0.59777769	0.8708	-6.50
258506_at	hypothetical protein predicted by g	---	AT3G06520	1.06	0.09	0.55	0.59772651	0.8708	-6.50
267052_at	unknown protein	---	AT2G38410	-1.05	-0.07	-0.55	0.59795341	0.8708	-6.50
258836_at	hypothetical protein predicted usin	---	AT3G07210	1.07	0.09	0.55	0.59810087	0.8709	-6.50
258221_at	Snf1-related protein kinase KIN11	AKIN11	AT3G29160	1.08	0.12	0.55	0.59809897	0.8709	-6.50
245441_at	decarboxylase like protein	PSD1	AT4G16700	-1.06	-0.08	-0.55	0.59814236	0.8709	-6.50
244922_s_at	hypothetical protein	---	AT2G07674	-1.06	-0.08	-0.55	0.59825557	0.8710	-6.50
265495_at	unknown protein predicted by gens	---	AT2G15695	-1.05	-0.06	-0.55	0.5984431	0.8711	-6.50
265215_at	hypothetical protein predicted by g	---	AT1G05040	-1.04	-0.05	-0.55	0.59847266	0.8711	-6.50
260070_at	putative helix-loop-helix DNA-bindi	BEE3	AT1G73830	-1.22	-0.29	-0.55	0.59835203	0.8711	-6.50
255671_at	Expressed protein ; supported by f	---	AT4G00355	1.05	0.07	0.55	0.59845112	0.8711	-6.50
246722_at	putative protein various predicted	---	---	-1.06	-0.08	-0.55	0.59836345	0.8711	-6.50
262662_at	hypothetical protein similar to hypo	---	AT1G13920	1.05	0.07	0.55	0.59856529	0.8711	-6.50
251657_at	putative protein MULTICOPY SUP	---	AT3G57000	-1.08	-0.11	-0.55	0.59867456	0.8711	-6.50
262020_at	polyprotein, putative similar to gag	---	---	1.04	0.05	0.55	0.59868989	0.8711	-6.50
256539_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.55	0.59864194	0.8711	-6.50
246948_at	cytochrome P450-like protein CYT	CYP71B12	AT5G25130	-1.04	-0.05	-0.55	0.59898316	0.8712	-6.50
247491_at	putative protein supported by cDN	---	AT5G61880	1.09	0.13	0.55	0.59901203	0.8712	-6.50

248524_s_at	putative protein contains similarity	---	AT5G50570	-1.16	-0.22	-0.55	0.59879968	0.8712	-6.50
247753_at	hexosyltransferase - like protein	---	AT5G59070	1.12	0.17	0.55	0.59892657	0.8712	-6.50
249695_at	putative protein similar to unknown	---	---	-1.04	-0.06	-0.55	0.5988822	0.8712	-6.50
262079_at	unknown protein ; supported by cD	ZCW7	AT1G59600	1.07	0.09	0.55	0.59876876	0.8712	-6.50
265163_at	putative OBP32pep protein	---	AT1G23580	1.03	0.05	0.55	0.59887868	0.8712	-6.50
258272_at	unknown protein similar to serine/	---	AT3G15610	-1.06	-0.09	-0.55	0.59896674	0.8712	-6.50
264418_at	nuclear ribonucleoprotein, putative	---	AT1G43190	-1.07	-0.09	-0.55	0.59908971	0.8712	-6.50
263247_at	unknown protein	---	AT2G31440	-1.04	-0.05	-0.55	0.59906893	0.8712	-6.50
266223_at	putative thaumatin ;supported by f	---	AT2G28790	-1.18	-0.23	-0.55	0.5991851	0.8712	-6.50
257237_at	DNA nick sensor, putative contain	---	AT3G14890	1.12	0.17	0.55	0.59920503	0.8712	-6.50
253723_at	extensin-like protein ;supported by	---	AT4G29240	1.05	0.07	0.55	0.59924659	0.8712	-6.50
253398_at	putative protein retinal pigment mi	CCD8	AT4G32810	-1.11	-0.16	-0.55	0.59931284	0.8713	-6.50
246731_at	putative protein RING finger rngB	ACBP5	AT5G27630	1.05	0.07	0.55	0.59937215	0.8713	-6.50
266921_at	putative cytochrome P450	CYP86A8	AT2G45970	1.13	0.18	0.55	0.59955568	0.8715	-6.50
265932_at	hypothetical protein predicted by g	LBD8	AT2G19510	1.03	0.05	0.55	0.5995661	0.8715	-6.50
255366_x_at	putative transposon protein	---	---	-1.05	-0.06	-0.55	0.59960997	0.8715	-6.50
255568_at	putative DNA-binding protein ; sup	WRKY22	AT4G01250	-1.17	-0.22	-0.55	0.5998489	0.8717	-6.50
263561_at	unknown protein	---	AT2G15360	-1.03	-0.05	-0.55	0.59979468	0.8717	-6.50
260023_at	unknown protein	ATGA2OX2	AT1G30040	-1.08	-0.11	-0.55	0.59990353	0.8717	-6.50
252858_at	puative protein various predicted p	---	AT4G39770	-1.05	-0.07	-0.55	0.59986758	0.8717	-6.50
265207_at	unknown protein	---	AT2G36680	1.04	0.06	0.55	0.59998065	0.8717	-6.51
245813_at	hypothetical protein contains simila	---	AT1G49920	-1.06	-0.09	-0.55	0.60003198	0.8717	-6.51
258920_at	class 2 non-symbiotic hemoglobin	---	AT1G04380	-1.10	-0.13	-0.55	0.60007964	0.8717	-6.51
258795_at	hypothetical protein similar to puta	---	AT3G04570	1.05	0.08	0.55	0.6000452	0.8717	-6.51
267604_at	hypothetical protein predicted by g	ZFN2	AT2G32930	-1.09	-0.13	-0.55	0.60022689	0.8718	-6.51
249837_at	Expressed protein ; supported by f	---	AT5G23480	-1.05	-0.06	-0.55	0.6002209	0.8718	-6.51
249250_at	arm repeat containing protein	---	AT5G42340	-1.04	-0.06	-0.55	0.60031862	0.8719	-6.51
252999_at	putative protein other Arabidopsis	---	AT4G38500	1.05	0.06	0.55	0.60037133	0.8719	-6.51
267288_at	similar to cold acclimation protein \	---	AT2G23680	1.15	0.20	0.55	0.60045439	0.8720	-6.51
251509_at	pectinesterase precursor-like prot	---	AT3G59010	1.13	0.18	0.55	0.60055058	0.8721	-6.51
254122_at	CER2 ;supported by full-length cD	CER2	AT4G24510	1.29	0.36	0.55	0.60075329	0.8722	-6.51
257144_at	glucose-6-phosphate 1-dehydroge	G6PD5	AT3G27300	1.04	0.06	0.55	0.60072102	0.8722	-6.51
256929_at	unknown protein	---	---	-1.05	-0.07	-0.55	0.60082015	0.8722	-6.51
255091_at	putative protein various predicted p	---	---	-1.04	-0.05	-0.55	0.60079944	0.8722	-6.51
247245_at	putative protein similar to unknown	---	AT5G64720	-1.04	-0.06	-0.55	0.60070319	0.8722	-6.51

256160_at	pyruvate dehydrogenase E1 beta	PDH-E1 BE	AT1G30120	-1.06	-0.09	-0.55	0.6010447	0.8723	-6.51
245994_at	putative protein various predicted	---	---	-1.05	-0.07	-0.55	0.60107822	0.8723	-6.51
266896_at	putative ATP-dependent RNA helic	---	AT2G45810	1.04	0.05	0.55	0.60107212	0.8723	-6.51
262376_at	unknown protein contains similarity	HTH	AT1G72970	-1.04	-0.06	-0.55	0.60105299	0.8723	-6.51
250729_at	ubiquitin activating enzyme 2 (UBA	UBA 2	AT5G06460	-1.04	-0.06	-0.55	0.60117081	0.8724	-6.51
262045_at	hypothetical protein predicted by g	---	AT1G80240 /	1.07	0.10	0.55	0.60130082	0.8726	-6.51
246645_at	putative protein ;supported by full-	---	AT5G35080	1.05	0.08	0.55	0.60137025	0.8726	-6.51
248563_at	anthocyanidin-3-glucoside rhamno	---	AT5G49690	-1.07	-0.10	-0.55	0.60144159	0.8726	-6.51
264432_at	hypothetical protein similar to hypo	---	AT1G61710	-1.04	-0.06	-0.55	0.6014479	0.8726	-6.51
258505_at	hypothetical protein predicted by g	---	AT3G06530	1.13	0.18	0.55	0.60165288	0.8727	-6.51
249932_at	unknown protein	---	AT5G22390	-1.13	-0.18	-0.55	0.60158834	0.8727	-6.51
251136_at	mRNA capping enzyme - like prot	---	AT5G01290	1.04	0.05	0.55	0.60165862	0.8727	-6.51
261003_at	hypothetical protein predicted by g	---	AT1G26500	1.05	0.08	0.55	0.60182825	0.8727	-6.51
245444_at	limonene cyclase like protein	ATTPS03	AT4G16740	1.06	0.08	0.55	0.60179541	0.8727	-6.51
265606_s_at	putative non-LTR retroelement rev	---	AT3G09510	1.04	0.06	0.55	0.60179134	0.8727	-6.51
258579_s_at	germin-like protein contains Pfam	---	AT3G04180 /	1.04	0.05	0.55	0.60166775	0.8727	-6.51
259901_at	disease resistance protein, putativ	AtRLP14	AT1G74180	-1.06	-0.08	-0.55	0.60183865	0.8727	-6.51
266080_at	hypothetical protein predicted by g	---	AT2G37840	-1.03	-0.05	-0.55	0.60179683	0.8727	-6.51
262943_at	inosine-5'-monophosphate dehydr	---	AT1G79470	-1.04	-0.06	-0.55	0.60249316	0.8727	-6.51
254076_at	putative protein immunophilin FKB	---	AT4G25340	1.08	0.12	0.55	0.6023365	0.8727	-6.51
246196_at	hypothetical protein ;supported by	---	AT4G37090	1.06	0.09	0.55	0.60229291	0.8727	-6.51
258883_at	unknown protein predicted by gen	---	AT3G09970	1.05	0.07	0.55	0.60201856	0.8727	-6.51
251308_at	putative protein several hypothetic	GAUT1	AT3G61130	1.04	0.06	0.55	0.6023651	0.8727	-6.51
254430_at	reticuline oxidase - like protein ret	---	AT4G20820	1.11	0.15	0.55	0.60221517	0.8727	-6.51
262278_at	transcription factor PERIANTHIA ic	PAN	AT1G68640	1.05	0.08	0.55	0.60191049	0.8727	-6.51
257169_at	Expressed protein ; supported by f	AtSec20	AT3G24315	1.05	0.07	0.55	0.60241308	0.8727	-6.51
262612_at	unknown protein location of ESTs	---	AT1G14150	-1.12	-0.16	-0.55	0.60234347	0.8727	-6.51
266333_at	putative ubiquitin activating enzym	AXL	AT2G32410	1.05	0.07	0.55	0.60248915	0.8727	-6.51
258562_at	unknown protein ;supported by ful	---	AT3G05980	1.04	0.05	0.55	0.60218408	0.8727	-6.51
245591_at	hypothetical protein	---	AT4G14530	-1.03	-0.05	-0.55	0.60217695	0.8727	-6.51
247850_at	receptor-like protein kinase	---	AT5G58150	1.15	0.20	0.55	0.60234695	0.8727	-6.51
251806_at	zinc finger protein OBP3 ; support	OBP3	AT3G55370	-1.04	-0.06	-0.55	0.60213451	0.8727	-6.51
252783_at	putative protein predicted proteins	---	---	1.04	0.05	0.55	0.60248968	0.8727	-6.51
261807_at	Expressed protein ; supported by f	---	AT1G30515	1.04	0.06	0.55	0.60219779	0.8727	-6.51
253960_at	putative protein various predicted	GAMT1	AT4G26420	1.05	0.07	0.55	0.60233706	0.8727	-6.51

257933_at	aminoalcoholphosphotransferase,	AAPT2	AT3G25585	1.08	0.11	0.55	0.60265167	0.8727	-6.51
255397_at	putative transposon protein	---	---	-1.06	-0.08	-0.55	0.60268928	0.8727	-6.51
248150_at	kinesin-like protein ; supported by	ATK3	AT5G54670	-1.11	-0.15	-0.55	0.60264489	0.8727	-6.51
257481_at	hypothetical protein identical to hy	ALMT1	AT1G08430	1.04	0.06	0.55	0.60268552	0.8727	-6.51
260721_at	hypothetical protein predicted by g	---	AT1G48060	1.04	0.06	0.55	0.60274395	0.8728	-6.51
253859_at	Expressed protein ; supported by f	---	AT4G27657	-1.34	-0.42	-0.55	0.60284234	0.8728	-6.51
250981_at	receptor like protein kinase recept	---	AT5G03140	1.06	0.09	0.55	0.60293325	0.8729	-6.51
246597_at	L-aspartate oxidase -like protein L	AO	AT5G14760	-1.15	-0.20	-0.55	0.60316202	0.8729	-6.51
264179_at	hypothetical protein predicted by g	---	AT1G02180	1.07	0.10	0.55	0.60315505	0.8729	-6.51
250790_at	putative protein similar to unknown	---	AT5G05640	-1.07	-0.09	-0.55	0.603069	0.8729	-6.51
250848_at	3-phosphoinositide-dependent pro	PDK1	AT5G04510	1.05	0.07	0.55	0.60297181	0.8729	-6.51
266722_at	unknown protein	FUT2	AT2G03210	1.05	0.07	0.55	0.60321185	0.8729	-6.51
259576_at	RING zinc finger protein, putative	---	AT1G35330	1.06	0.09	0.55	0.60304346	0.8729	-6.51
251612_at	putative protein hypothetical prote	---	AT3G57950	-1.05	-0.06	-0.55	0.60313504	0.8729	-6.51
258864_at	unknown protein	---	AT3G03210	-1.06	-0.08	-0.55	0.60321028	0.8729	-6.51
247064_at	putative protein contains similarity	---	AT5G66890	1.08	0.11	0.55	0.60330625	0.8730	-6.51
259376_at	unknown protein C-terminus simila	CDC27a	AT3G16320	1.04	0.06	0.54	0.60336085	0.8730	-6.51
249070_at	cellulose synthase catalytic subuni	CESA4	AT5G44030	1.05	0.08	0.54	0.60344576	0.8730	-6.51
259402_at	developmental protein, putative si	VPS46.1	AT1G17730	1.04	0.06	0.54	0.6034791	0.8730	-6.51
249111_at	unknown protein	---	AT5G43770	-1.04	-0.05	-0.54	0.60343013	0.8730	-6.51
252379_at	ABC-type transport protein-like pr	ATH1	AT3G47730	1.05	0.07	0.54	0.60360509	0.8730	-6.51
266081_at	putative protein kinase contains a	---	AT2G37840	-1.04	-0.06	-0.54	0.60353378	0.8730	-6.51
257908_at	unknown protein contains Pfam pr	---	AT3G25410	-1.05	-0.07	-0.54	0.60358293	0.8730	-6.51
245657_at	unknown protein similar to recepto	---	AT1G56720	1.12	0.17	0.54	0.60369991	0.8731	-6.51
258518_at	unknown protein ; supported by cl	---	AT3G06570	1.04	0.05	0.54	0.60373748	0.8731	-6.51
252227_at	putative protein various predicted	---	AT3G49900	1.04	0.06	0.54	0.6038343	0.8731	-6.51
247322_at	unknown protein	---	AT5G64090	-1.04	-0.06	-0.54	0.60380421	0.8731	-6.51
249355_at	hypothetical protein	---	AT5G40500	1.04	0.06	0.54	0.60388074	0.8731	-6.51
265708_at	unknown protein member of a larg	---	AT2G03380	1.04	0.06	0.54	0.60394113	0.8732	-6.51
254270_at	gamma-glutamylcysteine syntheta	GSH1	AT4G23100	-1.12	-0.16	-0.54	0.60423023	0.8732	-6.51
247167_at	unknown protein	---	AT5G65850	1.06	0.08	0.54	0.6041235	0.8732	-6.51
265919_at	putative retroelement pol polyprote	---	---	-1.05	-0.07	-0.54	0.60421132	0.8732	-6.51
256138_at	Nt-gh3 deduced protein, putative	---	AT1G48670	-1.06	-0.08	-0.54	0.60424637	0.8732	-6.51
254449_at	putative protein predicted protein,	HEN1	AT4G20910	-1.06	-0.08	-0.54	0.60414611	0.8732	-6.51
253514_at	putative protein DNA-binding prot	---	AT4G31805	-1.04	-0.05	-0.54	0.60420788	0.8732	-6.51

255361_at	hypothetical protein	---	---	-1.04	-0.05	-0.54	0.60401717	0.8732	-6.51
257471_at	G-box binding factor, putative sim	ATBZIP4	AT1G59530	-1.04	-0.05	-0.54	0.60414576	0.8732	-6.51
255852_at	unknown protein	SVL2	AT1G66970	-1.13	-0.17	-0.54	0.60435786	0.8732	-6.51
250548_at	myosin heavy chain-like protein ; s	MBP2C	AT5G08120	1.05	0.06	0.54	0.60435124	0.8732	-6.51
251248_at	P-glycoprotein-like proetin P-glycc	PGP21	AT3G62150	1.21	0.27	0.54	0.60440436	0.8732	-6.51
245782_at	60S ribosomal protein (fragment),	---	AT1G35200	-1.06	-0.09	-0.54	0.60453175	0.8734	-6.51
264112_at	putative 1,3-beta-D-glucan syntha	CALS5	AT2G13680	-1.05	-0.07	-0.54	0.60467875	0.8735	-6.51
254478_at	putative protein TRANSCRIPTION	---	AT4G20330	1.06	0.08	0.54	0.60466054	0.8735	-6.51
247282_at	putative protein strong similarity to	AtMC3	AT5G64240	-1.05	-0.07	-0.54	0.60472287	0.8735	-6.51
264912_at	auxin-induced protein, putative sir	---	AT1G60750	-1.04	-0.06	-0.54	0.60477014	0.8735	-6.51
256806_at	CCAAT-binding factor B chain, pu	NF-YA9	AT3G20910	1.05	0.07	0.54	0.60487338	0.8736	-6.51
249387_at	putative protein predicted proteins	---	AT5G40070	-1.06	-0.08	-0.54	0.6049272	0.8736	-6.51
254485_at	cell-cell signaling protein csgA - lik	---	AT4G20760	-1.06	-0.08	-0.54	0.6051828	0.8737	-6.51
251335_at	1-aminocyclopropane-1-carboxyla	---	AT3G61400	1.07	0.10	0.54	0.60520588	0.8737	-6.51
252806_at	putative protein	---	AT3G42390	-1.04	-0.06	-0.54	0.60518283	0.8737	-6.51
249374_at	20S proteasome beta subunit PBB	PBB2	AT5G40580	1.05	0.07	0.54	0.60508544	0.8737	-6.51
261274_at	myb-related protein, putative simil	MYB117	AT1G26780	1.04	0.05	0.54	0.60513174	0.8737	-6.51
249697_at	unknown protein	---	AT5G35510	-1.04	-0.06	-0.54	0.60513395	0.8737	-6.51
266929_at	putative AT-hook DNA-binding pro	---	AT2G45850	-1.04	-0.06	-0.54	0.60525392	0.8737	-6.51
247436_at	dehydrogenase ; supported by cD	ALDH12A1	AT5G62530	-1.06	-0.09	-0.54	0.60540545	0.8738	-6.51
245385_at	hypothetical protein ;supported by	---	AT4G14020	-1.07	-0.09	-0.54	0.60570933	0.8739	-6.51
261166_s_at	Expressed protein ; supported by f	---	AT1G34570 /	1.06	0.08	0.54	0.60611815	0.8739	-6.51
247996_at	putative protein contains similarity	---	AT5G56170	1.08	0.11	0.54	0.60595511	0.8739	-6.51
252496_at	putative protein several hypothetic	CRR2	AT3G46790	-1.07	-0.10	-0.54	0.60595506	0.8739	-6.51
258542_at	unknown protein	---	AT3G07030	1.05	0.07	0.54	0.60609885	0.8739	-6.51
250066_at	unknown protein	---	AT5G17930	-1.07	-0.10	-0.54	0.60595679	0.8739	-6.51
252911_at	cytochrome P450 -like protein cyt	CYP96A12	AT4G39510	-1.13	-0.17	-0.54	0.60596999	0.8739	-6.51
246939_at	AP2 domain containing protein AF	SHN2	AT5G25390	-1.05	-0.06	-0.54	0.60598536	0.8739	-6.51
262257_at	hypothetical protein predicted by g	---	AT1G53860	1.05	0.07	0.54	0.60562995	0.8739	-6.51
252040_at	putative protein hypothetical prote	---	AT3G52060	1.10	0.14	0.54	0.60569264	0.8739	-6.51
252727_s_at	putative protein predicted proteins	---	---	1.04	0.05	0.54	0.60554733	0.8739	-6.51
266032_x_at	putative replication protein A1	---	---	1.05	0.06	0.54	0.60612186	0.8739	-6.51
264536_at	hypothetical protein predicted by g	PRA1.G1	AT1G55640	1.07	0.10	0.54	0.60559051	0.8739	-6.51
265745_at	hypothetical protein predicted by g	---	---	-1.04	-0.05	-0.54	0.60605852	0.8739	-6.51
245487_at	phytochrome D	PHYD	AT4G16250	-1.05	-0.08	-0.54	0.60586536	0.8739	-6.51

264290_at	hypothetical protein predicted by g	---	AT1G78810	-1.06	-0.09	-0.54	0.60550005	0.8739	-6.51
249881_at	cytochrome P450-like protein	CYP86B1	AT5G23190	-1.04	-0.05	-0.54	0.60591931	0.8739	-6.51
247877_at	putative protein contains similarity	XBAT32	AT5G57740	1.08	0.11	0.54	0.60571603	0.8739	-6.51
266552_at	unknown protein ; supported by cD	AGP16	AT2G46330	1.07	0.09	0.54	0.6063439	0.8740	-6.51
262298_at	unknown protein Similar to gb|AF1	---	AT1G27530	-1.04	-0.05	-0.54	0.60632677	0.8740	-6.51
261869_at	hypothetical protein predicted by g	---	AT1G11470	-1.05	-0.07	-0.54	0.60631201	0.8740	-6.51
260270_at	putative disease resistance protein	---	AT1G63730	-1.04	-0.06	-0.54	0.60623351	0.8740	-6.51
249482_at	putative protein ;supported by full-	---	AT5G38980	-1.11	-0.15	-0.54	0.60643062	0.8740	-6.51
246854_at	mitochondrial carrier - like protein	---	AT5G26200	1.05	0.07	0.54	0.60650954	0.8740	-6.51
264404_at	putative cytochrome P450	CYP82F1	AT2G25160	-1.06	-0.08	-0.54	0.60652082	0.8740	-6.51
263273_x_at	En/Spm-like transposon protein re	---	---	-1.04	-0.06	-0.54	0.60650807	0.8740	-6.51
258039_at	unknown protein ;supported by ful	---	AT3G21200	1.04	0.06	0.54	0.60661809	0.8740	-6.51
264890_at	unknown protein	---	AT1G23180	1.06	0.09	0.54	0.60661401	0.8740	-6.51
249653_at	putative protein REPLICATION PF	---	---	1.04	0.06	0.54	0.60665289	0.8740	-6.51
262794_at	unknown protein EST gb|N37870 c	emb1745	AT1G13120	-1.05	-0.06	-0.54	0.60688035	0.8741	-6.51
250309_at	putative protein similar to unknown	---	AT5G12220	1.06	0.08	0.54	0.60687469	0.8741	-6.51
254177_at	putative protein gene T22C1.1, Ca	---	AT4G23860	1.06	0.09	0.54	0.60688116	0.8741	-6.51
256800_at	hypothetical protein predicted by g	---	AT3G20900	-1.05	-0.07	-0.54	0.60677191	0.8741	-6.51
248478_at	ubiquitin-conjugating enzyme-like p	UBC27	AT5G50870	-1.04	-0.05	-0.54	0.60699732	0.8743	-6.51
267557_at	unknown protein ; supported by cD	KRP4	AT2G32710	1.06	0.08	0.54	0.6071966	0.8744	-6.51
257573_at	putative SF16 protein {Helianthus a	iqd9	AT2G33990	1.07	0.09	0.54	0.60719326	0.8744	-6.51
246113_at	putative protein predicted proteins	---	---	1.04	0.06	0.54	0.60738871	0.8746	-6.51
263363_at	putative cold-regulated protein ;su	---	AT2G03850	-1.13	-0.18	-0.54	0.60735243	0.8746	-6.51
252777_at	hypothetical protein	---	AT3G42970	-1.04	-0.06	-0.54	0.60756355	0.8748	-6.51
262869_s_at	putative protein predicted protein,	GTG1	AT1G64990 /	1.05	0.07	0.54	0.60760014	0.8748	-6.51
247596_at	putative protein predicted protein,	---	AT5G60840	-1.08	-0.11	-0.54	0.60816905	0.8748	-6.51
267129_at	curly leaf protein (polycomb-group	CLF	AT2G23380	-1.04	-0.06	-0.53	0.61037045	0.8748	-6.51
256406_at	unknown protein	---	AT1G50710	-1.05	-0.07	-0.53	0.61048403	0.8748	-6.51
266704_at	putative N-acetyl-gamma-glutamyl	---	AT2G19940	1.05	0.08	0.54	0.60813872	0.8748	-6.51
263843_at	translin-like protein ; supported by	---	AT2G37020	-1.04	-0.06	-0.54	0.6092154	0.8748	-6.51
257687_at	hypothetical protein predicted by g	SDRB	AT3G12800	1.04	0.06	0.54	0.60971957	0.8748	-6.51
260480_at	Ser/Thr kinase ;supported by full-l	SNRK2.4	AT1G10940	1.03	0.05	0.54	0.60907048	0.8748	-6.51
247694_at	GTP cyclohydrolase II / 3,4-dihydr	---	AT5G59750	-1.05	-0.07	-0.53	0.6100957	0.8748	-6.51
262918_at	hypothetical protein predicted by g	---	AT1G65000	-1.05	-0.07	-0.54	0.60855725	0.8748	-6.51
252128_at	transcription factor-like protein Ara	MNP	AT3G50870	-1.04	-0.06	-0.54	0.60919506	0.8748	-6.51

249769_at	sigma-like factor (emb CAA77213.	SIGE	AT5G24120	1.06	0.09	0.54	0.60948564	0.8748	-6.51
247401_at	1-deoxy-D-xylulose 5-phosphate re	DXR	AT5G62790	1.07	0.09	0.54	0.60961063	0.8748	-6.51
246523_at	CONSTANS-like 1	COL1	AT5G15850	-1.07	-0.10	-0.54	0.60935493	0.8748	-6.51
255851_at	hypothetical protein predicted by g	---	AT1G67040	-1.05	-0.07	-0.54	0.60863691	0.8748	-6.51
264545_at	photosystem I subunit V precurso	PSAG	AT1G55670	1.03	0.05	0.54	0.60984853	0.8748	-6.51
251453_at	putative protein hypothetical prote	---	AT3G60070	-1.05	-0.06	-0.54	0.60913242	0.8748	-6.51
263583_at	putative NAD+ dependent isocitra	IDH2	AT2G17130	1.07	0.09	0.53	0.61017257	0.8748	-6.51
251507_at	putative protein CND41, chloropla	---	AT3G59080	1.21	0.27	0.54	0.60963748	0.8748	-6.51
245389_at	putative protein ;supported by full-l	---	AT4G17480	-1.05	-0.08	-0.53	0.61048546	0.8748	-6.51
245312_at	Expressed protein ; supported by f	---	AT4G14600	1.06	0.08	0.54	0.60980265	0.8748	-6.51
265454_at	putative ARF1 family auxin respon	ARF11	AT2G46530	1.14	0.19	0.53	0.61006456	0.8748	-6.51
259541_at	protein kinase, putative similar to	---	AT1G20650	1.07	0.10	0.54	0.60768413	0.8748	-6.51
249713_at	putative protein contains similarity	---	AT5G35690	-1.05	-0.07	-0.54	0.60792216	0.8748	-6.51
258806_at	unknown protein	---	AT3G04020	1.08	0.11	0.54	0.6096948	0.8748	-6.51
259647_at	acetyl-CoA synthetase, putative si	---	AT1G55325	1.05	0.07	0.53	0.6103091	0.8748	-6.51
260822_at	RNA polymerase, putative similar	---	AT1G06790	1.04	0.06	0.54	0.60948184	0.8748	-6.51
253515_at	auxin induced like-protein auxin-in	---	AT4G31320	-1.06	-0.08	-0.54	0.60826483	0.8748	-6.51
264167_at	unknown protein Location of EST g	---	AT1G02060	-1.06	-0.09	-0.54	0.60838062	0.8748	-6.51
252652_at	putative chloroplast prephenate de	ADT4	AT3G44720	-1.17	-0.23	-0.54	0.60808801	0.8748	-6.51
248034_at	serine threonine-specific protein ki	D6PK	AT5G55910	1.05	0.07	0.54	0.60926429	0.8748	-6.51
248645_at	unknown protein	GEX2	AT5G49150	-1.05	-0.07	-0.54	0.60810202	0.8748	-6.51
265587_at	putative pathogenesis-related prot	---	AT2G19980	1.04	0.06	0.53	0.60992936	0.8748	-6.51
266778_at	putative cytochrome P450	CYP707A2	AT2G29090	1.05	0.07	0.53	0.61049571	0.8748	-6.51
252258_at	putative protein several hypothetic	---	AT3G49450	-1.05	-0.08	-0.53	0.61012407	0.8748	-6.51
263654_at	unknown protein	---	AT1G04300	1.04	0.06	0.54	0.60896528	0.8748	-6.51
260484_at	putative zinc finger protein similar t	---	AT1G68360	-1.05	-0.07	-0.53	0.61024551	0.8748	-6.51
265640_at	putative cysteine proteinase	---	AT2G27395	1.04	0.05	0.54	0.60825417	0.8748	-6.51
256586_at	hypothetical protein	---	AT3G28770	-1.04	-0.05	-0.54	0.60822051	0.8748	-6.51
255740_at	wall-associated kinase, putative si	---	AT1G25390	-1.12	-0.16	-0.54	0.60836014	0.8748	-6.51
260320_at	hypothetical protein similar to puta	---	AT1G63930	1.06	0.09	0.54	0.60795091	0.8748	-6.51
260757_at	phytocyanin, putative similar to ph	---	AT1G48940	-1.04	-0.05	-0.53	0.6101537	0.8748	-6.51
262403_s_at	mutator-like transposase, putative	---	---	-1.04	-0.05	-0.54	0.60801083	0.8748	-6.51
266997_at	hypothetical protein predicted by g	---	AT2G34410	-1.07	-0.10	-0.54	0.60849953	0.8748	-6.51
255844_at	putative protein kinase contains a	---	AT2G33580	1.10	0.14	0.54	0.60842717	0.8748	-6.51
247163_at	Expressed protein ; supported by c	---	AT5G65685	-1.05	-0.07	-0.54	0.60958158	0.8748	-6.51

265152_s_at	hypothetical protein predicted by g	---	AT1G30935	1.04	0.05	0.53	0.61029708	0.8748	-6.51
252781_at	polygalacturonase -like protein po	---	AT3G42950	1.04	0.06	0.54	0.60796003	0.8748	-6.51
265621_at	NAM (no apical meristem)-like prot	NTL8	AT2G27300	1.04	0.06	0.53	0.61034173	0.8748	-6.51
245247_at	scarecrow-like 13 (SCL13) ; suppo	SCL13	AT4G17230	-1.13	-0.17	-0.54	0.60917463	0.8748	-6.51
246204_at	putative protein ; supported by cDN	---	AT4G37020	1.04	0.06	0.54	0.60788415	0.8748	-6.51
AFFX-TrpnX-5	B. subtilis /GEN=trpE, trpD /DB_XI	---	---	-1.04	-0.06	-0.54	0.60974863	0.8748	-6.51
252398_at	putative protein RING-H2 finger p	---	AT3G47990	-1.04	-0.06	-0.54	0.60861907	0.8748	-6.51
266985_at	putative geranylgeranyl transferase	PGGT-I	AT2G39550	1.05	0.07	0.53	0.60988965	0.8748	-6.51
266413_at	unknown protein ;supported by ful	---	AT2G38740	-1.05	-0.07	-0.54	0.60890002	0.8748	-6.51
256283_at	hypothetical protein	---	AT3G12540	-1.04	-0.06	-0.54	0.60820155	0.8748	-6.51
263051_s_at	En/Spm-like transposon protein rel	---	---	1.04	0.06	0.54	0.60971885	0.8748	-6.51
267117_at	unknown protein	---	AT2G32560	-1.04	-0.05	-0.53	0.61006678	0.8748	-6.51
259066_at	hypothetical protein predicted by g	---	AT3G07530	-1.06	-0.09	-0.54	0.60856389	0.8748	-6.51
267483_at	unknown protein ;supported by ful	UTR1	AT2G02810	1.16	0.22	0.54	0.6088385	0.8748	-6.51
255459_at	polyubiquitin (UBQ14) identical to	UBQ14	AT4G02890	1.04	0.06	0.54	0.60824912	0.8748	-6.51
AFFX-r2-Bs-lys	B. subtilis /GEN=lys /DB_XREF=gi	---	---	-1.11	-0.15	-0.54	0.60897027	0.8748	-6.51
261196_at	unknown protein	SCRM2	AT1G12860	1.09	0.12	0.54	0.60791684	0.8748	-6.51
255112_at	casein kinase I - Arabidopsis thali	---	AT4G08800	-1.04	-0.06	-0.54	0.60883659	0.8748	-6.51
251014_at	putative protein fimbriae-associate	---	AT5G02520	-1.04	-0.05	-0.54	0.60970012	0.8748	-6.51
255998_at	hypothetical protein contains simila	---	AT1G29780	1.04	0.05	0.54	0.60951694	0.8748	-6.51
251625_at	beta-1,3-glucanase 2 (BG2) (PR-2	BGL2	AT3G57260	1.70	0.77	0.53	0.61042961	0.8748	-6.51
263481_at	predicted protein	---	AT2G04025	-1.04	-0.05	-0.54	0.60873553	0.8748	-6.51
247088_at	unknown protein	---	AT5G66340	1.04	0.06	0.54	0.60830994	0.8748	-6.51
247736_at	actin 4 ;supported by full-length cI	ACT4	AT5G59370	-1.04	-0.06	-0.54	0.60928856	0.8748	-6.51
256414_at	putative nucleic acid binding protei	AL2	AT3G11200	1.04	0.06	0.54	0.60951937	0.8748	-6.51
257778_at	hypothetical protein predicted by g	---	---	-1.05	-0.07	-0.54	0.60911731	0.8748	-6.51
257482_x_at	hypothetical protein contains simila	---	AT1G27820	1.06	0.09	0.54	0.60977344	0.8748	-6.51
246336_at	putative protein putative integral m	ATCHX4	AT3G44900	-1.04	-0.05	-0.54	0.60982565	0.8748	-6.51
259925_at	thaumatin-like protein similar to tha	PR5	AT1G75040	1.61	0.69	0.54	0.60942145	0.8748	-6.51
261486_at	nucleic acid binding protein (alfin-	AL7	AT1G14510	1.05	0.06	0.54	0.60946709	0.8748	-6.51
258766_at	galactokinase-like protein similar t	---	AT3G10700	-1.04	-0.06	-0.53	0.61060848	0.8749	-6.51
253568_at	putative protein receptor-like kinas	---	AT4G31230	-1.04	-0.06	-0.53	0.61070888	0.8750	-6.51
259166_at	unknown protein ; supported by cI	---	AT3G01670	1.14	0.19	0.53	0.61102519	0.8751	-6.51
252667_at	protein kinase-like protein MSTK2	NEK6	AT3G44200	-1.06	-0.08	-0.53	0.61100805	0.8751	-6.51
245806_at	light-harvesting complex protein si	LHCA5	AT1G45474	-1.08	-0.11	-0.53	0.61086161	0.8751	-6.51

255833_at	unknown protein	---	AT2G33390	1.05	0.07	0.53	0.61083738	0.8751	-6.51
255880_at	hypothetical protein predicted by g	---	AT1G67060	-1.04	-0.06	-0.53	0.61104664	0.8751	-6.51
260983_at	hypothetical protein predicted by g	---	AT1G53560	-1.08	-0.11	-0.53	0.61080448	0.8751	-6.51
265787_at	Mutator-like transposase similar to	---	---	-1.06	-0.08	-0.53	0.61103864	0.8751	-6.51
250200_at	peroxidase ATP20a (emb|CAA673	---	AT5G14130	1.05	0.07	0.53	0.61093277	0.8751	-6.51
267073_at	unknown protein	---	AT2G41160	-1.06	-0.08	-0.53	0.61110402	0.8751	-6.52
261015_at	14-3-3 protein GF14iota (grf12) ide	GRF12	AT1G26480	1.04	0.06	0.53	0.61116497	0.8751	-6.52
251636_at	calcium-dependent protein kinase	CPK32	AT3G57530	1.15	0.20	0.53	0.61157943	0.8757	-6.52
250299_at	putative esterase - like protein cin	---	AT5G11910	1.04	0.06	0.53	0.61167521	0.8757	-6.52
255705_at	hypothetical protein ;supported by	---	AT4G00160	1.04	0.05	0.53	0.61167965	0.8757	-6.52
251192_at	alpha galactosyltransferase-like pr	XT1	AT3G62720	1.11	0.15	0.53	0.61178225	0.8758	-6.52
249585_at	5-oxoprolinase -like protein 5-oxo	OXP1	AT5G37830	1.04	0.06	0.53	0.61208341	0.8758	-6.52
257315_at	proline oxidase, mitochondrial pre	ERD5	AT3G30775	-1.17	-0.23	-0.53	0.61232672	0.8758	-6.52
251306_at	putative DNA-binding protein DNA	---	AT3G61260	1.06	0.08	0.53	0.61264221	0.8758	-6.52
248165_at	putative protein similar to unknown	PHOS32	AT5G54430	1.05	0.07	0.53	0.61195333	0.8758	-6.52
245709_at	putative protein	---	AT5G04320	1.06	0.08	0.53	0.6127645	0.8758	-6.52
250972_at	putative protein various Myb relate	LCL1	AT5G02840	1.07	0.10	0.53	0.61269998	0.8758	-6.52
249751_at	putative protein similar to unknown	---	AT5G24650	1.06	0.08	0.53	0.61210256	0.8758	-6.52
246560_at	putative protein hypothetical protei	---	AT5G15560	-1.04	-0.06	-0.53	0.61219915	0.8758	-6.52
254883_at	putative protein histidine-rich glyc	HAP2	AT4G11720	-1.05	-0.08	-0.53	0.612262	0.8758	-6.52
252804_at	putative protein	---	---	-1.04	-0.05	-0.53	0.61267955	0.8758	-6.52
248940_at	replication protein A1-like	---	AT5G45400	-1.05	-0.07	-0.53	0.61268177	0.8758	-6.52
266242_at	hypothetical protein predicted by g	---	AT2G27790	1.04	0.06	0.53	0.61252022	0.8758	-6.52
246531_at	MADS box protein AGL2 ; suppor	ספט-01	AT5G15800	1.05	0.07	0.53	0.61243939	0.8758	-6.52
266528_at	putative disease resistance protein	---	AT2G16870	-1.04	-0.05	-0.53	0.61199412	0.8758	-6.52
260130_s_at	beta-glucosidase, putative similar	BGLU21	AT1G66270 /	1.03	0.05	0.53	0.61212675	0.8758	-6.52
267191_at	similar to Mlo proteins from H. vulg	MLO15	AT2G44110	1.06	0.09	0.53	0.61266328	0.8758	-6.52
267407_at	unknown protein	MEE27	AT2G34880	1.05	0.06	0.53	0.61277197	0.8758	-6.52
251434_at	polygalacturonase-like protein pol	---	AT3G59850	-1.04	-0.06	-0.53	0.61269835	0.8758	-6.52
245511_at	hypothetical protein	---	AT4G15755	1.04	0.05	0.53	0.61254939	0.8758	-6.52
258793_at	hypothetical protein supported by f	---	AT3G04780	1.04	0.06	0.53	0.61261705	0.8758	-6.52
250071_at	putative protein similar to unknown	---	AT5G18000	-1.04	-0.05	-0.53	0.61269819	0.8758	-6.52
255374_at	hypothetical protein	---	---	-1.03	-0.05	-0.53	0.61260019	0.8758	-6.52
260269_at	putative disease resistance protein	---	AT1G63740	1.05	0.07	0.53	0.61222084	0.8758	-6.52
267067_at	unknown protein	---	AT2G41020	-1.06	-0.08	-0.53	0.61217354	0.8758	-6.52

246707_at	putative protein	---	---	-1.04	-0.06	-0.53	0.61207996	0.8758	-6.52
251530_at	putative protein several hypothetic	---	AT3G58520	1.06	0.09	0.53	0.61282398	0.8758	-6.52
257083_s_at	non-race specific disease resistan	---	AT3G20590	1.08	0.11	0.53	0.61295728	0.8760	-6.52
257983_at	unknown protein	---	AT3G20790	-1.12	-0.16	-0.53	0.61307514	0.8761	-6.52
258168_at	hypothetical protein predicted by g	---	AT3G21570	-1.04	-0.05	-0.53	0.61316763	0.8762	-6.52
259861_at	unknown protein similar to ribosom	---	AT1G80620	1.05	0.08	0.53	0.61332493	0.8762	-6.52
264888_at	hypothetical protein	---	AT1G23070	-1.04	-0.06	-0.53	0.61332086	0.8762	-6.52
247590_at	putative protein predicted proteins	---	AT5G60720	-1.05	-0.07	-0.53	0.61327513	0.8762	-6.52
258601_at	putative histidyl tRNA synthetase s	---	AT3G02760	-1.05	-0.07	-0.53	0.61352479	0.8764	-6.52
259168_at	unknown protein similar to hypothe	---	AT3G03570	-1.05	-0.07	-0.53	0.61354587	0.8764	-6.52
255620_at	putative copper-containing glycop	---	AT4G01380	-1.04	-0.05	-0.53	0.61349075	0.8764	-6.52
262709_at	unknown protein ESTs gb|F15498	SYP51	AT1G16240	1.05	0.07	0.53	0.61365828	0.8764	-6.52
250963_at	putative protein various predicted	---	AT5G03000	-1.06	-0.08	-0.53	0.61362747	0.8764	-6.52
252287_at	30S ribosomal protein S9 -like sim	---	AT3G49080	1.07	0.10	0.53	0.6138183	0.8765	-6.52
246609_at	putative receptor-like protein kinas	---	AT5G35390	-1.04	-0.05	-0.53	0.61379598	0.8765	-6.52
255438_at	putative oxidoreductase	AOP1	AT4G03070	-1.10	-0.14	-0.53	0.61379049	0.8765	-6.52
261967_at	En/Spm-like transposon protein, p	---	---	-1.06	-0.08	-0.53	0.61384804	0.8765	-6.52
253302_at	Expressed protein ; supported by f	---	AT4G33660	-1.06	-0.09	-0.53	0.61403677	0.8766	-6.52
248639_at	anthranilate N-benzoyltransferase	HCT	AT5G48930	-1.07	-0.10	-0.53	0.61400473	0.8766	-6.52
251149_at	putative protein CGI-77 protein, H	---	AT3G62940	-1.03	-0.05	-0.53	0.61400051	0.8766	-6.52
264246_at	trehalose-6-phosphate synthase,	ATTPS10	AT1G60140	1.13	0.18	0.53	0.61425068	0.8768	-6.52
245174_at	putative kinesin heavy chain	---	AT2G47500	-1.08	-0.11	-0.53	0.61423517	0.8768	-6.52
260663_at	hypothetical protein predicted by g	NFD5	AT1G19520	1.07	0.10	0.53	0.61430337	0.8768	-6.52
250861_at	putative protein predicted proteins	---	AT5G04740	1.05	0.07	0.53	0.61447618	0.8769	-6.52
255597_at	hypothetical protein	---	AT4G01730	-1.05	-0.07	-0.53	0.61446877	0.8769	-6.52
256578_at	peroxidase, putative similar to per	---	AT3G28200	-1.09	-0.12	-0.53	0.61483703	0.8770	-6.52
257652_at	unknown protein contains Pfam pr	APUM24	AT3G16810	-1.08	-0.12	-0.53	0.61495079	0.8770	-6.52
265943_at	putative cytidine deaminase ;supp	CDA1	AT2G19570	-1.09	-0.13	-0.53	0.61460698	0.8770	-6.52
246428_at	spindle pole body protein-like spin	---	AT5G17410	1.05	0.08	0.53	0.61492719	0.8770	-6.52
248078_at	putative protein contains similarity	---	AT5G55780	-1.04	-0.06	-0.53	0.6148361	0.8770	-6.52
254383_at	hypothetical protein	---	AT4G21950	-1.04	-0.06	-0.53	0.61494483	0.8770	-6.52
246532_at	putative protein beta-glucan-elicit	---	AT5G15870	1.18	0.24	0.53	0.61457044	0.8770	-6.52
257502_at	unknown protein	---	AT1G78110	1.09	0.13	0.53	0.6149185	0.8770	-6.52
257716_at	hypothetical protein predicted by g	---	AT3G18300	1.04	0.06	0.53	0.61470569	0.8770	-6.52
248601_at	putative protein contains similarity	---	AT5G49400	1.03	0.05	0.53	0.61487893	0.8770	-6.52

252339_at	hypothetical protein	---	AT3G48900	1.04	0.05	0.53	0.61477023	0.8770	-6.52
253210_at	putative protein predicted protein,	MTN2	AT4G34840	-1.04	-0.06	-0.53	0.6151907	0.8773	-6.52
255348_at	hypothetical protein	---	AT4G03820	1.05	0.06	0.53	0.61522049	0.8773	-6.52
263109_at	hypothetical protein similar to puta	---	AT1G65180	1.05	0.07	0.53	0.61529135	0.8773	-6.52
258476_at	hypothetical protein predicted by g	---	AT3G02400	-1.06	-0.08	-0.53	0.61534887	0.8774	-6.52
264126_at	hypothetical protein predicted by g	NUA	AT1G79280	-1.04	-0.05	-0.53	0.61545666	0.8774	-6.52
255202_at	putative polyprotein	---	---	-1.04	-0.06	-0.53	0.61543358	0.8774	-6.52
252861_at	hypothetical protein	---	AT4G39820	-1.07	-0.10	-0.53	0.61546825	0.8774	-6.52
262987_at	conserved hypothetical protein pro	---	AT1G23240	-1.07	-0.09	-0.53	0.61553675	0.8774	-6.52
247161_at	putative protein similar to unknown	---	AT5G65810	1.05	0.08	0.53	0.61583417	0.8775	-6.52
266588_at	putative proline-rich protein ; supp	AGP9	AT2G14890	1.25	0.32	0.53	0.61570929	0.8775	-6.52
256227_at	unknown protein ; supported by cD	---	AT1G56290	-1.04	-0.05	-0.53	0.61599353	0.8775	-6.52
260695_at	RNA helicase, putative similar to (	ESP3	AT1G32490	1.03	0.05	0.53	0.6158788	0.8775	-6.52
260847_s_at	alanine aminotransferase, putative	AlaAT1	AT1G17290 /	1.04	0.06	0.53	0.61582735	0.8775	-6.52
254958_at	nucleoside diphosphate kinase 3 (	NDPK3	AT4G11010	1.06	0.08	0.53	0.61602735	0.8775	-6.52
250890_at	3-oxoacyl-[acyl-carrier-protein] syr	---	AT5G04520	1.04	0.06	0.53	0.61572991	0.8775	-6.52
245545_at	UTP-glucose glucosyltransferase	UGT71B5	AT4G15280	-1.05	-0.08	-0.53	0.61588219	0.8775	-6.52
247567_at	putative protein various predicted	---	AT5G61190	-1.06	-0.08	-0.53	0.61593825	0.8775	-6.52
245609_at	disease resistance N like protein	---	AT4G14368 /	-1.05	-0.07	-0.53	0.61601498	0.8775	-6.52
249105_at	40S ribosomal protein S15	---	AT5G43640	-1.04	-0.06	-0.53	0.61596934	0.8775	-6.52
257576_at	hypothetical protein predicted by g	---	AT3G28280	-1.04	-0.06	-0.53	0.61578264	0.8775	-6.52
253479_at	ferredoxin-NADP+ reductase - like	---	AT4G32360	1.04	0.05	0.53	0.61617086	0.8775	-6.52
260344_at	polyneuridine aldehyde esterase,	MES15	AT1G69240	1.04	0.06	0.53	0.61610376	0.8775	-6.52
257180_at	sun protein (fmu protein), putative	---	AT3G13180	1.05	0.08	0.53	0.61613703	0.8775	-6.52
260088_at	tonoplast intrinsic protein, alpha (a	TIP3;1	AT1G73190	1.05	0.07	0.53	0.61636917	0.8775	-6.52
263597_at	hypothetical protein predicted by g	---	AT2G01870	1.11	0.15	0.52	0.61644514	0.8775	-6.52
245233_at	putative protein similarity to low-te	---	AT4G25580	-1.05	-0.07	-0.53	0.61632885	0.8775	-6.52
257115_at	kinesin-like protein contains Pfam	---	AT3G20150	1.04	0.06	0.52	0.61646915	0.8775	-6.52
251531_at	putative protein hypothetical prote	---	AT3G58550	-1.05	-0.07	-0.53	0.61640333	0.8775	-6.52
256662_at	male sterility protein 2 (MS2) nearl	MS2	AT3G11980	1.04	0.05	0.53	0.61630435	0.8775	-6.52
255334_at	putative transposon protein	---	---	-1.03	-0.05	-0.53	0.61628411	0.8775	-6.52
263646_at	Ac-like transposase related to Ac/D	---	---	1.03	0.05	0.52	0.6165883	0.8777	-6.52
248716_at	unknown protein ;supported by ful	---	AT5G48210	-1.05	-0.08	-0.52	0.61668614	0.8777	-6.52
247664_at	APETALA2 protein - like APETAL	TOE2	AT5G60120	-1.04	-0.06	-0.52	0.61671853	0.8777	-6.52
264348_at	putative NPK1-related protein kina	NRT1.1	AT1G12110	-1.27	-0.35	-0.52	0.61677232	0.8777	-6.52

259809_at	hypothetical protein predicted by g	---	AT1G49800	-1.06	-0.09	-0.52	0.61666613	0.8777	-6.52
263059_at	putative non-LTR retrolelement rev	---	---	-1.04	-0.06	-0.52	0.61678466	0.8777	-6.52
263662_at	ankyrin-like protein EST gb|ATTS0	---	AT1G04430	1.07	0.10	0.52	0.61687473	0.8777	-6.52
262429_at	polyprotein, putative similar to poly	---	---	-1.05	-0.07	-0.52	0.61691127	0.8777	-6.52
265496_at	copia-like retroelement pol polypro	---	---	1.03	0.05	0.52	0.61689579	0.8777	-6.52
254048_at	putative protein various predicted	---	AT4G25680	-1.07	-0.10	-0.52	0.61709394	0.8778	-6.52
256163_at	terpene cyclase, putative similar t	---	AT1G48820	1.03	0.05	0.52	0.61703246	0.8778	-6.52
259693_at	hypothetical protein predicted by g	---	AT1G63060	-1.05	-0.07	-0.52	0.61705975	0.8778	-6.52
254249_at	serine /threonine kinase - like prot	---	AT4G23280	-1.12	-0.16	-0.52	0.6172032	0.8778	-6.52
265426_at	hypothetical protein predicted by g	---	AT2G20740	1.05	0.07	0.52	0.6171971	0.8778	-6.52
248366_at	SCARECROW transcriptional regu	---	AT5G52510	1.05	0.07	0.52	0.61782112	0.8780	-6.52
255535_at	putative RNaseP-associated prote	---	AT4G01790	1.06	0.09	0.52	0.61766223	0.8780	-6.52
246090_at	putative protein BEM46 bem1/bud	WAV2	AT5G20520	1.08	0.11	0.52	0.61753533	0.8780	-6.52
257619_at	unknown protein	ICK3	AT3G24810	1.05	0.07	0.52	0.61780808	0.8780	-6.52
259229_at	unknown protein similar to transcri	ADA2A	AT3G07740	-1.05	-0.08	-0.52	0.61771146	0.8780	-6.52
253882_at	pelota (PEL1)	PEL1	AT4G27650	-1.05	-0.07	-0.52	0.61776845	0.8780	-6.52
248673_at	putative protein contains similarity	---	AT5G48780	1.04	0.05	0.52	0.61749855	0.8780	-6.52
259792_at	unknown protein ; supported by cD	CAD1	AT1G29690	-1.13	-0.17	-0.52	0.61763815	0.8780	-6.52
251761_at	glucuronosyl transferase - like pro	---	AT3G55700	1.06	0.08	0.52	0.61779227	0.8780	-6.52
248047_at	putative protein similar to unknown	---	AT5G56070	1.04	0.06	0.52	0.61763505	0.8780	-6.52
264872_at	putative floral homeotic protein, A	ספט-03	AT1G24260	1.06	0.09	0.52	0.61751995	0.8780	-6.52
252955_at	multiubiquitin chain binding protein	RPN10	AT4G38630	-1.03	-0.05	-0.52	0.61745696	0.8780	-6.52
249617_at	receptor protein kinase-like protein	---	AT5G37450	1.05	0.08	0.52	0.61756146	0.8780	-6.52
252968_at	putative protein unknown mRNA,	---	AT4G38890	1.06	0.09	0.52	0.61789936	0.8780	-6.52
266211_at	putative retroelement pol polyprote	---	---	-1.04	-0.06	-0.52	0.61799473	0.8781	-6.52
266562_at	unknown protein	---	AT2G23970	-1.06	-0.09	-0.52	0.618014	0.8781	-6.52
254045_at	pumilio-like protein abdominal seg	APUM6	AT4G25880	1.04	0.05	0.52	0.61866902	0.8782	-6.52
261062_at	transcription factor scarecrow-like	SCL14	AT1G07530	1.04	0.06	0.52	0.61860888	0.8782	-6.52
266806_at	unknown protein ;supported by ful	---	AT2G30000	1.05	0.08	0.52	0.61846607	0.8782	-6.52
257188_at	hypothetical protein contains Pfam	---	AT3G13150	-1.05	-0.07	-0.52	0.6184536	0.8782	-6.52
246693_at	putative protein	---	AT5G29070	1.04	0.06	0.52	0.61878642	0.8782	-6.52
265006_at	unknown protein similar to small zi	TIM13	AT1G61570	1.10	0.14	0.52	0.6186097	0.8782	-6.52
265222_at	putative endosomal protein ; supp	---	AT2G01970	-1.03	-0.05	-0.52	0.61844519	0.8782	-6.52
251884_at	embryonic abundant protein -like e	---	AT3G54150	1.22	0.29	0.52	0.61825055	0.8782	-6.52
261674_at	unknown protein	---	AT1G18270	1.08	0.11	0.52	0.61862019	0.8782	-6.52

249615_x_at	contains similarity to unknown prot	AGL105	AT5G37420	-1.04	-0.06	-0.52	0.61838626	0.8782	-6.52
253169_at	putative protein various predicted	---	AT4G35120	1.05	0.07	0.52	0.61851293	0.8782	-6.52
254658_at	putative protein predicted gene M	---	AT4G18230	1.04	0.06	0.52	0.61877348	0.8782	-6.52
259877_at	unknown protein C-terminal portion	SDG26	AT1G76710	1.05	0.07	0.52	0.61838114	0.8782	-6.52
249082_at	legumin-like protein	CRA1	AT5G44120	1.04	0.06	0.52	0.61850124	0.8782	-6.52
249522_at	putative protein similar to unknown	---	AT5G38700	-1.04	-0.06	-0.52	0.61830255	0.8782	-6.52
262034_at	hypothetical protein predicted by g	---	---	1.04	0.06	0.52	0.6184443	0.8782	-6.52
245843_at	unknown protein	---	AT1G26180	1.05	0.07	0.52	0.61875733	0.8782	-6.52
266437_at	unknown protein	---	AT2G43160	1.05	0.07	0.52	0.61868266	0.8782	-6.52
246241_at	patatin-like protein	PLP4	AT4G37050	-1.05	-0.07	-0.52	0.61851661	0.8782	-6.52
263139_at	hypothetical protein similar to hypo	---	AT1G65110	-1.03	-0.05	-0.52	0.6188502	0.8782	-6.52
262579_at	hypothetical protein predicted by g	---	AT1G15320	1.04	0.05	0.52	0.61887182	0.8782	-6.52
263314_at	putative membrane transporter	---	AT2G05760	1.03	0.05	0.52	0.61892531	0.8782	-6.52
246463_at	quinone oxidoreductase -like prote	AT-AER	AT5G16970	-1.07	-0.09	-0.52	0.61985206	0.8784	-6.52
246724_at	putative protein CDPK substrate p	---	AT5G29000	-1.05	-0.08	-0.52	0.61938532	0.8784	-6.52
258800_at	unknown protein predicted by gen	---	AT3G04550	-1.05	-0.07	-0.52	0.61913323	0.8784	-6.52
248700_at	ligand-gated ion channel protein-li	ATGLR1.2	AT5G48400	-1.05	-0.07	-0.52	0.61925752	0.8784	-6.52
259806_at	mysoin-like protein similar to GI:2	---	AT1G47900	1.06	0.09	0.52	0.61940818	0.8784	-6.52
263202_at	putative inositol 1,4,5-trisphospha	5PTASE13	AT1G05630	-1.11	-0.15	-0.52	0.62008959	0.8784	-6.52
265664_at	unknown protein predicted by gens	---	AT2G24420	1.05	0.07	0.52	0.61910269	0.8784	-6.52
266920_at	hypothetical protein predicted by g	---	AT2G45750	-1.05	-0.07	-0.52	0.61959561	0.8784	-6.52
246425_at	cellulose synthase catalytic subuni	IRX3	AT5G17420	1.10	0.13	0.52	0.62006222	0.8784	-6.52
246005_at	lipoic acid synthase - like protein I	---	AT5G08415	1.06	0.09	0.52	0.61975811	0.8784	-6.52
250869_at	Terminal flower1 (TFL1) ; supporte	TFL1	AT5G03840	-1.04	-0.06	-0.52	0.61925323	0.8784	-6.52
248257_at	putative protein similar to unknown	---	AT5G53410	-1.06	-0.08	-0.52	0.61988739	0.8784	-6.52
262628_at	glucan synthase, putative similar t	ATGSL07	AT1G06490	-1.05	-0.08	-0.52	0.61960661	0.8784	-6.52
266730_at	putative RNA-binding protein	---	AT2G03110	-1.04	-0.06	-0.52	0.61966062	0.8784	-6.52
263960_at	putative kinesin-related cytokinesis	---	AT2G36200	1.04	0.06	0.52	0.61992816	0.8784	-6.52
257091_at	DNA polymerase, putative C-term	POLGAMM	AT3G20540	-1.06	-0.08	-0.52	0.61995003	0.8784	-6.52
246141_at	TipD - like WD repeat protein TipL	---	AT5G19920	-1.05	-0.07	-0.52	0.61999745	0.8784	-6.52
267086_at	putative salt-inducible protein	---	AT2G32630	-1.05	-0.07	-0.52	0.61973321	0.8784	-6.52
266263_at	putative flavonol sulfotransferase	---	AT2G27570	1.04	0.06	0.52	0.61948128	0.8784	-6.52
250476_at	MADS box protein FLOWERING L	FLC	AT5G10140	-1.04	-0.06	-0.52	0.6200186	0.8784	-6.52
251111_at	putative protein different hypothetic	---	AT5G01310	1.05	0.07	0.52	0.61970058	0.8784	-6.52
266409_at	hypothetical protein predicted by g	---	AT2G38510	-1.05	-0.07	-0.52	0.61952331	0.8784	-6.52

259879_at	putative calmodulin similar to calm	CML38	AT1G76650	1.21	0.27	0.52	0.61947536	0.8784	-6.52
248648_at	putative protein similar to unknown	---	AT5G49220	-1.05	-0.07	-0.52	0.61993095	0.8784	-6.52
264725_at	Expressed protein ; supported by f	---	AT1G22885	1.09	0.12	0.52	0.61953753	0.8784	-6.52
254499_at	putative protein probable membra	---	AT4G20100	-1.04	-0.06	-0.52	0.6194527	0.8784	-6.52
258762_at	hypothetical protein	---	AT3G10750	1.06	0.08	0.52	0.61950108	0.8784	-6.52
251898_at	floral homeotic protein APETALA3	AP3	AT3G54340	1.03	0.05	0.52	0.62013771	0.8784	-6.52
259338_at	s-syntaxin-like protein similar to s-s	SYP131	AT3G03800	-1.04	-0.05	-0.52	0.62021186	0.8784	-6.52
248148_at	putative protein similar to unknown	---	AT5G54930	-1.07	-0.10	-0.52	0.62024369	0.8784	-6.52
262056_at	Expressed protein ; supported by f	---	AT1G80245	-1.04	-0.06	-0.52	0.62039094	0.8784	-6.52
262621_at	hypothetical protein	---	AT1G06530	-1.04	-0.06	-0.52	0.62048556	0.8784	-6.52
253354_at	putative protein RNA helicase DB	---	AT4G33370	1.08	0.11	0.52	0.620365	0.8784	-6.52
256993_at	unknown protein ; supported by cl	---	AT3G28670	-1.03	-0.05	-0.52	0.62047494	0.8784	-6.52
262139_at	mutator-like transposase, putative	AT1G52615	---	1.04	0.05	0.52	0.62047871	0.8784	-6.52
262679_at	unknown protein ; supported by cD	LCR67	AT1G75830	-1.05	-0.07	-0.52	0.62045794	0.8784	-6.52
245124_at	small nuclear ribonucleoprotein U1	U1A	AT2G47580	1.04	0.06	0.52	0.62065255	0.8785	-6.52
245397_at	auxin-responsive protein IAA1 ;sup	IAA1	AT4G14560	-1.12	-0.17	-0.52	0.62078229	0.8785	-6.52
246138_at	putative protein predicted proteins	---	AT5G19870	-1.03	-0.05	-0.52	0.6206704	0.8785	-6.52
253176_at	putative protein Human (H326) ml	---	AT4G35140	-1.07	-0.09	-0.52	0.62088219	0.8785	-6.52
251763_at	MYB transcription factor - like prot	MYB109	AT3G55730	1.05	0.07	0.52	0.62059568	0.8785	-6.52
262998_at	hypothetical protein predicted by g	---	AT1G54280	1.03	0.05	0.52	0.62088469	0.8785	-6.52
264834_at	unknown protein similar to ESTs g	---	AT1G03730	1.09	0.12	0.52	0.6207145	0.8785	-6.52
250702_at	peroxidase ;supported by full-leng	---	AT5G06730	-1.25	-0.32	-0.52	0.62083134	0.8785	-6.52
255976_at	hypothetical protein predicted by g	---	AT1G22010	-1.04	-0.05	-0.52	0.62078666	0.8785	-6.52
252072_at	putative protein protein kinase PK	---	AT3G51710	-1.04	-0.06	-0.52	0.62081259	0.8785	-6.52
266003_at	hypothetical protein predicted by g	---	AT2G37320	1.06	0.08	0.52	0.62100161	0.8785	-6.52
255661_at	hypothetical protein	ULP1B	AT4G00690	1.04	0.05	0.52	0.62101097	0.8785	-6.52
259561_at	hypothetical protein ; supported by	WAK1	AT1G21250	1.26	0.33	0.52	0.62098536	0.8785	-6.52
257825_at	protein kinase, putative contains P	---	AT3G26700	-1.04	-0.06	-0.52	0.62119927	0.8785	-6.52
266441_at	hypothetical protein predicted by g	---	AT2G43250	1.04	0.06	0.52	0.62131221	0.8785	-6.52
263692_at	unknown protein Location of ESTs	---	AT1G26850	1.04	0.06	0.52	0.62133902	0.8785	-6.52
245767_at	hypothetical protein similar to puta	---	AT1G33610	-1.03	-0.05	-0.52	0.62114993	0.8785	-6.52
267190_at	putative N-myristoyltransferase ; s	NMT2	AT2G44170	1.04	0.06	0.52	0.62126423	0.8785	-6.52
264831_at	hypothetical protein predicted by g	---	AT1G03687	-1.04	-0.06	-0.52	0.6213195	0.8785	-6.52
252024_at	monodehydroascorbate reductase	ATMDAR1	AT3G52880	1.05	0.08	0.52	0.62133778	0.8785	-6.52
245339_at	hypothetical protein ;supported by	COBL7	AT4G16120	-1.08	-0.11	-0.52	0.62167712	0.8786	-6.52

254593_s_at	putative protein IEF SSP 9502, Hc	---	AT4G18900 /	1.05	0.07	0.52	0.62162992	0.8786	-6.52
259603_at	Expressed protein ; supported by f	---	AT1G56500	1.07	0.09	0.52	0.62173391	0.8786	-6.52
251437_at	putative protein hypothetical prote	---	AT3G59910	1.04	0.05	0.52	0.62181117	0.8786	-6.52
252643_at	acidic ribosomal protein P2 -like a	---	AT3G44590	-1.11	-0.14	-0.52	0.62173749	0.8786	-6.52
245484_at	enoyl-CoA hydratase like protein	ECHIA	AT4G16210	-1.04	-0.06	-0.52	0.62186053	0.8786	-6.52
261170_at	growth regulator protein similar to (	---	AT1G04910	1.04	0.06	0.52	0.62164894	0.8786	-6.52
265772_at	putative protein kinase contains a	RKF3	AT2G48010	-1.06	-0.08	-0.52	0.62182154	0.8786	-6.52
263149_at	unknown protein	---	AT1G53970	1.04	0.06	0.52	0.62143927	0.8786	-6.52
246414_at	hypothetical protein similar to hypo	---	AT1G77340	1.04	0.05	0.52	0.62161187	0.8786	-6.52
244963_at	PSII cytochrome b559	---	---	-1.03	-0.05	-0.52	0.62188362	0.8786	-6.52
261756_at	Expressed protein ; supported by f	---	AT1G08315	1.09	0.13	0.52	0.62142603	0.8786	-6.52
255800_at	putative protein transposase, Ipon	---	AT4G10200	-1.04	-0.05	-0.52	0.62155026	0.8786	-6.52
255606_at	hypothetical protein similar to T3F	---	AT4G01110	-1.06	-0.08	-0.52	0.62170158	0.8786	-6.52
246700_at	cysteine synthase - like cysteine s	---	AT5G28030	-1.09	-0.12	-0.52	0.62210264	0.8787	-6.52
246846_at	putative protein	---	AT5G26760	1.04	0.05	0.52	0.62210549	0.8787	-6.52
265455_at	hypothetical protein predicted by g	---	AT2G46560	1.04	0.06	0.52	0.62207641	0.8787	-6.52
255559_at	putative NAK-like ser/thr protein k	---	AT4G02010	1.05	0.08	0.52	0.62216342	0.8787	-6.52
262629_at	heat shock protein, putative conta	ACD32.1	AT1G06460	-1.04	-0.05	-0.52	0.62243581	0.8788	-6.52
249953_at	FAR1 - like protein far-red impaire	FRS12	AT5G18960	1.05	0.07	0.52	0.62240811	0.8788	-6.52
247774_at	putative protein fruit ripening expr	---	AT5G58660	1.04	0.05	0.52	0.62237657	0.8788	-6.52
246248_at	hypothetical protein	---	AT4G36560	-1.04	-0.05	-0.52	0.62237953	0.8788	-6.52
267295_at	pregeranylgeranyl pyrophosphate	GGPS2	AT2G23800	1.04	0.05	0.52	0.62236654	0.8788	-6.52
258700_at	putative SF16 protein similar to SF	IQD1	AT3G09710	-1.04	-0.06	-0.52	0.62251796	0.8789	-6.52
255241_at	putative protein hypothetical prote	---	---	-1.03	-0.05	-0.52	0.62262472	0.8790	-6.52
245005_at	ribosomal protein S14	---	---	-1.07	-0.10	-0.52	0.62277442	0.8791	-6.53
267301_at	ubiquitin activating enzyme 1 (UBA	ATUBA1	AT2G30110	1.04	0.06	0.52	0.62275656	0.8791	-6.53
259565_at	hypothetical protein	---	AT1G20530	1.03	0.04	0.52	0.62279319	0.8791	-6.53
262294_at	hypothetical protein identical to hy	---	AT1G27610	-1.04	-0.06	-0.52	0.6229578	0.8791	-6.53
262085_at	hypothetical protein predicted by g	---	AT1G56060	1.21	0.27	0.52	0.62295382	0.8791	-6.53
254719_at	putative protein beta 1,3-glucanas	---	AT4G13600	1.05	0.06	0.52	0.62295141	0.8791	-6.53
252343_at	putative protein hypothetical prote	---	AT3G48610	-1.14	-0.19	-0.52	0.62301158	0.8792	-6.53
254394_at	subtilisin-like serine protease conta	---	AT4G21630	1.03	0.05	0.51	0.62304191	0.8792	-6.53
248689_at	SCARECROW gene regulator-like	PAT1	AT5G48150	1.05	0.07	0.51	0.62311664	0.8792	-6.53
257297_at	unknown protein contains Pfam pr	---	AT3G28040	1.11	0.15	0.51	0.62318567	0.8793	-6.53
251381_at	secretory protein - like 33 kDa sec	PDLP8	AT3G60720 /	-1.08	-0.11	-0.51	0.6233085	0.8794	-6.53

254850_at	putative protein predicted proteins	---	AT4G12000	-1.06	-0.09	-0.51	0.62334856	0.8794	-6.53
258416_at	hypothetical protein predicted by g	---	AT3G17310	-1.04	-0.06	-0.51	0.62357996	0.8796	-6.53
246060_at	rev interacting protein mis3 - like r	---	AT5G08420	1.03	0.05	0.51	0.62373734	0.8796	-6.53
266578_at	putative cinnamoyl CoA reductase	---	AT2G23910	-1.05	-0.07	-0.51	0.62367007	0.8796	-6.53
249420_at	NAC domain/ NAM like protein NA	anac094	AT5G39820	-1.04	-0.06	-0.51	0.62373519	0.8796	-6.53
256194_at	unknown protein	---	---	1.06	0.08	0.51	0.62367845	0.8796	-6.53
261688_at	unknown protein contains similarity	---	AT1G47380	-1.13	-0.18	-0.51	0.62426541	0.8797	-6.53
261248_at	calreticulin, putative similar to GB:	---	AT1G20030	1.11	0.15	0.51	0.62430225	0.8797	-6.53
258568_at	unknown protein contains Pfam pr	---	AT3G04470	1.04	0.06	0.51	0.62394116	0.8797	-6.53
264973_at	nitrate transporter, putative nitrate	---	AT1G27040	-1.05	-0.07	-0.51	0.62423301	0.8797	-6.53
254868_at	copper amine oxidase like protein	---	AT4G12270	-1.05	-0.07	-0.51	0.62396492	0.8797	-6.53
250894_s_at	putative protein proline-rich protei	---	AT5G03810 /	-1.05	-0.06	-0.51	0.62417331	0.8797	-6.53
259468_at	unknown protein	TTN10	AT1G19080 /	1.05	0.07	0.51	0.6239339	0.8797	-6.53
265875_at	unknown protein ; supported by cl	---	AT2G01690	-1.05	-0.07	-0.51	0.6241873	0.8797	-6.53
257620_at	hypothetical protein predicted by g	---	AT3G24850	1.05	0.07	0.51	0.62417829	0.8797	-6.53
260562_at	putative protein kinase contains a	---	AT2G43850	-1.06	-0.08	-0.51	0.62414189	0.8797	-6.53
250138_at	DRH1 DEAD box protein - like DR	---	AT5G14610	-1.04	-0.06	-0.51	0.62399456	0.8797	-6.53
260536_at	putative electron transfer flavoprot	ETFQO	AT2G43400	1.08	0.10	0.51	0.62393787	0.8797	-6.53
263269_at	En/Spm-like transposon protein re	---	---	1.04	0.06	0.51	0.62422185	0.8797	-6.53
254727_at	hypothetical protein	PTAC5	AT4G13670	1.03	0.05	0.51	0.6242299	0.8797	-6.53
257352_at	putative RING3 protein	IMB1	AT2G34900	1.05	0.07	0.51	0.62438404	0.8797	-6.53
250297_at	putative protein predicted protein,	---	AT5G11980	1.05	0.07	0.51	0.62445484	0.8798	-6.53
266899_at	hypothetical protein predicted by g	---	AT2G34620	1.11	0.15	0.51	0.62473767	0.8798	-6.53
265572_at	putative carbonic anhydrase	ATACA2	AT2G28210	-1.29	-0.37	-0.51	0.6246293	0.8798	-6.53
253803_at	putative protein hypothetical prote	---	AT4G28200	-1.04	-0.06	-0.51	0.62474003	0.8798	-6.53
250984_at	protein kinase - like protein kinase	---	AT5G02800	-1.03	-0.05	-0.51	0.62470322	0.8798	-6.53
259360_at	hypothetical protein predicted by g	---	AT1G13310	-1.04	-0.05	-0.51	0.62454485	0.8798	-6.53
244971_at	ATP-dependent protease subunit	---	---	1.04	0.06	0.51	0.62471605	0.8798	-6.53
248321_at	putative protein similar to unknown	---	AT5G52740	-1.04	-0.06	-0.51	0.62468611	0.8798	-6.53
261319_at	phytochrome A supressor spa1, p	SPA4	AT1G53090	1.03	0.04	0.51	0.62478386	0.8798	-6.53
266184_s_at	phosphate transporter (AtPT2) ide	ATPT2	AT2G38940 /	1.09	0.13	0.51	0.62487475	0.8799	-6.53
263325_at	putative RING zinc finger protein ;	XERICO	AT2G04240	1.09	0.12	0.51	0.62489262	0.8799	-6.53
257560_at	galactosyltransferase, putative co	---	AT3G14960	-1.03	-0.05	-0.51	0.62492506	0.8799	-6.53
246210_at	ribosomal protein ; supported by cl	---	AT4G36420	1.06	0.09	0.51	0.6250071	0.8799	-6.53
260108_at	hypothetical protein similar to puta	---	AT1G63280	-1.04	-0.06	-0.51	0.62508431	0.8800	-6.53

245825_at	protein kinase, putative similar to	ATSK42	AT1G57870	-1.04	-0.06	-0.51	0.62517804	0.8800	-6.53
250743_at	phosphate/phosphoenolpyruvate t	---	AT5G05820	1.05	0.07	0.51	0.62547289	0.8802	-6.53
263188_at	hypothetical protein predicted by g	---	AT1G36095	-1.04	-0.06	-0.51	0.62538742	0.8802	-6.53
248562_at	putative protein strong similarity to	---	AT5G49680	1.10	0.14	0.51	0.62549594	0.8802	-6.53
246729_at	putative protein	---	AT5G28070	-1.04	-0.06	-0.51	0.62549547	0.8802	-6.53
257085_at	ubiquitin-specific protease 14 (UB	UBP14	AT3G20630	-1.07	-0.10	-0.51	0.62539844	0.8802	-6.53
267095_at	putative AMP deaminase ; suppor	FAC1	AT2G38280	-1.05	-0.07	-0.51	0.62556946	0.8803	-6.53
254088_at	putative protein snurportin1 m3G-	---	AT4G24880	1.06	0.08	0.51	0.62587221	0.8803	-6.53
250591_at	alpha galactosyltransferase protei	---	AT5G07720	-1.05	-0.07	-0.51	0.62583184	0.8803	-6.53
257683_at	hypothetical protein predicted by g	---	AT3G13280	-1.04	-0.06	-0.51	0.62567976	0.8803	-6.53
248426_at	putative protein contains similarity	---	AT5G51740	-1.04	-0.05	-0.51	0.62584686	0.8803	-6.53
267195_at	putative protein kinase contains a	---	AT2G30940	1.06	0.08	0.51	0.62585587	0.8803	-6.53
267076_at	calcium binding protein (CaBP-22)	---	AT2G41090	1.23	0.30	0.51	0.62590712	0.8803	-6.53
254974_at	putative flavanone 3-beta-hydroxy	---	AT4G10490	1.04	0.05	0.51	0.62565626	0.8803	-6.53
251779_at	putative protein various predicted	---	---	-1.04	-0.06	-0.51	0.62574601	0.8803	-6.53
258442_at	hypothetical protein predicted by g	---	AT3G01015	1.04	0.05	0.51	0.62573814	0.8803	-6.53
246305_at	putative protein protein At2g4006(	---	AT3G51890	1.05	0.07	0.51	0.6261073	0.8803	-6.53
257420_at	hypothetical protein predicted by g	---	AT1G77250	-1.05	-0.07	-0.51	0.62604056	0.8803	-6.53
258650_at	putative protein kinase similar to p	---	AT3G09830	1.08	0.11	0.51	0.62637356	0.8803	-6.53
257212_at	zinc-binding dehydrogenase, puta	---	AT3G15090	-1.06	-0.08	-0.51	0.62606786	0.8803	-6.53
261635_at	tubulin alpha-6 chain, putative ide	---	AT1G50020	-1.05	-0.08	-0.51	0.62635841	0.8803	-6.53
257116_at	arginine methyltransferase, putati	PRMT6	AT3G20020	1.05	0.07	0.51	0.626354	0.8803	-6.53
250251_at	putative protein contains similarity	---	AT5G13670	-1.04	-0.06	-0.51	0.62616781	0.8803	-6.53
248727_at	cytochrome P450	CYP705A5	AT5G47990	-1.04	-0.05	-0.51	0.62622206	0.8803	-6.53
265302_at	Mutator-like transposase similar to	---	---	1.03	0.05	0.51	0.62631336	0.8803	-6.53
246498_at	stearoyl-acyl carrier protein desat	---	AT5G16230	-1.11	-0.15	-0.51	0.62615792	0.8803	-6.53
252432_at	hypothetical protein	---	AT3G47675	-1.03	-0.05	-0.51	0.62638902	0.8803	-6.53
251676_at	hypothetical protein	---	AT3G57320	1.06	0.09	0.51	0.62643435	0.8804	-6.53
252819_at	putative protein several hypothetic	---	---	-1.03	-0.05	-0.51	0.62652364	0.8804	-6.53
266177_at	putative phloem-specific lectin	ATPP2-B3	AT2G02270	1.05	0.08	0.51	0.62651275	0.8804	-6.53
262050_at	unknown protein ;supported by full	---	AT1G80130	-1.19	-0.25	-0.51	0.62681177	0.8806	-6.53
253357_at	Dem -like protein Dem (defective	---	AT4G33400	1.04	0.06	0.51	0.62677957	0.8806	-6.53
249367_at	putative protein predicted protein,	---	AT5G40630	-1.04	-0.06	-0.51	0.6269204	0.8806	-6.53
250003_at	hypothetical protein predicted prot	---	AT5G18710	-1.04	-0.05	-0.51	0.62676843	0.8806	-6.53
247872_at	putative protein similar to unknow	---	AT5G57670	-1.06	-0.08	-0.51	0.62687388	0.8806	-6.53

248412_at	putative protein contains similarity	---	AT5G51590	-1.04	-0.06	-0.51	0.62689743	0.8806	-6.53
258260_at	unknown protein ; supported by cI	---	AT3G26850	1.04	0.05	0.51	0.62733497	0.8807	-6.53
245543_at	glucosyltransferase	---	AT4G15260	1.05	0.07	0.51	0.62736801	0.8807	-6.53
249888_s_at	zinc finger protein-like ; supported	---	AT5G22480	1.04	0.06	0.51	0.62727141	0.8807	-6.53
260505_at	Cyclin, putative similar to GB:CAB	CYCA3;4	AT1G47230	-1.04	-0.05	-0.51	0.62729259	0.8807	-6.53
256108_at	hypothetical protein predicted by g	---	AT1G16940	-1.06	-0.08	-0.51	0.62717992	0.8807	-6.53
258017_at	unknown protein	---	AT3G19370	-1.08	-0.11	-0.51	0.62728124	0.8807	-6.53
260061_at	cell division protein kinase similar t	CDKD1;1	AT1G73690	-1.06	-0.09	-0.51	0.6271397	0.8807	-6.53
256021_at	unknown protein contains Pfam pr	ZW9	AT1G58270	1.06	0.09	0.51	0.62713958	0.8807	-6.53
254514_at	hypothetical protein	---	AT4G20250	-1.05	-0.07	-0.51	0.62715322	0.8807	-6.53
245165_at	unknown protein predicted by gens	---	AT2G33180	1.10	0.13	0.51	0.62712144	0.8807	-6.53
249928_at	CCR4-associated factor-like protei	---	AT5G22250	-1.26	-0.33	-0.51	0.6276731	0.8811	-6.53
261519_at	unknown protein ; supported by cD	---	AT1G71810	-1.06	-0.09	-0.51	0.62773614	0.8811	-6.53
262018_at	hypothetical protein predicted by g	---	AT1G35617	1.05	0.07	0.51	0.62784299	0.8812	-6.53
256945_at	hypothetical protein similar to exte	---	AT3G19020	1.04	0.06	0.51	0.62791923	0.8812	-6.53
261346_at	putative aspartyl protease contains	---	AT1G79720	1.04	0.06	0.51	0.6285719	0.8815	-6.53
258764_at	putative pectinesterase contains si	---	AT3G10720	-1.09	-0.13	-0.51	0.62941481	0.8815	-6.53
257157_at	syntaxin-like protein similar to syn	SYP32	AT3G24350	-1.06	-0.08	-0.51	0.62828826	0.8815	-6.53
247912_at	putative protein contains similarity	---	AT5G57480	1.09	0.12	0.51	0.62963323	0.8815	-6.53
261398_at	hypothetical protein contains simila	NHX6	AT1G79610	-1.04	-0.06	-0.51	0.62924878	0.8815	-6.53
245822_at	unknown protein ; supported by cD	---	AT1G26110	-1.05	-0.07	-0.51	0.62893138	0.8815	-6.53
260984_at	Expressed protein ; supported by f	---	AT1G53645	1.08	0.11	0.51	0.62963471	0.8815	-6.53
265092_at	hypothetical protein predicted by g	---	AT1G03910	-1.03	-0.05	-0.51	0.62944137	0.8815	-6.53
259924_at	putative DNA-binding protein simila	---	AT1G72740	1.05	0.07	0.51	0.62884831	0.8815	-6.53
267136_at	putative GTP-binding protein (extra	XLG1	AT2G23460	1.04	0.06	0.51	0.62966407	0.8815	-6.53
249787_at	putative protein contains similarity	---	AT5G24320	-1.04	-0.05	-0.51	0.6291969	0.8815	-6.53
255728_at	unknown protein	---	AT1G25500	-1.07	-0.10	-0.51	0.62959589	0.8815	-6.53
259626_at	bZIP transcription factor, putative	ATBZIP60	AT1G42990	1.16	0.21	0.51	0.62826348	0.8815	-6.53
245679_at	clathrin-associated protein, putativ	---	AT1G56590	1.04	0.06	0.51	0.62908416	0.8815	-6.53
267489_s_at	putative DNA2-NAM7 helicase fam	---	AT2G19120	-1.06	-0.09	-0.51	0.62858023	0.8815	-6.53
248469_at	putative protein similar to unknown	anac097	AT5G50820	-1.05	-0.08	-0.51	0.62925809	0.8815	-6.53
256007_at	allinase, putative similar to allinas	SAMC2	AT1G34065	-1.06	-0.08	-0.51	0.62937043	0.8815	-6.53
250301_at	putative protein predicted proteins	---	AT5G11970	1.06	0.08	0.51	0.62966708	0.8815	-6.53
264302_at	ATPase 70 kDa subunit, putative	VHA-A	AT1G78900	-1.05	-0.06	-0.51	0.62878111	0.8815	-6.53
257550_at	hypothetical protein similar to GB:A	---	AT3G18460	-1.05	-0.07	-0.51	0.62950866	0.8815	-6.53

251071_at	putative protein receptor protein ki	---	AT5G01950	-1.07	-0.10	-0.51	0.62838277	0.8815	-6.53
248822_at	peroxidase ;supported by full-leng	---	AT5G47000	-1.04	-0.05	-0.51	0.62958588	0.8815	-6.53
257590_s_at	hypothetical protein predicted by g	---	AT3G24870 /	-1.05	-0.07	-0.51	0.62934014	0.8815	-6.53
261780_at	cyclin, putative similar to B-like cy	CYCB2;4	AT1G76310	1.04	0.06	0.51	0.6288271	0.8815	-6.53
257895_at	dihydrolipoamide dehydrogenase,	LPD1	AT3G16950	1.08	0.12	0.51	0.62862733	0.8815	-6.53
257064_at	hypothetical protein predicted by g	---	AT3G18260	-1.05	-0.07	-0.51	0.62861611	0.8815	-6.53
249747_at	putative protein similar to unknown	---	AT5G24600	1.05	0.07	0.51	0.62883425	0.8815	-6.53
252744_at	putative protein hypothetical prote	---	AT3G43310	-1.04	-0.06	-0.51	0.62902447	0.8815	-6.53
250989_at	cytochrome P450 - like protein cyt	CYP96A13	AT5G02900	-1.03	-0.05	-0.51	0.62857035	0.8815	-6.53
258185_at	hypothetical protein similar to hypo	---	AT3G21580	-1.05	-0.07	-0.51	0.62901738	0.8815	-6.53
254586_at	TMV resistance protein N-like TM	---	AT4G19510	1.05	0.06	0.51	0.62840392	0.8815	-6.53
246347_at	putative protein probable chloropla	---	AT3G56830	1.04	0.06	0.51	0.62944684	0.8815	-6.53
265047_at	hypothetical protein similar to unkn	IQD27	AT1G51960	1.04	0.06	0.50	0.62969149	0.8815	-6.53
264874_at	unknown protein Location of EST g	---	AT1G24240	-1.04	-0.05	-0.51	0.62838279	0.8815	-6.53
249699_at	putative protein similar to unknown	---	AT5G35540	-1.03	-0.04	-0.51	0.629389	0.8815	-6.53
260265_at	hypothetical protein similar to hypo	LBD42	AT1G68510	1.05	0.07	0.51	0.62814057	0.8815	-6.53
257259_at	hypothetical protein predicted by g	---	AT3G22090	1.03	0.05	0.51	0.62961336	0.8815	-6.53
247557_at	putative protein	---	AT5G61050	1.03	0.05	0.51	0.62814771	0.8815	-6.53
252705_at	putative protein predicted proteins	---	---	-1.05	-0.07	-0.51	0.62844235	0.8815	-6.53
260554_at	putative zinc protease member of i	---	AT2G41790	-1.03	-0.05	-0.51	0.62874344	0.8815	-6.53
247666_at	putative protein various predicted	---	AT5G60140	-1.03	-0.05	-0.51	0.62880774	0.8815	-6.53
245322_at	Expressed protein ; supported by f	---	AT4G14815	1.08	0.12	0.51	0.62907496	0.8815	-6.53
258570_at	phosphoenolpyruvate carboxylase	PPCK2	AT3G04530	-1.05	-0.07	-0.50	0.62991967	0.8817	-6.53
246669_at	galactinol synthase, putative	---	AT5G30500	1.05	0.07	0.50	0.63002457	0.8818	-6.53
266470_at	putative non-LTR retroelement rev	---	---	-1.07	-0.10	-0.50	0.63018744	0.8820	-6.53
249558_at	hypothetical protein	---	AT5G38310	1.15	0.20	0.50	0.63024199	0.8820	-6.53
267377_at	beta-ketoacyl-CoA synthase (FIDL	KCS10	AT2G26250	1.09	0.12	0.50	0.63041483	0.8820	-6.53
259597_at	ATP-dependent RNA helicase, pu	---	AT1G27900	-1.05	-0.07	-0.50	0.63079612	0.8820	-6.53
267298_at	putative homeodomain transcriptio	BLH4	AT2G23760	-1.06	-0.08	-0.50	0.63049819	0.8820	-6.53
246782_at	putative protein PrMC3 - Pinus ra	GID1C	AT5G27320	1.08	0.12	0.50	0.63072217	0.8820	-6.53
262031_x_at	hypothetical protein similar to puta	---	---	1.04	0.06	0.50	0.63038144	0.8820	-6.53
260698_at	unknown protein contains similarity	---	AT1G32300	1.03	0.05	0.50	0.63029356	0.8820	-6.53
267328_at	putative receptor-like protein kinas	---	AT2G19230	1.05	0.07	0.50	0.63052773	0.8820	-6.53
267042_at	putative non-LTR retroelement rev	---	AT2G34320	-1.04	-0.06	-0.50	0.63062268	0.8820	-6.53
248775_at	receptor kinase-like protein	CCR4	AT5G47850	-1.23	-0.30	-0.50	0.63075771	0.8820	-6.53

260591_at	predicted protein	---	AT1G53325	1.03	0.05	0.50	0.63075837	0.8820	-6.53
260474_at	lysophospholipase isolog	---	AT1G11090	-1.05	-0.07	-0.50	0.630581	0.8820	-6.53
265350_at	unknown protein predicted by gens	---	AT2G22620	1.04	0.06	0.50	0.63078795	0.8820	-6.53
261546_at	hypothetical protein	---	AT1G63520	-1.04	-0.06	-0.50	0.63048044	0.8820	-6.53
263966_s_at	putative TNP2-like transposon prot	---	---	-1.04	-0.06	-0.50	0.63039514	0.8820	-6.53
266677_at	hypothetical protein predicted by g	---	AT2G29820	-1.05	-0.07	-0.50	0.63086016	0.8821	-6.53
265167_at	putative OBP32pep protein	---	AT1G23680	-1.04	-0.06	-0.50	0.63097279	0.8821	-6.53
252052_at	beta-fructofuranosidase	AtcwINV2	AT3G52600	-1.03	-0.05	-0.50	0.63102214	0.8821	-6.53
258279_at	putative self-incompatibility protei	---	AT3G26870	1.03	0.04	0.50	0.6310389	0.8821	-6.53
259999_at	hypothetical protein predicted by g	---	AT1G68080	1.06	0.08	0.50	0.63100903	0.8821	-6.53
255187_s_at	putative transposon protein	---	---	-1.04	-0.05	-0.50	0.63109116	0.8821	-6.53
256961_at	transcription initiation factor TFIID-	TBP1	AT3G13445	1.04	0.06	0.50	0.63121956	0.8822	-6.53
257358_at	unknown protein predicted by gens	---	AT2G40990	1.06	0.09	0.50	0.63123774	0.8822	-6.53
247865_at	Expressed protein ; supported by f	---	AT5G57815	1.04	0.05	0.50	0.63138194	0.8822	-6.53
266546_at	putative AT-hook DNA-binding pro	---	AT2G35270	-1.03	-0.05	-0.50	0.63143824	0.8822	-6.53
263103_at	putative Ta11-like non-LTR retroel	---	---	-1.04	-0.06	-0.50	0.63142858	0.8822	-6.53
256732_at	hypothetical protein predicted by g	---	---	1.04	0.05	0.50	0.63143711	0.8822	-6.53
265198_at	putative glucosyl transferase	UGT73C2	AT2G36760	-1.04	-0.05	-0.50	0.63135456	0.8822	-6.53
254193_at	putative protein predicted proteins	---	AT4G23870	-1.13	-0.17	-0.50	0.63155338	0.8823	-6.53
253930_at	embryo-specific protein 1 (ATS1)	ATS1	AT4G26740	-1.04	-0.06	-0.50	0.63166451	0.8824	-6.53
261492_at	acid phosphatase, putative similar	SBH2	AT1G14290	-1.05	-0.08	-0.50	0.63178622	0.8825	-6.53
262124_at	nucleoporin 98-like protein similar	---	AT1G59660	-1.03	-0.05	-0.50	0.63188978	0.8826	-6.53
249819_at	unknown protein	---	AT5G23640	1.04	0.05	0.50	0.63195172	0.8826	-6.53
265144_at	putative serine/threonine protein ki	---	AT1G51170	-1.06	-0.08	-0.50	0.63192574	0.8826	-6.53
255453_at	hypothetical protein similar to A. th	---	AT4G02900	1.05	0.08	0.50	0.63192637	0.8826	-6.53
261378_at	calcium-dependent protein kinase	ATCDPK1	AT1G18890	-1.06	-0.09	-0.50	0.6320498	0.8826	-6.53
253634_at	putative protein ENOD20 gene pro	---	AT4G30590	1.03	0.04	0.50	0.63203976	0.8826	-6.53
262681_at	anter-specific proline-rich -like prot	---	AT1G75890	-1.03	-0.05	-0.50	0.63210474	0.8826	-6.53
264640_at	pollen allergen, putative similar to	ATEXPB2	AT1G65680	-1.06	-0.09	-0.50	0.63222347	0.8827	-6.53
262782_at	Expressed protein ; supported by f	---	AT1G13195	1.04	0.05	0.50	0.63249042	0.8830	-6.53
263615_at	putative MYB family transcription f	MYB100	AT2G25230	-1.03	-0.05	-0.50	0.63261913	0.8830	-6.53
254946_at	putative protein proline-rich protei	---	AT4G10950	1.04	0.06	0.50	0.63257289	0.8830	-6.53
256580_s_at	hypothetical protein	---	AT3G28810	-1.04	-0.05	-0.50	0.6325298	0.8830	-6.53
256950_at	hypothetical protein similar to hypo	---	AT3G19080	1.08	0.12	0.50	0.63263217	0.8830	-6.53
250281_at	putative protein prdeicted proteins	---	AT5G13240	1.06	0.08	0.50	0.63273537	0.8831	-6.53

255502_at	contains similarity to a protein kina	---	AT4G02410	1.17	0.23	0.50	0.63278594	0.8831	-6.53
246300_at	putative transmembrane protein G	SAC8	AT3G51830	-1.04	-0.05	-0.50	0.63306191	0.8835	-6.53
267588_at	unknown protein	---	AT2G42060	1.03	0.05	0.50	0.63314032	0.8835	-6.53
252068_at	mucin -like protein hemomucin, D	---	AT3G51440	-1.12	-0.16	-0.50	0.63321235	0.8836	-6.53
259699_at	hypothetical protein predicted by g	---	AT1G68940	1.03	0.05	0.50	0.63328535	0.8836	-6.53
250878_at	maturase -like protein gene cob in	---	AT5G04050	-1.07	-0.09	-0.50	0.63337947	0.8837	-6.53
249840_at	unknown protein ; supported by cl	ATLCBK1	AT5G23450	-1.03	-0.05	-0.50	0.63346289	0.8837	-6.53
248228_at	unknown protein ;supported by ful	---	AT5G53800	-1.06	-0.08	-0.50	0.6336974	0.8839	-6.53
259012_at	hypothetical protein similar to hypo	PUB9	AT3G07360	-1.05	-0.08	-0.50	0.63372746	0.8839	-6.53
260282_at	putative N-terminal acetyltransfera	EMB2753	AT1G80410	1.04	0.06	0.50	0.63362381	0.8839	-6.53
248904_at	Expressed protein ; supported by f	---	AT5G46295	-1.04	-0.06	-0.50	0.6336968	0.8839	-6.53
263338_at	hypothetical protein predicted by g	---	---	1.04	0.06	0.50	0.63378341	0.8839	-6.53
245604_at	hypothetical protein	---	AT4G14290	1.04	0.06	0.50	0.63383865	0.8839	-6.53
266301_at	putative MYB family transcription f	AtMYB81	AT2G26960	-1.06	-0.08	-0.50	0.63391968	0.8840	-6.53
262454_at	bifunctional nuclease bfn1 almost i	BFN1	AT1G11190	1.22	0.29	0.50	0.6339353	0.8840	-6.53
248418_at	cleavage and polyadenylation spe	CPSF160	AT5G51660	1.04	0.06	0.50	0.6339838	0.8840	-6.53
255710_at	predicted protein of unknown funct	---	AT4G00030	1.07	0.10	0.50	0.63410689	0.8840	-6.53
263760_at	unknown protein ; supported by cl	SULA	AT2G21280	1.07	0.10	0.50	0.63413009	0.8840	-6.53
247713_at	putative protein nonspecific lipid-t	---	AT5G59330	-1.04	-0.06	-0.50	0.63426643	0.8840	-6.53
254960_at	predicted protein	---	AT4G10845	-1.04	-0.06	-0.50	0.63423831	0.8840	-6.53
260123_at	AIG1-like protein similar to AIG1 p	---	AT1G33890	1.04	0.06	0.50	0.63406192	0.8840	-6.53
247587_at	putative protein predicted proteins	---	AT5G60620	-1.04	-0.06	-0.50	0.63421224	0.8840	-6.53
256463_s_at	unknown protein	---	---	-1.04	-0.06	-0.50	0.63426442	0.8840	-6.53
261179_at	unknown protein	---	AT1G04985	-1.05	-0.07	-0.50	0.63433729	0.8840	-6.53
264956_at	unknown protein similar to putative	ACR3	AT1G76990	1.12	0.16	0.50	0.63439699	0.8841	-6.53
265541_at	hypothetical protein predicted by g	SQN	---	-1.04	-0.05	-0.50	0.63445568	0.8841	-6.53
246384_at	glutaredoxin, putative similar to gl	---	AT1G77370	-1.03	-0.05	-0.50	0.63483417	0.8842	-6.54
261038_at	unknown protein ; supported by ful	---	AT1G17490	-1.05	-0.07	-0.50	0.63480923	0.8842	-6.54
256210_at	hypothetical protein	---	AT1G50950	1.12	0.17	0.50	0.63463077	0.8842	-6.53
246891_at	putative protein various predicted	---	AT5G25490	-1.03	-0.05	-0.50	0.63486141	0.8842	-6.54
260860_at	hypothetical protein predicted by g	---	AT1G43810	-1.04	-0.06	-0.50	0.63455322	0.8842	-6.53
265473_at	Expressed protein ; supported by f	LCR10	AT2G15535	-1.04	-0.06	-0.50	0.63491478	0.8842	-6.54
261598_at	unknown protein contains similarity	---	AT1G49750	1.19	0.26	0.50	0.63492069	0.8842	-6.54
259091_at	hypothetical protein predicted by g	---	AT3G04890	-1.04	-0.06	-0.50	0.63477855	0.8842	-6.54
266334_at	hypothetical protein predicted by g	---	AT2G32380	1.07	0.09	0.50	0.63487891	0.8842	-6.54

263800_at	hypothetical protein predicted by g	---	AT2G24600	1.27	0.35	0.50	0.63481714	0.8842	-6.54
265134_at	putative acyl-CoA : 1-acylglycerol-	LPAT3	AT1G51260	1.06	0.08	0.50	0.63487367	0.8842	-6.54
248841_at	ubiquitin-specific protease 21 (UBF	UBP21	AT5G46740	-1.06	-0.09	-0.50	0.6350133	0.8842	-6.54
258016_at	hypothetical protein similar to poly(	MPC	AT3G19350	-1.04	-0.05	-0.50	0.63498099	0.8842	-6.54
264972_at	meiotic asynaptic mutant asy1, pu	ASY1	AT1G67370	1.06	0.09	0.50	0.63506528	0.8842	-6.54
254484_at	hypothetical protein	---	AT4G20760	-1.04	-0.05	-0.50	0.63518667	0.8842	-6.54
260999_at	hypothetical protein similar to puta	---	AT1G26580	1.04	0.05	0.50	0.63516981	0.8842	-6.54
250115_at	salt-inducible protein-like	---	AT5G16420	-1.06	-0.09	-0.50	0.63521011	0.8842	-6.54
254031_at	putative protein other hypothetical	---	AT4G25920	1.04	0.05	0.50	0.6353153	0.8843	-6.54
266976_at	putative phospholipase	---	AT2G39410	-1.06	-0.09	-0.50	0.63544026	0.8844	-6.54
261237_at	hypothetical protein contains simila	---	AT1G32980	-1.04	-0.06	-0.50	0.63555336	0.8844	-6.54
249425_at	putative protein 5'-AMP-ACTIVAT	---	AT5G39790	-1.08	-0.12	-0.50	0.63553107	0.8844	-6.54
248301_at	DnaJ protein-like	---	AT5G53150	-1.04	-0.05	-0.50	0.63549353	0.8844	-6.54
260297_at	unknown protein contains Pfam pr	---	AT1G80280	-1.04	-0.06	-0.50	0.63580891	0.8846	-6.54
251501_at	putative protein several hypothetic	---	AT3G59120	-1.04	-0.06	-0.50	0.63587861	0.8846	-6.54
262934_s_at	hypothetical protein contains simila	---	AT1G16270 /	1.05	0.08	0.50	0.63569556	0.8846	-6.54
252881_at	putative protein predicted proteins	---	AT4G39610	-1.06	-0.08	-0.50	0.63587872	0.8846	-6.54
253499_at	putative protein zinc-finger helicas	---	AT4G31900	-1.04	-0.05	-0.50	0.63586619	0.8846	-6.54
262524_at	tuftelin-interacting-like protein Simi	---	AT1G17070	-1.03	-0.05	-0.50	0.63575644	0.8846	-6.54
266273_at	putative zinc transporter	MTPB1	AT2G29410	-1.16	-0.21	-0.50	0.6359385	0.8846	-6.54
251591_at	carboxyl terminal protease - like p	---	AT3G57680	1.07	0.10	0.50	0.63597376	0.8846	-6.54
265890_s_at	En/Spm-like transposon protein rel	---	---	1.03	0.05	0.50	0.63599546	0.8846	-6.54
251382_at	pectinesterase - like protein pectir	---	AT3G60730	-1.03	-0.05	-0.50	0.6360694	0.8846	-6.54
256204_at	DNA polymerase A family protein,	POLGAMM	AT1G50840	-1.05	-0.07	-0.49	0.63674653	0.8848	-6.54
250866_at	Expressed protein ; supported by f	---	AT5G03905	-1.04	-0.06	-0.49	0.63639024	0.8848	-6.54
251578_at	putative protein contains alternativ	---	AT3G58180	1.04	0.05	0.49	0.63661897	0.8848	-6.54
251631_at	putative protein several hypothetic	---	AT3G57430	1.05	0.06	0.49	0.63683276	0.8848	-6.54
264929_at	auxin-induced protein, putative sir	---	AT1G60730	-1.19	-0.25	-0.49	0.63652483	0.8848	-6.54
263073_at	unknown protein ;supported by ful	---	AT2G17500	-1.36	-0.44	-0.49	0.63646948	0.8848	-6.54
258494_at	cell division protein FtsH-like prote	---	AT3G02450	1.05	0.07	0.49	0.63672559	0.8848	-6.54
265008_at	Mlo protein, putative similar to Mlo	MLO6	AT1G61560	-1.16	-0.21	-0.49	0.63683405	0.8848	-6.54
264395_at	putative GDP-dissociation inhibitor	---	AT1G12070	-1.05	-0.07	-0.49	0.63686499	0.8848	-6.54
267495_at	myb-like protein isolog	ETC2	AT2G30420	1.08	0.12	0.49	0.63666343	0.8848	-6.54
257915_at	superman protein identical to supe	SUP	AT3G23130	-1.05	-0.06	-0.49	0.6368912	0.8848	-6.54
252402_s_at	putative protein predicted proteins	---	AT3G48050 /	-1.03	-0.05	-0.50	0.63627129	0.8848	-6.54

256320_at	DnaJ protein, putative contains Pf	---	AT3G12170	-1.05	-0.07	-0.49	0.63674054	0.8848	-6.54
265355_at	hypothetical protein predicted by g	---	AT2G16760	-1.07	-0.09	-0.49	0.63648505	0.8848	-6.54
263070_at	unknown protein	---	AT2G17600	1.04	0.06	0.50	0.63634028	0.8848	-6.54
256246_at	betaine aldehyde dehydrogenase,	ALDH22a1	AT3G66658	1.05	0.07	0.49	0.63639366	0.8848	-6.54
267514_at	putative glycerate dehydrogenase	---	AT2G45630	-1.11	-0.15	-0.49	0.63656421	0.8848	-6.54
254714_at	myb-like protein snapdragon myb	AtMYB79	AT4G13480	-1.04	-0.05	-0.49	0.63664053	0.8848	-6.54
262288_at	unknown protein identical to residu	CRR23	AT1G70760	-1.11	-0.15	-0.49	0.63732639	0.8849	-6.54
261701_at	hypothetical protein similar to hypo	HAF01	AT1G32750	1.03	0.04	0.49	0.63711778	0.8849	-6.54
256276_at	geranylgeranyl transferase type II	---	AT3G12070	-1.04	-0.06	-0.49	0.63722994	0.8849	-6.54
246162_at	actin interacting protein ; supporte	---	AT4G36400	1.05	0.07	0.49	0.63737791	0.8849	-6.54
261224_at	subtilisin-like serine protease simil	ATSBT5.2	AT1G20160	1.11	0.15	0.49	0.63737865	0.8849	-6.54
249080_at	putative protein strong similarity to	SUVR2	AT5G43990	-1.05	-0.08	-0.49	0.63733011	0.8849	-6.54
263500_s_at	hypothetical protein	---	AT2G07672	-1.05	-0.06	-0.49	0.63721822	0.8849	-6.54
255155_at	hypothetical protein	---	AT4G08230	-1.05	-0.07	-0.49	0.63702918	0.8849	-6.54
255407_at	hypothetical protein similar to A. th	---	AT4G03480	-1.06	-0.08	-0.49	0.63724938	0.8849	-6.54
252857_at	putative protein various predicted	---	AT4G39756	1.04	0.05	0.49	0.63729446	0.8849	-6.54
262446_at	hypothetical protein predicted by g	---	AT1G49310	1.11	0.15	0.49	0.63721112	0.8849	-6.54
252406_at	putative protein pectinesterase - A	---	AT3G47670	1.03	0.05	0.49	0.63742378	0.8849	-6.54
262025_at	growth regulator, putative similar t	---	AT1G35510	-1.05	-0.07	-0.49	0.63757086	0.8850	-6.54
246467_at	UDP glucose:flavonoid 3-o-glucos	---	AT5G17040	-1.06	-0.09	-0.49	0.63760199	0.8850	-6.54
254205_at	putative protein kinesin heavy cha	---	AT4G24170	1.05	0.07	0.49	0.63774187	0.8852	-6.54
256085_at	hypothetical protein predicted by g	---	AT1G20760	1.03	0.05	0.49	0.63785402	0.8853	-6.54
265661_at	putative protein kinase contains a	---	AT2G24360	1.05	0.07	0.49	0.63790159	0.8853	-6.54
247477_at	putative protein 21K protein precu	---	AT5G62340	-1.06	-0.08	-0.49	0.63798955	0.8854	-6.54
260031_at	putative nuclear matrix constituent	LINC3	AT1G68790	-1.04	-0.06	-0.49	0.63807157	0.8854	-6.54
261359_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.49	0.63818803	0.8855	-6.54
259481_at	germin, putative similar to germin	GLP4	AT1G18970	1.09	0.12	0.49	0.63815079	0.8855	-6.54
266893_at	hypothetical protein predicted by g	RTE1	AT2G26070	1.04	0.06	0.49	0.63822838	0.8855	-6.54
249124_at	disease resistance protein ; suppo	---	AT5G43740	-1.04	-0.05	-0.49	0.63827081	0.8855	-6.54
252589_s_at	putative protein different transporte	NAXT1	AT3G45650	-1.11	-0.15	-0.49	0.63831041	0.8855	-6.54
263596_at	putative inositol polyphosphate-5-p	---	AT2G01900	1.03	0.05	0.49	0.63842905	0.8856	-6.54
265765_at	hypothetical protein predicted by g	---	AT2G48060	1.04	0.06	0.49	0.63851225	0.8856	-6.54
256216_at	calreticulin (crt1) identical to calreti	CRT1	AT1G56340	1.08	0.12	0.49	0.6385697	0.8857	-6.54
259618_at	myb-related transcription factor (c	MYB112	AT1G48000	-1.06	-0.08	-0.49	0.63865219	0.8857	-6.54
261809_at	rac GTPase activating protein, put	---	AT1G08340	-1.06	-0.08	-0.49	0.63867162	0.8857	-6.54

259330_at	hypothetical protein gene model pr	---	AT3G16270	-1.05	-0.07	-0.49	0.63872952	0.8857	-6.54
267168_at	putative alcohol dehydrogenase	---	AT2G37770	1.27	0.35	0.49	0.63874571	0.8857	-6.54
249849_at	putative protein similar to unknown	NIC2	AT5G23230	-1.05	-0.07	-0.49	0.63879789	0.8857	-6.54
253307_at	putative protein auxin-induced pro	---	AT4G33670	-1.05	-0.06	-0.49	0.63889023	0.8858	-6.54
250110_at	putative protein many predicted pr	---	AT5G15350	-1.10	-0.14	-0.49	0.63920588	0.8858	-6.54
264726_at	Expressed protein ; supported by f	---	AT1G22985	1.05	0.07	0.49	0.63926024	0.8858	-6.54
254339_at	glucosidase like protein furostanol	BGLU3	AT4G22100	-1.04	-0.05	-0.49	0.63935758	0.8858	-6.54
259689_x_at	unknown protein	---	AT1G63130	-1.07	-0.10	-0.49	0.63919292	0.8858	-6.54
249512_at	DNA repair protein RAD23 homolo	---	AT5G38470	1.03	0.04	0.49	0.6393698	0.8858	-6.54
252933_at	putative receptor-like protein kinas	---	AT4G39110	-1.05	-0.07	-0.49	0.63905232	0.8858	-6.54
265082_at	hypothetical protein predicted by g	---	AT1G03830	-1.04	-0.05	-0.49	0.63935638	0.8858	-6.54
261629_at	unknown protein	---	AT1G49980	-1.04	-0.05	-0.49	0.6391315	0.8858	-6.54
251777_s_at	pyruvate kinase - like protein pyru	---	AT3G55650 /	1.04	0.06	0.49	0.63929082	0.8858	-6.54
260415_at	putative protein kinase similar to pr	---	AT1G69790	1.07	0.10	0.49	0.63915632	0.8858	-6.54
246529_at	serine/threonine-specific protein ki	---	AT5G15730	-1.09	-0.13	-0.49	0.63934594	0.8858	-6.54
251607_at	hypothetical protein	---	AT3G57850	1.04	0.05	0.49	0.63928004	0.8858	-6.54
264533_s_at	H+/Ca2+ antiporter, putative simil	CAX5	AT1G55720 /	1.04	0.06	0.49	0.63953073	0.8858	-6.54
254148_at	hsp 70-like protein heat shock 70	cpHsc70-1	AT4G24280	1.04	0.06	0.49	0.63952963	0.8858	-6.54
266741_s_at	putative disease resistance protein	---	AT2G03030 /	-1.03	-0.05	-0.49	0.63953425	0.8858	-6.54
253332_at	peroxidase ATP17a -like protein p	---	AT4G33420	-1.13	-0.18	-0.49	0.6395048	0.8858	-6.54
260973_at	hypothetical protein predicted by g	---	AT1G53490	1.04	0.05	0.49	0.63965041	0.8859	-6.54
266140_at	nodulin-like protein ; supported by	---	AT2G28120	1.06	0.08	0.49	0.63978967	0.8860	-6.54
246275_at	putative protein ; supported by full-	BEE2	AT4G36540	1.22	0.29	0.49	0.63981819	0.8860	-6.54
256960_at	unknown protein ;supported by ful	---	AT3G13510	-1.05	-0.07	-0.49	0.63978723	0.8860	-6.54
266972_at	40S ribosomal protein S15A	---	AT2G39590	-1.04	-0.05	-0.49	0.6400065	0.8862	-6.54
266888_s_at	putative thiamin pyrophosphokinas	TPK1	AT1G02880 /	1.04	0.05	0.49	0.64006841	0.8862	-6.54
262665_at	xyloglucan fucosyltransferase, put	FUT7	AT1G14070	1.11	0.15	0.49	0.64048678	0.8863	-6.54
267550_at	putative protein kinase contains a	AP4.3A	AT2G32800	1.10	0.14	0.49	0.64051775	0.8863	-6.54
264914_at	clathrin adaptor medium chain pro	HAP13	AT1G60780	-1.04	-0.06	-0.49	0.64023745	0.8863	-6.54
252513_at	putative protein KIAA0776 protein	---	AT3G46220	-1.04	-0.06	-0.49	0.64047906	0.8863	-6.54
251276_at	putative protein hypothetical prote	SDG14	AT3G61740	-1.04	-0.05	-0.49	0.64040908	0.8863	-6.54
247039_at	putative protein contains similarity	ATEB1C	AT5G67270	-1.05	-0.08	-0.49	0.64055966	0.8863	-6.54
248317_at	unknown protein	---	AT5G52680	-1.04	-0.06	-0.49	0.6403166	0.8863	-6.54
259302_at	unknown protein	GID1A	AT3G05120	-1.06	-0.08	-0.49	0.64031443	0.8863	-6.54
265424_at	putative sugar transporter	---	AT2G20780	-1.04	-0.06	-0.49	0.64043176	0.8863	-6.54

252812_at	putative protein hypothetical protei	---	---	1.03	0.05	0.49	0.64032733	0.8863	-6.54
260054_at	putative transporter contains Pfam	UNE2	AT1G78130	-1.07	-0.10	-0.49	0.64054522	0.8863	-6.54
267597_at	putative leucine-rich repeat diseas	AtRLP24	AT2G33020	1.08	0.11	0.49	0.6403596	0.8863	-6.54
246810_at	putative protein many predicted pr	---	---	-1.04	-0.05	-0.49	0.64078783	0.8865	-6.54
266351_at	unknown protein ;supported by ful	---	AT2G01490	1.05	0.06	0.49	0.64087464	0.8866	-6.54
259963_at	phosphate/phosphoenolpyruvate t	---	AT1G53660	-1.04	-0.06	-0.49	0.64106188	0.8868	-6.54
255106_at	putative protein hypothetical protei	---	---	-1.03	-0.05	-0.49	0.6411116	0.8868	-6.54
246198_at	geranylgeranyl pyrophosphate syn	GGPS1	AT4G36810	-1.05	-0.08	-0.49	0.64136078	0.8869	-6.54
247843_at	aluminium tolerance associated - li	SVL4	AT5G58050	-1.05	-0.06	-0.49	0.64123589	0.8869	-6.54
265137_at	F-box protein family, AtFBX10 cor	---	AT1G51290	-1.04	-0.06	-0.49	0.64131271	0.8869	-6.54
245162_at	putative myosin heavy chain	XID	AT2G33240	1.07	0.09	0.49	0.64138	0.8869	-6.54
250452_at	putative protein KIAA1038 protein	---	AT5G10630	-1.04	-0.06	-0.49	0.64136186	0.8869	-6.54
248525_s_at	unknown protein	---	AT5G50610 /	1.04	0.06	0.49	0.64122345	0.8869	-6.54
246091_at	putative protein various predicted	---	AT5G20590	1.05	0.07	0.49	0.64159724	0.8871	-6.54
258558_at	hypothetical protein predicted by g	---	AT3G06000	-1.03	-0.04	-0.49	0.64161123	0.8871	-6.54
246973_at	putative protein UBIQUINONE BI	---	AT5G24970	1.06	0.09	0.49	0.64180212	0.8872	-6.54
256247_at	SRF-type transcription factor conta	AGL91	AT3G66656	-1.03	-0.05	-0.49	0.64181416	0.8872	-6.54
266914_at	putative beta-amylase	BAM7	AT2G45880	1.08	0.11	0.49	0.64176797	0.8872	-6.54
256505_at	unknown protein	---	AT1G75200	1.06	0.08	0.49	0.64186745	0.8872	-6.54
259559_at	hypothetical protein	WAK3	AT1G21240	1.06	0.09	0.49	0.64198923	0.8873	-6.54
264639_at	unknown protein similar to ubiquitir	UCH2	AT1G65650	1.05	0.07	0.49	0.6419744	0.8873	-6.54
259480_at	hypothetical protein predicted by g	---	AT1G19010	1.06	0.08	0.49	0.64209901	0.8874	-6.54
254428_at	putative protein Human mRNA for	ZAC	AT4G21160	1.04	0.05	0.49	0.64225316	0.8875	-6.54
264092_at	photosystem II polypeptide, putati	PSBR	AT1G79040 /	1.03	0.05	0.49	0.64221353	0.8875	-6.54
263527_at	putative thaumatin-like pathogenes	---	AT2G24810	1.07	0.09	0.49	0.6422885	0.8875	-6.54
263038_at	conserved hypothetical protein pro	---	AT1G23270	-1.04	-0.05	-0.49	0.64237613	0.8876	-6.54
260758_at	endo-beta-1,4-glucanase, putative	AtGH9C1	AT1G48930	-1.05	-0.07	-0.49	0.64241709	0.8876	-6.54
264946_at	hypothetical protein predicted by g	---	AT1G77010	1.05	0.07	0.49	0.64283067	0.8877	-6.54
250007_at	beta-amylase-like proten beta-am	BMY3	AT5G18670	1.17	0.22	0.49	0.64287411	0.8877	-6.54
251723_at	putative protein speckle-type prote	---	AT3G56230	1.05	0.07	0.49	0.64265873	0.8877	-6.54
262647_at	putative growth regulator protein s	---	AT1G14020	-1.06	-0.08	-0.49	0.64302943	0.8877	-6.54
250065_at	putative protein predicted proteins	---	AT5G17910	-1.06	-0.08	-0.49	0.64260779	0.8877	-6.54
248300_at	PP2A regulatory subunit ;supporte	TAP46	AT5G53000	-1.05	-0.07	-0.49	0.64258296	0.8877	-6.54
254239_at	water channel - like protein plasm	PIP1;5	AT4G23400	1.07	0.10	0.49	0.6429283	0.8877	-6.54
245001_at	PSII low MW protein	---	---	-1.04	-0.06	-0.49	0.64305026	0.8877	-6.54

255903_at	myb-like protein, putative similar t	MYB52	AT1G17950	-1.03	-0.05	-0.49	0.64297276	0.8877	-6.54
251867_at	SKP1 interacting partner 5 (SKIP5	SKIP5	AT3G54480	1.03	0.05	0.49	0.64295807	0.8877	-6.54
245177_at	annexin-like protein genmodel sup	---	AT5G12380	-1.04	-0.06	-0.49	0.64282078	0.8877	-6.54
266245_at	putative translation initiation factor	---	AT2G27700	-1.04	-0.06	-0.49	0.64287742	0.8877	-6.54
261916_at	jasmonic acid, putative similar to j	anac028	AT1G65910	1.05	0.07	0.49	0.64288197	0.8877	-6.54
266724_at	hypothetical protein predicted by g	---	AT2G03180	-1.03	-0.05	-0.49	0.64284771	0.8877	-6.54
249041_at	male sterility MS5; pollenless3	---	AT5G44330	-1.04	-0.06	-0.48	0.64310341	0.8877	-6.54
251176_at	Ca2+-transporting ATPase -like pr	---	AT3G63380	1.15	0.21	0.48	0.64330536	0.8877	-6.54
250965_at	putative protein various predicted	---	AT5G03020	1.03	0.05	0.48	0.6431751	0.8877	-6.54
256410_at	hypothetical protein	---	AT1G66630	-1.03	-0.04	-0.48	0.64326462	0.8877	-6.54
266025_at	putative retroelement pol polyprote	---	---	1.04	0.05	0.48	0.64321436	0.8877	-6.54
247782_at	putative protein predicted RNA bir	---	AT5G58790	1.03	0.05	0.48	0.64327668	0.8877	-6.54
251167_at	putative protein proteinase inhibito	---	AT3G63360	-1.03	-0.05	-0.48	0.64374231	0.8882	-6.54
250596_at	putative protein contains similarity	---	AT5G07780	-1.06	-0.08	-0.48	0.64371086	0.8882	-6.54
258136_at	hypothetical protein predicted by g	RSY3	AT3G24560	1.04	0.06	0.48	0.64388714	0.8882	-6.54
263075_at	hypothetical protein predicted by g	---	AT2G17570	1.06	0.08	0.48	0.64383933	0.8882	-6.54
246493_at	putative protein hypothetical protei	CRS1	AT5G16180	1.04	0.06	0.48	0.64385379	0.8882	-6.54
259263_at	putative UDP-glucose 6-dehydroge	---	AT3G01010	1.04	0.05	0.48	0.64397355	0.8883	-6.54
255425_s_at	putative protein	---	AT4G02950 /	-1.05	-0.07	-0.48	0.6440254	0.8883	-6.54
265296_at	hypothetical protein predicted by g	---	AT2G14060	-1.04	-0.05	-0.48	0.64412709	0.8884	-6.54
252160_at	proline-rich protein	---	AT3G50570	-1.05	-0.07	-0.48	0.64410809	0.8884	-6.54
246132_at	Rad51-like protein ; supported by	ATRAD51	AT5G20850	1.03	0.04	0.48	0.64419274	0.8884	-6.54
263969_at	putative VSF-1-like b-ZIP transcrip	UNE4	AT2G12940	-1.04	-0.06	-0.48	0.64424046	0.8884	-6.54
263922_s_at	putative pyruvate kinase ;supporte	---	AT2G36580 /	-1.03	-0.05	-0.48	0.6443411	0.8884	-6.54
249504_at	disease resistance protein - like di	---	AT5G38850	1.08	0.11	0.48	0.64433611	0.8884	-6.54
267542_at	hypothetical protein predicted by g	---	AT2G32740	-1.03	-0.05	-0.48	0.64439568	0.8885	-6.54
245910_at	putative protein ER66 - Lycopersi	EICBP.B	AT5G09410	1.04	0.05	0.48	0.64454693	0.8886	-6.54
263707_at	hypothetical protein Similar to gi|15	---	AT1G09300	1.06	0.08	0.48	0.64497342	0.8888	-6.54
245137_at	unknown protein	---	AT2G45460	-1.05	-0.07	-0.48	0.64488293	0.8888	-6.54
249506_at	putative protein	---	AT5G38880	1.04	0.06	0.48	0.64480974	0.8888	-6.54
260552_at	putative glyoxalase II ; supported	GLX2-1	AT2G43430	-1.03	-0.05	-0.48	0.64481466	0.8888	-6.54
254895_at	hypothetical protein	---	AT4G11870	1.05	0.07	0.48	0.64489623	0.8888	-6.54
256840_x_at	unknown protein similar to putative	---	---	1.03	0.04	0.48	0.64487499	0.8888	-6.54
260668_at	unknown protein ;supported by full	---	AT1G19530	-1.19	-0.25	-0.48	0.64494289	0.8888	-6.54
255860_at	putative protein heparanase, Hom	AtGUS3	AT5G34940	1.32	0.40	0.48	0.64508489	0.8889	-6.54

246977_at	putative protein CONSTANS-like	COL4	AT5G24930	-1.03	-0.05	-0.48	0.64515741	0.8890	-6.54
261209_at	unknown protein ; supported by cD	---	AT1G12810	1.05	0.07	0.48	0.64522891	0.8890	-6.54
246795_at	putative protein	---	AT5G27020	1.04	0.06	0.48	0.64526149	0.8890	-6.54
253644_at	putative protein predicted protein,	---	AT4G29870	1.05	0.08	0.48	0.64532774	0.8890	-6.54
251512_at	putative protein several hypothetic	---	AT3G59190	-1.04	-0.05	-0.48	0.64541547	0.8890	-6.54
267085_at	putative cellulose synthase	ATCSLB02	AT2G32620	-1.03	-0.04	-0.48	0.64567653	0.8890	-6.54
250544_at	syntaxin-like protein syntaxin-relat	SYP132	AT5G08080	1.05	0.07	0.48	0.6455786	0.8890	-6.54
254302_at	hypothetical protein	---	AT4G22800	1.03	0.04	0.48	0.64566159	0.8890	-6.54
264342_at	unknown protein ; supported by ful	---	AT1G12080	1.19	0.25	0.48	0.645452	0.8890	-6.54
263592_at	putative non-LTR retroelement rev	---	---	1.06	0.09	0.48	0.64563863	0.8890	-6.54
266165_at	putative copper/zinc superoxide dis	CSD2	AT2G28190	1.22	0.29	0.48	0.64565714	0.8890	-6.54
250681_at	unknown protein	---	AT5G06590	1.03	0.05	0.48	0.64538928	0.8890	-6.54
255213_at	putative athila transposon protein	---	---	-1.03	-0.04	-0.48	0.64553965	0.8890	-6.54
265980_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.48	0.64580164	0.8891	-6.54
260752_at	unknown protein contains similarity	---	AT1G49030	1.05	0.07	0.48	0.64584667	0.8891	-6.54
261723_at	unknown protein ; supported by ful	---	AT1G76200	1.04	0.05	0.48	0.64585802	0.8891	-6.54
254243_at	serine/threonine kinase - like prote	CRK13	AT4G23210	1.19	0.26	0.48	0.64596534	0.8892	-6.54
261497_x_at	hypothetical protein contains simila	AGL59	AT1G28460	1.04	0.06	0.48	0.6460959	0.8894	-6.54
258575_at	putative O-linked GlcNAc transfera	SEC	AT3G04240	-1.04	-0.05	-0.48	0.6462846	0.8894	-6.54
252699_at	hypothetical protein predicted prot	---	---	-1.07	-0.09	-0.48	0.6462227	0.8894	-6.54
AFFX-r2-P1-cre	Bacteriophage P1 /GEN=cre /DB_	---	---	-1.07	-0.09	-0.48	0.64620732	0.8894	-6.54
251822_at	centromere protein - like centrome	---	AT3G55060	-1.04	-0.05	-0.48	0.64626473	0.8894	-6.54
255905_at	tonoplast intrinsic protein, putative	BETA-TIP	AT1G17810	-1.07	-0.10	-0.48	0.64635006	0.8894	-6.54
255723_at	hypothetical protein	AFP3	AT3G29575	1.10	0.14	0.48	0.64656154	0.8895	-6.54
249655_at	putative helicase PIF1 protein - Ca	---	---	-1.04	-0.05	-0.48	0.64655086	0.8895	-6.54
254246_at	protein kinase - like protein recept	EMB1290	AT4G23250	1.03	0.05	0.48	0.64646676	0.8895	-6.54
254403_at	subtilisin-like serine protease conta	---	AT4G21323	1.03	0.04	0.48	0.64654989	0.8895	-6.54
259334_at	unknown protein similar to hect do	---	AT3G03790	-1.06	-0.08	-0.48	0.64656205	0.8895	-6.54
263586_at	unknown protein predicted by gens	---	AT2G25350	-1.05	-0.08	-0.48	0.64670161	0.8896	-6.54
254979_at	subtilisin-like serine protease conta	---	AT4G10550	-1.04	-0.06	-0.48	0.6469115	0.8898	-6.54
251950_at	zinc finger - like protein Zat11 zinc	---	AT3G53600	-1.24	-0.31	-0.48	0.64690866	0.8898	-6.54
260642_at	plastid protein, putative similar to	---	AT1G53260	-1.06	-0.08	-0.48	0.64702684	0.8898	-6.54
245750_at	histone H2A, putative similar to his	HTA10	AT1G51060	-1.08	-0.12	-0.48	0.64698848	0.8898	-6.54
266345_at	hypothetical protein predicted by g	---	AT2G01410	1.04	0.05	0.48	0.64735482	0.8899	-6.55
247691_at	heat shock protein 18 ;supported	HSP18.2	AT5G59720	-1.04	-0.06	-0.48	0.64744183	0.8899	-6.55

261450_s_at	O-methyltransferase, putative sim	---	AT1G21110	1.33	0.41	0.48	0.64743064	0.8899	-6.55
258146_at	putative WD-repeat protein (WDR	---	AT3G18060	1.04	0.06	0.48	0.64733451	0.8899	-6.55
250632_at	putative protein cyclin 2 - Trypano	CYCP4;3	AT5G07450	1.05	0.06	0.48	0.64740158	0.8899	-6.55
247609_at	cleavage stimulation factor 50K ch	---	AT5G60940	1.04	0.05	0.48	0.64724597	0.8899	-6.54
262388_at	unknown protein	---	AT1G49320	1.04	0.06	0.48	0.64730274	0.8899	-6.54
247531_at	putative protein protein kinase 1, F	---	AT5G61550	1.04	0.06	0.48	0.64731542	0.8899	-6.55
265616_at	hypothetical protein predicted by g	---	AT2G25500	-1.03	-0.04	-0.48	0.64736032	0.8899	-6.55
256228_at	phosphoglycerate kinase, putative	---	AT1G56190	-1.05	-0.07	-0.48	0.64783908	0.8899	-6.55
247187_at	putative protein similar to unknown	---	AT5G65490	1.04	0.05	0.48	0.64783367	0.8899	-6.55
262791_at	unknown protein EST gb|F13926 c	---	AT1G10830	-1.05	-0.07	-0.48	0.64773754	0.8899	-6.55
252998_at	probable H+-transporting ATPase	---	AT4G38510	1.04	0.06	0.48	0.64761344	0.8899	-6.55
264542_at	hypothetical protein predicted by g	---	AT1G55830	1.03	0.05	0.48	0.64765437	0.8899	-6.55
249098_at	DNA repair protein-like	---	AT5G43530	-1.04	-0.05	-0.48	0.64787816	0.8899	-6.55
262035_at	polyprotein, putative similar to poly	---	---	-1.03	-0.05	-0.48	0.64786756	0.8899	-6.55
263915_at	hypothetical protein predicted by g	---	AT2G36430	-1.12	-0.16	-0.48	0.64764416	0.8899	-6.55
255954_at	hypothetical protein predicted by g	emb2204	AT1G22090	1.04	0.05	0.48	0.64766926	0.8899	-6.55
255404_at	predicted protein	---	AT4G03153	1.04	0.06	0.48	0.64784581	0.8899	-6.55
254292_at	putative protein	---	AT4G23030	-1.12	-0.17	-0.48	0.64759927	0.8899	-6.55
255378_at	putative glucan synthase compon	ATGSL05	AT4G03550	-1.04	-0.05	-0.48	0.64808702	0.8899	-6.55
245509_at	hypothetical protein	---	AT4G15730	1.05	0.07	0.48	0.64812582	0.8899	-6.55
254223_at	putative protein Pennisetum ciliare	---	AT4G23730	1.03	0.05	0.48	0.64797649	0.8899	-6.55
247781_at	dehydrodolichyl diphosphate synth	---	AT5G58784	-1.05	-0.07	-0.48	0.64810811	0.8899	-6.55
266678_at	hypothetical protein predicted by g	---	AT2G25870	1.04	0.05	0.48	0.64795218	0.8899	-6.55
246869_at	putative protein various predicted	---	---	-1.03	-0.05	-0.48	0.64806046	0.8899	-6.55
256131_at	bZIP transcription factor, putative	AtbZIP58	AT1G13600	1.05	0.07	0.48	0.64818617	0.8900	-6.55
258921_at	unknown protein N-terminus simila	anac053	AT3G10500	-1.05	-0.07	-0.48	0.64917866	0.8900	-6.55
264836_at	unknown protein similar to hypothe	---	AT1G03610	-1.06	-0.09	-0.48	0.64852003	0.8900	-6.55
257880_at	AMP-binding protein, putative con	AAE7	AT3G16910	1.07	0.10	0.48	0.64890405	0.8900	-6.55
247520_at	cytochrome c oxidase subunit - lik	---	AT5G61310	1.07	0.10	0.48	0.64829728	0.8900	-6.55
247367_at	oxygen-independent coproporphyr	---	AT5G63290	1.07	0.09	0.48	0.64831683	0.8900	-6.55
259307_at	unknown protein similar to MICRO	---	AT3G05230	1.05	0.07	0.48	0.64864854	0.8900	-6.55
252959_at	putative protein NADH dehydroge	---	AT4G38640	1.04	0.06	0.48	0.64899396	0.8900	-6.55
247636_at	putative protein predicted proteins	---	AT5G60570	-1.04	-0.05	-0.48	0.64922908	0.8900	-6.55
255943_at	UDP-glucose glucosyltransferase,	AtUGT85A5	AT1G22370	1.13	0.17	0.48	0.64872512	0.8900	-6.55
256452_at	hypothetical protein predicted by g	AtHB33	AT1G75240	1.14	0.19	0.48	0.64860591	0.8900	-6.55

246600_at	putative protein disease resistanc	SAG101	AT5G14930	1.08	0.10	0.48	0.64919062	0.8900	-6.55
252131_at	BCS1 protein-like protein Homo s	BCS1	AT3G50930	-1.20	-0.26	-0.48	0.64886921	0.8900	-6.55
267264_at	putative serine carboxypeptidase I	SCPL11	AT2G22970	1.11	0.15	0.48	0.64856797	0.8900	-6.55
263968_s_at	PttA-like transposon protein no AT	---	---	-1.04	-0.06	-0.48	0.64898957	0.8900	-6.55
251315_at	putative protein protein kinase hor	---	AT3G61410	-1.05	-0.06	-0.48	0.64834384	0.8900	-6.55
263550_at	Expressed protein ; supported by c	---	AT2G17033	1.04	0.06	0.48	0.64903737	0.8900	-6.55
245423_at	putative protein	---	AT4G17483	-1.05	-0.06	-0.48	0.64837948	0.8900	-6.55
249696_at	copia-like retrotransposable eleme	---	---	1.03	0.05	0.48	0.64865596	0.8900	-6.55
250901_at	putative protein ; supported by cD	RABC2A	AT5G03530	1.14	0.18	0.48	0.64908016	0.8900	-6.55
256995_at	protein kinase, putative contains s	---	AT3G25840	1.04	0.06	0.48	0.64890439	0.8900	-6.55
260817_at	unknown protein	---	AT1G06900	1.04	0.06	0.48	0.64873197	0.8900	-6.55
259400_at	receptor-like protein kinase, putati	---	AT1G17750	-1.18	-0.24	-0.48	0.64880043	0.8900	-6.55
245380_at	hypothetical protein	---	AT4G17760	-1.05	-0.07	-0.48	0.64906176	0.8900	-6.55
265527_at	putative Athila retroelement ORF1	---	---	1.03	0.05	0.48	0.6491563	0.8900	-6.55
264617_at	unknown protein	---	AT2G17660	-1.08	-0.11	-0.48	0.64929758	0.8900	-6.55
266973_at	hypothetical protein predicted by g	---	AT2G39620	-1.04	-0.06	-0.48	0.64887414	0.8900	-6.55
249639_at	disease resistance like protein TM	---	AT5G36930	1.04	0.05	0.48	0.64858495	0.8900	-6.55
265558_at	putative non-LTR retroelement rev	---	---	1.03	0.04	0.48	0.64930306	0.8900	-6.55
267303_at	hookless1-like protein	---	AT2G30090	-1.03	-0.04	-0.48	0.64934758	0.8900	-6.55
259185_at	putative phosphate/phosphoenolpy	PPT2	AT3G01550	-1.16	-0.22	-0.48	0.64969586	0.8900	-6.55
264701_at	hypothetical protein similar to hypo	---	AT1G70160	1.04	0.06	0.47	0.65009024	0.8900	-6.55
261634_at	ATP-dependent Clp protease prote	CLPR1	AT1G49970	1.05	0.07	0.48	0.64979645	0.8900	-6.55
261905_at	hypothetical protein contains simila	---	AT1G65070	-1.04	-0.05	-0.48	0.64972849	0.8900	-6.55
264587_at	putative ligand-gated ion channel p	ATGLR3.4	AT1G05200	-1.14	-0.18	-0.48	0.6497924	0.8900	-6.55
266864_at	putative hydroxymethylglutaryl-CoA	---	AT2G26800	-1.05	-0.07	-0.48	0.64973985	0.8900	-6.55
253669_at	dihydropteroate synthase-like prot	---	AT4G30000	1.04	0.05	0.48	0.64958087	0.8900	-6.55
250208_at	unknown protein ;supported by ful	anac084	AT5G14000	-1.12	-0.16	-0.47	0.65002729	0.8900	-6.55
258128_at	chloroplast thylakoidal processing	PLSP1	AT3G24590	1.05	0.07	0.48	0.64953838	0.8900	-6.55
245184_at	F12A21.8 hypothetical protein	---	AT1G67790	-1.04	-0.06	-0.47	0.64990221	0.8900	-6.55
248752_at	unknown protein	---	AT5G47600	-1.04	-0.05	-0.47	0.65009018	0.8900	-6.55
252623_at	hypothetical protein	---	AT3G45320	-1.04	-0.06	-0.47	0.65003315	0.8900	-6.55
262150_at	hypothetical protein contains simila	FRS6	AT1G52520	1.04	0.06	0.47	0.64996884	0.8900	-6.55
261890_at	hypothetical protein predicted by g	---	AT1G80970	-1.07	-0.10	-0.47	0.65008675	0.8900	-6.55
262266_at	mudrA-like protein similar to mudrA	---	---	1.04	0.06	0.47	0.64999934	0.8900	-6.55
249196_at	unknown protein supported by full	---	AT5G42560	-1.04	-0.05	-0.47	0.64984067	0.8900	-6.55

245113_at	hypothetical protein predicted by g	MIZ1	AT2G41660	-1.05	-0.08	-0.48	0.64953564	0.8900	-6.55
266486_at	hypothetical protein predicted by g	---	AT2G47950	-1.20	-0.26	-0.47	0.64992003	0.8900	-6.55
250976_at	putative protein various predicted	---	AT5G03060	-1.03	-0.05	-0.47	0.65004425	0.8900	-6.55
262249_at	root hairless 1 (RHL1) similar to ro	RHL1	AT1G48380	-1.04	-0.06	-0.47	0.65026613	0.8900	-6.55
265962_at	nodulin-like protein ;supported by	---	AT2G37460	1.11	0.15	0.47	0.65023346	0.8900	-6.55
264776_at	unknown protein location of EST g	---	AT1G22860	-1.04	-0.05	-0.47	0.6502066	0.8900	-6.55
257585_at	hypothetical protein predicted by g	---	AT3G12420	-1.04	-0.06	-0.47	0.65026678	0.8900	-6.55
255506_at	predicted glycosyl transferase sim	GATL6	AT4G02130	1.08	0.11	0.47	0.65033325	0.8901	-6.55
264586_at	putative cytochrome P450 Similar	CYP88A3	AT1G05160	-1.04	-0.06	-0.47	0.65039639	0.8901	-6.55
267409_at	hypothetical protein predicted by g	---	AT2G34910	-1.03	-0.04	-0.47	0.65062125	0.8904	-6.55
247397_at	Dof zinc finger protein - like Dof zi	---	AT5G62940	-1.07	-0.09	-0.47	0.6507329	0.8904	-6.55
261096_at	4-coumarate:coenzyme A ligase,	ACOS5	AT1G62940	-1.04	-0.06	-0.47	0.65071813	0.8904	-6.55
251988_at	CYTOCHROME P450-like protein	CYP71B31	AT3G53300	1.03	0.04	0.47	0.65067303	0.8904	-6.55
248529_at	protein kinase ;supported by full-le	---	AT5G50000	-1.06	-0.08	-0.47	0.65089911	0.8904	-6.55
263988_at	floral homeodomain transcription fa	SHP2	AT2G42830	-1.04	-0.05	-0.47	0.65084947	0.8904	-6.55
251430_at	putative protein hypothetical prote	---	AT3G60110	1.04	0.06	0.47	0.65088534	0.8904	-6.55
250372_at	putative protein various predicted	---	AT5G11460	1.05	0.07	0.47	0.65087499	0.8904	-6.55
252868_at	putative protein tubulin-folding cof	POR	AT4G39920	1.03	0.05	0.47	0.65109787	0.8905	-6.55
258705_at	hypothetical protein predicted by g	---	AT3G09470	-1.04	-0.06	-0.47	0.651084	0.8905	-6.55
249254_at	unknown protein	---	AT5G42110	-1.04	-0.06	-0.47	0.65134217	0.8906	-6.55
262779_at	putative cytochrome P450 monoox	---	AT1G13070	-1.03	-0.04	-0.47	0.65128492	0.8906	-6.55
263967_at	En/Spm-like transposon protein	---	---	-1.03	-0.05	-0.47	0.65133646	0.8906	-6.55
247159_at	1-aminocyclopropane-1-carboxylat	ACS5	AT5G65800	1.03	0.04	0.47	0.65128407	0.8906	-6.55
255122_at	putative athila-like protein	---	---	1.05	0.07	0.47	0.65127308	0.8906	-6.55
247920_at	putative protein contains similarity	---	AT5G57670	1.05	0.07	0.47	0.65129266	0.8906	-6.55
254427_at	putative protein predicted protein,	emb1417	AT4G21190	1.07	0.09	0.47	0.65142709	0.8906	-6.55
257925_at	unknown protein ;supported by ful	---	AT3G23170	1.20	0.26	0.47	0.65290738	0.8906	-6.55
265011_at	putative chloroplast membrane pr	ALB4	AT1G24490	-1.03	-0.04	-0.47	0.65279812	0.8906	-6.55
257625_at	cytochrome P450, putative contai	CYP71B24	AT3G26230	1.20	0.27	0.47	0.65256961	0.8906	-6.55
266164_at	putative salt-inducible protein	---	AT2G28050	-1.06	-0.09	-0.47	0.65254931	0.8906	-6.55
253009_at	glycine hydroxymethyltransferase	SHM1	AT4G37930	-1.05	-0.07	-0.47	0.65180216	0.8906	-6.55
256272_at	unknown protein	---	AT3G12100	1.04	0.05	0.47	0.65226929	0.8906	-6.55
249943_at	putative protein similar to unknown	---	AT5G22280	1.08	0.11	0.47	0.65213958	0.8906	-6.55
261120_at	homeodomain protein BELL1, put	BLH3	AT1G75410	1.06	0.08	0.47	0.65224393	0.8906	-6.55
246771_at	putative protein putative replicatior	---	---	-1.03	-0.05	-0.47	0.65270068	0.8906	-6.55

260367_at	unknown protein ;supported by ful	---	AT1G69760	-1.11	-0.15	-0.47	0.65281231	0.8906	-6.55
257838_at	hypothetical protein contains Pfam	---	AT3G25210	1.03	0.05	0.47	0.65186684	0.8906	-6.55
245620_at	hypothetical protein	---	AT4G14050	-1.04	-0.06	-0.47	0.65281145	0.8906	-6.55
259946_at	putative TINY similar to TINY GB:(	---	AT1G71450	-1.03	-0.04	-0.47	0.65285829	0.8906	-6.55
265540_at	Mutator-like transposase similar to	---	---	1.03	0.05	0.47	0.65169333	0.8906	-6.55
246116_at	putative protein predicted proteins	---	AT5G20310	1.04	0.06	0.47	0.65253315	0.8906	-6.55
265762_at	hypothetical protein	---	AT2G01240	-1.05	-0.08	-0.47	0.6526175	0.8906	-6.55
245159_at	putative cellulose synthase	ATCSLD1	AT2G33100	1.05	0.06	0.47	0.65151854	0.8906	-6.55
248593_at	pectin methylesterase ;supported	---	AT5G49180	1.05	0.07	0.47	0.6523676	0.8906	-6.55
252279_at	1-aminocyclopropane-1-carboxyla	ACS9	AT3G49700	1.04	0.06	0.47	0.65207774	0.8906	-6.55
267294_at	hypothetical protein predicted by g	YCF37	AT2G23670	-1.05	-0.08	-0.47	0.6517621	0.8906	-6.55
248018_at	putative protein strong similarity to	---	AT5G56470	-1.04	-0.06	-0.47	0.65271305	0.8906	-6.55
254755_at	hypothetical protein	---	AT4G13220	1.04	0.06	0.47	0.65291758	0.8906	-6.55
265399_at	hypothetical protein predicted by g	---	AT2G11010	-1.08	-0.11	-0.47	0.65148828	0.8906	-6.55
252142_at	putative protein hypothetical prote	---	AT3G51120	-1.05	-0.06	-0.47	0.65287591	0.8906	-6.55
250474_at	annexin -like protein annexin (Anr	ANNAT7	AT5G10230	-1.03	-0.04	-0.47	0.65206966	0.8906	-6.55
252346_at	hypothetical protein	---	AT3G48650	-1.03	-0.04	-0.47	0.65217746	0.8906	-6.55
263562_at	hypothetical protein predicted by g	---	AT2G15420	1.03	0.04	0.47	0.65259808	0.8906	-6.55
255316_at	putative protein	---	---	-1.03	-0.05	-0.47	0.65213516	0.8906	-6.55
245973_at	putative protein predicted proteins	---	---	1.03	0.04	0.47	0.65281267	0.8906	-6.55
256555_at	hypothetical protein similar to puta	---	---	1.03	0.05	0.47	0.65256203	0.8906	-6.55
257493_at	unknown protein	---	AT1G48180	-1.06	-0.08	-0.47	0.65209216	0.8906	-6.55
252708_at	putative protein amine oxidase, C	---	AT3G43820	-1.05	-0.07	-0.47	0.65268648	0.8906	-6.55
250046_at	putative protein predicted proteins	---	AT5G17720	1.04	0.06	0.47	0.65285584	0.8906	-6.55
249877_at	transcription factor-like protein (gb	HUA2	AT5G23150	-1.03	-0.05	-0.47	0.6516255	0.8906	-6.55
251674_at	hypothetical protein	---	AT3G57250	-1.04	-0.05	-0.47	0.65160059	0.8906	-6.55
265269_at	hypothetical protein predicted by g	---	AT2G42950	1.04	0.06	0.47	0.65190678	0.8906	-6.55
244962_at	NADH dehydrogenase ND4	---	---	-1.03	-0.04	-0.47	0.65166645	0.8906	-6.55
262928_at	hypothetical protein	---	AT1G65760	-1.04	-0.06	-0.47	0.65258878	0.8906	-6.55
259159_at	unknown protein contains Pfam pr	ACBP4	AT3G05420	-1.05	-0.07	-0.47	0.65303375	0.8907	-6.55
245097_at	Expressed protein ; supported by f	---	AT2G40935	-1.03	-0.04	-0.47	0.65321824	0.8909	-6.55
256090_at	predicted protein	---	AT1G20816	-1.05	-0.07	-0.47	0.65329445	0.8910	-6.55
245766_at	En/Spm-like transposon protein, p	---	---	-1.04	-0.05	-0.47	0.65349204	0.8912	-6.55
258998_at	putative adenylate kinase similar to	---	AT3G01820	-1.05	-0.07	-0.47	0.65359881	0.8913	-6.55
265854_at	hypothetical protein predicted by g	---	AT2G42370	1.03	0.05	0.47	0.65374708	0.8914	-6.55

252323_at	putative protein probable transcrip	KING1	AT3G48530	-1.06	-0.08	-0.47	0.65377536	0.8914	-6.55
255022_at	NAM/NAP like protein nap gene, A	ANAC070	AT4G10350	1.03	0.05	0.47	0.65371544	0.8914	-6.55
260687_at	inner mitochondrial membrane pro	ATTIM23-1	AT1G17530	1.06	0.08	0.47	0.6538368	0.8914	-6.55
265166_at	putative OBP32pep protein	---	AT1G23640	-1.03	-0.05	-0.47	0.65387589	0.8914	-6.55
263270_at	putative replication protein A1	---	---	-1.03	-0.05	-0.47	0.65407543	0.8916	-6.55
266533_s_at	putative plasma membrane intrinsi	PIP2;8	AT2G16850 /	1.06	0.08	0.47	0.65413364	0.8916	-6.55
247197_at	receptor-like protein kinase	---	AT5G65240	1.09	0.12	0.47	0.65416203	0.8916	-6.55
247763_at	RNA polymerase II	NRPB7	AT5G59180	1.04	0.05	0.47	0.65420878	0.8916	-6.55
264979_s_at	disease resistance protein, putativ	---	AT1G27170 /	1.05	0.07	0.47	0.65425383	0.8916	-6.55
260260_at	putative reductase similar to cinna	---	AT1G68540	1.05	0.07	0.47	0.65428103	0.8916	-6.55
246674_at	bcnt-like protein ; supported by full	---	AT5G30490	-1.04	-0.05	-0.47	0.65443428	0.8917	-6.55
254947_at	putative retrotransposon polyprote	---	---	-1.06	-0.08	-0.47	0.65439775	0.8917	-6.55
249946_at	putative protein predicted proteins	---	AT5G19170	1.08	0.11	0.47	0.65441183	0.8917	-6.55
255925_at	unknown protein ;supported by full	---	AT1G22200	-1.05	-0.07	-0.47	0.65454776	0.8918	-6.55
257546_s_at	hypothetical protein predicted by g	---	AT3G28410 /	-1.03	-0.04	-0.47	0.65462869	0.8918	-6.55
251932_at	pasticcino 1 ; supported by cDNA:	PAS1	AT3G54010	1.04	0.05	0.47	0.65490749	0.8921	-6.55
260561_at	putative endochitinase	---	AT2G43580	-1.05	-0.07	-0.47	0.65487246	0.8921	-6.55
265761_at	putative stress protein	---	AT2G01330	1.04	0.05	0.47	0.65512009	0.8921	-6.55
254588_at	putative protein hypothetical protei	---	AT4G18840	-1.04	-0.05	-0.47	0.65507869	0.8921	-6.55
264217_at	hypothetical protein predicted by g	---	AT1G60190	-1.19	-0.25	-0.47	0.65513197	0.8921	-6.55
250560_at	replication factor A - like protein re	RPA70B	AT5G08020	1.07	0.10	0.47	0.65515319	0.8921	-6.55
246765_at	glutamic acid-rich protein hypothe	---	AT5G27330	-1.04	-0.06	-0.47	0.65515185	0.8921	-6.55
249586_at	putative protein predicted proteins	---	AT5G37840	-1.10	-0.13	-0.47	0.65506936	0.8921	-6.55
258042_at	hypothetical protein similar to hypo	---	AT3G21310	1.03	0.04	0.47	0.65525535	0.8922	-6.55
263841_at	putative xyloglucan endo-transglyc	---	AT2G36870	1.29	0.37	0.47	0.65533153	0.8923	-6.55
254619_at	myb - like protein transforming pro	MYB98	AT4G18770	-1.04	-0.05	-0.47	0.65544474	0.8924	-6.55
256031_at	choline kinase (GmCK2p), putativ	---	AT1G34100	1.04	0.05	0.47	0.65555333	0.8925	-6.55
253891_at	putative protein ;supported by full-	---	AT4G27720	1.08	0.11	0.47	0.65566563	0.8926	-6.55
254520_at	potassium transporter-like protein	---	AT4G19960	1.05	0.08	0.47	0.65600318	0.8926	-6.55
246056_at	katanin p80 subunit - like protein k	---	AT5G08390	-1.05	-0.06	-0.47	0.65599155	0.8926	-6.55
247975_at	putative protein similar to unknown	---	AT5G56800	-1.03	-0.04	-0.47	0.65600484	0.8926	-6.55
251358_at	shaggy-like kinase beta	---	AT3G61160	1.09	0.12	0.47	0.6558493	0.8926	-6.55
259904_at	hypothetical protein predicted by g	---	AT1G74150	1.04	0.06	0.47	0.65587948	0.8926	-6.55
262142_at	hypothetical protein predicted by g	---	AT1G52640	1.04	0.06	0.47	0.65586625	0.8926	-6.55
254885_at	putative protein various predicted	---	AT4G11745	-1.05	-0.07	-0.47	0.65601704	0.8926	-6.55

249520_at	putative protein similar to unknown	---	AT5G38670	-1.03	-0.04	-0.47	0.65585844	0.8926	-6.55
261172_at	hypothetical protein predicted by g	---	AT1G04840	-1.04	-0.06	-0.47	0.65616826	0.8928	-6.55
254607_at	hypothetical protein ;supported by	---	AT4G18920	-1.03	-0.05	-0.47	0.65628089	0.8929	-6.55
267017_at	unknown protein	SVR1	AT2G39140	1.09	0.12	0.47	0.65644153	0.8930	-6.55
264440_at	unknown protein similar to fim pro	---	AT1G27340	1.03	0.05	0.47	0.65648171	0.8930	-6.55
261090_at	protein kinase, putative contains P	---	AT1G07560	1.04	0.06	0.47	0.65642563	0.8930	-6.55
257796_at	hypothetical protein predicted by g	---	AT3G15930	-1.04	-0.06	-0.47	0.6565064	0.8930	-6.55
265683_at	putative auxin-regulated protein	---	AT2G24400	-1.04	-0.06	-0.47	0.65655786	0.8930	-6.55
260310_at	hypothetical protein predicted by g	---	AT1G70590	1.05	0.07	0.46	0.6566348	0.8930	-6.55
255293_at	putative zinc finger protein	---	AT4G04730	-1.04	-0.05	-0.46	0.65723443	0.8938	-6.55
245537_at	hypothetical protein	---	AT4G15200	-1.03	-0.05	-0.46	0.65750519	0.8940	-6.55
253192_at	putative protein nuclear phosphop	---	AT4G35370	-1.03	-0.05	-0.46	0.6574677	0.8940	-6.55
262747_at	hypothetical protein predicted by g	---	AT1G28540	-1.03	-0.05	-0.46	0.65744938	0.8940	-6.55
260809_at	hypothetical protein predicted by g	---	AT1G43730	-1.03	-0.05	-0.46	0.65761619	0.8940	-6.55
249767_at	acidic endochitinase (dbj|BAA2186	---	AT5G24090	-1.11	-0.14	-0.46	0.65759214	0.8940	-6.55
249215_at	dihydroflavonol 4-reductase	DFR	AT5G42800	1.06	0.08	0.46	0.65769108	0.8941	-6.55
252580_at	putative protein putative proteins -	---	AT3G45490	-1.03	-0.05	-0.46	0.65771025	0.8941	-6.55
247131_at	ferredoxin-NADP+ reductase	FNR1	AT5G66190	1.03	0.05	0.46	0.65777452	0.8941	-6.55
265340_at	putative AAA-type ATPase similar	---	AT2G18330	1.07	0.10	0.46	0.65787949	0.8941	-6.55
256766_at	Expressed protein ; supported by c	PCC1	AT3G22231	1.45	0.53	0.46	0.65793351	0.8941	-6.55
248642_at	putative protein similar to unknown	---	AT5G49120	-1.04	-0.05	-0.46	0.65789848	0.8941	-6.55
265993_at	putative disease resistance protein	---	AT2G24160	1.21	0.27	0.46	0.65783789	0.8941	-6.55
258206_at	hypothetical protein predicted by g	CID4	AT3G14010	1.04	0.05	0.46	0.65800587	0.8941	-6.55
255448_at	hypothetical protein	---	AT4G02810	-1.05	-0.07	-0.46	0.65806698	0.8941	-6.55
258301_at	hypothetical protein predicted by g	---	---	-1.03	-0.04	-0.46	0.65802918	0.8941	-6.55
250089_at	homeobox protein	HDG9	AT5G17320	-1.04	-0.06	-0.46	0.6582118	0.8942	-6.55
250391_at	putative protein predicted proteins	---	---	-1.04	-0.06	-0.46	0.65820992	0.8942	-6.55
249516_s_at	myrosinase binding protein-like; si	---	AT5G38540 /	-1.04	-0.06	-0.46	0.65831902	0.8943	-6.55
255862_at	hypothetical protein predicted by g	---	AT2G30300	-1.04	-0.05	-0.46	0.65838097	0.8943	-6.55
265700_at	putative MYB family transcription f	---	AT2G03470	1.03	0.04	0.46	0.65853149	0.8945	-6.55
251790_at	elicitor responsive/phloem -like pr	---	AT3G55470	1.04	0.06	0.46	0.65878583	0.8947	-6.55
256130_at	unknown protein contains Pfam pr	---	AT1G18170	1.04	0.06	0.46	0.65879829	0.8947	-6.55
259929_at	transcription factor, putative simila	---	AT1G34360	-1.04	-0.06	-0.46	0.65879384	0.8947	-6.55
258869_at	hypothetical protein similar to xylos	AtVGT1	AT3G03090	-1.04	-0.06	-0.46	0.65891656	0.8947	-6.55
246898_at	putative protein	---	AT5G25580	1.03	0.04	0.46	0.65889219	0.8947	-6.55

252423_at	putative protein putative hydrolyse	---	AT3G47590	1.03	0.05	0.46	0.65922694	0.8948	-6.55
264615_at	unknown protein ; supported by cl	---	AT1G04590	1.06	0.09	0.46	0.65918813	0.8948	-6.55
266308_at	putative cytochrome P450	CYP705A9	AT2G27010	1.04	0.06	0.46	0.6591362	0.8948	-6.55
256192_at	diadenosine 5,5-P1,P4-tetraphosp	ATNUDX25	AT1G30110	1.04	0.06	0.46	0.65921323	0.8948	-6.55
264706_at	hypothetical protein predicted by g	---	AT1G09720	-1.03	-0.04	-0.46	0.65919723	0.8948	-6.55
252846_at	putative protein several pectin met	---	AT3G42160	1.03	0.04	0.46	0.65924554	0.8948	-6.55
258378_at	hypothetical protein contains simila	---	AT3G17490	1.03	0.05	0.46	0.65914497	0.8948	-6.55
259313_at	hypothetical protein predicted by g	---	AT3G05090	1.04	0.06	0.46	0.65938214	0.8948	-6.55
247537_s_at	ABC transport protein - like ABC t	ATH15	AT5G61690	-1.04	-0.05	-0.46	0.65934907	0.8948	-6.55
266276_at	putative tropinone reductase	TRI	AT2G29330	-1.03	-0.04	-0.46	0.6593086	0.8948	-6.55
257472_at	hypothetical protein predicted by g	---	AT1G56040	1.03	0.05	0.46	0.65944698	0.8949	-6.55
249319_s_at	putative protein similar to unknown	---	AT5G40880	-1.04	-0.06	-0.46	0.65949512	0.8949	-6.55
249517_at	putative protein similar to unknown	---	AT5G38580	1.03	0.04	0.46	0.65953715	0.8949	-6.55
254189_at	putative protein cellulose synthase	CSLG2	AT4G24000	-1.11	-0.15	-0.46	0.65966955	0.8949	-6.55
257962_at	hypothetical protein predicted by g	---	AT3G19790	1.06	0.09	0.46	0.65979671	0.8949	-6.55
260443_at	Expressed protein ; supported by f	---	AT1G68185	1.03	0.04	0.46	0.65980365	0.8949	-6.55
257128_at	cytochrome P450, putative contai	CYP705A1	AT3G20080	1.05	0.07	0.46	0.65978956	0.8949	-6.55
245448_at	disease resistance RPP5 like prote	RPP4	AT4G16860	1.04	0.06	0.46	0.65978943	0.8949	-6.55
256287_at	hypothetical protein	---	AT3G12190	-1.04	-0.05	-0.46	0.6596846	0.8949	-6.55
261376_at	hypothetical protein contains simila	---	AT1G18660	-1.04	-0.06	-0.46	0.6598488	0.8949	-6.55
254589_at	hypothetical protein	---	AT4G18850	-1.04	-0.06	-0.46	0.65988896	0.8949	-6.55
260349_at	mitotic checkpoint protein, putative	---	AT1G69400	-1.04	-0.06	-0.46	0.66019304	0.8952	-6.55
248233_at	F-box protein family, AtFBL13 con	---	AT5G53840	-1.04	-0.05	-0.46	0.6601292	0.8952	-6.55
264620_at	putative bZIP transcription factor	ATBZIP27	AT2G17770	1.05	0.07	0.46	0.66016567	0.8952	-6.55
257858_at	hypothetical protein predicted by g	---	AT3G12920	1.07	0.10	0.46	0.66034674	0.8954	-6.55
249519_at	putative protein similar to unknown	APE1	AT5G38660	1.05	0.07	0.46	0.6604249	0.8954	-6.55
259857_at	hypothetical protein predicted by g	---	AT1G68430	1.04	0.05	0.46	0.66046465	0.8954	-6.55
260862_at	unknown protein	SEU	AT1G43850	-1.04	-0.05	-0.46	0.66053291	0.8954	-6.55
258232_at	unknown protein	---	AT3G27750	1.06	0.08	0.46	0.660579	0.8955	-6.56
253280_at	poly(A)-binding protein non-conse	PAB2	AT4G34110	1.03	0.05	0.46	0.6608963	0.8956	-6.56
258446_at	hypothetical protein predicted by g	---	AT3G22430	1.04	0.05	0.46	0.66086379	0.8956	-6.56
260424_at	putative receptor-like protein kinas	---	AT1G72460	-1.04	-0.05	-0.46	0.66086097	0.8956	-6.56
262059_at	DnaJ protein, putative similar to D	---	AT1G80030	-1.05	-0.08	-0.46	0.66081651	0.8956	-6.56
259345_s_at	hypothetical protein predicted by g	---	AT3G03700	1.09	0.12	0.46	0.66094217	0.8956	-6.56
255758_at	hypothetical protein predicted by g	---	AT1G16800	-1.03	-0.05	-0.46	0.6607367	0.8956	-6.56

246252_s_at	patatin-like protein ;supported by f	PLP1	AT4G37060 /	1.03	0.04	0.46	0.66093945	0.8956	-6.56
251967_at	putative protein DMR-N9 PROTEI	---	AT3G53390	1.03	0.05	0.46	0.66102418	0.8956	-6.56
248167_at	putative protein similar to unknown	---	AT5G54530	1.05	0.07	0.46	0.66113569	0.8957	-6.56
257839_at	hypothetical protein	---	AT3G25080	1.03	0.05	0.46	0.66109967	0.8957	-6.56
249279_at	SCARECROW gene regulator-like	---	AT5G41920	-1.03	-0.04	-0.46	0.66145155	0.8957	-6.56
261689_at	hypothetical protein contains simila	---	AT1G50140	1.05	0.07	0.46	0.6613207	0.8957	-6.56
259136_at	unknown protein	---	AT3G05470	1.05	0.07	0.46	0.66127502	0.8957	-6.56
265429_at	hypothetical protein predicted by g	---	AT2G20710	-1.05	-0.06	-0.46	0.66156154	0.8957	-6.56
259337_at	putative cationic amino acid transp	CAT4	AT3G03720	1.04	0.05	0.46	0.66157231	0.8957	-6.56
252430_at	CHLOROPHYLL A-B BINDING PI	LHCA4	AT3G47470	1.05	0.06	0.46	0.6615228	0.8957	-6.56
264035_at	hypothetical protein predicted by g	---	AT2G03630	-1.04	-0.06	-0.46	0.66144058	0.8957	-6.56
255085_at	putative protein several hypothetic	---	---	1.04	0.05	0.46	0.66147709	0.8957	-6.56
247969_at	putative protein similar to unknown	---	AT5G56700	1.06	0.09	0.46	0.66147184	0.8957	-6.56
252798_at	putative protein	---	AT3G42310	1.03	0.05	0.46	0.66151382	0.8957	-6.56
259414_at	hypothetical protein contains Pfam	---	AT1G02420	-1.04	-0.06	-0.46	0.66176696	0.8959	-6.56
250458_s_at	ACTIN 2/7 (sp|P53492) ; supporte	ACT7	AT5G09810	1.03	0.04	0.46	0.66191796	0.8961	-6.56
245521_at	Expressed protein ;supported by c	ESD4	AT4G15880	-1.03	-0.05	-0.46	0.66216633	0.8961	-6.56
258943_at	hypothetical protein predicted by g	---	AT3G10400	-1.04	-0.06	-0.46	0.66212738	0.8961	-6.56
247948_at	putative protein strong similarity to	---	AT5G57130	1.04	0.06	0.46	0.6620056	0.8961	-6.56
245727_at	hypothetical protein contains simila	---	AT1G73350	-1.04	-0.06	-0.46	0.66209073	0.8961	-6.56
251510_at	putative protein several hypothetic	---	AT3G59170	-1.03	-0.04	-0.46	0.6620216	0.8961	-6.56
258754_at	hypothetical protein similar to hypo	---	AT3G11920	1.04	0.06	0.46	0.66214549	0.8961	-6.56
254493_at	DAG-like protein DAG precursor, /	---	AT4G20020	1.07	0.09	0.46	0.66223478	0.8961	-6.56
264935_at	hypothetical protein predicted by g	---	AT1G61150	1.06	0.08	0.46	0.66227003	0.8961	-6.56
256660_at	hypothetical protein similar to hypo	---	AT3G12060	-1.04	-0.06	-0.46	0.66238002	0.8962	-6.56
246925_at	cytochrome P450 71B1 - like prote	CYP71B14	AT5G25180	-1.03	-0.05	-0.46	0.66256897	0.8963	-6.56
260033_at	putative mutT protein contains Pfa	ATNUDX1	AT1G68760	1.04	0.06	0.46	0.66257022	0.8963	-6.56
266897_at	remorin identical to GB:M25268, a	---	AT2G45820	-1.06	-0.09	-0.46	0.66253423	0.8963	-6.56
248956_at	unknown protein	---	AT5G45610	-1.04	-0.05	-0.46	0.66284553	0.8967	-6.56
258787_at	hypothetical protein predicted by g	PUB24	AT3G11840	1.18	0.24	0.46	0.6629954	0.8967	-6.56
258861_at	putative helicase similar to C-termi	---	AT3G02060	-1.05	-0.07	-0.46	0.66296704	0.8967	-6.56
263769_at	5S ribosomal RNA	---	---	-1.04	-0.06	-0.46	0.66309284	0.8967	-6.56
257437_s_at	hypothetical protein predicted by g	---	AT2G16290 /	-1.04	-0.05	-0.46	0.66309096	0.8967	-6.56
255921_at	hypothetical protein contains Pfam	APUM8	AT1G22240	-1.04	-0.05	-0.46	0.66296866	0.8967	-6.56
257069_at	hypothetical protein predicted by g	---	AT3G28170	-1.03	-0.05	-0.46	0.66309905	0.8967	-6.56

251733_at	copper homeostasis factor ;suppo	CCH	AT3G56240	1.04	0.06	0.46	0.66330846	0.8968	-6.56
263259_at	putative zinc-binding protein simila	PUB18	AT1G10560	1.07	0.10	0.46	0.66328346	0.8968	-6.56
258645_s_at	exopolygalacturonase identical to	---	AT3G07850	-1.04	-0.05	-0.46	0.66331412	0.8968	-6.56
260281_at	unknown protein	---	AT1G80500	1.04	0.06	0.45	0.66355634	0.8970	-6.56
265781_at	putative Athila retroelement ORF1	---	---	-1.03	-0.05	-0.45	0.66355623	0.8970	-6.56
259041_at	unknown protein similar to putative	ATCSLC6	AT3G07330	1.06	0.08	0.45	0.66362963	0.8970	-6.56
261002_at	hypothetical protein contains simila	---	AT1G26520	-1.04	-0.05	-0.45	0.66368748	0.8970	-6.56
245975_at	putative protein CGI-107 protein -	---	AT5G13070	-1.04	-0.06	-0.45	0.66375428	0.8970	-6.56
263683_at	putative NAM protein similar to GE	FEZ	AT1G26870	-1.04	-0.05	-0.45	0.66370842	0.8970	-6.56
248927_at	ubiquitin activating enzyme E1-like	APG7	AT5G45900	1.04	0.06	0.45	0.66372619	0.8970	-6.56
251611_at	putative protein several hypothetic	---	AT3G57940	-1.05	-0.07	-0.45	0.66387483	0.8971	-6.56
258150_at	hypothetical protein ;supported by	---	AT3G18160	-1.08	-0.10	-0.45	0.66401536	0.8973	-6.56
245938_at	putative protein protein phosphata	---	AT5G19680	-1.05	-0.07	-0.45	0.66413674	0.8974	-6.56
265910_at	putative vacuolar ATP synthase pr	---	AT2G25610	-1.04	-0.05	-0.45	0.66419089	0.8974	-6.56
249915_at	putative protein similar to unknown	---	AT5G22870	1.03	0.05	0.45	0.66439868	0.8976	-6.56
248544_at	putative protein contains similarity	PIMT2	AT5G50240	-1.07	-0.10	-0.45	0.6644145	0.8976	-6.56
262190_at	unknown protein	---	AT1G78030	-1.05	-0.07	-0.45	0.66441106	0.8976	-6.56
257323_at	hypothetical protein	---	AT2G07698	-1.10	-0.14	-0.45	0.66470296	0.8977	-6.56
252313_at	RNA-binding - like protein RNA-bi	CID10	AT3G49390	1.07	0.09	0.45	0.66460374	0.8977	-6.56
253483_at	putative protein anthranilate N-hyd	---	AT4G31910	-1.07	-0.09	-0.45	0.66469922	0.8977	-6.56
246618_at	putative protein similar to unknown	---	AT5G36280	-1.03	-0.04	-0.45	0.66465354	0.8977	-6.56
251063_at	protein kinase ATN1-like protein p	---	AT5G01850	-1.04	-0.05	-0.45	0.66476959	0.8978	-6.56
251277_at	dynamin-like protein phragmoplas	ADL1B	AT3G61760	-1.03	-0.04	-0.45	0.66497194	0.8980	-6.56
256293_at	pinhead-like protein similar to pinh	AGO7	AT1G69440	-1.06	-0.08	-0.45	0.66505152	0.8980	-6.56
256862_at	dihydroxyacid dehydratase, putati	---	AT3G23940	1.09	0.12	0.45	0.6653347	0.8982	-6.56
252634_x_at	putative protein predicted proteins	---	---	-1.04	-0.06	-0.45	0.66528067	0.8982	-6.56
263983_at	unknown protein ;supported by ful	---	AT2G42780	1.03	0.04	0.45	0.66518583	0.8982	-6.56
264073_at	putative replication protein A1	---	---	1.04	0.06	0.45	0.66538274	0.8982	-6.56
254373_at	hypothetical protein ;supported by	---	AT4G21730	1.03	0.05	0.45	0.66536529	0.8982	-6.56
247129_at	alpha-mannosidase	---	AT5G66150	1.06	0.08	0.45	0.6654096	0.8982	-6.56
252726_at	putative protein predicted proteins	---	---	1.05	0.08	0.45	0.66532703	0.8982	-6.56
265590_at	SKP1/ASK1 (At17), putative simila	MEO	AT2G20160	-1.03	-0.05	-0.45	0.66546133	0.8982	-6.56
262348_at	unknown protein similar to transcri	---	AT2G48160	-1.03	-0.05	-0.45	0.66552547	0.8982	-6.56
266650_at	unknown protein	---	AT2G25800	1.05	0.06	0.45	0.66711409	0.8982	-6.56
251494_at	protein kinase-like protein Pto kina	---	AT3G59350	-1.09	-0.12	-0.45	0.66709428	0.8982	-6.56

246988_at	putative protein strong similarity to	---	AT5G67340	-1.09	-0.13	-0.45	0.66570664	0.8982	-6.56
245744_at	unknown protein	---	AT1G51110	-1.10	-0.14	-0.45	0.66630885	0.8982	-6.56
259434_at	unknown protein	---	AT1G01490	1.03	0.05	0.45	0.66652434	0.8982	-6.56
251831_at	pectate lyase -like protein pectate	---	AT3G55140	1.03	0.04	0.45	0.66654577	0.8982	-6.56
258502_at	unknown protein	---	AT3G02490	1.06	0.09	0.45	0.66622192	0.8982	-6.56
245989_s_at	polyubiquitin (UBQ4) identical to G	UBQ4	AT5G20620	-1.04	-0.06	-0.45	0.66610159	0.8982	-6.56
259118_at	unknown protein similar to unknov	---	AT3G01310	1.05	0.07	0.45	0.66715905	0.8982	-6.56
260479_at	hypothetical protein predicted by g	---	AT1G11020	-1.03	-0.04	-0.45	0.66623512	0.8982	-6.56
258063_at	putative cytochrome P450 similar t	CYP72A8	AT3G14620	-1.12	-0.16	-0.45	0.66694327	0.8982	-6.56
245873_at	bHLH transcription factor GBOF-1	CIB5	AT1G26260	-1.05	-0.07	-0.45	0.66679455	0.8982	-6.56
252709_at	putative protein predicted proteins	---	AT3G43840	-1.03	-0.04	-0.45	0.66654581	0.8982	-6.56
262149_at	hypothetical protein predicted by g	---	AT1G52530	1.05	0.07	0.45	0.66708143	0.8982	-6.56
254291_at	putative protein UDP-galactose tra	UTR2	AT4G23010	1.06	0.08	0.45	0.66613794	0.8982	-6.56
267026_at	DREB-like AP2 domain transcriptio	---	AT2G38340	1.12	0.16	0.45	0.66708154	0.8982	-6.56
257865_at	protein kinase, putative contains P	---	AT3G17750	-1.03	-0.04	-0.45	0.66605294	0.8982	-6.56
254118_at	DNA polymerase III like protein DI	---	AT4G24790	-1.03	-0.05	-0.45	0.66688985	0.8982	-6.56
262293_at	heat-shock protein 90, putative ide	---	AT1G27640	-1.06	-0.08	-0.45	0.6658505	0.8982	-6.56
245832_at	chorismate synthase, putative sim	EMB1144	AT1G48850	-1.11	-0.16	-0.45	0.66644572	0.8982	-6.56
246023_at	ethylene-insensitive3-like2 (EIL2)	EIL2	AT5G21120	1.04	0.05	0.45	0.66627681	0.8982	-6.56
264366_at	unknown protein EST gb|N96383 c	---	AT1G03250	-1.05	-0.07	-0.45	0.66578756	0.8982	-6.56
255159_at	putative polyprotein	---	---	-1.05	-0.07	-0.45	0.66624228	0.8982	-6.56
249371_at	hypothetical protein	---	AT5G40750	-1.03	-0.04	-0.45	0.66603431	0.8982	-6.56
264317_at	spermidine synthase, putative sim	SPDS2	AT1G70310	1.04	0.05	0.45	0.66573652	0.8982	-6.56
261853_at	unknown protein	---	AT1G50660	1.05	0.07	0.45	0.66638303	0.8982	-6.56
255509_at	hypothetical protein identical to T1	---	AT4G02210	-1.06	-0.08	-0.45	0.66692472	0.8982	-6.56
250018_at	putative protein similar to unknown	---	AT5G18150	1.12	0.16	0.45	0.66677108	0.8982	-6.56
260650_at	Expressed protein ; supported by f	TOM2B	AT1G32370	1.03	0.05	0.45	0.66655092	0.8982	-6.56
256576_at	zinc finger protein (PMZ), putative	PMZ	AT3G28210	-1.13	-0.17	-0.45	0.66715411	0.8982	-6.56
263543_at	putative pectinesterase	PE11	AT2G21610	1.03	0.04	0.45	0.66605786	0.8982	-6.56
257298_at	hypothetical protein predicted by g	---	AT3G28155	1.05	0.07	0.45	0.66634486	0.8982	-6.56
245836_at	hypothetical protein similar to hypo	---	---	1.03	0.05	0.45	0.66626982	0.8982	-6.56
250802_at	pectinesterase	---	AT5G04970	-1.04	-0.05	-0.45	0.66696112	0.8982	-6.56
265014_at	hypothetical protein similar to dea	---	AT1G24430	-1.05	-0.08	-0.45	0.66675844	0.8982	-6.56
250926_at	Expressed protein ; supported by f	---	AT5G03555	1.08	0.12	0.45	0.66601598	0.8982	-6.56
246386_at	beta-galactosidase, putative simila	BGAL16	AT1G77410	1.05	0.07	0.45	0.66680889	0.8982	-6.56

253311_s_at	putative protein xylan endohydrola	---	AT4G33830	1.03	0.04	0.45	0.66654661	0.8982	-6.56
252729_at	putative protein replication protein	---	---	-1.03	-0.04	-0.45	0.66595539	0.8982	-6.56
249005_at	terpene cyclase/synthase	---	AT5G44630	1.03	0.04	0.45	0.66694268	0.8982	-6.56
251836_at	lipase -like protein monoglyceride	---	AT3G55190	1.03	0.04	0.45	0.66668539	0.8982	-6.56
259586_at	unknown protein	---	AT1G28100	-1.03	-0.05	-0.45	0.66901625	0.8983	-6.56
265991_at	chloroplast single subunit DNA-de	SCA3	AT2G24120	-1.07	-0.09	-0.45	0.66774747	0.8983	-6.56
245428_at	putative protein	---	AT4G17570	-1.04	-0.05	-0.45	0.66875687	0.8983	-6.56
265968_at	putative protein translocase ; supp	ATTIM17-2	AT2G37410	1.06	0.08	0.45	0.66849043	0.8983	-6.56
258139_at	heat shock transcription factor HS	HSFC1	AT3G24520	-1.05	-0.07	-0.45	0.66769476	0.8983	-6.56
267347_at	hypothetical protein predicted by g	---	AT2G39950	1.03	0.05	0.45	0.66796157	0.8983	-6.56
245676_at	nodule-specific protein, putative si	---	AT1G56670	1.04	0.05	0.45	0.66864566	0.8983	-6.56
257721_at	hypothetical protein predicted by g	---	AT3G18310	-1.03	-0.04	-0.45	0.66859062	0.8983	-6.56
264571_at	hypothetical protein predicted by g	---	AT1G05330	-1.03	-0.04	-0.45	0.66850455	0.8983	-6.56
251139_at	cell division - like protein JM23 pr	---	AT5G01230	1.05	0.06	0.45	0.66800372	0.8983	-6.56
257598_at	PRT1 identical to GB:CAA11891 f	PRT1	AT3G24800	-1.05	-0.07	-0.45	0.66897776	0.8983	-6.56
255865_at	unknown protein	---	AT2G30330	1.03	0.04	0.45	0.66903611	0.8983	-6.56
252502_at	copper transport protein - like prot	COPT2	AT3G46900	1.11	0.15	0.45	0.66892263	0.8983	-6.56
248101_at	chaperone GrpE-like protein ;supp	---	AT5G55200	-1.09	-0.12	-0.45	0.66835369	0.8983	-6.56
257081_at	RING zinc finger protein contains	---	AT3G30460	-1.03	-0.05	-0.45	0.66800035	0.8983	-6.56
257236_at	hypothetical protein	---	AT3G15095	-1.05	-0.07	-0.45	0.66740849	0.8983	-6.56
262668_at	flavin-containing amine oxidase co	LDL1	AT1G62830	1.04	0.05	0.45	0.66881151	0.8983	-6.56
245979_at	putative protein leucine zipper-cor	ATEXO70C	AT5G13150	-1.03	-0.04	-0.45	0.6677492	0.8983	-6.56
261097_at	protein kinase, putative contains p	---	AT1G62950	-1.06	-0.08	-0.45	0.66729934	0.8983	-6.56
257769_at	indoleacetic acid (IAA)-inducible g	IAA7	AT3G23050	-1.26	-0.33	-0.45	0.66726532	0.8983	-6.56
246878_at	putative protein self-incompatibility	---	AT5G26060	-1.05	-0.07	-0.45	0.6691049	0.8983	-6.56
254898_at	serine/threonine kinase-like protei	---	AT4G11480	1.15	0.21	0.45	0.66851491	0.8983	-6.56
254477_at	zinc-finger protein Lsd1 ;supporte	---	AT4G20380	-1.05	-0.07	-0.45	0.66915007	0.8983	-6.56
245082_at	hypothetical protein predicted by g	---	AT2G23270	-1.26	-0.33	-0.45	0.66884257	0.8983	-6.56
256619_at	hypothetical protein predicted by g	---	AT3G24460	1.03	0.05	0.45	0.66807981	0.8983	-6.56
257431_at	unknown protein	---	AT2G36360	1.04	0.05	0.45	0.66882641	0.8983	-6.56
262125_at	heat shock protein, putative simila	EDA1	AT1G59680	-1.04	-0.05	-0.45	0.66786286	0.8983	-6.56
249389_at	disease resistence like - protein d	---	AT5G40100	-1.05	-0.06	-0.45	0.66784161	0.8983	-6.56
263208_at	zinc finger protein 5, ZFP5 possib	ZFP5	AT1G10480	1.05	0.06	0.45	0.66888779	0.8983	-6.56
254994_at	putative methyltransferase	MTA	AT4G10760	-1.07	-0.09	-0.45	0.66883607	0.8983	-6.56
256162_at	hypothetical protein similar to hypo	---	AT1G55390	1.03	0.04	0.45	0.66902763	0.8983	-6.56

251450_at	squamosa promoter binding protei	SPL12	AT3G60030	-1.04	-0.06	-0.45	0.66765465	0.8983	-6.56
245613_at	hypothetical protein	---	AT4G14450	1.21	0.27	0.45	0.66879793	0.8983	-6.56
252224_at	putative protein various ADP-RIBC	ATARLA1B	AT3G49860	1.04	0.06	0.45	0.66785147	0.8983	-6.56
250807_at	helicase-like transcription factor-lik	---	AT5G05130	1.05	0.07	0.45	0.66918594	0.8983	-6.56
252642_at	putative protein predicted protein,	---	AT3G44580	1.03	0.04	0.45	0.66810319	0.8983	-6.56
254740_s_at	glycine hydroxymethyltransferase	---	AT2G42450	1.12	0.16	0.45	0.6684876	0.8983	-6.56
264492_at	unknown protein similar to unknov	---	AT1G27430	1.03	0.04	0.45	0.66768212	0.8983	-6.56
255115_at	putative protein probable regulato	APUM11	AT4G08840	1.03	0.05	0.45	0.66912686	0.8983	-6.56
245849_at	leukotriene-A4 hydrolase-like prot	---	AT5G13520	1.08	0.11	0.45	0.66767368	0.8983	-6.56
258147_at	beta-glucosidase, putative similar	BGLU43	AT3G18070	1.04	0.05	0.45	0.66830672	0.8983	-6.56
260771_at	serine/threonine protein kinase, pu	WNK7	AT1G49160	1.07	0.09	0.45	0.669062	0.8983	-6.56
262927_at	hypothetical protein shares similari	---	AT1G65810	1.03	0.05	0.45	0.6688054	0.8983	-6.56
266819_at	unknown protein ;supported by ful	---	AT2G44870	1.05	0.07	0.45	0.66875917	0.8983	-6.56
261980_at	hypothetical protein predicted by g	---	AT1G33820	1.03	0.04	0.45	0.6677572	0.8983	-6.56
264554_at	putative cinnamyl alcohol dehydro	---	AT1G09510	1.05	0.07	0.45	0.66850748	0.8983	-6.56
255757_at	putative protein	ROPGEF3	AT4G00460	1.03	0.05	0.45	0.66812788	0.8983	-6.56
255854_at	unknown protein ;supported by full	---	AT1G67050	1.10	0.14	0.45	0.66804083	0.8983	-6.56
246663_at	putative protein	---	AT5G35300	-1.03	-0.05	-0.45	0.667222	0.8983	-6.56
263436_at	hypothetical protein	---	AT2G28690	1.04	0.06	0.45	0.66812568	0.8983	-6.56
263166_at	putative protein destination factor S	---	AT1G03050	-1.03	-0.04	-0.45	0.66808782	0.8983	-6.56
261740_at	hypothetical protein similar to unkn	---	AT1G47740	-1.05	-0.07	-0.45	0.66991777	0.8983	-6.56
261819_at	receptor-like kinase, putative simil	---	AT1G11410	-1.03	-0.05	-0.45	0.67017322	0.8983	-6.56
263766_at	hypothetical protein predicted by g	---	AT2G21440	1.05	0.07	0.45	0.66980496	0.8983	-6.56
257092_at	unknown protein	DDL	AT3G20550	-1.05	-0.07	-0.45	0.66931182	0.8983	-6.56
255455_at	mitochondrial elongation factor Tu	---	AT4G02930	1.08	0.11	0.45	0.67013032	0.8983	-6.56
248669_at	putative protein contains similarity	---	AT5G48730	-1.05	-0.08	-0.45	0.66974713	0.8983	-6.56
254845_at	hydroxymethylglutaryl-CoA syntha	MVA1	AT4G11820	-1.05	-0.07	-0.45	0.66999877	0.8983	-6.56
257607_at	hypothetical protein predicted by g	---	AT3G13880	1.03	0.04	0.45	0.67024015	0.8983	-6.56
257950_at	putative UDP-glucose glucosyltran	UGT71B6	AT3G21780	1.12	0.17	0.45	0.66966354	0.8983	-6.56
265312_at	unknown protein	---	AT2G20240	-1.08	-0.11	-0.45	0.6696379	0.8983	-6.56
263661_at	unknown protein EST gb|T45093 c	---	AT1G04290	-1.06	-0.09	-0.45	0.6695608	0.8983	-6.56
245406_at	GTP-binding RAB2A like protein	ATRABB1A	AT4G17160	-1.03	-0.04	-0.45	0.67015061	0.8983	-6.56
261294_at	dihydroxyacetone kinase, putative	---	AT1G48430	1.05	0.07	0.45	0.66958021	0.8983	-6.56
256335_at	hypothetical protein predicted by g	---	AT1G72110	-1.04	-0.06	-0.45	0.66975201	0.8983	-6.56
260716_at	peroxiredoxin identical to SP:O040	ATPER1	AT1G48130	-1.05	-0.06	-0.45	0.67024915	0.8983	-6.56

251230_at	beta-glucosidase-like protein sevel	BGLU8	AT3G62750	-1.03	-0.04	-0.45	0.67016493	0.8983	-6.56
259465_at	hypothetical protein similar to puta	---	AT1G19025	-1.04	-0.06	-0.45	0.66933933	0.8983	-6.56
264066_at	Argonaute (AGO1)-like protein	AGO5	AT2G27880	1.04	0.05	0.45	0.6696931	0.8983	-6.56
261472_at	hypothetical protein predicted by g	---	AT1G14470	-1.03	-0.04	-0.45	0.67019597	0.8983	-6.56
256591_at	hypothetical protein	---	AT3G31910	-1.03	-0.04	-0.45	0.66984345	0.8983	-6.56
264650_at	putative transcription factor Similar	NF-YC9	AT1G08970	-1.04	-0.05	-0.45	0.66946372	0.8983	-6.56
257439_at	hypothetical protein similar to hypo	---	AT2G17000	-1.03	-0.04	-0.45	0.66969107	0.8983	-6.56
266902_at	hypothetical protein predicted by g	---	AT2G34580	1.03	0.04	0.45	0.66951993	0.8983	-6.56
253962_at	hypothetical protein	---	AT4G26460	1.04	0.05	0.45	0.67025735	0.8983	-6.56
257318_at	hypothetical protein	---	AT2G07777	-1.03	-0.05	-0.45	0.67005065	0.8983	-6.56
249730_at	calcium dependent protein kinase-	---	AT5G24430	1.08	0.11	0.45	0.66942724	0.8983	-6.56
248486_at	respiratory burst oxidase protein	RHD2	AT5G51060	-1.03	-0.04	-0.45	0.66985052	0.8983	-6.56
264399_at	postsynaptic protein CRIPT, putat	---	AT1G61780	1.03	0.04	0.44	0.67041478	0.8983	-6.56
257902_at	receptor kinase, putative similar to	---	AT3G28450	-1.06	-0.08	-0.44	0.67040717	0.8983	-6.56
254550_at	Fe(II) transport protein ;supported	IRT1	AT4G19690	1.03	0.04	0.44	0.67036346	0.8983	-6.56
267572_at	3-hydroxyisobutyryl-coenzyme A h	---	AT2G30660	-1.04	-0.05	-0.44	0.67058013	0.8984	-6.56
244969_at	ribosomal protein S18	---	---	1.08	0.11	0.44	0.67057946	0.8984	-6.56
251117_at	putative protein predicted protein,	---	AT3G63390	1.04	0.06	0.44	0.67071655	0.8985	-6.56
258312_at	putative long-chain acyl-CoA synth	---	AT3G16170	1.05	0.07	0.44	0.67074143	0.8985	-6.56
262578_at	hypothetical protein Similar to gi|22	---	---	-1.04	-0.05	-0.44	0.67072801	0.8985	-6.56
265145_at	unknown protein similar to GB:CA/	PLT2	AT1G51190	-1.04	-0.05	-0.44	0.67107835	0.8988	-6.56
255101_at	putative lipid transfer protein simil	---	AT4G08670	1.05	0.06	0.44	0.67109316	0.8988	-6.56
253983_at	putative protein SPF1 protein -Ipo	WRKY20	AT4G26640	-1.04	-0.06	-0.44	0.67104175	0.8988	-6.56
247965_at	putative protein similar to unknown	AGP14	AT5G56540	-1.06	-0.08	-0.44	0.67124143	0.8989	-6.56
265766_at	unknown protein	---	AT2G48080	-1.05	-0.07	-0.44	0.67117951	0.8989	-6.56
265997_at	Expressed protein ; supported by c	---	AT2G24250	-1.03	-0.05	-0.44	0.67124206	0.8989	-6.56
246213_at	serine C-palmitoyltransferase like p	ATLCB1	AT4G36480	1.04	0.06	0.44	0.67135259	0.8989	-6.56
259126_at	putative NADPH-ferrihemoprotein	---	AT3G02280	-1.03	-0.04	-0.44	0.6716655	0.8992	-6.56
252452_at	receptor protein kinase - like prote	---	AT3G47110	-1.03	-0.04	-0.44	0.67168281	0.8992	-6.56
256026_at	auxin response factor 1, putative s	---	AT1G34170	1.03	0.05	0.44	0.67164741	0.8992	-6.56
263997_at	hypothetical protein predicted by g	---	AT2G22520	-1.03	-0.04	-0.44	0.67159245	0.8992	-6.56
261115_at	hypothetical protein predicted by g	---	AT1G75360	1.03	0.04	0.44	0.67175886	0.8992	-6.56
247231_at	transcription factor-like protein	AtMYB53	AT5G65230	1.04	0.05	0.44	0.6720166	0.8995	-6.56
249296_at	kinesin-like protein	---	AT5G41310	1.04	0.06	0.44	0.67204179	0.8995	-6.56
245819_at	cauliflower identical to CAULIFLO	CAL	AT1G26310	1.04	0.05	0.44	0.67217079	0.8996	-6.56

262275_at	ATPase, putative similar to chrom	---	AT1G68710	-1.04	-0.06	-0.44	0.67238286	0.8996	-6.56
250347_at	putative protein	---	AT5G11960	-1.03	-0.05	-0.44	0.67231618	0.8996	-6.56
248618_at	myb-related transcription factor	AtMYB78	AT5G49620	-1.04	-0.06	-0.44	0.67237353	0.8996	-6.56
246203_at	putative protein ; supported by full-	---	AT4G36610	-1.07	-0.10	-0.44	0.67241224	0.8996	-6.56
265280_at	Expressed protein ; supported by f	LCR5	AT2G28355	-1.03	-0.05	-0.44	0.67239823	0.8996	-6.56
257013_at	hypothetical protein contains Pfam	---	AT3G26920	1.04	0.05	0.44	0.67237736	0.8996	-6.56
267635_at	rhodanese-like family protein ;supp	---	AT2G42220	1.06	0.09	0.44	0.6727023	0.8997	-6.56
251098_at	light-inducible protein ATLS1	---	AT5G01650	1.03	0.04	0.44	0.67282632	0.8997	-6.56
249583_at	CALMODULIN-RELATED PROTE	TCH2	AT5G37770	-1.14	-0.18	-0.44	0.67267687	0.8997	-6.56
245335_at	pore protein homolog ;supported b	ATOEP16-2	AT4G16160	-1.04	-0.06	-0.44	0.67278978	0.8997	-6.56
252067_at	protein phosphatase 2C -like prote	---	AT3G51370	1.04	0.06	0.44	0.67261476	0.8997	-6.56
261917_at	hypothetical protein similar to TMV	---	AT1G65920	-1.08	-0.11	-0.44	0.67275836	0.8997	-6.56
266558_at	putative polygalacturonase	---	AT2G23900	-1.03	-0.05	-0.44	0.67277766	0.8997	-6.56
265427_at	unknown protein	---	AT2G20740	1.05	0.06	0.44	0.67268493	0.8997	-6.56
254352_at	hypothetical protein	---	AT4G22320	1.03	0.04	0.44	0.67252734	0.8997	-6.56
246313_at	PPR-repeat protein, putative conta	---	AT1G31920	1.08	0.11	0.44	0.6729907	0.8998	-6.56
265102_at	putative peroxidase similar to catio	---	AT1G30870	1.04	0.06	0.44	0.67294391	0.8998	-6.56
263234_at	hypothetical protein predicted by g	---	AT1G10417	1.03	0.05	0.44	0.67300779	0.8998	-6.56
247019_at	AP2 domain transcription factor-lik	---	AT5G67010	-1.04	-0.05	-0.44	0.67306424	0.8998	-6.56
252408_at	putative transcription factor MYB94	ATMYB94	AT3G47600	-1.03	-0.04	-0.44	0.67321978	0.8999	-6.56
255441_at	putative cullin-like 1 protein similar	ATCUL1	AT4G02570	-1.03	-0.05	-0.44	0.6731954	0.8999	-6.56
264465_at	SKP1/ASK1 (At18), putative simila	ASK18	AT1G10230	1.03	0.04	0.44	0.6731874	0.8999	-6.56
251304_at	putative protein several O-methyltr	---	AT3G61990	1.13	0.17	0.44	0.67347441	0.8999	-6.56
266311_at	hypothetical protein predicted by g	---	AT2G27130	1.12	0.16	0.44	0.6733959	0.8999	-6.56
245605_at	ribonucleoprotein like protein	---	AT4G14300	1.03	0.04	0.44	0.67347371	0.8999	-6.56
262677_at	unknown protein	---	AT1G75860	-1.07	-0.09	-0.44	0.67329828	0.8999	-6.56
262248_at	hypothetical protein predicted by g	YSL8	AT1G48370	-1.07	-0.10	-0.44	0.673442	0.8999	-6.56
255248_at	Oxygen-evolving enhancer protein	PSBQ-2	AT4G05180	-1.03	-0.04	-0.44	0.67347869	0.8999	-6.56
264396_at	fumarylacetoacetate hydrolase-lik	---	AT1G12050	-1.03	-0.04	-0.44	0.67363909	0.9000	-6.56
246575_at	bystin, putative similar to bystin G	---	AT1G31660	-1.06	-0.08	-0.44	0.67367173	0.9000	-6.56
247179_at	putative protein contains similarity	---	AT5G65320	-1.03	-0.05	-0.44	0.67362954	0.9000	-6.56
255039_at	calmodulin-domain protein kinase	CPK4	AT4G09570	1.04	0.06	0.44	0.67381915	0.9001	-6.56
246880_s_at	myrosinase TGG2 ; supported by	TGG2	AT5G25980	-1.12	-0.16	-0.44	0.6739254	0.9002	-6.56
265620_at	unknown protein	---	AT2G27310	1.12	0.16	0.44	0.67393958	0.9002	-6.56
250237_at	putative protein strong similarity to	---	AT5G13560	-1.04	-0.06	-0.44	0.67399127	0.9002	-6.56

256063_at	Expressed protein ; supported by f	STN1	AT1G07130	1.04	0.05	0.44	0.67399214	0.9002	-6.56
255801_at	putative protein heat shock protein	---	AT4G10130	1.03	0.04	0.44	0.67432607	0.9004	-6.56
262988_at	putative alanine aminotrans	GGT1	AT1G23310	-1.03	-0.04	-0.44	0.67426769	0.9004	-6.56
256051_at	hypothetical protein similar to puta	CHX14	AT1G06970	1.04	0.06	0.44	0.67436835	0.9004	-6.56
265743_s_at	En/Spm-like transposon protein rel	---	---	-1.03	-0.04	-0.44	0.67438961	0.9004	-6.56
249605_at	putative protein predicted protein,	---	AT5G37240	-1.04	-0.06	-0.44	0.67433442	0.9004	-6.56
248858_at	AP47 50p (gb|AAB88283.1) ; supp	---	AT5G46630	1.04	0.05	0.44	0.6744276	0.9004	-6.56
257354_x_at	hypothetical protein predicted by g	---	---	1.04	0.06	0.44	0.67454372	0.9005	-6.57
256280_at	unknown protein	---	AT3G12590	1.04	0.06	0.44	0.67461293	0.9006	-6.57
259995_at	putative golgi transport complex p	---	AT1G67930	1.04	0.06	0.44	0.67549829	0.9007	-6.57
255842_at	putative serine carboxypeptidase I	scpl46	AT2G33530	1.09	0.12	0.44	0.67545605	0.9007	-6.57
263419_at	putative protein kinase contains a	---	AT2G17220	1.05	0.07	0.44	0.67554723	0.9007	-6.57
253297_at	beta-xylan endohydrolase -like pr	---	AT4G33810	1.03	0.05	0.44	0.67556855	0.9007	-6.57
256485_at	unknown protein	---	AT1G31440	1.03	0.05	0.44	0.67536809	0.9007	-6.57
259419_at	acyl-CoA oxidase ACX3, putative	ACX6	AT1G06310	-1.03	-0.05	-0.44	0.67513491	0.9007	-6.57
255426_at	putative protein	---	AT4G03370	-1.03	-0.05	-0.44	0.67497546	0.9007	-6.57
250880_at	putative protein Ube-1a, Mus mus	---	AT5G04070	1.03	0.04	0.44	0.67551621	0.9007	-6.57
267507_at	putative ribosomal protein S27 ;su	---	AT2G45710	1.06	0.08	0.44	0.67518702	0.9007	-6.57
244976_at	cytochrome B6	---	---	-1.03	-0.05	-0.44	0.67537449	0.9007	-6.57
267271_at	hypothetical protein predicted by g	ATHB21	AT2G02540	1.03	0.05	0.44	0.67555505	0.9007	-6.57
247273_at	unknown protein	CPuORF40	AT5G64340 /	-1.06	-0.08	-0.44	0.67502701	0.9007	-6.57
263308_at	hypothetical protein predicted by g	---	---	-1.03	-0.04	-0.44	0.67558748	0.9007	-6.57
245086_at	putative translation initiation factor	---	AT2G39820	-1.03	-0.05	-0.44	0.67534797	0.9007	-6.57
259651_at	unknown protein	---	AT1G55280	1.08	0.12	0.44	0.67541423	0.9007	-6.57
257688_at	Snf2-related CBP activator protein	PIE1	AT3G12810	1.03	0.04	0.44	0.67522457	0.9007	-6.57
266726_at	SKP1/ASK1 (At19), putative simila	ASK19	AT2G03160	-1.05	-0.07	-0.44	0.6751866	0.9007	-6.57
250601_at	putative protein contains similarity	---	AT5G07810	1.03	0.04	0.44	0.67540736	0.9007	-6.57
265751_at	putative retroelement pol polyprote	---	---	-1.03	-0.04	-0.44	0.67554046	0.9007	-6.57
247022_at	unknown protein	---	AT5G67050	-1.03	-0.05	-0.44	0.6747951	0.9007	-6.57
249813_at	acyltransferase ; supported by full	EMB3009	AT5G23940	-1.03	-0.04	-0.44	0.67558533	0.9007	-6.57
259716_at	unknown protein	---	AT1G60995 /	-1.05	-0.07	-0.44	0.67545173	0.9007	-6.57
264778_at	unknown protein similar to C-1 (Hc	AIP3	AT1G08780	1.03	0.05	0.44	0.67554026	0.9007	-6.57
264786_at	putative Ta11-like non-LTR retroel	---	AT2G17920	-1.03	-0.05	-0.44	0.67563819	0.9007	-6.57
255769_at	hypothetical protein predicted by g	---	AT1G18610	1.03	0.05	0.44	0.67566996	0.9007	-6.57
259728_at	putative coatomer zeta subunit sim	---	AT1G60970	-1.03	-0.05	-0.44	0.67572209	0.9007	-6.57

249212_at	putative protein strong similarity to	---	AT5G42690	-1.04	-0.05	-0.44	0.67582252	0.9007	-6.57
249968_at	putative protein predicted proteins	---	AT5G19070	-1.08	-0.11	-0.44	0.67585743	0.9007	-6.57
265055_at	hypothetical protein similar to hypo	---	---	-1.03	-0.05	-0.44	0.67580737	0.9007	-6.57
267602_at	unknown protein ; supported by cl	---	AT2G32970	-1.05	-0.07	-0.44	0.67591677	0.9007	-6.57
252978_at	galactosidase like protein ss-1,4-e	BGAL14	AT4G38590	-1.05	-0.06	-0.44	0.67620303	0.9008	-6.57
259423_at	unknown protein similar to putative	---	AT1G13880	1.05	0.07	0.44	0.67614683	0.9008	-6.57
249766_at	peroxidase-like protein	---	AT5G24070	-1.04	-0.05	-0.44	0.67618999	0.9008	-6.57
262301_at	ripening-induced protein, putative	---	AT1G70880	-1.04	-0.05	-0.44	0.6762254	0.9008	-6.57
252232_at	bZIP transcription factor - like prot	AtbZIP5	AT3G49760	1.03	0.04	0.44	0.67605392	0.9008	-6.57
252017_at	cytochrome P450 - like protein cyt	CYP76G1	AT3G52970	-1.04	-0.05	-0.44	0.6761757	0.9008	-6.57
256733_at	hypothetical protein predicted by g	---	AT3G30370	1.03	0.05	0.44	0.67626419	0.9008	-6.57
266499_at	hypothetical protein predicted by g	---	---	1.05	0.07	0.44	0.67636604	0.9009	-6.57
254875_at	putative protein various predicted	---	AT4G11590	-1.04	-0.05	-0.44	0.67647857	0.9010	-6.57
255682_at	putative dTDP-6-deoxy-L-mannose	---	AT4G00560	-1.04	-0.05	-0.44	0.67662472	0.9011	-6.57
245689_at	phosphoglycerate mutase - like pro	---	AT5G04120	-1.04	-0.05	-0.44	0.67658813	0.9011	-6.57
263066_at	unknown protein	---	AT2G17540	1.03	0.04	0.44	0.67679277	0.9011	-6.57
263013_at	knotted-like homeobox protein, pu	KNAT6	AT1G23380	-1.04	-0.06	-0.44	0.67673827	0.9011	-6.57
260339_at	putative serine/threonine kinase si	SIK1	AT1G69220	1.05	0.07	0.44	0.67677704	0.9011	-6.57
263576_at	hypothetical protein similar to hypo	---	AT2G17080	-1.03	-0.04	-0.44	0.67679048	0.9011	-6.57
266667_at	hypothetical protein predicted by g	---	AT2G29770	1.03	0.04	0.44	0.67684418	0.9011	-6.57
262213_at	hypothetical protein predicted by g	---	AT1G74870	-1.05	-0.07	-0.44	0.6769007	0.9011	-6.57
259516_at	hypothetical protein ; supported by	ERD10	AT1G20450	1.07	0.10	0.44	0.67694739	0.9011	-6.57
249901_at	histone deacetylase-like protein n	HD2B	AT5G22650	1.05	0.07	0.43	0.67769232	0.9012	-6.57
253096_at	cytochrome P450-like protein	CYP81D4	AT4G37330	-1.04	-0.06	-0.43	0.67731906	0.9012	-6.57
259075_at	putative N2,N2-dimethylguanosine	---	AT3G02320	1.04	0.05	0.44	0.67706927	0.9012	-6.57
259650_at	leucoanthocyanidin dioxygenase 2	---	AT1G55290	-1.04	-0.05	-0.43	0.67749955	0.9012	-6.57
252405_at	putative protein RNA helicase HE	---	AT3G48120	-1.04	-0.06	-0.43	0.67776075	0.9012	-6.57
254070_at	hypothetical protein	---	AT4G25430	-1.05	-0.07	-0.43	0.67760549	0.9012	-6.57
259216_at	hypothetical protein ; supported by	---	AT3G09000	1.08	0.10	0.43	0.67739193	0.9012	-6.57
265286_at	putative NADH-ubiquinone oxiredu	---	AT2G20360	-1.04	-0.05	-0.43	0.67729665	0.9012	-6.57
253616_at	blight-associated protein homolog	EXLB2	AT4G30380	-1.03	-0.04	-0.43	0.67731182	0.9012	-6.57
260917_at	unknown protein similar to hypothe	---	AT1G02700	-1.04	-0.06	-0.43	0.67766652	0.9012	-6.57
255746_at	heat shock transcription factor, pu	---	AT1G32020	1.03	0.04	0.43	0.67769063	0.9012	-6.57
250331_at	putative protein self-incompatibility	---	AT5G11820	-1.04	-0.05	-0.43	0.67750182	0.9012	-6.57
263012_at	homeotic protein, putative similar	KNAT6	AT1G23380	-1.03	-0.04	-0.43	0.67778834	0.9012	-6.57

250411_at	putative protein	---	AT5G11120	-1.03	-0.05	-0.43	0.67757302	0.9012	-6.57
256685_at	hypothetical protein predicted by g	---	AT3G32100	1.04	0.05	0.43	0.67718716	0.9012	-6.57
255423_at	putative calmodulin	---	AT4G03290	-1.03	-0.05	-0.43	0.67720122	0.9012	-6.57
266433_at	unknown protein	---	AT2G07110	-1.03	-0.04	-0.43	0.67774002	0.9012	-6.57
251452_at	putative protein male sterility prote	---	AT3G60060	-1.03	-0.04	-0.43	0.67763108	0.9012	-6.57
246388_at	hypothetical protein predicted by g	---	AT1G77405	-1.05	-0.07	-0.43	0.67768782	0.9012	-6.57
256884_at	hypothetical protein contains Pfam	---	AT3G15200	-1.06	-0.08	-0.43	0.67742083	0.9012	-6.57
263296_at	unknown protein	---	AT2G38800	-1.08	-0.10	-0.43	0.67787987	0.9012	-6.57
247238_at	histone acetyltransferase	HAM1	AT5G64610	1.03	0.04	0.43	0.67793142	0.9012	-6.57
248023_at	ADP/ATP translocase-like protein	---	AT5G56450	-1.04	-0.05	-0.43	0.67791965	0.9012	-6.57
261983_at	protein kinase, putative similar to	---	AT1G33770	1.06	0.08	0.43	0.67797914	0.9013	-6.57
260620_at	unknown protein	---	AT1G08070	1.04	0.05	0.43	0.67803443	0.9013	-6.57
267277_at	putative protein transport protein S	---	AT2G30050	1.04	0.05	0.43	0.67827647	0.9013	-6.57
246080_at	putative protein	---	AT5G20460	1.03	0.05	0.43	0.67818373	0.9013	-6.57
256235_at	cysteine proteinase inhibitor, puta	ATCYSB	AT3G12490	-1.03	-0.04	-0.43	0.67839709	0.9013	-6.57
262061_at	hypothetical protein contains simila	ATPP2-B11	AT1G80110	-1.04	-0.05	-0.43	0.67820615	0.9013	-6.57
257815_at	unknown protein	---	AT3G25130	1.04	0.05	0.43	0.67832075	0.9013	-6.57
256120_at	hypothetical protein contains simila	---	AT1G18130	-1.03	-0.04	-0.43	0.67838828	0.9013	-6.57
256124_at	hypothetical protein predicted by g	ATPUP9	AT1G18220	1.03	0.04	0.43	0.67831756	0.9013	-6.57
263147_at	polyubiquitin, putative similar to p	---	AT1G53980	-1.03	-0.04	-0.43	0.67822943	0.9013	-6.57
253727_at	profilin 2 ; supported by full-length	PFN2	AT4G29350	-1.04	-0.05	-0.43	0.67837279	0.9013	-6.57
266574_at	hypothetical protein predicted by g	---	AT2G23890	-1.07	-0.10	-0.43	0.67845808	0.9013	-6.57
262905_at	thioredoxin, putative similar to thio	ATH7	AT1G59730	-1.03	-0.04	-0.43	0.678575	0.9014	-6.57
254171_at	PsRT17-1 like protein PsRT17-1,	---	AT4G24530	-1.03	-0.04	-0.43	0.67862162	0.9014	-6.57
249472_at	hypothetical protein ;supported by	CRR7	AT5G39210	-1.06	-0.09	-0.43	0.67871137	0.9015	-6.57
246671_at	putative protein	---	---	1.03	0.04	0.43	0.67873583	0.9015	-6.57
255992_at	unknown protein	---	AT1G29790	1.04	0.06	0.43	0.67893689	0.9015	-6.57
246182_at	beta-1,3-glucanase - like protein p	---	AT5G20870	-1.04	-0.06	-0.43	0.67901722	0.9015	-6.57
263826_at	hypothetical protein predicted by g	---	AT2G40410	-1.05	-0.07	-0.43	0.67895998	0.9015	-6.57
264978_at	unknown protein contains Pfam pr	---	AT1G27120	1.07	0.10	0.43	0.67891991	0.9015	-6.57
267354_at	putative MYB family transcription f	MYB25	AT2G39880	-1.06	-0.08	-0.43	0.6789682	0.9015	-6.57
252684_at	disease resistence - like protein R	---	AT3G44400	-1.04	-0.05	-0.43	0.6790061	0.9015	-6.57
251340_at	actin - like protein actin 3, Drosop	ATARP7	AT3G60830	1.03	0.05	0.43	0.67909537	0.9016	-6.57
261244_at	subtilisin-like serine protease simil	---	AT1G20150	1.03	0.04	0.43	0.67913167	0.9016	-6.57
245299_at	ras-related small GTP-binding prot	ATRAB1C	AT4G17530	-1.05	-0.07	-0.43	0.67919537	0.9016	-6.57

254463_at	putative protein transcription initia	TAF11	AT4G20280	1.04	0.06	0.43	0.67923998	0.9016	-6.57
265654_s_at	En/Spm-like transposon protein rel	---	---	1.03	0.04	0.43	0.67930347	0.9017	-6.57
247709_at	D-xylose-H+ symporter - like prote	---	AT5G59250	-1.04	-0.06	-0.43	0.67959242	0.9018	-6.57
266876_at	hypothetical protein predicted by g	---	AT2G44820	-1.04	-0.05	-0.43	0.67947903	0.9018	-6.57
264904_s_at	putative thioredoxin reductase	NTRA	AT2G17420 /	1.05	0.07	0.43	0.67955928	0.9018	-6.57
258230_s_at	hypothetical protein similar to hyp	ARI13	AT3G27710 /	1.03	0.04	0.43	0.67963471	0.9018	-6.57
249299_at	E2, ubiquitin-conjugating enzyme	UBC4	AT5G41340	1.04	0.06	0.43	0.67962556	0.9018	-6.57
257444_at	hypothetical protein predicted by g	---	AT2G12550	-1.04	-0.06	-0.43	0.6798989	0.9019	-6.57
265446_at	unknown protein ;supported by ful	---	AT2G37110	1.04	0.05	0.43	0.68004566	0.9019	-6.57
257699_at	phosphoglycerate kinase, putative	PGK1	AT3G12780	1.04	0.06	0.43	0.68006149	0.9019	-6.57
267564_at	putative protein kinase contains a	---	AT2G30740	-1.04	-0.06	-0.43	0.67991573	0.9019	-6.57
253289_at	putative protein F10M10_100, Ara	---	AT4G34320	-1.03	-0.05	-0.43	0.6800432	0.9019	-6.57
247133_at	chalcone isomerase-like protein	---	AT5G66220	-1.07	-0.09	-0.43	0.67979903	0.9019	-6.57
252791_at	transposase - like protein putative	---	---	-1.03	-0.04	-0.43	0.67993419	0.9019	-6.57
259804_at	cytosolic factor, putative similar to	---	AT1G72160	1.07	0.09	0.43	0.6799456	0.9019	-6.57
251460_at	hypothetical protein	SAC9	AT3G59770	-1.03	-0.04	-0.43	0.67996111	0.9019	-6.57
249490_s_at	germin -like protein germin -like pr	---	AT5G39110 /	-1.10	-0.14	-0.43	0.68024925	0.9020	-6.57
245580_at	hypothetical protein	---	AT4G14820	-1.05	-0.07	-0.43	0.68023521	0.9020	-6.57
252569_at	receptor-like protein kinase recept	---	AT3G45420	-1.04	-0.05	-0.43	0.68024612	0.9020	-6.57
262910_at	unknown protein ;supported by full	---	AT1G59710	-1.05	-0.07	-0.43	0.68043421	0.9020	-6.57
244995_at	ATPase a subunit	---	---	-1.07	-0.10	-0.43	0.68076892	0.9020	-6.57
260425_at	hypothetical protein similar to CCA	EDA25	AT1G72440	1.09	0.12	0.43	0.6807473	0.9020	-6.57
261427_at	protein kinase, putative similar to	IBS1	AT1G18670	1.07	0.09	0.43	0.68043611	0.9020	-6.57
255760_at	vacuolar-type H+-translocating ino	---	AT1G16780	-1.04	-0.05	-0.43	0.68073823	0.9020	-6.57
250612_s_at	putative protein ARR2 protein - Ar	ARR13	AT2G27070 /	-1.05	-0.07	-0.43	0.68049384	0.9020	-6.57
249547_at	lipid transfer - like protein P48h-10	---	AT5G38160	-1.04	-0.06	-0.43	0.68074077	0.9020	-6.57
250635_at	glycine-rich protein glycine-rich pr	GRP14	AT5G07510	-1.04	-0.06	-0.43	0.68072352	0.9020	-6.57
259044_at	pollen allergen Bra r II identical to	---	AT3G03430	1.03	0.04	0.43	0.68056605	0.9020	-6.57
263835_at	putative eukaryotic translation initi	---	AT2G40290	-1.03	-0.05	-0.43	0.68070717	0.9020	-6.57
266577_at	predicted protein	---	AT2G23945	1.04	0.05	0.43	0.68056516	0.9020	-6.57
256046_at	unknown protein	---	AT1G07135	1.15	0.20	0.43	0.68067346	0.9020	-6.57
262995_s_at	hypothetical protein predicted by g	---	---	1.03	0.04	0.43	0.6804613	0.9020	-6.57
247272_at	GTP cyclohydrolase II; 3,4-dihydr	---	AT5G14040 /	-1.10	-0.13	-0.43	0.68082417	0.9020	-6.57
262613_at	putative DNA-binding protein simil	WRKY4	AT1G13960	1.03	0.05	0.43	0.68085781	0.9020	-6.57
261677_at	unknown protein ;supported by full	---	AT1G18470	-1.05	-0.08	-0.43	0.68089752	0.9020	-6.57

264384_at	putative chromodomain-helicase-D	PKL	AT2G25170	-1.03	-0.04	-0.43	0.68104876	0.9022	-6.57
261367_at	protein kinase, putative similar to r	---	AT1G53080	-1.20	-0.27	-0.43	0.68106796	0.9022	-6.57
260792_at	unknown protein ;supported by full	---	AT1G06270	-1.04	-0.05	-0.43	0.68130129	0.9022	-6.57
248616_at	putative protein contains similarity	---	AT5G49580	-1.05	-0.07	-0.43	0.68164806	0.9022	-6.57
252092_at	mucin-like protein hemomucin, Dr	SSL4	AT3G51420	1.06	0.09	0.43	0.68148282	0.9022	-6.57
263155_at	transcriptional activation factor TA	TAFII21	AT1G54140	1.04	0.06	0.43	0.68153633	0.9022	-6.57
254248_at	serine/threonine kinase serine/thre	---	AT4G23270	1.07	0.09	0.43	0.68141045	0.9022	-6.57
266397_at	unknown protein	---	AT2G38690	1.03	0.04	0.43	0.68124739	0.9022	-6.57
261198_at	nitrate transporter, putative similar	ATNRT2.5	AT1G12940	-1.03	-0.04	-0.43	0.68133622	0.9022	-6.57
266430_at	unknown protein	---	AT2G07200	-1.03	-0.04	-0.43	0.6816692	0.9022	-6.57
245576_at	hypothetical protein	TCX2	AT4G14770	1.05	0.07	0.43	0.68146451	0.9022	-6.57
245997_at	putative protein saur1 protein, Zea	---	AT5G20810	-1.05	-0.08	-0.43	0.68161784	0.9022	-6.57
258971_at	unknown protein similar to uridylyl	ACR6	AT3G01990	-1.09	-0.12	-0.43	0.68143614	0.9022	-6.57
245839_at	disease resistance protein, putativ	---	AT1G58390	-1.03	-0.04	-0.43	0.68121881	0.9022	-6.57
257342_at	pseudogene, putative polyprotein	---	---	1.06	0.08	0.43	0.68167402	0.9022	-6.57
252501_at	hypothetical protein	---	AT3G46880	-1.03	-0.05	-0.43	0.68129826	0.9022	-6.57
267025_at	unknown protein predicted by gens	---	AT2G38350	-1.03	-0.04	-0.43	0.68175581	0.9022	-6.57
249018_at	CHP-rich zinc finger protein-like	---	AT5G44770	1.05	0.08	0.43	0.68171741	0.9022	-6.57
245175_at	putative protein disulfide-isomeras	UNE5	AT2G47470	1.06	0.09	0.43	0.68181683	0.9023	-6.57
253560_at	putative protein KIAA0800 protein	DCAF1	AT4G31160	-1.04	-0.05	-0.43	0.6818656	0.9023	-6.57
252581_at	hypothetical protein	---	AT3G45500	-1.04	-0.05	-0.43	0.68192272	0.9023	-6.57
252782_at	putative protein predicted proteins	---	---	-1.03	-0.04	-0.43	0.68193367	0.9023	-6.57
256700_at	pseudouridine synthase, putative s	---	AT3G52260	1.03	0.05	0.43	0.68205304	0.9024	-6.57
251962_at	plasma membrane intrinsic protein	PIP2A	AT3G53420	-1.06	-0.09	-0.43	0.68210014	0.9024	-6.57
262978_at	tubulin beta-1 chain identical to G	TUB1	AT1G75780	-1.24	-0.31	-0.43	0.68233674	0.9024	-6.57
266107_at	hypothetical protein predicted by g	---	AT2G37910	-1.05	-0.08	-0.43	0.68226569	0.9024	-6.57
255410_at	putative rac GTPase activating pro	---	AT4G03100	-1.03	-0.05	-0.43	0.68231365	0.9024	-6.57
254338_s_at	pectate lyase like protein pectate l	---	AT4G22080 /	-1.03	-0.04	-0.43	0.68233366	0.9024	-6.57
257441_at	putative GDSL-motif lipase/hydrola	---	AT2G04020	-1.04	-0.06	-0.43	0.68231244	0.9024	-6.57
248008_at	transcription factor NtWRKY4-like	WRKY2	AT5G56270	1.05	0.07	0.43	0.68243108	0.9024	-6.57
260102_at	unknown protein	---	AT1G35470	1.04	0.06	0.43	0.68241053	0.9024	-6.57
260596_at	unknown protein	TIM50	AT1G55900	-1.06	-0.08	-0.43	0.68248935	0.9025	-6.57
253574_at	putative protein	---	AT4G31030	1.05	0.07	0.43	0.68260561	0.9026	-6.57
259405_at	Expressed protein ; supported by c	---	AT1G17744	1.05	0.07	0.43	0.68271489	0.9027	-6.57
246089_at	ring-box protein - like ring-box pro	RBX1	AT5G20570	1.03	0.04	0.43	0.68274533	0.9027	-6.57

252899_at	putative protein leaf protein, Ipom	---	AT4G39530	-1.04	-0.05	-0.43	0.68297031	0.9027	-6.57
AFFX-LysX-5_	B. subtilis /GEN=lys /DB_XREF=g	---	---	-1.07	-0.09	-0.43	0.68281623	0.9027	-6.57
255350_at	putative transposon protein similar	---	---	-1.03	-0.04	-0.43	0.68296441	0.9027	-6.57
248363_at	nodulin-like protein	---	AT5G52480	-1.03	-0.04	-0.43	0.68295551	0.9027	-6.57
266740_at	hypothetical protein predicted by g	---	AT2G46840	-1.04	-0.05	-0.43	0.68290489	0.9027	-6.57
263023_at	unknown protein	---	AT1G23960	-1.07	-0.10	-0.43	0.68306821	0.9028	-6.57
260331_at	hypothetical protein contains Pfam	---	AT1G80270	1.16	0.21	0.43	0.68311347	0.9028	-6.57
249899_at	putative protein similar to unknown	---	AT5G22620	-1.06	-0.09	-0.43	0.68333171	0.9030	-6.57
256948_at	unknown protein	---	AT3G18930	1.03	0.05	0.43	0.68360285	0.9030	-6.57
252383_at	ABC-type transport protein-like pr	ATH6	AT3G47780	1.10	0.14	0.43	0.68347981	0.9030	-6.57
256222_at	hypothetical protein predicted by g	---	AT1G56210	-1.05	-0.08	-0.43	0.68352979	0.9030	-6.57
257795_at	hypothetical protein predicted by g	---	AT3G15910	-1.04	-0.06	-0.43	0.68361095	0.9030	-6.57
250507_at	putative protein similar to unknown	---	AT5G09940	1.03	0.05	0.43	0.68341876	0.9030	-6.57
254887_at	putative protein various predicted	---	AT4G11770	1.04	0.05	0.43	0.68354988	0.9030	-6.57
247697_at	subtilisin-like protease - like protei	SBT5.4	AT5G59810	1.04	0.06	0.43	0.68348061	0.9030	-6.57
256761_at	hypothetical protein predicted by g	---	AT3G25670	1.04	0.06	0.43	0.68366568	0.9030	-6.57
267498_at	unknown protein	---	AT2G45720	1.05	0.07	0.43	0.68372117	0.9031	-6.57
257015_at	hypothetical protein predicted by g	---	AT3G28680	1.04	0.05	0.43	0.68393265	0.9033	-6.57
262897_at	hypothetical protein predicted by g	CCB4	AT1G59840	-1.09	-0.12	-0.43	0.68399605	0.9033	-6.57
245512_at	hypothetical protein	---	AT4G15770	1.06	0.08	0.42	0.68410631	0.9034	-6.57
248883_at	putative protein strong similarity to	---	AT5G46190	-1.03	-0.05	-0.42	0.68429931	0.9036	-6.57
257918_at	ethylene responsive element bind	---	AT3G23230	-1.32	-0.40	-0.42	0.68433642	0.9036	-6.57
261420_at	fatty acid elongase 3-ketoacyl-Co	KCS3	AT1G07720	1.08	0.11	0.42	0.68445174	0.9037	-6.57
257814_at	acyl-(acyl carrier protein) thioester	AtFaTA	AT3G25110	1.08	0.11	0.42	0.68445631	0.9037	-6.57
264688_at	hypothetical protein similar to LG2	---	AT1G09890	1.05	0.07	0.42	0.68457014	0.9037	-6.57
249459_at	peroxidase ATP24a	---	AT5G39580	1.21	0.27	0.42	0.68460171	0.9037	-6.57
256703_at	MADS-box transcription factor sim	AGL79	AT3G30260	1.03	0.04	0.42	0.68470607	0.9038	-6.57
266339_s_at	hypothetical protein predicted by g	---	AT2G01360	1.04	0.05	0.42	0.6846745	0.9038	-6.57
245619_at	hypothetical protein	---	AT4G13990	-1.05	-0.07	-0.42	0.68479395	0.9038	-6.57
257256_at	hypothetical protein contains Pfam	---	AT3G21970	-1.03	-0.04	-0.42	0.68478145	0.9038	-6.57
248479_at	unknown protein	---	AT5G50910	-1.03	-0.04	-0.42	0.68485428	0.9038	-6.57
247145_at	receptor protein kinase-like protein	---	AT5G65600	-1.20	-0.26	-0.42	0.68490484	0.9038	-6.57
255337_at	putative DNA-binding protein simil	WRKY42	AT4G04450	-1.05	-0.06	-0.42	0.68493373	0.9038	-6.57
246411_at	hypothetical protein contains simila	---	AT1G57770	-1.08	-0.11	-0.42	0.68541063	0.9040	-6.57
250012_x_at	auxin-induced protein-like	---	AT5G18060	1.20	0.26	0.42	0.68516682	0.9040	-6.57

246681_at	chloride channel-like protein chlor	---	AT5G33280	-1.03	-0.04	-0.42	0.68543764	0.9040	-6.57
255508_at	putative zinc finger protein identica	---	AT4G02220	1.04	0.06	0.42	0.6855219	0.9040	-6.57
249679_at	unknown protein	---	AT5G35980	1.03	0.04	0.42	0.68530806	0.9040	-6.57
265915_at	En/Spm-like transposon protein rel	---	---	1.03	0.04	0.42	0.68518448	0.9040	-6.57
267563_at	putative protein kinase contains a	---	AT2G30730	1.03	0.05	0.42	0.68524744	0.9040	-6.57
244991_s_at	NADH dehydrogenase ND2	---	---	1.03	0.05	0.42	0.68551771	0.9040	-6.57
247803_at	similar to unknown protein (gb|AAF	---	AT5G58340	-1.03	-0.04	-0.42	0.68555832	0.9040	-6.57
254760_at	putative protein hypothetical prote	---	AT4G13200	-1.03	-0.04	-0.42	0.68522512	0.9040	-6.57
248325_at	unknown protein	---	AT5G52800	1.03	0.04	0.42	0.68555855	0.9040	-6.57
252345_at	hypothetical protein	---	AT3G48640	1.05	0.07	0.42	0.68508591	0.9040	-6.57
261302_at	hypothetical protein predicted by g	---	AT1G48580	1.04	0.05	0.42	0.68541912	0.9040	-6.57
245976_at	WRKY-like protein WRKY DNA bi	WRKY75	AT5G13080	-1.16	-0.21	-0.42	0.6859746	0.9041	-6.57
251428_at	beta-glucosidase-like protein sever	DIN2	AT3G60140	1.26	0.34	0.42	0.6860757	0.9041	-6.57
251917_at	putative protein	---	AT3G53970	-1.03	-0.04	-0.42	0.6860121	0.9041	-6.57
245980_at	putative protein ;supported by full-	---	AT5G13140	1.26	0.33	0.42	0.68595745	0.9041	-6.57
257879_at	unknown protein	---	AT3G17160	1.06	0.08	0.42	0.68607808	0.9041	-6.57
251407_at	Arm repeat containing protein - lik	---	AT3G60350	-1.04	-0.05	-0.42	0.68597717	0.9041	-6.57
263321_at	ADP-ribosylation factor 1 ;support	ARF1A1C	AT2G47170	1.03	0.05	0.42	0.68579981	0.9041	-6.57
254700_at	hypothetical protein	---	AT4G18000	-1.04	-0.05	-0.42	0.68609122	0.9041	-6.57
248740_at	putative protein contains similarity	---	AT5G48130	-1.05	-0.06	-0.42	0.68572753	0.9041	-6.57
245820_at	allyl alcohol dehydrogenase, putat	---	AT1G26320	1.03	0.05	0.42	0.68582085	0.9041	-6.57
265862_at	putative S-locus glycoprotein	---	AT2G01780	1.04	0.05	0.42	0.68599121	0.9041	-6.57
246781_at	sugar transporter-like protein puta	SFP1	AT5G27350	-1.08	-0.11	-0.42	0.68620201	0.9042	-6.57
255266_at	receptor protein kinase - like prote	---	AT4G05200	1.03	0.05	0.42	0.68624896	0.9042	-6.57
259182_at	hypothetical protein predicted by g	---	AT3G01750	-1.06	-0.09	-0.42	0.68636558	0.9042	-6.57
245799_at	disease resistance protein, putativ	AtRLP6	AT1G45616	1.03	0.05	0.42	0.68635975	0.9042	-6.57
248792_at	ras-related small GTP-binding prot	ATRAB1A	AT5G47200	1.04	0.05	0.42	0.68640633	0.9042	-6.57
253189_at	putative protein	---	AT4G35335	1.05	0.08	0.42	0.68664841	0.9042	-6.57
248994_at	disease resistance protein-like	RPS4	AT5G45250	-1.04	-0.06	-0.42	0.68661381	0.9042	-6.57
254404_at	hypothetical protein	B70	AT4G21340	-1.03	-0.04	-0.42	0.68657625	0.9042	-6.57
255172_x_at	putative transposon protein simila	---	---	-1.05	-0.06	-0.42	0.68657285	0.9042	-6.57
246107_at	putative protein various predicted	---	---	1.03	0.05	0.42	0.68653114	0.9042	-6.57
262458_at	serine/threonine kinase, putative s	---	AT1G11280	1.03	0.05	0.42	0.6864918	0.9042	-6.57
253970_at	putative uracil phosphoribosyl tran	---	AT4G26510	1.04	0.05	0.42	0.68676858	0.9044	-6.57
251313_at	putative protein several hypothetic	---	AT3G61360	-1.04	-0.05	-0.42	0.68682582	0.9044	-6.57

257728_at	hypothetical protein predicted by g	---	AT3G18295	1.04	0.06	0.42	0.68687762	0.9044	-6.57
254298_at	putative protein ;supported by full-	PGR5-LIKE	AT4G22890	-1.05	-0.06	-0.42	0.68697391	0.9044	-6.57
257049_at	hypothetical protein predicted by g	---	AT3G15250	1.05	0.06	0.42	0.68693541	0.9044	-6.57
265303_at	hypothetical protein	---	---	1.03	0.05	0.42	0.68707747	0.9045	-6.57
266715_at	putative RNA-binding protein	---	AT2G46780	-1.04	-0.06	-0.42	0.68719812	0.9046	-6.57
255764_at	unknown protein	HCF173	AT1G16720	1.04	0.06	0.42	0.68752374	0.9046	-6.57
251801_at	cytosolic triosephosphatisomerase	TPI	AT3G55440	1.03	0.04	0.42	0.68729233	0.9046	-6.57
261226_at	expansin S2 precursor, putative si	ATEXPA11	AT1G20190	-1.25	-0.32	-0.42	0.68745674	0.9046	-6.57
258429_at	putative GTP-binding protein simila	TOC120	AT3G16620	1.03	0.05	0.42	0.68742603	0.9046	-6.57
257584_at	hypothetical protein similar to puta	---	---	-1.05	-0.07	-0.42	0.68738381	0.9046	-6.57
264998_at	unknown protein similar to hypothe	---	AT1G67330	-1.13	-0.17	-0.42	0.68738463	0.9046	-6.57
250352_at	beta-adaptin-like protein A ; suppo	---	AT5G11490	-1.03	-0.04	-0.42	0.68721492	0.9046	-6.57
249683_x_at	putative protein similar to unknown	---	---	1.04	0.06	0.42	0.68735254	0.9046	-6.57
250064_at	disease resistance protein - like d	DAR4	AT5G17890	1.05	0.06	0.42	0.68753076	0.9046	-6.57
263604_s_at	putative replication protein A1	---	---	1.02	0.04	0.42	0.68764674	0.9047	-6.57
245215_at	F12A21.4 similar to iEP4 gb|AAD1	ATFXG1	AT1G67830	1.08	0.11	0.42	0.68772617	0.9047	-6.57
260998_at	CAF protein similar to C2H2 zinc fi	---	AT1G26590	-1.03	-0.05	-0.42	0.68774987	0.9047	-6.57
246535_at	putative protein several hypothetic	---	AT5G15900	-1.05	-0.07	-0.42	0.68789466	0.9047	-6.57
256718_at	hypothetical protein predicted by g	---	AT2G34120	-1.03	-0.05	-0.42	0.68785817	0.9047	-6.57
257559_at	hypothetical protein contains Pfam	---	AT3G22050	1.03	0.05	0.42	0.68790199	0.9047	-6.57
245510_at	hypothetical protein	---	AT4G15740	1.06	0.08	0.42	0.6879534	0.9048	-6.57
254864_at	putative reverse transcriptase othe	---	---	-1.03	-0.04	-0.42	0.68813322	0.9049	-6.57
251912_at	protein kinase-like protein wall-ass	---	AT3G53840	-1.04	-0.05	-0.42	0.68832896	0.9052	-6.57
265976_at	putative Athila retroelement ORF1	---	---	-1.03	-0.05	-0.42	0.68839141	0.9052	-6.57
248701_at	ligand-gated ion channel protein-lik	GLR1.3	AT5G48410	1.03	0.05	0.42	0.68964727	0.9052	-6.58
267005_at	unknown protein ; supported by cD	---	AT2G34460	-1.03	-0.05	-0.42	0.68972209	0.9052	-6.58
251017_at	protein phosphatase - like protein	---	AT5G02760	1.22	0.29	0.42	0.68957208	0.9052	-6.58
249264_s_at	disease resistance protein-like	---	AT5G41740 /	-1.06	-0.09	-0.42	0.68941738	0.9052	-6.58
261624_at	nucleotide sugar epimerase, putat	GAE2	AT1G02000	-1.06	-0.09	-0.42	0.68907289	0.9052	-6.57
261365_at	proton pump interactor, putative s	---	AT1G53110	1.09	0.13	0.42	0.68953872	0.9052	-6.58
260107_at	fructokinase, putative similar to fru	---	AT1G66430	-1.14	-0.18	-0.42	0.68968744	0.9052	-6.58
246459_at	receptor protein kinase -like protei	---	AT5G16900	1.03	0.05	0.42	0.68919141	0.9052	-6.58
258391_at	hypothetical protein predicted by g	---	AT3G15420	1.05	0.07	0.42	0.68931568	0.9052	-6.58
252127_at	putative protein ATP binding prote	PLP3a	AT3G50960	-1.05	-0.07	-0.42	0.68897976	0.9052	-6.57
253533_at	putative protein cellulose synthase	ATCSLC5	AT4G31590	1.11	0.15	0.42	0.68849369	0.9052	-6.57

254992_at	putative transcriptional regulator	SPT16	AT4G10710	-1.05	-0.07	-0.42	0.68945104	0.9052	-6.58
259715_at	hypothetical protein predicted by g	---	AT1G60990	-1.04	-0.06	-0.42	0.68976022	0.9052	-6.58
253653_at	hypothetical protein	---	AT4G30050	-1.04	-0.05	-0.42	0.68906307	0.9052	-6.57
253940_at	putative protein other Arabidopsis	---	AT4G26950	1.04	0.06	0.42	0.68899322	0.9052	-6.57
246473_at	putative protein cathepsin L-like cy	---	AT5G17140	1.04	0.05	0.42	0.68965591	0.9052	-6.58
265611_at	unknown protein ;supported by ful	---	AT2G25510	1.06	0.09	0.42	0.68854986	0.9052	-6.57
259269_at	putative pectate lyase similar to pe	---	AT3G01270	-1.04	-0.05	-0.42	0.68911211	0.9052	-6.57
245996_at	putative protein predicted non-LTR	---	---	-1.03	-0.04	-0.42	0.68926536	0.9052	-6.58
257305_at	hypothetical protein predicted by g	---	---	-1.04	-0.06	-0.42	0.68905003	0.9052	-6.57
264771_at	phosphomethylpyrimidine kinase p	TH1	AT1G22940	1.03	0.04	0.42	0.68968301	0.9052	-6.58
250218_at	putative protein contains similarity	CHC1	AT5G14170	1.05	0.06	0.42	0.68886013	0.9052	-6.57
258098_at	hypothetical protein similar to kines	KINESIN-1	AT3G23670	1.05	0.07	0.42	0.68924031	0.9052	-6.58
248355_at	putative protein strong similarity to	ATEXO70A	AT5G52340	-1.03	-0.04	-0.42	0.68930865	0.9052	-6.58
252696_at	hypothetical protein predicted tran	---	---	-1.03	-0.04	-0.42	0.68886732	0.9052	-6.57
253380_at	hypothetical protein hypothetical p	PGSIP3	AT4G33330	1.04	0.05	0.42	0.68883084	0.9052	-6.57
261880_at	unknown protein	HIT1	AT1G50500	1.04	0.05	0.42	0.68924025	0.9052	-6.58
256042_at	hypothetical protein predicted by g	---	AT1G07220	-1.03	-0.04	-0.42	0.68906989	0.9052	-6.57
248033_s_at	putative protein similar to unknown	---	AT5G54330	-1.03	-0.04	-0.42	0.68886842	0.9052	-6.57
247150_at	putative protein similar to unknown	---	AT5G65650	-1.04	-0.06	-0.42	0.68937549	0.9052	-6.58
249358_at	sucrose cleavage protein -like suc	---	AT5G40510	-1.04	-0.05	-0.42	0.68979925	0.9052	-6.58
262841_at	aspartate-semialdehyde dehydrog	---	AT1G14810	-1.05	-0.07	-0.42	0.689356	0.9052	-6.58
260298_at	putative oxidoreductase contains F	---	AT1G80320	-1.03	-0.04	-0.42	0.68857986	0.9052	-6.57
250468_at	transcription factor TEIL/ethylene-	---	AT5G10120	-1.03	-0.04	-0.42	0.6886146	0.9052	-6.57
260149_at	putative oxidoreductase similar to a	---	AT1G52810	-1.08	-0.11	-0.42	0.68869642	0.9052	-6.57
251463_at	hypothetical protein	---	AT3G59800	1.04	0.05	0.42	0.69004291	0.9053	-6.58
261997_at	hypothetical protein similar C-term	---	---	-1.03	-0.04	-0.42	0.69006537	0.9053	-6.58
260091_at	putative serine carboxypeptidase s	scpl5	AT1G73290	-1.03	-0.04	-0.42	0.69004405	0.9053	-6.58
267050_at	putative RNA-binding protein ; sup	---	AT2G41060	1.04	0.05	0.42	0.69001042	0.9053	-6.58
266669_at	putative flavonol 3-O-glucosyltrans	UGT71C1	AT2G29750	-1.04	-0.06	-0.42	0.68992019	0.9053	-6.58
262145_at	unknown protein contains similarity	---	AT1G52730	1.04	0.06	0.42	0.69039957	0.9057	-6.58
260864_at	hypothetical protein predicted by g	---	---	1.04	0.05	0.42	0.6904874	0.9057	-6.58
255388_at	hypothetical protein similar to A. th	---	---	-1.03	-0.04	-0.42	0.69046531	0.9057	-6.58
253112_at	putative ascorbate peroxidase asc	APX5	AT4G35970	-1.05	-0.07	-0.42	0.69064829	0.9058	-6.58
249661_x_at	putative protein similar to unknown	---	---	-1.04	-0.05	-0.42	0.690632	0.9058	-6.58
263439_at	hypothetical protein predicted by g	ATEXO70H	AT2G28650	-1.04	-0.05	-0.42	0.69077734	0.9059	-6.58

244929_at	NADH dehydrogenase subunit 4	---	---	-1.05	-0.08	-0.42	0.69088318	0.9060	-6.58
259142_at	unknown protein similar to ankyrin	---	AT3G10200	1.04	0.05	0.42	0.69089961	0.9060	-6.58
251004_at	putative protein predicted protein,	---	AT5G02720	-1.03	-0.05	-0.42	0.69095588	0.9060	-6.58
266908_at	putative protein kinase contains a	PID	AT2G34650	-1.08	-0.12	-0.42	0.69100036	0.9060	-6.58
249726_at	unknown protein	---	AT5G35480	1.06	0.09	0.41	0.69109145	0.9060	-6.58
248277_at	ABC transporter-like protein	---	AT5G52860	-1.04	-0.06	-0.42	0.69105179	0.9060	-6.58
267057_at	hypothetical protein predicted by g	---	AT2G32500	-1.08	-0.12	-0.41	0.69121615	0.9061	-6.58
256003_at	Ta11 non-LTR retroelement prote	---	AT3G31430	1.04	0.05	0.41	0.69128969	0.9062	-6.58
250228_at	cell cycle switch protein	FZR3	AT5G13840	-1.04	-0.06	-0.41	0.69134398	0.9062	-6.58
267208_at	putative shaggy-like protein kinase	ASKdZeta	AT2G30980	1.03	0.04	0.41	0.69148791	0.9063	-6.58
254196_at	putative protein	---	AT4G24030	-1.04	-0.06	-0.41	0.69150855	0.9063	-6.58
252666_at	putative protein hypothetical protei	---	AT3G44180	-1.04	-0.05	-0.41	0.69147388	0.9063	-6.58
253847_at	putative protein CRP1, Zea mays,	---	AT4G28010	1.03	0.05	0.41	0.69154892	0.9063	-6.58
246516_at	putative protein auxin-independen	---	AT5G15740	1.12	0.16	0.41	0.69169477	0.9063	-6.58
260412_at	putative alpha-amylase similar to a	AMY3	AT1G69830	1.03	0.04	0.41	0.69173547	0.9063	-6.58
266425_at	putative strictosidine synthase	---	AT2G41300	1.04	0.05	0.41	0.69171127	0.9063	-6.58
253994_at	protein phosphatase ABI1 ; suppo	ABI1	AT4G26080	1.03	0.05	0.41	0.69208994	0.9065	-6.58
259033_at	putative pectinacetylesterase simil	---	AT3G09405	-1.20	-0.26	-0.41	0.6924145	0.9065	-6.58
267011_at	unknown protein	---	AT2G39230	1.05	0.06	0.41	0.69223974	0.9065	-6.58
266606_at	putative AP2 domain transcription	CRF5	AT2G46310	1.06	0.09	0.41	0.69200064	0.9065	-6.58
257269_at	unknown protein contains Pfam pr	NPSN13	AT3G17440	1.05	0.07	0.41	0.69205953	0.9065	-6.58
258697_at	putative minichromosome mainten	MCM8	AT3G09660	1.04	0.06	0.41	0.69234508	0.9065	-6.58
247046_at	unknown protein ; supported by cl	---	AT5G66540	-1.04	-0.05	-0.41	0.6923375	0.9065	-6.58
261111_at	homeodomain protein BELL1, put	BLH11	AT1G75430	1.03	0.04	0.41	0.69223644	0.9065	-6.58
257153_at	unknown protein ; supported by cl	---	AT3G27220	-1.05	-0.07	-0.41	0.69208937	0.9065	-6.58
249483_at	Expressed protein ; supported by c	---	AT5G38895	1.04	0.06	0.41	0.6925713	0.9065	-6.58
267487_at	putative non-LTR retroelement rev	---	---	-1.04	-0.05	-0.41	0.69235002	0.9065	-6.58
254532_at	putative protein regulatory protein	NPR4	AT4G19660	1.06	0.08	0.41	0.69246288	0.9065	-6.58
254330_at	predicted protein predicted gene	LBD32	AT4G22700	-1.03	-0.04	-0.41	0.69239011	0.9065	-6.58
265079_at	hypothetical protein contains simila	---	AT1G55460	1.03	0.04	0.41	0.69224146	0.9065	-6.58
255912_at	2,3-oxidosqualene-triterpenoid cy	---	AT1G66960	-1.04	-0.06	-0.41	0.69205829	0.9065	-6.58
265645_at	unknown protein	---	AT2G27370	-1.03	-0.05	-0.41	0.69264489	0.9065	-6.58
263936_at	putative ATP-dependent RNA helic	---	AT2G35920	-1.04	-0.06	-0.41	0.69268558	0.9065	-6.58
252772_at	hypothetical protein	---	---	1.03	0.05	0.41	0.69263753	0.9065	-6.58
253069_at	hexokinase - like protein hexokina	HKL3	AT4G37840	-1.03	-0.05	-0.41	0.69264746	0.9065	-6.58

256537_at	unknown protein	---	AT1G33340	1.09	0.12	0.41	0.69252084	0.9065	-6.58
265649_at	putative ferredoxin ; supported by	ATFD3	AT2G27510	-1.07	-0.09	-0.41	0.69293095	0.9066	-6.58
257532_at	hypothetical protein similar to hypo	---	AT3G04700	-1.13	-0.18	-0.41	0.69279679	0.9066	-6.58
264370_at	hybrid proline-rich protein, putative	---	AT1G12100	-1.03	-0.05	-0.41	0.69285456	0.9066	-6.58
251817_at	small GTP-binding protein - like (f	ARA6	AT3G54840	-1.03	-0.04	-0.41	0.69291398	0.9066	-6.58
256990_at	hypothetical protein predicted by g	---	AT3G28590	-1.05	-0.07	-0.41	0.69290116	0.9066	-6.58
249311_at	disease resistance protein-like	---	AT5G41540	-1.04	-0.05	-0.41	0.69297007	0.9066	-6.58
265639_at	putative reverse transcriptase	---	---	-1.03	-0.05	-0.41	0.69308289	0.9067	-6.58
247415_at	unknown protein	---	AT5G63060	-1.07	-0.09	-0.41	0.69327307	0.9069	-6.58
253453_at	protein phosphatase 2C - like prot	---	AT4G31860	1.03	0.04	0.41	0.69342288	0.9069	-6.58
248996_at	unknown protein	RRS1	AT5G45260	-1.05	-0.08	-0.41	0.69338404	0.9069	-6.58
249300_at	putative protein similar to unknown	---	AT5G41380	-1.03	-0.05	-0.41	0.6933927	0.9069	-6.58
266538_at	hypothetical protein predicted by g	---	AT2G35230	1.03	0.05	0.41	0.69351111	0.9070	-6.58
261695_at	Mg-chelatase, putative similar to M	CHLD	AT1G08520	-1.04	-0.05	-0.41	0.69365137	0.9071	-6.58
255624_at	MAP kinase 4 (MPK4) ;supported	ATMPK4	AT4G01370	1.04	0.06	0.41	0.69365681	0.9071	-6.58
267405_at	putative related to microbial divale	CUTA	AT2G33740	1.03	0.04	0.41	0.69379275	0.9072	-6.58
254555_at	putative protein curved DNA-bindi	---	AT4G19570	1.03	0.05	0.41	0.69381368	0.9072	-6.58
261702_at	unknown protein similar to hypothe	---	AT1G32760	1.03	0.05	0.41	0.69398621	0.9074	-6.58
263595_at	putative purple acid phosphatase c	PAP8	AT2G01890	1.37	0.45	0.41	0.69403058	0.9074	-6.58
258375_at	hypothetical protein predicted by g	---	AT3G17470	-1.03	-0.04	-0.41	0.69431251	0.9076	-6.58
262514_at	NAM(no apical meristem) protein,	anac017	AT1G34190	-1.03	-0.04	-0.41	0.69430849	0.9076	-6.58
249332_at	putative protein similar to unknown	---	AT5G40980	-1.04	-0.06	-0.41	0.69434576	0.9076	-6.58
255845_at	putative cinnamoyl-CoA reductase	---	AT2G33600	1.05	0.08	0.41	0.69432289	0.9076	-6.58
256391_at	hypothetical protein predicted by g	---	AT3G06090	-1.02	-0.04	-0.41	0.69445406	0.9077	-6.58
254949_at	hypothetical protein	---	AT4G11020	1.03	0.05	0.41	0.69463025	0.9078	-6.58
255336_at	putative transposon protein	---	---	-1.03	-0.04	-0.41	0.69470364	0.9079	-6.58
248393_at	putative protein contains similarity	ATBAG1	AT5G52060	-1.06	-0.08	-0.41	0.69570517	0.9079	-6.58
245929_at	alcohol dehydrogenase - like prote	---	AT5G24760	-1.11	-0.14	-0.41	0.69506993	0.9079	-6.58
258193_at	putative pectinesterase similar to p	PME31	AT3G29090	-1.03	-0.04	-0.41	0.69564314	0.9079	-6.58
254546_at	lectin like protein lectin 2, phloem-	PP2-A2	AT4G19850	-1.10	-0.13	-0.41	0.69499968	0.9079	-6.58
251985_at	thioredoxin -like protein cop c2, C	---	AT3G53220	-1.04	-0.06	-0.41	0.69495698	0.9079	-6.58
266950_at	expressed protein supported by ful	---	AT2G18910	-1.05	-0.07	-0.41	0.69567538	0.9079	-6.58
249285_at	unknown protein	---	AT5G41960	1.04	0.06	0.41	0.69551042	0.9079	-6.58
266790_at	expansin AtEx6 identical to GB U3	ATEXPA6	AT2G28950	1.17	0.22	0.41	0.6957509	0.9079	-6.58
266086_at	putative Na+-dependent inorganic	PHT4;2	AT2G38060	-1.03	-0.05	-0.41	0.69511969	0.9079	-6.58

264802_at	putative syntaxin-related protein (U	SYP111	AT1G08560	1.07	0.10	0.41	0.69556976	0.9079	-6.58
266522_at	putative ubiquitin-conjugating enzy	UBC23	AT2G16920	1.04	0.05	0.41	0.6949802	0.9079	-6.58
260151_at	unknown protein ;supported by ful	---	AT1G52910	1.12	0.16	0.41	0.69523721	0.9079	-6.58
265802_at	predicted protein	---	AT2G35733	-1.04	-0.06	-0.41	0.69546208	0.9079	-6.58
246761_at	embryonic abundant protein - like	---	AT5G27980	-1.03	-0.04	-0.41	0.69503039	0.9079	-6.58
250120_at	putative protein similar to unknown	RIC4	AT5G16490	-1.05	-0.07	-0.41	0.69531443	0.9079	-6.58
265046_s_at	mutator-like transposase, putative	---	---	-1.03	-0.05	-0.41	0.69563033	0.9079	-6.58
249543_at	Expressed protein ; supported by f	---	---	1.04	0.05	0.41	0.69571849	0.9079	-6.58
263360_at	unknown protein	---	AT2G03830	-1.03	-0.05	-0.41	0.69550849	0.9079	-6.58
251426_at	URIDYLATE KINASE-like protein	---	AT3G60180	1.04	0.05	0.41	0.69522559	0.9079	-6.58
265833_at	Mutator-like transposase similar to	---	---	-1.03	-0.04	-0.41	0.69538423	0.9079	-6.58
247148_at	auxin-induced protein IAA9 (pir |T0	IAA9	AT5G65670	-1.05	-0.07	-0.41	0.6949115	0.9079	-6.58
258236_at	hypothetical protein predicted by g	---	AT3G27800	-1.03	-0.04	-0.41	0.69521459	0.9079	-6.58
245823_at	hypothetical protein predicted by g	---	AT1G57906	1.04	0.05	0.41	0.69572323	0.9079	-6.58
258130_at	unknown protein	---	AT3G24510	1.03	0.05	0.41	0.69539925	0.9079	-6.58
245835_at	hypothetical protein similar to puta	---	AT1G42190	-1.03	-0.04	-0.41	0.69480281	0.9079	-6.58
264648_at	putative luminal binding protein Sir	BIP3	AT1G09080	-1.04	-0.06	-0.41	0.69532987	0.9079	-6.58
260106_at	unknown protein ;supported by full	---	AT1G35420	-1.03	-0.05	-0.41	0.69588406	0.9080	-6.58
252923_at	kinesin like protein kinesin motor p	---	AT4G39050	-1.05	-0.06	-0.41	0.69603375	0.9081	-6.58
252685_at	disease resistence - like protein R	---	AT3G44410	-1.06	-0.08	-0.41	0.69611938	0.9081	-6.58
246474_at	putative protein predicted protein,	---	AT5G17150	-1.03	-0.05	-0.41	0.69601815	0.9081	-6.58
256032_at	polyprotein, putative similar to poly	---	---	-1.02	-0.03	-0.41	0.69608682	0.9081	-6.58
251159_at	hypothetical protein	---	AT3G63230	1.05	0.06	0.41	0.69616427	0.9081	-6.58
249448_at	cdc2-like protein	cdc2cAt	AT5G39420	-1.04	-0.06	-0.41	0.69615386	0.9081	-6.58
251936_at	putative protein crp1 protein, Zea	MEE40	AT3G53700	1.04	0.06	0.41	0.69632019	0.9081	-6.58
248361_at	putative protein similar to unknown	EDA41	AT5G52460	-1.04	-0.05	-0.41	0.69635083	0.9081	-6.58
266564_at	putative serine carboxypeptidase I	scpl22	AT2G24000	1.04	0.06	0.41	0.69633266	0.9081	-6.58
258867_at	hypothetical protein predicted by g	---	AT3G03130	-1.03	-0.05	-0.41	0.69636453	0.9081	-6.58
261947_at	ubiquitin, putative similar to poly-u	---	AT1G64470	-1.04	-0.06	-0.41	0.69626203	0.9081	-6.58
262134_at	sulfate transporter, putative simila	AST56	AT1G77990	1.07	0.09	0.41	0.69659037	0.9083	-6.58
262292_at	hypothetical protein similar to hypo	---	AT1G27595	1.04	0.05	0.41	0.69665293	0.9083	-6.58
266659_at	putative poly(A) polymerase ; supp	---	AT2G25850	-1.03	-0.05	-0.41	0.69674554	0.9084	-6.58
256633_at	unknown protein	GATL10	AT3G28340	-1.17	-0.23	-0.41	0.69671617	0.9084	-6.58
254997_s_at	putative protein various predicted	---	AT4G09920 /	1.03	0.04	0.41	0.69685336	0.9085	-6.58
254970_at	chlorophyll a/b-binding protein - lik	LHCB5	AT4G10340	-1.03	-0.04	-0.41	0.69698115	0.9085	-6.58

249465_at	AIG2 - like protein AIG2, Arabidop	AIG2L	AT5G39720	1.04	0.05	0.41	0.69698013	0.9085	-6.58
263462_at	similar to Ariadne protein from Dro	ARI11	AT2G31780	-1.03	-0.04	-0.41	0.69695351	0.9085	-6.58
251145_at	putative protein predicted protein,	---	AT3G63500	-1.04	-0.05	-0.41	0.69702257	0.9085	-6.58
249554_at	CRS2 -like protein CRS2, Zea ma	---	AT5G38290	1.08	0.11	0.41	0.69710587	0.9085	-6.58
251699_at	cytochrome P450-like protein cyto	CYP94D2	AT3G56630	1.03	0.05	0.41	0.69742019	0.9085	-6.58
256436_at	hypothetical protein predicted by g	---	AT3G11150	-1.03	-0.05	-0.41	0.69746604	0.9085	-6.58
248497_at	putative protein strong similarity to	ATEXO70F	AT5G50380	1.05	0.07	0.41	0.69750913	0.9085	-6.58
257648_at	RNA helicase, putative similar to F	---	AT3G16840	-1.06	-0.08	-0.41	0.69739345	0.9085	-6.58
251788_at	putative protein	---	AT3G55420	-1.08	-0.11	-0.41	0.69738253	0.9085	-6.58
260521_at	putative villin 2	VLN2	AT2G41740	-1.05	-0.07	-0.41	0.6975023	0.9085	-6.58
263777_at	putative cyclic nucleotide-regulated	ATCNGC12	AT2G46450	-1.14	-0.19	-0.41	0.69730931	0.9085	-6.58
262919_at	unknown protein ; supported by cD	---	AT1G79380	-1.05	-0.06	-0.41	0.69725255	0.9085	-6.58
257228_at	NADPH:quinone oxidoreductase (N	NQR	AT3G27890	1.03	0.04	0.41	0.69719901	0.9085	-6.58
259731_at	unknown protein similar to unknow	---	AT1G77460	1.08	0.11	0.41	0.69747818	0.9085	-6.58
246593_at	putative protein predicted protein,	---	AT5G14790	1.05	0.07	0.41	0.69763808	0.9086	-6.58
255216_s_at	putative peptidase	---	AT4G07670 /	1.06	0.09	0.41	0.69757278	0.9086	-6.58
264652_at	putative sugar transport protein, E	---	AT1G08920	-1.09	-0.12	-0.41	0.69770708	0.9086	-6.58
267056_at	hypothetical protein predicted by g	---	AT2G32470	1.04	0.06	0.41	0.69765083	0.9086	-6.58
260838_at	hypothetical protein predicted by g	---	AT1G43680	1.03	0.04	0.41	0.69773024	0.9086	-6.58
262366_at	disease resistance protein, putativ	---	AT1G72890	-1.09	-0.12	-0.41	0.69780322	0.9086	-6.58
263716_at	26S proteasome regulatory subuni	RPN1A	AT2G20580	1.03	0.04	0.41	0.69783075	0.9086	-6.58
255843_at	unknown protein	CPL3	AT2G33540	-1.03	-0.04	-0.41	0.69789348	0.9086	-6.58
257606_at	root hair defective 3 (RHD3) ident	RHD3	AT3G13870	1.04	0.06	0.41	0.69793718	0.9086	-6.58
260856_at	TINY-like protein similar to TINY G	---	AT1G21910	-1.14	-0.19	-0.40	0.69816119	0.9086	-6.58
250167_at	myb-related protein - like myb-rela	ATMYB16	AT5G15310	-1.05	-0.07	-0.40	0.6989263	0.9086	-6.58
249188_at	N-hydroxycinnamoyl benzoyltransf	---	AT5G42830	1.09	0.12	0.40	0.69933092	0.9086	-6.58
259245_at	unknown protein predicted by gen	---	AT3G07660	1.04	0.05	0.40	0.69870735	0.9086	-6.58
265442_at	hypothetical protein predicted by g	---	AT2G20940	-1.06	-0.09	-0.40	0.69872828	0.9086	-6.58
252105_at	protein phosphatase 2C-like prote	---	AT3G51470	1.04	0.06	0.40	0.69886837	0.9086	-6.58
258911_at	unknown protein similar to hypoth	---	AT3G06470	1.04	0.05	0.40	0.69934904	0.9086	-6.58
252199_at	anthranilate N-hydroxycinnamoyl/I	---	AT3G50270	1.04	0.05	0.40	0.69876348	0.9086	-6.58
256776_at	multispanning membrane protein,	---	AT3G13772	-1.03	-0.04	-0.41	0.69801403	0.9086	-6.58
261446_at	unknown protein	SEC5B	AT1G21170	-1.04	-0.06	-0.40	0.69910269	0.9086	-6.58
245499_at	membrane transporter like protein	INT4	AT4G16480	1.03	0.04	0.40	0.69839335	0.9086	-6.58
246772_at	putative protein unknown protein T	---	AT5G27490	1.06	0.09	0.40	0.69893969	0.9086	-6.58

249702_at	axi 1 (auxin-independent growth pr	---	AT5G35570	-1.08	-0.12	-0.40	0.69911866	0.9086	-6.58
255290_at	coded for by A. thaliana cDNA AA(	ATPC1	AT4G04640	-1.03	-0.04	-0.40	0.698493	0.9086	-6.58
255327_at	putative malonyl-CoA decarboxyla	---	AT4G04320	1.03	0.04	0.40	0.69846734	0.9086	-6.58
259986_at	thaumatin-like protein similar to tha	---	AT1G75050	-1.04	-0.05	-0.40	0.69901275	0.9086	-6.58
260381_at	putative kinesin similar to kinesin-(	---	AT1G73860	1.04	0.05	0.40	0.69888427	0.9086	-6.58
251766_at	putative protein PA26, p53 regulat	---	AT3G55890 /	1.03	0.05	0.40	0.69855638	0.9086	-6.58
245238_at	putative protein similarity to cytoch	ACYB-2	AT4G25570	1.04	0.06	0.40	0.69932539	0.9086	-6.58
246293_at	SigA binding protein ; supported b	SIB1	AT3G56710	-1.15	-0.21	-0.40	0.69937213	0.9086	-6.58
259709_at	Expressed protein ; supported by f	---	AT1G77655	-1.04	-0.05	-0.40	0.69850439	0.9086	-6.58
265023_at	unknown protein weak similarity to	---	AT1G24440	-1.05	-0.06	-0.40	0.69889132	0.9086	-6.58
256373_at	hypothetical protein	SGA2	AT1G66740	-1.04	-0.06	-0.40	0.69936346	0.9086	-6.58
261231_at	unknown protein ; supported by cD	---	AT1G20110	-1.03	-0.04	-0.40	0.69931202	0.9086	-6.58
265752_at	putative Athila retroelement ORF1	---	---	-1.03	-0.04	-0.40	0.6980508	0.9086	-6.58
255234_at	contains similarity to Medicago tru	---	AT4G05500	-1.03	-0.05	-0.40	0.69844926	0.9086	-6.58
253006_at	putative amino acid transport prot	---	AT4G38250	1.04	0.05	0.40	0.69866444	0.9086	-6.58
261520_at	unknown protein ; supported by cD	SEC6	AT1G71820	1.03	0.04	0.40	0.69921054	0.9086	-6.58
245061_at	hypothetical protein ;supported by	RCA	AT2G39730	1.03	0.04	0.40	0.69819245	0.9086	-6.58
266412_at	hypothetical protein predicted by g	MAP65-5	AT2G38720	-1.03	-0.04	-0.40	0.69894817	0.9086	-6.58
252445_at	beta-D-glucan exohydrolase - like	---	AT3G47000	1.03	0.05	0.40	0.69918922	0.9086	-6.58
255391_at	hypothetical protein similar to T6P	---	---	1.03	0.04	0.40	0.69927339	0.9086	-6.58
249853_at	farnesyl cysteine carboxyl methyltr	ATSTE14A	AT5G23320	-1.03	-0.05	-0.40	0.69827651	0.9086	-6.58
246475_at	putative protein IFA-binding protei	---	AT5G16720	1.04	0.06	0.40	0.69813076	0.9086	-6.58
253168_at	putative protein various predicted	---	AT4G35070	-1.07	-0.10	-0.40	0.69825038	0.9086	-6.58
265992_at	putative receptor-like protein kinas	---	AT2G24130	-1.03	-0.04	-0.40	0.69852873	0.9086	-6.58
247016_at	putative protein contains similarity	---	AT5G66970	1.03	0.05	0.40	0.69944548	0.9086	-6.58
263300_at	Mutator-like transposase similar to	---	---	1.03	0.04	0.40	0.69947507	0.9086	-6.58
257254_at	salicylic acid carboxyl methyltrans	---	AT3G21950	-1.03	-0.04	-0.40	0.69950031	0.9086	-6.58
262420_at	hypothetical protein contains simila	TAF15	AT1G50300	-1.03	-0.04	-0.40	0.69956558	0.9087	-6.58
263454_at	putative cysteine proteinase	---	AT2G22160	-1.03	-0.05	-0.40	0.69960829	0.9087	-6.58
261088_at	DNA-binding protein, putative sim	---	AT1G07590	-1.04	-0.06	-0.40	0.69980784	0.9089	-6.58
260110_at	hypothetical protein similar to NBS	---	AT1G63350	1.03	0.04	0.40	0.69986992	0.9089	-6.58
259190_at	unknown protein est hit, predicted	TPLATE	AT3G01780	-1.05	-0.06	-0.40	0.69991895	0.9089	-6.58
264275_at	hypothetical protein predicted by g	anac024	AT1G60350	-1.03	-0.04	-0.40	0.70002841	0.9090	-6.58
264175_at	unknown protein Similar to rice ch	---	AT1G02050	1.04	0.06	0.40	0.70016606	0.9091	-6.58
252565_at	actin depolymerizing factor 2 (ADF	ADF2	AT3G46000	-1.03	-0.04	-0.40	0.70021392	0.9091	-6.58

245240_at	polyprotein, putative similar to poly	---	---	1.04	0.05	0.40	0.70022246	0.9091	-6.58
254347_at	putative protein DNA-binding prote	WRKY31	AT4G22070	-1.04	-0.06	-0.40	0.70020821	0.9091	-6.58
250305_at	putative protein contains similarity	---	AT5G12150	-1.04	-0.06	-0.40	0.70042557	0.9093	-6.58
256453_at	GSH-dependent dehydroascorbat	DHAR2	AT1G75270	-1.07	-0.09	-0.40	0.70050256	0.9093	-6.58
253418_at	putative protein tom-1B protein, G	---	AT4G32760	-1.03	-0.04	-0.40	0.70057666	0.9094	-6.58
262088_at	unknown protein	---	AT1G56020	-1.03	-0.04	-0.40	0.70064452	0.9094	-6.58
267040_at	unknown protein	---	AT2G34300	-1.08	-0.10	-0.40	0.7007462	0.9094	-6.58
266501_at	unknown protein ; supported by cl	HEN2	AT2G06990	1.04	0.05	0.40	0.70092428	0.9094	-6.58
245786_at	G-Box binding protein, putative sir	---	AT1G32150	-1.03	-0.04	-0.40	0.70103187	0.9094	-6.58
258928_at	unknown protein similar to hypothe	TAF12	AT3G10070	-1.04	-0.06	-0.40	0.70080697	0.9094	-6.58
250152_at	putative protein predicted proteins	---	AT5G15120	1.03	0.04	0.40	0.70099263	0.9094	-6.58
267167_at	putative C2H2-type zinc finger prot	ZFP10	AT2G37740	-1.03	-0.05	-0.40	0.70101607	0.9094	-6.58
245978_at	putative protein MORC microrchid	---	AT5G13130	-1.04	-0.05	-0.40	0.7010414	0.9094	-6.58
248164_at	putative protein similar to unknown	PBP1	AT5G54490	-1.20	-0.27	-0.40	0.70084321	0.9094	-6.58
246257_at	splicing factor-like protein	ATU2AF65	AT4G36690	1.03	0.05	0.40	0.70101971	0.9094	-6.58
257569_at	hypothetical protein	---	AT3G26350	-1.05	-0.06	-0.40	0.70110037	0.9095	-6.58
247501_at	putative protein predicted proteins	---	AT5G61920	-1.03	-0.04	-0.40	0.7012317	0.9095	-6.58
256036_at	fructose-2,6-bisphosphatase, puta	F2KP	AT1G07110	1.03	0.05	0.40	0.70118586	0.9095	-6.58
249263_at	putative protein contains similarity	---	AT5G41730	-1.03	-0.04	-0.40	0.70120647	0.9095	-6.58
264565_at	hypothetical protein Similar to hypo	---	AT1G05280	-1.04	-0.06	-0.40	0.70128683	0.9095	-6.58
260664_at	myb-related protein, putative simil	ATRL5	AT1G19510	1.07	0.10	0.40	0.70142202	0.9096	-6.58
255543_at	predicted protein of unknown funct	---	AT4G01870	1.09	0.13	0.40	0.70155411	0.9097	-6.58
263204_at	hypothetical protein contains simila	chr31	AT1G05490	-1.02	-0.03	-0.40	0.70159656	0.9098	-6.58
254529_at	ATP binding protein - like nucleoti	INDL	AT4G19540	1.03	0.04	0.40	0.70177652	0.9099	-6.58
262049_at	unknown protein ;supported by full	---	AT1G80180	1.04	0.05	0.40	0.70191083	0.9099	-6.58
258781_at	hypothetical protein predicted by g	---	AT3G11740	1.03	0.04	0.40	0.70194019	0.9099	-6.58
247326_at	peroxidase ATP3a homolog ;supp	---	AT5G64110	1.15	0.20	0.40	0.70183436	0.9099	-6.58
264345_at	Expressed protein ; supported by c	---	AT1G11915	1.04	0.06	0.40	0.70188379	0.9099	-6.58
263699_at	putative potassium transporter sim	KUP10	AT1G31120	-1.05	-0.07	-0.40	0.7020212	0.9099	-6.58
264249_at	vacuolar-type H+-translocating ino	AVP2	AT1G78920	1.04	0.05	0.40	0.70200626	0.9099	-6.58
257294_at	non-phototropic hypocotyl protein,	---	AT3G15570	1.05	0.07	0.40	0.70207926	0.9099	-6.58
253306_at	dynamin-like protein ADL2	DRP3A	AT4G33650	-1.03	-0.04	-0.40	0.70218591	0.9099	-6.58
258848_at	Expressed protein ; supported by f	DCL2	AT3G03300	1.03	0.04	0.40	0.70212101	0.9099	-6.58
245245_at	delta-aminolevulinic acid dehydrat	hemb2	AT1G44318	-1.03	-0.05	-0.40	0.70217486	0.9099	-6.58
259020_at	unknown protein ; supported by cl	---	AT3G07470	1.04	0.06	0.40	0.70259321	0.9100	-6.58

263924_at	enolase (2-phospho-D-glycerate hy	LOS2	AT2G36530	1.07	0.10	0.40	0.70234498	0.9100	-6.58
262854_at	unknown protein	---	AT1G20870	1.03	0.05	0.40	0.70283383	0.9100	-6.58
265369_s_at	putative retroelement pol polyprote	---	---	1.03	0.04	0.40	0.70271232	0.9100	-6.58
263079_at	putative retroelement pol polyprote	---	---	-1.03	-0.04	-0.40	0.70253515	0.9100	-6.58
259585_at	hypothetical protein contains simila	---	AT1G28090	1.03	0.04	0.40	0.70262094	0.9100	-6.58
263619_at	putative GDP-mannose pyrophosp	---	AT2G04650	-1.03	-0.05	-0.40	0.7023342	0.9100	-6.58
246318_at	putative protein predicted protein l	---	AT3G56740	1.04	0.05	0.40	0.70257287	0.9100	-6.58
259503_at	unknown protein ; supported by cD	---	AT1G15870	1.05	0.07	0.40	0.70271974	0.9100	-6.58
256233_at	ankyrin-like protein contains Pfam	ITN1	AT3G12360	1.03	0.04	0.40	0.70271904	0.9100	-6.58
265981_s_at	putative replication protein A1	---	---	1.04	0.06	0.40	0.70282154	0.9100	-6.58
256084_at	hypothetical protein predicted by g	---	AT1G20750	1.04	0.05	0.40	0.70241192	0.9100	-6.58
260393_at	putative lipase similar to lipase GB	---	AT1G73920	-1.04	-0.06	-0.40	0.7027158	0.9100	-6.58
250781_at	DREB2A (dbj|BAA33794.1) ; supp	DREB2A	AT5G05410	-1.06	-0.09	-0.40	0.70281205	0.9100	-6.58
264794_at	hypothetical protein predicted by g	---	AT1G08670	-1.03	-0.04	-0.40	0.70229204	0.9100	-6.58
254515_at	CLV1 receptor kinase like protein	BAM3	AT4G20270	1.03	0.04	0.40	0.70240845	0.9100	-6.58
266953_at	hypothetical protein predicted by g	---	AT2G34540	1.03	0.05	0.40	0.70295506	0.9101	-6.58
259979_at	unknown protein ;supported by ful	---	AT1G76600	1.07	0.10	0.40	0.70306139	0.9101	-6.58
254594_at	putative protein	---	AT4G18930	-1.05	-0.07	-0.40	0.70308367	0.9101	-6.58
263753_at	putative dehydrin ;supported by fu	LEA	AT2G21490	-1.02	-0.04	-0.40	0.70305119	0.9101	-6.58
252572_at	putative protein Mlo-h1 protein - H	MLO3	AT3G45290	1.06	0.08	0.40	0.70314966	0.9101	-6.58
263470_at	putative unconventional myosin	XIF	AT2G31900	1.03	0.04	0.40	0.70320423	0.9101	-6.58
250792_at	unknown protein ;supported by ful	---	AT5G05520	-1.03	-0.05	-0.40	0.70334349	0.9102	-6.58
245912_at	putative protein sulfate transporter	SULTR3;5	AT5G19600	-1.09	-0.12	-0.40	0.70334259	0.9102	-6.58
247688_at	putative protein predicted proteins	---	AT5G59760	-1.03	-0.04	-0.40	0.7033399	0.9102	-6.58
253508_at	putative protein various predicted	---	AT4G31680	-1.03	-0.05	-0.40	0.70353043	0.9103	-6.58
246856_at	nucleic acid binding protein - like r	AL4	AT5G26210	1.03	0.04	0.40	0.70434616	0.9104	-6.58
264510_at	putative phytochrome-associated p	PIF3	AT1G09530	1.06	0.08	0.40	0.7036708	0.9104	-6.58
247863_at	SKP1 interacting partner 1 (SKIP1	---	AT5G57890 /	-1.03	-0.05	-0.40	0.70385323	0.9104	-6.58
264560_at	hypothetical protein predicted by g	---	AT1G55820	-1.03	-0.04	-0.40	0.70435763	0.9104	-6.58
264674_at	Expressed protein ; supported by f	POLD4	AT1G09815	-1.04	-0.05	-0.40	0.70391985	0.9104	-6.58
253982_at	calcineurin B-like protein 3 ;suppo	ATCBL3	AT4G26570	-1.05	-0.07	-0.40	0.70379633	0.9104	-6.58
244989_s_at	hypothetical protein	---	---	-1.04	-0.06	-0.40	0.70410631	0.9104	-6.58
267517_at	unknown protein	RPT2	AT2G30520	1.04	0.05	0.40	0.70435157	0.9104	-6.58
256428_at	putative disease resistance protein	AtRLP35	AT3G11080	1.06	0.08	0.40	0.70406916	0.9104	-6.58
257039_at	tRNA isopentenyl transferase, put	ATIPT8	AT3G19160	1.04	0.05	0.40	0.70401308	0.9104	-6.58

252963_at	putative protein	---	AT4G38820	1.03	0.04	0.40	0.70419138	0.9104	-6.58
250670_at	polygalacturonase inhibiting protei	PGIP1	AT5G06860	1.10	0.13	0.40	0.70398449	0.9104	-6.58
247906_at	putative protein similar to unknown	IAA33	AT5G57420	1.04	0.06	0.40	0.70432997	0.9104	-6.58
264755_at	receptor kinase, putative similar to	---	AT1G61390	1.03	0.05	0.40	0.70374877	0.9104	-6.58
247227_at	putative protein contains similarity	---	AT5G65130	-1.03	-0.04	-0.40	0.7039202	0.9104	-6.58
261082_at	unknown protein ; supported by cD	---	AT1G07360	1.02	0.04	0.40	0.70421083	0.9104	-6.58
252591_at	putative protein senescence-asso	TET3	AT3G45600	1.06	0.08	0.40	0.70430686	0.9104	-6.58
250557_at	putative protein ankyrin, Rattus no	CPuORF16	AT5G07840 /	1.03	0.04	0.40	0.70432656	0.9104	-6.58
264110_at	unknown protein	---	---	1.02	0.03	0.40	0.70406984	0.9104	-6.58
258887_at	putative phospholipase D similar to	PLDP2	AT3G05630	1.05	0.07	0.40	0.70448463	0.9104	-6.58
246487_at	putative protein with poly glutamic	---	AT5G16030	1.06	0.09	0.40	0.70469899	0.9104	-6.58
254926_at	ACC synthase (AtACS-6) ; suppor	ACS6	AT4G11280	1.18	0.24	0.40	0.70481014	0.9104	-6.59
248289_at	unknown protein ; supported by cl	---	AT5G52880	-1.03	-0.04	-0.40	0.70478897	0.9104	-6.58
261154_at	unknown protein ;supported by full	---	AT1G04970	1.04	0.06	0.40	0.70471584	0.9104	-6.58
262262_at	unknown protein identical to unkno	---	AT1G70780 /	-1.05	-0.08	-0.40	0.70463336	0.9104	-6.58
256258_at	unknown protein	NF-YC11	AT3G12480	-1.03	-0.04	-0.40	0.7047734	0.9104	-6.58
248640_at	selenium-binding protein-like ; sup	---	AT5G48910	1.04	0.05	0.40	0.7047728	0.9104	-6.58
252904_at	putative protein crp1 protein, Zea	EMB2453	AT4G39620	-1.04	-0.05	-0.40	0.70457876	0.9104	-6.58
263417_at	putative C2H2-type zinc finger prot	---	AT2G17180	1.04	0.06	0.40	0.70459295	0.9104	-6.58
245241_at	hypothetical protein contains simila	---	AT1G44478	-1.03	-0.04	-0.40	0.70466272	0.9104	-6.58
258876_at	putative ADP-ribosylation factor sir	ATARFB1C	AT3G03120	-1.03	-0.04	-0.39	0.70531458	0.9106	-6.59
246817_at	putative protein various predicted	---	AT5G27240	1.04	0.05	0.39	0.70518176	0.9106	-6.59
264548_at	unknown protein ; supported by cD	---	AT1G55680	-1.03	-0.05	-0.39	0.70537301	0.9106	-6.59
267455_at	hypothetical protein predicted by g	---	AT2G33760	1.04	0.06	0.39	0.70533588	0.9106	-6.59
260014_at	hydroxypyruvate reductase (HPR)	HPR	AT1G68010	-1.04	-0.05	-0.39	0.70522587	0.9106	-6.59
265294_at	Mutator-like transposase similar to	---	---	1.04	0.05	0.39	0.70516173	0.9106	-6.59
258605_at	phi-1-like protein similar to phi-1 (p	EXL6	AT3G02970	1.04	0.05	0.39	0.7052021	0.9106	-6.59
245497_at	hypothetical protein	---	AT4G16460	-1.04	-0.05	-0.39	0.70519041	0.9106	-6.59
266191_at	putative peroxidase	---	AT2G39040	-1.03	-0.05	-0.39	0.7053085	0.9106	-6.59
252810_at	putative protein several hypothetic	---	---	-1.04	-0.05	-0.39	0.70514014	0.9106	-6.59
264015_at	putative XAP-5 protein [Homo sapi	XCT	AT2G21150	1.03	0.04	0.39	0.70522279	0.9106	-6.59
249675_at	putative protein myrosinase-bindin	---	AT5G35940	-1.02	-0.03	-0.39	0.70529793	0.9106	-6.59
253571_at	putative calmodulin-binding protei	---	AT4G31000	1.11	0.15	0.39	0.70577221	0.9106	-6.59
258368_at	subtilisin-like serine protease conta	---	AT3G14240	-1.07	-0.10	-0.39	0.70584084	0.9106	-6.59
260398_at	putative RNA-binding domain con	APUM23	AT1G72320	-1.05	-0.07	-0.39	0.70598079	0.9106	-6.59

251823_at	putative protein	---	AT3G55080	1.03	0.04	0.39	0.70562952	0.9106	-6.59
259119_at	transport protein SEC13, putative	---	AT3G01340	1.03	0.04	0.39	0.70571791	0.9106	-6.59
264535_at	Phosphatidylinositol Transfer Prot	---	AT1G55690	1.08	0.12	0.39	0.70600895	0.9106	-6.59
247014_at	RuvB DNA helicase-like protein ; s	---	AT5G67630	-1.07	-0.09	-0.39	0.70585052	0.9106	-6.59
256025_at	xylan endohydrolase, putative sim	RXF12	AT1G58370	1.05	0.07	0.39	0.70639137	0.9106	-6.59
248517_at	St12p protein	---	AT5G50550	1.03	0.04	0.39	0.70575328	0.9106	-6.59
251283_at	seven in absentia-like protein SIN	---	AT3G61790	1.03	0.04	0.39	0.70566834	0.9106	-6.59
250205_at	unknown protein	---	AT5G14020	-1.03	-0.04	-0.39	0.70622347	0.9106	-6.59
257718_at	organ separation protein, putative	anac058	AT3G18400	-1.03	-0.05	-0.39	0.705626	0.9106	-6.59
255736_at	unknown protein contains similarity	---	AT1G25380	-1.03	-0.05	-0.39	0.7062284	0.9106	-6.59
258597_x_at	hypothetical protein predicted by g	---	AT3G04390	1.03	0.04	0.39	0.70613704	0.9106	-6.59
256164_at	terpene cyclase, putative similar t	---	AT1G48800	1.03	0.04	0.39	0.70567964	0.9106	-6.59
251868_at	RNA polymerase 24kDa subunit -	RPB5E	AT3G54490	-1.03	-0.05	-0.39	0.70638041	0.9106	-6.59
261836_at	hypothetical protein contains simila	WAKL7	AT1G16090	-1.13	-0.17	-0.39	0.70559298	0.9106	-6.59
251162_at	putative protein hypothetical protei	---	AT3G63300	1.03	0.04	0.39	0.70622092	0.9106	-6.59
252311_at	calcium dependent protein kinase	---	AT3G49370	-1.08	-0.11	-0.39	0.70586077	0.9106	-6.59
254637_at	putative protein KIAA0244 gene, H	---	AT4G18720	-1.03	-0.05	-0.39	0.70609526	0.9106	-6.59
264174_s_at	hypothetical protein	ANAC004	AT1G02230	1.05	0.06	0.39	0.70625239	0.9106	-6.59
257367_at	hypothetical protein predicted by g	---	AT2G25780	-1.03	-0.05	-0.39	0.70641126	0.9106	-6.59
256044_at	protein phosphatase 2C, putative	---	AT1G07160	-1.19	-0.25	-0.39	0.70582399	0.9106	-6.59
254058_at	putative protein cylicin II - human,	---	AT4G25210	-1.04	-0.05	-0.39	0.70640702	0.9106	-6.59
254017_at	putative transcription factor	---	AT4G26170	1.02	0.03	0.39	0.70594824	0.9106	-6.59
250377_at	putative protein predicted proteins	---	AT5G11560	1.04	0.06	0.39	0.7063458	0.9106	-6.59
250153_at	putative protein TMV response-rel	WRKY72	AT5G15130	-1.08	-0.11	-0.39	0.70647192	0.9106	-6.59
267030_at	unknown protein	SCAR2	AT2G38440	-1.03	-0.04	-0.39	0.7065749	0.9106	-6.59
259667_at	unknown protein ; supported by cD	---	AT1G55270	-1.04	-0.05	-0.39	0.70659189	0.9106	-6.59
259950_at	hypothetical protein predicted by g	---	AT1G71410	-1.03	-0.05	-0.39	0.70672885	0.9107	-6.59
247222_at	ABC transporter protein 1-like ; su	ATGCN5	AT5G64840	1.05	0.08	0.39	0.70670544	0.9107	-6.59
251701_at	putative protein hypothetical prote	---	AT3G56650	1.03	0.05	0.39	0.70724074	0.9108	-6.59
258333_at	myosin heavy chain-like protein sir	MFP1	AT3G16000	-1.03	-0.05	-0.39	0.70704697	0.9108	-6.59
260916_at	predicted protein ; supported by cD	---	AT1G02475	1.03	0.05	0.39	0.70688742	0.9108	-6.59
258525_at	hypothetical protein predicted by g	IBR3	AT3G06810	-1.04	-0.06	-0.39	0.70724694	0.9108	-6.59
245700_at	carbonate dehydratase - like prote	ACA3	AT5G04180	-1.03	-0.04	-0.39	0.70731467	0.9108	-6.59
246796_at	putative protein myosin heavy cha	---	AT5G26770	1.04	0.06	0.39	0.70705044	0.9108	-6.59
267228_at	putative polygalacturonase	---	AT2G43890	-1.03	-0.04	-0.39	0.70736566	0.9108	-6.59

262156_at	hypothetical protein contains simila	---	AT1G52680	-1.03	-0.05	-0.39	0.70699102	0.9108	-6.59
266785_at	putative receptor-like protein kinas	---	AT2G28970	1.03	0.05	0.39	0.7070449	0.9108	-6.59
260887_at	ascorbate oxidase promoter-bindi	---	AT1G29160	1.11	0.15	0.39	0.70735203	0.9108	-6.59
249184_at	receptor kinase-like protein	---	AT5G43020	-1.05	-0.07	-0.39	0.70696233	0.9108	-6.59
251589_at	putative protein SINA2p zinc finge	SINAT2	AT3G58040	1.03	0.04	0.39	0.70720776	0.9108	-6.59
249193_at	putative protein similar to unknown	ARC6	AT5G42480	-1.03	-0.04	-0.39	0.70711639	0.9108	-6.59
254025_at	putative pathogenesis-related pro	---	AT4G25790	1.02	0.04	0.39	0.70733876	0.9108	-6.59
264449_at	hypothetical protein predicted by g	NPGR1	AT1G27460	1.06	0.08	0.39	0.70766611	0.9108	-6.59
257075_at	unknown protein contains Pfam pr	---	AT3G19670	1.04	0.06	0.39	0.70745187	0.9108	-6.59
247334_at	cdc2-like protein kinase-like protei	CDKE;1	AT5G63610	-1.02	-0.03	-0.39	0.7076895	0.9108	-6.59
250459_at	unknown protein ; supported by cl	---	AT5G09860	-1.03	-0.05	-0.39	0.70754137	0.9108	-6.59
245513_at	SYBL1 like protein	ATVAMP72	AT4G15780	1.06	0.09	0.39	0.70759369	0.9108	-6.59
267203_at	hypothetical protein predicted by g	---	AT2G31035	1.02	0.03	0.39	0.70767707	0.9108	-6.59
251887_at	FKBP12 interacting protein (FIP37	ATFIP37	AT3G54170	1.05	0.07	0.39	0.70768472	0.9108	-6.59
263992_at	putative retroelement pol polyprote	---	---	1.03	0.04	0.39	0.70769596	0.9108	-6.59
255210_at	may be a pseudogene	---	---	1.03	0.04	0.39	0.70775993	0.9109	-6.59
246370_at	hypothetical protein predicted by g	---	AT1G51920	-1.14	-0.19	-0.39	0.70797533	0.9109	-6.59
251583_at	putative protein several hypothetic	---	AT3G58590	1.05	0.07	0.39	0.70802314	0.9109	-6.59
257735_at	pectate lyase, putative similar to p	---	AT3G27400	-1.06	-0.08	-0.39	0.70804131	0.9109	-6.59
247279_at	arabinogalactan-protein (gb|AAC7	AGP1	AT5G64310	1.13	0.18	0.39	0.70782096	0.9109	-6.59
249539_at	putative protein AtPP - Brassica n	---	AT5G38100	-1.04	-0.05	-0.39	0.70795067	0.9109	-6.59
246981_at	unknown protein	---	AT5G04840	1.04	0.06	0.39	0.70800412	0.9109	-6.59
255164_at	hypothetical protein	---	---	1.03	0.04	0.39	0.70798732	0.9109	-6.59
254160_at	putative protein ;supported by full-	SLY1	AT4G24210	-1.04	-0.06	-0.39	0.70813444	0.9109	-6.59
260196_at	hypothetical protein similar to hypo	---	AT1G67570	1.02	0.04	0.39	0.70829223	0.9111	-6.59
259783_at	auxin-induced protein, putative sir	SAUR68	AT1G29510	1.16	0.21	0.39	0.70864874	0.9111	-6.59
255688_at	putative RNA helicase similar to A	---	AT4G00660	1.03	0.04	0.39	0.7084785	0.9111	-6.59
263788_at	putative sarcosine oxidase	---	AT2G24580	-1.05	-0.07	-0.39	0.70864915	0.9111	-6.59
245900_at	putative protein predicted proteins	---	AT5G11040	1.04	0.05	0.39	0.70863476	0.9111	-6.59
264089_at	actin depolymerizing factor 6 ;sup	ADF6	AT2G31200	-1.04	-0.06	-0.39	0.70867466	0.9111	-6.59
246202_at	methionyl aminopeptidase-like pro	MAP1D	AT4G37040	-1.05	-0.07	-0.39	0.70851193	0.9111	-6.59
244952_at	hypothetical protein	---	---	-1.04	-0.05	-0.39	0.70859009	0.9111	-6.59
256037_at	hypothetical protein predicted by g	---	AT1G19160	-1.04	-0.05	-0.39	0.70860545	0.9111	-6.59
249984_at	putative protein rsc43, Dictyosteliu	---	AT5G18400	-1.06	-0.09	-0.39	0.70860221	0.9111	-6.59
251922_at	protein kinase -like protein protein	---	AT3G54030	1.06	0.09	0.39	0.7095625	0.9111	-6.59

265260_at	NAM (no apical meristem)-like prot	anac042	AT2G43000	1.17	0.23	0.39	0.70912204	0.9111	-6.59
264645_at	unknown protein Similar to Saccha	---	AT1G08940	1.10	0.14	0.39	0.70933412	0.9111	-6.59
267219_at	putative transport protein ;support	---	AT2G02590	-1.04	-0.06	-0.39	0.70939445	0.9111	-6.59
264517_at	hypothetical protein predicted by g	---	AT1G10120	1.04	0.06	0.39	0.70877077	0.9111	-6.59
249828_at	succinyl-CoA synthetase, alpha su	---	AT5G23250	-1.04	-0.06	-0.39	0.70929557	0.9111	-6.59
250533_at	flavonol synthase (FLS) (sp|Q9633	FLS	AT5G08640	-1.03	-0.04	-0.39	0.70960769	0.9111	-6.59
251042_at	eceriferum3 (CER3)	PRT6	AT5G02310	-1.03	-0.04	-0.39	0.70885341	0.9111	-6.59
250568_at	putative protein several putative A	---	AT5G08110	1.03	0.05	0.39	0.70953271	0.9111	-6.59
261397_at	hexose transporter, putative simila	SGB1	AT1G79820	-1.06	-0.08	-0.39	0.70920899	0.9111	-6.59
246586_at	putative protein predicted protein,	---	AT5G14770	-1.04	-0.06	-0.39	0.70894982	0.9111	-6.59
263430_at	unknown protein ;supported by ful	---	AT2G22270	-1.04	-0.05	-0.39	0.70949894	0.9111	-6.59
261575_at	hypothetical protein contains simila	---	AT1G01130	-1.05	-0.07	-0.39	0.70942681	0.9111	-6.59
264860_at	hypothetical protein contains ATP/	---	AT1G24290	1.03	0.04	0.39	0.70929445	0.9111	-6.59
253599_at	putative protein ash1 protein, Dros	SDG4	AT4G30860	-1.05	-0.07	-0.39	0.70896584	0.9111	-6.59
265829_at	unknown protein	---	AT2G14490	-1.03	-0.04	-0.39	0.70958624	0.9111	-6.59
266269_at	putative glutathione S-transferase	ATGSTU2	AT2G29480	-1.09	-0.13	-0.39	0.70896198	0.9111	-6.59
254253_at	serine/threonine kinase - like prote	---	AT4G23320	-1.10	-0.14	-0.39	0.7092628	0.9111	-6.59
254775_at	hypothetical protein	---	AT4G13450	1.02	0.03	0.39	0.70914413	0.9111	-6.59
248979_at	putative protein contains similarity	AtPP2-A6	AT5G45080	-1.03	-0.05	-0.39	0.708828	0.9111	-6.59
263908_at	hypothetical protein predicted by g	---	AT2G36480	-1.03	-0.04	-0.39	0.70919421	0.9111	-6.59
265354_at	actin depolymerizing factor 5 ;sup	ADF5	AT2G16700	1.07	0.10	0.39	0.70898963	0.9111	-6.59
260893_at	hypothetical protein similar to hypo	---	AT1G29180	1.03	0.04	0.39	0.70916112	0.9111	-6.59
249823_s_at	putative protein contains similarity	---	AT5G23350 /	-1.05	-0.07	-0.39	0.7097814	0.9111	-6.59
265149_at	unknown protein ; supported by ful	---	AT1G51400	1.04	0.05	0.39	0.70970594	0.9111	-6.59
254242_at	serine /threonine kinase - like prot	---	AT4G23200	-1.11	-0.15	-0.39	0.70971428	0.9111	-6.59
245153_at	putative protein similarity to predic	---	AT5G12450	1.02	0.03	0.39	0.70978152	0.9111	-6.59
264253_at	putative kinesin similar to GB:AAB	---	AT1G09170	-1.05	-0.07	-0.39	0.70999508	0.9114	-6.59
254244_at	putative protein S-receptor kinase	---	AT4G23230	1.04	0.05	0.39	0.71006355	0.9114	-6.59
251377_at	putative protein	---	AT3G60650	-1.03	-0.04	-0.39	0.71012545	0.9114	-6.59
264115_at	hypothetical protein	---	AT2G31290	1.04	0.05	0.39	0.71031199	0.9116	-6.59
247300_at	unknown protein	FCLY	AT5G63910	1.03	0.05	0.39	0.71044281	0.9117	-6.59
250739_at	putative protein similar to unknown	EGY2	AT5G05740	-1.05	-0.07	-0.39	0.71067082	0.9118	-6.59
261004_at	hypothetical protein similar to puta	---	AT1G26450	-1.05	-0.07	-0.39	0.71062665	0.9118	-6.59
260246_at	hypothetical protein similar to GB:A	---	AT1G74220	-1.03	-0.04	-0.39	0.71070753	0.9118	-6.59
252900_at	shikimate kinase - like protein shik	---	AT4G39540	-1.04	-0.06	-0.39	0.71069483	0.9118	-6.59

265793_at	unknown protein	---	AT2G01220	-1.04	-0.06	-0.39	0.71057094	0.9118	-6.59
249369_at	putative protein Kelch motif contai	---	AT5G40680	1.03	0.04	0.39	0.71063524	0.9118	-6.59
247096_at	S-adenosyl-L-methionine:salicylic a	---	AT5G66430	-1.02	-0.03	-0.39	0.71074998	0.9118	-6.59
261041_at	hypothetical protein contains simila	EER4	AT1G17440	-1.03	-0.04	-0.39	0.71084416	0.9118	-6.59
246566_at	oligopeptide transporter -like prote	---	AT5G14940	1.06	0.08	0.39	0.71101564	0.9119	-6.59
266840_at	hypothetical protein predicted by g	---	AT2G26160	1.02	0.03	0.39	0.71097934	0.9119	-6.59
265625_at	hypothetical protein predicted by g	---	AT2G27240	-1.04	-0.05	-0.39	0.7110278	0.9119	-6.59
249348_at	unknown protein	---	AT5G40860	1.04	0.05	0.39	0.7110733	0.9119	-6.59
256394_at	unknown protein contains non-con	---	AT3G06290	1.03	0.04	0.39	0.711213	0.9120	-6.59
257018_at	unknown protein	---	AT3G19630	1.03	0.05	0.39	0.71120642	0.9120	-6.59
251638_at	40S ribosomal protein S2 homolog	---	AT3G57490	-1.06	-0.09	-0.39	0.71132302	0.9121	-6.59
246712_at	putative protein various predicted	---	---	-1.03	-0.04	-0.39	0.71134089	0.9121	-6.59
259082_at	unknown protein similar to hypothe	---	AT3G04820	1.05	0.07	0.39	0.71144726	0.9121	-6.59
262468_at	alanine--tRNA ligase, putative sim	ALATS	AT1G50200	1.04	0.06	0.39	0.71146334	0.9121	-6.59
259026_at	putative protein kinase similar to h	---	AT3G09240	1.03	0.05	0.39	0.71148772	0.9121	-6.59
254038_at	nitrogen fixation like protein nitrog	NFU3	AT4G25910	-1.03	-0.04	-0.39	0.71179707	0.9122	-6.59
265799_at	unknown protein ; supported by cI	---	AT2G35680	1.03	0.05	0.39	0.71164155	0.9122	-6.59
262548_at	unknown protein contains similarity	AGO2	AT1G31280	-1.04	-0.05	-0.39	0.71169078	0.9122	-6.59
260352_at	Expressed protein ; supported by f	PDCB4	AT1G69295	-1.03	-0.04	-0.39	0.71172886	0.9122	-6.59
245185_at	F12A21.11 similar to T-Complex p	---	AT1G67760	-1.04	-0.06	-0.39	0.71165268	0.9122	-6.59
253556_at	serine/threonine-specific protein k	---	AT4G31100	-1.02	-0.03	-0.39	0.71178051	0.9122	-6.59
267212_at	similar to late embryogenesis abur	---	AT2G44060	-1.03	-0.04	-0.39	0.71188239	0.9122	-6.59
250834_at	putative protein various predicted	DME	AT5G04560	-1.04	-0.06	-0.39	0.71194289	0.9122	-6.59
254699_at	putative protein predicted protein,	---	AT4G17990	-1.03	-0.05	-0.39	0.71193767	0.9122	-6.59
249063_at	NBD-like protein (gb|AAD20643.1)	POP1	AT5G44110	-1.04	-0.06	-0.39	0.71205872	0.9123	-6.59
252913_at	AtRer1A ; supported by full-length	ATRER1A	AT4G39220	-1.03	-0.04	-0.38	0.71224236	0.9124	-6.59
252786_at	putative protein putative DNA-heli	CHR38	AT3G42670	-1.06	-0.09	-0.38	0.7122912	0.9124	-6.59
248997_at	beta-amylase-like	BMY2	AT5G45300	1.05	0.06	0.38	0.71230915	0.9124	-6.59
258422_at	hypothetical protein predicted by g	---	AT3G16710	1.03	0.04	0.38	0.71223398	0.9124	-6.59
248154_at	putative protein strong similarity to	---	AT5G54400	-1.12	-0.17	-0.38	0.71239429	0.9125	-6.59
258752_at	hypothetical protein predicted by g	ATEXO70H	AT3G09520	-1.07	-0.09	-0.38	0.71244962	0.9125	-6.59
248168_at	beta-glucosidase	BGLU41	AT5G54570	-1.03	-0.05	-0.38	0.71248347	0.9125	-6.59
253521_at	multicatalytic endopeptidase comp	PBA1	AT4G31300	1.05	0.07	0.38	0.71254188	0.9125	-6.59
264576_at	unknown protein Similar to Arabido	---	AT1G05360	1.03	0.04	0.38	0.71259805	0.9126	-6.59
248110_at	wax synthase-like protein	---	AT5G55320	1.03	0.04	0.38	0.71272038	0.9126	-6.59

245494_at	salt-inducible protein homolog	---	AT4G16390	-1.03	-0.05	-0.38	0.71269842	0.9126	-6.59
256638_at	RNA-binding protein, putative sim	---	AT3G19090	-1.05	-0.06	-0.38	0.71271727	0.9126	-6.59
254684_at	glycine-rich RNA-binding protein A	GR-RBP2	AT4G13850	-1.05	-0.07	-0.38	0.71279003	0.9126	-6.59
249978_at	putative protein	---	AT5G18850	-1.03	-0.05	-0.38	0.712832	0.9126	-6.59
267315_at	putative CCAAT-binding transcripti	NF-YA4	AT2G34720	1.05	0.07	0.38	0.71307497	0.9128	-6.59
265423_at	unknown protein	---	AT2G20790	1.05	0.07	0.38	0.71318302	0.9128	-6.59
262880_at	hypothetical protein contains simila	---	AT1G64880	1.08	0.11	0.38	0.71320922	0.9128	-6.59
251299_at	putative protein transcription facto	---	AT3G61950	1.03	0.05	0.38	0.71324245	0.9128	-6.59
261631_at	unknown protein contains similarity	---	AT1G49940	-1.03	-0.04	-0.38	0.71325447	0.9128	-6.59
262979_s_at	unknown protein similar to histone	---	AT1G13370	1.03	0.05	0.38	0.71309962	0.9128	-6.59
253591_at	putative protein hypothetical prote	MUS81	AT4G30870	1.05	0.06	0.38	0.71332081	0.9129	-6.59
252701_at	hypothetical protein SPOP protein	ATBPM6	AT3G43700	1.04	0.06	0.38	0.71340441	0.9129	-6.59
263330_at	putative leucine-rich repeat diseas	---	AT2G15320	-1.07	-0.09	-0.38	0.71341362	0.9129	-6.59
247162_at	xyloglucan endo-transglycosylase-	---	AT5G65730	1.09	0.12	0.38	0.71361069	0.9130	-6.59
251685_at	putative protein unknown protein A	---	AT3G56430	-1.07	-0.10	-0.38	0.71360547	0.9130	-6.59
266448_s_at	unknown protein ;supported by ful	---	AT2G43210	1.03	0.04	0.38	0.71355674	0.9130	-6.59
261704_at	hypothetical protein identical to hy	---	AT1G32600	-1.03	-0.04	-0.38	0.71382855	0.9132	-6.59
262507_at	receptor-like protein kinase, putati	---	AT1G11330	1.04	0.05	0.38	0.7139051	0.9133	-6.59
262482_at	SRG1-like protein Strong homolog	SRG1	AT1G17020	-1.11	-0.15	-0.38	0.71409721	0.9134	-6.59
255612_at	hypothetical protein	---	AT4G01240	-1.04	-0.06	-0.38	0.71413069	0.9134	-6.59
260594_at	hypothetical protein predicted by g	---	AT1G55880	-1.02	-0.03	-0.38	0.7143055	0.9136	-6.59
251942_at	ABC transporter - like protein PDR	PDR9	AT3G53480	1.09	0.13	0.38	0.71431782	0.9136	-6.59
253193_at	putative protein SEC7 protein, Sa	---	AT4G35380	-1.04	-0.06	-0.38	0.71436438	0.9136	-6.59
250090_at	glutamate decarboxylase 1 (GAD 1	GAD	AT5G17330	1.15	0.20	0.38	0.71547236	0.9136	-6.59
261019_at	unknown protein ; supported by cD	---	AT1G26470	1.03	0.05	0.38	0.71524038	0.9136	-6.59
249811_at	unknown protein ;supported by ful	---	AT5G23760	-1.03	-0.04	-0.38	0.71545421	0.9136	-6.59
249356_at	putative protein predicted proteins	---	AT5G40520	-1.05	-0.07	-0.38	0.71479784	0.9136	-6.59
258313_at	unknown protein contains RanBP1	---	AT3G15970	-1.03	-0.04	-0.38	0.7159515	0.9136	-6.59
267532_at	unknown protein ;supported by ful	---	AT2G42040	-1.05	-0.08	-0.38	0.71541375	0.9136	-6.59
265123_at	hypothetical protein similar to puta	---	AT1G55440	1.03	0.04	0.38	0.71592733	0.9136	-6.59
247874_at	101 kDa heat shock protein; HSP1	---	AT5G57710	-1.05	-0.07	-0.38	0.71565752	0.9136	-6.59
256077_at	hypothetical protein contains simila	---	AT1G18090	-1.04	-0.05	-0.38	0.71454319	0.9136	-6.59
254273_at	glycoprotein endopeptidase - like	---	AT4G22720	1.05	0.07	0.38	0.71583487	0.9136	-6.59
248337_at	low-temperature-induced protein 7	LTI78	AT5G52310	-1.17	-0.22	-0.38	0.71529384	0.9136	-6.59
256497_at	ORF1, putative similar to ORF1 G	ECS1	AT1G31580	-1.06	-0.09	-0.38	0.71550084	0.9136	-6.59

258454_at	putative 40S ribosomal protein S1(	RPS10	AT3G22300	1.04	0.06	0.38	0.71568805	0.9136	-6.59
261829_at	P-glycoprotein, putative similar to	PGP10	AT1G10680	-1.04	-0.05	-0.38	0.71546083	0.9136	-6.59
262620_at	hypothetical protein predicted by g	---	AT1G06540	1.03	0.04	0.38	0.71578236	0.9136	-6.59
258073_at	putative auxin-resistance protein,	---	AT3G25880	-1.03	-0.04	-0.38	0.71596823	0.9136	-6.59
262797_at	putative sugar transporter protein	TMT1	AT1G20840	1.06	0.08	0.38	0.71449226	0.9136	-6.59
265418_at	AP2 domain transcription factor	---	AT2G20880	1.12	0.16	0.38	0.7146783	0.9136	-6.59
264310_at	hypothetical protein similar to hypo	---	AT1G62030	1.03	0.05	0.38	0.71585036	0.9136	-6.59
254590_at	hypothetical protein	---	AT4G18860	1.03	0.04	0.38	0.7152142	0.9136	-6.59
253229_at	putative protein ;supported by full-	---	AT4G34660	1.02	0.03	0.38	0.71591746	0.9136	-6.59
254768_at	hypothetical protein	---	AT4G13320	-1.03	-0.05	-0.38	0.71513808	0.9136	-6.59
261380_at	hypothetical protein predicted by g	---	AT1G05400	-1.04	-0.06	-0.38	0.71537053	0.9136	-6.59
250864_at	putative protein predicted proteins	---	AT5G03870	-1.03	-0.05	-0.38	0.71554888	0.9136	-6.59
256867_at	hypothetical protein predicted by g	---	AT3G26390	-1.03	-0.04	-0.38	0.71516021	0.9136	-6.59
246208_at	hypothetical protein ; supported by	SFH12	AT4G36490	-1.03	-0.04	-0.38	0.715034	0.9136	-6.59
253299_at	hypothetical protein ;supported by	---	AT4G33800	1.03	0.05	0.38	0.7146868	0.9136	-6.59
259040_at	putative glutathione transferase sir	ATGSTU8	AT3G09270	1.16	0.21	0.38	0.71544446	0.9136	-6.59
263464_at	putative ARI-like RING zinc finger	---	AT2G31760	1.03	0.05	0.38	0.71485624	0.9136	-6.59
266341_at	hypothetical protein predicted by g	---	AT2G01510	-1.03	-0.04	-0.38	0.71553819	0.9136	-6.59
260615_at	mitochondrial NAD-dependent mal	---	AT1G53240	1.06	0.09	0.38	0.71495468	0.9136	-6.59
252720_at	putative protein predicted protein,	---	AT3G43970	1.04	0.05	0.38	0.71499112	0.9136	-6.59
249863_at	putative protein contains similarity	VPS24.1	AT5G22950	1.02	0.03	0.38	0.71544765	0.9136	-6.59
245021_at	PSII component	---	---	1.04	0.06	0.38	0.71571174	0.9136	-6.59
246185_at	5-methyltetrahydropteroyltriglutam	ATMS3	AT5G20980	-1.03	-0.04	-0.38	0.71577964	0.9136	-6.59
266919_at	hypothetical protein predicted by g	AT2G4578(	---	-1.03	-0.04	-0.38	0.71574108	0.9136	-6.59
245041_at	AR781, similar to yeast pheromon	AR781	AT2G26530	-1.16	-0.21	-0.38	0.71503874	0.9136	-6.59
264564_at	hypothetical protein predicted by g	---	AT1G05290	1.02	0.03	0.38	0.71490694	0.9136	-6.59
255395_at	hypothetical protein	---	---	1.03	0.04	0.38	0.71526075	0.9136	-6.59
245192_at	F12A21.9 hypothetical protein	---	AT1G67780	1.03	0.04	0.38	0.716136	0.9137	-6.59
264846_at	senescence-associated protein co	---	AT2G17850	-1.03	-0.04	-0.38	0.71619352	0.9137	-6.59
255984_at	inositol polyphosphate 5-phospha	IP5PI	AT1G34120	-1.03	-0.04	-0.38	0.71625499	0.9137	-6.59
251307_at	putative protein ;supported by full-	---	AT3G61200	-1.04	-0.05	-0.38	0.716266	0.9137	-6.59
254901_at	serine/threonine kinase-like protei	---	AT4G11530	-1.03	-0.04	-0.38	0.71630397	0.9137	-6.59
256137_at	auxin-regulated protein, putative s	---	AT1G48690	1.03	0.04	0.38	0.71631122	0.9137	-6.59
265004_at	polyprotein, putative similar to pol	---	---	1.04	0.05	0.38	0.71608625	0.9137	-6.59
246557_at	putative protein hypothetical prote	---	AT5G15510	-1.03	-0.04	-0.38	0.71633305	0.9137	-6.59

262850_at	signal response protein (GAI) iden	GAI	AT1G14920	1.06	0.09	0.38	0.71691586	0.9138	-6.59
252130_at	putative protein 1 photosystem II c	PSBO2	AT3G50820	-1.03	-0.04	-0.38	0.71701086	0.9138	-6.59
247698_at	putative protein predicted proteins	---	AT5G59830	1.03	0.05	0.38	0.71697497	0.9138	-6.59
253010_at	ovule development protein aintegu	ANT	AT4G37750	1.03	0.05	0.38	0.7166705	0.9138	-6.59
255252_at	contains similarity to Gossypium hi	---	AT4G04990	1.03	0.04	0.38	0.71697686	0.9138	-6.59
252974_at	putative protein ; supported by cD	MTN1	AT4G38800	-1.03	-0.04	-0.38	0.71700473	0.9138	-6.59
255711_at	putative WD repeat membrane pro	---	AT4G00090	1.04	0.05	0.38	0.71668883	0.9138	-6.59
253155_at	putative protein predicted protein,	---	AT4G35720	-1.03	-0.05	-0.38	0.7169295	0.9138	-6.59
254842_at	putative protein other hypothetical	---	AT4G11950	-1.04	-0.05	-0.38	0.71696405	0.9138	-6.59
250636_at	glycine-rich protein atGRP	GRP18	AT5G07520	-1.03	-0.04	-0.38	0.71681996	0.9138	-6.59
253650_at	EST GB:N37377 spans last intron	---	AT4G30020	-1.19	-0.25	-0.38	0.71687692	0.9138	-6.59
254130_at	MADS-box protein AGL24 ; suppo	AGL24	AT4G24540	1.05	0.08	0.38	0.71659638	0.9138	-6.59
256610_at	hypothetical protein predicted by g	---	AT3G30845	1.02	0.04	0.38	0.71661404	0.9138	-6.59
257811_at	nitrate transporter, putative similar	---	AT3G25280	-1.03	-0.04	-0.38	0.7168765	0.9138	-6.59
264709_at	putative DNA-binding protein, Myb	ATCDC5	AT1G09770	-1.05	-0.07	-0.38	0.71730186	0.9140	-6.59
261687_at	hypothetical protein predicted by g	---	AT1G47280	-1.03	-0.04	-0.38	0.7171873	0.9140	-6.59
259242_at	putative actin similar to actin 1 GB	ATARP6	AT3G33520	1.03	0.04	0.38	0.71724229	0.9140	-6.59
254488_at	putative protein receptor-like prote	---	AT4G20790	1.02	0.03	0.38	0.7172905	0.9140	-6.59
258804_at	hypothetical protein similar to hypo	---	AT3G04760	1.04	0.06	0.38	0.71736345	0.9140	-6.59
248567_at	putative protein contains similarity	---	AT5G49750	-1.03	-0.04	-0.38	0.71743925	0.9141	-6.59
263184_at	UDP-glucose:indole-3-acetate bet	UGT75B1	AT1G05560	1.05	0.06	0.38	0.71766426	0.9142	-6.59
253605_at	putative protein probable membra	---	AT4G30990	1.04	0.06	0.38	0.71762855	0.9142	-6.59
252054_at	hypothetical protein ;supported by	OFP18	AT3G52540	-1.03	-0.05	-0.38	0.71766818	0.9142	-6.59
257615_at	unknown protein	---	AT3G26510	-1.05	-0.06	-0.38	0.71762398	0.9142	-6.59
258750_at	putative pectinacetylesterase simil	---	AT3G05910	-1.08	-0.11	-0.38	0.71778812	0.9142	-6.59
264093_at	hypothetical protein predicted by g	---	AT1G79220	-1.03	-0.04	-0.38	0.71780729	0.9142	-6.59
257899_at	P-glycoprotein, putative similar to	---	AT3G28345	1.03	0.04	0.38	0.717799	0.9142	-6.59
249976_at	Serine/arginine rich protein - like S	SCL28	AT5G18810	-1.03	-0.04	-0.38	0.71791643	0.9142	-6.59
260330_at	putative RING zinc finger protein c	---	AT1G80400	1.03	0.04	0.38	0.71792891	0.9142	-6.59
255103_at	putative phosphoglyceride transfe	---	AT4G08690	1.03	0.04	0.38	0.71811245	0.9144	-6.59
259296_at	putative aminopeptidase similar to	---	AT3G05350	-1.04	-0.05	-0.38	0.71811214	0.9144	-6.59
258455_at	unknown protein ;supported by ful	---	AT3G22440	1.05	0.06	0.38	0.7184758	0.9145	-6.59
251506_at	putative protein ; supported by cD	---	AT3G59090	1.02	0.04	0.38	0.71841791	0.9145	-6.59
245278_at	syntaxin ; supported by cDNA: gi_2	SYP23	AT4G17730	-1.04	-0.06	-0.38	0.71825491	0.9145	-6.59
251839_at	putative protein patatin, Solanum t	PLA IIIA	AT3G54950	1.05	0.07	0.38	0.71854295	0.9145	-6.59

255379_at	putative M-type thioredoxin simila	ATHM2	AT4G03520	1.02	0.04	0.38	0.71844883	0.9145	-6.59
256560_s_at	vetispiradiene synthase, putative,	---	AT3G31415	-1.03	-0.04	-0.38	0.71836396	0.9145	-6.59
260326_at	putative MYB family transcription f	AtMYB103	AT1G63910	1.03	0.05	0.38	0.71855353	0.9145	-6.59
260272_at	F-box protein family, AtFBL14 cor	---	AT1G80570	-1.04	-0.06	-0.38	0.71851788	0.9145	-6.59
247714_at	wuschel protein - like wuschel pro	WOX2	AT5G59340	-1.05	-0.07	-0.38	0.71850193	0.9145	-6.59
259825_at	RNA and export factor binding pro	---	AT1G66260	1.04	0.05	0.38	0.71878756	0.9146	-6.59
252853_at	hypothetical protein ; supported by	---	AT4G39710	-1.07	-0.10	-0.38	0.71876248	0.9146	-6.59
250759_at	unknown protein	---	AT5G06020	-1.03	-0.04	-0.38	0.7187518	0.9146	-6.59
248840_at	unknown protein ; supported by cl	---	AT5G46770	-1.04	-0.05	-0.38	0.71870543	0.9146	-6.59
250522_at	cleft lip and palate associated tran	---	AT5G08500	1.03	0.04	0.38	0.71892103	0.9146	-6.59
254771_at	hypothetical protein	MEE56	AT4G13380	-1.03	-0.04	-0.38	0.71891944	0.9146	-6.59
248755_at	putative protein strong similarity to	---	AT5G47690	-1.04	-0.06	-0.38	0.71895218	0.9146	-6.59
246520_at	putative protein RING-H2 finger p	---	AT5G15790	-1.03	-0.04	-0.37	0.71930713	0.9150	-6.59
261718_at	wall-associated kinase, putative s	---	AT1G18390	1.10	0.13	0.37	0.71938193	0.9151	-6.59
251679_at	putative protein strictosidine syntha	---	AT3G57030	-1.06	-0.08	-0.37	0.71975937	0.9153	-6.59
AFFX-Athal-GA	Arabidopsis thaliana /REF=M6411	GAPC1	---	1.06	0.09	0.37	0.71968282	0.9153	-6.59
246179_at	putative protein hypothetical prote	---	AT5G28440	1.04	0.06	0.37	0.71974406	0.9153	-6.59
257053_at	ethylene responsive element bindi	ERF4	AT3G15210	-1.11	-0.15	-0.37	0.71969981	0.9153	-6.59
255196_x_at	see GB:AF058826	---	---	-1.03	-0.04	-0.37	0.71974056	0.9153	-6.59
255516_at	hypothetical protein similar to exte	---	AT4G02270	1.04	0.06	0.37	0.72002968	0.9155	-6.59
262443_at	Expressed protein ; supported by f	---	AT1G47655	1.04	0.06	0.37	0.71998568	0.9155	-6.59
260789_s_at	acyl-CoA oxidase ACX3 identical t	ACX3	AT1G06290	1.03	0.04	0.37	0.72000392	0.9155	-6.59
260587_at	unknown protein ; supported by cD	---	AT1G53210	1.03	0.05	0.37	0.72021174	0.9157	-6.59
259554_at	hypothetical protein	---	---	-1.04	-0.06	-0.37	0.72055938	0.9160	-6.59
256040_at	hypothetical protein similar to puta	---	AT1G07270	1.03	0.04	0.37	0.72054808	0.9160	-6.59
245918_at	putative protein various predicted	---	---	-1.02	-0.04	-0.37	0.72053805	0.9160	-6.59
249567_at	SAMT-like protein S-adenosyl-L-m	---	AT5G38020	1.02	0.03	0.37	0.72069948	0.9161	-6.59
266970_at	hypothetical protein predicted by g	---	AT2G39560	1.03	0.04	0.37	0.72086039	0.9162	-6.59
257137_at	P-glycoprotein, putative similar to	ABCB19	AT3G28860	1.11	0.15	0.37	0.72101426	0.9163	-6.59
262272_at	unknown protein ; supported by cD	---	AT1G42440	-1.02	-0.03	-0.37	0.72122723	0.9163	-6.59
258025_at	putative D-3-phosphoglycerate deh	---	AT3G19480	1.05	0.07	0.37	0.72115933	0.9163	-6.59
254275_at	HSP associated protein like p48, H	AtHip1	AT4G22670	1.04	0.05	0.37	0.72125149	0.9163	-6.59
257763_s_at	disease resistance protein, putativ	AtRLP37	AT3G23110	1.09	0.13	0.37	0.72120746	0.9163	-6.59
258401_at	unknown protein ; supported by cl	---	AT3G15430	1.04	0.05	0.37	0.72118059	0.9163	-6.59
249717_at	unknown protein ;supported by ful	---	AT5G35730	-1.03	-0.04	-0.37	0.72093947	0.9163	-6.59

254507_at	Glu-rich protein mature-parasite-ir	---	AT4G20160	1.03	0.04	0.37	0.72111172	0.9163	-6.59
262103_at	glutathione S-transferase, putative	GSTF5	AT1G02940	-1.05	-0.07	-0.37	0.72114875	0.9163	-6.59
260093_at	putative serine carboxypeptidase	scpl6	AT1G73270	-1.03	-0.04	-0.37	0.72147736	0.9165	-6.60
265771_at	unknown protein ;supported by ful	---	AT2G48030	1.04	0.05	0.37	0.72157033	0.9166	-6.60
252668_at	hypothetical protein	---	AT3G44210	-1.03	-0.04	-0.37	0.7216811	0.9167	-6.60
250327_at	putative serine rich protein predict	---	AT5G12050	1.09	0.12	0.37	0.72185723	0.9167	-6.60
255808_at	putative protein predicted protein,	---	AT4G10280	1.03	0.04	0.37	0.72190845	0.9167	-6.60
245390_at	putative protein ;supported by full-l	---	AT4G17650	1.06	0.08	0.37	0.72183063	0.9167	-6.60
264207_at	unknown protein strong similarity t	---	AT1G22750	-1.04	-0.06	-0.37	0.72189074	0.9167	-6.60
257383_at	hypothetical protein predicted by g	---	AT2G19630	1.03	0.04	0.37	0.72188018	0.9167	-6.60
259964_at	glutathione transferase, putative s	ATGSTU28	AT1G53680	-1.03	-0.04	-0.37	0.7220899	0.9169	-6.60
265078_at	hypothetical protein contains simila	ECT4	AT1G55500	1.06	0.08	0.37	0.72220556	0.9169	-6.60
250095_at	phytoene synthase (gb|AAB65697	---	AT5G17230	1.06	0.08	0.37	0.72220959	0.9169	-6.60
252301_at	putative protein various predicted	EMB2261	---	1.04	0.05	0.37	0.72236252	0.9171	-6.60
263421_at	unknown protein ;supported by ful	EXL5	AT2G17230	-1.07	-0.10	-0.37	0.72244721	0.9171	-6.60
262152_s_at	hypothetical protein predicted by g	---	AT1G52430 /	1.03	0.04	0.37	0.72246838	0.9171	-6.60
253262_at	putative serine threonine protein ki	---	AT4G34440	1.03	0.04	0.37	0.72251034	0.9171	-6.60
245020_at	cytochrome f	---	---	1.03	0.04	0.37	0.72266279	0.9173	-6.60
267318_at	fatty acid hydroxylase (FAH1) iden	FAH1	AT2G34770	1.03	0.05	0.37	0.72278589	0.9173	-6.60
248877_at	putative protein similar to unknown	---	AT5G46140	-1.03	-0.04	-0.37	0.722789	0.9173	-6.60
258231_at	hypothetical protein contains Pfam	RCK	AT3G27730	-1.03	-0.04	-0.37	0.72277048	0.9173	-6.60
254191_at	hypothetical protein ;supported by	---	AT4G23900	-1.04	-0.05	-0.37	0.72283394	0.9173	-6.60
245597_at	salt-inducible protein homolog	---	AT4G14190	1.03	0.04	0.37	0.72295042	0.9173	-6.60
256738_at	geranylgeranyl pyrophosphate syr	---	AT3G29430	-1.03	-0.04	-0.37	0.72297329	0.9173	-6.60
249037_at	putative protein contains similarity	FLA13	AT5G44130	1.11	0.15	0.37	0.72311837	0.9174	-6.60
259934_at	unknown protein	---	AT1G71340	1.05	0.06	0.37	0.72310839	0.9174	-6.60
249179_at	Expressed protein ; supported by f	---	AT5G42955	1.03	0.05	0.37	0.72309535	0.9174	-6.60
252156_at	BCS1 protein-like protein BCS1 p	---	AT3G50940	1.04	0.05	0.37	0.72348545	0.9175	-6.60
252902_at	putative protein various predicted	---	AT4G39560	1.03	0.04	0.37	0.72342805	0.9175	-6.60
247305_at	Expressed protein ; supported by f	---	AT5G63905	1.08	0.12	0.37	0.72332893	0.9175	-6.60
265437_at	hypothetical protein predicted by g	MCM10	AT2G20980	-1.03	-0.04	-0.37	0.72345772	0.9175	-6.60
256768_at	hypothetical protein predicted by g	LDL2	AT3G13682	-1.03	-0.04	-0.37	0.72329298	0.9175	-6.60
263461_at	putative protein kinase contains a	---	AT2G31800	1.04	0.05	0.37	0.72346108	0.9175	-6.60
251715_at	putative protein putative WRKY-ty	---	AT3G56390	-1.03	-0.04	-0.37	0.72342176	0.9175	-6.60
247737_at	putative protein various predicted	---	AT5G59200	-1.02	-0.03	-0.37	0.72356965	0.9175	-6.60

264911_at	auxin-induced protein, putative sir	---	AT1G60690	-1.04	-0.06	-0.37	0.72356762	0.9175	-6.60
255457_at	putative photosystem I reaction ce	PSAD-1	AT4G02770	-1.02	-0.03	-0.37	0.72368828	0.9175	-6.60
248750_at	putative protein similar to unknown	---	AT5G47530	1.05	0.07	0.37	0.72363529	0.9175	-6.60
248278_at	putative protein similar to unknown	---	AT5G52890	1.03	0.05	0.37	0.7237123	0.9175	-6.60
251890_at	SCARECROW1 ; supported by cD	SCR	AT3G54220	1.03	0.04	0.37	0.72385604	0.9176	-6.60
257175_s_at	cyclopropane-fatty-acyl-phospholi	---	AT3G23470	1.03	0.04	0.37	0.72403273	0.9177	-6.60
261251_at	hypothetical protein predicted by g	---	AT1G05920	-1.05	-0.07	-0.37	0.72398302	0.9177	-6.60
250799_at	putative protein strong similarity to	---	AT5G05350	1.03	0.04	0.37	0.7240158	0.9177	-6.60
262469_s_at	hypothetical protein identical to hy	---	AT1G50190	-1.03	-0.04	-0.37	0.7239245	0.9177	-6.60
257204_at	Expressed protein ; supported by f	RALFL24	AT3G23805	1.08	0.11	0.37	0.72439158	0.9177	-6.60
261366_at	unknown protein	---	AT1G53100	-1.08	-0.11	-0.37	0.72439408	0.9177	-6.60
258052_at	putative hydrolase predicted by ge	---	AT3G16190	-1.03	-0.05	-0.37	0.72454924	0.9177	-6.60
249396_at	DegP protease contains similarity t	DegP9	AT5G40200	1.03	0.04	0.37	0.72457046	0.9177	-6.60
256219_at	hypothetical protein predicted by g	---	AT1G56260	1.03	0.04	0.37	0.7245345	0.9177	-6.60
265551_at	putative replication protein A1	---	---	-1.03	-0.04	-0.37	0.72441654	0.9177	-6.60
256028_at	poly(A)-binding protein, putative s	PAB1	AT1G34140	1.04	0.06	0.37	0.7242823	0.9177	-6.60
263241_at	arginine decarboxylase identical to	ADC1	AT2G16500	1.10	0.13	0.37	0.72453777	0.9177	-6.60
252584_at	putative protein several hypothetic	---	AT3G45560	-1.03	-0.04	-0.37	0.7245063	0.9177	-6.60
251698_at	putative protein	---	AT3G56610	1.02	0.03	0.37	0.72419324	0.9177	-6.60
249379_at	putative protein predicted protein,	---	AT5G40460	1.07	0.10	0.37	0.72433875	0.9177	-6.60
263737_at	unknown protein ;supported by full	---	AT1G60010	-1.04	-0.05	-0.37	0.72457381	0.9177	-6.60
256975_at	unknown protein similar to putative	---	AT3G21000	1.04	0.05	0.37	0.7242308	0.9177	-6.60
266359_at	putative phospholipid cytidylyltrans	CCT1	AT2G32260	1.03	0.04	0.37	0.72527793	0.9178	-6.60
251476_at	putative protein hypothetical prote	---	AT3G59670	1.05	0.07	0.37	0.72533154	0.9178	-6.60
265400_at	unknown protein ;supported by ful	---	AT2G10940	1.51	0.60	0.37	0.72513425	0.9178	-6.60
259670_at	protein kinase, putative similar to	---	AT1G52310	1.04	0.05	0.37	0.72523436	0.9178	-6.60
246627_s_at	5-enolpyruvylshikimate-3-phospha	---	AT1G48860	-1.08	-0.11	-0.37	0.72531984	0.9178	-6.60
262202_at	TATC-like protein similar to GB:AA	APG2	AT2G01110	-1.05	-0.06	-0.37	0.72530204	0.9178	-6.60
265635_at	hypothetical protein predicted by g	---	AT2G25360	1.02	0.03	0.37	0.72486105	0.9178	-6.60
258604_at	putative N-acetlytransferase conta	---	AT3G02980	-1.04	-0.05	-0.37	0.72521741	0.9178	-6.60
265501_at	putative glucosyltransferase	UGT73B4	AT2G15490	-1.09	-0.12	-0.37	0.7247873	0.9178	-6.60
256802_at	cytochrome P450, putative similar	CYP705A3	AT3G20950	-1.03	-0.04	-0.37	0.72518797	0.9178	-6.60
246706_at	putative protein predicted proteins	---	---	1.05	0.07	0.37	0.72502341	0.9178	-6.60
260975_at	receptor-like serine/threonine kina	---	AT1G53430	-1.08	-0.11	-0.37	0.72501028	0.9178	-6.60
245452_at	retrotransposon like protein	---	---	-1.03	-0.04	-0.37	0.72483925	0.9178	-6.60

257436_s_at	hypothetical protein predicted by g	---	AT2G24650 /	1.04	0.05	0.37	0.72490876	0.9178	-6.60
251455_at	citrate synthase-like protein citrate	CSY5	AT3G60100	1.02	0.04	0.37	0.72511816	0.9178	-6.60
257898_s_at	hypothetical protein predicted by g	---	---	1.02	0.03	0.37	0.72484512	0.9178	-6.60
259073_at	unknown protein contains zinc fing	---	AT3G02290	-1.06	-0.08	-0.37	0.72544489	0.9179	-6.60
253132_at	NAM / CUC2 -like protein nap gen	NTL9	AT4G35580	-1.04	-0.05	-0.37	0.72567171	0.9181	-6.60
257465_at	hypothetical protein predicted by g	---	AT1G13040	-1.02	-0.03	-0.37	0.72565297	0.9181	-6.60
251208_at	putative protein amino acid selecti	ATOEP16-4	AT3G62880	-1.03	-0.04	-0.37	0.72573582	0.9181	-6.60
256534_at	unknown protein	---	AT1G33270	1.03	0.04	0.37	0.72578839	0.9182	-6.60
260229_at	putative RING zinc finger protein c	---	AT1G74370	1.04	0.05	0.37	0.72605479	0.9183	-6.60
245217_at	retroelement pol polyprotein, puta	---	---	1.04	0.06	0.37	0.72602441	0.9183	-6.60
247838_at	ubiquitin-specific protease 23 (UB	UBP23	AT5G57990	-1.05	-0.07	-0.37	0.72600648	0.9183	-6.60
258309_at	putative transposase related protei	---	---	-1.03	-0.04	-0.37	0.72612185	0.9184	-6.60
247120_at	amino acid transporter protein-like	---	AT5G65990	-1.03	-0.04	-0.37	0.72620936	0.9184	-6.60
249032_at	putative protein contains similarity	---	AT5G44910	-1.13	-0.18	-0.37	0.72630144	0.9185	-6.60
265754_x_at	En/Spm transposon protein (mosa	---	---	1.03	0.04	0.36	0.72638025	0.9185	-6.60
254442_at	putative protein predicted protein	---	AT4G21060	-1.03	-0.04	-0.36	0.72650451	0.9187	-6.60
256354_at	dormancy related protein, putative	---	AT1G54870	1.04	0.05	0.36	0.72668521	0.9188	-6.60
265130_at	unknown protein similar to ESTs g	---	AT1G30890	1.02	0.03	0.36	0.72675953	0.9188	-6.60
251604_at	putative protein 60S RIBOSOMAL	---	AT3G57820	1.03	0.04	0.36	0.72677507	0.9188	-6.60
260996_at	NBS/LRR disease resistance prote	RFL1	AT1G12210	1.04	0.06	0.36	0.72704599	0.9188	-6.60
254559_at	putative protein glycine/proline-ric	---	AT4G19200	1.04	0.06	0.36	0.72703916	0.9188	-6.60
245824_at	hypothetical protein predicted by g	ATPUP17	AT1G57943	1.05	0.06	0.36	0.72718241	0.9188	-6.60
260329_at	putative cyclin similar to cyclin GB	CYCA2;4	AT1G80370	1.03	0.05	0.36	0.72710616	0.9188	-6.60
250947_at	putative protein	---	AT5G03450	-1.04	-0.05	-0.36	0.72714727	0.9188	-6.60
253739_at	putative protein predicted protein. /	---	AT4G28760	-1.04	-0.05	-0.36	0.72684308	0.9188	-6.60
266632_at	putative serpin	---	AT2G35570	-1.03	-0.04	-0.36	0.72696607	0.9188	-6.60
263506_s_at	hypothetical protein	---	---	-1.04	-0.05	-0.36	0.72711939	0.9188	-6.60
245408_at	putative protein	---	AT4G17180	1.04	0.05	0.36	0.72703145	0.9188	-6.60
262243_at	hypothetical protein predicted by g	---	---	1.04	0.05	0.36	0.72707374	0.9188	-6.60
264218_at	unknown protein	---	AT1G60200	1.02	0.03	0.36	0.72765224	0.9191	-6.60
248417_at	unknown protein	---	AT5G51650	-1.02	-0.03	-0.36	0.7276909	0.9191	-6.60
250791_at	nucleic acid binding protein-like ;s	AL1	AT5G05610	-1.03	-0.04	-0.36	0.72757509	0.9191	-6.60
258349_at	Expressed protein ; supported by f	HYH	AT3G17609	-1.07	-0.10	-0.36	0.7276745	0.9191	-6.60
259805_at	disease resistance protein, putativ	AtRLP7	AT1G47890	-1.04	-0.06	-0.36	0.72746422	0.9191	-6.60
249078_at	phytochelatin synthase (gb|AAD41	CAD1	AT5G44070	1.09	0.12	0.36	0.72755816	0.9191	-6.60

245222_at	contains similarity to En/Spm trans	---	---	-1.02	-0.03	-0.36	0.72764109	0.9191	-6.60
254265_s_at	serine threonine kinase - like prote	CRK6	AT4G23140 /	1.11	0.16	0.36	0.72795367	0.9192	-6.60
257922_at	ethylene receptor, putative (ETR2	ETR2	AT3G23150	-1.06	-0.08	-0.36	0.72781268	0.9192	-6.60
262596_at	putative phosphatidic acid phospha	LPP2	AT1G15080	1.03	0.05	0.36	0.72793442	0.9192	-6.60
263281_at	putative glycine-rich RNA-binding p	---	AT2G14160	-1.03	-0.04	-0.36	0.72796614	0.9192	-6.60
258096_at	hypothetical protein similar to puta	---	AT3G23650	1.03	0.04	0.36	0.72780043	0.9192	-6.60
254072_at	putative protein ClpC protease - S	---	AT4G25370	1.03	0.05	0.36	0.72788718	0.9192	-6.60
247405_at	Arac10 ; supported by cDNA: gi_3	ARAC10	AT5G62880	-1.03	-0.04	-0.36	0.72809358	0.9193	-6.60
265899_s_at	SKP1/ASK1 (At3), putative similar	ASK4	AT1G20140 /	-1.03	-0.05	-0.36	0.72812885	0.9193	-6.60
251919_at	putative protein Hsp70 binding pro	---	AT3G53800	1.05	0.07	0.36	0.72815283	0.9193	-6.60
249426_at	putative RNA helicase putative AT	---	AT5G39840	-1.07	-0.10	-0.36	0.72831729	0.9193	-6.60
256917_at	unknown protein contains Pfam pr	---	AT3G18930	1.03	0.04	0.36	0.72829039	0.9193	-6.60
254909_at	putative disease resistance respor	---	AT4G11210	1.03	0.05	0.36	0.72833405	0.9193	-6.60
263373_at	Expressed protein ; supported by f	---	AT2G20515	-1.05	-0.07	-0.36	0.72833015	0.9193	-6.60
266293_at	putative tropinone reductase ;supp	---	AT2G29360	1.03	0.04	0.36	0.7283838	0.9193	-6.60
246527_at	ribosomal protein-like 40S RIBOSO	---	AT5G15750	1.07	0.10	0.36	0.72846606	0.9193	-6.60
250754_at	arginine-tRNA-protein transferase	ATE1	AT5G05700	-1.03	-0.04	-0.36	0.72845398	0.9193	-6.60
245308_at	putative protein ; supported by cDN	---	AT4G17486	1.03	0.04	0.36	0.72864449	0.9193	-6.60
247740_at	receptor-like protein kinase precur	CRCK1	AT5G58940	1.09	0.12	0.36	0.72889777	0.9193	-6.60
246736_at	putative protein hypothetical prote	---	AT5G27560	-1.03	-0.04	-0.36	0.72884216	0.9193	-6.60
247888_at	phytocyanin/early nodulin-like prot	---	AT5G57920	1.03	0.04	0.36	0.72858502	0.9193	-6.60
259751_at	putative transcription factor similar	MYBL2	AT1G71030	1.03	0.04	0.36	0.72872194	0.9193	-6.60
256642_at	hypothetical protein similar to hypo	---	AT3G32280	-1.03	-0.04	-0.36	0.72866954	0.9193	-6.60
249623_at	putative protein Ariadne-2 protein	---	AT5G37560	-1.02	-0.03	-0.36	0.72886376	0.9193	-6.60
261035_at	hypothetical protein contains Pfam	---	---	-1.02	-0.03	-0.36	0.72880764	0.9193	-6.60
259953_at	putative anion exchanger contains	BOR5	AT1G74810	1.04	0.06	0.36	0.728586	0.9193	-6.60
255972_at	hypothetical protein similar to hypo	---	---	1.02	0.03	0.36	0.72875939	0.9193	-6.60
259753_at	putative isoprenylated protein simil	---	AT1G71050	1.04	0.06	0.36	0.72909427	0.9194	-6.60
267568_at	hypothetical protein predicted by g	---	AT2G30780	1.03	0.04	0.36	0.72916206	0.9194	-6.60
259407_at	protein phosphatase 2A regulatory	PP2AA3	AT1G13320	1.02	0.03	0.36	0.72901935	0.9194	-6.60
247559_at	histone deacetylase - like GR AF-	HDA18	AT5G61070	-1.02	-0.04	-0.36	0.7291305	0.9194	-6.60
258759_at	putative bZIP transcription factor c	BZIP28	AT3G10800	-1.03	-0.04	-0.36	0.72913099	0.9194	-6.60
251514_at	pirin-like protein pirin - Lycopersic	---	AT3G59260	-1.03	-0.04	-0.36	0.72910229	0.9194	-6.60
250011_at	putative protein crp1 protein, maiz	---	AT5G18475	-1.03	-0.04	-0.36	0.72972929	0.9197	-6.60
262342_at	unknown protein similar to hypothe	---	AT1G64150	1.05	0.07	0.36	0.72968856	0.9197	-6.60

260300_at	gibberellin 3 beta-hydroxylase ider	GA3OX2	AT1G80340	-1.05	-0.07	-0.36	0.72956198	0.9197	-6.60
253152_at	putative protein predicted proteins	---	AT4G35690	1.03	0.05	0.36	0.72963188	0.9197	-6.60
260495_at	unknown protein similar to T11A07	---	AT2G41810	1.04	0.06	0.36	0.72961608	0.9197	-6.60
265622_at	unknown protein	---	AT2G27280	-1.02	-0.03	-0.36	0.7297038	0.9197	-6.60
248712_at	unknown protein	---	AT5G48280	-1.03	-0.04	-0.36	0.72950544	0.9197	-6.60
262405_at	hypothetical protein contains simila	HDG10	AT1G34650	1.03	0.05	0.36	0.729893	0.9198	-6.60
250302_at	fructosidase - like protein fructosic	AtcwINV6	AT5G11920	1.15	0.21	0.36	0.72989542	0.9198	-6.60
255230_at	ferredoxin--NADP+ reductase - lik	ATRFNR1	AT4G05390	1.11	0.15	0.36	0.73014178	0.9198	-6.60
266017_at	unknown protein ; supported by cI	---	AT2G18690	1.08	0.12	0.36	0.73053844	0.9198	-6.60
245711_at	putative c2h2 zinc finger transcript	ZAT6	AT5G04340	1.11	0.15	0.36	0.73044765	0.9198	-6.60
264597_at	unknown protein	---	AT1G04620	-1.04	-0.06	-0.36	0.73079092	0.9198	-6.60
264751_at	putative superoxide-generating NA	FRO3	AT1G23020	-1.10	-0.14	-0.36	0.73068769	0.9198	-6.60
249720_at	fimbrin ; supported by cDNA: gi_1	FIM2	AT5G35700	-1.03	-0.04	-0.36	0.73085304	0.9198	-6.60
258894_at	putative disease resistance protein	AtRLP32	AT3G05650	-1.07	-0.10	-0.36	0.73033101	0.9198	-6.60
267156_at	hypothetical protein predicted by g	---	AT2G37610	1.03	0.04	0.36	0.73089607	0.9198	-6.60
247092_at	putative protein contains similarity	ATFOLT1	AT5G66380	-1.04	-0.05	-0.36	0.73021917	0.9198	-6.60
245407_at	GTP-binding RAB2A like protein	RABB1C	AT4G17170	1.03	0.04	0.36	0.73050618	0.9198	-6.60
264649_at	hypothetical protein Similar to Vicia	---	AT1G09060	-1.03	-0.05	-0.36	0.72998846	0.9198	-6.60
254440_at	putative protein desiccation-relate	---	AT4G21020	-1.03	-0.04	-0.36	0.73029304	0.9198	-6.60
262048_at	cytochrome c oxidase subunit, put	---	AT1G80230	1.03	0.05	0.36	0.73076953	0.9198	-6.60
254063_at	receptor kinase-like protein recept	---	AT4G25390	1.06	0.09	0.36	0.73046287	0.9198	-6.60
245898_at	ser/thr specific protein kinase-like	---	AT5G11020	-1.04	-0.05	-0.36	0.73085812	0.9198	-6.60
266870_at	putative heterogeneous nuclear rib	---	AT2G44710	-1.04	-0.06	-0.36	0.72999908	0.9198	-6.60
261899_at	cinnamoyl CoA reductase, putativ	CCR2	AT1G80820	-1.18	-0.24	-0.36	0.73024629	0.9198	-6.60
257575_at	hypothetical protein similar to hypo	---	---	-1.03	-0.04	-0.36	0.73080319	0.9198	-6.60
262899_at	ABC transporter, putative similar t	PEN3	AT1G59870	-1.03	-0.04	-0.36	0.73091427	0.9198	-6.60
245200_at	F12A21.2 hypothetical protein; sup	---	AT1G67850	-1.06	-0.08	-0.36	0.73063747	0.9198	-6.60
259115_at	hypothetical protein predicted by g	---	AT3G01360	1.03	0.05	0.36	0.73068178	0.9198	-6.60
252145_at	putative protein several putative pr	---	AT3G51200	1.03	0.04	0.36	0.7302866	0.9198	-6.60
245838_at	disease resistance protein, putativ	---	AT1G58410	1.03	0.04	0.36	0.73080981	0.9198	-6.60
263191_at	polyprotein, putative similar to poly	---	---	1.03	0.05	0.36	0.73095229	0.9198	-6.60
247901_at	ubiquinone/menaquinone biosynth	---	AT5G57300	-1.03	-0.04	-0.36	0.73053901	0.9198	-6.60
258361_at	unknown protein similar to hypothe	---	AT3G14270	1.05	0.07	0.36	0.73020596	0.9198	-6.60
256889_at	PHD-finger protein, putative conta	ING1	AT3G24010	1.02	0.03	0.36	0.73105385	0.9199	-6.60
253907_at	putative protein dihydrokaempferc	---	AT4G27250	-1.04	-0.06	-0.36	0.73106092	0.9199	-6.60

260808_at	polyprotein, putative similar to poly	---	---	-1.02	-0.04	-0.36	0.73114577	0.9199	-6.60
253656_at	putative protein hypothetical prote	emb1353	AT4G30090	1.03	0.04	0.36	0.73111361	0.9199	-6.60
257295_at	serine/threonine protein kinase, pu	GPK1	AT3G17420	-1.05	-0.07	-0.36	0.7312838	0.9200	-6.60
254660_at	receptor serine/threonine kinase-li	---	AT4G18250	1.05	0.07	0.36	0.73150433	0.9201	-6.60
254569_s_at	hypothetical protein	---	---	1.02	0.04	0.36	0.73152061	0.9201	-6.60
255547_at	putative CHP-rich zinc finger prote	---	AT4G01920	1.04	0.06	0.36	0.73152977	0.9201	-6.60
257242_at	9-cis-epoxycarotenoid dioxygenas	NCED6	AT3G24220	1.03	0.04	0.36	0.73151829	0.9201	-6.60
248240_at	CUC2 (dbj|BAA19529.1)	CUC2	AT5G53950	1.03	0.04	0.36	0.73147451	0.9201	-6.60
260022_at	unknown protein	---	AT1G30020	1.03	0.04	0.36	0.73158382	0.9201	-6.60
248441_at	putative protein contains similarity	---	AT5G51270	-1.02	-0.03	-0.36	0.73179584	0.9203	-6.60
255026_at	hypothetical protein	MES12	AT4G09900	-1.06	-0.08	-0.36	0.73192013	0.9203	-6.60
260163_at	putative carnitine/acylcarnitine tran	BAC2	AT1G79900	1.09	0.13	0.36	0.73193329	0.9203	-6.60
249412_at	putative protein predicted proteins	---	AT5G40410	-1.03	-0.05	-0.36	0.73193042	0.9203	-6.60
250052_at	putative protein predicted proteins	---	AT5G17830	1.03	0.05	0.36	0.73228393	0.9207	-6.60
258030_at	hypothetical protein predicted by g	---	AT3G27590	-1.03	-0.05	-0.36	0.73261718	0.9210	-6.60
267016_at	hypothetical protein predicted by g	---	AT2G39160 /	-1.03	-0.04	-0.36	0.73259794	0.9210	-6.60
257912_at	formin-like protein AHF1 identical t	AFH1	AT3G25500	1.07	0.09	0.36	0.73281681	0.9211	-6.60
262055_at	unknown protein ; supported by ful	---	AT1G79970	1.03	0.04	0.36	0.73276179	0.9211	-6.60
265336_at	hypothetical protein predicted by g	APC10	AT2G18290	1.03	0.04	0.36	0.73276759	0.9211	-6.60
266282_at	putative protein kinase contains a p	---	AT2G29220	1.02	0.03	0.36	0.7328277	0.9211	-6.60
264237_at	hypothetical protein predicted by g	---	AT1G54700	-1.02	-0.03	-0.36	0.7329466	0.9212	-6.60
250526_at	pyruvate kinase	---	AT5G08570	-1.03	-0.04	-0.36	0.73300064	0.9212	-6.60
244998_at	RNA polymerase beta' subunit-1	---	---	-1.04	-0.06	-0.36	0.73313731	0.9212	-6.60
246648_at	putative protein predicted proteins	---	---	-1.03	-0.04	-0.36	0.7331457	0.9212	-6.60
260319_at	hypothetical protein predicted by g	---	AT1G63950	-1.03	-0.05	-0.36	0.73311974	0.9212	-6.60
249073_at	vegetative storage protein-like ;su	---	AT5G44020	1.08	0.11	0.36	0.73342658	0.9213	-6.60
247528_at	MIM protein ; supported by cDNA;	MIM	AT5G61460	1.03	0.05	0.36	0.73336991	0.9213	-6.60
249869_at	acetyl-CoA synthetase-like protein	AAE17	AT5G23050	1.04	0.06	0.36	0.73338386	0.9213	-6.60
252360_at	putative protein predicted protein,	---	AT3G48480	-1.04	-0.05	-0.36	0.73328093	0.9213	-6.60
248937_at	putative protein contains similarity	AtRLP55	AT5G45770	-1.04	-0.06	-0.36	0.73344983	0.9213	-6.60
263524_x_at	hypothetical protein predicted by g	---	---	-1.04	-0.05	-0.36	0.73337945	0.9213	-6.60
255401_at	hypothetical protein ;supported by	---	AT4G03600	-1.04	-0.05	-0.36	0.73332527	0.9213	-6.60
250231_at	AP2/EREBP-like transcription factc	LEP	AT5G13910	-1.03	-0.04	-0.35	0.7335992	0.9213	-6.60
252784_at	putative protein predicted proteins	---	---	1.02	0.03	0.35	0.7337191	0.9213	-6.60
265557_at	unknown protein	---	---	-1.03	-0.05	-0.35	0.73373429	0.9213	-6.60

267322_at	putative leucine-rich-repeat protein	---	AT2G19330	1.02	0.04	0.35	0.73362761	0.9213	-6.60
256022_at	amino acid permease I identical to	AAP1	AT1G58360	-1.08	-0.11	-0.35	0.73361771	0.9213	-6.60
259470_at	unknown protein	---	AT1G19110	1.02	0.03	0.35	0.733688	0.9213	-6.60
254435_at	putative protein	MS5	AT4G20900	1.03	0.04	0.35	0.7337317	0.9213	-6.60
255108_at	hypothetical protein	---	AT4G08740	1.04	0.05	0.35	0.7338116	0.9213	-6.60
259730_at	unknown protein similar to hypothe	---	AT1G77660	1.08	0.11	0.35	0.73447777	0.9214	-6.60
255767_at	ribosomal protein L20, putative sir	---	AT1G16740	1.03	0.04	0.35	0.73391368	0.9214	-6.60
246558_at	putative protein IDN3-B - Homo sa	EMB2773	AT5G15540	1.03	0.05	0.35	0.73437241	0.9214	-6.60
245504_at	glutaredoxin	---	AT4G15660	1.05	0.07	0.35	0.73415487	0.9214	-6.60
249055_at	calmodulin-like protein	---	AT5G44460	1.02	0.03	0.35	0.73429828	0.9214	-6.60
248758_at	RNA-binding protein-like ;supporte	---	AT5G47620	1.03	0.05	0.35	0.73445379	0.9214	-6.60
265020_at	putative cytochrome P450 similar	CYP86C1	AT1G24540	-1.02	-0.04	-0.35	0.73455876	0.9214	-6.60
257527_at	hypothetical protein similar to hyp	---	AT3G01880	-1.03	-0.04	-0.35	0.73409119	0.9214	-6.60
260750_at	light repressible receptor protein k	---	AT1G49100	1.03	0.04	0.35	0.73401305	0.9214	-6.60
263307_at	hypothetical protein similar to myo	---	---	-1.03	-0.04	-0.35	0.73429999	0.9214	-6.60
262141_s_at	hypothetical protein predicted by g	---	AT1G52440 /	1.02	0.03	0.35	0.73457741	0.9214	-6.60
245419_at	putative protein	MSH4	AT4G17380	1.02	0.03	0.35	0.73425621	0.9214	-6.60
264610_at	Expressed protein ; supported by f	---	AT1G04645	1.03	0.04	0.35	0.73451929	0.9214	-6.60
259329_at	putative two-component phosphor	AHP4	AT3G16360	1.07	0.10	0.35	0.73413153	0.9214	-6.60
259339_at	putative adenylylsulfate kinase sim	---	AT3G03900	-1.04	-0.05	-0.35	0.73457805	0.9214	-6.60
261830_at	protein kinase, putative similar to	---	AT1G10620	1.03	0.04	0.35	0.73448828	0.9214	-6.60
255450_at	putative protein similar to T5J8.18	---	AT4G02850	1.03	0.04	0.35	0.73438829	0.9214	-6.60
257126_at	E2, ubiquitin-conjugating enzyme,	UBC19	AT3G20060	1.04	0.05	0.35	0.7345153	0.9214	-6.60
250349_at	putative receptor - like kinase rece	---	AT5G12000	-1.03	-0.04	-0.35	0.73467506	0.9214	-6.60
267248_at	hypothetical protein predicted by g	---	AT2G30120	-1.04	-0.05	-0.35	0.73473178	0.9214	-6.60
247480_at	KED - like protein KED, Nicotiana	ATBAG7	AT5G62390	1.04	0.05	0.35	0.73487843	0.9215	-6.60
263727_at	putative cap-binding protein ; supp	ABH1	AT2G13540	1.04	0.05	0.35	0.73492566	0.9215	-6.60
253796_at	hypothetical protein	---	AT4G28460	-1.16	-0.21	-0.35	0.73489523	0.9215	-6.60
252906_at	putative gamma-glutamyltransfera	GGT1	AT4G39640	1.05	0.08	0.35	0.73494743	0.9215	-6.60
265489_at	hypothetical protein predicted by g	---	AT2G15640	-1.04	-0.06	-0.35	0.73486965	0.9215	-6.60
255979_at	hypothetical protein	UPF3	AT1G33980	1.03	0.04	0.35	0.73503377	0.9215	-6.60
262805_at	putative DNA-binding protein simi	ESC	AT1G20900	1.03	0.04	0.35	0.73526868	0.9218	-6.60
264102_at	hypothetical protein predicted by g	ECT8	AT1G79270	-1.04	-0.06	-0.35	0.73549386	0.9220	-6.60
259221_s_at	putative phospholipase similar to	NPC5	AT3G03530 /	1.17	0.23	0.35	0.73550865	0.9220	-6.60
251945_at	dTDP-glucose 4-6-dehydratase -li	UXS1	AT3G53520	-1.03	-0.04	-0.35	0.73579174	0.9220	-6.60

253447_at	hypothetical protein	---	AT4G32630	1.02	0.03	0.35	0.73573691	0.9220	-6.60
246066_at	putative protein predicted proteins	SMG7	AT5G19400	-1.03	-0.04	-0.35	0.73580325	0.9220	-6.60
253271_s_at	SKP1/ASK1 (At11), putative simila	ASK12	AT4G34210	1.04	0.05	0.35	0.73564393	0.9220	-6.60
259890_at	inner mitochondrial membrane pro	ATTIM23-2	AT1G72750	1.05	0.07	0.35	0.73579579	0.9220	-6.60
256558_at	hypothetical protein predicted by g	---	---	-1.03	-0.04	-0.35	0.73569271	0.9220	-6.60
255359_at	putative glucose-6-phosphate/phos	---	AT4G03950	-1.03	-0.04	-0.35	0.73597171	0.9220	-6.60
260066_at	putative lipase/acylhydrolase conta	---	AT1G73610	-1.07	-0.10	-0.35	0.73594781	0.9220	-6.60
261143_at	unknown protein	ATPUP14	AT1G19770	1.05	0.07	0.35	0.73585736	0.9220	-6.60
262268_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.35	0.73596442	0.9220	-6.60
250027_at	putative protein similar to unknown	---	AT5G18250	1.04	0.05	0.35	0.73605492	0.9221	-6.60
253404_at	putative pyrophosphate--fructose-	PFK6	AT4G32840	-1.03	-0.05	-0.35	0.73629581	0.9221	-6.60
260308_at	putative ABC transporter contains	ATTAP1	AT1G70610	-1.06	-0.08	-0.35	0.73630231	0.9221	-6.60
259674_at	thaumatin-like protein similar to tha	---	AT1G77700	-1.03	-0.05	-0.35	0.73621982	0.9221	-6.60
256123_at	hypothetical protein predicted by g	GC2	AT1G18190	-1.02	-0.03	-0.35	0.73631143	0.9221	-6.60
259856_at	unknown protein ;supported by ful	---	AT1G68440	-1.07	-0.10	-0.35	0.73616103	0.9221	-6.60
254596_at	putative protein proline-rich protei	---	AT4G18975	-1.03	-0.04	-0.35	0.73611588	0.9221	-6.60
249176_at	thioredoxin (clone GIF1) (pir||S581	ATTRX3	AT5G42980	1.02	0.03	0.35	0.7366109	0.9223	-6.60
245951_at	aspartate aminotransferase Asp2	ASP2	AT5G19550	1.05	0.07	0.35	0.73672434	0.9223	-6.60
261837_s_at	transcriptional regulator, putative s	---	AT1G15910	-1.04	-0.05	-0.35	0.73671475	0.9223	-6.60
262334_at	hypothetical protein similar to puta	---	AT1G64010	-1.03	-0.04	-0.35	0.73655708	0.9223	-6.60
266537_at	Expressed protein ; supported by f	---	AT2G16860	-1.03	-0.04	-0.35	0.7366486	0.9223	-6.60
254379_at	putative protein calmodulin-bindin	---	AT4G21820	1.02	0.03	0.35	0.73656803	0.9223	-6.60
261243_at	hypothetical protein predicted by g	---	AT1G20180	1.08	0.11	0.35	0.73658782	0.9223	-6.60
260167_at	hypothetical protein predicted by g	---	AT1G71970	-1.03	-0.05	-0.35	0.73685973	0.9223	-6.60
259409_at	hypothetical protein contains simila	---	AT1G13330	1.03	0.04	0.35	0.73679019	0.9223	-6.60
260703_at	syntaxin, putative similar to syntax	ATSYP24	AT1G32270	-1.02	-0.03	-0.35	0.73686227	0.9223	-6.60
247671_at	putative protein slow myosin heav	---	AT5G60210	-1.02	-0.03	-0.35	0.73695509	0.9223	-6.60
252771_at	receptor protein kinase -like protei	---	AT3G42880	1.03	0.04	0.35	0.73695155	0.9223	-6.60
257463_at	phosphatidylinositol/phosphatidylc	---	AT1G14820	-1.04	-0.05	-0.35	0.73704344	0.9223	-6.60
253929_s_at	putative protein H+-transporting A	---	AT2G16030	1.03	0.04	0.35	0.73699958	0.9223	-6.60
254802_at	endoxyloglucan transferase-like p	---	AT4G13090	1.04	0.05	0.35	0.73707797	0.9223	-6.60
254902_at	putative protein several hypothetic	---	AT4G11550	-1.03	-0.04	-0.35	0.73712017	0.9223	-6.60
247328_at	unknown protein ;supported by ful	---	AT5G64130	-1.04	-0.06	-0.35	0.73745554	0.9225	-6.60
261261_at	putative aldehyde oxidase	---	AT1G26730	-1.11	-0.15	-0.35	0.73733564	0.9225	-6.60
255092_s_at	putative protein various predicted p	---	---	-1.03	-0.04	-0.35	0.73744784	0.9225	-6.60

261061_at	DNA-binding protein, putative con	TRFL2	AT1G07540	1.03	0.04	0.35	0.73732589	0.9225	-6.60
252535_at	hypothetical protein	---	AT3G46150	-1.05	-0.07	-0.35	0.73745424	0.9225	-6.60
255446_at	hypothetical protein similar to A. th	---	AT4G02750	1.03	0.04	0.35	0.73763033	0.9225	-6.60
247380_at	4-coumarate-CoA ligase-like prote	---	AT5G63380	1.04	0.05	0.35	0.73781758	0.9225	-6.60
256420_at	unknown protein	---	AT1G33475 /	1.04	0.05	0.35	0.73768765	0.9225	-6.60
251235_at	putative protein lysophospholipase	---	AT3G62860	1.05	0.07	0.35	0.73763226	0.9225	-6.60
259988_at	Athila ORF 1, putative simlar to G	---	---	-1.02	-0.03	-0.35	0.73782883	0.9225	-6.60
267424_at	hypothetical protein predicted by g	---	AT2G34800	-1.02	-0.03	-0.35	0.73780411	0.9225	-6.60
267512_at	hypothetical protein predicted by g	SSE1	AT2G45690	1.03	0.04	0.35	0.73763244	0.9225	-6.60
248156_at	unknown protein	---	AT5G54410	-1.02	-0.03	-0.35	0.73776698	0.9225	-6.60
247320_at	photosystem I reaction centre subu	PSAN	AT5G64040	1.03	0.04	0.35	0.7379112	0.9226	-6.60
248853_at	protein kinase-like protein	BSK2	AT5G46570	1.04	0.05	0.35	0.73796534	0.9226	-6.60
251238_at	putative protein several hypothetic	---	AT3G62430	1.03	0.05	0.35	0.73816417	0.9228	-6.60
262666_at	xyloglucan fucosyltransferase, put	FUT6	AT1G14080	-1.06	-0.08	-0.35	0.73816597	0.9228	-6.60
249278_at	putative protein strong similarity to	---	AT5G41900	1.20	0.27	0.35	0.73834605	0.9228	-6.60
267275_at	putative Na H antiporter	ATCHX13	AT2G30240	-1.04	-0.05	-0.35	0.73848395	0.9228	-6.60
262461_at	myosin, putative similar to myosin	VIIIA	AT1G50360	1.05	0.07	0.35	0.7384402	0.9228	-6.60
255464_s_at	putative protein similar to T4I9.17	AT7SL-1	AT4G02970 /	1.02	0.04	0.35	0.73855274	0.9228	-6.60
246970_at	cytochrome P450-like protein fatty	CYP714A2	AT5G24900	1.05	0.07	0.35	0.73852633	0.9228	-6.60
251829_at	putative protein KIAA0882 protein	---	AT3G55020	1.06	0.09	0.35	0.73834204	0.9228	-6.60
253179_at	putative protein various predicted	---	AT4G35200	1.02	0.03	0.35	0.7383831	0.9228	-6.60
263747_at	putative ubiquitin activating enzym	SAE2	AT2G21470	-1.02	-0.03	-0.35	0.7385296	0.9228	-6.60
246631_at	unknown protein ; supported by ful	---	AT1G50740	1.03	0.04	0.35	0.73861254	0.9229	-6.60
248748_at	putative protein contains similarity	AMK2	AT5G47840	1.03	0.04	0.35	0.73865424	0.9229	-6.60
253926_at	hnRNP-like protein ; supported by	---	AT4G26650	-1.03	-0.04	-0.35	0.73878181	0.9229	-6.60
248437_at	putative protein similar to unknown	EMF2	AT5G51230	-1.04	-0.05	-0.35	0.73872836	0.9229	-6.60
248783_at	putative protein contains similarity	---	AT5G47360	1.05	0.07	0.35	0.73879709	0.9229	-6.60
259664_at	unknown protein ; supported by ful	AGP21	AT1G55330	-1.19	-0.24	-0.35	0.73890063	0.9229	-6.60
247422_at	putative protein	PEX14	AT5G62810	-1.03	-0.04	-0.35	0.73888536	0.9229	-6.60
248182_at	putative protein contains similarity	---	AT5G54030	-1.02	-0.03	-0.35	0.73902038	0.9230	-6.60
260018_at	hypothetical protein predicted by g	---	AT1G41820	1.03	0.04	0.35	0.73898267	0.9230	-6.60
251700_at	putative protein exocyst complex p	---	AT3G56640	1.05	0.07	0.35	0.73907419	0.9230	-6.60
249052_at	antifungal protein-like (PDF1.2)	PDF1.2	AT5G44420	1.13	0.17	0.35	0.73940589	0.9231	-6.61
248028_at	putative protein similar to unknown	---	AT5G55620	1.07	0.10	0.35	0.73937651	0.9231	-6.60
253913_at	myosin heavy chain - like protein r	VIIIB	AT4G27370	1.03	0.04	0.35	0.73933096	0.9231	-6.60

253641_at	hypothetical protein ;supported by	---	AT4G29980	-1.03	-0.05	-0.35	0.73945248	0.9231	-6.61
251232_at	shock protein SRC2-like shock pr	---	AT3G62780	1.09	0.13	0.35	0.73930617	0.9231	-6.60
251891_at	aintegumaenta-like protein ovule	WRI1	AT3G54320	-1.02	-0.03	-0.35	0.73944248	0.9231	-6.61
263316_s_at	putative ligand-gated ion channel	ATGLR2.3	AT2G24710	1.03	0.04	0.35	0.73935504	0.9231	-6.60
245863_s_at	hypothetical protein contains simila	---	AT1G58050	1.03	0.05	0.35	0.73956058	0.9231	-6.61
245371_at	hypothetical protein ;supported by	---	AT4G15750	1.03	0.05	0.35	0.73952204	0.9231	-6.61
251317_at	putative protein polygalacturonase	---	AT3G61490	1.04	0.06	0.35	0.73975324	0.9233	-6.61
266693_at	unknown protein predicted by gens	MIOX2	AT2G19800	-1.16	-0.21	-0.35	0.73988892	0.9234	-6.61
250512_at	Expressed protein ; supported by f	---	AT5G09995	-1.03	-0.05	-0.35	0.73997306	0.9234	-6.61
266221_at	putative nucleotide-sugar dehydrat	UXS6	AT2G28760	1.13	0.18	0.35	0.74001192	0.9234	-6.61
264346_at	putative amino-cyclopropane-carbo	---	AT1G12010	-1.03	-0.04	-0.35	0.73994193	0.9234	-6.61
252813_at	putative protein several hypothetic	---	---	1.03	0.04	0.35	0.74017115	0.9236	-6.61
264029_at	unknown protein	MRH6	AT2G03720	-1.03	-0.04	-0.35	0.74018275	0.9236	-6.61
246052_at	putative protein predicted proteins	---	AT5G08310	1.04	0.05	0.35	0.7404554	0.9237	-6.61
252960_at	hypothetical protein	---	AT4G38750	1.05	0.07	0.35	0.74045869	0.9237	-6.61
250242_at	putative protein similar to unknown	---	AT5G13620	1.03	0.04	0.35	0.74048155	0.9237	-6.61
249323_at	unknown protein	FLA20	AT5G40940	1.03	0.04	0.35	0.74047562	0.9237	-6.61
249194_at	kinesin heavy chain-like protein	---	AT5G42490	1.02	0.03	0.35	0.74039396	0.9237	-6.61
262211_at	AP2 domain containing protein, pu	ORA47	AT1G74930	-1.11	-0.15	-0.35	0.74059216	0.9237	-6.61
257946_at	hypothetical protein predicted by g	---	AT3G21710	1.03	0.04	0.35	0.74057487	0.9237	-6.61
264796_at	unknown protein similar to ESTs g	ZIGA4	AT1G08680	-1.03	-0.04	-0.35	0.74061018	0.9237	-6.61
266662_at	hypothetical protein predicted by g	---	AT2G25830	1.04	0.05	0.34	0.74118044	0.9238	-6.61
247830_at	putative protein predicted proteins	---	AT5G58530	-1.04	-0.06	-0.34	0.74094007	0.9238	-6.61
260025_at	unknown protein ;supported by full	---	AT1G30070	-1.05	-0.06	-0.34	0.74089141	0.9238	-6.61
259517_at	hypothetical protein ; supported by	CAT1	AT1G20630	1.04	0.06	0.34	0.7412135	0.9238	-6.61
248509_at	Expressed protein ; supported by f	---	AT5G50335	-1.30	-0.38	-0.34	0.74120491	0.9238	-6.61
266755_at	putative alcohol dehydrogenase	---	AT2G47150	1.03	0.04	0.34	0.740972	0.9238	-6.61
256012_at	unknown protein similar to dimethy	FMO1	AT1G19250	-1.25	-0.33	-0.34	0.74091523	0.9238	-6.61
257929_at	RNA Polymerase II subunit 14.5 k	NRPB9A	AT3G16980	1.03	0.04	0.34	0.7410259	0.9238	-6.61
259151_at	kinesin-like protein similar to carbo	---	AT3G10310	1.04	0.05	0.34	0.74122101	0.9238	-6.61
256181_at	light repressible receptor protein k	---	AT1G51820	-1.09	-0.13	-0.34	0.74122615	0.9238	-6.61
253771_at	hypothetical protein ;supported by	---	AT4G28430	-1.03	-0.04	-0.34	0.74111612	0.9238	-6.61
246658_at	putative protein predicted proteins	---	---	1.03	0.04	0.34	0.74111987	0.9238	-6.61
263718_at	putative CCAAT-box binding tranc	NF-YB7	AT2G13570	-1.03	-0.05	-0.34	0.74145219	0.9240	-6.61
254307_at	putative protein various predicted	---	AT4G22400	-1.05	-0.06	-0.34	0.74144184	0.9240	-6.61

258901_at	putative protein phosphatase-2C s	---	AT3G05640	-1.14	-0.18	-0.34	0.74149523	0.9240	-6.61
252840_at	putative protein various predicted	---	---	1.02	0.04	0.34	0.74153369	0.9240	-6.61
254274_at	putative DNA binding protein DNA	---	AT4G22770	1.04	0.06	0.34	0.74178973	0.9242	-6.61
253228_at	putative protein ;supported by full	---	AT4G34630	-1.08	-0.11	-0.34	0.74174727	0.9242	-6.61
250917_at	fructose-bisphosphate aldolase -li	---	AT5G03690	-1.03	-0.05	-0.34	0.74178358	0.9242	-6.61
251998_at	putative protein KIAA0010 protein	UPL7	AT3G53090	1.03	0.04	0.34	0.74191833	0.9242	-6.61
256195_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.34	0.74192914	0.9242	-6.61
265763_at	unknown protein	---	AT2G48060	1.02	0.03	0.34	0.74186678	0.9242	-6.61
246073_at	ribosomal protein L36-like riboson	---	AT5G20180	-1.03	-0.04	-0.34	0.74197496	0.9242	-6.61
264568_at	putative O-GlcNAc transferase sim	---	AT1G05150	1.04	0.05	0.34	0.74219615	0.9243	-6.61
247138_at	3-dehydroquinate synthase-like pr	---	AT5G66120	-1.04	-0.06	-0.34	0.74210177	0.9243	-6.61
265038_at	putative protein kinase highly simi	---	AT1G03920	-1.03	-0.04	-0.34	0.74212675	0.9243	-6.61
267643_at	hypothetical protein predicted by g	RALFL17	AT2G32890	1.02	0.03	0.34	0.74217858	0.9243	-6.61
254896_at	MADS-box protein AGL14	AGL14	AT4G11880	-1.02	-0.03	-0.34	0.74237986	0.9244	-6.61
261029_at	unknown protein	---	AT1G17330	-1.04	-0.05	-0.34	0.74238759	0.9244	-6.61
248721_at	putative protein strong similarity to	GAUT4	AT5G47780	-1.02	-0.03	-0.34	0.74251825	0.9246	-6.61
262261_at	CLE17, putative CLAVATA3/ESR-	CLE17	AT1G70895	-1.03	-0.05	-0.34	0.74264401	0.9246	-6.61
261180_at	hypothetical protein predicted by g	---	---	-1.03	-0.04	-0.34	0.74265428	0.9246	-6.61
261137_at	auxin-induced protein, putative sir	---	AT1G19830	1.02	0.03	0.34	0.74266104	0.9246	-6.61
266043_at	hypothetical protein	---	AT2G07724	-1.04	-0.05	-0.34	0.74287953	0.9248	-6.61
267360_at	unknown protein ;supported by ful	---	AT2G40060	-1.03	-0.05	-0.34	0.74291634	0.9248	-6.61
250956_at	putative protein	---	AT5G03210	-1.04	-0.06	-0.34	0.74296792	0.9248	-6.61
258528_at	unknown protein contains Pfam pr	---	AT3G06770	-1.07	-0.09	-0.34	0.74318719	0.9250	-6.61
262207_at	hypothetical protein predicted by g	PTAC2	AT1G74850	1.04	0.05	0.34	0.74340748	0.9251	-6.61
251319_at	putative protein POSSIBLE APOS	---	AT3G61610	-1.04	-0.06	-0.34	0.74338328	0.9251	-6.61
266462_at	unknown protein ; supported by cl	---	AT2G47770	1.08	0.12	0.34	0.74339765	0.9251	-6.61
260052_at	14-3-3 protein (grf13), putative co	GRF13	AT1G78220	-1.03	-0.04	-0.34	0.74326215	0.9251	-6.61
255215_at	putative athila transposon protein	---	---	-1.02	-0.03	-0.34	0.74328988	0.9251	-6.61
262636_at	DEIH-box RNA/DNA helicase iden	NIH	AT1G06670	1.03	0.05	0.34	0.74378077	0.9251	-6.61
260372_at	unknown protein contains a region	---	AT1G73980	1.03	0.04	0.34	0.74385133	0.9251	-6.61
263260_at	putative protein-tyrosine phosphat	OTS2	AT1G10570	-1.02	-0.04	-0.34	0.74391665	0.9251	-6.61
248067_at	unknown protein	---	AT5G55600	-1.03	-0.05	-0.34	0.7438837	0.9251	-6.61
257930_at	hypothetical protein	---	AT3G17010	-1.04	-0.05	-0.34	0.74394626	0.9251	-6.61
248726_at	RAS superfamily GTP-binding prot	ATRABA4C	AT5G47960	1.13	0.18	0.34	0.74395461	0.9251	-6.61
248333_at	photoassimilate-responsive protein	---	AT5G52390	-1.13	-0.18	-0.34	0.74376972	0.9251	-6.61

247868_at	Myb-related transcription factor-like	MYB36	AT5G57620	-1.03	-0.04	-0.34	0.74396216	0.9251	-6.61
246545_at	pectate lyase -like protein pectate	---	AT5G15110	-1.02	-0.03	-0.34	0.74357727	0.9251	-6.61
252648_at	disease resistance protein homolo	---	AT3G44630	-1.03	-0.04	-0.34	0.74369838	0.9251	-6.61
265830_at	putative helicase	---	---	1.03	0.05	0.34	0.74364325	0.9251	-6.61
244974_at	PSII low MW protein	---	---	-1.03	-0.04	-0.34	0.74373608	0.9251	-6.61
265866_at	unknown protein ;supported by ful	---	AT2G01710	1.03	0.04	0.34	0.74349452	0.9251	-6.61
260317_at	E2, ubiquitin-conjugating enzyme	UBC5	AT1G63800	1.05	0.07	0.34	0.7440972	0.9252	-6.61
256473_at	unknown protein	---	---	1.03	0.04	0.34	0.74415787	0.9252	-6.61
251532_at	putative protein F-box protein Fbl2	---	AT3G58530	1.03	0.04	0.34	0.74426519	0.9253	-6.61
250700_at	CDK5 activator-binding protein-like	---	AT5G06830	1.03	0.04	0.34	0.74433711	0.9254	-6.61
260485_at	putative amp-binding protein simila	---	AT1G68270	-1.03	-0.04	-0.34	0.7444257	0.9254	-6.61
267155_at	CLE7, putative CLAVATA3/ESR-r	---	AT2G30925	-1.03	-0.04	-0.34	0.74444922	0.9254	-6.61
256015_at	PSI type II chlorophyll a/b-binding	LHCA6	AT1G19150	-1.12	-0.16	-0.34	0.74473848	0.9254	-6.61
262245_at	unknown protein	NPSN12	AT1G48240	-1.04	-0.05	-0.34	0.74478052	0.9254	-6.61
259762_at	hypothetical protein predicted by g	---	AT1G77600	-1.03	-0.04	-0.34	0.74476297	0.9254	-6.61
246167_at	putative protein	---	---	-1.03	-0.05	-0.34	0.74466572	0.9254	-6.61
258653_at	hypothetical protein similar to auxi	---	AT3G09870	1.03	0.05	0.34	0.74475513	0.9254	-6.61
260759_at	hypothetical protein contains simila	---	AT1G49180	-1.05	-0.07	-0.34	0.74476518	0.9254	-6.61
260278_at	hypothetical protein predicted by g	WRKY66	AT1G80590	-1.05	-0.06	-0.34	0.74455581	0.9254	-6.61
247466_at	putative protein predicted proteins	---	AT5G62090	-1.04	-0.06	-0.34	0.7445203	0.9254	-6.61
246258_at	PPR-repeat protein, putative conta	---	AT1G31840	1.03	0.04	0.34	0.74490146	0.9255	-6.61
248530_at	putative protein strong similarity to	---	AT5G49945	1.03	0.05	0.34	0.74502723	0.9255	-6.61
263684_at	hypothetical protein predicted by g	---	AT1G26900	1.03	0.04	0.34	0.74500506	0.9255	-6.61
260467_at	unknown protein	---	AT1G10890	-1.02	-0.03	-0.34	0.74498121	0.9255	-6.61
256772_at	galactosidase, putative similar to E	BGAL1	AT3G13750	1.10	0.13	0.34	0.74511849	0.9255	-6.61
250855_at	putative protein predicted proteins	---	AT5G04730	-1.03	-0.04	-0.34	0.74515915	0.9255	-6.61
255247_at	hypothetical protein	---	---	-1.02	-0.03	-0.34	0.74517952	0.9255	-6.61
247747_at	putative protein predicted proteins	---	AT5G59000	-1.04	-0.05	-0.34	0.74523952	0.9256	-6.61
266257_at	putative chorismate mutase/prephe	PD1	AT2G27820	-1.04	-0.05	-0.34	0.74529095	0.9256	-6.61
261972_at	hypothetical protein predicted by g	---	AT1G64600	-1.05	-0.07	-0.34	0.7453952	0.9256	-6.61
265105_s_at	unknown protein contains similarity	---	AT1G62580 /	1.02	0.03	0.34	0.74535547	0.9256	-6.61
256617_at	unknown protein ; supported by fu	---	AT3G22240	1.07	0.10	0.34	0.7455357	0.9257	-6.61
263695_at	putative phosphoribosylglycinamid	---	AT1G31220	-1.03	-0.04	-0.34	0.74558505	0.9257	-6.61
257680_at	aspartate carbamoyltransferase p	---	AT3G20330	-1.04	-0.05	-0.34	0.74566465	0.9258	-6.61
265978_at	putative retroelement pol polyprote	---	---	-1.02	-0.03	-0.34	0.74584559	0.9260	-6.61

252111_at	propable disease resistance prote	---	AT3G51570	1.04	0.06	0.34	0.74592633	0.9260	-6.61
267169_at	putative oxidoreductase	---	AT2G37540	-1.06	-0.08	-0.33	0.74805384	0.9261	-6.61
264524_at	tat-binding protein, putative Highly	ATBCAT-2	AT1G10070	-1.12	-0.16	-0.33	0.74803362	0.9261	-6.61
262649_at	unknown protein contains similarity	---	AT1G14040	1.08	0.10	0.34	0.74755744	0.9261	-6.61
256093_at	predicted protein ; supported by cD	---	AT1G20823	-1.10	-0.13	-0.34	0.74765958	0.9261	-6.61
250549_at	N-hydroxycinnamoyl benzoyltrans	---	AT5G07860	1.04	0.06	0.34	0.74716004	0.9261	-6.61
261483_at	hypothetical protein predicted by g	---	AT1G14270	-1.03	-0.04	-0.34	0.74770813	0.9261	-6.61
252770_at	putative protein cellular nucleic ac	---	AT3G42860	-1.03	-0.04	-0.34	0.74688884	0.9261	-6.61
255021_at	hypothetical protein	---	AT4G10330	1.03	0.04	0.34	0.74616916	0.9261	-6.61
252938_at	hypothetical protein	---	AT4G39190	1.08	0.12	0.33	0.74801365	0.9261	-6.61
256976_at	unknown protein similar to putative	---	---	-1.04	-0.06	-0.34	0.74639102	0.9261	-6.61
251773_at	putative protein HSPC058, Homo	---	AT3G55960	-1.05	-0.06	-0.34	0.74730157	0.9261	-6.61
259910_at	putative P-type transporting ATPas	---	AT1G72700	-1.05	-0.08	-0.34	0.74618484	0.9261	-6.61
264557_at	putative pectinacetylesterase prec	---	AT1G09550	-1.04	-0.06	-0.33	0.74790704	0.9261	-6.61
265951_at	hypothetical protein predicted by g	OFP7	AT2G18500	1.05	0.06	0.34	0.74744878	0.9261	-6.61
250401_at	putative protein HSPC184, Homo	---	AT5G10780	1.02	0.03	0.34	0.74626	0.9261	-6.61
260647_at	hypothetical protein predicted by g	---	AT1G08030	-1.03	-0.05	-0.33	0.74787659	0.9261	-6.61
247574_at	putative protein predicted protein,	---	AT5G61228 /	-1.03	-0.04	-0.33	0.74802681	0.9261	-6.61
255029_x_at	hypothetical protein	---	AT4G09470	1.02	0.03	0.34	0.74651501	0.9261	-6.61
253823_at	putative protein ;supported by full-	---	AT4G28030	1.02	0.03	0.34	0.74705939	0.9261	-6.61
255532_at	hypothetical protein similar to orf a	---	AT4G02170	1.04	0.05	0.34	0.74722538	0.9261	-6.61
254451_at	adrenodoxin - like protein adrenoc	---	AT4G21090	-1.02	-0.03	-0.33	0.74797599	0.9261	-6.61
248071_at	unknown protein	---	AT5G55670	-1.03	-0.04	-0.34	0.74655787	0.9261	-6.61
254317_at	hypothetical protein	---	AT4G22510	-1.02	-0.03	-0.34	0.74645722	0.9261	-6.61
252629_at	cytochrome P450 - like protein cyt	---	AT3G44970	1.02	0.03	0.34	0.74603585	0.9261	-6.61
261885_at	unknown protein	---	AT1G80930	-1.03	-0.04	-0.34	0.74676598	0.9261	-6.61
255863_s_at	putative GDSL-motif lipase/hydrola	---	AT2G30220 /	-1.02	-0.03	-0.34	0.74729612	0.9261	-6.61
247913_at	unknown protein	---	AT5G57510	-1.16	-0.21	-0.33	0.74799578	0.9261	-6.61
247462_at	A9 protein precursor - like A9 prot	---	AT5G62080	-1.03	-0.04	-0.33	0.74794965	0.9261	-6.61
245762_at	ATP-dependent DNA helicase Re	---	AT1G27880	-1.02	-0.03	-0.34	0.74749852	0.9261	-6.61
266402_at	hypothetical protein predicted by g	---	AT2G38780	1.04	0.06	0.33	0.74804764	0.9261	-6.61
250219_at	putative protein similar to unknown	MPL1	AT5G14180	1.07	0.09	0.34	0.74647273	0.9261	-6.61
247363_at	unknown protein	---	AT5G63200	-1.03	-0.04	-0.34	0.74761402	0.9261	-6.61
267077_at	unknown protein similar to cytoske	---	AT2G40970	-1.04	-0.05	-0.34	0.74643338	0.9261	-6.61
252284_at	putative protein various predicted	---	AT3G49020	-1.03	-0.04	-0.34	0.74748544	0.9261	-6.61

263102_at	unknown protein	---	AT2G05270	-1.02	-0.03	-0.34	0.74650381	0.9261	-6.61
249905_at	unknown protein	---	AT5G22710	-1.03	-0.04	-0.34	0.7477579	0.9261	-6.61
246811_at	putative protein	---	AT5G27170	1.03	0.04	0.34	0.74608322	0.9261	-6.61
264997_at	hypothetical protein contains simila	HAC2	AT1G67220	1.03	0.05	0.33	0.74793273	0.9261	-6.61
261992_at	unknown protein	---	AT1G33680	1.03	0.04	0.34	0.74779552	0.9261	-6.61
249744_at	beta-glucosidase	BGLU32	AT5G24550	1.04	0.05	0.34	0.74678468	0.9261	-6.61
248588_at	unknown protein ; supported by cl	---	AT5G49540	1.02	0.04	0.34	0.74763514	0.9261	-6.61
260845_at	transcription factor, putative simila	---	AT1G17310	-1.03	-0.04	-0.34	0.74700049	0.9261	-6.61
252763_at	Expressed protein ; supported by c	---	AT3G42725	-1.03	-0.04	-0.34	0.74704267	0.9261	-6.61
249451_s_at	hypothetical protein	---	AT5G39480 /	1.02	0.03	0.33	0.74805832	0.9261	-6.61
263198_at	lipase, putative similar to lipase G	GLIP3	AT1G53990	1.04	0.05	0.34	0.74638424	0.9261	-6.61
252816_at	putative protein several putative pr	---	AT3G42550	1.02	0.03	0.33	0.74805664	0.9261	-6.61
264596_at	unknown protein similar to polygala	---	AT1G04625	1.03	0.05	0.33	0.74787482	0.9261	-6.61
264632_at	DegP protease contains similarity t	DegP4	AT1G65640	1.02	0.03	0.33	0.74789816	0.9261	-6.61
248825_at	ATP synthase delta chain, mitoch	---	AT5G47030	1.03	0.04	0.34	0.74750697	0.9261	-6.61
246805_at	putative protein various predicted	AGL101	AT5G27050	1.03	0.04	0.34	0.74689355	0.9261	-6.61
246431_at	calcium-binding protein calcium bi	APC1	AT5G17480	1.02	0.03	0.34	0.74775647	0.9261	-6.61
267607_s_at	epoxide hydrolase (ATsEH) identic	ATSEH	AT2G26740 /	1.05	0.07	0.33	0.74837798	0.9261	-6.61
251395_at	unknown protein ;supported by ful	FLA8	AT2G45470	1.20	0.27	0.33	0.74819683	0.9261	-6.61
263086_at	putative non-LTR retrolelement rev	---	AT2G16110	-1.03	-0.04	-0.33	0.74827928	0.9261	-6.61
261024_at	hypothetical protein predicted by g	---	AT1G12190	-1.02	-0.03	-0.33	0.74825336	0.9261	-6.61
257696_at	protein kinase, putative similar to	AGC1.5	AT3G12690	-1.04	-0.06	-0.33	0.7482326	0.9261	-6.61
265684_at	unknown protein	---	AT2G24410	-1.02	-0.03	-0.33	0.74839008	0.9261	-6.61
256925_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.33	0.74834213	0.9261	-6.61
256527_at	thionin, putative similar to thionin	---	AT1G66100	-1.04	-0.06	-0.33	0.74851421	0.9263	-6.61
257993_at	hypothetical protein similar to hypo	---	AT3G19890	-1.02	-0.04	-0.33	0.74856705	0.9263	-6.61
256797_at	DEAD box helicase protein, putati	---	AT3G18600	1.04	0.06	0.33	0.74872474	0.9263	-6.61
260137_at	unknown protein ;supported by full	---	AT1G66330	-1.04	-0.06	-0.33	0.74864763	0.9263	-6.61
254567_s_at	hypothetical protein	---	AT4G19260 /	-1.02	-0.03	-0.33	0.74872146	0.9263	-6.61
255386_at	hypothetical protein	---	AT4G03620	1.02	0.04	0.33	0.74877354	0.9263	-6.61
254844_at	hypothetical protein supported by f	---	AT4G11790	1.04	0.06	0.33	0.74885605	0.9264	-6.61
250586_at	putative protein similar to unknown	---	AT5G07630	-1.03	-0.05	-0.33	0.74897112	0.9264	-6.61
267313_at	putative protein phosphatase 2C	---	AT2G34740	-1.03	-0.05	-0.33	0.74894906	0.9264	-6.61
250118_at	putative protein similar to unknown	---	AT5G16460	-1.03	-0.04	-0.33	0.74901641	0.9264	-6.61
258033_at	unknown protein similar to MRP-lik	MRP6	AT3G21250	-1.05	-0.07	-0.33	0.74914192	0.9265	-6.61

251333_at	putative protein putative protein F	---	AT3G61690	-1.02	-0.03	-0.33	0.74920947	0.9265	-6.61
246664_at	putative protein predicted proteins	---	---	1.03	0.04	0.33	0.74918119	0.9265	-6.61
256116_at	unknown protein contains similarity	CPuORF55	AT1G16858	1.03	0.04	0.33	0.75005552	0.9265	-6.61
245334_at	Expressed protein ; supported by f	RALFL33	AT4G15800	1.06	0.08	0.33	0.74959549	0.9265	-6.61
255959_at	phosphatidylinositol-4-phosphate	ATPIP5K1	AT1G21980	1.10	0.14	0.33	0.74945247	0.9265	-6.61
262026_at	calcium-dependent protein kinase	ATCDPK2	AT1G35670	1.03	0.05	0.33	0.74976004	0.9265	-6.61
257300_at	unknown protein ; supported by fu	---	AT3G28080	-1.05	-0.07	-0.33	0.74963275	0.9265	-6.61
257883_at	calmodulin-binding protein, putativ	---	AT3G16940	1.04	0.05	0.33	0.74968173	0.9265	-6.61
251321_at	RING finger protein ;supported by	BRH1	AT3G61460	1.04	0.06	0.33	0.7499764	0.9265	-6.61
253349_at	putative protein	---	---	-1.02	-0.03	-0.33	0.74942075	0.9265	-6.61
250766_at	putative protein similar to unknown	---	AT5G05550	1.03	0.04	0.33	0.74951072	0.9265	-6.61
267541_at	hypothetical protein predicted by g	---	AT2G32750	-1.03	-0.05	-0.33	0.75002203	0.9265	-6.61
258439_at	lipoamide dehydrogenase precurs	mtLPD2	AT3G17240	-1.04	-0.06	-0.33	0.74942333	0.9265	-6.61
254149_at	putative protein hypothetical prote	---	AT4G24300	-1.04	-0.05	-0.33	0.75007066	0.9265	-6.61
253649_at	putative protein predicted protein,	---	AT4G29790	-1.05	-0.07	-0.33	0.74942613	0.9265	-6.61
266209_at	similar to terminal flower ; support	ATC	AT2G27550	-1.04	-0.06	-0.33	0.74993369	0.9265	-6.61
265775_at	Mutator-like transposase similar to	---	---	1.04	0.06	0.33	0.74971206	0.9265	-6.61
264868_at	unknown protein	---	AT1G24090	-1.06	-0.08	-0.33	0.74983207	0.9265	-6.61
255192_at	hypothetical protein	---	AT4G07380	1.02	0.04	0.33	0.74983392	0.9265	-6.61
251543_at	putative protein	---	AT3G58770	1.03	0.04	0.33	0.7500105	0.9265	-6.61
253292_at	Expressed protein ; supported by f	---	AT4G33985	1.04	0.06	0.33	0.75007527	0.9265	-6.61
264713_at	hypothetical protein Similar to N. ta	---	AT1G09820	-1.03	-0.04	-0.33	0.74940854	0.9265	-6.61
259973_at	hypothetical protein contains Pfam	---	AT1G76630	-1.04	-0.06	-0.33	0.74970616	0.9265	-6.61
259246_s_at	hypothetical protein predicted by g	---	AT3G07730	1.04	0.05	0.33	0.75021951	0.9266	-6.61
247438_at	unknown protein ; supported by cl	---	AT5G62460	-1.05	-0.07	-0.33	0.75024134	0.9266	-6.61
246755_at	F-box protein family contains simila	---	AT5G27920	-1.06	-0.09	-0.33	0.75061692	0.9267	-6.61
249368_at	putative protein predicted proteins	---	AT5G40640	-1.04	-0.05	-0.33	0.75045517	0.9267	-6.61
261612_at	fucosyltransferase c3 protein, puta	FUT12	AT1G49710	-1.02	-0.04	-0.33	0.75062311	0.9267	-6.61
264016_at	putative auxin-regulated protein	---	AT2G21220	1.03	0.04	0.33	0.75061178	0.9267	-6.61
245048_at	orf within trnK intron orf within trnK	---	---	-1.04	-0.05	-0.33	0.75044146	0.9267	-6.61
259803_at	cytosolic factor, putative similar to	PATL1	AT1G72150	-1.03	-0.04	-0.33	0.75040346	0.9267	-6.61
246827_at	copper binding - like protein mavic	---	AT5G26330	-1.03	-0.04	-0.33	0.75060747	0.9267	-6.61
260071_at	putative proline-rich protein precur	ESP1	AT1G73840	1.02	0.03	0.33	0.75050419	0.9267	-6.61
266186_at	unknown protein	AERO2	AT2G38960	-1.02	-0.03	-0.33	0.75072174	0.9267	-6.61
256073_at	terminal Flower 1 (TFL1), putative	E12A11	AT1G18100	-1.03	-0.04	-0.33	0.75072676	0.9267	-6.61

AFFX-r2-Bs-lys	B. subtilis /GEN=lys /DB_XREF=g	---	---	1.08	0.12	0.33	0.75095092	0.9270	-6.61
257029_at	dem-like protein similar to dem G	---	AT3G19240	1.03	0.04	0.33	0.75107852	0.9271	-6.61
261812_at	hypothetical protein contains simila	---	AT1G08270	1.02	0.03	0.33	0.75122556	0.9272	-6.61
262692_at	hypothetical protein predicted by g	---	---	1.03	0.04	0.33	0.75130556	0.9272	-6.61
253102_at	Expressed protein ; supported by f	---	AT4G36105	-1.04	-0.05	-0.33	0.75138149	0.9273	-6.61
256169_at	receptor protein kinase, putative c	---	AT1G51800	-1.12	-0.17	-0.33	0.75149444	0.9274	-6.61
254107_at	putative protein putative glycerol-3	---	AT4G25220	-1.03	-0.05	-0.33	0.7515269	0.9274	-6.61
254007_s_at	putative protein RNA-directed DN	---	AT1G60720	-1.02	-0.03	-0.33	0.75155946	0.9274	-6.61
247485_at	putative protein ARR1, Arabidops	ARR23	AT5G62120	-1.02	-0.03	-0.33	0.75182059	0.9274	-6.61
252731_at	putative protein predicted proteins	---	---	1.04	0.05	0.33	0.7517155	0.9274	-6.61
255529_at	CTP synthase - like protein	---	AT4G02120	1.03	0.04	0.33	0.75180382	0.9274	-6.61
253056_at	SHORT-ROOT (SHR)	SHR	AT4G37650	1.05	0.07	0.33	0.75175832	0.9274	-6.61
255823_at	unknown protein ;supported by ful	LBD15	AT2G40470	1.08	0.11	0.33	0.7517586	0.9274	-6.61
247936_at	lycopene epsilon cyclase ; suppor	LUT2	AT5G57030	-1.04	-0.05	-0.33	0.75194996	0.9275	-6.61
266595_at	hypothetical protein predicted by g	GC4	AT2G46180	-1.03	-0.04	-0.33	0.75192821	0.9275	-6.61
252226_at	putative protein transcribed gene	---	AT3G49880	1.02	0.03	0.33	0.75204365	0.9276	-6.61
251404_at	putative protein	---	AT3G60310	-1.03	-0.04	-0.33	0.75210487	0.9276	-6.61
249809_at	unknown protein	---	AT5G23910	-1.02	-0.03	-0.33	0.75212719	0.9276	-6.61
257176_s_at	cyclopropane-fatty-acyl-phospholi	---	AT3G23510	1.09	0.13	0.33	0.75219953	0.9276	-6.61
257033_at	metalloprotease, putative similar t	ATPREP1	AT3G19170	1.05	0.08	0.33	0.75227314	0.9276	-6.61
263335_x_at	hypothetical protein	---	---	1.02	0.03	0.33	0.7523461	0.9276	-6.61
249526_at	putative protein contains similarity	---	AT5G38560	-1.03	-0.05	-0.33	0.75235682	0.9276	-6.61
258812_at	unknown protein similar to GB:AAL	ECT1	AT3G03950	1.03	0.04	0.33	0.75250755	0.9276	-6.61
246461_at	putative protein AAA family protei	---	AT5G16930	1.07	0.10	0.33	0.75255224	0.9276	-6.61
252022_at	fructose bisphosphate aldolase - l	---	AT3G52930	1.04	0.06	0.33	0.75257178	0.9276	-6.61
255273_at	putative protein various predicted	---	---	1.02	0.03	0.33	0.75255081	0.9276	-6.61
252190_at	putative protein various predicted	---	AT3G50170	1.02	0.03	0.33	0.75242025	0.9276	-6.61
252191_at	putative protein various predicted	---	AT3G50180	-1.03	-0.04	-0.33	0.75281048	0.9278	-6.61
257121_at	hypothetical protein similar to auxi	---	AT3G20220	1.03	0.04	0.33	0.75280391	0.9278	-6.61
253375_at	hypothetical protein	---	AT4G33280	1.03	0.04	0.33	0.75275735	0.9278	-6.61
264958_at	unknown protein ; supported by cD	---	AT1G76960	-1.04	-0.06	-0.33	0.75285372	0.9278	-6.61
257779_at	protein kinase, putative similar to	CDG1	AT3G26940	-1.02	-0.03	-0.33	0.75297554	0.9278	-6.61
254009_at	pyruvate kinase like protein pyruv	---	AT4G26390	-1.04	-0.06	-0.33	0.75317203	0.9278	-6.61
252099_at	putative protein senescence-asso	---	AT3G51250	-1.03	-0.04	-0.33	0.75307391	0.9278	-6.61
256691_at	hypothetical protein predicted by g	---	---	1.02	0.03	0.33	0.75313306	0.9278	-6.61

253997_at	disease resistance protein RPS2 ;	RPS2	AT4G26090	1.08	0.12	0.33	0.75314482	0.9278	-6.61
246845_at	glutamyl-tRNA synthetase ; suppo	---	AT5G26710	-1.02	-0.03	-0.33	0.75319801	0.9278	-6.61
255935_at	hypothetical protein contains Pfam	---	AT1G12700	1.03	0.04	0.33	0.7530917	0.9278	-6.61
251422_at	transport protein subunit - like S61	---	AT3G60540	1.07	0.09	0.33	0.75293842	0.9278	-6.61
263948_at	similar to harpin-induced protein hi	YLS9	AT2G35980	-1.08	-0.11	-0.33	0.75341478	0.9279	-6.61
262959_at	protein translation factor Sui1 hom	---	AT1G54290	-1.03	-0.04	-0.33	0.75338432	0.9279	-6.61
265208_at	putative giberellin beta-hydroxylas	---	AT2G36690	-1.08	-0.11	-0.33	0.75338896	0.9279	-6.61
262753_at	putative 3-deoxy-D-manno-2-octul	ATKDSA2	AT1G16340	1.03	0.04	0.33	0.75368035	0.9280	-6.61
247366_at	putative protein contains similarity	---	AT5G63260	1.03	0.05	0.33	0.75385342	0.9280	-6.61
257840_at	protein kinase, putative contains P	AGC2-1	AT3G25250	-1.14	-0.19	-0.33	0.75368742	0.9280	-6.61
260586_at	unknown protein predicted by gene	---	AT2G43630	1.03	0.04	0.33	0.75370061	0.9280	-6.61
262013_s_at	mudrA-like protein similar to Mu tra	---	---	1.03	0.05	0.33	0.75384895	0.9280	-6.61
257748_at	hypothetical protein predicted by g	PUB29	AT3G18710	1.18	0.24	0.33	0.7537693	0.9280	-6.61
257120_at	protein kinase, putative contains P	---	AT3G20200	1.03	0.04	0.33	0.75378357	0.9280	-6.61
250619_at	A9 ;supported by full-length cDNA	---	AT5G07230	-1.02	-0.03	-0.33	0.75362081	0.9280	-6.61
267427_at	putative WRKY-type DNA binding	WRKY35	AT2G34830	1.02	0.03	0.33	0.7535383	0.9280	-6.61
246133_at	aldehyde oxidase AAO1 ; support	AAO1	AT5G20960	-1.08	-0.11	-0.33	0.75414074	0.9282	-6.61
250303_at	putative protein similar to unknown	---	AT5G12100	-1.05	-0.07	-0.33	0.75421734	0.9282	-6.61
264383_at	putative glutathione peroxidase C	ATGPX1	AT2G25080	-1.03	-0.05	-0.33	0.75440086	0.9282	-6.61
256122_at	hypothetical protein predicted by g	---	AT1G18180	1.03	0.04	0.33	0.75440254	0.9282	-6.61
246164_at	putative protein predicted proteins	---	---	-1.03	-0.04	-0.33	0.75406313	0.9282	-6.61
252008_at	hypothetical protein ; supported by	---	AT3G52610	-1.03	-0.04	-0.33	0.75431298	0.9282	-6.61
267433_at	putative peroxisome assembly pro	PEX10	AT2G26350	-1.03	-0.04	-0.33	0.75403863	0.9282	-6.61
255700_at	putative transcription factor similar	---	AT4G00200	1.05	0.07	0.33	0.75428193	0.9282	-6.61
264347_at	putative extensin strong similarity t	LRX1	AT1G12040	1.02	0.03	0.33	0.75428129	0.9282	-6.61
263670_at	hypothetical protein predicted by g	---	AT2G04840	-1.02	-0.03	-0.33	0.75419115	0.9282	-6.61
260475_at	Serine carboxypeptidase isolog	scpl31	AT1G11080	-1.06	-0.08	-0.33	0.7544024	0.9282	-6.61
260857_at	unknown protein contains Pfam pr	LYM1	AT1G21880	-1.06	-0.09	-0.33	0.75473255	0.9284	-6.61
254144_at	putative protein	---	AT4G24690	-1.03	-0.04	-0.33	0.75470814	0.9284	-6.61
259266_at	hypothetical protein predicted by g	---	AT3G01240	-1.02	-0.03	-0.33	0.75469035	0.9284	-6.61
260783_at	ethylene response factor, putative	ORA59	AT1G06160	-1.08	-0.12	-0.33	0.75498976	0.9286	-6.61
258472_at	unknown protein identical to unkno	---	AT3G06080	-1.04	-0.06	-0.33	0.75500666	0.9286	-6.61
252320_at	endoxyloglucan transferase-like p	---	AT3G48580	-1.06	-0.09	-0.32	0.75623325	0.9290	-6.61
258390_at	unknown protein similar to leucine-	---	AT3G15410	-1.03	-0.04	-0.32	0.75671131	0.9290	-6.61
263995_at	putative MADS-box protein	SVP	AT2G22540	1.03	0.05	0.32	0.7559807	0.9290	-6.61

245330_at	hypothetical protein ;supported by	---	AT4G14930	-1.03	-0.05	-0.32	0.7564075	0.9290	-6.61
257658_at	unknown protein ; supported by fu	---	AT3G13230	1.07	0.09	0.32	0.75561477	0.9290	-6.61
258635_at	unknown protein	---	AT3G08020	-1.02	-0.03	-0.32	0.75651996	0.9290	-6.61
246568_at	E2F transcription factor -like prote	DEL2	AT5G14960	-1.03	-0.04	-0.32	0.75618296	0.9290	-6.61
256777_at	hypothetical protein predicted by g	---	AT3G13780	-1.03	-0.04	-0.32	0.75589931	0.9290	-6.61
267083_at	calmodulin-like protein identical to	TCH3	AT2G41100	1.06	0.08	0.32	0.75655492	0.9290	-6.61
261543_at	unknown protein contains Pfam pr	---	AT1G63550	-1.03	-0.05	-0.32	0.75627273	0.9290	-6.61
246035_at	succinyl-CoA-ligase alpha subunit	---	AT5G08300	-1.07	-0.09	-0.32	0.75552485	0.9290	-6.61
252267_at	putative protein NITROGEN REG	---	AT3G49640	-1.04	-0.05	-0.32	0.75673304	0.9290	-6.61
253085_s_at	putative protein hypothetical prote	---	AT4G36270	1.04	0.06	0.32	0.75552987	0.9290	-6.61
257107_at	transmembrane trafficking protein	---	AT3G29070	1.03	0.04	0.32	0.75590825	0.9290	-6.61
251219_at	putative protein several hypothetic	---	AT3G62390	-1.05	-0.07	-0.32	0.75620454	0.9290	-6.61
254929_at	putative protein mitochondrial carr	---	AT4G11440	-1.03	-0.04	-0.32	0.75641704	0.9290	-6.61
265737_at	putative phosphatidic acid phospha	ATPAP1	AT2G01180	-1.11	-0.15	-0.32	0.75593319	0.9290	-6.61
256372_at	cell division protein kinase, putativ	CAK4	AT1G66750	-1.04	-0.05	-0.32	0.75672449	0.9290	-6.61
249166_at	CHP-rich zinc finger protein-like	---	AT5G42840	-1.03	-0.04	-0.32	0.75560426	0.9290	-6.61
249620_at	putative protein predicted proteins	---	AT5G37520	-1.02	-0.03	-0.32	0.75544432	0.9290	-6.61
247060_at	succinate dehydrogenase flavopro	SDH1-1	AT5G66760	-1.08	-0.11	-0.32	0.75635672	0.9290	-6.61
246228_at	peroxidase like protein	---	AT4G36430	1.11	0.15	0.32	0.75656368	0.9290	-6.61
259767_s_at	unknown protein	---	AT1G29350	1.02	0.04	0.32	0.75607863	0.9290	-6.61
255166_at	putative protein putative centrome	---	---	1.02	0.03	0.32	0.75611836	0.9290	-6.61
256621_at	unknown protein ; supported by fu	---	AT3G24450	-1.03	-0.04	-0.32	0.7557107	0.9290	-6.61
261755_at	histone H2B, putative similar to GI	---	AT1G08170	-1.03	-0.05	-0.32	0.75677099	0.9290	-6.61
265124_at	hypothetical protein similar to puta	---	AT1G55430	1.03	0.04	0.32	0.75627809	0.9290	-6.61
255492_at	hypothetical protein similar to A. th	EOL1	AT4G02680	1.03	0.04	0.32	0.75623883	0.9290	-6.61
254450_at	putative protein prolamin box bind	---	AT4G21080	1.03	0.04	0.32	0.75626622	0.9290	-6.61
267325_at	unknown protein predicted by gens	---	AT2G19360	-1.03	-0.04	-0.32	0.75663921	0.9290	-6.61
265407_at	F-box protein family, AtFBX8 cont	---	AT2G16810	1.04	0.06	0.32	0.75662254	0.9290	-6.61
262827_at	putative cytochrome P450 monoox	CYP71B29	AT1G13100	1.05	0.08	0.32	0.75574949	0.9290	-6.61
246256_at	glucosyltransferase-like protein	---	AT4G36770	-1.04	-0.06	-0.32	0.75544632	0.9290	-6.61
262015_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.32	0.7554802	0.9290	-6.61
251236_at	putative protein hypothetical protei	---	AT3G62380	-1.02	-0.03	-0.32	0.75563137	0.9290	-6.61
249339_at	putative protein similar to unknown	---	AT5G41100	1.09	0.12	0.32	0.75662635	0.9290	-6.61
246605_at	putative protein predicted proteins	---	---	-1.03	-0.04	-0.32	0.7555445	0.9290	-6.61
266429_at	hypothetical protein predicted by g	---	AT2G07190	1.03	0.04	0.32	0.75683424	0.9290	-6.61

257595_at	hypothetical protein predicted by g	---	AT3G24750	1.02	0.04	0.32	0.75691169	0.9290	-6.61
261762_at	hypothetical protein predicted by g	---	AT1G15510	1.05	0.07	0.32	0.75781267	0.9292	-6.61
247213_at	unknown protein ; supported by fu	PROPEP1	AT5G64900	-1.09	-0.13	-0.32	0.75756521	0.9292	-6.61
259838_at	unknown protein ;supported by full	---	AT1G52220	1.02	0.03	0.32	0.75756217	0.9292	-6.61
263609_at	putative LRR receptor protein kina	---	AT2G16250	-1.02	-0.03	-0.32	0.7577411	0.9292	-6.61
263243_at	putative glyoxalase II	GLX2-5	AT2G31350	1.03	0.04	0.32	0.75724118	0.9292	-6.61
249286_at	transcription factor-like protein	---	AT5G41580	-1.03	-0.04	-0.32	0.75756995	0.9292	-6.61
264661_at	hypothetical protein Similar to Nico	---	AT1G09950	-1.05	-0.07	-0.32	0.75750899	0.9292	-6.61
250388_at	putative protein various predicted	---	AT5G11310	1.06	0.08	0.32	0.75773985	0.9292	-6.61
246427_at	ADP/ATP translocase-like protein	ER-ANT1	AT5G17400	-1.03	-0.04	-0.32	0.75719255	0.9292	-6.61
248329_at	putative protein similar to unknown	---	AT5G52780	-1.04	-0.05	-0.32	0.75734138	0.9292	-6.61
251758_at	transcription factor L2 ;supported	---	AT3G55770	1.03	0.04	0.32	0.75768426	0.9292	-6.61
249533_at	putative protein predicted protein,	---	AT5G38790	-1.03	-0.04	-0.32	0.75718745	0.9292	-6.61
246481_s_at	cold and ABA inducible protein kin	KIN1	AT5G15960	-1.15	-0.20	-0.32	0.75732201	0.9292	-6.61
249449_at	unknown protein	---	AT5G39430	1.02	0.03	0.32	0.75759323	0.9292	-6.61
246938_at	cyclin 3a	CYCA2;1	AT5G25380	-1.03	-0.04	-0.32	0.75757863	0.9292	-6.61
267124_at	putative acetone-cyanohydrin lyas	MES19	AT2G23570	1.03	0.04	0.32	0.75781296	0.9292	-6.61
260488_at	flowering protein CONSTANS, put	TIFY2A	AT1G51600	-1.03	-0.05	-0.32	0.75735155	0.9292	-6.61
250797_at	unknown protein	---	AT5G05310	1.03	0.04	0.32	0.75766521	0.9292	-6.61
266793_at	homeotic protein AGL30	AGL30	AT2G03060	-1.05	-0.06	-0.32	0.7577241	0.9292	-6.61
267023_at	putative protein transport protein S	---	AT2G34250	1.03	0.04	0.32	0.75787827	0.9292	-6.61
249086_at	putative protein strong similarity to	---	AT5G44180	1.03	0.04	0.32	0.75801792	0.9292	-6.61
258311_at	transport inhibitor response 1 (TIR	AFB2	AT3G26810	1.03	0.04	0.32	0.75798908	0.9292	-6.61
261056_at	hypothetical protein similar to hypo	---	AT1G01360	-1.04	-0.05	-0.32	0.75793906	0.9292	-6.61
265706_at	unknown protein	---	AT2G03390	1.03	0.05	0.32	0.75806993	0.9293	-6.61
253402_at	HD-zip transcription factor (athb-8)	ATHB-8	AT4G32880	-1.04	-0.06	-0.32	0.75817443	0.9293	-6.61
246172_s_at	fragment of 1-aminocyclopropane	ACS1	AT3G61510	1.04	0.05	0.32	0.75817836	0.9293	-6.61
266491_at	putative retroelement pol polyprote	---	---	-1.02	-0.03	-0.32	0.75832198	0.9293	-6.61
259624_at	hypothetical protein similar to unkn	---	AT1G43020	-1.03	-0.04	-0.32	0.75830999	0.9293	-6.61
255235_at	contains similarity to transposases	---	---	1.03	0.05	0.32	0.75825189	0.9293	-6.61
248744_at	putative protein contains similarity	---	AT5G48250	-1.04	-0.05	-0.32	0.75836804	0.9293	-6.61
245969_at	putative protein nuclear gene for c	---	AT5G19830	-1.05	-0.07	-0.32	0.75856222	0.9295	-6.61
255999_at	DNA-binding protein, putative sim	WRKY71	AT1G29860	1.07	0.09	0.32	0.7590679	0.9295	-6.62
256852_at	unknown protein contains Pfam pr	ATRANGAP	AT3G18610	-1.04	-0.05	-0.32	0.75905437	0.9295	-6.62
262189_at	GTPase, putative similar to GTPa	---	AT1G78010	-1.03	-0.04	-0.32	0.75899431	0.9295	-6.62

248265_at	putative protein contains similarity	SDG29	AT5G53430	-1.04	-0.05	-0.32	0.75889333	0.9295	-6.62
258289_at	hypothetical protein predicted by g	---	AT3G23450	-1.02	-0.03	-0.32	0.75907571	0.9295	-6.62
246676_at	putative protein	---	---	-1.02	-0.03	-0.32	0.75894726	0.9295	-6.62
263569_at	putative chromosome associated p	TTN7	AT2G27170	1.04	0.06	0.32	0.75904896	0.9295	-6.62
267113_at	hypothetical protein predicted by g	---	AT2G14850	-1.02	-0.03	-0.32	0.75892787	0.9295	-6.62
260304_at	unknown protein identical to most	---	AT1G70480	-1.04	-0.06	-0.32	0.7590502	0.9295	-6.62
266066_at	putative xyloglucan endo-transglyc	XTH21	AT2G18800	-1.04	-0.05	-0.32	0.75896669	0.9295	-6.62
254271_at	serine/threonine kinase - like prote	---	AT4G23150	-1.06	-0.08	-0.32	0.75903055	0.9295	-6.62
245028_at	unknown protein	---	AT2G26570	-1.04	-0.05	-0.32	0.75865693	0.9295	-6.61
251979_at	caffeic acid O-methyltransferase -	LUT1	AT3G53130	-1.03	-0.04	-0.32	0.75928126	0.9297	-6.62
245017_at	PSI I protein	---	---	-1.03	-0.04	-0.32	0.75933673	0.9298	-6.62
255090_at	putative protein disease resistanc	---	AT4G09360	-1.03	-0.04	-0.32	0.75941335	0.9298	-6.62
255340_at	putative receptor-like protein kinas	---	AT4G04490	1.10	0.14	0.32	0.75961243	0.9300	-6.62
263154_at	Expressed protein ; supported by f	---	AT1G54110	-1.03	-0.04	-0.32	0.75963581	0.9300	-6.62
262030_s_at	mutator-like transposase, putative	---	---	-1.03	-0.04	-0.32	0.75965961	0.9300	-6.62
259144_at	putative kinesin-like centromere pr	---	AT3G10180	-1.02	-0.03	-0.32	0.75981191	0.9301	-6.62
256716_at	hypothetical protein predicted by g	---	AT2G34100	-1.03	-0.04	-0.32	0.75983626	0.9301	-6.62
258328_at	putative zinc finger protein similar t	---	AT3G16090	-1.02	-0.03	-0.32	0.7599465	0.9302	-6.62
246767_at	putative protein CG6949 - Drosop	---	AT5G27395	1.07	0.09	0.32	0.76001991	0.9302	-6.62
264710_at	putative phytochelatin synthetase s	COBL6	AT1G09790	1.02	0.04	0.32	0.76010169	0.9302	-6.62
250605_at	glycine/proline-rich protein flagellif	---	AT5G07570	-1.03	-0.04	-0.32	0.76007504	0.9302	-6.62
260028_at	unknown protein ; supported by cD	---	AT1G29980	1.11	0.15	0.32	0.76049055	0.9303	-6.62
245773_at	hypothetical protein predicted by g	---	AT1G30290	1.03	0.04	0.32	0.76040144	0.9303	-6.62
258524_at	acetyl-coA dehydrogenase, putati	IBR3	AT3G06810	-1.03	-0.04	-0.32	0.76026781	0.9303	-6.62
255770_at	hypothetical protein predicted by g	---	AT1G18560	-1.03	-0.04	-0.32	0.76057099	0.9303	-6.62
261710_at	hypothetical protein identical to hy	---	AT1G32730	1.03	0.04	0.32	0.76036275	0.9303	-6.62
251364_at	anthranilate phosphoribosyltransfe	---	AT3G61300	1.03	0.04	0.32	0.76049833	0.9303	-6.62
264268_at	hypothetical protein predicted by g	ULP1D	AT1G60220	-1.02	-0.03	-0.32	0.7606476	0.9303	-6.62
265733_at	unknown protein ;supported by ful	---	AT2G01190	1.03	0.04	0.32	0.76063384	0.9303	-6.62
259829_at	oligopeptide transporter, putative s	---	---	-1.03	-0.05	-0.32	0.76065654	0.9303	-6.62
252807_at	putative replication protein various	---	---	1.02	0.03	0.32	0.76065268	0.9303	-6.62
246723_at	putative protein various predicted	---	AT5G29030	1.03	0.04	0.32	0.76043751	0.9303	-6.62
264765_at	receptor kinase, putative similar to	---	AT1G61430	-1.03	-0.04	-0.32	0.7604258	0.9303	-6.62
260558_at	putative endochitinase	---	AT2G43600	-1.03	-0.05	-0.32	0.7607986	0.9304	-6.62
251032_at	putative homeodomain protein sev	RPL	AT5G02030	1.06	0.09	0.32	0.76094801	0.9305	-6.62

247364_at	putative protein similar to unknown	---	AT5G63200	1.02	0.03	0.32	0.76092362	0.9305	-6.62
259015_at	unknown protein similar to hypothe	---	AT3G07350	-1.07	-0.09	-0.32	0.76104362	0.9305	-6.62
258606_at	unknown protein ;supported by ful	---	AT3G02840	-1.19	-0.25	-0.32	0.76111586	0.9306	-6.62
254479_at	putative protein hypothetical prote	---	AT4G20350	1.03	0.04	0.32	0.76116385	0.9306	-6.62
246923_at	putative multispanning membrane	---	AT5G25100	-1.03	-0.04	-0.32	0.76153336	0.9306	-6.62
250072_at	putative protein similar to unknown	---	AT5G17210	1.04	0.05	0.32	0.76157791	0.9306	-6.62
264021_at	putative auxin-regulated protein ;s	---	AT2G21200	-1.06	-0.08	-0.32	0.7614238	0.9306	-6.62
251776_at	eukaryotic translation initiation fac	emb1624	AT3G55620	-1.04	-0.05	-0.32	0.76156479	0.9306	-6.62
266180_at	putative PHD-type zinc finger prote	AL6	AT2G02470	1.03	0.05	0.32	0.76153635	0.9306	-6.62
264462_at	putative transcription factor simila	WLIM1	AT1G10200	-1.04	-0.06	-0.32	0.76132265	0.9306	-6.62
253613_at	PR-1-like protein gene PR-1 prote	---	AT4G30320	-1.03	-0.04	-0.32	0.76136222	0.9306	-6.62
266692_at	Ac-like transposase related to Ac [	---	AT2G19960	1.02	0.03	0.32	0.76161029	0.9306	-6.62
262444_at	hypothetical protein similar to puta	---	AT1G47480	-1.05	-0.07	-0.32	0.76147494	0.9306	-6.62
254585_at	resistence protein - like downy mil	---	AT4G19500	-1.02	-0.03	-0.32	0.76137215	0.9306	-6.62
262816_at	alkylation repair-like protein	---	AT1G11780	-1.04	-0.05	-0.32	0.76163544	0.9306	-6.62
256493_at	hypothetical protein predicted by g	---	AT1G31600	-1.03	-0.04	-0.32	0.76169223	0.9306	-6.62
264690_at	hypothetical protein similar to hypo	SNL4	AT1G70060	-1.03	-0.05	-0.32	0.76182837	0.9307	-6.62
250725_at	putative protein similar to unknown	---	AT5G06400	-1.03	-0.04	-0.32	0.76183081	0.9307	-6.62
249455_s_at	putative protein predicted proteins	---	AT1G50870 /	1.02	0.03	0.32	0.76183533	0.9307	-6.62
261223_at	hypothetical protein predicted by g	HVA22H	AT1G19950	-1.02	-0.03	-0.32	0.76187635	0.9307	-6.62
245213_at	photosystem II 22kDa protein, put	NPQ4	AT1G44575	-1.07	-0.09	-0.31	0.76232868	0.9307	-6.62
254991_at	putative protein conserved hypoth	---	AT4G10620	-1.03	-0.04	-0.32	0.76221494	0.9307	-6.62
250135_at	putative protein	---	AT5G15360	1.03	0.04	0.32	0.76227183	0.9307	-6.62
254481_at	hypothetical protein ; supported by	---	AT4G20480	1.04	0.06	0.31	0.76232401	0.9307	-6.62
264077_at	putative RAD51B-like DNA repair p	RAD51B	AT2G28560	-1.02	-0.04	-0.32	0.7621753	0.9307	-6.62
253786_at	receptor protein kinase-like protei	---	AT4G28650	-1.03	-0.04	-0.32	0.76213342	0.9307	-6.62
251298_at	hypothetical protein contains non-c	---	AT3G62040	-1.06	-0.08	-0.32	0.76228348	0.9307	-6.62
261963_at	hypothetical protein predicted by g	---	---	1.03	0.04	0.32	0.76211285	0.9307	-6.62
259975_at	putative cinnamoyl-CoA reductase	---	AT1G76470	-1.08	-0.11	-0.32	0.76221138	0.9307	-6.62
256492_at	hypothetical protein contains simila	---	AT1G31490	1.03	0.04	0.32	0.761998	0.9307	-6.62
259707_at	thylakoid-bound ascorbate peroxid	TAPX	AT1G77490	1.04	0.05	0.31	0.76254319	0.9308	-6.62
256825_at	unknown protein similar to cell wal	CWLP	AT3G22120	1.22	0.29	0.31	0.76250256	0.9308	-6.62
262413_at	hypothetical protein contains simila	ATAPRL4	AT1G34780	-1.03	-0.05	-0.31	0.76251412	0.9308	-6.62
247597_at	GTP-binding protein - like GTP-bi	AtRABA1f	AT5G60860	1.06	0.08	0.31	0.76276472	0.9309	-6.62
248157_at	putative protein similar to unknown	---	AT5G54420	1.03	0.04	0.31	0.76269873	0.9309	-6.62

264287_at	hypothetical protein similar to hypo	---	AT1G61930	-1.03	-0.04	-0.31	0.762731	0.9309	-6.62
258246_s_at	hypothetical protein similar to puta	---	---	1.02	0.03	0.31	0.76277463	0.9309	-6.62
247114_at	unknown protein ; supported by cl	---	AT5G65910	-1.03	-0.04	-0.31	0.76289982	0.9310	-6.62
245866_s_at	unknown protein	---	AT1G57980	-1.11	-0.15	-0.31	0.76299863	0.9310	-6.62
255332_at	predicted protein of unknown funct	---	AT4G04340	-1.02	-0.03	-0.31	0.76296149	0.9310	-6.62
265080_at	overlap with bases 100,099-109,1	sks12	AT1G55570	-1.03	-0.05	-0.31	0.76298586	0.9310	-6.62
265170_at	putative carbonic anhydrase	BCA3	AT1G23730	-1.15	-0.21	-0.31	0.76306556	0.9310	-6.62
262724_s_at	PC-MYB2, putative similar to PC-I	---	AT1G43330	-1.02	-0.03	-0.31	0.76325937	0.9312	-6.62
265503_at	putative non-LTR retroelement rev	---	---	1.03	0.05	0.31	0.7632563	0.9312	-6.62
255028_at	putative protein Arabidopsis thalia	PMP	AT3G24160	1.05	0.08	0.31	0.76347513	0.9312	-6.62
253333_at	2-dehydro-3-deoxyphosphohepton	DHS2	AT4G33510	1.03	0.04	0.31	0.76347049	0.9312	-6.62
263888_at	unknown protein	---	AT2G37000	-1.03	-0.05	-0.31	0.76333433	0.9312	-6.62
266128_at	hypothetical protein predicted by g	EMB2766	---	-1.03	-0.04	-0.31	0.76343085	0.9312	-6.62
258310_at	unknown protein	ICE1	AT3G26744	1.03	0.04	0.31	0.76341013	0.9312	-6.62
259893_at	putative disease resistance protein	AtRLP11	AT1G71390	-1.03	-0.04	-0.31	0.76369022	0.9313	-6.62
248698_at	receptor-like protein kinase ; suppo	---	AT5G48380	-1.04	-0.06	-0.31	0.76367746	0.9313	-6.62
251689_at	putative protein motif in hypothetic	---	AT3G56500	-1.09	-0.13	-0.31	0.763746	0.9314	-6.62
252557_at	putative protein cim1 induced alle	ATEXLA3	AT3G45960	-1.02	-0.03	-0.31	0.76385902	0.9314	-6.62
246773_at	protein kinase-like protein MAP3K	---	AT5G27510	-1.04	-0.05	-0.31	0.76383846	0.9314	-6.62
250892_at	putative protein beta-(1-3)-glucosy	ATCSLA09	AT5G03760	-1.19	-0.25	-0.31	0.76404151	0.9314	-6.62
251190_at	RING-H2 zinc finger protein ATL5	ATL5	AT3G62690	1.05	0.07	0.31	0.76421403	0.9314	-6.62
249956_at	putative protein CGI-66 protein, H	---	AT5G18940	1.02	0.03	0.31	0.7639134	0.9314	-6.62
248553_at	putative protein strong similarity to	---	AT5G50170	-1.05	-0.07	-0.31	0.76420925	0.9314	-6.62
249139_at	Cys2/His2-type zinc finger protein	AZF3	AT5G43170	-1.06	-0.08	-0.31	0.76410634	0.9314	-6.62
257249_at	unknown protein	---	AT3G24180	1.04	0.05	0.31	0.76422722	0.9314	-6.62
266498_at	1-aminocyclopropane-1-carboxylat	---	AT2G06960	-1.02	-0.03	-0.31	0.76412973	0.9314	-6.62
259772_at	hypothetical protein predicted by g	---	AT1G29480	1.02	0.03	0.31	0.7642096	0.9314	-6.62
267555_at	Expressed protein ; supported by f	SUMO5	AT2G32765	1.03	0.04	0.31	0.7641893	0.9314	-6.62
255965_at	14-3-3 protein (grf14), putative sin	---	AT1G22290	-1.02	-0.03	-0.31	0.76431716	0.9314	-6.62
265209_at	putative DNA binding protein with I	ATHB22	AT2G36610	1.02	0.03	0.31	0.76429788	0.9314	-6.62
246409_at	CRK1 protein, putative similar to C	---	AT1G57700	1.04	0.05	0.31	0.76436125	0.9314	-6.62
253150_at	putative protein predicted protein,	---	AT4G35660	-1.02	-0.03	-0.31	0.76450445	0.9314	-6.62
261103_s_at	O-methyltransferase 1, putative si	---	AT1G62900	-1.03	-0.04	-0.31	0.76451895	0.9314	-6.62
257872_at	P-glycoprotein, putative similar to	PGP16	AT3G28360	1.02	0.03	0.31	0.76459412	0.9314	-6.62
258840_at	unknown protein similar to unknow	---	AT3G04620	-1.02	-0.03	-0.31	0.76456387	0.9314	-6.62

267642_at	unknown protein	---	AT2G32905 /	-1.02	-0.03	-0.31	0.7645147	0.9314	-6.62
258124_at	Expressed protein ; supported by c	---	AT3G18215	1.04	0.06	0.31	0.76463913	0.9315	-6.62
253809_at	putative (1-4)-beta-mannan endoh	---	AT4G28320	1.03	0.05	0.31	0.7647302	0.9315	-6.62
266843_at	hypothetical protein predicted by g	---	AT2G26135	1.02	0.03	0.31	0.7647948	0.9315	-6.62
263817_at	hypothetical protein predicted by g	---	---	1.03	0.04	0.31	0.76483462	0.9315	-6.62
264618_at	hypothetical protein predicted by g	---	AT2G17680	1.02	0.03	0.31	0.76490949	0.9316	-6.62
254834_at	flavonoid 3,5-hydroxylase -like pro	CYP706A4	AT4G12300	-1.03	-0.05	-0.31	0.76564035	0.9317	-6.62
259544_at	hypothetical protein ; supported by	CAT3	AT1G20620	1.02	0.03	0.31	0.76548605	0.9317	-6.62
246327_at	receptor-like serine/threonine kina	---	AT1G16670	1.03	0.05	0.31	0.76560876	0.9317	-6.62
265321_at	putative Tub family protein	AtTLP2	AT2G18280	1.02	0.03	0.31	0.76546269	0.9317	-6.62
258908_at	putative dehydroquinase shikimate	MEE32	AT3G06350	1.04	0.05	0.31	0.76517087	0.9317	-6.62
247973_at	putative protein contains similarity	---	AT5G56770	-1.02	-0.03	-0.31	0.76561424	0.9317	-6.62
260510_at	hypothetical protein predicted by g	---	AT1G51580	1.04	0.06	0.31	0.76555528	0.9317	-6.62
245432_at	putative serine protease-like protei	---	AT4G17100	1.02	0.03	0.31	0.76555153	0.9317	-6.62
267443_at	hypothetical protein predicted by g	---	AT2G19000	-1.02	-0.03	-0.31	0.7653619	0.9317	-6.62
260173_at	NAM-like protein similar to NAM G	VND7	AT1G71930	1.03	0.04	0.31	0.76534505	0.9317	-6.62
254497_at	Phosphoribosylanthranilate transf	---	AT4G20080	1.04	0.06	0.31	0.76521431	0.9317	-6.62
249321_at	disease resistance protein-like	---	AT5G40920	1.03	0.05	0.31	0.76539213	0.9317	-6.62
261079_s_at	transcription factor IIA large subun	---	AT1G07470 /	-1.03	-0.04	-0.31	0.76528368	0.9317	-6.62
251045_s_at	putative protein various predicted	---	AT2G13910 /	1.02	0.03	0.31	0.76513011	0.9317	-6.62
254539_s_at	chitinase - like protein chitinase / l	---	AT4G19750 /	-1.02	-0.03	-0.31	0.76540686	0.9317	-6.62
250527_at	serine/threonine-protein kinase	SNRK2.1	AT5G08590	-1.02	-0.03	-0.31	0.76569502	0.9317	-6.62
250841_at	putative protein CGI-01 protein, H	---	AT5G04610	1.04	0.06	0.31	0.7657831	0.9318	-6.62
252674_at	cytochrome P450-like protein CYT	CYP71B38	AT3G44250	1.02	0.03	0.31	0.76591648	0.9319	-6.62
248908_at	receptor kinase-like protein	MEE62	AT5G45800	1.08	0.10	0.31	0.7661394	0.9319	-6.62
246109_at	hypothetical protein (fragment?)	---	AT5G20120	-1.03	-0.04	-0.31	0.76604208	0.9319	-6.62
250286_at	auxin-responsive - like protein Nt-	PBS3	AT5G13320	1.16	0.21	0.31	0.76613848	0.9319	-6.62
257341_at	pseudogene, Mutator-like transpo	---	---	-1.02	-0.03	-0.31	0.76622467	0.9319	-6.62
256946_at	hypothetical protein contains Pfam	HAF2	AT3G19040	1.04	0.06	0.31	0.76606048	0.9319	-6.62
259600_at	hypothetical protein predicted by g	---	AT1G35220	1.03	0.05	0.31	0.76620945	0.9319	-6.62
251747_at	putative protein various predicted	---	AT3G55670	-1.02	-0.03	-0.31	0.76619195	0.9319	-6.62
247686_at	receptor-like protein kinase precu	---	AT5G59700	-1.08	-0.11	-0.31	0.76651739	0.9319	-6.62
265577_at	unknown protein	---	AT2G20100	-1.02	-0.03	-0.31	0.76644304	0.9319	-6.62
264944_at	hypothetical protein similar to hypo	---	AT1G76940	-1.04	-0.05	-0.31	0.76634399	0.9319	-6.62
249414_at	putative transcription factor MYB8	MYB89	AT5G39700	-1.03	-0.04	-0.31	0.76635323	0.9319	-6.62

260253_at	disease resistance protein, putativ	AtRLP15	AT1G74190	-1.02	-0.03	-0.31	0.76649137	0.9319	-6.62
249998_at	putative protein unnamed ORF, M	FASS	AT5G18580	1.02	0.03	0.31	0.76638031	0.9319	-6.62
252307_at	putative protein SAE1-S9-protein,	---	---	-1.03	-0.04	-0.31	0.76646251	0.9319	-6.62
256270_at	unknown protein ; supported by cD	---	AT3G12300	1.03	0.04	0.31	0.7666238	0.9320	-6.62
259827_at	hypothetical protein	---	AT1G72270	-1.02	-0.03	-0.31	0.76661944	0.9320	-6.62
252414_at	putative protein sn-glycerol-3-phos	---	AT3G47420	1.04	0.05	0.31	0.76682559	0.9320	-6.62
249898_at	alkaline/neutral invertase ; suppor	---	AT5G22510	-1.04	-0.05	-0.31	0.7668074	0.9320	-6.62
250239_at	ABC transporter-like protein	---	AT5G13580	1.03	0.05	0.31	0.76678042	0.9320	-6.62
246118_at	beta-1,3-glucanase bg5	BG5	AT5G20340	1.03	0.04	0.31	0.76685697	0.9320	-6.62
256783_at	casein kinase, putative similar to c	---	AT3G13670	-1.02	-0.03	-0.31	0.76685434	0.9320	-6.62
247739_at	40S ribosomal protein S8 - like 40	---	AT5G59240	-1.03	-0.05	-0.31	0.76693147	0.9320	-6.62
250030_at	putative protein contains similarity	ATAPRL7	AT5G18120	1.02	0.03	0.31	0.76695505	0.9320	-6.62
259375_at	putative APG protein similar to ant	---	AT3G16370	-1.26	-0.33	-0.31	0.76702842	0.9321	-6.62
246632_at	hypothetical protein similar to puta	---	AT1G29710	-1.03	-0.04	-0.31	0.76730745	0.9323	-6.62
262438_at	hypothetical protein identical to hy	---	AT1G47410	1.05	0.07	0.31	0.76729275	0.9323	-6.62
254310_at	putative protein predicted protein,	---	AT4G22430	1.02	0.03	0.31	0.76735696	0.9323	-6.62
258460_at	unknown protein	ECT6	AT3G17330	1.03	0.04	0.31	0.767464	0.9324	-6.62
249458_at	putative protein predicted proteins	---	AT5G39560	-1.02	-0.03	-0.31	0.76744778	0.9324	-6.62
252334_at	mitochondrial phosphate transpor	---	AT3G48850	1.12	0.16	0.31	0.7677158	0.9324	-6.62
256934_at	unknown protein contains Pfam pr	---	AT3G22530	-1.03	-0.04	-0.31	0.76820515	0.9324	-6.62
259725_at	Expressed protein ; supported by f	---	AT1G61065	-1.04	-0.06	-0.31	0.76759849	0.9324	-6.62
251148_at	hypothetical protein	TKL	AT3G63180	1.02	0.03	0.31	0.76831078	0.9324	-6.62
256606_at	hypothetical protein	---	AT3G32960	1.02	0.03	0.31	0.76781786	0.9324	-6.62
253342_at	Expressed protein ; supported by c	PAA1	AT4G33520	-1.06	-0.08	-0.31	0.76829922	0.9324	-6.62
261493_at	DNA-binding protein p24, putative	WHY1	AT1G14410	1.04	0.05	0.31	0.76806044	0.9324	-6.62
260958_at	unknown protein identical to unkno	---	AT1G06060	1.03	0.04	0.31	0.76768695	0.9324	-6.62
264166_at	unknown protein ; supported by cD	---	AT1G65370	-1.03	-0.04	-0.31	0.76817617	0.9324	-6.62
250224_at	putative protein similar to unknown	---	AT5G14150	-1.03	-0.05	-0.31	0.76778298	0.9324	-6.62
247582_at	putative protein various predicted	---	AT5G60760	-1.03	-0.04	-0.31	0.76790064	0.9324	-6.62
256507_at	hypothetical protein predicted by g	---	AT1G75150	-1.03	-0.04	-0.31	0.76808911	0.9324	-6.62
259947_at	putative protein kinase similar to p	---	AT1G71530	-1.03	-0.04	-0.31	0.76808494	0.9324	-6.62
246705_x_at	putative protein predicted resistan	---	---	-1.03	-0.04	-0.31	0.76784198	0.9324	-6.62
255964_at	hypothetical protein predicted by g	ZYP1b	AT1G22275	-1.02	-0.03	-0.31	0.76802419	0.9324	-6.62
261690_at	branched-chain amino acid amino	---	AT1G50090	-1.02	-0.03	-0.31	0.76771179	0.9324	-6.62
250249_at	putative protein similar to unknown	---	AT5G13760	-1.03	-0.04	-0.31	0.76829658	0.9324	-6.62

261918_at	hypothetical protein	---	AT1G65940	-1.02	-0.03	-0.31	0.76803179	0.9324	-6.62
264695_at	lipid transfer protein, putative simi	---	AT1G70250	1.03	0.04	0.31	0.76818323	0.9324	-6.62
263634_at	putative retroelement gag/pol polyp	---	---	1.02	0.03	0.31	0.76861938	0.9327	-6.62
264225_at	hypothetical protein predicted by g	---	AT1G67420	1.04	0.06	0.31	0.7685934	0.9327	-6.62
257111_x_at	hypothetical protein	---	---	1.02	0.03	0.31	0.76872581	0.9328	-6.62
247202_at	GTP-binding protein ; supported b	AtRABA4a	AT5G65270	1.03	0.04	0.31	0.7690264	0.9329	-6.62
245437_at	RNA helicase like protein	---	AT4G16630	1.04	0.05	0.31	0.76905798	0.9329	-6.62
261092_at	unknown protein	---	AT1G62870	1.02	0.03	0.31	0.76899462	0.9329	-6.62
249252_at	putative protein contains similarity	---	AT5G42010	-1.09	-0.12	-0.31	0.7690654	0.9329	-6.62
248500_at	unknown protein	---	AT5G50410	1.03	0.04	0.31	0.7688272	0.9329	-6.62
251588_at	putative protein several putative pr	---	AT3G58090	-1.03	-0.04	-0.31	0.7690356	0.9329	-6.62
245469_at	reverse transcriptase like protein	---	---	-1.02	-0.03	-0.31	0.76899228	0.9329	-6.62
267284_at	unknown protein predicted by gens	---	AT2G23700	-1.03	-0.05	-0.31	0.76914884	0.9329	-6.62
257826_at	RING zinc finger protein, putative	---	AT3G26730	1.02	0.03	0.31	0.76922323	0.9329	-6.62
247751_at	putative protein	---	AT5G59050	1.05	0.07	0.31	0.76923246	0.9329	-6.62
261245_at	anter-specific proline-rich protein A	---	AT1G20130 /	1.02	0.03	0.31	0.76930345	0.9329	-6.62
255810_at	hypothetical protein ; supported by	---	AT4G10140	-1.02	-0.04	-0.31	0.76938896	0.9330	-6.62
259960_at	cell division control protein, putativ	---	AT1G53710	-1.03	-0.05	-0.31	0.76935032	0.9330	-6.62
263900_at	unknown protein ;supported by ful	---	AT2G36290	1.03	0.04	0.31	0.76952793	0.9330	-6.62
249239_at	MAP kinase ; supported by cDNA	CPuORF58	AT5G41990 /	1.02	0.03	0.31	0.7694997	0.9330	-6.62
247354_at	flavonol synthase ;supported by fu	FLS3	AT5G63590	-1.02	-0.03	-0.31	0.76950212	0.9330	-6.62
267309_at	Expressed protein ; supported by f	---	AT2G19385	1.04	0.05	0.30	0.76998232	0.9330	-6.62
266614_at	unknown protein	---	AT2G14910	1.03	0.04	0.30	0.77004873	0.9330	-6.62
255931_at	hypothetical protein similar to puta	AtPP2-A12	AT1G12710	1.04	0.06	0.30	0.77000802	0.9330	-6.62
266571_at	unknown protein	---	AT2G23830	1.05	0.07	0.30	0.76985041	0.9330	-6.62
250146_at	putative protein polypeptide defor	PDF1B	AT5G14660	-1.04	-0.06	-0.30	0.76994055	0.9330	-6.62
248083_at	unknown protein	---	AT5G55420	1.08	0.12	0.30	0.76997625	0.9330	-6.62
249940_at	NAC-domain protein-like ;supporte	anac090	AT5G22380	-1.03	-0.04	-0.30	0.7700166	0.9330	-6.62
260422_at	hypothetical protein predicted by g	---	AT1G69630	-1.02	-0.03	-0.30	0.76984131	0.9330	-6.62
260016_at	Athila ORF 1, putative simlar to G	---	---	-1.02	-0.03	-0.30	0.76988822	0.9330	-6.62
265783_at	putative Athila retroelement ORF1	---	---	-1.03	-0.04	-0.30	0.76987107	0.9330	-6.62
263511_at	En/Spm-like transposon protein rel	---	---	-1.02	-0.03	-0.30	0.76988732	0.9330	-6.62
260180_at	E2, ubiquitin-conjugating enzyme,	MMZ2	AT1G70660	1.04	0.05	0.30	0.77000592	0.9330	-6.62
251960_at	GTPase AtRAB8 ;supported by fu	HEMB1	AT1G69740 /	1.02	0.04	0.30	0.77045668	0.9334	-6.62
249402_at	Expressed protein ; supported by f	---	AT5G40155	-1.02	-0.04	-0.30	0.77045278	0.9334	-6.62

250216_at	unknown protein	---	AT5G14090	-1.03	-0.04	-0.30	0.77055074	0.9334	-6.62
265223_at	putative pectinesterase	---	AT2G36700	-1.02	-0.03	-0.30	0.77055245	0.9334	-6.62
264038_at	putative ubiquinone biosynthesis p	---	AT2G03690	-1.03	-0.05	-0.30	0.77066571	0.9335	-6.62
263232_at	putative light repressible receptor	---	AT1G05700	-1.02	-0.03	-0.30	0.77072965	0.9335	-6.62
261017_at	UDP-glucose dehydrogenase, put	UGD1	AT1G26570	-1.03	-0.04	-0.30	0.77079009	0.9335	-6.62
263820_at	hypothetical protein predicted by g	---	---	-1.04	-0.05	-0.30	0.77081269	0.9335	-6.62
256328_at	6-phosphogluconate dehydrogena	---	AT3G02360	-1.05	-0.07	-0.30	0.77093956	0.9335	-6.62
247143_at	unknown protein	---	AT5G65580	1.04	0.06	0.30	0.77089235	0.9335	-6.62
254743_at	potassium transporter - like protei	HAK5	AT4G13420	-1.19	-0.24	-0.30	0.7709208	0.9335	-6.62
261944_at	unknown protein	---	AT1G64650	-1.03	-0.05	-0.30	0.77100486	0.9336	-6.62
250899_at	putative protein ; supported by cD	---	AT5G03340	1.04	0.05	0.30	0.77115598	0.9337	-6.62
248545_at	cysteine proteinase similar to cyste	---	AT5G50260	-1.02	-0.03	-0.30	0.77124896	0.9338	-6.62
247494_at	calnexin - like protein calnexin hor	CNX1	AT5G61790	-1.08	-0.11	-0.30	0.77136609	0.9339	-6.62
252463_at	putative protein ;supported by full-	---	AT3G47070	1.05	0.07	0.30	0.77142236	0.9339	-6.62
263201_at	putative ADP-glucose pyrophosph	APS2	AT1G05610	-1.03	-0.04	-0.30	0.77148661	0.9339	-6.62
257732_at	unknown protein contains Pfam pr	AtCASP	AT3G18480	-1.02	-0.04	-0.30	0.7716148	0.9340	-6.62
247194_at	putative protein similar to unknown	---	AT5G65480	1.04	0.05	0.30	0.77177766	0.9341	-6.62
245753_at	hypothetical protein similar to puta	---	---	-1.02	-0.03	-0.30	0.77173886	0.9341	-6.62
254583_at	hypothetical protein	---	AT4G19480	1.02	0.03	0.30	0.77171694	0.9341	-6.62
261727_at	S-adenosyl-methionine-sterol-C-m	SMT3	AT1G76090	1.05	0.07	0.30	0.77197308	0.9341	-6.62
259824_at	copper homeostasis factor, putativ	ATX1	AT1G66240	-1.02	-0.03	-0.30	0.7719624	0.9341	-6.62
254437_s_at	putative protein	---	AT3G06433	-1.04	-0.06	-0.30	0.77198145	0.9341	-6.62
255141_at	putative protein several hypothetic	---	---	1.02	0.03	0.30	0.77190098	0.9341	-6.62
260471_at	hypothetical protein predicted by g	---	AT1G11070	-1.02	-0.03	-0.30	0.77203546	0.9341	-6.62
256564_at	alpha/beta hydrolase, putative cor	MES11	AT3G29770	1.06	0.09	0.30	0.77208701	0.9341	-6.62
249058_at	disease resistance protein-like	TAO1	AT5G44510	1.03	0.04	0.30	0.77213595	0.9341	-6.62
252439_at	pectinesterase-like protein pectine	---	AT3G47400	1.02	0.03	0.30	0.77228129	0.9343	-6.62
265631_at	putative helicase	---	---	1.02	0.03	0.30	0.77232899	0.9343	-6.62
258441_at	hypothetical protein predicted by g	AT3G17265	---	-1.02	-0.03	-0.30	0.77237455	0.9343	-6.62
252375_at	rac GTP binding protein Arac8 ; su	ROP10	AT3G48040	-1.03	-0.04	-0.30	0.77290245	0.9343	-6.62
258658_at	putative adenosine kinase similar t	ADK1	AT3G09820	1.06	0.08	0.30	0.77259065	0.9343	-6.62
259316_at	unknown protein	---	AT3G01175	1.03	0.04	0.30	0.772482	0.9343	-6.62
267194_s_at	putative ARP2/3 protein complex s	ARPC1A	AT2G30910	1.02	0.04	0.30	0.77282384	0.9343	-6.62
256381_at	lipid transfer protein, putative cont	---	AT1G66850	-1.03	-0.04	-0.30	0.77295001	0.9343	-6.62
256224_at	GTP-binding protein (SAR1B) iden	ATSAR1B	AT1G56330	1.04	0.05	0.30	0.77294347	0.9343	-6.62

264741_at	aspartic protease, putative similar	---	AT1G62290	1.08	0.11	0.30	0.77257251	0.9343	-6.62
252482_at	glucosyltransferase-like protein UI	UGT76E11	AT3G46670	-1.09	-0.12	-0.30	0.77262534	0.9343	-6.62
257682_at	hypothetical protein predicted by g	---	AT3G13240	-1.02	-0.03	-0.30	0.77283033	0.9343	-6.62
265520_at	hypothetical protein predicted by g	---	AT2G06020	-1.03	-0.04	-0.30	0.77278312	0.9343	-6.62
246397_at	hypothetical protein contains simila	AtRLP9	AT1G58190	1.02	0.03	0.30	0.77264757	0.9343	-6.62
264827_at	hypothetical protein similar to anth	---	AT1G03390	1.02	0.03	0.30	0.77273614	0.9343	-6.62
257603_at	unknown protein	---	AT3G13820	-1.02	-0.03	-0.30	0.77286636	0.9343	-6.62
264158_at	hypothetical protein contains simila	PTAC4	AT1G65260	1.03	0.04	0.30	0.77312108	0.9344	-6.62
262655_s_at	putative mandelonitrile lyase simil	---	AT1G14185 /	1.02	0.03	0.30	0.77310405	0.9344	-6.62
256893_x_at	unknown protein	---	---	1.02	0.03	0.30	0.77307399	0.9344	-6.62
263949_at	E2, ubiquitin-conjugating enzyme,	MMZ3	AT2G36060	1.02	0.03	0.30	0.77320514	0.9345	-6.62
250188_at	putative protein COP9 complex su	COP13	AT5G14250	1.02	0.03	0.30	0.77344494	0.9347	-6.62
263630_at	Expressed protein ; supported by f	---	AT2G04845	1.02	0.03	0.30	0.77365382	0.9349	-6.62
266480_at	unknown protein ; supported by cl	---	AT2G31130	1.02	0.03	0.30	0.77379698	0.9349	-6.62
254457_at	putative protein various predicted	---	AT4G21170	-1.03	-0.05	-0.30	0.7741552	0.9349	-6.62
262129_at	mutM homologue-1 identical to mu	ATMMH-1	AT1G52500	-1.03	-0.04	-0.30	0.7740791	0.9349	-6.62
260952_at	hypothetical protein predicted by g	---	AT1G06140	-1.03	-0.05	-0.30	0.77412427	0.9349	-6.62
258332_at	putative transport protein similar to	---	AT3G16180	-1.07	-0.09	-0.30	0.77377575	0.9349	-6.62
253869_at	hypothetical protein	---	AT4G27510	1.03	0.04	0.30	0.77417629	0.9349	-6.62
246784_at	signal peptidase ; supported by cD	---	AT5G27430	-1.02	-0.03	-0.30	0.77428833	0.9349	-6.62
259573_at	hypothetical protein	---	---	-1.02	-0.03	-0.30	0.77418862	0.9349	-6.62
256630_at	unknown protein	---	AT3G28230	1.02	0.04	0.30	0.77418871	0.9349	-6.62
256403_at	unknown protein similar to SPOP (	BPM2	AT3G06190	-1.02	-0.03	-0.30	0.77404036	0.9349	-6.62
246485_at	putative protein cell death associa	AtCXE17	AT5G16080	1.10	0.14	0.30	0.7742923	0.9349	-6.62
245677_at	hypothetical protein predicted by g	---	AT1G56660	-1.02	-0.03	-0.30	0.77427702	0.9349	-6.62
265851_at	hypothetical protein predicted by g	---	AT2G42340	1.02	0.03	0.30	0.77384011	0.9349	-6.62
255372_at	putative reverse transcriptase	---	---	-1.04	-0.05	-0.30	0.77385281	0.9349	-6.62
265755_at	En/Spm transposon hypothetical p	---	---	-1.02	-0.03	-0.30	0.7739415	0.9349	-6.62
254776_at	3-hydroxyisobutyryl-coenzyme A h	---	AT4G13360	1.02	0.03	0.30	0.77450708	0.9349	-6.62
256866_at	unknown protein similar to alpha g	---	AT3G26380	-1.03	-0.05	-0.30	0.77463386	0.9349	-6.62
249011_at	putative protein strong similarity to	---	AT5G44670	1.06	0.08	0.30	0.77462946	0.9349	-6.62
247055_at	putative protein similar to unknown	---	AT5G66740	-1.03	-0.04	-0.30	0.774529	0.9349	-6.62
249804_at	galactinol synthase	AtGolS5	AT5G23790	1.02	0.03	0.30	0.77441157	0.9349	-6.62
254098_at	superoxide dismutase (EC 1.15.1.1	FSD1	AT4G25100	1.03	0.04	0.30	0.77463685	0.9349	-6.62
252248_at	putative protein resistance gene H	AtRLP44	AT3G49750	1.04	0.06	0.30	0.77455322	0.9349	-6.62

255981_at	hypothetical protein ;supported by	---	AT1G34020	1.03	0.04	0.30	0.7745839	0.9349	-6.62
265230_s_at	hypothetical protein	---	AT2G07707	-1.03	-0.05	-0.30	0.77473979	0.9349	-6.62
267065_at	hypothetical protein predicted by g	---	AT2G41080	-1.03	-0.04	-0.30	0.77476084	0.9349	-6.62
266629_at	putative serpin	---	AT2G35590	-1.02	-0.03	-0.30	0.77475179	0.9349	-6.62
246011_at	putative protein auxin-induced bas	---	AT5G08330	-1.05	-0.07	-0.30	0.77487869	0.9350	-6.62
263113_at	unknown protein Belongs to PF|00	---	AT1G03150	-1.02	-0.03	-0.30	0.77488029	0.9350	-6.62
254419_at	NADH dehydrogenase like protein	NDB3	AT4G21490	1.02	0.03	0.30	0.77489143	0.9350	-6.62
247811_at	leucine zipper-containing protein l	ATEXO70B	AT5G58430	-1.06	-0.08	-0.30	0.77510492	0.9352	-6.62
267109_at	hypothetical protein predicted by g	---	AT2G14810	1.03	0.04	0.30	0.77530386	0.9354	-6.62
261301_at	hypothetical protein predicted by g	---	AT1G48570	1.06	0.08	0.30	0.77545487	0.9354	-6.62
261068_at	tropinone reductase-I, putative sin	---	AT1G07450	-1.02	-0.03	-0.30	0.77541632	0.9354	-6.62
263819_x_at	putative TNP2-like transposon prot	---	---	1.02	0.03	0.30	0.77539254	0.9354	-6.62
251310_at	homeobox protein Anthocyaninles	HDG1	AT3G61150	1.03	0.04	0.30	0.7755678	0.9355	-6.62
258418_at	unknown protein	---	AT3G16660	1.09	0.12	0.30	0.77566692	0.9355	-6.62
256981_at	brassinosteroid receptor kinase, p	BRL3	AT3G13380	-1.04	-0.06	-0.30	0.77580816	0.9356	-6.62
251157_at	mRNA binding protein precursor -	CSP41A	AT3G63140	-1.04	-0.05	-0.30	0.77589018	0.9356	-6.62
258214_at	amidase, putative similar to amida	atToc64-III	AT3G17970	1.04	0.06	0.30	0.77591815	0.9356	-6.62
252903_at	putative protein various predicted	---	AT4G39570	1.04	0.06	0.30	0.77588939	0.9356	-6.62
258420_at	putative RNA polymerase similar t	---	AT3G16680	1.02	0.03	0.30	0.77589148	0.9356	-6.62
253670_at	putative protein ; supported by full	---	AT4G30010	1.03	0.04	0.30	0.77594452	0.9356	-6.62
247021_at	putative protein similar to unknown	---	AT5G67040	-1.03	-0.04	-0.30	0.7761504	0.9357	-6.62
254677_at	chloroplast protein cs/ch-42	---	AT4G18490	1.03	0.04	0.30	0.77611542	0.9357	-6.62
256322_at	unknown protein ; supported by cD	AXR4	AT1G54990	1.05	0.07	0.30	0.7762253	0.9358	-6.62
256089_at	hypothetical protein predicted by g	---	AT1G20830	1.04	0.05	0.30	0.77629337	0.9358	-6.62
258552_at	putative pectate lyase similar to pe	---	AT3G07010	1.15	0.20	0.30	0.77639901	0.9359	-6.62
257402_at	hypothetical protein similar to puta	---	AT1G23570	-1.02	-0.03	-0.30	0.77651755	0.9360	-6.62
266172_at	putative aquaporin (water channel	PIP2E	AT2G39010	1.05	0.07	0.30	0.77657368	0.9360	-6.62
255765_at	protein kinase, putative contains P	---	AT1G16760	1.02	0.03	0.30	0.77664196	0.9360	-6.62
248143_at	putative protein similar to unknown	---	AT5G55040	-1.02	-0.03	-0.30	0.7766536	0.9360	-6.62
251971_at	glucosyltransferase - like protein g	UGT73C7	AT3G53160	-1.13	-0.18	-0.30	0.77673925	0.9360	-6.62
258948_at	putative sulfite oxidase similar to s	SOX	AT3G01910	-1.02	-0.03	-0.30	0.7768269	0.9361	-6.62
246154_at	putative protein predicted protein,	---	AT5G19940	-1.02	-0.03	-0.29	0.77711716	0.9361	-6.62
246732_at	putative protein hypothetical prote	---	AT5G27650	1.03	0.04	0.29	0.7770964	0.9361	-6.62
254916_at	putative protein hypothetical prote	---	AT4G11340	-1.02	-0.03	-0.29	0.77706068	0.9361	-6.62
262425_at	hypothetical protein predicted by g	---	AT1G47660	-1.02	-0.03	-0.29	0.77712269	0.9361	-6.62

252681_at	NAC domain -like protein Tobacc	anac061	AT3G44350	1.03	0.04	0.29	0.77707594	0.9361	-6.62
264720_at	hypothetical protein similar to vetis	---	AT1G70080	-1.03	-0.04	-0.29	0.77701418	0.9361	-6.62
246716_s_at	putative protein	---	AT5G28910 /	1.02	0.03	0.29	0.77691819	0.9361	-6.62
258161_at	hypothetical protein predicted by g	---	AT3G17930	-1.03	-0.04	-0.29	0.77721213	0.9362	-6.62
251968_at	putative protein proline-rich protei	---	AT3G53100	-1.03	-0.05	-0.29	0.77743973	0.9363	-6.62
251147_at	kinesin heavy chain - like protein k	---	AT3G63480	-1.02	-0.03	-0.29	0.77742568	0.9363	-6.62
246657_at	putative protein predicted proteins	---	---	-1.02	-0.03	-0.29	0.77755028	0.9364	-6.62
247542_at	autophagocytosis protein - like au	ATG3	AT5G61500	1.03	0.04	0.29	0.77768488	0.9364	-6.62
251939_at	putative protein MICRONUCLEAR	---	AT3G53440	-1.04	-0.05	-0.29	0.77766574	0.9364	-6.62
265410_at	putative protein kinase contains a	---	AT2G16620	1.02	0.03	0.29	0.77765434	0.9364	-6.62
253393_at	Expressed protein ; supported by c	GLB3	AT4G32690	1.03	0.04	0.29	0.777812	0.9365	-6.62
259673_at	putative phorbol ester / diacylglyce	---	AT1G77800	1.03	0.04	0.29	0.77820983	0.9365	-6.62
265154_at	putative GTP-binding protein, ER(	---	AT1G30960	1.05	0.07	0.29	0.77796452	0.9365	-6.62
250751_at	glucuronosyl transferase-like prote	---	AT5G05890	-1.03	-0.04	-0.29	0.7779825	0.9365	-6.62
252863_at	myo-inositol-1-phosphate synthase	MIPS1	AT4G39800	-1.12	-0.17	-0.29	0.77822196	0.9365	-6.62
262126_at	disease resistance protein, putativ	CW9	AT1G59620	-1.03	-0.05	-0.29	0.77785858	0.9365	-6.62
263728_at	gamma-adaptin, putative similar to	---	AT1G60070	-1.02	-0.03	-0.29	0.77777248	0.9365	-6.62
265886_at	putative protein phosphatase 2C ;	---	AT2G25610 /	-1.05	-0.07	-0.29	0.77815577	0.9365	-6.62
256997_at	subtilisin-like serine protease, puta	---	AT3G14067	-1.04	-0.05	-0.29	0.7782086	0.9365	-6.62
256344_at	C2H2-type zinc finger protein, put	TFIIIA	AT1G72050	1.03	0.04	0.29	0.77796942	0.9365	-6.62
249664_at	putative protein histone stem-loop	---	AT5G36722 /	-1.02	-0.03	-0.29	0.77815791	0.9365	-6.62
256561_s_at	hypothetical protein similar to puta	---	---	-1.02	-0.03	-0.29	0.77816627	0.9365	-6.62
252869_at	putative protein	---	AT4G39930	-1.02	-0.03	-0.29	0.77826412	0.9365	-6.62
267054_at	hypothetical protein	---	AT2G38370	-1.04	-0.06	-0.29	0.77847849	0.9366	-6.62
253118_at	ras-related small GTP-binding pro	ARAC6	AT4G35950	1.03	0.04	0.29	0.77854924	0.9366	-6.62
267049_at	putative transcription elongation fa	---	AT2G34210	1.04	0.06	0.29	0.7784441	0.9366	-6.62
266507_at	unknown protein EST matches on	---	AT2G47860	1.02	0.03	0.29	0.77851078	0.9366	-6.62
261529_at	hypothetical protein contains simila	---	AT1G14430	1.02	0.03	0.29	0.77840908	0.9366	-6.62
253038_at	homeobox protein HAT22 ;suppor	HAT22	AT4G37790	1.04	0.06	0.29	0.77871981	0.9367	-6.62
252728_at	putative protein various predicted	---	---	1.02	0.03	0.29	0.77869361	0.9367	-6.62
247454_at	unknown protein	---	AT5G62440	1.05	0.07	0.29	0.77894134	0.9369	-6.62
256095_at	hypothetical protein contains Pfam	---	AT1G13630	-1.05	-0.06	-0.29	0.7789178	0.9369	-6.62
259989_at	hypothetical protein predicted by g	---	---	1.03	0.04	0.29	0.77899072	0.9369	-6.62
255939_at	hypothetical protein predicted by g	---	AT1G12730	-1.03	-0.05	-0.29	0.77915698	0.9370	-6.62
258493_at	Expressed protein ; supported by f	---	AT3G02555	1.02	0.04	0.29	0.77922998	0.9371	-6.62

252745_at	putative protein Sh3yl1 mRNA, Mu	---	AT3G43230	1.03	0.04	0.29	0.77959331	0.9375	-6.62
249858_at	myb-related transcription factor-like	MYB37	AT5G23000	-1.03	-0.04	-0.29	0.77977398	0.9375	-6.62
263672_at	putative retroelement pol polyprote	---	---	-1.02	-0.03	-0.29	0.77979092	0.9375	-6.62
265617_at	putative phosphate/phosphoenolpy	---	AT2G25520	1.05	0.06	0.29	0.77980797	0.9375	-6.62
263827_at	unknown protein	---	AT2G40420	-1.04	-0.05	-0.29	0.77968004	0.9375	-6.62
254672_at	hypothetical protein	---	---	-1.03	-0.04	-0.29	0.77977336	0.9375	-6.62
264316_at	unknown protein ; supported by cD	ENT1,AT	AT1G70330	-1.03	-0.04	-0.29	0.78001904	0.9375	-6.62
259250_at	unknown protein	---	AT3G07580	1.04	0.05	0.29	0.77989615	0.9375	-6.62
258242_at	hypothetical protein predicted by g	---	AT3G27640	-1.02	-0.03	-0.29	0.78001896	0.9375	-6.62
259448_at	hypothetical protein similar to trans	---	AT1G13790	1.03	0.04	0.29	0.77993722	0.9375	-6.62
255824_at	hypothetical protein predicted by g	---	AT2G40530	-1.07	-0.10	-0.29	0.78008355	0.9375	-6.62
262825_at	putative chloroplast prephenate de	ADT1	AT1G11790	-1.04	-0.06	-0.29	0.78030031	0.9378	-6.62
257859_at	Expressed protein ; supported by f	---	AT3G12955	1.03	0.04	0.29	0.78035034	0.9378	-6.63
262999_at	NAM protein, putative similar to N	ANAC020	AT1G54330	-1.03	-0.05	-0.29	0.78049464	0.9379	-6.63
252340_at	myb-like protein	AtMYB45	AT3G48920	1.04	0.05	0.29	0.78055268	0.9379	-6.63
255346_at	hypothetical protein	---	---	-1.02	-0.02	-0.29	0.78061077	0.9379	-6.63
253427_at	putative protein phosphate/phospl	---	AT4G32390	-1.02	-0.03	-0.29	0.7806733	0.9379	-6.63
247373_at	unknown protein ;supported by ful	---	AT5G63150	1.03	0.04	0.29	0.78082334	0.9379	-6.63
263353_at	hypothetical protein predicted by g	---	AT2G22070	1.02	0.03	0.29	0.78089264	0.9379	-6.63
247733_at	putative protein heat shock protein	---	AT5G59610	-1.04	-0.05	-0.29	0.78072061	0.9379	-6.63
257412_at	unknown protein	---	AT1G22980	1.02	0.03	0.29	0.78090994	0.9379	-6.63
263187_at	athila ORF 1, putative similar to A	---	---	1.02	0.03	0.29	0.780903	0.9379	-6.63
249680_s_at	putative protein strong similarity to	---	AT3G61730 /	-1.02	-0.02	-0.29	0.78083382	0.9379	-6.63
258555_at	fatty acid multifunctional protein (A	MFP2	AT3G06860	-1.03	-0.04	-0.29	0.78097246	0.9380	-6.63
261876_at	pirin-like protein similar to pirin GB	---	AT1G50590	1.06	0.09	0.29	0.78103787	0.9380	-6.63
259464_at	hypothetical protein predicted by g	---	AT1G18990	1.02	0.03	0.29	0.78113227	0.9380	-6.63
259078_at	unknown protein predicted by gene	HST	AT3G05040	-1.02	-0.03	-0.29	0.78110302	0.9380	-6.63
245646_x_at	F5A9.9 hypothetical protein	---	AT1G24851 /	1.02	0.03	0.29	0.78113037	0.9380	-6.63
247314_at	3(2),5-bisphosphate nucleotidase	SAL2	AT5G64000	1.06	0.09	0.29	0.78147318	0.9380	-6.63
254263_at	Expressed protein ; supported by f	---	AT4G23493	-1.02	-0.03	-0.29	0.78141177	0.9380	-6.63
260616_at	hypothetical protein contains Pfam	---	AT1G53280	1.03	0.05	0.29	0.78139687	0.9380	-6.63
260377_at	unknown protein	---	AT1G73930	-1.02	-0.03	-0.29	0.78135141	0.9380	-6.63
252776_at	putative protein predicted proteins	---	AT3G42940	-1.03	-0.04	-0.29	0.78144711	0.9380	-6.63
251521_at	putative protein receptor kinase h	ACR4	AT3G59420	-1.03	-0.04	-0.29	0.78146881	0.9380	-6.63
250206_at	mitochondrial phosphate transloca	---	AT5G14040	-1.04	-0.06	-0.29	0.78133891	0.9380	-6.63

250677_at	putative protein similar to unknown	---	AT5G06520	-1.02	-0.03	-0.29	0.78120394	0.9380	-6.63
260347_at	DHHC-type zinc finger protein, pu	---	AT1G69420	-1.04	-0.05	-0.29	0.78158029	0.9381	-6.63
264752_at	unknown protein similar to Bacillu	LPR1	AT1G23010	-1.02	-0.03	-0.29	0.78165619	0.9381	-6.63
260447_at	hypothetical protein similar to N-te	---	AT1G72410	1.02	0.03	0.29	0.78183936	0.9382	-6.63
263387_at	unknown protein ; supported by cl	---	AT2G40160	-1.03	-0.04	-0.29	0.78183947	0.9382	-6.63
267226_at	unknown protein	---	AT2G44010	-1.06	-0.08	-0.29	0.78206243	0.9384	-6.63
254039_at	putative protein Human GS1 (prot	GPP1	AT4G25840	1.03	0.04	0.29	0.7820063	0.9384	-6.63
252278_at	NAC2-like protein NAC2 - Arabido	anac062	AT3G49530	1.06	0.08	0.29	0.78208341	0.9384	-6.63
253026_at	hypothetical protein	---	AT4G38120	-1.03	-0.05	-0.29	0.78213663	0.9384	-6.63
257246_at	pectinesterase, putative contains	---	AT3G24130	-1.02	-0.03	-0.29	0.78218023	0.9384	-6.63
255177_at	strong similarity to 1-aminocyclopr	ACS11	AT4G08040	1.08	0.10	0.29	0.78261332	0.9385	-6.63
248315_at	selenium-binding protein-like	MEF1	AT5G52630	-1.02	-0.03	-0.29	0.78316769	0.9385	-6.63
260313_at	putative disease resistance protein	---	AT1G63870	-1.03	-0.04	-0.29	0.78317616	0.9385	-6.63
262155_at	glycosyl transferase, putative simi	---	AT1G52420	1.03	0.04	0.29	0.78288148	0.9385	-6.63
245206_at	putative protein similarity to NCA2	DGS1	AT5G12290	1.03	0.04	0.29	0.78266125	0.9385	-6.63
262711_at	hypothetical protein predicted by g	---	AT1G16500	-1.04	-0.05	-0.29	0.78232682	0.9385	-6.63
248186_at	unknown protein ;supported by ful	---	AT5G53880	1.10	0.13	0.29	0.78268667	0.9385	-6.63
262576_at	unknown protein ESTs gb|R90323	---	AT1G15280	-1.02	-0.03	-0.29	0.78267645	0.9385	-6.63
264879_at	cotton fiber expressed protein, put	---	AT1G61260	1.06	0.08	0.29	0.78308405	0.9385	-6.63
255289_at	score=11/3, E=0.23, N=1 contains	---	AT4G04690	-1.02	-0.03	-0.29	0.78318983	0.9385	-6.63
262483_at	putative translation initiation factor	FUG1	AT1G17220	1.02	0.03	0.29	0.78307181	0.9385	-6.63
247677_at	oxysterol-binding protein - like oxy	ORP3C	AT5G59420	1.02	0.03	0.29	0.78235046	0.9385	-6.63
246554_at	HSP100/ClpB, putative similar to	CLPB3	AT5G15450	1.03	0.04	0.29	0.7826205	0.9385	-6.63
246899_at	putative protein various predicted	---	AT5G25590	1.02	0.03	0.29	0.78314722	0.9385	-6.63
258746_at	germin-like protein similar to germi	---	AT3G05950	-1.02	-0.03	-0.29	0.78293242	0.9385	-6.63
252243_at	putative protein some putative prot	---	AT3G50120	-1.05	-0.07	-0.29	0.78300034	0.9385	-6.63
267282_at	unknown protein ; supported by cl	---	AT2G19390	-1.03	-0.04	-0.29	0.78308538	0.9385	-6.63
259205_at	hypothetical protein similar to puta	---	AT3G09030	-1.03	-0.04	-0.29	0.78280432	0.9385	-6.63
260517_at	unknown protein	SPP1	AT1G51420	1.02	0.03	0.29	0.78296826	0.9385	-6.63
263814_at	putative TNP2-like transposon prot	---	---	1.02	0.03	0.29	0.78271919	0.9385	-6.63
256086_at	hypothetical protein predicted by g	---	AT1G20770	1.02	0.03	0.29	0.78269286	0.9385	-6.63
256758_at	hypothetical protein similar to Athil	---	---	1.03	0.04	0.29	0.78322656	0.9385	-6.63
256395_at	putative helix-loop-helix DNA-bindi	MUTE	AT3G06120	-1.02	-0.04	-0.29	0.7826463	0.9385	-6.63
252532_at	glucosidase-like protein GLUCAN	---	AT3G46570	1.04	0.05	0.29	0.78250113	0.9385	-6.63
260427_at	hypothetical protein predicted by g	---	AT1G72430	-1.06	-0.08	-0.29	0.78341628	0.9386	-6.63

262877_at	unknown protein ;supported by full	---	AT1G64850	-1.03	-0.04	-0.29	0.78343575	0.9386	-6.63
252489_at	disease resistance protein RPP8-l	---	AT3G46710	-1.03	-0.04	-0.29	0.783436	0.9386	-6.63
262848_at	unknown protein ; supported by cD	BPC2	AT1G14685	1.02	0.03	0.29	0.78357857	0.9387	-6.63
261050_at	transcription factor MYC7E, putati	---	AT1G01260	1.04	0.05	0.29	0.78367781	0.9387	-6.63
252655_at	hypothetical protein with predicted	---	AT3G44760	-1.02	-0.03	-0.29	0.78370901	0.9387	-6.63
267499_at	hypothetical protein predicted by g	---	AT2G45500	-1.02	-0.03	-0.29	0.78383987	0.9388	-6.63
247924_at	Expressed protein	---	AT5G57655	-1.05	-0.07	-0.29	0.78380168	0.9388	-6.63
253318_at	extensin-like protein extensin-like	---	AT4G33970	-1.02	-0.03	-0.29	0.78388292	0.9388	-6.63
257938_at	cell elongation protein, Dwarf1 ide	DWF1	AT3G19820	1.10	0.14	0.28	0.78430441	0.9388	-6.63
262198_at	pectin methylesterase (PMEU1), p	ATPME2	AT1G53830	-1.08	-0.10	-0.28	0.7842728	0.9388	-6.63
262224_at	hypothetical protein contains Pfam	OTP43	AT1G74900	1.02	0.03	0.29	0.78403092	0.9388	-6.63
265648_at	putative beta-1,3-glucanase ;supp	---	AT2G27500	1.05	0.07	0.28	0.78433842	0.9388	-6.63
248121_at	putative protein contains similarity	GAUT12	AT5G54690	-1.03	-0.05	-0.28	0.7843165	0.9388	-6.63
264865_at	DNAJ-like heatshock protein simila	ARL1	AT1G24120	1.02	0.03	0.29	0.78405344	0.9388	-6.63
255145_at	hypothetical protein	---	---	-1.03	-0.04	-0.28	0.78424933	0.9388	-6.63
263812_at	putative replication protein A1	---	---	-1.02	-0.03	-0.28	0.78427139	0.9388	-6.63
265690_at	hypothetical protein predicted by g	---	AT2G24320	-1.03	-0.04	-0.28	0.78434519	0.9388	-6.63
261345_at	hypothetical protein predicted by g	DTA4	AT1G79760	1.03	0.04	0.28	0.78429704	0.9388	-6.63
246661_at	putative protein various predicted	---	---	1.02	0.03	0.28	0.78439878	0.9388	-6.63
254366_s_at	LTR retrotransposon like protein r	---	---	1.02	0.03	0.28	0.78434919	0.9388	-6.63
264358_at	hypothetical protein predicted by g	---	AT1G03180	-1.03	-0.04	-0.28	0.78442924	0.9388	-6.63
260995_at	unknown protein	---	AT1G12120	-1.02	-0.03	-0.28	0.78463535	0.9389	-6.63
251389_at	putative protein	---	AT3G60850	-1.02	-0.03	-0.28	0.78462661	0.9389	-6.63
258761_at	unknown protein	---	AT3G10760	-1.04	-0.05	-0.28	0.7846167	0.9389	-6.63
246250_at	cysteine proteinase similar to cyste	CP1	AT4G36880	-1.13	-0.17	-0.28	0.78473999	0.9390	-6.63
252116_at	putative protein ;supported by full-	---	AT3G51510	1.03	0.04	0.28	0.784814	0.9390	-6.63
246504_at	hypothetical protein ;supported by	---	AT5G16160	-1.02	-0.03	-0.28	0.78489638	0.9390	-6.63
262032_at	biotin holocarboxylase synthetase	HCS2	AT1G37150	-1.02	-0.03	-0.28	0.78481867	0.9390	-6.63
256208_at	hypothetical protein predicted by g	---	AT1G50930	-1.02	-0.02	-0.28	0.78488033	0.9390	-6.63
259120_at	unknown protein	---	AT3G02240	1.15	0.20	0.28	0.78498476	0.9390	-6.63
260170_at	putative sucrose transport protein	SUC5	AT1G71890	-1.03	-0.05	-0.28	0.78507821	0.9391	-6.63
245765_at	hypothetical protein similar to puta	---	AT1G33600	1.08	0.11	0.28	0.78516331	0.9391	-6.63
253256_at	putative protein endothelin conver	---	AT4G34360	1.03	0.04	0.28	0.78516443	0.9391	-6.63
258404_at	ribosomal protein L3	RPL3P	AT3G17465	1.03	0.04	0.28	0.78522702	0.9391	-6.63
262436_at	En/Spm-like transposon protein, p	---	AT1G47610	1.04	0.06	0.28	0.78526509	0.9391	-6.63

246145_at	peroxidase peroxidase, Lycopersi	---	AT5G19880	-1.07	-0.09	-0.28	0.78531072	0.9391	-6.63
247767_at	putative protein various predicted	AGL82	AT5G58890	-1.02	-0.03	-0.28	0.78558268	0.9394	-6.63
255367_at	putative transposon protein	---	---	-1.02	-0.03	-0.28	0.78569551	0.9395	-6.63
266279_at	putative tropinone reductase	---	AT2G29290	1.03	0.04	0.28	0.78627458	0.9395	-6.63
265347_at	similar to mammalian MHC III regi	SUVH6	AT2G22740	1.02	0.03	0.28	0.78614947	0.9395	-6.63
256620_at	disease resistance protein, putativ	---	AT3G24480	-1.04	-0.06	-0.28	0.78619438	0.9395	-6.63
245103_at	putative Ta11-like non-LTR retroel	---	AT2G41590	-1.02	-0.03	-0.28	0.78600004	0.9395	-6.63
257833_at	transcriptional regulator protein, p	LWD2	AT3G26640	1.02	0.03	0.28	0.78619687	0.9395	-6.63
259847_at	unknown protein	---	AT1G72170	1.03	0.04	0.28	0.78612468	0.9395	-6.63
253887_at	putative protein isp4 protein, Schi	OPT6	AT4G27730	1.06	0.08	0.28	0.78601443	0.9395	-6.63
267247_at	hypothetical protein predicted by g	---	AT2G30170	1.03	0.04	0.28	0.78618211	0.9395	-6.63
257819_at	Expressed protein ; supported by f	RALFL25	AT3G25165	-1.02	-0.03	-0.28	0.78618083	0.9395	-6.63
249851_at	MADS-box transcription factor-like	TT16	AT5G23260	-1.02	-0.02	-0.28	0.78626264	0.9395	-6.63
260926_at	unknown protein	GLTP2	AT1G21360	-1.02	-0.03	-0.28	0.78581325	0.9395	-6.63
252630_at	putative protein	---	AT3G44980	1.02	0.03	0.28	0.78587725	0.9395	-6.63
249646_at	SEN1-like protein SEN1 - Saccha	---	AT5G37030	1.02	0.03	0.28	0.78618436	0.9395	-6.63
265140_at	F-box protein family, AtFBX11 cor	---	AT1G51320	1.02	0.03	0.28	0.78643791	0.9397	-6.63
247215_at	Expressed protein ; supported by f	PROPEP3	AT5G64905	1.14	0.18	0.28	0.78648337	0.9397	-6.63
256675_at	putative protein DNA-binding prot	---	AT3G52170	1.04	0.06	0.28	0.78654987	0.9397	-6.63
267047_at	putative selenium-binding protein	---	AT2G34370	-1.02	-0.03	-0.28	0.78664399	0.9398	-6.63
265313_at	unknown protein	---	AT2G20210	-1.03	-0.04	-0.28	0.7867171	0.9398	-6.63
249856_at	serine carboxypeptidase	scpl47	AT5G22980	-1.04	-0.05	-0.28	0.78688422	0.9399	-6.63
257740_at	hypothetical protein predicted by g	---	AT3G27330	-1.02	-0.02	-0.28	0.78685736	0.9399	-6.63
264869_at	hypothetical protein similar to hypo	---	AT1G24350	-1.02	-0.03	-0.28	0.78696183	0.9400	-6.63
254710_at	multidrug resistance protein/P-gly	PGP9	AT4G18050	-1.04	-0.06	-0.28	0.78705578	0.9400	-6.63
250615_at	putative protein ankyrins - different	---	AT5G07270	-1.03	-0.04	-0.28	0.78732643	0.9403	-6.63
252154_at	putative DNA-3-methyladenine gly	---	AT3G50880	1.03	0.05	0.28	0.78742757	0.9404	-6.63
264763_at	hypothetical protein contains simila	---	AT1G61450	-1.02	-0.03	-0.28	0.78750406	0.9404	-6.63
262704_at	hypothetical protein predicted by g	ASL9	AT1G16530	-1.05	-0.07	-0.28	0.78755829	0.9404	-6.63
255571_at	hypothetical protein ; supported by	---	AT4G01220	-1.04	-0.05	-0.28	0.78809561	0.9406	-6.63
259436_at	hypothetical protein predicted by g	---	AT1G01500	-1.02	-0.03	-0.28	0.78786548	0.9406	-6.63
247892_at	putative protein contains similarity	---	AT5G57970	-1.04	-0.05	-0.28	0.78826899	0.9406	-6.63
246507_at	lipase-like protein monoglyceride l	---	AT5G16120	1.04	0.05	0.28	0.78810634	0.9406	-6.63
258344_at	hypothetical protein similar to hypo	CEG	AT3G22650	-1.02	-0.03	-0.28	0.78823465	0.9406	-6.63
246862_at	E2, ubiquitin-conjugating enzyme,	PEX4	AT5G25760	1.02	0.03	0.28	0.7879716	0.9406	-6.63

249297_at	unknown protein	---	AT5G41320	1.02	0.03	0.28	0.7880686	0.9406	-6.63
263213_at	unknown protein Strong similarity t	---	AT1G30560	-1.03	-0.04	-0.28	0.78801984	0.9406	-6.63
249590_at	putative protein SIAH1, Brassica r	---	AT5G37870	1.02	0.03	0.28	0.78813703	0.9406	-6.63
251061_at	putative protein hypothetical prote	---	AT5G01830	-1.06	-0.08	-0.28	0.78826425	0.9406	-6.63
252703_at	leucine-rich repeat protein LRP -li	---	AT3G43740	-1.02	-0.03	-0.28	0.78828552	0.9406	-6.63
265746_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.28	0.78790001	0.9406	-6.63
246966_at	DNA photolyase - like protein DNA	CRY3	AT5G24850	1.03	0.05	0.28	0.78774584	0.9406	-6.63
246160_at	putative protein predicted protein,	FBX2	AT5G21040	1.02	0.03	0.28	0.78808221	0.9406	-6.63
259122_at	unknown protein similar to putativ	COBL1	AT3G02210	-1.03	-0.04	-0.28	0.78783578	0.9406	-6.63
246748_at	putative protein predicted protein,	---	AT5G27730	-1.02	-0.03	-0.28	0.7885002	0.9408	-6.63
251209_at	putative protein several hypothetic	---	AT3G62890	1.03	0.04	0.28	0.78865047	0.9409	-6.63
249065_at	putative protein similar to unknown	---	AT5G44260	-1.04	-0.06	-0.28	0.78894801	0.9410	-6.63
250777_at	putative protein similar to unknown	---	AT5G05440	1.10	0.13	0.28	0.78895981	0.9410	-6.63
252716_at	putative protein CAF protein, Arab	DCL3	AT3G43920	1.03	0.04	0.28	0.78880883	0.9410	-6.63
250756_at	putative protein strong similarity to	ROPGEF5	AT5G05940	-1.02	-0.03	-0.28	0.78895775	0.9410	-6.63
248051_at	Atmyb103 (gb|AAD40692.1)	ATMYB103	AT5G56110	1.02	0.03	0.28	0.78898827	0.9410	-6.63
262950_at	transcription initiation factor, putat	---	AT1G75510	1.02	0.03	0.28	0.78881345	0.9410	-6.63
263652_at	unknown protein EST gb|H76414 c	---	AT1G04330	-1.02	-0.03	-0.28	0.78885655	0.9410	-6.63
246325_at	hypothetical protein contains simila	ABA3	AT1G16540	-1.06	-0.08	-0.28	0.78903501	0.9410	-6.63
257816_at	glycosyl transferase, putative cont	QUA1	AT3G25140	1.02	0.04	0.28	0.78923228	0.9410	-6.63
247659_at	DNA-directed RNA polymerase - I	NRPC1	AT5G60040	1.06	0.08	0.28	0.78949716	0.9410	-6.63
248357_at	putative protein similar to unknown	---	AT5G52380	-1.05	-0.06	-0.28	0.78917088	0.9410	-6.63
262716_at	multicatalytic endopeptidase ident	PAB1	AT1G16470	1.03	0.04	0.28	0.78946821	0.9410	-6.63
259169_at	unknown protein similar to unknow	---	AT3G03520	-1.07	-0.10	-0.28	0.78947294	0.9410	-6.63
251585_at	putative protein hypothetical prote	---	AT3G58630	-1.04	-0.06	-0.28	0.78943594	0.9410	-6.63
252149_at	putative protein hypothetical prote	---	AT3G51290	-1.02	-0.03	-0.28	0.78935828	0.9410	-6.63
247515_at	ABC family transporter - like prote	ATH14	AT5G61740	-1.02	-0.03	-0.28	0.78915775	0.9410	-6.63
253491_at	RNA lariat debranching enzyme -	---	AT4G31770	-1.04	-0.06	-0.28	0.78924952	0.9410	-6.63
264385_at	unknown protein	---	AT1G12020	-1.04	-0.05	-0.28	0.78931134	0.9410	-6.63
265546_at	putative proline/hydroxyproline-rich	---	AT2G28240	-1.02	-0.03	-0.28	0.7894112	0.9410	-6.63
247057_at	SCARECROW gene regulator	---	AT5G66770	1.06	0.09	0.28	0.78961643	0.9411	-6.63
251923_at	reductase-like protein abscisic aci	---	AT3G53880	-1.05	-0.07	-0.28	0.78984266	0.9413	-6.63
254679_at	putative protein Mei2-like protein,	AML3	AT4G18120	-1.02	-0.03	-0.28	0.79000024	0.9414	-6.63
253987_at	pyrophosphate-dependent phosph	PFK3	AT4G26270	-1.05	-0.07	-0.28	0.79046669	0.9415	-6.63
260239_at	putative receptor protein kinase si	---	AT1G74360	1.11	0.15	0.28	0.79059801	0.9415	-6.63

246308_at	chlorophyll synthetase ; supported	G4	AT3G51820	-1.03	-0.04	-0.28	0.7907729	0.9415	-6.63
252473_s_at	hypothetical protein several hypoth	---	AT3G46610	1.03	0.05	0.28	0.79068198	0.9415	-6.63
254421_at	VP1 like protein transcription activ	VAL3	AT4G21550	-1.03	-0.05	-0.28	0.79077	0.9415	-6.63
249711_at	putative protein contains similarity	---	AT5G35680	-1.03	-0.04	-0.28	0.79051338	0.9415	-6.63
258615_at	putative aspartyl protease contains	---	AT3G02740	1.03	0.04	0.28	0.79091459	0.9415	-6.63
250255_at	sigma-like factor (gb|AAC97954.1)	SIG4	AT5G13730	1.05	0.06	0.28	0.79042077	0.9415	-6.63
250713_at	putative protein similar to unknown	---	AT5G06130	-1.02	-0.03	-0.28	0.79091975	0.9415	-6.63
249771_at	receptor-like protein kinase ; supp	---	AT5G24080	1.04	0.05	0.28	0.79021413	0.9415	-6.63
264767_at	hypothetical protein similar to puta	SD1-29	AT1G61380	1.06	0.08	0.28	0.79089975	0.9415	-6.63
264111_at	hypothetical protein predicted by g	---	AT2G13690	1.02	0.03	0.28	0.79019731	0.9415	-6.63
265085_at	hypothetical protein predicted by g	TPX2	AT1G03780	1.03	0.05	0.28	0.79051318	0.9415	-6.63
264603_at	hypothetical protein predicted by g	---	AT1G04670	1.02	0.03	0.28	0.79027557	0.9415	-6.63
252518_at	receptor-like protein kinase homol	---	AT3G46350	1.02	0.03	0.28	0.79093651	0.9415	-6.63
251097_at	receptor like protein kinase recept	LECRKA4.3	AT5G01560	-1.09	-0.12	-0.28	0.79096713	0.9415	-6.63
262543_at	Expressed protein ; supported by f	---	AT1G34245	-1.02	-0.04	-0.28	0.79047057	0.9415	-6.63
251005_at	putative protein various predicted	---	AT5G02590	-1.06	-0.09	-0.28	0.79018289	0.9415	-6.63
261382_at	hypothetical protein contains simila	CVP2	AT1G05470	1.03	0.04	0.28	0.7908102	0.9415	-6.63
262564_at	anionic peroxidase, putative simila	---	AT1G34330	-1.02	-0.03	-0.28	0.79060577	0.9415	-6.63
265811_at	unknown protein possibly related t	EDA2	AT2G18080	-1.02	-0.03	-0.28	0.79065687	0.9415	-6.63
250086_at	NAM (no apical meristem)-like prot	anac086	AT5G17260	1.02	0.03	0.28	0.79024184	0.9415	-6.63
245588_at	putative protein	---	AT4G15030	1.03	0.05	0.28	0.79041764	0.9415	-6.63
260622_at	hypothetical protein predicted by g	NF-YC10	AT1G07980	1.02	0.03	0.28	0.7913443	0.9417	-6.63
252416_at	chromosome assembly protein ho	ATSMC2	AT3G47460	1.02	0.02	0.28	0.79127193	0.9417	-6.63
245417_at	phosphoribosylglycinamide formylt	---	AT4G17360	-1.04	-0.05	-0.28	0.7913792	0.9417	-6.63
249652_at	putative protein hypothetical protei	---	AT5G37070	-1.03	-0.04	-0.28	0.79137462	0.9417	-6.63
252607_at	xyloglucan endo-transglycosylase	XTR8	AT3G44990	-1.04	-0.06	-0.28	0.79155181	0.9419	-6.63
260832_at	unknown protein ; supported by cD	GAUT6	AT1G06780	-1.02	-0.04	-0.27	0.79159475	0.9419	-6.63
246263_at	unknown protein	---	AT1G31780	1.03	0.04	0.27	0.79169903	0.9420	-6.63
265514_s_at	Mutator-like transposase similar to	---	---	1.02	0.03	0.27	0.79178381	0.9420	-6.63
253755_at	26S proteasome subunit 4-like pro	RPT2a	AT4G29040	-1.02	-0.03	-0.27	0.79202873	0.9422	-6.63
263346_at	En/Spm-like transposon protein rel	---	---	-1.02	-0.03	-0.27	0.79204058	0.9422	-6.63
263064_at	putative bZIP transcription factor c	CPuORF1	AT2G18160	-1.03	-0.04	-0.27	0.79213325	0.9423	-6.63
259614_at	dioxygenase, putative similar to di	ATGA2OX4	AT1G47990	-1.02	-0.03	-0.27	0.79227971	0.9423	-6.63
261297_at	hypothetical protein predicted by g	JAZ4	AT1G48500	-1.02	-0.03	-0.27	0.79226334	0.9423	-6.63
261173_at	hypothetical protein predicted by g	---	AT1G04830	1.02	0.03	0.27	0.79220309	0.9423	-6.63

249880_at	putative protein similar to unknown	---	AT5G23180	1.02	0.03	0.27	0.79232363	0.9423	-6.63
245022_at	PSII L protein	---	---	1.03	0.05	0.27	0.79248065	0.9425	-6.63
246408_at	hypothetical protein predicted by g	---	AT1G57680	-1.03	-0.04	-0.27	0.79260122	0.9425	-6.63
244988_s_at	ribosomal protein L23	---	---	1.03	0.04	0.27	0.79257428	0.9425	-6.63
266292_at	putative tropinone reductase ;supp	SAG13	AT2G29350	1.15	0.20	0.27	0.79272828	0.9426	-6.63
251511_at	putative protein several hypothetic	---	AT3G59180	-1.02	-0.03	-0.27	0.7928201	0.9427	-6.63
252231_at	hypothetical protein ;supported by	---	AT3G49720	-1.03	-0.04	-0.27	0.79346708	0.9428	-6.63
261551_at	ATP dependent copper transporte	HMA5	AT1G63440	1.02	0.03	0.27	0.7934542	0.9428	-6.63
244942_at	hypothetical protein	---	---	-1.02	-0.03	-0.27	0.79335829	0.9428	-6.63
263757_at	cysteine proteinase similar to cyst	---	AT2G21430	1.04	0.05	0.27	0.79315667	0.9428	-6.63
257702_at	CTP-synthetase, putative similar t	emb2742	AT3G12670	-1.03	-0.04	-0.27	0.7932656	0.9428	-6.63
252636_at	putative protein triacylglycerol lipa	---	AT3G44510	1.02	0.03	0.27	0.79349065	0.9428	-6.63
251210_at	hypothetical protein ;supported by	---	AT3G62810	-1.03	-0.04	-0.27	0.79351422	0.9428	-6.63
252801_at	putative protein various predicted	---	---	-1.02	-0.03	-0.27	0.79327459	0.9428	-6.63
258346_at	hypothetical protein predicted by g	---	AT3G22690	-1.02	-0.04	-0.27	0.793268	0.9428	-6.63
267444_at	hypothetical protein predicted by g	---	AT2G19180	1.03	0.04	0.27	0.79345034	0.9428	-6.63
253666_at	xyloglucan endo-1,4-beta-D-gluca	MERI5B	AT4G30270	1.02	0.03	0.27	0.79329812	0.9428	-6.63
251002_at	putative protein predicted proteins	---	AT5G02680	1.02	0.03	0.27	0.79325044	0.9428	-6.63
261716_at	kinesin-related protein, putative si	---	AT1G18410	-1.02	-0.03	-0.27	0.79305106	0.9428	-6.63
254519_at	putative protein W15DMY30S	---	AT4G19940	-1.03	-0.04	-0.27	0.79322589	0.9428	-6.63
254103_at	putative protein ;supported by full-	---	AT4G25030	-1.06	-0.08	-0.27	0.79356229	0.9428	-6.63
266854_at	putative C2H2-type zinc finger prot	---	AT2G26940	-1.03	-0.04	-0.27	0.79366855	0.9428	-6.63
260608_at	putative polygalacturonase	---	AT2G43870	-1.19	-0.25	-0.27	0.79364568	0.9428	-6.63
246906_at	Expressed protein ; supported by f	---	AT5G25475	1.02	0.03	0.27	0.79375232	0.9429	-6.63
263420_at	unknown protein ; supported by fu	---	AT2G17240	1.02	0.03	0.27	0.79381661	0.9429	-6.63
246382_at	hypothetical protein	---	---	-1.03	-0.04	-0.27	0.79395366	0.9429	-6.63
265072_at	hypothetical protein predicted by g	LAS	AT1G55580	-1.03	-0.04	-0.27	0.79392867	0.9429	-6.63
263107_at	putative cytochrome P450	CYP705A6	AT2G05180	-1.02	-0.03	-0.27	0.79392202	0.9429	-6.63
251753_at	putative protein predicted protein,	---	AT3G55760	1.05	0.08	0.27	0.79410498	0.9430	-6.63
253724_at	Expressed protein ; supported by f	LCR24	AT4G29285	-1.02	-0.03	-0.27	0.79407976	0.9430	-6.63
265780_at	Mutator-like transposase similar to	---	---	-1.02	-0.03	-0.27	0.79424546	0.9431	-6.63
257322_at	hypothetical protein	AT2G0766	---	-1.02	-0.03	-0.27	0.79425172	0.9431	-6.63
253995_at	Col-0 casein kinase I-like protein ;	CK1	AT4G26100	-1.03	-0.04	-0.27	0.79435254	0.9432	-6.63
261822_at	unknown protein ;supported by full	---	AT1G11380	-1.04	-0.06	-0.27	0.79463192	0.9434	-6.63
261212_at	hypothetical protein predicted by g	atnudt12	AT1G12880	-1.03	-0.05	-0.27	0.79469179	0.9434	-6.63

250053_at	potassium-dependent sodium-calc	---	AT5G17850	-1.03	-0.04	-0.27	0.79469755	0.9434	-6.63
264085_at	putative glutamyl tRNA reductase	HEMA3	AT2G31250	-1.02	-0.03	-0.27	0.79482135	0.9435	-6.63
254101_at	alpha-amylase - like protein alpha	AMY1	AT4G25000	-1.07	-0.09	-0.27	0.79488232	0.9435	-6.63
267326_at	putative RNA-binding protein	---	AT2G19380	-1.02	-0.03	-0.27	0.79494763	0.9435	-6.63
263276_at	putative cytochrome P450	CYP705A1	AT2G14100	1.02	0.03	0.27	0.79494423	0.9435	-6.63
262606_at	hypothetical protein predicted by g	---	AT1G15190	-1.03	-0.04	-0.27	0.79505408	0.9436	-6.63
249743_at	beta-glucosidase	BGLU31	AT5G24540	-1.13	-0.18	-0.27	0.79509158	0.9436	-6.63
265516_at	putative Athila retroelement ORF1	---	---	-1.02	-0.03	-0.27	0.79513193	0.9436	-6.63
253748_at	putative protein RNA-binding prote	---	AT4G28990	-1.03	-0.04	-0.27	0.79517481	0.9436	-6.63
252412_at	Expressed protein ; supported by f	---	AT3G47295	-1.04	-0.06	-0.27	0.79530966	0.9437	-6.63
249340_at	putative protein contains similarity	---	AT5G41140	-1.03	-0.04	-0.27	0.79545518	0.9438	-6.63
245447_at	triacylglycerol lipase like protein	---	AT4G16820	-1.07	-0.10	-0.27	0.79543847	0.9438	-6.63
257353_at	hypothetical protein predicted by g	NPY4	AT2G23050	1.02	0.03	0.27	0.79562911	0.9439	-6.63
254260_at	hypothetical protein	---	AT4G23440	-1.03	-0.05	-0.27	0.79574338	0.9440	-6.63
256301_at	unknown protein ;supported by full	---	AT1G69510	1.02	0.03	0.27	0.79586453	0.9441	-6.63
246471_s_at	putative protein predicted proteins	---	AT5G17100 /	1.02	0.03	0.27	0.79586205	0.9441	-6.63
258087_at	putative peroxiredoxin similar to pe	ATPRX Q	AT3G26060	1.03	0.05	0.27	0.7960728	0.9442	-6.63
261216_at	catechol O-methyltransferase, put	---	AT1G33030	-1.07	-0.10	-0.27	0.79602719	0.9442	-6.63
264123_at	unknown protein ; supported by cD	---	AT1G02270	-1.02	-0.04	-0.27	0.79606274	0.9442	-6.63
246955_at	calcium-dependent protein kinase	CPK1	AT5G04870	1.05	0.08	0.27	0.79616472	0.9442	-6.63
255409_at	NDX1 homeobox protein homolog	---	AT4G03090	-1.02	-0.02	-0.27	0.79623897	0.9443	-6.63
266753_at	auxin-induced protein (IAA20) iden	IAA20	AT2G46990	-1.02	-0.03	-0.27	0.79632387	0.9443	-6.63
257767_at	hypothetical protein predicted by g	---	AT3G23040	1.03	0.04	0.27	0.79640995	0.9444	-6.63
263199_at	hypothetical protein Similar to hex	HEXO2	AT1G05590	1.03	0.04	0.27	0.79653814	0.9444	-6.63
247009_at	unknown protein ;supported by ful	---	AT5G67600	1.04	0.06	0.27	0.79652221	0.9444	-6.63
251575_at	putative protein basic leucine zipp	BZIP61	AT3G58120	1.06	0.09	0.27	0.79666181	0.9445	-6.63
256677_at	unknown protein contains Pfam pr	PHF1	AT3G52190	-1.02	-0.04	-0.27	0.79677468	0.9445	-6.63
246793_at	putative protein seven transmemb	---	AT5G27210	1.02	0.03	0.27	0.7967285	0.9445	-6.63
253864_at	hypothetical protein	---	AT4G27460	1.03	0.04	0.27	0.79679987	0.9445	-6.63
253197_at	putative protein Cyanophora para	---	AT4G35250	1.03	0.05	0.27	0.79704002	0.9446	-6.63
248916_at	receptor protein kinase-like protein	---	AT5G45840	-1.05	-0.07	-0.27	0.7970457	0.9446	-6.63
263368_at	putative protein kinase contains a	---	AT2G20470	-1.03	-0.04	-0.27	0.79692691	0.9446	-6.63
245004_at	hypothetical protein	---	---	1.03	0.04	0.27	0.79701443	0.9446	-6.63
244949_at	hypothetical protein	---	---	-1.02	-0.03	-0.27	0.79714917	0.9447	-6.63
266148_x_at	En/Spm-like transposon protein rel	---	---	-1.02	-0.04	-0.27	0.79713176	0.9447	-6.63

258225_at	unknown protein ; supported by cl	---	AT3G15630	1.05	0.08	0.27	0.79868182	0.9447	-6.63
261025_at	Expressed protein ; supported by f	---	AT1G01225	1.04	0.06	0.27	0.79843928	0.9447	-6.63
259675_at	unknown protein similar to hypothe	---	AT1G77710	1.02	0.03	0.26	0.79917834	0.9447	-6.63
256117_at	unknown protein ; supported by cD	---	AT1G16840	1.02	0.03	0.27	0.79890638	0.9447	-6.63
255557_at	hypothetical protein ; supported by	---	AT4G01990	1.03	0.05	0.26	0.79929828	0.9447	-6.63
254087_at	brefeldin A-sensitive Golgi protein	---	AT4G24840	-1.02	-0.03	-0.26	0.79967781	0.9447	-6.63
250858_at	I-box binding factor - like protein I-	---	AT5G04760	1.03	0.05	0.26	0.79989314	0.9447	-6.63
249028_at	DNA-damage-inducible protein P	POLH	AT5G44740	1.03	0.04	0.27	0.79759858	0.9447	-6.63
255607_at	putative acetyltransferase similar t	---	AT4G01130	-1.04	-0.05	-0.26	0.79936666	0.9447	-6.63
256978_at	phosphoribosyamidoimidazole-su	PUR7	AT3G21110	-1.04	-0.06	-0.26	0.79992801	0.9447	-6.63
265284_at	unknown protein ;supported by ful	---	AT2G20230	1.02	0.03	0.26	0.79958042	0.9447	-6.63
261178_at	synaptobrevin 7B, putative similar	ATVAMP72	AT1G04760	1.02	0.03	0.26	0.79901709	0.9447	-6.63
246192_at	translation initiation factor eIF-2 be	EIF2 BETA	AT5G20920	-1.02	-0.03	-0.26	0.79995091	0.9447	-6.63
263326_at	unknown protein ; supported by cl	---	AT2G04280	1.03	0.04	0.26	0.79958683	0.9447	-6.63
248010_at	peroxisomal targeting signal type 1	PEX5	AT5G56290	-1.02	-0.03	-0.26	0.80000525	0.9447	-6.63
246460_at	cellulose synthase catalytic subun	CSLD2	AT5G16910	-1.04	-0.05	-0.26	0.79909061	0.9447	-6.63
263042_at	conserved hypothetical protein pro	---	AT1G23340	-1.02	-0.03	-0.27	0.79837331	0.9447	-6.63
266915_at	hypothetical protein predicted by g	---	AT2G45870	-1.02	-0.03	-0.27	0.79862783	0.9447	-6.63
260630_at	subtilisin-like serine protease conta	ALE1	AT1G62340	-1.03	-0.04	-0.27	0.79763319	0.9447	-6.63
248458_at	putative protein contains similarity	EYE	AT5G51430	1.02	0.03	0.26	0.80008327	0.9447	-6.63
252101_at	rac-like GTP binding protein Arac1	ROP1	AT3G51300	1.02	0.03	0.26	0.7990276	0.9447	-6.63
254157_at	putative protein protein induced u	VEP1	AT4G24220	-1.02	-0.03	-0.27	0.79725401	0.9447	-6.63
256020_at	glutamyl-tRNA reductase, putative	HEMA1	AT1G58290	1.03	0.05	0.26	0.79912733	0.9447	-6.63
259079_at	unknown protein	---	AT3G04950	1.03	0.04	0.27	0.79814124	0.9447	-6.63
267327_at	putative protein kinase contains a	---	AT2G19410	1.02	0.03	0.26	0.79939709	0.9447	-6.63
267292_at	hypothetical protein predicted by g	---	AT2G23740	-1.02	-0.03	-0.27	0.79869717	0.9447	-6.63
261114_at	bZIP transcription factor ATB2, pu	AtbZIP44	AT1G75388	1.13	0.18	0.27	0.79843644	0.9447	-6.63
265343_at	unknown protein ; supported by ful	NIC1	AT2G22570	1.04	0.06	0.26	0.79970554	0.9447	-6.63
257404_at	hypothetical protein predicted by g	SUVR1	AT1G04050	1.02	0.03	0.27	0.79761631	0.9447	-6.63
245225_at	mitochondrial protein-like; contains	---	AT3G29800	-1.03	-0.04	-0.26	0.7997966	0.9447	-6.63
260079_s_at	helix-loop-helix protein 1A, putativ	---	AT1G35460	1.02	0.03	0.27	0.79738163	0.9447	-6.63
247923_at	porin-like protein ;supported by ful	VDAC4	AT5G57490	-1.02	-0.03	-0.26	0.79935722	0.9447	-6.63
248686_at	33 kDa secretory protein-like ; sup	---	AT5G48540	-1.08	-0.11	-0.27	0.79842654	0.9447	-6.63
254517_at	putative protein conserved hypoth	---	AT4G20310	-1.02	-0.03	-0.27	0.79779373	0.9447	-6.63
249511_at	putative protein contains similarity	---	AT5G38500	-1.02	-0.03	-0.26	0.79958853	0.9447	-6.63

256448_s_at	unknown protein	MED21	AT4G04780 /	-1.02	-0.03	-0.27	0.79742902	0.9447	-6.63
261026_at	hypothetical protein predicted by g	---	AT1G01240	1.03	0.04	0.26	0.79938834	0.9447	-6.63
249712_at	eIF4Eiso protein (emb|CAA71579.	LSP1	AT5G35620	-1.03	-0.04	-0.27	0.79886277	0.9447	-6.63
245363_at	hypothetical protein ;supported by	---	AT4G15120	-1.07	-0.10	-0.26	0.80003786	0.9447	-6.63
247319_at	glutamate-tRNA ligase ; supported	ERS	AT5G64050	1.02	0.03	0.26	0.7992337	0.9447	-6.63
264896_at	Hypothetical protein similar to end	AtGH9B6	AT1G23210	-1.02	-0.03	-0.26	0.79965646	0.9447	-6.63
266644_at	unknown protein ;supported by ful	---	AT2G29660	1.03	0.04	0.27	0.79883266	0.9447	-6.63
267032_at	putative protein kinase contains a	CIPK22	AT2G38490	-1.03	-0.05	-0.27	0.79832677	0.9447	-6.63
266354_at	putative homeodomain transcriptio	PFS2	AT2G01500	-1.02	-0.03	-0.26	0.7992002	0.9447	-6.63
264194_at	putative wall-associated kinase co	---	AT1G22720	-1.02	-0.03	-0.27	0.79856252	0.9447	-6.63
265859_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.27	0.79843916	0.9447	-6.63
256775_at	hypothetical protein predicted by g	---	AT3G13770	1.03	0.05	0.26	0.8000916	0.9447	-6.63
265526_x_at	putative Athila retroelement ORF1	---	---	1.02	0.02	0.26	0.8000193	0.9447	-6.63
247490_at	LFY floral meristem identity contro	LFY	AT5G61850	1.02	0.03	0.26	0.7989725	0.9447	-6.63
255189_at	hypothetical protein	---	AT4G07350	1.02	0.03	0.26	0.80002304	0.9447	-6.63
251253_at	putative zinc-finger protein zinc-fir	---	AT3G62240	-1.03	-0.05	-0.26	0.799401	0.9447	-6.63
247931_at	putative protein similar to unknown	---	AT5G57040	1.03	0.04	0.26	0.80009523	0.9447	-6.63
265757_x_at	putative PttA2-like transposon prot	---	---	1.03	0.04	0.27	0.7975059	0.9447	-6.63
255945_at	putative protein	---	AT5G28610	-1.03	-0.04	-0.27	0.79796824	0.9447	-6.63
263230_at	putative indole-3-acetate beta-gluc	---	AT1G05670	-1.04	-0.06	-0.27	0.79777588	0.9447	-6.63
267394_s_at	putative cellulase	AtGH9B9	AT2G44540 /	1.02	0.03	0.26	0.79998571	0.9447	-6.63
257316_at	hypothetical protein predicted by g	---	---	1.02	0.03	0.27	0.79837543	0.9447	-6.63
260181_at	endo-1,4-beta-glucanase identical	ATGH9B1	AT1G70710	1.05	0.07	0.27	0.79859582	0.9447	-6.63
256129_at	calcium-binding protein, putative s	---	AT1G18210	-1.04	-0.06	-0.27	0.797907	0.9447	-6.63
265456_at	Expressed protein ; supported by f	SDH4	AT2G46505	1.02	0.03	0.27	0.79788047	0.9447	-6.63
255793_at	Expressed protein ; supported by c	---	AT2G33250	-1.03	-0.04	-0.26	0.79995758	0.9447	-6.63
258711_at	ubiquitin-like protein (UBQ8) ident	UBQ8	AT3G09790	-1.02	-0.03	-0.26	0.80000535	0.9447	-6.63
259636_at	RNA pseudouridylate synthase, p	---	AT1G56345	-1.04	-0.06	-0.27	0.79875549	0.9447	-6.63
267103_at	putative UDP-N-acetylglucosamine	GPT	AT2G41490	1.02	0.03	0.27	0.79815872	0.9447	-6.63
266597_at	putative WRKY-type DNA binding	WRKY43	AT2G46130	1.02	0.02	0.27	0.79770894	0.9447	-6.63
255807_at	probable wound-induced protein v	---	AT4G10270	-1.02	-0.02	-0.26	0.80008824	0.9447	-6.63
261485_at	unknown protein ;supported by full	UTR3	AT1G14360	1.06	0.08	0.26	0.79947047	0.9447	-6.63
245955_at	hypothetical protein	BGLU24	AT5G28510	1.02	0.03	0.27	0.79814197	0.9447	-6.63
252603_at	putative protein	---	AT3G45050	1.03	0.04	0.27	0.79778498	0.9447	-6.63
266706_at	hypothetical protein predicted by g	---	AT2G03320	-1.02	-0.03	-0.27	0.79721307	0.9447	-6.63

258839_at	unknown protein ; supported by cl	---	AT3G07170	1.02	0.03	0.26	0.79895907	0.9447	-6.63
256402_at	hypothetical protein ; supported by	---	AT3G06130	-1.05	-0.06	-0.26	0.80026927	0.9447	-6.63
248429_at	putative protein contains similarity	---	AT5G51770	-1.04	-0.06	-0.26	0.80028116	0.9447	-6.63
248131_at	unknown protein	---	AT5G54830	1.04	0.06	0.26	0.80021942	0.9447	-6.63
267002_s_at	putative photosystem II type I chlo	LHB1B1	AT2G34420	1.02	0.02	0.26	0.80029557	0.9447	-6.63
259851_at	kinesin, putative	---	AT1G72250	1.02	0.03	0.26	0.80041311	0.9447	-6.63
250638_at	glycine-rich protein atGRP-6	GRP16	AT5G07540	-1.03	-0.04	-0.26	0.80038564	0.9447	-6.63
252091_at	putative protein NADH dehydroge	---	AT3G51390	1.02	0.03	0.26	0.80042954	0.9447	-6.63
263906_at	plastid division protein (FtsZ) ident	FTSZ2-1	AT2G36250	1.02	0.03	0.26	0.80049509	0.9448	-6.63
245947_at	spermine synthase (ACL5) ;suppo	ACL5	AT5G19530	-1.04	-0.05	-0.26	0.80059729	0.9448	-6.63
252898_at	cytochrome P450 -like protein sim	CYP96A11	AT4G39500	1.02	0.03	0.26	0.80060976	0.9448	-6.63
265186_at	Expressed protein ; supported by f	---	AT1G23560	-1.03	-0.04	-0.26	0.80083099	0.9450	-6.63
252837_at	putative protein hypothetical protei	---	---	-1.02	-0.03	-0.26	0.80079289	0.9450	-6.63
264424_at	unknown protein similar to hypothe	---	AT1G61740	1.03	0.04	0.26	0.80140156	0.9450	-6.63
263108_at	hypothetical protein similar to puta	---	AT1G65240	-1.07	-0.10	-0.26	0.80158139	0.9450	-6.63
253948_at	Avr9 elicitor response like protein	---	AT4G26940	1.02	0.03	0.26	0.80143775	0.9450	-6.63
261060_at	unknown protein	---	AT1G17340	1.03	0.04	0.26	0.80100693	0.9450	-6.63
264320_at	unknown protein	---	AT1G04090	1.02	0.02	0.26	0.80125593	0.9450	-6.63
253284_at	putative protein hydroxyproline-ric	---	AT4G34150	-1.05	-0.06	-0.26	0.80123289	0.9450	-6.63
259951_at	unknown protein	---	AT1G71490	-1.02	-0.03	-0.26	0.80156374	0.9450	-6.63
247649_at	KED - like protein KED, Nicotiana	---	AT5G60030	-1.02	-0.03	-0.26	0.80099147	0.9450	-6.63
266688_at	hypothetical protein	---	AT2G19660	-1.02	-0.02	-0.26	0.80138487	0.9450	-6.63
256431_s_at	putative disease resistance protein	AtRLP34	AT3G11010	1.04	0.06	0.26	0.80123069	0.9450	-6.63
260139_at	Myb-related transcription factor, p	MYB114	AT1G66380	-1.02	-0.03	-0.26	0.80112622	0.9450	-6.63
254562_at	cytochrome P450 cytochrome P45	CYP707A1	AT4G19230	-1.05	-0.07	-0.26	0.8012475	0.9450	-6.63
258589_at	putative GDSL-motif lipase/acylhyd	LTL1	AT3G04290	-1.02	-0.04	-0.26	0.80124819	0.9450	-6.63
254252_at	serine/threonine kinase - like prote	---	AT4G23310	-1.03	-0.04	-0.26	0.80104721	0.9450	-6.63
253449_at	putative protein hypothetical prote	---	AT4G32700	1.02	0.03	0.26	0.80139632	0.9450	-6.63
259355_at	hypothetical protein predicted by g	---	AT3G05240	1.02	0.03	0.26	0.80151009	0.9450	-6.63
253488_at	putative protein reproductive meri	REM1	AT4G31610	1.03	0.04	0.26	0.80150153	0.9450	-6.63
252939_at	NAD(P)H oxidoreductase, isoflavo	---	AT4G39230	1.08	0.10	0.26	0.80171638	0.9450	-6.63
264737_at	unknown protein	---	AT1G62210	-1.03	-0.04	-0.26	0.80174768	0.9450	-6.63
266306_at	hypothetical protein predicted by g	---	AT2G26970	-1.02	-0.03	-0.26	0.8017506	0.9450	-6.63
260743_at	unknown protein	---	AT1G15030	-1.04	-0.06	-0.26	0.80163393	0.9450	-6.63
252481_at	putative protein DCL PROTEIN, C	---	AT3G46630	-1.02	-0.03	-0.26	0.80195513	0.9450	-6.63

253738_at	photosystem I subunit PSI-E - like	PSAE-1	AT4G28750	-1.02	-0.02	-0.26	0.80195088	0.9450	-6.63
256326_at	RING zinc-finger protein, putative	---	AT3G02340	1.03	0.04	0.26	0.80185647	0.9450	-6.63
247702_at	putative protein ;supported by full-	---	AT5G59500	1.02	0.03	0.26	0.80195928	0.9450	-6.63
263762_at	putative kinesin heavy chain ; sup	---	AT2G21380	1.03	0.05	0.26	0.80184808	0.9450	-6.63
257583_at	hypothetical protein	PMI2	AT1G66480	-1.09	-0.12	-0.26	0.80200694	0.9450	-6.63
263233_at	hypothetical protein similar to Na/H	---	AT1G05577	1.02	0.02	0.26	0.80206143	0.9450	-6.63
255358_at	hypothetical protein	---	AT4G03940	1.02	0.03	0.26	0.80210914	0.9450	-6.63
257155_at	hypothetical protein predicted by g	---	AT3G27290	-1.03	-0.04	-0.26	0.80217184	0.9451	-6.63
253505_at	Cytochrome P450-like protein flav	CYP82C2	AT4G31970	-1.03	-0.04	-0.26	0.80227378	0.9451	-6.63
249870_at	unknown protein	TGH	AT5G23080	1.05	0.07	0.26	0.80225312	0.9451	-6.63
263651_at	unknown protein Similar to Nicotia	---	AT1G04340	-1.03	-0.04	-0.26	0.80235293	0.9451	-6.63
257375_at	unknown protein	---	AT2G38640	1.06	0.09	0.26	0.80231806	0.9451	-6.63
250606_s_at	pectin methyl-esterase-like protei	PPME1	AT1G69940	1.02	0.03	0.26	0.80239701	0.9451	-6.63
265482_at	hypothetical protein contains a dor	---	AT2G15780	-1.17	-0.23	-0.26	0.80245153	0.9451	-6.63
255110_at	peroxidase C2 precursor like prote	---	AT4G08770	1.11	0.15	0.26	0.80258142	0.9452	-6.63
246335_at	lethal leaf-spot 1 homolog Lls1	ACD1	AT3G44880	-1.03	-0.04	-0.26	0.80262077	0.9452	-6.63
262601_at	hypothetical protein similar to GB:F	ATHSRP54	AT1G15310	-1.03	-0.04	-0.26	0.80254839	0.9452	-6.63
253598_at	ribosomal protein S11 - like ribosc	---	AT4G30800	-1.06	-0.08	-0.26	0.80269078	0.9452	-6.63
255697_at	hypothetical protein	---	AT4G00130	-1.03	-0.04	-0.26	0.80270859	0.9452	-6.63
254692_at	putative protein predicted protein,	---	AT4G17860	1.02	0.03	0.26	0.80305043	0.9454	-6.63
250438_at	putative protein predicted protein,	---	AT5G10580	-1.02	-0.03	-0.26	0.80301891	0.9454	-6.63
247066_at	DNA binding protein-like	---	AT5G66940	1.02	0.02	0.26	0.80300633	0.9454	-6.63
257032_at	zinc finger protein, putative simila	---	AT3G19140	1.02	0.02	0.26	0.80307836	0.9454	-6.63
253146_at	putative protein predicted protein,	---	AT4G35590	1.02	0.03	0.26	0.80302037	0.9454	-6.63
263312_at	putative replication protein A1	---	---	1.02	0.03	0.26	0.80316865	0.9454	-6.63
247199_at	DNA binding protein TGA1a homo	TGA1	AT5G65210	1.04	0.06	0.26	0.80321114	0.9454	-6.63
249843_at	putative protein similar to unknow	SGS3	AT5G23570	-1.03	-0.04	-0.26	0.80347281	0.9455	-6.63
260423_at	unknown protein	ATEXO70D	AT1G72470	-1.05	-0.07	-0.26	0.80390109	0.9455	-6.63
252527_at	dTDP-glucose 4-6-dehydratases-l	UXS5	AT3G46440	1.02	0.04	0.26	0.80398662	0.9455	-6.63
249054_at	unknown protein	---	AT5G02870	-1.02	-0.03	-0.26	0.80390879	0.9455	-6.63
258560_at	hypothetical protein predicted by g	---	AT3G06020	-1.03	-0.04	-0.26	0.80379576	0.9455	-6.63
263195_at	non-specific lipid transfer protein,	---	AT1G36150	-1.03	-0.04	-0.26	0.80352613	0.9455	-6.63
261167_at	disulfide isomerase-related protei	ATPDIL2-2	AT1G04980	1.07	0.10	0.26	0.80364779	0.9455	-6.63
257896_at	basic chitinase, putative similar to	---	AT3G16920	1.08	0.11	0.26	0.80395463	0.9455	-6.63
266783_at	putative laccase (diphenol oxidase	LAC2	AT2G29130	1.03	0.04	0.26	0.80341504	0.9455	-6.63

259004_at	putative protein kinase C-terminal	---	AT3G01840	1.02	0.03	0.26	0.8036159	0.9455	-6.63
248159_at	unknown protein	---	AT5G54460	-1.02	-0.02	-0.26	0.80374233	0.9455	-6.63
253442_at	H+-transporting ATPase - like pro	---	AT4G32530	-1.02	-0.03	-0.26	0.80345269	0.9455	-6.63
264974_at	unknown protein contains Pfam pr	ATHB54	AT1G27050	-1.02	-0.03	-0.26	0.80386978	0.9455	-6.63
246991_at	peroxidase (emb|CAA66967.1)	---	AT5G67400	1.02	0.03	0.26	0.80395345	0.9455	-6.63
254381_at	putative protein membrane-associ	---	AT4G21880	1.02	0.04	0.26	0.80375514	0.9455	-6.63
251515_at	putative protein several hypothetic	---	AT3G59270	1.02	0.02	0.26	0.80360334	0.9455	-6.63
247646_at	putative protein various predicted	---	AT5G59990	1.02	0.03	0.26	0.80354876	0.9455	-6.63
254003_at	hypothetical protein	---	AT4G26290	-1.02	-0.03	-0.26	0.80391564	0.9455	-6.63
257038_at	longevity factor-like protein similar	LOH2	AT3G19260	-1.04	-0.06	-0.26	0.80426531	0.9456	-6.63
264451_s_at	putative lectin receptor kinase very	---	---	1.02	0.03	0.26	0.804177	0.9456	-6.63
262244_at	serine threonine kinase, putative s	CIPK17	AT1G48260	-1.10	-0.13	-0.26	0.80424082	0.9456	-6.63
256393_at	hypothetical protein	---	AT3G06280	-1.02	-0.03	-0.26	0.80427176	0.9456	-6.63
262669_at	hypothetical protein	---	AT1G62850	-1.02	-0.03	-0.26	0.80429579	0.9456	-6.63
260222_at	putative alpha galactosyltransferas	XXT5	AT1G74380	-1.04	-0.06	-0.26	0.80462072	0.9457	-6.64
245277_at	glucosyltransferase like protein ; su	IAGLU	AT4G15550	-1.04	-0.06	-0.26	0.80472388	0.9457	-6.64
248162_at	1,4-benzoquinone reductase-like;	FQR1	AT5G54500	1.04	0.05	0.26	0.8048979	0.9457	-6.64
254303_at	predicted protein	---	AT4G22830	-1.02	-0.03	-0.26	0.80510641	0.9457	-6.64
247771_at	Ran binding protein 1 homolog - li	RANBP1	AT5G58590	1.02	0.03	0.26	0.80469805	0.9457	-6.64
259659_at	hypothetical protein contains simila	---	AT1G55170	-1.03	-0.04	-0.26	0.80472215	0.9457	-6.64
262586_at	hypothetical protein predicted by g	---	AT1G15480	-1.04	-0.05	-0.26	0.80497368	0.9457	-6.64
259198_at	hypothetical protein similar to F1N2	---	AT3G03610	-1.02	-0.03	-0.26	0.80514449	0.9457	-6.64
250991_at	metallothionein 2b ; supported by	MT2B	AT5G02380	1.02	0.03	0.26	0.80519988	0.9457	-6.64
251396_at	transketolase - like protein transke	---	AT3G60750	-1.02	-0.03	-0.26	0.80516941	0.9457	-6.64
250715_at	splicing factor 3a ; supported by c	ATO	AT5G06160	-1.03	-0.04	-0.26	0.80466713	0.9457	-6.64
254987_s_at	hypothetical protein	---	AT4G10660 /	-1.02	-0.02	-0.26	0.80471509	0.9457	-6.64
247795_at	putative protein zinc finger transcr	---	AT5G58620	-1.02	-0.03	-0.26	0.80503189	0.9457	-6.64
258631_at	putative polygalacturonase similar	QRT2	AT3G07970	1.07	0.09	0.26	0.80516472	0.9457	-6.64
258035_at	putative Ca2+-transporting ATPase	ACA9	AT3G21180	-1.02	-0.03	-0.26	0.80448621	0.9457	-6.64
267018_at	unknown protein	SVR1	AT2G39140	-1.03	-0.05	-0.26	0.80505898	0.9457	-6.64
256351_at	NPK1-related protein kinase, puta	ANP2	AT1G54960	-1.02	-0.03	-0.26	0.8045719	0.9457	-6.64
257425_at	hypothetical protein similar to heat	---	AT1G60400	1.03	0.04	0.26	0.80490136	0.9457	-6.64
257462_at	hypothetical protein	---	AT1G65740	-1.02	-0.03	-0.26	0.80522094	0.9457	-6.64
249182_at	putative protein similar to unknown	---	AT5G42960	1.02	0.03	0.26	0.80509768	0.9457	-6.64
267491_at	unknown protein predicted by gens	---	---	-1.03	-0.04	-0.26	0.80530857	0.9457	-6.64

247911_at	putative protein contains similarity	XRCC3	AT5G57450	-1.02	-0.03	-0.26	0.80539178	0.9458	-6.64
259608_at	unknown protein	ECT9	AT1G27960	1.02	0.03	0.26	0.80568797	0.9461	-6.64
246027_at	homoserine dehydrogenase-like p	---	AT5G21060	1.03	0.05	0.26	0.80576796	0.9461	-6.64
264543_at	hypothetical protein predicted by g	---	AT1G55780	-1.03	-0.04	-0.26	0.80576279	0.9461	-6.64
251981_at	putative protein BETA-GALACTO	---	AT3G53080	1.02	0.03	0.26	0.80582628	0.9461	-6.64
250311_at	unknown protein	---	AT5G12240	1.02	0.02	0.26	0.80589152	0.9461	-6.64
265283_at	unknown protein predicted by gene	MUR3	AT2G20370	1.03	0.04	0.25	0.80634542	0.9462	-6.64
262052_at	hypothetical protein identical to hy	---	---	-1.02	-0.03	-0.26	0.80620489	0.9462	-6.64
258990_at	unknown protein ;supported by ful	---	AT3G08840	-1.03	-0.05	-0.26	0.80633154	0.9462	-6.64
258176_at	B regulatory subunit of PP2A, puta	---	AT3G21650	1.04	0.06	0.26	0.80619921	0.9462	-6.64
248151_at	Lhcb3 chlorophyll a/b binding prote	LHCB3	AT5G54270	1.04	0.06	0.26	0.80629297	0.9462	-6.64
260960_at	calcium-binding protein, putative s	---	AT1G05990	-1.02	-0.03	-0.26	0.80611966	0.9462	-6.64
258173_at	putative protein kinase similar to s	CERK1	AT3G21630	1.02	0.03	0.26	0.8059871	0.9462	-6.64
263874_at	putative ATP synthase ;supported	---	AT2G21870	-1.03	-0.04	-0.26	0.80608792	0.9462	-6.64
247956_at	cytokinin oxidase ; supported by c	CKX3	AT5G56970	1.02	0.03	0.25	0.80637692	0.9462	-6.64
255534_at	CHP-rich hypothetical protein simil	---	AT4G02190	-1.02	-0.03	-0.26	0.80628624	0.9462	-6.64
262855_at	putative inorganic phosphate trans	---	AT1G20860	-1.03	-0.04	-0.26	0.8062217	0.9462	-6.64
258171_at	unknown protein	---	AT3G21610	1.02	0.03	0.25	0.80656085	0.9463	-6.64
AFFX-r2-At-GA	Arabidopsis thaliana /REF=M6411	---	---	1.04	0.06	0.25	0.80677076	0.9465	-6.64
249486_at	receptor protein kinase - like prote	---	AT5G39030	-1.02	-0.03	-0.25	0.80675663	0.9465	-6.64
248100_at	beta-1,3-glucanase-like protein ;s	---	AT5G55180	1.06	0.09	0.25	0.80716256	0.9465	-6.64
265974_at	unknown protein	---	---	1.04	0.05	0.25	0.80710071	0.9465	-6.64
255224_at	putative protein hypothetical prote	---	AT4G05400	1.03	0.04	0.25	0.80686444	0.9465	-6.64
246433_at	glutamine-rich protein predicted p	---	AT5G17510	-1.03	-0.04	-0.25	0.80691825	0.9465	-6.64
247476_at	putative protein	---	AT5G62330	1.02	0.03	0.25	0.80713723	0.9465	-6.64
264672_at	hypothetical protein predicted by g	---	AT1G09750	1.19	0.25	0.25	0.80701003	0.9465	-6.64
257133_at	hypothetical protein predicted by g	---	AT3G17190	1.02	0.02	0.25	0.80696466	0.9465	-6.64
266015_at	putative carbonyl reductase	---	AT2G24190	-1.02	-0.03	-0.25	0.80709748	0.9465	-6.64
258703_at	unknown protein	---	AT3G09750	-1.02	-0.03	-0.25	0.80701603	0.9465	-6.64
249833_at	putative protein contains similarity	---	AT5G23430	-1.03	-0.04	-0.25	0.80730426	0.9465	-6.64
246849_at	putative protein various predicted	---	AT5G26850	1.05	0.07	0.25	0.80729679	0.9465	-6.64
264985_at	unknown protein ;supported by full	---	AT1G27150	-1.04	-0.05	-0.25	0.80730528	0.9465	-6.64
263520_at	putative protein kinase contains a	---	AT2G42640	-1.02	-0.03	-0.25	0.80747368	0.9466	-6.64
250907_at	putative protein predicted proteins	---	AT5G03670	-1.02	-0.03	-0.25	0.80749487	0.9466	-6.64
259099_at	unknown protein similar to GB:AAE	---	AT3G05010	1.02	0.03	0.25	0.80745093	0.9466	-6.64

252702_at	putative protein predicted proteins	---	---	1.02	0.03	0.25	0.80749084	0.9466	-6.64
261283_s_at	hypothetical protein predicted by g	---	---	1.02	0.02	0.25	0.80762585	0.9467	-6.64
260245_at	putative RNA-binding protein simil	GR-RBP5	AT1G74230	1.02	0.02	0.25	0.80776405	0.9467	-6.64
247287_at	unknown protein ; supported by cl	---	AT5G64230	1.04	0.05	0.25	0.80771557	0.9467	-6.64
258403_at	hypothetical protein predicted by g	---	AT3G15380	-1.02	-0.03	-0.25	0.80779322	0.9467	-6.64
255341_at	putative receptor-like protein kinas	---	AT4G04500	1.13	0.17	0.25	0.80781677	0.9467	-6.64
249638_at	acetyl-CoA synthetase ; supporte	---	AT5G36880	-1.05	-0.07	-0.25	0.80789858	0.9467	-6.64
261384_at	hypothetical protein predicted by g	---	AT1G05440	1.02	0.03	0.25	0.80800716	0.9467	-6.64
248055_at	serine/threonine-specific kinase lik	---	AT5G55830	-1.02	-0.03	-0.25	0.8080338	0.9467	-6.64
258598_at	hypothetical protein predicted by g	---	AT3G04410	-1.03	-0.04	-0.25	0.80796662	0.9467	-6.64
253144_at	putative protein transcription facto	---	AT4G35540	1.02	0.03	0.25	0.80815391	0.9468	-6.64
255942_at	UDP-glucose glucosyltransferase i	AtUGT85A2	AT1G22360	-1.07	-0.10	-0.25	0.80812687	0.9468	-6.64
246984_at	cytochrome P450	CYP81G1	AT5G67310	1.07	0.10	0.25	0.80830961	0.9468	-6.64
247866_at	endoxyloglucan transferase (gb|AA	XTR3	AT5G57550	-1.07	-0.09	-0.25	0.8084195	0.9468	-6.64
264766_at	receptor kinase, putative similar to	---	AT1G61420	1.05	0.07	0.25	0.80847611	0.9468	-6.64
263993_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.25	0.80845968	0.9468	-6.64
259135_at	hypothetical protein predicted by g	RAD9	AT3G05480	-1.03	-0.04	-0.25	0.8082443	0.9468	-6.64
257934_at	serine carboxypeptidase, putative	scpl21	AT3G25420	1.03	0.04	0.25	0.80837819	0.9468	-6.64
261123_at	hypothetical protein predicted by g	---	AT1G62860	1.03	0.04	0.25	0.80843546	0.9468	-6.64
255545_at	putative polygalacturonidase simil	---	AT4G01890	1.02	0.03	0.25	0.8085617	0.9469	-6.64
263091_at	unknown protein	---	AT2G16200	1.02	0.03	0.25	0.80866269	0.9469	-6.64
248453_at	unknown protein	---	AT5G51340	1.02	0.03	0.25	0.8087734	0.9470	-6.64
247921_at	CONSTANS-like B-box zinc finger	COL5	AT5G57660	-1.03	-0.04	-0.25	0.8088314	0.9470	-6.64
267179_at	putative ADP ribosylation factor 1 (	AGD7	AT2G37550	1.03	0.04	0.25	0.80892603	0.9471	-6.64
249666_at	phytochrome C (sp|P14714)	PHYC	AT5G35840	1.03	0.04	0.25	0.80900306	0.9471	-6.64
255555_at	putative protein transport factor ; s	---	AT4G01810	1.02	0.03	0.25	0.80901228	0.9471	-6.64
256101_at	hypothetical protein predicted by g	---	AT1G13760	-1.02	-0.03	-0.25	0.80900068	0.9471	-6.64
246375_at	light repressible receptor protein k	---	AT1G51830	-1.03	-0.04	-0.25	0.80913179	0.9472	-6.64
245740_at	amino acid permease, putative alr	AAP5	AT1G44100	1.03	0.04	0.25	0.80929861	0.9473	-6.64
252577_at	putative protein putative proteins -	---	AT3G45460	1.02	0.02	0.25	0.80932965	0.9473	-6.64
266639_at	defender against cell death protein	DAD2	AT2G35520	1.02	0.03	0.25	0.80945124	0.9474	-6.64
257187_at	hypothetical protein predicted by g	---	AT3G13140	-1.02	-0.03	-0.25	0.80953827	0.9474	-6.64
245840_at	hypothetical protein predicted by g	---	AT1G58420	1.05	0.07	0.25	0.80952816	0.9474	-6.64
248280_at	putative protein similar to unknown	---	AT5G52950	-1.02	-0.03	-0.25	0.80961051	0.9474	-6.64
266016_at	putative RING zinc finger protein ;	---	AT2G18670	1.02	0.03	0.25	0.80966139	0.9474	-6.64

258363_at	putative pectin methylesterase sim	ATPMEPCI	AT3G14300	-1.02	-0.03	-0.25	0.80973151	0.9475	-6.64
253871_at	protochlorophyllide reductase prec	PORB	AT4G27440	-1.03	-0.04	-0.25	0.81013002	0.9476	-6.64
261788_at	unknown protein ;supported by full	NDF1	AT1G15980	1.04	0.05	0.25	0.81008614	0.9476	-6.64
266792_at	putative sucrose/H+ symporter	SUT2	AT2G02860	1.05	0.07	0.25	0.81014367	0.9476	-6.64
262557_at	photosystem I subunit III precurso	---	AT1G31330	-1.02	-0.03	-0.25	0.81012063	0.9476	-6.64
264534_at	hypothetical protein predicted by g	---	AT1G55700	1.03	0.04	0.25	0.81014895	0.9476	-6.64
264407_at	unknown protein similar to EST gb	---	AT1G10180	-1.02	-0.03	-0.25	0.8099739	0.9476	-6.64
258492_at	unknown protein	---	AT3G02390	1.02	0.03	0.25	0.81010165	0.9476	-6.64
256582_at	unknown protein	---	AT3G28840	-1.02	-0.03	-0.25	0.80993699	0.9476	-6.64
260314_at	unknown protein similar to putative	---	AT1G63830	-1.04	-0.05	-0.25	0.8102418	0.9476	-6.64
246147_s_at	26S proteasome AAA-ATPase su	RPT6A	AT5G19990	1.02	0.03	0.25	0.81031681	0.9477	-6.64
257535_at	hypothetical protein predicted by g	---	AT3G09490	-1.04	-0.06	-0.25	0.81045931	0.9478	-6.64
261351_at	hypothetical protein predicted by g	---	AT1G79790	-1.02	-0.03	-0.25	0.81054622	0.9478	-6.64
252470_at	protein kinase 6-like protein protei	---	AT3G46930	1.06	0.08	0.25	0.81072322	0.9478	-6.64
245467_at	hypothetical protein	---	AT4G16610	1.03	0.04	0.25	0.81085367	0.9478	-6.64
259752_at	spore coat protein-like protein simi	LPR2	AT1G71040	-1.03	-0.04	-0.25	0.81087817	0.9478	-6.64
251224_at	hypothetical protein	---	AT3G62620	-1.02	-0.03	-0.25	0.81089857	0.9478	-6.64
256340_at	DnaJ protein, putative contains Pf	---	AT1G72070	1.02	0.03	0.25	0.81096253	0.9478	-6.64
250276_at	putative protein mRNA, Moritella r	---	AT5G13030	1.02	0.03	0.25	0.8109316	0.9478	-6.64
249770_at	unknown protein ;supported by full	WRKY30	AT5G24110	-1.12	-0.16	-0.25	0.81086124	0.9478	-6.64
252748_at	putative protein putative proteins -	---	---	-1.02	-0.03	-0.25	0.81083722	0.9478	-6.64
245102_at	putative non-LTR retroelement rev	---	---	-1.03	-0.04	-0.25	0.81062885	0.9478	-6.64
255174_at	putative Athila-like protein	---	---	-1.02	-0.02	-0.25	0.81096073	0.9478	-6.64
258178_at	hypothetical protein predicted by g	---	AT3G21680	1.02	0.02	0.25	0.81071514	0.9478	-6.64
260583_x_at	putative polyribonucleotide phosph	---	AT2G47220	1.03	0.04	0.25	0.81101244	0.9478	-6.64
247042_at	putative protein similar to unknown	---	AT5G67220	1.02	0.03	0.25	0.81113383	0.9478	-6.64
257742_at	hypothetical protein predicted by g	SDH2-1	AT3G27380	-1.02	-0.03	-0.25	0.81109709	0.9478	-6.64
263402_at	hypothetical protein similar to hypo	---	AT2G04050	-1.08	-0.11	-0.25	0.81125342	0.9479	-6.64
265240_s_at	hypothetical protein	---	AT2G07691	1.02	0.03	0.25	0.8112888	0.9479	-6.64
248697_at	putative protein contains similarity	---	AT5G48370	-1.04	-0.05	-0.25	0.81133632	0.9479	-6.64
251872_at	putative protein predicted protein A	---	AT3G54570	1.02	0.03	0.25	0.81148187	0.9481	-6.64
260391_at	putative strictosidine synthase extr	SS2	AT1G74020	-1.02	-0.03	-0.25	0.81159879	0.9481	-6.64
246169_at	putative protein predicted protein,	---	AT5G32470	-1.02	-0.03	-0.25	0.81171546	0.9481	-6.64
256888_at	hypothetical protein predicted by g	---	AT3G15160	-1.02	-0.03	-0.25	0.81174595	0.9481	-6.64
260623_at	high-affinity nitrate transporter NR	ATNRT2:1	AT1G08090	-1.02	-0.03	-0.25	0.81171262	0.9481	-6.64

245923_at	putative protein predicted proteins	---	AT5G28820	-1.02	-0.03	-0.25	0.81170967	0.9481	-6.64
258609_at	unknown protein ;supported by ful	---	AT3G02910	1.02	0.03	0.25	0.81232829	0.9482	-6.64
252650_at	putative protein	---	AT3G44690	-1.02	-0.03	-0.25	0.81221618	0.9482	-6.64
246232_at	hypothetical protein	EMB2754	AT4G36630	-1.02	-0.03	-0.25	0.81201832	0.9482	-6.64
263659_at	unknown protein EST gb|ATTS567	---	AT1G04470	1.02	0.03	0.25	0.81227583	0.9482	-6.64
254531_at	putative protein predicted protein,	---	AT4G19650	1.03	0.04	0.25	0.81207074	0.9482	-6.64
251966_at	receptor lectin kinase -like protein	---	AT3G53380	1.03	0.04	0.25	0.81227586	0.9482	-6.64
259898_at	hypothetical protein predicted by g	---	AT1G71200	1.02	0.03	0.25	0.81194543	0.9482	-6.64
253127_at	putative Myc-type transcription fac	---	AT4G36060	-1.02	-0.03	-0.25	0.8122242	0.9482	-6.64
258763_s_at	putative beta-mannan endohydrola	---	AT3G10900 /	1.02	0.02	0.25	0.81203859	0.9482	-6.64
264398_at	unknown protein similar to hypothe	---	AT1G61730	-1.02	-0.03	-0.25	0.81214889	0.9482	-6.64
256702_at	unknown protein contains Pfam pr	---	AT3G30380	-1.03	-0.04	-0.25	0.81230681	0.9482	-6.64
256039_at	hypothetical protein contains simila	---	AT1G19190	1.03	0.04	0.25	0.81196919	0.9482	-6.64
252641_at	putative protein predicted protein,	---	AT3G44570	1.02	0.03	0.25	0.81196743	0.9482	-6.64
254578_at	putative pectinacetylesterase prot	---	AT4G19400 /	1.03	0.05	0.25	0.81243184	0.9482	-6.64
250395_at	putative protein cylicin II, bovine, F	---	AT5G10950	-1.03	-0.04	-0.25	0.81251643	0.9482	-6.64
250336_at	alpha-glucosidase 1 ; supported b	---	AT5G11720	1.02	0.03	0.25	0.81247715	0.9482	-6.64
265696_at	putative molybdopterin biosynthesi	CNX2	AT2G31955	1.04	0.05	0.25	0.81244081	0.9482	-6.64
256694_at	hypothetical protein predicted gens	---	---	1.02	0.03	0.25	0.81264758	0.9483	-6.64
266975_at	hypothetical protein predicted by g	ATEXO70H	AT2G39380	-1.05	-0.07	-0.25	0.81268062	0.9483	-6.64
260702_at	calmodulin, putative similar to caln	---	AT1G32250	1.02	0.03	0.25	0.81278717	0.9484	-6.64
264830_at	hypothetical protein predicted by g	---	AT1G03710	-1.02	-0.03	-0.25	0.81292584	0.9485	-6.64
260693_at	peptide transporter PTR2-B, putat	NRT1.5	AT1G32450	-1.05	-0.07	-0.25	0.81301473	0.9485	-6.64
247798_at	subtilisin-like serine protease conta	---	AT5G58830	-1.02	-0.02	-0.25	0.81303012	0.9485	-6.64
253993_at	mitogen activated protein kinase ki	MEK1	AT4G26070	1.04	0.05	0.25	0.81317624	0.9486	-6.64
262660_at	putative protein kinase	VIK	AT1G14000	-1.02	-0.03	-0.25	0.81316101	0.9486	-6.64
264232_at	putative protein kinase Pfam HMM	---	AT1G67470	1.07	0.10	0.25	0.81324995	0.9486	-6.64
257627_at	cytochrome P450, putative contair	CYP71B25	AT3G26270	-1.02	-0.03	-0.25	0.81345873	0.9488	-6.64
260503_at	proteasome, 30 kda subunit (ec 3.	PAF2	AT1G47250	-1.02	-0.03	-0.25	0.81367332	0.9490	-6.64
250043_at	putative protein proline-rich protei	---	AT5G18430	1.02	0.03	0.25	0.81365142	0.9490	-6.64
264940_at	galactinol synthase, putative simila	AtGolS4	AT1G60470	-1.06	-0.09	-0.24	0.81376523	0.9490	-6.64
258960_at	hypothetical protein similar to myb	---	AT3G10590	-1.02	-0.03	-0.24	0.81381812	0.9490	-6.64
266251_s_at	unknown protein	---	AT2G18320 /	-1.02	-0.02	-0.24	0.81387504	0.9491	-6.64
258066_at	hypothetical protein predicted by g	---	AT3G25970	1.02	0.02	0.24	0.81392218	0.9491	-6.64
257105_at	unknown protein	---	AT3G15300	1.03	0.04	0.24	0.81401246	0.9491	-6.64

249118_at	putative protein similar to unknown	---	AT5G43870	1.02	0.04	0.24	0.81426322	0.9491	-6.64
252121_at	GDP-D-mannose-4,6-dehydratase	MUR1	AT3G51160	1.04	0.06	0.24	0.8141587	0.9491	-6.64
252692_at	cysteine proteinase contains simil	---	AT3G43960	-1.05	-0.07	-0.24	0.81414648	0.9491	-6.64
255314_at	putative transposon protein	---	---	1.02	0.03	0.24	0.81415545	0.9491	-6.64
252533_at	putative protein predicted proteins	---	AT3G46110	-1.06	-0.08	-0.24	0.81422194	0.9491	-6.64
251065_at	lipid-transfer protein-like lipid-trans	---	AT5G01870	1.02	0.03	0.24	0.81425947	0.9491	-6.64
250091_at	unknown protein	---	AT5G17340	1.02	0.02	0.24	0.81435694	0.9492	-6.64
254790_at	probable photosystem I chain XI p	PSAL	AT4G12800	-1.02	-0.03	-0.24	0.8145545	0.9493	-6.64
267091_at	Expressed protein ; supported by f	---	AT2G38185	1.03	0.04	0.24	0.81460176	0.9493	-6.64
247402_at	putative protein predicted proteins	---	AT5G62750	-1.02	-0.03	-0.24	0.81454975	0.9493	-6.64
246037_at	putative protein predicted chromos	---	AT5G19420	-1.02	-0.03	-0.24	0.8145677	0.9493	-6.64
254600_at	4-coumarate-CoA ligase - like 4-c	---	AT4G19010	-1.03	-0.05	-0.24	0.81465457	0.9493	-6.64
255335_at	putative transposon protein	---	---	1.02	0.03	0.24	0.81480321	0.9493	-6.64
257243_at	pectate lyase, putative similar to G	---	AT3G24230	1.01	0.02	0.24	0.8148085	0.9493	-6.64
258137_at	Expressed protein ; supported by c	UBC37	AT3G24515	1.02	0.02	0.24	0.81477447	0.9493	-6.64
250034_at	apyrase (gb|AAF00612.1) ; suppo	ATAPY2	AT5G18280	-1.02	-0.03	-0.24	0.81486573	0.9493	-6.64
252742_at	putative protein glyceraldehyde-3-	---	AT3G43290	-1.02	-0.03	-0.24	0.81504178	0.9495	-6.64
262984_at	hypothetical protein predicted by g	---	AT1G54460	-1.04	-0.05	-0.24	0.81512865	0.9495	-6.64
250481_at	putative protein	---	AT5G10310	-1.02	-0.03	-0.24	0.81522119	0.9496	-6.64
261488_at	Expressed protein ; supported by f	---	AT1G14345	-1.02	-0.03	-0.24	0.81524691	0.9496	-6.64
257964_at	hypothetical protein similar to hypo	---	AT3G19850	-1.03	-0.05	-0.24	0.81544335	0.9496	-6.64
261806_at	ferrodoxin NADP oxidoreductase,	ATRFNR2	AT1G30510	1.04	0.05	0.24	0.81538168	0.9496	-6.64
256252_at	glucosyl transferase, putative simi	---	AT3G11340	1.12	0.17	0.24	0.81549925	0.9496	-6.64
257571_at	hypothetical protein predicted by g	---	AT3G16870	-1.04	-0.05	-0.24	0.8155151	0.9496	-6.64
248987_at	dimethylaniline monooxygenase (N	---	AT5G45180	-1.02	-0.03	-0.24	0.81554397	0.9496	-6.64
266335_at	putative cytochrome P450 ; suppo	KAO2	AT2G32440	1.03	0.05	0.24	0.81534955	0.9496	-6.64
245239_at	putative homeodomain-protein sin	FWA	AT4G25530	-1.02	-0.03	-0.24	0.81542445	0.9496	-6.64
264377_at	similar to early nodulins	---	AT2G25060	-1.02	-0.02	-0.24	0.81567762	0.9497	-6.64
248286_at	putative protein similar to unknown	---	AT5G52870	1.05	0.06	0.24	0.81582619	0.9498	-6.64
248082_at	fimbrin	---	AT5G55400	-1.04	-0.05	-0.24	0.81598573	0.9499	-6.64
260816_at	hypothetical protein predicted by g	---	AT1G06930	-1.03	-0.04	-0.24	0.81600579	0.9499	-6.64
258370_at	Expressed protein ; supported by f	---	AT3G14395	-1.02	-0.03	-0.24	0.81597533	0.9499	-6.64
266316_at	unknown protein ; supported by cl	---	AT2G27080	-1.10	-0.14	-0.24	0.81617593	0.9500	-6.64
262474_at	hypothetical protein identical to hy	FU	AT1G50240	-1.02	-0.03	-0.24	0.8163863	0.9502	-6.64
249221_at	serine/threonine protein kinase-like	---	AT5G42440	-1.02	-0.04	-0.24	0.81650315	0.9503	-6.64

264414_s_at	putative protein several hypothetic	---	---	1.03	0.05	0.24	0.81658908	0.9504	-6.64
251559_at	putative protein hypothetical prote	---	AT3G58010	1.03	0.04	0.24	0.81672621	0.9505	-6.64
245276_at	DNA-binding homeotic protein Athl	ATHB-2	AT4G16780	-1.02	-0.03	-0.24	0.81713187	0.9506	-6.64
259743_at	hypothetical protein predicted by g	---	AT1G71140	-1.08	-0.11	-0.24	0.81695107	0.9506	-6.64
262645_at	unknown protein similar to elongat	SCO1	AT1G62750	-1.02	-0.04	-0.24	0.8172396	0.9506	-6.64
245888_at	putative protein DNA-binding prote	---	AT5G09450	1.02	0.03	0.24	0.81720954	0.9506	-6.64
257713_at	succinate dehydrogenase iron-pro	SDH2-1	AT3G27380	-1.03	-0.05	-0.24	0.81698095	0.9506	-6.64
257331_at	hypothetical protein	---	---	-1.02	-0.03	-0.24	0.81710681	0.9506	-6.64
254277_at	myb-like protein myb-related trans	MYB85	AT4G22680	-1.06	-0.09	-0.24	0.81711424	0.9506	-6.64
260097_at	putative transporter similar to orga	AtOCT1	AT1G73220	-1.12	-0.16	-0.24	0.81703674	0.9506	-6.64
252651_at	putative protein several hypothetic	---	AT3G44700	1.02	0.03	0.24	0.81721949	0.9506	-6.64
247729_at	1-aminocyclopropane-1-carboxyla	---	AT5G59530	1.04	0.05	0.24	0.81767512	0.9508	-6.64
262802_at	putative cell division control protei	CDKB2;2	AT1G20930	-1.02	-0.02	-0.24	0.81786888	0.9508	-6.64
251944_at	ABC transporter -like protein brea	---	AT3G53510	1.03	0.04	0.24	0.81754227	0.9508	-6.64
261711_at	unknown protein similar to hypothe	---	AT1G32700	1.02	0.03	0.24	0.81761593	0.9508	-6.64
250537_at	Expressed protein ; supported by f	---	AT5G08565	1.03	0.05	0.24	0.81748058	0.9508	-6.64
261719_at	hypothetical protein similar to hypo	---	AT1G18390	1.06	0.08	0.24	0.81788103	0.9508	-6.64
249051_at	berberine bridge enzyme-like prote	---	AT5G44390	-1.02	-0.03	-0.24	0.8175731	0.9508	-6.64
256422_at	unknown protein	MOS2	AT1G33520	1.02	0.03	0.24	0.81784421	0.9508	-6.64
246766_at	hypothetical protein	---	AT5G27340	-1.03	-0.04	-0.24	0.81795724	0.9508	-6.64
245154_at	putative protein similarity to predict	---	AT5G12460	1.02	0.03	0.24	0.81777784	0.9508	-6.64
265462_at	putative vetispiradiene synthase	---	AT2G37140	1.02	0.03	0.24	0.81755926	0.9508	-6.64
263450_at	putative calcium-dependent protein	CPK24	AT2G31500	1.02	0.02	0.24	0.81794426	0.9508	-6.64
254528_at	hypothetical protein	---	AT4G19620	-1.02	-0.03	-0.24	0.81785761	0.9508	-6.64
262520_at	putative polygalacturonase After fi	---	AT1G17150	-1.02	-0.03	-0.24	0.81787231	0.9508	-6.64
249765_at	putative protein contains similarity	SLAH3	AT5G24030	1.07	0.09	0.24	0.81801049	0.9508	-6.64
253390_at	hypothetical protein ;supported by	---	AT4G32750	1.03	0.04	0.24	0.81804095	0.9508	-6.64
265249_at	putative C2H2-type zinc finger prot	SGR5	AT2G01940	-1.05	-0.07	-0.24	0.81817544	0.9509	-6.64
250191_at	kinase - like protein RING3 protein	ATBET9	AT5G14270	-1.02	-0.03	-0.24	0.81823632	0.9509	-6.64
247738_at	putative protein myosin heavy cha	---	AT5G59210	1.02	0.03	0.24	0.81841211	0.9511	-6.64
260244_at	putative choline kinase similar to G	---	AT1G74320	-1.02	-0.03	-0.24	0.8185194	0.9512	-6.64
247015_at	protease-like	---	AT5G66960	-1.03	-0.04	-0.24	0.81856679	0.9512	-6.64
245204_at	1-AMINOCYCLOPROPANE-1-CA	---	AT5G12270	-1.03	-0.04	-0.24	0.81864063	0.9512	-6.64
259463_at	hypothetical protein predicted by g	---	AT1G18950	1.03	0.05	0.24	0.81888968	0.9514	-6.64
249291_at	glutathione transferase AtGST 10 (	ATGSTT1	AT5G41210	-1.02	-0.03	-0.24	0.81886483	0.9514	-6.64

248533_at	putative protein contains similarity	---	AT5G50020	-1.03	-0.04	-0.24	0.81894587	0.9514	-6.64
257221_at	MYB family transcription factor (G	ATMYB0	AT3G27920	-1.02	-0.04	-0.24	0.81899482	0.9514	-6.64
255263_at	4-coumarate--CoA ligase - like pro	---	AT4G05160	1.02	0.02	0.24	0.81908311	0.9515	-6.64
263578_at	F-box protein family, AtFBL10 con	---	AT2G17020	1.02	0.02	0.24	0.81917157	0.9515	-6.64
254146_at	endo-1,4-beta-glucanase like prot	ATGH9A3	AT4G24260	-1.02	-0.03	-0.24	0.81922996	0.9516	-6.64
258229_at	unknown protein contains Pfam pr	---	AT3G27700	1.02	0.02	0.24	0.81936973	0.9516	-6.64
258007_at	putative tyrosine phosphatase simi	ATPEN2	AT3G19420	1.03	0.04	0.24	0.81932806	0.9516	-6.64
248958_at	unknown protein ; supported by fu	---	AT5G45590	-1.03	-0.04	-0.24	0.81943467	0.9516	-6.64
247101_at	apospory-associated protein C-like	---	AT5G66530	-1.03	-0.04	-0.24	0.81952309	0.9517	-6.64
267038_at	expressed protein supported by c	---	AT2G38480	-1.05	-0.07	-0.24	0.81959223	0.9517	-6.64
255169_x_at	hypothetical protein	---	AT4G07940	1.02	0.03	0.24	0.81967975	0.9517	-6.64
265749_at	putative retroelement pol polyprote	---	---	-1.02	-0.03	-0.24	0.81963657	0.9517	-6.64
248574_at	putative protein strong similarity to	---	AT5G49830	1.02	0.02	0.24	0.81968521	0.9517	-6.64
261430_at	hypothetical protein predicted by g	---	AT1G18830	-1.03	-0.04	-0.24	0.81981248	0.9518	-6.64
245569_at	RNA polymerase II fifth largest sub	NRPE7	AT4G14660	1.02	0.02	0.24	0.82014957	0.9519	-6.64
261195_at	transport inhibitor response 1 (TIR	AFB3	AT1G12820	-1.02	-0.03	-0.24	0.82005369	0.9519	-6.64
258980_at	putative reversibly glycosylatable p	RGP3	AT3G08900	-1.02	-0.03	-0.24	0.8201747	0.9519	-6.64
247941_at	putative protein strong similarity to	---	AT5G57200	-1.02	-0.02	-0.24	0.82021794	0.9519	-6.64
267634_at	putative actin	---	AT2G42100	-1.02	-0.02	-0.24	0.82017405	0.9519	-6.64
256687_x_at	hypothetical protein predicted by g	---	AT3G32120	-1.02	-0.02	-0.24	0.82020676	0.9519	-6.64
259764_at	transcription factor inhibitor I kapp	NPR1	AT1G64280	1.03	0.04	0.24	0.82023729	0.9519	-6.64
248604_at	protein kinase	---	AT5G49470	1.03	0.05	0.24	0.81996409	0.9519	-6.64
251762_at	sedoheptulose-bisphosphatase pre	SBPASE	AT3G55800	-1.02	-0.03	-0.24	0.82044537	0.9519	-6.64
248630_at	putative protein strong similarity to	---	AT5G48990	1.02	0.03	0.24	0.82046339	0.9519	-6.64
253188_at	putative sugar transporter protein	TMT2	AT4G35300	1.02	0.03	0.24	0.82042911	0.9519	-6.64
256830_at	eukaryotic translation initiation fac	TIF3C2	AT3G22860	-1.02	-0.03	-0.24	0.82031176	0.9519	-6.64
246806_at	putative cdc20 protein	---	AT5G27080	1.02	0.03	0.24	0.82046533	0.9519	-6.64
257313_at	gamma tonoplast intrinsic protein r	TIP2	AT3G26520	-1.02	-0.03	-0.24	0.82100693	0.9521	-6.64
258291_at	putative protein kinase similar to p	---	AT3G23310	-1.02	-0.03	-0.24	0.82081617	0.9521	-6.64
265109_s_at	NBS/LRR disease resistance prot	---	AT1G62630	1.03	0.04	0.24	0.821164	0.9521	-6.64
258686_at	putative polygalacturonase similar	---	AT3G07840	1.02	0.02	0.24	0.82065295	0.9521	-6.64
251874_at	putative protein (fragment) esteras	---	AT3G54240	-1.02	-0.04	-0.24	0.82073533	0.9521	-6.64
264473_at	hypothetical protein predicted by g	---	AT1G67180	1.04	0.05	0.24	0.82072675	0.9521	-6.64
262465_at	hypothetical protein similar to hypo	---	AT1G50270	-1.02	-0.02	-0.24	0.8209336	0.9521	-6.64
257810_at	TOM20, putative similar to TOM2	TOM20-1	AT3G27070	1.02	0.03	0.24	0.82084841	0.9521	-6.64

264181_at	ubiquitin, putative similar to ubiqui	UBQ13	AT1G65350	-1.01	-0.02	-0.24	0.82113642	0.9521	-6.64
246734_at	putative protein WRN (Werner syr	RECQSIM	AT5G27680	1.02	0.03	0.24	0.82107261	0.9521	-6.64
263798_at	putative ubiquitin carboxyl terminal	UBP19	AT2G24640	1.02	0.02	0.24	0.82112622	0.9521	-6.64
265278_at	hypothetical protein predicted by g	---	AT2G28330	-1.02	-0.04	-0.24	0.82109986	0.9521	-6.64
257510_at	unknown protein	---	AT1G55360	-1.05	-0.07	-0.24	0.82109557	0.9521	-6.64
257552_at	cellulase, putative contains Pfam	---	AT3G26130	1.02	0.02	0.24	0.82115145	0.9521	-6.64
251363_at	putative transcription factor (MYB1	AtMYB17	AT3G61250	-1.03	-0.05	-0.23	0.82131301	0.9522	-6.64
263055_at	unknown protein	---	---	1.02	0.02	0.23	0.82136195	0.9522	-6.64
264497_at	hypothetical protein predicted by g	ATPUP4	AT1G30840	-1.03	-0.04	-0.23	0.82159614	0.9524	-6.64
249955_at	sugar transporter - like protein pro	---	AT5G18840	-1.05	-0.07	-0.23	0.8217155	0.9525	-6.64
246349_at	Expressed protein ; supported by f	---	AT1G51915	1.05	0.07	0.23	0.82175798	0.9525	-6.64
261230_at	beta tubulin 1, putative similar to (	TUB5	AT1G20010	-1.02	-0.02	-0.23	0.82195595	0.9525	-6.64
246441_at	putative protein ;supported by full-	---	AT5G17560	-1.02	-0.02	-0.23	0.82187557	0.9525	-6.64
265477_at	hypothetical protein predicted by g	GAUT2	AT2G46480	-1.02	-0.03	-0.23	0.82183669	0.9525	-6.64
257581_s_at	RAV-like DNA-binding protein, put	---	AT1G50680	1.02	0.02	0.23	0.8219923	0.9525	-6.64
248503_at	putative protein contains similarity	NF-YC7	AT5G50470	-1.03	-0.04	-0.23	0.82193661	0.9525	-6.64
244961_at	hypothetical protein	---	---	-1.02	-0.02	-0.23	0.8220399	0.9525	-6.64
246105_at	putative protein predicted helicase	---	---	-1.01	-0.02	-0.23	0.8221344	0.9526	-6.64
265293_at	hypothetical protein predicted by g	---	---	-1.02	-0.03	-0.23	0.82228109	0.9527	-6.64
258222_at	putative zinc finger protein contain	---	AT3G15680	1.04	0.05	0.23	0.82235736	0.9528	-6.64
250760_at	unknown protein	---	AT5G06040	1.02	0.03	0.23	0.82246929	0.9528	-6.64
246412_at	phosphoglucomutase-like protein	---	AT5G17530	1.03	0.05	0.23	0.82266079	0.9530	-6.64
263530_at	HSP100/ClpB, putative similar to I	---	AT2G25030	-1.02	-0.03	-0.23	0.82276137	0.9531	-6.64
260289_at	CAD ATPase (AAA1) identical to (	ERH3	AT1G80350	-1.01	-0.02	-0.23	0.82287512	0.9531	-6.64
253014_at	MADS-box protein AGL17 -like pr	AGL21	AT4G37940	-1.02	-0.02	-0.23	0.82284659	0.9531	-6.64
260266_at	putative B-box zinc finger protein c	---	AT1G68520	-1.03	-0.04	-0.23	0.82306114	0.9531	-6.64
265898_at	hypothetical protein predicted by g	---	AT2G25690	1.03	0.05	0.23	0.82319283	0.9531	-6.64
255966_at	14-3-3 protein GF14epsilon (grf10	GRF10	AT1G22300	1.02	0.03	0.23	0.82308982	0.9531	-6.64
246624_at	flavin-containing monooxygenase,	YUC10	AT1G48910	1.02	0.03	0.23	0.82304764	0.9531	-6.64
252333_at	putative protein N-terminus: sever	---	AT3G48830	-1.02	-0.02	-0.23	0.82315116	0.9531	-6.64
254766_at	putative protein predicted protein,	TPS12	AT4G13280	1.02	0.02	0.23	0.82317246	0.9531	-6.64
265432_at	hypothetical protein predicted by g	---	AT2G20650	1.02	0.03	0.23	0.82319368	0.9531	-6.64
264819_at	hypothetical protein similar to mem	---	AT1G03510	1.03	0.04	0.23	0.82336474	0.9532	-6.64
254001_at	putative protein PRE87 mRNA, Pi	MIOX4	AT4G26260	-1.06	-0.08	-0.23	0.82336037	0.9532	-6.64
246570_at	putative protein nonmuscle myosi	---	AT5G14990	1.02	0.03	0.23	0.823242	0.9532	-6.64

257813_at	Cdc45-like protein similar to Cdc4	CDC45	AT3G25100	1.02	0.02	0.23	0.82335409	0.9532	-6.64
248914_at	Rab-type small GTP-binding protei	AtRABA1c	AT5G45750	-1.03	-0.05	-0.23	0.82564115	0.9532	-6.64
253255_at	putative auxin-regulated protein a	---	AT4G34760	-1.08	-0.10	-0.23	0.82436504	0.9532	-6.64
253422_at	putative protein ;supported by full-	---	AT4G32240	-1.02	-0.03	-0.23	0.82451166	0.9532	-6.64
266716_at	unknown protein ;supported by ful	PSI-P	AT2G46820	1.02	0.03	0.23	0.82480066	0.9532	-6.64
246070_at	ribosomal protein L7Ae-like NHP2	---	AT5G20160	-1.03	-0.04	-0.23	0.82632472	0.9532	-6.64
258716_at	unknown protein similar to a regior	---	AT3G09700	1.03	0.04	0.23	0.82372169	0.9532	-6.64
260316_at	hypothetical protein similar to hypo	---	AT1G63810	-1.02	-0.03	-0.23	0.82574648	0.9532	-6.64
247249_at	putative protein similar to unknowr	---	AT5G64670	1.03	0.04	0.23	0.82561946	0.9532	-6.64
256696_at	unknown protein	---	AT3G20650	-1.02	-0.02	-0.23	0.82625352	0.9532	-6.64
265941_s_at	recA, putative similar to GB:CAA3	---	AT2G19490 /	1.03	0.04	0.23	0.82599597	0.9532	-6.64
250073_at	unknown protein ; supported by cl	ENH1	AT5G17170	-1.04	-0.06	-0.23	0.82578332	0.9532	-6.64
262775_at	unknown protein	---	AT1G13000	1.02	0.02	0.23	0.82406259	0.9532	-6.64
254192_at	acyl-CoA synthetase - like protein	---	AT4G23850	-1.02	-0.03	-0.23	0.82603771	0.9532	-6.64
246612_at	putative protein ;supported by full-	---	AT5G35320	-1.02	-0.03	-0.23	0.82583879	0.9532	-6.64
248064_at	unknown protein	---	AT5G55570	-1.05	-0.07	-0.23	0.8261656	0.9532	-6.64
264441_at	Expressed protein ; supported by f	---	AT1G27435	1.02	0.03	0.23	0.82528366	0.9532	-6.64
247880_at	putative protein similar to unknowr	---	AT5G57780	1.07	0.10	0.23	0.82572154	0.9532	-6.64
255093_s_at	putative microfibril-associated prot	---	AT4G08580 /	-1.02	-0.02	-0.23	0.82566305	0.9532	-6.64
267182_at	unknown protein	---	AT2G23360	-1.02	-0.03	-0.23	0.82493856	0.9532	-6.64
251876_at	TATA box binding protein (TBP) a	RGD3	AT3G54280	-1.02	-0.03	-0.23	0.8248668	0.9532	-6.64
252179_at	putative protein UDP-glucose:(glu	GATL2	AT3G50760	-1.03	-0.04	-0.23	0.82457999	0.9532	-6.64
267448_at	putative protein phosphatase 2C	---	AT2G33700	-1.01	-0.02	-0.23	0.82626995	0.9532	-6.64
262640_at	hypothetical protein	---	AT1G62760	-1.16	-0.21	-0.23	0.82425422	0.9532	-6.64
264945_at	MADS-box protein (MADS2), puta	MAF1	AT1G77080	1.04	0.05	0.23	0.82596138	0.9532	-6.64
246030_at	Expressed protein genomic seque	---	AT5G21105	-1.02	-0.03	-0.23	0.82501105	0.9532	-6.64
245643_at	myb-related transcription factor (c	MYB116	AT1G25340	1.02	0.03	0.23	0.82358691	0.9532	-6.64
267125_at	putative acetone-cyanohydrin lyas	MES4	AT2G23580	1.02	0.02	0.23	0.82582916	0.9532	-6.64
252187_at	putative protein UV inducible prote	---	AT3G50850	1.02	0.03	0.23	0.82359717	0.9532	-6.64
251380_at	putative protein	---	AT3G60700	1.02	0.02	0.23	0.82449979	0.9532	-6.64
259016_at	unknown protein HMM hit: 2Fe-2S	---	AT3G07480	1.02	0.03	0.23	0.82633349	0.9532	-6.64
257357_at	hypothetical protein predicted by g	---	AT2G41050	1.02	0.03	0.23	0.82536933	0.9532	-6.64
249707_at	putative protein similar to unknowr	---	AT5G35640	1.03	0.04	0.23	0.8243837	0.9532	-6.64
261045_at	pathogenesis related protein, puta	---	AT1G01310	1.01	0.02	0.23	0.82535071	0.9532	-6.64
255270_at	putative protein (ubiquitin like) to v	---	AT4G05250	1.02	0.02	0.23	0.82459838	0.9532	-6.64

256567_at	amino acid permease, putative co	---	AT3G19553	1.02	0.03	0.23	0.82527285	0.9532	-6.64
245273_at	hypothetical protein ; supported by	---	AT4G14950	-1.02	-0.03	-0.23	0.82538203	0.9532	-6.64
260113_at	hypothetical protein predicted by g	---	AT1G63300	1.02	0.02	0.23	0.8238623	0.9532	-6.64
256827_at	hypothetical protein contains simila	---	AT3G18570	-1.02	-0.02	-0.23	0.82543666	0.9532	-6.64
261001_at	hypothetical protein similar to hypo	---	AT1G26530	-1.02	-0.03	-0.23	0.82432943	0.9532	-6.64
251949_at	receptor protein kinase -like protei	---	AT3G53590	-1.02	-0.03	-0.23	0.82584352	0.9532	-6.64
262885_at	alpha-tubulin, putative similar to a	TUA1	AT1G64740	1.02	0.03	0.23	0.82470759	0.9532	-6.64
259432_at	myb-related protein, putative simil	---	AT1G01520	-1.02	-0.03	-0.23	0.82645842	0.9532	-6.64
251052_at	DP-2 transcription factor - like tran	DPA	AT5G02470	1.02	0.03	0.23	0.82632979	0.9532	-6.64
257387_s_at	putative receptor-like protein kinas	---	AT2G14440	-1.02	-0.03	-0.23	0.82392173	0.9532	-6.64
259734_at	unknown protein similar to GB:AAD	---	AT1G77500	-1.04	-0.06	-0.23	0.82352423	0.9532	-6.64
264867_at	unknown protein	FH4	AT1G24150	-1.04	-0.06	-0.23	0.82638942	0.9532	-6.64
264197_at	unknown protein Similar to hypothe	ATSAC1	AT1G22620	1.01	0.02	0.23	0.82399194	0.9532	-6.64
260185_at	hypothetical protein similar to hypo	---	AT1G36030	-1.01	-0.02	-0.23	0.82629329	0.9532	-6.64
265560_at	putative glycine-rich protein	GRP-3	AT2G05520	1.02	0.02	0.23	0.82573244	0.9532	-6.64
255251_at	see GB:U95973 similar to a family	---	AT4G04980	-1.01	-0.02	-0.23	0.82637872	0.9532	-6.64
250285_at	putative protein GCN4-compleme	SFC	AT5G13300	-1.03	-0.04	-0.23	0.82379102	0.9532	-6.64
255875_s_at	putative protein kinase contains a	---	AT2G40500	1.02	0.03	0.23	0.82505258	0.9532	-6.64
265111_at	similar to 14KD proline-rich protein	---	AT1G62510	-1.10	-0.14	-0.23	0.82351707	0.9532	-6.64
263724_at	putative Ta11-like non-LTR retroel	---	AT2G13510	-1.02	-0.02	-0.23	0.82446074	0.9532	-6.64
262865_at	cytochrome p450, putative similar	CYP89A7	AT1G64930	-1.02	-0.03	-0.23	0.82610616	0.9532	-6.64
259271_at	Expressed protein ; supported by f	---	AT3G01170	1.02	0.03	0.23	0.82569464	0.9532	-6.64
254841_at	putative protein predicted proteins	---	AT4G11940	-1.02	-0.03	-0.23	0.8240411	0.9532	-6.64
263616_at	unknown protein	---	AT2G04680	-1.02	-0.03	-0.23	0.82464585	0.9532	-6.64
249867_at	2-isopropylmalate synthase-like pr	IMS2	AT5G23020	-1.09	-0.13	-0.23	0.82537886	0.9532	-6.64
266879_at	putative phragmoplastin	ADL1D	AT2G44590	1.02	0.03	0.23	0.82579036	0.9532	-6.64
260186_at	hypothetical protein predicted by g	---	AT1G36020	1.02	0.03	0.23	0.82486863	0.9532	-6.64
248145_at	unknown protein ;supported by ful	---	AT5G54880	-1.02	-0.03	-0.23	0.82583057	0.9532	-6.64
247678_at	putative zinc transporter ZIP2 - like	ZIP2	AT5G59520	-1.03	-0.05	-0.23	0.82368218	0.9532	-6.64
249934_at	peroxidase ATP14a homolog	---	AT5G22410	1.02	0.02	0.23	0.82349605	0.9532	-6.64
255068_at	Arabidopsis thaliana flavin-type bl	CRY1	AT4G08920	-1.01	-0.02	-0.23	0.82644226	0.9532	-6.64
261312_at	putative NPK1-related protein kina	---	AT1G05790	1.02	0.03	0.23	0.82389641	0.9532	-6.64
266392_at	late embryogenesis abundant M10	M10	AT2G41280	-1.02	-0.02	-0.23	0.82611998	0.9532	-6.64
248422_at	putative protein strong similarity to	YLS7	AT5G51640	-1.01	-0.02	-0.23	0.82620918	0.9532	-6.64
255313_at	putative transposon protein	---	---	1.02	0.03	0.23	0.82504064	0.9532	-6.64

261200_at	60S ribosomal protein L27a, putat	---	AT1G12960	1.02	0.03	0.23	0.82502709	0.9532	-6.64
245837_at	peptidylprolyl isomerase, putative	---	AT1G58450	-1.02	-0.02	-0.23	0.82602305	0.9532	-6.64
254777_at	putative protein hypothetical prote	---	AT4G12960	1.02	0.03	0.23	0.82478359	0.9532	-6.64
254795_at	putative protein	---	AT4G12990	-1.02	-0.02	-0.23	0.82416522	0.9532	-6.64
256632_at	hypothetical protein	---	AT3G28330	1.02	0.03	0.23	0.82450324	0.9532	-6.64
247864_s_at	anthranilate synthase beta chain ;	---	AT1G24807 /	-1.07	-0.10	-0.23	0.82681436	0.9534	-6.64
254308_at	putative protein snRNP assembly	---	AT4G22410	1.02	0.03	0.23	0.82673611	0.9534	-6.64
261437_at	hypothetical protein predicted by g	RAD51D	AT1G07745	1.02	0.03	0.23	0.82681278	0.9534	-6.64
246314_at	promoter-binding factor-like protei	AREB3	AT3G56850	1.02	0.03	0.23	0.82682441	0.9534	-6.64
260000_at	unknown protein similar to C-term	ATMAP70-	AT1G68060	1.02	0.03	0.23	0.82714364	0.9534	-6.64
266116_at	unknown protein ;supported by ful	TOM3	AT2G02180	1.02	0.03	0.23	0.82728254	0.9534	-6.64
266592_at	putative fatty acid desaturase/cyto	---	AT2G46210	-1.02	-0.02	-0.23	0.82787344	0.9534	-6.64
263145_at	hypothetical protein predicted by g	ATEXO70D	AT1G54090	-1.02	-0.04	-0.23	0.82721027	0.9534	-6.64
251885_at	fructose-bisphosphatase precurso	---	AT3G54050	1.03	0.04	0.23	0.82821985	0.9534	-6.64
249393_at	disease resistance - like protein re	AtRLP54	AT5G40170	-1.04	-0.05	-0.23	0.8273952	0.9534	-6.64
250761_at	ankyrin-like protein	---	AT5G06050	1.02	0.03	0.23	0.82773197	0.9534	-6.64
265770_at	Expressed protein ; supported by f	---	AT2G48100	1.02	0.03	0.23	0.82749475	0.9534	-6.64
254524_at	hypothetical protein	---	AT4G20000	-1.07	-0.09	-0.23	0.82714641	0.9534	-6.64
247237_at	auxin-independent growth promote	---	AT5G64600	1.02	0.03	0.23	0.82771458	0.9534	-6.64
245074_at	putative protein kinase contains a	---	AT2G23200	1.06	0.09	0.23	0.82722238	0.9534	-6.64
262494_at	myosin-like protein similar to myos	---	AT1G21810	-1.02	-0.03	-0.23	0.82806711	0.9534	-6.64
264455_at	hypothetical protein predicted by g	---	AT1G10330	-1.02	-0.03	-0.23	0.82723775	0.9534	-6.64
266925_at	unknown protein ;supported by ful	PEX11D	AT2G45740	-1.02	-0.02	-0.23	0.82750889	0.9534	-6.64
253133_at	DNA-directed RNA polymerase (E	NRPB1	AT4G35800	1.02	0.03	0.23	0.82815217	0.9534	-6.64
245833_at	transposon protein, putative simila	---	---	-1.02	-0.03	-0.23	0.82792791	0.9534	-6.64
259779_s_at	hypothetical protein predicted by g	---	AT1G29620 /	1.02	0.03	0.23	0.82731188	0.9534	-6.64
259443_at	chitinase, putative similar to chitin	---	AT1G02360	1.04	0.06	0.23	0.82810394	0.9534	-6.64
266101_at	unknown protein ; supported by cl	---	AT2G37940	-1.05	-0.07	-0.23	0.82797031	0.9534	-6.64
252635_at	putative protein predicted proteins	---	AT3G44510	1.02	0.03	0.23	0.82793337	0.9534	-6.64
265393_at	unknown protein ; supported by cl	---	AT2G20830	-1.03	-0.05	-0.23	0.82823268	0.9534	-6.64
256439_at	putative [Mn] superoxide dismutas	MSD1	AT3G10920	-1.02	-0.03	-0.23	0.8276762	0.9534	-6.64
246366_at	light repressible receptor protein k	---	AT1G51850	-1.03	-0.04	-0.23	0.82753858	0.9534	-6.64
255212_at	putative athila transposon protein	---	---	-1.02	-0.02	-0.23	0.82696697	0.9534	-6.64
261964_at	hypothetical protein similar to enve	---	---	-1.01	-0.02	-0.23	0.82715109	0.9534	-6.64
247003_at	putative protein similar to unknown	---	AT5G67550	-1.02	-0.03	-0.23	0.82749558	0.9534	-6.64

262735_at	hypothetical protein	---	AT1G28630	1.02	0.03	0.23	0.8272519	0.9534	-6.64
250128_at	zinc finger protein 3 (gb|AAD2787	ZFN3	AT5G16540	1.03	0.04	0.23	0.82795908	0.9534	-6.64
245519_at	retrotransposon like protein	---	---	1.01	0.02	0.23	0.82821114	0.9534	-6.64
248464_at	putative protein similar to unknown	---	AT5G51160	-1.03	-0.04	-0.23	0.82800782	0.9534	-6.64
258307_x_at	hypothetical protein predicted by g	---	---	1.02	0.03	0.23	0.82761107	0.9534	-6.64
259522_at	hypothetical protein	---	AT1G12490	1.02	0.02	0.23	0.82780207	0.9534	-6.64
264411_at	mutator-like transposase, putative	---	---	1.01	0.02	0.23	0.82769006	0.9534	-6.64
266134_s_at	putative beta-expansin	---	AT1G65680 /	1.02	0.03	0.23	0.82837666	0.9535	-6.64
256126_at	hypothetical protein similar to MuD	---	AT1G18050	1.03	0.04	0.23	0.82843337	0.9536	-6.64
249551_at	putative protein predicted proteins	---	AT5G38220	1.02	0.03	0.23	0.82851889	0.9536	-6.64
252621_at	putative protein Ac-like transposas	---	---	-1.02	-0.03	-0.23	0.82849261	0.9536	-6.64
250085_at	unknown protein	---	AT5G17250	-1.02	-0.03	-0.23	0.82856638	0.9536	-6.64
245563_at	SNF1 like protein kinase ; supporte	CIPK4	AT4G14580	-1.05	-0.07	-0.22	0.82876234	0.9537	-6.64
260599_at	cytochrome P450, putative similar	CYP708A1	AT1G55940	1.01	0.02	0.22	0.82872951	0.9537	-6.64
247616_at	putative protein various predicted	---	AT5G60260	-1.02	-0.03	-0.22	0.8288258	0.9537	-6.64
250851_at	putative protein rngB protein, Dicty	---	AT5G04420	-1.02	-0.03	-0.22	0.82890674	0.9537	-6.64
267074_s_at	hypothetical protein predicted by g	---	AT2G40955 /	1.02	0.02	0.22	0.82892099	0.9537	-6.64
249885_at	putative protein strong similarity to	F8H	AT5G22940	1.03	0.05	0.22	0.82902004	0.9538	-6.64
253151_at	putative polygalacturonase polyga	---	AT4G35670	1.02	0.02	0.22	0.82910477	0.9538	-6.64
247116_at	Mlo protein-like ; supported by cDN	MLO10	AT5G65970	1.02	0.03	0.22	0.82925754	0.9540	-6.64
256531_at	cystathionine gamma-synthase, p	---	AT1G33320	1.02	0.02	0.22	0.82935513	0.9540	-6.64
261563_at	polyphosphoinositide binding prot	---	AT1G01630	1.02	0.03	0.22	0.8302629	0.9541	-6.64
253066_at	1-aminocyclopropane-1-carboxyla	ACS8	AT4G37770	1.08	0.11	0.22	0.83037126	0.9541	-6.64
248743_at	unknown protein	---	AT5G48240	-1.03	-0.04	-0.22	0.83001827	0.9541	-6.64
266157_at	unknown protein	ATFUC1	AT2G28100	1.01	0.02	0.22	0.82977857	0.9541	-6.64
260878_at	scarecrow-like 1 identical to scared	SCL1	AT1G21450	1.03	0.04	0.22	0.82956849	0.9541	-6.64
259739_at	unknown protein supported by cDN	SEH1H	AT1G64350	-1.02	-0.03	-0.22	0.82987049	0.9541	-6.64
263840_at	Expressed protein ; supported by f	---	AT2G36885	-1.03	-0.04	-0.22	0.82959231	0.9541	-6.64
249453_at	v-SNARE AtVTI1a	SGR4	AT5G39510	1.01	0.02	0.22	0.8297177	0.9541	-6.64
251933_at	putative protein mucin MUC3, Hor	---	AT3G54060	-1.02	-0.03	-0.22	0.82989562	0.9541	-6.64
267566_at	unknown protein predicted by gens	---	AT2G30760	1.01	0.02	0.22	0.82998651	0.9541	-6.64
257727_at	unknown protein	---	AT3G18380	-1.02	-0.02	-0.22	0.83011168	0.9541	-6.64
265784_at	hypothetical protein predicted by g	---	AT2G07280	-1.02	-0.02	-0.22	0.82965004	0.9541	-6.64
250447_at	putative protein KIAA0332 gene, H	---	AT5G10800	1.02	0.02	0.22	0.82989979	0.9541	-6.64
247419_at	unknown protein	---	AT5G63080	1.02	0.03	0.22	0.83013964	0.9541	-6.64

263746_at	putative retroelement pol polyprote	---	---	1.02	0.02	0.22	0.83033186	0.9541	-6.64
262057_at	unknown protein ;supported by full	---	AT1G80040	-1.02	-0.03	-0.22	0.82996696	0.9541	-6.64
261637_at	DNA-binding protein PcMYB1, put	TRB1	AT1G49950	-1.02	-0.03	-0.22	0.83014159	0.9541	-6.64
AFFX-Athal-5S	Arabidopsis thaliana /REF=M6513	---	---	1.02	0.02	0.22	0.83027806	0.9541	-6.64
266940_at	unknown protein	---	AT2G18970	1.02	0.03	0.22	0.83029866	0.9541	-6.64
247622_at	putative protein	---	AT5G60350	-1.02	-0.02	-0.22	0.83035523	0.9541	-6.64
248416_at	putative protein disease resistance	---	AT5G51630	1.02	0.03	0.22	0.83011528	0.9541	-6.64
252706_at	putative protein predicted proteins	---	---	1.01	0.02	0.22	0.82957757	0.9541	-6.64
246604_at	putative protein	---	---	-1.02	-0.02	-0.22	0.83047921	0.9542	-6.64
257720_at	hypothetical protein similar to GB:A	---	AT3G18450	-1.02	-0.03	-0.22	0.83054972	0.9543	-6.64
252525_at	putative protein hypothetical protei	---	AT3G46450	-1.02	-0.03	-0.22	0.83060164	0.9543	-6.64
261769_at	plastocyanin identical to plastocya	PETE1	AT1G76100	-1.02	-0.03	-0.22	0.83082213	0.9543	-6.64
256922_at	hypothetical protein contains simil	---	AT3G19010	-1.04	-0.06	-0.22	0.83075081	0.9543	-6.64
252289_at	putative protein pre-mRNA splicin	---	AT3G49130	-1.03	-0.04	-0.22	0.83079337	0.9543	-6.64
245536_at	hypothetical protein	SDG2	AT4G15180	-1.02	-0.02	-0.22	0.83075338	0.9543	-6.64
255157_at	hypothetical protein	---	---	1.01	0.02	0.22	0.8306876	0.9543	-6.64
259892_at	germin-like protein similar to germi	GER1	AT1G72610	1.08	0.12	0.22	0.83089891	0.9543	-6.64
265827_at	hypothetical protein predicted by g	VOZ2	AT2G42400	1.01	0.02	0.22	0.83092267	0.9543	-6.64
262562_at	hypothetical protein predicted by g	---	AT1G34220	1.02	0.02	0.22	0.83127784	0.9546	-6.64
264453_at	putative GTP-binding protein simil	---	AT1G10300	1.01	0.02	0.22	0.83123968	0.9546	-6.64
266927_at	aquaporin (plasma membrane intr	PIP1B	AT2G45960	-1.02	-0.03	-0.22	0.83141091	0.9546	-6.64
250044_at	disease resistance protein RPP1-\	---	AT5G17680	1.03	0.04	0.22	0.83143655	0.9546	-6.64
255708_at	predicted protein	---	AT4G00232	1.02	0.03	0.22	0.83136226	0.9546	-6.64
248637_at	DNAJ-like protein	---	AT5G49060	-1.02	-0.02	-0.22	0.83153074	0.9547	-6.64
258135_at	Expressed protein ; supported by f	---	AT3G24506	1.02	0.03	0.22	0.83154216	0.9547	-6.64
250015_at	N-acetylglucosamine-phosphate m	DRT101	AT5G18070	1.03	0.05	0.22	0.83178788	0.9549	-6.64
260797_at	neoxanthin cleavage enzyme, put	NCED9	AT1G78390	1.02	0.03	0.22	0.8318738	0.9550	-6.64
246456_at	telomerase reverse transcriptase	ATTERT	AT5G16850	-1.02	-0.02	-0.22	0.83202644	0.9550	-6.64
246787_s_at	cdc20-like protein putative cdc20	---	AT5G27570	1.01	0.02	0.22	0.83205089	0.9550	-6.64
259145_at	hypothetical protein predicted by g	---	AT3G10180	1.01	0.02	0.22	0.83203611	0.9550	-6.64
256327_at	unknown protein ;supported by full	GAUT9	AT3G02350	-1.02	-0.03	-0.22	0.83236807	0.9551	-6.65
254784_at	growth factor like protein antisens	NUDT7	AT4G12720	1.04	0.06	0.22	0.83301549	0.9551	-6.65
245626_at	unknown protein ;supported by full	---	AT1G56700	1.03	0.04	0.22	0.83289112	0.9551	-6.65
258238_at	unknown protein	RST1	AT3G27670	1.01	0.02	0.22	0.83265034	0.9551	-6.65
249088_at	selenium-binding protein-like	---	AT5G44230	-1.02	-0.04	-0.22	0.83235631	0.9551	-6.65

266637_at	hypothetical protein ;supported by	BRXL1	AT2G35600	-1.03	-0.04	-0.22	0.8326906	0.9551	-6.65
245555_at	HSR201 like protein	---	AT4G15390	-1.02	-0.02	-0.22	0.83285195	0.9551	-6.65
259905_s_at	hypothetical protein predicted by g	---	AT1G74130	-1.01	-0.02	-0.22	0.83313159	0.9551	-6.65
258010_at	unknown protein similar to recepto	---	AT3G19300	-1.02	-0.02	-0.22	0.83312114	0.9551	-6.65
247764_at	subtilisin-like serine protease conta	---	AT5G59190	-1.02	-0.03	-0.22	0.83226467	0.9551	-6.65
264900_at	putative auxin transport protein str	PIN7	AT1G23080	1.03	0.04	0.22	0.83269078	0.9551	-6.65
252953_at	putative phosphatidylinositol synth	PIS2	AT4G38570	1.02	0.02	0.22	0.83279784	0.9551	-6.65
246770_at	putative protein DNA-binding prote	---	AT5G27460	-1.02	-0.03	-0.22	0.83290893	0.9551	-6.65
246000_at	putative protein predicted proteins	---	AT5G20820	-1.03	-0.05	-0.22	0.83250716	0.9551	-6.65
254595_at	floral homeotic protein agamous (A	AG	AT4G18960	-1.01	-0.02	-0.22	0.8327556	0.9551	-6.65
248130_at	unknown protein	---	AT5G54790	-1.02	-0.02	-0.22	0.83296409	0.9551	-6.65
265466_at	putative CCAAT-box binding tranc	NF-YB8	AT2G37060	1.02	0.03	0.22	0.83229503	0.9551	-6.65
265339_at	putative inorganic pyrophosphatas	AtPPa2	AT2G18230	-1.03	-0.04	-0.22	0.83243414	0.9551	-6.65
265408_at	Mutator-like transposase similar to	---	---	-1.01	-0.02	-0.22	0.83250764	0.9551	-6.65
257943_at	SKP1/ASK1 (At7), putative similar	ASK7	AT3G21840	1.02	0.03	0.22	0.83247554	0.9551	-6.65
254124_at	hypothetical protein ; supported by	---	AT4G24500	1.02	0.03	0.22	0.8331201	0.9551	-6.65
247727_at	putative ripening-related protein - I	---	AT5G59490	1.02	0.03	0.22	0.83287257	0.9551	-6.65
252687_at	putative protein predicted protein,	---	---	1.02	0.03	0.22	0.83244062	0.9551	-6.65
246876_at	putative protein various predicted	---	AT5G26140	1.02	0.02	0.22	0.83233088	0.9551	-6.65
251592_at	zinc finger - like protein finger prot	NTT	AT3G57670	1.02	0.02	0.22	0.83302294	0.9551	-6.65
248319_at	unknown protein	---	AT5G52710	1.02	0.02	0.22	0.83322908	0.9551	-6.65
266023_at	copia-like retroelement pol polypro	---	---	1.02	0.03	0.22	0.8332107	0.9551	-6.65
259757_at	putative thioredoxin similar to prote	ATPDIL1-2	AT1G77510	1.06	0.08	0.22	0.83344681	0.9551	-6.65
263129_at	unknown protein ;supported by full	---	AT1G78620	1.02	0.02	0.22	0.83332783	0.9551	-6.65
262766_at	hypothetical protein predicted by g	---	AT1G13160	1.03	0.04	0.22	0.8335386	0.9551	-6.65
266771_s_at	unknown protein	---	AT2G03010	-1.02	-0.02	-0.22	0.83352868	0.9551	-6.65
249148_at	unknown protein ; supported by cl	---	AT5G43260	-1.03	-0.04	-0.22	0.83333108	0.9551	-6.65
260859_at	serine carboxypeptidase II, putativ	scpl44	AT1G43780	-1.02	-0.03	-0.22	0.83349793	0.9551	-6.65
248210_at	ethylene-forming-enzyme-like diox	---	AT5G54000	1.02	0.02	0.22	0.83340476	0.9551	-6.65
247854_at	contains similarity to phosphoester	---	AT5G58200	-1.02	-0.03	-0.22	0.83396297	0.9552	-6.65
263291_at	unknown protein	---	AT2G10920	-1.02	-0.02	-0.22	0.83398285	0.9552	-6.65
264075_at	envelope-like protein identical to G	---	---	-1.02	-0.03	-0.22	0.83398346	0.9552	-6.65
246126_at	putative protein predicted protein,	ATNUDX19	AT5G20070	-1.04	-0.05	-0.22	0.83399461	0.9552	-6.65
259634_at	hypothetical protein	---	AT1G56380	-1.01	-0.02	-0.22	0.83396732	0.9552	-6.65
257443_at	hypothetical protein predicted by g	---	AT2G22050	1.02	0.02	0.22	0.83400981	0.9552	-6.65

256554_at	hypothetical protein similar to puta	---	---	1.02	0.03	0.22	0.83380683	0.9552	-6.65
247662_at	protein kinase - like protein kinase	---	AT5G60090	1.02	0.04	0.22	0.83375637	0.9552	-6.65
258092_at	Expressed protein ; supported by f	---	AT3G14595	1.03	0.04	0.22	0.83413987	0.9553	-6.65
248358_at	cytochrome P-450-like protein	CYP715A1	AT5G52400	-1.04	-0.06	-0.22	0.83428393	0.9555	-6.65
266220_at	putative dTDP-glucose 4-6-dehydr	---	AT2G28755	1.02	0.03	0.22	0.83435179	0.9555	-6.65
248938_at	receptor-like protein kinase	---	AT5G45780	1.02	0.02	0.22	0.83443477	0.9555	-6.65
250443_at	Pto kinase interactor - like protein	RBK1	AT5G10520	1.09	0.12	0.22	0.83469806	0.9557	-6.65
264630_at	hypothetical protein predicted by g	FAS1	AT1G65470	1.02	0.03	0.22	0.83464215	0.9557	-6.65
254762_at	Expressed protein ; supported by f	---	AT4G13230	1.02	0.03	0.22	0.83466506	0.9557	-6.65
264522_at	putative xylan endohydrolase simi	---	AT1G10050	-1.02	-0.03	-0.22	0.83485278	0.9557	-6.65
255949_at	hypothetical protein predicted by g	---	AT1G22080	1.01	0.02	0.22	0.83479106	0.9557	-6.65
245594_at	acylaminoacyl-peptidase like prote	---	AT4G14570	-1.03	-0.04	-0.22	0.8348262	0.9557	-6.65
258338_at	putative L-asparaginase similar to	---	AT3G16150	-1.03	-0.04	-0.22	0.83498349	0.9557	-6.65
260522_x_at	hypothetical protein predicted by g	---	AT2G41730	1.10	0.13	0.22	0.83553066	0.9557	-6.65
251667_at	putative protein DYSKERIN (NUC	NAP57	AT3G57150	-1.04	-0.06	-0.22	0.83534543	0.9557	-6.65
265662_at	putative C2H2-type zinc finger prot	FZF	AT2G24500	-1.02	-0.03	-0.22	0.83589904	0.9557	-6.65
255567_at	hypothetical protein ; supported by	---	AT4G01150	-1.02	-0.02	-0.21	0.83625419	0.9557	-6.65
253876_at	COP1-interacting protein 7 (CIP7)	CIP7	AT4G27430	-1.03	-0.04	-0.21	0.83627817	0.9557	-6.65
250404_at	CCR4-ASSOCIATED FACTOR -l	---	AT5G10960	-1.01	-0.02	-0.22	0.83501991	0.9557	-6.65
253648_at	pathogenesis related homeodomai	PRHA	AT4G29940	-1.01	-0.02	-0.22	0.83586406	0.9557	-6.65
245040_at	hypothetical protein predicted by g	---	AT2G26520	1.02	0.03	0.22	0.83521164	0.9557	-6.65
249385_at	thioredoxin ; supported by full-leng	ATTRX2	AT5G39950	1.02	0.03	0.22	0.83523253	0.9557	-6.65
261775_at	hypothetical protein predicted by g	---	AT1G76280	1.02	0.03	0.22	0.83520783	0.9557	-6.65
247254_at	CLE21, putative CLAVATA3/ESR-	CLE21	AT5G64800	-1.03	-0.05	-0.21	0.83615424	0.9557	-6.65
253581_at	stress responsive protein homolog	---	AT4G30660	1.04	0.05	0.22	0.83583374	0.9557	-6.65
262863_at	rhamnosyltransferase, putative sir	---	AT1G64910	1.02	0.03	0.22	0.83599949	0.9557	-6.65
257551_at	hypothetical protein contains simila	---	---	-1.02	-0.03	-0.21	0.83640522	0.9557	-6.65
254361_at	Expressed protein ; supported by f	---	AT4G22212	1.02	0.03	0.22	0.83612854	0.9557	-6.65
259306_at	unknown protein ;supported by ful	PNC1	AT3G05290	-1.02	-0.02	-0.22	0.83535498	0.9557	-6.65
253735_at	putative protein SNF7 protein - Sa	SNF7.1	AT4G29160	-1.02	-0.02	-0.22	0.83585392	0.9557	-6.65
249632_at	caffeic acid O-methyltransferase-l	---	AT5G37170	1.02	0.02	0.22	0.83504313	0.9557	-6.65
254067_at	hypothetical protein	NAP8	AT4G25450	1.02	0.02	0.22	0.83593144	0.9557	-6.65
256688_at	non-LTR reverse transcriptase, pu	---	AT3G32130	-1.01	-0.02	-0.22	0.83604293	0.9557	-6.65
260067_at	putative lipid transfer protein simila	---	AT1G73780	1.02	0.03	0.21	0.83632262	0.9557	-6.65
247879_at	unknown protein	---	AT5G57770	1.01	0.02	0.22	0.83578369	0.9557	-6.65

249074_at	putative protein contains similarity	---	AT5G44080	1.02	0.02	0.22	0.83589575	0.9557	-6.65
250496_at	inorganic pyrophosphatase - like p	AtPPa6	AT5G09650	-1.05	-0.07	-0.21	0.83620462	0.9557	-6.65
260432_at	putative DNA binding protein simila	WRKY9	AT1G68150	-1.02	-0.03	-0.22	0.83491187	0.9557	-6.65
250363_at	putative protein predicted proteins	---	AT5G11390	-1.03	-0.04	-0.22	0.83554698	0.9557	-6.65
263575_at	hypothetical protein similar to hypo	---	AT2G17070	-1.02	-0.02	-0.22	0.83556856	0.9557	-6.65
265701_at	unknown protein related to uncharа	---	AT2G03460	1.02	0.02	0.22	0.83595376	0.9557	-6.65
249896_at	unknown protein ; supported by cI	---	AT5G22530	-1.02	-0.03	-0.22	0.83550875	0.9557	-6.65
248803_at	selenium-binding protein-like	---	AT5G47460	1.02	0.03	0.21	0.83615674	0.9557	-6.65
259814_at	zinc finger protein ATZF1, putative	---	AT1G49900	1.03	0.04	0.21	0.83637325	0.9557	-6.65
261679_at	polyprotein, putative similar to poly	---	---	1.01	0.02	0.22	0.83535643	0.9557	-6.65
249848_at	putative protein similar to unknown	NIC3	AT5G23220	1.02	0.03	0.21	0.83624831	0.9557	-6.65
245982_at	senescence-associated protein (SA	SAG29	AT5G13170	-1.09	-0.12	-0.22	0.83591991	0.9557	-6.65
249155_at	unknown protein	---	AT5G43480	1.01	0.02	0.21	0.83635884	0.9557	-6.65
250185_at	putative protein esterase HDE, Pe	AtCXE16	AT5G14310	-1.02	-0.03	-0.22	0.83573351	0.9557	-6.65
257923_at	hypothetical protein predicted by g	---	AT3G23160	1.05	0.07	0.21	0.83681126	0.9558	-6.65
250905_at	protein kinase -like protein protein	---	AT5G03640	1.01	0.02	0.21	0.83680853	0.9558	-6.65
248229_at	caffeic acid 3-O-methyltransferase	---	AT5G53810	-1.02	-0.03	-0.21	0.83674438	0.9558	-6.65
245516_at	hypothetical protein	---	AT4G15820	1.02	0.03	0.21	0.8367197	0.9558	-6.65
251051_at	putative zinc finger protein zinc fin	---	AT5G02460	-1.02	-0.03	-0.21	0.83677105	0.9558	-6.65
255896_at	basic blue protein, putative similar	---	AT1G17800	1.01	0.02	0.21	0.83684176	0.9558	-6.65
256303_at	disease resistance protein, putativ	---	AT1G69550	-1.02	-0.03	-0.21	0.83675588	0.9558	-6.65
257257_at	hypothetical protein contains Pfam	---	AT3G22020	-1.01	-0.02	-0.21	0.83661377	0.9558	-6.65
255188_at	contains similarity to Xenopus laev	---	---	1.01	0.02	0.21	0.8365519	0.9558	-6.65
253274_at	Phosphoglycerate dehydrogenase	EDA9	AT4G34200	-1.10	-0.14	-0.21	0.83710741	0.9559	-6.65
247762_at	cell wall protein	---	AT5G59170	1.04	0.06	0.21	0.8371832	0.9559	-6.65
267434_at	3-beta-hydroxysteroid dehydrogen	AT3BETAH	AT2G26260	1.02	0.03	0.21	0.83711037	0.9559	-6.65
258786_at	putative syntaxin contains Pfam pr	SYP121	AT3G11820	1.04	0.06	0.21	0.8370545	0.9559	-6.65
261095_at	unknown protein	---	AT1G62930	1.02	0.03	0.21	0.83714733	0.9559	-6.65
246717_at	putative protein	---	AT5G28920	-1.02	-0.02	-0.21	0.83702699	0.9559	-6.65
254690_at	N-acetylornithine deacetylase-like	---	AT4G17830	-1.01	-0.02	-0.21	0.8369755	0.9559	-6.65
253044_at	hypothetical protein ;supported by	---	AT4G37290	1.11	0.15	0.21	0.8378342	0.9559	-6.65
246447_at	putative protein SART-1 protein -	DOT2	AT5G16780	1.02	0.03	0.21	0.83743364	0.9559	-6.65
254633_at	putative protein (fragment)	MRH1	AT4G18640	-1.03	-0.04	-0.21	0.83777035	0.9559	-6.65
248988_at	putative protein contains similarity	---	AT5G45190	1.02	0.03	0.21	0.83740457	0.9559	-6.65
245191_at	F12A21.10 similar to terminal ear1	TEL2	AT1G67770	1.03	0.04	0.21	0.83725643	0.9559	-6.65

245647_at	F5A9.22 hypothetical protein	---	AT1G24706	1.01	0.02	0.21	0.83765109	0.9559	-6.65
262367_at	hypothetical protein contains simila	VPS46.2	AT1G73030	1.02	0.03	0.21	0.83769259	0.9559	-6.65
244911_at	hypothetical protein	---	---	-1.02	-0.03	-0.21	0.83796552	0.9559	-6.65
252306_at	hypothetical protein	---	AT3G49270	1.01	0.02	0.21	0.83785712	0.9559	-6.65
248432_at	putative protein similar to unknown	---	AT5G51390	-1.04	-0.06	-0.21	0.83740251	0.9559	-6.65
267453_at	putative homeodomain transcriptio	HB-3	AT2G33880	1.02	0.04	0.21	0.83732553	0.9559	-6.65
258224_at	LEA76 homologue type2 identical	---	AT3G15670	-1.02	-0.02	-0.21	0.83799429	0.9559	-6.65
266118_at	protease inhibitor II ; supported by	LCR68	AT2G02130	-1.05	-0.06	-0.21	0.83769722	0.9559	-6.65
257283_at	hypothetical protein predicted by g	---	AT3G29750	-1.01	-0.02	-0.21	0.83755704	0.9559	-6.65
259676_at	hypothetical protein similar to puta	---	AT1G77730	1.02	0.02	0.21	0.83780456	0.9559	-6.65
260661_at	hypothetical protein predicted by g	---	AT1G19500	-1.02	-0.03	-0.21	0.83754499	0.9559	-6.65
256079_at	hypothetical protein predicted by g	---	AT1G20680	-1.01	-0.02	-0.21	0.83790794	0.9559	-6.65
256923_at	hypothetical protein	---	AT3G29635	-1.02	-0.03	-0.21	0.8380054	0.9559	-6.65
249197_at	putative protein contains similarity	CML37	AT5G42380	-1.12	-0.17	-0.21	0.83762401	0.9559	-6.65
260786_s_at	unknown protein similar to Cryptos	MEE5	AT1G06220	1.02	0.03	0.21	0.83813951	0.9559	-6.65
261915_at	amp-binding protein, putative simi	BZO1	AT1G65880	-1.01	-0.02	-0.21	0.83812316	0.9559	-6.65
263453_at	hypothetical protein predicted by g	---	AT2G22180	-1.01	-0.02	-0.21	0.83815237	0.9559	-6.65
267034_at	unknown protein ;supported by ful	---	AT2G38310	1.05	0.07	0.21	0.838264	0.9560	-6.65
262980_at	endo-beta-1,4-glucanase, putative	AtGH9B7	AT1G75680	1.08	0.11	0.21	0.83830399	0.9560	-6.65
251710_at	putative protein several hypothetic	---	AT3G56930	-1.03	-0.05	-0.21	0.83885311	0.9563	-6.65
248507_at	putative protein strong similarity to	---	AT5G50420	1.02	0.03	0.21	0.83867915	0.9563	-6.65
251681_at	putative protein hypothetical prote	---	AT3G57100	-1.02	-0.03	-0.21	0.8390745	0.9563	-6.65
245631_at	tRNA-glutamine synthetase, putat	OVA9	AT1G25350	1.02	0.02	0.21	0.8391331	0.9563	-6.65
248246_at	putative protein contains similarity	TRY	AT5G53200	1.02	0.03	0.21	0.83901821	0.9563	-6.65
260842_at	19S proteosome subunit 9, putativ	ATS9	AT1G29150	-1.02	-0.03	-0.21	0.83886325	0.9563	-6.65
249789_at	putative protein similar to unknown	---	AT5G24340	-1.02	-0.03	-0.21	0.8391631	0.9563	-6.65
266683_at	hypothetical protein predicted by g	GC1	AT2G19950	1.02	0.02	0.21	0.83896466	0.9563	-6.65
260136_at	hypothetical protein predicted by g	---	AT1G66360	1.02	0.02	0.21	0.83912827	0.9563	-6.65
252403_at	hypothetical protein	---	AT3G48080	-1.01	-0.02	-0.21	0.83870668	0.9563	-6.65
251769_at	receptor kinase - like protein rece	CCR3	AT3G55950	-1.09	-0.13	-0.21	0.83909361	0.9563	-6.65
253157_at	putative protein DNA helicase TP	RecQl3	AT4G35740	-1.02	-0.03	-0.21	0.83867366	0.9563	-6.65
261523_at	protein tyrosine phosphatase iden	PTP1	AT1G71860	-1.02	-0.02	-0.21	0.83895281	0.9563	-6.65
253951_at	putative Proline synthetase assoc	---	AT4G26860	1.03	0.04	0.21	0.83914066	0.9563	-6.65
248876_at	putative protein similar to unknown	---	---	1.01	0.02	0.21	0.83921983	0.9563	-6.65
245014_at	ATPase beta subunit	---	---	-1.01	-0.02	-0.21	0.83932887	0.9564	-6.65

264212_at	putative tRNA adenylyltransferase	---	AT1G22660	1.03	0.04	0.21	0.83938818	0.9564	-6.65
252133_at	hypothetical protein hypothetical p	---	AT3G50900	1.06	0.08	0.21	0.83956463	0.9564	-6.65
254408_at	serine/threonine kinase - like prote	B120	AT4G21390	1.10	0.14	0.21	0.83968801	0.9564	-6.65
261938_at	hypothetical protein predicted by g	---	AT1G22510	-1.03	-0.05	-0.21	0.83982755	0.9564	-6.65
256653_at	hypothetical protein predicted by g	---	AT3G18870	1.02	0.02	0.21	0.83976886	0.9564	-6.65
259249_at	hypothetical protein predicted by g	---	AT3G07790	-1.02	-0.04	-0.21	0.83972053	0.9564	-6.65
249952_at	putative protein predicted proteins	---	AT5G18950	-1.02	-0.03	-0.21	0.83979135	0.9564	-6.65
257014_at	hypothetical protein predicted by g	---	AT3G26930	1.02	0.03	0.21	0.83964183	0.9564	-6.65
256985_at	myb-related protein 5 identical to (	ATMYB5	AT3G13540	-1.02	-0.03	-0.21	0.83967296	0.9564	-6.65
262822_at	putative membrane-associated sal	---	AT1G11630	-1.02	-0.02	-0.21	0.83981272	0.9564	-6.65
263362_at	putative selenium-binding protein	---	AT2G03880	1.01	0.02	0.21	0.83955613	0.9564	-6.65
255944_at	putative protein	---	---	-1.02	-0.03	-0.21	0.83990988	0.9565	-6.65
251188_at	putative protein DESSICATION-R	---	AT3G62730	1.02	0.03	0.21	0.83999924	0.9565	-6.65
251668_at	putative protein strictosidine syntha	---	AT3G57010	-1.04	-0.05	-0.21	0.83998464	0.9565	-6.65
254954_at	hypothetical protein ;supported by	---	AT4G10910	1.05	0.07	0.21	0.84028413	0.9566	-6.65
264050_at	putative non-LTR retroelement rev	---	---	-1.02	-0.03	-0.21	0.84024045	0.9566	-6.65
264787_at	putative senescence-associated pr	ERD7	AT2G17840	-1.03	-0.04	-0.21	0.84031469	0.9566	-6.65
261260_at	hypothetical protein predicted by g	---	AT1G26680	-1.02	-0.02	-0.21	0.84032465	0.9566	-6.65
249390_at	60S RIBOSOMAL PROTEIN L5 -l	---	AT5G40130	-1.01	-0.02	-0.21	0.84024651	0.9566	-6.65
247813_at	NADP-dependent malate dehydrog	---	AT5G58330	-1.02	-0.02	-0.21	0.84040541	0.9567	-6.65
257601_at	hypothetical protein predicted by g	---	AT3G24820	-1.02	-0.02	-0.21	0.84053338	0.9567	-6.65
248796_at	VAMP (vesicle-associated membra	---	AT5G47180	-1.03	-0.04	-0.21	0.84052472	0.9567	-6.65
262834_at	hypothetical protein predicted by g	MAP65-7	AT1G14690	1.02	0.02	0.21	0.84054113	0.9567	-6.65
267556_at	putative beta-galactosidase ; supp	BGAL9	AT2G32810	1.02	0.03	0.21	0.84068761	0.9568	-6.65
260504_at	Cyclin similar to GB:CAB77269 fro	CYCA3;3	AT1G47220	-1.02	-0.03	-0.21	0.84073262	0.9568	-6.65
246708_at	putative protein various predicted	---	AT5G28150	-1.02	-0.03	-0.21	0.84102119	0.9568	-6.65
266240_at	putative RNA-binding protein ; sup	---	AT2G29580	1.01	0.02	0.21	0.84109106	0.9568	-6.65
248551_at	putative protein similar to unknown	WR3	AT5G50200	1.05	0.07	0.21	0.84096092	0.9568	-6.65
256864_at	topoisomerase II identical to topoi	TOPII	AT3G23890	-1.02	-0.03	-0.21	0.84107499	0.9568	-6.65
251416_at	putative protein various predicted	---	AT3G60400	-1.02	-0.02	-0.21	0.84083615	0.9568	-6.65
252855_at	putative protein alpha-amino-epsil	AGT2	AT4G39660	1.02	0.03	0.21	0.84085123	0.9568	-6.65
266610_at	Ac-like transposase related to Ac/D	---	---	1.01	0.02	0.21	0.84099776	0.9568	-6.65
257479_at	hypothetical protein contains simila	WAKL4	AT1G16150	-1.03	-0.04	-0.21	0.84104798	0.9568	-6.65
259531_at	hypothetical protein	---	AT1G12460	1.03	0.04	0.21	0.84133253	0.9569	-6.65
260734_at	disease resistance protein RPP1-W	---	AT1G17600	-1.02	-0.03	-0.21	0.84133319	0.9569	-6.65

249344_at	prohibitin (gb AAC49691.1) ;suppo	ATPHB3	AT5G40770	1.03	0.04	0.21	0.84139616	0.9569	-6.65
256938_at	LEA protein, putative similar to LE	ATECP31	AT3G22500	-1.02	-0.03	-0.21	0.84133333	0.9569	-6.65
266143_at	Expressed protein ; supported by c	---	AT2G38905	1.02	0.03	0.21	0.8412455	0.9569	-6.65
265017_at	unknown protein similar to EST em	---	AT1G24390	-1.02	-0.02	-0.21	0.84139026	0.9569	-6.65
258993_at	putative chlorophyll a/b-binding pr	LHCB4.2	AT3G08940	1.02	0.03	0.21	0.84154258	0.9570	-6.65
255205_at	putative transposon protein	---	---	-1.01	-0.02	-0.21	0.84151059	0.9570	-6.65
259163_at	putative protein kinase similar to A	---	AT3G01490	1.02	0.03	0.21	0.84176058	0.9570	-6.65
245171_at	hypothetical protein predicted by g	---	AT2G47560	-1.02	-0.03	-0.21	0.84172863	0.9570	-6.65
259777_at	zinc finger protein, putative similar	---	AT1G29570	-1.02	-0.02	-0.21	0.8417397	0.9570	-6.65
259343_s_at	putative methionine synthase simil	ATMS2	AT3G03780 /	1.03	0.04	0.21	0.84168301	0.9570	-6.65
246223_at	UDP-glucuronyltransferase-like pro	IRX14	AT4G36890	1.01	0.02	0.21	0.84186319	0.9571	-6.65
252600_at	putative protein unknown protein (	VPS24.2	AT3G45000	-1.02	-0.03	-0.21	0.84202806	0.9572	-6.65
259956_at	unknown protein ;supported by ful	RRA2	AT1G75110	1.02	0.02	0.21	0.84210806	0.9573	-6.65
252761_at	putative protein several hypothetic	---	AT3G42770	1.03	0.04	0.21	0.84234455	0.9575	-6.65
253740_at	Expressed protein ; supported by c	---	AT4G28706	-1.02	-0.03	-0.21	0.84248478	0.9576	-6.65
253088_at	ferulate-5-hydroxylase (FAH1) ; su	FAH1	AT4G36220	-1.04	-0.05	-0.21	0.84288152	0.9579	-6.65
257211_at	exonuclease, putative contains Pf	---	AT3G15080	1.02	0.03	0.21	0.84303527	0.9579	-6.65
260644_at	hypothetical protein contains simila	---	AT1G53290	1.02	0.03	0.21	0.84290662	0.9579	-6.65
257009_at	unknown protein ; supported by cl	---	AT3G14160	1.01	0.02	0.21	0.84301593	0.9579	-6.65
264221_s_at	unknown protein contains similarity	emb1220	AT1G60170 /	-1.02	-0.02	-0.21	0.84318627	0.9579	-6.65
246651_at	adenylate kinase -like protein ade	---	AT5G35170	1.02	0.03	0.21	0.8429658	0.9579	-6.65
262861_at	hypothetical protein similar to hypo	---	AT1G64820	1.02	0.02	0.21	0.84305191	0.9579	-6.65
254518_at	downy mildew resistance-like prot	---	AT4G19910	-1.02	-0.02	-0.21	0.84308482	0.9579	-6.65
265094_at	putative cruciferin 12S seed stora	---	AT1G03890	1.01	0.02	0.21	0.84324431	0.9579	-6.65
252732_at	putative protein predicted proteins	---	---	-1.02	-0.02	-0.21	0.84321381	0.9579	-6.65
263468_at	hypothetical protein predicted by g	---	AT2G31930	-1.02	-0.03	-0.21	0.84317967	0.9579	-6.65
266024_at	En/Spm-like transposon protein rel	---	---	-1.01	-0.02	-0.21	0.84289294	0.9579	-6.65
259550_at	hypothetical protein ;supported by	AGP5	AT1G35230	1.07	0.09	0.21	0.84333458	0.9579	-6.65
266703_at	unknown protein predicted by gens	---	AT2G19880	-1.03	-0.04	-0.21	0.84355679	0.9581	-6.65
249154_at	Nicotiana EREBP-3 like	---	AT5G43410	1.07	0.10	0.21	0.84356332	0.9581	-6.65
256647_at	unknown protein contains similarity	---	AT3G13610	-1.14	-0.20	-0.20	0.84376974	0.9582	-6.65
256315_at	hypothetical protein predicted by g	---	AT1G35880	-1.02	-0.02	-0.20	0.84372608	0.9582	-6.65
249883_at	Na+/H+ antiporter-like protein	CHX3	AT5G22900	1.01	0.02	0.20	0.84378024	0.9582	-6.65
249352_at	putative transcription factor MYB22	MYB22	AT5G40430	-1.01	-0.02	-0.20	0.8437298	0.9582	-6.65
266194_at	unknown protein	---	AT2G39090	1.01	0.02	0.20	0.84423276	0.9582	-6.65

254476_at	putative protein gamma-SNAP pr	GSNAP	AT4G20410	-1.02	-0.02	-0.20	0.84448513	0.9582	-6.65
248526_at	putative protein contains similarity	---	AT5G50740	1.02	0.03	0.20	0.84453977	0.9582	-6.65
261511_at	polyadenylate-binding protein 5 ide	PAB5	AT1G71770	1.02	0.03	0.20	0.84402835	0.9582	-6.65
245305_at	Expressed protein ; supported by f	---	AT4G17215	-1.06	-0.09	-0.20	0.84432444	0.9582	-6.65
253124_at	putative protein unknown protein A	ARO3	AT4G36030	1.05	0.07	0.20	0.8445034	0.9582	-6.65
245329_at	Expressed protein ; supported by f	---	AT4G14365	1.04	0.06	0.20	0.84449907	0.9582	-6.65
248859_at	putative protein contains similarity	---	AT5G46660	1.02	0.03	0.20	0.84422606	0.9582	-6.65
247308_at	receptor-like protein kinase	---	AT5G63930	1.02	0.02	0.20	0.8444296	0.9582	-6.65
262350_at	putative glutathione peroxidase ;s	ATGPX4	AT2G48150	1.02	0.02	0.20	0.84429742	0.9582	-6.65
255577_at	putative hypoersensitive response	---	AT4G01410	1.06	0.08	0.20	0.84434732	0.9582	-6.65
267120_at	hypothetical protein predicted by g	---	AT2G23530	1.02	0.03	0.20	0.84456385	0.9582	-6.65
251329_at	putative protein hypothetical prote	SYP73	AT3G61450	1.02	0.03	0.20	0.8439846	0.9582	-6.65
256540_at	polyprotein, putative similar to pol	---	---	1.01	0.02	0.20	0.84425145	0.9582	-6.65
257159_at	protein kinase, putative similar to	---	AT3G24400	-1.03	-0.04	-0.20	0.84412929	0.9582	-6.65
256851_at	hypothetical protein predicted by g	---	AT3G27930	-1.01	-0.02	-0.20	0.84399345	0.9582	-6.65
247870_at	calmodulin-binding protein ; suppo	---	AT5G57580	-1.01	-0.02	-0.20	0.8445006	0.9582	-6.65
255201_at	putative transposon protein	---	---	-1.01	-0.02	-0.20	0.84461003	0.9582	-6.65
253338_at	somatic embryogenesis receptor-l	BAK1	AT4G33430	1.02	0.02	0.20	0.84465725	0.9583	-6.65
254414_at	hypothetical protein	HSA32	AT4G21320	-1.02	-0.03	-0.20	0.84476241	0.9583	-6.65
261790_at	unknown protein ; supported by ful	---	AT1G16000	1.03	0.04	0.20	0.84478185	0.9583	-6.65
266443_at	putative myb-related transcription f	---	AT2G43270	1.01	0.02	0.20	0.84479477	0.9583	-6.65
251243_at	putative protein hypothetical prote	---	AT3G61870	1.02	0.03	0.20	0.84494654	0.9583	-6.65
245927_at	sterol glucosyltransferase - like pr	---	AT5G24750	-1.01	-0.02	-0.20	0.84501245	0.9583	-6.65
261586_at	hypothetical protein predicted by g	---	AT1G01640	1.04	0.05	0.20	0.84490961	0.9583	-6.65
262012_s_at	integral membrane protein, putativ	---	AT1G35625 A	-1.02	-0.02	-0.20	0.84484683	0.9583	-6.65
263030_at	hypothetical protein predicted by g	---	AT1G24060	-1.01	-0.02	-0.20	0.84500821	0.9583	-6.65
252498_at	putative protein several hypothetic	---	AT3G46810	1.01	0.02	0.20	0.84512018	0.9583	-6.65
248402_at	dihydrodipicolinate reductase-like p	crr1	AT5G52100	1.03	0.04	0.20	0.84556007	0.9584	-6.65
249677_at	DNA helicase-like	---	AT5G35970	-1.03	-0.04	-0.20	0.84561207	0.9584	-6.65
248833_at	Bax inhibitor-1 like ;supported by f	ATBI1	AT5G47120	-1.02	-0.03	-0.20	0.84569585	0.9584	-6.65
261698_at	unknown protein identical to hypot	---	AT1G32630	-1.02	-0.03	-0.20	0.84568098	0.9584	-6.65
253565_at	predicted protein DAN26, Homo s	---	AT4G31200	-1.02	-0.03	-0.20	0.84546888	0.9584	-6.65
246224_at	putative MADS-box protein ;suppo	---	AT4G36590	1.02	0.03	0.20	0.84541361	0.9584	-6.65
261508_at	unknown protein	---	AT1G71730	1.02	0.02	0.20	0.84563199	0.9584	-6.65
255630_at	putative phosphoribosylanthranilat	---	AT4G00700	1.14	0.19	0.20	0.84563009	0.9584	-6.65

257978_at	putative serine/threonine protein ki	ATNEK5	AT3G20860	-1.05	-0.08	-0.20	0.84557283	0.9584	-6.65
256546_at	hypothetical protein contains simila	---	AT3G14820	1.02	0.02	0.20	0.84563874	0.9584	-6.65
253611_at	RNase L inhibitor-like protein ribor	NAP15	AT4G30300	1.02	0.02	0.20	0.84525438	0.9584	-6.65
252384_at	ABC-type transport protein-like pr	ATH7	AT3G47790	-1.01	-0.02	-0.20	0.84535208	0.9584	-6.65
250195_at	putative protein	---	AT5G14560	1.01	0.02	0.20	0.84575681	0.9584	-6.65
247927_at	unknown protein	---	AT5G57310	-1.02	-0.02	-0.20	0.84578047	0.9584	-6.65
251006_at	putative protein predicted proteins	---	AT5G02600	1.02	0.03	0.20	0.84590022	0.9585	-6.65
256833_at	calmodulin-stimulated calcium-AT	---	AT3G22910	1.07	0.09	0.20	0.84589025	0.9585	-6.65
264646_at	hypothetical protein Similar to Hom	BON3	AT1G08860	-1.02	-0.02	-0.20	0.84596695	0.9585	-6.65
251902_at	uncoupling protein (ucp/PUMP) ; s	PUMP1	AT3G54110	-1.04	-0.05	-0.20	0.84608684	0.9586	-6.65
250658_at	C3HC4-type RING zinc finger prot	---	AT5G07040	-1.02	-0.03	-0.20	0.84627802	0.9588	-6.65
265089_at	hypothetical protein similar to hypo	SUVR1	AT1G04050	-1.02	-0.02	-0.20	0.84636872	0.9588	-6.65
262752_at	putative mitotic cyclin similar to gb	CYCB3;1	AT1G16330	-1.02	-0.03	-0.20	0.84647274	0.9589	-6.65
253854_at	putative protein zinc-finger protein	---	AT4G27900	1.04	0.06	0.20	0.84667341	0.9590	-6.65
253331_at	nucellin -like protein nucellin - Hor	---	AT4G33490	-1.02	-0.03	-0.20	0.84666712	0.9590	-6.65
249302_at	putative protein similar to unknown	---	AT5G41450	1.02	0.03	0.20	0.84672586	0.9590	-6.65
256992_at	hypothetical protein predicted by g	---	AT3G28630	-1.02	-0.02	-0.20	0.84685973	0.9590	-6.65
249568_at	glucosyltransferase-like protein UI	---	AT5G38040	-1.02	-0.03	-0.20	0.84678112	0.9590	-6.65
257501_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.20	0.84682604	0.9590	-6.65
246097_at	putative protein CGI-45 protein - H	HHP1	AT5G20270	-1.04	-0.06	-0.20	0.84696979	0.9590	-6.65
254701_at	putative protein predicted protein,	---	AT4G18030	1.03	0.04	0.20	0.84716923	0.9590	-6.65
266181_at	putative glutathione S-transferase	ATGSTZ1	AT2G02390	1.02	0.03	0.20	0.84717237	0.9590	-6.65
263085_at	hypothetical protein predicted by g	ARI12	AT2G16090	1.02	0.03	0.20	0.84715084	0.9590	-6.65
262382_at	virus resistance protein, putative s	---	AT1G72920	1.08	0.12	0.20	0.8472523	0.9590	-6.65
252264_at	putative protein hypothetical prote	---	AT3G49590	-1.02	-0.02	-0.20	0.84728493	0.9590	-6.65
246668_at	putative protein	---	---	-1.01	-0.02	-0.20	0.84707282	0.9590	-6.65
251182_at	putative protein HIRA interacting p	ATERDJ3B	AT3G62600	-1.05	-0.07	-0.20	0.84720161	0.9590	-6.65
253461_at	cytochrome p450 - like protein cyt	CYP96A2	AT4G32170	1.01	0.02	0.20	0.84715469	0.9590	-6.65
255123_at	putative lipid transfer protein	---	AT4G08530	1.02	0.02	0.20	0.84726853	0.9590	-6.65
257632_at	cytochrome P450, putative similar	CYP71B21	AT3G26190	1.03	0.04	0.20	0.8474178	0.9591	-6.65
248211_at	flavonol 3-O-glucosyltransferase-li	---	AT5G54010	-1.01	-0.02	-0.20	0.84761081	0.9593	-6.65
264638_at	flowering signals mediating protein	FT	AT1G65480	-1.05	-0.06	-0.20	0.84781688	0.9594	-6.65
259283_at	putative transcription factor similar	MYB65	AT3G11440	-1.02	-0.02	-0.20	0.84786649	0.9594	-6.65
249854_at	putative protein contains similarity	---	AT5G22960	-1.02	-0.03	-0.20	0.84777192	0.9594	-6.65
244964_at	PSII cytochrome b559	---	---	1.01	0.02	0.20	0.8478299	0.9594	-6.65

249306_at	RING zinc finger protein-like ;supp	---	AT5G41400	-1.04	-0.06	-0.20	0.84902528	0.9594	-6.65
248344_at	hyaluronan mediated motility recep	---	AT5G52280	1.03	0.04	0.20	0.84893837	0.9594	-6.65
249845_at	putative protein similar to unknown	---	AT5G23610	-1.01	-0.02	-0.20	0.84794595	0.9594	-6.65
266860_at	putative phospholipase C	---	AT2G26870	-1.03	-0.04	-0.20	0.84847072	0.9594	-6.65
249244_at	FtsH protease, putative similar to	VAR1	AT5G42270	1.02	0.02	0.20	0.84903693	0.9594	-6.65
251412_at	RING-H2 zinc finger protein ATL4	ATL4	AT3G60220	-1.04	-0.05	-0.20	0.84833327	0.9594	-6.65
258586_s_at	putative trypsin inhibitor similar to t	---	AT3G04320 /	-1.04	-0.06	-0.20	0.84806429	0.9594	-6.65
264354_s_at	unknown protein similar to Lambda	---	AT1G03200 /	-1.02	-0.02	-0.20	0.84852907	0.9594	-6.65
254634_at	putative protein transcription facto	---	AT4G18650	-1.02	-0.02	-0.20	0.84881247	0.9594	-6.65
261429_at	hypothetical protein contains simila	WRKY61	AT1G18860	1.02	0.02	0.20	0.84847069	0.9594	-6.65
248425_at	ACC synthase; 1-aminocyclopropa	ACS12	AT5G51690	-1.02	-0.03	-0.20	0.84924291	0.9594	-6.65
256680_at	unknown protein ; supported by ful	---	AT3G52230	1.02	0.03	0.20	0.84922906	0.9594	-6.65
247433_at	E2, ubiquitin-conjugating enzyme	UBC3	AT5G62540	1.02	0.04	0.20	0.84905817	0.9594	-6.65
260891_at	cysteine protease contains similari	---	AT1G29080	-1.02	-0.02	-0.20	0.84873017	0.9594	-6.65
250707_at	putative protein similar to unknown	MEE60	AT5G05950	1.02	0.03	0.20	0.84880065	0.9594	-6.65
260335_at	putative strictosidine synthase sim	SS3	AT1G74000	-1.04	-0.06	-0.20	0.84895044	0.9594	-6.65
259156_at	hypothetical protein predicted by g	SEC8	AT3G10380	1.01	0.02	0.20	0.84856843	0.9594	-6.65
255223_at	putative protein predicted proteins	---	AT4G05370	1.01	0.02	0.20	0.84860216	0.9594	-6.65
248949_at	putative protein strong similarity to	---	AT5G45570	1.01	0.02	0.20	0.84916909	0.9594	-6.65
255191_at	may be a pseudogene	---	---	-1.01	-0.02	-0.20	0.84898065	0.9594	-6.65
250392_at	putative protein multifunctional am	---	AT5G10880	-1.01	-0.02	-0.20	0.84885507	0.9594	-6.65
262955_at	unknown protein ;supported by full	---	AT1G54520	-1.02	-0.03	-0.20	0.84853077	0.9594	-6.65
249097_at	putative protein strong similarity to	---	AT5G43520	1.02	0.03	0.20	0.84860826	0.9594	-6.65
258595_at	unknown protein contains Pfam pr	---	AT3G04500	1.02	0.02	0.20	0.8487287	0.9594	-6.65
259258_at	putative ribulose-1,5-bisphosphate	---	AT3G07670	1.03	0.04	0.20	0.84828953	0.9594	-6.65
254397_at	gibberellin 3 beta-hydroxylase - lik	GA3OX3	AT4G21690	-1.03	-0.04	-0.20	0.84808145	0.9594	-6.65
261182_at	hypothetical protein predicted by g	---	AT1G34575	1.01	0.02	0.20	0.84866631	0.9594	-6.65
248090_at	putative protein contains similarity	MAPKKK15	AT5G55090	1.01	0.02	0.20	0.84858295	0.9594	-6.65
261358_s_at	hypothetical protein predicted by g	---	AT1G41920 /	1.02	0.02	0.20	0.84834069	0.9594	-6.65
252153_at	putative protein several hypothetic	---	AT3G51360	-1.02	-0.03	-0.20	0.84911629	0.9594	-6.65
261659_at	unknown protein contains similarity	TOR	AT1G50030	-1.01	-0.02	-0.20	0.84907198	0.9594	-6.65
264149_at	NAM (no apical meristem)-like pro	anac005	AT1G02250	-1.02	-0.02	-0.20	0.84917232	0.9594	-6.65
246476_at	putative protein predicted proteins	---	AT5G16730	1.02	0.03	0.20	0.84938039	0.9595	-6.65
260164_at	putative D-isomer specific 2-hydro	---	AT1G79870	1.02	0.02	0.20	0.84934114	0.9595	-6.65
264521_at	unknown protein Location of EST g	---	AT1G10020	1.04	0.05	0.20	0.84955457	0.9595	-6.65

246911_at	transcription factor TINY	tny	AT5G25810	-1.04	-0.06	-0.20	0.84958595	0.9595	-6.65
259441_at	cathepsin B-like cysteine protease	---	AT1G02300	1.02	0.03	0.20	0.84961744	0.9595	-6.65
263081_at	putative homeodomain transcriptio	BLH5	AT2G27220	-1.01	-0.02	-0.20	0.84955861	0.9595	-6.65
246841_at	nectarin - like protein nectarin I pr	---	AT5G26700	1.03	0.04	0.20	0.84948246	0.9595	-6.65
252838_at	hypothetical protein	---	---	-1.01	-0.02	-0.20	0.84973689	0.9596	-6.65
248336_at	unknown protein ; supported by cl	---	AT5G52420	-1.03	-0.04	-0.20	0.84989928	0.9598	-6.65
264083_at	ethylene reponse factor-like AP2 d	ATERF15	AT2G31230	-1.06	-0.08	-0.20	0.84994179	0.9598	-6.65
245384_at	glycoprotein homolog ;supported b	---	AT4G16790	-1.03	-0.04	-0.20	0.85000325	0.9598	-6.65
262263_at	auxin transport protein REH1, puta	PIN3	AT1G70940	1.05	0.07	0.20	0.85022445	0.9598	-6.65
251856_at	Peptidase - like protein ileal peptic	AMP1	AT3G54720	-1.03	-0.04	-0.20	0.85021135	0.9598	-6.65
252994_at	putative protein gene PC326 prote	---	AT4G38480	-1.04	-0.05	-0.20	0.85021141	0.9598	-6.65
264759_at	receptor protein kinase (IRK1), pu	---	AT1G61480	-1.02	-0.02	-0.20	0.85026413	0.9598	-6.65
257920_at	hypothetical protein predicted by g	---	AT3G23260	-1.01	-0.02	-0.20	0.85016027	0.9598	-6.65
246683_at	putative protein chromokinesin KI	---	AT5G33300	1.02	0.02	0.20	0.85012645	0.9598	-6.65
245172_at	hypothetical protein predicted by g	---	AT2G47540	1.01	0.02	0.20	0.85038385	0.9598	-6.65
250269_at	anthranilate phosphoribosyltransfe	---	AT5G12970	-1.02	-0.02	-0.20	0.85035856	0.9598	-6.65
246616_at	aspartyl protease-like	---	AT5G36260	-1.03	-0.04	-0.20	0.85049237	0.9599	-6.65
249681_s_at	putative protein strong similarity to	---	---	-1.02	-0.03	-0.20	0.85057516	0.9600	-6.65
248706_at	unknown protein	---	AT5G48530	-1.02	-0.03	-0.20	0.85070795	0.9601	-6.65
261282_at	hypothetical protein predicted by g	APUM10	AT1G35750	1.02	0.03	0.20	0.85091913	0.9602	-6.65
247689_at	putative protein protein tyrosine pl	---	AT5G59770	1.02	0.03	0.20	0.85090889	0.9602	-6.65
257871_at	hypothetical protein predicted by g	---	AT3G28350	1.01	0.02	0.20	0.85088186	0.9602	-6.65
258929_at	unknown protein Pfam HMM hit: FI	---	AT3G10060	-1.04	-0.06	-0.20	0.8511	0.9602	-6.65
249926_at	E1, ubiquitin-like activating enzym	ECR1	AT5G19180	1.02	0.03	0.20	0.85111566	0.9602	-6.65
255952_at	MADS-box protein (ZAP1), putativ	AGL104	AT1G22130	1.01	0.02	0.19	0.8511726	0.9602	-6.65
249498_at	putative protein motif in transcriptic	---	AT5G39230	1.02	0.02	0.19	0.85116145	0.9602	-6.65
257308_at	unknown protein	---	AT3G28120	1.01	0.02	0.19	0.85127324	0.9603	-6.65
244967_at	PSI J protein	---	---	1.03	0.05	0.19	0.85123572	0.9603	-6.65
245331_at	hypothetical protein ;supported by	---	AT4G14410	1.01	0.02	0.19	0.85149331	0.9603	-6.65
258926_s_at	unknown protein N-terminus simila	anac052	AT3G10480	-1.02	-0.03	-0.19	0.85153658	0.9603	-6.65
263089_at	putative retroelement pol polyprote	---	---	-1.02	-0.03	-0.19	0.85143514	0.9603	-6.65
254523_at	putative protein hypothetical prote	FRS1	AT4G19990	1.02	0.03	0.19	0.85137854	0.9603	-6.65
253963_at	putative protein probable calcium-	---	AT4G26470	1.03	0.04	0.19	0.85150244	0.9603	-6.65
249038_at	putative protein contains similarity	RING1A	AT5G44280	-1.02	-0.02	-0.19	0.85162587	0.9604	-6.65
248695_at	putative protein similar to unknowr	---	AT5G48350	1.02	0.03	0.19	0.85167405	0.9604	-6.65

253671_at	serine threonine-specific receptor	---	AT4G29990	-1.02	-0.03	-0.19	0.85178809	0.9605	-6.65
256881_at	hypothetical protein ; supported by	---	AT3G26410	-1.02	-0.02	-0.19	0.85184255	0.9605	-6.65
254167_at	serine/threonine kinase-like protei	CIPK8	AT4G24400	1.02	0.02	0.19	0.85187568	0.9605	-6.65
261669_at	unknown protein similar to hypothe	---	AT1G18490	-1.01	-0.02	-0.19	0.85202555	0.9606	-6.65
260706_at	oxidase, putative similar to oxidas	AOX1D	AT1G32350	-1.12	-0.17	-0.19	0.85244998	0.9607	-6.65
264756_at	receptor protein kinase (IRK1), pu	---	AT1G61370	-1.06	-0.08	-0.19	0.85252896	0.9607	-6.65
253729_at	beta-1,3-glucanase-like protein be	---	AT4G29360	-1.02	-0.03	-0.19	0.8523546	0.9607	-6.65
260761_at	hypothetical protein predicted by g	---	AT1G49150	-1.03	-0.04	-0.19	0.85233299	0.9607	-6.65
247551_at	ras-GTPase-activating protein SH	---	AT5G60980	1.01	0.02	0.19	0.85254707	0.9607	-6.65
262844_at	unknown protein similar to pectines	---	AT1G14890	-1.04	-0.06	-0.19	0.85243055	0.9607	-6.65
251140_at	lectin - like protein lectin precurso	---	AT5G01090	-1.02	-0.02	-0.19	0.85232066	0.9607	-6.65
267413_at	putative amino acid transporter	CAT5	AT2G34960	-1.03	-0.04	-0.19	0.8525698	0.9607	-6.65
251043_s_at	putative protein various predicted	---	AT5G02330	-1.02	-0.02	-0.19	0.85215226	0.9607	-6.65
259509_at	mutator-like transposase, putative	---	---	-1.01	-0.02	-0.19	0.85253451	0.9607	-6.65
247203_at	unknown protein ; supported by cl	---	AT5G65180	1.01	0.02	0.19	0.85227749	0.9607	-6.65
263328_at	hypothetical protein similar to hypo	---	AT2G15280	-1.02	-0.03	-0.19	0.8527954	0.9608	-6.65
266910_at	unknown protein	---	AT2G45920	1.04	0.05	0.19	0.85277149	0.9608	-6.65
260206_at	putative protein kinase contains Pf	---	AT1G70740	1.04	0.05	0.19	0.85278475	0.9608	-6.65
261843_at	unknown protein	---	AT1G16180	-1.01	-0.02	-0.19	0.85292615	0.9609	-6.65
245552_at	cytochrome P450 like protein	CYP705A3	AT4G15360	1.01	0.02	0.19	0.85293348	0.9609	-6.65
255565_at	putative CHP-rich zinc finger prote	---	AT4G01760	1.01	0.02	0.19	0.85304026	0.9609	-6.65
245829_at	hypothetical protein predicted by g	---	AT1G57780	-1.02	-0.02	-0.19	0.85301672	0.9609	-6.65
257968_at	hypothetical protein predicted by g	---	AT3G27550	-1.02	-0.03	-0.19	0.85311141	0.9609	-6.65
249960_at	squamosa promoter binding protei	SPL7	AT5G18830	-1.02	-0.02	-0.19	0.85324233	0.9610	-6.65
257593_at	phosphatidylinositol transfer prote	---	AT3G24840	1.01	0.02	0.19	0.85327113	0.9610	-6.65
263143_at	hypothetical protein Contains PF|0	---	AT1G03100	-1.02	-0.02	-0.19	0.85369526	0.9610	-6.65
260585_at	unknown protein	EMB2777	AT2G43650	1.03	0.05	0.19	0.85354552	0.9610	-6.65
261676_at	Expressed protein ; supported by f	---	AT1G18480	-1.02	-0.03	-0.19	0.85367613	0.9610	-6.65
259747_at	putative dehydrogenase similar to	---	AT1G71170	1.02	0.03	0.19	0.85370508	0.9610	-6.65
255930_at	hypothetical protein predicted by g	---	AT1G12660	-1.01	-0.02	-0.19	0.85361386	0.9610	-6.65
252856_at	putative protein ; supported by cDN	---	AT4G39690	1.01	0.02	0.19	0.85365859	0.9610	-6.65
247160_at	putative protein contains similarity	---	AT5G65820	1.01	0.02	0.19	0.85333877	0.9610	-6.65
254206_at	thaumatin-like protein thaumatin-li	---	AT4G24180	1.02	0.03	0.19	0.85342952	0.9610	-6.65
248266_at	putative protein similar to unknown	---	AT5G53440	1.01	0.02	0.19	0.85344732	0.9610	-6.65
266810_at	hypothetical protein predicted by g	---	AT2G44880	-1.01	-0.02	-0.19	0.85359917	0.9610	-6.65

265485_at	putative Ta11-like non-LTR retroel	---	---	-1.02	-0.03	-0.19	0.85375718	0.9610	-6.65
260906_at	hypothetical protein predicted by g	---	AT1G02540	1.01	0.02	0.19	0.85382731	0.9611	-6.65
264730_at	hypothetical protein similar to puta	---	AT1G62085	1.02	0.02	0.19	0.85390568	0.9611	-6.65
256780_at	RNase L inhibitor, putative similar	ATRLI1	AT3G13640	-1.02	-0.02	-0.19	0.85395246	0.9611	-6.65
246404_at	hypothetical protein contains simila	---	AT1G57600	1.01	0.02	0.19	0.85400506	0.9611	-6.65
253286_at	hypothetical protein	FUC95A	AT4G34260	1.06	0.09	0.19	0.8540769	0.9611	-6.65
251593_at	DNA-directed RNA polymerase I 1	NRPA1	AT3G57660	1.03	0.04	0.19	0.85420964	0.9611	-6.65
251725_at	putative protein	---	AT3G56260	1.02	0.04	0.19	0.85441592	0.9611	-6.65
264641_at	ATP-dependent Clp protease prot	---	AT1G09130	1.02	0.02	0.19	0.85435891	0.9611	-6.65
252211_at	putative protein predicted proteins	---	AT3G50220	1.02	0.02	0.19	0.8542455	0.9611	-6.65
266111_at	unknown protein	---	AT2G02060	1.02	0.02	0.19	0.85444993	0.9611	-6.65
264937_at	hypothetical protein contains simila	SCPL32	AT1G61130	-1.02	-0.02	-0.19	0.85444521	0.9611	-6.65
259591_at	unknown protein ;supported by full	---	AT1G28150	1.01	0.02	0.19	0.85428842	0.9611	-6.65
246641_s_at	Expressed protein ; supported by f	---	AT5G34883	1.02	0.02	0.19	0.85424872	0.9611	-6.65
249500_at	expansin-like protein expansin - P	ATEXPA21	AT5G39260	1.02	0.03	0.19	0.85447023	0.9611	-6.65
253252_at	amidophosphoribosyltransferase 2	ATASE2	AT4G34740	-1.02	-0.03	-0.19	0.85439558	0.9611	-6.65
261338_at	hypothetical protein predicted by g	---	AT1G44920	-1.02	-0.03	-0.19	0.85456379	0.9612	-6.65
258159_at	receptor kinase, putative similar to	RLK902	AT3G17840	-1.03	-0.04	-0.19	0.85492768	0.9613	-6.65
266048_at	putative thioredoxin H contains a th	ATCXXS2	AT2G40790	1.02	0.02	0.19	0.85486067	0.9613	-6.65
245281_at	DEF (CLA1) protein ; supported by	CLA1	AT4G15560	-1.02	-0.03	-0.19	0.8548186	0.9613	-6.65
260296_at	putative disease resistance protein	---	AT1G63750	1.05	0.08	0.19	0.85486626	0.9613	-6.65
248899_at	carboxy-terminal proteinase D1-like	---	AT5G46390	-1.02	-0.02	-0.19	0.85490466	0.9613	-6.65
256418_at	hypothetical protein	---	AT3G06160	1.01	0.02	0.19	0.85472221	0.9613	-6.65
262267_at	hypothetical protein predicted by g	---	---	-1.01	-0.02	-0.19	0.85496703	0.9613	-6.65
248892_at	unknown protein	---	AT5G46300	1.01	0.02	0.19	0.85518762	0.9615	-6.65
247638_at	arabinogalactan protein - like arab	FLA12	AT5G60490	-1.03	-0.05	-0.19	0.85526581	0.9615	-6.65
262441_at	hypothetical protein similar to hypo	OSB1	AT1G47720	1.02	0.03	0.19	0.85534204	0.9616	-6.65
259749_at	putative ribose 5-phosphate isome	RSW10	AT1G71100	-1.03	-0.05	-0.19	0.85541143	0.9616	-6.65
263869_at	unknown protein	PROPEP6	AT2G22000	-1.01	-0.02	-0.19	0.85555106	0.9617	-6.65
266852_at	hypothetical protein predicted by g	---	AT2G26810	1.01	0.02	0.19	0.85558269	0.9617	-6.65
247934_at	putative protein similar to unknown	---	AT5G57000	1.02	0.02	0.19	0.85573897	0.9617	-6.65
266366_at	unknown protein	---	AT2G41420	1.02	0.03	0.19	0.85573206	0.9617	-6.65
258118_at	unknown protein	---	AT3G14710	1.02	0.03	0.19	0.85573548	0.9617	-6.65
261999_at	hypothetical protein predicted by g	---	AT1G33800	-1.02	-0.03	-0.19	0.85606831	0.9621	-6.65
265613_at	putative DnaJ protein ; supported	---	AT2G25560	1.02	0.03	0.19	0.85624729	0.9622	-6.65

261279_at	class I chitinase, putative similar t	POM1	AT1G05850	1.07	0.10	0.19	0.85643856	0.9623	-6.65
251727_at	putative protein	---	AT3G56290	-1.03	-0.05	-0.19	0.85637488	0.9623	-6.65
249725_at	unknown protein	---	AT5G35470	1.01	0.02	0.19	0.85644286	0.9623	-6.65
254295_at	putative protein predicted protein,	---	AT4G23080	-1.01	-0.02	-0.19	0.85657946	0.9624	-6.65
255083_s_at	hypothetical protein	---	---	-1.02	-0.03	-0.19	0.85682839	0.9626	-6.65
254942_at	putative protein predicted proteins	---	AT4G10880	-1.01	-0.02	-0.19	0.85679252	0.9626	-6.65
262371_at	putative glycosyl transferase conta	---	AT1G73160	1.01	0.02	0.19	0.8568935	0.9626	-6.65
267422_at	putative protein kinase contains a	---	AT2G35050	-1.01	-0.02	-0.19	0.85691378	0.9626	-6.65
258064_at	putative cytochrome P450 similar t	CYP72A14	AT3G14680	1.04	0.06	0.19	0.85706225	0.9626	-6.65
254115_at	putative protein binding protein HF	---	AT4G24710	-1.01	-0.02	-0.19	0.85701982	0.9626	-6.65
245046_at	putative membrane transporter ; s	PDE135	AT2G26510	1.02	0.02	0.19	0.8570988	0.9626	-6.65
262585_at	hypothetical protein Is a member o	BOR4	AT1G15460	1.02	0.03	0.19	0.85727185	0.9627	-6.65
261683_at	hypothetical protein similar to hypo	---	AT1G47300	-1.01	-0.02	-0.19	0.85728231	0.9627	-6.65
266380_at	unknown protein	MEE13	AT2G14680	-1.02	-0.02	-0.19	0.85722639	0.9627	-6.65
249429_at	putative protein	---	AT5G39880	-1.01	-0.02	-0.19	0.85739262	0.9628	-6.65
261541_at	unknown protein contains Pfam pr	---	AT1G63600	-1.02	-0.02	-0.19	0.85773706	0.9628	-6.65
259745_at	unknown protein	SAG18	AT1G71190	1.02	0.02	0.19	0.85772432	0.9628	-6.65
249903_at	disease resistance protein-like	---	AT5G22690	-1.05	-0.07	-0.19	0.85761465	0.9628	-6.65
264499_at	Expressed protein ; supported by f	---	AT1G30795	1.02	0.02	0.19	0.85760617	0.9628	-6.65
266765_at	putative inorganic pyrophosphatas	AtPPa3	AT2G46860	-1.01	-0.02	-0.19	0.85767242	0.9628	-6.65
246216_at	cytochrome P450 like protein ; sup	ROT3	AT4G36380	-1.02	-0.03	-0.19	0.85773842	0.9628	-6.65
257995_at	putative monosaccharide transpor	---	AT3G19940	1.02	0.03	0.19	0.85771646	0.9628	-6.65
257282_at	TNP2-like transposon protein, put	---	---	1.02	0.02	0.19	0.85754387	0.9628	-6.65
257273_at	hypothetical protein contains Pfam	UVH3	AT3G28030	1.02	0.03	0.19	0.85786321	0.9628	-6.65
264493_at	unknown protein similar to multiple	GUT2	AT1G27440	1.03	0.04	0.19	0.8578674	0.9628	-6.65
253007_at	putative protein hypothetical prote	---	AT4G38090	1.02	0.03	0.19	0.85784459	0.9628	-6.65
247712_at	E2, ubiquitin-conjugating enzyme	UBC7	AT5G59300	-1.02	-0.02	-0.19	0.85792322	0.9628	-6.65
258443_at	unknown protein	---	AT3G22290	1.02	0.02	0.19	0.85811477	0.9629	-6.65
262707_at	hypothetical protein	---	AT1G16290	1.02	0.03	0.19	0.85809335	0.9629	-6.65
265908_at	contains similarity to S. cerevisiae	---	AT4G00270	1.02	0.03	0.19	0.85819997	0.9630	-6.65
245861_at	GTL1 - like protein GTL1, Arabido	---	AT5G28300	1.03	0.05	0.19	0.85850689	0.9630	-6.65
259331_at	putative auxin-induced protein sim	---	AT3G03840	-1.02	-0.03	-0.19	0.85827107	0.9630	-6.65
245226_at	gene_id:K17E7.15~unknown prote	---	AT3G29970	-1.07	-0.10	-0.19	0.85834238	0.9630	-6.65
257488_s_at	putative RING-finger protein	---	AT1G36950	1.01	0.02	0.19	0.85846582	0.9630	-6.65
251596_at	1-acylcerol-3-phosphate acyltrans	LPAT2	AT3G57650	1.01	0.02	0.19	0.85854217	0.9630	-6.65

264139_at	hypothetical protein contains simila	---	AT1G78940	-1.01	-0.02	-0.19	0.85847534	0.9630	-6.65
252917_at	putative zinc finger protein zinc fin	---	AT4G38960	-1.02	-0.03	-0.19	0.85838553	0.9630	-6.65
249893_at	Expressed protein ; supported by f	---	AT5G22555	-1.02	-0.02	-0.19	0.85844689	0.9630	-6.65
259616_at	hypothetical protein contains simila	C/VIF1	AT1G47960	1.02	0.03	0.18	0.85874259	0.9631	-6.65
266049_at	putative translation initiation factor	---	AT2G40780	1.01	0.02	0.18	0.85869285	0.9631	-6.65
260811_s_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.18	0.85875486	0.9631	-6.65
250970_at	putative protein ; supported by cD	---	AT5G02770	1.01	0.02	0.18	0.85886607	0.9632	-6.65
252908_at	putative protein	---	AT4G39670	-1.08	-0.12	-0.18	0.85893659	0.9632	-6.65
265292_s_at	hypothetical protein predicted by g	---	---	-1.01	-0.02	-0.18	0.85897981	0.9632	-6.65
251323_at	delta-8 sphingolipid desaturase ;s	---	AT3G61580	-1.02	-0.02	-0.18	0.85916564	0.9633	-6.65
258698_at	unknown protein	---	AT3G09690	1.02	0.02	0.18	0.85916699	0.9633	-6.65
260836_at	hypothetical protein predicted by g	---	---	-1.01	-0.02	-0.18	0.85914188	0.9633	-6.65
250554_at	unknown protein ;supported by ful	---	AT5G07900	1.02	0.02	0.18	0.85926283	0.9633	-6.65
250918_at	putative protein proline-rich protei	---	AT5G03610	1.07	0.09	0.18	0.85936151	0.9634	-6.65
249169_at	putative protein strong similarity to	---	AT5G42880	-1.01	-0.02	-0.18	0.85937134	0.9634	-6.65
251581_at	putative protein CARBON CATAB	---	AT3G58560	1.02	0.02	0.18	0.85943671	0.9634	-6.65
257562_at	hypothetical protein	---	---	1.02	0.02	0.18	0.85952901	0.9634	-6.65
247164_at	NifS-like aminotranfserase ; suppo	NFS1	AT5G65720	-1.02	-0.02	-0.18	0.85965058	0.9635	-6.65
261181_at	monosaccharide transporter, puta	---	AT1G34580	1.02	0.03	0.18	0.85975812	0.9636	-6.65
255339_at	hypothetical protein similar to A. th	---	AT4G04480	-1.03	-0.04	-0.18	0.85976165	0.9636	-6.65
254940_at	putative protein predicted proteins	---	AT4G10820	-1.01	-0.02	-0.18	0.85982082	0.9636	-6.65
250186_at	putative protein apospory-associa	---	AT5G14500	1.02	0.03	0.18	0.85993043	0.9636	-6.65
258127_at	unknown protein	---	AT3G24570	1.01	0.02	0.18	0.85998567	0.9637	-6.65
253799_at	putative DNA-binding protein AP2	---	AT4G28140	1.09	0.12	0.18	0.86017395	0.9637	-6.65
253750_at	putative transcription factor legher	---	AT4G29000	1.02	0.03	0.18	0.86018422	0.9637	-6.65
245236_at	putative DNA mismatch repair pro	MSH3	AT4G25540	-1.01	-0.02	-0.18	0.86015252	0.9637	-6.65
261396_at	hypothetical protein contains simila	---	AT1G79800	-1.02	-0.02	-0.18	0.86024876	0.9638	-6.65
257348_at	hypothetical protein predicted by g	---	AT2G42140	-1.03	-0.04	-0.18	0.86027946	0.9638	-6.65
266234_at	SKP1 interacting partner 3 (SKIP3	SKIP3	AT2G02350	-1.02	-0.02	-0.18	0.86032518	0.9638	-6.65
250710_at	MYB family transcription factor-like	MYB33	AT5G06100	1.01	0.02	0.18	0.86050492	0.9639	-6.65
248016_at	putative protein similar to unknown	---	AT5G56380	-1.02	-0.03	-0.18	0.86058824	0.9640	-6.65
248275_at	isp4 protein	ATOPT8	AT5G53520	1.01	0.02	0.18	0.86070204	0.9640	-6.65
260227_at	unknown protein similar to hypoth	---	AT1G74450	1.04	0.06	0.18	0.86069933	0.9640	-6.65
254296_at	hypothetical protein	---	AT4G23090	1.02	0.03	0.18	0.86079486	0.9640	-6.65
260932_s_at	hypothetical protein contains simila	PGP12	AT1G02520	-1.06	-0.08	-0.18	0.86090319	0.9641	-6.65

AFFX-r2-Bs-da	B. subtilis /GEN=jojG /DB_XREF=(	---	---	-1.02	-0.03	-0.18	0.86114007	0.9642	-6.65
248443_at	gibberellin 20-oxidase-like protein	---	AT5G51310	1.01	0.02	0.18	0.86114209	0.9642	-6.65
251053_at	Ca2+/H+ exchanger-like protein C	CAX4	AT5G01490	1.03	0.04	0.18	0.861102	0.9642	-6.65
266424_at	unknown protein	---	AT2G41330	-1.02	-0.04	-0.18	0.86124795	0.9643	-6.65
255946_at	glycine hydroxymethyltransferase,	SHM6	AT1G22020	-1.01	-0.02	-0.18	0.86133562	0.9643	-6.65
AFFX-Athal-Ac	Arabidopsis thaliana /REF=U3728	ACT7	---	1.01	0.02	0.18	0.86137029	0.9643	-6.65
248056_at	unknown protein ; supported by cI	XYLT	AT5G55500	-1.01	-0.02	-0.18	0.86134356	0.9643	-6.65
261339_at	protein kinase, putative similar to	---	AT1G35710	1.03	0.04	0.18	0.86137907	0.9643	-6.65
245369_at	Expressed protein ; supported by f	---	AT4G15975	1.03	0.04	0.18	0.86142286	0.9643	-6.65
262058_at	Expressed protein ; supported by f	---	AT1G79990	-1.01	-0.02	-0.18	0.86176053	0.9644	-6.65
265073_at	unknown protein similar to putative	---	AT1G55480	1.03	0.04	0.18	0.86176024	0.9644	-6.65
254810_at	putative protein pectinesterase - C	PME1	AT4G12390	1.03	0.05	0.18	0.86163734	0.9644	-6.65
256081_at	hypothetical protein contains Pfam	WOX14	AT1G20700	-1.02	-0.02	-0.18	0.86177724	0.9644	-6.65
260631_at	hypothetical protein predicted by g	---	AT1G62350	1.02	0.02	0.18	0.86173559	0.9644	-6.65
247681_at	serine/threonine-specific protein k	---	---	-1.02	-0.03	-0.18	0.86177035	0.9644	-6.65
245293_at	HSP like protein ; supported by cD	---	AT4G16660	1.05	0.06	0.18	0.86182782	0.9644	-6.65
251415_at	putative protein	---	AT3G60380	1.01	0.02	0.18	0.86187979	0.9644	-6.65
258676_at	hypothetical protein predicted by g	---	AT3G08600	1.02	0.02	0.18	0.86227787	0.9644	-6.65
246858_at	receptor-like protein kinase - like r	---	AT5G25930	-1.05	-0.07	-0.18	0.86216005	0.9644	-6.65
246861_at	putative protein phytochrome-ass	IAA28	AT5G25890	-1.01	-0.02	-0.18	0.86225627	0.9644	-6.65
247265_at	putative protein strong similarity to	CPuORF22	AT5G64550 /	-1.03	-0.05	-0.18	0.86253956	0.9644	-6.65
264855_at	3-hydroxy-3-methylglutaryl-coenzy	HSK	AT2G17265	-1.01	-0.02	-0.18	0.86250645	0.9644	-6.65
252524_at	putative protein mitochondrial ATF	---	AT3G46430	1.02	0.02	0.18	0.86211886	0.9644	-6.65
251718_at	putative protein hypothetical protei	MRLK	AT3G56100	-1.02	-0.03	-0.18	0.86244958	0.9644	-6.65
247594_at	putative protein farnesylated prote	---	AT5G60800	-1.02	-0.03	-0.18	0.86254329	0.9644	-6.65
266622_at	hypothetical protein predicted by g	---	AT2G35430	-1.02	-0.02	-0.18	0.86197359	0.9644	-6.65
264915_at	hypothetical protein predicted by g	---	AT1G60790	-1.01	-0.02	-0.18	0.86245512	0.9644	-6.65
256319_at	trehalose-phosphatase, putative c	---	AT1G35910	-1.05	-0.06	-0.18	0.86229193	0.9644	-6.65
265513_at	hypothetical protein	---	---	-1.01	-0.02	-0.18	0.86248099	0.9644	-6.65
247756_at	subtilisin-like serine protease conta	---	AT5G59100	-1.01	-0.02	-0.18	0.86213925	0.9644	-6.65
247562_at	putative protein	---	AT5G61120	1.01	0.02	0.18	0.86253776	0.9644	-6.65
266027_at	En/Spm-like transposon protein rel	---	---	1.01	0.02	0.18	0.86252617	0.9644	-6.65
258678_at	E2, ubiquitin-conjugating enzyme	UBC11	AT3G08690	1.02	0.03	0.18	0.86263436	0.9645	-6.65
244979_at	ribosomal protein S11	---	---	1.01	0.02	0.18	0.86268067	0.9645	-6.65
259282_at	unknown protein similar to unknow	GPAT5	AT3G11430	-1.02	-0.03	-0.18	0.8627469	0.9645	-6.65

248190_at	unknown protein	---	AT5G54130	1.01	0.02	0.18	0.86286482	0.9646	-6.65
247981_at	putative protein similar to unknown	MIOX5	AT5G56640	-1.01	-0.02	-0.18	0.86298991	0.9646	-6.65
258314_at	putative RAS-related GTP-binding	ATRABG3(	AT3G16100	-1.02	-0.02	-0.18	0.86297588	0.9646	-6.65
254005_at	subtilisin-like serine protease cont	UNE17	AT4G26330	-1.02	-0.03	-0.18	0.86297733	0.9646	-6.65
257070_at	hypothetical protein predicted by g	---	AT3G28190	-1.01	-0.02	-0.18	0.86285767	0.9646	-6.65
255111_at	peroxidase C2 precursor like prote	---	AT4G08780	-1.11	-0.15	-0.18	0.86314629	0.9646	-6.65
264211_at	putative gigantea protein strong sir	GI	AT1G22770	-1.01	-0.02	-0.18	0.86329886	0.9646	-6.65
248884_at	putative protein similar to unknown	---	AT5G46030	-1.01	-0.02	-0.18	0.86308914	0.9646	-6.65
247749_at	myb-related protein - like myb-rela	MYB119	AT5G58850	-1.02	-0.03	-0.18	0.86327325	0.9646	-6.65
260719_at	unknown protein	---	AT1G48090	1.02	0.03	0.18	0.86323168	0.9646	-6.65
259997_at	unknown protein similar to N-acety	---	AT1G67880	1.03	0.05	0.18	0.86306949	0.9646	-6.65
264885_s_at	NBS/LRR disease resistance prot	---	AT1G61180 /	-1.02	-0.02	-0.18	0.86328003	0.9646	-6.65
250362_at	1-D-deoxyxylulose 5-phosphate s	DXPS3	AT5G11380	-1.01	-0.02	-0.18	0.86343045	0.9647	-6.65
263083_at	purple acid phosphatase precurso	PAP12	AT2G27190	1.01	0.02	0.18	0.8635727	0.9647	-6.65
255347_at	putative retrotransposon protein	---	---	-1.01	-0.02	-0.18	0.86354752	0.9647	-6.65
262526_at	putative prenyl transferase (preph	SPS2	AT1G17050	-1.04	-0.06	-0.18	0.8636185	0.9647	-6.65
249178_at	putative protein similar to unknown	SCP2	AT5G42890	1.01	0.02	0.18	0.8648637	0.9648	-6.65
253474_at	hypothetical protein	---	AT4G32270	-1.02	-0.02	-0.18	0.86415385	0.9648	-6.65
255560_at	hypothetical protein similar to C. e	---	AT4G02030	1.01	0.02	0.18	0.86484652	0.9648	-6.65
263856_at	unknown protein	---	AT2G04410	1.02	0.03	0.18	0.86397123	0.9648	-6.65
258223_at	unknown protein ; supported by cl	PIFI	AT3G15840	-1.02	-0.02	-0.18	0.86460524	0.9648	-6.65
249859_at	serine protein kinase-like protein ;	---	AT5G22840 /	-1.03	-0.04	-0.18	0.86479052	0.9648	-6.65
263776_s_at	putative cyclic nucleotide-regulated	ATCNGC3	AT2G46430 /	1.07	0.09	0.18	0.86394868	0.9648	-6.65
261457_at	Expressed protein ; supported by f	---	AT1G21065 /	1.02	0.02	0.18	0.86459765	0.9648	-6.65
245725_at	sucrose synthase, putative similar	SUS6	AT1G73370	1.03	0.04	0.18	0.86428483	0.9648	-6.65
256822_at	unknown protein contains PF0061	IQD5	AT3G22190	-1.02	-0.02	-0.18	0.86390859	0.9648	-6.65
255892_at	hypothetical protein contains simila	---	AT1G17910	1.01	0.02	0.18	0.86417136	0.9648	-6.65
254691_at	hypothetical protein ; supported by	---	AT4G17840	-1.02	-0.03	-0.18	0.86455132	0.9648	-6.65
247894_at	putative protein similar to unknown	CPL4	AT5G58000 /	1.02	0.04	0.18	0.86400466	0.9648	-6.65
246798_at	putative protein various predicted	---	AT5G26930	1.01	0.02	0.18	0.86422269	0.9648	-6.65
250493_at	putative protein various predicted	---	AT5G09800	-1.10	-0.13	-0.18	0.86479222	0.9648	-6.65
254597_at	hypothetical protein	---	AT4G18980	-1.02	-0.03	-0.18	0.86454802	0.9648	-6.65
261617_s_at	hypothetical protein predicted by g	---	AT1G33090 /	1.01	0.02	0.18	0.86474937	0.9648	-6.65
251731_at	manganese superoxide dismutase	---	AT3G56350	1.02	0.03	0.18	0.86375193	0.9648	-6.65
257145_at	esterase, putative similar to estera	---	AT3G27320	-1.02	-0.03	-0.18	0.8643768	0.9648	-6.65

254473_s_at	putative protein kinase like protein	---	AT4G20520 /	-1.01	-0.02	-0.18	0.86456511	0.9648	-6.65
260446_at	unknown protein	---	AT1G72420	1.02	0.02	0.18	0.86390417	0.9648	-6.65
261908_at	stig1-like protein similar to Stig1 G	---	AT1G50650	-1.02	-0.02	-0.18	0.86413793	0.9648	-6.65
256594_at	hypothetical protein similar to puta	---	AT3G28520	1.01	0.02	0.18	0.8647626	0.9648	-6.65
256289_s_at	serine carboxypeptidase, putative	scpl14	AT3G12230 /	-1.04	-0.05	-0.18	0.86418067	0.9648	-6.65
256290_at	serine carboxypeptidase, putative	scpl17	AT3G12203	1.01	0.02	0.18	0.86421064	0.9648	-6.65
245230_at	hypothetical protein Contains Zinc	---	AT4G25610	1.02	0.03	0.18	0.86429664	0.9648	-6.65
256593_at	hypothetical protein similar to puta	---	AT3G28510	1.04	0.06	0.18	0.864835	0.9648	-6.65
249781_at	unknown protein	---	AT5G24250	-1.02	-0.02	-0.18	0.86464635	0.9648	-6.65
264008_at	unknown protein	---	AT2G21120	-1.02	-0.03	-0.18	0.86494101	0.9649	-6.65
256014_at	hypothetical protein predicted by g	---	AT1G19200	1.04	0.06	0.18	0.86517972	0.9650	-6.65
248711_at	putative protein similar to unknown	---	AT5G48270	-1.02	-0.02	-0.18	0.86515974	0.9650	-6.65
261521_at	protein kinase, putative similar to	SERK1	AT1G71830	1.04	0.05	0.18	0.86513752	0.9650	-6.65
258590_at	putative response regulator protei	ARR22	AT3G04280	-1.01	-0.02	-0.18	0.86527946	0.9650	-6.65
259437_at	protein serine/threonine kinase, pu	---	AT1G01540	-1.03	-0.04	-0.18	0.86540198	0.9651	-6.65
259461_at	unknown protein	---	AT1G18900	1.02	0.03	0.18	0.86542407	0.9651	-6.65
265125_at	hypothetical protein similar to puta	---	AT1G55410	1.01	0.02	0.18	0.86540863	0.9651	-6.65
254019_at	putative protein mature-parasite-in	---	AT4G26190	1.01	0.02	0.18	0.86553897	0.9651	-6.65
263964_at	putative CCHC-type zinc finger pro	---	AT2G12880	-1.02	-0.02	-0.18	0.865634	0.9652	-6.65
255382_at	putative pre-mRNA splicing factor	EMB2770	AT4G03430	-1.01	-0.02	-0.18	0.86568494	0.9652	-6.65
263729_at	hypothetical protein predicted by g	---	AT1G60080	-1.01	-0.02	-0.18	0.86579394	0.9652	-6.65
256202_s_at	hypothetical protein	---	AT1G48150 /	-1.01	-0.02	-0.18	0.8657928	0.9652	-6.65
256535_at	unknown protein	ANAC015	AT1G33280	1.02	0.03	0.18	0.86587402	0.9653	-6.65
260010_at	putative trehalose-6-phosphate syn	ATTPS6	AT1G68020	-1.02	-0.03	-0.18	0.86610633	0.9655	-6.66
247333_at	1-aminocyclopropane-1-carboxylic	FLS5	AT5G63600	1.03	0.04	0.17	0.86644285	0.9657	-6.66
267280_at	diacylglycerol O-acyltransferase ; s	TAG1	AT2G19450	-1.02	-0.03	-0.17	0.86637549	0.9657	-6.66
246321_at	unknown protein	---	AT1G16640	-1.01	-0.02	-0.17	0.86642623	0.9657	-6.66
266612_at	22 kDa peroxisomal membrane pro	---	AT2G14860	-1.01	-0.02	-0.17	0.86632851	0.9657	-6.66
254064_at	putative protein hypothetical prote	---	AT4G25410	1.01	0.02	0.17	0.86646548	0.9657	-6.66
256954_at	E2, ubiquitin-conjugating enzyme,	FUS9	AT3G13550	-1.02	-0.02	-0.17	0.86689617	0.9661	-6.66
251820_at	putative protein In2-1 protein, Zea	GSTL2	AT3G55040	1.03	0.04	0.17	0.86703257	0.9662	-6.66
258799_at	putative 40S ribosomal protein ide	RPSAb	AT3G04770	1.02	0.03	0.17	0.86711904	0.9662	-6.66
245780_at	unknown protein ;supported by full	---	AT1G45688	1.02	0.02	0.17	0.86820093	0.9663	-6.66
267559_at	putative cytochrome P450	CYP76C2	AT2G45570	-1.06	-0.09	-0.17	0.8685691	0.9663	-6.66
266284_at	putative pumilio/Mpt5 family RNA-b	APUM2	AT2G29190	1.02	0.02	0.17	0.8674824	0.9663	-6.66

252688_at	putative protein	---	AT3G44020	-1.02	-0.02	-0.17	0.86733227	0.9663	-6.66
263939_at	hypothetical protein predicted by g	ATTIM44-2	AT2G36070	-1.01	-0.02	-0.17	0.86810512	0.9663	-6.66
255586_at	hypothetical protein ;supported by	MEE49	AT4G01560	-1.02	-0.03	-0.17	0.8680753	0.9663	-6.66
253988_at	putative protein elongation factor I	---	AT4G26310	1.01	0.02	0.17	0.86870924	0.9663	-6.66
254675_at	RNA helicase - like protein Cdc28	---	AT4G18465	1.02	0.03	0.17	0.86867122	0.9663	-6.66
259736_at	endo-beta-1,4-glucanase, putative	AtGH9C2	AT1G64390	-1.07	-0.10	-0.17	0.86741497	0.9663	-6.66
260459_at	hypothetical protein predicted by g	---	AT1G68240	1.01	0.02	0.17	0.8687726	0.9663	-6.66
262467_at	hypothetical protein similar to hypo	FU	AT1G50240	-1.02	-0.02	-0.17	0.86857302	0.9663	-6.66
265257_at	succinyl-CoA ligase beta subunit ;	---	AT2G20420	1.03	0.04	0.17	0.86725387	0.9663	-6.66
256392_at	putative glycosyl transferase conta	GATL4	AT3G06260	-1.02	-0.02	-0.17	0.8680961	0.9663	-6.66
257350_x_at	hypothetical protein predicted by g	RALFL12	AT2G19040	-1.01	-0.02	-0.17	0.86809973	0.9663	-6.66
263834_at	hypothetical protein	---	AT2G40316	1.02	0.02	0.17	0.86815342	0.9663	-6.66
251394_at	endosperm specific protein - like e	FLA10	AT3G60900	-1.02	-0.02	-0.17	0.86846569	0.9663	-6.66
246356_x_at	hypothetical protein, 5' partial	---	---	-1.01	-0.02	-0.17	0.86770842	0.9663	-6.66
259147_at	putative RNA binding protein simila	APUM4	AT3G10360	1.02	0.03	0.17	0.86868724	0.9663	-6.66
255126_at	putative protein hypothetical prote	---	AT4G08270	-1.01	-0.02	-0.17	0.8684806	0.9663	-6.66
252788_at	putative protein several hypothetic	---	---	-1.01	-0.02	-0.17	0.86870911	0.9663	-6.66
262004_at	calcineurin B-like protein similar to	CBL8	AT1G64480	-1.02	-0.03	-0.17	0.86777168	0.9663	-6.66
258177_at	ubiquitin-regulatory protein, putati	---	AT3G21660	1.01	0.02	0.17	0.86875848	0.9663	-6.66
248341_at	unknown protein	---	AT5G52220	1.02	0.03	0.17	0.86828266	0.9663	-6.66
248769_at	putative protein strong similarity to	---	AT5G47730	-1.05	-0.07	-0.17	0.86773347	0.9663	-6.66
248778_at	unknown protein	---	AT5G47940	1.01	0.02	0.17	0.86833299	0.9663	-6.66
258758_at	putative RING zinc finger protein c	---	AT3G10810	1.02	0.03	0.17	0.86847228	0.9663	-6.66
266144_at	hypothetical protein	---	AT2G12170	1.01	0.02	0.17	0.86819588	0.9663	-6.66
248543_at	putative protein similar to unknown	---	AT5G50230	-1.01	-0.02	-0.17	0.86862089	0.9663	-6.66
247602_at	S-receptor kinase homolog 2 prec	RLK1	AT5G60900	-1.04	-0.06	-0.17	0.86845932	0.9663	-6.66
262755_at	unknown protein	---	AT1G16360	-1.01	-0.02	-0.17	0.86852315	0.9663	-6.66
257704_at	myb-related transcription factor, p	ATMYB67	AT3G12720	-1.01	-0.02	-0.17	0.86768346	0.9663	-6.66
256375_at	unknown protein	---	AT1G66720	1.01	0.02	0.17	0.86783399	0.9663	-6.66
257464_at	hypothetical protein predicted by g	---	AT1G20940	-1.01	-0.02	-0.17	0.86736256	0.9663	-6.66
252721_at	putative protein predicted proteins	---	AT3G43990	-1.02	-0.03	-0.17	0.86761461	0.9663	-6.66
248661_at	putative protein contains similarity	AGL80	AT5G48670	1.02	0.03	0.17	0.86876632	0.9663	-6.66
252497_at	putative protein several putative pr	---	AT3G46800	-1.01	-0.02	-0.17	0.86752893	0.9663	-6.66
254836_at	flavonoid 3,5-hydroxylase like prot	CYP706A7	AT4G12330	-1.01	-0.02	-0.17	0.86842296	0.9663	-6.66
261641_at	hypothetical protein similar to hypo	---	AT1G27670	1.03	0.04	0.17	0.86728103	0.9663	-6.66

265297_at	putative disease resistance protein	---	AT2G14080	-1.01	-0.02	-0.17	0.86887999	0.9664	-6.66
249099_at	putative protein similar to unknown	---	AT5G43550	-1.01	-0.01	-0.17	0.86892696	0.9664	-6.66
262223_at	hypothetical protein predicted by g	---	AT1G74680	-1.02	-0.03	-0.17	0.86930743	0.9664	-6.66
265019_at	putative myosin heavy chain simila	---	AT1G24560	-1.01	-0.02	-0.17	0.86906193	0.9664	-6.66
252478_at	putative protein mitotic phosphopr	---	AT3G46540	1.02	0.03	0.17	0.86912726	0.9664	-6.66
256503_at	myb-related protein similar to GI:7	ATRL6	AT1G75250	-1.05	-0.07	-0.17	0.86930279	0.9664	-6.66
259510_at	hypothetical protein predicted by g	---	AT1G43970	1.01	0.01	0.17	0.86930389	0.9664	-6.66
265248_at	unknown protein ; supported by cl	PIF4	AT2G43010	1.02	0.03	0.17	0.8693189	0.9664	-6.66
262011_at	hypothetical protein predicted by g	---	AT1G35614	-1.02	-0.03	-0.17	0.86929899	0.9664	-6.66
249857_at	C2H2-type zinc finger protein-like	---	AT5G22990	1.02	0.02	0.17	0.869197	0.9664	-6.66
250877_at	putative protein predicted protein,	SDP1	AT5G04040	-1.02	-0.03	-0.17	0.86941259	0.9664	-6.66
266479_at	unknown protein ; supported by cl	LSH3	AT2G31160	1.05	0.07	0.17	0.86939004	0.9664	-6.66
250203_at	alpha-mannosidase	---	AT5G13980	1.02	0.03	0.17	0.86954937	0.9665	-6.66
245221_s_at	polyprotein, putative similar to poly	---	---	1.01	0.02	0.17	0.86962635	0.9666	-6.66
250202_at	putative protein similar to unknown	---	AT5G13970	1.02	0.02	0.17	0.8696697	0.9666	-6.66
249502_s_at	expansin-like protein expansin - P	ATEXPA23	AT5G39280	1.02	0.02	0.17	0.86985216	0.9667	-6.66
260826_at	hypothetical protein predicted by g	---	AT1G06710	1.01	0.02	0.17	0.86992006	0.9668	-6.66
252808_at	putative protein various predicted	---	---	1.02	0.02	0.17	0.87024024	0.9671	-6.66
259557_at	hypothetical protein	WAK4	AT1G21210	1.01	0.02	0.17	0.87029889	0.9671	-6.66
264148_at	NAM (no apical meristem)-like pro	ANAC003	AT1G02220	1.12	0.16	0.17	0.87045862	0.9671	-6.66
259457_at	auxin response factor 1, putative s	ARF23	AT1G43950	1.01	0.02	0.17	0.87040545	0.9671	-6.66
259042_at	RGA1-like protein similar to RGA1	RGL2	AT3G03450	-1.02	-0.03	-0.17	0.87041918	0.9671	-6.66
246912_at	putative protein various predicted	---	AT5G25820	-1.04	-0.05	-0.17	0.87050509	0.9671	-6.66
247839_at	eukaryotic initiation factor 4, eIF4-	---	AT5G57870	1.02	0.03	0.17	0.87057197	0.9672	-6.66
247552_at	phytochelatin synthetase - like pro	COB	AT5G60920	1.02	0.03	0.17	0.87065949	0.9672	-6.66
259043_at	unknown protein similar to putative	---	AT3G03440	1.02	0.03	0.17	0.8706512	0.9672	-6.66
266071_at	unknown protein	---	AT2G18670	1.05	0.07	0.17	0.87076895	0.9672	-6.66
260458_at	unknown protein	---	AT1G68250	-1.01	-0.02	-0.17	0.87091385	0.9674	-6.66
253207_at	putative protein small auxin up-reg	---	AT4G34770	-1.04	-0.06	-0.17	0.87100744	0.9674	-6.66
252723_at	hypothetical protein ; supported by	---	AT3G43520	-1.01	-0.02	-0.17	0.87114047	0.9674	-6.66
264136_at	leucine-rich repeat transmembran	SRF5	AT1G78980	1.02	0.03	0.17	0.87111785	0.9674	-6.66
253243_at	putative protein	---	AT4G34560	-1.05	-0.08	-0.17	0.87113189	0.9674	-6.66
256618_at	hypothetical protein	VRN5	AT3G24440	-1.03	-0.04	-0.17	0.87108511	0.9674	-6.66
265667_at	putative CCAAT-binding transcripti	NF-YB11	AT2G27470	-1.01	-0.02	-0.17	0.87124186	0.9674	-6.66
252862_at	putative L-ascorbate oxidase L-as	---	AT4G39830	-1.04	-0.05	-0.17	0.8713009	0.9675	-6.66

264459_at	putative reverse transcriptase simi	---	---	1.02	0.03	0.17	0.87142422	0.9675	-6.66
251294_at	zinc transporter-like protein zinc tr	MTPA1	AT3G61940	1.01	0.02	0.17	0.87141088	0.9675	-6.66
256297_at	cytochrome P450, putative contair	---	AT1G69500	-1.02	-0.02	-0.17	0.87167299	0.9677	-6.66
249598_at	putative protein AtPP protein, Bras	---	AT5G37970	-1.01	-0.02	-0.17	0.87170639	0.9677	-6.66
266473_at	unknown protein	---	AT2G31110	-1.04	-0.06	-0.17	0.87177077	0.9677	-6.66
267587_at	unknown protein	---	AT2G42080	-1.02	-0.03	-0.17	0.87184193	0.9677	-6.66
266750_s_at	putative pectinesterase	VGDH1	AT2G47030	-1.01	-0.02	-0.17	0.87183609	0.9677	-6.66
249017_at	C2 domain-containing protein-like	---	AT5G44760	1.02	0.02	0.17	0.87191926	0.9678	-6.66
251116_at	serin carboxypeptidase - like prote	scpl40	AT3G63470	-1.02	-0.02	-0.17	0.87204534	0.9678	-6.66
266553_at	unknown protein ; supported by cl	---	AT2G46170	-1.02	-0.02	-0.17	0.87203785	0.9678	-6.66
249436_at	putative protein crp1 protein - Zea	---	AT5G39980	-1.02	-0.03	-0.17	0.8722019	0.9678	-6.66
253774_at	NAM / CUC2 -like protein No apic	anac074	AT4G28530	-1.02	-0.03	-0.17	0.87213501	0.9678	-6.66
262087_at	hypothetical protein predicted by g	---	AT1G56030	-1.01	-0.02	-0.17	0.87216855	0.9678	-6.66
253630_at	putative protein putative ATPase -	---	AT4G30490	1.02	0.02	0.17	0.87251381	0.9681	-6.66
263386_at	unknown protein ; supported by cl	---	AT2G40150	-1.03	-0.04	-0.17	0.8726806	0.9682	-6.66
259711_at	putative DNA-binding protein simil	---	AT1G77570	1.03	0.04	0.17	0.87274901	0.9682	-6.66
263302_at	hypothetical protein predicted by g	---	---	-1.01	-0.02	-0.17	0.87276033	0.9682	-6.66
260105_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.17	0.87272624	0.9682	-6.66
256226_at	unknown protein ; supported by cD	ATDI19	AT1G56280	-1.02	-0.03	-0.17	0.87292195	0.9683	-6.66
265565_at	putative retroelement pol polyprote	---	---	-1.01	-0.02	-0.17	0.87289399	0.9683	-6.66
247200_at	unknown protein ;supported by ful	---	AT5G65120	-1.02	-0.02	-0.17	0.87296981	0.9683	-6.66
253450_at	putative protein MUS308 gene, Dr	---	AT4G32700	1.01	0.02	0.17	0.87295628	0.9683	-6.66
259010_at	unknown protein contains helix-loo	---	AT3G07340	1.02	0.03	0.17	0.87303041	0.9683	-6.66
252879_at	putative protein predicted proteins	NST-K1	AT4G39390	-1.03	-0.05	-0.17	0.87326842	0.9683	-6.66
253870_at	putative protein	---	AT4G27530	1.01	0.02	0.17	0.87324088	0.9683	-6.66
259680_at	putative AUX1-like permease simi	LAX3	AT1G77690	-1.06	-0.09	-0.17	0.87312931	0.9683	-6.66
251694_s_at	putative protein NAM (no apical m	anac063	AT3G55210	-1.01	-0.02	-0.17	0.87332795	0.9683	-6.66
249461_at	putative protein predicted proteins	---	AT5G39640	1.01	0.02	0.17	0.87335287	0.9683	-6.66
261121_at	hypothetical protein predicted by g	---	AT1G75340	-1.01	-0.02	-0.17	0.8733119	0.9683	-6.66
251384_at	putative protein	---	AT3G60760	-1.01	-0.02	-0.17	0.87325779	0.9683	-6.66
261990_at	unknown protein	---	AT1G33660	-1.01	-0.02	-0.17	0.87340968	0.9683	-6.66
263122_at	prenyltransferase, putative similar	SPS1	AT1G78510	1.02	0.02	0.16	0.87379988	0.9685	-6.66
245716_at	Expressed protein ; supported by c	NDC1	AT5G08740	1.02	0.03	0.17	0.87373725	0.9685	-6.66
261991_at	hypothetical protein predicted by g	---	AT1G33700	1.02	0.02	0.16	0.8738326	0.9685	-6.66
256689_at	hypothetical protein predicted by g	---	AT3G32150	1.01	0.02	0.17	0.8736513	0.9685	-6.66

262857_at	major latex homologue type2 ident	---	AT1G14930	1.01	0.02	0.17	0.8737609	0.9685	-6.66
246273_at	globulin-like protein	---	AT4G36700	-1.01	-0.02	-0.17	0.87376781	0.9685	-6.66
254165_at	putative protein hypothetical prote	---	AT4G24330	-1.02	-0.03	-0.16	0.87379302	0.9685	-6.66
253502_at	Cytochrome P450-like protein cyt	CYP82C4	AT4G31940	1.01	0.02	0.16	0.8740004	0.9686	-6.66
249217_at	ubiquitin-like protein ; supported b	UBL5	AT5G42300	1.01	0.01	0.16	0.87412405	0.9686	-6.66
262479_at	leucine-rich repeat transmembran	SUB	AT1G11130	-1.01	-0.02	-0.16	0.87414641	0.9686	-6.66
253532_at	putative protein centromere protei	---	AT4G31570	1.01	0.02	0.16	0.87416256	0.9686	-6.66
253475_at	putative protein predicted protein,	---	AT4G32290	-1.03	-0.04	-0.16	0.87423142	0.9687	-6.66
249128_at	1-aminocyclopropane-1-carboxylat	---	AT5G43440	1.01	0.02	0.16	0.87444458	0.9687	-6.66
260027_at	unknown protein	CPuORF34	AT1G29950	1.02	0.03	0.16	0.87442691	0.9687	-6.66
253848_at	putative protein regulator protein,	---	AT4G28020	-1.02	-0.03	-0.16	0.87441312	0.9687	-6.66
251370_at	putative protein prib5, Ribes nigru	---	AT3G60450	-1.04	-0.05	-0.16	0.87443768	0.9687	-6.66
262901_at	hypothetical protein predicted by g	---	AT1G59910	1.03	0.05	0.16	0.87457707	0.9688	-6.66
254602_at	hypothetical protein	EDR2	AT4G19040	-1.01	-0.02	-0.16	0.87474503	0.9688	-6.66
266355_at	hypothetical protein predicted by g	---	AT2G01400	1.03	0.04	0.16	0.87474502	0.9688	-6.66
257878_at	hypothetical protein predicted by g	---	AT3G17150	-1.01	-0.02	-0.16	0.8747546	0.9688	-6.66
267202_s_at	putative oxysterol-binding protein	ORP1A	AT2G31020	1.02	0.03	0.16	0.87473974	0.9688	-6.66
258383_at	hypothetical protein predicted by g	---	AT3G15440	1.03	0.04	0.16	0.8748197	0.9689	-6.66
248471_at	unknown protein	---	AT5G50840	1.02	0.02	0.16	0.87486968	0.9689	-6.66
246455_at	putative protein predicted protein	---	AT5G16790	1.01	0.02	0.16	0.87492829	0.9689	-6.66
249042_at	ethylene-regulated nuclear protein	---	AT5G44350	-1.03	-0.04	-0.16	0.87497078	0.9689	-6.66
245268_at	hypothetical protein ; supported by	PRMT7	AT4G16570	1.02	0.03	0.16	0.87508036	0.9689	-6.66
258951_at	putative phosphatidylinositolglycar	---	AT3G01380	1.01	0.02	0.16	0.87505787	0.9689	-6.66
249326_at	unknown protein ; supported by cl	SYN2	AT5G40840	1.01	0.02	0.16	0.87515534	0.9689	-6.66
245008_at	hypothetical protein	---	---	1.01	0.02	0.16	0.87544404	0.9690	-6.66
265750_x_at	putative Athila retroelement ORF1	---	---	-1.02	-0.03	-0.16	0.87529601	0.9690	-6.66
252399_at	putative cyclic nucleotide-gated ch	CNGC16	AT3G48010	-1.01	-0.02	-0.16	0.87528218	0.9690	-6.66
249156_s_at	putative protein similar to unknown	---	AT5G43490	-1.01	-0.02	-0.16	0.87549809	0.9690	-6.66
262842_at	xyloglucan endo-transglycosylase	XTR2	AT1G14720	-1.03	-0.04	-0.16	0.87546425	0.9690	-6.66
247581_at	receptor-like protein kinase precu	---	AT5G61350	-1.01	-0.02	-0.16	0.87546337	0.9690	-6.66
259692_at	unknown protein	---	AT1G63080	1.01	0.02	0.16	0.87549592	0.9690	-6.66
258415_at	putative s-adenosylmethionine syn	MTO3	AT3G17390	1.03	0.04	0.16	0.87573353	0.9691	-6.66
245108_at	putative cytokinin oxidase	CKX1	AT2G41510	1.01	0.02	0.16	0.87578334	0.9691	-6.66
250962_at	putative protein various predicted	---	AT5G02990	-1.01	-0.02	-0.16	0.87586402	0.9691	-6.66
258271_at	hypothetical protein predicted by g	---	AT3G15605	-1.01	-0.02	-0.16	0.87585062	0.9691	-6.66

253902_at	NWMU4 - 2S albumin 4 precursor	---	AT4G27170	-1.01	-0.02	-0.16	0.87587433	0.9691	-6.66
260072_at	unknown protein supported by cDN	---	AT1G73650	1.01	0.02	0.16	0.87567984	0.9691	-6.66
261527_at	hypothetical protein similar to puta	---	AT1G14390	-1.02	-0.02	-0.16	0.87565443	0.9691	-6.66
259635_at	purple acid phosphatase, putative	PAP6	AT1G56360	1.01	0.02	0.16	0.87595211	0.9691	-6.66
250939_at	putative protein various predicted	iqd2	AT5G03040	-1.02	-0.03	-0.16	0.87703615	0.9692	-6.66
264757_at	receptor protein kinase (IRK1), pu	---	AT1G61360	1.06	0.08	0.16	0.87723777	0.9692	-6.66
252246_at	putative protein various predicted p	---	AT3G49725 /	1.01	0.02	0.16	0.87748272	0.9692	-6.66
254827_at	putative protein KIAA0255 gene, h	---	AT4G12650	1.01	0.02	0.16	0.87688637	0.9692	-6.66
265675_at	70kD heat shock protein ;supporte	HSP70T-2	AT2G32120	-1.02	-0.03	-0.16	0.87699646	0.9692	-6.66
258701_at	putative RNA helicase similar to R	---	AT3G09720	-1.02	-0.03	-0.16	0.87626619	0.9692	-6.66
253319_at	putative protein various predicted	EMB2758	AT4G33990	-1.02	-0.03	-0.16	0.87627256	0.9692	-6.66
247898_at	F-box protein ZTL/LFK1/ADO1, At	ZTL	AT5G57360	-1.01	-0.02	-0.16	0.8769212	0.9692	-6.66
264464_at	putative heat-shock protein similar	---	AT1G10350	-1.01	-0.02	-0.16	0.87694187	0.9692	-6.66
250460_at	putative protein similar to unknown	---	AT5G09850	-1.01	-0.02	-0.16	0.87746227	0.9692	-6.66
267389_at	putative beta-glucosidase	BGLU28	AT2G44460	-1.12	-0.17	-0.16	0.87717664	0.9692	-6.66
259335_s_at	unknown protein similar to unknow	---	AT3G03930 /	-1.02	-0.02	-0.16	0.87689601	0.9692	-6.66
265331_at	similar to gibberellin-regulated prot	---	AT2G18420	-1.01	-0.02	-0.16	0.87742269	0.9692	-6.66
262217_at	hypothetical protein predicted by g	---	AT1G74770	1.01	0.01	0.16	0.87657194	0.9692	-6.66
260814_at	histidine decarboxylase, putative s	emb1075	AT1G43710	1.01	0.02	0.16	0.87696147	0.9692	-6.66
258341_at	unknown protein similar to centrom	---	AT3G22790	1.04	0.06	0.16	0.87695626	0.9692	-6.66
249478_at	germin - like protein GLP6 germin	---	AT5G38950	-1.01	-0.02	-0.16	0.87645115	0.9692	-6.66
264216_at	hypothetical protein similar to hypo	---	AT1G60180	1.01	0.02	0.16	0.87635433	0.9692	-6.66
246534_at	putative protein several hypothetic	---	AT5G15890	-1.02	-0.02	-0.16	0.8765031	0.9692	-6.66
258533_at	hypothetical protein	---	AT3G06670	-1.01	-0.02	-0.16	0.87689049	0.9692	-6.66
245633_at	unknown protein similar to putative	AtTLP10	AT1G25280	1.01	0.01	0.16	0.87613701	0.9692	-6.66
248013_at	putative protein contains similarity	ACA8	AT5G56330	-1.02	-0.03	-0.16	0.87664068	0.9692	-6.66
259298_at	putative disease resistance protein	AtRLP31	AT3G05370	1.06	0.08	0.16	0.87698125	0.9692	-6.66
263943_at	putative mitochondrial carrier prote	---	AT2G35800	1.02	0.02	0.16	0.87673438	0.9692	-6.66
262740_at	lipase, putative contains Pfam pro	---	AT1G28590	-1.01	-0.02	-0.16	0.87738891	0.9692	-6.66
250492_at	putative protein Requiem protein,	ATXR5	AT5G09790	-1.01	-0.02	-0.16	0.87686135	0.9692	-6.66
263883_at	hypothetical protein predicted by g	---	AT2G21830	-1.01	-0.02	-0.16	0.87701751	0.9692	-6.66
262311_at	homeodomain leucine zipper prote	ATHB18	AT1G70920	-1.01	-0.02	-0.16	0.87727643	0.9692	-6.66
250040_at	putative protein predicted proteins	---	AT5G18390	1.01	0.02	0.16	0.87705645	0.9692	-6.66
257095_at	unknown protein ; supported by cl	ATPDIL5-3	AT3G20560	-1.02	-0.02	-0.16	0.87694411	0.9692	-6.66
255144_at	putative protein predicted proteins	---	---	-1.01	-0.01	-0.16	0.87712683	0.9692	-6.66

256142_at	hypothetical protein predicted by g	---	AT1G48790	-1.01	-0.02	-0.16	0.87616175	0.9692	-6.66
244960_at	ribosomal protein L32	---	---	-1.03	-0.04	-0.16	0.87734529	0.9692	-6.66
252814_at	putative protein several hypothetic	---	---	-1.01	-0.02	-0.16	0.87706958	0.9692	-6.66
267272_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.16	0.87732377	0.9692	-6.66
259201_at	hypothetical protein predicted usin	---	AT3G09080	1.02	0.03	0.16	0.87755382	0.9692	-6.66
256057_at	unknown protein contains similarity	NDA1	AT1G07180	-1.03	-0.04	-0.16	0.87807318	0.9692	-6.66
259257_at	unknown protein ;supported by ful	---	AT3G07760	1.01	0.02	0.16	0.87828345	0.9692	-6.66
257310_at	ATP-dependent RNA helicase, pu	---	AT3G26560	-1.01	-0.02	-0.16	0.87792557	0.9692	-6.66
258964_at	putative 3-phosphoinositide-depen	---	AT3G10540	-1.01	-0.02	-0.16	0.87834499	0.9692	-6.66
252256_at	PRE-MRNA SPLICING FACTOR	SRp34a	AT3G49430	1.02	0.02	0.16	0.87830084	0.9692	-6.66
256321_at	lipoxygenase, putative similar to li	LOX1	AT1G55020	-1.06	-0.08	-0.16	0.87797439	0.9692	-6.66
264526_at	putative calcium ATPase very sim	ECA3	AT1G10130	1.01	0.02	0.16	0.87834286	0.9692	-6.66
258410_at	putative ribosomal protein similar t	---	AT3G16780	1.03	0.05	0.16	0.87832712	0.9692	-6.66
267463_at	Expressed protein ; supported by f	---	AT2G33845	1.02	0.03	0.16	0.87796361	0.9692	-6.66
265703_at	putative ankyrin	---	AT2G03430	1.02	0.02	0.16	0.87835656	0.9692	-6.66
255380_at	putative calcium channel ; suppor	ATTPC1	AT4G03560	1.02	0.03	0.16	0.87800849	0.9692	-6.66
260080_at	putative RNA-binding protein cont	APUM7	AT1G78160	1.01	0.02	0.16	0.87811406	0.9692	-6.66
256949_at	hypothetical protein predicted by g	---	AT3G19070	1.01	0.01	0.16	0.87826974	0.9692	-6.66
253639_at	putative protein component of anil	---	AT4G30550	-1.02	-0.03	-0.16	0.87828701	0.9692	-6.66
254175_at	putative protein CGI-82 protein - H	---	AT4G24050	-1.01	-0.02	-0.16	0.87775187	0.9692	-6.66
257161_at	hypothetical protein predicted by g	SMAP2	AT3G24280	-1.01	-0.02	-0.16	0.87843016	0.9692	-6.66
266314_at	Argonaute (AGO1)-like protein ; s	AGO4	AT2G27040	-1.02	-0.03	-0.16	0.87785937	0.9692	-6.66
261976_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.16	0.87847839	0.9692	-6.66
265562_at	hypothetical protein predicted by g	---	AT2G05500	-1.01	-0.01	-0.16	0.87780556	0.9692	-6.66
261647_at	hypothetical protein similar to hypo	---	AT1G27740	-1.02	-0.02	-0.16	0.8784493	0.9692	-6.66
257400_s_at	hypothetical protein	---	AT1G23810 /	1.01	0.01	0.16	0.8776455	0.9692	-6.66
252919_at	putative endo-1,4-beta-glucanase	AtGH9B16	AT4G38990	-1.02	-0.02	-0.16	0.87873946	0.9693	-6.66
252760_x_at	putative protein several hypothetic	---	---	-1.01	-0.02	-0.16	0.8787153	0.9693	-6.66
251312_at	MADS-box protein AGL13 ; suppo	AGL13	AT3G61120	-1.01	-0.02	-0.16	0.87868648	0.9693	-6.66
264079_at	putative seed storage protein (vicil	---	AT2G28490	1.01	0.02	0.16	0.87875028	0.9693	-6.66
265727_at	putative DNA topoisomerase III be	---	AT2G32000	-1.01	-0.02	-0.16	0.87878892	0.9693	-6.66
264448_at	putative sensory transduction histi	AHK3	AT1G27320	-1.01	-0.02	-0.16	0.87887527	0.9694	-6.66
261534_at	unknown protein ;supported by full	PEX11C	AT1G01820	1.01	0.02	0.16	0.87900146	0.9695	-6.66
267111_s_at	hypothetical protein predicted by g	---	---	-1.02	-0.02	-0.16	0.8791374	0.9695	-6.66
AFFX-r2-At-Act	Arabidopsis thaliana /REF=U3728	---	---	1.01	0.02	0.16	0.8790992	0.9695	-6.66

261545_at	unknown protein	---	AT1G63530	1.01	0.02	0.16	0.87909458	0.9695	-6.66
261288_at	hypothetical protein predicted by g	---	AT1G37010	-1.01	-0.02	-0.16	0.87905014	0.9695	-6.66
261031_at	hypothetical protein predicted by g	---	AT1G17360	-1.03	-0.04	-0.16	0.87929189	0.9695	-6.66
258305_at	hypothetical protein predicted by g	---	---	1.01	0.01	0.16	0.87928651	0.9695	-6.66
254276_at	predicted protein PVPR3 protein,	---	AT4G22820	1.03	0.04	0.16	0.87932064	0.9695	-6.66
250574_at	putative protein putative transcript	---	AT5G08230	1.01	0.02	0.16	0.87950357	0.9697	-6.66
253673_at	putative protein putative phosphat	---	AT4G29530	-1.01	-0.02	-0.16	0.87973072	0.9698	-6.66
258665_at	thioredoxin-like protein similar to th	ATH9	AT3G08710	-1.02	-0.03	-0.16	0.87965543	0.9698	-6.66
248212_at	CHP-rich zinc finger protein-like	---	AT5G54020	1.01	0.02	0.16	0.87970588	0.9698	-6.66
261474_at	anionic peroxidase, putative simila	---	AT1G14540	1.08	0.11	0.16	0.87983768	0.9698	-6.66
264583_at	putative AVR9 elicitor response pr	---	AT1G05170	1.02	0.02	0.16	0.88001401	0.9700	-6.66
257306_at	hypothetical protein contains regio	---	AT3G30200	1.01	0.02	0.16	0.88014189	0.9701	-6.66
251456_at	beta-glucosidase-like protein sever	BGLU27	AT3G60120	1.11	0.15	0.16	0.8803456	0.9702	-6.66
265970_at	Mutator-like transposase similar to	---	---	-1.01	-0.02	-0.16	0.88030361	0.9702	-6.66
258408_at	unknown protein similar to putative	ATCHX19	AT3G17630	-1.01	-0.02	-0.16	0.88040005	0.9702	-6.66
264219_at	unknown protein contains similarity	---	AT1G60420	1.02	0.03	0.16	0.88066305	0.9703	-6.66
251879_at	putative protein hin1 protein, Nico	---	AT3G54200	-1.03	-0.04	-0.16	0.88062304	0.9703	-6.66
263518_at	Expressed protein ; supported by f	---	AT2G21655	1.01	0.02	0.16	0.88067137	0.9703	-6.66
264042_at	putative steroid sulfotransferase ;	ST	AT2G03760	-1.06	-0.08	-0.16	0.88052807	0.9703	-6.66
262099_s_at	auxin-regulated protein GH3, puta	GH3.4	AT1G59500	1.07	0.10	0.16	0.88073576	0.9703	-6.66
256358_at	unknown protein	---	AT1G66470	1.01	0.02	0.16	0.88074683	0.9703	-6.66
260155_at	unknown protein	---	AT1G52870	-1.03	-0.04	-0.16	0.88059815	0.9703	-6.66
247481_at	putative protein predicted protein,	---	AT5G62400	1.01	0.02	0.16	0.88085061	0.9704	-6.66
257744_at	hypothetical protein contains Pfam	---	AT3G29230	-1.02	-0.02	-0.16	0.88094538	0.9704	-6.66
254785_at	putative pollen surface protein enc	FLA2	AT4G12730	-1.05	-0.08	-0.15	0.88234943	0.9704	-6.66
263231_at	putative indole-3-acetate beta-gluc	---	AT1G05680	-1.11	-0.16	-0.15	0.88246822	0.9704	-6.66
262706_at	putative ATP-dependent RNA helic	---	AT1G16280	-1.02	-0.02	-0.16	0.88121038	0.9704	-6.66
254911_at	putative protein ;supported by full-	---	AT4G11100	-1.01	-0.02	-0.15	0.88196141	0.9704	-6.66
264920_at	hypothetical protein contains simila	ECHID	AT1G60550	1.01	0.02	0.15	0.88243897	0.9704	-6.66
266253_at	unknown protein contains non-con	HDT4	AT2G27840	1.02	0.04	0.15	0.88181368	0.9704	-6.66
264022_at	Expressed protein ; supported by f	---	AT2G21185	-1.02	-0.02	-0.15	0.88226356	0.9704	-6.66
259294_at	hypothetical protein predicted by g	ATN	AT3G05330	-1.02	-0.03	-0.16	0.88115705	0.9704	-6.66
260416_at	putative cullin similar to cullin 3 GB	CUL3B	AT1G69670	1.01	0.02	0.15	0.88206258	0.9704	-6.66
263435_at	putative ATP-dependent RNA helic	---	AT2G28600	1.02	0.03	0.15	0.88269711	0.9704	-6.66
249023_at	putative protein strong similarity to	---	AT5G44850	-1.03	-0.04	-0.15	0.88191406	0.9704	-6.66

258888_at	putative pectinesterase similar to p	---	AT3G05620	1.02	0.03	0.16	0.88118318	0.9704	-6.66
257312_at	Expressed protein ; supported by f	AT3G2659(	---	1.01	0.02	0.15	0.88265576	0.9704	-6.66
259415_at	hypothetical protein contains simila	---	AT1G02330	-1.02	-0.02	-0.15	0.88198646	0.9704	-6.66
257528_at	hypothetical protein predicted by g	---	AT3G02125	1.01	0.02	0.15	0.88166552	0.9704	-6.66
255260_at	score=63.7, E=3.9e-15, N=8 ; sup	---	AT4G05040	1.02	0.02	0.16	0.88104341	0.9704	-6.66
248702_at	unknown protein	---	AT5G48420	1.01	0.02	0.16	0.88101022	0.9704	-6.66
260392_at	putative enolase similar to ENOLA	---	AT1G74030	-1.07	-0.09	-0.15	0.88201001	0.9704	-6.66
258208_at	putative acetyltransferase similar t	---	AT3G13930	-1.02	-0.03	-0.15	0.88218793	0.9704	-6.66
255369_at	putative NifU-like metallocluster as	ISU3	AT4G04080	-1.01	-0.02	-0.15	0.88155134	0.9704	-6.66
250068_at	CHP-rich zinc finger protein-like	---	AT5G17960	1.01	0.02	0.15	0.88253385	0.9704	-6.66
258268_at	putative WD-repeat protein contai	WSIP2	AT3G15880	-1.02	-0.03	-0.15	0.88191148	0.9704	-6.66
265841_at	putative glycogenin	---	AT2G35710	-1.06	-0.08	-0.15	0.8823799	0.9704	-6.66
254336_at	aspartic proteinase like protein ory	---	AT4G22050	-1.02	-0.02	-0.15	0.88149899	0.9704	-6.66
246635_at	hypothetical protein predicted by g	---	AT1G31720	-1.02	-0.03	-0.15	0.88246708	0.9704	-6.66
247985_at	putative protein contains similarity	---	AT5G56790	-1.01	-0.02	-0.15	0.88188139	0.9704	-6.66
265218_at	putative transcription factor	GTF2H2	AT1G05055	1.01	0.01	0.15	0.88254034	0.9704	-6.66
248001_at	calcineurin B-like protein 2 (gb|AA(	CBL2	AT5G55990	1.02	0.02	0.15	0.88205468	0.9704	-6.66
263587_at	putative synaptobrevin	ATVAMP71	AT2G25340	1.01	0.02	0.15	0.88163651	0.9704	-6.66
258306_at	putative transcription factor similar	ATBZIP42	AT3G30530	-1.01	-0.01	-0.15	0.88143934	0.9704	-6.66
253142_at	putative protein methyl-directed m	MLH3	AT4G35520	1.01	0.02	0.15	0.88164987	0.9704	-6.66
264153_at	disease resistance protein RPS4,	ATPP2-A5	AT1G65390	1.03	0.04	0.15	0.88176028	0.9704	-6.66
251555_at	shatterproof 1 (SHP1)/ agamous -l	SHP1	AT3G58780	1.01	0.02	0.16	0.88133491	0.9704	-6.66
245931_at	major pollen allergen-like protein p	---	AT5G09280	1.02	0.02	0.15	0.88137535	0.9704	-6.66
260376_at	putative cytochrome P-450 similar	CYP78A10	AT1G74110	1.01	0.02	0.15	0.88213994	0.9704	-6.66
253439_at	dimethylaniline monooxygenase -	YUC1	AT4G32540	-1.01	-0.02	-0.15	0.88253263	0.9704	-6.66
259098_at	putative ribose 5-phosphate isome	---	AT3G04790	1.02	0.03	0.15	0.88176714	0.9704	-6.66
250098_at	putative protein ;supported by full-	---	AT5G17350	-1.08	-0.11	-0.15	0.8826845	0.9704	-6.66
261468_s_at	hypothetical protein predicted by g	---	AT1G27860 /	-1.02	-0.02	-0.16	0.88129069	0.9704	-6.66
263217_at	putative reticuline oxidase-like pro	---	AT1G30740	1.01	0.02	0.15	0.88266604	0.9704	-6.66
245071_at	putative vetispiradiene synthase	---	AT2G23230	1.02	0.02	0.15	0.88224385	0.9704	-6.66
258043_at	unknown protein ; supported by cl	---	AT3G21290	1.01	0.01	0.15	0.88274603	0.9704	-6.66
245644_at	unknown protein similar to putative	---	AT1G25320	-1.01	-0.02	-0.15	0.88284391	0.9705	-6.66
258974_at	unknown protein similar to brahma	---	AT3G01890	-1.01	-0.02	-0.15	0.88296708	0.9705	-6.66
267618_at	putative cyclin ; supported by cDN	CYCB1;4	AT2G26760	1.01	0.02	0.15	0.88298102	0.9705	-6.66
253415_at	putative protein peptidyl-prolyl cis-	---	AT4G33060	-1.02	-0.03	-0.15	0.88289783	0.9705	-6.66

254534_at	putative Fe(II) transport protein Fe	IRT2	AT4G19680	-1.01	-0.01	-0.15	0.88291654	0.9705	-6.66
266540_at	hypothetical protein predicted by g	---	AT2G35310	1.01	0.02	0.15	0.88308758	0.9705	-6.66
247621_at	putative protein predicted proteins	---	AT5G60340	1.01	0.02	0.15	0.88306077	0.9705	-6.66
252854_at	ubiquitin-specific protease 27 (UB	UBP27	AT4G39370	1.01	0.01	0.15	0.88329048	0.9707	-6.66
248584_at	putative protein similar to unknown	---	AT5G49960	1.02	0.03	0.15	0.88335276	0.9707	-6.66
247555_at	putative protein various predicted p	ECT3	AT5G61020	1.02	0.03	0.15	0.88356465	0.9708	-6.66
260813_at	VirE2-interacting protein VIP1 iden	VIP1	AT1G43700	1.02	0.02	0.15	0.88356206	0.9708	-6.66
256799_at	unknown protein ; supported by cl	---	AT3G18560	-1.03	-0.04	-0.15	0.88374552	0.9710	-6.66
260138_at	calmodulin-4 identical to GB:Q035	CAM4	AT1G66410	-1.01	-0.02	-0.15	0.88380577	0.9710	-6.66
250928_at	putative protein	EIN2	AT5G03280	1.01	0.02	0.15	0.88391011	0.9710	-6.66
261113_at	hypothetical protein predicted by g	---	AT1G75400	-1.02	-0.02	-0.15	0.8843527	0.9710	-6.66
258283_at	hypothetical protein predicted by g	---	AT3G26750	-1.01	-0.02	-0.15	0.88405249	0.9710	-6.66
246800_at	glycine hydroxymethyltransferase	SHM2	AT5G26780	-1.02	-0.02	-0.15	0.8843011	0.9710	-6.66
260261_at	unknown protein	---	AT1G68450	1.05	0.07	0.15	0.88416661	0.9710	-6.66
266952_at	putative gibberellin 2-oxidase	ATGA2OX3	AT2G34555	-1.01	-0.02	-0.15	0.88409132	0.9710	-6.66
257361_at	putative Ta11-like non-LTR retroel	---	---	1.01	0.02	0.15	0.88429453	0.9710	-6.66
246589_at	glucosyltransferase -like protein g	---	AT5G14860	-1.01	-0.02	-0.15	0.88402547	0.9710	-6.66
266105_at	putative transport protein SEC61 b	SEC61 BE	AT2G45070	1.02	0.02	0.15	0.88439303	0.9710	-6.66
262731_at	hypothetical protein similar to gb|A	MC8	AT1G16420	-1.09	-0.13	-0.15	0.88444126	0.9710	-6.66
261410_at	metallothionein-like protein identica	MT1C	AT1G07610	-1.04	-0.05	-0.15	0.88417546	0.9710	-6.66
245012_at	NADH dehydrogenase D3	---	---	-1.02	-0.02	-0.15	0.88408012	0.9710	-6.66
252047_at	putative protein heat shock protei	---	AT3G52490	-1.01	-0.02	-0.15	0.8844443	0.9710	-6.66
264369_at	Ste-20 related kinase SPAK, puta	---	AT1G70430	1.01	0.02	0.15	0.88428305	0.9710	-6.66
247417_at	putative protein similar to unknown	---	AT5G63040	1.01	0.02	0.15	0.88391048	0.9710	-6.66
245140_at	unknown protein predicted by gene	LBD18	AT2G45420	1.01	0.01	0.15	0.88464938	0.9710	-6.66
249228_at	SKP1/ASK1 (At2) identical to UIP2	ASK2	AT5G42190	-1.02	-0.02	-0.15	0.88460457	0.9710	-6.66
257664_at	hypothetical protein predicted by g	EMB2743	AT3G20400	1.02	0.02	0.15	0.88457544	0.9710	-6.66
252446_at	beta-D-glucan exohydrolase - like	---	AT3G47010	1.01	0.01	0.15	0.8846677	0.9710	-6.66
254554_at	hypothetical protein	---	AT4G19550	-1.01	-0.02	-0.15	0.88467865	0.9710	-6.66
255023_at	hypothetical protein	---	AT4G09850	-1.01	-0.02	-0.15	0.88485948	0.9712	-6.66
250679_at	putative protein contains similarity	---	AT5G06550	-1.02	-0.03	-0.15	0.88498994	0.9712	-6.66
263650_at	hypothetical protein predicted by g	---	AT1G04360	-1.01	-0.02	-0.15	0.8849846	0.9712	-6.66
262239_at	unknown protein similar to putative	---	AT1G48230	1.02	0.03	0.15	0.8852353	0.9714	-6.66
255743_at	unknown protein ; supported by cD	---	AT1G25375	-1.01	-0.02	-0.15	0.88545008	0.9716	-6.66
248195_at	membrane associated protein ; su	ATMAMI	AT5G54110	-1.01	-0.02	-0.15	0.88549397	0.9716	-6.66

255137_at	extensin-like protein extensin prec	---	AT4G08370	1.01	0.02	0.15	0.88570231	0.9718	-6.66
254483_at	putative protein CRP1, Zea mays,	---	AT4G20740	1.02	0.02	0.15	0.88590985	0.9718	-6.66
248309_at	putative protein contains similarity	---	AT5G52540	1.03	0.05	0.15	0.88590015	0.9718	-6.66
258862_at	putative mitochondrial processing	MPPBETA	AT3G02090	1.01	0.02	0.15	0.88592922	0.9718	-6.66
265808_at	hypothetical protein predicted by g	---	AT2G17960	1.01	0.02	0.15	0.88614765	0.9718	-6.66
250642_at	receptor-like protein kinase severa	ERL2	AT5G07180	1.01	0.01	0.15	0.88596645	0.9718	-6.66
263094_at	hypothetical protein predicted by g	---	AT2G16020	-1.01	-0.02	-0.15	0.88604282	0.9718	-6.66
246828_at	putative protein hypothetical prote	---	---	-1.01	-0.02	-0.15	0.88577659	0.9718	-6.66
251848_at	Expressed protein ; supported by c	BZIP25	AT3G54620	1.01	0.02	0.15	0.88597915	0.9718	-6.66
247217_s_at	MADS box transcription factors-like	MAF3	AT5G65050 /	-1.01	-0.01	-0.15	0.88613462	0.9718	-6.66
260202_at	hypothetical protein predicted by g	---	---	-1.01	-0.01	-0.15	0.88613351	0.9718	-6.66
262777_at	hypothetical protein predicted by g	---	AT1G13030	-1.02	-0.03	-0.15	0.88643616	0.9720	-6.66
246424_at	Exportin1 (XPO1) protein ; suppor	XPO1A	AT5G17020	1.01	0.02	0.15	0.88648543	0.9720	-6.66
250247_at	unknown protein	---	AT5G13720	1.01	0.01	0.15	0.88635952	0.9720	-6.66
256656_at	hypothetical protein similar to hypo	---	AT3G18900	-1.01	-0.02	-0.15	0.88645477	0.9720	-6.66
267332_at	hypothetical protein predicted by g	---	AT2G19290	-1.01	-0.01	-0.15	0.8864007	0.9720	-6.66
247990_at	unknown protein ;supported by ful	---	AT5G56360	1.01	0.02	0.15	0.8866443	0.9720	-6.66
245649_at	F5A9.21 unknown protein; similar	---	AT1G24706	1.01	0.02	0.15	0.8866234	0.9720	-6.66
267001_at	putative urease accessory protein	UREG	AT2G34470	-1.02	-0.02	-0.15	0.88668304	0.9720	-6.66
249189_at	putative protein similar to unknown	AtHB27	AT5G42780	1.02	0.03	0.15	0.88678791	0.9721	-6.66
256082_at	hypothetical protein predicted by g	---	AT1G20720	1.02	0.03	0.15	0.88694804	0.9722	-6.66
254178_at	hypothetical protein	---	AT4G23880	1.05	0.07	0.15	0.8872091	0.9724	-6.66
265368_at	hypothetical protein identical to hy	---	AT2G13350	1.02	0.02	0.15	0.88719532	0.9724	-6.66
265591_at	hypothetical protein predicted by g	---	AT2G20150	1.02	0.02	0.15	0.88729296	0.9725	-6.66
266733_at	similar to axi 1 protein from Nicotia	---	AT2G03280	1.01	0.02	0.15	0.88745501	0.9726	-6.66
249491_at	germin - like protein germin-like pr	---	AT5G39130	-1.01	-0.02	-0.15	0.88746852	0.9726	-6.66
267646_at	putative phosphate transporter	PHT5	AT2G32830	1.02	0.03	0.15	0.88779636	0.9726	-6.66
245489_at	FCA gamma protein	FCA	AT4G16280	1.01	0.02	0.15	0.88777916	0.9726	-6.66
247205_at	unknown protein ;supported by ful	PROPEP2	AT5G64890	1.06	0.08	0.15	0.8876842	0.9726	-6.66
251302_at	RAV-like protein DNA-binding pro	NGA2	AT3G61970	1.01	0.01	0.15	0.88763912	0.9726	-6.66
264483_at	unknown protein	---	AT1G77230	-1.02	-0.02	-0.15	0.88759497	0.9726	-6.66
252793_at	hypothetical protein	---	---	-1.01	-0.01	-0.15	0.88778122	0.9726	-6.66
267302_at	putative unknown protein, leucine-	---	AT2G30100	-1.01	-0.01	-0.15	0.88768659	0.9726	-6.66
248905_at	putative protein contains similarity	---	AT5G46250	-1.01	-0.02	-0.15	0.88805118	0.9726	-6.66
251500_at	receptor-like protein kinase recept	---	AT3G59110	-1.01	-0.02	-0.15	0.88824094	0.9726	-6.66

257540_at	hypothetical protein	---	AT3G21520	1.01	0.02	0.15	0.88824503	0.9726	-6.66
258819_at	unknown protein similar to putativ	---	AT3G04590	-1.01	-0.02	-0.15	0.88824042	0.9726	-6.66
266837_x_at	unknown protein	---	AT2G25990	-1.01	-0.01	-0.15	0.8883221	0.9726	-6.66
259589_at	unknown protein	---	AT1G28135	-1.01	-0.02	-0.15	0.88832662	0.9726	-6.66
261185_at	cytochrome p450, putative similar	CYP94D1	AT1G34540	1.01	0.02	0.15	0.88792201	0.9726	-6.66
246337_at	putative protein putative integral m	CHX12	AT3G44910	-1.02	-0.02	-0.15	0.88830821	0.9726	-6.66
260187_at	hypothetical protein	LBD5	AT1G36000	-1.01	-0.01	-0.15	0.88809942	0.9726	-6.66
250312_at	unknown protein	---	AT5G12260	1.01	0.02	0.15	0.88834623	0.9726	-6.66
260854_at	CCAAT-box binding factor HAP3 h	LEC1	AT1G21970	1.02	0.02	0.15	0.88804459	0.9726	-6.66
249495_at	germin - like protein GLP6 exon 2	GLP6	AT5G39100	-1.01	-0.02	-0.15	0.88803907	0.9726	-6.66
247195_at	putative protein contains similarity	---	AT5G65500	1.01	0.02	0.15	0.88840787	0.9727	-6.66
245698_at	phosphate/phosphoenolpyruvate tr	---	AT5G04160	1.02	0.03	0.15	0.88855243	0.9728	-6.66
263220_at	hypothetical protein predicted by g	emb2279	AT1G30610	-1.01	-0.02	-0.15	0.88859345	0.9728	-6.66
253421_at	putative protein predicted proteins	---	AT4G32340	1.02	0.02	0.15	0.88873999	0.9729	-6.66
249095_at	myosin heavy chain MYA2 (pir||S5	MYA2	AT5G43900	1.02	0.03	0.15	0.88886775	0.9730	-6.66
245271_at	transcription factor like protein ; su	---	AT4G16430	1.01	0.01	0.15	0.88888937	0.9730	-6.66
250913_at	3-deoxy-D-manno-octulosonic aci	---	AT5G03770	-1.01	-0.02	-0.14	0.889	0.9730	-6.66
249493_at	acyltransferase -like protein Anthc	---	AT5G39080	-1.02	-0.03	-0.14	0.89046387	0.9731	-6.66
246792_at	putative protein predicted proteins	---	AT5G27290	1.03	0.04	0.14	0.88971226	0.9731	-6.66
262433_s_at	DNA binding protein, putative simi	ATRBP47C	AT1G47490 /	-1.01	-0.01	-0.14	0.89017085	0.9731	-6.66
259899_at	hypothetical protein predicted by g	---	AT1G71210	1.02	0.02	0.14	0.88938327	0.9731	-6.66
253033_at	putative protein aminoacylase I - S	---	AT4G38220	-1.01	-0.02	-0.14	0.8906966	0.9731	-6.66
250220_at	receptor protein kinase-like protein	---	AT5G14210	1.03	0.04	0.14	0.89010103	0.9731	-6.66
265626_at	unknown protein ;supported by ful	---	AT2G27260	-1.01	-0.02	-0.14	0.89082316	0.9731	-6.66
258015_at	unknown protein	---	AT3G19340	-1.01	-0.02	-0.14	0.89027359	0.9731	-6.66
249974_at	putative protein predicted proteins	---	AT5G18780	1.02	0.03	0.14	0.88940442	0.9731	-6.66
246901_at	putative protein Leaf protein, Phar	---	AT5G25630	1.01	0.02	0.14	0.89036416	0.9731	-6.66
259496_at	hypothetical protein predicted by g	---	AT1G15900	1.01	0.02	0.14	0.89012259	0.9731	-6.66
252421_at	endochitinase-like protein BASIC	---	AT3G47540	1.07	0.09	0.14	0.89079337	0.9731	-6.66
264859_at	glucose-6-phosphate 1-dehydroge	G6PD3	AT1G24280	-1.04	-0.05	-0.14	0.88996988	0.9731	-6.66
259902_at	disease resistance protein, putativ	AtRLP13	AT1G74170	1.03	0.04	0.14	0.89041193	0.9731	-6.66
253986_at	putative protein predicted protein,	---	AT4G26210	1.02	0.03	0.14	0.89008334	0.9731	-6.66
246088_at	putative protein	---	AT5G20600	1.02	0.02	0.14	0.890083	0.9731	-6.66
258023_at	cinnamyl alcohol dehydrogenase i	ATCAD4	AT3G19450	-1.03	-0.04	-0.14	0.8907296	0.9731	-6.66
250744_at	putative protein strong similarity to	---	AT5G05840	-1.01	-0.02	-0.14	0.8892943	0.9731	-6.66

255175_at	putative glucosyltransferase ;supp	ATCSLC12	AT4G07960	1.01	0.02	0.14	0.88971475	0.9731	-6.66
252455_at	putative protein various predicted	---	AT3G47140	-1.01	-0.01	-0.14	0.88961412	0.9731	-6.66
249936_at	putative protein similar to unknown	---	AT5G22450	-1.01	-0.02	-0.14	0.89051254	0.9731	-6.66
249288_at	unknown protein ;supported by ful	---	AT5G41050	-1.04	-0.05	-0.14	0.89005248	0.9731	-6.66
248810_at	disease resistance protein-like	ADR1-L3	AT5G47280	1.01	0.01	0.14	0.89080797	0.9731	-6.66
263658_at	unknown protein EST gb|T21788 c	---	AT1G04490	-1.01	-0.02	-0.14	0.88941741	0.9731	-6.66
264165_at	hypothetical protein contains simila	ATNAP11	AT1G65410	1.01	0.01	0.14	0.88992397	0.9731	-6.66
258019_at	hypothetical protein predicted by g	---	AT3G19470	1.01	0.02	0.14	0.88938782	0.9731	-6.66
266029_at	putative serine carboxypeptidase I	scpl38	AT2G05850	1.01	0.02	0.14	0.89081173	0.9731	-6.66
257068_at	non-LTR reverse transcriptase, pu	---	---	1.01	0.01	0.14	0.89084062	0.9731	-6.66
245577_at	kinase like protein	---	AT4G14780	1.01	0.02	0.14	0.8903349	0.9731	-6.66
249431_at	polygalacturonase-like protein pol	---	AT5G39910	-1.02	-0.03	-0.14	0.88925096	0.9731	-6.66
262097_at	hypothetical protein predicted by g	---	AT1G55990	-1.01	-0.02	-0.14	0.88927413	0.9731	-6.66
250689_at	putative protein similar to unknown	---	AT5G06610	1.03	0.04	0.14	0.89061616	0.9731	-6.66
253914_at	putative protein late embryogenes	---	AT4G27400	1.02	0.02	0.14	0.88958587	0.9731	-6.66
260456_at	hypothetical protein	---	AT1G72490	-1.01	-0.02	-0.14	0.89077886	0.9731	-6.66
261993_at	unknown protein	---	AT1G33860	1.01	0.02	0.14	0.8894936	0.9731	-6.66
255109_s_at	hypothetical protein	---	AT4G08760	-1.01	-0.01	-0.14	0.89014237	0.9731	-6.66
259476_at	Myb-related transcription activator	---	AT1G19000	1.02	0.02	0.14	0.89004578	0.9731	-6.66
261978_at	Athila retroelment ORF 1, putative	---	---	1.01	0.01	0.14	0.89054803	0.9731	-6.66
248734_at	putative protein similar to unknown	ELP1	AT5G48090	-1.02	-0.02	-0.14	0.89052	0.9731	-6.66
264074_at	putative retroelement pol polyprote	---	---	-1.01	-0.02	-0.14	0.89002317	0.9731	-6.66
255899_at	zinc-finger protein (C-terminal), pu	---	AT1G17970	-1.02	-0.03	-0.14	0.89026725	0.9731	-6.66
257386_at	hypothetical protein predicted by g	---	AT2G42440	1.01	0.01	0.14	0.88944711	0.9731	-6.66
247502_at	putative protein predicted proteins	---	AT5G61940	1.01	0.02	0.14	0.89097809	0.9732	-6.66
247576_at	putative protein predicted protein,	---	AT5G61280	-1.01	-0.01	-0.14	0.89104646	0.9732	-6.66
255496_at	putative protein similar to plant nuc	BZO2H1	AT4G02640	-1.02	-0.02	-0.14	0.89118162	0.9733	-6.66
252141_at	putative protein	---	AT3G51100	-1.01	-0.01	-0.14	0.89132581	0.9734	-6.66
253906_at	putative protein disease resistanc	---	AT4G27220	1.02	0.02	0.14	0.89137295	0.9734	-6.66
262965_at	hypothetical protein predicted by g	---	AT1G54310	1.02	0.02	0.14	0.8915007	0.9734	-6.66
255256_at	see GB:AC003952 similar to a fam	---	AT4G05080	1.01	0.02	0.14	0.89147063	0.9734	-6.66
258767_at	putative (1-4)-beta-mannan endoh	---	AT3G10890	-1.01	-0.02	-0.14	0.89149863	0.9734	-6.66
248345_at	unknown protein	SHOC1	AT5G52290	-1.01	-0.01	-0.14	0.8914906	0.9734	-6.66
262077_at	dynamin-like protein similar to dyn	ADL3	AT1G59610	-1.01	-0.01	-0.14	0.89157834	0.9734	-6.66
247700_at	RNA-binding protein - like cold-ind	---	AT5G59860	1.01	0.01	0.14	0.89158869	0.9734	-6.66

260478_at	DnaJ isolog	---	AT1G11040	-1.01	-0.01	-0.14	0.89165141	0.9734	-6.66
253551_at	Expressed protein ; supported by c	---	AT4G30996	1.01	0.02	0.14	0.89183834	0.9735	-6.66
245062_at	hypothetical protein predicted by g	BPM3	AT2G39760	-1.01	-0.01	-0.14	0.89186184	0.9735	-6.66
259134_at	hypothetical protein predicted by g	---	AT3G05390	1.04	0.05	0.14	0.89183068	0.9735	-6.66
259479_at	Expressed protein ; supported by f	---	AT1G19020	1.05	0.07	0.14	0.89204417	0.9735	-6.66
250602_s_at	unknown protein	---	AT5G07940	1.01	0.02	0.14	0.89227143	0.9735	-6.66
245229_at	putative protein contains EST gb:T	---	AT4G25620	1.02	0.03	0.14	0.89219366	0.9735	-6.66
264964_at	hypothetical protein predicted by g	---	AT1G60460	-1.01	-0.02	-0.14	0.89222458	0.9735	-6.66
246551_at	putative protein predicted proteins	---	AT5G15070	-1.01	-0.02	-0.14	0.89225035	0.9735	-6.66
264096_at	Expressed protein ; supported by f	---	AT1G78995	-1.02	-0.03	-0.14	0.89236119	0.9735	-6.66
263052_at	unknown protein	---	AT2G13430	-1.01	-0.01	-0.14	0.89231774	0.9735	-6.66
254342_at	receptor like protein (fragment) ES	---	AT4G22140	-1.01	-0.01	-0.14	0.89227733	0.9735	-6.66
265035_at	hypothetical protein contains Pfam	---	AT1G61620	1.01	0.02	0.14	0.89232542	0.9735	-6.66
246688_at	putative protein predicted proteins	---	---	-1.01	-0.01	-0.14	0.89225555	0.9735	-6.66
255170_at	hypothetical protein similar to A. th	---	---	-1.01	-0.02	-0.14	0.89207355	0.9735	-6.66
263754_at	putative DnaJ protein ;supported b	---	AT2G21510	1.03	0.04	0.14	0.89244525	0.9736	-6.66
259196_at	putative ribosomal protein S2 simil	RPS2	AT3G03600	1.02	0.02	0.14	0.89251404	0.9736	-6.66
261459_at	O-methyltransferase, putative sim	---	AT1G21100	-1.06	-0.08	-0.14	0.89295029	0.9737	-6.66
265735_at	putative aldolase ;supported by fu	---	AT2G01140	1.02	0.02	0.14	0.89274051	0.9737	-6.66
246199_at	putative protein ;supported by full-l	---	AT4G36530	1.02	0.02	0.14	0.89274448	0.9737	-6.66
260944_at	beta-galactosidase, putative simila	BGAL5	AT1G45130	-1.07	-0.10	-0.14	0.8929944	0.9737	-6.66
246418_at	quinone oxidoreductase -like prote	---	AT5G16960	1.01	0.02	0.14	0.89288279	0.9737	-6.66
245257_at	calmodulin ; supported by cDNA: g	CAM8	AT4G14640	1.01	0.02	0.14	0.8929717	0.9737	-6.66
262847_at	unknown protein similar to myosin	ATMAP70-4	AT1G14840	1.02	0.03	0.14	0.89280288	0.9737	-6.66
251911_at	putative C2H2-type zinc finger prot	---	AT3G53820	1.01	0.02	0.14	0.89286084	0.9737	-6.66
254870_at	KI domain interacting kinase 1 -lik	---	AT4G11900	1.02	0.03	0.14	0.89271376	0.9737	-6.66
245189_at	F12A21.18 hypothetical protein	---	AT1G67670	1.01	0.01	0.14	0.89315344	0.9738	-6.66
254806_at	putative trehalose-6-phosphate ph	---	AT4G12430	-1.01	-0.02	-0.14	0.89334319	0.9739	-6.66
260710_at	protein phosphatase 2C, putative	---	AT1G17545	1.01	0.01	0.14	0.89326311	0.9739	-6.66
252437_at	putative protein pectinesterase ho	---	AT3G47380	-1.03	-0.05	-0.14	0.89339054	0.9739	-6.66
247352_at	serine/threonine-protein kinase ;su	SNRK2.5	AT5G63650	-1.03	-0.04	-0.14	0.89336214	0.9739	-6.66
260889_at	hypothetical protein predicted by g	---	AT1G29120	1.01	0.01	0.14	0.89350759	0.9740	-6.66
248470_at	unknown protein	---	AT5G50830	-1.01	-0.02	-0.14	0.89351358	0.9740	-6.66
261766_at	auxin-induced protein IAA5, putati	IAA5	AT1G15580	1.03	0.05	0.14	0.89357813	0.9740	-6.66
250954_at	putative protein ;supported by full-	ATRAB8C	AT5G03520	-1.01	-0.02	-0.14	0.89377635	0.9740	-6.66

260148_at	putative oxidoreductase similar to	---	AT1G52800	1.02	0.02	0.14	0.89381083	0.9740	-6.66
261883_at	protein kinase, putative similar to	---	AT1G80870	-1.01	-0.02	-0.14	0.8937466	0.9740	-6.66
265659_at	putative disease resistance protein	AtRLP20	AT2G25440	-1.03	-0.04	-0.14	0.89372778	0.9740	-6.66
249226_at	GDSL-motif lipase/hydrolase-like p	---	AT5G42170	-1.01	-0.01	-0.14	0.89365112	0.9740	-6.66
261438_at	metallothionein-like protein identica	---	AT1G07590	1.01	0.01	0.14	0.8939179	0.9741	-6.66
245123_at	unknown protein ; supported by cl	CAO	AT2G47450	-1.01	-0.02	-0.14	0.89404235	0.9741	-6.66
246546_at	voltage-dependent anion-selective	VDAC3	AT5G15090	1.02	0.02	0.14	0.89401888	0.9741	-6.66
245475_at	hypothetical protein	---	AT4G16080	-1.01	-0.01	-0.14	0.89420066	0.9742	-6.66
262241_at	hypothetical protein predicted by g	---	AT1G48390	1.01	0.01	0.14	0.89428316	0.9743	-6.66
246131_at	MOLYBDOPTERIN BIOSYNTHES	B73	AT5G20990	-1.01	-0.01	-0.14	0.89450914	0.9744	-6.66
255581_at	putative transposon protein simila	---	---	-1.01	-0.02	-0.14	0.89445703	0.9744	-6.66
253787_at	serine/threonine kinase-like protei	---	AT4G28670	1.01	0.02	0.14	0.89448417	0.9744	-6.66
255292_s_at	putative calcium dependent protein	CPK22	AT4G04710	1.01	0.02	0.14	0.89457341	0.9744	-6.66
257817_at	putative RNA-binding protein cont	---	AT3G25150	1.01	0.02	0.14	0.89471397	0.9744	-6.66
254645_at	putative protein	---	AT4G18520	-1.01	-0.02	-0.14	0.89486565	0.9744	-6.66
248312_at	unknown protein	---	AT5G52580	-1.01	-0.02	-0.14	0.89488838	0.9744	-6.66
261476_at	hypothetical protein contains simila	---	AT1G14480	1.02	0.04	0.14	0.89479748	0.9744	-6.66
254395_at	subtilisin-like protease subtilisin-lik	---	AT4G21640	-1.01	-0.01	-0.14	0.89489368	0.9744	-6.66
249618_at	putative protein predicted proteins	---	AT5G37490	-1.07	-0.10	-0.14	0.89488265	0.9744	-6.66
255486_at	AtMlo-h1-like protein	MLO1	AT4G02600	-1.01	-0.02	-0.14	0.89485867	0.9744	-6.66
265568_s_at	hypothetical protein predicted by g	---	---	-1.01	-0.02	-0.14	0.89467314	0.9744	-6.66
248936_at	heat shock transcription factor	RHA1	AT5G45710	-1.02	-0.02	-0.14	0.89500987	0.9744	-6.66
255517_at	putative endo-1,4-beta glucanase	AtGH9B13	AT4G02290	1.01	0.02	0.14	0.89502325	0.9744	-6.66
253678_at	cytidine deaminase 7	---	AT4G29600	1.01	0.01	0.14	0.89495403	0.9744	-6.66
248765_at	MutT domain protein-like ; suppor	ATNUDT2	AT5G47650	1.01	0.01	0.14	0.89514096	0.9744	-6.66
245587_at	putative protein	---	AT4G15020	-1.02	-0.03	-0.14	0.8951456	0.9744	-6.66
248609_at	unknown protein ; supported by cl	---	AT5G49440	-1.01	-0.02	-0.14	0.89520678	0.9744	-6.66
257523_at	hypothetical protein similar to puta	---	AT3G01620	-1.01	-0.02	-0.14	0.89524706	0.9744	-6.66
251334_at	putative protein several hypothetic	---	AT3G61390	-1.01	-0.02	-0.14	0.89522996	0.9744	-6.66
265190_at	unknown protein ; supported by cl	---	AT1G23780	-1.01	-0.01	-0.14	0.89550029	0.9745	-6.66
266823_at	hypothetical protein predicted by g	---	AT2G44930	-1.01	-0.02	-0.14	0.89555727	0.9745	-6.66
250296_at	heat shock protein 17.6-II ;suppor	HSP17.6II	AT5G12020	-1.03	-0.04	-0.14	0.89555174	0.9745	-6.66
267493_at	unknown protein	OFP2	AT2G30400	-1.02	-0.02	-0.14	0.89542939	0.9745	-6.66
264903_at	putative phosphoglucomutase sim	---	AT1G23190	1.01	0.02	0.14	0.89537389	0.9745	-6.66
253267_at	putative protein TEB4 protein, Hor	---	AT4G34100	-1.01	-0.02	-0.14	0.89545647	0.9745	-6.66

261495_at	hypothetical protein predicted by g	---	AT1G28410	-1.01	-0.02	-0.14	0.89562133	0.9745	-6.66
261413_at	unknown protein ;supported by full	PLL5	AT1G07630	1.03	0.04	0.14	0.89573449	0.9745	-6.66
246608_at	putative protein various predicted	---	AT5G35380	1.01	0.02	0.14	0.89592175	0.9745	-6.66
261597_at	hypothetical protein predicted by g	PUB26	AT1G49780	-1.04	-0.06	-0.14	0.8958112	0.9745	-6.66
260228_at	putative cytochrome P450 similar t	CYP98A8	AT1G74540	1.01	0.02	0.14	0.8958003	0.9745	-6.66
249107_at	unknown protein	---	AT5G43680	-1.01	-0.02	-0.14	0.89587919	0.9745	-6.66
253525_at	predicted protein ; supported by c	---	AT4G31330	1.01	0.02	0.14	0.89586324	0.9745	-6.66
261645_at	hypothetical protein similar to hypo	---	---	1.01	0.01	0.14	0.89584919	0.9745	-6.66
255856_at	unknown protein identical to unkno	---	AT1G66940	-1.05	-0.06	-0.14	0.89623358	0.9745	-6.66
257724_at	hypothetical protein predicted by g	---	AT3G18510	-1.01	-0.02	-0.13	0.89686136	0.9745	-6.66
254187_at	putative protein hypothetical prote	---	AT4G23890	1.01	0.01	0.13	0.89689096	0.9745	-6.66
251837_s_at	spliceosomal - like protein spliceo	---	AT3G55200 /	1.01	0.02	0.14	0.89650361	0.9745	-6.66
246960_at	unknown protein	---	AT5G24710	-1.01	-0.01	-0.13	0.89691372	0.9745	-6.66
245396_at	hypothetical protein ;supported by	---	AT4G14870	-1.02	-0.03	-0.14	0.89629679	0.9745	-6.66
249546_at	putative protein chromosome segr	PMI15	AT5G38150	1.02	0.03	0.14	0.89611463	0.9745	-6.66
256613_at	hypothetical protein predicted by g	emb2076	AT3G29290	1.01	0.02	0.14	0.89651644	0.9745	-6.66
258978_at	unknown protein ; supported by cl	---	AT3G09320	1.01	0.01	0.13	0.89683497	0.9745	-6.66
263868_at	hypothetical protein predicted by g	---	AT2G36840	-1.01	-0.02	-0.13	0.89680998	0.9745	-6.66
249168_at	putative protein strong similarity to	---	AT5G42870	1.01	0.02	0.14	0.89639446	0.9745	-6.66
252669_at	putative protein hypothetical prote	---	AT3G44100	1.01	0.02	0.14	0.89607565	0.9745	-6.66
253114_at	GTP-binding protein GB2 ;suppor	ATGB2	AT4G35860	1.01	0.02	0.14	0.89642889	0.9745	-6.66
251577_at	putative protein several hypothetic	---	AT3G58350	-1.01	-0.02	-0.13	0.89673909	0.9745	-6.66
255629_at	stress-induced protein OZI1 precu	ATOZI1	AT4G00860	-1.02	-0.02	-0.14	0.89644074	0.9745	-6.66
251279_at	hypothetical protein	---	AT3G61800	-1.02	-0.03	-0.14	0.896453	0.9745	-6.66
254792_at	putative protein nucleoid DNA-bin	---	AT4G12920	-1.01	-0.02	-0.13	0.89688889	0.9745	-6.66
266769_s_at	putative reverse transcriptase	---	---	1.01	0.02	0.13	0.89656552	0.9745	-6.66
250641_at	putative bZIP protein bZIP protein	---	AT5G07160	-1.01	-0.02	-0.13	0.8967122	0.9745	-6.66
266586_s_at	putative protein	---	---	-1.01	-0.01	-0.13	0.89679122	0.9745	-6.66
265665_at	cysteine proteinase contains simila	---	AT2G27420	-1.01	-0.01	-0.13	0.89688078	0.9745	-6.66
246328_at	putative protein hexamer-binding	---	AT3G43590	-1.01	-0.02	-0.14	0.8964106	0.9745	-6.66
264924_at	RNA polymerase subunit identical	ATRPAC43	AT1G60620	1.01	0.01	0.13	0.89697464	0.9746	-6.66
257240_at	monooxygenase, putatve contains	---	AT3G24200	-1.01	-0.01	-0.13	0.89700897	0.9746	-6.66
247487_at	putative protein predicted protein,	---	AT5G62150	-1.05	-0.07	-0.13	0.8970729	0.9746	-6.66
262456_at	glucose transporter almost identica	STP1	AT1G11260	-1.02	-0.03	-0.13	0.89710602	0.9746	-6.66
257997_at	hypothetical protein similar to hypo	---	AT3G27500	1.01	0.01	0.13	0.8971938	0.9746	-6.66

257139_at	disease resistance protein, putativ	AtRLP43	AT3G28890	-1.02	-0.02	-0.13	0.89727274	0.9747	-6.66
264916_at	ATP citrate-lyase, putative similar	ACLA-2	AT1G60810	1.02	0.02	0.13	0.89792786	0.9750	-6.66
265682_at	similar to avrRpt2-induced protein	---	AT2G24390	1.01	0.02	0.13	0.89787061	0.9750	-6.66
246067_at	membrane transporter - like protei	---	AT5G19410	-1.01	-0.01	-0.13	0.89777022	0.9750	-6.66
249213_at	unknown protein	---	AT5G42700	1.01	0.01	0.13	0.89791705	0.9750	-6.66
255211_at	may be a pseudogene	---	---	-1.01	-0.01	-0.13	0.89763988	0.9750	-6.66
247411_at	putative protein contains similarity	---	AT5G63000	-1.01	-0.02	-0.13	0.89783568	0.9750	-6.66
253164_at	Expressed protein ; supported by f	---	AT4G35725	-1.01	-0.01	-0.13	0.89766111	0.9750	-6.66
245779_at	hypothetical protein predicted by g	---	AT1G73510	1.01	0.01	0.13	0.8979452	0.9750	-6.66
AFFX-r2-Bs-ph	B. subtilis /GEN=pheA /DB_XREF=	---	---	-1.03	-0.04	-0.13	0.89773937	0.9750	-6.66
254891_at	putative protein Fly Fas-associate	SAY1	AT4G11740	-1.01	-0.01	-0.13	0.89811464	0.9751	-6.66
246502_at	stearoyl-acyl carrier protein desatu	---	AT5G16240	-1.02	-0.02	-0.13	0.89818089	0.9751	-6.66
257415_at	hypothetical protein similar to hypo	---	AT1G70040	1.01	0.02	0.13	0.89824249	0.9752	-6.66
264141_at	hypothetical protein predicted by g	---	AT1G79090	1.01	0.01	0.13	0.89833196	0.9752	-6.66
260900_s_at	branched-chain alpha keto-acid de	---	AT1G21400 /	1.02	0.03	0.13	0.89891197	0.9753	-6.66
263411_at	putative C2H2-type zinc finger prot	---	AT2G28710	1.02	0.03	0.13	0.89862402	0.9753	-6.66
253992_at	putative protein ;supported by full-	---	AT4G26060	-1.01	-0.02	-0.13	0.89877333	0.9753	-6.66
258174_at	hypothetical protein contains Pfam	---	AT3G21470	1.01	0.02	0.13	0.89848379	0.9753	-6.66
257856_at	hypothetical protein predicted by g	---	AT3G12930	-1.01	-0.01	-0.13	0.89864369	0.9753	-6.66
260351_at	hypothetical protein predicated by	---	AT1G69380	-1.02	-0.03	-0.13	0.89889615	0.9753	-6.66
247033_at	SKP1 interacting partner 2 (SKIP2	SKIP2	AT5G67250	-1.01	-0.02	-0.13	0.89863561	0.9753	-6.66
252534_at	Myb DNA binding protein -like MY	MYB111	AT3G46130	-1.01	-0.01	-0.13	0.89890799	0.9753	-6.66
246894_at	heat-shock protein - like heat-sho	---	AT5G25530	-1.02	-0.02	-0.13	0.89866879	0.9753	-6.66
248610_at	SRP54 (signal recognition particle	---	AT5G49500	1.01	0.01	0.13	0.8988735	0.9753	-6.66
251215_at	putative protein region within disul	---	AT3G62510	-1.01	-0.01	-0.13	0.89883568	0.9753	-6.66
260720_at	hypothetical protein predicted by g	---	AT1G48095	1.01	0.02	0.13	0.89886381	0.9753	-6.66
245743_at	hypothetical protein contains simil	---	AT1G51080	1.02	0.02	0.13	0.89902053	0.9753	-6.66
250491_at	putative protein predicted proteins	---	AT5G09780	-1.02	-0.02	-0.13	0.89903477	0.9753	-6.66
267283_at	Mutator-like transposase similar to	---	---	1.01	0.01	0.13	0.89912322	0.9754	-6.66
247189_at	unknown protein ;supported by ful	AGP7	AT5G65390	-1.03	-0.04	-0.13	0.8992308	0.9754	-6.66
245445_at	apetala2 domain TINY like protein	---	AT4G16750	1.03	0.04	0.13	0.89924312	0.9754	-6.66
262705_at	putative wall-associated kinase sin	---	AT1G16260	-1.04	-0.06	-0.13	0.89929128	0.9754	-6.66
252493_at	hypothetical protein	---	AT3G46750	1.01	0.02	0.13	0.89941763	0.9755	-6.66
253546_at	hypothetical protein ;supported by	---	AT4G31030 /	-1.01	-0.02	-0.13	0.89947302	0.9755	-6.66
258203_at	hypothetical protein predicted by g	---	AT3G13950	1.05	0.07	0.13	0.90020938	0.9755	-6.66

251273_at	serine/threonine-protein kinase-lik	---	AT3G61960	-1.02	-0.02	-0.13	0.90002811	0.9755	-6.66
252181_at	Expressed protein ; supported by f	---	AT3G50685	-1.01	-0.01	-0.13	0.9002175	0.9755	-6.66
262968_at	hypothetical protein predicted by g	---	AT1G75720	-1.01	-0.01	-0.13	0.89996666	0.9755	-6.66
266207_at	unknown protein ; supported by cl	---	AT2G27680	1.01	0.02	0.13	0.89997674	0.9755	-6.66
258556_at	UDP-glucose:sterol glucosyltransfe	---	AT3G07020	1.01	0.02	0.13	0.90019237	0.9755	-6.66
254787_at	putative protein hypothetical protei	---	AT4G12690	-1.02	-0.03	-0.13	0.89968225	0.9755	-6.66
266236_at	putative glutathione S-transferase	ATGSTZ2	AT2G02380	1.01	0.01	0.13	0.8996564	0.9755	-6.66
254774_at	hypothetical protein	---	AT4G13440	-1.02	-0.03	-0.13	0.8997611	0.9755	-6.66
262889_at	hypothetical protein	---	AT1G14800	1.01	0.02	0.13	0.89981964	0.9755	-6.66
259052_at	unknown protein	PEX19-1	AT3G03490	-1.01	-0.01	-0.13	0.89971385	0.9755	-6.66
259931_at	hypothetical protein predicted by g	---	AT1G34400	-1.01	-0.02	-0.13	0.89960561	0.9755	-6.66
266559_at	unknown protein	---	AT2G23920	1.01	0.02	0.13	0.89965845	0.9755	-6.66
248227_at	ABA-inducible protein-like ;suppor	---	AT5G53820	-1.01	-0.02	-0.13	0.90020542	0.9755	-6.66
253117_at	Expressed protein ; supported by f	---	AT4G35905	-1.01	-0.02	-0.13	0.90002916	0.9755	-6.66
257292_s_at	hypothetical protein contains Pfam	---	---	1.01	0.01	0.13	0.9002116	0.9755	-6.66
263250_at	putative fructokinase ; supported b	---	AT2G31390	-1.02	-0.03	-0.13	0.90016593	0.9755	-6.66
254486_at	putative protein crp1 protein, Zea	---	AT4G20770	-1.01	-0.02	-0.13	0.90032533	0.9756	-6.66
260942_s_at	hypothetical protein contains simila	---	AT1G45190 /	-1.01	-0.02	-0.13	0.90029976	0.9756	-6.66
264431_at	RNA polymerase II subunit (hsRP	---	AT1G61700	-1.01	-0.02	-0.13	0.90049812	0.9757	-6.66
257577_at	hypothetical protein predicted by g	---	---	1.01	0.02	0.13	0.90061144	0.9758	-6.66
257277_at	disease resistance protein, putativ	---	AT3G14470	1.01	0.02	0.13	0.90068688	0.9758	-6.66
266002_at	hypothetical protein predicted by g	---	AT2G37310	-1.01	-0.02	-0.13	0.9008389	0.9758	-6.66
252969_at	putative protein vsf-1 protein, Lyc	---	AT4G38900	1.01	0.01	0.13	0.9008658	0.9758	-6.66
261933_at	3-deoxy-D-arabino-heptulosonate	---	AT1G22410	1.02	0.03	0.13	0.90080618	0.9758	-6.66
257846_at	unknown protein	---	AT3G12910	-1.04	-0.06	-0.13	0.90076414	0.9758	-6.66
258540_at	hypothetical protein predicted by g	---	AT3G06990	1.01	0.01	0.13	0.90092446	0.9758	-6.66
254930_at	putative protein hypothetical prote	---	AT4G11450	-1.02	-0.03	-0.13	0.90099855	0.9759	-6.66
251221_at	putative protein ER6 protein - Lyc	---	AT3G62550	1.01	0.02	0.13	0.90110422	0.9759	-6.66
248641_at	unknown protein	---	AT5G49110	-1.01	-0.02	-0.13	0.90129284	0.9761	-6.66
261590_at	hypothetical protein predicted by g	ROPGEF2	AT1G01700	-1.01	-0.01	-0.13	0.90136318	0.9761	-6.66
266979_at	unknown protein ;supported by ful	PPL2	AT2G39470	-1.04	-0.06	-0.13	0.9015652	0.9762	-6.66
250453_at	putative protein predicted protein,	---	AT5G10620	1.01	0.02	0.13	0.90158767	0.9762	-6.66
257841_at	nitrate transporter, putative similar	---	AT3G25260	-1.01	-0.01	-0.13	0.90154809	0.9762	-6.66
257541_at	hypothetical protein predicted by g	---	AT3G25950	-1.02	-0.03	-0.13	0.90157992	0.9762	-6.66
253046_at	cytochrome P450 - like protein cyt	CYP81D8	AT4G37370	-1.04	-0.06	-0.13	0.90230218	0.9762	-6.66

259431_at	plasma membrane intrinsic protein	PIP1C	AT1G01620	1.04	0.06	0.13	0.90185852	0.9762	-6.66
248420_at	receptor-like protein kinase ;suppo	---	AT5G51560	1.03	0.04	0.13	0.90224829	0.9762	-6.66
264048_at	unknown protein	---	AT2G22400	1.01	0.02	0.13	0.90189289	0.9762	-6.66
252754_at	putative protein hypothetical prote	---	---	-1.02	-0.03	-0.13	0.90218289	0.9762	-6.66
247610_at	putative protein predicted protein,	---	AT5G60630	-1.06	-0.08	-0.13	0.90214386	0.9762	-6.66
248295_at	putative protein contains similarity	---	AT5G53070	-1.01	-0.02	-0.13	0.90223645	0.9762	-6.66
251616_at	putative protein	---	AT3G57990	-1.01	-0.01	-0.13	0.90221776	0.9762	-6.66
255265_at	kinesin - like protein kinesin like p	ATK5	AT4G05190	1.01	0.02	0.13	0.90175736	0.9762	-6.66
265132_at	unknown protein ; supported by cl	---	AT1G23830	-1.02	-0.03	-0.13	0.90230979	0.9762	-6.66
245076_at	unknown protein	GH3.3	AT2G23170	1.06	0.09	0.13	0.90230897	0.9762	-6.66
263818_at	putative retroelement pol polyprote	---	---	1.01	0.01	0.13	0.90197938	0.9762	-6.66
249507_at	similar to unknown protein (pir||T02	---	AT5G38370	1.01	0.01	0.13	0.90193167	0.9762	-6.66
246053_at	putative protein farnesyl cysteine (	---	AT5G08340	1.01	0.02	0.13	0.90207813	0.9762	-6.66
264488_s_at	unknown protein similar to EST gb	---	AT1G27330 /	1.02	0.02	0.13	0.90231974	0.9762	-6.66
267217_at	hypothetical protein	---	AT2G02610	-1.01	-0.01	-0.13	0.90185046	0.9762	-6.66
266171_at	putative CCAAT-binding transcripti	NF-YB1	AT2G38880	-1.01	-0.02	-0.13	0.90253254	0.9764	-6.66
266758_at	unknown protein	POL	AT2G46920	-1.01	-0.02	-0.13	0.90262751	0.9764	-6.66
258986_at	putative heat shock protein similar	---	AT3G08910	1.01	0.02	0.13	0.90265257	0.9764	-6.66
251135_at	putative protein proteophosphogly	---	AT5G01280	1.01	0.01	0.13	0.90255395	0.9764	-6.66
262817_at	putative reticuline oxidase strong s	---	AT1G11770	1.01	0.02	0.13	0.90261483	0.9764	-6.66
266307_at	putative cytochrome P450	CYP705A8	AT2G27000	1.01	0.02	0.13	0.90269983	0.9764	-6.66
248970_at	urea active transporter-like protein	---	AT5G45380	1.02	0.03	0.13	0.9035428	0.9764	-6.66
246057_at	putative protein predicted proteins	---	AT5G08400	1.01	0.01	0.13	0.90276318	0.9764	-6.66
265172_at	putative spermidine synthase	SPDS1	AT1G23820	-1.01	-0.01	-0.13	0.90301628	0.9764	-6.66
255821_at	putative initiator tRNA phosphoribo	---	AT2G40570	-1.01	-0.02	-0.13	0.90311758	0.9764	-6.66
255677_at	putative calmodulin-binding heat sl	---	AT4G00500	-1.02	-0.02	-0.13	0.90336491	0.9764	-6.66
245732_at	unknown protein contains similarity	---	AT1G73440	1.01	0.01	0.13	0.90295067	0.9764	-6.66
249577_at	calmodulin-binding heat-shock pro	---	AT5G37710	1.02	0.02	0.13	0.90354192	0.9764	-6.66
246385_at	mitotic cyclin a2-type, putative sim	CYCA1;2	AT1G77390	-1.02	-0.04	-0.13	0.90343069	0.9764	-6.66
261786_at	cyclic nucleotide and calmodulin-r	ATCNGC7	AT1G15990	-1.01	-0.01	-0.13	0.90348659	0.9764	-6.66
262659_at	putative nucleoside triphosphatase	---	AT1G14240	-1.01	-0.01	-0.13	0.90343269	0.9764	-6.66
266235_at	putative phloem-specific lectin	AtPP2-B10	AT2G02360	1.01	0.02	0.13	0.90356195	0.9764	-6.66
263229_s_at	putative polygalacturonase similar	---	AT1G05650 /	-1.01	-0.01	-0.13	0.90325917	0.9764	-6.66
260637_at	ACC oxidase, putative similar to A	ACO2	AT1G62380	-1.03	-0.04	-0.13	0.90353779	0.9764	-6.66
255285_at	putative protein A. thaliana hypoth	---	AT4G04630	1.03	0.05	0.13	0.90316597	0.9764	-6.66

258745_at	unknown protein ; supported by ful	---	AT3G05920	-1.01	-0.02	-0.13	0.9029444	0.9764	-6.66
253675_at	hypothetical protein	---	AT4G29560	1.01	0.01	0.13	0.90321238	0.9764	-6.66
248323_at	unknown protein	---	AT5G52770	1.01	0.01	0.13	0.90350023	0.9764	-6.66
245212_at	hypothetical protein predicted by g	AT1G4422	---	1.01	0.02	0.13	0.90284242	0.9764	-6.66
262228_at	protein kinase, putative similar to	---	AT1G68690	1.04	0.05	0.13	0.9031628	0.9764	-6.66
253472_at	hypothetical protein	---	AT4G32230	-1.01	-0.01	-0.13	0.90280885	0.9764	-6.66
259577_at	unknown protein	---	AT1G35340	1.01	0.02	0.13	0.90365131	0.9764	-6.66
264528_at	hypothetical protein similar to Hum	---	AT1G30810	1.01	0.01	0.13	0.90366771	0.9764	-6.66
254080_at	fibrillarin 2 (AtFib2) identical to fibr	FIB2	AT4G25630	1.03	0.04	0.13	0.90372378	0.9764	-6.66
258038_at	unknown protein ;supported by ful	---	AT3G21260	-1.02	-0.03	-0.13	0.9037642	0.9764	-6.66
248276_at	EspB-like protein	YSL3	AT5G53550	-1.01	-0.02	-0.13	0.90404757	0.9764	-6.66
255142_at	stromal ascorbate peroxidase ; su	SAPX	AT4G08390	1.04	0.06	0.13	0.90413582	0.9764	-6.66
251534_at	ATP-dependent RNA helicase-like	---	AT3G58510	-1.02	-0.02	-0.13	0.90393653	0.9764	-6.66
258315_at	Expressed protein ; supported by f	---	AT3G16175	1.01	0.02	0.13	0.90417105	0.9764	-6.66
262042_at	polygalacturonase, putative simila	---	AT1G80140	-1.01	-0.01	-0.13	0.9040273	0.9764	-6.66
249137_at	putative protein contains similarity	---	AT5G43140	1.02	0.02	0.13	0.90400848	0.9764	-6.66
249834_at	putative protein contains similarity	FTRA1	AT5G23440	-1.01	-0.02	-0.13	0.90414603	0.9764	-6.66
261385_at	lipid-transfer protein, putative simi	---	AT1G05450	1.01	0.01	0.13	0.90403669	0.9764	-6.66
265341_at	hypothetical protein predicted by g	---	AT2G18360	1.01	0.02	0.13	0.90397027	0.9764	-6.66
262972_at	unknown protein	---	AT1G75620	1.01	0.02	0.12	0.90447931	0.9766	-6.66
248176_at	putative protein contains similarity	Fh5	AT5G54650	-1.02	-0.03	-0.12	0.9043878	0.9766	-6.66
267221_at	similar to prokaryotic DNA polymer	STI	AT2G02480	1.01	0.01	0.12	0.90449546	0.9766	-6.66
250078_at	putative protein	ORC3	AT5G16690	-1.01	-0.02	-0.12	0.90447348	0.9766	-6.66
261394_at	wall-associated kinase 2, putative	---	AT1G79680	1.05	0.07	0.12	0.90469358	0.9767	-6.66
259176_at	putative cell division control protei	CDC48C	AT3G01610	1.01	0.01	0.12	0.90474722	0.9767	-6.66
252034_at	putative protein ;supported by full-	---	AT3G52040	1.02	0.03	0.12	0.90483935	0.9767	-6.66
254014_at	NPR1 like protein regulatory prote	---	AT4G26120	1.02	0.03	0.12	0.90498676	0.9767	-6.66
249914_at	protease-like protein	---	AT5G22850	-1.01	-0.02	-0.12	0.90476725	0.9767	-6.66
265986_at	putative receptor-like protein kinas	---	AT2G24230	-1.01	-0.02	-0.12	0.90498351	0.9767	-6.66
245015_at	large subunit of riblose-1,5-bispho	---	---	1.02	0.02	0.12	0.90485687	0.9767	-6.66
245534_at	hypothetical protein	---	AT4G15150	-1.01	-0.02	-0.12	0.90508309	0.9767	-6.66
246592_at	putative protein predicted protein,	---	AT5G14890	-1.01	-0.02	-0.12	0.90509285	0.9767	-6.66
247341_at	unknown protein	---	AT5G63720	-1.01	-0.01	-0.12	0.90497479	0.9767	-6.66
267363_at	putative peroxisomal membrane ca	---	AT2G39970	1.01	0.01	0.12	0.9050591	0.9767	-6.66
257411_s_at	hypothetical protein predicted by g	---	AT1G61320	-1.01	-0.01	-0.12	0.90515717	0.9768	-6.66

267371_at	Expressed protein ; supported by c	---	AT2G44510	-1.02	-0.02	-0.12	0.9053416	0.9768	-6.66
255033_at	putative protein phosphonopyruva	---	AT4G09520	1.01	0.02	0.12	0.90534552	0.9768	-6.66
250640_at	putative protein protein kinase Xa	---	AT5G07150	1.02	0.03	0.12	0.90536211	0.9768	-6.66
260060_at	feebly-like protein similar to feebly	---	AT1G73680	1.01	0.02	0.12	0.90548019	0.9769	-6.66
253577_at	putative protein	---	AT4G31080	1.02	0.02	0.12	0.90561307	0.9769	-6.66
263808_at	hypothetical protein predicted by g	---	AT2G04340	-1.01	-0.01	-0.12	0.90563412	0.9769	-6.66
264660_at	putative glutamyl-tRNA reductase	HEMA2	AT1G09940	-1.03	-0.04	-0.12	0.90566982	0.9769	-6.66
261953_at	UDP-galactose 4-epimerase, puta	RHD1	AT1G64440	-1.02	-0.03	-0.12	0.90558729	0.9769	-6.66
252541_at	putative protein hypothetical prote	---	AT3G45750	-1.01	-0.01	-0.12	0.90555961	0.9769	-6.66
254384_at	heat shock protein - like heat shoc	---	AT4G21870	-1.03	-0.04	-0.12	0.90577865	0.9769	-6.66
262466_at	hypothetical protein similar to hypo	NTMC2T5.	AT1G50260	1.01	0.02	0.12	0.90593552	0.9769	-6.66
255858_at	zinc finger protein (ZFP6) identical	ZFP6	AT1G67030	1.01	0.02	0.12	0.9059487	0.9769	-6.66
258768_at	hypothetical protein predicted by g	---	AT3G10880	-1.01	-0.01	-0.12	0.90591292	0.9769	-6.66
252438_at	putative protein riboflavin biosynth	---	AT3G47390	-1.01	-0.01	-0.12	0.90587828	0.9769	-6.66
265709_at	hypothetical protein predicted by g	---	---	-1.03	-0.04	-0.12	0.90586572	0.9769	-6.66
247435_at	glutathione S-transferase-like prote	ATGSTU9	AT5G62480	1.06	0.08	0.12	0.90606354	0.9770	-6.66
259853_at	leucine-rich receptor-like protein k	---	AT1G72300	-1.01	-0.02	-0.12	0.90609553	0.9770	-6.66
260306_at	hypothetical protein predicted by g	EDA24	AT1G70540	-1.01	-0.01	-0.12	0.90612352	0.9770	-6.66
266795_at	unknown protein	---	AT2G03070	-1.01	-0.02	-0.12	0.90622672	0.9770	-6.66
264540_at	hypothetical protein predicted by g	---	AT1G55630	1.01	0.01	0.12	0.90633408	0.9771	-6.66
266431_at	Mutator-like transposase similar to	---	---	-1.01	-0.01	-0.12	0.90649396	0.9772	-6.66
250318_at	dihydropyrimidinase ; supported b	---	AT5G12200	-1.01	-0.02	-0.12	0.906545	0.9772	-6.66
253165_at	putative protein predicted protein,	---	AT4G35320	1.02	0.03	0.12	0.90684694	0.9773	-6.66
253057_at	putative protein amino-acid N-ace	---	AT4G37670	-1.03	-0.04	-0.12	0.90690806	0.9773	-6.66
248269_at	putative protein contains similarity	ACBP1	AT5G53470	1.01	0.02	0.12	0.90663289	0.9773	-6.66
254748_at	unknown protein	---	---	1.01	0.01	0.12	0.90673098	0.9773	-6.66
262993_at	hypothetical protein contains simila	---	AT1G54230	1.01	0.01	0.12	0.90688409	0.9773	-6.66
259028_at	putative C2H2-type zinc finger pro	TAC1	AT3G09290	1.01	0.02	0.12	0.90686188	0.9773	-6.66
259387_at	histone H3 protein, putative simila	---	AT1G13370	1.01	0.01	0.12	0.90671076	0.9773	-6.66
249935_at	acyl CoA reductase-like protein	FAR7	AT5G22420	-1.01	-0.01	-0.12	0.90681022	0.9773	-6.66
255955_at	hypothetical protein predicted by g	---	AT1G22030	-1.02	-0.03	-0.12	0.90702214	0.9773	-6.66
247026_at	protein kinase-like protein	MAPKKK19	AT5G67080	-1.05	-0.08	-0.12	0.90720875	0.9775	-6.66
252700_at	hypothetical protein envelope-like	---	---	1.01	0.02	0.12	0.90722231	0.9775	-6.66
258736_at	unknown protein	---	AT3G05900	1.02	0.02	0.12	0.90733236	0.9775	-6.66
254284_at	putative fizzy-related protein fizzy-	FZR2	AT4G22910	1.01	0.02	0.12	0.90728215	0.9775	-6.66

246362_at	hypothetical protein	---	---	1.01	0.01	0.12	0.90735832	0.9775	-6.66
246371_at	unknown protein contains similarity	---	AT1G51940	1.01	0.02	0.12	0.90752426	0.9775	-6.66
258545_at	putative GTPase contains Pfam pr	---	AT3G07050	1.02	0.02	0.12	0.90773972	0.9775	-6.66
257381_at	unknown protein	---	AT2G37950	1.02	0.03	0.12	0.90759153	0.9775	-6.66
260560_at	putative endochitinase	---	AT2G43590	-1.02	-0.02	-0.12	0.90773109	0.9775	-6.66
253420_at	H+-transporting ATP synthase cha	---	AT4G32260	1.01	0.02	0.12	0.90760238	0.9775	-6.66
256857_at	NAM-like protein similar to NAM (n	CUC1	AT3G15170	1.01	0.01	0.12	0.90775414	0.9775	-6.66
265834_at	hypothetical protein predicted by g	---	AT2G14410	-1.01	-0.01	-0.12	0.90765529	0.9775	-6.66
249569_at	putative protein Pit1 - Arabidopsis	---	AT5G38070	1.01	0.02	0.12	0.90746225	0.9775	-6.66
253180_at	putative protein various predicted	---	AT4G35210	-1.01	-0.01	-0.12	0.90777523	0.9775	-6.66
256349_at	late embryogenesis protein, putati	---	AT1G54890	-1.09	-0.12	-0.12	0.9079192	0.9775	-6.66
256474_at	unknown protein	---	---	1.01	0.02	0.12	0.9079381	0.9775	-6.66
246380_at	cytochrome P450, putative similar	CYP96A15	AT1G57750	1.01	0.02	0.12	0.90791997	0.9775	-6.66
261311_at	disease resistance protein RTM1,	---	AT1G05770	-1.01	-0.02	-0.12	0.90801965	0.9776	-6.66
263977_at	hypothetical protein predicted by g	---	AT2G42660	-1.01	-0.02	-0.12	0.90805814	0.9776	-6.66
264995_at	mutator-like transposase, putative	---	---	-1.01	-0.02	-0.12	0.90813247	0.9776	-6.66
255675_at	MYC1 transcription factor	ATMYC1	AT4G00480	-1.01	-0.01	-0.12	0.90822824	0.9776	-6.66
256427_at	hypothetical protein predicted by g	LBD21	AT3G11090	-1.02	-0.03	-0.12	0.90823319	0.9776	-6.66
247214_at	putative protein similar to unknown	---	AT5G64850	1.03	0.04	0.12	0.908504	0.9778	-6.66
249709_at	putative protein similar to unknown	iqd33	AT5G35670	1.01	0.02	0.12	0.90858396	0.9778	-6.66
254799_at	putative protein various predicted p	---	AT4G13060	-1.01	-0.01	-0.12	0.90851697	0.9778	-6.66
244994_at	NADH dehydrogenase ND5	---	---	1.01	0.02	0.12	0.90859272	0.9778	-6.66
255296_at	hypothetical protein	---	AT4G04790	-1.02	-0.03	-0.12	0.90871253	0.9779	-6.66
263895_at	hypothetical protein predicted by g	---	AT2G21920	-1.01	-0.01	-0.12	0.9087705	0.9779	-6.66
263886_at	hypothetical protein predicted by g	TKI1	AT2G36960	1.01	0.01	0.12	0.90882448	0.9779	-6.66
254959_at	predicted protein	UGE5	AT4G10955 /	1.01	0.02	0.12	0.90894387	0.9779	-6.66
252882_at	Expressed protein ; supported by f	---	AT4G39675	1.01	0.01	0.12	0.90885886	0.9779	-6.66
255146_at	putative protein disease resistanc	---	AT4G08450	-1.01	-0.01	-0.12	0.90894346	0.9779	-6.66
258724_at	unknown protein	---	AT3G09600	-1.01	-0.01	-0.12	0.90880862	0.9779	-6.66
261940_at	hypothetical protein predicted by g	---	AT1G22520	1.01	0.02	0.12	0.9091338	0.9780	-6.66
245602_at	Expressed protein ;supported by c	---	AT4G14270	1.01	0.02	0.12	0.90936307	0.9781	-6.66
248488_at	putative protein contains similarity	---	AT5G51080	-1.01	-0.01	-0.12	0.90930001	0.9781	-6.66
250809_at	putative protein contains similarity	---	AT5G05140	-1.02	-0.03	-0.12	0.90919282	0.9781	-6.66
259324_at	unknown protein	MIRO3	AT3G05310	1.01	0.02	0.12	0.90925244	0.9781	-6.66
249157_at	unknown protein	---	AT5G43510 /	1.01	0.01	0.12	0.90935071	0.9781	-6.66

253160_at	putative protein predicted protein,	---	AT4G35760	1.01	0.02	0.12	0.909791	0.9781	-6.66
258637_at	putative RHO GDP-dissociation inl	---	AT3G07880	-1.01	-0.02	-0.12	0.90953613	0.9781	-6.66
256742_at	transcription initiation factor IIB, pu	---	AT3G29380	1.01	0.01	0.12	0.90977518	0.9781	-6.66
265927_at	hypothetical protein	---	AT2G18590	-1.01	-0.02	-0.12	0.90989851	0.9781	-6.66
247914_at	xyloglucan endotransglycosylase	---	AT5G57540	1.01	0.01	0.12	0.90970444	0.9781	-6.66
250758_at	eukaryotic translation initiation fact	EIF3G2	AT5G06000	-1.01	-0.02	-0.12	0.90983734	0.9781	-6.66
253503_at	cytochrome P450-like protein cyto	CYP82C3	AT4G31950	1.02	0.02	0.12	0.90951637	0.9781	-6.66
261291_at	hypothetical protein predicted by g	---	AT1G36970	-1.01	-0.02	-0.12	0.90976499	0.9781	-6.66
255416_at	hypothetical protein	---	AT4G03170	-1.01	-0.01	-0.12	0.90991147	0.9781	-6.66
263896_at	hypothetical protein predicted by g	---	AT2G21930	-1.01	-0.02	-0.12	0.9096498	0.9781	-6.66
256234_at	50S ribosomal protein L10, putativ	---	AT3G12370	1.01	0.01	0.12	0.90959146	0.9781	-6.66
266399_at	putative phospholipid cytidylyltrans	PECT1	AT2G38670	1.01	0.02	0.12	0.9099121	0.9781	-6.66
252558_at	actin depolymerising like protein A	---	AT3G45990	-1.01	-0.01	-0.12	0.90995676	0.9781	-6.66
251439_at	putative protein unknown protein A	---	AT3G59950	1.01	0.01	0.12	0.91010186	0.9782	-6.66
264816_at	hypothetical protein similar to mem	---	AT1G03560	-1.02	-0.03	-0.12	0.91006664	0.9782	-6.66
264185_at	unknown protein ;supported by full	---	AT1G54780	-1.01	-0.01	-0.12	0.91028936	0.9783	-6.66
258467_at	unknown protein contains Pfam pr	---	AT3G06060	1.01	0.02	0.12	0.9104564	0.9784	-6.66
246497_at	putative protein hypothetical protei	---	AT5G16220	1.02	0.03	0.12	0.91044932	0.9784	-6.66
251929_at	sigma factor SigC ; supported by	SIGC	AT3G53920	-1.01	-0.01	-0.12	0.91051198	0.9784	-6.66
265821_at	putative homeodomain transcriptio	WUS	AT2G17950	1.01	0.02	0.12	0.91055584	0.9784	-6.66
257103_at	hypothetical protein contains Pfam	---	AT3G25060	1.01	0.01	0.12	0.91067675	0.9785	-6.66
249247_at	maize crp1 protein-like	---	AT5G42310	-1.01	-0.02	-0.12	0.91073617	0.9785	-6.66
257405_at	putative calmodulin similar to EST	---	AT1G24620	-1.01	-0.01	-0.12	0.91091981	0.9787	-6.66
261460_at	MAP kinase, putative similar to GE	ATMPK13	AT1G07880	-1.01	-0.01	-0.12	0.91100178	0.9787	-6.66
257926_at	unknown protein contains Pfam pr	---	AT3G23280	1.01	0.01	0.12	0.91107194	0.9787	-6.66
253681_at	cytidine deaminase 3 (CDA3)	---	AT4G29630	1.01	0.01	0.12	0.91114892	0.9788	-6.66
255642_at	hypothetical protein	iqd17	AT4G00820	1.02	0.02	0.12	0.91122915	0.9788	-6.66
246794_s_at	putative protein predicted proteins	---	AT5G06350	-1.02	-0.03	-0.12	0.91132757	0.9789	-6.66
250351_at	heat shock protein 17.6A	AT-HSP17.	AT5G12030	1.03	0.04	0.12	0.91168894	0.9789	-6.66
259787_at	auxin-induced protein, putative sir	---	AT1G29460	1.03	0.04	0.12	0.91141827	0.9789	-6.66
250523_at	putative protein strong similarity to	---	AT5G08510	-1.01	-0.01	-0.12	0.91154824	0.9789	-6.66
258959_at	putative amino acid transporter sim	CAT7	AT3G10600	1.01	0.01	0.12	0.91153897	0.9789	-6.66
257448_s_at	putative protein various predicted p	---	AT2G11620	1.01	0.01	0.12	0.91166415	0.9789	-6.66
258234_at	hypothetical protein similar to myb-	MYB118	AT3G27785	-1.01	-0.01	-0.12	0.91164251	0.9789	-6.66
247348_at	beta-galactosidase (emb CAB6474	BGAL10	AT5G63810	-1.01	-0.02	-0.12	0.91165228	0.9789	-6.66

246048_at	putative protein	---	---	1.01	0.01	0.12	0.9116609	0.9789	-6.66
259840_at	photosystem I subunit VI precurso	PSAH2	AT1G52230	-1.01	-0.02	-0.11	0.91185244	0.9789	-6.66
257063_s_at	unknown protein ;supported by ful	---	AT3G18240	1.01	0.01	0.11	0.91180157	0.9789	-6.66
259062_at	unknown protein est hits to gensca	---	AT3G07440	1.01	0.02	0.11	0.9118987	0.9789	-6.66
251697_at	putative protein hypothetical prote	---	AT3G56600	1.01	0.01	0.11	0.91193862	0.9789	-6.66
265298_s_at	putative retroelement pol polyprote	---	---	-1.01	-0.01	-0.11	0.91194524	0.9789	-6.66
251199_at	transport inhibitor response 1 (TIR	TIR1	AT3G62980	1.02	0.02	0.11	0.91223162	0.9791	-6.66
252487_at	glucosyltransferase-like protein UI	UGT76E12	AT3G46660	-1.04	-0.06	-0.11	0.91221423	0.9791	-6.66
267428_at	putative coatomer epsilon subunit	---	AT2G34840	1.01	0.01	0.11	0.91220411	0.9791	-6.66
246744_at	putative protein predicted protein,	---	AT5G27760	-1.03	-0.04	-0.11	0.91229857	0.9791	-6.66
257041_at	unknown protein	---	AT3G28550	-1.01	-0.02	-0.11	0.91235753	0.9791	-6.66
259086_at	hypothetical protein predicted by g	---	AT3G04990	1.01	0.01	0.11	0.91237259	0.9791	-6.66
259466_at	response regulator 5, putative sim	ARR7	AT1G19050	1.03	0.05	0.11	0.9125522	0.9792	-6.67
249343_at	succinate dehydrogenase iron-pro	SDH2-2	AT5G40650	-1.01	-0.02	-0.11	0.91252217	0.9792	-6.66
266723_at	SKP1/ASK1 (At16), putative simila	ASK16	AT2G03190	1.01	0.01	0.11	0.91254035	0.9792	-6.67
255859_at	putative protein embryonic abunda	---	AT5G34930	-1.01	-0.02	-0.11	0.91268768	0.9793	-6.67
249271_at	myosin heavy chain-like protein	CIP1	AT5G41790	1.01	0.02	0.11	0.91287391	0.9794	-6.67
255173_at	putative transposon protein simila	---	---	1.01	0.01	0.11	0.91297318	0.9795	-6.67
249450_at	serine/threonine-specific protein k	SnRK1.3	AT5G39440	-1.01	-0.01	-0.11	0.91305374	0.9795	-6.67
246407_at	disease resistance protein RPS4,	---	AT1G57670	1.01	0.01	0.11	0.91330196	0.9797	-6.67
250123_at	putative protein contains similarity	PIN5	AT5G16530	-1.01	-0.02	-0.11	0.91328317	0.9797	-6.67
249658_s_at	N-glyceraldehyde-2-phosphotransf	---	AT5G36700	1.01	0.02	0.11	0.91344419	0.9798	-6.67
264260_at	putative calcium-binding protein, c	---	AT1G09210	1.02	0.03	0.11	0.91344919	0.9798	-6.67
263847_at	putative glucosyltransferase ; supp	---	AT2G36970	-1.03	-0.05	-0.11	0.913724	0.9798	-6.67
250232_at	unknown protein	---	AT5G13950	1.01	0.01	0.11	0.91368963	0.9798	-6.67
245160_at	putative leucine-rich repeat diseas	AtRLP28	AT2G33080	-1.01	-0.01	-0.11	0.91371206	0.9798	-6.67
254713_at	hypothetical protein	---	AT4G18090	-1.01	-0.02	-0.11	0.91358939	0.9798	-6.67
251166_at	heat shock transcription factor-like	AT-HSFA7I	AT3G63350	-1.01	-0.01	-0.11	0.91359072	0.9798	-6.67
248761_at	Expressed protein ; supported by f	---	AT5G47635	1.02	0.02	0.11	0.91371946	0.9798	-6.67
251488_at	calmodulin-like protein calcium-bir	---	AT3G59440	1.01	0.01	0.11	0.91379791	0.9798	-6.67
257766_at	auxin-inducible gene (IAA2) identi	IAA2	AT3G23030	1.01	0.02	0.11	0.91384622	0.9798	-6.67
263095_at	Ac-like transposase related to Ac/D	---	AT2G16040	-1.01	-0.01	-0.11	0.91401531	0.9799	-6.67
257359_x_at	putative protein kinase contains a	---	AT2G34290	1.01	0.01	0.11	0.91401127	0.9799	-6.67
256411_at	ATP-dependent Clp protease prote	CLPP3	AT1G66670	1.01	0.02	0.11	0.91409304	0.9800	-6.67
267161_at	hypothetical protein predicted by g	---	AT2G37680	1.01	0.01	0.11	0.91422792	0.9800	-6.67

246189_at	ABI3-interacting protein 2 ;suppor	---	AT5G20910	1.01	0.02	0.11	0.91421396	0.9800	-6.67
257170_at	beta-1,3-glucanase, putative simil	---	AT3G23770	-1.01	-0.02	-0.11	0.9141976	0.9800	-6.67
261053_at	hypothetical protein predicted by g	---	AT1G01320	1.01	0.02	0.11	0.91465075	0.9801	-6.67
262143_at	unknown protein	---	AT1G52630	1.01	0.01	0.11	0.9144618	0.9801	-6.67
261681_at	hypothetical protein similar to hypo	---	AT1G47340	1.01	0.02	0.11	0.91445056	0.9801	-6.67
260597_at	hypothetical protein predicted by g	---	AT1G55915	1.01	0.02	0.11	0.91463962	0.9801	-6.67
251362_at	DEAD box RNA helicase RH12	---	AT3G61240	-1.01	-0.01	-0.11	0.91478047	0.9801	-6.67
262799_at	hypothetical protein predicted by g	---	AT1G20970	1.01	0.02	0.11	0.914831	0.9801	-6.67
255239_at	contains similarity to Arabidopsis th	---	---	1.01	0.01	0.11	0.91459419	0.9801	-6.67
262083_at	hypothetical protein predicted by g	---	AT1G56100	1.01	0.01	0.11	0.91468986	0.9801	-6.67
248431_at	auxin-responsive GH3-like protein	---	AT5G51470	-1.01	-0.01	-0.11	0.91476058	0.9801	-6.67
249897_at	putative protein strong similarity to	---	AT5G22550	1.01	0.01	0.11	0.91483583	0.9801	-6.67
250592_at	putative protein contains similarity	---	AT5G07740	-1.01	-0.02	-0.11	0.91472334	0.9801	-6.67
263258_at	putative permease similar to putati	---	AT1G10540	1.01	0.02	0.11	0.9149281	0.9801	-6.67
255057_at	hypothetical protein	---	AT4G09840	1.01	0.01	0.11	0.91495749	0.9801	-6.67
252094_at	multicatalytic endopeptidase comp	PAD1	AT3G51260	1.01	0.02	0.11	0.91507652	0.9802	-6.67
246903_at	putative protein	---	AT5G25750	-1.01	-0.01	-0.11	0.91508931	0.9802	-6.67
250257_at	putative protein similar to unknown	---	AT5G13770	1.01	0.01	0.11	0.91514512	0.9802	-6.67
252327_at	MTN3-like protein MtN3 gene proc	---	AT3G48740	-1.01	-0.02	-0.11	0.91519835	0.9802	-6.67
250405_at	ubiquitin-specific protease 22 (UB	UBP22	AT5G10790	-1.01	-0.02	-0.11	0.91532701	0.9803	-6.67
247359_at	acyltransferase-like protein ;suppo	---	AT5G63560	-1.01	-0.02	-0.11	0.91538222	0.9803	-6.67
260315_at	hypothetical protein similar to C-te	---	AT1G63820	1.01	0.01	0.11	0.91542357	0.9803	-6.67
252194_at	putative tyrosine phosphatase pho	ATPEN3	AT3G50110	1.01	0.01	0.11	0.9157159	0.9804	-6.67
254984_s_at	putative protein Homo sapiens de	UBP10	AT4G10570	-1.01	-0.01	-0.11	0.91571342	0.9804	-6.67
263678_at	hypothetical protein Similar to Bab	---	AT1G04420	-1.01	-0.02	-0.11	0.91572606	0.9804	-6.67
259203_at	hypothetical protein predicted by g	---	AT3G09130	1.01	0.01	0.11	0.91566433	0.9804	-6.67
258220_at	DnaJ, putative similar to DnaJ GB	---	AT3G17830	1.01	0.02	0.11	0.91565497	0.9804	-6.67
257410_at	hypothetical protein similar to polyl	emb2421	AT1G24340	-1.01	-0.02	-0.11	0.91582088	0.9805	-6.67
246072_at	PISTILLATA ; supported by full-le	PI	AT5G20240	1.01	0.01	0.11	0.91604859	0.9805	-6.67
267022_at	hypothetical protein predicted by g	---	AT2G34230	-1.01	-0.01	-0.11	0.91600176	0.9805	-6.67
263892_at	putative MYB family transcription f	RAX2	AT2G36890	1.01	0.01	0.11	0.91606096	0.9805	-6.67
261332_s_at	hypothetical protein contains simila	---	---	1.01	0.01	0.11	0.91597004	0.9805	-6.67
266396_at	unknown protein	---	AT2G38790	1.01	0.02	0.11	0.91634164	0.9807	-6.67
247383_at	putative protein contains similarity	---	AT5G63410	1.02	0.02	0.11	0.91630915	0.9807	-6.67
253221_at	peptidylprolyl isomerase (cyclophil	ROC5	AT4G34870	-1.01	-0.02	-0.11	0.91636462	0.9807	-6.67

254538_at	putative protein chitinase / lysozyr	---	AT4G19740	1.01	0.01	0.11	0.91631472	0.9807	-6.67
257470_at	hypothetical protein predicted by g	---	AT1G53770	1.01	0.02	0.11	0.91640898	0.9807	-6.67
262966_at	ER lumen protein retaining recept	---	AT1G75760	-1.01	-0.01	-0.11	0.91654287	0.9808	-6.67
255165_at	putative protein putative centrome	---	---	-1.02	-0.02	-0.11	0.91656596	0.9808	-6.67
246398_at	auxin-induced basic helix-loop-hel	---	AT1G58100	-1.01	-0.01	-0.11	0.91677764	0.9809	-6.67
260936_at	hypothetical protein predicted by g	---	AT1G45150	1.01	0.01	0.11	0.91696544	0.9809	-6.67
267398_at	putative glucanase	AtGH9B11	AT2G44560	1.01	0.01	0.11	0.91695919	0.9809	-6.67
256809_at	hypothetical protein predicted by g	ALY3	AT3G21430	-1.01	-0.02	-0.11	0.91693303	0.9809	-6.67
250768_at	signal recognition particle receptor	---	AT5G05670	1.01	0.02	0.11	0.91679752	0.9809	-6.67
258382_at	hypothetical protein	UBC25	AT3G15355	-1.01	-0.02	-0.11	0.91689432	0.9809	-6.67
252474_at	putative protein several hypothetic	---	AT3G46620	1.02	0.04	0.11	0.91701221	0.9809	-6.67
253409_at	putative protein	---	AT4G32960	-1.01	-0.01	-0.11	0.91713923	0.9810	-6.67
267392_at	putative beta-glucosidase	PEN2	AT2G44490	1.01	0.02	0.11	0.91718406	0.9810	-6.67
249057_at	putative protein contains similarity	DUR	AT5G44480	1.03	0.04	0.11	0.91758	0.9810	-6.67
246064_at	DNA binding protein ACBF - like D	---	AT5G19350	1.01	0.01	0.11	0.9175312	0.9810	-6.67
247580_at	putative protein traube, Mus musc	---	AT5G61330	-1.01	-0.01	-0.11	0.91762705	0.9810	-6.67
248576_at	methionine S-methyltransferase (g	MMT	AT5G49810	1.01	0.01	0.11	0.91760521	0.9810	-6.67
258727_at	ethylene-responsive protein, putat	---	AT3G11930	-1.01	-0.01	-0.11	0.91750038	0.9810	-6.67
266010_at	putative C2H2-type zinc finger prot	---	AT2G37430	-1.06	-0.09	-0.11	0.91739003	0.9810	-6.67
261996_at	AIG1-like protein similar to AIG1 p	---	AT1G33830	1.01	0.01	0.11	0.91762996	0.9810	-6.67
262894_at	disease resistance protein, putativ	---	AT1G59780	-1.01	-0.01	-0.11	0.91747491	0.9810	-6.67
246377_at	low-temperature-specific protein, p	---	AT1G57550	-1.01	-0.02	-0.11	0.91754993	0.9810	-6.67
256693_at	hypothetical protein predicted by g	---	---	1.01	0.01	0.11	0.91746734	0.9810	-6.67
253829_at	Medicago nodulin N21-like protein	---	AT4G28040	1.03	0.04	0.11	0.91782362	0.9810	-6.67
260134_at	Myb-related transcription factor, p	MYB113	AT1G66370	-1.01	-0.02	-0.11	0.91772303	0.9810	-6.67
255009_at	putative DNA-directed RNA polym	---	AT4G10070	1.01	0.02	0.11	0.91798758	0.9810	-6.67
248230_at	putative protein similar to unknown	---	AT5G53830	1.02	0.02	0.11	0.91811698	0.9810	-6.67
252552_at	putative protein	---	AT3G45900	1.01	0.02	0.11	0.91794842	0.9810	-6.67
265263_at	putative DNA binding protein	---	AT2G42940	-1.01	-0.01	-0.11	0.91825332	0.9810	-6.67
257884_at	hypothetical protein predicted by g	---	AT3G16960	-1.01	-0.01	-0.11	0.91783547	0.9810	-6.67
261793_at	unknown protein ; supported by cD	---	AT1G16080	-1.02	-0.03	-0.11	0.91784857	0.9810	-6.67
265039_at	unknown protein Location of ESTs	---	AT1G04000	1.01	0.01	0.11	0.91834033	0.9810	-6.67
263403_at	hypothetical protein similar to hypo	TX1	AT2G04040	-1.05	-0.06	-0.11	0.91836934	0.9810	-6.67
264478_at	hypothetical protein predicted by g	---	AT1G77270	1.01	0.01	0.11	0.91822171	0.9810	-6.67
251091_at	pyridoxine biosynthesis protein - lik	RSR4	AT5G01410	-1.02	-0.03	-0.11	0.91805302	0.9810	-6.67

257612_at	unknown protein	ARO4	AT3G26600	1.02	0.03	0.11	0.91818943	0.9810	-6.67
264795_at	unknown protein similar to ESTs e	ZIGA4	AT1G08680	-1.02	-0.02	-0.11	0.91785609	0.9810	-6.67
267372_at	putative protein kinase contains a	ARSK1	AT2G26290	-1.03	-0.04	-0.11	0.91828596	0.9810	-6.67
265487_at	hypothetical protein	---	---	1.01	0.01	0.11	0.91820841	0.9810	-6.67
264502_at	putative 12-oxophytodienoate red	---	AT1G09400	1.01	0.02	0.11	0.91833586	0.9810	-6.67
266882_at	unknown protein ;supported by ful	---	AT2G44670	1.02	0.03	0.11	0.91847926	0.9811	-6.67
256804_at	hypothetical protein predicted by g	---	AT3G20920	-1.01	-0.01	-0.11	0.918646	0.9812	-6.67
260679_at	unknown protein	---	AT1G07990	1.01	0.01	0.11	0.91886774	0.9812	-6.67
258398_at	thioredoxin m4 identical to GB:AAF	TRX-M4	AT3G15360	-1.01	-0.01	-0.11	0.91878589	0.9812	-6.67
254151_at	F-box protein family, AtFBX14 sim	---	AT4G24390	1.01	0.01	0.11	0.9188351	0.9812	-6.67
247952_at	salt-inducible protein-like	CYP71B10	AT5G57250	1.01	0.01	0.11	0.91885185	0.9812	-6.67
257117_at	geranyl geranyl pyrophosphate sy	---	AT3G20160	-1.01	-0.01	-0.11	0.91881385	0.9812	-6.67
260619_at	glyoxalase I, putative similar to GE	---	AT1G08110	1.01	0.02	0.11	0.91912198	0.9813	-6.67
263009_at	hypothetical protein contains simila	NHX5	AT1G54370	1.01	0.01	0.11	0.91908521	0.9813	-6.67
263463_at	putative ARI-like RING zinc finger	---	AT2G31770	-1.01	-0.01	-0.11	0.91899417	0.9813	-6.67
250081_at	unknown protein	---	AT5G17180	1.01	0.01	0.11	0.91915051	0.9813	-6.67
260907_at	hypothetical protein predicted by g	---	AT1G02570	-1.01	-0.01	-0.11	0.91904753	0.9813	-6.67
257784_at	geranylgeranylated protein, putati	MUB4	AT3G26980	-1.03	-0.04	-0.11	0.91940593	0.9815	-6.67
263214_at	hypothetical protein predicted by g	---	AT1G30660	-1.01	-0.01	-0.11	0.91939033	0.9815	-6.67
265812_at	hypothetical protein predicted by g	---	AT2G18070	-1.01	-0.01	-0.11	0.9194323	0.9815	-6.67
245558_at	hypothetical protein	---	AT4G15430	-1.01	-0.01	-0.10	0.9195281	0.9815	-6.67
253586_s_at	putative protein hypothetical prote	---	AT4G30710	-1.01	-0.02	-0.10	0.91952757	0.9815	-6.67
265236_s_at	hypothetical protein	---	AT2G07714	1.01	0.01	0.10	0.91961498	0.9815	-6.67
266041_s_at	hypothetical protein	---	---	-1.01	-0.01	-0.10	0.91958568	0.9815	-6.67
258484_at	sterol-C5-desaturase identical to G	STE1	AT3G02580	1.01	0.01	0.10	0.91993122	0.9815	-6.67
258877_at	putative expansin precursor simila	ATEXPA13	AT3G03220	1.02	0.03	0.10	0.92012373	0.9815	-6.67
255465_at	hypothetical protein similar to A. th	---	AT4G02990	-1.01	-0.01	-0.10	0.92161649	0.9815	-6.67
246282_at	ATPase-like protein	---	AT4G36580	1.01	0.02	0.10	0.92294928	0.9815	-6.67
248177_at	putative protein strong similarity to	---	AT5G54630	-1.01	-0.01	-0.10	0.92068469	0.9815	-6.67
247625_at	zinc finger protein - like dof6 zinc f	---	AT5G60200	-1.01	-0.02	-0.10	0.9221335	0.9815	-6.67
265907_at	unknown protein ;supported by ful	---	AT2G25650	-1.01	-0.01	-0.10	0.92310094	0.9815	-6.67
246012_at	Pspzf zinc finger protein - like DN	---	AT5G10650	1.01	0.02	0.10	0.92163334	0.9815	-6.67
245758_at	unknown protein contains similarity	KAN2	AT1G32240	1.01	0.02	0.10	0.92140173	0.9815	-6.67
255578_at	predicted protein of unknown func	---	AT4G01450	-1.02	-0.03	-0.10	0.92069867	0.9815	-6.67
253849_at	putative protein 150-kD protein, D	---	AT4G28080	-1.01	-0.01	-0.10	0.92297312	0.9815	-6.67

245581_at	hypothetical protein	---	AT4G14840	-1.01	-0.01	-0.10	0.92052462	0.9815	-6.67
254495_at	hypothetical protein	EMB1895	AT4G20060	-1.01	-0.02	-0.10	0.92216237	0.9815	-6.67
264475_s_at	hypothetical protein predicted by g	---	AT1G77150 /	-1.01	-0.02	-0.10	0.92063103	0.9815	-6.67
257667_at	1,4-alpha-glucan branching enzyn	EMB2729	AT3G20440	-1.01	-0.02	-0.10	0.9229773	0.9815	-6.67
251324_at	plasma membrane intrinsic protein	PIP1A	AT3G61430	-1.01	-0.01	-0.10	0.92024272	0.9815	-6.67
248907_at	putative protein contains similarity	---	AT5G46340	-1.01	-0.01	-0.10	0.9218241	0.9815	-6.67
248445_at	unknown protein ;supported by ful	---	AT5G51170	1.01	0.01	0.10	0.9209155	0.9815	-6.67
247999_at	E2, ubiquitin-conjugating enzyme,	UBC30	AT5G56150	-1.01	-0.01	-0.10	0.92067896	0.9815	-6.67
256928_at	unknown protein	---	AT3G22590	-1.01	-0.01	-0.10	0.92162778	0.9815	-6.67
255208_at	see GB:AL022580	---	---	-1.01	-0.01	-0.10	0.92298343	0.9815	-6.67
262810_at	putative salt-inducible protein simil	---	AT1G11710	-1.01	-0.02	-0.10	0.92134064	0.9815	-6.67
265381_at	putative non-LTR retroelement rev	---	---	1.01	0.02	0.10	0.92225799	0.9815	-6.67
251712_at	putative protein non-consensus T	---	AT3G56120	1.01	0.01	0.10	0.92176684	0.9815	-6.67
256590_at	recombination signal sequence re	ATHMG	AT3G28730	1.01	0.02	0.10	0.92070825	0.9815	-6.67
247285_at	putative protein similar to unknown	---	AT5G64400	1.01	0.01	0.10	0.9214633	0.9815	-6.67
263225_at	putative DNA-binding protein simil	WRKY14	AT1G30650	1.01	0.01	0.10	0.922753	0.9815	-6.67
259309_at	putative cyclin-dependent protein k	---	AT3G05050	-1.01	-0.02	-0.10	0.92084583	0.9815	-6.67
255012_at	putative protein ;supported by full-	---	AT4G10030	1.01	0.02	0.10	0.92254194	0.9815	-6.67
252401_at	putative protein predicted proteins	---	AT3G48030	-1.01	-0.01	-0.10	0.92207594	0.9815	-6.67
264026_at	glycine-rich protein (AtGRP2) Sam	ATGRP2B	AT2G21060	1.02	0.02	0.10	0.92180548	0.9815	-6.67
249793_at	putative protein contains similarity	---	AT5G23680	1.01	0.02	0.10	0.92004257	0.9815	-6.67
260388_at	hypothetical protein predicted by g	---	AT1G74070	-1.02	-0.02	-0.10	0.92294319	0.9815	-6.67
266204_at	hypothetical protein predicted by g	---	AT2G02410	1.01	0.02	0.10	0.92258506	0.9815	-6.67
255047_at	AX110P -like protein AX110P -Da	---	AT4G09670	1.01	0.01	0.10	0.92076008	0.9815	-6.67
249442_at	putative protein ; supported by cD	---	AT5G39590	-1.02	-0.03	-0.10	0.92075293	0.9815	-6.67
259641_at	putative protease similar to protea	---	AT1G69020	1.01	0.01	0.10	0.92282656	0.9815	-6.67
248627_at	putative protein similar to unknown	---	AT5G48950	-1.01	-0.02	-0.10	0.9226969	0.9815	-6.67
254897_at	serine/threonine kinase-like protei	---	AT4G11470	-1.02	-0.03	-0.10	0.92272877	0.9815	-6.67
264801_at	hypothetical protein gene overlaps	emb2411	AT1G08840	-1.01	-0.01	-0.10	0.92041286	0.9815	-6.67
254156_at	Rab geranylgeranyl transferase lik	---	AT4G24490	1.01	0.02	0.10	0.92164467	0.9815	-6.67
253939_at	putative myb-related protein myb-	MYB97	AT4G26930	-1.01	-0.02	-0.10	0.9224099	0.9815	-6.67
262765_at	putative cytochrome P450 monoox	CYP86C4	AT1G13150	-1.01	-0.01	-0.10	0.92262311	0.9815	-6.67
248120_at	putative protein similar to unknown	---	AT5G54540	-1.01	-0.01	-0.10	0.92254669	0.9815	-6.67
265994_at	putative multispanning membrane	---	AT2G24170	1.02	0.03	0.10	0.9218683	0.9815	-6.67
262723_at	hypothetical protein predicted by g	---	AT1G43630	-1.01	-0.02	-0.10	0.9222519	0.9815	-6.67

251211_s_at	putative protein several hypothetic	---	AT3G62470	-1.02	-0.03	-0.10	0.92124123	0.9815	-6.67
263284_at	unknown protein	---	AT2G36100	-1.01	-0.01	-0.10	0.92311211	0.9815	-6.67
261862_at	DNA-binding protein, putative sim	---	AT1G50410	-1.01	-0.02	-0.10	0.92198861	0.9815	-6.67
265704_at	hypothetical protein predicted by g	---	AT2G03420	1.01	0.02	0.10	0.92004713	0.9815	-6.67
266670_at	putative flavonol 3-O-glucosyltrans	UGT71C2	AT2G29740	-1.01	-0.01	-0.10	0.92273687	0.9815	-6.67
246121_at	putative protein motif in PGPS/D1	---	AT5G20370	1.01	0.01	0.10	0.92298764	0.9815	-6.67
249437_at	putative protein predicted proteins	---	AT5G39990	-1.01	-0.01	-0.10	0.92066036	0.9815	-6.67
247294_at	putative protein similar to unknown	XRCC2	AT5G64520	-1.01	-0.01	-0.10	0.92162284	0.9815	-6.67
255168_at	putative protein hypothetical prote	---	---	1.01	0.01	0.10	0.92302002	0.9815	-6.67
252576_s_at	clpC-like protein AtClpC - Arabido	---	AT3G45450	-1.01	-0.02	-0.10	0.92257048	0.9815	-6.67
257828_at	unknown protein	---	AT3G26670	-1.01	-0.02	-0.10	0.92171082	0.9815	-6.67
258618_at	Expressed protein ; supported by c	GASA5	AT3G02885	1.01	0.02	0.10	0.9205924	0.9815	-6.67
246721_at	putative protein glycine-rich protei	---	---	1.01	0.01	0.10	0.91992502	0.9815	-6.67
246726_at	putative protein predicted protein,	---	AT5G29050	1.01	0.01	0.10	0.92139598	0.9815	-6.67
262022_at	hypothetical protein predicted by g	---	AT1G35490	-1.01	-0.01	-0.10	0.92063388	0.9815	-6.67
260772_at	unknown protein contains similarity	---	AT1G49050	1.01	0.01	0.10	0.92281627	0.9815	-6.67
249072_at	putative protein similar to unknown	---	AT5G44060	-1.03	-0.04	-0.10	0.92260641	0.9815	-6.67
265652_x_at	hypothetical protein predicted by g	---	---	-1.01	-0.01	-0.10	0.92164338	0.9815	-6.67
250610_at	glycine-rich protein PUTG1 ;suppo	GRP19	AT5G07550	-1.01	-0.02	-0.10	0.92235161	0.9815	-6.67
262750_at	unknown protein ; supported by cD	---	AT1G28710	-1.01	-0.01	-0.10	0.92101296	0.9815	-6.67
257088_at	unknown protein	---	AT3G20510	1.02	0.03	0.10	0.9224803	0.9815	-6.67
250142_at	polygalacturonase - like protein po	---	AT5G14650	-1.02	-0.02	-0.10	0.92310932	0.9815	-6.67
245733_at	hypothetical protein predicted by g	---	AT1G73380	-1.01	-0.02	-0.10	0.92255603	0.9815	-6.67
255075_at	putative protein RING-H2 zinc fing	---	AT4G09110	1.01	0.01	0.10	0.92268612	0.9815	-6.67
254506_at	leucine rich repeat-like protein Cf-	GSO1	AT4G20140	1.01	0.02	0.10	0.92269298	0.9815	-6.67
265692_at	hypothetical protein predicted by g	---	AT2G24340	-1.01	-0.01	-0.10	0.92311045	0.9815	-6.67
247165_at	transcription factor-like protein ; su	MYB68	AT5G65790	-1.01	-0.01	-0.10	0.92112113	0.9815	-6.67
263537_at	CONSTANS-like B-box zinc finger	COL3	AT2G24790	-1.01	-0.01	-0.10	0.92190111	0.9815	-6.67
252730_at	putative protein	---	AT3G43110	-1.01	-0.02	-0.10	0.92061592	0.9815	-6.67
248444_at	putative protein similar to unknown	---	---	-1.01	-0.01	-0.10	0.92220154	0.9815	-6.67
251900_at	putative protein lateral root primor	SRS6	AT3G54430	-1.01	-0.01	-0.10	0.92061866	0.9815	-6.67
265555_at	putative Mutator-like transposase r	---	---	-1.01	-0.01	-0.10	0.92099126	0.9815	-6.67
261827_at	unknown protein contains similarity	---	AT1G11480	1.01	0.01	0.10	0.92102265	0.9815	-6.67
256556_at	mutator-like transposase, putative	---	---	1.01	0.01	0.10	0.91984262	0.9815	-6.67
262812_at	hypothetical protein predicted by g	---	AT1G11690	1.01	0.01	0.10	0.92315531	0.9815	-6.67

251435_at	putative protein hypothetical protei	---	---	1.01	0.01	0.10	0.92330354	0.9817	-6.67
247204_at	GTP binding protein-like	AtRABH1a	AT5G64990	-1.01	-0.01	-0.10	0.92335365	0.9817	-6.67
258773_at	hypothetical protein predicted by g	---	AT3G10730	-1.01	-0.01	-0.10	0.92371355	0.9818	-6.67
247637_at	putative protein gcpE protein, Chl	HDS	AT5G60600	1.01	0.02	0.10	0.92355035	0.9818	-6.67
245720_at	RNA binding protein - like	---	AT5G04210	-1.01	-0.01	-0.10	0.92378312	0.9818	-6.67
257927_at	ethylene response factor 1 (ERF1)	ERF1	AT3G23240	1.06	0.09	0.10	0.92350232	0.9818	-6.67
252722_at	putative protein hypothetical prote	---	---	-1.01	-0.01	-0.10	0.92375139	0.9818	-6.67
261281_at	hypothetical protein predicted by g	---	AT1G35740	-1.01	-0.01	-0.10	0.92371321	0.9818	-6.67
260850_at	glucose 6 phosphate/phosphate tr	---	AT1G21870	-1.01	-0.01	-0.10	0.92379117	0.9818	-6.67
257508_at	bZIP transcription factor, putative	---	AT1G64320	1.01	0.01	0.10	0.9237451	0.9818	-6.67
245105_at	hypothetical protein predicted by g	---	AT2G41610	1.01	0.02	0.10	0.9238597	0.9818	-6.67
250181_at	tRNA synthase - like protein tRNA	---	AT5G14460	-1.01	-0.01	-0.10	0.92422736	0.9821	-6.67
264113_at	unknown protein	APG9	AT2G31260	1.01	0.01	0.10	0.92420463	0.9821	-6.67
255835_at	unknown protein	---	AT2G33420	-1.01	-0.01	-0.10	0.92434533	0.9821	-6.67
257230_at	DegP protease contains similarity t	DegP11	AT3G16540	-1.01	-0.01	-0.10	0.92431911	0.9821	-6.67
259439_at	1-aminocyclopropane-1-carboxylat	ACS2	AT1G01480	1.04	0.06	0.10	0.92445921	0.9821	-6.67
247270_at	ER66 protein-like	---	AT5G64220	-1.01	-0.01	-0.10	0.92448657	0.9821	-6.67
259427_at	MADS-box transcription factor, pu	AGL28	AT1G01530	1.01	0.01	0.10	0.92442081	0.9821	-6.67
260382_at	unknown protein	---	AT1G73850	-1.01	-0.01	-0.10	0.92463841	0.9822	-6.67
255554_at	Expressed protein ; supported by f	---	AT4G01897	1.01	0.01	0.10	0.9246347	0.9822	-6.67
247393_at	unknown protein	---	AT5G63130	1.03	0.05	0.10	0.9248303	0.9822	-6.67
259794_at	unknown protein	---	AT1G64330	-1.01	-0.01	-0.10	0.92470458	0.9822	-6.67
254138_at	hypothetical protein	---	AT4G24950	1.01	0.01	0.10	0.92485679	0.9822	-6.67
260333_at	putative polygalacturonase similar	---	AT1G70500	1.01	0.02	0.10	0.92473507	0.9822	-6.67
266381_at	putative sucrose-proton symporter	ATSUC8	AT2G14670	-1.01	-0.01	-0.10	0.92482975	0.9822	-6.67
247601_at	zinc finger protein OBP4 - like zin	OBP4	AT5G60850	1.01	0.02	0.10	0.92507502	0.9823	-6.67
255777_at	glycine-rich RNA-binding protein,	GR-RBP6	AT1G18630	-1.01	-0.01	-0.10	0.92507102	0.9823	-6.67
265406_at	En/Spm-like transposon protein rel	---	---	-1.01	-0.01	-0.10	0.92496109	0.9823	-6.67
256514_at	oxidoreductase, putative contains	---	AT1G66130	1.01	0.02	0.10	0.92505753	0.9823	-6.67
253733_at	hypothetical protein	ATMND1	AT4G29170	-1.01	-0.01	-0.10	0.92549869	0.9823	-6.67
262476_at	phosphoprotein phosphatase ident	---	AT1G50370	1.01	0.01	0.10	0.9254812	0.9823	-6.67
253125_at	DnaJ-like protein DnaJ-like protei	---	AT4G36040	1.01	0.01	0.10	0.92535467	0.9823	-6.67
255866_at	hypothetical protein predicted by g	---	AT2G30350	-1.01	-0.01	-0.10	0.92527438	0.9823	-6.67
265036_at	unknown protein Contains similari	PRP39	AT1G04080	-1.01	-0.01	-0.10	0.92548013	0.9823	-6.67
249242_at	alcohol dehydrogenase	---	AT5G42250	-1.01	-0.01	-0.10	0.9252983	0.9823	-6.67

267421_at	putative phosphoribosylaminoimida	---	AT2G35040	-1.01	-0.01	-0.10	0.92540379	0.9823	-6.67
257845_at	unknown protein GC donor splice s	---	AT3G28430	1.01	0.01	0.10	0.9254336	0.9823	-6.67
265168_at	putative Ser/Thr protein kinase	---	AT1G23700	-1.01	-0.01	-0.10	0.92518649	0.9823	-6.67
255888_at	hypothetical protein contains simila	---	AT1G20300	1.02	0.03	0.10	0.92557626	0.9823	-6.67
257701_at	unknown protein contains similarity	---	AT3G12710	-1.03	-0.05	-0.10	0.92565458	0.9823	-6.67
263476_at	putative poly(ADP-ribose) glycohy	TEJ	AT2G31870	-1.01	-0.01	-0.10	0.92567221	0.9823	-6.67
255396_at	hypothetical protein	---	---	1.01	0.01	0.10	0.92566027	0.9823	-6.67
245274_at	ankyrin like protein ; supported by	---	AT4G14360	-1.01	-0.01	-0.10	0.9257522	0.9823	-6.67
256850_at	hypothetical protein similar to hypo	---	---	1.01	0.01	0.10	0.92591497	0.9825	-6.67
259652_at	unknown protein	HUB2	AT1G55250	-1.01	-0.02	-0.10	0.9259681	0.9825	-6.67
262517_at	putative glutathione transferase Se	ATGSTU25	AT1G17180	1.05	0.07	0.10	0.92606541	0.9825	-6.67
256626_at	hypothetical protein, 5' partial	---	AT3G20015	1.02	0.03	0.10	0.92603819	0.9825	-6.67
253707_at	hypothetical protein	---	AT4G29200	1.01	0.01	0.10	0.92609978	0.9825	-6.67
263485_at	putative villin ; supported by cDNA	VLN1	AT2G29890	-1.01	-0.01	-0.10	0.92624477	0.9826	-6.67
248014_at	putative protein similar to unknown	---	AT5G56340	-1.01	-0.01	-0.10	0.9263145	0.9826	-6.67
258202_at	unknown protein	---	AT3G13940	1.01	0.02	0.10	0.926512	0.9827	-6.67
261605_at	CDPK-related protein kinase, puta	---	AT1G49580	1.01	0.01	0.10	0.92650891	0.9827	-6.67
261159_s_at	cyclin, putative similar to GB:AAB	CYCB1;5	AT1G34460	1.01	0.01	0.10	0.92651957	0.9827	-6.67
255343_at	hypothetical protein	---	---	1.01	0.01	0.10	0.92654606	0.9827	-6.67
245834_at	transposon protein, putative simila	---	---	1.01	0.01	0.10	0.92657177	0.9827	-6.67
264666_at	hypothetical protein Similar to N. ta	---	AT1G09680	-1.01	-0.01	-0.10	0.92661924	0.9827	-6.67
266285_at	unknown protein	---	AT2G29180	1.02	0.02	0.10	0.9268698	0.9828	-6.67
266176_at	lectin-like protein	AtPP2-B2	AT2G02250	-1.01	-0.01	-0.10	0.92687079	0.9828	-6.67
252005_at	purple acid phosphatase-like prote	PAP21	AT3G52810	-1.01	-0.01	-0.10	0.92686912	0.9828	-6.67
245251_at	calcineurin B-like protein 1 ; suppo	CBL1	AT4G17615	-1.02	-0.03	-0.10	0.92692622	0.9828	-6.67
250165_at	putative protein many predicted pr	---	AT5G15290	-1.01	-0.01	-0.10	0.92701256	0.9829	-6.67
264634_at	cytochrome P450, putative	CYP702A1	AT1G65670	-1.01	-0.01	-0.09	0.92721758	0.9830	-6.67
263794_at	similar to S-locus glycoproteins	---	AT2G24620	1.01	0.01	0.09	0.92727686	0.9830	-6.67
259187_at	putative transcription factor similar	AtMYB57	AT3G01530	1.01	0.01	0.09	0.92735618	0.9831	-6.67
257010_at	Expressed protein ; supported by c	ATEXO70D	AT3G14090	-1.01	-0.02	-0.09	0.92740212	0.9831	-6.67
257787_at	actin related protein, putative simi	ARP2	AT3G27000	-1.01	-0.01	-0.09	0.92753524	0.9831	-6.67
263914_at	unknown protein	AtGRF3	AT2G36400	-1.01	-0.02	-0.09	0.9275903	0.9831	-6.67
254572_at	putative protein predicted protein	---	AT4G19380	-1.01	-0.01	-0.09	0.92746403	0.9831	-6.67
248475_at	unknown protein	---	AT5G50880	-1.01	-0.01	-0.09	0.92756552	0.9831	-6.67
261131_at	unknown protein	---	AT1G19835	-1.01	-0.02	-0.09	0.92772259	0.9832	-6.67

255918_at	putative protein	---	---	-1.01	-0.01	-0.09	0.9277146	0.9832	-6.67
258520_at	hypothetical protein predicted by g	---	AT3G06710	-1.01	-0.01	-0.09	0.92780705	0.9832	-6.67
254735_at	putative disease resistance protei	AtRLP47	AT4G13810	-1.01	-0.01	-0.09	0.927845	0.9832	-6.67
264313_at	carbonic anhydrase, putative simi	BCA4	AT1G70410	1.01	0.01	0.09	0.9280717	0.9832	-6.67
261206_at	heat shock factor protein hsf8, put	---	AT1G12800	1.01	0.01	0.09	0.9279464	0.9832	-6.67
256989_at	hypothetical protein predicted by g	---	AT3G28580	1.04	0.06	0.09	0.92801425	0.9832	-6.67
260116_at	AIG1 identical to AIG1 (exhibits R	AIG1	AT1G33960	1.01	0.01	0.09	0.92805535	0.9832	-6.67
258999_at	putative D-ribulose-5-phosphate 3-	---	AT3G01850	-1.01	-0.01	-0.09	0.92816926	0.9833	-6.67
254522_at	hypothetical protein	---	AT4G19980	-1.01	-0.01	-0.09	0.92821785	0.9833	-6.67
260188_at	Mutator-like transposase similar to	---	---	-1.01	-0.01	-0.09	0.92833083	0.9834	-6.67
261022_at	unknown protein similar to NAM lik	ANAC007	AT1G12260	-1.01	-0.01	-0.09	0.92840122	0.9834	-6.67
251473_at	putative protein myrosinase-bindi	---	AT3G59610	-1.01	-0.01	-0.09	0.92846523	0.9834	-6.67
259888_at	hypothetical protein similar to nodu	---	AT1G76350	-1.02	-0.03	-0.09	0.92856179	0.9835	-6.67
252647_at	protein-tyrosine-phosphatase-like	---	AT3G44620	1.01	0.02	0.09	0.92864872	0.9835	-6.67
263610_at	putative beta-1,3-glucanase	---	AT2G16230	-1.01	-0.01	-0.09	0.92884945	0.9836	-6.67
252746_at	sucrose synthase -like protein SU	SUS4	AT3G43190	-1.01	-0.01	-0.09	0.92880114	0.9836	-6.67
252631_s_at	putative protein predicted proteins	---	---	-1.01	-0.01	-0.09	0.9288521	0.9836	-6.67
257218_at	unknown protein similar to DAG pr	---	AT3G15000	-1.01	-0.01	-0.09	0.92921118	0.9836	-6.67
251233_at	putative protein hypothetical prote	DRB4	AT3G62800	-1.01	-0.01	-0.09	0.92970983	0.9836	-6.67
254639_at	putative protein various predicted	DOT4	AT4G18750	1.01	0.01	0.09	0.92917262	0.9836	-6.67
248886_at	phosphate/triose-phosphate transl	APE2	AT5G46110	-1.01	-0.01	-0.09	0.92929746	0.9836	-6.67
261139_at	homeodomain protein, putative sir	BEL10	AT1G19700	1.01	0.01	0.09	0.92960918	0.9836	-6.67
254422_at	putative protein hypothetical prote	VPS28-1	AT4G21560	1.01	0.02	0.09	0.92946888	0.9836	-6.67
260328_at	putative aspartate aminotransferas	---	AT1G80360	-1.01	-0.01	-0.09	0.92916349	0.9836	-6.67
266100_at	similar to axi 1 protein from Nicotia	---	AT2G37980	-1.01	-0.02	-0.09	0.92899514	0.9836	-6.67
252252_at	putative protein GTP-binding prote	RID3	AT3G49180	1.01	0.02	0.09	0.92940039	0.9836	-6.67
262917_at	hypothetical protein contains simila	---	AT1G64800	-1.01	-0.01	-0.09	0.92915592	0.9836	-6.67
248934_at	serine/threonine protein kinase-like	---	AT5G46080	-1.03	-0.04	-0.09	0.92906927	0.9836	-6.67
245763_at	transposon protein, putative simila	---	AT1G27850	-1.01	-0.01	-0.09	0.92971841	0.9836	-6.67
262506_at	unknown protein Similar to gb|X84	NADK2	AT1G21640	1.01	0.02	0.09	0.92967145	0.9836	-6.67
247472_at	cytokinesis regulating protein - like	MAP65-9	AT5G62250	1.01	0.01	0.09	0.92921218	0.9836	-6.67
252845_at	vacuolar H(+)-ATPase subunit-like	---	AT3G42050	-1.01	-0.01	-0.09	0.92967213	0.9836	-6.67
258624_at	unknown protein ; supported by cl	---	AT3G02950	1.01	0.01	0.09	0.92959768	0.9836	-6.67
266324_at	putative rac GTPase activating pro	---	AT2G46710	1.03	0.04	0.09	0.92980264	0.9836	-6.67
254861_at	putative protein zinc finger protein	---	AT4G12040	-1.01	-0.01	-0.09	0.92901025	0.9836	-6.67

250295_at	putative protein	NEF1	AT5G13390	1.01	0.01	0.09	0.92976294	0.9836	-6.67
257911_at	hypothetical protein contains simila	GLYR1	AT3G25530	-1.01	-0.01	-0.09	0.92978114	0.9836	-6.67
248844_s_at	extA (emb CAA47807.1)	---	AT5G46890	-1.01	-0.01	-0.09	0.92955529	0.9836	-6.67
247561_at	putative protein	---	AT5G61110	-1.01	-0.01	-0.09	0.92940496	0.9836	-6.67
267146_at	hypothetical protein predicted by g	---	AT2G38160	-1.01	-0.01	-0.09	0.92989301	0.9836	-6.67
250067_at	unknown protein	---	AT5G17950	1.01	0.01	0.09	0.92990811	0.9836	-6.67
247603_at	microtubule-associated motor - lik	---	AT5G60930	-1.01	-0.01	-0.09	0.92995795	0.9836	-6.67
254856_at	putative ribosomal protein (fragme	---	AT4G12160	1.01	0.01	0.09	0.93003242	0.9837	-6.67
249749_at	unknown protein	BIN4	AT5G24630	1.01	0.01	0.09	0.93008156	0.9837	-6.67
247274_at	putative protein similar to unknown	---	AT5G64360	1.01	0.01	0.09	0.93010638	0.9837	-6.67
250059_at	peroxidase ATP13a ; supported b	---	AT5G17820	-1.01	-0.01	-0.09	0.93026928	0.9838	-6.67
262903_at	NADPH-dependent codeinone rec	---	AT1G59950	1.03	0.04	0.09	0.9306565	0.9840	-6.67
259060_at	hypothetical protein predicted by g	---	AT3G07400	1.01	0.01	0.09	0.93068679	0.9840	-6.67
245429_at	Bax inhibitor-1-like protein	---	AT4G17580	-1.01	-0.01	-0.09	0.93064826	0.9840	-6.67
248493_at	putative protein contains similarity	FSD2	AT5G51100	1.01	0.01	0.09	0.93062402	0.9840	-6.67
258893_at	putative disease resistance protein	AtRLP33	AT3G05660	-1.03	-0.04	-0.09	0.9307236	0.9840	-6.67
266446_at	hypothetical protein predicted by g	---	AT2G43310	1.01	0.01	0.09	0.93074806	0.9840	-6.67
255368_at	hypothetical protein	---	---	1.01	0.01	0.09	0.93092238	0.9842	-6.67
255901_at	GDP-L-fucose synthetase, putativ	GER2	AT1G17890	-1.01	-0.02	-0.09	0.93108021	0.9842	-6.67
253167_at	calmodulin-domain protein kinase	CPK5	AT4G35310	1.01	0.01	0.09	0.9314171	0.9842	-6.67
255752_at	secretory carrier membrane protei	---	AT1G32050	1.01	0.01	0.09	0.93167369	0.9842	-6.67
245224_at	gene_id:K17E7.8~unknown protein	---	AT3G29796	-1.01	-0.01	-0.09	0.93112902	0.9842	-6.67
252126_at	putative disease resistance protein	---	AT3G50950	1.01	0.01	0.09	0.93120545	0.9842	-6.67
255621_at	hypothetical protein	---	AT4G01390	1.03	0.04	0.09	0.93150742	0.9842	-6.67
258878_at	hypothetical protein predicted by g	---	AT3G03170	1.01	0.01	0.09	0.93157462	0.9842	-6.67
261985_at	terpene synthase, putative similar	---	AT1G33750	-1.01	-0.01	-0.09	0.93146199	0.9842	-6.67
257371_at	putative CCAAT-box binding tranc	NF-YB5	AT2G47810	-1.01	-0.01	-0.09	0.93105423	0.9842	-6.67
261929_at	hypothetical protein similar to axi 1	---	AT1G22460	-1.01	-0.01	-0.09	0.93163175	0.9842	-6.67
254390_at	calcium-dependent protein kinase	CPK15	AT4G21940	-1.01	-0.01	-0.09	0.93157878	0.9842	-6.67
252757_at	putative protein several hypothetic	---	---	1.01	0.01	0.09	0.9315168	0.9842	-6.67
247519_at	NAM, no apical meristem, - like pr	ANAC100	AT5G61430	-1.01	-0.01	-0.09	0.93116197	0.9842	-6.67
265666_at	putative rac GTPase activating pro	---	AT2G27440	1.01	0.01	0.09	0.93144683	0.9842	-6.67
259264_at	putative aldose 1-epimerase show	---	AT3G01260	-1.01	-0.01	-0.09	0.93145784	0.9842	-6.67
254941_s_at	putative protein various reverse tra	---	---	-1.01	-0.01	-0.09	0.93161809	0.9842	-6.67
256472_at	unknown protein	---	---	-1.01	-0.01	-0.09	0.9316162	0.9842	-6.67

248225_at	unknown protein	---	AT5G53740	-1.01	-0.01	-0.09	0.9317728	0.9842	-6.67
258730_at	putative GTP-binding protein (ATF	ATFP8	AT3G11730	1.01	0.01	0.09	0.93187095	0.9843	-6.67
252459_s_at	1-phosphatidylinositol-4,5-bisphos	PLC9	AT3G47220 /	-1.01	-0.01	-0.09	0.93183846	0.9843	-6.67
261310_at	hypothetical protein predicted by g	PDE247	AT1G05750	1.01	0.01	0.09	0.93206254	0.9844	-6.67
256574_at	hypothetical protein similar to callo	---	AT3G14780	1.01	0.02	0.09	0.9321781	0.9845	-6.67
245131_s_at	unknown protein	emb1067	AT2G45330 /	1.01	0.01	0.09	0.93230608	0.9846	-6.67
265056_at	mitochondrial processing peptidas	---	AT1G51980	1.01	0.01	0.09	0.93236314	0.9846	-6.67
266808_at	Expressed protein ; supported by f	---	AT2G29995	-1.01	-0.01	-0.09	0.93316366	0.9846	-6.67
259533_at	hypothetical protein	---	AT1G12530	-1.01	-0.01	-0.09	0.93288013	0.9846	-6.67
252484_at	glucuronosyl transferase-like prote	---	AT3G46690	1.01	0.01	0.09	0.93290734	0.9846	-6.67
250160_at	putative protein various predicted	ATHB30	AT5G15210	1.02	0.02	0.09	0.93320156	0.9846	-6.67
254037_at	hypothetical protein hypothetical p	ATGDU2	AT4G25760	-1.01	-0.01	-0.09	0.93260969	0.9846	-6.67
259240_at	unknown protein ; supported by cl	---	AT3G11590	-1.01	-0.01	-0.09	0.93294672	0.9846	-6.67
249513_at	glucosyltransferase-like protein ; s	---	AT5G38460	1.01	0.01	0.09	0.93294474	0.9846	-6.67
256746_at	alpha-glucan phosphorylase, puta	---	AT3G29320	1.01	0.01	0.09	0.93284567	0.9846	-6.67
248654_at	importin alpha	IMPA-5	AT5G49310	1.01	0.01	0.09	0.93273702	0.9846	-6.67
257011_at	predicted protein	CAX9	AT3G14070	1.01	0.02	0.09	0.93299258	0.9846	-6.67
265401_at	hypothetical protein predicted by g	---	AT2G10970	-1.01	-0.01	-0.09	0.93304853	0.9846	-6.67
245549_at	cellulose synthase like protein	ATCSLB06	AT4G15320	-1.01	-0.01	-0.09	0.93288612	0.9846	-6.67
246477_at	putative transcription factor (MYB9	AtMYB9	AT5G16770	1.01	0.02	0.09	0.93251863	0.9846	-6.67
248993_at	putative protein contains similarity	---	AT5G45240	1.01	0.01	0.09	0.93313268	0.9846	-6.67
252598_at	putative protein putative proteins /	---	---	1.01	0.01	0.09	0.93258977	0.9846	-6.67
247523_at	ribulose-5-phosphate-3-epimerase	RPE	AT5G61410	1.01	0.01	0.09	0.93321245	0.9846	-6.67
249802_at	putative protein similar to unknown	---	AT5G23770	1.01	0.01	0.09	0.93305154	0.9846	-6.67
245561_at	indole-3-acetate beta-glucosyltrans	UGT84A4	AT4G15500	1.01	0.01	0.09	0.93258321	0.9846	-6.67
263822_at	hypothetical protein predicted by g	---	AT2G40240	-1.01	-0.01	-0.09	0.93275761	0.9846	-6.67
253275_at	Expressed protein ; supported by f	---	AT4G34215	1.01	0.01	0.09	0.93330443	0.9847	-6.67
246438_at	putative protein non-phototropic h	---	AT5G17580	1.01	0.01	0.09	0.93334599	0.9847	-6.67
267609_at	unknown protein similar to GP|522	---	AT2G26780	1.01	0.01	0.09	0.93351363	0.9848	-6.67
256908_at	hypothetical protein similar to muci	---	AT3G24040	-1.01	-0.01	-0.09	0.93361192	0.9848	-6.67
257459_at	unknown protein	---	AT1G24040	-1.01	-0.01	-0.09	0.93359949	0.9848	-6.67
256396_at	unknown protein	---	AT3G06150	-1.01	-0.02	-0.08	0.93489789	0.9848	-6.67
257076_at	unknown protein	---	AT3G19680	-1.02	-0.02	-0.08	0.93485595	0.9848	-6.67
255651_at	putative protein	---	AT4G00940	1.01	0.01	0.09	0.9344822	0.9848	-6.67
256528_at	C2H2-type zinc finger protein, put	ZFP4	AT1G66140	1.01	0.01	0.08	0.93491431	0.9848	-6.67

253912_at	putative protein met-10+ protein, M	---	AT4G27340	-1.01	-0.01	-0.09	0.93388866	0.9848	-6.67
258845_at	unknown protein ; supported by fu	---	AT3G03150	-1.01	-0.01	-0.09	0.93448488	0.9848	-6.67
256149_at	zinc finger protein, putative similar	AtIDD7	AT1G55110	1.01	0.01	0.09	0.93451177	0.9848	-6.67
255495_at	predicted protein of unknown func	---	AT4G02720	1.01	0.01	0.08	0.93476935	0.9848	-6.67
257280_at	9-cis-epoxycarotenoid dioxygenas	NCED3	AT3G14440	-1.01	-0.02	-0.09	0.93397786	0.9848	-6.67
251119_at	putative protein nifR3 protein, Azo	---	AT3G63510	1.01	0.01	0.09	0.9345723	0.9848	-6.67
249265_at	E2, ubiquitin-conjugating enzyme	---	AT5G41080	-1.01	-0.01	-0.08	0.93494476	0.9848	-6.67
259202_at	putative mRNA capping enzyme, l	---	AT3G09100	-1.01	-0.01	-0.08	0.93495683	0.9848	-6.67
248342_at	unknown protein	MBD13	AT5G52230	-1.01	-0.01	-0.09	0.93378991	0.9848	-6.67
248542_at	putative protein similar to unknown	AT5G5019(	---	1.01	0.01	0.09	0.93455086	0.9848	-6.67
257067_at	unknown protein contains Pfam pr	CYP77A5P	AT3G18270	-1.01	-0.01	-0.09	0.93386954	0.9848	-6.67
247564_at	RNA helicase - like protein RNA h	---	AT5G61140	1.01	0.01	0.09	0.93397446	0.9848	-6.67
253433_s_at	nodulin - like protein nodulin (clon	---	AT4G28365	1.01	0.01	0.09	0.9344621	0.9848	-6.67
254505_at	Expressed protein ; supported by f	---	AT4G19985	-1.01	-0.01	-0.09	0.93402718	0.9848	-6.67
265494_at	putative calmodulin-like protein	---	AT2G15680	1.01	0.01	0.09	0.93373835	0.9848	-6.67
246101_at	putative protein	---	---	1.01	0.01	0.08	0.93492686	0.9848	-6.67
251034_at	putative protein ;supported by full-	PRA1.A1	AT5G02040	-1.01	-0.01	-0.09	0.93383225	0.9848	-6.67
248935_at	salt-inducible protein-like	---	AT5G46100	-1.01	-0.01	-0.09	0.93441253	0.9848	-6.67
257390_x_at	hypothetical protein predicted by g	---	---	1.01	0.01	0.09	0.93367022	0.9848	-6.67
267558_at	unknown protein ; supported by cl	LUH	AT2G32700	1.01	0.01	0.08	0.93494197	0.9848	-6.67
246799_at	putative protein various predicted t	---	AT5G26940	-1.01	-0.01	-0.09	0.93445142	0.9848	-6.67
262352_at	hypothetical protein similar to hypo	---	---	1.01	0.02	0.09	0.93428667	0.9848	-6.67
260512_at	unknown protein	---	AT1G51520	-1.01	-0.01	-0.09	0.93409721	0.9848	-6.67
253725_at	profilin 3 ;supported by full-length	PRF4	AT4G29340	-1.01	-0.01	-0.09	0.93438386	0.9848	-6.67
259217_at	unknown protein similar to F16N3	---	AT3G03620	-1.01	-0.01	-0.09	0.93413237	0.9848	-6.67
263280_x_at	hypothetical protein predicted by g	---	---	1.01	0.01	0.08	0.93476484	0.9848	-6.67
256844_s_at	En/Spm transposon protein, putat	---	---	1.01	0.01	0.09	0.93448855	0.9848	-6.67
263223_at	coatomer-like protein, epsilon sub	---	AT1G30630	1.01	0.01	0.08	0.93502389	0.9848	-6.67
247067_at	putative protein strong similarity to	---	AT5G66950	-1.01	-0.01	-0.08	0.93508546	0.9849	-6.67
256128_at	laccase, putative similar to high-pl	LAC1	AT1G18140	1.01	0.01	0.08	0.93513089	0.9849	-6.67
256788_at	cytochrome P450, putative similar	CYP90D1	AT3G13730	-1.03	-0.04	-0.08	0.93523907	0.9849	-6.67
251468_at	epsin-like protein Af10-protein - A	---	AT3G59290	-1.01	-0.01	-0.08	0.93546677	0.9850	-6.67
266408_at	putative retroelement pol polyprote	---	---	1.01	0.01	0.08	0.93535839	0.9850	-6.67
250037_at	disease resistance protein -like dis	---	AT5G18350	-1.01	-0.01	-0.08	0.93544571	0.9850	-6.67
253181_at	amino acid permease - like protein	LHT7	AT4G35180	-1.03	-0.04	-0.08	0.93548689	0.9850	-6.67

246873_at	putative protein	---	AT5G26100	-1.01	-0.01	-0.08	0.93550119	0.9850	-6.67
246511_at	UDP-glucose dehydrogenase-like	---	AT5G15490	1.02	0.02	0.08	0.93561712	0.9851	-6.67
260169_at	hypothetical protein predicted by	FUT13	AT1G71990	1.01	0.02	0.08	0.93578675	0.9852	-6.67
262935_at	hypothetical protein similar to puta	AtOCT5	AT1G79410	1.02	0.03	0.08	0.93601539	0.9852	-6.67
255037_at	DNA-binding protein ;supported by	ATMYB6	AT4G09460	1.01	0.02	0.08	0.93612052	0.9852	-6.67
248809_at	GTP-binding protein-like	AtRABA5a	AT5G47520	1.01	0.01	0.08	0.9358383	0.9852	-6.67
257629_at	cellulase, putative contains Pfam	---	AT3G26140	-1.01	-0.01	-0.08	0.93610611	0.9852	-6.67
262391_at	geranyl geranyl pyrophosphate sy	GGPS6	AT1G49530	-1.01	-0.01	-0.08	0.93592194	0.9852	-6.67
255655_at	contains similarity to gag proteins	---	AT4G00980	-1.01	-0.02	-0.08	0.93613042	0.9852	-6.67
248119_at	serine/threonine-specific protein ki	---	AT5G54590	-1.01	-0.01	-0.08	0.93613557	0.9852	-6.67
265428_at	hypothetical protein predicted by g	---	AT2G20720	1.01	0.02	0.08	0.93612305	0.9852	-6.67
265643_at	hypothetical protein predicted by g	---	AT2G27390	1.01	0.02	0.08	0.93619031	0.9852	-6.67
259913_at	putative GTP-binding protein simila	---	AT1G72660	1.01	0.01	0.08	0.936283	0.9853	-6.67
250539_at	WD-repeat protein-like ; supported	---	AT5G08560	-1.01	-0.01	-0.08	0.93643374	0.9854	-6.67
257340_at	pseudogene, retroelement pol pol	---	---	-1.01	-0.01	-0.08	0.93651292	0.9854	-6.67
247744_at	putative protein various predicted	---	AT5G59020	1.01	0.01	0.08	0.936616	0.9855	-6.67
247044_at	MAP protein kinase ; supported by	MAPKKK5	AT5G66850	-1.01	-0.01	-0.08	0.93665538	0.9855	-6.67
247595_at	ring finger protein - like ring finger	---	AT5G60820	1.01	0.01	0.08	0.93683178	0.9855	-6.67
259662_at	Expressed protein ; supported by f	HUB2	AT1G55250	-1.01	-0.01	-0.08	0.93674097	0.9855	-6.67
255040_at	putative protein hypothetical prote	---	AT4G09580	-1.01	-0.01	-0.08	0.93680567	0.9855	-6.67
255873_at	hypothetical protein predicted by g	LBD13	AT2G30340	1.01	0.01	0.08	0.93685169	0.9855	-6.67
261601_at	ARP protein, putative similar to AF	NQR	AT1G49670	-1.01	-0.01	-0.08	0.93693265	0.9855	-6.67
259365_at	unknown protein ; supported by cD	---	AT1G13300	1.03	0.04	0.08	0.93696142	0.9855	-6.67
258516_at	myb-related protein, putative simil	MYB108	AT3G06490	-1.02	-0.03	-0.08	0.93707307	0.9856	-6.67
246942_at	anion exchanger-like protein chlor	---	AT5G25430	-1.01	-0.01	-0.08	0.93708536	0.9856	-6.67
258290_at	hypothetical protein predicted by g	---	AT3G23460	-1.01	-0.01	-0.08	0.93711844	0.9856	-6.67
257377_at	unknown protein	PLL4	AT2G28890	-1.01	-0.02	-0.08	0.9372662	0.9857	-6.67
261518_at	peroxidase ATP4a identical to GB:	---	AT1G71695	1.01	0.01	0.08	0.93735348	0.9857	-6.67
250867_at	putative protein predicted protein,	---	AT5G03880	1.01	0.01	0.08	0.93731664	0.9857	-6.67
264494_at	hypothetical protein predicted by g	---	AT1G27461	-1.01	-0.01	-0.08	0.93740641	0.9857	-6.67
244983_at	ribosomal protein L16	---	---	-1.01	-0.02	-0.08	0.93750281	0.9857	-6.67
254432_at	reticuline oxidase -like protein reti	---	AT4G20830	1.02	0.03	0.08	0.93751751	0.9857	-6.67
259076_at	hypothetical protein predicted by g	TMAC2	AT3G02140	-1.03	-0.04	-0.08	0.93760954	0.9858	-6.67
258946_at	hypothetical protein predicted by g	---	AT3G10650	1.01	0.01	0.08	0.93781214	0.9859	-6.67
252690_at	putative protein	---	---	-1.01	-0.01	-0.08	0.93793514	0.9860	-6.67

258844_at	hypothetical protein predicted by g	SWP	AT3G04740	1.01	0.01	0.08	0.93793463	0.9860	-6.67
264878_at	unknown protein	---	AT2G17410	-1.01	-0.01	-0.08	0.93811183	0.9860	-6.67
257143_at	cytochrome P450, putative contair	CYP705A2(	AT3G20110	1.01	0.01	0.08	0.93839587	0.9860	-6.67
262212_at	response regulator 7, putative sim	ARR15	AT1G74890	1.01	0.01	0.08	0.93819564	0.9860	-6.67
263717_at	malate oxidoreductase (malic enzy	---	AT2G13560	-1.01	-0.01	-0.08	0.93832135	0.9860	-6.67
246102_at	putative protein various predicted	---	AT5G32590	-1.01	-0.01	-0.08	0.93825509	0.9860	-6.67
247318_at	3(2),5-bisphosphate nucleotidase	---	AT5G63990	1.02	0.02	0.08	0.93824291	0.9860	-6.67
246069_at	zinc finger protein ;supported by f	---	AT5G20220	-1.01	-0.02	-0.08	0.93805853	0.9860	-6.67
248375_at	potassium/proton antiporter-like pr	KEA5	AT5G51710	1.01	0.01	0.08	0.93833719	0.9860	-6.67
255072_at	outer envelope membrane protein	TOC75-IV	AT4G09080	-1.01	-0.01	-0.08	0.9385241	0.9860	-6.67
247883_at	unknown protein	---	AT5G57790	1.01	0.01	0.08	0.93855799	0.9860	-6.67
263682_at	hypothetical protein similar to reve	AT5G49590	---	1.01	0.01	0.08	0.93849207	0.9860	-6.67
257931_at	hypothetical protein predicted by g	---	AT3G17030	-1.01	-0.01	-0.08	0.93856657	0.9860	-6.67
249203_at	cytochrome P450	CYP71A16	AT5G42590	1.01	0.01	0.08	0.93850787	0.9860	-6.67
249556_at	Expressed protein ; supported by f	---	AT5G38195	1.01	0.01	0.08	0.93858191	0.9860	-6.67
251881_at	DIPHOSPHOMEVALONATE DEC	---	AT3G54250	-1.01	-0.02	-0.08	0.93881494	0.9861	-6.67
264156_at	unknown protein	---	AT1G65280	1.00	0.01	0.08	0.93881095	0.9861	-6.67
245205_at	putative protein similarity to splicir	---	AT5G12280	1.01	0.01	0.08	0.93872616	0.9861	-6.67
255831_at	hypothetical protein predicted by g	---	AT2G33350	-1.01	-0.01	-0.08	0.93888998	0.9861	-6.67
260835_at	protein kinase interactor, putative	---	AT1G06700	-1.01	-0.01	-0.08	0.93885229	0.9861	-6.67
260440_at	hypothetical protein predicted by g	---	AT1G68160	1.01	0.01	0.08	0.93895789	0.9861	-6.67
245654_at	disease resistance protein, putativ	---	AT1G56540	-1.01	-0.01	-0.08	0.93903503	0.9862	-6.67
261399_at	receptor protein kinase, putative s	---	AT1G79620	1.01	0.01	0.08	0.93919634	0.9863	-6.67
245691_at	zinc finger protein - like	ELF6	AT5G04240	-1.01	-0.01	-0.08	0.93925604	0.9863	-6.67
250720_at	putative protein similar to unknowr	---	AT5G06180	1.01	0.01	0.08	0.93935017	0.9864	-6.67
252451_at	hypothetical protein	---	AT3G47100	-1.01	-0.01	-0.08	0.93942329	0.9864	-6.67
249404_at	ankyrin repeat protein EMB506 ; s	EMB506	AT5G40160	-1.01	-0.01	-0.08	0.93959537	0.9864	-6.67
264809_at	superoxidase dismutase identical t	CSD1	AT1G08830	1.02	0.03	0.08	0.93951139	0.9864	-6.67
265322_at	hypothetical protein predicted by g	---	AT2G18270	-1.01	-0.01	-0.08	0.93958627	0.9864	-6.67
248247_at	putative protein contains similarity	SPCH	AT5G53210	1.01	0.01	0.08	0.93967913	0.9865	-6.67
255857_at	unknown protein ;supported by full	ABA4	AT1G67080	1.01	0.01	0.08	0.93986239	0.9865	-6.67
250385_at	aspartate aminotransferase (Asp3)	ASP3	AT5G11520	1.01	0.02	0.08	0.93994645	0.9865	-6.67
246562_at	putative protein unknown protein I	LNG1	AT5G15580	1.04	0.05	0.08	0.93980636	0.9865	-6.67
248084_at	sodium proton exchanger	NHX3	AT5G55470	1.01	0.01	0.08	0.93998746	0.9865	-6.67
249578_at	putative protein predicted protein,	---	AT5G37730	1.00	0.01	0.08	0.93986121	0.9865	-6.67

255238_at	see GB:AL022580)	---	---	-1.00	-0.01	-0.08	0.93985839	0.9865	-6.67
245570_at	heat shock protein 101 (HSP101),	CLPB2	AT4G14670	-1.01	-0.01	-0.08	0.93997191	0.9865	-6.67
256915_at	unknown protein	---	AT3G23900	-1.01	-0.01	-0.08	0.94017029	0.9866	-6.67
263383_at	putative protein kinase contains a	---	AT2G40120	1.01	0.01	0.08	0.94013596	0.9866	-6.67
260405_at	putative glutathione transferase sir	ATGSTU11	AT1G69930	-1.04	-0.06	-0.08	0.94038151	0.9866	-6.67
253249_at	GATA transcription factor 3	---	AT4G34680	1.01	0.01	0.08	0.941061	0.9866	-6.67
262837_at	dynamin, putative similar to dynar	ADL1C	AT1G14830	-1.01	-0.01	-0.08	0.9405146	0.9866	-6.67
259278_at	hypothetical protein predicted by g	---	AT3G01160	1.01	0.01	0.08	0.94094034	0.9866	-6.67
246262_at	hypothetical protein	---	AT1G31790	-1.01	-0.01	-0.08	0.94166458	0.9866	-6.67
246120_at	tetratricopeptide repeat protein tet	---	AT5G20360	1.01	0.01	0.08	0.94166039	0.9866	-6.67
254990_at	RNA-binding protein ;supported b	CID12	AT4G10610	1.00	0.01	0.08	0.94092246	0.9866	-6.67
259830_at	hypothetical protein predicted by g	---	AT1G80630	-1.01	-0.01	-0.08	0.94174478	0.9866	-6.67
246971_at	Protein phosphatase 2C-like prote	---	AT5G24940	-1.01	-0.01	-0.08	0.94183244	0.9866	-6.67
260707_s_at	Expressed protein ; supported by f	---	AT1G32410	1.01	0.01	0.08	0.94127905	0.9866	-6.67
246270_at	putative protein	---	AT4G36500	-1.02	-0.03	-0.08	0.94138971	0.9866	-6.67
267625_at	putative RNA-binding protein	---	AT2G42240	-1.01	-0.01	-0.08	0.9410374	0.9866	-6.67
247998_at	unknown protein	---	AT5G56200	-1.01	-0.02	-0.08	0.94123741	0.9866	-6.67
252370_at	putative protein	---	AT3G48600	-1.01	-0.02	-0.08	0.94177849	0.9866	-6.67
259839_at	peptide transporter, putative simila	---	AT1G52190	-1.03	-0.05	-0.08	0.94143737	0.9866	-6.67
250693_at	ubiquitin-specific protease 12 (UB	UBP12	AT5G06600	-1.01	-0.01	-0.08	0.94197605	0.9866	-6.67
254613_at	ankyrin-like protein ankyrin 3, Mus	---	AT4G19150	-1.01	-0.01	-0.08	0.9412581	0.9866	-6.67
255330_s_at	putative polyprotein	---	---	-1.00	-0.01	-0.08	0.94154593	0.9866	-6.67
263318_at	Expressed protein ; supported by f	AtGDU4	AT2G24762	1.03	0.04	0.08	0.94178073	0.9866	-6.67
249719_at	Expressed protein ; supported by f	---	AT5G35735	-1.02	-0.03	-0.08	0.94157731	0.9866	-6.67
263726_at	putative ABC transporter ;support	---	AT2G13610	-1.03	-0.04	-0.08	0.94132264	0.9866	-6.67
256735_at	hypothetical protein predicted by g	ATEXO70E	AT3G29400	-1.01	-0.01	-0.08	0.94195361	0.9866	-6.67
251835_at	lipase -like protein monoglyceride	---	AT3G55180	-1.01	-0.01	-0.08	0.94069407	0.9866	-6.67
254556_at	putative protein various predicted	---	AT4G19220	-1.01	-0.01	-0.08	0.94160476	0.9866	-6.67
245235_at	putative protein similarity to predic	---	AT4G25550	-1.01	-0.01	-0.08	0.9404477	0.9866	-6.67
253355_at	putative protein	---	AT4G33380	1.01	0.01	0.08	0.94079034	0.9866	-6.67
266255_at	putative selenium-binding protein	---	AT2G27610	-1.01	-0.01	-0.08	0.94032194	0.9866	-6.67
245090_at	putative integral membrane protein	---	AT2G40900	1.01	0.01	0.08	0.94193741	0.9866	-6.67
257118_at	hypothetical protein	---	AT3G20180	-1.01	-0.01	-0.08	0.94194516	0.9866	-6.67
248414_at	50S ribosomal protein L11-like	---	AT5G51610	-1.01	-0.01	-0.08	0.94149089	0.9866	-6.67
267343_at	hypothetical protein predicted by g	---	AT2G44260	1.03	0.04	0.08	0.94103173	0.9866	-6.67

255713_s_at	predicted protein	---	AT4G00234 /	-1.01	-0.01	-0.08	0.94177351	0.9866	-6.67
262527_at	SRG1-like protein Strong homolog	---	AT1G17010	-1.01	-0.01	-0.08	0.94191389	0.9866	-6.67
253301_at	pathogenesis-related protein 1 pre	---	AT4G33720	-1.02	-0.03	-0.08	0.94029693	0.9866	-6.67
245220_at	hypothetical protein contains simila	---	AT1G59171	1.01	0.01	0.08	0.94080288	0.9866	-6.67
245990_at	putative protein predicted proteins	---	AT5G20640	1.01	0.01	0.08	0.94078052	0.9866	-6.67
263169_at	hypothetical protein similar to unkn	---	AT1G03010	1.01	0.01	0.08	0.94152181	0.9866	-6.67
254998_at	choline kinase GmCK2p -like prot	---	AT4G09760	1.01	0.02	0.08	0.94068013	0.9866	-6.67
262896_at	chromaffin granule ATPase II hom	ALA3	AT1G59820	-1.01	-0.01	-0.08	0.94036698	0.9866	-6.67
253030_at	hypothetical protein	FRS5	AT4G38180	1.01	0.01	0.08	0.94048006	0.9866	-6.67
249657_at	sen1-like protein SEN1 - Sacchar	---	AT5G37140	-1.00	-0.01	-0.08	0.94183899	0.9866	-6.67
246415_at	putative protein (fragment) predict	---	AT5G17160	-1.01	-0.01	-0.08	0.94203507	0.9866	-6.67
247224_at	MADS box transcription factor-like	MAF5	AT5G65080	1.01	0.01	0.08	0.9421372	0.9866	-6.67
257529_at	hypothetical protein predicted by g	---	AT3G03290	-1.01	-0.01	-0.08	0.94214003	0.9866	-6.67
262201_at	unknown protein	ORC4	AT2G01120	1.01	0.01	0.08	0.94220094	0.9867	-6.67
245336_at	Expressed protein ; supported by f	---	AT4G16515	1.03	0.04	0.08	0.94227831	0.9867	-6.67
251819_at	phosphatidylglycerophosphate sy	PGPS2	AT3G55030	1.01	0.01	0.08	0.94234296	0.9867	-6.67
248868_at	putative protein similar to unknown	---	AT5G46780	1.01	0.02	0.07	0.94244584	0.9868	-6.67
254913_at	putative protein beta-transducin re	---	AT4G11270	1.01	0.01	0.07	0.94254383	0.9868	-6.67
267376_at	putative receptor-like protein kinas	ER	AT2G26330	-1.02	-0.03	-0.07	0.94273567	0.9868	-6.67
266749_at	putative protein kinase contains a	---	AT2G47060	-1.01	-0.02	-0.07	0.94266596	0.9868	-6.67
255727_at	hypothetical protein similar to unkn	---	AT1G25510	-1.01	-0.01	-0.07	0.9426147	0.9868	-6.67
262106_at	hypothetical protein similar to Wee	WEE1	AT1G02970	1.01	0.01	0.07	0.94273622	0.9868	-6.67
262276_at	hypothetical protein predicted by g	---	AT1G68700	1.01	0.01	0.07	0.94269664	0.9868	-6.67
249895_at	male sterility 2-like protein (emb|C/	FAR1	AT5G22500	-1.02	-0.03	-0.07	0.94285385	0.9869	-6.67
260787_at	Ring3-like bromodomain protein s	GTE4	AT1G06230	-1.01	-0.01	-0.07	0.94284982	0.9869	-6.67
256302_at	Expressed protein ; supported by f	---	AT1G69526	-1.01	-0.01	-0.07	0.94290153	0.9869	-6.67
251096_at	receptor like protein kinase recept	LECRKA4.2	AT5G01550	-1.01	-0.01	-0.07	0.94300345	0.9869	-6.67
253140_at	RING-H2 finger protein RHA3b ;su	RHA3B	AT4G35480	-1.01	-0.01	-0.07	0.94305467	0.9869	-6.67
261331_at	hypothetical protein predicted by g	---	---	1.01	0.01	0.07	0.94302599	0.9869	-6.67
261461_at	hypothetical protein predicted by g	---	AT1G07860	-1.01	-0.01	-0.07	0.94333513	0.9870	-6.67
263514_at	putative poly(ADP-ribose) glycohy	---	AT2G31860	-1.01	-0.01	-0.07	0.94336128	0.9870	-6.67
266647_at	hypothetical protein predicted by g	---	AT2G25870	1.01	0.01	0.07	0.94331402	0.9870	-6.67
264374_at	putative two-component response	ARR12	AT2G25180	1.01	0.01	0.07	0.94326562	0.9870	-6.67
264119_at	myb-related protein, putative simil	MYB63	AT1G79180	1.00	0.01	0.07	0.94323909	0.9870	-6.67
247953_at	cytochrome P450	CYP71B10	AT5G57260	1.00	0.01	0.07	0.94343208	0.9870	-6.67

255389_at	putative reverse transcriptase	---	---	1.00	0.01	0.07	0.94343334	0.9870	-6.67
245831_at	unknown protein	---	AT1G48840	-1.01	-0.01	-0.07	0.94350099	0.9870	-6.67
256940_at	unknown protein	QQS	AT3G30720	-1.01	-0.01	-0.07	0.94354922	0.9870	-6.67
253827_at	Expressed protein ; supported by c	---	AT4G28085	-1.02	-0.03	-0.07	0.94382351	0.9870	-6.67
250685_at	kinesin heavy chain-like protein	---	AT5G06670	-1.00	-0.01	-0.07	0.94367914	0.9870	-6.67
267518_at	unknown protein	---	AT2G30500	1.02	0.02	0.07	0.94379061	0.9870	-6.67
245701_at	ferredoxin-dependent glutamate sy	GLU1	AT5G04140	1.01	0.01	0.07	0.94365418	0.9870	-6.67
261030_at	unknown protein contains similarity	---	AT1G17410	1.01	0.01	0.07	0.94370888	0.9870	-6.67
262122_at	polygalacturonase, putative simila	PGA4	AT1G02790	-1.01	-0.01	-0.07	0.94373754	0.9870	-6.67
250334_at	NADH dehydrogenase (ubiquinone	---	AT5G11770	1.01	0.01	0.07	0.94388765	0.9870	-6.67
248681_at	pectate lyase non-consensus AG c	---	AT5G48900	1.05	0.07	0.07	0.94397861	0.9871	-6.67
260406_at	putative glutathione transferase sir	ATGSTU12	AT1G69920	-1.04	-0.06	-0.07	0.94418129	0.9872	-6.67
259903_at	unknown protein	---	AT1G74160	1.01	0.01	0.07	0.94415547	0.9872	-6.67
248518_at	putative protein similar to unknown	---	AT5G50560	1.01	0.01	0.07	0.94431782	0.9873	-6.67
245940_at	putative protein predicted proteins	---	AT5G19630	-1.01	-0.01	-0.07	0.94438217	0.9873	-6.67
266406_at	hypothetical protein predicted by g	---	AT2G38570	1.01	0.01	0.07	0.9444244	0.9873	-6.67
247073_at	33 kDa polypeptide of oxygen-evol	PSBO1	AT5G66570	1.00	0.01	0.07	0.94469927	0.9874	-6.67
258491_at	unknown protein ;supported by ful	---	AT3G02700	1.01	0.01	0.07	0.94489384	0.9874	-6.67
264359_at	hypothetical protein predicted by g	---	AT1G03320	1.01	0.01	0.07	0.94479815	0.9874	-6.67
253261_at	putative protein mRNA, partial cds	CHB3	AT4G34430	-1.01	-0.01	-0.07	0.94495936	0.9874	-6.67
260204_at	hypothetical protein predicted by g	---	AT1G52900	1.01	0.01	0.07	0.94514715	0.9874	-6.67
264182_at	MADS-box protein, putative simila	AGL23	AT1G65360	-1.01	-0.01	-0.07	0.94468848	0.9874	-6.67
248116_at	putative protein contains similarity	MYB120	AT5G55020	1.01	0.01	0.07	0.94510701	0.9874	-6.67
252448_at	beta-D-glucan exohydrolase - like	---	AT3G47050	-1.01	-0.01	-0.07	0.94486025	0.9874	-6.67
247807_at	similar to unknown protein (gb|AAE	OFP3	AT5G58360	1.01	0.01	0.07	0.94500379	0.9874	-6.67
264758_at	late embryogenesis abundant prot	---	AT1G61340	-1.03	-0.04	-0.07	0.94492842	0.9874	-6.67
262553_at	hypothetical protein similar to hypo	RECQL2	AT1G31360	-1.01	-0.01	-0.07	0.94470927	0.9874	-6.67
248660_at	RNA-binding protein-like	---	AT5G48650	1.01	0.01	0.07	0.94506271	0.9874	-6.67
245470_at	retrotransposon like protein	---	---	1.01	0.01	0.07	0.94492428	0.9874	-6.67
260672_at	Expressed protein ; supported by f	---	AT1G19480	-1.01	-0.01	-0.07	0.94502495	0.9874	-6.67
249416_at	putative protein DNA DAMAGE-R	---	AT5G39570	-1.01	-0.01	-0.07	0.94523032	0.9874	-6.67
262008_s_at	CACTA-element, putative similar t	---	---	1.01	0.01	0.07	0.94523542	0.9874	-6.67
250773_at	putative protein similar to unknown	---	AT5G05430	-1.01	-0.01	-0.07	0.94532489	0.9875	-6.67
250197_at	isocitrate dehydrogenase - like pro	---	AT5G14590	1.01	0.01	0.07	0.94542477	0.9875	-6.67
264671_at	unknown protein ; supported by fu	---	AT1G09920	1.01	0.01	0.07	0.94540317	0.9875	-6.67

252043_at	putative protein mttC protein, Esch	---	AT3G52390	1.01	0.01	0.07	0.94547482	0.9875	-6.67
250870_at	hypothetical protein	---	AT5G03920	1.01	0.01	0.07	0.94558843	0.9876	-6.67
265319_at	auxin-regulated protein (IAA8) ;su	IAA8	AT2G22670	1.01	0.02	0.07	0.94571507	0.9876	-6.67
250260_at	putative protein contains similarity	---	AT5G13810	-1.01	-0.01	-0.07	0.94568779	0.9876	-6.67
252073_at	hypothetical protein	---	AT3G51750	-1.02	-0.03	-0.07	0.9458576	0.9877	-6.67
249663_s_at	unknown protein	---	---	1.01	0.01	0.07	0.94586916	0.9877	-6.67
258841_at	hypothetical protein similar to hypo	---	AT3G04660	1.01	0.01	0.07	0.94596252	0.9878	-6.67
259072_at	unknown protein similar to unknow	FLA18	AT3G11700	-1.01	-0.01	-0.07	0.94627871	0.9878	-6.67
257684_s_at	unknown protein contains Pfam pr	VCS	AT3G13290 /	1.01	0.01	0.07	0.94628765	0.9878	-6.67
254044_at	putative xyloglucan endo-1,4-beta	XTR9	AT4G25820	-1.01	-0.01	-0.07	0.94620528	0.9878	-6.67
266907_at	Expressed protein ; supported by f	ATGA2OX3	---	-1.01	-0.01	-0.07	0.94622975	0.9878	-6.67
256504_at	cytosolic IMP-GMP specific 5'-nuc	---	AT1G75210	1.01	0.01	0.07	0.94607785	0.9878	-6.67
245125_at	putative histidine kinase identical t	CKI1	AT2G47430	-1.01	-0.01	-0.07	0.94625138	0.9878	-6.67
263455_at	hypothetical protein predicted by g	---	AT2G22320	1.01	0.01	0.07	0.94625518	0.9878	-6.67
258389_at	hypothetical protein predicted by g	SDE5	AT3G15390	-1.01	-0.01	-0.07	0.94647476	0.9878	-6.67
250942_at	putative protein	---	AT5G03350	1.05	0.07	0.07	0.94664503	0.9878	-6.67
263345_s_at	putative chlorophyll a/b binding pro	LHCB2.1	AT2G05070 /	1.01	0.02	0.07	0.94656093	0.9878	-6.67
257148_at	cytochrome c, putative similar to c	---	AT3G27240	1.01	0.01	0.07	0.94642976	0.9878	-6.67
261779_at	hypothetical protein predicted by g	---	AT1G76230	1.00	0.01	0.07	0.94664609	0.9878	-6.67
260256_at	putative type II intron maturase cor	---	AT1G74350	-1.01	-0.01	-0.07	0.94651114	0.9878	-6.67
262191_at	hypothetical protein contains simila	---	---	-1.01	-0.01	-0.07	0.94644844	0.9878	-6.67
253915_at	putative protein centrin, Marsilea v	---	AT4G27280	1.03	0.04	0.07	0.94659663	0.9878	-6.67
258285_at	photosystem I subunit VI precurso	PSAH-1	AT3G16140	1.00	0.01	0.07	0.94688355	0.9878	-6.67
250060_at	chromo domain protein polycomb-	TFL2	AT5G17690	-1.01	-0.01	-0.07	0.94697689	0.9878	-6.67
251814_at	chlorophyll a/b-binding protein ; su	LHCA1	AT3G54890	1.00	0.01	0.07	0.94691815	0.9878	-6.67
264592_at	putative prolyl 4-hydroxylase, alph	---	AT2G17720	1.01	0.02	0.07	0.94679108	0.9878	-6.67
256088_at	putative FKBP-type peptidyl-prolyl	---	AT1G20810	-1.01	-0.01	-0.07	0.94700468	0.9878	-6.67
267046_at	hypothetical protein	---	AT2G34360	1.01	0.01	0.07	0.94695537	0.9878	-6.67
267039_at	hypothetical protein predicted by g	---	AT2G34270	-1.01	-0.01	-0.07	0.94671574	0.9878	-6.67
260124_at	E2, ubiquitin-conjugating enzyme,	UBC31	AT1G36340	-1.01	-0.01	-0.07	0.94684565	0.9878	-6.67
245967_at	proline-rich protein extensins	---	AT5G19800	-1.01	-0.01	-0.07	0.94712456	0.9879	-6.67
266811_at	unknown protein	---	AT2G44850	1.01	0.01	0.07	0.94721875	0.9879	-6.67
248592_at	unknown protein ;supported by ful	---	AT5G49280	-1.01	-0.02	-0.07	0.94734169	0.9880	-6.67
264055_at	putative protein kinase contains a	---	AT2G28590	1.01	0.01	0.07	0.94733742	0.9880	-6.67
260607_at	putative receptor protein kinase	---	AT2G43700	1.01	0.01	0.07	0.94761832	0.9880	-6.67

263039_at	mak16-like protein-related similar	---	AT1G23280	1.01	0.01	0.07	0.94764589	0.9880	-6.67
260566_at	cysteine synthase (cpACS1) ;supp	OASB	AT2G43750	-1.01	-0.01	-0.07	0.94743835	0.9880	-6.67
250785_at	unknown protein	---	AT5G05510	1.01	0.01	0.07	0.94739998	0.9880	-6.67
251619_at	putative protein hypothetical prote	---	AT3G58050	-1.00	-0.01	-0.07	0.94763481	0.9880	-6.67
263951_at	putative harpin-induced protein ;su	NHL12	AT2G35960	-1.02	-0.03	-0.07	0.94755736	0.9880	-6.67
264829_at	hypothetical protein predicted by g	ANAC006	AT1G03490	-1.00	-0.01	-0.07	0.94764173	0.9880	-6.67
264875_at	putative glucanase	AKR2B	AT2G17390	-1.00	-0.01	-0.07	0.94771355	0.9880	-6.67
267196_at	FtsH protease (VAR2) identical to	VAR2	AT2G30950	-1.01	-0.01	-0.07	0.94776442	0.9880	-6.67
245559_at	glycine-rich protein like	---	AT4G15460	1.00	0.01	0.07	0.94782456	0.9880	-6.67
253019_at	putative protein crp1-hcf111 allele	---	AT4G38010	-1.01	-0.01	-0.07	0.94793043	0.9881	-6.67
266332_at	hypothetical protein predicted by g	---	AT2G32415	-1.01	-0.01	-0.07	0.94798096	0.9881	-6.67
256447_at	nitrate transporter NTL1, putative	---	AT1G33440	1.01	0.01	0.07	0.94803519	0.9881	-6.67
255287_at	see T10M13.1 (GB:AF001308) sim	---	AT4G04660	1.01	0.01	0.07	0.94805834	0.9881	-6.67
267261_at	unknown protein ;supported by ful	---	AT2G23120	-1.01	-0.01	-0.07	0.9482402	0.9881	-6.67
255667_at	phospholipase D, putative	PLDBETA2	AT4G00240	1.01	0.01	0.07	0.94823636	0.9881	-6.67
250821_at	putative protein similar to unknown	---	AT5G05190	1.01	0.01	0.07	0.94815632	0.9881	-6.67
263606_at	putative beta-ketoacyl-CoA syntha	KCS9	AT2G16280	1.01	0.01	0.07	0.94896023	0.9883	-6.67
264704_at	unknown protein similar to putative	LGT8	AT1G70090	-1.01	-0.01	-0.07	0.94873103	0.9883	-6.67
256853_at	hypothetical protein predicted by g	---	AT3G18640	-1.00	-0.01	-0.07	0.94898569	0.9883	-6.67
256238_at	unknown protein ; supported by ful	ELC	AT3G12400	1.01	0.01	0.07	0.94867066	0.9883	-6.67
264256_at	putative importin alpha similar to G	IMPA-4	AT1G09270	-1.00	-0.01	-0.07	0.94893272	0.9883	-6.67
253746_at	putative protein hypothetical prote	---	AT4G29100	-1.01	-0.02	-0.07	0.94898644	0.9883	-6.67
259478_at	germin, putative similar to germin	---	AT1G18980	-1.03	-0.05	-0.07	0.94879706	0.9883	-6.67
256868_at	eukaryotic translation initiation fac	EIF4B1	AT3G26400	1.01	0.01	0.07	0.94891727	0.9883	-6.67
248054_at	unknown protein	---	AT5G55820	1.01	0.01	0.07	0.94867724	0.9883	-6.67
263782_at	hypothetical protein predicted by g	---	AT2G46380	1.01	0.01	0.07	0.94902455	0.9883	-6.67
261010_at	hypothetical protein predicted by g	---	AT1G26350	1.01	0.01	0.07	0.94902362	0.9883	-6.67
254367_at	hypothetical protein	---	AT4G21700	-1.01	-0.01	-0.07	0.94893436	0.9883	-6.67
253211_at	amidase - like protein amidase, Ba	---	AT4G34880	1.00	0.01	0.07	0.94856704	0.9883	-6.67
261642_at	ADP-glucose pyrophosphorylase,	APL2	AT1G27680	-1.01	-0.01	-0.07	0.94877534	0.9883	-6.67
252326_at	putative protein ferripyochelin bind	GAMMA CA	AT3G48680	-1.01	-0.01	-0.07	0.94908039	0.9883	-6.67
246106_at	receptor-like protein kinase precu	---	AT5G28680	-1.00	-0.01	-0.07	0.94913886	0.9884	-6.67
250644_at	protein phosphatase 2C-like ;supp	---	AT5G06750	-1.01	-0.01	-0.07	0.94922692	0.9884	-6.67
257774_at	short-chain alcohol dehydrogenas	---	AT3G29250	-1.01	-0.01	-0.07	0.9492023	0.9884	-6.67
251007_at	ribosomal protein L35 - like riboso	---	AT5G02610	1.01	0.01	0.07	0.94951934	0.9884	-6.67

257102_at	endoxyloglucan transferase, putat	XTH3	AT3G25050	1.00	0.01	0.07	0.94954102	0.9884	-6.67
259351_at	putative sugar transporter similar t	---	AT3G05150	1.01	0.01	0.07	0.94938368	0.9884	-6.67
249241_at	serine carboxypeptidase-II like	scpl41	AT5G42230	1.00	0.01	0.07	0.94946752	0.9884	-6.67
265525_at	putative Ty3-gypsy-like retroeleme	---	---	-1.01	-0.01	-0.07	0.94942124	0.9884	-6.67
262430_s_at	unknown protein	---	AT1G47550 /	1.01	0.01	0.07	0.94948502	0.9884	-6.67
252341_at	remorin -like protein remorin, Sola	---	AT3G48940	-1.00	-0.01	-0.07	0.94945078	0.9884	-6.67
258884_at	threonine dehydratase/deaminase	OMR1	AT3G10050	-1.01	-0.01	-0.07	0.94967593	0.9884	-6.67
248218_at	unknown protein ;supported by full	---	AT5G53710	1.01	0.01	0.07	0.94963777	0.9884	-6.67
259562_at	hypothetical protein ; supported by	---	AT1G21200	1.01	0.01	0.07	0.94988311	0.9884	-6.67
248305_at	putative protein similar to unknown	ATUSP	AT5G52560	1.01	0.01	0.07	0.95002626	0.9884	-6.67
265838_at	putative spliceosome associated p	---	AT2G14550	1.00	0.01	0.07	0.94982081	0.9884	-6.67
260827_at	mudrA-like protein similar to Mu tra	AT1G06750	---	-1.01	-0.01	-0.07	0.94984523	0.9884	-6.67
255295_at	putative sugar transporter	---	AT4G04760	1.00	0.01	0.07	0.94999704	0.9884	-6.67
249731_at	RNA-binding protein-like	CID13	AT5G24440	1.01	0.01	0.07	0.95002257	0.9884	-6.67
262836_at	hypothetical protein predicted by g	---	AT1G14680	-1.00	-0.01	-0.07	0.95001863	0.9884	-6.67
252049_at	putative protein putative and hypot	---	AT3G52510	1.00	0.01	0.07	0.95005409	0.9884	-6.67
258437_at	unknown protein contains protein p	---	AT3G16560	-1.01	-0.01	-0.06	0.95020607	0.9885	-6.67
266757_at	unknown protein	---	AT2G46940	1.01	0.01	0.06	0.95017911	0.9885	-6.67
249440_at	protein kinase -like protein probab	---	AT5G40030	1.00	0.01	0.06	0.95026765	0.9885	-6.67
248179_at	receptor-protein kinase-like protein	THE1	AT5G54380	-1.01	-0.02	-0.06	0.95076637	0.9885	-6.67
263287_at	Expressed protein ; supported by f	---	AT2G36145	-1.01	-0.02	-0.06	0.95134468	0.9885	-6.67
263533_at	putative Rieske iron-sulfur protein	TIC55	AT2G24820	1.00	0.01	0.06	0.95088646	0.9885	-6.67
253954_at	putative aconitase Pumpkin mRNA	---	AT4G26970	-1.01	-0.01	-0.06	0.95079592	0.9885	-6.67
258381_at	kinesin-like protein similar to mitoti	KINESIN-1	AT3G16630	1.01	0.01	0.06	0.95080741	0.9885	-6.67
251379_at	putative protein various predicted /	---	AT3G60680	1.01	0.01	0.06	0.95138993	0.9885	-6.67
267092_at	unknown protein ;supported by ful	AUX1	AT2G38120	-1.01	-0.02	-0.06	0.95140345	0.9885	-6.67
255194_at	score=37.6, E=2.9e-07, N=3	---	AT4G07410	-1.01	-0.01	-0.06	0.9513928	0.9885	-6.67
263909_at	hypothetical protein predicted by g	DML1	AT2G36490	-1.01	-0.01	-0.06	0.95127078	0.9885	-6.67
261203_at	Expressed protein ; supported by f	---	AT1G12845	-1.02	-0.03	-0.06	0.95127604	0.9885	-6.67
253139_at	ankyrin repeat-containing protein 2	AKR2	AT4G35450	-1.00	-0.01	-0.06	0.9516781	0.9885	-6.67
262939_s_at	glyceraldehyde-3-phosphate dehy	GAPCP-2	AT1G16300 /	1.02	0.03	0.06	0.95089608	0.9885	-6.67
258931_at	hypothetical protein similar to hyp	DML2	AT3G10010	1.01	0.01	0.06	0.95109465	0.9885	-6.67
250225_at	Expressed protein ; supported by f	---	AT5G14105	1.01	0.01	0.06	0.95127413	0.9885	-6.67
252217_at	putative protein some putative prot	---	AT3G50140	1.01	0.01	0.06	0.95174683	0.9885	-6.67
266075_s_at	unknown protein	---	AT2G40710 /	1.01	0.01	0.06	0.95164015	0.9885	-6.67

263933_s_at	putative harpin-induced protein	---	AT2G35970	1.01	0.01	0.06	0.95160908	0.9885	-6.67
264496_at	putative polyprotein similar to GB:A	---	---	1.01	0.01	0.06	0.95103978	0.9885	-6.67
251901_at	putative protein axi1 protein, Nicot	---	AT3G54100	-1.01	-0.01	-0.06	0.95147694	0.9885	-6.67
256605_at	hypothetical protein predicted by g	---	AT3G32940	-1.01	-0.01	-0.06	0.95116533	0.9885	-6.67
265159_at	unknown protein similar to EST gb	---	AT1G31060	-1.01	-0.01	-0.06	0.95081366	0.9885	-6.67
261246_at	unknown protein	SYTB	AT1G20080	1.01	0.01	0.06	0.95036326	0.9885	-6.67
259940_at	hypothetical protein	---	AT1G71290	1.00	0.01	0.06	0.95047499	0.9885	-6.67
248149_at	Expressed protein ; supported by f	---	AT5G54855	-1.00	-0.01	-0.06	0.95172495	0.9885	-6.67
267351_at	unknown protein	NRPD1B	AT2G40030	-1.01	-0.01	-0.06	0.95155406	0.9885	-6.67
264416_at	hypothetical protein similar to puta	---	AT1G43140	1.01	0.01	0.06	0.95113644	0.9885	-6.67
255148_at	putative mitogen-activated protein	MAPKKK1(	AT4G08470	1.01	0.02	0.06	0.95076602	0.9885	-6.67
264743_at	receptor-like protein kinase, putati	---	AT1G62090	-1.00	-0.01	-0.06	0.95143458	0.9885	-6.67
248454_at	receptor protein kinase-like	---	AT5G51350	-1.01	-0.01	-0.06	0.95170761	0.9885	-6.67
259111_at	alpha subunit of F-actin capping pr	---	AT3G05520	1.01	0.01	0.06	0.95086637	0.9885	-6.67
260242_at	putative transcription factor similar	EGL3	AT1G63650	-1.00	-0.01	-0.06	0.95128778	0.9885	-6.67
257936_at	hypothetical protein contains simila	---	---	-1.01	-0.01	-0.06	0.95147036	0.9885	-6.67
259798_at	hypothetical protein predicted by g	---	AT1G64310	1.01	0.01	0.06	0.95067831	0.9885	-6.67
261388_at	Expressed protein ; supported by c	---	AT1G05385	1.00	0.01	0.06	0.95034815	0.9885	-6.67
259520_at	hypothetical protein	---	AT1G12320	1.01	0.01	0.06	0.951833	0.9886	-6.67
262325_at	dirigent protein, putative similar to	---	AT1G64160	-1.01	-0.02	-0.06	0.95185157	0.9886	-6.67
246391_at	unknown protein ; supported by cD	---	AT1G77350	-1.01	-0.01	-0.06	0.95193358	0.9886	-6.67
266368_at	putative embryo-abundant protein	---	AT2G41380	1.03	0.04	0.06	0.95208315	0.9887	-6.67
249758_at	putative protein similar to unknown	---	AT5G24350	-1.01	-0.01	-0.06	0.95210592	0.9887	-6.67
265259_at	putative WD-40 repeat protein sim	---	AT2G20330	1.01	0.01	0.06	0.95224043	0.9888	-6.67
256678_at	RNA-binding protein (cp33) identi	CP33	AT3G52380	1.01	0.01	0.06	0.95231033	0.9888	-6.67
246365_at	hypothetical protein	---	---	1.01	0.01	0.06	0.95247542	0.9888	-6.67
250788_at	putative protein similar to unknown	---	AT5G05570	1.01	0.01	0.06	0.9524538	0.9888	-6.67
258513_at	protein kinase, putative contains P	---	AT3G06630	1.00	0.01	0.06	0.95241648	0.9888	-6.67
263142_at	unknown protein	---	AT1G65230	1.01	0.01	0.06	0.95253066	0.9889	-6.67
247997_at	putative protein contains similarity	ATARP8	AT5G56180	-1.01	-0.01	-0.06	0.95265727	0.9889	-6.67
255537_at	protoporphyrinogen oxidase ; sup	PPOX	AT4G01690	1.01	0.01	0.06	0.95272003	0.9890	-6.67
263274_at	putative protein kinase contains a	CRCK3	AT2G11520	1.01	0.01	0.06	0.95282348	0.9890	-6.67
263723_at	putative Ta11-like non-LTR retroel	---	AT2G13500	-1.00	-0.01	-0.06	0.95285584	0.9890	-6.67
256203_at	hypothetical protein	---	AT1G50800	1.01	0.01	0.06	0.95287553	0.9890	-6.67
257258_at	hypothetical protein contains Pfam	---	AT3G22040	1.01	0.01	0.06	0.95296018	0.9890	-6.67

256107_at	hypothetical protein predicted by g	---	AT1G16830	-1.00	-0.01	-0.06	0.95313393	0.9891	-6.67
245651_s_at	F5A9.18 unknown protein; similar	---	AT1G24793	-1.01	-0.01	-0.06	0.95313362	0.9891	-6.67
256508_at	unknown protein	---	AT1G75140	-1.00	-0.01	-0.06	0.95322762	0.9892	-6.67
259571_at	hypothetical protein	---	AT1G20410	1.01	0.01	0.06	0.95349991	0.9893	-6.67
264667_s_at	hypothetical protein identical to hy	ZW18	AT1G09980	-1.00	-0.01	-0.06	0.9534393	0.9893	-6.67
262485_at	kinesin-like protein Similar to gb|U	---	AT1G21730	-1.00	-0.01	-0.06	0.95349932	0.9893	-6.67
252886_at	cellulose synthase catalytic subuni	CESA2	AT4G39350	1.01	0.01	0.06	0.9538013	0.9893	-6.67
250695_at	lectin-like protein kinase	---	AT5G06740	1.01	0.02	0.06	0.95359185	0.9893	-6.67
247008_at	ADP-ribosylation factor-like protein	ATARLA1D	AT5G67560	1.00	0.01	0.06	0.95364891	0.9893	-6.67
257020_at	mitotic checkpoint protein, putative	---	AT3G19590	1.01	0.01	0.06	0.95382749	0.9893	-6.67
248347_at	putative protein contains similarity	---	AT5G52250	-1.00	-0.01	-0.06	0.95389467	0.9893	-6.67
263703_at	unknown protein ;supported by ful	SRX	AT1G31170	-1.01	-0.01	-0.06	0.95371492	0.9893	-6.67
261444_at	hypothetical protein predicted by g	SYP61	AT1G28490	-1.00	-0.01	-0.06	0.95366807	0.9893	-6.67
256846_at	pectin methylesterase, putative si	---	AT3G27980	1.00	0.01	0.06	0.95386603	0.9893	-6.67
256069_at	hypothetical protein predicted by g	AFP2	AT1G13740	-1.01	-0.01	-0.06	0.95379647	0.9893	-6.67
266732_at	unknown protein	---	AT2G03240	-1.01	-0.01	-0.06	0.95403049	0.9893	-6.67
259227_at	putative 3 exoribonuclease contai	---	AT3G07750	1.01	0.02	0.06	0.95405642	0.9893	-6.67
265576_at	unknown protein	CLASP	AT2G20190	-1.00	-0.01	-0.06	0.95406243	0.9893	-6.67
264235_at	myosin, putative similar to myosin	XIE	AT1G54560	1.01	0.01	0.06	0.95411267	0.9893	-6.67
253883_at	hypothetical protein	---	AT4G27660	-1.00	-0.01	-0.06	0.95407858	0.9893	-6.67
262452_at	hypothetical protein similar to hypo	---	AT1G11210	-1.00	-0.01	-0.06	0.95463746	0.9893	-6.67
247427_at	putative protein similar to unknown	---	AT5G62580	-1.01	-0.01	-0.06	0.95478803	0.9893	-6.67
266984_at	unknown protein ; supported by cl	---	AT2G39570	1.01	0.01	0.06	0.9554829	0.9893	-6.67
252338_at	putative progesterone-binding prot	MAPR3	AT3G48890	1.02	0.02	0.06	0.95556986	0.9893	-6.67
252031_at	putative protein 150-kD protein clu	---	AT3G52140	-1.00	-0.01	-0.06	0.9547344	0.9893	-6.67
245685_at	Expressed protein ; supported by c	E2F1	AT5G22220	1.00	0.01	0.06	0.95462078	0.9893	-6.67
266728_at	similar to late embryogenesis abur	---	AT2G03140	-1.00	-0.01	-0.06	0.95549983	0.9893	-6.67
253866_at	putative protein various putative pr	---	AT4G27480	-1.01	-0.01	-0.06	0.95487874	0.9893	-6.67
258640_at	hypothetical protein predicted by g	---	AT3G07930	-1.01	-0.01	-0.06	0.95553448	0.9893	-6.67
254603_at	putative protein hypothetical prote	---	AT4G19045	-1.01	-0.01	-0.06	0.95490921	0.9893	-6.67
255792_at	AT-hook DNA-binding protein (AHI	---	AT2G33620	-1.01	-0.01	-0.06	0.95556789	0.9893	-6.67
257270_at	unknown protein ; supported by fu	---	AT3G28140	-1.00	-0.01	-0.06	0.95517867	0.9893	-6.67
260288_at	nodulin-like protein similar to nodu	---	AT1G80530	-1.01	-0.01	-0.06	0.95548136	0.9893	-6.67
264707_at	unknown protein	---	AT1G09730	1.00	0.01	0.06	0.95559132	0.9893	-6.67
263426_at	putative glutathione peroxidase ;s	ATGPX2	AT2G31570	1.01	0.01	0.06	0.95561158	0.9893	-6.67

264898_at	Unknown protein ; supported by fu	---	AT1G23205	-1.01	-0.01	-0.06	0.95537094	0.9893	-6.67
265609_at	hypothetical protein predicted by g	---	AT2G25420	1.01	0.01	0.06	0.9542172	0.9893	-6.67
257301_at	hypothetical protein predicted by g	---	---	-1.00	-0.01	-0.06	0.95549497	0.9893	-6.67
262982_at	unknown protein ;supported by full	ING2	AT1G54390	-1.00	-0.01	-0.06	0.95506505	0.9893	-6.67
264063_at	unknown protein	---	AT2G27900	-1.00	-0.01	-0.06	0.95471593	0.9893	-6.67
246626_at	hypothetical protein contains simila	---	AT1G48870	-1.01	-0.01	-0.06	0.95513437	0.9893	-6.67
246680_at	putative protein predicted proteins	---	---	1.01	0.01	0.06	0.95520038	0.9893	-6.67
256709_at	hypothetical protein predicted by g	---	---	1.00	0.01	0.06	0.95549326	0.9893	-6.67
257492_at	hypothetical protein contains simila	ARR19	AT1G49190	-1.00	-0.01	-0.06	0.95422656	0.9893	-6.67
250501_at	carboxypeptidase - like protein G(	SCPL19	AT5G09640	-1.00	-0.01	-0.06	0.95564735	0.9893	-6.67
259714_at	putative gibberellin 20-oxidase sim	ATGA20OX	AT1G60980	-1.00	-0.01	-0.06	0.95481426	0.9893	-6.67
255658_at	hypothetical protein ;supported by	---	AT4G00770	1.01	0.01	0.06	0.95507093	0.9893	-6.67
255282_at	putative polyprotein	---	---	1.00	0.01	0.06	0.95486861	0.9893	-6.67
257490_x_at	Myb homolog (CPC), putative sim	ETC1	AT1G01380	1.00	0.00	0.06	0.9546676	0.9893	-6.67
259556_at	hypothetical protein	---	---	-1.00	-0.01	-0.06	0.9550756	0.9893	-6.67
253712_at	putative protein putative NADH ox	DER1	AT4G29330	-1.00	-0.01	-0.06	0.95547572	0.9893	-6.67
260662_at	2-hydroxyisoflavone reductase, pu	---	AT1G19540	1.01	0.01	0.06	0.95452441	0.9893	-6.67
257957_at	wall-associated serine/threonine k	---	AT3G25490	1.01	0.01	0.06	0.95484464	0.9893	-6.67
252299_at	putative protein various predicted	---	AT3G49150	1.01	0.01	0.06	0.9545109	0.9893	-6.67
264125_at	hypothetical protein predicted by g	EMB1135	AT1G79350	-1.01	-0.01	-0.06	0.95543587	0.9893	-6.67
267070_at	putative DnaJ protein	---	AT2G41000	-1.01	-0.01	-0.06	0.9557336	0.9894	-6.67
253555_at	putative protein predicted proetein	---	AT4G31080	-1.01	-0.01	-0.06	0.95583652	0.9894	-6.67
259938_at	hypothetical protein predicted by g	---	AT1G71310	-1.00	-0.01	-0.06	0.95589667	0.9894	-6.67
260778_at	splicing factor, putative similar to h	---	AT1G14640	-1.01	-0.01	-0.06	0.95585757	0.9894	-6.67
254182_at	putative protein various npredicted	---	AT4G23950	-1.01	-0.01	-0.06	0.95595897	0.9894	-6.67
263748_at	putative protein kinase contains a	---	AT2G21480	1.00	0.01	0.06	0.95606616	0.9895	-6.67
256658_at	unknown protein	---	AT3G12010	-1.00	-0.01	-0.06	0.95614258	0.9895	-6.67
256305_at	glutathione S-conjugate transportir	MRP1	AT1G30400	1.01	0.01	0.06	0.95653822	0.9896	-6.67
253238_at	putative protein (fragment)	---	AT4G34480	-1.01	-0.01	-0.06	0.95688643	0.9896	-6.67
258054_at	delta tonoplast integral protein (de	DELTA-TIP	AT3G16240	1.03	0.04	0.06	0.95640777	0.9896	-6.67
248106_at	putative protein similar to unknown	---	AT5G55100	-1.00	-0.01	-0.06	0.95648515	0.9896	-6.67
246918_at	putative protein hypothetical prote	---	AT5G25340	1.01	0.01	0.06	0.95647225	0.9896	-6.67
250515_at	putative protein	---	AT5G09570	-1.00	0.00	-0.06	0.95664333	0.9896	-6.67
250114_s_at	AMP-binding protein	AAE5	AT5G16340	1.01	0.01	0.06	0.95621491	0.9896	-6.67
254325_at	putative protein various predicted	---	AT4G22650	-1.01	-0.01	-0.06	0.95678949	0.9896	-6.67

257672_at	unknown protein ;supported by ful	---	AT3G20300	-1.01	-0.01	-0.06	0.95660313	0.9896	-6.67
246752_at	putative protein predicted proteins	---	AT5G27890	-1.00	-0.01	-0.06	0.95649227	0.9896	-6.67
257179_at	topoisomerase VIA (SPO11 gene	---	AT3G13160	-1.00	-0.01	-0.06	0.95667261	0.9896	-6.67
267334_at	hypothetical protein predicted by g	---	AT2G19420	-1.00	-0.01	-0.06	0.95648506	0.9896	-6.67
248123_at	putative protein similar to unknown	---	AT5G54720	-1.00	-0.01	-0.06	0.9568705	0.9896	-6.67
259855_at	putative asparaginyl-tRNA synthet	---	AT1G68420	1.00	0.01	0.06	0.95679748	0.9896	-6.67
252628_at	putative protein	---	AT3G44960	-1.00	-0.01	-0.06	0.95642331	0.9896	-6.67
254125_at	putative alliin lyase alliin lyase (EC	TAR2	AT4G24670	-1.01	-0.01	-0.06	0.95666747	0.9896	-6.67
265327_at	unknown protein	---	AT2G18210	1.02	0.03	0.06	0.95681273	0.9896	-6.67
266946_at	putative protein kinase contains a	---	AT2G18890	1.01	0.01	0.06	0.95730948	0.9896	-6.67
261935_at	phosphoribosylanthranilate transfe	---	AT1G22610	-1.00	-0.01	-0.06	0.95700872	0.9896	-6.67
256544_at	Mlo-like protein similar to Mlo [Hor	MLO9	AT1G42560	1.01	0.01	0.06	0.95729851	0.9896	-6.67
262221_at	hypothetical protein predicted by g	ARC3	AT1G75010	-1.01	-0.01	-0.06	0.95731401	0.9896	-6.67
263639_at	unknown protein	---	AT2G25300	-1.00	-0.01	-0.06	0.95735205	0.9896	-6.67
264570_at	unknown protein Similar to Caenor	---	AT1G05350	1.01	0.01	0.06	0.95729181	0.9896	-6.67
252222_at	putative protein various predicted	---	AT3G49840	1.01	0.01	0.06	0.95733498	0.9896	-6.67
256278_at	unknown protein ; supported by ful	---	AT3G12130	1.00	0.01	0.06	0.95722879	0.9896	-6.67
248963_at	unknown protein	---	AT5G45700	1.00	0.01	0.06	0.95716388	0.9896	-6.67
259907_at	GCN4-complementing protein, pu	AGD2	AT1G60860	-1.01	-0.01	-0.06	0.95703107	0.9896	-6.67
261847_at	hypothetical protein predicted by g	---	AT1G11560	-1.01	-0.01	-0.06	0.95742173	0.9896	-6.67
247685_at	serine/threonine-specific protein k	---	AT5G59680	1.01	0.02	0.06	0.95768918	0.9898	-6.67
249634_at	putative protein several hypothetic	---	---	1.00	0.01	0.06	0.95767966	0.9898	-6.67
254665_at	beta-1,3-glucanase-like protein str	---	AT4G18340	-1.01	-0.01	-0.05	0.95830997	0.9898	-6.67
258009_at	unknown protein	---	AT3G19440	-1.00	0.00	-0.05	0.95795893	0.9898	-6.67
255043_at	putative protein several hypothetic	---	AT4G09640	-1.01	-0.01	-0.05	0.9577813	0.9898	-6.67
252038_at	gamma response I protein ; suppo	---	AT3G52120	-1.01	-0.01	-0.05	0.95824742	0.9898	-6.67
265796_at	Expressed protein ; supported by f	---	AT2G35730	-1.02	-0.03	-0.05	0.9580905	0.9898	-6.67
246895_at	putative protein predicted protein,	CID6	AT5G25540	1.00	0.01	0.05	0.95823941	0.9898	-6.67
245013_at	ATPase epsilon subunit	---	---	1.00	0.01	0.05	0.9579621	0.9898	-6.67
249499_at	hypothetical protein	---	AT5G39250	1.00	0.01	0.05	0.95821213	0.9898	-6.67
256389_at	hypothetical protein predicted by g	---	AT3G06220	1.00	0.01	0.05	0.95811096	0.9898	-6.67
250528_at	putative protein strong similarity to	---	AT5G08600	-1.00	0.00	-0.05	0.9583148	0.9898	-6.67
252523_at	putative protein light repressible re	---	AT3G46400	1.01	0.01	0.05	0.95786656	0.9898	-6.67
257440_at	unknown protein	---	AT2G24880	1.00	0.01	0.05	0.9580848	0.9898	-6.67
251095_at	putative protein hypothetical prote	---	AT5G01510	-1.01	-0.01	-0.05	0.9582813	0.9898	-6.67

256495_at	hypothetical protein contains simila	---	AT1G31530	1.01	0.01	0.05	0.95829529	0.9898	-6.67
258684_at	putative protein kinase contains P	---	AT3G08680	-1.01	-0.01	-0.05	0.95848344	0.9899	-6.67
247801_at	putative protein ; supported by full-	---	AT5G58560	1.00	0.01	0.05	0.95866115	0.9899	-6.67
248659_at	cyclin C-like protein	---	AT5G48640	1.00	0.01	0.05	0.95907357	0.9899	-6.67
245738_at	nucellin, putative similar to nucelli	---	AT1G44130	-1.01	-0.01	-0.05	0.95896395	0.9899	-6.67
263105_at	putative N-acetylglucosaminyltrans	---	AT2G05320	-1.00	-0.01	-0.05	0.95892762	0.9899	-6.67
262324_at	hypothetical protein similar to hypo	ATCHX16	AT1G64170	1.02	0.03	0.05	0.95890871	0.9899	-6.67
247209_at	putative protein contains similarity	---	AT5G64830	1.00	0.01	0.05	0.95875508	0.9899	-6.67
261835_at	hypothetical protein contains simila	---	AT1G16040	1.00	0.01	0.05	0.95907506	0.9899	-6.67
256013_at	unknown protein	DA1	AT1G19270	1.01	0.01	0.05	0.95898934	0.9899	-6.67
245286_at	cytosolic O-acetylserine(thiol)lyase	OASA1	AT4G14880	-1.00	-0.01	-0.05	0.95875877	0.9899	-6.67
255638_at	predicted protein of unknown funct	---	AT4G00740	-1.01	-0.01	-0.05	0.95867779	0.9899	-6.67
258032_at	hypothetical protein predicted by g	---	AT3G21170	1.01	0.01	0.05	0.95879612	0.9899	-6.67
245151_at	putative pectinesterase ;supporte	---	AT2G47550	1.03	0.04	0.05	0.95869352	0.9899	-6.67
257801_at	mitogen activated protein kinase k	WNK6	AT3G18750	1.00	0.01	0.05	0.95875713	0.9899	-6.67
266179_at	putative phloem-specific lectin	AtPP2-B5	AT2G02300	-1.00	-0.01	-0.05	0.95892703	0.9899	-6.67
265569_at	unknown protein ;supported by ful	PGR5	AT2G05620	1.00	0.01	0.05	0.95920522	0.9900	-6.67
250825_at	putative protein similar to unknown	---	AT5G05210	1.00	0.01	0.05	0.95925414	0.9900	-6.67
266510_at	unknown protein	SWA1	AT2G47990	-1.01	-0.01	-0.05	0.95947519	0.9901	-6.67
263429_at	putative aspartate aminotransferas	AAT	AT2G22250	-1.01	-0.02	-0.05	0.95974884	0.9901	-6.67
251080_at	putative protein hypothetical protei	ROPGEF7	AT5G02010	1.01	0.01	0.05	0.95958603	0.9901	-6.67
258509_at	protein kinase, putative similar to	---	AT3G06620	1.01	0.01	0.05	0.95966836	0.9901	-6.67
256421_at	hypothetical protein predicted by g	---	AT1G33500	-1.00	-0.01	-0.05	0.95969354	0.9901	-6.67
261555_s_at	hypothetical protein predicted by g	---	AT1G63230	1.00	0.00	0.05	0.95950284	0.9901	-6.67
263084_at	hypothetical protein predicted by g	---	AT2G27180	-1.00	-0.01	-0.05	0.9597168	0.9901	-6.67
245603_at	hypothetical protein	---	AT4G14280	-1.00	-0.01	-0.05	0.95969337	0.9901	-6.67
261636_at	branched-chain amino acid amino	---	AT1G50110	-1.00	-0.01	-0.05	0.95952835	0.9901	-6.67
256731_at	hypothetical protein contains Pfam	---	AT3G30340	-1.00	-0.01	-0.05	0.95991467	0.9902	-6.67
245827_at	disease resistance protein RPS4,	---	AT1G57830	1.00	0.01	0.05	0.96000917	0.9902	-6.67
252336_at	putative protein N7 protein - Medi	---	AT3G48880	-1.00	-0.01	-0.05	0.9600248	0.9902	-6.67
265165_at	putative OBP32pep protein	---	AT1G23610	1.00	0.01	0.05	0.9599037	0.9902	-6.67
254576_at	putative protein ;supported by full-	EMB3006	AT4G19350	1.00	0.01	0.05	0.95993814	0.9902	-6.67
246508_at	sugar transporter-like protein puta	PGLCT	AT5G16150	1.01	0.01	0.05	0.96007664	0.9902	-6.67
246702_at	putative cytidine deaminase - like	---	AT5G28050	1.01	0.02	0.05	0.96017296	0.9902	-6.67
253576_at	putative protein various predicted	---	AT4G31070	-1.00	-0.01	-0.05	0.96020169	0.9902	-6.67

251775_s_at	delta-1-pyrroline-5-carboxylate syn	P5CS1	AT2G39800 /	1.01	0.01	0.05	0.96014684	0.9902	-6.67
258239_at	putative chlorophyll A-B binding pr	LHCB2.3	AT3G27690	-1.02	-0.03	-0.05	0.96029631	0.9902	-6.67
245304_at	hypothetical protein ; supported by	---	AT4G15630	1.01	0.02	0.05	0.96044715	0.9902	-6.67
264716_at	matrix metalloproteinase, putative	MMP	AT1G70170	-1.01	-0.02	-0.05	0.9604369	0.9902	-6.67
264919_at	hypothetical protein contains simila	---	AT1G60540	1.00	0.01	0.05	0.96039645	0.9902	-6.67
245801_at	hypothetical protein similar to hypo	---	AT1G46912	-1.00	-0.01	-0.05	0.96045901	0.9902	-6.67
256136_s_at	lectin receptor kinase, putative sin	---	AT1G48720	-1.00	0.00	-0.05	0.96056768	0.9903	-6.67
258889_at	putative pectinesterase similar to p	---	AT3G05610	-1.01	-0.01	-0.05	0.9606487	0.9903	-6.67
250896_at	putative protein ; supported by cD	---	AT5G03560	-1.01	-0.01	-0.05	0.96081748	0.9904	-6.67
257539_at	hypothetical protein predicted by g	---	AT3G29150	1.00	0.01	0.05	0.96089552	0.9904	-6.67
247667_at	putative protein predicted protein,	---	AT5G60150	-1.00	-0.01	-0.05	0.96072581	0.9904	-6.67
257077_at	PR-1 protein, putative similar to P	---	AT3G19690	-1.01	-0.01	-0.05	0.96089321	0.9904	-6.67
256895_at	zinc-finger protein, putative almos	---	---	1.00	0.01	0.05	0.96093068	0.9904	-6.67
260694_at	NAD+ dependent isocitrate dehyd	---	AT1G32480	1.00	0.00	0.05	0.96084576	0.9904	-6.67
258501_at	hypothetical protein predicted by g	---	AT3G06780	-1.01	-0.01	-0.05	0.96097827	0.9904	-6.67
253685_at	putative protein nucleotide pyroph	---	AT4G29710	1.00	0.01	0.05	0.9611069	0.9904	-6.67
256481_at	elicitor response protein, putative	---	AT1G33430	-1.00	-0.01	-0.05	0.96110624	0.9904	-6.67
247608_at	replication protein A1 - like probab	---	AT5G60990	1.00	0.01	0.05	0.96194439	0.9905	-6.67
258735_at	low temperature and salt responsiv	RCI2A	AT3G05880	-1.01	-0.01	-0.05	0.96124714	0.9905	-6.67
263941_at	unknown protein	---	---	-1.00	-0.01	-0.05	0.96170434	0.9905	-6.67
251293_at	hypothetical protein	---	AT3G61930	-1.03	-0.04	-0.05	0.96152149	0.9905	-6.67
245584_at	amine oxidase like protein	ATAO1	AT4G14940	-1.00	0.00	-0.05	0.96151598	0.9905	-6.67
257168_at	mrp protein, putative similar to mr	HCF101	AT3G24430	1.01	0.01	0.05	0.96184016	0.9905	-6.67
256707_at	hypothetical protein predicted by g	---	---	1.00	0.00	0.05	0.96186007	0.9905	-6.67
250240_at	unknown protein	---	AT5G13590	1.01	0.01	0.05	0.96179719	0.9905	-6.67
256748_x_at	En/Spm transposon protein, putat	---	---	1.00	0.01	0.05	0.96168413	0.9905	-6.67
250865_at	putative protein predicted protein,	---	AT5G03900	-1.01	-0.01	-0.05	0.96173148	0.9905	-6.67
246934_at	putative protein several hypothetic	---	AT5G25290	-1.00	-0.01	-0.05	0.96125775	0.9905	-6.67
261340_at	hypothetical protein predicted by g	APUM9	AT1G35730	-1.00	-0.01	-0.05	0.96185394	0.9905	-6.67
256968_at	unknown protein	NADK1	AT3G21070	-1.02	-0.03	-0.05	0.96179159	0.9905	-6.67
263932_at	unknown protein	---	AT2G35990	1.00	0.01	0.05	0.9613519	0.9905	-6.67
265756_at	putative bZIP transcription factor s	---	AT2G13150	-1.00	0.00	-0.05	0.9619035	0.9905	-6.67
248851_s_at	disease resistance protein-like ; su	---	AT5G46260 /	-1.00	-0.01	-0.05	0.96174039	0.9905	-6.67
254964_at	98b like protein 98b - Daucus carc	---	AT4G11080	1.00	0.01	0.05	0.96155104	0.9905	-6.67
266524_at	putative importin, beta subunit	---	AT2G16960	1.00	0.01	0.05	0.96136606	0.9905	-6.67

252826_at	hypothetical protein ; supported by	---	AT4G40050	-1.00	-0.01	-0.05	0.96200719	0.9905	-6.67
267170_at	putative RING zinc finger protein	---	AT2G37585	1.01	0.01	0.05	0.96230908	0.9906	-6.67
258062_at	unknown protein ; supported by cl	---	AT3G26000	-1.01	-0.01	-0.05	0.96230221	0.9906	-6.67
263424_at	putative RING zinc finger protein	---	AT2G31510	-1.00	-0.01	-0.05	0.96219566	0.9906	-6.67
249206_at	putative protein similar to unknown	ATS	AT5G42630	-1.00	-0.01	-0.05	0.96227682	0.9906	-6.67
255362_at	putative reverse transcriptase	---	---	1.00	0.00	0.05	0.96238623	0.9906	-6.67
245058_at	hypothetical protein predicted by g	---	AT2G39790	-1.00	-0.01	-0.05	0.96240366	0.9906	-6.67
264881_s_at	lysine and histidine specific transp	---	AT1G61270 /	1.00	0.00	0.05	0.96246158	0.9906	-6.67
245881_at	putative protein	---	AT5G09460 /	1.01	0.01	0.05	0.96255498	0.9907	-6.67
248824_at	putative protein contains similarity	---	AT5G46940	1.05	0.06	0.05	0.96253506	0.9907	-6.67
265967_at	nodulin-like protein ; supported by	---	AT2G37450	-1.01	-0.01	-0.05	0.96278001	0.9908	-6.67
245488_at	peroxidase like protein	---	AT4G16270	1.00	0.01	0.05	0.96279842	0.9908	-6.67
247278_at	fructose-bisphosphatase-like prote	---	AT5G64380	-1.00	-0.01	-0.05	0.96285156	0.9908	-6.67
252485_at	disease resistance protein RPP13	RPP13	AT3G46530	1.00	0.01	0.05	0.96289802	0.9908	-6.67
263315_at	Expressed protein ; supported by f	---	AT2G05755	1.00	0.00	0.05	0.9630077	0.9909	-6.67
247773_at	putative protein	---	AT5G58630	-1.00	-0.01	-0.05	0.96309804	0.9909	-6.67
265048_at	jasmonate inducible protein, puta	---	AT1G52050	1.00	0.01	0.05	0.96307329	0.9909	-6.67
249341_at	salt-inducible protein-like	---	AT5G41170	-1.01	-0.01	-0.05	0.96306819	0.9909	-6.67
250817_at	SET-domain protein-like ; support	SUVH1	AT5G04940	-1.00	-0.01	-0.05	0.96329301	0.9910	-6.67
265954_at	putative WRKY-type DNA binding	TTG2	AT2G37260	-1.00	-0.01	-0.05	0.96326284	0.9910	-6.67
266300_at	putative auxin transport protein ; s	PIN4	AT2G01420	-1.01	-0.02	-0.05	0.96337728	0.9910	-6.67
259350_at	putative serine/threonine protein ki	RBK2	AT3G05140	1.00	0.01	0.05	0.96342327	0.9910	-6.67
258004_at	unknown protein similar to putative	MYB110	AT3G29020	-1.00	-0.01	-0.05	0.96365517	0.9910	-6.67
262583_at	putative phosphatidylserine syntha	---	AT1G15110	-1.00	-0.01	-0.05	0.96356624	0.9910	-6.67
257703_at	unknown protein ; supported by ful	---	AT3G12640	1.00	0.00	0.05	0.96368751	0.9910	-6.67
257245_at	hypothetical protein contains Pfam	---	AT3G24110	-1.00	-0.01	-0.05	0.96349864	0.9910	-6.67
266445_at	unknown protein	---	AT2G43070	1.00	0.01	0.05	0.96367972	0.9910	-6.67
247778_at	wounding stress induced protein -	---	AT5G58750	-1.00	0.00	-0.05	0.96359876	0.9910	-6.67
253183_at	putative protein predicted protein,	---	AT4G35220	1.00	0.00	0.05	0.96387506	0.9911	-6.67
246135_at	putative protein non-consensus do	---	AT5G20885	1.01	0.01	0.05	0.9639537	0.9911	-6.67
254509_at	terpene cyclase like protein 5-epi-	---	AT4G20200	-1.00	0.00	-0.05	0.96384564	0.9911	-6.67
263331_at	unknown protein ; supported by cl	---	AT2G15270	-1.00	-0.01	-0.05	0.9638134	0.9911	-6.67
248823_s_at	unknown protein ;supported by ful	---	AT5G46950 /	1.03	0.04	0.05	0.96395097	0.9911	-6.67
259891_at	putative Eukaryotic initiation factor	---	AT1G72730	-1.00	-0.01	-0.05	0.96402562	0.9911	-6.67
250668_at	unknown protein ; supported by fu	---	AT5G07020	1.01	0.01	0.05	0.96411502	0.9911	-6.67

260323_at	putative U3 small nucleolar ribonu	IMP4	AT1G63780	1.01	0.01	0.05	0.96416692	0.9912	-6.67
246871_at	extensin - like protein pAP8 protei	---	AT5G26070	1.00	0.00	0.05	0.96456331	0.9912	-6.67
259490_at	hypothetical protein preedicted by	---	AT1G15800	-1.00	-0.01	-0.05	0.96450662	0.9912	-6.67
253888_at	hypothetical protein	ISI1	AT4G27750	-1.00	0.00	-0.05	0.96431186	0.9912	-6.67
249609_at	putative protein predicted proteins	---	---	-1.00	0.00	-0.05	0.9645338	0.9912	-6.67
264598_at	putative dimethylaniline monooxyg	---	AT1G04610	-1.00	0.00	-0.05	0.96436264	0.9912	-6.67
246158_at	Expressed protein ; supported by f	---	AT5G19855	1.01	0.01	0.05	0.96430641	0.9912	-6.67
263323_at	putative receptor-like protein kinas	---	AT2G04300	1.00	0.01	0.05	0.96446573	0.9912	-6.67
252196_at	putative protein predicted protein,	---	AT3G50200	1.00	0.01	0.05	0.96444887	0.9912	-6.67
254905_at	RPP1-WsA-like disease resistanc	---	AT4G11170	-1.01	-0.02	-0.05	0.96462631	0.9912	-6.67
264685_at	endo-1,4-beta-glucanase, putative	KOR2	AT1G65610	1.00	0.01	0.05	0.96476655	0.9913	-6.67
250340_at	putative protein predicted proteins	---	AT5G11840	-1.00	-0.01	-0.05	0.9649728	0.9914	-6.67
259260_at	unknown protein similar to unknow	---	AT3G11370	1.00	0.01	0.05	0.96495932	0.9914	-6.67
257955_at	unknown protein ; supported by cl	---	AT3G21810	-1.01	-0.01	-0.05	0.96503138	0.9915	-6.67
253443_at	putative protein beta transducin-lik	LUG	AT4G32551	-1.00	0.00	-0.05	0.96513045	0.9915	-6.67
246079_at	putative protein unconventional m	---	AT5G20450	1.00	0.01	0.05	0.96511048	0.9915	-6.67
266461_at	glutathione S-transferase (GST6)	ATGSTF8	AT2G47730	-1.01	-0.01	-0.04	0.96555935	0.9915	-6.67
250381_at	putative protein various predicted	---	AT5G11610	1.01	0.01	0.04	0.96542917	0.9915	-6.67
261584_at	CAF protein identical to RNA helic	DCL1	AT1G01040	1.01	0.01	0.04	0.96561954	0.9915	-6.67
261574_at	cytochrome P450, putative similar	CYP78A8	AT1G01190	1.01	0.01	0.04	0.96565614	0.9915	-6.67
247752_at	putative protein	---	AT5G59060	1.00	0.00	0.04	0.96563542	0.9915	-6.67
266529_at	putative salt-inducible protein	---	AT2G16880	-1.00	-0.01	-0.04	0.96553077	0.9915	-6.67
247425_at	unknown protein	---	AT5G62550	1.00	0.00	0.05	0.96531373	0.9915	-6.67
246581_at	hypothetical protein predicted by g	---	AT1G31760	-1.00	-0.01	-0.05	0.96540826	0.9915	-6.67
267386_at	unknown protein	---	AT2G44430	1.01	0.01	0.04	0.96559319	0.9915	-6.67
260050_at	hypothetical protein predicted by g	AGL64	AT1G29960	1.00	0.01	0.04	0.96553035	0.9915	-6.67
255722_at	hypothetical protein	---	AT3G29570	-1.00	-0.01	-0.05	0.96519784	0.9915	-6.67
267316_at	homeodomain transcription factor (	PHB	AT2G34710	1.01	0.01	0.04	0.96543631	0.9915	-6.67
267600_at	mitochondrial F1-ATPase, gamma	---	AT2G33040	-1.01	-0.01	-0.04	0.96578029	0.9915	-6.67
245883_at	ribosomal protein S15-like riboson	---	AT5G09500	1.00	0.00	0.04	0.96573744	0.9915	-6.67
257543_at	hypothetical protein predicted by g	---	AT3G28960	1.00	0.01	0.04	0.96579381	0.9915	-6.67
260514_at	hypothetical protein predicted by g	---	AT1G51480	-1.00	0.00	-0.04	0.96587922	0.9915	-6.67
258695_at	putative ascorbate peroxidase stro	APX2	AT3G09640	1.00	0.01	0.04	0.96597521	0.9916	-6.67
264519_at	putative reverse transcriptase simi	---	AT1G10000	-1.00	-0.01	-0.04	0.96608725	0.9916	-6.67
255228_at	F-box protein family, AtFBL21 cor	---	AT4G05470	1.00	0.00	0.04	0.96605419	0.9916	-6.67

248430_at	putative protein similar to unknown	---	AT5G51800	1.00	0.01	0.04	0.96617373	0.9916	-6.67
248703_at	dermal glycoprotein precursor, ext	---	AT5G48430	-1.03	-0.04	-0.04	0.96623772	0.9917	-6.67
254145_at	hypothetical protein	---	AT4G24700	1.01	0.01	0.04	0.96642647	0.9917	-6.67
253080_at	hypothatical protein	---	---	1.00	0.00	0.04	0.96639794	0.9917	-6.67
258833_at	unknown protein	---	---	1.00	0.01	0.04	0.96634284	0.9917	-6.67
263343_at	putative replication protein A1	---	---	-1.00	0.00	-0.04	0.96633811	0.9917	-6.67
245759_at	hypothetical protein predicted by g	---	AT1G66900	1.00	0.01	0.04	0.96652381	0.9917	-6.67
251606_at	hypothetical protein	---	AT3G57840	-1.00	-0.01	-0.04	0.96663658	0.9918	-6.67
245298_at	hypothetical protein ; supported by	---	AT4G15010	-1.00	0.00	-0.04	0.96669291	0.9918	-6.67
253595_at	putative protein M1 protein, Strept	---	AT4G30830	-1.00	0.00	-0.04	0.96684609	0.9919	-6.67
262300_at	ripening-induced protein, putative	---	AT1G70870	-1.00	0.00	-0.04	0.96690937	0.9920	-6.67
249521_at	putative protein strong similarity to	---	AT5G38690	-1.00	0.00	-0.04	0.96700392	0.9920	-6.67
255489_at	predicted protein destination facto	---	AT4G02650 /	-1.00	-0.01	-0.04	0.96698932	0.9920	-6.67
256551_at	unknown protein	---	---	1.00	0.01	0.04	0.96708846	0.9920	-6.67
263975_at	hypothetical protein predicted by g	---	AT2G42710	-1.00	-0.01	-0.04	0.96722155	0.9920	-6.67
255558_at	P II nitrogen sensing protein GLB I	GLB1	AT4G01900	1.00	0.01	0.04	0.96722299	0.9920	-6.67
248779_at	acetoacyl-CoA-thiolase ;supported	---	AT5G47720	-1.01	-0.01	-0.04	0.96726942	0.9920	-6.67
259740_at	phytochrome, putative similar to G	---	AT1G64300	1.01	0.01	0.04	0.9673607	0.9920	-6.67
256565_at	hypothetical protein	AT3G19515	---	-1.00	0.00	-0.04	0.96732009	0.9920	-6.67
248764_at	putative protein contains similarity	NF-YB2	AT5G47640	-1.00	-0.01	-0.04	0.96730099	0.9920	-6.67
253638_at	cinnamoyl-CoA reductase - like pr	---	AT4G30470	1.01	0.01	0.04	0.96750214	0.9920	-6.67
253052_at	cytochrome P450-like protein ; sup	CYP81H1	AT4G37310	-1.01	-0.01	-0.04	0.96748321	0.9920	-6.67
265178_at	Pto kinase interactor, putative sim	---	AT1G23540	1.00	0.01	0.04	0.96749609	0.9920	-6.67
267364_at	unknown protein ;supported by ful	ELF4	AT2G40080	-1.00	-0.01	-0.04	0.96781781	0.9920	-6.67
263942_at	unknown protein	FLA16	AT2G35860	1.02	0.03	0.04	0.9676834	0.9920	-6.67
257215_at	RING zinc finger protein, putative	---	AT3G15070	-1.00	0.00	-0.04	0.96775144	0.9920	-6.67
266060_at	unknown protein unusual splice sit	---	AT2G18630	1.00	0.01	0.04	0.9676575	0.9920	-6.67
251567_at	putative protein several hypothetic	---	AT3G58230	1.00	0.01	0.04	0.96773545	0.9920	-6.67
245752_at	hypothetical protein similar to Ac-li	---	AT1G35150	-1.00	0.00	-0.04	0.9676817	0.9920	-6.67
246299_at	embryonic abundant protein AtEm	EM1	AT3G51810	1.00	0.00	0.04	0.96781796	0.9920	-6.67
247679_at	1-aminocyclopropane-1-carboxyla	---	AT5G59540	1.01	0.01	0.04	0.96790615	0.9921	-6.67
246740_at	putative protein	---	AT5G27810	1.00	0.00	0.04	0.96803113	0.9921	-6.67
257026_at	hypothetical protein predicted by g	---	AT3G19200	1.00	0.01	0.04	0.96800833	0.9921	-6.67
266872_at	unknown protein	---	AT2G44730	-1.00	-0.01	-0.04	0.96810011	0.9922	-6.67
266992_at	similar to Mlo proteins from H. vulg	MLO12	AT2G39200	1.01	0.02	0.04	0.96834176	0.9923	-6.67

258852_at	unknown protein similar to C-termi	AT-P4H-2	AT3G06300	-1.00	-0.01	-0.04	0.96831195	0.9923	-6.67
256701_at	transcription initiation factor IIF, be	---	AT3G52270	1.00	0.01	0.04	0.96836454	0.9923	-6.67
246238_at	sugar transporter like protein	---	AT4G36670	1.01	0.01	0.04	0.96843703	0.9923	-6.67
265828_at	hypothetical protein predicted by g	---	AT2G14520	-1.00	0.00	-0.04	0.96948759	0.9925	-6.67
261197_at	putative calcium-binding protein, c	GAPA-2	AT1G12900	-1.00	-0.01	-0.04	0.96926109	0.9925	-6.67
259590_at	hypothetical protein contains simila	---	AT1G28160	1.00	0.00	0.04	0.96947191	0.9925	-6.67
267355_at	putative LIM-domain protein	---	AT2G39900	-1.00	-0.01	-0.04	0.96937497	0.9925	-6.67
247289_at	2-oxoglutarate/malate translocator	DIT2.1	AT5G64290	1.00	0.01	0.04	0.96889394	0.9925	-6.67
255538_at	putative transcription factor ; supp	MYB55	AT4G01680	1.01	0.01	0.04	0.96899186	0.9925	-6.67
266260_at	putative ATPase skd1 family; supp	SKD1	AT2G27600	1.00	0.00	0.04	0.96943312	0.9925	-6.67
263364_at	unknown protein predicted by gens	---	AT2G20540	-1.00	0.00	-0.04	0.96890699	0.9925	-6.67
254021_at	putative protein cell death suppres	ACD1-LIKE	AT4G25650	1.00	0.01	0.04	0.96889169	0.9925	-6.67
245848_at	putative protein predicted proteins	FY	AT5G13480	-1.00	0.00	-0.04	0.96928013	0.9925	-6.67
247995_at	putative protein contains similarity	---	AT5G56160	-1.00	-0.01	-0.04	0.96925077	0.9925	-6.67
256562_at	Ty1/Copia-type retroelement polyp	---	---	1.00	0.00	0.04	0.9692405	0.9925	-6.67
261371_at	ubiquitin-conjugating enzyme, put	UBC26	AT1G53020	1.00	0.00	0.04	0.96941409	0.9925	-6.67
249259_at	putative protein similar to unknown	---	AT5G41660	-1.01	-0.02	-0.04	0.96887127	0.9925	-6.67
245741_at	hypothetical protein similar to unkn	---	AT1G44120	1.00	0.00	0.04	0.9691228	0.9925	-6.67
249370_at	zinc finger - like protein predicted	---	AT5G40710	-1.00	0.00	-0.04	0.9689886	0.9925	-6.67
248814_at	putative protein similar to unknown	---	AT5G46910	1.01	0.02	0.04	0.96912291	0.9925	-6.67
261157_at	peroxidase ATP13a, putative simi	---	AT1G34510	-1.00	0.00	-0.04	0.96927841	0.9925	-6.67
255084_s_at	putative protein same aa sequence	---	AT4G09220 /	-1.00	0.00	-0.04	0.96940753	0.9925	-6.67
260340_at	putative dihydropterin pyrophospho	---	AT1G69190	1.00	0.00	0.04	0.96945999	0.9925	-6.67
264143_at	latex-abundant protein, putative si	ATMC5	AT1G79330	-1.00	0.00	-0.04	0.96958997	0.9926	-6.67
262983_at	hypothetical protein similar to unkn	---	AT1G54550	-1.00	0.00	-0.04	0.96974016	0.9927	-6.67
264394_at	aminomethyltransferase-like precu	---	AT1G11860	-1.00	-0.01	-0.04	0.9698035	0.9927	-6.67
262051_at	putative coatomer protein complex	---	AT1G79990	-1.00	-0.01	-0.04	0.96991818	0.9927	-6.67
248784_at	putative protein similar to unknown	---	AT5G47380	-1.00	-0.01	-0.04	0.96985666	0.9927	-6.67
261707_at	unknown protein	---	AT1G32650	1.00	0.00	0.04	0.96991128	0.9927	-6.67
248847_at	disease resistance protein-like	---	AT5G46510	1.00	0.00	0.04	0.96997419	0.9927	-6.67
267459_at	unknown protein ;supported by ful	---	AT2G33850	1.00	0.00	0.04	0.97003671	0.9927	-6.67
AFFX-r2-Bs-lys	B. subtilis /GEN=lys /DB_XREF=g	---	---	-1.01	-0.01	-0.04	0.97021978	0.9928	-6.67
256640_at	hypothetical protein predicted by g	---	AT3G32260	-1.00	-0.01	-0.04	0.97022297	0.9928	-6.67
253022_at	putative protein	---	AT4G38060	-1.01	-0.01	-0.04	0.97056293	0.9931	-6.67
266635_at	unknown protein ;supported by ful	---	AT2G35470	1.00	0.01	0.04	0.97055502	0.9931	-6.67

253566_at	DNA topoisomerase like- protein B	---	AT4G31210	-1.01	-0.01	-0.04	0.9706505	0.9931	-6.67
245939_at	oxoglutarate/malate translocator-li	---	AT5G19760	-1.00	0.00	-0.04	0.97072015	0.9931	-6.67
250559_at	putative protein condensin subuni	---	AT5G08010	1.00	0.01	0.04	0.97080886	0.9931	-6.67
263740_at	hypothetical protein predicted by g	RALFL14	AT2G20660	-1.00	-0.01	-0.04	0.97078809	0.9931	-6.67
252517_at	receptor-like protein kinase homol	---	AT3G46340	-1.00	0.00	-0.04	0.97085803	0.9932	-6.67
266742_at	predicted by genefinder and gensc	---	AT2G03050	1.00	0.00	0.04	0.97091244	0.9932	-6.67
262210_at	hypothetical protein predicted by g	IQD31	AT1G74690	-1.01	-0.01	-0.04	0.97117703	0.9932	-6.67
249612_at	putative protein CG14881, Drosop	---	AT5G37290	-1.01	-0.01	-0.04	0.97126957	0.9932	-6.67
259982_at	putative RING zinc finger protein c	ATL8	AT1G76410	1.01	0.01	0.04	0.97132035	0.9932	-6.67
245869_at	hypothetical protein predicted by g	---	AT1G26330	-1.00	0.00	-0.04	0.97129292	0.9932	-6.67
259987_at	thaumatin-like protein (PR-5) simila	ATLP-3	AT1G75030	1.00	0.01	0.04	0.97130828	0.9932	-6.67
265855_at	unknown protein ;supported by ful	---	AT2G42390	-1.00	0.00	-0.04	0.97130861	0.9932	-6.67
265608_at	hypothetical protein predicted by g	---	AT2G25380	1.00	0.00	0.04	0.97105852	0.9932	-6.67
255541_s_at	P-glycoprotein-like protein pgp3 sir	PGP5	AT4G01820 /	1.00	0.00	0.04	0.97128543	0.9932	-6.67
247889_at	putative protein similar to unknown	APO2	AT5G57930	-1.00	0.00	-0.04	0.97135372	0.9932	-6.67
252109_at	putative protein mucin 5AC, Homo	---	AT3G51540	1.01	0.01	0.04	0.97108266	0.9932	-6.67
246852_at	putative protein various predicted b	---	AT5G26880	-1.00	0.00	-0.04	0.97142847	0.9932	-6.67
252001_at	plastid division protein FtsZ-like F	FTSZ2-2	AT3G52750	1.01	0.01	0.04	0.97159292	0.9932	-6.67
246226_at	thiol-disulfide interchange like prot	HCF164	AT4G37200	-1.00	-0.01	-0.04	0.97156256	0.9932	-6.67
253403_at	putative serine/threonine protein k	AtAUR1	AT4G32830	-1.00	-0.01	-0.04	0.97150789	0.9932	-6.67
250079_at	putative protein similar to unknown	---	AT5G16650	-1.00	0.00	-0.04	0.97176788	0.9934	-6.67
259788_at	lipase/hydrolase, putative contains	---	AT1G29670	1.01	0.02	0.04	0.97197088	0.9934	-6.67
261277_at	hypothetical protein predicted by g	---	AT1G20230	1.00	0.00	0.04	0.97192192	0.9934	-6.67
257423_at	hypothetical protein predicted by g	---	AT1G62010	1.00	0.00	0.04	0.97202484	0.9934	-6.67
251535_at	hypothetical protein ;supported by	---	AT3G58540	1.00	0.01	0.04	0.972081	0.9934	-6.67
264034_s_at	unknown protein	ATUPS1	AT2G03590 /	-1.00	0.00	-0.04	0.97206759	0.9934	-6.67
252697_at	nodulin - like protein nodulin-21, G	---	AT3G43660	-1.00	0.00	-0.04	0.97205562	0.9934	-6.67
257818_at	hypothetical protein predicted by g	---	AT3G25120	-1.00	0.00	-0.04	0.97214719	0.9934	-6.67
258940_at	putative lipase acylhydrolase conta	---	AT3G09930	-1.00	0.00	-0.04	0.97254081	0.9935	-6.67
254230_at	polyprenyltransferase like protein	AtPPT1	AT4G23660	-1.00	0.00	-0.04	0.9723925	0.9935	-6.67
259177_at	hypothetical protein similar to puta	---	AT3G01630	1.00	0.00	0.04	0.97246946	0.9935	-6.67
254670_at	teosinte branched1 - like protein te	---	AT4G18390	-1.00	-0.01	-0.04	0.97255754	0.9935	-6.67
257853_at	hypothetical protein predicted by g	---	AT3G12960	-1.00	0.00	-0.04	0.97246829	0.9935	-6.67
247296_at	unknown protein ;supported by ful	---	AT5G64160	-1.00	-0.01	-0.04	0.97237927	0.9935	-6.67
258256_at	unknown protein ; supported by cl	---	AT3G26890	1.00	0.00	0.04	0.97259056	0.9935	-6.67

264334_at	calcium-dependent protein kinase	CPK19	AT1G61950	-1.00	0.00	-0.04	0.97258805	0.9935	-6.67
252515_at	heat shock protein 17 ; supported	HSP17.4	AT3G46230	1.01	0.02	0.04	0.97282479	0.9937	-6.67
245170_at	60S ribosomal protein L18, 5'parti	---	AT2G47570	-1.00	0.00	-0.04	0.97295335	0.9937	-6.67
258610_at	IAA-amino acid hydrolase (ILR1) ic	ILR1	AT3G02875	1.01	0.01	0.04	0.97296585	0.9937	-6.67
246170_at	putative protein various predicted	---	AT5G32450	-1.00	0.00	-0.04	0.97288401	0.9937	-6.67
263710_at	unknown protein ;supported by ful	---	AT1G09330	1.00	0.00	0.04	0.97300389	0.9937	-6.67
264229_at	unknown protein	---	AT1G67480	-1.00	-0.01	-0.04	0.97290604	0.9937	-6.67
245585_at	hypothetical	---	AT4G14970	1.00	0.00	0.04	0.97308152	0.9937	-6.67
244909_at	hypothetical protein	---	---	-1.00	0.00	-0.03	0.97315178	0.9938	-6.67
246316_at	putative protein predicted proteins	---	AT3G56890	-1.00	0.00	-0.03	0.97359885	0.9939	-6.67
250912_at	histone deacetylase -like protein h	HD2C	AT5G03740	1.01	0.01	0.03	0.97365128	0.9939	-6.67
249256_at	putative protein strong similarity to	---	AT5G41620	-1.00	-0.01	-0.03	0.9734609	0.9939	-6.67
254932_at	putative translation elongation fac	---	AT4G11120	-1.00	-0.01	-0.03	0.97339228	0.9939	-6.67
251582_at	putative protein CARBON CATAB	---	AT3G58580	1.00	0.00	0.03	0.9736441	0.9939	-6.67
255098_at	hypothetical protein	---	AT4G08640	1.00	0.00	0.03	0.97366241	0.9939	-6.67
245567_at	germin precursor oxalate oxidase	GLP9	AT4G14630	1.01	0.02	0.03	0.97340397	0.9939	-6.67
263041_at	putative alliinase similar to alliinase	TAR1	AT1G23320	-1.00	0.00	-0.03	0.97364852	0.9939	-6.67
251343_at	phosphatidate cytidylyltransferase	---	AT3G60620	-1.01	-0.01	-0.03	0.97337131	0.9939	-6.67
265926_at	RUB1-conjugating enzyme, putati	---	AT2G18600	-1.00	-0.01	-0.03	0.97375523	0.9939	-6.67
255595_at	putative chitinase similar to peanu	---	AT4G01700	-1.01	-0.01	-0.03	0.97383078	0.9939	-6.67
245805_at	hypothetical protein predicted by g	---	AT1G46336	1.00	0.00	0.03	0.97382144	0.9939	-6.67
251197_at	glutaredoxin -like protein glutared	---	AT3G62960	1.01	0.01	0.03	0.97389135	0.9939	-6.67
266121_at	unknown protein ; supported by cl	---	AT2G02160	1.00	0.01	0.03	0.97394413	0.9939	-6.67
252608_at	putative protein 2-phosphoglycera	---	AT3G45090	-1.00	0.00	-0.03	0.97410163	0.9940	-6.67
257548_s_at	hypothetical protein	LBD23	AT3G26620	1.00	0.00	0.03	0.97412424	0.9940	-6.67
260747_at	unknown protein ; supported by cD	---	AT1G78420	-1.00	0.00	-0.03	0.97421107	0.9941	-6.67
264010_at	putative disease resistance respor	---	AT2G21100	1.00	0.01	0.03	0.97424761	0.9941	-6.67
256125_at	pathogenesis-related group 5 prot	ATLP-1	AT1G18250	-1.00	-0.01	-0.03	0.97434819	0.9941	-6.67
246916_at	disease resistance protein - like di	AtRLP52	AT5G25910	1.00	0.00	0.03	0.97431791	0.9941	-6.67
248433_at	putative protein strong similarity to	---	AT5G51400	-1.00	0.00	-0.03	0.97501601	0.9942	-6.67
250038_at	disease resistance protein -like dis	---	AT5G18360	1.00	0.01	0.03	0.97519311	0.9942	-6.67
261582_at	unknown protein ; supported by cD	GIF2	AT1G01160	1.00	0.00	0.03	0.97476976	0.9942	-6.67
264637_at	allyl alcohol dehydrogenase, putat	---	AT1G65560	-1.00	-0.01	-0.03	0.97479682	0.9942	-6.67
245216_at	Expressed protein non-consensus	IMPA-2	AT4G16143	1.00	0.00	0.03	0.97458483	0.9942	-6.67
254695_at	putative protein predicted protein,	ATL4H	AT4G17905	-1.00	0.00	-0.03	0.97452272	0.9942	-6.67

267548_at	putative disease resistance protein	AtRLP22	AT2G32660	-1.01	-0.01	-0.03	0.97481541	0.9942	-6.67
265265_at	unknown protein	---	AT2G42900	1.00	0.01	0.03	0.97491651	0.9942	-6.67
251857_at	RNA binding protein - like SEB4 p	---	AT3G54770	1.00	0.00	0.03	0.97499818	0.9942	-6.67
255143_at	putative protein several hypothetic	---	AT4G08430	1.00	0.00	0.03	0.97519116	0.9942	-6.67
248894_at	unknown protein	---	AT5G46320	1.00	0.00	0.03	0.97510399	0.9942	-6.67
251523_at	putative protein several hypothetic	---	AT3G58975	1.00	0.00	0.03	0.97494599	0.9942	-6.67
256814_at	beta-glucosidase, putative similar	BGLU19	AT3G21370	-1.00	-0.01	-0.03	0.97482157	0.9942	-6.67
261280_at	hypothetical protein predicted by g	---	AT1G05860	1.00	0.01	0.03	0.97479729	0.9942	-6.67
264655_at	unknown protein Similar to Glycin	SRC2	AT1G09070	-1.01	-0.01	-0.03	0.97474735	0.9942	-6.67
266178_at	putative phloem-specific lectin	AtPP2-B4	AT2G02280	-1.00	0.00	-0.03	0.9751234	0.9942	-6.67
255124_at	putative self-incompatability RNA-b	APUM15	AT4G08560	-1.00	0.00	-0.03	0.97516863	0.9942	-6.67
261042_at	GTP-binding protein, putative simi	ATRABA3	AT1G01200	1.00	0.00	0.03	0.97528203	0.9942	-6.67
252883_at	GTP-binding - like protein GTP-bi	---	AT4G39520	-1.00	0.00	-0.03	0.97537592	0.9942	-6.67
260240_at	putative tRNA isopentenyl transfer	ATIPT1	AT1G68460	1.00	0.00	0.03	0.97533752	0.9942	-6.67
266831_at	putative squalene epoxidase	SQE2	AT2G22830	1.01	0.01	0.03	0.97563398	0.9943	-6.67
266114_at	hypothetical protein predicted by g	---	AT2G02150	-1.00	0.00	-0.03	0.97561591	0.9943	-6.67
247256_at	putative protein contains similarity	---	AT5G64730	-1.00	0.00	-0.03	0.97571944	0.9943	-6.67
256538_x_at	hypothetical protein predicted by g	---	---	-1.00	0.00	-0.03	0.97550295	0.9943	-6.67
264176_at	bZIP-like protein similar to bZIP (l	---	AT1G02110	1.00	0.01	0.03	0.97570407	0.9943	-6.67
263007_at	hypothetical protein contains simila	---	AT1G54260	1.00	0.00	0.03	0.97560524	0.9943	-6.67
245664_at	hypothetical protein predicted by g	---	AT1G28327	1.00	0.00	0.03	0.97576335	0.9943	-6.67
247384_at	protein kinase ; supported by cDN	---	AT5G63370	-1.00	-0.01	-0.03	0.97582911	0.9944	-6.67
249077_at	alcohol dehydrogenase (EC 1.1.1.	HOT5	AT5G43940	-1.00	0.00	-0.03	0.97595875	0.9944	-6.67
247467_at	putative protein predicted proteins	---	AT5G62130	1.01	0.01	0.03	0.9759273	0.9944	-6.67
248220_at	26S proteasome regulatory particle	---	AT5G53540	-1.00	0.00	-0.03	0.97600805	0.9944	-6.67
257413_at	putative RNA-binding protein cont	---	AT1G22910	-1.00	-0.01	-0.03	0.97618765	0.9945	-6.67
263804_at	putative protein kinase contains a	---	AT2G40270	-1.00	0.00	-0.03	0.97618126	0.9945	-6.67
254800_at	putative protein several hypothetic	---	AT4G13070	1.00	0.01	0.03	0.97617647	0.9945	-6.67
266150_s_at	hypothetical protein	---	AT2G12290	1.01	0.01	0.03	0.97636645	0.9945	-6.67
248528_at	putative protein similar to unknown	---	AT5G50760	1.01	0.02	0.03	0.97632953	0.9945	-6.67
247783_at	light harvesting pigment - like prot	---	AT5G58800	1.00	0.01	0.03	0.97642617	0.9946	-6.67
265009_at	putative protein kinase similar to C	---	AT1G24650	-1.00	0.00	-0.03	0.97653567	0.9946	-6.67
260267_at	very-long-chain fatty acid condens	KCS6	AT1G68530	-1.01	-0.01	-0.03	0.97666308	0.9947	-6.67
252366_at	Expressed protein ; supported by f	---	AT3G48420	1.01	0.01	0.03	0.97670699	0.9947	-6.67
265512_at	hypothetical protein predicted by g	---	AT2G05590	1.00	0.00	0.03	0.9766774	0.9947	-6.67

250274_at	putative protein predicted protein,	---	AT5G13020	1.00	0.00	0.03	0.97681111	0.9947	-6.67
265385_at	putative diacylglycerol kinase ;sup	---	AT2G20900	1.00	0.01	0.03	0.97681041	0.9947	-6.67
260194_at	hypothetical protein similar to hypo	---	AT1G67530	1.00	0.01	0.03	0.97682187	0.9947	-6.67
262739_at	lipase, putative contains Pfam pro	---	AT1G28650	1.00	0.01	0.03	0.97691074	0.9947	-6.67
260834_at	sugar kinase, putative similar to ri	---	AT1G06730	-1.00	0.00	-0.03	0.97703791	0.9948	-6.67
245208_at	lateral root primordia (LRP1)	LRP1	AT5G12330	-1.00	0.00	-0.03	0.97708469	0.9948	-6.67
258688_at	putative eukaryotic translation initia	---	AT3G07920	-1.00	0.00	-0.03	0.9771499	0.9948	-6.67
256589_at	cytochrome P450, putative contair	CYP81D1	AT3G28740	1.01	0.02	0.03	0.9773349	0.9950	-6.67
267296_at	hypothetical protein predicted by g	LBD10	AT2G23660	-1.00	0.00	-0.03	0.97754214	0.9950	-6.67
249595_at	putative protein SIAH1 protein, Br	---	AT5G37930	1.00	0.00	0.03	0.97742731	0.9950	-6.67
253596_s_at	hypothetical protein ; supported by	---	AT4G30730 /	1.00	0.01	0.03	0.97753147	0.9950	-6.67
245566_at	disease resistance RPS2 like prote	---	AT4G14610	-1.00	0.00	-0.03	0.97747205	0.9950	-6.67
252901_at	putative protein various predicted	---	AT4G39550	-1.00	0.00	-0.03	0.97760952	0.9950	-6.67
262632_at	23 kDa polypeptide of oxygen-evol	PSBP-1	AT1G06680	1.00	0.00	0.03	0.97767793	0.9950	-6.67
250951_at	putative protein	---	AT5G03550	1.01	0.01	0.03	0.97767084	0.9950	-6.67
253627_at	low temperature and salt responsi	---	AT4G30650	-1.01	-0.02	-0.03	0.97795242	0.9950	-6.67
264309_at	coatomer alpha subunit, putative s	---	AT1G62020	-1.00	0.00	-0.03	0.978075	0.9950	-6.67
260945_at	hypothetical protein predicted by g	---	AT1G05950	1.00	0.00	0.03	0.97783198	0.9950	-6.67
248519_at	11-beta-hydroxysteroid dehydroge	AtHSD7	AT5G50590 /	-1.00	0.00	-0.03	0.97802435	0.9950	-6.67
244955_at	hypothetical protein	---	---	-1.00	0.00	-0.03	0.97784257	0.9950	-6.67
261673_at	lipid transfer protein, putative simi	---	AT1G18280	1.01	0.01	0.03	0.97783695	0.9950	-6.67
245956_s_at	luminal binding protein ; supporte	BIP2	AT5G28540 /	1.01	0.01	0.03	0.97809473	0.9950	-6.67
266621_at	unknown protein	---	AT2G35450	1.00	0.01	0.03	0.97805915	0.9950	-6.67
248754_at	putative protein contains similarity	NF-YB6	AT5G47670	1.00	0.00	0.03	0.97793955	0.9950	-6.67
259356_at	unknown protein	---	AT3G05250	1.00	0.00	0.03	0.97820314	0.9951	-6.67
245149_at	putative SWI/SNF family transcript	ATSWI3A	AT2G47620	-1.00	0.00	-0.03	0.978285	0.9951	-6.67
265532_at	hypothetical protein predicted by g	---	---	1.00	0.00	0.03	0.97830925	0.9951	-6.67
249939_at	unknown protein ;supported by ful	---	AT5G22430	-1.00	0.00	-0.03	0.97844367	0.9952	-6.67
252347_at	ribosomal protein L13 homolog rib	---	AT3G48130	1.00	0.00	0.03	0.97851197	0.9952	-6.67
260359_at	hypothetical protein predicted by g	---	AT1G69210	1.00	0.00	0.03	0.97864765	0.9953	-6.67
264413_s_at	hypothetical protein similar to hypo	---	---	-1.00	0.00	-0.03	0.9787058	0.9953	-6.67
264813_at	putative Ca2+-dependent ser/thr p	CPK16	AT2G17890	-1.00	0.00	-0.03	0.9787153	0.9953	-6.67
245232_at	actin depolymerizing factor-like pr	ADF7	AT4G25590	-1.00	0.00	-0.03	0.978686	0.9953	-6.67
252842_at	putative protein hypothetical protei	---	---	-1.00	0.00	-0.03	0.97884046	0.9953	-6.67
259180_at	unknown protein	---	AT3G01680	-1.01	-0.01	-0.03	0.97895154	0.9954	-6.67

261782_at	unknown protein	---	AT1G76110	1.00	0.00	0.03	0.97905137	0.9955	-6.67
257533_at	putative alpha/beta hydrolase cont	---	AT3G10840	-1.00	-0.01	-0.03	0.97910601	0.9955	-6.67
248377_at	unknown protein ; supported by fu	---	AT5G51720	1.00	0.01	0.03	0.97980863	0.9955	-6.67
254221_at	putative polygalacturonase polyga	---	AT4G23820	1.01	0.01	0.03	0.97940131	0.9955	-6.67
264324_at	myosin heavy chain MYA2 Strong	XIB	AT1G04160	1.00	0.01	0.03	0.97976171	0.9955	-6.67
252066_at	receptor-protein kinase-like protei	FER	AT3G51550	-1.00	0.00	-0.03	0.97954739	0.9955	-6.67
246211_at	G-box-binding factor 1 ; supported	GBF1	AT4G36730	1.00	0.01	0.03	0.97944251	0.9955	-6.67
263579_at	hypothetical protein similar to hypo	---	AT2G17030	-1.00	0.00	-0.03	0.97951503	0.9955	-6.67
265195_at	hypothetical protein	---	AT2G36730	1.00	0.00	0.03	0.97950593	0.9955	-6.67
266028_at	hypothetical protein predicted by g	---	AT2G06000	-1.00	0.00	-0.03	0.9797204	0.9955	-6.67
246086_at	beta-1,3-glucanase - like protein b	---	AT5G20560	1.00	0.00	0.03	0.97960878	0.9955	-6.67
267488_at	putative cadmium-transporting ATF	HMA4	AT2G19110	-1.00	0.00	-0.03	0.97949594	0.9955	-6.67
265705_at	unknown protein related to MO25 (	---	AT2G03410	-1.01	-0.01	-0.03	0.97978397	0.9955	-6.67
247902_at	plasma membrane ATPase 3 (prot	AHA3	AT5G57350	-1.00	0.00	-0.03	0.97959444	0.9955	-6.67
257210_at	hypothetical protein	TTL2	AT3G14950	1.00	0.00	0.03	0.97962177	0.9955	-6.67
254289_at	putative protein predicted protein,	---	AT4G22980	-1.01	-0.01	-0.03	0.97930398	0.9955	-6.67
260559_at	putative polygalacturonase	---	AT2G43860	1.00	0.00	0.03	0.97949766	0.9955	-6.67
259451_at	synaptosomal associated protein (	SNAP30	AT1G13890	1.00	0.00	0.03	0.97980842	0.9955	-6.67
252620_at	hypothetical protein	---	---	-1.00	0.00	-0.03	0.97985226	0.9955	-6.67
256756_at	ATPase II, putative similar to GB:A	---	AT3G25610	1.00	0.01	0.03	0.98060445	0.9955	-6.67
265853_at	putative RING zinc finger protein	---	AT2G42360	-1.01	-0.01	-0.03	0.98023854	0.9955	-6.67
261363_at	pectinesterase, putative similar to	SKS6	AT1G41830	-1.01	-0.02	-0.03	0.98061136	0.9955	-6.67
245130_at	putative receptor-like protein kinas	---	AT2G45340	1.00	0.00	0.03	0.97998341	0.9955	-6.67
265100_at	hypothetical protein predicted by g	OSB4	AT1G31010	1.00	0.00	0.03	0.980256	0.9955	-6.67
247295_at	putative protein similar to unknown	---	AT5G64180	1.00	0.00	0.02	0.98079866	0.9955	-6.67
246762_at	cyclin H-like protein cycH (CAK as	CYCH;1	AT5G27620	1.00	0.00	0.03	0.98064713	0.9955	-6.67
246136_at	peptide transporter - like protein p	---	AT5G28470	-1.00	0.00	-0.03	0.9804392	0.9955	-6.67
267402_at	putative SF16 protein {Helianthus a	IQD6	AT2G26180	1.00	0.00	0.03	0.98075734	0.9955	-6.67
267100_at	unknown protein	---	AT2G41470	1.00	0.00	0.03	0.98048029	0.9955	-6.67
262670_s_at	transposase [Escherichia coli] mus	---	---	-1.00	0.00	-0.03	0.98062035	0.9955	-6.67
255315_at	hypothetical protein	---	---	-1.00	0.00	-0.03	0.98016748	0.9955	-6.67
253936_at	STIG1 like protein STIG1 protein -	---	AT4G26880	-1.00	0.00	-0.03	0.98008251	0.9955	-6.67
246271_at	photosystem II oxygen-evolving co	---	AT4G37230	-1.00	0.00	-0.03	0.98055883	0.9955	-6.67
255884_at	hypothetical protein predicted by g	---	AT1G20310	-1.01	-0.01	-0.02	0.98087283	0.9955	-6.67
264231_at	hypothetical protein similar to hypo	---	AT1G67450	-1.00	0.00	-0.02	0.98080305	0.9955	-6.67

256338_at	hypothetical protein similar to seed	---	AT1G72100	-1.00	0.00	-0.02	0.98088164	0.9955	-6.67
245856_at	putative protein predicted proteins	---	---	1.00	0.00	0.02	0.98081419	0.9955	-6.67
252240_at	putative protein several hypothetic	---	AT3G50010	1.00	0.00	0.03	0.98019183	0.9955	-6.67
247230_at	putative protein similar to unknown	---	AT5G65170	1.00	0.00	0.03	0.98010302	0.9955	-6.67
248413_at	putative protein strong similarity to	PLE	AT5G51600	1.00	0.00	0.03	0.98000387	0.9955	-6.67
266624_s_at	phosphoribosyl pyrophosphate syn	---	AT1G32380 /	-1.00	-0.01	-0.03	0.98073099	0.9955	-6.67
245173_at	putative AP2 domain transcription	---	AT2G47520	1.01	0.01	0.03	0.98070949	0.9955	-6.67
263795_at	putative cyclic nucleotide-regulated	ATCNGC14	AT2G24610	-1.00	0.00	-0.02	0.98093494	0.9955	-6.67
246061_at	RAN GTPase activating protein 2	RANGAP2	AT5G19320	1.00	0.00	0.02	0.98106954	0.9956	-6.67
257976_at	putative transcription factor contai	PLT1	AT3G20840	-1.00	0.00	-0.02	0.98104905	0.9956	-6.67
259069_at	lysyl-tRNA synthetase identical to l	ATKRS-1	AT3G11710	1.00	0.00	0.02	0.98118631	0.9956	-6.67
249778_at	Expressed protein ; supported by f	---	AT5G24165	-1.00	0.00	-0.02	0.98139246	0.9957	-6.67
247002_at	putative protein strong similarity to	HOS15	AT5G67320	1.00	0.00	0.02	0.98143623	0.9957	-6.67
261965_at	athila ORF 1, putative similar to at	---	---	-1.00	0.00	-0.02	0.98140222	0.9957	-6.67
255392_at	hypothetical protein	---	---	-1.00	0.00	-0.02	0.98143401	0.9957	-6.67
263970_at	putative cytochrome P450	CYP718	AT2G42850	1.00	0.00	0.02	0.98149513	0.9957	-6.67
258394_at	unknown protein ;supported by ful	---	AT3G15530	1.00	0.01	0.02	0.98186503	0.9958	-6.67
266288_s_at	putative pumilio/Mpt5 family RNA-l	APUM1	AT2G29140 /	1.00	0.00	0.02	0.98192094	0.9958	-6.67
262913_at	NADPH-dependent codeinone red	---	AT1G59960	-1.01	-0.01	-0.02	0.98179726	0.9958	-6.67
265179_at	unknown protein predicted by gene	---	AT1G23650	1.00	0.00	0.02	0.98180242	0.9958	-6.67
246234_at	putative protein	---	AT4G37280	1.00	0.00	0.02	0.9816769	0.9958	-6.67
265519_at	hypothetical protein	---	AT2G06040	-1.00	0.00	-0.02	0.98193511	0.9958	-6.67
249805_at	putative protein similar to unknown	---	AT5G23800	-1.00	0.00	-0.02	0.98186941	0.9958	-6.67
246495_at	putative protein hypothetical prote	---	AT5G16200	-1.01	-0.01	-0.02	0.98169707	0.9958	-6.67
266900_at	hypothetical protein predicted by g	---	AT2G34610	1.00	0.00	0.02	0.98168787	0.9958	-6.67
262907_at	hypothetical protein predicted by g	CRR28	AT1G59720	1.00	0.00	0.02	0.98208734	0.9958	-6.67
251792_at	probable serine/threonine-specific	---	AT3G55550	-1.00	0.00	-0.02	0.98207984	0.9958	-6.67
254489_at	putative protein berberine bridge e	---	AT4G20800	-1.00	0.00	-0.02	0.98215495	0.9959	-6.67
256242_at	actin-like protein contains Pfam pr	ATARP5	AT3G12380	-1.00	0.00	-0.02	0.98220688	0.9959	-6.67
246919_at	putative protein hypothetical prote	---	AT5G25460	1.01	0.02	0.02	0.98277048	0.9960	-6.67
263756_at	putative ubiquitin fusion-degradatic	---	AT2G21270	-1.00	0.00	-0.02	0.98271532	0.9960	-6.67
266633_at	putative DnaJ protein	---	AT2G35540	1.00	0.00	0.02	0.98257129	0.9960	-6.67
267552_at	putative purple acid phosphatase p	PAP13	AT2G32770	1.00	0.00	0.02	0.98244804	0.9960	-6.67
260040_at	Expressed protein ; supported by f	IDA	AT1G68765	1.01	0.01	0.02	0.98277341	0.9960	-6.67
263857_at	unknown protein	---	AT2G04380	-1.00	0.00	-0.02	0.98256478	0.9960	-6.67

252028_at	hypothetical protein	---	AT3G52640	1.00	0.00	0.02	0.98271524	0.9960	-6.67
256811_at	serine/threonine-specific protein k	---	AT3G21340	1.00	0.00	0.02	0.98260377	0.9960	-6.67
259540_at	nodule inception protein, putative	---	AT1G20640	1.00	0.00	0.02	0.98249192	0.9960	-6.67
263469_at	putative Na+/H+ antiporter	ATCHX21	AT2G31910	1.00	0.00	0.02	0.98257384	0.9960	-6.67
248787_at	putative protein similar to unknown	---	AT5G47420	1.00	0.00	0.02	0.98295875	0.9961	-6.67
258875_at	unknown protein ;supported by ful	---	AT3G03160	1.00	0.00	0.02	0.98298263	0.9961	-6.67
261658_at	hypothetical protein predicted by g	---	AT1G50040	1.00	0.01	0.02	0.98369489	0.9962	-6.67
247488_at	putative protein MtN19, Medicago	---	AT5G61820	1.00	0.00	0.02	0.98321413	0.9962	-6.67
267567_at	putative cytochrome P450	CYP71A13	AT2G30770	-1.01	-0.02	-0.02	0.98485308	0.9962	-6.67
266270_at	putative glutathione S-transferase	ATGSTU3	AT2G29470	-1.01	-0.02	-0.02	0.98482195	0.9962	-6.67
252355_at	putative protein various predicted	---	AT3G48250	1.00	0.00	0.02	0.98416754	0.9962	-6.67
262136_at	auxin response factor, putative sir	ARF17	AT1G77850	1.00	0.00	0.02	0.98372248	0.9962	-6.67
263538_at	hypothetical protein predicted by g	---	AT2G25010	-1.00	0.00	-0.02	0.98363016	0.9962	-6.67
249173_at	unknown protein	---	AT5G43000	1.00	0.00	0.02	0.98435073	0.9962	-6.67
253695_at	arginine methyltransferase (pam1)	PRMT11	AT4G29510	-1.00	0.00	-0.02	0.9840277	0.9962	-6.67
255402_at	Expressed protein	hemf2	AT4G03205	1.00	0.00	0.02	0.98397415	0.9962	-6.67
262246_at	leaf development protein Argonaut	AGO1	AT1G48410	1.00	0.00	0.02	0.98452178	0.9962	-6.67
265480_at	similar to cold acclimation protein \	COR413-PI	AT2G15970	-1.00	0.00	-0.02	0.98399036	0.9962	-6.67
254545_at	putative protein FKBP-type peptid	---	AT4G19830	1.00	0.00	0.02	0.98353408	0.9962	-6.67
248463_at	putative protein contains similarity	---	AT5G51130	-1.00	-0.01	-0.02	0.98408573	0.9962	-6.67
249069_at	unknown protein	---	AT5G44010	-1.00	-0.01	-0.02	0.98369093	0.9962	-6.67
245853_at	putative protein predicted protein /	---	AT5G13500	-1.00	0.00	-0.02	0.98449447	0.9962	-6.67
257939_at	monosaccharide transport protein	STP4	AT3G19930	-1.00	0.00	-0.02	0.98424037	0.9962	-6.67
244935_at	NADH dehydrogenase subunit	---	---	1.00	0.00	0.02	0.98350489	0.9962	-6.67
261599_at	hypothetical protein similar to hypo	---	AT1G49700	-1.00	0.00	-0.02	0.98449217	0.9962	-6.67
257183_at	ABC transporter contains Pfam pro	---	AT3G13220	-1.00	0.00	-0.02	0.98392957	0.9962	-6.67
265893_at	putative disease resistance protein	---	AT2G15040 /	-1.00	-0.01	-0.02	0.98469378	0.9962	-6.67
245529_at	SEN1 like protein	MAA3	AT4G15570	-1.00	0.00	-0.02	0.98465586	0.9962	-6.67
263552_x_at	unknown protein proline, tyrosine,	---	AT2G24980	1.00	0.00	0.02	0.98481984	0.9962	-6.67
263688_at	unknown protein Location of EST	---	AT1G26920	1.01	0.01	0.02	0.98423407	0.9962	-6.67
265809_at	unknown protein	---	AT2G18100	1.00	0.00	0.02	0.9832291	0.9962	-6.67
253780_at	protein phosphatase 2C-like prote	---	AT4G28400	-1.00	-0.01	-0.02	0.98352224	0.9962	-6.67
251863_at	kinesin-like protein kinesin, Synce	MRH2	AT3G54870	-1.00	0.00	-0.02	0.98390461	0.9962	-6.67
257134_at	hypothetical protein similar to oxid	---	AT3G12870	1.00	0.00	0.02	0.98357147	0.9962	-6.67
256264_at	unknown protein ; supported by ful	---	AT3G12210	-1.00	0.00	-0.02	0.98431736	0.9962	-6.67

257090_at	protein kinase, putative contains P	---	AT3G20530	-1.00	0.00	-0.02	0.98379322	0.9962	-6.67
264631_at	DegP protease contains similarity t	DegP3	AT1G65630	1.00	0.00	0.02	0.98463418	0.9962	-6.67
266200_at	hypothetical protein predicted by g	---	AT2G38920	-1.00	0.00	-0.02	0.98426083	0.9962	-6.67
256769_at	protein kinase, putative similar to	---	AT3G13690	1.00	0.00	0.02	0.98483891	0.9962	-6.67
261894_at	unknown protein ;supported by full	MGT1	AT1G80900	-1.00	0.00	-0.02	0.98484389	0.9962	-6.67
257893_at	E2, ubiquitin-conjugating enzyme,	UBC32	AT3G17000	-1.00	0.00	-0.02	0.98365626	0.9962	-6.67
264068_at	putative homeodomain transcriptio	BLH8	AT2G27990	-1.00	0.00	-0.02	0.98467568	0.9962	-6.67
251574_at	putative protein GLUCAN ENDO-1	PDCB5	AT3G58100	-1.00	0.00	-0.02	0.98447964	0.9962	-6.67
248166_at	putative protein contains similarity	---	AT5G54520	1.00	0.00	0.02	0.98443211	0.9962	-6.67
253323_at	putative protein protein phosphata	---	AT4G33920	-1.00	-0.01	-0.02	0.98361597	0.9962	-6.67
247570_at	putative protein heparanase, Hom	AtGUS1	AT5G61250	-1.00	-0.01	-0.02	0.98341385	0.9962	-6.67
266756_at	putative cytochrome P450	CYP709B2	AT2G46950	-1.01	-0.01	-0.02	0.98443733	0.9962	-6.67
263245_at	hypothetical protein predicted by g	---	AT2G31470	1.00	0.00	0.02	0.98446721	0.9962	-6.67
262230_at	alpha-xylosidase precursor identica	XYL1	AT1G68560	1.00	0.01	0.02	0.98510055	0.9962	-6.67
253135_at	cytoplasmatic aconitate hydratase	---	AT4G35830	1.00	0.00	0.02	0.98504173	0.9962	-6.67
246312_at	G-protein, putative contains Pfam	XLG3	AT1G31930	1.00	0.01	0.02	0.9851004	0.9962	-6.67
260957_at	delta 9 desaturase identical to delt	ADS1	AT1G06080	1.00	0.00	0.02	0.98501979	0.9962	-6.67
265839_at	putative serpin	---	AT2G14540	-1.00	0.00	-0.02	0.98508076	0.9962	-6.67
253424_at	putative protein ; supported by cDN	---	AT4G32330	1.00	0.00	0.02	0.9856973	0.9962	-6.67
257365_x_at	putative antifungal protein	PDF1.2b	AT2G26020	1.01	0.01	0.02	0.98544555	0.9962	-6.67
259677_at	putative phosphatidylinositol-4-pho	---	AT1G77740	-1.00	0.00	-0.02	0.98569158	0.9962	-6.67
260645_at	hypothetical protein predicted by g	TTL1	AT1G53300	1.00	0.00	0.02	0.98565636	0.9962	-6.67
263605_at	hypothetical protein predicted by g	---	AT2G16485	-1.00	0.00	-0.02	0.98565253	0.9962	-6.67
249557_at	receptor serine/threonine kinase P	PR5K	AT5G38280	1.00	0.00	0.02	0.98522005	0.9962	-6.67
249407_at	putative protein predicted proteins	---	AT5G40320	-1.00	0.00	-0.02	0.98572521	0.9962	-6.67
262546_at	iron-regulated transporter protein,	ZIP10	AT1G31260	1.00	0.00	0.02	0.98531938	0.9962	-6.67
254268_at	putative protein FAF1, Mus muscu	---	AT4G23040	-1.00	0.00	-0.02	0.98527103	0.9962	-6.67
248459_at	putative protein similar to unknown	CRL	AT5G51020	1.00	0.00	0.02	0.98543084	0.9962	-6.67
246363_at	hypothetical protein	---	AT1G40390	-1.00	0.00	-0.02	0.98528829	0.9962	-6.67
254024_at	putative pathogenesis-related prot	---	AT4G25780	1.00	0.00	0.02	0.9856469	0.9962	-6.67
246556_at	putative protein hypothetical prote	---	AT5G15480	-1.00	0.00	-0.02	0.98546557	0.9962	-6.67
263272_at	hypothetical protein predicted by g	---	---	1.00	0.00	0.02	0.98546868	0.9962	-6.67
251252_at	putative protein several hypothetic	---	AT3G62230	1.00	0.00	0.02	0.98583521	0.9963	-6.67
252372_at	aldehyde dehydrogenase (NAD+)	ALDH2B4	AT3G48000	-1.00	0.00	-0.02	0.98591463	0.9963	-6.67
250420_at	HY5(bZIP transcription factor famil	HY5	AT5G11260	-1.00	0.00	-0.02	0.98601279	0.9964	-6.67

250967_at	putative protein In2, Zea mays, EM	---	AT5G02790	-1.00	0.00	-0.02	0.98625415	0.9965	-6.67
263170_at	putative peroxisome assembly fact	PEX6	AT1G03000	-1.00	0.00	-0.02	0.98623005	0.9965	-6.67
260084_at	chromatin structure regulator, puta	---	AT1G63210	1.00	0.00	0.02	0.98616879	0.9965	-6.67
249724_at	disease resistance protein	---	AT5G35450	1.00	0.00	0.02	0.98635114	0.9965	-6.67
253223_at	L-ascorbate peroxidase ;supported	APX3	AT4G35000	1.00	0.00	0.02	0.98634388	0.9965	-6.67
246967_at	FPF1 protein	FPF1	AT5G24860	-1.00	0.00	-0.02	0.98643696	0.9965	-6.67
253324_at	Expressed protein ; supported by f	---	AT4G33940	-1.00	0.00	-0.02	0.98651889	0.9966	-6.67
245977_at	glucose-6-phosphate 1-dehydroge	G6PD2	AT5G13110	1.00	0.00	0.02	0.98661613	0.9966	-6.67
260628_at	hypothetical protein predicted by g	---	AT1G62320	-1.00	0.00	-0.02	0.98669918	0.9967	-6.67
255690_at	probable cytochrome P450	CYP86A2	AT4G00360	-1.01	-0.01	-0.02	0.98689032	0.9967	-6.67
259969_at	putative pyrophosphate-dependen	---	AT1G76550	1.00	0.00	0.02	0.98683079	0.9967	-6.67
262177_at	isochorismate synthase (icsI) iden	EDS16	AT1G74710	-1.00	-0.01	-0.02	0.98689946	0.9967	-6.67
253341_at	putative protein ; supported by cD	---	AT4G33410	-1.00	0.00	-0.02	0.98684706	0.9967	-6.67
249894_at	unknown protein ; supported by cl	---	AT5G22580	1.02	0.03	0.02	0.98701349	0.9967	-6.67
255649_at	contains region of similarity to mou	---	AT4G00920	1.00	0.00	0.02	0.98701555	0.9967	-6.67
266709_at	unknown protein ;supported by ful	ATSPP	AT2G03120	-1.00	0.00	-0.02	0.98707013	0.9967	-6.67
261047_at	hypothetical protein predicted by g	APUM22	AT1G01410	1.00	0.00	0.02	0.98721648	0.9968	-6.67
258561_at	putative hexose transporter similar	STP6	AT3G05960	1.00	0.00	0.02	0.98718314	0.9968	-6.67
251169_at	putative protein putative protein A	MARD1	AT3G63210	-1.00	0.00	-0.02	0.98748562	0.9969	-6.67
263301_x_at	hypothetical protein predicted by g	---	---	-1.00	0.00	-0.02	0.98746908	0.9969	-6.67
257605_at	hypothetical protein predicted by g	---	AT3G13840	-1.00	0.00	-0.02	0.98748597	0.9969	-6.67
254465_at	tapetum-specific A3 like protein A	---	AT4G20420	-1.00	0.00	-0.02	0.98736216	0.9969	-6.67
257195_at	hypothetical protein predicted by g	---	AT3G23680	-1.00	0.00	-0.02	0.98755612	0.9969	-6.67
263495_at	cold-regulated protein cor15b prec	COR15B	AT2G42530	1.00	0.01	0.02	0.98766914	0.9970	-6.67
246286_at	unknown protein	---	AT1G31910	1.00	0.00	0.02	0.98778082	0.9970	-6.67
264921_at	RNA binding protein, putative simi	---	AT1G60650	-1.00	0.00	-0.02	0.98780822	0.9970	-6.67
245485_at	proline-rich, APG like protein	---	AT4G16230	-1.00	0.00	-0.02	0.98785051	0.9970	-6.67
263755_at	unknown protein ;supported by ful	---	AT2G21340	1.00	0.00	0.02	0.98788966	0.9970	-6.67
257678_at	RNA helicase, putative contains P	RTL2	AT3G20420	1.00	0.00	0.02	0.98801742	0.9970	-6.67
264352_at	unknown protein Strong similarity t	---	AT1G03270	-1.00	0.00	-0.02	0.9880329	0.9970	-6.67
254736_at	putative disease resistance protei	---	AT4G13820	-1.00	0.00	-0.02	0.98801565	0.9970	-6.67
255841_at	putative tyrosine-specific transport	---	AT2G33260	-1.00	0.00	-0.02	0.98792006	0.9970	-6.67
250328_at	putative protein	---	AT5G11780	1.00	0.00	0.02	0.98825751	0.9972	-6.67
264822_at	putative ribonucleoprotein	---	AT1G03457	1.00	0.00	0.02	0.9883619	0.9972	-6.67
251800_at	putative protein various predicted p	RBL	AT3G55510	-1.00	0.00	-0.02	0.9884334	0.9973	-6.67

266582_at	unknown protein ; supported by cl	---	AT2G46090	1.00	0.00	0.01	0.98847449	0.9973	-6.67
255445_at	hypothetical protein	---	AT4G02740	1.00	0.00	0.01	0.98857987	0.9973	-6.67
258179_at	integral membrane protein, putativ	---	AT3G21690	-1.00	0.00	-0.01	0.98871293	0.9974	-6.67
247400_at	putative protein ;supported by full-	---	AT5G62840	1.00	0.00	0.01	0.98883626	0.9975	-6.67
253198_at	putative protein various predicted p	---	AT4G35360	1.00	0.00	0.01	0.98885663	0.9975	-6.67
264409_s_at	hypothetical protein similar to hypo	---	---	1.00	0.00	0.01	0.9889751	0.9975	-6.67
265942_at	putative casein kinase I ;supporte	ckl5	AT2G19470	1.00	0.00	0.01	0.98915605	0.9976	-6.67
254877_at	putative protein threonine dehydra	ATSR	AT4G11640	-1.00	0.00	-0.01	0.98916871	0.9976	-6.67
253436_at	ubiquinol-cytochrome c reductase	---	AT4G32470	-1.00	0.00	-0.01	0.98920019	0.9976	-6.67
262872_at	hypothetical protein predicted by g	---	AT1G64690	-1.00	0.00	-0.01	0.98938745	0.9977	-6.67
256139_at	Nt-gh3 deduced protein, putative s	---	AT1G48660	1.00	0.00	0.01	0.9894068	0.9977	-6.67
248614_at	putative protein similar to unknown	---	AT5G49560	-1.00	0.00	-0.01	0.98940828	0.9977	-6.67
266076_at	ATP-dependent RNA helicase ide	---	AT2G40700	1.00	0.00	0.01	0.98969554	0.9977	-6.67
259994_at	putative C2H2-type zinc finger pro	AtIDD14	AT1G68130	1.00	0.00	0.01	0.98950677	0.9977	-6.67
247432_at	microtubule-associated protein EB	ATEB1B	AT5G62500	-1.00	0.00	-0.01	0.98969696	0.9977	-6.67
256547_at	receptor-like serine/threonine kina	---	AT3G14840	1.00	0.00	0.01	0.98959522	0.9977	-6.67
256896_at	hypothetical protein predicted by g	---	AT3G24630	-1.00	0.00	-0.01	0.98973497	0.9977	-6.67
256282_at	unknown protein	---	AT3G12550	-1.00	0.00	-0.01	0.98962	0.9977	-6.67
257428_at	hypothetical protein predicted by g	---	AT1G78990	-1.00	0.00	-0.01	0.98957513	0.9977	-6.67
249360_at	putative protein KIAA0409 protein	---	AT5G40530	1.00	0.00	0.01	0.98985276	0.9978	-6.67
257395_at	putative salt-inducible protein	---	AT2G15630	-1.00	0.00	-0.01	0.98995916	0.9979	-6.67
265877_at	unknown protein ; supported by cl	BZIP34	AT2G42380	-1.00	0.00	-0.01	0.99040144	0.9979	-6.67
253027_at	putative protein leaf protein (PnC4	---	AT4G38150	-1.00	0.00	-0.01	0.99024552	0.9979	-6.67
251138_at	putative protein various predicted p	---	AT5G01160	1.00	0.00	0.01	0.990383	0.9979	-6.67
253265_at	putative protein RING-finger prote	---	AT4G34040	1.00	0.00	0.01	0.99026461	0.9979	-6.67
252802_at	putative protein	---	---	-1.00	0.00	-0.01	0.99030029	0.9979	-6.67
259045_at	calmodulin-like protein similar to c	---	AT3G03410	1.00	0.00	0.01	0.99007636	0.9979	-6.67
254204_at	putative protein CGI-58 protein - H	---	AT4G24160	-1.00	0.00	-0.01	0.99022006	0.9979	-6.67
245772_at	hypothetical protein similar to puta	---	AT1G30300	-1.00	0.00	-0.01	0.99031502	0.9979	-6.67
258734_at	putative DNA-binding protein simila	---	AT3G05860	1.00	0.00	0.01	0.99030638	0.9979	-6.67
260924_at	hypothetical protein similar to Pto k	---	AT1G21590	1.00	0.00	0.01	0.99061845	0.9980	-6.67
253042_at	formamidase - like protein formam	---	AT4G37550	-1.00	0.00	-0.01	0.99096325	0.9980	-6.67
266330_at	unknown protein ; supported by cl	MLP329	AT2G01530	1.00	0.00	0.01	0.99073728	0.9980	-6.67
258219_at	thioredoxin, putative similar to TH	ATTDX	AT3G17880	-1.00	0.00	-0.01	0.99157807	0.9980	-6.67
250674_at	laccase-like protein laccase - Pop	LAC13	AT5G07130	-1.00	0.00	-0.01	0.99140012	0.9980	-6.67

252260_at	putative protein several hypothetic	---	AT3G49480	-1.00	0.00	-0.01	0.99150193	0.9980	-6.67
267636_at	hypothetical protein predicted by g	---	AT2G42110	1.00	0.00	0.01	0.99134347	0.9980	-6.67
257347_at	pseudogene, gene_id:K17E7.6	---	---	-1.00	0.00	-0.01	0.99091681	0.9980	-6.67
256712_at	unknown protein similar to T14G11	---	AT2G34020	1.00	0.00	0.01	0.99104344	0.9980	-6.67
264703_at	serine threonine protein phosphata	PP2A	AT1G69960	-1.00	0.00	-0.01	0.99145805	0.9980	-6.67
255712_at	hypothetical protein similar to A. th	---	AT4G00280	-1.00	0.00	-0.01	0.99155791	0.9980	-6.67
249603_at	putative protein predicted proteins	---	AT5G37210	1.00	0.00	0.01	0.9914926	0.9980	-6.67
264241_at	hypothetical protein contains simila	---	AT1G54840	-1.00	0.00	-0.01	0.99111428	0.9980	-6.67
260421_at	acid phosphatase, putative similar	SBH1	AT1G69640	1.00	0.00	0.01	0.99104978	0.9980	-6.67
248742_at	unknown protein	---	AT5G48200	1.00	0.00	0.01	0.99061505	0.9980	-6.67
250432_at	putative protein various predicted	---	AT5G10420	1.00	0.00	0.01	0.99084624	0.9980	-6.67
261943_at	plasma membrane ATPase, putat	AHA9	AT1G80660	1.00	0.00	0.01	0.99077593	0.9980	-6.67
247047_at	putative protein contains similarity	---	AT5G66650	1.00	0.01	0.01	0.99090232	0.9980	-6.67
253345_at	putative protein	BCA5	AT4G33580	-1.00	0.00	-0.01	0.99141568	0.9980	-6.67
262078_at	hypothetical protein predicted by g	CW7	AT1G59520	-1.00	0.00	-0.01	0.99147163	0.9980	-6.67
261868_s_at	hypothetical protein contains simila	---	AT1G11450 /	1.00	0.00	0.01	0.99107268	0.9980	-6.67
251440_at	SKP1/ASK1 (At13), putative simila	ASK13	AT3G60010	1.00	0.00	0.01	0.99062234	0.9980	-6.67
254632_at	putative protein predicted protein,	---	AT4G18630	1.00	0.00	0.01	0.99115576	0.9980	-6.67
245203_at	hypothetical protein similar to prote	---	---	1.00	0.00	0.01	0.99146475	0.9980	-6.67
255217_s_at	hypothetical protein	---	---	-1.00	0.00	-0.01	0.99149819	0.9980	-6.67
265995_at	hypothetical protein predicted by g	---	AT2G24140	1.00	0.00	0.01	0.99170889	0.9981	-6.67
247439_at	plasma membrane proton ATPase	AHA11	AT5G62670	-1.00	0.00	-0.01	0.99176983	0.9981	-6.67
246149_at	peroxidase ATP N ;supported by f	---	AT5G19890	1.00	0.01	0.01	0.99190173	0.9982	-6.67
255614_at	putative myb-related DNA-binding	---	AT4G01280	-1.00	0.00	-0.01	0.99198944	0.9982	-6.67
266601_at	hypothetical protein predicted by g	---	AT2G46060	-1.00	0.00	-0.01	0.99213251	0.9983	-6.67
257434_at	hypothetical protein predicted by g	---	AT2G21740	1.00	0.00	0.01	0.99212149	0.9983	-6.67
251027_at	putative protein hypothetical prote	---	AT5G02210	1.00	0.00	0.01	0.99211546	0.9983	-6.67
261858_at	Expressed protein ; supported by f	---	AT1G50570	-1.00	0.00	-0.01	0.9923786	0.9983	-6.67
250741_at	putative protein contains similarity	---	AT5G05790	-1.00	0.00	-0.01	0.99233416	0.9983	-6.67
250583_at	zinc finger transcription factor ; su	PEI1	AT5G07500	1.00	0.00	0.01	0.99237844	0.9983	-6.67
261327_at	transcription factor, putative conta	---	AT1G44830	-1.00	-0.01	-0.01	0.99236761	0.9983	-6.67
250736_s_at	putative protein contains similarity	---	AT1G01350 /	1.00	0.00	0.01	0.99230701	0.9983	-6.67
256024_at	unknown protein contains Pfam pr	ZF14	AT1G58340	1.00	0.00	0.01	0.99249655	0.9983	-6.67
259691_at	hypothetical protein predicted by g	---	AT1G63200	1.00	0.00	0.01	0.99244831	0.9983	-6.67
259183_at	hypothetical protein similar to puta	---	AT3G01580	-1.00	0.00	-0.01	0.99250487	0.9983	-6.67

264321_at	unknown protein Contains similarit	---	AT1G04200	1.00	0.00	0.01	0.99289203	0.9983	-6.67
259444_at	hypothetical protein predicted by g	---	AT1G02370	-1.00	0.00	-0.01	0.99261799	0.9983	-6.67
259321_at	unknown protein	GAUT13	AT3G01040	-1.00	0.00	-0.01	0.9927976	0.9983	-6.67
247471_at	putative protein receptor-like prote	ERL1	AT5G62230	1.00	0.00	0.01	0.99286682	0.9983	-6.67
257643_at	AP2 domain transcription factor co	---	AT3G25730	1.00	0.00	0.01	0.99286229	0.9983	-6.67
263057_at	hypothetical protein predicted by g	---	AT2G09840	-1.00	0.00	-0.01	0.99291294	0.9983	-6.67
264477_at	amp-binding protein, putative simi	---	AT1G77240	1.00	0.00	0.01	0.99279248	0.9983	-6.67
259214_at	Expressed protein ; supported by f	---	AT3G09085	-1.00	0.00	-0.01	0.99276296	0.9983	-6.67
266775_at	putative SCARECROW gene regu	---	AT2G29060	1.00	0.00	0.01	0.99323927	0.9984	-6.67
245318_at	Expressed protein ; supported by f	---	AT4G16980	1.00	0.01	0.01	0.99326336	0.9984	-6.67
245341_at	Expressed protein ; supported by f	---	AT4G16447	1.00	0.00	0.01	0.99323603	0.9984	-6.67
263792_at	putative retroelement pol polyprote	---	---	-1.00	0.00	-0.01	0.993014	0.9984	-6.67
259921_at	putative protein kinase similar to pi	---	AT1G72540	-1.00	0.00	-0.01	0.99310592	0.9984	-6.67
261067_at	lectin, putative contains Pfam prof	---	AT1G07460	1.00	0.00	0.01	0.99309566	0.9984	-6.67
245085_at	putative poly(A) binding protein ; s	PAB4	AT2G23350	-1.00	0.00	-0.01	0.99313977	0.9984	-6.67
266922_s_at	SKP1/ASK1-related, putative simi	ASK20	AT2G45950 /	-1.00	0.00	-0.01	0.99348831	0.9986	-6.67
262956_at	eukaryotic translation initiation fac	EIF4A-2	AT1G54270	-1.00	0.00	-0.01	0.99356612	0.9986	-6.67
251281_at	putative protein hypothetical prote	AGP20	AT3G61640	-1.00	0.00	-0.01	0.99376634	0.9987	-6.67
253240_at	putative ketoacyl-CoA synthase fa	KCS17	AT4G34510	1.00	0.00	0.01	0.99388357	0.9987	-6.67
262840_at	linker histone protein, putative cor	HMGA	AT1G14900	1.00	0.00	0.01	0.99379384	0.9987	-6.67
257785_at	geranylgeranylated protein, putati	MUB4	AT3G26980	1.00	0.00	0.01	0.99375069	0.9987	-6.67
248428_at	protein phosphatase-2C; PP2C-lik	AHG1	AT5G51760	1.00	0.00	0.01	0.99389849	0.9987	-6.67
267593_at	similar to disease resistance protei	AtRLP25	AT2G33030	-1.00	0.00	-0.01	0.99381959	0.9987	-6.67
264635_at	unknown protein ;supported by full	---	AT1G65500	-1.00	0.00	-0.01	0.99488769	0.9990	-6.67
247497_at	Peter Pan - like protein Peter Pan	PPAN	AT5G61770	-1.00	0.00	-0.01	0.99510858	0.9990	-6.67
265187_at	putative ADP-ribosylation factor ;	---	AT1G23490 /	1.00	0.00	0.01	0.99514429	0.9990	-6.67
259936_at	putative UDP-glucose:glycoprotein	EBS1	AT1G71220	-1.00	0.00	-0.01	0.99505769	0.9990	-6.67
267520_at	putative integral membrane protein	---	AT2G30460	1.00	0.00	0.01	0.99459707	0.9990	-6.67
257886_at	pectinesterase, putative similar to	---	AT3G17060	-1.00	0.00	-0.01	0.99549332	0.9990	-6.67
258056_at	hypothetical protein similar to GB:A	---	AT3G29010	1.00	0.00	0.01	0.99449858	0.9990	-6.67
246835_at	putative protein putative APC11 a	---	AT5G26640	1.00	0.00	0.01	0.99528442	0.9990	-6.67
260556_at	putative endochitinase	---	AT2G43620	-1.00	0.00	-0.01	0.9952776	0.9990	-6.67
256819_at	unknown protein contains Pfam pr	---	AT3G21390	-1.00	0.00	-0.01	0.9951079	0.9990	-6.67
261126_at	TATA binding protein-associated f	TAF6	AT1G04950	1.00	0.00	0.01	0.99572094	0.9990	-6.67
265543_at	unknown protein	---	AT2G28270	1.00	0.00	0.01	0.99572013	0.9990	-6.67

260717_at	serine/threonine phosphatase PP1	---	AT1G48120	1.00	0.00	0.01	0.99508365	0.9990	-6.67
250796_at	putative protein similar to unknown	---	AT5G05300	1.00	0.00	0.01	0.99543405	0.9990	-6.67
267255_at	putative Ca2+-ATPase	---	AT2G22950	-1.00	0.00	-0.01	0.9946191	0.9990	-6.67
261910_at	zinc finger protein identical to GB:A	ZFP1	AT1G80730	1.00	0.00	0.01	0.99474916	0.9990	-6.67
256176_at	hypothetical protein predicted by g	ATEXO70G	AT1G51640	-1.00	0.00	-0.01	0.99469748	0.9990	-6.67
267641_at	Argonaute (AGO1)-like protein	AGO6	AT2G32940	1.00	0.00	0.01	0.99474834	0.9990	-6.67
252342_at	endo-polygalacturonase - like prot	---	AT3G48950	1.00	0.00	0.01	0.99571028	0.9990	-6.67
258969_at	hypothetical protein predicted by g	---	AT3G10680	-1.00	0.00	-0.01	0.99471248	0.9990	-6.67
252138_at	peroxidase-like protein peroxidase	---	AT3G50990	-1.00	0.00	-0.01	0.994853	0.9990	-6.67
248670_at	receptor protein kinase-like protein	---	AT5G48740	1.00	0.00	0.01	0.99493537	0.9990	-6.67
247530_at	glycosylasparaginase - like protein	---	AT5G61540	-1.00	0.00	-0.01	0.99499824	0.9990	-6.67
253744_s_at	putative protein hypothetical prote	---	---	1.00	0.00	0.01	0.99506276	0.9990	-6.67
255206_at	putative transposon protein	---	---	1.00	0.00	0.01	0.99564132	0.9990	-6.67
252689_at	putative protein predicted proteins	---	AT3G44030	-1.00	0.00	-0.01	0.99526407	0.9990	-6.67
264500_at	hypothetical protein predicted by g	---	AT1G09370	1.00	0.00	0.01	0.9954088	0.9990	-6.67
263540_at	unknown protein	---	AT2G24780	-1.00	0.00	-0.01	0.99432177	0.9990	-6.67
251811_at	APETALA2 - like protein APETAL	SMZ	AT3G54990	1.00	0.00	0.01	0.99505632	0.9990	-6.67
251682_s_at	hypothetical protein	---	AT3G57110 /	-1.00	0.00	-0.01	0.99495852	0.9990	-6.67
249588_at	protein kinase - like protein Pto kin	---	AT5G37790	1.00	0.00	0.01	0.99556327	0.9990	-6.67
259854_at	RING-H2 zinc finger protein ATL3	---	AT1G72200	1.00	0.00	0.01	0.99539819	0.9990	-6.67
262408_at	protein phosphatase type 2C, puta	---	AT1G34750	-1.00	0.00	-0.01	0.99527316	0.9990	-6.67
263257_at	putative DNA polymerase Beta sim	---	AT1G10520	-1.00	0.00	-0.01	0.99475029	0.9990	-6.67
245381_at	MYB transcription factor like protei	MYB39	AT4G17785	-1.00	0.00	-0.01	0.99567426	0.9990	-6.67
247079_at	Expressed protein ; supported by c	AKRP	AT5G66055	-1.00	0.00	-0.01	0.99590139	0.9991	-6.67
250478_at	non-phototropic hypocotyl 3-like p	DOT3	AT5G10250	1.00	0.00	0.00	0.99618575	0.9993	-6.67
253528_s_at	putative protein bcop gene produc	---	AT4G31480 /	1.00	0.00	0.00	0.99652884	0.9993	-6.67
254334_at	predicted protein	---	AT4G22760	-1.00	0.00	0.00	0.99645485	0.9993	-6.67
262421_at	hypothetical protein predicted by g	---	AT1G50290	-1.00	0.00	0.00	0.99631706	0.9993	-6.67
250055_at	NADH-cytochrome b5 reductase ;	ATCBR	AT5G17770	1.00	0.00	0.00	0.9961976	0.9993	-6.67
247443_at	putative protein predicted proteins	---	AT5G62720	1.00	0.00	0.00	0.99615826	0.9993	-6.67
249570_at	hypothetical protein	---	AT5G38080	-1.00	0.00	0.00	0.99652992	0.9993	-6.67
266618_at	unknown protein	---	AT2G35480	-1.00	0.00	0.00	0.99657001	0.9993	-6.67
247394_at	putative protein predicted proteins	---	AT5G62860	1.00	0.00	0.00	0.99645109	0.9993	-6.67
263816_at	putative CCHC-type zinc finger pro	---	---	1.00	0.00	0.00	0.99659046	0.9993	-6.67
245461_at	hypothetical protein	---	AT4G17000	-1.00	0.00	0.00	0.99626876	0.9993	-6.67

251947_at	putative protein various predicted	---	AT3G53550	1.00	0.00	0.00	0.99641581	0.9993	-6.67
262683_at	anter-specific proline-rich -like prot	---	AT1G75920	1.00	0.00	0.00	0.99674749	0.9994	-6.67
261124_at	hypothetical protein predicted by g	---	AT1G04900	1.00	0.00	0.00	0.9975161	0.9994	-6.67
265718_at	putative WRKY DNA-binding prote	WRKY3	AT2G03340	-1.00	0.00	0.00	0.99716972	0.9994	-6.67
261300_at	hypothetical protein predicted by g	---	AT1G48560	-1.00	0.00	0.00	0.99716972	0.9994	-6.67
264490_at	putative protein import receptor si	TOM20-2	AT1G27390	1.00	0.00	0.00	0.99722335	0.9994	-6.67
262778_at	hypothetical protein predicted by g	---	AT1G13050	-1.00	0.00	0.00	0.99682711	0.9994	-6.67
262253_s_at	unknown protein contains similarity	---	AT1G53880 /	1.00	0.00	0.00	0.99774861	0.9994	-6.67
257182_s_at	crn-like protein similar to crn GB:C	---	AT3G13210 /	1.00	0.00	0.00	0.99728723	0.9994	-6.67
263344_at	unknown protein ;supported by ful	---	AT2G04940	1.00	0.00	0.00	0.99731667	0.9994	-6.67
260841_at	Expressed protein ; supported by f	---	AT1G29195	-1.00	0.00	0.00	0.99777316	0.9994	-6.67
264547_at	unknown protein ; supported by cD	CLC-F	AT1G55620	1.00	0.00	0.00	0.99697685	0.9994	-6.67
249705_at	serine/threonine protein kinase-like	---	AT5G35580	1.00	0.00	0.00	0.9977853	0.9994	-6.67
259332_at	putative auxin-induced protein sim	---	AT3G03830	-1.00	0.00	0.00	0.99764555	0.9994	-6.67
266532_at	putative glucosyltransferase ;supp	---	AT2G16890	-1.00	0.00	0.00	0.99711698	0.9994	-6.67
265632_at	hypothetical protein predicted by g	---	AT2G14290	-1.00	0.00	0.00	0.99776075	0.9994	-6.67
252259_at	putative protein acidic ribosomal p	---	AT3G49460	1.00	0.00	0.00	0.99759384	0.9994	-6.67
256907_at	hydoxyethylthiazole kinase, putati	---	AT3G24030	1.00	0.00	0.00	0.99770476	0.9994	-6.67
256053_at	UDP-glucose glucosyltransferase,	UGT71C3	AT1G07260	1.00	0.00	0.00	0.99708077	0.9994	-6.67
256762_at	Expressed protein ; supported by f	IDL1	AT3G25655	-1.00	0.00	0.00	0.99737491	0.9994	-6.67
250630_at	hypothetical protein	---	AT5G07400	1.00	0.00	0.00	0.99747408	0.9994	-6.67
247772_at	putative protein various predicted	---	AT5G58610	-1.00	0.00	0.00	0.99749893	0.9994	-6.67
261706_at	hypothetical protein similar to hypo	---	---	-1.00	0.00	0.00	0.9974294	0.9994	-6.67
264104_at	En/Spm-like transposon protein rel	---	---	1.00	0.00	0.00	0.99777639	0.9994	-6.67
251568_at	putative protein several hypothetic	---	AT3G58280	1.00	0.00	0.00	0.99692554	0.9994	-6.67
263689_at	ribonuclease, RNS3 identical to ril	RNS3	AT1G26820	1.00	0.00	0.00	0.99809602	0.9995	-6.67
265289_at	unknown protein predicted by gens	---	AT2G22690	-1.00	0.00	0.00	0.99801911	0.9995	-6.67
261128_at	ubiquitin-specific protease 2 (UBP2	UBP2	AT1G04860	1.00	0.00	0.00	0.99804541	0.9995	-6.67
256464_at	late-embryogenesis abundant pro	---	AT1G32560	1.00	0.00	0.00	0.99792598	0.9995	-6.67
250772_at	putative protein contains similarity	---	AT5G05420	-1.00	0.00	0.00	0.99806274	0.9995	-6.67
252614_at	serpin-like protein serpin - Hordeu	---	AT3G45220	-1.00	0.00	0.00	0.99791223	0.9995	-6.67
248827_at	calcium sensor protein, calcineuri	CBL9	AT5G47100	-1.00	0.00	0.00	0.99824061	0.9995	-6.67
267451_at	putative AP2 domain transcription	---	AT2G33710	1.00	0.00	0.00	0.99815796	0.9995	-6.67
249280_at	unknown protein	---	AT5G41940	-1.00	0.00	0.00	0.99824429	0.9995	-6.67
245035_at	unknown protein similar to GP|224	ATARD3	AT2G26400	1.00	0.00	0.00	0.99833434	0.9995	-6.67

257202_at	receptor-like kinase, putative simil	---	AT3G23750	1.00	0.00	0.00	0.99847958	0.9996	-6.67
261708_at	unknown protein similar to hypothe	---	AT1G32740	-1.00	0.00	0.00	0.99869272	0.9996	-6.67
262559_at	unknown protein similar to hypothe	---	AT1G31300	-1.00	0.00	0.00	0.99909547	0.9996	-6.67
261507_at	RIBOSOMAL PROTEIN, putative	---	AT1G71720	-1.00	0.00	0.00	0.99849189	0.9996	-6.67
258026_at	abscisic acid responsive elements-	ABF4	AT3G19290	1.00	0.00	0.00	0.99888625	0.9996	-6.67
263994_at	putative VSF-1-like b-ZIP transcrip	---	AT2G12900	1.00	0.00	0.00	0.99924682	0.9996	-6.67
258704_at	putative protein kinase similar to P	CCR1	AT3G09780	-1.00	0.00	0.00	0.99923881	0.9996	-6.67
263773_at	putative xylulose kinase	---	AT2G21370	-1.00	0.00	0.00	0.99901933	0.9996	-6.67
251168_at	putative protein several hypothetic	---	AT3G63370	1.00	0.00	0.00	0.99873336	0.9996	-6.67
250051_at	MYB56 R2R3-MYB factor family m	AtMYB56	AT5G17800	1.00	0.00	0.00	0.99856697	0.9996	-6.67
255470_at	hypothetical protein	---	AT4G03040	-1.00	0.00	0.00	0.99917237	0.9996	-6.67
254530_at	small GTP-binding protein - like G	ARA7	AT4G19640	-1.00	0.00	0.00	0.9991156	0.9996	-6.67
265813_at	putative NAM (no apical meristem	VND1	AT2G18060	1.00	0.00	0.00	0.99866432	0.9996	-6.67
248598_at	putative protein contains similarity	---	AT5G49370	-1.00	0.00	0.00	0.99863068	0.9996	-6.67
262642_at	hypothetical protein predicted by g	---	AT1G62690	1.00	0.00	0.00	0.99909956	0.9996	-6.67
248902_at	unknown protein	---	AT5G46440	1.00	0.00	0.00	0.99877071	0.9996	-6.67
261066_at	hypothetical protein predicted by g	---	AT1G07485	1.00	0.00	0.00	0.9989269	0.9996	-6.67
255354_at	putative transposon protein	---	---	-1.00	0.00	0.00	0.99914298	0.9996	-6.67
255383_at	hypothetical protein	---	AT4G03570	1.00	0.00	0.00	0.99914467	0.9996	-6.67
259726_at	Expressed protein ; supported by f	SCRL6	AT1G60985	1.00	0.00	0.00	0.99903639	0.9996	-6.67
259625_at	glyceraldehyde-3-phosphate dehy	GAPB	AT1G42970	-1.00	0.00	0.00	0.99933508	0.9996	-6.67
261962_s_at	hypothetical protein predicted by g	---	---	1.00	0.00	0.00	0.9994464	0.9997	-6.67
252389_at	Expressed protein ; supported by f	---	AT3G47833	-1.00	0.00	0.00	0.99957225	0.9997	-6.67
250280_at	putative protein many predicted pr	---	AT5G13230	-1.00	0.00	0.00	0.99974463	0.9999	-6.67
249068_at	putative protein similar to unknowr	PDLP1	AT5G43980	1.00	0.00	0.00	0.99990249	1.0000	-6.67
247779_at	putative protein damage-specific I	DDB2	AT5G58760	1.00	0.00	0.00	0.99997198	1.0000	-6.67
252170_at	hypothetical protein ; supported by	HR4	AT3G26560	1.00	0.00	0.00	1	1.0000	-6.67

	mut.72 vs wt.72								
ID	Description	Gene Sym	AGI	FC	logFC	t	P.Value	adj.P.Val	B
262595_at	putative ethylene responsive element Si	SHN1	AT1G15360	313.40	8.29	71.28	6.12E-11	0.000001	10.16
257774_at	short-chain alcohol dehydrogenase, put	---	AT3G29250	16.74	4.07	28.10	3.14E-08	0.000358	8.41
253101_at	cytochrome P450 monooxygenase (CYP	CYP91A2	AT4G37430	22.14	4.47	20.03	3.00E-07	0.002279	7.07
248701_at	ligand-gated ion channel protein-like; glu	GLR1.3	AT5G48410	4.53	2.18	18.33	5.40E-07	0.002314	6.65
262811_at	unknown protein ESTs gb|R65381 and g	---	AT1G11700	-4.93	-2.30	-18.73	4.68E-07	0.002314	6.76
256771_at	unknown protein	---	AT3G13700 /	3.46	1.79	17.65	6.92E-07	0.002314	6.47
260408_at	putative thioredoxin similar to thioredoxi	ATH8	AT1G69880	5.37	2.42	17.58	7.10E-07	0.002314	6.45
266967_at	unknown protein	---	AT2G39530	3.12	1.64	17.07	8.63E-07	0.002462	6.30
259272_at	unknown protein similar to hypothetical p	---	AT3G01290	4.88	2.29	16.41	1.12E-06	0.002585	6.10
261335_at	nodulin protein, putative similar to GB:2	---	AT1G44800	2.80	1.48	16.38	1.13E-06	0.002585	6.09
259150_at	unknown protein similar to unknown pro	---	AT3G10320	3.15	1.66	15.54	1.60E-06	0.002832	5.81
263475_at	Expressed protein ; supported by full-ler	---	AT2G31945	4.19	2.07	15.52	1.61E-06	0.002832	5.80
262599_at	unknown protein ESTs gb|R65145, gb|I	---	AT1G15350	3.39	1.76	15.66	1.52E-06	0.002832	5.85
263809_at	putative GDSL-motif lipase/hydrolase si	---	AT2G04570	18.27	4.19	15.32	1.76E-06	0.002866	5.73
256964_at	unknown protein ;supported by full-leng	AGP12	AT3G13520	3.53	1.82	14.47	2.56E-06	0.003241	5.42
248700_at	ligand-gated ion channel protein-like; glu	ATGLR1.2	AT5G48400	3.89	1.96	14.50	2.53E-06	0.003241	5.43
265724_at	hypothetical protein predicted by gensca	OFP16	AT2G32100	-6.07	-2.60	-14.69	2.31E-06	0.003241	5.51
259418_at	unknown protein ; supported by cDNA: g	GPAT2	AT1G02390	4.69	2.23	14.76	2.25E-06	0.003241	5.53
266551_at	unknown protein ; supported by cDNA:	---	AT2G35260	-2.35	-1.23	-14.04	3.12E-06	0.003337	5.25
263180_at	unknown protein ;supported by full-leng	URH2	AT1G05620	3.29	1.72	14.11	3.02E-06	0.003337	5.28
256062_at	unknown protein ;supported by full-lengt	LSH6	AT1G07090	-2.73	-1.45	-14.11	3.02E-06	0.003337	5.28
252097_at	putative protein hypothetical protein F16	---	AT3G51090	2.70	1.43	13.89	3.35E-06	0.003337	5.19
245642_at	Expressed protein ; supported by full-ler	---	AT1G25275	2.48	1.31	13.79	3.50E-06	0.003337	5.15
264614_s_a	putative aldehyde oxidase similar to GB	---	AT1G02590 /	3.08	1.62	13.78	3.51E-06	0.003337	5.15
254453_at	amino acid transport protein AAT1	AAT1	AT4G21120	5.53	2.47	13.65	3.74E-06	0.003347	5.10
264685_at	endo-1,4-beta-glucanase, putative simil	KOR2	AT1G65610	3.33	1.73	13.61	3.82E-06	0.003347	5.08
261819_at	receptor-like kinase, putative similar to	---	AT1G11410	-2.80	-1.49	-13.43	4.16E-06	0.003498	5.00
248918_at	senescence-specific cysteine protease S	SAG12	AT5G45890	4.14	2.05	13.36	4.29E-06	0.003498	4.98
251706_at	nodulin-like protein MtN21 - Medicago t	---	AT3G56620	3.44	1.78	13.17	4.72E-06	0.003711	4.89
266247_at	hypothetical protein predicted by gensca	---	AT2G27660	3.74	1.90	13.03	5.07E-06	0.003855	4.83
245130_at	putative receptor-like protein kinase	---	AT2G45340	-2.41	-1.27	-12.86	5.51E-06	0.003927	4.76
255074_at	putative protein RING-H2 zinc finger pr	---	AT4G09100	2.91	1.54	12.92	5.35E-06	0.003927	4.78
256436_at	hypothetical protein predicted by genefir	---	AT3G11150	2.85	1.51	12.78	5.74E-06	0.003965	4.72

245010_at	NADH dehydrogenase subunit	---	---	-3.24	-1.69	-12.72	5.91E-06	0.003965	4.69
262603_at	hypothetical protein Is a member of the	---	AT1G15380	10.73	3.42	12.44	6.84E-06	0.004056	4.56
252303_at	putative protein hypothetical protein Rv	---	AT3G49210	2.50	1.32	12.56	6.43E-06	0.004056	4.62
255403_at	putative GH3-like protein similar to soyb	DFL2	AT4G03400	-3.59	-1.84	-12.41	6.93E-06	0.004056	4.55
247723_at	protein phosphatase 2C - like ABA indu	---	AT5G59220	6.98	2.80	12.62	6.23E-06	0.004056	4.65
254305_at	potassium channel protein AKT3 ; supp	AKT2/3	AT4G22200	-2.20	-1.14	-12.48	6.69E-06	0.004056	4.58
250646_at	peroxidase (emb|CAA68212.1) ;suppor	---	AT5G06720	3.96	1.99	12.28	7.44E-06	0.004245	4.49
256631_at	At14a-like protein similar to At14a protei	---	AT3G28320	-6.51	-2.70	-12.21	7.72E-06	0.004294	4.45
263680_at	unknown protein	---	AT1G26930	2.15	1.10	12.01	8.58E-06	0.004350	4.36
245362_at	homeobox-leucine zipper protein HAT1	HAT1	AT4G17460	-3.96	-1.98	-12.12	8.12E-06	0.004350	4.41
259735_at	Expressed protein ; supported by full-ler	---	AT1G64405	5.20	2.38	12.08	8.26E-06	0.004350	4.39
259399_at	hypothetical protein similar to putative p	---	AT1G17710	3.55	1.83	12.05	8.43E-06	0.004350	4.37
244997_at	RNA polymerase beta' subunit-2	---	---	-2.72	-1.44	-11.95	8.89E-06	0.004407	4.32
252118_at	putative protein various predicted prote	---	AT3G51400	-2.08	-1.05	-11.83	9.48E-06	0.004561	4.26
248927_at	ubiquitin activating enzyme E1-like prote	APG7	AT5G45900	2.84	1.50	11.81	9.60E-06	0.004561	4.25
253268_s_a	glucosyltransferase -like protein immed	UGT73B2	AT4G34131 /	5.43	2.44	11.37	1.22E-05	0.004734	4.03
245011_at	photosystem II G protein	---	---	-2.51	-1.33	-11.46	1.16E-05	0.004734	4.08
251096_at	receptor like protein kinase receptor like	LECRKA4	AT5G01550	4.90	2.29	11.40	1.20E-05	0.004734	4.04
257765_at	hypothetical protein contains Pfam profil	---	AT3G23020	-2.26	-1.18	-11.59	1.08E-05	0.004734	4.14
257697_at	hypothetical protein predicted by genem	---	AT3G12700	4.06	2.02	11.41	1.20E-05	0.004734	4.05
251642_at	imbibition protein homolog probable iml	AtSIP2	AT3G57520	2.72	1.44	11.61	1.07E-05	0.004734	4.15
245730_at	unknown protein ;supported by full-lengt	---	AT1G73470	-2.37	-1.24	-11.68	1.03E-05	0.004734	4.19
248564_at	putative protein contains similarity to AT	---	AT5G49700	3.58	1.84	11.37	1.22E-05	0.004734	4.03
256050_at	leucine zipper protein, putative similar t	ATEXO70I	AT1G07000	2.57	1.36	11.50	1.13E-05	0.004734	4.10
256602_at	unknown protein	---	AT3G28310	-3.42	-1.77	-11.49	1.14E-05	0.004734	4.09
247340_at	unknown protein	---	AT5G63700	-2.24	-1.16	-11.56	1.10E-05	0.004734	4.13
245317_at	hypothetical protein ; supported by full-le	---	AT4G15610	2.52	1.33	11.14	1.40E-05	0.005306	3.90
267266_at	putative metal ion transporter (NRAMP)	NRAMP3	AT2G23150	2.35	1.23	11.06	1.46E-05	0.005455	3.86
260391_at	putative strictosidine synthase extremely	SS2	AT1G74020	2.83	1.50	10.78	1.72E-05	0.005627	3.70
260581_at	MYB transcription factor (Atmyb2)	MYB2	AT2G47190	3.58	1.84	10.93	1.57E-05	0.005627	3.79
257650_at	protein phosphatase, putative similar to	---	AT3G16800	-3.25	-1.70	-10.87	1.63E-05	0.005627	3.76
263184_at	UDP-glucose:indole-3-acetate beta-D-g	UGT75B1	AT1G05560	3.60	1.85	10.89	1.61E-05	0.005627	3.77
249727_at	putative protein similar to unknown prote	MRU1	AT5G35490	-2.11	-1.08	-10.61	1.91E-05	0.005627	3.61
248624_at	unknown protein ; supported by cDNA:	---	AT5G48790	-2.21	-1.15	-10.65	1.86E-05	0.005627	3.63
245616_at	kinase like protein	---	AT4G14480	-5.03	-2.33	-10.63	1.88E-05	0.005627	3.62

245016_at	carboxytransferase beta subunit	---	---	-2.19	-1.13	-10.67	1.84E-05	0.005627	3.64
245003_at	PSII 43 KDa protein	---	---	-2.47	-1.30	-10.72	1.78E-05	0.005627	3.67
256818_at	hypothetical protein contains Pfam profil	---	AT3G21420	2.13	1.09	10.58	1.94E-05	0.005627	3.59
261551_at	ATP dependent copper transporter, put	HMA5	AT1G63440	2.27	1.18	10.59	1.93E-05	0.005627	3.60
259133_at	sugar transporter, putative similar to int	---	AT3G05400	6.13	2.62	10.65	1.86E-05	0.005627	3.63
256024_at	unknown protein contains Pfam profile:	ZF14	AT1G58340	9.30	3.22	10.77	1.73E-05	0.005627	3.70
257363_at	hypothetical protein predicted by gensca	BAP2	AT2G45760	3.12	1.64	10.57	1.95E-05	0.005627	3.59
260023_at	unknown protein	ATGA2OX	AT1G30040	4.32	2.11	10.74	1.76E-05	0.005627	3.68
249193_at	putative protein similar to unknown prote	ARC6	AT5G42480	-1.98	-0.99	-10.67	1.84E-05	0.005627	3.64
263715_at	unknown protein ; supported by cDNA:	GPRI1	AT2G20570	-2.32	-1.22	-10.64	1.87E-05	0.005627	3.63
252511_at	putative protein serine/threonine-specifi	---	AT3G46280	9.71	3.28	10.75	1.75E-05	0.005627	3.69
260364_at	putative alliinase similar to aliinase prec	TAA1	AT1G70560	-3.37	-1.75	-10.52	2.01E-05	0.005634	3.56
246057_at	putative protein predicted proteins, Aral	---	AT5G08400	-2.17	-1.12	-10.54	1.99E-05	0.005634	3.57
264360_at	putative isoamylase Similar to gi|16527	DBE1	AT1G03310	-2.83	-1.50	-10.47	2.07E-05	0.005634	3.53
257632_at	cytochrome P450, putative similar to cy	CYP71B21	AT3G26190	4.92	2.30	10.50	2.04E-05	0.005634	3.54
264573_at	putative pectin methylesterase Similar to	---	AT1G05310	3.04	1.60	10.49	2.05E-05	0.005634	3.54
247899_at	Expressed protein ; supported by full-ler	---	AT5G57345	-2.76	-1.46	-10.43	2.13E-05	0.005709	3.50
265945_at	putative cytokinin oxidase ; supported b	CKX2	AT2G19500	2.21	1.15	10.37	2.21E-05	0.005807	3.47
259443_at	chitinase, putative similar to chitinase G	---	AT1G02360	6.68	2.74	10.36	2.21E-05	0.005807	3.47
253630_at	putative protein putative ATPase - Haer	---	AT4G30490	2.87	1.52	10.34	2.24E-05	0.005811	3.45
253903_at	kinesin-related protein katB ; supported	ATK2	AT4G27180	-1.88	-0.91	-10.32	2.28E-05	0.005835	3.44
248563_at	anthocyanidin-3-glucoside rhamnosyltra	---	AT5G49690	3.85	1.94	10.29	2.31E-05	0.005864	3.42
249123_at	beta-ketoacyl-CoA synthase ; supporte	KCS20	AT5G43760	1.88	0.91	10.24	2.39E-05	0.005984	3.39
245569_at	RNA polymerase II fifth largest subunit I	NRPE7	AT4G14660	-1.94	-0.96	-10.14	2.54E-05	0.006099	3.33
245712_at	pullulanase-like protein (starch debranch	ATLDA	AT5G04360	-2.13	-1.09	-10.14	2.55E-05	0.006099	3.33
265699_at	putative esterase (contains an esterase/	---	AT2G03550	-2.31	-1.21	-10.13	2.57E-05	0.006099	3.32
257890_s_a	putative protein peroxidase - Lycopers	---	AT3G17070 /	-3.02	-1.59	-10.14	2.55E-05	0.006099	3.33
251634_at	putative protein putative zinc finger prot	---	AT3G57480	2.31	1.21	10.13	2.56E-05	0.006099	3.33
247586_at	mipC protein - like (aquaporin) mipC pr	PIP2;4	AT5G60660	2.25	1.17	10.10	2.61E-05	0.006104	3.31
258586_s_a	putative trypsin inhibitor similar to trypsi	---	AT3G04320 /	7.64	2.93	10.09	2.62E-05	0.006104	3.30
253609_at	H+-transporting ATPase type 2, plasma	AHA2	AT4G30190	2.58	1.37	10.04	2.71E-05	0.006253	3.27
252374_at	response reactor 2 (ATRR2) ; supporte	ARR5	AT3G48100	4.06	2.02	10.00	2.77E-05	0.006267	3.25
254938_at	putative oligopeptide transporter similar	OPT7	AT4G10770	-2.13	-1.09	-10.00	2.78E-05	0.006267	3.25
252543_at	nonphototropic hypocotyl 1 ; supported	PHOT1	AT3G45780	-1.97	-0.98	-9.99	2.80E-05	0.006267	3.24
255332_at	predicted protein of unknown function ;	---	AT4G04340	-1.97	-0.98	-9.93	2.90E-05	0.006426	3.20

253273_at	putative protein hypothetical protein slr2	---	AT4G34180	2.03	1.02	9.89	2.98E-05	0.006534	3.18
245108_at	putative cytokinin oxidase	CKX1	AT2G41510	-2.11	-1.07	-9.86	3.04E-05	0.006534	3.16
253632_at	senescence-associated protein homolo	TET9	AT4G30430	1.84	0.88	9.87	3.02E-05	0.006534	3.17
245008_at	hypothetical protein	---	---	-2.00	-1.00	-9.78	3.20E-05	0.006579	3.11
252355_at	putative protein various predicted prote	---	AT3G48250	-2.15	-1.10	-9.81	3.14E-05	0.006579	3.13
264107_s_a	putative receptor-like protein kinase	SERK5	AT2G13790 /	2.36	1.24	9.79	3.18E-05	0.006579	3.12
246001_at	putative protein predicted protein, Arabi	---	AT5G20790	5.27	2.40	9.81	3.13E-05	0.006579	3.13
254687_at	cytochrome P450 monooxygenase (CYP	CYP83A1	AT4G13770 /	-3.25	-1.70	-9.79	3.18E-05	0.006579	3.12
266712_at	unknown protein	---	AT2G46750	2.61	1.38	9.73	3.31E-05	0.006725	3.08
267356_at	putative isoamylase	ISA1	AT2G39930	-2.21	-1.15	-9.71	3.36E-05	0.006725	3.06
245501_at	hypothetical protein	---	AT4G15620	5.94	2.57	9.72	3.33E-05	0.006725	3.07
250613_at	putative protein SF16 protein, pollen sp	IQD24	AT5G07240	-2.57	-1.36	-9.67	3.43E-05	0.006744	3.04
246366_at	light repressible receptor protein kinase	---	AT1G51850	2.95	1.56	9.68	3.41E-05	0.006744	3.05
248753_at	acyl carrier protein-like	mtACP3	AT5G47630	-2.07	-1.05	-9.63	3.52E-05	0.006803	3.02
255733_at	unknown protein similar to unknown pro	---	AT1G25400	3.71	1.89	9.64	3.50E-05	0.006803	3.02
250287_at	putative protein AP2 domain containing	Rap2.6L	AT5G13330	3.21	1.68	9.52	3.80E-05	0.006847	2.94
264195_at	putative gibberellin-regulated protein co	---	AT1G22690	-3.87	-1.95	-9.56	3.71E-05	0.006847	2.97
266132_at	hypothetical protein predicted by gensca	SPX3	AT2G45130	5.49	2.46	9.54	3.74E-05	0.006847	2.96
266197_at	hypothetical protein predicted by gensca	---	AT2G39120	-2.07	-1.05	-9.57	3.68E-05	0.006847	2.97
264053_at	hypothetical protein predicted by gensca	---	AT2G22560	2.76	1.46	9.53	3.77E-05	0.006847	2.95
267134_at	putative protein kinase contains a protei	---	AT2G23450	1.77	0.82	9.50	3.84E-05	0.006847	2.93
256873_at	cytochrome P450, putative contains Pfa	CYP71B34	AT3G26300 /	-2.27	-1.18	-9.56	3.70E-05	0.006847	2.97
248540_at	FRO1 and FRO2-like protein	FRO8	AT5G50160	-1.85	-0.89	-9.51	3.83E-05	0.006847	2.93
262736_at	lipase, putative contains Pfam profile: P	---	AT1G28570	-2.05	-1.03	-9.54	3.75E-05	0.006847	2.95
267496_at	putative lipase ; supported by full-length	---	AT2G30550	2.83	1.50	9.55	3.72E-05	0.006847	2.96
259942_at	unknown protein	ATWHY2	AT1G71260	-1.79	-0.84	-9.48	3.90E-05	0.006893	2.92
260235_at	putative SET protein, phospatase 2A in	NRP1	AT1G74560	-1.89	-0.92	-9.45	3.97E-05	0.006893	2.90
245346_at	putative beta-amylase ;supported by full	CT-BMY	AT4G17090	-2.51	-1.33	-9.45	3.99E-05	0.006893	2.89
257824_at	unknown protein ; supported by cDNA:	---	AT3G25290	4.36	2.13	9.46	3.96E-05	0.006893	2.90
262648_at	putative ribulose-1,5 bisphosphate carb	---	AT1G14030	-2.06	-1.04	-9.39	4.15E-05	0.007124	2.85
258395_at	putative jasmonic acid regulatory protein	ANAC055	AT3G15500	3.94	1.98	9.33	4.32E-05	0.007194	2.82
255070_at	isoamylase-like protein probable isoam	ISA3	AT4G09020	-1.96	-0.97	-9.34	4.28E-05	0.007194	2.82
251762_at	sedoheptulose-bisphosphatase precurs	SBPASE	AT3G55800	-2.17	-1.12	-9.32	4.33E-05	0.007194	2.81
256499_at	unknown protein	---	AT1G36640	4.06	2.02	9.34	4.28E-05	0.007194	2.83
253054_at	probable N-acetyltransferase hookless 1	HLS1	AT4G37580	-2.03	-1.02	-9.31	4.36E-05	0.007194	2.81

251839_at	putative protein patatin, Solanum tuber	PLA IIIA	AT3G54950	3.40	1.77	9.31	4.38E-05	0.007194	2.80
245018_at	hypothetical protein	---	---	-1.89	-0.92	-9.29	4.43E-05	0.007194	2.79
267337_at	putative anthocyanin 5-aromatic acyltran	---	AT2G39980	3.13	1.65	9.28	4.47E-05	0.007194	2.78
245002_at	PSII D2 protein	---	---	-2.51	-1.33	-9.25	4.54E-05	0.007194	2.77
254262_at	putative protein annexin VII, Dictyosteli	---	AT4G23470	2.52	1.34	9.27	4.49E-05	0.007194	2.78
254952_at	UDP-galactose 4-epimerase - like prote	UGE5	AT4G10955 /	2.36	1.24	9.25	4.54E-05	0.007194	2.77
256489_at	unknown protein	---	AT1G31550	-1.80	-0.85	-9.22	4.66E-05	0.007276	2.74
262653_at	dioxygenase-like protein very similar to	---	AT1G14130	1.84	0.88	9.19	4.75E-05	0.007276	2.72
251155_at	putative protein outer envelope membra	---	AT3G63160	-1.87	-0.91	-9.19	4.75E-05	0.007276	2.72
248910_at	serine threonine protein kinase ; suppor	CIPK20	AT5G45820	-3.83	-1.94	-9.22	4.65E-05	0.007276	2.74
245845_at	Pto kinase interactor, putative similar to	PERK10	AT1G26150	-2.06	-1.04	-9.20	4.72E-05	0.007276	2.73
262380_at	threonine synthase, putative similar to t	---	AT1G72810	-2.28	-1.19	-9.17	4.82E-05	0.007329	2.71
250327_at	putative serine rich protein predicted pr	---	AT5G12050	-8.39	-3.07	-9.12	4.96E-05	0.007350	2.68
257131_at	mitochondrial carrier protein, putative c	---	AT3G20240	-1.88	-0.91	-9.12	4.97E-05	0.007350	2.68
254181_at	FtsH protease, putative contains similar	---	AT4G23940	-1.86	-0.89	-9.13	4.93E-05	0.007350	2.69
246568_at	E2F transcription factor -like protein E2	DEL2	AT5G14960	-2.40	-1.26	-9.11	4.99E-05	0.007350	2.67
245525_at	dynein light chain like protein	---	AT4G15930	-1.76	-0.81	-9.12	4.96E-05	0.007350	2.68
245112_at	glycerol-3-phosphate dehydrogenase ;s	GPDHC1	AT2G41540	8.21	3.04	9.10	5.05E-05	0.007381	2.66
266072_at	putative trehalose-6-phosphate synthas	ATTPS11	AT2G18700	3.51	1.81	9.08	5.12E-05	0.007424	2.65
252183_at	UTP-glucose glucosyltransferase - like	UGT72E1	AT3G50740	-2.54	-1.35	-9.06	5.18E-05	0.007424	2.64
259370_at	hypothetical protein predicted by gensca	---	AT1G69050	2.41	1.27	9.05	5.21E-05	0.007424	2.63
246701_at	cysteine synthase ;supported by full-len	CYSD2	AT5G28020	-2.35	-1.23	-9.06	5.19E-05	0.007424	2.63
258920_at	class 2 non-symbiotic hemoglobin identi	---	AT1G04380 /	-4.49	-2.17	-9.04	5.25E-05	0.007444	2.62
266279_at	putative tropinone reductase	---	AT2G29290	-2.58	-1.36	-9.02	5.32E-05	0.007487	2.61
260089_at	putative ATPase contains Pfam profile:	---	AT1G73170	-1.81	-0.85	-9.00	5.41E-05	0.007565	2.59
250196_at	polynucleotide phosphorylase	---	AT5G14580	-2.40	-1.26	-8.97	5.53E-05	0.007596	2.57
248315_at	selenium-binding protein-like	MEF1	AT5G52630	-2.11	-1.08	-8.96	5.57E-05	0.007596	2.56
257280_at	9-cis-epoxycarotenoid dioxygenase, pu	NCED3	AT3G14440	3.36	1.75	8.95	5.59E-05	0.007596	2.56
249876_at	putative protein similar to unknown prote	CaS	AT5G23060	-2.40	-1.26	-8.96	5.58E-05	0.007596	2.56
250158_at	putative protein	---	AT5G15190	3.51	1.81	8.96	5.58E-05	0.007596	2.56
262259_s_a	hypothetical protein predicted by genem	---	AT1G53870 /	-3.11	-1.64	-8.93	5.66E-05	0.007612	2.55
253860_at	hypothetical protein ;supported by full-le	---	AT4G27700	-1.92	-0.94	-8.93	5.67E-05	0.007612	2.54
260101_at	putative trypsin inhibitor similar to trypsi	---	AT1G73260	2.82	1.50	8.85	6.01E-05	0.007831	2.49
258975_at	putative WRKY-like transcriptional regul	WRKY45	AT3G01970	2.29	1.20	8.81	6.16E-05	0.007831	2.46
264951_at	unknown protein contains similarity to se	---	AT1G76970	1.76	0.82	8.83	6.08E-05	0.007831	2.48

254133_at	putative protein various predicted ABC-t	---	AT4G24810	-1.82	-0.87	-8.83	6.10E-05	0.007831	2.47
255572_at	hypothetical protein ; supported by cDN	---	AT4G01050	-1.72	-0.78	-8.78	6.32E-05	0.007831	2.44
252353_at	putative protein KIAA0226 gene produc	---	AT3G48200	-2.07	-1.05	-8.83	6.10E-05	0.007831	2.47
265726_at	putative inositol polyphosphate 5'-phosp	---	AT2G32010	-2.71	-1.44	-8.78	6.30E-05	0.007831	2.44
260167_at	hypothetical protein predicted by gensca	---	AT1G71970	-2.27	-1.18	-8.80	6.22E-05	0.007831	2.45
249035_at	putative protein contains similarity to un	GLK2	AT5G44190	-2.30	-1.20	-8.79	6.27E-05	0.007831	2.45
260648_at	unknown protein	---	AT1G08050	3.46	1.79	8.79	6.28E-05	0.007831	2.44
266560_at	putative LRR receptor protein kinase	---	AT2G23950	-2.36	-1.24	-8.80	6.21E-05	0.007831	2.45
254742_at	putative protein various predicted 3-isop	IIL1	AT4G13430	-1.76	-0.82	-8.82	6.12E-05	0.007831	2.47
247618_at	receptor like protein kinase receptor like	---	AT5G60280	2.13	1.09	8.84	6.06E-05	0.007831	2.48
262925_at	hypothetical protein	YSL7	AT1G65730	2.14	1.10	8.83	6.11E-05	0.007831	2.47
266466_at	hypothetical protein The first 3 exons is	---	AT2G47790	-1.98	-0.98	-8.76	6.39E-05	0.007873	2.43
259430_at	hypothetical protein similar to unknown	GPAT4	AT1G01610	2.94	1.56	8.71	6.63E-05	0.008128	2.39
263737_at	unknown protein ;supported by full-lengt	---	AT1G60010	-2.31	-1.21	-8.70	6.67E-05	0.008130	2.38
265121_at	similar to flavin-containing monooxyger	FMO GS-(	AT1G62560	-3.57	-1.84	-8.68	6.78E-05	0.008225	2.37
266319_s_a	putative beta-ketoacyl-CoA synthase	KCS13	AT2G46720 /	-2.98	-1.58	-8.65	6.94E-05	0.008290	2.34
261525_at	hypothetical protein predicted by genem	---	AT1G14330	2.49	1.32	8.65	6.91E-05	0.008290	2.35
256880_at	major latex protein, putative similar to n	---	AT3G26450	-3.36	-1.75	-8.65	6.94E-05	0.008290	2.34
257756_at	uridylate kinase, putative similar to UMI	---	AT3G18680	-2.19	-1.13	-8.63	7.04E-05	0.008366	2.33
266707_at	hypothetical protein predicted by gensca	---	AT2G03310	-1.90	-0.93	-8.61	7.14E-05	0.008399	2.31
259596_at	auxin-regulated GH3 protein, putative s	GH3.17	AT1G28130	4.73	2.24	8.61	7.11E-05	0.008399	2.32
245025_at	ATPase I subunit	---	---	-1.66	-0.74	-8.59	7.22E-05	0.008402	2.30
265024_at	Expressed protein ; supported by full-ler	---	AT1G24600	4.30	2.11	8.60	7.20E-05	0.008402	2.31
249120_at	unknown protein ;supported by full-leng	---	AT5G43750	-2.00	-1.00	-8.57	7.35E-05	0.008510	2.29
245738_at	nucellin, putative similar to nucellin GI:2	---	AT1G44130	3.16	1.66	8.55	7.45E-05	0.008536	2.27
244992_s_a	ribosomal protein S7	---	---	-2.10	-1.07	-8.55	7.45E-05	0.008536	2.27
260805_at	glutathione transferase, putative similar	ATGSTU2	AT1G78320	-1.78	-0.83	-8.53	7.58E-05	0.008583	2.25
247549_at	putative transcription factor MYB28 ; su	MYB28	AT5G61420	-3.05	-1.61	-8.53	7.58E-05	0.008583	2.25
253722_at	putative protein zinc finger transcription	---	AT4G29190	-2.27	-1.19	-8.52	7.60E-05	0.008583	2.25
256466_at	plastid protein, putative similar to GI:22	---	AT1G32580	-1.76	-0.81	-8.51	7.65E-05	0.008601	2.25
250213_at	H-protein promoter binding factor-1 (gb|	TBP1	AT5G13820	2.63	1.39	8.48	7.83E-05	0.008755	2.22
247074_at	putative protein contains similarity to pat	---	AT5G66590	-2.60	-1.38	-8.43	8.15E-05	0.009004	2.18
245019_at	hypothetical protein	---	---	-1.71	-0.78	-8.43	8.11E-05	0.009004	2.19
253971_at	fructose-bisphosphate aldolase - like pr	---	AT4G26530	-4.23	-2.08	-8.42	8.17E-05	0.009004	2.18
253485_at	Expressed protein ; supported by full-ler	WRKY18	AT4G31800	4.39	2.13	8.39	8.39E-05	0.009168	2.15

254347_at	putative protein DNA-binding protein AE	WRKY31	AT4G22070	2.25	1.17	8.39	8.40E-05	0.009168	2.15
264467_at	unknown protein similar to EST gb|AA59	---	AT1G10140	2.06	1.05	8.38	8.46E-05	0.009193	2.14
257407_at	unknown protein	---	AT1G27100	1.90	0.93	8.36	8.58E-05	0.009279	2.13
249377_at	putative protein predicted proteins, Aral	---	AT5G40690	3.46	1.79	8.34	8.67E-05	0.009285	2.12
246952_at	putative protein similar to unknown prote	OFP13	AT5G04820	-2.29	-1.20	-8.35	8.66E-05	0.009285	2.12
263902_at	phosphoribosylformimino-5-aminoimidaz	APG10	AT2G36230	-1.90	-0.93	-8.33	8.78E-05	0.009356	2.11
257196_at	AMP-binding protein, putative similar to	---	AT3G23790	2.34	1.23	8.27	9.13E-05	0.009478	2.07
250180_at	early nodule-specific protein - like early	---	AT5G14450	-1.93	-0.95	-8.25	9.29E-05	0.009478	2.05
264313_at	carbonic anhydrase, putative similar to	BCA4	AT1G70410	-1.72	-0.78	-8.30	8.97E-05	0.009478	2.08
257164_at	mismatch binding protein, putative simil	MSH1	AT3G24320	-1.98	-0.99	-8.30	8.98E-05	0.009478	2.08
247386_at	putative protein similar to unknown prote	emb2746	AT5G63420	-1.86	-0.89	-8.25	9.33E-05	0.009478	2.05
263483_at	putative heat shock protein ; supported	CR88	AT2G04030	-1.99	-1.00	-8.23	9.46E-05	0.009478	2.03
249115_at	PINHEAD (gb|AAD40098.1); translation	ZLL	AT5G43810	-1.74	-0.80	-8.27	9.18E-05	0.009478	2.06
262947_at	unknown protein ;supported by full-lengt	GASA1	AT1G75750	-1.67	-0.74	-8.23	9.47E-05	0.009478	2.03
263696_at	putative aspartate kinase-homoserine d	AK-HSDH	AT1G31230	-2.92	-1.55	-8.24	9.37E-05	0.009478	2.04
262232_at	unknown protein ; supported by cDNA: g	---	AT1G68600	-2.82	-1.50	-8.25	9.32E-05	0.009478	2.05
250975_at	putative protein	---	AT5G03050	-2.24	-1.17	-8.25	9.28E-05	0.009478	2.05
257670_at	unknown protein	---	AT3G20340	4.50	2.17	8.23	9.47E-05	0.009478	2.03
252274_at	branched-chain-amino-acid transamina	BCAT3	AT3G49680	-1.90	-0.93	-8.29	9.02E-05	0.009478	2.08
248566_s_a	FRO2-like protein; NADPH oxidase-like	ATFRO7	AT5G49730 /	-3.54	-1.82	-8.28	9.13E-05	0.009478	2.07
264280_at	beta-glucosidase, putative similar to be	BGLU46	AT1G61820	4.12	2.04	8.20	9.62E-05	0.009545	2.01
266684_at	40S ribosomal protein S15A	rps15ab	AT2G19720	-1.75	-0.80	-8.21	9.59E-05	0.009545	2.02
245840_at	hypothetical protein predicted by genem	---	AT1G58420	4.90	2.29	8.19	9.70E-05	0.009580	2.01
257022_at	zinc finger protein, putative similar to C	AZF2	AT3G19580	2.32	1.21	8.15	0.0001	0.009612	1.97
250680_at	putative protein similar to unknown prote	---	AT5G06570	4.26	2.09	8.15	0.0001	0.009612	1.97
267562_at	unknown protein similar to hypothetical	---	AT2G39670	-1.81	-0.86	-8.17	9.88E-05	0.009612	1.99
264835_at	unknown protein similar to unknown pro	---	AT1G03550	-1.65	-0.72	-8.17	9.90E-05	0.009612	1.98
246122_at	putative protein brain specific Na+-depe	PHT4;5	AT5G20380	2.10	1.07	8.16	9.97E-05	0.009612	1.98
245743_at	hypothetical protein contains similarity t	---	AT1G51080	-2.54	-1.34	-8.18	9.78E-05	0.009612	2.00
266857_at	putative Na+ dependent ileal bile acid tr	---	AT2G26900	-1.84	-0.88	-8.15	0.0001	0.009612	1.97
256622_at	unknown protein	AtHB34	AT3G28920	-1.70	-0.77	-8.14	0.000101	0.009612	1.96
265182_at	putative auxin-induced protein ;support	---	AT1G23740	-2.55	-1.35	-8.13	0.000102	0.009612	1.96
258977_s_a	putative aspartate kinase similar to aspa	AK3	AT3G02020 /	-2.78	-1.47	-8.13	0.000102	0.009612	1.96
266929_at	putative AT-hook DNA-binding protein ;	---	AT2G45850	-1.92	-0.94	-8.14	0.000101	0.009612	1.97
257061_at	hypothetical protein predicted by gensca	---	AT3G18250	3.22	1.69	8.10	0.000104	0.009614	1.93

258616_at	putative protein kinase contains Pfam p	---	AT3G02880	2.27	1.18	8.08	0.000105	0.009614	1.92
261350_at	hypothetical protein predicted by genem	---	AT1G79770	-2.72	-1.44	-8.09	0.000105	0.009614	1.93
254645_at	putative protein	---	AT4G18520	-2.03	-1.02	-8.11	0.000103	0.009614	1.94
262717_s_a	putative cytochrome P450 similar to gbl	CYP79F2	AT1G16400 /	-2.68	-1.42	-8.08	0.000106	0.009614	1.92
247239_at	pectin methylesterase-like protein suppo	---	AT5G64640	-2.02	-1.02	-8.11	0.000104	0.009614	1.94
253257_at	extra-large G-protein - like extra-large G	XLG2	AT4G34390	2.18	1.12	8.10	0.000104	0.009614	1.94
257911_at	hypothetical protein contains similarity to	GLYR1	AT3G25530	-1.71	-0.78	-8.09	0.000105	0.009614	1.92
255331_at	hypothetical protein ; supported by cDN	---	AT4G04330	-1.95	-0.96	-8.08	0.000106	0.009614	1.92
254862_at	putative transport protein Na(+) depend	---	AT4G12030	-3.21	-1.68	-8.07	0.000106	0.009620	1.91
260693_at	peptide transporter PTR2-B, putative si	NRT1.5	AT1G32450	5.37	2.42	8.06	0.000107	0.009636	1.91
254724_at	putative protein IFA-binding protein, Ara	---	AT4G13630	2.12	1.09	8.06	0.000107	0.009636	1.90
263142_at	unknown protein	---	AT1G65230	-2.01	-1.01	-8.05	0.000109	0.009638	1.89
250429_at	putative protein TH65 protein, Arabidop	---	AT5G10470	-1.92	-0.94	-8.05	0.000109	0.009638	1.89
256676_at	putative protein ;supported by full-lengt	SEX4	AT3G52180	-2.83	-1.50	-8.05	0.000108	0.009638	1.89
258334_at	hypothetical protein predicted by gensca	---	AT3G16010	-1.92	-0.94	-8.04	0.000109	0.009658	1.88
245705_at	zinc finger transcription factor-like protei	---	AT5G04390	1.78	0.83	8.02	0.000111	0.009658	1.87
259701_at	unknown protein similar to GB:AAC2818	---	AT1G77770	2.24	1.16	8.02	0.000111	0.009658	1.87
250177_at	putative protein copine I, Homo sapiens	RGLG2	AT5G14420	2.10	1.07	8.03	0.00011	0.009658	1.88
245388_at	hypothetical protein ;supported by full-le	---	AT4G16410	-1.74	-0.80	-7.99	0.000113	0.009744	1.85
267388_at	putative beta-glucosidase	BGLU15	AT2G44450	3.50	1.81	7.99	0.000113	0.009744	1.85
247853_at	non phototropic hypocotyl 1-like ; suppo	PHOT2	AT5G58140	-2.01	-1.01	-8.00	0.000113	0.009744	1.86
251063_at	protein kinase ATN1-like protein protein	---	AT5G01850	1.88	0.91	7.99	0.000113	0.009744	1.85
248060_at	putative protein contains similarity to NR	---	AT5G55560	1.90	0.93	7.95	0.000117	0.009833	1.82
261588_at	hypothetical protein predicted by genem	---	AT1G01670	-1.66	-0.74	-7.95	0.000117	0.009833	1.82
267300_at	putative glucosyltransferase	---	AT2G30140	1.79	0.84	7.97	0.000115	0.009833	1.83
258534_at	thioredoxin, putative similar to thioredox	---	AT3G06730	-1.80	-0.85	-7.97	0.000116	0.009833	1.83
247903_at	unknown protein ; supported by cDNA:	---	AT5G57340	-2.27	-1.19	-7.95	0.000116	0.009833	1.82
261373_at	CMP-KDO synthetase, putative similar	---	AT1G53000	-1.82	-0.86	-7.95	0.000117	0.009833	1.82
259759_at	hypothetical protein similar to GB:CAB5	---	AT1G77550	-1.89	-0.92	-7.94	0.000117	0.009851	1.81
252688_at	putative protein	---	AT3G44020	-2.02	-1.01	-7.93	0.000118	0.009871	1.80
247468_at	ARF1-binding protein ; supported by cD	ARF2	AT5G62000	-1.96	-0.97	-7.93	0.000119	0.009871	1.80
266098_at	hypothetical protein predicted by gensca	---	AT2G37870	2.47	1.31	7.92	0.00012	0.009939	1.79
246316_at	putative protein predicted proteins - Ara	---	AT3G56890	-1.64	-0.71	-7.88	0.000123	0.009987	1.76
255716_at	coded for by A. thaliana cDNA R30513	CRCK2	AT4G00330	1.61	0.68	7.88	0.000123	0.009987	1.76
258259_s_a	unknown protein ; supported by cDNA:	---	AT3G26820 /	1.93	0.95	7.90	0.000122	0.009987	1.78

253458_at	putative protein predicted protein, Arabi	---	AT4G32070	2.80	1.49	7.90	0.000121	0.009987	1.78
267548_at	putative disease resistance protein	AtRLP22	AT2G32660	6.34	2.67	7.89	0.000122	0.009987	1.77
264111_at	hypothetical protein predicted by gensca	---	AT2G13690	-1.71	-0.78	-7.89	0.000122	0.009987	1.77
266685_at	hypothetical protein	---	AT2G19710	1.89	0.92	7.88	0.000123	0.009987	1.76
255887_at	hypothetical protein contains Pfam profil	---	AT1G20370	-1.72	-0.78	-7.86	0.000125	0.009995	1.75
258109_at	hypothetical protein contains Pfam profil	HGL1	AT3G23640	-1.91	-0.93	-7.87	0.000124	0.009995	1.76
245784_at	hypothetical protein similar to hypothetic	---	AT1G32190	-1.97	-0.98	-7.87	0.000125	0.009995	1.75
266227_at	unknown protein ;supported by full-leng	---	AT2G28870	-1.65	-0.72	-7.86	0.000125	0.009995	1.75
265985_at	hypothetical protein predicted by gensca	ATPUP5	AT2G24220	-1.74	-0.80	-7.85	0.000126	0.010010	1.74
245209_at	putative protein similarity to predicted p	---	AT5G12340	9.23	3.21	7.85	0.000126	0.010010	1.74
258957_at	feebly-like protein contains similarity to f	DOX1	AT3G01420	2.47	1.30	7.83	0.000129	0.010094	1.72
253669_at	dihydropteroate synthase-like protein p	---	AT4G30000	-1.79	-0.84	-7.83	0.000129	0.010094	1.72
260922_at	hypothetical protein predicted by genem	---	AT1G21560	-1.84	-0.88	-7.83	0.000129	0.010094	1.72
255521_at	putative sucrose synthetase similar to s	SUS3	AT4G02280	2.76	1.46	7.82	0.000129	0.010111	1.71
263851_at	putative retroelement pol polyprotein	---	---	5.21	2.38	7.79	0.000132	0.010244	1.69
265998_at	putative NADP-dependent glyceraldehy	ALDH11A3	AT2G24270	-1.94	-0.96	-7.80	0.000132	0.010244	1.69
264047_at	hypothetical protein predicted by gensca	---	AT2G22410	-1.85	-0.88	-7.77	0.000134	0.010330	1.68
259658_at	hypothetical protein predicted by genem	NDF5	AT1G55370	-2.50	-1.32	-7.78	0.000134	0.010330	1.68
251200_at	putative protein PrMC3, Pinus radiata,	GID1B	AT3G63010	2.24	1.16	7.67	0.000145	0.010473	1.60
266993_at	nodulin-like protein ; supported by cDNA	---	AT2G39210	3.09	1.63	7.71	0.000141	0.010473	1.62
265067_at	hypothetical protein predicted by genefin	---	AT1G03850	7.27	2.86	7.67	0.000146	0.010473	1.59
251472_at	putative protein nodule inception protei	---	AT3G59580	-1.77	-0.82	-7.64	0.000149	0.010473	1.57
256661_at	hypothetical protein similar to putative p	---	AT3G11964	-1.77	-0.83	-7.64	0.000149	0.010473	1.57
250217_at	nodulin-like protein	---	AT5G14120	2.33	1.22	7.71	0.000142	0.010473	1.62
254187_at	putative protein hypothetical protein, Sy	---	AT4G23890	-1.68	-0.75	-7.63	0.00015	0.010473	1.56
255446_at	hypothetical protein similar to A. thalian	---	AT4G02750	-1.96	-0.97	-7.64	0.00015	0.010473	1.57
262937_at	FtsH protease, putative contains similar	FTSH12	AT1G79560	-1.71	-0.78	-7.69	0.000143	0.010473	1.61
260100_at	Expressed protein ; supported by full-ler	BNS	AT1G73177	-1.69	-0.75	-7.70	0.000142	0.010473	1.62
262162_at	unknown protein ;supported by full-lengt	---	AT1G78020	-2.28	-1.19	-7.67	0.000145	0.010473	1.59
260058_at	unknown protein ; supported by cDNA:	---	AT1G78100	-1.94	-0.96	-7.64	0.000149	0.010473	1.57
260968_at	hypothetical protein predicted by genem	---	AT1G12250	-2.06	-1.05	-7.71	0.000141	0.010473	1.62
249510_at	putative protein similar to unknown prote	---	AT5G38510	-1.90	-0.93	-7.66	0.000147	0.010473	1.58
253020_at	hypothetical protein	---	AT4G38020	-2.25	-1.17	-7.64	0.000149	0.010473	1.57
267361_at	hypothetical protein predicted by gensca	---	AT2G39920	-2.83	-1.50	-7.68	0.000144	0.010473	1.60
244940_at	ribosomal protein S12 (trans-splice part	---	---	-2.11	-1.08	-7.64	0.000149	0.010473	1.57

248298_at	putative protein similar to unknown prote	---	AT5G53110	2.75	1.46	7.64	0.00015	0.010473	1.56
253218_at	subtilisin-like serine protease similar to	SLP2	AT4G34980	-3.36	-1.75	-7.65	0.000148	0.010473	1.57
260385_at	putative flavonol sulfotransferase similar	SOT18	AT1G74090	-2.13	-1.09	-7.73	0.000139	0.010473	1.64
264185_at	unknown protein ;supported by full-lengt	---	AT1G54780	-1.80	-0.84	-7.71	0.000141	0.010473	1.63
265670_s_a	unknown protein ;supported by full-leng	---	AT2G32190 /	6.70	2.74	7.63	0.00015	0.010473	1.56
251766_at	putative protein PA26, p53 regulated PA	---	AT3G55890 /	1.85	0.88	7.72	0.00014	0.010473	1.63
264619_at	putative chloroplast nucleoid DNA-bindi	---	AT2G17760	1.98	0.98	7.69	0.000144	0.010473	1.61
254612_at	putative protein hypothetical protein sll0	---	AT4G19100	-1.65	-0.72	-7.64	0.000149	0.010473	1.57
255302_at	putative protein similar to transcriptional	ATMSRB5	AT4G04830	-2.43	-1.28	-7.71	0.000141	0.010473	1.63
263363_at	putative cold-regulated protein ;support	---	AT2G03850	6.06	2.60	7.67	0.000145	0.010473	1.59
265584_at	unknown protein	PIL5	AT2G20180	-1.70	-0.77	-7.65	0.000148	0.010473	1.58
250821_at	putative protein similar to unknown prote	---	AT5G05190	2.02	1.01	7.70	0.000142	0.010473	1.62
266110_at	putative C2H2-type zinc finger protein	AtIDD4	AT2G02080	-1.93	-0.95	-7.68	0.000145	0.010473	1.60
264800_at	hypothetical protein similar to IFA-bindin	---	AT1G08800	2.11	1.07	7.63	0.000151	0.010473	1.56
248422_at	putative protein strong similarity to unkn	YLS7	AT5G51640	1.61	0.69	7.72	0.00014	0.010473	1.63
251478_at	putative protein SF16 protein, pollen sp	IQD13	AT3G59690	1.68	0.75	7.62	0.000151	0.010475	1.55
257193_at	Expressed protein ; supported by full-ler	---	AT3G13160	-1.69	-0.76	-7.61	0.000153	0.010499	1.54
262180_at	phosphoglycerate mutase, putative sim	PGM	AT1G78050	1.74	0.80	7.61	0.000152	0.010499	1.55
252250_at	putative protein predicted protein, Arabi	---	AT3G49790	2.62	1.39	7.61	0.000153	0.010499	1.54
267256_s_a	putative serine carboxypeptidase I ;sup	scpl10	AT2G23000 /	-2.15	-1.10	-7.55	0.000161	0.010536	1.49
263236_at	putative response regulator 3 similar to	ARR4	AT1G10470	2.79	1.48	7.60	0.000154	0.010536	1.53
259884_at	hypothetical protein predicted by gensca	---	AT1G76390	1.72	0.78	7.54	0.000162	0.010536	1.48
245612_at	carnitine racemase like protein	HCD1	AT4G14440	6.94	2.79	7.53	0.000163	0.010536	1.48
256336_at	unknown protein	---	AT1G72030	-2.23	-1.15	-7.59	0.000155	0.010536	1.53
263674_at	hypothetical protein predicted by genefin	---	AT2G04790	-1.92	-0.94	-7.59	0.000155	0.010536	1.53
252468_at	starch phosphorylase H (cytosolic form	PHS2	AT3G46970	-2.23	-1.16	-7.54	0.000161	0.010536	1.49
247541_at	structural protein - like glycine-rich cell w	---	AT5G61660	-2.02	-1.01	-7.54	0.000162	0.010536	1.48
252181_at	Expressed protein ; supported by full-ler	---	AT3G50685	-1.77	-0.82	-7.56	0.000159	0.010536	1.50
258911_at	unknown protein similar to hypothetical	---	AT3G06470	1.92	0.94	7.54	0.000161	0.010536	1.49
248971_at	putative protein contains similarity to dis	---	AT5G45000	2.62	1.39	7.54	0.000162	0.010536	1.48
246099_at	blue copper binding protein ;supported	ATBCB	AT5G20230	3.06	1.62	7.58	0.000157	0.010536	1.52
252922_at	putative protein	---	AT4G39040	-1.81	-0.85	-7.57	0.000158	0.010536	1.51
262483_at	putative translation initiation factor IF2 I	FUG1	AT1G17220	-1.74	-0.80	-7.54	0.000162	0.010536	1.48
267226_at	unknown protein	---	AT2G44010	4.10	2.04	7.54	0.000162	0.010536	1.48
263477_at	putative glucosyltransferase ; supported	---	AT2G31790	-2.49	-1.31	-7.56	0.00016	0.010536	1.50

267385_at	unknown protein highly similar to GP|24	---	AT2G44380	2.85	1.51	7.57	0.000158	0.010536	1.51
257064_at	hypothetical protein predicted by genem	---	AT3G18260	2.12	1.08	7.58	0.000156	0.010536	1.52
264580_at	unknown protein EST gb|ATTS0295 cor	---	AT1G05340	3.77	1.92	7.57	0.000157	0.010536	1.51
254928_at	putative protein hypothetical protein - B	---	AT4G11410	-1.86	-0.90	-7.56	0.000159	0.010536	1.50
256170_at	receptor protein kinase, putative contai	---	AT1G51790	2.81	1.49	7.53	0.000163	0.010536	1.48
251011_at	putative protein histone H2A, garden pe	HTA12	AT5G02560	-1.71	-0.77	-7.52	0.000165	0.010574	1.47
260068_at	putative calmodulin-binding protein simi	---	AT1G73805	6.65	2.73	7.52	0.000164	0.010574	1.47
267538_at	putative DNA binding protein ; supporte	---	AT2G41870	-1.66	-0.73	-7.51	0.000165	0.010594	1.46
266575_at	putative chloroplast initiation factor 3 ;s	---	AT2G24060	-1.93	-0.95	-7.51	0.000166	0.010594	1.46
260635_at	unknown protein	---	AT1G62420 /	2.16	1.11	7.51	0.000166	0.010597	1.46
249797_at	putative protein contains similarity to rer	---	AT5G23750	-2.20	-1.14	-7.50	0.000167	0.010625	1.45
266264_at	Expressed protein ; supported by full-ler	---	AT2G27775	-1.73	-0.79	-7.49	0.000169	0.010676	1.44
258730_at	putative GTP-binding protein (ATFP8) ic	ATFP8	AT3G11730	-1.58	-0.66	-7.49	0.000169	0.010676	1.44
245026_at	ATPase III subunit	---	---	-1.70	-0.77	-7.47	0.000171	0.010682	1.43
260915_at	hypothetical protein similar to hypothetic	---	AT1G02660	4.11	2.04	7.48	0.00017	0.010682	1.43
258800_at	unknown protein predicted by genscan,	---	AT3G04550	-2.00	-1.00	-7.47	0.000171	0.010682	1.43
244993_s_a	hypothetical protein	---	---	-2.11	-1.08	-7.48	0.00017	0.010682	1.44
255488_at	putative serine/threonine protein kinase	---	AT4G02630	-2.19	-1.13	-7.46	0.000172	0.010698	1.42
246997_at	putative protein similar to unknown prote	---	AT5G67390	-2.42	-1.28	-7.46	0.000172	0.010698	1.42
256383_at	hypothetical protein ; supported by full-le	---	AT1G66820	-2.00	-1.00	-7.46	0.000173	0.010698	1.42
246947_at	cytochrome P450-like protein CYTOCH	CYP71B11	AT5G25120	-1.75	-0.81	-7.45	0.000174	0.010749	1.41
255948_at	hypothetical protein predicted by gensca	---	AT1G22060	-1.64	-0.71	-7.45	0.000174	0.010749	1.41
263228_at	putative reticuline oxidase-like protein s	---	AT1G30700	3.21	1.68	7.44	0.000175	0.010770	1.40
261242_at	subtilisin-like serine protease contains s	SBT3.3	AT1G32960	2.83	1.50	7.43	0.000177	0.010787	1.39
255662_at	putative protein	GPAT8	AT4G00400	3.36	1.75	7.42	0.000179	0.010787	1.38
254527_at	putative protein KIAA0682 protein, Hom	---	AT4G19610	-1.60	-0.68	-7.44	0.000176	0.010787	1.40
248680_at	pantoate-beta-alanine ligase ;supporte	PANC	AT5G48840	-1.94	-0.96	-7.42	0.000178	0.010787	1.39
248713_at	putative protein contains similarity to jas	NSP5	AT5G48180	3.76	1.91	7.43	0.000177	0.010787	1.39
251524_at	3-isopropylmalate dehydratase-like prot	---	AT3G58980 /	-3.75	-1.91	-7.42	0.000178	0.010787	1.38
266293_at	putative tropinone reductase ;supporte	---	AT2G29360	-1.73	-0.79	-7.42	0.000178	0.010787	1.38
255647_at	Ca2+-transporting ATPase - like protein	ECA2	AT4G00900	2.08	1.06	7.39	0.000182	0.010817	1.36
265828_at	hypothetical protein predicted by gensca	---	AT2G14520	-1.69	-0.76	-7.39	0.000183	0.010817	1.36
259081_at	putative sodium proton exchanger simila	NHX2	AT3G05030	-2.07	-1.05	-7.38	0.000184	0.010817	1.35
259838_at	unknown protein ;supported by full-lengt	---	AT1G52220	-1.66	-0.74	-7.36	0.000187	0.010817	1.33
258993_at	putative chlorophyll a/b-binding protein	LHCB4.2	AT3G08940	-1.98	-0.99	-7.38	0.000184	0.010817	1.35

257856_at	hypothetical protein predicted by gensc	---	AT3G12930	-1.63	-0.70	-7.38	0.000184	0.010817	1.35
254564_at	neoxanthin cleavage enzyme-like prote	NCED4	AT4G19170	-2.69	-1.43	-7.35	0.000189	0.010817	1.33
248792_at	ras-related small GTP-binding protein-lik	ATRAB1A	AT5G47200	1.85	0.89	7.35	0.000189	0.010817	1.33
255080_at	arabinogalactan-protein homolog arabir	AGP10	AT4G09030	2.83	1.50	7.37	0.000185	0.010817	1.35
251712_at	putative protein non-consensus TT don	---	AT3G56120	-1.64	-0.71	-7.38	0.000184	0.010817	1.35
247486_at	putative protein	---	AT5G62140	-2.48	-1.31	-7.36	0.000187	0.010817	1.33
247059_at	UTP-glucose glucosyltransferase ;supp	UGT72E2	AT5G66690	1.76	0.82	7.35	0.000188	0.010817	1.33
264543_at	hypothetical protein predicted by genem	---	AT1G55780	2.08	1.06	7.36	0.000188	0.010817	1.33
259863_at	hypothetical protein ;supported by full-le	ELF4-L2	AT1G72630	-1.75	-0.80	-7.37	0.000187	0.010817	1.34
255456_at	hypothetical protein ;supported by full-le	---	AT4G02920	-1.79	-0.84	-7.37	0.000185	0.010817	1.35
246799_at	putative protein various predicted bacter	---	AT5G26940	2.23	1.16	7.36	0.000188	0.010817	1.33
266277_at	putative tropinone reductase	---	AT2G29310	-1.91	-0.94	-7.38	0.000184	0.010817	1.35
251497_at	putative protein phytochrome-associate	PIL6	AT3G59060	-1.90	-0.93	-7.35	0.000189	0.010817	1.33
247571_at	snap25a ;supported by full-length cDNA	SNAP33	AT5G61210	1.66	0.73	7.35	0.000189	0.010817	1.33
247040_at	anthranilate N-hydroxycinnamoyl/benzo	---	AT5G67150	-2.13	-1.09	-7.38	0.000185	0.010817	1.35
265674_at	unknown protein ; supported by full-leng	---	AT2G32190	6.50	2.70	7.33	0.000192	0.010990	1.31
253812_at	putative wound induced protein wound-	---	AT4G28240	-1.99	-0.99	-7.32	0.000193	0.010996	1.30
250751_at	glucuronosyl transferase-like protein	---	AT5G05890	-1.94	-0.96	-7.31	0.000194	0.011035	1.29
258475_at	putative tyrosyl-tRNA synthetase similar	emb2768	AT3G02660	-1.71	-0.77	-7.31	0.000194	0.011035	1.30
250523_at	putative protein strong similarity to unkn	---	AT5G08510	-1.61	-0.68	-7.29	0.000199	0.011164	1.27
255028_at	putative protein Arabidopsis thaliana ch	PMP	AT3G24160 /	-3.42	-1.77	-7.29	0.000199	0.011164	1.27
261300_at	hypothetical protein predicted by genem	---	AT1G48560	-1.93	-0.95	-7.29	0.000198	0.011164	1.28
257253_at	unknown protein ; supported by cDNA:	---	AT3G24190	-1.88	-0.91	-7.29	0.000198	0.011164	1.28
253061_at	putative protein SPOP, Homo sapiens,	BT5	AT4G37610	2.90	1.54	7.28	0.0002	0.011187	1.27
259848_at	leucine-rich receptor-like protein kinase	---	AT1G72180	-2.08	-1.05	-7.27	0.000201	0.011230	1.26
252862_at	putative L-ascorbate oxidase L-ascorba	---	AT4G39830	4.79	2.26	7.27	0.000201	0.011230	1.26
256981_at	brassinosteroid receptor kinase, putativ	BRL3	AT3G13380	2.61	1.38	7.27	0.000202	0.011230	1.26
260696_at	unknown protein	---	AT1G32520	-1.86	-0.89	-7.25	0.000205	0.011234	1.24
264693_at	hypothetical protein predicted by genem	CLE26	AT1G69970	-1.76	-0.81	-7.26	0.000204	0.011234	1.25
254075_at	DRE CRT-binding protein DREB1C invo	CBF2	AT4G25470	-2.72	-1.44	-7.26	0.000203	0.011234	1.25
261118_at	protease, putative similar to SP:P36774	---	AT1G75460	-1.81	-0.86	-7.26	0.000203	0.011234	1.25
249346_at	amino acid permease	LTH1	AT5G40780	2.07	1.05	7.25	0.000205	0.011234	1.24
266672_at	putative Na+-dependent inorganic phos	PHT4;1	AT2G29650	-1.74	-0.80	-7.26	0.000204	0.011234	1.25
255583_at	hypothetical protein similar to C. elegan	ARV2	AT4G01510	-1.91	-0.93	-7.24	0.000206	0.011256	1.23
250257_at	putative protein similar to unknown prote	---	AT5G13770	-1.97	-0.98	-7.25	0.000206	0.011256	1.24

254869_at	protein kinase - like protein KI domain i	---	AT4G11890	3.83	1.94	7.24	0.000207	0.011296	1.23
246927_s_a	nodulin - like protein nodulin, Glycine m	---	AT5G25250 /	2.71	1.44	7.23	0.000208	0.011315	1.22
250441_at	oligopeptidase A - like protein oligopept	---	AT5G10540	-1.60	-0.68	-7.23	0.000209	0.011347	1.22
263866_at	putative farnesylated protein ;supported	---	AT2G36950	2.54	1.35	7.21	0.000212	0.011392	1.21
264512_at	Expressed protein ; supported by cDNA	---	AT1G09575	1.91	0.93	7.21	0.000212	0.011392	1.20
261973_at	hypothetical protein predicted by genem	---	AT1G64610	2.38	1.25	7.20	0.000214	0.011392	1.20
259625_at	glyceraldehyde-3-phosphate dehydroge	GAPB	AT1G42970	-2.06	-1.04	-7.20	0.000213	0.011392	1.20
264938_at	unknown protein contains similarity to S	---	AT1G60610	1.80	0.85	7.20	0.000214	0.011392	1.20
247216_at	4-alpha-glucanotransferase ; supported	DPE1	AT5G64860	-2.20	-1.13	-7.21	0.000213	0.011392	1.20
258607_at	thioredoxin f1 identical to thioredoxin f1	TRXF1	AT3G02730	-2.10	-1.07	-7.21	0.000213	0.011392	1.20
253140_at	RING-H2 finger protein RHA3b ;suppor	RHA3B	AT4G35480	2.05	1.04	7.20	0.000213	0.011392	1.20
250415_at	putative protein GLUR3 ligand-gated ch	GLR2.5	AT5G11210	6.26	2.65	7.20	0.000215	0.011393	1.19
251336_at	putative protein hypothetical protein F4	BAP1	AT3G61190	3.50	1.81	7.18	0.000217	0.011447	1.18
255742_at	DNA-binding protein RAV2, putative sin	TEM1	AT1G25560	1.69	0.76	7.18	0.000218	0.011447	1.18
264365_s_a	unknown protein Strong similarity to gb	---	AT1G03220 /	4.33	2.11	7.19	0.000216	0.011447	1.18
250005_at	putative protein predicted proteins, Ara	---	AT5G18760	-1.66	-0.73	-7.18	0.000218	0.011447	1.18
267505_at	putative cytochrome P450 ;supported b	CYP76C1	AT2G45560	-1.94	-0.96	-7.18	0.000218	0.011447	1.18
245150_at	photolyase/blue-light receptor (PHR2) ;	PHR2	AT2G47590	-1.95	-0.97	-7.17	0.000219	0.011469	1.17
245349_at	cyanohydrin lyase like protein ;supporte	MES16	AT4G16690	3.67	1.88	7.17	0.00022	0.011477	1.17
245027_at	heme oxygenase 2 (HO2)	HO2	AT2G26550	-1.74	-0.80	-7.16	0.000222	0.011554	1.16
264099_at	replicase, putative similar to replicase G	---	AT1G79050	-1.82	-0.86	-7.14	0.000225	0.011648	1.15
250243_at	cobalamin biosynthesis protein	GUN5	AT5G13630	-2.21	-1.14	-7.14	0.000226	0.011648	1.14
255436_at	Expressed protein ; supported by cDNA	---	AT4G03150	-1.56	-0.64	-7.14	0.000226	0.011648	1.14
260199_at	unknown protein similar to putative DNA	---	AT1G67590	-1.66	-0.73	-7.14	0.000225	0.011648	1.14
254597_at	hypothetical protein	---	AT4G18980	2.35	1.23	7.13	0.000228	0.011722	1.13
259275_at	unknown protin ;supported by full-lengt	---	AT3G01060	-2.74	-1.45	-7.12	0.000228	0.011722	1.13
257940_at	putative UDP-glucose glucosyltransfera	---	AT3G21790	2.02	1.01	7.12	0.000229	0.011730	1.13
260203_at	NAM-like protein similar to NAM (no api	ANAC019	AT1G52890	2.82	1.50	7.11	0.00023	0.011770	1.12
259751_at	putative transcription factor similar to my	MYBL2	AT1G71030	-1.79	-0.84	-7.11	0.000231	0.011773	1.12
265029_at	zinc finger protein 7, ZFP7 ; supported	ZFP7	AT1G24625	-2.21	-1.15	-7.10	0.000232	0.011834	1.11
246809_s_a	SAR DNA-binding protein - like SAR DN	---	AT5G27120 /	-1.56	-0.64	-7.09	0.000235	0.011837	1.10
261951_at	hypothetical protein predicted by genem	---	AT1G64490	-1.78	-0.83	-7.10	0.000234	0.011837	1.11
257891_at	hypothetical protein predicted by genem	RFC3	AT3G17170	-2.45	-1.29	-7.07	0.000239	0.011837	1.08
263912_at	starch branching enzyme II	SBE2.1	AT2G36390	-2.10	-1.07	-7.08	0.000237	0.011837	1.09
258333_at	myosin heavy chain-like protein similar t	MFP1	AT3G16000	-1.78	-0.83	-7.07	0.000238	0.011837	1.09

263761_at	putative fructose bisphosphate aldolase	---	AT2G21330	-2.18	-1.12	-7.07	0.000238	0.011837	1.09
258027_at	hypothetical protein predicted by genem	---	AT3G19515	-1.76	-0.82	-7.08	0.000237	0.011837	1.09
265943_at	putative cytidine deaminase ;supported	CDA1	AT2G19570	3.30	1.72	7.08	0.000236	0.011837	1.09
253692_at	putative protein Cs protein, Drosophila	ATPAO5	AT4G29720	-1.58	-0.66	-7.08	0.000237	0.011837	1.09
264959_at	hypothetical protein predicted by genem	---	AT1G77090	-1.91	-0.93	-7.09	0.000236	0.011837	1.10
244998_at	RNA polymerase beta' subunit-1	---	---	-2.16	-1.11	-7.09	0.000235	0.011837	1.10
264839_at	putative protochlorophyllide reductase s	POR C	AT1G03630	-2.26	-1.17	-7.07	0.000239	0.011837	1.08
266120_at	putative C2H2-type zinc finger protein ;	AtIDD5	AT2G02070	-1.84	-0.88	-7.10	0.000234	0.011837	1.11
250485_at	Expressed protein ; supported by full-ler	PROPEP5	AT5G09990	-2.75	-1.46	-7.05	0.000242	0.011853	1.07
262220_at	calcium-dependent protein kinase, puta	CPK30	AT1G74740	1.65	0.72	7.05	0.000242	0.011853	1.07
259087_at	hypothetical protein, contains DnaJ mot	---	AT3G04980	-1.57	-0.65	-7.05	0.000242	0.011853	1.07
260567_at	putative glucosyltransferase ;supported	UGT74F2	AT2G43820	2.43	1.28	7.06	0.00024	0.011853	1.08
248124_at	putative protein contains similarity to unl	ATG18F	AT5G54730	1.85	0.88	7.06	0.000242	0.011853	1.07
246371_at	unknown protein contains similarity to pr	---	AT1G51940	-1.86	-0.89	-7.05	0.000244	0.011901	1.06
263412_at	putative histone H2B ;supported by full-	---	AT2G28720	-1.74	-0.80	-7.04	0.000246	0.011924	1.05
257932_at	unknown protein contains Pfam profile:	HCF107	AT3G17040	-1.90	-0.93	-7.03	0.000246	0.011924	1.05
254398_at	photosystem II oxygen-evolving comple	PSBQA	AT4G21280	-1.83	-0.87	-7.04	0.000245	0.011924	1.06
258573_at	hypothetical protein contains Pfam profil	PTAC3	AT3G04260	-1.60	-0.68	-7.04	0.000246	0.011924	1.05
257746_at	chorismate mutase identical to chorisma	CM1	AT3G29200	1.65	0.73	7.02	0.000248	0.011929	1.04
255904_at	lemir (miraculin), putative similar to lem	---	AT1G17860	2.07	1.05	7.03	0.000248	0.011929	1.04
248510_at	Expressed protein ; supported by full-ler	---	---	-1.58	-0.66	-7.03	0.000247	0.011929	1.05
258919_at	Expressed protein ; supported by full-ler	---	AT3G10525	-2.08	-1.06	-7.02	0.000248	0.011929	1.04
262671_at	calcium-dependent protein kinase, puta	CPK29	AT1G76040	2.11	1.07	7.02	0.000249	0.011946	1.04
260209_at	putative AP2 domain transcription factor	CPuORF5	AT1G68550 /	-1.87	-0.90	-7.01	0.000251	0.011983	1.03
263953_at	hypothetical protein predicted by genefir	OFP15	AT2G36050	-2.89	-1.53	-7.00	0.000253	0.012005	1.02
261838_at	heat shock protein hsp70, putative simi	Hsp70b	AT1G16030	-1.75	-0.81	-6.98	0.000258	0.012005	1.00
246943_at	putative protein kinase serine/threonine	---	AT5G25440	2.46	1.30	6.97	0.00026	0.012005	0.99
264506_at	germin-like protein Identical to Arabidop	GLP5	AT1G09560	1.91	0.93	6.98	0.000259	0.012005	1.00
259138_s_a	putative DNA gyrase subunit B similar to	---	AT3G10270 /	-1.80	-0.84	-6.97	0.000261	0.012005	0.99
259768_at	expressed protein supported by cDNA: (	COR314-T	AT1G29390	-1.53	-0.61	-6.97	0.00026	0.012005	0.99
260283_at	hypothetical protein predicted by gensc	PTAC17	AT1G80480	-1.56	-0.64	-6.98	0.000257	0.012005	1.01
261746_at	unknown protein ;supported by full-lengt	PSAO	AT1G08380	-1.62	-0.70	-6.99	0.000256	0.012005	1.01
266636_at	glycine decarboxylase complex H-protei	GDCH	AT2G35370	-1.88	-0.91	-6.98	0.000258	0.012005	1.00
252179_at	putative protein UDP-glucose:(glucosyl	GATL2	AT3G50760	2.34	1.23	6.97	0.00026	0.012005	1.00
253647_at	putative protein KIAA0210 gene, Homo	---	AT4G29950	1.94	0.96	6.98	0.000257	0.012005	1.01

259351_at	putative sugar transporter similar to put	---	AT3G05150	1.72	0.78	7.00	0.000253	0.012005	1.02
246154_at	putative protein predicted protein, Arabi	---	AT5G19940	-1.73	-0.79	-6.97	0.00026	0.012005	1.00
256746_at	alpha-glucan phosphorylase, putative s	---	AT3G29320	-2.29	-1.19	-6.99	0.000255	0.012005	1.01
251181_at	putative protein pectinesterase homolog	---	AT3G62820	-2.07	-1.05	-6.99	0.000255	0.012005	1.02
244996_at	ribosomal protein S2	---	---	-1.87	-0.91	-6.98	0.000258	0.012005	1.00
255809_at	putative protein predicted protein, Arabi	---	AT4G10300	-1.90	-0.92	-6.97	0.000261	0.012005	0.99
254271_at	serine/threonine kinase - like protein KI	---	AT4G23150	3.55	1.83	6.98	0.000258	0.012005	1.00
259038_at	unknown protein predicted by genscan;	PTAC13	AT3G09210	-1.78	-0.83	-7.00	0.000254	0.012005	1.02
265571_s_a	unknown protein	---	AT2G28020 /	-1.66	-0.74	-6.96	0.000262	0.012017	0.99
259835_at	unknown protein	TRZ3	AT1G52160	-1.70	-0.76	-6.95	0.000264	0.012031	0.98
250969_at	putative protein ;supported by full-lengt	---	AT5G02740	-1.68	-0.75	-6.95	0.000264	0.012031	0.98
257044_at	hypothetical protein predicted by gensca	ARC5	AT3G19720	-1.98	-0.99	-6.96	0.000263	0.012031	0.98
249866_at	2-isopropylmalate synthase-like; homoc	MAM1	AT5G23010	-3.11	-1.64	-6.94	0.000266	0.012103	0.97
257763_s_a	disease resistance protein, putative sim	AtRLP37	AT3G23110 /	5.32	2.41	6.94	0.000267	0.012131	0.97
265253_at	putative peptide/amino acid transporter	---	AT2G02020	-1.62	-0.70	-6.93	0.000269	0.012194	0.96
249472_at	hypothetical protein ;supported by full-le	CRR7	AT5G39210	-2.67	-1.42	-6.93	0.00027	0.012219	0.96
258292_at	hypothetical protein predicted by genem	---	AT3G23330	-1.93	-0.95	-6.92	0.000271	0.012230	0.95
245201_at	F12A21.3 unknown protein; similar to E	CSK	AT1G67840	-1.81	-0.86	-6.92	0.000272	0.012239	0.95
251804_at	beta-1,3-glucanase - like protein probat	---	AT3G55430	2.21	1.14	6.92	0.000273	0.012261	0.95
267061_at	unknown protein ;supported by full-leng	---	AT2G32480	-1.71	-0.77	-6.91	0.000274	0.012261	0.94
253791_at	early auxin-inducible protein 11 (IAA11)	IAA11	AT4G28640	-2.02	-1.02	-6.91	0.000274	0.012261	0.94
249494_at	acyltransferase - like protein Anthocyan	---	AT5G39050	3.78	1.92	6.89	0.000278	0.012298	0.92
250787_at	meiotic check point regulator-like protein	EMB2771	AT5G05560	-1.66	-0.73	-6.90	0.000278	0.012298	0.93
246829_at	putative protein pyruvate water dikinase	ATGWD3	AT5G26570	-1.65	-0.72	-6.90	0.000276	0.012298	0.93
259761_at	putative acyl-CoA synthetase similar to I	LACS9	AT1G77590	2.27	1.18	6.90	0.000276	0.012298	0.93
263177_at	hypothetical protein predicted by genem	---	AT1G05540	-1.70	-0.76	-6.90	0.000277	0.012298	0.93
251230_at	beta-glucosidase-like protein several be	BGLU8	AT3G62750	-1.59	-0.67	-6.90	0.000277	0.012298	0.93
248149_at	Expressed protein ; supported by full-ler	---	AT5G54855	-1.64	-0.71	-6.89	0.000278	0.012298	0.92
250582_at	transcription factor-like protein ethylene	---	AT5G07580	-3.01	-1.59	-6.89	0.00028	0.012332	0.92
264031_at	unknown protein	---	AT2G03780	-1.93	-0.95	-6.88	0.00028	0.012349	0.92
262175_at	unknown protein ; supported by cDNA: g	NDH-O	AT1G74880	-2.11	-1.08	-6.87	0.000283	0.012425	0.91
249230_at	putative protein similar to unknown prote	---	AT5G42070	-1.98	-0.99	-6.87	0.000284	0.012439	0.90
263706_s_a	3-methyladenine DNA glycosylase, puta	---	AT1G31180 /	-2.51	-1.33	-6.84	0.00029	0.012615	0.88
262369_at	hypothetical protein predicted by genem	---	AT1G73010	10.46	3.39	6.84	0.000291	0.012615	0.88
255600_s_a	putative protein predicted protein, Arabi	---	AT4G01020 /	-1.59	-0.67	-6.84	0.000291	0.012615	0.88

264201_at	unknown protein ;supported by full-lengt	---	AT1G22630	-2.33	-1.22	-6.84	0.00029	0.012615	0.88
257401_at	hypothetical protein identical to hypothe	SRO2	AT1G23550	2.03	1.02	6.85	0.000289	0.012615	0.89
260793_at	unknown protein ;supported by full-lengt	---	AT1G06190	-1.73	-0.79	-6.84	0.00029	0.012615	0.88
255457_at	putative photosystem I reaction center s	PSAD-1	AT4G02770	-1.56	-0.64	-6.84	0.000291	0.012615	0.88
258935_at	unknown protein predicted by genscan-	---	AT3G10120	-2.70	-1.43	-6.83	0.000293	0.012642	0.87
257236_at	hypothetical protein	---	AT3G15095	-2.02	-1.01	-6.83	0.000294	0.012682	0.87
245094_at	4-alpha-glucanotransferase	DPE2	AT2G40840	-2.01	-1.00	-6.82	0.000296	0.012760	0.86
265139_at	unknown protein	---	AT1G51310	-1.91	-0.93	-6.82	0.000297	0.012762	0.86
256813_at	unknown protein	---	AT3G21360	-1.76	-0.82	-6.81	0.000298	0.012762	0.85
267592_at	unknown protein similar to GP 2245012	---	AT2G39710	1.57	0.65	6.81	0.0003	0.012814	0.85
266884_at	phytocyanin identical to GB:U90428; su	UCC2	AT2G44790	4.59	2.20	6.79	0.000305	0.012814	0.83
263433_at	putative myo-inositol 1-phosphate synth	MIPS2	AT2G22240	-2.31	-1.21	-6.78	0.000306	0.012814	0.82
258953_at	hypothetical protein predicted by gensca	---	AT3G01430	1.90	0.93	6.79	0.000305	0.012814	0.83
254649_at	pherophorin - like protein pherophorin-S	---	AT4G18570	-1.82	-0.86	-6.78	0.000307	0.012814	0.82
260799_at	UDP-glucose glucosyltransferase, puta	AtUGT85A	AT1G78270	-1.90	-0.92	-6.79	0.000304	0.012814	0.83
254524_at	hypothetical protein	---	AT4G20000	6.71	2.75	6.78	0.000306	0.012814	0.82
248230_at	putative protein similar to unknown prote	---	AT5G53830	2.97	1.57	6.78	0.000306	0.012814	0.83
262247_at	unknown protein contains similarity to 1-	D-CDES	AT1G48420	-1.69	-0.76	-6.78	0.000306	0.012814	0.83
246860_at	putative protein various predicted prote	---	AT5G25840	-4.36	-2.12	-6.78	0.000307	0.012814	0.82
257205_at	putative glucosyltransferase similar to U	UGT88A1	AT3G16520	-1.68	-0.75	-6.79	0.000305	0.012814	0.83
261934_at	UDP-glucose glucosyltransferase, puta	UGT85A1	AT1G22400	5.02	2.33	6.80	0.000301	0.012814	0.84
258173_at	putative protein kinase similar to serine	CERK1	AT3G21630	1.73	0.79	6.80	0.000301	0.012814	0.84
254244_at	putative protein S-receptor kinase 8 pre	---	AT4G23230	1.89	0.92	6.80	0.000303	0.012814	0.84
256932_at	unknown protein	---	AT3G22520	-1.65	-0.72	-6.77	0.000309	0.012858	0.82
251021_at	thaumatin-like protein thaumatin-like pr	---	AT5G02140	2.74	1.45	6.77	0.000309	0.012858	0.82
245794_at	endoxyloglucan transferase, putative si	XTR4	AT1G32170	2.01	1.01	6.77	0.00031	0.012863	0.81
265728_at	hypothetical protein predicted by gensca	---	AT2G31990	2.10	1.07	6.77	0.000311	0.012863	0.81
255720_at	phosphoribulokinase precursor identical	PRK	AT1G32060	-1.76	-0.82	-6.77	0.000311	0.012863	0.81
246631_at	unknown protein ; supported by full-leng	---	AT1G50740	1.65	0.72	6.76	0.000311	0.012867	0.81
261292_at	hypothetical protein predicted by genem	---	AT1G36940	-1.88	-0.91	-6.76	0.000312	0.012870	0.81
253558_at	kinase binding protein - like Skb1 protei	SKB1	AT4G31120	-1.84	-0.88	-6.76	0.000313	0.012871	0.80
261769_at	plastocyanin identical to plastocyanin G	PETE1	AT1G76100	-1.93	-0.95	-6.75	0.000314	0.012900	0.80
244979_at	ribosomal protein S11	---	---	-1.53	-0.62	-6.75	0.000315	0.012911	0.80
248968_at	pectin acetylesterase ;supported by full	---	AT5G45280	3.01	1.59	6.72	0.000323	0.012988	0.77
260292_at	putative UDP-N-acetylmuramoylalanyl-	MURE	AT1G63680	-1.52	-0.60	-6.73	0.000321	0.012988	0.78

263049_at	unknown protein ;supported by full-leng	---	AT2G05260	1.73	0.79	6.72	0.000322	0.012988	0.77
250753_at	glucuronosyl transferase-like protein ; s	UGT76C2	AT5G05860	2.02	1.01	6.74	0.000317	0.012988	0.79
260902_at	hypothetical protein similar to carboxyvi	---	AT1G21440	-2.59	-1.37	-6.73	0.000322	0.012988	0.77
247450_at	ripening-related protein - like ripening-r	---	AT5G62350	-1.99	-0.99	-6.73	0.000321	0.012988	0.78
265965_at	putative glutamate/ornithine acetyltransf	---	AT2G37500	-1.76	-0.82	-6.74	0.000318	0.012988	0.79
258554_at	putative DEAD/DEAH box helicase cont	---	AT3G06980	-1.63	-0.70	-6.73	0.000322	0.012988	0.77
263014_at	unknown protein similar to hypothetical	CAF2	AT1G23400	-1.72	-0.78	-6.72	0.000322	0.012988	0.77
261090_at	protein kinase, putative contains Pfam	---	AT1G07560	1.87	0.90	6.73	0.000321	0.012988	0.78
256156_at	phosphoinositide specific phospholipase	ATPLC2	AT3G08510	-1.68	-0.75	-6.73	0.000321	0.012988	0.78
245050_at	PSII K protein	---	---	-1.51	-0.60	-6.72	0.000324	0.013006	0.77
261891_at	transcriptional regulator, putative simila	---	AT1G80790	-1.56	-0.64	-6.72	0.000325	0.013009	0.76
253473_at	putative protein mixed-lineage protein k	---	AT4G32250	2.80	1.49	6.71	0.000326	0.013010	0.76
259591_at	unknown protein ;supported by full-lengt	---	AT1G28150	-1.50	-0.59	-6.71	0.000326	0.013010	0.76
252367_at	putative protein MEL-26, Caenorhabditi	BT2	AT3G48360	5.83	2.54	6.71	0.000326	0.013010	0.76
263053_at	similar to glucose inhibited division prote	---	AT2G13440	-1.74	-0.80	-6.71	0.000327	0.013033	0.76
254255_at	serine/threonine kinase - like protein se	---	AT4G23220	4.33	2.11	6.70	0.000329	0.013082	0.75
251355_at	putative protein hypothetical protein T1	---	AT3G61100	-1.99	-0.99	-6.69	0.000331	0.013129	0.74
251321_at	RING finger protein ;supported by full-le	BRH1	AT3G61460	-2.34	-1.23	-6.69	0.000333	0.013195	0.74
263676_at	putative RNA-binding protein Identical t	CRB	AT1G09340	-2.07	-1.05	-6.67	0.000338	0.013354	0.72
256356_s_a	hypothetical protein	---	AT1G66500 /	1.79	0.84	6.67	0.000338	0.013354	0.72
267178_at	unknown protein ; supported by full-leng	---	AT2G37750	8.36	3.06	6.66	0.00034	0.013363	0.71
244972_at	PSII 47KDa protein	---	---	-3.96	-1.99	-6.67	0.000339	0.013363	0.72
264317_at	spermidine synthase, putative similar to	SPDS2	AT1G70310	-1.70	-0.77	-6.66	0.000341	0.013363	0.71
252409_at	putative protein bundle sheath defective	---	AT3G47650	-1.72	-0.78	-6.66	0.000341	0.013363	0.71
259878_at	putative catechol O-methyltransferase s	---	AT1G76790	-3.31	-1.73	-6.65	0.000345	0.013376	0.70
251278_at	putative protein hypothetical protein - A	emb1703	AT3G61780	-1.84	-0.88	-6.65	0.000346	0.013376	0.70
247187_at	putative protein similar to unknown prote	---	AT5G65490	-1.68	-0.75	-6.65	0.000344	0.013376	0.70
247357_at	receptor-like protein kinase ; supported	---	AT5G63710	-1.73	-0.79	-6.65	0.000345	0.013376	0.70
252084_at	wax synthase-like protein wax synthase	AtSAT1	AT3G51970	1.94	0.95	6.64	0.000346	0.013376	0.70
267089_at	unknown protein	---	AT2G38300	-2.03	-1.02	-6.66	0.000343	0.013376	0.71
255857_at	unknown protein ;supported by full-lengt	ABA4	AT1G67080	-1.56	-0.64	-6.64	0.000347	0.013376	0.70
262879_at	plastid RNA polymerase sigma-subunit	SIGA	AT1G64860	-1.79	-0.84	-6.64	0.000347	0.013376	0.69
262784_at	unknown protein strong similarity to gbl	SEX1	AT1G10760	-2.32	-1.21	-6.66	0.000343	0.013376	0.71
248459_at	putative protein similar to unknown prote	CRL	AT5G51020	-1.70	-0.76	-6.65	0.000345	0.013376	0.70
262539_at	unknown protein Location of est 136A23	---	AT1G17200	-2.17	-1.12	-6.64	0.000348	0.013382	0.69

252010_at	hypothetical protein ; supported by cDN	---	AT3G52740	-2.01	-1.01	-6.64	0.000349	0.013388	0.69
262942_at	hypothetical protein similar to unknown	ALIS5	AT1G79450	3.89	1.96	6.63	0.00035	0.013393	0.69
247891_at	GTP binding protein-like	---	AT5G57960	-1.68	-0.75	-6.63	0.00035	0.013393	0.69
248449_at	putative protein similar to unknown prote	---	AT5G51110	-1.58	-0.66	-6.63	0.000351	0.013393	0.68
245797_at	defective chloroplasts and leaves (DCL	---	AT1G45230	-1.48	-0.56	-6.62	0.000352	0.013394	0.68
261230_at	beta tubulin 1, putative similar to GB:AA	TUB5	AT1G20010	-1.63	-0.70	-6.62	0.000353	0.013394	0.68
267462_at	Expressed protein ; supported by full-ler	---	AT2G33735	-2.64	-1.40	-6.62	0.000353	0.013394	0.68
244935_at	NADH dehydrogenase subunit	---	---	-1.64	-0.71	-6.63	0.000352	0.013394	0.68
248956_at	unknown protein	---	AT5G45610	-1.73	-0.79	-6.61	0.000356	0.013405	0.67
262699_at	unknown protein	---	AT1G75980	-1.72	-0.78	-6.61	0.000356	0.013405	0.67
264186_at	hypothetical protein predicted by genem	---	AT1G54570	3.98	1.99	6.62	0.000355	0.013405	0.67
260979_at	MAP kinase ATMPK9, putative similar t	ATMPK18	AT1G53510	-1.64	-0.71	-6.61	0.000356	0.013405	0.67
253335_at	putative protein YHR077c (NMD2,IFS1	---	AT4G33500	-1.79	-0.84	-6.62	0.000354	0.013405	0.67
256595_x_a	hypothetical protein	---	AT3G28530	-1.85	-0.89	-6.60	0.000361	0.013541	0.65
266078_at	putative two-component response regul	ARR16	AT2G40670	1.67	0.74	6.60	0.000361	0.013541	0.65
256999_at	hypothetical protein predicted by genem	---	AT3G14200	-1.67	-0.74	-6.59	0.000363	0.013562	0.65
246478_at	putative protein several hypothetical pro	---	AT5G15980	-1.64	-0.71	-6.59	0.000363	0.013562	0.65
254790_at	probable photosystem I chain XI precur	PSAL	AT4G12800	-1.60	-0.68	-6.59	0.000363	0.013562	0.65
264383_at	putative glutathione peroxidase Contair	ATGPX1	AT2G25080	-1.93	-0.95	-6.58	0.000366	0.013627	0.64
265884_at	unknown protein	---	AT2G42320	-1.94	-0.96	-6.58	0.000367	0.013657	0.64
245745_at	unknown protein contains similarity to ar	---	AT1G51110	-2.19	-1.13	-6.57	0.000369	0.013687	0.63
245195_at	F12A21.13 putative photosystem II Cor	PSBY	AT1G67740	-1.66	-0.74	-6.57	0.000369	0.013687	0.63
247954_at	beta-galactosidase (emb|CAB64740.1)	BGAL4	AT5G56870	1.90	0.92	6.56	0.000373	0.013739	0.62
267005_at	unknown protein ; supported by cDNA: g	---	AT2G34460	-1.68	-0.75	-6.53	0.000383	0.013739	0.59
256655_at	hypothetical protein predicted by genem	---	AT3G18890	-2.26	-1.18	-6.54	0.00038	0.013739	0.60
259791_at	unknown protein ; supported by cDNA: g	---	AT1G29700	-2.58	-1.37	-6.53	0.000383	0.013739	0.59
263410_at	predicted protein ;supported by full-leng	---	AT2G04039	-2.41	-1.27	-6.53	0.000384	0.013739	0.59
244995_at	ATPase a subunit	---	---	-2.73	-1.45	-6.55	0.000378	0.013739	0.60
260754_at	unknown protein	---	AT1G49000	3.46	1.79	6.53	0.000382	0.013739	0.59
257300_at	unknown protein ; supported by full-leng	---	AT3G28080	-2.59	-1.37	-6.54	0.000381	0.013739	0.60
254038_at	nitrogen fixation like protein nitrogen fix	NFU3	AT4G25910	-1.59	-0.67	-6.53	0.000384	0.013739	0.59
246249_at	salt-inducible like protein	---	AT4G36680	-1.93	-0.95	-6.55	0.000377	0.013739	0.61
251935_at	fructokinase - like protein fructokinase,	---	AT3G54090	-2.15	-1.11	-6.56	0.000374	0.013739	0.62
260268_at	unknown protein ;supported by full-leng	---	AT1G68490	-1.62	-0.70	-6.56	0.000373	0.013739	0.62
255227_at	D123 -like protein protein D123, Rattus	EDA35	AT4G05440	-1.97	-0.98	-6.56	0.000374	0.013739	0.62

265569_at	unknown protein ;supported by full-leng	PGR5	AT2G05620	-1.70	-0.77	-6.54	0.00038	0.013739	0.60
258495_at	unknown protein ;supported by full-leng	---	AT3G02690	-1.61	-0.68	-6.53	0.000385	0.013739	0.59
246434_at	root cap 1 (RCP1) ;supported by full-ler	RCP1	AT5G17520	-2.03	-1.02	-6.57	0.000371	0.013739	0.62
253009_at	glycine hydroxymethyltransferase like p	SHM1	AT4G37930	-2.04	-1.03	-6.56	0.000373	0.013739	0.62
256876_at	hypothetical protein predicted by genem	---	AT3G26360	-1.48	-0.57	-6.54	0.000379	0.013739	0.60
256433_at	unknown protein	SAG20	AT3G10985	2.16	1.11	6.55	0.000378	0.013739	0.61
253981_at	putative protein ;supported by full-length	---	AT4G26670	-1.61	-0.69	-6.53	0.000385	0.013739	0.59
246454_at	Expressed protein ; supported by full-ler	DHAR3	AT5G16710	-1.68	-0.75	-6.55	0.000377	0.013739	0.61
250580_at	glutamate dehydrogenase 2 ; supporte	GDH2	AT5G07440	3.33	1.74	6.54	0.000382	0.013739	0.60
260633_at	protein kinase, putative similar to protei	HT1	AT1G62400	-1.65	-0.72	-6.56	0.000375	0.013739	0.61
254697_at	putative protein predicted protein, Arabi	---	AT4G17970	-1.58	-0.66	-6.53	0.000384	0.013739	0.59
265200_s_a	putative glucosyl transferase an EST ma	UGT73C6	AT2G36790 /	3.96	1.99	6.52	0.000386	0.013745	0.58
255462_at	hypothetical protein similar to A. thalian	---	AT4G02940	2.55	1.35	6.52	0.000388	0.013761	0.58
266280_at	putative tropinone reductase	---	AT2G29260	-1.52	-0.61	-6.51	0.000389	0.013761	0.58
251008_at	putative protein ;supported by full-length	---	AT5G02710	-1.86	-0.90	-6.52	0.000388	0.013761	0.58
248981_at	regulatory protein NPR1-like; transcripti	NPR3	AT5G45110	1.69	0.76	6.52	0.000389	0.013761	0.58
250575_at	putative protein	---	AT5G08240	2.53	1.34	6.51	0.000389	0.013761	0.58
251853_at	putative protein various Arabidopsis tha	---	AT3G54790	-1.61	-0.69	-6.51	0.00039	0.013762	0.57
259535_at	hypothetical protein	---	AT1G12280	-2.15	-1.11	-6.51	0.00039	0.013762	0.57
253264_at	protein kinase - like protein protein kina	OST1	AT4G33950	-1.56	-0.64	-6.51	0.000392	0.013782	0.57
254779_at	hypothetical protein	---	AT4G12760	-1.58	-0.66	-6.50	0.000393	0.013794	0.56
262136_at	auxin response factor, putative similar t	ARF17	AT1G77850	-1.62	-0.70	-6.50	0.000393	0.013794	0.56
257848_at	hypothetical protein predicted by gensca	---	AT3G13030	-1.90	-0.92	-6.50	0.000394	0.013794	0.56
258263_at	unknown protein	---	AT3G15780	-2.51	-1.33	-6.50	0.000395	0.013803	0.56
251519_at	putative protein hypothetical protein 23	GUN4	AT3G59400	-1.98	-0.99	-6.49	0.000397	0.013828	0.55
264657_at	putative 26S protease regulatory subun	RPT5B	AT1G09100	-1.64	-0.71	-6.49	0.000398	0.013828	0.55
258120_at	hypothetical protein predicted by genma	---	AT3G14730	-1.56	-0.64	-6.49	0.000399	0.013828	0.55
255465_at	hypothetical protein similar to A. thalian	---	AT4G02990	-1.88	-0.91	-6.49	0.000398	0.013828	0.55
255718_at	unknown protein ;supported by full-lengt	ATNSI	AT1G32070	-1.70	-0.77	-6.48	0.0004	0.013828	0.55
245017_at	PSI I protein	---	---	-1.80	-0.85	-6.48	0.0004	0.013828	0.55
257066_at	lipid transfer protein, putative similar to	---	AT3G18280	3.84	1.94	6.49	0.000397	0.013828	0.56
267010_at	putative AP2 domain transcription factor	SNZ	AT2G39250	-1.91	-0.94	-6.48	0.0004	0.013828	0.55
257608_at	chaperonin, putative similar to CHAPEF	HSP60-3A	AT3G13860	-1.69	-0.76	-6.47	0.000404	0.013930	0.54
253866_at	putative protein various putative protein	---	AT4G27480	1.80	0.85	6.47	0.000405	0.013954	0.53
251447_at	U6 snRNA-associated Sm-like protein U	---	AT3G59810	-1.53	-0.61	-6.44	0.000415	0.013996	0.51

247696_at	MYB27 protein - like MYB27 protein, Ar	MYB59	AT5G59780	-3.32	-1.73	-6.45	0.000413	0.013996	0.51
261190_at	ribosomal protein L11, putative similar t	PRPL11	AT1G32990	-1.73	-0.79	-6.45	0.000412	0.013996	0.52
251936_at	putative protein crp1 protein, Zea mays	MEE40	AT3G53700	-1.90	-0.93	-6.45	0.000414	0.013996	0.51
252886_at	cellulose synthase catalytic subunit (Ath	CESA2	AT4G39350	-1.79	-0.84	-6.45	0.000414	0.013996	0.51
251360_at	putative protein embryonic abundant pr	---	AT3G61210	-1.63	-0.71	-6.46	0.000409	0.013996	0.52
246021_at	ascorbate oxidase-like protein ascorbat	---	AT5G21100	-2.29	-1.19	-6.45	0.000414	0.013996	0.51
263114_at	putative photosystem I reaction center s	PSAD-2	AT1G03130	-1.73	-0.79	-6.44	0.000415	0.013996	0.51
256309_at	photosystem I subunit X precursor ident	PSAK	AT1G30380	-1.59	-0.67	-6.46	0.00041	0.013996	0.52
263488_at	hypothetical protein predicted by gensca	---	AT2G31840	-1.99	-0.99	-6.46	0.000409	0.013996	0.52
253635_at	putative protein hypothetical protein - A	---	AT4G30620	-1.58	-0.66	-6.46	0.000409	0.013996	0.52
256215_at	unknown protein ;supported by full-lengt	---	AT1G50900	-1.72	-0.79	-6.44	0.000415	0.013996	0.51
261323_at	hypothetical protein predicted by genem	---	AT1G44760	-2.34	-1.22	-6.46	0.00041	0.013996	0.52
258424_at	hypothetical protein predicted by genem	---	AT3G16750	-1.79	-0.84	-6.46	0.000409	0.013996	0.52
255844_at	putative protein kinase contains a protei	---	AT2G33580	3.08	1.62	6.46	0.000411	0.013996	0.52
251621_at	protein kinase - like protein wall-associa	---	AT3G57700	2.55	1.35	6.43	0.00042	0.014060	0.50
249839_at	Expressed protein ; supported by cDNA	---	AT5G23405	-1.77	-0.82	-6.44	0.000418	0.014060	0.50
266589_at	hypothetical protein predicted by gensca	---	AT2G46250	-2.03	-1.02	-6.43	0.00042	0.014060	0.50
258285_at	photosystem I subunit VI precursor iden	PSAH-1	AT3G16140	-1.55	-0.64	-6.43	0.000421	0.014060	0.49
245020_at	cytochrome f	---	---	-1.68	-0.75	-6.43	0.00042	0.014060	0.50
247826_at	beta 1-3 glucanase - like protein beta 1	---	AT5G58480	-1.68	-0.74	-6.43	0.000421	0.014060	0.49
259793_at	AP2-containing DNA-binding protein cor	---	AT1G64380	4.31	2.11	6.42	0.000424	0.014069	0.48
261824_at	DAG protein, putative similar to DAG pr	---	AT1G11430	-1.55	-0.63	-6.42	0.000424	0.014069	0.49
245137_at	unknown protein	---	AT2G45460	-1.97	-0.98	-6.42	0.000424	0.014069	0.49
250832_at	nicotianamine synthase (dbj|BAA74589.	NAS1	AT5G04950	-7.16	-2.84	-6.42	0.000425	0.014069	0.48
251652_at	putative protein hypothetical protein T3	---	AT3G57380	2.25	1.17	6.42	0.000425	0.014069	0.48
247835_at	putative protein similar to unknown prote	---	AT5G57910	2.78	1.48	6.42	0.000425	0.014069	0.48
263000_at	hypothetical protein similar to hypothetic	---	AT1G54350	-1.77	-0.82	-6.42	0.000426	0.014069	0.48
259945_at	unknown protein	---	AT1G71460	-1.80	-0.85	-6.41	0.000427	0.014100	0.48
253740_at	Expressed protein ; supported by cDNA	---	AT4G28706	-1.83	-0.87	-6.40	0.000433	0.014181	0.46
255543_at	predicted protein of unknown function si	---	AT4G01870	4.12	2.04	6.40	0.000433	0.014181	0.46
255829_at	putative potassium transporter ; suppor	KT2	AT2G40540	-1.53	-0.62	-6.40	0.000431	0.014181	0.47
248330_at	putative protein contains similarity to orr	---	AT5G52810	2.73	1.45	6.40	0.000431	0.014181	0.47
265335_at	Expressed protein ; supported by full-ler	---	AT2G18245	-1.49	-0.57	-6.40	0.000431	0.014181	0.47
256678_at	RNA-binding protein (cp33) identical to	CP33	AT3G52380	-1.73	-0.79	-6.39	0.000436	0.014243	0.46
264930_at	receptor-like kinase, putative similar to	NIK3	AT1G60800	-1.95	-0.97	-6.39	0.000436	0.014243	0.46

258209_at	expressed protein supported by cDNA: (	GAPC1	AT3G04120 /	3.42	1.77	6.39	0.000436	0.014243	0.46
250194_at	putative protein various predicted prote	---	AT5G14550	-1.65	-0.72	-6.38	0.00044	0.014291	0.45
246197_at	caltractin-like protein ;supported by full-l	CEN2	AT4G37010	5.27	2.40	6.38	0.000439	0.014291	0.45
263543_at	putative pectinesterase	PE11	AT2G21610	1.54	0.63	6.38	0.00044	0.014291	0.45
259952_at	putative disease resistance protein simil	AtRLP12	AT1G71400	2.59	1.37	6.36	0.00045	0.014566	0.42
258167_at	UDP-glucose:indole-3-acetate beta-D-g	UGT84A2	AT3G21560	2.64	1.40	6.36	0.000449	0.014566	0.42
247819_at	MAP kinase ; supported by cDNA: gi_14	WNK4	AT5G58350	2.14	1.10	6.35	0.000452	0.014613	0.42
260595_at	unknown protein	---	AT1G55890	-1.79	-0.84	-6.34	0.000456	0.014682	0.41
254639_at	putative protein various predicted prote	DOT4	AT4G18750	-1.71	-0.78	-6.34	0.000456	0.014682	0.41
245024_at	ATPase alpha subunit	---	---	-1.54	-0.62	-6.34	0.000457	0.014682	0.41
248619_at	amino acid permease 6 (emb CAA6505	AAP6	AT5G49630	-2.00	-1.00	-6.34	0.000457	0.014682	0.41
262630_at	unknown protein ;supported by full-leng	GPAT1	AT1G06520	6.33	2.66	6.34	0.000457	0.014682	0.41
257203_at	xyloglucan endotransglycosylase, putat	---	AT3G23730	1.59	0.67	6.33	0.000459	0.014689	0.40
251309_at	putative protein carbonyl reductase (NA	---	AT3G61220	-1.81	-0.86	-6.33	0.000459	0.014689	0.40
267210_at	dihydroxypolyprenylbenzoate methyltrar	ATCOQ3	AT2G30920	-1.48	-0.56	-6.34	0.000459	0.014689	0.40
252940_at	receptor protein kinase - like protein rec	---	AT4G39270	2.34	1.22	6.32	0.000464	0.014741	0.39
265946_s_a	putative WD-40 repeat protein, MSI4 al	FVE	AT2G19520 /	-1.57	-0.65	-6.32	0.000464	0.014741	0.39
246808_at	putative protein many predicted protein	---	AT5G27110	-1.64	-0.71	-6.32	0.000463	0.014741	0.39
246681_at	chloride channel-like protein chloride ch	---	AT5G33280	-1.54	-0.62	-6.32	0.000463	0.014741	0.39
246272_at	hydroxynitrile lyase like protein	MES9	AT4G37150	4.16	2.06	6.32	0.000463	0.014741	0.39
254638_at	hypothetical protein	---	AT4G18740	-2.18	-1.12	-6.31	0.000469	0.014762	0.38
260390_at	unknown protein ; supported by full-leng	---	AT1G73940	-1.76	-0.81	-6.31	0.000468	0.014762	0.38
247312_at	putative protein strong similarity to unkn	---	AT5G63970	1.85	0.89	6.32	0.000467	0.014762	0.38
248242_at	aldo/keto reductase-like protein	---	AT5G53580	-1.91	-0.93	-6.31	0.000469	0.014762	0.38
251353_at	putative protein hypothetical protein - S	---	AT3G61080	-1.92	-0.94	-6.31	0.000468	0.014762	0.38
257773_at	hypothetical protein predicted by genem	---	AT3G29185	-1.72	-0.78	-6.31	0.000469	0.014762	0.38
252004_at	purple acid phosphatase-like protein pu	PAP20	AT3G52780	2.96	1.56	6.31	0.000469	0.014762	0.38
248878_at	50S ribosomal protein L14	---	AT5G46160	-1.60	-0.68	-6.31	0.00047	0.014765	0.38
260442_at	unknown protein ; supported by full-leng	---	AT1G68220	-1.92	-0.94	-6.30	0.000472	0.014813	0.37
260431_at	putative zinc finger protein similar to zin	---	AT1G68190	-1.49	-0.58	-6.30	0.000474	0.014825	0.37
248237_at	receptor protein kinase-like protein	---	AT5G53890	-1.88	-0.91	-6.30	0.000473	0.014825	0.37
254011_at	putative protein transcription terminatio	---	AT4G26370	-1.74	-0.80	-6.30	0.000474	0.014825	0.37
258453_at	RNA polymerase I, II and III 24.3 kDa s	NRPB5	AT3G22320	-1.53	-0.62	-6.29	0.000476	0.014827	0.36
249335_at	putative protein contains similarity to me	NRPB12	AT5G41010	-1.66	-0.73	-6.30	0.000476	0.014827	0.36
261628_at	hypothetical protein predicted by genem	---	AT1G50000	-1.54	-0.63	-6.29	0.000476	0.014827	0.36

256204_at	DNA polymerase A family protein, putat	POLGAMM	AT1G50840	-1.90	-0.93	-6.29	0.00048	0.014876	0.35
266338_at	putative ligand-gated ion channel subun	GLR5	AT2G32400	-1.88	-0.91	-6.29	0.00048	0.014876	0.36
251859_at	putative protein proteophosphoglycan,	---	AT3G54680	1.70	0.77	6.28	0.000483	0.014876	0.35
257855_at	hypothetical protein predicted by genefir	---	AT3G13040	-1.61	-0.69	-6.28	0.000483	0.014876	0.35
265880_at	unknown protein	---	AT2G42300	-2.10	-1.07	-6.28	0.000483	0.014876	0.35
253966_at	fructose-bisphosphate aldolase	---	AT4G26520	-1.95	-0.96	-6.28	0.000482	0.014876	0.35
262727_at	thaumatin, putative contains Pfam profi	---	AT1G75800	-1.59	-0.66	-6.28	0.000483	0.014876	0.35
255342_at	putative receptor-like protein kinase	---	AT4G04510	1.79	0.84	6.28	0.000484	0.014876	0.35
248828_at	Lil3 protein	---	AT5G47110	-1.53	-0.61	-6.28	0.000483	0.014876	0.35
264923_s_a	peroxiredoxin, putative similar to type 2	---	AT1G60740 /	3.01	1.59	6.27	0.000489	0.015008	0.34
261086_at	hypothetical protein predicted by genem	TRFL3	AT1G17460	-1.55	-0.63	-6.26	0.00049	0.015032	0.33
254727_at	hypothetical protein	PTAC5	AT4G13670	-1.50	-0.59	-6.26	0.000491	0.015047	0.33
264605_at	putative auxin-induced protein, IAA12 s	IAA12	AT1G04550	-1.69	-0.75	-6.26	0.000493	0.015067	0.33
256675_at	putative protein DNA-binding protein PI	---	AT3G52170	-2.62	-1.39	-6.25	0.000495	0.015110	0.32
248889_at	unknown protein ;supported by full-lengt	---	AT5G46230	2.33	1.22	6.25	0.000496	0.015110	0.32
249404_at	ankyrin repeat protein EMB506 ; suppo	EMB506	AT5G40160	-1.95	-0.97	-6.25	0.000497	0.015110	0.32
265287_at	putative photosystem I reaction center s	PSAE-2	AT2G20260	-1.48	-0.57	-6.25	0.000496	0.015110	0.32
259422_at	unknown protein	---	AT1G13810	-2.09	-1.06	-6.24	0.0005	0.015118	0.31
255749_at	p68 RNA helicase, putative similar to p	STRS1	AT1G31970	-1.63	-0.70	-6.24	0.0005	0.015118	0.31
260412_at	putative alpha-amylase similar to alpha-	AMY3	AT1G69830	-1.50	-0.58	-6.24	0.0005	0.015118	0.31
244974_at	PSII low MW protein	---	---	-1.65	-0.72	-6.25	0.000498	0.015118	0.32
266957_at	unknown protein	PTAC12	AT2G34640	-1.81	-0.85	-6.23	0.000504	0.015161	0.30
260106_at	unknown protein ;supported by full-lengt	---	AT1G35420	-1.66	-0.73	-6.24	0.000503	0.015161	0.31
251107_at	putative protein several hypothetical pro	---	AT5G01610	1.81	0.86	6.23	0.000504	0.015161	0.31
258880_at	hypothetical protein similar to symbiosis	ATG8H	AT3G06420	3.14	1.65	6.24	0.000503	0.015161	0.31
247297_at	peroxidase ATP3a (emb|CAA67340.1)	---	AT5G64100	3.91	1.97	6.23	0.000505	0.015173	0.30
251179_at	putative protein ABP130 protein, Homo	---	AT3G63460	1.49	0.57	6.23	0.000506	0.015173	0.30
261443_at	glutaredoxin, putative similar to glutared	GRX480	AT1G28480	4.55	2.19	6.23	0.000506	0.015175	0.30
264072_at	hypothetical protein	---	---	-1.56	-0.64	-6.23	0.000507	0.015183	0.30
254503_at	hypothetical protein ;supported by full-le	PTAC9	AT4G20010	-1.71	-0.77	-6.22	0.000509	0.015189	0.29
264648_at	putative luminal binding protein Similar t	BIP3	AT1G09080	1.92	0.94	6.22	0.000509	0.015189	0.30
264258_at	hypothetical protein predicted by genefir	---	AT1G09220	-1.70	-0.76	-6.22	0.00051	0.015195	0.29
250385_at	aspartate aminotransferase (Asp3) ; su	ASP3	AT5G11520	2.65	1.40	6.22	0.00051	0.015195	0.29
260672_at	Expressed protein ; supported by full-ler	---	AT1G19480	-1.57	-0.66	-6.22	0.000511	0.015206	0.29
252305_at	putative protein CRP1 protein, Zea may	emb1796	AT3G49240	-2.09	-1.06	-6.22	0.000512	0.015219	0.29

252723_at	hypothetical protein ; supported by full-l	---	AT3G43520	-1.51	-0.60	-6.21	0.000514	0.015235	0.28
253911_at	putative receptor protein kinase recepto	---	AT4G27300	-3.19	-1.67	-6.21	0.000516	0.015241	0.28
263471_at	hypothetical protein predicted by genscа	RAP	AT2G31890	-1.74	-0.80	-6.21	0.000516	0.015241	0.28
258046_at	MAP kinase kinase 5 identical to GB:BA	MKK5	AT3G21220	1.66	0.73	6.21	0.000515	0.015241	0.28
256874_at	cytochrome P450, putative contains Pfa	CYP71B36	AT3G26320	-1.74	-0.80	-6.21	0.000517	0.015241	0.28
252350_at	ataxia-telangiectasia mutated protein A	ATM	AT3G48190	-1.53	-0.62	-6.21	0.000517	0.015241	0.28
262751_at	hypothetical protein predicted by genscа	---	AT1G16310	-1.55	-0.63	-6.20	0.000521	0.015251	0.27
261948_at	unknown protein ;supported by full-lengt	---	AT1G64680	-2.42	-1.28	-6.20	0.000521	0.015251	0.27
246736_at	putative protein hypothetical protein slr	---	AT5G27560	-1.70	-0.76	-6.20	0.00052	0.015251	0.27
253188_at	putative sugar transporter protein sugar	TMT2	AT4G35300	-1.70	-0.77	-6.20	0.000519	0.015251	0.27
255088_at	putative protein heat shock protein dna	---	AT4G09350	-2.29	-1.20	-6.20	0.000519	0.015251	0.27
266716_at	unknown protein ;supported by full-leng	PSI-P	AT2G46820	-1.68	-0.74	-6.19	0.000524	0.015318	0.26
248628_at	putative protein contains similarity to 5'-	---	AT5G48960	-1.68	-0.75	-6.18	0.000528	0.015425	0.26
266033_at	putative translation initiation factor eIF-2	---	AT2G05830	-1.87	-0.90	-6.18	0.000531	0.015436	0.25
260137_at	unknown protein ;supported by full-lengt	---	AT1G66330	-2.09	-1.06	-6.18	0.00053	0.015436	0.25
249152_s_a	inorganic phosphate transporter (dbj|BA	APT1	AT5G43350 /	2.13	1.09	6.18	0.00053	0.015436	0.25
259911_at	putative cinnamyl-alcohol dehydrogenas	CAD1	AT1G72680	2.07	1.05	6.17	0.000535	0.015540	0.24
262113_at	late embryogenis abundant protein, put	---	AT1G02820	-2.81	-1.49	-6.17	0.000537	0.015589	0.24
260046_at	Expressed protein ; supported by cDNA	---	AT1G73805	7.78	2.96	6.16	0.000538	0.015602	0.24
248984_at	DNA-directed RNA polymerase subunit	NRPC2	AT5G45140	-1.87	-0.90	-6.16	0.00054	0.015635	0.23
265336_at	hypothetical protein predicted by genscа	APC10	AT2G18290	-1.57	-0.65	-6.16	0.000543	0.015635	0.23
266126_at	putative metalloproteinase ; supported	---	AT2G45040	2.30	1.20	6.16	0.000541	0.015635	0.23
264279_s_a	glycoprotein(EP1), putative similar to gl	---	AT1G78820 /	1.97	0.98	6.16	0.000542	0.015635	0.23
256181_at	light repressible receptor protein kinase	---	AT1G51820	4.86	2.28	6.16	0.000542	0.015635	0.23
253440_at	putative protein ;supported by full-length	TIFY8	AT4G32570	-1.46	-0.54	-6.15	0.000545	0.015654	0.22
255047_at	AX110P -like protein AX110P -Daucus	---	AT4G09670	-1.63	-0.71	-6.15	0.000545	0.015654	0.22
253495_at	putative protein crp1 protein, Zea mays	PGR3	AT4G31850	-2.10	-1.07	-6.15	0.000548	0.015712	0.22
252921_at	putative protein DNA damage-inducible	EDS5	AT4G39030	2.99	1.58	6.14	0.000552	0.015813	0.21
254598_at	xyloglucan endo-transglycosylase - like	---	AT4G18990	2.89	1.53	6.14	0.000553	0.015814	0.21
255116_at	receptor protein kinase-like protein rece	---	AT4G08850	2.00	1.00	6.13	0.000555	0.015814	0.20
254350_at	putative protein hypothetical protein, ch	---	AT4G22280	-1.49	-0.58	-6.13	0.000556	0.015814	0.20
258617_at	putative calmodulin similar to calmodulin	---	AT3G03000	1.51	0.59	6.13	0.000554	0.015814	0.20
245321_at	Expressed protein ; supported by full-ler	---	AT4G15545	-1.51	-0.59	-6.13	0.000556	0.015814	0.20
247889_at	putative protein similar to unknown prote	APO2	AT5G57930	-1.65	-0.73	-6.13	0.000554	0.015814	0.21
255068_at	Arabidopsis thaliana flavin-type blue-lig	CRY1	AT4G08920	-1.47	-0.56	-6.13	0.000557	0.015832	0.20

266761_at	putative alcohol dehydrogenase	---	AT2G47130	3.31	1.73	6.13	0.000558	0.015833	0.20
247176_at	acyl-CoA oxidase (gb|AAC13497.1) ; su	ACX2	AT5G65110	2.16	1.11	6.12	0.000559	0.015833	0.20
261075_at	unknown protein	---	AT1G07280	-1.71	-0.77	-6.12	0.000561	0.015864	0.19
264746_at	unknown protein similar to putative DNA	WRKY6	AT1G62300	4.05	2.02	6.09	0.000575	0.015983	0.17
263679_at	RNA helicase, putative similar to RNA h	---	AT1G59990	-1.81	-0.86	-6.09	0.000576	0.015983	0.17
245323_at	cysteine proteinase inhibitor like protein	---	AT4G16500	1.85	0.89	6.10	0.000574	0.015983	0.17
259285_at	hypothetical protein similar to putative p	---	AT3G11460	-1.59	-0.67	-6.10	0.000574	0.015983	0.17
256603_at	unknown protein similar to At14a protein	---	AT3G28270	-3.16	-1.66	-6.11	0.000567	0.015983	0.18
253912_at	putative protein met-10+ protein, Neuro	---	AT4G27340	-1.78	-0.83	-6.10	0.000571	0.015983	0.17
255046_at	H+-transporting ATP synthase-like prot	ATPD	AT4G09650	-1.74	-0.80	-6.10	0.000572	0.015983	0.17
267553_s_a	hypothetical protein predicted by genefin	---	AT2G32180 /	-2.10	-1.07	-6.11	0.000569	0.015983	0.18
259160_at	unknown protein	---	AT3G05410	-1.71	-0.78	-6.11	0.000567	0.015983	0.18
256343_at	unknown protein ; supported by cDNA: g	---	AT1G72090	-1.76	-0.82	-6.10	0.000573	0.015983	0.17
247320_at	photosystem I reaction centre subunit ps	PSAN	AT5G64040	-1.61	-0.68	-6.11	0.000568	0.015983	0.18
261048_at	flavonol 3-o-glucosyltransferase, putativ	UGT72B3	AT1G01420	-1.75	-0.81	-6.09	0.000575	0.015983	0.17
265704_at	hypothetical protein predicted by genscan	---	AT2G03420	-2.04	-1.03	-6.10	0.000571	0.015983	0.17
263168_at	putative glutaredoxin Strong similarity to	---	AT1G03020	-4.87	-2.28	-6.10	0.000574	0.015983	0.17
261189_at	hypothetical protein contains similarity to	NACA5	AT1G33040	-1.66	-0.73	-6.10	0.000571	0.015983	0.17
266331_at	putative RGA1, giberellin repsonse mod	RGA1	AT2G01570	-1.81	-0.86	-6.09	0.000576	0.015983	0.16
265446_at	unknown protein ;supported by full-leng	---	AT2G37110	1.65	0.72	6.09	0.000577	0.016000	0.16
263557_at	putative homeodomain transcription fact	BLH7	AT2G16400	-1.84	-0.88	-6.09	0.000579	0.016014	0.16
257587_at	3'-5' exonuclease, putative contains Pfa	---	AT1G56310	-1.56	-0.64	-6.08	0.000581	0.016056	0.16
258815_at	putative short-chain type dehydrogenas	---	AT3G04000	2.42	1.28	6.07	0.000586	0.016083	0.15
255440_at	predicted protein of unknown function ;	---	AT4G02530	-1.77	-0.83	-6.08	0.000584	0.016083	0.15
258281_at	putative shikimate kinase similar to shiki	---	AT3G26900	-1.46	-0.54	-6.08	0.000584	0.016083	0.15
251885_at	fructose-bisphosphatase precursor ; su	---	AT3G54050	-2.19	-1.13	-6.08	0.000585	0.016083	0.15
263864_at	hypothetical protein predicted by genscan	CPZ	AT2G04530	-1.66	-0.73	-6.08	0.000584	0.016083	0.15
245736_at	Dr4(protease inhibitor) identical to Dr4 C	ATDR4	AT1G73330	-3.08	-1.63	-6.08	0.000586	0.016083	0.15
257635_at	cytochrome P450 monooxygenase (CY	CYP71B4	AT3G26280	-1.81	-0.85	-6.07	0.000587	0.016101	0.14
266832_at	putative protein kinase contains a protei	MAPKKK1	AT2G30040	2.16	1.11	6.07	0.000591	0.016188	0.14
261804_at	UDP glucose:flavonoid 3-o-glucosyltran	UGT78D1	AT1G30530	-2.11	-1.08	-6.06	0.000593	0.016230	0.13
252300_at	pyruvate kinase -like protein various pyr	---	AT3G49160	2.47	1.31	6.05	0.000599	0.016279	0.12
247575_at	RNA-binding protein - like RNA-binding	GR-RBP3	AT5G61030	-1.91	-0.93	-6.05	0.000602	0.016279	0.12
255668_s_a	predicted protein ; supported by full-leng	---	AT4G00238 /	-1.85	-0.89	-6.05	0.000601	0.016279	0.12
249315_at	unknown protein	---	AT5G41190	-1.52	-0.61	-6.04	0.000608	0.016279	0.11

248307_at	selenium-binding protein-like	---	AT5G52850	-1.72	-0.79	-6.04	0.000608	0.016279	0.11
256253_at	60S acidic ribosomal protein, putative s	---	AT3G11250	-1.69	-0.76	-6.04	0.000604	0.016279	0.12
260343_at	fructokinase (Frk1), putative similar to fr	---	AT1G69200	-1.99	-0.99	-6.04	0.000605	0.016279	0.11
258193_at	putative pectinesterase similar to pectin	PME31	AT3G29090	-1.53	-0.61	-6.04	0.000604	0.016279	0.11
258396_at	unknown protein similar to unknown pro	---	AT3G15460	-2.57	-1.36	-6.04	0.000608	0.016279	0.11
256607_at	unknown protein ; supported by cDNA: g	---	AT3G32930	-1.53	-0.61	-6.05	0.000598	0.016279	0.12
245198_at	Expressed protein ; supported by full-ler	---	AT1G67700	-1.59	-0.67	-6.04	0.000606	0.016279	0.11
257699_at	phosphoglycerate kinase, putative simil	PGK1	AT3G12780	-1.80	-0.85	-6.04	0.000604	0.016279	0.11
262738_at	hypothetical protein	---	AT1G28530	-1.81	-0.85	-6.04	0.000603	0.016279	0.12
253387_at	P-Protein - like protein P-Protein precur	AtGLDP1	AT4G33010	-2.83	-1.50	-6.04	0.000608	0.016279	0.11
254643_at	putative protein DNA polymerase III hol	---	AT4G18820	-1.66	-0.73	-6.04	0.000608	0.016279	0.11
260904_at	unknown protein	NIMIN1	AT1G02450	5.72	2.52	6.05	0.000602	0.016279	0.12
260956_at	salt-tolerance protein identical to salt-tol	STO	AT1G06040	-1.55	-0.64	-6.05	0.0006	0.016279	0.12
246547_at	seed maturation -like protein seed matu	---	AT5G14970	-1.93	-0.95	-6.04	0.000605	0.016279	0.11
256617_at	unknown protein ; supported by full-leng	---	AT3G22240	3.34	1.74	6.03	0.000615	0.016293	0.10
252291_s_a	peroxidase ;supported by full-length cD	PRXCB	AT3G49110 /	2.50	1.32	6.02	0.000616	0.016293	0.09
262288_at	unknown protein identical to residues 1	CRR23	AT1G70760	-3.45	-1.79	-6.03	0.000612	0.016293	0.10
253803_at	putative protein hypothetical protein - S	---	AT4G28200	-1.58	-0.66	-6.03	0.000612	0.016293	0.10
263122_at	prenyltransferase, putative similar to pr	SPS1	AT1G78510	-1.79	-0.84	-6.03	0.000612	0.016293	0.10
263249_at	delta 9 desaturase ALMOST identical (4	ADS2	AT2G31360	-1.54	-0.62	-6.03	0.000611	0.016293	0.10
265330_at	unknown protein	GUT15	---	-1.72	-0.78	-6.03	0.000614	0.016293	0.10
250676_at	harpin-induced protein-like ; supported	NHL3	AT5G06320	2.28	1.19	6.03	0.000614	0.016293	0.10
255644_at	coded for by A. thaliana cDNA T43872 s	---	AT4G00870	-1.57	-0.65	-6.03	0.00061	0.016293	0.10
264658_at	hypothetical protein similar to LG27/30-l	---	AT1G09910	-1.65	-0.72	-6.02	0.000616	0.016293	0.09
262237_at	hypothetical protein predicted by genem	---	AT1G48320	2.46	1.30	6.01	0.000622	0.016410	0.08
260981_at	hypothetical protein predicted by gensca	---	AT1G53460	-1.79	-0.84	-6.01	0.000621	0.016410	0.08
249690_at	acyl-peptide hydrolase-like	---	AT5G36210	-1.58	-0.66	-6.01	0.000623	0.016430	0.08
260179_at	unknown protein similar to hypothetical	HWI1	AT1G70690	2.91	1.54	6.01	0.000624	0.016445	0.08
254710_at	multidrug resistance protein/P-glycopro	PGP9	AT4G18050	2.28	1.19	6.01	0.000626	0.016450	0.08
251083_at	hypothetical protein ; supported by cDN	---	AT5G01590	-1.64	-0.71	-6.01	0.000625	0.016450	0.08
263298_at	unknown protein ; supported by cDNA:	TIC21	AT2G15290	-1.52	-0.60	-6.00	0.000628	0.016458	0.07
248590_at	receptor protein kinase	---	AT5G49660	-1.58	-0.66	-6.00	0.000627	0.016458	0.07
256796_at	hypothetical protein predicted by gensca	---	AT3G22210	-2.30	-1.20	-6.00	0.000628	0.016458	0.07
252441_at	putative protein ; supported by cDNA: g	PTAC16	AT3G46780	-2.11	-1.07	-6.00	0.000632	0.016482	0.07
249264_s_a	disease resistance protein-like	---	AT5G41740 /	2.44	1.29	6.00	0.000631	0.016482	0.07

261422_at	unknown protein	NDF6	AT1G18730	-1.78	-0.83	-6.00	0.000631	0.016482	0.07
261674_at	unknown protein	---	AT1G18270	2.35	1.23	5.99	0.000634	0.016500	0.06
248595_at	drought-induced protein Di19-like protei	HRB1	AT5G49230	-1.66	-0.73	-5.99	0.000634	0.016500	0.06
248036_at	nucleolar protein-like	OLI2	AT5G55920	-1.98	-0.99	-5.99	0.000635	0.016518	0.06
258079_at	hypothetical protein predicted by gensca	---	AT3G25940	-1.62	-0.70	-5.99	0.000637	0.016520	0.06
259392_at	hypothetical protein similar to hypothetic	---	AT1G06380	-1.53	-0.62	-5.99	0.000637	0.016520	0.06
248854_at	putative protein contains similarity to sal	---	AT5G46580	-1.76	-0.82	-5.99	0.000637	0.016520	0.06
250529_at	RNA helicase-like protein	---	AT5G08610	-1.97	-0.97	-5.98	0.00064	0.016551	0.05
257294_at	non-phototropic hypocotyl protein, puta	---	AT3G15570	-2.13	-1.09	-5.98	0.000641	0.016551	0.05
254933_at	putative RNA-directed RNA polymerase	RDR2	AT4G11130	-1.77	-0.83	-5.98	0.000641	0.016551	0.05
255880_at	hypothetical protein predicted by gensca	---	AT1G67060	1.55	0.63	5.98	0.000641	0.016551	0.05
256107_at	hypothetical protein predicted by gensca	---	AT1G16830	-1.52	-0.61	-5.98	0.000643	0.016558	0.05
255957_at	unknown protein ;supported by full-lengt	---	AT1G22160	-3.51	-1.81	-5.98	0.000643	0.016558	0.05
252277_at	alpha NAC-like protein Nascent polype	NACA2	AT3G49470	-1.46	-0.54	-5.98	0.000644	0.016559	0.05
256049_at	unknown protein	---	AT1G07010	-1.87	-0.90	-5.97	0.000645	0.016577	0.04
249433_at	putative protein hypothetical protein - S	---	AT5G39940	-1.94	-0.96	-5.97	0.000648	0.016611	0.04
254778_at	putative protein	---	AT4G12750	-1.84	-0.88	-5.97	0.000648	0.016611	0.04
258610_at	IAA-amino acid hydrolase (ILR1) identic	ILR1	AT3G02875	2.36	1.24	5.96	0.000653	0.016723	0.03
250906_at	1,4-alpha-glucan branching enzyme pro	SBE2.2	AT5G03650	-1.69	-0.75	-5.96	0.000655	0.016725	0.03
245047_at	PSII 32 KDa protein	---	---	-1.56	-0.65	-5.96	0.000655	0.016725	0.03
262552_at	hypothetical protein similar to hypothetic	---	AT1G31350	2.20	1.14	5.96	0.000657	0.016774	0.03
251137_at	putative protein several hypothetical pro	---	AT5G01300	-1.96	-0.97	-5.95	0.000658	0.016777	0.02
261582_at	unknown protein ; supported by cDNA: g	GIF2	AT1G01160	-1.55	-0.64	-5.95	0.00066	0.016814	0.02
267452_at	auxin response transcription factor 3 (E	ETT	AT2G33860	-1.66	-0.73	-5.95	0.000661	0.016814	0.02
259840_at	photosystem I subunit VI precursor iden	PSAH2	AT1G52230	-1.81	-0.86	-5.94	0.000665	0.016866	0.01
246673_at	ribosomal protein S1 ;supported by full-l	RPS1	AT5G30510	-1.54	-0.62	-5.94	0.000665	0.016866	0.01
255795_at	putative calcium-binding EF-hand protei	RD20	AT2G33380	3.22	1.69	5.94	0.000666	0.016867	0.01
259442_at	(1-4)-beta-mannan endohydrolase prec	---	AT1G02310	2.31	1.21	5.94	0.000666	0.016867	0.01
254515_at	CLV1 receptor kinase like protein CLA	BAM3	AT4G20270	-1.57	-0.65	-5.94	0.000668	0.016880	0.01
255936_at	calcium dependent protein kinase, puta	---	AT1G12680 /	-1.59	-0.66	-5.94	0.000669	0.016904	0.01
265511_at	putative glycine-rich protein ; supported	---	AT2G05540	2.03	1.02	5.93	0.000675	0.016936	0.00
255623_at	putative L5 ribosomal protein ;supporte	---	AT4G01310	-1.56	-0.64	-5.93	0.000673	0.016936	0.00
254167_at	serine/threonine kinase-like protein ser	CIPK8	AT4G24400	1.68	0.75	5.93	0.000674	0.016936	0.00
262753_at	putative 3-deoxy-D-manno-2-octulosona	ATKDSA2	AT1G16340	-1.58	-0.66	-5.93	0.000675	0.016936	0.00
265186_at	Expressed protein ; supported by full-ler	---	AT1G23560	1.85	0.89	5.93	0.000674	0.016936	0.00

265059_at	unknown protein ; supported by cDNA: g	AR791	AT1G52080	1.91	0.93	5.93	0.000672	0.016936	0.00
248173_at	putative protein contains similarity to RN	---	AT5G54580	-1.56	-0.64	-5.92	0.000677	0.016956	-0.01
253181_at	amino acid permease - like protein Lily	LHT7	AT4G35180	7.61	2.93	5.92	0.000677	0.016956	-0.01
263248_at	putative endonuclease ;supported by fu	ATNTH1	AT2G31450	-1.57	-0.65	-5.92	0.000683	0.017081	-0.02
266896_at	putative ATP-dependent RNA helicase	---	AT2G45810	-1.47	-0.56	-5.92	0.000684	0.017081	-0.02
266903_at	hypothetical protein predicted by gensca	MEE21	AT2G34570	-1.52	-0.60	-5.91	0.000688	0.017165	-0.02
250752_at	cytochrome P450 90A1 (sp|Q42569) ; s	CPD	AT5G05690	-1.79	-0.84	-5.90	0.000691	0.017217	-0.03
258538_at	putative tRNA pseudouridine synthase s	---	AT3G06950	-1.55	-0.63	-5.90	0.000692	0.017223	-0.03
264584_at	unknown protein Similar to Synechocyst	---	AT1G05140	-1.69	-0.76	-5.90	0.000692	0.017223	-0.03
245492_at	putative protein	SPK1	AT4G16340	-1.63	-0.70	-5.90	0.000694	0.017234	-0.03
251109_at	ferritin 1 precursor ;supported by full-ler	FER1	AT5G01600	2.75	1.46	5.90	0.000695	0.017237	-0.03
266353_at	unknown protein ;supported by full-leng	MLP328	AT2G01520	2.24	1.16	5.90	0.000695	0.017237	-0.03
266184_s_a	phosphate transporter (AtPT2) identical	ATPT2	AT2G38940 /	2.74	1.46	5.90	0.000697	0.017242	-0.04
262287_at	unknown protein ;supported by full-lengt	---	AT1G68660	-1.67	-0.74	-5.90	0.000697	0.017242	-0.04
254101_at	alpha-amylase - like protein alpha-amyl	AMY1	AT4G25000	4.14	2.05	5.89	0.000699	0.017267	-0.04
256002_at	carbamoylphosphate synthetase, putati	CARB	AT1G29900	-1.63	-0.71	-5.89	0.0007	0.017267	-0.04
250884_at	signal recognition particle 54CP protein	CPSRP54	AT5G03940	-1.54	-0.62	-5.89	0.0007	0.017267	-0.04
259749_at	putative ribose 5-phosphate isomerase	RSW10	AT1G71100	2.67	1.42	5.89	0.000702	0.017285	-0.04
250498_at	microbody NAD-dependent malate dehy	PMDH2	AT5G09660	-2.13	-1.09	-5.88	0.000704	0.017333	-0.05
261762_at	hypothetical protein predicted by genem	---	AT1G15510	-2.47	-1.31	-5.88	0.000706	0.017344	-0.05
266874_at	unknown protein	---	AT2G44760	-1.47	-0.55	-5.88	0.000706	0.017344	-0.05
250526_at	pyruvate kinase	---	AT5G08570	-1.58	-0.66	-5.88	0.000707	0.017344	-0.05
254026_at	putative calmodulin-binding protein caln	---	AT4G25800	-1.46	-0.55	-5.87	0.000714	0.017379	-0.06
262581_at	unknown protein ESTs gb|T22508, gb|H	---	AT1G15370	1.46	0.54	5.87	0.000714	0.017379	-0.06
247158_at	branched-chain amino acid aminotransf	ATBCAT-5	AT5G65780	-1.54	-0.62	-5.87	0.000715	0.017379	-0.06
252282_at	6-phosphogluconolactonase - like prote	---	AT3G49360	-1.51	-0.59	-5.87	0.000714	0.017379	-0.06
253768_at	putative protein	---	AT4G28550	2.08	1.06	5.87	0.000714	0.017379	-0.06
247347_at	putative protein similar to unknown prote	SHA1	AT5G63780	-3.12	-1.64	-5.88	0.000711	0.017379	-0.06
246768_at	putative protein hypothetical proteins - d	---	AT5G27400	-1.42	-0.51	-5.87	0.000714	0.017379	-0.06
260943_at	thioredoxin, putative similar to thioredox	ATTRX5	AT1G45145	2.01	1.01	5.87	0.000711	0.017379	-0.06
254664_at	initiation factor-2Bepsilon-like protein in	---	AT4G18300	-1.68	-0.75	-5.87	0.000716	0.017382	-0.06
262680_at	anter-specific proline-rich -like protein (A	---	AT1G75880	-2.17	-1.12	-5.87	0.000716	0.017382	-0.06
255294_at	putative sugar transporter	---	AT4G04750	-1.62	-0.70	-5.86	0.000723	0.017527	-0.07
246510_at	cyclic nucleotide-gated cation channel ;	DND1	AT5G15410	-1.69	-0.76	-5.85	0.000727	0.017539	-0.08
245348_at	trehalose-6-phosphate synthase like pro	ATTPS5	AT4G17770	-1.94	-0.96	-5.85	0.000726	0.017539	-0.08

248941_s_a	putative protein similar to unknown prote	---	AT5G45460 /	1.77	0.83	5.85	0.000726	0.017539	-0.08
251038_at	putative protein unknown protein At2g3	---	AT5G02240	-1.52	-0.61	-5.85	0.000725	0.017539	-0.08
259179_at	hypothetical protein similar to putative p	---	AT3G01660	-1.85	-0.89	-5.85	0.000732	0.017642	-0.09
251929_at	sigma factor SigC ; supported by cDNA	SIGC	AT3G53920	-1.57	-0.65	-5.84	0.000732	0.017642	-0.09
255870_at	hypothetical protein predicted by gensca	---	AT2G30280	-1.56	-0.64	-5.84	0.000735	0.017672	-0.09
245168_at	3-ketoacyl-CoA thiolase ;supported by f	PKT3	AT2G33150	1.78	0.83	5.84	0.000735	0.017672	-0.09
249628_at	putative protein tropomyosin gene 1, isc	---	AT5G37590	-1.77	-0.83	-5.84	0.000737	0.017688	-0.09
265338_at	putative ribosomal protein L6 ; supporte	---	AT2G18400	-1.59	-0.67	-5.84	0.000738	0.017699	-0.10
262875_at	gamma-tocopherol methyltransferase al	G-TMT	AT1G64970	-1.71	-0.78	-5.83	0.00074	0.017720	-0.10
253401_at	putative protein hypothetical protein F1	---	AT4G32870	16.13	4.01	5.83	0.000741	0.017736	-0.10
262754_at	putative inosine-5-monophosphate dehy	---	AT1G16350	-1.71	-0.78	-5.83	0.000743	0.017762	-0.10
251841_at	putative protein CRP1, Zea mays, PIR2	---	AT3G54980	-2.16	-1.11	-5.83	0.000744	0.017762	-0.10
261006_at	unknown protein similar to reticuline oxi	---	AT1G26410	3.16	1.66	5.82	0.000747	0.017831	-0.11
266889_at	hypothetical protein predicted by gensca	---	AT2G44640	-1.67	-0.74	-5.82	0.000751	0.017897	-0.11
254234_at	putative major latex protein major latex	---	AT4G23680	4.06	2.02	5.81	0.000755	0.017904	-0.12
251157_at	mRNA binding protein precursor - like r	CSP41A	AT3G63140	-1.97	-0.98	-5.82	0.000754	0.017904	-0.12
255604_at	hypothetical protein	---	AT4G01080	-2.06	-1.04	-5.81	0.000757	0.017904	-0.12
258009_at	unknown protein	---	AT3G19440	-1.44	-0.53	-5.82	0.000752	0.017904	-0.12
253857_at	putative protein hypothetical chloroplas	---	AT4G27990	-1.61	-0.69	-5.81	0.00076	0.017904	-0.13
262629_at	heat shock protein, putative contains Pf	ACD32.1	AT1G06460	-1.52	-0.60	-5.81	0.000757	0.017904	-0.12
249694_at	glucose-6-phosphate dehydrogenase ;s	G6PD1	AT5G35790	-1.45	-0.54	-5.81	0.000756	0.017904	-0.12
266703_at	unknown protein predicted by genscan a	---	AT2G19880	2.04	1.03	5.82	0.000753	0.017904	-0.12
262491_at	putative SecA-type chloroplast protein tr	---	AT1G21650	-1.67	-0.74	-5.81	0.000759	0.017904	-0.13
262464_at	hypothetical protein contains similarity to	---	AT1G50280	-2.32	-1.21	-5.81	0.000761	0.017904	-0.13
254835_s_a	flavonoid 3,5-hydroxylase -like protein f	CYP706A5	AT4G12310 /	-2.49	-1.31	-5.81	0.000758	0.017904	-0.12
245273_at	hypothetical protein ; supported by cDN	---	AT4G14950	1.73	0.79	5.81	0.00076	0.017904	-0.13
246988_at	putative protein strong similarity to unkn	---	AT5G67340	3.20	1.68	5.80	0.000763	0.017915	-0.13
255278_at	putative WD-repeat membrane protein	---	AT4G04940	-2.08	-1.06	-5.80	0.000763	0.017915	-0.13
249843_at	putative protein similar to unknown prote	SGS3	AT5G23570	-2.00	-1.00	-5.80	0.000764	0.017915	-0.13
245049_at	ribosomal protein S16	---	---	-2.09	-1.06	-5.80	0.000764	0.017915	-0.13
258275_at	unknown protein ;supported by full-leng	---	AT3G15760	2.26	1.17	5.80	0.000765	0.017916	-0.13
266600_at	putative mitogen-activated protein kinas	MPK12	AT2G46070	-2.15	-1.11	-5.80	0.000766	0.017927	-0.14
262930_at	hypothetical protein similar to hin1 GB:Y	---	AT1G65690	2.54	1.34	5.80	0.000768	0.017932	-0.14
258747_at	unknown protein ; supported by full-leng	---	AT3G05810	-1.89	-0.91	-5.80	0.000769	0.017932	-0.14
254723_at	ammonium transport protein (AMT1) ; s	AMT1;1	AT4G13510	1.89	0.92	5.80	0.000768	0.017932	-0.14

256064_at	Expressed protein ; supported by full-ler	---	AT1G07020	1.58	0.66	5.79	0.000773	0.018003	-0.14
245701_at	ferredoxin-dependent glutamate synthas	GLU1	AT5G04140	-1.96	-0.97	-5.79	0.000775	0.018029	-0.15
247943_at	light-inducible protein ATLS1-like ;supp	---	AT5G57170	-2.25	-1.17	-5.79	0.000777	0.018065	-0.15
258380_at	PP1/PP2A phosphatases pleiotropic reg	---	AT3G16650	-1.63	-0.71	-5.78	0.000778	0.018081	-0.15
254189_at	putative protein cellulose synthase cata	CSLG2	AT4G24000	3.78	1.92	5.78	0.000783	0.018082	-0.16
262433_s_a	DNA binding protein, putative similar to	ATRBP47(	AT1G47490 /	-1.51	-0.60	-5.78	0.000784	0.018082	-0.16
259295_at	hypothetical protein predicted by gensca	---	AT3G05340	-1.79	-0.84	-5.78	0.000783	0.018082	-0.16
251130_at	oligopeptide transporter - like protein pe	PTR5	AT5G01180	-1.49	-0.58	-5.77	0.000786	0.018082	-0.16
260806_at	RNA recognition motif-containing protei	---	AT1G78260	1.45	0.54	5.77	0.000785	0.018082	-0.16
261351_at	hypothetical protein predicted by genem	---	AT1G79790	-1.67	-0.74	-5.77	0.000785	0.018082	-0.16
253827_at	Expressed protein ; supported by cDNA	---	AT4G28085	3.99	2.00	5.77	0.000785	0.018082	-0.16
255645_at	coded for by A. thaliana cDNA T43845 s	---	AT4G00880	-2.15	-1.10	-5.78	0.00078	0.018082	-0.16
256698_at	unknown protein	---	AT3G20680	-1.74	-0.80	-5.78	0.000783	0.018082	-0.16
252362_at	hypothetical protein	PDE312	AT3G48500	-2.17	-1.12	-5.77	0.000789	0.018118	-0.17
254356_at	hypothetical protein ;supported by full-le	---	AT4G22190	-1.76	-0.81	-5.77	0.000788	0.018118	-0.17
248739_at	DnaJ protein-like ;supported by full-leng	GFA2	AT5G48030	-1.51	-0.59	-5.77	0.000792	0.018134	-0.17
249128_at	1-aminocyclopropane-1-carboxylate oxi	---	AT5G43440	-1.56	-0.64	-5.77	0.000791	0.018134	-0.17
255290_at	coded for by A. thaliana cDNA AA04114	ATPC1	AT4G04640	-1.42	-0.51	-5.77	0.000791	0.018134	-0.17
248552_at	RNA-binding protein-like ; supported by	---	AT5G50250	-1.59	-0.66	-5.76	0.000793	0.018136	-0.17
263537_at	CONSTANS-like B-box zinc finger prote	COL3	AT2G24790	-1.54	-0.62	-5.76	0.000796	0.018195	-0.18
260236_at	geranylgeranyl reductase identical to ge	---	AT1G74470	-1.46	-0.55	-5.76	0.000798	0.018228	-0.18
253545_at	AIG2-like protein AIG2 protein, Arabido	---	AT4G31310	-1.84	-0.88	-5.76	0.0008	0.018244	-0.18
258313_at	unknown protein contains RanBP1 dom	---	AT3G15970	-1.51	-0.59	-5.75	0.000801	0.018253	-0.18
267202_s_a	putative oxysterol-binding protein	ORP1A	AT2G31020 /	2.17	1.12	5.75	0.000802	0.018253	-0.18
267586_at	hypothetical protein predicted by genfin	---	AT2G41950	-1.86	-0.90	-5.75	0.000804	0.018285	-0.19
247866_at	endoxyloglucan transferase (gb|AAD45	XTR3	AT5G57550	4.47	2.16	5.75	0.000808	0.018318	-0.19
261750_at	hypothetical protein contains similarity t	---	AT1G76120	-1.74	-0.80	-5.74	0.000809	0.018318	-0.19
266207_at	unknown protein ; supported by cDNA:	---	AT2G27680	-1.82	-0.86	-5.75	0.000808	0.018318	-0.19
245329_at	Expressed protein ; supported by full-ler	---	AT4G14365	3.28	1.71	5.75	0.000808	0.018318	-0.19
251906_at	putative protein several hypothetical Na	ATCHX20	AT3G53720	-1.85	-0.89	-5.74	0.000812	0.018333	-0.20
250981_at	receptor like protein kinase receptor like	---	AT5G03140	-1.90	-0.92	-5.74	0.000812	0.018333	-0.20
256829_at	unknown protein similar to aluminum-inc	---	AT3G22850	2.18	1.12	5.74	0.00081	0.018333	-0.19
250305_at	putative protein contains similarity to unl	---	AT5G12150	-1.76	-0.82	-5.74	0.000816	0.018401	-0.20
260386_at	putative strictosidine synthase similar to	---	AT1G74010	5.02	2.33	5.73	0.000823	0.018453	-0.21
261803_at	transcription factor, putative similar to tr	NF-YA7	AT1G30500	-1.90	-0.93	-5.73	0.000819	0.018453	-0.21

250504_at	putative protein similar to unknown prote	---	AT5G09840	-1.76	-0.82	-5.73	0.000821	0.018453	-0.21
246435_at	hypothetical protein ; supported by cDN	---	AT5G17460	-1.46	-0.55	-5.73	0.000823	0.018453	-0.21
266079_at	unknown protein	LCD1	AT2G37860	-1.77	-0.82	-5.73	0.000822	0.018453	-0.21
258162_at	dehydrogenase, putative similar to dihy	---	AT3G17810	1.88	0.91	5.73	0.000823	0.018453	-0.21
258599_at	L-allo-threonine aldolase, putative simil	THA2	AT3G04520	2.11	1.08	5.73	0.000824	0.018468	-0.21
265895_at	unknown protein ;supported by full-leng	---	AT2G15000	-1.67	-0.74	-5.72	0.000828	0.018521	-0.22
247266_at	beta-xylosidase	XYL4	AT5G64570	2.22	1.15	5.72	0.000828	0.018521	-0.22
266932_s_a	putative RNA helicase	---	AT1G63250 /	-2.09	-1.06	-5.71	0.000836	0.018651	-0.23
261498_at	receptor kinase, putative similar to rece	HSL1	AT1G28440	-1.82	-0.86	-5.71	0.000836	0.018651	-0.23
251030_at	putative protein kinesin light chain - Ple	NDP1	AT5G02130	-1.97	-0.98	-5.71	0.00084	0.018726	-0.23
263906_at	plastid division protein (FtsZ) identical to	FTSZ2-1	AT2G36250	-1.67	-0.74	-5.70	0.000843	0.018782	-0.24
253004_at	putative protein	---	AT4G38280 /	-1.89	-0.91	-5.70	0.000845	0.018794	-0.24
254229_at	hypothetical protein ; supported by cDN	---	AT4G23610	4.33	2.12	5.70	0.000849	0.018855	-0.24
250484_at	asparagine synthetase ASN3 ; supporte	ASN3	AT5G10240	-1.55	-0.63	-5.70	0.000849	0.018855	-0.24
264515_at	hypothetical protein similar to hypothetic	---	AT1G10090	-1.41	-0.50	-5.69	0.00085	0.018855	-0.24
267008_at	putative ABC transporter	---	AT2G39350	2.07	1.05	5.69	0.000856	0.018858	-0.25
264708_at	putative ER6 protein similar to GB:AAD	---	AT1G09740	1.87	0.91	5.69	0.000857	0.018858	-0.25
258682_at	putative ribosomal-protein S6 kinase (A	S6K2	AT3G08720	3.20	1.68	5.69	0.000857	0.018858	-0.25
264239_at	hypothetical protein predicted by genem	---	AT1G54770	-1.48	-0.57	-5.69	0.000854	0.018858	-0.25
267064_at	calmodulin (cam2)	CAM2	AT2G41110	2.51	1.33	5.69	0.000853	0.018858	-0.25
247131_at	ferredoxin-NADP+ reductase	FNR1	AT5G66190	-1.50	-0.59	-5.69	0.000854	0.018858	-0.25
248541_at	protein kinase ATN1-like protein	---	AT5G50180	-1.88	-0.91	-5.69	0.000855	0.018858	-0.25
249726_at	unknown protein	---	AT5G35480	-2.27	-1.18	-5.69	0.000854	0.018858	-0.25
251612_at	putative protein hypothetical protein T2	---	AT3G57950	1.59	0.67	5.69	0.000855	0.018858	-0.25
251848_at	Expressed protein ; supported by cDNA	BZIP25	AT3G54620	1.61	0.68	5.68	0.000859	0.018868	-0.26
251743_at	Yippee-like protein Yippee protein, Hon	---	AT3G55890	2.75	1.46	5.68	0.000862	0.018916	-0.26
245422_at	putative protein	---	AT4G17470	-4.51	-2.17	-5.68	0.000863	0.018928	-0.26
258643_at	unknown protein ;supported by full-leng	ATAB2	AT3G08010	-1.47	-0.55	-5.68	0.000864	0.018928	-0.26
262062_s_a	hypothetical protein	emb1427	AT1G20570 /	-1.60	-0.68	-5.67	0.000868	0.018990	-0.27
259207_at	unknown protein	---	AT3G09050	-1.76	-0.82	-5.67	0.000868	0.018990	-0.27
264415_at	AP2 domain containing protein, putative	RAP2.6	AT1G43160	1.76	0.82	5.67	0.000871	0.019017	-0.27
261845_at	metal ion transporter, putative similar to	NRAMP6	AT1G15960	-1.92	-0.94	-5.67	0.000871	0.019017	-0.27
264188_at	histone H2A, putative similar to histone	GAMMA-H	AT1G54690	-2.57	-1.36	-5.67	0.000874	0.019031	-0.27
247139_at	unknown protein ;supported by full-leng	---	AT5G66090	-1.60	-0.68	-5.67	0.000873	0.019031	-0.27
246922_at	serine/threonine protein kinase-like prot	CIPK25	AT5G25110	-2.06	-1.05	-5.67	0.000874	0.019031	-0.28

266608_at	hypothetical protein predicted by genefir	---	AT2G35500	-1.84	-0.88	-5.67	0.000875	0.019037	-0.28
251427_at	beta-glucosidase-like protein several be	BGLU16	AT3G60130	1.92	0.94	5.66	0.000881	0.019120	-0.28
264014_at	putative auxin-regulated protein	---	AT2G21210	-4.31	-2.11	-5.66	0.000883	0.019120	-0.29
250852_at	putative protein BRL protein, Homo sap	---	AT5G04670	-1.46	-0.55	-5.66	0.000883	0.019120	-0.29
251134_at	hypothetical protein RNA polymerase II	AtQSOX2	AT2G01270 /	-1.59	-0.67	-5.66	0.000883	0.019120	-0.29
253251_at	putative protein similarity predicted prot	---	AT4G34730	-1.90	-0.92	-5.66	0.000883	0.019120	-0.29
265314_at	hypothetical protein predicted by gensca	---	AT2G20210	-1.63	-0.71	-5.65	0.000885	0.019129	-0.29
258264_at	unknown protein	MBD11	AT3G15790	-1.74	-0.80	-5.65	0.000886	0.019139	-0.29
261728_at	pectinesterase, putative similar to pecti	sks5	AT1G76160	2.16	1.11	5.64	0.0009	0.019160	-0.31
245325_at	xyloglucan endotransglycosylase-relate	XTR7	AT4G14130	8.76	3.13	5.65	0.000893	0.019160	-0.30
254543_at	putative chitinase chitinase (EC 3.2.1.1	---	AT4G19810	4.49	2.17	5.64	0.000897	0.019160	-0.30
258161_at	hypothetical protein predicted by genem	---	AT3G17930	-1.65	-0.72	-5.64	0.0009	0.019160	-0.31
249527_at	proline oxidase, mitochondrial precurso	---	AT5G38710	1.97	0.98	5.64	0.000894	0.019160	-0.30
263958_at	putative salt-inducible protein	---	AT2G36240	-1.43	-0.51	-5.64	0.000896	0.019160	-0.30
247508_at	auxin response factor - like protein auxi	ARF2	AT5G62000	-1.93	-0.95	-5.64	0.0009	0.019160	-0.31
258365_s_a	putative diaminopimelate decarboxylase	---	AT3G14390 /	-1.63	-0.71	-5.64	0.000899	0.019160	-0.30
248075_at	selenium-binding protein-like	CRR21	AT5G55740	-2.02	-1.02	-5.64	0.000894	0.019160	-0.30
259293_at	putative DNA binding protein similarity t	---	AT3G11580	2.21	1.15	5.64	0.000895	0.019160	-0.30
245795_at	unknown protein contains similarity to ol	---	AT1G32160	-1.51	-0.59	-5.64	0.000899	0.019160	-0.30
267384_at	unknown protein highly similar to GP|24	---	AT2G44370	5.67	2.50	5.64	0.000898	0.019160	-0.30
245595_at	hypothetical protein	---	AT4G14170	-1.49	-0.58	-5.65	0.000888	0.019160	-0.29
261481_at	nucleoside triphosphatase, putative sim	---	AT1G14260	1.80	0.85	5.65	0.000891	0.019160	-0.30
261629_at	unknown protein	---	AT1G49980	-1.50	-0.59	-5.65	0.000892	0.019160	-0.30
265873_at	putative beta-1,3-glucanase ;supported	---	AT2G01630	-1.72	-0.78	-5.65	0.000892	0.019160	-0.30
245367_at	Expressed protein ; supported by full-ler	NRPB9B	AT4G16265	-1.60	-0.68	-5.63	0.000903	0.019203	-0.31
266052_at	putative WRKY-type DNA binding protei	WRKY55	AT2G40740	2.33	1.22	5.63	0.000904	0.019210	-0.31
265305_at	putative tyrosine decarboxylase	---	AT2G20340	-1.78	-0.83	-5.63	0.00091	0.019296	-0.32
251699_at	cytochrome P450-like protein cytochror	CYP94D2	AT3G56630	-1.61	-0.68	-5.62	0.000912	0.019296	-0.32
254628_at	Expressed protein ; supported by full-ler	---	AT4G18593	-1.42	-0.51	-5.63	0.000912	0.019296	-0.32
256244_at	sulphate transporter, putative similar to	SULTR4;2	AT3G12520	-1.51	-0.59	-5.62	0.000912	0.019296	-0.32
263843_at	translin-like protein ; supported by cDN/	---	AT2G37020	-1.53	-0.62	-5.62	0.000913	0.019310	-0.32
258049_at	hypothetical protein similar to CGI-18 pr	---	AT3G16220	1.46	0.55	5.62	0.000914	0.019314	-0.32
246214_at	heat shock transcription factor HSF4 ; s	HSF4	AT4G36988 /	1.86	0.89	5.62	0.000915	0.019315	-0.32
251541_at	citrate synthase -like protein citrate syn	CSY2	AT3G58750	1.86	0.89	5.62	0.000917	0.019324	-0.32
261119_at	chloroplast 50S ribosomal protein L31,	emb2184	AT1G75350	-1.39	-0.47	-5.62	0.000919	0.019354	-0.33

260062_at	hypothetical protein contains Pfam profil	---	AT1G73710	-1.71	-0.77	-5.61	0.000925	0.019474	-0.33
250688_at	transcription factor-like protein ;support	NF-YA10	AT5G06510	-1.50	-0.58	-5.61	0.00093	0.019529	-0.34
251744_at	putative protein CHLOROPLAST 30S R	---	AT3G56010	-1.73	-0.79	-5.61	0.00093	0.019529	-0.34
261322_at	hypothetical protein predicted by genem	ATPUP11	AT1G44750	-1.64	-0.71	-5.60	0.000932	0.019548	-0.34
261420_at	fatty acid elongase 3-ketoacyl-CoA syn	KCS3	AT1G07720	2.66	1.41	5.60	0.000936	0.019608	-0.35
254894_at	putative phospholipase D-gamma phos	PLDGAMM	AT4G11840	1.97	0.98	5.60	0.000936	0.019608	-0.35
259541_at	protein kinase, putative similar to protei	---	AT1G20650	-2.09	-1.06	-5.60	0.000937	0.019608	-0.35
264591_at	hypothetical protein contains similarity to	---	AT2G17670	-1.58	-0.66	-5.60	0.000939	0.019629	-0.35
260328_at	putative aspartate aminotransferase sim	---	AT1G80360	1.44	0.53	5.59	0.000941	0.019658	-0.35
248292_at	putative protein similar to unknown prote	---	AT5G53030	-1.98	-0.99	-5.59	0.000946	0.019735	-0.36
257478_at	hypothetical protein similar to putative s	WAKL2	AT1G16130	2.79	1.48	5.59	0.000947	0.019747	-0.36
258283_at	hypothetical protein predicted by genem	---	AT3G26750	-1.58	-0.66	-5.59	0.000948	0.019749	-0.36
251970_at	glucosyltransferase - like protein glucos	UGT73D1	AT3G53150	2.18	1.12	5.58	0.00095	0.019781	-0.36
262682_at	anter-specific proline-rich -like protein (A	---	AT1G75900	4.40	2.14	5.58	0.000954	0.019801	-0.37
253438_at	glycine hydroxymethyltransferase (EC 2	SHM3	AT4G32520	-1.80	-0.85	-5.58	0.000953	0.019801	-0.37
256405_at	calcium-dependent protein kinase simila	CPK33	AT1G50700	-1.49	-0.58	-5.58	0.000955	0.019801	-0.37
254641_at	ras-like GTP-binding protein strong hon	ATRABA1	AT4G18800	2.01	1.01	5.58	0.000953	0.019801	-0.37
261564_at	NAC domain protein, putative similar to	ATAF1	AT1G01720	1.89	0.92	5.58	0.000956	0.019813	-0.37
259043_at	unknown protein similar to putative prote	---	AT3G03440	2.02	1.02	5.58	0.000958	0.019819	-0.37
257021_at	branched-chain amino acid aminotrans	BCAT4	AT3G19710	-2.68	-1.42	-5.57	0.000961	0.019876	-0.37
255619_s_a	putative CHP-rich zinc finger protein sir	---	AT4G01350 /	-1.83	-0.87	-5.57	0.000963	0.019900	-0.38
257903_at	unknown protein	---	AT3G28460	-1.53	-0.61	-5.57	0.000965	0.019912	-0.38
253738_at	photosystem I subunit PSI-E - like prote	PSAE-1	AT4G28750	-1.41	-0.49	-5.56	0.000969	0.019984	-0.38
255685_s_a	putative tetrahydrofolate synthase simila	---	AT4G00600 /	-2.05	-1.03	-5.56	0.000971	0.020014	-0.39
247694_at	GTP cyclohydrolase II / 3,4-dihydroxy-2	---	AT5G59750	-1.60	-0.68	-5.56	0.000973	0.020021	-0.39
260989_at	unknown protein ; supported by cDNA: g	---	AT1G53450	-1.80	-0.85	-5.56	0.000974	0.020024	-0.39
255026_at	hypothetical protein	MES12	AT4G09900	-2.37	-1.24	-5.56	0.000974	0.020024	-0.39
248493_at	putative protein contains similarity to iro	FSD2	AT5G51100	-1.63	-0.71	-5.56	0.000978	0.020087	-0.39
252178_at	putative protein various predicted protei	---	AT3G50750	-2.91	-1.54	-5.55	0.00098	0.020103	-0.40
262099_s_a	auxin-regulated protein GH3, putative s	GH3.4	AT1G59500 /	11.70	3.55	5.55	0.000983	0.020141	-0.40
262878_at	hypothetical protein predicted by genem	NDF2	AT1G64770	-1.68	-0.75	-5.55	0.000985	0.020163	-0.40
249977_at	chaperonin 60 alpha chain - like protein	EMB3007	AT5G18820	-1.82	-0.87	-5.55	0.000988	0.020196	-0.40
246145_at	peroxidase peroxidase, Lycopersicon e	---	AT5G19880	3.51	1.81	5.55	0.000987	0.020196	-0.40
251739_at	putative protein protein of unknown fun	CAN	AT3G56170	1.83	0.87	5.54	0.000992	0.020255	-0.41
258299_at	unknown protein contains GMC oxidore	---	AT3G23410	-1.90	-0.92	-5.54	0.000994	0.020279	-0.41

264504_at	unknown protein similar to ATP-citrate-	ACLA-3	AT1G09430	1.52	0.60	5.54	0.000996	0.020297	-0.41
244939_at	ribosomal protein S12 (trans-splice part	---	---	-2.08	-1.06	-5.54	0.000997	0.020297	-0.41
266065_at	phytochrome B Identical to GB:X17342	PHYB	AT2G18790	-1.66	-0.74	-5.54	0.000998	0.020300	-0.41
251119_at	putative protein nifR3 protein, Azospirill	---	AT3G63510	-1.88	-0.91	-5.54	0.000999	0.020300	-0.42
264254_at	unknown protein	---	AT1G09150	-1.43	-0.51	-5.53	0.001	0.020303	-0.42
251525_at	putative protein several hypothetical pro	---	AT3G59000	-1.65	-0.72	-5.53	0.001	0.020303	-0.42
250486_at	putative protein predicted proteins, Arat	---	AT5G09670 /	-1.58	-0.66	-5.53	0.001008	0.020421	-0.43
254680_at	phytochrome E	PHYE	AT4G18130	-1.78	-0.83	-5.53	0.001008	0.020421	-0.43
247232_at	ABC transporter-like	ATH13	AT5G64940	-1.79	-0.84	-5.52	0.00101	0.020434	-0.43
264384_at	putative chromodomain-helicase-DNA-	PKL	AT2G25170	-1.44	-0.53	-5.52	0.001012	0.020458	-0.43
251149_at	putative protein CGI-77 protein, Homo s	---	AT3G62940	-1.41	-0.49	-5.52	0.001013	0.020467	-0.43
259347_at	putative GAR1 protein similar to GB:P28	---	AT3G03920	-1.52	-0.60	-5.52	0.001017	0.020498	-0.43
248765_at	MutT domain protein-like ; supported by	ATNUDT2	AT5G47650	-1.48	-0.57	-5.52	0.001016	0.020498	-0.43
245875_at	hypothetical protein predicted by genem	---	AT1G26240	1.70	0.76	5.52	0.001017	0.020498	-0.43
249927_at	Glucose-1-phosphate adenylyltransferas	APL1	AT5G19220	-2.08	-1.06	-5.50	0.001032	0.020527	-0.45
265720_at	unknown protein	---	AT2G40110	2.53	1.34	5.50	0.001035	0.020527	-0.45
251713_at	putative protein several hypothetical pro	---	AT3G56080	-1.78	-0.83	-5.51	0.001023	0.020527	-0.44
254784_at	growth factor like protein antisense bas	NUDT7	AT4G12720	2.87	1.52	5.50	0.001033	0.020527	-0.45
258355_at	hypothetical protein predicted by gensca	---	AT3G14330	-1.90	-0.92	-5.51	0.001028	0.020527	-0.45
267101_at	putative peroxidase	---	AT2G41480	-1.84	-0.88	-5.50	0.001034	0.020527	-0.45
257964_at	hypothetical protein similar to hypothetic	---	AT3G19850	-2.04	-1.03	-5.51	0.001025	0.020527	-0.44
249247_at	maize crp1 protein-like	---	AT5G42310	-1.75	-0.81	-5.50	0.001035	0.020527	-0.45
251295_at	putative protein several O-methyltransfe	---	AT3G62000	-1.81	-0.85	-5.51	0.001025	0.020527	-0.44
263405_s_a	hypothetical protein similar to hypothetic	---	AT2G04066 /	-1.44	-0.53	-5.51	0.00102	0.020527	-0.44
258890_at	putative transcription factor similar to GE	NF-YA2	AT3G05690	-2.14	-1.10	-5.50	0.001033	0.020527	-0.45
254716_at	putative protein LEA protein , Cicer arie	UNE15	AT4G13560	-1.92	-0.94	-5.51	0.001028	0.020527	-0.45
264586_at	putative cytochrome P450 Similar to GB	CYP88A3	AT1G05160	-1.57	-0.65	-5.51	0.001026	0.020527	-0.44
261014_at	unknown protein ;supported by full-lengt	---	AT1G26460	-1.55	-0.64	-5.51	0.001021	0.020527	-0.44
260411_at	hypothetical protein similar to GB:AAB6	---	AT1G69890	2.61	1.38	5.50	0.001033	0.020527	-0.45
258113_at	putative cytochrome P450 similar to GB	CYP72A11	AT3G14650	-2.06	-1.04	-5.51	0.001027	0.020527	-0.44
253795_at	tyrosine transaminase-like protein tyros	---	AT4G28420	1.61	0.68	5.51	0.001026	0.020527	-0.44
248770_at	unknown protein	---	AT5G47740	1.73	0.79	5.50	0.001034	0.020527	-0.45
256797_at	DEAD box helicase protein, putative sir	---	AT3G18600	-2.00	-1.00	-5.50	0.001036	0.020529	-0.45
256130_at	unknown protein contains Pfam profile:	---	AT1G18170	-1.67	-0.74	-5.50	0.001037	0.020542	-0.46
248094_at	trigger factor-like protein	---	AT5G55220	-1.79	-0.84	-5.50	0.001039	0.020562	-0.46

248134_at	putative protein contains similarity to int	---	AT5G54860	2.29	1.20	5.50	0.001041	0.020570	-0.46
267415_at	putative translation initiation factor eIF-2	---	AT2G34970	-1.45	-0.53	-5.49	0.001043	0.020578	-0.46
245982_at	senescence-associated protein (SAG29	SAG29	AT5G13170	8.82	3.14	5.49	0.001043	0.020578	-0.46
245188_at	F12A21.19 unknown protein; similar to	---	AT1G67660	-1.59	-0.67	-5.49	0.001044	0.020582	-0.46
247855_at	similar to unknown protein (sp|P23253)	---	AT5G58210	-1.79	-0.84	-5.49	0.001048	0.020586	-0.47
267013_at	putative protein kinase contains a protei	CCR2	AT2G39180	-1.57	-0.65	-5.49	0.001049	0.020586	-0.47
247154_at	receptor protein kinase-like protein	HSL2	AT5G65710	-1.50	-0.58	-5.49	0.001048	0.020586	-0.47
263216_s_a	putative reticuline oxidase-like protein s	---	AT1G30720 /	10.31	3.37	5.49	0.001047	0.020586	-0.46
250301_at	putative protein predicted proteins, Arat	---	AT5G11970	1.87	0.90	5.49	0.001046	0.020586	-0.46
252199_at	anthranilate N-hydroxycinnamoyl/benzo	---	AT3G50270	-1.66	-0.73	-5.49	0.001051	0.020610	-0.47
266395_at	3-isopropylmalate dehydratase, small s	---	AT2G43100	-3.27	-1.71	-5.48	0.001054	0.020659	-0.47
249783_at	calcium sensor homolog (gb|AAC26110	SOS3	AT5G24270	2.51	1.33	5.48	0.001057	0.020681	-0.48
259235_at	hypothetical protein predicted by gensca	---	AT3G11600	2.89	1.53	5.48	0.001057	0.020681	-0.48
246060_at	rev interacting protein mis3 - like rev int	---	AT5G08420	-1.44	-0.52	-5.48	0.001062	0.020683	-0.48
254502_at	hypothetical protein	PTAC14	AT4G20130	-1.69	-0.76	-5.48	0.001059	0.020683	-0.48
260014_at	hydroxypyruvate reductase (HPR) identi	HPR	AT1G68010	-1.66	-0.73	-5.48	0.001062	0.020683	-0.48
250763_at	short chain alcohol dehydrogenase-like	---	AT5G06060	-1.65	-0.72	-5.48	0.00106	0.020683	-0.48
250383_at	putative GTP-binding protein GTP-bind	---	AT5G11480	-1.89	-0.92	-5.48	0.001061	0.020683	-0.48
256863_at	CCHC-type zinc finger protein, putative	---	AT3G24070	-1.44	-0.52	-5.47	0.001063	0.020683	-0.48
246052_at	putative protein predicted proteins, Arat	---	AT5G08310	-1.74	-0.80	-5.47	0.001064	0.020699	-0.48
250621_at	membrane protein membrane protein -	ATRBL3	AT5G07250	-1.58	-0.66	-5.47	0.001066	0.020720	-0.48
266461_at	glutathione S-transferase (GST6) identi	ATGSTF8	AT2G47730	2.18	1.12	5.47	0.001068	0.020729	-0.49
249026_at	Expressed protein ; supported by full-ler	OSB3	AT5G44785	-1.75	-0.81	-5.47	0.00107	0.020762	-0.49
265147_at	hypothetical protein	---	AT1G51380	-1.91	-0.93	-5.47	0.001072	0.020766	-0.49
250987_at	putative protein crp1 protein, Zea mays	---	AT5G02860	-1.65	-0.72	-5.47	0.001072	0.020766	-0.49
259297_at	putative disease resistance protein simil	AtRLP30	AT3G05360	3.08	1.62	5.46	0.001074	0.020772	-0.49
252929_at	putative fructose-bisphosphate aldolase	---	AT4G38970	-1.53	-0.61	-5.46	0.001075	0.020772	-0.49
253224_at	invertase - like protein mRNA, Lilium lo	---	AT4G34860	-1.97	-0.98	-5.46	0.001076	0.020772	-0.49
265172_at	putative spermidine synthase	SPDS1	AT1G23820	-1.45	-0.53	-5.46	0.001076	0.020772	-0.49
267363_at	putative peroxisomal membrane carrier	---	AT2G39970	1.52	0.61	5.46	0.001078	0.020788	-0.50
257685_at	unknown protein	---	AT3G12770	-1.68	-0.75	-5.46	0.001082	0.020825	-0.50
244966_at	cytochrome b6-f complex, subunit V	---	---	-1.93	-0.95	-5.46	0.001081	0.020825	-0.50
251022_at	putative protein Hsp70 binding protein h	---	AT5G02150	1.63	0.70	5.46	0.001084	0.020852	-0.50
261788_at	unknown protein ;supported by full-lengt	NDF1	AT1G15980	-2.28	-1.19	-5.45	0.001092	0.020977	-0.51
251670_at	putative protein translation releasing fa	---	AT3G57190	-1.73	-0.79	-5.44	0.001101	0.021131	-0.52

260276_at	unknown protein	---	AT1G80450	2.82	1.50	5.44	0.001102	0.021144	-0.52
258622_at	unknown protein contains Pfam profile:	---	AT3G02720	-1.52	-0.60	-5.44	0.001103	0.021150	-0.52
261722_at	acyl-(acyl carrier protein) thioesterase,	FATB	AT1G08510	1.46	0.54	5.43	0.001108	0.021187	-0.53
258809_at	NAM-like protein (no apical meristem) s	anac047	AT3G04070	3.03	1.60	5.43	0.00111	0.021187	-0.53
266635_at	unknown protein ;supported by full-leng	---	AT2G35470	-1.72	-0.79	-5.43	0.001109	0.021187	-0.53
264475_s_a	hypothetical protein predicted by genem	---	AT1G77150 /	-1.74	-0.80	-5.43	0.00111	0.021187	-0.53
250724_at	harpin-induced protein-like	---	AT5G06330	2.06	1.04	5.43	0.001109	0.021187	-0.53
246228_at	peroxidase like protein	---	AT4G36430	5.53	2.47	5.43	0.001111	0.021189	-0.53
261482_at	unknown protein ;supported by full-leng	THH1	AT1G14530	1.57	0.65	5.43	0.001113	0.021197	-0.53
264613_at	lipoyltransferase identical to GB:BAA78	LIP2	AT1G04640	-1.58	-0.66	-5.43	0.001113	0.021197	-0.53
247406_at	response regulator 6 (ARR6) ; supporte	ARR6	AT5G62920	3.06	1.61	5.43	0.001116	0.021200	-0.53
248942_at	putative protein similar to unknown prote	---	AT5G45480	1.64	0.72	5.43	0.001116	0.021200	-0.53
262455_at	Mlo protein, putative similar to Mlo prote	MLO2	AT1G11310	1.84	0.88	5.43	0.001116	0.021200	-0.53
252450_s_a	receptor kinase-like protein receptor kin	---	AT3G47090 /	2.41	1.27	5.42	0.00112	0.021252	-0.54
265961_at	unknown protein ;supported by full-leng	---	AT2G37400	-1.98	-0.98	-5.42	0.001121	0.021262	-0.54
254563_at	putative protein several hypothetical pro	ERD3	AT4G19120	-1.80	-0.85	-5.42	0.001128	0.021364	-0.54
256296_at	hypothetical protein	---	AT1G69480	1.46	0.55	5.41	0.001132	0.021419	-0.55
254066_at	transcriptional activator CBF1-like prote	DREB1A	AT4G25480	-3.44	-1.78	-5.41	0.001133	0.021420	-0.55
259908_at	RNA polymerase subunit identical to GI:	ATRPAC4	AT1G60850	-1.84	-0.88	-5.41	0.001135	0.021443	-0.55
248418_at	cleavage and polyadenylation specificity	CPSF160	AT5G51660	-1.58	-0.66	-5.41	0.00114	0.021526	-0.56
258149_at	hypothetical protein contains Pfam profi	EMB1270	AT3G18110	-1.69	-0.76	-5.41	0.001141	0.021526	-0.56
259149_at	putative phenylalanine ammonia-lyase s	PAL4	AT3G10340	7.09	2.83	5.40	0.001143	0.021545	-0.56
244978_at	RNA polymerase alpha subunit	---	---	-1.49	-0.57	-5.40	0.001144	0.021555	-0.56
265326_at	unknown protein predicted by genscan	---	AT2G18220	-1.82	-0.87	-5.39	0.001155	0.021589	-0.57
247015_at	protease-like	---	AT5G66960	-1.77	-0.82	-5.39	0.001155	0.021589	-0.57
256858_at	hypothetical protein predicted by genem	---	AT3G15140	-1.89	-0.92	-5.40	0.001152	0.021589	-0.57
254052_at	UMP/CMP kinase like protein UMP/CM	---	AT4G25280	-1.65	-0.73	-5.40	0.001151	0.021589	-0.57
262631_at	hypothetical protein predicted by genem	---	AT1G06500	-1.50	-0.59	-5.40	0.00115	0.021589	-0.56
264893_at	unknown protein similar to unknown pro	---	AT1G23140	1.72	0.78	5.40	0.001151	0.021589	-0.57
265660_at	putative disease resistance protein	AtRLP21	AT2G25470	1.89	0.92	5.40	0.001152	0.021589	-0.57
AFFX-DapX	B. subtilis /GEN=jojG /DB_XREF=gb:L3	---	---	-1.68	-0.75	-5.40	0.001153	0.021589	-0.57
256134_at	aminoalcoholphosphotransferase identi	AAPT1	AT1G13560	-1.47	-0.56	-5.40	0.001153	0.021589	-0.57
267606_at	putative beta-ketoacyl-CoA synthase	KCS11	AT2G26640	-1.46	-0.54	-5.39	0.001157	0.021606	-0.57
254040_at	possible apospory-associated like prote	---	AT4G25900	2.05	1.04	5.39	0.001164	0.021698	-0.58
256979_at	Expressed protein ; supported by full-ler	PSBTN	AT3G09550 /	-1.60	-0.68	-5.39	0.001163	0.021698	-0.58

254050_s_a	hypothetical protein ; supported by cDN	---	AT4G25670 /	1.53	0.61	5.39	0.001164	0.021698	-0.58
264514_at	putative cinnamyl alcohol dehydrogena	---	AT1G09500	8.94	3.16	5.38	0.001167	0.021708	-0.58
252246_at	putative protein various predicted protei	---	AT3G49725 /	-1.58	-0.66	-5.38	0.001167	0.021708	-0.58
245007_at	PSI P700 apoprotein A1	---	---	-2.19	-1.13	-5.38	0.001171	0.021770	-0.58
251140_at	lectin - like protein lectin precursor LEC	---	AT5G01090	-1.59	-0.67	-5.38	0.001178	0.021881	-0.59
249710_at	glutamate-ammonia ligase (EC 6.3.1.2)	GS2	AT5G35630	-1.57	-0.65	-5.37	0.001181	0.021911	-0.59
251206_at	putative protein various predicted proet	---	AT3G63090	-1.92	-0.94	-5.37	0.001183	0.021922	-0.59
266104_at	putative phosphatidate cytidylyltransfera	---	AT2G45150	-1.60	-0.68	-5.37	0.001185	0.021922	-0.60
246074_at	hypothetical protein ; supported by full-l	---	AT5G20130	-1.48	-0.57	-5.37	0.001185	0.021922	-0.60
266673_at	putative thiamin biosynthesis protein	THIC	AT2G29630	-2.02	-1.01	-5.37	0.001184	0.021922	-0.60
254250_at	serine/threonine kinase - like protein se	---	AT4G23290	-2.41	-1.27	-5.37	0.001188	0.021969	-0.60
258849_at	putative UDP-glucose pyrophosphorylas	UGP	AT3G03250	-1.74	-0.80	-5.36	0.001191	0.021995	-0.60
256014_at	hypothetical protein predicted by genem	---	AT1G19200	3.62	1.86	5.36	0.001198	0.022093	-0.61
252632_s_a	disease resistance protein -like disease	RPP1	AT3G44480 /	1.59	0.66	5.36	0.001198	0.022093	-0.61
245061_at	hypothetical protein ;supported by full-le	RCA	AT2G39730	-1.43	-0.52	-5.36	0.001199	0.022098	-0.61
256407_at	sucrose-proton symporter, putative sim	ATSUC7	AT1G66570	4.52	2.18	5.36	0.001201	0.022108	-0.61
247455_at	MYB96 transcription factor-like protein	MYB96	AT5G62470	2.08	1.06	5.35	0.001208	0.022213	-0.62
261474_at	anionic peroxidase, putative similar to a	---	AT1G14540	11.99	3.58	5.35	0.001209	0.022222	-0.62
261925_at	oligopeptide transporter, putative simila	---	AT1G22540	-1.53	-0.62	-5.35	0.001213	0.022272	-0.62
258474_at	hypothetical protein predicted by gensca	---	AT3G02650	-1.92	-0.94	-5.34	0.001216	0.022281	-0.62
248105_at	cell division protein FtsZ chloroplast hon	FTSZ1-1	AT5G55280	-1.77	-0.83	-5.34	0.001216	0.022281	-0.62
267644_s_a	unknown protein highly similar to T21L1	---	AT2G32870 /	-1.92	-0.94	-5.35	0.001215	0.022281	-0.62
253422_at	putative protein ;supported by full-lengt	---	AT4G32240	-1.57	-0.65	-5.34	0.001218	0.022283	-0.62
256468_at	ferredoxin, putative similar to GB:D909	---	AT1G32550	-1.65	-0.72	-5.34	0.001218	0.022283	-0.63
246030_at	Expressed protein genomic sequence i	---	AT5G21105	1.53	0.61	5.34	0.001222	0.022316	-0.63
257225_s_a	50S ribosomal protein L12-C identical t	RPL12-C	AT3G27830 /	-1.48	-0.56	-5.34	0.001222	0.022316	-0.63
255886_at	plastocyanin, putative similar to plastoc	DRT112	AT1G20340	-1.48	-0.56	-5.34	0.001226	0.022367	-0.63
251059_at	serine/threonine protein kinase ATPK10	CIPK15	AT5G01810	3.22	1.69	5.34	0.001228	0.022367	-0.63
246110_at	putative protein predicted proteins - Ara	---	AT5G20140	-1.97	-0.98	-5.33	0.001229	0.022367	-0.63
249459_at	peroxidase ATP24a	---	AT5G39580	10.76	3.43	5.34	0.001227	0.022367	-0.63
253908_at	GH3 like protein GH3 protein, Glycine r	WES1	AT4G27260	6.56	2.71	5.33	0.001231	0.022400	-0.64
261540_at	unknown protein	---	AT1G63610	-1.61	-0.69	-5.33	0.001233	0.022401	-0.64
249101_at	unknown protein	---	AT5G43580	3.31	1.73	5.33	0.001237	0.022442	-0.64
260496_at	putative ABC transporter	---	AT2G41700	-1.43	-0.51	-5.33	0.001236	0.022442	-0.64
266284_at	putative pumilio/Mpt5 family RNA-bindin	APUM2	AT2G29190	-1.59	-0.67	-5.33	0.001239	0.022462	-0.64

247716_at	putative protein predicted protein, Arabi	---	AT5G59350	-1.95	-0.97	-5.33	0.001241	0.022462	-0.64
247786_at	putative protein various predicted prote	PMR5	AT5G58600	-1.45	-0.54	-5.32	0.001242	0.022462	-0.65
246252_s_a	patatin-like protein ;supported by full-len	PLP1	AT4G37060 /	1.42	0.50	5.32	0.001242	0.022462	-0.65
249658_s_a	N-glyceraldehyde-2-phosphotransferase	---	AT5G36700 /	-1.84	-0.88	-5.32	0.001247	0.022531	-0.65
253657_at	cadmium-transporting ATPase-like prot	HMA2	AT4G30110	-3.03	-1.60	-5.32	0.001248	0.022546	-0.65
248362_at	fibrillarin 1 (AtFib1) identical to fibrillarin	FIB1	AT5G52470	-1.50	-0.58	-5.32	0.001252	0.022558	-0.65
251985_at	thioredoxin -like protein cop c2, Coprin	---	AT3G53220	-1.69	-0.75	-5.32	0.001252	0.022558	-0.65
258403_at	hypothetical protein predicted by gensca	---	AT3G15380	-1.51	-0.59	-5.32	0.001252	0.022558	-0.65
262632_at	23 kDa polypeptide of oxygen-evolving c	PSBP-1	AT1G06680	-1.52	-0.60	-5.31	0.001256	0.022604	-0.66
260605_at	hypothetical protein predicted by genefir	---	AT2G43780	-1.50	-0.58	-5.31	0.00126	0.022647	-0.66
265258_at	hypothetical protein predicted by genefir	---	AT2G20390	-1.42	-0.51	-5.31	0.00126	0.022647	-0.66
264115_at	hypothetical protein	---	AT2G31290	-1.67	-0.74	-5.31	0.001262	0.022659	-0.66
248906_at	putative protein similar to unknown prote	---	AT5G46420	-1.51	-0.59	-5.31	0.001264	0.022689	-0.66
248589_at	von Hippel-Lindau binding protein (VHL	PDF3	AT5G49510	-1.46	-0.55	-5.31	0.001265	0.022691	-0.67
246282_at	ATPase-like protein	---	AT4G36580	-2.03	-1.02	-5.30	0.001269	0.022714	-0.67
262941_at	hypothetical protein predicted by genem	EMB2217	AT1G79490	-1.88	-0.91	-5.30	0.001269	0.022714	-0.67
265673_at	unknown protein ;supported by full-leng	---	AT2G32090	-1.71	-0.78	-5.30	0.00127	0.022714	-0.67
249470_at	putative protein predicted proteins, Arat	---	AT5G39350	-1.67	-0.74	-5.30	0.001273	0.022746	-0.67
256129_at	calcium-binding protein, putative similar	---	AT1G18210	2.14	1.10	5.30	0.001273	0.022746	-0.67
246453_at	syntaxin homologue ;supported by full-l	SYP21	AT5G16830	1.58	0.66	5.30	0.001276	0.022778	-0.67
257311_at	phosphate transporter, putative contain	PHT2;1	AT3G26570	-1.56	-0.64	-5.30	0.001277	0.022778	-0.68
258927_at	putative folylpolyglutamate synthetase s	DFC	AT3G10160	-1.51	-0.59	-5.30	0.001279	0.022790	-0.68
253001_at	Expressed protein ; supported by cDNA	---	AT4G38490	-1.39	-0.48	-5.29	0.001285	0.022870	-0.68
249162_at	Expressed protein ; supported by full-ler	---	AT5G42765	-1.80	-0.85	-5.29	0.001287	0.022870	-0.68
248500_at	unknown protein	---	AT5G50410	-1.66	-0.73	-5.29	0.001286	0.022870	-0.68
257846_at	unknown protein	---	AT3G12910	5.23	2.39	5.29	0.001286	0.022870	-0.68
263064_at	putative bZIP transcription factor contair	CPuORF1	AT2G18160 /	-1.82	-0.86	-5.29	0.001289	0.022884	-0.69
246327_at	receptor-like serine/threonine kinase, p	---	AT1G16670	1.71	0.78	5.29	0.00129	0.022884	-0.69
265865_at	hypothetical protein predicted by gensca	---	AT2G01740	-1.43	-0.51	-5.29	0.001293	0.022885	-0.69
247073_at	33 kDa polypeptide of oxygen-evolving c	PSBO1	AT5G66570	-1.43	-0.52	-5.28	0.001296	0.022885	-0.69
267590_at	putative expansin ;supported by full-len	ATEXPA4	AT2G39700	2.34	1.23	5.29	0.001292	0.022885	-0.69
253308_at	putative protein aminotransferase (Asp	AGD2	AT4G33680	-1.48	-0.57	-5.28	0.001295	0.022885	-0.69
260772_at	unknown protein contains similarity to nu	---	AT1G49050	1.66	0.74	5.28	0.001296	0.022885	-0.69
259017_at	unknown protein ; supported by full-leng	---	AT3G07310	-1.56	-0.64	-5.28	0.001295	0.022885	-0.69
266641_at	Expressed protein ; supported by full-ler	---	AT2G35605	-1.54	-0.62	-5.28	0.001299	0.022913	-0.69

266117_at	hypothetical protein ; supported by cDN	---	AT2G02170	-1.46	-0.55	-5.28	0.001303	0.022952	-0.70
263564_s_a	DNA-directed RNA polymerase II, third	NRPB3	AT2G15400 /	-1.54	-0.62	-5.28	0.001303	0.022952	-0.70
255692_at	putative protein	GPAT8	AT4G00400	3.91	1.97	5.28	0.001305	0.022963	-0.70
254804_at	putative protein putative oxidoreductase	---	AT4G13010	-1.61	-0.69	-5.28	0.001308	0.023005	-0.70
251325_s_a	Lhca2 protein ;supported by full-length	LHCA2	AT3G61470 /	-1.38	-0.46	-5.27	0.00131	0.023029	-0.70
262456_at	glucose transporter almost identical to g	STP1	AT1G11260	2.25	1.17	5.27	0.001315	0.023068	-0.71
256274_at	GTPase, putative contains Pfam profile	emb2738	AT3G12080	-1.47	-0.55	-5.27	0.001314	0.023068	-0.71
258392_at	anther development protein, ATA20 ide	ATA20	AT3G15400	-1.73	-0.79	-5.27	0.001318	0.023100	-0.71
258134_at	rubisco expression protein, putative sim	---	AT3G24530	1.82	0.86	5.27	0.001319	0.023112	-0.71
259856_at	unknown protein ;supported by full-leng	---	AT1G68440	2.78	1.47	5.26	0.001323	0.023154	-0.71
249067_at	putative protein similar to unknown prote	---	AT5G43960	-1.53	-0.61	-5.26	0.001325	0.023177	-0.71
255760_at	vacuolar-type H+-translocating inorgani	---	AT1G16780	-1.53	-0.61	-5.26	0.001331	0.023263	-0.72
247709_at	D-xylose-H+ symporter - like protein D-	---	AT5G59250	-1.68	-0.75	-5.25	0.001337	0.023359	-0.72
257636_at	cytochrome P450, putative contains Pfa	CYP71B22	AT3G26200	2.72	1.45	5.25	0.001346	0.023424	-0.73
250798_at	peroxidase	---	AT5G05340	12.53	3.65	5.25	0.001343	0.023424	-0.73
260294_at	GMP synthase similar to GMP synthase	---	AT1G63660	-1.46	-0.55	-5.25	0.001345	0.023424	-0.73
248558_at	permease	---	AT5G49990	-1.97	-0.98	-5.25	0.001345	0.023424	-0.73
262170_at	hypothetical protein predicted by genem	---	AT1G74940	-1.90	-0.93	-5.25	0.001346	0.023424	-0.73
254877_at	putative protein threonine dehydratase	ATSR	AT4G11640	-1.58	-0.66	-5.24	0.001352	0.023513	-0.74
252972_at	auxin-induced protein - like auxin-induc	---	AT4G38840	-2.76	-1.46	-5.24	0.001355	0.023541	-0.74
264084_at	putative kinesin light chain	---	AT2G31240	-1.52	-0.61	-5.24	0.001359	0.023597	-0.74
249827_at	unknown protein ;supported by full-leng	---	AT5G23330	-1.64	-0.72	-5.24	0.001364	0.023635	-0.74
252412_at	Expressed protein ; supported by full-ler	---	AT3G47295	-2.10	-1.07	-5.24	0.001363	0.023635	-0.74
267126_s_a	putative acetone-cyanohydrin lyase	ACL	AT2G23590 /	-1.97	-0.98	-5.23	0.001366	0.023649	-0.75
254460_at	putative protein sigma70 operon, Staph	ATRP1	AT4G21210	-1.73	-0.79	-5.23	0.001366	0.023649	-0.75
256785_at	unknown protein ;supported by full-leng	PRA8	AT3G13720	1.81	0.85	5.23	0.001371	0.023702	-0.75
267506_at	unknown protein ;supported by full-leng	---	AT2G45520	-1.46	-0.54	-5.23	0.001372	0.023702	-0.75
253099_s_a	peroxidase - like protein peroxidase, Ar	---	AT4G37520 /	1.64	0.71	5.23	0.001376	0.023716	-0.75
250694_at	putative protein contains similarity to hol	HAT14	AT5G06710	-1.71	-0.77	-5.23	0.001375	0.023716	-0.75
263491_at	phosphoenolpyruvate carboxylase	ATPPC2	AT2G42600	-1.59	-0.67	-5.23	0.001374	0.023716	-0.75
250817_at	SET-domain protein-like ; supported by	SUVH1	AT5G04940	-1.49	-0.57	-5.23	0.001379	0.023758	-0.76
248347_at	putative protein contains similarity to phe	---	AT5G52250	1.42	0.51	5.22	0.001381	0.023764	-0.76
264900_at	putative auxin transport protein strongly	PIN7	AT1G23080	-1.98	-0.98	-5.22	0.001381	0.023764	-0.76
253505_at	Cytochrome P450-like protein flavonoid	CYP82C2	AT4G31970	1.77	0.82	5.22	0.00139	0.023787	-0.77
247101_at	apospory-associated protein C-like	---	AT5G66530	-1.75	-0.81	-5.22	0.001388	0.023787	-0.76

256793_at	unknown protein ;supported by full-leng	---	AT3G22160	2.63	1.40	5.22	0.001394	0.023787	-0.77
248605_at	putative protein similar to unknown prote	---	AT5G49410	-1.97	-0.98	-5.22	0.001389	0.023787	-0.76
249741_at	putative protein contains similarity to two	APRR5	AT5G24470	-1.38	-0.46	-5.22	0.001393	0.023787	-0.77
246700_at	cysteine synthase - like cysteine syntha	---	AT5G28030	-2.33	-1.22	-5.22	0.001392	0.023787	-0.77
247333_at	1-aminocyclopropane-1-carboxylic acid	FLS5	AT5G63600	2.51	1.33	5.22	0.001386	0.023787	-0.76
264177_at	hypothetical protein contains Pfam profil	---	AT1G02150	-1.50	-0.58	-5.22	0.001394	0.023787	-0.77
250791_at	nucleic acid binding protein-like ;suppor	AL1	AT5G05610	-1.47	-0.56	-5.21	0.001394	0.023787	-0.77
259841_at	unknown protein ; supported by full-leng	---	AT1G52200	1.74	0.80	5.22	0.001386	0.023787	-0.76
257180_at	sun protein (fmu protein), putative simil	---	AT3G13180	-1.69	-0.76	-5.22	0.001386	0.023787	-0.76
259592_at	lipid transfer protein, putative contains	LTPG1	AT1G27950	3.57	1.84	5.21	0.001403	0.023831	-0.78
256220_at	unknown protein	---	AT1G56230	-1.69	-0.76	-5.21	0.001405	0.023831	-0.78
254796_at	putative protein protein kinase homolog	---	AT4G13000	1.63	0.70	5.21	0.001403	0.023831	-0.78
266948_at	unknown protein	---	AT2G18850	-2.06	-1.04	-5.21	0.001404	0.023831	-0.78
261933_at	3-deoxy-D-arabino-heptulosonate 7-pho	---	AT1G22410	2.36	1.24	5.21	0.001401	0.023831	-0.77
246348_at	putative protein putative glycerol-3-phos	---	AT3G56840	-1.36	-0.44	-5.21	0.001405	0.023831	-0.78
262620_at	hypothetical protein predicted by gensca	---	AT1G06540	1.43	0.52	5.21	0.001402	0.023831	-0.77
262183_at	unknown protein	---	AT1G77890	1.49	0.57	5.21	0.001403	0.023831	-0.78
250679_at	putative protein contains similarity to unl	---	AT5G06550	-1.88	-0.91	-5.21	0.001406	0.023831	-0.78
263736_at	nucleic acid-binding protein, putative sir	---	AT1G60000	-1.82	-0.86	-5.20	0.001409	0.023847	-0.78
263442_at	hypothetical protein	---	AT2G28605	-1.44	-0.52	-5.21	0.001409	0.023847	-0.78
253674_at	UDP-N-acetylglucosamine O-acyltransf	---	AT4G29540	-1.51	-0.59	-5.20	0.001411	0.023852	-0.78
254045_at	pumilio-like protein abdominal segment	APUM6	AT4G25880	-1.46	-0.54	-5.20	0.001415	0.023868	-0.78
261166_s_a	Expressed protein ; supported by full-ler	---	AT1G34570 /	-1.75	-0.80	-5.20	0.001413	0.023868	-0.78
253452_at	hypothetical protein ; supported by cDN/	---	AT4G31930	-1.50	-0.58	-5.20	0.001414	0.023868	-0.78
252289_at	putative protein pre-mRNA splicing fact	---	AT3G49130	1.89	0.92	5.20	0.001416	0.023868	-0.78
253137_at	protein kinase - like protein protein kina	---	AT4G35500	1.71	0.78	5.20	0.001422	0.023955	-0.79
262098_at	transcription factor, putative similar to T	NF-YC2	AT1G56170	-1.72	-0.79	-5.20	0.001424	0.023973	-0.79
262823_at	ATP-dependent Clp protease proteolytic	CLPP6	AT1G11750	-1.49	-0.58	-5.19	0.001427	0.024008	-0.79
262943_at	inosine-5'-monophosphate dehydrogen	---	AT1G79470	-1.49	-0.57	-5.19	0.00143	0.024018	-0.80
261931_at	alcohol dehydrogenase ADH, putative s	---	AT1G22430	-1.44	-0.52	-5.19	0.001429	0.024018	-0.79
249906_at	unknown protein	---	AT5G22730	-1.42	-0.51	-5.19	0.001431	0.024018	-0.80
259690_at	replication factor, putative similar to GI:	---	AT1G63160	-1.94	-0.96	-5.19	0.001436	0.024065	-0.80
259639_at	unknown protein ;supported by full-lengt	---	AT1G52380	-1.58	-0.66	-5.19	0.001435	0.024065	-0.80
265175_at	hypothetical protein similar to putative g	ATCSLA03	AT1G23480	-2.01	-1.01	-5.19	0.001437	0.024067	-0.80
244936_at	NADH dehydrogenase ND1	---	---	-1.49	-0.58	-5.19	0.001439	0.024084	-0.80

257338_s_a	NADH dehydrogenase subunit 5 (nad5)	---	AT2G07711 /	-1.80	-0.84	-5.18	0.001441	0.024102	-0.80
251151_at	hypothetical protein ; supported by full-le	---	AT3G63170	-1.65	-0.72	-5.18	0.001443	0.024104	-0.81
256958_at	unknown protein contains Pfam profile:	---	AT3G13430	1.96	0.97	5.18	0.001443	0.024104	-0.80
250905_at	protein kinase -like protein protein kinas	---	AT5G03640	-1.42	-0.50	-5.18	0.001449	0.024111	-0.81
264022_at	Expressed protein ; supported by full-ler	---	AT2G21185	-1.72	-0.78	-5.18	0.001452	0.024111	-0.81
259491_at	chlorophyll binding protein, putative sim	LHCB6	AT1G15820	-1.59	-0.67	-5.18	0.001449	0.024111	-0.81
264133_at	hypothetical protein predicted by genem	---	AT1G79080	-1.52	-0.61	-5.18	0.001448	0.024111	-0.81
254020_at	beta-carotene hydroxylase ; supported	BETA-OH/	AT4G25700	4.09	2.03	5.18	0.001452	0.024111	-0.81
266018_at	putative preprotein translocase SECY p	SCY1	AT2G18710	-1.44	-0.52	-5.18	0.001452	0.024111	-0.81
251334_at	putative protein several hypothetical pro	---	AT3G61390	1.68	0.75	5.18	0.001451	0.024111	-0.81
255248_at	Oxygen-evolving enhancer protein 3 pr	PSBQ-2	AT4G05180	-1.38	-0.46	-5.18	0.001452	0.024111	-0.81
249188_at	N-hydroxycinnamoyl benzoyltransferase	---	AT5G42830	2.94	1.56	5.17	0.001462	0.024188	-0.82
264689_at	hypothetical protein predicted by gensca	---	AT1G09900	-1.83	-0.87	-5.17	0.001462	0.024188	-0.82
251076_at	putative protein putative protein At2g30	---	AT5G01970	1.93	0.95	5.17	0.001459	0.024188	-0.82
247795_at	putative protein zinc finger transcription	---	AT5G58620	1.60	0.68	5.17	0.001462	0.024188	-0.82
256600_at	hypothetical protein predicted by genem	---	AT3G14850	4.07	2.03	5.17	0.00146	0.024188	-0.82
258585_at	unknown protein C-term similar to cell d	emb2458	AT3G04340	-1.49	-0.58	-5.17	0.001466	0.024230	-0.82
253659_at	hypothetical protein	---	AT4G30150	-1.52	-0.60	-5.16	0.001471	0.024291	-0.82
263929_at	hypothetical protein predicted by genefir	URH1	AT2G36310	1.59	0.67	5.16	0.001474	0.024305	-0.83
261457_at	Expressed protein ; supported by full-ler	---	AT1G21065 /	-1.56	-0.64	-5.16	0.001473	0.024305	-0.83
251914_at	putative protein serine/threonine-specifi	---	AT3G53930	1.51	0.59	5.16	0.001476	0.024327	-0.83
254750_at	putative protein	---	AT4G13150	-1.69	-0.75	-5.16	0.001481	0.024390	-0.83
245006_at	PSI P700 apoprotein A2	---	---	-1.36	-0.45	-5.16	0.001483	0.024401	-0.83
256425_at	disease resistance protein, putative sim	ADR1	AT1G33560	1.80	0.85	5.16	0.001486	0.024435	-0.84
247326_at	peroxidase ATP3a homolog ;supported	---	AT5G64110	5.78	2.53	5.15	0.00149	0.024488	-0.84
253988_at	putative protein elongation factor P (efp	---	AT4G26310	-1.46	-0.55	-5.15	0.001493	0.024512	-0.84
255588_at	hypothetical protein	---	AT4G01570	-1.83	-0.87	-5.15	0.001498	0.024563	-0.84
257185_at	ABC transporter, putative similar to AtM	ATMRP7	AT3G13100	2.05	1.04	5.15	0.001498	0.024563	-0.84
261886_s_a	hypothetical protein predicted by gensca	---	AT1G80700 /	-1.39	-0.47	-5.15	0.0015	0.024583	-0.85
264190_at	heme activated protein, putative similar	NF-YC3	AT1G54830	-1.39	-0.47	-5.14	0.001509	0.024709	-0.85
262345_at	hypothetical protein similar to hypothetic	---	AT1G64180	-1.56	-0.64	-5.14	0.001512	0.024744	-0.85
246775_at	putative protein GTP-binding proteins at	MIRO1	AT5G27540	-1.40	-0.49	-5.14	0.001516	0.024782	-0.86
264142_at	hypothetical protein predicted by gensca	---	AT1G78930	-1.83	-0.87	-5.13	0.001521	0.024832	-0.86
251416_at	putative protein various predicted prote	---	AT3G60400	-1.47	-0.55	-5.13	0.001524	0.024832	-0.86
266863_at	putative ripening-associated protein ; su	ATCDPME	AT2G26930	-1.46	-0.55	-5.13	0.001523	0.024832	-0.86

250245_at	alpha-N-acetylglucosaminidase	---	AT5G13690	-1.66	-0.73	-5.13	0.00152	0.024832	-0.86
251019_at	putative protein predicted proteins, Arat	---	AT5G02420	1.56	0.64	5.13	0.001522	0.024832	-0.86
246194_at	putative protein ;supported by full-length	ACD2	AT4G37000	-1.73	-0.79	-5.13	0.001526	0.024838	-0.86
261815_at	leucine zipper protein, putative similar t	---	AT1G08320	1.69	0.76	5.13	0.001529	0.024878	-0.87
261669_at	unknown protein similar to hypothetical p	---	AT1G18490	-1.36	-0.45	-5.13	0.001533	0.024918	-0.87
256076_at	unknown protein ; supported by cDNA: g	---	AT1G18060	-1.97	-0.98	-5.12	0.001538	0.024978	-0.87
263334_at	putative nonsense-mediated mRNA dec	---	AT2G03820	-1.51	-0.59	-5.12	0.00154	0.024978	-0.87
263605_at	hypothetical protein predicted by genscа	---	AT2G16485	-1.65	-0.72	-5.12	0.001541	0.024978	-0.87
254905_at	RPP1-WsA-like disease resistance prot	---	AT4G11170	3.92	1.97	5.12	0.001539	0.024978	-0.87
255719_at	unknown protein ;supported by full-lengt	---	AT1G32080	-2.46	-1.30	-5.12	0.001543	0.024994	-0.88
245136_at	putative auxin-regulated protein	---	AT2G45210	2.80	1.49	5.12	0.001545	0.025018	-0.88
247497_at	Peter Pan - like protein Peter Pan, Dros	PPAN	AT5G61770	-1.87	-0.90	-5.12	0.001548	0.025019	-0.88
261378_at	calcium-dependent protein kinase, puta	ATCDPK1	AT1G18890	1.90	0.93	5.12	0.001548	0.025019	-0.88
252829_at	homeodomain - like protein ; supported	ATHB16	AT4G40060	-1.66	-0.73	-5.12	0.001549	0.025019	-0.88
246463_at	quinone oxidoreductase -like protein pr	AT-AER	AT5G16970	1.87	0.90	5.11	0.001554	0.025044	-0.88
264806_at	hypothetical protein predicted by genscа	---	AT1G08610	-2.24	-1.16	-5.11	0.001552	0.025044	-0.88
244933_at	NADH dehydrogenase ND4L	---	---	-1.54	-0.63	-5.11	0.001554	0.025044	-0.88
246982_s_a	unknown protein	---	AT2G10560 /	2.33	1.22	5.11	0.001557	0.025087	-0.89
253871_at	protochlorophyllide reductase precursor	PORB	AT4G27440	-1.88	-0.91	-5.11	0.001564	0.025151	-0.89
263863_at	3-oxoacyl carrier protein synthase	---	AT2G04540	-1.39	-0.47	-5.11	0.001565	0.025151	-0.89
246268_at	cytochrome P450, putative contains Pfa	CYP97A3	AT1G31800	-1.69	-0.75	-5.11	0.001564	0.025151	-0.89
264987_at	unknown protein ; supported by cDNA: g	---	AT1G27030	-2.48	-1.31	-5.11	0.001567	0.025157	-0.89
257698_at	regulatory protein of P-starvation acclim	---	AT3G12730	-1.52	-0.61	-5.11	0.001567	0.025157	-0.89
248704_at	putative protein pectinesterase-like; also	sks3	AT5G48450	1.75	0.80	5.10	0.001572	0.025170	-0.90
249641_at	DegP protease contains similarity to De	DegP10	AT5G36950	-1.57	-0.65	-5.10	0.001572	0.025170	-0.90
253607_at	small nuclear ribonucleoprotein homolo	---	AT4G30330	-1.74	-0.80	-5.10	0.00157	0.025170	-0.89
251815_at	putative protein thioredoxin-like protein,	CXIP1	AT3G54900	-1.62	-0.69	-5.10	0.001572	0.025170	-0.90
255595_at	putative chitinase similar to peanut type	---	AT4G01700	4.19	2.07	5.10	0.001574	0.025173	-0.90
253872_at	putative protein Arabidopsis thaliana na	RD26	AT4G27410	1.92	0.94	5.10	0.001575	0.025173	-0.90
251833_at	putative protein various predicted protei	---	AT3G55160	-1.47	-0.55	-5.10	0.001582	0.025232	-0.90
264308_at	hypothetical protein similar to hypothetic	---	AT1G61990	-1.35	-0.43	-5.10	0.001581	0.025232	-0.90
249265_at	E2, ubiquitin-conjugating enzyme 8 (UB	---	AT5G41080 /	-1.38	-0.47	-5.10	0.00158	0.025232	-0.90
267534_at	putative CCCH-type zinc finger protein a	---	AT2G41900	-1.46	-0.55	-5.10	0.001584	0.025238	-0.90
263574_at	putative tetracycline transporter protein	---	AT2G16990	-1.44	-0.52	-5.10	0.001584	0.025238	-0.90
262970_at	unknown protein	---	AT1G75690	-1.50	-0.59	-5.09	0.001591	0.025240	-0.91

261309_at	phosphoethanolamine N-methyltransfe	CPuORF3	AT1G48598 /	-2.02	-1.01	-5.09	0.00159	0.025240	-0.91
250937_at	putative protein various predicted prote	---	AT5G03230	-2.03	-1.02	-5.09	0.001587	0.025240	-0.91
261419_at	hypothetical protein predicted by genem	---	AT1G07840	-1.39	-0.47	-5.09	0.001587	0.025240	-0.91
264458_at	unknown protein similar to ESTs gb|N96	---	AT1G10410	1.49	0.58	5.09	0.001591	0.025240	-0.91
249625_at	hypothetical protein ;supported by full-le	---	AT5G37480	1.48	0.56	5.09	0.001593	0.025240	-0.91
250016_at	Cu/Zn superoxide dismutase-like protein	CSD3	AT5G18100	-1.53	-0.61	-5.09	0.001593	0.025240	-0.91
253377_at	putative protein NBS/LRR disease resis	ADR1-L1	AT4G33300	1.56	0.64	5.09	0.001592	0.025240	-0.91
265582_at	putative RING zinc finger protein	---	AT2G20030	1.61	0.69	5.09	0.001597	0.025280	-0.91
248162_at	1,4-benzoquinone reductase-like; Trp re	FQR1	AT5G54500	2.01	1.01	5.09	0.001602	0.025341	-0.92
253804_at	putative protein	---	AT4G28230	-1.58	-0.66	-5.08	0.001604	0.025348	-0.92
267305_at	high affinity K+ transporter (AtKUP1/AtK	ATKT1	AT2G30070	-2.21	-1.14	-5.08	0.001605	0.025352	-0.92
249065_at	putative protein similar to unknown prote	---	AT5G44260	-2.18	-1.12	-5.08	0.00161	0.025413	-0.92
256070_at	hypothetical protein predicted by genscа	---	AT1G13730	-1.46	-0.54	-5.08	0.001612	0.025425	-0.92
257686_at	unknown protein similar to unknown pro	SDRB	AT3G12800	1.57	0.65	5.08	0.001619	0.025499	-0.93
267435_at	30S ribosomal protein S5 ; supported b	---	AT2G33800	-1.43	-0.52	-5.08	0.001618	0.025499	-0.93
253743_at	putative protein vegetative storage prot	---	AT4G28940	1.36	0.44	5.08	0.00162	0.025499	-0.93
250938_at	putative protein various predicted prote	---	AT5G03180	-1.76	-0.81	-5.07	0.001628	0.025606	-0.93
248273_at	putative protein contains similarity to unl	---	AT5G53500	-2.10	-1.07	-5.07	0.001634	0.025675	-0.94
266578_at	putative cinnamoyl CoA reductase ;sup	---	AT2G23910	1.63	0.70	5.07	0.001634	0.025675	-0.94
250382_at	putative protein rjs protein, Mus muscul	---	AT5G11580	-1.37	-0.46	-5.06	0.001639	0.025724	-0.94
247099_at	putative protein contains similarity to sel	---	AT5G66500	-1.59	-0.67	-5.06	0.00164	0.025724	-0.94
252853_at	hypothetical protein ; supported by cDN/	---	AT4G39710	-2.54	-1.34	-5.06	0.001647	0.025828	-0.95
260438_at	putative bifunctional nuclease similar to	ENDO 2	AT1G68290	2.78	1.48	5.06	0.001649	0.025836	-0.95
258314_at	putative RAS-related GTP-binding prote	ATRABG3	AT3G16100	-1.54	-0.63	-5.06	0.001652	0.025855	-0.95
251538_at	putative protein PBK1 protein, Homo sa	---	AT3G58660	-1.95	-0.97	-5.06	0.001653	0.025867	-0.95
252986_at	putative protein T19C21.18 Arabidopsis	---	AT4G38380	-1.36	-0.44	-5.05	0.001656	0.025891	-0.95
247745_at	copper transport protein	COPT1	AT5G59030	-1.39	-0.48	-5.05	0.001659	0.025892	-0.95
247862_at	similar to unknown protein (sp|P72777)	---	AT5G58250	-1.50	-0.58	-5.05	0.00166	0.025892	-0.95
249779_at	putative protein similar to unknown prote	---	AT5G24230	1.44	0.53	5.05	0.001658	0.025892	-0.95
247258_at	expressed protein similar to unknown pr	---	AT5G64816	-1.60	-0.67	-5.05	0.001662	0.025901	-0.95
262951_at	nodulin-like protein similar to MtN21 GE	---	AT1G75500	-1.69	-0.76	-5.05	0.001662	0.025901	-0.95
261912_s_a	unknown protein	---	AT1G66000 /	-1.59	-0.67	-5.05	0.001672	0.026027	-0.96
259198_at	hypothetical protein similar to F1N21.1 (	---	AT3G03610	1.53	0.61	5.04	0.001674	0.026052	-0.96
247609_at	cleavage stimulation factor 50K chain c	---	AT5G60940	-1.49	-0.58	-5.04	0.001677	0.026079	-0.96
247668_at	pseudo-response regulator - like pseud	APRR3	AT5G60100	-1.39	-0.48	-5.04	0.00168	0.026107	-0.97

249821_at	putative protein contains similarity to pol	---	AT5G23690	-2.01	-1.01	-5.04	0.001685	0.026107	-0.97
248065_at	putative protein similar to unknown prote	---	AT5G55580	-1.73	-0.79	-5.04	0.001683	0.026107	-0.97
249091_at	AtCLH2 (gb|AAF27046.1) ; supported b	CLH2	AT5G43860	-1.51	-0.60	-5.04	0.001684	0.026107	-0.97
252520_at	receptor-like protein kinase homolog lig	---	AT3G46370	-2.54	-1.35	-5.04	0.001684	0.026107	-0.97
245793_at	unknown protein ;supported by full-lengt	---	AT1G32220	-2.32	-1.22	-5.03	0.001693	0.026145	-0.97
245747_at	hypothetical protein predicted by genem	---	AT1G51100	-1.76	-0.81	-5.03	0.001692	0.026145	-0.97
265464_at	putative myosin heavy chain	---	AT2G37080	-1.39	-0.48	-5.04	0.001692	0.026145	-0.97
258915_at	unknown protein similar to hypothetical	VPS60.1	AT3G10640	1.64	0.72	5.03	0.001693	0.026145	-0.97
264867_at	unknown protein	FH4	AT1G24150	2.62	1.39	5.04	0.001691	0.026145	-0.97
246083_at	zinc finger protein - like probable zinc fi	AL5	AT5G20510	-1.44	-0.53	-5.03	0.001696	0.026157	-0.98
258683_at	putative protein kinase contains Pfam pr	ATSIK	AT3G08760	2.07	1.05	5.03	0.001697	0.026157	-0.98
255793_at	Expressed protein ; supported by cDNA	---	AT2G33250	-1.64	-0.72	-5.03	0.001696	0.026157	-0.98
248951_at	putative protein similar to unknown prote	---	AT5G45550	1.64	0.71	5.03	0.001699	0.026160	-0.98
261381_at	hypothetical protein predicted by genem	SDE3	AT1G05460	-1.41	-0.49	-5.03	0.001701	0.026160	-0.98
251400_at	putative protein prib5, Ribes nigrum, EM	---	AT3G60420	5.30	2.41	5.03	0.001702	0.026160	-0.98
260380_at	hypothetical protein predicted by gensca	---	AT1G73870	-2.28	-1.19	-5.03	0.001703	0.026160	-0.98
262719_at	hypothetical protein predicted by gensca	---	---	1.51	0.59	5.03	0.001702	0.026160	-0.98
253537_at	putative protein ; supported by full-leng	HCF153	AT4G31560	-1.54	-0.63	-5.03	0.001707	0.026185	-0.98
258524_at	acetyl-coA dehydrogenase, putative sim	IBR3	AT3G06810	1.58	0.66	5.03	0.001706	0.026185	-0.98
247747_at	putative protein predicted proteins, Ara	---	AT5G59000	-1.72	-0.78	-5.03	0.001709	0.026197	-0.98
260047_at	putative UDP-N-acetylglucosamine--N-a	---	AT1G73740	1.48	0.57	5.02	0.001711	0.026197	-0.99
262086_at	GTP-binding protein, putative similar to	---	AT1G56050	-1.63	-0.70	-5.03	0.00171	0.026197	-0.98
264811_at	hypothetical protein predicted by gensca	---	AT1G08640	-1.41	-0.49	-5.02	0.001714	0.026205	-0.99
255547_at	putative CHP-rich zinc finger protein sim	---	AT4G01920	1.76	0.81	5.02	0.001713	0.026205	-0.99
248507_at	putative protein strong similarity to unkn	---	AT5G50420	-1.64	-0.71	-5.02	0.001717	0.026234	-0.99
248721_at	putative protein strong similarity to unkn	GAUT4	AT5G47780	-1.35	-0.44	-5.02	0.001719	0.026253	-0.99
249354_at	nuclear pore protein -like nuclear pore p	EMB3012	AT5G40480	-1.84	-0.88	-5.02	0.001724	0.026286	-0.99
250554_at	unknown protein ;supported by full-leng	---	AT5G07900	-1.50	-0.59	-5.02	0.001723	0.026286	-0.99
261102_at	unknown protein	---	AT1G62880	-1.43	-0.52	-5.02	0.001728	0.026326	-1.00
263039_at	mak16-like protein-related similar to MA	---	AT1G23280	-1.80	-0.85	-5.02	0.001729	0.026326	-1.00
245682_at	Expressed protein ; supported by cDNA	---	AT5G08750	1.51	0.59	5.01	0.001735	0.026402	-1.00
260427_at	hypothetical protein predicted by genefi	---	AT1G72430	-2.67	-1.42	-5.01	0.00174	0.026447	-1.00
255447_at	hypothetical protein similar to A. thalian	---	AT4G02790	-2.10	-1.07	-5.01	0.00174	0.026447	-1.00
255650_s_a	hypothetical protein	CIP4.1	AT4G00930 /	-1.60	-0.68	-5.01	0.001743	0.026447	-1.00
262921_at	transfactor, putative similar to transfact	APL	AT1G79430	-1.49	-0.57	-5.01	0.001742	0.026447	-1.00

249256_at	putative protein strong similarity to unkn	---	AT5G41620	-1.75	-0.81	-5.01	0.001746	0.026483	-1.01
258247_at	hypothetical protein predicted by genem	---	AT3G29130	-1.34	-0.42	-5.00	0.001748	0.026493	-1.01
245789_at	hypothetical protein similar to hypothetic	---	AT1G32090	2.27	1.18	5.00	0.001749	0.026493	-1.01
263705_at	unknown protein contains similarity to gi	IMPL1	AT1G31190	-1.73	-0.79	-5.00	0.001751	0.026500	-1.01
260651_at	hypothetical protein predicted by genem	---	AT1G32460	1.46	0.55	5.00	0.001752	0.026507	-1.01
260938_at	hypothetical protein contains similarity to	---	AT1G45170	-1.62	-0.69	-5.00	0.001754	0.026513	-1.01
266799_at	unknown protein	ATPSK2	AT2G22860	2.18	1.13	5.00	0.001757	0.026546	-1.01
262454_at	bifunctional nuclease bfn1 almost identi	BFN1	AT1G11190	7.31	2.87	5.00	0.001764	0.026635	-1.02
266962_at	hypothetical protein predicted by gensca	---	AT2G39435 /	1.50	0.58	5.00	0.001767	0.026652	-1.02
263937_at	putative RING zinc finger protein	---	AT2G35910	1.53	0.61	4.99	0.001768	0.026662	-1.02
248678_at	U6 snRNA-associated Sm-like protein-li	SAD1	AT5G48870	-1.53	-0.62	-4.99	0.001774	0.026730	-1.02
259598_at	sphingosine-1-phosphate lyase, putativ	DPL1	AT1G27980	1.59	0.67	4.99	0.001776	0.026736	-1.02
250286_at	auxin-responsive - like protein Nt-gh3 d	PBS3	AT5G13320	10.27	3.36	4.99	0.001781	0.026801	-1.03
245067_at	S-like ribonuclease RNS2 identical to ri	RNS2	AT2G39780	1.53	0.62	4.99	0.001782	0.026802	-1.03
249089_at	ATPase, calcium-transporting	---	AT5G44240	1.36	0.44	4.99	0.001784	0.026814	-1.03
256890_at	glycine-rich RNA binding protein, putati	GRP4	AT3G23830	-2.41	-1.27	-4.98	0.00179	0.026846	-1.03
255764_at	unknown protein	HCF173	AT1G16720	-1.65	-0.72	-4.98	0.001794	0.026846	-1.04
256613_at	hypothetical protein predicted by genem	emb2076	AT3G29290	-1.67	-0.74	-4.98	0.001793	0.026846	-1.03
257888_at	seed maturation protein, putative simila	---	AT3G16990	2.02	1.01	4.98	0.001792	0.026846	-1.03
251599_at	adenylosuccinate synthetase ;supporte	ADSS	AT3G57610	-1.52	-0.60	-4.98	0.001792	0.026846	-1.03
261325_at	hypothetical protein predicted by genem	---	AT1G44780	-1.37	-0.45	-4.98	0.00179	0.026846	-1.03
266004_at	unknown protein predicted by genscan a	ALS3	AT2G37330	-1.39	-0.47	-4.98	0.001795	0.026855	-1.04
253999_at	1-aminocyclopropane-1-carboxylate syr	ACS7	AT4G26200	2.36	1.24	4.98	0.001798	0.026861	-1.04
251900_at	putative protein lateral root primordia (L	SRS6	AT3G54430	-1.65	-0.72	-4.98	0.001798	0.026861	-1.04
259515_at	hypothetical protein ; supported by cDN	---	AT1G20430	-1.40	-0.49	-4.97	0.00181	0.026867	-1.04
260020_at	hydrophilic protein, putative similar to G	PDF6	AT1G29990	-1.39	-0.47	-4.97	0.001812	0.026867	-1.05
265826_at	hypothetical protein predicted by genefir	---	AT2G35795	-1.41	-0.50	-4.97	0.00182	0.026867	-1.05
251184_at	small nuclear ribonucleoprotein-like pro	---	AT3G62840	-1.38	-0.46	-4.98	0.001803	0.026867	-1.04
252319_at	putative protein putative protein - Arabi	---	AT3G48710	-1.75	-0.81	-4.97	0.001818	0.026867	-1.05
251094_at	putative protein ;supported by full-lengt	---	AT5G01350	1.55	0.63	4.97	0.001816	0.026867	-1.05
260245_at	putative RNA-binding protein similar to F	GR-RBP5	AT1G74230	-1.40	-0.48	-4.97	0.001818	0.026867	-1.05
253612_at	putative protein D-ribulokinase - Klebsie	---	AT4G30310	-1.45	-0.53	-4.97	0.00182	0.026867	-1.05
261923_at	UDP-glucose glucosyltransferase, puta	AtUGT85A	AT1G22380	1.56	0.64	4.97	0.00182	0.026867	-1.05
253886_at	cytochrome P450 - like protein cytochro	CYP709B3	AT4G27710	-1.44	-0.53	-4.97	0.001817	0.026867	-1.05
261784_at	hypothetical protein predicted by genem	---	AT1G08220	-1.45	-0.54	-4.97	0.001822	0.026867	-1.05

248248_at	spermidine synthase ;supported by full-	SPDS3	AT5G53120	2.01	1.01	4.97	0.001821	0.026867	-1.05
261681_at	hypothetical protein similar to hypothetic	---	AT1G47340	-1.90	-0.93	-4.97	0.001807	0.026867	-1.04
250412_at	putative protein synaptobrevin-like prote	ATVAMP7	AT5G11150	-1.67	-0.74	-4.97	0.001819	0.026867	-1.05
258128_at	chloroplast thylakoidal processing pepti	PLSP1	AT3G24590	-1.64	-0.71	-4.97	0.001822	0.026867	-1.05
252661_at	putative protein	---	AT3G44450	-3.40	-1.77	-4.97	0.001812	0.026867	-1.05
253620_at	receptor-like kinase homolog somatic e	---	AT4G30520	-1.54	-0.62	-4.97	0.001817	0.026867	-1.05
262507_at	receptor-like protein kinase, putative sir	---	AT1G11330	1.63	0.71	4.97	0.001814	0.026867	-1.05
260807_at	hypothetical protein predicted by genem	---	AT1G78310	1.36	0.44	4.97	0.001813	0.026867	-1.05
256593_at	hypothetical protein similar to putative m	---	AT3G28510	2.99	1.58	4.97	0.001815	0.026867	-1.05
258947_at	hypothetical protein similar to calmoduli	---	AT3G01830	8.46	3.08	4.97	0.001824	0.026880	-1.05
265169_x_a	unknown protein	---	AT1G23720	1.50	0.58	4.96	0.00183	0.026951	-1.06
251791_at	expansin-like protein expansin At-EXP6	ATEXPA1(	AT3G55500	2.59	1.37	4.96	0.001841	0.027077	-1.06
260498_at	putative AP2 domain transcription factor	---	AT2G41710	-1.64	-0.71	-4.96	0.001841	0.027077	-1.06
258549_at	putative arginine methyltransferase simi	PRMT4B	AT3G06930	-1.38	-0.46	-4.96	0.001844	0.027085	-1.06
255025_at	putative host response protein pir7a pro	MES12	AT4G09900	-1.99	-0.99	-4.96	0.001844	0.027085	-1.06
248196_at	putative protein similar to unknown prote	---	AT5G54150	-1.43	-0.51	-4.95	0.001846	0.027102	-1.07
263750_at	unknown protein	---	AT2G21530	-1.69	-0.76	-4.95	0.001848	0.027102	-1.07
261871_at	similar to serine/threonine protein kinase	---	AT1G11440	-1.58	-0.66	-4.95	0.00185	0.027119	-1.07
261536_at	K Efflux antiporter KEA1 identical to GB	KEA1	AT1G01790	-1.71	-0.78	-4.95	0.001853	0.027149	-1.07
246821_at	calmodulin-binding - like protein calmod	CBP60G	AT5G26920	4.68	2.23	4.95	0.001855	0.027159	-1.07
252975_s_a	putative protein other predicted proteins	ROPGEF1	AT4G38430	-1.44	-0.53	-4.95	0.001857	0.027169	-1.07
264351_at	unknown protein Contains similarity to g	---	AT1G03370	1.51	0.60	4.94	0.00187	0.027316	-1.08
245876_at	chaperonin precursor, putative similar t	---	AT1G26230	-2.04	-1.03	-4.94	0.00187	0.027316	-1.08
246492_at	CRS2-like protein CRS2 - Zea mays, E	---	AT5G16140	-1.78	-0.83	-4.94	0.001871	0.027316	-1.08
261124_at	hypothetical protein predicted by genem	---	AT1G04900	-1.47	-0.56	-4.94	0.001876	0.027368	-1.08
255679_at	putative acetyl CoA thioesterase	---	AT4G00520	-1.72	-0.78	-4.94	0.001878	0.027368	-1.08
257232_at	phytochrome-associated protein 1 (PAP	PAP1	AT3G16500	-1.62	-0.69	-4.94	0.001877	0.027368	-1.08
252377_at	putative peptide transporter peptide tra	---	AT3G47960	-1.67	-0.74	-4.94	0.001884	0.027435	-1.09
249900_at	unknown protein	emb1211	AT5G22640	-1.45	-0.54	-4.93	0.001887	0.027472	-1.09
267406_at	unknown protein	MEE22	AT2G34780	-1.59	-0.67	-4.93	0.001894	0.027547	-1.09
246313_at	PPR-repeat protein, putative contains n	---	AT1G31920	-2.43	-1.28	-4.93	0.001897	0.027585	-1.10
254363_at	pectinesterase like protein pectinestera	sks4	AT4G22010	1.93	0.95	4.93	0.0019	0.027608	-1.10
249231_at	putative protein similar to unknown prote	ABIL4	AT5G42030	-1.54	-0.62	-4.93	0.001902	0.027611	-1.10
249965_at	putative protein predicted proteins, Ara	---	AT5G19020	-1.34	-0.43	-4.92	0.001911	0.027688	-1.10
247041_at	floral homeotic protein apetala2-like ;su	TOE3	AT5G67180	-1.56	-0.64	-4.92	0.001909	0.027688	-1.10

249988_at	putative protein predicted proteins, Dro	---	AT5G18310	1.66	0.73	4.92	0.001912	0.027688	-1.10
263703_at	unknown protein ;supported by full-leng	SRX	AT1G31170	-1.58	-0.66	-4.92	0.00191	0.027688	-1.10
262060_at	polygalacturonase, putative similar to p	---	AT1G80170	-1.51	-0.59	-4.92	0.001916	0.027729	-1.11
249283_at	amino acid permease-like protein; prolin	---	AT5G41800	1.75	0.81	4.92	0.001919	0.027749	-1.11
246901_at	putative protein Leaf protein, Pharbitis r	---	AT5G25630	-1.45	-0.54	-4.92	0.00192	0.027749	-1.11
265274_at	putative RNA methyltransferase	---	AT2G28450	-1.60	-0.68	-4.92	0.001922	0.027751	-1.11
253337_at	putative protein acetylpolyamine amino	hda14	AT4G33470	-1.96	-0.97	-4.92	0.001922	0.027751	-1.11
264442_at	hypothetical protein similar to lecithin:ch	---	AT1G27480	-1.87	-0.91	-4.92	0.001924	0.027761	-1.11
246993_at	Cys2/His2-type zinc finger protein 1 (dbj	AZF1	AT5G67450	3.74	1.90	4.92	0.001926	0.027777	-1.11
265908_at	contains similarity to S. cerevisiae ADR1	---	AT4G00270	-1.78	-0.84	-4.91	0.001931	0.027820	-1.11
245775_at	serine/threonine kinase, putative simila	CIPK23	AT1G30270	1.48	0.57	4.91	0.001939	0.027909	-1.12
249691_at	translation releasing factor RF-2 ;suppo	HCF109	AT5G36170	-1.38	-0.46	-4.91	0.001939	0.027909	-1.12
262151_at	hypothetical protein predicted by genem	---	AT1G52510	-2.18	-1.12	-4.91	0.00195	0.027998	-1.12
249393_at	disease resistance - like protein resista	AtRLP54	AT5G40170	2.21	1.14	4.91	0.001947	0.027998	-1.12
246909_at	putative protein predicted protein, Oryz	---	AT5G25770	2.60	1.38	4.91	0.001949	0.027998	-1.12
248738_at	unknown protein ;supported by full-leng	---	AT5G48020	1.48	0.57	4.91	0.00195	0.027998	-1.12
249785_at	soluble starch synthase	SSI1	AT5G24300	-1.52	-0.61	-4.90	0.001957	0.028058	-1.13
245933_at	putative protein KIAA1521 - Homo sapi	VPS9B	AT5G09320	-1.41	-0.50	-4.90	0.001964	0.028058	-1.13
257487_at	hypothetical protein predicted by genem	---	AT1G71850	-2.10	-1.07	-4.90	0.001963	0.028058	-1.13
262988_at	putative alanine aminotransferas	GGT1	AT1G23310	-1.41	-0.50	-4.90	0.001961	0.028058	-1.13
265073_at	unknown protein similar to putative tyros	---	AT1G55480	-2.10	-1.07	-4.90	0.001961	0.028058	-1.13
263570_at	aldehyde oxidase identical to GP:31720	AAO3	AT2G27150	1.96	0.97	4.90	0.001961	0.028058	-1.13
260639_at	hypothetical protein predicted by genem	---	AT1G53180	2.65	1.41	4.90	0.001965	0.028058	-1.13
253432_at	putative protein various predicted protei	---	AT4G32450	-1.40	-0.49	-4.90	0.001963	0.028058	-1.13
248823_s_a	unknown protein ;supported by full-leng	---	AT5G46950 /	17.65	4.14	4.90	0.001966	0.028058	-1.13
252344_s_a	putative protein	---	AT3G44160 /	-1.45	-0.54	-4.90	0.001969	0.028094	-1.13
256978_at	phosphoribosyamidoimidazole-succino	PUR7	AT3G21110	-2.12	-1.09	-4.89	0.001978	0.028206	-1.14
252985_at	putative protein Niemann-Pick C diseas	---	AT4G38350	-1.46	-0.55	-4.89	0.001982	0.028216	-1.14
254535_at	aspartate kinase-homoserine dehydrog	AK-HSDH	AT4G19710	-1.41	-0.50	-4.89	0.001981	0.028216	-1.14
249606_at	putative protein DNA-binding protein C	RVE2	AT5G37260	1.50	0.58	4.89	0.001985	0.028252	-1.14
252901_at	putative protein various predicted prote	---	AT4G39550	-1.44	-0.52	-4.88	0.001995	0.028269	-1.15
262931_at	small nuclear ribonucleoprotein, putativ	---	AT1G65700	-1.50	-0.58	-4.89	0.001994	0.028269	-1.15
260145_at	putative G protein-coupled receptor simi	GPCR	AT1G52920	-1.36	-0.44	-4.89	0.001994	0.028269	-1.15
265053_at	myrosinase binding protein, putative sir	---	AT1G52000	-2.17	-1.12	-4.89	0.001992	0.028269	-1.15
266141_at	protease inhibitor II contains a gamma-t	PDF2.1	AT2G02120	1.41	0.50	4.89	0.001988	0.028269	-1.14

249139_at	Cys2/His2-type zinc finger protein 3 (db	AZF3	AT5G43170	2.38	1.25	4.89	0.00199	0.028269	-1.15
265618_at	hypothetical protein predicted by gensca	---	AT2G25460	1.53	0.61	4.89	0.001991	0.028269	-1.15
261796_at	non-phototropic hypocotyl, putative sim	---	AT1G30440	1.47	0.56	4.88	0.002001	0.028290	-1.15
264192_at	hypothetical protein predicted by genem	ATATG18I	AT1G54710	1.37	0.45	4.88	0.002	0.028290	-1.15
245183_at	putative protein similarity to predicted p	---	AT5G12440	-1.68	-0.75	-4.88	0.002	0.028290	-1.15
265345_at	copia-like retroelement pol polyprotein	---	AT2G22680	1.46	0.54	4.88	0.002002	0.028298	-1.15
253301_at	pathogenesis-related protein 1 precurso	---	AT4G33720	3.15	1.66	4.88	0.002006	0.028328	-1.15
245158_at	hypothetical protein predicted by genefir	RALFL18	AT2G33130	1.76	0.81	4.88	0.002015	0.028441	-1.16
261591_at	protein kinase, putative similar to protei	---	AT1G01740	-1.69	-0.76	-4.87	0.00202	0.028489	-1.16
249103_at	N-carbamyl-L-amino acid amidohydrolas	UAH	AT5G43600	-1.50	-0.59	-4.87	0.002022	0.028512	-1.16
266767_at	Expressed protein ; supported by full-ler	---	AT2G46910	-1.67	-0.74	-4.87	0.002027	0.028549	-1.16
250879_at	putative protein various predicted prote	---	AT5G04060	-1.67	-0.74	-4.87	0.002028	0.028549	-1.17
259000_at	hypothetical protein predicted by gensca	---	AT3G01860	-2.31	-1.21	-4.87	0.00203	0.028566	-1.17
266100_at	similar to axi 1 protein from Nicotiana ta	---	AT2G37980	1.96	0.97	4.87	0.002037	0.028643	-1.17
264571_at	hypothetical protein predicted by genefir	---	AT1G05330	1.37	0.45	4.86	0.00204	0.028665	-1.17
249342_at	putative protein ATP12 protein precurso	---	AT5G40660	-1.54	-0.62	-4.86	0.002041	0.028668	-1.17
254848_at	putative protein hypothetical protein F7	PGRL1B	AT4G11960	-1.48	-0.56	-4.86	0.002043	0.028684	-1.17
264774_at	unknown protein	---	AT1G22890	2.69	1.43	4.86	0.002045	0.028684	-1.17
246856_at	nucleic acid binding protein - like nuclei	AL4	AT5G26210	-1.38	-0.46	-4.86	0.002046	0.028690	-1.18
262914_at	auxin response factor 1 identical to auxi	ARF1	AT1G59750	-1.50	-0.59	-4.86	0.002049	0.028711	-1.18
264652_at	putative sugar transport protein, ERD6	---	AT1G08920	2.69	1.43	4.86	0.002052	0.028735	-1.18
256677_at	unknown protein contains Pfam profile:	PHF1	AT3G52190	1.55	0.64	4.86	0.002055	0.028757	-1.18
258087_at	putative peroxiredoxin similar to peroxire	ATPRX Q	AT3G26060	-1.81	-0.85	-4.86	0.00206	0.028768	-1.18
259661_at	Expressed protein ; supported by full-ler	---	AT1G55265	1.69	0.76	4.85	0.002062	0.028768	-1.18
258976_at	putative dehydrogenase contains Pfam	---	AT3G01980	-1.40	-0.49	-4.86	0.002059	0.028768	-1.18
256514_at	oxidoreductase, putative contains Pfam	---	AT1G66130	-1.89	-0.92	-4.86	0.002057	0.028768	-1.18
249422_at	putative protein predicted proteins, Ara	AtHB23	AT5G39760	-1.59	-0.67	-4.85	0.002062	0.028768	-1.18
249524_at	putative protein similar to unknown prote	---	AT5G38520	-1.87	-0.91	-4.85	0.002065	0.028797	-1.18
245096_at	putative cysteine proteinase inhibitor B (	ATCYSA	AT2G40880	-1.54	-0.62	-4.85	0.002072	0.028869	-1.19
266570_at	putative chloroplast ribosomal protein L3	---	AT2G24090	-1.43	-0.52	-4.85	0.002081	0.028982	-1.19
257680_at	aspartate carbamoyltransferase precurs	---	AT3G20330	-1.66	-0.74	-4.85	0.002083	0.028987	-1.19
252116_at	putative protein ;supported by full-lengt	---	AT3G51510	-1.58	-0.66	-4.84	0.002087	0.029025	-1.20
251996_at	beta-galactosidase precursor - like prot	BGAL2	AT3G52840	-1.58	-0.66	-4.84	0.002093	0.029087	-1.20
264487_at	vacuolar protein sorting homolog almost	VPS45	AT1G77140	1.39	0.48	4.84	0.002095	0.029103	-1.20
267378_at	hypothetical protein	---	AT2G26200	-1.38	-0.47	-4.84	0.002101	0.029119	-1.20

249993_at	GTP-binding protein obg -like GTP-bind	---	AT5G18570	-1.36	-0.44	-4.84	0.002101	0.029119	-1.20
254610_at	putative protein predicted protein, Arabi	---	AT4G18890	1.50	0.58	4.84	0.0021	0.029119	-1.20
255908_s_a	unknown protein ;supported by full-lengt	---	AT1G18000 /	-1.49	-0.57	-4.84	0.002101	0.029119	-1.20
248698_at	receptor-like protein kinase ; supported	---	AT5G48380	1.90	0.93	4.84	0.002104	0.029134	-1.20
255437_at	putative oxidoreductase similar to P. vu	AOP2	AT4G03060	-3.16	-1.66	-4.83	0.002113	0.029248	-1.21
255118_at	nitrilase 1 like protein nitrilase 1 - Mus r	---	AT4G08790	-1.58	-0.66	-4.83	0.002122	0.029343	-1.21
245124_at	small nuclear ribonucleoprotein U1A ide	U1A	AT2G47580	-1.49	-0.58	-4.83	0.002123	0.029343	-1.21
258359_s_a	putative glycolate oxidase similar to glyc	---	AT3G14415 /	-1.62	-0.69	-4.83	0.002127	0.029389	-1.22
252677_at	nitrilase 3 ;supported by full-length cDN	NIT3	AT3G44320	1.99	0.99	4.83	0.002131	0.029430	-1.22
247279_at	arabinogalactan-protein (gb|AAC77823.	AGP1	AT5G64310	4.72	2.24	4.82	0.002133	0.029440	-1.22
247493_at	copine - like protein copine I, Homo sap	BON1	AT5G61900	2.12	1.08	4.82	0.002136	0.029461	-1.22
264677_at	hypothetical protein predicted by genefi	HYL1	AT1G09700	-1.35	-0.43	-4.82	0.002154	0.029677	-1.23
251664_at	leucine zipper-containing protein AT103	CRD1	AT3G56940	-1.56	-0.64	-4.82	0.002155	0.029677	-1.23
253465_at	putative protein ATAC98, Arabidopsis t	---	AT4G32120	-1.64	-0.71	-4.82	0.002156	0.029677	-1.23
266235_at	putative phloem-specific lectin	AtPP2-B1(	AT2G02360	1.68	0.75	4.81	0.002158	0.029691	-1.23
249594_at	putative protein SIAH1 protein, Brassica	---	AT5G37910	1.42	0.50	4.81	0.002169	0.029747	-1.24
257189_at	hypothetical protein	GIP1	AT3G13222	-1.40	-0.48	-4.81	0.002166	0.029747	-1.24
259417_at	unknown protein contains similarity to pl	HFR1	AT1G02340	-1.90	-0.93	-4.81	0.002168	0.029747	-1.24
254195_at	putative protein various predicted prote	NLP7	AT4G24020	1.46	0.54	4.81	0.002168	0.029747	-1.24
260403_at	hypothetical protein predicted by genscal	WRKY36	AT1G69810	1.39	0.48	4.81	0.002165	0.029747	-1.24
249947_at	FVT1 - like protein follicular lymphoma	---	AT5G19200	1.39	0.48	4.81	0.002171	0.029749	-1.24
259927_at	unknown protein ; supported by cDNA:	JAC1	AT1G75100	-1.88	-0.91	-4.81	0.002172	0.029749	-1.24
248710_at	unknown protein ;supported by full-leng	---	AT5G48480	-1.66	-0.73	-4.81	0.002176	0.029766	-1.24
254004_at	arginyl-tRNA synthetase	emb1027	AT4G26300	-1.34	-0.42	-4.81	0.002176	0.029766	-1.24
249421_at	DegP protease contains similarity to De	DEG8	AT5G39830	-1.53	-0.61	-4.81	0.002177	0.029766	-1.24
249941_at	putative protein similar to unknown prote	---	AT5G22270	1.67	0.74	4.80	0.00218	0.029782	-1.24
258850_at	putative cellulose synthase catalytic sub	CSLD3	AT3G03050	1.49	0.57	4.81	0.00218	0.029782	-1.24
257687_at	hypothetical protein predicted by genem	SDRB	AT3G12800	1.46	0.55	4.80	0.002182	0.029786	-1.24
246439_at	RING-H2 zinc finger protein-like RING-	---	AT5G17600	-2.91	-1.54	-4.80	0.002183	0.029786	-1.24
251432_at	putative protein leucine zipper-EF-hand	---	AT3G59820	-1.80	-0.85	-4.80	0.002186	0.029788	-1.25
250897_at	putative protein ; supported by cDNA: g	---	AT5G03430	-1.46	-0.54	-4.80	0.002187	0.029788	-1.25
247553_at	MAD box containing protein NAP1-1 - li	AGL8	AT5G60910	-2.11	-1.07	-4.80	0.002187	0.029788	-1.25
253856_at	hypothetical protein ;supported by full-le	---	AT4G28100	-1.38	-0.46	-4.80	0.002194	0.029862	-1.25
248299_at	unknown protein ;supported by full-leng	---	AT5G53080	-1.47	-0.56	-4.80	0.002198	0.029896	-1.25
258965_at	hypothetical protein similar to hypotheti	---	AT3G10530	-2.14	-1.10	-4.80	0.002203	0.029896	-1.25

265002_at	putative lysine/histidine-specific permea	LHT2	AT1G24400	-1.77	-0.82	-4.80	0.002204	0.029896	-1.25
257540_at	hypothetical protein	---	AT3G21520	1.52	0.61	4.80	0.002203	0.029896	-1.25
253124_at	putative protein unknown protein Arabic	ARO3	AT4G36030	3.05	1.61	4.80	0.002201	0.029896	-1.25
249337_at	putative protein contains similarity to un	---	AT5G41080	4.34	2.12	4.80	0.002202	0.029896	-1.25
254889_at	osmotin precursor ;supported by full-ler	ATOSM34	AT4G11650	1.90	0.93	4.79	0.002206	0.029900	-1.25
257218_at	unknown protein similar to DAG protein	---	AT3G15000	-1.43	-0.51	-4.79	0.002211	0.029915	-1.26
258072_at	unknown protein	RGS1	AT3G26090	1.39	0.48	4.79	0.002209	0.029915	-1.26
256967_at	hypothetical protein predicted by genen	---	AT3G21060	-1.53	-0.61	-4.79	0.00221	0.029915	-1.26
257451_at	hypothetical protein predicted by genefir	BT3	AT1G05690	-1.48	-0.57	-4.79	0.002215	0.029944	-1.26
260897_at	ER lumen protein retaining receptor ider	ERD2	AT1G29330	1.46	0.55	4.79	0.002219	0.029974	-1.26
266182_at	hypothetical protein predicted by gensca	---	AT2G02370	1.67	0.74	4.79	0.002219	0.029974	-1.26
263375_s_a	putative prohibitin ;supported by full-len	ATPHB6	AT2G20530 /	-1.55	-0.64	-4.79	0.002227	0.030052	-1.26
258640_at	hypothetical protein predicted by gensca	---	AT3G07930	-1.62	-0.69	-4.79	0.002228	0.030052	-1.27
245788_at	hypothetical protein similar to hypothetic	---	AT1G32120 /	2.46	1.30	4.78	0.002234	0.030110	-1.27
267083_at	calmodulin-like protein identical to GB:D	TCH3	AT2G41100	2.25	1.17	4.78	0.002236	0.030125	-1.27
260824_at	unknown protein	---	AT1G06720	-2.14	-1.10	-4.78	0.002239	0.030130	-1.27
248538_at	putative protein contains similarity to glu	---	AT5G50110	-1.65	-0.72	-4.78	0.002239	0.030130	-1.27
264375_at	putative protein kinase contains a protei	CIPK16	AT2G25090	3.02	1.59	4.78	0.002243	0.030169	-1.27
265483_at	hypothetical protein ; supported by cDN	SQN	AT2G15790	-1.73	-0.79	-4.77	0.002257	0.030267	-1.28
258132_at	protein kinase, putative similar to GB:B	ATPERK1	AT3G24550	1.75	0.81	4.78	0.002254	0.030267	-1.28
253547_at	chloroplast omega-6 fatty acid desatura	FAD6	AT4G30950	-1.45	-0.53	-4.77	0.002256	0.030267	-1.28
251461_at	putative protein	---	AT3G59780	-1.61	-0.69	-4.77	0.002257	0.030267	-1.28
254921_at	putative protein hypothetical protein F1	---	AT4G11300	1.81	0.85	4.77	0.002257	0.030267	-1.28
265594_at	50S ribosomal protein L4 ;supported by	---	AT2G20060	-1.86	-0.90	-4.77	0.00226	0.030287	-1.28
253283_at	hypothetical protein ; supported by cDN	---	AT4G34090	-1.74	-0.80	-4.77	0.002261	0.030287	-1.28
253698_at	nucleotide pyrophosphatase - like prote	---	AT4G29680	-1.44	-0.52	-4.77	0.002265	0.030326	-1.28
247816_at	similar to unknown protein (pir||S75584)	---	AT5G58260	-2.38	-1.25	-4.77	0.002275	0.030413	-1.29
259738_at	predicted protein	---	AT1G64355	-1.49	-0.57	-4.77	0.002274	0.030413	-1.29
250985_at	putative protein various predicted prote	---	AT5G02830	-1.40	-0.49	-4.77	0.002277	0.030414	-1.29
255021_at	hypothetical protein	---	AT4G10330	-1.47	-0.55	-4.77	0.002279	0.030414	-1.29
254636_at	putative protein kinase ; supported by c	CIPK12	AT4G18700	-1.40	-0.48	-4.77	0.002278	0.030414	-1.29
250527_at	serine/threonine-protein kinase	SNRK2.1	AT5G08590	-1.40	-0.49	-4.77	0.00228	0.030414	-1.29
266828_at	putative flavonol 3-O-glucosyltransferas	---	AT2G22930	-1.38	-0.46	-4.76	0.002284	0.030452	-1.29
247979_at	pollen specific protein SF21 ;supported	---	AT5G56750	1.56	0.65	4.76	0.002286	0.030453	-1.29
260771_at	serine/threonine protein kinase, putative	WNK7	AT1G49160	2.01	1.00	4.76	0.002288	0.030462	-1.29

267559_at	putative cytochrome P450	CYP76C2	AT2G45570	5.36	2.42	4.76	0.002294	0.030529	-1.30
247182_at	putative protein contains similarity to unl	HB25	AT5G65410	-1.55	-0.63	-4.76	0.002299	0.030558	-1.30
254810_at	putative protein pectinesterase - Citrus	PME1	AT4G12390	-2.41	-1.27	-4.76	0.002298	0.030558	-1.30
248607_at	NaCl-inducible Ca2+-binding protein-like	ATCP1	AT5G49480	2.68	1.42	4.76	0.002305	0.030602	-1.30
253338_at	somatic embryogenesis receptor-like ki	BAK1	AT4G33430	1.48	0.56	4.76	0.002304	0.030602	-1.30
264799_at	putative violaxanthin de-epoxidase prec	NPQ1	AT1G08550	-1.58	-0.66	-4.75	0.00231	0.030645	-1.30
266285_at	unknown protein	---	AT2G29180	-2.11	-1.08	-4.75	0.002311	0.030645	-1.30
262402_at	unknown protein ; supported by cDNA: g	TOM6	AT1G49410	-1.64	-0.72	-4.75	0.002313	0.030651	-1.30
254670_at	teosinte branched1 - like protein teosint	---	AT4G18390	-1.92	-0.94	-4.75	0.002314	0.030651	-1.31
256930_at	O-acetylserine(thiol) lyase, putative sim	OASA2	AT3G22460	1.59	0.67	4.75	0.002322	0.030686	-1.31
251583_at	putative protein several hypothetical pro	---	AT3G58590	-1.74	-0.80	-4.75	0.00232	0.030686	-1.31
246159_at	Expressed protein ; supported by full-ler	---	AT5G20935	-2.04	-1.03	-4.75	0.002318	0.030686	-1.31
250727_at	putative protein similar to unknown prote	---	AT5G06430	-1.40	-0.49	-4.75	0.002321	0.030686	-1.31
250733_at	2-cys peroxiredoxin-like protein ;suppor	2-Cys Prx	AT5G06290	-1.58	-0.66	-4.75	0.002329	0.030760	-1.31
263779_at	putative photomorphogenesis repressor	SPA1	AT2G46340	-1.55	-0.63	-4.74	0.002333	0.030798	-1.31
264831_at	hypothetical protein predicted by gensca	---	AT1G03687	-1.48	-0.56	-4.74	0.002336	0.030817	-1.32
267624_at	putative protein kinase	BIK1	AT2G39660	2.34	1.23	4.74	0.002338	0.030828	-1.32
265472_at	putative RING-H2 zinc finger protein ;su	---	AT2G15580	-1.59	-0.66	-4.74	0.002341	0.030837	-1.32
260629_at	unknown protein	---	AT1G62330	-1.55	-0.63	-4.74	0.002341	0.030837	-1.32
264913_at	hypothetical protein predicted by genem	---	AT1G60770	-1.90	-0.92	-4.74	0.002348	0.030840	-1.32
252770_at	putative protein cellular nucleic acid bin	---	AT3G42860	-1.52	-0.61	-4.74	0.002344	0.030840	-1.32
267017_at	unknown protein	SVR1	AT2G39140	-2.31	-1.21	-4.74	0.002348	0.030840	-1.32
267357_at	putative nematode-resistance protein ;s	HSPRO2	AT2G40000	2.62	1.39	4.74	0.002349	0.030840	-1.32
257722_at	putative chloroplast nucleoid DNA-bindi	---	AT3G18490	-1.96	-0.97	-4.74	0.002345	0.030840	-1.32
262309_at	phosphoglucomutase, putative similar t	---	AT1G70820	-2.17	-1.11	-4.74	0.002352	0.030872	-1.32
246417_at	quinone oxidoreductase - like protein pr	---	AT5G16990	-1.74	-0.80	-4.74	0.002355	0.030889	-1.32
255055_at	hypothetical protein	---	AT4G09810	-1.64	-0.72	-4.73	0.002359	0.030921	-1.33
259789_at	Expressed protein ; supported by full-ler	COR414-T	AT1G29395	-1.52	-0.61	-4.73	0.002366	0.031003	-1.33
261433_s_a	endoplasmic reticulum-type calcium-trar	---	AT1G07670 /	1.36	0.44	4.73	0.002369	0.031016	-1.33
251191_at	putative protein putative protein F15G1	---	AT3G62590	2.11	1.08	4.73	0.002371	0.031032	-1.33
251701_at	putative protein hypothetical protein F2	---	AT3G56650	-1.50	-0.59	-4.73	0.002381	0.031045	-1.34
249015_at	Dreg-2 like protein	---	AT5G44730	-1.47	-0.56	-4.73	0.002381	0.031045	-1.34
266950_at	expressed protein supported by full-leng	---	AT2G18910	-1.79	-0.84	-4.73	0.002378	0.031045	-1.33
246450_at	Heat Shock Factor 3	HSF3	AT5G16820	-1.40	-0.49	-4.73	0.002374	0.031045	-1.33
254608_at	major intrinsic protein (MIP)- like noduli	NIP1;2	AT4G18910	2.47	1.31	4.73	0.002382	0.031045	-1.34

252751_at	putative protein RING-H2 zinc finger pr	---	AT3G43430	2.21	1.15	4.73	0.002383	0.031045	-1.34
264745_at	5'-adenylylphosphosulfate reductase, p	אפר-02	AT1G62180	-1.90	-0.93	-4.73	0.002383	0.031045	-1.34
252391_at	putative protein ; supported by cDNA: g	---	AT3G47860	-1.58	-0.66	-4.73	0.002382	0.031045	-1.34
255438_at	putative oxidoreductase	AOP1	AT4G03070	-2.35	-1.23	-4.73	0.002385	0.031056	-1.34
246572_at	putative protein predicted proteins, Aral	---	AT5G15010	-1.49	-0.57	-4.72	0.002389	0.031083	-1.34
247077_at	putative protein similar to unknown prote	---	AT5G66420	-1.56	-0.64	-4.72	0.002392	0.031106	-1.34
249424_s_a	hypothetical protein ; supported by full-l	---	AT5G39800 /	-1.54	-0.62	-4.72	0.002398	0.031167	-1.34
258861_at	putative helicase similar to C-terminal ha	---	AT3G02060	-1.69	-0.76	-4.72	0.002403	0.031185	-1.35
247834_at	cinnamoyl-CoA reductase - like protein	---	AT5G58490	-1.39	-0.48	-4.72	0.002402	0.031185	-1.35
251759_at	tetrahydrofolylpolyglutamate synthase p	ATDFD	AT3G55630	-2.01	-1.01	-4.72	0.002405	0.031185	-1.35
266001_at	hypothetical protein predicted by genefi	HHP3	AT2G24150	-1.39	-0.48	-4.72	0.002403	0.031185	-1.35
245512_at	hypothetical protein	---	AT4G15770	-1.82	-0.87	-4.72	0.002409	0.031200	-1.35
259536_s_a	putative protein hypothetical proteins - d	ATCOAB	AT1G12350 /	-1.34	-0.43	-4.71	0.002415	0.031200	-1.35
248329_at	putative protein similar to unknown prote	---	AT5G52780	-1.72	-0.78	-4.71	0.002415	0.031200	-1.35
250789_at	putative protein contains similarity to cat	---	AT5G05630	-1.48	-0.57	-4.72	0.002411	0.031200	-1.35
262830_at	purple acid phosphatase, putative conta	PAP3	AT1G14700	-1.84	-0.88	-4.71	0.002414	0.031200	-1.35
263494_at	14-3-3 protein GF14mu (grf9) identical	GRF9	AT2G42590	-1.39	-0.48	-4.72	0.00241	0.031200	-1.35
257036_at	hypothetical protein predicted by genem	---	AT3G19120	-1.41	-0.49	-4.71	0.002416	0.031200	-1.35
246792_at	putative protein predicted proteins, Aral	---	AT5G27290	-2.27	-1.18	-4.71	0.002418	0.031212	-1.35
258526_at	DAG protein, putative similar to DAG P	---	AT3G06790	-1.48	-0.56	-4.71	0.002419	0.031212	-1.35
248409_at	putative protein contains similarity to en	LPA2	AT5G51540 /	-1.58	-0.66	-4.71	0.002423	0.031219	-1.35
261161_at	hypothetical protein contains Pfam prof	---	AT1G34420	1.93	0.95	4.71	0.002422	0.031219	-1.35
247311_at	DNA polymerase III catalytic subunit	EMB2780	AT5G63960	-1.49	-0.58	-4.71	0.002427	0.031237	-1.36
249905_at	unknown protein	---	AT5G22710	-1.45	-0.54	-4.71	0.002426	0.031237	-1.36
258813_at	NAM-like protein (no apical meristem) si	anac046	AT3G04060	1.71	0.77	4.71	0.002432	0.031252	-1.36
267535_at	putative C2H2-type zinc finger protein li	ZFP8	AT2G41940	-2.03	-1.02	-4.71	0.00243	0.031252	-1.36
254298_at	putative protein ;supported by full-lengt	PGR5-LIK	AT4G22890	-1.64	-0.71	-4.71	0.002432	0.031252	-1.36
255522_at	putative GTP pyrophosphokinase simila	RSH1	AT4G02260	-1.49	-0.58	-4.71	0.002439	0.031323	-1.36
249122_at	putative protein similar to unknown prote	ARD4	AT5G43850	-1.73	-0.79	-4.70	0.002441	0.031331	-1.36
261480_at	phytochrome kinase substrate 1, putati	PKS2	AT1G14280	-4.02	-2.01	-4.70	0.002452	0.031434	-1.37
262501_at	putative replication factor Similar to gb|	emb1968	AT1G21690	-1.53	-0.62	-4.70	0.002451	0.031434	-1.37
258493_at	Expressed protein ; supported by full-ler	---	AT3G02555	-1.49	-0.57	-4.70	0.002456	0.031476	-1.37
248815_at	putative protein contains similarity to ma	---	AT5G46920	-1.74	-0.80	-4.70	0.00246	0.031491	-1.37
247788_at	putative protein carbohydrate kinase, p	---	AT5G58730	1.84	0.88	4.70	0.00246	0.031491	-1.37
245618_at	hypothetical protein	---	AT4G14510	-1.56	-0.64	-4.70	0.002462	0.031499	-1.37

261315_at	AP2 domain containing protein, putative	ERF8	AT1G53170	2.25	1.17	4.70	0.002467	0.031536	-1.37
252858_at	puative protein various predicted protein	---	AT4G39770	-1.53	-0.62	-4.70	0.002468	0.031536	-1.37
246528_at	putative mitochondrial carrier protein M	---	AT5G15640	1.92	0.94	4.69	0.00247	0.031552	-1.37
255607_at	putative acetyltransferase similar to Dig	---	AT4G01130	-1.91	-0.94	-4.69	0.002473	0.031561	-1.38
252357_at	putative protein predicted proteins, Aral	---	AT3G48410	-1.75	-0.81	-4.69	0.002478	0.031608	-1.38
255557_at	hypothetical protein ; supported by cDN	---	AT4G01990	-1.82	-0.86	-4.69	0.002483	0.031657	-1.38
250125_at	biotin carboxyl carrier protein of acetyl-C	CAC1	AT5G16390	-1.46	-0.55	-4.69	0.002491	0.031693	-1.38
245528_at	pyruvate,orthophosphate dikinase	PPDK	AT4G15530	1.59	0.67	4.69	0.002495	0.031693	-1.39
245749_at	proline-rich protein, putative similar to p	---	AT1G51090	-3.15	-1.65	-4.68	0.002517	0.031693	-1.39
246173_s_a	putative protein hypothetical protein F2	---	AT3G61520 /	-1.70	-0.77	-4.68	0.002503	0.031693	-1.39
257730_at	unknown protein contains Pfam profile:	---	AT3G18420	-1.70	-0.77	-4.68	0.002514	0.031693	-1.39
255799_at	Deetiolated1 (DET1) light signal transdu	DET1	AT4G10180	-1.49	-0.58	-4.68	0.002501	0.031693	-1.39
265383_at	putative WD-40 repeat protein, MSI2 ;s	MSI2	AT2G16780	-1.70	-0.77	-4.68	0.002505	0.031693	-1.39
252971_at	extensin - like protein proline-rich protei	PRP4	AT4G38770	11.15	3.48	4.68	0.002507	0.031693	-1.39
263419_at	putative protein kinase contains a protei	---	AT2G17220	1.73	0.79	4.68	0.002518	0.031693	-1.40
259188_at	unknown protein ;supported by full-leng	---	AT3G01510	-1.71	-0.77	-4.68	0.002498	0.031693	-1.39
248547_at	putative protein contains similarity to sal	EMB1006	AT5G50280	-1.86	-0.89	-4.68	0.002515	0.031693	-1.39
258851_at	glutathione S-transferase identical to glu	ATGSTF1	AT3G03190	-2.39	-1.26	-4.68	0.002509	0.031693	-1.39
257198_at	DNA-binding protein, putative similar to	---	AT3G23690	-1.55	-0.63	-4.69	0.002488	0.031693	-1.38
250256_at	GTP-binding protein typA (tyrosine phos	---	AT5G13650	-1.43	-0.51	-4.68	0.002517	0.031693	-1.39
255487_at	tryptophan synthase alpha 1-like protei	---	AT4G02610	-1.52	-0.60	-4.69	0.002489	0.031693	-1.38
246746_at	putative protein predicted proteins, Ory	---	AT5G27820	-1.53	-0.61	-4.68	0.002517	0.031693	-1.39
248174_at	50S ribosomal protein L24, chloroplast	---	AT5G54600	-1.46	-0.55	-4.69	0.002496	0.031693	-1.39
252348_at	B12D-like protein B12D protein - Horde	---	AT3G48140	1.42	0.50	4.68	0.002516	0.031693	-1.39
252068_at	mucin -like protein hemomucin, Drosop	---	AT3G51440	2.79	1.48	4.68	0.002516	0.031693	-1.39
250465_at	putative protein various predicted protei	---	AT5G10070	-1.35	-0.44	-4.68	0.002516	0.031693	-1.39
254760_at	putative protein hypothetical protein sll1	---	AT4G13200	-1.41	-0.49	-4.68	0.002503	0.031693	-1.39
258782_at	putative dihydroneopterin aldolase simil	---	AT3G11750	-1.66	-0.73	-4.68	0.002516	0.031693	-1.39
259499_at	PRLI-interacting factor L, putative simil	---	AT1G15730	-1.61	-0.69	-4.68	0.002516	0.031693	-1.39
264696_at	unknown protein	---	AT1G70230	-2.47	-1.31	-4.68	0.002519	0.031698	-1.40
247247_at	50S ribosomal protein L17 ;supported b	---	AT5G64650	-1.41	-0.50	-4.67	0.002529	0.031731	-1.40
266348_at	putative MAP kinase	ATMPK17	AT2G01450	1.62	0.69	4.67	0.002528	0.031731	-1.40
252130_at	putative protein 1 photosystem II oxyge	PSBO2	AT3G50820	-1.46	-0.55	-4.67	0.002526	0.031731	-1.40
261864_s_a	10-formyltetrahydrofolate synthetase ide	THFS	AT1G50480 /	-1.49	-0.57	-4.67	0.002528	0.031731	-1.40
265707_at	unknown protein	---	AT2G03390	-1.55	-0.63	-4.67	0.00253	0.031731	-1.40

259947_at	putative protein kinase similar to protein	---	AT1G71530	1.56	0.64	4.67	0.002527	0.031731	-1.40
258805_at	putative beta-1,3-glucanase similar to b	---	AT3G04010	1.74	0.80	4.67	0.002536	0.031778	-1.40
263326_at	unknown protein ; supported by cDNA:	---	AT2G04280	-1.73	-0.79	-4.67	0.002538	0.031791	-1.40
266296_at	putative glutathione S-transferase ;supp	ATGSTU7	AT2G29420	1.58	0.66	4.67	0.002541	0.031813	-1.40
257956_at	unknown protein	---	AT3G25400	-1.62	-0.70	-4.67	0.002546	0.031851	-1.41
264094_at	unknown protein ;supported by full-lengt	---	AT1G79200	-1.50	-0.59	-4.66	0.002554	0.031874	-1.41
248920_at	magnesium chelatase subunit of protoc	CHLI2	AT5G45930	-1.49	-0.57	-4.66	0.002554	0.031874	-1.41
256741_at	hypothetical protein predicted by genem	---	AT3G29375	-1.72	-0.78	-4.66	0.002565	0.031874	-1.42
265760_at	unknown protein	---	AT2G01220	-1.47	-0.55	-4.66	0.002556	0.031874	-1.41
253782_at	hypothetical protein	---	AT4G28590	-1.36	-0.44	-4.66	0.002565	0.031874	-1.41
258174_at	hypothetical protein contains Pfam profi	---	AT3G21470	-1.48	-0.56	-4.66	0.002559	0.031874	-1.41
247193_at	putative protein strong similarity to unkn	---	AT5G65380	1.67	0.74	4.66	0.002566	0.031874	-1.42
258956_at	hypothetical protein predicted by gensca	---	AT3G01440	-3.04	-1.60	-4.66	0.002566	0.031874	-1.42
256784_at	hypothetical protein predicted by genem	---	AT3G13674	-1.40	-0.48	-4.67	0.002553	0.031874	-1.41
248399_at	putative protein strong similarity to unkn	---	AT5G52010	-1.42	-0.50	-4.66	0.002557	0.031874	-1.41
251496_at	putative protein crp1 protein, involved in	---	AT3G59040	-1.40	-0.48	-4.66	0.002561	0.031874	-1.41
259247_at	unknown protein predicted by genefind	---	AT3G07570	1.61	0.68	4.66	0.002562	0.031874	-1.41
247813_at	NADP-dependent malate dehydrogenas	---	AT5G58330	-1.45	-0.54	-4.66	0.002561	0.031874	-1.41
251785_at	ABC transporter - like protein breast ca	ATWBC19	AT3G55130	-2.24	-1.16	-4.66	0.002567	0.031875	-1.42
258250_at	putative delta 9 desaturase similar to de	FAD5	AT3G15850	-1.38	-0.46	-4.66	0.002571	0.031912	-1.42
263532_s_a	putative protein RIO1 protein, Saccharo	---	AT2G24990 /	-1.68	-0.74	-4.66	0.002577	0.031945	-1.42
245981_at	putative protein ;supported by full-lengt	---	AT5G13100	1.52	0.60	4.66	0.00258	0.031945	-1.42
265149_at	unknown protein ; supported by full-leng	---	AT1G51400	-1.52	-0.60	-4.66	0.00258	0.031945	-1.42
256266_at	unknown protein ; supported by cDNA: g	---	AT3G12320	-2.09	-1.06	-4.66	0.002578	0.031945	-1.42
263701_at	putative protein kinase C inhibitor (Zinc-	---	AT1G31160	-1.37	-0.46	-4.65	0.002583	0.031952	-1.42
267516_at	unknown protein	RPT2	AT2G30520	-1.55	-0.63	-4.66	0.002582	0.031952	-1.42
249807_at	pectinacetylesterase	---	AT5G23870	-1.74	-0.80	-4.65	0.002585	0.031963	-1.42
260783_at	ethylene response factor, putative simil	ORA59	AT1G06160	-3.15	-1.66	-4.65	0.002593	0.032004	-1.43
255087_at	putative protein proteins of this bac	---	AT4G09340	-1.39	-0.47	-4.65	0.002592	0.032004	-1.43
246019_at	putative protein predicted proteins, Ara	---	AT5G10690	-1.62	-0.70	-4.65	0.002592	0.032004	-1.43
262571_at	hypothetical protein predicted by gensca	---	AT1G15430	2.40	1.26	4.65	0.002595	0.032019	-1.43
253493_at	putative protein various predicted protei	ENP	AT4G31820	-1.90	-0.93	-4.65	0.002605	0.032121	-1.43
262706_at	putative ATP-dependent RNA helicase s	---	AT1G16280	-1.65	-0.72	-4.65	0.002609	0.032132	-1.43
257788_at	unknown protein	TCP20	AT3G27010	1.61	0.69	4.65	0.002608	0.032132	-1.43
250669_at	polygalacturonase inhibiting protein ;su	PGIP2	AT5G06870	3.01	1.59	4.64	0.002613	0.032169	-1.43

246518_at	acetyltransferase-like protein Glucosam	AtGNA1	AT5G15770	-1.43	-0.51	-4.64	0.002621	0.032233	-1.44
252325_at	acetolactate synthase ; supported by cI	CSR1	AT3G48560	-1.35	-0.43	-4.64	0.002621	0.032233	-1.44
251240_at	putative protein	---	AT3G62450	-1.40	-0.48	-4.64	0.002628	0.032297	-1.44
254263_at	Expressed protein ; supported by full-ler	---	AT4G23493	-1.41	-0.49	-4.64	0.002632	0.032308	-1.44
245242_at	chlorophyll a oxygenase identical to chlo	CH1	AT1G44446	-1.63	-0.71	-4.64	0.002631	0.032308	-1.44
260678_at	hypothetical protein predicted by genem	---	AT1G07970	-1.34	-0.43	-4.64	0.002638	0.032319	-1.44
256152_at	ethylene-responsive RNA helicase, puta	---	AT1G55150	-1.36	-0.44	-4.64	0.002635	0.032319	-1.44
255701_at	predicted protein of unknown function	JLO	AT4G00220	1.38	0.47	4.64	0.002637	0.032319	-1.44
257615_at	unknown protein	---	AT3G26510	-1.72	-0.78	-4.64	0.002638	0.032319	-1.44
264728_at	unknown protein location of EST gb|T45	---	AT1G22850	-1.55	-0.63	-4.63	0.002643	0.032340	-1.45
252463_at	putative protein ;supported by full-lengt	---	AT3G47070	-2.09	-1.07	-4.64	0.002641	0.032340	-1.45
253197_at	putative protein Cyanophora paradoxa	---	AT4G35250	-1.72	-0.79	-4.63	0.002645	0.032350	-1.45
256706_at	auxin-independent growth promoter, pu	---	AT3G30300	-1.49	-0.57	-4.63	0.002648	0.032358	-1.45
251556_at	putative protein predicted proteins, Met	---	AT3G58840	-1.66	-0.73	-4.63	0.002649	0.032358	-1.45
252876_at	putative protein ;supported by full-lengt	---	AT4G39970	-1.82	-0.86	-4.63	0.002664	0.032410	-1.45
250126_at	ubiquitin C-terminal hydrolase-like prote	UCH1	AT5G16310	-1.55	-0.63	-4.63	0.002656	0.032410	-1.45
265270_at	putative ribose phosphate pyrophospho	---	AT2G42910	-1.43	-0.51	-4.63	0.002654	0.032410	-1.45
259444_at	hypothetical protein predicted by gensca	---	AT1G02370	-2.34	-1.22	-4.63	0.00266	0.032410	-1.45
258804_at	hypothetical protein similar to hypothetic	---	AT3G04760	-1.67	-0.74	-4.63	0.002664	0.032410	-1.46
262248_at	hypothetical protein predicted by gensca	YSL8	AT1G48370	2.03	1.02	4.63	0.002657	0.032410	-1.45
267430_at	unknown protein	EDA3	AT2G34860	-1.74	-0.80	-4.63	0.002663	0.032410	-1.45
258661_at	unknown protein	---	AT3G02930	2.37	1.25	4.63	0.002663	0.032410	-1.45
251415_at	putative protein	---	AT3G60380	-1.42	-0.50	-4.63	0.002671	0.032481	-1.46
245248_at	Expressed protein ; supported by cDNA	ATB' GAM	AT4G15415	-1.31	-0.39	-4.62	0.002676	0.032498	-1.46
247598_at	UVB-resistance protein UVR8 - like UV	---	AT5G60870	-1.46	-0.54	-4.62	0.002675	0.032498	-1.46
262291_at	zinc finger and C2 domain protein, puta	---	AT1G70790	-1.40	-0.48	-4.62	0.002685	0.032568	-1.46
257772_at	unknown protein C-term similar to phosp	---	AT3G23080	-1.53	-0.62	-4.62	0.002686	0.032568	-1.46
263558_at	putative phosphatidylinositol/phosphatid	---	AT2G16380	-1.67	-0.74	-4.62	0.002684	0.032568	-1.46
245350_at	nuclear antigen homolog ;supported by	---	AT4G16830	-1.52	-0.60	-4.62	0.002694	0.032628	-1.47
245281_at	DEF (CLA1) protein ; supported by cDN	CLA1	AT4G15560	-1.53	-0.61	-4.62	0.002693	0.032628	-1.47
259248_at	putative heat-shock protein similar to he	---	AT3G07770	-2.28	-1.19	-4.62	0.002695	0.032629	-1.47
263693_at	hypothetical protein predicted by genefir	ATPP2-A9	AT1G31200	-2.54	-1.34	-4.62	0.0027	0.032648	-1.47
255117_s_a	putative protein various hypothetical pro	ATPUP13	AT4G08700 /	-1.34	-0.43	-4.62	0.002701	0.032648	-1.47
255866_at	hypothetical protein predicted by gensca	---	AT2G30350	-1.48	-0.57	-4.62	0.002701	0.032648	-1.47
249899_at	putative protein similar to unknown prote	---	AT5G22620	-1.95	-0.96	-4.61	0.002704	0.032667	-1.47

248467_at	MtN3-like protein ;supported by full-leng	---	AT5G50800	-2.73	-1.45	-4.61	0.002709	0.032716	-1.47
247572_at	putative protein ; supported by full-leng	---	AT5G61220	-1.39	-0.47	-4.61	0.002715	0.032765	-1.48
251037_at	putative protein oxysterol-binding protei	UNE18	AT5G02100	-1.77	-0.83	-4.61	0.002717	0.032778	-1.48
250971_at	putative protein ABI3-interacting protein	PRR7	AT5G02810	-1.47	-0.56	-4.61	0.002719	0.032784	-1.48
246479_at	hypothetical protein	---	AT5G16060	-1.45	-0.54	-4.61	0.002721	0.032788	-1.48
248050_at	unknown protein	---	AT5G56100	2.07	1.05	4.61	0.002725	0.032801	-1.48
255951_at	unknown protein contains similarity to ul	MUB6	AT1G22050	-1.56	-0.65	-4.61	0.002725	0.032801	-1.48
250168_at	putative protein predicted protein, Arabi	---	AT5G15320	-1.42	-0.50	-4.61	0.002727	0.032808	-1.48
254215_at	putative Na+/H+-exchanging protein Na	ATCHX17	AT4G23700	4.50	2.17	4.61	0.002732	0.032848	-1.48
255340_at	putative receptor-like protein kinase	---	AT4G04490	3.87	1.95	4.61	0.002733	0.032848	-1.48
245532_at	cytochrome P450 like protein	CYP97B3	AT4G15110	-1.33	-0.41	-4.60	0.002739	0.032886	-1.48
266801_at	putative nucleotide-binding protein ;sup	EMB2001	AT2G22870	-2.11	-1.08	-4.60	0.002738	0.032886	-1.48
263758_s_a	putative NADPH dependent mannose 6-	---	AT2G21250 /	-1.39	-0.48	-4.60	0.002746	0.032946	-1.49
266824_at	homeodomain transcription factor (HAT9	HAT9	AT2G22800	-1.40	-0.49	-4.60	0.002749	0.032947	-1.49
261060_at	unknown protein	---	AT1G17340	1.56	0.64	4.60	0.002752	0.032947	-1.49
250031_at	transfactor-like protein ; supported by c	MYR1	AT5G18240	-1.69	-0.76	-4.60	0.002753	0.032947	-1.49
257168_at	mrp protein, putative similar to mrp prot	HCF101	AT3G24430	-2.25	-1.17	-4.60	0.002748	0.032947	-1.49
254642_at	putative protein hypothetical protein, Sy	---	AT4G18810	-1.92	-0.94	-4.60	0.00275	0.032947	-1.49
254623_at	protein ch-42 precursor, chloroplast ;su	CHLI1	AT4G18480	-1.66	-0.73	-4.60	0.002757	0.032954	-1.49
256536_at	peptide chain release factor, putative si	---	AT1G33330	-1.41	-0.49	-4.60	0.002756	0.032954	-1.49
249222_at	putative protein similar to unknown prote	---	AT5G42450	-1.34	-0.42	-4.60	0.002759	0.032964	-1.49
252570_at	isovaleryl-CoA-dehydrogenase precurso	IVD	AT3G45300	2.24	1.16	4.60	0.002761	0.032973	-1.49
250186_at	putative protein apospory-associated pr	---	AT5G14500	-1.57	-0.65	-4.60	0.002766	0.032980	-1.49
251227_at	ABC transporter-like protein glutathione	ATMRP10	AT3G62700	-1.91	-0.94	-4.60	0.002765	0.032980	-1.49
252410_at	putative protein br-1 protein (NITRIC O	NOA1	AT3G47450	-1.58	-0.66	-4.60	0.002765	0.032980	-1.49
261488_at	Expressed protein ; supported by full-ler	---	AT1G14345	-1.58	-0.66	-4.59	0.00277	0.033006	-1.50
266476_at	unknown protein ;supported by full-leng	---	AT2G31090	1.64	0.72	4.59	0.002773	0.033035	-1.50
251961_at	inorganic pyrophosphatase -like protein	AtPPa4	AT3G53620	2.00	1.00	4.59	0.00278	0.033095	-1.50
264491_at	hypothetical protein predicted by gensca	---	AT1G27410	-1.42	-0.50	-4.59	0.002782	0.033107	-1.50
252214_at	putative protein EREBP-3 homolog, Sty	CEJ1	AT3G50260	2.48	1.31	4.59	0.002791	0.033196	-1.50
257463_at	phosphatidylinositol/phosphatidylcholin	---	AT1G14820	-1.59	-0.67	-4.59	0.002795	0.033217	-1.51
261112_at	unknown protein	---	AT1G75420	-1.53	-0.62	-4.59	0.002796	0.033222	-1.51
256735_at	hypothetical protein predicted by genem	ATEXO70I	AT3G29400	1.55	0.63	4.58	0.002799	0.033234	-1.51
267419_at	putative thioredoxin	ATO1	AT2G35010	-1.46	-0.54	-4.58	0.002807	0.033312	-1.51
265777_at	hypothetical protein predicted by genefir	---	AT2G07340	-1.39	-0.48	-4.58	0.002808	0.033312	-1.51

261913_at	flavin-containing monooxygenase FMO	FMO GS-(	AT1G65860	-2.35	-1.23	-4.58	0.002812	0.033336	-1.51
258025_at	putative D-3-phosphoglycerate dehydro(	---	AT3G19480	-1.87	-0.90	-4.58	0.002819	0.033405	-1.52
246490_at	S-adenosylmethionine decarboxylase (a	CPuORF1	AT5G15948 /	-1.66	-0.73	-4.58	0.002826	0.033450	-1.52
253305_at	Expressed protein ; supported by full-ler	---	AT4G33666	2.58	1.37	4.58	0.002826	0.033450	-1.52
262397_at	hypothetical protein predicted by genem	---	AT1G49380	-1.87	-0.91	-4.57	0.002836	0.033554	-1.52
258041_at	Expressed protein ; supported by full-ler	ZML1	AT3G21175	-1.47	-0.55	-4.57	0.00284	0.033579	-1.52
265384_at	unknown protein ;supported by full-leng	---	AT2G20760	1.34	0.42	4.57	0.002847	0.033635	-1.53
261338_at	hypothetical protein predicted by genem	---	AT1G44920	-1.54	-0.63	-4.57	0.002847	0.033635	-1.53
249847_at	serine carboxypeptidase II-like protein	SCPL34	AT5G23210	-1.77	-0.82	-4.57	0.00286	0.033725	-1.53
255819_s_a	40S ribosomal protein S26	---	AT2G40510 /	-1.43	-0.52	-4.57	0.002858	0.033725	-1.53
253614_at	putative protein heat shock protein 101	---	AT4G30350	1.90	0.93	4.57	0.002858	0.033725	-1.53
249187_at	cysteine proteinase RD21A similar to cy	---	AT5G43060	2.44	1.29	4.57	0.002861	0.033725	-1.53
247206_at	putative protein similar to unknown prote	---	AT5G64950	-1.31	-0.39	-4.57	0.002862	0.033726	-1.53
262482_at	SRG1-like protein Strong homology to S	SRG1	AT1G17020	3.58	1.84	4.56	0.002878	0.033852	-1.54
262794_at	unknown protein EST gb|N37870 comes	emb1745	AT1G13120	-1.46	-0.54	-4.56	0.002882	0.033852	-1.54
260261_at	unknown protein	---	AT1G68450	4.01	2.00	4.56	0.002879	0.033852	-1.54
267517_at	unknown protein	RPT2	AT2G30520	-1.51	-0.60	-4.56	0.002878	0.033852	-1.54
251193_at	translation releasing factor RF-1 -like pr	APG3	AT3G62910	-1.71	-0.78	-4.56	0.002876	0.033852	-1.54
266747_at	predicted by genefinder and genscan ;	---	AT2G02870	1.54	0.63	4.56	0.002882	0.033852	-1.54
266732_at	unknown protein	---	AT2G03240	1.72	0.78	4.56	0.00289	0.033898	-1.54
249014_at	putative protein similar to unknown prote	---	AT5G44710	-1.57	-0.65	-4.56	0.002889	0.033898	-1.54
253943_at	putative protein gene F19K23.12 of BA(	---	AT4G27030	-2.80	-1.48	-4.56	0.002889	0.033898	-1.54
257071_at	unknown protein ; supported by cDNA:	ATCSLC04	AT3G28180	1.77	0.82	4.56	0.002896	0.033940	-1.54
264026_at	glycine-rich protein (AtGRP2) Same as (	ATGRP2B	AT2G21060	1.98	0.98	4.55	0.002897	0.033940	-1.54
254673_at	membrane-bound small GTP-binding -	AtRABA1e	AT4G18430	2.94	1.56	4.55	0.002901	0.033952	-1.55
262586_at	hypothetical protein predicted by gensca	---	AT1G15480	-1.87	-0.90	-4.55	0.002901	0.033952	-1.55
245439_at	hypothetical protein	---	AT4G16670	2.14	1.09	4.55	0.002905	0.033963	-1.55
251438_s_a	putative protein hypothetical protein F1(	---	AT3G59930 /	6.70	2.74	4.55	0.002905	0.033963	-1.55
259512_at	hypothetical protein ; supported by cDN/	KEU	AT1G12360	1.35	0.44	4.55	0.002907	0.033966	-1.55
259502_at	unknown protein ; supported by cDNA: g	---	AT1G15670	2.16	1.11	4.55	0.002922	0.034124	-1.55
250796_at	putative protein similar to unknown prote	---	AT5G05300	5.37	2.43	4.55	0.002931	0.034209	-1.56
263352_at	En/Spm-like transposon protein related	---	AT2G22080	-1.73	-0.79	-4.54	0.002933	0.034221	-1.56
246457_at	WD40-repeat protein transducin homol(	TOZ	AT5G16750	-1.46	-0.55	-4.54	0.002944	0.034315	-1.56
251518_at	putative protein protein CG15643 - Dros	---	AT3G59390	-1.46	-0.54	-4.54	0.002943	0.034315	-1.56
266327_at	homeodomain transcription factor (ATH	ATHB-7	AT2G46680	2.15	1.11	4.54	0.002965	0.034361	-1.57

250326_at	putative protein strong similarity to unkn	MSL10	AT5G12080	-1.65	-0.72	-4.54	0.002956	0.034361	-1.57
256512_at	Expressed protein ; supported by full-ler	---	AT1G33265	-1.55	-0.63	-4.54	0.00296	0.034361	-1.57
262509_at	hypothetical protein similar to hypothetic	CRR22	AT1G11290	-1.50	-0.58	-4.54	0.002962	0.034361	-1.57
261771_at	hypothetical protein contains similarity to	---	AT1G76150	1.32	0.40	4.54	0.002964	0.034361	-1.57
259466_at	response regulator 5, putative similar to	ARR7	AT1G19050	3.87	1.95	4.54	0.002962	0.034361	-1.57
261195_at	transport inhibitor response 1 (TIR1), pu	AFB3	AT1G12820	-1.45	-0.54	-4.54	0.002951	0.034361	-1.56
258786_at	putative syntaxin contains Pfam profile:	SYP121	AT3G11820	2.26	1.18	4.54	0.002961	0.034361	-1.57
255939_at	hypothetical protein predicted by genem	---	AT1G12730	-1.70	-0.77	-4.54	0.002958	0.034361	-1.57
263072_at	putative protein kinase contains a protei	---	AT2G17530	1.41	0.50	4.54	0.002954	0.034361	-1.56
266582_at	unknown protein ; supported by cDNA:	---	AT2G46090	-1.57	-0.65	-4.54	0.002957	0.034361	-1.57
251611_at	putative protein several hypothetical pro	---	AT3G57940	-1.67	-0.74	-4.53	0.002973	0.034439	-1.57
250563_at	putative protein predicted protein, Arabi	---	AT5G08050	-1.73	-0.79	-4.53	0.002977	0.034447	-1.57
254647_at	hypothetical protein	---	AT4G18540	1.33	0.41	4.53	0.002975	0.034447	-1.57
266442_at	hypothetical protein	---	AT2G43260	-1.33	-0.41	-4.53	0.002982	0.034490	-1.57
267383_at	unknown protein	---	AT2G44360	1.34	0.42	4.53	0.002983	0.034490	-1.58
246949_at	cytochrome P450-like protein CYTOCH	CYP71B13	AT5G25140	-3.09	-1.63	-4.53	0.002986	0.034497	-1.58
251340_at	actin - like protein actin 3, Drosophila m	ATARP7	AT3G60830	-1.43	-0.52	-4.53	0.002987	0.034497	-1.58
260607_at	putative receptor protein kinase	---	AT2G43700	-1.61	-0.69	-4.53	0.002989	0.034498	-1.58
264199_at	unknown protein contains similarity to y	---	AT1G22700	-1.50	-0.58	-4.53	0.002996	0.034568	-1.58
263716_at	26S proteasome regulatory subunit S2 c	RPN1A	AT2G20580	-1.34	-0.43	-4.53	0.002999	0.034580	-1.58
256585_at	hypothetical protein	---	AT3G28760	-1.73	-0.79	-4.52	0.003006	0.034613	-1.58
252508_at	putative protein tRNA nucleotidyltransfe	---	AT3G46210	-1.79	-0.84	-4.52	0.003004	0.034613	-1.58
262283_at	unknown protein ;supported by full-lengt	---	AT1G68590	-1.62	-0.70	-4.52	0.003006	0.034613	-1.58
259970_at	putative chlorophyll A-B binding protein	---	AT1G76570	-1.81	-0.86	-4.52	0.003013	0.034663	-1.59
253172_at	putative protein ;supported by full-length	---	AT4G35060	2.72	1.44	4.52	0.003013	0.034663	-1.59
261881_at	nodulin-like protein similar to nodulin GE	NIP6;1	AT1G80760	-1.85	-0.89	-4.52	0.003015	0.034668	-1.59
267436_at	putative receptor-like protein kinase	FRK1	AT2G19190	3.34	1.74	4.52	0.003017	0.034673	-1.59
255224_at	putative protein hypothetical protein, Ar	---	AT4G05400	-1.57	-0.65	-4.52	0.003024	0.034730	-1.59
256480_at	unknown protein	SAR1	AT1G33410	-1.56	-0.64	-4.52	0.003032	0.034774	-1.59
246308_at	chlorophyll synthetase ; supported by c	G4	AT3G51820	-1.57	-0.65	-4.52	0.003032	0.034774	-1.59
264702_at	hypothetical protein contains similarity to	---	AT1G70190	-1.49	-0.58	-4.52	0.003033	0.034774	-1.59
246026_at	putative protein predicted protein - Oryz	---	AT5G21070	-1.42	-0.51	-4.52	0.003034	0.034774	-1.59
245613_at	hypothetical protein	---	AT4G14450 /	6.83	2.77	4.51	0.003037	0.034774	-1.59
252122_at	putative protein hypothetical protein - S	---	AT3G51140	-1.47	-0.56	-4.51	0.003037	0.034774	-1.59
248634_at	isoleucyl-tRNA synthetase	OVA2	AT5G49030	-1.58	-0.66	-4.51	0.00304	0.034797	-1.60

265931_at	unknown protein ;supported by full-leng	---	AT2G18520	-1.60	-0.68	-4.51	0.003048	0.034866	-1.60
255994_at	hypothetical protein predicted by gensca	---	AT1G29760	1.38	0.47	4.51	0.00305	0.034871	-1.60
266566_at	unknown protein	---	AT2G24040	1.50	0.58	4.51	0.003052	0.034874	-1.60
249410_at	receptor-like protein kinase receptor-lik	---	AT5G40380	-2.04	-1.03	-4.51	0.003057	0.034881	-1.60
246058_at	putative protein predicted proteins, Aral	---	AT5G08430	-1.47	-0.56	-4.51	0.003056	0.034881	-1.60
253849_at	putative protein 150-kD protein, Dictyos	---	AT4G28080	-1.40	-0.48	-4.51	0.003055	0.034881	-1.60
258106_at	ribonucleoside-diphosphate reductase s	RNR2A	AT3G23580	-1.55	-0.63	-4.51	0.003059	0.034888	-1.60
245227_s_a	gunknown protein contains non-consens	---	AT1G08410	-1.74	-0.80	-4.51	0.003065	0.034943	-1.60
266131_at	putative SCARECROW gene regulator	---	AT2G45160	-1.73	-0.79	-4.51	0.003069	0.034967	-1.61
265214_at	unkown protein ESTs gb|H36249, gb|A	---	AT1G05000	2.32	1.22	4.50	0.003077	0.035023	-1.61
252496_at	putative protein several hypothetical pro	CRR2	AT3G46790	-1.76	-0.82	-4.50	0.00308	0.035023	-1.61
258051_at	hypothetical protein predicted by genem	TRZ4	AT3G16260	-1.60	-0.68	-4.50	0.003076	0.035023	-1.61
267588_at	unknown protein	---	AT2G42060	1.36	0.45	4.50	0.00308	0.035023	-1.61
263948_at	similar to harpin-induced protein hin1 fro	YLS9	AT2G35980	2.81	1.49	4.50	0.003088	0.035046	-1.61
258338_at	putative L-asparaginase similar to L-ASI	---	AT3G16150	1.90	0.92	4.50	0.003086	0.035046	-1.61
246007_at	Expressed protein ; supported by full-ler	FTRA2	AT5G08410	-1.53	-0.61	-4.50	0.003088	0.035046	-1.61
250644_at	protein phosphatase 2C-like ;supported	---	AT5G06750	1.76	0.81	4.50	0.003088	0.035046	-1.61
259012_at	hypothetical protein similar to hypothetic	PUB9	AT3G07360	-1.62	-0.69	-4.50	0.003092	0.035076	-1.61
249282_at	CMP-sialic acid transporter-like protein	---	AT5G41760	-1.62	-0.70	-4.50	0.003098	0.035085	-1.62
256319_at	trehalose-phosphatase, putative contai	---	AT1G35910	3.06	1.61	4.50	0.003098	0.035085	-1.62
245408_at	putative protein	---	AT4G17180	-1.54	-0.62	-4.50	0.003097	0.035085	-1.61
261146_at	hypothetical protein predicted by genem	---	AT1G19620	-1.62	-0.70	-4.50	0.003101	0.035094	-1.62
253147_at	protein kinase - like protein serine/threo	CONNEXI	AT4G35600	1.90	0.92	4.50	0.003102	0.035094	-1.62
256441_at	unknown protein ;supported by full-leng	---	AT3G10940	-1.96	-0.97	-4.49	0.00311	0.035121	-1.62
258151_at	beta-glucosidase, putative similar to be	BGLU44	AT3G18080	-2.02	-1.02	-4.49	0.00311	0.035121	-1.62
245064_at	Expressed protein ; supported by full-ler	---	AT2G39725	1.86	0.89	4.49	0.003108	0.035121	-1.62
252001_at	plastid division protein FtsZ-like FtsZ pr	FTSZ2-2	AT3G52750	-2.00	-1.00	-4.49	0.00311	0.035121	-1.62
249558_at	hypothetical protein	---	AT5G38310	3.54	1.82	4.49	0.003114	0.035147	-1.62
261902_at	unknown protein ; supported by full-leng	PLMT	AT1G80860	-1.39	-0.48	-4.49	0.00312	0.035202	-1.62
261981_at	unknown protein	---	AT1G33811	-3.17	-1.67	-4.49	0.003124	0.035225	-1.62
257659_at	Expressed protein ; supported by full-ler	---	AT3G13226	-1.36	-0.44	-4.49	0.003132	0.035293	-1.63
265920_s_a	unknown protein	---	AT2G15120 /	2.46	1.30	4.49	0.00314	0.035343	-1.63
252945_at	putative protein ;supported by full-lengt	---	AT4G39140	1.50	0.59	4.49	0.003141	0.035343	-1.63
247720_at	dTDP-glucose 4-6-dehydratase - like pr	UXS3	AT5G59290	1.51	0.60	4.49	0.00314	0.035343	-1.63
266822_at	60S ribosomal protein L30 ;supported b	---	AT2G44860	-1.69	-0.76	-4.48	0.003143	0.035355	-1.63

253249_at	GATA transcription factor 3	---	AT4G34680	-1.61	-0.68	-4.48	0.003148	0.035385	-1.63
267233_s_a	unknown protein	---	AT2G43910 /	-1.70	-0.77	-4.48	0.003151	0.035412	-1.63
252400_at	hypothetical protein	---	AT3G48020	2.16	1.11	4.48	0.003157	0.035435	-1.64
246756_at	protein phosphatase - like protein phos	---	AT5G27930	-1.58	-0.66	-4.48	0.003156	0.035435	-1.63
253410_at	putative protein various predicted prote	---	AT4G32970	-1.60	-0.68	-4.48	0.003163	0.035476	-1.64
247746_at	uncoupling protein AtUCP2 ;supported	ATUCP2	AT5G58970	-1.62	-0.70	-4.48	0.003163	0.035476	-1.64
252542_at	nuclear receptor binding factor-like prot	---	AT3G45770	-1.36	-0.44	-4.48	0.003167	0.035479	-1.64
265643_at	hypothetical protein predicted by genefi	---	AT2G27390 /	1.98	0.99	4.48	0.003167	0.035479	-1.64
252064_at	putative protein various predicted prote	---	AT3G51520	-1.41	-0.49	-4.48	0.00317	0.035501	-1.64
251657_at	putative protein MULTICOPY SUPPRE	---	AT3G57000	-1.83	-0.87	-4.48	0.003173	0.035516	-1.64
265581_at	putative cAMP-dependent protein kinas	---	AT2G20050	-1.39	-0.47	-4.47	0.003185	0.035626	-1.64
251225_at	putative protein glycosyl transferase lgt	GATL7	AT3G62660	-1.67	-0.74	-4.47	0.003188	0.035648	-1.65
247705_at	putative protein ;supported by full-lengt	---	AT5G59460	-1.42	-0.50	-4.47	0.003194	0.035694	-1.65
252058_at	putative protein hin1 protein -Nicotiana	---	AT3G52470	1.80	0.85	4.47	0.003197	0.035695	-1.65
248231_at	putative protein contains similarity to top	---	AT5G53770	-1.48	-0.57	-4.47	0.003197	0.035695	-1.65
262957_s_a	RNA polymerase II subunit, putative sir	NRPB8A	AT1G54250 /	-1.31	-0.39	-4.47	0.003199	0.035698	-1.65
245314_at	Expressed protein ; supported by full-ler	---	AT4G16745	1.44	0.53	4.47	0.003202	0.035710	-1.65
247577_at	putative protein flavin-containing monoc	---	AT5G61290	-1.46	-0.55	-4.47	0.003203	0.035710	-1.65
247222_at	ABC transporter protein 1-like ; support	ATGCN5	AT5G64840	-1.82	-0.86	-4.47	0.003205	0.035714	-1.65
262047_at	hypothetical protein predicted by genem	---	AT1G80160	4.30	2.10	4.47	0.003212	0.035779	-1.65
245417_at	phosphoribosylglycinamide formyltransf	---	AT4G17360	-1.78	-0.83	-4.46	0.003221	0.035857	-1.66
251790_at	elicitor responsive/phloem -like protein	---	AT3G55470	1.50	0.59	4.46	0.003223	0.035859	-1.66
256787_at	beta-fructofuranosidase 1 identical to GI	ATBFRUC	AT3G13790	2.02	1.01	4.46	0.003232	0.035895	-1.66
249828_at	succinyl-CoA synthetase, alpha subunit	---	AT5G23250	-1.55	-0.63	-4.46	0.003235	0.035895	-1.66
258366_at	DNA-binding protein contains AP2 dom	RAP2.2	AT3G14230	-1.48	-0.56	-4.46	0.003234	0.035895	-1.66
266924_at	unknown protein ;supported by full-leng	---	AT2G45730	-1.55	-0.63	-4.46	0.003236	0.035895	-1.66
253395_at	protein kinase AME3 ; supported by cD	AME3	AT4G32660	-1.35	-0.43	-4.46	0.003234	0.035895	-1.66
252904_at	putative protein crp1 protein, Zea mays	EMB2453	AT4G39620	-1.48	-0.57	-4.46	0.00323	0.035895	-1.66
255694_at	putative transcriptional regulator	UNE10	AT4G00050	-1.59	-0.67	-4.46	0.003237	0.035895	-1.66
250559_at	putative protein condensin subunit SMC	---	AT5G08010	-1.51	-0.59	-4.46	0.003254	0.036066	-1.67
250941_at	putative protein	---	AT5G03320	1.56	0.64	4.45	0.003257	0.036079	-1.67
257074_at	unknown protein	---	AT3G19660	2.08	1.06	4.45	0.003259	0.036085	-1.67
254419_at	NADH dehydrogenase like protein NAD	NDB3	AT4G21490	1.34	0.42	4.45	0.003262	0.036099	-1.67
246908_at	dehydration-induced protein RD22 ; sup	RD22	AT5G25610	4.82	2.27	4.45	0.003265	0.036099	-1.67
249842_at	putative protein contains similarity to unl	---	AT5G23550	-1.38	-0.46	-4.45	0.003264	0.036099	-1.67

253443_at	putative protein beta transducin-like pro	LUG	AT4G32551	-1.31	-0.39	-4.45	0.003268	0.036112	-1.67
249826_at	iron superoxide dismutase 3 (gb|AAC24	FSD3	AT5G23310	-1.65	-0.73	-4.45	0.003281	0.036207	-1.68
253834_at	protein phosphatase homolog (PPH1)	---	AT4G27800	-1.50	-0.58	-4.45	0.003278	0.036207	-1.68
261638_at	Expressed protein ; supported by full-ler	---	AT1G49975	-2.05	-1.03	-4.45	0.003281	0.036207	-1.68
250718_at	unknown protein	emb2735	AT5G06240	-1.42	-0.51	-4.45	0.003285	0.036212	-1.68
263755_at	unknown protein ;supported by full-leng	---	AT2G21340	-1.61	-0.68	-4.45	0.003284	0.036212	-1.68
259517_at	hypothetical protein ; supported by cDN	CAT1	AT1G20630	1.75	0.80	4.45	0.003286	0.036215	-1.68
254105_at	magnesium-protoporphyrin IX methyltra	CHLM	AT4G25080	-1.48	-0.57	-4.45	0.003291	0.036226	-1.68
264766_at	receptor kinase, putative similar to rece	---	AT1G61420	2.21	1.15	4.45	0.003289	0.036226	-1.68
248093_at	putative protein similar to unknown prote	---	AT5G55210	-1.50	-0.59	-4.44	0.003299	0.036295	-1.68
264782_at	putative transcription factor similar to GI	MYB60	AT1G08810	-1.59	-0.67	-4.44	0.003301	0.036305	-1.68
246702_at	putative cytidine deaminase - like putati	---	AT5G28050	2.68	1.42	4.44	0.003307	0.036356	-1.68
258716_at	unknown protein similar to a region of D	---	AT3G09700	-1.77	-0.82	-4.44	0.003309	0.036359	-1.69
252671_at	putative protein dehydrogenases of bac	---	AT3G44190	1.58	0.66	4.44	0.003313	0.036381	-1.69
246200_at	putative protein ;supported by full-length	---	AT4G37240	1.98	0.99	4.44	0.00333	0.036384	-1.69
256293_at	pinhead-like protein similar to pinhead [A	AGO7	AT1G69440	-1.71	-0.77	-4.44	0.003326	0.036384	-1.69
256892_at	hypothetical protein contains similarity t	---	AT3G19000	-1.89	-0.92	-4.44	0.003322	0.036384	-1.69
258097_at	transport protein, putative similar to tran	---	AT3G23660	1.35	0.43	4.44	0.003315	0.036384	-1.69
258502_at	unknown protein	---	AT3G02490	-1.85	-0.89	-4.44	0.003317	0.036384	-1.69
262428_at	hypothetical protein predicted by genem	---	AT1G47570	-1.41	-0.49	-4.44	0.003324	0.036384	-1.69
246977_at	putative protein CONSTANS-like protei	COL4	AT5G24930	-1.35	-0.44	-4.44	0.003319	0.036384	-1.69
245347_at	ferredoxin ;supported by full-length cDN	---	AT4G14890	-1.60	-0.68	-4.44	0.003324	0.036384	-1.69
261141_at	unknown protein contains Pfam profile: I	---	AT1G19740	-1.49	-0.58	-4.43	0.003333	0.036384	-1.69
261828_at	unknown protein ; supported by cDNA: g	---	AT1G11360	-1.40	-0.48	-4.44	0.003327	0.036384	-1.69
253053_at	putative protein beta-ketoadipate enol-l	---	AT4G37470	-1.58	-0.66	-4.43	0.003333	0.036384	-1.69
256096_at	unknown protein	---	AT1G13650	-2.21	-1.15	-4.43	0.003334	0.036384	-1.69
251643_at	guanylate kinase-like protein guanylate	AGK2	AT3G57550	2.36	1.24	4.44	0.003329	0.036384	-1.69
250515_at	putative protein	---	AT5G09570	1.30	0.38	4.43	0.003338	0.036394	-1.69
253398_at	putative protein retinal pigment microso	CCD8	AT4G32810	2.37	1.25	4.43	0.003338	0.036394	-1.69
259746_at	hypothetical protein predicted by gensca	---	AT1G71060	-1.65	-0.72	-4.43	0.003343	0.036430	-1.70
263117_at	putative lipoamide dehydrogenase com	---	AT1G03040	-1.34	-0.42	-4.43	0.003348	0.036461	-1.70
266719_at	MYB-related transcription factor (CCA1)	CCA1	AT2G46830	-1.57	-0.65	-4.43	0.003349	0.036461	-1.70
244934_at	NADH dehydrogenase ND6	---	---	-2.09	-1.06	-4.43	0.003361	0.036564	-1.70
252984_at	cinnamyl-alcohol dehydrogenase ELI3-2	ELI3-2	AT4G37990	3.06	1.61	4.43	0.003361	0.036564	-1.70
250936_at	putative protein ;supported by full-lengt	---	AT5G03120	-2.04	-1.03	-4.43	0.003366	0.036596	-1.70

263158_at	CCAAT-binding factor B subunit, putativ	NF-YA5	AT1G54160	-1.42	-0.51	-4.43	0.003369	0.036602	-1.70
252187_at	putative protein UV inducible protein UV	---	AT3G50850	1.51	0.59	4.43	0.00337	0.036602	-1.70
266795_at	unknown protein	---	AT2G03070	-1.51	-0.59	-4.42	0.003372	0.036604	-1.71
259677_at	putative phosphatidylinositol-4-phospha	---	AT1G77740	1.60	0.67	4.42	0.003382	0.036642	-1.71
257063_s_a	unknown protein ;supported by full-leng	---	AT3G18240 /	-1.35	-0.43	-4.42	0.003379	0.036642	-1.71
260172_s_a	putative histidinol-phosphate aminotrans	---	AT1G71920 /	-1.61	-0.69	-4.42	0.00338	0.036642	-1.71
260718_at	unknown protein	ECT7	AT1G48110	1.31	0.39	4.42	0.003381	0.036642	-1.71
260814_at	histidine decarboxylase, putative simila	emb1075	AT1G43710	-1.39	-0.48	-4.42	0.003398	0.036808	-1.71
259344_at	putative polynucleotide phosphorylase	RIF10	AT3G03710	-1.53	-0.62	-4.42	0.003401	0.036816	-1.71
251969_at	Cytochrom P450 -like protein CYTOCH	LUT1	AT3G53130	-1.57	-0.66	-4.42	0.003403	0.036821	-1.71
266881_at	putative casein kinase II beta subunit ;s	CKB4	AT2G44680	-1.42	-0.51	-4.41	0.003411	0.036888	-1.72
245502_at	hypothetical protein	---	AT4G15640	-1.55	-0.64	-4.41	0.003418	0.036930	-1.72
250444_at	beta-xylosidase - like protein beta-xylos	---	AT5G10560	-1.46	-0.55	-4.41	0.003416	0.036930	-1.72
265484_at	unknown protein ; supported by cDNA:	OTP51	AT2G15820	-1.45	-0.53	-4.41	0.003424	0.036957	-1.72
265100_at	hypothetical protein predicted by gensca	OSB4	AT1G31010	-1.66	-0.73	-4.41	0.003423	0.036957	-1.72
254452_at	UV-damaged DNA-binding protein- like	DDB1B	AT4G21100	-1.57	-0.65	-4.41	0.003429	0.036998	-1.72
262346_at	unknown protein similar to hypothetical	---	AT1G63980	-1.61	-0.68	-4.41	0.003437	0.037055	-1.73
250813_at	GTP-binding protein (gb|AAD09203.1)	TOC34	AT5G05000	-1.53	-0.61	-4.41	0.003437	0.037055	-1.73
266357_at	putative beta-amylase	BAM6	AT2G32290	-2.77	-1.47	-4.41	0.003443	0.037094	-1.73
257672_at	unknown protein ;supported by full-leng	---	AT3G20300	-1.89	-0.92	-4.41	0.003444	0.037094	-1.73
259274_at	putative homeobox-leucine zipper prote	ATHB20	AT3G01220	1.38	0.46	4.41	0.003446	0.037099	-1.73
256573_at	hypothetical protein predicted by genem	---	AT3G14860	-1.41	-0.50	-4.40	0.003453	0.037148	-1.73
246086_at	beta-1,3-glucanase - like protein beta-1	---	AT5G20560	1.35	0.44	4.40	0.003471	0.037308	-1.74
254982_at	putative protein ; supported by cDNA: g	---	AT4G10470	-1.52	-0.61	-4.40	0.003471	0.037308	-1.74
257035_at	cytochrome P450, putative similar to cy	CYP707A4	AT3G19270	-1.48	-0.57	-4.40	0.003473	0.037311	-1.74
255928_at	unknown protein	---	AT1G12640	1.73	0.79	4.40	0.003478	0.037346	-1.74
248798_at	putative protein contains similarity to pla	---	AT5G47190	-1.45	-0.53	-4.40	0.003481	0.037350	-1.74
258369_at	putative pectin methylesterase similar to	ATPME3	AT3G14310	-1.49	-0.58	-4.40	0.003481	0.037350	-1.74
247278_at	fructose-bisphosphatase-like protein ;su	---	AT5G64380	-1.53	-0.61	-4.39	0.003493	0.037460	-1.74
263411_at	putative C2H2-type zinc finger protein li	---	AT2G28710	1.97	0.98	4.39	0.003496	0.037479	-1.74
248709_at	unknown protein ;supported by full-leng	---	AT5G48470	-1.85	-0.89	-4.39	0.003498	0.037483	-1.74
260373_at	unknown protein	---	AT1G73970	-1.41	-0.50	-4.39	0.003501	0.037494	-1.75
252234_at	putative protein ; supported by full-leng	ATPSK4	AT3G49780	3.97	1.99	4.39	0.003506	0.037515	-1.75
254198_at	hypothetical protein	---	AT4G24090	-1.46	-0.54	-4.39	0.003506	0.037515	-1.75
259410_at	hypothetical protein predicted by genem	---	AT1G13340	2.48	1.31	4.39	0.003514	0.037545	-1.75

255636_at	homeodomain protein AHDP ; supporte	ANL2	AT4G00730	-1.52	-0.60	-4.39	0.003514	0.037545	-1.75
255691_at	hypothetical protein	ANTR2	AT4G00370	-1.48	-0.57	-4.39	0.003514	0.037545	-1.75
249777_at	putative protein similar to unknown prote	---	AT5G24210	1.60	0.68	4.39	0.003516	0.037545	-1.75
249375_at	putative protein predicted proteins, Arat	AGP24	AT5G40730	-1.43	-0.52	-4.39	0.003518	0.037546	-1.75
257713_at	succinate dehydrogenase iron-protein s	SDH2-1	AT3G27380	1.81	0.86	4.39	0.003519	0.037546	-1.75
254132_at	putative protein hypothetical protein T8	ATHB22	AT4G24660	-1.74	-0.80	-4.39	0.003523	0.037566	-1.75
263449_at	unknown protein	AtRABA5d	AT2G31670 /	-1.39	-0.47	-4.39	0.003529	0.037618	-1.75
263136_at	trehalose-6-phosphate synthase, putati	ATTPS1	AT1G78580	-1.43	-0.52	-4.38	0.003537	0.037664	-1.76
251666_at	CYSTATHIONINE BETA-LYASE PREC	CBL	AT3G57050	-1.58	-0.66	-4.38	0.003538	0.037664	-1.76
259250_at	unknown protein	---	AT3G07580	1.74	0.80	4.38	0.003538	0.037664	-1.76
250723_at	lysine decarboxylase-like protein	---	AT5G06300	-1.63	-0.70	-4.38	0.003544	0.037684	-1.76
266391_at	putative strictosidine synthase identical	---	AT2G41290	-1.57	-0.65	-4.38	0.003542	0.037684	-1.76
258203_at	hypothetical protein predicted by genem	---	AT3G13950	5.18	2.37	4.38	0.003553	0.037767	-1.76
246114_at	seed imbitition protein-like seed imbititi	DIN10	AT5G20250	1.81	0.86	4.38	0.003557	0.037785	-1.76
261084_at	tropinone reductase-I, putative similar t	---	AT1G07440	-1.81	-0.85	-4.38	0.003566	0.037873	-1.76
261544_at	unknown protein	---	AT1G63540	-1.61	-0.68	-4.38	0.003572	0.037893	-1.77
255567_at	hypothetical protein ; supported by cDN	---	AT4G01150	-1.42	-0.51	-4.38	0.00357	0.037893	-1.77
255763_at	hypothetical protein predicted by genem	---	AT1G16730	-1.52	-0.61	-4.38	0.003573	0.037893	-1.77
260745_at	2,4-D inducible glutathione S-transferas	ATGSTU2	AT1G78370	-2.60	-1.38	-4.37	0.003577	0.037915	-1.77
250856_at	putative protein salt-inducible protein, n	---	AT5G04810	-1.55	-0.63	-4.37	0.003584	0.037921	-1.77
261559_at	LIM domain protein, putative similar to I	---	AT1G01780	1.48	0.56	4.37	0.003582	0.037921	-1.77
266003_at	hypothetical protein predicted by gensca	---	AT2G37320	-1.61	-0.69	-4.37	0.003581	0.037921	-1.77
263931_at	unknown protein ;supported by full-leng	---	AT2G36220	2.46	1.30	4.37	0.003584	0.037921	-1.77
261078_at	unknown protein identical to SP:O50061	RPL4	AT1G07320	-1.41	-0.50	-4.37	0.003592	0.037987	-1.77
265913_at	Expressed protein ; supported by full-ler	---	AT2G25625	2.51	1.33	4.37	0.003594	0.037993	-1.77
253089_at	putative protein hypothetical protein, Ar	---	AT4G36290	-1.35	-0.44	-4.37	0.003599	0.038025	-1.77
247446_at	unknown protein ; supported by cDNA:	---	AT5G62650	-1.35	-0.44	-4.37	0.003603	0.038046	-1.78
247351_at	putative protein contains similarity to NA	ANAC102	AT5G63790	2.50	1.32	4.37	0.003607	0.038051	-1.78
266916_at	hypothetical protein predicted by gensca	---	AT2G45860	-1.73	-0.79	-4.37	0.003609	0.038051	-1.78
264855_at	3-hydroxy-3-methylglutaryl-coenzyme A	HSK	AT2G17265	-1.37	-0.46	-4.37	0.003612	0.038051	-1.78
262238_at	hypothetical protein predicted by genem	---	AT1G48300	-1.78	-0.83	-4.37	0.003606	0.038051	-1.78
251198_at	putative protein PGP237-11, Petunia x	---	AT3G62970	-1.39	-0.47	-4.37	0.003612	0.038051	-1.78
252890_at	brassinosteroid insensitive 1 gene (BRI1	BRI1	AT4G39400	-1.38	-0.47	-4.36	0.003621	0.038099	-1.78
248172_at	unknown protein ;supported by full-leng	---	AT5G54660	-1.89	-0.92	-4.36	0.003618	0.038099	-1.78
264887_at	unknown protein similar to ripening-indu	---	AT1G23120	1.71	0.78	4.36	0.003621	0.038099	-1.78

248192_at	IAA-amino acid hydrolase homolog ILL3	ILL3	AT5G54140	1.39	0.48	4.36	0.003628	0.038137	-1.78
265154_at	putative GTP-binding protein, ERG sim	---	AT1G30960	-1.97	-0.98	-4.36	0.003627	0.038137	-1.78
248726_at	RAS superfamily GTP-binding protein-lil	ATRABA4(	AT5G47960	4.81	2.27	4.36	0.003635	0.038189	-1.78
266289_at	putative C-4 sterol methyl oxidase ;sup	SMO2-2	AT2G29390	-1.40	-0.48	-4.36	0.003638	0.038209	-1.79
245277_at	glucosyltransferase like protein ; suppor	IAGLU	AT4G15550	2.04	1.03	4.36	0.00364	0.038210	-1.79
252504_at	telomere repeat-binding protein homolo	TRFL1	AT3G46590	-1.39	-0.48	-4.36	0.003642	0.038210	-1.79
266758_at	unknown protein	POL	AT2G46920	-1.46	-0.55	-4.36	0.003648	0.038257	-1.79
252031_at	putative protein 150-kD protein cluA - D	---	AT3G52140	-1.38	-0.47	-4.35	0.003668	0.038261	-1.79
259514_at	hypothetical protein ; supported by cDN	OZS1	AT1G12480	-1.43	-0.52	-4.35	0.003663	0.038261	-1.79
260786_s_a	unknown protein similar to Cryptosporid	MEE5	AT1G06220 /	-1.53	-0.61	-4.36	0.003658	0.038261	-1.79
255449_at	hypothetical protein	---	AT4G02820	-1.61	-0.68	-4.36	0.003653	0.038261	-1.79
256061_at	unknown protein ;supported by full-lengt	---	AT1G07040	1.78	0.83	4.36	0.003653	0.038261	-1.79
266598_at	3-methyl-2-oxobutanoate hydroxy-methy	KPHMT1	AT2G46110	-1.56	-0.64	-4.35	0.003665	0.038261	-1.79
249994_at	putative protein cell polarity protein tea1	---	AT5G18590	-1.44	-0.53	-4.35	0.003668	0.038261	-1.79
251742_at	putative protein kinase serine threonine	---	AT3G56050	-1.40	-0.48	-4.36	0.00366	0.038261	-1.79
250057_at	putative protein ; supported by full-lengt	---	AT5G17840	-1.35	-0.43	-4.36	0.00366	0.038261	-1.79
250994_at	dnaK-type molecular chaperone hsc70.	---	AT5G02490	2.67	1.42	4.35	0.003663	0.038261	-1.79
253334_at	putative protein dihydrokaempferol 4-re	---	AT4G33360	1.73	0.79	4.35	0.003668	0.038261	-1.79
252057_at	putative protein ;supported by full-lengt	---	AT3G52480	1.93	0.95	4.36	0.003657	0.038261	-1.79
249008_at	putative protein contains similarity to DN	---	AT5G44680	-1.84	-0.88	-4.35	0.003676	0.038326	-1.80
253765_at	hypothetical protein ;supported by full-le	---	AT4G28740	-1.90	-0.93	-4.35	0.003689	0.038441	-1.80
261296_at	unknown protein	---	AT1G48460	-1.92	-0.94	-4.35	0.003691	0.038445	-1.80
246440_at	glycine/proline-rich protein glycine/proli	---	AT5G17650	2.07	1.05	4.35	0.003698	0.038497	-1.80
262207_at	hypothetical protein predicted by gensca	PTAC2	AT1G74850	-1.56	-0.64	-4.34	0.003707	0.038561	-1.81
248964_at	cytochrome P450	CYP707A3	AT5G45340	2.73	1.45	4.34	0.003706	0.038561	-1.81
252245_at	putative protein various predicted prote	---	AT3G49710	-1.80	-0.85	-4.34	0.00371	0.038572	-1.81
254675_at	RNA helicase - like protein Cdc28p, Sc	---	AT4G18465	-1.72	-0.78	-4.34	0.003716	0.038614	-1.81
257724_at	hypothetical protein predicted by genem	---	AT3G18510	-1.50	-0.58	-4.34	0.003725	0.038629	-1.81
244980_at	ribosomal protein L36	---	---	-1.41	-0.50	-4.34	0.003732	0.038629	-1.81
252559_at	RNA binding protein -like COLD-INDUC	---	AT3G46020	-1.33	-0.41	-4.34	0.003729	0.038629	-1.81
260780_at	valyl-tRNA synthetase, putative similar	TWN2	AT1G14610	-1.34	-0.42	-4.34	0.003723	0.038629	-1.81
251958_at	putative protein predicted proteins, Ara	---	AT3G53560	-1.92	-0.94	-4.34	0.003728	0.038629	-1.81
245031_at	putative mitochondrial carrier protein	---	AT2G26360	-1.34	-0.42	-4.34	0.003731	0.038629	-1.81
263503_s_a	hypothetical protein	---	AT2G07676	-1.37	-0.45	-4.34	0.003731	0.038629	-1.81
262165_at	putative acyl-CoA:1-acylglycerol-3-phos	LPAT4	AT1G75020	1.80	0.84	4.34	0.003719	0.038629	-1.81

259976_at	hypothetical protein ;supported by full-l	CP12-3	AT1G76560	1.85	0.88	4.34	0.003726	0.038629	-1.81
256106_at	unknown protein	---	AT1G16870	-1.38	-0.46	-4.34	0.003735	0.038638	-1.81
266760_at	putative RAV-like B3 domain DNA bindi	NGA1	AT2G46870	-1.56	-0.64	-4.34	0.003737	0.038641	-1.81
250394_at	putative protein yllC, Enterococcus faec	---	AT5G10910	-1.52	-0.60	-4.34	0.003742	0.038662	-1.82
252126_at	putative disease resistance protein	---	AT3G50950	1.64	0.71	4.34	0.003742	0.038662	-1.82
255010_at	lipase-like protein monoglyceride lipase	---	AT4G10050	-1.37	-0.46	-4.33	0.003754	0.038762	-1.82
257174_at	uracil phosphoribosyltransferase, putati	---	AT3G27190	1.57	0.66	4.33	0.003757	0.038762	-1.82
262112_at	unknown protein ;supported by full-lengt	---	AT1G02870	-1.60	-0.68	-4.33	0.003758	0.038762	-1.82
257723_at	hypothetical protein predicted by genem	---	AT3G18500	-1.57	-0.66	-4.33	0.003759	0.038762	-1.82
251760_at	Expressed protein ; supported by full-ler	---	AT3G55605	-1.90	-0.93	-4.33	0.003764	0.038785	-1.82
255029_x_a	hypothetical protein	---	AT4G09470	1.31	0.39	4.33	0.003765	0.038785	-1.82
247487_at	putative protein predicted protein, Arabi	---	AT5G62150	4.57	2.19	4.33	0.003773	0.038823	-1.82
249898_at	alkaline/neutral invertase ; supported by	---	AT5G22510	-1.64	-0.71	-4.33	0.003773	0.038823	-1.82
250885_at	ABC transporter -like protein ABC-type	ATH12	AT5G03910	-1.38	-0.46	-4.33	0.003773	0.038823	-1.82
245732_at	unknown protein contains similarity to ca	---	AT1G73440	-1.40	-0.48	-4.33	0.003777	0.038838	-1.83
266951_at	putative salt-inducible protein ; supporte	---	AT2G18940	-1.34	-0.42	-4.33	0.003787	0.038895	-1.83
245567_at	germin precursor oxalate oxidase	GLP9	AT4G14630	4.28	2.10	4.33	0.003787	0.038895	-1.83
252033_at	putative protein ;supported by full-lengt	---	AT3G51950	-1.84	-0.88	-4.33	0.003787	0.038895	-1.83
251029_at	putative protein gene product of suAprg	---	AT5G02050	-2.05	-1.04	-4.33	0.003791	0.038904	-1.83
246387_at	hypothetical protein predicted by gensca	---	AT1G77400	-1.59	-0.67	-4.32	0.003794	0.038904	-1.83
246554_at	HSP100/ClpB, putative similar to HSP1	CLPB3	AT5G15450	-1.46	-0.55	-4.32	0.003795	0.038904	-1.83
263632_at	Expressed protein ; supported by cDNA	---	AT2G04795	-2.54	-1.34	-4.33	0.003792	0.038904	-1.83
250174_at	agp6	AGP6	AT5G14380	1.36	0.44	4.32	0.003802	0.038948	-1.83
255782_at	transcription factor identical to transcript	MP	AT1G19850	2.03	1.02	4.32	0.003803	0.038948	-1.83
262168_at	unknown protein ;supported by full-lengt	---	AT1G74730	-1.43	-0.51	-4.32	0.003805	0.038956	-1.83
263132_at	unknown protein ;supported by full-lengt	---	AT1G78560	-1.34	-0.42	-4.32	0.003809	0.038977	-1.83
256855_at	30S ribosomal protein S20 contains Pfa	---	AT3G15190	-1.53	-0.61	-4.32	0.003816	0.039015	-1.84
246152_at	IPP transferase - like protein tRNA delta	IPT9	AT5G20040	-1.39	-0.48	-4.32	0.003815	0.039015	-1.84
245276_at	DNA-binding homeotic protein Athb-2 ; s	ATHB-2	AT4G16780	-1.51	-0.59	-4.32	0.003823	0.039064	-1.84
254117_at	putative protein	---	AT4G24750	-1.60	-0.68	-4.32	0.003824	0.039064	-1.84
249552_s_a	receptor serine/threonine protein kinase	---	AT5G38240 /	1.88	0.91	4.32	0.003838	0.039189	-1.84
259873_s_a	putative translation initiation factor IF-2 s	---	AT1G76720 /	-1.59	-0.67	-4.31	0.00384	0.039193	-1.84
265132_at	unknown protein ; supported by cDNA:	---	AT1G23830	1.92	0.94	4.31	0.003842	0.039193	-1.84
249047_at	berberine bridge enzyme-like protein	---	AT5G44410	-1.46	-0.54	-4.31	0.003851	0.039272	-1.85
264128_at	unknown protein	---	AT1G79190	-1.40	-0.48	-4.31	0.003854	0.039277	-1.85

264864_at	hypothetical protein predicted by gensca	---	AT1G24310	-1.76	-0.81	-4.31	0.003857	0.039297	-1.85
256530_at	unknown protein	---	AT1G33290	-1.41	-0.49	-4.31	0.00386	0.039306	-1.85
260374_at	unknown protein	TAF2	AT1G73960	-1.40	-0.48	-4.31	0.003868	0.039357	-1.85
259550_at	hypothetical protein ;supported by full-le	AGP5	AT1G35230	3.96	1.99	4.31	0.003867	0.039357	-1.85
254576_at	putative protein ;supported by full-lengt	EMB3006	AT4G19350	-1.37	-0.45	-4.31	0.003871	0.039370	-1.85
266728_at	similar to late embryogenesis abundant	---	AT2G03140	-1.40	-0.48	-4.31	0.003873	0.039374	-1.85
256756_at	ATPase II, putative similar to GB:AAD3	---	AT3G25610	2.24	1.16	4.31	0.003878	0.039397	-1.85
264840_at	unknown protein similar to leucine-rich r	---	AT1G03440	-1.38	-0.46	-4.30	0.003885	0.039435	-1.86
263808_at	hypothetical protein predicted by gensca	---	AT2G04340	-1.40	-0.48	-4.31	0.003884	0.039435	-1.86
246094_at	putative protein predicted proteins, H. s	---	AT5G19300	-1.76	-0.81	-4.30	0.003893	0.039500	-1.86
251957_at	putative protein predicted proteins, Ara	---	AT3G53690	-1.46	-0.54	-4.30	0.003896	0.039511	-1.86
245817_at	hypothetical protein similar to unknown	---	AT1G26160	-1.34	-0.42	-4.30	0.003899	0.039527	-1.86
256482_at	protein kinase, putative contains Pfam	FEI1	AT1G31420	-1.40	-0.49	-4.30	0.003901	0.039528	-1.86
246050_s_a	protein phosphatase 2A regulatory subu	---	AT5G28850 /	-1.32	-0.40	-4.30	0.00391	0.039583	-1.86
266620_at	unknown protein	---	AT2G35450	-1.51	-0.59	-4.30	0.003908	0.039583	-1.86
258866_at	unknown protein	---	AT3G03180	-1.35	-0.43	-4.30	0.003915	0.039616	-1.86
255482_at	putative chloroplast outer envelope 86-	TOC159	AT4G02510	-1.38	-0.47	-4.30	0.003929	0.039647	-1.87
249307_s_a	DNA excision repair cross-complementi	XPB1	AT5G41360 /	-1.41	-0.50	-4.30	0.003926	0.039647	-1.87
254732_at	hypothetical protein	---	AT4G13750	-1.65	-0.73	-4.29	0.003932	0.039647	-1.87
248021_at	RuBisCO subunit binding-protein beta s	---	AT5G56500	-1.91	-0.93	-4.29	0.003935	0.039647	-1.87
245852_at	ribosomal protein L10-like ribosomal pr	---	AT5G13510	-1.53	-0.61	-4.30	0.003928	0.039647	-1.87
248207_at	tyrosine aminotransferase	---	AT5G53970	2.75	1.46	4.30	0.003925	0.039647	-1.87
257600_at	hypothetical protein predicted by gensca	CLE41	AT3G24770	1.53	0.61	4.29	0.003933	0.039647	-1.87
259460_at	unknown protein ; supported by cDNA: g	---	AT1G44000	-1.91	-0.94	-4.30	0.003921	0.039647	-1.87
260406_at	putative glutathione transferase similar t	ATGSTU1	AT1G69920	9.57	3.26	4.30	0.003921	0.039647	-1.87
263452_at	putative trehalose-6-phosphate phospha	---	AT2G22190	-1.93	-0.95	-4.29	0.003934	0.039647	-1.87
244926_s_a	maturase	---	AT2G07711 /	1.51	0.60	4.29	0.003955	0.039679	-1.87
246596_at	CARBONIC ANHYDRASE 2 ; supporte	CA2	AT5G14740	-1.39	-0.48	-4.29	0.003964	0.039679	-1.88
255365_at	putative phosphofructokinase beta subu	MEE51	AT4G04040	-1.37	-0.46	-4.29	0.003956	0.039679	-1.87
250978_at	putative protein contains transmembrar	---	AT5G03080	1.32	0.40	4.29	0.003958	0.039679	-1.88
260316_at	hypothetical protein similar to hypothetic	---	AT1G63810	-1.54	-0.63	-4.29	0.003944	0.039679	-1.87
245249_at	acyl-CoA oxidase like protein ; supporte	ACX1	AT4G16760	1.63	0.71	4.29	0.003954	0.039679	-1.87
263143_at	hypothetical protein Contains PF|00637	---	AT1G03100	-1.47	-0.56	-4.29	0.003952	0.039679	-1.87
245575_at	centromere protein homolog	---	AT4G14760	-1.40	-0.48	-4.29	0.003961	0.039679	-1.88
266181_at	putative glutathione S-transferase ; sup	ATGSTZ1	AT2G02390	1.52	0.60	4.29	0.003951	0.039679	-1.87

263618_at	hypothetical protein predicted by gensca	APC2	AT2G04660	-1.53	-0.61	-4.29	0.003965	0.039679	-1.88
246317_at	putative protein unnamed ORF - Homo	---	AT3G56900	-1.66	-0.73	-4.29	0.003966	0.039679	-1.88
257260_at	hypothetical protein predicted by genem	---	AT3G22104	-1.61	-0.69	-4.29	0.003966	0.039679	-1.88
250595_at	unknown protein	---	AT5G07770	1.71	0.77	4.29	0.003947	0.039679	-1.87
260972_at	hypothetical protein contains similarity to	---	AT1G53530	-1.40	-0.49	-4.29	0.003955	0.039679	-1.87
260036_at	putative protein kinase Pfam HMM hit: E	STN7	AT1G68830	-1.51	-0.59	-4.29	0.003951	0.039679	-1.87
254251_at	serine/threonine kinase - like protein KI	---	AT4G23300	-1.52	-0.60	-4.29	0.003947	0.039679	-1.87
250058_at	plastid-specific ribosomal protein 6 prec	PSRP6	AT5G17870	-1.54	-0.62	-4.29	0.003969	0.039689	-1.88
247760_at	subtilisin-like serine protease contains s	---	AT5G59130	-4.07	-2.03	-4.29	0.003972	0.039706	-1.88
254299_at	hypothetical protein ;supported by full-le	NYE1	AT4G22920	2.00	1.00	4.29	0.003977	0.039737	-1.88
249234_at	putative protein similar to unknown prote	---	AT5G42200	-1.88	-0.91	-4.28	0.00398	0.039748	-1.88
261191_at	starch synthase, putative similar to star	---	AT1G32900	-1.99	-0.99	-4.28	0.003986	0.039773	-1.88
249268_at	Expressed protein ; supported by cDNA	---	AT5G41685	-1.36	-0.45	-4.28	0.003986	0.039773	-1.88
262910_at	unknown protein ;supported by full-lengt	---	AT1G59710	1.60	0.68	4.28	0.004001	0.039910	-1.89
245357_at	putative protein ;supported by full-length	---	AT4G17560	-1.58	-0.66	-4.28	0.004007	0.039945	-1.89
248004_at	putative protein similar to unknown prote	PRA1.G2	AT5G56230	2.00	1.00	4.28	0.004009	0.039953	-1.89
260877_at	unknown protein ; supported by full-leng	---	AT1G21500	-1.64	-0.72	-4.28	0.004011	0.039954	-1.89
259981_at	unknown protein ; supported by full-leng	---	AT1G76450	-1.50	-0.59	-4.28	0.004021	0.040021	-1.89
245545_at	UTP-glucose glucosyltransferase	UGT71B5	AT4G15280	1.54	0.62	4.28	0.004021	0.040021	-1.89
263636_at	unknown protein ; supported by full-leng	---	AT2G11910	-1.45	-0.54	-4.27	0.004037	0.040115	-1.90
259070_at	digalactosyldiacylglycerol synthase iden	DGD1	AT3G11670	-1.98	-0.99	-4.27	0.004037	0.040115	-1.90
265092_at	hypothetical protein predicted by gensca	---	AT1G03910	-1.33	-0.41	-4.27	0.004036	0.040115	-1.90
245952_at	putative protein predicted proteins, Aral	---	AT5G28500	-1.54	-0.62	-4.27	0.004038	0.040115	-1.90
247156_at	lysosomal Pro-X carboxypeptidase	---	AT5G65760	-1.42	-0.51	-4.27	0.004049	0.040155	-1.90
255801_at	putative protein heat shock protein dna	---	AT4G10130	-1.35	-0.43	-4.27	0.004051	0.040155	-1.90
266488_at	putative pectinesterase ; supported by f	---	AT2G47670	-1.70	-0.77	-4.27	0.004044	0.040155	-1.90
264926_at	cytochrome b5, putative similar to cytoc	CB5LP	AT1G60660	-1.41	-0.50	-4.27	0.004048	0.040155	-1.90
249834_at	putative protein contains similarity to fer	FTRA1	AT5G23440	-1.58	-0.66	-4.27	0.004046	0.040155	-1.90
247115_at	kinesin-like calmodulin-binding protein ;	ZWI	AT5G65930	-1.52	-0.61	-4.27	0.004057	0.040197	-1.90
257475_at	hypothetical protein predicted by gensca	---	AT1G80880	-1.31	-0.38	-4.27	0.004058	0.040197	-1.90
259091_at	hypothetical protein predicted by gensca	---	AT3G04890	-1.45	-0.53	-4.27	0.004064	0.040236	-1.90
254147_at	putative protein similarity Human mRNA	---	AT4G24270	-1.74	-0.80	-4.26	0.004078	0.040351	-1.91
259924_at	putative DNA-binding protein similar to D	---	AT1G72740	-1.46	-0.55	-4.26	0.004081	0.040351	-1.91
247025_at	zeaxanthin epoxidase precursor ; suppo	ABA1	AT5G67030	-1.54	-0.62	-4.26	0.004081	0.040351	-1.91
265076_at	Rubisco subunit binding-protein beta su	CPN60B	AT1G55490	-1.86	-0.89	-4.26	0.004093	0.040438	-1.91

252429_at	H-protein promoter binding factor-2a ;s	CDF3	AT3G47500	-1.70	-0.76	-4.26	0.004093	0.040438	-1.91
246370_at	hypothetical protein predicted by genem	---	AT1G51920	4.24	2.08	4.26	0.004098	0.040461	-1.91
262370_at	hypothetical protein predicted by genem	---	AT1G73090	-1.58	-0.66	-4.26	0.004099	0.040463	-1.91
258048_at	FtsH protease, putative contains similar	EMB2083	AT3G16290	-1.42	-0.51	-4.26	0.004105	0.040498	-1.91
265212_at	putative sugar transporter protein Simila	---	AT1G05030	-1.40	-0.49	-4.26	0.004111	0.040526	-1.92
245009_at	ribosomal protein S4	---	---	-1.32	-0.40	-4.26	0.00411	0.040526	-1.92
254148_at	hsp 70-like protein heat shock 70 protei	cpHsc70-1	AT4G24280	-1.41	-0.49	-4.26	0.004118	0.040576	-1.92
259594_at	unknown protein contains similarity to cy	---	AT1G28140	-1.37	-0.46	-4.26	0.004122	0.040601	-1.92
252173_at	scarecrow-like 7 (SCL7)	---	AT3G50650	1.88	0.91	4.25	0.004127	0.040626	-1.92
257083_s_a	non-race specific disease resistance pr	---	AT3G20590 /	1.87	0.90	4.25	0.004134	0.040672	-1.92
253310_at	hypothetical protein ; supported by cDN	EX1	AT4G33630	-1.37	-0.45	-4.25	0.004135	0.040672	-1.92
259013_at	unknown protein similar to putative prote	emb1990	AT3G07430	-1.39	-0.47	-4.25	0.004141	0.040700	-1.92
255458_at	small nuclear riboprotein Sm-D1-like pr	---	AT4G02840	-1.34	-0.43	-4.25	0.004143	0.040700	-1.92
262177_at	isochorismate synthase (icsI) identical t	EDS16	AT1G74710	2.81	1.49	4.25	0.004142	0.040700	-1.92
254200_at	putative protein predicted proteins, Aral	---	AT4G24110	4.60	2.20	4.25	0.004152	0.040770	-1.93
254726_at	isoflavone reductase-like protein isoflav	PRR2	AT4G13660	2.31	1.21	4.25	0.004155	0.040784	-1.93
261206_at	heat shock factor protein hsf8, putative	---	AT1G12800	-1.52	-0.60	-4.25	0.004158	0.040788	-1.93
263209_at	Expressed protein ; supported by full-ler	---	AT1G10522	-1.96	-0.97	-4.25	0.004163	0.040810	-1.93
259194_at	RNA helicase, DRH1 identical to RNA h	DRH1	AT3G01540	1.32	0.40	4.25	0.004163	0.040810	-1.93
256091_at	Expressed protein ; supported by full-ler	HMGB2	AT1G20693	-1.41	-0.49	-4.24	0.004177	0.040887	-1.93
260359_at	hypothetical protein predicted by genem	---	AT1G69210	-1.58	-0.66	-4.24	0.004179	0.040887	-1.93
250371_at	putative protein 23 kDa polypeptide of	---	AT5G11450	-1.49	-0.58	-4.24	0.004177	0.040887	-1.93
261081_at	transformer-SR ribonucleoprotein, puta	---	AT1G07350	-1.73	-0.79	-4.24	0.004178	0.040887	-1.93
267018_at	unknown protein	SVR1	AT2G39140	-1.73	-0.79	-4.24	0.00418	0.040887	-1.93
259880_at	hypothetical protein similar to hypotheti	---	AT1G76730	-1.67	-0.74	-4.24	0.004186	0.040929	-1.93
251233_at	putative protein hypothetical protein At2	DRB4	AT3G62800	-1.40	-0.49	-4.24	0.004191	0.040941	-1.94
246781_at	sugar transporter-like protein putative s	SFP1	AT5G27350	2.13	1.09	4.24	0.004191	0.040941	-1.94
256542_at	unknown protein	PMI1	AT1G42550	-1.55	-0.63	-4.24	0.004198	0.040977	-1.94
263085_at	hypothetical protein predicted by gensca	ARI12	AT2G16090	-1.57	-0.65	-4.24	0.004198	0.040977	-1.94
251100_at	aldose reductase-like protein aldose red	---	AT5G01670	1.86	0.90	4.24	0.004203	0.041005	-1.94
255839_at	putative CONSTANS-like B-box zinc fing	---	AT2G33500	-1.34	-0.43	-4.23	0.004225	0.041096	-1.94
246748_at	putative protein predicted protein, Dros	---	AT5G27730	-1.41	-0.49	-4.23	0.004225	0.041096	-1.94
266519_at	unknown protein ; supported by cDNA:	---	AT2G35155	-1.46	-0.54	-4.23	0.004228	0.041096	-1.95
262415_at	40S ribosomal protein S17, putative sim	emb1129	AT1G49400	-1.53	-0.62	-4.24	0.004221	0.041096	-1.94
255507_at	AtKAP alpha similar to AtKAP, GenBan	MOS6	AT4G02150	-1.32	-0.40	-4.23	0.004231	0.041096	-1.95

261429_at	hypothetical protein contains similarity t	WRKY61	AT1G18860	1.39	0.48	4.24	0.004218	0.041096	-1.94
267197_at	hypothetical protein predicted by gensca	---	AT2G30960	-1.37	-0.46	-4.23	0.004229	0.041096	-1.95
265247_at	50S ribosomal protein L3 ;supported by	---	AT2G43030	-1.36	-0.44	-4.23	0.004232	0.041096	-1.95
254783_at	hydrolase-like protein 2-hydroxy-6-oxoh	---	AT4G12830	-2.17	-1.12	-4.24	0.00422	0.041096	-1.94
247901_at	ubiquinone/menaquinone biosynthesis r	---	AT5G57300	-1.37	-0.46	-4.23	0.004229	0.041096	-1.95
260260_at	putative reductase similar to cinnamoyl	---	AT1G68540	-1.56	-0.64	-4.24	0.004214	0.041096	-1.94
263729_at	hypothetical protein predicted by genem	---	AT1G60080	-1.31	-0.39	-4.23	0.004238	0.041114	-1.95
246322_at	S-locus protein, putative similar to S-loc	---	AT1G16680	-1.37	-0.45	-4.23	0.004236	0.041114	-1.95
250532_at	putative protein similar to unknown prote	---	AT5G08540	-1.49	-0.58	-4.23	0.00424	0.041122	-1.95
251036_at	putative protein ; supported by cDNA: g	---	AT5G02160	1.46	0.54	4.23	0.004259	0.041201	-1.95
258982_at	putative serine/threonine protein kinase	---	AT3G08870	1.73	0.79	4.23	0.004257	0.041201	-1.95
259172_at	O-acetylserine (thiol) lyase identical to C	CS26	AT3G03630	-1.96	-0.97	-4.23	0.00426	0.041201	-1.95
245134_s_a	unknown protein	---	AT2G45250 /	-1.40	-0.49	-4.23	0.004262	0.041201	-1.95
262760_at	hypothetical protein contains similarity t	---	AT1G10770	-3.06	-1.61	-4.23	0.00426	0.041201	-1.95
260484_at	putative zinc finger protein similar to zin	---	AT1G68360	1.44	0.52	4.23	0.004251	0.041201	-1.95
261970_at	glutamate decarboxylase (gad), putativ	GAD2	AT1G65960	-1.59	-0.67	-4.23	0.00426	0.041201	-1.95
264434_at	hypothetical protein predicted by gensca	---	AT1G10340	3.16	1.66	4.23	0.004263	0.041201	-1.95
251118_at	putative chloroplast inner envelope prot	APG1	AT3G63410	-1.55	-0.64	-4.23	0.004266	0.041219	-1.95
245494_at	salt-inducible protein homolog	---	AT4G16390	-1.45	-0.53	-4.23	0.00427	0.041238	-1.96
246020_at	putative protein ; supported by cDNA: g	---	AT5G10710	-1.39	-0.48	-4.22	0.004279	0.041266	-1.96
255734_at	hypothetical protein similar to putative tv	---	AT1G25550	1.62	0.70	4.22	0.004275	0.041266	-1.96
249171_at	putative protein contains similarity to RI	---	AT5G42940	1.53	0.62	4.22	0.00428	0.041266	-1.96
246111_at	putative protein	---	AT5G20170	-1.42	-0.51	-4.22	0.004278	0.041266	-1.96
266818_at	unknown protein	HUB1	AT2G44950	-1.49	-0.58	-4.22	0.004287	0.041299	-1.96
260363_at	unknown protein similar to hypothetical	---	AT1G70550	-1.52	-0.61	-4.22	0.004287	0.041299	-1.96
263472_at	molybdopterin synthase (CNX2) ;suppo	CNX2	AT2G31955	1.53	0.61	4.22	0.004291	0.041318	-1.96
251446_at	Expressed protein ; supported by full-ler	---	AT3G59840	-1.34	-0.42	-4.22	0.004294	0.041325	-1.96
245418_at	putative protein	---	AT4G17370	-1.58	-0.66	-4.22	0.004296	0.041326	-1.96
248613_at	phytoene dehydrogenase-like	---	AT5G49555	-1.61	-0.68	-4.22	0.004299	0.041341	-1.96
247376_at	nucleotide diphosphate kinase Ia (emb|	NDPK2	AT5G63310	-1.35	-0.44	-4.22	0.004301	0.041347	-1.96
259253_at	hypothetical protein predicted by gensca	---	AT3G07640	-1.31	-0.38	-4.22	0.004313	0.041420	-1.97
253467_at	putative protein hypothetical protein YD	---	AT4G32140	1.46	0.55	4.22	0.004311	0.041420	-1.97
259178_at	unknown protein similar to hypothetical	RGLG1	AT3G01650	1.55	0.63	4.22	0.004316	0.041437	-1.97
261197_at	putative calcium-binding protein, calreti	GAPA-2	AT1G12900	-1.45	-0.54	-4.22	0.004322	0.041459	-1.97
263846_at	putative RNA polymerase sigma-70 fact	SIGF	AT2G36990	-1.64	-0.72	-4.22	0.004321	0.041459	-1.97

256366_at	protein kinase, putative contains Pfam	---	AT1G66880	2.08	1.06	4.21	0.004331	0.041488	-1.97
251800_at	putative protein various predicted protei	RBL	AT3G55510	-1.99	-0.99	-4.21	0.004339	0.041488	-1.97
261930_at	alcohol dehydrogenase ADH, putative s	---	AT1G22440	1.63	0.70	4.21	0.004336	0.041488	-1.97
253295_at	putative aspartate--tRNA ligase asparta	---	AT4G33760	-1.66	-0.74	-4.21	0.004333	0.041488	-1.97
266439_s_a	hypothetical protein predicted by grail	---	AT2G43200	-1.41	-0.49	-4.21	0.004327	0.041488	-1.97
251819_at	phosphatidylglycerophosphate synthas	PGPS2	AT3G55030	-1.42	-0.51	-4.21	0.004331	0.041488	-1.97
262591_at	hypothetical protein Similar to gb|X8256	CCMH	AT1G15220	-1.36	-0.45	-4.21	0.00434	0.041488	-1.97
249002_at	putative protein contains similarity to rib	---	AT5G44520	-1.52	-0.60	-4.21	0.00434	0.041488	-1.97
250459_at	unknown protein ; supported by cDNA:	---	AT5G09860	-1.41	-0.50	-4.21	0.004343	0.041500	-1.97
253629_at	glycine-rich protein glycine-rich cell wal	---	AT4G30450	-1.51	-0.59	-4.21	0.004357	0.041559	-1.98
264057_at	putative AP2 domain transcription factor	RAP2.7	AT2G28550	-1.71	-0.77	-4.21	0.004359	0.041559	-1.98
254134_at	argininosuccinate synthase -like protein	---	AT4G24830	-1.86	-0.89	-4.21	0.004353	0.041559	-1.98
245474_at	hypothetical protein	---	AT4G16060	-1.50	-0.58	-4.21	0.00436	0.041559	-1.98
259564_at	hypothetical protein	---	AT1G20540	-1.33	-0.41	-4.21	0.004353	0.041559	-1.98
247150_at	putative protein similar to unknown prote	---	AT5G65650	-1.51	-0.59	-4.21	0.004359	0.041559	-1.98
249938_at	Ruv DNA-helicase-like protein ;support	RIN1	AT5G22330	-1.37	-0.45	-4.21	0.004367	0.041580	-1.98
252193_at	R2R3-MYB transcription factor ; suppor	MYB77	AT3G50060	2.51	1.33	4.21	0.004368	0.041580	-1.98
250114_s_a	AMP-binding protein	AAE5	AT5G16340 /	1.72	0.79	4.21	0.004368	0.041580	-1.98
259063_at	putative 5B-anther specific protein simila	---	AT3G07450	1.31	0.38	4.21	0.004371	0.041595	-1.98
253174_at	catalase ; supported by cDNA: gi_1545	CAT2	AT4G35090	-1.49	-0.58	-4.21	0.004374	0.041608	-1.98
258555_at	fatty acid multifunctional protein (AtMFP	MFP2	AT3G06860	1.46	0.54	4.21	0.004379	0.041624	-1.98
265675_at	70kD heat shock protein ;supported by	HSP70T-2	AT2G32120	-1.59	-0.67	-4.21	0.00438	0.041624	-1.98
254445_at	3-hydroxyisobutyrate dehydrogenase -l	---	AT4G20930	1.42	0.50	4.20	0.004388	0.041688	-1.98
253373_at	lysine-ketoglutarate reductase/saccharo	---	AT4G33150	2.64	1.40	4.20	0.00439	0.041692	-1.99
253668_at	snRNP Sm protein F - like Sm protein	RUXF	AT4G30220	-1.48	-0.56	-4.20	0.004401	0.041736	-1.99
247429_at	putative protein strong similarity to unkn	---	AT5G62620	1.59	0.67	4.20	0.004399	0.041736	-1.99
257447_at	hypothetical protein predicted by gensca	---	AT2G04230	-1.29	-0.37	-4.20	0.0044	0.041736	-1.99
261903_at	chromomethylase identical to GB:AAC0	CMT1	AT1G80740	1.32	0.40	4.20	0.004406	0.041775	-1.99
254417_at	putative protein	ATFMN/FH	AT4G21470	1.65	0.73	4.20	0.00441	0.041778	-1.99
265474_at	Expressed protein ; supported by cDNA	---	AT2G15690	-1.77	-0.82	-4.20	0.00441	0.041778	-1.99
262398_at	hypothetical protein predicted by genem	---	AT1G49350	-1.32	-0.40	-4.19	0.004436	0.042004	-2.00
259497_at	unknown protein	---	AT1G15860	1.31	0.38	4.19	0.00444	0.042024	-2.00
262712_at	mercaptopyruvate sulfurtransferase (Ms	ATRDH2	AT1G16460	-1.47	-0.56	-4.19	0.004446	0.042060	-2.00
263582_at	unknown protein similar to hypothetical	LYM2	AT2G17120	1.71	0.77	4.19	0.004467	0.042245	-2.00
257779_at	protein kinase, putative similar to PROT	CDG1	AT3G26940	1.29	0.36	4.19	0.004472	0.042272	-2.00

267220_at	putative sugar nucleotide phosphorylase	ISPD	AT2G02500	-1.50	-0.58	-4.19	0.004481	0.042337	-2.01
260405_at	putative glutathione transferase similar t	ATGSTU1	AT1G69930	8.32	3.06	4.19	0.004483	0.042342	-2.01
265374_at	hypothetical protein ;supported by full-le	PSBX	AT2G06520	-1.32	-0.40	-4.19	0.004485	0.042348	-2.01
249677_at	DNA helicase-like	---	AT5G35970	-1.84	-0.88	-4.18	0.004493	0.042402	-2.01
256143_at	40S ribosomal protein S7 homolog, put	---	AT1G48830	-1.54	-0.62	-4.18	0.004504	0.042402	-2.01
246261_at	unknown protein	---	AT1G31810	-1.43	-0.51	-4.18	0.0045	0.042402	-2.01
251755_at	putative protein predicted protein, Arabi	---	AT3G55790	1.72	0.78	4.18	0.004503	0.042402	-2.01
262209_at	hypothetical protein contains similarity to	---	AT1G74720	-1.50	-0.58	-4.18	0.004499	0.042402	-2.01
258154_at	unknown protein ; supported by cDNA:	---	AT3G18210	-1.51	-0.59	-4.18	0.004497	0.042402	-2.01
262000_at	Expressed protein ; supported by full-ler	---	AT1G33810	-1.47	-0.56	-4.18	0.004504	0.042402	-2.01
260792_at	unknown protein ;supported by full-lengt	---	AT1G06270	-1.43	-0.51	-4.18	0.004513	0.042437	-2.01
250562_at	putative protein	TOM5	AT5G08040	-1.49	-0.57	-4.18	0.004512	0.042437	-2.01
265266_at	putative RNA-binding protein ; supporte	AML2	AT2G42890	1.50	0.59	4.18	0.004512	0.042437	-2.01
250268_s_a	putative protein putative secreted prote	---	AT5G12950 /	-1.59	-0.67	-4.18	0.004525	0.042495	-2.02
263356_at	putative RNA-binding protein ; supporte	UBA1A	AT2G22090	1.33	0.42	4.18	0.004525	0.042495	-2.02
264845_at	putative thioredoxin-m similar to thiored	ATHM1	AT1G03680	-1.44	-0.52	-4.18	0.004524	0.042495	-2.02
260620_at	unknown protein	---	AT1G08070	-1.39	-0.48	-4.18	0.00453	0.042512	-2.02
255219_at	hypothetical protein	---	AT4G07720	1.34	0.42	4.18	0.004531	0.042512	-2.02
266002_at	hypothetical protein predicted by gensca	---	AT2G37310	-1.40	-0.49	-4.18	0.004538	0.042563	-2.02
257207_at	hypothetical protein predicted by genem	---	AT3G14900	-1.47	-0.56	-4.17	0.004547	0.042617	-2.02
253733_at	hypothetical protein	ATMND1	AT4G29170	-1.47	-0.56	-4.17	0.004549	0.042617	-2.02
258126_at	hypothetical protein predicted by genem	---	AT3G24490	-1.44	-0.53	-4.17	0.004548	0.042617	-2.02
262038_at	invertase, putative similar to neutral inv	CINV1	AT1G35580	1.74	0.80	4.17	0.004551	0.042618	-2.02
248523_s_a	ubiquitin activating enzyme ;supported	SAE1B	AT5G50580 /	-1.50	-0.58	-4.17	0.004554	0.042624	-2.02
254532_at	putative protein regulatory protein NPR	NPR4	AT4G19660	1.74	0.80	4.17	0.004558	0.042645	-2.02
263773_at	putative xylulose kinase	---	AT2G21370	-1.57	-0.65	-4.17	0.004563	0.042678	-2.03
251243_at	putative protein hypothetical protein - S	---	AT3G61870	-1.60	-0.68	-4.17	0.004567	0.042692	-2.03
249475_at	putative protein CGI-108 protein, Homo	---	AT5G38890	-1.56	-0.64	-4.17	0.004572	0.042694	-2.03
247977_at	putative protein similar to unknown prote	---	AT5G56850	-1.59	-0.67	-4.17	0.004572	0.042694	-2.03
264069_at	putative rubisco subunit binding-protein	CPN60A	AT2G28000	-1.69	-0.76	-4.17	0.004573	0.042694	-2.03
262521_at	unknown protein Location of est 278F3T	---	AT1G17130	-1.40	-0.49	-4.17	0.004577	0.042717	-2.03
262134_at	sulfate transporter, putative similar to su	AST56	AT1G77990	-1.91	-0.93	-4.17	0.004584	0.042754	-2.03
253284_at	putative protein hydroxyproline-rich glyc	---	AT4G34150	2.03	1.02	4.17	0.004585	0.042754	-2.03
248676_at	putative protein similar to unknown prote	ATSDI1	AT5G48850	-3.32	-1.73	-4.17	0.004588	0.042770	-2.03
248338_at	HCF106 (gb|AAD32652.1) ; supported	HCF106	AT5G52440	-1.48	-0.56	-4.17	0.004592	0.042784	-2.03

267308_at	putative malonyl-CoA:Acyl carrier protei	---	AT2G30200	-1.48	-0.56	-4.17	0.004594	0.042789	-2.03
261222_at	anter-specific proline-rich protein APG p	---	AT1G20120	-1.35	-0.44	-4.16	0.004605	0.042871	-2.04
259303_at	hypothetical protein predicted by gensca	---	AT3G05130	-1.28	-0.35	-4.16	0.004607	0.042875	-2.04
263655_at	hypothetical protein predicted by genefir	---	AT1G04500	1.38	0.46	4.16	0.004609	0.042880	-2.04
267336_at	putative small heat shock protein ;supp	---	AT2G19310	-1.61	-0.69	-4.16	0.004614	0.042904	-2.04
258542_at	unknown protein	---	AT3G07030	-1.48	-0.57	-4.16	0.004616	0.042908	-2.04
262055_at	unknown protein ; supported by full-leng	---	AT1G79970	1.35	0.43	4.16	0.00462	0.042925	-2.04
252366_at	Expressed protein ; supported by full-ler	---	AT3G48420	-2.18	-1.12	-4.16	0.004623	0.042936	-2.04
249850_at	putative protein similar to unknown prote	---	AT5G23240	-1.32	-0.40	-4.16	0.00463	0.042951	-2.04
248933_at	putative protein contains similarity to gu	---	AT5G46070	-1.37	-0.45	-4.16	0.004645	0.042951	-2.04
265272_at	unknown protein	ARF10	AT2G28350	-1.62	-0.69	-4.16	0.004645	0.042951	-2.05
266410_at	unknown protein	EMB2765	AT2G38770	-1.35	-0.43	-4.16	0.004641	0.042951	-2.04
249845_at	putative protein similar to unknown prote	---	AT5G23610	-1.36	-0.45	-4.16	0.004645	0.042951	-2.05
259176_at	putative cell division control protein sim	CDC48C	AT3G01610	-1.41	-0.50	-4.16	0.004634	0.042951	-2.04
252015_at	putative protein growth-regulating facto	AtGRF4	AT3G52910	-1.29	-0.37	-4.16	0.004633	0.042951	-2.04
254656_at	putative protein ;supported by full-lengt	---	AT4G18070	-1.62	-0.69	-4.16	0.004645	0.042951	-2.05
251919_at	putative protein Hsp70 binding protein h	---	AT3G53800	-1.68	-0.75	-4.16	0.004633	0.042951	-2.04
256428_at	putative disease resistance protein simil	AtRLP35	AT3G11080	1.81	0.85	4.16	0.004639	0.042951	-2.04
255798_at	unknown protein predicted by genefinde	---	AT2G33255	-1.43	-0.52	-4.16	0.004642	0.042951	-2.04
264322_at	unknown protein Contains similarity to te	---	AT1G04190	-1.46	-0.54	-4.16	0.00465	0.042973	-2.05
260243_at	hypothetical protein similar to putative p	---	AT1G63720	2.31	1.21	4.15	0.004653	0.042992	-2.05
246343_at	putative protein	---	AT3G56720	-1.28	-0.36	-4.15	0.004662	0.043018	-2.05
252944_at	hypothetical protein ;supported by full-le	---	AT4G39320	1.36	0.45	4.15	0.00466	0.043018	-2.05
260876_at	hypothetical protein contains similarity to	---	AT1G21460	-1.65	-0.73	-4.15	0.004661	0.043018	-2.05
255501_at	hypothetical protein	---	AT4G02400	-1.67	-0.74	-4.15	0.004668	0.043052	-2.05
258742_at	hypothetical protein predicted by gensca	---	AT3G05800	1.92	0.94	4.15	0.004673	0.043064	-2.05
260404_at	unknown protein similar to activator-like	---	---	-1.74	-0.80	-4.15	0.004675	0.043064	-2.05
254063_at	receptor kinase-like protein receptor-lik	---	AT4G25390	2.05	1.03	4.15	0.004672	0.043064	-2.05
254821_at	hypothetical protein	---	AT4G12540	1.34	0.43	4.15	0.004677	0.043067	-2.05
258449_s_a	putative RNA helicase similar to RNA he	PMH1	AT3G22310 /	-1.64	-0.71	-4.15	0.00468	0.043068	-2.05
246985_at	putative protein contains similarity to unl	---	AT5G67290	-1.43	-0.52	-4.15	0.004681	0.043068	-2.05
253175_at	WD-40 repeat protein (MSI3) ; supporte	MSI3	AT4G35050	-1.77	-0.82	-4.15	0.004688	0.043107	-2.05
254943_at	putative protein predicted proteins, Aral	---	AT4G10890	-1.38	-0.47	-4.15	0.004695	0.043107	-2.06
254112_at	putative protein KIAA0136 gene, Homo	---	AT4G24970	1.39	0.48	4.15	0.004692	0.043107	-2.06
252121_at	GDP-D-mannose-4,6-dehydratase (MU	MUR1	AT3G51160	1.94	0.95	4.15	0.004696	0.043107	-2.06

251942_at	ABC transporter - like protein PDR5-like	PDR9	AT3G53480	2.57	1.36	4.15	0.004696	0.043107	-2.06
264698_at	unknown protein	---	AT1G70200	-1.38	-0.47	-4.15	0.004696	0.043107	-2.06
260946_at	hypothetical protein predicted by genem	---	AT1G06010	-1.47	-0.55	-4.15	0.004709	0.043155	-2.06
265301_s_a	putative MYB family transcription factor	---	AT2G13960 /	-1.41	-0.50	-4.15	0.004709	0.043155	-2.06
250741_at	putative protein contains similarity to I-b	---	AT5G05790	-1.96	-0.97	-4.15	0.004704	0.043155	-2.06
257188_at	hypothetical protein contains Pfam profil	---	AT3G13150	-1.45	-0.54	-4.14	0.004713	0.043155	-2.06
251753_at	putative protein predicted protein, Arabi	---	AT3G55760	-2.25	-1.17	-4.14	0.004712	0.043155	-2.06
250547_at	asparaginase ; supported by cDNA: gi_	---	AT5G08100	-1.41	-0.50	-4.15	0.004707	0.043155	-2.06
254505_at	Expressed protein ; supported by full-ler	---	AT4G19985	-1.62	-0.70	-4.14	0.004716	0.043164	-2.06
255978_at	hypothetical protein	---	AT1G34010	-1.34	-0.43	-4.14	0.004719	0.043181	-2.06
267077_at	unknown protein similar to cytoskeletal p	---	AT2G40970	-1.56	-0.64	-4.14	0.004726	0.043221	-2.06
262279_at	hypothetical protein predicted by gensca	---	AT1G68630	2.02	1.02	4.14	0.004739	0.043321	-2.07
252942_at	putative protein ;supported by full-lengt	---	AT4G39300	-1.46	-0.55	-4.14	0.004756	0.043333	-2.07
256255_at	MYB-family transcription factor, putative	---	AT3G11280	-1.30	-0.38	-4.14	0.004752	0.043333	-2.07
265947_at	putative WD-40 repeat protein ; suppor	---	AT2G19540	-1.73	-0.79	-4.14	0.004758	0.043333	-2.07
254228_at	putative protein ; supported by full-leng	---	AT4G23620	-1.38	-0.47	-4.14	0.00476	0.043333	-2.07
251500_at	receptor-like protein kinase receptor-like	---	AT3G59110	-1.37	-0.45	-4.14	0.004753	0.043333	-2.07
249224_at	mitochondrial carrier protein-like	---	AT5G42130	-1.32	-0.40	-4.14	0.00476	0.043333	-2.07
256045_at	MAP3K gamma protein kinase, putative	MAPKKK1	AT1G07150	1.44	0.53	4.14	0.004748	0.043333	-2.07
260211_at	hypothetical protein similar to YGL010w	---	AT1G74440	2.86	1.52	4.14	0.004745	0.043333	-2.07
263868_at	hypothetical protein predicted by genefir	---	AT2G36840	-1.44	-0.52	-4.14	0.004761	0.043333	-2.07
256828_at	unknown protein	---	AT3G22968 /	-1.98	-0.98	-4.14	0.004745	0.043333	-2.07
259302_at	unknown protein	GID1A	AT3G05120	-1.62	-0.69	-4.14	0.004761	0.043333	-2.07
261240_at	subtilisin-like serine protease contains s	SBT3.5	AT1G32940	2.40	1.26	4.13	0.004769	0.043392	-2.07
260465_at	membrane-associated salt-inducible pro	---	AT1G10910	-1.28	-0.36	-4.13	0.004776	0.043400	-2.07
245877_at	unknown protein	---	AT1G26220	-1.58	-0.66	-4.13	0.004774	0.043400	-2.07
252716_at	putative protein CAF protein, Arabidops	DCL3	AT3G43920	-1.50	-0.58	-4.13	0.004776	0.043400	-2.07
267499_at	hypothetical protein predicted by gensca	---	AT2G45500	1.41	0.49	4.13	0.004781	0.043428	-2.08
258921_at	unknown protein N-terminus similar to u	anac053	AT3G10500	1.54	0.62	4.13	0.004787	0.043464	-2.08
257270_at	unknown protein ; supported by full-leng	---	AT3G28140	-1.32	-0.40	-4.13	0.00479	0.043480	-2.08
257744_at	hypothetical protein contains Pfam profil	---	AT3G29230	-1.50	-0.59	-4.13	0.004794	0.043501	-2.08
253696_at	cytokinin oxidase - like protein cytokinin	CKX4	AT4G29740	2.28	1.19	4.13	0.0048	0.043537	-2.08
254546_at	lectin like protein lectin 2, phloem-speci	PP2-A2	AT4G19850	-2.53	-1.34	-4.13	0.004806	0.043568	-2.08
257706_at	Expressed protein ; supported by cDNA	---	AT3G12685	-1.72	-0.79	-4.13	0.00481	0.043586	-2.08
256852_at	unknown protein contains Pfam profile:	ATRANGA	AT3G18610	-1.60	-0.68	-4.13	0.004821	0.043658	-2.08

247528_at	MIM protein ; supported by cDNA: gi_5	MIM	AT5G61460	-1.46	-0.55	-4.13	0.004821	0.043658	-2.08
253917_at	hypothetical protein ;supported by full-l	---	AT4G27380	-1.64	-0.71	-4.12	0.004842	0.043810	-2.09
250729_at	ubiquitin activating enzyme 2 (UBA2) id	UBA 2	AT5G06460	-1.39	-0.47	-4.12	0.004842	0.043810	-2.09
246515_at	putative protein unusual floral organs p	---	AT5G15710	-1.29	-0.37	-4.12	0.004848	0.043851	-2.09
253319_at	putative protein various predicted prote	EMB2758	AT4G33990	-1.67	-0.74	-4.12	0.004852	0.043867	-2.09
258999_at	putative D-ribulose-5-phosphate 3-epim	---	AT3G01850	-1.39	-0.47	-4.12	0.00486	0.043901	-2.09
265776_at	hypothetical protein predicted by genefi	---	AT2G07340	-1.33	-0.42	-4.12	0.00486	0.043901	-2.09
251305_at	peptidylprolyl isomerase ROC4 ;suppor	ROC4	AT3G62030	-1.67	-0.74	-4.12	0.004862	0.043901	-2.09
266763_at	unknown protein	SPL1	AT2G47070	-1.47	-0.56	-4.12	0.00487	0.043957	-2.10
258646_at	MATE efflux family protein, putative cor	FRD3	AT3G08040	1.35	0.43	4.12	0.004875	0.043989	-2.10
266934_at	unknown protein	---	AT2G18900	-1.45	-0.54	-4.12	0.00488	0.044012	-2.10
254693_at	bHLH protein - like bHLH protein, Arabi	---	AT4G17880	-2.79	-1.48	-4.12	0.004884	0.044036	-2.10
245565_at	hypothetical protein	---	AT4G14605	-1.42	-0.50	-4.11	0.004894	0.044103	-2.10
267102_at	putative small nuclear ribonucleoprotein	LIS	AT2G41500	-1.43	-0.51	-4.11	0.004903	0.044146	-2.10
250146_at	putative protein polypeptide deformylas	PDF1B	AT5G14660	-1.73	-0.79	-4.11	0.004903	0.044146	-2.10
251484_at	putative protein putative protein At2g43	---	AT3G59640	1.33	0.41	4.11	0.004904	0.044146	-2.10
259244_at	unknown protein similar to zinc finger pr	COL9	AT3G07650	2.09	1.06	4.11	0.004907	0.044152	-2.10
261071_at	unknown protein	---	AT1G07380	-1.50	-0.58	-4.11	0.00491	0.044160	-2.10
264118_at	unknown protein	---	AT1G79150	-2.13	-1.09	-4.11	0.004915	0.044165	-2.10
248035_at	sucrose cleavage protein-like ;supporte	---	AT5G55900	-1.36	-0.45	-4.11	0.004915	0.044165	-2.10
250914_at	myb -like protein telomeric DNA binding	TRFL10	AT5G03780	-1.44	-0.53	-4.11	0.004916	0.044165	-2.11
257764_at	disease resistance protein, putative sim	AtRLP36	AT3G23010	1.80	0.85	4.11	0.004926	0.044238	-2.11
263799_at	unknown protein ; supported by cDNA:	---	AT2G24550	1.65	0.72	4.11	0.004935	0.044257	-2.11
264173_at	unknown protein	---	AT1G02160	-1.36	-0.44	-4.11	0.004933	0.044257	-2.11
245015_at	large subunit of riblose-1,5-bisphospha	---	---	-1.72	-0.78	-4.11	0.004932	0.044257	-2.11
255151_at	putative protein oxysterol-binding prote	ORP1C	AT4G08180	1.28	0.35	4.11	0.004936	0.044257	-2.11
258656_at	putative Ras-like GTP-binding protein c	ATRABE1	AT3G09900	-1.60	-0.67	-4.11	0.004938	0.044261	-2.11
266702_at	hexokinase (ATHXK2) ; supported by c	HXK2	AT2G19860	-1.37	-0.45	-4.10	0.004946	0.044294	-2.11
256306_at	lipase, putative contains Pfam profile: P	---	AT1G30370	10.37	3.37	4.11	0.004944	0.044294	-2.11
258701_at	putative RNA helicase similar to RNA h	---	AT3G09720	-1.76	-0.82	-4.10	0.004955	0.044341	-2.11
260753_at	RING-H2 finger protein RHA3a, putativ	---	AT1G49230	-2.24	-1.17	-4.10	0.004957	0.044341	-2.11
265867_at	unknown protein ;supported by full-leng	MEE11	AT2G01620	-1.47	-0.56	-4.10	0.004959	0.044341	-2.11
266621_at	unknown protein	---	AT2G35450	-1.70	-0.77	-4.10	0.004954	0.044341	-2.11
253975_at	putative protein proliferating-cell nucleo	---	AT4G26600	-2.14	-1.10	-4.10	0.00497	0.044400	-2.12
262618_at	unknown protein	---	AT1G06560	-1.31	-0.39	-4.10	0.004984	0.044400	-2.12

257154_at	unknown protein ; supported by cDNA:	---	AT3G27210	-1.53	-0.61	-4.10	0.004984	0.044400	-2.12
246199_at	putative protein ;supported by full-length	---	AT4G36530	-1.64	-0.72	-4.10	0.004984	0.044400	-2.12
253237_at	putative aldehyde dehydrogenase aldel	ALDH3I1	AT4G34240	-1.70	-0.76	-4.10	0.004978	0.044400	-2.12
257721_at	hypothetical protein predicted by genem	---	AT3G18310	-1.31	-0.39	-4.10	0.004978	0.044400	-2.12
251396_at	transketolase - like protein transketolas	---	AT3G60750	-1.36	-0.44	-4.10	0.004969	0.044400	-2.12
252060_at	putative protein other hypothetical prote	PAD4	AT3G52430	3.11	1.64	4.10	0.004985	0.044400	-2.12
250503_at	putative protein similar to unknown prote	---	AT5G09820	-1.60	-0.68	-4.10	0.004978	0.044400	-2.12
247119_at	ATP-dependent RNA helicase-like ; sup	---	AT5G65900	-1.29	-0.37	-4.10	0.004981	0.044400	-2.12
254427_at	putative protein predicted protein, Arabi	emb1417	AT4G21190	-1.76	-0.82	-4.10	0.004992	0.044424	-2.12
249329_at	putative protein similar to unknown prote	---	AT5G40960	1.54	0.62	4.10	0.004991	0.044424	-2.12
255670_at	Expressed protein ; supported by full-ler	RHB1A	AT4G00335	-1.31	-0.39	-4.10	0.004997	0.044450	-2.12
263478_at	putative receptor-like protein kinase ; su	---	AT2G31880	2.66	1.41	4.10	0.005	0.044462	-2.12
264857_at	putative glycosyl transferase similar to G	LGT9	AT1G24170	1.64	0.71	4.09	0.005012	0.044553	-2.13
256331_at	GT-like trihelix DNA-binding protein, pu	---	AT1G76880	-1.37	-0.45	-4.09	0.005019	0.044598	-2.13
262229_at	unknown protein ; supported by cDNA: g	---	AT1G68620	2.48	1.31	4.09	0.00503	0.044641	-2.13
260682_at	hypothetical protein predicted by genem	---	AT1G17510	-1.38	-0.47	-4.09	0.005032	0.044641	-2.13
261145_at	thioredoxin identical to GB:CAA84610 f	ATTRX4	AT1G19730	-1.39	-0.48	-4.09	0.005034	0.044641	-2.13
265415_at	unknown protein ;supported by full-leng	PSB29	AT2G20890	-1.42	-0.51	-4.09	0.005036	0.044641	-2.13
266964_at	putative ABC transporter related to mult	PGP6	AT2G39480	1.28	0.36	4.09	0.005026	0.044641	-2.13
259129_at	unknown protein predicted by genscan,	PTF1	AT3G02150	2.13	1.09	4.09	0.005034	0.044641	-2.13
260959_at	unknown protein ;supported by full-lengt	---	AT1G06050	1.38	0.47	4.09	0.005042	0.044678	-2.13
250685_at	kinesin heavy chain-like protein	---	AT5G06670	-1.28	-0.35	-4.09	0.005044	0.044684	-2.13
246296_at	putative protein hypothetical protein At2	---	AT3G56750	-1.34	-0.43	-4.09	0.005051	0.044729	-2.13
254753_at	putative protein Pto kinase interactor 1	---	AT4G13190	1.32	0.40	4.09	0.005054	0.044737	-2.13
253058_at	ribosomal - like protein ribosomal protei	---	AT4G37660	-1.63	-0.70	-4.09	0.00506	0.044774	-2.14
249134_at	unknown protein	---	AT5G43150	-1.77	-0.83	-4.09	0.005065	0.044777	-2.14
247919_at	putative protein similar to unknown prote	---	AT5G57650	1.44	0.53	4.09	0.005064	0.044777	-2.14
249201_at	putative protein similar to unknown prote	---	AT5G42370	-1.54	-0.62	-4.08	0.005068	0.044791	-2.14
251536_at	ketol-acid reductoisomerase ; supporte	---	AT3G58610	-1.42	-0.50	-4.08	0.005073	0.044803	-2.14
250482_at	putative protein	---	AT5G10320	-1.50	-0.58	-4.08	0.005072	0.044803	-2.14
256965_at	branched chain alpha-keto acid dehydr	DIN4	AT3G13450	2.05	1.04	4.08	0.005077	0.044820	-2.14
246800_at	glycine hydroxymethyltransferase - like	SHM2	AT5G26780	-1.50	-0.59	-4.08	0.005086	0.044843	-2.14
256013_at	unknown protein	DA1	AT1G19270	1.52	0.60	4.08	0.005082	0.044843	-2.14
249137_at	putative protein contains similarity to 22	---	AT5G43140	-1.69	-0.75	-4.08	0.005086	0.044843	-2.14
266963_at	unknown protein	MTP11	AT2G39450	-1.42	-0.51	-4.08	0.005092	0.044872	-2.14

258553_at	hypothetical protein ; supported by cDN	PDE320	AT3G06960	-1.34	-0.42	-4.08	0.005093	0.044872	-2.14
254948_at	putative protein various predicted prote	---	AT4G11000	1.43	0.52	4.08	0.005098	0.044897	-2.14
260653_at	pyruvate kinase, plastid isozyme, putati	PKp3	AT1G32440	-1.41	-0.50	-4.08	0.00511	0.044987	-2.15
265939_at	putative Ta11-like non-LTR retroelemen	---	AT2G19650	-1.65	-0.72	-4.08	0.005116	0.045006	-2.15
253589_at	puative protein membrane-associated s	---	AT4G30825	-1.59	-0.67	-4.08	0.005115	0.045006	-2.15
249864_at	putative protein similar to unknown prot	ATMGT10	AT5G22830	-1.31	-0.39	-4.08	0.005121	0.045013	-2.15
259300_at	hypothetical protein predicted by gensca	---	AT3G05100	-1.37	-0.45	-4.08	0.005123	0.045013	-2.15
261696_at	unknown protein similar to hypothetical	---	AT1G08470	-1.65	-0.72	-4.08	0.005122	0.045013	-2.15
246098_at	ethylene-forming-enzyme-like dioxygen	---	AT5G20400	1.72	0.78	4.08	0.005129	0.045021	-2.15
262473_at	chloroplast FtsH protease almost identi	FTSH1	AT1G50250	-1.52	-0.61	-4.08	0.00513	0.045021	-2.15
251061_at	putative protein hypothetical protein AR	---	AT5G01830	2.23	1.16	4.08	0.00513	0.045021	-2.15
261177_at	hypothetical protein predicted by genem	---	AT1G04770	-1.77	-0.82	-4.07	0.005133	0.045029	-2.15
258525_at	hypothetical protein predicted by genem	IBR3	AT3G06810	1.58	0.66	4.07	0.005138	0.045049	-2.15
257127_at	hypothetical protein predicted by genem	TTN9	AT3G20070	-1.48	-0.56	-4.07	0.005141	0.045049	-2.15
265259_at	putative WD-40 repeat protein similar to	---	AT2G20330	-1.41	-0.50	-4.07	0.00514	0.045049	-2.15
261483_at	hypothetical protein predicted by genem	---	AT1G14270	-1.44	-0.52	-4.07	0.005146	0.045054	-2.15
249672_at	nucleolar protein-like	---	AT5G35910	-1.50	-0.59	-4.07	0.005147	0.045054	-2.15
266617_at	unknown protein ; supported by cDNA:	---	AT2G29670	-2.09	-1.06	-4.07	0.005147	0.045054	-2.15
262275_at	ATPase, putative similar to chromaffin g	---	AT1G68710	1.43	0.52	4.07	0.005154	0.045077	-2.16
264158_at	hypothetical protein contains similarity t	PTAC4	AT1G65260	-1.49	-0.57	-4.07	0.005154	0.045077	-2.16
250283_at	putative protein many hypothetical prot	---	AT5G13270	-1.41	-0.50	-4.07	0.005163	0.045138	-2.16
249987_at	putative protein predicted proteins, Ara	---	AT5G18490	1.71	0.78	4.07	0.00517	0.045185	-2.16
248287_at	putative protein similar to unknown prot	---	AT5G52970	-1.60	-0.68	-4.07	0.005179	0.045223	-2.16
262544_at	hypothetical protein predicted by gensca	---	AT1G15420	-1.46	-0.55	-4.07	0.005179	0.045223	-2.16
258592_at	hypothetical protein contains Pfam profi	---	AT3G04130	-1.43	-0.52	-4.07	0.00518	0.045223	-2.16
256511_at	RNA helicase, putative similar to GI:174	---	AT1G33390	-1.35	-0.43	-4.07	0.005186	0.045238	-2.16
257002_at	oligouridylate binding protein, putative s	---	AT3G14100	-1.51	-0.59	-4.07	0.005186	0.045238	-2.16
256503_at	myb-related protein similar to GI:798138	ATRL6	AT1G75250	-3.33	-1.74	-4.07	0.005189	0.045244	-2.16
245976_at	WRKY-like protein WRKY DNA binding	WRKY75	AT5G13080	4.18	2.06	4.07	0.005191	0.045246	-2.16
261639_at	tubulin alpha-2/alpha-4 chain, putative	TUA2	AT1G50010	2.69	1.43	4.06	0.005202	0.045295	-2.17
255791_at	plastid protein identical to GB:Z86094; s	DAL1	AT2G33430	-1.56	-0.64	-4.06	0.005203	0.045295	-2.17
247348_at	beta-galactosidase (emb CAB64746.1)	BGAL10	AT5G63810	-1.50	-0.59	-4.06	0.005199	0.045295	-2.16
245428_at	putative protein	---	AT4G17570	-1.38	-0.47	-4.06	0.005214	0.045303	-2.17
247400_at	putative protein ;supported by full-lengt	---	AT5G62840	-1.57	-0.65	-4.06	0.005216	0.045303	-2.17
267640_at	photomorphogenesis repressor (COP1)	COP1	AT2G32950	-1.52	-0.60	-4.06	0.005211	0.045303	-2.17

253170_at	putative protein various predicted prote	---	AT4G35130	-1.31	-0.39	-4.06	0.005211	0.045303	-2.17
247699_at	GTP-binding protein ara-3 GTP-binding	---	AT5G59840	1.77	0.82	4.06	0.005214	0.045303	-2.17
254755_at	hypothetical protein	---	AT4G13220	-1.44	-0.53	-4.06	0.005206	0.045303	-2.17
250182_at	putative protein predicted proteins, Arat	---	AT5G14470	2.55	1.35	4.06	0.005219	0.045312	-2.17
254911_at	putative protein ;supported by full-lengt	---	AT4G11100	-1.35	-0.44	-4.06	0.005226	0.045329	-2.17
246240_at	nucleoporin-like protein	---	AT4G37130	-1.30	-0.37	-4.06	0.005224	0.045329	-2.17
245004_at	hypothetical protein	---	---	-1.53	-0.62	-4.06	0.005224	0.045329	-2.17
254357_at	nifU-like protein nifU protein homolog Y	ISU1	AT4G22220	-1.28	-0.35	-4.06	0.005232	0.045362	-2.17
245178_at	putative protein similarity to cDNA clone	FIS1B	AT5G12390	1.33	0.41	4.06	0.005241	0.045364	-2.17
262645_at	unknown protein similar to elongation fa	SCO1	AT1G62750	-1.51	-0.60	-4.06	0.005239	0.045364	-2.17
246916_at	disease resistance protein - like disease	AtRLP52	AT5G25910	1.31	0.39	4.06	0.005238	0.045364	-2.17
249626_at	putative protein nucleoid DNA-binding p	---	AT5G37540	1.89	0.92	4.06	0.005242	0.045364	-2.17
263044_at	spore germination protein c2 similar to 1	---	AT1G23360	-1.40	-0.48	-4.06	0.005241	0.045364	-2.17
262733_s_a	lipase identical to lipase GB:AAA93262	---	AT1G28660 /	-1.46	-0.54	-4.06	0.005252	0.045370	-2.18
251516_s_a	putative protein hypothetical protein SP	---	AT3G59310 /	-1.42	-0.51	-4.06	0.005256	0.045370	-2.18
251768_at	phosphoinositide-specific phospholipas	---	AT3G55940	-1.84	-0.88	-4.06	0.005247	0.045370	-2.17
245711_at	putative c2h2 zinc finger transcription fa	ZAT6	AT5G04340	3.18	1.67	4.06	0.005256	0.045370	-2.18
262996_at	hypothetical protein predicted by gensca	---	AT1G54440	-1.37	-0.46	-4.06	0.00525	0.045370	-2.17
253790_at	photosystem II protein W - like photosy	PSB28	AT4G28660	-1.74	-0.80	-4.06	0.005256	0.045370	-2.18
259568_at	hypothetical protein	---	AT1G20490	-1.34	-0.42	-4.06	0.005257	0.045370	-2.18
260487_at	RNA-binding protein, putative similar to	Y14	AT1G51510	-1.36	-0.44	-4.05	0.005269	0.045457	-2.18
253626_at	F-box protein family, AtFBL19 contains	---	AT4G30640	1.73	0.79	4.05	0.005272	0.045465	-2.18
249426_at	putative RNA helicase putative ATP-de	---	AT5G39840	-2.13	-1.09	-4.05	0.005283	0.045491	-2.18
246003_at	chloroplast Cpn21 protein ; supported b	CPN20	AT5G20720	-1.43	-0.52	-4.05	0.00528	0.045491	-2.18
258497_at	putative flowering-time gene CONSTAN	COL2	AT3G02380	-1.40	-0.49	-4.05	0.005283	0.045491	-2.18
252724_at	putative protein hypothetical protein slr1	---	AT3G43540	-1.48	-0.57	-4.05	0.005281	0.045491	-2.18
253758_at	Expressed protein ;supported by cDNA:	emb2726	AT4G29060	-1.48	-0.56	-4.05	0.005296	0.045582	-2.18
261742_at	hypothetical protein predicted by genem	---	AT1G08390	-1.33	-0.41	-4.05	0.005303	0.045626	-2.19
253294_at	hypothetical protein	---	AT4G33740	-1.40	-0.48	-4.05	0.00531	0.045655	-2.19
258324_at	putative DNA binding protein identical to	TSO1	AT3G22780	-1.32	-0.40	-4.05	0.00531	0.045655	-2.19
250825_at	putative protein similar to unknown prote	---	AT5G05210	-1.36	-0.44	-4.05	0.005317	0.045699	-2.19
266017_at	unknown protein ; supported by cDNA:	---	AT2G18690	2.49	1.32	4.05	0.005322	0.045712	-2.19
245052_at	putative pectinesterase	---	AT2G26440	1.51	0.59	4.04	0.005325	0.045712	-2.19
261204_s_a	Eukaryotic peptide chain release factor s	ERF1-2	AT1G12920 /	-1.28	-0.36	-4.04	0.005327	0.045712	-2.19
255682_at	putative dTDP-6-deoxy-L-mannose-deh	---	AT4G00560	-1.38	-0.47	-4.04	0.005325	0.045712	-2.19

255960_at	unknown protein ; supported by cDNA: g	---	AT1G22140	-1.52	-0.60	-4.04	0.005329	0.045713	-2.19
259505_at	hypothetical protein contains similarity to	---	AT1G15810	-1.53	-0.61	-4.04	0.005332	0.045719	-2.19
265819_at	Expressed protein ; supported by full-ler	---	AT2G17972	-1.46	-0.54	-4.04	0.005334	0.045719	-2.19
259979_at	unknown protein ;supported by full-leng	---	AT1G76600	2.07	1.05	4.04	0.005341	0.045764	-2.19
264314_at	unknown protein ; supported by cDNA: g	---	AT1G70420	-1.72	-0.78	-4.04	0.005354	0.045856	-2.20
247401_at	1-deoxy-D-xylulose 5-phosphate reducto	DXR	AT5G62790	-1.64	-0.71	-4.04	0.00536	0.045896	-2.20
255872_at	putative protein kinase contains a protei	SIP4	AT2G30360	2.29	1.19	4.04	0.005366	0.045915	-2.20
267196_at	FtsH protease (VAR2) identical to zinc d	VAR2	AT2G30950	-1.38	-0.47	-4.04	0.005366	0.045915	-2.20
244983_at	ribosomal protein L16	---	---	-1.81	-0.86	-4.04	0.005376	0.045943	-2.20
253592_at	hypothetical protein ;supported by full-le	---	AT4G30840	-1.34	-0.42	-4.04	0.005376	0.045943	-2.20
256654_at	ribosomal protein, putative similar to 40	---	AT3G18880	-1.61	-0.69	-4.04	0.005375	0.045943	-2.20
256249_at	26S proteasome regulatory subunit S12	MEE34	AT3G11270	-1.40	-0.48	-4.04	0.005379	0.045954	-2.20
246400_at	hypothetical protein contains similarity to	---	AT1G57540	-1.32	-0.40	-4.03	0.005391	0.046025	-2.20
250353_at	putative protein predicted proteins, Arat	---	AT5G11630	-1.44	-0.53	-4.03	0.005391	0.046025	-2.20
247004_at	putative protein similar to unknown prote	DG1	AT5G67570	-1.42	-0.50	-4.03	0.005398	0.046067	-2.20
257315_at	proline oxidase, mitochondrial precurso	ERD5	AT3G30775	3.28	1.71	4.03	0.005406	0.046090	-2.21
247194_at	putative protein similar to unknown prote	---	AT5G65480	-1.62	-0.70	-4.03	0.005407	0.046090	-2.21
265795_at	putative serine carboxypeptidase II ;sup	scpl26	AT2G35780	-1.41	-0.50	-4.03	0.005411	0.046090	-2.21
245065_at	unknown protein ; supported by cDNA:	---	AT2G39750	-1.31	-0.39	-4.03	0.005411	0.046090	-2.21
249078_at	phytochelatin synthase (gb|AAD41794.1	CAD1	AT5G44070	2.56	1.35	4.03	0.005409	0.046090	-2.21
255885_at	sterol-C-methyltransferase identical to s	SMT2	AT1G20330	1.37	0.46	4.03	0.005416	0.046111	-2.21
251007_at	ribosomal protein L35 - like ribosomal p	---	AT5G02610	-1.47	-0.56	-4.03	0.005422	0.046135	-2.21
258317_at	hypothetical protein predicted by genem	---	AT3G22670	-1.35	-0.43	-4.03	0.005429	0.046135	-2.21
246237_at	putative protein	---	AT4G36390	-1.44	-0.53	-4.03	0.005426	0.046135	-2.21
254416_at	receptor-like serine/threonine protein kir	ARK3	AT4G21380	2.86	1.52	4.03	0.005427	0.046135	-2.21
262635_at	4-hydroxyphenylpyruvate dioxygenase (	PDS1	AT1G06570	1.91	0.94	4.03	0.005425	0.046135	-2.21
264394_at	aminomethyltransferase-like precursor	---	AT1G11860	-1.64	-0.72	-4.03	0.00544	0.046155	-2.21
247779_at	putative protein damage-specific DNA b	DDB2	AT5G58760	-1.48	-0.56	-4.03	0.005439	0.046155	-2.21
260525_at	putative pre-mRNA splicing factor RNA	---	AT2G47250	-1.33	-0.41	-4.03	0.005441	0.046155	-2.21
257004_s_a	glycolate oxidase, putative similar to GE	---	AT3G14130 /	-1.32	-0.40	-4.03	0.005443	0.046155	-2.21
261617_s_a	hypothetical protein predicted by genem	---	AT1G33090 /	1.32	0.40	4.03	0.005437	0.046155	-2.21
250040_at	putative protein predicted proteins, Arat	---	AT5G18390	-1.32	-0.40	-4.03	0.005433	0.046155	-2.21
262316_at	pale cress protein identical to GB:CAA6	PAC	AT2G48120	-1.61	-0.69	-4.03	0.005445	0.046155	-2.21
248663_at	putative protein strong similarity to unkn	---	AT5G48590	-1.29	-0.37	-4.03	0.005452	0.046198	-2.21
252949_at	putative thaumatin-like protein thaumati	---	AT4G38670	-1.85	-0.88	-4.02	0.005457	0.046218	-2.22

260683_at	ribosomal protein, putative similar to GE	HLL	AT1G17560	-1.40	-0.48	-4.02	0.00546	0.046230	-2.22
250323_at	putative protein hydroxyproline-rich glyc	---	AT5G12880	3.29	1.72	4.02	0.005471	0.046304	-2.22
249140_at	F-box protein family, AtFBX6 contains s	---	AT5G43190	1.57	0.65	4.02	0.005473	0.046305	-2.22
246815_at	putative protein integrin analogue, Sacc	---	AT5G27220	-1.32	-0.40	-4.02	0.005489	0.046426	-2.22
255603_at	hypothetical protein	---	AT4G01040	-1.32	-0.41	-4.02	0.005501	0.046497	-2.22
260789_s_a	acyl-CoA oxidase ACX3 identical to acy	ACX3	AT1G06290 /	1.31	0.39	4.02	0.005502	0.046497	-2.22
266215_at	putative endoxyloglucan glycosyltransfe	EXGT-A1	AT2G06850	2.68	1.42	4.02	0.005506	0.046507	-2.23
248303_at	FtsH protease, putative similar to ATP-d	FTSH11	AT5G53170	-1.39	-0.48	-4.02	0.005511	0.046507	-2.23
250739_at	putative protein similar to unknown prote	EGY2	AT5G05740	-1.61	-0.68	-4.02	0.005508	0.046507	-2.23
245427_at	putative protein	---	AT4G17550	-1.56	-0.64	-4.02	0.00551	0.046507	-2.23
253949_at	grpE like protein ;supported by full-leng	AR192	AT4G26780	-2.32	-1.22	-4.01	0.005524	0.046581	-2.23
245866_s_a	unknown protein	---	AT1G57980 /	3.71	1.89	4.01	0.005526	0.046581	-2.23
250530_at	unknown protein	---	AT5G08630	1.40	0.49	4.01	0.005526	0.046581	-2.23
244982_at	ribosomal protein L14	---	---	-1.45	-0.54	-4.01	0.005548	0.046633	-2.23
262964_at	hypothetical protein predicted by genem	---	AT1G54380	-1.62	-0.70	-4.01	0.005541	0.046633	-2.23
247608_at	replication protein A1 - like probable rep	---	AT5G60990	-1.48	-0.57	-4.01	0.005543	0.046633	-2.23
261098_at	unknown protein	---	AT1G62970	-1.37	-0.45	-4.01	0.005548	0.046633	-2.23
265276_at	hypothetical protein predicted by gensca	---	AT2G28400	1.67	0.74	4.01	0.005551	0.046633	-2.23
247902_at	plasma membrane ATPase 3 (proton pu	AHA3	AT5G57350	-1.45	-0.54	-4.01	0.005549	0.046633	-2.23
254413_at	myb-related protein M4 ;supported by f	ATMYB10	AT4G21440	1.70	0.76	4.01	0.005538	0.046633	-2.23
267152_at	hypothetical protein predicted by grail; s	---	AT2G31040	-1.58	-0.66	-4.01	0.005549	0.046633	-2.23
256414_at	putative nucleic acid binding protein sim	AL2	AT3G11200	1.37	0.45	4.01	0.005543	0.046633	-2.23
260051_at	hypothetical protein	---	AT1G78210	2.02	1.02	4.01	0.005554	0.046648	-2.23
266587_at	unknown protein ; supported by full-leng	---	AT2G14880	-1.44	-0.53	-4.01	0.005564	0.046692	-2.24
249816_at	cleavage and polyadenylation specificity	CPSF100	AT5G23880	-1.55	-0.63	-4.01	0.005564	0.046692	-2.24
264725_at	Expressed protein ; supported by full-ler	---	AT1G22885	1.92	0.94	4.01	0.005566	0.046693	-2.24
256207_at	GTP-binding protein, putative similar to	---	AT1G50920	-1.52	-0.60	-4.01	0.005575	0.046702	-2.24
254032_at	predicted protein destination factor syna	---	AT4G25940	1.52	0.60	4.01	0.005573	0.046702	-2.24
251616_at	putative protein	---	AT3G57990	-1.31	-0.39	-4.01	0.005578	0.046702	-2.24
266337_at	putative ligand-gated ion channel subun	ATGLR3.5	AT2G32390	-1.35	-0.43	-4.01	0.005576	0.046702	-2.24
251941_at	putative protein ribosomal protein S25,	---	AT3G53470	-1.38	-0.46	-4.01	0.005578	0.046702	-2.24
260481_at	ferredoxin precusor isolog ;supported b	ATFD1	AT1G10960	-1.77	-0.82	-4.01	0.005579	0.046702	-2.24
261344_at	hypothetical protein similar to hypothetic	---	AT1G79710	1.36	0.45	4.01	0.005585	0.046733	-2.24
250842_at	putative protein predicted proteins, Arch	VTE5	AT5G04490	-1.55	-0.63	-4.00	0.005603	0.046783	-2.24
248136_at	RNA helicase-like protein	---	AT5G54910	-1.79	-0.84	-4.00	0.005597	0.046783	-2.24

253665_at	hypothetical protein	---	AT4G30230	1.77	0.83	4.00	0.005596	0.046783	-2.24
263914_at	unknown protein	AtGRF3	AT2G36400	-1.78	-0.83	-4.00	0.005597	0.046783	-2.24
257666_at	bactericidal permeability-increasing pro	---	AT3G20270	1.72	0.78	4.00	0.005603	0.046783	-2.24
247937_at	Ca2+-transporting ATPase-like protein (	ACA8	AT5G57110	-1.82	-0.87	-4.00	0.0056	0.046783	-2.24
253605_at	putative protein probable membrane pr	---	AT4G30990	-1.56	-0.64	-4.00	0.005611	0.046832	-2.25
265036_at	unknown protein Contains similarity to p	PRP39	AT1G04080	-1.33	-0.41	-4.00	0.005613	0.046832	-2.25
265876_at	putative receptor-like protein kinase	---	AT2G42290	-1.33	-0.41	-4.00	0.005616	0.046841	-2.25
266490_at	unknown protein	---	AT2G07000	-1.47	-0.56	-4.00	0.005624	0.046887	-2.25
263448_at	putative importin (nuclear transport facto	SAD2	AT2G31660	-1.46	-0.55	-4.00	0.005635	0.046965	-2.25
245076_at	unknown protein	GH3.3	AT2G23170	6.80	2.77	4.00	0.005638	0.046971	-2.25
263867_at	putative aquaporin (tonoplast intrinsic pr	GAMMA-T	AT2G36830	1.91	0.94	4.00	0.005646	0.046990	-2.25
248291_at	putative protein similar to unknown prote	---	AT5G53020	-1.39	-0.48	-4.00	0.005647	0.046990	-2.25
251287_at	putative protein nucleoid DNA-binding p	---	AT3G61820	-1.68	-0.75	-4.00	0.005646	0.046990	-2.25
246303_at	putative carrier protein peroxisomal Ca-	---	AT3G51870	1.71	0.77	4.00	0.00565	0.047000	-2.25
251241_s_a	putative protein hypothetical proteins - A	---	AT3G62460 /	-1.56	-0.64	-4.00	0.005652	0.047000	-2.25
258518_at	unknown protein ; supported by cDNA:	---	AT3G06570	-1.31	-0.39	-4.00	0.00566	0.047037	-2.25
264680_at	hypothetical protein predicted by genem	---	AT1G65510	1.98	0.99	4.00	0.00566	0.047037	-2.25
251110_at	putative protein various alpha amylases	---	AT5G01260	-1.70	-0.77	-3.99	0.005669	0.047093	-2.26
249610_at	putative protein	---	AT5G37360	-1.93	-0.95	-3.99	0.005675	0.047111	-2.26
248386_at	DNA-directed RNA polymerase II subun	NRPB6A	AT5G51940	-1.40	-0.48	-3.99	0.005676	0.047111	-2.26
246621_at	putative protein strong similarity to unkn	---	AT5G36230	-1.27	-0.35	-3.99	0.005678	0.047114	-2.26
252098_at	putative protein several hypothetical pro	---	AT3G51330	3.00	1.59	3.99	0.005685	0.047157	-2.26
253136_at	putative protein leucine-rich protein - He	---	AT4G35470	-1.40	-0.49	-3.99	0.005714	0.047249	-2.26
265649_at	putative ferredoxin ; supported by full-le	ATFD3	AT2G27510	1.84	0.88	3.99	0.005722	0.047249	-2.27
257530_at	unknown protein	---	AT3G03040	-1.35	-0.43	-3.99	0.005718	0.047249	-2.27
246061_at	RAN GTPase activating protein 2 ; supp	RANGAP2	AT5G19320	-1.28	-0.35	-3.99	0.005714	0.047249	-2.26
260168_at	unknown protein contains zinc finger, C	---	AT1G71980	-1.51	-0.59	-3.99	0.005711	0.047249	-2.26
248380_at	phosphoglucomutase (emb|CAB64725.1	PGM	AT5G51820	-1.89	-0.92	-3.99	0.00572	0.047249	-2.27
245364_at	hypothetical protein ;supported by full-le	---	AT4G15790	-1.48	-0.57	-3.99	0.005717	0.047249	-2.27
255707_at	predicted protein	MEE50	AT4G00231	-1.32	-0.40	-3.99	0.00571	0.047249	-2.26
249242_at	alcohol dehydrogenase	---	AT5G42250	1.47	0.56	3.99	0.005716	0.047249	-2.26
257831_at	unknown protein ;supported by full-leng	CCB1	AT3G26710	-1.46	-0.55	-3.99	0.0057	0.047249	-2.26
258807_at	transfactor-like similar to transfactor GB	---	AT3G04030	-1.72	-0.79	-3.99	0.005723	0.047249	-2.27
261640_at	permease, putative similar to permease	---	AT1G49960	1.44	0.52	3.99	0.005714	0.047249	-2.26
255554_at	Expressed protein ; supported by full-ler	---	AT4G01897	-1.37	-0.45	-3.99	0.005708	0.047249	-2.26

255078_at	putative protein ascorbate peroxidase -	APX4	AT4G09010	-1.57	-0.65	-3.99	0.005726	0.047256	-2.27
259705_at	GRAB1-like protein similar to GRAB1 p	anac032	AT1G77450	1.72	0.78	3.99	0.005729	0.047260	-2.27
250848_at	3-phosphoinositide-dependent protein k	PDK1	AT5G04510	-1.40	-0.49	-3.98	0.005743	0.047364	-2.27
257073_at	hypothetical protein predicted by gensca	---	AT3G19650	-1.50	-0.58	-3.98	0.005749	0.047377	-2.27
258989_at	rhodanese-like family protein contains rh	---	AT3G08920	-1.44	-0.52	-3.98	0.005747	0.047377	-2.27
263766_at	hypothetical protein predicted by gensca	---	AT2G21440	-1.53	-0.61	-3.98	0.005757	0.047424	-2.27
267247_at	hypothetical protein predicted by gensca	---	AT2G30170	-1.45	-0.54	-3.98	0.005761	0.047428	-2.27
265583_at	unknown protein	---	AT2G20010	1.30	0.38	3.98	0.005762	0.047428	-2.27
262897_at	hypothetical protein predicted by genem	CCB4	AT1G59840	-2.18	-1.12	-3.98	0.005767	0.047457	-2.27
263566_at	hypothetical protein predicted by genefir	---	AT2G15340	1.43	0.52	3.98	0.005772	0.047479	-2.28
262610_at	putative mitochondrial uncoupling protei	---	AT1G14140	-1.28	-0.36	-3.98	0.005774	0.047481	-2.28
262525_at	putative cytochrome P450 41% identica	CYP72C1	AT1G17060	1.74	0.80	3.98	0.005777	0.047484	-2.28
264222_at	hypothetical protein predicted by genem	---	AT1G60230	-1.36	-0.44	-3.98	0.005779	0.047484	-2.28
250013_at	putative protein similar to unknown prote	---	AT5G18040	-1.34	-0.42	-3.98	0.005792	0.047562	-2.28
256755_at	calmodulin, putative similar to GB:P074	---	AT3G25600	1.87	0.90	3.98	0.005792	0.047562	-2.28
253854_at	putative protein zinc-finger protein S125	---	AT4G27900	-2.38	-1.25	-3.98	0.005801	0.047612	-2.28
256986_at	unknown protein	---	AT3G28700	-1.56	-0.64	-3.97	0.005806	0.047629	-2.28
254605_at	protein kinase - like protein protein kina	---	AT4G18950	2.16	1.11	3.97	0.005809	0.047629	-2.28
252404_at	glycine--tRNA ligase precursor, chlorop	EDD1	AT3G48110	-1.36	-0.44	-3.97	0.005809	0.047629	-2.28
248320_at	putative protein similar to unknown prote	---	AT5G52720	1.42	0.51	3.97	0.005822	0.047721	-2.28
251209_at	putative protein several hypothetical pro	---	AT3G62890	-1.48	-0.57	-3.97	0.005835	0.047794	-2.29
263980_at	hypothetical protein predicted by grail;su	---	AT2G42770	-1.49	-0.58	-3.97	0.005834	0.047794	-2.29
265225_at	putative PHD-type zinc finger protein	---	AT2G36720	-1.36	-0.45	-3.97	0.00584	0.047801	-2.29
260226_at	hypothetical protein predicted by genefir	MIF1	AT1G74660	-1.47	-0.56	-3.97	0.005839	0.047801	-2.29
266745_at	unknown protein ; supported by cDNA:	PKS1	AT2G02950	-2.20	-1.14	-3.97	0.005852	0.047822	-2.29
253208_at	putative protein	---	AT4G34830	-1.34	-0.43	-3.97	0.005856	0.047822	-2.29
254958_at	nucleoside diphosphate kinase 3 (ndpk3	NDPK3	AT4G11010	-1.56	-0.64	-3.97	0.005852	0.047822	-2.29
254901_at	serine/threonine kinase-like protein (fra	---	AT4G11530	1.37	0.46	3.97	0.005848	0.047822	-2.29
259633_at	hypothetical protein	---	AT1G56500	-1.50	-0.58	-3.97	0.005848	0.047822	-2.29
254860_at	putative C-4 sterol methyl oxidase C-4	SMO1-1	AT4G12110	-1.44	-0.53	-3.97	0.005856	0.047822	-2.29
246791_at	putative protein predicted proteins, Aral	---	AT5G27280	-1.44	-0.52	-3.97	0.005868	0.047910	-2.29
256529_at	protein kinase, putative contains Pfam p	---	AT1G33260	1.85	0.89	3.97	0.005873	0.047927	-2.29
251183_at	putative protein putative protein At2g15	---	AT3G62630	-2.69	-1.43	-3.96	0.005879	0.047962	-2.29
264330_at	multi-drug resistance protein Strong sim	ATMRP5	AT1G04120	1.36	0.44	3.96	0.005892	0.048035	-2.30
257042_s_a	hypothetical protein predicted by genem	---	AT3G28640 /	-1.33	-0.41	-3.96	0.00589	0.048035	-2.30

255317_at	putative vesicle transfer ATPase	---	AT4G04180	-1.76	-0.82	-3.96	0.005909	0.048117	-2.30
266552_at	unknown protein ; supported by cDNA: g	AGP16	AT2G46330	1.60	0.68	3.96	0.005907	0.048117	-2.30
249579_at	ADP-ribosylation factor - like protein AD	ATARLA1A	AT5G37680	-1.37	-0.45	-3.96	0.005908	0.048117	-2.30
260076_at	putative calmodulin similar to calmodulir	---	AT1G73630	-1.66	-0.73	-3.96	0.005914	0.048143	-2.30
249253_at	putative protein similar to unknown prote	---	AT5G42060	-1.42	-0.51	-3.96	0.00592	0.048155	-2.30
252596_at	receptor-like protein kinase receptor like	---	AT3G45330	1.31	0.39	3.96	0.00592	0.048155	-2.30
252334_at	mitochondrial phosphate transporter mi	---	AT3G48850	4.26	2.09	3.96	0.005926	0.048193	-2.30
262114_at	unknown protein contains similarity to pe	NLA	AT1G02860	1.78	0.83	3.96	0.005936	0.048256	-2.30
248515_at	putative protein strong similarity to unkn	---	AT5G50530 /	1.43	0.51	3.95	0.005962	0.048416	-2.31
245644_at	unknown protein similar to putative rece	---	AT1G25320	-1.45	-0.53	-3.95	0.005961	0.048416	-2.31
246484_at	UVB-resistance protein-like UVB-resista	---	AT5G16040	-1.41	-0.50	-3.95	0.005967	0.048416	-2.31
256459_at	acetyl-CoA carboxylase, putative simila	ACC2	AT1G36180	-1.49	-0.57	-3.95	0.005969	0.048416	-2.31
247993_at	putative protein similar to unknown prote	---	AT5G56130	-1.48	-0.56	-3.95	0.005965	0.048416	-2.31
265679_at	putative myosin heavy chain ; supporte	---	AT2G32235 /	1.40	0.49	3.95	0.005966	0.048416	-2.31
257211_at	exonuclease, putative contains Pfam pr	---	AT3G15080	-1.52	-0.61	-3.95	0.005972	0.048422	-2.31
259984_at	putative RNA-binding protein contains F	---	AT1G76460	-1.43	-0.52	-3.95	0.005979	0.048468	-2.31
251117_at	putative protein predicted protein, Caer	---	AT3G63390	-1.47	-0.56	-3.95	0.005984	0.048470	-2.31
251725_at	putative protein	---	AT3G56260	1.66	0.73	3.95	0.005983	0.048470	-2.31
252534_at	Myb DNA binding protein -like MYB59,	MYB111	AT3G46130	-1.35	-0.43	-3.95	0.005988	0.048489	-2.31
256648_at	ribosomal protein, putative similar to 60	---	AT3G13580	-1.56	-0.64	-3.95	0.006001	0.048574	-2.32
260407_at	putative protein kinase Pfam HMM hit: E	---	AT1G69910	1.31	0.39	3.94	0.006025	0.048750	-2.32
260618_at	flower development protein cycloidea (c	TCP3	AT1G53230	-1.46	-0.54	-3.94	0.006034	0.048804	-2.32
249197_at	putative protein contains similarity to cal	CML37	AT5G42380	8.51	3.09	3.94	0.006044	0.048874	-2.32
255686_at	putative potassium/H+ antiporter	KEA2	AT4G00630	-1.48	-0.56	-3.94	0.006056	0.048950	-2.33
262955_at	unknown protein ;supported by full-lengt	---	AT1G54520	-1.45	-0.54	-3.94	0.006063	0.048971	-2.33
260324_at	unknown protein similar to hypothetical p	ISPF	AT1G63970	-1.48	-0.57	-3.94	0.006061	0.048971	-2.33
260453_s_a	unknown protein	---	AT1G72510 /	-1.52	-0.61	-3.94	0.006071	0.049002	-2.33
254493_at	DAG-like protein DAG precursor, Antirrl	---	AT4G20020	-1.75	-0.80	-3.94	0.006072	0.049002	-2.33
245307_at	gibberellin oxidase-like protein non-cons	---	AT4G16770	-1.44	-0.53	-3.94	0.006073	0.049002	-2.33
265656_at	putative nonspecific lipid-transfer protein	---	AT2G13820	2.13	1.09	3.94	0.006083	0.049044	-2.33
245714_at	RNA-binding protein-like	---	AT5G04280	-1.37	-0.45	-3.94	0.006081	0.049044	-2.33
248952_at	putative protein similar to unknown prote	---	AT5G45410	1.42	0.51	3.94	0.006096	0.049107	-2.33
245758_at	unknown protein contains similarity to tra	KAN2	AT1G32240	-1.64	-0.72	-3.94	0.006098	0.049107	-2.33
247563_at	putative protein various predicted prote	PDCB1	AT5G61130	-1.52	-0.60	-3.94	0.0061	0.049107	-2.33
262839_at	PhD-finger protein, putative contains Pf	---	AT1G14770	-1.73	-0.79	-3.93	0.0061	0.049107	-2.33

265719_at	unknown protein related to putative two-	---	AT2G03500	-1.33	-0.41	-3.93	0.006101	0.049107	-2.33
263962_at	putative protein kinase contains a protei	---	AT2G36350	-1.57	-0.65	-3.93	0.006109	0.049137	-2.34
247029_at	TINY-like protein	---	AT5G67190	1.52	0.60	3.93	0.006109	0.049137	-2.34
252002_at	hypothetical protein YIP1 protein, Sacc	---	AT3G52760	-1.35	-0.43	-3.93	0.006114	0.049160	-2.34
266447_at	putative calcium binding protein ;suppor	MSS3	AT2G43290	2.31	1.21	3.93	0.006119	0.049177	-2.34
262189_at	GTPase, putative similar to GTPase GI	---	AT1G78010	-1.38	-0.46	-3.93	0.006135	0.049292	-2.34
251883_at	ribosomal protein L17 -like protein ribos	---	AT3G54210	-1.36	-0.45	-3.93	0.006137	0.049292	-2.34
264920_at	hypothetical protein contains similarity t	ECHID	AT1G60550	-1.43	-0.52	-3.93	0.006168	0.049521	-2.35
257751_at	hypothetical protein predicted by genem	MKS1	AT3G18690	2.95	1.56	3.93	0.00617	0.049521	-2.35
256235_at	cysteine proteinase inhibitor, putative s	ATCYSB	AT3G12490	1.29	0.36	3.93	0.006172	0.049521	-2.35
263118_at	putative 3-methylcrotonyl-CoA carboxyl	MCCA	AT1G03090	2.20	1.14	3.92	0.006179	0.049557	-2.35
265262_at	putative chloroplast nucleoid DNA bindi	---	AT2G42980	1.49	0.57	3.92	0.006182	0.049566	-2.35
252516_at	histidyl-tRNA synthetase ; supported by	ATHRS1	AT3G46100	-1.42	-0.50	-3.92	0.006186	0.049578	-2.35
265948_at	1-aminocyclopropane-1-carboxylate oxi	ACO1	AT2G19590	1.40	0.49	3.92	0.006194	0.049593	-2.35
254997_s_a	putative protein various predicted prote	---	AT4G09920 /	-1.33	-0.41	-3.92	0.006194	0.049593	-2.35
252175_at	zinc finger protein zinc finger protein ID	AtIDD2	AT3G50700	-1.29	-0.37	-3.92	0.006191	0.049593	-2.35
254991_at	putative protein conserved hypothetical	---	AT4G10620	-1.46	-0.55	-3.92	0.006212	0.049639	-2.35
261049_at	hypothetical protein similar to hypothetic	---	AT1G01430	-1.63	-0.71	-3.92	0.006214	0.049639	-2.35
254751_at	hypothetical protein	---	AT4G13150	-1.33	-0.41	-3.92	0.00621	0.049639	-2.35
257928_at	hypothetical protein contains Pfam profi	PPR40	AT3G16890	-1.28	-0.36	-3.92	0.006217	0.049639	-2.35
255435_at	putative component of cytochrome B6-F	PETC	AT4G03280	-1.39	-0.48	-3.92	0.006205	0.049639	-2.35
264105_x_a	hypothetical protein	---	AT2G13760	1.43	0.51	3.92	0.00622	0.049639	-2.35
255328_at	putative leucyl tRNA synthetase	EMB2369	AT4G04350	-1.53	-0.61	-3.92	0.006205	0.049639	-2.35
263780_at	hypothetical protein predicted by genefi	SPA1	AT2G46340	-1.76	-0.82	-3.92	0.006209	0.049639	-2.35
245328_at	Expressed protein ; supported by full-ler	---	AT4G14465	1.35	0.44	3.92	0.006218	0.049639	-2.35
248793_at	mutT domain protein-like ;supported by	atnudt8	AT5G47240	-2.09	-1.06	-3.92	0.006228	0.049689	-2.36
247213_at	unknown protein ; supported by full-leng	PROPEP1	AT5G64900	2.90	1.54	3.92	0.006239	0.049726	-2.36
247722_at	GTP-binding protein rab11 - like GTP-b	ATRABA2	AT5G59150	1.38	0.46	3.92	0.006237	0.049726	-2.36
262085_at	hypothetical protein predicted by genem	---	AT1G56060	4.17	2.06	3.92	0.006238	0.049726	-2.36
255044_at	putative protein	---	AT4G09680	-1.40	-0.48	-3.91	0.006255	0.049817	-2.36
257717_at	unknown protein	EMB1865	AT3G18390	-1.48	-0.57	-3.91	0.006255	0.049817	-2.36
249454_at	expressed protein predicted protein, Sy	---	AT5G39520	2.90	1.54	3.91	0.006262	0.049825	-2.36
246817_at	putative protein various predicted prote	---	AT5G27240	-1.42	-0.50	-3.91	0.006263	0.049825	-2.36
261304_at	unknown protein ;supported by full-lengt	---	AT1G48440	-1.28	-0.35	-3.91	0.006261	0.049825	-2.36
250495_at	ribsomal protein - like chloroplast ribos	---	AT5G09770	-1.48	-0.57	-3.91	0.006274	0.049886	-2.36

253695_at	arginine methyltransferase (pam1) ; su	PRMT11	AT4G29510	-1.57	-0.65	-3.91	0.006275	0.049886	-2.36
245498_at	hypothetical protein	---	AT4G16470	-1.31	-0.39	-3.91	0.006277	0.049886	-2.36
245932_at	3'(2'),5'-bisphosphate nucleotidase-like	---	AT5G09290	2.02	1.01	3.91	0.006286	0.049941	-2.37
246576_at	hypothetical protein predicted by genem	ROPGEF1	AT1G31650	-1.29	-0.37	-3.91	0.006293	0.049981	-2.37
259039_at	unknown protein ;supported by full-leng	---	AT3G09250	-1.35	-0.43	-3.91	0.006298	0.050006	-2.37
261653_at	subtilisin-like serine protease, putative	SBTI1.1	AT1G01900	2.18	1.13	3.91	0.006305	0.050033	-2.37
257352_at	putative RING3 protein	IMB1	AT2G34900	-1.45	-0.54	-3.91	0.006306	0.050033	-2.37
253193_at	putative protein SEC7 protein, Sacchar	---	AT4G35380	1.56	0.64	3.91	0.00631	0.050049	-2.37
257395_at	putative salt-inducible protein	---	AT2G15630	-1.52	-0.60	-3.91	0.006323	0.050103	-2.37
266580_at	unknown protein ;supported by full-leng	---	AT2G46260	1.40	0.48	3.91	0.006322	0.050103	-2.37
253710_at	putative protein hypothetical protein F2	anac075	AT4G29230	1.47	0.55	3.91	0.006324	0.050103	-2.37
257816_at	glycosyl transferase, putative contains	QUA1	AT3G25140	-1.41	-0.49	-3.91	0.006333	0.050107	-2.37
247913_at	unknown protein	---	AT5G57510	5.56	2.48	3.91	0.006327	0.050107	-2.37
248023_at	ADP/ATP translocase-like protein ;supp	---	AT5G56450	-1.39	-0.47	-3.91	0.006331	0.050107	-2.37
255280_at	score=179, E=5.7e-06, N=1)	---	AT4G04960	1.98	0.98	3.91	0.006333	0.050107	-2.37
265676_at	putative CCR4-associated factor ; supp	---	AT2G32070	-1.33	-0.41	-3.90	0.006337	0.050123	-2.37
267596_s_a	putative leucine-rich repeat disease resi	AtRLP26	AT2G33050 /	-2.24	-1.16	-3.90	0.006346	0.050171	-2.38
248107_at	small Ras-like GTP-binding protein (gb|	RAN3	AT5G55190	-1.30	-0.38	-3.90	0.00636	0.050268	-2.38
254072_at	putative protein ClpC protease - Spinac	---	AT4G25370	-1.40	-0.49	-3.90	0.006368	0.050313	-2.38
248095_at	putative protein strong similarity to unkn	ATMAP65	AT5G55230	-1.53	-0.61	-3.90	0.00637	0.050313	-2.38
254593_s_a	putative protein IEF SSP 9502, Homo s	---	AT4G18900 /	-1.45	-0.54	-3.90	0.006376	0.050339	-2.38
258655_at	putative isocitrate dehydrogenase (NAD	---	AT3G09810	1.55	0.64	3.90	0.006379	0.050349	-2.38
257147_at	unknown protein	---	AT3G27270	1.57	0.65	3.90	0.006386	0.050383	-2.38
252093_at	putative protein predicted protein, Oryz	---	AT3G51500	-1.39	-0.48	-3.90	0.006389	0.050388	-2.38
250408_at	serine/threonine protein kinase -like pro	CIPK5	AT5G10930	-1.74	-0.80	-3.90	0.006395	0.050420	-2.38
257517_at	unknown protein	---	AT3G16330	2.99	1.58	3.90	0.006399	0.050439	-2.38
258995_at	putative ribosomal protein L13 similar to	---	AT3G01790	-1.57	-0.65	-3.90	0.006407	0.050478	-2.39
254438_at	translation initiation factor eIF3 - like pr	---	AT4G20980	-1.48	-0.56	-3.90	0.006411	0.050494	-2.39
261748_at	hypothetical protein predicted by genem	---	AT1G76070	3.00	1.58	3.89	0.006416	0.050515	-2.39
245893_at	hypothetical protein ;supported by full-le	---	AT5G09270	-1.35	-0.44	-3.89	0.006427	0.050566	-2.39
262633_at	Expressed protein ; supported by full-ler	---	AT1G06630	-1.32	-0.40	-3.89	0.006424	0.050566	-2.39
267365_at	putative phosphoribosyl pyrophosphate	---	AT2G44530	-1.28	-0.36	-3.89	0.006431	0.050580	-2.39
252707_at	transporter-like protein multidrug-efflux	ZIFL2	AT3G43790	-1.47	-0.55	-3.89	0.006442	0.050643	-2.39
257914_at	Expressed protein ; supported by cDNA	---	AT3G25545	-1.45	-0.54	-3.89	0.006443	0.050643	-2.39
267162_s_a	putative phosphoribosylaminoimidazole	---	AT2G05140 /	-1.61	-0.69	-3.89	0.006456	0.050644	-2.39

258687_at	unknown protein	---	AT3G07860	-1.54	-0.63	-3.89	0.006452	0.050644	-2.39
251551_at	transcriptional coactivator - like protein	MBF1B	AT3G58680	-1.27	-0.35	-3.89	0.00645	0.050644	-2.39
264878_at	unknown protein	---	AT2G17410	-1.30	-0.38	-3.89	0.006448	0.050644	-2.39
251288_at	exonuclease RRP41 ; supported by cDI	RRP41	AT3G61620	-1.54	-0.62	-3.89	0.006456	0.050644	-2.39
245755_at	hypothetical protein predicted by genem	---	AT1G35210	6.42	2.68	3.89	0.006456	0.050644	-2.39
250418_at	putative protein predicted proteins, Hon	---	AT5G11240	-1.84	-0.88	-3.89	0.006467	0.050708	-2.40
252953_at	putative phosphatidylinositol synthase p	PIS2	AT4G38570	-1.35	-0.44	-3.89	0.006472	0.050730	-2.40
263134_at	dTDP-glucose 4,6-dehydratase, putativ	RHM1	AT1G78570	1.56	0.65	3.89	0.006474	0.050733	-2.40
244944_s_a	ribosomal protein L16	---	---	-1.57	-0.65	-3.89	0.006484	0.050752	-2.40
247721_at	elongin - like protein elongin C, Drosopl	---	AT5G59140	-1.28	-0.36	-3.89	0.006483	0.050752	-2.40
255500_at	NAD+ ADP-ribosyltransferase	APP	AT4G02390	-1.49	-0.58	-3.89	0.006486	0.050752	-2.40
248009_at	transcription factor-like; similar to CH6 a	CSN6A	AT5G56280	-1.36	-0.44	-3.89	0.006483	0.050752	-2.40
254955_at	putative protein RNA polymerase II tran	KELP	AT4G10920	-1.33	-0.41	-3.88	0.006525	0.051005	-2.41
262532_at	hypothetical protein predicted by gensca	---	AT1G17210	-1.37	-0.45	-3.88	0.006522	0.051005	-2.40
246895_at	putative protein predicted protein, Arabi	CID6	AT5G25540	1.34	0.42	3.88	0.006525	0.051005	-2.41
255093_s_a	putative microfibril-associated protein	---	AT4G08580 /	-1.30	-0.38	-3.88	0.006528	0.051016	-2.41
248938_at	receptor-like protein kinase	---	AT5G45780	-1.31	-0.39	-3.88	0.00654	0.051091	-2.41
262056_at	Expressed protein ; supported by full-ler	---	AT1G80245	-1.39	-0.47	-3.88	0.006555	0.051133	-2.41
253095_at	putative protein ribonuclease III, Bacillu	---	AT4G37510	-1.38	-0.46	-3.88	0.00655	0.051133	-2.41
252981_at	putative protein gene T10 protein - mou	---	AT4G38260	1.52	0.60	3.88	0.006549	0.051133	-2.41
267471_at	putative ferrochelatase precusor ; supp	FC2	AT2G30390	-1.71	-0.77	-3.88	0.006554	0.051133	-2.41
264738_at	unknown protein contains similarity to pe	---	AT1G62250	-1.46	-0.55	-3.88	0.006562	0.051175	-2.41
254013_at	putative leucine-rich-repeat protein leuc	---	AT4G26050	1.59	0.67	3.88	0.006566	0.051189	-2.41
247498_at	peroxisomal Ca-dependent solute carrie	---	AT5G61810	-1.50	-0.58	-3.88	0.006572	0.051214	-2.41
250071_at	putative protein similar to unknown prote	---	AT5G18000	1.29	0.37	3.87	0.00658	0.051261	-2.41
255657_at	acidic ribosomal protein p1 similar to aci	---	AT4G00810	-1.43	-0.51	-3.87	0.006586	0.051287	-2.41
261337_at	unknown protein ; supported by cDNA: g	---	AT1G44810	-1.76	-0.81	-3.87	0.006595	0.051292	-2.42
265664_at	unknown protein predicted by genscan;	---	AT2G24420	-1.43	-0.52	-3.87	0.006593	0.051292	-2.42
252174_at	putative protein APRIL protein, Homo s	---	AT3G50690	-1.30	-0.38	-3.87	0.006594	0.051292	-2.42
254388_at	Expressed protein ; supported by full-ler	MSRB2	AT4G21860	-1.36	-0.45	-3.87	0.006591	0.051292	-2.42
264975_at	hypothetical protein predicted by genem	---	AT1G27070	-1.37	-0.46	-3.87	0.006598	0.051292	-2.42
261610_at	hypothetical protein predicted by genem	---	AT1G49560	-1.68	-0.75	-3.87	0.006608	0.051337	-2.42
260434_at	hypothetical protein predicted by gensca	---	AT1G68330	1.66	0.73	3.87	0.006606	0.051337	-2.42
266188_at	unknown protein	---	AT2G39000	-1.43	-0.51	-3.87	0.006616	0.051380	-2.42
251139_at	cell division - like protein JM23 protein,	---	AT5G01230	-1.46	-0.55	-3.87	0.006634	0.051503	-2.42

261218_at	ferredoxin--NADP reductase precursor,	FNR2	AT1G20020	-1.66	-0.73	-3.87	0.006637	0.051514	-2.42
263371_at	unknown protein ;supported by full-leng	NOP10	AT2G20490	-1.48	-0.56	-3.87	0.006652	0.051554	-2.43
265521_at	hypothetical protein predicted by gensca	ORG4	AT2G06010	-1.44	-0.53	-3.87	0.006654	0.051554	-2.43
262933_at	polyamine oxidase, putative similar to p	ATPAO4	AT1G65840	1.67	0.74	3.87	0.006647	0.051554	-2.42
248961_at	subtilisin-like protease	---	AT5G45650	-2.48	-1.31	-3.87	0.006647	0.051554	-2.42
256251_at	hypothetical protein predicted by genem	---	AT3G11330	1.50	0.58	3.87	0.006653	0.051554	-2.43
265597_at	Expressed protein ; supported by cDNA	---	AT2G20142	2.66	1.41	3.86	0.006662	0.051596	-2.43
255821_at	putative initiator tRNA phosphoribosyl-tr	---	AT2G40570	-1.37	-0.46	-3.86	0.006665	0.051608	-2.43
263252_at	putative CONSTANS-like B-box zinc fing	STH	AT2G31380	-1.68	-0.74	-3.86	0.006679	0.051698	-2.43
248442_at	DEAD-box protein abstrakt	---	AT5G51280	-1.45	-0.53	-3.86	0.00669	0.051720	-2.43
257661_at	unknown protein contains Pfam profile:	---	AT3G13340	-1.27	-0.35	-3.86	0.006693	0.051720	-2.43
261002_at	hypothetical protein contains similarity to	---	AT1G26520	-1.36	-0.44	-3.86	0.006687	0.051720	-2.43
261644_s_a	hypothetical protein contains similarity to	ATCSA-1	AT1G19750 /	-1.40	-0.49	-3.86	0.006693	0.051720	-2.43
261946_at	unknown protein	---	AT1G64560	-1.46	-0.55	-3.86	0.006691	0.051720	-2.43
245316_at	hypothetical protein ;supported by full-le	---	AT4G14000	-1.39	-0.47	-3.86	0.006702	0.051736	-2.43
260415_at	putative protein kinase similar to protein	---	AT1G69790	1.74	0.80	3.86	0.006702	0.051736	-2.43
259447_s_a	ADP-ribosylation factor, putative similar	ATARFD1/	AT1G02430 /	1.35	0.43	3.86	0.006701	0.051736	-2.43
248289_at	unknown protein ; supported by cDNA:	---	AT5G52880	-1.33	-0.41	-3.86	0.006706	0.051739	-2.43
251834_at	ribosomal protein L35 -like various ribos	---	AT3G55170	-1.34	-0.43	-3.86	0.006707	0.051739	-2.43
259428_at	MAP kinase, putative similar to MAP kir	ATMPK11	AT1G01560	4.95	2.31	3.86	0.006727	0.051876	-2.44
262802_at	putative cell division control protein, cdc	CDKB2;2	AT1G20930	1.28	0.36	3.85	0.006746	0.052002	-2.44
250110_at	putative protein many predicted protein	---	AT5G15350	2.14	1.10	3.85	0.006755	0.052013	-2.44
246831_at	hexose transporter - like protein hexose	MSS1	AT5G26340	1.71	0.77	3.85	0.006752	0.052013	-2.44
267044_at	nodulin-like protein	---	AT2G34357	-1.72	-0.78	-3.85	0.006759	0.052013	-2.44
255444_at	LUMINIDEPENDENS protein ; supporte	LD	AT4G02560	-1.35	-0.43	-3.85	0.006757	0.052013	-2.44
250999_at	putative protein predicted proyeins, Ara	---	AT5G02630	1.51	0.60	3.85	0.006751	0.052013	-2.44
265817_at	histone H1 ;supported by full-length cDI	HIS1-3	AT2G18050	-2.30	-1.20	-3.85	0.006765	0.052021	-2.44
255319_at	putative disease resistance protein simil	AtRLP46	AT4G04220	1.92	0.94	3.85	0.006764	0.052021	-2.44
259587_at	unknown protein ;supported by full-lengt	---	AT1G28120	-1.38	-0.46	-3.85	0.006767	0.052021	-2.44
257299_at	unknown protein ;supported by full-leng	---	AT3G28050	-1.41	-0.50	-3.85	0.006792	0.052138	-2.45
248669_at	putative protein contains similarity to sal	---	AT5G48730	-1.58	-0.66	-3.85	0.006803	0.052138	-2.45
255688_at	putative RNA helicase similar to ATP-de	---	AT4G00660	-1.35	-0.43	-3.85	0.006805	0.052138	-2.45
263975_at	hypothetical protein predicted by genefir	---	AT2G42710	-1.40	-0.48	-3.85	0.006794	0.052138	-2.45
245341_at	Expressed protein ; supported by full-ler	---	AT4G16447	-2.31	-1.21	-3.85	0.006802	0.052138	-2.45
263963_at	putative DNA-binding protein RAV2	---	AT2G36080	1.59	0.67	3.85	0.006804	0.052138	-2.45

250322_at	putative transcription factor (MYB46)	MYB46	AT5G12870	1.28	0.36	3.85	0.006803	0.052138	-2.45
245285_s_a	selenium-binding protein like ; supporte	SBP1	AT4G14030 /	-1.33	-0.41	-3.85	0.00679	0.052138	-2.45
267421_at	putative phosphoribosylaminoimidazole	---	AT2G35040	-1.48	-0.57	-3.85	0.006791	0.052138	-2.45
251963_at	protein kinase (AME2/AFC1) ; supporte	AFC1	AT3G53570	-1.32	-0.41	-3.85	0.006789	0.052138	-2.45
247918_at	putative protein contains similarity to pr	---	AT5G57610	-1.48	-0.57	-3.85	0.006816	0.052188	-2.45
264361_at	unknown protein Strong similarity to T08	---	AT1G03300	-1.37	-0.46	-3.85	0.006814	0.052188	-2.45
252411_at	putative protein PMP31 protein - Candi	PEX11B	AT3G47430	-1.90	-0.92	-3.85	0.006826	0.052215	-2.45
248402_at	dihydrodipicolinate reductase-like protei	crr1	AT5G52100	-1.68	-0.75	-3.85	0.006826	0.052215	-2.45
264019_at	cyclophilin (CYP2) Same as GB: AF020	---	AT2G21130	-1.46	-0.55	-3.85	0.006823	0.052215	-2.45
248625_at	3-keto-acyl-CoA thiolase 2 (gb|AAC178	PKT2	AT5G48880	-1.88	-0.91	-3.84	0.006837	0.052280	-2.45
246368_at	light repressible receptor protein kinase	---	AT1G51890	2.67	1.42	3.84	0.006845	0.052325	-2.46
256754_at	unknown protein	CHUP1	AT3G25690	-1.41	-0.49	-3.84	0.006851	0.052355	-2.46
264211_at	putative gigantea protein strong similarit	GI	AT1G22770	-1.29	-0.37	-3.84	0.006865	0.052422	-2.46
264331_at	hypothetical protein contains non-conse	---	AT1G04130	-1.36	-0.45	-3.84	0.006863	0.052422	-2.46
267279_at	hypothetical protein predicted by genefi	---	AT2G19460	1.96	0.97	3.84	0.006873	0.052452	-2.46
261062_at	transcription factor scarecrow-like 14, p	SCL14	AT1G07530	-1.35	-0.43	-3.84	0.006872	0.052452	-2.46
254318_at	putative protein embryo-abundant prote	---	AT4G22530	3.13	1.65	3.84	0.006889	0.052555	-2.46
253897_at	putative protein	---	AT4G27120	-1.33	-0.41	-3.84	0.006892	0.052557	-2.46
267057_at	hypothetical protein predicted by gensca	---	AT2G32500	-2.12	-1.09	-3.84	0.006894	0.052558	-2.46
261277_at	hypothetical protein predicted by gensca	---	AT1G20230	-1.43	-0.52	-3.84	0.006899	0.052558	-2.46
261268_at	unknown protein similar to 50S ribosom	---	AT1G26740	-1.42	-0.51	-3.84	0.006898	0.052558	-2.46
247931_at	putative protein similar to unknown prote	---	AT5G57040	-1.46	-0.54	-3.84	0.006912	0.052626	-2.47
252562_s_a	Histone H4 - like protein histone H4, Ze	---	AT3G45930 /	-1.37	-0.45	-3.84	0.006912	0.052626	-2.47
261319_at	phytochrome A supressor spa1, putativ	SPA4	AT1G53090	-1.26	-0.33	-3.83	0.006935	0.052771	-2.47
262181_at	xylosidase, putative similar to xylosidas	---	AT1G78060	-2.20	-1.14	-3.83	0.006936	0.052771	-2.47
251163_at	putative protein S1R protein - Homo sa	---	AT3G63310	1.28	0.35	3.83	0.006939	0.052777	-2.47
246912_at	putative protein various predicted prote	---	AT5G25820	2.21	1.14	3.83	0.006953	0.052869	-2.47
246984_at	cytochrome P450	CYP81G1	AT5G67310	2.97	1.57	3.83	0.006961	0.052876	-2.47
249592_at	putative protein SIAH1 protein, Brassica	---	AT5G37890	-1.43	-0.52	-3.83	0.006961	0.052876	-2.47
265461_at	unknown protein similarity to ubiquitin fa	---	AT2G46500	1.36	0.44	3.83	0.006959	0.052876	-2.47
260688_at	hypothetical protein similar to dehydroge	---	AT1G17665	-1.39	-0.48	-3.83	0.006975	0.052942	-2.48
251866_at	putative protein MSP58 - nucleolar prot	emb1967	AT3G54350	-1.30	-0.38	-3.83	0.006974	0.052942	-2.48
261572_at	unknown protein	---	AT1G01170	-1.43	-0.52	-3.83	0.006979	0.052947	-2.48
257533_at	putative alpha/beta hydrolase contains F	---	AT3G10840	-1.71	-0.78	-3.83	0.00698	0.052947	-2.48
259819_at	unknown protein ; supported by cDNA: g	ATMTK	AT1G49820	-1.28	-0.36	-3.83	0.006991	0.052998	-2.48

263583_at	putative NAD+ dependent isocitrate del	IDH2	AT2G17130	1.59	0.67	3.83	0.006991	0.052998	-2.48
251959_at	putative protein KIAA0544 protein, Hom	---	AT3G53410	-1.33	-0.41	-3.83	0.006994	0.053000	-2.48
247478_at	DC1.2 homologue - like protein DC1.2 I	---	AT5G62360	-2.61	-1.38	-3.82	0.007014	0.053040	-2.48
251740_at	peptidylprolyl isomerase	ROC2	AT3G56070	-1.86	-0.90	-3.82	0.007021	0.053040	-2.48
261844_at	hypothetical protein predicted by genem	---	AT1G15940	-1.69	-0.76	-3.82	0.007007	0.053040	-2.48
264205_at	hypothetical protein identical to hypothe	---	AT1G22790	-1.30	-0.38	-3.82	0.007022	0.053040	-2.48
258260_at	unknown protein ; supported by cDNA:	---	AT3G26850	-1.31	-0.39	-3.82	0.007022	0.053040	-2.48
253836_at	putative protein hypothetical protein F2	---	AT4G27840	-1.35	-0.43	-3.83	0.007003	0.053040	-2.48
254463_at	putative protein transcription initiation fa	TAF11	AT4G20280	-1.44	-0.52	-3.82	0.007016	0.053040	-2.48
262668_at	flavin-containing amine oxidase contains	LDL1	AT1G62830	-1.37	-0.45	-3.82	0.007006	0.053040	-2.48
262984_at	hypothetical protein predicted by genem	---	AT1G54460	1.77	0.82	3.82	0.00701	0.053040	-2.48
264000_at	putative mitochondrial dicarboxylate car	UCP5	AT2G22500	3.16	1.66	3.82	0.007021	0.053040	-2.48
246844_at	transcription factor ATMYB4 ; supporte	ATMYB86	AT5G26660	1.43	0.51	3.82	0.00703	0.053082	-2.48
253364_at	F-box protein family, AtFBX13 cotains s	---	AT4G33160	1.28	0.36	3.82	0.007038	0.053106	-2.49
253417_at	putative protein	PC-MYB1	AT4G32730	1.35	0.43	3.82	0.007036	0.053106	-2.48
250545_at	serine/threonine protein kinase ;suppor	ATPK3	AT5G08160	1.31	0.39	3.82	0.007042	0.053119	-2.49
267353_at	En/Spm-like transposon protein related	---	AT2G40070	-1.47	-0.56	-3.82	0.007045	0.053119	-2.49
261507_at	RIBOSOMAL PROTEIN, putative simila	---	AT1G71720	-1.34	-0.42	-3.82	0.007052	0.053143	-2.49
249685_at	putative protein similar to unknown prote	CCB3	AT5G36120	-1.30	-0.38	-3.82	0.007052	0.053143	-2.49
258896_at	putative syntaxin protein, AtSNAP33 sir	SYP43	AT3G05710	1.39	0.47	3.82	0.007058	0.053166	-2.49
263517_at	unknown protein ;supported by full-leng	RD2	AT2G21620	1.60	0.67	3.82	0.00707	0.053243	-2.49
249001_at	putative protein strong similarity to unkn	---	AT5G44990	2.70	1.43	3.82	0.007078	0.053280	-2.49
253942_at	putative protein	---	AT4G27010	-1.65	-0.72	-3.82	0.007082	0.053281	-2.49
254562_at	cytochrome P450 cytochrome P450, Ar	CYP707A1	AT4G19230	2.06	1.04	3.82	0.007082	0.053281	-2.49
250133_at	thioredoxin f2 (gb|AAD35004.1) ; suppo	TRXF2	AT5G16400	-1.75	-0.80	-3.81	0.0071	0.053354	-2.49
258223_at	unknown protein ; supported by cDNA:	PIFI	AT3G15840	-1.41	-0.50	-3.81	0.007099	0.053354	-2.49
247177_at	unknown protein ; supported by cDNA: g	---	AT5G65300	2.60	1.38	3.81	0.007101	0.053354	-2.49
264250_at	gamma glutamyl hydrolase, putative sir	ATGGH2	AT1G78680	-1.41	-0.50	-3.81	0.007099	0.053354	-2.49
262348_at	unknown protein similar to transcription	---	AT2G48160	-1.31	-0.39	-3.81	0.007106	0.053375	-2.50
258663_at	hypothetical protein	---	AT3G08670	-1.30	-0.38	-3.81	0.007113	0.053400	-2.50
266668_at	hypothetical protein predicted by grail	---	AT2G29760	-1.85	-0.89	-3.81	0.007115	0.053400	-2.50
247676_at	putative protein RNaseP protein p30, M	---	AT5G59980	-1.71	-0.78	-3.81	0.007126	0.053469	-2.50
250335_at	lysophospholipase - like protein lysopho	---	AT5G11650	1.67	0.74	3.81	0.007136	0.053527	-2.50
261725_at	small nuclear ribonucleoprotein, putativ	SmD3	AT1G76300	-1.52	-0.60	-3.81	0.00714	0.053539	-2.50
254679_at	putative protein Mei2-like protein, Arabi	AML3	AT4G18120	-1.37	-0.45	-3.81	0.007146	0.053546	-2.50

267637_at	unknown protein predicted by genscan;	---	AT2G42190	-1.59	-0.67	-3.81	0.007145	0.053546	-2.50
257291_at	DNA-binding protein, putative similar to	---	AT3G15590	-1.98	-0.99	-3.81	0.007157	0.053593	-2.50
246632_at	hypothetical protein similar to putative s	---	AT1G29710	-1.38	-0.47	-3.81	0.007156	0.053593	-2.50
250540_at	unknown protein ; supported by cDNA:	---	AT5G08580	-1.53	-0.62	-3.81	0.00716	0.053600	-2.50
253835_at	putative beta-glucosidase beta-glucosid	BGLU9	AT4G27820	-1.41	-0.50	-3.81	0.007165	0.053616	-2.50
252459_s_a	1-phosphatidylinositol-4,5-bisphosphate	PLC9	AT3G47220 /	1.30	0.38	3.81	0.007178	0.053698	-2.51
267309_at	Expressed protein ; supported by full-ler	---	AT2G19385	-1.57	-0.65	-3.81	0.007181	0.053703	-2.51
244999_at	RNA polymerase beta subunit	---	---	-1.63	-0.71	-3.80	0.007184	0.053711	-2.51
253233_at	putative protein various predicted protei	---	AT4G34290	-1.67	-0.74	-3.80	0.00719	0.053739	-2.51
257828_at	unknown protein	---	AT3G26670	1.72	0.79	3.80	0.007213	0.053893	-2.51
260264_at	hypothetical protein predicted by genefi	---	AT1G68500	-1.54	-0.62	-3.80	0.00722	0.053922	-2.51
255786_at	unknown protein contains similarity to cl	ATCLH1	AT1G19670	-2.13	-1.09	-3.80	0.007223	0.053932	-2.51
263783_at	putative WRKY-type DNA binding protei	WRKY46	AT2G46400	3.62	1.86	3.80	0.00723	0.053966	-2.51
264678_at	putative U2 small nuclear ribonucleopro	U2A'	AT1G09760	-1.36	-0.45	-3.80	0.007236	0.053988	-2.51
259762_at	hypothetical protein predicted by gensca	---	AT1G77600	-1.40	-0.48	-3.80	0.007238	0.053988	-2.51
255495_at	predicted protein of unknown function s	---	AT4G02720	-1.35	-0.44	-3.80	0.007253	0.054082	-2.52
264286_at	unknown protein ;supported by full-lengt	PPR336	AT1G61870	-1.71	-0.77	-3.79	0.007282	0.054129	-2.52
257178_at	hemolysin-like protein similar to hemoly	---	AT3G13070	1.39	0.48	3.80	0.007274	0.054129	-2.52
259140_at	lycopene beta cyclase identical to lycop	LYC	AT3G10230	-1.31	-0.39	-3.79	0.007283	0.054129	-2.52
247822_at	putative protein sorting nexin 2, Homo s	SNX2a	AT5G58440	-1.43	-0.51	-3.79	0.00728	0.054129	-2.52
260735_at	disease resistance protein, putative sim	---	AT1G17610	1.80	0.85	3.79	0.007284	0.054129	-2.52
248633_at	arginine methyltransferase-like protein	PRMT4A	AT5G49020	-1.39	-0.47	-3.80	0.007262	0.054129	-2.52
250137_at	rRNA methylase - like protein rRNA me	---	AT5G15390	-1.36	-0.44	-3.79	0.007285	0.054129	-2.52
254320_at	putative protein various predicted prote	---	AT4G22580	-1.30	-0.38	-3.80	0.007274	0.054129	-2.52
254432_at	reticuline oxidase -like protein reticuline	---	AT4G20830 /	2.73	1.45	3.80	0.007268	0.054129	-2.52
257367_at	hypothetical protein predicted by gensca	---	AT2G25780	-1.37	-0.45	-3.79	0.007283	0.054129	-2.52
249312_at	disease resistance protein-like	---	AT5G41550	1.48	0.56	3.80	0.007264	0.054129	-2.52
263048_s_a	unknown protein ;supported by full-leng	---	AT2G05310 /	-1.43	-0.51	-3.79	0.007292	0.054164	-2.52
256011_at	respiratory burst oxidase protein, putati	---	AT1G19230	1.36	0.44	3.79	0.007296	0.054172	-2.52
264832_at	unknown unknown	---	AT1G03660	1.50	0.59	3.79	0.007299	0.054172	-2.52
267072_at	unknown protein	---	AT2G41170	1.45	0.54	3.79	0.007303	0.054172	-2.52
248615_at	putative protein contains similarity to pe	AtPNG1	AT5G49570	1.64	0.71	3.79	0.007302	0.054172	-2.52
249318_at	uridine kinase-like protein	AtUK/UPR	AT5G40870	-1.35	-0.43	-3.79	0.007308	0.054177	-2.52
245421_at	hypothetical protein	---	AT4G17430	-1.28	-0.36	-3.79	0.007308	0.054177	-2.52
253585_at	putative protein hypothetical protein - S	---	AT4G30720	-1.32	-0.40	-3.79	0.007323	0.054233	-2.53

250678_at	selenium-binding protein-like	---	AT5G06540	-1.30	-0.38	-3.79	0.007319	0.054233	-2.53
249408_at	myb-related protein	MYB23	AT5G40330	-1.44	-0.52	-3.79	0.007323	0.054233	-2.53
253117_at	Expressed protein ; supported by full-ler	---	AT4G35905	-1.46	-0.55	-3.79	0.007343	0.054365	-2.53
266127_s_a	putative mitochondrial translation elonga	---	AT1G45332 /	-1.53	-0.62	-3.79	0.007366	0.054439	-2.53
252619_at	putative protein several hypothetical pro	---	AT3G45210	-1.77	-0.82	-3.79	0.007367	0.054439	-2.53
266152_s_a	hypothetical protein predicted by gensca	---	AT2G12050 /	1.30	0.38	3.79	0.00736	0.054439	-2.53
251576_at	putative protein several hypothetical pro	---	AT3G58200	-1.32	-0.40	-3.79	0.007361	0.054439	-2.53
247793_at	putative protein ; supported by cDNA: g	PSY1	AT5G58650	1.57	0.65	3.79	0.007363	0.054439	-2.53
259906_at	unknown protein	---	AT1G74120	-1.30	-0.38	-3.79	0.007366	0.054439	-2.53
248046_at	receptor protein kinase-like protein	---	AT5G56040	-1.51	-0.60	-3.78	0.007376	0.054478	-2.53
262199_at	unknown protein ; supported by cDNA: g	---	AT1G53800	-1.51	-0.60	-3.78	0.007379	0.054478	-2.54
AFFX-r2-Bs	B. subtilis /GEN=dapB /DB_XREF=gb:L	---	---	-1.86	-0.90	-3.78	0.00738	0.054478	-2.54
258853_at	unknown protein similar to GB:AAD552	---	AT3G06440	-1.34	-0.42	-3.78	0.007389	0.054510	-2.54
253115_at	putative protein ;supported by full-lengt	---	AT4G35910	-1.32	-0.40	-3.78	0.007389	0.054510	-2.54
256043_at	hypothetical protein contains Pfam profil	---	AT1G07210	-1.57	-0.65	-3.78	0.007395	0.054536	-2.54
257702_at	CTP-synthetase, putative similar to CTP	emb2742	AT3G12670	-1.42	-0.51	-3.78	0.007423	0.054724	-2.54
261431_at	Myb-related transcription factor mixta, p	AtMYB47	AT1G18710	-2.74	-1.45	-3.78	0.007442	0.054793	-2.54
255243_at	putative protein hypothetical protein - A	---	AT4G05590	1.34	0.42	3.78	0.007443	0.054793	-2.54
250966_at	putative protein various predicted prote	---	AT5G02910	-1.44	-0.53	-3.78	0.007436	0.054793	-2.54
266051_at	rhodanese-like family protein	---	AT2G40760	-1.54	-0.62	-3.78	0.00744	0.054793	-2.54
250029_at	galactose-1-phosphate uridyl transferas	---	AT5G18200	-1.44	-0.52	-3.78	0.007444	0.054793	-2.54
255838_at	unknown protein	---	AT2G33490	1.33	0.41	3.78	0.007451	0.054826	-2.55
250745_at	putative protein strong similarity to unkn	---	AT5G05850	1.59	0.67	3.77	0.007465	0.054913	-2.55
251330_at	putative protein putative protein At2g461	---	AT3G61550	1.55	0.63	3.77	0.007469	0.054925	-2.55
267056_at	hypothetical protein predicted by gensca	---	AT2G32470	1.49	0.57	3.77	0.007475	0.054948	-2.55
245719_at	DNA gyrase subunit B - like protein	---	AT5G04110	-1.33	-0.41	-3.77	0.007488	0.055027	-2.55
248932_at	peptide transporter	PTR3	AT5G46050	3.06	1.61	3.77	0.007496	0.055067	-2.55
260746_at	glutathione transferase, putative similar	ATGSTU1	AT1G78380	1.36	0.45	3.77	0.007502	0.055086	-2.55
253992_at	putative protein ;supported by full-lengt	---	AT4G26060	1.37	0.46	3.77	0.007503	0.055086	-2.55
250546_at	nhp2-like protein high mobility group-like	---	AT5G08180	-1.84	-0.88	-3.77	0.007507	0.055096	-2.55
247652_at	histone H2B - like protein histone H2B,	HTB4	AT5G59910	-1.45	-0.54	-3.77	0.007517	0.055150	-2.55
253543_at	hypothetical protein	---	AT4G31270	-1.34	-0.42	-3.77	0.007528	0.055215	-2.56
264575_at	putative chloroplast 50S ribosomal prot	emb2394	AT1G05190	-1.36	-0.44	-3.77	0.007538	0.055248	-2.56
250489_s_a	putative protein predicted proteins, Arat	---	AT5G09710 /	1.42	0.51	3.77	0.007536	0.055248	-2.56
262072_at	hypothetical protein predicted by genem	ZCF37	AT1G59590	2.15	1.11	3.77	0.007546	0.055295	-2.56

252759_at	putative protein hypothetical proteins - A	---	AT3G42630	-1.27	-0.34	-3.76	0.007566	0.055421	-2.56
246904_at	DNA methyltransferase PMT1 - like pro	DNMT2	AT5G25480	-1.42	-0.50	-3.76	0.007584	0.055516	-2.56
252586_at	dof6 zinc finger protein	---	AT3G45610	1.38	0.46	3.76	0.007583	0.055516	-2.56
264645_at	unknown protein Similar to Saccharomy	---	AT1G08940	2.52	1.33	3.76	0.007597	0.055585	-2.57
251593_at	DNA-directed RNA polymerase I 190K	NRPA1	AT3G57660	-1.66	-0.73	-3.76	0.007598	0.055585	-2.57
253706_at	putative protein D-threonine dehydroge	---	AT4G29120	-1.33	-0.41	-3.76	0.007607	0.055631	-2.57
248611_at	putative protein contains similarity to WF	WRKY48	AT5G49520	2.63	1.39	3.76	0.00763	0.055783	-2.57
266813_at	unknown protein	---	AT2G44920	-1.45	-0.53	-3.76	0.007639	0.055832	-2.57
260228_at	putative cytochrome P450 similar to cyt	CYP98A8	AT1G74540	1.36	0.44	3.76	0.007646	0.055862	-2.57
253381_at	Tic22 -like protein strong homology to T	---	AT4G33350	-1.40	-0.49	-3.75	0.007668	0.056005	-2.58
262612_at	unknown protein location of ESTs 144D	---	AT1G14150	-2.15	-1.10	-3.75	0.007687	0.056126	-2.58
263287_at	Expressed protein ; supported by full-ler	---	AT2G36145	-2.35	-1.23	-3.75	0.007692	0.056143	-2.58
263104_at	unknown protein	---	AT2G05120	-1.39	-0.48	-3.75	0.0077	0.056188	-2.58
249025_at	putative protein contains similarity to unl	---	AT5G44720	-1.74	-0.80	-3.75	0.007709	0.056235	-2.58
247327_at	peroxidase (emb|CAA67551.1) ;suppor	---	AT5G64120	3.79	1.92	3.75	0.007712	0.056237	-2.58
259008_at	metallothionein-like protein similar to me	MT2A	AT3G09390	1.39	0.48	3.75	0.007719	0.056251	-2.58
259193_at	putative thylakoid lumen rotamase simil	CYP38	AT3G01480	-1.54	-0.63	-3.75	0.007717	0.056251	-2.58
260269_at	putative disease resistance protein simil	---	AT1G63740	1.44	0.52	3.75	0.007734	0.056343	-2.58
250181_at	tRNA synthase - like protein tRNA pseu	---	AT5G14460	-1.36	-0.45	-3.75	0.00774	0.056350	-2.59
255401_at	hypothetical protein ;supported by full-le	---	AT4G03600	-1.44	-0.53	-3.75	0.007739	0.056350	-2.59
245629_at	hypothetical protein predicted by genem	---	AT1G56580	-1.49	-0.57	-3.74	0.007755	0.056359	-2.59
253424_at	putative protein ; supported by cDNA: gi	---	AT4G32330	-1.45	-0.54	-3.74	0.007756	0.056359	-2.59
254360_at	CDP-diacylglycerol synthetase-like prot	---	AT4G22340	-1.33	-0.42	-3.75	0.007751	0.056359	-2.59
262517_at	putative glutathione transferase Second	ATGSTU2	AT1G17180	5.78	2.53	3.75	0.007745	0.056359	-2.59
248285_at	putative protein similar to unknown prote	---	AT5G52960	-1.26	-0.33	-3.75	0.007752	0.056359	-2.59
245354_at	Lil3 protein ;supported by full-length cDI	LIL3:1	AT4G17600	-1.42	-0.50	-3.75	0.007753	0.056359	-2.59
252608_at	putative protein 2-phosphoglycerate kin	---	AT3G45090	1.39	0.48	3.74	0.007758	0.056359	-2.59
261005_at	hypothetical protein similar to reticuline	---	AT1G26420	2.34	1.23	3.74	0.007767	0.056379	-2.59
254574_at	expressed protein supported by cDNA:	---	AT4G19430	-3.36	-1.75	-3.74	0.007768	0.056379	-2.59
262368_at	unknown protein ;supported by full-lengt	---	AT1G73060 /	-1.63	-0.71	-3.74	0.007769	0.056379	-2.59
265193_at	unknown protein ESTs gb|T144077 and	---	AT1G05070	-1.32	-0.40	-3.74	0.007773	0.056395	-2.59
260073_at	putative protein kinase contains Pfam pr	---	AT1G73660	-1.48	-0.56	-3.74	0.007777	0.056408	-2.59
265104_at	unknown protein 3'-end of protein conta	ATO2	AT1G31020	-1.35	-0.44	-3.74	0.00778	0.056408	-2.59
264048_at	unknown protein	---	AT2G22400	-1.54	-0.63	-3.74	0.007791	0.056453	-2.59
249304_at	folylpolyglutamate synthase-like protein	GLA1	AT5G41480	-1.49	-0.58	-3.74	0.007791	0.056453	-2.59

252991_at	protein kinase like protein protein kinas	---	AT4G38470	2.66	1.41	3.74	0.007813	0.056594	-2.60
263797_at	putative WRKY-type DNA binding protei	WRKY17	AT2G24570	2.85	1.51	3.74	0.007817	0.056602	-2.60
262135_at	AP2 domain containing protein, putative	RAP2.4	AT1G78080	1.81	0.85	3.74	0.007837	0.056735	-2.60
250250_at	putative protein similar to unknown prote	---	AT5G13610	-1.38	-0.46	-3.74	0.007847	0.056753	-2.60
250695_at	lectin-like protein kinase	---	AT5G06740	2.32	1.21	3.74	0.007844	0.056753	-2.60
262408_at	protein phosphatase type 2C, putative s	---	AT1G34750	2.02	1.01	3.74	0.007847	0.056753	-2.60
262636_at	DEIH-box RNA/DNA helicase identical t	NIH	AT1G06670	-1.42	-0.50	-3.73	0.007857	0.056801	-2.60
251892_at	putative protein	WRI1	AT3G54320	-1.52	-0.61	-3.73	0.007866	0.056852	-2.60
247453_at	putative protein similar to unknown prote	---	AT5G62440	-1.47	-0.56	-3.73	0.007871	0.056854	-2.60
255967_at	protein phosphatase type 2C, putative s	---	AT1G22280	1.44	0.53	3.73	0.007871	0.056854	-2.60
246405_at	disease resistance protein RPP1-WsB,	---	AT1G57630	4.70	2.23	3.73	0.007881	0.056905	-2.60
255614_at	putative myb-related DNA-binding prote	---	AT4G01280	-1.32	-0.40	-3.73	0.007899	0.057015	-2.61
259085_at	unknown protein similar to GB:CAB0554	---	AT3G05000	-1.35	-0.43	-3.73	0.007905	0.057025	-2.61
267448_at	putative protein phosphatase 2C	---	AT2G33700	1.27	0.35	3.73	0.007904	0.057025	-2.61
259082_at	unknown protein similar to hypothetical	---	AT3G04820	-1.65	-0.72	-3.73	0.007916	0.057084	-2.61
253973_at	Expressed protein ; supported by cDNA	---	AT4G26555	-1.25	-0.32	-3.73	0.007927	0.057126	-2.61
251645_at	putative protein polygalacturonase (EC	---	AT3G57790	-1.39	-0.47	-3.73	0.007929	0.057126	-2.61
252131_at	BCS1 protein-like protein Homo sapien	BCS1	AT3G50930	4.12	2.04	3.73	0.007926	0.057126	-2.61
258461_at	hypothetical protein predicted by genefi	---	AT3G17340	1.29	0.37	3.73	0.007932	0.057129	-2.61
254431_at	reticuline oxidase - like protein reticuline	---	AT4G20840	-1.64	-0.71	-3.73	0.007948	0.057228	-2.61
261954_at	plastid ribosomal protein S6, putative si	---	AT1G64510	-1.35	-0.43	-3.72	0.00799	0.057510	-2.62
252156_at	BCS1 protein-like protein BCS1 protein	---	AT3G50940	-1.45	-0.54	-3.72	0.008007	0.057618	-2.62
265991_at	chloroplast single subunit DNA-depende	SCA3	AT2G24120	-1.69	-0.76	-3.72	0.008012	0.057632	-2.62
255785_at	sulfate adenylyltransferase identical to s	APS2	AT1G19920	-1.36	-0.45	-3.72	0.00803	0.057743	-2.62
246306_at	putative protein hypothetical proteins -	ATBAG4	AT3G51780	-1.26	-0.33	-3.72	0.008041	0.057768	-2.63
260841_at	Expressed protein ; supported by full-ler	---	AT1G29195	1.43	0.52	3.72	0.008039	0.057768	-2.63
265615_at	putative dioxygenase ; supported by cD	---	AT2G25450	1.41	0.50	3.72	0.008036	0.057768	-2.63
261650_at	envelope Ca2+-ATPase identical to env	ACA1	AT1G27770	1.71	0.78	3.72	0.008055	0.057848	-2.63
246134_at	protein kinase tousled ; supported by cI	TSL	AT5G20930	-1.44	-0.53	-3.71	0.008066	0.057876	-2.63
252055_at	putative ribosomal protein S14 ribosom	---	AT3G52580	-1.45	-0.53	-3.71	0.008063	0.057876	-2.63
260582_at	hypothetical protein predicted by genefi	---	AT2G47200	1.39	0.48	3.71	0.008065	0.057876	-2.63
245757_at	phosphate-induced (phi-1) protein, puta	PHI-1	AT1G35140	4.78	2.26	3.71	0.008071	0.057896	-2.63
253329_at	hypothetical protein	---	AT4G33480	-1.30	-0.37	-3.71	0.008082	0.057957	-2.63
262155_at	glycosyl transferase, putative similar to	---	AT1G52420	-1.40	-0.49	-3.71	0.008094	0.058022	-2.63
264318_at	putative beta-ketoacyl-CoA synthase St	KCS2	AT1G04220	1.80	0.85	3.71	0.008104	0.058057	-2.63

265900_at	unknown protein	---	AT2G25730	-1.25	-0.32	-3.71	0.008107	0.058057	-2.63
248868_at	putative protein similar to unknown prote	---	AT5G46780	1.95	0.96	3.71	0.008102	0.058057	-2.63
263934_at	hypothetical protein predicted by genefir	EDA12	AT2G35950	-1.27	-0.34	-3.71	0.00811	0.058061	-2.63
250647_at	putative protein contains similarity to unl	---	AT5G06770	-1.35	-0.44	-3.71	0.008124	0.058130	-2.64
249786_at	putative protein strong similarity to unkn	ABIL3	AT5G24310	-1.77	-0.82	-3.71	0.008126	0.058130	-2.64
264553_s_a	putative cinnamyl alcohol dehydrogena	---	AT1G09480 /	1.42	0.51	3.71	0.00813	0.058130	-2.64
258882_at	unknown protein ; supported by full-leng	---	AT3G06330	-1.37	-0.46	-3.71	0.008132	0.058130	-2.64
260163_at	putative carnitine/acylcarnitine transloca	BAC2	AT1G79900	2.52	1.33	3.71	0.008131	0.058130	-2.64
253920_at	histone H2A- like protein histone H2A.4	HTA2	AT4G27230	-1.56	-0.65	-3.71	0.008152	0.058233	-2.64
266811_at	unknown protein	---	AT2G44850	-1.32	-0.40	-3.71	0.008149	0.058233	-2.64
258282_at	unknown protein	---	AT3G26910	2.20	1.14	3.70	0.008165	0.058312	-2.64
253643_at	hypothetical protein ;supported by full-le	---	AT4G29780	2.89	1.53	3.70	0.008181	0.058405	-2.64
250472_at	putative protein	---	AT5G10210	1.47	0.56	3.70	0.008186	0.058427	-2.64
247510_at	putative protein predicted proteins, D.m	---	AT5G62030	-1.44	-0.53	-3.70	0.00819	0.058436	-2.65
256248_at	hypothetical protein	---	AT3G66652	-1.55	-0.63	-3.70	0.008201	0.058492	-2.65
261435_at	GTP-binding protein, putative similar to	---	AT1G07615 /	-1.66	-0.73	-3.70	0.008204	0.058499	-2.65
254764_at	putative protein ; supported by cDNA: g	---	AT4G13250	1.93	0.95	3.70	0.008209	0.058517	-2.65
258810_at	hypothetical protein similar to hypothetic	---	AT3G03970	1.39	0.48	3.70	0.008215	0.058530	-2.65
266240_at	putative RNA-binding protein ; supporte	---	AT2G29580	-1.26	-0.33	-3.70	0.008216	0.058530	-2.65
253688_at	putative protein ;supported by full-lengt	---	AT4G29590	-1.54	-0.63	-3.70	0.008229	0.058586	-2.65
258436_at	putative RING zinc finger protein similar	ATL2	AT3G16720	2.30	1.20	3.70	0.008228	0.058586	-2.65
254483_at	putative protein CRP1, Zea mays, PID:g	---	AT4G20740	-1.51	-0.59	-3.70	0.008241	0.058653	-2.65
264673_at	Expressed protein ; supported by full-ler	ATATP-PR	AT1G09795	-1.35	-0.43	-3.70	0.008254	0.058724	-2.65
259258_at	putative ribulose-1,5-bisphosphate carb	---	AT3G07670	-1.67	-0.74	-3.70	0.008259	0.058739	-2.65
245202_at	F12A21.14 similar to receptor protein ki	---	AT1G67720	-1.45	-0.54	-3.70	0.008264	0.058760	-2.65
265385_at	putative diacylglycerol kinase ;supporte	---	AT2G20900	1.68	0.75	3.69	0.008272	0.058795	-2.66
247277_at	putative protein similar to unknown prote	---	AT5G64420	-1.35	-0.44	-3.69	0.008284	0.058803	-2.66
252147_at	putative protein several hypothetical pro	---	AT3G51270	-1.56	-0.64	-3.69	0.008284	0.058803	-2.66
255138_at	extensin-like protein extensin class 1 pr	---	AT4G08380	1.30	0.37	3.69	0.008286	0.058803	-2.66
266318_at	Mutator-like transposase similar to MUF	FRS3	AT2G27110	-1.25	-0.32	-3.69	0.008276	0.058803	-2.66
245446_at	enoyl-CoA hydratase	---	AT4G16800	-1.36	-0.44	-3.69	0.00828	0.058803	-2.66
254204_at	putative protein CGI-58 protein - Homo	---	AT4G24160	1.90	0.93	3.69	0.008298	0.058871	-2.66
251663_at	putative protein hypothetical protein At2	---	AT3G57070	-1.34	-0.43	-3.69	0.008305	0.058889	-2.66
255627_at	Expressed protein ; supported by full-ler	---	AT4G00955	1.29	0.37	3.69	0.008305	0.058889	-2.66
252548_at	kinesin-related protein - like kinesin-rela	---	AT3G45850	-1.39	-0.47	-3.69	0.008314	0.058896	-2.66

248310_at	putative protein similar to unknown prote	CPuORF1	AT5G52550 /	-1.31	-0.39	-3.69	0.00831	0.058896	-2.66
252205_at	hypothetical protein various predicted p	---	AT3G50350	-1.47	-0.55	-3.69	0.008312	0.058896	-2.66
261646_at	putative lipase similar to hypothetical pr	---	AT1G27690	-1.35	-0.44	-3.69	0.008322	0.058930	-2.66
261122_at	ornithine carbamoyltransferase precurso	OTC	AT1G75330	-1.50	-0.59	-3.69	0.008327	0.058949	-2.66
246509_at	valine--tRNA ligase-like protein several I	EMB2247	AT5G16715	-1.63	-0.71	-3.69	0.008336	0.058999	-2.66
263678_at	hypothetical protein Similar to Babesia a	---	AT1G04420	-1.62	-0.70	-3.69	0.008345	0.059042	-2.67
251072_at	putative protein wound-inducible protein	---	AT5G01740	-1.85	-0.89	-3.69	0.008351	0.059065	-2.67
251522_at	hypothetical protein	---	AT3G59430	-1.38	-0.46	-3.69	0.008357	0.059088	-2.67
263200_at	hypothetical protein predicted by gensca	---	AT1G05600	-1.48	-0.57	-3.68	0.008377	0.059210	-2.67
262663_at	hypothetical protein identical to hypothe	---	AT1G13940	-1.38	-0.46	-3.68	0.00839	0.059287	-2.67
253114_at	GTP-binding protein GB2 ;supported by	ATGB2	AT4G35860	1.40	0.49	3.68	0.008406	0.059379	-2.67
260676_at	integral membrane protein, putative sim	---	AT1G19450	-1.77	-0.83	-3.68	0.008427	0.059511	-2.68
262640_at	hypothetical protein	---	AT1G62760	9.94	3.31	3.68	0.00846	0.059721	-2.68
263268_at	unknown protein	---	---	-1.35	-0.43	-3.68	0.008462	0.059721	-2.68
248693_at	regulator of chromosome condensation	---	AT5G48330	-1.55	-0.63	-3.68	0.008466	0.059732	-2.68
264455_at	hypothetical protein predicted by gensca	---	AT1G10330	-1.41	-0.50	-3.68	0.008469	0.059736	-2.68
260462_at	ZIP4, a putative zinc transporter per su	ZIP4	AT1G10970	-1.71	-0.78	-3.68	0.008481	0.059796	-2.68
246190_at	hypothetical protein (fragment) ;supporte	ATBPM5	AT5G21010	-1.27	-0.34	-3.67	0.008484	0.059799	-2.68
258696_at	hypothetical protein predicted by gensca	HCF152	AT3G09650	-1.61	-0.68	-3.67	0.008496	0.059835	-2.68
260215_at	unknown protein	---	AT1G74530	-1.34	-0.42	-3.67	0.008501	0.059835	-2.68
254126_at	RNA-binding protein RNP-T precursor ;	RBP31	AT4G24770	-1.36	-0.44	-3.67	0.008492	0.059835	-2.68
251814_at	chlorophyll a/b-binding protein ; suppor	LHCA1	AT3G54890	-1.25	-0.32	-3.67	0.008502	0.059835	-2.68
250262_at	putative protein peptidyl-prolyl cis-trans	---	AT5G13410	-1.68	-0.75	-3.67	0.0085	0.059835	-2.68
249093_at	putative protein similar to unknown prote	---	AT5G43880	-1.28	-0.36	-3.67	0.008518	0.059884	-2.69
258787_at	hypothetical protein predicted by gensca	PUB24	AT3G11840	3.92	1.97	3.67	0.008525	0.059884	-2.69
262846_at	endomembrane protein, putative simila	---	AT1G14670	1.37	0.45	3.67	0.008527	0.059884	-2.69
246070_at	ribosomal protein L7Ae-like NHP2/RS6	---	AT5G20160	-1.58	-0.66	-3.67	0.008523	0.059884	-2.69
250522_at	cleft lip and palate associated transmem	---	AT5G08500	-1.31	-0.39	-3.67	0.00853	0.059884	-2.69
267375_at	G protein alpha subunit 1 (GPA1) identi	GP ALPHA	AT2G26300	1.40	0.48	3.67	0.008528	0.059884	-2.69
263019_at	trehalose 6-phosphate synthase, putati	ATTPS9	AT1G23870	2.36	1.24	3.67	0.008511	0.059884	-2.69
252011_at	carbonic anhydrase (CAH1) ; supported	ACA1	AT3G52720	-1.53	-0.61	-3.67	0.008528	0.059884	-2.69
245605_at	ribonucleoprotein like protein	---	AT4G14300	-1.27	-0.34	-3.67	0.008538	0.059907	-2.69
245885_at	putative protein phi-1 - Nicotiana tabacu	EXL4	AT5G09440	1.73	0.79	3.67	0.008537	0.059907	-2.69
248757_at	putative protein contains similarity to un	---	AT5G47680	-1.29	-0.37	-3.67	0.008564	0.060023	-2.69
249291_at	glutathione transferase AtGST 10 (embl	ATGSTT1	AT5G41210	-1.38	-0.46	-3.67	0.008567	0.060023	-2.69

246564_at	putative protein hypothetical protein F1	---	AT5G15610	-1.27	-0.35	-3.67	0.008562	0.060023	-2.69
245628_at	anthocyanin2, putative similar to anthoc	PAP1	AT1G56650	-1.59	-0.67	-3.67	0.008559	0.060023	-2.69
255910_at	unknown protein contains similarity to pr	---	AT1G18030	-1.34	-0.42	-3.67	0.008568	0.060023	-2.69
252566_at	cytoplasmic ribosomal protein S15a -lik	RPS15AD	AT3G46040	-1.47	-0.55	-3.67	0.008584	0.060061	-2.69
257345_s_a	pseudogene	---	---	1.27	0.35	3.67	0.008582	0.060061	-2.69
261132_at	hypothetical protein predicted by genem	TGD1	AT1G19800	-1.32	-0.40	-3.67	0.008583	0.060061	-2.69
253951_at	putative Proline synthetase associated	---	AT4G26860	-1.58	-0.66	-3.67	0.008581	0.060061	-2.69
260626_at	storage protein, putative similar to GB:(	---	AT1G08040	-1.39	-0.48	-3.66	0.008592	0.060101	-2.70
259734_at	unknown protein similar to GB:AAD4142	---	AT1G77500	1.93	0.95	3.66	0.008598	0.060120	-2.70
266995_at	putative cytochrome P450	CYP710A1	AT2G34500	3.60	1.85	3.66	0.008605	0.060125	-2.70
249092_at	putative protein similar to unknown prote	---	AT5G43710	-1.39	-0.48	-3.66	0.008602	0.060125	-2.70
249417_at	calcium-binding protein - like cbp1 calci	---	AT5G39670	5.47	2.45	3.66	0.008606	0.060125	-2.70
250381_at	putative protein various predicted prote	---	AT5G11610	-1.74	-0.80	-3.66	0.008618	0.060191	-2.70
255899_at	zinc-finger protein (C-terminal), putative	---	AT1G17970	-1.58	-0.66	-3.66	0.008634	0.060280	-2.70
247726_at	telomere repeat-binding protein	TRP1	AT5G59430	1.45	0.54	3.66	0.008638	0.060285	-2.70
250996_at	putative protein BcDNA.LD24793, Dros	---	AT5G02530	-1.31	-0.39	-3.66	0.00864	0.060285	-2.70
258181_at	nitrate transporter identical to nitrate tra	---	AT3G21670	-1.56	-0.64	-3.66	0.008654	0.060370	-2.70
247734_at	putative protein predicted protein, Arabi	---	AT5G59400	1.37	0.46	3.66	0.008664	0.060416	-2.70
266137_at	unknown protein ;supported by full-leng	---	AT2G45010	1.33	0.41	3.66	0.008673	0.060440	-2.71
257966_at	unknown protein ;supported by full-leng	---	AT3G19800	-1.53	-0.62	-3.66	0.008672	0.060440	-2.71
250111_at	acetolactate synthase-like protein	---	AT5G16290	-1.55	-0.63	-3.66	0.008681	0.060481	-2.71
252032_at	putative protein RNA-binding protein 30	---	AT3G52150	-1.28	-0.36	-3.66	0.008694	0.060540	-2.71
253486_at	putative protein KIAA0260 gene, humar	---	AT4G31600	-1.34	-0.42	-3.66	0.008695	0.060540	-2.71
247507_at	putative protein predicted protein, Arabi	APO3	AT5G61930	-1.79	-0.84	-3.65	0.00872	0.060659	-2.71
251003_at	putative protein	---	AT5G02690	1.35	0.44	3.65	0.008723	0.060659	-2.71
251810_at	putative protein predicted pectate-lyase	---	AT3G55250	-1.46	-0.54	-3.65	0.008721	0.060659	-2.71
246703_at	mitogen activated protein kinase - like p	WNK9	AT5G28080	-2.46	-1.30	-3.65	0.008715	0.060659	-2.71
266422_at	hypothetical protein predicted by gensca	GAUT7	AT2G38650	-1.32	-0.40	-3.65	0.008735	0.060677	-2.71
267509_at	MADS-box protein (AGL20) ; supported	AGL20	AT2G45660	-1.53	-0.62	-3.65	0.008728	0.060677	-2.71
248238_at	putative protein similar to unknown prote	---	AT5G53900	-1.51	-0.59	-3.65	0.008736	0.060677	-2.71
250036_at	putative protein predicted proteins, Arat	---	AT5G18340	-1.47	-0.56	-3.65	0.008733	0.060677	-2.71
266579_at	putative small nuclear ribonucleoprotein	SNRNP-G	AT2G23930	-1.43	-0.52	-3.65	0.008744	0.060684	-2.71
248103_at	ubiquitin-like protein SMT3-like ; suppo	SUMO2	AT5G55160	-1.55	-0.63	-3.65	0.008746	0.060684	-2.71
257926_at	unknown protein contains Pfam profile:	---	AT3G23280	-1.26	-0.33	-3.65	0.008747	0.060684	-2.71
267293_at	hypothetical protein	TET8	AT2G23810	1.68	0.75	3.65	0.008741	0.060684	-2.71

266216_at	putative DOF zinc finger protein	---	AT2G28810	-1.38	-0.46	-3.65	0.008765	0.060788	-2.72
250088_at	APG5 (autophagy 5)-like protein	APG5	AT5G17290	1.34	0.42	3.65	0.00879	0.060943	-2.72
267140_at	putative GT-1-like transcription factor	---	AT2G38250	1.70	0.76	3.65	0.008801	0.060999	-2.72
251172_at	putative protein chloroplast ribosome re	RRF	AT3G63190	-1.31	-0.39	-3.64	0.008827	0.061158	-2.72
253331_at	nucellin -like protein nucellin - Hordeum	---	AT4G33490	-1.54	-0.62	-3.64	0.008831	0.061170	-2.72
250202_at	putative protein similar to unknown prote	---	AT5G13970	-1.39	-0.47	-3.64	0.008844	0.061244	-2.73
251302_at	RAV-like protein DNA-binding protein R	NGA2	AT3G61970	-1.25	-0.33	-3.64	0.008856	0.061308	-2.73
251697_at	putative protein hypothetical protein At2	---	AT3G56600	1.26	0.33	3.64	0.008867	0.061362	-2.73
246623_at	nuM1 protein, putative similar to nuM1	ATNUC-L1	AT1G48920	-1.48	-0.57	-3.64	0.008878	0.061421	-2.73
259311_at	putative SAR DNA-binding protein-1 sim	---	AT3G05060	-1.76	-0.82	-3.64	0.008882	0.061431	-2.73
261787_at	hypothetical protein predicted by genem	---	AT1G16020	-1.34	-0.42	-3.64	0.008891	0.061453	-2.73
254682_at	putative protein WERBP-1 - Nicotiana t	UNE16	AT4G13640	-1.38	-0.47	-3.64	0.008888	0.061453	-2.73
255549_at	predicted protein of unknown function	GPAT3	AT4G01950	4.07	2.03	3.64	0.008895	0.061466	-2.73
263638_at	unknown protein	---	AT2G25310	-1.26	-0.34	-3.64	0.008901	0.061487	-2.73
260852_at	transmembrane protein, putative similar	---	AT1G21900	1.29	0.36	3.64	0.008908	0.061501	-2.73
259914_at	hypothetical protein predicted by genefir	---	AT1G72640	-1.44	-0.53	-3.64	0.008906	0.061501	-2.73
253958_at	putative protein RING zinc finger protei	---	AT4G26400	1.37	0.45	3.64	0.008913	0.061516	-2.73
255902_at	transcription factor, putative similar to tr	---	AT1G17880	-1.33	-0.41	-3.64	0.008923	0.061567	-2.74
253531_at	putative protein tomato leucine zipper-c	ATEXO70(	AT4G31540	-1.32	-0.40	-3.63	0.008935	0.061612	-2.74
261622_at	hypothetical protein predicted by genem	---	AT1G01970	-1.36	-0.44	-3.63	0.008935	0.061612	-2.74
247249_at	putative protein similar to unknown prote	---	AT5G64670	-1.51	-0.60	-3.63	0.008938	0.061615	-2.74
250470_at	(3R)-hydroxymyristoyl-[acyl carrier prote	---	AT5G10160	1.43	0.52	3.63	0.008947	0.061631	-2.74
264045_at	putative GTP cyclohydrolase	---	AT2G22450	-1.31	-0.39	-3.63	0.008949	0.061631	-2.74
259335_s_a	unknown protein similar to unknown pro	---	AT3G03930 /	-1.45	-0.54	-3.63	0.008947	0.061631	-2.74
251098_at	light-inducible protein ATLS1	---	AT5G01650	-1.27	-0.34	-3.63	0.008959	0.061649	-2.74
265577_at	unknown protein	---	AT2G20100	-1.30	-0.38	-3.63	0.008959	0.061649	-2.74
247205_at	unknown protein ;supported by full-leng	PROPEP2	AT5G64890	4.15	2.05	3.63	0.008955	0.061649	-2.74
263128_at	zinc finger protein, putative similar to zi	LZF1	AT1G78600	-1.69	-0.75	-3.63	0.008982	0.061782	-2.74
264042_at	putative steroid sulfotransferase ; suppo	ST	AT2G03760	3.78	1.92	3.63	0.008988	0.061788	-2.74
263845_at	phenylalanine ammonia lyase (PAL1) ;	pal1	AT2G37040	2.74	1.46	3.63	0.008986	0.061788	-2.74
267358_at	proline transporter 1 ;supported by full-l	PROT1	AT2G39890	-1.42	-0.51	-3.63	0.009004	0.061865	-2.75
245359_at	carnitine racemase like protein ;supporte	IBR10	AT4G14430	1.71	0.77	3.63	0.009004	0.061865	-2.75
255586_at	hypothetical protein ;supported by full-le	MEE49	AT4G01560	-1.65	-0.72	-3.63	0.009019	0.061944	-2.75
247295_at	putative protein similar to unknown prote	---	AT5G64180	-1.36	-0.44	-3.63	0.00903	0.062003	-2.75
259242_at	putative actin similar to actin 1 GB:P025	ATARP6	AT3G33520	-1.31	-0.38	-3.63	0.009038	0.062041	-2.75

262059_at	DnaJ protein, putative similar to DnaJ h	---	AT1G80030	-1.51	-0.59	-3.63	0.009046	0.062076	-2.75
264471_at	hypothetical protein predicted by genem	---	AT1G67120	-1.69	-0.76	-3.62	0.009067	0.062185	-2.75
257005_at	hypothetical protein predicted by gensca	---	AT3G14190	-1.41	-0.49	-3.62	0.009068	0.062185	-2.75
261388_at	Expressed protein ; supported by cDNA	---	AT1G05385	-1.30	-0.37	-3.62	0.00907	0.062185	-2.75
256394_at	unknown protein contains non-consensu	---	AT3G06290	-1.31	-0.39	-3.62	0.009074	0.062192	-2.75
266892_at	putative glycine dehydrogenase	AtGLDP2	AT2G26080	-1.45	-0.54	-3.62	0.009086	0.062248	-2.75
262946_at	hypothetical protein predicted by gensca	---	AT1G79390	-1.34	-0.43	-3.62	0.009088	0.062248	-2.76
266808_at	Expressed protein ; supported by full-ler	---	AT2G29995	1.46	0.55	3.62	0.009093	0.062249	-2.76
256430_at	DREB2B transcription factor identical to	DREB2B	AT3G11020	-1.32	-0.40	-3.62	0.009092	0.062249	-2.76
263829_at	unknown protein	---	AT2G40435	-2.29	-1.19	-3.62	0.009097	0.062255	-2.76
262452_at	hypothetical protein similar to hypothetic	---	AT1G11210	-1.34	-0.42	-3.62	0.009107	0.062304	-2.76
247449_at	putative protein swelling-induced chlori	---	AT5G62290	-1.66	-0.73	-3.62	0.009117	0.062304	-2.76
246262_at	hypothetical protein	---	AT1G31790	-1.51	-0.60	-3.62	0.009114	0.062304	-2.76
256398_at	putative major intrinsic protein contains	NIP7;1	AT3G06100	1.26	0.33	3.62	0.009114	0.062304	-2.76
259251_at	unknown protein identical to residues 23	---	AT3G07600	2.40	1.26	3.62	0.009118	0.062304	-2.76
262622_at	hypothetical protein predicted by genem	---	AT1G06510	-1.29	-0.37	-3.62	0.009129	0.062361	-2.76
248336_at	unknown protein ; supported by cDNA:	---	AT5G52420	-1.61	-0.69	-3.62	0.00914	0.062420	-2.76
252239_at	putative protein putative protein - Drosc	---	AT3G49990	-1.63	-0.70	-3.62	0.009145	0.062437	-2.76
264850_at	unknown protein similar to F5J6.8 and C	---	AT2G17340	-1.32	-0.40	-3.62	0.009151	0.062459	-2.76
247212_at	putative protein similar to unknown prote	---	AT5G65040	1.28	0.36	3.62	0.009156	0.062475	-2.76
260619_at	glyoxalase I, putative similar to GB:Y13	---	AT1G08110	-1.45	-0.54	-3.62	0.00916	0.062475	-2.76
250128_at	zinc finger protein 3 (gb|AAD27875.1) ;	ZFN3	AT5G16540	-1.56	-0.64	-3.62	0.009162	0.062475	-2.76
266717_at	Expressed protein ; supported by full-ler	---	AT2G46735	1.33	0.41	3.61	0.009171	0.062504	-2.76
244986_at	ribosomal protein S19	---	---	-1.59	-0.67	-3.61	0.00917	0.062504	-2.76
247287_at	unknown protein ; supported by cDNA:	---	AT5G64230	1.72	0.78	3.61	0.009178	0.062528	-2.77
257459_at	unknown protein	---	AT1G24040	-1.33	-0.42	-3.61	0.009184	0.062552	-2.77
257700_at	unknown protein similar to unknown pro	ALIS1	AT3G12740	1.40	0.49	3.61	0.009198	0.062554	-2.77
247464_at	putative protein various predicted prote	IQD23	AT5G62070	1.64	0.71	3.61	0.009195	0.062554	-2.77
264946_at	hypothetical protein predicted by genem	---	AT1G77010	-1.42	-0.50	-3.61	0.009195	0.062554	-2.77
251451_s_a	putative protein several hypothetical pro	---	AT3G60040 /	-1.35	-0.43	-3.61	0.009197	0.062554	-2.77
262728_at	receptor kinase (CLV1) identical to rece	CLV1	AT1G75820	-1.70	-0.76	-3.61	0.00919	0.062554	-2.77
253779_at	receptor-like protein kinase 5 precursor	HAE	AT4G28490	1.87	0.90	3.61	0.009203	0.062570	-2.77
257228_at	NADPH:quinone oxidoreductase (NQR)	NQR	AT3G27890	1.30	0.38	3.61	0.009209	0.062592	-2.77
251662_at	putative protein DNA-DIRECTED RNA	NRPE5	AT3G57080	-1.43	-0.52	-3.61	0.009213	0.062602	-2.77
251479_at	serine/threonine-specific kinase lecRK1	ATHLECR	AT3G59700	2.17	1.11	3.61	0.009226	0.062621	-2.77

255426_at	putative protein	---	AT4G03370	1.32	0.40	3.61	0.009226	0.062621	-2.77
253444_at	putative protein ring finger protein, Horc	---	AT4G32600	-1.29	-0.37	-3.61	0.009225	0.062621	-2.77
265470_at	putative protein with C-terminal RING fir	---	AT2G37150	1.41	0.50	3.61	0.009227	0.062621	-2.77
255926_at	AP2 domain containing protein RAP2, p	---	AT1G22190	1.86	0.90	3.61	0.009246	0.062673	-2.77
258390_at	unknown protein similar to leucine-rich r	---	AT3G15410	-1.32	-0.40	-3.61	0.009248	0.062673	-2.77
250190_at	ribosomal protein precursor - like ribosc	---	AT5G14320	-1.31	-0.39	-3.61	0.009245	0.062673	-2.77
246548_at	putative protein ;supported by full-lengt	---	AT5G14910	-1.36	-0.44	-3.61	0.009241	0.062673	-2.77
259982_at	putative RING zinc finger protein contai	ATL8	AT1G76410	2.26	1.17	3.61	0.009244	0.062673	-2.77
262381_at	virus resistance protein, putative similar	---	AT1G72900	3.26	1.70	3.61	0.009253	0.062684	-2.77
248606_at	putative protein contains similarity to bZ	CPuORF4	AT5G49448 /	1.65	0.72	3.61	0.009258	0.062701	-2.77
258225_at	unknown protein ; supported by cDNA:	---	AT3G15630	2.03	1.02	3.61	0.009269	0.062720	-2.78
251407_at	Arm repeat containing protein - like arm	---	AT3G60350	-1.36	-0.44	-3.61	0.00927	0.062720	-2.78
264371_at	pEARLI 1-like protein may be induced w	ELP	AT1G12090	-1.77	-0.83	-3.61	0.00927	0.062720	-2.78
245830_at	hypothetical protein predicted by genem	---	AT1G57790	-1.29	-0.37	-3.61	0.009272	0.062720	-2.78
260566_at	cysteine synthase (cpACS1) ;supported	OASB	AT2G43750	-1.42	-0.51	-3.60	0.009312	0.062973	-2.78
257799_at	protein kinase, putative similar to soma	---	AT3G15890	-1.35	-0.43	-3.60	0.009317	0.062990	-2.78
248167_at	putative protein similar to unknown prote	---	AT5G54530	-1.49	-0.58	-3.60	0.009322	0.063001	-2.78
260457_at	unknown protein	---	AT1G72480	-1.33	-0.42	-3.60	0.009325	0.063007	-2.78
252552_at	putative protein	---	AT3G45900	-1.50	-0.58	-3.60	0.009335	0.063045	-2.78
262228_at	protein kinase, putative similar to protei	---	AT1G68690	2.77	1.47	3.60	0.009338	0.063045	-2.78
249457_s_a	zinc finger -like protein transcription fac	VIM4	AT1G66040 /	1.48	0.56	3.60	0.009339	0.063045	-2.78
267578_at	Expressed protein ; supported by cDNA	---	AT2G30695	-1.74	-0.80	-3.60	0.009347	0.063078	-2.78
266417_at	putative non-green plastid inner envelop	---	AT2G38550	-1.42	-0.50	-3.60	0.009354	0.063108	-2.79
261044_at	molybdopterin biosynthesis CNX3 prote	CNX3	AT1G01290	-1.36	-0.45	-3.60	0.009362	0.063124	-2.79
255035_at	putative protein	---	AT4G09550	-1.51	-0.60	-3.60	0.00936	0.063124	-2.79
252602_at	putative protein KIAA1094 protein, Hom	---	AT3G45040	1.38	0.46	3.60	0.009377	0.063207	-2.79
254599_at	putative protein hypothetical protein YP	---	AT4G19000	1.37	0.45	3.60	0.009387	0.063256	-2.79
259278_at	hypothetical protein predicted by gensca	---	AT3G01160	-1.39	-0.47	-3.60	0.009395	0.063290	-2.79
253166_at	putative protein putative ligand-gated ic	GLUR2	AT4G35290	-1.57	-0.65	-3.60	0.009401	0.063309	-2.79
253445_at	putative protein pAFD103 mRNA, Malu	---	AT4G32605 /	-1.38	-0.47	-3.59	0.009422	0.063423	-2.79
255585_at	putative NAM-like protein	anac069	AT4G01550	-1.57	-0.65	-3.59	0.009423	0.063423	-2.79
255260_at	score=63.7, E=3.9e-15, N=8 ; supporte	---	AT4G05040	-1.44	-0.52	-3.59	0.009432	0.063460	-2.79
256341_at	deoxyguanosine kinase, putative simila	---	AT1G72040	-1.74	-0.80	-3.59	0.009434	0.063460	-2.79
266034_at	Expressed protein ; supported by full-ler	FIP1	AT2G06005	-1.28	-0.36	-3.59	0.009466	0.063653	-2.80
266509_at	DegP2 protease identical to DegP2 prot	DEGP2	AT2G47940	-1.38	-0.47	-3.59	0.009474	0.063692	-2.80

265340_at	putative AAA-type ATPase similar to 26	---	AT2G18330	-1.70	-0.77	-3.59	0.009489	0.063772	-2.80
255883_at	unknown protein similar to putative prol	---	AT1G20270	-1.42	-0.50	-3.59	0.009521	0.063931	-2.80
245678_at	unknown protein	---	AT1G56610	-1.48	-0.56	-3.59	0.009519	0.063931	-2.80
246213_at	serine C-palmitoyltransferase like protei	ATLCB1	AT4G36480	1.43	0.51	3.59	0.009519	0.063931	-2.80
253216_at	cyclophilin - like protein cyclophilin, Ara	---	AT4G34960	-1.41	-0.49	-3.58	0.009536	0.064015	-2.81
261259_at	unknown protein	---	AT1G26660	-1.35	-0.43	-3.58	0.009552	0.064101	-2.81
254116_at	hypothetical protein	---	AT4G24730	1.30	0.38	3.58	0.009561	0.064144	-2.81
260664_at	myb-related protein, putative similar to (	ATRL5	AT1G19510	-1.83	-0.88	-3.58	0.009565	0.064150	-2.81
259571_at	hypothetical protein	---	AT1G20410	-1.47	-0.56	-3.58	0.009577	0.064213	-2.81
248687_at	ADPG pyrophosphorylase small subunit	ADG1	AT5G48300	-1.79	-0.84	-3.58	0.009583	0.064236	-2.81
245790_at	glycerol-3-phosphate acyltransferase ide	ATS1	AT1G32200	-1.40	-0.48	-3.58	0.009601	0.064335	-2.81
259540_at	nodule inception protein, putative simila	---	AT1G20640	-1.65	-0.72	-3.58	0.009614	0.064401	-2.81
252272_at	receptor protein kinase - like protein CL	BAM2	AT3G49670	-1.84	-0.88	-3.58	0.009622	0.064427	-2.82
255288_at	coded for by A. thaliana cDNA T41604	---	AT4G04670	-1.56	-0.64	-3.58	0.009626	0.064427	-2.82
247777_at	putative protein MNUDC protein, Homo	---	AT5G58740	-1.28	-0.36	-3.58	0.009626	0.064427	-2.82
266718_at	putative zinc transporter ;supported by	ZAT	AT2G46800	1.34	0.42	3.58	0.009637	0.064479	-2.82
261266_at	expansin 10 identical to GB:AAF61712 f	ATEXPA1(	AT1G26770	1.50	0.59	3.58	0.009646	0.064521	-2.82
245252_at	ethylene responsive element binding fac	ATERF-1	AT4G17500	2.44	1.29	3.57	0.009668	0.064631	-2.82
266402_at	hypothetical protein predicted by genefir	---	AT2G38780	-1.59	-0.67	-3.57	0.009666	0.064631	-2.82
247198_at	unknown protein	---	AT5G65290	1.30	0.38	3.57	0.009672	0.064643	-2.82
263432_at	putative beta-hydroxyacyl-ACP dehydra	---	AT2G22230	-1.45	-0.53	-3.57	0.00968	0.064658	-2.82
254847_at	putative phospholipase D-gamma phos	PLDGAMM	AT4G11850	2.04	1.03	3.57	0.009683	0.064658	-2.82
252964_at	receptor-like protein kinase - like protei	---	AT4G38830	1.32	0.40	3.57	0.009682	0.064658	-2.82
245592_at	CCAAT-binding transcription factor subu	NF-YB3	AT4G14540	-1.49	-0.58	-3.57	0.00969	0.064668	-2.82
262315_at	unknown protein ;supported by full-lengt	---	AT1G70990	1.83	0.88	3.57	0.009689	0.064668	-2.82
263873_at	unknown protein predicted by genscan;s	---	AT2G21860	-1.43	-0.51	-3.57	0.009705	0.064746	-2.82
258689_at	putative GTPase activating protein conta	---	AT3G07940	-1.29	-0.36	-3.57	0.009713	0.064785	-2.83
252943_at	cinnamyl-alcohol dehydrogenase CAD1	CAD9	AT4G39330	7.36	2.88	3.57	0.009723	0.064810	-2.83
247844_at	ARR2 - like protein ARR2 protein, Arab	ARR18	AT5G58080	1.28	0.36	3.57	0.009722	0.064810	-2.83
253396_at	putative protein RNA-binding protein LA	AtLa1	AT4G32720	-1.32	-0.40	-3.57	0.009738	0.064818	-2.83
251784_at	putative protein photosystem II oxygen	PPL1	AT3G55330	-1.60	-0.68	-3.57	0.009732	0.064818	-2.83
252092_at	mucin-like protein hemomucin, Drosoph	SSL4	AT3G51420	-1.65	-0.72	-3.57	0.009734	0.064818	-2.83
265854_at	hypothetical protein predicted by gensca	---	AT2G42370	-1.28	-0.36	-3.57	0.009738	0.064818	-2.83
249336_at	putative protein similar to unknown prote	DRB5	AT5G41070	1.64	0.71	3.57	0.009729	0.064818	-2.83
263259_at	putative zinc-binding protein similar to zi	PUB18	AT1G10560	1.71	0.77	3.57	0.009757	0.064924	-2.83

267393_at	similar to axi 1 protein from Nicotiana ta	---	AT2G44500	1.69	0.75	3.56	0.009801	0.065195	-2.83
267180_at	unknown protein ; supported by cDNA:	SLT1	AT2G37570	-1.34	-0.42	-3.56	0.009804	0.065195	-2.84
262584_at	hypothetical protein Strong similarity to	---	AT1G15440	-1.88	-0.91	-3.56	0.009834	0.065356	-2.84
247489_at	carbonyl reductase - like protein inducit	---	AT5G61830	-1.37	-0.45	-3.56	0.009831	0.065356	-2.84
261395_at	unknown protein similar to putative AP2	---	AT1G79700	2.02	1.01	3.56	0.009853	0.065430	-2.84
252977_at	Phospholipase like protein Arabidopsis	---	AT4G38560	2.18	1.13	3.56	0.009851	0.065430	-2.84
259401_at	hypothetical protein contains similarity t	CSTF77	AT1G17760	-1.63	-0.70	-3.56	0.009851	0.065430	-2.84
266662_at	hypothetical protein predicted by gensca	---	AT2G25830	-1.46	-0.54	-3.56	0.009857	0.065436	-2.84
245597_at	salt-inducible protein homolog	---	AT4G14190	-1.32	-0.40	-3.56	0.009866	0.065475	-2.84
260309_at	putative alanine aminotransferase simila	AOAT2	AT1G70580	-1.45	-0.54	-3.56	0.009869	0.065478	-2.84
263597_at	hypothetical protein predicted by gensca	---	AT2G01870	-2.04	-1.03	-3.56	0.009874	0.065494	-2.84
251186_at	putative protein unknown protein At2g4	---	AT3G62790	-1.25	-0.32	-3.56	0.009882	0.065524	-2.84
250139_at	putative protein de novo DNA methyltra	DRM2	AT5G14620	-1.25	-0.32	-3.56	0.009895	0.065589	-2.84
264082_at	unknown protein ;supported by full-leng	---	AT2G28570	1.32	0.40	3.56	0.009898	0.065589	-2.85
258148_s_a	DNA-directed RNA polymerase II secor	NRPD2B	AT3G18090 /	-1.63	-0.70	-3.56	0.009903	0.065589	-2.85
265082_at	hypothetical protein predicted by genefi	---	AT1G03830	-1.32	-0.40	-3.56	0.009901	0.065589	-2.85
258081_at	Expressed protein ; supported by full-ler	---	AT3G26085	-1.33	-0.41	-3.56	0.009908	0.065602	-2.85
256510_at	ATP-dependent Clp protease ATP-bind	---	AT1G33360	1.37	0.45	3.55	0.009921	0.065650	-2.85
262956_at	eukaryotic translation initiation factor 4A	EIF4A-2	AT1G54270	1.38	0.47	3.55	0.009919	0.065650	-2.85
264633_at	step II splicing factor, putative similar to	SMP1	AT1G65660	-1.34	-0.42	-3.55	0.009933	0.065708	-2.85
248440_at	acid phosphatase	---	AT5G51260	1.40	0.48	3.55	0.009955	0.065839	-2.85
267635_at	rhodanese-like family protein ;supported	---	AT2G42220	-1.63	-0.71	-3.55	0.009961	0.065857	-2.85
258104_at	hypothetical protein predicted by genem	---	AT3G23620	-1.59	-0.67	-3.55	0.009967	0.065879	-2.85
257016_at	protein kinase, putative similar to PROT	---	AT3G28690	-1.37	-0.46	-3.55	0.009995	0.065972	-2.86
250238_at	unknown protein	DCP2	AT5G13570	-1.31	-0.39	-3.55	0.009996	0.065972	-2.86
254289_at	putative protein predicted protein, Arabi	---	AT4G22980	3.35	1.75	3.55	0.009986	0.065972	-2.85
258188_at	unknown protein ;supported by full-leng	---	AT3G17800	-1.42	-0.51	-3.55	0.009992	0.065972	-2.86
256177_at	protein kinase, putative contains Pfam p	---	AT1G51620	2.34	1.22	3.55	0.009992	0.065972	-2.86
249782_at	dipeptidyl peptidase IV-like protein	---	AT5G24260	1.33	0.41	3.55	0.010007	0.066025	-2.86
264899_at	unknown protein similar to ripening-indu	---	AT1G23130	-1.77	-0.83	-3.55	0.01003	0.066158	-2.86
261129_at	tubulin alpha-2/alpha-4 chain identical to	TUA4	AT1G04820	2.09	1.07	3.54	0.010049	0.066269	-2.86
259192_at	unknown protein ;supported by full-leng	---	AT3G01740	-1.40	-0.49	-3.54	0.010058	0.066296	-2.86
252228_at	porin - like protein porin, Mesembryanth	VDAC5	AT3G49920	-1.28	-0.35	-3.54	0.010062	0.066296	-2.86
263373_at	Expressed protein ; supported by full-ler	---	AT2G20515	-1.61	-0.69	-3.54	0.01006	0.066296	-2.86
250555_at	putative protein ferredoxin (2Fe-2S), Ar	---	AT5G07950	-1.50	-0.59	-3.54	0.010078	0.066380	-2.86

252474_at	putative protein several hypothetical pro	---	AT3G46620	2.24	1.17	3.54	0.010103	0.066525	-2.87
250097_at	putative protein similar to unknown prote	---	AT5G17280	1.40	0.49	3.54	0.010106	0.066531	-2.87
259776_s_a	eukaryotic translation initiation factor 4E	---	AT1G29550 /	-1.32	-0.40	-3.54	0.010111	0.066542	-2.87
254014_at	NPR1 like protein regulatory protein NP	---	AT4G26120	2.00	1.00	3.54	0.010121	0.066581	-2.87
261043_at	hypothetical protein similar to unknown	---	AT1G01220	-1.41	-0.50	-3.54	0.010123	0.066581	-2.87
258454_at	putative 40S ribosomal protein S10 simi	RPS10	AT3G22300	-1.49	-0.58	-3.54	0.010132	0.066591	-2.87
262340_at	Expressed protein ; supported by full-ler	ANAC027	AT1G64100 /	-1.30	-0.37	-3.54	0.010129	0.066591	-2.87
251112_s_a	pyruvate decarboxylase-like protein pyr	PDC3	AT5G01320 /	-1.49	-0.58	-3.54	0.010133	0.066591	-2.87
251669_at	putative protein hypothetical protein - A	---	AT3G57180	-1.79	-0.84	-3.54	0.010142	0.066623	-2.87
249379_at	putative protein predicted protein, Arabi	---	AT5G40460	1.92	0.94	3.54	0.010144	0.066623	-2.87
254226_at	putative disease resistance response p	---	AT4G23690	5.11	2.35	3.54	0.010148	0.066633	-2.87
248487_at	ATP-dependent Clp protease ATP-bind	ERD1	AT5G51070	1.37	0.45	3.54	0.010158	0.066679	-2.87
256340_at	DnaJ protein, putative contains Pfam pr	---	AT1G72070	1.37	0.46	3.54	0.010162	0.066683	-2.87
253948_at	Avr9 elicitor response like protein Avr9	---	AT4G26940	1.32	0.40	3.53	0.010182	0.066794	-2.87
252269_at	putative protein ;supported by full-lengt	LSU1	AT3G49580	-2.22	-1.15	-3.53	0.010187	0.066811	-2.88
251245_at	putative protein phytochrome-associate	PIL2	AT3G62090	-2.35	-1.23	-3.53	0.010203	0.066896	-2.88
267026_at	DREB-like AP2 domain transcription fac	---	AT2G38340	2.44	1.29	3.53	0.010213	0.066930	-2.88
255524_at	hypothetical protein similar to pectineste	ATPMEPC	AT4G02330	3.75	1.91	3.53	0.010215	0.066930	-2.88
250249_at	putative protein similar to unknown prote	---	AT5G13760	1.38	0.47	3.53	0.010217	0.066930	-2.88
266821_at	putative ethylene response element bin	ERF13	AT2G44840	4.31	2.11	3.53	0.010221	0.066934	-2.88
254966_at	COP1 like protein photomorphogenesis	SPA2	AT4G11110	-1.24	-0.31	-3.53	0.010231	0.066985	-2.88
260290_at	hypothetical protein predicted by gensc	---	AT1G80510	1.34	0.43	3.53	0.010235	0.066990	-2.88
260075_at	putative integral membrane protein cont	---	AT1G73700	-1.44	-0.52	-3.53	0.010267	0.067177	-2.88
260238_at	AtHVA22a identical to AtHVA22a GB:A	ATHVA22/	AT1G74520	-1.43	-0.52	-3.53	0.010286	0.067284	-2.89
263250_at	putative fructokinase ; supported by full	---	AT2G31390	1.83	0.87	3.52	0.010305	0.067393	-2.89
246460_at	cellulose synthase catalytic subunit -like	CSLD2	AT5G16910	1.60	0.68	3.52	0.01031	0.067403	-2.89
262116_at	Expressed protein ; supported by full-ler	---	AT1G02816	1.81	0.86	3.52	0.010328	0.067496	-2.89
249396_at	DegP protease contains similarity to De	DegP9	AT5G40200	-1.28	-0.35	-3.52	0.01033	0.067496	-2.89
258823_at	putative RING zinc finger protein contai	---	AT3G07200	-1.45	-0.53	-3.52	0.010338	0.067530	-2.89
266536_at	hypothetical protein predicted by genefir	---	AT2G16900	2.31	1.21	3.52	0.010362	0.067549	-2.89
250148_at	putative protein various predicted prote	---	AT5G14530	-1.36	-0.45	-3.52	0.010371	0.067549	-2.89
249901_at	histone deacetylase-like protein non-co	HD2B	AT5G22650	-1.49	-0.58	-3.52	0.010375	0.067549	-2.89
260157_at	unknown protein ; supported by cDNA:	---	AT1G52930	-1.87	-0.90	-3.52	0.01037	0.067549	-2.89
250406_at	enhancer of rudimentary ; supported by	ER	AT5G10810	-1.49	-0.58	-3.52	0.010347	0.067549	-2.89
259583_at	hypothetical protein	---	AT1G28070	-1.38	-0.47	-3.52	0.010362	0.067549	-2.89

265162_at	hypothetical protein predicted by gensca	---	AT1G30910	-1.36	-0.44	-3.52	0.010367	0.067549	-2.89
257879_at	unknown protein	---	AT3G17160	-1.60	-0.68	-3.52	0.010355	0.067549	-2.89
260642_at	plastid protein, putative similar to plastic	---	AT1G53260	1.51	0.59	3.52	0.010378	0.067549	-2.89
248945_at	putative protein strong similarity to unkn	---	AT5G45510	1.40	0.49	3.52	0.010367	0.067549	-2.89
264941_at	auxin-induced protein, putative similar t	---	AT1G60680	1.64	0.72	3.52	0.010373	0.067549	-2.89
AFFX-r2-Bs	B. subtilis /GEN=dapB, jojF /DB_XREF=	---	---	-1.67	-0.74	-3.52	0.01036	0.067549	-2.89
255040_at	putative protein hypothetical protein - A	---	AT4G09580	1.35	0.43	3.52	0.01038	0.067549	-2.90
261526_at	protein kinase identical to protein kinase	APK2A	AT1G14370	1.66	0.73	3.52	0.010398	0.067609	-2.90
245152_at	putative mitochondrial carrier protein sim	---	AT2G47490	1.33	0.41	3.52	0.010394	0.067609	-2.90
254153_at	putative protein hypothetical protein R1	PWD	AT4G24450	-1.73	-0.79	-3.52	0.010397	0.067609	-2.90
248387_at	unknown protein	---	AT5G51960	-1.39	-0.47	-3.52	0.010408	0.067655	-2.90
245761_at	hypothetical protein predicted by genem	---	AT1G66890	-1.33	-0.41	-3.52	0.010418	0.067685	-2.90
247173_at	poly(A)-binding protein II-like ; supporte	---	AT5G65260	-1.39	-0.48	-3.52	0.010418	0.067685	-2.90
247851_at	outer membrane lipoprotein - like outer	TIL	AT5G58070	-1.80	-0.85	-3.51	0.010445	0.067838	-2.90
262160_at	hypothetical protein predicted by genem	---	AT1G52590	-1.68	-0.75	-3.51	0.010454	0.067877	-2.90
253281_at	predicted protein	UGT73B1	AT4G34138	1.85	0.89	3.51	0.010464	0.067894	-2.90
248128_at	thiazole biosynthetic enzyme precursor	THI1	AT5G54770	-1.44	-0.52	-3.51	0.010468	0.067894	-2.90
261463_at	hypothetical protein predicted by gensca	---	AT1G07730 /	-1.28	-0.35	-3.51	0.010468	0.067894	-2.90
258577_at	putative disease resistance protein simil	---	AT3G04220	1.84	0.88	3.51	0.010468	0.067894	-2.90
264183_at	unknown protein	CLV2	AT1G65380	-1.36	-0.45	-3.51	0.01048	0.067949	-2.91
259910_at	putative P-type transporting ATPase sim	---	AT1G72700	1.74	0.80	3.51	0.010497	0.068040	-2.91
248913_at	unknown protein ;supported by full-leng	---	AT5G45760	-1.31	-0.39	-3.51	0.010504	0.068065	-2.91
253351_at	putative protein hemolysin, 38K, Synec	---	AT4G33700	-1.34	-0.42	-3.51	0.010507	0.068069	-2.91
262703_at	putative auxin-induced protein similar to	---	AT1G16510	1.53	0.62	3.51	0.010516	0.068076	-2.91
245627_at	water stress-induced protein, putative s	AtGolS2	AT1G56600	-1.83	-0.87	-3.51	0.010511	0.068076	-2.91
264549_at	putative ser/thr protein kinase similar to	---	AT1G09440	-1.30	-0.38	-3.51	0.010517	0.068076	-2.91
257369_at	hypothetical protein predicted by gensca	BPC7	AT2G35550	-1.36	-0.44	-3.51	0.010531	0.068108	-2.91
261672_at	unknown protein contains similarity to a	ATARP4	AT1G18450	-1.46	-0.55	-3.51	0.010529	0.068108	-2.91
264717_at	hypothetical protein predicted by genem	ATFH8	AT1G70140	1.76	0.82	3.51	0.010528	0.068108	-2.91
248976_at	putative protein strong similarity to unkn	ARAD2	AT5G44930	-1.42	-0.50	-3.51	0.01055	0.068120	-2.91
263178_at	hypothetical protein predicted by genem	---	AT1G05550	-1.38	-0.46	-3.51	0.010548	0.068120	-2.91
254849_at	putative protein RNA splicing-related pr	---	AT4G11970	-1.25	-0.33	-3.51	0.010538	0.068120	-2.91
254975_at	putative Fe(II)/ascorbate oxidase SRG1	---	AT4G10500	11.58	3.53	3.51	0.010551	0.068120	-2.91
263165_at	putataive transport protein Similar to gb	---	AT1G03060	1.26	0.34	3.51	0.01055	0.068120	-2.91
261659_at	unknown protein contains similarity to pl	TOR	AT1G50030	-1.29	-0.37	-3.51	0.010542	0.068120	-2.91

265570_at	unknown protein	---	AT2G28310	-1.42	-0.50	-3.51	0.010558	0.068144	-2.91
248473_at	small zinc finger-like protein ;supported	TIM8	AT5G50810	-1.41	-0.50	-3.51	0.010573	0.068201	-2.91
264849_at	putative ribosomal protein S4 contains r	---	AT2G17360	-1.40	-0.49	-3.51	0.010571	0.068201	-2.91
244937_at	NADH dehydrogenase 49KDa protein	---	---	-1.66	-0.73	-3.50	0.010586	0.068228	-2.92
258560_at	hypothetical protein predicted by genefi	---	AT3G06020	1.48	0.57	3.50	0.010585	0.068228	-2.92
254278_at	Expressed protein ; supported by full-ler	---	AT4G22740	-1.35	-0.43	-3.50	0.010582	0.068228	-2.92
262523_at	ubiquitin-specific protease 15 (UBP15)	UBP15	AT1G17110	-1.25	-0.33	-3.50	0.010591	0.068243	-2.92
253608_at	xyloglucan endo-1,4-beta-D-glucanase-	XTH19	AT4G30290	2.52	1.33	3.50	0.01061	0.068327	-2.92
266093_at	unknown protein ;supported by full-leng	---	AT2G37990	-1.53	-0.61	-3.50	0.010619	0.068327	-2.92
245734_at	lysophospholipase homolog, putative si	---	AT1G73480	-1.64	-0.71	-3.50	0.010616	0.068327	-2.92
256193_at	hypothetical protein similar to hypothetic	---	AT1G30200	-1.30	-0.38	-3.50	0.010615	0.068327	-2.92
256616_at	hypothetical protein similar to unknown	---	AT3G22260	1.55	0.63	3.50	0.010618	0.068327	-2.92
252039_at	Expressed protein ; supported by cDNA	---	AT3G52155	-1.38	-0.47	-3.50	0.010625	0.068348	-2.92
252217_at	putative protein some putative proteins -	---	AT3G50140	1.51	0.59	3.50	0.010631	0.068367	-2.92
251256_at	putative protein hypothetical proteins - A	---	AT3G62300	-1.42	-0.51	-3.50	0.010638	0.068376	-2.92
253909_at	putative protein LEDI-3 protein, Lithosp	---	AT4G27270	1.40	0.48	3.50	0.010639	0.068376	-2.92
246842_at	Expressed protein ; supported by full-ler	---	AT5G26731	1.63	0.70	3.50	0.010645	0.068377	-2.92
267526_at	photosystem II reaction center 6.1KD pr	PSBW	AT2G30570	-1.24	-0.31	-3.50	0.010644	0.068377	-2.92
260266_at	putative B-box zinc finger protein contai	---	AT1G68520	-1.48	-0.56	-3.50	0.010648	0.068378	-2.92
260598_at	unknown protein	---	AT1G55930	-1.51	-0.59	-3.50	0.010662	0.068408	-2.92
261749_at	dehydrin, putative similar to dehydrin G	ERD14	AT1G76180	1.30	0.38	3.50	0.010659	0.068408	-2.92
254521_at	putative protein similar to unknown prote	---	AT5G44820	1.33	0.41	3.50	0.010656	0.068408	-2.92
258254_at	unknown protein contains Pfam profile:	---	AT3G26780 /	-1.46	-0.55	-3.50	0.010678	0.068476	-2.93
247201_at	50S ribosomal protein L29 ; supported	---	AT5G65220	-1.41	-0.50	-3.50	0.010677	0.068476	-2.92
245770_at	hypothetical protein predicted by genem	---	AT1G30240	-1.61	-0.69	-3.50	0.010685	0.068500	-2.93
259882_at	unknown protein similar to hypothetical	---	AT1G76670	-1.35	-0.43	-3.50	0.010691	0.068518	-2.93
252786_at	putative protein putative DNA-helicase	CHR38	AT3G42670	-1.71	-0.77	-3.50	0.010697	0.068521	-2.93
245051_at	putative WRKY-type DNA-binding protei	WRKY15	AT2G23320	1.93	0.95	3.50	0.010697	0.068521	-2.93
252437_at	putative protein pectinesterase homolo	---	AT3G47380	2.20	1.14	3.50	0.01071	0.068581	-2.93
253063_at	plasma membrane-type calcium ATPase	ACA2	AT4G37640	1.66	0.73	3.50	0.010718	0.068613	-2.93
253052_at	cytochrome P450-like protein ; supporte	CYP81H1	AT4G37310	1.94	0.95	3.49	0.010726	0.068647	-2.93
249087_at	DNA binding protein EREBP-3-like prote	ERF9	AT5G44210	-1.56	-0.64	-3.49	0.010744	0.068702	-2.93
257789_at	unknown protein ;supported by full-leng	YSL6	AT3G27020	1.57	0.65	3.49	0.010743	0.068702	-2.93
245831_at	unknown protein	---	AT1G48840	-1.35	-0.43	-3.49	0.01074	0.068702	-2.93
261387_at	hypothetical protein predicted by genem	---	AT1G05410	-1.63	-0.71	-3.49	0.010759	0.068766	-2.93

251995_at	nuclear envelope membrane protein - li	FK	AT3G52940	-1.27	-0.35	-3.49	0.01076	0.068766	-2.93
254669_at	HhoA protease precursor, putative iden	DEG5	AT4G18370	-1.47	-0.55	-3.49	0.010763	0.068768	-2.93
263798_at	putative ubiquitin carboxyl terminal hydr	UBP19	AT2G24640	1.27	0.35	3.49	0.010769	0.068786	-2.93
255535_at	putative RNaseP-associated protein sir	---	AT4G01790	-1.50	-0.59	-3.49	0.010772	0.068787	-2.93
249886_at	unknown protein ; supported by cDNA:	---	AT5G22320	-1.53	-0.62	-3.49	0.010775	0.068788	-2.93
254857_at	putative protein acetylcholine regulator	SEC1B	AT4G12120	1.37	0.45	3.49	0.010781	0.068809	-2.94
251413_at	bZIP protein ; supported by cDNA: gi_6	---	AT3G60320	-1.41	-0.49	-3.49	0.010789	0.068810	-2.94
260239_at	putative receptor protein kinase similar	---	AT1G74360	3.65	1.87	3.49	0.01079	0.068810	-2.94
251289_at	auxin response factor-like protein auxin	ARF18	AT3G61830	-1.43	-0.52	-3.49	0.010794	0.068810	-2.94
253796_at	hypothetical protein	---	AT4G28460	4.33	2.11	3.49	0.010792	0.068810	-2.94
259732_at	putative replication factor C similar to re	---	AT1G77470	-1.35	-0.43	-3.49	0.010811	0.068847	-2.94
251578_at	putative protein contains alternative dor	---	AT3G58180	-1.30	-0.38	-3.49	0.010806	0.068847	-2.94
248871_at	putative protein strong similarity to unkn	---	AT5G46680	-1.36	-0.44	-3.49	0.01081	0.068847	-2.94
256609_at	hypothetical protein predicted by genem	---	---	1.27	0.35	3.49	0.010811	0.068847	-2.94
247215_at	Expressed protein ; supported by full-ler	PROPEP3	AT5G64905	4.85	2.28	3.49	0.010821	0.068886	-2.94
251956_at	RNA-binding protein cp29 protein ;supp	CP29	AT3G53460	-1.32	-0.40	-3.49	0.010829	0.068922	-2.94
257275_at	RNA-binding protein, putative contains	CID9	AT3G14450	-1.64	-0.71	-3.49	0.010832	0.068922	-2.94
263882_at	putative ribonucleoside-diphosphate red	RNR1	AT2G21790	-1.94	-0.96	-3.49	0.010838	0.068938	-2.94
265596_at	hypothetical protein predicted by gensca	CAF1	AT2G20020	-1.80	-0.84	-3.49	0.010844	0.068958	-2.94
257840_at	protein kinase, putative contains Pfam p	AGC2-1	AT3G25250	4.04	2.02	3.48	0.010862	0.069054	-2.94
245106_at	unknown protein	---	AT2G41650	-1.39	-0.48	-3.48	0.010871	0.069091	-2.94
256889_at	PHD-finger protein, putative contains P	ING1	AT3G24010	-1.26	-0.33	-3.48	0.010879	0.069120	-2.94
251930_at	putative protein several hypothetical pro	ATRBL4	AT3G53780	1.41	0.49	3.48	0.010882	0.069121	-2.94
259577_at	unknown protein	---	AT1G35340	-1.43	-0.52	-3.48	0.010887	0.069123	-2.95
259943_at	unknown protein	---	AT1G71480	-1.56	-0.64	-3.48	0.010888	0.069123	-2.95
250358_at	putative protein gibberellin-responsive p	AGP15	AT5G11740	1.44	0.53	3.48	0.010931	0.069224	-2.95
261695_at	Mg-chelatase, putative similar to Mg-ch	CHLD	AT1G08520	-1.38	-0.46	-3.48	0.01092	0.069224	-2.95
247698_at	putative protein predicted proteins, Aral	---	AT5G59830	-1.36	-0.45	-3.48	0.010909	0.069224	-2.95
263804_at	putative protein kinase contains a protei	---	AT2G40270	1.42	0.51	3.48	0.010913	0.069224	-2.95
257787_at	actin related protein, putative similar to	ARP2	AT3G27000	-1.24	-0.31	-3.48	0.01093	0.069224	-2.95
251508_at	putative protein mitochondrial RNA spli	---	AT3G58970	-1.40	-0.49	-3.48	0.010917	0.069224	-2.95
262003_at	unknown protein	---	AT1G64460	1.33	0.41	3.48	0.010912	0.069224	-2.95
253573_at	putative protein BEM46 PROTEIN, Sch	---	AT4G31020	1.38	0.46	3.48	0.01093	0.069224	-2.95
252043_at	putative protein mttC protein, Escherich	---	AT3G52390	-1.37	-0.45	-3.48	0.01093	0.069224	-2.95
245993_at	putative protein predicted proteins, Aral	---	AT5G20700	-1.57	-0.65	-3.48	0.010948	0.069274	-2.95

245228_at	phytochelatin synthetase-like protein ge	COBL2	AT3G29810	1.93	0.95	3.48	0.010948	0.069274	-2.95
250089_at	homeobox protein	HDG9	AT5G17320	1.39	0.47	3.48	0.010944	0.069274	-2.95
253619_at	glycine-rich protein glycine-rich cell wal	---	AT4G30460	-1.50	-0.58	-3.48	0.010959	0.069304	-2.95
249489_at	acyltransferase -like protein anthocyan	---	AT5G39090	1.42	0.51	3.48	0.010958	0.069304	-2.95
251849_at	Expressed protein ; supported by cDNA	HAG1	AT3G54610	-1.36	-0.44	-3.48	0.010963	0.069306	-2.95
256299_at	expansin (At-EXP1) identical to expansi	ATEXPA1	AT1G69530	3.36	1.75	3.48	0.010978	0.069385	-2.95
262590_at	putative RING-H2 zinc finger protein ES	RHA2A	AT1G15100	1.36	0.45	3.48	0.010985	0.069410	-2.95
244965_at	hypothetical protein	---	---	-1.50	-0.58	-3.48	0.010988	0.069412	-2.96
247936_at	lycopene epsilon cyclase ; supported by	LUT2	AT5G57030	-1.49	-0.58	-3.48	0.010998	0.069455	-2.96
261418_at	mitochondrial ribosomal protein, putativ	---	AT1G07830	-1.52	-0.61	-3.48	0.011002	0.069460	-2.96
250458_s_a	ACTIN 2/7 (sp|P53492) ; supported by	ACT7	AT5G09810	-1.25	-0.32	-3.47	0.011019	0.069544	-2.96
248694_at	unknown protein	---	AT5G48340	-1.30	-0.37	-3.47	0.011037	0.069640	-2.96
265220_at	histidine transport protein (PTR2-B) ; su	PTR2	AT2G02040	1.27	0.34	3.47	0.011049	0.069694	-2.96
247841_at	putative protein predicted proteins, Dro	ATFIP1[V]	AT5G58040	-1.35	-0.43	-3.47	0.011054	0.069694	-2.96
265837_at	unknown protein	LURP1	AT2G14560	7.88	2.98	3.47	0.011053	0.069694	-2.96
257712_at	hypothetical protein predicted by genem	---	AT3G27420	-1.24	-0.31	-3.47	0.011077	0.069819	-2.96
254969_at	hypothetical protein ;supported by full-le	---	AT4G10360	1.29	0.36	3.47	0.011096	0.069877	-2.97
246418_at	quinone oxidoreductase -like protein pr	---	AT5G16960	1.42	0.50	3.47	0.011095	0.069877	-2.97
259181_at	unknown protein similar to putative prote	---	AT3G01690	-1.47	-0.56	-3.47	0.011093	0.069877	-2.97
266876_at	hypothetical protein predicted by genefir	---	AT2G44820	-1.35	-0.43	-3.47	0.011099	0.069877	-2.97
244973_at	PSII T protein	---	---	-1.91	-0.93	-3.47	0.011105	0.069898	-2.97
246789_at	long-chain-fatty-acid--CoA ligase-like pr	LACS7	AT5G27600	1.29	0.36	3.47	0.011114	0.069916	-2.97
253160_at	putative protein predicted protein, Syne	---	AT4G35760	-1.54	-0.62	-3.47	0.011114	0.069916	-2.97
259094_at	putative cysteine synthase similar to cys	CYSD1	AT3G04940	-1.52	-0.60	-3.47	0.011119	0.069927	-2.97
256089_at	hypothetical protein predicted by gensca	---	AT1G20830	-1.53	-0.61	-3.47	0.011135	0.070010	-2.97
259553_x_a	hypothetical protein	ATEXT3	AT1G21310	2.01	1.01	3.47	0.01115	0.070042	-2.97
265916_at	hypothetical protein similar to En/Spm-li	---	---	1.30	0.38	3.47	0.011145	0.070042	-2.97
254355_at	Ribosomal protein L7Ae - like NHP2/RS	---	AT4G22380	-1.55	-0.63	-3.47	0.01115	0.070042	-2.97
250863_at	F1F0-ATPase inhibitor - like protein F1I	---	AT5G04750	1.26	0.33	3.46	0.011163	0.070106	-2.97
249096_at	putative protein similar to unknown prote	---	AT5G43910	1.69	0.75	3.46	0.011166	0.070106	-2.97
259148_at	putative ATPase similar to ATPase GB1	---	AT3G10350	-1.40	-0.48	-3.46	0.01117	0.070110	-2.97
267371_at	Expressed protein ; supported by cDNA	---	AT2G44510	-1.55	-0.64	-3.46	0.011178	0.070142	-2.97
251095_at	putative protein hypothetical protein At2	---	AT5G01510	-1.48	-0.56	-3.46	0.011197	0.070245	-2.97
246015_at	putative protein predicted proteins, Dro	---	AT5G10700	-1.29	-0.37	-3.46	0.011203	0.070252	-2.98
250255_at	sigma-like factor (gb|AAC97954.1) ; su	SIG4	AT5G13730	-1.76	-0.81	-3.46	0.011205	0.070252	-2.98

256805_at	unknown protein contains similarity to p	---	AT3G20930	-1.80	-0.85	-3.46	0.01121	0.070268	-2.98
251951_s_a	putative protein predicted proteins, Aral	---	AT1G55710 /	-1.33	-0.41	-3.46	0.011225	0.070341	-2.98
251884_at	embryonic abundant protein -like embry	---	AT3G54150	3.82	1.93	3.46	0.011269	0.070587	-2.98
264363_at	hypothetical protein predicted by genefir	---	AT1G03170	1.36	0.44	3.46	0.01127	0.070587	-2.98
267494_at	TCP1-chaperonin cofactor A isolog ;sup	KIS	AT2G30410	-1.32	-0.40	-3.46	0.011289	0.070681	-2.98
244977_at	cytochrome b/f	---	---	-1.71	-0.78	-3.45	0.011302	0.070746	-2.98
251895_at	class IV chitinase (CHIV)	ATEP3	AT3G54420	2.10	1.07	3.45	0.011307	0.070756	-2.99
263624_at	putative ferredoxin-thioredoxin reductas	---	AT2G04700	-1.41	-0.50	-3.45	0.011315	0.070792	-2.99
262244_at	serine threonine kinase, putative simila	CIPK17	AT1G48260	3.45	1.79	3.45	0.01132	0.070802	-2.99
263212_at	unknown protein similar to ribonuclease	emb2004	AT1G10510	-1.32	-0.40	-3.45	0.011355	0.070968	-2.99
253578_at	putative protein diacylglycerol kinase io	ATDGK7	AT4G30340	1.51	0.60	3.45	0.011356	0.070968	-2.99
265480_at	similar to cold acclimation protein WCOI	COR413-F	AT2G15970	-1.60	-0.68	-3.45	0.011353	0.070968	-2.99
259036_at	putative laccase similar to laccase GB:C	LAC7	AT3G09220	1.27	0.34	3.45	0.011361	0.070982	-2.99
257809_at	ribonucleotide reductase small subunit,	TSO2	AT3G27060	-1.50	-0.58	-3.45	0.011371	0.070990	-2.99
257727_at	unknown protein	---	AT3G18380	-1.30	-0.38	-3.45	0.011368	0.070990	-2.99
265353_at	unknown protein ;supported by full-leng	---	AT2G16800	-1.26	-0.33	-3.45	0.011372	0.070990	-2.99
247261_at	ZW10-like protein ; supported by cDNA	---	AT5G64460	-1.30	-0.38	-3.45	0.011379	0.071015	-2.99
258026_at	abscisic acid responsive elements-bindi	ABF4	AT3G19290	-1.45	-0.53	-3.45	0.011388	0.071050	-2.99
265697_at	hypothetical protein predicted by gensca	---	AT2G32170	-1.29	-0.37	-3.45	0.011393	0.071060	-2.99
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.55	-0.64	-3.45	0.011397	0.071070	-2.99
263097_at	hypothetical protein predicted by gensca	PDV2	AT2G16070	-1.41	-0.50	-3.45	0.011405	0.071095	-2.99
250886_at	putative protein	---	AT5G04440	-1.36	-0.44	-3.45	0.011412	0.071096	-3.00
262526_at	putative prenyl transferase (prephytoen	SPS2	AT1G17050	-2.10	-1.07	-3.45	0.011409	0.071096	-2.99
247225_at	inositol-1, 4, 5-trisphosphate 5-phospha	BST1	AT5G65090	-1.36	-0.45	-3.45	0.011414	0.071096	-3.00
262485_at	kinesin-like protein Similar to gb|U06698	---	AT1G21730	-1.27	-0.34	-3.45	0.011444	0.071262	-3.00
267381_at	unknown protein ; supported by cDNA:	---	AT2G26190	3.61	1.85	3.44	0.011449	0.071278	-3.00
253539_at	putative protein RING-finger protein - L	---	AT4G31450	-1.35	-0.43	-3.44	0.011463	0.071344	-3.00
256576_at	zinc finger protein (PMZ), putative ident	PMZ	AT3G28210	2.48	1.31	3.44	0.011467	0.071350	-3.00
248720_at	protein kinase (EC 2.7.1.37) 5 (pir||JN05	D6PKL2	AT5G47750	-1.30	-0.38	-3.44	0.01148	0.071408	-3.00
255041_at	putative protein hypothetical protein F6	---	AT4G09620	-1.39	-0.48	-3.44	0.011496	0.071472	-3.00
254668_at	neoxanthin cleavage enzyme - like prot	NCED2	AT4G18350	1.41	0.50	3.44	0.011496	0.071472	-3.00
251855_at	sugar-phosphate isomerase - like prote	---	AT3G54690	1.75	0.81	3.44	0.011504	0.071492	-3.00
258005_at	cysteine proteinase contains similarity t	---	AT3G19390	2.97	1.57	3.44	0.011506	0.071492	-3.00
248295_at	putative protein contains similarity to rib	---	AT5G53070	-1.34	-0.42	-3.44	0.011509	0.071495	-3.00
264096_at	Expressed protein ; supported by full-ler	---	AT1G78995	-1.76	-0.82	-3.44	0.011532	0.071568	-3.01

266778_at	putative cytochrome P450	CYP707A2	AT2G29090	-1.39	-0.48	-3.44	0.011528	0.071568	-3.01
265628_at	hypothetical protein predicted by genefir	---	AT2G27290	-1.60	-0.68	-3.44	0.011528	0.071568	-3.01
251315_at	putative protein protein kinase homolog	---	AT3G61410	1.37	0.46	3.44	0.011534	0.071568	-3.01
267591_at	Expressed protein ; supported by full-ler	RTFL8	AT2G39705	-2.18	-1.13	-3.44	0.011549	0.071605	-3.01
254108_at	putative protein	RIN2	AT4G25230	1.37	0.45	3.44	0.011547	0.071605	-3.01
264939_at	receptor kinase, putative similar to rece	---	AT1G60630	-1.32	-0.40	-3.44	0.011547	0.071605	-3.01
251868_at	RNA polymerase 24kDa subunit -like pr	RPB5E	AT3G54490	1.34	0.42	3.44	0.011554	0.071614	-3.01
246965_at	methyltransferase-like protein methyltra	---	AT5G24840	-1.55	-0.63	-3.44	0.011559	0.071628	-3.01
254261_at	beta adaptin - like protein beta-adaptin	---	AT4G23460	1.28	0.35	3.44	0.011563	0.071632	-3.01
264113_at	unknown protein	APG9	AT2G31260	1.38	0.47	3.44	0.011589	0.071774	-3.01
265453_at	putative cellular apoptosis susceptibility	---	AT2G46520	-1.39	-0.48	-3.44	0.011599	0.071778	-3.01
246041_at	phospholipase - like protein various prec	---	AT5G19290	1.25	0.32	3.44	0.011597	0.071778	-3.01
260872_at	hypothetical protein predicted by genem	---	AT1G21350	-1.52	-0.60	-3.44	0.011594	0.071778	-3.01
AFFX-r2-Bs	B. subtilis /GEN=thrC /DB_XREF=gb:X0	---	---	-1.84	-0.88	-3.43	0.011604	0.071788	-3.01
265057_at	unknown protein ;supported by full-lengt	---	AT1G52140	-1.34	-0.42	-3.43	0.011614	0.071829	-3.01
266604_at	E2, ubiquitin-conjugating enzyme 6 (UB	UBC6	AT2G46030	1.68	0.74	3.43	0.011635	0.071922	-3.02
248799_at	ethylene responsive element binding fac	ERF5	AT5G47230	4.32	2.11	3.43	0.011635	0.071922	-3.02
257535_at	hypothetical protein predicted by gensca	---	AT3G09490	1.79	0.84	3.43	0.01165	0.071997	-3.02
260536_at	putative electron transfer flavoprotein ub	ETFQO	AT2G43400	1.63	0.70	3.43	0.011653	0.071997	-3.02
252430_at	CHLOROPHYLL A-B BINDING PROTE	LHCA4	AT3G47470	-1.40	-0.49	-3.43	0.011657	0.071998	-3.02
261003_at	hypothetical protein predicted by genem	---	AT1G26500	-1.39	-0.47	-3.43	0.011668	0.072050	-3.02
245771_at	hypothetical protein predicted by genem	---	AT1G30250	4.26	2.09	3.43	0.01168	0.072101	-3.02
255018_at	hypothetical protein ; supported by full-l	---	AT4G10090	-1.43	-0.52	-3.43	0.011697	0.072180	-3.02
253144_at	putative protein transcription factor IIIB	---	AT4G35540	-1.30	-0.38	-3.43	0.011702	0.072180	-3.02
245138_at	unknown protein predicted by genscan;	AFO	AT2G45190	-1.58	-0.66	-3.43	0.011702	0.072180	-3.02
249975_s_a	ribosomal protein L33 - like ribosomal p	---	AT3G06320 /	-1.62	-0.70	-3.43	0.011723	0.072211	-3.02
246929_at	putative protein ; supported by full-lengt	---	AT5G25210	-1.45	-0.53	-3.43	0.011721	0.072211	-3.02
256191_at	unknown protein similar to hypothetical p	---	AT1G30130	1.35	0.43	3.43	0.011716	0.072211	-3.02
245167_s_a	putative synaptobrevin ;supported by fu	ATVAMP7	AT2G33110 /	1.26	0.34	3.43	0.011718	0.072211	-3.02
253802_at	putative protein	---	AT4G28180	-1.31	-0.39	-3.43	0.011719	0.072211	-3.02
259152_at	hypothetical protein similar to putative p	---	AT3G10210	-1.24	-0.31	-3.43	0.011744	0.072288	-3.03
253212_s_a	xanthine dehydrogenase - like protein x	XDH1	AT4G34890 /	1.44	0.52	3.43	0.011749	0.072288	-3.03
252606_at	carboxypeptidase precursor-like protein	scpl48	AT3G45010	2.04	1.03	3.43	0.011751	0.072288	-3.03
265659_at	putative disease resistance protein	AtRLP20	AT2G25440	1.88	0.91	3.43	0.011748	0.072288	-3.03
247006_at	unknown protein ;supported by full-leng	---	AT5G67490	1.23	0.29	3.43	0.01174	0.072288	-3.02

257654_at	DnaJ protein, putative contains Pfam pr	---	AT3G13310	2.39	1.26	3.42	0.011779	0.072440	-3.03
246892_at	putative protein predicted protein, Oryz	---	AT5G25500	-1.33	-0.42	-3.42	0.011785	0.072458	-3.03
249964_at	MAP kinase -like protein ATMPK9, Aral	MPK16	AT5G19010	-1.31	-0.38	-3.42	0.011798	0.072478	-3.03
246307_at	putative nuclear DNA-binding protein G2	ATG2	AT3G51800	-1.52	-0.61	-3.42	0.011801	0.072478	-3.03
251499_at	putative protein putative callose syntha	ATGSL11	AT3G59100	1.30	0.38	3.42	0.011801	0.072478	-3.03
245156_at	calcium-dependent protein kinase-like p	CPK7	AT5G12480	1.32	0.40	3.42	0.011796	0.072478	-3.03
252320_at	endoxyloglucan transferase-like protein	---	AT3G48580	1.94	0.96	3.42	0.011809	0.072505	-3.03
263629_at	hypothetical protein predicted by gensca	---	AT2G04850	-1.57	-0.65	-3.42	0.011818	0.072540	-3.03
267382_at	unknown protein	---	AT2G44300	1.54	0.63	3.42	0.011824	0.072561	-3.03
247448_at	putative protein predicted proteins, Aral	---	AT5G62770	2.53	1.34	3.42	0.011829	0.072574	-3.03
246113_at	putative protein predicted proteins - Aral	---	---	1.28	0.35	3.42	0.011841	0.072628	-3.03
263739_at	putative CONSTANS-like B-box zinc fing	---	AT2G21320	-1.69	-0.76	-3.42	0.01185	0.072660	-3.03
252475_s_a	putative protein several hypothetical pro	PCL1	AT3G46640 /	1.41	0.49	3.42	0.011862	0.072709	-3.04
259141_at	putative cytoskeleton-associated protein	---	AT3G10220	-1.32	-0.40	-3.42	0.011864	0.072709	-3.04
258196_at	hypothetical protein predicted by genem	---	AT3G13980	-2.29	-1.20	-3.42	0.011871	0.072733	-3.04
245803_at	cysteine proteinase RD21A identical to t	RD21	AT1G47128	1.42	0.50	3.42	0.01188	0.072745	-3.04
267286_at	putative seed maturation protein	---	AT2G23640	1.26	0.33	3.42	0.011878	0.072745	-3.04
247393_at	unknown protein	---	AT5G63130	3.30	1.72	3.42	0.011893	0.072788	-3.04
259076_at	hypothetical protein predicted by gensca	TMAC2	AT3G02140	3.14	1.65	3.42	0.011891	0.072788	-3.04
253994_at	protein phosphatase ABI1 ; supported b	ABI1	AT4G26080	1.32	0.40	3.42	0.011906	0.072846	-3.04
250668_at	unknown protein ; supported by full-leng	---	AT5G07020	-1.45	-0.54	-3.41	0.011914	0.072878	-3.04
246674_at	bcnt-like protein ; supported by full-lengt	---	AT5G30490	-1.31	-0.39	-3.41	0.011925	0.072923	-3.04
256792_at	hypothetical protein predicted by genem	---	AT3G22150	-1.83	-0.87	-3.41	0.011936	0.072957	-3.04
266022_at	subtilisin-like serine protease, putative c	---	AT2G05920	-1.52	-0.61	-3.41	0.011937	0.072957	-3.04
252951_at	disease resistance response like protei	---	AT4G38700	-1.56	-0.64	-3.41	0.011945	0.072989	-3.04
263794_at	similar to S-locus glycoproteins	---	AT2G24620	1.26	0.33	3.41	0.011957	0.073044	-3.04
262094_at	SAR DNA binding protein, putative simi	NOP56	AT1G56110	-1.81	-0.86	-3.41	0.011967	0.073081	-3.04
251774_at	nematode resistance protein-like protei	---	AT3G55840	2.79	1.48	3.41	0.011974	0.073107	-3.05
257374_at	hypothetical protein predicted by gensca	---	AT2G43280	-1.46	-0.55	-3.41	0.011987	0.073168	-3.05
262780_at	putative cytochrome P450 monooxyger	CYP71B28	AT1G13090	-1.43	-0.52	-3.41	0.011997	0.073211	-3.05
259955_s_a	unknown protein ;supported by full-leng	BZR1	AT1G19350 /	-1.35	-0.43	-3.41	0.012014	0.073276	-3.05
260164_at	putative D-isomer specific 2-hydroxyaci	---	AT1G79870	-1.31	-0.39	-3.41	0.012012	0.073276	-3.05
266556_at	hypothetical protein predicted by gensca	---	AT2G46230	-1.38	-0.46	-3.41	0.012049	0.073405	-3.05
253881_at	putative protein Ran_GTP binding prote	---	AT4G27640	-1.29	-0.37	-3.41	0.012046	0.073405	-3.05
249430_at	GTP-binding protein-like GTP-binding p	---	AT5G39900	-1.51	-0.60	-3.41	0.012043	0.073405	-3.05

245867_at	ATP phosphoribosyl transferase identica	ATATP-PR	AT1G58080	-1.35	-0.43	-3.41	0.012048	0.073405	-3.05
260895_at	unknown protein similar to unknown pro	---	AT1G29250	-1.72	-0.78	-3.41	0.012054	0.073417	-3.05
264270_at	beta-glucosidase, putative similar to be	---	---	-1.26	-0.34	-3.41	0.012058	0.073422	-3.05
263949_at	E2, ubiquitin-conjugating enzyme, putat	MMZ3	AT2G36060	-1.25	-0.33	-3.40	0.012094	0.073626	-3.06
257541_at	hypothetical protein predicted by genem	---	AT3G25950	1.90	0.93	3.40	0.012098	0.073629	-3.06
253492_at	enoyl-CoA hydratase - like protein enoy	---	AT4G31810	-1.96	-0.97	-3.40	0.012102	0.073635	-3.06
251293_at	hypothetical protein	---	AT3G61930	5.58	2.48	3.40	0.012107	0.073641	-3.06
254201_at	putative protein predicted proteins	---	AT4G24130	1.44	0.53	3.40	0.01211	0.073642	-3.06
262741_at	hypothetical protein	---	AT1G28760	-1.28	-0.35	-3.40	0.012121	0.073668	-3.06
265923_at	putative protein kinase contains a protei	---	AT2G18470	-1.25	-0.32	-3.40	0.01212	0.073668	-3.06
261088_at	DNA-binding protein, putative similar to	---	AT1G07590	-1.39	-0.47	-3.40	0.012129	0.073686	-3.06
267477_at	putative receptor-like protein kinase	PLPB	AT2G02710	1.69	0.76	3.40	0.01213	0.073686	-3.06
260728_at	Pto kinase interactor 1, putative similar	---	AT1G48210	1.72	0.79	3.40	0.012135	0.073697	-3.06
251922_at	protein kinase -like protein protein kinas	---	AT3G54030	1.70	0.77	3.40	0.01214	0.073703	-3.06
263875_at	unknown protein ;supported by full-leng	ogo-02	AT2G21970	-1.53	-0.61	-3.40	0.012143	0.073703	-3.06
256034_at	unknown protein ; supported by cDNA: g	---	AT1G07080	-1.28	-0.35	-3.40	0.012146	0.073703	-3.06
248466_at	putative protein similar to unknown prote	HVA22E	AT5G50720	-1.62	-0.70	-3.40	0.012176	0.073810	-3.06
264435_at	putative glutathione S-transferase TSI-1	ATGSTU1	AT1G10360	-1.62	-0.70	-3.40	0.012168	0.073810	-3.06
247677_at	oxysterol-binding protein - like oxystero	ORP3C	AT5G59420	1.27	0.34	3.40	0.012171	0.073810	-3.06
264292_at	hypothetical protein predicted by genem	---	AT1G78790	-1.37	-0.45	-3.40	0.012175	0.073810	-3.06
250080_at	translocon Tic40-like protein ; supporte	TIC40	AT5G16620	-1.25	-0.32	-3.40	0.012194	0.073876	-3.06
255884_at	hypothetical protein predicted by genem	---	AT1G20310	3.38	1.76	3.40	0.012191	0.073876	-3.06
246733_at	serine protease-like protein serine prote	---	AT5G27660	-1.35	-0.43	-3.40	0.012206	0.073931	-3.07
248334_s_a	unknown protein ; supported by cDNA:	---	AT5G52370 /	-1.62	-0.69	-3.40	0.012216	0.073971	-3.07
253941_at	putative protein	---	AT4G26980	-1.27	-0.35	-3.40	0.012229	0.074029	-3.07
253279_at	putative protein B subunit of propionyl-(	MCCB	AT4G34030	1.69	0.76	3.39	0.012239	0.074069	-3.07
266510_at	unknown protein	SWA1	AT2G47990	-1.76	-0.82	-3.39	0.01225	0.074071	-3.07
254830_at	putative protein predicted protein, Sacc	---	AT4G12590	-1.24	-0.30	-3.39	0.012248	0.074071	-3.07
258827_at	hypothetical protein predicted by genefir	---	AT3G07150	-1.46	-0.55	-3.39	0.012248	0.074071	-3.07
267065_at	hypothetical protein predicted by genefir	---	AT2G41080	-1.37	-0.45	-3.39	0.012252	0.074071	-3.07
259792_at	unknown protein ; supported by cDNA: g	CAD1	AT1G29690	2.19	1.13	3.39	0.012264	0.074125	-3.07
AFFX-DapX	B. subtilis /GEN=dapB, jojF /DB_XREF=	---	---	-1.56	-0.64	-3.39	0.012279	0.074192	-3.07
255424_at	putative glycosylation enzyme similar to	---	AT4G03340	1.30	0.38	3.39	0.012284	0.074202	-3.07
245961_at	putative protein predicted proteins - Ara	---	AT5G19670	-1.37	-0.46	-3.39	0.01229	0.074220	-3.07
253867_at	putative protein tRNA nucleotidyltransfe	---	AT4G27490	-1.57	-0.65	-3.39	0.012301	0.074269	-3.07

266898_at	unknown protein ; supported by cDNA: g	---	AT2G45990	-1.38	-0.47	-3.39	0.012312	0.074315	-3.07
260822_at	RNA polymerase, putative similar to DI	---	AT1G06790	-1.30	-0.38	-3.39	0.012315	0.074315	-3.08
247748_at	putative protein ;supported by full-lengt	---	AT5G58920	-1.32	-0.40	-3.39	0.012327	0.074355	-3.08
251485_at	putative protein rad21 mitotic cohesin -	SYN3	AT3G59550	1.26	0.33	3.39	0.012335	0.074355	-3.08
248201_at	putative protein similar to unknown prote	PTAC15	AT5G54180	-1.77	-0.83	-3.39	0.012332	0.074355	-3.08
262420_at	hypothetical protein contains similarity to	TAF15	AT1G50300	-1.24	-0.31	-3.39	0.012333	0.074355	-3.08
254665_at	beta-1,3-glucanase-like protein strong s	---	AT4G18340	1.64	0.71	3.39	0.01237	0.074545	-3.08
264615_at	unknown protein ; supported by cDNA:	---	AT1G04590	-1.54	-0.62	-3.39	0.012373	0.074545	-3.08
245774_at	hypothetical protein contains similarity to	TCP24	AT1G30210	-1.28	-0.35	-3.38	0.012405	0.074716	-3.08
265118_at	beta-fructosidase nearly identical to beta	---	AT1G62660	1.58	0.66	3.38	0.012414	0.074753	-3.08
256015_at	PSI type II chlorophyll a/b-binding prote	LHCA6	AT1G19150	-3.05	-1.61	-3.38	0.012421	0.074756	-3.08
246485_at	putative protein cell death associated p	AtCXE17	AT5G16080	2.99	1.58	3.38	0.012419	0.074756	-3.08
248026_at	putative protein similar to unknown prote	---	AT5G55710	-1.35	-0.44	-3.38	0.012432	0.074803	-3.08
245863_s_a	hypothetical protein contains similarity to	---	AT1G58050 /	-1.36	-0.44	-3.38	0.012461	0.074957	-3.09
248227_at	ABA-inducible protein-like ;supported b	---	AT5G53820	1.32	0.40	3.38	0.012468	0.074979	-3.09
266990_at	putative ABC transporter	ATATH8	AT2G39190	-1.69	-0.75	-3.38	0.012504	0.075175	-3.09
256422_at	unknown protein	MOS2	AT1G33520	-1.31	-0.39	-3.38	0.012511	0.075182	-3.09
249513_at	glucosyltransferase-like protein ; suppor	---	AT5G38460	-1.30	-0.37	-3.38	0.012512	0.075182	-3.09
246699_at	putative protein predicted proteins, Sac	---	AT5G27990	-1.48	-0.56	-3.38	0.012521	0.075206	-3.09
257601_at	hypothetical protein predicted by genem	---	AT3G24820	-1.28	-0.35	-3.38	0.012522	0.075206	-3.09
264130_at	hypothetical protein predicted by genem	---	AT1G79160	1.40	0.49	3.38	0.012536	0.075269	-3.09
266291_at	putative tropinone reductase ;supported	---	AT2G29320	-1.68	-0.75	-3.38	0.01254	0.075271	-3.09
262570_at	unknown protein EST gb|H77143 comes	---	AT1G15200	-1.31	-0.39	-3.38	0.012544	0.075280	-3.09
260617_at	Expressed protein ; supported by full-ler	---	AT1G53345	-1.37	-0.46	-3.38	0.012555	0.075305	-3.10
260674_at	unknown protein ; supported by cDNA: g	---	AT1G19370	-1.31	-0.39	-3.38	0.012555	0.075305	-3.10
265101_at	unknown protein similar to ESTs gb|R30	---	AT1G30880	-1.57	-0.65	-3.38	0.012561	0.075322	-3.10
244961_at	hypothetical protein	---	---	-1.25	-0.33	-3.37	0.012566	0.075331	-3.10
255714_at	contains weak similarity to S. cerevisiae	---	AT4G00300	1.35	0.44	3.37	0.012595	0.075463	-3.10
246286_at	unknown protein	---	AT1G31910	-1.28	-0.35	-3.37	0.012595	0.075463	-3.10
253369_at	F-box protein family, AtFBL15 contains	---	AT4G33210	-1.23	-0.29	-3.37	0.012599	0.075466	-3.10
264882_at	NAM protein, putative similar to NAM pr	anac025	AT1G61110	1.28	0.35	3.37	0.012614	0.075536	-3.10
259707_at	thylakoid-bound ascorbate peroxidase ic	TAPX	AT1G77490	-1.48	-0.57	-3.37	0.012619	0.075547	-3.10
260127_at	hypothetical protein similar to hypotheti	---	AT1G36320	-1.46	-0.55	-3.37	0.012631	0.075565	-3.10
254231_at	putative protein AR411 - Arabidopsis th	WRKY53	AT4G23810	4.47	2.16	3.37	0.012632	0.075565	-3.10
249563_at	similar to unknown protein (pir |T03994)	---	AT5G38360	-1.29	-0.36	-3.37	0.012632	0.075565	-3.10

252376_at	L-galactono-1,4-lactone dehydrogenase	ATGLDH	AT3G47930	-1.46	-0.54	-3.37	0.012636	0.075573	-3.10
262775_at	unknown protein	---	AT1G13000	1.28	0.36	3.37	0.012644	0.075599	-3.10
256633_at	unknown protein	GATL10	AT3G28340	3.68	1.88	3.37	0.012692	0.075868	-3.11
260468_at	transcription factor RUSH-1alpha isolog	---	AT1G11100	1.45	0.54	3.37	0.012697	0.075873	-3.11
265199_s_a	putative glucosyl transferase	---	AT2G36770 /	1.56	0.64	3.37	0.012705	0.075894	-3.11
266154_at	putative cytochrome p450	---	AT2G12190	1.49	0.58	3.37	0.012707	0.075894	-3.11
245100_at	ubiquitin-specific protease 5 (UBP5), pu	UBP5	AT2G40930	-1.30	-0.37	-3.37	0.012726	0.075981	-3.11
259879_at	putative calmodulin similar to calmodulir	CML38	AT1G76650	3.38	1.76	3.37	0.012728	0.075981	-3.11
256246_at	betaine aldehyde dehydrogenase, puta	ALDH22a1	AT3G66658	-1.42	-0.51	-3.36	0.012733	0.075990	-3.11
261719_at	hypothetical protein similar to hypothetic	---	AT1G18390	2.29	1.19	3.36	0.012738	0.076002	-3.11
255479_at	coded for by A. thaliana cDNA T46835	SAG21	AT4G02380	2.94	1.56	3.36	0.01275	0.076036	-3.11
245744_at	unknown protein	---	AT1G51110	-2.03	-1.02	-3.36	0.012748	0.076036	-3.11
262419_at	hypothetical protein identical to hypothe	---	AT1G50380	-1.44	-0.53	-3.36	0.012754	0.076039	-3.11
253952_at	ubiquitin-like protein ubiquitin-like prote	SUMO1	AT4G26840	-1.30	-0.38	-3.36	0.012759	0.076049	-3.11
264120_at	latex-abundant protein, putative similar	AtMC4	AT1G79340	1.25	0.32	3.36	0.012772	0.076065	-3.11
248505_at	putative protein similar to unknown prote	---	AT5G50360	1.38	0.47	3.36	0.012773	0.076065	-3.11
254163_s_a	putative protein storage protein - Popul	---	AT4G24340 /	-3.08	-1.62	-3.36	0.012768	0.076065	-3.11
251133_at	LAX1 / AUX1 -like permease	---	AT5G01240	-1.49	-0.58	-3.36	0.012775	0.076065	-3.11
266796_at	predicted by genscan	---	AT2G02880	-1.30	-0.38	-3.36	0.012818	0.076259	-3.12
252053_at	syntaxin-like protein synt4 ;supported b	SYP122	AT3G52400	2.37	1.24	3.36	0.012815	0.076259	-3.12
261616_at	NAC domain containing protein, putativ	ANAC014	AT1G33060	-1.22	-0.29	-3.36	0.012817	0.076259	-3.12
262164_at	unknown protein ; supported by cDNA: g	---	AT1G78070	-1.43	-0.52	-3.36	0.01283	0.076312	-3.12
254485_at	cell-cell signaling protein csgA - like cel	---	AT4G20760	-1.42	-0.51	-3.36	0.01285	0.076389	-3.12
266979_at	unknown protein ;supported by full-leng	PPL2	AT2G39470	-2.88	-1.53	-3.36	0.012849	0.076389	-3.12
252273_at	putative WD-40 repeat - protein beta-tra	---	AT3G49660	-1.33	-0.41	-3.36	0.012893	0.076616	-3.12
247443_at	putative protein predicted proteins, Aral	---	AT5G62720	-1.51	-0.60	-3.36	0.012895	0.076616	-3.12
249076_at	putative protein similar to unknown prote	TOM22-V	AT5G43970	-1.45	-0.54	-3.36	0.012901	0.076632	-3.12
263621_at	putative DNA-directed RNA polymerase	NRPB6B	AT2G04630	-1.33	-0.41	-3.35	0.012911	0.076673	-3.12
257937_at	hypothetical protein predicted by gensca	---	AT3G19810	-1.25	-0.33	-3.35	0.012923	0.076724	-3.13
252220_at	putative protein hypothetical protein - A	LBD38	AT3G49940	1.56	0.65	3.35	0.012927	0.076728	-3.13
258673_at	unknown protein	---	AT3G08620	-1.48	-0.56	-3.35	0.012946	0.076787	-3.13
253761_at	putative protein thyroid receptor interac	---	AT4G28820	-1.36	-0.45	-3.35	0.012942	0.076787	-3.13
246539_at	putative protein geranylgeranylated pro	MUB2	AT5G15460	-1.24	-0.31	-3.35	0.012947	0.076787	-3.13
244962_at	NADH dehydrogenase ND4	---	---	-1.23	-0.30	-3.35	0.01296	0.076845	-3.13
266856_at	putative ABC transporter related to mult	PDR4	AT2G26910	1.69	0.76	3.35	0.012969	0.076856	-3.13

263565_at	unknown protein	FUT4	AT2G15390	2.45	1.30	3.35	0.012989	0.076856	-3.13
258067_at	putative mitotic checkpoint protein simil	---	AT3G25980	1.29	0.37	3.35	0.012985	0.076856	-3.13
257324_at	hypothetical protein	---	---	-2.12	-1.09	-3.35	0.012977	0.076856	-3.13
245400_at	ATP-dependent Clp protease proteolyti	---	AT4G17040	-1.39	-0.48	-3.35	0.012978	0.076856	-3.13
253060_at	putative protein predicted protein, Arabi	---	AT4G37710	1.92	0.94	3.35	0.012981	0.076856	-3.13
250867_at	putative protein predicted protein, Arabi	---	AT5G03880	-1.49	-0.58	-3.35	0.012971	0.076856	-3.13
246329_at	putative protein gamma-tubulin interact	---	AT3G43610	-1.35	-0.43	-3.35	0.012987	0.076856	-3.13
264161_at	antigen receptor, putative similar to anti	---	AT1G65420	-1.32	-0.40	-3.35	0.012992	0.076856	-3.13
254079_at	putative protein pmt2 methyltransferase	---	AT4G25730	-1.66	-0.73	-3.35	0.013018	0.076956	-3.13
260523_at	putative salt-inducible protein	EMB2654	AT2G41720	-1.47	-0.56	-3.35	0.013019	0.076956	-3.13
261408_s_a	histone H4 identical to GB:M36659 from	---	AT1G07660 /	-1.45	-0.53	-3.35	0.013019	0.076956	-3.13
259490_at	hypothetical protein preedicted by gener	---	AT1G15800	1.30	0.38	3.35	0.013026	0.076975	-3.13
248403_at	arginine-aspartate-rich RNA binding pro	---	AT5G51410	-1.31	-0.39	-3.35	0.013048	0.077047	-3.14
257248_at	hypothetical protein predicted by gensca	---	AT3G24150	-1.45	-0.53	-3.35	0.013048	0.077047	-3.14
265008_at	Mlo protein, putative similar to Mlo prote	MLO6	AT1G61560	2.69	1.43	3.35	0.013042	0.077047	-3.14
267068_at	unknown protein	---	AT2G41020	-1.39	-0.47	-3.35	0.013058	0.077084	-3.14
251531_at	putative protein hypothetical protein F4	---	AT3G58550	1.35	0.43	3.34	0.013079	0.077189	-3.14
246498_at	stearoyl-acyl carrier protein desaturase	---	AT5G16230	1.94	0.95	3.34	0.013089	0.077230	-3.14
252941_at	phenylalanyl-trna synthetase - like prote	---	AT4G39280	-1.26	-0.34	-3.34	0.013093	0.077233	-3.14
255384_at	hypothetical protein	---	AT4G03580	1.24	0.31	3.34	0.013107	0.077274	-3.14
260102_at	unknown protein	---	AT1G35470	-1.36	-0.44	-3.34	0.013104	0.077274	-3.14
255296_at	hypothetical protein	---	AT4G04790	-1.69	-0.75	-3.34	0.013115	0.077300	-3.14
251904_at	Machado-Joseph disease MJD1a -like p	---	AT3G54130	1.43	0.52	3.34	0.013123	0.077327	-3.14
261377_at	unknown protein ;supported by full-lengt	---	AT1G18850	-1.76	-0.82	-3.34	0.013137	0.077393	-3.14
259439_at	1-aminocyclopropane-1-carboxylate syn	ACS2	AT1G01480	4.14	2.05	3.34	0.013153	0.077412	-3.14
266599_at	unknown protein	---	AT2G46100	-1.27	-0.35	-3.34	0.013154	0.077412	-3.14
246223_at	UDP-glucuronyltransferase-like protein	IRX14	AT4G36890	-1.27	-0.34	-3.34	0.013153	0.077412	-3.14
266283_at	putative proline-rich protein	---	AT2G29210	-1.33	-0.41	-3.34	0.013152	0.077412	-3.14
255894_at	nuclear poly(A) polymerase, putative sir	---	AT1G17980	-1.31	-0.39	-3.34	0.013159	0.077422	-3.14
245780_at	unknown protein ;supported by full-lengt	---	AT1G45688	1.36	0.44	3.34	0.013167	0.077448	-3.15
258185_at	hypothetical protein similar to hypothetic	---	AT3G21580	-1.41	-0.49	-3.34	0.013175	0.077475	-3.15
253451_at	putative myb-protein transforming prote	PC-MYB1	AT4G32730	1.29	0.36	3.34	0.013188	0.077533	-3.15
249908_at	putative protein similar to unknown prote	---	AT5G22760	-1.28	-0.36	-3.34	0.013202	0.077592	-3.15
261269_at	unknown protein ; supported by full-leng	---	AT1G26690	1.36	0.45	3.34	0.013207	0.077600	-3.15
266751_at	putative peptide chain release factor	---	AT2G47020	-1.29	-0.37	-3.34	0.013222	0.077670	-3.15

251259_at	putative protein phosphoprotein phosph	---	AT3G62260	1.55	0.63	3.34	0.013239	0.077749	-3.15
248771_at	unknown protein	---	AT5G47790	-1.37	-0.45	-3.33	0.013257	0.077802	-3.15
253972_at	putative protein Uvi31, Schizosaccharo	CPSUFE	AT4G26500	-1.22	-0.29	-3.33	0.01326	0.077802	-3.15
254863_at	putative protein predicted protein W02C	ATNUDX1	AT4G11980	-1.36	-0.44	-3.33	0.013261	0.077802	-3.15
254125_at	putative alliin lyase alliin lyase (EC 4.4.	TAR2	AT4G24670	-1.74	-0.80	-3.33	0.01326	0.077802	-3.15
257325_at	hypothetical protein	---	AT2G07798	-1.89	-0.92	-3.33	0.013267	0.077802	-3.15
259170_at	hypothetical protein similar to putative p	---	AT3G03510	-1.27	-0.35	-3.33	0.013268	0.077802	-3.15
245387_at	nuclear RNA binding protein A-like prote	---	AT4G17520	-1.42	-0.50	-3.33	0.013277	0.077813	-3.15
248814_at	putative protein similar to unknown prote	---	AT5G46910	3.27	1.71	3.33	0.013276	0.077813	-3.15
249849_at	putative protein similar to unknown prote	NIC2	AT5G23230	-1.39	-0.48	-3.33	0.013281	0.077816	-3.15
263345_s_a	putative chlorophyll a/b binding protein	LHCB2.1	AT2G05070 /	-2.01	-1.01	-3.33	0.013286	0.077823	-3.15
262313_at	unknown protein ;supported by full-lengt	---	AT1G70900	-1.47	-0.56	-3.33	0.013304	0.077883	-3.16
261027_at	cyclic nucleotide and calmodulin-regula	ATCNGC1	AT1G01340	2.20	1.13	3.33	0.013301	0.077883	-3.16
248959_at	putative protein similar to unknown prote	---	AT5G45630	2.02	1.02	3.33	0.013306	0.077883	-3.16
248436_at	putative protein contains similarity to unl	---	AT5G51220	-1.29	-0.37	-3.33	0.01332	0.077943	-3.16
252701_at	hypothetical protein SPOP protein, Hon	ATBPM6	AT3G43700	-1.39	-0.48	-3.33	0.013335	0.078012	-3.16
265450_at	hypothetical protein predicted by genefin	---	AT2G46620	1.54	0.62	3.33	0.013347	0.078064	-3.16
245269_at	hypothetical protein ; supported by cDNA	---	AT4G14500	1.32	0.41	3.33	0.013361	0.078085	-3.16
260425_at	hypothetical protein similar to CCAAT-b	EDA25	AT1G72440	-1.89	-0.92	-3.33	0.013355	0.078085	-3.16
253479_at	ferredoxin-NADP+ reductase - like prote	---	AT4G32360	-1.26	-0.34	-3.33	0.01336	0.078085	-3.16
259334_at	unknown protein similar to hect domain	---	AT3G03790	1.48	0.57	3.33	0.013366	0.078097	-3.16
244981_at	ribosomal protein S8	---	---	-1.37	-0.46	-3.33	0.01337	0.078098	-3.16
260812_at	nodulin-like protein similar to MtN21 GE	---	AT1G43650	-1.55	-0.63	-3.33	0.013393	0.078210	-3.16
265974_at	unknown protein	---	---	1.57	0.65	3.33	0.013401	0.078237	-3.16
255128_at	putative protein glutamic acid-rich prote	---	AT4G08310	-1.40	-0.49	-3.33	0.01341	0.078272	-3.16
254093_at	putative protein extensin, Catharanthus	AtMC2	AT4G25110	2.05	1.04	3.33	0.013416	0.078283	-3.16
250471_at	myo-inositol-1-phosphate synthase -like	MIPS3	AT5G10170	-1.52	-0.61	-3.32	0.013431	0.078330	-3.17
245180_at	putative protein similarity to proteins of u	---	AT5G12410	-1.50	-0.58	-3.32	0.013433	0.078330	-3.17
262953_at	hypothetical protein predicted by genem	---	AT1G75670	-1.59	-0.67	-3.32	0.013434	0.078330	-3.17
250494_at	embryogenic callus protein - like embry	HAM2	AT5G09740	-1.39	-0.47	-3.32	0.013455	0.078434	-3.17
262029_at	50S ribosomal protein L21 chloroplast p	---	AT1G35680	-1.42	-0.50	-3.32	0.013507	0.078635	-3.17
256238_at	unknown protein ; supported by full-leng	ELC	AT3G12400	1.42	0.51	3.32	0.013501	0.078635	-3.17
265388_s_a	unknown protein ;supported by full-leng	---	AT2G20990 /	-1.28	-0.36	-3.32	0.013505	0.078635	-3.17
251986_at	putative protein various predicted prote	---	AT3G53310	-1.78	-0.83	-3.32	0.013501	0.078635	-3.17
256192_at	diadenosine 5,5-P1,P4-tetraphosphate	ATNUDX2	AT1G30110	1.33	0.41	3.32	0.0135	0.078635	-3.17

260627_at	hypothetical protein predicted by genem	---	AT1G62310	-1.51	-0.59	-3.32	0.013522	0.078701	-3.17
246476_at	putative protein predicted proteins - Ara	---	AT5G16730	-1.47	-0.55	-3.32	0.013529	0.078726	-3.17
252104_at	putative protein KIAA0851 protein, Hom	RHD4	AT3G51460	1.38	0.47	3.32	0.013561	0.078891	-3.18
246575_at	bystin, putative similar to bystin GI:116	---	AT1G31660	-1.54	-0.63	-3.32	0.013567	0.078906	-3.18
266202_at	putative cinnamoyl-CoA reductase	---	AT2G02400	-1.27	-0.34	-3.32	0.013571	0.078907	-3.18
246064_at	DNA binding protein ACBF - like DNA b	---	AT5G19350	-1.30	-0.38	-3.32	0.013594	0.078998	-3.18
246879_at	endopeptidase - like protein O-sialoglyc	---	AT5G26110	-1.31	-0.39	-3.32	0.013593	0.078998	-3.18
246144_at	dynein light chain - like protein dynein li	---	AT5G20110	-1.56	-0.64	-3.32	0.013605	0.079044	-3.18
246192_at	translation initiation factor eIF-2 beta ch	EIF2 BETA	AT5G20920	-1.26	-0.33	-3.31	0.013637	0.079171	-3.18
251138_at	putative protein various predicted protei	---	AT5G01160	-1.33	-0.42	-3.31	0.013633	0.079171	-3.18
254455_at	hypothetical protein	---	AT4G21140	-1.52	-0.60	-3.31	0.013636	0.079171	-3.18
258166_at	WD-repeat protein, putative contains Pf	---	AT3G21540	-1.71	-0.78	-3.31	0.013642	0.079177	-3.18
249360_at	putative protein KIAA0409 protein, Hom	---	AT5G40530	-1.30	-0.37	-3.31	0.013663	0.079272	-3.18
248622_at	xylosidase	---	AT5G01980 /	1.90	0.93	3.31	0.013665	0.079272	-3.18
260882_at	DNA binding protein, putative similar to	WRKY65	AT1G29280	1.68	0.75	3.31	0.013677	0.079322	-3.19
252075_at	putative protein saposin precursor - Hor	---	AT3G51730	1.44	0.53	3.31	0.013694	0.079352	-3.19
256779_at	beta-fructofuranosidase, putative simila	AtcwINV5	AT3G13784	1.23	0.30	3.31	0.013693	0.079352	-3.19
264911_at	auxin-induced protein, putative similar t	---	AT1G60690	-1.42	-0.51	-3.31	0.013692	0.079352	-3.19
254057_at	putative protein ;supported by full-lengt	---	AT4G25170	1.63	0.70	3.31	0.013696	0.079352	-3.19
257726_at	hypothetical protein predicted by genem	---	AT3G18360	1.28	0.36	3.31	0.013704	0.079377	-3.19
250156_at	putative protein predicted proteins, Hom	---	AT5G15170	-1.25	-0.33	-3.31	0.013707	0.079377	-3.19
249705_at	serine/threonine protein kinase-like	---	AT5G35580	1.50	0.58	3.31	0.013716	0.079408	-3.19
249546_at	putative protein chromosome segregati	PMI15	AT5G38150	-1.54	-0.62	-3.31	0.013739	0.079517	-3.19
248039_at	putative protein similar to unknown prote	---	AT5G55950	1.24	0.31	3.31	0.013766	0.079578	-3.19
256268_at	retinoblastoma-related protein, putative	RBR1	AT3G12280	-1.41	-0.49	-3.31	0.013766	0.079578	-3.19
260274_at	putative glycerol kinase similar to GLYC	NHO1	AT1G80460	1.40	0.49	3.31	0.013754	0.079578	-3.19
260921_at	amp-binding protein, putative similar to	---	AT1G21540	-1.52	-0.60	-3.31	0.013764	0.079578	-3.19
247420_at	unknown protein	---	AT5G63100	-1.46	-0.54	-3.31	0.013762	0.079578	-3.19
259316_at	unknown protein	---	AT3G01175	1.40	0.48	3.31	0.013771	0.079584	-3.19
256883_at	unknown protein ; supported by cDNA:	---	AT3G26440	2.24	1.16	3.31	0.013781	0.079613	-3.19
253079_s_a	putative protein F56F10.1, Caenorhabd	---	AT4G36190 /	-1.43	-0.52	-3.31	0.013787	0.079613	-3.19
257641_s_a	hypothetical protein	AOC1	AT3G25760 /	-1.67	-0.74	-3.31	0.013784	0.079613	-3.19
249066_at	WD-repeat protein-like	---	AT5G43920	-1.24	-0.31	-3.30	0.013811	0.079735	-3.20
261256_at	disease resistance protein RTM1 identi	RTM1	AT1G05760	1.40	0.49	3.30	0.013817	0.079749	-3.20
252863_at	myo-inositol-1-phosphate synthase ;sup	MIPS1	AT4G39800	-3.72	-1.90	-3.30	0.013833	0.079821	-3.20

262737_at	hypothetical protein	SRD2	AT1G28560	-1.36	-0.44	-3.30	0.013845	0.079851	-3.20
256870_at	cytochrome P450, putative contains Pfa	CYP71B34	AT3G26300	-1.64	-0.72	-3.30	0.013844	0.079851	-3.20
256753_at	unknown protein contains Pfam profile:	GHS1	AT3G27160	-1.39	-0.47	-3.30	0.013853	0.079877	-3.20
246246_at	putative protein	---	AT4G37170	-1.40	-0.48	-3.30	0.013873	0.079927	-3.20
249143_at	putative protein strong similarity to unkn	---	AT5G43230	1.24	0.31	3.30	0.01387	0.079927	-3.20
264624_at	zinc finger protein ATZF1, putative iden	ERD6	AT1G08930	1.45	0.53	3.30	0.013871	0.079927	-3.20
249862_at	PGPD14 protein ;supported by full-leng	---	AT5G22920	1.76	0.81	3.30	0.013879	0.079929	-3.20
260480_at	Ser/Thr kinase ;supported by full-length	SNRK2.4	AT1G10940	-1.23	-0.30	-3.30	0.013883	0.079929	-3.20
250758_at	eukaryotic translation initiation factor 3 s	EIF3G2	AT5G06000	-1.45	-0.54	-3.30	0.01388	0.079929	-3.20
260593_at	poly(A)-specific ribonuclease, putative s	AHG2	AT1G55870	-1.41	-0.49	-3.30	0.013899	0.079972	-3.20
256625_at	uteroglobin promoter-binding protein, R	---	AT3G20010	-1.56	-0.64	-3.30	0.013898	0.079972	-3.20
256548_at	hypothetical protein contains similarity to	---	AT3G14770	4.05	2.02	3.30	0.013901	0.079972	-3.20
258179_at	integral membrane protein, putative cor	---	AT3G21690	1.49	0.57	3.30	0.01391	0.079989	-3.20
262202_at	TATC-like protein similar to GB:AAD339	APG2	AT2G01110	-1.49	-0.58	-3.30	0.013911	0.079989	-3.20
255850_at	putative chloroplast 50S ribosomal prote	---	AT2G33450	-1.36	-0.44	-3.29	0.013989	0.080048	-3.21
267099_at	DNA-(apurinic or apyrimidinic site) lyase	ARP	AT2G41460	-1.52	-0.61	-3.30	0.013942	0.080048	-3.21
251678_at	putative protein conserved hypothetical	EDA7	AT3G56990	-1.26	-0.34	-3.30	0.013979	0.080048	-3.21
247032_at	putative protein strong similarity to unkn	SDN3	AT5G67240	-1.28	-0.36	-3.29	0.013985	0.080048	-3.21
245773_at	hypothetical protein predicted by gensca	---	AT1G30290	-1.30	-0.38	-3.30	0.013945	0.080048	-3.21
267442_at	unknown protein ;supported by full-leng	---	AT2G19080	-1.26	-0.33	-3.30	0.013959	0.080048	-3.21
266189_at	unknown protein	---	AT2G39020	-1.24	-0.31	-3.29	0.013988	0.080048	-3.21
264336_at	hypothetical protein contains similarity to	---	AT1G70360	-1.36	-0.44	-3.30	0.013968	0.080048	-3.21
260443_at	Expressed protein ; supported by full-ler	---	AT1G68185	-1.24	-0.31	-3.29	0.01399	0.080048	-3.21
253662_at	transcription factor-like protein Arabidop	ARF16	AT4G30080	-1.32	-0.40	-3.29	0.013992	0.080048	-3.21
252383_at	ABC-type transport protein-like protein	ATH6	AT3G47780	2.10	1.07	3.30	0.013967	0.080048	-3.21
261793_at	unknown protein ; supported by cDNA: g	---	AT1G16080	-1.83	-0.87	-3.30	0.013975	0.080048	-3.21
257132_at	hypothetical protein predicted by genem	---	AT3G20230	-1.29	-0.37	-3.30	0.013957	0.080048	-3.21
255638_at	predicted protein of unknown function ;	---	AT4G00740	-1.42	-0.51	-3.30	0.013968	0.080048	-3.21
251689_at	putative protein motif in hypothetical pro	---	AT3G56500	2.52	1.33	3.30	0.013937	0.080048	-3.20
247168_at	putative protein contains similarity to pro	---	AT5G65860	-1.38	-0.47	-3.30	0.013939	0.080048	-3.20
254280_at	Expressed protein ; supported by full-ler	SMO1-2	AT4G22756	-1.49	-0.58	-3.29	0.01398	0.080048	-3.21
249800_at	MtN3-like protein ; supported by cDNA:	MTN3	AT5G23660	-1.31	-0.38	-3.30	0.013932	0.080048	-3.20
249007_at	unknown protein ;supported by full-leng	---	AT5G44650	-1.57	-0.65	-3.30	0.013938	0.080048	-3.20
247605_at	DNA binding protein - like putative basi	TCP5	AT5G60970	-1.37	-0.45	-3.29	0.013986	0.080048	-3.21
265959_at	unknown protein ;supported by full-leng	---	AT2G37240	-1.76	-0.82	-3.29	0.014001	0.080081	-3.21

257857_s_a	unknown protein contains an RNase_PH	RRP45a	AT3G12990 /	-1.50	-0.58	-3.29	0.014022	0.080182	-3.21
245287_at	imidazoleglycerol-phosphate dehydratas	---	AT4G14910	-1.45	-0.54	-3.29	0.014029	0.080201	-3.21
254306_at	putative protein ; supported by cDNA: g	ATCES1	AT4G22330	1.24	0.31	3.29	0.014055	0.080308	-3.21
262440_at	serpin, putative similar to serpin GB:X9	---	AT1G47710	-1.47	-0.55	-3.29	0.014052	0.080308	-3.21
245602_at	Expressed protein ;supported by cDNA:	---	AT4G14270	-1.49	-0.58	-3.29	0.01406	0.080315	-3.21
263225_at	putative DNA-binding protein similar to	WRKY14	AT1G30650	1.34	0.42	3.29	0.014063	0.080315	-3.21
256401_at	putative guanylate kinase similar to gua	---	AT3G06200	-1.22	-0.29	-3.29	0.014071	0.080332	-3.21
249149_at	casein kinase I ; supported by cDNA: gi_	ckl8	AT5G43320	1.23	0.30	3.29	0.014073	0.080332	-3.22
263495_at	cold-regulated protein cor15b precursor	COR15B	AT2G42530	-2.66	-1.41	-3.29	0.014097	0.080427	-3.22
266253_at	unknown protein contains non-consensu	HDT4	AT2G27840	-1.68	-0.75	-3.29	0.014095	0.080427	-3.22
265586_at	pathogenesis-related protein (PR-1) cor	PR-1-LIKE	AT2G19990	1.38	0.47	3.29	0.014103	0.080445	-3.22
258332_at	putative transport protein similar to trans	---	AT3G16180	-2.06	-1.04	-3.29	0.014107	0.080447	-3.22
257573_at	putative SF16 protein {Helianthus annu	iqd9	AT2G33990	-1.47	-0.56	-3.29	0.014135	0.080586	-3.22
266882_at	unknown protein ;supported by full-leng	---	AT2G44670	-1.97	-0.98	-3.29	0.014146	0.080627	-3.22
250818_at	Expressed protein ; supported by cDNA	ALA1	AT5G04930	1.44	0.52	3.29	0.014151	0.080634	-3.22
261070_at	disease resistance protein, putative sim	AtRLP1	AT1G07390	-1.39	-0.48	-3.28	0.014173	0.080738	-3.22
248748_at	putative protein contains similarity to ad	AMK2	AT5G47840	-1.31	-0.39	-3.28	0.01418	0.080762	-3.22
259717_at	putative cleavage and polyadenylation s	CPSF73-I	AT1G61010	-1.35	-0.44	-3.28	0.014191	0.080803	-3.22
267031_at	hypothetical protein predicted by gensca	---	AT2G38420	-1.27	-0.35	-3.28	0.014196	0.080809	-3.22
253183_at	putative protein predicted protein, Arabi	---	AT4G35220	-1.25	-0.32	-3.28	0.014208	0.080859	-3.23
262967_at	hypothetical protein predicted by genem	---	AT1G75730	-1.32	-0.41	-3.28	0.014224	0.080925	-3.23
267550_at	putative protein kinase contains a protei	AP4.3A	AT2G32800	1.88	0.91	3.28	0.014227	0.080925	-3.23
253042_at	formamidase - like protein formamidase	---	AT4G37550	-1.56	-0.65	-3.28	0.014237	0.080965	-3.23
248900_at	putative protein strong similarity to unkn	PRP39-2	AT5G46400	-1.46	-0.55	-3.28	0.014246	0.080994	-3.23
259113_at	hypothetical protein predicted by genen	---	AT3G05510	-1.35	-0.43	-3.28	0.014263	0.081069	-3.23
253932_at	putative protein other Arabidopsis putati	---	AT4G26800	-1.25	-0.32	-3.28	0.014269	0.081084	-3.23
260768_at	Expressed protein ; supported by full-ler	---	AT1G49245	-1.31	-0.39	-3.28	0.014294	0.081206	-3.23
252310_at	GTPase activating -like protein GTPase	---	AT3G49350	1.67	0.74	3.28	0.014309	0.081269	-3.23
267238_at	unknown protein ;supported by full-leng	---	AT2G44130	3.01	1.59	3.28	0.014327	0.081356	-3.23
266705_at	40S ribosomal protein S30 ; supported	---	AT2G19750	-1.49	-0.57	-3.28	0.014334	0.081369	-3.23
263550_at	Expressed protein ; supported by cDNA	---	AT2G17033	-1.35	-0.43	-3.28	0.014337	0.081369	-3.23
264869_at	hypothetical protein similar to hypothetic	---	AT1G24350	1.29	0.37	3.28	0.01434	0.081370	-3.23
259534_at	hypothetical protein	---	AT1G12290	1.36	0.45	3.28	0.014358	0.081430	-3.24
255081_at	MLH1 protein ; supported by cDNA: gi_	MLH1	AT4G09140	-1.59	-0.67	-3.28	0.014355	0.081430	-3.24
249288_at	unknown protein ;supported by full-leng	---	AT5G41050	-2.21	-1.15	-3.27	0.014363	0.081434	-3.24

263711_at	putative protein phosphatase 2C ;suppo	---	AT2G20630	1.31	0.38	3.27	0.01437	0.081458	-3.24
267288_at	similar to cold acclimation protein WCOI	---	AT2G23680	2.33	1.22	3.27	0.014384	0.081513	-3.24
256256_at	unknown protein ; supported by full-leng	---	AT3G11230	1.31	0.39	3.27	0.014411	0.081626	-3.24
256052_at	spliceosomal protein (U2B), putative sir	---	AT1G06960	-1.31	-0.39	-3.27	0.014407	0.081626	-3.24
248532_at	Expressed protein ; supported by cDNA	NFU2	AT5G49940	-1.36	-0.45	-3.27	0.014427	0.081680	-3.24
255053_at	putative protein RNA helicase -Mus mu	---	AT4G09730	-1.93	-0.95	-3.27	0.014427	0.081680	-3.24
259062_at	unknown protein est hits to genscan mo	---	AT3G07440	-1.45	-0.54	-3.27	0.014441	0.081715	-3.24
256148_at	hypothetical protein similar to putative g	---	AT1G55090	-1.23	-0.30	-3.27	0.014439	0.081715	-3.24
253420_at	H+-transporting ATP synthase chain 9 -	---	AT4G32260	-1.35	-0.43	-3.27	0.014455	0.081773	-3.24
264377_at	similar to early nodulins	---	AT2G25060	1.25	0.33	3.27	0.014474	0.081843	-3.24
255652_at	putative protein	MEE47	AT4G00950	-2.27	-1.18	-3.27	0.014473	0.081843	-3.24
254736_at	putative disease resistance protein Cf-2	---	AT4G13820	1.62	0.70	3.27	0.014509	0.082017	-3.25
252281_at	putative protein various predicted protei	---	AT3G49320	-1.43	-0.52	-3.27	0.014521	0.082067	-3.25
263157_at	aldehyde dehydrogenase homolog, put	ALDH7B4	AT1G54100	1.60	0.68	3.27	0.014537	0.082117	-3.25
249747_at	putative protein similar to unknown prote	---	AT5G24600	1.36	0.44	3.27	0.014536	0.082117	-3.25
245543_at	glucosyltransferase	---	AT4G15260	1.35	0.44	3.27	0.014547	0.082152	-3.25
248223_at	unknown protein ; supported by cDNA:	---	AT5G53620	-1.22	-0.29	-3.26	0.014558	0.082195	-3.25
265090_at	putative protein phosphatase 2A Highly	---	AT1G03960	-1.30	-0.38	-3.26	0.01458	0.082298	-3.25
261522_at	RIBOSOMAL PROTEIN, putative simila	---	AT1G71710	-1.70	-0.76	-3.26	0.014608	0.082435	-3.25
256943_at	hypothetical protein similar to hypothetic	---	AT3G18910	-1.26	-0.33	-3.26	0.014652	0.082664	-3.26
253358_at	gamma-VPE (vacuolar processing enzy	GAMMA-V	AT4G32940	-1.29	-0.37	-3.26	0.01466	0.082688	-3.26
267096_at	unknown protein ; supported by cDNA:	---	AT2G38180	-1.66	-0.73	-3.26	0.014669	0.082720	-3.26
253276_at	caffeoyl-CoA O-methyltransferase - like	---	AT4G34050	1.48	0.56	3.26	0.014683	0.082776	-3.26
259935_at	putative GDSL-motif lipase/acylhydrolas	---	AT1G71250	1.35	0.43	3.26	0.014689	0.082789	-3.26
250706_at	deoxyhypusine synthase ;supported by	DHS	AT5G05920	-1.36	-0.44	-3.26	0.014717	0.082931	-3.26
257580_at	hypothetical protein	---	AT3G06210	-1.32	-0.40	-3.26	0.014733	0.082996	-3.26
260992_at	hypothetical protein predicted by genem	---	AT1G12150	-1.25	-0.32	-3.26	0.014739	0.083009	-3.26
249057_at	putative protein contains similarity to UD	DUR	AT5G44480	2.49	1.31	3.26	0.014749	0.083015	-3.26
262414_at	acyl CoA synthetase, putative similar to	LACS2	AT1G49430	2.76	1.47	3.25	0.014754	0.083015	-3.26
249285_at	unknown protein	---	AT5G41960	-1.36	-0.45	-3.26	0.014748	0.083015	-3.26
261718_at	wall-associated kinase, putative similar	---	AT1G18390	2.21	1.15	3.26	0.014752	0.083015	-3.26
255635_at	Shaggy related protein kinase tetha ; su	ATSK32	AT4G00720	-1.33	-0.41	-3.25	0.014763	0.083044	-3.27
247440_at	peptide transporter	---	AT5G62680	1.27	0.35	3.25	0.014797	0.083201	-3.27
263810_at	putative translation initiation factor eIF-1	---	AT2G04520	-1.24	-0.31	-3.25	0.014801	0.083201	-3.27
246654_s_a	putative protein predicted protein from S	EGY1	AT5G35210 /	-1.22	-0.29	-3.25	0.014802	0.083201	-3.27

251455_at	citrate synthase-like protein citrate synt	CSY5	AT3G60100	1.24	0.31	3.25	0.014807	0.083208	-3.27
258887_at	putative phospholipase D similar to phos	PLDP2	AT3G05630	1.47	0.55	3.25	0.014817	0.083225	-3.27
263425_at	putative preprotein translocase SECY p	EMB2289	AT2G31530	-1.35	-0.43	-3.25	0.014815	0.083225	-3.27
261168_at	unknown protein	---	AT1G04940 /	-1.60	-0.68	-3.25	0.014834	0.083238	-3.27
256284_at	unknown protein	PSF2	AT3G12530	-1.49	-0.58	-3.25	0.014824	0.083238	-3.27
246391_at	unknown protein ; supported by cDNA: g	---	AT1G77350	-1.36	-0.44	-3.25	0.014828	0.083238	-3.27
265269_at	hypothetical protein predicted by gensca	---	AT2G42950	1.35	0.43	3.25	0.014832	0.083238	-3.27
264999_at	hypothetical protein contains similarity to	---	AT1G67310	-1.27	-0.35	-3.25	0.014841	0.083253	-3.27
261888_at	ribosomal protein, putative similar to rib	---	AT1G80800	-1.33	-0.41	-3.25	0.014844	0.083253	-3.27
247390_at	putative protein similar to unknown prote	---	AT5G63520	-1.25	-0.33	-3.25	0.014855	0.083296	-3.27
266106_at	putative microtubule-associated protein	ATATG8E	AT2G45170	1.52	0.60	3.25	0.01486	0.083304	-3.27
255678_at	predicted protein with unknown function	AT4G0052	---	-1.32	-0.40	-3.25	0.014874	0.083358	-3.27
253412_at	putative protein (fragment) calcineurin B	CBL10	AT4G33000	-1.37	-0.46	-3.25	0.014891	0.083435	-3.27
264748_at	hypothetical protein predicted by genem	EMB25	AT1G70070	-1.24	-0.31	-3.25	0.014902	0.083475	-3.27
248391_at	putative protein similar to unknown prote	---	AT5G52030	-1.32	-0.40	-3.25	0.014912	0.083513	-3.28
250359_at	putative protein predicted proteins, Arat	---	AT5G11350	-1.27	-0.34	-3.25	0.014932	0.083591	-3.28
251629_at	villin 3 fragment ; supported by cDNA: g	VLN3	AT3G57410	1.40	0.48	3.25	0.014934	0.083591	-3.28
247554_at	putative protein leucine zipper-containir	ATEXO70I	AT5G61010	2.00	1.00	3.25	0.01494	0.083606	-3.28
259800_at	Expressed protein ; supported by full-ler	---	AT1G72175	-1.37	-0.46	-3.24	0.014972	0.083698	-3.28
249550_at	protein kinase - like protein wall-associa	---	AT5G38210	1.68	0.75	3.24	0.014963	0.083698	-3.28
263712_at	Expressed protein ; supported by full-ler	NFD6	AT2G20585	-1.47	-0.56	-3.24	0.014975	0.083698	-3.28
251559_at	putative protein hypothetical protein T2	---	AT3G58010	-1.41	-0.49	-3.24	0.014968	0.083698	-3.28
248235_at	unknown protein ;supported by full-lengt	emb2737	AT5G53860	-1.24	-0.31	-3.24	0.014974	0.083698	-3.28
255660_at	Expressed protein ; supported by full-ler	---	AT4G00755	-1.34	-0.42	-3.24	0.014995	0.083778	-3.28
256922_at	hypothetical protein contains similarity t	---	AT3G19010	1.82	0.87	3.24	0.015	0.083778	-3.28
251207_at	putative protein ;supported by full-lengt	---	AT3G63050	1.62	0.70	3.24	0.014999	0.083778	-3.28
247988_at	putative protein similar to unknown prote	---	AT5G56910	-1.50	-0.58	-3.24	0.015017	0.083853	-3.28
251391_at	putative protein weak homology with pr	---	AT3G60910	-1.36	-0.45	-3.24	0.015025	0.083878	-3.28
265284_at	unknown protein ;supported by full-leng	---	AT2G20230	-1.33	-0.41	-3.24	0.01503	0.083884	-3.28
264638_at	flowering signals mediating protein FT ic	FT	AT1G65480	2.05	1.04	3.24	0.015044	0.083921	-3.28
258949_at	unknown protein	ATCFM2	AT3G01370	-1.41	-0.50	-3.24	0.015043	0.083921	-3.28
259411_at	hypothetical protein contains Pfam profil	---	AT1G13410	-1.29	-0.37	-3.24	0.01505	0.083934	-3.29
247568_at	putative protein predicted proteins, Arat	---	AT5G61260	1.69	0.75	3.24	0.015059	0.083964	-3.29
260177_at	hypothetical protein predicted by gensca	---	AT1G70650	-1.51	-0.59	-3.24	0.015066	0.083985	-3.29
259645_at	putative DNA-binding protein predicted	BIM2	AT1G69010	-1.41	-0.50	-3.24	0.015074	0.083996	-3.29

246607_at	receptor-like protein kinase - like protei	---	AT5G35370	1.83	0.87	3.24	0.015076	0.083996	-3.29
252654_at	similar to glycyl tRNA synthetase	---	AT3G44740	-1.24	-0.31	-3.24	0.015088	0.084046	-3.29
257009_at	unknown protein ; supported by cDNA:	---	AT3G14160	-1.26	-0.33	-3.24	0.015107	0.084126	-3.29
246858_at	receptor-like protein kinase - like recept	---	AT5G25930	2.37	1.24	3.24	0.015123	0.084181	-3.29
249177_at	unknown protein ;supported by full-leng	---	AT5G42850	1.28	0.36	3.24	0.015124	0.084181	-3.29
259225_at	putative small nuclear ribonucleoprotein	---	AT3G07590	-1.94	-0.96	-3.23	0.015171	0.084361	-3.29
260499_at	unknown protein ; supported by cDNA:	---	AT2G41760	-1.26	-0.34	-3.23	0.015162	0.084361	-3.29
260237_at	putative MYB family transcription factor	MYB95	AT1G74430	-1.90	-0.93	-3.23	0.015167	0.084361	-3.29
252698_at	amine oxidase -like protein amine oxida	---	AT3G43670	-1.37	-0.45	-3.23	0.01517	0.084361	-3.29
248786_at	unknown protein	---	AT5G47410	-1.58	-0.66	-3.23	0.01518	0.084394	-3.29
247641_at	imidazoleglycerol-phosphate synthase s	PDX2	AT5G60540	-1.31	-0.39	-3.23	0.015196	0.084458	-3.30
261756_at	Expressed protein ; supported by full-ler	---	AT1G08315	1.74	0.80	3.23	0.015212	0.084529	-3.30
265119_at	flavin-containing monooxygenase, puta	FMO GS-(	AT1G62570	1.75	0.80	3.23	0.015239	0.084649	-3.30
254346_at	symbiosis-related like protein symbiosis	APG8A	AT4G21980	1.57	0.65	3.23	0.015248	0.084649	-3.30
263151_at	hypothetical protein predicted by genem	---	AT1G54120	-1.93	-0.95	-3.23	0.015249	0.084649	-3.30
261982_at	hypothetical protein predicted by genem	---	AT1G33780	-1.26	-0.33	-3.23	0.015243	0.084649	-3.30
259849_at	phosphoglycerate dehydrogenase, puta	---	AT1G72190	-1.23	-0.30	-3.23	0.015259	0.084684	-3.30
248800_at	40S ribosomal protein S19 ; supported	RPS19	AT5G47320	-1.30	-0.38	-3.23	0.015266	0.084703	-3.30
264400_at	glucose-6-phosphate/phosphate-translo	GPT2	AT1G61800	4.55	2.19	3.23	0.015286	0.084792	-3.30
246295_at	calmodulin-binding protein ; supported	CIP111	AT3G56690	-1.41	-0.49	-3.23	0.01529	0.084795	-3.30
254370_at	L1 specific homeobox gene ATML1/ovu	ATML1	AT4G21750	1.40	0.48	3.23	0.015326	0.084963	-3.30
264299_s_a	hypothetical protein predicted by genem	---	AT1G78850 /	1.84	0.88	3.23	0.015331	0.084963	-3.30
260464_at	disease resistance protein RPM1 isolog	LOV1	AT1G10920	1.26	0.33	3.23	0.015331	0.084963	-3.30
264178_at	latex-abundant protein, putative similar	AMC1	AT1G02170	1.33	0.41	3.23	0.015337	0.084974	-3.31
257963_at	hypothetical protein predicted by genem	---	AT3G19840	-1.60	-0.68	-3.23	0.015341	0.084978	-3.31
263145_at	hypothetical protein predicted by genem	ATEXO70I	AT1G54090	1.41	0.50	3.23	0.015356	0.085038	-3.31
260297_at	unknown protein contains Pfam profile:	---	AT1G80280	1.32	0.40	3.22	0.015382	0.085158	-3.31
251584_at	putative protein At2g42580 - Arabidops	TTL4	AT3G58620	-1.90	-0.93	-3.22	0.015409	0.085208	-3.31
257000_at	hypothetical protein predicted by genem	---	AT3G14120	-1.50	-0.59	-3.22	0.015396	0.085208	-3.31
260660_at	hypothetical protein contains Pfam profi	---	AT1G19485	-1.38	-0.46	-3.22	0.015413	0.085208	-3.31
265725_at	putative alanine acetyl transferase	---	AT2G32030	6.24	2.64	3.22	0.015406	0.085208	-3.31
254490_at	CTP synthase like protein CTP synthas	---	AT4G20320	1.51	0.60	3.22	0.01541	0.085208	-3.31
245601_at	hypothetical protein	---	AT4G14240	-1.33	-0.42	-3.22	0.015403	0.085208	-3.31
261303_at	unknown protein contains DNA-binding	HON5	AT1G48620	-1.23	-0.30	-3.22	0.015418	0.085214	-3.31
259543_at	hypothetical protein ; supported by full-le	---	AT1G20580	-1.34	-0.42	-3.22	0.015421	0.085214	-3.31

263015_at	hypothetical protein similar to hypothetic	---	AT1G23440	1.33	0.41	3.22	0.015434	0.085262	-3.31
252625_at	putative histone deacetylase similar to n	HDA3	AT3G44750	-2.05	-1.03	-3.22	0.015459	0.085362	-3.31
254076_at	putative protein immunophilin FKBP46	---	AT4G25340	-1.62	-0.69	-3.22	0.015456	0.085362	-3.31
264131_at	unknown protein	---	AT1G79150	-1.48	-0.56	-3.22	0.01547	0.085399	-3.31
253576_at	putative protein various predicted prote	---	AT4G31070	-1.24	-0.31	-3.22	0.015484	0.085433	-3.32
254730_at	putative protein GTPase activating prot	---	AT4G13730	-1.25	-0.32	-3.22	0.015484	0.085433	-3.32
257406_at	hypothetical protein predicted by genen	---	AT1G27060	-1.37	-0.46	-3.22	0.015492	0.085460	-3.32
264875_at	putative glucanase	AKR2B	AT2G17390	-1.22	-0.29	-3.22	0.015505	0.085508	-3.32
255621_at	hypothetical protein	---	AT4G01390	-3.03	-1.60	-3.22	0.015513	0.085534	-3.32
264772_at	unknown protein location of EST gb|H3	---	AT1G22930	1.32	0.40	3.22	0.015532	0.085597	-3.32
262376_at	unknown protein contains similarity to m	HTH	AT1G72970	-1.26	-0.34	-3.22	0.015529	0.085597	-3.32
266986_at	putative dolichyl-phosphate beta-glucos	---	AT2G39630	-1.24	-0.32	-3.22	0.015543	0.085637	-3.32
263193_at	acetyl-CoA carboxylase, putative simila	---	AT1G36050	1.27	0.35	3.22	0.015553	0.085657	-3.32
265441_at	unknown protein ;supported by full-leng	---	AT2G20870	1.41	0.49	3.22	0.015554	0.085657	-3.32
254265_s_a	serine threonine kinase - like protein KI	CRK6	AT4G23140 /	2.62	1.39	3.22	0.015569	0.085718	-3.32
260933_at	hypothetical protein contains non-conse	---	AT1G02470	2.65	1.40	3.21	0.015594	0.085734	-3.32
259859_at	putative protein phosphatase similar to p	---	AT1G68410	1.90	0.92	3.21	0.015594	0.085734	-3.32
247886_at	branched-chain amino acid aminotransf	---	AT5G57850	-1.44	-0.53	-3.21	0.015598	0.085734	-3.32
256094_at	hypothetical protein predicted by genem	SAUL1	AT1G20780	1.29	0.37	3.21	0.015588	0.085734	-3.32
266806_at	unknown protein ;supported by full-leng	---	AT2G30000	-1.38	-0.47	-3.21	0.015607	0.085734	-3.32
255596_at	putative DNA-binding protein similar to	WRKY47	AT4G01720	1.85	0.89	3.21	0.015576	0.085734	-3.32
258916_at	putative ABC transporter ATPase simila	ATNAP7	AT3G10670	-1.28	-0.35	-3.21	0.015583	0.085734	-3.32
246266_at	30S ribosomal protein S11, putative co	NFD3	AT1G31817	-1.43	-0.52	-3.21	0.015602	0.085734	-3.32
258511_at	unknown protein ;supported by full-leng	---	AT3G06590	-1.36	-0.44	-3.21	0.015609	0.085734	-3.32
261874_at	ethylene responsive element binding fac	ERF3	AT1G50640	1.36	0.45	3.21	0.015606	0.085734	-3.32
266414_at	mevalonate diphosphate decarboxylase	MVD1	AT2G38700	1.31	0.39	3.21	0.015637	0.085854	-3.33
263995_at	putative MADS-box protein	SVP	AT2G22540	-1.36	-0.45	-3.21	0.015642	0.085854	-3.33
260414_at	nitrate transporter (NTL1) identical to nit	ATNRT1:2	AT1G69850	-1.34	-0.42	-3.21	0.015643	0.085854	-3.33
258766_at	galactokinase-like protein similar to gal	---	AT3G10700	1.26	0.34	3.21	0.015661	0.085936	-3.33
264933_at	hypothetical protein predicted by genem	---	AT1G61160	1.33	0.41	3.21	0.015675	0.085971	-3.33
248695_at	putative protein similar to unknown prote	---	AT5G48350	1.45	0.53	3.21	0.015675	0.085971	-3.33
250715_at	splicing factor 3a ; supported by cDNA:	ATO	AT5G06160	-1.42	-0.51	-3.21	0.01568	0.085978	-3.33
264635_at	unknown protein ;supported by full-lengt	---	AT1G65500	2.05	1.04	3.21	0.015697	0.086051	-3.33
266329_at	unknown protein ; supported by cDNA:	CRR3	AT2G01590	-1.69	-0.75	-3.21	0.015713	0.086116	-3.33
246407_at	disease resistance protein RPS4, putat	---	AT1G57670	1.24	0.31	3.21	0.015731	0.086192	-3.33

266225_at	putative membrane channel protein ;su	ATOEP16-	AT2G28900	-1.88	-0.91	-3.21	0.01574	0.086194	-3.33
245358_at	PRL1 protein ;supported by full-length c	PRL1	AT4G15900	-1.34	-0.43	-3.21	0.015746	0.086194	-3.33
249151_at	inorganic phosphate transporter (dbj|BA	PHT3	AT5G43360	1.29	0.37	3.21	0.015737	0.086194	-3.33
246069_at	zinc finger protein ;supported by full-len	---	AT5G20220	-1.55	-0.63	-3.21	0.015742	0.086194	-3.33
256838_at	ADP-ribosylation factor, putative similar	ATARFC1	AT3G22950	1.35	0.43	3.21	0.015753	0.086209	-3.33
257648_at	RNA helicase, putative similar to RNA h	---	AT3G16840	-1.58	-0.66	-3.21	0.015763	0.086246	-3.33
249391_at	putative protein predicted proteins, Arat	---	AT5G40140	-1.43	-0.52	-3.21	0.015771	0.086270	-3.33
258055_at	putative 2Fe-2S iron-sulfur cluster prote	NDF4	AT3G16250	-2.09	-1.06	-3.20	0.015786	0.086328	-3.34
253519_at	predicted protein red-1 gene, M.muscul	---	AT4G31240	1.66	0.73	3.20	0.015792	0.086339	-3.34
255481_at	T14P8.6 ; supported by cDNA: gi_1561	PMS1	AT4G02460	-1.40	-0.48	-3.20	0.015812	0.086368	-3.34
254335_at	putative protein alternative oxidase, Ma	IM	AT4G22260	-1.26	-0.33	-3.20	0.015809	0.086368	-3.34
254826_at	putative protein predicted protein, Arabi	---	AT4G12640	-1.36	-0.44	-3.20	0.015812	0.086368	-3.34
260741_at	hypothetical protein contains Pfam profil	---	AT1G15040	8.04	3.01	3.20	0.01581	0.086368	-3.34
260288_at	nodulin-like protein similar to nodule-spe	---	AT1G80530	-1.48	-0.57	-3.20	0.015819	0.086386	-3.34
263265_at	hypothetical protein predicted by gensca	---	AT2G38820	1.52	0.60	3.20	0.015834	0.086447	-3.34
250673_at	serine threonine protein kinase-like prot	CIPK2	AT5G07070	1.42	0.51	3.20	0.015851	0.086473	-3.34
258447_at	hypothetical protein predicted by genem	---	AT3G22450	-1.25	-0.32	-3.20	0.015853	0.086473	-3.34
258327_at	unknown protein contains similarity to m	PAP85	AT3G22640	1.24	0.31	3.20	0.015858	0.086473	-3.34
263791_at	putative plasma membrane proton ATPa	AHA5	AT2G24520	-1.51	-0.60	-3.20	0.015851	0.086473	-3.34
249351_at	MAP kinase kinase 3 (ATMKK3) 10.01.(	ATMKK3	AT5G40440	-1.31	-0.39	-3.20	0.015857	0.086473	-3.34
250493_at	putative protein various predicted prote	---	AT5G09800	5.20	2.38	3.20	0.015893	0.086645	-3.34
266495_at	cycloartenol synthase identical to SP:P3	CAS1	AT2G07050	-1.33	-0.41	-3.20	0.015905	0.086691	-3.34
248339_at	prolyl tRNA synthetase	OVA6	AT5G52520	-1.31	-0.39	-3.20	0.015926	0.086781	-3.34
260575_at	hypothetical protein predicted by genefin	---	AT2G47300	-1.30	-0.38	-3.20	0.01593	0.086783	-3.34
259307_at	unknown protein similar to MICROSOM/	---	AT3G05230	1.40	0.48	3.20	0.015955	0.086898	-3.35
247033_at	SKP1 interacting partner 2 (SKIP2) iden	SKIP2	AT5G67250	1.33	0.41	3.20	0.01599	0.087071	-3.35
247240_at	putative protein strong similarity to unkn	CMPG2	AT5G64660	3.79	1.92	3.20	0.015999	0.087097	-3.35
260500_at	Expressed protein ; supported by cDNA	---	AT2G41705	-1.24	-0.31	-3.19	0.016004	0.087106	-3.35
250875_at	putative protein fimbriae-associated pro	---	AT5G04020	1.92	0.94	3.19	0.016015	0.087142	-3.35
250232_at	unknown protein	---	AT5G13950	-1.26	-0.34	-3.19	0.016026	0.087181	-3.35
250388_at	putative protein various predicted prote	---	AT5G11310	-1.79	-0.84	-3.19	0.016062	0.087359	-3.35
266847_at	hypothetical protein predicted by grail;su	emb1345	AT2G26060	-1.37	-0.46	-3.19	0.016067	0.087365	-3.35
260984_at	Expressed protein ; supported by full-ler	---	AT1G53645	-1.62	-0.70	-3.19	0.016075	0.087367	-3.35
261823_at	hypothetical protein predicted by genem	PYM	AT1G11400	1.29	0.36	3.19	0.016074	0.087367	-3.35
252637_at	WD repeat domain protein nuclear prot	HIRA	AT3G44530	1.34	0.42	3.19	0.016081	0.087379	-3.35

251667_at	putative protein DYSKERIN (NUCLEOL	NAP57	AT3G57150	-1.81	-0.86	-3.19	0.016113	0.087518	-3.36
246910_at	exonuclease - like protein ribonuclease	---	AT5G25800	-1.48	-0.56	-3.19	0.016117	0.087518	-3.36
253737_at	Expressed protein ; supported by full-ler	---	AT4G28703	2.09	1.06	3.19	0.016118	0.087518	-3.36
259928_at	DNA polymerase type I, putative similar	---	AT1G34380	-1.55	-0.63	-3.19	0.016134	0.087558	-3.36
256680_at	unknown protein ; supported by full-leng	---	AT3G52230	-1.45	-0.54	-3.19	0.016132	0.087558	-3.36
252899_at	putative protein leaf protein, Ipomoea n	---	AT4G39530	-1.32	-0.40	-3.19	0.016148	0.087597	-3.36
258398_at	thioredoxin m4 identical to GB:AAF1595	TRX-M4	AT3G15360	-1.25	-0.33	-3.19	0.016148	0.087597	-3.36
251097_at	receptor like protein kinase receptor like	LECRKA4	AT5G01560	2.72	1.44	3.19	0.016161	0.087644	-3.36
245404_at	putative protein	---	AT4G17610	-1.38	-0.46	-3.19	0.016169	0.087665	-3.36
254328_at	adenine phosphoribosyltransferase (EC	APT3	AT4G22570	-1.66	-0.73	-3.19	0.016189	0.087690	-3.36
253549_at	Expressed protein ; supported by full-ler	NFD1	AT4G30930	-1.53	-0.61	-3.19	0.0162	0.087690	-3.36
257199_at	Tic22, putative similar to Tic22 GB:AAC	---	AT3G23710	-1.34	-0.42	-3.18	0.016219	0.087690	-3.36
259566_at	hypothetical protein	---	AT1G20520	1.24	0.31	3.19	0.016183	0.087690	-3.36
245792_at	pinoresinol-lariciresinol reductase, puta	PRR1	AT1G32100	2.21	1.14	3.19	0.01618	0.087690	-3.36
247989_at	pyruvate kinase ;supported by full-lengt	---	AT5G56350	1.44	0.52	3.19	0.01619	0.087690	-3.36
262745_at	lipase, putative contains Pfam profile: P	---	AT1G28600	1.38	0.47	3.19	0.016216	0.087690	-3.36
253282_at	putative protein hypothetical protein, Ar	LEJ1	AT4G34120	1.23	0.30	3.19	0.016212	0.087690	-3.36
265164_at	putative OBP32pep protein	---	AT1G23600	1.25	0.33	3.19	0.016202	0.087690	-3.36
251352_at	putative protein hypothetical protein At2	PEX11E	AT3G61070	1.40	0.48	3.19	0.016208	0.087690	-3.36
253411_at	homeobox gene ATH1	ATH1	AT4G32980	-1.66	-0.73	-3.19	0.016193	0.087690	-3.36
255492_at	hypothetical protein similar to A. thalian	EOL1	AT4G02680	-1.30	-0.38	-3.19	0.016206	0.087690	-3.36
247457_at	putative protein various predicted prote	---	AT5G62170	1.25	0.32	3.18	0.016226	0.087697	-3.36
257025_at	hypothetical protein predicted by genem	ATG2	AT3G19190	1.43	0.51	3.18	0.016228	0.087697	-3.36
265678_at	putative RAD50 DNA repair protein ; su	RAD50	AT2G31970	-1.50	-0.59	-3.18	0.016235	0.087710	-3.36
249922_at	aluminium-induced protein - like alumin	AILP1	AT5G19140	-1.28	-0.35	-3.18	0.016247	0.087757	-3.37
264429_at	hypothetical protein similar to membrane	---	AT1G61670	-1.25	-0.32	-3.18	0.016266	0.087816	-3.37
256285_at	hypothetical protein predicted by gensca	---	AT3G12510	1.45	0.54	3.18	0.016263	0.087816	-3.37
264071_at	putative carboxypeptidase ; supported b	SCPL51	AT2G27920	1.58	0.66	3.18	0.016271	0.087823	-3.37
245332_at	isomerase like protein ;supported by full	---	AT4G15940	1.21	0.28	3.18	0.01628	0.087852	-3.37
250244_at	putative protein similar to unknown prote	ABO1	AT5G13680	-1.54	-0.62	-3.18	0.016311	0.087995	-3.37
248839_at	putative protein contains similarity to bH	bHLH071	AT5G46690	-1.96	-0.97	-3.18	0.016316	0.088005	-3.37
248914_at	Rab-type small GTP-binding protein-like	AtRABA1c	AT5G45750	1.54	0.63	3.18	0.016326	0.088032	-3.37
251176_at	Ca2+-transporting ATPase -like protein	---	AT3G63380	2.54	1.35	3.18	0.016333	0.088032	-3.37
246191_at	T-complex protein 1, beta subunit T-CC	---	AT5G20890	-1.37	-0.45	-3.18	0.01633	0.088032	-3.37
260978_at	17.6 kDa heat shock protein (AA 1-156	---	AT1G53540	1.83	0.87	3.18	0.01634	0.088049	-3.37

245882_at	mitochondrial carrier-like protein mitoch	DIC3	AT5G09470	1.34	0.42	3.18	0.016344	0.088052	-3.37
266105_at	putative transport protein SEC61 beta-s	SEC61 BE	AT2G45070	1.42	0.51	3.18	0.016369	0.088144	-3.37
264063_at	unknown protein	---	AT2G27900	-1.28	-0.35	-3.18	0.016369	0.088144	-3.37
264722_at	unknown protein location of EST emb|F	---	AT1G22970	-1.40	-0.49	-3.18	0.016385	0.088169	-3.37
249831_at	putative protein contains similarity to glu	---	AT5G23340	1.61	0.69	3.18	0.01638	0.088169	-3.37
257866_at	dihydroxyacetone kinase, putative simil	---	AT3G17770	1.82	0.86	3.18	0.016384	0.088169	-3.37
265040_at	G-box binding factor, GBF4 Identical to	GBF4	AT1G03970	-1.41	-0.50	-3.18	0.016399	0.088222	-3.38
266366_at	unknown protein	---	AT2G41420	1.37	0.46	3.17	0.016454	0.088496	-3.38
252022_at	fructose bisphosphate aldolase - like pr	---	AT3G52930	1.46	0.55	3.17	0.01647	0.088563	-3.38
262208_at	hypothetical protein predicted by gensca	---	AT1G74800	-1.34	-0.42	-3.17	0.016481	0.088598	-3.38
266076_at	ATP-dependent RNA helicase identical	---	AT2G40700	-1.59	-0.67	-3.17	0.016488	0.088618	-3.38
258378_at	hypothetical protein contains similarity t	---	AT3G17490	1.25	0.32	3.17	0.016518	0.088757	-3.38
260734_at	disease resistance protein RPP1-WsB,	---	AT1G17600	1.37	0.45	3.17	0.016548	0.088900	-3.38
265495_at	unknown protein predicted by genscan	---	AT2G15695	-1.29	-0.37	-3.17	0.016557	0.088907	-3.39
265039_at	unknown protein Location of ESTs 203	---	AT1G04000	1.27	0.35	3.17	0.016558	0.088907	-3.39
256179_at	ubiquitin-specific protease 6 (UBP6), pu	UBP6	AT1G51710	1.25	0.32	3.17	0.016563	0.088915	-3.39
245914_at	putative protein outer membrane protei	OEP80	AT5G19620	-1.31	-0.39	-3.17	0.01657	0.088932	-3.39
257919_at	myb-related transcription factor, putativ	MYB15	AT3G23250	3.94	1.98	3.17	0.016578	0.088952	-3.39
253581_at	stress responsive protein homolog low	---	AT4G30660	-1.74	-0.80	-3.17	0.016586	0.088977	-3.39
258456_at	putative protein kinase similar to mitoge	WNK2	AT3G22420	-1.99	-0.99	-3.17	0.016597	0.089016	-3.39
264906_at	putative mitochondrial phosphate transl	---	AT2G17270	-1.42	-0.51	-3.17	0.016619	0.089110	-3.39
246389_at	amino acid carrier, putative similar to ar	AAP3	AT1G77380	1.43	0.52	3.17	0.01663	0.089128	-3.39
253404_at	putative pyrophosphate--fructose-6-pho	PFK6	AT4G32840	-1.36	-0.44	-3.17	0.016626	0.089128	-3.39
264572_at	unknown protein ESTs gb|AA042402,g	---	AT1G05320	1.31	0.39	3.17	0.016659	0.089263	-3.39
265268_at	putative protein kinase contains a protei	---	AT2G42960	-1.29	-0.37	-3.16	0.016682	0.089365	-3.39
259098_at	putative ribose 5-phosphate isomerase	---	AT3G04790	-1.51	-0.60	-3.16	0.016689	0.089381	-3.39
254861_at	putative protein zinc finger protein ZNF	---	AT4G12040	1.42	0.50	3.16	0.016703	0.089434	-3.39
258152_at	chaperonin subunit, putative similar to c	---	AT3G18190	-1.33	-0.42	-3.16	0.016733	0.089493	-3.40
264821_at	hypothetical protein predicted by genefi	---	AT1G03470	1.53	0.62	3.16	0.016731	0.089493	-3.40
251152_at	RAN GTPase activating protein 1 protei	RANGAP1	AT3G63130	-1.48	-0.56	-3.16	0.01673	0.089493	-3.40
252652_at	putative chloroplast prephenate dehydra	ADT4	AT3G44720	2.53	1.34	3.16	0.01673	0.089493	-3.40
253546_at	hypothetical protein ;supported by full-l	---	AT4G31030 /	-1.36	-0.44	-3.16	0.016731	0.089493	-3.40
255045_at	putative protein hypothetical protein T1	---	AT4G09690	1.32	0.40	3.16	0.016741	0.089514	-3.40
259308_at	putative nodulin similar to nodulin GB:A	---	AT3G05180	-1.56	-0.64	-3.16	0.016749	0.089536	-3.40
257092_at	unknown protein	DDL	AT3G20550	-1.39	-0.47	-3.16	0.016761	0.089580	-3.40

261553_at	hypothetical protein	---	AT1G63420	-1.33	-0.41	-3.16	0.01679	0.089714	-3.40
246824_at	drought-induced protein - like non-cons	---	AT5G26990	1.25	0.32	3.16	0.016804	0.089740	-3.40
265403_at	putative Ta11-like non-LTR retroelemen	---	---	1.32	0.40	3.16	0.016816	0.089740	-3.40
256936_at	prefoldin-like protein similar to prefoldin	PDF2	AT3G22480	-1.29	-0.36	-3.16	0.016803	0.089740	-3.40
266878_at	putative RING zinc finger protein	---	AT2G44580	1.29	0.37	3.16	0.016816	0.089740	-3.40
263003_at	protein phosphatase 2A 72 kDa regulat	---	AT1G54450	1.23	0.30	3.16	0.016809	0.089740	-3.40
249484_at	cytochrome P450 - like protein cytochro	BR6OX1	AT5G38970	-1.26	-0.33	-3.16	0.016819	0.089740	-3.40
250284_at	protein kinase precursor - like receptor-	CRN	AT5G13290	-1.47	-0.55	-3.16	0.016828	0.089770	-3.40
247123_at	unknown protein	---	AT5G66050	1.45	0.53	3.16	0.016836	0.089787	-3.40
263409_at	predicted protein	---	AT2G04063	-1.28	-0.35	-3.16	0.016845	0.089814	-3.40
264676_at	unknown protein EST gb|R64758 comes	---	AT1G09870	1.24	0.31	3.16	0.016874	0.089867	-3.40
250075_at	putative protein	---	AT5G17670	-1.59	-0.67	-3.16	0.016874	0.089867	-3.40
256885_at	chaperone-like ATPase contains Pfam p	---	AT3G15120	-1.34	-0.42	-3.16	0.016863	0.089867	-3.40
245057_at	En/Spm-like transposon protein related	---	AT2G26490	1.21	0.28	3.16	0.016874	0.089867	-3.40
248518_at	putative protein similar to unknown prote	---	AT5G50560 /	1.47	0.56	3.16	0.01686	0.089867	-3.40
262104_at	hypothetical protein predicted by genem	LPA1	AT1G02910	-1.29	-0.37	-3.15	0.016903	0.089998	-3.41
247673_at	tRNA intron endonuclease - like protein	SEN2	AT5G60230	-1.22	-0.29	-3.15	0.016912	0.090025	-3.41
245304_at	hypothetical protein ; supported by full-le	---	AT4G15630	2.10	1.07	3.15	0.016922	0.090045	-3.41
266616_at	putative CDC6 protein ; supported by c	CDC6	AT2G29680	-1.26	-0.34	-3.15	0.016923	0.090045	-3.41
254684_at	glycine-rich RNA-binding protein AtGRF	GR-RBP2	AT4G13850	-1.46	-0.55	-3.15	0.01693	0.090058	-3.41
265844_at	putative receptor-like protein kinase	FEI2	AT2G35620	-1.44	-0.53	-3.15	0.016953	0.090131	-3.41
245666_at	hypothetical protein predicted by genem	---	AT1G28280	1.66	0.74	3.15	0.016955	0.090131	-3.41
256257_at	arginine-tRNA-protein transferase, puta	ATE2	AT3G11240	-1.25	-0.32	-3.15	0.016948	0.090131	-3.41
245148_at	putative pectinesterase ; supported by	---	AT2G45220	3.10	1.63	3.15	0.016981	0.090146	-3.41
261317_at	cytochrome C oxidase assembly protei	---	AT1G53030	1.29	0.37	3.15	0.016963	0.090146	-3.41
267181_at	putative alcohol dehydrogenase ; suppo	---	AT2G37760	1.62	0.70	3.15	0.017005	0.090146	-3.41
264441_at	Expressed protein ; supported by full-ler	---	AT1G27435	-1.34	-0.43	-3.15	0.016994	0.090146	-3.41
261126_at	TATA binding protein-associated factor	TAF6	AT1G04950	-1.25	-0.33	-3.15	0.017004	0.090146	-3.41
264355_at	unknown protein similar to PHZF, catal	---	AT1G03210	1.48	0.56	3.15	0.017	0.090146	-3.41
248030_at	transcription regulator Sir2-like protein ;	SRT1	AT5G55760	-1.42	-0.50	-3.15	0.016974	0.090146	-3.41
256781_at	dirigent protein, putative similar to dirige	---	AT3G13650	6.37	2.67	3.15	0.017	0.090146	-3.41
253801_at	hypothetical protein	---	AT4G28170	1.28	0.35	3.15	0.016985	0.090146	-3.41
262296_at	putative cyclin similar to cyclin GB:4502	CYCT1;3	AT1G27630	-1.26	-0.34	-3.15	0.017006	0.090146	-3.41
249743_at	beta-glucosidase	BGLU31	AT5G24540	4.22	2.08	3.15	0.016967	0.090146	-3.41
245759_at	hypothetical protein predicted by genem	---	AT1G66900	-1.38	-0.47	-3.15	0.016987	0.090146	-3.41

265109_s_a	NBS/LRR disease resistance protein, p	---	AT1G62630 /	-1.52	-0.60	-3.15	0.01702	0.090200	-3.41
257803_at	unknown protein	---	AT3G18790	-1.26	-0.34	-3.15	0.017033	0.090247	-3.41
255258_at	contains similarity to Arabidopsis thalian	---	AT4G05060	1.32	0.40	3.15	0.017042	0.090275	-3.42
254559_at	putative protein glycine/proline-rich prot	---	AT4G19200	1.45	0.54	3.15	0.017058	0.090318	-3.42
257187_at	hypothetical protein predicted by gensca	---	AT3G13140	1.27	0.35	3.15	0.017062	0.090318	-3.42
246459_at	receptor protein kinase -like protein ser	---	AT5G16900	1.27	0.35	3.15	0.017058	0.090318	-3.42
256221_at	DnaJ protein, putative contains Pfam pr	---	AT1G56300	-1.26	-0.33	-3.15	0.017068	0.090330	-3.42
259818_at	unknown protein ; supported by cDNA: g	---	AT1G49890	-1.43	-0.52	-3.15	0.017084	0.090375	-3.42
249085_at	putative protein similar to unknown prote	---	AT5G44170	-1.31	-0.39	-3.15	0.017084	0.090375	-3.42
259862_at	hypothetical protein ;supported by full-le	TRFL6	AT1G72650	-1.36	-0.44	-3.15	0.017096	0.090415	-3.42
261909_at	hypothetical protein predicted by genem	SAR3	AT1G80680	-1.36	-0.45	-3.15	0.017104	0.090415	-3.42
266998_at	hypothetical protein predicted by gensca	---	AT2G34400	-1.29	-0.37	-3.15	0.017102	0.090415	-3.42
267298_at	putative homeodomain transcription fact	BLH4	AT2G23760	-1.43	-0.51	-3.15	0.017116	0.090457	-3.42
252754_at	putative protein hypothetical protein ret	---	---	-1.55	-0.63	-3.15	0.017122	0.090469	-3.42
251503_at	ABC transporter-like protein putative m	ATMRP14	AT3G59140	-1.57	-0.65	-3.14	0.017148	0.090545	-3.42
261578_at	acidic ribosomal protein, putative simila	---	AT1G01100	-1.39	-0.48	-3.14	0.017148	0.090545	-3.42
262140_at	hypothetical protein predicted by genem	---	AT1G52470	1.25	0.32	3.14	0.017143	0.090545	-3.42
255827_at	unknown protein ; supported by cDNA:	---	AT2G40600	1.33	0.41	3.14	0.017152	0.090545	-3.42
250510_at	15.9 kDa subunit of RNA polymerase II	NRPB4	AT5G09920	-1.26	-0.33	-3.14	0.01716	0.090563	-3.42
264137_at	lupeol synthase, putative similar to lupe	ATLUP2	AT1G78960	-1.48	-0.57	-3.14	0.017165	0.090569	-3.42
251972_at	nodulin / glutamate-ammonia ligase - lik	---	AT3G53170	-1.31	-0.39	-3.14	0.01718	0.090629	-3.42
246651_at	adenylate kinase -like protein adenylate	---	AT5G35170	-1.42	-0.51	-3.14	0.017195	0.090686	-3.42
258776_at	putative T-complex protein 1, ETA subu	---	AT3G11830	-1.33	-0.42	-3.14	0.017207	0.090706	-3.43
251146_at	neoxanthin cleavage enzyme nc1	CCD1	AT3G63520	-1.41	-0.50	-3.14	0.017205	0.090706	-3.43
263763_at	Expressed protein ; supported by cDNA	---	AT2G21385	-1.58	-0.66	-3.14	0.017218	0.090744	-3.43
263221_at	UDP-galactose 4-epimerase-like protein	MUR4	AT1G30620	2.15	1.11	3.14	0.017241	0.090845	-3.43
261907_at	4-coumarate:CoA ligase 3 identical to 4-	4CL3	AT1G65060	2.00	1.00	3.14	0.017246	0.090848	-3.43
249612_at	putative protein CG14881, Drosophila r	---	AT5G37290	-1.62	-0.70	-3.14	0.017261	0.090907	-3.43
261927_at	RING-H2 zinc finger protein ATL5, puta	---	AT1G22500	-1.78	-0.83	-3.14	0.017273	0.090949	-3.43
264006_at	homeodomain transcription factor (ATHI	ATHB6	AT2G22430	-1.45	-0.54	-3.14	0.017307	0.091106	-3.43
254368_at	DNA-directed RNA polymerase (EC 2.7.	NRPB2	AT4G21710	-1.27	-0.34	-3.14	0.017319	0.091129	-3.43
258150_at	hypothetical protein ;supported by full-le	---	AT3G18160	-1.65	-0.72	-3.14	0.017317	0.091129	-3.43
248568_at	receptor protein kinase-like	---	AT5G49760	1.35	0.43	3.14	0.017324	0.091134	-3.43
245284_at	phytoene dehydrogenase precursor (phy	PDS3	AT4G14210	-1.44	-0.53	-3.14	0.017337	0.091180	-3.43
252392_s_a	putative protein various predicted prote	---	AT3G47890 /	-1.40	-0.48	-3.14	0.017359	0.091224	-3.43

264238_at	hypothetical protein predicted by gensca	---	AT1G54740	1.78	0.83	3.14	0.017353	0.091224	-3.43
245769_at	hypothetical protein similar to putative s	INT2	AT1G30220	1.25	0.32	3.14	0.017361	0.091224	-3.43
257939_at	monosaccharide transport protein, STP	STP4	AT3G19930	1.56	0.64	3.14	0.017356	0.091224	-3.43
260206_at	putative protein kinase contains Pfam p	---	AT1G70740	1.79	0.84	3.13	0.017367	0.091237	-3.44
257088_at	unknown protein	---	AT3G20510	1.82	0.86	3.13	0.017374	0.091252	-3.44
266290_at	putative glutathione S-transferase ;supp	ATGSTU1	AT2G29490	3.92	1.97	3.13	0.017383	0.091276	-3.44
254110_at	putative protein pectinesterase - Citrus	---	AT4G25260	-1.87	-0.90	-3.13	0.017392	0.091282	-3.44
265964_at	putative RNA-binding protein ; supporte	---	AT2G37510	-1.30	-0.38	-3.13	0.017391	0.091282	-3.44
245088_at	subtilisin-like serine protease contains s	---	AT2G39850	-1.77	-0.83	-3.13	0.017396	0.091283	-3.44
265794_at	unknown protein	---	AT2G01310	-1.23	-0.30	-3.13	0.017423	0.091402	-3.44
253391_at	hypothetical protein ; supported by cDN	---	AT4G32590	-1.46	-0.55	-3.13	0.017435	0.091425	-3.44
251726_at	protein kinase NPK1-related protein kin	---	AT3G56280	1.21	0.27	3.13	0.017439	0.091425	-3.44
258984_at	putative DnaJ protein Pfam HMM hit: D	ATERDJ3A	AT3G08970	1.35	0.43	3.13	0.017435	0.091425	-3.44
265075_at	hypothetical protein similar to embryo-al	---	AT1G55450	2.52	1.33	3.13	0.017453	0.091457	-3.44
265841_at	putative glycogenin	---	AT2G35710	3.24	1.70	3.13	0.01745	0.091457	-3.44
251476_at	putative protein hypothetical protein F6	---	AT3G59670	-1.52	-0.61	-3.13	0.017464	0.091492	-3.44
253701_at	choline monooxygenase - like protein c	---	AT4G29890	-1.38	-0.47	-3.13	0.017473	0.091515	-3.44
249195_s_a	disease resistance response protein-like	---	AT5G42500 /	1.47	0.55	3.13	0.017482	0.091546	-3.44
266983_at	putative phospholipase ; supported by c	---	AT2G39400	1.48	0.56	3.13	0.017502	0.091603	-3.44
259641_at	putative protease similar to protease II (	---	AT1G69020	-1.36	-0.44	-3.13	0.017505	0.091603	-3.44
246289_at	putative protein predicted protein At2g4	---	AT3G56880	1.59	0.67	3.13	0.017501	0.091603	-3.44
254342_at	receptor like protein (fragment) ES43 p	---	AT4G22140	-1.24	-0.31	-3.13	0.017549	0.091809	-3.45
258883_at	unknown protein predicted by genscan,	---	AT3G09970	-1.32	-0.40	-3.13	0.01756	0.091811	-3.45
260094_at	GDP-4-keto-6-deoxy-D-mannose-3,5-e	GER1	AT1G73250	1.38	0.46	3.13	0.017561	0.091811	-3.45
260993_at	hypothetical protein predicted by genem	FMO GS-(	AT1G12140	1.22	0.28	3.13	0.017555	0.091811	-3.45
248640_at	selenium-binding protein-like ; supporte	---	AT5G48910	-1.33	-0.41	-3.13	0.017567	0.091822	-3.45
253386_at	sulfolipid biosynthesis protein SQD1 ; s	SQD1	AT4G33030	-1.42	-0.51	-3.13	0.017574	0.091838	-3.45
248145_at	unknown protein ;supported by full-leng	---	AT5G54880	-1.31	-0.39	-3.13	0.017578	0.091838	-3.45
261116_at	sec14 cytosolic factor, putative similar t	---	AT1G75370	-1.28	-0.35	-3.12	0.017609	0.091977	-3.45
254111_at	putative protein acid phosphatase (EC	PAP24	AT4G24890	1.47	0.55	3.12	0.017644	0.092137	-3.45
263987_at	putative lipase ; supported by cDNA: gi	---	AT2G42690	-1.41	-0.50	-3.12	0.017652	0.092140	-3.45
265912_at	hypothetical protein predicted by gensca	---	AT2G25565 /	-1.28	-0.36	-3.12	0.017652	0.092140	-3.45
259937_s_a	putative ABC transporter contains Pfam	ATNAP5	AT1G71330 /	1.29	0.37	3.12	0.017679	0.092191	-3.45
249077_at	alcohol dehydrogenase (EC 1.1.1.1) cla	HOT5	AT5G43940	-1.31	-0.39	-3.12	0.017683	0.092191	-3.45
263379_at	putative CCCH-type zinc finger protein a	CZF1	AT2G40140	2.81	1.49	3.12	0.017687	0.092191	-3.45

262583_at	putative phosphatidylserine synthase Si	---	AT1G15110	1.38	0.47	3.12	0.017669	0.092191	-3.45
255942_at	UDP-glucose glucosyltransferase identi	AtUGT85A	AT1G22360	2.33	1.22	3.12	0.017686	0.092191	-3.45
258516_at	myb-related protein, putative similar to	MYB108	AT3G06490	2.22	1.15	3.12	0.017691	0.092191	-3.45
251370_at	putative protein prib5, Ribes nigrum, EM	---	AT3G60450	2.05	1.04	3.12	0.017681	0.092191	-3.45
253640_at	putative protein ;supported by full-lengt	---	AT4G30630	-1.24	-0.31	-3.12	0.017715	0.092298	-3.46
267093_at	high affinity Ca2+ antiporter identical to	CAX1	AT2G38170	-1.51	-0.59	-3.12	0.01772	0.092301	-3.46
252906_at	putative gamma-glutamyltransferase ga	GGT1	AT4G39640	1.58	0.66	3.12	0.017756	0.092471	-3.46
258136_at	hypothetical protein predicted by genem	RSY3	AT3G24560	-1.33	-0.41	-3.12	0.017767	0.092485	-3.46
263420_at	unknown protein ; supported by full-leng	---	AT2G17240	-1.25	-0.33	-3.12	0.017765	0.092485	-3.46
252813_at	putative protein several hypothetical pro	---	---	1.26	0.33	3.12	0.017778	0.092518	-3.46
249434_at	putative protein GTP-binding proteins -	---	AT5G39960	-1.41	-0.50	-3.12	0.017795	0.092589	-3.46
267048_at	hypothetical protein predicted by genefi	---	AT2G34200	-1.40	-0.49	-3.12	0.01781	0.092644	-3.46
258405_at	unknown protein almost identical to SN	BSH	AT3G17590	-1.44	-0.53	-3.12	0.017821	0.092681	-3.46
260931_at	hypothetical protein predicted by genem	---	AT1G02550	1.35	0.43	3.12	0.017832	0.092694	-3.46
265566_at	hypothetical protein predicted by genefi	---	AT2G05600	1.31	0.39	3.12	0.017828	0.092694	-3.46
258817_at	hypothetical protein similar to hypotheti	---	AT3G04750	-1.23	-0.30	-3.12	0.017839	0.092709	-3.46
261411_at	histone H2B identical to GB:CAA73156	HTB1	AT1G07790	-1.46	-0.55	-3.11	0.017854	0.092767	-3.46
267029_at	unknown protein	ATIREG1	AT2G38460	-1.34	-0.42	-3.11	0.017937	0.093179	-3.47
247136_at	senescence-associated protein contains	---	AT5G66170	2.72	1.44	3.11	0.017949	0.093219	-3.47
260730_at	lipoamide dehydrogenase precursor ide	mtLPD1	AT1G48030	-1.41	-0.49	-3.11	0.017953	0.093220	-3.47
265993_at	putative disease resistance protein	---	AT2G24160	3.58	1.84	3.11	0.017967	0.093268	-3.47
247863_at	SKP1 interacting partner 1 (SKIP1) iden	---	AT5G57890 /	1.29	0.37	3.11	0.017975	0.093290	-3.47
257987_at	fertilization-independent endosperm pro	FIE	AT3G20740	-1.27	-0.34	-3.11	0.018014	0.093424	-3.47
257829_at	unknown protein	SNM1	AT3G26680	1.56	0.64	3.11	0.018016	0.093424	-3.47
250742_at	putative protein similar to unknown prote	---	AT5G05800	-1.31	-0.39	-3.11	0.018017	0.093424	-3.47
252345_at	hypothetical protein	---	AT3G48640	1.46	0.55	3.11	0.018016	0.093424	-3.47
265070_at	branched-chain alpha-keto acid decarbo	BCDH BET	AT1G55510	1.81	0.85	3.11	0.018022	0.093427	-3.47
246487_at	putative protein with poly glutamic acid	---	AT5G16030	-1.62	-0.69	-3.11	0.018026	0.093427	-3.47
255728_at	unknown protein	---	AT1G25500	1.56	0.64	3.11	0.018034	0.093433	-3.47
251695_at	putative protein hypothetical proteins - A	---	AT3G56590	-1.51	-0.60	-3.11	0.018039	0.093433	-3.47
258943_at	hypothetical protein predicted by genefi	---	AT3G10400	1.32	0.40	3.11	0.018035	0.093433	-3.47
266156_at	hypothetical protein predicted by gensca	FRA8	AT2G28110	2.26	1.18	3.11	0.018044	0.093436	-3.47
247047_at	putative protein contains similarity to unl	---	AT5G66650	3.02	1.59	3.11	0.018052	0.093454	-3.48
259871_at	nodulin-like protein similar to nodulin GB	---	AT1G76800	-1.81	-0.86	-3.11	0.018056	0.093457	-3.48
267174_at	60S ribosomal protein L36 ;supported b	---	AT2G37600	-1.57	-0.65	-3.11	0.018076	0.093508	-3.48

252406_at	putative protein pectinesterase - Arabid	---	AT3G47670	1.22	0.29	3.11	0.018078	0.093508	-3.48
253456_at	putative protein norbin, Rattus norvegic	---	AT4G32050	-1.37	-0.45	-3.11	0.018083	0.093508	-3.48
252425_at	putative protein auxin-induced basic he	AtTCP14	AT3G47620	-1.47	-0.56	-3.11	0.01808	0.093508	-3.48
248092_at	ubiquitin-like protein	SUMO3	AT5G55170	2.16	1.11	3.10	0.018102	0.093587	-3.48
262809_at	putative glycogen synthase strong simila	ATSS3	AT1G11720	-1.87	-0.90	-3.10	0.018114	0.093630	-3.48
263255_at	unknown protein similar to steroid recep	---	AT1G10490	-1.41	-0.49	-3.10	0.018137	0.093726	-3.48
260025_at	unknown protein ;supported by full-lengt	---	AT1G30070	-1.50	-0.58	-3.10	0.018146	0.093753	-3.48
245987_at	NAM-like protein hypothetical protein S	ANAC083	AT5G13180	1.31	0.39	3.10	0.018193	0.093757	-3.48
258719_at	putative pectate lyase simliar to pectate	---	AT3G09540	-1.78	-0.83	-3.10	0.018163	0.093757	-3.48
251665_at	responce reactor 4 ; supported by cDNA	ARR9	AT3G57040	1.94	0.96	3.10	0.018168	0.093757	-3.48
256957_at	hypothetical protein predicted by gensca	---	AT3G13420	1.28	0.36	3.10	0.018187	0.093757	-3.48
245509_at	hypothetical protein	---	AT4G15730	-1.34	-0.43	-3.10	0.018198	0.093757	-3.48
257224_at	P-type ATPase, putative similar to ATP	---	AT3G27870	1.32	0.40	3.10	0.018156	0.093757	-3.48
262918_at	hypothetical protein predicted by genem	---	AT1G65000	-1.31	-0.39	-3.10	0.018183	0.093757	-3.48
261958_at	peptide transporter, putative predicted p	---	AT1G64500	-1.66	-0.73	-3.10	0.018201	0.093757	-3.48
261651_at	unknown protein similar to unknown pro	SAT32	AT1G27760	1.63	0.71	3.10	0.018156	0.093757	-3.48
264381_at	putative ribonuclease large subunit sim	---	AT2G25100	-1.46	-0.55	-3.10	0.018182	0.093757	-3.48
252278_at	NAC2-like protein NAC2 - Arabidopsis t	anac062	AT3G49530	1.88	0.91	3.10	0.01819	0.093757	-3.48
245924_at	Tha4 protein - like Tha4 protein, Pisum	---	AT5G28750	-1.24	-0.31	-3.10	0.018194	0.093757	-3.48
258207_at	putative GTP pyrophosphokinase simila	RSH2	AT3G14050	1.68	0.75	3.10	0.018168	0.093757	-3.48
247550_at	putative protein many predicted proteins	---	AT5G61370	-1.23	-0.30	-3.10	0.018219	0.093769	-3.48
267147_at	putative anthocyanidin synthase ;suppo	---	AT2G38240	2.87	1.52	3.10	0.018212	0.093769	-3.48
251837_s_a	spliceosomal - like protein spliceosoma	---	AT3G55200 /	-1.35	-0.43	-3.10	0.018219	0.093769	-3.49
260148_at	putative oxidoreductase similar to gibbe	---	AT1G52800	-1.46	-0.55	-3.10	0.018209	0.093769	-3.48
251422_at	transport protein subunit - like S61B_AI	---	AT3G60540	1.83	0.87	3.10	0.018232	0.093812	-3.49
266992_at	similar to Mlo proteins from H. vulgare ;	MLO12	AT2G39200	2.82	1.50	3.10	0.018291	0.094095	-3.49
248931_at	peptide transporter	---	AT5G46040	1.22	0.29	3.10	0.018314	0.094177	-3.49
247505_at	signal recognition particle - like protein	---	AT5G61970	-1.22	-0.29	-3.10	0.018315	0.094177	-3.49
256627_at	unknown protein ; supported by cDNA:	---	AT3G19970	2.80	1.48	3.10	0.018321	0.094187	-3.49
255526_at	hypothetical protein	---	AT4G02350	1.33	0.41	3.10	0.018332	0.094222	-3.49
247284_at	Isp4-like protein ; supported by full-leng	OPT4	AT5G64410	1.75	0.81	3.09	0.018341	0.094245	-3.49
252878_at	mitochondrial carrier - like protein AgPE	SAMC1	AT4G39460	-1.28	-0.36	-3.09	0.018355	0.094299	-3.49
247925_at	TCH4 protein (gb|AAA92363.1) ; suppo	TCH4	AT5G57560	2.86	1.51	3.09	0.018379	0.094397	-3.49
247256_at	putative protein contains similarity to un	---	AT5G64730	-1.23	-0.30	-3.09	0.018393	0.094450	-3.49
246779_at	putative protein peroxisomal integral me	PNC2	AT5G27520	1.59	0.67	3.09	0.018431	0.094602	-3.50

260935_at	hypothetical protein predicted by genem	---	AT1G45110	-1.37	-0.45	-3.09	0.018429	0.094602	-3.50
256379_at	hypothetical protein predicted by gensca	---	AT1G66840	-1.42	-0.51	-3.09	0.018447	0.094663	-3.50
247597_at	GTP-binding protein - like GTP-binding	AtRABA1f	AT5G60860	1.77	0.83	3.09	0.018458	0.094700	-3.50
256252_at	glucosyl transferase, putative similar to	---	AT3G11340	4.40	2.14	3.09	0.018483	0.094806	-3.50
253538_at	putative protein ribosomal protein YmL1	---	AT4G31460	-1.23	-0.30	-3.09	0.018491	0.094827	-3.50
260542_at	putative FKBP type peptidyl-prolyl cis-tra	---	AT2G43560	-1.55	-0.63	-3.09	0.018508	0.094890	-3.50
249355_at	hypothetical protein	---	AT5G40500	-1.26	-0.33	-3.09	0.018516	0.094912	-3.50
266226_at	histone H4 identical to GB:M17133 and	HIS4	AT2G28740	-1.50	-0.58	-3.09	0.018528	0.094949	-3.50
251729_at	alpha-galactosidase-like protein alpha g	---	AT3G56310	1.57	0.65	3.09	0.01855	0.095024	-3.50
251052_at	DP-2 transcription factor - like transcrip	DPA	AT5G02470	-1.31	-0.39	-3.09	0.018551	0.095024	-3.50
250550_at	N-hydroxycinnamoyl benzoyltransferas	---	AT5G07870	1.71	0.77	3.09	0.018561	0.095054	-3.50
264789_at	putative glycine-rich, zinc-finger DNA-b	---	AT2G17870	-1.23	-0.29	-3.09	0.01858	0.095132	-3.51
266481_at	unknown protein ; supported by cDNA:	TCP10	AT2G31070	-1.39	-0.48	-3.08	0.018604	0.095215	-3.51
246294_at	ribosomal protein, chloroplast ribosoma	PSRP5	AT3G56910	-1.26	-0.33	-3.08	0.018617	0.095215	-3.51
264007_at	putative proline-rich protein	ATPRP2	AT2G21140	4.30	2.10	3.08	0.018614	0.095215	-3.51
259240_at	unknown protein ; supported by cDNA:	---	AT3G11590	-1.40	-0.49	-3.08	0.018617	0.095215	-3.51
263722_at	putative vanadate resistance protein	GONST1	AT2G13650	1.29	0.37	3.08	0.018615	0.095215	-3.51
258929_at	unknown protein Pfam HMM hit: FKBP-t	---	AT3G10060	-1.93	-0.95	-3.08	0.018645	0.095230	-3.51
250222_at	putative protein similar to unknown prote	---	AT5G14050	-1.50	-0.59	-3.08	0.018625	0.095230	-3.51
255434_at	predicted protein of unknown function ;	---	AT4G03180	-1.28	-0.36	-3.08	0.018644	0.095230	-3.51
247963_at	beta-1,3-glucanase-like protein	---	AT5G56590	-1.26	-0.33	-3.08	0.018641	0.095230	-3.51
266062_at	putative diacylglycerol kinase	---	AT2G18730	-1.21	-0.28	-3.08	0.01863	0.095230	-3.51
249746_at	NAC2-like protein	TIP	AT5G24590	1.33	0.41	3.08	0.018643	0.095230	-3.51
262166_at	myb-related transcription activator, puta	---	AT1G74840	-1.38	-0.46	-3.08	0.018651	0.095237	-3.51
266421_at	putative nonspecific lipid-transfer protein	LP1	AT2G38540	2.32	1.21	3.08	0.018665	0.095287	-3.51
250961_at	putative protein various predicted prote	---	AT5G02980	1.28	0.35	3.08	0.018682	0.095356	-3.51
245250_at	ethylene responsive element binding fac	ATERF6	AT4G17490	4.01	2.01	3.08	0.01869	0.095374	-3.51
259326_at	putative mitochondrial processing pepti	MPPalpha	AT3G16480	-1.24	-0.31	-3.08	0.01871	0.095452	-3.51
265394_at	predicted protein ; supported by cDNA:	---	AT2G20725	-1.33	-0.42	-3.08	0.018739	0.095581	-3.51
259673_at	putative phorbol ester / diacylglycerol bi	---	AT1G77800	-1.39	-0.47	-3.08	0.018773	0.095642	-3.52
258379_at	putative decarboxilase similar to 5-oxo-	---	AT3G16700	1.43	0.52	3.08	0.018775	0.095642	-3.52
245256_at	Expressed protein ; supported by cDNA	FAR1	AT4G15090	-1.33	-0.41	-3.08	0.01876	0.095642	-3.52
267088_at	30S ribosomal protein S31 ;supported b	PSRP4	AT2G38140	-1.37	-0.45	-3.08	0.018762	0.095642	-3.52
261163_x_a	auxin response factor, putative similar t	ARF21	AT1G34410	1.21	0.28	3.08	0.018776	0.095642	-3.52
248528_at	putative protein similar to unknown prote	---	AT5G50760	4.35	2.12	3.08	0.018772	0.095642	-3.52

246196_at	hypothetical protein ;supported by full-le	---	AT4G37090	-1.42	-0.51	-3.08	0.018842	0.095954	-3.52
245415_at	G2484-1 protein	ATG2484-	AT4G17330	-1.24	-0.31	-3.08	0.018847	0.095960	-3.52
247355_at	unknown protein ; supported by full-leng	SPT42	AT5G63670	-1.26	-0.33	-3.07	0.018856	0.095985	-3.52
264860_at	hypothetical protein contains ATP/GTP-	---	AT1G24290	-1.23	-0.30	-3.07	0.018863	0.096000	-3.52
256720_at	putative DOF zinc finger protein	---	AT2G34140	1.65	0.72	3.07	0.018879	0.096059	-3.52
260913_at	s-adenosylmethionine synthetase identi	SAM1	AT1G02500	1.52	0.61	3.07	0.018888	0.096061	-3.52
260017_at	hypothetical protein predicted by genem	---	---	1.49	0.58	3.07	0.018896	0.096061	-3.52
260082_at	putative mitochondrial carrier protein co	---	AT1G78180	-1.37	-0.46	-3.07	0.018896	0.096061	-3.52
252373_at	disease resistance protein EDS1 ; supp	EDS1	AT3G48090	2.15	1.11	3.07	0.018887	0.096061	-3.52
254747_at	serine/threonine-specific protein kinase	MHK	AT4G13020	-1.29	-0.36	-3.07	0.018911	0.096115	-3.52
256649_at	serine/arginine-rich protein, putative sin	SCL30A	AT3G13570	-1.37	-0.46	-3.07	0.018964	0.096340	-3.53
251984_at	phenylalanine ammonia-lyase ;supporte	PAL2	AT3G53260	2.67	1.42	3.07	0.018964	0.096340	-3.53
251637_at	hypothetical protein	---	AT3G57570	-1.30	-0.38	-3.07	0.018971	0.096355	-3.53
245082_at	hypothetical protein predicted by genefin	---	AT2G23270	4.85	2.28	3.07	0.018983	0.096394	-3.53
255037_at	DNA-binding protein ;supported by full-	ATMYB6	AT4G09460	1.71	0.78	3.07	0.018994	0.096418	-3.53
261577_at	ribonucleoprotein, putative similar to 33	---	AT1G01080	-1.43	-0.51	-3.07	0.018996	0.096418	-3.53
251705_at	DNA-binding protein-like DNA-binding p	WRKY70	AT3G56400	5.84	2.55	3.07	0.019002	0.096429	-3.53
259162_at	unknown protein similar to unknown pro	---	AT3G01640	1.35	0.43	3.07	0.019008	0.096433	-3.53
246139_at	putative protein predicted protein, Dros	---	AT5G19900	-1.33	-0.41	-3.07	0.019017	0.096458	-3.53
250634_at	putative protein 2-oxoglutarate-depende	---	AT5G07480	1.25	0.32	3.07	0.019026	0.096486	-3.53
246777_at	RING-H2 zinc finger protein-like RING-	---	AT5G27420	3.20	1.68	3.07	0.019033	0.096500	-3.53
253349_at	putative protein	---	---	-1.23	-0.30	-3.07	0.019043	0.096529	-3.53
249752_at	putative protein similar to unknown prote	LSU2	AT5G24660	-1.35	-0.44	-3.07	0.019052	0.096550	-3.53
259481_at	germin, putative similar to germin GI:17	GLP4	AT1G18970	1.67	0.74	3.07	0.019064	0.096590	-3.53
253388_at	putative protein ; supported by cDNA: g	---	AT4G32910	-1.44	-0.52	-3.07	0.019077	0.096637	-3.53
265011_at	putative chloroplast membrane protein,	ALB4	AT1G24490	-1.21	-0.28	-3.07	0.019104	0.096719	-3.53
259380_at	putative ABC transporter similar to ABC	PDR1	AT3G16340	1.35	0.43	3.06	0.019111	0.096719	-3.53
264018_at	putative triosephosphate isomerase ;su	TIM	AT2G21170	-1.27	-0.35	-3.06	0.01911	0.096719	-3.53
265027_at	putative ribonuclease III similar to ESTs	NFD2	AT1G24450	-1.37	-0.46	-3.06	0.01911	0.096719	-3.53
258485_at	putative stearoyl-acyl carrier protein des	---	AT3G02630	-1.20	-0.26	-3.06	0.019126	0.096775	-3.54
259996_at	hypothetical protein predicted by genefin	---	AT1G67910	-1.38	-0.47	-3.06	0.019143	0.096803	-3.54
AFFX-r2-Bs	B. subtilis /GEN=jojG /DB_XREF=gb:L3	---	---	-1.50	-0.58	-3.06	0.019144	0.096803	-3.54
261280_at	hypothetical protein predicted by genem	---	AT1G05860	-1.42	-0.51	-3.06	0.019139	0.096803	-3.54
266521_at	unknown protein ; supported by cDNA:	---	AT2G24020	-1.24	-0.31	-3.06	0.019194	0.097014	-3.54
253969_at	putative protein hypothetical protein YC	CSN6B	AT4G26430	-1.54	-0.62	-3.06	0.019193	0.097014	-3.54

263415_at	hypothetical protein similar to GB:AAB8(	EMB2762	AT2G17250	-1.41	-0.50	-3.06	0.019224	0.097143	-3.54
254932_at	putative translation elongation factor ts	---	AT4G11120	-1.47	-0.55	-3.06	0.019234	0.097148	-3.54
253773_s_a	Expressed protein ; supported by full-ler	---	AT1G52370 /	-1.34	-0.42	-3.06	0.019232	0.097148	-3.54
266572_at	unknown protein	---	AT2G23840	-1.44	-0.52	-3.06	0.01925	0.097204	-3.54
264563_s_a	unknown protein	---	AT1G55750 /	-1.30	-0.38	-3.06	0.019254	0.097204	-3.54
254447_at	berberine bridge enzyme - like protein ;	---	AT4G20860	2.40	1.26	3.06	0.019258	0.097204	-3.54
266119_at	protease inhibitor II identical to GB:X69	LCR69	AT2G02100	2.42	1.27	3.06	0.019276	0.097276	-3.54
264327_at	putative translation initiation factor eIF-1	EIF2 GAM	AT1G04170	-1.25	-0.32	-3.06	0.019297	0.097361	-3.54
253048_at	formamidase - like protein formamidase	---	AT4G37560	-1.95	-0.97	-3.06	0.019304	0.097372	-3.55
257209_at	hypothetical protein	---	AT3G14920	1.22	0.28	3.06	0.019309	0.097376	-3.55
266368_at	putative embryo-abundant protein	---	AT2G41380	3.98	1.99	3.06	0.019326	0.097443	-3.55
263668_at	putative 1-aminocyclopropane-1-carbox	---	AT1G04350	-1.32	-0.40	-3.06	0.019344	0.097508	-3.55
254763_at	ribosomal protein L13a like protein ribo	---	AT4G13170	-1.37	-0.45	-3.06	0.01935	0.097520	-3.55
261664_s_a	hypothetical protein contains similarity to	---	AT1G18320 /	-1.43	-0.52	-3.06	0.019372	0.097538	-3.55
259105_at	stress related protein, putative similar to	---	AT3G05500	1.41	0.49	3.06	0.019372	0.097538	-3.55
249138_at	putative protein contains similarity to MF	WPP1	AT5G43070	1.26	0.34	3.06	0.019366	0.097538	-3.55
258933_at	unknown protein similar to unknown pro	---	AT3G09980	-1.28	-0.36	-3.06	0.019372	0.097538	-3.55
257734_at	unknown protein contains Pfam profile: I	ATSYTF	AT3G18370	1.22	0.29	3.05	0.019375	0.097538	-3.55
252990_at	putative protein	---	AT4G38440	-1.65	-0.72	-3.05	0.019385	0.097567	-3.55
257948_at	hypothetical protein predicted by genem	APO4	AT3G21740	-1.30	-0.38	-3.05	0.019396	0.097579	-3.55
265189_at	unknown protein ; supported by cDNA:	---	AT1G23840	1.69	0.76	3.05	0.019392	0.097579	-3.55
260732_at	myb-related DNA-binding protein, putat	---	AT1G17520	-1.25	-0.32	-3.05	0.019448	0.097755	-3.55
262092_at	unknown protein	---	AT1G56150	-2.12	-1.08	-3.05	0.019444	0.097755	-3.55
263260_at	putative protein-tyrosine phosphatase 2	OTS2	AT1G10570	-1.24	-0.32	-3.05	0.019444	0.097755	-3.55
246973_at	putative protein UBIQUINONE BIOSYN	---	AT5G24970	-1.46	-0.54	-3.05	0.019448	0.097755	-3.55
246980_at	peptidylprolyl isomerase (cyclophilin)-lik	---	AT5G67530	-1.26	-0.33	-3.05	0.019455	0.097760	-3.55
259764_at	transcription factor inhibitor I kappa B, p	NPR1	AT1G64280	1.46	0.55	3.05	0.019458	0.097760	-3.55
253119_at	Expressed protein ; supported by full-ler	---	AT4G35980	-1.25	-0.32	-3.05	0.019481	0.097853	-3.55
257337_at	NADH dehydrogenase subunit 5 (nad5)	---	---	-1.70	-0.77	-3.05	0.019509	0.097882	-3.56
249528_at	putative protein predicted protein, Dros	---	AT5G38720	-1.49	-0.57	-3.05	0.019496	0.097882	-3.56
264452_at	unknown protein similar to salt-inducible	GRP23	AT1G10270	-2.06	-1.04	-3.05	0.019502	0.097882	-3.56
263727_at	putative cap-binding protein ; supported	ABH1	AT2G13540	-1.36	-0.44	-3.05	0.019511	0.097882	-3.56
264407_at	unknown protein similar to EST gb|N960	---	AT1G10180	-1.33	-0.42	-3.05	0.019501	0.097882	-3.56
246141_at	TipD - like WD repeat protein TipD, Dic	---	AT5G19920	-1.34	-0.42	-3.05	0.019512	0.097882	-3.56
263154_at	Expressed protein ; supported by full-ler	---	AT1G54110	-1.34	-0.42	-3.05	0.019519	0.097896	-3.56

258545_at	putative GTPase contains Pfam profile:	---	AT3G07050	-1.51	-0.59	-3.05	0.019538	0.097946	-3.56
258604_at	putative N-acetlytransferase contains Pf	---	AT3G02980	-1.33	-0.42	-3.05	0.019537	0.097946	-3.56
252928_at	putative protein more than 30 predicted	---	AT4G38940	1.64	0.72	3.05	0.019546	0.097950	-3.56
261417_at	Expressed protein ; supported by cDNA	---	AT1G07700	-1.26	-0.33	-3.05	0.019547	0.097950	-3.56
244943_at	NADH dehydrogenase subunit 9	---	ATMG00070	-1.39	-0.48	-3.05	0.019563	0.097991	-3.56
264005_at	unknown protein ; supported by cDNA:	AGP2	AT2G22470	3.85	1.94	3.05	0.019564	0.097991	-3.56
256612_at	hypothetical protein predicted by genem	---	AT3G29280	-1.34	-0.42	-3.05	0.019576	0.098030	-3.56
250426_at	ovule development protein - like ovule d	AIL6	AT5G10510	1.24	0.31	3.05	0.019604	0.098125	-3.56
263883_at	hypothetical protein predicted by gensca	---	AT2G21830	-1.29	-0.37	-3.05	0.019602	0.098125	-3.56
266675_s_a	hypothetical protein predicted by gensca	---	AT2G29610 /	1.20	0.27	3.05	0.019615	0.098139	-3.56
246445_at	glucose 6 phosphate/phosphate translo	---	AT5G17630	-1.32	-0.40	-3.05	0.019615	0.098139	-3.56
250028_at	putative protein similar to unknown prote	---	AT5G18130	-1.27	-0.35	-3.05	0.019626	0.098152	-3.56
259714_at	putative gibberellin 20-oxidase similar to	ATGA20O	AT1G60980	1.29	0.37	3.05	0.019623	0.098152	-3.56
259868_at	thioredoxin-like protein similar to thiored	ATY1	AT1G76760	1.25	0.33	3.05	0.01964	0.098198	-3.56
260271_at	unknown protein similar to unknown pro	---	AT1G63690	-1.26	-0.33	-3.04	0.019652	0.098215	-3.56
249910_at	chorismate mutase/prephenate dehydra	ADT5	AT5G22630	2.07	1.05	3.04	0.019651	0.098215	-3.56
260156_at	NAM-like protein similar to NAM (no apic	NAM	AT1G52880	-1.52	-0.60	-3.04	0.019683	0.098349	-3.57
257525_at	hypothetical protein predicted by gensca	---	AT3G04900	1.32	0.40	3.04	0.019693	0.098377	-3.57
249529_at	putative protein predicted proteins, Arat	---	AT5G38730	-1.44	-0.52	-3.04	0.019716	0.098452	-3.57
250135_at	putative protein	---	AT5G15360	-1.28	-0.35	-3.04	0.019721	0.098452	-3.57
258085_at	unknown protein ; supported by cDNA:	---	AT3G26100	1.32	0.40	3.04	0.019719	0.098452	-3.57
250095_at	phytoene synthase (gb|AAB65697.1) ;s	---	AT5G17230	-1.58	-0.66	-3.04	0.019729	0.098452	-3.57
253173_at	putative protein pEARLI 4, Arabidopsis	---	AT4G35110	2.06	1.04	3.04	0.019726	0.098452	-3.57
254145_at	hypothetical protein	---	AT4G24700	-1.68	-0.75	-3.04	0.019745	0.098488	-3.57
249918_at	putative protein predicted protein, Arabi	---	AT5G19240	2.16	1.11	3.04	0.019744	0.098488	-3.57
247556_at	putative protein predicted protein, Arabi	---	AT5G61040	-1.36	-0.44	-3.04	0.01976	0.098540	-3.57
253093_at	putative protein SPINDLY protein, Petu	SRFR1	AT4G37460	-1.27	-0.35	-3.04	0.019784	0.098637	-3.57
266893_at	hypothetical protein predicted by gensca	RTE1	AT2G26070	-1.30	-0.38	-3.04	0.019792	0.098643	-3.57
267322_at	putative leucine-rich-repeat protein	---	AT2G19330	1.23	0.30	3.04	0.019793	0.098643	-3.57
267440_at	putative anthranilate N-hydroxycinnamo	SHT	AT2G19070	-1.27	-0.35	-3.04	0.019815	0.098729	-3.57
248115_at	putative protein strong similarity to unkn	---	AT5G54870	1.55	0.63	3.04	0.019839	0.098806	-3.57
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=gb:M	---	---	-1.59	-0.67	-3.04	0.019838	0.098806	-3.57
248659_at	cyclin C-like protein	---	AT5G48640	1.32	0.40	3.04	0.019859	0.098885	-3.57
264170_at	hypothetical protein	---	AT1G02260	1.28	0.36	3.04	0.019867	0.098900	-3.58
259161_at	carbonic anhydrase, chloroplast precur	CA1	AT3G01500	-1.95	-0.96	-3.04	0.01989	0.098971	-3.58

251285_at	putative protein several hypothetical pro	---	AT3G61770	-1.27	-0.35	-3.04	0.019889	0.098971	-3.58
249754_at	flavanone 3-hydroxylase-like protein ; s	DMR6	AT5G24530	3.19	1.68	3.04	0.019904	0.099019	-3.58
263083_at	purple acid phosphatase precursor iden	PAP12	AT2G27190	-1.27	-0.34	-3.04	0.019911	0.099026	-3.58
259721_at	putative phosphatidylinositol-4-phospha	---	AT1G60890	1.43	0.51	3.03	0.019922	0.099026	-3.58
266780_at	putative ligand-gated ion channel protei	ATGLR2.8	AT2G29110	1.47	0.56	3.03	0.019917	0.099026	-3.58
246283_at	putative protein	---	AT4G36860	-1.34	-0.42	-3.03	0.019922	0.099026	-3.58
264716_at	matrix metalloproteinase, putative simil	MMP	AT1G70170	1.95	0.96	3.03	0.019954	0.099162	-3.58
266883_at	putative triacylglycerol lipase	DAD1	AT2G44810	1.26	0.34	3.03	0.019969	0.099214	-3.58
258796_at	unknown protein ;supported by full-leng	WDL1	AT3G04630	1.72	0.78	3.03	0.019987	0.099245	-3.58
246345_at	calcium-dependent protein kinase-like (	---	AT3G56760	-1.36	-0.44	-3.03	0.019997	0.099245	-3.58
257350_x_a	hypothetical protein predicted by gensca	RALFL12	AT2G19040	1.28	0.35	3.03	0.019981	0.099245	-3.58
263805_at	unknown protein ; supported by cDNA:	---	AT2G40400	-1.22	-0.29	-3.03	0.019995	0.099245	-3.58
249586_at	putative protein predicted proteins, Aral	---	AT5G37840	1.83	0.87	3.03	0.019988	0.099245	-3.58
258444_at	expressed protein supported by cDNA: g	TIC	AT3G22380	-1.27	-0.35	-3.03	0.020003	0.099254	-3.58
250920_at	putative protein ;supported by full-lengt	---	AT5G03390	1.55	0.63	3.03	0.020018	0.099308	-3.58
249945_at	60S ribosomal protein L10A ; supported	---	AT5G22440	-1.71	-0.77	-3.03	0.020027	0.099328	-3.58
251685_at	putative protein unknown protein At2g4	---	AT3G56430	-1.73	-0.79	-3.03	0.020036	0.099350	-3.58
247323_at	putative protein similar to unknown prote	---	AT5G64170	-1.42	-0.51	-3.03	0.020056	0.099388	-3.59
264527_at	putative reticuline oxidase-like protein s	---	AT1G30760	1.72	0.79	3.03	0.020056	0.099388	-3.59
250258_at	floral homeotic protein AGL15 (sp|Q388	AGL15	AT5G13790	1.29	0.37	3.03	0.020048	0.099388	-3.58
245621_at	AMP-binding protein	AAE15	AT4G14070	-1.43	-0.51	-3.03	0.020072	0.099446	-3.59
245039_at	putative beta-1,3-glucanase ;supported	---	AT2G26600	-1.28	-0.35	-3.03	0.020087	0.099498	-3.59
258908_at	putative dehydroquinase shikimate dehy	MEE32	AT3G06350	1.42	0.50	3.03	0.020107	0.099575	-3.59
267159_at	putative SCARECROW gene regulator	---	AT2G37650	-1.28	-0.36	-3.03	0.020129	0.099660	-3.59
251265_at	ATP-dependent RNA helicase-like prote	---	AT3G62310	-1.37	-0.46	-3.03	0.02015	0.099745	-3.59
250557_at	putative protein ankyrin, Rattus norvegi	CPuORF1	AT5G07840 /	-1.24	-0.31	-3.03	0.020182	0.099879	-3.59
247491_at	putative protein supported by cDNA: Ce	---	AT5G61880	-1.61	-0.69	-3.02	0.020192	0.099889	-3.59
259681_at	nitrate reductase 1 (NR1) identical to nit	NIA1	AT1G77760	5.73	2.52	3.02	0.020196	0.099889	-3.59
265034_at	unknown protein ;supported by full-lengt	---	AT1G61660	1.31	0.39	3.02	0.020201	0.099889	-3.59
264778_at	unknown protein similar to C-1 (Homo s	AIP3	AT1G08780	-1.26	-0.33	-3.02	0.020199	0.099889	-3.59
259883_at	putative ribophorin I (dolichyl-diphospho	---	AT1G76400	-1.34	-0.43	-3.02	0.020211	0.099916	-3.59
245671_at	purine permease identical to purine perr	PUP1	AT1G28230	-1.25	-0.32	-3.02	0.020217	0.099925	-3.59
251641_at	protease-like protein INSULIN-DEGRAI	---	AT3G57470	-1.42	-0.50	-3.02	0.020237	0.099980	-3.59
265382_at	putative gluconokinase ;supported by fu	---	AT2G16790	1.55	0.63	3.02	0.020233	0.099980	-3.59
245521_at	Expressed protein ;supported by cDNA:	ESD4	AT4G15880	-1.25	-0.32	-3.02	0.020251	0.100007	-3.60

249200_at	5-3 exoribonuclease 2 ; supported by cD	XRN2	AT5G42540	-1.36	-0.44	-3.02	0.020251	0.100007	-3.60
247410_at	putative protein similar to unknown prote	emb1692	AT5G62990	-1.58	-0.66	-3.02	0.020256	0.100007	-3.60
252851_at	putative protein CLATHRIN COAT ASS	---	AT4G40080	1.85	0.89	3.02	0.020288	0.100144	-3.60
253557_at	putative protein wall-associated kinase	---	AT4G31110 /	-1.22	-0.29	-3.02	0.020308	0.100224	-3.60
267512_at	hypothetical protein predicted by genscа	SSE1	AT2G45690	-1.30	-0.38	-3.02	0.020327	0.100296	-3.60
253726_at	ribosomal protein S15a homolog riboso	rps15ae	AT4G29430	-1.69	-0.75	-3.02	0.020337	0.100320	-3.60
247125_at	putative protein contains similarity to unl	---	AT5G66070	1.91	0.93	3.02	0.020347	0.100350	-3.60
255783_at	hypothetical protein contains Pfam profil	iqd32	AT1G19870	-1.43	-0.52	-3.02	0.020356	0.100370	-3.60
264289_at	hypothetical protein similar to hypothetic	---	AT1G61890	1.88	0.91	3.02	0.020389	0.100513	-3.60
245296_at	isp4 like protein ; supported by cDNA: g	ATOPT3	AT4G16370	-1.54	-0.63	-3.02	0.020395	0.100520	-3.60
259419_at	acyl-CoA oxidase ACX3, putative simila	ACX6	AT1G06310	1.26	0.33	3.02	0.020408	0.100559	-3.60
262401_at	small GTP-binding protein, putative sim	RABG3E	AT1G49300	-1.22	-0.28	-3.02	0.020412	0.100559	-3.60
257220_at	MYB family transcription factor (Atmyb3	ATMYB21	AT3G27810	1.33	0.42	3.02	0.020441	0.100681	-3.60
265354_at	actin depolymerizing factor 5 ;supporte	ADF5	AT2G16700	1.73	0.79	3.02	0.020445	0.100681	-3.61
267040_at	unknown protein	---	AT2G34300	1.73	0.79	3.02	0.020451	0.100689	-3.61
263553_at	putative purple acid phosphatase precu	PAP10	AT2G16430	1.34	0.42	3.02	0.020458	0.100701	-3.61
266097_at	unknown protein ; supported by cDNA:	SOUL-1	AT2G37970	1.76	0.81	3.01	0.020495	0.100860	-3.61
257708_at	hypothetical protein predicted by genscа	---	AT3G13330	1.26	0.34	3.01	0.0205	0.100866	-3.61
253535_at	putaive DNA-binding protein DNA-bindi	WRKY11	AT4G31550	2.48	1.31	3.01	0.020541	0.101015	-3.61
248774_at	unknown protein	---	AT5G47830	-1.24	-0.31	-3.01	0.020542	0.101015	-3.61
245654_at	disease resistance protein, putative sim	---	AT1G56540	1.28	0.36	3.01	0.020544	0.101015	-3.61
254629_at	Expressed protein ; supported by full-ler	---	AT4G18425	1.37	0.46	3.01	0.020558	0.101063	-3.61
260007_at	unknown protein contains non-consensu	---	AT1G67870	-1.61	-0.69	-3.01	0.020571	0.101104	-3.61
267001_at	putative urease accessory protein ; supp	UREG	AT2G34470	-1.39	-0.48	-3.01	0.020577	0.101114	-3.61
261439_at	Expressed protein ; supported by full-ler	---	AT1G28395	-1.59	-0.67	-3.01	0.020626	0.101310	-3.61
246232_at	hypothetical protein	EMB2754	AT4G36630	-1.26	-0.34	-3.01	0.020624	0.101310	-3.61
246075_at	monogalactosyldiacylglycerol synthase	MGD2	AT5G20410	-2.06	-1.05	-3.01	0.020638	0.101347	-3.61
258171_at	unknown protein	---	AT3G21610	1.27	0.35	3.01	0.020664	0.101431	-3.62
259569_at	hypothetical protein	---	AT1G20480	1.31	0.39	3.01	0.020661	0.101431	-3.62
261614_at	poly(A)-binding protein, putative similar	PAB8	AT1G49760	-1.40	-0.48	-3.01	0.020683	0.101502	-3.62
259670_at	protein kinase, putative similar to GI:75	---	AT1G52310	-1.34	-0.42	-3.01	0.020697	0.101549	-3.62
245389_at	putative protein ;supported by full-length	---	AT4G17480	1.35	0.43	3.01	0.020712	0.101580	-3.62
253597_at	putative protein translation initiation fac	---	AT4G30690	-1.54	-0.63	-3.01	0.020712	0.101580	-3.62
261282_at	hypothetical protein predicted by genscа	APUM10	AT1G35750	-1.37	-0.45	-3.01	0.02073	0.101589	-3.62
248053_at	putative protein similar to unknown prote	AtNMNAT	AT5G55810	-1.30	-0.38	-3.01	0.020732	0.101589	-3.62

267188_at	6,7-dimethyl-8-ribityllumazine synthase	COS1	AT2G44050 /	-1.27	-0.35	-3.01	0.02072	0.101589	-3.62
244971_at	ATP-dependent protease subunit	---	---	-1.27	-0.34	-3.01	0.020731	0.101589	-3.62
257038_at	longevity factor-like protein similar to LA	LOH2	AT3G19260	1.56	0.64	3.01	0.020747	0.101640	-3.62
256996_at	unknown protein similar to unknown pro	---	AT3G25850	1.22	0.28	3.00	0.02077	0.101730	-3.62
263899_at	hypothetical protein predicted by genscа	EMB2219	AT2G21710	-1.34	-0.43	-3.00	0.020787	0.101792	-3.62
267036_at	Expressed protein ; supported by full-ler	---	AT2G38465	-1.55	-0.63	-3.00	0.020797	0.101809	-3.62
261552_at	receptor protein kinase, putative contai	---	AT1G63430	-1.30	-0.38	-3.00	0.020799	0.101809	-3.62
253480_at	putative protein ENOD16, Medicago tru	---	AT4G31840	1.26	0.33	3.00	0.020808	0.101829	-3.62
254798_at	oleoyl-[acyl-carrier-protein] hydrolase-li	---	AT4G13050	-1.52	-0.61	-3.00	0.020826	0.101896	-3.62
255411_at	putative ribonucleoprotein similarity to c	---	AT4G03110	1.32	0.40	3.00	0.020884	0.102127	-3.63
255617_at	putative protein kinase	---	AT4G01330	-1.35	-0.44	-3.00	0.0209	0.102127	-3.63
250021_at	casein kinase-like protein	---	AT5G18190	-1.20	-0.26	-3.00	0.020894	0.102127	-3.63
246956_at	unknown protein ; supported by cDNA:	RTM2	AT5G04890	1.27	0.35	3.00	0.02089	0.102127	-3.63
255420_at	putative frataxin-like protein similar to fra	FH	AT4G03240	-1.23	-0.29	-3.00	0.020881	0.102127	-3.63
247823_at	putative protein predicted proteins from	---	AT5G58450	-1.21	-0.27	-3.00	0.020897	0.102127	-3.63
245443_at	limonene cyclase like protein	---	AT4G16730	8.75	3.13	3.00	0.020906	0.102136	-3.63
248010_at	peroxisomal targeting signal type 1 rece	PEX5	AT5G56290	-1.23	-0.30	-3.00	0.02092	0.102181	-3.63
250027_at	putative protein similar to unknown prote	---	AT5G18250	-1.36	-0.44	-3.00	0.020933	0.102223	-3.63
253332_at	peroxidase ATP17a -like protein peroxi	---	AT4G33420	2.13	1.09	3.00	0.02094	0.102236	-3.63
249064_at	putative protein contains similarity to unl	---	AT5G44250	-1.22	-0.29	-3.00	0.020946	0.102241	-3.63
257125_at	t-complex polypeptide 1 homologue ider	ATTCP-1	AT3G20050	-1.33	-0.41	-3.00	0.02096	0.102265	-3.63
252483_at	scarecrow-like protein scarecrow-like 1	---	AT3G46600	1.78	0.83	3.00	0.020956	0.102265	-3.63
259071_at	unknown protein similar to hin1 GB:CAA	NHL2	AT3G11650	1.50	0.59	3.00	0.020994	0.102412	-3.63
247385_at	putative protein similar to unknown prote	emb2746	AT5G63420	-1.41	-0.50	-3.00	0.021013	0.102460	-3.63
248129_at	putative protein contains similarity to GT	---	AT5G54780	1.31	0.39	3.00	0.021013	0.102460	-3.63
249456_at	unknown protein ;supported by full-leng	---	AT5G39410	-1.29	-0.37	-3.00	0.021032	0.102510	-3.63
247302_at	unknown protein ;supported by full-leng	VPS20.1	AT5G63880	1.26	0.33	3.00	0.021032	0.102510	-3.63
249485_at	receptor protein kinase - like protein rec	---	AT5G39020	1.98	0.99	2.99	0.021083	0.102564	-3.64
251888_at	putative protein GTP-binding regulatory	---	AT3G54190	-1.23	-0.29	-2.99	0.021084	0.102564	-3.64
251741_at	putative protein predicted protein, Arabi	UGP3	AT3G56040	-1.65	-0.72	-2.99	0.021066	0.102564	-3.64
247241_at	unknown protein	---	AT5G64680	-1.56	-0.64	-2.99	0.021071	0.102564	-3.64
263333_at	unknown protein ; supported by cDNA:	---	AT2G03890	-1.39	-0.48	-2.99	0.021077	0.102564	-3.64
257423_at	hypothetical protein predicted by genem	---	AT1G62010	-1.32	-0.40	-2.99	0.021052	0.102564	-3.64
251783_at	ribosomal L23a - like protein various rib	RPL23AB	AT3G55280	-1.67	-0.74	-2.99	0.021069	0.102564	-3.64
247602_at	S-receptor kinase homolog 2 precursor	RLK1	AT5G60900	2.01	1.01	2.99	0.021061	0.102564	-3.64

256232_at	unknown protein ; supported by full-leng	FYD	AT3G12570	1.20	0.26	2.99	0.021061	0.102564	-3.64
262900_at	hypothetical protein contains similarity t	SNL5	AT1G59890	1.32	0.40	2.99	0.021119	0.102700	-3.64
267284_at	unknown protein predicted by genscan	---	AT2G23700	1.36	0.44	2.99	0.021121	0.102700	-3.64
251786_at	phosphatase - like protein DUAL SPEC	MKP1	AT3G55270	1.24	0.31	2.99	0.021137	0.102719	-3.64
267445_at	hypothetical protein predicted by gensc	---	AT2G33680	-1.30	-0.38	-2.99	0.021138	0.102719	-3.64
247785_at	subtilisin-like serine protease contains s	---	AT5G58820	1.21	0.28	2.99	0.021129	0.102719	-3.64
250663_at	putative protein prenylated rab accepto	PRA1.B6	AT5G07110	1.26	0.33	2.99	0.021154	0.102729	-3.64
256757_at	membrane transporter, putative similar	---	AT3G25620	-1.28	-0.36	-2.99	0.021152	0.102729	-3.64
252902_at	putative protein various predicted prote	---	AT4G39560	-1.27	-0.34	-2.99	0.021149	0.102729	-3.64
257759_at	hypothetical protein	---	AT3G23070	-1.44	-0.53	-2.99	0.0212	0.102933	-3.64
245363_at	hypothetical protein ;supported by full-le	---	AT4G15120	2.22	1.15	2.99	0.021214	0.102979	-3.64
260548_at	biotin synthase (Bio B) ;supported by fu	BIO2	AT2G43360	-1.46	-0.55	-2.99	0.021236	0.102997	-3.64
249244_at	FtsH protease, putative similar to FtsH	VAR1	AT5G42270	-1.28	-0.36	-2.99	0.021228	0.102997	-3.64
249365_at	putative protein predicted protein, Arabi	---	AT5G40600	-1.26	-0.34	-2.99	0.021232	0.102997	-3.64
264776_at	unknown protein location of EST gb|T46	---	AT1G22860	-1.27	-0.34	-2.99	0.021226	0.102997	-3.64
245301_at	farnesyl-pyrophosphate synthetase FPS	FPS2	AT4G17190	-1.62	-0.69	-2.99	0.021241	0.103001	-3.64
254646_at	putative protein	---	AT4G18530	-1.37	-0.45	-2.99	0.021286	0.103196	-3.65
259551_at	hypothetical protein	---	AT1G21190	-1.26	-0.33	-2.99	0.021296	0.103220	-3.65
254035_at	putative phosphatidylserine decarboxyla	PSD3	AT4G25970 /	-1.26	-0.34	-2.99	0.021305	0.103222	-3.65
260079_s_a	helix-loop-helix protein 1A, putative sim	---	AT1G35460 /	-1.27	-0.35	-2.99	0.021302	0.103222	-3.65
260570_at	stearoyl-ACP desaturase ; supported by	SSI2	AT2G43710	-1.43	-0.52	-2.99	0.021314	0.103242	-3.65
259050_at	hypothetical protein similar to GB:AAC2	---	AT3G03356 /	1.20	0.26	2.99	0.021322	0.103261	-3.65
245723_at	hypothetical protein predicted by genem	---	AT1G73400	-1.36	-0.44	-2.98	0.021342	0.103271	-3.65
259424_at	hypothetical protein contains similarity t	---	AT1G13830	1.42	0.51	2.98	0.021344	0.103271	-3.65
254321_at	trehalose-6-phosphate phosphatase - li	CPuORF2	AT4G22590 /	1.53	0.61	2.98	0.021351	0.103271	-3.65
253161_at	senescence-associated protein sen1 ide	SEN1	AT4G35770	1.89	0.92	2.99	0.021331	0.103271	-3.65
265161_at	putative vacuolar sorting receptor simila	---	AT1G30900	2.60	1.38	2.98	0.021349	0.103271	-3.65
265658_at	putative aspartate aminotransferase ; su	ALD1	AT2G13810	2.63	1.40	2.98	0.021351	0.103271	-3.65
246925_at	cytochrome P450 71B1 - like protein cy	CYP71B14	AT5G25180	-1.25	-0.32	-2.98	0.021363	0.103304	-3.65
250887_at	putative protein	---	---	-1.29	-0.37	-2.98	0.021374	0.103336	-3.65
248163_at	auxin-responsive-like protein ; supporte	DFL1	AT5G54510	3.11	1.64	2.98	0.021389	0.103388	-3.65
253421_at	putative protein predicted proteins, Arat	---	AT4G32340	-1.37	-0.45	-2.98	0.021399	0.103412	-3.65
257960_at	S-adenosylmethionine decarboxylase, p	---	AT3G25570 /	-1.22	-0.29	-2.98	0.021406	0.103428	-3.65
255062_at	hypothetical protein	---	AT4G08940	-1.33	-0.41	-2.98	0.021421	0.103478	-3.65
248530_at	putative protein strong similarity to unkn	---	AT5G49945	-1.33	-0.41	-2.98	0.021435	0.103514	-3.65

264936_at	hypothetical protein predicted by genem	EDA16	AT1G61140	1.24	0.31	2.98	0.021438	0.103514	-3.65
265853_at	putative RING zinc finger protein	---	AT2G42360	2.21	1.14	2.98	0.021453	0.103520	-3.66
251048_at	putative protein potassium channel regu	---	AT5G02410	1.31	0.39	2.98	0.021447	0.103520	-3.65
250691_at	glycolate oxidase subunit D-like; D-lacta	---	AT5G06580	-1.21	-0.27	-2.98	0.021449	0.103520	-3.65
249019_at	unknown protein	---	AT5G44780	-1.78	-0.83	-2.98	0.021474	0.103555	-3.66
260896_at	flower pigmentation protein ATAN11 sim	---	AT1G29310	1.60	0.68	2.98	0.021474	0.103555	-3.66
263325_at	putative RING zinc finger protein ; supp	XERICO	AT2G04240	-1.62	-0.70	-2.98	0.021478	0.103555	-3.66
247350_at	unknown protein	---	AT5G63830	-1.29	-0.37	-2.98	0.021467	0.103555	-3.66
256568_at	hypothetical protein ;supported by full-le	---	AT3G19520	-1.25	-0.32	-2.98	0.021498	0.103622	-3.66
248890_at	disease resistance protein-like	---	AT5G46270	-1.25	-0.32	-2.98	0.021501	0.103622	-3.66
256751_at	CLC-b chloride channel protein identica	CLC-B	AT3G27170	-1.64	-0.71	-2.98	0.021524	0.103653	-3.66
266595_at	hypothetical protein predicted by gensca	GC4	AT2G46180	-1.30	-0.37	-2.98	0.021516	0.103653	-3.66
265236_s_a	hypothetical protein	---	AT2G07714	1.27	0.34	2.98	0.02152	0.103653	-3.66
266009_at	putative kinesin heavy chain	---	AT2G37420	1.27	0.34	2.98	0.021526	0.103653	-3.66
261413_at	unknown protein ;supported by full-lengt	PLL5	AT1G07630	1.78	0.83	2.98	0.021544	0.103720	-3.66
258752_at	hypothetical protein predicted by gensca	ATEXO70I	AT3G09520	1.64	0.71	2.98	0.021553	0.103742	-3.66
248028_at	putative protein similar to unknown prote	---	AT5G55620	-1.81	-0.86	-2.98	0.021579	0.103821	-3.66
247081_at	AtRAD17 (dbj|BAA90479.1) ; supported	ATRAD17	AT5G66130	-1.32	-0.40	-2.98	0.021577	0.103821	-3.66
262589_s_a	hypothetical protein Strong similarity to g	---	AT1G15150 /	-1.25	-0.33	-2.98	0.021584	0.103821	-3.66
256442_at	hypothetical protein predicted by genefir	---	AT3G10930	3.34	1.74	2.98	0.021595	0.103856	-3.66
254301_at	predicted protein predicted protein, Ara	---	AT4G22790	-1.44	-0.52	-2.98	0.021619	0.103925	-3.66
250725_at	putative protein similar to unknown prote	---	AT5G06400	-1.32	-0.40	-2.98	0.021618	0.103925	-3.66
265798_at	unknown protein ; supported by cDNA: g	---	AT2G35790	-1.44	-0.52	-2.97	0.02164	0.103982	-3.66
245113_at	hypothetical protein predicted by genefir	MIZ1	AT2G41660	1.39	0.48	2.97	0.021639	0.103982	-3.66
261627_at	arsA homolog (hASNA-I), putative simil	---	AT1G01910	1.23	0.30	2.97	0.021645	0.103986	-3.66
254879_at	hypothetical protein	---	AT4G11670	1.28	0.35	2.97	0.02166	0.104035	-3.67
256183_at	MAP kinase kinase 4 (ATMKK4) identica	MKK4	AT1G51660	1.88	0.91	2.97	0.02168	0.104089	-3.67
246146_at	receptor-like protein kinase - like protei	---	AT5G20050	1.38	0.46	2.97	0.02168	0.104089	-3.67
253686_at	putative protein predicted proteins, Ara	---	AT4G29750	-1.32	-0.40	-2.97	0.021687	0.104089	-3.67
260125_at	putative heat shock protein similar to Gr	---	AT1G36390	-1.40	-0.48	-2.97	0.021689	0.104089	-3.67
262538_at	Expressed protein ; supported by full-ler	---	AT1G17140	1.58	0.66	2.97	0.021697	0.104105	-3.67
258054_at	delta tonoplast integral protein (delta-TI	DELTA-TIP	AT3G16240	4.55	2.19	2.97	0.021724	0.104213	-3.67
259700_at	unknown protein	---	AT1G68980	-1.20	-0.26	-2.97	0.021739	0.104240	-3.67
252976_s_a	Phospholipase like protein Arabidopsis	---	AT4G38550	1.53	0.62	2.97	0.021735	0.104240	-3.67
257951_at	putative SGP1 monomeric G-protein sim	SGP2	AT3G21700	1.77	0.82	2.97	0.021781	0.104420	-3.67

256881_at	hypothetical protein ; supported by cDN	---	AT3G26410	-1.26	-0.34	-2.97	0.021786	0.104423	-3.67
250463_at	transcription factor OBF4	TGA4	AT5G10030	-1.32	-0.40	-2.97	0.021811	0.104496	-3.67
253715_at	RIBOSOMAL PROTEIN S30 homolog F	---	AT4G29390	-1.30	-0.38	-2.97	0.021809	0.104496	-3.67
255301_at	putative protein similar to transcriptional	ATMSRB3	AT4G04800	1.55	0.63	2.97	0.021816	0.104501	-3.67
263880_at	unknown protein ;supported by full-leng	---	AT2G21960	-1.40	-0.48	-2.97	0.021862	0.104662	-3.67
256438_s_a	ribosomal protein L41 identical to riboso	---	AT2G40205 /	-1.68	-0.75	-2.97	0.021865	0.104662	-3.67
247610_at	putative protein predicted protein, Arabi	---	AT5G60630	3.72	1.90	2.97	0.021868	0.104662	-3.67
259312_at	putative RING-H2 zinc finger protein AT	ATL6	AT3G05200	1.96	0.97	2.97	0.021865	0.104662	-3.67
253139_at	ankyrin repeat-containing protein 2 ;sup	AKR2	AT4G35450	-1.23	-0.30	-2.97	0.021896	0.104773	-3.68
267304_at	putative Fe(II) transport protein	ZIP6	AT2G30080	-1.36	-0.44	-2.97	0.021906	0.104795	-3.68
253983_at	putative protein SPF1 protein -Ipomoea	WRKY20	AT4G26640	-1.32	-0.40	-2.97	0.021912	0.104795	-3.68
248176_at	putative protein contains similarity to unl	Fh5	AT5G54650	1.61	0.69	2.97	0.021916	0.104795	-3.68
263754_at	putative DnaJ protein ;supported by full	---	AT2G21510	1.79	0.84	2.97	0.021919	0.104795	-3.68
254480_at	translation elongation factor EF-Tu prec	ATRABE1	AT4G20360	-1.30	-0.38	-2.97	0.02193	0.104825	-3.68
264885_s_a	NBS/LRR disease resistance protein, p	---	AT1G61180 /	-1.32	-0.40	-2.96	0.021938	0.104843	-3.68
265576_at	unknown protein	CLASP	AT2G20190	-1.23	-0.30	-2.96	0.021952	0.104888	-3.68
256060_at	hypothetical protein contains similarity to	---	AT1G07050	-1.45	-0.54	-2.96	0.021957	0.104889	-3.68
263735_s_a	hypothetical protein predicted by genem	AGL50	AT1G59810 /	1.22	0.29	2.96	0.021969	0.104924	-3.68
246420_at	putative protein various predicted protei	---	AT5G16870	-1.33	-0.41	-2.96	0.021986	0.104984	-3.68
259218_at	hypothetical protein similar to putative p	---	AT3G03580	-1.30	-0.37	-2.96	0.021992	0.104991	-3.68
259753_at	putative isoprenylated protein similar to	---	AT1G71050	1.43	0.52	2.96	0.022	0.104997	-3.68
AFFX-DapX	B. subtilis /GEN=dapB /DB_XREF=gb:L	---	---	-1.64	-0.71	-2.96	0.022003	0.104997	-3.68
265634_at	hypothetical protein predicted by gensca	---	AT2G25530	1.27	0.35	2.96	0.022013	0.105024	-3.68
254157_at	putative protein protein induced upon w	VEP1	AT4G24220	1.28	0.35	2.96	0.022043	0.105143	-3.68
247210_at	annexin ;supported by full-length cDNA	ANNAT2	AT5G65020	-1.63	-0.71	-2.96	0.022071	0.105147	-3.68
258601_at	putative histidyl tRNA synthetase similar	---	AT3G02760	-1.31	-0.39	-2.96	0.022063	0.105147	-3.68
251456_at	beta-glucosidase-like protein several be	BGLU27	AT3G60120	7.56	2.92	2.96	0.022067	0.105147	-3.68
264834_at	unknown protein similar to ESTs gb|AA6	---	AT1G03730	1.62	0.69	2.96	0.022053	0.105147	-3.68
245917_at	putative protein HCNP, Homo sapiens,	---	AT5G28740	-1.28	-0.36	-2.96	0.022051	0.105147	-3.68
245243_at	hypothetical protein predicted by genem	---	AT1G44414	-1.23	-0.30	-2.96	0.02207	0.105147	-3.68
252908_at	putative protein	---	AT4G39670	3.68	1.88	2.96	0.022087	0.105200	-3.69
250303_at	putative protein similar to unknown prote	---	AT5G12100	-1.55	-0.63	-2.96	0.022116	0.105315	-3.69
259520_at	hypothetical protein	---	AT1G12320	1.50	0.59	2.96	0.022145	0.105415	-3.69
247815_at	ribosomal protein S4 - like ribosomal pr	---	AT5G58420	-1.43	-0.51	-2.96	0.022146	0.105415	-3.69
257041_at	unknown protein	---	AT3G28550	1.38	0.46	2.96	0.022173	0.105524	-3.69

266985_at	putative geranylgeranyl transferase type	PGGT-I	AT2G39550	1.32	0.40	2.96	0.022192	0.105592	-3.69
263800_at	hypothetical protein predicted by gensca	---	AT2G24600	4.18	2.06	2.96	0.022203	0.105622	-3.69
250170_at	putative protein ribulose-1,5-bisphospha	---	AT5G14260	-1.30	-0.38	-2.96	0.022224	0.105694	-3.69
261715_at	hypothetical protein similar to hypothetic	---	AT1G18485	-1.27	-0.35	-2.96	0.022228	0.105694	-3.69
251218_at	CP12 protein precursor-like protein CP	CP12-2	AT3G62410	-1.36	-0.45	-2.95	0.022252	0.105789	-3.69
252961_at	putative protein KIAA0169 gene, Homo	---	AT4G38760	-1.31	-0.39	-2.95	0.022293	0.105962	-3.69
259889_at	predicted protein ; supported by cDNA:	---	AT1G76405	-1.40	-0.49	-2.95	0.022306	0.105999	-3.70
254155_at	putative protein kinase putative protein	---	AT4G24480	-1.31	-0.39	-2.95	0.022318	0.106011	-3.70
257748_at	hypothetical protein predicted by genem	PUB29	AT3G18710	4.57	2.19	2.95	0.022315	0.106011	-3.70
252139_at	putative protein hypothetical protein L1	---	AT3G51050	-1.25	-0.32	-2.95	0.022323	0.106016	-3.70
257267_at	unknown protein similar to TCP3 GB:AA	TCP4	AT3G15030	-1.30	-0.37	-2.95	0.02234	0.106073	-3.70
262281_at	peptide transporter, putative similar to P	---	AT1G68570	-1.86	-0.90	-2.95	0.022361	0.106153	-3.70
247280_at	phi-1-like protein ;supported by full-leng	EXL2	AT5G64260	1.66	0.73	2.95	0.022373	0.106158	-3.70
262687_at	PPR-repeat protein contains multiple PF	---	AT1G62670	-1.22	-0.28	-2.95	0.022381	0.106158	-3.70
261458_at	unknown protein contains DNA-J domai	---	AT1G21080	1.33	0.41	2.95	0.022377	0.106158	-3.70
260207_at	putative phosphoglucomutase similar to	---	AT1G70730	-1.39	-0.47	-2.95	0.022369	0.106158	-3.70
256667_at	hypothetical protein predicted by genem	---	AT3G32180	1.20	0.26	2.95	0.022415	0.106296	-3.70
255485_at	predicted protein of unknown function s	---	AT4G02550	1.25	0.33	2.95	0.022442	0.106403	-3.70
262396_at	unknown protein ;supported by full-lengt	---	AT1G49470	-1.65	-0.73	-2.95	0.022456	0.106447	-3.70
267011_at	unknown protein	---	AT2G39230	-1.37	-0.46	-2.95	0.022474	0.106487	-3.70
262598_at	unknown protein EST gb|N65467 comes	---	AT1G15260	1.43	0.51	2.95	0.022474	0.106487	-3.70
249473_at	His-Asp Phosphotransfer Signal Transd	AHP3	AT5G39340	-1.29	-0.37	-2.95	0.022481	0.106498	-3.70
247364_at	putative protein similar to unknown prote	---	AT5G63200	-1.23	-0.30	-2.95	0.022485	0.106498	-3.70
245390_at	putative protein ;supported by full-length	---	AT4G17650	1.60	0.67	2.95	0.022512	0.106602	-3.71
265295_at	putative DNA replication licensing factor	MCM9	AT2G14050	-1.33	-0.41	-2.95	0.022523	0.106631	-3.71
261252_at	RAS-related protein ARA-1 identical to S	RABA5E	AT1G05810	1.35	0.43	2.95	0.022539	0.106664	-3.71
251444_at	putative protein ETHIONINE AMINOPE	MAP2B	AT3G59990	-1.23	-0.30	-2.95	0.022538	0.106664	-3.71
263887_at	hypothetical protein predicted by gensca	---	AT2G36980	-1.35	-0.44	-2.95	0.022548	0.106684	-3.71
262855_at	putative inorganic phosphate transporte	---	AT1G20860	1.38	0.47	2.94	0.02256	0.106717	-3.71
245926_at	VPS13 - like protein VPS13, Saccharor	---	AT5G24740	-1.27	-0.35	-2.94	0.022574	0.106719	-3.71
254058_at	putative protein cylicin II - human, PID:g	---	AT4G25210	-1.31	-0.39	-2.94	0.02257	0.106719	-3.71
247441_at	receptor - like protein kinase - like prote	---	AT5G62710	-1.30	-0.38	-2.94	0.022567	0.106719	-3.71
250846_at	sulphite reductase ; supported by cDNA	SIR	AT5G04590	-1.57	-0.65	-2.94	0.022581	0.106727	-3.71
262385_at	root hair defective, putative similar to ro	---	AT1G72960	1.21	0.27	2.94	0.022615	0.106821	-3.71
265907_at	unknown protein ;supported by full-leng	---	AT2G25650	-1.31	-0.39	-2.94	0.022611	0.106821	-3.71

247990_at	unknown protein ;supported by full-leng	---	AT5G56360	-1.23	-0.30	-2.94	0.022608	0.106821	-3.71
258899_at	Expressed protein ; supported by full-ler	---	AT3G05675	-1.34	-0.42	-2.94	0.022636	0.106898	-3.71
250784_at	unknown protein ; supported by cDNA: g	---	AT5G05480	-1.33	-0.41	-2.94	0.022652	0.106945	-3.71
252154_at	putative DNA-3-methyladenine glycosid	---	AT3G50880	-1.39	-0.47	-2.94	0.022655	0.106945	-3.71
251074_at	putative protein hypothetical protein T1	---	AT5G01800	1.31	0.39	2.94	0.022676	0.107020	-3.71
264870_at	hypothetical protein ;supported by full-le	---	AT1G24210	-1.30	-0.37	-2.94	0.022686	0.107035	-3.71
250161_at	putative protein amino acid transport pr	---	AT5G15240	1.52	0.60	2.94	0.022688	0.107035	-3.71
248965_at	nodulin-like protein	---	AT5G45370	1.35	0.43	2.94	0.022693	0.107036	-3.71
266478_at	putative cysteinyl-tRNA synthetase ; sup	SYCO ARA	AT2G31170	-1.46	-0.54	-2.94	0.022702	0.107056	-3.71
249903_at	disease resistance protein-like	---	AT5G22690	2.09	1.06	2.94	0.02273	0.107166	-3.72
246727_at	major latex protein homolog - like major	---	AT5G28010	-1.37	-0.45	-2.94	0.022736	0.107171	-3.72
251879_at	putative protein hin1 protein, Nicotiana	---	AT3G54200	1.60	0.68	2.94	0.022766	0.107271	-3.72
262777_at	hypothetical protein predicted by gensca	---	AT1G13030	-1.45	-0.54	-2.94	0.022762	0.107271	-3.72
259367_at	hypothetical protein predicted by genem	---	AT1G69070	-1.45	-0.54	-2.94	0.022783	0.107304	-3.72
260757_at	phytocyanin, putative similar to phytocy	---	AT1G48940	1.23	0.29	2.94	0.022781	0.107304	-3.72
264587_at	putative ligand-gated ion channel protei	ATGLR3.4	AT1G05200	-2.20	-1.14	-2.94	0.022803	0.107376	-3.72
265226_at	unknown protein ; supported by cDNA:	---	AT2G28430	-1.22	-0.28	-2.94	0.022828	0.107471	-3.72
245594_at	acylaminoacyl-peptidase like protein	---	AT4G14570	-1.42	-0.51	-2.94	0.022834	0.107481	-3.72
247520_at	cytochrome c oxidase subunit - like cyt	---	AT5G61310	-1.53	-0.62	-2.94	0.022865	0.107501	-3.72
248639_at	anthranilate N-benzoyltransferase ;supp	HCT	AT5G48930	1.46	0.55	2.94	0.022844	0.107501	-3.72
251690_at	putative protein TATA-binding protein-b	---	AT3G56510	-1.26	-0.34	-2.94	0.022848	0.107501	-3.72
261056_at	hypothetical protein similar to hypothetic	---	AT1G01360	-1.40	-0.49	-2.94	0.022867	0.107501	-3.72
261307_at	unknown protein similar to Glu-tRNAGln	GATB	AT1G48520	-1.25	-0.32	-2.94	0.022867	0.107501	-3.72
259737_at	acyl-CoA synthetase, putative similar to	---	AT1G64400	2.10	1.07	2.94	0.022861	0.107501	-3.72
261814_at	unknown protein	---	AT1G08310	3.03	1.60	2.93	0.022881	0.107546	-3.72
262566_at	auxin response factor 1, putative simila	ARF12	AT1G34310	1.42	0.50	2.93	0.022907	0.107621	-3.72
248234_at	putative protein contains similarity to en	---	AT5G53850	-1.23	-0.29	-2.93	0.022902	0.107621	-3.72
255931_at	hypothetical protein similar to putative p	AtPP2-A12	AT1G12710	-1.49	-0.58	-2.93	0.022922	0.107651	-3.72
250837_at	8-amino-7-oxononanoate synthase - lik	ATBIOF	AT5G04620	-1.35	-0.44	-2.93	0.022919	0.107651	-3.72
252993_at	monooxygenase 2 (MO2)	---	AT4G38540	1.62	0.70	2.93	0.022928	0.107653	-3.72
261724_at	Expressed protein ; supported by full-ler	---	AT1G76185	-1.25	-0.33	-2.93	0.022944	0.107707	-3.72
245290_at	hypothetical protein ; supported by cDN	---	AT4G16490	-1.40	-0.48	-2.93	0.022957	0.107722	-3.73
248715_at	ATFP4, putative	---	AT5G48290	1.40	0.49	2.93	0.022953	0.107722	-3.73
259365_at	unknown protein ; supported by cDNA: g	---	AT1G13300	2.56	1.35	2.93	0.022964	0.107736	-3.73
261281_at	hypothetical protein predicted by genem	---	AT1G35740	-1.22	-0.29	-2.93	0.022984	0.107808	-3.73

250516_at	putative protein predicted proteins, Arat	---	AT5G09620	1.26	0.33	2.93	0.022992	0.107822	-3.73
262778_at	hypothetical protein predicted by genefir	---	AT1G13050	-1.21	-0.28	-2.93	0.023053	0.108085	-3.73
251056_at	putative protein KIAA1303 protein - Hor	RAPTOR2	AT5G01770	1.34	0.43	2.93	0.023076	0.108173	-3.73
255269_at	putative protein various predicted prote	---	AT4G05240	1.26	0.34	2.93	0.023085	0.108191	-3.73
264193_at	CRK1 protein, putative similar to CRK1	---	AT1G54610	-1.21	-0.27	-2.93	0.023109	0.108282	-3.73
247607_at	putative protein various predicted prote	---	AT5G60960	-1.55	-0.63	-2.93	0.023119	0.108287	-3.73
253065_at	putative protein predicted proteins, Arat	AtGRF2	AT4G37740	-1.38	-0.46	-2.93	0.023119	0.108287	-3.73
260830_at	histone H1, putative similar to histone H	---	AT1G06760	-1.51	-0.59	-2.93	0.023133	0.108329	-3.73
250122_at	unknown protein	---	AT5G16520	-1.28	-0.36	-2.93	0.023146	0.108368	-3.73
259650_at	leucoanthocyanidin dioxygenase 2, puta	---	AT1G55290	1.26	0.34	2.93	0.023152	0.108371	-3.73
260656_at	hypothetical protein predicted by genem	---	AT1G19380	2.44	1.28	2.93	0.023168	0.108424	-3.73
263730_at	beta-glucosidase, putative similar to be	BGLU4	AT1G60090	-1.23	-0.30	-2.93	0.023173	0.108425	-3.74
252037_at	putative calmodulin calmodulin - Tetrah	CAM9	AT3G51920	1.46	0.54	2.93	0.02318	0.108436	-3.74
248322_at	putative protein similar to unknown prote	---	AT5G52760	6.12	2.61	2.92	0.023199	0.108502	-3.74
266791_at	unknown protein	---	AT2G02960	1.25	0.32	2.92	0.023207	0.108518	-3.74
260293_at	unknown protein predicted by genscan-	---	AT1G63670	-1.32	-0.41	-2.92	0.023241	0.108643	-3.74
246406_at	disease resistance protein RPP1-WsA,	---	AT1G57650	1.19	0.25	2.92	0.023243	0.108643	-3.74
263082_at	putative nucleotide-binding protein	---	AT2G27200	1.21	0.27	2.92	0.023254	0.108672	-3.74
266535_s_a	50S ribosomal protein L27 ;supported b	---	AT2G16930 /	-1.36	-0.44	-2.92	0.023264	0.108694	-3.74
256700_at	pseudouridine synthase, putative simila	---	AT3G52260	-1.24	-0.31	-2.92	0.023272	0.108709	-3.74
249084_at	unknown protein	---	AT5G44150	-1.28	-0.36	-2.92	0.023283	0.108742	-3.74
248962_at	putative protein contains similarity to FK	FKBP13	AT5G45680	-1.48	-0.56	-2.92	0.023322	0.108834	-3.74
252923_at	kinesin like protein kinesin motor protei	---	AT4G39050	1.38	0.46	2.92	0.023317	0.108834	-3.74
265037_at	putative prohibitin 2 B-cell receptor asso	ATPHB2	AT1G03860	-1.32	-0.40	-2.92	0.023318	0.108834	-3.74
261969_at	hypothetical protein contains similarity to	---	AT1G65950	-1.23	-0.30	-2.92	0.023322	0.108834	-3.74
258531_at	importin alpha identical to GB:AAC2764	IMPA-1	AT3G06720	-1.23	-0.29	-2.92	0.023339	0.108886	-3.74
257786_at	hypothetical protein predicted by genem	---	AT3G26990	-1.37	-0.46	-2.92	0.023345	0.108886	-3.74
258774_at	putative alpha-L-arabinofuranosidase co	ASD1	AT3G10740	2.00	1.00	2.92	0.023348	0.108886	-3.74
260731_at	P-type ATPase, putative similar to GB:A	---	AT1G17500	1.31	0.39	2.92	0.02336	0.108920	-3.74
251980_at	putative protein endopeptidase Clp ATP	---	AT3G53270	-1.21	-0.28	-2.92	0.023372	0.108954	-3.74
249158_at	electron transfer flavoprotein beta-subur	ETFBETA	AT5G43430	1.22	0.29	2.92	0.023381	0.108976	-3.74
251255_at	putative protein early nodule-specific pr	---	AT3G62280	1.22	0.28	2.92	0.023392	0.109002	-3.74
259345_s_a	hypothetical protein predicted by genefir	---	AT3G03700 /	1.69	0.75	2.92	0.023435	0.109181	-3.75
252487_at	glucosyltransferase-like protein UDP-gl	UGT76E12	AT3G46660	2.89	1.53	2.92	0.02345	0.109231	-3.75
254210_at	putative protein zinc finger protein, Arat	---	AT4G23450	1.59	0.67	2.92	0.023487	0.109330	-3.75

247465_at	RNA helicase ; supported by cDNA: gi_	PRH75	AT5G62190	-1.48	-0.57	-2.92	0.023492	0.109330	-3.75
265184_at	unknown protein ;supported by full-leng	---	AT1G23710	2.49	1.31	2.92	0.023497	0.109330	-3.75
255154_at	putative protein several hypothetical pro	---	---	-1.21	-0.27	-2.92	0.023486	0.109330	-3.75
251232_at	shock protein SRC2-like shock protein	---	AT3G62780	2.10	1.07	2.92	0.023478	0.109330	-3.75
248556_at	unknown protein	---	AT5G50350	1.33	0.41	2.92	0.0235	0.109330	-3.75
256363_at	unknown protein ; supported by cDNA: g	---	AT1G66510	-1.56	-0.64	-2.92	0.023513	0.109368	-3.75
261618_at	unknown protein	---	AT1G33110	1.68	0.75	2.91	0.02353	0.109404	-3.75
256583_at	hypothetical protein	---	AT3G28850	1.73	0.79	2.91	0.023531	0.109404	-3.75
258650_at	putative protein kinase similar to protein	---	AT3G09830	1.52	0.60	2.91	0.023539	0.109420	-3.75
258400_at	unknown protein ; supported by cDNA:	---	AT3G15470	-1.34	-0.43	-2.91	0.023558	0.109474	-3.75
259059_at	hypothetical protein	---	AT3G07300	-1.26	-0.33	-2.91	0.02356	0.109474	-3.75
258329_at	putative protein disulfide isomerase simi	ATPDIL1-6	AT3G16110	-1.25	-0.33	-2.91	0.02361	0.109681	-3.75
266274_at	putative protein phosphatase 2C	---	AT2G29380	1.26	0.33	2.91	0.023644	0.109817	-3.76
245101_at	putative cytochrome P450 ; supported b	CYP98A3	AT2G40890	1.41	0.50	2.91	0.023656	0.109853	-3.76
264268_at	hypothetical protein predicted by genem	ULP1D	AT1G60220	-1.23	-0.30	-2.91	0.023662	0.109856	-3.76
262350_at	putative glutathione peroxidase ;suppor	ATGPX4	AT2G48150	1.24	0.32	2.91	0.02369	0.109964	-3.76
267374_at	putative uricase subunit similar to nodu	---	AT2G26230	1.22	0.28	2.91	0.023704	0.110009	-3.76
251301_at	cytochrome p450 (CYP78A9) ;supporte	CYP78A9	AT3G61880	-1.30	-0.38	-2.91	0.023733	0.110112	-3.76
253654_at	putative protein several hypothetical pro	---	AT4G30060	1.66	0.73	2.91	0.023736	0.110112	-3.76
260420_at	unknown protein	---	AT1G69610	1.26	0.34	2.91	0.023788	0.110285	-3.76
248668_at	putative protein similar to unknown prote	XRI1	AT5G48720	-1.48	-0.57	-2.91	0.023788	0.110285	-3.76
255389_at	putative reverse transcriptase	---	---	-1.20	-0.26	-2.91	0.023783	0.110285	-3.76
250449_at	embryonic abundant protein -like embry	---	AT5G10830	1.66	0.73	2.91	0.023796	0.110300	-3.76
261698_at	unknown protein identical to hypothetica	---	AT1G32630	-1.33	-0.41	-2.91	0.023801	0.110301	-3.76
267268_at	hypothetical protein predicted by gensca	---	AT2G02570	-1.27	-0.34	-2.91	0.023809	0.110314	-3.76
252859_at	putative protein AP2 domain containing	---	AT4G39780	1.48	0.56	2.91	0.023826	0.110374	-3.76
256483_at	hypothetical protein	---	AT1G31410	-1.33	-0.42	-2.90	0.023851	0.110430	-3.76
267338_at	26S proteasome regulatory subunit ; su	EIF2	AT2G39990	-1.31	-0.39	-2.90	0.02385	0.110430	-3.76
255509_at	hypothetical protein identical to T10M13	---	AT4G02210	-1.44	-0.53	-2.90	0.023853	0.110430	-3.77
262876_at	unknown protein ;supported by full-lengt	ATDSS1(I	AT1G64750	1.34	0.43	2.90	0.023876	0.110467	-3.77
253113_at	putative protein physical impedance inc	---	AT4G35985	-1.50	-0.58	-2.90	0.023875	0.110467	-3.77
260709_at	hypothetical protein predicted by genem	ATNAP6	AT1G32500	-1.30	-0.37	-2.90	0.02387	0.110467	-3.77
267027_at	hypothetical protein	---	AT2G38330	-1.37	-0.45	-2.90	0.023891	0.110514	-3.77
263650_at	hypothetical protein predicted by gensca	---	AT1G04360	1.26	0.33	2.90	0.023934	0.110649	-3.77
267451_at	putative AP2 domain transcription factor	---	AT2G33710	3.42	1.77	2.90	0.023928	0.110649	-3.77

267257_at	putative casein kinase II catalytic (alpha	---	AT2G23080	-1.19	-0.25	-2.90	0.023933	0.110649	-3.77
257149_at	prohibitin, putative similar to prohibitin (	ATPHB4	AT3G27280	-1.62	-0.70	-2.90	0.023952	0.110709	-3.77
247027_at	subtilisin-like serine protease contains s	---	AT5G67090	1.21	0.28	2.90	0.023963	0.110715	-3.77
250009_at	putative protein nuclear FMRP interacti	---	AT5G18440	-1.64	-0.71	-2.90	0.023959	0.110715	-3.77
249875_at	photosystem II stability/assembly factor	HCF136	AT5G23120	-1.46	-0.54	-2.90	0.023969	0.110717	-3.77
257950_at	putative UDP-glucose glucosyltransfera	UGT71B6	AT3G21780	2.14	1.10	2.90	0.023979	0.110727	-3.77
266771_s_a	unknown protein	---	AT2G03010 /	-1.24	-0.31	-2.90	0.023985	0.110727	-3.77
266241_s_a	hypothetical protein predicted by gensca	---	AT2G27800 /	-1.29	-0.37	-2.90	0.023981	0.110727	-3.77
251544_at	putative protein general stress protein g	GAUT15	AT3G58790	-1.41	-0.50	-2.90	0.024043	0.110924	-3.77
254241_at	serine/threonine kinase - like protein se	CRK11	AT4G23190	2.25	1.17	2.90	0.02405	0.110924	-3.77
251860_at	Gluthatione reductase, chloroplast prec	GR	AT3G54660	-1.20	-0.27	-2.90	0.024042	0.110924	-3.77
245505_at	glutaredoxin	---	AT4G15690	1.87	0.90	2.90	0.024039	0.110924	-3.77
250809_at	putative protein contains similarity to unl	---	AT5G05140	1.66	0.73	2.90	0.024052	0.110924	-3.77
254715_at	putative protein hypothetical protein, Sy	---	AT4G13550	-1.42	-0.50	-2.90	0.02406	0.110938	-3.77
252133_at	hypothetical protein hypothetical protein	---	AT3G50900	2.12	1.08	2.90	0.024066	0.110942	-3.77
245968_at	proline-rich protein extensins	---	AT5G19800 /	1.32	0.40	2.90	0.024101	0.110967	-3.78
259694_at	uridine diphosphate glucose epimerase	UGE3	AT1G63180	1.95	0.96	2.90	0.02408	0.110967	-3.77
253739_at	putative protein predicted protein. Arabi	---	AT4G28760	-1.34	-0.42	-2.90	0.0241	0.110967	-3.78
257967_at	hypothetical protein predicted by genem	---	AT3G19910	1.24	0.31	2.90	0.024092	0.110967	-3.78
257665_at	unknown protein	---	AT3G20430	-1.24	-0.31	-2.90	0.024096	0.110967	-3.78
258182_at	1-D-deoxyxylulose 5-phosphate syntha	DXPS1	AT3G21500	1.99	0.99	2.90	0.024098	0.110967	-3.78
257807_at	glyceraldehyde 3-phosphate dehydroge	GAPA	AT3G26650	-1.23	-0.30	-2.90	0.024147	0.111159	-3.78
260042_at	hypothetical protein C-term similar to C-	---	AT1G68820	1.47	0.56	2.89	0.024184	0.111309	-3.78
253097_at	cytochrome P450-like protein	CYP81D5	AT4G37320	1.88	0.91	2.89	0.024218	0.111442	-3.78
251507_at	putative protein CND41, chloroplast nu	---	AT3G59080	2.78	1.48	2.89	0.024229	0.111455	-3.78
244970_at	ribosomal protein L20	---	---	-1.52	-0.61	-2.89	0.024231	0.111455	-3.78
267467_at	putative C3HC4 zinc finger protein ; sup	DRIP2	AT2G30580	1.27	0.35	2.89	0.024239	0.111470	-3.78
266867_at	putative signal recognition particle recep	CPFTSY	AT2G45770	-1.27	-0.34	-2.89	0.024251	0.111501	-3.78
257222_at	DegP protease almost identical to DegF	DEGP1	AT3G27925	-1.34	-0.42	-2.89	0.024268	0.111557	-3.78
245165_at	unknown protein predicted by genscan	---	AT2G33180	-1.68	-0.75	-2.89	0.024283	0.111605	-3.78
266563_at	nodulin-like protein	---	AT2G23990	1.25	0.32	2.89	0.024301	0.111610	-3.78
250066_at	unknown protein	---	AT5G17930	-1.46	-0.55	-2.89	0.024309	0.111610	-3.78
247524_at	thioredoxin-like 3 ; supported by cDNA:	ACHT5	AT5G61440	2.05	1.04	2.89	0.024303	0.111610	-3.78
266633_at	putative DnaJ protein	---	AT2G35540	-1.30	-0.38	-2.89	0.024306	0.111610	-3.78
264340_at	unknown protein similar to hypothetical p	---	AT1G70280	-1.31	-0.39	-2.89	0.02429	0.111610	-3.78

252326_at	putative protein ferripyochelin binding p	GAMMA C	AT3G48680	-1.28	-0.35	-2.89	0.024319	0.111635	-3.79
245166_at	putative receptor-like protein kinase	---	AT2G33170	1.29	0.36	2.89	0.024344	0.111728	-3.79
263172_at	hypothetical protein predicted by genem	CID3	AT1G54170	1.19	0.26	2.89	0.024361	0.111783	-3.79
246447_at	putative protein SART-1 protein - Homo	DOT2	AT5G16780	-1.29	-0.37	-2.89	0.024392	0.111863	-3.79
267579_at	metallothionein-like protein	---	AT2G42000	-1.21	-0.27	-2.89	0.024396	0.111863	-3.79
266054_at	hypothetical protein predicted by genefir	---	AT2G40640	-1.34	-0.42	-2.89	0.024398	0.111863	-3.79
265632_at	hypothetical protein predicted by gensca	---	AT2G14290	3.67	1.88	2.89	0.024388	0.111863	-3.79
265342_at	hypothetical protein predicted by gensca	---	AT2G18300	-1.55	-0.63	-2.89	0.02442	0.111879	-3.79
252887_at	putative protein various predicted prote	---	AT4G39240	-1.20	-0.26	-2.89	0.024414	0.111879	-3.79
251371_at	putative protein CGI-94 protein, Homo s	EDA14	AT3G60360	-1.49	-0.58	-2.89	0.024409	0.111879	-3.79
254870_at	KI domain interacting kinase 1 -like prot	---	AT4G11900	1.58	0.66	2.89	0.024421	0.111879	-3.79
263170_at	putative peroxisome assembly factor-2 I	PEX6	AT1G03000	-1.20	-0.26	-2.89	0.024451	0.111995	-3.79
261652_at	dimethyladenosine transferase, putative	PFC1	AT1G01860	-1.29	-0.37	-2.89	0.024483	0.112119	-3.79
249914_at	protease-like protein	---	AT5G22850	1.35	0.43	2.89	0.024497	0.112159	-3.79
266938_at	hypothetical protein predicted by genefir	HPT1	AT2G18950	1.33	0.41	2.89	0.024505	0.112173	-3.79
262844_at	unknown protein similar to pectinesteras	---	AT1G14890	1.88	0.91	2.89	0.024521	0.112222	-3.79
245508_at	hypothetical protein	---	AT4G15720	-1.20	-0.27	-2.88	0.024546	0.112314	-3.79
261216_at	catechol O-methyltransferase, putative	---	AT1G33030	2.11	1.08	2.88	0.024555	0.112333	-3.80
266288_s_a	putative pumilio/Mpt5 family RNA-bindin	APUM1	AT2G29140 /	-1.31	-0.39	-2.88	0.024576	0.112410	-3.80
252422_at	putative protein PIT1 - Arabidopsis thali	---	AT3G47550	1.41	0.50	2.88	0.024585	0.112425	-3.80
253876_at	COP1-interacting protein 7 (CIP7) ; sup	CIP7	AT4G27430	-1.44	-0.53	-2.88	0.024606	0.112457	-3.80
266484_at	putative putative sister-chromatide cohe	SCC3	AT2G47980	-1.27	-0.35	-2.88	0.024626	0.112457	-3.80
246653_at	putative protein clathrin assembly prote	---	AT5G35200	1.26	0.34	2.88	0.02461	0.112457	-3.80
266050_at	putative SNF2/SWI2 family transcription	---	AT2G40770	-1.22	-0.29	-2.88	0.024606	0.112457	-3.80
252832_at	ubiquitin-specific protease 3 (UBP3) ide	ATUBP3	AT4G39910	1.20	0.26	2.88	0.024615	0.112457	-3.80
248001_at	calcineurin B-like protein 2 (gb|AAC260	CBL2	AT5G55990	-1.35	-0.43	-2.88	0.024623	0.112457	-3.80
249867_at	2-isopropylmalate synthase-like protein	IMS2	AT5G23020	-3.11	-1.64	-2.88	0.024624	0.112457	-3.80
253947_at	putative protein hypothetical protein, Ar	MAP65-2	AT4G26760	-1.30	-0.38	-2.88	0.024665	0.112611	-3.80
266229_at	putative RING zinc finger ankyrin protei	---	AT2G28840	-1.23	-0.30	-2.88	0.024706	0.112689	-3.80
246521_at	N2,N2-dimethylguanine tRNA methyltra	---	AT5G15810	-1.35	-0.43	-2.88	0.024699	0.112689	-3.80
249769_at	sigma-like factor (emb CAA77213.1)	SIGE	AT5G24120	-1.39	-0.48	-2.88	0.024707	0.112689	-3.80
248158_at	unknown protein	---	AT5G54440	-1.20	-0.27	-2.88	0.024705	0.112689	-3.80
263954_at	unknown protein ; supported by cDNA:	---	AT2G35840	-1.33	-0.42	-2.88	0.024695	0.112689	-3.80
245038_at	similar to latex allergen from Hevea bras	PLA2A	AT2G26560	2.16	1.11	2.88	0.024717	0.112692	-3.80
251421_at	enoyl-CoA-hydratase - like protein enoy	---	AT3G60510	1.26	0.33	2.88	0.024716	0.112692	-3.80

258514_at	unknown protein ; supported by full-leng	---	AT3G06610	-1.23	-0.29	-2.88	0.024724	0.112700	-3.80
258463_at	putative protein kinase similar to Pto kin	---	AT3G17410	1.32	0.40	2.88	0.024752	0.112804	-3.80
258780_at	putative ubiquitin carboxyl-terminal hydr	UBP13	AT3G11910	-1.20	-0.26	-2.88	0.024772	0.112853	-3.80
245943_at	putative protein permease family protei	---	AT5G19500	-1.35	-0.44	-2.88	0.024772	0.112853	-3.80
250836_at	putative protein various predicted prote	DME	AT5G04560	1.21	0.27	2.88	0.024803	0.112962	-3.81
248790_at	membrane channel protein-like; aquapo	TIP2;3	AT5G47450	1.41	0.49	2.88	0.024806	0.112962	-3.81
261887_at	CCR4-associated factor, putative\0CCF	---	AT1G80780	-1.21	-0.27	-2.88	0.02483	0.113047	-3.81
247438_at	unknown protein ; supported by cDNA:	---	AT5G62460	1.50	0.59	2.88	0.024844	0.113091	-3.81
251143_at	putative protein SqdX protein, Synecho	SQD2	AT5G01220	-1.57	-0.65	-2.87	0.024872	0.113196	-3.81
249385_at	thioredoxin ; supported by full-length cD	ATTRX2	AT5G39950	1.33	0.41	2.87	0.024887	0.113218	-3.81
263626_at	transcription factor ZAP1 identical to GP	ZAP1	AT2G04880	-1.21	-0.28	-2.87	0.024887	0.113218	-3.81
261569_at	DNA-binding protein, putative similar to	LHY	AT1G01060	1.30	0.38	2.87	0.024901	0.113256	-3.81
254353_s_a	putative protein probable membrane pr	---	AT4G22285 /	-1.38	-0.46	-2.87	0.024908	0.113270	-3.81
259860_at	putative protein kinase similar to leucine	---	AT1G80640	-1.39	-0.47	-2.87	0.024917	0.113285	-3.81
247768_at	I-box binding factor - like protein I-box b	---	AT5G58900	-2.01	-1.00	-2.87	0.024944	0.113369	-3.81
254103_at	putative protein ;supported by full-lengt	---	AT4G25030	1.80	0.85	2.87	0.024945	0.113369	-3.81
265909_at	unknown protein ;supported by full-leng	---	AT2G25720	-1.28	-0.36	-2.87	0.024954	0.113387	-3.81
247335_at	RNA helicase	---	AT5G63630	-1.26	-0.34	-2.87	0.025014	0.113613	-3.81
252557_at	putative protein cim1 induced allergen,	ATEXLA3	AT3G45960	1.24	0.31	2.87	0.025024	0.113613	-3.81
258557_at	hypothetical protein similar to receptor	---	AT3G05990	1.24	0.32	2.87	0.025017	0.113613	-3.81
253429_at	putative protein CDC28/cdc2-like kinas	---	AT4G32420	-1.25	-0.32	-2.87	0.025024	0.113613	-3.81
251154_at	tRNA isopentenyl transferase -like prote	ATIPT3	AT3G63110	-1.83	-0.87	-2.87	0.02505	0.113709	-3.82
267446_s_a	putative tyrosyl-tRNA synthetase	---	AT1G28350 /	-1.23	-0.29	-2.87	0.025068	0.113733	-3.82
245704_at	glycine-rich protein	KTF1	AT5G04290	-1.21	-0.28	-2.87	0.025085	0.113733	-3.82
248997_at	beta-amylase-like	BMY2	AT5G45300	-1.40	-0.48	-2.87	0.025084	0.113733	-3.82
253080_at	hypothatical protein	---	---	-1.24	-0.31	-2.87	0.025079	0.113733	-3.82
265229_s_a	hypothetical protein	---	AT2G07701	-1.23	-0.30	-2.87	0.025072	0.113733	-3.82
259320_at	putative DNA-binding protein similar to N	WRKY58	AT3G01080	1.96	0.97	2.87	0.025074	0.113733	-3.82
250960_at	putative protein	---	AT5G02940	-1.54	-0.62	-2.87	0.025093	0.113734	-3.82
265499_at	putative glucosyltransferase	UGT73B5	AT2G15480	2.38	1.25	2.87	0.0251	0.113734	-3.82
254150_at	putative protein storage protein - Popul	---	AT4G24350	-3.30	-1.72	-2.87	0.025096	0.113734	-3.82
256069_at	hypothetical protein predicted by gensca	AFP2	AT1G13740	1.53	0.62	2.87	0.025123	0.113816	-3.82
259965_at	transcriptional regulator, putative found	MSRB1	AT1G53670	-1.33	-0.41	-2.87	0.025139	0.113843	-3.82
250185_at	putative protein esterase HDE, Petroleu	AtCXE16	AT5G14310	1.31	0.39	2.87	0.025139	0.113843	-3.82
259404_at	type 2A protein serine/threonine phosph	ATB BETA	AT1G17720	1.19	0.25	2.87	0.025159	0.113888	-3.82

265219_at	unknown protein ; supported by full-leng	---	AT2G02050	1.32	0.41	2.87	0.025159	0.113888	-3.82
AFFX-ThrX-	B. subtilis /GEN=thrC /DB_XREF=gb:X0	---	---	-1.57	-0.65	-2.87	0.025167	0.113902	-3.82
247191_at	homeobox-leucine zipper protein ATHB-	ATHB5	AT5G65310	-1.49	-0.57	-2.87	0.025194	0.113998	-3.82
265869_at	putative two-component response regul	ARR14	AT2G01760	-1.35	-0.43	-2.87	0.025213	0.114064	-3.82
263922_s_a	putative pyruvate kinase ;supported by	---	AT2G36580 /	1.22	0.29	2.86	0.025224	0.114089	-3.82
257031_at	fucosyltransferase, putative similar to F	FUT11	AT3G19280	-1.27	-0.34	-2.86	0.025241	0.114144	-3.82
248985_at	GTP-binding protein-like; root hair defec	---	AT5G45160	-1.22	-0.29	-2.86	0.025255	0.114188	-3.82
263911_at	hypothetical protein predicted by genefir	---	AT2G36560	-1.22	-0.29	-2.86	0.025293	0.114302	-3.83
253751_at	hypothetical protein ;supported by full-le	---	AT4G29070	-1.56	-0.64	-2.86	0.025287	0.114302	-3.83
252982_at	Histone deacetylase ; supported by cDI	HD1	AT4G38130	-1.26	-0.33	-2.86	0.025296	0.114302	-3.83
257795_at	hypothetical protein predicted by gensca	---	AT3G15910	1.34	0.42	2.86	0.025305	0.114322	-3.83
260867_at	hypothetical protein predicted by genem	TED6	AT1G43790	2.14	1.10	2.86	0.025323	0.114378	-3.83
252086_at	hypothetical protein	---	AT3G52030	-1.26	-0.34	-2.86	0.025331	0.114393	-3.83
249436_at	putative protein crp1 protein - Zea mays	---	AT5G39980	-1.43	-0.52	-2.86	0.025353	0.114470	-3.83
249258_at	putative protein similar to unknown prote	---	AT5G41650	-1.21	-0.28	-2.86	0.025378	0.114559	-3.83
255630_at	putative phosphoribosylanthranilate tran	---	AT4G00700	6.33	2.66	2.86	0.025388	0.114584	-3.83
245338_at	Expressed protein ; supported by full-ler	---	AT4G16442	-1.36	-0.45	-2.86	0.025396	0.114596	-3.83
251116_at	serin carboxypeptidase - like protein ca	scpl40	AT3G63470	1.32	0.40	2.86	0.025405	0.114612	-3.83
245000_at	hypothetical protein	---	---	-1.25	-0.33	-2.86	0.02542	0.114660	-3.83
254662_at	putative protein phospho-N-acetylmura	TRANS11	AT4G18270	-1.43	-0.51	-2.86	0.025433	0.114693	-3.83
247912_at	putative protein contains similarity to AA	---	AT5G57480	1.63	0.70	2.86	0.02544	0.114704	-3.83
257652_at	unknown protein contains Pfam profile:F	APUM24	AT3G16810	-1.55	-0.63	-2.86	0.025446	0.114707	-3.83
245476_at	hypothetical protein	---	AT4G16090	1.27	0.34	2.86	0.025451	0.114707	-3.83
AFFX-ThrX-	B. subtilis /GEN=thrC, thrB /DB_XREF=	---	---	-1.67	-0.74	-2.86	0.025466	0.114754	-3.83
264761_at	hypothetical protein predicted by genem	---	AT1G61280	-1.23	-0.30	-2.86	0.025474	0.114765	-3.83
262441_at	hypothetical protein similar to hypothetic	OSB1	AT1G47720	-1.30	-0.38	-2.86	0.025525	0.114952	-3.84
247655_at	zinc finger protein Zat12 ;supported by	RHL41	AT5G59820	2.47	1.30	2.86	0.025523	0.114952	-3.84
259385_at	hypothetical protein predicted by gensca	---	AT1G13470	5.10	2.35	2.86	0.025534	0.114964	-3.84
249889_at	putative protein strong similarity to unkn	---	AT5G22540	2.04	1.03	2.86	0.025538	0.114964	-3.84
262561_at	late embryogenesis abundant protein (E	---	AT1G34340	-1.26	-0.33	-2.86	0.025565	0.115063	-3.84
261808_at	DNA damage repair protein, putative si	DRT111	AT1G30480	-1.23	-0.30	-2.85	0.025584	0.115124	-3.84
265088_at	hypothetical protein similar to DNA Helic	SWI2	AT1G03750	-1.20	-0.26	-2.85	0.025649	0.115348	-3.84
265153_at	unusual floral organ (UFO), AtFBX1 aln	UFO	AT1G30950	-1.28	-0.36	-2.85	0.025647	0.115348	-3.84
264752_at	unknown protein similar to Bacillus spo	LPR1	AT1G23010	1.21	0.27	2.85	0.025643	0.115348	-3.84
258939_at	unknown protein predicted by genefinde	---	AT3G10020	1.59	0.67	2.85	0.025661	0.115379	-3.84

266185_at	unknown protein	---	AT2G38950	-1.23	-0.30	-2.85	0.025679	0.115440	-3.84
254575_at	putative protein various predicted prote	---	AT4G19460	1.78	0.83	2.85	0.02569	0.115465	-3.84
245582_at	hypothetical protein	LOI1	AT4G14850	-1.38	-0.46	-2.85	0.025742	0.115654	-3.84
262308_at	unknown protein	---	AT1G71010	1.30	0.38	2.85	0.025742	0.115654	-3.84
253336_at	putative protein Caenorhabditis elegans	EIF3K	AT4G33250	-1.28	-0.35	-2.85	0.025754	0.115685	-3.84
253996_at	nucleosome assembly protein I-like prot	NAP1;1	AT4G26110	-1.29	-0.37	-2.85	0.025771	0.115692	-3.85
259363_at	methionine aminopeptidase I (MAP1), p	MAP1C	AT1G13270	-1.27	-0.35	-2.85	0.025768	0.115692	-3.84
253997_at	disease resistance protein RPS2 ; supp	RPS2	AT4G26090	2.03	1.02	2.85	0.025767	0.115692	-3.84
260784_at	MYB-related protein identical to GB:CA	ATMYB13	AT1G06180	1.60	0.68	2.85	0.025814	0.115795	-3.85
266614_at	unknown protein	---	AT2G14910	-1.28	-0.36	-2.85	0.025809	0.115795	-3.85
264862_at	hypothetical protein predicted by gensca	---	AT1G24330	-1.41	-0.50	-2.85	0.025809	0.115795	-3.85
246209_at	BEL1-like homeobox 2 protein (BLH2) ;	BLH2	AT4G36870	-1.46	-0.55	-2.85	0.02581	0.115795	-3.85
252948_at	putative protein NLS receptor - Oryza s	KAK	AT4G38600	1.28	0.35	2.85	0.025827	0.115831	-3.85
264675_at	putative phosphoribosylglycinamide syr	---	AT1G09830	-1.24	-0.31	-2.85	0.025852	0.115910	-3.85
247428_at	unknown protein	---	AT5G62600	-1.21	-0.27	-2.85	0.025855	0.115910	-3.85
254487_at	calcium-binding protein - like calcium-bi	---	AT4G20780	2.38	1.25	2.85	0.025865	0.115933	-3.85
260250_at	putative phosphoribosylformylglycinamic	PUR4	AT1G74260	-1.32	-0.40	-2.85	0.025874	0.115952	-3.85
263443_at	putative fatty acid elongase ;supported	KCS12	AT2G28630	2.43	1.28	2.85	0.025903	0.116057	-3.85
248132_at	SGP1 monomeric G-protein (emb|CAB5	SGP1	AT5G54840	1.42	0.50	2.84	0.025944	0.116081	-3.85
247926_at	protein carboxyl methylase-like	---	AT5G57280	-1.62	-0.70	-2.84	0.025937	0.116081	-3.85
246536_at	putative protein KIAA0594 - Homo sapi	---	AT5G15920	-1.74	-0.80	-2.84	0.025936	0.116081	-3.85
258637_at	putative RHO GDP-dissociation inhibitor	---	AT3G07880	-1.32	-0.40	-2.84	0.025941	0.116081	-3.85
258645_s_a	exopolygalacturonase identical to exop	---	AT3G07850 /	1.26	0.33	2.85	0.02592	0.116081	-3.85
264970_at	glyoxalase I, putative similar to glyoxala	---	AT1G67280	-1.23	-0.30	-2.84	0.025949	0.116081	-3.85
245623_s_a	hypothetical protein	---	AT4G14096 /	-1.24	-0.30	-2.84	0.025936	0.116081	-3.85
262907_at	hypothetical protein predicted by genem	CRR28	AT1G59720	-1.27	-0.34	-2.84	0.025937	0.116081	-3.85
249929_at	unknown protein	---	AT5G22340	-1.32	-0.40	-2.84	0.025961	0.116096	-3.85
246053_at	putative protein farnesyl cysteine carbo	---	AT5G08340	-1.34	-0.43	-2.84	0.025963	0.116096	-3.85
252358_at	putative protein cfxY protein, Alcaligene	---	AT3G48425	-1.23	-0.30	-2.84	0.026011	0.116254	-3.85
246962_s_a	transcription factor-like protein light-indu	BZIP9	AT5G24800	1.51	0.59	2.84	0.026005	0.116254	-3.85
261176_at	hypothetical protein predicted by genem	---	AT1G04780	1.22	0.29	2.84	0.026013	0.116254	-3.85
259226_at	unknown protein similar to hypothetical	---	AT3G07700	1.34	0.42	2.84	0.026049	0.116393	-3.86
248177_at	putative protein strong similarity to unkn	---	AT5G54630	-1.23	-0.30	-2.84	0.026056	0.116401	-3.86
248585_at	unknown protein	---	AT5G49640	-1.25	-0.33	-2.84	0.026088	0.116522	-3.86
262899_at	ABC transporter, putative similar to ABC	PEN3	AT1G59870	1.28	0.35	2.84	0.026136	0.116712	-3.86

247495_at	putative protein predicted protein, Arabi	IPK2BETA	AT5G61760	-1.31	-0.39	-2.84	0.026185	0.116887	-3.86
250105_at	putative protein contains similarity to DN	RAD4	AT5G16630	-1.53	-0.61	-2.84	0.026185	0.116887	-3.86
261254_at	Expressed protein ; supported by full-ler	---	AT1G05805	-1.27	-0.35	-2.84	0.026205	0.116950	-3.86
261682_at	unknown protein similar to hypothetical p	---	AT1G47330	-1.31	-0.38	-2.84	0.02623	0.117039	-3.86
262607_at	unknown protein ;supported by full-lengt	---	AT1G13990	1.33	0.41	2.84	0.026243	0.117074	-3.86
267355_at	putative LIM-domain protein	---	AT2G39900	-1.37	-0.45	-2.84	0.026254	0.117100	-3.86
246561_at	putative protein hypothetical protein F14	---	AT5G15570	-1.26	-0.33	-2.84	0.026292	0.117246	-3.87
248533_at	putative protein contains similarity to unl	---	AT5G50020	-1.38	-0.46	-2.83	0.026305	0.117285	-3.87
247540_at	ethylene responsive element binding fa	---	AT5G61590	-1.69	-0.76	-2.83	0.026323	0.117315	-3.87
248044_at	putative protein similar to unknown prote	---	AT5G56020	-1.25	-0.32	-2.83	0.02632	0.117315	-3.87
249841_at	unknown protein	---	AT5G23520	1.25	0.33	2.83	0.026351	0.117419	-3.87
257536_at	unknown protein	---	AT3G02800	3.07	1.62	2.83	0.026379	0.117452	-3.87
256650_at	hypothetical protein contains similarity to	---	AT3G13620	-1.29	-0.36	-2.83	0.026378	0.117452	-3.87
247938_at	putative protein similar to unknown prote	---	AT5G57140 /	-1.23	-0.30	-2.83	0.026376	0.117452	-3.87
257139_at	disease resistance protein, putative sim	AtRLP43	AT3G28890	1.40	0.49	2.83	0.026364	0.117452	-3.87
251445_at	putative protein hypothetical protein F6	---	AT3G59870	-1.21	-0.27	-2.83	0.02639	0.117468	-3.87
252806_at	putative protein	---	AT3G42390	1.25	0.32	2.83	0.026393	0.117468	-3.87
258876_at	putative ADP-ribosylation factor similar t	ATARFB1(	AT3G03120	-1.21	-0.28	-2.83	0.026412	0.117532	-3.87
252712_at	glutathione transferase-like protein glut	ATGSTU2	AT3G43800	-1.50	-0.58	-2.83	0.026423	0.117556	-3.87
259922_at	protein phosphatase 2C (AtP2C-HA) id	HAB1	AT1G72770	1.42	0.50	2.83	0.026431	0.117569	-3.87
251066_at	putative protein RING-H2 finger protein	---	AT5G01880	-1.45	-0.54	-2.83	0.026453	0.117643	-3.87
248950_at	ATP-dependent Clp protease proteolytic	CLPP4	AT5G45390	-1.30	-0.38	-2.83	0.02647	0.117694	-3.87
255651_at	putative protein	---	AT4G00940	-1.26	-0.34	-2.83	0.026486	0.117714	-3.87
266158_at	putative ABC transporter	---	AT2G28070	-1.37	-0.46	-2.83	0.026489	0.117714	-3.87
254700_at	hypothetical protein	---	AT4G18000	1.28	0.35	2.83	0.026485	0.117714	-3.87
258764_at	putative pectinesterase contains similari	---	AT3G10720	1.65	0.72	2.83	0.026498	0.117727	-3.87
262046_at	hypothetical protein predicted by genem	OFP14	AT1G79960	1.33	0.41	2.83	0.026512	0.117746	-3.87
258350_at	unknown protein similar to serine/threon	CIPK1	AT3G17510	1.62	0.70	2.83	0.026509	0.117746	-3.87
258050_at	unknown protein	---	AT3G16200	-1.31	-0.39	-2.83	0.026525	0.117779	-3.87
259057_at	unknown protein ; supported by cDNA:	---	AT3G03310	1.35	0.43	2.83	0.026537	0.117788	-3.88
263719_at	hypothetical protein predicted by gensca	---	AT2G13600	-1.22	-0.28	-2.83	0.026535	0.117788	-3.88
259763_at	unknown protein similar to GB:AAB8167	---	AT1G77630	-1.42	-0.50	-2.83	0.026545	0.117800	-3.88
245147_at	putative RAD51C-like DNA repair protei	ATRAD51(	AT2G45280	-1.55	-0.63	-2.83	0.026605	0.117884	-3.88
252318_at	glutamate-1-semialdehyde aminotransfe	GSA2	AT3G48730	-1.43	-0.52	-2.83	0.026591	0.117884	-3.88
250854_at	aspartyl aminopeptidase -like protein as	---	AT5G04710	-1.32	-0.40	-2.83	0.026603	0.117884	-3.88

247238_at	histone acetyltransferase	HAM1	AT5G64610	-1.21	-0.27	-2.83	0.0266	0.117884	-3.88
263426_at	putative glutathione peroxidase ;suppor	ATGPX2	AT2G31570	1.41	0.50	2.83	0.026579	0.117884	-3.88
249519_at	putative protein similar to unknown prote	APE1	AT5G38660	-1.34	-0.42	-2.83	0.026594	0.117884	-3.88
258954_at	unknown protein contains Pfam profile:	---	AT3G01400	-1.19	-0.25	-2.83	0.026604	0.117884	-3.88
256837_at	hypothetical protein similar to DNA-direc	NRPD7	AT3G22900	-1.48	-0.57	-2.83	0.026578	0.117884	-3.88
262701_at	hypothetical protein predicted by gensca	---	AT1G16480	-1.30	-0.38	-2.83	0.026621	0.117908	-3.88
260096_at	hypothetical protein predicted by genefi	---	AT1G73240	-1.31	-0.39	-2.83	0.026617	0.117908	-3.88
254073_at	splicing factor At-SRp40 contains EST	RSP35	AT4G25500	-1.27	-0.35	-2.83	0.026649	0.117984	-3.88
254218_at	putative receptor kinase receptor-like p	---	AT4G23740	-1.27	-0.34	-2.83	0.026654	0.117984	-3.88
253628_at	xyloglucan endo-1,4-beta-D-glucanase-	XTH18	AT4G30280	4.97	2.31	2.83	0.026659	0.117984	-3.88
259083_at	putative kinase similar to NIMA-related k	ATNEK2	AT3G04810	-1.24	-0.31	-2.83	0.026659	0.117984	-3.88
253271_s_a	SKP1/ASK1 (At11), putative similar to S	ASK12	AT4G34210 /	1.32	0.40	2.83	0.026669	0.118006	-3.88
253893_at	putative protein hypothetical protein, Sy	---	AT4G27390	-1.37	-0.45	-2.82	0.026683	0.118045	-3.88
263344_at	unknown protein ;supported by full-leng	---	AT2G04940	-1.34	-0.42	-2.82	0.026697	0.118085	-3.88
249144_at	squamosa promoter binding protein-like	SPL2	AT5G43270	-1.27	-0.34	-2.82	0.026715	0.118128	-3.88
262221_at	hypothetical protein predicted by genem	ARC3	AT1G75010	-1.34	-0.43	-2.82	0.026717	0.118128	-3.88
249778_at	Expressed protein ; supported by full-ler	---	AT5G24165	-1.23	-0.30	-2.82	0.026758	0.118287	-3.88
252036_at	putative protein ;supported by full-lengt	---	AT3G52070	-1.34	-0.42	-2.82	0.02684	0.118626	-3.89
247529_at	monosaccharide transporter STP3	---	AT5G61520	-1.25	-0.33	-2.82	0.026874	0.118753	-3.89
253203_at	arginine decarboxylase SPE2 ; support	ADC2	AT4G34710	1.89	0.92	2.82	0.026915	0.118910	-3.89
261942_at	unknown protein similar to putative DNA	AGL87	AT1G22590	-1.55	-0.63	-2.82	0.02697	0.119132	-3.89
258528_at	unknown protein contains Pfam profile:F	---	AT3G06770	-1.71	-0.78	-2.82	0.027028	0.119293	-3.89
247175_at	G protein-coupled receptor-like protein	GCL1	AT5G65280	-1.86	-0.90	-2.82	0.027024	0.119293	-3.89
256446_at	RING zinc finger protein contains Pfam	---	AT3G11110	-1.49	-0.57	-2.82	0.027032	0.119293	-3.89
258728_at	unknown protein ; supported by cDNA:	---	AT3G11800	1.22	0.29	2.82	0.027013	0.119293	-3.89
256121_at	MAP kinase, putative similar to MAP3K	---	AT1G18160	-1.26	-0.33	-2.82	0.027036	0.119293	-3.89
259805_at	disease resistance protein, putative sim	AtRLP7	AT1G47890	1.38	0.46	2.82	0.027038	0.119293	-3.89
254526_at	putative protein cyclin C homolog 1, Sc	CYCT1;4	AT4G19600	-1.23	-0.30	-2.81	0.027065	0.119388	-3.90
264329_at	unknown protein Contains similarity to r	---	AT1G04140	-1.22	-0.29	-2.81	0.027101	0.119523	-3.90
265620_at	unknown protein	---	AT2G27310	2.03	1.02	2.81	0.027131	0.119609	-3.90
255341_at	putative receptor-like protein kinase	---	AT4G04500	3.83	1.94	2.81	0.027127	0.119609	-3.90
249784_at	putative protein similar to unknown prote	---	AT5G24280	-1.38	-0.47	-2.81	0.027139	0.119623	-3.90
262374_s_a	flax rust resistance protein, putative sim	TIR	AT1G72910 /	2.24	1.17	2.81	0.027157	0.119679	-3.90
256799_at	unknown protein ; supported by cDNA:	---	AT3G18560	1.73	0.79	2.81	0.027174	0.119704	-3.90
260670_at	Expressed protein ; supported by full-ler	NFD5	AT1G19520	-1.42	-0.51	-2.81	0.02717	0.119704	-3.90

260329_at	putative cyclin similar to cyclin GB:S530	CYCA2;4	AT1G80370	1.29	0.37	2.81	0.027203	0.119812	-3.90
256772_at	galactosidase, putative similar to BETA	BGAL1	AT3G13750	2.16	1.11	2.81	0.027223	0.119865	-3.90
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=gb:M	---	---	-1.63	-0.71	-2.81	0.027226	0.119865	-3.90
246522_at	bZIP DNA-binding protein-like putative	AtbZIP3	AT5G15830	-1.80	-0.85	-2.81	0.027243	0.119902	-3.90
260027_at	unknown protein	CPuORF3	AT1G29950 /	-1.36	-0.45	-2.81	0.027245	0.119902	-3.90
245632_at	unknown protein contains similarity to m	ATRBL10	AT1G25290	-1.26	-0.33	-2.81	0.027252	0.119910	-3.90
266653_at	hypothetical protein predicted by gensca	---	AT2G25740	-1.28	-0.35	-2.81	0.02728	0.119988	-3.90
260379_at	putative glucosyltransferase similar to gl	UGT89B1	AT1G73880 /	1.36	0.44	2.81	0.027291	0.119988	-3.90
265864_at	putative myosin heavy chain-like protein	ATMAP70	AT2G01750	-1.37	-0.46	-2.81	0.027296	0.119988	-3.90
260384_at	putative 2-isopropylmalate synthase sim	IMS1	AT1G74040	-1.25	-0.32	-2.81	0.027296	0.119988	-3.90
256769_at	protein kinase, putative similar to protei	---	AT3G13690	-1.51	-0.60	-2.81	0.027292	0.119988	-3.90
247776_at	phosphoinositide-specific phospholipas	PLC4	AT5G58700	1.33	0.41	2.81	0.027306	0.120011	-3.90
249809_at	unknown protein	---	AT5G23910	1.21	0.27	2.81	0.027323	0.120062	-3.91
259747_at	putative dehydrogenase similar to D-thre	---	AT1G71170	1.29	0.37	2.81	0.027333	0.120084	-3.91
246415_at	putative protein (fragment) predicted pr	---	AT5G17160	1.42	0.51	2.81	0.02735	0.120134	-3.91
263101_s_a	hypothetical protein predicted by gensca	---	AT2G05230 /	-1.24	-0.31	-2.81	0.02736	0.120154	-3.91
263179_at	unknown protein similar to unknown pro	---	AT1G05710	1.53	0.61	2.81	0.027381	0.120223	-3.91
249874_at	putative protein contains similarity to thy	---	AT5G23070	-1.49	-0.58	-2.81	0.027424	0.120391	-3.91
260585_at	unknown protein	EMB2777	AT2G43650	-1.60	-0.68	-2.80	0.027432	0.120402	-3.91
247932_at	putative protein similar to unknown prote	---	AT5G56920	1.20	0.27	2.80	0.027459	0.120433	-3.91
265967_at	nodulin-like protein ; supported by cDN/	---	AT2G37450	-1.37	-0.45	-2.80	0.027461	0.120433	-3.91
263247_at	unknown protein	---	AT2G31440	-1.21	-0.27	-2.80	0.027458	0.120433	-3.91
253663_at	putative villin	VLN4	AT4G30160	1.27	0.34	2.80	0.027451	0.120433	-3.91
249577_at	calmodulin-binding heat-shock protein -	---	AT5G37710	1.42	0.50	2.80	0.02748	0.120474	-3.91
254746_at	putative protein hypothetical protein - A	---	AT4G12980	-1.54	-0.63	-2.80	0.027478	0.120474	-3.91
246011_at	putative protein auxin-induced basic he	---	AT5G08330	-1.59	-0.67	-2.80	0.027509	0.120569	-3.91
265195_at	hypothetical protein	---	AT2G36730	-1.21	-0.28	-2.80	0.027518	0.120569	-3.91
265855_at	unknown protein ;supported by full-leng	---	AT2G42390	-1.22	-0.29	-2.80	0.027514	0.120569	-3.91
253808_at	predicted proline-rich protein hydroxypr	---	AT4G28300	1.33	0.41	2.80	0.027526	0.120580	-3.91
258466_at	hypothetical protein contains similarity t	---	AT3G06040	-1.30	-0.38	-2.80	0.02757	0.120729	-3.91
249055_at	calmodulin-like protein	---	AT5G44460	1.20	0.26	2.80	0.02757	0.120729	-3.91
258992_at	unknown protein similar to unknown pro	---	AT3G08930	1.19	0.25	2.80	0.027585	0.120748	-3.92
259219_at	hypothetical protein predicted by gensca	---	AT3G03560	1.41	0.50	2.80	0.027581	0.120748	-3.92
262084_at	hypothetical protein predicted by genem	---	AT1G56080	1.29	0.36	2.80	0.027593	0.120760	-3.92
250197_at	isocitrate dehydrogenase - like protein i	---	AT5G14590	-1.22	-0.28	-2.80	0.027606	0.120791	-3.92

261346_at	putative aspartyl protease contains Pfar	---	AT1G79720	-1.27	-0.34	-2.80	0.027644	0.120913	-3.92
248461_s_a	fumarate hydratase ; supported by cDN	FUM1	AT2G47510 /	-1.30	-0.37	-2.80	0.027644	0.120913	-3.92
247518_at	putative protein many predicted protein	---	AT5G61800	-1.28	-0.36	-2.80	0.027652	0.120925	-3.92
251537_at	putative protein several hypothetical pro	---	AT3G58470	-1.50	-0.58	-2.80	0.02769	0.121068	-3.92
250398_at	putative protein predicted proteins, Aral	---	AT5G11000	1.56	0.64	2.80	0.027725	0.121195	-3.92
260486_at	F-box protein ZEITLUPE/FKF/LKP/ADA	---	AT1G51550	-1.26	-0.33	-2.80	0.027761	0.121331	-3.92
255176_s_a	putative DNA-directed RNA polymerase	---	AT1G01210 /	-1.24	-0.31	-2.80	0.027768	0.121336	-3.92
254977_s_a	subtilisin-like serine protease contains s	---	AT4G10520 /	1.19	0.25	2.80	0.027774	0.121336	-3.92
267103_at	putative UDP-N-acetylglucosamine--dol	GPT	AT2G41490	1.25	0.32	2.80	0.027778	0.121336	-3.92
265682_at	similar to avrRpt2-induced protein 2	---	AT2G24390	-1.36	-0.44	-2.80	0.027787	0.121352	-3.92
267340_at	unknown protein	ACD11	AT2G34690	-1.23	-0.29	-2.80	0.027802	0.121395	-3.92
265387_at	unknown protein ;supported by full-leng	---	AT2G20670	1.83	0.87	2.79	0.027859	0.121595	-3.93
264224_at	hypothetical protein predicted by genem	emb1688	AT1G67440	-1.28	-0.35	-2.79	0.027857	0.121595	-3.93
255291_at	putative calcium dependent protein kina	CPK27	AT4G04700	1.28	0.36	2.79	0.027911	0.121799	-3.93
256909_at	hypothetical protein predicted by genem	---	AT3G24060	1.30	0.38	2.79	0.02794	0.121905	-3.93
259079_at	unknown protein	---	AT3G04950	-1.35	-0.44	-2.79	0.027982	0.122041	-3.93
257745_at	unknown protein ;supported by full-leng	---	AT3G29240	1.89	0.92	2.79	0.027978	0.122041	-3.93
261675_at	hypothetical protein predicted by genem	---	AT1G18290	1.25	0.32	2.79	0.028003	0.122106	-3.93
248531_at	putative protein contains similarity to alp	---	AT5G49950	1.26	0.33	2.79	0.028027	0.122190	-3.93
254970_at	chlorophyll a/b-binding protein - like chl	LHCB5	AT4G10340	-1.24	-0.31	-2.79	0.028042	0.122232	-3.93
264466_at	Expressed protein ; supported by full-ler	---	AT1G10380	-1.61	-0.68	-2.79	0.028048	0.122234	-3.93
267504_at	unknown protein ;supported by full-leng	---	AT2G45530	-1.31	-0.39	-2.79	0.028063	0.122275	-3.93
264924_at	RNA polymerase subunit identical to RN	ATRPAC4	AT1G60620	-1.22	-0.29	-2.79	0.028094	0.122377	-3.93
251798_at	putative RNA binding protein Serine/arg	SCL30	AT3G55460	-1.24	-0.31	-2.79	0.028097	0.122377	-3.93
255859_at	putative protein embryonic abundant pr	---	AT5G34930	1.42	0.51	2.79	0.028111	0.122416	-3.93
262766_at	hypothetical protein predicted by gensca	---	AT1G13160	-1.49	-0.57	-2.79	0.028156	0.122515	-3.94
245694_at	EF - hand Calcium binding protein - like	---	AT5G04170	1.23	0.29	2.79	0.028144	0.122515	-3.94
262502_at	unknown protein similar to hypothetical	PTAC6	AT1G21600	-1.25	-0.32	-2.79	0.028158	0.122515	-3.94
255881_at	phosphomannose isomerase, putative s	DIN9	AT1G67070	1.99	0.99	2.79	0.02816	0.122515	-3.94
259126_at	putative NADPH-ferrihemoprotein reduc	---	AT3G02280	-1.21	-0.28	-2.79	0.028161	0.122515	-3.94
260323_at	putative U3 small nucleolar ribonucleopr	IMP4	AT1G63780	-1.55	-0.63	-2.78	0.028213	0.122708	-3.94
250290_at	putative protein ;supported by full-lengt	---	AT5G13310	-1.22	-0.29	-2.78	0.028216	0.122708	-3.94
248357_at	putative protein similar to unknown prote	---	AT5G52380	-1.56	-0.64	-2.78	0.028248	0.122776	-3.94
266742_at	predicted by genefinder and genscan	---	AT2G03050	-1.24	-0.31	-2.78	0.028247	0.122776	-3.94
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.75	-0.80	-2.78	0.028239	0.122776	-3.94

259361_at	glyceraldehyde-3-phosphate dehydroge	GAPC2	AT1G13440	-1.28	-0.35	-2.78	0.02826	0.122805	-3.94
245383_at	SUPERMAN like protein	---	AT4G17810	-1.50	-0.59	-2.78	0.028266	0.122811	-3.94
258662_at	unknown protein	---	AT3G02900	1.61	0.68	2.78	0.028278	0.122838	-3.94
254759_at	short-chain alcohol dehydrogenase like	---	AT4G13180	1.41	0.49	2.78	0.028299	0.122896	-3.94
258416_at	hypothetical protein predicted by genefi	---	AT3G17310	-1.26	-0.33	-2.78	0.028302	0.122896	-3.94
265657_at	unknown protein ; supported by cDNA:	---	AT2G13840	-1.27	-0.35	-2.78	0.028328	0.122972	-3.94
255797_at	putative steroid dehydrogenase ; suppo	---	AT2G33630	1.40	0.48	2.78	0.02833	0.122972	-3.94
254549_at	putative protein various predicted protei	---	AT4G19880	1.37	0.46	2.78	0.028346	0.122982	-3.94
265818_at	putative peptidyl-prolyl cis-trans isomera	PIN1AT	AT2G18040	-1.23	-0.30	-2.78	0.028349	0.122982	-3.94
254552_at	putative protein several hypothetical pro	---	AT4G19900	-1.24	-0.31	-2.78	0.028345	0.122982	-3.94
258860_at	putative potassium transporter similar to	KUP3	AT3G02050	-1.46	-0.55	-2.78	0.028367	0.123015	-3.94
259429_at	cytochrome P450, putative similar to cy	CYP86A4	AT1G01600	2.36	1.24	2.78	0.028365	0.123015	-3.94
267179_at	putative ADP ribosylation factor 1 GTPa	AGD7	AT2G37550	1.38	0.47	2.78	0.028444	0.123325	-3.95
261301_at	hypothetical protein predicted by genem	---	AT1G48570	-1.69	-0.76	-2.78	0.028463	0.123383	-3.95
248282_at	unknown protein ;supported by full-leng	---	AT5G52900	-2.12	-1.09	-2.78	0.028473	0.123403	-3.95
265887_at	biotin holocarboxylase synthetase identi	HCS1	AT2G25710	-1.31	-0.39	-2.78	0.028481	0.123415	-3.95
255656_at	putative protein (fragment) DNA-binding	---	AT4G00990	-1.28	-0.36	-2.78	0.0285	0.123461	-3.95
263428_at	ubiquitin-specific protease 4 (UBP4) ide	ATUBP4	AT2G22310	-1.27	-0.35	-2.78	0.028503	0.123461	-3.95
250762_at	putative protein similar to unknown prote	---	AT5G05990	-1.63	-0.70	-2.78	0.028513	0.123483	-3.95
256589_at	cytochrome P450, putative contains Pfa	CYP81D1	AT3G28740	3.10	1.63	2.78	0.02854	0.123495	-3.95
254208_at	Expressed protein ; supported by full-ler	---	AT4G24175	-1.28	-0.36	-2.78	0.028529	0.123495	-3.95
265432_at	hypothetical protein predicted by grail	---	AT2G20650	1.29	0.37	2.78	0.028529	0.123495	-3.95
250452_at	putative protein KIAA1038 protein, Hom	---	AT5G10630	-1.28	-0.35	-2.78	0.028543	0.123495	-3.95
265918_at	putative fatty acid elongase	KCS8	AT2G15090	-2.37	-1.25	-2.78	0.028537	0.123495	-3.95
260663_at	hypothetical protein predicted by gensca	NFD5	AT1G19520	-1.44	-0.53	-2.78	0.028557	0.123507	-3.95
257422_at	hypothetical protein Contains similarity t	---	AT1G11940	1.22	0.29	2.78	0.028554	0.123507	-3.95
249568_at	glucosyltransferase-like protein UDP-gl	---	AT5G38040	-1.30	-0.37	-2.78	0.028598	0.123662	-3.95
264037_at	putative steroid sulfotransferase ;suppo	---	AT2G03750	-1.31	-0.39	-2.77	0.028626	0.123702	-3.95
260430_at	putative zinc finger protein similar to CC	---	AT1G68200	1.21	0.27	2.77	0.028624	0.123702	-3.95
247283_at	2-nitropropane dioxygenase-like protein	---	AT5G64250	1.27	0.35	2.77	0.028629	0.123702	-3.95
255236_at	score=11.7, E=0.66,N=1	ATEHD2	AT4G05520	-1.45	-0.53	-2.78	0.028613	0.123702	-3.95
251770_at	leucoanthocyanidin dioxygenase -like p	---	AT3G55970	2.87	1.52	2.77	0.028686	0.123927	-3.96
250330_at	putative protein	---	AT5G11810	-1.28	-0.35	-2.77	0.028694	0.123938	-3.96
255723_at	hypothetical protein	AFP3	AT3G29575	1.72	0.78	2.77	0.028716	0.124008	-3.96
245861_at	GTL1 - like protein GTL1, Arabidopsis t	---	AT5G28300	-1.60	-0.68	-2.77	0.028732	0.124010	-3.96

256186_at	4-coumarate:CoA ligase 1 identical to 4-	4CL1	AT1G51680	1.75	0.81	2.77	0.028736	0.124010	-3.96
245438_at	growth regulator like protein	---	AT4G16650	-1.24	-0.31	-2.77	0.028734	0.124010	-3.96
247008_at	ADP-ribosylation factor-like protein ;sup	ATARLA1I	AT5G67560	-1.23	-0.30	-2.77	0.028744	0.124010	-3.96
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.49	-0.58	-2.77	0.028743	0.124010	-3.96
267556_at	putative beta-galactosidase ; supported	BGAL9	AT2G32810	-1.29	-0.37	-2.77	0.028749	0.124010	-3.96
245351_at	casein kinase II beta chain CKB2 ;suppo	CKB2	AT4G17640	-1.26	-0.33	-2.77	0.028757	0.124019	-3.96
261133_at	DYW7 protein identical to DYW7 protei	---	AT1G19715	-1.42	-0.50	-2.77	0.028767	0.124034	-3.96
259357_at	unknown protein ;supported by full-lengt	---	AT1G13380	-1.30	-0.38	-2.77	0.028771	0.124034	-3.96
255941_at	mitochondrial inner membrane transloc	ATTIM17-1	AT1G20350	1.43	0.51	2.77	0.028792	0.124102	-3.96
253648_at	pathogenesis related homeodomain pro	PRHA	AT4G29940	-1.21	-0.27	-2.77	0.0288	0.124114	-3.96
261085_at	hypothetical protein similar to hypothetic	IQD7	AT1G17480	1.22	0.29	2.77	0.028809	0.124116	-3.96
253923_at	hypothetical protein Arabidopsis thalian	TOR1	AT4G27060	-1.25	-0.33	-2.77	0.028812	0.124116	-3.96
258505_at	hypothetical protein predicted by gensca	---	AT3G06530	-1.90	-0.92	-2.77	0.028844	0.124187	-3.96
260622_at	hypothetical protein predicted by genem	NF-YC10	AT1G07980	-1.22	-0.29	-2.77	0.028834	0.124187	-3.96
266839_at	unknown protein	ELF3	AT2G25930	-1.22	-0.29	-2.77	0.028844	0.124187	-3.96
260681_at	hypothetical protein predicted by genem	AT1G0803	---	-1.22	-0.29	-2.77	0.028864	0.124245	-3.96
248239_at	ribosomal protein L11 methyltransferase	---	AT5G53920	-1.40	-0.49	-2.77	0.028887	0.124325	-3.96
260706_at	oxidase, putative similar to oxidase GB	AOX1D	AT1G32350	5.36	2.42	2.77	0.0289	0.124330	-3.96
263633_at	putative SCARECROW gene regulator ;	SCL21	AT2G04890	-1.31	-0.39	-2.77	0.028905	0.124330	-3.96
252073_at	hypothetical protein	---	AT3G51750	-2.37	-1.25	-2.77	0.028901	0.124330	-3.96
262748_at	lipase, putative contains Pfam profile: P	---	AT1G28610	-1.49	-0.57	-2.77	0.028919	0.124367	-3.96
267503_at	unknown protein ; supported by full-leng	---	AT2G45600	-1.45	-0.53	-2.77	0.028935	0.124379	-3.96
256328_at	6-phosphogluconate dehydrogenase, p	---	AT3G02360	1.51	0.60	2.77	0.028927	0.124379	-3.96
248015_at	putative protein similar to unknown prote	---	AT5G56370	1.24	0.31	2.77	0.028938	0.124379	-3.96
266056_at	hypothetical protein predicted by gensca	ATATG18(	AT2G40810	-1.21	-0.28	-2.77	0.028946	0.124391	-3.96
258075_at	homocysteine S-methyltransferase AtHI	HMT-1	AT3G25900	2.84	1.51	2.77	0.028978	0.124502	-3.97
266506_at	unknown protein	---	AT2G47850	-1.23	-0.30	-2.77	0.028989	0.124505	-3.97
247980_at	putative protein similar to unknown prote	GNC	AT5G56860	-1.85	-0.89	-2.77	0.028989	0.124505	-3.97
265852_at	putative RING zinc finger protein	---	AT2G42350	1.49	0.58	2.76	0.029021	0.124596	-3.97
256195_at	hypothetical protein predicted by genem	---	---	-1.19	-0.25	-2.76	0.029022	0.124596	-3.97
248169_at	ankyrin-repeat-containing protein-like	ANK	AT5G54610	4.13	2.05	2.76	0.029035	0.124630	-3.97
263239_at	amidophosphoribosyltransferase identic	ATASE1	AT2G16570	1.27	0.35	2.76	0.029044	0.124645	-3.97
255664_at	putative protein	---	AT4G00440	-1.21	-0.27	-2.76	0.029069	0.124732	-3.97
246839_at	putative protein	---	AT5G26720	-1.26	-0.33	-2.76	0.029079	0.124747	-3.97
264390_at	putative DNA-binding protein Contains s	---	AT1G11950	-1.31	-0.39	-2.76	0.029096	0.124754	-3.97

247842_at	SPP30 - like protein SPP30, Solanum c	---	AT5G58030	-1.21	-0.27	-2.76	0.029086	0.124754	-3.97
251542_at	putative protein protein-tyrosine kinase,	---	AT3G58760	-1.32	-0.40	-2.76	0.029097	0.124754	-3.97
261475_at	anionic peroxidase, putative similar to a	---	AT1G14550	1.44	0.53	2.76	0.029112	0.124798	-3.97
260446_at	unknown protein	---	AT1G72420	-1.27	-0.35	-2.76	0.029123	0.124820	-3.97
255249_at	3(2),5-BISPHOSPHATE NUCLEOTIDA	---	AT4G05090	-1.44	-0.52	-2.76	0.029153	0.124925	-3.97
247034_at	cyclin D3-like protein ;supported by full-l	CYCD3;2	AT5G67260	-1.37	-0.45	-2.76	0.029158	0.124925	-3.97
251787_at	2-oxoglutarate dehydrogenase, E1 subu	---	AT3G55410	1.30	0.37	2.76	0.029166	0.124933	-3.97
247865_at	Expressed protein ; supported by full-ler	---	AT5G57815	-1.23	-0.30	-2.76	0.029235	0.125058	-3.98
266074_at	putative small nuclear ribonucleoprotein	---	AT2G18740	-1.44	-0.52	-2.76	0.029202	0.125058	-3.97
258241_at	hypothetical protein similar to hypothetic	LBD25	AT3G27650	1.35	0.44	2.76	0.029239	0.125058	-3.98
247628_at	putative protein	---	AT5G60400	1.36	0.44	2.76	0.029231	0.125058	-3.98
260899_at	hypothetical protein predicted by genem	---	AT1G21370	1.31	0.39	2.76	0.029214	0.125058	-3.97
253666_at	xyloglucan endo-1,4-beta-D-glucanase	MERI5B	AT4G30270	1.22	0.29	2.76	0.02923	0.125058	-3.98
261615_at	unknown protein	---	AT1G33050	1.27	0.35	2.76	0.029215	0.125058	-3.97
267302_at	putative unknown protein, leucine-rich r	---	AT2G30100	-1.20	-0.26	-2.76	0.029229	0.125058	-3.97
246514_at	DNA-directed RNA polymerase (mitocho	---	AT5G15700	-1.42	-0.50	-2.76	0.029253	0.125097	-3.98
245288_at	transcriptional adaptor like protein ; supp	ADA2B	AT4G16420	-1.24	-0.31	-2.76	0.029261	0.125106	-3.98
267055_at	unknown protein	PRA1.B4	AT2G38360	1.80	0.85	2.76	0.029304	0.125268	-3.98
245660_at	unknown protein	---	AT1G28240	1.44	0.53	2.76	0.029311	0.125272	-3.98
254588_at	putative protein hypothetical proteins - A	---	AT4G18840	-1.23	-0.30	-2.76	0.029329	0.125325	-3.98
251283_at	seven in absentia-like protein SINAH1 p	---	AT3G61790	-1.23	-0.30	-2.76	0.029348	0.125383	-3.98
252924_at	putative zinc finger protein salt-toleranc	---	AT4G39070	1.77	0.82	2.76	0.029354	0.125388	-3.98
248392_at	integral membrane protein-like	---	AT5G52050	3.16	1.66	2.76	0.029372	0.125440	-3.98
260044_at	Expressed protein ; supported by full-ler	---	AT1G73655	-1.25	-0.32	-2.76	0.029378	0.125444	-3.98
260006_at	phosphatidylinositol synthase (PIS1) ide	ATPIS1	AT1G68000	1.19	0.25	2.76	0.029403	0.125527	-3.98
249808_at	unknown protein	---	AT5G23890	-1.53	-0.62	-2.75	0.029443	0.125673	-3.98
246850_at	Lon protease homolog 2 precursor almo	LON1	AT5G26860	-1.62	-0.69	-2.75	0.029453	0.125676	-3.98
266787_at	putative receptor-like protein kinase	---	AT2G28990	1.21	0.27	2.75	0.029455	0.125676	-3.98
262026_at	calcium-dependent protein kinase identi	ATCDPK2	AT1G35670	1.32	0.40	2.75	0.029463	0.125687	-3.98
264076_at	unknown protein	---	AT2G28540	-1.19	-0.25	-2.75	0.029487	0.125728	-3.98
252226_at	putative protein transcribed gene of unk	---	AT3G49880	-1.22	-0.28	-2.75	0.029487	0.125728	-3.98
267069_at	unknown protein	ATCAMBP	AT2G41010	2.07	1.05	2.75	0.029489	0.125728	-3.98
264447_at	hypothetical protein predicted by gensca	---	AT1G27300	1.60	0.68	2.75	0.029514	0.125810	-3.98
259231_at	protein phosphatase 2C (PP2C) identica	PP2CA	AT3G11410	1.50	0.58	2.75	0.029529	0.125827	-3.99
262901_at	hypothetical protein predicted by genem	---	AT1G59910	1.71	0.78	2.75	0.029526	0.125827	-3.99

258480_at	unknown protein ;supported by full-leng	---	AT3G02640	1.27	0.34	2.75	0.029547	0.125857	-3.99
253772_at	Expressed protein ; supported by full-ler	A7	AT4G28395	1.19	0.25	2.75	0.029545	0.125857	-3.99
253544_at	hypothetical protein	---	AT4G31280	1.21	0.27	2.75	0.029559	0.125887	-3.99
246347_at	putative protein probable chloroplast all	---	AT3G56830	-1.25	-0.32	-2.75	0.029568	0.125900	-3.99
265712_s_a	unknown protein	---	AT2G03330 /	-1.24	-0.31	-2.75	0.029584	0.125902	-3.99
252292_at	RNA polymerase III subunit - like protei	---	AT3G49000	-1.27	-0.35	-2.75	0.029585	0.125902	-3.99
248576_at	methionine S-methyltransferase (gb|AA	MMT	AT5G49810	-1.23	-0.30	-2.75	0.029574	0.125902	-3.99
253321_at	putative protein prolyl 4-hydroxylase alp	---	AT4G33910	1.23	0.29	2.75	0.029606	0.125966	-3.99
267569_at	putative photosystem II oxygen-evolving	PSBP-2	AT2G30790	-1.47	-0.56	-2.75	0.029619	0.125973	-3.99
248249_at	protein phosphatase 2C-like ; supporte	---	AT5G53140	-1.24	-0.31	-2.75	0.029624	0.125973	-3.99
250446_at	nucleoid DNA-binding protein cnd41 - li	---	AT5G10770	1.50	0.59	2.75	0.029619	0.125973	-3.99
245729_at	unknown protein	---	AT1G73490	-1.30	-0.38	-2.75	0.029647	0.126033	-3.99
248886_at	phosphate/triose-phosphate translocato	APE2	AT5G46110	-1.26	-0.33	-2.75	0.029649	0.126033	-3.99
245673_at	hypothetical protein similar to putative s	---	AT1G56690	-1.28	-0.36	-2.75	0.029655	0.126034	-3.99
250671_at	transcription factor HBP-1b homolog (sp	AHBP-1B	AT5G06950	-1.22	-0.29	-2.75	0.029682	0.126127	-3.99
252738_at	putative protein predicted protein, Dros	---	AT3G43240	-1.22	-0.29	-2.75	0.029699	0.126175	-3.99
253703_at	putative protein origin recognition comp	ORC5	AT4G29910	-1.27	-0.34	-2.75	0.029727	0.126266	-3.99
246364_at	hypothetical protein	---	---	1.21	0.27	2.75	0.029731	0.126266	-3.99
252034_at	putative protein ;supported by full-lengt	---	AT3G52040	-1.53	-0.62	-2.75	0.02974	0.126277	-3.99
256833_at	calmodulin-stimulated calcium-ATPase	---	AT3G22910	2.36	1.24	2.75	0.02976	0.126338	-3.99
260308_at	putative ABC transporter contains Pfam	ATTAP1	AT1G70610	1.56	0.64	2.75	0.029785	0.126398	-3.99
265706_at	unknown protein	---	AT2G03390	-1.34	-0.42	-2.75	0.029779	0.126398	-3.99
255257_at	score=526.5, E=1.9e-154, N=3 ;suppo	UBQ11	AT4G05050	1.20	0.27	2.75	0.029804	0.126455	-4.00
247309_at	putative protein contains similarity to pro	---	AT5G63940	-1.39	-0.47	-2.75	0.029813	0.126471	-4.00
248975_at	unknown protein ; supported by cDNA:	---	AT5G45040	-1.25	-0.32	-2.75	0.029832	0.126526	-4.00
263300_at	Mutator-like transposase similar to MUF	---	---	1.20	0.26	2.75	0.029849	0.126576	-4.00
266805_at	hypothetical protein ;supported by full-le	---	AT2G30010	3.77	1.91	2.74	0.029939	0.126936	-4.00
261576_at	unknown protein ;supported by full-lengt	---	AT1G01070	-1.66	-0.73	-2.74	0.029946	0.126941	-4.00
265648_at	putative beta-1,3-glucanase ;supporte	---	AT2G27500	1.64	0.72	2.74	0.029967	0.127006	-4.00
261159_s_a	cyclin, putative similar to GB:AAB02028	CYCB1;5	AT1G34460 /	-1.30	-0.38	-2.74	0.029994	0.127099	-4.00
249581_at	glutamate--ammonia ligase ; supported	GSR 1	AT5G37600	1.23	0.30	2.74	0.030012	0.127136	-4.00
258720_at	putative ankyrin similar to ankyrin GB:A	---	AT3G09550	-1.30	-0.38	-2.74	0.030014	0.127136	-4.00
258708_at	putative oxidoreductase similar to phyto	---	AT3G09580	-1.41	-0.49	-2.74	0.030049	0.127257	-4.00
246555_at	putative protein 68 kDa protein - Cicer a	GAUT14	AT5G15470	1.40	0.49	2.74	0.030084	0.127360	-4.00
250874_at	putative protein	---	AT5G04010	1.27	0.35	2.74	0.030081	0.127360	-4.00

249386_at	disease resistance -like protein downy r	---	AT5G40060	-1.24	-0.31	-2.74	0.030095	0.127382	-4.01
251192_at	alpha galactosyltransferase-like protein	XT1	AT3G62720	1.72	0.78	2.74	0.030104	0.127395	-4.01
255305_at	putative ABC transporter similar to Guil	ATABC1	AT4G04770	-1.34	-0.42	-2.74	0.030117	0.127428	-4.01
266010_at	putative C2H2-type zinc finger protein li	---	AT2G37430	4.62	2.21	2.74	0.030141	0.127505	-4.01
260160_at	putative RNA-binding protein contains R	---	AT1G79880	-1.23	-0.29	-2.74	0.030162	0.127572	-4.01
245809_at	squalene monooxygenase, putative sim	XF1	AT1G58440	-1.30	-0.38	-2.74	0.030203	0.127692	-4.01
246636_at	acid phosphatase-like protein purple ac	PAP26	AT5G34850	1.35	0.44	2.74	0.030207	0.127692	-4.01
261579_at	soluble inorganic pyrophosphatase, put	AtPPa1	AT1G01050	-1.20	-0.27	-2.74	0.030207	0.127692	-4.01
261077_at	protein phosphatase 2C, putative simila	---	AT1G07430	1.42	0.50	2.74	0.030229	0.127762	-4.01
258413_at	unknown protein ;supported by full-leng	---	AT3G17300	-1.29	-0.36	-2.74	0.030242	0.127792	-4.01
258725_at	putative RNA helicase similar to RNA h	---	AT3G09620	1.21	0.28	2.74	0.030254	0.127820	-4.01
263391_at	putative monogalactosyldiacylglycerol s	MGDC	AT2G11810	1.49	0.58	2.73	0.030279	0.127901	-4.01
256742_at	transcription initiation factor IIB, putative	---	AT3G29380	1.23	0.30	2.73	0.030306	0.127990	-4.01
248856_at	putative protein similar to unknown prote	---	AT5G46620	-1.21	-0.28	-2.73	0.030333	0.128083	-4.01
264408_at	hypothetical protein predicted by genefir	FRS11	AT1G10240	-1.23	-0.30	-2.73	0.030348	0.128120	-4.01
255064_at	putative phi-1-like phosphate-induced pr	EXO	AT4G08950	2.34	1.23	2.73	0.030382	0.128180	-4.01
254529_at	ATP binding protein - like nucleotide-bir	INDL	AT4G19540	-1.21	-0.28	-2.73	0.030384	0.128180	-4.01
254092_at	respiratory burst oxidase - like protein r	---	AT4G25090	1.18	0.24	2.73	0.03037	0.128180	-4.01
266037_at	putative protein kinase contains a protei	---	AT2G05940	1.97	0.98	2.73	0.030384	0.128180	-4.01
249348_at	unknown protein	---	AT5G40860	1.30	0.37	2.73	0.030394	0.128196	-4.02
249028_at	DNA-damage-inducible protein P ; supp	POLH	AT5G44740	-1.32	-0.40	-2.73	0.0304	0.128200	-4.02
255807_at	probable wound-induced protein wound	---	AT4G10270	-1.19	-0.25	-2.73	0.030406	0.128201	-4.02
263504_s_a	hypothetical protein	---	AT2G07677	-1.22	-0.28	-2.73	0.030438	0.128313	-4.02
255575_at	predicted protein of unknown function s	---	AT4G01430	1.85	0.88	2.73	0.03049	0.128439	-4.02
248816_at	prematurely terminated mRNA decay fa	LBA1	AT5G47010	-1.22	-0.28	-2.73	0.030491	0.128439	-4.02
250600_at	dimethylaniline monooxygenase-like pro	---	AT5G07800	1.23	0.29	2.73	0.03048	0.128439	-4.02
254658_at	putative protein predicted gene M02B7.1	---	AT4G18230	-1.24	-0.31	-2.73	0.030489	0.128439	-4.02
266606_at	putative AP2 domain transcription factor	CRF5	AT2G46310	1.48	0.57	2.73	0.030499	0.128449	-4.02
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.50	-0.59	-2.73	0.030526	0.128517	-4.02
263594_at	putative purple acid phosphatase contai	PAP7	AT2G01880	1.65	0.72	2.73	0.030521	0.128517	-4.02
250670_at	polygalacturonase inhibiting protein 1; P	PGIP1	AT5G06860	1.88	0.91	2.73	0.030533	0.128522	-4.02
248901_at	putative protein contains similarity to (pi	---	AT5G46410	1.30	0.38	2.73	0.030567	0.128640	-4.02
253925_at	putative protein ; supported by cDNA: gi	SHV3	AT4G26690	1.52	0.60	2.73	0.030603	0.128716	-4.02
250019_at	putative protein similar to unknown prote	---	AT5G18160	1.29	0.37	2.73	0.030604	0.128716	-4.02
253245_at	bZIP transcription factor ATB2	GBF6	AT4G34588 /	-1.77	-0.83	-2.73	0.030602	0.128716	-4.02

267379_at	unknown protein ; supported by cDNA:	---	AT2G26340	-1.41	-0.50	-2.73	0.030612	0.128716	-4.02
259221_s_a	putative phospholipase similar to unkno	NPC5	AT3G03530 /	3.39	1.76	2.73	0.030613	0.128716	-4.02
257510_at	unknown protein	---	AT1G55360	-1.81	-0.85	-2.73	0.030623	0.128734	-4.02
252464_at	RNA-binding protein-like protein various	---	AT3G47160	-1.33	-0.42	-2.73	0.030636	0.128763	-4.02
267532_at	unknown protein ;supported by full-leng	---	AT2G42040	-1.45	-0.54	-2.73	0.030651	0.128806	-4.02
251169_at	putative protein putative protein At2g25	MARD1	AT3G63210	-1.63	-0.71	-2.73	0.030661	0.128806	-4.02
249216_at	serine carboxypeptidase II-like ; suppor	scpl42	AT5G42240	-1.54	-0.62	-2.73	0.030663	0.128806	-4.02
251918_at	photoassimilate-responsive protein PAF	---	AT3G54040	1.22	0.29	2.73	0.030681	0.128835	-4.02
252470_at	protein kinase 6-like protein protein kina	---	AT3G46930	1.83	0.87	2.73	0.03068	0.128835	-4.02
246976_s_a	putative protein UBIQUINONE BIOSYN	---	AT5G24810	1.42	0.50	2.73	0.03069	0.128849	-4.03
253993_at	mitogen activated protein kinase kinase	MEK1	AT4G26070	1.50	0.59	2.73	0.0307	0.128868	-4.03
261394_at	wall-associated kinase 2, putative simila	---	AT1G79680	3.06	1.61	2.72	0.030734	0.128940	-4.03
257658_at	unknown protein ; supported by full-leng	---	AT3G13230	-1.70	-0.77	-2.72	0.030734	0.128940	-4.03
254095_at	oleosin, 18.5K	OLEO1	AT4G25140	1.25	0.32	2.72	0.030729	0.128940	-4.03
251392_at	dihydrodipicolinate synthase precursor	DHDPS1	AT3G60880	-1.23	-0.29	-2.72	0.03078	0.129026	-4.03
253447_at	hypothetical protein	---	AT4G32630	1.19	0.25	2.72	0.030767	0.129026	-4.03
264156_at	unknown protein	---	AT1G65280	-1.18	-0.24	-2.72	0.030789	0.129026	-4.03
246893_at	PHD finger protein - like PHD finger pro	---	AT5G25520	-1.18	-0.24	-2.72	0.030781	0.129026	-4.03
252825_at	small GTP-binding protein - like SR1 Nt	AtRABH1c	AT4G39890	1.66	0.73	2.72	0.030765	0.129026	-4.03
259637_at	protein disulfide isomerase precursor, p	ATPDIL1-5	AT1G52260	-1.34	-0.43	-2.72	0.030784	0.129026	-4.03
259213_at	putative receptor ser/thr protein kinase s	---	AT3G09010	2.21	1.14	2.72	0.030819	0.129107	-4.03
264406_at	putative phragmoplastin similar to dyna	ADL6	AT1G10290	1.27	0.35	2.72	0.030817	0.129107	-4.03
258157_at	putative MYB family transcription factor	MYB4R1	AT3G18100	-1.40	-0.48	-2.72	0.030854	0.129227	-4.03
255304_at	putative potassium transporter similar t	KEA3	AT4G04850	-1.44	-0.53	-2.72	0.030867	0.129261	-4.03
258205_at	unknown protein	---	AT3G13965	1.23	0.30	2.72	0.030876	0.129274	-4.03
258269_at	putative acetyl-CoA carboxylase biotin-c	---	AT3G15690	-1.23	-0.30	-2.72	0.030888	0.129298	-4.03
264259_at	hypothetical protein This gene is continu	---	AT1G09290	-1.40	-0.48	-2.72	0.030913	0.129379	-4.03
259989_at	hypothetical protein predicted by genem	---	---	1.27	0.34	2.72	0.030918	0.129379	-4.03
266930_at	hypothetical protein predicted by gensca	---	AT2G45930	1.30	0.38	2.72	0.030932	0.129411	-4.03
264705_at	putative leucyl-tRNA synthetase Strong	---	AT1G09620	-1.28	-0.35	-2.72	0.030973	0.129537	-4.03
267584_at	putative protein kinase contains a protei	---	AT2G41930	1.24	0.31	2.72	0.030973	0.129537	-4.03
256898_at	abscisic acid-insensitive protein 3 ident	ABI3	AT3G24650	1.21	0.28	2.72	0.031002	0.129633	-4.04
253523_at	putative protein myosin heavy chain, ne	---	AT4G31340	1.25	0.32	2.72	0.03101	0.129645	-4.04
252854_at	ubiquitin-specific protease 27 (UBP27),	UBP27	AT4G39370	-1.20	-0.26	-2.72	0.031023	0.129675	-4.04
246124_at	putative protein acyl-protein thioesteras	---	AT5G20060	1.18	0.24	2.72	0.031038	0.129712	-4.04

251684_at	putative protein	---	AT3G56410	1.45	0.53	2.72	0.031046	0.129723	-4.04
266254_at	putative membrane transporter	NAT12	AT2G27810	-1.33	-0.41	-2.72	0.031078	0.129814	-4.04
251221_at	putative protein ER6 protein - Lycopers	---	AT3G62550	-1.25	-0.32	-2.72	0.031105	0.129814	-4.04
261513_at	unknown protein contains Pfam profile:	---	AT1G71840	-1.27	-0.35	-2.72	0.031082	0.129814	-4.04
256816_at	unknown protein	---	AT3G21400	-1.26	-0.34	-2.72	0.031095	0.129814	-4.04
246399_at	bZIP transcription factor similar to bZIP	---	AT1G58110	1.27	0.34	2.72	0.031098	0.129814	-4.04
254910_at	translation initiation factor IF-1, putative	---	AT4G11175	-1.21	-0.27	-2.72	0.031108	0.129814	-4.04
258706_at	unknown protein similar to putative prote	---	AT3G09570	1.24	0.32	2.72	0.031093	0.129814	-4.04
251830_at	phosphoribosylformylglycinamidine cycl	PUR5	AT3G55010	-1.48	-0.57	-2.72	0.031143	0.129938	-4.04
260467_at	unknown protein	---	AT1G10890	1.19	0.25	2.71	0.03115	0.129946	-4.04
250214_at	endoxyloglucan transferase (dbj|BAA81	EXGT-A4	AT5G13870	-1.29	-0.37	-2.71	0.031162	0.129946	-4.04
246455_at	putative protein predicted protein F13E	---	AT5G16790	-1.26	-0.34	-2.71	0.031161	0.129946	-4.04
262981_at	unknown protein ;supported by full-lengt	---	AT1G75590	1.33	0.41	2.71	0.031173	0.129967	-4.04
250234_at	transaldolase - like protein transaldolas	---	AT5G13420	1.37	0.45	2.71	0.031183	0.129987	-4.04
263994_at	putative VSF-1-like b-ZIP transcription fa	---	AT2G12900	1.20	0.26	2.71	0.031281	0.130321	-4.04
263181_at	unknown protein ;supported by full-leng	---	AT1G05720	-1.21	-0.28	-2.71	0.031282	0.130321	-4.04
260381_at	putative kinesin similar to kinesin-C GB:	---	AT1G73860	1.28	0.35	2.71	0.031283	0.130321	-4.04
259296_at	putative aminopeptidase similar to X-pro	---	AT3G05350	-1.29	-0.37	-2.71	0.031286	0.130321	-4.04
267000_at	Expressed protein ; supported by full-ler	---	AT2G34310	-1.49	-0.58	-2.71	0.03131	0.130383	-4.05
260110_at	hypothetical protein similar to NBS/LRR	---	AT1G63350	1.21	0.27	2.71	0.031312	0.130383	-4.05
254131_at	protein kinase (AFC2) ; supported by cI	AFC2	AT4G24740	-1.28	-0.35	-2.71	0.031324	0.130408	-4.05
248894_at	unknown protein	---	AT5G46320	1.26	0.33	2.71	0.031354	0.130507	-4.05
250247_at	unknown protein	---	AT5G13720	-1.21	-0.27	-2.71	0.031407	0.130680	-4.05
267112_at	putative adenosine phosphosulfate kina	APK	AT2G14750	-1.60	-0.68	-2.71	0.031405	0.130680	-4.05
264687_at	cysteine protease XBCP3 identical to pa	XBCP3	AT1G09850	-1.20	-0.26	-2.71	0.031423	0.130726	-4.05
249331_at	50S ribosomal protein L27 ;supported b	RPL27	AT5G40950	-1.25	-0.32	-2.71	0.031434	0.130746	-4.05
254464_at	putative protein retinoblastoma binding	---	AT4G20400	-1.36	-0.44	-2.71	0.031467	0.130791	-4.05
245600_at	hypothetical protein	---	AT4G14230	-1.32	-0.40	-2.71	0.031468	0.130791	-4.05
255459_at	polyubiquitin (UBQ14) identical to GI:16	UBQ14	AT4G02890	1.23	0.29	2.71	0.031464	0.130791	-4.05
245697_at	latex-abundant protein - like ;supported	AtMC9	AT5G04200	2.68	1.42	2.71	0.031451	0.130791	-4.05
261233_at	hypothetical protein similar to hypothetic	---	AT1G32810	-1.27	-0.35	-2.71	0.031476	0.130801	-4.05
263066_at	unknown protein	---	AT2G17540	-1.19	-0.25	-2.71	0.031482	0.130801	-4.05
253475_at	putative protein predicted protein, Arabi	---	AT4G32290	-1.52	-0.61	-2.71	0.031546	0.131020	-4.05
266820_at	putative AP2 domain transcription factor	---	AT2G44940	-1.78	-0.84	-2.71	0.031544	0.131020	-4.05
245886_at	ribosomal protein S15-like ribosomal pr	---	AT5G09510	-1.20	-0.26	-2.71	0.031559	0.131043	-4.05

267639_at	putative squamosa-promoter binding pr	SPL9	AT2G42200	-1.21	-0.27	-2.71	0.031563	0.131043	-4.05
252950_at	putative protein phospholipase C (EC 3	---	AT4G38690	-1.63	-0.70	-2.70	0.031597	0.131088	-4.06
253019_at	putative protein crp1-hcf111 allele,enco	---	AT4G38010	-1.23	-0.30	-2.70	0.031593	0.131088	-4.05
247031_at	UDP-glucuronyltransferase-like protein	---	AT5G67230	-1.37	-0.45	-2.70	0.031594	0.131088	-4.06
249313_at	unknown protein	---	AT5G41560	1.21	0.27	2.71	0.031583	0.131088	-4.05
258697_at	putative minichromosome maintenance	MCM8	AT3G09660	-1.29	-0.37	-2.70	0.031616	0.131142	-4.06
253572_at	hypothetical protein	---	AT4G31010	-1.26	-0.33	-2.70	0.031648	0.131201	-4.06
245023_at	PSII I protein	---	---	-1.45	-0.54	-2.70	0.031649	0.131201	-4.06
251439_at	putative protein unknown protein At2g4	---	AT3G59950	1.27	0.34	2.70	0.031646	0.131201	-4.06
245327_at	hypothetical protein ; supported by full-le	---	AT4G16850	-1.22	-0.29	-2.70	0.031658	0.131201	-4.06
250576_at	cytochrome P450-like protein several cy	---	AT5G08250	1.25	0.33	2.70	0.031658	0.131201	-4.06
262235_at	ribosomal protein L18, putative similar t	---	AT1G48350	-1.38	-0.46	-2.70	0.031673	0.131218	-4.06
248555_at	DNA repair protein-like	---	AT5G50340	-1.25	-0.32	-2.70	0.031691	0.131218	-4.06
263035_at	splicing factor, putative similar to RSZp	RSZP21	AT1G23860	-1.33	-0.41	-2.70	0.03169	0.131218	-4.06
247964_at	profilin-like protein ; supported by full-ler	PRF3	AT5G56600	-1.38	-0.47	-2.70	0.031683	0.131218	-4.06
246171_at	putative protein centrosomal Nek2-assc	---	AT5G32440	1.21	0.28	2.70	0.031679	0.131218	-4.06
250965_at	putative protein various predicted prote	---	AT5G03020	1.21	0.27	2.70	0.031708	0.131263	-4.06
254182_at	putative protein various npredicted prot	---	AT4G23950	-1.29	-0.37	-2.70	0.031732	0.131337	-4.06
253980_at	sucrase-like protein sucrose cleavage p	---	AT4G26620	-1.43	-0.51	-2.70	0.031758	0.131400	-4.06
262498_at	8-oxoguanine DNA glycosylase-like prot	OGG1	AT1G21710	-1.26	-0.34	-2.70	0.031756	0.131400	-4.06
261899_at	cinnamoyl CoA reductase, putative sim	CCR2	AT1G80820	3.45	1.79	2.70	0.031771	0.131430	-4.06
258467_at	unknown protein contains Pfam profile:	---	AT3G06060	1.28	0.36	2.70	0.031798	0.131494	-4.06
256199_at	unknown protein	SAB	AT1G58250	-1.32	-0.40	-2.70	0.031798	0.131494	-4.06
256461_s_a	adenylosuccinate lyase - like protein ade	---	AT1G36280 /	-1.90	-0.93	-2.70	0.031846	0.131570	-4.06
249742_at	putative protein contains similarity to rib	---	AT5G24490	-1.30	-0.37	-2.70	0.031839	0.131570	-4.06
267035_at	putative beta-alanine-pyruvate aminotra	AGT3	AT2G38400	1.92	0.94	2.70	0.031845	0.131570	-4.06
247740_at	receptor-like protein kinase precursor -	CRCK1	AT5G58940	1.89	0.92	2.70	0.031836	0.131570	-4.06
248759_at	putative protein similar to unknown prote	---	AT5G47610	-1.65	-0.72	-2.70	0.031825	0.131570	-4.06
256728_at	glutamyl-tRNA amidotransferase subun	---	AT3G25660	-1.36	-0.44	-2.70	0.031912	0.131820	-4.07
264803_at	hypothetical protein predicted by gensca	---	AT1G08580	-1.36	-0.45	-2.70	0.031919	0.131826	-4.07
266109_at	putative mitochondrial carrier protein	---	AT2G37890	-1.52	-0.61	-2.70	0.031972	0.131988	-4.07
246558_at	putative protein IDN3-B - Homo sapiens	EMB2773	AT5G15540	-1.29	-0.37	-2.70	0.031976	0.131988	-4.07
252784_at	putative protein predicted proteins, Aral	---	---	1.18	0.24	2.70	0.031974	0.131988	-4.07
258245_at	hypothetical protein	---	AT3G29075	1.24	0.31	2.70	0.031988	0.132016	-4.07
255982_at	hypothetical protein contains similarity to	OHP2	AT1G34000	-1.22	-0.29	-2.69	0.03204	0.132207	-4.07

251876_at	TATA box binding protein (TBP) associ	RGD3	AT3G54280	-1.25	-0.32	-2.69	0.032051	0.132221	-4.07
246803_at	tSNARE AtTLG2a ; supported by cDNA	SYP41	AT5G26980	-1.22	-0.29	-2.69	0.032055	0.132221	-4.07
264209_at	RAS-related protein, RAB7 identical GE	RABG3B	AT1G22740	-1.30	-0.38	-2.69	0.032068	0.132225	-4.07
263639_at	unknown protein	---	AT2G25300	-1.27	-0.34	-2.69	0.032064	0.132225	-4.07
255667_at	phospholipase D, putative	PLDBETA	AT4G00240	1.23	0.29	2.69	0.032081	0.132254	-4.07
260704_at	glycine cleavage system H protein prec	---	AT1G32470	-1.90	-0.92	-2.69	0.032101	0.132256	-4.07
265332_at	hypothetical protein predicted by genefi	---	AT2G18410	-1.29	-0.37	-2.69	0.032097	0.132256	-4.07
259733_at	nucellin-like protein similar to nucellin G	---	AT1G77480	-1.43	-0.52	-2.69	0.032089	0.132256	-4.07
251224_at	hypothetical protein	---	AT3G62620	-1.27	-0.34	-2.69	0.032104	0.132256	-4.07
266449_at	hypothetical protein predicted by gensc	AT-P4H-1	AT2G43080	1.28	0.35	2.69	0.032129	0.132308	-4.07
262457_at	hypothetical protein similar to hypothetic	---	AT1G11200	1.46	0.54	2.69	0.032126	0.132308	-4.07
250880_at	putative protein Ube-1a, Mus musculus	---	AT5G04070	-1.20	-0.26	-2.69	0.032136	0.132314	-4.07
247504_at	putative protein various predicted prote	---	AT5G61990	-1.36	-0.45	-2.69	0.03216	0.132389	-4.07
248040_at	putative protein contains similarity to un	---	AT5G55970	1.60	0.68	2.69	0.032178	0.132414	-4.07
251379_at	putative protein various predicted Arabic	---	AT3G60680	1.45	0.53	2.69	0.032184	0.132414	-4.07
264228_at	hypothetical protein contains similarity t	GCS1	AT1G67490	-1.24	-0.31	-2.69	0.03218	0.132414	-4.07
257172_at	hypothetical protein predicted by genen	---	AT3G23700	-1.32	-0.40	-2.69	0.0322	0.132418	-4.07
253892_at	hypothetical protein ;supported by full-l	---	AT4G27620	-1.22	-0.29	-2.69	0.032208	0.132418	-4.07
253816_at	hypothetical protein ;supported by full-l	emb1923	AT4G28210	-1.29	-0.37	-2.69	0.032201	0.132418	-4.07
265711_at	unknown protein	---	AT2G03360	1.20	0.26	2.69	0.032206	0.132418	-4.07
259200_at	unknown protein similar to hypothetical	---	AT3G09070	1.23	0.30	2.69	0.032227	0.132476	-4.08
245456_at	disease resistance RPP5 like protein	RPP5	AT4G16950	1.30	0.38	2.69	0.032241	0.132506	-4.08
250267_at	putative protein predicted proteins	---	AT5G12930	2.42	1.27	2.69	0.032308	0.132531	-4.08
255788_at	auxin regulated protein (IAA13) GB:S58	IAA13	AT2G33310	-1.34	-0.43	-2.69	0.032265	0.132531	-4.08
255977_at	ribosomal protein S18, putative similar	---	AT1G34030	-1.34	-0.42	-2.69	0.032302	0.132531	-4.08
255582_at	putative DNA-binding protein similar to A	NGA4	AT4G01500	-1.21	-0.28	-2.69	0.032328	0.132531	-4.08
248684_at	Expressed protein ; supported by full-ler	DIR1	AT5G48485	-1.88	-0.91	-2.69	0.032275	0.132531	-4.08
264942_at	unknown protein ; supported by cDNA: g	---	AT1G67340	-1.34	-0.42	-2.69	0.032312	0.132531	-4.08
246507_at	lipase-like protein monoglyceride lipase	---	AT5G16120	1.39	0.48	2.69	0.032323	0.132531	-4.08
247492_at	putative protein AP2 domain containing	---	AT5G61890	1.82	0.86	2.69	0.032276	0.132531	-4.08
249795_at	40S ribosomal protein S11 ;supported b	RPS11-BE	AT5G23740	-1.51	-0.59	-2.69	0.032299	0.132531	-4.08
261033_at	unknown protein ;supported by full-leng	JAZ5	AT1G17380	2.27	1.18	2.69	0.03232	0.132531	-4.08
260155_at	unknown protein	---	AT1G52870	-1.63	-0.70	-2.69	0.032311	0.132531	-4.08
258527_at	branched chain alpha-keto acid dehydr	BCE2	AT3G06850	2.04	1.03	2.69	0.032303	0.132531	-4.08
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XREF=gb:M	---	---	-1.76	-0.81	-2.69	0.0323	0.132531	-4.08

246444_at	putative protein predicted protein T21P	---	AT5G17570	-1.39	-0.47	-2.69	0.032318	0.132531	-4.08
260095_at	putative transcription factor BTF3 (RNA	---	AT1G73230	-1.38	-0.46	-2.69	0.03234	0.132554	-4.08
245888_at	putative protein DNA-binding protein - T	---	AT5G09450	-1.25	-0.32	-2.69	0.032367	0.132644	-4.08
255225_at	U3 snoRNP-associated -like protein U3	---	AT4G05410	-1.64	-0.71	-2.69	0.032394	0.132684	-4.08
267289_at	putative protein kinase contains a protei	---	AT2G23770	1.20	0.27	2.69	0.032389	0.132684	-4.08
265879_at	hypothetical protein predicted by gensca	---	AT2G42450	-1.20	-0.27	-2.69	0.032387	0.132684	-4.08
248082_at	fimbrin	---	AT5G55400	1.47	0.56	2.69	0.03245	0.132719	-4.08
257076_at	unknown protein	---	AT3G19680	-1.62	-0.69	-2.69	0.032446	0.132719	-4.08
261019_at	unknown protein ; supported by cDNA: g	---	AT1G26470	-1.26	-0.33	-2.69	0.03244	0.132719	-4.08
245289_at	Expressed protein ; supported by cDNA	---	AT4G15470	1.19	0.25	2.69	0.032436	0.132719	-4.08
263295_at	putative MADS-box protein ANR1	AGL44	AT2G14210	-1.20	-0.26	-2.69	0.032436	0.132719	-4.08
247093_at	zinc finger protein SHI-like ; supported	SHI	AT5G66350	-1.35	-0.43	-2.69	0.032448	0.132719	-4.08
248834_at	unknown protein ;supported by full-leng	---	AT5G47090	-1.24	-0.31	-2.69	0.032414	0.132719	-4.08
256526_at	disease resistance protein, putative sim	---	AT1G66090	1.25	0.32	2.69	0.032423	0.132719	-4.08
251120_at	chloroplast ribosomal L1 - like protein ri	---	AT3G63490	-1.31	-0.39	-2.69	0.032466	0.132761	-4.08
256374_at	DNA ligase I, putative similar to DNA lig	---	AT1G66730	-1.28	-0.35	-2.68	0.032497	0.132864	-4.08
264054_at	unknown protein	SVP	AT2G22540	-1.28	-0.35	-2.68	0.032503	0.132866	-4.08
259489_at	unknown protein	---	AT1G15790	1.48	0.56	2.68	0.032518	0.132904	-4.08
246966_at	DNA photolyase - like protein DNA pho	CRY3	AT5G24850	1.37	0.45	2.68	0.032559	0.133033	-4.09
262604_at	unknown protein similar to unknown pro	---	AT1G15060	-1.18	-0.24	-2.68	0.032561	0.133033	-4.09
258792_at	hypothetical protein predicted by genefi	---	AT3G04640	2.04	1.03	2.68	0.032578	0.133078	-4.09
251228_at	beta-D-glucan exohydrolase-like protei	---	AT3G62710	1.22	0.29	2.68	0.032636	0.133289	-4.09
249718_at	putative protein contains similarity to be	---	AT5G35740	1.29	0.37	2.68	0.032647	0.133310	-4.09
256992_at	hypothetical protein predicted by genem	---	AT3G28630	1.25	0.32	2.68	0.032656	0.133326	-4.09
266671_at	anthranilate synthase, alpha subunit ide	ASA2	AT2G29690	-1.26	-0.34	-2.68	0.032669	0.133353	-4.09
250054_at	potassium-dependent sodium-calcium e	CAX7	AT5G17860	1.77	0.83	2.68	0.032677	0.133364	-4.09
256169_at	receptor protein kinase, putative contai	---	AT1G51800	2.58	1.37	2.68	0.032692	0.133401	-4.09
246162_at	actin interacting protein ; supported by c	---	AT4G36400	1.32	0.40	2.68	0.032715	0.133468	-4.09
255412_at	auxin-binding protein 1 precursor ;supp	ABP1	AT4G02980	-1.24	-0.31	-2.68	0.032722	0.133470	-4.09
250719_at	putative protein contains similarity to RA	---	AT5G06250	1.29	0.36	2.68	0.032727	0.133470	-4.09
262852_at	hypothetical protein predicted by gensca	---	AT1G20910	-1.23	-0.29	-2.68	0.032768	0.133585	-4.09
258090_at	putative 60S ribosomal protein L18A sin	---	AT3G14600	-1.34	-0.43	-2.68	0.032774	0.133585	-4.09
251031_at	one helix protein (OHP) ;supported by f	OHP	AT5G02120	-1.27	-0.35	-2.68	0.032778	0.133585	-4.09
249075_at	putative protein similar to unknown prote	---	AT5G44000	-1.32	-0.40	-2.68	0.032768	0.133585	-4.09
263351_at	hypothetical protein predicted by grail ar	---	AT2G22120	-1.18	-0.24	-2.68	0.03279	0.133609	-4.09

246822_at	putative protein predicted proteins, Arat	---	AT5G26960	-1.27	-0.35	-2.68	0.032804	0.133637	-4.09
248164_at	putative protein similar to unknown prote	PBP1	AT5G54490	3.42	1.77	2.68	0.032809	0.133637	-4.09
259092_at	putative zeta-carotene desaturase precu	ZDS	AT3G04870	-1.18	-0.24	-2.68	0.032821	0.133662	-4.09
253213_at	RNA helicase (RH16)	---	AT4G34910	-1.24	-0.31	-2.68	0.032834	0.133667	-4.09
251454_at	putative protein COP1-interacting prote	---	AT3G60080	1.32	0.40	2.68	0.032831	0.133667	-4.09
256219_at	hypothetical protein predicted by genem	---	AT1G56260	-1.24	-0.31	-2.68	0.032853	0.133724	-4.10
248007_at	S-adenosylmethionine:2-demethylmena	---	AT5G56260	1.20	0.26	2.68	0.032906	0.133914	-4.10
266101_at	unknown protein ; supported by cDNA:	---	AT2G37940	1.84	0.88	2.68	0.032914	0.133922	-4.10
252364_at	hypothetical protein ;supported by full-le	---	AT3G48450	2.17	1.11	2.68	0.032933	0.133977	-4.10
261375_at	transcription factor, putative similar to G	SPL4	AT1G53160	-2.45	-1.30	-2.68	0.03294	0.133981	-4.10
262230_at	alpha-xylosidase precursor identical to a	XYL1	AT1G68560	-1.65	-0.72	-2.67	0.032983	0.134130	-4.10
260602_at	serine acetyltransferase identical to GB	ATSERAT	AT1G55920	1.27	0.35	2.67	0.032989	0.134132	-4.10
259605_at	unknown protein	PUB45	AT1G27910	-1.47	-0.56	-2.67	0.033002	0.134161	-4.10
267492_at	histone H1 ;supported by full-length cDN	---	AT2G30620	-1.33	-0.42	-2.67	0.033016	0.134192	-4.10
259711_at	putative DNA-binding protein similarity t	---	AT1G77570	-1.64	-0.71	-2.67	0.033021	0.134192	-4.10
261511_at	polyadenylate-binding protein 5 identica	PAB5	AT1G71770	1.27	0.34	2.67	0.033052	0.134267	-4.10
246656_at	hypothetical protein	---	---	1.26	0.34	2.67	0.033047	0.134267	-4.10
265966_at	putative RNA-binding protein ; supporte	---	AT2G37220	-1.32	-0.40	-2.67	0.033067	0.134307	-4.10
250795_at	RING zinc finger protein-like	CPuORF6	AT5G05280 /	-1.27	-0.34	-2.67	0.033078	0.134324	-4.10
247461_at	putative protein various predicted prote	ATBAG2	AT5G62100	-1.31	-0.39	-2.67	0.033121	0.134382	-4.10
256865_at	NAD dependent epimerase, putative co	GAE6	AT3G23820	-1.51	-0.59	-2.67	0.033114	0.134382	-4.10
251823_at	putative protein	---	AT3G55080	-1.20	-0.26	-2.67	0.033109	0.134382	-4.10
261817_at	hypothetical protein predicted by genem	---	AT1G08180	-1.60	-0.67	-2.67	0.033111	0.134382	-4.10
255906_at	hypothetical protein similar to RING3-lik	---	AT1G17790	-1.24	-0.30	-2.67	0.033121	0.134382	-4.10
256042_at	hypothetical protein predicted by genem	---	AT1G07220	1.19	0.25	2.67	0.033141	0.134435	-4.10
265048_at	jasmonate inducible protein, putative s	---	AT1G52050	1.29	0.36	2.67	0.033146	0.134435	-4.10
265989_at	unknown protein	---	AT2G24260	1.22	0.29	2.67	0.033176	0.134533	-4.11
255338_at	PEROXISOMAL MEMBRANE PROTEIN	PMP22	AT4G04470	-1.20	-0.26	-2.67	0.033195	0.134537	-4.11
252252_at	putative protein GTP-binding protein be	RID3	AT3G49180	-1.51	-0.60	-2.67	0.033201	0.134537	-4.11
247422_at	putative protein	PEX14	AT5G62810	-1.22	-0.29	-2.67	0.033186	0.134537	-4.11
AFFX-PheX	B. subtilis /GEN=pheB /DB_XREF=gb:M	---	---	-1.39	-0.48	-2.67	0.0332	0.134537	-4.11
267062_at	putative spliceosome associated protein	---	AT2G32600	-1.30	-0.37	-2.67	0.033223	0.134581	-4.11
251010_at	putative protein ;supported by full-lengt	---	AT5G02550	1.32	0.40	2.67	0.033219	0.134581	-4.11
262068_at	splicing factor Prp8, putative similar to s	SUS2	AT1G80070	-1.35	-0.44	-2.67	0.03323	0.134584	-4.11
252328_at	Expressed protein ; supported by cDNA	---	AT3G48570	1.23	0.30	2.67	0.033243	0.134589	-4.11

258609_at	unknown protein ;supported by full-leng	---	AT3G02910	-1.28	-0.35	-2.67	0.033237	0.134589	-4.11
248775_at	receptor kinase-like protein	CCR4	AT5G47850	3.02	1.60	2.67	0.033273	0.134685	-4.11
250931_at	putative protein various predicted prote	---	AT5G03200	-1.79	-0.84	-2.67	0.033309	0.134808	-4.11
248102_at	putative protein contains similarity to 50	---	AT5G55140	-1.35	-0.43	-2.67	0.033328	0.134840	-4.11
259581_at	RING zinc finger protein, putative conta	---	AT1G28040	1.26	0.34	2.67	0.033329	0.134840	-4.11
259627_at	unknown protein ; supported by cDNA: g	---	AT1G42960	-1.27	-0.34	-2.67	0.033341	0.134864	-4.11
247026_at	protein kinase-like protein	MAPKKK1	AT5G67080	3.18	1.67	2.67	0.03335	0.134879	-4.11
264226_at	hypothetical protein similar to putative re	---	AT1G67510	-1.24	-0.32	-2.67	0.033364	0.134889	-4.11
261556_s_a	unknown protein	---	AT1G62600 /	1.32	0.40	2.67	0.033365	0.134889	-4.11
265187_at	putative ADP-ribosylation factor ; suppo	---	AT1G23490 /	1.17	0.23	2.67	0.033389	0.134965	-4.11
255279_at	putative thioredoxin ; supported by cDN	---	AT4G04950	-1.40	-0.49	-2.67	0.033409	0.134999	-4.11
247921_at	CONSTANS-like B-box zinc finger prote	COL5	AT5G57660	-1.36	-0.44	-2.67	0.033406	0.134999	-4.11
261885_at	unknown protein	---	AT1G80930	-1.28	-0.35	-2.67	0.033426	0.135041	-4.11
257144_at	glucose-6-phosphate 1-dehydrogenase	G6PD5	AT3G27300	-1.22	-0.29	-2.66	0.033447	0.135060	-4.11
247164_at	NifS-like aminotranfserase ; supported	NFS1	AT5G65720	-1.24	-0.32	-2.66	0.033443	0.135060	-4.11
255609_s_a	hypothetical protein	---	AT4G01180 /	1.19	0.25	2.66	0.033448	0.135060	-4.11
264965_at	hypothetical protein predicted by genem	---	AT1G60560	-1.30	-0.38	-2.66	0.033456	0.135060	-4.11
253785_s_a	ABC transporter - like protein ABC tran	ATM2	AT4G28620 /	-1.24	-0.31	-2.66	0.03346	0.135060	-4.11
258093_at	unknown protein ; supported by cDNA:	---	AT3G14750	-1.29	-0.37	-2.66	0.033507	0.135155	-4.12
253138_at	ribosomal protein L11 homolog several	MRPL11	AT4G35490	-1.21	-0.27	-2.66	0.033509	0.135155	-4.12
260303_at	putative protein kinase similar to C-term	---	AT1G70520	1.57	0.65	2.66	0.033511	0.135155	-4.12
264636_at	hypothetical protein predicted by genem	---	AT1G65490	1.60	0.68	2.66	0.033497	0.135155	-4.12
249998_at	putative protein unnamed ORF, Mus m	FASS	AT5G18580	-1.22	-0.29	-2.66	0.033513	0.135155	-4.12
250166_at	putative protein many predicted protein	---	AT5G15300	-1.22	-0.28	-2.66	0.033538	0.135233	-4.12
253092_at	putative protein various predicted prote	---	AT4G37380	-1.45	-0.53	-2.66	0.033565	0.135316	-4.12
253272_at	putative protein ;supported by full-lengt	סעס-01	AT4G34190	-1.37	-0.46	-2.66	0.033591	0.135397	-4.12
263533_at	putative Rieske iron-sulfur protein ;supp	TIC55	AT2G24820	-1.18	-0.24	-2.66	0.033605	0.135430	-4.12
267172_at	unknown protein ;supported by full-leng	---	AT2G37660	-1.31	-0.39	-2.66	0.033625	0.135484	-4.12
245095_at	putative protein kinase contains a protei	---	AT2G40860	-1.36	-0.45	-2.66	0.033631	0.135487	-4.12
262093_at	receptor protein kinase, putative contai	---	AT1G56145	1.41	0.49	2.66	0.033659	0.135567	-4.12
256919_at	hypothetical protein predicted by genem	---	AT3G18970	-1.26	-0.34	-2.66	0.033663	0.135567	-4.12
260223_at	putative exonuclease contains Pfam pro	---	AT1G74390	-1.23	-0.30	-2.66	0.033675	0.135593	-4.12
258884_at	threonine dehydratase/deaminase (OM	OMR1	AT3G10050	-1.50	-0.58	-2.66	0.033716	0.135708	-4.12
248271_at	putative protein similar to unknown prote	---	AT5G53420	-1.66	-0.73	-2.66	0.033716	0.135708	-4.12
249856_at	serine carboxypeptidase	scpl47	AT5G22980	1.39	0.47	2.66	0.033723	0.135713	-4.12

259479_at	Expressed protein ; supported by full-ler	---	AT1G19020	2.47	1.30	2.66	0.033743	0.135768	-4.12
255406_at	hypothetical protein similar to hypotheti	---	AT4G03450	1.80	0.85	2.66	0.033826	0.136079	-4.13
265739_at	unknown protein ; supported by cDNA:	AtQSOX2	AT2G01270	-1.18	-0.24	-2.66	0.033837	0.136082	-4.13
264838_at	putative AHP2 similar to GB:BAA36336;	AHP5	AT1G03430	-1.17	-0.23	-2.66	0.033839	0.136082	-4.13
253246_at	putative protein	---	AT4G34600	-1.28	-0.36	-2.66	0.033857	0.136131	-4.13
248806_at	putative protein contains similarity to un	---	AT5G47490	-1.21	-0.28	-2.66	0.03387	0.136161	-4.13
253979_at	putative protein other putative proteins f	---	AT4G26680	-1.25	-0.32	-2.66	0.033883	0.136184	-4.13
259601_s_a	CACTA-element transposase, putative	---	---	-1.21	-0.28	-2.66	0.033888	0.136184	-4.13
246398_at	auxin-induced basic helix-loop-helix tra	---	AT1G58100	1.18	0.24	2.65	0.033915	0.136269	-4.13
251528_at	putative protein hypothetical protein F2	---	AT3G58600	1.29	0.37	2.65	0.033931	0.136308	-4.13
247942_at	putative protein similar to unknown prote	---	AT5G57120	-1.36	-0.44	-2.65	0.033989	0.136467	-4.13
266792_at	putative sucrose/H+ symporter	SUT2	AT2G02860	1.64	0.72	2.65	0.033978	0.136467	-4.13
262273_at	hypothetical protein predicted by gensca	---	AT1G68730	-1.20	-0.27	-2.65	0.033985	0.136467	-4.13
264566_at	hypothetical protein predicted by genefir	---	AT1G05270	1.26	0.34	2.65	0.034	0.136467	-4.13
252006_at	purple acid phosphatase-like protein pu	PAP22	AT3G52820	2.66	1.41	2.65	0.033998	0.136467	-4.13
264664_at	putative elongation factor similar to GB:A	---	AT1G09660	-1.37	-0.46	-2.65	0.034036	0.136580	-4.13
258803_at	unknown protein similar to elicitor respo	WRKY39	AT3G04670	1.25	0.32	2.65	0.03404	0.136580	-4.13
256288_at	arginine N-methyltransferase 3, putative	PRMT3	AT3G12270	-1.61	-0.69	-2.65	0.034049	0.136592	-4.13
267475_at	expressed protein ; supported by full-ler	---	AT2G02730	1.29	0.36	2.65	0.03408	0.136660	-4.13
250131_at	unknown protein ; supported by cDNA:	---	AT5G16550	-1.40	-0.48	-2.65	0.034084	0.136660	-4.13
249228_at	SKP1/ASK1 (At2) identical to UIP2 GI:3	ASK2	AT5G42190	-1.34	-0.42	-2.65	0.034072	0.136660	-4.13
254852_at	putative disease resistance protein DNA	WRKY19	AT4G12020	1.18	0.24	2.65	0.034106	0.136724	-4.13
261798_at	hypothetical protein similar to hypothetic	CPSF30	AT1G30460	-1.27	-0.34	-2.65	0.034127	0.136785	-4.13
256494_at	hypothetical protein predicted by genem	---	AT1G31520	1.21	0.28	2.65	0.034156	0.136864	-4.13
266275_at	putative tropinone reductase	---	AT2G29370	1.30	0.38	2.65	0.034159	0.136864	-4.14
254219_at	putative protein	---	AT4G23760	-1.23	-0.30	-2.65	0.034195	0.136983	-4.14
251686_at	putative protein hypothetical protein - di	ATATG18I	AT3G56440	1.21	0.28	2.65	0.034213	0.136993	-4.14
264660_at	putative glutamyl-tRNA reductase 2 pre	HEMA2	AT1G09940	1.79	0.84	2.65	0.034215	0.136993	-4.14
248953_at	serine/threonine-protein kinase Mak (ma	---	AT5G45428 /	-1.22	-0.29	-2.65	0.034209	0.136993	-4.14
260900_s_a	branched-chain alpha keto-acid dehydr	---	AT1G21400 /	1.50	0.58	2.65	0.034236	0.137047	-4.14
266345_at	hypothetical protein predicted by genefir	---	AT2G01410	1.21	0.28	2.65	0.034259	0.137047	-4.14
250664_at	putative protein 10-deacetylbaccatin III-	---	AT5G07080	1.61	0.69	2.65	0.034244	0.137047	-4.14
254275_at	HSP associated protein like p48, Homo	AtHip1	AT4G22670	-1.30	-0.38	-2.65	0.034247	0.137047	-4.14
246140_at	SOH1 - like protein SOH1, Saccharomy	---	AT5G19910	-1.18	-0.24	-2.65	0.034269	0.137047	-4.14
257247_at	helix-loop-helix DNA-binding protein cor	FMA	AT3G24140	-1.34	-0.42	-2.65	0.034271	0.137047	-4.14

246359_x_a	hypothetical protein	---	---	1.31	0.39	2.65	0.034258	0.137047	-4.14
267185_at	unknown protein ; supported by cDNA:	OEP37	AT2G43950	-1.26	-0.33	-2.65	0.034288	0.137092	-4.14
266171_at	putative CCAAT-binding transcription fa	NF-YB1	AT2G38880	-1.30	-0.38	-2.65	0.034313	0.137167	-4.14
250191_at	kinase - like protein RING3 protein, Hor	ATBET9	AT5G14270	-1.26	-0.33	-2.65	0.034323	0.137182	-4.14
249767_at	acidic endochitinase (dbj|BAA21861.1)	---	AT5G24090	1.77	0.83	2.65	0.034338	0.137219	-4.14
250087_at	putative protein contains similarity to un	---	AT5G17270	-1.44	-0.53	-2.65	0.034358	0.137227	-4.14
259077_s_a	reversibly glycosylated polypeptide-1 ide	RGP1	AT3G02230 /	1.51	0.59	2.65	0.034354	0.137227	-4.14
249770_at	unknown protein ;supported by full-lengt	WRKY30	AT5G24110	3.34	1.74	2.65	0.034364	0.137227	-4.14
247148_at	auxin-induced protein IAA9 (pir |T05902	IAA9	AT5G65670	-1.39	-0.48	-2.65	0.034357	0.137227	-4.14
247754_at	putative protein	---	AT5G59080	-1.69	-0.76	-2.64	0.034404	0.137313	-4.14
AFFX-r2-Bs	B. subtilis /GEN=pheB /DB_XREF=gb:M	---	---	-1.43	-0.52	-2.65	0.034392	0.137313	-4.14
257959_at	somatic embryogenesis receptor-like ki	NIK2	AT3G25560	-1.54	-0.62	-2.64	0.034402	0.137313	-4.14
256055_at	mitochondrial carrier protein, putative si	---	AT1G07030	1.22	0.28	2.64	0.034434	0.137337	-4.14
262499_at	unknown protein EST gb|T41993 comes	---	AT1G21770	1.34	0.42	2.64	0.034421	0.137337	-4.14
265547_at	hypothetical protein similar to hypothetic	---	AT2G28305	1.56	0.64	2.64	0.034423	0.137337	-4.14
247217_s_a	MADS box transcription factors-like prot	MAF3	AT5G65050 /	1.18	0.24	2.64	0.03444	0.137337	-4.14
247382_at	adenylate kinase ;supported by full-leng	ADK1	AT5G63400	1.31	0.39	2.64	0.034431	0.137337	-4.14
262362_at	disease resistance protein, putative sim	---	AT1G72840	-1.22	-0.28	-2.64	0.034465	0.137390	-4.14
257499_at	hypothetical protein similar to hypothetic	---	AT1G63850	-1.50	-0.59	-2.64	0.034461	0.137390	-4.14
262126_at	disease resistance protein, putative sim	CW9	AT1G59620	1.34	0.43	2.64	0.034487	0.137433	-4.14
264669_at	putative RAS-related protein, RAB11C	ATRAB11(	AT1G09630	1.39	0.47	2.64	0.034488	0.137433	-4.14
245246_at	hypothetical protein predicted by genem	---	AT1G44224	1.21	0.27	2.64	0.034542	0.137601	-4.15
250288_at	auxin-responsive - like protein Nt-gh3 d	---	AT5G13350	1.25	0.32	2.64	0.034538	0.137601	-4.15
264320_at	unknown protein	---	AT1G04090	1.18	0.24	2.64	0.034583	0.137740	-4.15
258930_at	unknown protein predicted by genscan,	---	AT3G10040	-1.22	-0.29	-2.64	0.034597	0.137771	-4.15
257266_at	RNA-binding protein contains Pfam pro	---	AT3G15010	-1.21	-0.27	-2.64	0.034611	0.137804	-4.15
263231_at	putative indole-3-acetate beta-glucosyltr	---	AT1G05680	6.41	2.68	2.64	0.03462	0.137805	-4.15
253184_at	putative protein protein kinase APK1, A	BSK1	AT4G35230	1.25	0.32	2.64	0.034623	0.137805	-4.15
248608_at	ATP citrate lyase ; supported by cDNA:	ACLB-2	AT5G49460	1.28	0.36	2.64	0.034637	0.137833	-4.15
247476_at	putative protein	---	AT5G62330	1.22	0.29	2.64	0.034643	0.137833	-4.15
247288_at	non-phototropic hypocotyl 3 (gb|AAF05	NPH3	AT5G64330	-1.96	-0.97	-2.64	0.03468	0.137947	-4.15
AFFX-r2-Bs	B. subtilis /GEN=thrB /DB_XREF=gb:X0	---	---	-1.42	-0.50	-2.64	0.034683	0.137947	-4.15
262014_at	unknown protein	---	AT1G35660	-1.48	-0.57	-2.64	0.034692	0.137957	-4.15
254158_at	putative protein dihydrofolate reductase	---	AT4G24380	2.45	1.29	2.64	0.034699	0.137961	-4.15
260679_at	unknown protein	---	AT1G07990	-1.21	-0.27	-2.64	0.034724	0.138039	-4.15

259632_at	nicotianamine synathase, putative simil	NAS4	AT1G56430	-1.71	-0.78	-2.64	0.034744	0.138092	-4.15
264777_at	unknown protein similar to L-allo-threor	THA1	AT1G08630	2.36	1.24	2.64	0.034762	0.138116	-4.15
258726_at	Expressed protein ; supported by full-ler	---	AT3G11745	-1.21	-0.27	-2.64	0.034762	0.138116	-4.15
250586_at	putative protein similar to unknown prote	---	AT5G07630	-1.29	-0.36	-2.64	0.034831	0.138366	-4.16
246762_at	cyclin H-like protein cycH (CAK associa	CYCH;1	AT5G27620	-1.39	-0.48	-2.64	0.034855	0.138435	-4.16
254711_at	putative protein	---	AT4G18060	-1.27	-0.34	-2.64	0.034877	0.138469	-4.16
248453_at	unknown protein	---	AT5G51340	-1.23	-0.30	-2.64	0.034881	0.138469	-4.16
267262_at	putative serine carboxypeptidase I ; sup	SNG1	AT2G22990	-1.36	-0.44	-2.64	0.034876	0.138469	-4.16
253820_at	hypothetical protein	---	AT4G28370	1.23	0.29	2.63	0.034903	0.138531	-4.16
247617_at	receptor like protein kinase receptor like	---	AT5G60270	1.63	0.71	2.63	0.034921	0.138579	-4.16
250231_at	AP2/EREBP-like transcription factor LE/	LEP	AT5G13910	1.21	0.27	2.63	0.034955	0.138666	-4.16
258088_at	hypothetical protein predicted by genma	---	AT3G14580	-1.22	-0.28	-2.63	0.034951	0.138666	-4.16
260549_at	Expressed protein ; supported by full-ler	---	AT2G43535	-1.90	-0.92	-2.63	0.03497	0.138701	-4.16
247014_at	RuvB DNA helicase-like protein ; suppo	---	AT5G67630	-1.54	-0.62	-2.63	0.035015	0.138856	-4.16
255552_at	S-adenosylmethionine synthase 2 ;sup	SAM-2	AT4G01850	1.25	0.32	2.63	0.035024	0.138865	-4.16
252515_at	heat shock protein 17 ; supported by cI	HSP17.4	AT3G46230	2.28	1.19	2.63	0.035048	0.138931	-4.16
262801_at	unknown protein ;supported by full-leng	---	AT1G21010	1.71	0.78	2.63	0.035053	0.138931	-4.16
246543_at	putative protein	---	AT5G15060	1.18	0.24	2.63	0.035131	0.139218	-4.16
249425_at	putative protein 5'-AMP-ACTIVATED P	---	AT5G39790	-1.53	-0.62	-2.63	0.035144	0.139244	-4.16
265903_at	putative potassium transporter/channel	SPIK	AT2G25600	1.21	0.27	2.63	0.035208	0.139450	-4.17
254083_at	PROTEIN TRANSPORT PROTEIN SE	---	AT4G24920	1.36	0.44	2.63	0.035204	0.139450	-4.17
262383_at	disease resistance protein, putative sim	---	AT1G72940	2.78	1.48	2.63	0.035242	0.139560	-4.17
247214_at	putative protein similar to unknown prote	---	AT5G64850	-1.74	-0.80	-2.63	0.035261	0.139612	-4.17
253956_at	fimbrin-like protein (ATFIM1) ; supporte	FIM1	AT4G26700	-1.43	-0.52	-2.63	0.035277	0.139652	-4.17
250454_at	unknown protein ; supported by full-leng	---	AT5G09830	-1.17	-0.23	-2.63	0.035298	0.139686	-4.17
265402_at	hypothetical protein predicted by gensca	---	AT2G10950	-1.22	-0.29	-2.63	0.035296	0.139686	-4.17
252823_at	Expressed protein ; supported by full-ler	---	AT4G40045	-1.24	-0.31	-2.63	0.03531	0.139691	-4.17
252419_at	putative protein	---	AT3G47510	-1.59	-0.67	-2.63	0.035312	0.139691	-4.17
264516_at	unknown protein	---	AT1G10090	-1.22	-0.28	-2.63	0.035339	0.139775	-4.17
267004_at	hypothetical protein predicted by genefir	---	AT2G34260	-1.91	-0.93	-2.63	0.035346	0.139777	-4.17
261609_at	unknown protein similar to MAP3K-like p	---	AT1G49740	1.41	0.49	2.63	0.035352	0.139777	-4.17
257045_at	dynamin-like protein similar to phragmo	ARC5	AT3G19720	-1.41	-0.49	-2.63	0.035373	0.139835	-4.17
246612_at	putative protein ;supported by full-lengt	---	AT5G35320	-1.29	-0.36	-2.62	0.035391	0.139875	-4.17
246598_at	dolichyl-phosphate-mannose--glycolipid	---	AT5G14850	-1.30	-0.38	-2.62	0.035412	0.139875	-4.17
252509_at	putative protein serine/threonine-specif	---	AT3G46240	1.18	0.24	2.62	0.035397	0.139875	-4.17

252336_at	putative protein N7 protein - Medicago t	---	AT3G48880	1.21	0.27	2.62	0.035418	0.139875	-4.17
260546_at	putative trypsin inhibitor ;supported by f	ATTI2	AT2G43520	-2.30	-1.20	-2.62	0.035401	0.139875	-4.17
248278_at	putative protein similar to unknown prote	---	AT5G52890	-1.27	-0.35	-2.62	0.035419	0.139875	-4.17
263435_at	putative ATP-dependent RNA helicase	---	AT2G28600	-1.47	-0.55	-2.62	0.035427	0.139881	-4.17
257190_at	30S ribosomal protein S10, putative sim	---	AT3G13120	-1.38	-0.47	-2.62	0.03547	0.140025	-4.17
247664_at	APETALA2 protein - like APETALA2 pr	TOE2	AT5G60120	-1.23	-0.30	-2.62	0.035496	0.140103	-4.17
254504_at	putative protein RNPL, Homo sapiens,	---	AT4G20030	-1.41	-0.49	-2.62	0.035525	0.140195	-4.18
245029_at	hypothetical protein predicted by genscа	YAB5	AT2G26580	-1.65	-0.72	-2.62	0.035574	0.140338	-4.18
249763_at	receptor-protein kinase-like protein	---	AT5G24010	-1.42	-0.50	-2.62	0.035571	0.140338	-4.18
263182_at	Expressed protein ; supported by full-ler	---	AT1G05575	3.84	1.94	2.62	0.035607	0.140421	-4.18
258811_at	unknown protein similar to putative prote	---	AT3G03990	1.39	0.48	2.62	0.035605	0.140421	-4.18
250869_at	Terminal flower1 (TFL1) ; supported by	TFL1	AT5G03840	1.23	0.30	2.62	0.035624	0.140463	-4.18
247753_at	hexosyltransferase - like protein	---	AT5G59070	1.72	0.79	2.62	0.035633	0.140475	-4.18
266576_at	hypothetical protein predicted by genscа	---	AT2G23940	-1.23	-0.30	-2.62	0.035651	0.140521	-4.18
247325_at	putative protein contains similarity to spl	SC35	AT5G64200	-1.21	-0.27	-2.62	0.035665	0.140552	-4.18
252134_at	putative protein ; supported by cDNA: g	---	AT3G50910	1.68	0.75	2.62	0.035682	0.140594	-4.18
266592_at	putative fatty acid desaturase/cytochrom	---	AT2G46210	1.22	0.29	2.62	0.035694	0.140595	-4.18
255267_at	putative protein LpxD gene, Brucella ab	---	AT4G05210	-1.18	-0.24	-2.62	0.035689	0.140595	-4.18
255544_at	predicted protein of unknown function	---	AT4G01880	-1.31	-0.39	-2.62	0.035704	0.140610	-4.18
255036_at	putative protein similarity RING zinc fing	---	AT4G09560	-1.44	-0.53	-2.62	0.035718	0.140616	-4.18
258852_at	unknown protein similar to C-terminal pc	AT-P4H-2	AT3G06300	1.36	0.44	2.62	0.035716	0.140616	-4.18
261911_at	ribosomal protein L7, putative similar to	---	AT1G80750	-1.51	-0.60	-2.62	0.035732	0.140646	-4.18
267246_at	putative WRKY-type DNA binding protei	WRKY25	AT2G30250	1.49	0.58	2.62	0.035739	0.140648	-4.18
266415_at	putative nonspecific lipid-transfer protein	LTP2	AT2G38530	2.71	1.44	2.62	0.035751	0.140648	-4.18
258499_at	putative RAD23 similar to RAD23 protei	RAD23-3	AT3G02540	-1.24	-0.31	-2.62	0.035749	0.140648	-4.18
249095_at	myosin heavy chain MYA2 (pir||S51824	MYA2	AT5G43900	1.41	0.49	2.62	0.035797	0.140806	-4.18
253393_at	Expressed protein ; supported by cDNA	GLB3	AT4G32690	-1.25	-0.32	-2.62	0.035835	0.140878	-4.18
246311_at	high mobility group protein 2-like ; supp	HMGB1	AT3G51880	-1.26	-0.33	-2.62	0.035846	0.140878	-4.18
257621_at	calmodulin-domain protein kinase CDPK	CPK9	AT3G20410	1.48	0.56	2.62	0.035825	0.140878	-4.18
253598_at	ribosomal protein S11 - like ribosomal p	---	AT4G30800	-1.80	-0.85	-2.62	0.035838	0.140878	-4.18
246505_at	putative protein hypothetical protein F1	---	AT5G16250	1.45	0.54	2.62	0.035841	0.140878	-4.18
246874_at	arabinosidase - like protein arabinosida	ASD2	AT5G26120	1.25	0.32	2.62	0.035864	0.140898	-4.18
259683_at	unknown protein	---	AT1G63050	-1.40	-0.49	-2.62	0.035859	0.140898	-4.18
258507_at	neutral invertase, putative similar to neu	---	AT3G06500	1.64	0.71	2.62	0.03587	0.140899	-4.19
266756_at	putative cytochrome P450	CYP709B2	AT2G46950	2.84	1.51	2.62	0.035886	0.140937	-4.19

249271_at	myosin heavy chain-like protein	CIP1	AT5G41790	-1.39	-0.48	-2.61	0.035912	0.141014	-4.19
247209_at	putative protein contains similarity to unl	---	AT5G64830	-1.22	-0.29	-2.61	0.035937	0.141074	-4.19
260275_at	hypothetical protein predicted by grail	---	AT1G80610	1.23	0.29	2.61	0.035942	0.141074	-4.19
264651_at	putative histone H2A Strong similarity t	H2AXA	AT1G08880	-1.44	-0.53	-2.61	0.035946	0.141074	-4.19
255963_at	unknown protein	MBD8	AT1G22310	-1.23	-0.30	-2.61	0.035953	0.141078	-4.19
265737_at	putative phosphatidic acid phosphatase	ATPAP1	AT2G01180	2.31	1.21	2.61	0.035966	0.141104	-4.19
258744_at	hypothetical protein similar to plant IF-li	---	AT3G05830	1.27	0.35	2.61	0.035992	0.141183	-4.19
247685_at	serine/threonine-specific protein kinase	---	AT5G59680	1.82	0.87	2.61	0.036011	0.141235	-4.19
262938_at	hypothetical protein predicted by genem	---	AT1G79540	-1.26	-0.33	-2.61	0.036018	0.141235	-4.19
249341_at	salt-inducible protein-like	---	AT5G41170	1.45	0.53	2.61	0.036031	0.141263	-4.19
248032_at	myosin heavy chain-like	---	AT5G55860	-1.31	-0.39	-2.61	0.036061	0.141358	-4.19
254080_at	fibrillarin 2 (AtFib2) identical to fibrillarin	FIB2	AT4G25630	-1.82	-0.86	-2.61	0.036078	0.141400	-4.19
257141_at	60S ribosomal protein L34, putative sim	---	AT3G28900	-1.47	-0.56	-2.61	0.036103	0.141409	-4.19
258907_at	putative sodium proton exchanger simila	NHX4	AT3G06370	1.26	0.33	2.61	0.036093	0.141409	-4.19
254545_at	putative protein FKBP-type peptidyl-pro	---	AT4G19830	-1.44	-0.52	-2.61	0.036112	0.141409	-4.19
262747_at	hypothetical protein predicted by genem	---	AT1G28540	-1.20	-0.26	-2.61	0.036109	0.141409	-4.19
248358_at	cytochrome P-450-like protein	CYP715A1	AT5G52400	1.63	0.70	2.61	0.036101	0.141409	-4.19
256479_at	unknown protein	---	AT1G33400	-1.32	-0.41	-2.61	0.036176	0.141637	-4.19
257965_at	unknown protein ;supported by full-leng	---	AT3G19900	1.38	0.46	2.61	0.036188	0.141653	-4.19
246267_at	Acyl CoA binding protein, putative conta	ACBP6	AT1G31812	-1.19	-0.25	-2.61	0.036193	0.141653	-4.19
259158_at	hypothetical protein predicted by gensc	---	AT3G05430	-1.19	-0.25	-2.61	0.036201	0.141657	-4.19
248181_at	cytochrome c biogenesis protein precurs	---	AT5G54290	-1.34	-0.42	-2.61	0.036206	0.141657	-4.19
252457_at	zinc-finger protein-like protein DNA binc	---	AT3G47180	1.21	0.27	2.61	0.036228	0.141694	-4.20
257838_at	hypothetical protein contains Pfam profil	---	AT3G25210	-1.20	-0.27	-2.61	0.036224	0.141694	-4.20
254972_at	putative protein more than 10 putative p	---	AT4G10440	1.25	0.32	2.61	0.036237	0.141705	-4.20
254571_at	hypothetical protein	---	AT4G19370	2.28	1.19	2.61	0.036259	0.141766	-4.20
259616_at	hypothetical protein contains similarity to	C/VIF1	AT1G47960	-1.40	-0.49	-2.61	0.036274	0.141802	-4.20
247038_at	anthranilate N-hydroxycinnamoyl/benzo	EPS1	AT5G67160	-1.33	-0.41	-2.61	0.036315	0.141881	-4.20
265960_at	putative histone H2B ;supported by full-	---	AT2G37470	-1.48	-0.57	-2.61	0.036326	0.141881	-4.20
265454_at	putative ARF1 family auxin responsive t	ARF11	AT2G46530	-1.92	-0.94	-2.61	0.036306	0.141881	-4.20
246224_at	putative MADS-box protein ;supported b	---	AT4G36590	1.32	0.40	2.61	0.036307	0.141881	-4.20
267392_at	putative beta-glucosidase	PEN2	AT2G44490	1.39	0.47	2.61	0.036322	0.141881	-4.20
246786_at	putative amino acid aminotransferase b	---	AT5G27410	-1.27	-0.35	-2.61	0.036347	0.141941	-4.20
245710_at	ferulate-5-hydroxylase	---	AT5G04330	1.34	0.42	2.60	0.036497	0.142478	-4.20
249443_at	putative protein ; supported by cDNA: g	---	AT5G39600	-1.32	-0.40	-2.60	0.036503	0.142478	-4.20

262919_at	unknown protein ; supported by cDNA: g	---	AT1G79380	1.33	0.41	2.60	0.036499	0.142478	-4.20
251175_at	homocysteine S-methyltransferase AtHM	HMT2	AT3G63250	-1.23	-0.30	-2.60	0.03651	0.142479	-4.20
245515_at	hypothetical protein	---	AT4G15810	-1.46	-0.54	-2.60	0.036519	0.142489	-4.20
247895_at	putative protein bHLH transcription fact	---	AT5G58010	1.22	0.29	2.60	0.036529	0.142505	-4.20
262749_at	lipase, putative contains Pfam profile: P	---	AT1G28580	1.23	0.30	2.60	0.036554	0.142577	-4.20
250953_at	putative protein ;supported by full-lengt	DPB	AT5G03415	-1.37	-0.45	-2.60	0.036609	0.142745	-4.21
245633_at	unknown protein similar to putative Tub	AtTLP10	AT1G25280	1.17	0.23	2.60	0.036608	0.142745	-4.21
250757_at	tetrahydrofolylpolyglutamate synthase-li	ATDFB	AT5G05980	-1.23	-0.30	-2.60	0.03662	0.142762	-4.21
245213_at	photosystem II 22kDa protein, putative	NPQ4	AT1G44575	-1.71	-0.78	-2.60	0.036634	0.142793	-4.21
251290_at	transcription factor BBFa	DAG1	AT3G61850	1.26	0.33	2.60	0.036651	0.142833	-4.21
262157_at	unknown protein contains similarity to bi	---	AT1G52670	-1.25	-0.32	-2.60	0.036677	0.142913	-4.21
250604_at	putative protein heparanase precursor,	PIP1B	AT2G45960 /	-1.38	-0.46	-2.60	0.036721	0.143042	-4.21
260466_at	phosphatidylinositol-4-phosphate 5-kina	---	AT1G10900	-1.57	-0.65	-2.60	0.036723	0.143042	-4.21
256432_at	hypothetical protein similar to hypothetic	---	AT3G10990	1.20	0.26	2.60	0.036778	0.143209	-4.21
258353_s_a	unknown protein similar to GB:AAD4976	YSL5	AT3G17650 /	-1.32	-0.41	-2.60	0.036779	0.143209	-4.21
258156_at	unknown protein ; supported by cDNA:	---	AT3G18050	-1.51	-0.60	-2.60	0.036796	0.143252	-4.21
251573_at	phenylalanine-tRNA synthetase-like pro	---	AT3G58140	-1.24	-0.32	-2.60	0.03683	0.143362	-4.21
245841_s_a	ribosomal protein S2, putative similar to	XW6	AT1G58380 /	-1.40	-0.48	-2.60	0.036855	0.143381	-4.21
245308_at	putative protein ; supported by cDNA: gi	---	AT4G17486	1.20	0.26	2.60	0.03685	0.143381	-4.21
252861_at	hypothetical protein	---	AT4G39820	1.40	0.48	2.60	0.03685	0.143381	-4.21
249339_at	putative protein similar to unknown prote	---	AT5G41100	1.94	0.96	2.60	0.03686	0.143381	-4.21
254140_at	putative protein	---	AT4G24610	-1.36	-0.44	-2.60	0.036918	0.143531	-4.21
247829_at	protein kinase - like protein kinase ATN	---	AT5G58520	-1.33	-0.41	-2.60	0.036909	0.143531	-4.21
259280_at	putative polypyrimidine tract-binding pro	PTB1	AT3G01150	-1.19	-0.25	-2.60	0.036912	0.143531	-4.21
254078_at	putative protein various predicted prote	---	AT4G25710	1.26	0.33	2.60	0.03693	0.143543	-4.21
261370_at	cell division-related protein, putative sim	---	AT1G53050	-1.21	-0.28	-2.60	0.036933	0.143543	-4.21
249124_at	disease resistance protein ; supported b	---	AT5G43740	1.22	0.29	2.59	0.036941	0.143548	-4.22
251023_at	putative protein amino acid transport pr	---	AT5G02170	1.26	0.34	2.59	0.036966	0.143619	-4.22
251672_at	MADS-box transcription factor-like prote	AGL16	AT3G57230	1.21	0.28	2.59	0.036996	0.143711	-4.22
266237_at	DNA-directed RNA polymerase 14 kDa	ATRPC14	AT2G29540	-1.40	-0.48	-2.59	0.037018	0.143750	-4.22
264871_at	pyruvate dehydrogenase E1 alpha subu	IAR4	AT1G24180	1.44	0.53	2.59	0.037014	0.143750	-4.22
257988_at	unknown protein ; supported by cDNA:	---	AT3G20870	-1.23	-0.30	-2.59	0.037064	0.143904	-4.22
260951_at	hypothetical protein similar to hypothetic	---	AT1G06145 /	-1.29	-0.37	-2.59	0.037148	0.144198	-4.22
258606_at	unknown protein ;supported by full-leng	---	AT3G02840	4.15	2.05	2.59	0.037159	0.144198	-4.22
250824_at	putative protein contains similarity to unl	---	AT5G05200	-1.32	-0.40	-2.59	0.037154	0.144198	-4.22

255540_at	putative SecA-type chloroplast protein tr	---	AT4G01800	-1.36	-0.44	-2.59	0.037172	0.144223	-4.22
252513_at	putative protein KIAA0776 protein, Hom	---	AT3G46220	-1.23	-0.30	-2.59	0.037179	0.144227	-4.22
245991_at	24 kDa vacuolar protein - like 24 kDa va	---	AT5G20660	-1.21	-0.28	-2.59	0.03719	0.144246	-4.22
254019_at	putative protein mature-parasite-infecte	---	AT4G26190	-1.17	-0.23	-2.59	0.037202	0.144266	-4.22
262231_at	putative receptor protein similar to viral	---	AT1G68740	-1.64	-0.72	-2.59	0.037218	0.144305	-4.22
254999_at	putative protein ; supported by full-lengt	---	AT4G09830	-1.31	-0.39	-2.59	0.037238	0.144337	-4.22
258642_at	unknown protein ;supported by full-leng	---	AT3G07910	-1.20	-0.26	-2.59	0.037239	0.144337	-4.22
267265_at	putative serine carboxypeptidase I ; sup	SCPL13	AT2G22980	-1.36	-0.45	-2.59	0.037261	0.144372	-4.22
263515_at	unknown protein	---	AT2G21640	2.04	1.03	2.59	0.037255	0.144372	-4.22
259770_s_a	phosphoribosylanthranilate isomerase i	PAI3	AT1G07780 /	-1.39	-0.47	-2.59	0.037299	0.144496	-4.23
258848_at	Expressed protein ; supported by full-ler	DCL2	AT3G03300 /	-1.22	-0.28	-2.59	0.037352	0.144678	-4.23
247345_at	putative protein contains similarity to AR	---	AT5G63760	-1.27	-0.35	-2.59	0.037373	0.144733	-4.23
267414_at	putative berberine bridge enzyme	MEE23	AT2G34790	1.44	0.52	2.59	0.037442	0.144956	-4.23
263469_at	putative Na+/H+ antiporter	ATCHX21	AT2G31910	1.21	0.28	2.59	0.037443	0.144956	-4.23
262031_x_a	hypothetical protein similar to putative A	---	---	1.23	0.29	2.59	0.037461	0.144999	-4.23
246441_at	putative protein ;supported by full-lengt	---	AT5G17560	-1.21	-0.27	-2.58	0.037492	0.145083	-4.23
258758_at	putative RING zinc finger protein contai	---	AT3G10810	-1.37	-0.46	-2.58	0.037495	0.145083	-4.23
260493_at	hypothetical protein predicted by gensca	---	AT2G41830	1.45	0.54	2.58	0.037525	0.145175	-4.23
264202_at	TINY-like transcription factor Contains s	---	AT1G22810	1.91	0.94	2.58	0.03754	0.145208	-4.23
253850_at	pectinesterase like protein pectinestera	sks10	AT4G28090	1.30	0.38	2.58	0.037568	0.145291	-4.23
259232_at	unknown protein similar to hypothetical p	---	AT3G11420	1.39	0.48	2.58	0.037576	0.145297	-4.23
258615_at	putative aspartyl protease contains Pfam	---	AT3G02740	1.30	0.38	2.58	0.037584	0.145303	-4.23
258818_at	putative ethylene receptor (EIN4) simila	EIN4	AT3G04580	1.27	0.35	2.58	0.037601	0.145343	-4.23
246421_at	TOM (target of myb1) -like protein TOM	---	AT5G16880	1.27	0.35	2.58	0.037625	0.145414	-4.23
248228_at	unknown protein ;supported by full-leng	---	AT5G53800	-1.32	-0.40	-2.58	0.037643	0.145433	-4.23
257389_at	hypothetical protein predicted by gensca	---	AT2G17970	-1.20	-0.27	-2.58	0.03764	0.145433	-4.23
262773_at	putative nuclear matrix constituent prote	LINC2	AT1G13220	-1.26	-0.33	-2.58	0.037658	0.145467	-4.23
256484_at	PPR-repeat protein contains multiple PF	---	AT1G31430	-1.25	-0.33	-2.58	0.037673	0.145495	-4.24
265797_at	Expressed protein ; supported by full-ler	---	AT2G35710	2.34	1.23	2.58	0.037678	0.145495	-4.24
254606_at	nodulin-26 - like protein major intrinsic p	NLM1	AT4G19030	1.19	0.25	2.58	0.03769	0.145517	-4.24
261694_at	60S ribosomal protein L10A, putative si	---	AT1G08360	-1.34	-0.43	-2.58	0.037698	0.145523	-4.24
265740_at	RING-H2 finger protein RHA2b identical	RHA2B	AT2G01150	-1.61	-0.69	-2.58	0.03774	0.145660	-4.24
254500_at	vacuolar sorting receptor-like protein BP	---	AT4G20110	1.59	0.67	2.58	0.037751	0.145676	-4.24
245731_at	MAP kinase, putative similar to MAP kir	MKK9	AT1G73500	1.53	0.62	2.58	0.037789	0.145783	-4.24
259765_at	unknown protein ;supported by full-lengt	---	AT1G64370	-1.35	-0.43	-2.58	0.037791	0.145783	-4.24

262616_at	oxidoreductase, putative contains Pfam	---	AT1G06620	1.51	0.59	2.58	0.037798	0.145784	-4.24
258733_at	unknown protein	---	---	1.20	0.26	2.58	0.037825	0.145864	-4.24
252931_at	putative ubiquitin-dependent proteolytic	---	AT4G38930	1.23	0.29	2.58	0.037853	0.145947	-4.24
244959_s_a	hypothetical protein	---	AT2G07708	-1.31	-0.39	-2.58	0.037895	0.146062	-4.24
266972_at	40S ribosomal protein S15A	---	AT2G39590	-1.20	-0.27	-2.58	0.037894	0.146062	-4.24
249757_at	Expressed protein ; supported by full-ler	---	AT5G24316	1.26	0.34	2.58	0.037958	0.146278	-4.24
262058_at	Expressed protein ; supported by full-ler	---	AT1G79990	1.18	0.23	2.58	0.037972	0.146279	-4.24
260603_at	membrane related protein CP5, putative	---	AT1G55960	1.38	0.46	2.58	0.037977	0.146279	-4.24
252222_at	putative protein various predicted prote	---	AT3G49840 /	1.54	0.62	2.58	0.037971	0.146279	-4.24
256513_at	unknown protein similar to phospholipas	SGR2	AT1G31480	-1.21	-0.28	-2.58	0.037991	0.146292	-4.24
264639_at	unknown protein similar to ubiquitin C-te	UCH2	AT1G65650	-1.28	-0.35	-2.58	0.037994	0.146292	-4.24
258812_at	unknown protein similar to GB:AAD1064	ECT1	AT3G03950	-1.27	-0.34	-2.57	0.038007	0.146319	-4.24
260522_x_a	hypothetical protein predicted by genefir	---	AT2G41730	2.98	1.57	2.57	0.03803	0.146382	-4.24
262558_at	Expressed protein ; supported by full-ler	---	AT1G31335	-1.25	-0.33	-2.57	0.038062	0.146482	-4.25
266815_at	F-box protein family, AtFBX5 contains s	---	AT2G44900	-1.27	-0.34	-2.57	0.038078	0.146517	-4.25
255556_at	putative NifU-like metallocluster assem	NFU1	AT4G01940	-1.31	-0.38	-2.57	0.038095	0.146560	-4.25
253594_at	Expressed protein ; supported by full-ler	---	AT4G30820	-1.27	-0.34	-2.57	0.03811	0.146591	-4.25
246028_at	AKIN beta1 ; supported by full-length cl	---	AT5G21170	1.39	0.47	2.57	0.038127	0.146609	-4.25
246059_at	putative protein KED, Nicotiana tabacu	---	AT5G08450	-1.21	-0.27	-2.57	0.038124	0.146609	-4.25
265715_s_a	expressed protein non-consensus GA d	---	AT1G13860 /	-1.47	-0.55	-2.57	0.038142	0.146642	-4.25
264424_at	unknown protein similar to hypothetical	---	AT1G61740	-1.29	-0.37	-2.57	0.038164	0.146701	-4.25
258736_at	unknown protein	---	AT3G05900	-1.38	-0.47	-2.57	0.0382	0.146765	-4.25
249607_at	putative protein RING-H2 finger protein	---	AT5G37280	1.21	0.27	2.57	0.0382	0.146765	-4.25
254386_at	peroxidase prxr1 ;supported by full-leng	PRXR1	AT4G21960	-1.50	-0.59	-2.57	0.038194	0.146765	-4.25
260049_at	DNA-directed RNA polymerase subunit	NRPA2	AT1G29940	-1.49	-0.58	-2.57	0.038223	0.146829	-4.25
259106_at	unknown protein ;supported by full-leng	RALFL22	AT3G05490	1.64	0.72	2.57	0.038231	0.146830	-4.25
260445_at	ARG1 protein (Altered Response to Gra	ARG1	AT1G68370	1.27	0.34	2.57	0.038236	0.146830	-4.25
246326_at	unknown protein ; supported by cDNA: g	REV7	AT1G16590	-1.20	-0.27	-2.57	0.038249	0.146855	-4.25
249810_at	unknown protein	---	AT5G23920	-1.38	-0.47	-2.57	0.038258	0.146866	-4.25
257319_at	hypothetical protein	---	---	-1.34	-0.42	-2.57	0.03827	0.146886	-4.25
267130_at	hypothetical protein predicted by gensca	---	AT2G23390	-1.34	-0.42	-2.57	0.038319	0.147049	-4.25
260335_at	putative strictosidine synthase similar to	SS3	AT1G74000	1.67	0.74	2.57	0.038347	0.147133	-4.25
246532_at	putative protein beta-glucan-elicitor rec	---	AT5G15870	2.28	1.19	2.57	0.038388	0.147263	-4.25
248170_at	ankyrin-repeat-containing protein-like	---	AT5G54620	1.32	0.40	2.57	0.038399	0.147280	-4.25
265753_at	putative Athila retroelement ORF1 prote	---	---	-1.17	-0.22	-2.57	0.038406	0.147282	-4.25

258563_at	putative long-chain-fatty-acid--CoA ligas	LACS6	AT3G05970	1.24	0.32	2.57	0.038416	0.147296	-4.26
265244_at	putative amine oxidase	ATPAO2	AT2G43018 /	-1.49	-0.58	-2.57	0.038425	0.147306	-4.26
247648_at	laccase - like protein laccase LAC2-4, L	LAC17	AT5G60020	1.26	0.34	2.57	0.038452	0.147338	-4.26
245687_at	unknown protein	DEG15	AT1G28320	-1.17	-0.23	-2.57	0.038452	0.147338	-4.26
250893_at	putative protein predicted proteins - Aral	EMB175	AT5G03795 /	1.20	0.26	2.57	0.038441	0.147338	-4.26
255247_at	hypothetical protein	---	---	-1.17	-0.23	-2.57	0.038474	0.147396	-4.26
258202_at	unknown protein	---	AT3G13940	-1.42	-0.50	-2.57	0.03853	0.147510	-4.26
262039_at	adenine phosphoribosyltransferase almo	APT2	AT1G80050	1.32	0.40	2.57	0.03852	0.147510	-4.26
258862_at	putative mitochondrial processing peptid	MPPBETA	AT3G02090	1.23	0.30	2.57	0.038529	0.147510	-4.26
251812_at	hypothetical protein ;supported by full-le	---	AT3G54970	-1.32	-0.40	-2.57	0.038513	0.147510	-4.26
263644_at	hypothetical protein predicted by gensca	---	AT2G04730	1.23	0.30	2.57	0.038547	0.147553	-4.26
245141_at	putative flavonol reductase	BEN1	AT2G45400	-1.26	-0.34	-2.56	0.038598	0.147723	-4.26
255071_at	putative protein putative chloroplast 31	---	AT4G09040	-1.25	-0.32	-2.56	0.038606	0.147728	-4.26
253828_at	putative protein predicted protein, Arabi	SLAH2	AT4G27970	1.30	0.38	2.56	0.03863	0.147737	-4.26
264213_at	hypothetical protein contains similarity to	ATPP2-A5	AT1G65390	2.86	1.51	2.56	0.038641	0.147737	-4.26
263284_at	unknown protein	---	AT2G36100	1.22	0.29	2.56	0.038624	0.147737	-4.26
254160_at	putative protein ;supported by full-lengt	SLY1	AT4G24210	-1.30	-0.38	-2.56	0.038622	0.147737	-4.26
248821_at	protein serine threonine kinase-like	---	AT5G47070	1.59	0.67	2.56	0.038637	0.147737	-4.26
246782_at	putative protein PrMC3 - Pinus radiata,	GID1C	AT5G27320	-1.51	-0.59	-2.56	0.038658	0.147779	-4.26
262107_at	hypothetical protein predicted by genem	---	AT1G02750	1.20	0.27	2.56	0.038685	0.147819	-4.26
266335_at	putative cytochrome P450 ; supported b	KAO2	AT2G32440	-1.43	-0.51	-2.56	0.038684	0.147819	-4.26
259548_at	hypothetical protein similar to ripening-in	MLP165	AT1G35260	1.64	0.72	2.56	0.038688	0.147819	-4.26
250004_at	putative protein predicted proteins - Aral	---	AT5G18750	-1.32	-0.40	-2.56	0.038698	0.147833	-4.26
258375_at	hypothetical protein predicted by genesc	---	AT3G17470	-1.20	-0.27	-2.56	0.038706	0.147839	-4.26
251122_at	protein kinase -like protein serine/threo	---	AT5G01020	-1.34	-0.42	-2.56	0.038728	0.147898	-4.26
264523_at	unknown protein Location of EST gb|T4	ERG28	AT1G10030	-1.20	-0.26	-2.56	0.038749	0.147952	-4.26
245093_at	hypothetical protein predicted by gensca	---	AT2G40815 /	-1.23	-0.30	-2.56	0.038794	0.148097	-4.27
263704_at	unknown protein similar to unknown pro	---	AT1G31130	1.28	0.36	2.56	0.038875	0.148382	-4.27
250034_at	apyrase (gb|AAF00612.1) ; supported b	ATAPY2	AT5G18280	1.26	0.33	2.56	0.038889	0.148399	-4.27
265990_at	putative prolylcarboxypeptidase	---	AT2G24280	-1.39	-0.47	-2.56	0.038892	0.148399	-4.27
252808_at	putative protein various predicted prote	---	---	1.26	0.33	2.56	0.038908	0.148433	-4.27
262625_at	hypothetical protein predicted by genem	---	AT1G06440	-1.19	-0.25	-2.56	0.03893	0.148468	-4.27
247237_at	auxin-independent growth promoter-like	---	AT5G64600	-1.26	-0.33	-2.56	0.038927	0.148468	-4.27
260849_at	pectinesterase, putative similar to pecti	sks7	AT1G21860	1.19	0.25	2.56	0.038967	0.148587	-4.27
259090_at	putative ribosomal protein s19 or s24 sir	---	AT3G04920	-1.42	-0.51	-2.56	0.038977	0.148598	-4.27

259723_at	putative iron-regulated transporter simila	IRT3	AT1G60960	-1.57	-0.65	-2.56	0.03904	0.148783	-4.27
262245_at	unknown protein	NPSN12	AT1G48240	-1.30	-0.38	-2.56	0.039045	0.148783	-4.27
258892_at	unknown protein	---	AT3G05670	-1.21	-0.28	-2.56	0.039039	0.148783	-4.27
248575_at	ATP-dependent Clp protease ATP-bind	---	AT5G49840	-1.20	-0.26	-2.56	0.039059	0.148810	-4.27
261450_s_a	O-methyltransferase, putative similar to	---	AT1G21110 /	4.51	2.17	2.56	0.03907	0.148828	-4.27
256553_at	hypothetical protein contains similarity to	---	---	1.22	0.29	2.56	0.039082	0.148849	-4.27
258099_at	unknown protein similar to hypothetical	---	AT3G23540	1.22	0.28	2.56	0.039091	0.148857	-4.27
259628_at	hypothetical protein contains Pfam profil	---	AT1G56440	-1.34	-0.43	-2.55	0.039119	0.148892	-4.27
249299_at	E2, ubiquitin-conjugating enzyme 4 (UB	UBC4	AT5G41340	-1.28	-0.36	-2.55	0.039117	0.148892	-4.27
255869_at	unknown protein	---	AT2G30270	1.25	0.33	2.55	0.039109	0.148892	-4.27
247407_at	putative protein predicted proteins, Aral	---	AT5G62900	1.31	0.39	2.55	0.039141	0.148949	-4.27
249700_at	40S ribosomal protein S3 ; supported b	---	AT5G35530	-1.30	-0.38	-2.55	0.039152	0.148966	-4.27
249403_at	putative protein intracellular protein Mg	---	AT5G40270	-1.30	-0.38	-2.55	0.039196	0.149108	-4.28
251624_at	hypothetical protein ;supported by full-le	---	AT3G57280	1.29	0.37	2.55	0.039236	0.149236	-4.28
252910_at	putative protein various predicted prote	---	AT4G39590	-1.18	-0.24	-2.55	0.039248	0.149257	-4.28
252421_at	endochitinase-like protein BASIC ENDO	---	AT3G47540	3.11	1.64	2.55	0.039257	0.149269	-4.28
251756_at	putative protein	---	AT3G55820	1.20	0.26	2.55	0.039293	0.149378	-4.28
AFFX-ThrX-	B. subtilis /GEN=thrB /DB_XREF=gb:X0	---	---	-1.42	-0.50	-2.55	0.03931	0.149418	-4.28
258962_at	putative cytochrome P450 similar to cyto	CYP77A6	AT3G10570	2.88	1.53	2.55	0.039326	0.149454	-4.28
253566_at	DNA topoisomerase like- protein Bacillu	---	AT4G31210	-1.76	-0.81	-2.55	0.039342	0.149466	-4.28
251173_at	putative protein hypothetical protein AT	---	AT3G63270	-1.18	-0.24	-2.55	0.039339	0.149466	-4.28
260790_at	hypothetical protein predicted by gensca	---	AT1G06240	-1.39	-0.47	-2.55	0.039435	0.149794	-4.28
259956_at	unknown protein ;supported by full-leng	RRA2	AT1G75110	-1.21	-0.28	-2.55	0.03946	0.149821	-4.28
261867_at	unknown protein ; supported by cDNA: g	---	AT1G50575	-1.25	-0.33	-2.55	0.03945	0.149821	-4.28
248855_at	NAM-like	anac096	AT5G46590	1.45	0.53	2.55	0.039462	0.149821	-4.28
256399_at	hypothetical protein predicted by genefir	---	AT3G06240	-1.22	-0.29	-2.55	0.039472	0.149834	-4.28
259642_at	hypothetical protein predicted by gensca	---	AT1G69030	1.36	0.45	2.55	0.039528	0.149959	-4.28
246260_at	amino acid permease, putative contains	---	AT1G31820	-1.32	-0.40	-2.55	0.039538	0.149959	-4.28
256916_at	GATA transcription factor 1 (AtGATA-1)	---	AT3G24050	1.29	0.37	2.55	0.039529	0.149959	-4.28
260887_at	ascorbate oxidase promoter-binding pro	---	AT1G29160	1.96	0.97	2.55	0.039529	0.149959	-4.28
246257_at	splicing factor-like protein	ATU2AF65	AT4G36690	-1.22	-0.29	-2.55	0.039535	0.149959	-4.28
245237_at	putative protein similarity to ALR - Homo	SLK1	AT4G25520	-1.20	-0.27	-2.55	0.039556	0.150002	-4.28
263545_at	unknown protein	---	AT2G21560	-1.64	-0.71	-2.55	0.039568	0.150025	-4.29
258544_at	disease resistance gene (RPM1) identic	RPM1	AT3G07040	1.44	0.53	2.55	0.039585	0.150037	-4.29
254613_at	ankyrin-like protein ankyrin 3, Mus mus	---	AT4G19150	-1.23	-0.30	-2.55	0.039583	0.150037	-4.29

264818_at	hypothetical protein similar to hypothetic	NAF1	AT1G03530	-1.56	-0.64	-2.55	0.039598	0.150064	-4.29
259597_at	ATP-dependent RNA helicase, putative	---	AT1G27900	-1.26	-0.33	-2.55	0.039607	0.150071	-4.29
262050_at	unknown protein ;supported by full-lengt	---	AT1G80130	-2.39	-1.26	-2.55	0.039634	0.150150	-4.29
258775_at	hydroxyacylglutathione hydrolase cytop	GLY2	AT3G10850	-1.22	-0.29	-2.55	0.039642	0.150155	-4.29
254233_at	98b like protein 98b - Daucus carota (ca	---	AT4G23800	1.41	0.49	2.55	0.039652	0.150169	-4.29
263658_at	unknown protein EST gb|T21788 comes	---	AT1G04490	1.21	0.27	2.55	0.039659	0.150171	-4.29
253229_at	putative protein ;supported by full-lengt	---	AT4G34660	1.16	0.21	2.54	0.039728	0.150405	-4.29
254551_at	lectin like protein lectin phloem protein	ATPP2-A1	AT4G19840	-1.28	-0.36	-2.54	0.039736	0.150411	-4.29
266270_at	putative glutathione S-transferase ; sup	ATGSTU3	AT2G29470	3.84	1.94	2.54	0.039747	0.150422	-4.29
266482_at	putative small nuclear ribonucleoprotein	---	AT2G47640	-1.30	-0.38	-2.54	0.03978	0.150422	-4.29
263322_at	putative ribonuclease E	RNEE/G	AT2G04270	-1.40	-0.48	-2.54	0.039775	0.150422	-4.29
261592_at	double-stranded RNA-specific editase,	---	AT1G01760	1.25	0.32	2.54	0.039777	0.150422	-4.29
248758_at	RNA-binding protein-like ;supported by	---	AT5G47620	-1.27	-0.35	-2.54	0.03976	0.150422	-4.29
247445_at	putative protein similar to unknown prote	---	AT5G62640	1.23	0.30	2.54	0.039785	0.150422	-4.29
266908_at	putative protein kinase contains a protei	PID	AT2G34650	1.64	0.71	2.54	0.039762	0.150422	-4.29
251867_at	SKP1 interacting partner 5 (SKIP5)	SKIP5	AT3G54480	1.20	0.26	2.54	0.03982	0.150530	-4.29
251185_at	60S RIBOSOMAL PROTEIN L7A prote	---	AT3G62870	-1.31	-0.39	-2.54	0.039853	0.150593	-4.29
253167_at	calmodulin-domain protein kinase CDPK	CPK5	AT4G35310	1.28	0.36	2.54	0.039848	0.150593	-4.29
260416_at	putative cullin similar to cullin 3 GB:4503	CUL3B	AT1G69670	-1.22	-0.28	-2.54	0.039857	0.150593	-4.29
260535_at	hypothetical protein predicted by gensca	---	AT2G43390	1.18	0.24	2.54	0.039872	0.150627	-4.29
255702_at	subtilisin-like serine protease XSP1 iden	XSP1	AT4G00230	1.36	0.44	2.54	0.039889	0.150641	-4.29
249237_at	putative protein similar to unknown prote	---	AT5G42050	1.37	0.45	2.54	0.039884	0.150641	-4.29
246778_at	mevalonate kinase supported by full-len	MK	AT5G27450	1.26	0.33	2.54	0.03991	0.150694	-4.29
261255_at	hypothetical protein contains similarity to	ATNTH2	AT1G05900	-1.26	-0.33	-2.54	0.039922	0.150714	-4.29
259672_at	DNA-directed RNA polymerase identica	---	AT1G68990	-1.67	-0.74	-2.54	0.039989	0.150933	-4.30
262506_at	unknown protein Similar to gb|X84260 F	NADK2	AT1G21640	-1.34	-0.42	-2.54	0.039993	0.150933	-4.30
250079_at	putative protein similar to unknown prote	---	AT5G16650	1.27	0.34	2.54	0.040035	0.151025	-4.30
262547_at	hypothetical protein predicted by genem	---	AT1G31270	1.18	0.23	2.54	0.040037	0.151025	-4.30
262111_at	hypothetical protein predicted by genem	---	AT1G02960	-1.21	-0.28	-2.54	0.040035	0.151025	-4.30
256113_at	unknown protein ;supported by full-lengt	---	AT1G16810	-1.26	-0.33	-2.54	0.040056	0.151070	-4.30
263031_at	glucosyltransferase, putative similar to	ATCSLA1(	AT1G24070	-2.55	-1.35	-2.54	0.040071	0.151077	-4.30
253021_at	putative protein permease 1 - Mesembr	---	AT4G38050	-1.25	-0.32	-2.54	0.040069	0.151077	-4.30
266452_at	hypothetical protein predicted by gensca	---	AT2G43320	1.37	0.45	2.54	0.04008	0.151085	-4.30
255208_at	see GB:AL022580	---	---	1.22	0.29	2.54	0.040112	0.151160	-4.30
253806_at	putative protein Arabidopsis thaliana RI	---	AT4G28270	-1.29	-0.36	-2.54	0.040113	0.151160	-4.30

262462_at	hypothetical protein predicted by genem	---	AT1G50350	1.19	0.26	2.54	0.040133	0.151188	-4.30
266399_at	putative phospholipid cytidylyltransferas	PECT1	AT2G38670	-1.28	-0.35	-2.54	0.040129	0.151188	-4.30
251342_at	putative protein SAUR-AC1, Arabidopsi	---	AT3G60690	-1.33	-0.41	-2.54	0.04015	0.151225	-4.30
266819_at	unknown protein ;supported by full-leng	---	AT2G44870	-1.30	-0.38	-2.54	0.040176	0.151257	-4.30
251869_at	putative protein	---	AT3G54500	-1.42	-0.50	-2.54	0.040171	0.151257	-4.30
249916_at	histone H2B like protein (emb|CAA6902	HTB2	AT5G22880	-1.38	-0.47	-2.54	0.040178	0.151257	-4.30
267397_at	hypothetical protein predicted by gensca	---	AT1G76170	-1.44	-0.53	-2.54	0.040188	0.151268	-4.30
258183_at	unknown protein ;supported by full-leng	---	AT3G21550	1.96	0.97	2.54	0.040212	0.151334	-4.30
256231_at	unknown protein ; supported by full-leng	---	AT3G12630	1.21	0.27	2.53	0.040254	0.151467	-4.30
246344_at	putative protein predicted proteins - Ara	---	AT3G56730	-1.47	-0.56	-2.53	0.040262	0.151474	-4.30
252395_at	H+-transporting ATPase - like protein H	AHA4	AT3G47950	-1.37	-0.45	-2.53	0.040274	0.151491	-4.30
262883_at	ammonium transporter, puitative similar	ATAMT1;2	AT1G64780	-1.42	-0.51	-2.53	0.040296	0.151549	-4.30
245810_at	axi 1 protein, putative similar to axi 1 pr	---	AT1G38065 /	-1.24	-0.31	-2.53	0.040314	0.151592	-4.30
259899_at	hypothetical protein predicted by gensca	---	AT1G71210	-1.31	-0.39	-2.53	0.040334	0.151609	-4.30
266149_x_a	En/Spm-like transposon protein related	---	---	1.22	0.29	2.53	0.040345	0.151609	-4.31
266497_at	putative retroelement pol polyprotein	---	---	1.25	0.32	2.53	0.040339	0.151609	-4.30
266349_at	unknown protein predicted by genscan	---	AT2G01460	1.23	0.30	2.53	0.040337	0.151609	-4.30
245599_at	RING-H2 finger protein RHF1a	RHF1A	AT4G14220	1.37	0.46	2.53	0.040366	0.151644	-4.31
252200_at	anthranilate N-hydroxycinnamoyl/benzo	---	AT3G50280	1.84	0.88	2.53	0.040373	0.151644	-4.31
260588_at	unknown protein contains similarity to tu	AtTLP7	AT1G53320	-1.28	-0.35	-2.53	0.040374	0.151644	-4.31
248764_at	putative protein contains similarity to CC	NF-YB2	AT5G47640	-1.29	-0.37	-2.53	0.040384	0.151656	-4.31
250792_at	unknown protein ;supported by full-leng	---	AT5G05520	-1.23	-0.30	-2.53	0.040424	0.151756	-4.31
265929_s_a	putative flavonol 3-O-glucosyltransferas	---	AT2G18560 /	-1.44	-0.52	-2.53	0.040418	0.151756	-4.31
265003_at	protein kinase, putative similar to protei	---	AT1G26970	1.17	0.22	2.53	0.040432	0.151763	-4.31
265723_at	putative disease resistance protein	---	AT2G32140	1.18	0.24	2.53	0.040471	0.151884	-4.31
254442_at	putative protein predicted protein T7N9	---	AT4G21060	-1.21	-0.28	-2.53	0.040499	0.151918	-4.31
252502_at	copper transport protein - like protein c	COPT2	AT3G46900	-1.79	-0.84	-2.53	0.040493	0.151918	-4.31
257749_at	actin 2 identical to GB:AAB37098 from	ACT2	AT3G18780	1.20	0.26	2.53	0.0405	0.151918	-4.31
266265_at	putative tropinone reductase ; supporte	---	AT2G29340	-1.38	-0.47	-2.53	0.040555	0.152098	-4.31
257607_at	hypothetical protein predicted by gensca	---	AT3G13880	-1.18	-0.23	-2.53	0.040604	0.152181	-4.31
260143_at	sucrose transport protein SUC1 identica	SUC1	AT1G71880	1.63	0.70	2.53	0.040598	0.152181	-4.31
251727_at	putative protein	---	AT3G56290	-1.58	-0.66	-2.53	0.040598	0.152181	-4.31
259026_at	putative protein kinase similar to hypoth	---	AT3G09240	1.25	0.32	2.53	0.040599	0.152181	-4.31
262480_at	receptor kinase, putative similar to rece	---	AT1G11340	-1.47	-0.55	-2.53	0.04063	0.152254	-4.31
261034_s_a	hypothetical protein predicted by genem	---	AT1G17450 /	-1.31	-0.39	-2.53	0.040653	0.152291	-4.31

250492_at	putative protein Requiem protein, Xeno	ATXR5	AT5G09790	1.24	0.31	2.53	0.040648	0.152291	-4.31
264433_at	beta-glucosidase, putative similar to be	BGLU45	AT1G61810	2.64	1.40	2.53	0.04067	0.152310	-4.31
255379_at	putative M-type thioredoxin similar to A	ATHM2	AT4G03520	-1.18	-0.24	-2.53	0.040672	0.152310	-4.31
266523_at	putative transportin	TRN1	AT2G16950	1.21	0.27	2.53	0.040688	0.152345	-4.31
250883_at	putative protein predicted proteins, Aral	---	AT5G03970	-1.30	-0.38	-2.53	0.040698	0.152358	-4.31
245123_at	unknown protein ; supported by cDNA:	CAO	AT2G47450	-1.26	-0.33	-2.53	0.040723	0.152381	-4.31
247701_at	putative protein many predicted protein	---	AT5G59900	-1.21	-0.27	-2.53	0.040731	0.152381	-4.31
253204_at	GTP binding protein beta subunit ; supp	AGB1	AT4G34460	1.18	0.24	2.53	0.040724	0.152381	-4.31
245279_at	putative protein ; supported by cDNA: gi	---	AT4G17270	1.21	0.28	2.53	0.040731	0.152381	-4.31
245144_at	putative methionine aminopeptidase ;su	MAP1A	AT2G45240	-1.24	-0.31	-2.53	0.040746	0.152413	-4.32
267116_at	unknown protein	---	AT2G32560	-1.48	-0.57	-2.53	0.040788	0.152546	-4.32
256289_s_a	serine carboxypeptidase, putative conta	scpl14	AT3G12230 /	1.66	0.73	2.53	0.0408	0.152566	-4.32
267067_at	unknown protein	---	AT2G41020	-1.31	-0.39	-2.53	0.04081	0.152578	-4.32
250386_at	MYB like protein MYB like protein, Dicty	MYB3R-4	AT5G11510	1.28	0.36	2.52	0.040831	0.152605	-4.32
252398_at	putative protein RING-H2 finger protein	---	AT3G47990	-1.23	-0.30	-2.52	0.040829	0.152605	-4.32
267023_at	putative protein transport protein SEC61	---	AT2G34250	1.28	0.35	2.52	0.040886	0.152788	-4.32
245193_at	F12A21.6 hypothetical protein	SUFE2	AT1G67810	2.09	1.07	2.52	0.040925	0.152906	-4.32
247285_at	putative protein similar to unknown prote	---	AT5G64400	1.20	0.27	2.52	0.040947	0.152965	-4.32
267405_at	putative related to microbial divalent cat	CUTA	AT2G33740	-1.20	-0.26	-2.52	0.040955	0.152970	-4.32
259436_at	hypothetical protein predicted by genem	---	AT1G01500	-1.22	-0.28	-2.52	0.040983	0.153025	-4.32
247009_at	unknown protein ;supported by full-leng	---	AT5G67600	1.51	0.59	2.52	0.040981	0.153025	-4.32
248199_at	membrane related protein-like ;supporte	---	AT5G54170	1.55	0.64	2.52	0.041043	0.153197	-4.32
258863_at	unknown protein similar to RNA helicase	DCL2	AT3G03300	-1.40	-0.49	-2.52	0.041037	0.153197	-4.32
246423_at	putative protein ribosomal protein L18,	---	AT5G16950	-1.30	-0.38	-2.52	0.041062	0.153244	-4.32
250513_at	protein kinase ;supported by full-length	---	AT5G09890	1.22	0.28	2.52	0.041083	0.153271	-4.32
245034_at	putative serpin	---	AT2G26390	1.30	0.37	2.52	0.041076	0.153271	-4.32
260834_at	sugar kinase, putative similar to ribokina	---	AT1G06730	-1.28	-0.36	-2.52	0.041106	0.153311	-4.32
247137_at	calcium-dependent protein kinase ;supp	CPK28	AT5G66210	1.60	0.68	2.52	0.041107	0.153311	-4.32
264223_s_a	receptor kinase, putative similar to rece	---	AT1G67520 /	1.66	0.73	2.52	0.041132	0.153360	-4.32
256976_at	unknown protein similar to putative retro	---	---	-1.34	-0.43	-2.52	0.041133	0.153360	-4.32
251925_at	hypothetical protein ;supported by full-le	---	AT3G54000	1.38	0.47	2.52	0.041149	0.153368	-4.33
254059_at	Arabidopsis mitochondrion-localized sm	ATHSP23.	AT4G25200	1.29	0.37	2.52	0.041148	0.153368	-4.33
251024_at	putative protein hypothetical proteins - A	---	AT5G02180	1.28	0.35	2.52	0.041167	0.153384	-4.33
249295_at	putative protein contains similarity to un	---	AT5G41280	1.18	0.24	2.52	0.041163	0.153384	-4.33
250649_at	thioredoxin-like ; supported by cDNA: g	WCRKC1	AT5G06690	-1.26	-0.33	-2.52	0.041187	0.153432	-4.33

267312_at	unknown protein	---	AT2G34750	-1.31	-0.38	-2.52	0.041257	0.153668	-4.33
251964_at	hypothetical protein ; supported by cDN	---	AT3G53370	-1.38	-0.47	-2.52	0.041276	0.153715	-4.33
260537_at	hypothetical protein predicted by gensca	---	AT2G43450	1.17	0.23	2.52	0.041309	0.153778	-4.33
266700_at	60S ribosomal protein L31 ; supported	---	AT2G19740	-1.32	-0.40	-2.52	0.041328	0.153778	-4.33
246352_at	hypothetical protein	---	---	1.17	0.23	2.52	0.041333	0.153778	-4.33
260785_at	hypothetical protein predicted by gensca	---	AT1G06200	-1.22	-0.28	-2.52	0.041318	0.153778	-4.33
259191_at	unknown protein	---	AT3G01720	1.28	0.36	2.52	0.041302	0.153778	-4.33
262805_at	putative DNA-binding protein similar to	ESC	AT1G20900	1.21	0.27	2.52	0.041322	0.153778	-4.33
251082_at	chlorophyll a/b-binding protein CP29 ; s	---	AT5G01530	-1.16	-0.22	-2.52	0.041365	0.153870	-4.33
256984_at	hypothetical protein predicted by gensca	---	AT3G13480	-1.26	-0.33	-2.52	0.041372	0.153870	-4.33
267490_at	putative receptor-like protein kinase	---	AT2G19130	1.49	0.57	2.52	0.041399	0.153947	-4.33
246917_at	serine-rich protein ;supported by full-ler	---	AT5G25280	-1.48	-0.56	-2.51	0.041488	0.154253	-4.33
263709_at	unknown protein ESTs gb|T20589, gb|T	---	AT1G09310	2.92	1.54	2.51	0.041531	0.154273	-4.33
244949_at	hypothetical protein	---	---	-1.24	-0.31	-2.51	0.041521	0.154273	-4.33
266425_at	putative strictosidine synthase	---	AT2G41300	1.24	0.31	2.51	0.041513	0.154273	-4.33
251313_at	putative protein several hypothetical pro	---	AT3G61360	-1.23	-0.30	-2.51	0.041536	0.154273	-4.33
254247_at	putative protein receptor protein kinase	---	AT4G23260	1.52	0.61	2.51	0.041504	0.154273	-4.33
259097_at	unknown protein similar to GB:AAD491(	---	AT3G04830	-1.20	-0.26	-2.51	0.041536	0.154273	-4.33
262028_at	DNA binding protein, putative similar to	---	AT1G35560	-1.21	-0.27	-2.51	0.041541	0.154273	-4.33
250720_at	putative protein similar to unknown prote	---	AT5G06180	-1.34	-0.42	-2.51	0.041552	0.154290	-4.34
259580_at	oxidoreductase, putative contains Pfam	---	AT1G28030	1.29	0.36	2.51	0.041559	0.154290	-4.34
264851_at	putative calmodulin-domain protein kina	CPK6	AT2G17290	1.45	0.54	2.51	0.041587	0.154345	-4.34
266852_at	hypothetical protein predicted by gensca	---	AT2G26810	-1.21	-0.28	-2.51	0.041586	0.154345	-4.34
251345_at	putative protein hypothetical proteins - A	---	AT3G60940	1.22	0.29	2.51	0.0416	0.154366	-4.34
260221_at	GAST1-like protein similar to GAST1 pr	---	AT1G74670	2.68	1.42	2.51	0.041647	0.154372	-4.34
267315_at	putative CCAAT-binding transcription fa	NF-YA4	AT2G34720	-1.37	-0.45	-2.51	0.041617	0.154372	-4.34
259441_at	cathepsin B-like cysteine protease, puta	---	AT1G02300	-1.29	-0.36	-2.51	0.041614	0.154372	-4.34
249666_at	phytochrome C (sp|P14714)	PHYC	AT5G35840	-1.29	-0.36	-2.51	0.041646	0.154372	-4.34
254371_at	beta-glucosidase -like protein beta-gluc	BGLU47	AT4G21760	1.20	0.26	2.51	0.041626	0.154372	-4.34
263404_s_a	hypothetical protein similar to hypothetic	---	AT2G04090 /	1.93	0.95	2.51	0.041642	0.154372	-4.34
249034_at	putative protein contains similarity to zin	NUC	AT5G44160	-1.24	-0.31	-2.51	0.041649	0.154372	-4.34
267136_at	putative GTP-binding protein (extra larg	XLG1	AT2G23460	-1.23	-0.30	-2.51	0.04168	0.154438	-4.34
246945_s_a	putative membrane protein hypothetica	---	AT5G25040 /	1.24	0.31	2.51	0.04168	0.154438	-4.34
265871_at	unknown protein ;supported by full-leng	---	AT2G01680	-1.31	-0.39	-2.51	0.041704	0.154500	-4.34
260714_at	chaperonin CPN10 identical to SP:P348	CPN10	AT1G14980	-1.46	-0.55	-2.51	0.041712	0.154505	-4.34

259603_at	Expressed protein ; supported by full-ler	---	AT1G56500	-1.36	-0.44	-2.51	0.041744	0.154524	-4.34
249059_at	subtilisin-like serine protease contains s	---	AT5G44530	-1.38	-0.47	-2.51	0.041732	0.154524	-4.34
256766_at	Expressed protein ; supported by cDNA	PCC1	AT3G22231	7.38	2.88	2.51	0.041741	0.154524	-4.34
261892_at	transcription factor, putative similar to W	WRKY40	AT1G80840	3.49	1.80	2.51	0.041742	0.154524	-4.34
248308_at	putative protein similar to unknown prote	---	AT5G52530	1.21	0.27	2.51	0.041851	0.154850	-4.34
264956_at	unknown protein similar to putative uridy	ACR3	AT1G76990	-1.73	-0.79	-2.51	0.041841	0.154850	-4.34
266431_at	Mutator-like transposase similar to MUF	---	---	-1.22	-0.28	-2.51	0.041852	0.154850	-4.34
265602_at	putative retroelement pol polyprotein	---	---	1.25	0.33	2.51	0.04191	0.155038	-4.34
263108_at	hypothetical protein similar to putative a	---	AT1G65240	1.93	0.95	2.51	0.041941	0.155064	-4.34
259919_at	putative exportin, tRNA (nuclear export	PSD	AT1G72560	-1.31	-0.39	-2.51	0.04195	0.155064	-4.34
251502_at	putative protein several hypothetical pro	---	AT3G59130	1.19	0.25	2.51	0.041924	0.155064	-4.34
260677_at	translation elongation factor EF-1 alpha	RNL	AT1G07910	-1.41	-0.50	-2.51	0.041951	0.155064	-4.34
257402_at	hypothetical protein similar to putative C	---	AT1G23570	1.22	0.28	2.51	0.041942	0.155064	-4.34
267082_at	CPDK-related protein kinase CDPK:calc	CRK1	AT2G41140	-1.19	-0.26	-2.51	0.041964	0.155086	-4.35
257461_at	hypothetical protein predicted by gensca	ATPUP15	AT1G75470	1.17	0.23	2.51	0.041984	0.155135	-4.35
250993_at	putative protein HSPC172, Homo sapie	---	AT5G02280	-1.24	-0.31	-2.50	0.042014	0.155222	-4.35
260031_at	putative nuclear matrix constituent prote	LINC3	AT1G68790	-1.24	-0.31	-2.50	0.042055	0.155347	-4.35
264300_at	gamma glutamyl hydrolase, putative sir	ATGGH3	AT1G78670	-1.21	-0.28	-2.50	0.042134	0.155514	-4.35
256279_at	protein phosphatase 2C, putative conta	---	AT3G12620	1.16	0.22	2.50	0.04213	0.155514	-4.35
257023_at	RNA helicase, putative similar to RNA h	---	AT3G19760	-1.22	-0.29	-2.50	0.04213	0.155514	-4.35
254707_at	putative protein inositol polyphosphate	AT5PTASE	AT4G18010	1.67	0.74	2.50	0.042133	0.155514	-4.35
251483_at	putative protein hypothetical protein SP	---	AT3G59650	-1.26	-0.33	-2.50	0.042123	0.155514	-4.35
267645_at	putative beta-glucosidase	BGLU33	AT2G32860	-1.75	-0.81	-2.50	0.04215	0.155548	-4.35
264147_at	receptor-like protein glossy1 (gl1), puta	CER1	AT1G02205	4.52	2.18	2.50	0.042202	0.155716	-4.35
259476_at	Myb-related transcription activator, puta	---	AT1G19000	-1.30	-0.38	-2.50	0.042248	0.155857	-4.35
261036_at	developmentally regulated GTP-binding	ATDRG1	AT1G17470	-1.19	-0.25	-2.50	0.042286	0.155925	-4.35
257935_at	unknown protein	---	AT3G25440	-1.21	-0.28	-2.50	0.042286	0.155925	-4.35
266360_at	Mutator-like transposase similar to MUF	FRS2	AT2G32250	1.52	0.61	2.50	0.04228	0.155925	-4.35
246245_at	putative protein	---	AT4G36440	-1.22	-0.28	-2.50	0.042303	0.155963	-4.35
261821_at	thioredoxin h, putative similar to thiored	ATCXXS1	AT1G11530	-1.23	-0.30	-2.50	0.042324	0.155989	-4.35
265721_at	putative ABC1 protein identical to EGA	ATATH9	AT2G40090	1.32	0.41	2.50	0.042319	0.155989	-4.35
247460_at	AtOXA1 ;supported by full-length cDNA	OXA1	AT5G62050	-1.16	-0.21	-2.50	0.04239	0.156181	-4.36
259576_at	RING zinc finger protein, putative conta	---	AT1G35330	1.32	0.40	2.50	0.042384	0.156181	-4.36
246527_at	ribosomal protein-like 40S RIBOSOMAL	---	AT5G15750	-1.60	-0.68	-2.50	0.04248	0.156487	-4.36
254086_at	putative proteasome regulatory subunit	---	AT4G24820	1.18	0.23	2.50	0.042487	0.156487	-4.36

254077_at	putative protein NorM, Vibrio parahaem	---	AT4G25640	1.28	0.36	2.50	0.0425	0.156511	-4.36
259099_at	unknown protein similar to GB:AAB6107	---	AT3G05010	-1.23	-0.30	-2.50	0.042525	0.156576	-4.36
253747_at	serine threonine-specific kinase like pro	---	AT4G29050	1.47	0.56	2.50	0.04254	0.156608	-4.36
251730_at	N2,N2-dimethylguanosine tRNA methyl	---	AT3G56330	-1.28	-0.36	-2.50	0.042567	0.156655	-4.36
250061_at	chloroplast GrpE protein ; supported by	EMB1241	AT5G17710	-1.27	-0.35	-2.50	0.042562	0.156655	-4.36
263155_at	transcriptional activation factor TAFII32	TAFII21	AT1G54140	-1.25	-0.32	-2.50	0.042575	0.156660	-4.36
256491_at	hypothetical protein contains similarity to	---	AT1G31500	-1.24	-0.31	-2.49	0.04267	0.156985	-4.36
256033_at	UDP-glucose glucosyltransferase, puta	UGT71C4	AT1G07250	-1.21	-0.28	-2.49	0.042698	0.157054	-4.36
253118_at	ras-related small GTP-binding protein r	ARAC6	AT4G35950	-1.29	-0.37	-2.49	0.042703	0.157054	-4.36
255615_at	hypothetical protein	---	AT4G01290	-1.16	-0.22	-2.49	0.042716	0.157078	-4.36
247523_at	ribulose-5-phosphate-3-epimerase ; su	RPE	AT5G61410	-1.26	-0.34	-2.49	0.042726	0.157087	-4.36
264392_at	hypothetical protein Similar to salt-induc	---	AT1G11900	-1.27	-0.35	-2.49	0.042734	0.157094	-4.36
251058_at	putative protein	---	AT5G01790	-2.01	-1.01	-2.49	0.04275	0.157121	-4.36
255730_at	dihydroflavonol 4-reductase, putative si	---	AT1G25460	1.21	0.28	2.49	0.042755	0.157121	-4.36
245377_at	hypothetical protein	---	AT4G17700	1.22	0.29	2.49	0.042768	0.157141	-4.36
256265_at	serine carboxypeptidase, putative conta	scpl16	---	1.28	0.35	2.49	0.042779	0.157156	-4.36
248977_at	putative protein strong similarity to unkn	---	AT5G45020	-1.31	-0.39	-2.49	0.042797	0.157199	-4.37
251864_at	pectate lyase - like protein pectate lyas	PMR6	AT3G54920	-1.29	-0.36	-2.49	0.042805	0.157202	-4.37
259875_s_a	12-oxophytodienoate reductase (OPR2)	OPR1	AT1G76680 /	1.80	0.84	2.49	0.042851	0.157346	-4.37
249693_at	histidine kinase-like protein ; supported	AHK2	AT5G35750	-1.40	-0.49	-2.49	0.042868	0.157382	-4.37
258232_at	unknown protein	---	AT3G27750	-1.35	-0.43	-2.49	0.042914	0.157528	-4.37
252644_at	putative protein KIAA0073, Homo sapie	CYP71	AT3G44600	-1.27	-0.35	-2.49	0.042962	0.157677	-4.37
246666_at	hypothetical protein	---	AT5G34830	1.17	0.23	2.49	0.042997	0.157781	-4.37
252873_at	putative protein myosin heavy chain, O	---	AT4G40020	1.25	0.32	2.49	0.043004	0.157781	-4.37
256504_at	cytosolic IMP-GMP specific 5'-nucleotid	---	AT1G75210	-1.22	-0.29	-2.49	0.043015	0.157796	-4.37
250264_at	glucosyltransferase -like protein glucos	---	AT5G12890	1.16	0.22	2.49	0.043072	0.157979	-4.37
262467_at	hypothetical protein similar to hypothetic	FU	AT1G50240	1.26	0.34	2.49	0.043085	0.158000	-4.37
262100_s_a	hypothetical protein similar to hypothetic	---	AT1G59550 /	1.30	0.38	2.49	0.043096	0.158015	-4.37
253278_at	receptor protein kinase - like protein pro	---	AT4G34220	-1.90	-0.93	-2.49	0.043114	0.158058	-4.37
254990_at	RNA-binding protein ;supported by full-l	CID12	AT4G10610	-1.17	-0.23	-2.49	0.043152	0.158169	-4.37
259967_at	putative DNA-binding protein contains P	---	AT1G76510	-1.19	-0.25	-2.49	0.043178	0.158242	-4.37
258455_at	unknown protein ;supported by full-leng	---	AT3G22440	-1.34	-0.42	-2.48	0.043239	0.158417	-4.38
248877_at	putative protein similar to unknown prote	---	AT5G46140	1.21	0.27	2.48	0.043245	0.158417	-4.38
254501_at	hypothetical protein	PTAC14	AT4G20130	-1.40	-0.49	-2.48	0.043254	0.158417	-4.38
253266_s_a	putative protein predicted protein, Arabi	---	AT2G45260 /	-1.26	-0.33	-2.48	0.043251	0.158417	-4.38

261445_at	unknown protein ; supported by cDNA: g	NSL1	AT1G28380	1.60	0.68	2.48	0.043286	0.158511	-4.38
265235_s_a	hypothetical protein	---	AT2G07719	1.24	0.31	2.48	0.043299	0.158530	-4.38
264788_at	putative DnaJ protein ;supported by full	---	AT2G17880	1.82	0.86	2.48	0.043319	0.158578	-4.38
263131_at	ribosomal protein L13, putative similar t	emb1473	AT1G78630	-1.22	-0.28	-2.48	0.043348	0.158657	-4.38
246446_at	putative protein hypothetical protein T2	---	AT5G17640	-1.28	-0.36	-2.48	0.043354	0.158657	-4.38
267204_at	putative blue copper-binding protein	---	AT2G31050	1.23	0.30	2.48	0.043362	0.158661	-4.38
250520_at	putative protein contains similarity to AT	PEX1	AT5G08470	-1.17	-0.23	-2.48	0.043381	0.158703	-4.38
265544_at	putative cyclic nucleotide and calmodul	ATCNGC1	AT2G28260	-1.31	-0.39	-2.48	0.04339	0.158712	-4.38
247132_at	putative protein strong similarity to unkn	ARO2	AT5G66200	1.31	0.39	2.48	0.043409	0.158757	-4.38
265545_at	putative protein kinase contains a protei	NCRK	AT2G28250	1.25	0.32	2.48	0.043426	0.158792	-4.38
245129_at	hypothetical protein predicted by genefi	CRR4	AT2G45350	-1.17	-0.22	-2.48	0.043472	0.158936	-4.38
259305_at	unknown protein ;supported by full-leng	---	AT3G05070	-1.22	-0.29	-2.48	0.043482	0.158945	-4.38
261960_at	hypothetical protein similar to putative re	---	---	-1.16	-0.22	-2.48	0.043494	0.158964	-4.38
247458_at	putative protein PrMC3, Pinus radiata,	AtCXE20	AT5G62180	1.44	0.53	2.48	0.043517	0.159022	-4.38
245033_at	putative disease resistance protein	---	AT2G26380	1.21	0.27	2.48	0.043556	0.159140	-4.38
252572_at	putative protein Mlo-h1 protein - Hordeu	MLO3	AT3G45290	1.42	0.50	2.48	0.043624	0.159263	-4.38
257509_at	unknown protein	---	AT1G63190	-1.24	-0.31	-2.48	0.043607	0.159263	-4.38
247594_at	putative protein farnesylated protein GN	---	AT5G60800	1.29	0.37	2.48	0.043597	0.159263	-4.38
255700_at	putative transcription factor similar to Ar	---	AT4G00200	1.43	0.51	2.48	0.043624	0.159263	-4.38
252120_at	putative protein lin-10 protein - Rattus n	---	AT3G51130	1.24	0.31	2.48	0.043613	0.159263	-4.38
258404_at	ribosomal protein L3	RPL3P	AT3G17465	-1.27	-0.35	-2.48	0.043657	0.159356	-4.39
258409_at	hypothetical protein similar to GB:AAB9	---	AT3G17640	-1.46	-0.55	-2.48	0.043678	0.159408	-4.39
264551_at	unknown protein similar to beta-1,3-glu	---	AT1G09460	1.46	0.55	2.48	0.04374	0.159531	-4.39
255706_at	putative ribosomal protein S13 similar to	ATRPS13/	AT4G00100	-1.35	-0.44	-2.48	0.043731	0.159531	-4.39
244931_at	hypothetical protein	---	---	-1.33	-0.42	-2.48	0.04373	0.159531	-4.39
257053_at	ethylene responsive element binding fac	ERF4	AT3G15210	1.95	0.97	2.48	0.043737	0.159531	-4.39
265190_at	unknown protein ; supported by cDNA:	---	AT1G23780	-1.18	-0.24	-2.48	0.043766	0.159582	-4.39
264396_at	fumarylacetoacetate hydrolase-like prot	---	AT1G12050	-1.19	-0.25	-2.48	0.043768	0.159582	-4.39
266000_at	putative cytochrome P450 identical to G	CYP71B6	AT2G24180	1.49	0.58	2.48	0.043806	0.159671	-4.39
267028_at	putative WRKY-type DNA binding protei	WRKY33	AT2G38470	2.82	1.50	2.48	0.043806	0.159671	-4.39
253567_at	protein kinase-like protein serine/threon	---	AT4G31230	1.30	0.38	2.48	0.04385	0.159804	-4.39
263824_at	putative WD-40 repeat protein	---	AT2G40360	-1.42	-0.51	-2.47	0.043949	0.160142	-4.39
265941_s_a	recA, putative similar to GB:CAA39098	---	AT2G19490 /	-1.38	-0.47	-2.47	0.044038	0.160375	-4.39
261225_at	unknown protein ;supported by full-lengt	---	AT1G20100	1.20	0.26	2.47	0.044045	0.160375	-4.39
261165_at	dihydrolipoamide S-acetyltransferase, p	EMB3003	AT1G34430	-1.22	-0.29	-2.47	0.044049	0.160375	-4.39

249676_at	serine/threonine protein kinase-like	---	AT5G35960	1.25	0.32	2.47	0.044041	0.160375	-4.39
266648_at	putative trytophanyl-tRNA synthetase	OVA4	AT2G25840	-1.20	-0.26	-2.47	0.044022	0.160375	-4.39
246926_at	putative protein	---	AT5G25240	-1.42	-0.51	-2.47	0.044073	0.160439	-4.39
262222_at	unknown protein	TRZ1	AT1G74700	-1.23	-0.30	-2.47	0.044092	0.160481	-4.40
249792_at	putative protein contains similarity to Ds	PHS1	AT5G23720	-1.20	-0.26	-2.47	0.044101	0.160490	-4.40
257844_at	prolyl 4-hydroxylase, putative similar to	---	AT3G28480	1.31	0.39	2.47	0.04412	0.160534	-4.40
266005_at	unknown protein	RSZ33	AT2G37340	-1.30	-0.38	-2.47	0.044149	0.160537	-4.40
267110_at	hypothetical protein predicted by gensca	---	AT2G14800	-1.28	-0.35	-2.47	0.044136	0.160537	-4.40
266208_at	putative tRNA isopentenylpyrophosphat	ATIPT2	AT2G27760	-1.39	-0.48	-2.47	0.044135	0.160537	-4.40
259656_at	protein kinase, putative contains Pfam	---	AT1G55200	-1.20	-0.27	-2.47	0.044149	0.160537	-4.40
249482_at	putative protein ;supported by full-lengt	---	AT5G38980	-1.60	-0.68	-2.47	0.04418	0.160603	-4.40
256597_at	acidic ribosomal protein P2b (rpp2b), p	---	AT3G28500	-1.63	-0.70	-2.47	0.044202	0.160603	-4.40
244920_s_a	NADH dehydrogenase subunit 3 Protein	---	AT2G07751	-1.25	-0.32	-2.47	0.04419	0.160603	-4.40
256937_at	hypothetical protein predicted by genem	---	AT3G22620	3.78	1.92	2.47	0.044182	0.160603	-4.40
252482_at	glucosyltransferase-like protein UDP-gl	UGT76E1	AT3G46670	1.99	0.99	2.47	0.044203	0.160603	-4.40
248747_at	ribosomal protein S27 ;supported by full	---	AT5G47930	-1.32	-0.40	-2.47	0.044232	0.160684	-4.40
246790_at	putative protein unknown protein F22F7	---	AT5G27610	1.30	0.38	2.47	0.044252	0.160731	-4.40
263961_at	F-box protein family, AtFBL11 contains	---	AT2G36370	-1.28	-0.35	-2.47	0.044266	0.160755	-4.40
245037_at	putative phosphatidylinositol-4-phospha	PIP5K3	AT2G26420	1.18	0.23	2.47	0.044273	0.160756	-4.40
254352_at	hypothetical protein	---	AT4G22320	1.19	0.25	2.47	0.044303	0.160838	-4.40
247593_at	ABC transporter homolog PnATH - like	GCN1	AT5G60790	1.23	0.30	2.47	0.044367	0.161022	-4.40
265680_at	putative hydrolase ; supported by cDNA	---	AT2G32150	1.42	0.50	2.47	0.044365	0.161022	-4.40
260398_at	putative RNA-binding domain contains	APUM23	AT1G72320	-1.35	-0.44	-2.47	0.044428	0.161215	-4.40
247488_at	putative protein MtN19, Medicago trunc	---	AT5G61820	1.35	0.44	2.47	0.044458	0.161246	-4.40
258966_at	putative DNA gyrase subunit A similar to	---	AT3G10690	-1.44	-0.53	-2.47	0.044461	0.161246	-4.40
257334_at	hypothetical protein	---	---	-1.62	-0.70	-2.47	0.044445	0.161246	-4.40
245041_at	AR781, similar to yeast pheromone rec	AR781	AT2G26530	2.55	1.35	2.47	0.044464	0.161246	-4.40
247426_at	putative protein contains similarity to cal	---	AT5G62570	1.47	0.56	2.47	0.044492	0.161321	-4.40
249257_at	unknown protein	---	AT5G41640	1.16	0.22	2.46	0.044532	0.161440	-4.41
255103_at	putative phosphoglyceride transfer prot	---	AT4G08690	1.21	0.27	2.46	0.044567	0.161528	-4.41
261521_at	protein kinase, putative similar to recep	SERK1	AT1G71830	1.64	0.71	2.46	0.044571	0.161528	-4.41
260345_at	receptor protein kinase, putative similar	RPK1	AT1G69270	1.35	0.43	2.46	0.044591	0.161549	-4.41
260967_at	unknown protein contains similarity to tr	---	AT1G12230	-1.28	-0.36	-2.46	0.04459	0.161549	-4.41
256928_at	unknown protein	---	AT3G22590	-1.22	-0.29	-2.46	0.044619	0.161600	-4.41
266083_at	hypothetical protein predicted by gensca	---	AT2G37820	1.17	0.22	2.46	0.044617	0.161600	-4.41

266917_at	unknown protein	DTA2	AT2G45830	-1.20	-0.26	-2.46	0.04463	0.161616	-4.41
267054_at	hypothetical protein	---	AT2G38370	-1.38	-0.47	-2.46	0.044678	0.161736	-4.41
258950_at	unknown protein contains Pfam profile:	MBD9	AT3G01460	-1.16	-0.21	-2.46	0.044672	0.161736	-4.41
248081_at	putative protein similar to unknown prote	EDM2	AT5G55390	-1.18	-0.24	-2.46	0.044703	0.161750	-4.41
264160_at	hypothetical protein predicted by genem	---	AT1G65450	1.26	0.34	2.46	0.044696	0.161750	-4.41
254291_at	putative protein UDP-galactose transpo	UTR2	AT4G23010	1.36	0.45	2.46	0.044696	0.161750	-4.41
248879_at	ornithine aminotransferase	DELTA-OA	AT5G46180	1.28	0.36	2.46	0.044716	0.161774	-4.41
266272_at	hypothetical protein predicted by gensca	---	AT2G29600	1.22	0.29	2.46	0.044724	0.161775	-4.41
264221_s_a	unknown protein contains similarity to sp	emb1220	AT1G60170 /	-1.23	-0.30	-2.46	0.044742	0.161813	-4.41
256729_at	hypothetical protein predicted by genem	---	AT3G25680	-1.23	-0.30	-2.46	0.044752	0.161824	-4.41
253588_at	putative protein	---	AT4G30790	1.24	0.31	2.46	0.044779	0.161896	-4.41
259971_at	unknown protein similar to SPL1-relate	---	AT1G76580	-1.34	-0.42	-2.46	0.044836	0.162077	-4.41
247737_at	putative protein various predicted prote	---	AT5G59200	-1.16	-0.21	-2.46	0.044862	0.162146	-4.41
254430_at	reticuline oxidase - like protein reticulin	---	AT4G20820	-1.60	-0.68	-2.46	0.044892	0.162228	-4.41
262847_at	unknown protein similar to myosin heav	ATMAP70	AT1G14840	-1.51	-0.59	-2.46	0.044901	0.162237	-4.41
257111_x_a	hypothetical protein	---	---	1.19	0.25	2.46	0.044926	0.162299	-4.41
254043_at	putative protein ; supported by cDNA: gi	CIL	AT4G25990	-1.83	-0.88	-2.46	0.04496	0.162386	-4.42
251924_at	histone H4-like protein several histone H	---	AT3G53730	-1.33	-0.41	-2.46	0.044964	0.162386	-4.42
251148_at	hypothetical protein	TKL	AT3G63180	-1.21	-0.27	-2.46	0.044973	0.162392	-4.42
250538_at	RNA helicase (emb|CAA09212.1) ; sup	STRS2	AT5G08620	-1.39	-0.48	-2.46	0.044985	0.162410	-4.42
255250_at	MYB - like protein cM4 myb transcriptio	AtMYB74	AT4G05100	2.12	1.08	2.46	0.045036	0.162569	-4.42
263957_at	unknown protein ; supported by cDNA:	---	AT2G35880	-1.19	-0.25	-2.46	0.045046	0.162578	-4.42
262299_at	unknown protein Similar to gb|U04299	---	AT1G27520	-1.21	-0.28	-2.46	0.045057	0.162594	-4.42
247184_at	putative protein contains similarity to ubi	UBP17	AT5G65450	-1.28	-0.36	-2.46	0.045082	0.162659	-4.42
263637_at	hypothetical protein predicted by gensca	---	AT2G11890	-1.19	-0.26	-2.46	0.045097	0.162660	-4.42
249159_at	Nicotiana lesion-inducing like ; supporte	---	AT5G43460	-1.32	-0.40	-2.46	0.045091	0.162660	-4.42
247444_at	putative protein strong similarity to unkn	HIPL2	AT5G62630	1.64	0.71	2.46	0.045106	0.162667	-4.42
260898_at	plastid ribosomal protein L34 precursor	---	AT1G29070	-1.30	-0.38	-2.45	0.045168	0.162866	-4.42
247126_at	protein phosphatase 2C-like protein	---	AT5G66080	-1.35	-0.43	-2.45	0.045186	0.162903	-4.42
264153_at	disease resistance protein RPS4, putat	ATPP2-A5	AT1G65390	1.59	0.66	2.45	0.045193	0.162904	-4.42
246517_at	ribosomal protein 3 precursor-like prote	---	AT5G15760	-1.26	-0.33	-2.45	0.045245	0.163040	-4.42
247163_at	Expressed protein ; supported by cDNA	---	AT5G65685	-1.26	-0.33	-2.45	0.04524	0.163040	-4.42
262366_at	disease resistance protein, putative sim	---	AT1G72890	1.65	0.72	2.45	0.045279	0.163134	-4.42
251260_at	putative protein ISOPENICILLIN N EPI	---	AT3G62130	-1.38	-0.47	-2.45	0.045296	0.163134	-4.42
255830_at	putative PRP19-like spliceosomal protei	---	AT2G33340	-1.45	-0.54	-2.45	0.045291	0.163134	-4.42

247821_at	WD-40 repeat protein MSI1 (sp|O22467	MSI1	AT5G58230	-1.24	-0.31	-2.45	0.0453	0.163134	-4.42
261992_at	unknown protein	---	AT1G33680	-1.22	-0.29	-2.45	0.04531	0.163143	-4.42
266370_at	hypothetical protein predicted by gensca	---	AT2G41350	-1.17	-0.23	-2.45	0.045321	0.163157	-4.42
265087_at	hypothetical protein predicted by genefi	---	AT1G03760	-1.42	-0.51	-2.45	0.045337	0.163163	-4.42
250871_at	putative protein	---	AT5G03930	1.25	0.32	2.45	0.045335	0.163163	-4.42
264770_at	unknown protein similar to unknown pro	---	AT1G23030	1.52	0.60	2.45	0.045375	0.163277	-4.42
247007_at	porin-like protein ;supported by full-leng	VDAC2	AT5G67500	1.27	0.35	2.45	0.045406	0.163361	-4.43
266737_at	putative alcohol dehydrogenase ; suppo	---	AT2G47140	1.24	0.32	2.45	0.045422	0.163393	-4.43
256198_at	Myb-family transcription factor, putative	---	AT1G58220	-1.31	-0.39	-2.45	0.04543	0.163395	-4.43
255095_at	MEKK1/MAP kinase kinase kinase ; su	MEKK1	AT4G08500	1.34	0.43	2.45	0.045448	0.163437	-4.43
252481_at	putative protein DCL PROTEIN, CHLO	---	AT3G46630	-1.26	-0.33	-2.45	0.04549	0.163507	-4.43
257108_x_a	hypothetical protein	---	---	1.18	0.24	2.45	0.045481	0.163507	-4.43
266596_at	hypothetical protein predicted by gensca	---	AT2G46150	1.64	0.71	2.45	0.04549	0.163507	-4.43
265007_s_a	Expressed protein ; supported by full-le	RALFL8	AT1G61563 /	1.16	0.22	2.45	0.045524	0.163605	-4.43
266071_at	unknown protein	---	AT2G18670 /	1.97	0.98	2.45	0.04557	0.163694	-4.43
245806_at	light-harvesting complex protein similar	LHCA5	AT1G45474	-1.40	-0.49	-2.45	0.045561	0.163694	-4.43
251857_at	RNA binding protein - like SEB4 protein	---	AT3G54770	1.22	0.28	2.45	0.045564	0.163694	-4.43
248378_at	unknown protein ;supported by full-leng	---	AT5G51840	-1.20	-0.26	-2.45	0.045583	0.163715	-4.43
265260_at	NAM (no apical meristem)-like protein	anac042	AT2G43000	2.68	1.42	2.45	0.045595	0.163733	-4.43
258351_at	hypothetical protein contains similarity t	CNBT1	AT3G17700	1.36	0.44	2.45	0.04565	0.163778	-4.43
263332_at	putative snRNP splicing factor ;support	---	AT2G03870	-1.20	-0.26	-2.45	0.045662	0.163778	-4.43
260331_at	hypothetical protein contains Pfam profi	---	AT1G80270	-2.31	-1.21	-2.45	0.045646	0.163778	-4.43
253307_at	putative protein auxin-induced protein,	---	AT4G33670	-1.25	-0.32	-2.45	0.045664	0.163778	-4.43
250828_at	unknown protein ; supported by cDNA: g	---	AT5G05250	-2.88	-1.53	-2.45	0.045665	0.163778	-4.43
253928_at	phosphoprotein phosphatase (PPX-1)	PPX1	AT4G26720	-1.22	-0.28	-2.45	0.045652	0.163778	-4.43
263573_at	unknown protein similar to A. thaliana hy	---	AT2G17150	-1.31	-0.39	-2.45	0.045616	0.163778	-4.43
257465_at	hypothetical protein predicted by gensca	---	AT1G13040	-1.17	-0.22	-2.45	0.045641	0.163778	-4.43
264602_at	putative Ser/Thr protein kinase similar to	---	AT1G04700	-1.21	-0.27	-2.45	0.045691	0.163845	-4.43
251282_at	putative protein transcription factor Pti6	CRF6	AT3G61630	-1.60	-0.68	-2.45	0.04575	0.164031	-4.43
251546_at	putative protein predicted proteins, yea	---	AT3G58830	-1.36	-0.44	-2.45	0.045768	0.164070	-4.43
256960_at	unknown protein ;supported by full-leng	---	AT3G13510	-1.29	-0.37	-2.44	0.045854	0.164352	-4.43
255601_at	putative protein (fragment) various hypo	---	AT4G01030	-1.24	-0.31	-2.44	0.045953	0.164549	-4.44
264625_at	hypothetical protein Contains similarity t	SNF4	AT1G09020	1.21	0.28	2.44	0.045945	0.164549	-4.44
248810_at	disease resistance protein-like	ADR1-L3	AT5G47280	1.18	0.24	2.44	0.045936	0.164549	-4.44
262563_at	somatic embryogenesis receptor-like ki	SERK2	AT1G34210	-1.28	-0.36	-2.44	0.045946	0.164549	-4.44

261143_at	unknown protein	ATPUP14	AT1G19770	1.43	0.51	2.44	0.045945	0.164549	-4.44
245556_at	HSR201 like protein	---	AT4G15400	1.18	0.23	2.44	0.045935	0.164549	-4.44
250702_at	peroxidase ;supported by full-length cD	---	AT5G06730	2.88	1.52	2.44	0.045986	0.164644	-4.44
255520_at	putative ribosomal protein L19 similar to	---	AT4G02230	-1.40	-0.49	-2.44	0.046042	0.164819	-4.44
246906_at	Expressed protein ; supported by full-ler	---	AT5G25475	-1.21	-0.27	-2.44	0.046087	0.164936	-4.44
254703_at	putative protein ; supported by full-leng	---	AT4G17960	-1.31	-0.39	-2.44	0.046097	0.164936	-4.44
263542_at	putative protein transport protein SEC23	---	AT2G21630	-1.32	-0.40	-2.44	0.046095	0.164936	-4.44
246738_at	replication factor C - like replication fact	EMB2775	AT5G27740	-1.21	-0.28	-2.44	0.046117	0.164983	-4.44
263786_at	putative auxin-responsive protein ; supp	JAR1	AT2G46370	-1.16	-0.21	-2.44	0.046133	0.164988	-4.44
258191_at	putative vesicle transport protein similar	VTI13	AT3G29100	-1.18	-0.24	-2.44	0.046126	0.164988	-4.44
254652_at	DNA binding-like protein SPF1 protein,	WRKY28	AT4G18170	2.54	1.35	2.44	0.046165	0.165076	-4.44
247831_at	putative protein serine/threonine-specif	---	AT5G58540	1.41	0.50	2.44	0.046203	0.165187	-4.44
247178_at	Expressed protein ; supported by cDNA	---	AT5G65205	-1.57	-0.65	-2.44	0.046256	0.165350	-4.44
265897_at	hypothetical protein predicted by gensca	MOT1	AT2G25680	1.39	0.48	2.44	0.046294	0.165460	-4.44
264597_at	unknown protein	---	AT1G04620	-1.30	-0.38	-2.44	0.04634	0.165523	-4.45
252331_s_a	serine palmitoyltransferase-like protein	SPT1	AT3G48780 /	1.24	0.31	2.44	0.046323	0.165523	-4.45
253863_at	putative protein D.melanogaster P elem	---	AT4G27420	1.25	0.32	2.44	0.046348	0.165523	-4.45
266437_at	unknown protein	---	AT2G43160	1.25	0.32	2.44	0.046341	0.165523	-4.45
247738_at	putative protein myosin heavy chain, D	---	AT5G59210	-1.24	-0.31	-2.44	0.04633	0.165523	-4.45
262881_at	unknown protein ; supported by cDNA: g	---	AT1G64890	-1.43	-0.51	-2.44	0.046373	0.165588	-4.45
257954_at	putative UDP-glucose glucosyltransfera	---	AT3G21760	-1.25	-0.32	-2.44	0.046408	0.165687	-4.45
247474_at	putative protein predicted proteins, Ara	---	AT5G62280	-3.29	-1.72	-2.44	0.046427	0.165728	-4.45
251656_at	putative protein N-ACETYLGLUCOSAM	---	AT3G57170	-1.22	-0.29	-2.44	0.046443	0.165759	-4.45
251414_at	hypothetical protein	---	AT3G60370	-1.28	-0.36	-2.43	0.0465	0.165918	-4.45
257839_at	hypothetical protein	---	AT3G25080	-1.18	-0.24	-2.43	0.046502	0.165918	-4.45
265930_at	putative spliceosome associated protein	emb2444	AT2G18510	-1.23	-0.30	-2.43	0.046518	0.165950	-4.45
256493_at	hypothetical protein predicted by genem	---	AT1G31600	-1.26	-0.33	-2.43	0.046533	0.165975	-4.45
266562_at	unknown protein	---	AT2G23970	1.33	0.41	2.43	0.046552	0.166019	-4.45
260029_at	endoplasmic reticulum alpha-mannosid	---	AT1G30000	1.19	0.25	2.43	0.046566	0.166043	-4.45
247870_at	calmodulin-binding protein ; supported	---	AT5G57580	1.19	0.26	2.43	0.046617	0.166198	-4.45
254122_at	CER2 ;supported by full-length cDNA: (	CER2	AT4G24510	3.07	1.62	2.43	0.046628	0.166211	-4.45
247043_at	protein kinase, 41K (EC 2.7.1.-) (pir||S7	SNRK2.3	AT5G66880	-1.37	-0.46	-2.43	0.046666	0.166319	-4.45
253028_at	putative protein	pde191	AT4G38160	-1.21	-0.28	-2.43	0.046682	0.166352	-4.45
256696_at	unknown protein	---	AT3G20650	-1.20	-0.26	-2.43	0.04671	0.166400	-4.45
262270_x_a	polyprotein, putative similar to polyprote	---	---	1.17	0.22	2.43	0.046706	0.166400	-4.45

264904_s_a	putative thioredoxin reductase	NTRA	AT2G17420 /	1.30	0.38	2.43	0.046732	0.166452	-4.45
259664_at	unknown protein ; supported by full-leng	AGP21	AT1G55330	3.28	1.71	2.43	0.046769	0.166558	-4.45
253425_at	putative protein myosin heavy chain-B,	---	AT4G32190	-1.39	-0.48	-2.43	0.046846	0.166804	-4.46
245235_at	putative protein similarity to predicted p	---	AT4G25550	-1.22	-0.29	-2.43	0.04686	0.166831	-4.46
264655_at	unknown protein Similar to Glycine SR(	SRC2	AT1G09070	1.51	0.59	2.43	0.046906	0.166967	-4.46
264101_at	unknown protein similar to putative CRE	HAC1	AT1G79000	-1.26	-0.33	-2.43	0.046917	0.166981	-4.46
263689_at	ribonuclease, RNS3 identical to ribonuc	RNS3	AT1G26820	1.40	0.48	2.43	0.04695	0.167045	-4.46
265501_at	putative glucosyltransferase	UGT73B4	AT2G15490	1.74	0.80	2.43	0.046944	0.167045	-4.46
262714_s_a	unknown protein similar to gb|AJ224359	---	AT1G07950 /	-1.19	-0.26	-2.43	0.046978	0.167093	-4.46
260441_at	unknown protein ;supported by full-leng	---	AT1G68260	1.57	0.65	2.43	0.046985	0.167093	-4.46
248483_at	putative protein contains similarity to sel	---	AT5G50990	-1.31	-0.39	-2.43	0.04698	0.167093	-4.46
266590_at	hypothetical protein predicted by gensca	BAG6	AT2G46240	-1.40	-0.48	-2.43	0.047001	0.167122	-4.46
266797_at	unknown protein	AtGRF1	AT2G22840	-1.55	-0.63	-2.43	0.047051	0.167276	-4.46
252633_x_a	putative protein HISTONE DEACETYLA	hda17	AT3G44490 /	-1.17	-0.22	-2.43	0.047064	0.167293	-4.46
256046_at	unknown protein	---	AT1G07135	2.16	1.11	2.43	0.047089	0.167357	-4.46
252646_at	protein kinase-like protein protein kinas	---	AT3G44610	-1.19	-0.25	-2.43	0.047102	0.167379	-4.46
251054_at	receptor like protein kinase receptor like	LECRKA4	AT5G01540	2.48	1.31	2.43	0.047127	0.167440	-4.46
261278_at	hypothetical protein predicted by genem	DGL	AT1G05800	1.20	0.26	2.42	0.047164	0.167531	-4.46
250728_at	putative protein similar to unknown prote	---	AT5G06440	-1.25	-0.32	-2.42	0.047167	0.167531	-4.46
258460_at	unknown protein	ECT6	AT3G17330	-1.27	-0.35	-2.42	0.047188	0.167578	-4.46
263073_at	unknown protein ;supported by full-leng	---	AT2G17500	4.51	2.17	2.42	0.047249	0.167769	-4.47
245297_at	hypothetical protein ; supported by cDN/	---	AT4G16510	-1.25	-0.33	-2.42	0.047257	0.167773	-4.47
266469_at	myb-related protein	MYB14	AT2G31180	1.21	0.28	2.42	0.047318	0.167962	-4.47
245573_at	hypothetical protein	---	AT4G14730	-1.17	-0.23	-2.42	0.047335	0.167996	-4.47
265718_at	putative WRKY DNA-binding protein ; s	WRKY3	AT2G03340	-1.23	-0.30	-2.42	0.047348	0.168016	-4.47
259121_at	unknown protein	---	AT3G02220	-1.28	-0.36	-2.42	0.047387	0.168098	-4.47
259528_at	hypothetical protein	---	AT1G12330	-1.33	-0.41	-2.42	0.047405	0.168098	-4.47
249925_at	putative protein predicted proteins, Hon	---	AT5G19150	-1.32	-0.40	-2.42	0.047384	0.168098	-4.47
264357_at	hypothetical protein Similar to hypothetic	ATRRP4	AT1G03360	-1.73	-0.79	-2.42	0.047408	0.168098	-4.47
252017_at	cytochrome P450 - like protein cytochro	CYP76G1	AT3G52970	1.23	0.30	2.42	0.047397	0.168098	-4.47
247063_at	unknown protein	---	AT5G66820	-1.34	-0.42	-2.42	0.04742	0.168113	-4.47
264298_at	hypothetical protein contains similarity to	---	AT1G78690	-1.22	-0.28	-2.42	0.047455	0.168211	-4.47
267622_at	hypothetical protein predicted by gensca	---	AT2G39690	1.21	0.27	2.42	0.047468	0.168231	-4.47
257646_at	methionine aminopeptidase, putative sil	MAP1B	AT3G25740	-1.46	-0.54	-2.42	0.047482	0.168256	-4.47
256505_at	unknown protein	---	AT1G75200	-1.31	-0.39	-2.42	0.047579	0.168447	-4.47

258211_at	hypothetical protein predicted by genem	---	AT3G17890	-1.30	-0.37	-2.42	0.047595	0.168447	-4.47
252828_at	DnaJ - like protein DnaJ-like protein, Pi	---	AT4G39960	-1.24	-0.31	-2.42	0.047565	0.168447	-4.47
263218_at	putative serine/threonine protein kinase	---	AT1G30570	-1.29	-0.37	-2.42	0.047572	0.168447	-4.47
250309_at	putative protein similar to unknown prote	---	AT5G12220	-1.30	-0.38	-2.42	0.047589	0.168447	-4.47
254561_at	putative protein ; supported by cDNA: g	---	AT4G19160	1.36	0.45	2.42	0.047566	0.168447	-4.47
262945_at	unknown protein ;supported by full-lengt	---	AT1G79510	-1.44	-0.52	-2.42	0.047591	0.168447	-4.47
257473_at	unknown protein	---	AT1G33840	1.30	0.38	2.42	0.04757	0.168447	-4.47
254806_at	putative trehalose-6-phosphate phosph	---	AT4G12430 /	-1.22	-0.29	-2.42	0.047652	0.168623	-4.47
263036_at	hypothetical protein predicted by genem	---	AT1G23890	1.25	0.32	2.42	0.047678	0.168688	-4.47
251277_at	dynamin-like protein phragmoplastin 5 -	ADL1B	AT3G61760	1.16	0.21	2.42	0.047698	0.168706	-4.47
246884_at	putative protein cation transport protein	---	AT5G26220	-1.49	-0.57	-2.42	0.047696	0.168706	-4.47
249624_at	putative protein predicted proteins, Arat	---	AT5G37570	-1.29	-0.37	-2.42	0.047715	0.168714	-4.48
261625_at	hypothetical protein predicted by genem	---	AT1G01930	-1.18	-0.24	-2.42	0.047711	0.168714	-4.48
255430_at	putative chloroplast protein import com	tic20-IV	AT4G03320	1.47	0.56	2.42	0.047742	0.168784	-4.48
257516_at	unknown protein	ACR4	AT1G69040	-1.36	-0.44	-2.42	0.047764	0.168836	-4.48
260884_at	unknown protein similar to unknown pro	---	AT1G29240	1.59	0.67	2.42	0.047788	0.168841	-4.48
253414_at	putative protein	EDA39	AT4G33050	2.59	1.37	2.42	0.047782	0.168841	-4.48
257802_at	unknown protein	---	AT3G18770	-1.29	-0.37	-2.42	0.047795	0.168841	-4.48
245164_at	mitochondrial chaperonin (HSP60)	HSP60-2	AT2G33210	-1.60	-0.68	-2.42	0.047792	0.168841	-4.48
250721_at	putative protein contains similarity to RN	---	AT5G06210	-1.19	-0.25	-2.42	0.047804	0.168845	-4.48
248410_at	putative protein similar to unknown prote	---	AT5G51570	1.20	0.27	2.41	0.047857	0.169008	-4.48
260358_at	unknown protein ; supported by cDNA: g	---	AT1G69340	-1.19	-0.25	-2.41	0.047866	0.169015	-4.48
260134_at	Myb-related transcription factor, putativ	MYB113	AT1G66370	1.28	0.36	2.41	0.047892	0.169080	-4.48
255590_at	cathepsin B-like cysteine protease, puta	---	AT4G01610	1.27	0.35	2.41	0.047919	0.169120	-4.48
246143_at	lipophosphoglycan biosynthetic protein	---	AT5G19980	1.32	0.40	2.41	0.047916	0.169120	-4.48
250306_at	putative protein similar to unknown prote	---	AT5G12170	1.34	0.42	2.41	0.047941	0.169173	-4.48
264662_at	putative sucrose/H+ symporter similar to	SUT4	AT1G09960	1.32	0.40	2.41	0.047949	0.169175	-4.48
258052_at	putative hydrolase predicted by genema	---	AT3G16190	-1.24	-0.31	-2.41	0.047958	0.169181	-4.48
257674_at	translational inhibitor protein, putative s	---	AT3G20390	-1.20	-0.26	-2.41	0.048042	0.169398	-4.48
262272_at	unknown protein ; supported by cDNA: g	---	AT1G42440	-1.17	-0.22	-2.41	0.048039	0.169398	-4.48
256041_at	unknown protein	---	AT1G07230	-1.29	-0.36	-2.41	0.04804	0.169398	-4.48
262216_at	hypothetical protein contains similarity to	---	AT1G74780	-1.25	-0.33	-2.41	0.048066	0.169458	-4.48
244902_at	NADH dehydrogenase subunit 4L	---	ATMG00650	-1.24	-0.31	-2.41	0.048097	0.169541	-4.48
260885_at	protein kinase PK4, putative similar to p	CIPK18	AT1G29230	1.26	0.34	2.41	0.048122	0.169603	-4.48
257003_at	unknown protein ;supported by full-leng	FLU	AT3G14110	-1.32	-0.40	-2.41	0.048144	0.169653	-4.48

264910_at	resistance protein, putative similar to re	---	AT1G61100	1.50	0.59	2.41	0.048159	0.169679	-4.48
265575_at	proline iminopeptidase identical to GP:1	PIP	AT2G14260	-1.19	-0.25	-2.41	0.048189	0.169706	-4.49
247830_at	putative protein predicted proteins, Aral	---	AT5G58530	-1.36	-0.44	-2.41	0.048188	0.169706	-4.49
246544_at	auxin transport protein - like auxin trans	PIN8	AT5G15100	1.18	0.24	2.41	0.048178	0.169706	-4.48
249824_at	putative protein similar to unknown prote	---	AT5G23380	1.20	0.27	2.41	0.048202	0.169728	-4.49
267352_at	hypothetical protein predicted by gensca	---	AT2G40050	1.18	0.24	2.41	0.048233	0.169809	-4.49
267205_at	unknown protein	---	AT2G30820	1.23	0.30	2.41	0.048268	0.169908	-4.49
262161_at	signal peptidase subunit, putative simila	---	AT1G52600	-1.19	-0.26	-2.41	0.04828	0.169924	-4.49
262588_at	unknown protein Similar to gb|AJ00507	---	AT1G15130	1.22	0.29	2.41	0.048302	0.169973	-4.49
252456_at	hypersensitivity-related protein-like prote	---	AT3G47170	1.22	0.29	2.41	0.048327	0.170036	-4.49
245312_at	Expressed protein ; supported by full-ler	---	AT4G14600	-1.28	-0.36	-2.41	0.048347	0.170079	-4.49
248106_at	putative protein similar to unknown prote	---	AT5G55100	1.18	0.24	2.41	0.04837	0.170133	-4.49
264264_at	unknown protein ESTs gb|T04610, gb|N	---	AT1G09250	1.53	0.62	2.41	0.048385	0.170150	-4.49
258103_at	hypothetical protein contains Pfam profil	IPT7	AT3G23630	-1.27	-0.35	-2.41	0.048389	0.170150	-4.49
253926_at	hnRNP-like protein ; supported by cDNA	---	AT4G26650	1.20	0.26	2.41	0.048405	0.170171	-4.49
247265_at	putative protein strong similarity to unkn	CPuORF2	AT5G64550 /	-1.53	-0.62	-2.41	0.048417	0.170171	-4.49
251627_at	glucan endo-1,3-beta-D-glucosidase-lik	BG1	AT3G57270	1.22	0.29	2.41	0.048418	0.170171	-4.49
267016_at	hypothetical protein predicted by gensca	---	AT2G39160 /	1.20	0.27	2.41	0.048453	0.170267	-4.49
250958_at	laccase precursor - like laccase precurs	LAC11	AT5G03260	1.83	0.88	2.41	0.048463	0.170279	-4.49
264236_at	hypothetical protein predicted by genem	---	AT1G54680	1.23	0.29	2.41	0.048488	0.170338	-4.49
261673_at	lipid transfer protein, putative similar to	---	AT1G18280	2.15	1.11	2.41	0.048503	0.170365	-4.49
250272_at	callose synthase catalytic subunit -like p	ATGSL12	AT5G13000	-1.27	-0.34	-2.40	0.048532	0.170441	-4.49
251189_at	putative protein putative mitochondrial c	---	AT3G62650	-1.31	-0.39	-2.40	0.048568	0.170538	-4.49
266031_at	hypothetical protein predicted by genefir	---	---	1.19	0.25	2.40	0.048577	0.170538	-4.49
263528_at	putative peroxidase	---	AT2G24800	-1.23	-0.29	-2.40	0.048582	0.170538	-4.49
261037_at	lipoxygenase identical to GB:CAB56692	LOX3	AT1G17420	2.47	1.30	2.40	0.048598	0.170568	-4.49
250946_at	putative protein	---	AT5G03420	-1.20	-0.26	-2.40	0.048606	0.170568	-4.49
265451_at	unknown protein	---	AT2G46490	1.17	0.23	2.40	0.048647	0.170689	-4.49
246591_at	putative cation transport protein putativ	---	AT5G14880	-1.26	-0.33	-2.40	0.048679	0.170774	-4.50
250198_at	expressed protein contains similarity to	NAP14	AT5G14100	-1.35	-0.43	-2.40	0.048721	0.170867	-4.50
AFFX-LysX-	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.38	-0.46	-2.40	0.048716	0.170867	-4.50
251161_at	putative protein hypothetical protein Sb	---	AT3G63290	-1.23	-0.29	-2.40	0.048729	0.170870	-4.50
248785_at	unknown protein	---	AT5G47400	-1.17	-0.22	-2.40	0.048752	0.170870	-4.50
258945_at	calmodulin-domain protein kinase CDP	CPK2	AT3G10660	1.17	0.23	2.40	0.048737	0.170870	-4.50
257521_at	hypothetical protein predicted by genefir	---	AT3G09140	1.18	0.23	2.40	0.048748	0.170870	-4.50

263856_at	unknown protein	---	AT2G04410	-1.30	-0.38	-2.40	0.048797	0.170932	-4.50
250130_at	amylogenin; reversibly glycosylatable pc	---	AT5G16510	1.30	0.38	2.40	0.048793	0.170932	-4.50
250599_at	unknown protein ; supported by cDNA:	---	AT5G07730	1.30	0.38	2.40	0.048799	0.170932	-4.50
256437_s_a	putative clathrin heavy chain similar to c	---	AT3G08530 /	1.18	0.23	2.40	0.04878	0.170932	-4.50
264952_at	Tub family protein, putative contains Pf	AtTLP1	AT1G76900	1.18	0.24	2.40	0.048827	0.171003	-4.50
260388_at	hypothetical protein predicted by gensc	---	AT1G74070	-1.48	-0.57	-2.40	0.04884	0.171024	-4.50
252184_at	steroid 22-alpha-hydroxylase (DWF4) ;	DWF4	AT3G50660	-1.30	-0.38	-2.40	0.048853	0.171041	-4.50
250829_at	disease resistance - like protein rpp8, A	ADR1-L2	AT5G04720	1.25	0.33	2.40	0.048892	0.171126	-4.50
247060_at	succinate dehydrogenase flavoprotein a	SDH1-1	AT5G66760	1.80	0.85	2.40	0.04889	0.171126	-4.50
259724_at	putative serine/threonine-protein kinase	SNRK2.10	AT1G60940	-1.29	-0.37	-2.40	0.048993	0.171430	-4.50
262117_at	ribosomal protein L19, putative similar t	emb2386	AT1G02780	-1.27	-0.35	-2.40	0.048994	0.171430	-4.50
248768_at	60S acidic ribosomal protein P1-like pro	---	AT5G47700	-1.38	-0.47	-2.40	0.049013	0.171443	-4.50
253840_at	putative acyl-CoA binding protein strong	ACBP2	AT4G27780	1.28	0.35	2.40	0.049005	0.171443	-4.50
248549_at	putative protein contains similarity to un	---	AT5G50310	-1.20	-0.27	-2.40	0.049028	0.171470	-4.50
250794_at	putative protein contains similarity to cha	---	AT5G05270	1.20	0.26	2.40	0.04904	0.171486	-4.50
254192_at	acyl-CoA synthetase - like protein acyl-	---	AT4G23850	1.21	0.28	2.40	0.049061	0.171532	-4.50
266014_s_a	hypothetical protein	---	AT2G07722	-1.49	-0.58	-2.40	0.049082	0.171580	-4.50
252946_at	Expressed protein ; supported by full-ler	---	AT4G39235	-1.36	-0.45	-2.40	0.049142	0.171762	-4.50
256906_at	hypothetical protein contains Pfam profil	---	AT3G24000	-1.27	-0.34	-2.40	0.049152	0.171771	-4.51
249633_at	sucrose synthase-like protein sucrose s	SUS5	AT5G37180	-1.19	-0.25	-2.40	0.04921	0.171920	-4.51
256522_at	unknown protein ;supported by full-lengt	CMPG1	AT1G66160	2.69	1.43	2.40	0.049207	0.171920	-4.51
258091_at	hypothetical protein predicted by genma	---	AT3G14560	1.82	0.86	2.39	0.049217	0.171920	-4.51
255639_at	putative protein	APRR8	AT4G00760	-1.27	-0.35	-2.39	0.049315	0.172209	-4.51
254967_at	putative protein various predicted prote	---	AT4G10410	1.20	0.26	2.39	0.049312	0.172209	-4.51
249119_at	unknown protein ;supported by full-leng	---	AT5G43720	-1.16	-0.22	-2.39	0.049361	0.172292	-4.51
253864_at	hypothetical protein	---	AT4G27460	1.26	0.33	2.39	0.049347	0.172292	-4.51
254634_at	putative protein transcription factor OBF	---	AT4G18650	1.23	0.30	2.39	0.049355	0.172292	-4.51
256782_at	dirigent protein, putative similar to dirige	---	AT3G13660	1.17	0.22	2.39	0.049393	0.172376	-4.51
258657_at	hypothetical protein predicted by gensca	---	AT3G09890	-1.33	-0.41	-2.39	0.049417	0.172433	-4.51
247300_at	unknown protein	FCLY	AT5G63910	-1.23	-0.29	-2.39	0.049487	0.172654	-4.51
252458_at	putative protein various predicted prote	---	AT3G47210	1.20	0.26	2.39	0.049503	0.172681	-4.51
255038_at	neutral invertase like protein Daucus ca	CINV2	AT4G09510	-1.55	-0.63	-2.39	0.049512	0.172688	-4.51
245398_at	hydroxyproline-rich glycoprotein homolo	---	AT4G14900	1.37	0.46	2.39	0.049581	0.172753	-4.51
250293_s_a	auxin reponsive - like protein Nt-gh3 de	---	AT5G13360 /	1.56	0.64	2.39	0.049556	0.172753	-4.51
266330_at	unknown protein ; supported by cDNA:	MLP329	AT2G01530	-1.35	-0.43	-2.39	0.049613	0.172753	-4.51

263687_at	unknown protein ;supported by full-leng	---	AT1G26940	-1.31	-0.39	-2.39	0.049618	0.172753	-4.51
257010_at	Expressed protein ; supported by cDNA	ATEXO70I	AT3G14090	1.35	0.43	2.39	0.049622	0.172753	-4.51
260489_at	hypothetical protein ; supported by cDN	---	AT1G51610	-1.20	-0.26	-2.39	0.049578	0.172753	-4.51
265969_at	En/Spm-like transposon protein related	---	---	1.21	0.27	2.39	0.049588	0.172753	-4.51
260394_at	putative transcription factor similar to OS	MYB122	AT1G74080	2.59	1.37	2.39	0.049597	0.172753	-4.51
266945_at	hypothetical protein predicted by genefir	VEL2	AT2G18880	1.18	0.24	2.39	0.049564	0.172753	-4.51
252681_at	NAC domain -like protein Tobacco elicit	anac061	AT3G44350	1.25	0.32	2.39	0.049601	0.172753	-4.51
264135_at	S-locus protein, putative similar to S-loc	---	AT1G79030	-1.20	-0.26	-2.39	0.049585	0.172753	-4.51
254685_at	SAUR-AC - like protein (small auxin up	---	AT4G13790	1.63	0.71	2.39	0.049556	0.172753	-4.51
252316_at	putative protein PrMC3 - Pinus radiata,	ATCXE13	AT3G48700	1.20	0.26	2.39	0.049655	0.172840	-4.52
247452_at	H-protein promoter binding factor-like pr	CDF1	AT5G62430	-1.35	-0.43	-2.39	0.049699	0.172969	-4.52
246002_at	ripening-related protein - like grip28 ripe	---	AT5G20740	1.51	0.60	2.39	0.049718	0.173010	-4.52
259284_at	putative cell division related protein simi	---	AT3G11450	1.24	0.31	2.39	0.049775	0.173180	-4.52
258973_at	putative cytochrome P450 similar to cyt	CYP94B2	AT3G01900	1.23	0.30	2.39	0.049843	0.173365	-4.52
261353_at	hypothetical protein contains similarity t	---	AT1G79600	1.33	0.41	2.39	0.049842	0.173365	-4.52
248557_at	transport inhibitor response 1 (TIR1), pu	AFB5	AT5G49980	-1.24	-0.31	-2.38	0.049938	0.173669	-4.52
266315_at	unknown protein ; supported by cDNA:	SE	AT2G27100	-1.17	-0.23	-2.38	0.049973	0.173682	-4.52
248884_at	putative protein similar to unknown prote	---	AT5G46030	-1.17	-0.23	-2.38	0.049954	0.173682	-4.52
264542_at	hypothetical protein predicted by genem	---	AT1G55830	-1.17	-0.23	-2.38	0.049969	0.173682	-4.52
257660_at	unknown protein ; supported by cDNA:	WIP3	AT3G13360	-1.17	-0.22	-2.38	0.04996	0.173682	-4.52
253809_at	putative (1-4)-beta-mannan endohydrol	---	AT4G28320	-1.30	-0.38	-2.38	0.050033	0.173864	-4.52
249136_at	putative protein similar to unknown prote	---	AT5G43180	-1.41	-0.50	-2.38	0.050075	0.173986	-4.52
259318_at	unknown protein similar to HYP1 GB:CA	HYP1	AT3G01100	-1.27	-0.35	-2.38	0.050121	0.174020	-4.52
245913_at	predicted protein	---	AT5G19860	1.23	0.29	2.38	0.05012	0.174020	-4.52
258570_at	phosphoenolpyruvate carboxylase kina	PPCK2	AT3G04530	1.27	0.34	2.38	0.050107	0.174020	-4.52
249751_at	putative protein similar to unknown prote	---	AT5G24650	-1.27	-0.35	-2.38	0.050131	0.174020	-4.53
250860_at	amino acid transport - like protein amin	CAT6	AT5G04770	1.51	0.59	2.38	0.050106	0.174020	-4.52
249160_at	putative protein similar to unknown prote	---	AT5G42660	-1.19	-0.25	-2.38	0.050126	0.174020	-4.52
245954_at	far-red impaired response protein (FAR	FRS10	AT5G28530	-1.23	-0.30	-2.38	0.050167	0.174120	-4.53
261341_s_a	putative purple acid phosphatase simila	PAP5	AT1G52940 /	1.16	0.21	2.38	0.050205	0.174224	-4.53
265245_at	unknown protein	---	AT2G43060	-1.43	-0.52	-2.38	0.05028	0.174406	-4.53
248630_at	putative protein strong similarity to unkn	---	AT5G48990	-1.21	-0.28	-2.38	0.050266	0.174406	-4.53
258228_at	unknown protein similar to unknown pro	---	AT3G27610	1.18	0.24	2.38	0.050277	0.174406	-4.53
253005_at	hypothetical protein ;supported by full-le	---	AT4G38100	-1.35	-0.43	-2.38	0.05034	0.174586	-4.53
265814_at	hypothetical protein similar to hypotheti	---	AT2G17930	-1.21	-0.28	-2.38	0.050353	0.174606	-4.53

246841_at	nectarin - like protein nectarin I precurs	---	AT5G26700	1.42	0.51	2.38	0.050364	0.174617	-4.53
253922_at	putative protein ; supported by cDNA: g	VTC2	AT4G26850	-1.34	-0.43	-2.38	0.050373	0.174620	-4.53
266553_at	unknown protein ; supported by cDNA:	---	AT2G46170	1.25	0.32	2.38	0.050467	0.174920	-4.53
246511_at	UDP-glucose dehydrogenase-like prote	---	AT5G15490	1.57	0.65	2.38	0.050476	0.174926	-4.53
255143_at	putative protein several hypothetical pro	---	AT4G08430	1.15	0.20	2.38	0.050551	0.175157	-4.53
264947_at	heat shock protein DnaJ, putative simila	---	AT1G77020	1.28	0.35	2.38	0.050572	0.175206	-4.53
247272_at	GTP cyclohydrolase II; 3,4-dihydroxy-2-	---	AT5G14040 /	1.67	0.74	2.38	0.050595	0.175258	-4.53
248165_at	putative protein similar to unknown prote	PHOS32	AT5G54430	-1.26	-0.33	-2.38	0.050655	0.175438	-4.54
255599_at	cyclic nucleotide gated channel (CNGC	ATCNGC1	AT4G01010	1.47	0.56	2.37	0.050699	0.175463	-4.54
246867_at	putative protein various predicted prote	---	AT5G25990	-1.17	-0.23	-2.37	0.050699	0.175463	-4.54
260097_at	putative transporter similar to organic ca	AtOCT1	AT1G73220	3.03	1.60	2.37	0.050701	0.175463	-4.54
261889_at	unknown protein	---	AT1G80810	-1.23	-0.30	-2.37	0.050685	0.175463	-4.54
AFFX-PheX	B. subtilis /GEN=pheA /DB_XREF=gb:M	---	---	-1.52	-0.60	-2.37	0.050699	0.175463	-4.54
261407_at	unknown protein ;supported by full-lengt	---	AT1G18810	-1.36	-0.44	-2.37	0.050713	0.175481	-4.54
258402_at	unknown protein very similar to unknow	---	AT3G15450	1.57	0.65	2.37	0.050764	0.175630	-4.54
266314_at	Argonaute (AGO1)-like protein ; suppor	AGO4	AT2G27040	-1.30	-0.37	-2.37	0.050854	0.175913	-4.54
247502_at	putative protein predicted proteins, Arat	---	AT5G61940	-1.19	-0.25	-2.37	0.050862	0.175915	-4.54
249554_at	CRS2 -like protein CRS2, Zea mays, E	---	AT5G38290	-1.59	-0.67	-2.37	0.050903	0.176031	-4.54
266139_at	Expressed protein ; supported by full-ler	---	AT2G28085	1.49	0.57	2.37	0.050986	0.176289	-4.54
264948_at	RNA helicase, putative similar to RNA h	---	AT1G77030	1.19	0.25	2.37	0.051018	0.176373	-4.54
261440_at	hypothetical protein predicted by genem	---	AT1G28510	1.20	0.27	2.37	0.051026	0.176377	-4.54
264533_s_a	H+/Ca2+ antiporter, putative similar to	CAX5	AT1G55720 /	1.21	0.28	2.37	0.051094	0.176584	-4.54
251467_at	putative protein putative proteins - Arabi	---	AT3G59470	-1.26	-0.33	-2.37	0.051118	0.176614	-4.54
260301_at	hypothetical protein ;supported by full-le	---	AT1G80290	1.24	0.31	2.37	0.051118	0.176614	-4.54
260254_at	putative glycerophosphodiester phospho	---	AT1G74210	1.20	0.26	2.37	0.051162	0.176725	-4.55
256158_at	hypothetical protein contains similarity to	ATPSK1	AT1G13590	1.19	0.26	2.37	0.051166	0.176725	-4.55
261861_at	hypothetical protein predicted by genem	---	AT1G50450	-1.49	-0.58	-2.37	0.051176	0.176735	-4.55
258243_at	carbamoyl phosphate synthetase small	CARA	AT3G27740	-1.33	-0.41	-2.37	0.051203	0.176746	-4.55
245665_at	unknown protein ;supported by full-lengt	---	AT1G28250	1.23	0.30	2.37	0.051193	0.176746	-4.55
267073_at	unknown protein	---	AT2G41160	1.28	0.35	2.37	0.051211	0.176746	-4.55
249618_at	putative protein predicted proteins, Arat	---	AT5G37490	3.31	1.73	2.37	0.051208	0.176746	-4.55
251854_at	putative protein various predicted prote	---	AT3G54800	1.19	0.25	2.37	0.051269	0.176920	-4.55
254469_at	hypothetical protein	---	AT4G20470	1.20	0.26	2.37	0.051287	0.176957	-4.55
253618_at	nodulin-like protein MtN21 gene produc	---	AT4G30420	-1.16	-0.22	-2.37	0.051295	0.176957	-4.55
245420_at	hypothetical protein	---	AT4G17410	-1.23	-0.30	-2.37	0.051329	0.177047	-4.55

247017_at	putative protein similar to unknown prote	---	AT5G66980	1.16	0.22	2.36	0.051396	0.177253	-4.55
263584_at	NAM (no apical meristem)-like protein si	anac036	AT2G17040	1.82	0.86	2.36	0.051425	0.177326	-4.55
259340_at	hypothetical protein predicted using gen	PYK10	AT3G03870 /	-1.24	-0.31	-2.36	0.051487	0.177444	-4.55
255890_at	rhodanese-like family protein predicted l	---	AT1G17850	-1.39	-0.47	-2.36	0.051498	0.177444	-4.55
264589_at	hypothetical protein	---	AT2G17650	-1.27	-0.35	-2.36	0.05149	0.177444	-4.55
259804_at	cytosolic factor, putative similar to GI:80	---	AT1G72160	-1.42	-0.50	-2.36	0.051492	0.177444	-4.55
253012_at	putative protein Caenorhabditis elegans	---	AT4G37900	1.21	0.28	2.36	0.051487	0.177444	-4.55
255020_at	isoleucine-tRNA ligase - like protein iso	---	AT4G10320	-1.16	-0.21	-2.36	0.051575	0.177571	-4.55
261846_at	hypothetical protein similar to hypothetic	---	AT1G11540	1.23	0.30	2.36	0.051582	0.177571	-4.55
264879_at	cotton fiber expressed protein, putative	---	AT1G61260	1.56	0.64	2.36	0.051571	0.177571	-4.55
262659_at	putative nucleoside triphosphatase simi	---	AT1G14240	1.21	0.27	2.36	0.051569	0.177571	-4.55
256854_at	hypothetical protein predicted by genem	---	AT3G15180	-1.19	-0.26	-2.36	0.051572	0.177571	-4.55
261194_at	unknown protein contains Pfam profiles	---	AT1G12770 /	-1.15	-0.20	-2.36	0.051571	0.177571	-4.55
253829_at	Medicago nodulin N21-like protein MtN2	---	AT4G28040	1.91	0.93	2.36	0.051597	0.177597	-4.55
253366_at	putative protein predicted protein, Arabi	---	AT4G33180	1.28	0.36	2.36	0.051617	0.177639	-4.55
256071_at	ubiquitin, putative similar to ubiquitin GI	---	AT1G13640	-1.34	-0.42	-2.36	0.051628	0.177651	-4.55
259909_at	unknown protein ; supported by full-leng	MEE9	AT1G60870	-1.19	-0.25	-2.36	0.051643	0.177673	-4.55
253116_at	putative protein CRP1, Zea mays, gb:A	---	AT4G35850	-1.42	-0.50	-2.36	0.051654	0.177686	-4.56
252866_at	putative protein	---	AT4G39840	1.69	0.75	2.36	0.051719	0.177877	-4.56
259775_at	hypothetical protein predicted by genem	---	AT1G29530	-1.38	-0.47	-2.36	0.051725	0.177877	-4.56
266991_at	putative CDP-diacylglycerol--glycerol-3-	PGP1	AT2G39290	-1.16	-0.22	-2.36	0.051756	0.177954	-4.56
255473_at	putative protein similar to several protein	---	AT4G02450	-1.18	-0.23	-2.36	0.051808	0.178000	-4.56
259338_at	s-syntaxin-like protein similar to s-syntax	SYP131	AT3G03800	1.18	0.23	2.36	0.051783	0.178000	-4.56
267470_at	cinnamate-4-hydroxylase molecular mar	C4H	AT2G30490	1.70	0.76	2.36	0.051799	0.178000	-4.56
255498_at	putative vacuolar ATPase similar to vac	---	AT4G02620	1.15	0.20	2.36	0.051804	0.178000	-4.56
257375_at	unknown protein	---	AT2G38640	1.75	0.80	2.36	0.051805	0.178000	-4.56
245416_at	putative protein	---	AT4G17350	-1.25	-0.32	-2.36	0.051882	0.178110	-4.56
247519_at	NAM, no apical meristem, - like protein	ANAC100	AT5G61430	1.26	0.33	2.36	0.051887	0.178110	-4.56
248349_at	progesterone-binding protein-like ; supp	MSBP1	AT5G52240	1.30	0.38	2.36	0.051865	0.178110	-4.56
256233_at	ankyrin-like protein contains Pfam profile	ITN1	AT3G12360	1.18	0.23	2.36	0.05188	0.178110	-4.56
251603_at	putative protein wall-associated kinase	---	AT3G57760	1.62	0.69	2.36	0.051859	0.178110	-4.56
260133_at	ethylene-response protein, ETR1 identi	ETR1	AT1G66340	1.17	0.22	2.36	0.051861	0.178110	-4.56
261402_at	wall-associated kinase 4, putative simila	RFO1	AT1G79670	1.40	0.48	2.36	0.051903	0.178139	-4.56
258797_at	auxin-induced protein identical to GB:AA	IAA16	AT3G04730	-1.31	-0.39	-2.36	0.051937	0.178174	-4.56
260182_at	unknown protein similar to IFA-binding p	---	AT1G70750	1.23	0.29	2.36	0.051932	0.178174	-4.56

253003_s_a	putative protein tapetum specific protein	---	AT4G38300 /	-1.23	-0.30	-2.36	0.051924	0.178174	-4.56
248795_at	Myb-related transcription activator-like ;	---	AT5G47390	-1.17	-0.23	-2.36	0.051987	0.178319	-4.56
248508_at	histone acetyltransferase ;supported by	ELO3	AT5G50320	-1.29	-0.36	-2.36	0.052003	0.178319	-4.56
252323_at	putative protein probable transcription r	KING1	AT3G48530	-1.34	-0.42	-2.36	0.051996	0.178319	-4.56
262592_at	unknown protein ESTs gb|H37295 and g	---	AT1G15400	1.31	0.39	2.36	0.052015	0.178334	-4.56
255240_at	coded for by A. thaliana cDNA Z18000	IBR1	AT4G05530	-1.20	-0.26	-2.36	0.052096	0.178559	-4.56
260356_at	unknown protein ; supported by full-leng	ATMINE1	AT1G69390	-1.20	-0.27	-2.36	0.052091	0.178559	-4.56
249010_at	unknown protein ; supported by cDNA:	---	AT5G44580	-1.38	-0.47	-2.36	0.052112	0.178588	-4.56
261955_at	proteasome regulatory subunit, putative	RPN12a	AT1G64520	-1.17	-0.23	-2.35	0.052144	0.178671	-4.56
261524_at	hypothetical protein predicted by genem	---	AT1G14300	-1.24	-0.31	-2.35	0.052177	0.178757	-4.57
260912_at	ATP-dependent Clp protease proteolytic	CLPP5	AT1G02560	-1.19	-0.25	-2.35	0.052245	0.178937	-4.57
262965_at	hypothetical protein predicted by genem	---	AT1G54310	-1.30	-0.37	-2.35	0.052245	0.178937	-4.57
261405_at	unknown protein ;supported by full-lengt	---	AT1G18740	1.47	0.55	2.35	0.052276	0.179016	-4.57
247907_at	unknown protein	---	AT5G57460	1.18	0.24	2.35	0.052286	0.179022	-4.57
260171_at	hypothetical protein predicted by gensca	---	AT1G71910	1.59	0.67	2.35	0.052298	0.179035	-4.57
261021_at	hypothetical protein similar to reticuline	---	AT1G26380	2.39	1.26	2.35	0.052334	0.179107	-4.57
250502_at	heat shock protein 70 (Hsc70-5) ; supp	MTHSC70	AT5G09590	-1.52	-0.60	-2.35	0.052335	0.179107	-4.57
245460_at	disease resistance RPP5 like protein (fr	RLM3	AT4G16990	-1.45	-0.54	-2.35	0.052356	0.179141	-4.57
266532_at	putative glucosyltransferase ;supported	---	AT2G16890	2.61	1.38	2.35	0.05236	0.179141	-4.57
254892_at	putative protein other hypothetical prote	---	AT4G11800	1.25	0.32	2.35	0.052387	0.179205	-4.57
255136_s_a	putative protein chromatin structural pro	---	AT4G08350 /	-1.24	-0.31	-2.35	0.052413	0.179267	-4.57
253464_at	putative protein ; supported by full-leng	---	AT4G32030	1.28	0.36	2.35	0.052443	0.179318	-4.57
254867_at	hypothetical proteins	---	AT4G12240	-1.31	-0.39	-2.35	0.052442	0.179318	-4.57
256819_at	unknown protein contains Pfam profile:	---	AT3G21390	-1.19	-0.25	-2.35	0.052455	0.179324	-4.57
265299_at	putative retroelement pol polyprotein co	---	---	1.32	0.40	2.35	0.052461	0.179324	-4.57
251901_at	putative protein axi1 protein, Nicotiana	---	AT3G54100	1.26	0.33	2.35	0.052478	0.179358	-4.57
259237_at	putative 2-cys peroxiredoxin BAS1 prec	---	AT3G11630	-1.30	-0.38	-2.35	0.052512	0.179410	-4.57
257865_at	protein kinase, putative contains Pfam	---	AT3G17750	-1.17	-0.22	-2.35	0.052525	0.179410	-4.57
247946_at	putative protein similar to unknown prot	CIA2	AT5G57180	-1.64	-0.72	-2.35	0.052519	0.179410	-4.57
252445_at	beta-D-glucan exohydrolase - like prote	---	AT3G47000	-1.21	-0.28	-2.35	0.052516	0.179410	-4.57
257051_at	squamosa promoter binding protein-like	SPL5	AT3G15270	-1.79	-0.84	-2.35	0.052534	0.179412	-4.57
256250_at	integral membrane protein, putative cor	---	AT3G11320	1.29	0.36	2.35	0.052572	0.179516	-4.57
256545_at	hypothetical protein predicted by genem	---	---	-1.21	-0.28	-2.35	0.052605	0.179575	-4.57
256038_at	hypothetical protein similar to polygalact	---	AT1G19170	-1.25	-0.32	-2.35	0.052604	0.179575	-4.57
248831_at	putative protein contains similarity to SE	---	AT5G47160	-1.22	-0.29	-2.35	0.052616	0.179584	-4.57

255452_at	hypothetical protein similar to A. thalian	---	AT4G02880	-1.18	-0.24	-2.35	0.052633	0.179590	-4.57
251086_at	putative protein hypothetical protein At2	---	AT5G01450	1.29	0.36	2.35	0.052628	0.179590	-4.57
252013_at	putative protein	---	AT3G52860	-1.19	-0.25	-2.35	0.052653	0.179632	-4.57
251803_at	putative protein predicted proteins, Arat	---	AT3G55350	-1.28	-0.35	-2.35	0.052698	0.179733	-4.58
261857_at	hypothetical protein predicted by gensca	---	AT1G50620	-1.53	-0.62	-2.35	0.052695	0.179733	-4.58
250340_at	putative protein predicted proteins in Sy	---	AT5G11840	-1.29	-0.37	-2.35	0.052743	0.179831	-4.58
254214_at	putative potassium transport protein (TI	TRH1	AT4G23640	1.24	0.31	2.35	0.052739	0.179831	-4.58
263648_at	hypothetical protein predicted by gensca	---	AT1G04390	-1.26	-0.33	-2.35	0.052779	0.179927	-4.58
264055_at	putative protein kinase contains a protei	---	AT2G28590	-1.24	-0.31	-2.35	0.052803	0.179982	-4.58
260351_at	hypothetical protein predicated by genso	---	AT1G69380	-1.48	-0.57	-2.35	0.052826	0.180030	-4.58
257969_at	hypothetical protein predicted by genem	---	AT3G27520	-1.38	-0.47	-2.35	0.052836	0.180030	-4.58
263660_at	unknown protein ESTs gb|N65789,gb|T	MPI7	AT1G04260	1.20	0.26	2.35	0.052841	0.180030	-4.58
261046_at	flavonol 3-o-glucosyltransferase, putativ	---	AT1G01390	-1.34	-0.42	-2.35	0.052896	0.180155	-4.58
256917_at	unknown protein contains Pfam profile:	---	AT3G18930	1.18	0.24	2.35	0.052893	0.180155	-4.58
250843_at	putative RNA-binding protein astrocytic	BTR1L	AT5G04430	-1.18	-0.24	-2.34	0.052901	0.180155	-4.58
266772_s_a	predicted by genefinder	---	AT2G03020 /	-1.34	-0.43	-2.34	0.052915	0.180176	-4.58
257634_s_a	cytochrome P450, putative similar to cy	CYP71B19	AT3G26170 /	1.46	0.55	2.34	0.052966	0.180178	-4.58
265283_at	unknown protein predicted by genefinde	MUR3	AT2G20370	1.32	0.41	2.34	0.052977	0.180178	-4.58
256826_at	hypothetical protein predicted by genem	---	AT3G18540	1.16	0.22	2.34	0.052925	0.180178	-4.58
258822_s_a	unknown protein contains Pfam profile:	---	AT3G07220 /	-1.38	-0.46	-2.34	0.052988	0.180178	-4.58
249958_at	plasma membrane associated protein -	---	AT5G18970	1.30	0.38	2.34	0.052957	0.180178	-4.58
265102_at	putative peroxidase similar to cationic pe	---	AT1G30870	1.23	0.29	2.34	0.052989	0.180178	-4.58
266696_at	copia-like retroelement pol polyprotein ;	---	AT2G19680	-1.25	-0.32	-2.34	0.052935	0.180178	-4.58
246024_at	putative protein predicted protein - Arab	---	AT5G21130	1.25	0.32	2.34	0.052995	0.180178	-4.58
262481_at	unknown protein Location of ests 147K	---	AT1G17080	1.22	0.28	2.34	0.052951	0.180178	-4.58
262579_at	hypothetical protein predicted by gensca	---	AT1G15320	-1.18	-0.24	-2.34	0.052981	0.180178	-4.58
246198_at	geranylgeranyl pyrophosphate synthase	GGPS1	AT4G36810	-1.29	-0.36	-2.34	0.053015	0.180198	-4.58
247708_at	putative protein COP1-interacting prote	---	AT5G59550	2.04	1.03	2.34	0.053016	0.180198	-4.58
259480_at	hypothetical protein predicted by gensca	---	AT1G19010	1.30	0.38	2.34	0.053037	0.180239	-4.58
246840_at	putative protein ;supported by full-lengt	---	AT5G26610	-1.16	-0.21	-2.34	0.053046	0.180243	-4.58
253043_at	putative protein predicted protein, Arabi	LBD39	AT4G37540	-1.43	-0.52	-2.34	0.053059	0.180261	-4.58
252797_at	putative protein	---	---	1.30	0.37	2.34	0.053082	0.180313	-4.58
247394_at	putative protein predicted proteins, Arat	---	AT5G62860	1.48	0.56	2.34	0.053092	0.180319	-4.58
246230_at	SCARECROW-like protein	---	AT4G36710	-1.19	-0.26	-2.34	0.053116	0.180345	-4.58
247771_at	Ran binding protein 1 homolog - like Ra	RANBP1	AT5G58590	-1.23	-0.30	-2.34	0.05313	0.180345	-4.58

259229_at	unknown protein similar to transcriptiona	ADA2A	AT3G07740	-1.27	-0.34	-2.34	0.053131	0.180345	-4.58
257437_s_a	hypothetical protein predicted by gensca	---	AT2G16290 /	-1.19	-0.26	-2.34	0.053115	0.180345	-4.58
255794_at	putative NAM (no apical meristem)-like p	ANAC041	AT2G33480	1.54	0.62	2.34	0.053147	0.180372	-4.58
248433_at	putative protein strong similarity to unkn	---	AT5G51400	1.18	0.24	2.34	0.053162	0.180375	-4.58
264791_at	predicted protein	---	AT2G17845	-1.16	-0.22	-2.34	0.053163	0.180375	-4.58
261701_at	hypothetical protein similar to hypothetic	HAF01	AT1G32750	-1.16	-0.21	-2.34	0.053224	0.180470	-4.59
255042_at	putative protein hypothetical protein T1	---	AT4G09630	1.20	0.26	2.34	0.05322	0.180470	-4.59
257474_at	DNA-3-methyladenine glycosidase, put	---	AT1G80850	1.24	0.30	2.34	0.05322	0.180470	-4.59
262090_at	CREB-binding protein, putative similar t	HAC4	AT1G55970	-1.21	-0.27	-2.34	0.053231	0.180470	-4.59
259111_at	alpha subunit of F-actin capping protein	---	AT3G05520	-1.27	-0.35	-2.34	0.053217	0.180470	-4.59
249585_at	5-oxoprolinase -like protein 5-oxoprolina	OXP1	AT5G37830	-1.20	-0.26	-2.34	0.05327	0.180558	-4.59
255578_at	predicted protein of unknown function s	---	AT4G01450	-1.52	-0.60	-2.34	0.053279	0.180558	-4.59
251530_at	putative protein several hypothetical pro	---	AT3G58520	-1.30	-0.38	-2.34	0.053283	0.180558	-4.59
260719_at	unknown protein	---	AT1G48090	-1.26	-0.34	-2.34	0.053297	0.180558	-4.59
249211_at	putative protein similar to unknown prote	---	AT5G42680	-1.50	-0.58	-2.34	0.053294	0.180558	-4.59
251383_at	beta-tubulin cofactor - like protein beta-	TTN1	AT3G60740	-1.34	-0.43	-2.34	0.053316	0.180569	-4.59
266844_at	hypothetical protein predicted by genefir	---	AT2G26120	-1.22	-0.29	-2.34	0.053316	0.180569	-4.59
266704_at	putative N-acetyl-gamma-glutamyl-phos	---	AT2G19940	-1.25	-0.33	-2.34	0.053328	0.180573	-4.59
260488_at	flowering protein CONSTANS, putative	TIFY2A	AT1G51600	-1.26	-0.34	-2.34	0.053333	0.180573	-4.59
247805_at	ATGP1-like protein	ATYKT62	AT5G58180	1.33	0.41	2.34	0.053356	0.180624	-4.59
249575_at	low-molecular-weight heat shock protei	---	AT5G37670	-1.33	-0.41	-2.34	0.053408	0.180735	-4.59
260878_at	scarecrow-like 1 identical to scarecrow-l	SCL1	AT1G21450	1.31	0.39	2.34	0.053423	0.180735	-4.59
264686_at	shaggy-like protien kinase, kappa Ident	ATSK41	AT1G09840	-1.16	-0.22	-2.34	0.053424	0.180735	-4.59
261403_at	unknown protein ;supported by full-lengt	SYP52	AT1G79590	-1.18	-0.23	-2.34	0.053428	0.180735	-4.59
257217_at	phosphoenolpyruvate carboxylase (PPC	ATPPC3	AT3G14940	-1.30	-0.38	-2.34	0.053398	0.180735	-4.59
262764_at	putative cytochrome P450 monooxygen	CYP86C3	AT1G13140	1.19	0.26	2.34	0.053474	0.180862	-4.59
255019_at	putative protein IB1C3-1 protein, Arabic	---	AT4G10210	1.19	0.25	2.34	0.053501	0.180929	-4.59
246378_at	integral membrane protein, putative sim	---	AT1G57620	1.18	0.24	2.34	0.053522	0.180972	-4.59
256524_at	glutamine synthetase, putative similar t	ATGSR2	AT1G66200	1.22	0.29	2.33	0.053685	0.181476	-4.59
265668_at	putative alanine acetyl transferase ;sup	---	AT2G32020	1.95	0.97	2.33	0.053687	0.181476	-4.59
252822_at	Expressed protein ; supported by full-ler	---	AT4G39955	-1.24	-0.31	-2.33	0.053728	0.181574	-4.59
255792_at	AT-hook DNA-binding protein (AHP1) al	---	AT2G33620	-1.26	-0.34	-2.33	0.053732	0.181574	-4.59
247098_at	GTP-binding protein-like	---	AT5G66470	-1.35	-0.43	-2.33	0.053751	0.181613	-4.60
253046_at	cytochrome P450 - like protein cytochro	CYP81D8	AT4G37370	2.13	1.09	2.33	0.053773	0.181661	-4.60
260890_at	cysteine proteinase contains similarity to	---	AT1G29090	1.31	0.39	2.33	0.053808	0.181750	-4.60

252613_at	putative protein hypothetical protein At2	---	AT3G45190	-1.17	-0.22	-2.33	0.05395	0.182201	-4.60
261448_at	tonoplast intrinsic protein, alpha (alpha-	---	AT1G21140	1.35	0.43	2.33	0.054086	0.182636	-4.60
263291_at	unknown protein	---	AT2G10920	-1.20	-0.26	-2.33	0.054105	0.182673	-4.60
266416_at	unknown protein ; supported by full-leng	---	AT2G38710	1.31	0.39	2.33	0.054138	0.182756	-4.60
248225_at	unknown protein	---	AT5G53740	1.19	0.26	2.33	0.054197	0.182928	-4.60
259449_at	hypothetical protein similar to putative s	---	AT1G13800	-1.24	-0.31	-2.33	0.054231	0.183018	-4.60
261414_at	Expressed protein ; supported by full-ler	---	AT1G07795	1.32	0.40	2.33	0.054271	0.183124	-4.60
265179_at	unknown protein predicted by genemark	---	AT1G23650	1.27	0.34	2.33	0.054296	0.183183	-4.61
254486_at	putative protein crp1 protein, Zea mays	---	AT4G20770	-1.23	-0.30	-2.33	0.054328	0.183262	-4.61
261905_at	hypothetical protein contains similarity to	---	AT1G65070	-1.20	-0.26	-2.33	0.054337	0.183267	-4.61
264578_at	hypothetical protein predicted by genem	---	AT1G05370	1.17	0.22	2.33	0.054359	0.183313	-4.61
250925_at	putative protein ; supported by full-leng	---	AT5G03370	-1.25	-0.33	-2.33	0.054374	0.183337	-4.61
264212_at	putative tRNA adenylyltransferase Simil	---	AT1G22660	-1.33	-0.42	-2.33	0.054396	0.183383	-4.61
255836_at	putative splicing factor U2AF large chair	---	AT2G33440	-1.30	-0.37	-2.33	0.054416	0.183424	-4.61
264561_at	uracil phosphoribosyltransferase, putati	---	AT1G55810	1.31	0.39	2.33	0.054448	0.183503	-4.61
260596_at	unknown protein	TIM50	AT1G55900	-1.37	-0.46	-2.32	0.054463	0.183527	-4.61
265366_at	putative N-acetylglucosaminyltransferas	---	AT2G13290	-1.22	-0.28	-2.32	0.054471	0.183529	-4.61
261100_at	RNA polymerase IIA large subunit, puta	NRPD1A	AT1G63020	1.21	0.28	2.32	0.05453	0.183591	-4.61
254248_at	serine/threonine kinase serine/threonine	---	AT4G23270	1.41	0.49	2.32	0.054499	0.183591	-4.61
251971_at	glucosyltransferase - like protein glucos	UGT73C7	AT3G53160	2.61	1.38	2.32	0.05453	0.183591	-4.61
264847_at	clathrin assembly protein AP19, small s	AP19	AT2G17380	1.15	0.21	2.32	0.054528	0.183591	-4.61
263427_at	hypothetical protein predicted by gensca	---	AT2G22260	-1.18	-0.23	-2.32	0.054511	0.183591	-4.61
249148_at	unknown protein ; supported by cDNA:	---	AT5G43260	1.37	0.46	2.32	0.054546	0.183619	-4.61
261349_at	Expressed protein ; supported by full-ler	AT1G7961	---	1.17	0.23	2.32	0.054567	0.183661	-4.61
262859_at	hypothetical protein predicted by genem	---	AT1G64790	-1.21	-0.27	-2.32	0.054587	0.183674	-4.61
262954_at	rubredoxin, putative similar to rubredox	---	AT1G54500	-1.26	-0.34	-2.32	0.054595	0.183674	-4.61
255134_at	putative protein	---	AT4G08330	-1.22	-0.29	-2.32	0.054582	0.183674	-4.61
247854_at	contains similarity to phosphoesterase	---	AT5G58200	-1.22	-0.29	-2.32	0.054614	0.183699	-4.61
259118_at	unknown protein similar to unknown pro	---	AT3G01310	-1.26	-0.34	-2.32	0.054619	0.183699	-4.61
252884_at	SEC14 - like protein phosphatidylinosito	---	AT4G39170	-1.24	-0.31	-2.32	0.054647	0.183767	-4.61
247789_at	putative protein various predicted prote	---	AT5G58680	1.24	0.31	2.32	0.054766	0.184141	-4.61
246552_at	putative protein	---	AT5G15420	-1.45	-0.53	-2.32	0.054784	0.184175	-4.61
257153_at	unknown protein ; supported by cDNA:	---	AT3G27220	-1.31	-0.39	-2.32	0.054861	0.184405	-4.62
263283_at	hypothetical protein predicted by gensca	---	AT2G36090	-1.20	-0.26	-2.32	0.054911	0.184543	-4.62
266666_at	hypothetical protein predicted by gensca	---	AT2G29780	-1.19	-0.26	-2.32	0.054918	0.184543	-4.62

255628_at	coded for by A. thaliana cDNA T45454	GIF3	AT4G00850	-1.21	-0.27	-2.32	0.054934	0.184569	-4.62
250531_at	GTP-binding protein LepA homolog	---	AT5G08650	-1.33	-0.41	-2.32	0.055	0.184763	-4.62
246379_s_a	60S ribosomal protein L21, putative sim	---	AT1G57660 /	-1.33	-0.42	-2.32	0.055043	0.184881	-4.62
247375_at	Expressed protein ; supported by full-ler	---	AT5G63135	-1.15	-0.21	-2.32	0.055054	0.184890	-4.62
245342_at	ribosomal protein ;supported by full-leng	---	AT4G16720	-1.31	-0.39	-2.32	0.055095	0.185001	-4.62
259626_at	bZIP transcription factor, putative conta	ATBZIP60	AT1G42990	1.97	0.98	2.32	0.055118	0.185023	-4.62
247310_at	putative protein contains similarity to SN	CHR24	AT5G63950	-1.30	-0.37	-2.32	0.055115	0.185023	-4.62
255194_at	score=37.6, E=2.9e-07, N=3	---	AT4G07410	-1.32	-0.40	-2.32	0.05513	0.185037	-4.62
257373_at	hypothetical protein predicted by genefir	---	AT2G43140	1.27	0.34	2.32	0.055204	0.185260	-4.62
262763_at	hypothetical protein	---	AT1G28690	-1.28	-0.36	-2.31	0.055251	0.185391	-4.62
245825_at	protein kinase, putative similar to protei	ATSK42	AT1G57870	-1.21	-0.27	-2.31	0.055295	0.185508	-4.62
258857_at	putative serine carboxypeptidase II simil	scpl25	AT3G02110	1.89	0.92	2.31	0.055343	0.185636	-4.62
244968_at	ribosomal protein L33	---	---	-1.23	-0.30	-2.31	0.055349	0.185636	-4.62
263610_at	putative beta-1,3-glucanase	---	AT2G16230	1.24	0.31	2.31	0.055395	0.185765	-4.63
262818_at	hypothetical protein predicted by gensca	---	AT1G11755 /	-1.20	-0.26	-2.31	0.055446	0.185889	-4.63
257310_at	ATP-dependent RNA helicase, putative	---	AT3G26560	-1.23	-0.30	-2.31	0.055449	0.185889	-4.63
250320_at	CCAAT box binding factor/ transcription	NF-YA1	AT5G12840	-1.21	-0.28	-2.31	0.055465	0.185917	-4.63
261996_at	AIG1-like protein similar to AIG1 protein	---	AT1G33830	-1.16	-0.21	-2.31	0.05548	0.185940	-4.63
265028_at	hypothetical protein predicted by genefir	---	AT1G24530	1.85	0.89	2.31	0.055502	0.185956	-4.63
257644_at	unknown protein ;supported by full-leng	AOC3	AT3G25780	2.10	1.07	2.31	0.055495	0.185956	-4.63
245155_at	putative protein similarity to predicted p	---	AT5G12470	-1.33	-0.41	-2.31	0.055539	0.186028	-4.63
252844_at	putative protein several hypothetical pro	---	AT3G42140	1.23	0.30	2.31	0.055539	0.186028	-4.63
267629_at	putative DNA polymerase delta small su	POLD2	AT2G42120	-1.29	-0.37	-2.31	0.05557	0.186105	-4.63
254617_s_a	ribosomal protein L11, cytosolic ;suppo	RPL16B	AT4G18730 /	-1.33	-0.41	-2.31	0.055594	0.186156	-4.63
251526_at	putative protein several serine/threonine	---	AT3G58640	1.24	0.31	2.31	0.055655	0.186307	-4.63
251132_at	putative protein Myb-related transcriptio	---	AT5G01200	-1.29	-0.37	-2.31	0.055653	0.186307	-4.63
247291_at	unknown protein	---	AT5G64480	-1.21	-0.27	-2.31	0.055698	0.186423	-4.63
246523_at	CONSTANS-like 1	COL1	AT5G15850	-1.35	-0.43	-2.31	0.05571	0.186435	-4.63
257176_s_a	cyclopropane-fatty-acyl-phospholipid sy	---	AT3G23510 /	1.86	0.89	2.31	0.055768	0.186602	-4.63
257892_at	unknown protein similar to ER6 protein (	---	AT3G17020	-1.20	-0.26	-2.31	0.055821	0.186751	-4.63
261310_at	hypothetical protein predicted by genem	PDE247	AT1G05750	-1.27	-0.34	-2.31	0.055839	0.186785	-4.63
251688_at	putative protein hypothetical protein At2	---	AT3G56480	1.50	0.58	2.31	0.055874	0.186875	-4.63
254184_at	hypothetical protein	---	AT4G23970	1.20	0.26	2.31	0.055913	0.186977	-4.63
253238_at	putative protein (fragment)	---	AT4G34480	1.24	0.31	2.31	0.055932	0.187006	-4.64
261476_at	hypothetical protein contains similarity to	---	AT1G14480	1.50	0.59	2.31	0.055938	0.187006	-4.64

257351_at	putative mitochondrial carrier protein	MBAC1	AT2G33820	-1.26	-0.33	-2.31	0.055955	0.187035	-4.64
255598_at	putative protein similar to nucleolin prote	---	AT4G00830	-1.27	-0.34	-2.31	0.055965	0.187042	-4.64
248452_at	putative protein contains similarity to tra	---	AT5G51300	-1.16	-0.21	-2.31	0.056009	0.187161	-4.64
252378_at	receptor kinase-like protein protein kina	---	AT3G47570	1.34	0.42	2.31	0.056036	0.187186	-4.64
267106_s_a	putative vacuolar sorting receptor identi	ATVSR3	AT2G14720 /	1.26	0.33	2.31	0.056028	0.187186	-4.64
265339_at	putative inorganic pyrophosphatase ;su	AtPPa2	AT2G18230	-1.38	-0.46	-2.31	0.056041	0.187186	-4.64
246103_at	putative protein	AN3	AT5G28640	1.15	0.21	2.30	0.056053	0.187197	-4.64
246339_at	RP19 gene for chloroplast ribosomal pro	RPL9	AT3G44890	-1.22	-0.29	-2.30	0.056109	0.187357	-4.64
251769_at	receptor kinase - like protein receptor k	CCR3	AT3G55950	2.66	1.41	2.30	0.056134	0.187414	-4.64
261069_at	small G protein, putative similar to GB:Z	ATRABA2	AT1G07410	1.16	0.22	2.30	0.056186	0.187456	-4.64
262298_at	unknown protein Similar to gb|AF15188	---	AT1G27530	-1.17	-0.22	-2.30	0.056164	0.187456	-4.64
263037_at	conserved hypothetical protein	---	AT1G23230	-1.25	-0.32	-2.30	0.056179	0.187456	-4.64
261661_at	lysophospholipase homolog, putative si	---	AT1G18360	-1.35	-0.43	-2.30	0.056159	0.187456	-4.64
248187_at	zinc-binding protein-like ; supported by	---	AT5G53940	-1.22	-0.28	-2.30	0.056187	0.187456	-4.64
264554_at	putative cinnamyl alcohol dehydrogena	---	AT1G09510	1.27	0.34	2.30	0.056254	0.187650	-4.64
256745_at	UDP-glucose dehydrogenase, putative	---	AT3G29360	1.25	0.32	2.30	0.05629	0.187720	-4.64
258459_at	hypothetical protein predicted by genma	---	---	1.21	0.28	2.30	0.056291	0.187720	-4.64
252433_at	putative protein putative hydrolyse - Ara	---	AT3G47560	-1.33	-0.41	-2.30	0.056375	0.187869	-4.64
262354_at	H+-transporting ATPase protein, putativ	VHA-E3	AT1G64200	1.52	0.61	2.30	0.056363	0.187869	-4.64
248594_at	unknown protein ; supported by full-leng	---	AT5G49210	-1.32	-0.41	-2.30	0.056385	0.187869	-4.64
261495_at	hypothetical protein predicted by genem	---	AT1G28410	-1.21	-0.27	-2.30	0.05638	0.187869	-4.64
255541_s_a	P-glycoprotein-like protein pgp3 similar	PGP5	AT4G01820 /	-1.17	-0.23	-2.30	0.056373	0.187869	-4.64
263032_at	unknown protein ;supported by full-lengt	---	AT1G23850	1.56	0.64	2.30	0.056355	0.187869	-4.64
265522_at	putative TPR repeat nuclear phosphopr	ELF8	AT2G06210	-1.23	-0.29	-2.30	0.056396	0.187877	-4.64
266800_at	hypothetical protein predicted by genefir	---	AT2G22880	3.59	1.84	2.30	0.056411	0.187899	-4.64
247235_at	putative protein contains similarity to Fts	---	AT5G64580	-1.39	-0.48	-2.30	0.056424	0.187915	-4.64
261952_at	unknown protein	---	AT1G64430	-1.16	-0.21	-2.30	0.05645	0.187955	-4.64
261241_at	subtilisin-like serine protease contains s	---	AT1G32950	1.19	0.25	2.30	0.056461	0.187955	-4.64
251326_at	putative protein stamina pistilloidia (Stp	HWS	AT3G61590	-1.28	-0.36	-2.30	0.056453	0.187955	-4.64
264106_at	unknown protein	SERK4	AT2G13790	1.18	0.24	2.30	0.056527	0.188120	-4.65
246585_at	myb transcription factor werewolf (WER	ATMYB66	AT5G14750	-1.18	-0.23	-2.30	0.056527	0.188120	-4.65
265662_at	putative C2H2-type zinc finger protein li	FZF	AT2G24500	-1.28	-0.35	-2.30	0.056539	0.188134	-4.65
248034_at	serine threonine-specific protein kinase	D6PK	AT5G55910	-1.22	-0.29	-2.30	0.056553	0.188143	-4.65
257357_at	hypothetical protein predicted by gensca	---	AT2G41050	1.19	0.25	2.30	0.056558	0.188143	-4.65
247780_at	dehydrodolichyl diphosphate - like prote	---	AT5G58770	-1.68	-0.75	-2.30	0.056597	0.188243	-4.65

248419_at	putative protein similar to unknown prote	EXL3	AT5G51550	1.40	0.48	2.30	0.056645	0.188350	-4.65
265442_at	hypothetical protein predicted by genefir	---	AT2G20940	-1.43	-0.51	-2.30	0.056645	0.188350	-4.65
262690_at	PPR-repeat protein contains multiple PF	---	AT1G62720	-1.19	-0.25	-2.30	0.056684	0.188450	-4.65
247374_at	topoisomerase-like protein ;supported b	---	AT5G63190	1.33	0.41	2.30	0.056762	0.188641	-4.65
264548_at	unknown protein ; supported by cDNA: g	---	AT1G55680	-1.20	-0.26	-2.30	0.056766	0.188641	-4.65
244988_s_a	ribosomal protein L23	---	---	-1.25	-0.32	-2.30	0.056765	0.188641	-4.65
265563_s_a	hypothetical protein predicted by gensca	---	---	1.15	0.20	2.30	0.056794	0.188678	-4.65
250312_at	unknown protein	---	AT5G12260	-1.23	-0.30	-2.30	0.05679	0.188678	-4.65
261708_at	unknown protein similar to hypothetical p	---	AT1G32740	1.19	0.25	2.30	0.056814	0.188719	-4.65
261663_at	hypothetical protein similar to hypothetic	EPR1	AT1G18330 /	-1.75	-0.80	-2.29	0.056887	0.188904	-4.65
245374_at	hypothetical protein	---	AT4G17620	-1.22	-0.29	-2.29	0.05688	0.188904	-4.65
255380_at	putative calcium channel ; supported by	ATTPC1	AT4G03560	-1.30	-0.37	-2.29	0.056903	0.188932	-4.65
254314_at	extensin - like protein hybrid proline-rich	---	AT4G22470	3.55	1.83	2.29	0.056959	0.189089	-4.65
247985_at	putative protein contains similarity to pro	---	AT5G56790	-1.24	-0.31	-2.29	0.056981	0.189135	-4.65
251015_at	putative protein predicted protein, Arabi	---	AT5G02480	1.18	0.23	2.29	0.057004	0.189182	-4.65
257870_at	prolyl 4-hydroxylase, putative similar to	---	AT3G28490	1.15	0.20	2.29	0.057017	0.189200	-4.65
249464_at	putative protein crp1, Zea mays, PIR:T0	EMB2745	AT5G39710	-1.57	-0.65	-2.29	0.057124	0.189528	-4.66
258838_at	unknown protein ; supported by cDNA:	---	AT3G07140	-1.18	-0.24	-2.29	0.057161	0.189621	-4.66
248499_at	putative protein contains similarity to un	PAP27	AT5G50400	-1.17	-0.22	-2.29	0.057169	0.189622	-4.66
247987_at	putative protein similar to unknown prote	---	AT5G56900	-1.22	-0.28	-2.29	0.057191	0.189638	-4.66
250768_at	signal recognition particle receptor beta	---	AT5G05670	-1.29	-0.36	-2.29	0.057185	0.189638	-4.66
260927_at	hypothetical protein predicted by genem	CAT9	AT1G05940	-1.25	-0.32	-2.29	0.057286	0.189859	-4.66
250918_at	putative protein proline-rich protein AP0	---	AT5G03610	2.24	1.16	2.29	0.057273	0.189859	-4.66
263720_at	putative Na/H antiporter	ATCHX15	AT2G13620	1.17	0.23	2.29	0.05728	0.189859	-4.66
250342_at	putative protein predicted protein, Arabi	---	AT5G11870	1.29	0.37	2.29	0.057299	0.189859	-4.66
246158_at	Expressed protein ; supported by full-ler	---	AT5G19855	1.34	0.42	2.29	0.057292	0.189859	-4.66
265917_at	putative disease resistance protein	AtRLP19	AT2G15080	1.27	0.34	2.29	0.057381	0.190059	-4.66
249674_at	unknown protein	---	AT5G35930	-1.17	-0.22	-2.29	0.057384	0.190059	-4.66
250098_at	putative protein ;supported by full-lengt	---	AT5G17350	3.05	1.61	2.29	0.057372	0.190059	-4.66
258677_at	putative ribosomal-protein S6 kinase (A	PK1	AT3G08730	1.23	0.30	2.29	0.05741	0.190116	-4.66
265847_at	unknown protein	---	AT2G35750	-1.18	-0.23	-2.29	0.057451	0.190226	-4.66
258432_at	unknown protein ;supported by full-leng	RALFL23	AT3G16570	-1.36	-0.45	-2.29	0.057466	0.190247	-4.66
251993_at	peroxiredoxin - like protein peroxiredoxi	---	AT3G52960	-1.24	-0.31	-2.29	0.057574	0.190521	-4.66
265021_at	unknown protein ;supported by full-leng	---	AT1G24610	-1.16	-0.22	-2.29	0.057567	0.190521	-4.66
259630_at	peptide chain release factor 2, putative	---	AT1G56350	-1.33	-0.41	-2.29	0.057573	0.190521	-4.66

248138_at	pyruvate decarboxylase (gb|AAB16855.	PDC2	AT5G54960	-1.29	-0.37	-2.29	0.057623	0.190583	-4.66
245517_at	hypothetical protein	---	AT4G15840	-1.15	-0.20	-2.29	0.057626	0.190583	-4.67
265637_at	unknown protein	ATCOAE	AT2G27490	1.20	0.26	2.29	0.057602	0.190583	-4.66
249074_at	putative protein contains similarity to G-	---	AT5G44080	-1.20	-0.26	-2.29	0.05762	0.190583	-4.66
246486_at	putative protein ;supported by full-lengt	---	AT5G15910	-1.20	-0.27	-2.29	0.057649	0.190632	-4.67
267330_at	unknown protein	---	AT2G19270	-1.14	-0.19	-2.29	0.057682	0.190713	-4.67
253714_at	putative protein adaptor protein - Homo	---	AT4G29380	1.20	0.26	2.28	0.057722	0.190789	-4.67
251034_at	putative protein ;supported by full-lengt	PRA1.A1	AT5G02040	1.21	0.28	2.28	0.05773	0.190789	-4.67
257945_at	SKP1/ASK1 (At10), putative similar to S	ASK10	AT3G21860	1.20	0.26	2.28	0.057723	0.190789	-4.67
249619_at	stelar K+ outward rectifying channel (SI	GORK	AT5G37500	-1.31	-0.39	-2.28	0.057756	0.190846	-4.67
254498_at	membrane-associated salt-inducible-lik	EMB1025	AT4G20090	-1.31	-0.39	-2.28	0.057787	0.190894	-4.67
253223_at	L-ascorbate peroxidase ;supported by fu	APX3	AT4G35000	-1.18	-0.24	-2.28	0.057782	0.190894	-4.67
246231_at	putative protein	---	AT4G37080	-1.28	-0.36	-2.28	0.057823	0.190979	-4.67
254249_at	serine /threonine kinase - like protein se	---	AT4G23280	1.61	0.69	2.28	0.057846	0.190979	-4.67
250959_at	F-box protein family, AtFBL25 contains	---	AT5G02920	1.20	0.27	2.28	0.057842	0.190979	-4.67
264743_at	receptor-like protein kinase, putative sir	---	AT1G62090	1.17	0.23	2.28	0.057837	0.190979	-4.67
250289_at	putative protein ;supported by full-lengt	---	AT5G13190	1.54	0.63	2.28	0.057898	0.191121	-4.67
252618_at	lipoxygenase AtLOX2 ; supported by cI	LOX2	AT3G45140	-1.29	-0.37	-2.28	0.057932	0.191134	-4.67
246335_at	lethal leaf-spot 1 homolog Lls1	ACD1	AT3G44880	1.28	0.35	2.28	0.057935	0.191134	-4.67
266634_at	putative G-box binding bZIP transcriptio	---	AT2G35530	1.18	0.24	2.28	0.057928	0.191134	-4.67
265738_at	NADC homolog identical to GP|121607	QPT	AT2G01350	1.21	0.28	2.28	0.057932	0.191134	-4.67
258613_at	putative myo-inositol monophosphatase	VTC4	AT3G02870	-1.40	-0.48	-2.28	0.057957	0.191177	-4.67
260217_at	hypothetical protein contains Pfam profil	---	AT1G74600	-1.17	-0.22	-2.28	0.057993	0.191251	-4.67
262621_at	hypothetical protein	---	AT1G06530	-1.20	-0.26	-2.28	0.057996	0.191251	-4.67
258490_at	hypothetical protein predicted by genefir	---	AT3G02670	1.19	0.25	2.28	0.05801	0.191271	-4.67
266814_at	homeodomain transcription factor (ATHI	ATHB4	AT2G44910	-1.15	-0.20	-2.28	0.058033	0.191291	-4.67
264359_at	hypothetical protein predicted by genefir	---	AT1G03320	1.23	0.29	2.28	0.058031	0.191291	-4.67
245583_at	hypothetical protein	---	AT4G14920	-1.20	-0.27	-2.28	0.058043	0.191296	-4.67
265051_at	jasmonate inducible protein, putative sil	---	AT1G52100	1.27	0.35	2.28	0.058062	0.191326	-4.67
264326_at	unknown protein	---	AT1G04230	-1.24	-0.31	-2.28	0.058069	0.191326	-4.67
266656_at	putative CCCH-type zinc finger protein i	ATCTH	AT2G25900	1.30	0.37	2.28	0.058085	0.191336	-4.67
262962_at	NADP-isocitrate dehydrogenase, putati	ICDH	AT1G54340	1.15	0.20	2.28	0.058089	0.191336	-4.67
254393_at	putative NADPH quinone oxidoreductas	---	AT4G21580	1.19	0.26	2.28	0.058115	0.191369	-4.67
264217_at	hypothetical protein predicted by genem	---	AT1G60190	2.30	1.20	2.28	0.058108	0.191369	-4.67
246390_at	1-aminocyclopropane-1-carboxylate ox	---	AT1G77330	1.28	0.36	2.28	0.05817	0.191519	-4.67

265708_at	unknown protein member of a large unc	---	AT2G03380	-1.19	-0.25	-2.28	0.058178	0.191519	-4.67
261827_at	unknown protein contains similarity to e	---	AT1G11480	1.19	0.25	2.28	0.058193	0.191541	-4.67
254345_at	hypothetical protein ;supported by full-le	---	AT4G22000	-1.34	-0.42	-2.28	0.058257	0.191696	-4.68
244938_at	ribosomal protein S15	---	---	-1.39	-0.47	-2.28	0.05825	0.191696	-4.68
246085_at	putative protein predicted proteins, Aral	ATBRXL4	AT5G20540	1.24	0.31	2.28	0.058292	0.191783	-4.68
250683_x_a	putative protein similar to unknown prote	---	AT5G06640	1.31	0.39	2.28	0.058312	0.191794	-4.68
245068_at	putative glucosyltransferase	UGT84B1	AT2G23260	1.20	0.27	2.28	0.058308	0.191794	-4.68
250700_at	CDK5 activator-binding protein-like	---	AT5G06830	-1.21	-0.27	-2.28	0.058374	0.191949	-4.68
246202_at	methionyl aminopeptidase-like protein ;s	MAP1D	AT4G37040	-1.30	-0.38	-2.28	0.058376	0.191949	-4.68
255581_at	putative transposon protein similar to A	---	---	1.25	0.32	2.28	0.05839	0.191967	-4.68
253323_at	putative protein protein phosphatase W	---	AT4G33920	1.62	0.70	2.28	0.058406	0.191995	-4.68
248195_at	membrane associated protein ; support	ATMAMI	AT5G54110	1.25	0.32	2.28	0.058463	0.192153	-4.68
255789_at	60S ribosomal protein L23 ;supported b	---	AT2G33370	-1.59	-0.67	-2.28	0.058479	0.192179	-4.68
253039_at	squalene epoxidase - like protein squal	SQE3	AT4G37760	-1.45	-0.54	-2.28	0.058513	0.192263	-4.68
254286_at	putative MADS Box / AGL protein MAD	AGL19	AT4G22950	-1.38	-0.46	-2.27	0.058566	0.192407	-4.68
263474_at	hypothetical protein predicted by gensca	---	AT2G31725	-1.26	-0.33	-2.27	0.05863	0.192591	-4.68
250786_at	putative protein strong similarity to unkn	SDN2	AT5G05540	-1.28	-0.36	-2.27	0.058674	0.192706	-4.68
256590_at	recombination signal sequence recogni	ATHMG	AT3G28730	-1.27	-0.34	-2.27	0.05877	0.192828	-4.68
260505_at	Cyclin, putative similar to GB:CAB7726	CYCA3;4	AT1G47230	-1.18	-0.24	-2.27	0.058762	0.192828	-4.68
248337_at	low-temperature-induced protein 78 (sp	LTI78	AT5G52310	-2.52	-1.34	-2.27	0.058765	0.192828	-4.68
261453_at	O-methyltransferase, putative similar to	---	AT1G21130	1.53	0.62	2.27	0.058749	0.192828	-4.68
259903_at	unknown protein	---	AT1G74160	-1.35	-0.43	-2.27	0.058732	0.192828	-4.68
256000_at	glycyl tRNA synthetase, putative similar	---	AT1G29880	-1.22	-0.29	-2.27	0.058746	0.192828	-4.68
251108_at	putative protein several hypothetical pro	---	AT5G01620	1.32	0.40	2.27	0.058749	0.192828	-4.68
258253_at	putative short chain alcohol dehydrogen	---	AT3G26760	1.18	0.24	2.27	0.05886	0.193098	-4.69
245524_at	cytochrome c oxidoreductase like protei	---	AT4G15920	-1.68	-0.75	-2.27	0.058926	0.193286	-4.69
252113_at	putative protein predicted protein, Arabi	---	AT3G51620	-1.17	-0.22	-2.27	0.058941	0.193306	-4.69
254980_at	putative ribosomal protein L9, cytosolic	---	AT4G10450	-1.47	-0.55	-2.27	0.058957	0.193330	-4.69
266450_s_a	hypothetical protein predicted by gensca	---	AT2G43190	-1.28	-0.36	-2.27	0.05898	0.193349	-4.69
256304_at	Expressed protein ; supported by cDNA	---	AT1G69523	-1.38	-0.46	-2.27	0.058974	0.193349	-4.69
266835_at	putative NADH dehydrogenase (ubiquin	NDA2	AT2G29990	1.67	0.74	2.27	0.059002	0.193396	-4.69
251845_at	Expressed protein ; supported by full-ler	ATGCN4	AT3G54540	-1.28	-0.35	-2.27	0.059027	0.193448	-4.69
255537_at	protoporphyrinogen oxidase ; supported	PPOX	AT4G01690	-1.25	-0.33	-2.27	0.059074	0.193548	-4.69
262952_at	hypothetical protein predicted by genem	---	AT1G75770	-1.25	-0.32	-2.27	0.059069	0.193548	-4.69
252107_at	sugar transporter-like protein sugar tran	TMT3	AT3G51490	1.28	0.36	2.27	0.059103	0.193563	-4.69

254141_at	glucose-6-phosphate isomerase glucos	PGI1	AT4G24620	-1.19	-0.25	-2.27	0.059104	0.193563	-4.69
263749_at	putative phosphatidylinositol/phosphatid	---	AT2G21520	1.22	0.28	2.27	0.059092	0.193563	-4.69
265619_at	hypothetical protein	---	AT2G27320	1.26	0.34	2.27	0.059133	0.193630	-4.69
259165_at	homeobox-leucine zipper protein HAT5	ATHB-1	AT3G01470 /	1.45	0.53	2.27	0.05917	0.193724	-4.69
251150_at	putative protein Sb34 (PREG-like prote	CYCP1;1	AT3G63120	-1.22	-0.29	-2.27	0.059181	0.193730	-4.69
257489_at	hypothetical protein predicted by genem	---	AT1G07330	1.19	0.25	2.27	0.059225	0.193793	-4.69
248934_at	serine/threonine protein kinase-like prot	---	AT5G46080	2.05	1.04	2.27	0.059218	0.193793	-4.69
255974_at	hypothetical protein	---	---	1.23	0.30	2.27	0.059214	0.193793	-4.69
261018_at	unknown protein contains similarity to p	---	AT1G26550	-1.15	-0.20	-2.27	0.059283	0.193953	-4.69
259016_at	unknown protein HMM hit: 2Fe-2S iron-s	---	AT3G07480	1.27	0.34	2.27	0.059307	0.194004	-4.69
255292_s_a	putative calcium dependent protein kina	CPK22	AT4G04710 /	-1.26	-0.34	-2.27	0.059341	0.194089	-4.69
261231_at	unknown protein ; supported by cDNA: g	---	AT1G20110	1.16	0.21	2.27	0.059372	0.194162	-4.69
249021_at	putative protein similar to unknown prote	---	AT5G44820	1.35	0.44	2.27	0.059387	0.194183	-4.70
261949_at	hypothetical protein predicted by genem	BDG1	AT1G64670	1.58	0.66	2.26	0.059419	0.194232	-4.70
264146_at	hypothetical protein contains similarity t	CER1	AT1G02205	5.47	2.45	2.26	0.059417	0.194232	-4.70
261173_at	hypothetical protein predicted by genem	---	AT1G04830	-1.20	-0.26	-2.26	0.059439	0.194271	-4.70
264866_at	putative metalloproteinase similar to GB	---	AT1G24140	2.74	1.46	2.26	0.059451	0.194281	-4.70
255812_at	potassium uptake transporter - like prot	HKT1	AT4G10310	1.38	0.47	2.26	0.059475	0.194331	-4.70
260636_at	hypothetical protein contains similarity t	ATCDS1	AT1G62430	-1.39	-0.48	-2.26	0.059503	0.194366	-4.70
247467_at	putative protein predicted proteins, D.m	---	AT5G62130	-1.44	-0.53	-2.26	0.059495	0.194366	-4.70
248491_at	unknown protein ;supported by full-leng	---	AT5G51010	-1.30	-0.38	-2.26	0.059526	0.194392	-4.70
259921_at	putative protein kinase similar to protein	---	AT1G72540	2.00	1.00	2.26	0.059529	0.194392	-4.70
262319_s_a	unknown protein similar to unknown pro	---	AT1G27540 /	1.37	0.45	2.26	0.059536	0.194392	-4.70
253637_at	putative protein ; supported by full-leng	---	AT4G30390	1.33	0.42	2.26	0.059578	0.194487	-4.70
264345_at	Expressed protein ; supported by cDNA	---	AT1G11915	1.26	0.34	2.26	0.059582	0.194487	-4.70
253189_at	putative protein	---	AT4G35335	-1.32	-0.41	-2.26	0.059592	0.194489	-4.70
249147_at	cytosolic malate dehydrogenase ;suppo	---	AT5G43330	-1.27	-0.34	-2.26	0.059654	0.194663	-4.70
260409_at	Expressed protein ; supported by full-ler	SHW1	AT1G69935	-1.36	-0.45	-2.26	0.059673	0.194670	-4.70
245530_at	splicing factor like protein	---	---	1.23	0.29	2.26	0.059671	0.194670	-4.70
247930_at	putative protein similar to unknown prote	---	AT5G57060	1.31	0.39	2.26	0.0597	0.194731	-4.70
259619_at	hypothetical protein	---	AT1G42980	-1.23	-0.30	-2.26	0.059767	0.194921	-4.70
257264_at	hypothetical protein contains Pfam profil	---	AT3G22060	2.11	1.08	2.26	0.059786	0.194958	-4.70
252166_at	protein kinase SPK-2 ;supported by full	SNRK2.2	AT3G50500	-1.25	-0.32	-2.26	0.059836	0.195093	-4.70
255303_at	predicted protein of unknown function ;	DER2.2	AT4G04860	-1.20	-0.26	-2.26	0.059882	0.195200	-4.70
262169_at	hypothetical protein predicted by genem	---	AT1G74860	-1.23	-0.30	-2.26	0.059886	0.195200	-4.70

249190_at	unknown protein ;supported by full-leng	BKI1	AT5G42750	-1.22	-0.29	-2.26	0.059905	0.195231	-4.70
248492_at	putative protein similar to unknown prote	---	AT5G51040	1.17	0.23	2.26	0.05997	0.195369	-4.70
253921_at	glutamine amidotransferase/cyclase ; s	AT-HF	AT4G26900	-1.22	-0.29	-2.26	0.059969	0.195369	-4.70
262958_at	water stress-induced protein, putative s	---	AT1G54410	-1.23	-0.30	-2.26	0.059973	0.195369	-4.70
245796_at	unknown protein similar to unknown pro	RCD1	AT1G32230	1.20	0.26	2.26	0.060008	0.195458	-4.71
263106_at	hypothetical protein predicted by gensca	---	AT2G05160	1.25	0.32	2.26	0.060044	0.195544	-4.71
265307_at	hypothetical protein predicted by gensca	RIN13	AT2G20310	-1.22	-0.29	-2.26	0.060077	0.195598	-4.71
262075_at	hypothetical protein contains similarity t	ZCF61	AT1G59560	-1.32	-0.40	-2.26	0.060077	0.195598	-4.71
251511_at	putative protein several hypothetical pro	---	AT3G59180	1.17	0.23	2.26	0.06011	0.195678	-4.71
246722_at	putative protein various predicted prote	---	---	1.25	0.32	2.26	0.060123	0.195690	-4.71
257818_at	hypothetical protein predicted by gensca	---	AT3G25120	-1.22	-0.29	-2.26	0.060134	0.195699	-4.71
258789_at	Mutator-like transposase similar to MUR	---	---	-1.20	-0.26	-2.26	0.060165	0.195743	-4.71
248328_at	putative protein contains similarity to MY	---	AT5G52660	-1.17	-0.22	-2.26	0.060159	0.195743	-4.71
256520_at	hypothetical protein	CYP96A14	AT1G66030	1.19	0.24	2.26	0.060194	0.195812	-4.71
264004_at	Expressed protein ; supported by full-ler	---	AT2G22425	1.23	0.30	2.26	0.060213	0.195846	-4.71
260299_at	putative gibberellin 3 beta-hydroxylase s	GA3OX4	AT1G80330	1.15	0.20	2.26	0.060231	0.195851	-4.71
246334_at	putative protein serine kinase SRPK2, I	---	AT3G44850	-1.31	-0.39	-2.26	0.060232	0.195851	-4.71
259665_at	unknown protein ; supported by cDNA: g	---	AT1G55160	-1.27	-0.34	-2.25	0.060262	0.195919	-4.71
257833_at	transcriptional regulator protein, putativ	LWD2	AT3G26640	-1.16	-0.22	-2.25	0.060278	0.195940	-4.71
267223_at	hypothetical protein predicted by grail	AtITPK4	AT2G43980	1.21	0.28	2.25	0.060293	0.195940	-4.71
247583_at	putative protein predicted protein, Syne	---	AT5G60750	1.19	0.25	2.25	0.060294	0.195940	-4.71
262853_at	unknown protein Location of ESTs OAC	---	AT1G20890	-1.21	-0.27	-2.25	0.060308	0.195958	-4.71
262188_at	Avr9 elicitor response protein, putative	---	AT1G77810	1.23	0.30	2.25	0.060328	0.195994	-4.71
247185_at	putative protein contains similarity to kin	---	AT5G65460	-1.24	-0.31	-2.25	0.060357	0.196062	-4.71
260638_at	unknown protein similar to putative cyto	---	AT1G62390	-1.36	-0.44	-2.25	0.060374	0.196090	-4.71
257216_at	4-methyl-5(b-hydroxyethyl)-thiazole mo	---	AT3G14990	1.49	0.57	2.25	0.060457	0.196262	-4.71
258114_at	putative cytochrome P450 similar to GB	CYP72A13	AT3G14660	-1.19	-0.26	-2.25	0.060472	0.196262	-4.71
247349_at	putative protein similar to unknown prote	---	AT5G63820	1.18	0.24	2.25	0.060452	0.196262	-4.71
263400_s_a	40S ribosomal protein; contains C-termi	---	AT2G31610 /	-1.24	-0.31	-2.25	0.060441	0.196262	-4.71
255918_at	putative protein	---	---	1.17	0.22	2.25	0.060479	0.196262	-4.71
266529_at	putative salt-inducible protein	---	AT2G16880	-1.22	-0.29	-2.25	0.060478	0.196262	-4.71
260654_at	hypothetical protein predicted by genem	---	AT1G19290	-1.26	-0.34	-2.25	0.060538	0.196425	-4.71
258034_at	hypothetical protein predicted by genem	---	AT3G21300	-1.54	-0.63	-2.25	0.060549	0.196434	-4.71
256866_at	unknown protein similar to alpha galacto	---	AT3G26380	-1.27	-0.34	-2.25	0.060609	0.196580	-4.72
266049_at	putative translation initiation factor	---	AT2G40780	-1.19	-0.25	-2.25	0.060611	0.196580	-4.72

249600_s_a	oxidoreductase-like protein zeta-crystal	---	AT5G37940 /	1.15	0.20	2.25	0.060629	0.196608	-4.72
248762_at	Expressed protein ; supported by full-ler	---	AT5G47455	-1.35	-0.43	-2.25	0.060673	0.196617	-4.72
247762_at	cell wall protein	---	AT5G59170	1.53	0.61	2.25	0.060665	0.196617	-4.72
250266_at	histone H3 -like protein histone H3, whe	---	AT5G12910	1.22	0.28	2.25	0.060678	0.196617	-4.72
265736_at	putative ribosomal protein L7 ;supporte	---	AT2G01250	-1.43	-0.52	-2.25	0.060683	0.196617	-4.72
261057_at	hypothetical protein predicted by genem	---	AT1G01230	-1.20	-0.26	-2.25	0.060662	0.196617	-4.72
250008_at	triacylglycerol lipase-like protein triacylg	---	AT5G18630	1.44	0.53	2.25	0.060649	0.196617	-4.72
261938_at	hypothetical protein predicted by gensca	---	AT1G22510	1.44	0.52	2.25	0.060716	0.196696	-4.72
249398_at	RING finger -like protein RING-H2 zinc	---	AT5G40250	1.22	0.29	2.25	0.060729	0.196709	-4.72
265216_at	putative NPK1-related MAP kinase simil	MAPKKK1	AT1G05100	1.36	0.45	2.25	0.06074	0.196719	-4.72
250912_at	histone deacetylase -like protein histon	HD2C	AT5G03740	-1.43	-0.52	-2.25	0.060756	0.196741	-4.72
259075_at	putative N2,N2-dimethylguanosine tRN	---	AT3G02320	-1.22	-0.28	-2.25	0.060767	0.196748	-4.72
263790_at	hypothetical protein predicted by genefir	---	AT2G24530	-1.26	-0.33	-2.25	0.060794	0.196808	-4.72
264367_at	unknown protein ESTs gb|T21276, gb|T	---	AT1G03350	1.18	0.24	2.25	0.060806	0.196817	-4.72
262666_at	xyloglucan fucosyltransferase, putative	FUT6	AT1G14080	1.43	0.52	2.25	0.060814	0.196817	-4.72
251057_at	putative protein alkB protein - Escherich	---	AT5G01780	-1.15	-0.20	-2.25	0.060848	0.196899	-4.72
251492_at	putative protein CGI-136 protein - Hom	TXR1	AT3G59280	1.16	0.21	2.25	0.060891	0.197011	-4.72
258735_at	low temperature and salt responsive pro	RCI2A	AT3G05880	1.35	0.43	2.25	0.061005	0.197350	-4.72
257546_s_a	hypothetical protein predicted by genem	---	AT3G28410 /	-1.15	-0.21	-2.25	0.061017	0.197362	-4.72
259348_at	hypothetical protein may contain C-term	---	AT3G03770	-1.35	-0.43	-2.25	0.061088	0.197564	-4.72
248836_at	NBS/LRR disease resistance protein	---	AT5G47260	1.26	0.33	2.25	0.061107	0.197597	-4.72
254737_at	fatty acid elongase - like protein (cer2-li	---	AT4G13840	-1.63	-0.71	-2.25	0.06113	0.197636	-4.72
259117_at	unknown protein similar to hypothetical	SNL1	AT3G01320	-1.18	-0.24	-2.25	0.061136	0.197636	-4.72
264574_at	putative zinc transporter Similar to Arabi	ZIP5	AT1G05300	-1.46	-0.54	-2.24	0.061166	0.197675	-4.72
258934_at	putative RecA protein similar to RecA pr	RECA3	AT3G10140	-1.22	-0.28	-2.24	0.061165	0.197675	-4.72
252968_at	putative protein unknown mRNA, Homo	---	AT4G38890	-1.31	-0.39	-2.24	0.061218	0.197815	-4.73
249963_at	putative protein SPECKLE-TYPE POZ	ATBPM1	AT5G19000	1.24	0.31	2.24	0.061231	0.197830	-4.73
265731_at	putative RNA helicase A 3' end of this g	---	AT2G01130	-1.16	-0.21	-2.24	0.061254	0.197877	-4.73
256891_at	hypothetical protein contains similarity to	---	AT3G19030	1.27	0.35	2.24	0.061284	0.197945	-4.73
248921_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G45950	1.61	0.69	2.24	0.061317	0.197995	-4.73
250144_at	putative protein various predicted prote	---	AT5G14680	-1.37	-0.45	-2.24	0.061316	0.197995	-4.73
245291_at	Expressed protein ; supported by cDNA	---	AT4G16155	-1.19	-0.26	-2.24	0.061329	0.198006	-4.73
254102_at	acyl carrier - like protein acyl carrier pro	ACP4	AT4G25050	-1.24	-0.31	-2.24	0.06136	0.198021	-4.73
262911_s_a	heat shock protein, putative similar to h	---	AT1G07400 /	1.83	0.87	2.24	0.061362	0.198021	-4.73
258654_at	unknown protein	---	AT3G09860	-1.33	-0.41	-2.24	0.061368	0.198021	-4.73

257272_at	unknown protein ; supported by cDNA:	---	AT3G28130	-1.22	-0.28	-2.24	0.061342	0.198021	-4.73
247469_at	Expressed protein ; supported by cDNA	AGL42	AT5G62165	-2.39	-1.26	-2.24	0.061385	0.198048	-4.73
252009_at	zinc finger - like protein zinc finger prote	---	AT3G52800	1.31	0.39	2.24	0.061411	0.198102	-4.73
262721_at	thioredoxin, putative similar to thioredox	Aty2	AT1G43560	-1.24	-0.31	-2.24	0.061437	0.198158	-4.73
255496_at	putative protein similar to plant nucleic a	BZO2H1	AT4G02640	-1.28	-0.36	-2.24	0.061453	0.198182	-4.73
262129_at	mutM homologue-1 identical to mutM ho	ATMMH-1	AT1G52500	-1.25	-0.32	-2.24	0.061467	0.198201	-4.73
262940_at	unknown protein	---	AT1G79520	-1.32	-0.40	-2.24	0.061505	0.198266	-4.73
244921_s_a	hypothetical protein	---	AT2G07674 /	-1.31	-0.39	-2.24	0.0615	0.198266	-4.73
267168_at	putative alcohol dehydrogenase	---	AT2G37770	2.98	1.58	2.24	0.061526	0.198306	-4.73
250420_at	HY5(bZIP transcription factor family) ide	HY5	AT5G11260	1.23	0.30	2.24	0.061553	0.198364	-4.73
265629_at	unknown protein ; supported by cDNA:	LHW	AT2G27228 /	-1.33	-0.41	-2.24	0.061641	0.198621	-4.73
256008_s_a	allinase, putative similar to allinase GI:1	---	AT1G34040 /	-1.20	-0.26	-2.24	0.061664	0.198665	-4.73
253326_at	putative protein polygalacturonase(EC 3	---	AT4G33440	-1.20	-0.27	-2.24	0.061705	0.198769	-4.73
261362_s_a	ribosomal protein identical to GB:CAB81	---	AT1G41880 /	-1.36	-0.45	-2.24	0.061714	0.198771	-4.73
263862_at	putative protein phosphatase	IBR5	AT2G04550	1.19	0.25	2.24	0.06175	0.198859	-4.73
249210_at	unknown protein	---	AT5G42670	-1.17	-0.22	-2.24	0.061784	0.198942	-4.73
254981_at	putative alpha NAC stong similarity to N	---	AT4G10480	-1.37	-0.45	-2.24	0.061808	0.198991	-4.74
253553_at	putative protein LipB gene, Prochloroth	---	AT4G31050	-1.22	-0.29	-2.24	0.061844	0.199077	-4.74
258900_at	putative 60S ribosomal protein L18 simil	RPL18	AT3G05590	-1.38	-0.46	-2.24	0.061941	0.199361	-4.74
258991_at	unknown protein contains Pfam profile:	---	AT3G08820	-1.20	-0.26	-2.24	0.061969	0.199396	-4.74
252546_at	DNA-binding protein - like DNA-binding	---	AT3G45830	-1.19	-0.25	-2.24	0.061965	0.199396	-4.74
265580_at	putative protein phosphatase 2C	---	AT2G20050	-1.24	-0.31	-2.24	0.061987	0.199425	-4.74
AFFX-Athal	Arabidopsis thaliana /REF=U37281 /DE	ACT7	---	-1.18	-0.24	-2.24	0.06202	0.199504	-4.74
257482_x_a	hypothetical protein contains similarity to	---	AT1G27820	1.29	0.37	2.23	0.062086	0.199688	-4.74
260816_at	hypothetical protein predicted by gensca	---	AT1G06930	1.26	0.33	2.23	0.062119	0.199764	-4.74
247718_at	nonspecific lipid-transfer protein precur	LTP4	AT5G59310	1.28	0.35	2.23	0.062137	0.199795	-4.74
249208_at	allene oxide synthase (emb CAA73184.	AOS	AT5G42650	-1.65	-0.72	-2.23	0.062151	0.199812	-4.74
263090_at	hypothetical protein predicted by gensca	---	AT2G16190	-1.17	-0.23	-2.23	0.062164	0.199827	-4.74
254010_at	putative protein ;supported by full-lengt	---	AT1G72125 /	1.18	0.24	2.23	0.062199	0.199893	-4.74
261974_at	protein kinase, putative similar to mitog	CPuORF5	AT1G64628 /	-1.19	-0.25	-2.23	0.062203	0.199893	-4.74
253858_at	carbohydrate kinase - like protein phos	---	AT4G27600	-1.17	-0.23	-2.23	0.062228	0.199947	-4.74
265183_at	unknown protein ;supported by full-leng	---	AT1G23750	-1.35	-0.44	-2.23	0.062241	0.199961	-4.74
256914_at	hypothetical protein	---	AT3G23880	-1.33	-0.41	-2.23	0.062261	0.199995	-4.74
259116_at	putative peptide transporter similar to pe	---	AT3G01350	-1.37	-0.46	-2.23	0.062273	0.200007	-4.74
252913_at	AtRer1A ; supported by full-length cDN	ATRER1A	AT4G39220	1.19	0.25	2.23	0.062319	0.200043	-4.74

252473_s_a	hypothetical protein several hypothetica	---	AT3G46610 /	-1.31	-0.39	-2.23	0.062314	0.200043	-4.74
248911_at	tumor-related protein-like	DOG1	AT5G45830	-1.28	-0.35	-2.23	0.062294	0.200043	-4.74
249891_at	unknown protein	---	AT5G22590	-1.14	-0.19	-2.23	0.062316	0.200043	-4.74
265709_at	hypothetical protein predicted by gensca	---	---	1.64	0.71	2.23	0.062338	0.200073	-4.74
250704_at	Expressed protein ; supported by full-ler	---	AT5G06265	-1.25	-0.32	-2.23	0.062408	0.200132	-4.74
248019_at	putative protein similar to unknown prote	---	AT5G56480	1.19	0.26	2.23	0.062384	0.200132	-4.74
265120_at	3-ketoacyl-acyl carrier protein synthase	KAS III	AT1G62640	-1.24	-0.32	-2.23	0.062377	0.200132	-4.74
261775_at	hypothetical protein predicted by genem	---	AT1G76280	-1.21	-0.28	-2.23	0.062409	0.200132	-4.74
265103_at	UDP-N-acetylglucosamine pyrophosph	---	AT1G31070	-1.25	-0.32	-2.23	0.062399	0.200132	-4.74
261193_at	unknown protein ; supported by cDNA: g	---	AT1G32920	1.69	0.76	2.23	0.06239	0.200132	-4.74
253477_at	L-ascorbate peroxidase - like protein val	APX6	AT4G32320	-1.39	-0.48	-2.23	0.06244	0.200206	-4.75
267580_at	unknown protein	---	AT2G41990	1.23	0.30	2.23	0.062456	0.200227	-4.75
AFFX-r2-Bs	B. subtilis /GEN=thrC, thrB /DB_XREF=	---	---	-1.43	-0.52	-2.23	0.062489	0.200305	-4.75
267612_at	putative nitrate transporter	---	AT2G26690	1.67	0.74	2.23	0.062503	0.200323	-4.75
261519_at	unknown protein ; supported by cDNA: g	---	AT1G71810	-1.30	-0.37	-2.23	0.062554	0.200456	-4.75
258006_at	cysteine proteinase non-consensus AT	---	AT3G19400	-1.28	-0.35	-2.23	0.06259	0.200540	-4.75
260907_at	hypothetical protein predicted by gensca	---	AT1G02570	-1.17	-0.23	-2.23	0.062597	0.200540	-4.75
264679_s_a	putative 60S ribosomal protein L21 Sim	---	AT1G09590 /	-1.36	-0.44	-2.23	0.062613	0.200563	-4.75
257893_at	E2, ubiquitin-conjugating enzyme, putat	UBC32	AT3G17000	1.34	0.43	2.23	0.062632	0.200593	-4.75
246480_at	TCP-1 chaperonin-like protein t-comple	---	AT5G16070	-1.27	-0.35	-2.23	0.062641	0.200597	-4.75
257235_at	ras-related GTP-binding protein contain	AtRABA1g	AT3G15060	1.88	0.91	2.23	0.062661	0.200632	-4.75
246622_at	protein phosphatase-2C PP2C-like ; su	---	AT5G36250	-1.16	-0.22	-2.23	0.062707	0.200751	-4.75
247949_at	cytochrome P450	CYP81F2	AT5G57220	2.31	1.21	2.23	0.062727	0.200786	-4.75
266231_at	putative protein kinase	PSKR1	AT2G02220	1.80	0.85	2.23	0.062753	0.200830	-4.75
264890_at	unknown protein	---	AT1G23180	-1.28	-0.35	-2.23	0.062758	0.200830	-4.75
266045_s_a	hypothetical protein	---	AT2G07727	-1.28	-0.35	-2.23	0.062785	0.200888	-4.75
254405_at	putative protein arm repeat containing p	PUB8	AT4G21350	-1.31	-0.39	-2.23	0.062796	0.200895	-4.75
251683_at	putative protein several hypothetical pro	---	AT3G57120	1.47	0.56	2.23	0.062817	0.200935	-4.75
250224_at	putative protein similar to unknown prote	---	AT5G14150	1.27	0.34	2.23	0.062882	0.201086	-4.75
259814_at	zinc finger protein ATZF1, putative simi	---	AT1G49900	1.34	0.43	2.23	0.062875	0.201086	-4.75
265116_at	unknown protein ; supported by full-leng	---	AT1G62480	2.33	1.22	2.23	0.062915	0.201163	-4.75
247106_at	WD repeat protein-like ;supported by ful	---	AT5G66240	-1.21	-0.28	-2.23	0.062935	0.201165	-4.75
247695_at	putative protein Not2p, Homo sapiens,	VIP2	AT5G59710	-1.17	-0.22	-2.23	0.062938	0.201165	-4.75
261988_at	single-strand nucleic acid-binding prote	---	AT1G33680	-1.28	-0.36	-2.22	0.062942	0.201165	-4.75
245662_at	hypothetical protein predicted by genem	---	AT1G28190	1.96	0.97	2.22	0.062991	0.201292	-4.75

246073_at	ribosomal protein L36-like ribosomal pr	---	AT5G20180	-1.21	-0.28	-2.22	0.063022	0.201364	-4.75
259973_at	hypothetical protein contains Pfam profil	---	AT1G76630	-1.34	-0.42	-2.22	0.063092	0.201558	-4.76
245054_at	unknown protein	---	AT2G26460	-1.23	-0.30	-2.22	0.063107	0.201559	-4.76
250395_at	putative protein cylicin II, bovine, PIR:I4	---	AT5G10950	-1.32	-0.40	-2.22	0.063115	0.201559	-4.76
260315_at	hypothetical protein similar to C-termina	---	AT1G63820	-1.18	-0.24	-2.22	0.063119	0.201559	-4.76
247221_at	Expressed protein ; supported by cDNA	LIP1	AT5G64813	1.15	0.20	2.22	0.063132	0.201574	-4.76
250339_at	NADP dependent malic enzyme - like p	ATNADP-M	AT5G11670	-1.27	-0.34	-2.22	0.063147	0.201593	-4.76
259657_at	phospholipase D alpha, putative similar	PLDEPSIL	AT1G55180	1.18	0.24	2.22	0.063298	0.202047	-4.76
254689_at	putative pectate lyase A11 ; supported	---	AT4G13710	1.29	0.36	2.22	0.06332	0.202061	-4.76
250025_at	putative protein similar to unknown prote	SIP1;2	AT5G18290	1.28	0.36	2.22	0.063312	0.202061	-4.76
253638_at	cinnamoyl-CoA reductase - like protein	---	AT4G30470	1.64	0.71	2.22	0.063379	0.202220	-4.76
246433_at	glutamine-rich protein predicted protein	---	AT5G17510	-1.29	-0.37	-2.22	0.063389	0.202224	-4.76
248012_at	putative protein strong similarity to unkn	---	AT5G56310	-1.26	-0.33	-2.22	0.063401	0.202236	-4.76
264727_at	putative cytochrome C strong similarity t	CYTC-1	AT1G22840	1.47	0.56	2.22	0.063416	0.202252	-4.76
246693_at	putative protein	---	AT5G29070	1.18	0.24	2.22	0.063431	0.202271	-4.76
253503_at	cytochrome P450-like protein cytochror	CYP82C3	AT4G31950	1.38	0.47	2.22	0.063439	0.202271	-4.76
248970_at	urea active transporter-like protein	---	AT5G45380	1.53	0.62	2.22	0.063451	0.202279	-4.76
266503_at	unknown protein	---	AT2G47780	1.44	0.53	2.22	0.063475	0.202328	-4.76
250548_at	myosin heavy chain-like protein ; suppo	MBP2C	AT5G08120	-1.20	-0.27	-2.22	0.063496	0.202367	-4.76
264731_at	hypothetical protein predicted by genem	---	AT1G62150	-1.21	-0.27	-2.22	0.063549	0.202508	-4.76
255023_at	hypothetical protein	---	AT4G09850	1.20	0.26	2.22	0.06357	0.202518	-4.76
250788_at	putative protein similar to unknown prote	---	AT5G05570	-1.26	-0.34	-2.22	0.063563	0.202518	-4.76
256711_at	unknown protein contains Pfam profile:	---	AT3G30390	1.34	0.42	2.22	0.063602	0.202593	-4.76
259602_at	disease resistance protein, putative sim	---	AT1G56520	1.16	0.22	2.22	0.063654	0.202729	-4.76
262890_at	nucleoporin, putative similar to nuclear	NUP155	AT1G14850	-1.31	-0.39	-2.22	0.063674	0.202736	-4.76
248666_at	cyclin C-like protein ;supported by full-le	---	AT5G48630	-1.25	-0.32	-2.22	0.063666	0.202736	-4.76
245299_at	ras-related small GTP-binding protein R	ATRAB1C	AT4G17530	1.27	0.35	2.22	0.063727	0.202793	-4.77
258760_at	putative membrane protein similar to int	---	AT3G10780	1.40	0.48	2.22	0.063705	0.202793	-4.77
266826_at	putative amino acid acetyltransferase	---	AT2G22910	-1.45	-0.54	-2.22	0.06372	0.202793	-4.77
247230_at	putative protein similar to unknown prote	---	AT5G65170	1.17	0.22	2.22	0.063716	0.202793	-4.77
251931_at	putative protein glyoxal oxidase (glx2) -	---	AT3G53950	1.34	0.42	2.22	0.063776	0.202845	-4.77
258384_at	hypothetical protein predicted by gensca	---	AT3G15490	1.18	0.24	2.22	0.063755	0.202845	-4.77
245035_at	unknown protein similar to GP|2244827	ATARD3	AT2G26400	1.54	0.62	2.22	0.063778	0.202845	-4.77
254257_s_a	putative protein predicted proteins, Arat	---	AT4G23350 /	-1.18	-0.24	-2.22	0.063779	0.202845	-4.77
252117_at	mucin -like protein hemomucin, Drosop	YLS2	AT3G51430	1.34	0.42	2.22	0.063823	0.202955	-4.77

249309_at	homeotic protein BEL1 homolog ; supp	BEL1	AT5G41410	-1.23	-0.30	-2.22	0.063856	0.202977	-4.77
249990_at	hypothetical protein	---	AT5G18540	-1.18	-0.24	-2.22	0.063843	0.202977	-4.77
251738_at	PROBABLE EUKARYOTIC TRANSLAT	EIF3C	AT3G56150	-1.18	-0.24	-2.22	0.06385	0.202977	-4.77
256752_at	hypothetical protein predicted by genem	---	AT3G27180	-1.35	-0.43	-2.21	0.063879	0.202992	-4.77
266631_at	putative serpin	---	AT2G35570	1.15	0.20	2.21	0.063877	0.202992	-4.77
251437_at	putative protein hypothetical protein At2	---	AT3G59910	-1.17	-0.22	-2.21	0.063895	0.203014	-4.77
255472_at	82.09 and 30.80) similar to alternative s	---	AT4G02430	-1.19	-0.25	-2.21	0.063913	0.203044	-4.77
245173_at	putative AP2 domain transcription factor	---	AT2G47520	1.56	0.64	2.21	0.063956	0.203153	-4.77
261581_at	serine/threonine kinase, putative simila	CIPK9	AT1G01140	-1.28	-0.36	-2.21	0.063994	0.203190	-4.77
247939_at	putative protein contains similarity to DN	ATLIG4	AT5G57160	-1.19	-0.25	-2.21	0.063987	0.203190	-4.77
262171_at	unknown protein ;supported by full-leng	TIFY10B	AT1G74950	-1.33	-0.41	-2.21	0.063989	0.203190	-4.77
264819_at	hypothetical protein similar to membran	---	AT1G03510	-1.32	-0.40	-2.21	0.064017	0.203210	-4.77
251532_at	putative protein F-box protein Fbl2 - Ho	---	AT3G58530	-1.19	-0.25	-2.21	0.064019	0.203210	-4.77
260383_s_a	putative 60S ribosomal protein L6 simila	---	AT1G74050 /	-1.28	-0.36	-2.21	0.064048	0.203275	-4.77
244924_at	hypothetical protein	---	---	-1.21	-0.27	-2.21	0.064122	0.203481	-4.77
246566_at	oligopeptide transporter -like protein oli	---	AT5G14940	-1.40	-0.48	-2.21	0.064176	0.203624	-4.77
249204_at	unknown protein ;supported by full-leng	---	AT5G42570	1.18	0.24	2.21	0.064208	0.203699	-4.77
258587_at	hypothetical protein predicted by gensca	---	AT3G04310	-1.39	-0.48	-2.21	0.064244	0.203769	-4.77
263643_at	unknown protein predicted by genefinde	---	AT2G04740	-1.31	-0.39	-2.21	0.064248	0.203769	-4.77
256090_at	predicted protein	---	AT1G20816	-1.24	-0.31	-2.21	0.064293	0.203883	-4.77
249570_at	hypothetical protein	---	AT5G38080	1.23	0.29	2.21	0.064326	0.203953	-4.77
266907_at	Expressed protein ; supported by full-ler	ATGA2OX	---	1.23	0.30	2.21	0.064342	0.203953	-4.78
255605_at	hypothetical protein	---	AT4G01090	1.34	0.42	2.21	0.064338	0.203953	-4.77
246708_at	putative protein various predicted prote	---	AT5G28150	-1.25	-0.33	-2.21	0.064371	0.204015	-4.78
261167_at	disulfide isomerase-related protein, put	ATPDIL2-2	AT1G04980	1.78	0.83	2.21	0.064427	0.204164	-4.78
252549_at	protein kinase - like receptor-like protei	---	AT3G45860	-1.56	-0.64	-2.21	0.064455	0.204198	-4.78
258620_at	putative MYB family transcription factor	MYB107	AT3G02940	1.14	0.19	2.21	0.064453	0.204198	-4.78
252100_at	crooked neck-like protein crooked neck	---	AT3G51110	-1.38	-0.46	-2.21	0.064469	0.204213	-4.78
264169_at	hypothetical protein predicted by gensca	---	AT1G02020	-1.14	-0.19	-2.21	0.064518	0.204339	-4.78
247916_at	adenosylmethionine-8-amino-7-oxonona	BIO1	AT5G57590	-1.20	-0.26	-2.21	0.064531	0.204352	-4.78
247574_at	putative protein predicted protein, Arab	---	AT5G61228 /	-1.20	-0.26	-2.21	0.064575	0.204464	-4.78
247127_at	putative protein similar to unknown prote	---	AT5G66100	-1.18	-0.24	-2.21	0.064602	0.204520	-4.78
264837_at	unknown protein similar to ESTs emb|Z	---	AT1G03600	-1.37	-0.45	-2.21	0.064634	0.204581	-4.78
247202_at	GTP-binding protein ; supported by full-	AtRABA4a	AT5G65270	1.23	0.30	2.21	0.064642	0.204581	-4.78
260375_at	unknown protein	---	AT1G73950	-1.20	-0.26	-2.21	0.064648	0.204581	-4.78

249240_at	putative protein similar to unknown prote	---	AT5G42220	-1.23	-0.30	-2.21	0.064705	0.204734	-4.78
254212_at	putative protein many putative proteins,	---	AT4G23580	1.18	0.24	2.21	0.064749	0.204789	-4.78
257733_at	unknown protein ; supported by cDNA:	---	AT3G18350	1.21	0.28	2.21	0.064737	0.204789	-4.78
248140_at	putative protein similar to unknown prote	---	AT5G54980	-1.20	-0.26	-2.21	0.064749	0.204789	-4.78
251574_at	putative protein GLUCAN ENDO-1,3-BI	PDCB5	AT3G58100	-1.22	-0.29	-2.20	0.064798	0.204913	-4.78
263996_at	unknown protein	---	AT2G22530	-1.22	-0.29	-2.20	0.064891	0.205180	-4.78
244969_at	ribosomal protein S18	---	---	-1.48	-0.57	-2.20	0.064921	0.205247	-4.78
261739_at	hypothetical protein similar to hypothetic	PEX11A	AT1G47750	1.16	0.22	2.20	0.064979	0.205401	-4.78
259646_at	n-calpain-1 large subunit, putative simil	DEK1	AT1G55350	-1.18	-0.24	-2.20	0.065055	0.205612	-4.79
245956_s_a	luminal binding protein ; supported by c	BIP2	AT5G28540 /	1.74	0.80	2.20	0.065079	0.205660	-4.79
259519_at	hypothetical protein	---	AT1G12270	-1.25	-0.32	-2.20	0.065115	0.205745	-4.79
256125_at	pathogenesis-related group 5 protein, p	ATLP-1	AT1G18250	1.29	0.37	2.20	0.065159	0.205766	-4.79
261208_at	unknown protein ; supported by cDNA: g	---	AT1G12930	-1.27	-0.34	-2.20	0.065164	0.205766	-4.79
260961_at	unknown protein similar to hypothetical	---	AT1G05960	-1.15	-0.21	-2.20	0.065167	0.205766	-4.79
248189_at	DNA mismatch repair protein MutS2-like	---	AT5G54090	-1.24	-0.31	-2.20	0.065146	0.205766	-4.79
258385_at	putative jasmonic acid regulatory protein	ATNAC2	AT3G15510	1.30	0.37	2.20	0.065134	0.205766	-4.79
246097_at	putative protein CGI-45 protein - Homo	HHP1	AT5G20270	1.58	0.66	2.20	0.065191	0.205814	-4.79
264027_at	putative AAA-type ATPase similar to CD	CDC48B	AT2G03670	-1.27	-0.34	-2.20	0.065244	0.205954	-4.79
249636_at	beta-glucosidase -like protein prunasin	BGLU42	AT5G36890	-1.20	-0.26	-2.20	0.065285	0.206027	-4.79
260428_at	putative translation initiation factor EIF-2	---	AT1G72340	-1.28	-0.35	-2.20	0.065286	0.206027	-4.79
255968_at	Expressed protein ; supported by full-ler	---	AT1G22270	-1.23	-0.30	-2.20	0.065299	0.206042	-4.79
259259_at	spindly (gibberellin signal transduction p	SPY	AT3G11540	-1.19	-0.26	-2.20	0.065327	0.206100	-4.79
258160_at	glutamine synthetase, putative similar t	GLN1.3	AT3G17820	1.37	0.45	2.20	0.065347	0.206137	-4.79
267095_at	putative AMP deaminase ; supported b	FAC1	AT2G38280	-1.22	-0.29	-2.20	0.06538	0.206212	-4.79
258076_at	50S ribosomal protein L15, chloroplast	RPL15	AT3G25920	-1.29	-0.36	-2.20	0.065434	0.206350	-4.79
258665_at	thioredoxin-like protein similar to thiored	ATH9	AT3G08710	1.39	0.47	2.20	0.065442	0.206350	-4.79
246428_at	spindle pole body protein-like spindle p	---	AT5G17410	-1.24	-0.31	-2.20	0.065454	0.206359	-4.79
246877_at	putative protein various predicted prote	---	AT5G26150	1.15	0.20	2.20	0.065474	0.206394	-4.79
252561_at	histone H2B ;supported by full-length c	HTB9	AT3G45980	-1.29	-0.37	-2.20	0.065523	0.206520	-4.79
266952_at	putative gibberellin 2-oxidase	ATGA2OX	AT2G34555	1.21	0.28	2.20	0.065535	0.206528	-4.79
263788_at	putative sarcosine oxidase	---	AT2G24580	1.33	0.41	2.20	0.065585	0.206658	-4.79
262297_at	hypothetical protein similar to hypothetic	---	AT1G27600	1.16	0.21	2.20	0.065621	0.206726	-4.79
263764_at	putative vacuolar proton-ATPase subun	VHA-A2	AT2G21410	-1.23	-0.30	-2.20	0.065625	0.206726	-4.79
266059_at	predicted protein ;supported by cDNA:	---	AT2G40765	1.42	0.51	2.20	0.065662	0.206814	-4.80
267296_at	hypothetical protein predicted by genefi	LBD10	AT2G23660	1.19	0.25	2.20	0.065674	0.206822	-4.80

266359_at	putative phospholipid cytidylyltransferas	CCT1	AT2G32260	-1.17	-0.23	-2.20	0.065686	0.206833	-4.80
251745_at	putative protein zinc finger transcription	SZF1	AT3G55980	2.62	1.39	2.20	0.06571	0.206878	-4.80
256236_at	hypothetical protein predicted by genem	---	AT3G12350	-1.22	-0.29	-2.20	0.065718	0.206878	-4.80
252094_at	multicatalytic endopeptidase complex a	PAD1	AT3G51260	-1.30	-0.38	-2.20	0.065737	0.206909	-4.80
259507_at	unknown protein	---	AT1G43910	1.63	0.71	2.19	0.065752	0.206925	-4.80
255283_at	putative symbiosis-related protein ;supp	ATG8B	AT4G04620	1.30	0.38	2.19	0.065764	0.206935	-4.80
253478_at	putative protein trichohyalin - human, P	---	AT4G32350	-1.35	-0.43	-2.19	0.06582	0.206999	-4.80
253561_at	aspartate--tRNA ligase - like protein asp	---	AT4G31180	-1.17	-0.23	-2.19	0.065802	0.206999	-4.80
261139_at	homeodomain protein, putative similar t	BEL10	AT1G19700	-1.17	-0.22	-2.19	0.065795	0.206999	-4.80
260987_at	hypothetical protein predicted by genem	NTMC2T6	AT1G53590	-1.25	-0.32	-2.19	0.065818	0.206999	-4.80
253087_at	purple acid phosphatase like protein	PAP25	AT4G36350	1.21	0.28	2.19	0.065849	0.207060	-4.80
263666_at	putative pre-mRNA splicing factor PRP1	---	AT1G04510	-1.28	-0.36	-2.19	0.065923	0.207186	-4.80
255003_at	AIG1-like protein AIG1 - Arabidopsis tha	---	AT4G09950	1.17	0.22	2.19	0.065918	0.207186	-4.80
248578_at	putative protein contains similarity to un	emb1879	AT5G49820	-1.27	-0.34	-2.19	0.065925	0.207186	-4.80
249259_at	putative protein similar to unknown prote	---	AT5G41660	1.92	0.94	2.19	0.065903	0.207186	-4.80
261438_at	metallothionein-like protein identical to S	---	AT1G07590 /	1.16	0.22	2.19	0.065975	0.207257	-4.80
248061_at	putative protein contains similarity to wa	---	AT5G55340	1.15	0.20	2.19	0.065961	0.207257	-4.80
250236_at	delta subunit of mitochondrial F1-ATPas	---	AT5G13450	1.22	0.29	2.19	0.065973	0.207257	-4.80
258520_at	hypothetical protein predicted by genem	---	AT3G06710	-1.27	-0.35	-2.19	0.065997	0.207292	-4.80
257582_at	hypothetical protein	---	AT1G50720	-1.16	-0.21	-2.19	0.066005	0.207292	-4.80
257792_at	TOM20, putative similar to TOM20 GB:	TOM20-3	AT3G27080	-1.23	-0.30	-2.19	0.066063	0.207420	-4.80
267621_at	unknown protein	---	---	-1.23	-0.30	-2.19	0.066061	0.207420	-4.80
250462_at	receptor protein kinase -like(fragment) r	---	AT5G10020	-1.14	-0.19	-2.19	0.066084	0.207455	-4.80
262729_at	rac-like GTP binding protein (ARAC5) id	ARAC5	AT1G75840	-1.27	-0.34	-2.19	0.066181	0.207733	-4.80
255072_at	outer envelope membrane protein OEP	TOC75-IV	AT4G09080	-1.22	-0.29	-2.19	0.066239	0.207857	-4.80
247956_at	cytokinin oxidase ; supported by cDNA:	CKX3	AT5G56970	-1.19	-0.25	-2.19	0.066233	0.207857	-4.80
245967_at	proline-rich protein extensins	---	AT5G19800	1.18	0.24	2.19	0.066275	0.207930	-4.80
246010_at	putative protein predicted proteins, Ara	---	AT5G08440	-1.15	-0.21	-2.19	0.06628	0.207930	-4.80
257647_at	Expressed protein ; supported by cDNA	---	AT3G25805	-1.37	-0.46	-2.19	0.066321	0.207987	-4.81
256682_at	putative protein dihydrolipoamide S-ace	LTA3	AT3G52200	1.16	0.21	2.19	0.066324	0.207987	-4.81
261152_at	hypothetical protein predicted by genem	---	AT1G04930	-1.31	-0.39	-2.19	0.066326	0.207987	-4.81
260220_at	putative MYB family transcription factor	MYB31	AT1G74650	1.30	0.38	2.19	0.066426	0.208259	-4.81
249877_at	transcription factor-like protein (gb|AAD	HUA2	AT5G23150	1.16	0.21	2.19	0.066431	0.208259	-4.81
267581_at	putative RING zinc finger protein	---	AT2G41980	-1.35	-0.43	-2.19	0.066498	0.208439	-4.81
264013_at	unknown protein	FIO1	AT2G21070	-1.15	-0.20	-2.19	0.066613	0.208771	-4.81

256686_at	non-LTR reverse transcriptase, putative	---	---	-1.15	-0.20	-2.19	0.066665	0.208813	-4.81
263451_at	putative triacylglycerol lipase	---	AT2G31690	1.14	0.20	2.19	0.066668	0.208813	-4.81
250882_at	putative protein ;supported by full-lengt	---	AT5G04000	-1.18	-0.23	-2.19	0.066642	0.208813	-4.81
262549_at	hypothetical protein similar to hypothetic	---	AT1G31290	1.17	0.23	2.19	0.066653	0.208813	-4.81
245247_at	scarecrow-like 13 (SCL13) ; supported b	SCL13	AT4G17230	1.62	0.70	2.19	0.066672	0.208813	-4.81
255214_at	hypothetical protein	---	---	1.16	0.21	2.18	0.066722	0.208942	-4.81
247649_at	KED - like protein KED, Nicotiana tabac	---	AT5G60030	-1.21	-0.28	-2.18	0.066739	0.208966	-4.81
247328_at	unknown protein ;supported by full-leng	---	AT5G64130	1.32	0.40	2.18	0.066761	0.209005	-4.81
253536_at	RSZp22 splicing factor ;supported by ful	SRZ-22	AT4G31580	-1.15	-0.20	-2.18	0.066783	0.209046	-4.81
261295_at	unknown protein	---	AT1G48450	-1.16	-0.22	-2.18	0.066815	0.209119	-4.81
263380_at	hypothetical protein	---	AT2G40200	1.18	0.24	2.18	0.066826	0.209122	-4.81
264123_at	unknown protein ; supported by cDNA: g	---	AT1G02270	-1.22	-0.28	-2.18	0.066845	0.209155	-4.81
257908_at	unknown protein contains Pfam profile: I	---	AT3G25410	-1.21	-0.27	-2.18	0.066866	0.209163	-4.81
260673_at	unknown protein ; supported by full-leng	---	AT1G19330	-1.39	-0.47	-2.18	0.06686	0.209163	-4.81
267314_at	putative myosin heavy chain	---	AT2G34730	1.27	0.34	2.18	0.066891	0.209183	-4.81
247637_at	putative protein gcpE protein, Chlamydi	HDS	AT5G60600	-1.26	-0.34	-2.18	0.066887	0.209183	-4.81
251997_at	60S ribosomal protein - like 60S riboso	STV1	AT3G53020	-1.27	-0.35	-2.18	0.066939	0.209303	-4.81
259173_at	beta-glucosidase identical to beta-gluco	BGLU25	AT3G03640	-1.37	-0.46	-2.18	0.066948	0.209304	-4.81
252168_at	putative protein pir7a protein - Oryza sa	MES10	AT3G50440	-1.75	-0.80	-2.18	0.066965	0.209328	-4.81
257677_at	unknown protein contains Pfam profiles:	ATEHD1	AT3G20290	-1.21	-0.28	-2.18	0.066982	0.209353	-4.81
266555_at	G-box binding bZIP transcription factor i	GBF3	AT2G46270	1.50	0.59	2.18	0.066996	0.209367	-4.82
249314_at	receptor kinase-like protein	---	AT5G41180	1.23	0.30	2.18	0.067115	0.209713	-4.82
247427_at	putative protein similar to unknown prote	---	AT5G62580	1.37	0.46	2.18	0.067134	0.209718	-4.82
256397_at	putative dual-specificity protein phospha	MKP2	AT3G06110	-1.18	-0.23	-2.18	0.067143	0.209718	-4.82
245870_at	hypothetical protein similar to hypothetic	---	AT1G26300	1.17	0.23	2.18	0.067165	0.209718	-4.82
265207_at	unknown protein	---	AT2G36680	1.17	0.22	2.18	0.067148	0.209718	-4.82
250106_at	putative protein strong similarity to unkn	---	AT5G16640	-1.17	-0.23	-2.18	0.067161	0.209718	-4.82
253341_at	putative protein ; supported by cDNA: g	---	AT4G33410	-1.21	-0.27	-2.18	0.067172	0.209718	-4.82
258229_at	unknown protein contains Pfam profile: I	---	AT3G27700	-1.17	-0.23	-2.18	0.067212	0.209812	-4.82
266458_at	unknown protein ;supported by full-leng	---	AT2G47710	-1.16	-0.22	-2.18	0.067232	0.209846	-4.82
251793_at	regulator of chromosome condensation	---	AT3G55580	-1.15	-0.20	-2.18	0.067352	0.210191	-4.82
248006_at	unknown protein	HAP8	AT5G56250	-1.18	-0.24	-2.18	0.067378	0.210218	-4.82
262960_at	unknown protein ; supported by cDNA: g	---	AT1G54320	1.19	0.25	2.18	0.067371	0.210218	-4.82
260333_at	putative polygalacturonase similar to po	---	AT1G70500	1.31	0.39	2.18	0.067391	0.210228	-4.82
252760_x_a	putative protein several hypothetical pro	---	---	1.17	0.22	2.18	0.067412	0.210266	-4.82

246238_at	sugar transporter like protein	---	AT4G36670	1.56	0.64	2.18	0.067422	0.210266	-4.82
252115_at	non-specific lipid transfer protein ;suppo	LTP5	AT3G51600	1.24	0.31	2.18	0.067465	0.210345	-4.82
254067_at	hypothetical protein	NAP8	AT4G25450	1.16	0.22	2.18	0.067462	0.210345	-4.82
245641_at	Expressed protein ; supported by full-ler	---	AT1G25370	2.02	1.02	2.18	0.067478	0.210356	-4.82
248448_at	putative protein contains similarity to eth	---	AT5G51190	2.24	1.16	2.18	0.067552	0.210557	-4.82
253275_at	Expressed protein ; supported by full-ler	---	AT4G34215	-1.21	-0.28	-2.18	0.067587	0.210609	-4.82
246092_at	glutaredoxin ;supported by full-length c	---	AT5G20500	1.21	0.27	2.18	0.067581	0.210609	-4.82
260339_at	putative serine/threonine kinase similar	SIK1	AT1G69220	-1.28	-0.36	-2.18	0.06766	0.210807	-4.82
254624_at	hypothetical protein ;supported by full-le	---	AT4G18580	-1.19	-0.25	-2.17	0.067711	0.210938	-4.83
247620_at	receptor like protein kinase receptor like	---	AT5G60310	1.20	0.27	2.17	0.067731	0.210972	-4.83
262263_at	auxin transport protein REH1, putative	PIN3	AT1G70940	-1.66	-0.74	-2.17	0.067788	0.211093	-4.83
252925_at	ES43 like protein ES43 protein - barley	SHL1	AT4G39100	-1.24	-0.32	-2.17	0.067785	0.211093	-4.83
257219_at	uroporphyrinogen decarboxylase, putat	HEME1	AT3G14930	-1.28	-0.36	-2.17	0.067817	0.211127	-4.83
264070_at	putative cyclin-dependent kinase regula	CKS1	AT2G27960	-1.29	-0.37	-2.17	0.067827	0.211127	-4.83
255981_at	hypothetical protein ;supported by full-le	---	AT1G34020	-1.23	-0.29	-2.17	0.067822	0.211127	-4.83
260551_at	putative trypsin inhibitor ; supported by	ATTI1	AT2G43510	1.52	0.60	2.17	0.067866	0.211147	-4.83
256887_at	hypothetical protein predicted by genem	---	AT3G15150	-1.22	-0.28	-2.17	0.067844	0.211147	-4.83
250622_at	putative transcription factor AP2 domain	---	AT5G07310	1.17	0.22	2.17	0.067871	0.211147	-4.83
252065_at	putative protein ;supported by full-lengt	---	AT3G51610	-1.23	-0.30	-2.17	0.067859	0.211147	-4.83
264232_at	putative protein kinase Pfam HMM hit: E	---	AT1G67470	1.81	0.86	2.17	0.067937	0.211324	-4.83
255518_at	putative pectinesterase similar to severa	---	AT4G02300	1.20	0.26	2.17	0.067948	0.211329	-4.83
267493_at	unknown protein	OFP2	AT2G30400	1.31	0.39	2.17	0.067982	0.211406	-4.83
259109_at	putative serine threonine protein phosph	---	AT3G05580	1.31	0.39	2.17	0.068019	0.211494	-4.83
256227_at	unknown protein ; supported by cDNA: g	---	AT1G56290	-1.16	-0.22	-2.17	0.06804	0.211530	-4.83
253728_at	putative protein unknown protein chrom	---	AT4G29410	-1.32	-0.40	-2.17	0.068061	0.211567	-4.83
251981_at	putative protein BETA-GALACTOSIDAS	---	AT3G53080	1.19	0.25	2.17	0.068193	0.211947	-4.83
256644_at	unknown protein similar to hypothetical	---	---	1.17	0.23	2.17	0.068241	0.212068	-4.83
265975_at	putative citrate synthetase	---	AT2G11270	1.25	0.32	2.17	0.068265	0.212113	-4.83
261782_at	unknown protein	---	AT1G76110	-1.25	-0.32	-2.17	0.068276	0.212114	-4.83
255925_at	unknown protein ;supported by full-lengt	---	AT1G22200	-1.25	-0.32	-2.17	0.068291	0.212114	-4.83
258548_at	hypothetical protein	ULP1A	AT3G06910	-1.25	-0.32	-2.17	0.068293	0.212114	-4.83
267343_at	hypothetical protein predicted by grail; s	---	AT2G44260	2.39	1.26	2.17	0.068311	0.212141	-4.83
248905_at	putative protein contains similarity to RN	---	AT5G46250	-1.18	-0.24	-2.17	0.06837	0.212294	-4.84
264243_at	hypothetical protein predicted by genem	---	AT1G54650	-1.28	-0.35	-2.17	0.068388	0.212321	-4.84
254780_s_a	auxilin-like protein auxilin - bovine, Pir2	---	AT4G12770	1.31	0.39	2.17	0.068402	0.212338	-4.84

260616_at	hypothetical protein contains Pfam profil	---	AT1G53280	-1.27	-0.34	-2.17	0.068425	0.212378	-4.84
265465_at	hypothetical protein predicted by genefir	---	AT2G37070	1.51	0.60	2.17	0.068455	0.212430	-4.84
263778_at	putative cytochrome oxidase biogenesis	OXA1L	AT2G46470	-1.21	-0.28	-2.17	0.06846	0.212430	-4.84
258482_at	putative chaperonin similar to chaperoni	---	AT3G02530	-1.23	-0.29	-2.17	0.068548	0.212615	-4.84
244911_at	hypothetical protein	---	---	-1.20	-0.27	-2.17	0.068546	0.212615	-4.84
264868_at	unknown protein	---	AT1G24090	1.45	0.53	2.17	0.068532	0.212615	-4.84
253190_at	UDP-galactose transporter - like protein	---	AT4G35335	-1.20	-0.26	-2.17	0.068567	0.212646	-4.84
254659_at	starch synthase-like protein bacterial ar	SS4	AT4G18240	-1.32	-0.41	-2.17	0.068581	0.212662	-4.84
256315_at	hypothetical protein predicted by genem	---	AT1G35880	1.17	0.23	2.17	0.068628	0.212775	-4.84
251592_at	zinc finger - like protein finger protein p	NTT	AT3G57670	1.16	0.22	2.17	0.068636	0.212775	-4.84
251870_at	putative protein Various predicted prote	---	AT3G54510	1.17	0.23	2.16	0.068665	0.212834	-4.84
250957_at	photoreceptor-interacting protein - like r	---	AT5G03250	-1.15	-0.20	-2.16	0.068699	0.212910	-4.84
254373_at	hypothetical protein ;supported by full-le	---	AT4G21730	1.17	0.23	2.16	0.068725	0.212962	-4.84
249467_at	NAM / CUC2 - like protein CUC2, Arabi	ATNAC6	AT5G39610	1.77	0.82	2.16	0.068801	0.213167	-4.84
250438_at	putative protein predicted protein, Arabi	---	AT5G10580	1.16	0.21	2.16	0.06881	0.213167	-4.84
256131_at	bZIP transcription factor, putative simila	AtbZIP58	AT1G13600	1.24	0.31	2.16	0.06884	0.213232	-4.84
263857_at	unknown protein	---	AT2G04380	1.14	0.19	2.16	0.068893	0.213338	-4.84
251874_at	putative protein (fragment) esterase, Ps	---	AT3G54240	1.25	0.32	2.16	0.068888	0.213338	-4.84
252694_at	nodulin -like protein nodulin-21, Glycine	---	AT3G43630	-1.19	-0.25	-2.16	0.068911	0.213365	-4.84
257313_at	gamma tonoplast intrinsic protein nearly	TIP2	AT3G26520	1.24	0.31	2.16	0.068939	0.213424	-4.84
266089_at	hypothetical protein predicted by gensca	---	AT2G38010	-1.41	-0.50	-2.16	0.068956	0.213447	-4.84
267565_at	putative cytochrome P450	CYP71A12	AT2G30750	2.05	1.04	2.16	0.068991	0.213510	-4.84
263126_at	hypothetical protein predicted by genem	---	AT1G78460	-1.79	-0.84	-2.16	0.068995	0.213510	-4.84
258064_at	putative cytochrome P450 similar to GB	CYP72A14	AT3G14680	-1.60	-0.68	-2.16	0.069026	0.213577	-4.84
254926_at	ACC synthase (AtACS-6) ; supported b	ACS6	AT4G11280	2.48	1.31	2.16	0.06913	0.213785	-4.85
266601_at	hypothetical protein predicted by gensca	---	AT2G46060	-1.35	-0.43	-2.16	0.069103	0.213785	-4.85
245119_at	unknown protein ; supported by cDNA:	---	AT2G41640	2.21	1.14	2.16	0.069131	0.213785	-4.85
257024_at	CDPK-related kinase identical to GB:2A	---	AT3G19100	1.29	0.36	2.16	0.069125	0.213785	-4.85
245014_at	ATPase beta subunit	---	---	-1.15	-0.20	-2.16	0.069258	0.214120	-4.85
249347_at	putative protein similar to unknown prote	---	AT5G40830	-1.40	-0.49	-2.16	0.069251	0.214120	-4.85
255699_at	putative pectinesterase	PME38	AT4G00190	1.16	0.22	2.16	0.069268	0.214120	-4.85
256727_at	hypothetical protein	---	AT3G52240	1.22	0.29	2.16	0.069325	0.214239	-4.85
263520_at	putative protein kinase contains a protei	---	AT2G42640	-1.18	-0.24	-2.16	0.069316	0.214239	-4.85
260399_at	putative lipoxygenase similar to lipoxyge	---	AT1G72520	2.72	1.44	2.16	0.069367	0.214341	-4.85
259431_at	plasma membrane intrinsic protein 1c, p	PIP1C	AT1G01620	1.98	0.99	2.16	0.069514	0.214455	-4.85

255690_at	probable cytochrome P450	CYP86A2	AT4G00360	2.31	1.21	2.16	0.06947	0.214455	-4.85
261238_at	hypothetical protein predicted by genem	---	AT1G32810	-1.19	-0.26	-2.16	0.069439	0.214455	-4.85
265440_at	pEARLI 4 protein Same as GB: L43081;	pEARLI4	AT2G20960	1.37	0.45	2.16	0.0695	0.214455	-4.85
246513_at	hypothetical protein	---	AT5G15680	-1.16	-0.22	-2.16	0.069441	0.214455	-4.85
254688_at	DnaJ-like protein DnaJ-like protein, Pha	J20	AT4G13830	-1.18	-0.24	-2.16	0.069447	0.214455	-4.85
266130_at	putative transcription activator	---	AT2G44980	1.32	0.40	2.16	0.06943	0.214455	-4.85
254739_at	putative disease resistance protein Hcr	AtRLP48	AT4G13880	1.18	0.23	2.16	0.069487	0.214455	-4.85
255896_at	basic blue protein, putative similar to ba	---	AT1G17800	1.16	0.21	2.16	0.069495	0.214455	-4.85
263282_at	Expressed protein ; supported by full-ler	---	AT2G14095	1.19	0.25	2.16	0.069455	0.214455	-4.85
255427_at	hypothetical protein	---	AT4G03380	-1.14	-0.19	-2.16	0.069474	0.214455	-4.85
260369_at	60S ribosomal protein L34, putative sim	RPL34	AT1G69620	-1.28	-0.35	-2.16	0.069517	0.214455	-4.85
256497_at	ORF1, putative similar to ORF1 GI:457	ECS1	AT1G31580	1.42	0.50	2.16	0.069585	0.214637	-4.85
251270_at	putative protein	---	AT3G62370	1.30	0.37	2.15	0.069676	0.214857	-4.85
262198_at	pectin methylesterase (PMEU1), putati	ATPME2	AT1G53830	1.73	0.79	2.15	0.069694	0.214857	-4.85
247313_at	3(2),5-bisphosphate nucleotidase ; sup	SAL1	AT5G63980	-1.28	-0.36	-2.15	0.069669	0.214857	-4.85
249701_at	putative protein similar to unknown prote	---	AT5G35460	-1.17	-0.23	-2.15	0.069686	0.214857	-4.85
259368_at	aspartic protease, putative similar to as	---	AT1G69100	1.17	0.23	2.15	0.069776	0.215072	-4.86
264735_s_a	hypothetical protein similar to hypothetic	---	AT1G62000 /	-1.25	-0.32	-2.15	0.069792	0.215072	-4.86
253317_at	putative protein	---	AT4G33960	-1.49	-0.58	-2.15	0.069785	0.215072	-4.86
252025_at	putative protein chromosome assembly	---	AT3G52900	1.20	0.26	2.15	0.069863	0.215262	-4.86
254965_at	putative protein other hypothetical prote	---	AT4G11090	-1.16	-0.22	-2.15	0.069879	0.215278	-4.86
253122_at	hypothetical protein	---	AT4G35987	-1.20	-0.26	-2.15	0.069887	0.215278	-4.86
256372_at	cell division protein kinase, putative sim	CAK4	AT1G66750	-1.26	-0.34	-2.15	0.069935	0.215396	-4.86
258963_at	putative myotubularin similar to myotubu	---	AT3G10550	1.21	0.27	2.15	0.069959	0.215415	-4.86
255864_at	putative pseudouridine synthase	---	AT2G30320	-1.21	-0.28	-2.15	0.06996	0.215415	-4.86
247338_at	pyruvate kinase	---	AT5G63680	1.18	0.24	2.15	0.069986	0.215435	-4.86
252041_at	DNA-directed RNA polymerase II 13.6K	NRPB11	AT3G52090	-1.19	-0.25	-2.15	0.069988	0.215435	-4.86
255067_at	putative phosphotyrosyl phosphatase ac	---	AT4G08960	-1.15	-0.20	-2.15	0.069995	0.215435	-4.86
247068_at	putative protein similar to unknown prote	---	AT5G66800	1.22	0.28	2.15	0.070018	0.215476	-4.86
262840_at	linker histone protein, putative contains	HMGA	AT1G14900	-1.21	-0.28	-2.15	0.070029	0.215482	-4.86
247959_at	unknown protein	---	AT5G57080	-1.27	-0.35	-2.15	0.070046	0.215503	-4.86
258235_at	alternative oxidase 1c precursor identica	AOX1C	AT3G27620	1.21	0.27	2.15	0.070068	0.215544	-4.86
251987_at	CYTOCHROME P450 71B5 ; supporte	CYP71B5	AT3G53280	-1.22	-0.29	-2.15	0.070092	0.215558	-4.86
260916_at	predicted protein ; supported by cDNA:	---	AT1G02475	-1.20	-0.26	-2.15	0.070088	0.215558	-4.86
249116_at	putative protein similar to unknown prote	---	AT5G43820 /	-1.24	-0.31	-2.15	0.070165	0.215755	-4.86

254963_at	putative protein single strand DNA-bind	MTSSB	AT4G11060	-1.21	-0.28	-2.15	0.070176	0.215758	-4.86
255467_at	putative leucine-rich repeat protein simi	---	AT4G03010	-1.19	-0.25	-2.15	0.070188	0.215767	-4.86
260787_at	Ring3-like bromodomain protein similar	GTE4	AT1G06230	-1.20	-0.26	-2.15	0.070229	0.215864	-4.86
247849_at	putative protein fibrinogen-binding prote	---	AT5G58130	-1.24	-0.31	-2.15	0.070263	0.215940	-4.86
249279_at	SCARECROW gene regulator-like prote	---	AT5G41920	-1.15	-0.21	-2.15	0.070283	0.215971	-4.86
249049_at	tubulin beta-4 chain (sp|P24636) ; supp	TUB4	AT5G44340	1.29	0.37	2.15	0.070308	0.216018	-4.86
254185_at	cellulose synthase catalytic subunit - lik	CSLG3	AT4G23990	1.32	0.40	2.15	0.070366	0.216170	-4.86
254025_at	putative pathogenesis-related protein g	---	AT4G25790	1.14	0.20	2.15	0.070383	0.216191	-4.86
248079_at	unknown protein	---	AT5G55790	-1.27	-0.35	-2.15	0.070444	0.216349	-4.86
258437_at	unknown protein contains protein phosp	---	AT3G16560	-1.31	-0.39	-2.15	0.070458	0.216362	-4.87
256310_at	unknown protein ; supported by cDNA: g	ERD4	AT1G30360	-1.30	-0.37	-2.15	0.070557	0.216578	-4.87
267508_at	hypothetical protein predicted by gensca	---	AT2G45700	-1.18	-0.23	-2.15	0.070549	0.216578	-4.87
246204_at	putative protein ; supported by cDNA: gi	---	AT4G37020	-1.19	-0.25	-2.15	0.070566	0.216578	-4.87
251633_at	putative protein metalloendopeptidase I	---	AT3G57460	1.40	0.49	2.15	0.070557	0.216578	-4.87
259662_at	Expressed protein ; supported by full-ler	HUB2	AT1G55250	-1.26	-0.33	-2.15	0.070662	0.216756	-4.87
262066_at	hypothetical protein contains similarity to	---	AT1G79950	-1.38	-0.46	-2.15	0.07066	0.216756	-4.87
245240_at	polyprotein, putative similar to polyprote	---	---	1.22	0.29	2.15	0.070645	0.216756	-4.87
257519_at	unknown protein	---	AT3G01210	-1.22	-0.28	-2.15	0.070644	0.216756	-4.87
266752_at	putative ABC transporter related to mult	ABCB4	AT2G47000	2.62	1.39	2.14	0.070758	0.216963	-4.87
266183_at	unknown protein	ATPT2	AT2G38940	1.24	0.31	2.14	0.070749	0.216963	-4.87
260556_at	putative endochitinase	---	AT2G43620	2.77	1.47	2.14	0.070743	0.216963	-4.87
258256_at	unknown protein ; supported by cDNA:	---	AT3G26890	-1.20	-0.27	-2.14	0.070781	0.217005	-4.87
254853_at	putative DNA-binding protein AT-hook p	---	AT4G12080	1.25	0.33	2.14	0.070928	0.217425	-4.87
248222_at	GTPase activator protein of Rab-like sm	---	AT5G53570	1.24	0.31	2.14	0.070997	0.217608	-4.87
266853_at	putative salt-inducible protein	---	AT2G26790	-1.17	-0.22	-2.14	0.071048	0.217735	-4.87
257381_at	unknown protein	---	AT2G37950	-1.37	-0.46	-2.14	0.071069	0.217741	-4.87
246206_at	Expressed protein ; supported by cDNA	ATPBRP	---	1.17	0.23	2.14	0.07106	0.217741	-4.87
261087_at	hypothetical protein similar to unknown	---	AT1G17350	-1.31	-0.39	-2.14	0.071097	0.217768	-4.87
247389_at	putative protein strong similarity to unkn	---	AT5G63490	1.27	0.35	2.14	0.071087	0.217768	-4.87
264091_at	hypothetical protein predicted by gensca	---	AT1G79110	-1.50	-0.59	-2.14	0.071159	0.217929	-4.87
257777_x_a	hypothetical protein	---	---	1.21	0.27	2.14	0.071179	0.217962	-4.88
262518_at	putative glutathione transferase One of	ATGSTU2	AT1G17170	3.86	1.95	2.14	0.071245	0.218136	-4.88
259881_at	Expressed protein ; supported by cDNA	---	AT1G76820	-1.29	-0.37	-2.14	0.071279	0.218150	-4.88
265956_at	hypothetical protein predicted by gensca	---	AT2G37290	1.14	0.19	2.14	0.071267	0.218150	-4.88
266196_at	putative protein kinase contains a protei	---	AT2G39110	-1.18	-0.24	-2.14	0.071288	0.218150	-4.88

256323_at	unknown protein ; supported by cDNA: g	---	AT1G54920	-1.25	-0.33	-2.14	0.071275	0.218150	-4.88
256478_at	unknown protein	---	---	1.20	0.27	2.14	0.071337	0.218218	-4.88
266352_at	unknown protein	---	AT2G01610	1.66	0.73	2.14	0.07133	0.218218	-4.88
254348_at	putative protein p47 - Homo sapiens,PI	PUX3	AT4G22150	-1.16	-0.22	-2.14	0.071339	0.218218	-4.88
246036_at	alpha-galactosidase - like protein alpha	AtAGAL2	AT5G08370	-1.44	-0.52	-2.14	0.071359	0.218250	-4.88
245756_at	hyoscyamine 6-dioxygenase hydroxylas	---	AT1G35190	1.29	0.36	2.14	0.071388	0.218308	-4.88
253967_at	putative protein probable membrane pr	---	AT4G26550	1.29	0.37	2.14	0.071402	0.218320	-4.88
265327_at	unknown protein	---	AT2G18210	2.41	1.27	2.14	0.071479	0.218529	-4.88
263484_at	putative presenilin	---	AT2G29900	-1.15	-0.21	-2.14	0.07152	0.218623	-4.88
247972_at	histone acetyltransferase HAT B	HAG2	AT5G56740	-1.27	-0.35	-2.14	0.0716	0.218840	-4.88
267412_at	putative vacuolar sorting receptor	---	AT2G34940	1.69	0.75	2.14	0.071625	0.218862	-4.88
254276_at	predicted protein PVPR3 protein, Phae	---	AT4G22820	1.42	0.51	2.14	0.071627	0.218862	-4.88
254705_at	putative protein ; supported by cDNA: g	---	AT4G17870	-1.31	-0.39	-2.14	0.071709	0.219084	-4.88
261767_s_a	adenine nucleotide translocase, putativ	NTT1	AT1G15500 /	1.22	0.29	2.13	0.071738	0.219144	-4.88
266968_at	putative protein kinase contains a protei	---	AT2G39360	1.50	0.59	2.13	0.071762	0.219176	-4.88
266623_at	unknown protein	---	AT2G35390	1.26	0.33	2.13	0.071768	0.219176	-4.88
252446_at	beta-D-glucan exohydrolase - like prote	---	AT3G47010	-1.16	-0.21	-2.13	0.071784	0.219195	-4.88
248986_at	putative protein similar to unknown prote	---	AT5G45170	-1.24	-0.31	-2.13	0.071889	0.219488	-4.88
254259_s_a	putative protein rape mRNA, Brassica r	---	AT4G23420 /	-1.30	-0.37	-2.13	0.071961	0.219678	-4.89
250017_at	unknown protein	---	AT5G18140	-1.32	-0.41	-2.13	0.071975	0.219690	-4.89
246946_at	putative protein	---	AT5G25070	-1.15	-0.21	-2.13	0.072035	0.219816	-4.89
250030_at	putative protein contains similarity to pro	ATAPRL7	AT5G18120	-1.17	-0.23	-2.13	0.072031	0.219816	-4.89
262646_at	aspartate aminotransferase nearly iden	ASP4	AT1G62800	-1.41	-0.50	-2.13	0.072057	0.219853	-4.89
262503_at	hypothetical protein predicted by gensca	---	AT1G21670	1.42	0.50	2.13	0.072092	0.219930	-4.89
255004_at	putative protein	---	AT4G09970	-1.25	-0.32	-2.13	0.072108	0.219948	-4.89
265058_s_a	myrosinase-binding protein homolog, p	MBP2	AT1G52030 /	-2.57	-1.36	-2.13	0.072163	0.220087	-4.89
259273_s_a	serine/threonine specific protein kinase	---	AT3G01300 /	-1.18	-0.24	-2.13	0.072192	0.220117	-4.89
252501_at	hypothetical protein	---	AT3G46880	1.18	0.23	2.13	0.072192	0.220117	-4.89
252415_at	glutamine-dependent asparagine synthe	ASN1	AT3G47340	3.14	1.65	2.13	0.072204	0.220126	-4.89
250302_at	fructosidase - like protein fructosidase,	AtcwINV6	AT5G11920	2.33	1.22	2.13	0.072215	0.220130	-4.89
261879_at	cytochrome P450, putative similar to CY	CYP705A2	AT1G50520	1.16	0.22	2.13	0.07226	0.220236	-4.89
253683_at	cytidine deaminase 4 (CDA4)	---	AT4G29650	1.18	0.23	2.13	0.072336	0.220298	-4.89
266323_at	putative calcium-dependent protein kina	CRK3	AT2G46700	1.20	0.26	2.13	0.072348	0.220298	-4.89
262782_at	Expressed protein ; supported by full-ler	---	AT1G13195	1.17	0.23	2.13	0.072317	0.220298	-4.89
253682_at	cytidine deaminase 5 (CDA5)	---	AT4G29640	1.23	0.30	2.13	0.072308	0.220298	-4.89

246270_at	putative protein	---	AT4G36500	1.84	0.88	2.13	0.072338	0.220298	-4.89
263555_at	unknown protein ;supported by full-leng	---	AT2G16460	1.17	0.23	2.13	0.072335	0.220298	-4.89
252299_at	putative protein various predicted prote	---	AT3G49150	1.22	0.28	2.13	0.072315	0.220298	-4.89
265033_at	PSI type III chlorophyll a/b-binding prot	LHCA3	AT1G61520	-1.14	-0.19	-2.13	0.072359	0.220304	-4.89
258452_at	alternative oxidase 1a precursor identica	AOX1A	AT3G22370	1.74	0.80	2.13	0.07239	0.220337	-4.89
260649_at	storage protein, putative similar to GB:(	ACA7	AT1G08080	1.17	0.23	2.13	0.072387	0.220337	-4.89
248820_at	putative protein similar to unknown prote	---	AT5G47060	-1.26	-0.33	-2.13	0.072438	0.220425	-4.89
261038_at	unknown protein ; supported by full-leng	---	AT1G17490	-1.23	-0.30	-2.13	0.072433	0.220425	-4.89
260594_at	hypothetical protein predicted by gensca	---	AT1G55880	-1.14	-0.19	-2.13	0.072473	0.220504	-4.89
245579_at	hypothetical protein	---	AT4G14810	1.16	0.21	2.13	0.072533	0.220657	-4.89
253474_at	hypothetical protein	---	AT4G32270	-1.22	-0.29	-2.13	0.072561	0.220703	-4.89
245897_at	potassium transport protein-like several	KUP7	AT5G09400	1.26	0.34	2.13	0.072577	0.220703	-4.89
257957_at	wall-associated serine/threonine kinase	---	AT3G25490	1.28	0.35	2.13	0.072575	0.220703	-4.89
267327_at	putative protein kinase contains a protei	---	AT2G19410	1.16	0.22	2.13	0.072589	0.220707	-4.89
256126_at	hypothetical protein similar to MuDR tra	---	AT1G18050	1.27	0.35	2.13	0.072605	0.220728	-4.89
264739_at	hypothetical protein predicted by genem	---	AT1G62260	-1.21	-0.28	-2.13	0.072649	0.220833	-4.90
258712_s_a	putative 40S ribosomal protein S23 sim	---	AT3G09680 /	-1.24	-0.31	-2.13	0.072685	0.220894	-4.90
252494_at	receptor-like protein kinase receptor like	---	AT3G46760	1.19	0.26	2.13	0.072689	0.220894	-4.90
264790_at	putative histidine kinase histidine kinase	ATHK1	AT2G17820	-1.23	-0.30	-2.13	0.072721	0.220924	-4.90
261707_at	unknown protein	---	AT1G32650	-1.17	-0.22	-2.13	0.072716	0.220924	-4.90
255576_at	predicted protein of unknown function s	---	AT4G01440	-1.34	-0.42	-2.13	0.072728	0.220924	-4.90
252000_at	hypothetical protein predicted protein, A	---	AT3G52710	-1.24	-0.31	-2.13	0.072752	0.220970	-4.90
247091_at	peroxidase (emb CAA66964.1)	---	AT5G66390	1.20	0.27	2.12	0.072831	0.221151	-4.90
251068_at	putative protein several protein kinases	STN8	AT5G01920	-1.32	-0.40	-2.12	0.072824	0.221151	-4.90
266048_at	putative thioredoxin H contains a thiored	ATCXXS2	AT2G40790	1.20	0.26	2.12	0.072856	0.221195	-4.90
267623_at	unknown protein	---	AT2G39650	2.03	1.02	2.12	0.07288	0.221240	-4.90
266757_at	unknown protein	---	AT2G46940	1.36	0.44	2.12	0.072903	0.221279	-4.90
260815_at	chloroplast inner envelope protein, puta	TIC110	AT1G06950	-1.33	-0.41	-2.12	0.072951	0.221345	-4.90
251579_at	putative protein Bet1 homolog - Rattus	BS14A	AT3G58170	-1.17	-0.23	-2.12	0.072954	0.221345	-4.90
257393_at	unknown protein	---	AT2G20080	1.14	0.19	2.12	0.072946	0.221345	-4.90
261348_at	hypothetical protein contains similarity t	TED3	AT1G79810	-1.16	-0.22	-2.12	0.072971	0.221368	-4.90
266361_at	putative O-GlcNAc transferase	---	AT2G32450	-1.39	-0.48	-2.12	0.073027	0.221508	-4.90
252389_at	Expressed protein ; supported by full-ler	---	AT3G47833	1.38	0.46	2.12	0.073107	0.221721	-4.90
259034_at	putative pectinacetylesterase similar to	---	AT3G09410	-1.31	-0.39	-2.12	0.073135	0.221746	-4.90
266302_at	ethylene-insensitive3-like1 (EIL1) identi	EIL1	AT2G27050	-1.23	-0.30	-2.12	0.073132	0.221746	-4.90

245615_at	reverse transcriptase like protein	---	---	1.17	0.22	2.12	0.073152	0.221769	-4.90
263539_at	putative tyrosine aminotransferase ;sup	TAT3	AT2G24850	2.97	1.57	2.12	0.07318	0.221815	-4.90
251585_at	putative protein hypothetical protein F9	---	AT3G58630	-1.35	-0.43	-2.12	0.073196	0.221815	-4.90
261099_at	expansin At-EXP6, putative similar to G	ATEXPA1	AT1G62980	1.23	0.30	2.12	0.073189	0.221815	-4.90
256516_at	receptor protein kinase (TMK1), putativ	TMK1	AT1G66150	-1.32	-0.40	-2.12	0.073214	0.221840	-4.90
264718_at	receptor-like kinase, putative similar to	---	AT1G70130	1.15	0.20	2.12	0.073232	0.221866	-4.90
249054_at	unknown protein	---	AT5G02870 /	-1.22	-0.29	-2.12	0.073251	0.221894	-4.90
256877_at	unknown protein ;supported by full-leng	---	AT3G26470	1.59	0.67	2.12	0.073294	0.221993	-4.90
249166_at	CHP-rich zinc finger protein-like	---	AT5G42840	-1.20	-0.26	-2.12	0.073364	0.222146	-4.91
257897_at	HAL3A protein identical to GB:AAD5161	HAL3A	AT3G18030	-1.26	-0.33	-2.12	0.073359	0.222146	-4.90
248147_at	putative protein contains similarity to pol	ATRBP45/	AT5G54900	-1.19	-0.25	-2.12	0.073405	0.222217	-4.91
266300_at	putative auxin transport protein ; suppo	PIN4	AT2G01420	-1.80	-0.85	-2.12	0.073407	0.222217	-4.91
258354_at	putative zinc finger protein similar to RIN	---	AT3G14320	1.15	0.20	2.12	0.073437	0.222279	-4.91
252455_at	putative protein various predicted prote	---	AT3G47140	1.15	0.20	2.12	0.073456	0.222279	-4.91
263734_at	permease, putative similar to permease	NAT7	AT1G60030	1.27	0.34	2.12	0.073451	0.222279	-4.91
250041_at	putative protein p53 inducible protein P	PIR121	AT5G18410	-1.14	-0.19	-2.12	0.07354	0.222502	-4.91
247864_s_a	anthranilate synthase beta chain ;suppo	---	AT1G24807 /	1.87	0.90	2.12	0.073554	0.222507	-4.91
249406_at	putative protein MtN21, Medicago trunc	---	AT5G40210	1.22	0.29	2.12	0.07358	0.222507	-4.91
251886_at	putative protein various predicted prote	---	AT3G54260	1.33	0.41	2.12	0.073563	0.222507	-4.91
257109_s_a	hypothetical protein	---	---	1.15	0.20	2.12	0.073575	0.222507	-4.91
263414_at	putative bZIP transcription factor contair	---	AT2G21230	-1.18	-0.23	-2.12	0.073644	0.222629	-4.91
264545_at	photosystem I subunit V precursor, puta	PSAG	AT1G55670	-1.14	-0.19	-2.12	0.07365	0.222629	-4.91
264483_at	unknown protein	---	AT1G77230	-1.24	-0.31	-2.12	0.073642	0.222629	-4.91
245891_at	amino acid transport protein AAP2 ;sup	AAP2	AT5G09220	-1.58	-0.66	-2.12	0.073662	0.222635	-4.91
253652_at	putative protein nucleoid DNA-binding p	---	AT4G30040	1.14	0.19	2.12	0.07368	0.222660	-4.91
251078_at	putative protein hypothetical proteins - A	---	AT5G01990	1.31	0.39	2.12	0.073734	0.222795	-4.91
262850_at	signal response protein (GAI) identical t	GAI	AT1G14920	-1.39	-0.48	-2.12	0.073751	0.222810	-4.91
260519_at	unknown protein	---	AT1G51540	1.15	0.20	2.12	0.073759	0.222810	-4.91
247145_at	receptor protein kinase-like protein	---	AT5G65600	2.49	1.31	2.12	0.073775	0.222828	-4.91
253390_at	hypothetical protein ;supported by full-le	---	AT4G32750	-1.25	-0.33	-2.11	0.073854	0.223038	-4.91
261660_at	kinesin heavy chain isolog, putative sim	HIK	AT1G18370	1.16	0.21	2.11	0.073889	0.223115	-4.91
253530_at	putative protein hypothetical protein - A	---	AT4G31530	-1.36	-0.45	-2.11	0.073899	0.223115	-4.91
250094_at	2-hydroxyphytanoyl-CoA lyase-like prote	---	AT5G17380	1.53	0.61	2.11	0.07392	0.223119	-4.91
261196_at	unknown protein	SCRM2	AT1G12860	-1.40	-0.49	-2.11	0.073919	0.223119	-4.91
263831_at	putative ferritin	ATFER4	AT2G40300	1.31	0.39	2.11	0.073961	0.223184	-4.91

261654_at	hypothetical protein contains similarity t	---	AT1G01920	-1.25	-0.32	-2.11	0.073955	0.223184	-4.91
250115_at	salt-inducible protein-like	---	AT5G16420	-1.29	-0.36	-2.11	0.07398	0.223211	-4.91
255100_at	putative MuDR-like transposon protein	---	---	-1.15	-0.20	-2.11	0.074044	0.223376	-4.91
246396_at	carbonic anhydrase, putative similar to	BCA6	AT1G58180	1.30	0.38	2.11	0.074065	0.223411	-4.91
266542_at	unknown protein	ARAD1	AT2G35100	-1.16	-0.21	-2.11	0.074094	0.223466	-4.91
247447_at	nitrate transporter NTL1 - like protein ni	---	AT5G62730	1.51	0.60	2.11	0.074132	0.223494	-4.92
267380_at	putative thromboxane-A synthase ; sup	CYP711A1	AT2G26170	1.45	0.54	2.11	0.074131	0.223494	-4.92
265893_at	putative disease resistance protein	---	AT2G15040 /	1.56	0.64	2.11	0.074142	0.223494	-4.92
246606_at	putative protein	---	---	1.14	0.19	2.11	0.074142	0.223494	-4.92
255568_at	putative DNA-binding protein ; supporte	WRKY22	AT4G01250	1.81	0.86	2.11	0.074193	0.223500	-4.92
244929_at	NADH dehydrogenase subunit 4	---	---	-1.30	-0.38	-2.11	0.074183	0.223500	-4.92
249721_at	Expressed protein ; supported by full-ler	LSU4	AT5G24655	-1.14	-0.19	-2.11	0.074186	0.223500	-4.92
245340_at	elicitor like protein ; supported by full-ler	---	AT4G14420	1.29	0.37	2.11	0.074173	0.223500	-4.92
251299_at	putative protein transcription factor MY(	---	AT3G61950	-1.20	-0.26	-2.11	0.074188	0.223500	-4.92
260141_at	gibberellin regulatory protein, putative s	RGL1	AT1G66350	1.87	0.90	2.11	0.074207	0.223514	-4.92
261017_at	UDP-glucose dehydrogenase, putative	UGD1	AT1G26570	1.21	0.28	2.11	0.074239	0.223580	-4.92
256365_at	arginyl-tRNA synthetase nearly identical	---	AT1G66530	-1.32	-0.40	-2.11	0.074325	0.223750	-4.92
263559_at	putative non-LTR retroelement reverse t	---	---	1.17	0.23	2.11	0.074313	0.223750	-4.92
246297_at	putative protein hypothetical protein F1	---	AT3G51760	-1.28	-0.35	-2.11	0.074318	0.223750	-4.92
266658_at	Expressed protein ; supported by full-ler	---	AT2G25735	2.38	1.25	2.11	0.074353	0.223806	-4.92
263013_at	knotted-like homeobox protein, putative	KNAT6	AT1G23380	1.21	0.28	2.11	0.074377	0.223817	-4.92
266550_s_a	Expressed protein ; supported by cDNA	---	AT2G35070 /	-1.78	-0.83	-2.11	0.074375	0.223817	-4.92
260400_at	putative peptide transporter similar to pe	---	AT1G69860	1.15	0.20	2.11	0.074411	0.223863	-4.92
253400_at	putative protein unknown protein T02O(	---	AT4G32860	1.16	0.21	2.11	0.074408	0.223863	-4.92
253506_at	putative protein EREBP-4 homolog, Ara	---	AT4G31980	1.33	0.41	2.11	0.074433	0.223896	-4.92
266766_at	hypothetical protein predicted by genscal	PAP14	AT2G46880	1.38	0.46	2.11	0.074503	0.224078	-4.92
259321_at	unknown protein	GAUT13	AT3G01040	1.26	0.33	2.11	0.074565	0.224160	-4.92
264376_at	putative protein phosphatase 2C ;suppo	---	AT2G25070	-1.26	-0.34	-2.11	0.074543	0.224160	-4.92
262377_at	rubisco activase, putative similar to rubi	---	AT1G73110	-1.37	-0.46	-2.11	0.074569	0.224160	-4.92
249984_at	putative protein rsc43, Dictyostelium dis	---	AT5G18400	1.40	0.48	2.11	0.074569	0.224160	-4.92
247117_at	3-hydroxyisobutyryl-coenzyme A hydrola	CHY1	AT5G65940	-1.26	-0.33	-2.11	0.074637	0.224334	-4.92
245854_at	adenosine nucleotide translocator ; sup	AAC2	AT5G13490	2.34	1.22	2.11	0.074674	0.224414	-4.92
264251_at	hypothetical protein identical to GB:AAC	---	AT1G09190	-1.26	-0.34	-2.11	0.074683	0.224414	-4.92
252045_at	putative protein arm repeat containing p	PUB22	AT3G52450	2.69	1.43	2.11	0.074719	0.224490	-4.92
249951_at	S-adenosyl-L-methionine decarboxylas	BUD2	AT5G18930	-1.30	-0.38	-2.11	0.074744	0.224537	-4.92

252960_at	hypothetical protein	---	AT4G38750	-1.34	-0.43	-2.11	0.07478	0.224558	-4.92
256247_at	SRF-type transcription factor contains P	AGL91	AT3G66656	1.16	0.21	2.11	0.074777	0.224558	-4.92
249293_at	protein kinase-like	---	AT5G41260	-1.23	-0.30	-2.11	0.074777	0.224558	-4.92
249895_at	male sterility 2-like protein (emb|CAA68	FAR1	AT5G22500	1.79	0.84	2.11	0.074823	0.224627	-4.92
248749_at	eukaryotic release factor 1 homolog (gb	ERF1-1	AT5G47880	1.16	0.21	2.11	0.074862	0.224627	-4.92
265319_at	auxin-regulated protein (IAA8) ;support	IAA8	AT2G22670	-1.41	-0.50	-2.11	0.074855	0.224627	-4.92
251932_at	pasticcino 1 ; supported by cDNA: gi_1	PAS1	AT3G54010	-1.17	-0.23	-2.11	0.074855	0.224627	-4.92
264810_at	putative GPI-anchor transamidase (U32	---	AT1G08750	-1.21	-0.28	-2.11	0.074834	0.224627	-4.92
262841_at	aspartate-semialdehyde dehydrogenas	---	AT1G14810	-1.29	-0.37	-2.11	0.074839	0.224627	-4.92
256502_at	Eukaryotic translation initiation factor 5,	---	AT1G36730 /	-1.27	-0.34	-2.11	0.074905	0.224696	-4.93
248414_at	50S ribosomal protein L11-like	---	AT5G51610	-1.20	-0.26	-2.11	0.074898	0.224696	-4.93
247270_at	ER66 protein-like	---	AT5G64220	1.16	0.22	2.10	0.074929	0.224737	-4.93
267444_at	hypothetical protein predicted by gensca	---	AT2G19180	-1.26	-0.33	-2.10	0.07502	0.224980	-4.93
264490_at	putative protein import receptor similar	TOM20-2	AT1G27390	-1.32	-0.41	-2.10	0.075098	0.225145	-4.93
264463_at	unknown protein similar to ESTs gb|T2(	---	AT1G10150	1.24	0.31	2.10	0.07509	0.225145	-4.93
263869_at	unknown protein	PROPEP6	AT2G22000	-1.15	-0.20	-2.10	0.075104	0.225145	-4.93
249481_at	frnE protein - like frnE protein, Deinoco	---	AT5G38900	1.94	0.95	2.10	0.075147	0.225218	-4.93
248998_at	unknown protein	---	AT5G45320	1.16	0.22	2.10	0.075161	0.225218	-4.93
249009_at	unknown protein ; supported by full-leng	MAP18	AT5G44610	1.32	0.41	2.10	0.075168	0.225218	-4.93
264897_at	dynein light subunit lc6, flagellar outer a	---	AT1G23220	-1.21	-0.28	-2.10	0.075178	0.225218	-4.93
264758_at	late embryogenesis abundant protein, p	---	AT1G61340	2.28	1.19	2.10	0.075168	0.225218	-4.93
254744_at	Expressed protein ; supported by cDNA	MEE55	AT4G13345	-1.28	-0.35	-2.10	0.075211	0.225288	-4.93
264781_at	putative plastid RNA polymerase sigma-	SIG2	AT1G08540	-1.26	-0.33	-2.10	0.075266	0.225423	-4.93
251296_at	putative protein paladin - Mus musculus	---	AT3G62010	-1.20	-0.26	-2.10	0.075276	0.225424	-4.93
266514_at	putative zinc-finger protein (B-box zinc f	---	AT2G47890	-1.26	-0.34	-2.10	0.075347	0.225590	-4.93
261626_at	unknown protein ; supported by cDNA: g	---	AT1G01990	-1.22	-0.29	-2.10	0.075352	0.225590	-4.93
256384_at	hypothetical protein	---	AT1G66660	-1.21	-0.27	-2.10	0.075373	0.225624	-4.93
261620_s_a	ribosomal protein L9, putative similar to	PGY2	AT1G33120 /	-1.25	-0.33	-2.10	0.075441	0.225768	-4.93
258257_at	putative short chain alcohol dehydrogen	---	AT3G26770	1.15	0.20	2.10	0.075434	0.225768	-4.93
262667_at	amine oxidase, putative similar to amin	---	AT1G62810	-1.30	-0.38	-2.10	0.075451	0.225770	-4.93
252603_at	putative protein	---	AT3G45050	-1.24	-0.31	-2.10	0.075479	0.225824	-4.93
261447_at	transcription factor, putative similar to G	---	AT1G21160	1.18	0.24	2.10	0.075503	0.225835	-4.93
248804_at	nodulin-like protein	---	AT5G47470	1.19	0.25	2.10	0.07551	0.225835	-4.93
252083_at	putative protein hypothetical protein M4	---	AT3G51960	1.50	0.59	2.10	0.075513	0.225835	-4.93
250056_at	putative protein predicted proteins, Syn	---	AT5G17660	-1.45	-0.53	-2.10	0.075529	0.225854	-4.93

264261_at	putative nicotianamine synthase similar	NAS3	AT1G09240	1.94	0.95	2.10	0.075542	0.225865	-4.93
256611_at	unknown protein similar to putative RIN(	---	AT3G29270	-1.22	-0.29	-2.10	0.075584	0.225929	-4.93
263560_s_a	unknown protein	FUT5	AT2G15350 /	-1.20	-0.27	-2.10	0.075583	0.225929	-4.93
256385_at	60S ribosomal protein L10, putative cor	---	AT1G66580	1.34	0.42	2.10	0.075639	0.226007	-4.94
253815_at	putative beta-expansin/allergen protein	ATEXPB3	AT4G28250	1.29	0.37	2.10	0.075621	0.226007	-4.93
254904_at	putative translation initiation factor IF-2	---	AT4G11160	-1.27	-0.34	-2.10	0.07564	0.226007	-4.94
245574_at	hypothetical protein	IQD19	AT4G14750	1.27	0.35	2.10	0.075705	0.226150	-4.94
250164_at	putative protein various predicted prote	---	AT5G15280	-1.25	-0.32	-2.10	0.075726	0.226150	-4.94
265267_at	hypothetical protein predicted by gensca	---	AT2G42920	-1.23	-0.30	-2.10	0.075727	0.226150	-4.94
246397_at	hypothetical protein contains similarity t	AtRLP9	AT1G58190	1.16	0.21	2.10	0.075713	0.226150	-4.94
258071_s_a	unknown protein	---	AT3G26070 /	-1.28	-0.36	-2.10	0.075775	0.226265	-4.94
266147_at	putative C-1-tetrahydrofolate synthase	---	AT2G12230	1.13	0.18	2.10	0.07583	0.226398	-4.94
245683_at	ubiquitin-specific protease 8 (UBP8), pu	UBP8	AT5G22030	-1.16	-0.21	-2.10	0.075871	0.226460	-4.94
261339_at	protein kinase, putative similar to many	---	AT1G35710	1.35	0.44	2.10	0.075866	0.226460	-4.94
253783_at	putative protein predicted protein, Arabi	NPGR2	AT4G28600	1.20	0.26	2.10	0.075894	0.226501	-4.94
246767_at	putative protein CG6949 - Drosophila m	---	AT5G27395	-1.54	-0.62	-2.10	0.07599	0.226698	-4.94
248014_at	putative protein similar to unknown prote	---	AT5G56340	1.24	0.31	2.10	0.075983	0.226698	-4.94
266321_at	putative cytochrome P450	CYP78A6	AT2G46660	-1.25	-0.32	-2.10	0.075972	0.226698	-4.94
246960_at	unknown protein	---	AT5G24710	1.17	0.22	2.09	0.076027	0.226738	-4.94
256100_at	unknown protein	---	AT1G13750	1.68	0.75	2.09	0.076025	0.226738	-4.94
256172_at	hypothetical protein	---	AT1G51745	1.16	0.21	2.09	0.076033	0.226738	-4.94
254029_at	putative protein other hypothetical prote	---	AT4G25870	-1.21	-0.27	-2.09	0.076098	0.226900	-4.94
245311_at	ribosomal protein ; supported by full-len	---	AT4G14320	-1.30	-0.37	-2.09	0.07612	0.226937	-4.94
262804_at	putative RNA-binding protein similar to	---	AT1G20880	1.23	0.30	2.09	0.076161	0.226941	-4.94
247255_at	putative protein similar to unknown prote	---	AT5G64780	1.38	0.46	2.09	0.076159	0.226941	-4.94
259001_at	hypothetical protein predicted by gensca	---	AT3G01960	-1.58	-0.66	-2.09	0.076136	0.226941	-4.94
266528_at	putative disease resistance protein	---	AT2G16870	1.15	0.20	2.09	0.076171	0.226941	-4.94
248236_at	putative protein contains similarity to phy	---	AT5G53870	2.15	1.10	2.09	0.076166	0.226941	-4.94
256803_at	cytochrome P450, putative similar to cy	CYP705A3	AT3G20960	1.16	0.21	2.09	0.076236	0.227015	-4.94
248883_at	putative protein strong similarity to unkn	---	AT5G46190	-1.17	-0.22	-2.09	0.076224	0.227015	-4.94
250065_at	putative protein predicted proteins, Arat	---	AT5G17910	1.27	0.34	2.09	0.076235	0.227015	-4.94
267085_at	putative cellulose synthase	ATCSLB02	AT2G32620	-1.14	-0.19	-2.09	0.076227	0.227015	-4.94
257707_at	hypothetical protein predicted by genem	---	AT3G12650	-1.17	-0.22	-2.09	0.076282	0.227124	-4.94
259215_at	unknown protein largely predicted by ge	DEX1	AT3G09090	-1.17	-0.22	-2.09	0.076416	0.227492	-4.95
261127_at	unknown protein ; supported by cDNA: g	---	AT1G04790	-1.24	-0.31	-2.09	0.076489	0.227679	-4.95

253502_at	Cytochrome P450-like protein cytochro	CYP82C4	AT4G31940	1.16	0.21	2.09	0.076571	0.227895	-4.95
258216_at	unknown protein contains Pfam profile:F	---	AT3G17980	1.24	0.31	2.09	0.076605	0.227966	-4.95
261131_at	unknown protein	---	AT1G19835	-1.35	-0.43	-2.09	0.076625	0.227995	-4.95
258226_at	putative phospholipase D similar to pho	PLDALPHA	AT3G15730	-1.19	-0.25	-2.09	0.076682	0.228081	-4.95
260999_at	hypothetical protein similar to putative M	---	AT1G26580	-1.16	-0.21	-2.09	0.076684	0.228081	-4.95
245848_at	putative protein predicted proteins - diffe	FY	AT5G13480	-1.18	-0.23	-2.09	0.076665	0.228081	-4.95
248773_at	kinesin-like protein	FRA1	AT5G47820	-1.24	-0.31	-2.09	0.076822	0.228464	-4.95
245361_at	hypothetical protein ;supported by full-le	---	AT4G17790	1.38	0.47	2.09	0.076849	0.228512	-4.95
253526_at	putative zinc finger protein hypothetical	---	AT4G31420	1.17	0.23	2.09	0.076872	0.228553	-4.95
262993_at	hypothetical protein contains similarity to	---	AT1G54230	-1.16	-0.21	-2.09	0.076902	0.228575	-4.95
246274_at	transcription factor like protein	---	AT4G36620	1.22	0.29	2.09	0.076899	0.228575	-4.95
252536_at	putative transporter protein peptide tran	---	AT3G45700	1.22	0.29	2.09	0.07691	0.228575	-4.95
267329_at	hypothetical protein	---	AT2G19250	-1.18	-0.24	-2.09	0.076925	0.228592	-4.95
264078_at	putative beta-galactosidase	BGAL8	AT2G28470	-1.77	-0.82	-2.09	0.076954	0.228624	-4.95
263350_at	alanine-glyoxylate aminotransferase ;su	AGT	AT2G13360	-1.30	-0.37	-2.09	0.076964	0.228624	-4.95
254626_at	hypothetical protein ; supported by full-l	---	AT4G18400	-1.21	-0.27	-2.09	0.076973	0.228624	-4.95
246404_at	hypothetical protein contains similarity to	---	AT1G57600	-1.16	-0.21	-2.09	0.076986	0.228624	-4.95
248503_at	putative protein contains similarity to tra	NF-YC7	AT5G50470	1.32	0.40	2.09	0.076984	0.228624	-4.95
246951_at	unknown protein	---	AT5G04880	-1.42	-0.50	-2.09	0.077	0.228633	-4.95
262825_at	putative chloroplast prephenate dehydra	ADT1	AT1G11790	1.34	0.43	2.09	0.077035	0.228708	-4.95
252161_at	proline-rich protein	---	AT3G50580	-1.14	-0.19	-2.09	0.077072	0.228728	-4.95
259861_at	unknown protein similar to ribosomal pro	---	AT1G80620	-1.23	-0.30	-2.09	0.077056	0.228728	-4.95
256905_at	mitochondrial chaperonin hsp60 identic	HSP60	AT3G23990	-1.48	-0.57	-2.09	0.077062	0.228728	-4.95
260937_at	hypothetical protein contains similarity to	---	AT1G45160	-1.14	-0.19	-2.08	0.077174	0.228998	-4.95
259712_at	putative 20S proteasome beta subunit P	PBC2	AT1G77440	-1.16	-0.21	-2.08	0.077183	0.228998	-4.96
260932_s_a	hypothetical protein contains similarity to	PGP12	AT1G02520 /	1.86	0.90	2.08	0.077208	0.229044	-4.96
258421_at	MtN3-like protein similar to MtN3 GB:CA	---	AT3G16690	-1.40	-0.49	-2.08	0.077236	0.229073	-4.96
265770_at	Expressed protein ; supported by full-ler	---	AT2G48100	-1.23	-0.30	-2.08	0.077255	0.229073	-4.96
262884_at	membrane related protein CP5, putative	CP5	AT1G64720	-1.18	-0.24	-2.08	0.077258	0.229073	-4.96
256490_at	unknown protein ;supported by full-lengt	---	AT1G31460	-1.27	-0.34	-2.08	0.077239	0.229073	-4.96
261333_at	hypothetical protein predicted by genem	---	AT1G44910	-1.28	-0.36	-2.08	0.077307	0.229163	-4.96
247621_at	putative protein predicted proteins from	---	AT5G60340	1.17	0.22	2.08	0.077309	0.229163	-4.96
265868_at	unknown protein ;supported by full-leng	PUX2	AT2G01650	1.25	0.33	2.08	0.07733	0.229198	-4.96
251087_at	putative protein unknown protein T16O	---	AT5G01460	1.16	0.21	2.08	0.077364	0.229265	-4.96
266494_at	putative receptor-like protein kinase	PRK2A	AT2G07040	-1.17	-0.22	-2.08	0.077373	0.229265	-4.96

260914_at	beta-xylosidase, putative similar to beta	BXL2	AT1G02640	1.54	0.63	2.08	0.077404	0.229297	-4.96
264437_at	unknown protein EST gb|N65787 comes	---	AT1G27510	-1.19	-0.25	-2.08	0.077398	0.229297	-4.96
259755_at	unknown protein similar to glucosaminyl	---	AT1G71070	1.22	0.28	2.08	0.077432	0.229351	-4.96
256762_at	Expressed protein ; supported by full-ler	IDL1	AT3G25655	2.37	1.24	2.08	0.077445	0.229360	-4.96
253372_at	pectinesterase - like protein pectinester	PME44	AT4G33220	1.55	0.63	2.08	0.077489	0.229430	-4.96
246155_at	putative protein predicted proteins, Arat	---	AT5G20030	1.15	0.20	2.08	0.077488	0.229430	-4.96
252298_at	putative protein various predicted prote	---	AT3G49060	1.16	0.21	2.08	0.077559	0.229547	-4.96
250951_at	putative protein	---	AT5G03550	1.51	0.60	2.08	0.077551	0.229547	-4.96
263166_at	putative protein destination factor Simila	---	AT1G03050	1.15	0.20	2.08	0.077549	0.229547	-4.96
250716_at	sucrose transporter protein	ATSUC9	AT5G06170	1.17	0.22	2.08	0.077615	0.229666	-4.96
253575_at	putative protein TINY, Arabidopsis thali	---	AT4G31060	-1.18	-0.23	-2.08	0.077619	0.229666	-4.96
255147_at	hypothetical protein	---	AT4G08460	-1.19	-0.25	-2.08	0.077689	0.229842	-4.96
262120_at	glutathione-S-transferase, putative simi	ATGSTF4	AT1G02950	1.25	0.32	2.08	0.077915	0.230463	-4.96
254161_at	hypothetical protein ;supported by full-le	---	AT4G24370	1.18	0.24	2.08	0.077919	0.230463	-4.96
261117_at	unknown protein	AUL1	AT1G75310	-1.31	-0.39	-2.08	0.077944	0.230509	-4.96
263152_at	hypothetical protein predicted by genem	ASIL1	AT1G54060	-1.27	-0.35	-2.08	0.077963	0.230533	-4.96
251374_at	homeobox-leucine zipper protein HAT3	HAT3	AT3G60390	-1.41	-0.50	-2.08	0.07801	0.230583	-4.97
252486_at	arm repeat containing protein homolog	PUB13	AT3G46510	1.19	0.25	2.08	0.07801	0.230583	-4.97
265759_at	putative membrane transporter	---	AT2G13100	-1.15	-0.20	-2.08	0.078008	0.230583	-4.97
266464_at	glutathione-conjugate transporter AtMRI	ATMRP4	AT2G47800	2.32	1.21	2.08	0.078084	0.230678	-4.97
246794_s_a	putative protein predicted proteins, Arat	---	AT5G06350 /	-1.38	-0.47	-2.08	0.078091	0.230678	-4.97
252965_at	putative auxin-induced protein auxin-ind	---	AT4G38860	-1.52	-0.60	-2.08	0.078088	0.230678	-4.97
253234_at	Expressed protein ; supported by full-ler	---	AT4G34265	-1.19	-0.25	-2.08	0.078078	0.230678	-4.97
266543_at	hypothetical protein predicted by gensca	---	AT2G35075	-1.14	-0.18	-2.08	0.078093	0.230678	-4.97
253489_at	monogalactosyldiacylglycerol synthase	MGD1	AT4G31780	-1.28	-0.36	-2.08	0.078116	0.230699	-4.97
256723_at	unknown protein ;supported by full-leng	---	AT2G34160	-1.14	-0.20	-2.08	0.078138	0.230699	-4.97
249748_at	thaumatin-like protein	---	AT5G24620	1.20	0.26	2.08	0.07815	0.230699	-4.97
257705_at	unknown protein ; supported by cDNA:	---	AT3G12760	1.13	0.18	2.08	0.078128	0.230699	-4.97
260045_at	putative MAP kinase similar to mitogen-	ATMPK15	AT1G73670	1.14	0.19	2.08	0.078148	0.230699	-4.97
257150_at	unknown protein ;supported by full-leng	---	AT3G27230	-1.23	-0.30	-2.08	0.078208	0.230840	-4.97
261265_at	hypothetical protein predicted by gensca	---	AT1G26800	-1.35	-0.43	-2.08	0.078252	0.230940	-4.97
264604_at	hypothetical protein predicted by gensca	---	AT1G04650	-1.25	-0.32	-2.07	0.078273	0.230970	-4.97
266081_at	putative protein kinase contains a protei	---	AT2G37840	1.17	0.23	2.07	0.078399	0.231306	-4.97
257382_at	hypothetical protein predicted by gensca	WRKY54	AT2G40750	3.12	1.64	2.07	0.078407	0.231306	-4.97
261570_at	fatty acid elongase 3-ketoacyl-CoA synt	KCS1	AT1G01120	2.13	1.09	2.07	0.07843	0.231338	-4.97

257107_at	transmembrane trafficking protein, puta	---	AT3G29070	1.20	0.26	2.07	0.078438	0.231338	-4.97
265805_s_a	60S ribosomal protein L2	EMB2296	AT2G18020 /	-1.26	-0.34	-2.07	0.078458	0.231367	-4.97
261968_at	disease resistance protein RPP1-WsB,	---	AT1G65850	1.14	0.19	2.07	0.078515	0.231448	-4.97
263030_at	hypothetical protein predicted by gensca	---	AT1G24060	-1.14	-0.19	-2.07	0.078516	0.231448	-4.97
247681_at	serine/threonine-specific protein kinase	---	---	1.24	0.32	2.07	0.078513	0.231448	-4.97
258168_at	hypothetical protein predicted by genem	---	AT3G21570	1.15	0.20	2.07	0.078562	0.231555	-4.97
257583_at	hypothetical protein	PMI2	AT1G66480	1.93	0.95	2.07	0.0786	0.231635	-4.97
251915_at	putative protein peroxisomal Ca-depen	---	AT3G53940	-1.24	-0.31	-2.07	0.07867	0.231766	-4.97
257055_at	Expressed protein ; supported by full-ler	---	AT3G15351	-1.18	-0.23	-2.07	0.078675	0.231766	-4.97
253265_at	putative protein RING-finger protein, Lo	---	AT4G34040	-1.15	-0.20	-2.07	0.07866	0.231766	-4.97
258819_at	unknown protein similar to putative DNA	---	AT3G04590	-1.23	-0.29	-2.07	0.07869	0.231781	-4.97
252888_at	glucose-1-phosphate adenylyltransferas	APL3	AT4G39210	-1.51	-0.59	-2.07	0.078704	0.231792	-4.97
249720_at	fimbrin ; supported by cDNA: gi_15027	FIM2	AT5G35700	1.17	0.23	2.07	0.078737	0.231830	-4.97
256913_at	unknown protein	---	AT3G23870	-1.32	-0.40	-2.07	0.078727	0.231830	-4.97
252747_at	putative protein retrotransposon finger	---	---	1.20	0.26	2.07	0.078758	0.231862	-4.97
262912_at	oligopeptide transporter, putative simila	---	AT1G59740	1.82	0.86	2.07	0.078788	0.231908	-4.98
262896_at	chromaffin granule ATPase II homolog,	ALA3	AT1G59820	1.21	0.28	2.07	0.078794	0.231908	-4.98
264694_at	receptor serine/threonine kinase PR5, p	---	AT1G70250	1.15	0.20	2.07	0.078815	0.231940	-4.98
252465_x_a	putative protein several hypothetical pro	---	---	1.17	0.23	2.07	0.078854	0.231973	-4.98
258692_at	unknown protein	---	AT3G08640	-1.35	-0.43	-2.07	0.078857	0.231973	-4.98
259900_at	c-Jun coactivator-like protein (AJH2) ide	CSN5B	AT1G71230	-1.14	-0.19	-2.07	0.078854	0.231973	-4.98
245309_at	putative protein ; supported by cDNA: gi	---	AT4G15140	1.32	0.40	2.07	0.078872	0.231988	-4.98
250703_at	putative protein similar to unknown prote	---	AT5G06360	-1.24	-0.31	-2.07	0.078994	0.232318	-4.98
266384_at	hypothetical protein predicted by gensca	---	AT2G14660	-1.20	-0.27	-2.07	0.079053	0.232460	-4.98
245204_at	1-AMINOCYCLOPROPANE-1-CARBO	---	AT5G12270	1.28	0.36	2.07	0.079112	0.232604	-4.98
246008_at	putative protein predicted proteins, Hon	---	AT5G08320	-1.22	-0.28	-2.07	0.079191	0.232703	-4.98
262070_at	far-red impaired response protein, puta	FRS8	AT1G80010	-1.16	-0.22	-2.07	0.079186	0.232703	-4.98
265328_at	unknown protein	---	AT2G18200	1.13	0.18	2.07	0.079156	0.232703	-4.98
253038_at	homeobox protein HAT22 ;supported by	HAT22	AT4G37790	1.34	0.43	2.07	0.079191	0.232703	-4.98
247860_at	bis(5'-adenosyl)-triphosphatase-like; als	---	AT5G58240	1.17	0.23	2.07	0.079197	0.232703	-4.98
246081_s_a	myosin-like protein unconventional myo	---	AT5G20470 /	1.28	0.36	2.07	0.079226	0.232761	-4.98
267248_at	hypothetical protein predicted by genefi	---	AT2G30120	-1.23	-0.30	-2.07	0.079245	0.232784	-4.98
261314_at	putative GTP-binding protein similar to N	---	AT1G52980	-1.28	-0.36	-2.07	0.079282	0.232863	-4.98
263748_at	putative protein kinase contains a protei	---	AT2G21480	1.19	0.25	2.07	0.079307	0.232907	-4.98
258904_at	putative ATPase (ISW2-like) similar to I	CHR11	AT3G06400	-1.19	-0.26	-2.07	0.07935	0.233003	-4.98

256006_at	hypothetical protein	---	AT1G34070	1.16	0.21	2.07	0.079393	0.233099	-4.98
245578_at	RNA helicase like protein	ATSUV3	AT4G14790	-1.22	-0.29	-2.06	0.079408	0.233115	-4.98
246005_at	lipoic acid synthase - like protein lipoic a	---	AT5G08415	-1.27	-0.34	-2.06	0.079446	0.233196	-4.98
264176_at	bZIP-like protein similar to bZIP (leucine	---	AT1G02110	-1.32	-0.40	-2.06	0.079545	0.233425	-4.98
267142_at	putative ammonium transporter	ATAMT2	AT2G38290	1.37	0.45	2.06	0.079537	0.233425	-4.98
249311_at	disease resistance protein-like	---	AT5G41540	1.21	0.27	2.06	0.079584	0.233509	-4.99
250826_at	unknown protein ; supported by cDNA: g	---	AT5G05220	1.19	0.25	2.06	0.079611	0.233537	-4.99
259748_at	putative dehydrogenase similar to D-thre	---	AT1G71180	-1.20	-0.26	-2.06	0.079613	0.233537	-4.99
247741_at	putative protein predicted proteins, Arat	GIL1	AT5G58960	-1.37	-0.45	-2.06	0.07965	0.233614	-4.99
246219_at	aminopeptidase-like protein ; supported	APP1	AT4G36760	1.27	0.34	2.06	0.079693	0.233680	-4.99
265293_at	hypothetical protein predicted by genscа	---	---	1.19	0.25	2.06	0.079689	0.233680	-4.99
267497_at	putative glutaredoxin ;supported by full-	---	AT2G30540	1.42	0.50	2.06	0.07976	0.233800	-4.99
266374_at	putative retroelement pol polyprotein	---	---	1.24	0.31	2.06	0.079751	0.233800	-4.99
245690_at	phenylalanine ammonia-lyase PAL3	PAL3	AT5G04230	-1.36	-0.45	-2.06	0.079765	0.233800	-4.99
267557_at	unknown protein ; supported by cDNA:	KRP4	AT2G32710	-1.23	-0.30	-2.06	0.079801	0.233846	-4.99
258917_at	unknown protein C-terminal portion simi	---	AT3G10630	-1.13	-0.18	-2.06	0.079797	0.233846	-4.99
247367_at	oxygen-independent coproporphyrinoge	---	AT5G63290	-1.31	-0.39	-2.06	0.079892	0.234072	-4.99
257078_at	putative MAP kinase very similar to BnM	---	AT3G15220	-1.17	-0.23	-2.06	0.079898	0.234072	-4.99
255995_at	receptor-like serine/threonine kinase, p	RKF1	AT1G29750	1.23	0.30	2.06	0.079959	0.234220	-4.99
255843_at	unknown protein	CPL3	AT2G33540	1.15	0.20	2.06	0.07997	0.234221	-4.99
245557_at	phosphatase like protein	PUX5	AT4G15410	-1.14	-0.18	-2.06	0.080001	0.234253	-4.99
249518_at	putative protein similar to unknown prote	---	AT5G38610	1.18	0.23	2.06	0.08	0.234253	-4.99
262005_at	ABC transporter protein, putative simila	ATGCN3	AT1G64550	-1.26	-0.33	-2.06	0.080012	0.234255	-4.99
255753_at	myb factor, putative similar to myb facto	MYB51	AT1G18570	2.50	1.32	2.06	0.080039	0.234280	-4.99
246376_at	auxin regulated protein IAA18, putative	IAA18	AT1G51950	-1.25	-0.33	-2.06	0.080052	0.234280	-4.99
245151_at	putative pectinesterase ;supported by fu	---	AT2G47550	2.72	1.44	2.06	0.080045	0.234280	-4.99
246930_at	KNAT3 homeodomain protein ;supporte	KNAT3	AT5G25220	-1.22	-0.29	-2.06	0.080062	0.234280	-4.99
266471_at	putative GTP-binding protein	---	AT2G31060	-1.31	-0.39	-2.06	0.080125	0.234291	-4.99
259421_at	disease resistance protein, putative sim	---	AT1G13910	-1.22	-0.29	-2.06	0.080097	0.234291	-4.99
245518_at	ATP-dependent RNA helicase like prote	ATRH1	AT4G15850	-1.32	-0.40	-2.06	0.080148	0.234291	-4.99
265152_s_a	hypothetical protein predicted by genscа	---	AT1G30935 /	1.15	0.20	2.06	0.080121	0.234291	-4.99
258713_at	Expressed protein ; supported by full-ler	---	AT3G09735	1.16	0.22	2.06	0.080101	0.234291	-4.99
266454_at	putative bHLH transcription factor	---	AT2G22750	1.18	0.24	2.06	0.080145	0.234291	-4.99
263276_at	putative cytochrome P450	CYP705A1	AT2G14100	1.18	0.23	2.06	0.080098	0.234291	-4.99
255823_at	unknown protein ;supported by full-leng	LBD15	AT2G40470	1.60	0.68	2.06	0.080147	0.234291	-4.99

256584_at	unknown protein	---	AT3G28750	1.17	0.22	2.06	0.08016	0.234296	-4.99
266396_at	unknown protein	---	AT2G38790	-1.27	-0.35	-2.06	0.080186	0.234312	-4.99
259954_at	cytochrome P450, putative similar to GI	CYP721A1	AT1G75130	1.30	0.38	2.06	0.08018	0.234312	-4.99
256185_at	dof zinc finger protein identical to dof zir	ADOF1	AT1G51700	1.64	0.71	2.06	0.080203	0.234331	-4.99
266630_at	putative serpin	---	AT2G35580	1.16	0.21	2.06	0.080265	0.234484	-4.99
249040_at	eukaryotic translation initiation factor 3 s	---	AT5G44320	-1.18	-0.24	-2.06	0.080319	0.234602	-4.99
261424_at	unknown protein	---	AT1G18700	-1.14	-0.19	-2.06	0.080336	0.234602	-4.99
249890_at	putative protein contains similarity to DN	WRKY38	AT5G22570	2.87	1.52	2.06	0.080332	0.234602	-4.99
251252_at	putative protein several hypothetical pro	---	AT3G62230	1.17	0.23	2.06	0.080373	0.234679	-4.99
267511_at	unknown protein	---	AT2G45670	1.17	0.23	2.06	0.080392	0.234702	-5.00
251910_at	serine/threonine-specific kinase like pro	---	AT3G53810	1.86	0.90	2.06	0.080451	0.234818	-5.00
246234_at	putative protein	---	AT4G37280	-1.21	-0.27	-2.06	0.080452	0.234818	-5.00
263511_at	En/Spm-like transposon protein related	---	---	1.16	0.22	2.06	0.080477	0.234863	-5.00
266044_s_a	hypothetical protein	---	AT2G07725	-1.38	-0.47	-2.06	0.080506	0.234884	-5.00
263787_at	unknown protein ; supported by cDNA:	---	AT2G46420	-1.28	-0.35	-2.06	0.080516	0.234884	-5.00
251430_at	putative protein hypothetical protein At2	---	AT3G60110	1.19	0.25	2.06	0.080507	0.234884	-5.00
264929_at	auxin-induced protein, putative similar t	---	AT1G60730	2.05	1.04	2.05	0.080652	0.235161	-5.00
247056_at	SWI2/SNF2-like protein (gb|AAD28303.	CHR1	AT5G66750	-1.18	-0.24	-2.05	0.080646	0.235161	-5.00
245355_at	60S ribosomal protein L15 homolog ;sup	---	AT4G17390	-1.44	-0.53	-2.05	0.080641	0.235161	-5.00
258197_at	hypothetical protein predicted by genem	ATBRXL2	AT3G14000	-1.21	-0.28	-2.05	0.080638	0.235161	-5.00
249325_at	urophorphyrin III methylase (gb|AAB926	UPM1	AT5G40850	-1.24	-0.31	-2.05	0.080778	0.235376	-5.00
249086_at	putative protein strong similarity to unkn	---	AT5G44180	-1.18	-0.24	-2.05	0.080787	0.235376	-5.00
253037_at	putative protein other predicted Arabido	GAUT3	AT4G38270	-1.17	-0.23	-2.05	0.080737	0.235376	-5.00
266794_at	hypothetical protein	---	AT2G02980	-1.16	-0.22	-2.05	0.080785	0.235376	-5.00
254127_at	NADPH-ferrihemoprotein reductase ATF	ATR1	AT4G24520	1.22	0.28	2.05	0.080767	0.235376	-5.00
261692_at	calreticulin, putative similar to calreticul	CRT3	AT1G08450	1.38	0.46	2.05	0.080747	0.235376	-5.00
262577_at	unknown protein ESTs gb|F20110 and g	---	AT1G15290	-1.25	-0.32	-2.05	0.080809	0.235408	-5.00
255043_at	putative protein several hypothetical pro	---	AT4G09640	-1.34	-0.42	-2.05	0.080825	0.235423	-5.00
256856_at	Expressed protein ; supported by full-ler	---	AT3G15110	-1.28	-0.35	-2.05	0.080834	0.235423	-5.00
245333_at	Expressed protein ; supported by full-ler	---	AT4G14615	-1.13	-0.18	-2.05	0.080869	0.235494	-5.00
248005_at	unknown protein	---	AT5G56240	-1.23	-0.29	-2.05	0.080921	0.235615	-5.00
265825_at	ubiquitin-like (UBQ7), putative similar to	UBQ7	AT2G35635	-1.19	-0.25	-2.05	0.080955	0.235654	-5.00
250179_at	putative protein	---	AT5G14440	-1.21	-0.27	-2.05	0.08095	0.235654	-5.00
252290_at	putative protein various predicted prote	---	AT3G49140	-1.21	-0.27	-2.05	0.080984	0.235708	-5.00
263847_at	putative glucosyltransferase ; supporte	---	AT2G36970	-1.84	-0.88	-2.05	0.081105	0.236030	-5.00

267362_at	hypothetical protein predicted by genefir	---	AT2G39910	-1.15	-0.20	-2.05	0.081181	0.236211	-5.00
264989_at	unknown protein ; supported by cDNA: g	---	AT1G27200	-1.26	-0.34	-2.05	0.081188	0.236211	-5.00
254018_at	putative mitochondrial carrier protein G	---	AT4G26180	-1.19	-0.25	-2.05	0.081199	0.236213	-5.00
256159_at	Expressed protein ; supported by full-ler	JAZ8	AT1G30135	2.10	1.07	2.05	0.081239	0.236299	-5.01
259699_at	hypothetical protein predicted by genefir	---	AT1G68940	1.15	0.20	2.05	0.081289	0.236416	-5.01
265013_at	unknown protein similar to EST gb|T761	---	AT1G24460	1.17	0.22	2.05	0.081301	0.236419	-5.01
253446_at	putative protein predicted protein T10M	---	AT4G32620	-1.19	-0.25	-2.05	0.08133	0.236474	-5.01
255344_s_a	putative receptor-like protein kinase	---	AT4G04540 /	1.57	0.65	2.05	0.081374	0.236572	-5.01
266642_at	putative chloroplast RNA binding protein	---	AT2G35410	-1.18	-0.24	-2.05	0.081428	0.236698	-5.01
247643_at	auxin response factor 4 ; supported by	ARF4	AT5G60450	-1.30	-0.38	-2.05	0.081478	0.236813	-5.01
261806_at	ferrodoxin NADP oxidoreductase, putat	ATRFNR2	AT1G30510	-1.37	-0.46	-2.05	0.081537	0.236956	-5.01
248797_at	putative protein similar to unknown prote	---	AT5G47210	-1.21	-0.27	-2.05	0.081563	0.237002	-5.01
248743_at	unknown protein	---	AT5G48240	-1.31	-0.39	-2.05	0.081626	0.237153	-5.01
252479_at	small zinc finger-like protein TIM9 ;supp	TIM9	AT3G46560	-1.27	-0.34	-2.05	0.081652	0.237189	-5.01
250984_at	protein kinase - like protein kinase APK	---	AT5G02800	-1.15	-0.20	-2.05	0.081659	0.237189	-5.01
256763_at	unknown protein	COBL8	AT3G16860	1.69	0.75	2.05	0.081671	0.237193	-5.01
247792_at	Expressed protein ; supported by full-ler	---	AT5G58787	-1.32	-0.40	-2.05	0.081685	0.237204	-5.01
254300_at	Translation factor EF-1 alpha - like prot	ACR7	AT4G22780	1.28	0.36	2.05	0.081731	0.237306	-5.01
251124_s_a	laccase -like protein lac110 laccase, Po	LAC8	AT5G01040 /	2.19	1.13	2.04	0.081752	0.237337	-5.01
249333_at	GDSL-motif lipase/hydrolase-like protein	GLIP1	AT5G40990	1.90	0.92	2.04	0.081779	0.237386	-5.01
265078_at	hypothetical protein contains similarity to	ECT4	AT1G55500	-1.37	-0.45	-2.04	0.081796	0.237404	-5.01
250297_at	putative protein predicted protein, Dros	---	AT5G11980	1.20	0.27	2.04	0.081822	0.237444	-5.01
256853_at	hypothetical protein predicted by genem	---	AT3G18640	-1.16	-0.22	-2.04	0.08183	0.237444	-5.01
247383_at	putative protein contains similarity to rec	---	AT5G63410	-1.36	-0.44	-2.04	0.081841	0.237446	-5.01
260781_at	decoy identical to GB:AAB51588 GI:193	DECOY	AT1G14620	-1.62	-0.70	-2.04	0.081896	0.237545	-5.01
252204_at	putative protein predicted protein, Arabi	---	AT3G50340	-1.60	-0.67	-2.04	0.081895	0.237545	-5.01
252919_at	putative endo-1,4-beta-glucanase endo	AtGH9B16	AT4G38990	1.24	0.31	2.04	0.081907	0.237546	-5.01
246374_at	light repressible receptor protein kinase	---	AT1G51840	1.14	0.19	2.04	0.081928	0.237578	-5.01
247525_at	pseudo-response regulator 1 ; supporte	TOC1	AT5G61380	1.14	0.19	2.04	0.081947	0.237602	-5.01
261106_at	homeodomain-containing protein HD1,	KNAT7	AT1G62990	1.16	0.21	2.04	0.08209	0.237987	-5.02
256190_at	9-cis-epoxycarotenoid dioxygenase, pu	NCED5	AT1G30100	-1.17	-0.23	-2.04	0.082102	0.237990	-5.02
256118_at	hypothetical protein predicted by genem	KU70	AT1G16970	-1.23	-0.30	-2.04	0.082249	0.238161	-5.02
248784_at	putative protein similar to unknown prote	---	AT5G47380	1.28	0.36	2.04	0.082255	0.238161	-5.02
263355_at	putative RNA-binding protein ;supporte	---	AT2G22100	-1.23	-0.29	-2.04	0.082215	0.238161	-5.02
266256_at	60S acidic ribosomal protein P2 ;suppo	---	AT2G27710	-1.35	-0.43	-2.04	0.082207	0.238161	-5.02

266364_at	unknown protein	---	AT2G41230	2.03	1.02	2.04	0.08224	0.238161	-5.02
252827_at	cytochrome P450 - like protein cytochro	CYP79B2	AT4G39950	2.02	1.01	2.04	0.082203	0.238161	-5.02
250124_at	putative protein contains similarity to tyr	---	AT5G16480	1.20	0.26	2.04	0.082212	0.238161	-5.02
265317_at	unknown protein	BRK1	AT2G22640	-1.17	-0.23	-2.04	0.082255	0.238161	-5.02
265650_at	hypothetical protein predicted by gensca	---	AT2G27460	-1.18	-0.23	-2.04	0.082244	0.238161	-5.02
257609_at	Expressed protein ; supported by full-ler	---	AT3G13845	-1.20	-0.27	-2.04	0.082297	0.238253	-5.02
247727_at	putative ripening-related protein - like pu	---	AT5G59490	1.24	0.31	2.04	0.082342	0.238352	-5.02
252740_at	pectinesterase -like protein PECTINES	---	AT3G43270	-1.30	-0.38	-2.04	0.082376	0.238420	-5.02
251428_at	beta-glucosidase-like protein several be	DIN2	AT3G60140	3.09	1.63	2.04	0.082431	0.238432	-5.02
259689_x_a	unknown protein	---	AT1G63130	-1.33	-0.41	-2.04	0.082451	0.238432	-5.02
258990_at	unknown protein ;supported by full-leng	---	AT3G08840	-1.31	-0.39	-2.04	0.08246	0.238432	-5.02
258053_at	unknown protein similar to CGI-18 prote	---	AT3G16230	-1.14	-0.19	-2.04	0.082416	0.238432	-5.02
261001_at	hypothetical protein similar to hypothetic	---	AT1G26530	-1.21	-0.28	-2.04	0.082397	0.238432	-5.02
261389_s_a	hypothetical protein identical to hypothe	---	---	-1.15	-0.20	-2.04	0.082418	0.238432	-5.02
248707_at	putative protein similar to unknown prote	---	AT5G48550	-1.19	-0.25	-2.04	0.082463	0.238432	-5.02
256290_at	serine carboxypeptidase, putative conta	scpl17	AT3G12203	-1.16	-0.22	-2.04	0.082439	0.238432	-5.02
255999_at	DNA-binding protein, putative similar to	WRKY71	AT1G29860	1.50	0.58	2.04	0.082508	0.238528	-5.02
247555_at	putative protein various predicted protei	ECT3	AT5G61020	-1.32	-0.40	-2.04	0.082519	0.238528	-5.02
248099_at	DNA topoisomerase I (sp P30181)	TOP1ALPI	AT5G55300	-1.15	-0.21	-2.04	0.082528	0.238528	-5.02
253560_at	putative protein KIAA0800 protein, Hom	DCAF1	AT4G31160	-1.19	-0.25	-2.04	0.08255	0.238560	-5.02
252675_at	putative protein hypothetical proteins - A	---	---	1.17	0.22	2.04	0.082651	0.238824	-5.02
259027_at	hypothetical protein predicted by gensca	---	AT3G09280	1.14	0.18	2.04	0.0827	0.238934	-5.02
259290_at	putative cyclin similar to cyclin cyc1b GE	CYCB1;3	AT3G11520	1.26	0.33	2.04	0.082722	0.238969	-5.02
251821_at	protein phosphatase 2C - like protein pr	---	AT3G55050	1.40	0.48	2.04	0.082743	0.238998	-5.02
252958_at	putative transcription factor (MYB4) ; su	MYB4	AT4G38620	1.54	0.62	2.04	0.082762	0.239022	-5.02
253757_at	rac GTP binding protein Arac7 ; suppor	ROP9	AT4G28950	1.20	0.27	2.04	0.082789	0.239072	-5.02
245275_at	beta-amylase ; supported by cDNA: gi_1	BAM5	AT4G15210	1.49	0.57	2.04	0.082858	0.239227	-5.02
250402_at	putative protein unnamed ORF cDNA F	---	AT5G10940	-1.16	-0.22	-2.04	0.082875	0.239227	-5.02
267303_at	hookless1-like protein	---	AT2G30090	-1.13	-0.17	-2.04	0.082869	0.239227	-5.02
265188_at	putative aldehyde dehydrogenase ; sup	ALDH2B7	AT1G23800	1.24	0.31	2.04	0.08291	0.239299	-5.03
256843_at	hypothetical protein predicted by genem	---	---	1.17	0.23	2.03	0.082978	0.239464	-5.03
251004_at	putative protein predicted protein, Arab	---	AT5G02720	1.18	0.24	2.03	0.083001	0.239500	-5.03
247046_at	unknown protein ; supported by cDNA:	---	AT5G66540	-1.19	-0.25	-2.03	0.083035	0.239538	-5.03
256018_at	plastid heme oxygenase, putative simila	ho4	AT1G58300	-1.30	-0.38	-2.03	0.083025	0.239538	-5.03
252775_s_a	putative protein various predicted prote	---	---	-1.17	-0.23	-2.03	0.083047	0.239543	-5.03

245266_at	hypothetical protein ; supported by cDN	---	AT4G17070	1.32	0.40	2.03	0.083107	0.239661	-5.03
252218_at	putative protein some putative proteins -	---	AT3G50150	1.16	0.22	2.03	0.083109	0.239661	-5.03
246967_at	FPF1 protein	FPF1	AT5G24860	1.31	0.39	2.03	0.083148	0.239744	-5.03
258284_at	putative ribosomal protein similar to ribo	---	AT3G16080	-1.43	-0.51	-2.03	0.083182	0.239756	-5.03
252038_at	gamma response I protein ; supported I	---	AT3G52120	1.25	0.32	2.03	0.08319	0.239756	-5.03
261262_at	hypothetical protein predicted by genem	SDG35	AT1G26760	-1.15	-0.20	-2.03	0.08317	0.239756	-5.03
261134_at	cytochrome P450, putative similar to GI	CYP722A1	AT1G19630	1.17	0.22	2.03	0.083201	0.239756	-5.03
245727_at	hypothetical protein contains similarity t	---	AT1G73350	-1.21	-0.28	-2.03	0.083205	0.239756	-5.03
248620_at	putative protein similar to unknown prote	---	AT5G49320	1.17	0.23	2.03	0.083384	0.240210	-5.03
257433_at	hypothetical protein predicted by genefir	---	AT2G21990	-1.15	-0.20	-2.03	0.083375	0.240210	-5.03
259675_at	unknown protein similar to hypothetical	---	AT1G77710	-1.16	-0.22	-2.03	0.083433	0.240293	-5.03
248446_at	putative protein similar to unknown prote	---	AT5G51140	-1.17	-0.22	-2.03	0.083434	0.240293	-5.03
261412_at	L-ascorbate peroxidase identical to GB	APX1	AT1G07890	1.36	0.44	2.03	0.083467	0.240358	-5.03
247372_at	unknown protein ;supported by full-leng	---	AT5G63280	-1.28	-0.36	-2.03	0.083486	0.240384	-5.03
249181_at	putative protein contains similarity to unl	---	AT5G42920	-1.18	-0.24	-2.03	0.083501	0.240396	-5.03
248465_at	putative protein contains similarity to unl	---	AT5G51200	-1.27	-0.34	-2.03	0.083535	0.240462	-5.03
259067_at	F-box protein family, AtFBL12 contains	---	AT3G07550	-1.15	-0.21	-2.03	0.083561	0.240477	-5.03
247580_at	putative protein traube, Mus musculus,	---	AT5G61330	-1.21	-0.27	-2.03	0.083552	0.240477	-5.03
247543_at	DNA binding protein - like DNA binding	---	AT5G61600	1.66	0.73	2.03	0.083572	0.240480	-5.03
255817_at	unknown protein ;supported by full-leng	PDLP3	AT2G33330	-1.40	-0.48	-2.03	0.083626	0.240596	-5.03
252460_at	putative protein predicted protein, Arabi	---	---	-1.13	-0.18	-2.03	0.083634	0.240596	-5.03
255767_at	ribosomal protein L20, putative similar t	---	AT1G16740	-1.17	-0.23	-2.03	0.083704	0.240767	-5.03
262453_at	hypothetical protein predicted by genem	---	AT1G11240	-1.14	-0.19	-2.03	0.083732	0.240817	-5.03
253044_at	hypothetical protein ;supported by full-le	---	AT4G37290	2.63	1.39	2.03	0.083806	0.241001	-5.04
251089_at	heat shock protein 40-like heat shock p	---	AT5G01390	-1.16	-0.22	-2.03	0.083867	0.241145	-5.04
252927_at	cysteine proteinase RD19A identical to	RD19	AT4G39090	1.15	0.20	2.03	0.083888	0.241150	-5.04
259876_at	putative DnaJ protein similar to dnaJ-lik	---	AT1G76700	1.35	0.43	2.03	0.08389	0.241150	-5.04
246581_at	hypothetical protein predicted by genem	---	AT1G31760	-1.18	-0.23	-2.03	0.083913	0.241188	-5.04
259014_at	putative glucan endo-1-3-beta-glucosida	---	AT3G07320	1.29	0.37	2.03	0.083928	0.241199	-5.04
262678_at	hypothetical protein ;supported by full-le	---	AT1G75810	1.25	0.32	2.03	0.084004	0.241358	-5.04
257075_at	unknown protein contains Pfam profile:F	---	AT3G19670	-1.24	-0.31	-2.03	0.083994	0.241358	-5.04
260078_at	hypothetical protein predicted by genefir	---	AT1G73790	-1.19	-0.25	-2.03	0.084094	0.241584	-5.04
253359_at	putative protein kinase protein kinase, S	---	AT4G33080	-1.22	-0.29	-2.03	0.084134	0.241658	-5.04
248241_at	unknown protein	---	AT5G53960	1.16	0.22	2.03	0.084141	0.241658	-5.04
246250_at	cysteine proteinase similar to cysteine p	CP1	AT4G36880	2.33	1.22	2.02	0.084153	0.241664	-5.04

260109_at	hypothetical protein predicted by gensca	TET10	AT1G63260	1.22	0.29	2.02	0.084186	0.241698	-5.04
260165_at	30S ribosomal protein S17, chloroplast	RPS17	AT1G79850	-1.25	-0.32	-2.02	0.084186	0.241698	-5.04
254953_at	Expressed protein ; supported by full-ler	---	AT4G10925	1.18	0.24	2.02	0.084197	0.241698	-5.04
260065_at	putative RING zinc finger protein contai	---	AT1G73760	1.19	0.26	2.02	0.084215	0.241719	-5.04
246500_at	putative protein HR21spA protein involv	SYN4	AT5G16270	-1.19	-0.25	-2.02	0.084269	0.241843	-5.04
248512_at	protein translocation complex Sec61 ga	SIG2	AT1G08540 /	1.39	0.48	2.02	0.084319	0.241957	-5.04
253168_at	putative protein various predicted prote	---	AT4G35070	1.40	0.48	2.02	0.08433	0.241959	-5.04
249316_s_a	glutathione transferase-like ;supported b	ATGSTT2	AT5G41220 /	-1.18	-0.24	-2.02	0.084343	0.241964	-5.04
259891_at	putative Eukaryotic initiation factor 4A s	---	AT1G72730	1.21	0.27	2.02	0.084372	0.242018	-5.04
250865_at	putative protein predicted protein, Syne	---	AT5G03900	-1.27	-0.34	-2.02	0.084386	0.242026	-5.04
263024_at	hypothetical protein predicted by genem	---	AT1G23980	-1.23	-0.30	-2.02	0.084401	0.242040	-5.04
247984_s_a	IAA-amino acid hydrolase homolog 1 pr	ILL1	AT5G56650 /	-1.26	-0.33	-2.02	0.084459	0.242175	-5.04
265439_at	senescence-associated protein contains	---	AT2G21045	-1.91	-0.93	-2.02	0.084491	0.242236	-5.04
251005_at	putative protein various predicted prote	---	AT5G02590	-1.56	-0.64	-2.02	0.084506	0.242250	-5.04
248025_at	NOI protein, nitrate-induced	NOI	AT5G55850	1.21	0.28	2.02	0.08454	0.242316	-5.04
259343_s_a	putative methionine synthase similar to	ATMS2	AT3G03780 /	-1.29	-0.37	-2.02	0.084569	0.242370	-5.04
259938_at	hypothetical protein predicted by gensca	---	AT1G71310	-1.18	-0.24	-2.02	0.084581	0.242374	-5.04
262797_at	putative sugar transporter protein nearl	TMT1	AT1G20840	1.33	0.41	2.02	0.084615	0.242440	-5.05
247319_at	glutamate-tRNA ligase ; supported by cl	ERS	AT5G64050	-1.18	-0.24	-2.02	0.084677	0.242586	-5.05
260056_at	hypothetical protein predicted by gensca	---	AT1G78140	-1.28	-0.36	-2.02	0.0847	0.242622	-5.05
256048_at	hypothetical protein contains similarity t	---	AT1G07025	1.16	0.21	2.02	0.084714	0.242633	-5.05
252413_at	40S ribosomal protein S20-like protein	---	AT3G47370	-1.39	-0.47	-2.02	0.08473	0.242648	-5.05
265431_at	(1-4)-beta-mannan endohydrolase	---	AT2G20680	-1.17	-0.22	-2.02	0.08479	0.242657	-5.05
259227_at	putative 3 exoribonuclease contains Pfa	---	AT3G07750	-1.54	-0.62	-2.02	0.084778	0.242657	-5.05
261089_at	protein kinase APK1A identical to SP:Q	APK1A	AT1G07570	1.29	0.37	2.02	0.084797	0.242657	-5.05
258824_at	unknown protein	---	AT3G07190	-1.24	-0.31	-2.02	0.084746	0.242657	-5.05
250783_at	cytochrome P450 ; supported by cDNA	CYP79A2	AT5G05260	1.20	0.26	2.02	0.084785	0.242657	-5.05
256740_at	hypothetical protein predicted by genem	---	AT3G29330	-1.15	-0.20	-2.02	0.084796	0.242657	-5.05
245625_at	transport protein	---	AT4G14160	1.17	0.23	2.02	0.084822	0.242667	-5.05
265733_at	unknown protein ;supported by full-leng	---	AT2G01190	1.20	0.26	2.02	0.08482	0.242667	-5.05
253178_at	putative protein predicted protein, Arabi	---	AT4G35170	1.21	0.27	2.02	0.084869	0.242773	-5.05
263708_at	unknown protein	---	AT1G09320	-1.17	-0.23	-2.02	0.084925	0.242882	-5.05
258478_at	unknown protein	---	AT3G02710	-1.17	-0.23	-2.02	0.084943	0.242882	-5.05
262903_at	NADPH-dependent codeinone reductas	---	AT1G59950	-1.96	-0.97	-2.02	0.08495	0.242882	-5.05
263973_at	60S ribosomal protein L11B	RPL16A	AT2G42740	-1.33	-0.41	-2.02	0.084941	0.242882	-5.05

256264_at	unknown protein ; supported by full-leng	---	AT3G12210	-1.26	-0.33	-2.02	0.084964	0.242892	-5.05
253083_at	aldehyde dehydrogenase like protein al	ALDH3F1	AT4G36250	1.39	0.48	2.02	0.084996	0.242949	-5.05
262789_at	putative auxin-induced protein strong sir	---	AT1G10810	1.15	0.21	2.02	0.085005	0.242949	-5.05
247332_at	unknown protein ; supported by cDNA:	---	AT5G63440	-1.22	-0.29	-2.02	0.085051	0.243050	-5.05
252477_at	glucosyltransferase-like protein UDP-gl	---	AT3G46680	1.24	0.32	2.02	0.085086	0.243119	-5.05
256147_at	hypothetical protein predicted by genem	---	AT1G55080	1.23	0.29	2.02	0.085127	0.243206	-5.05
264164_at	Expressed protein ; supported by full-ler	---	AT1G65295	-1.22	-0.28	-2.02	0.085164	0.243279	-5.05
259154_at	unknown protein similar to unknown pro	---	AT3G10260	-1.17	-0.23	-2.02	0.0852	0.243291	-5.05
249940_at	NAC-domain protein-like ;supported by	anac090	AT5G22380	1.19	0.25	2.02	0.085191	0.243291	-5.05
256844_s_a	En/Spm transposon protein, putative sir	---	---	1.16	0.22	2.02	0.085179	0.243291	-5.05
264763_at	hypothetical protein contains similarity to	---	AT1G61450	1.14	0.19	2.02	0.085233	0.243354	-5.05
260764_at	unknown protein	---	AT1G48950	-1.22	-0.28	-2.02	0.08527	0.243430	-5.05
267483_at	unknown protein ;supported by full-leng	UTR1	AT2G02810	1.76	0.81	2.02	0.085289	0.243454	-5.05
250566_at	putative helix-loop-helix DNA binding pr	TCP17	AT5G08070	-1.26	-0.33	-2.02	0.085301	0.243458	-5.05
256440_at	unknown protein ;supported by full-leng	---	AT3G10970	-1.16	-0.22	-2.02	0.085312	0.243458	-5.05
261561_at	unknown protein ;supported by full-lengt	---	AT1G01730	1.26	0.34	2.02	0.085338	0.243502	-5.05
260874_at	hypothetical protein predicted by genem	emb2170	AT1G21390	1.21	0.28	2.01	0.085382	0.243598	-5.05
246796_at	putative protein myosin heavy chain, ch	---	AT5G26770	-1.24	-0.32	-2.01	0.085397	0.243610	-5.05
250481_at	putative protein	---	AT5G10310	-1.17	-0.23	-2.01	0.085437	0.243664	-5.05
254118_at	DNA polymerase III like protein DNA po	---	AT4G24790	-1.15	-0.21	-2.01	0.085434	0.243664	-5.05
249580_at	putative protein predicted proteins, Arat	---	AT5G37740	1.23	0.30	2.01	0.085482	0.243672	-5.06
263378_at	protein phosphatase 2C (AthPP2C5)	ATHPP2C	AT2G40180	1.28	0.36	2.01	0.085479	0.243672	-5.06
263933_s_a	putative harpin-induced protein	---	AT2G35970 /	1.18	0.24	2.01	0.085469	0.243672	-5.05
252386_at	putative protein various predicted proet	---	AT3G47840	-1.22	-0.29	-2.01	0.085483	0.243672	-5.06
261113_at	hypothetical protein predicted by genem	---	AT1G75400	-1.24	-0.31	-2.01	0.085526	0.243755	-5.06
251042_at	eceriferum3 (CER3)	PRT6	AT5G02310	-1.16	-0.21	-2.01	0.085533	0.243755	-5.06
265458_at	unknown protein ;supported by full-leng	---	AT2G46580	-1.20	-0.27	-2.01	0.085573	0.243807	-5.06
255355_at	hypothetical protein	---	---	-1.18	-0.24	-2.01	0.085572	0.243807	-5.06
249362_at	putative protein predicted protein, Arabi	---	AT5G40550	-1.50	-0.58	-2.01	0.085601	0.243856	-5.06
251196_at	glutaredoxin -like protein glutaredoxin, c	---	AT3G62950	1.64	0.71	2.01	0.085633	0.243887	-5.06
263027_at	hypothetical protein predicted by genem	---	AT1G24010	1.14	0.19	2.01	0.085624	0.243887	-5.06
256518_at	hypothetical protein	---	AT1G66080	-1.21	-0.28	-2.01	0.085657	0.243924	-5.06
248850_at	putative protein contains similarity to kin	---	AT5G46550	-1.18	-0.24	-2.01	0.085717	0.244066	-5.06
245631_at	tRNA-glutamine synthetase, putative sir	OVA9	AT1G25350	-1.16	-0.21	-2.01	0.08574	0.244069	-5.06
263725_at	unknown protein	---	AT2G13550	1.14	0.19	2.01	0.085732	0.244069	-5.06

262306_s_a	asparaginyl-tRNA synthetase(SYNC1)	SYNC3	AT1G70980 /	-1.23	-0.29	-2.01	0.085777	0.244144	-5.06
249793_at	putative protein contains similarity to unl	---	AT5G23680	-1.26	-0.33	-2.01	0.085814	0.244219	-5.06
256035_at	Ran-binding protein (atranbp1a) identica	SIRANBP	AT1G07140	1.20	0.26	2.01	0.085855	0.244306	-5.06
261535_at	Expressed protein ; supported by full-ler	---	AT1G01725	-1.22	-0.28	-2.01	0.085884	0.244358	-5.06
261781_at	far-red impaired response protein, puta	FRS4	AT1G76320	-1.22	-0.28	-2.01	0.085897	0.244363	-5.06
266012_s_a	predicted protein	---	AT2G07699 /	-1.37	-0.46	-2.01	0.085942	0.244402	-5.06
264093_at	hypothetical protein predicted by genem	---	AT1G79220	-1.17	-0.23	-2.01	0.085942	0.244402	-5.06
267046_at	hypothetical protein	---	AT2G34360	1.26	0.33	2.01	0.085942	0.244402	-5.06
257623_at	cytochrome P450, putative contains Pfa	CYP71B23	AT3G26210	1.64	0.71	2.01	0.086018	0.244467	-5.06
259471_at	hypothetical protein contains similarity to	---	AT1G19040	1.14	0.18	2.01	0.08603	0.244467	-5.06
245709_at	putative protein	---	AT5G04320	-1.23	-0.30	-2.01	0.086027	0.244467	-5.06
248843_at	homeobox protein	HB-7	AT5G46880	1.20	0.26	2.01	0.086002	0.244467	-5.06
247157_at	nuclear matrix constituent protein 1 (NM	LINC4	AT5G65770	-1.17	-0.23	-2.01	0.085995	0.244467	-5.06
247463_at	embryo-specific protein - like embryo-sp	---	AT5G62210	1.19	0.25	2.01	0.085998	0.244467	-5.06
248369_at	arginine/serine-rich splicing factor RSP4	ATRSP41	AT5G52040	-1.23	-0.30	-2.01	0.086078	0.244544	-5.06
258382_at	hypothetical protein	UBC25	AT3G15355	1.23	0.30	2.01	0.086072	0.244544	-5.06
252329_at	putative protein several hypothetical pro	---	AT3G48760	1.15	0.20	2.01	0.086096	0.244563	-5.06
256760_at	SKP1/ASK1 (At15), putative similar to S	ASK15	AT3G25650	-1.13	-0.18	-2.01	0.086203	0.244839	-5.06
267193_at	hypothetical protein predicted by grail	---	AT2G30900	1.17	0.23	2.01	0.086226	0.244873	-5.06
259727_at	ferrodoxin precursor identical to FERRE	FED A	AT1G60950	-1.15	-0.20	-2.01	0.086338	0.245160	-5.06
258434_at	AP2 domain containing protein RAP2.3	ATEBP	AT3G16770	-1.28	-0.35	-2.01	0.086366	0.245210	-5.07
247432_at	microtubule-associated protein EB1-like	ATEB1B	AT5G62500	1.19	0.25	2.01	0.086458	0.245409	-5.07
256637_at	unknown protein similar to membrane pr	---	AT3G12030	1.25	0.32	2.01	0.086452	0.245409	-5.07
264854_at	putative RING zinc finger protein ; suppo	RHA3A	AT2G17450	1.20	0.26	2.01	0.08648	0.245442	-5.07
267212_at	similar to late embryogenesis abundant	---	AT2G44060	-1.15	-0.21	-2.01	0.086566	0.245578	-5.07
265614_at	Expressed protein ; supported by cDNA	---	AT2G25355	-1.23	-0.30	-2.01	0.086587	0.245578	-5.07
259934_at	unknown protein	---	AT1G71340	-1.27	-0.35	-2.01	0.086589	0.245578	-5.07
254068_at	putative protein similarity to multidrug re	NAP8	AT4G25450	1.19	0.25	2.01	0.086552	0.245578	-5.07
253525_at	predicted protein ; supported by cDNA:	---	AT4G31330	-1.19	-0.25	-2.01	0.086593	0.245578	-5.07
257592_at	leucine-rich repeat disease resistance p	---	AT3G24982	1.17	0.23	2.01	0.086548	0.245578	-5.07
256744_at	ATHP2, putative similar to ATHP2 GB:E	AHP2	AT3G29350	-1.21	-0.27	-2.01	0.086616	0.245582	-5.07
267369_at	unknown protein ;supported by full-leng	---	AT2G44420	1.20	0.26	2.01	0.086609	0.245582	-5.07
255759_at	hypothetical protein predicted by genem	---	AT1G16790	-1.18	-0.24	-2.00	0.086673	0.245651	-5.07
246743_at	putative protein predicted proteins, Ara	---	AT5G27750	-1.20	-0.26	-2.00	0.086661	0.245651	-5.07
267367_at	unknown protein ;supported by full-leng	---	AT2G44210	-1.27	-0.34	-2.00	0.086663	0.245651	-5.07

252959_at	putative protein NADH dehydrogenase	---	AT4G38640	-1.18	-0.23	-2.00	0.086751	0.245809	-5.07
244932_at	PSI 9KDa protein	---	---	-1.20	-0.27	-2.00	0.086761	0.245809	-5.07
251558_at	putative protein ;supported by full-leng	---	AT3G57810	-1.35	-0.44	-2.00	0.086745	0.245809	-5.07
263895_at	hypothetical protein predicted by gensca	---	AT2G21920	1.14	0.18	2.00	0.086776	0.245821	-5.07
256396_at	unknown protein	---	AT3G06150	-1.33	-0.41	-2.00	0.086806	0.245863	-5.07
262089_s_a	hypothetical protein predicted by genem	---	AT1G55980 /	-1.25	-0.32	-2.00	0.086823	0.245863	-5.07
250002_at	proline-richh protein predicted protein F	AGP25	AT5G18690	-1.62	-0.70	-2.00	0.086817	0.245863	-5.07
262892_at	succinic semialdehyde dehydrogenase	ALDH5F1	AT1G79440	-1.16	-0.21	-2.00	0.086863	0.245947	-5.07
258287_at	putative sulfate transporter similar to sul	SULTR3;4	AT3G15990	1.54	0.62	2.00	0.086883	0.245973	-5.07
246031_at	putative protein KIAA0731 - Homo sapi	---	AT5G21160	-1.20	-0.26	-2.00	0.086959	0.246157	-5.07
251187_at	putative protein putative proteins - differ	AtATG18a	AT3G62770	1.14	0.18	2.00	0.086999	0.246216	-5.07
258036_at	unknown protein	---	AT3G21210	1.14	0.19	2.00	0.087002	0.246216	-5.07
248382_at	peroxidase	---	AT5G51890	1.79	0.84	2.00	0.087052	0.246330	-5.07
260555_at	hypothetical protein predicted by genefi	---	AT2G41780	1.55	0.63	2.00	0.087082	0.246351	-5.07
261906_at	hypothetical protein predicted by gensca	---	AT1G65080	-1.32	-0.40	-2.00	0.087092	0.246351	-5.07
261776_at	hypothetical protein similar to putative a	---	AT1G76190	-1.24	-0.31	-2.00	0.087072	0.246351	-5.07
263979_at	En/Spm-like transposon protein related	PDF1	AT2G42840	1.26	0.33	2.00	0.087122	0.246375	-5.07
267583_at	unknown protein	---	AT2G41960	-1.14	-0.18	-2.00	0.08712	0.246375	-5.07
258255_at	hypothetical protein predicted by genem	---	AT3G26800	-1.15	-0.21	-2.00	0.087134	0.246378	-5.07
247405_at	Arac10 ; supported by cDNA: gi_37029	ARAC10	AT5G62880	-1.18	-0.24	-2.00	0.087157	0.246381	-5.07
259409_at	hypothetical protein contains similarity t	---	AT1G13330	-1.16	-0.22	-2.00	0.087146	0.246381	-5.07
266407_at	putative elongation factor	TFIIS	AT2G38560	1.17	0.22	2.00	0.087175	0.246401	-5.07
247775_at	phosphoinositide-specific phospholipas	PLC5	AT5G58690	-1.33	-0.41	-2.00	0.087237	0.246546	-5.07
256485_at	unknown protein	---	AT1G31440	-1.17	-0.22	-2.00	0.087348	0.246830	-5.08
255889_at	ABC transporter, putative similar to ABC	WBC11	AT1G17840	-1.26	-0.33	-2.00	0.087361	0.246837	-5.08
266499_at	hypothetical protein predicted by gensca	---	---	1.25	0.32	2.00	0.087388	0.246882	-5.08
251826_at	ABC transporter - like protein ATP-bind	---	AT3G55110	-1.19	-0.25	-2.00	0.087437	0.246929	-5.08
263718_at	putative CCAAT-box binding trancriptior	NF-YB7	AT2G13570	1.21	0.27	2.00	0.087434	0.246929	-5.08
253252_at	amidophosphoribosyltransferase 2 prec	ATASE2	AT4G34740	-1.28	-0.36	-2.00	0.087426	0.246929	-5.08
255551_at	putative potassium channel ;supported	KCO5	AT4G01840	1.14	0.19	2.00	0.087517	0.247123	-5.08
263601_s_a	dihydrofolate reductase-thymidylate syn	THY-1	AT2G16370 /	-1.23	-0.30	-2.00	0.087533	0.247139	-5.08
256044_at	protein phosphatase 2C, putative simila	---	AT1G07160	2.40	1.26	2.00	0.087553	0.247163	-5.08
245706_at	putative protein	---	AT5G04310	1.17	0.23	2.00	0.087623	0.247209	-5.08
265114_at	hypothetical protein contains similarity t	LRX2	AT1G62440	1.36	0.45	2.00	0.087615	0.247209	-5.08
254164_at	putative protein ;supported by full-lengt	TIFY1	AT4G24470	-1.18	-0.23	-2.00	0.087584	0.247209	-5.08

253564_at	protein kinase - like protein protein kina	---	AT4G31170	1.19	0.25	2.00	0.087602	0.247209	-5.08
251084_at	putative protein putative proteins - Arabi	---	AT5G01520	1.37	0.46	2.00	0.08762	0.247209	-5.08
258685_at	putative polygalacturonase similar to po	---	AT3G07830	1.23	0.29	2.00	0.087701	0.247399	-5.08
261648_at	salt-tolerance zinc finger protein identica	STZ	AT1G27730	1.95	0.96	2.00	0.087715	0.247407	-5.08
258638_at	unknown protein ;supported by full-leng	---	AT3G07950	1.16	0.21	2.00	0.08774	0.247447	-5.08
254937_at	putative aldolase similar to 2,4-dihydrox	---	AT4G10750	-1.15	-0.20	-2.00	0.087778	0.247492	-5.08
254591_at	heat shock transcription factor - like pro	---	AT4G18870	1.12	0.17	2.00	0.08777	0.247492	-5.08
257925_at	unknown protein ;supported by full-leng	---	AT3G23170	2.13	1.09	2.00	0.0878	0.247494	-5.08
253078_at	putative receptor protein kinase Cf-2.1	---	AT4G36180	-1.32	-0.40	-2.00	0.0878	0.247494	-5.08
263129_at	unknown protein ;supported by full-lengt	---	AT1G78620	1.17	0.22	2.00	0.087832	0.247522	-5.08
262711_at	hypothetical protein predicted by gensca	---	AT1G16500	1.27	0.35	2.00	0.087832	0.247522	-5.08
266102_at	unknown protein	---	AT2G40720	-1.18	-0.24	-2.00	0.087846	0.247531	-5.08
250525_at	putative protein contains similarity to unl	ILP1	AT5G08550	-1.16	-0.22	-2.00	0.08786	0.247539	-5.08
258671_at	putative vacuolar ATP synthase subunit	VHA-E2	AT3G08560	1.23	0.29	2.00	0.08788	0.247544	-5.08
253644_at	putative protein predicted protein, Arabi	---	AT4G29870	-1.25	-0.32	-2.00	0.087883	0.247544	-5.08
264015_at	putative XAP-5 protein [Homo sapiens]	XCT	AT2G21150	1.17	0.22	1.99	0.087923	0.247627	-5.08
261984_at	TINY-like protein similar to TINY GB: CA	---	AT1G33760	1.23	0.30	1.99	0.087977	0.247687	-5.08
251144_at	anthranilate N-benzoyltransferase - like	---	AT5G01210	1.37	0.46	1.99	0.087962	0.247687	-5.08
255073_at	beta-1,3-glucanase-like protein probabl	---	AT4G09090	-1.15	-0.20	-1.99	0.087967	0.247687	-5.08
247102_at	putative protein similar to unknown prote	---	AT5G66550	-1.20	-0.26	-1.99	0.087997	0.247692	-5.08
260883_at	hypothetical protein predicted by genem	---	AT1G29270	1.13	0.17	1.99	0.088001	0.247692	-5.08
245598_at	hypothetical protein	---	AT4G14200	1.24	0.31	1.99	0.088028	0.247738	-5.08
262705_at	putative wall-associated kinase similar t	---	AT1G16260	1.79	0.84	1.99	0.088087	0.247874	-5.08
248275_at	isp4 protein	ATOPT8	AT5G53520	1.14	0.19	1.99	0.088125	0.247950	-5.08
263785_at	unknown protein ; supported by cDNA:	---	AT2G46390	1.18	0.24	1.99	0.088144	0.247974	-5.09
246383_at	hypothetical protein predicted by genem	---	AT1G77360	-1.32	-0.40	-1.99	0.088302	0.248388	-5.09
264661_at	hypothetical protein Similar to Nicotiana	---	AT1G09950	1.33	0.41	1.99	0.088371	0.248466	-5.09
262052_at	hypothetical protein identical to hypothe	---	---	-1.19	-0.25	-1.99	0.088346	0.248466	-5.09
262492_at	unknown protein Contains similarity to g	---	AT1G21630	1.18	0.23	1.99	0.088355	0.248466	-5.09
264204_at	putative sucrose transport protein, SUC	SUC2	AT1G22710	-1.26	-0.33	-1.99	0.088374	0.248466	-5.09
247688_at	putative protein predicted proteins, Arat	---	AT5G59760	1.15	0.21	1.99	0.088389	0.248479	-5.09
248258_at	putative protein contains similarity to nu	---	AT5G53400	-1.37	-0.46	-1.99	0.088415	0.248520	-5.09
250877_at	putative protein predicted protein, Arabi	SDP1	AT5G04040	1.25	0.33	1.99	0.088455	0.248602	-5.09
256458_at	integral membrane protein, putative sim	---	AT1G75220	1.31	0.39	1.99	0.088535	0.248766	-5.09
263220_at	hypothetical protein predicted by genscа	emb2279	AT1G30610	-1.22	-0.29	-1.99	0.088529	0.248766	-5.09

244912_at	cytochrome c biogenesis orf382 Protein	---	AT2G07783	-1.25	-0.33	-1.99	0.088616	0.248932	-5.09
254309_s_a	putative protein predicted protein, Arabi	---	AT4G22390 /	-1.21	-0.27	-1.99	0.088605	0.248932	-5.09
256307_at	pectate lyase, putative contains Pfam p	---	AT1G30350	-1.14	-0.19	-1.99	0.088648	0.248961	-5.09
265815_at	predicted protein	---	AT2G17975	-1.13	-0.17	-1.99	0.088646	0.248961	-5.09
253633_at	putative protein tetratricopeptide repeat	---	AT4G30480	-1.20	-0.27	-1.99	0.088668	0.248986	-5.09
248597_at	DNA (cytosine-5)-methyltransferase (DN	MET1	AT5G49160	1.44	0.52	1.99	0.08874	0.249159	-5.09
262704_at	hypothetical protein predicted by genscа	ASL9	AT1G16530	1.44	0.52	1.99	0.088774	0.249222	-5.09
266643_s_a	putative flavonol 3-O-glucosyltransferas	---	AT2G29710 /	1.23	0.30	1.99	0.088844	0.249306	-5.09
247342_at	ARI-like RING zinc finger protein-like	---	AT5G63730	1.16	0.22	1.99	0.088845	0.249306	-5.09
259277_at	putative glycogen synthase similar to gly	AtSS2	AT3G01180	-1.28	-0.35	-1.99	0.088847	0.249306	-5.09
248151_at	Lhcb3 chlorophyll a/b binding protein (gi	LHCB3	AT5G54270	-1.35	-0.43	-1.99	0.088829	0.249306	-5.09
245485_at	proline-rich, APG like protein	---	AT4G16230	1.19	0.25	1.99	0.088864	0.249323	-5.09
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281 /DE	---	---	-1.17	-0.23	-1.99	0.088933	0.249484	-5.09
250062_at	BCS1 - like protein h-bcs1, Homo sapie	---	AT5G17760	1.31	0.39	1.99	0.088957	0.249522	-5.09
262124_at	nucleoporin 98-like protein similar to nuc	---	AT1G59660	-1.14	-0.19	-1.99	0.089023	0.249676	-5.09
250090_at	glutamate decarboxylase 1 (GAD 1) (sp	GAD	AT5G17330	2.07	1.05	1.99	0.089057	0.249738	-5.10
256300_at	unknown protein similar to N-term half o	NAP	AT1G69490	1.78	0.83	1.99	0.089085	0.249738	-5.10
251630_at	putative protein unknown protein - Arbi	---	AT3G57420	1.15	0.20	1.99	0.089089	0.249738	-5.10
247057_at	SCARECROW gene regulator	---	AT5G66770	-1.54	-0.62	-1.99	0.089076	0.249738	-5.10
262575_at	putative ABC transporter Similar to gb|Z	PDR7	AT1G15210	1.18	0.24	1.99	0.089118	0.249788	-5.10
255329_at	hypothetical protein	---	AT4G04370	-1.14	-0.19	-1.99	0.08913	0.249793	-5.10
258249_s_a	unknown protein ; supported by full-leng	---	AT3G15820 /	-1.27	-0.34	-1.99	0.089144	0.249801	-5.10
250614_at	putative protein homeodomain protein h	---	AT5G07260	-1.12	-0.17	-1.99	0.089155	0.249801	-5.10
259997_at	unknown protein similar to N-acetylgluco	---	AT1G67880	1.41	0.50	1.99	0.089177	0.249833	-5.10
266500_at	Expressed protein ; supported by full-ler	PLA2-ALP	AT2G06925	-1.33	-0.41	-1.98	0.089216	0.249880	-5.10
254752_at	putative protein IFA-binding protein - Ar	---	AT4G13160	-1.18	-0.24	-1.98	0.089206	0.249880	-5.10
261842_at	hypothetical protein contains similarity to	WAKL5	AT1G16160	1.23	0.30	1.98	0.089284	0.250039	-5.10
246604_at	putative protein	---	---	1.17	0.22	1.98	0.089303	0.250061	-5.10
248064_at	unknown protein	---	AT5G55570	-1.49	-0.57	-1.98	0.089397	0.250294	-5.10
262861_at	hypothetical protein similar to hypothetic	---	AT1G64820	1.17	0.23	1.98	0.089409	0.250297	-5.10
264382_at	unknown protein similarity to stromal ce	SDF2	AT2G25110	1.31	0.39	1.98	0.08946	0.250409	-5.10
256334_at	oligopeptide transporter, putative simila	---	AT1G72120 /	1.26	0.33	1.98	0.089581	0.250717	-5.10
248454_at	receptor protein kinase-like	---	AT5G51350	-1.28	-0.35	-1.98	0.089604	0.250751	-5.10
257725_at	DNA mismatch repair protein MSH2, 5'	MSH2	AT3G18524	-1.25	-0.32	-1.98	0.089627	0.250751	-5.10
245985_at	peptidylprolyl isomerase-like protein chl	---	AT5G13120	-1.22	-0.29	-1.98	0.089621	0.250751	-5.10

257578_x_a	unknown protein similar to hypothetical	---	AT3G30160	1.15	0.20	1.98	0.089637	0.250751	-5.10
247018_at	AP2 domain transcription factor-like	---	AT5G67000	-1.13	-0.17	-1.98	0.0897	0.250895	-5.10
262569_at	hypothetical protein Strong similarity to	---	AT1G15180	-1.29	-0.37	-1.98	0.089762	0.251038	-5.10
260996_at	NBS/LRR disease resistance protein ide	RFL1	AT1G12210	1.24	0.31	1.98	0.089858	0.251277	-5.10
248860_at	putative protein contains similarity to CH	---	AT5G46670	1.16	0.22	1.98	0.089882	0.251313	-5.10
253977_at	putative protein various Caenorhabditis	---	AT4G26630	-1.27	-0.35	-1.98	0.089956	0.251469	-5.10
254844_at	hypothetical protein supported by full-ler	---	AT4G11790	-1.29	-0.37	-1.98	0.08996	0.251469	-5.10
246239_at	putative protein	---	AT4G36790	1.16	0.22	1.98	0.09015	0.251970	-5.11
266537_at	Expressed protein ; supported by full-ler	---	AT2G16860	-1.17	-0.23	-1.98	0.090203	0.252086	-5.11
251796_at	synaptic glycoprotein SC2-like protein s	---	AT3G55360	1.30	0.38	1.98	0.090327	0.252402	-5.11
265263_at	putative DNA binding protein	---	AT2G42940	1.16	0.22	1.98	0.09034	0.252407	-5.11
264787_at	putative senescence-associated protein	ERD7	AT2G17840	-1.33	-0.41	-1.98	0.090367	0.252452	-5.11
249118_at	putative protein similar to unknown prote	---	AT5G43870	-1.22	-0.29	-1.98	0.090403	0.252511	-5.11
245878_at	hypothetical protein contains similarity to	---	AT1G26190	-1.20	-0.26	-1.98	0.09041	0.252511	-5.11
266140_at	nodulin-like protein ; supported by cDN	---	AT2G28120	1.24	0.32	1.97	0.090516	0.252745	-5.11
251640_at	putative protein ;supported by full-lengt	---	AT3G57450	1.83	0.87	1.97	0.09051	0.252745	-5.11
252916_at	kinesin like protein kinesin-related prote	---	AT4G38950	1.17	0.22	1.97	0.090532	0.252759	-5.11
253399_at	putative poly(A) polymerase polynucleo	nPAP	AT4G32850	-1.15	-0.20	-1.97	0.090559	0.252773	-5.11
262095_at	hypothetical protein predicted by genem	---	AT1G56090	-1.24	-0.31	-1.97	0.090552	0.252773	-5.11
251842_at	extensin precursor -like protein extensi	---	AT3G54580	1.48	0.56	1.97	0.090578	0.252794	-5.11
244985_at	ribosomal protein L22	---	---	-1.28	-0.35	-1.97	0.090596	0.252812	-5.11
265411_at	unknown protein	---	AT2G16630	1.74	0.80	1.97	0.090629	0.252874	-5.11
256102_at	unknown protein	---	AT1G13680	-1.15	-0.20	-1.97	0.090647	0.252894	-5.11
264736_at	oligopeptide transporter, putative simila	---	AT1G62200	1.24	0.31	1.97	0.090765	0.253049	-5.11
262143_at	unknown protein	---	AT1G52630	-1.18	-0.24	-1.97	0.090733	0.253049	-5.11
266725_at	SKP1/ASK1 (At14), putative similar to S	ASK14	AT2G03170	1.16	0.21	1.97	0.090739	0.253049	-5.11
256088_at	putative FKBP-type peptidyl-prolyl cis-tr	---	AT1G20810	-1.27	-0.34	-1.97	0.090728	0.253049	-5.11
247160_at	putative protein contains similarity to sal	---	AT5G65820	-1.15	-0.21	-1.97	0.090769	0.253049	-5.11
259359_at	B regulatory subunit of protein phospha	---	AT1G13460	-1.18	-0.24	-1.97	0.090769	0.253049	-5.11
267396_at	hypothetical protein predicted by grail ar	---	AT2G44270	-1.21	-0.28	-1.97	0.09081	0.253132	-5.11
248631_at	putative protein strong similarity to unkn	---	AT5G49000	-1.21	-0.27	-1.97	0.090882	0.253301	-5.11
267150_at	putative anthranilate N-hydroxycinnamo	SDT	AT2G23510	-1.14	-0.18	-1.97	0.090951	0.253463	-5.12
256009_at	AP2 domain transcription factor, putativ	---	AT1G19210	1.78	0.83	1.97	0.090969	0.253481	-5.12
255455_at	mitochondrial elongation factor Tu	---	AT4G02930	-1.38	-0.47	-1.97	0.091012	0.253571	-5.12
245679_at	clathrin-associated protein, putative sim	---	AT1G56590	-1.18	-0.24	-1.97	0.091079	0.253674	-5.12

259458_at	glycine-rich protein, putative similar to g	---	AT1G44085	1.19	0.25	1.97	0.091082	0.253674	-5.12
258319_at	hypothetical protein similar to hypothetic	---	AT3G22700	1.15	0.21	1.97	0.091065	0.253674	-5.12
249744_at	beta-glucosidase	BGLU32	AT5G24550	1.23	0.30	1.97	0.091108	0.253684	-5.12
260835_at	protein kinase interactor, putative simila	---	AT1G06700	-1.17	-0.22	-1.97	0.091104	0.253684	-5.12
259975_at	putative cinnamoyl-CoA reductase simil	---	AT1G76470	1.62	0.70	1.97	0.091134	0.253726	-5.12
245639_at	unknown protein contains similarity to 6	---	AT1G25260	-1.33	-0.41	-1.97	0.091183	0.253739	-5.12
265369_s_a	putative retroelement pol polyprotein co	---	---	-1.16	-0.21	-1.97	0.091173	0.253739	-5.12
250697_at	putative protein contains similarity to tra	---	AT5G06800	-1.20	-0.26	-1.97	0.091171	0.253739	-5.12
258044_at	Dof zinc finger protein identical to GB:B/	ADOF2	AT3G21270	-1.40	-0.49	-1.97	0.091184	0.253739	-5.12
261455_at	unknown protein ;supported by full-lengt	---	AT1G21070	1.30	0.37	1.97	0.091215	0.253777	-5.12
263757_at	cysteine proteinase similar to cysteine p	---	AT2G21430	1.29	0.36	1.97	0.091219	0.253777	-5.12
266615_s_a	putative monooxygenase ;supported by	CTF2A	AT2G29720 /	1.76	0.81	1.97	0.09125	0.253831	-5.12
260033_at	putative mutT protein contains Pfam pr	ATNUDX1	AT1G68760	-1.20	-0.26	-1.97	0.091271	0.253859	-5.12
250427_at	putative protein myosin heavy chain for	---	AT5G10500	-1.14	-0.19	-1.97	0.091312	0.253940	-5.12
247570_at	putative protein heparanase, Homo sap	AtGUS1	AT5G61250	1.49	0.57	1.97	0.091354	0.254027	-5.12
262413_at	hypothetical protein contains similarity t	ATAPRL4	AT1G34780	-1.22	-0.29	-1.97	0.091409	0.254149	-5.12
248087_at	unknown protein	---	AT5G55060	1.13	0.18	1.97	0.091428	0.254172	-5.12
247480_at	KED - like protein KED, Nicotiana tabac	ATBAG7	AT5G62390	1.22	0.29	1.97	0.091478	0.254278	-5.12
255127_at	nodulin-like protein nodulin gene MtN21	---	AT4G08300	1.76	0.82	1.97	0.091511	0.254321	-5.12
246045_at	putative protein predicted proteins, Dro	---	AT5G19430	-1.23	-0.30	-1.97	0.091515	0.254321	-5.12
264191_at	integral membrane protein, putative	---	AT1G54730	-1.28	-0.36	-1.97	0.091547	0.254377	-5.12
247833_at	putative protein	---	AT5G58575	-1.14	-0.19	-1.97	0.091584	0.254449	-5.12
253360_at	aminopeptidase- like protein aminopept	APM1	AT4G33090	1.19	0.25	1.97	0.091716	0.254786	-5.12
263510_s_a	hypothetical protein	---	AT2G07681 /	-1.14	-0.19	-1.97	0.091761	0.254786	-5.12
253986_at	putative protein predicted protein, Arabi	---	AT4G26210	-1.31	-0.39	-1.97	0.091749	0.254786	-5.12
248880_at	putative protein contains similarity to ca	---	AT5G46200	1.15	0.21	1.97	0.091738	0.254786	-5.12
260973_at	hypothetical protein predicted by genem	---	AT1G53490	1.15	0.20	1.97	0.091755	0.254786	-5.12
258901_at	putative protein phosphatase-2C similar	---	AT3G05640	2.07	1.05	1.96	0.091818	0.254838	-5.12
247843_at	aluminium tolerance associated - like pr	SVL4	AT5G58050	1.20	0.26	1.97	0.091796	0.254838	-5.12
250336_at	alpha-glucosidase 1 ; supported by cDN	---	AT5G11720	-1.21	-0.27	-1.96	0.091824	0.254838	-5.12
262425_at	hypothetical protein predicted by gensca	---	AT1G47660	1.15	0.21	1.96	0.091822	0.254838	-5.12
258731_at	unknown protein ; supported by cDNA:	---	AT3G11880	-1.16	-0.22	-1.96	0.091841	0.254854	-5.12
260352_at	Expressed protein ; supported by full-ler	PDCB4	AT1G69295	1.16	0.22	1.96	0.091881	0.254933	-5.13
266148_x_a	En/Spm-like transposon protein related	---	---	1.20	0.26	1.96	0.091916	0.254998	-5.13
259309_at	putative cyclin-dependent protein kinase	---	AT3G05050	1.23	0.30	1.96	0.091931	0.255009	-5.13

266084_at	hypothetical protein predicted by gensca	---	AT2G37810	1.22	0.29	1.96	0.091987	0.255080	-5.13
258487_at	unknown protein ;supported by full-leng	LBD41	AT3G02550	1.91	0.93	1.96	0.09199	0.255080	-5.13
258873_at	hypothetical protein similar to unknown	---	AT3G03240	1.22	0.28	1.96	0.091985	0.255080	-5.13
246403_at	pectinacetylesterase precursor, putative	---	AT1G57590	-1.27	-0.35	-1.96	0.092027	0.255151	-5.13
256020_at	glutamyl-tRNA reductase, putative simil	HEMA1	AT1G58290	-1.27	-0.34	-1.96	0.092043	0.255165	-5.13
250006_at	putative protein 2'-hydroxyisoflavone re	PCB2	AT5G18660	-1.52	-0.61	-1.96	0.092097	0.255283	-5.13
261485_at	unknown protein ;supported by full-leng	UTR3	AT1G14360	1.52	0.60	1.96	0.092144	0.255382	-5.13
263486_at	AP2 domain transcription factor	---	AT2G22200	-1.16	-0.21	-1.96	0.092255	0.255659	-5.13
247108_at	ReMembR-H2 protein JR700 (gb|AAF32	RMR1	AT5G66160	-1.20	-0.26	-1.96	0.092309	0.255779	-5.13
254230_at	polyprenyltransferase like protein para-	AtPPT1	AT4G23660	-1.17	-0.23	-1.96	0.092354	0.255871	-5.13
253945_at	putative protein gene F23F1.15 Arabido	---	AT4G27050	-1.13	-0.18	-1.96	0.092372	0.255891	-5.13
255318_at	hypothetical protein	---	AT4G04190	-1.20	-0.26	-1.96	0.092385	0.255896	-5.13
258316_at	unknown protein	---	AT3G22660	-1.28	-0.35	-1.96	0.092407	0.255926	-5.13
245686_at	Expressed protein ; supported by cDNA	J2	AT5G22060	1.38	0.47	1.96	0.092431	0.255960	-5.13
255776_at	60S ribosomal protein L6, putative simil	---	AT1G18540	-1.43	-0.51	-1.96	0.092486	0.256083	-5.13
249252_at	putative protein contains similarity to un	---	AT5G42010	1.72	0.78	1.96	0.092578	0.256307	-5.13
246732_at	putative protein hypothetical protein F2	---	AT5G27650	-1.22	-0.28	-1.96	0.092662	0.256507	-5.13
251813_at	Expressed protein ; supported by full-ler	TON1A	AT3G55000	-1.22	-0.28	-1.96	0.092701	0.256583	-5.13
261924_at	peptide transporter, putative similar to p	---	AT1G22550	-1.48	-0.56	-1.96	0.092755	0.256702	-5.13
247970_at	cytosolic malate dehydrogenase	---	AT5G56720	-1.16	-0.21	-1.96	0.092788	0.256720	-5.13
260827_at	mudrA-like protein similar to Mu transpo	AT1G0675	---	-1.25	-0.33	-1.96	0.092795	0.256720	-5.14
249107_at	unknown protein	---	AT5G43680	-1.17	-0.22	-1.96	0.092787	0.256720	-5.13
261270_at	initiation factor 5A-4, putative similar to	FBR12	AT1G26630	-1.15	-0.20	-1.96	0.092864	0.256874	-5.14
259123_at	unknown protein	---	AT3G02200	-1.15	-0.20	-1.96	0.092873	0.256874	-5.14
250024_at	NAM (no apical meristem)-like protein	ANAC087	AT5G18270	1.30	0.37	1.96	0.092914	0.256955	-5.14
259137_at	unknown protein Pfam HMM hit: EF han	---	AT3G10300	1.29	0.37	1.96	0.092961	0.257054	-5.14
258723_at	putative MYB-related protein similar to M	---	AT3G09600	-1.16	-0.22	-1.96	0.092989	0.257101	-5.14
248769_at	putative protein strong similarity to unkn	---	AT5G47730	1.69	0.76	1.96	0.093045	0.257223	-5.14
256528_at	C2H2-type zinc finger protein, putative	ZFP4	AT1G66140	-1.27	-0.34	-1.96	0.093114	0.257227	-5.14
260332_at	hypothetical protein predicted by genefir	---	AT1G70470	1.13	0.17	1.96	0.093064	0.257227	-5.14
262886_at	hypothetical protein	KNATM	AT1G14760	1.22	0.29	1.96	0.093082	0.257227	-5.14
265681_at	putative protein kinase contains a protei	---	AT2G24370	1.15	0.20	1.96	0.093104	0.257227	-5.14
246079_at	putative protein unconventional myosin	---	AT5G20450	-1.21	-0.28	-1.96	0.093073	0.257227	-5.14
263288_at	cyclophilin-like protein ;supported by ful	---	AT2G36130	-1.21	-0.27	-1.96	0.0931	0.257227	-5.14
258580_at	germin-like protein contains Pfam profile	---	AT3G04170	1.18	0.23	1.96	0.093125	0.257227	-5.14

259586_at	unknown protein	---	AT1G28100	-1.16	-0.22	-1.96	0.093149	0.257252	-5.14
245949_at	elongation factor 1B alpha-subunit ;sup	---	AT5G19510	-1.23	-0.29	-1.95	0.093157	0.257252	-5.14
257019_at	unknown protein	---	AT3G19640	-1.13	-0.17	-1.95	0.093181	0.257257	-5.14
258501_at	hypothetical protein predicted by genem	---	AT3G06780	1.26	0.34	1.95	0.093171	0.257257	-5.14
247076_at	ferripyochelin-binding protein-like ;supp	GAMMA C	AT5G66510	1.16	0.21	1.95	0.09321	0.257306	-5.14
254721_at	hypothetical protein ;supported by full-l	SMAP1	AT4G13520	-1.18	-0.23	-1.95	0.093253	0.257362	-5.14
255512_at	Expressed protein ; supported by cDNA	SYP42	AT4G02195	-1.22	-0.29	-1.95	0.093246	0.257362	-5.14
244960_at	ribosomal protein L32	---	---	-1.42	-0.51	-1.95	0.093265	0.257364	-5.14
264670_s_a	unknown protein Similar to elongation f	---	AT1G09640 /	-1.21	-0.27	-1.95	0.093314	0.257454	-5.14
260173_at	NAM-like protein similar to NAM GB:CA	VND7	AT1G71930	-1.19	-0.25	-1.95	0.093326	0.257454	-5.14
250067_at	unknown protein	---	AT5G17950	1.13	0.18	1.95	0.093331	0.257454	-5.14
249974_at	putative protein predicted proteins, Ara	---	AT5G18780	1.37	0.45	1.95	0.093371	0.257471	-5.14
248616_at	putative protein contains similarity to un	---	AT5G49580	-1.23	-0.30	-1.95	0.093354	0.257471	-5.14
255287_at	see T10M13.1 (GB:AF001308) similar t	---	AT4G04660	1.18	0.24	1.95	0.093362	0.257471	-5.14
264691_s_a	putative reverse transcriptase	---	---	-1.17	-0.22	-1.95	0.093384	0.257475	-5.14
249427_at	40S ribosomal protein S9-like 40S ribos	---	AT5G39850	-1.52	-0.60	-1.95	0.093427	0.257562	-5.14
254898_at	serine/threonine kinase-like protein rec	---	AT4G11480	1.86	0.90	1.95	0.093492	0.257711	-5.14
256591_at	hypothetical protein	---	AT3G31910	1.13	0.17	1.95	0.093524	0.257769	-5.14
246538_at	40S RIBOSOMAL PROTEIN S19 - like	---	AT5G15520	-1.30	-0.37	-1.95	0.093553	0.257817	-5.14
255510_at	polycomb group - like protein similar to	SWN	AT4G02020	-1.24	-0.31	-1.95	0.093689	0.257911	-5.14
256068_at	hypothetical protein contains similarity t	ATE1	AT1G13690	-1.15	-0.21	-1.95	0.093607	0.257911	-5.14
263279_x_a	hypothetical protein predicted by gensca	---	---	1.18	0.23	1.95	0.093671	0.257911	-5.14
266518_at	hypothetical protein predicted by gensca	---	AT2G35170	1.18	0.24	1.95	0.093657	0.257911	-5.14
265457_at	unknown protein ; supported by full-leng	---	AT2G46550	-1.22	-0.28	-1.95	0.093649	0.257911	-5.14
254556_at	putative protein various predicted prote	---	AT4G19220	-1.25	-0.33	-1.95	0.093642	0.257911	-5.14
254917_at	putative protein various hypothetical pro	---	AT4G11350	1.28	0.36	1.95	0.093685	0.257911	-5.14
260769_at	Expressed protein ; supported by full-ler	---	AT1G49010	-1.32	-0.40	-1.95	0.093689	0.257911	-5.14
261506_at	choline kinase, putative similar to CHO	ATCK1	AT1G71697	1.35	0.44	1.95	0.093631	0.257911	-5.14
247263_at	putative protein similar to unknown prot	---	AT5G64470	-1.24	-0.31	-1.95	0.093712	0.257912	-5.14
247940_at	phosphatidylserine decarboxylase	PSD2	AT5G57190	1.58	0.66	1.95	0.09371	0.257912	-5.14
260477_at	Ser/Thr protein kinase isolog	---	AT1G11050	1.89	0.92	1.95	0.09375	0.257955	-5.14
264985_at	unknown protein ;supported by full-leng	---	AT1G27150	-1.32	-0.40	-1.95	0.093748	0.257955	-5.14
265318_at	putative D-amino acid dehydrogenase	---	AT2G22650	-1.25	-0.32	-1.95	0.093771	0.257982	-5.15
260818_at	unknown protein	---	AT1G06890	1.13	0.18	1.95	0.093818	0.258049	-5.15
247011_at	putative protein contains similarity to NA	FRO1	AT5G67590	1.30	0.38	1.95	0.093816	0.258049	-5.15

249928_at	CCR4-associated factor-like protein	---	AT5G22250	2.40	1.26	1.95	0.093846	0.258095	-5.15
265044_at	hypothetical protein Similar to human B	VPS2.3	AT1G03950	1.22	0.28	1.95	0.093887	0.258144	-5.15
257095_at	unknown protein ; supported by cDNA:	ATPDIL5-3	AT3G20560	-1.22	-0.28	-1.95	0.093878	0.258144	-5.15
245117_at	putative Ca2+-ATPase ; supported by c	ACA4	AT2G41560	-1.25	-0.32	-1.95	0.093949	0.258283	-5.15
250954_at	putative protein ;supported by full-lengt	ATRAB8C	AT5G03520	-1.23	-0.30	-1.95	0.094049	0.258528	-5.15
247371_at	histone deacetylase ;supported by full-l	HDA6	AT5G63110	-1.17	-0.22	-1.95	0.094114	0.258674	-5.15
245272_at	hypothetical protein ; supported by cDN	---	AT4G17250	1.37	0.46	1.95	0.094154	0.258753	-5.15
246095_at	homeotic gene regulator - like protein h	---	AT5G19310	-1.28	-0.36	-1.95	0.094194	0.258832	-5.15
256145_at	lipid transfer protein, putative similar to	---	AT1G48750	1.46	0.55	1.95	0.094206	0.258835	-5.15
263659_at	unknown protein EST gb|ATTS5672 cor	---	AT1G04470	1.17	0.23	1.95	0.0943	0.259029	-5.15
253384_at	Expressed protein ; supported by full-ler	---	AT4G32915	-1.20	-0.26	-1.95	0.094299	0.259029	-5.15
250533_at	flavonol synthase (FLS) (sp|Q96330) ;s	FLS	AT5G08640	1.15	0.20	1.95	0.094331	0.259084	-5.15
259816_at	RING-H2 finger protein RHY1a identica	---	AT1G49850	-1.17	-0.23	-1.95	0.094406	0.259228	-5.15
246130_at	putative protein various predicted prote	---	---	1.26	0.33	1.95	0.094405	0.259228	-5.15
261472_at	hypothetical protein predicted by genem	---	AT1G14470	-1.12	-0.17	-1.95	0.094434	0.259273	-5.15
253040_at	endo-xyloglucan transferase - like prote	---	AT4G37800	-1.72	-0.78	-1.95	0.094453	0.259293	-5.15
257483_at	hypothetical protein contains similarity t	ICK5	AT1G49620	1.17	0.22	1.95	0.094464	0.259293	-5.15
262158_at	somatic embryogenesis receptor-like ki	---	AT1G52540	1.27	0.35	1.95	0.094507	0.259347	-5.15
261990_at	unknown protein	---	AT1G33660	1.17	0.22	1.95	0.094506	0.259347	-5.15
260760_at	hypothetical protein predicted by genem	---	AT1G49170	-1.22	-0.28	-1.94	0.094611	0.259572	-5.15
248424_at	unknown protein	---	AT5G51680	1.64	0.71	1.94	0.094604	0.259572	-5.15
256624_at	hypothetical protein predicted by genem	---	AT3G19990	1.15	0.21	1.94	0.094661	0.259638	-5.15
249982_at	putative protein predicted proteins, Aral	---	AT5G18520	1.16	0.22	1.94	0.09465	0.259638	-5.15
244964_at	PSII cytochrome b559	---	---	-1.12	-0.17	-1.94	0.094669	0.259638	-5.15
259907_at	GCN4-complementing protein, putative	AGD2	AT1G60860	-1.32	-0.40	-1.94	0.0947	0.259690	-5.15
260606_at	putative splicing factor	---	AT2G43770	-1.27	-0.34	-1.94	0.094712	0.259693	-5.15
258001_at	AIG2-like protein similar to AIG2 protein	---	AT3G28950	-1.16	-0.21	-1.94	0.09473	0.259711	-5.16
263502_s_a	hypothetical protein	---	AT2G07675	-1.28	-0.36	-1.94	0.094749	0.259731	-5.16
253153_at	hypothetical protein	---	AT4G35700	-1.16	-0.21	-1.94	0.094762	0.259737	-5.16
253916_at	hypothetical protein ;supported by full-le	---	AT4G27240	-1.34	-0.42	-1.94	0.094784	0.259740	-5.16
252287_at	30S ribosomal protein S9 -like similar to	---	AT3G49080	-1.28	-0.35	-1.94	0.094793	0.259740	-5.16
247802_at	putative protein RING-H2 zinc finger pr	ATL63	AT5G58580	-1.19	-0.25	-1.94	0.094798	0.259740	-5.16
247687_at	protein serine /threonine kinase - like pr	---	AT5G59740	-1.18	-0.24	-1.94	0.094874	0.259919	-5.16
248936_at	heat shock transcription factor	RHA1	AT5G45710	1.25	0.32	1.94	0.094911	0.259987	-5.16
263054_at	putative cation transport protein	---	AT2G04620	-1.16	-0.22	-1.94	0.094943	0.260027	-5.16

248824_at	putative protein contains similarity to inv	---	AT5G46940	5.80	2.54	1.94	0.094948	0.260027	-5.16
266155_at	cytochrome p450, putative similar to cy	CYP89A5	AT1G64950 /	1.44	0.52	1.94	0.095022	0.260170	-5.16
257918_at	ethylene responsive element binding pr	---	AT3G23230	3.51	1.81	1.94	0.095023	0.260170	-5.16
259434_at	unknown protein	---	AT1G01490	-1.15	-0.21	-1.94	0.0951	0.260347	-5.16
246944_at	ubiquinol--cytochrome-c reductase-like	---	AT5G25450	1.18	0.24	1.94	0.095111	0.260347	-5.16
246040_at	peptidyl-prolyl cis-trans isomerase - like	---	AT5G19370	-1.16	-0.22	-1.94	0.095155	0.260375	-5.16
263321_at	ADP-ribosylation factor 1 ;supported by	ARF1A1C	AT2G47170	1.16	0.22	1.94	0.09515	0.260375	-5.16
245620_at	hypothetical protein	---	AT4G14050	-1.19	-0.25	-1.94	0.095137	0.260375	-5.16
256473_at	unknown protein	---	---	1.17	0.22	1.94	0.095255	0.260616	-5.16
265626_at	unknown protein ;supported by full-leng	---	AT2G27260	1.18	0.24	1.94	0.095304	0.260710	-5.16
261843_at	unknown protein	---	AT1G16180	1.15	0.20	1.94	0.095312	0.260710	-5.16
259527_at	hypothetical protein	---	AT1G12600	1.13	0.18	1.94	0.09534	0.260733	-5.16
256983_at	chaperonin 60 beta, putative very simila	---	AT3G13470	-1.47	-0.55	-1.94	0.095354	0.260733	-5.16
245464_at	hypothetical protein	UGLYAH	AT4G17050	-1.24	-0.31	-1.94	0.095352	0.260733	-5.16
251358_at	shaggy-like kinase beta	---	AT3G61160	-1.43	-0.52	-1.94	0.095406	0.260842	-5.16
254976_at	subtilisin-like serine protease contains s	---	AT4G10510	1.16	0.21	1.94	0.095462	0.260912	-5.16
255203_at	hypothetical protein	---	---	-1.23	-0.29	-1.94	0.095465	0.260912	-5.16
256410_at	hypothetical protein	---	AT1G66630	1.12	0.17	1.94	0.095451	0.260912	-5.16
265911_at	unknown protein ;supported by full-leng	---	AT2G25670	-1.14	-0.19	-1.94	0.095486	0.260935	-5.16
267320_at	hypothetical protein predicted by gensca	---	AT2G19300	1.17	0.23	1.94	0.095554	0.261092	-5.16
267184_at	unknown protein ; supported by cDNA:	ASHH3	AT2G44150	-1.15	-0.21	-1.94	0.09559	0.261159	-5.16
253202_at	Expressed protein ; supported by full-ler	---	AT4G34555	-1.37	-0.46	-1.94	0.095617	0.261202	-5.16
246251_at	cold acclimation protein homolog	---	AT4G37220	1.51	0.60	1.94	0.095629	0.261203	-5.16
261205_at	hypothetical protein predicted by genem	---	AT1G12790	1.29	0.37	1.94	0.09569	0.261337	-5.16
254408_at	serine/threonine kinase - like protein se	B120	AT4G21390	2.48	1.31	1.94	0.095712	0.261366	-5.17
264049_at	putative GTP-binding protein	---	AT2G22390	-1.25	-0.33	-1.94	0.095729	0.261382	-5.17
246888_at	putative protein	---	AT5G26270	1.14	0.19	1.94	0.095741	0.261382	-5.17
259120_at	unknown protein	---	AT3G02240	2.61	1.38	1.94	0.095766	0.261388	-5.17
247096_at	S-adenosyl-L-methionine:salicylic acid c	---	AT5G66430	-1.12	-0.17	-1.94	0.09576	0.261388	-5.17
266292_at	putative tropinone reductase ;supported	SAG13	AT2G29350	2.72	1.44	1.93	0.095992	0.261631	-5.17
257008_at	myrosinase-associated protein, putative	ESM1	AT3G14210	-2.05	-1.04	-1.93	0.095977	0.261631	-5.17
260334_at	homeotic protein (ATK1) identical to hor	KNAT2	AT1G70510	1.14	0.20	1.93	0.095982	0.261631	-5.17
261105_at	unknown protein ;supported by full-lengt	NRS/ER	AT1G63000	-1.22	-0.29	-1.93	0.095971	0.261631	-5.17
245941_at	putative protein karyopherin beta 3 - Ho	emb2734	AT5G19820	-1.19	-0.25	-1.93	0.095988	0.261631	-5.17
244984_at	ribosomal protein S3	---	---	-1.26	-0.34	-1.93	0.095987	0.261631	-5.17

263304_at	hypothetical protein predicted by gensca	---	AT2G01920	1.16	0.21	1.93	0.095919	0.261631	-5.17
247419_at	unknown protein	---	AT5G63080	-1.22	-0.29	-1.93	0.095944	0.261631	-5.17
256022_at	amino acid permease I identical to amin	AAP1	AT1G58360	1.51	0.59	1.93	0.095954	0.261631	-5.17
256540_at	polyprotein, putative similar to polyprote	---	---	-1.14	-0.19	-1.93	0.095971	0.261631	-5.17
265686_at	hypothetical protein predicted by gensca	---	AT2G24460	1.14	0.19	1.93	0.095952	0.261631	-5.17
245022_at	PSII L protein	---	---	-1.25	-0.32	-1.93	0.095927	0.261631	-5.17
260357_at	unknown protein ;supported by full-lengt	AFP1	AT1G69260	1.22	0.29	1.93	0.096029	0.261700	-5.17
248908_at	receptor kinase-like protein	MEE62	AT5G45800	1.57	0.65	1.93	0.096046	0.261714	-5.17
246843_at	putative protein various predicted prote	---	AT5G26740	-1.15	-0.20	-1.93	0.096081	0.261753	-5.17
251638_at	40S ribosomal protein S2 homolog 40S	---	AT3G57490	-1.36	-0.45	-1.93	0.096099	0.261753	-5.17
251367_at	SKP1 interacting partner 4 (SKIP4), put	SKIP4	AT3G61350	-1.20	-0.27	-1.93	0.096093	0.261753	-5.17
263943_at	putative mitochondrial carrier protein	---	AT2G35800	-1.20	-0.26	-1.93	0.096106	0.261753	-5.17
250350_at	putative protein predicted proteins, Aral	---	AT5G12010	1.38	0.46	1.93	0.096187	0.261868	-5.17
262224_at	hypothetical protein contains Pfam profil	OTP43	AT1G74900	-1.14	-0.19	-1.93	0.096165	0.261868	-5.17
262731_at	hypothetical protein similar to gb|AF098	MC8	AT1G16420	3.11	1.64	1.93	0.096194	0.261868	-5.17
260739_at	serine carboxypeptidase precursor, put	scpl50	AT1G15000	-1.37	-0.45	-1.93	0.096191	0.261868	-5.17
263123_at	beta-Amyrin Synthase, putative similar	---	AT1G78500	1.16	0.22	1.93	0.096216	0.261895	-5.17
262450_at	hypothetical protein identical to hypothe	---	AT1G11320	-1.20	-0.26	-1.93	0.096228	0.261897	-5.17
259584_at	hypothetical protein predicted by genem	---	AT1G28080	1.14	0.19	1.93	0.096334	0.262154	-5.17
259739_at	unknown protein supported by cDNA: C	SEH1H	AT1G64350	-1.17	-0.23	-1.93	0.096453	0.262447	-5.17
262048_at	cytochrome c oxidase subunit, putative	---	AT1G80230	1.18	0.24	1.93	0.096519	0.262595	-5.17
247904_at	putative protein contains similarity to unl	AIL5	AT5G57390	1.22	0.29	1.93	0.096538	0.262615	-5.17
250223_at	glutaredoxin-like protein ;supported by f	ROXY2	AT5G14070	1.15	0.21	1.93	0.096563	0.262652	-5.17
256878_at	major latex protein, putative similar to m	---	AT3G26460	-1.21	-0.27	-1.93	0.096576	0.262657	-5.17
256065_at	ribosomal protein, putative similar to rib	---	AT1G07070	-1.36	-0.45	-1.93	0.096589	0.262661	-5.17
260775_at	14-3-3 protein GF14omega (grf2) identic	GRF2	AT1G78300	1.22	0.28	1.93	0.096632	0.262746	-5.17
266224_at	chloroplast membrane protein (ALBINO3	ALB3	AT2G28800	-1.14	-0.19	-1.93	0.096695	0.262860	-5.17
246304_at	acyl-coA dehydrogenase Mus musculus	ACX4	AT3G51840	1.24	0.31	1.93	0.096697	0.262860	-5.17
262336_at	hypothetical protein predicted be genem	TOM7-2	AT1G64220	-1.13	-0.18	-1.93	0.09673	0.262899	-5.18
252533_at	putative protein predicted proteins, Aral	---	AT3G46110	1.55	0.64	1.93	0.096734	0.262899	-5.18
250769_at	putative protein similar to unknown prote	---	AT5G05680	-1.32	-0.40	-1.93	0.09676	0.262937	-5.18
262133_at	high affinity sulphate transporter, putati	SULTR1;2	AT1G78000	-1.67	-0.74	-1.93	0.096829	0.263061	-5.18
254292_at	putative protein	---	AT4G23030	1.60	0.68	1.93	0.096819	0.263061	-5.18
259830_at	hypothetical protein predicted by gensca	---	AT1G80630	-1.18	-0.23	-1.93	0.096866	0.263132	-5.18
257344_s_a	pseudogene, putative mutator-like tran	---	---	1.25	0.32	1.93	0.096907	0.263147	-5.18

246101_at	putative protein	---	---	1.18	0.24	1.93	0.096896	0.263147	-5.18
257268_at	unknown protein	---	AT3G17450	-1.25	-0.32	-1.93	0.096912	0.263147	-5.18
251033_at	hypothetical protein ;supported by full-le	---	AT5G01960	1.13	0.17	1.93	0.096918	0.263147	-5.18
266834_s_a	putative protein phosphatase 2C	---	AT2G05050 /	2.16	1.11	1.93	0.096973	0.263265	-5.18
262395_at	hypothetical protein similar to hypothetic	---	AT1G49540	-1.35	-0.43	-1.93	0.096995	0.263292	-5.18
262922_at	hypothetical protein predicted by genem	---	AT1G79420	1.23	0.29	1.93	0.09701	0.263304	-5.18
261743_s_a	protein serine/threonine phosphatase a	BSL2	AT1G08420 /	1.16	0.21	1.93	0.097067	0.263395	-5.18
264843_at	putative 1-aminocyclopropane-1-carbox	---	AT1G03400	1.30	0.38	1.93	0.097063	0.263395	-5.18
261869_at	hypothetical protein predicted by genem	---	AT1G11470	1.18	0.24	1.93	0.097124	0.263517	-5.18
258021_at	hypothetical protein predicted genemark	PUB25	AT3G19380	1.60	0.68	1.93	0.097257	0.263848	-5.18
249411_at	raffinose synthase -like protein raffinose	SIP1	AT5G40390	1.50	0.58	1.92	0.09737	0.264100	-5.18
250732_at	putative protein contains similarity to unl	---	AT5G06480	-1.31	-0.39	-1.92	0.097373	0.264100	-5.18
258582_at	germin-like protein contains Pfam profile	---	AT3G04150	1.13	0.17	1.92	0.09739	0.264115	-5.18
253542_at	putative protein deubiquitinating enzym	UBP18	AT4G31670	-1.16	-0.21	-1.92	0.09741	0.264138	-5.18
253847_at	putative protein CRP1, Zea mays, AF07	---	AT4G28010	-1.16	-0.21	-1.92	0.097435	0.264174	-5.18
252855_at	putative protein alpha-amino-epsilon-ca	AGT2	AT4G39660	-1.21	-0.28	-1.92	0.09745	0.264182	-5.18
266699_at	putative ribosomal protein L28 ; suppor	---	AT2G19730	-1.28	-0.36	-1.92	0.097478	0.264212	-5.18
245395_at	hypothetical protein ;supported by full-le	---	AT4G17420	-1.20	-0.27	-1.92	0.097484	0.264212	-5.18
250439_at	14-3-3 protein GF14lambda (grf6/AFT1)	GRF6	AT5G10450	1.17	0.23	1.92	0.097499	0.264221	-5.18
263552_x_a	unknown protein proline, tyrosine, and s	---	AT2G24980	1.24	0.32	1.92	0.09752	0.264247	-5.18
245200_at	F12A21.2 hypothetical protein; supporte	---	AT1G67850	1.35	0.43	1.92	0.097602	0.264406	-5.18
251626_at	UDP-GlcNAc:dolichol phosphate N-ace	---	AT3G57220	-1.17	-0.23	-1.92	0.097601	0.264406	-5.18
265323_at	putative syntaxin	SYP112	AT2G18260	-1.22	-0.29	-1.92	0.097618	0.264417	-5.18
245225_at	mitochondrial protein-like; contains simil	---	AT3G29800	1.23	0.29	1.92	0.097689	0.264578	-5.18
258974_at	unknown protein similar to brahma asso	---	AT3G01890	-1.18	-0.24	-1.92	0.097769	0.264720	-5.19
267561_at	putative protein kinase contains a protei	---	AT2G45590	-1.30	-0.38	-1.92	0.097776	0.264720	-5.19
265056_at	mitochondrial processing peptidase alp	---	AT1G51980	1.22	0.29	1.92	0.097771	0.264720	-5.19
262651_at	hypothetical protein One of a cluster of	FUT9	AT1G14100 /	1.19	0.25	1.92	0.097797	0.264747	-5.19
261505_at	carboxypeptidase, putative similar to ca	SOL1	AT1G71696	1.22	0.29	1.92	0.097823	0.264785	-5.19
253330_at	putative potassium transporter AtKT5p (	KUP5	AT4G33530	1.16	0.21	1.92	0.097863	0.264863	-5.19
253617_at	hypothetical protein	---	AT4G30410	1.52	0.60	1.92	0.097885	0.264872	-5.19
252683_at	putative protein predicted proteins, Arat	---	AT3G44380	-1.21	-0.28	-1.92	0.097891	0.264872	-5.19
249343_at	succinate dehydrogenase iron-protein s	SDH2-2	AT5G40650	1.23	0.29	1.92	0.097901	0.264872	-5.19
263635_at	hypothetical protein predicted by gensca	---	---	1.13	0.17	1.92	0.097939	0.264941	-5.19
251205_at	glutathione peroxidase -like protein pho	ATGPX5	AT3G63080	1.21	0.28	1.92	0.097982	0.264995	-5.19

246264_at	hypothetical protein	FRL2	AT1G31814	-1.17	-0.23	-1.92	0.097979	0.264995	-5.19
265492_at	hypothetical protein	AGL95	AT2G15660	1.16	0.22	1.92	0.098007	0.265033	-5.19
264865_at	DNAJ-like heatshock protein similar to C	ARL1	AT1G24120	-1.14	-0.19	-1.92	0.098089	0.265221	-5.19
253219_at	MYB-like protein myb-related protein Y4	AtMYB32	AT4G34990	-1.32	-0.40	-1.92	0.098135	0.265284	-5.19
253959_at	putative protein	---	AT4G26410	-1.15	-0.20	-1.92	0.098135	0.265284	-5.19
245746_at	bHLH transcription factor, putative simil	---	AT1G51070	1.21	0.28	1.92	0.098148	0.265287	-5.19
255478_at	putative protein ;supported by full-lengt	EID1	AT4G02440	1.18	0.24	1.92	0.098163	0.265295	-5.19
262597_at	unknown protein Strong similarity to gb	---	AT1G15470	-1.22	-0.29	-1.92	0.098199	0.265363	-5.19
265780_at	Mutator-like transposase similar to MUF	---	---	1.16	0.22	1.92	0.098221	0.265391	-5.19
257431_at	unknown protein	---	AT2G36360	1.17	0.22	1.92	0.098313	0.265608	-5.19
252223_at	MYB -like protein DNA-binding protein I	TRB3	AT3G49850	-1.26	-0.33	-1.92	0.098344	0.265660	-5.19
249238_at	GAMM1 protein-like ; supported by cDN	---	AT5G41970	-1.16	-0.22	-1.92	0.098401	0.265781	-5.19
251327_at	prolyl aminopeptidase-like protein proly	---	AT3G61540	-1.13	-0.17	-1.92	0.098428	0.265824	-5.19
251780_s_a	beta-ketoacyl-ACP reductase - like prot	---	AT3G55290 /	-1.30	-0.38	-1.92	0.098465	0.265892	-5.19
262722_at	sterol glucosyltransferase, putative simi	---	AT1G43620	-1.15	-0.20	-1.92	0.09849	0.265928	-5.19
248777_at	putative protein similar to unknown prote	---	AT5G47920	1.18	0.24	1.92	0.09858	0.266121	-5.19
267428_at	putative coatomer epsilon subunit	---	AT2G34840	-1.18	-0.24	-1.92	0.098597	0.266121	-5.19
248937_at	putative protein contains similarity to unl	AtRLP55	AT5G45770	1.25	0.32	1.92	0.098595	0.266121	-5.19
258964_at	putative 3-phosphoinositide-dependent	---	AT3G10540	1.17	0.23	1.92	0.098639	0.266186	-5.19
262159_at	hypothetical protein predicted by genem	---	AT1G52720	1.43	0.52	1.92	0.098668	0.266186	-5.19
261446_at	unknown protein	SEC5B	AT1G21170	1.23	0.30	1.92	0.09866	0.266186	-5.19
253646_at	MAP kinase kinase 2 ; supported by cD	ATMKK2	AT4G29810	1.29	0.37	1.92	0.098665	0.266186	-5.19
264307_at	hypothetical protein contains similarity to	---	AT1G61900	-1.20	-0.27	-1.92	0.098692	0.266203	-5.19
264023_at	Expressed protein ; supported by full-ler	---	AT2G21195	-1.30	-0.38	-1.92	0.098697	0.266203	-5.19
259896_at	unknown protein ;supported by full-lengt	---	AT1G71500	-1.18	-0.24	-1.91	0.09879	0.266423	-5.20
252261_at	RNA-directed RNA polymerase RNA-dir	RDR6	AT3G49500	-1.18	-0.24	-1.91	0.098819	0.266437	-5.20
262430_s_a	unknown protein	---	AT1G47550 /	-1.17	-0.23	-1.91	0.098809	0.266437	-5.20
246584_at	putative protein predicted protein, Arabi	---	AT5G14730	1.74	0.80	1.91	0.09884	0.266462	-5.20
254402_at	putative protein predicted protein, Arabi	---	AT4G21310	1.27	0.34	1.91	0.098916	0.266637	-5.20
264353_at	hypothetical protein predicted by gensca	---	AT1G03260	1.16	0.22	1.91	0.098945	0.266683	-5.20
262822_at	putative membrane-associated salt-indu	---	AT1G11630	-1.17	-0.22	-1.91	0.098968	0.266712	-5.20
252375_at	rac GTP binding protein Arac8 ; suppor	ROP10	AT3G48040	-1.18	-0.24	-1.91	0.098985	0.266728	-5.20
258014_at	hypothetical protein predicted by genem	---	AT3G19330	-1.26	-0.33	-1.91	0.099077	0.266945	-5.20
258399_at	early auxin-induced protein, IAA19 iden	IAA19	AT3G15540	1.73	0.79	1.91	0.099108	0.266977	-5.20
265949_at	putative vicilin storage protein (globulin-	---	AT2G18540	-1.13	-0.18	-1.91	0.099113	0.266977	-5.20

259134_at	hypothetical protein predicted by gensca	---	AT3G05390	1.61	0.69	1.91	0.099147	0.267039	-5.20
249912_at	putative protein similar to unknown prote	RER1	AT5G22790	-1.41	-0.49	-1.91	0.099184	0.267105	-5.20
251711_at	phosphatidylinositol-4-phosphate 5-kina	PIP5K4	AT3G56960	-1.22	-0.28	-1.91	0.099234	0.267210	-5.20
261398_at	hypothetical protein contains similarity to	NHX6	AT1G79610	1.17	0.22	1.91	0.099299	0.267324	-5.20
260586_at	unknown protein predicted by genefinde	---	AT2G43630	-1.18	-0.24	-1.91	0.0993	0.267324	-5.20
253889_at	forever young gene (FEY)	FEY	AT4G27760	1.14	0.19	1.91	0.09934	0.267401	-5.20
262303_at	homeobox protein, putative similar to h	ATHB18	AT1G70920	1.29	0.37	1.91	0.099357	0.267415	-5.20
266504_at	hypothetical protein predicted by gensca	---	AT2G47820	1.20	0.26	1.91	0.099428	0.267573	-5.20
257616_at	hypothetical protein contains Pfam profil	---	AT3G26540	-1.21	-0.28	-1.91	0.099525	0.267802	-5.20
260189_at	putative urease similar to urease GB:22	URE	AT1G67550	-1.20	-0.26	-1.91	0.099564	0.267875	-5.20
267474_at	hypothetical protein predicted by gensca	WHY3	AT2G02740	-1.19	-0.25	-1.91	0.099596	0.267932	-5.20
249730_at	calcium dependent protein kinase-like p	---	AT5G24430	1.38	0.46	1.91	0.09963	0.267991	-5.20
260641_at	hypothetical protein predicted by gensca	---	AT1G53200	-1.33	-0.42	-1.91	0.099664	0.268031	-5.20
248051_at	Atmyb103 (gb|AAD40692.1)	ATMYB10	AT5G56110	1.17	0.22	1.91	0.099668	0.268031	-5.20
265071_at	transcription initiation factor TFIID-2 ider	TBP2	AT1G55520	-1.17	-0.22	-1.91	0.099706	0.268101	-5.20
257562_at	hypothetical protein	---	---	1.20	0.26	1.91	0.099756	0.268140	-5.21
264927_at	phosphatidylinositol 3-kinase, putative s	VPS34	AT1G60490	-1.12	-0.17	-1.91	0.099752	0.268140	-5.20
258636_at	putative GTPase activator protein conta	---	AT3G07890	-1.17	-0.23	-1.91	0.099734	0.268140	-5.20
256301_at	unknown protein ;supported by full-lengt	---	AT1G69510	-1.16	-0.22	-1.91	0.099856	0.268346	-5.21
250650_at	anthranilate phosphoribosyltransferase-	---	AT5G06850	-1.27	-0.35	-1.91	0.099847	0.268346	-5.21
256262_at	unknown protein	---	AT3G12150	1.21	0.28	1.91	0.099973	0.268554	-5.21
245260_at	kinase like protein ; supported by cDNA	---	AT4G16360	-1.14	-0.19	-1.91	0.099981	0.268554	-5.21
255339_at	hypothetical protein similar to A. thalian	---	AT4G04480	1.34	0.42	1.91	0.099965	0.268554	-5.21
251792_at	probable serine/threonine-specific prote	---	AT3G55550	-1.16	-0.22	-1.91	0.099946	0.268554	-5.21
264620_at	putative bZIP transcription factor	ATBZIP27	AT2G17770	1.21	0.27	1.91	0.100006	0.268590	-5.21
260568_at	endochitinase isolog	---	AT2G43570	3.25	1.70	1.91	0.100038	0.268613	-5.21
258012_at	unknown protein similar to GB:CAB167	---	AT3G19310	1.13	0.17	1.91	0.100031	0.268613	-5.21
258923_at	putative glucose acyltransferase similar	SCPL7	AT3G10450	1.40	0.48	1.91	0.100072	0.268648	-5.21
263016_at	ubiquitin extension protein, putative sim	---	AT1G23410	-1.18	-0.24	-1.91	0.100075	0.268648	-5.21
262966_at	ER lumen protein retaining receptor, pu	---	AT1G75760	-1.16	-0.22	-1.91	0.100138	0.268787	-5.21
259033_at	putative pectinacetylesterase similar to	---	AT3G09405 /	2.33	1.22	1.90	0.100194	0.268904	-5.21
263160_at	oligouridylate binding protein, putative s	UBP1A	AT1G54080	-1.17	-0.23	-1.90	0.10022	0.268942	-5.21
264807_at	putative presenilin similar to presenilin G	---	AT1G08700	1.22	0.29	1.90	0.10028	0.269008	-5.21
256722_at	hypothetical protein predicted by genefi	---	AT2G34050	-1.34	-0.42	-1.90	0.100268	0.269008	-5.21
248664_at	peptidyl-prolyl cis-trans isomerase-like p	FKBP15-2	AT5G48580	-1.25	-0.32	-1.90	0.10027	0.269008	-5.21

250274_at	putative protein predicted protein, Arabi	---	AT5G13020	-1.18	-0.24	-1.90	0.100343	0.269085	-5.21
264557_at	putative pectinacetylesterase precursor	---	AT1G09550	1.24	0.31	1.90	0.100342	0.269085	-5.21
259019_at	hypothetical protein similar to serologica	CHIP	AT3G07370	1.17	0.23	1.90	0.100335	0.269085	-5.21
264508_at	putative phytochrome A similar to GB:A/	PHYA	AT1G09570	-1.30	-0.38	-1.90	0.100361	0.269100	-5.21
251654_at	putative protein several hypothetical pro	SDP1-LIKI	AT3G57140	1.14	0.19	1.90	0.100375	0.269106	-5.21
264462_at	putative transcription factor similar to tra	WLIM1	AT1G10200	-1.27	-0.35	-1.90	0.100417	0.269124	-5.21
249323_at	unknown protein	FLA20	AT5G40940	1.16	0.22	1.90	0.100402	0.269124	-5.21
257978_at	putative serine/threonine protein kinase	ATNEK5	AT3G20860	1.64	0.71	1.90	0.100407	0.269124	-5.21
245326_at	Expressed protein ; supported by full-ler	---	AT4G14100	-1.22	-0.29	-1.90	0.100555	0.269442	-5.21
264815_at	hypothetical protein similar to hypothetic	---	AT1G03620	-1.37	-0.46	-1.90	0.100559	0.269442	-5.21
251506_at	putative protein ; supported by cDNA: g	---	AT3G59090	1.13	0.18	1.90	0.100608	0.269503	-5.21
260583_x_a	putative polyribonucleotide phosphoryla	---	AT2G47220	-1.23	-0.30	-1.90	0.100618	0.269503	-5.21
254531_at	putative protein predicted protein, Arabi	---	AT4G19650	-1.23	-0.30	-1.90	0.100601	0.269503	-5.21
247836_at	putative protein similar to unknown prote	---	AT5G57860	-1.19	-0.25	-1.90	0.100647	0.269517	-5.21
246503_at	40S ribosomal protein S7-like 40S ribos	---	AT5G16130	-1.35	-0.43	-1.90	0.100642	0.269517	-5.21
251806_at	zinc finger protein OBP3 ; supported by	OBP3	AT3G55370	1.15	0.20	1.90	0.100735	0.269723	-5.21
247037_at	putative protein similar to unknown prote	RALFL34	AT5G67070	2.11	1.08	1.90	0.100797	0.269856	-5.22
266687_at	putative arginine N-methyltransferase	PRMT1A	AT2G19670	-1.33	-0.41	-1.90	0.100841	0.269942	-5.22
265356_at	putative TRAP protein	---	AT2G16595	1.22	0.28	1.90	0.100929	0.270083	-5.22
260037_at	putative DNA-binding protein (RAV2-like	RAV2	AT1G68840	1.81	0.86	1.90	0.100924	0.270083	-5.22
251680_at	putative protein 13S condensin XCAP-I	---	AT3G57060	-1.15	-0.20	-1.90	0.100922	0.270083	-5.22
250625_at	calnexin homolog	---	AT5G07340	-1.24	-0.31	-1.90	0.100955	0.270120	-5.22
247271_at	nuclear protein-like	---	AT5G64270	-1.19	-0.25	-1.90	0.10098	0.270155	-5.22
252082_at	putative protein	---	AT3G51940	-1.14	-0.18	-1.90	0.101044	0.270296	-5.22
261083_at	unknown protein ; supported by cDNA: g	---	AT1G07310	1.19	0.25	1.90	0.101087	0.270378	-5.22
267214_at	unknown protein ; supported by cDNA:	---	AT2G43970	-1.23	-0.29	-1.90	0.101114	0.270405	-5.22
253236_at	putative protein ARI protein, Drosophila	ARI1	AT4G34370	-1.14	-0.18	-1.90	0.101123	0.270405	-5.22
264889_at	unknown protein	---	AT1G23050	-1.19	-0.25	-1.90	0.101132	0.270405	-5.22
261053_at	hypothetical protein predicted by genem	---	AT1G01320	-1.23	-0.30	-1.90	0.10119	0.270431	-5.22
254797_at	putative protein	---	AT4G13030	-1.30	-0.37	-1.90	0.101179	0.270431	-5.22
252439_at	pectinesterase-like protein pectinestera	---	AT3G47400	1.14	0.18	1.90	0.101173	0.270431	-5.22
247924_at	Expressed protein	---	AT5G57655	1.38	0.47	1.90	0.101184	0.270431	-5.22
265539_at	unknown protein	---	AT2G15830	-1.48	-0.56	-1.90	0.101216	0.270470	-5.22
254232_at	tyrosine transaminase like protein tyros	CORI3	AT4G23600	-1.70	-0.77	-1.90	0.101245	0.270486	-5.22
258611_at	unknown protein ;supported by full-leng	---	AT3G02860	-1.17	-0.22	-1.90	0.101244	0.270486	-5.22

263314_at	putative membrane transporter	---	AT2G05760	1.13	0.18	1.90	0.101275	0.270503	-5.22
249814_at	putative protein similar to unknown prote	---	AT5G23840	-1.14	-0.19	-1.90	0.101276	0.270503	-5.22
247632_at	protein transport protein subunit - like p	---	AT5G60460	1.19	0.25	1.90	0.10131	0.270563	-5.22
250989_at	cytochrome P450 - like protein cytochro	CYP96A13	AT5G02900	1.12	0.17	1.90	0.101338	0.270605	-5.22
257145_at	esterase, putative similar to esterase H	---	AT3G27320	-1.22	-0.29	-1.90	0.101462	0.270875	-5.22
264477_at	amp-binding protein, putative similar to	---	AT1G77240	1.24	0.31	1.90	0.10146	0.270875	-5.22
255000_at	S18.A ribosomal protein ;supported by	RPS18C	AT4G09800	-1.26	-0.33	-1.90	0.101522	0.271001	-5.22
264347_at	putative extensin strong similarity to exte	LRX1	AT1G12040	1.12	0.16	1.90	0.101535	0.271005	-5.22
254021_at	putative protein cell death suppressor p	ACD1-LIKE	AT4G25650	-1.20	-0.26	-1.90	0.101596	0.271136	-5.22
250150_at	putative protein ;supported by full-length	---	AT5G14710	-1.25	-0.32	-1.89	0.101695	0.271338	-5.22
251954_at	putative protein predicted protein, Arabi	CPuORF5	AT3G53668 /	1.41	0.49	1.89	0.101685	0.271338	-5.22
251843_x_a	extensin precursor -like protein extensin	ATHRGP1	AT3G54590	1.33	0.42	1.89	0.101744	0.271437	-5.22
252232_at	bZIP transcription factor - like protein bZ	AtbZIP5	AT3G49760	1.13	0.18	1.89	0.101807	0.271573	-5.22
247601_at	zinc finger protein OBP4 - like zinc finge	OBP4	AT5G60850	-1.26	-0.33	-1.89	0.101851	0.271626	-5.23
266080_at	hypothetical protein predicted by gensca	---	AT2G37840	-1.12	-0.17	-1.89	0.10184	0.271626	-5.22
261257_at	tat-binding protein, putative similar to G	---	AT1G05910	-1.21	-0.28	-1.89	0.101874	0.271657	-5.23
255805_at	zinc-finger - like protein zinc-finger prot	---	AT4G10240	1.16	0.22	1.89	0.101912	0.271725	-5.23
246226_at	thiol-disulfide interchange like protein	HCF164	AT4G37200	-1.24	-0.31	-1.89	0.101965	0.271836	-5.23
250187_at	putative protein predicted proteins, Arat	---	AT5G14370	-1.31	-0.39	-1.89	0.102008	0.271919	-5.23
257202_at	receptor-like kinase, putative similar to	---	AT3G23750	1.20	0.27	1.89	0.102048	0.271993	-5.23
258274_at	putative cytochrome c oxidase subunit V	---	AT3G15640	1.19	0.26	1.89	0.102117	0.272082	-5.23
255032_at	putative protein anthocyanin rhamnosyl	---	AT4G09500	-1.22	-0.29	-1.89	0.102108	0.272082	-5.23
259870_at	putative heat shock protein predicted by	---	AT1G76780	-1.13	-0.17	-1.89	0.102116	0.272082	-5.23
255729_at	hypothetical protein similar to putative A	---	AT1G25470 /	-1.17	-0.22	-1.89	0.102138	0.272106	-5.23
245199_at	Expressed protein ; supported by full-ler	KCR1	AT1G67730	1.20	0.26	1.89	0.102176	0.272174	-5.23
254951_at	putative protein various kinesin light cha	---	AT4G10840	1.14	0.19	1.89	0.102274	0.272341	-5.23
263870_at	unknown protein	RKP	AT2G22010	-1.18	-0.23	-1.89	0.102272	0.272341	-5.23
260107_at	fructokinase, putative similar to fructoki	---	AT1G66430	-1.78	-0.83	-1.89	0.102258	0.272341	-5.23
255546_at	putative CHP-rich zinc finger protein sim	---	AT4G01910	1.43	0.52	1.89	0.102348	0.272507	-5.23
263760_at	unknown protein ; supported by cDNA:	SULA	AT2G21280	-1.29	-0.36	-1.89	0.102427	0.272684	-5.23
260103_at	unknown protein	---	AT1G35430	1.16	0.21	1.89	0.102496	0.272804	-5.23
256521_at	AMP-binding enzyme, putative contains	---	AT1G66120	1.16	0.21	1.89	0.102489	0.272804	-5.23
266554_s_a	eukaryotic translation initiation factor 3 c	---	AT2G46280 /	-1.21	-0.27	-1.89	0.102513	0.272817	-5.23
251088_at	putative protein several hypothetical pro	---	AT5G01480	1.26	0.33	1.89	0.102633	0.272978	-5.23
249020_at	helicase-like protein	CHR4	AT5G44800	-1.19	-0.25	-1.89	0.102625	0.272978	-5.23

262382_at	virus resistance protein, putative similar	---	AT1G72920	2.14	1.09	1.89	0.102611	0.272978	-5.23
245013_at	ATPase epsilon subunit	---	---	-1.13	-0.17	-1.89	0.102605	0.272978	-5.23
262906_at	unknown protein contains similarity to he	---	AT1G59760	-1.22	-0.28	-1.89	0.102623	0.272978	-5.23
265536_at	unknown protein contains a domain rela	---	AT2G15880	1.42	0.50	1.89	0.102685	0.273085	-5.23
256223_at	unknown protein ;supported by full-lengt	emb1303	AT1G56200	-1.19	-0.25	-1.89	0.102702	0.273097	-5.23
262449_at	hypothetical protein similar to hypothetic	---	AT1G11160	1.13	0.17	1.89	0.102771	0.273248	-5.23
258717_at	unknown protein ; supported by cDNA:	SYP71	AT3G09740	1.13	0.17	1.89	0.102802	0.273300	-5.23
267426_at	hypothetical protein predicted by gensca	---	AT2G34820	1.15	0.20	1.89	0.102833	0.273350	-5.23
246958_at	putative protein similar to unknown prote	---	AT5G24690	-1.23	-0.30	-1.89	0.102856	0.273381	-5.23
260686_at	unknown protein ; supported by cDNA: g	---	AT1G17620	1.39	0.48	1.89	0.102869	0.273382	-5.23
263792_at	putative retroelement pol polyprotein	---	---	1.21	0.27	1.89	0.102928	0.273508	-5.24
259618_at	myb-related transcription factor (cpm10	MYB112	AT1G48000	1.24	0.31	1.89	0.103012	0.273699	-5.24
245295_at	hypothetical protein ; supported by cDN	---	AT4G16100	-1.20	-0.26	-1.89	0.10306	0.273794	-5.24
266064_at	expressed protein	---	AT2G18780	-1.22	-0.28	-1.88	0.103154	0.273948	-5.24
256254_at	hypothetical protein predicted by gensca	---	AT3G11290	-1.21	-0.28	-1.88	0.103146	0.273948	-5.24
266567_at	putative eukaryotic initiation factor 4, el	---	AT2G24050	-1.25	-0.32	-1.88	0.103151	0.273948	-5.24
250779_at	eukaryotic translation initiation factor 2 a	EIF2 ALPH	AT5G05470	-1.27	-0.34	-1.88	0.103184	0.273997	-5.24
257343_s_a	pseudogene, polyprotein similar to GB:	---	---	1.12	0.16	1.88	0.103207	0.274026	-5.24
266638_at	putative fibrillin ;supported by full-length	---	AT2G35490	-1.17	-0.23	-1.88	0.103299	0.274237	-5.24
250007_at	beta-amylase-like proten beta-amylase	BMY3	AT5G18670	1.83	0.87	1.88	0.103343	0.274268	-5.24
245824_at	hypothetical protein predicted by genem	ATPUP17	AT1G57943	1.26	0.33	1.88	0.103346	0.274268	-5.24
248202_at	unknown protein	---	AT5G54220	1.24	0.31	1.88	0.103326	0.274268	-5.24
252510_at	putative protein serine/threonine-specifi	---	AT3G46270	1.16	0.21	1.88	0.103398	0.274373	-5.24
250803_at	putative protein contains similarity to inc	---	AT5G04980	1.27	0.35	1.88	0.103422	0.274385	-5.24
254619_at	myb - like protein transforming protein r	MYB98	AT4G18770	1.16	0.21	1.88	0.103427	0.274385	-5.24
263978_at	unknown protein ;supported by full-lengt	MBF1A	AT2G42680	-1.15	-0.20	-1.88	0.103514	0.274522	-5.24
250735_at	putative protein similar to unknown prote	---	AT5G06280	-1.16	-0.22	-1.88	0.103497	0.274522	-5.24
261632_at	hypothetical protein predicted by genem	---	AT1G50120	1.18	0.24	1.88	0.103514	0.274522	-5.24
259360_at	hypothetical protein predicted by genem	---	AT1G13310	1.15	0.20	1.88	0.103601	0.274696	-5.24
258422_at	hypothetical protein predicted by gensca	---	AT3G16710	1.15	0.20	1.88	0.103604	0.274696	-5.24
250073_at	unknown protein ; supported by cDNA:	ENH1	AT5G17170	-1.37	-0.45	-1.88	0.10364	0.274760	-5.24
257399_at	putative OBP32pep protein	---	AT1G23690	-1.12	-0.16	-1.88	0.103716	0.274928	-5.24
266574_at	hypothetical protein predicted by gensca	---	AT2G23890	-1.36	-0.45	-1.88	0.103829	0.275196	-5.24
247275_at	beta-ureidopropionase	BETA-UP	AT5G64370	1.30	0.38	1.88	0.103846	0.275209	-5.24
258667_at	hypothetical protein	---	AT3G08750	-1.15	-0.20	-1.88	0.103928	0.275395	-5.24

246038_s_a	putative protein thiamin pyrophosphokir	atnudt20	AT5G19460 /	-1.23	-0.29	-1.88	0.10402	0.275607	-5.25
245484_at	enoyl-CoA hydratase like protein	ECHIA	AT4G16210	1.16	0.21	1.88	0.104088	0.275754	-5.25
262880_at	hypothetical protein contains similarity to	---	AT1G64880	-1.46	-0.55	-1.88	0.104122	0.275781	-5.25
248967_at	unknown protein ;supported by full-lengt	---	AT5G45350	1.21	0.27	1.88	0.104121	0.275781	-5.25
265778_at	unknown protein	---	AT2G07360	1.14	0.19	1.88	0.10415	0.275815	-5.25
260532_at	putative ATP-dependent RNA helicase	---	AT2G47330	-1.13	-0.18	-1.88	0.104159	0.275815	-5.25
246305_at	putative protein protein At2g40060 - Ara	---	AT3G51890	1.19	0.26	1.88	0.104239	0.275930	-5.25
261211_at	uridine diphosphate glucose epimerase	UGE1	AT1G12780	1.30	0.38	1.88	0.104217	0.275930	-5.25
249423_at	Expressed protein ; supported by full-ler	---	AT5G39785	1.22	0.28	1.88	0.104228	0.275930	-5.25
259301_at	hypothetical protein predicted by genscа	---	AT3G05110	-1.23	-0.30	-1.88	0.104264	0.275963	-5.25
257755_at	unknown protein ; supported by full-leng	---	AT3G18760	-1.30	-0.38	-1.88	0.104312	0.275994	-5.25
248397_at	unknown protein	---	AT5G52140	1.16	0.22	1.88	0.104293	0.275994	-5.25
257370_at	hypothetical protein predicted by genscа	---	AT2G35080	1.16	0.22	1.88	0.1043	0.275994	-5.25
262991_at	hypothetical protein predicted by genscа	BRX-LIKE	AT1G54180	1.13	0.18	1.88	0.104329	0.276009	-5.25
255486_at	AtMlo-h1-like protein	MLO1	AT4G02600	-1.17	-0.22	-1.88	0.10443	0.276243	-5.25
266340_at	similar to axi 1 protein from Nicotiana ta	---	AT2G01480	1.13	0.17	1.88	0.104495	0.276383	-5.25
256645_at	hypothetical protein predicted by genem	---	AT3G24250	1.14	0.18	1.88	0.104557	0.276435	-5.25
253260_at	hypothetical protein	---	AT4G34420 /	-1.17	-0.23	-1.88	0.104531	0.276435	-5.25
261052_at	hypothetical protein similar to hypothetic	---	AT1G01440	1.21	0.27	1.88	0.104566	0.276435	-5.25
259484_at	calcium-dependent protein kinase, puta	PEPKR1	AT1G12580	1.21	0.27	1.88	0.104556	0.276435	-5.25
255211_at	may be a pseudogene	---	---	1.13	0.18	1.87	0.104611	0.276435	-5.25
262378_at	CCAAT-binding factor B subunit homol	NF-YA3	AT1G72830	-1.23	-0.30	-1.88	0.104597	0.276435	-5.25
251600_at	protein kinase - like protein wall-associa	---	AT3G57710	-1.12	-0.17	-1.88	0.104589	0.276435	-5.25
252821_at	putative protein ;supported by full-lengt	---	AT4G39860	-1.44	-0.53	-1.87	0.104611	0.276435	-5.25
258252_at	putative polygalacturonase similar to po	---	AT3G15720	-1.36	-0.44	-1.87	0.104645	0.276459	-5.25
263762_at	putative kinesin heavy chain ; supporte	---	AT2G21380	-1.27	-0.35	-1.87	0.104636	0.276459	-5.25
265722_at	putative chlorophyll a/b binding protein	LHCB4.3	AT2G40100	1.29	0.37	1.87	0.104662	0.276473	-5.25
258806_at	unknown protein	---	AT3G04020	-1.30	-0.37	-1.87	0.104708	0.276529	-5.25
250015_at	N-acetylglucosamine-phosphate mutase	DRT101	AT5G18070	1.34	0.42	1.87	0.104707	0.276529	-5.25
247948_at	putative protein strong similarity to unkn	---	AT5G57130	1.20	0.26	1.87	0.104763	0.276644	-5.25
253672_at	mRNA cleavage factor subunit - like pro	CFIM-25	AT4G29820	-1.21	-0.27	-1.87	0.104822	0.276652	-5.25
260436_at	unknown protein	---	AT1G68140	1.20	0.27	1.87	0.104826	0.276652	-5.25
267399_at	hypothetical protein predicted by genscа	---	AT2G44195	-1.13	-0.17	-1.87	0.104839	0.276652	-5.25
263392_at	putative PttA-like transposon protein rela	---	---	-1.13	-0.18	-1.87	0.104811	0.276652	-5.25
248381_at	fructokinase 1 ; supported by cDNA: gi_	---	AT5G51830	1.36	0.44	1.87	0.104839	0.276652	-5.25

260881_at	unknown protein contains similarity to ca	---	AT1G21550	2.00	1.00	1.87	0.104819	0.276652	-5.25
265476_at	putative thioredoxin M ; supported by cI	ATHM3	AT2G15570	1.14	0.18	1.87	0.104888	0.276748	-5.25
255165_at	putative protein putative centromeric pr	---	---	1.30	0.38	1.87	0.104919	0.276798	-5.25
259416_at	Expressed protein ; supported by cDNA	---	AT1G02305	1.21	0.28	1.87	0.105012	0.276995	-5.25
254308_at	putative protein snRNP assembly factor	---	AT4G22410	-1.16	-0.21	-1.87	0.105018	0.276995	-5.25
266298_at	unknown protein ;supported by full-leng	---	AT2G29590	-1.19	-0.25	-1.87	0.105094	0.277165	-5.26
265999_at	unknown protein ; supported by cDNA:	---	AT2G24100	1.23	0.29	1.87	0.105117	0.277192	-5.26
254178_at	hypothetical protein	---	AT4G23880	-1.86	-0.89	-1.87	0.105197	0.277339	-5.26
257308_at	unknown protein	---	AT3G28120	1.13	0.17	1.87	0.105196	0.277339	-5.26
255577_at	putative hypoersensitive response prote	---	AT4G01410	1.68	0.75	1.87	0.105216	0.277357	-5.26
262935_at	hypothetical protein similar to putative tr	AtOCT5	AT1G79410	1.54	0.62	1.87	0.105251	0.277385	-5.26
263514_at	putative poly(ADP-ribose) glycohydrolas	---	AT2G31860	1.16	0.22	1.87	0.105251	0.277385	-5.26
267377_at	beta-ketoacyl-CoA synthase (FIDDLEHE	KCS10	AT2G26250	1.38	0.46	1.87	0.105285	0.277443	-5.26
265968_at	putative protein translocase ; supported	ATTIM17-2	AT2G37410	-1.26	-0.34	-1.87	0.105312	0.277482	-5.26
249699_at	putative protein similar to unknown prote	---	AT5G35540	1.12	0.17	1.87	0.105461	0.277842	-5.26
247130_at	putative protein contains similarity to nu	---	AT5G66180	-1.34	-0.42	-1.87	0.105561	0.277881	-5.26
255637_at	hypothetical protein	---	AT4G00750	1.25	0.32	1.87	0.105537	0.277881	-5.26
247898_at	F-box protein ZTL/LFK1/ADO1, AtFBX2	ZTL	AT5G57360	-1.16	-0.22	-1.87	0.105501	0.277881	-5.26
264607_at	putative K+ channel, beta subunit simila	KAB1	AT1G04690	-1.13	-0.17	-1.87	0.105552	0.277881	-5.26
260040_at	Expressed protein ; supported by full-ler	IDA	AT1G68765	2.01	1.01	1.87	0.105542	0.277881	-5.26
256012_at	unknown protein similar to dimethylanilir	FMO1	AT1G19250	3.40	1.77	1.87	0.105508	0.277881	-5.26
262078_at	hypothetical protein predicted by gensca	CW7	AT1G59520	-1.13	-0.18	-1.87	0.10552	0.277881	-5.26
257289_at	hypothetical protein	---	AT3G29690	1.14	0.19	1.87	0.105607	0.277971	-5.26
246580_at	ABC transporter, putative contains Pfar	---	AT1G31770	-1.21	-0.27	-1.87	0.105626	0.277989	-5.26
261170_at	growth regulator protein similar to GB:X	---	AT1G04910	-1.16	-0.22	-1.87	0.105644	0.278005	-5.26
248579_at	mitotic checkpoint protein-like	---	AT5G49880	-1.24	-0.31	-1.87	0.105664	0.278025	-5.26
259135_at	hypothetical protein predicted by genem	RAD9	AT3G05480	1.25	0.32	1.87	0.105689	0.278046	-5.26
253108_at	putative bZIP transcription factor Dc3 p	FD	AT4G35900	-1.32	-0.40	-1.87	0.105697	0.278046	-5.26
265361_at	putative retroelement pol polyprotein	---	---	1.15	0.20	1.87	0.10571	0.278049	-5.26
267372_at	putative protein kinase contains a protei	ARSK1	AT2G26290	1.72	0.78	1.87	0.105765	0.278163	-5.26
251417_at	putative protein prib5, Ribes nigrum, EM	AT3G6042	---	1.13	0.18	1.87	0.105778	0.278165	-5.26
264472_at	hypothetical protein predicted by genem	SWEETIE	AT1G67140	-1.21	-0.27	-1.87	0.10581	0.278216	-5.26
254042_at	xyloglucan endo-1,4-beta-D-glucanase	XTR6	AT4G25810	2.02	1.02	1.87	0.105858	0.278280	-5.26
267165_at	putative receptor-like protein kinase sam	RLK	AT2G37710	1.45	0.53	1.87	0.10585	0.278280	-5.26
267454_at	putative U5 small nuclear ribonucleopro	---	AT2G33730	-1.15	-0.20	-1.87	0.105891	0.278333	-5.26

260840_at	hypothetical protein similar to hypothetic	---	AT1G29050	-1.20	-0.27	-1.87	0.105941	0.278400	-5.26
267525_at	putative glycine-rich protein	---	AT2G30560	1.12	0.17	1.87	0.10594	0.278400	-5.26
261563_at	polyphosphoinositide binding protein, p	---	AT1G01630	1.18	0.24	1.87	0.105994	0.278410	-5.26
249407_at	putative protein predicted proteins, Arat	---	AT5G40320	1.14	0.19	1.87	0.105961	0.278410	-5.26
257662_at	low affinity calcium antiporter CAX2 alm	CAX2	AT3G13320	1.15	0.20	1.87	0.10599	0.278410	-5.26
251099_at	putative protein KIAA0132 - Homo sapi	---	AT5G01660	-1.15	-0.20	-1.87	0.105988	0.278410	-5.26
249164_at	U2 snRNP auxiliary factor, small subun	U2AF35B	AT5G42820	-1.19	-0.25	-1.87	0.106077	0.278598	-5.26
249466_at	ribosomal protein L5 - like ribosomal pr	RPL5B	AT5G39740	-1.27	-0.34	-1.87	0.106096	0.278615	-5.26
262432_at	unknown protein	---	AT1G47530	1.33	0.41	1.87	0.10611	0.278619	-5.26
250227_at	FtsJ (dbj|BAA83750.1)	---	AT5G13830	1.19	0.25	1.86	0.106153	0.278700	-5.26
245776_at	hypothetical protein predicted by gensca	---	AT1G30260	1.31	0.39	1.86	0.106218	0.278839	-5.27
246153_s_a	RAN1 small Ras-like GTP-binding nucle	RAN-1	AT5G20010 /	-1.29	-0.36	-1.86	0.106336	0.279109	-5.27
247890_at	cyclic nucleotide and calmodulin-regulat	ATCNGC5	AT5G57940	-1.19	-0.25	-1.86	0.106345	0.279109	-5.27
259139_at	hypothetical protein similar to F16N3.1 (	---	AT3G10240	1.15	0.21	1.86	0.106437	0.279319	-5.27
265471_at	putative peroxidase ATP2a ;supported	---	AT2G37130	-1.44	-0.53	-1.86	0.106551	0.279585	-5.27
254776_at	3-hydroxyisobutyryl-coenzyme A hydrol	---	AT4G13360	-1.12	-0.17	-1.86	0.106662	0.279811	-5.27
261494_at	homeobox transcription factor Hox7, pu	HB-1	AT1G28420	-1.18	-0.24	-1.86	0.106661	0.279811	-5.27
260424_at	putative receptor-like protein kinase cor	---	AT1G72460	1.15	0.21	1.86	0.106754	0.279988	-5.27
249453_at	v-SNARE AtVTI1a	SGR4	AT5G39510	-1.13	-0.18	-1.86	0.106749	0.279988	-5.27
264372_at	lactoylglutathione lyase-like protein Sim	ATGLX1	AT1G11840	-1.26	-0.33	-1.86	0.106778	0.280020	-5.27
252590_at	putative protein kinase NPK1-related pr	---	AT3G45670	1.16	0.22	1.86	0.106795	0.280032	-5.27
251331_s_a	tubulin gamma-1 chain	TUBG1	AT3G61650 /	-1.46	-0.54	-1.86	0.106873	0.280203	-5.27
246350_at	hypothetical protein predicted by genem	---	AT1G16650	1.19	0.25	1.86	0.106967	0.280418	-5.27
262807_at	unknown protein strong similarity to gi|3	---	AT1G11740	1.21	0.28	1.86	0.106997	0.280465	-5.27
262451_at	receptor-associated kinase isolog	SUB	AT1G11130	1.29	0.37	1.86	0.107055	0.280585	-5.27
261732_at	hypothetical protein predicted by genem	---	AT1G47770	1.16	0.21	1.86	0.10708	0.280618	-5.27
246258_at	PPR-repeat protein, putative contains n	---	AT1G31840	-1.15	-0.20	-1.86	0.107158	0.280759	-5.27
253157_at	putative protein DNA helicase TPS1, Sa	RecQl3	AT4G35740	-1.19	-0.25	-1.86	0.107158	0.280759	-5.27
249198_s_a	putative protein similar to unknown prote	---	AT5G42350 /	1.16	0.21	1.86	0.107189	0.280805	-5.27
260225_at	putative glutathione S-transferase simila	GSTU10	AT1G74590	1.92	0.94	1.86	0.107263	0.280969	-5.27
256140_at	hypothetical protein contains similarity to	---	AT1G48650	-1.25	-0.32	-1.86	0.107284	0.280992	-5.27
259337_at	putative cationic amino acid transporter	CAT4	AT3G03720	1.15	0.20	1.86	0.107311	0.281029	-5.28
261790_at	unknown protein ; supported by full-leng	---	AT1G16000	-1.26	-0.34	-1.86	0.107353	0.281107	-5.28
257126_at	E2, ubiquitin-conjugating enzyme, putat	UBC19	AT3G20060	1.21	0.28	1.86	0.107367	0.281112	-5.28
263010_at	T76725 come from this gene.	---	AT1G23330	1.14	0.19	1.86	0.107403	0.281174	-5.28

255359_at	putative glucose-6-phosphate/phosphat	---	AT4G03950	1.16	0.21	1.86	0.107436	0.281226	-5.28
266135_at	putative transcription factor IIIB 70 KD s	---	AT2G45100	-1.29	-0.36	-1.86	0.107462	0.281264	-5.28
257694_at	nucleolar protein, putative nucleolar pro	---	AT3G12860	-1.15	-0.20	-1.86	0.107475	0.281265	-5.28
245375_at	NAK like protein kinase	---	AT4G17660	1.17	0.23	1.86	0.107516	0.281340	-5.28
260685_at	Expressed protein ; supported by full-ler	GLYR2	AT1G17650	-1.24	-0.31	-1.86	0.107573	0.281456	-5.28
245718_at	putative protein	---	AT5G04110	-1.20	-0.27	-1.86	0.107597	0.281487	-5.28
254461_at	receptor kinase - like protein SRK3 rece	---	AT4G21230	1.24	0.31	1.86	0.107659	0.281564	-5.28
266324_at	putative rac GTPase activating protein	---	AT2G46710	-1.69	-0.76	-1.86	0.107663	0.281564	-5.28
252591_at	putative protein senescence-associated	TET3	AT3G45600	-1.30	-0.38	-1.86	0.107639	0.281564	-5.28
249236_at	putative protein similar to unknown prote	---	AT5G41950	1.14	0.18	1.85	0.107686	0.281590	-5.28
248857_at	putative protein contains similarity to AT	---	AT5G46640	1.34	0.42	1.85	0.10774	0.281700	-5.28
253821_at	extensin-like protein extensin-like prote	---	AT4G28380	1.17	0.22	1.85	0.107973	0.282260	-5.28
257320_at	hypothetical protein	---	AT2G07749	-1.18	-0.24	-1.85	0.107979	0.282260	-5.28
255947_at	hypothetical protein contains Pfam profil	---	AT1G22040	-1.16	-0.21	-1.85	0.108048	0.282408	-5.28
258302_at	hypothetical protein predicted by genem	---	---	1.14	0.19	1.85	0.108065	0.282420	-5.28
265922_at	putative sugar transporter	---	AT2G18480	-1.15	-0.20	-1.85	0.10816	0.282602	-5.28
246502_at	stearoyl-acyl carrier protein desaturase	---	AT5G16240	-1.23	-0.30	-1.85	0.108158	0.282602	-5.28
265541_at	hypothetical protein predicted by gensca	SQN	---	1.14	0.19	1.85	0.108292	0.282916	-5.28
264219_at	unknown protein contains similarity to try	---	AT1G60420	-1.25	-0.32	-1.85	0.108363	0.283070	-5.28
254785_at	putative pollen surface protein endospe	FLA2	AT4G12730	1.88	0.91	1.85	0.108429	0.283082	-5.29
259892_at	germin-like protein similar to germin pre	GER1	AT1G72610	1.95	0.96	1.85	0.108387	0.283082	-5.28
265296_at	hypothetical protein predicted by genefin	---	AT2G14060	1.14	0.19	1.85	0.108419	0.283082	-5.29
266113_x_a	hypothetical protein predicted by gensca	---	---	1.19	0.25	1.85	0.108426	0.283082	-5.29
248269_at	putative protein contains similarity to acy	ACBP1	AT5G53470	-1.20	-0.26	-1.85	0.10843	0.283082	-5.29
246496_at	putative protein KIAA1468 - Homo sapi	---	AT5G16210	-1.17	-0.23	-1.85	0.108513	0.283206	-5.29
256767_at	hypothetical protein predicted by genem	---	AT3G13680	1.15	0.20	1.85	0.108515	0.283206	-5.29
256168_at	receptor protein kinase, putative contai	---	AT1G51805	-1.41	-0.50	-1.85	0.108492	0.283206	-5.29
254661_at	unknown protein multidrug resistance p	---	AT4G18260	-1.17	-0.23	-1.85	0.108563	0.283298	-5.29
247962_at	protein kinase MEK1 homolog	MKK6	AT5G56580	1.15	0.20	1.85	0.108615	0.283338	-5.29
258124_at	Expressed protein ; supported by cDNA	---	AT3G18215	-1.27	-0.34	-1.85	0.108605	0.283338	-5.29
249465_at	AIG2 - like protein AIG2, Arabidopsis th	AIG2L	AT5G39720	1.18	0.23	1.85	0.108605	0.283338	-5.29
262489_at	unknown protein EST gb|T21171 comes	---	AT1G21830	1.23	0.29	1.85	0.108665	0.283408	-5.29
262361_at	unknown protein contains similarity to fe	GTE3	AT1G73150	-1.15	-0.21	-1.85	0.108667	0.283408	-5.29
254890_at	phospholipid hydroperoxide glutathione	ATGPX6	AT4G11600	1.16	0.22	1.85	0.108697	0.283449	-5.29
257526_s_a	hypothetical protein similar to putative p	---	AT3G09330 /	1.14	0.18	1.85	0.108707	0.283449	-5.29

247418_at	glutaredoxin-like protein ; supported by	---	AT5G63030	1.21	0.28	1.85	0.108743	0.283511	-5.29
247262_at	putative protein contains similarity to glu	AtFAAH	AT5G64440	1.17	0.22	1.85	0.10877	0.283547	-5.29
252978_at	galactosidase like protein ss-1,4-exoga	BGAL14	AT4G38590	1.21	0.27	1.85	0.108808	0.283615	-5.29
253013_at	heat shock protein 70 like protein dnaK	mtHsc70-1	AT4G37910	-1.33	-0.41	-1.85	0.108924	0.283859	-5.29
255862_at	hypothetical protein predicted by genefi	---	AT2G30300	1.16	0.21	1.85	0.108927	0.283859	-5.29
255676_at	putative beta-amylase similar to the fam	BAM2	AT4G00490	-1.42	-0.50	-1.85	0.109007	0.283966	-5.29
257671_at	hypothetical protein predicted by gensca	---	AT3G20450	1.19	0.25	1.85	0.109014	0.283966	-5.29
255717_at	coded for by A. thaliana cDNA H76622	---	AT4G00350	-1.15	-0.20	-1.85	0.109023	0.283966	-5.29
250121_at	protein kinase-like protein	---	AT5G16500	1.13	0.18	1.85	0.109004	0.283966	-5.29
254136_at	putative protein various predicted prote	---	AT4G24860	1.15	0.20	1.85	0.10903	0.283966	-5.29
259333_at	putative auxin-independent growth prom	EDA30	AT3G03810	1.18	0.24	1.85	0.109078	0.284059	-5.29
245432_at	putative serine protease-like protein	---	AT4G17100	-1.13	-0.18	-1.85	0.109113	0.284116	-5.29
253569_at	receptor kinase - like protein receptor k	---	AT4G31250	-1.20	-0.26	-1.85	0.10913	0.284130	-5.29
250692_at	putative protein strong similarity to unkn	---	AT5G06560	1.17	0.23	1.85	0.109167	0.284192	-5.29
255953_at	transcription factor identical to transcript	TGA3	AT1G22070	-1.22	-0.29	-1.85	0.109187	0.284212	-5.29
262821_at	unknown protein EST gb|F14156 comes	---	AT1G11800	-1.11	-0.16	-1.85	0.109224	0.284276	-5.29
258825_at	unknown protein	---	AT3G07180	-1.14	-0.19	-1.85	0.109252	0.284317	-5.29
258457_at	Expressed protein ; supported by full-ler	IGPD	AT3G22425	-1.21	-0.28	-1.84	0.109304	0.284322	-5.29
265255_at	unknown protein ; supported by cDNA:	---	AT2G28420	-1.29	-0.37	-1.84	0.1093	0.284322	-5.29
264750_at	hypothetical protein predicted by gensca	---	AT1G22870	1.14	0.18	1.84	0.1093	0.284322	-5.29
255555_at	putative protein transport factor ; suppo	---	AT4G01810	1.18	0.24	1.84	0.109285	0.284322	-5.29
251217_at	Sar1-like GTP binding protein small GT	---	AT3G62560	-1.17	-0.23	-1.84	0.109346	0.284366	-5.29
252710_at	cellulase-like protein cellulase, Sambuc	AtGH9A4	AT3G43860	1.14	0.19	1.84	0.109335	0.284366	-5.29
253610_at	putative protein ; supported by cDNA: g	VEL1	AT4G30200	1.18	0.24	1.84	0.109363	0.284378	-5.29
266928_at	putative phosphomannomutase ;suppo	PMM	AT2G45790	-1.23	-0.30	-1.84	0.109392	0.284423	-5.29
246437_at	putative protein hypersensitivity-related	---	AT5G17540	1.14	0.19	1.84	0.109407	0.284427	-5.29
264175_at	unknown protein Similar to rice chalcon	---	AT1G02050	-1.20	-0.26	-1.84	0.109471	0.284465	-5.29
264700_at	hypothetical protein predicted by genem	---	AT1G70100	-1.20	-0.26	-1.84	0.10948	0.284465	-5.29
247042_at	putative protein similar to unknown prote	---	AT5G67220	1.15	0.20	1.84	0.109481	0.284465	-5.29
252690_at	putative protein	---	---	1.21	0.28	1.84	0.109484	0.284465	-5.29
261063_at	transcription factor scarecrow-like 14, p	---	AT1G07520	1.70	0.77	1.84	0.109455	0.284465	-5.29
263593_at	hypothetical protein predicted by gensca	EMB975	AT2G01860	-1.20	-0.26	-1.84	0.109499	0.284473	-5.29
251319_at	putative protein POSSIBLE APOSPOR	---	AT3G61610	1.23	0.30	1.84	0.109518	0.284489	-5.29
250707_at	putative protein similar to unknown prote	MEE60	AT5G05950	-1.23	-0.30	-1.84	0.109597	0.284662	-5.30
259175_at	unknown protein	---	AT3G01560	-1.19	-0.25	-1.84	0.109616	0.284678	-5.30

246161_at	putative protein predicted proteins, Aral	JAZ12	AT5G20900	-1.23	-0.30	-1.84	0.109673	0.284794	-5.30
257742_at	hypothetical protein predicted by genem	SDH2-1	AT3G27380	1.16	0.21	1.84	0.109728	0.284907	-5.30
260903_at	polygalacturonase PG1, putative simila	---	AT1G02460	1.86	0.90	1.84	0.109745	0.284918	-5.30
267002_s_a	putative photosystem II type I chlorophy	LHB1B1	AT2G34420 /	-1.12	-0.16	-1.84	0.109777	0.284967	-5.30
260562_at	putative protein kinase contains a protei	---	AT2G43850	-1.22	-0.29	-1.84	0.109823	0.285055	-5.30
266211_at	putative retroelement pol polyprotein	---	---	1.16	0.21	1.84	0.109846	0.285081	-5.30
259254_at	putative P-protein: chorismate mutase,	ADT2	AT3G07630	-1.18	-0.24	-1.84	0.109894	0.285141	-5.30
251470_at	putative protein hypothetical protein At2	---	AT3G59570	1.20	0.26	1.84	0.109893	0.285141	-5.30
254120_at	putative mitochondrial uncoupling prote	DIC2	AT4G24570	2.79	1.48	1.84	0.109913	0.285160	-5.30
246553_at	putative protein hypothetical protein T2(	EDL1	AT5G15440	-1.17	-0.23	-1.84	0.109939	0.285193	-5.30
260286_at	putative acetylornithine transaminase si	WIN1	AT1G80600	-1.20	-0.26	-1.84	0.109951	0.285193	-5.30
267273_at	putative non-LTR retroelement reverse t	---	AT2G02520	1.12	0.17	1.84	0.110029	0.285361	-5.30
265020_at	putative cytochrome P450 similar to GE	CYP86C1	AT1G24540	1.14	0.18	1.84	0.110043	0.285366	-5.30
262557_at	photosystem I subunit III precursor, put	---	AT1G31330 /	-1.16	-0.22	-1.84	0.110131	0.285561	-5.30
264713_at	hypothetical protein Similar to N. tabacu	---	AT1G09820	-1.17	-0.23	-1.84	0.11016	0.285605	-5.30
254260_at	hypothetical protein	---	AT4G23440	1.26	0.33	1.84	0.110233	0.285730	-5.30
249944_at	NAM (no apical meristem)-like protein ;	anac089	AT5G22290	-1.43	-0.52	-1.84	0.11023	0.285730	-5.30
259414_at	hypothetical protein contains Pfam profil	---	AT1G02420	-1.19	-0.25	-1.84	0.110375	0.286065	-5.30
249966_at	putative protein COLD-INDUCIBLE RN	---	AT5G19030	-1.32	-0.40	-1.84	0.110414	0.286132	-5.30
262576_at	unknown protein ESTs gb|R90323, gb|I	---	AT1G15280	-1.13	-0.18	-1.84	0.110466	0.286225	-5.30
263263_at	putative guanylate binding protein	---	AT2G38840	1.21	0.27	1.84	0.110475	0.286225	-5.30
254565_at	replication A protein-like replication prot	---	AT4G19130	-1.12	-0.17	-1.84	0.110488	0.286226	-5.30
247080_at	20S proteasome subunit PAD2 (gb|AAC	PAD2	AT5G66140	-1.17	-0.22	-1.84	0.110509	0.286249	-5.30
259163_at	putative protein kinase similar to ATMR	---	AT3G01490	-1.21	-0.27	-1.84	0.110562	0.286291	-5.30
246807_at	ion channel - like protein ligand gated c	GLR2.1	AT5G27100	1.23	0.30	1.84	0.110563	0.286291	-5.30
266073_at	putative signal recognition particle recep	---	AT2G18770	-1.15	-0.21	-1.84	0.110542	0.286291	-5.30
261833_at	ATP citrate-lyase, putative similar to AT	ACLA-1	AT1G10670	1.16	0.21	1.84	0.110633	0.286336	-5.30
246117_at	CAF-like protein CAF protein - Arabidop	DCL4	AT5G20320	-1.25	-0.32	-1.84	0.110609	0.286336	-5.30
249830_at	dihydroorotate dehydrogenase precurso	PYRD	AT5G23300	-1.33	-0.41	-1.84	0.110646	0.286336	-5.30
248096_at	embryo-specific protein 1; Ca2+-binding	---	AT5G55240	1.15	0.20	1.84	0.110655	0.286336	-5.30
AFFX-Athal-	Arabidopsis thaliana /REF=M65137 /DE	---	---	-1.14	-0.19	-1.84	0.110646	0.286336	-5.30
252497_at	putative protein several putative protein	---	AT3G46800	-1.13	-0.18	-1.84	0.110607	0.286336	-5.30
250285_at	putative protein GCN4-complementing	SFC	AT5G13300	-1.26	-0.34	-1.84	0.110673	0.286349	-5.30
260112_at	unknown protein similar to unknown pro	---	AT1G63310	1.21	0.27	1.84	0.110701	0.286356	-5.30
252418_at	hypothetical protein	---	AT3G47490	-1.20	-0.27	-1.84	0.110699	0.286356	-5.30

250199_at	putative protein contains similarity to lipa	MPL1	AT5G14180	1.66	0.73	1.84	0.110843	0.286691	-5.31
264507_at	Expressed protein ; supported by cDNA	NIMIN-3	AT1G09415	1.21	0.28	1.83	0.11087	0.286728	-5.31
257545_at	hypothetical protein predicted by genscan	---	AT3G23200	1.24	0.31	1.83	0.110924	0.286836	-5.31
261406_at	unknown protein contains similarity to se	NRP2	AT1G18800	-1.26	-0.33	-1.83	0.110949	0.286848	-5.31
256344_at	C2H2-type zinc finger protein, putative	TFIIIA	AT1G72050	-1.19	-0.25	-1.83	0.110954	0.286848	-5.31
253289_at	putative protein F10M10_100, Arabidop	---	AT4G34320	-1.16	-0.21	-1.83	0.110976	0.286872	-5.31
246319_at	putative protein HYPOTHETICAL PRO	---	AT3G56680	-1.15	-0.20	-1.83	0.111015	0.286907	-5.31
251475_at	putative protein other hypothetical prote	---	AT3G59660	1.28	0.36	1.83	0.111002	0.286907	-5.31
266987_at	unknown protein	---	AT2G39280	-1.12	-0.17	-1.83	0.111043	0.286948	-5.31
266926_at	unknown protein predicted by genscan a	---	AT2G46000	1.21	0.28	1.83	0.111074	0.286995	-5.31
265519_at	hypothetical protein	---	AT2G06040	-1.15	-0.20	-1.83	0.111223	0.287316	-5.31
259084_at	putative inner mitochondrial membrane	ATTIM23-3	AT3G04800	1.16	0.21	1.83	0.111214	0.287316	-5.31
260421_at	acid phosphatase, putative similar to G	SBH1	AT1G69640	-1.16	-0.21	-1.83	0.111311	0.287511	-5.31
248852_at	unknown protein	---	AT5G46560	-1.12	-0.17	-1.83	0.111336	0.287529	-5.31
264465_at	SKP1/ASK1 (At18), putative similar to S	ASK18	AT1G10230	-1.13	-0.18	-1.83	0.111343	0.287529	-5.31
264445_at	unknown protein similar to ESTs gb|T42	---	AT1G27290	1.29	0.37	1.83	0.11136	0.287539	-5.31
259164_at	hypothetical protein contains bromodon	ATBET10	AT3G01770	-1.23	-0.29	-1.83	0.111457	0.287566	-5.31
248352_at	low-temperature-induced 65 kD protein	LTI65	AT5G52300	1.66	0.73	1.83	0.111458	0.287566	-5.31
264103_at	unknown protein	---	AT2G13660	-1.17	-0.23	-1.83	0.111427	0.287566	-5.31
258230_s_a	hypothetical protein similar to hypotheti	ARI13	AT3G27710 /	1.13	0.18	1.83	0.111443	0.287566	-5.31
258035_at	putative Ca2+-transporting ATPase simi	ACA9	AT3G21180	1.18	0.23	1.83	0.111394	0.287566	-5.31
248464_at	putative protein similar to unknown prote	---	AT5G51160	1.23	0.29	1.83	0.111437	0.287566	-5.31
256780_at	RNase L inhibitor, putative similar to RN	ATRLI1	AT3G13640	-1.15	-0.21	-1.83	0.111448	0.287566	-5.31
247951_at	oxysterol-binding protein-like	ORP4C	AT5G57240	-1.15	-0.20	-1.83	0.111487	0.287574	-5.31
261376_at	hypothetical protein contains similarity to	---	AT1G18660	-1.17	-0.23	-1.83	0.111479	0.287574	-5.31
251950_at	zinc finger - like protein Zat11 zinc finge	---	AT3G53600	2.26	1.18	1.83	0.111523	0.287634	-5.31
257033_at	metalloprotease, putative similar to met	ATPREP1	AT3G19170	-1.34	-0.43	-1.83	0.111554	0.287667	-5.31
247095_at	dehydrin RAB18-like protein (sp P30185	RAB18	AT5G66400	-1.43	-0.51	-1.83	0.111561	0.287667	-5.31
256273_at	senescence-assocated protein, putative	TET6	AT3G12090	-1.19	-0.25	-1.83	0.111634	0.287823	-5.31
254374_at	hypothetical protein ;supported by full-le	---	AT4G21780	-1.14	-0.18	-1.83	0.111664	0.287868	-5.31
257556_at	hypothetical protein predicted by genem	---	AT3G28100	1.45	0.54	1.83	0.111711	0.287956	-5.31
245989_s_a	polyubiquitin (UBQ4) identical to GI:176	UBQ4	AT5G20620	-1.17	-0.23	-1.83	0.111813	0.288188	-5.31
247692_s_a	histone H4 - like protein histone H4, Ze	---	AT5G59690 /	-1.34	-0.43	-1.83	0.111837	0.288215	-5.31
245853_at	putative protein predicted protein At2g2	---	AT5G13500	1.21	0.28	1.83	0.111879	0.288293	-5.32
252565_at	actin depolymerizing factor 2 (ADF2) ; s	ADF2	AT3G46000	-1.13	-0.17	-1.83	0.111893	0.288296	-5.32

262580_at	hypothetical protein Similar to gb|U4071	---	AT1G15330	1.23	0.29	1.83	0.111911	0.288308	-5.32
245283_at	Expressed protein ; supported by cDNA	AT-HSFA5	AT4G13980	1.17	0.22	1.83	0.111979	0.288453	-5.32
254577_at	putative protein ;supported by full-lengt	---	AT4G19450	-1.24	-0.31	-1.83	0.112026	0.288541	-5.32
265475_at	ferredoxin--nitrite reductase ; supported	NIR1	AT2G15620	-1.25	-0.32	-1.83	0.112045	0.288556	-5.32
250208_at	unknown protein ;supported by full-leng	anac084	AT5G14000	1.55	0.63	1.83	0.112102	0.288606	-5.32
267617_at	heme oxygenase 1 (HO1) identical to G	TED4	AT2G26670	1.27	0.34	1.83	0.112099	0.288606	-5.32
261449_at	putative ATPase similar to GB:AAF2835	---	AT1G21120	1.29	0.37	1.83	0.112086	0.288606	-5.32
257612_at	unknown protein	ARO4	AT3G26600	1.43	0.52	1.83	0.112332	0.289164	-5.32
249729_at	6-phosphogluconolactonase-like protein	---	AT5G24410	1.16	0.22	1.83	0.112372	0.289236	-5.32
265389_at	putative riboflavin synthase alpha chain	---	AT2G20690	-1.18	-0.24	-1.83	0.112424	0.289337	-5.32
246885_at	putative protein predicted protein, Arabi	---	AT5G26230	1.47	0.56	1.82	0.112488	0.289468	-5.32
265846_at	putative serine carboxypeptidase II	scpl28	AT2G35770	-1.17	-0.22	-1.82	0.112624	0.289787	-5.32
262233_at	hypothetical protein contains similarity to	CHR18	AT1G48310	-1.14	-0.19	-1.82	0.112657	0.289838	-5.32
263222_at	putative protein kinase Strong similarity	---	AT1G30640	1.25	0.32	1.82	0.112678	0.289860	-5.32
256653_at	hypothetical protein predicted by genem	---	AT3G18870	-1.16	-0.21	-1.82	0.112712	0.289914	-5.32
248672_at	disease resistance protein	---	AT5G48770	1.18	0.23	1.82	0.112728	0.289922	-5.32
250352_at	beta-adaptin-like protein A ; supported l	---	AT5G11490	-1.13	-0.17	-1.82	0.112762	0.289977	-5.32
260267_at	very-long-chain fatty acid condensing e	KCS6	AT1G68530	1.38	0.47	1.82	0.11283	0.290065	-5.32
262371_at	putative glycosyl transferase contains P	---	AT1G73160	1.14	0.19	1.82	0.112834	0.290065	-5.32
247373_at	unknown protein ;supported by full-leng	---	AT5G63150	-1.19	-0.25	-1.82	0.112809	0.290065	-5.32
260886_at	hypothetical protein contains similarity to	---	AT1G29200	1.13	0.18	1.82	0.113054	0.290570	-5.33
263306_at	putative serine carboxypeptidase II	SCPL43	AT2G12480	1.14	0.20	1.82	0.113056	0.290570	-5.33
250221_at	protoporphyrinogen oxidase - like prote	HEMG2	AT5G14220	-1.26	-0.33	-1.82	0.113074	0.290583	-5.33
257690_at	unknown protein contains similarity to a	---	AT3G12830	1.47	0.56	1.82	0.113091	0.290594	-5.33
247454_at	unknown protein	---	AT5G62440	-1.33	-0.41	-1.82	0.113173	0.290760	-5.33
251911_at	putative C2H2-type zinc finger protein p	---	AT3G53820	1.16	0.21	1.82	0.113181	0.290760	-5.33
265006_at	unknown protein similar to small zinc fin	TIM13	AT1G61570	-1.40	-0.48	-1.82	0.113196	0.290767	-5.33
252023_at	putative protein various predicted prote	---	AT3G52920	1.44	0.52	1.82	0.113239	0.290817	-5.33
253516_at	hypothetical protein	---	AT4G31360	-1.26	-0.33	-1.82	0.113241	0.290817	-5.33
245986_at	protein kinase-like protein kinase 1 PnP	PBS1	AT5G13160	1.13	0.18	1.82	0.113289	0.290853	-5.33
247944_at	putative protein similar to unknown prote	---	AT5G57100	-1.19	-0.25	-1.82	0.113294	0.290853	-5.33
252883_at	GTP-binding - like protein GTP-binding	---	AT4G39520	-1.21	-0.28	-1.82	0.113287	0.290853	-5.33
256098_at	unknown protein similar to 6-phosphoglu	---	AT1G13700	1.34	0.42	1.82	0.113348	0.290862	-5.33
255775_at	hypothetical protein predicted by gensca	RBL12	AT1G18600	1.15	0.20	1.82	0.113337	0.290862	-5.33
258875_at	unknown protein ;supported by full-leng	---	AT3G03160	1.23	0.29	1.82	0.113324	0.290862	-5.33

260631_at	hypothetical protein predicted by genem	---	AT1G62350	-1.18	-0.24	-1.82	0.113316	0.290862	-5.33
259358_at	hypothetical protein similar to putative g	GATL3	AT1G13250	1.56	0.65	1.82	0.113397	0.290888	-5.33
253049_at	putative protein ; supported by cDNA: gi	MEE59	AT4G37300	-1.37	-0.45	-1.82	0.113385	0.290888	-5.33
259472_at	hypothetical protein contains similarity t	---	AT1G18910	1.15	0.20	1.82	0.113383	0.290888	-5.33
247612_at	ATPase - like protein ATPase, Solanum	---	AT5G60730	-1.17	-0.22	-1.82	0.113457	0.290911	-5.33
265129_at	putative zinc finger protein similar to zin	SUF4	AT1G30970	1.16	0.22	1.82	0.11345	0.290911	-5.33
245898_at	ser/thr specific protein kinase-like prote	---	AT5G11020	-1.20	-0.26	-1.82	0.113422	0.290911	-5.33
263746_at	putative retroelement pol polyprotein	---	---	-1.14	-0.19	-1.82	0.113447	0.290911	-5.33
262504_at	putative protein disulfide isomerase pre	ATPDIL1-1	AT1G21750	1.25	0.33	1.82	0.113475	0.290925	-5.33
263125_at	hypothetical protein predicted by genem	---	AT1G78470	1.15	0.20	1.82	0.113515	0.290995	-5.33
245187_s_a	F12A21.17 similar to signal recognition	---	AT1G67650 /	1.15	0.20	1.82	0.113568	0.291100	-5.33
265381_at	putative non-LTR retroelement reverse t	---	---	1.22	0.29	1.82	0.113646	0.291267	-5.33
261396_at	hypothetical protein contains similarity t	---	AT1G79800	1.16	0.22	1.82	0.113674	0.291305	-5.33
256095_at	hypothetical protein contains Pfam profil	---	AT1G13630	-1.32	-0.40	-1.82	0.113706	0.291354	-5.33
249192_at	brain and reproductive organ-expressed	---	AT5G42470	-1.12	-0.17	-1.82	0.113722	0.291362	-5.33
252163_at	hypothetical protein	---	AT3G50610	1.16	0.22	1.82	0.113759	0.291397	-5.33
256017_at	unknown protein ;supported by full-lengt	JAZ1	AT1G19180	1.59	0.67	1.82	0.113761	0.291397	-5.33
261747_at	unknown protein similar to putative endo	---	AT1G08350	-1.21	-0.28	-1.82	0.113826	0.291498	-5.33
266709_at	unknown protein ;supported by full-leng	ATSPP	AT2G03120	1.23	0.30	1.82	0.113815	0.291498	-5.33
257079_at	unknown protein	---	AT3G15240	1.13	0.18	1.82	0.113892	0.291633	-5.33
261957_at	methionine/cystathionine gamma lyase	ATMGL	AT1G64660	1.36	0.44	1.82	0.113925	0.291685	-5.33
255051_at	RNA-directed DNA polymerase -like pro	---	---	1.26	0.33	1.82	0.113956	0.291732	-5.33
251025_at	putative protein CND41, chloroplast nu	PCS1	AT5G02190	1.21	0.27	1.82	0.114028	0.291824	-5.33
253306_at	dynamin-like protein ADL2	DRP3A	AT4G33650	-1.14	-0.19	-1.82	0.11402	0.291824	-5.33
256831_at	hypothetical protein	---	AT3G22870	1.16	0.21	1.82	0.11403	0.291824	-5.33
252434_s_a	putative protein mudrA protein - maize	---	---	1.16	0.22	1.81	0.114137	0.292033	-5.33
267258_at	hypothetical protein predicted by gensca	---	AT2G23140	1.14	0.19	1.81	0.114136	0.292033	-5.33
256110_at	Ser Thr protein kinase, putative similar	---	AT1G16900	-1.23	-0.30	-1.81	0.114255	0.292302	-5.34
254008_at	hypothetical protein various predicted p	---	AT4G26380	1.16	0.21	1.81	0.114289	0.292355	-5.34
261711_at	unknown protein similar to hypothetical	---	AT1G32700	-1.17	-0.22	-1.81	0.114354	0.292489	-5.34
253913_at	myosin heavy chain - like protein myosi	VIIIB	AT4G27370	1.14	0.19	1.81	0.114383	0.292530	-5.34
264350_at	putative seryl-tRNA synthetase similar t	SRS	AT1G11870	-1.25	-0.32	-1.81	0.1144	0.292541	-5.34
251459_at	putative protein hypothetical proteins A	---	AT3G60200	1.50	0.59	1.81	0.114442	0.292616	-5.34
259824_at	copper homeostasis factor, putative sim	ATX1	AT1G66240	-1.14	-0.19	-1.81	0.114476	0.292669	-5.34
257100_at	disease resistance protein, putative sim	AtRLP41	AT3G25010	1.19	0.26	1.81	0.114492	0.292677	-5.34

256057_at	unknown protein contains similarity to al	NDA1	AT1G07180	-1.37	-0.46	-1.81	0.114637	0.292877	-5.34
245255_at	COP9 protein ; supported by cDNA: gi_	COP9	AT4G14110	-1.16	-0.22	-1.81	0.114671	0.292877	-5.34
251262_at	hypothetical protein ; supported by cDN	---	AT3G62080	-1.26	-0.33	-1.81	0.114632	0.292877	-5.34
266401_s_a	putative cell division control protein kina	CDKB1;2	AT2G38620 /	1.13	0.17	1.81	0.114697	0.292877	-5.34
262024_at	protein disulfide isomerase, putative sir	ATPDIL5-2	AT1G35620	-1.19	-0.26	-1.81	0.114645	0.292877	-5.34
261384_at	hypothetical protein predicted by genem	---	AT1G05440	1.16	0.21	1.81	0.114623	0.292877	-5.34
262596_at	putative phosphatidic acid phosphatase	LPP2	AT1G15080	-1.18	-0.24	-1.81	0.114655	0.292877	-5.34
245721_s_a	hypothetical protein similar to Ser-Thr pr	---	AT1G73450 /	-1.23	-0.29	-1.81	0.114641	0.292877	-5.34
259445_at	dioxygenase, putative similar to dioxyge	GA2OX6	AT1G02400	2.34	1.23	1.81	0.114684	0.292877	-5.34
257348_at	hypothetical protein predicted by genefir	---	AT2G42140	1.30	0.38	1.81	0.114699	0.292877	-5.34
261093_at	non-LTR reverse transcriptase, putative	AT1G6288	---	1.19	0.25	1.81	0.114737	0.292944	-5.34
248542_at	putative protein similar to unknown prote	AT5G5019	---	1.14	0.19	1.81	0.114753	0.292951	-5.34
254193_at	putative protein predicted proteins, Aral	---	AT4G23870	-1.53	-0.62	-1.81	0.114802	0.293044	-5.34
253716_at	hypothetical protein	---	AT4G29420	-1.18	-0.23	-1.81	0.114824	0.293066	-5.34
262484_at	putative transcriptional regulatory prote	ATSWI3C	AT1G21700	-1.11	-0.16	-1.81	0.11485	0.293067	-5.34
256822_at	unknown protein contains PF00612 IQ:I	IQD5	AT3G22190	-1.18	-0.24	-1.81	0.114849	0.293067	-5.34
262865_at	cytochrome p450, putative similar to cy	CYP89A7	AT1G64930	1.17	0.22	1.81	0.114873	0.293093	-5.34
256777_at	hypothetical protein predicted by genem	---	AT3G13780	-1.15	-0.20	-1.81	0.114897	0.293121	-5.34
261109_at	cytokinin oxidase, putative similar to GE	CKX5	AT1G75450	1.91	0.94	1.81	0.11495	0.293172	-5.34
246795_at	putative protein	---	AT5G27020	1.16	0.21	1.81	0.114947	0.293172	-5.34
263455_at	hypothetical protein predicted by genefir	---	AT2G22320	1.27	0.34	1.81	0.114955	0.293172	-5.34
246998_at	putative protein similar to unknown prote	---	AT5G67370	-1.32	-0.40	-1.81	0.115061	0.293375	-5.34
260958_at	unknown protein identical to unknown p	---	AT1G06060	-1.18	-0.23	-1.81	0.115059	0.293375	-5.34
266297_at	putative proliferating cell nuclear antige	PCNA2	AT2G29570	-1.66	-0.73	-1.81	0.115074	0.293376	-5.34
249835_s_a	putative protein similar to unknown prote	---	AT5G23490 /	1.34	0.42	1.81	0.115116	0.293451	-5.34
261273_at	unknown protein ; supported by cDNA: g	---	AT1G26650	-1.25	-0.32	-1.81	0.115174	0.293565	-5.34
254814_at	hypothetical protein ; supported by cDN	---	AT4G12340	-1.12	-0.16	-1.81	0.115232	0.293647	-5.34
265313_at	unknown protein	---	AT2G20210	-1.18	-0.24	-1.81	0.115223	0.293647	-5.34
248767_at	putative protein contains similarity to GT	---	AT5G47710	-1.18	-0.24	-1.81	0.115271	0.293715	-5.34
266116_at	unknown protein ;supported by full-leng	TOM3	AT2G02180	1.21	0.28	1.81	0.115302	0.293736	-5.34
255534_at	CHP-rich hypothetical protein similar to	---	AT4G02190	1.15	0.20	1.81	0.115305	0.293736	-5.34
266308_at	putative cytochrome P450	CYP705A9	AT2G27010	-1.18	-0.24	-1.81	0.115374	0.293879	-5.34
259448_at	hypothetical protein similar to transcripti	---	AT1G13790	-1.18	-0.24	-1.81	0.115395	0.293900	-5.34
246483_at	receptor protein kinase-like protein prot	NIK1	AT5G16000	-1.40	-0.49	-1.81	0.115489	0.294074	-5.35
266501_at	unknown protein ; supported by cDNA:	HEN2	AT2G06990	-1.18	-0.24	-1.81	0.115489	0.294074	-5.35

257780_at	hypothetical protein predicted by genem	---	AT3G27100	-1.19	-0.25	-1.81	0.115504	0.294079	-5.35
262800_at	putative ATP-dependent RNA helicase	emb1507	AT1G20960	-1.16	-0.22	-1.81	0.115531	0.294114	-5.35
264303_s_a	E2, ubiquitin-conjugating enzyme, putat	UBC35	AT1G16890 /	1.15	0.21	1.81	0.115561	0.294157	-5.35
254522_at	hypothetical protein	---	AT4G19980	1.12	0.16	1.81	0.115592	0.294204	-5.35
248373_at	MADS box transcription factor-like prote	---	AT5G51860	-1.20	-0.26	-1.81	0.115607	0.294209	-5.35
256575_at	dTDP-glucose 4,6-dehydratase, putativ	RHM3	AT3G14790	1.23	0.29	1.81	0.115673	0.294280	-5.35
258918_at	putative cytochrome P450 similar to cyt	UNE9	AT3G10560	1.24	0.31	1.81	0.115673	0.294280	-5.35
260573_at	putative pectinesterase	---	AT2G47280	1.17	0.22	1.81	0.115662	0.294280	-5.35
250109_at	GASA4 ; supported by cDNA: gi_95009	GASA4	AT5G15230	2.32	1.22	1.81	0.115703	0.294323	-5.35
247274_at	putative protein similar to unknown prote	---	AT5G64360	-1.19	-0.25	-1.81	0.115718	0.294326	-5.35
256857_at	NAM-like protein similar to NAM (no apic	CUC1	AT3G15170	1.12	0.16	1.81	0.115744	0.294359	-5.35
252934_at	Inositol monophosphatase - like protein	IMPL2	AT4G39120	-1.21	-0.28	-1.80	0.115934	0.294810	-5.35
249515_at	tryptophan synthase beta chain	---	AT5G38530	1.64	0.71	1.80	0.115974	0.294867	-5.35
249223_at	receptor lectin kinase-like protein	---	AT5G42120	-1.17	-0.23	-1.80	0.115982	0.294867	-5.35
254749_at	putative protein various predicted prote	---	AT4G13130	1.11	0.16	1.80	0.116055	0.295021	-5.35
260004_at	unknown protein ;supported by full-leng	---	AT1G67860	1.29	0.37	1.80	0.116069	0.295023	-5.35
251644_at	putative protein putative DNA binding p	---	AT3G57540	-1.32	-0.40	-1.80	0.116165	0.295233	-5.35
267269_at	unknown protein	CAND1	AT2G02560	-1.17	-0.22	-1.80	0.116229	0.295265	-5.35
245649_at	F5A9.21 unknown protein; similar to ES	---	AT1G24706	-1.19	-0.25	-1.80	0.116229	0.295265	-5.35
262479_at	leucine-rich repeat transmembrane prot	SUB	AT1G11130	1.13	0.17	1.80	0.116202	0.295265	-5.35
260652_at	putative MYB family transcription factor	---	AT1G32360	-1.14	-0.18	-1.80	0.116227	0.295265	-5.35
253915_at	putative protein centrin, Marsilea vestita	---	AT4G27280	1.94	0.96	1.80	0.116251	0.295288	-5.35
258138_at	Expressed protein GC donor splice site	MSH7	AT3G24495	-1.13	-0.18	-1.80	0.116335	0.295370	-5.35
250216_at	unknown protein	---	AT5G14090	1.20	0.26	1.80	0.116329	0.295370	-5.35
250845_at	rna binding protein - like rna binding pro	---	AT5G04600	-1.24	-0.31	-1.80	0.116327	0.295370	-5.35
265636_at	putative calcium binding protein	---	AT2G27480	1.17	0.23	1.80	0.116335	0.295370	-5.35
264522_at	putative xylan endohydrolase similar to	---	AT1G10050	-1.19	-0.25	-1.80	0.116411	0.295530	-5.35
247233_at	mitochondrial carrier protein-like	---	AT5G64970	-1.18	-0.24	-1.80	0.11645	0.295595	-5.35
247021_at	putative protein similar to unknown prote	---	AT5G67040	1.16	0.22	1.80	0.116504	0.295700	-5.35
263942_at	unknown protein	FLA16	AT2G35860	2.26	1.17	1.80	0.116569	0.295831	-5.35
255810_at	hypothetical protein ; supported by full-le	---	AT4G10140	1.15	0.21	1.80	0.116596	0.295840	-5.35
253010_at	ovule development protein aintegumenta	ANT	AT4G37750	1.17	0.22	1.80	0.116598	0.295840	-5.35
265417_at	unknown protein	---	AT2G20920	1.28	0.36	1.80	0.116612	0.295843	-5.35
263838_at	putative s-adenosylmethionine synthetas	MAT3	AT2G36880	1.43	0.52	1.80	0.116649	0.295903	-5.35
265701_at	unknown protein related to uncharacteri	---	AT2G03460	1.14	0.19	1.80	0.116695	0.295986	-5.36

254384_at	heat shock protein - like heat shock pro	---	AT4G21870	-1.55	-0.63	-1.80	0.116758	0.296115	-5.36
247434_at	Expressed protein ; supported by full-ler	---	AT5G62575	-1.14	-0.18	-1.80	0.116815	0.296159	-5.36
251552_at	ribosomal protein L11 -like ribosomal pr	---	AT3G58700	-1.30	-0.38	-1.80	0.116811	0.296159	-5.36
250173_at	MYB40 - putative transcription factor	AtMYB40	AT5G14340	1.18	0.23	1.80	0.116806	0.296159	-5.36
245194_at	F12A21.5 similar to protein phosphatase	---	AT1G67820	-1.30	-0.38	-1.80	0.11693	0.296353	-5.36
259974_at	putative phosphate transporter similar to	---	AT1G76430	1.19	0.26	1.80	0.116913	0.296353	-5.36
260439_at	hypothetical protein predicted by gensca	---	AT1G68340	1.33	0.41	1.80	0.116922	0.296353	-5.36
249097_at	putative protein strong similarity to unkn	---	AT5G43520	-1.17	-0.23	-1.80	0.116963	0.296403	-5.36
254054_at	putative protein DNA-binding protein PD	---	AT4G25320	-1.23	-0.30	-1.80	0.117096	0.296673	-5.36
261180_at	hypothetical protein predicted by genem	---	---	1.15	0.20	1.80	0.117084	0.296673	-5.36
249344_at	prohibitin (gb AAC49691.1) ;supported b	ATPHB3	AT5G40770	-1.29	-0.36	-1.80	0.117176	0.296816	-5.36
252443_at	putative helicase helicase SKI2W - hum	---	AT3G46960	-1.17	-0.23	-1.80	0.117178	0.296816	-5.36
247089_at	dimethyladenosine transferase-like prote	---	AT5G66360	-1.17	-0.23	-1.80	0.117308	0.297029	-5.36
249112_at	ATP sulfurylase precursor (gb|AAD2663	APS4	AT5G43780	1.32	0.40	1.80	0.117277	0.297029	-5.36
266887_at	unknown protein ; supported by cDNA:	CHL-CPN1	AT2G44650	-1.19	-0.25	-1.80	0.117314	0.297029	-5.36
262555_at	hypothetical protein	---	AT1G31400	1.13	0.17	1.80	0.117296	0.297029	-5.36
252056_at	ubiquitin extension protein (UBQ1) iden	UBQ1	AT3G52590	-1.15	-0.20	-1.80	0.117382	0.297138	-5.36
250193_at	putative protein proline-rich protein M14	---	AT5G14540	1.16	0.21	1.80	0.117396	0.297138	-5.36
250380_at	putative protein	---	AT5G11600	-1.15	-0.20	-1.80	0.117396	0.297138	-5.36
258684_at	putative protein kinase contains Pfam p	---	AT3G08680	-1.21	-0.28	-1.79	0.117448	0.297203	-5.36
249241_at	serine carboxypeptidase-II like	scpl41	AT5G42230	1.13	0.18	1.79	0.117439	0.297203	-5.36
250623_at	peroxisomal Ca-dependent solute carrie	---	AT5G07320	-1.15	-0.21	-1.79	0.117608	0.297576	-5.36
253852_at	putative protein diacylglycerol kinase ze	---	AT4G28130	1.14	0.18	1.79	0.117682	0.297730	-5.36
246597_at	L-aspartate oxidase -like protein L-aspa	AO	AT5G14760	1.59	0.67	1.79	0.117745	0.297823	-5.36
250189_at	putative protein ;supported by full-lengt	---	AT5G14410	-1.27	-0.34	-1.79	0.117742	0.297823	-5.36
261972_at	hypothetical protein predicted by genem	---	AT1G64600	-1.28	-0.35	-1.79	0.117798	0.297863	-5.36
256109_at	hypothetical protein predicted by genem	---	AT1G16950	1.29	0.37	1.79	0.117799	0.297863	-5.36
259817_at	hypothetical protein predicted by genem	---	AT1G49880	-1.15	-0.21	-1.79	0.1178	0.297863	-5.36
249894_at	unknown protein ; supported by cDNA:	---	AT5G22580	6.73	2.75	1.79	0.117872	0.297979	-5.36
247743_at	protein kinase - like serine/threonine/tyr	---	AT5G59010	-1.20	-0.26	-1.79	0.117861	0.297979	-5.36
249267_at	putative protein contains similarity to 24	BTI3	AT5G41600	-1.27	-0.34	-1.79	0.117897	0.298010	-5.36
262843_at	Expressed protein ; supported by full-ler	AtHB32	AT1G14687	-1.24	-0.31	-1.79	0.11795	0.298110	-5.37
264665_at	unknown protein ESTs gb|H37208,gb|H	---	AT1G09660	-1.18	-0.24	-1.79	0.117977	0.298144	-5.37
249401_at	putative protein LIM7, Lily, EMBL:LLOR	---	AT5G40260	1.13	0.18	1.79	0.118046	0.298255	-5.37
254648_at	lipase-like protein Pn47p, Ipomoea nil,	---	AT4G18550	1.14	0.19	1.79	0.118047	0.298255	-5.37

253984_at	isp4 like protein isp4 protein -Schizosac	OPT5	AT4G26590	1.16	0.22	1.79	0.118063	0.298264	-5.37
261686_at	unknown protein ;supported by full-lengt	---	AT1G47310	-1.15	-0.21	-1.79	0.118077	0.298264	-5.37
248675_at	putative protein similar to unknown prote	ICK6	AT5G48820	1.27	0.34	1.79	0.118129	0.298341	-5.37
245833_at	transposon protein, putative similar to E	---	---	1.17	0.23	1.79	0.118133	0.298341	-5.37
266970_at	hypothetical protein predicted by genefir	---	AT2G39560	1.16	0.21	1.79	0.11822	0.298528	-5.37
254654_at	translation initiation factor eIF4E ;suppo	EIF4E	AT4G18040	-1.16	-0.22	-1.79	0.118243	0.298553	-5.37
247578_at	putative protein predicted protein, Arabi	---	AT5G61300	-1.18	-0.24	-1.79	0.118317	0.298671	-5.37
255009_at	putative DNA-directed RNA polymerase	---	AT4G10070	-1.23	-0.30	-1.79	0.118339	0.298671	-5.37
262819_at	putative cytochrome P450 strong similar	CYP77B1	AT1G11600	-1.14	-0.18	-1.79	0.118334	0.298671	-5.37
265091_s_a	hypothetical protein similar to Anthocyar	---	AT1G03495 /	1.20	0.27	1.79	0.118342	0.298671	-5.37
262776_at	unknown protein EST gb|T22808 comes	---	AT1G13020	1.19	0.25	1.79	0.118382	0.298710	-5.37
262360_at	receptor protein kinase, putative similar	---	AT1G73080 /	1.82	0.86	1.79	0.118384	0.298710	-5.37
263802_at	unknown protein ;supported by full-leng	---	AT2G40430	-1.29	-0.37	-1.79	0.118427	0.298787	-5.37
245216_at	Expressed protein non-consensus GG d	IMPA-2	AT4G16143	-1.11	-0.16	-1.79	0.118462	0.298809	-5.37
249952_at	putative protein predicted proteins, Arat	---	AT5G18950	-1.17	-0.23	-1.79	0.118454	0.298809	-5.37
252018_at	putative protein various predicted prote	AtPP2-A15	AT3G53000	1.22	0.29	1.79	0.118527	0.298938	-5.37
247339_at	unknown protein	---	AT5G63690	-1.19	-0.25	-1.79	0.118565	0.299002	-5.37
250341_at	MAP3K delta-1 protein kinase	---	AT5G11850	1.13	0.17	1.79	0.118597	0.299050	-5.37
252405_at	putative protein RNA helicase HEL117,	---	AT3G48120	-1.18	-0.24	-1.79	0.118655	0.299163	-5.37
249357_at	ribonucleoprotein -like ribonucleoprotein	---	AT5G40490	-1.18	-0.24	-1.79	0.118696	0.299232	-5.37
247604_at	putative phytochelatin synthetase - like	COBL5	AT5G60950	1.98	0.99	1.79	0.118717	0.299251	-5.37
254412_at	putative protein chloroplast DNA-bindin	B160	AT4G21430	-1.26	-0.33	-1.79	0.118852	0.299559	-5.37
249762_at	putative protein contains similarity to unl	---	AT5G24000	-1.14	-0.19	-1.79	0.11891	0.299674	-5.37
261289_at	hypothetical protein predicted by genem	---	AT1G37000	-1.13	-0.18	-1.79	0.118967	0.299752	-5.37
253132_at	NAM / CUC2 -like protein nap gene, Ara	NTL9	AT4G35580	-1.19	-0.25	-1.79	0.118968	0.299752	-5.37
250460_at	putative protein similar to unknown prote	---	AT5G09850	1.13	0.18	1.78	0.119153	0.300186	-5.38
247735_at	thymidylate kinase - like protein thymidy	ZEU1	AT5G59440	-1.34	-0.42	-1.78	0.119214	0.300206	-5.38
245368_at	hypothetical protein ; supported by full-le	---	AT4G15510	-1.27	-0.34	-1.78	0.11921	0.300206	-5.38
258373_at	20S proteasome subunit PAE2 identical	PAE2	AT3G14290	-1.15	-0.20	-1.78	0.119209	0.300206	-5.38
264794_at	hypothetical protein predicted by genscar	---	AT1G08670	1.13	0.18	1.78	0.119194	0.300206	-5.38
263692_at	unknown protein Location of ESTs 108	---	AT1G26850	1.15	0.20	1.78	0.119259	0.300253	-5.38
245463_at	allergen like protein	ATEXLB1	AT4G17030	-1.37	-0.45	-1.78	0.119253	0.300253	-5.38
257327_at	hypothetical protein	---	---	1.28	0.36	1.78	0.119317	0.300333	-5.38
251369_at	putative protein ;supported by full-lengt	---	AT3G60480	-1.17	-0.23	-1.78	0.119311	0.300333	-5.38
253814_at	putative protein ;supported by full-lengt	---	AT4G28290	1.25	0.32	1.78	0.119436	0.300539	-5.38

265696_at	putative molybdopterin biosynthesis CN	CNX2	AT2G31955	1.30	0.38	1.78	0.119451	0.300539	-5.38
253670_at	putative protein ; supported by full-leng	---	AT4G30010	1.16	0.22	1.78	0.119445	0.300539	-5.38
257555_at	hypothetical protein predicted by gensca	---	AT3G24780	1.21	0.28	1.78	0.119439	0.300539	-5.38
254385_s_a	putative protein CGI-131 protein, Homo	ATMSRB7	AT4G21830 /	3.23	1.69	1.78	0.119545	0.300741	-5.38
251389_at	putative protein	---	AT3G60850	-1.14	-0.18	-1.78	0.119571	0.300760	-5.38
245142_at	putative O-sialoglycoprotein endopeptid	---	AT2G45270	-1.16	-0.21	-1.78	0.119579	0.300760	-5.38
255264_at	putative protein ethylene responsive EF	---	AT4G05170	-1.17	-0.23	-1.78	0.119633	0.300862	-5.38
249712_at	eIF4Eiso protein (emb|CAA71579.1) ;su	LSP1	AT5G35620	-1.22	-0.29	-1.78	0.119702	0.300973	-5.38
250801_at	pectinesterase	---	AT5G04960	-1.14	-0.19	-1.78	0.119703	0.300973	-5.38
265773_at	unknown protein ; supported by cDNA:	RPH1	AT2G48070	-1.17	-0.22	-1.78	0.119753	0.301032	-5.38
255135_at	putative protein several hypothetical pro	---	---	1.16	0.21	1.78	0.119741	0.301032	-5.38
254188_at	UDPglucose 4-epimerase - like protein	UGE2	AT4G23920	-1.37	-0.45	-1.78	0.119766	0.301032	-5.38
262860_at	unknown protein	APO1	AT1G64810	-1.20	-0.26	-1.78	0.11981	0.301108	-5.38
249873_at	ATP-dependent Clp protease proteolyti	NCLPP7	AT5G23140	1.17	0.22	1.78	0.119899	0.301300	-5.38
258868_at	putative exportin1 (XPO1) protein simila	XPO1B	AT3G03110	-1.17	-0.22	-1.78	0.119961	0.301354	-5.38
262131_at	hypothetical protein predicted by genem	RALF1	AT1G02900	1.65	0.72	1.78	0.119966	0.301354	-5.38
250349_at	putative receptor - like kinase receptor-	---	AT5G12000	1.17	0.22	1.78	0.119949	0.301354	-5.38
265690_at	hypothetical protein predicted by gensca	---	AT2G24320	1.19	0.25	1.78	0.119974	0.301354	-5.38
258715_at	putative 60S ribosomal protein L1 strong	---	AT3G09630	-1.23	-0.30	-1.78	0.120009	0.301410	-5.38
253221_at	peptidylprolyl isomerase (cyclophilin) ;s	ROC5	AT4G34870	-1.20	-0.26	-1.78	0.120034	0.301440	-5.38
251939_at	putative protein MICRONUCLEAR LINK	---	AT3G53440	-1.24	-0.31	-1.78	0.120112	0.301601	-5.38
261029_at	unknown protein	---	AT1G17330	1.21	0.27	1.78	0.120141	0.301641	-5.38
265248_at	unknown protein ; supported by cDNA:	PIF4	AT2G43010	-1.28	-0.35	-1.78	0.120159	0.301653	-5.38
266238_at	phosphoprotein phosphatase, type 1 ca	TOPP1	AT2G29400	1.25	0.33	1.78	0.120189	0.301695	-5.38
266779_at	putative ligand-gated ion channel protei	ATGLR2.9	AT2G29100	1.17	0.23	1.78	0.120202	0.301695	-5.38
266733_at	similar to axi 1 protein from Nicotiana ta	---	AT2G03280	-1.15	-0.20	-1.78	0.120223	0.301715	-5.38
246716_s_a	putative protein	---	AT5G28910 /	-1.12	-0.17	-1.78	0.12024	0.301724	-5.38
246163_at	putative protein predicted proteins, Aral	---	---	-1.19	-0.25	-1.78	0.120271	0.301770	-5.38
248560_at	putative protein contains similarity to pyr	ATPPOX	AT5G49970	-1.20	-0.26	-1.78	0.120297	0.301801	-5.38
260153_at	putative lipase similar to monoglyceride	---	AT1G52760	1.32	0.41	1.78	0.120369	0.301883	-5.38
266239_at	unknown protein ; supported by cDNA:	---	AT2G29530	-1.36	-0.45	-1.78	0.120344	0.301883	-5.38
255309_at	hypothetical protein	SFR6	AT4G04920	1.13	0.17	1.78	0.120367	0.301883	-5.38
246847_at	putative protein ferroportin1, Mus musc	ATIREG3	AT5G26820	-1.28	-0.36	-1.78	0.120473	0.302110	-5.39
245497_at	hypothetical protein	---	AT4G16460	1.17	0.22	1.78	0.120507	0.302131	-5.39
259171_at	hypothetical protein predicted by genefir	---	AT3G03590	-1.16	-0.22	-1.78	0.120508	0.302131	-5.39

252835_at	putative protein several hypothetical pro	---	AT3G42060	1.17	0.23	1.78	0.120533	0.302160	-5.39
262342_at	unknown protein similar to hypothetical	---	AT1G64150	-1.28	-0.35	-1.78	0.120606	0.302309	-5.39
260855_at	phosphatidylinositol-4-phosphate 5-kina	---	AT1G21920	1.23	0.30	1.78	0.120755	0.302650	-5.39
249950_at	protein kinase - like protein Pto kinase i	---	AT5G18910	1.13	0.17	1.78	0.120782	0.302684	-5.39
258323_at	unknown protein similar to putative prote	---	AT3G22750	1.22	0.29	1.78	0.120842	0.302702	-5.39
254602_at	hypothetical protein	EDR2	AT4G19040	1.15	0.20	1.78	0.120803	0.302702	-5.39
254800_at	putative protein several hypothetical pro	---	AT4G13070	-1.25	-0.32	-1.78	0.120841	0.302702	-5.39
266624_s_a	phosphoribosyl pyrophosphate syntheta	---	AT1G32380 /	1.38	0.46	1.78	0.120829	0.302702	-5.39
247715_at	putative protein predicted protein, Arabi	---	AT5G59360	1.25	0.32	1.77	0.12089	0.302788	-5.39
245300_at	hypothetical protein ; supported by cDN/	CBL6	AT4G16350	1.13	0.17	1.77	0.120928	0.302852	-5.39
250147_at	putative protein predicted proteins, Dros	---	AT5G14600	-1.24	-0.31	-1.77	0.120958	0.302892	-5.39
254603_at	putative protein hypothetical protein YIL	---	AT4G19045 /	1.17	0.23	1.77	0.120977	0.302906	-5.39
262347_at	unknown protein similar to hypothetical	---	AT1G64110	1.17	0.23	1.77	0.121078	0.303093	-5.39
254837_at	putative protein	---	AT4G12360	1.18	0.24	1.77	0.121071	0.303093	-5.39
264374_at	putative two-component response regu	ARR12	AT2G25180	-1.16	-0.21	-1.77	0.121091	0.303093	-5.39
265105_s_a	unknown protein contains similarity to F	---	AT1G62580 /	1.12	0.16	1.77	0.121144	0.303193	-5.39
264257_at	unknown protein	---	AT1G09230	-1.18	-0.24	-1.77	0.121195	0.303252	-5.39
248071_at	unknown protein	---	AT5G55670	-1.15	-0.21	-1.77	0.121192	0.303252	-5.39
247199_at	DNA binding protein TGA1a homolog ;s	TGA1	AT5G65210	1.33	0.41	1.77	0.121221	0.303285	-5.39
252012_at	ubiquinol--cytochrome-c reductase-like	---	AT3G52730	1.14	0.19	1.77	0.121238	0.303295	-5.39
251046_at	kinesin -like protein kinesin, Xenopus la	---	AT5G02370	1.13	0.17	1.77	0.121261	0.303319	-5.39
245365_at	hypothetical protein ;supported by full-le	---	AT4G17720	1.27	0.35	1.77	0.121331	0.303461	-5.39
257032_at	zinc finger protein, putative similar to R	---	AT3G19140	1.12	0.16	1.77	0.121349	0.303472	-5.39
263253_at	bZIP transcription factor (POSF21) iden	---	AT2G31370	-1.20	-0.26	-1.77	0.121387	0.303534	-5.39
246027_at	homoserine dehydrogenase-like protein	---	AT5G21060	-1.25	-0.32	-1.77	0.121465	0.303696	-5.39
247952_at	salt-inducible protein-like	CYP71B1(	AT5G57250 /	-1.16	-0.21	-1.77	0.121479	0.303698	-5.39
249287_at	putative protein strong similarity to unkn	---	AT5G41250	1.17	0.23	1.77	0.121518	0.303728	-5.39
257094_at	hypothetical protein similar to tetraacyld	---	AT3G20480	-1.24	-0.31	-1.77	0.121514	0.303728	-5.39
246090_at	putative protein BEM46 bem1/bud5 sup	WAV2	AT5G20520	-1.31	-0.38	-1.77	0.121614	0.303919	-5.39
266539_at	similar to mammalian MHC III region pro	SUVH5	AT2G35160	1.17	0.22	1.77	0.121621	0.303919	-5.39
257613_at	polygalacturonase, putative similar to p	---	AT3G26610	-1.14	-0.18	-1.77	0.121681	0.304035	-5.39
258905_at	unknown protein similar to hypothetical	---	AT3G06390	1.27	0.34	1.77	0.121778	0.304245	-5.40
255871_at	putative small nuclear ribonucleoprotein	U2B"	AT2G30260	-1.16	-0.22	-1.77	0.121814	0.304245	-5.40
255272_at	putative protein (ubiquitin like) to various	---	AT4G05270	-1.12	-0.17	-1.77	0.121818	0.304245	-5.40
266741_s_a	putative disease resistance protein	---	AT2G03030 /	1.13	0.17	1.77	0.121806	0.304245	-5.40

262327_at	hypothetical protein similar to hypothetic	---	AT1G64130	1.15	0.20	1.77	0.121886	0.304382	-5.40
267533_at	unknown protein ;supported by full-leng	ATNUDX2	AT2G42070	-1.16	-0.22	-1.77	0.121926	0.304416	-5.40
250433_at	histone H3 - like protein histone H3, Ara	---	AT5G10400	-1.18	-0.23	-1.77	0.121923	0.304416	-5.40
250225_at	Expressed protein ; supported by full-ler	---	AT5G14105	-1.20	-0.27	-1.77	0.121956	0.304424	-5.40
254622_at	hypothetical protein contains similarity to	---	AT4G18375	-1.26	-0.34	-1.77	0.121951	0.304424	-5.40
245799_at	disease resistance protein, putative sim	AtRLP6	AT1G45616	-1.14	-0.19	-1.77	0.121971	0.304426	-5.40
256364_at	wrky-type DNA binding protein, putative	WRKY67	AT1G66550	1.17	0.23	1.77	0.121996	0.304441	-5.40
260460_at	unknown protein	---	AT1G68230	1.15	0.21	1.77	0.122003	0.304441	-5.40
253192_at	putative protein nuclear phosphoprotein	---	AT4G35370	1.13	0.18	1.77	0.122106	0.304665	-5.40
262344_at	cytochrome b245 beta chain homolog P	ATRBOH I	AT1G64060	1.49	0.58	1.77	0.12212	0.304666	-5.40
256453_at	GSH-dependent dehydroascorbate red	DHAR2	AT1G75270	1.33	0.41	1.77	0.122202	0.304703	-5.40
246489_at	14-3-3 protein GF14upsilon (grf5) identi	GRF5	AT5G16050	-1.16	-0.22	-1.77	0.122151	0.304703	-5.40
252108_at	putative protein various predicted prote	---	AT3G51530	-1.15	-0.20	-1.77	0.122195	0.304703	-5.40
250968_at	putative protein ;supported by full-lengt	---	AT5G02890	1.39	0.47	1.77	0.122165	0.304703	-5.40
248688_at	indole-3-glycerol phosphate synthase ;	---	AT5G48220	-1.21	-0.28	-1.77	0.122185	0.304703	-5.40
257537_at	hypothetical protein predicted by genma	---	AT3G22350	1.20	0.27	1.77	0.122258	0.304776	-5.40
265503_at	putative non-LTR retroelement reverse t	---	---	1.20	0.26	1.77	0.122245	0.304776	-5.40
247085_at	kinesin heavy chain DNA binding protein	---	AT5G66310	-1.16	-0.21	-1.77	0.122302	0.304854	-5.40
263327_at	putative receptor-like protein kinase	---	AT2G15300	1.13	0.17	1.77	0.122359	0.304961	-5.40
251945_at	dTDP-glucose 4-6-dehydratase -like pr	UXS1	AT3G53520	1.15	0.20	1.77	0.122439	0.305127	-5.40
252905_at	putative protein predicted protein, Arabi	---	AT4G39720	1.20	0.26	1.77	0.122469	0.305170	-5.40
262203_at	transfactor-like protein similar to transfa	---	AT2G01060	-1.16	-0.22	-1.77	0.122495	0.305191	-5.40
263440_at	unknown protein predicted by genscan	ATEXO70I	AT2G28640	1.11	0.16	1.77	0.122505	0.305191	-5.40
257097_at	hypothetical protein predicted by genem	---	---	1.13	0.18	1.77	0.12254	0.305245	-5.40
263199_at	hypothetical protein Similar to hexosam	HEXO2	AT1G05590	-1.20	-0.27	-1.77	0.122597	0.305321	-5.40
246410_at	hypothetical protein predicted by genem	---	AT1G57760	1.13	0.18	1.77	0.12259	0.305321	-5.40
266836_at	hypothetical protein predicted by grail	---	AT2G26000	-1.21	-0.27	-1.77	0.122629	0.305353	-5.40
249868_at	senescence-associated protein 5-like pr	TET12	AT5G23030	1.15	0.21	1.76	0.122636	0.305353	-5.40
254509_at	terpene cyclase like protein 5-epi-aristo	---	AT4G20200	-1.14	-0.18	-1.76	0.12267	0.305369	-5.40
251564_at	myosin heavy chain MYA3	XIJ	AT3G58160	-1.16	-0.22	-1.76	0.122664	0.305369	-5.40
245414_at	hypothetical protein	---	AT4G17310	1.19	0.25	1.76	0.122763	0.305567	-5.40
258940_at	putative lipase acylhydrolase contains P	---	AT3G09930	1.12	0.16	1.76	0.122812	0.305656	-5.40
264362_at	unknown protein ESTs gb|H36966, gb|I	---	AT1G03290	1.23	0.30	1.76	0.122841	0.305688	-5.40
246072_at	PISTILLATA ; supported by full-length c	PI	AT5G20240	1.13	0.18	1.76	0.122851	0.305688	-5.40
263497_at	cold-regulated protein cor15a precursor	COR15A	AT2G42540	-2.17	-1.12	-1.76	0.122926	0.305839	-5.40

263261_at	putative pre-mRNA splicing factor simila	---	AT1G10580	-1.11	-0.15	-1.76	0.12297	0.305860	-5.40
254813_at	putative transcription factor myb-relatec	MYB42	AT4G12350	1.13	0.17	1.76	0.122969	0.305860	-5.40
257830_at	MutT-like protein contains Pfam profile:	ATNUDX1	AT3G26690	1.32	0.40	1.76	0.122974	0.305860	-5.40
262172_at	ribosomal protein S9, putative similar to	RPS9	AT1G74970	-1.15	-0.20	-1.76	0.123014	0.305923	-5.41
257317_at	hypothetical protein	AT2G0774	---	-1.17	-0.23	-1.76	0.123026	0.305923	-5.41
257194_at	serine acetyltransferase (Sat-1) identica	ATSERAT	AT3G13110	-1.16	-0.21	-1.76	0.12309	0.306014	-5.41
252294_at	60S ribosomal protein L13, BBC1 prote	ATBBC1	AT3G49010	-1.41	-0.49	-1.76	0.123084	0.306014	-5.41
252136_at	calmodulin-like protein flagellar calmod	---	AT3G50770	2.15	1.11	1.76	0.123138	0.306100	-5.41
249068_at	putative protein similar to unknown prote	PDLP1	AT5G43980	1.14	0.19	1.76	0.123198	0.306216	-5.41
245992_at	receptor protein kinase - like receptor-li	---	AT5G20690	1.12	0.16	1.76	0.123364	0.306597	-5.41
261372_at	zinc finger protein, putative similar to G	---	AT1G53010	1.17	0.23	1.76	0.123393	0.306635	-5.41
251493_at	putative protein hypothetical protein T2	---	AT3G59300	1.19	0.25	1.76	0.12341	0.306642	-5.41
259794_at	unknown protein	---	AT1G64330	-1.17	-0.22	-1.76	0.123491	0.306745	-5.41
251065_at	lipid-transfer protein-like lipid-transfer p	---	AT5G01870	1.19	0.25	1.76	0.123483	0.306745	-5.41
262184_at	hypothetical protein contains similarity to	---	AT1G77910	1.12	0.16	1.76	0.123477	0.306745	-5.41
245472_at	hypothetical protein	---	AT4G16040	1.19	0.25	1.76	0.123581	0.306922	-5.41
250581_at	copine-like protein copine VII protein - H	BON2	AT5G07300	1.14	0.19	1.76	0.12359	0.306922	-5.41
255808_at	putative protein predicted protein, Arabi	---	AT4G10280	-1.16	-0.21	-1.76	0.123615	0.306952	-5.41
249266_at	6-phosphogluconate dehydrogenase ;s	---	AT5G41670	-1.22	-0.28	-1.76	0.123647	0.306997	-5.41
255094_at	putative zinc finger protein	ORTHL	AT4G08590	-1.26	-0.34	-1.76	0.123665	0.307009	-5.41
248728_at	cytochrome P450-like protein	CYP708A2	AT5G48000	1.16	0.21	1.76	0.123712	0.307061	-5.41
246332_at	putative protein phosphatidylcholine--st	---	AT3G44830	1.19	0.26	1.76	0.123713	0.307061	-5.41
258653_at	hypothetical protein similar to auxin-ind	---	AT3G09870	1.19	0.25	1.76	0.123772	0.307168	-5.41
257907_at	hemolysin, putative similar to hemolysir	---	AT3G25470	-1.12	-0.16	-1.76	0.123783	0.307168	-5.41
249185_at	CHP-rich zinc finger protein-like	---	AT5G43030	1.15	0.20	1.76	0.123799	0.307176	-5.41
245581_at	hypothetical protein	---	AT4G14840	1.18	0.24	1.76	0.123904	0.307368	-5.41
249780_at	ubiquitin	---	AT5G24240	1.19	0.25	1.76	0.123903	0.307368	-5.41
254827_at	putative protein KIAA0255 gene, Homo	---	AT4G12650	1.16	0.21	1.76	0.123944	0.307434	-5.41
253691_at	putative protein predicted proteins, Arat	EMB2752	AT4G29660	-1.12	-0.16	-1.76	0.123964	0.307449	-5.41
256016_at	hypothetical protein predicted by genscа	---	AT1G19240	-1.18	-0.24	-1.76	0.124017	0.307548	-5.41
266261_at	putative zinc finger protein ;supported b	---	AT2G27580	1.12	0.16	1.76	0.124031	0.307548	-5.41
260015_at	putative S-adenosyl-L-methionine:trans-	CCOAMT	AT1G67980	1.75	0.81	1.76	0.124108	0.307652	-5.41
265860_at	hypothetical protein predicted by genscа	---	AT2G01810	1.13	0.18	1.76	0.124113	0.307652	-5.41
262873_at	hypothetical protein predicted by genem	---	AT1G64700	-1.15	-0.21	-1.76	0.124103	0.307652	-5.41
246905_at	putative protein ;supported by full-lengt	---	AT5G25570	-1.34	-0.42	-1.76	0.124201	0.307837	-5.41

256929_at	unknown protein	---	---	1.17	0.23	1.76	0.124272	0.307916	-5.41
246018_at	Expressed protein ; supported by full-ler	---	AT5G10695	1.57	0.65	1.76	0.124306	0.307916	-5.42
261820_at	hypothetical protein predicted by genem	---	AT1G11420	-1.22	-0.29	-1.76	0.124304	0.307916	-5.42
258147_at	beta-glucosidase, putative similar to be	BGLU43	AT3G18070	-1.15	-0.20	-1.76	0.124296	0.307916	-5.42
261602_at	hydrogenase protein, putative similar to	ATPREP2	AT1G49630	1.13	0.17	1.76	0.124282	0.307916	-5.41
264469_at	hypothetical protein similar to hypothetic	LBD40	AT1G67100	-1.13	-0.18	-1.76	0.124314	0.307916	-5.42
263286_at	40S ribosomal protein S14 ;supported b	---	AT2G36160	-1.24	-0.31	-1.75	0.124423	0.308119	-5.42
250035_at	putative protein contains similarity to tra	---	AT5G18230	-1.13	-0.17	-1.75	0.124412	0.308119	-5.42
264760_at	syntaxin-related protein Nt-syr1, putativ	SYP124	AT1G61290	1.21	0.28	1.75	0.124553	0.308409	-5.42
250738_at	anthranilate synthase component I-1 pre	ASA1	AT5G05730	1.56	0.64	1.75	0.124587	0.308424	-5.42
266091_at	hypothetical protein predicted by gensca	emb1513	AT2G37920	-1.19	-0.25	-1.75	0.124585	0.308424	-5.42
260086_at	hypothetical protein predicted by gensca	---	AT1G63240	-1.22	-0.28	-1.75	0.124706	0.308687	-5.42
249972_at	tRNA isopentenyltransferase -like prote	IPT5	AT5G19040	-1.15	-0.20	-1.75	0.124772	0.308815	-5.42
251211_s_a	putative protein several hypothetical pro	---	AT3G62470 /	-1.35	-0.43	-1.75	0.124858	0.308996	-5.42
259715_at	hypothetical protein predicted by gensc	---	AT1G60990	-1.19	-0.25	-1.75	0.124907	0.309047	-5.42
246091_at	putative protein various predicted prote	---	AT5G20590	-1.18	-0.24	-1.75	0.124946	0.309047	-5.42
245048_at	orf within trnK intron orf within trnK intro	---	---	-1.22	-0.29	-1.75	0.124947	0.309047	-5.42
248120_at	putative protein similar to unknown prote	---	AT5G54540	-1.16	-0.22	-1.75	0.124916	0.309047	-5.42
254287_at	putative protein similaritry to hypothetic	---	AT4G22960	1.13	0.18	1.75	0.124947	0.309047	-5.42
263421_at	unknown protein ;supported by full-leng	EXL5	AT2G17230	1.39	0.48	1.75	0.125039	0.309050	-5.42
259696_at	unknown protein ; supported by cDNA: g	---	AT1G63150	-1.15	-0.20	-1.75	0.125022	0.309050	-5.42
252297_at	cytosolic ribosomal protein S11 ;suppor	EMB1080	AT3G48930	-1.31	-0.39	-1.75	0.125036	0.309050	-5.42
255419_at	putative receptor kinase	---	AT4G03230	-1.16	-0.22	-1.75	0.124973	0.309050	-5.42
250018_at	putative protein similar to unknown prote	---	AT5G18150	1.54	0.63	1.75	0.124977	0.309050	-5.42
250251_at	putative protein contains similarity to Mt	---	AT5G13670	-1.15	-0.20	-1.75	0.125043	0.309050	-5.42
259796_at	hypothetical protein predicted by genem	---	---	-1.17	-0.23	-1.75	0.124997	0.309050	-5.42
247065_s_a	disease resistance protein-like	---	AT5G66900 /	1.20	0.26	1.75	0.125077	0.309101	-5.42
248551_at	putative protein similar to unknown prote	WR3	AT5G50200	1.49	0.58	1.75	0.125115	0.309162	-5.42
266715_at	putative RNA-binding protein	---	AT2G46780	1.18	0.23	1.75	0.125154	0.309192	-5.42
259666_at	unknown protein ; supported by cDNA: g	SR33	AT1G55310	-1.15	-0.20	-1.75	0.125154	0.309192	-5.42
247298_at	glucosidase II alpha subunit	RSW3	AT5G63840	-1.14	-0.19	-1.75	0.125257	0.309411	-5.42
245426_at	hypothetical protein	---	AT4G17540	-1.18	-0.24	-1.75	0.125307	0.309502	-5.42
262118_at	beta-glucosidase, putative similar to be	BGLU11	AT1G02850	-1.57	-0.65	-1.75	0.125519	0.309665	-5.42
256314_at	hypothetical protein	TOC75-I	AT1G35860	1.15	0.21	1.75	0.125536	0.309665	-5.42
251861_at	putative protein GATA transcription fact	BME3	AT3G54810	1.56	0.64	1.75	0.125437	0.309665	-5.42

251486_at	60S RIBOSOMAL PROTEIN L38-like p	---	AT3G59540	-1.25	-0.33	-1.75	0.125516	0.309665	-5.42
264012_at	hypothetical protein predicted by gensca	---	AT2G21080	1.19	0.25	1.75	0.125432	0.309665	-5.42
255737_at	unknown protein ;supported by full-lengt	---	AT1G25420	-1.16	-0.21	-1.75	0.12546	0.309665	-5.42
259913_at	putative GTP-binding protein similar to G	---	AT1G72660	1.12	0.16	1.75	0.125519	0.309665	-5.42
252731_at	putative protein predicted proteins, Aral	---	---	1.21	0.27	1.75	0.125496	0.309665	-5.42
250218_at	putative protein contains similarity to un	CHC1	AT5G14170	-1.20	-0.27	-1.75	0.125387	0.309665	-5.42
266486_at	hypothetical protein predicted by gensca	---	AT2G47950	1.95	0.96	1.75	0.125532	0.309665	-5.42
262626_at	FtsH protease, putative similar to zinc d	FTSH8	AT1G06430	-1.20	-0.27	-1.75	0.125497	0.309665	-5.42
260298_at	putative oxidoreductase contains Pfam p	---	AT1G80320	1.13	0.17	1.75	0.125443	0.309665	-5.42
262049_at	unknown protein ;supported by full-lengt	---	AT1G80180	-1.17	-0.22	-1.75	0.125555	0.309679	-5.42
258336_at	putative ethylene-inducible protein simila	PDX1.2	AT3G16050	-1.34	-0.43	-1.75	0.125587	0.309725	-5.42
250329_at	putative potassium transport protein glu	KEA6	AT5G11800	-1.16	-0.21	-1.75	0.125611	0.309750	-5.42
264454_at	unknown protein similar to U2 small nuc	---	AT1G10320	-1.17	-0.23	-1.75	0.12567	0.309862	-5.43
246820_at	putative protein predicted proteins, Aral	---	AT5G26910	-1.12	-0.16	-1.75	0.125724	0.309901	-5.43
262132_at	ribosomal protein L22, putative similar t	---	AT1G02830	1.14	0.19	1.75	0.125707	0.309901	-5.43
260908_at	maternal embryogenesis control protein	MEA	AT1G02580	1.30	0.38	1.75	0.125726	0.309901	-5.43
252818_at	putative protein several hypothetical pro	---	---	1.17	0.23	1.75	0.125786	0.309950	-5.43
261239_at	Avr9 elicitor response protein, putative	---	AT1G32930	1.13	0.18	1.75	0.125766	0.309950	-5.43
259999_at	hypothetical protein predicted by genefir	---	AT1G68080	-1.23	-0.29	-1.75	0.125787	0.309950	-5.43
248049_at	putative protein contains similarity to cyt	COX15	AT5G56090	-1.36	-0.44	-1.75	0.125896	0.310083	-5.43
248832_at	putative protein similar to unknown prote	---	AT5G47170	1.12	0.17	1.75	0.125874	0.310083	-5.43
258902_at	putative pyruvate dehydrogenase kinas	PDK	AT3G06483	-1.13	-0.17	-1.75	0.125879	0.310083	-5.43
247766_at	FtsH protease, putative contains similar	ftsh9	AT5G58870	-1.17	-0.22	-1.75	0.125887	0.310083	-5.43
258559_at	putative transcriptional regulator similar	ATCHR12	AT3G06010	-1.19	-0.25	-1.75	0.125914	0.310094	-5.43
251111_at	putative protein different hypothetical pr	---	AT5G01310	1.17	0.22	1.75	0.125974	0.310210	-5.43
258262_at	hypothetical protein	---	AT3G15770	1.18	0.24	1.75	0.126083	0.310443	-5.43
258690_at	putative phosphatidylinositol-4-phospha	---	AT3G07960	1.14	0.19	1.75	0.126168	0.310586	-5.43
257887_at	protein phosphatase-2c, putative simila	---	AT3G17090	-1.18	-0.24	-1.75	0.126155	0.310586	-5.43
256940_at	unknown protein	QQS	AT3G30720	-1.18	-0.24	-1.75	0.126193	0.310613	-5.43
245783_s_a	hypothetical protein similar to hypothetic	---	AT1G35170 /	1.48	0.56	1.74	0.126219	0.310645	-5.43
263630_at	Expressed protein ; supported by full-ler	---	AT2G04845	-1.13	-0.18	-1.74	0.126258	0.310708	-5.43
250743_at	phosphate/phosphoenolpyruvate translo	---	AT5G05820	1.17	0.22	1.74	0.126359	0.310923	-5.43
261557_at	kinesin-like protein C-terminal region is s	---	AT1G63640	-1.21	-0.28	-1.74	0.126389	0.310928	-5.43
255550_at	putative raffinose synthase or seed imb	AtSTS	AT4G01970	1.13	0.18	1.74	0.126376	0.310928	-5.43
251501_at	putative protein several hypothetical pro	---	AT3G59120	1.14	0.19	1.74	0.126447	0.311038	-5.43

251142_at	Expressed protein ; supported by full-ler	---	AT5G01015	1.16	0.21	1.74	0.126481	0.311056	-5.43
251850_at	F-box protein family, AtFBL17 contains	FBL17	AT3G54650	1.22	0.29	1.74	0.126473	0.311056	-5.43
256075_at	mitogen-activated protein kinase, putati	ATMPK8	AT1G18150	-1.18	-0.24	-1.74	0.126512	0.311093	-5.43
250868_at	malate synthase -like protein malate sy	MLS	AT5G03860	-1.23	-0.30	-1.74	0.126532	0.311093	-5.43
260531_at	putative acyl-CoA synthetase ; supporte	CER8	AT2G47240	1.21	0.27	1.74	0.126538	0.311093	-5.43
260591_at	predicted protein	---	AT1G53325	1.12	0.16	1.74	0.126569	0.311137	-5.43
263759_at	hypothetical protein predicted by genefi	---	AT2G21290	-1.16	-0.21	-1.74	0.126629	0.311223	-5.43
264502_at	putative 12-oxophytodienoate reductas	---	AT1G09400	1.19	0.25	1.74	0.126632	0.311223	-5.43
258364_at	unknown protein	GLIP4	AT3G14225	1.32	0.40	1.74	0.126668	0.311280	-5.43
264165_at	hypothetical protein contains similarity t	ATNAP11	AT1G65410	-1.13	-0.18	-1.74	0.126805	0.311558	-5.43
261464_at	disease resistance response protein, pu	---	AT1G07730 /	-1.17	-0.23	-1.74	0.126808	0.311558	-5.43
256862_at	dihydroxyacid dehydratase, putative sir	---	AT3G23940	-1.39	-0.48	-1.74	0.1269	0.311748	-5.43
265810_at	unknown protein	---	AT2G18090	1.25	0.33	1.74	0.126935	0.311802	-5.43
263590_at	putative receptor-like protein kinase	---	AT2G01820	-1.14	-0.18	-1.74	0.126961	0.311831	-5.44
252247_at	putative protein various predicted protei	---	AT3G49740	-1.14	-0.19	-1.74	0.127054	0.312026	-5.44
248346_at	GTP-binding protein-like ;supported by	ATGB1	AT5G52210	1.27	0.35	1.74	0.127087	0.312073	-5.44
263647_at	unknown protein	---	AT2G04690	-1.20	-0.27	-1.74	0.127145	0.312183	-5.44
258674_at	putative elongation factor P (EF-P) simil	---	AT3G08740	-1.25	-0.32	-1.74	0.127202	0.312289	-5.44
256733_at	hypothetical protein predicted by genem	---	AT3G30370	1.14	0.19	1.74	0.127267	0.312414	-5.44
258985_at	hypothetical protein similar to hypotheti	---	AT3G08960	1.13	0.18	1.74	0.127289	0.312435	-5.44
263932_at	unknown protein	---	AT2G35990	1.13	0.18	1.74	0.127327	0.312495	-5.44
255523_at	pectinesterase - like protein similar to ba	---	AT4G02320	-1.15	-0.20	-1.74	0.127425	0.312701	-5.44
247013_at	putative protein strong similarity to unkn	BT4	AT5G67480	1.28	0.36	1.74	0.127449	0.312727	-5.44
264208_at	putative polyA-binding protein, PAB3 st	PAB3	AT1G22760	1.25	0.32	1.74	0.12748	0.312771	-5.44
261763_at	ABC transporter, putative similar to ABC	PDR12	AT1G15520	1.83	0.87	1.74	0.127586	0.312997	-5.44
246758_at	60S ribosomal protein - like 60S riboso	---	AT5G27850	-1.28	-0.36	-1.74	0.127621	0.313048	-5.44
261987_at	hypothetical protein predicted by genem	---	AT1G33710	1.11	0.15	1.74	0.127667	0.313128	-5.44
245104_at	hypothetical protein predicted by genefi	---	AT2G41600	-1.14	-0.19	-1.74	0.12769	0.313150	-5.44
245720_at	RNA binding protein - like	---	AT5G04210	1.14	0.19	1.74	0.127708	0.313152	-5.44
255155_at	hypothetical protein	---	AT4G08230	1.17	0.23	1.74	0.127718	0.313152	-5.44
245397_at	auxin-responsive protein IAA1 ;supporte	IAA1	AT4G14560	-1.48	-0.57	-1.74	0.127757	0.313197	-5.44
248614_at	putative protein similar to unknown prote	---	AT5G49560	-1.14	-0.19	-1.74	0.127764	0.313197	-5.44
247112_at	unknown protein	---	AT5G65950	-1.16	-0.21	-1.74	0.127796	0.313211	-5.44
257443_at	hypothetical protein predicted by gensca	---	AT2G22050	-1.14	-0.18	-1.74	0.127797	0.313211	-5.44
252151_at	putative protein several hypothetical pro	---	AT3G51320	-1.12	-0.17	-1.74	0.127852	0.313253	-5.44

253929_s_a	putative protein H+-transporting ATP sy	---	AT2G16030 /	1.16	0.21	1.74	0.127833	0.313253	-5.44
246243_at	trichohyalin like protein	---	AT4G36520	1.12	0.17	1.74	0.127855	0.313253	-5.44
267277_at	putative protein transport protein SEC13	---	AT2G30050	1.15	0.20	1.74	0.127916	0.313348	-5.44
267032_at	putative protein kinase contains a protei	CIPK22	AT2G38490	1.25	0.32	1.74	0.127922	0.313348	-5.44
267237_s_a	unknown protein ;supported by full-leng	---	AT2G44040 /	-1.36	-0.44	-1.74	0.127992	0.313452	-5.44
245171_at	hypothetical protein predicted by gensca	---	AT2G47560	-1.16	-0.21	-1.74	0.127985	0.313452	-5.44
254284_at	putative fizzy-related protein fizzy-relate	FZR2	AT4G22910	1.23	0.30	1.73	0.128053	0.313535	-5.44
249948_at	eIF-4AII - like protein EUKARYOTIC IN	---	AT5G19210	-1.20	-0.26	-1.73	0.128052	0.313535	-5.44
254390_at	calcium-dependent protein kinase - like	CPK15	AT4G21940	1.15	0.20	1.73	0.12811	0.313640	-5.44
249239_at	MAP kinase ; supported by cDNA: gi_1	CPuORF5	AT5G41990 /	1.13	0.18	1.73	0.128177	0.313766	-5.44
254203_at	putative protein various predicted prote	AtGRF8	AT4G24150	-1.13	-0.18	-1.73	0.128189	0.313766	-5.44
258761_at	unknown protein	---	AT3G10760	-1.24	-0.31	-1.73	0.128227	0.313825	-5.44
250409_at	putative protein 110K5.11, unknown pro	---	AT5G10860	-1.15	-0.20	-1.73	0.128271	0.313900	-5.44
245376_at	peroxidase like protein	---	AT4G17690	1.13	0.17	1.73	0.128318	0.313980	-5.45
255234_at	contains similarity to Medicago truncatul	---	AT4G05500	1.15	0.20	1.73	0.128333	0.313985	-5.45
263938_at	hypothetical protein predicted by genefir	---	AT2G35900	-1.14	-0.19	-1.73	0.128384	0.314075	-5.45
249595_at	putative protein SIAH1 protein, Brassica	---	AT5G37930	-1.21	-0.27	-1.73	0.128424	0.314139	-5.45
258491_at	unknown protein ;supported by full-leng	---	AT3G02700	1.23	0.30	1.73	0.128442	0.314150	-5.45
252939_at	NAD(P)H oxidoreductase, isoflavone re	---	AT4G39230	1.62	0.69	1.73	0.128473	0.314160	-5.45
245063_at	Expressed protein ; supported by full-ler	---	AT2G39795	-1.39	-0.47	-1.73	0.128467	0.314160	-5.45
259477_at	unknown protein ;supported by full-lengt	---	AT1G19120	-1.13	-0.17	-1.73	0.128534	0.314273	-5.45
267244_at	putative reverse transcriptase	---	AT2G02650	1.14	0.18	1.73	0.128613	0.314434	-5.45
258584_at	hypothetical protein predicted by gensca	SIP1A	AT3G04090	1.11	0.15	1.73	0.128638	0.314458	-5.45
245910_at	putative protein ER66 - Lycopersicon es	EICBP.B	AT5G09410	-1.14	-0.19	-1.73	0.128651	0.314458	-5.45
254387_at	putative protein CGI-131 protein, Homo	ATMSRB9	AT4G21850	2.45	1.29	1.73	0.12867	0.314471	-5.45
258125_s_a	hypothetical protein contains Pfam profil	---	AT3G23510 /	1.43	0.52	1.73	0.128734	0.314561	-5.45
260135_at	calmodulin-related protein similar to GB	---	AT1G66400	1.57	0.65	1.73	0.128731	0.314561	-5.45
248224_at	thylakoid lumenal 17.4 kD protein, chlor	---	AT5G53490	-1.22	-0.29	-1.73	0.128764	0.314599	-5.45
246280_at	hypothetical protein	---	AT4G36660	-1.35	-0.43	-1.73	0.1288	0.314655	-5.45
264592_at	putative prolyl 4-hydroxylase, alpha sub	---	AT2G17720	1.43	0.52	1.73	0.128835	0.314705	-5.45
246950_at	transcription initiation factor IID-associa	TAF5	AT5G25150	-1.12	-0.17	-1.73	0.129048	0.315192	-5.45
250602_s_a	unknown protein	---	AT5G07940 /	-1.15	-0.20	-1.73	0.129101	0.315255	-5.45
247680_s_a	glycine-rich protein - like glycine-rich pr	---	AT1G61210 /	-1.15	-0.20	-1.73	0.129099	0.315255	-5.45
251291_at	putative protein auxin-induced protein S	---	AT3G61900	-1.14	-0.19	-1.73	0.129133	0.315266	-5.45
246728_at	putative protein various predicted prote	---	AT5G28040	-1.12	-0.16	-1.73	0.12912	0.315266	-5.45

265784_at	hypothetical protein predicted by gensca	---	AT2G07280	-1.14	-0.18	-1.73	0.129203	0.315368	-5.45
247769_at	laccase precursor - like protein laccase	LAC16	AT5G58910	1.13	0.18	1.73	0.129199	0.315368	-5.45
262664_at	hypothetical protein predicted by genem	---	AT1G13970	-1.15	-0.20	-1.73	0.129251	0.315426	-5.45
263770_at	Mutator-like transposase similar to MUF	---	---	1.22	0.29	1.73	0.129278	0.315426	-5.45
262213_at	hypothetical protein predicted by genem	---	AT1G74870	1.20	0.27	1.73	0.129282	0.315426	-5.45
264276_at	hypothetical protein contains similarity t	---	AT1G60380	1.13	0.17	1.73	0.129264	0.315426	-5.45
259600_at	hypothetical protein predicted by gensca	---	AT1G35220	1.20	0.26	1.73	0.129311	0.315464	-5.45
261566_at	unknown protein ;supported by full-lengt	---	AT1G33230	-1.19	-0.25	-1.73	0.129353	0.315508	-5.45
247188_at	14-3-3 protein GF14kappa (grf8) identic	GRF8	AT5G65430	-1.16	-0.22	-1.73	0.129357	0.315508	-5.45
249368_at	putative protein predicted proteins, Arat	---	AT5G40640	-1.20	-0.27	-1.73	0.129372	0.315511	-5.45
258300_at	putative casein kinase I similar to casein	ckl10	AT3G23340	-1.23	-0.30	-1.73	0.129476	0.315712	-5.45
261667_at	unknown protein similar to putative lipas	---	AT1G18460	-1.22	-0.28	-1.73	0.129482	0.315712	-5.45
AFFX-Athal-	Arabidopsis thaliana /REF=X52320 /DE	---	---	1.21	0.27	1.73	0.129533	0.315719	-5.45
259096_at	putative 40S ribosomal protein S3A (S p	---	AT3G04840	-1.37	-0.45	-1.73	0.129554	0.315719	-5.45
248735_at	laccase (diphenol oxidase)	TT10	AT5G48100	1.14	0.18	1.73	0.129562	0.315719	-5.45
260628_at	hypothetical protein predicted by genem	---	AT1G62320	1.13	0.18	1.73	0.129559	0.315719	-5.45
250022_at	Brn1-like protein	---	AT5G18210	-1.28	-0.36	-1.73	0.129568	0.315719	-5.45
260986_at	glyoxalase II, putative similar to GI:164	GLY3	AT1G53580	1.26	0.33	1.73	0.129504	0.315719	-5.45
251660_at	Expressed protein ; supported by full-ler	---	AT3G57160	1.22	0.28	1.73	0.129616	0.315735	-5.45
255956_at	Expressed protein ; supported by full-ler	DD46	AT1G22015	1.16	0.22	1.73	0.129606	0.315735	-5.45
258451_at	alternative oxidase 1b precursor identica	AOX1B	AT3G22360	1.18	0.24	1.73	0.129603	0.315735	-5.45
266842_at	FtsH protease, putative contains similar	ftsh4	AT2G26140	-1.17	-0.23	-1.73	0.129638	0.315756	-5.45
260361_at	unknown protein ; supported by cDNA: g	---	AT1G69360	-1.21	-0.28	-1.73	0.12968	0.315789	-5.46
261285_at	Ca2+-dependent membrane-binding pro	ANNAT1	AT1G35720	-1.45	-0.53	-1.73	0.129673	0.315789	-5.45
254743_at	potassium transporter - like protein pota	HAK5	AT4G13420	2.63	1.39	1.73	0.12974	0.315902	-5.46
245919_at	putative protein various predicted prote	---	AT5G28780	1.12	0.16	1.73	0.129766	0.315932	-5.46
264830_at	hypothetical protein predicted by genefir	---	AT1G03710	1.17	0.23	1.73	0.129853	0.316110	-5.46
260024_at	beta-1,3-glucanase precursor, putative	---	AT1G30080	-1.11	-0.16	-1.73	0.129886	0.316155	-5.46
250104_at	unknown protein	---	AT5G16610	-1.21	-0.28	-1.72	0.129903	0.316163	-5.46
250542_at	hypothetical protein (fragment at BAC e	---	AT5G08270	-1.30	-0.38	-1.72	0.129978	0.316245	-5.46
250998_at	ankyrin - like protein ankyrin G119, Hor	---	AT5G02620	-1.22	-0.29	-1.72	0.129952	0.316245	-5.46
246493_at	putative protein hypothetical proteins - A	CRS1	AT5G16180	-1.17	-0.23	-1.72	0.129977	0.316245	-5.46
266413_at	unknown protein ;supported by full-leng	---	AT2G38740	-1.17	-0.22	-1.72	0.130014	0.316299	-5.46
249098_at	DNA repair protein-like	---	AT5G43530	-1.14	-0.19	-1.72	0.13005	0.316352	-5.46
247584_at	60S ribosomal protein L12 - like 60S RI	---	AT5G60670	-1.40	-0.49	-1.72	0.130066	0.316357	-5.46

262163_at	ribosomal protein L30, putative similar t	---	AT1G77940	-1.37	-0.45	-1.72	0.13013	0.316479	-5.46
251807_at	methionyl-tRNA synthetase (AtcpMetRS	OVA1	AT3G55400	-1.19	-0.25	-1.72	0.130155	0.316508	-5.46
267519_at	putative VP1/ABI3 family regulatory prot	HSI2	AT2G30470	-1.21	-0.28	-1.72	0.130169	0.316508	-5.46
266129_at	hypothetical protein predicted by gensca	CCD7	AT2G44990	1.55	0.64	1.72	0.130229	0.316585	-5.46
262724_s_a	PC-MYB2, putative similar to PC-MYB2	---	AT1G43330 /	1.13	0.17	1.72	0.130218	0.316585	-5.46
263382_at	putative anthranilate N-hydroxycinnamo	---	AT2G40230	-1.19	-0.25	-1.72	0.130261	0.316629	-5.46
245638_s_a	F5A9.10 unknown protein; similar to ES	---	AT1G24822 /	1.15	0.20	1.72	0.130297	0.316682	-5.46
256276_at	geranylgeranyl transferase type II beta	---	AT3G12070	-1.15	-0.21	-1.72	0.130326	0.316720	-5.46
261361_at	hypothetical protein predicted by gensca	---	---	-1.16	-0.22	-1.72	0.130382	0.316822	-5.46
263606_at	putative beta-ketoacyl-CoA synthase	KCS9	AT2G16280	1.23	0.30	1.72	0.13047	0.316988	-5.46
266336_at	putative Fe(II) transporter identical to G	ZIP3	AT2G32270	1.19	0.25	1.72	0.130478	0.316988	-5.46
249332_at	putative protein similar to unknown prote	---	AT5G40980	1.18	0.24	1.72	0.130565	0.317167	-5.46
263907_at	abscisic acid insensitive 5 (ABI5) contai	ABI5	AT2G36270	1.19	0.25	1.72	0.130593	0.317200	-5.46
249073_at	vegetative storage protein-like ;support	---	AT5G44020	1.44	0.53	1.72	0.130687	0.317321	-5.46
261248_at	calreticulin, putative similar to GB:AAF0	---	AT1G20030	-1.43	-0.51	-1.72	0.130686	0.317321	-5.46
256643_at	unknown protein similar to putative retro	---	---	-1.15	-0.20	-1.72	0.130698	0.317321	-5.46
247494_at	calnexin - like protein calnexin homolog	CNX1	AT5G61790	1.53	0.61	1.72	0.130688	0.317321	-5.46
251471_at	putative protein GTPASE-ACTIVATING	---	AT3G59570	1.16	0.21	1.72	0.13072	0.317339	-5.46
245750_at	histone H2A, putative similar to histone	HTA10	AT1G51060	-1.33	-0.42	-1.72	0.130749	0.317362	-5.46
248648_at	putative protein similar to unknown prote	---	AT5G49220	-1.16	-0.22	-1.72	0.130764	0.317362	-5.46
255484_at	putative protein similar to A. thaliana hy	---	AT4G02540	1.18	0.23	1.72	0.130785	0.317362	-5.46
255566_s_a	hypothetical protein	---	AT3G48670 /	-1.16	-0.21	-1.72	0.130773	0.317362	-5.46
267290_at	putative SET-domain transcriptional reg	---	AT2G23740	-1.18	-0.24	-1.72	0.130957	0.317745	-5.46
255796_at	similar to mammalian MHC III region pro	SUVH2	AT2G33290	-1.15	-0.20	-1.72	0.131047	0.317930	-5.46
255993_at	hypothetical protein contains similarity to	---	AT1G29770	1.13	0.17	1.72	0.131074	0.317962	-5.47
259216_at	hypothetical protein ; supported by cDNA	---	AT3G09000	1.33	0.41	1.72	0.131137	0.318070	-5.47
245768_at	hypothetical protein similar to putative d	---	AT1G33590	1.37	0.45	1.72	0.131146	0.318070	-5.47
262639_at	calmodulin, putative similar to calmodul	---	AT1G62820	1.23	0.30	1.72	0.13117	0.318094	-5.47
260454_at	RING-H2 zinc finger protein (ATL3) iden	ATL3	AT1G72310	-1.33	-0.42	-1.72	0.131213	0.318163	-5.47
256402_at	hypothetical protein ; supported by cDN	---	AT3G06130	1.34	0.42	1.72	0.131267	0.318261	-5.47
245206_at	putative protein similarity to NCA2 prote	DGS1	AT5G12290	-1.16	-0.22	-1.72	0.131375	0.318455	-5.47
246845_at	glutamyl-tRNA synthetase ; supported b	---	AT5G26710	-1.12	-0.17	-1.72	0.131368	0.318455	-5.47
265742_at	putative ribose 5-phosphate isomerase	---	AT2G01290	-1.23	-0.29	-1.72	0.1314	0.318474	-5.47
251055_at	putative protein putative protein F4P12.	---	AT5G01710 /	-1.13	-0.18	-1.72	0.131425	0.318474	-5.47
248537_at	putative protein similar to unknown prote	---	AT5G50100	-1.20	-0.26	-1.72	0.131417	0.318474	-5.47

259349_at	unknown protein ; supported by cDNA:	ATAPRL5	AT3G03860	-1.13	-0.17	-1.72	0.131448	0.318498	-5.47
266086_at	putative Na+-dependent inorganic phos	PHT4;2	AT2G38060	1.15	0.21	1.72	0.131468	0.318512	-5.47
255298_at	putative protein similar to transcriptional	ATMSRB6	AT4G04840	-1.65	-0.72	-1.72	0.131511	0.318582	-5.47
256578_at	peroxidase, putative similar to peroxida	---	AT3G28200	-1.31	-0.39	-1.72	0.13162	0.318654	-5.47
247380_at	4-coumarate-CoA ligase-like protein	---	AT5G63380	-1.20	-0.26	-1.72	0.131608	0.318654	-5.47
258159_at	receptor kinase, putative similar to rece	RLK902	AT3G17840	1.31	0.39	1.72	0.13157	0.318654	-5.47
260502_at	putative Tub family protein contains Pfa	AtTLP6	AT1G47270	1.17	0.22	1.72	0.131625	0.318654	-5.47
263683_at	putative NAM protein similar to GB:AAD	FEZ	AT1G26870	1.15	0.20	1.72	0.13159	0.318654	-5.47
256178_s_a	auxin conjugate hydrolase (ILL5) identic	ILL5	AT1G51760 /	1.59	0.67	1.72	0.131574	0.318654	-5.47
255140_x_a	extensin-like protein hydroxyproline-rich	---	AT4G08410	1.24	0.31	1.72	0.131719	0.318848	-5.47
263900_at	unknown protein ;supported by full-leng	---	AT2G36290	-1.19	-0.25	-1.72	0.131735	0.318855	-5.47
246481_s_a	cold and ABA inducible protein kin1 ;su	KIN1	AT5G15960 /	-2.09	-1.06	-1.72	0.131779	0.318926	-5.47
255574_at	putative calcium-regulated protein phos	CBL5	AT4G01420	-1.15	-0.20	-1.71	0.131911	0.319213	-5.47
256321_at	lipoxygenase, putative similar to lipoxyg	LOX1	AT1G55020	1.84	0.88	1.71	0.132109	0.319623	-5.47
249486_at	receptor protein kinase - like protein rec	---	AT5G39030	1.17	0.23	1.71	0.132097	0.319623	-5.47
267209_at	unknown protein ;supported by full-leng	---	AT2G30930	-1.19	-0.25	-1.71	0.13219	0.319750	-5.47
257590_s_a	hypothetical protein predicted by gensca	---	AT3G24870 /	-1.19	-0.25	-1.71	0.132176	0.319750	-5.47
263858_at	hypothetical protein predicted by gensca	---	AT2G04370	1.13	0.17	1.71	0.132224	0.319799	-5.47
248679_at	unknown protein ;supported by full-leng	---	AT5G48830	-1.23	-0.30	-1.71	0.132241	0.319807	-5.47
250665_at	unknown protein ;supported by full-leng	---	AT5G06980	-1.19	-0.25	-1.71	0.132267	0.319833	-5.47
262816_at	alkylation repair-like protein	---	AT1G11780	-1.22	-0.28	-1.71	0.13228	0.319833	-5.47
267431_at	unknown protein ;supported by full-leng	MEE26	AT2G34870	1.16	0.21	1.71	0.132327	0.319913	-5.47
260039_at	CLE12 CLAVATA3/ESR-Related 12; su	CLE12	AT1G68795	1.18	0.24	1.71	0.132357	0.319952	-5.47
261224_at	subtilisin-like serine protease similar to s	ATSBT5.2	AT1G20160	-1.44	-0.53	-1.71	0.132402	0.319965	-5.47
267441_at	putative receptor-like protein kinase	---	AT2G19210	1.13	0.17	1.71	0.132389	0.319965	-5.47
245645_at	F5A9.19 unknown protein; similar to ES	ATMAP70	AT1G24764	-1.22	-0.29	-1.71	0.132405	0.319965	-5.47
256240_at	unknown protein ; supported by cDNA: g	atnudt16	AT3G12600	1.15	0.20	1.71	0.132423	0.319974	-5.47
255779_at	unknown protein similar to beta-1,3-glu	PDCB3	AT1G18650	-1.35	-0.43	-1.71	0.132436	0.319974	-5.47
248861_at	senescence-associated protein 5-like pr	TRN2	AT5G46700	1.56	0.64	1.71	0.132476	0.320037	-5.48
263534_at	putative steroid binding protein ;suppor	AtMAPR2	AT2G24940 /	-1.16	-0.22	-1.71	0.132525	0.320120	-5.48
247050_at	At14a protein-like	---	AT5G66660	1.21	0.28	1.71	0.132543	0.320131	-5.48
248939_at	tyrosine-specific protein phosphatase-lik	---	AT5G45790	-1.15	-0.20	-1.71	0.132578	0.320180	-5.48
250896_at	putative protein ; supported by cDNA: g	---	AT5G03560	-1.22	-0.28	-1.71	0.13262	0.320180	-5.48
265205_at	putative poly(A) binding protein	PAB7	AT2G36660	1.14	0.18	1.71	0.132617	0.320180	-5.48
247425_at	unknown protein	---	AT5G62550	1.12	0.16	1.71	0.132609	0.320180	-5.48

266061_at	putative translation initiation factor eIF-2	---	AT2G18720	1.15	0.21	1.71	0.132651	0.320221	-5.48
261425_at	peptide transporter, putative similar to p	---	AT1G18880	-1.35	-0.43	-1.71	0.13267	0.320234	-5.48
258924_at	putative diadenosine 5',5'''-P1,P4-tetrap	ATNUDX2	AT3G10620	-1.13	-0.18	-1.71	0.13274	0.320327	-5.48
267146_at	hypothetical protein predicted by gensca	---	AT2G38160	1.14	0.18	1.71	0.132751	0.320327	-5.48
250689_at	putative protein similar to unknown prote	---	AT5G06610	-1.42	-0.51	-1.71	0.132727	0.320327	-5.48
260712_at	protein phosphatase 2C, putative simila	HAB2	AT1G17550	1.21	0.27	1.71	0.13281	0.320415	-5.48
252626_at	putative protein predicted protein, Arabi	---	AT3G44940	1.19	0.25	1.71	0.132815	0.320415	-5.48
258038_at	unknown protein ;supported by full-leng	---	AT3G21260	-1.27	-0.35	-1.71	0.132871	0.320515	-5.48
250163_at	putative protein various predicted prote	---	AT5G15270	-1.16	-0.22	-1.71	0.132916	0.320590	-5.48
265233_s_a	hypothetical protein	---	AT2G07718	1.15	0.20	1.71	0.13302	0.320806	-5.48
245120_at	hypothetical protein predicted by gensca	HOS1	AT2G39810	-1.18	-0.24	-1.71	0.133104	0.320906	-5.48
245238_at	putative protein similarity to cytochrome	ACYB-2	AT4G25570	-1.18	-0.24	-1.71	0.1331	0.320906	-5.48
259684_at	unknown protein	---	AT1G63070	-1.14	-0.19	-1.71	0.133083	0.320906	-5.48
247611_at	putative protein predicted proteins	---	AT5G60710	-1.12	-0.17	-1.71	0.133175	0.321046	-5.48
265761_at	putative stress protein	---	AT2G01330	1.14	0.19	1.71	0.133226	0.321132	-5.48
252070_at	short-chain alcohol dehydrogenase-like	---	AT3G51680	1.18	0.24	1.71	0.133255	0.321170	-5.48
254171_at	PsRT17-1 like protein PsRT17-1, Pisun	---	AT4G24530	-1.12	-0.17	-1.71	0.133276	0.321187	-5.48
253907_at	putative protein dihydrokaempferol 4-re	---	AT4G27250	1.20	0.27	1.71	0.133325	0.321236	-5.48
247665_at	putative protein various predicted prote	---	AT5G60130	-1.12	-0.17	-1.71	0.133339	0.321236	-5.48
247929_at	apospory-associated protein C	---	AT5G57330	-1.18	-0.24	-1.71	0.133321	0.321236	-5.48
264820_at	putative coproporphyrinogen III oxidase	LIN2	AT1G03475	-1.11	-0.15	-1.71	0.133397	0.321343	-5.48
259004_at	putative protein kinase C-terminal regio	---	AT3G01840	1.14	0.19	1.71	0.133539	0.321650	-5.48
261794_at	hypothetical protein contains similarity to	---	AT1G16060	-1.18	-0.24	-1.71	0.133648	0.321879	-5.48
261164_at	hypothetical protein ;supported by full-le	---	AT1G34470	-1.16	-0.21	-1.70	0.133691	0.321881	-5.48
245441_at	decarboxylase like protein	PSD1	AT4G16700	-1.20	-0.26	-1.70	0.13369	0.321881	-5.48
254307_at	putative protein various predicted prote	---	AT4G22400	1.24	0.32	1.71	0.133687	0.321881	-5.48
262341_at	E2, ubiquitin-conjugating enzyme, puta	UBC28	AT1G64230	-1.17	-0.23	-1.70	0.133748	0.321916	-5.48
253047_at	Expressed protein ; supported by full-ler	---	AT4G37295	1.28	0.36	1.70	0.133728	0.321916	-5.48
262292_at	hypothetical protein similar to hypothetic	---	AT1G27595	1.16	0.21	1.70	0.133748	0.321916	-5.48
264438_at	putative 60S ribosomal protein L17 simil	---	AT1G27400	-1.27	-0.34	-1.70	0.133766	0.321924	-5.48
251281_at	putative protein hypothetical protein At2	AGP20	AT3G61640	1.42	0.51	1.70	0.133816	0.322011	-5.48
261860_at	scarecrow-like protein similar to SCARE	SCL5	AT1G50600	-1.18	-0.24	-1.70	0.133836	0.322025	-5.48
262411_at	hypothetical protein predicted by genem	---	AT1G34640	-1.16	-0.21	-1.70	0.133931	0.322220	-5.49
261243_at	hypothetical protein predicted by genem	---	AT1G20180	1.46	0.55	1.70	0.133998	0.322346	-5.49
263223_at	coatomer-like protein, epsilon subunit s	---	AT1G30630	1.16	0.22	1.70	0.134045	0.322401	-5.49

254757_at	putative protein other putative or hypoth	ROPGEF9	AT4G13240	1.14	0.19	1.70	0.134049	0.322401	-5.49
264611_at	putative pectate lyase A11 similar to GB	---	AT1G04680	1.74	0.80	1.70	0.134124	0.322443	-5.49
261183_at	hypothetical protein predicted by genem	EMB2756	AT1G34550	-1.18	-0.24	-1.70	0.134102	0.322443	-5.49
250944_at	putative protein	---	AT5G03380	1.63	0.71	1.70	0.134156	0.322443	-5.49
247141_at	putative protein strong similarity to unkn	---	AT5G65560	-1.23	-0.30	-1.70	0.134154	0.322443	-5.49
247976_at	unknown protein	---	---	1.17	0.23	1.70	0.134165	0.322443	-5.49
255372_at	putative reverse transcriptase	---	---	1.24	0.31	1.70	0.134129	0.322443	-5.49
248450_at	putative protein contains similarity to unl	---	AT5G51290	1.16	0.22	1.70	0.134161	0.322443	-5.49
257801_at	mitogen activated protein kinase kinase	WNK6	AT3G18750	-1.16	-0.21	-1.70	0.134251	0.322615	-5.49
252679_at	CCR4-associated factor 1-like protein C	---	AT3G44260	2.01	1.01	1.70	0.134302	0.322703	-5.49
263413_at	unknown protein ;supported by full-leng	BPC4	AT2G21240	-1.17	-0.22	-1.70	0.134316	0.322704	-5.49
265192_at	hypothetical protein predicted by gensca	---	AT1G05060	1.19	0.25	1.70	0.134379	0.322788	-5.49
260529_at	putative chloroplast protein CP12 ; supp	CP12-1	AT2G47400	1.12	0.16	1.70	0.134373	0.322788	-5.49
260600_at	hypothetical protein predicted by genem	---	AT1G55950	1.16	0.21	1.70	0.134417	0.322844	-5.49
258377_at	hypothetical protein contains similarity to	CNGC19	AT3G17690	1.16	0.21	1.70	0.134551	0.323131	-5.49
247294_at	putative protein similar to unknown prote	XRCC2	AT5G64520	1.13	0.17	1.70	0.134612	0.323246	-5.49
257102_at	endoxyloglucan transferase, putative si	XTH3	AT3G25050	1.12	0.16	1.70	0.134709	0.323374	-5.49
252478_at	putative protein mitotic phosphoprotein	---	AT3G46540	-1.26	-0.33	-1.70	0.134686	0.323374	-5.49
260234_at	putative lipase/acylhydrolase contains P	---	AT1G74460	1.20	0.27	1.70	0.134697	0.323374	-5.49
260995_at	unknown protein	---	AT1G12120	-1.14	-0.19	-1.70	0.1348	0.323493	-5.49
260539_at	putative peroxidase	---	AT2G43480	1.12	0.16	1.70	0.134788	0.323493	-5.49
249946_at	putative protein predicted proteins, Arat	---	AT5G19170	1.33	0.41	1.70	0.134778	0.323493	-5.49
247573_at	anthocyanin 5-aromatic acyltransferase	AACT1	AT5G61160	-2.11	-1.08	-1.70	0.134875	0.323637	-5.49
250496_at	inorganic pyrophosphatase - like protei	AtPPa6	AT5G09650	-1.43	-0.52	-1.70	0.134894	0.323648	-5.49
267568_at	hypothetical protein predicted by gensca	---	AT2G30780	-1.15	-0.21	-1.70	0.135108	0.324057	-5.49
259966_at	unknown protein	SOB3	AT1G76500	1.16	0.21	1.70	0.135135	0.324057	-5.49
253593_at	putative protein hypothetical protein F9	---	AT4G30760	-1.16	-0.22	-1.70	0.135114	0.324057	-5.49
251208_at	putative protein amino acid selective ch	ATOEP16-	AT3G62880	-1.14	-0.19	-1.70	0.135131	0.324057	-5.49
260099_at	unknown protein ;supported by full-leng	---	AT1G73180	-1.13	-0.17	-1.70	0.13512	0.324057	-5.49
254433_at	putative protein tripeptidyl-peptidase II,	TPP2	AT4G20850	1.12	0.16	1.70	0.13518	0.324088	-5.49
260128_at	hypothetical protein similar to Yml014wp	---	AT1G36310	-1.16	-0.21	-1.70	0.135185	0.324088	-5.49
266376_at	putative endoxyloglucan glycosyltransfe	---	AT2G14620	1.19	0.25	1.70	0.135191	0.324088	-5.49
254089_at	putative protein apoptosis gene MA3, S	---	AT4G24800	-1.15	-0.20	-1.70	0.135275	0.324174	-5.49
265418_at	AP2 domain transcription factor	---	AT2G20880	1.65	0.72	1.70	0.135283	0.324174	-5.49
248567_at	putative protein contains similarity to elic	---	AT5G49750	1.13	0.18	1.70	0.135283	0.324174	-5.49

267021_at	hypothetical protein predicted by genefi	---	AT2G39300	1.12	0.16	1.70	0.135245	0.324174	-5.49
266629_at	putative serpin	---	AT2G35590	1.14	0.19	1.70	0.135343	0.324283	-5.50
257323_at	hypothetical protein	---	AT2G07698	-1.44	-0.53	-1.70	0.135394	0.324370	-5.50
248586_at	putative protein similar to unknown prote	---	AT5G49610	-1.15	-0.20	-1.70	0.13545	0.324471	-5.50
257864_at	hypothetical protein predicted by genem	---	AT3G17740	-1.21	-0.28	-1.70	0.135476	0.324498	-5.50
259561_at	hypothetical protein ; supported by cDN	WAK1	AT1G21250	2.11	1.08	1.70	0.13549	0.324498	-5.50
256173_at	unknown protein	---	AT1G51730	-1.12	-0.17	-1.69	0.135625	0.324787	-5.50
264674_at	Expressed protein ; supported by full-ler	POLD4	AT1G09815	1.16	0.21	1.69	0.135684	0.324895	-5.50
262627_at	hypothetical protein	---	AT1G06580	-1.16	-0.21	-1.69	0.135709	0.324920	-5.50
262417_at	hypothetical protein similar to hypothetic	ATSIRB	AT1G50170	-1.11	-0.15	-1.69	0.135814	0.325138	-5.50
259842_at	phosphoethanolamine N-methyltransfe	CPuORF3	AT1G73600 /	-2.69	-1.43	-1.69	0.135847	0.325183	-5.50
262985_s_a	60s ribosomal protein l27a. similar to 60	RPL27AB	AT1G23290 /	-1.26	-0.33	-1.69	0.135883	0.325236	-5.50
252317_at	putative protein hypersensitivity-related	---	AT3G48720	1.67	0.74	1.69	0.135969	0.325408	-5.50
259035_at	hypothetical protein predicted by genefi	---	AT3G09430	1.13	0.17	1.69	0.135984	0.325410	-5.50
267398_at	putative glucanase	AtGH9B11	AT2G44560	1.16	0.22	1.69	0.136068	0.325538	-5.50
250338_at	putative protein ; supported by cDNA: g	---	AT5G11760	-1.13	-0.17	-1.69	0.136081	0.325538	-5.50
253833_at	putative calcium binding protein taipoxi	---	AT4G27790	1.25	0.32	1.69	0.136057	0.325538	-5.50
257512_at	unknown protein	---	AT1G35250	1.13	0.17	1.69	0.13613	0.325621	-5.50
246356_x_a	hypothetical protein, 5' partial	---	---	1.13	0.17	1.69	0.136215	0.325790	-5.50
256674_at	unknown protein ;supported by full-lengt	---	AT3G52360	1.23	0.30	1.69	0.136239	0.325813	-5.50
255618_at	hypothetical protein	---	AT4G01340	1.11	0.15	1.69	0.136263	0.325837	-5.50
261367_at	protein kinase, putative similar to many	---	AT1G53080	2.06	1.05	1.69	0.136306	0.325905	-5.50
254922_at	RING-H2 finger protein RHA1a -like pro	RHA1A	AT4G11370	2.21	1.15	1.69	0.136343	0.325938	-5.50
259475_at	unknown protein ;supported by full-lengt	---	AT1G19140	-1.26	-0.33	-1.69	0.136348	0.325938	-5.50
254051_at	putative protein other Arabidopsis putati	---	AT4G25270	-1.14	-0.19	-1.69	0.136378	0.325945	-5.50
246828_at	putative protein hypothetical protein, Pl	---	---	-1.14	-0.19	-1.69	0.13638	0.325945	-5.50
247548_at	putative protein various predicted prote	---	AT5G61400	-1.20	-0.26	-1.69	0.136478	0.326077	-5.50
256387_at	hypothetical protein	---	AT3G06170	-1.19	-0.25	-1.69	0.136469	0.326077	-5.50
250203_at	alpha-mannosidase	---	AT5G13980	-1.24	-0.31	-1.69	0.136476	0.326077	-5.50
256417_s_a	omega-3 fatty acid desaturase, chlorop	FAD7	AT3G11170 /	-1.27	-0.35	-1.69	0.136528	0.326095	-5.50
245611_at	hypothetical protein	---	AT4G14390	1.22	0.29	1.69	0.136502	0.326095	-5.50
263803_at	hypothetical protein predicted by gensca	---	AT2G40440	1.13	0.18	1.69	0.136514	0.326095	-5.50
245121_at	60S ribosomal protein L7A ;supported b	---	AT2G47610	-1.30	-0.38	-1.69	0.136596	0.326154	-5.50
256308_s_a	ABC transporter, putative contains Pfar	ATMRP13	AT1G30410 /	1.26	0.33	1.69	0.136595	0.326154	-5.50
262617_at	unknown protein	POR C	AT1G03630 /	-1.14	-0.18	-1.69	0.136589	0.326154	-5.50

258698_at	unknown protein	---	AT3G09690	1.16	0.22	1.69	0.136614	0.326164	-5.50
258315_at	Expressed protein ; supported by full-ler	---	AT3G16175	-1.16	-0.21	-1.69	0.136712	0.326346	-5.50
246278_at	tubulin-like protein	---	AT4G37190	-1.34	-0.42	-1.69	0.136719	0.326346	-5.50
260538_at	60S ribosomal protein L38	---	AT2G43460	-1.23	-0.30	-1.69	0.136814	0.326539	-5.51
263278_at	dynamin-like protein	DRP3B	AT2G14120	-1.16	-0.22	-1.69	0.136923	0.326731	-5.51
267194_s_a	putative ARP2/3 protein complex subun	ARPC1A	AT2G30910 /	-1.15	-0.20	-1.69	0.136917	0.326731	-5.51
248655_at	60S ribosomal protein L13a ;supported	---	AT5G48760	-1.21	-0.27	-1.69	0.136938	0.326732	-5.51
247286_at	2-oxoglutarate/malate translocator ; sup	DiT2.2	AT5G64280	-1.15	-0.20	-1.69	0.136976	0.326788	-5.51
259224_at	putative thymidine kinase similar to thyn	---	AT3G07800	1.20	0.27	1.69	0.137018	0.326855	-5.51
263893_at	putative WRKY-type DNA binding protei	WRKY59	AT2G21900	1.20	0.26	1.69	0.137063	0.326904	-5.51
266996_at	putative cytochrome P450 ;supported b	CYP710A2	AT2G34490	-2.17	-1.12	-1.69	0.137067	0.326904	-5.51
266686_at	hypothetical protein	---	AT2G19700	1.15	0.20	1.69	0.137114	0.326981	-5.51
245459_at	hypothetical protein	---	---	-1.23	-0.30	-1.69	0.137147	0.327025	-5.51
246773_at	protein kinase-like protein MAP3Ka ME	---	AT5G27510	1.21	0.27	1.69	0.137162	0.327026	-5.51
246442_at	hypothetical protein ;supported by full-le	---	AT5G17610	-1.13	-0.17	-1.69	0.137184	0.327046	-5.51
262109_at	hypothetical protein similar to cellulose s	ATCSLD5	AT1G02730	1.30	0.37	1.69	0.137203	0.327057	-5.51
249931_at	putative protein similar to unknown prote	QQT1	AT5G22370	-1.21	-0.28	-1.69	0.13722	0.327064	-5.51
261898_at	hypothetical protein predicted by genem	---	AT1G80720	-1.32	-0.40	-1.69	0.137275	0.327125	-5.51
254273_at	glycoprotein endopeptidase - like protei	---	AT4G22720	-1.22	-0.29	-1.69	0.137267	0.327125	-5.51
254491_at	putative protein hypothetical protein Ara	---	AT4G20300	1.21	0.27	1.69	0.137329	0.327220	-5.51
266973_at	hypothetical protein predicted by grail	---	AT2G39620	-1.16	-0.21	-1.69	0.137365	0.327271	-5.51
265713_at	putative integral membrane protein	UPS2	AT2G03530	1.49	0.57	1.69	0.137391	0.327299	-5.51
265831_at	unknown protein	---	AT2G14460	-1.35	-0.44	-1.69	0.137502	0.327530	-5.51
251668_at	putative protein strictosidine synthase (E	---	AT3G57010	1.35	0.43	1.69	0.137537	0.327579	-5.51
256899_at	putative kinase-like protein TMKL1 prec	TMKL1	AT3G24660	-1.15	-0.20	-1.68	0.137632	0.327770	-5.51
263099_at	putative non-LTR retroelement reverse t	---	---	1.19	0.26	1.68	0.137675	0.327794	-5.51
266316_at	unknown protein ; supported by cDNA:	---	AT2G27080	1.94	0.95	1.68	0.137691	0.327794	-5.51
246649_at	putative protein predicted proteins, Aral	---	---	1.13	0.18	1.68	0.137699	0.327794	-5.51
252346_at	hypothetical protein	---	AT3G48650	1.12	0.16	1.68	0.137688	0.327794	-5.51
256269_at	transcription factor HBP-1B-like nearly id	TGA6	AT3G12250	-1.13	-0.18	-1.68	0.137778	0.327946	-5.51
255666_at	putative protein ;supported by full-lengt	---	AT4G00390	1.17	0.23	1.68	0.137793	0.327949	-5.51
263891_at	putative glucan synthase	GSL8	AT2G36850	-1.13	-0.18	-1.68	0.137832	0.328008	-5.51
253027_at	putative protein leaf protein (PnC401) -	---	AT4G38150	-1.25	-0.32	-1.68	0.137862	0.328043	-5.51
247627_at	cysteine proteinase AALP identical to A/	AALP	AT5G60360	1.12	0.17	1.68	0.137972	0.328210	-5.51
248126_at	protein translation factor Sui1 homolog (	ROC5	AT4G34870 /	-1.11	-0.15	-1.68	0.137975	0.328210	-5.51

257850_at	putative protein kinase leucine-rich repe	SRF4	AT3G13065	-1.13	-0.18	-1.68	0.137974	0.328210	-5.51
246911_at	transcription factor TINY	tny	AT5G25810	1.39	0.48	1.68	0.138055	0.328333	-5.51
265462_at	putative vetispiradiene synthase	---	AT2G37140	1.15	0.21	1.68	0.138053	0.328333	-5.51
248649_at	putative protein contains similarity to twc	APRR4	AT5G49240	1.16	0.21	1.68	0.13815	0.328524	-5.51
265325_at	putative integral membrane protein	---	AT2G18240	1.19	0.25	1.68	0.138202	0.328614	-5.51
262851_at	putative RNA helicase Contains DEAD-I	---	AT1G20920	-1.17	-0.22	-1.68	0.138333	0.328890	-5.52
250988_at	putative protein thyroid receptor interac	UPL4	AT5G02880	1.12	0.16	1.68	0.138361	0.328903	-5.52
257689_at	myb-related protein, putative myb-relate	AtMYB10	AT3G12820	1.15	0.20	1.68	0.138367	0.328903	-5.52
259122_at	unknown protein similar to putative phy	COBL1	AT3G02210	1.17	0.23	1.68	0.138414	0.328979	-5.52
248944_at	putative protein similar to unknown prote	---	AT5G45500	1.19	0.25	1.68	0.138432	0.328990	-5.52
252420_at	putative protein several hypothetical pro	---	AT3G47530	-1.23	-0.29	-1.68	0.138489	0.329083	-5.52
263398_at	putative RAS superfamily GTP-binding p	AtRABA5d	AT2G31680	1.15	0.20	1.68	0.138501	0.329083	-5.52
246747_at	ribosomal protein S21 - like ribosomal p	---	AT5G27700	-1.22	-0.28	-1.68	0.138659	0.329426	-5.52
260348_at	PPR-repeat protein, putative contains P	---	AT1G69350	-1.21	-0.27	-1.68	0.13871	0.329478	-5.52
261741_at	transcription factor, putative similar to tr	ATE2F2	AT1G47870	1.15	0.20	1.68	0.138709	0.329478	-5.52
262290_at	Expressed protein ; supported by full-ler	---	AT1G70985	-1.22	-0.29	-1.68	0.138784	0.329618	-5.52
252080_at	putative protein polyphosphoinositide b	---	AT3G51670	-1.26	-0.33	-1.68	0.138874	0.329800	-5.52
249036_at	nuclear cap-binding protein; CBP20 (gb	CBP20	AT5G44200	-1.17	-0.22	-1.68	0.138902	0.329831	-5.52
254258_at	hypothetical protein	TET5	AT4G23410	-1.17	-0.23	-1.68	0.138925	0.329851	-5.52
263579_at	hypothetical protein similar to hypothetic	---	AT2G17030	-1.20	-0.26	-1.68	0.138955	0.329889	-5.52
263233_at	hypothetical protein similar to Na/H antip	---	AT1G05577	1.12	0.16	1.68	0.139034	0.330042	-5.52
254878_at	heat shock transcription factor - like pro	AT-HSFB2	AT4G11660	-1.26	-0.34	-1.68	0.139109	0.330049	-5.52
265112_at	hypothetical protein predicted by gensca	---	AT1G62530	1.11	0.15	1.68	0.13911	0.330049	-5.52
255327_at	putative malonyl-CoA decarboxylase	---	AT4G04320	1.12	0.16	1.68	0.139084	0.330049	-5.52
259066_at	hypothetical protein predicted by genefir	---	AT3G07530	-1.20	-0.27	-1.68	0.139085	0.330049	-5.52
259214_at	Expressed protein ; supported by full-ler	---	AT3G09085	1.15	0.20	1.68	0.139093	0.330049	-5.52
262619_at	3-hydroxyisobutyryl-coenzyme A hydrol	---	AT1G06550	1.51	0.60	1.68	0.139179	0.330179	-5.52
245122_at	putative dimethyladenosine transferase	---	AT2G47420	-1.16	-0.21	-1.68	0.139203	0.330189	-5.52
261318_at	Expressed protein ; supported by full-ler	---	AT1G53035	-1.77	-0.82	-1.68	0.139212	0.330189	-5.52
267129_at	curly leaf protein (polycomb-group) iden	CLF	AT2G23380	1.13	0.18	1.68	0.139265	0.330264	-5.52
245499_at	membrane transporter like protein	INT4	AT4G16480	1.13	0.18	1.68	0.139273	0.330264	-5.52
263217_at	putative reticuline oxidase-like protein s	---	AT1G30740	1.13	0.17	1.68	0.139299	0.330292	-5.52
247625_at	zinc finger protein - like dof6 zinc finger	---	AT5G60200	1.20	0.26	1.68	0.139327	0.330325	-5.52
258922_at	putative 40S ribosomal protein S17 simi	---	AT3G10610	-1.41	-0.49	-1.68	0.139377	0.330409	-5.52
260377_at	unknown protein	---	AT1G73930	1.11	0.16	1.68	0.139468	0.330590	-5.52

261220_at	ER lumen protein-retaining receptor sim	---	AT1G19970	1.36	0.45	1.68	0.1395	0.330598	-5.52
254832_at	pEARLI 1-like protein Arabidopsis thalia	---	AT4G12490	2.22	1.15	1.68	0.139517	0.330598	-5.52
245998_at	sucrose-UDP glucosyltransferase	SUS1	AT5G20830	1.31	0.39	1.68	0.13953	0.330598	-5.52
255853_at	hypothetical protein predicted by gensca	---	AT1G67020	-1.12	-0.17	-1.68	0.139513	0.330598	-5.52
259364_at	DNA-binding protein RAV1 identical to R	RAV1	AT1G13260	1.17	0.22	1.67	0.139685	0.330933	-5.52
264436_at	putative glutathione S-transferase TSI-1	ERD9	AT1G10370	1.65	0.72	1.67	0.139723	0.330988	-5.52
264922_s_a	U2 snRNP auxiliary factor, large subuni	---	AT1G60830 /	-1.12	-0.16	-1.67	0.13976	0.331040	-5.53
252643_at	acidic ribosomal protein P2 -like acidic r	---	AT3G44590	-1.38	-0.47	-1.67	0.139801	0.331104	-5.53
267075_at	putative bZIP transcription factor contair	EEL	AT2G41070	1.12	0.17	1.67	0.139834	0.331146	-5.53
260796_at	glutathione transferase, putative similar	ATGSTU2	AT1G78360	1.19	0.25	1.67	0.139875	0.331210	-5.53
254404_at	hypothetical protein	B70	AT4G21340	1.11	0.15	1.67	0.139917	0.331276	-5.53
266355_at	hypothetical protein predicted by gensca	---	AT2G01400	-1.30	-0.38	-1.67	0.139936	0.331287	-5.53
262810_at	putative salt-inducible protein similar to (	---	AT1G11710	-1.23	-0.30	-1.67	0.139997	0.331362	-5.53
258335_at	unknown protein	---	AT3G16020	-1.12	-0.16	-1.67	0.139987	0.331362	-5.53
264285_at	symbiosis-related protein, putative simil	ATG8C	AT1G62040	-1.16	-0.21	-1.67	0.140015	0.331370	-5.53
250053_at	potassium-dependent sodium-calcium e	---	AT5G17850	1.17	0.23	1.67	0.140076	0.331480	-5.53
251457_s_a	multi resistance protein homolog multi r	ATMRP9	AT3G60160 /	-1.14	-0.19	-1.67	0.140147	0.331613	-5.53
256053_at	UDP-glucose glucosyltransferase, puta	UGT71C3	AT1G07260	-1.50	-0.59	-1.67	0.140226	0.331766	-5.53
259052_at	unknown protein	PEX19-1	AT3G03490	1.14	0.18	1.67	0.140282	0.331863	-5.53
256823_at	hypothetical protein predicted by gensca	---	AT3G22220	-1.16	-0.22	-1.67	0.14037	0.332038	-5.53
267060_at	unknown protein ; supported by full-leng	---	AT2G32580	-1.23	-0.30	-1.67	0.140421	0.332105	-5.53
246062_at	putative protein VAC8 protein, Sacchar	---	AT5G19330	1.13	0.18	1.67	0.140427	0.332105	-5.53
258705_at	hypothetical protein predicted by genefir	---	AT3G09470	-1.15	-0.20	-1.67	0.14047	0.332172	-5.53
258023_at	cinnamyl alcohol dehydrogenase identic	ATCAD4	AT3G19450	-1.40	-0.48	-1.67	0.140532	0.332191	-5.53
260777_at	mitochondrial carrier protein, putative si	---	AT1G14560	-1.15	-0.20	-1.67	0.140496	0.332191	-5.53
259483_at	hypothetical protein predicted by genem	---	AT1G43980	-1.13	-0.18	-1.67	0.140521	0.332191	-5.53
264244_at	pantothenate kinase, putative similar to	ATPANK1	AT1G60440	1.14	0.19	1.67	0.140537	0.332191	-5.53
267080_at	unknown protein ; supported by cDNA:	---	AT2G41190	1.41	0.50	1.67	0.140588	0.332279	-5.53
248958_at	unknown protein ; supported by full-leng	---	AT5G45590	-1.21	-0.27	-1.67	0.140634	0.332283	-5.53
258625_at	hypothetical protein predicted by genem	PDLP4	AT3G04370	1.14	0.19	1.67	0.140609	0.332283	-5.53
252531_at	actin 12	ACT12	AT3G46520	-1.13	-0.18	-1.67	0.140627	0.332283	-5.53
246957_at	unknown protein	---	AT5G24670	1.11	0.15	1.67	0.140661	0.332313	-5.53
250315_at	putative protein contains similarity to tra	PDE149	AT5G12130	-1.28	-0.36	-1.67	0.140679	0.332319	-5.53
264092_at	photosystem II polypeptide, putative sir	PSBR	AT1G79040 /	-1.13	-0.17	-1.67	0.140719	0.332380	-5.53
253081_at	putative protein F35D11.3, Caenorhabd	---	AT4G36210	1.18	0.24	1.67	0.140733	0.332380	-5.53

246133_at	aldehyde oxidase AAO1 ; supported by	AAO1	AT5G20960	1.48	0.57	1.67	0.140769	0.332430	-5.53
246871_at	extensin - like protein pAP8 protein, Nic	---	AT5G26070	1.12	0.16	1.67	0.140823	0.332503	-5.53
263595_at	putative purple acid phosphatase contai	PAP8	AT2G01890	3.57	1.83	1.67	0.140829	0.332503	-5.53
263299_s_a	hypothetical protein predicted by gensca	---	AT2G11570	-1.14	-0.18	-1.67	0.140848	0.332512	-5.53
261530_at	unknown protein contains Pfam profile: I	---	AT1G63460	1.19	0.25	1.67	0.140863	0.332515	-5.53
252129_at	putative protein hypothetical protein T8I	AtHB28	AT3G50890	1.16	0.21	1.67	0.140897	0.332560	-5.53
248629_at	mitochondrial carrier protein-like	---	AT5G48970	1.20	0.26	1.67	0.140949	0.332648	-5.53
254121_at	putative protein putative protein F6I18_	---	AT4G24760	-1.27	-0.35	-1.67	0.141062	0.332845	-5.53
255330_s_a	putative polyprotein	---	---	1.11	0.16	1.67	0.141059	0.332845	-5.53
264757_at	receptor protein kinase (IRK1), putative	---	AT1G61360	1.78	0.83	1.67	0.141092	0.332882	-5.53
247935_at	30S ribosomal protein S16 ; supported	---	AT5G56940	-1.20	-0.26	-1.67	0.141153	0.332993	-5.53
247623_at	receptor-like protein kinase receptor-lik	---	AT5G60320	1.13	0.18	1.67	0.141169	0.332995	-5.53
250672_at	DnaJ homologue (gb|AAB91418.1|) ; su	ATJ6	AT5G06910	-1.11	-0.15	-1.67	0.141201	0.333037	-5.53
252507_at	putative protein predicted protein, Sacc	aTNUDT9	AT3G46200	-1.22	-0.29	-1.67	0.141278	0.333148	-5.54
265010_at	T-complex chaperonin protein , epsilon	---	AT1G24510	-1.22	-0.29	-1.67	0.141271	0.333148	-5.54
256628_at	membrane import protein, putative simi	TOM40	AT3G20000	-1.24	-0.31	-1.67	0.141311	0.333183	-5.54
266910_at	unknown protein	---	AT2G45920	1.37	0.46	1.67	0.141322	0.333183	-5.54
254741_s_a	putative disease resistance protein Hcr	AtRLP49	AT4G13900 /	-1.12	-0.16	-1.67	0.141362	0.333244	-5.54
249981_at	putative protein predicted proteins, Arat	---	AT5G18510	1.18	0.24	1.67	0.141377	0.333245	-5.54
249652_at	putative protein hypothetical proteins - A	---	AT5G37070	1.18	0.24	1.67	0.141434	0.333344	-5.54
256112_at	guanine nucleotide regulatory protein, p	ATRABA1	AT1G16920	1.46	0.55	1.67	0.141478	0.333344	-5.54
255284_at	5-adenylylsulfate reductase ;supported	אפר-01	AT4G04610	-1.56	-0.64	-1.67	0.141473	0.333344	-5.54
264903_at	putative phosphoglucomutase similar to	---	AT1G23190	1.16	0.22	1.67	0.141457	0.333344	-5.54
260530_at	putative peptidyl-prolyl cis-trans isomera	---	AT2G47320	-1.12	-0.17	-1.67	0.141496	0.333354	-5.54
265927_at	hypothetical protein	---	AT2G18590	1.17	0.23	1.67	0.141517	0.333367	-5.54
255277_at	putative homeotic protein ; supported b	PDF2	AT4G04890	1.20	0.26	1.66	0.141618	0.333572	-5.54
259110_at	unknown protein	---	AT3G05570	-1.21	-0.27	-1.66	0.141671	0.333628	-5.54
248042_at	putative protein similar to unknown prote	---	AT5G55960	-1.18	-0.24	-1.66	0.141669	0.333628	-5.54
250127_at	putative protein similar to unknown prote	---	AT5G16380	-1.18	-0.24	-1.66	0.14173	0.333733	-5.54
254667_at	glycine-rich cell wall protein-like glycine	---	AT4G18280	1.30	0.38	1.66	0.141804	0.333837	-5.54
251523_at	putative protein several hypothetical pro	---	AT3G58975	-1.14	-0.19	-1.66	0.141799	0.333837	-5.54
253555_at	putative protein predicted proetein, Arat	---	AT4G31080	-1.21	-0.28	-1.66	0.14186	0.333934	-5.54
259291_at	unknown protein similar to unknown pro	---	AT3G11550	1.17	0.23	1.66	0.141889	0.333970	-5.54
264841_at	putative protein kinase similar to (Z717(	---	AT1G03740	1.35	0.44	1.66	0.141941	0.334057	-5.54
258187_at	HSC70-interacting protein, putative sim	ATTDX	AT3G17880	-1.14	-0.19	-1.66	0.141963	0.334073	-5.54

264172_at	unknown protein	VAD1	AT1G02120	1.22	0.29	1.66	0.142002	0.334130	-5.54
248024_at	putative protein contains similarity to sal	---	AT5G55840	-1.18	-0.24	-1.66	0.14202	0.334139	-5.54
265606_s_a	putative non-LTR retroelement reverse t	---	AT3G09510	1.13	0.18	1.66	0.142048	0.334161	-5.54
257989_at	unknown protein ; supported by cDNA: g	VPS9A	AT3G19770	1.15	0.20	1.66	0.142073	0.334161	-5.54
250772_at	putative protein contains similarity to pe	---	AT5G05420	-1.23	-0.30	-1.66	0.142074	0.334161	-5.54
264773_at	putative disease resistance response pr	---	AT1G22900	1.45	0.54	1.66	0.142127	0.334184	-5.54
246897_at	putative protein predicted proteins, Aral	---	AT5G25560	1.17	0.23	1.66	0.142126	0.334184	-5.54
247142_at	putative protein strong similarity to unkn	---	AT5G65570	-1.15	-0.20	-1.66	0.142117	0.334184	-5.54
259426_at	hypothetical protein contains similarity to	LEA14	AT1G01470	1.16	0.21	1.66	0.142156	0.334217	-5.54
246780_at	seryl-tRNA synthetase ; supported by c	---	AT5G27470	-1.15	-0.20	-1.66	0.142182	0.334243	-5.54
259073_at	unknown protein contains zinc finger m	---	AT3G02290	1.28	0.36	1.66	0.142363	0.334634	-5.54
254657_s_a	putative protein W15DMY32F, W25DM	---	AT4G18210 /	1.30	0.38	1.66	0.142416	0.334725	-5.54
248417_at	unknown protein	---	AT5G51650	1.11	0.15	1.66	0.142432	0.334729	-5.54
255273_at	putative protein various predicted prote	---	---	1.12	0.16	1.66	0.142454	0.334745	-5.54
245813_at	hypothetical protein contains similarity to	---	AT1G49920	1.20	0.27	1.66	0.142473	0.334755	-5.54
256078_at	hypothetical protein predicted by genem	---	AT1G20670	1.15	0.20	1.66	0.142497	0.334778	-5.54
265953_at	unknown protein	---	AT2G37478 /	-1.13	-0.18	-1.66	0.142537	0.334802	-5.54
252342_at	endo-polygalacturonase - like protein e	---	AT3G48950	1.10	0.14	1.66	0.142535	0.334802	-5.54
262533_at	hypothetical protein Pfam	---	AT1G17090	-1.15	-0.20	-1.66	0.142613	0.334938	-5.54
265901_at	putative selenium-binding protein	---	AT2G25580	-1.17	-0.22	-1.66	0.142624	0.334938	-5.54
255997_s_a	photosystem II type I chlorophyll a /b b	CAB3	AT1G29910 /	-1.22	-0.29	-1.66	0.142665	0.334966	-5.54
245838_at	disease resistance protein, putative sim	---	AT1G58410	1.14	0.19	1.66	0.142662	0.334966	-5.54
246611_at	putative protein predicted proteins, Aral	MBD02	AT5G35330	-1.26	-0.34	-1.66	0.142732	0.335084	-5.54
251512_at	putative protein several hypothetical pro	---	AT3G59190	-1.14	-0.18	-1.66	0.142745	0.335084	-5.54
250399_at	putative protein predicted proteins, Aral	---	AT5G10750	-1.19	-0.25	-1.66	0.142948	0.335527	-5.55
258710_s_a	putative coatomer zeta subunit (zeta-co	---	AT3G09800 /	-1.13	-0.17	-1.66	0.142982	0.335571	-5.55
250480_at	protein serine/threonine kinase-like pro	---	AT5G10290	-1.41	-0.50	-1.66	0.143053	0.335635	-5.55
251328_at	putative protein putative protein At2g46	ATPOB1	AT3G61600	1.12	0.16	1.66	0.143043	0.335635	-5.55
249588_at	protein kinase - like protein Pto kinase i	---	AT5G37790	-1.20	-0.26	-1.66	0.143029	0.335635	-5.55
253777_at	SOF1 protein-like protein SOF1 (involve	---	AT4G28450	-1.39	-0.48	-1.66	0.143164	0.335834	-5.55
263163_at	fructokinase, putative predicted by gene	FZL	AT1G03160	-1.33	-0.42	-1.66	0.143168	0.335834	-5.55
258391_at	hypothetical protein predicted by gensca	---	AT3G15420	-1.23	-0.30	-1.66	0.143189	0.335850	-5.55
245672_at	polygalacturonase, putative similar to p	---	AT1G56710	-1.19	-0.26	-1.66	0.143306	0.336089	-5.55
249440_at	protein kinase -like protein probable pro	---	AT5G40030	1.13	0.18	1.66	0.143377	0.336221	-5.55
252363_at	lipase - like protein lipase Arab-1, Arabi	---	AT3G48460	-1.50	-0.59	-1.66	0.143401	0.336243	-5.55

260069_at	unknown protein	---	AT1G73820	-1.13	-0.18	-1.66	0.143508	0.336424	-5.55
265203_at	unknown protein	---	AT2G36630	1.17	0.23	1.66	0.143506	0.336424	-5.55
254326_at	putative protein AIR1, Arabidopsis thali	---	AT4G22610	1.15	0.20	1.66	0.143528	0.336438	-5.55
261023_at	unknown protein similar to unknown pro	---	AT1G12200	1.17	0.23	1.66	0.143566	0.336457	-5.55
250653_at	putative protein strong similarity to unkn	---	AT5G06930	1.36	0.45	1.66	0.143559	0.336457	-5.55
266462_at	unknown protein ; supported by cDNA:	---	AT2G47770	1.48	0.57	1.66	0.143613	0.336533	-5.55
255973_at	hypothetical protein predicted by gensca	---	AT3G32400	-1.11	-0.15	-1.65	0.143819	0.336981	-5.55
263646_at	Ac-like transposase related to Ac/Ds tra	---	---	-1.11	-0.15	-1.65	0.143839	0.336994	-5.55
260200_at	unknown protein ; supported by full-leng	---	AT1G67620	-1.15	-0.20	-1.65	0.143877	0.337048	-5.55
258458_at	Expressed protein ; supported by cDNA	---	AT3G22435	-1.22	-0.29	-1.65	0.143985	0.337163	-5.55
250325_s_a	putative protein contains similarity to S1	---	AT5G12060 /	1.12	0.16	1.65	0.143951	0.337163	-5.55
266015_at	putative carbonyl reductase	---	AT2G24190	-1.16	-0.21	-1.65	0.143985	0.337163	-5.55
266090_at	unknown protein	---	AT2G38000	-1.17	-0.23	-1.65	0.143962	0.337163	-5.55
267219_at	putative transport protein ;supported by	---	AT2G02590	-1.20	-0.26	-1.65	0.144015	0.337183	-5.55
264583_at	putative AVR9 elicitor response protein	---	AT1G05170	1.18	0.24	1.65	0.144045	0.337183	-5.55
246763_at	NHE1 Na+/H+ exchanger ; supported b	NHX1	AT5G27150	1.25	0.32	1.65	0.144053	0.337183	-5.55
255092_s_a	putative protein various predicted protei	---	---	1.13	0.18	1.65	0.144038	0.337183	-5.55
253243_at	putative protein	---	AT4G34560	-1.67	-0.74	-1.65	0.144118	0.337301	-5.55
246955_at	calcium-dependent protein kinase ; sup	CPK1	AT5G04870	1.38	0.46	1.65	0.14415	0.337340	-5.55
257834_at	alpha-mannosidase, putative similar to	---	AT3G26720	-1.11	-0.15	-1.65	0.144203	0.337429	-5.55
261401_at	kinase, putative similar to Ste-20 relate	---	AT1G79640	1.19	0.25	1.65	0.144286	0.337590	-5.55
261834_at	polygalacturonase PG1, putative simila	---	AT1G10640	1.12	0.17	1.65	0.144323	0.337642	-5.56
256241_at	nascent polypeptide associated comple	---	AT3G12390	-1.27	-0.35	-1.65	0.144344	0.337656	-5.56
251318_at	putative protein putative protein At2g46	GDAP1	AT3G61570	1.13	0.17	1.65	0.144376	0.337697	-5.56
257843_at	hypothetical protein predicted by genen	---	---	1.12	0.16	1.65	0.144429	0.337750	-5.56
253469_at	putative protein gene C42D8.3, Caenor	ATPANK2	AT4G32180	-1.14	-0.19	-1.65	0.14442	0.337750	-5.56
245479_at	extensin like protein	---	AT4G16140	1.15	0.20	1.65	0.144566	0.337933	-5.56
250991_at	metallothionein 2b ; supported by full-le	MT2B	AT5G02380	1.15	0.21	1.65	0.14456	0.337933	-5.56
251659_at	hypothetical protein ;supported by full-l	BIGYIN	AT3G57090	1.15	0.20	1.65	0.14453	0.337933	-5.56
250377_at	putative protein predicted proteins, Hon	---	AT5G11560	1.19	0.25	1.65	0.144541	0.337933	-5.56
264500_at	hypothetical protein predicted by genefi	---	AT1G09370	1.11	0.15	1.65	0.144605	0.337988	-5.56
245680_at	hypothetical protein contains similarity t	---	AT1G56570	-1.14	-0.18	-1.65	0.144649	0.338057	-5.56
260936_at	hypothetical protein predicted by genem	---	AT1G45150	1.15	0.20	1.65	0.144696	0.338133	-5.56
251090_at	putative protein ACR1-protein - Saccha	---	AT5G01340	1.47	0.56	1.65	0.144713	0.338135	-5.56
254874_at	putative protein beta-phosphoglucomut	---	AT4G11570	-1.19	-0.25	-1.65	0.144741	0.338135	-5.56

248580_at	chloride channel (emb|CAA70310.1)	CLC-C	AT5G49890	1.19	0.25	1.65	0.144734	0.338135	-5.56
259612_at	60S ribosomal protein L37, putative sim	---	AT1G52300	-1.31	-0.39	-1.65	0.144777	0.338183	-5.56
250259_at	putative protein similar to unknown prote	---	AT5G13800	1.20	0.26	1.65	0.144807	0.338220	-5.56
252627_at	putative protein	---	AT3G44950	-1.16	-0.22	-1.65	0.144834	0.338248	-5.56
254788_at	putative protein other predicted proteins	---	AT4G12790	1.12	0.17	1.65	0.144905	0.338309	-5.56
262448_at	En/Spm-like transposon protein, putativ	---	AT1G49450	1.14	0.19	1.65	0.144885	0.338309	-5.56
246832_at	putative protein isopenicillin N epimeras	---	AT5G26600	1.16	0.22	1.65	0.144899	0.338309	-5.56
265477_at	hypothetical protein predicted by gensca	GAUT2	AT2G46480	1.15	0.20	1.65	0.145009	0.338518	-5.56
248882_at	cullin ;supported by full-length cDNA: Ce	CUL4	AT5G46210	-1.12	-0.16	-1.65	0.145087	0.338665	-5.56
263034_at	pollen allergen-like protein similar to ma	MLP423	AT1G24020	1.30	0.38	1.65	0.145151	0.338675	-5.56
267507_at	putative ribosomal protein S27 ;support	---	AT2G45710	-1.22	-0.29	-1.65	0.145138	0.338675	-5.56
258567_at	apyrase (Atapy1) identical to apyrase (A	ATAPY1	AT3G04080	1.18	0.24	1.65	0.145149	0.338675	-5.56
249698_at	unknown protein	MIS12	AT5G35520	-1.21	-0.27	-1.65	0.145136	0.338675	-5.56
260613_at	unknown protein	---	AT1G53380	-1.15	-0.20	-1.65	0.145171	0.338687	-5.56
252426_at	putative protein proline transport helper	---	AT3G47630	-1.17	-0.22	-1.65	0.145208	0.338688	-5.56
255837_at	unknown protein	RIC1	AT2G33460	1.14	0.19	1.65	0.145215	0.338688	-5.56
246752_at	putative protein predicted proteins, Arat	---	AT5G27890	1.15	0.20	1.65	0.145222	0.338688	-5.56
256902_s_a	HAPp48,5 protein identical to HAPp48,5	---	AT3G23910 /	-1.23	-0.29	-1.65	0.14523	0.338688	-5.56
262468_at	alanine--tRNA ligase, putative similar to	ALATS	AT1G50200	-1.20	-0.26	-1.65	0.145322	0.338867	-5.56
249319_s_a	putative protein similar to unknown prote	---	AT5G40880 /	1.16	0.22	1.65	0.145368	0.338938	-5.56
256933_at	unknown protein contains Pfam profile:P	---	AT3G22600	2.65	1.40	1.65	0.145432	0.339054	-5.56
249400_at	putative protein MtN24 gene, Medicago	---	AT5G40300	-1.18	-0.24	-1.65	0.145484	0.339140	-5.56
251604_at	putative protein 60S RIBOSOMAL PRO	---	AT3G57820	1.12	0.16	1.65	0.145533	0.339221	-5.56
254560_at	kinase-like protein protein kinase rck, M	---	AT4G19110 /	1.11	0.15	1.65	0.145583	0.339302	-5.56
264167_at	unknown protein Location of EST gb|N9	---	AT1G02060	-1.20	-0.26	-1.65	0.145611	0.339334	-5.56
259582_at	hypothetical protein	---	AT1G28060	-1.17	-0.23	-1.65	0.14565	0.339388	-5.56
264296_at	protein transport protein sec61 alpha su	---	AT1G78720	1.23	0.29	1.64	0.145703	0.339477	-5.56
250505_at	cellulose synthase catalytic subunit	CESA5	AT5G09870	1.21	0.27	1.64	0.145731	0.339507	-5.56
260929_at	transcription factor TFIID, putative simil	TAF13	AT1G02680	-1.21	-0.28	-1.64	0.145829	0.339534	-5.56
253240_at	putative ketoacyl-CoA synthase fatty ac	KCS17	AT4G34510	1.12	0.16	1.64	0.145809	0.339534	-5.56
257701_at	unknown protein contains similarity to 3-	---	AT3G12710	1.72	0.78	1.64	0.145831	0.339534	-5.56
259538_at	putative serine/threonine kinase ; suppo	---	AT1G12310	1.17	0.23	1.64	0.145761	0.339534	-5.56
256907_at	hydoxyethylthiazole kinase, putative sim	---	AT3G24030	-1.22	-0.29	-1.64	0.145827	0.339534	-5.56
247704_at	Expressed protein ; supported by full-ler	RTFL5	AT5G59510	1.43	0.52	1.64	0.145794	0.339534	-5.56
260055_at	unknown protein similar to putative prote	---	AT1G78150	-1.12	-0.17	-1.64	0.145914	0.339692	-5.57

257894_at	unknown protein ; supported by cDNA: g	---	AT3G17100	1.29	0.37	1.64	0.14594	0.339717	-5.57
264809_at	superoxidase dismutase identical to GB	CSD1	AT1G08830	1.54	0.62	1.64	0.145966	0.339744	-5.57
259685_at	unknown protein	AtPP2-A1	AT1G63090	-1.25	-0.33	-1.64	0.146013	0.339818	-5.57
263588_s_a	unknown protein	---	AT2G25320 /	-1.14	-0.19	-1.64	0.146072	0.339853	-5.57
246121_at	putative protein motif in PGPS/D10 - Pe	---	AT5G20370	1.15	0.20	1.64	0.146073	0.339853	-5.57
246349_at	Expressed protein ; supported by full-ler	---	AT1G51915	1.43	0.51	1.64	0.146062	0.339853	-5.57
258069_at	hypothetical protein predicted by genem	---	AT3G26010	1.19	0.25	1.64	0.146156	0.339976	-5.57
267066_at	hypothetical protein predicted by genefir	---	AT2G41040	-1.21	-0.27	-1.64	0.146149	0.339976	-5.57
265627_at	Expressed protein ; supported by full-ler	---	AT2G27285	-1.15	-0.21	-1.64	0.146171	0.339977	-5.57
250400_at	protein phosphatase 2C -like protein pr	---	AT5G10740	1.24	0.31	1.64	0.146264	0.340091	-5.57
259482_at	receptor-like serine/threonine kinase, p	RKF2	AT1G19090	1.15	0.20	1.64	0.146253	0.340091	-5.57
246160_at	putative protein predicted protein, Oryz	FBX2	AT5G21040	-1.13	-0.17	-1.64	0.146243	0.340091	-5.57
249345_at	putative protein ; supported by cDNA: g	---	AT5G40740	-1.15	-0.20	-1.64	0.146297	0.340097	-5.57
263267_at	putative vacuolar proton-ATPase 16 kDa	---	AT2G16510	1.14	0.19	1.64	0.146283	0.340097	-5.57
265136_at	hypothetical protein similar to disease re	---	AT1G51270	1.11	0.14	1.64	0.146312	0.340097	-5.57
248691_at	putative protein strong similarity to unkn	---	AT5G48310	1.13	0.18	1.64	0.146335	0.340117	-5.57
267232_at	hypothetical protein predicted by gensca	EDE1	AT2G44190	1.15	0.20	1.64	0.14643	0.340302	-5.57
252382_at	ABC-type transport protein-like protein /	ATH5	AT3G47770	-1.11	-0.15	-1.64	0.146493	0.340415	-5.57
260947_at	fructokinase, putative similar to fructoki	---	AT1G06020	1.11	0.15	1.64	0.146523	0.340450	-5.57
259562_at	hypothetical protein ; supported by cDN/	---	AT1G21200	-1.14	-0.19	-1.64	0.146575	0.340497	-5.57
260749_at	hypothetical protein predicted by genem	---	AT1G49110	1.16	0.21	1.64	0.146565	0.340497	-5.57
247871_at	xyloglucan endotransglycosylase ; supp	---	AT5G57530	1.12	0.16	1.64	0.146588	0.340497	-5.57
248047_at	putative protein similar to unknown prote	---	AT5G56070	1.13	0.18	1.64	0.146695	0.340710	-5.57
250278_at	2-oxoglutarate/malate translocator prec	DiT1	AT5G12860	-1.26	-0.33	-1.64	0.146742	0.340784	-5.57
264086_at	unknown protein ;supported by full-leng	---	AT2G31190	-1.18	-0.24	-1.64	0.146762	0.340796	-5.57
252286_at	putative protein	---	AT3G49070	1.10	0.14	1.64	0.146833	0.340858	-5.57
260558_at	putative endochitinase	---	AT2G43600	1.18	0.24	1.64	0.146826	0.340858	-5.57
249815_at	60S ribosomal protein L13 ; supported b	---	AT5G23900	-1.22	-0.29	-1.64	0.146827	0.340858	-5.57
248434_at	mitochondrial heat shock 22 kd protein-l	---	AT5G51440	2.02	1.01	1.64	0.146854	0.340871	-5.57
251386_at	putative protein rec, Homo sapiens, EM	---	AT3G60800	1.11	0.15	1.64	0.146891	0.340923	-5.57
254034_at	P-glycoprotein-2 (pgp2)	PGP2	AT4G25960	1.21	0.28	1.64	0.146987	0.341100	-5.57
250636_at	glycine-rich protein atGRP	GRP18	AT5G07520	1.14	0.19	1.64	0.146998	0.341100	-5.57
252737_at	putative protein KIAA0274 protein, Hom	---	AT3G43220	-1.13	-0.17	-1.64	0.14702	0.341117	-5.57
256325_at	hypothetical protein	---	AT3G02330	-1.17	-0.22	-1.64	0.147086	0.341201	-5.57
267124_at	putative acetone-cyanohydrin lyase	MES19	AT2G23570	-1.16	-0.21	-1.64	0.147082	0.341201	-5.57

245409_at	putative protein	---	AT4G17200	1.10	0.14	1.64	0.147125	0.341258	-5.57
262634_at	unknown protein ; supported by cDNA: g	---	AT1G06690	-1.40	-0.48	-1.64	0.147164	0.341279	-5.57
255985_at	putative protein contains similarity to ps	---	AT1G34150	1.12	0.16	1.64	0.147164	0.341279	-5.57
253565_at	predicted protein DAN26, Homo sapien	---	AT4G31200	-1.18	-0.24	-1.64	0.147192	0.341309	-5.57
264741_at	aspartic protease, putative similar to as	---	AT1G62290	1.51	0.60	1.64	0.147212	0.341320	-5.57
247667_at	putative protein predicted protein, Arabi	---	AT5G60150	1.16	0.21	1.64	0.147276	0.341434	-5.57
266286_at	putative tropinone reductase	---	AT2G29160 /	-1.15	-0.20	-1.64	0.147368	0.341613	-5.57
264980_at	receptor kinase, putative similar to CLV	---	AT1G27190	-1.17	-0.22	-1.64	0.147402	0.341657	-5.57
248863_at	zinc finger protein Glo3-like	AGD9	AT5G46750	-1.12	-0.16	-1.64	0.147454	0.341742	-5.58
249978_at	putative protein	---	AT5G18850	-1.15	-0.20	-1.64	0.147499	0.341812	-5.58
249516_s_a	myrosinase binding protein-like; similar t	---	AT5G38540 /	1.15	0.20	1.64	0.147553	0.341901	-5.58
260081_at	unknown protein	---	AT1G78170	1.82	0.87	1.64	0.147571	0.341908	-5.58
248665_at	Expressed protein ; supported by full-ler	---	AT5G48655	1.12	0.16	1.64	0.147606	0.341956	-5.58
265850_at	putative DnaJ protein	---	AT2G35720	-1.20	-0.26	-1.64	0.147675	0.342080	-5.58
246852_at	putative protein various predicted bacter	---	AT5G26880	-1.13	-0.17	-1.64	0.147784	0.342265	-5.58
252864_at	putative protein regulatory protein prrC,	---	AT4G39740	-1.28	-0.35	-1.64	0.147778	0.342265	-5.58
258068_at	putative DNA-binding protein, GT-1 sim	---	AT3G25990	1.13	0.18	1.63	0.147807	0.342282	-5.58
261336_at	unknown protein ;supported by full-lengt	---	AT1G44790	1.22	0.29	1.63	0.14795	0.342333	-5.58
266036_s_a	20S proteasome subunit (PAA2) identica	PAA2	AT2G05840 /	-1.13	-0.18	-1.63	0.147961	0.342333	-5.58
259959_at	hypothetical protein predicted by genscа	CYP59	AT1G53720	-1.16	-0.22	-1.63	0.147938	0.342333	-5.58
255562_at	G/T DNA mismatch repair enzyme simil	MSH6	AT4G02070	-1.18	-0.24	-1.63	0.147975	0.342333	-5.58
255976_at	hypothetical protein predicted by genem	---	AT1G22010	1.13	0.17	1.63	0.147979	0.342333	-5.58
264793_at	unknown protein similar to beta-galacto	---	AT1G08660	-1.21	-0.28	-1.63	0.14791	0.342333	-5.58
245622_at	A6 anther-specific protein	MEE48	AT4G14080	1.15	0.20	1.63	0.147944	0.342333	-5.58
249490_s_a	germin -like protein germin -like protein	---	AT5G39110 /	1.46	0.54	1.63	0.147918	0.342333	-5.58
259196_at	putative ribosomal protein S2 similar to	RPS2	AT3G03600	-1.20	-0.26	-1.63	0.147858	0.342333	-5.58
258864_at	unknown protein	---	AT3G03210	-1.18	-0.24	-1.63	0.147931	0.342333	-5.58
267434_at	3-beta-hydroxysteroid dehydrogenase	AT3BETAI	AT2G26260	1.16	0.22	1.63	0.148045	0.342450	-5.58
249458_at	putative protein predicted proteins, Ara	---	AT5G39560	1.13	0.17	1.63	0.148095	0.342531	-5.58
259652_at	unknown protein	HUB2	AT1G55250	-1.20	-0.27	-1.63	0.148272	0.342878	-5.58
258020_at	unknown protein ;supported by full-leng	NHD1	AT3G19490	-1.14	-0.19	-1.63	0.148275	0.342878	-5.58
250831_at	unknown protein	---	AT5G04920	1.13	0.18	1.63	0.148464	0.343246	-5.58
265894_at	putative lipid transfer protein	LTP	AT2G15050	-1.43	-0.52	-1.63	0.148455	0.343246	-5.58
256897_at	hypothetical protein predicted by genscа	---	AT3G24640	1.12	0.16	1.63	0.148516	0.343331	-5.58
251469_at	putative protein strictosidine synthase -	---	AT3G59530	1.12	0.17	1.63	0.148637	0.343546	-5.58

253601_at	hypothetical protein	---	AT4G30900	-1.11	-0.15	-1.63	0.148639	0.343546	-5.58
258741_at	Lon protease, putative similar to Lon pr	LON4	AT3G05790	-1.12	-0.16	-1.63	0.148662	0.343564	-5.58
265444_s_a	aquaporin (plasma membrane intrinsic p	RD28	AT2G37170 /	1.30	0.38	1.63	0.148762	0.343667	-5.58
261210_at	vacuolar ATP synthase subunit C, puta	DET3	AT1G12840	1.11	0.15	1.63	0.148747	0.343667	-5.58
260098_at	tumor-related protein, putative similar to	---	AT1G73320	-1.26	-0.34	-1.63	0.148724	0.343667	-5.58
245231_at	hypothetical protein	---	AT4G25600	-1.16	-0.22	-1.63	0.148767	0.343667	-5.58
262418_at	thioredoxin, putative similar to thioredox	ATHX	AT1G50320	-1.22	-0.29	-1.63	0.14885	0.343824	-5.58
255774_at	unknown protein	---	AT1G18620	-1.34	-0.42	-1.63	0.149033	0.344160	-5.58
247558_at	histone deacetylase - like histone deac	HDA05	AT5G61060	-1.14	-0.19	-1.63	0.149047	0.344160	-5.58
246051_at	epimerase/dehydratase - like protein dT	GME	AT5G28840	-1.18	-0.24	-1.63	0.149021	0.344160	-5.58
262732_at	putative protein kinase similar to gb|J04	---	AT1G16440	1.16	0.21	1.63	0.149056	0.344160	-5.59
247482_at	chromosomal protein - like chromosom	SMC2	AT5G62410	1.16	0.21	1.63	0.149156	0.344358	-5.59
264168_at	unknown protein Similar to yeast genera	---	AT1G02080	-1.15	-0.20	-1.63	0.149266	0.344547	-5.59
254317_at	hypothetical protein	---	AT4G22510	1.11	0.15	1.63	0.149268	0.344547	-5.59
259609_at	myosin-like protein contains Pfam profil	TSA1	AT1G52410	-1.79	-0.84	-1.63	0.149287	0.344555	-5.59
250898_at	putative protein ; supported by cDNA: g	ADK2	AT5G03300	-1.18	-0.24	-1.63	0.149367	0.344705	-5.59
261207_at	peroxisomal targeting signal type 2 rece	---	AT1G12830	-1.22	-0.29	-1.63	0.14946	0.344884	-5.59
248152_at	DNA repair and meiosis protein Mre11 (	MRE11	AT5G54260	-1.20	-0.26	-1.63	0.149513	0.344936	-5.59
266332_at	hypothetical protein predicted by gensca	---	AT2G32415	1.14	0.19	1.63	0.149507	0.344936	-5.59
249913_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G22810	-1.15	-0.21	-1.63	0.149572	0.345002	-5.59
261015_at	14-3-3 protein GF14iota (grf12) identica	GRF12	AT1G26480	-1.13	-0.18	-1.63	0.149565	0.345002	-5.59
258376_at	hypothetical protein similar to GB:AAD4	---	AT3G17680	1.12	0.16	1.63	0.149605	0.345010	-5.59
263047_at	putative phosphoserine aminotransferas	---	AT2G17630	-1.31	-0.39	-1.63	0.149595	0.345010	-5.59
248063_at	RNA-binding protein-like ; supported by	---	AT5G55550	-1.13	-0.18	-1.63	0.149645	0.345032	-5.59
265292_s_a	hypothetical protein predicted by gensca	---	---	-1.11	-0.15	-1.63	0.149635	0.345032	-5.59
246499_at	putative protein Tat-SF1 - Homo sapien	---	AT5G16260	-1.18	-0.24	-1.63	0.149706	0.345137	-5.59
253029_at	hypothetical protein	FRS9	AT4G38170	-1.32	-0.40	-1.63	0.149887	0.345382	-5.59
263828_at	putative GDSL-motif lipase/hydrolase si	---	AT2G40250	1.18	0.24	1.63	0.149874	0.345382	-5.59
250149_at	cinnamoyl CoA reductase - like protein	---	AT5G14700	1.93	0.95	1.63	0.149841	0.345382	-5.59
265278_at	hypothetical protein predicted by gensca	---	AT2G28330	-1.18	-0.24	-1.63	0.149854	0.345382	-5.59
252697_at	nodulin - like protein nodulin-21, Glycin	---	AT3G43660	-1.15	-0.21	-1.63	0.149864	0.345382	-5.59
264593_at	putative GTP-binding protein ; supporte	ARAC1	AT2G17800	-1.14	-0.19	-1.62	0.149918	0.345416	-5.59
253258_at	putative protein NF-180, Petromyzon m	---	AT4G34400	1.16	0.21	1.62	0.150037	0.345656	-5.59
267007_at	60S ribosomal protein L18A ; supported	---	AT2G34480	-1.24	-0.31	-1.62	0.150081	0.345722	-5.59
260868_at	unknown protein ;supported by full-leng	---	AT1G43860	-1.18	-0.24	-1.62	0.150133	0.345773	-5.59

266092_at	hypothetical protein predicted by gensca	---	AT2G37880	1.14	0.19	1.62	0.150129	0.345773	-5.59
260426_at	putative 40S ribosomal protein SA (lami	P40	AT1G72370	-1.27	-0.35	-1.62	0.150199	0.345855	-5.59
253963_at	putative protein probable calcium-depe	---	AT4G26470	1.27	0.35	1.62	0.15019	0.345855	-5.59
245802_at	hypothetical protein similar to hypothetic	---	AT1G46840	-1.11	-0.15	-1.62	0.150248	0.345909	-5.59
246872_at	extensin - like protein hydroxyproline-ric	---	AT5G26080	1.16	0.22	1.62	0.150253	0.345909	-5.59
250740_at	t-SNARE SED5 (gb|AAC06291.1) ; sup	SYP31	AT5G05760	1.11	0.16	1.62	0.150294	0.345921	-5.59
255115_at	putative protein probable regulatory pro	APUM11	AT4G08840	1.12	0.17	1.62	0.150303	0.345921	-5.59
251182_at	putative protein HIRA interacting protei	ATERDJ3I	AT3G62600	1.52	0.61	1.62	0.150289	0.345921	-5.59
251258_at	PECTINESTERASE-like protein PECTI	VGDH2	AT3G62170	1.16	0.22	1.62	0.150387	0.346079	-5.59
247387_at	unknown protein	---	AT5G63460	-1.13	-0.18	-1.62	0.150482	0.346261	-5.59
247717_at	nonspecific lipid-transfer protein precur	LTP3	AT5G59320	1.34	0.42	1.62	0.150552	0.346388	-5.59
253664_at	NADPH-ferrihemoprotein reductase (AT	ATR2	AT4G30210	1.48	0.57	1.62	0.150567	0.346389	-5.59
250084_at	unknown protein	SDG40	AT5G17240	-1.22	-0.28	-1.62	0.150612	0.346456	-5.59
252578_at	putative protein Ariadne protein (ARI) -	---	AT3G45480	1.12	0.16	1.62	0.150639	0.346483	-5.59
258986_at	putative heat shock protein similar to he	---	AT3G08910	1.14	0.19	1.62	0.150669	0.346517	-5.59
260327_at	putative RING zinc finger protein Pfam	---	AT1G63840	1.24	0.32	1.62	0.150724	0.346610	-5.60
246055_at	alpha-galactosidase - like protein alpha	AtAGAL1	AT5G08380	-1.34	-0.43	-1.62	0.150748	0.346629	-5.60
258598_at	hypothetical protein predicted by gensca	---	AT3G04410	1.18	0.24	1.62	0.150779	0.346666	-5.60
252774_at	putative protein predicted proteins, Arat	---	---	1.17	0.23	1.62	0.150825	0.346736	-5.60
253775_at	putative protein T01B08.14 gene, BAC	---	AT4G28440	-1.12	-0.16	-1.62	0.15106	0.347165	-5.60
246759_at	putative protein kinesin heavy chain-like	---	AT5G27950	-1.20	-0.26	-1.62	0.151085	0.347165	-5.60
265863_at	putative membrane protein	VIT1	AT2G01770	1.18	0.24	1.62	0.151065	0.347165	-5.60
245640_at	helix-loop-helix protein homolog, putativ	---	AT1G25330	1.13	0.18	1.62	0.151083	0.347165	-5.60
261444_at	hypothetical protein predicted by genem	SYP61	AT1G28490	-1.13	-0.18	-1.62	0.15109	0.347165	-5.60
259288_at	putative small nuclear ribonucleoprotein	---	AT3G11500	-1.14	-0.19	-1.62	0.151103	0.347165	-5.60
265377_at	putative beta-1,3-glucanase	---	AT2G05790	1.92	0.94	1.62	0.151236	0.347436	-5.60
262535_at	trehalose-6-phosphate synthase, putati	ATTPS3	AT1G17000	-1.10	-0.14	-1.62	0.151263	0.347463	-5.60
266096_at	putative vacuolar protein sorting-associa	VCL1	AT2G38020	1.13	0.17	1.62	0.151314	0.347545	-5.60
252257_at	putative protein several hypothetical pro	---	AT3G49440	1.11	0.16	1.62	0.151333	0.347554	-5.60
250195_at	putative protein	---	AT5G14560	-1.10	-0.14	-1.62	0.151351	0.347561	-5.60
248127_at	transport protein particle component Bet	---	AT5G54750	-1.12	-0.17	-1.62	0.151433	0.347713	-5.60
261508_at	unknown protein	---	AT1G71730	-1.15	-0.20	-1.62	0.151458	0.347736	-5.60
258139_at	heat shock transcription factor HSF1, p	HSFC1	AT3G24520	-1.18	-0.24	-1.62	0.151478	0.347747	-5.60
256103_at	hypothetical protein similar to hypothetic	---	AT1G13540	-1.10	-0.14	-1.62	0.151526	0.347823	-5.60
265215_at	hypothetical protein predicted by gensca	---	AT1G05040	1.11	0.15	1.62	0.151562	0.347870	-5.60

254834_at	flavonoid 3,5-hydroxylase -like protein f	CYP706A4	AT4G12300	-1.18	-0.24	-1.62	0.151596	0.347913	-5.60
267161_at	hypothetical protein predicted by genefir	---	AT2G37680	-1.12	-0.16	-1.62	0.151683	0.348078	-5.60
252541_at	putative protein hypothetical protein At2	---	AT3G45750	-1.13	-0.17	-1.62	0.151705	0.348092	-5.60
248948_at	putative protein strong similarity to unkn	---	AT5G45560	-1.20	-0.27	-1.62	0.151733	0.348115	-5.60
263544_at	putative ADP-glucose pyrophosphorylas	APL4	AT2G21590	-1.16	-0.22	-1.62	0.151745	0.348115	-5.60
247324_at	putative protein strong similarity to unkn	---	AT5G64190	1.63	0.70	1.62	0.151763	0.348120	-5.60
245197_at	F12A21.7 hypothetical protein;supporte	---	AT1G67800	1.13	0.18	1.62	0.151784	0.348134	-5.60
257046_at	ATPase, putative similar to spastin prot	---	AT3G19740	-1.19	-0.26	-1.62	0.151801	0.348139	-5.60
267114_at	Expressed protein ; supported by full-ler	---	AT2G14835	1.13	0.18	1.62	0.151838	0.348188	-5.60
250750_at	glucuronosyl transferase-like protein	UGT76C2	AT5G05860 /	-1.14	-0.19	-1.62	0.151886	0.348263	-5.60
248243_at	unknown protein	CPuORF5	AT5G53588 /	1.11	0.15	1.62	0.151964	0.348372	-5.60
264627_at	hypothetical protein similar to carnitine r	ECI1	AT1G65520	1.15	0.21	1.62	0.151962	0.348372	-5.60
250626_at	putative protein p100 co-activator - Mus	---	AT5G07350	1.14	0.19	1.62	0.152018	0.348461	-5.60
254530_at	small GTP-binding protein - like GTP-bi	ARA7	AT4G19640	1.12	0.17	1.61	0.152126	0.348672	-5.60
252109_at	putative protein mucin 5AC, Homo sapi	---	AT3G51540	1.33	0.42	1.61	0.152141	0.348672	-5.60
266267_at	putative glutathione S-transferase ; sup	ATGSTU4	AT2G29460	1.88	0.91	1.61	0.152327	0.348928	-5.61
246253_at	myb-related protein	MYB73	AT4G37260	1.20	0.26	1.61	0.152316	0.348928	-5.61
260491_at	hypothetical protein predicted by genem	---	AT1G51440	1.21	0.27	1.61	0.152408	0.348928	-5.61
262932_at	glutathione-s-transferase, putative simil	---	AT1G65820	1.19	0.25	1.61	0.152373	0.348928	-5.61
247624_at	aspartyl aminopeptidase - like protein a	---	AT5G60160	-1.11	-0.15	-1.61	0.152385	0.348928	-5.61
252449_at	FtsH protease, putative contains similar	ftsh7	AT3G47060	1.11	0.15	1.61	0.152374	0.348928	-5.61
263238_at	putative auxin-induced protein	---	AT2G16580	1.11	0.16	1.61	0.152321	0.348928	-5.61
262465_at	hypothetical protein similar to hypothetic	---	AT1G50270	-1.12	-0.16	-1.61	0.152416	0.348928	-5.61
258095_at	dual-specificity protein phosphatase ide	---	AT3G23610	-1.16	-0.22	-1.61	0.152403	0.348928	-5.61
248455_at	unknown protein	---	AT5G51360	1.12	0.16	1.61	0.152308	0.348928	-5.60
246557_at	putative protein hypothetical protein TE	---	AT5G15510	-1.13	-0.18	-1.61	0.152421	0.348928	-5.61
263699_at	putative potassium transporter similar to	KUP10	AT1G31120	-1.21	-0.28	-1.61	0.152441	0.348940	-5.61
265529_at	hypothetical protein predicted by gensca	---	---	1.12	0.16	1.61	0.152533	0.349115	-5.61
248573_at	cellulase homolog OR16pep precursor (	ATGH9A1	AT5G49720	1.16	0.21	1.61	0.152561	0.349145	-5.61
255907_at	homeobox protein, putative similar to h	HDG12	AT1G17920	1.12	0.16	1.61	0.152595	0.349186	-5.61
252288_at	hypothetical protein	---	AT3G49080	-1.20	-0.26	-1.61	0.152634	0.349207	-5.61
259069_at	lysyl-tRNA synthetase identical to lysyl-t	ATKRS-1	AT3G11710	-1.17	-0.23	-1.61	0.152627	0.349207	-5.61
247592_at	high affinity nitrate transporter protein -	NRT2.3	AT5G60780	1.12	0.16	1.61	0.15275	0.349435	-5.61
262328_at	hypothetical protein similar to hypothetic	---	AT1G64100	-1.10	-0.14	-1.61	0.152808	0.349533	-5.61
246641_s_a	Expressed protein ; supported by full-ler	---	AT5G34883 /	1.14	0.19	1.61	0.152859	0.349616	-5.61

251710_at	putative protein several hypothetical pro	---	AT3G56930	1.28	0.36	1.61	0.152971	0.349765	-5.61
246586_at	putative protein predicted protein, Arabi	---	AT5G14770	-1.19	-0.25	-1.61	0.152961	0.349765	-5.61
252042_at	putative serine/threonine protein kinase	---	AT3G51990	1.17	0.22	1.61	0.152953	0.349765	-5.61
252379_at	ABC-type transport protein-like protein /	ATH1	AT3G47730	1.15	0.20	1.61	0.152995	0.349785	-5.61
261928_at	uclacyanin II, putative similar to uclacya	---	AT1G22480	1.21	0.28	1.61	0.153093	0.349976	-5.61
254159_at	putative DNA-binding protein DNA-bind	WRKY7	AT4G24240	1.31	0.39	1.61	0.153185	0.350149	-5.61
260821_at	unknown protein contains Pfam profile:F	CRTISO	AT1G06820	-1.17	-0.22	-1.61	0.153204	0.350160	-5.61
250363_at	putative protein predicted proteins, Ory	---	AT5G11390	-1.26	-0.33	-1.61	0.153226	0.350164	-5.61
250977_at	importin alpha - like protein importin alp	IMPA-9	AT5G03070	-1.16	-0.21	-1.61	0.153237	0.350164	-5.61
258219_at	thioredoxin, putative similar to THIORE	ATTDX	AT3G17880	-1.13	-0.18	-1.61	0.153283	0.350207	-5.61
244927_at	hypothetical protein	---	AT2G07776	1.18	0.24	1.61	0.153287	0.350207	-5.61
245740_at	amino acid permease, putative almost i	AAP5	AT1G44100	1.18	0.24	1.61	0.15338	0.350386	-5.61
264534_at	hypothetical protein predicted by genem	---	AT1G55700	1.19	0.26	1.61	0.153532	0.350697	-5.61
266309_at	unknown protein ;supported by full-leng	---	AT2G27140	1.20	0.26	1.61	0.153599	0.350805	-5.61
267574_at	hypothetical protein predicted by gensca	---	AT2G30680	1.20	0.26	1.61	0.15361	0.350805	-5.61
258783_at	unknown protein	---	AT3G11760	1.15	0.20	1.61	0.153666	0.350892	-5.61
252918_at	putative protein	---	AT4G38980	-1.11	-0.15	-1.61	0.153679	0.350892	-5.61
262832_s_a	unknown protein	---	AT1G14870 /	3.10	1.63	1.61	0.153734	0.350982	-5.61
265613_at	putative DnaJ protein ; supported by cD	---	AT2G25560	-1.17	-0.22	-1.61	0.153801	0.351101	-5.61
264231_at	hypothetical protein similar to hypothetic	---	AT1G67450	1.11	0.15	1.61	0.153848	0.351173	-5.61
256845_x_a	hypothetical protein similar to putative re	---	---	-1.13	-0.18	-1.61	0.153894	0.351242	-5.61
246881_at	putative protein histone deacetylase/Ac	HDA2	AT5G26040	-1.24	-0.30	-1.61	0.153938	0.351307	-5.61
259003_at	hypothetical protein similar to hypotheti	---	AT3G02010	-1.21	-0.28	-1.61	0.154014	0.351447	-5.62
248895_at	receptor protein kinase	FLS2	AT5G46330	-1.34	-0.42	-1.61	0.15408	0.351502	-5.62
263518_at	Expressed protein ; supported by full-ler	---	AT2G21655	1.13	0.18	1.61	0.154084	0.351502	-5.62
257130_at	vacuolar processing enzyme/asparagin	DELTA-VP	AT3G20210	1.11	0.15	1.61	0.154066	0.351502	-5.62
266981_at	60S ribosomal protein L23A identical to	RPL23AA	AT2G39460	-1.30	-0.38	-1.61	0.154118	0.351544	-5.62
245449_at	retrotransposon like protein	---	---	1.24	0.31	1.61	0.154176	0.351641	-5.62
255337_at	putative DNA-binding protein similar to	WRKY42	AT4G04450	1.18	0.24	1.60	0.154352	0.352007	-5.62
248327_at	putative protein similar to unknown prote	---	AT5G52750	2.11	1.08	1.60	0.154448	0.352137	-5.62
260166_at	homeobox protein (GLABRA2) identical	GL2	AT1G79840	-1.12	-0.16	-1.60	0.154427	0.352137	-5.62
258206_at	hypothetical protein predicted by genem	CID4	AT3G14010	-1.14	-0.18	-1.60	0.154456	0.352137	-5.62
249150_at	inorganic phosphate transporter (dbj|BA	PHT6	AT5G43340	1.12	0.16	1.60	0.154482	0.352163	-5.62
250038_at	disease resistance protein -like disease	---	AT5G18360	1.21	0.27	1.60	0.154539	0.352256	-5.62
265824_at	putative glucosyltransferase ;supported	ATCSLA07	AT2G35650	1.19	0.25	1.60	0.154568	0.352288	-5.62

261244_at	subtilisin-like serine protease similar to s	---	AT1G20150	1.10	0.14	1.60	0.154589	0.352300	-5.62
248835_at	NBS/LRR disease resistance protein	---	AT5G47250	-1.25	-0.33	-1.60	0.154654	0.352378	-5.62
267547_at	putative synaptobrevin	ATVAMP7	AT2G32670	1.18	0.24	1.60	0.154647	0.352378	-5.62
252736_at	kinesin -like protein kinesin-like protein	TES	AT3G43210	1.13	0.17	1.60	0.15477	0.352607	-5.62
252564_at	actin depolymerizing factor 1 (ADF1) ;s	ADF1	AT3G46010	1.14	0.19	1.60	0.154801	0.352642	-5.62
252563_at	putative protein cim1 induced allergen,	ATEXLA1	AT3G45970	1.50	0.58	1.60	0.154866	0.352652	-5.62
263691_at	60s ribosomal protein L34 identical to G	---	AT1G26880	-1.28	-0.35	-1.60	0.154874	0.352652	-5.62
247542_at	autophagocytosis protein - like autopha	ATG3	AT5G61500	-1.16	-0.22	-1.60	0.154873	0.352652	-5.62
249805_at	putative protein similar to unknown prote	---	AT5G23800	1.13	0.17	1.60	0.154882	0.352652	-5.62
252467_at	putative protein predicted proteins, Aral	---	AT3G47080	1.19	0.25	1.60	0.154827	0.352652	-5.62
265422_at	putative NADH-ubiquinone oxireductase	NDB4	AT2G20800	1.15	0.20	1.60	0.154981	0.352841	-5.62
253517_at	predicted protein hypothetical protein sl	---	AT4G31390	-1.19	-0.25	-1.60	0.155003	0.352856	-5.62
249081_at	protein phosphatase 2A 62 kDa B regula	---	AT5G44090	1.13	0.18	1.60	0.155026	0.352874	-5.62
258837_at	putative 60S ribosomal protein L13A sin	---	AT3G07110	-1.36	-0.44	-1.60	0.155159	0.353141	-5.62
247818_at	contains similarity to GTP-binding protei	---	AT5G58370	-1.14	-0.18	-1.60	0.155351	0.353543	-5.62
259682_at	transcription factor DREB1A, putative s	---	AT1G63040	1.20	0.26	1.60	0.155388	0.353592	-5.62
254277_at	myb-like protein myb-related transcripti	MYB85	AT4G22680	1.51	0.59	1.60	0.155467	0.353736	-5.62
250351_at	heat shock protein 17.6A	AT-HSP17	AT5G12030	1.43	0.52	1.60	0.15551	0.353763	-5.62
254310_at	putative protein predicted protein, Arabi	---	AT4G22430	1.10	0.14	1.60	0.1555	0.353763	-5.62
247876_at	unknown protein	---	AT5G57730	-1.12	-0.16	-1.60	0.155529	0.353771	-5.62
258298_at	unknown protein ; supported by cDNA:	---	AT3G23300	1.19	0.25	1.60	0.155568	0.353805	-5.62
247847_at	putative protein predicted proteins, Hon	---	AT5G58110	-1.22	-0.29	-1.60	0.155575	0.353805	-5.62
258556_at	UDP-glucose:sterol glucosyltransferase	---	AT3G07020	-1.16	-0.21	-1.60	0.155605	0.353838	-5.62
246826_at	UTP-glucose glucosyltransferase - like	UGT72E3	AT5G26310	1.13	0.18	1.60	0.155655	0.353876	-5.63
249156_s_a	putative protein similar to unknown prote	---	AT5G43490 /	1.11	0.15	1.60	0.155668	0.353876	-5.63
245263_at	PSII D1 protein processing enzyme ; su	---	AT4G17740	-1.12	-0.17	-1.60	0.155668	0.353876	-5.63
254745_at	putative protein G9A protein, Mus musc	SUVH9	AT4G13460	-1.10	-0.13	-1.60	0.155755	0.354038	-5.63
263274_at	putative protein kinase contains a protei	CRCK3	AT2G11520	1.16	0.21	1.60	0.155772	0.354042	-5.63
250345_at	subtilisin-like serine protease contains s	---	AT5G11940	1.14	0.19	1.60	0.155858	0.354201	-5.63
262693_at	unknown protein	---	AT1G62780	-1.31	-0.39	-1.60	0.155875	0.354204	-5.63
252920_at	putative endo-1,4-beta-glucanase endo	AtGH9B17	AT4G39000	1.15	0.21	1.60	0.155947	0.354262	-5.63
250508_at	selenium-binding protein-like	---	AT5G09950	-1.13	-0.18	-1.60	0.155938	0.354262	-5.63
249715_at	putative protein similar to unknown prote	---	AT5G35760	1.17	0.22	1.60	0.15592	0.354262	-5.63
247619_at	putative protein	---	AT5G60290	-1.19	-0.25	-1.60	0.155989	0.354322	-5.63
259222_at	putative phosphoribosylanthranilate tra	---	AT3G03680	-1.17	-0.23	-1.60	0.156019	0.354353	-5.63

255841_at	putative tyrosine-specific transport prote	---	AT2G33260	1.20	0.27	1.60	0.156033	0.354353	-5.63
267299_at	putative glucosyltransferase	---	AT2G30150	-1.18	-0.24	-1.60	0.156066	0.354357	-5.63
258089_at	hypothetical protein predicted by gensca	---	AT3G14740	-1.29	-0.36	-1.60	0.156056	0.354357	-5.63
249479_at	germin - like protein probable germin ty	---	AT5G38960	1.18	0.23	1.60	0.156215	0.354660	-5.63
258386_at	hypothetical protein predicted by gensca	---	AT3G15520	-1.20	-0.27	-1.60	0.156252	0.354708	-5.63
253463_at	Expressed protein ; supported by full-ler	---	AT4G32105	1.13	0.18	1.60	0.15635	0.354896	-5.63
265677_at	putative purine-rich single-stranded DNA	PUR ALPH	AT2G32080	-1.12	-0.16	-1.60	0.156396	0.354964	-5.63
264119_at	myb-related protein, putative similar to	MYB63	AT1G79180	1.11	0.15	1.60	0.156451	0.355054	-5.63
267411_at	putative disease resistance protein	---	AT2G34930	2.00	1.00	1.59	0.156516	0.355166	-5.63
257624_at	cytochrome P450 monooxygenase (CY	CYP71B3	AT3G26220	1.63	0.70	1.59	0.156535	0.355174	-5.63
265072_at	hypothetical protein predicted by genem	LAS	AT1G55580	1.19	0.25	1.59	0.156572	0.355223	-5.63
251681_at	putative protein hypothetical protein F1	---	AT3G57100	1.16	0.21	1.59	0.156589	0.355225	-5.63
252967_at	amidophosphoribosyltransferase - like p	ATASE3	AT4G38880	1.14	0.19	1.59	0.156605	0.355228	-5.63
260479_at	hypothetical protein predicted by genefir	---	AT1G11020	-1.11	-0.16	-1.59	0.156683	0.355369	-5.63
265612_at	hypothetical protein predicted by gensca	---	AT2G25390 /	-1.12	-0.17	-1.59	0.156777	0.355547	-5.63
254994_at	putative methyltransferase	MTA	AT4G10760	-1.26	-0.33	-1.59	0.156819	0.355605	-5.63
246948_at	cytochrome P450-like protein CYTOCH	CYP71B12	AT5G25130	1.11	0.16	1.59	0.156859	0.355661	-5.63
258635_at	unknown protein	---	AT3G08020	-1.11	-0.15	-1.59	0.157	0.355840	-5.63
245372_at	ribosomal protein ;supported by full-leng	---	AT4G15000	-1.28	-0.36	-1.59	0.156984	0.355840	-5.63
251976_at	disease resistance - like protein disease	AtRLP45	AT3G53240	-1.16	-0.22	-1.59	0.156986	0.355840	-5.63
253484_at	Transcription factor II homolog ;support	TAFII15	AT4G31720	-1.11	-0.15	-1.59	0.15696	0.355840	-5.63
260474_at	lysophospholipase isolog	---	AT1G11090	-1.16	-0.21	-1.59	0.157051	0.355875	-5.63
257663_at	hypothetical protein predicted by gensca	---	AT3G20260	-1.14	-0.18	-1.59	0.15704	0.355875	-5.63
258037_at	putative 4-coumarate:CoA ligase 2 simil	4CL5	AT3G21230	1.97	0.98	1.59	0.157062	0.355875	-5.63
259144_at	putative kinesin-like centromere protein	---	AT3G10180	1.13	0.17	1.59	0.157093	0.355909	-5.63
262040_at	receptor protein kinase, putative similar	TMM	AT1G80080	-1.14	-0.19	-1.59	0.157213	0.356145	-5.63
245486_x_a	glycine-rich protein homolog	---	AT4G16240	1.13	0.18	1.59	0.157239	0.356169	-5.63
249787_at	putative protein contains similarity to unl	---	AT5G24320	-1.12	-0.16	-1.59	0.157454	0.356621	-5.64
264601_at	hypothetical protein similar to hypothetic	---	AT1G04540	1.14	0.19	1.59	0.157516	0.356726	-5.64
245547_at	cytochrome P450 like protein	CYP702A2	AT4G15300	1.12	0.16	1.59	0.157577	0.356825	-5.64
252790_at	putative protein various predicted transp	---	---	1.12	0.16	1.59	0.157591	0.356825	-5.64
259104_at	unknown protein ;supported by full-leng	LNG2	AT3G02170	-1.25	-0.32	-1.59	0.157697	0.356872	-5.64
248265_at	putative protein contains similarity to zin	SDG29	AT5G53430	-1.19	-0.25	-1.59	0.157666	0.356872	-5.64
265030_at	receptor-like kinase, putative similar to	---	AT1G61610	1.31	0.39	1.59	0.157715	0.356872	-5.64
252725_at	putative protein mudrA transposase, Ze	---	---	1.13	0.17	1.59	0.157722	0.356872	-5.64

251877_at	synaptobrevin -like protein vesicle-asso	ATVAMP7	AT3G54300	1.16	0.21	1.59	0.157707	0.356872	-5.64
256200_at	hypothetical protein predicted by genem	EMB1674	AT1G58210	-1.14	-0.19	-1.59	0.157686	0.356872	-5.64
257366_s_a	unknown protein	---	AT2G03040 /	1.14	0.19	1.59	0.157713	0.356872	-5.64
247303_at	histidinol dehydrogenase ;supported by	ATHDH	AT5G63890	-1.19	-0.25	-1.59	0.157753	0.356907	-5.64
260564_at	putative small nuclear ribonucleoprotein	---	AT2G43810	-1.16	-0.21	-1.59	0.157854	0.356966	-5.64
258952_at	putative RNase H contains Pfam profile:	---	AT3G01410	1.16	0.21	1.59	0.157807	0.356966	-5.64
246118_at	beta-1,3-glucanase bg5	BG5	AT5G20340	1.15	0.20	1.59	0.157872	0.356966	-5.64
261755_at	histone H2B, putative similar to GB:AA(	---	AT1G08170	1.18	0.24	1.59	0.157872	0.356966	-5.64
258788_at	unknown protein ;supported by full-leng	---	AT3G11780	1.14	0.19	1.59	0.157856	0.356966	-5.64
261596_at	hypothetical protein predicted by genem	---	AT1G33080	-1.14	-0.19	-1.59	0.157811	0.356966	-5.64
255991_at	unknown protein	---	AT1G29820	-1.24	-0.31	-1.59	0.157915	0.357027	-5.64
249395_at	putative protein	---	AT5G40190	-1.11	-0.15	-1.59	0.158001	0.357186	-5.64
249027_at	ATP dependent copper transporter ; su	RAN1	AT5G44790	1.17	0.23	1.59	0.158048	0.357257	-5.64
250123_at	putative protein contains similarity to au	PIN5	AT5G16530	-1.16	-0.22	-1.59	0.158117	0.357376	-5.64
250253_at	putative protein contains similarity to un	PDAT	AT5G13640	-1.16	-0.21	-1.59	0.158157	0.357433	-5.64
264917_at	unknown protein contains Pfam profile:	---	AT1G60500	1.11	0.15	1.59	0.158232	0.357567	-5.64
264245_at	galactinol synthase, putative similar to g	AtGolS7	AT1G60450	-1.12	-0.17	-1.59	0.158293	0.357668	-5.64
250401_at	putative protein HSPC184, Homo sapie	---	AT5G10780	-1.12	-0.16	-1.59	0.158373	0.357814	-5.64
253220_s_a	putative protein phospholipase C, Liste	---	AT4G34920 /	-1.19	-0.25	-1.59	0.1585	0.358065	-5.64
260444_at	unknown protein ;supported by full-leng	---	AT1G68300	1.15	0.20	1.59	0.158556	0.358142	-5.64
259754_at	hypothetical protein predicted by gensca	---	AT1G71090	-1.15	-0.20	-1.59	0.158597	0.358142	-5.64
253011_at	putative protein retrotransposon -like pr	EDA40	AT4G37890	1.29	0.37	1.59	0.158588	0.358142	-5.64
262537_s_a	putative ubiquitin-conjugating enzyme F	UBC34	AT1G17280 /	-1.21	-0.28	-1.59	0.158578	0.358142	-5.64
254630_at	glycolate oxidase - like protein (S)-2-hy	---	AT4G18360	1.71	0.77	1.59	0.158638	0.358193	-5.64
252124_at	hypothetical protein ;supported by full-le	---	AT3G51010	-1.17	-0.23	-1.59	0.158651	0.358193	-5.64
247231_at	transcription factor-like protein	AtMYB53	AT5G65230	1.13	0.18	1.58	0.158768	0.358422	-5.64
264654_s_a	putative sugar transport protein, ERD6	---	AT1G08890 /	-1.24	-0.31	-1.58	0.15882	0.358504	-5.64
250361_at	putative protein various predicted prote	---	AT5G11370	1.11	0.15	1.58	0.158841	0.358516	-5.64
245126_at	putative MYB family transcription factor	MYB12	AT2G47460	1.12	0.17	1.58	0.158938	0.358699	-5.64
250141_at	protein kinase MSK-3 - like protein kina	SK13	AT5G14640	1.17	0.22	1.58	0.158982	0.358729	-5.64
256619_at	hypothetical protein predicted by gensca	---	AT3G24460	1.13	0.17	1.58	0.158978	0.358729	-5.64
264134_at	unknown protein contains similarity to al	---	AT1G79070	-1.11	-0.14	-1.58	0.159002	0.358736	-5.64
246138_at	putative protein predicted proteins from	---	AT5G19870	1.10	0.14	1.58	0.159037	0.358736	-5.64
252521_at	hypothetical protein	---	AT3G46380	-1.21	-0.28	-1.58	0.159035	0.358736	-5.64
255245_at	hypothetical protein	---	AT4G05630	-1.13	-0.17	-1.58	0.159048	0.358736	-5.64

246818_at	putative protein crp1, Zea mays, PIR:T(	EMB976	AT5G27270	-1.30	-0.38	-1.58	0.159083	0.358743	-5.65
248226_at	putative protein strong similarity to unkn	---	AT5G53750	1.48	0.57	1.58	0.159077	0.358743	-5.64
253636_at	putative protein predicted protein, Arabi	---	AT4G30500	1.71	0.77	1.58	0.159161	0.358884	-5.65
264087_at	hypothetical protein predicted by gensca	emb1381	AT2G31340	-1.13	-0.17	-1.58	0.15924	0.359026	-5.65
258914_at	hypothetical protein predicted by genefi	AGP27	AT3G06360	1.11	0.16	1.58	0.159281	0.359082	-5.65
256161_at	unknown protein ; supported by cDNA: g	---	AT1G30090	1.14	0.19	1.58	0.159354	0.359140	-5.65
261800_at	HD-Zip protein identical to HD-Zip prote	PHV	AT1G30490	-1.16	-0.21	-1.58	0.159351	0.359140	-5.65
262466_at	hypothetical protein similar to hypothetic	NTMC2T5	AT1G50260	1.18	0.24	1.58	0.159343	0.359140	-5.65
262197_at	AP2 domain containing protein, putative	RAP2.12	AT1G53910	1.25	0.32	1.58	0.159425	0.359266	-5.65
247846_at	putative protein	---	AT5G58100	-1.13	-0.18	-1.58	0.159474	0.359314	-5.65
262305_at	hypothetical protein predicted by genem	---	AT1G70950	1.13	0.17	1.58	0.159478	0.359314	-5.65
249703_at	putative protein strong similarity to unkn	---	AT5G35560	-1.12	-0.16	-1.58	0.15962	0.359572	-5.65
264246_at	trehalose-6-phosphate synthase, putati	ATTPS10	AT1G60140	1.45	0.54	1.58	0.159624	0.359572	-5.65
260475_at	Serine carboxypeptidase isolog	scpl31	AT1G11080	1.31	0.39	1.58	0.159653	0.359602	-5.65
245506_at	glutaredoxin homolog	---	AT4G15700	1.33	0.41	1.58	0.159679	0.359625	-5.65
259688_at	membrane protein, putative similar to G	ATRBL2	AT1G63120	-1.21	-0.28	-1.58	0.1598	0.359862	-5.65
251926_at	60S RIBOSOMAL PROTEIN L36 homo	---	AT3G53740	-1.27	-0.34	-1.58	0.15988	0.359923	-5.65
251797_at	putative protein AT-hook protein 1 (AHP	AGF2	AT3G55560	1.19	0.25	1.58	0.159879	0.359923	-5.65
262862_at	hypothetical protein predicted by genem	---	AT1G64830	1.21	0.27	1.58	0.159922	0.359923	-5.65
251442_at	putative protein multisynthetase comple	---	AT3G59980	-1.23	-0.29	-1.58	0.159911	0.359923	-5.65
259329_at	putative two-component phosphorelay r	AHP4	AT3G16360	-1.38	-0.46	-1.58	0.159856	0.359923	-5.65
264932_at	hypothetical protein similar to hypothetic	---	AT1G61240	-1.19	-0.25	-1.58	0.159903	0.359923	-5.65
266812_at	putative protein kinase contains a protei	---	AT2G44830	1.18	0.24	1.58	0.159995	0.360052	-5.65
250970_at	putative protein ; supported by cDNA: g	---	AT5G02770	-1.12	-0.16	-1.58	0.160075	0.360087	-5.65
250403_at	argininosuccinate lyase (AtArgH) ; supp	---	AT5G10920	-1.27	-0.34	-1.58	0.160053	0.360087	-5.65
258678_at	E2, ubiquitin-conjugating enzyme 11 (U	UBC11	AT3G08690	1.18	0.24	1.58	0.160058	0.360087	-5.65
254264_at	putative protein various predicted prote	---	AT4G23510	1.12	0.17	1.58	0.160062	0.360087	-5.65
260980_at	hypothetical protein predicted by genem	---	AT1G53600	-1.19	-0.25	-1.58	0.160089	0.360087	-5.65
250511_at	putative protein similar to unknown prote	---	AT5G09960	-1.14	-0.19	-1.58	0.160107	0.360091	-5.65
261865_at	sterol delta7 reductase identical to GB:A	DWF5	AT1G50430	1.23	0.30	1.58	0.160145	0.360141	-5.65
250917_at	fructose-bisphosphate aldolase -like pr	---	AT5G03690	1.17	0.22	1.58	0.160196	0.360221	-5.65
266557_at	unknown protein ; supported by cDNA:	---	AT2G46080	1.10	0.14	1.58	0.160225	0.360241	-5.65
248990_at	disease resistance protein-like	---	AT5G45210	1.13	0.18	1.58	0.160237	0.360241	-5.65
257377_at	unknown protein	PLL4	AT2G28890	1.31	0.39	1.58	0.160263	0.360264	-5.65
248371_at	gibberellin 20-oxidase (emb|CAA58294.	GA20OX2	AT5G51810	-1.38	-0.46	-1.58	0.160283	0.360274	-5.65

245330_at	hypothetical protein ;supported by full-le	---	AT4G14930	1.17	0.22	1.58	0.160345	0.360341	-5.65
247660_at	ankyrin-like protein ankyrin 3, Mus mus	---	AT5G60070	1.12	0.16	1.58	0.160338	0.360341	-5.65
263396_at	unknown protein ;supported by full-leng	---	AT2G31710	-1.14	-0.19	-1.58	0.160372	0.360366	-5.65
266007_at	unknown protein	---	AT2G37380	-1.16	-0.22	-1.58	0.1604	0.360394	-5.65
253298_at	putative protein ;supported by full-lengt	---	AT4G33560	-1.14	-0.19	-1.58	0.160553	0.360704	-5.65
258510_at	hypothetical protein predicted by genem	---	AT3G06600	-1.15	-0.20	-1.58	0.160676	0.360908	-5.65
262352_at	hypothetical protein similar to hypothetic	---	---	1.24	0.31	1.58	0.160663	0.360908	-5.65
266099_at	putative alpha-carboxyltransferase ; su	CAC3	AT2G38040	-1.20	-0.26	-1.58	0.160704	0.360936	-5.65
260341_at	squamosa-promoter binding protein, pu	---	AT1G69170	-1.19	-0.25	-1.58	0.160735	0.360970	-5.65
266162_at	putative bHLH transcription factor	FRU	AT2G28160	1.14	0.19	1.58	0.160769	0.361009	-5.65
248203_at	Myb-related transcription factor-like prot	MYB49	AT5G54230	1.10	0.14	1.58	0.160788	0.361017	-5.65
254022_at	putative membrane transporter Bactroc	---	AT4G25750	-1.15	-0.20	-1.58	0.160818	0.361050	-5.65
250211_at	unknown protein ; supported by cDNA:	---	AT5G13880	1.13	0.18	1.58	0.160854	0.361093	-5.66
255013_at	putative protein ;supported by full-lengt	---	AT4G10000	-1.16	-0.21	-1.58	0.160922	0.361181	-5.66
247252_at	unknown protein	---	AT5G64770	-1.64	-0.72	-1.58	0.160924	0.361181	-5.66
256239_at	hypothetical protein predicted by genem	---	AT3G12470	1.15	0.20	1.58	0.160942	0.361185	-5.66
247781_at	dehydrodolichyl diphosphate synthase	---	AT5G58784	1.18	0.24	1.58	0.160965	0.361200	-5.66
246954_at	unknown protein ; supported by cDNA:	---	AT5G04830	1.11	0.16	1.57	0.161028	0.361268	-5.66
247409_at	dihydroneopterin aldolase-like protein	---	AT5G62980	-1.22	-0.28	-1.57	0.161053	0.361268	-5.66
256380_at	pheromone receptor, putative (AR401)	AR401	AT1G66680	1.16	0.21	1.57	0.161019	0.361268	-5.66
257388_at	putative non-LTR retroelement reverse t	---	---	-1.10	-0.13	-1.57	0.161058	0.361268	-5.66
266172_at	putative aquaporin (water channel prote	PIP2E	AT2G39010	-1.31	-0.39	-1.57	0.161095	0.361280	-5.66
249229_at	putative protein similar to unknown prote	---	AT5G42090	1.14	0.18	1.57	0.161112	0.361280	-5.66
254395_at	subtilisin-like protease subtilisin-like pro	---	AT4G21640	1.11	0.15	1.57	0.161127	0.361280	-5.66
258121_s_a	putative geranylgeranyl pyrophosphate	GGPS3	AT3G14530 /	-1.16	-0.21	-1.57	0.161121	0.361280	-5.66
267131_at	hypothetical protein predicted by gensca	---	AT2G23400	-1.11	-0.15	-1.57	0.161259	0.361505	-5.66
251145_at	putative protein predicted protein, Arabi	---	AT3G63500	1.16	0.21	1.57	0.161244	0.361505	-5.66
256968_at	unknown protein	NADK1	AT3G21070	1.84	0.88	1.57	0.16128	0.361517	-5.66
263628_at	unknown protein ;supported by full-leng	FLA7	AT2G04780	1.59	0.67	1.57	0.161308	0.361545	-5.66
245467_at	hypothetical protein	---	AT4G16610	1.22	0.28	1.57	0.161339	0.361559	-5.66
248809_at	GTP-binding protein-like	AtRABA5a	AT5G47520	-1.15	-0.21	-1.57	0.161346	0.361559	-5.66
250701_at	bZIP transcription factor-like protein	---	AT5G06839	1.15	0.20	1.57	0.161498	0.361864	-5.66
249604_x_a	putative protein RING-H2 finger protein	---	AT5G37230	1.14	0.19	1.57	0.161546	0.361935	-5.66
265694_at	hypothetical protein predicted by gensca	---	AT2G24440	-1.15	-0.20	-1.57	0.161583	0.361947	-5.66
256657_at	unknown protein contains similarity to pl	---	AT3G18860	-1.13	-0.18	-1.57	0.161571	0.361947	-5.66

257414_at	hypothetical protein similar to hypothetic	---	AT1G62110	1.13	0.18	1.57	0.161599	0.361948	-5.66
261032_at	unknown protein ;supported by full-lengt	---	AT1G17430	1.44	0.53	1.57	0.161616	0.361949	-5.66
258729_at	putative amino acid transporter protein s	ANT1	AT3G11900	1.12	0.16	1.57	0.161648	0.361987	-5.66
261154_at	unknown protein ;supported by full-lengt	---	AT1G04970	1.18	0.24	1.57	0.161734	0.362036	-5.66
255508_at	putative zinc finger protein identical to T	---	AT4G02220	-1.15	-0.21	-1.57	0.161734	0.362036	-5.66
258981_at	hypothetical protein predicted by gensca	---	AT3G08880	-1.11	-0.15	-1.57	0.161693	0.362036	-5.66
251653_at	putative protein regulatory protein NPR	BOP1	AT3G57130	1.16	0.21	1.57	0.161714	0.362036	-5.66
258033_at	unknown protein similar to MRP-like AB	MRP6	AT3G21250	1.26	0.33	1.57	0.161812	0.362177	-5.66
255975_at	hypothetical protein	---	---	1.16	0.22	1.57	0.161857	0.362240	-5.66
248398_at	sorbitol dehydrogenase-like protein ;su	---	AT5G51970	-1.16	-0.21	-1.57	0.161935	0.362380	-5.66
245066_at	putative serine/threonine protein phosph	TOPP4	AT2G39840	-1.14	-0.19	-1.57	0.161967	0.362416	-5.66
246771_at	putative protein putative replication prot	---	---	1.11	0.16	1.57	0.162083	0.362640	-5.66
245176_at	unknown protein similar to GP|2104534	---	AT2G47440	-1.37	-0.45	-1.57	0.162163	0.362748	-5.66
252635_at	putative protein predicted proteins, Ara	---	AT3G44510	1.16	0.21	1.57	0.162155	0.362748	-5.66
254243_at	serine/threonine kinase - like protein se	CRK13	AT4G23210	1.78	0.84	1.57	0.162188	0.362768	-5.66
257505_at	hypothetical protein	---	AT1G47940	1.10	0.14	1.57	0.162345	0.363085	-5.66
267084_at	unknown protein ; supported by cDNA:	---	AT2G41180	-1.61	-0.69	-1.57	0.162404	0.363180	-5.66
244917_at	hypothetical protein	---	---	1.12	0.17	1.57	0.162434	0.363211	-5.66
266611_at	putative auxin-regulated protein	GH3.1	AT2G14960	-1.13	-0.18	-1.57	0.162526	0.363381	-5.66
254410_at	serine/threonine kinase - like protein	---	AT4G21410	1.40	0.49	1.57	0.162577	0.363460	-5.66
259643_at	putative menaquinone biosynthesis pro	---	AT1G68890	1.12	0.16	1.57	0.162598	0.363471	-5.67
252338_at	putative progesterone-binding protein h	MAPR3	AT3G48890	1.51	0.60	1.57	0.162733	0.363702	-5.67
247551_at	ras-GTPase-activating protein SH3-don	---	AT5G60980	-1.11	-0.15	-1.57	0.162727	0.363702	-5.67
263667_at	putative 40S ribosomal protein S15 Str	RPS15	AT1G04270	-1.18	-0.24	-1.57	0.162785	0.363733	-5.67
266451_at	3-isopropylmalate dehydratase, small s	---	AT2G43090	1.13	0.17	1.57	0.162777	0.363733	-5.67
259238_at	putative eukaryotic translation initiation f	EIF3G1	AT3G11400	-1.13	-0.18	-1.57	0.162797	0.363733	-5.67
259030_at	putative alpha-hemolysin similar to alph	---	AT3G09310	-1.10	-0.14	-1.57	0.162811	0.363733	-5.67
265435_s_a	putative major intrinsic (channel) protein	---	AT1G31885 /	1.17	0.23	1.57	0.162836	0.363753	-5.67
245405_at	hypothetical protein	---	AT4G17150	-1.11	-0.15	-1.57	0.162889	0.363836	-5.67
263529_at	ADP-ribosylation factor 3	ARF3	AT2G24765	-1.12	-0.16	-1.57	0.16291	0.363849	-5.67
267086_at	putative salt-inducible protein	---	AT2G32630	-1.17	-0.22	-1.57	0.162946	0.363892	-5.67
264321_at	unknown protein Contains similarity to g	---	AT1G04200	1.19	0.25	1.57	0.163039	0.364066	-5.67
263105_at	putative N-acetylglucosaminyltransferas	---	AT2G05320	-1.11	-0.16	-1.56	0.163329	0.364546	-5.67
263384_at	hypothetical protein predicted by gensca	---	AT2G40130	-1.15	-0.20	-1.56	0.163351	0.364546	-5.67
257177_at	cyanate lyase (CYN) identical to cyanas	CYN	AT3G23490	-1.20	-0.27	-1.56	0.16329	0.364546	-5.67

262779_at	putative cytochrome P450 monooxygen	---	AT1G13070	1.10	0.14	1.56	0.163346	0.364546	-5.67
261042_at	GTP-binding protein, putative similar to	ATRABA3	AT1G01200	1.16	0.21	1.56	0.163346	0.364546	-5.67
254003_at	hypothetical protein	---	AT4G26290	1.14	0.19	1.56	0.163318	0.364546	-5.67
253586_s_a	putative protein hypothetical protein T2	---	AT4G30710 /	-1.23	-0.30	-1.56	0.163656	0.365170	-5.67
247807_at	similar to unknown protein (gb|AAB630	OFP3	AT5G58360	-1.15	-0.20	-1.56	0.163662	0.365170	-5.67
252235_at	60S RIBOSOMAL PROTEIN - like 60S	---	AT3G49910	-1.27	-0.35	-1.56	0.163726	0.365206	-5.67
262688_at	PPR-repeat protein contains multiple PF	---	AT1G62680	-1.12	-0.16	-1.56	0.163719	0.365206	-5.67
256560_s_a	vetispiradiene synthase, putative, 5' par	---	AT3G31415 /	-1.12	-0.17	-1.56	0.163704	0.365206	-5.67
245974_at	putative protein	---	---	1.22	0.29	1.56	0.163763	0.365253	-5.67
246438_at	putative protein non-phototropic hypoco	---	AT5G17580	-1.11	-0.14	-1.56	0.163795	0.365288	-5.67
247672_at	senescence-associated protein - like se	TET4	AT5G60220	-1.10	-0.14	-1.56	0.16385	0.365376	-5.67
254537_at	putative protein chitinase / lysozyme PZ	---	AT4G19730	1.14	0.19	1.56	0.163879	0.365403	-5.67
264804_at	putative receptor kinase, CLV1 similar t	---	AT1G08590	1.16	0.22	1.56	0.163904	0.365425	-5.67
247506_at	Mei2-like protein Mei2-like protein, Arab	AML1	AT5G61960	1.11	0.15	1.56	0.163941	0.365470	-5.67
266234_at	SKP1 interacting partner 3 (SKIP3), put	SKIP3	AT2G02350	1.15	0.20	1.56	0.164043	0.365661	-5.67
245103_at	putative Ta11-like non-LTR retroelemen	---	AT2G41590	1.11	0.16	1.56	0.164127	0.365813	-5.67
265750_x_a	putative Athila retroelement ORF1 prote	---	---	1.21	0.27	1.56	0.164177	0.365890	-5.67
246593_at	putative protein predicted protein, Arabi	---	AT5G14790	1.19	0.26	1.56	0.164256	0.365937	-5.67
264918_at	interferon-induced GTP-binding protein	---	AT1G60530	1.13	0.17	1.56	0.164254	0.365937	-5.67
263879_at	hypothetical protein predicted by genefi	---	AT2G22030	-1.11	-0.16	-1.56	0.164225	0.365937	-5.67
262421_at	hypothetical protein predicted by genem	---	AT1G50290	-1.20	-0.26	-1.56	0.164263	0.365937	-5.67
246236_at	hypothetical protein	---	AT4G36470	1.16	0.21	1.56	0.164305	0.365996	-5.67
264520_at	putative amino acid permease GC splic	AAP8	AT1G10010	1.22	0.29	1.56	0.164321	0.365996	-5.67
250574_at	putative protein putative transcription fa	---	AT5G08230	-1.12	-0.16	-1.56	0.164471	0.366259	-5.68
252172_at	putative protein predicted proteins, Arab	---	AT3G50640	1.13	0.18	1.56	0.16446	0.366259	-5.68
252588_at	putative protein potential transcriptional	---	AT3G45630	-1.12	-0.16	-1.56	0.164567	0.366436	-5.68
259831_at	hypothetical protein predicted by genem	ZFHD1	AT1G69600	1.12	0.17	1.56	0.164695	0.366686	-5.68
249209_at	major surface glycoprotein-like ; suppor	---	AT5G42620	-1.14	-0.19	-1.56	0.164718	0.366701	-5.68
256122_at	hypothetical protein predicted by gensca	---	AT1G18180	1.14	0.19	1.56	0.164744	0.366723	-5.68
246244_at	receptor kinase-like protein	---	AT4G37250	-1.12	-0.17	-1.56	0.164841	0.366840	-5.68
254440_at	putative protein desiccation-related pro	---	AT4G21020	1.12	0.16	1.56	0.16482	0.366840	-5.68
244925_at	NADH dehydrogenase subunit 7	---	---	-1.16	-0.22	-1.56	0.164845	0.366840	-5.68
264227_at	hypothetical protein contains similarity to	ATREV3	AT1G67500	1.13	0.18	1.56	0.164863	0.366844	-5.68
255464_s_a	putative protein similar to T4I9.17	AT7SL-1	AT4G02970 /	1.12	0.16	1.56	0.164925	0.366947	-5.68
266588_at	putative proline-rich protein ; supported	AGP9	AT2G14890	1.93	0.95	1.56	0.164946	0.366957	-5.68

264979_s_a	disease resistance protein, putative sim	---	AT1G27170 /	1.16	0.22	1.56	0.165001	0.367045	-5.68
252170_at	hypothetical protein ; supported by cDN	HR4	AT3G26560 /	1.17	0.22	1.56	0.165031	0.367074	-5.68
254088_at	putative protein snurportin1 m3G-cap-s	---	AT4G24880	-1.19	-0.25	-1.56	0.165065	0.367094	-5.68
267271_at	hypothetical protein predicted by gensca	ATHB21	AT2G02540	1.13	0.17	1.56	0.165071	0.367094	-5.68
266218_s_a	putative cytochrome P450	CYP710A4	AT2G28850 /	1.13	0.17	1.56	0.165089	0.367096	-5.68
249125_at	1-aminocyclopropane-1-carboxylate oxi	---	AT5G43450	-1.22	-0.29	-1.56	0.165153	0.367167	-5.68
263634_at	putative retroelement gag/pol polyprotei	---	---	1.13	0.18	1.56	0.165137	0.367167	-5.68
254389_s_a	putative protein various predicted protei	---	AT4G21903 /	-1.36	-0.44	-1.56	0.165211	0.367261	-5.68
258074_at	unknown protein	---	AT3G25890	-1.40	-0.49	-1.56	0.165309	0.367372	-5.68
254475_at	putative snRNP protein small nuclear ri	smB	AT4G20440	-1.25	-0.32	-1.56	0.165297	0.367372	-5.68
245764_s_a	hypothetical protein contains similarity t	ATCSA-1	AT1G19750 /	-1.12	-0.16	-1.56	0.165306	0.367372	-5.68
251679_at	putative protein strictosidine synthase (E	---	AT3G57030	-1.27	-0.34	-1.56	0.16538	0.367492	-5.68
247565_at	putative protein Atu, Drosophila melanc	VIP4	AT5G61150	-1.13	-0.17	-1.56	0.165444	0.367571	-5.68
249474_s_a	germin-like protein (GLP2a) copy2 ; sup	GER2	AT5G39130 /	-1.16	-0.21	-1.56	0.165447	0.367571	-5.68
253403_at	putative serine/threonine protein kinase	AtAUR1	AT4G32830	1.16	0.21	1.56	0.165529	0.367681	-5.68
252555_at	putative protein alpha-xylosidase, Arabi	---	AT3G45940	1.10	0.14	1.56	0.165517	0.367681	-5.68
260241_at	putative cytochrome P450 similar to cyt	CYP86A7	AT1G63710	1.19	0.25	1.56	0.165595	0.367791	-5.68
255988_at	putative protein	---	---	1.13	0.17	1.55	0.165637	0.367804	-5.68
246744_at	putative protein predicted protein, Arabi	---	AT5G27760	1.50	0.58	1.55	0.165649	0.367804	-5.68
245550_at	cytochrome P450 like protein	CYP705A1	AT4G15330	-1.13	-0.18	-1.55	0.165619	0.367804	-5.68
254253_at	serine/threonine kinase - like protein se	---	AT4G23320	1.46	0.55	1.55	0.165677	0.367830	-5.68
249141_at	putative protein similar to unknown prote	---	AT5G43200	-1.11	-0.16	-1.55	0.165734	0.367920	-5.68
256541_at	ligand-gated ion channel, putative conta	GLR3.3	AT1G42540	-1.18	-0.24	-1.55	0.165754	0.367930	-5.68
250188_at	putative protein COP9 complex subunit	COP13	AT5G14250	-1.13	-0.17	-1.55	0.165795	0.367950	-5.68
267368_at	citrate synthase similar to GB:X17528,	ATCS	AT2G44350	1.15	0.20	1.55	0.165788	0.367950	-5.68
253481_at	aspartate aminotransferase ;supported	ASP5	AT4G31990	-1.14	-0.18	-1.55	0.165854	0.367989	-5.68
253325_at	Expressed protein ; supported by full-ler	---	AT4G33925	1.28	0.35	1.55	0.165845	0.367989	-5.68
250362_at	1-D-deoxyxylulose 5-phosphate syntha	DXPS3	AT5G11380	-1.12	-0.16	-1.55	0.165861	0.367989	-5.68
247437_at	AtHVA22b-like protein ; supported by c	HVA22B	AT5G62490	1.16	0.22	1.55	0.165985	0.368224	-5.68
263215_at	putative reticuline oxidase-like protein s	---	AT1G30710	1.14	0.20	1.55	0.165999	0.368224	-5.68
264108_at	hypothetical protein predicted by gensca	CALS5	AT2G13680	-1.12	-0.16	-1.55	0.1662	0.368597	-5.69
266941_at	peroxidase (ATP22a) identical to GB:Y0	---	AT2G18980	1.17	0.22	1.55	0.166197	0.368597	-5.69
258286_at	kinesin-like protein similar to kinesin hea	---	AT3G16060	-1.15	-0.20	-1.55	0.166325	0.368838	-5.69
258144_at	hypothetical protein	---	AT3G18180	-1.11	-0.15	-1.55	0.166371	0.368847	-5.69
251902_at	uncoupling protein (ucp/PUMP) ; suppo	PUMP1	AT3G54110	1.34	0.42	1.55	0.166378	0.368847	-5.69

247782_at	putative protein predicted RNA binding	---	AT5G58790	-1.11	-0.15	-1.55	0.16637	0.368847	-5.69
255573_at	hypothetical protein	---	AT4G01400	1.10	0.14	1.55	0.166617	0.369342	-5.69
247456_at	iron-regulated transporter - like protein	AtZIP12	AT5G62160	1.13	0.17	1.55	0.166675	0.369362	-5.69
245473_at	hypothetical protein	---	AT4G16050	-1.11	-0.15	-1.55	0.166664	0.369362	-5.69
245843_at	unknown protein	---	AT1G26180	-1.15	-0.20	-1.55	0.166651	0.369362	-5.69
247774_at	putative protein fruit ripening expressed	---	AT5G58660	1.12	0.16	1.55	0.166838	0.369653	-5.69
260139_at	Myb-related transcription factor, putativ	MYB114	AT1G66380	1.12	0.16	1.55	0.166824	0.369653	-5.69
262431_at	trypsin inhibitor 2, putative similar to try	---	AT1G47540	1.12	0.17	1.55	0.166889	0.369730	-5.69
251873_at	putative protein KIAA0122 gene , Homo	---	AT3G54230	-1.10	-0.14	-1.55	0.166954	0.369801	-5.69
246936_at	putative protein hypothetical protein Sb	---	AT5G25360	-1.13	-0.17	-1.55	0.166951	0.369801	-5.69
245674_at	chitinase, putative similar to chitinase G	---	AT1G56680	1.12	0.16	1.55	0.167021	0.369842	-5.69
255961_at	UDP-glucose glucosyltransferase, puta	AtUGT85A	AT1G22340	1.24	0.31	1.55	0.167014	0.369842	-5.69
256827_at	hypothetical protein contains similarity to	---	AT3G18570	1.11	0.15	1.55	0.16699	0.369842	-5.69
259778_at	hypothetical protein predicted by genem	---	AT1G29610	-1.12	-0.16	-1.55	0.167081	0.369939	-5.69
265505_at	putative RING zinc finger protein	---	AT2G15530	-1.12	-0.16	-1.55	0.167163	0.370085	-5.69
258489_at	14-3-3 protein GF14nu (grf7) identical to	GRF7	AT3G02520	1.11	0.15	1.55	0.167216	0.370144	-5.69
256077_at	hypothetical protein contains similarity to	---	AT1G18090	-1.16	-0.22	-1.55	0.167222	0.370144	-5.69
262461_at	myosin, putative similar to myosin GB:(	VIIIA	AT1G50360	1.25	0.32	1.55	0.167253	0.370177	-5.69
258937_at	putative ribosomal protein S28 similar to	---	AT3G10090	-1.22	-0.28	-1.55	0.167316	0.370280	-5.69
263401_at	hypothetical protein similar to hypothetic	---	AT2G04070	1.22	0.29	1.55	0.167341	0.370299	-5.69
255990_at	glycyl tRNA synthetase, putative similar	---	AT1G29870	1.14	0.18	1.55	0.167373	0.370335	-5.69
250440_at	40S ribsomal protein S6 ; supported by	EMB3010	AT5G10360	-1.19	-0.25	-1.55	0.167427	0.370419	-5.69
252256_at	PRE-MRNA SPLICING FACTOR SF2-I	SRp34a	AT3G49430	-1.17	-0.22	-1.55	0.167556	0.370668	-5.69
267325_at	unknown protein predicted by genscan a	---	AT2G19360	1.14	0.19	1.55	0.167576	0.370677	-5.69
253890_s_a	putative protein contains similarity to sto	---	AT4G27585 /	1.34	0.42	1.55	0.167593	0.370677	-5.69
255186_at	putative transposon protein similar to Ar	---	---	1.21	0.28	1.55	0.167622	0.370705	-5.69
251376_at	scarecrow - like protein scarecrow-like (	---	AT3G60630	-1.22	-0.29	-1.55	0.167642	0.370714	-5.69
257931_at	hypothetical protein predicted by genem	---	AT3G17030	-1.13	-0.17	-1.55	0.167659	0.370715	-5.69
253571_at	putative calmodulin-binding protein calr	---	AT4G31000	1.49	0.57	1.55	0.167736	0.370815	-5.69
262375_at	unknown protein ; supported by cDNA: g	SUVH3	AT1G73100	-1.16	-0.21	-1.55	0.167728	0.370815	-5.69
252802_at	putative protein	---	---	-1.10	-0.13	-1.55	0.167805	0.370930	-5.69
247547_at	putative protein	---	AT5G61360	1.22	0.28	1.55	0.167824	0.370937	-5.69
253823_at	putative protein ;supported by full-lengt	---	AT4G28030	-1.11	-0.14	-1.55	0.167851	0.370961	-5.69
251595_at	putative protein galactose oxidase prec	---	AT3G57620	1.14	0.18	1.55	0.167889	0.371008	-5.69
265115_at	rho GDP-dissociation inhibitor, putative	---	AT1G62450	-1.13	-0.18	-1.55	0.16794	0.371085	-5.69

247159_at	1-aminocyclopropane-1-carboxylate syn	ACS5	AT5G65800	-1.11	-0.15	-1.54	0.168038	0.371266	-5.70
261012_at	CLE9, putative CLAVATA3/ESR-Relate	CLE9	AT1G26600	-1.10	-0.14	-1.54	0.168099	0.371292	-5.70
262609_at	unknown protein ;supported by full-lengt	---	AT1G13930	-1.15	-0.20	-1.54	0.168082	0.371292	-5.70
259901_at	disease resistance protein, putative sim	AtRLP14	AT1G74180	-1.18	-0.23	-1.54	0.168086	0.371292	-5.70
250112_at	low density lipoprotein B-like protein	---	AT5G16300	1.12	0.16	1.54	0.168209	0.371463	-5.70
250435_at	putative protein various predicted prote	RING1	AT5G10380	1.30	0.38	1.54	0.168195	0.371463	-5.70
258778_s_a	hypothetical protein predicted by genefi	---	AT3G11860 /	-1.15	-0.21	-1.54	0.168366	0.371775	-5.70
250891_at	fatty acid elongase - like protein KCS1	KCS19	AT5G04530	1.16	0.22	1.54	0.168515	0.372066	-5.70
257631_at	cytochrome P450, putative similar to cy	CYP71B17	AT3G26160	1.20	0.26	1.54	0.168544	0.372095	-5.70
245058_at	hypothetical protein predicted by genefi	---	AT2G39790	1.12	0.17	1.54	0.168587	0.372154	-5.70
254984_s_a	putative protein Homo sapiens deubiqu	UBP10	AT4G10570 /	1.10	0.13	1.54	0.168686	0.372305	-5.70
252230_at	putative protein various predicted prote	---	AT3G49810	1.50	0.58	1.54	0.168688	0.372305	-5.70
264996_at	nuclear matrix constituent protein 1, put	LINC1	AT1G67230	1.16	0.21	1.54	0.168766	0.372332	-5.70
253868_at	proton pump interactor non-consensus (	PPI1	AT4G27500	1.15	0.20	1.54	0.168759	0.372332	-5.70
267255_at	putative Ca2+-ATPase	---	AT2G22950	1.17	0.23	1.54	0.16872	0.372332	-5.70
250909_at	S-receptor kinase - like protein S-recep	---	AT5G03700	1.55	0.63	1.54	0.168756	0.372332	-5.70
251575_at	putative protein basic leucine zipper tra	BZIP61	AT3G58120	1.41	0.50	1.54	0.168837	0.372439	-5.70
253762_at	putative protein conserved hypothetical	---	AT4G28830	-1.13	-0.18	-1.54	0.168846	0.372439	-5.70
261558_at	unknown protein	---	AT1G01770	1.22	0.29	1.54	0.168939	0.372534	-5.70
248029_at	beta-amylase ; supported by cDNA: gi_	BAM4	AT5G55700	1.14	0.19	1.54	0.168928	0.372534	-5.70
245074_at	putative protein kinase contains a protei	---	AT2G23200	1.53	0.62	1.54	0.16891	0.372534	-5.70
260950_s_a	delta 9 desaturase, putative similar to d	---	AT1G06090 /	1.15	0.21	1.54	0.168979	0.372537	-5.70
255641_at	contains region of similarity to beta trans	---	AT4G00800	1.13	0.18	1.54	0.168979	0.372537	-5.70
258951_at	putative phosphatidylinositolglycan class	---	AT3G01380	-1.14	-0.19	-1.54	0.168989	0.372537	-5.70
257567_at	hypothetical protein predicted by gensca	---	AT3G23930	-1.10	-0.13	-1.54	0.169017	0.372563	-5.70
259350_at	putative serine/threonine protein kinase	RBK2	AT3G05140	1.15	0.20	1.54	0.169039	0.372574	-5.70
248731_at	phosphoribosylanthranilate transferase-	---	AT5G48060	1.15	0.20	1.54	0.169067	0.372600	-5.70
245536_at	hypothetical protein	SDG2	AT4G15180	1.12	0.17	1.54	0.169084	0.372602	-5.70
262594_at	putative 60s ribosomal protein L37 almo	---	AT1G15250	-1.40	-0.49	-1.54	0.16912	0.372645	-5.70
260801_at	hypothetical protein predicted by genem	---	AT1G78430	1.10	0.14	1.54	0.169136	0.372645	-5.70
262338_at	Expressed protein ; supported by full-ler	---	AT1G64185	-1.19	-0.25	-1.54	0.169185	0.372716	-5.70
250404_at	CCR4-ASSOCIATED FACTOR -like pr	---	AT5G10960	-1.11	-0.15	-1.54	0.169225	0.372753	-5.70
250299_at	putative esterase - like protein cinI prot	---	AT5G11910	-1.13	-0.18	-1.54	0.169234	0.372753	-5.70
253143_at	putative protein	---	AT4G35530	-1.17	-0.22	-1.54	0.169255	0.372763	-5.70
253074_at	putative disease resistance protein TM	---	AT4G36140	-1.10	-0.14	-1.54	0.169276	0.372773	-5.70

264295_at	hypothetical protein predicted by genem	---	AT1G78740	1.10	0.14	1.54	0.169326	0.372807	-5.70
259252_at	hypothetical protein similar to hypotheti	IBM1	AT3G07610	-1.12	-0.16	-1.54	0.16934	0.372807	-5.70
246770_at	putative protein DNA-binding protein - T	---	AT5G27460	-1.17	-0.23	-1.54	0.169318	0.372807	-5.70
249954_at	putative protein ;supported by full-lengt	---	AT5G18920	-1.10	-0.13	-1.54	0.16936	0.372815	-5.70
259867_at	hypothetical protein predicted by genefir	---	AT1G76740	1.10	0.14	1.54	0.169409	0.372886	-5.70
263292_at	putative Ta11-like non-LTR retroelemen	---	---	1.13	0.18	1.54	0.169453	0.372947	-5.70
263717_at	malate oxidoreductase (malic enzyme)	---	AT2G13560	1.10	0.14	1.54	0.16947	0.372949	-5.70
247485_at	putative protein ARR1, Arabidopsis thal	ARR23	AT5G62120	1.10	0.14	1.54	0.169492	0.372961	-5.70
264921_at	RNA binding protein, putative similar to	---	AT1G60650	-1.14	-0.19	-1.54	0.169547	0.373046	-5.70
250895_at	RIBOSOMAL PROTEIN S28- like ribos	---	AT5G03850	-1.22	-0.28	-1.54	0.169568	0.373057	-5.70
249838_at	unknown protein ;supported by full-leng	---	AT5G23460	-1.18	-0.24	-1.54	0.169614	0.373058	-5.70
266306_at	hypothetical protein predicted by grail	---	AT2G26970	-1.14	-0.19	-1.54	0.169618	0.373058	-5.70
257250_at	transfactor, putative similar to GB:BAA7	---	AT3G24120	-1.14	-0.19	-1.54	0.169616	0.373058	-5.70
248943_s_a	putative protein similar to unknown prote	---	AT5G45440 /	1.32	0.40	1.54	0.169664	0.373099	-5.70
245929_at	alcohol dehydrogenase - like protein alc	---	AT5G24760	1.46	0.54	1.54	0.169702	0.373099	-5.70
261532_at	amino acid permease, putative similar t	---	AT1G71680	1.12	0.16	1.54	0.169691	0.373099	-5.70
252453_at	putative RNA-binding protein various pu	---	AT3G47120	-1.11	-0.15	-1.54	0.169684	0.373099	-5.70
249389_at	disease resistence like - protein downy	---	AT5G40100	1.17	0.22	1.54	0.169777	0.373228	-5.70
265331_at	similar to gibberellin-regulated proteins	---	AT2G18420	1.13	0.17	1.54	0.16993	0.373483	-5.71
260470_at	hypothetical protein predicted by genefir	---	AT1G11120	-1.16	-0.22	-1.54	0.169926	0.373483	-5.71
257486_at	unknown protein	---	AT1G63590	1.11	0.15	1.54	0.169942	0.373483	-5.71
246009_at	Expressed protein ; supported by cDNA	ATSTE14B	AT5G08335	1.18	0.24	1.54	0.17004	0.373661	-5.71
247814_at	polyneuridine aldehyde esterase-like; al	MES18	AT5G58310	-1.69	-0.76	-1.54	0.170179	0.373809	-5.71
263367_at	putative retroelement pol polyprotein	---	---	1.15	0.20	1.54	0.170139	0.373809	-5.71
266660_at	hypothetical protein predicted by gensca	---	AT2G25920	-1.22	-0.29	-1.54	0.170189	0.373809	-5.71
251359_at	putative protein several hypothetical pro	---	AT3G61170	-1.12	-0.16	-1.54	0.17016	0.373809	-5.71
251588_at	putative protein several putative proteins	---	AT3G58090	-1.16	-0.21	-1.54	0.170153	0.373809	-5.71
263772_at	Expressed protein ; supported by full-ler	ELF4-L3	AT2G06255	-1.25	-0.32	-1.54	0.170205	0.373809	-5.71
261607_at	unknown protein similar to putative este	AtCXE5	AT1G49660	-1.38	-0.46	-1.54	0.170324	0.374033	-5.71
264460_at	hypothetical protein similar to transcripti	ATNFXL1	AT1G10170	1.17	0.22	1.53	0.170377	0.374088	-5.71
251050_at	putative protein	---	AT5G02440	1.15	0.20	1.53	0.170381	0.374088	-5.71
255687_at	hypothetical protein	KEA2	AT4G00630	-1.28	-0.35	-1.53	0.170437	0.374174	-5.71
251002_at	putative protein predicted proteins, Aral	---	AT5G02680	1.11	0.15	1.53	0.170468	0.374207	-5.71
245957_at	putative protein predicted proteins - Aral	---	AT5G19590	-1.11	-0.15	-1.53	0.170518	0.374262	-5.71
255468_at	putative WD-repeat protein similar to L.	---	AT4G03020	-1.12	-0.17	-1.53	0.170526	0.374262	-5.71

256144_at	guanine nucleotide-binding protein, put	RACK1B_	AT1G48630	-1.42	-0.51	-1.53	0.170567	0.374315	-5.71
255516_at	hypothetical protein similar to extensin-	---	AT4G02270	1.20	0.26	1.53	0.170587	0.374322	-5.71
259143_at	calmodulin-like protein similar to calmo	---	AT3G10190	1.18	0.24	1.53	0.170652	0.374430	-5.71
264859_at	glucose-6-phosphate 1-dehydrogenase	G6PD3	AT1G24280	-1.47	-0.56	-1.53	0.170699	0.374497	-5.71
264816_at	hypothetical protein similar to membran	---	AT1G03560	-1.35	-0.43	-1.53	0.170756	0.374586	-5.71
255927_at	transcriptional activator CBF1, putative	---	AT1G12630	1.24	0.31	1.53	0.170782	0.374606	-5.71
248651_at	unknown protein	---	AT5G49260	1.11	0.15	1.53	0.170851	0.374685	-5.71
261287_at	hypothetical protein predicted by genem	---	AT1G37020	1.10	0.13	1.53	0.170842	0.374685	-5.71
260423_at	unknown protein	ATEXO70I	AT1G72470	1.33	0.41	1.53	0.170899	0.374720	-5.71
255416_at	hypothetical protein	---	AT4G03170	-1.11	-0.14	-1.53	0.170893	0.374720	-5.71
252583_at	putative protein several hypothetical pro	---	AT3G45540	1.13	0.18	1.53	0.170957	0.374799	-5.71
248817_at	putative protein strong similarity to unkn	---	AT5G47020	1.15	0.20	1.53	0.170968	0.374799	-5.71
246174_s_a	putative protein hypothetical protein T2	---	AT5G28340 /	-1.11	-0.15	-1.53	0.171116	0.375081	-5.71
247352_at	serine/threonine-protein kinase ;suppor	SNRK2.5	AT5G63650	1.37	0.46	1.53	0.17113	0.375081	-5.71
259047_at	unknown protein	DegP7	AT3G03380	-1.10	-0.14	-1.53	0.171416	0.375672	-5.71
252601_s_a	40S ribsomomal protein 40S ribsomom	---	AT3G45030 /	-1.26	-0.33	-1.53	0.171519	0.375797	-5.71
247431_at	putative protein similar to unknown prot	SRO5	AT5G62520	1.32	0.40	1.53	0.171522	0.375797	-5.71
250543_at	DR1-like protein TATA-binding protein-	NF-YB12	AT5G08190	-1.13	-0.18	-1.53	0.171517	0.375797	-5.71
262071_at	unknown protein ;supported by full-leng	CF9	AT1G59510	-1.15	-0.20	-1.53	0.171552	0.375812	-5.71
260313_at	putative disease resistance protein simil	---	AT1G63870	1.17	0.22	1.53	0.171562	0.375812	-5.71
259470_at	unknown protein	---	AT1G19110	-1.10	-0.14	-1.53	0.171635	0.375936	-5.71
253235_at	putative protein hypothetical protein, Sy	HDR	AT4G34350	1.27	0.35	1.53	0.171737	0.376123	-5.71
263688_at	unknown protein Location of EST 228A	---	AT1G26920	-1.50	-0.58	-1.53	0.171794	0.376211	-5.72
259708_at	lysophospholipase isolog, putative simi	---	AT1G77420	-1.17	-0.23	-1.53	0.172004	0.376276	-5.72
248421_at	unknown protein ;supported by full-leng	---	AT5G51510	-1.13	-0.18	-1.53	0.171846	0.376276	-5.72
266944_at	unknown protein predicted by genefinde	---	AT2G18870 /	1.14	0.19	1.53	0.171992	0.376276	-5.72
255356_x_a	putative transposon protein	---	---	1.14	0.18	1.53	0.171995	0.376276	-5.72
263390_at	hypothetical protein similar to Ta1-1 rev	---	---	1.11	0.15	1.53	0.172019	0.376276	-5.72
248437_at	putative protein similar to unknown prot	EMF2	AT5G51230	1.18	0.24	1.53	0.171921	0.376276	-5.72
249024_at	putative protein strong similarity to unkn	---	AT5G44860	1.12	0.17	1.53	0.171962	0.376276	-5.72
255530_at	hypothetical protein	---	AT4G02140	1.13	0.17	1.53	0.171958	0.376276	-5.72
246044_at	calcium-dependent protein kinase ; sup	CDPK19	AT5G19450	-1.17	-0.23	-1.53	0.171859	0.376276	-5.72
263999_at	hypothetical protein predicted by genefi	---	AT2G22370	-1.14	-0.19	-1.53	0.172021	0.376276	-5.72
262520_at	putative polygalacturonase After first 29	---	AT1G17150	1.16	0.21	1.53	0.171941	0.376276	-5.72
260833_at	lipase, putative similar to lipase GB:AA	---	AT1G06800	1.34	0.42	1.53	0.171909	0.376276	-5.72

261135_at	defensin AMP1, putative similar to PIR:	PDF1.4	AT1G19610	1.75	0.80	1.53	0.172101	0.376389	-5.72
266276_at	putative tropinone reductase	TRI	AT2G29330	-1.11	-0.15	-1.53	0.172106	0.376389	-5.72
250827_at	cellulose synthase catalytic subunit (gb|	CEV1	AT5G05170	-1.19	-0.25	-1.53	0.172144	0.376436	-5.72
267078_at	unknown protein ;supported by full-leng	---	AT2G40960	-1.13	-0.18	-1.53	0.172236	0.376565	-5.72
247218_at	asparagine synthetase (gb|AAC72837.1	ASN2	AT5G65010	-1.60	-0.68	-1.53	0.172235	0.376565	-5.72
249829_at	c-myc binding protein MM-1-like protein	PDF5	AT5G23290	-1.13	-0.17	-1.53	0.172307	0.376577	-5.72
253002_at	phosphoinositide-specific phospholipase	ATPLC1	AT4G38530	-1.15	-0.20	-1.53	0.172307	0.376577	-5.72
265796_at	Expressed protein ; supported by full-ler	---	AT2G35730	1.94	0.96	1.53	0.172286	0.376577	-5.72
261947_at	ubiquitin, putative similar to poly-ubiquit	---	AT1G64470	1.16	0.22	1.53	0.172265	0.376577	-5.72
247316_at	ankyrin-like protein	---	AT5G64030	-1.12	-0.17	-1.53	0.172336	0.376603	-5.72
250816_at	coatomer delta subunit (delta-coat prote	---	AT5G05010	1.17	0.23	1.53	0.172401	0.376673	-5.72
249799_at	serine palmitoyltransferase ; supported	LCB2	AT5G23670	-1.10	-0.14	-1.53	0.172397	0.376673	-5.72
260401_at	unknown protein similar to hypothetical	---	AT1G69840	1.16	0.21	1.53	0.17245	0.376708	-5.72
267160_at	putative WD-40 repeat protein	---	AT2G37670	1.11	0.15	1.53	0.172439	0.376708	-5.72
AFFX-r2-At-	Arabidopsis thaliana /REF=M64116 /DE	---	---	1.36	0.45	1.53	0.172511	0.376804	-5.72
260129_at	hypothetical protein similar to vanilloid re	---	AT1G36380	-1.11	-0.16	-1.53	0.172604	0.376968	-5.72
245766_at	En/Spm-like transposon protein, putativ	---	---	1.12	0.17	1.53	0.172619	0.376968	-5.72
249388_at	putative protein downy mildew resistan	---	AT5G40090	-1.14	-0.19	-1.53	0.172642	0.376982	-5.72
249334_at	putative protein strong similarity to unkn	YSL4	AT5G41000	1.20	0.26	1.52	0.172858	0.377408	-5.72
256081_at	hypothetical protein contains Pfam profil	WOX14	AT1G20700	1.14	0.19	1.52	0.172886	0.377408	-5.72
252103_at	putative protein various predicted prote	---	AT3G51410	-1.11	-0.15	-1.52	0.172886	0.377408	-5.72
266906_at	Expressed protein ; supported by full-ler	---	AT2G34585	1.19	0.25	1.52	0.172998	0.377615	-5.72
253600_at	SERINE CARBOXYPEPTIDASE II - like	scpl29	AT4G30810	-1.13	-0.17	-1.52	0.173017	0.377620	-5.72
263519_at	40S ribosomal protein S25 ; supported	---	AT2G21580	-1.27	-0.34	-1.52	0.173071	0.377649	-5.72
249858_at	myb-related transcription factor-like	MYB37	AT5G23000	1.18	0.23	1.52	0.17308	0.377649	-5.72
256990_at	hypothetical protein predicted by genem	---	AT3G28590	1.19	0.25	1.52	0.173066	0.377649	-5.72
266441_at	hypothetical protein predicted by gensca	---	AT2G43250	-1.13	-0.17	-1.52	0.173133	0.377729	-5.72
255346_at	hypothetical protein	---	---	1.09	0.13	1.52	0.173165	0.377764	-5.72
254256_at	serine/threonine kinase -like protein ser	CRK10	AT4G23180	1.22	0.28	1.52	0.173265	0.377945	-5.72
248761_at	Expressed protein ; supported by full-ler	---	AT5G47635	1.23	0.30	1.52	0.173308	0.378004	-5.72
249350_at	MYB -like protein MYB22, Arabidopsis t	MYB115	AT5G40360	-1.12	-0.17	-1.52	0.173508	0.378403	-5.72
252123_at	flavanone 3-hydroxylase (FH3) ;suppor	F3H	AT3G51240	1.12	0.16	1.52	0.173567	0.378494	-5.72
266880_at	hypothetical protein predicted by genefir	---	AT2G44770	-1.15	-0.20	-1.52	0.173686	0.378646	-5.73
256056_at	hypothetical protein contains similarity to	---	AT1G07190	1.11	0.15	1.52	0.173656	0.378646	-5.73
251364_at	anthranilate phosphoribosyltransferase-	---	AT3G61300	1.14	0.18	1.52	0.173683	0.378646	-5.73

260945_at	hypothetical protein predicted by genem	---	AT1G05950	1.15	0.20	1.52	0.173763	0.378778	-5.73
264373_at	putative vesicle transport protein Contai	SEC22	AT1G11890	-1.18	-0.23	-1.52	0.173786	0.378788	-5.73
258153_at	Expressed protein ; supported by full-ler	MOS4	AT3G18165	-1.16	-0.21	-1.52	0.173801	0.378788	-5.73
254893_at	putative phospholipase D-gamma phos	PLDGAMM	AT4G11830	-1.23	-0.30	-1.52	0.173886	0.378938	-5.73
265732_at	predicted by genscan and genefinder ;s	---	AT2G01300	2.00	1.00	1.52	0.173979	0.379103	-5.73
257902_at	receptor kinase, putative similar to rece	---	AT3G28450	1.22	0.29	1.52	0.174004	0.379123	-5.73
245107_at	putative heat shock transcription factor	AT-HSFB3	AT2G41690	1.38	0.47	1.52	0.17406	0.379180	-5.73
245733_at	hypothetical protein predicted by genem	---	AT1G73380	-1.20	-0.27	-1.52	0.174064	0.379180	-5.73
267166_at	unknown protein	---	AT2G37720	1.09	0.13	1.52	0.174113	0.379198	-5.73
264509_at	unknown protein Location of EST gb|Z3	---	AT1G09520	-1.14	-0.19	-1.52	0.174101	0.379198	-5.73
258816_at	putative T-complex protein 1, theta sub	---	AT3G03960	-1.20	-0.26	-1.52	0.174122	0.379198	-5.73
265038_at	putative protein kinase highly similar to	---	AT1G03920	1.13	0.18	1.52	0.174167	0.379261	-5.73
256429_at	unknown protein	---	AT3G11040	1.17	0.22	1.52	0.174216	0.379331	-5.73
248896_at	putative protein contains similarity to WF	WRKY8	AT5G46350	1.54	0.63	1.52	0.174274	0.379384	-5.73
254012_at	putative ribosomal protein ribosomal pr	---	AT4G26230	-1.27	-0.34	-1.52	0.174259	0.379384	-5.73
248940_at	replication protein A1-like	---	AT5G45400	-1.14	-0.19	-1.52	0.174298	0.379400	-5.73
260717_at	serine/threonine phosphatase PP7, put	---	AT1G48120	-1.17	-0.23	-1.52	0.174364	0.379508	-5.73
248270_at	putative protein similar to unknown prote	ORG1	AT5G53450	-1.31	-0.39	-1.52	0.1744	0.379551	-5.73
263383_at	putative protein kinase contains a protei	---	AT2G40120	1.15	0.20	1.52	0.174469	0.379665	-5.73
259009_at	thioglucosidase 3D precursor identical t	PYK10	AT3G09260	1.22	0.29	1.52	0.174508	0.379677	-5.73
267642_at	unknown protein	---	AT2G32905 /	-1.10	-0.14	-1.52	0.174499	0.379677	-5.73
265892_at	hypothetical protein predicted by gensca	---	AT2G15020	-1.26	-0.33	-1.52	0.17455	0.379731	-5.73
261676_at	Expressed protein ; supported by full-ler	---	AT1G18480	1.16	0.22	1.52	0.17466	0.379899	-5.73
258057_at	unknown protein	AAR3	AT3G28970	-1.11	-0.15	-1.52	0.174651	0.379899	-5.73
250020_at	putative protein contains similarity to GA	---	AT5G18180	1.15	0.21	1.52	0.174732	0.380019	-5.73
263927_s_a	putative cinnamyl-alcohol dehydrogenas	CAD2	AT2G21730 /	-1.17	-0.22	-1.52	0.174822	0.380178	-5.73
248121_at	putative protein contains similarity to un	GAUT12	AT5G54690	1.20	0.26	1.52	0.17485	0.380203	-5.73
267476_at	putative pectate lyase	---	AT2G02720	1.12	0.16	1.52	0.174917	0.380313	-5.73
267037_at	hypothetical protein ; supported by cDN	---	AT2G38320	1.14	0.19	1.52	0.174986	0.380426	-5.73
248898_at	outward rectifying potassium channel K(	KCO2	AT5G46370	-1.15	-0.20	-1.52	0.17505	0.380515	-5.73
250528_at	putative protein strong similarity to unkn	---	AT5G08600	-1.10	-0.14	-1.52	0.17506	0.380515	-5.73
249651_at	auxin response factor 8 (ARF8) ; suppo	ARF8	AT5G37020	-1.25	-0.32	-1.52	0.175092	0.380548	-5.73
252907_at	putative gamma-glutamyltransferase ga	GGT2	AT4G39650	1.11	0.16	1.52	0.175144	0.380624	-5.73
265979_at	putative replication protein A1	---	---	-1.13	-0.18	-1.52	0.175168	0.380641	-5.73
257719_at	unknown protein	AtALMT9	AT3G18440	1.18	0.24	1.52	0.17523	0.380739	-5.73

253679_at	cytidine deaminase 6 (CDA6)	---	AT4G29610	1.34	0.42	1.51	0.175357	0.380979	-5.73
259951_at	unknown protein	---	AT1G71490	1.12	0.16	1.51	0.175414	0.381066	-5.73
260429_at	unknown protein ;supported by full-leng	JAZ6	AT1G72450	-1.34	-0.43	-1.51	0.175497	0.381211	-5.73
247022_at	unknown protein	---	AT5G67050	-1.11	-0.16	-1.51	0.175548	0.381284	-5.73
251795_at	putative protein MtN24, Medicago trunc	---	AT3G55390	1.20	0.27	1.51	0.175628	0.381420	-5.74
248874_at	putative protein strong similarity to unkn	---	AT5G46460	-1.20	-0.27	-1.51	0.175644	0.381420	-5.74
252337_at	CELL DIVISION CONTROL PROTEIN 2	CDC2	AT3G48750	-1.22	-0.28	-1.51	0.175679	0.381448	-5.74
266435_s_a	hypothetical protein predicted by gensca	---	AT2G07130 /	-1.13	-0.17	-1.51	0.17569	0.381448	-5.74
262108_at	unknown protein similar to unknown pro	---	AT1G02740	-1.15	-0.21	-1.51	0.17581	0.381672	-5.74
248175_at	histone H2A (gb|AAF64418.1) ; support	RAT5	AT5G54640	1.14	0.19	1.51	0.175849	0.381719	-5.74
259750_at	hypothetical protein predicted by gensc	---	AT1G71130	-1.21	-0.27	-1.51	0.175925	0.381742	-5.74
249269_at	cell cycle control crn (crooked neck) pro	---	AT5G41770	-1.17	-0.23	-1.51	0.175926	0.381742	-5.74
253693_at	Thioredoxin - like protein thioredoxin;Lili	ACHT2	AT4G29670	1.22	0.29	1.51	0.175883	0.381742	-5.74
258680_at	adenylate translocator identical to adeny	AAC1	AT3G08580	1.23	0.29	1.51	0.175924	0.381742	-5.74
253976_at	putative protein kinase protein kinase -/	D6PKL1	AT4G26610	1.10	0.14	1.51	0.176077	0.381772	-5.74
254650_at	hypothetical protein	---	---	1.11	0.15	1.51	0.176068	0.381772	-5.74
262246_at	leaf development protein Argonaute ider	AGO1	AT1G48410	-1.14	-0.19	-1.51	0.176108	0.381772	-5.74
244948_at	hypothetical protein	---	---	-1.11	-0.16	-1.51	0.17612	0.381772	-5.74
249775_at	squalene monooxygenase 1,2 (squalen	SQE6	AT5G24160	1.22	0.29	1.51	0.176085	0.381772	-5.74
249719_at	Expressed protein ; supported by full-ler	---	AT5G35735	1.43	0.52	1.51	0.176076	0.381772	-5.74
252771_at	receptor protein kinase -like protein rec	---	AT3G42880	1.13	0.18	1.51	0.176067	0.381772	-5.74
253437_at	putative protein mRNAs from Ricinus c	---	AT4G32460	1.40	0.48	1.51	0.175978	0.381772	-5.74
263724_at	putative Ta11-like non-LTR retroelemen	---	AT2G13510	1.12	0.16	1.51	0.176038	0.381772	-5.74
266816_at	unknown protein identical to GB:AAC31	---	AT2G44970	1.11	0.15	1.51	0.176124	0.381772	-5.74
266177_at	putative phloem-specific lectin	ATPP2-B3	AT2G02270	1.17	0.23	1.51	0.176085	0.381772	-5.74
260028_at	unknown protein ; supported by cDNA: g	---	AT1G29980	1.62	0.70	1.51	0.176174	0.381783	-5.74
264056_at	putative DOF zinc finger protein ;suppo	---	AT2G28510	1.19	0.25	1.51	0.176153	0.381783	-5.74
249896_at	unknown protein ; supported by cDNA:	---	AT5G22530	1.16	0.21	1.51	0.176179	0.381783	-5.74
246461_at	putative protein AAA family protein Bor	---	AT5G16930	-1.36	-0.45	-1.51	0.176286	0.381977	-5.74
247082_at	putative protein contains similarity to my	ATGRIP	AT5G66030	-1.14	-0.19	-1.51	0.17634	0.382059	-5.74
248924_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G45960	1.11	0.16	1.51	0.176448	0.382184	-5.74
250277_at	putative protein DRT100 protein precur	---	AT5G12940	1.89	0.92	1.51	0.176435	0.382184	-5.74
253689_at	hypothetical protein ;supported by full-le	---	AT4G29770	-1.12	-0.17	-1.51	0.176438	0.382184	-5.74
256311_at	auxin response factor 6 (ARF6) identica	ARF6	AT1G30330	-1.23	-0.30	-1.51	0.176515	0.382287	-5.74
251488_at	calmodulin-like protein calcium-binding	---	AT3G59440	1.10	0.13	1.51	0.176529	0.382287	-5.74

260232_at	unknown protein contains Pfam profile:	---	AT1G74640	1.24	0.31	1.51	0.176624	0.382455	-5.74
252253_at	Expressed protein ; supported by full-ler	---	AT3G49300	-1.10	-0.14	-1.51	0.17665	0.382477	-5.74
259239_at	putative 40S ribosomal protein s14 simil	---	AT3G11510	-1.37	-0.45	-1.51	0.176703	0.382554	-5.74
266927_at	aquaporin (plasma membrane intrinsic	PIP1B	AT2G45960	-1.16	-0.22	-1.51	0.176731	0.382578	-5.74
258574_at	hypothetical protein	---	AT3G04250	1.13	0.17	1.51	0.176756	0.382596	-5.74
264621_at	putative protein kinase contains a protei	---	AT2G17700	-1.14	-0.19	-1.51	0.176793	0.382605	-5.74
247172_at	anthocyanidin-3-glucoside rhamnosyltra	---	AT5G65550	1.12	0.16	1.51	0.176793	0.382605	-5.74
266775_at	putative SCARECROW gene regulator	---	AT2G29060	1.28	0.36	1.51	0.17695	0.382834	-5.74
251788_at	putative protein	---	AT3G55420	1.33	0.41	1.51	0.176934	0.382834	-5.74
251419_at	putative protein various predicted prote	---	AT3G60470	-1.12	-0.16	-1.51	0.176925	0.382834	-5.74
259211_at	unknown protein identical to GB:AAD56	---	AT3G09020	1.54	0.63	1.51	0.177016	0.382941	-5.74
249439_at	thaumatin-like protein thaumatin-like pr	---	AT5G40020	1.27	0.34	1.51	0.177043	0.382964	-5.74
266269_at	putative glutathione S-transferase ; sup	ATGSTU2	AT2G29480	1.41	0.50	1.51	0.177106	0.383027	-5.74
245233_at	putative protein similarity to low-temper	---	AT4G25580	1.14	0.19	1.51	0.1771	0.383027	-5.74
266487_at	hypothetical protein predicted by gensca	---	AT2G47660	1.10	0.13	1.51	0.177146	0.383078	-5.74
251348_at	putative protein hypothetical protein F9	---	AT3G61010	1.20	0.26	1.51	0.177181	0.383080	-5.74
253725_at	profilin 3 ;supported by full-length cDNA	PRF4	AT4G29340	1.13	0.17	1.51	0.177165	0.383080	-5.74
262193_at	eukaryotic initiation factor 5 (eIF-5), put	---	AT1G77840	1.19	0.25	1.51	0.177289	0.383242	-5.74
252880_at	putative protein ;supported by full-length	---	AT4G39730	-1.23	-0.29	-1.51	0.177274	0.383242	-5.74
247725_at	putative Rab5-interacting protein - like p	---	AT5G59410	-1.21	-0.27	-1.51	0.177329	0.383254	-5.74
249202_at	cytochrome P450	CYP705A1	AT5G42580	-1.11	-0.16	-1.51	0.177317	0.383254	-5.74
266271_at	putative glutathione S-transferase ; sup	ATGSTU6	AT2G29440	1.51	0.60	1.51	0.177378	0.383281	-5.74
257618_at	protein kinase, putative similar to TYRC	---	AT3G24715	1.10	0.14	1.51	0.177437	0.383281	-5.74
252061_at	hypothetical protein phosphate actyltrar	---	AT3G52620	1.11	0.16	1.51	0.17742	0.383281	-5.74
252040_at	putative protein hypothetical protein F1	---	AT3G52060	1.31	0.39	1.51	0.177393	0.383281	-5.74
246189_at	ABI3-interacting protein 2 ;supported by	---	AT5G20910	1.18	0.24	1.51	0.177442	0.383281	-5.74
261962_s_a	hypothetical protein predicted by genem	---	---	1.13	0.18	1.51	0.177366	0.383281	-5.74
251702_at	transcription factor-like protein motif in t	BZIP49	AT3G56660	1.17	0.23	1.51	0.177518	0.383372	-5.74
257998_at	hypothetical protein similar to hypothetic	---	AT3G27510	1.10	0.14	1.51	0.177513	0.383372	-5.74
251297_at	germin-like protein (GLP10)	GLP10	AT3G62020	1.38	0.47	1.51	0.177583	0.383476	-5.75
248153_at	cyclic nucleotide and calmodulin-regulat	ATCNGC4	AT5G54250	-1.14	-0.19	-1.51	0.17761	0.383499	-5.75
252607_at	xyloglucan endo-transglycosylase ; sup	XTR8	AT3G44990	1.26	0.34	1.51	0.177651	0.383551	-5.75
258551_at	hypothetical protein predicted by gensca	---	AT3G06890	1.10	0.14	1.50	0.177811	0.383860	-5.75
261565_at	beta-1,3-glucanase, putative similar to I	---	AT1G33220	1.10	0.14	1.50	0.177891	0.383887	-5.75
251032_at	putative homeodomain protein several h	RPL	AT5G02030	-1.34	-0.43	-1.50	0.177865	0.383887	-5.75

250292_at	putative protein predicted proteins, Arat	JAZ10	AT5G13220	1.73	0.79	1.50	0.177876	0.383887	-5.75
251495_at	putative protein RanBP7/importin 7 - Ho	---	AT3G59020	1.18	0.24	1.50	0.177841	0.383887	-5.75
254049_at	putative ribosomal protein S10 40S ribo	---	AT4G25740	-1.26	-0.33	-1.50	0.178001	0.384075	-5.75
247531_at	putative protein protein kinase 1, PnPK	---	AT5G61550	1.14	0.19	1.50	0.178028	0.384075	-5.75
251764_at	putative protein exostose-related protei	EPC1	AT3G55830	1.16	0.21	1.50	0.178022	0.384075	-5.75
247934_at	putative protein similar to unknown prote	---	AT5G57000	-1.13	-0.18	-1.50	0.178079	0.384149	-5.75
265647_at	hypothetical protein predicted by genefir	---	AT2G27410	1.12	0.17	1.50	0.178144	0.384252	-5.75
265166_at	putative OBP32pep protein	---	AT1G23640	-1.11	-0.15	-1.50	0.178181	0.384295	-5.75
255113_at	putative protein various hypothetical pro	---	---	1.12	0.16	1.50	0.178253	0.384368	-5.75
248849_at	multidrug resistance p-glycoprotein	PGP7	AT5G46540	1.11	0.15	1.50	0.178265	0.384368	-5.75
266334_at	hypothetical protein predicted by genefir	---	AT2G32380	1.22	0.29	1.50	0.178252	0.384368	-5.75
265858_at	putative ribophorin I	---	AT2G01720	-1.16	-0.21	-1.50	0.178332	0.384440	-5.75
260032_at	putative phosphoenolpyruvate carboxyla	ATPPC4	AT1G68750	-1.13	-0.18	-1.50	0.178332	0.384440	-5.75
255170_at	hypothetical protein similar to A. thaliana	---	---	1.12	0.17	1.50	0.178363	0.384471	-5.75
252195_at	putative protein various predicted prote	---	AT3G50190	1.15	0.20	1.50	0.178398	0.384508	-5.75
263364_at	unknown protein predicted by genscan	---	AT2G20540	-1.10	-0.14	-1.50	0.178519	0.384734	-5.75
254720_at	DNA (cytosine-5-)-methyltransferase - I	MEE57	AT4G13610	1.14	0.19	1.50	0.178593	0.384856	-5.75
254604_at	cadmium-induced protein	---	AT4G19070	-1.14	-0.19	-1.50	0.178633	0.384906	-5.75
260808_at	polyprotein, putative similar to polyprote	---	---	1.11	0.15	1.50	0.178715	0.385048	-5.75
260355_at	transcription factor CRC identical to tran	CRC	AT1G69180	1.17	0.23	1.50	0.178797	0.385187	-5.75
254401_at	putative protein various predicted prote	---	AT4G21300	-1.12	-0.17	-1.50	0.178867	0.385283	-5.75
253596_s_a	hypothetical protein ; supported by cDN	---	AT4G30730 /	-1.20	-0.26	-1.50	0.178876	0.385283	-5.75
258794_at	ankyrin-like protein similar to ankyrin pr	---	AT3G04710	-1.31	-0.39	-1.50	0.17898	0.385471	-5.75
245352_at	indole-3-acetate beta-glucosyltransferas	UGT84A3	AT4G15490	1.24	0.30	1.50	0.179075	0.385567	-5.75
245881_at	putative protein	---	AT5G09460 /	-1.20	-0.27	-1.50	0.17905	0.385567	-5.75
250810_at	putative protein contains similarity to unl	---	AT5G05090	-1.22	-0.29	-1.50	0.179072	0.385567	-5.75
256267_at	unknown protein ; supported by cDNA: g	---	AT3G12260	-1.12	-0.16	-1.50	0.179127	0.385642	-5.75
254594_at	putative protein	---	AT4G18930	-1.21	-0.28	-1.50	0.179167	0.385693	-5.75
246325_at	hypothetical protein contains similarity to	ABA3	AT1G16540	1.34	0.42	1.50	0.17928	0.385899	-5.75
247086_at	GATA-binding transcription factor-like pr	---	AT5G66320	1.63	0.70	1.50	0.179334	0.385979	-5.75
259704_at	putative 3'-5' exoribonuclease similar to	---	AT1G77680	1.16	0.21	1.50	0.179359	0.385983	-5.75
252752_s_a	putative protein hypothetical protein At2	---	AT3G43470 /	1.11	0.15	1.50	0.179369	0.385983	-5.75
261111_at	homeodomain protein BELL1, putative	BLH11	AT1G75430	1.10	0.14	1.50	0.179484	0.386181	-5.75
267638_at	unknown protein ; supported by full-leng	OEP16-3	AT2G42210	1.10	0.14	1.50	0.179496	0.386181	-5.75
246996_at	putative protein similar to unknown prote	LBD37	AT5G67420	-1.22	-0.29	-1.50	0.179535	0.386229	-5.76

260774_at	serine-threonine protein kinase, putativ	---	AT1G78290	-1.39	-0.47	-1.50	0.179615	0.386250	-5.76
265857_s_a	serine threonine protein phosphatase P	PP2A-4	AT2G42500 /	-1.14	-0.19	-1.50	0.179595	0.386250	-5.76
267292_at	hypothetical protein predicted by genefi	---	AT2G23740	1.13	0.18	1.50	0.179598	0.386250	-5.76
249498_at	putative protein motif in transcription init	---	AT5G39230	1.13	0.17	1.50	0.1796	0.386250	-5.76
263714_at	putative tyrosine aminotransferase ; su	SUR1	AT2G20610	-1.26	-0.33	-1.50	0.179629	0.386250	-5.76
245939_at	oxoglutarate/malate translocator-like pr	---	AT5G19760	-1.13	-0.18	-1.50	0.179677	0.386289	-5.76
257006_at	hypothetical protein predicted by genem	---	AT3G14075	1.12	0.16	1.50	0.179681	0.386289	-5.76
263654_at	unknown protein	---	AT1G04300	-1.13	-0.17	-1.50	0.17972	0.386337	-5.76
252351_at	putative protein ;supported by full-lengt	---	AT3G48210	1.16	0.22	1.50	0.179758	0.386358	-5.76
260257_at	putative dolichyl-phosphate mannosyltra	---	AT1G74340	1.12	0.16	1.50	0.179799	0.386358	-5.76
260623_at	high-affinity nitrate transporter NRT2 ide	ATNRT2:1	AT1G08090	-1.15	-0.20	-1.50	0.179813	0.386358	-5.76
263205_at	Ca2+-dependent lipid-binding protein, p	NTMC2T2	AT1G05500	-1.12	-0.16	-1.50	0.179802	0.386358	-5.76
248783_at	putative protein contains similarity to sal	---	AT5G47360	-1.22	-0.29	-1.50	0.179815	0.386358	-5.76
258060_at	protein phosphatase 2A regulatory subu	ATB' DELT	AT3G26030	1.11	0.15	1.50	0.179901	0.386412	-5.76
255784_at	hypothetical protein predicted by gensca	---	AT1G19860	-1.12	-0.16	-1.50	0.179908	0.386412	-5.76
263904_at	putative ABC transporter related to mult	PDR6	AT2G36380	-1.42	-0.51	-1.50	0.179904	0.386412	-5.76
248204_at	myosin heavy chain	ATM2	AT5G54280	1.16	0.22	1.50	0.179859	0.386412	-5.76
256579_at	hypothetical protein	---	AT3G28720	-1.11	-0.15	-1.50	0.180095	0.386777	-5.76
246429_at	farnesylated protein ATFP6-like protein	---	AT5G17450	1.36	0.45	1.50	0.18014	0.386801	-5.76
254558_at	Expressed protein ; supported by full-ler	---	AT4G19185	1.11	0.16	1.50	0.180123	0.386801	-5.76
248915_at	putative protein strong similarity to unkn	---	AT5G45690	1.14	0.19	1.50	0.180165	0.386819	-5.76
259617_at	hypothetical protein predicted by genem	---	AT1G47970	-1.15	-0.20	-1.50	0.18023	0.386922	-5.76
262030_s_a	mutator-like transposase, putative simil	---	---	1.13	0.18	1.49	0.180345	0.387132	-5.76
255814_at	unknown protein	---	AT1G19900	-1.11	-0.15	-1.49	0.180518	0.387431	-5.76
256369_at	hypothetical protein predicted by genem	---	AT1G66790 /	-1.09	-0.13	-1.49	0.180502	0.387431	-5.76
266252_at	hypothetical protein predicted by gensca	---	AT2G27520	1.13	0.18	1.49	0.180575	0.387516	-5.76
258750_at	putative pectinacetylesterase similar to (	---	AT3G05910	1.34	0.42	1.49	0.180595	0.387523	-5.76
256271_at	unknown protein	---	AT3G12140	-1.18	-0.24	-1.49	0.180618	0.387536	-5.76
248283_at	pyruvate kinase ;supported by full-lengt	PKP-BETA	AT5G52920	-1.24	-0.31	-1.49	0.180737	0.387681	-5.76
263275_at	putative methylmalonate semi-aldehyde	ALDH6B2	AT2G14170	1.19	0.25	1.49	0.180726	0.387681	-5.76
258360_at	hypothetical protein predicted by genem	---	AT3G14250	-1.12	-0.17	-1.49	0.180722	0.387681	-5.76
259202_at	putative mRNA capping enzyme, RNA (	---	AT3G09100	-1.14	-0.18	-1.49	0.180842	0.387871	-5.76
262494_at	myosin-like protein similar to myosin hea	---	AT1G21810	1.16	0.21	1.49	0.180942	0.388022	-5.76
254168_at	Mlo-like protein Mlo protein - Hordeum	MLO13	AT4G24250	-1.14	-0.19	-1.49	0.180947	0.388022	-5.76
259283_at	putative transcription factor similar to GA	MYB65	AT3G11440	1.13	0.18	1.49	0.181064	0.388157	-5.76

265349_at	putative kinesin heavy chain	---	AT2G22610	1.14	0.19	1.49	0.181078	0.388157	-5.76
263374_at	putative heat shock protein ;supported	---	AT2G20560	-1.28	-0.35	-1.49	0.181044	0.388157	-5.76
249042_at	ethylene-regulated nuclear protein ERT	---	AT5G44350	1.30	0.38	1.49	0.181061	0.388157	-5.76
254947_at	putative retrotransposon polyprotein va	---	---	1.20	0.27	1.49	0.181214	0.388412	-5.76
246422_at	ADP-ribosylation factor -like protein AD	ATARFB1I	AT5G17060	1.29	0.37	1.49	0.181241	0.388434	-5.76
253752_at	putative protein ;supported by full-lengt	---	AT4G28910	-1.16	-0.22	-1.49	0.181285	0.388492	-5.76
251203_at	putative protein putative transcription fa	---	AT3G63070	1.11	0.15	1.49	0.181333	0.388521	-5.76
262122_at	polygalacturonase, putative similar to p	PGA4	AT1G02790	1.13	0.18	1.49	0.181328	0.388521	-5.76
250800_at	ubiquinol-cytochrome C reductase comp	HPR	AT1G68010 /	1.31	0.39	1.49	0.181359	0.388525	-5.76
267148_at	hypothetical protein predicted by gensca	---	AT2G23470	-1.16	-0.21	-1.49	0.181368	0.388525	-5.76
252091_at	putative protein NADH dehydrogenase	---	AT3G51390	-1.11	-0.15	-1.49	0.1814	0.388556	-5.76
248068_at	unknown protein	---	AT5G55610	1.19	0.25	1.49	0.181472	0.388673	-5.76
252885_at	glycine-rich protein (clone AtGRP8) ; su	GR-RBP8	AT4G39260	-1.20	-0.26	-1.49	0.181515	0.388693	-5.77
262018_at	hypothetical protein predicted by gensca	---	AT1G35617	-1.15	-0.20	-1.49	0.181512	0.388693	-5.77
264337_at	hypothetical protein predicted by gensca	---	AT1G70350	-1.12	-0.17	-1.49	0.181575	0.388785	-5.77
261773_at	hypothetical protein predicted by gensca	---	AT1G76250	1.18	0.23	1.49	0.181636	0.388880	-5.77
266095_at	3-oxo-5-alpha-steroid 4-dehydrogenase	DET2	AT2G38050	-1.18	-0.24	-1.49	0.18171	0.389001	-5.77
266221_at	putative nucleotide-sugar dehydratase	UXS6	AT2G28760	1.72	0.78	1.49	0.181834	0.389202	-5.77
246183_at	beta-glucosidase - like protein beta-glu	---	AT5G20940	1.14	0.19	1.49	0.18185	0.389202	-5.77
253742_at	putative protein retrofit - Oryza longista	---	---	1.14	0.19	1.49	0.181855	0.389202	-5.77
254607_at	hypothetical protein ;supported by full-l	---	AT4G18920	1.11	0.16	1.49	0.181887	0.389233	-5.77
263910_at	hypothetical protein predicted by gensca	---	AT2G36550	1.12	0.16	1.49	0.181913	0.389254	-5.77
265304_at	putative AP2 domain transcription factor	---	AT2G20350	-1.10	-0.14	-1.49	0.181933	0.389259	-5.77
250655_at	transcription factor HBP-1b (gb|AAD243	OBF5	AT5G06960	1.11	0.15	1.49	0.182003	0.389336	-5.77
250907_at	putative protein predicted proteins, Aral	---	AT5G03670	1.11	0.15	1.49	0.181986	0.389336	-5.77
266398_at	hypothetical protein predicted by genefir	---	AT2G38680	-1.30	-0.38	-1.49	0.182062	0.389426	-5.77
251092_at	putative protein ;supported by full-lengt	---	AT5G01470	-1.13	-0.17	-1.49	0.182117	0.389437	-5.77
251691_at	putative protein hypothetical protein SE	---	AT3G56520	1.15	0.20	1.49	0.182126	0.389437	-5.77
250373_at	putative protein	---	AT5G11470	-1.10	-0.14	-1.49	0.182127	0.389437	-5.77
260278_at	hypothetical protein predicted by gensc	WRKY66	AT1G80590	1.21	0.28	1.49	0.182136	0.389437	-5.77
262522_at	putative amino acid transporter Very sim	CAT8	AT1G17120	1.14	0.19	1.49	0.182184	0.389505	-5.77
252587_at	putative protein Human (H326) translat	---	AT3G45620	1.26	0.33	1.49	0.182207	0.389517	-5.77
265589_at	hypothetical protein predicted by gensca	---	AT2G20170	1.13	0.18	1.49	0.182252	0.389577	-5.77
248636_at	putative protein similar to unknown prot	---	---	-1.13	-0.18	-1.49	0.182315	0.389674	-5.77
256724_at	unknown protein ;supported by full-leng	---	AT2G34040	-1.14	-0.19	-1.49	0.182342	0.389697	-5.77

256525_at	unknown protein ;supported by full-lengt	---	AT1G66180	-1.27	-0.35	-1.49	0.182426	0.389807	-5.77
264121_at	putative GTP-binding protein Carboxyl-	TOC33	AT1G02280	-1.15	-0.20	-1.49	0.182428	0.389807	-5.77
251606_at	hypothetical protein	---	AT3G57840	1.16	0.21	1.49	0.182533	0.389995	-5.77
255820_at	putative protein kinase contains a protei	---	AT2G40580	1.14	0.19	1.49	0.182666	0.390242	-5.77
246559_at	putative protein YTM1 - Homo sapiens,	---	AT5G15550	-1.21	-0.28	-1.49	0.182689	0.390254	-5.77
261837_s_a	transcriptional regulator, putative simila	---	AT1G15910 /	-1.17	-0.23	-1.49	0.182715	0.390274	-5.77
265875_at	unknown protein ; supported by cDNA:	---	AT2G01690	1.16	0.21	1.49	0.18276	0.390334	-5.77
254815_at	putative pollen-specific protein pollen-s	SKU5	AT4G12420	1.24	0.31	1.49	0.182789	0.390358	-5.77
257862_s_a	unknown protein similar to N-terminal pc	---	AT3G17720 /	1.10	0.14	1.48	0.182843	0.390437	-5.77
249986_at	putative protein predicted proteins, Aral	---	AT5G18460	-1.32	-0.40	-1.48	0.182862	0.390441	-5.77
262021_at	unknown protein	AT1G3554	---	-1.14	-0.19	-1.48	0.182975	0.390646	-5.77
263148_at	ubiquitin, putative similar to ubiquitin GI	---	AT1G53950	1.13	0.18	1.48	0.183008	0.390680	-5.77
253919_at	putative protein ; supported by full-lengt	---	AT4G27350	1.27	0.35	1.48	0.183093	0.390824	-5.77
246087_at	putative protein predicted protein, Arabi	---	AT5G20580	-1.20	-0.26	-1.48	0.183123	0.390853	-5.77
245471_at	probable ribosomal protein	---	AT4G16030	-1.11	-0.15	-1.48	0.18328	0.391151	-5.77
263822_at	hypothetical protein predicted by gensca	---	AT2G40240	-1.16	-0.22	-1.48	0.183384	0.391337	-5.77
244951_s_a	cytochrome c biogenesis orf452	---	AT2G07723	-1.27	-0.35	-1.48	0.183513	0.391480	-5.77
250736_s_a	putative protein contains similarity to zin	---	AT1G01350 /	-1.18	-0.24	-1.48	0.18349	0.391480	-5.77
247174_at	unknown protein ; supported by cDNA:	---	AT5G65250	-1.11	-0.16	-1.48	0.183477	0.391480	-5.77
264754_at	receptor kinase, putative similar to rece	---	AT1G61400	1.14	0.19	1.48	0.18352	0.391480	-5.77
264711_at	hypothetical protein predicted by gensca	---	AT1G09800	-1.12	-0.17	-1.48	0.183593	0.391584	-5.78
245493_at	hypothetical protein	---	---	-1.11	-0.15	-1.48	0.183603	0.391584	-5.78
264443_at	Expressed protein ; supported by full-ler	---	AT1G27385	-1.18	-0.23	-1.48	0.183623	0.391589	-5.78
263311_at	hypothetical protein predicted by genefir	---	AT2G10340	1.14	0.19	1.48	0.183669	0.391599	-5.78
265671_at	40S ribosomal protein S12 ;supported b	---	AT2G32060	-1.30	-0.38	-1.48	0.183679	0.391599	-5.78
251394_at	endosperm specific protein - like endos	FLA10	AT3G60900	1.16	0.21	1.48	0.183675	0.391599	-5.78
264967_at	unknown protein ;supported by full-lengt	---	AT1G67250	-1.11	-0.15	-1.48	0.18383	0.391884	-5.78
266905_at	putative katanin ;supported by full-lengt	---	AT2G34560	-1.19	-0.25	-1.48	0.183875	0.391943	-5.78
247566_at	40S ribsomal protein S19 - like 40S ribs	---	AT5G61170	-1.31	-0.38	-1.48	0.183944	0.392054	-5.78
264666_at	hypothetical protein Similar to N. tabacu	---	AT1G09680	-1.16	-0.22	-1.48	0.183979	0.392092	-5.78
267400_at	unknown protein	---	AT2G26240	1.17	0.22	1.48	0.184018	0.392139	-5.78
264637_at	allyl alcohol dehydrogenase, putative si	---	AT1G65560	-1.20	-0.26	-1.48	0.18406	0.392192	-5.78
248756_at	sodium-dicarboxylate cotransporter-like	TDT	AT5G47560	1.27	0.34	1.48	0.184177	0.392380	-5.78
249317_at	glutathione transferase	ATGSTT2	AT5G41240	-1.12	-0.16	-1.48	0.184183	0.392380	-5.78
254142_at	putative protein other predicted or hypo	---	AT4G24630	1.13	0.18	1.48	0.184223	0.392429	-5.78

260543_at	putative membrane transporter	INT1	AT2G43330	1.20	0.27	1.48	0.184248	0.392446	-5.78
245385_at	hypothetical protein ;supported by full-le	---	AT4G14020	1.19	0.25	1.48	0.184295	0.392509	-5.78
255161_at	putative reverse transcriptase	---	---	-1.12	-0.16	-1.48	0.184326	0.392539	-5.78
261487_at	hypothetical protein predicted by genem	---	AT1G14340	-1.12	-0.16	-1.48	0.184346	0.392543	-5.78
248190_at	unknown protein	---	AT5G54130	-1.13	-0.17	-1.48	0.184389	0.392562	-5.78
252535_at	hypothetical protein	---	AT3G46150	-1.24	-0.31	-1.48	0.184386	0.392562	-5.78
247152_at	oligopeptidase A ; supported by cDNA:	---	AT5G65620	-1.11	-0.15	-1.48	0.184498	0.392758	-5.78
257129_at	cytochrome P450, putative contains Pfa	CYP705A1	AT3G20100	-1.22	-0.29	-1.48	0.184543	0.392808	-5.78
259524_at	hypothetical protein	---	AT1G12550	-1.19	-0.25	-1.48	0.184565	0.392808	-5.78
266429_at	hypothetical protein predicted by gensca	---	AT2G07190	1.13	0.18	1.48	0.184573	0.392808	-5.78
265685_at	NAM (no apical meristem)-like protein	ANAC038	AT2G24430	1.15	0.21	1.48	0.184707	0.393055	-5.78
253548_at	Expressed protein ; supported by full-ler	---	AT4G30993	-1.18	-0.24	-1.48	0.184725	0.393058	-5.78
267619_at	putative receptor-like protein kinase ; su	---	AT2G26730	-1.25	-0.32	-1.48	0.184782	0.393113	-5.78
260022_at	unknown protein	---	AT1G30020	1.13	0.17	1.48	0.184786	0.393113	-5.78
265426_at	hypothetical protein predicted by genefir	---	AT2G20740	-1.14	-0.19	-1.48	0.184817	0.393144	-5.78
250280_at	putative protein many predicted protein	---	AT5G13230	-1.15	-0.20	-1.48	0.184856	0.393189	-5.78
258410_at	putative ribosomal protein similar to ribo	---	AT3G16780	-1.34	-0.42	-1.48	0.184882	0.393208	-5.78
258186_s_a	protein kinase, putative similar to serine	---	AT1G48490 /	1.11	0.16	1.48	0.184946	0.393307	-5.78
257753_at	60S ribosomal protein, putative similar t	---	AT3G18740	-1.20	-0.26	-1.48	0.184977	0.393322	-5.78
257823_at	integral membrane protein, putative cor	---	AT3G25190	1.14	0.18	1.48	0.185039	0.393322	-5.78
257561_at	hypothetical protein predicted by genem	APUM25	AT3G24270	1.13	0.18	1.48	0.185033	0.393322	-5.78
261040_at	oligouridylate binding protein, putative s	UBP1B	AT1G17370	-1.12	-0.17	-1.48	0.185031	0.393322	-5.78
261236_at	importin alpha, putative similar to impor	---	AT1G32880	1.12	0.16	1.48	0.185017	0.393322	-5.78
247850_at	receptor-like protein kinase	---	AT5G58150	1.46	0.55	1.48	0.185147	0.393515	-5.78
246866_at	putative protein various predicted prote	---	AT5G25960	1.12	0.17	1.48	0.185167	0.393522	-5.78
250074_at	UDP-glucose pyrophosphorylase ; supp	---	AT5G17310	-1.18	-0.24	-1.48	0.185209	0.393574	-5.78
253631_at	nucleotide sugar epimerase-like protein	GAE1	AT4G30440	-1.17	-0.22	-1.48	0.185228	0.393578	-5.78
259463_at	hypothetical protein predicted by genem	---	AT1G18950	-1.23	-0.30	-1.48	0.185268	0.393625	-5.78
252743_at	guanine nucleotide-exchange - like prot	ATMIN7	AT3G43300	1.11	0.15	1.48	0.185344	0.393751	-5.78
260001_at	putative S-adenosyl-L-methionine:trans-	TSM1	AT1G67990	1.16	0.21	1.48	0.185375	0.393780	-5.78
247908_at	GS1-like protein ;supported by full-lengt	GS1	AT5G57440	-1.30	-0.38	-1.47	0.185471	0.393935	-5.78
262505_at	unknown protein ESTs gb|N96028, gb|I	---	AT1G21680	-1.14	-0.19	-1.47	0.185483	0.393935	-5.78
256230_at	FKBP-type peptidyl-prolyl cis-trans ison	---	AT3G12340	-1.16	-0.22	-1.47	0.185565	0.394000	-5.78
246210_at	ribosomal protein ; supported by cDNA:	---	AT4G36420	-1.19	-0.25	-1.47	0.185552	0.394000	-5.78
247104_at	putative protein similar to unknown prote	DAR6	AT5G66620	1.19	0.25	1.47	0.185558	0.394000	-5.78

249644_at	putative serine-rich protein hypothetical	---	AT5G37010	1.15	0.20	1.47	0.185622	0.394083	-5.79
248445_at	unknown protein ;supported by full-leng	---	AT5G51170	-1.16	-0.21	-1.47	0.18564	0.394085	-5.79
254944_at	putative protein proliferation potential p	---	AT4G10930	-1.09	-0.12	-1.47	0.185714	0.394205	-5.79
249221_at	serine/threonine protein kinase-like prot	---	AT5G42440	1.16	0.21	1.47	0.185789	0.394235	-5.79
267599_at	putative serine/threonine protein kinase	---	AT2G32850	1.11	0.15	1.47	0.185784	0.394235	-5.79
251398_at	zinc finger protein - like ZPT3-3, Petuni	---	AT3G60580	1.16	0.21	1.47	0.185797	0.394235	-5.79
249567_at	SAMT-like protein S-adenosyl-L-methio	---	AT5G38020	1.10	0.14	1.47	0.18577	0.394235	-5.79
246696_at	putative protein predicted protein, Arabi	---	---	1.12	0.17	1.47	0.185827	0.394263	-5.79
263387_at	unknown protein ; supported by cDNA:	---	AT2G40160	-1.14	-0.18	-1.47	0.185859	0.394293	-5.79
266711_at	unknown protein	---	AT2G46740	1.11	0.15	1.47	0.185928	0.394404	-5.79
262762_at	phosphoribosyl diphosphate synthase id	---	AT1G10700	1.62	0.69	1.47	0.185963	0.394440	-5.79
261245_at	anter-specific proline-rich protein APG p	---	AT1G20130 /	-1.11	-0.15	-1.47	0.18607	0.394632	-5.79
264828_at	hypothetical protein predicted by genscа	ATATG18(	AT1G03380	-1.18	-0.24	-1.47	0.186215	0.394902	-5.79
248980_at	putative protein similar to unknown prote	AtPP2-A7	AT5G45090	1.16	0.21	1.47	0.186275	0.394993	-5.79
267616_at	unknown protein ;supported by full-leng	---	AT2G26680	-1.13	-0.18	-1.47	0.186409	0.395175	-5.79
254175_at	putative protein CGI-82 protein - Homo	---	AT4G24050	-1.12	-0.16	-1.47	0.186394	0.395175	-5.79
261501_at	wall-associated kinase 1, putative simila	---	AT1G28390	1.18	0.24	1.47	0.186413	0.395175	-5.79
266533_s_a	putative plasma membrane intrinsic prot	PIP2;8	AT2G16850 /	1.19	0.25	1.47	0.18646	0.395237	-5.79
254770_at	extensin-like protein extensin-like prote	---	AT4G13340	1.34	0.42	1.47	0.186502	0.395260	-5.79
254706_at	putative protein DNA-binding protein PI	---	AT4G17950	-1.17	-0.23	-1.47	0.186511	0.395260	-5.79
263859_at	hypothetical protein predicted by genscа	---	AT2G04360	-1.19	-0.26	-1.47	0.186523	0.395260	-5.79
259983_at	3-hydroxy-3-methylglutaryl CoA reducta	HMG1	AT1G76490	1.13	0.18	1.47	0.18655	0.395282	-5.79
248554_at	putative protein contains similarity to AB	---	AT5G50330	1.17	0.23	1.47	0.186595	0.395341	-5.79
267014_at	unknown protein	---	AT2G39170	-1.10	-0.13	-1.47	0.186623	0.395362	-5.79
254698_at	NAM (no apical meristem) - like protein	anac071	AT4G17980	1.09	0.13	1.47	0.186651	0.395385	-5.79
256713_at	putative peroxidase	---	AT2G34060	1.22	0.28	1.47	0.186732	0.395520	-5.79
257679_at	glycine-rich protein, putative identical to	GRP5	AT3G20470	1.46	0.54	1.47	0.186767	0.395558	-5.79
251916_at	transporter-like protein oligopeptide trar	---	AT3G53960	-1.20	-0.26	-1.47	0.186804	0.395587	-5.79
263878_s_a	unknown protein	---	AT2G22040 /	-1.15	-0.20	-1.47	0.186815	0.395587	-5.79
259578_at	unknown protein	---	AT1G27990	1.20	0.27	1.47	0.186836	0.395594	-5.79
261893_at	unknown protein ;supported by full-lengt	---	AT1G80690	1.12	0.17	1.47	0.186857	0.395600	-5.79
258494_at	cell division protein FtsH-like protein sim	---	AT3G02450	-1.16	-0.21	-1.47	0.186979	0.395823	-5.79
263556_at	hypothetical protein predicted by genscа	---	AT2G16365	-1.14	-0.19	-1.47	0.187005	0.395840	-5.79
266255_at	putative selenium-binding protein	---	AT2G27610	-1.12	-0.16	-1.47	0.187032	0.395861	-5.79
249739_at	Ttg1 protein (emb CAB45372.1)	TTG1	AT5G24520	-1.11	-0.15	-1.47	0.187065	0.395896	-5.79

257761_at	unknown protein	---	AT3G23090	1.25	0.32	1.47	0.187145	0.395991	-5.79
261013_at	fatty acid elongase 3-ketoacyl-CoA synt	ATUPS5	AT1G26440	1.18	0.24	1.47	0.187142	0.395991	-5.79
246089_at	ring-box protein - like ring-box protein-li	RBX1	AT5G20570	-1.09	-0.13	-1.47	0.187193	0.396056	-5.79
251204_at	putative protein HMW prekininogen, Mu	AT3G6309	---	1.13	0.18	1.47	0.187289	0.396191	-5.79
263360_at	unknown protein	---	AT2G03830	-1.12	-0.17	-1.47	0.187309	0.396191	-5.79
247061_at	putative protein similar to unknown prote	---	AT5G66780	1.20	0.26	1.47	0.187299	0.396191	-5.79
253574_at	putative protein	---	AT4G31030	-1.18	-0.24	-1.47	0.187342	0.396224	-5.79
258925_at	unknown protein similar to hypothetical	---	AT3G10420	1.15	0.20	1.47	0.187404	0.396317	-5.79
254931_at	serine/threonine kinase-like protein rec	---	AT4G11460	1.17	0.23	1.47	0.187511	0.396507	-5.79
267231_at	putative inositol polyphosphate 5'-phosp	---	AT2G43900	-1.13	-0.17	-1.47	0.187536	0.396523	-5.79
258414_at	unknown protein ;supported by full-leng	---	AT3G17380	1.13	0.18	1.47	0.187666	0.396761	-5.80
265221_s_a	putative glutamate decarboxylase ; sup	GAD3	AT2G02000 /	1.55	0.63	1.47	0.187715	0.396791	-5.80
254252_at	serine/threonine kinase - like protein KI	---	AT4G23310	1.18	0.24	1.47	0.18771	0.396791	-5.80
257372_at	hypothetical protein predicted by gensca	---	AT2G43220	1.11	0.16	1.47	0.187859	0.397059	-5.80
252575_at	receptor like protein kinase receptor like	---	AT3G45440	1.18	0.24	1.47	0.187895	0.397099	-5.80
260216_at	hypothetical protein contains Pfam profi	---	AT1G74580	-1.12	-0.17	-1.47	0.187913	0.397099	-5.80
258172_at	unknown protein similar to HYP1 GB:CA	---	AT3G21620	-1.11	-0.15	-1.47	0.187979	0.397203	-5.80
256606_at	hypothetical protein	---	AT3G32960	1.12	0.16	1.47	0.187997	0.397205	-5.80
253874_at	putative protein stem-specific protein -	---	AT4G27450	1.34	0.42	1.47	0.188019	0.397212	-5.80
259156_at	hypothetical protein predicted by genefi	SEC8	AT3G10380	1.12	0.16	1.46	0.188037	0.397214	-5.80
245899_at	putative protein	ALF4	AT5G11030	1.13	0.17	1.46	0.188094	0.397262	-5.80
255410_at	putative rac GTPase activating protein	---	AT4G03100	-1.13	-0.17	-1.46	0.188085	0.397262	-5.80
252700_at	hypothetical protein envelope-like, Glyc	---	---	1.14	0.18	1.46	0.188167	0.397378	-5.80
263098_at	Expressed protein ; supported by full-ler	---	AT2G16005	1.11	0.15	1.46	0.188256	0.397523	-5.80
263946_at	hypothetical protein ;supported by full-le	---	AT2G36000	-1.14	-0.19	-1.46	0.188288	0.397523	-5.80
258675_at	putative nonspecific lipid-transfer protein	LTP6	AT3G08770	1.13	0.17	1.46	0.188286	0.397523	-5.80
247827_at	putative protein various predicted prote	LSH5	AT5G58500	-1.15	-0.21	-1.46	0.188402	0.397690	-5.80
249670_at	unknown protein	---	AT5G35890	1.12	0.17	1.46	0.188395	0.397690	-5.80
247183_at	putative protein strong similarity to unkn	---	AT5G65440	1.11	0.15	1.46	0.18851	0.397716	-5.80
256908_at	hypothetical protein similar to mucin cor	---	AT3G24040	-1.13	-0.18	-1.46	0.188519	0.397716	-5.80
258180_at	unknown protein	---	AT3G21480	-1.22	-0.29	-1.46	0.188437	0.397716	-5.80
266204_at	hypothetical protein predicted by gensca	---	AT2G02410	-1.17	-0.23	-1.46	0.188498	0.397716	-5.80
255589_s_a	hypothetical protein	---	AT4G01590 /	-1.19	-0.25	-1.46	0.188496	0.397716	-5.80
257331_at	hypothetical protein	---	---	-1.15	-0.20	-1.46	0.188484	0.397716	-5.80
246408_at	hypothetical protein predicted by genem	---	AT1G57680	-1.16	-0.22	-1.46	0.188557	0.397760	-5.80

251349_s_a	putative protein several hypothetical pro	---	AT3G11030 /	-1.17	-0.23	-1.46	0.188668	0.397932	-5.80
266541_at	unknown protein	GRL	AT2G35110	-1.15	-0.20	-1.46	0.188673	0.397932	-5.80
265413_s_a	hypothetical protein predicted by gensca	---	AT2G16650 /	1.14	0.18	1.46	0.188698	0.397947	-5.80
255270_at	putative protein (ubiquitin like) to various	---	AT4G05250	1.10	0.14	1.46	0.18877	0.398062	-5.80
258155_at	protein kinase C-receptor/G-protein, pu	RACK1C_	AT3G18130	-1.43	-0.52	-1.46	0.188813	0.398116	-5.80
262239_at	unknown protein similar to putative phos	---	AT1G48230	-1.19	-0.25	-1.46	0.188842	0.398140	-5.80
253524_at	predicted protein ; supported by cDNA:	---	AT4G31430	-1.13	-0.18	-1.46	0.188888	0.398143	-5.80
258571_at	hypothetical protein predicted by genem	anac048	AT3G04420	-1.14	-0.19	-1.46	0.18889	0.398143	-5.80
245462_at	transcription factor like protein	---	AT4G17020	-1.13	-0.18	-1.46	0.188896	0.398143	-5.80
262877_at	unknown protein ;supported by full-lengt	---	AT1G64850	-1.16	-0.21	-1.46	0.188943	0.398206	-5.80
245707_at	NAC2-like protein	anac077	AT5G04400	-1.14	-0.19	-1.46	0.188978	0.398207	-5.80
262201_at	unknown protein	ORC4	AT2G01120	-1.11	-0.15	-1.46	0.188965	0.398207	-5.80
253527_at	pathogenesis-related protein homolog p	---	AT4G31470	1.13	0.18	1.46	0.189066	0.398302	-5.80
256621_at	unknown protein ; supported by full-leng	---	AT3G24450	1.13	0.18	1.46	0.189075	0.398302	-5.80
246265_at	phosphoribosyl-ATP pyrophosphohydro	AT-IE	AT1G31860	-1.28	-0.36	-1.46	0.189064	0.398302	-5.80
266645_at	hypothetical protein	---	AT2G29880	-1.11	-0.15	-1.46	0.189112	0.398343	-5.80
247071_at	putative protein similar to unknown prote	DAR3	AT5G66640	1.46	0.55	1.46	0.189269	0.398625	-5.80
263840_at	Expressed protein ; supported by full-ler	---	AT2G36885	1.19	0.25	1.46	0.189281	0.398625	-5.80
266299_at	glutathione S-transferase identical to GE	ATGSTU5	AT2G29450	1.28	0.36	1.46	0.189514	0.399078	-5.80
248122_at	unknown protein	---	AT5G54700	-1.12	-0.16	-1.46	0.189582	0.399184	-5.80
265094_at	putative cruciferin 12S seed storage pro	---	AT1G03890	1.11	0.15	1.46	0.189601	0.399188	-5.80
244953_s_a	NADH dehydrogenase subunit 6	---	AT2G07731	-1.21	-0.27	-1.46	0.189637	0.399227	-5.80
263836_at	unknown protein ;supported by full-leng	---	AT2G40330	1.48	0.56	1.46	0.189655	0.399228	-5.80
253987_at	pyrophosphate-dependent phosphofruc	PFK3	AT4G26270	1.30	0.38	1.46	0.189698	0.399263	-5.80
249420_at	NAC domain/ NAM like protein NAC do	anac094	AT5G39820	1.12	0.16	1.46	0.189721	0.399263	-5.80
255163_at	putative polyprotein	---	---	-1.11	-0.16	-1.46	0.189724	0.399263	-5.80
247545_at	putative protein rhoGAP, Homo sapiens	---	AT5G61530	1.11	0.15	1.46	0.189769	0.399321	-5.80
245874_at	unknown protein	---	AT1G26250	1.13	0.18	1.46	0.189839	0.399431	-5.81
246331_at	non-phototropic hypocotyl 3-like protein	---	AT3G44820	-1.15	-0.20	-1.46	0.189902	0.399526	-5.81
265093_at	unknown protein similar to NBD-like pro	---	AT1G03905	1.16	0.22	1.46	0.189985	0.399663	-5.81
261357_at	hypothetical protein predicted by genem	---	---	1.10	0.14	1.46	0.190004	0.399666	-5.81
264983_at	hypothetical protein predicted by gensca	---	AT1G27240	1.11	0.15	1.46	0.190042	0.399711	-5.81
259533_at	hypothetical protein	---	AT1G12530	-1.10	-0.13	-1.46	0.19013	0.399830	-5.81
252734_at	putative protein merozoite surface prote	MEE38	AT3G43160	1.13	0.17	1.46	0.190134	0.399830	-5.81
255725_at	hypothetical protein similar to putative p	PFT1	AT1G25540	1.10	0.13	1.46	0.190213	0.399960	-5.81

246341_x_a	putative protein predicted proteins, Arat	---	AT3G43150	1.16	0.21	1.46	0.190308	0.400123	-5.81
261745_at	unknown protein identical to unknown pr	---	AT1G08500	1.35	0.43	1.46	0.190455	0.400395	-5.81
245078_at	putative AP2 domain transcription factor	---	AT2G23340	1.38	0.47	1.46	0.19053	0.400441	-5.81
250761_at	ankyrin-like protein	---	AT5G06050	-1.13	-0.18	-1.46	0.190525	0.400441	-5.81
256989_at	hypothetical protein predicted by genem	---	AT3G28580	1.97	0.98	1.46	0.190508	0.400441	-5.81
255326_at	hypothetical protein	---	---	-1.10	-0.13	-1.46	0.190565	0.400479	-5.81
251794_at	mannose-1-phosphate guanylyltransfer	---	AT3G55590	1.11	0.15	1.46	0.190624	0.400528	-5.81
265546_at	putative proline/hydroxyproline-rich glyc	---	AT2G28240	-1.13	-0.18	-1.46	0.190612	0.400528	-5.81
246165_at	putative protein	---	---	-1.10	-0.14	-1.46	0.190661	0.400570	-5.81
267259_at	Expressed protein ; supported by full-ler	---	AT2G23090 /	1.13	0.18	1.45	0.19075	0.400666	-5.81
266122_at	putative helicase ; supported by cDNA:	ETL1	AT2G02090	-1.12	-0.16	-1.45	0.190813	0.400666	-5.81
262866_at	cytochrome p450, putative similar to cy	CYP89A6	AT1G64940	1.10	0.14	1.45	0.190803	0.400666	-5.81
249989_at	putative protein FACTOR ASSOCIATE	---	AT5G18525	-1.14	-0.19	-1.45	0.190779	0.400666	-5.81
267153_at	glutathione S-transferase identical to GE	ATGSTF9	AT2G30860	-1.18	-0.24	-1.45	0.190813	0.400666	-5.81
249936_at	putative protein similar to unknown prote	---	AT5G22450	1.14	0.19	1.45	0.190791	0.400666	-5.81
257179_at	topoisomerase VIA (SPO11 gene 1), pu	---	AT3G13160 /	1.10	0.14	1.45	0.190864	0.400738	-5.81
247220_at	cdc2-like protein kinase ; supported by	CDKC2	AT5G64960	-1.12	-0.17	-1.45	0.190886	0.400746	-5.81
263289_at	ubiquitin extension protein (UBQ2) iden	---	AT2G36170	-1.24	-0.31	-1.45	0.190918	0.400777	-5.81
267127_at	putative acetone-cyanohydrin lyase	MES3	AT2G23610	-1.13	-0.18	-1.45	0.190997	0.400905	-5.81
262623_at	integral membrane protein, putative cor	---	AT1G06470	-1.15	-0.20	-1.45	0.19117	0.401232	-5.81
258101_at	unknown protein	RFR1	AT3G23590	-1.26	-0.33	-1.45	0.191199	0.401257	-5.81
256074_at	unknown protein ; supported by cDNA: g	---	AT1G18260	1.14	0.19	1.45	0.191266	0.401359	-5.81
254365_at	putative protein hypothetical protein DL	---	AT4G22030	1.12	0.16	1.45	0.191366	0.401531	-5.81
250210_at	putative protein similar to unknown prote	---	AT5G13890	-1.14	-0.19	-1.45	0.191389	0.401544	-5.81
261212_at	hypothetical protein predicted by genem	atnudt12	AT1G12880	-1.20	-0.26	-1.45	0.191447	0.401628	-5.81
255069_s_a	Met2-type cytosine DNA-methyltransfer	---	AT4G08990 /	1.20	0.27	1.45	0.19153	0.401765	-5.81
261284_at	hypothetical protein predicted by gensca	---	---	-1.13	-0.18	-1.45	0.19155	0.401770	-5.81
252898_at	cytochrome P450 -like protein simialrity	CYP96A11	AT4G39500	1.10	0.14	1.45	0.191608	0.401808	-5.81
267413_at	putative amino acid transporter	CAT5	AT2G34960	1.21	0.28	1.45	0.19162	0.401808	-5.81
263700_at	unknown protein EST gb|Z33866 comes	---	AT1G31150	-1.17	-0.23	-1.45	0.191588	0.401808	-5.81
265530_at	12-oxophytodienoate-10,11-reductase	OPR3	AT2G06050	1.37	0.46	1.45	0.191676	0.401832	-5.81
260862_at	unknown protein	SEU	AT1G43850	-1.12	-0.16	-1.45	0.191763	0.401832	-5.81
248737_at	unknown protein	---	AT5G48120	-1.18	-0.24	-1.45	0.191734	0.401832	-5.81
264538_at	hypothetical protein predicted by genem	WRKY10	AT1G55600	1.15	0.20	1.45	0.191736	0.401832	-5.81
266781_at	putative protein kinase contains a protei	---	AT2G28940	-1.17	-0.22	-1.45	0.191736	0.401832	-5.81

267333_at	putative WD-40 repeat protein contains	---	AT2G19430	-1.11	-0.15	-1.45	0.191729	0.401832	-5.81
256973_at	unknown protein similar to putative retro	---	AT3G20980	1.12	0.16	1.45	0.191773	0.401832	-5.81
262469_s_a	hypothetical protein identical to hypothe	---	AT1G50190 /	-1.11	-0.15	-1.45	0.191747	0.401832	-5.81
258123_at	putative MAP kinase similar to blast and	MPK9	AT3G18040	-1.26	-0.33	-1.45	0.191808	0.401832	-5.81
257124_at	hexokinase, putative similar to hexokina	ATHXK4	AT3G20040	1.12	0.17	1.45	0.191802	0.401832	-5.81
256712_at	unknown protein similar to T14G11.15	---	AT2G34020	1.10	0.13	1.45	0.191875	0.401934	-5.81
252611_at	oxidosqualene cyclase - like protein oxi	LAS1	AT3G45130	1.34	0.42	1.45	0.191956	0.402068	-5.82
260695_at	RNA helicase, putative similar to GB:D5	ESP3	AT1G32490	-1.09	-0.13	-1.45	0.192006	0.402135	-5.82
251174_at	putative protein latex protein allergen H	PLP9	AT3G63200	1.27	0.35	1.45	0.192045	0.402181	-5.82
249934_at	peroxidase ATP14a homolog	---	AT5G22410	1.10	0.14	1.45	0.192082	0.402220	-5.82
251622_at	dnaJ-like protein DNAJ protein - Schizo	---	AT3G57340	-1.10	-0.14	-1.45	0.192135	0.402295	-5.82
263417_at	putative C2H2-type zinc finger protein li	---	AT2G17180	1.17	0.22	1.45	0.192223	0.402441	-5.82
249106_at	protein transport protein SEC23 ; suppo	---	AT5G43670	-1.19	-0.25	-1.45	0.192336	0.402641	-5.82
256730_at	floral homeotic protein AGL8, putative s	AGL79	AT3G30260	-1.10	-0.13	-1.45	0.192362	0.402660	-5.82
265433_at	unknown protein	---	AT2G20950	1.17	0.23	1.45	0.192392	0.402686	-5.82
259847_at	unknown protein	---	AT1G72170	-1.15	-0.20	-1.45	0.192428	0.402724	-5.82
248130_at	unknown protein	---	AT5G54790	-1.11	-0.15	-1.45	0.192474	0.402782	-5.82
257771_at	SNF1 related protein kinase (ATSRPK1	CIPK7	AT3G23000	-1.44	-0.52	-1.45	0.192527	0.402856	-5.82
259478_at	germin, putative similar to germin GI:17	---	AT1G18980	2.01	1.01	1.45	0.192593	0.402959	-5.82
266278_at	putative tropinone reductase	---	AT2G29300	-1.36	-0.44	-1.45	0.192694	0.403131	-5.82
262695_at	vacuolor sorting protein 35, putative sim	VPS35B	AT1G75850	-1.11	-0.15	-1.45	0.192715	0.403138	-5.82
252672_at	hypothetical protein	---	AT3G44230	1.10	0.14	1.45	0.192832	0.403309	-5.82
246964_at	putative protein crp1 protein - Zea mays	---	AT5G24830	-1.14	-0.19	-1.45	0.192827	0.403309	-5.82
256275_at	actin 11 (ACT11) identical to actin 11 (A	ACT11	AT3G12110	1.19	0.25	1.45	0.192894	0.403366	-5.82
246854_at	mitochondrial carrier - like protein mitoc	---	AT5G26200	-1.13	-0.18	-1.45	0.192889	0.403366	-5.82
249630_s_a	sen1-like protein SEN1 - Saccharomyce	---	AT5G37150 /	1.10	0.13	1.45	0.193008	0.403568	-5.82
267409_at	hypothetical protein predicted by genefir	---	AT2G34910	1.10	0.13	1.45	0.193044	0.403605	-5.82
263009_at	hypothetical protein contains similarity to	NHX5	AT1G54370	-1.11	-0.16	-1.45	0.193102	0.403689	-5.82
255216_s_a	putative peptidase	---	AT4G07670 /	-1.25	-0.32	-1.45	0.193195	0.403847	-5.82
254903_at	H+-transporting ATPase chain E, vacuo	TUF	AT4G11150	1.14	0.19	1.45	0.19322	0.403861	-5.82
264915_at	hypothetical protein predicted by genem	---	AT1G60790	-1.10	-0.13	-1.45	0.193273	0.403936	-5.82
255008_at	putative protein hypothetical protein sll1	---	AT4G10060	-1.12	-0.17	-1.45	0.193325	0.403985	-5.82
266913_at	hypothetical protein predicted by genscar	ROPGEF4	AT2G45890	1.10	0.14	1.44	0.193368	0.403985	-5.82
258066_at	hypothetical protein predicted by genem	---	AT3G25970	1.09	0.13	1.44	0.193364	0.403985	-5.82
263277_at	hypothetical protein predicted by genscar	---	AT2G14110	-1.11	-0.15	-1.45	0.193361	0.403985	-5.82

264427_at	hypothetical protein predicted by genem	---	AT1G61770	1.14	0.19	1.44	0.193398	0.404012	-5.82
247996_at	putative protein contains similarity to GF	---	AT5G56170	1.22	0.29	1.44	0.193466	0.404117	-5.82
261554_at	PPR-repeat protein contains multiple PF	---	AT1G63400	-1.09	-0.13	-1.44	0.193671	0.404508	-5.82
260440_at	hypothetical protein predicted by gensca	---	AT1G68160	-1.11	-0.16	-1.44	0.19376	0.404620	-5.82
258694_at	putative non-phototropic hypocotyl simil	---	AT3G08660	-1.25	-0.32	-1.44	0.193757	0.404620	-5.82
261985_at	terpene synthase, putative similar to DE	---	AT1G33750	1.10	0.14	1.44	0.194034	0.405156	-5.82
246900_at	putative protein flavin-containing monoc	YUC6	AT5G25620	-1.17	-0.22	-1.44	0.194106	0.405268	-5.83
258691_at	unknown protein	---	AT3G08630	1.36	0.45	1.44	0.194308	0.405542	-5.83
249869_at	acetyl-CoA synthetase-like protein	AAE17	AT5G23050	1.19	0.25	1.44	0.19428	0.405542	-5.83
254959_at	predicted protein	UGE5	AT4G10955 /	1.20	0.26	1.44	0.194303	0.405542	-5.83
257656_at	Expressed protein ; supported by full-ler	---	AT3G13228	1.10	0.14	1.44	0.194277	0.405542	-5.83
249970_at	dermal glycoprotein precursor -like prot	---	AT5G19100	1.24	0.31	1.44	0.194332	0.405556	-5.83
265611_at	unknown protein ;supported by full-leng	---	AT2G25510	1.23	0.30	1.44	0.194417	0.405692	-5.83
254907_at	putative disease resistance response p	---	AT4G11190	1.12	0.16	1.44	0.194433	0.405692	-5.83
249942_at	Nitrilase 4 (sp|P46011) ; supported by f	GAPB	AT1G42970 /	2.16	1.11	1.44	0.194467	0.405725	-5.83
262939_s_a	glyceraldehyde-3-phosphate dehydroge	GAPCP-2	AT1G16300 /	1.60	0.68	1.44	0.194504	0.405765	-5.83
253343_at	putative protein	---	AT4G33540	1.35	0.43	1.44	0.194586	0.405898	-5.83
260726_at	signal recognition particle 19 kDa prote	---	AT1G48160	-1.17	-0.23	-1.44	0.194624	0.405941	-5.83
258755_at	hypothetical protein identical to hypothe	---	AT3G11945 /	-1.14	-0.19	-1.44	0.194694	0.405956	-5.83
247955_at	nucleosome assembly protein	NAP1;3	AT5G56950	-1.15	-0.20	-1.44	0.194674	0.405956	-5.83
257629_at	cellulase, putative contains Pfam profile	---	AT3G26140	1.13	0.18	1.44	0.194702	0.405956	-5.83
257085_at	ubiquitin-specific protease 14 (UBP14),	UBP14	AT3G20630	-1.21	-0.27	-1.44	0.194668	0.405956	-5.83
258998_at	putative adenylate kinase similar to AdK	---	AT3G01820	1.15	0.20	1.44	0.194801	0.406126	-5.83
253841_at	putative beta-glucosidase beta-glucosid	BGLU10	AT4G27830	1.18	0.24	1.44	0.1949	0.406294	-5.83
254074_at	transcriptional activator CBF1 CRT CRI	CBF1	AT4G25490	-1.29	-0.37	-1.44	0.194972	0.406408	-5.83
257869_at	ER lumen protein retaining receptor, pu	---	AT3G25160	1.10	0.14	1.44	0.195057	0.406548	-5.83
260766_at	unknown protein similar to hypothetical	---	AT1G48960	1.13	0.17	1.44	0.195138	0.406679	-5.83
254206_at	thaumatin-like protein thaumatin-like pr	---	AT4G24180	-1.14	-0.19	-1.44	0.195197	0.406765	-5.83
254831_at	Ribosomal protein L7Ae -like various L7	---	AT4G12600	-1.29	-0.36	-1.44	0.195314	0.406944	-5.83
258759_at	putative bZIP transcription factor contair	BZIP28	AT3G10800	1.11	0.15	1.44	0.195319	0.406944	-5.83
258295_at	unknown protein ;supported by full-leng	---	AT3G23400	-1.19	-0.25	-1.44	0.195374	0.407022	-5.83
254686_at	putative protein putative oncogene prot	---	AT4G13720	-1.14	-0.18	-1.44	0.19541	0.407059	-5.83
249320_at	disease resistance protein-like non-cons	---	AT5G40910	-1.19	-0.25	-1.44	0.195505	0.407220	-5.83
251251_at	serine/threonine protein kinase-like prot	---	AT3G62220	-1.13	-0.18	-1.44	0.195567	0.407311	-5.83
AFFX-Athal	Arabidopsis thaliana /REF=U84969 /DE	---	---	1.13	0.18	1.44	0.19561	0.407365	-5.83

247053_at	protein kinase ATN1-like protein	---	AT5G66710	1.10	0.13	1.44	0.195672	0.407420	-5.83
262826_at	putative cytochrome P450 monooxyger	CYP71B2	AT1G13080	-1.29	-0.37	-1.44	0.195671	0.407420	-5.83
267025_at	unknown protein predicted by genscan	---	AT2G38350	1.09	0.13	1.44	0.195775	0.407559	-5.83
254580_at	putative protein ; supported by cDNA: g	---	AT4G19390	-1.12	-0.16	-1.44	0.195772	0.407559	-5.83
266397_at	unknown protein	---	AT2G38690	1.11	0.15	1.44	0.195817	0.407576	-5.83
249199_at	putative protein similar to unknown prote	BPC6	AT5G42520	-1.12	-0.17	-1.44	0.195819	0.407576	-5.83
260949_at	F-box protein family contains similarity t	SKIP16	AT1G06110	1.12	0.17	1.44	0.195859	0.407623	-5.83
257871_at	hypothetical protein predicted by gensca	---	AT3G28350	1.10	0.14	1.44	0.195908	0.407687	-5.83
245331_at	hypothetical protein ;supported by full-le	---	AT4G14410	1.11	0.16	1.44	0.195932	0.407700	-5.83
246046_at	putative protein predicted proteins, Aral	---	---	1.13	0.18	1.44	0.195969	0.407739	-5.83
264954_at	carboxyphosphonoenolpyruvate mutase	---	AT1G77060	-1.18	-0.23	-1.44	0.196045	0.407837	-5.83
259037_at	hypothetical protein predicted by gensca	---	AT3G09350	1.48	0.57	1.44	0.196051	0.407837	-5.83
261496_at	ethylene responsive element binding fa	ERF12	AT1G28360	1.14	0.19	1.43	0.196091	0.407882	-5.83
265016_at	unknown protein similar to deacetylvind	---	AT1G24420	1.10	0.13	1.43	0.196252	0.408143	-5.83
253195_at	putative protein dihydroflavonol-4-reduc	---	AT4G35420	1.13	0.18	1.43	0.196243	0.408143	-5.83
252428_at	putative protein rjs - Mus musculus, EM	---	AT3G47660	1.14	0.19	1.43	0.196539	0.408702	-5.84
246899_at	putative protein various predicted prote	---	AT5G25590	1.12	0.16	1.43	0.196641	0.408876	-5.84
252062_at	hypothetical protein KIAA0253 protein,	---	AT3G52640	-1.17	-0.22	-1.43	0.196672	0.408903	-5.84
246293_at	SigA binding protein ; supported by cDN	SIB1	AT3G56710	1.66	0.73	1.43	0.196722	0.408951	-5.84
261022_at	unknown protein similar to NAM like pro	ANAC007	AT1G12260	1.12	0.17	1.43	0.19673	0.408951	-5.84
246769_at	hypothetical protein	---	AT5G27440	-1.11	-0.16	-1.43	0.196778	0.408991	-5.84
266058_at	glycerol-3-phosphate dehydrogenase ;	GLY1	AT2G40690	-1.17	-0.22	-1.43	0.196786	0.408991	-5.84
247001_at	natural resistance-associated macropha	NRAMP4	AT5G67330	-1.14	-0.18	-1.43	0.19681	0.409005	-5.84
249321_at	disease resistance protein-like	---	AT5G40920	1.17	0.23	1.43	0.196839	0.409028	-5.84
261095_at	unknown protein	---	AT1G62930	-1.14	-0.18	-1.43	0.196875	0.409065	-5.84
256875_at	cytochrome P450, putative contains Pfa	CYP71B37	AT3G26330	-1.13	-0.18	-1.43	0.196924	0.409129	-5.84
263981_at	unknown protein ;supported by full-leng	PAR1	AT2G42870	1.46	0.55	1.43	0.19701	0.409272	-5.84
248472_at	cyclin-dependent protein kinase-like	---	AT5G50860	-1.13	-0.18	-1.43	0.197063	0.409306	-5.84
254312_s_a	hypothetical protein	---	---	1.14	0.19	1.43	0.197061	0.409306	-5.84
247055_at	putative protein similar to unknown prote	---	AT5G66740	1.15	0.20	1.43	0.197092	0.409330	-5.84
265896_at	unknown protein	emb2410	AT2G25660	-1.13	-0.17	-1.43	0.197156	0.409388	-5.84
248304_at	polypyrimidine tract-binding RNA transp	PTB2	AT5G53180	-1.10	-0.14	-1.43	0.19715	0.409388	-5.84
260224_at	hypothetical protein contains Pfam profil	---	AT1G74400	-1.10	-0.13	-1.43	0.1972	0.409443	-5.84
257138_at	hypothetical protein predicted by genem	---	AT3G28870	-1.10	-0.14	-1.43	0.197224	0.409455	-5.84
254295_at	putative protein predicted protein, Arabi	---	AT4G23080	1.10	0.13	1.43	0.197368	0.409715	-5.84

246880_s_a	myrosinase TGG2 ; supported by cDNA	TGG2	AT5G25980 /	1.44	0.53	1.43	0.197405	0.409718	-5.84
265716_at	unknown protein ;supported by full-leng	---	AT2G03350	-1.17	-0.23	-1.43	0.197395	0.409718	-5.84
265256_at	hypothetical protein predicted by gensca	---	AT2G28390	-1.09	-0.13	-1.43	0.197492	0.409766	-5.84
263796_at	unknown protein ;supported by full-leng	AFR	AT2G24540	-1.22	-0.28	-1.43	0.197452	0.409766	-5.84
262885_at	alpha-tubulin, putative similar to alpha-t	TUA1	AT1G64740	1.14	0.19	1.43	0.19747	0.409766	-5.84
252112_at	putative protein merozoite surface antig	---	AT3G51580	1.14	0.19	1.43	0.1975	0.409766	-5.84
247439_at	plasma membrane proton ATPase-like	AHA11	AT5G62670	-1.27	-0.34	-1.43	0.197537	0.409770	-5.84
249583_at	CALMODULIN-RELATED PROTEIN 2,	TCH2	AT5G37770	1.51	0.59	1.43	0.197529	0.409770	-5.84
258743_s_a	shaggy related protein kinase, ASK-GA	ATSK12	AT3G05840 /	-1.14	-0.19	-1.43	0.19761	0.409835	-5.84
265641_at	putative RNA-binding glycine rich protei	---	AT2G27330	-1.14	-0.19	-1.43	0.197623	0.409835	-5.84
255597_at	hypothetical protein	---	AT4G01730	1.13	0.18	1.43	0.197606	0.409835	-5.84
263403_at	hypothetical protein similar to hypothetic	TX1	AT2G04040	1.82	0.86	1.43	0.197731	0.410022	-5.84
262948_at	DNA-binding protein similar to cellular n	---	AT1G75560	-1.12	-0.17	-1.43	0.197786	0.410099	-5.84
252848_at	putative protein several hypothetical pro	---	---	1.14	0.19	1.43	0.197829	0.410151	-5.84
248475_at	unknown protein	---	AT5G50880	-1.10	-0.13	-1.43	0.19786	0.410178	-5.84
251357_at	ribosomal protein S27 ; supported by cl	ARS27A	AT3G61110	-1.23	-0.30	-1.43	0.197909	0.410242	-5.84
258714_at	putative RING zinc finger protein contai	---	AT3G09770	-1.18	-0.24	-1.43	0.198025	0.410446	-5.84
250674_at	laccase-like protein laccase - Populus t	LAC13	AT5G07130	1.20	0.27	1.43	0.198055	0.410447	-5.84
247305_at	Expressed protein ; supported by full-ler	---	AT5G63905	1.37	0.45	1.43	0.198062	0.410447	-5.84
253441_at	putative protein Fidipidine, Drosophila r	---	AT4G32560	-1.12	-0.16	-1.43	0.198113	0.410516	-5.84
255811_at	heat shock protein 22.0 ; supported by c	ATHSP22.	AT4G10250	1.15	0.20	1.43	0.198191	0.410602	-5.84
264206_at	putative topoisomerase strong similarity	---	AT1G22730	1.15	0.20	1.43	0.198177	0.410602	-5.84
245832_at	chorismate synthase, putative similar to	EMB1144	AT1G48850	1.41	0.50	1.43	0.198311	0.410749	-5.84
260026_at	60S ribosomal protein L18A, putative si	RPL18AA	AT1G29970	1.12	0.17	1.43	0.198363	0.410749	-5.84
267120_at	hypothetical protein predicted by genefir	---	AT2G23530	-1.14	-0.19	-1.43	0.198388	0.410749	-5.84
259563_s_a	hypothetical protein	---	AT1G20590 /	1.10	0.14	1.43	0.198335	0.410749	-5.84
257812_at	hypothetical protein	---	AT3G25090	1.14	0.19	1.43	0.198377	0.410749	-5.84
258734_at	putative DNA-binding protein similar to M	---	AT3G05860	1.11	0.14	1.43	0.198343	0.410749	-5.84
253067_at	myb transcription factor - like protein	MYB87	AT4G37780	1.11	0.16	1.43	0.198371	0.410749	-5.84
255323_at	putative transposon protein	---	---	-1.10	-0.14	-1.43	0.198648	0.411251	-5.85
266748_at	putative squamosa-promoter binding pro	SPL1	AT2G47070	-1.20	-0.27	-1.43	0.198676	0.411272	-5.85
246182_at	beta-1,3-glucanase - like protein probab	---	AT5G20870	1.15	0.20	1.42	0.198971	0.411806	-5.85
253062_at	putative protein predicted protein, Arabi	NPY5	AT4G37590	-1.35	-0.43	-1.42	0.198988	0.411806	-5.85
260019_at	polyprotein, putative simlar to GI:46801	---	---	-1.10	-0.14	-1.42	0.198966	0.411806	-5.85
251639_at	acetylglutamate kinase-like protein acet	---	AT3G57560	1.15	0.20	1.42	0.199063	0.411830	-5.85

246600_at	putative protein disease resistance prot	SAG101	AT5G14930	1.24	0.31	1.42	0.199072	0.411830	-5.85
253522_at	predicted protein cation transport protei	---	AT4G31290	1.38	0.47	1.42	0.19902	0.411830	-5.85
250552_at	putative protein microtubule binding pro	---	AT5G07890	-1.11	-0.15	-1.42	0.199037	0.411830	-5.85
266774_at	hypothetical protein predicted by genefir	ATRBL1	AT2G29050	1.16	0.21	1.42	0.199155	0.411964	-5.85
247024_at	Expressed protein ; supported by full-ler	---	AT5G66985	1.15	0.20	1.42	0.199206	0.412032	-5.85
246180_at	putative protein predicted proteins, Arat	---	AT5G20840	-1.11	-0.15	-1.42	0.19932	0.412193	-5.85
258439_at	lipoamide dehydrogenase precursor ide	mtLPD2	AT3G17240	1.19	0.25	1.42	0.199304	0.412193	-5.85
245657_at	unknown protein similar to receptor-like	---	AT1G56720	1.35	0.44	1.42	0.199424	0.412279	-5.85
265429_at	hypothetical protein predicted by gensca	---	AT2G20710	-1.15	-0.20	-1.42	0.199452	0.412279	-5.85
264216_at	hypothetical protein similar to hypothetic	---	AT1G60180	1.10	0.14	1.42	0.199384	0.412279	-5.85
249062_at	putative protein contains similarity to unl	---	AT5G44270	1.13	0.17	1.42	0.199438	0.412279	-5.85
247421_at	SIAH1 - like protein SIAH1, Brassica na	---	AT5G62800	1.14	0.19	1.42	0.199432	0.412279	-5.85
255987_s_a	putative protein predicted proteins, Arat	---	AT5G35050	-1.10	-0.14	-1.42	0.199623	0.412595	-5.85
251408_at	palmitoyl-protein thioesterase precursor	---	AT3G60340	-1.15	-0.21	-1.42	0.199777	0.412798	-5.85
263140_at	hypothetical protein predicted by genem	---	AT1G65120	-1.09	-0.13	-1.42	0.199762	0.412798	-5.85
267410_at	hypothetical protein predicted by gensca	EDA18	AT2G34920	1.23	0.30	1.42	0.199794	0.412798	-5.85
254651_at	potassium channel - like protein kco1, A	KCO6	AT4G18160	-1.15	-0.21	-1.42	0.199751	0.412798	-5.85
251933_at	putative protein mucin MUC3, Homo sa	---	AT3G54060	1.15	0.20	1.42	0.199883	0.412939	-5.85
257011_at	predicted protein	CAX9	AT3G14070	1.27	0.35	1.42	0.199898	0.412939	-5.85
267317_at	putative proline-rich glycoprotein	---	AT2G34700	1.11	0.16	1.42	0.199958	0.413026	-5.85
245118_at	putative thioredoxin reductase The last	NTRC	AT2G41680	-1.11	-0.15	-1.42	0.199994	0.413062	-5.85
248881_at	unknown protein ;supported by full-leng	---	AT5G46020	-1.10	-0.14	-1.42	0.200022	0.413083	-5.85
256415_at	unknown protein ; supported by full-leng	---	AT3G11210	1.40	0.48	1.42	0.200064	0.413094	-5.85
246886_at	CLC-d chloride channel protein	CLC-D	AT5G26240	1.13	0.17	1.42	0.200048	0.413094	-5.85
266862_at	putative MYB family transcription factor	AtMYB104	AT2G26950	1.10	0.13	1.42	0.200087	0.413105	-5.85
250279_at	ABA-responsive protein - like ABA-resp	---	AT5G13200	1.21	0.27	1.42	0.200179	0.413258	-5.85
245576_at	hypothetical protein	TCX2	AT4G14770	1.18	0.24	1.42	0.200215	0.413295	-5.85
265043_at	Expressed protein ; supported by cDNA	ATNAP4	AT1G03900	1.13	0.17	1.42	0.200355	0.413514	-5.85
261786_at	cyclic nucleotide and calmodulin-regula	ATCNGC7	AT1G15990	1.12	0.16	1.42	0.200358	0.413514	-5.85
247857_at	peroxidase	---	AT5G58400	1.13	0.18	1.42	0.200398	0.413560	-5.85
258133_at	ethylene-responsive transcriptional coa	MBF1C	AT3G24500	-1.17	-0.23	-1.42	0.200523	0.413780	-5.85
254803_at	putative protein several hypothetical pro	---	AT4G13100	-1.19	-0.25	-1.42	0.200564	0.413803	-5.85
251000_at	putative protein	---	AT5G02650	-1.13	-0.17	-1.42	0.20057	0.413803	-5.85
259803_at	cytosolic factor, putative similar to GI:8(	PATL1	AT1G72150	-1.11	-0.16	-1.42	0.200605	0.413837	-5.85
248333_at	photoassimilate-responsive protein PAR	---	AT5G52390	1.67	0.74	1.42	0.200737	0.414034	-5.86

249435_at	putative protein tail-specific thyroid horr	---	AT5G39970	-1.10	-0.13	-1.42	0.200737	0.414034	-5.86
267189_at	putative methionine aminopeptidase ; s	MAP2A	AT2G44180	1.28	0.36	1.42	0.200842	0.414084	-5.86
254245_at	serine/threonine kinase - like protein se	---	AT4G23240	-1.11	-0.15	-1.42	0.200786	0.414084	-5.86
262771_at	hypothetical protein predicted by gensca	---	AT1G13200	1.14	0.19	1.42	0.200817	0.414084	-5.86
258435_at	unknown protein ;supported by full-leng	---	AT3G16740	-1.13	-0.18	-1.42	0.200852	0.414084	-5.86
248983_at	ras-related GTP-binding protein RHA1 (	RHA1	AT5G45130	1.11	0.15	1.42	0.200851	0.414084	-5.86
253365_at	putative protein various predicted prote	---	AT4G33170	-1.12	-0.16	-1.42	0.200884	0.414112	-5.86
249469_at	UDP-glucose dehydrogenase-like prote	---	AT5G39320	1.31	0.39	1.42	0.200933	0.414177	-5.86
245382_at	hypothetical protein	---	AT4G17800	1.12	0.16	1.42	0.201	0.414278	-5.86
251822_at	centromere protein - like centromere pr	---	AT3G55060	1.11	0.15	1.42	0.201054	0.414352	-5.86
258768_at	hypothetical protein predicted by gensca	---	AT3G10880	-1.10	-0.14	-1.42	0.201083	0.414375	-5.86
259946_at	putative TINY similar to TINY GB:CAA6	---	AT1G71450	1.09	0.12	1.42	0.201108	0.414387	-5.86
248073_at	pectate lyase	---	AT5G55720	1.12	0.16	1.42	0.201146	0.414429	-5.86
258996_at	putative ribosome recycling factor simila	---	AT3G01800	-1.16	-0.21	-1.42	0.201197	0.414471	-5.86
259933_at	Expressed protein ; supported by full-ler	---	AT1G34350	-1.16	-0.21	-1.42	0.201203	0.414471	-5.86
253724_at	Expressed protein ; supported by full-ler	LCR24	AT4G29285	1.10	0.14	1.42	0.201229	0.414487	-5.86
255629_at	stress-induced protein OZI1 precursor ;	ATOZI1	AT4G00860	1.19	0.25	1.42	0.201275	0.414545	-5.86
247817_at	Expressed protein ; supported by full-ler	---	AT5G58375	1.14	0.19	1.42	0.201418	0.414690	-5.86
259402_at	developmental protein, putative similar	VPS46.1	AT1G17730	-1.11	-0.15	-1.42	0.201391	0.414690	-5.86
254422_at	putative protein hypothetical protein YP	VPS28-1	AT4G21560	1.24	0.31	1.42	0.201398	0.414690	-5.86
265280_at	Expressed protein ; supported by full-ler	LCR5	AT2G28355	1.11	0.15	1.42	0.201412	0.414690	-5.86
267515_at	putative PCF2-like DNA binding protein	---	AT2G45680	-1.15	-0.20	-1.42	0.201483	0.414748	-5.86
247658_at	actin depolymerizing factor 3 - like prote	ADF3	AT5G59880	1.10	0.14	1.42	0.201473	0.414748	-5.86
250464_at	hypothetical protein	---	AT5G10040	1.09	0.12	1.42	0.201583	0.414916	-5.86
259893_at	putative disease resistance protein simil	AtRLP11	AT1G71390	1.13	0.18	1.42	0.201626	0.414968	-5.86
253770_at	protein kinase ADK1-like protein protein	CKL6	AT4G28540	1.10	0.14	1.41	0.201728	0.415069	-5.86
252799_at	putative protein various predicted Helic	---	---	-1.09	-0.12	-1.41	0.20173	0.415069	-5.86
260668_at	unknown protein ;supported by full-lengt	---	AT1G19530	1.65	0.73	1.41	0.201714	0.415069	-5.86
262920_at	2-dehydro-3-deoxyphosphooctonate ald	---	AT1G79500	-1.29	-0.37	-1.41	0.201878	0.415277	-5.86
252658_at	hypothetical protein	---	AT3G44800	1.15	0.21	1.41	0.201885	0.415277	-5.86
244975_at	PSII 10KDa phosphoprotein	---	---	-1.13	-0.18	-1.41	0.201855	0.415277	-5.86
249888_s_a	zinc finger protein-like ; supported by fu	---	AT5G22480 /	-1.12	-0.17	-1.41	0.201939	0.415350	-5.86
265273_at	unknown protein	---	AT2G28320	1.13	0.17	1.41	0.201992	0.415421	-5.86
261041_at	hypothetical protein contains similarity to	EER4	AT1G17440	-1.12	-0.16	-1.41	0.202075	0.415555	-5.86
250192_at	pescadillo - like protein embryonic deve	---	AT5G14520	-1.20	-0.26	-1.41	0.20222	0.415815	-5.86

260273_at	unknown protein	---	AT1G80550	-1.14	-0.19	-1.41	0.202264	0.415847	-5.86
248088_at	2-oxoglutarate dehydrogenase E2 subu	---	AT5G55070	1.18	0.23	1.41	0.202273	0.415847	-5.86
260183_at	hypothetical protein similar to DNA sequ	---	---	-1.09	-0.13	-1.41	0.20229	0.415847	-5.86
267528_at	MADS-box protein (AGL6) ; supported	AGL6	AT2G45650	1.12	0.16	1.41	0.202311	0.415853	-5.86
252785_at	putative protein AND-1 protein - Homo	---	AT3G42660	1.23	0.30	1.41	0.202367	0.415931	-5.86
259185_at	putative phosphate/phosphoenolpyruvat	PPT2	AT3G01550	1.56	0.64	1.41	0.202477	0.416118	-5.86
255745_at	hypothetical protein predicted by genem	---	AT1G32030	-1.09	-0.12	-1.41	0.202611	0.416318	-5.86
251212_at	putative protein hypothetical protein At2	---	---	-1.11	-0.15	-1.41	0.202604	0.416318	-5.86
257606_at	root hair defective 3 (RHD3) identical to	RHD3	AT3G13870	1.15	0.20	1.41	0.202647	0.416355	-5.86
263599_at	putative histidine kinase ; supported by	WOL	AT2G01830	1.19	0.26	1.41	0.202739	0.416406	-5.86
257413_at	putative RNA-binding protein contains R	---	AT1G22910	1.19	0.25	1.41	0.202695	0.416406	-5.86
246462_at	putative protein predicted protein, Dros	---	AT5G16940	-1.20	-0.26	-1.41	0.202721	0.416406	-5.86
264505_at	putative nodulin protein, N21 Similar to	---	AT1G09380	1.18	0.24	1.41	0.202744	0.416406	-5.86
256281_at	myb-family transcription factor, putative	TRFL9	AT3G12560	1.15	0.20	1.41	0.203054	0.417004	-5.87
248309_at	putative protein contains similarity to unl	---	AT5G52540	1.38	0.46	1.41	0.203156	0.417164	-5.87
250153_at	putative protein TMV response-related	WRKY72	AT5G15130	1.32	0.40	1.41	0.203168	0.417164	-5.87
256457_at	3-methyladenine DNA glycosylase, puta	---	AT1G75230	-1.25	-0.33	-1.41	0.203221	0.417235	-5.87
257182_s_a	crn-like protein similar to crn GB:CAA41	---	AT3G13210 /	-1.17	-0.22	-1.41	0.203256	0.417268	-5.87
257596_at	unknown protein	---	AT3G24760	-1.13	-0.18	-1.41	0.203287	0.417294	-5.87
255933_at	membrane protein, putative similar to m	ATRBL6	AT1G12750	-1.20	-0.26	-1.41	0.203427	0.417432	-5.87
260983_at	hypothetical protein predicted by genem	---	AT1G53560	1.23	0.30	1.41	0.203389	0.417432	-5.87
255587_at	putative inorganic phosphatase ; suppo	AtPPa5	AT4G01480	1.16	0.22	1.41	0.203405	0.417432	-5.87
247557_at	putative protein	---	AT5G61050	1.09	0.13	1.41	0.203414	0.417432	-5.87
250176_at	putative protein cytochrome P450 CYP	CYP724A1	AT5G14400	-1.16	-0.22	-1.41	0.203461	0.417455	-5.87
257254_at	salicylic acid carboxyl methyltransferas	---	AT3G21950	1.11	0.15	1.41	0.203475	0.417455	-5.87
245994_at	putative protein various predicted prote	---	---	1.13	0.18	1.41	0.203519	0.417507	-5.87
264310_at	hypothetical protein similar to hypothetic	---	AT1G62030	-1.14	-0.18	-1.41	0.203631	0.417701	-5.87
265935_at	putative senescence-associated protein	TET2	AT2G19580	-1.21	-0.27	-1.41	0.203662	0.417726	-5.87
246878_at	putative protein self-incompatibility prot	---	AT5G26060	1.15	0.21	1.41	0.203685	0.417736	-5.87
247882_at	Expressed protein ; supported by full-ler	---	AT5G57785	1.46	0.55	1.41	0.203835	0.417993	-5.87
262658_at	ribonuclease contains similarity to S-like	---	AT1G14220	1.10	0.14	1.41	0.203847	0.417993	-5.87
253985_at	caffeoyl-CoA O-methyltransferase - like	---	AT4G26220	-1.14	-0.19	-1.41	0.203874	0.418010	-5.87
250348_at	putative protein	---	AT5G11990	1.15	0.20	1.41	0.204059	0.418352	-5.87
252550_at	putative protein MtN21, Medicago trunc	---	AT3G45870	-1.14	-0.19	-1.41	0.204103	0.418361	-5.87
258928_at	unknown protein similar to hypothetical	TAF12	AT3G10070	-1.16	-0.21	-1.41	0.204137	0.418361	-5.87

253112_at	putative ascorbate peroxidase ascorbat	APX5	AT4G35970	1.19	0.25	1.41	0.204098	0.418361	-5.87
264749_at	hypothetical protein Contains similarity t	---	AT1G22830	-1.21	-0.28	-1.41	0.204136	0.418361	-5.87
248470_at	unknown protein	---	AT5G50830	1.12	0.16	1.41	0.204199	0.418452	-5.87
251887_at	FKBP12 interacting protein (FIP37) ; su	ATFIP37	AT3G54170	-1.18	-0.24	-1.41	0.204299	0.418619	-5.87
252815_at	hypothetical protein	---	---	-1.14	-0.19	-1.41	0.204378	0.418742	-5.87
260219_at	hypothetical protein contains Pfam profil	---	AT1G74630	-1.11	-0.15	-1.41	0.204436	0.418825	-5.87
252436_x_a	putative protein several hypothetical pro	---	---	1.23	0.30	1.40	0.204569	0.419012	-5.87
260802_at	exopolygalacturonase, putative similar t	---	AT1G78400	-1.09	-0.13	-1.40	0.204597	0.419012	-5.87
253433_s_a	nodulin - like protein nodulin (clone Gm	---	AT4G28365 /	1.14	0.19	1.40	0.204601	0.419012	-5.87
249478_at	germin - like protein GLP6 germin - like	---	AT5G38950	1.12	0.16	1.40	0.204598	0.419012	-5.87
248171_at	putative protein similar to unknown prote	ILR3	AT5G54680	-1.10	-0.14	-1.40	0.204665	0.419066	-5.87
249920_at	putative protein various predicted protei	---	AT5G19260	1.34	0.42	1.40	0.204659	0.419066	-5.87
247973_at	putative protein contains similarity to tra	---	AT5G56770	1.11	0.15	1.40	0.204692	0.419085	-5.87
258521_at	ribosomal protein L29, putative similar t	---	AT3G06680	-1.32	-0.40	-1.40	0.204731	0.419128	-5.87
255343_at	hypothetical protein	---	---	1.09	0.12	1.40	0.204883	0.419401	-5.87
266342_at	hypothetical protein predicted by grail	---	AT2G01540	1.17	0.23	1.40	0.204956	0.419512	-5.87
247475_at	IRE (root hair elongation)	IRE	AT5G62310	1.11	0.15	1.40	0.205065	0.419699	-5.87
260190_at	putative lipoxygenase similar to 13-lipox	---	AT1G67560	1.21	0.28	1.40	0.205091	0.419713	-5.87
258979_at	heat-shock protein (At-hsc70-3) identica	---	AT3G09440	1.25	0.32	1.40	0.205123	0.419729	-5.87
250588_at	SMC-like protein	---	AT5G07660	-1.11	-0.15	-1.40	0.205136	0.419729	-5.87
260893_at	hypothetical protein similar to hypothetic	---	AT1G29180	1.11	0.15	1.40	0.205212	0.419847	-5.87
257318_at	hypothetical protein	---	AT2G07777	-1.11	-0.15	-1.40	0.205275	0.419939	-5.87
267520_at	putative integral membrane protein	---	AT2G30460	-1.21	-0.27	-1.40	0.205295	0.419943	-5.87
257783_at	unknown protein	---	AT3G26950	-1.12	-0.16	-1.40	0.205315	0.419946	-5.88
256535_at	unknown protein	ANAC015	AT1G33280	1.15	0.20	1.40	0.205349	0.419978	-5.88
267090_at	unknown protein ; supported by full-leng	CXIP2	AT2G38270	-1.10	-0.13	-1.40	0.205443	0.420132	-5.88
250565_at	putative protein various predicted prote	E13L3	AT5G08000	1.15	0.20	1.40	0.205485	0.420144	-5.88
256683_at	unknown protein ; supported by cDNA: g	---	AT3G52220	-1.10	-0.13	-1.40	0.205472	0.420144	-5.88
247207_at	putative protein similar to unknown prote	---	AT5G65000	1.09	0.13	1.40	0.205684	0.420332	-5.88
249582_at	calmodulin 1 (CAM1) ; supported by cD	CAM1	AT5G37780	-1.15	-0.20	-1.40	0.205688	0.420332	-5.88
245219_at	viral resistance protein, putative similar	---	AT1G58807 /	-1.11	-0.15	-1.40	0.205663	0.420332	-5.88
250862_s_a	40S ribosomal protein S17 -like 40S rib	---	AT2G04390 /	-1.21	-0.28	-1.40	0.205643	0.420332	-5.88
254696_at	hypothetical protein	---	AT4G17930	1.10	0.14	1.40	0.205642	0.420332	-5.88
259957_at	putative protein kinase C-terminal regior	---	AT1G67890	-1.24	-0.31	-1.40	0.205682	0.420332	-5.88
251825_at	ABC transporter - like protein ATP-bind	---	AT3G55100	1.12	0.17	1.40	0.205709	0.420338	-5.88

263235_at	serine/threonine protein phosphatase, F	PP2A-2	AT1G10430	1.13	0.17	1.40	0.205755	0.420394	-5.88
266727_at	putative calmodulin	emb1579	AT2G03150	-1.14	-0.19	-1.40	0.205856	0.420562	-5.88
257356_s_a	hypothetical protein predicted by gensca	---	AT2G32490 /	1.13	0.17	1.40	0.205876	0.420566	-5.88
246365_at	hypothetical protein	---	---	1.12	0.17	1.40	0.205913	0.420604	-5.88
263377_at	AP2 domain transcription factor (ABI4:a	ABI4	AT2G40220	1.10	0.14	1.40	0.205938	0.420617	-5.88
258664_at	E2, ubiquitin-conjugating enzyme, putat	UBC12	AT3G08700	1.13	0.17	1.40	0.206005	0.420716	-5.88
257819_at	Expressed protein ; supported by full-ler	RALFL25	AT3G25165	1.11	0.15	1.40	0.206084	0.420839	-5.88
263203_at	hypothetical protein predicted by genem	chr31	AT1G05490	1.09	0.12	1.40	0.206116	0.420868	-5.88
254839_at	stress-induced protein sti1 -like protein	---	AT4G12400	-1.32	-0.40	-1.40	0.206179	0.420957	-5.88
253017_at	cinnamyl alcohol dehydrogenase -like p	CAD6	AT4G37970	1.10	0.14	1.40	0.206231	0.421000	-5.88
249879_at	serine/threonine protein kinase-like prot	---	AT5G23170	-1.12	-0.16	-1.40	0.206236	0.421000	-5.88
257411_s_a	hypothetical protein predicted by genem	---	AT1G61320 /	1.09	0.13	1.40	0.206299	0.421052	-5.88
254582_at	putative protein TMV resistance protein	---	AT4G19470	1.11	0.14	1.40	0.206292	0.421052	-5.88
263935_at	unknown protein	PUB23	AT2G35930	1.99	0.99	1.40	0.206353	0.421124	-5.88
252270_at	putative protein ;supported by full-lengt	---	AT3G49560	-1.14	-0.19	-1.40	0.206404	0.421192	-5.88
255409_at	NDX1 homeobox protein homolog	---	AT4G03090	-1.09	-0.12	-1.40	0.206589	0.421531	-5.88
257882_at	hypothetical protein predicted by genem	---	AT3G16930	-1.13	-0.17	-1.40	0.206782	0.421865	-5.88
246862_at	E2, ubiquitin-conjugating enzyme, putat	PEX4	AT5G25760	-1.11	-0.15	-1.40	0.20679	0.421865	-5.88
257676_at	unknown protein ;supported by full-leng	TGD2	AT3G20320	-1.12	-0.16	-1.40	0.206861	0.421973	-5.88
247500_at	putative protein B2 protein, Daucus car	---	AT5G61910	1.18	0.24	1.40	0.207086	0.422394	-5.88
252182_at	U1 snRNP 70K protein ; supported by c	U1-70K	AT3G50670	-1.11	-0.16	-1.40	0.207162	0.422511	-5.88
261550_at	hypothetical protein	---	AT1G63450	1.11	0.15	1.40	0.207232	0.422523	-5.88
256708_at	hypothetical protein predicted by genem	---	AT3G30320	1.10	0.14	1.40	0.207206	0.422523	-5.88
254098_at	superoxide dismutase (EC 1.15.1.1) (Fe	FSD1	AT4G25100	-1.15	-0.21	-1.40	0.20726	0.422523	-5.88
260300_at	gibberellin 3 beta-hydroxylase identical t	GA3OX2	AT1G80340	-1.21	-0.28	-1.40	0.207216	0.422523	-5.88
249973_at	GPAA1 - like protein glycosylphosphati	---	AT5G19130	-1.13	-0.18	-1.40	0.207258	0.422523	-5.88
264963_at	hypothetical protein predicted by genem	ABC4	AT1G60600	-1.18	-0.24	-1.40	0.207286	0.422538	-5.88
262990_at	E2, ubiquitin-conjugating enzyme, putat	MMZ1	AT1G23260	1.11	0.15	1.39	0.207377	0.422684	-5.88
254457_at	putative protein various predicted prote	---	AT4G21170	-1.16	-0.21	-1.39	0.207416	0.422726	-5.88
265567_at	unknown protein predicted by genefinde	---	AT2G05580	-1.14	-0.19	-1.39	0.207455	0.422769	-5.88
257458_at	hypothetical protein predicted by gensca	---	AT2G05400	1.09	0.13	1.39	0.207497	0.422816	-5.88
254998_at	choline kinase GmCK2p -like protein ch	---	AT4G09760	-1.23	-0.30	-1.39	0.207594	0.422976	-5.88
248674_at	non-phototropic hypocotyl-like protein	---	AT5G48800	-1.24	-0.31	-1.39	0.207643	0.423038	-5.88
259298_at	putative disease resistance protein simil	AtRLP31	AT3G05370	1.59	0.67	1.39	0.207683	0.423083	-5.89
257214_at	hypothetical protein ;supported by full-le	---	AT3G15040	1.14	0.19	1.39	0.207923	0.423458	-5.89

249048_at	auxin-repressed protein-like ;supported	---	AT5G44300	1.12	0.16	1.39	0.207921	0.423458	-5.89
246757_at	Expressed protein ; supported by full-ler	WPP3	AT5G27940	1.09	0.13	1.39	0.207892	0.423458	-5.89
262304_at	major latex protein (MLP149), putative	MLP43	AT1G70890	-1.76	-0.82	-1.39	0.207966	0.423506	-5.89
253270_at	cyclin delta-3	CYCD3;1	AT4G34160	1.18	0.24	1.39	0.208115	0.423621	-5.89
266406_at	hypothetical protein predicted by gensca	---	AT2G38570	-1.14	-0.19	-1.39	0.208101	0.423621	-5.89
265809_at	unknown protein	---	AT2G18100	1.14	0.18	1.39	0.208105	0.423621	-5.89
254781_at	putative protein putative protein F28j12	---	AT4G12840	-1.11	-0.15	-1.39	0.208064	0.423621	-5.89
256119_at	guanine nucleotide regulatory protein, p	---	AT1G18070	-1.12	-0.17	-1.39	0.208114	0.423621	-5.89
245955_at	hypothetical protein	BGLU24	AT5G28510	1.11	0.15	1.39	0.208161	0.423678	-5.89
264968_at	stress related protein, putative similar t	---	AT1G67360	1.30	0.38	1.39	0.208256	0.423833	-5.89
265434_at	predicted protein	---	AT2G20805	1.10	0.13	1.39	0.208397	0.424081	-5.89
248527_at	putative protein contains similarity to AT	---	AT5G50740	-1.12	-0.17	-1.39	0.208449	0.424150	-5.89
253242_at	isoflavone reductase - like protein isofla	CIB1	AT4G34530 /	-1.22	-0.29	-1.39	0.208467	0.424150	-5.89
245905_at	putative protein predicted proteins, Ara	---	AT5G11090	1.12	0.17	1.39	0.208518	0.424214	-5.89
258389_at	hypothetical protein predicted by gensca	SDE5	AT3G15390	1.15	0.20	1.39	0.208626	0.424359	-5.89
246898_at	putative protein	---	AT5G25580	-1.09	-0.13	-1.39	0.208624	0.424359	-5.89
260350_at	Eukaryotic initiation factor 5A , putative	ELF5A-3	AT1G69410	1.17	0.23	1.39	0.208649	0.424367	-5.89
246819_at	WD-repeat protein - like WD-repeat pro	---	AT5G26900	-1.12	-0.17	-1.39	0.208693	0.424420	-5.89
255646_at	hypothetical protein	---	AT4G00890	1.12	0.17	1.39	0.208731	0.424459	-5.89
257534_at	hypothetical protein predicted by gensca	---	AT3G09670	1.11	0.15	1.39	0.208812	0.424586	-5.89
248584_at	putative protein similar to unknown prot	---	AT5G49960	-1.19	-0.25	-1.39	0.208851	0.424626	-5.89
263493_at	putative ATP-dependent RNA helicase	---	AT2G42520	1.17	0.23	1.39	0.208908	0.424682	-5.89
247837_at	N-hydroxycinnamoyl/benzoyltransferase	---	AT5G57840	-1.17	-0.22	-1.39	0.208915	0.424682	-5.89
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=gb:X17	---	---	-1.41	-0.49	-1.39	0.209038	0.424856	-5.89
249731_at	RNA-binding protein-like	CID13	AT5G24440	1.15	0.21	1.39	0.209021	0.424856	-5.89
248603_at	WD-40 repeat protein-like	---	AT5G49430	-1.10	-0.14	-1.39	0.209175	0.425059	-5.89
262251_at	hypothetical protein predicted by genem	---	AT1G53760	1.22	0.29	1.39	0.20916	0.425059	-5.89
254450_at	putative protein prolamin box binding fa	---	AT4G21080	1.12	0.16	1.39	0.209215	0.425101	-5.89
262257_at	hypothetical protein predicted by genem	---	AT1G53860	1.12	0.17	1.39	0.209255	0.425146	-5.89
249322_at	protein import receptor TOM20, mitoch	TOM20-4	AT5G40930	-1.10	-0.14	-1.39	0.209296	0.425152	-5.89
258855_at	unknown protein	---	AT3G02070	1.21	0.27	1.39	0.20928	0.425152	-5.89
250686_at	gamma-tubulin interacting protein-like	SPC98	AT5G06680	-1.18	-0.24	-1.39	0.209314	0.425152	-5.89
252067_at	protein phosphatase 2C -like protein pr	---	AT3G51370	-1.13	-0.18	-1.39	0.209366	0.425220	-5.89
255098_at	hypothetical protein	---	AT4G08640	1.09	0.13	1.39	0.209408	0.425266	-5.89
254281_at	predicted protein ileal sodium-depende	---	AT4G22840	-1.41	-0.50	-1.39	0.209525	0.425466	-5.89

246501_at	putative protein KIAA1012 protein - Hor	---	AT5G16280	-1.11	-0.16	-1.39	0.209603	0.425470	-5.89
257741_at	hypothetical protein predicted by genem	---	AT3G27340	-1.17	-0.23	-1.39	0.209613	0.425470	-5.89
254270_at	gamma-glutamylcysteine synthetase ; s	GSH1	AT4G23100	1.33	0.41	1.39	0.209615	0.425470	-5.89
253156_at	putative protein mRNA for KIAA0174 ge	---	AT4G35730	1.13	0.18	1.39	0.209597	0.425470	-5.89
256142_at	hypothetical protein predicted by genem	---	AT1G48790	-1.12	-0.17	-1.39	0.20962	0.425470	-5.89
248559_at	unknown protein	---	AT5G50010 /	1.12	0.16	1.39	0.20973	0.425617	-5.89
259400_at	receptor-like protein kinase, putative sir	---	AT1G17750	1.64	0.71	1.39	0.20972	0.425617	-5.89
250159_at	40S ribosomal protein - like 40S riboso	---	AT5G15200	-1.18	-0.24	-1.39	0.209856	0.425650	-5.89
247144_at	DOF zinc finger protein-like	---	AT5G65590	1.18	0.24	1.39	0.209788	0.425650	-5.89
247812_at	peroxidase ;supported by full-length cDN	---	AT5G58390	1.40	0.49	1.39	0.209858	0.425650	-5.89
257653_at	hypothetical protein	---	AT3G13225	-1.14	-0.19	-1.39	0.209824	0.425650	-5.89
255622_at	putative flavonol glucosyltransferase sir	GT72B1	AT4G01070	1.15	0.21	1.39	0.209797	0.425650	-5.89
245271_at	transcription factor like protein ; support	---	AT4G16430	-1.10	-0.14	-1.39	0.209846	0.425650	-5.89
258484_at	sterol-C5-desaturase identical to GB:AA	STE1	AT3G02580	-1.12	-0.16	-1.39	0.210071	0.426044	-5.90
246932_at	ethylene-responsive element - like prot	---	AT5G25190	1.30	0.38	1.39	0.210193	0.426253	-5.90
266922_s_a	SKP1/ASK1-related, putative similar to	ASK20	AT2G45950 /	-1.21	-0.28	-1.38	0.210312	0.426456	-5.90
261147_at	unknown protein ;supported by full-lengt	---	AT1G19690	-1.21	-0.28	-1.38	0.210487	0.426774	-5.90
251865_at	protein phosphatase 2A regulatory subu	---	AT3G54930	-1.10	-0.14	-1.38	0.21056	0.426884	-5.90
263848_at	putative reverse transcriptase	---	---	1.13	0.18	1.38	0.210714	0.427159	-5.90
258291_at	putative protein kinase similar to protein	---	AT3G23310	-1.13	-0.18	-1.38	0.210832	0.427245	-5.90
251128_at	putative protein crp1 protein, Zea mays	---	AT5G01110	-1.09	-0.13	-1.38	0.210795	0.427245	-5.90
260132_s_a	hypothetical protein	---	AT1G66320 /	1.09	0.13	1.38	0.210827	0.427245	-5.90
265639_at	putative reverse transcriptase	---	---	1.11	0.15	1.38	0.210809	0.427245	-5.90
251153_at	putative protein predicted protein, Arabi	NPL41	AT3G63000	1.14	0.19	1.38	0.210995	0.427538	-5.90
250866_at	Expressed protein ; supported by full-ler	---	AT5G03905	1.12	0.17	1.38	0.211063	0.427601	-5.90
259691_at	hypothetical protein predicted by genem	---	AT1G63200	1.17	0.23	1.38	0.211058	0.427601	-5.90
256938_at	LEA protein, putative similar to LEA pro	ATECP31	AT3G22500	1.13	0.17	1.38	0.211309	0.427946	-5.90
263951_at	putative harpin-induced protein ;suppor	NHL12	AT2G35960	-1.46	-0.54	-1.38	0.211282	0.427946	-5.90
248286_at	putative protein similar to unknown prote	---	AT5G52870	1.29	0.37	1.38	0.211272	0.427946	-5.90
253415_at	putative protein peptidyl-prolyl cis-trans	---	AT4G33060	-1.18	-0.24	-1.38	0.211298	0.427946	-5.90
259406_at	hypothetical protein predicted by genem	---	AT1G17690	-1.10	-0.14	-1.38	0.211409	0.428072	-5.90
248813_at	Expressed protein ; supported by full-ler	VAM3	AT5G46860	-1.17	-0.23	-1.38	0.211395	0.428072	-5.90
245092_at	putative TGACG-sequence-specific bZIP	BZIP17	AT2G40950	-1.14	-0.19	-1.38	0.21149	0.428088	-5.90
260832_at	unknown protein ; supported by cDNA: g	GAUT6	AT1G06780	-1.13	-0.18	-1.38	0.211516	0.428088	-5.90
246761_at	embryonic abundant protein - like embr	---	AT5G27980	1.10	0.14	1.38	0.211493	0.428088	-5.90

267502_at	putative cytochrome P450	CYP76C4	AT2G45550	1.10	0.14	1.38	0.211537	0.428088	-5.90
261515_at	cleavage stimulation factor, putative sin	---	AT1G71800	1.10	0.14	1.38	0.211492	0.428088	-5.90
247561_at	putative protein	---	AT5G61110	1.11	0.15	1.38	0.211474	0.428088	-5.90
247171_at	unknown protein	---	AT5G65540	-1.10	-0.14	-1.38	0.211548	0.428088	-5.90
264038_at	putative ubiquinone biosynthesis protein	---	AT2G03690	1.15	0.21	1.38	0.211586	0.428127	-5.90
247640_at	putative protein various predicted prote	---	AT5G60610	-1.12	-0.16	-1.38	0.211613	0.428144	-5.90
264709_at	putative DNA-binding protein, Myb Iden	ATCDC5	AT1G09770	-1.20	-0.26	-1.38	0.211711	0.428178	-5.90
250903_at	putative protein coil protein PO22, micr	---	AT5G03600	1.16	0.21	1.38	0.211722	0.428178	-5.90
260584_at	putative beta-1,3-glucanase, C terminal	---	AT2G43660	1.10	0.14	1.38	0.211724	0.428178	-5.90
262145_at	unknown protein contains similarity to W	---	AT1G52730	-1.14	-0.19	-1.38	0.211702	0.428178	-5.90
265218_at	putative transcription factor	GTF2H2	AT1G05055	-1.10	-0.13	-1.38	0.211654	0.428178	-5.90
247140_at	putative protein similar to unknown prote	---	AT5G66250	1.11	0.15	1.38	0.21181	0.428302	-5.90
251890_at	SCARECROW1 ; supported by cDNA:	SCR	AT3G54220	-1.12	-0.16	-1.38	0.211841	0.428302	-5.90
265601_at	hypothetical protein predicted by gensca	---	AT2G14390	1.12	0.16	1.38	0.211839	0.428302	-5.90
246108_at	putative protein retinal glutamic acid-ric	---	AT5G28630	1.29	0.37	1.38	0.21203	0.428644	-5.90
261752_at	putative AMP-binding protein contains P	---	AT1G76290	1.12	0.16	1.38	0.2121	0.428713	-5.90
252963_at	putative protein	---	AT4G38820	1.10	0.14	1.38	0.212101	0.428713	-5.90
267404_at	hypothetical protein predicted by genefir	atnudt22	AT2G33980	-1.12	-0.16	-1.38	0.212154	0.428782	-5.90
256451_s_a	unknown protein	---	AT1G75170 /	1.36	0.44	1.38	0.212193	0.428823	-5.90
255433_at	putative xyloglucan endotransglycosylas	XTH9	AT4G03210	-1.29	-0.37	-1.38	0.212336	0.428913	-5.90
267346_at	coronatine-insensitive 1 (COI1), AtFBL2	COI1	AT2G39940	-1.16	-0.21	-1.38	0.212334	0.428913	-5.90
265346_at	hypothetical protein	---	---	1.11	0.15	1.38	0.212348	0.428913	-5.90
252917_at	putative zinc finger protein zinc finger p	---	AT4G38960	1.16	0.22	1.38	0.212345	0.428913	-5.90
252630_at	putative protein	---	AT3G44980	-1.10	-0.14	-1.38	0.212351	0.428913	-5.90
267597_at	putative leucine-rich repeat disease resi	AtRLP24	AT2G33020	1.23	0.30	1.38	0.212258	0.428913	-5.90
264993_at	glyoxal oxidase (glx1), putative similar t	---	AT1G67290	1.21	0.28	1.38	0.2124	0.428975	-5.90
247656_at	actin depolymerizing factor 4 - like prote	ADF4	AT5G59890	1.15	0.20	1.38	0.212522	0.429183	-5.91
249949_at	SAE1-S9-protein - like SAE1-S9-protein	---	AT5G18880	-1.11	-0.16	-1.38	0.212575	0.429253	-5.91
253158_at	putative protein protein kinase 6, Glycin	---	AT4G35780	1.15	0.20	1.38	0.212598	0.429261	-5.91
249186_at	CHP-rich zinc finger protein-like	---	AT5G43040	1.11	0.15	1.38	0.212679	0.429386	-5.91
264874_at	unknown protein Location of EST gb|Z2	---	AT1G24240	-1.10	-0.14	-1.38	0.212719	0.429429	-5.91
264848_at	unknown protein ;supported by full-leng	---	AT2G17350	-1.09	-0.13	-1.38	0.212783	0.429521	-5.91
257691_at	hypothetical protein predicted by genem	FLA14	AT3G12660	1.17	0.23	1.38	0.212847	0.429601	-5.91
266039_s_a	hypothetical protein	---	AT2G07739	-1.14	-0.18	-1.38	0.21286	0.429601	-5.91
263492_at	putative seed maturation protein	---	AT2G42560	-1.12	-0.17	-1.38	0.21288	0.429603	-5.91

264895_at	putative 10kd chaperonin strongly simila	---	AT1G23100	-1.31	-0.39	-1.38	0.212906	0.429617	-5.91
261704_at	hypothetical protein identical to hypothe	---	AT1G32600	-1.10	-0.14	-1.38	0.213009	0.429787	-5.91
248494_at	putative protein contains similarity to oxi	AtHSD6	AT5G50770	-1.12	-0.17	-1.38	0.213106	0.429869	-5.91
245001_at	PSII low MW protein	---	---	-1.13	-0.17	-1.38	0.213098	0.429869	-5.91
245298_at	hypothetical protein ; supported by cDN	---	AT4G15010	1.11	0.15	1.38	0.213069	0.429869	-5.91
261209_at	unknown protein ; supported by cDNA: g	---	AT1G12810	1.16	0.21	1.37	0.213197	0.430013	-5.91
261136_at	ribokinase, putative similar to GB:AAD0	---	AT1G19600	-1.10	-0.14	-1.37	0.213307	0.430178	-5.91
251399_at	putative protein	---	AT3G60590	-1.14	-0.19	-1.37	0.213316	0.430178	-5.91
253205_at	putative cyclase associated protein CA	ATCAP1	AT4G34490	1.22	0.29	1.37	0.213409	0.430251	-5.91
247967_at	putative protein similar to unknown prote	anac099	AT5G56620	1.09	0.13	1.37	0.213391	0.430251	-5.91
246934_at	putative protein several hypothetical pro	---	AT5G25290	-1.14	-0.19	-1.37	0.213389	0.430251	-5.91
263242_at	unknown protein	---	AT2G31400	1.12	0.17	1.37	0.213451	0.430269	-5.91
256454_at	NADPH oxidoreductase, putative simila	---	AT1G75280	-1.35	-0.44	-1.37	0.213455	0.430269	-5.91
247318_at	3(2),5-bisphosphate nucleotidase ;sup	---	AT5G63990	1.33	0.41	1.37	0.213497	0.430314	-5.91
246617_at	GSH-dependent dehydroascorbate redu	---	AT5G36270	-1.12	-0.16	-1.37	0.213532	0.430346	-5.91
248048_at	nicotianamine synthase	NAS2	AT5G56080	-1.12	-0.16	-1.37	0.213678	0.430603	-5.91
264095_at	mercaptopyruvate sulfurtransferase (Ms	MST1	AT1G79230	-1.10	-0.14	-1.37	0.213732	0.430674	-5.91
248583_at	putative protein strong similarity to unkn	emb1441	AT5G49930	-1.14	-0.18	-1.37	0.213754	0.430679	-5.91
245339_at	hypothetical protein ;supported by full-le	COBL7	AT4G16120	1.23	0.29	1.37	0.213806	0.430748	-5.91
258709_at	putative 60S ribosomal protein L35 simi	---	AT3G09500	-1.25	-0.32	-1.37	0.213945	0.430950	-5.91
258309_at	putative transposase related protein sim	---	---	1.10	0.14	1.37	0.213935	0.430950	-5.91
251333_at	putative protein putative protein F26O1	---	AT3G61690	-1.09	-0.12	-1.37	0.213965	0.430952	-5.91
266320_at	hypothetical protein predicted by gensca	---	AT2G46640	-1.20	-0.27	-1.37	0.213993	0.430967	-5.91
257120_at	protein kinase, putative contains Pfam	---	AT3G20200	-1.12	-0.16	-1.37	0.21401	0.430967	-5.91
255112_at	casein kinase I - Arabidopsis thaliana,P	---	AT4G08800	-1.12	-0.16	-1.37	0.21403	0.430969	-5.91
267295_at	pregeranylgeranyl pyrophosphate synth	GGPS2	AT2G23800	1.11	0.15	1.37	0.214107	0.431087	-5.91
259322_at	unknown protein	---	AT3G05270	-1.15	-0.20	-1.37	0.214127	0.431089	-5.91
251276_at	putative protein hypothetical protein T1	SDG14	AT3G61740	-1.10	-0.14	-1.37	0.214182	0.431117	-5.91
250092_at	putative protein	---	AT5G17360	-1.09	-0.13	-1.37	0.214198	0.431117	-5.91
249072_at	putative protein similar to unknown prote	---	AT5G44060	1.43	0.51	1.37	0.21419	0.431117	-5.91
264513_at	putative glucose-6-phosphate dehydrog	G6PD4	AT1G09420	-1.12	-0.16	-1.37	0.214227	0.431139	-5.91
254238_at	putative protein probable membrane pr	---	AT4G23540	-1.15	-0.20	-1.37	0.214292	0.431230	-5.91
261872_s_a	hypthetical protein contains similarity to	---	AT1G11520 /	-1.12	-0.17	-1.37	0.214479	0.431404	-5.91
260289_at	CAD ATPase (AAA1) identical to CAD A	ERH3	AT1G80350	-1.09	-0.12	-1.37	0.214419	0.431404	-5.91
265438_at	hypothetical protein	---	AT2G20970	1.09	0.13	1.37	0.214529	0.431404	-5.91

261932_at	hypothetical protein predicted by genem	---	AT1G22420	1.10	0.13	1.37	0.214447	0.431404	-5.91
251505_at	putative protein polyamine oxidase (EC	CPuORF1	AT3G59050 /	-1.20	-0.26	-1.37	0.214489	0.431404	-5.91
259501_at	unknown protein ; supported by cDNA: g	TPL	AT1G15750	1.14	0.19	1.37	0.214513	0.431404	-5.91
249909_s_a	alpha-adaptin	---	AT5G22770 /	1.14	0.19	1.37	0.214449	0.431404	-5.91
252659_at	putative protein	---	AT3G44430	-1.13	-0.18	-1.37	0.214508	0.431404	-5.91
258412_at	unknown protein similar to pop3 peptide	HS1	AT3G17210	-1.12	-0.17	-1.37	0.214563	0.431434	-5.91
263959_at	hypothetical protein predicted by gensca	---	AT2G36210	1.10	0.14	1.37	0.214722	0.431715	-5.91
266243_at	hypothetical protein predicted by gensca	---	AT2G27750	1.10	0.14	1.37	0.214818	0.431870	-5.91
257119_at	receptor kinase protein, putative similar	---	AT3G20190	1.11	0.15	1.37	0.214945	0.432088	-5.92
266112_x_a	hypothetical protein predicted by gensca	---	---	1.13	0.18	1.37	0.215037	0.432143	-5.92
250730_at	C3HC4-type RING zinc finger protein-lik	---	AT5G06490	1.12	0.16	1.37	0.215048	0.432143	-5.92
266768_s_a	ubiquitin extension protein (UBQ6) ident	UBQ6	AT2G47110 /	-1.18	-0.24	-1.37	0.214995	0.432143	-5.92
263416_at	hypothetical protein contains protein kin	---	AT2G17170	1.12	0.16	1.37	0.215024	0.432143	-5.92
255564_s_a	hypothetical protein T15B16.8	RGXT2	AT4G01750 /	1.12	0.17	1.37	0.215134	0.432238	-5.92
255860_at	putative protein heparanase, Homo sap	AtGUS3	AT5G34940	2.19	1.13	1.37	0.215123	0.432238	-5.92
254541_at	putative LTR retrotransposon Brassica	---	---	1.09	0.13	1.37	0.215158	0.432249	-5.92
261153_at	unknown protein ;supported by full-lengt	---	AT1G04850	1.11	0.16	1.37	0.215262	0.432420	-5.92
253267_at	putative protein TEB4 protein, Homo sa	---	AT4G34100	-1.13	-0.18	-1.37	0.215321	0.432500	-5.92
264277_at	polygalacturonase isoenzyme 1 beta su	---	AT1G60390	1.12	0.16	1.37	0.215422	0.432627	-5.92
266460_at	unknown protein ; supported by cDNA: g	AGP26	AT2G47930	2.11	1.07	1.37	0.215416	0.432627	-5.92
261465_at	unknown protein	---	AT1G07705	-1.10	-0.14	-1.37	0.215503	0.432752	-5.92
255515_at	putative pistil-specific protein similar to	---	AT4G02250	-1.10	-0.14	-1.37	0.21556	0.432827	-5.92
263876_at	putative RAS superfamily GTP-binding p	ATRAB7A	AT2G21880	1.17	0.22	1.37	0.215631	0.432895	-5.92
263697_at	hypothetical protein contains similarity to	---	AT1G31080	-1.14	-0.19	-1.37	0.215629	0.432895	-5.92
262477_at	hypothetical protein contains similarity to	---	AT1G11220	1.18	0.24	1.37	0.215704	0.433003	-5.92
266743_at	ribonuclease, RNS1 identical to ribonuc	RNS1	AT2G02990 /	1.73	0.79	1.37	0.215793	0.433143	-5.92
245303_at	hypothetical protein ; supported by full-le	---	AT4G17010	-1.10	-0.14	-1.37	0.215831	0.433179	-5.92
253970_at	putative uracil phosphoribosyl transfera	---	AT4G26510	-1.12	-0.16	-1.37	0.215849	0.433179	-5.92
261604_at	unknown protein contains similarity to fo	---	AT1G49590	-1.13	-0.18	-1.37	0.215879	0.433202	-5.92
249250_at	arm repeat containing protein	---	AT5G42340	1.10	0.14	1.37	0.215922	0.433249	-5.92
253590_at	putative protein various predicted protei	HHP2	AT4G30850	1.16	0.22	1.37	0.215984	0.433335	-5.92
250645_at	putative protein strong similarity to unkn	---	AT5G06700	-1.22	-0.29	-1.37	0.216037	0.433404	-5.92
261611_at	hypothetical protein predicted by genem	---	AT1G49730	1.23	0.30	1.36	0.216175	0.433528	-5.92
259006_at	putative 60S acidic ribosomal protein P0	---	AT3G09200	-1.20	-0.27	-1.36	0.216154	0.433528	-5.92
245951_at	aspartate aminotransferase Asp2 ; supp	ASP2	AT5G19550	1.21	0.28	1.36	0.216135	0.433528	-5.92

249189_at	putative protein similar to unknown prote	AtHB27	AT5G42780	1.17	0.23	1.36	0.216166	0.433528	-5.92
260740_at	thioredoxin, putative contains Pfam pro	ATQSOX1	AT1G15020	1.09	0.13	1.36	0.216235	0.433610	-5.92
253340_s_a	WD-repeat protein -like protein WD-rep	CDC20.2	AT4G33260 /	-1.11	-0.15	-1.36	0.216325	0.433678	-5.92
247128_at	atfp6-like protein	---	AT5G66110	-1.17	-0.22	-1.36	0.216315	0.433678	-5.92
252814_at	putative protein several hypothetical pro	---	---	1.12	0.17	1.36	0.216291	0.433678	-5.92
266899_at	hypothetical protein predicted by genefir	---	AT2G34620	-1.32	-0.40	-1.36	0.216376	0.433740	-5.92
258530_at	hypothetical protein predicted by genem	---	AT3G06840	1.13	0.18	1.36	0.21644	0.433830	-5.92
265400_at	unknown protein ;supported by full-leng	---	AT2G10940	4.66	2.22	1.36	0.216461	0.433835	-5.92
258762_at	hypothetical protein	---	AT3G10750	1.15	0.20	1.36	0.216592	0.434059	-5.92
258773_at	hypothetical protein predicted by gensca	---	AT3G10730	1.09	0.12	1.36	0.216756	0.434339	-5.92
259199_at	putative signal peptidase similar to MITC	---	AT3G08980	-1.10	-0.14	-1.36	0.216769	0.434339	-5.92
247030_at	putative protein similar to unknown prote	---	AT5G67210	1.09	0.13	1.36	0.21679	0.434342	-5.92
256105_at	hypothetical protein predicted by genem	LSH8	AT1G16910	-1.13	-0.18	-1.36	0.216844	0.434401	-5.92
259065_at	unknown protein similar to putative gluta	GLR1.4	AT3G07520	1.21	0.28	1.36	0.216858	0.434401	-5.92
263547_at	hypothetical protein predicted by genefir	---	AT2G21680	-1.13	-0.18	-1.36	0.217024	0.434628	-5.92
256582_at	unknown protein	---	AT3G28840	1.11	0.15	1.36	0.217006	0.434628	-5.92
264249_at	vacuolar-type H+-translocating inorganic	AVP2	AT1G78920	1.13	0.17	1.36	0.217028	0.434628	-5.92
258576_at	putative 40S ribosomal protein S16 simi	---	AT3G04230	-1.16	-0.22	-1.36	0.217132	0.434760	-5.92
246321_at	unknown protein	---	AT1G16640	1.12	0.17	1.36	0.217132	0.434760	-5.92
246669_at	galactinol synthase, putative	---	AT5G30500	1.15	0.20	1.36	0.217182	0.434821	-5.92
250593_at	putative protein similar to unknown prote	---	AT5G07740	1.10	0.14	1.36	0.217275	0.434969	-5.92
264117_at	hypothetical protein predicted by genefir	---	AT2G31210	1.10	0.14	1.36	0.217347	0.435076	-5.93
264628_at	hypothetical protein contains similarity to	---	AT1G65540	1.09	0.12	1.36	0.217511	0.435365	-5.93
250384_at	putative protein various predicted prote	---	AT5G11500	1.11	0.15	1.36	0.217604	0.435514	-5.93
264937_at	hypothetical protein contains similarity to	SCPL32	AT1G61130	1.11	0.15	1.36	0.217643	0.435522	-5.93
262928_at	hypothetical protein	---	AT1G65760	1.13	0.18	1.36	0.217646	0.435522	-5.93
245488_at	peroxidase like protein	---	AT4G16270	1.11	0.15	1.36	0.217713	0.435616	-5.93
264931_at	polygalacturonase, putative similar to p	---	AT1G60590	1.12	0.16	1.36	0.217742	0.435636	-5.93
250417_at	putative protein predicted proteins, Arat	---	AT5G11230	1.14	0.19	1.36	0.217845	0.435804	-5.93
263567_at	hypothetical protein predicted by genefir	---	AT2G15440	-1.13	-0.18	-1.36	0.217866	0.435807	-5.93
259182_at	hypothetical protein predicted by genefir	---	AT3G01750	-1.21	-0.28	-1.36	0.217894	0.435826	-5.93
246565_at	biotin carboxyl carrier protein precursor	BCCP2	AT5G15530	1.12	0.16	1.36	0.217993	0.435987	-5.93
265605_at	putative cellulose synthase catalytic sub	CESA10	AT2G25540	1.09	0.12	1.36	0.218034	0.436029	-5.93
264703_at	serine threonine protein phosphatase (ty	PP2A	AT1G69960	1.10	0.13	1.36	0.218083	0.436041	-5.93
255945_at	putative protein	---	AT5G28610	1.14	0.20	1.36	0.218097	0.436041	-5.93

266683_at	hypothetical protein predicted by gensca	GC1	AT2G19950	1.11	0.15	1.36	0.218075	0.436041	-5.93
249302_at	putative protein similar to unknown prote	---	AT5G41450	1.14	0.19	1.36	0.218172	0.436153	-5.93
260178_at	hypothetical protein similar to unknown	---	AT1G70720	1.12	0.16	1.36	0.218239	0.436249	-5.93
246914_at	putative protein various predicted prote	---	AT5G25860	1.15	0.20	1.36	0.218281	0.436277	-5.93
248736_at	terpene synthase	---	AT5G48110	1.11	0.15	1.36	0.218292	0.436277	-5.93
266798_at	putative embryo-abundant protein conta	AtbZIP6	AT2G22850	-1.24	-0.31	-1.36	0.218311	0.436277	-5.93
255536_at	Expressed protein ; supported by full-ler	---	AT4G01575	1.20	0.26	1.36	0.218332	0.436281	-5.93
261944_at	unknown protein	---	AT1G64650	-1.16	-0.21	-1.36	0.218391	0.436361	-5.93
248686_at	33 kDa secretory protein-like ; supporte	---	AT5G48540	1.46	0.55	1.36	0.218413	0.436367	-5.93
262254_at	unknown protein similar to GDSL-motif l	GLIP5	AT1G53920	1.25	0.33	1.36	0.218564	0.436397	-5.93
258296_at	putative ribosomal protein similar to ribo	---	AT3G23390	-1.27	-0.35	-1.36	0.218548	0.436397	-5.93
249774_at	squalene monooxygenase	SQP1	AT5G24150	-1.21	-0.28	-1.36	0.21862	0.436397	-5.93
261271_at	Expressed protein ; supported by full-ler	---	AT1G26795	1.12	0.17	1.36	0.218602	0.436397	-5.93
249463_s_a	putative protein predicted proteins, Arat	anac064	AT3G56530 /	1.12	0.16	1.36	0.218574	0.436397	-5.93
266817_at	hypothetical protein similar to hypothetic	HUB1	AT2G44950	-1.16	-0.21	-1.36	0.218499	0.436397	-5.93
263305_at	unknown protein ;supported by full-leng	BPC1	AT2G01930	-1.17	-0.22	-1.36	0.218455	0.436397	-5.93
245143_at	unknown protein ;supported by full-leng	ZPR1	AT2G45450	1.26	0.33	1.36	0.218613	0.436397	-5.93
245322_at	Expressed protein ; supported by full-ler	---	AT4G14815	1.24	0.31	1.36	0.21861	0.436397	-5.93
252706_at	putative protein predicted proteins, Arat	---	---	1.09	0.12	1.36	0.21853	0.436397	-5.93
253303_at	putative protein ; supported by full-lengt	---	AT4G33780	1.12	0.16	1.36	0.218683	0.436472	-5.93
265787_at	Mutator-like transposase similar to MUF	---	---	1.15	0.21	1.36	0.218772	0.436472	-5.93
259654_at	hypothetical protein predicted by genem	---	AT1G55220	1.12	0.17	1.36	0.21877	0.436472	-5.93
263307_at	hypothetical protein similar to myosin-lik	---	---	-1.12	-0.17	-1.36	0.218766	0.436472	-5.93
266646_at	unknown protein ;supported by full-leng	ATPH1	AT2G29700	1.12	0.17	1.36	0.218741	0.436472	-5.93
263388_at	En/Spm-like transposon protein related	---	---	1.14	0.18	1.36	0.218746	0.436472	-5.93
264701_at	hypothetical protein similar to hypothetic	---	AT1G70160	-1.12	-0.17	-1.36	0.218829	0.436509	-5.93
266219_at	putative para-aminobenzoate synthase	emb1997	AT2G28880	1.11	0.15	1.36	0.218828	0.436509	-5.93
262572_at	unknown protein Contains a PF|00175 (	---	AT1G15140	-1.15	-0.20	-1.36	0.218848	0.436510	-5.93
255497_at	hypothetical protein similar to A. thalian	UNE12	AT4G02590	-1.11	-0.15	-1.36	0.218873	0.436522	-5.93
252979_at	Expressed protein ; supported by full-ler	---	AT4G38225	-1.19	-0.25	-1.36	0.218933	0.436603	-5.93
251385_at	putative protein various predicted prote	---	AT3G60790	1.12	0.16	1.36	0.218986	0.436670	-5.93
245045_at	unknown protein similar to glycoprotein	---	AT2G26590	1.10	0.13	1.36	0.219035	0.436692	-5.93
261995_at	unknown protein similar to N-terminal ha	---	AT1G33850 /	-1.09	-0.12	-1.36	0.219025	0.436692	-5.93
260729_at	regulatory protein, putative contains Pfa	KU80	AT1G48050	-1.09	-0.13	-1.36	0.219098	0.436740	-5.93
250120_at	putative protein similar to unknown prote	RIC4	AT5G16490	1.19	0.25	1.36	0.219094	0.436740	-5.93

260813_at	VirE2-interacting protein VIP1 identical t	VIP1	AT1G43700	-1.17	-0.22	-1.35	0.219142	0.436790	-5.93
256392_at	putative glycosyl transferase contains P	GATL4	AT3G06260	1.12	0.17	1.35	0.219161	0.436790	-5.93
250311_at	unknown protein	---	AT5G12240	1.09	0.13	1.35	0.21923	0.436889	-5.93
264011_at	unknown protein	---	AT2G21090	-1.12	-0.17	-1.35	0.219341	0.437073	-5.93
266057_at	putative methionyl-tRNA synthetase ; s	---	AT2G40660	-1.10	-0.14	-1.35	0.219407	0.437166	-5.93
248708_at	putative protein contains similarity to un	---	AT5G48560	1.27	0.34	1.35	0.219433	0.437176	-5.93
252322_at	putative protein putative zinc-finger pro	---	AT3G48550	-1.26	-0.34	-1.35	0.21949	0.437176	-5.93
248592_at	unknown protein ;supported by full-leng	---	AT5G49280	1.31	0.39	1.35	0.219464	0.437176	-5.93
255740_at	wall-associated kinase, putative similar	---	AT1G25390	1.33	0.41	1.35	0.219508	0.437176	-5.93
254330_at	predicted protein predicted gene F5I14.	LBD32	AT4G22700	1.11	0.14	1.35	0.219476	0.437176	-5.93
267213_at	60S ribosomal protein L7 ;supported by	---	AT2G44120	-1.23	-0.30	-1.35	0.219562	0.437206	-5.93
248160_at	putative protein similar to unknown prote	---	AT5G54470	-1.17	-0.22	-1.35	0.219555	0.437206	-5.93
261347_at	unknown protein	ELF7	AT1G79730	-1.13	-0.17	-1.35	0.219693	0.437429	-5.93
267359_at	hypothetical protein predicted by genefi	---	AT2G40020	-1.16	-0.21	-1.35	0.219739	0.437483	-5.93
248692_s_a	hypothetical protein	---	AT4G15070 /	1.12	0.16	1.35	0.21977	0.437506	-5.93
246848_at	putative protein	---	AT5G26840	-1.12	-0.16	-1.35	0.219791	0.437511	-5.93
263149_at	unknown protein	---	AT1G53970	1.11	0.15	1.35	0.219833	0.437557	-5.94
247133_at	chalcone isomerase-like protein	---	AT5G66220	1.22	0.29	1.35	0.219867	0.437585	-5.94
254376_at	putative protein ; supported by cDNA: g	TOM1	AT4G21790	1.09	0.12	1.35	0.219973	0.437758	-5.94
247075_at	putative protein contains similarity to AT	PLP3b	AT5G66410	1.13	0.18	1.35	0.220016	0.437805	-5.94
253430_at	putative protein	---	AT4G32430	-1.13	-0.17	-1.35	0.220039	0.437812	-5.94
252090_at	5B protein like protein cysteine-rich 5B	---	AT3G52130	1.10	0.14	1.35	0.220081	0.437823	-5.94
246328_at	putative protein hexamer-binding protei	---	AT3G43590	-1.12	-0.16	-1.35	0.220082	0.437823	-5.94
261286_at	unknown protein ; supported by cDNA: g	---	AT1G35780	-1.15	-0.20	-1.35	0.220108	0.437836	-5.94
262744_at	anthranilate N-hydroxycinnamoyl/benzo	---	AT1G28680	1.21	0.28	1.35	0.220195	0.437972	-5.94
256564_at	alpha/beta hydrolase, putative contains	MES11	AT3G29770	1.31	0.39	1.35	0.220334	0.438209	-5.94
263577_at	putative protein kinase identical to hypo	SSP	AT2G17090	1.14	0.18	1.35	0.220401	0.438284	-5.94
265859_at	hypothetical protein predicted by gensca	---	---	-1.11	-0.15	-1.35	0.22041	0.438284	-5.94
256872_at	non-phototropic hypocotyl, putative sim	---	AT3G26490	-1.11	-0.15	-1.35	0.220436	0.438298	-5.94
254466_at	subtilisin-like serine protease contains s	---	AT4G20430	-1.16	-0.21	-1.35	0.220543	0.438471	-5.94
255558_at	P II nitrogen sensing protein GLB I ; su	GLB1	AT4G01900	-1.13	-0.17	-1.35	0.220606	0.438558	-5.94
263040_at	conserved hypothetical protein predicte	---	AT1G23300	-1.11	-0.15	-1.35	0.220719	0.438745	-5.94
246524_at	Carboxylesterase-like protein sterol est	ATPCME	AT5G15860	1.17	0.23	1.35	0.220777	0.438788	-5.94
254506_at	leucine rich repeat-like protein Cf-2.2, L	GSO1	AT4G20140	-1.15	-0.21	-1.35	0.220779	0.438788	-5.94
251520_at	protein kinase like GCN2 - Saccharomy	---	AT3G59410	-1.10	-0.14	-1.35	0.220825	0.438804	-5.94

261423_at	homeodomain transcription factor, puta	AGL65	AT1G18750	-1.14	-0.19	-1.35	0.220825	0.438804	-5.94
251080_at	putative protein hypothetical proteins - A	ROPGEF7	AT5G02010	-1.29	-0.37	-1.35	0.22085	0.438815	-5.94
256812_at	hypothetical protein contains similarity to	---	AT3G21350	-1.10	-0.14	-1.35	0.220912	0.438898	-5.94
266325_at	putative extensin	---	AT2G46630	1.43	0.52	1.35	0.220935	0.438906	-5.94
245251_at	calcineurin B-like protein 1 ; supported b	CBL1	AT4G17615	1.37	0.46	1.35	0.221052	0.438938	-5.94
262373_at	hypothetical protein predicted by genefir	---	AT1G73120	1.27	0.35	1.35	0.221072	0.438938	-5.94
251875_at	putative protein various predicted prote	---	AT3G54270	1.14	0.19	1.35	0.221085	0.438938	-5.94
265158_at	hypothetical protein predicted by genefir	---	AT1G31040	1.09	0.13	1.35	0.22102	0.438938	-5.94
256500_at	Ty1/copia-element polyprotein	---	---	1.12	0.16	1.35	0.221061	0.438938	-5.94
258724_at	unknown protein	---	AT3G09600	-1.09	-0.13	-1.35	0.221022	0.438938	-5.94
247922_at	putative protein similar to unknown prote	---	AT5G57500	1.31	0.39	1.35	0.221008	0.438938	-5.94
253130_at	putative protein ;supported by full-lengt	---	AT4G35510	-1.20	-0.26	-1.35	0.221115	0.438958	-5.94
264484_at	hypothetical protein similar to ankyrin lik	---	AT1G77260	-1.10	-0.14	-1.35	0.22118	0.439012	-5.94
245116_at	unknown protein ; supported by cDNA:	---	AT2G41620	-1.25	-0.32	-1.35	0.221179	0.439012	-5.94
265551_at	putative replication protein A1	---	---	1.10	0.14	1.35	0.221245	0.439102	-5.94
250705_at	diadenosine 5,5-P1,P4-tetraphosphate	ATNUDX2	AT5G06340	-1.14	-0.19	-1.35	0.221316	0.439205	-5.94
266347_at	putative ATP-dependent DNA helicase I	---	AT2G01440	-1.15	-0.20	-1.35	0.221339	0.439212	-5.94
260736_at	hypothetical protein predicted by genem	---	AT1G17630	-1.10	-0.14	-1.35	0.221433	0.439360	-5.94
264531_at	hypothetical protein predicted by gensca	---	AT1G30790	1.11	0.15	1.35	0.221488	0.439431	-5.94
256587_at	histone-H4-like protein similar to H41 ge	---	AT3G28780	1.12	0.16	1.35	0.221585	0.439516	-5.94
266679_at	putative helicase ; supported by cDNA:	---	AT2G03270	1.12	0.17	1.35	0.221587	0.439516	-5.94
249113_at	putative protein similar to unknown prote	---	AT5G43790	-1.16	-0.21	-1.35	0.221589	0.439516	-5.94
258833_at	unknown protein	---	---	-1.13	-0.18	-1.35	0.221608	0.439517	-5.94
248947_at	putative protein similar to unknown prote	---	AT5G45540	1.15	0.20	1.35	0.221655	0.439572	-5.94
255387_at	putative nodulin similar to M. truncatula	---	AT4G03630	1.15	0.20	1.35	0.221745	0.439712	-5.94
262536_at	SOUL-like protein Similar to SOUL Prot	---	AT1G17100	-1.25	-0.32	-1.35	0.222035	0.440249	-5.94
267577_at	unknown protein ; supported by cDNA:	---	AT2G30710	-1.09	-0.12	-1.35	0.222058	0.440256	-5.94
245767_at	hypothetical protein similar to putative d	---	AT1G33610	1.08	0.12	1.35	0.222156	0.440413	-5.94
258078_at	unknown protein ;supported by full-leng	---	AT3G25870	1.25	0.33	1.34	0.22221	0.440442	-5.94
259526_at	hypothetical protein	---	AT1G12570	1.25	0.32	1.34	0.222197	0.440442	-5.94
255610_at	putative phosphatidylinositol kinase sim	ATPIPK10	AT4G01190	1.11	0.15	1.34	0.222241	0.440463	-5.94
255183_at	hypothetical protein	---	AT4G08140	1.13	0.18	1.34	0.222259	0.440463	-5.94
256569_at	hypothetical protein ; supported by full-l	---	AT3G19550	-1.37	-0.45	-1.34	0.222318	0.440541	-5.94
264067_x_a	putative chloroplast nucleoid DNA bindir	---	AT2G28010	-1.14	-0.19	-1.34	0.222347	0.440560	-5.94
253461_at	cytochrome p450 - like protein cytochro	CYP96A2	AT4G32170	1.10	0.14	1.34	0.222391	0.440609	-5.95

250598_at	transcription factor-like protein ; suppor	ATMYB29	AT5G07690	-1.18	-0.24	-1.34	0.222443	0.440659	-5.95
263366_at	unknown protein	---	AT2G20440	1.12	0.17	1.34	0.222454	0.440659	-5.95
265617_at	putative phosphate/phosphoenolpyruvat	---	AT2G25520	1.23	0.29	1.34	0.222506	0.440723	-5.95
263110_at	unknown protein ;supported by full-lengt	---	AT1G65220	1.15	0.20	1.34	0.22255	0.440772	-5.95
254162_at	transcription factor IIA small subunit ;su	---	AT4G24440	-1.16	-0.21	-1.34	0.222639	0.440801	-5.95
246300_at	putative transmembrane protein G5p ye	SAC8	AT3G51830	-1.10	-0.14	-1.34	0.222605	0.440801	-5.95
262325_at	dirigent protein, putative similar to dirige	---	AT1G64160	-1.26	-0.34	-1.34	0.222661	0.440801	-5.95
246704_at	putative protein	---	AT5G28090	1.11	0.15	1.34	0.222595	0.440801	-5.95
267433_at	putative peroxisome assembly protein P	PEX10	AT2G26350	-1.12	-0.16	-1.34	0.222657	0.440801	-5.95
253232_at	hypothetical protein ;supported by full-le	TAF8	AT4G34340	1.12	0.17	1.34	0.222804	0.441007	-5.95
254423_at	Lsd1 like protein zinc-finger protein Lsd	LOL2	AT4G21610	1.15	0.20	1.34	0.222791	0.441007	-5.95
266720_s_a	hypothetical protein predicted by genefir	APRR9	AT2G46670 /	-1.24	-0.31	-1.34	0.222876	0.441111	-5.95
265178_at	Pto kinase interactor, putative similar to	---	AT1G23540	1.12	0.16	1.34	0.222906	0.441132	-5.95
264529_at	CTP synthase-like protein similar to ctp	---	AT1G30820	1.28	0.36	1.34	0.222952	0.441185	-5.95
261700_at	hypothetical protein similar to hypothetic	---	AT1G32690	-1.15	-0.20	-1.34	0.223014	0.441269	-5.95
265455_at	hypothetical protein predicted by gensca	---	AT2G46560	-1.10	-0.14	-1.34	0.223109	0.441381	-5.95
250876_at	hypothetical protein	---	AT5G04030	-1.10	-0.14	-1.34	0.223094	0.441381	-5.95
258164_at	surfeit 1 identical to GB:AAF19609 from	SURF1	AT3G17910	-1.18	-0.24	-1.34	0.223147	0.441417	-5.95
255924_at	unknown protein contains similarity to pl	---	AT1G22170	1.14	0.18	1.34	0.223167	0.441419	-5.95
262755_at	unknown protein	---	AT1G16360	-1.11	-0.15	-1.34	0.223208	0.441461	-5.95
263080_at	hypothetical protein predicted by gensca	---	---	-1.13	-0.17	-1.34	0.223257	0.441520	-5.95
246474_at	putative protein predicted protein, Arabi	---	AT5G17150	1.11	0.15	1.34	0.223276	0.441520	-5.95
245043_at	putative cyclin ;supported by full-length	RCY1	AT2G26430	-1.20	-0.26	-1.34	0.223335	0.441567	-5.95
257410_at	hypothetical protein similar to polyketide	emb2421	AT1G24340	-1.16	-0.22	-1.34	0.223339	0.441567	-5.95
259703_at	putative endo-1,3-beta-glucanase simila	---	AT1G77790	1.11	0.15	1.34	0.223381	0.441613	-5.95
252845_at	vacuolar H(+)-ATPase subunit-like prot	---	AT3G42050	-1.10	-0.14	-1.34	0.223465	0.441740	-5.95
245437_at	RNA helicase like protein	---	AT4G16630	-1.18	-0.23	-1.34	0.223623	0.442013	-5.95
250265_at	putative protein predicted proteins, Arat	---	AT5G12900	-1.17	-0.23	-1.34	0.223695	0.442080	-5.95
256431_s_a	putative disease resistance protein simil	AtRLP34	AT3G11010 /	1.24	0.30	1.34	0.223678	0.442080	-5.95
248272_at	Expressed protein ; supported by full-ler	---	AT5G53480	-1.15	-0.20	-1.34	0.223741	0.442133	-5.95
248805_at	putative protein similar to unknown prote	---	AT5G47480	-1.10	-0.14	-1.34	0.223783	0.442177	-5.95
254767_s_a	cytochrome p450 - like protein cytochro	CYP71A19	AT4G13290 /	-1.09	-0.13	-1.34	0.223804	0.442181	-5.95
261149_s_a	GSH-dependent dehydroascorbate red	DHAR1	AT1G19550 /	-1.20	-0.26	-1.34	0.223836	0.442205	-5.95
252824_at	histone H3.3 ; supported by cDNA: gi_1	---	AT4G40030	-1.12	-0.17	-1.34	0.223907	0.442307	-5.95
251337_at	proteasome component C5 ;supported	PBF1	AT3G60820	-1.09	-0.13	-1.34	0.22417	0.442750	-5.95

264419_s_a	hypothetical protein contains similarity to	---	AT1G43310 /	-1.32	-0.40	-1.34	0.224159	0.442750	-5.95
258856_at	hypothetical protein predicted by genefir	SRG3	AT3G02040	1.27	0.35	1.34	0.224271	0.442912	-5.95
256146_at	delta-adaptin, putative similar to delta-a	delta-ADR	AT1G48760	-1.10	-0.14	-1.34	0.224303	0.442917	-5.95
251136_at	mRNA capping enzyme - like protein m	---	AT5G01290	1.09	0.13	1.34	0.224313	0.442917	-5.95
267278_at	unknown protein ; supported by full-leng	---	AT2G19350	-1.08	-0.12	-1.34	0.224388	0.442955	-5.95
247105_at	putative protein similar to unknown prote	DAR5	AT5G66630	1.16	0.21	1.34	0.22439	0.442955	-5.95
247170_at	putative protein contains similarity to lec	---	AT5G65530	1.09	0.13	1.34	0.224369	0.442955	-5.95
248478_at	ubiquitin-conjugating enzyme-like protei	UBC27	AT5G50870	-1.09	-0.13	-1.34	0.224467	0.443068	-5.95
244901_at	hypothetical protein	---	ATMG00640	1.13	0.17	1.34	0.224527	0.443148	-5.95
252416_at	chromosome assembly protein homolog	ATSMC2	AT3G47460	1.08	0.12	1.34	0.224609	0.443272	-5.95
266534_at	putative splicing factor ;supported by fu	---	AT2G16940	-1.10	-0.13	-1.34	0.224844	0.443697	-5.95
247659_at	DNA-directed RNA polymerase - like pr	NRPC1	AT5G60040	-1.30	-0.37	-1.34	0.22494	0.443847	-5.95
247885_at	putative protein similar to unknown prote	---	AT5G57830	1.19	0.25	1.34	0.224986	0.443862	-5.96
259604_at	20S proteasome beta subunit (PBG1) id	PBG1	AT1G56450	-1.11	-0.15	-1.34	0.224985	0.443862	-5.96
251361_at	LIM domain protein LIM domain protein	---	AT3G61230	1.14	0.19	1.34	0.225046	0.443941	-5.96
244923_s_a	orf153b orf153b	---	AT2G07674	-1.20	-0.26	-1.34	0.225075	0.443960	-5.96
247679_at	1-aminocyclopropane-1-carboxylate oxi	---	AT5G59540	-1.25	-0.33	-1.34	0.225191	0.444037	-5.96
261685_at	3-beta-hydroxysteroid dehydrogenase,	AT3BETAI	AT1G47290	1.26	0.34	1.34	0.22519	0.444037	-5.96
260185_at	hypothetical protein similar to hypothetic	---	AT1G36030	1.09	0.12	1.34	0.225187	0.444037	-5.96
250407_at	chorismate mutase CM2 ; supported by	ATCM2	AT5G10870	-1.11	-0.15	-1.34	0.225155	0.444037	-5.96
264197_at	unknown protein Similar to hypothetical	ATSAC1	AT1G22620	-1.09	-0.12	-1.34	0.225241	0.444097	-5.96
247414_at	unknown protein	EMB2759	AT5G63050	-1.14	-0.19	-1.33	0.225268	0.444112	-5.96
246080_at	putative protein	---	AT5G20460	-1.11	-0.15	-1.33	0.225295	0.444125	-5.96
262684_s_a	vacuolar ATP synthase subunit B identic	---	AT1G20260 /	-1.13	-0.18	-1.33	0.22539	0.444255	-5.96
259262_at	unknown protein similar to nifU-like prot	ISU2	AT3G01020	-1.10	-0.14	-1.33	0.225399	0.444255	-5.96
260846_at	unknown protein	---	AT1G17300	1.12	0.16	1.33	0.225485	0.444384	-5.96
262593_at	putative ubiquinol--cytochrome-c reducta	---	AT1G15120	1.19	0.25	1.33	0.225519	0.444414	-5.96
265185_at	OBP32pep protein, putative identical to	---	AT1G23670	1.13	0.17	1.33	0.225743	0.444816	-5.96
256149_at	zinc finger protein, putative similar to zi	AtIDD7	AT1G55110	-1.16	-0.22	-1.33	0.225799	0.444888	-5.96
245182_at	putative protein similarity to TETRATRI	---	AT5G12430	-1.17	-0.23	-1.33	0.225888	0.445025	-5.96
252915_at	EF-Hand containing protein -like strond	---	AT4G38810	1.14	0.19	1.33	0.225954	0.445117	-5.96
247435_at	glutathione S-transferase-like protein ; s	ATGSTU9	AT5G62480	1.84	0.88	1.33	0.225978	0.445125	-5.96
248935_at	salt-inducible protein-like	---	AT5G46100	-1.13	-0.17	-1.33	0.226024	0.445178	-5.96
250660_at	RNA-binding protein-like	---	AT5G07060	-1.09	-0.12	-1.33	0.226098	0.445285	-5.96
258909_at	putative DnaJ protein Pfam HMM hit: D	---	AT3G06340	-1.09	-0.12	-1.33	0.226184	0.445417	-5.96

259130_at	putative ribosomal protein L39 similar to	---	AT3G02190	-1.13	-0.17	-1.33	0.226228	0.445426	-5.96
256164_at	terpene cyclase, putative similar to terp	---	AT1G48800	-1.09	-0.13	-1.33	0.22622	0.445426	-5.96
252867_at	putative protein hypothetical protein, Sc	---	AT4G39870	-1.13	-0.18	-1.33	0.226381	0.445689	-5.96
246563_at	putative protein	---	AT5G15581	1.13	0.18	1.33	0.226641	0.446039	-5.96
258063_at	putative cytochrome P450 similar to GB	CYP72A8	AT3G14620	1.39	0.47	1.33	0.226617	0.446039	-5.96
248180_at	unknown protein ;supported by full-leng	AGD5	AT5G54310	1.09	0.13	1.33	0.226642	0.446039	-5.96
246142_at	putative protein	---	AT5G19970	-1.10	-0.13	-1.33	0.226657	0.446039	-5.96
264273_s_a	hypothetical protein contains similarity to	---	AT1G60300 /	-1.16	-0.21	-1.33	0.226607	0.446039	-5.96
255360_at	putative protein ;supported by full-lengt	---	AT4G03960	-1.11	-0.15	-1.33	0.226751	0.446056	-5.96
253423_at	Expressed protein ; supported by cDNA	IAA29	AT4G32280	-1.70	-0.76	-1.33	0.226779	0.446056	-5.96
266198_at	unknown protein predicted by genscan a	---	AT2G38890	1.11	0.15	1.33	0.226782	0.446056	-5.96
246448_at	putative protein putative N-acetlytransfe	---	AT5G16800	1.12	0.16	1.33	0.226772	0.446056	-5.96
253655_at	Expressed protein ;supported by cDNA:	LCR59	AT4G30070	1.09	0.12	1.33	0.226771	0.446056	-5.96
249418_at	putative protein predicted protein, Arabi	---	AT5G39785	1.09	0.13	1.33	0.22671	0.446056	-5.96
260804_at	hypothetical protein predicted by genem	---	AT1G78410	2.21	1.14	1.33	0.22697	0.446297	-5.96
264753_at	receptor kinase, putative similar to rece	---	AT1G61490	-1.09	-0.12	-1.33	0.22697	0.446297	-5.96
247773_at	putative protein	---	AT5G58630	1.11	0.15	1.33	0.226931	0.446297	-5.96
266190_at	unknown protein	---	AT2G38840	1.11	0.15	1.33	0.226983	0.446297	-5.96
266094_at	Expressed protein ; supported by full-ler	---	AT2G37975	1.12	0.17	1.33	0.227026	0.446343	-5.96
246412_at	phosphoglucomutase-like protein phosp	---	AT5G17530	-1.20	-0.26	-1.33	0.227113	0.446474	-5.96
260820_at	receptor protein kinase, putative similar	---	AT1G06840	1.22	0.29	1.33	0.227156	0.446521	-5.96
251943_at	splicing factor - like protein splicing fact	RSZ32	AT3G53500	-1.09	-0.12	-1.33	0.227236	0.446639	-5.96
250571_at	hypothetical protein	---	AT5G08200	1.16	0.22	1.33	0.227404	0.446888	-5.96
259342_at	unknown protein ;supported by full-leng	---	AT3G03890	1.16	0.21	1.33	0.227421	0.446888	-5.96
265574_at	putative replication protein A1	---	---	-1.10	-0.14	-1.33	0.227382	0.446888	-5.96
266803_at	putative protein kinase contains a protei	APK1B	AT2G28930	-1.28	-0.36	-1.33	0.227444	0.446894	-5.96
262351_at	beta-galactosidase (BGAL), putative sir	BGAL17	AT1G72990	-1.09	-0.13	-1.33	0.227479	0.446926	-5.96
245911_at	oligosaccharyl transferase STT3-like pr	STT3A	AT5G19690	1.09	0.13	1.33	0.227532	0.446951	-5.96
262613_at	putative DNA-binding protein similar to \	WRKY4	AT1G13960	1.11	0.15	1.33	0.227523	0.446951	-5.96
264984_at	unknown protein ;supported by full-lengt	---	AT1G27000	1.09	0.13	1.33	0.227593	0.447032	-5.97
252879_at	putative protein predicted proteins, Arat	NST-K1	AT4G39390	1.31	0.39	1.33	0.227693	0.447129	-5.97
254557_at	hypothetical protein ;supported by full-le	---	AT4G19140	1.23	0.30	1.33	0.227662	0.447129	-5.97
253885_at	putative protein essential for embryoge	VPS26B	AT4G27690	-1.14	-0.19	-1.33	0.2277	0.447129	-5.97
258372_at	ubiquitin-specific protease 25 (UBP25) s	UBP25	AT3G14400	-1.10	-0.14	-1.33	0.227746	0.447179	-5.97
254028_s_a	putative protein N.crassa mRNA for put	ORP4B	AT4G25850 /	1.10	0.14	1.33	0.227783	0.447214	-5.97

246603_at	copper amine oxidase, putative similar	---	AT1G31690	1.16	0.22	1.33	0.227805	0.447218	-5.97
255709_at	putative YABBY3 axial regulator ; supp	YAB3	AT4G00180	-1.13	-0.18	-1.33	0.227889	0.447343	-5.97
245563_at	SNF1 like protein kinase ; supported by	CIPK4	AT4G14580	-1.34	-0.42	-1.33	0.227908	0.447343	-5.97
245444_at	limonene cyclase like protein	ATTPS03	AT4G16740	1.15	0.20	1.33	0.227974	0.447397	-5.97
245862_at	putative protein	---	AT5G01010	1.13	0.17	1.33	0.227964	0.447397	-5.97
252796_at	putative protein predicted proteins, Ara	---	---	1.17	0.22	1.33	0.228086	0.447540	-5.97
254128_at	ubiquitin-specific protease 16 (UBP16),	UBP16	AT4G24560	-1.09	-0.12	-1.33	0.228085	0.447540	-5.97
257827_at	unknown protein contains Pfam profile:	---	AT3G26630	-1.20	-0.26	-1.33	0.228193	0.447595	-5.97
247923_at	porin-like protein ;supported by full-leng	VDAC4	AT5G57490	1.13	0.17	1.33	0.228148	0.447595	-5.97
259521_at	ATP-dependent Clp protease proteolytic	CLP2	AT1G12410	-1.14	-0.19	-1.33	0.228174	0.447595	-5.97
262982_at	unknown protein ;supported by full-lengt	ING2	AT1G54390	1.10	0.13	1.33	0.228182	0.447595	-5.97
254420_at	hypothetical protein	---	AT4G21500	1.15	0.20	1.33	0.228244	0.447657	-5.97
261851_at	hexokinase, putative similar to chloropl	HKL1	AT1G50460	1.23	0.29	1.33	0.228289	0.447675	-5.97
251545_at	zinc transporter -like protein zinc transp	MTPA2	AT3G58810	1.16	0.22	1.33	0.228293	0.447675	-5.97
260871_at	hypothetical protein predicted by genem	---	AT1G29040	1.09	0.12	1.32	0.228414	0.447835	-5.97
263061_at	putative AAA-type ATPase	---	AT2G18190	1.12	0.17	1.32	0.228396	0.447835	-5.97
259080_at	putative mitogen activated protein kinas	WNK1	AT3G04910	-1.13	-0.18	-1.32	0.22849	0.447853	-5.97
260070_at	putative helix-loop-helix DNA-binding pr	BEE3	AT1G73830	-1.61	-0.69	-1.32	0.228504	0.447853	-5.97
263871_at	hypothetical protein predicted by gensca	RKP	AT2G22010	-1.13	-0.18	-1.32	0.228521	0.447853	-5.97
266075_s_a	unknown protein	---	AT2G40710 /	-1.14	-0.19	-1.32	0.228494	0.447853	-5.97
262007_at	hypothetical protein predicted by gensca	---	AT1G64580	-1.11	-0.15	-1.32	0.228511	0.447853	-5.97
260253_at	disease resistance protein, putative sim	AtRLP15	AT1G74190	1.10	0.13	1.32	0.228568	0.447907	-5.97
246650_at	putative protein p76, Homo sapiens, EM	---	AT5G35160	1.12	0.16	1.32	0.228628	0.447948	-5.97
259044_at	pollen allergen Bra r II identical to polle	---	AT3G03430	1.10	0.14	1.32	0.22861	0.447948	-5.97
253382_at	putative protein AT.I.24, Arabidopsis th	---	AT4G33040	-1.15	-0.20	-1.32	0.228688	0.448004	-5.97
260762_at	I-box binding factor, putative similar to I	---	AT1G49015	-1.11	-0.15	-1.32	0.228696	0.448004	-5.97
261452_s_a	hypothetical protein predicted by genem	---	---	1.11	0.15	1.32	0.228791	0.448151	-5.97
250861_at	putative protein predicted proteins, Ara	---	AT5G04740	1.13	0.17	1.32	0.228892	0.448211	-5.97
252742_at	putative protein glyceraldehyde-3-phos	---	AT3G43290	1.14	0.19	1.32	0.228847	0.448211	-5.97
251948_at	diaminopimelate epimerase - like protei	---	AT3G53580	-1.13	-0.17	-1.32	0.228937	0.448211	-5.97
263986_at	putative citrate synthase ;supported by	CSY3	AT2G42790	1.15	0.21	1.32	0.228861	0.448211	-5.97
247736_at	actin 4 ;supported by full-length cDNA:	ACT4	AT5G59370	-1.10	-0.14	-1.32	0.228922	0.448211	-5.97
251274_at	putative protein hypothetical protein At2	---	AT3G61700	-1.20	-0.26	-1.32	0.228939	0.448211	-5.97
265741_at	putative membrane transporter ; suppo	---	AT2G01320	-1.22	-0.29	-1.32	0.228968	0.448229	-5.97
246127_s_a	putative protein	---	---	1.09	0.12	1.32	0.229089	0.448366	-5.97

251703_at	putative protein hypothetical proteins - A	---	AT3G56670	1.15	0.20	1.32	0.229092	0.448366	-5.97
247330_at	putative protein contains similarity to ac	GAMMA C	AT5G63510	-1.09	-0.12	-1.32	0.229097	0.448366	-5.97
259287_at	putative rac GTPase activating protein s	---	AT3G11490	-1.13	-0.18	-1.32	0.229157	0.448406	-5.97
266282_at	putative protein kinase contains a protei	---	AT2G29220	1.09	0.13	1.32	0.229144	0.448406	-5.97
260576_at	putative FCA-related protein	---	AT2G47310	-1.15	-0.20	-1.32	0.229226	0.448502	-5.97
254135_at	putative protein MSP1 protein, Sacchar	---	AT4G24860	1.12	0.16	1.32	0.229252	0.448515	-5.97
262496_at	unknown protein ; supported by full-leng	---	AT1G21790	-1.22	-0.29	-1.32	0.229279	0.448530	-5.97
260794_at	unknown protein ; supported by cDNA: g	---	AT1G06210	1.12	0.16	1.32	0.2293	0.448531	-5.97
265703_at	putative ankyrin	---	AT2G03430	-1.14	-0.19	-1.32	0.229377	0.448610	-5.97
252871_at	proliferating-cell nucleolar antigen - like	---	AT4G40000	-1.11	-0.15	-1.32	0.229398	0.448610	-5.97
263669_at	putative cryptochrome 2 apoprotein Mat	CRY2	AT1G04400	-1.10	-0.14	-1.32	0.229399	0.448610	-5.97
259874_at	unknown protein	---	AT1G76660	-1.16	-0.22	-1.32	0.229509	0.448787	-5.97
254458_at	putative protein heat shock protein dna	ATERDJ2I	AT4G21180	1.20	0.26	1.32	0.229556	0.448840	-5.97
267200_at	hypothetical protein predicted by genefi	---	AT2G31010	-1.13	-0.18	-1.32	0.229649	0.448884	-5.97
253879_s_a	UDP rhamnose--anthocyanidin-3-gluco	---	AT4G27560 /	-1.25	-0.32	-1.32	0.229696	0.448884	-5.97
265479_at	hypothetical protein ;supported by full-le	---	AT2G15760	1.62	0.69	1.32	0.229628	0.448884	-5.97
257678_at	RNA helicase, putative contains Pfam p	RTL2	AT3G20420	-1.13	-0.18	-1.32	0.229667	0.448884	-5.97
251655_at	hypothetical protein	AT3G5715	---	1.15	0.20	1.32	0.229604	0.448884	-5.97
252850_at	putative protein ;supported by full-lengt	---	AT4G39880	-1.15	-0.20	-1.32	0.229687	0.448884	-5.97
247002_at	putative protein strong similarity to unkn	HOS15	AT5G67320	-1.13	-0.17	-1.32	0.229757	0.448964	-5.97
257854_at	putative CREB-binding protein similar to	HAC5	AT3G12980	1.11	0.15	1.32	0.229806	0.448982	-5.97
251298_at	hypothetical protein contains non-conse	---	AT3G62040	-1.25	-0.32	-1.32	0.229795	0.448982	-5.97
248247_at	putative protein contains similarity to hel	SPCH	AT5G53210	1.10	0.14	1.32	0.230015	0.449353	-5.97
246661_at	putative protein various predicted prote	---	---	-1.10	-0.13	-1.32	0.230101	0.449482	-5.97
255089_at	nucleoside-diphosphate kinase ;suppor	NDPK1	AT4G09320	-1.17	-0.22	-1.32	0.230124	0.449489	-5.97
257333_at	cytochrome c oxidase subunit 1	---	---	1.24	0.31	1.32	0.230185	0.449530	-5.97
261655_at	hypothetical protein predicted by genem	---	AT1G01940	-1.16	-0.21	-1.32	0.230171	0.449530	-5.97
263861_at	hypothetical protein	---	AT2G04560	-1.17	-0.23	-1.32	0.230273	0.449665	-5.98
256072_at	WD-40 repeat protein identical to WD-4(	ATARCA	AT1G18080	-1.24	-0.31	-1.32	0.230375	0.449825	-5.98
258397_at	Expressed protein ; supported by full-ler	---	AT3G15357	-1.10	-0.14	-1.32	0.230423	0.449840	-5.98
257026_at	hypothetical protein predicted by genem	---	AT3G19200	1.12	0.16	1.32	0.230442	0.449840	-5.98
247051_at	At14a protein-like	---	AT5G66670	-1.12	-0.16	-1.32	0.230412	0.449840	-5.98
255132_at	inositol 1,3,4-trisphosphate 5/6-kinase-l	---	AT4G08170	-1.14	-0.19	-1.32	0.230511	0.449936	-5.98
AFFX-r2-At-	Arabidopsis thaliana /REF=U84969 /DE	---	---	1.08	0.11	1.32	0.230551	0.449976	-5.98
257874_at	hypothetical protein	---	AT3G17110	1.12	0.17	1.32	0.230573	0.449981	-5.98

252769_at	arabinose kinase - like protein putative	---	AT3G42850	-1.11	-0.15	-1.32	0.230639	0.450072	-5.98
248112_at	wax synthase-like protein	---	AT5G55350	1.14	0.19	1.32	0.230715	0.450181	-5.98
265045_s_a	putative protein kinase, ADK1 dual spe	ADK1	AT1G03930 /	-1.22	-0.29	-1.32	0.230759	0.450228	-5.98
264230_at	hypothetical protein predicted by genem	---	AT1G67460	1.10	0.14	1.32	0.230792	0.450253	-5.98
253843_at	putative protein MLL protein, Gallus gal	SDG16	AT4G27910	1.09	0.13	1.32	0.230889	0.450405	-5.98
262864_at	anthocyanidin-3-glucoside rhamnosyltra	---	AT1G64920	-1.12	-0.16	-1.32	0.230959	0.450466	-5.98
246362_at	hypothetical protein	---	---	-1.08	-0.12	-1.32	0.23096	0.450466	-5.98
261649_at	putative clathrin-coat assembly protein s	---	AT1G27700	-1.11	-0.15	-1.32	0.230988	0.450481	-5.98
256487_at	disease resistance gene, putative simila	---	AT1G31540	1.16	0.21	1.32	0.231087	0.450635	-5.98
266021_at	unknown protein	---	AT2G05910	1.18	0.24	1.32	0.231128	0.450679	-5.98
251158_at	rac-GTP binding protein -like RACC sm	MIRO2	AT3G63150	-1.10	-0.14	-1.32	0.231207	0.450793	-5.98
259987_at	thaumatin-like protein (PR-5) similar to t	ATLP-3	AT1G75030	1.15	0.20	1.32	0.231246	0.450830	-5.98
247415_at	unknown protein	---	AT5G63060	-1.23	-0.30	-1.32	0.231379	0.450975	-5.98
257667_at	1,4-alpha-glucan branching enzyme, pu	EMB2729	AT3G20440	-1.18	-0.24	-1.32	0.23136	0.450975	-5.98
259455_x_a	unknown protein	---	AT1G44030	1.15	0.20	1.32	0.23137	0.450975	-5.98
247809_at	unknown protein	---	AT5G58280	-1.12	-0.17	-1.32	0.231428	0.451032	-5.98
259649_at	Serine/arginine-rich protein, putative sir	TAF7	AT1G55300	-1.11	-0.14	-1.32	0.231483	0.451075	-5.98
254411_at	hypothetical protein	---	---	1.12	0.17	1.32	0.23149	0.451075	-5.98
251514_at	pirin-like protein pirin - Lycopersicon es	---	AT3G59260	1.12	0.16	1.32	0.231525	0.451106	-5.98
264260_at	putative calcium-binding protein, calreti	---	AT1G09210	1.30	0.38	1.31	0.231556	0.451127	-5.98
249310_at	putative protein contains similarity to 40	---	AT5G41520	-1.12	-0.17	-1.31	0.231596	0.451165	-5.98
261589_at	hypothetical protein predicted by gensca	---	AT1G01690	1.14	0.18	1.31	0.231686	0.451303	-5.98
258029_at	serine/threonine-protein kinase, PK7 id	ATPK7	AT3G27580	1.10	0.13	1.31	0.231806	0.451498	-5.98
246520_at	putative protein RING-H2 finger protein	---	AT5G15790	-1.10	-0.13	-1.31	0.231838	0.451522	-5.98
265954_at	putative WRKY-type DNA binding protei	TTG2	AT2G37260	-1.10	-0.14	-1.31	0.231899	0.451602	-5.98
267540_at	hypothetical protein predicted by gensca	---	AT2G32760	-1.10	-0.13	-1.31	0.231919	0.451603	-5.98
252283_at	60S ribosomal protein L13 (BBC1) - like	---	AT3G48960	-1.11	-0.15	-1.31	0.231946	0.451617	-5.98
262786_at	putative lipase similar to gb|X02844 lipa	---	AT1G10740	1.16	0.21	1.31	0.231976	0.451637	-5.98
266784_at	putative receptor-like protein kinase	---	AT2G28960	1.09	0.12	1.31	0.232018	0.451642	-5.98
245169_at	unknown protein predicted by genefinde	---	AT2G33220	-1.09	-0.12	-1.31	0.232001	0.451642	-5.98
265559_at	putative glycine-rich protein	---	AT2G05530	1.13	0.18	1.31	0.232095	0.451753	-5.98
261919_at	type 2 peroxiredoxin, putative similar to	TPX1	AT1G65980	-1.13	-0.18	-1.31	0.232171	0.451863	-5.98
267074_s_a	hypothetical protein predicted by gensca	---	AT2G40955 /	-1.10	-0.14	-1.31	0.232438	0.452342	-5.98
260227_at	unknown protein similar to hypothetical	---	AT1G74450	1.32	0.40	1.31	0.232485	0.452395	-5.98
246469_at	putative protein predicted protein, Dros	---	AT5G17070	-1.10	-0.14	-1.31	0.232508	0.452402	-5.98

249572_at	chromosome condensation protein -like	EMB2656	AT5G37630	1.14	0.19	1.31	0.232584	0.452511	-5.98
255494_at	predicted protein of unknown function s	---	AT4G02710	-1.10	-0.14	-1.31	0.232621	0.452545	-5.98
252048_at	expressed protein supported by cDNA: g	---	AT3G52500	-1.16	-0.21	-1.31	0.232716	0.452572	-5.98
255474_at	coded for by A. thaliana cDNA T75804	---	AT4G02480	-1.11	-0.15	-1.31	0.232689	0.452572	-5.98
260317_at	E2, ubiquitin-conjugating enzyme 5 (UB	UBC5	AT1G63800	-1.19	-0.25	-1.31	0.232708	0.452572	-5.98
251818_at	vacuolar protein sorting protein 33a-like	ATVPS33	AT3G54860	1.11	0.15	1.31	0.232734	0.452572	-5.98
262524_at	tuftelin-interacting-like protein Similar to	---	AT1G17070	-1.09	-0.12	-1.31	0.232706	0.452572	-5.98
257638_at	terpene synthase-related protein contair	ATTPS-CI	AT3G25820 /	1.10	0.14	1.31	0.232781	0.452586	-5.98
254424_at	hypothetical protein ;supported by full-le	---	AT4G21510	1.20	0.26	1.31	0.232764	0.452586	-5.98
255680_at	hypothetical protein	---	AT4G00530	-1.14	-0.19	-1.31	0.232843	0.452647	-5.98
255698_at	scarecrow-like 6 (SCL6)	---	AT4G00150	-1.15	-0.20	-1.31	0.232852	0.452647	-5.98
254467_at	receptor protein kinase - like protein se	---	AT4G20450	-1.13	-0.17	-1.31	0.232901	0.452664	-5.99
264765_at	receptor kinase, putative similar to rece	---	AT1G61430	1.12	0.17	1.31	0.232899	0.452664	-5.99
264024_at	hypothetical protein predicted by genefi	---	AT2G21180	1.23	0.30	1.31	0.233067	0.452916	-5.99
267518_at	unknown protein	---	AT2G30500	1.34	0.42	1.31	0.233099	0.452916	-5.99
263052_at	unknown protein	---	AT2G13430	-1.10	-0.14	-1.31	0.23313	0.452916	-5.99
252745_at	putative protein Sh3yl1 mRNA, Mus mu	---	AT3G43230	1.12	0.16	1.31	0.233099	0.452916	-5.99
257934_at	serine carboxypeptidase, putative simil	scpl21	AT3G25420	1.17	0.22	1.31	0.233111	0.452916	-5.99
248135_at	putative protein similar to unknown prote	---	AT5G54890	-1.15	-0.20	-1.31	0.233191	0.452997	-5.99
261201_at	unknown protein ;supported by full-lengt	---	AT1G12850	-1.12	-0.16	-1.31	0.233221	0.453017	-5.99
263444_at	putative MADS-box protein	AGL46	AT2G28700	1.13	0.17	1.31	0.233304	0.453140	-5.99
245293_at	HSP like protein ; supported by cDNA: g	---	AT4G16660	1.38	0.46	1.31	0.233425	0.453335	-5.99
259978_at	putative cell division control protein cdc2	CDKB2;1	AT1G76540	1.18	0.23	1.31	0.233503	0.453449	-5.99
260541_at	putative trypsin inhibitor	---	AT2G43530	-1.40	-0.49	-1.31	0.233608	0.453552	-5.99
252225_at	ADP-RIBOSYLATION FACTOR -like pr	ATARLA1(	AT3G49870	1.10	0.14	1.31	0.233605	0.453552	-5.99
256297_at	cytochrome P450, putative contains Pfa	---	AT1G69500	-1.13	-0.18	-1.31	0.233616	0.453552	-5.99
265077_at	hypothetical protein similar to RING-H2	---	AT1G55530	1.17	0.22	1.31	0.233655	0.453588	-5.99
265592_at	hypothetical protein predicted by genefi	---	AT2G20110	-1.12	-0.16	-1.31	0.233722	0.453680	-5.99
258879_at	unknown protein ; supported by full-leng	---	AT3G03270	1.25	0.32	1.31	0.233757	0.453710	-5.99
249639_at	disease resistance like protein TMV res	---	AT5G36930	-1.10	-0.14	-1.31	0.234185	0.454501	-5.99
258042_at	hypothetical protein similar to hypothetic	---	AT3G21310	1.09	0.12	1.31	0.23431	0.454697	-5.99
251464_at	farnesyltransferase subunit A (FTA) ; su	FTA	AT3G59380	-1.13	-0.18	-1.31	0.234326	0.454697	-5.99
259931_at	hypothetical protein predicted by gensca	---	AT1G34400	1.12	0.16	1.31	0.234382	0.454767	-5.99
264468_at	unknown protein similar to daunorubicin	---	AT1G10310	-1.14	-0.19	-1.31	0.234448	0.454857	-5.99
263196_at	hypothetical protein predicted by genem	---	AT1G36070	-1.18	-0.24	-1.31	0.234492	0.454905	-5.99

262534_at	unknown protein contains Pfam profile:	SHA	AT1G17040	-1.15	-0.20	-1.31	0.234613	0.455100	-5.99
260174_at	unknown protein ;supported by full-leng	---	AT1G71940	1.10	0.14	1.31	0.234719	0.455194	-5.99
259826_at	arm repeat-containing protein, putative	PUB17	AT1G29340	1.18	0.24	1.31	0.234689	0.455194	-5.99
259953_at	putative anion exchanger contains Pfam	BOR5	AT1G74810	-1.16	-0.22	-1.31	0.234721	0.455194	-5.99
266527_at	hypothetical protein predicted by gensca	---	---	1.14	0.18	1.30	0.234747	0.455206	-5.99
261744_at	nitrogen fixation protein (nifS), putative	CPNIFS	AT1G08490	1.12	0.16	1.30	0.234789	0.455247	-5.99
254272_at	predicted protein hypothetical protein, S	---	AT4G22850	1.09	0.12	1.30	0.234817	0.455264	-5.99
259169_at	unknown protein similar to unknown pro	---	AT3G03520	-1.38	-0.47	-1.30	0.234841	0.455271	-5.99
257249_at	unknown protein	---	AT3G24180	1.16	0.22	1.30	0.234893	0.455334	-5.99
263844_at	unknown protein ; supported by cDNA:	---	AT2G36930	-1.26	-0.34	-1.30	0.234944	0.455393	-5.99
263793_at	putative glucosyltransferase	ATCSLC0	AT2G24630	-1.24	-0.31	-1.30	0.234985	0.455419	-5.99
267059_at	putative carboxymethylenebutenolidase	---	AT2G32520	1.11	0.15	1.30	0.234997	0.455419	-5.99
264440_at	unknown protein similar to fim protein; s	---	AT1G27340	-1.10	-0.13	-1.30	0.235031	0.455445	-5.99
265496_at	copia-like retroelement pol polyprotein	---	---	-1.08	-0.12	-1.30	0.235173	0.455683	-5.99
264971_at	Expressed protein ; supported by full-ler	---	AT1G67210	-1.09	-0.12	-1.30	0.235196	0.455689	-5.99
250608_at	pectin methyl-esterase-like protein pect	---	AT5G07420	-1.09	-0.13	-1.30	0.23524	0.455735	-5.99
259852_at	disulfide bond formation protein, putativ	AERO1	AT1G72280	1.26	0.34	1.30	0.235319	0.455782	-5.99
248524_s_a	putative protein contains similarity to sq	---	AT5G50570 /	1.42	0.51	1.30	0.235324	0.455782	-5.99
253455_at	putative protein	---	AT4G32020	1.20	0.27	1.30	0.235289	0.455782	-5.99
261229_at	RAC-like GTP-binding protein ARAC4 ic	ROP2	AT1G20090	-1.09	-0.12	-1.30	0.235351	0.455786	-5.99
247744_at	putative protein various predicted prote	---	AT5G59020	1.15	0.20	1.30	0.235366	0.455786	-5.99
250910_at	heat shock transcription factor -like prot	HSFA3	AT5G03720	-1.37	-0.45	-1.30	0.235414	0.455839	-5.99
264690_at	hypothetical protein similar to hypothetic	SNL4	AT1G70060	1.14	0.19	1.30	0.235491	0.455950	-5.99
266445_at	unknown protein	---	AT2G43070	1.14	0.19	1.30	0.235607	0.456137	-6.00
247307_at	UVB-resistance protein UVR8 (gb|AAD4	---	AT5G21326 /	-1.10	-0.14	-1.30	0.235678	0.456197	-6.00
245115_at	putative esterase D ;supported by full-le	SFGH	AT2G41530	-1.18	-0.24	-1.30	0.235677	0.456197	-6.00
260450_at	hypothetical protein predicted by gensca	---	AT1G72390	-1.16	-0.22	-1.30	0.235769	0.456328	-6.00
267076_at	calcium binding protein (CaBP-22) ident	---	AT2G41090	1.69	0.75	1.30	0.235786	0.456328	-6.00
265271_at	hypothetical protein predicted by gensca	---	AT2G28360	1.12	0.17	1.30	0.235807	0.456329	-6.00
266146_at	En/Spm-like transposon protein related	---	---	1.09	0.12	1.30	0.235877	0.456426	-6.00
258566_at	putative glutamate receptor (GLR1) iden	GLR1.1	AT3G04110	-1.20	-0.26	-1.30	0.235956	0.456540	-6.00
254418_at	glucose transporter glucose transport p	---	AT4G21480	-1.11	-0.15	-1.30	0.236027	0.456601	-6.00
263538_at	hypothetical protein predicted by genefir	---	AT2G25010	-1.16	-0.21	-1.30	0.236013	0.456601	-6.00
251375_at	putative protein various predicted prote	---	AT3G60410	1.16	0.22	1.30	0.236151	0.456802	-6.00
261900_at	unknown protein ;supported by full-lengt	---	AT1G80940	-1.11	-0.15	-1.30	0.236217	0.456829	-6.00

253552_at	ubiquitin-specific protease 24 (UBP24),	UBP24	AT4G30890	-1.10	-0.14	-1.30	0.236206	0.456829	-6.00
251734_at	putative protein Centrosome- and Golgi	---	AT3G56270	-1.26	-0.33	-1.30	0.236225	0.456829	-6.00
257466_at	hypothetical protein predicted by genem	---	AT1G62840	1.31	0.39	1.30	0.236327	0.456892	-6.00
252693_s_a	ribosomal protein S29 - like ribosomal p	---	AT3G43980 /	-1.10	-0.14	-1.30	0.236282	0.456892	-6.00
247958_at	putative protein similar to unknown prote	---	AT5G57070	1.12	0.16	1.30	0.236304	0.456892	-6.00
258342_at	hypothetical protein similar to extensin-li	---	AT3G22800	1.22	0.29	1.30	0.236338	0.456892	-6.00
253428_at	cellulose synthase catalytic subunit (RS	CESA1	AT4G32410	-1.15	-0.21	-1.30	0.236473	0.457113	-6.00
253621_at	putative protein component of aniline di	---	AT4G30540	1.11	0.15	1.30	0.23672	0.457514	-6.00
248447_at	putative protein contains similarity to pol	PABN1	AT5G51120	1.10	0.13	1.30	0.236712	0.457514	-6.00
245940_at	putative protein predicted proteins - diffe	---	AT5G19630	-1.13	-0.18	-1.30	0.236789	0.457532	-6.00
249790_at	putative protein similar to unknown prote	---	AT5G24290	-1.53	-0.61	-1.30	0.236788	0.457532	-6.00
262436_at	En/Spm-like transposon protein, putativ	---	AT1G47610	-1.22	-0.29	-1.30	0.236789	0.457532	-6.00
245868_at	hypothetical protein	CAT2	AT1G58030	1.13	0.18	1.30	0.236887	0.457668	-6.00
265746_at	hypothetical protein predicted by gensca	---	---	-1.11	-0.15	-1.30	0.2369	0.457668	-6.00
259958_at	leucine-rich repeat transmembrane prot	SRF6	AT1G53730	-1.12	-0.16	-1.30	0.237055	0.457890	-6.00
251199_at	transport inhibitor response 1 (TIR1), A	TIR1	AT3G62980	1.20	0.26	1.30	0.237048	0.457890	-6.00
252952_at	putative protein cylicin II - bovine, PIR2	---	AT4G38710	-1.15	-0.20	-1.30	0.237161	0.458056	-6.00
257994_at	unknown protein	---	AT3G19920	1.16	0.21	1.30	0.237198	0.458089	-6.00
250549_at	N-hydroxycinnamoyl benzoyltransferas	---	AT5G07860	1.18	0.24	1.30	0.237333	0.458155	-6.00
263733_at	polyprotein, putative similar to polyprote	---	---	1.08	0.11	1.30	0.237321	0.458155	-6.00
253076_at	NAM like protein P.hybrida NAM gene,	ANAC076	AT4G36160	1.11	0.15	1.30	0.237311	0.458155	-6.00
247645_at	late embryonic abundant protein - like la	---	AT5G60530	1.10	0.14	1.30	0.237258	0.458155	-6.00
253133_at	DNA-directed RNA polymerase (EC 2.7.	NRPB1	AT4G35800	-1.11	-0.15	-1.30	0.237277	0.458155	-6.00
258681_at	unknown protein ; supported by full-leng	---	AT3G08610	-1.12	-0.16	-1.30	0.237386	0.458180	-6.00
260338_at	putative RNA-binding protein similar to p	---	AT1G69250	1.10	0.13	1.30	0.237368	0.458180	-6.00
247600_at	Myb transcription factor homolog (ATR1	MYB34	AT5G60890	-1.31	-0.39	-1.30	0.237471	0.458266	-6.00
251840_at	protein disulfide-isomerase-like protein	ATPDIL1-3	AT3G54960	1.23	0.30	1.30	0.23747	0.458266	-6.00
254421_at	VP1 like protein transcription activator V	VAL3	AT4G21550	-1.16	-0.22	-1.30	0.237525	0.458332	-6.00
253577_at	putative protein	---	AT4G31080	-1.19	-0.25	-1.30	0.237565	0.458370	-6.00
264077_at	putative RAD51B-like DNA repair protei	RAD51B	AT2G28560	1.11	0.15	1.30	0.237689	0.458571	-6.00
256531_at	cystathionine gamma-synthase, putativ	---	AT1G33320	1.09	0.13	1.30	0.237782	0.458713	-6.00
260614_at	hypothetical protein contains Pfam profil	---	AT1G53390	1.09	0.13	1.30	0.237918	0.458934	-6.00
266489_at	unknown protein ; supported by cDNA:	NPSN11	AT2G35190	1.19	0.25	1.29	0.238092	0.459134	-6.00
248232_at	putative protein contains similarity to sal	MLO11	AT5G53760	-1.14	-0.19	-1.29	0.238045	0.459134	-6.00
247329_at	putative protein similar to unknown prote	---	AT5G64150	-1.21	-0.27	-1.29	0.238102	0.459134	-6.00

253939_at	putative myb-related protein myb-relate	MYB97	AT4G26930	1.15	0.20	1.29	0.238093	0.459134	-6.00
252680_at	putative protein predicted protein, C.ele	---	AT3G44330	1.09	0.12	1.29	0.238133	0.459156	-6.00
265145_at	unknown protein similar to GB:CAA8763	PLT2	AT1G51190	1.12	0.16	1.29	0.238159	0.459167	-6.00
254409_at	serine/threonine protein kinase - like pr	---	AT4G21400	1.41	0.50	1.29	0.238183	0.459175	-6.00
261386_at	unknown protein ;supported by full-lengt	---	AT1G05430	-1.13	-0.17	-1.29	0.238221	0.459209	-6.00
265714_at	putative integral membrane protein	ATUPS4	AT2G03520	1.09	0.13	1.29	0.238359	0.459437	-6.01
261634_at	ATP-dependent Clp protease proteolytic	CLPR1	AT1G49970	-1.15	-0.20	-1.29	0.238401	0.459440	-6.01
262215_at	hypothetical protein contains similarity t	---	AT1G74790	1.27	0.34	1.29	0.238401	0.459440	-6.01
256647_at	unknown protein contains similarity to D	---	AT3G13610	2.35	1.23	1.29	0.238512	0.459615	-6.01
261294_at	dihydroxyacetone kinase, putative simil	---	AT1G48430	-1.16	-0.21	-1.29	0.238603	0.459752	-6.01
249441_at	avirulence induced gene (AIG) - like pro	---	AT5G39730	1.14	0.19	1.29	0.238695	0.459890	-6.01
249088_at	selenium-binding protein-like	---	AT5G44230	-1.16	-0.21	-1.29	0.238751	0.459959	-6.01
263732_at	hypothetical protein predicted by genem	ARL2	AT1G59980	-1.12	-0.16	-1.29	0.238807	0.460027	-6.01
262343_at	phosphoprotein phosphatase 1 identical	TOPP3	AT1G64040	-1.10	-0.14	-1.29	0.238907	0.460031	-6.01
265752_at	putative Athila retroelement ORF1 prote	---	---	1.10	0.14	1.29	0.238884	0.460031	-6.01
267227_at	hypothetical protein predicted by gensca	---	AT2G44030	-1.14	-0.19	-1.29	0.238847	0.460031	-6.01
249995_at	protein kinase -like protein protein kinas	---	AT5G18610	-1.09	-0.13	-1.29	0.238882	0.460031	-6.01
255084_s_a	putative protein same aa sequence as p	---	AT4G09220 /	-1.10	-0.14	-1.29	0.23891	0.460031	-6.01
261518_at	peroxidase ATP4a identical to GB:CAA6	---	AT1G71695	-1.13	-0.18	-1.29	0.238981	0.460125	-6.01
256945_at	hypothetical protein similar to extensin-li	---	AT3G19020	1.11	0.15	1.29	0.239019	0.460125	-6.01
265751_at	putative retroelement pol polyprotein	---	---	1.09	0.13	1.29	0.239013	0.460125	-6.01
253239_at	putative serine/threonine protein kinase	---	AT4G34500	1.18	0.23	1.29	0.23918	0.460358	-6.01
262987_at	conserved hypothetical protein protein s	---	AT1G23240	1.17	0.23	1.29	0.23917	0.460358	-6.01
249801_at	calcium-dependent protein kinase (pir||S	CDPK9	AT5G23580	-1.11	-0.15	-1.29	0.239248	0.460450	-6.01
249571_at	putative protein predicted proteins, Aral	---	AT5G37620	1.09	0.13	1.29	0.239294	0.460499	-6.01
267199_at	hypothetical protein predicted by genefir	---	AT2G30990	1.39	0.48	1.29	0.239334	0.460505	-6.01
257501_at	hypothetical protein predicted by genem	---	---	-1.08	-0.11	-1.29	0.239338	0.460505	-6.01
252639_at	acyl CoA reductase -like protein acyl C	FAR5	AT3G44550	-1.09	-0.12	-1.29	0.239396	0.460579	-6.01
246989_at	unknown protein	---	AT5G67350	1.31	0.39	1.29	0.239441	0.460626	-6.01
265788_at	putative auxin-induced protein	IAA32	AT2G01200	-1.09	-0.12	-1.29	0.239464	0.460632	-6.01
258312_at	putative long-chain acyl-CoA synthetase	---	AT3G16170	-1.16	-0.21	-1.29	0.239515	0.460651	-6.01
253745_at	putative protein the C-terminus of the R	---	AT4G29090	1.10	0.14	1.29	0.239505	0.460651	-6.01
247536_at	PREG-like - like protein PREG-like prot	CYCP4;2	AT5G61650	1.13	0.18	1.29	0.239555	0.460651	-6.01
264795_at	unknown protein similar to ESTs emb|Z	ZIGA4	AT1G08680	-1.23	-0.30	-1.29	0.239537	0.460651	-6.01
247642_at	putative protein various predicted protei	---	AT5G60590	1.10	0.14	1.29	0.239652	0.460798	-6.01

266294_at	putative small heat shock protein ;supp	---	AT2G29500	1.61	0.69	1.29	0.239722	0.460856	-6.01
261061_at	DNA-binding protein, putative contains	TRFL2	AT1G07540	1.11	0.15	1.29	0.239721	0.460856	-6.01
246375_at	light repressible receptor protein kinase	---	AT1G51830	-1.16	-0.22	-1.29	0.239888	0.461136	-6.01
247296_at	unknown protein ;supported by full-leng	---	AT5G64160	1.14	0.19	1.29	0.240031	0.461373	-6.01
253667_at	peroxidase ATP8a ;supported by full-le	---	AT4G30170	1.10	0.14	1.29	0.240113	0.461491	-6.01
255744_at	hypothetical protein predicted by genem	---	---	-1.08	-0.11	-1.29	0.240196	0.461611	-6.01
250726_at	putative protein similar to unknown prote	---	AT5G06410	-1.13	-0.18	-1.29	0.240445	0.462042	-6.01
258431_at	hypothetical protein predicted by genefir	---	AT3G16580	1.10	0.13	1.29	0.24046	0.462042	-6.01
263270_at	putative replication protein A1	---	---	1.10	0.14	1.29	0.240534	0.462144	-6.01
249566_at	cytochrome P450-like protein	CYP735A1	AT5G38450	1.11	0.14	1.29	0.240597	0.462226	-6.01
256406_at	unknown protein	---	AT1G50710	1.12	0.16	1.29	0.240761	0.462503	-6.01
262252_at	RING-H2 zinc finger protein ATL3, puta	---	AT1G53820	1.10	0.14	1.29	0.240786	0.462511	-6.01
248502_at	putative protein strong similarity to unkn	---	AT5G50450	-1.15	-0.20	-1.29	0.240818	0.462535	-6.01
251425_at	putative protein chloroplast Cpn21 prote	---	AT3G60210	-1.12	-0.16	-1.29	0.240878	0.462612	-6.01
265845_at	unknown protein	---	AT2G35610	1.08	0.11	1.29	0.240923	0.462659	-6.01
259644_at	unknown protein	---	AT1G68910	-1.13	-0.18	-1.29	0.240999	0.462766	-6.01
252394_at	heat shock protein-like protein heat-sho	---	AT3G47940	-1.15	-0.20	-1.29	0.241224	0.463159	-6.02
245373_s_a	Expressed protein ; supported by full-ler	ATARD2	AT4G14710 /	-1.11	-0.15	-1.28	0.241334	0.463330	-6.02
261810_at	ligase I, putative similar to ligase I GI:11	ATLIG1	AT1G08130	-1.22	-0.29	-1.28	0.241507	0.463623	-6.02
254936_at	predicted protein of unknown function	---	AT4G10790	-1.09	-0.12	-1.28	0.241568	0.463701	-6.02
245765_at	hypothetical protein similar to putative d	---	AT1G33600	1.39	0.48	1.28	0.241659	0.463833	-6.02
256840_x_a	unknown protein similar to putative Athil	---	---	-1.09	-0.12	-1.28	0.241677	0.463833	-6.02
256188_at	unknown protein similar to hypothetical	---	AT1G30160	-1.22	-0.29	-1.28	0.241832	0.464091	-6.02
257642_at	putative HLH DNA-binding protein conta	BHLH32	AT3G25710	-1.14	-0.18	-1.28	0.241913	0.464208	-6.02
251051_at	putative zinc finger protein zinc finger p	---	AT5G02460	-1.12	-0.16	-1.28	0.241941	0.464223	-6.02
264143_at	latex-abundant protein, putative similar	ATMC5	AT1G79330	1.10	0.14	1.28	0.241993	0.464284	-6.02
265085_at	hypothetical protein predicted by gensca	TPX2	AT1G03780	1.16	0.21	1.28	0.242016	0.464288	-6.02
250838_at	cytochrome P450 - like protein cytochro	CYP77A9	AT5G04630	-1.09	-0.12	-1.28	0.242132	0.464472	-6.02
266823_at	hypothetical protein predicted by gensca	---	AT2G44930	1.11	0.15	1.28	0.242276	0.464708	-6.02
245818_at	cytochrome b561, putative similar to cy	---	AT1G26100	-1.21	-0.28	-1.28	0.242303	0.464721	-6.02
255673_at	Similar to receptor-like protein kinase p	RLK4	AT4G00340	-1.11	-0.14	-1.28	0.242378	0.464802	-6.02
249399_at	putative protein intracellular protein Mg	---	AT5G40290	1.08	0.11	1.28	0.242386	0.464802	-6.02
265988_at	hypothetical protein predicted by genefir	---	AT2G24255	-1.10	-0.14	-1.28	0.242442	0.464871	-6.02
263418_at	putative selenium-binding protein	---	AT2G17210	-1.10	-0.14	-1.28	0.242546	0.464991	-6.02
265174_s_a	polygalacturonase, putative similar to p	---	AT1G23460 /	-1.17	-0.22	-1.28	0.242538	0.464991	-6.02

258105_at	Expressed protein ; supported by full-ler	---	AT3G23605	1.22	0.28	1.28	0.242587	0.464992	-6.02
260974_at	receptor-like serine/threonine kinase, p	---	AT1G53440	-1.24	-0.31	-1.28	0.242587	0.464992	-6.02
257985_at	hypothetical protein predicted by gensca	---	AT3G20810	1.14	0.18	1.28	0.242757	0.465279	-6.02
258871_at	putative 26S proteosome regulatory sub	---	AT3G03060	-1.27	-0.34	-1.28	0.242792	0.465307	-6.02
255321_at	putative ES43-like protein	---	AT4G04260	-1.11	-0.15	-1.28	0.242861	0.465360	-6.02
248002_at	Expressed protein ; supported by full-ler	ATARP8	AT5G56180	1.15	0.21	1.28	0.242848	0.465360	-6.02
263302_at	hypothetical protein predicted by gensca	---	---	-1.08	-0.12	-1.28	0.242919	0.465434	-6.02
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281 /DE	---	---	-1.09	-0.13	-1.28	0.24302	0.465588	-6.02
249534_at	bZIP transcription factor - like protein p	AtbZIP43	AT5G38800	1.09	0.13	1.28	0.24307	0.465645	-6.02
250873_at	lipase -like protein lipase Arab-1, Arabi	---	AT5G03980	1.11	0.15	1.28	0.243164	0.465708	-6.02
259376_at	unknown protein C-terminus similar to C	CDC27a	AT3G16320	1.11	0.14	1.28	0.243148	0.465708	-6.02
260694_at	NAD+ dependent isocitrate dehydroger	---	AT1G32480	-1.09	-0.12	-1.28	0.243153	0.465708	-6.02
263581_at	hypothetical protein identical to hypothe	---	AT2G17160	1.13	0.17	1.28	0.243217	0.465729	-6.02
259354_at	unknown protein	---	AT3G05220	1.18	0.24	1.28	0.243208	0.465729	-6.02
248517_at	St12p protein	---	AT5G50550 /	-1.11	-0.15	-1.28	0.243252	0.465758	-6.02
252650_at	putative protein	---	AT3G44690	-1.10	-0.13	-1.28	0.24338	0.465926	-6.02
262226_at	Expressed protein ; supported by full-ler	---	AT1G53885 /	-1.32	-0.40	-1.28	0.24337	0.465926	-6.02
259485_at	ATP synthase gamma-subunit, putative	ATPC2	AT1G15700	-1.25	-0.33	-1.28	0.243418	0.465959	-6.02
265653_at	hypothetical protein	---	---	1.09	0.12	1.28	0.243468	0.466016	-6.02
253150_at	putative protein predicted protein, Arabi	---	AT4G35660	1.08	0.11	1.28	0.243576	0.466153	-6.02
249502_s_a	expansin-like protein expansin - Prunus	ATEXPA2	AT5G39280 /	1.13	0.17	1.28	0.243581	0.466153	-6.02
244916_at	hypothetical protein	ORF187	ATMG00880	1.10	0.13	1.28	0.243607	0.466163	-6.02
265771_at	unknown protein ;supported by full-leng	---	AT2G48030	1.13	0.18	1.28	0.243688	0.466208	-6.02
261670_at	hypothetical protein contains similarity to	TET11	AT1G18520	1.09	0.12	1.28	0.243675	0.466208	-6.02
249298_at	putative protein similar to unknown prote	---	AT5G41330	-1.10	-0.14	-1.28	0.243691	0.466208	-6.02
247880_at	putative protein similar to unknown prote	---	AT5G57780	-1.45	-0.54	-1.28	0.243717	0.466218	-6.02
265870_at	hypothetical protein predicted by genefir	PDLP6	AT2G01660	-1.09	-0.13	-1.28	0.243851	0.466435	-6.02
248955_at	putative protein contains similarity to unl	GAS41	AT5G45600	-1.10	-0.14	-1.28	0.243967	0.466548	-6.02
264059_at	Expressed protein ; supported by full-ler	INH3	AT2G31305	1.11	0.15	1.28	0.243937	0.466548	-6.02
245254_at	ATP-sulfurylase ; supported by cDNA: g	APS3	AT4G14680	-1.51	-0.59	-1.28	0.243971	0.466548	-6.02
245558_at	hypothetical protein	---	AT4G15430	1.09	0.12	1.28	0.244018	0.466598	-6.03
267107_at	hypothetical protein predicted by gensca	---	---	1.11	0.15	1.28	0.244048	0.466616	-6.03
261492_at	acid phosphatase, putative similar to ac	SBH2	AT1G14290	1.14	0.19	1.28	0.244157	0.466629	-6.03
261390_at	hypothetical protein similar to hypothetic	---	AT1G35040	1.09	0.13	1.28	0.244152	0.466629	-6.03
247560_at	putative protein predicted proteins, from	---	AT5G61090	1.14	0.18	1.28	0.244157	0.466629	-6.03

262662_at	hypothetical protein similar to hypothetic	---	AT1G13920	1.12	0.17	1.28	0.244116	0.466629	-6.03
245083_at	putative integral membrane protein ;sup	ATRER1C	AT2G23310	-1.11	-0.15	-1.28	0.244154	0.466629	-6.03
262004_at	calcineurin B-like protein similar to CAL	CBL8	AT1G64480	1.15	0.20	1.28	0.244362	0.466982	-6.03
249450_at	serine/threonine-specific protein kinase	SnRK1.3	AT5G39440	-1.10	-0.14	-1.28	0.244494	0.467195	-6.03
261160_at	hypothetical protein	---	AT1G34480	1.10	0.14	1.28	0.244524	0.467213	-6.03
263731_at	metalloproteinase, putative similar to m	---	AT1G59970	1.37	0.46	1.28	0.24455	0.467225	-6.03
253719_at	putative protein, fragment prolidase - S	---	AT4G29490	-1.08	-0.12	-1.27	0.244626	0.467291	-6.03
257170_at	beta-1,3-glucanase, putative similar to I	---	AT3G23770	-1.15	-0.21	-1.27	0.244619	0.467291	-6.03
266480_at	unknown protein ; supported by cDNA:	---	AT2G31130	-1.09	-0.13	-1.27	0.24467	0.467335	-6.03
267530_at	putative receptor-like protein kinase	---	AT2G41890	-1.27	-0.34	-1.27	0.244798	0.467499	-6.03
261816_at	unknown protein	CHX6B	AT1G08135	1.10	0.14	1.27	0.244779	0.467499	-6.03
257747_at	hypothetical protein predicted by genem	---	AT3G18700	1.09	0.12	1.27	0.244817	0.467499	-6.03
258676_at	hypothetical protein predicted by gensca	---	AT3G08600	-1.13	-0.17	-1.27	0.244915	0.467627	-6.03
262726_at	hypothetical protein similar to putative T	AtTLP5	AT1G43640	1.13	0.18	1.27	0.244925	0.467627	-6.03
245814_at	mitotic checkpoint protein, putative simi	---	AT1G49910	1.13	0.18	1.27	0.244951	0.467638	-6.03
262176_at	3-ketoacyl-ACP synthase, putative simi	FAB1	AT1G74960	-1.13	-0.17	-1.27	0.244979	0.467651	-6.03
259041_at	unknown protein similar to putative gluc	ATCSLC6	AT3G07330	1.16	0.22	1.27	0.245073	0.467791	-6.03
245947_at	spermine synthase (ACL5) ;supported b	ACL5	AT5G19530	-1.19	-0.25	-1.27	0.245175	0.467846	-6.03
253901_at	ribosomal protein L14 -like protein ribos	---	AT4G27090	-1.18	-0.24	-1.27	0.245123	0.467846	-6.03
252558_at	actin depolymerising like protein Actin d	---	AT3G45990	1.10	0.14	1.27	0.245183	0.467846	-6.03
257385_at	hypothetical protein predicted by gensca	---	AT2G01800	-1.12	-0.16	-1.27	0.245183	0.467846	-6.03
257007_at	Expressed protein ; supported by cDNA	---	AT3G14205	1.09	0.12	1.27	0.245223	0.467882	-6.03
263686_at	putative 60s ribosomal protein L10 Nea	---	AT1G26910	1.18	0.23	1.27	0.245276	0.467945	-6.03
257163_at	DNA-binding protein, putative similar to	MYB305	AT3G24310	1.11	0.14	1.27	0.245366	0.468077	-6.03
254375_at	putative protein (fragment) ATP(GTP)-b	QQT2	AT4G21800	-1.11	-0.14	-1.27	0.245495	0.468206	-6.03
261840_at	hypothetical protein contains similarity to	AtTLP8	AT1G16070	1.10	0.13	1.27	0.245491	0.468206	-6.03
257776_at	terpene synthase-related protein contain	---	AT3G29190	-1.12	-0.16	-1.27	0.245468	0.468206	-6.03
245105_at	hypothetical protein predicted by gensca	---	AT2G41610	1.19	0.25	1.27	0.245667	0.468303	-6.03
245798_at	hypothetical protein predicted by genem	---	AT1G45545	-1.08	-0.11	-1.27	0.245631	0.468303	-6.03
250535_at	putative protein similar to unknown prote	---	AT5G08480	1.11	0.15	1.27	0.245614	0.468303	-6.03
251838_at	cysteine proteinase non-consensus AG	---	AT3G54940	1.12	0.17	1.27	0.245599	0.468303	-6.03
246373_at	receptor-like protein kinase, putative sir	---	AT1G51860	1.17	0.23	1.27	0.245594	0.468303	-6.03
257241_at	hypothetical protein contains Pfam profil	---	AT3G24210	1.13	0.18	1.27	0.245669	0.468303	-6.03
250616_at	receptor-like protein kinase-like protein	EMS1	AT5G07280	1.13	0.17	1.27	0.245694	0.468311	-6.03
265012_at	putative b-keto acyl reductase similar to	KCR2	AT1G24470	1.11	0.15	1.27	0.245742	0.468351	-6.03

252472_at	GTP-binding protein Rab11 ; supported	ATRABA2	AT3G46830	-1.12	-0.17	-1.27	0.245765	0.468351	-6.03
245215_at	F12A21.4 similar to iEP4 gb|AAD11468	ATFXG1	AT1G67830	-1.25	-0.32	-1.27	0.245776	0.468351	-6.03
262474_at	hypothetical protein identical to hypothe	FU	AT1G50240	1.12	0.16	1.27	0.245825	0.468404	-6.03
254592_at	heat shock transcription factor - like pro	HSF A4A	AT4G18880	1.37	0.46	1.27	0.245999	0.468659	-6.03
267167_at	putative C2H2-type zinc finger protein li	ZFP10	AT2G37740	1.11	0.15	1.27	0.246	0.468659	-6.03
250780_at	expansin At-EXP2 (gb|AAB38073.1) ; s	ATEXPA2	AT5G05290	-1.15	-0.21	-1.27	0.246035	0.468684	-6.03
267313_at	putative protein phosphatase 2C	---	AT2G34740	-1.14	-0.18	-1.27	0.246054	0.468684	-6.03
266690_at	malate oxidoreductase (malic enzyme)	ATNADP-M	AT2G19900	1.10	0.14	1.27	0.246093	0.468719	-6.03
254358_at	putative protein light induced protein ho	---	AT4G22310	-1.08	-0.11	-1.27	0.246145	0.468779	-6.03
254137_at	hypothetical protein	---	AT4G24930	-1.20	-0.26	-1.27	0.246314	0.469062	-6.03
258881_at	unknown protein ; supported by full-leng	---	AT3G06310	-1.11	-0.15	-1.27	0.246398	0.469146	-6.03
264218_at	unknown protein	---	AT1G60200	1.09	0.12	1.27	0.2464	0.469146	-6.03
264421_at	ribosomal protein identical to ribosomal	ARP1	AT1G43170	-1.16	-0.21	-1.27	0.24654	0.469375	-6.03
251880_at	hypothetical protein ;supported by full-le	---	AT3G54290	-1.15	-0.20	-1.27	0.246565	0.469384	-6.03
264659_at	unknown protein Similar to S. pombe IS	ATOPT2	AT1G09930	1.10	0.14	1.27	0.246587	0.469386	-6.03
255310_at	Expressed protein ; supported by full-ler	ATALN	AT4G04955	-1.29	-0.36	-1.27	0.246613	0.469396	-6.03
256664_at	DNA-3-methlyadenine glycosylase (MA	---	AT3G12040	1.14	0.19	1.27	0.246652	0.469430	-6.03
259387_at	histone H3 protein, putative similar to h	---	AT1G13370	-1.09	-0.13	-1.27	0.246672	0.469430	-6.03
266260_at	putative ATPase skd1 family; supported	SKD1	AT2G27600	1.09	0.12	1.27	0.24672	0.469464	-6.03
249713_at	putative protein contains similarity to zin	---	AT5G35690	1.13	0.17	1.27	0.246731	0.469464	-6.03
264928_at	auxin-induced protein, putative similar t	ATB2	AT1G60710	-1.11	-0.15	-1.27	0.246765	0.469475	-6.03
246798_at	putative protein various predicted prote	---	AT5G26930	1.09	0.13	1.27	0.246778	0.469475	-6.03
250682_x_a	putative protein similar to unknown prote	---	AT5G06630	1.27	0.34	1.27	0.246903	0.469634	-6.04
249126_at	Expressed protein ; supported by cDNA	TOPP6	AT5G43380	1.25	0.32	1.27	0.246887	0.469634	-6.04
265734_at	predicted by genscan and genefinder ;s	---	AT2G01260	-1.10	-0.14	-1.27	0.246977	0.469736	-6.04
263482_at	putative GDSL-motif lipase/hydrolase si	---	AT2G03980	-1.61	-0.69	-1.27	0.247034	0.469766	-6.04
259631_at	heat shock protein, putative similar to h	ERD2	AT1G56410	-1.09	-0.12	-1.27	0.247018	0.469766	-6.04
256912_at	hypothetical protein predicted by genem	---	AT3G23850	1.11	0.15	1.27	0.247077	0.469808	-6.04
249537_at	cysteine-tRNA ligase -like protein cyste	---	AT5G38830	1.14	0.19	1.27	0.24711	0.469833	-6.04
254635_at	extensin-like protein extensin-like prote	---	AT4G18670	1.12	0.17	1.27	0.247178	0.469923	-6.04
255362_at	putative reverse transcriptase	---	---	1.09	0.12	1.27	0.247203	0.469931	-6.04
256205_at	hypothetical protein	---	AT1G50890	1.10	0.14	1.27	0.247246	0.469973	-6.04
260120_at	hypothetical protein	ATPP2-A4	AT1G33920	1.11	0.15	1.27	0.247301	0.470002	-6.04
265585_at	CDC27/NUC2-like protein TPR-repeat p	HBT	AT2G20000	-1.13	-0.18	-1.27	0.247302	0.470002	-6.04
254566_at	hypothetical protein	---	AT4G19240	-1.14	-0.19	-1.27	0.247385	0.470059	-6.04

264388_at	hypothetical protein contains similarity to	---	AT1G11970	1.13	0.17	1.27	0.247405	0.470059	-6.04
255108_at	hypothetical protein	---	AT4G08740	1.14	0.19	1.27	0.247415	0.470059	-6.04
245918_at	putative protein various predicted prote	---	---	-1.09	-0.12	-1.27	0.247401	0.470059	-6.04
247806_at	ABC transporter-like protein ; supported	STA1	AT5G58270	1.10	0.14	1.27	0.247519	0.470219	-6.04
253255_at	putative auxin-regulated protein auxin-i	---	AT4G34760	-1.49	-0.57	-1.27	0.247676	0.470320	-6.04
251268_at	putative protein hypothetical proteins - A	---	AT3G62350	-1.12	-0.16	-1.27	0.247717	0.470320	-6.04
263230_at	putative indole-3-acetate beta-glucosyltr	---	AT1G05670	1.21	0.28	1.27	0.247643	0.470320	-6.04
255414_at	hypothetical protein	---	AT4G03156	-1.08	-0.12	-1.27	0.24764	0.470320	-6.04
252900_at	shikimate kinase - like protein shikimate	---	AT4G39540	-1.15	-0.20	-1.27	0.247705	0.470320	-6.04
249735_at	putative protein contains similarity to ge	---	AT5G24450	1.14	0.19	1.27	0.247646	0.470320	-6.04
263057_at	hypothetical protein predicted by genefir	---	AT2G09840	1.15	0.20	1.27	0.247707	0.470320	-6.04
259736_at	endo-beta-1,4-glucanase, putative simil	AtGH9C2	AT1G64390	1.69	0.76	1.27	0.247821	0.470440	-6.04
254377_at	subtilisin proteinase - like subtilisin-like	---	AT4G21650	1.67	0.74	1.27	0.24782	0.470440	-6.04
249967_at	putative protein	---	AT5G19050	1.11	0.15	1.27	0.247901	0.470512	-6.04
256561_s_a	hypothetical protein similar to putative re	---	---	-1.09	-0.13	-1.27	0.247893	0.470512	-6.04
256656_at	hypothetical protein similar to hypothetic	---	AT3G18900	1.10	0.14	1.26	0.248025	0.470709	-6.04
258192_at	putative terpene synthase-related prote	---	AT3G29110	1.09	0.12	1.26	0.248116	0.470833	-6.04
250039_at	disease resistance protein -like disease	---	AT5G18370	-1.13	-0.17	-1.26	0.248132	0.470833	-6.04
265391_at	Expressed protein ; supported by cDNA	GAUT10	AT2G20810	-1.09	-0.12	-1.26	0.24816	0.470847	-6.04
247690_at	putative protein	MBD7	AT5G59800	-1.21	-0.27	-1.26	0.248331	0.471133	-6.04
262959_at	protein translation factor Sui1 homolog,	---	AT1G54290	1.12	0.16	1.26	0.248514	0.471442	-6.04
265062_at	receptor kinase, putative similar to rece	---	AT1G61550	1.19	0.25	1.26	0.248615	0.471593	-6.04
262963_at	dihydrolipoamide S-acetyltransferase, p	---	AT1G54220	-1.09	-0.13	-1.26	0.248684	0.471612	-6.04
251636_at	calcium-dependent protein kinase calci	CPK32	AT3G57530	1.39	0.48	1.26	0.248647	0.471612	-6.04
247417_at	putative protein similar to unknown prote	---	AT5G63040	-1.10	-0.14	-1.26	0.248687	0.471612	-6.04
251835_at	lipase -like protein monoglyceride lipase	---	AT3G55180	1.10	0.13	1.26	0.248722	0.471639	-6.04
248732_at	xyloglucan endo-1,4-beta-D-glucanase	XTH20	AT5G48070	-1.13	-0.18	-1.26	0.248743	0.471641	-6.04
249104_at	sucrose transporter protein	ATSUC6	AT5G43610	-1.10	-0.14	-1.26	0.248804	0.471717	-6.04
256775_at	hypothetical protein predicted by genem	---	AT3G13770	-1.18	-0.24	-1.26	0.248875	0.471812	-6.04
252615_at	serine/proline-rich protein	---	AT3G45230	-1.17	-0.23	-1.26	0.249073	0.472031	-6.04
255892_at	hypothetical protein contains similarity to	---	AT1G17910	1.10	0.13	1.26	0.249068	0.472031	-6.04
258163_at	aldose 1-epimerase, putative similar to	---	AT3G17940	-1.10	-0.14	-1.26	0.249012	0.472031	-6.04
256539_at	hypothetical protein predicted by genem	---	---	1.09	0.13	1.26	0.249073	0.472031	-6.04
247289_at	2-oxoglutarate/malate translocator ; sup	DIT2.1	AT5G64290	-1.13	-0.18	-1.26	0.249331	0.472404	-6.04
250473_at	annexin -like protein annexin (AnnAt2),	ANN6	AT5G10220	1.08	0.12	1.26	0.249301	0.472404	-6.04

247308_at	receptor-like protein kinase	---	AT5G63930	1.11	0.15	1.26	0.249332	0.472404	-6.04
250113_at	putative protein similar to unknown prote	FRL1	AT5G16320	-1.10	-0.14	-1.26	0.249451	0.472590	-6.04
254891_at	putative protein Fly Fas-associated fact	SAY1	AT4G11740	-1.09	-0.13	-1.26	0.249603	0.472839	-6.04
249740_at	unknown protein	---	AT5G24500	-1.16	-0.21	-1.26	0.249704	0.472950	-6.04
260214_at	hypothetical protein contains Pfam profil	---	AT1G74510	-1.10	-0.14	-1.26	0.249696	0.472950	-6.04
263771_at	putative Athila retroelement ORF1 prote	---	---	1.08	0.11	1.26	0.249827	0.473120	-6.05
267558_at	unknown protein ; supported by cDNA:	LUH	AT2G32700	-1.09	-0.13	-1.26	0.249835	0.473120	-6.05
246401_at	DNA-binding protein, putative similar to	AtMYB50	AT1G57560	1.18	0.24	1.26	0.249926	0.473214	-6.05
266723_at	SKP1/ASK1 (At16), putative similar to S	ASK16	AT2G03190	1.09	0.12	1.26	0.249925	0.473214	-6.05
247654_at	cytoplasmic ribosomal protein S15a - lik	---	AT5G59850	-1.29	-0.36	-1.26	0.250056	0.473343	-6.05
267554_at	E2, ubiquitin-conjugating enzyme, putat	---	AT2G32790	1.13	0.17	1.26	0.250047	0.473343	-6.05
267389_at	putative beta-glucosidase	BGLU28	AT2G44460	-2.47	-1.30	-1.26	0.250045	0.473343	-6.05
252996_s_a	geranylgeranyl pyrophosphate synthase	GGR	AT4G38460	1.12	0.16	1.26	0.250158	0.473496	-6.05
245392_at	glutaredoxin ;supported by full-length cD	---	AT4G15680	1.47	0.56	1.26	0.250211	0.473504	-6.05
246512_at	putative phytochelatin synthetase putat	IRX6	AT5G15630	1.14	0.18	1.26	0.250185	0.473504	-6.05
247392_at	glutamate-1-semialdehyde 2,1-aminom	GSA1	AT5G63570	1.17	0.22	1.26	0.250224	0.473504	-6.05
265096_at	unknown protein Location of ESTs 40C	---	AT1G04030	-1.12	-0.16	-1.26	0.250339	0.473681	-6.05
245262_at	predicted protein ; supported by cDNA:	---	AT4G16563	-1.19	-0.25	-1.26	0.25036	0.473683	-6.05
258888_at	putative pectinesterase similar to pectin	---	AT3G05620	1.19	0.25	1.26	0.250478	0.473867	-6.05
258588_s_a	glyceraldehyde-3-phosphate dehydroge	GAPC1	AT3G04120	1.24	0.31	1.26	0.250504	0.473876	-6.05
247653_at	transcriptional coactivator - like protein	---	AT5G59950	-1.09	-0.13	-1.26	0.25056	0.473943	-6.05
252665_at	valine-rich protein	---	AT3G44140	1.12	0.16	1.26	0.250627	0.474030	-6.05
264902_at	unknown protein Location of EST gb|T2	---	AT1G23060	-1.24	-0.30	-1.26	0.250798	0.474313	-6.05
AFFX-Athal-	Arabidopsis thaliana /REF=M64116 /DE	GAPC1	---	1.17	0.23	1.26	0.250923	0.474459	-6.05
249687_at	putative protein oxidosqualene cyclase;	ATPEN3	AT5G36150	1.10	0.14	1.26	0.250898	0.474459	-6.05
263923_at	Expressed protein ; supported by cDNA	---	AT2G36485	-1.15	-0.20	-1.26	0.250937	0.474459	-6.05
249405_at	beta subunit of protein farnesyl transfera	ERA1	AT5G40280	-1.10	-0.13	-1.26	0.251021	0.474541	-6.05
246870_at	ferrochelatase-I	FC1	AT5G26030	1.38	0.47	1.26	0.251022	0.474541	-6.05
247526_at	putative protein C2H2 zinc-finger protei	---	AT5G61470	1.10	0.13	1.26	0.251074	0.474600	-6.05
258960_at	hypothetical protein similar to myb-relat	---	AT3G10590	1.10	0.14	1.26	0.251219	0.474834	-6.05
256291_at	protein kinase, putative contains Pfam p	AtNek7	AT3G12200	-1.12	-0.17	-1.26	0.25127	0.474892	-6.05
249487_at	ABC transporter -like protein TAP-like A	TAP2	AT5G39040	1.21	0.27	1.26	0.251294	0.474898	-6.05
250774_at	ATP-dependent RNA helicase-like prote	---	AT5G05450	-1.15	-0.20	-1.25	0.251421	0.475099	-6.05
251723_at	putative protein speckle-type protein, S	---	AT3G56230	1.13	0.17	1.25	0.251491	0.475191	-6.05
249511_at	putative protein contains similarity to unl	---	AT5G38500	1.09	0.13	1.25	0.251568	0.475298	-6.05

262486_at	putative bzip-like transcription factor sir	---	AT1G21740	1.16	0.21	1.25	0.251647	0.475408	-6.05
266303_at	putative receptor-like protein kinase	---	AT2G27060	-1.20	-0.26	-1.25	0.25173	0.475485	-6.05
246082_at	receptor protein kinase - like protein kir	EFR	AT5G20480	1.34	0.42	1.25	0.25172	0.475485	-6.05
261175_at	unknown protein	---	AT1G04800	-1.11	-0.15	-1.25	0.251891	0.475751	-6.05
264547_at	unknown protein ; supported by cDNA: g	CLC-F	AT1G55620	-1.16	-0.21	-1.25	0.251918	0.475762	-6.05
266581_at	putative desiccation related protein ; su	---	AT2G46140	1.59	0.67	1.25	0.252057	0.475797	-6.05
252491_at	disease resistance protein RPP8-like p	---	AT3G46730	-1.09	-0.12	-1.25	0.252021	0.475797	-6.05
245966_at	AP2 domain containing protein RAP2.1	RAP2.11	AT5G19790	1.11	0.15	1.25	0.252012	0.475797	-6.05
257657_at	Expressed protein ; supported by full-ler	---	AT3G13235	1.09	0.13	1.25	0.252021	0.475797	-6.05
252720_at	putative protein predicted protein, Arabi	---	AT3G43970	-1.12	-0.17	-1.25	0.251961	0.475797	-6.05
256194_at	unknown protein	---	---	-1.14	-0.19	-1.25	0.252062	0.475797	-6.05
249301_at	putative protein similar to unknown prote	---	AT5G41440	1.13	0.17	1.25	0.25217	0.475922	-6.05
253933_at	hypothetical protein	---	AT4G26820	1.12	0.16	1.25	0.252164	0.475922	-6.05
250859_at	cytochrom P450 - like protein cytochror	CYP77A4	AT5G04660	-1.08	-0.11	-1.25	0.252236	0.476008	-6.05
257206_at	putative lectin similar to lectin SP:P0287	---	AT3G16530	1.64	0.71	1.25	0.252416	0.476277	-6.05
263137_at	gamma glutamyl hydrolase, putative sir	ATGGH1	AT1G78660	1.23	0.30	1.25	0.25242	0.476277	-6.05
253509_at	putative protein kainate receptor, Rattus	GLR2.4	AT4G31710	1.11	0.15	1.25	0.252447	0.476287	-6.05
245442_at	hypothetical protein	---	AT4G16710	-1.09	-0.12	-1.25	0.252565	0.476472	-6.05
262837_at	dynamin, putative similar to dynamin-1	ADL1C	AT1G14830	1.11	0.15	1.25	0.252714	0.476660	-6.05
248637_at	DNAJ-like protein	---	AT5G49060	-1.10	-0.13	-1.25	0.252728	0.476660	-6.05
254961_at	putative acyl-CoA synthetase acyl-CoA	---	AT4G11030	1.11	0.15	1.25	0.252725	0.476660	-6.05
248395_at	putative protein contains similarity to un	AtPP2-A14	AT5G52120	-1.15	-0.20	-1.25	0.252791	0.476739	-6.06
263888_at	unknown protein	---	AT2G37000	1.14	0.19	1.25	0.25293	0.476961	-6.06
255538_at	putative transcription factor ; supported	MYB55	AT4G01680	1.31	0.39	1.25	0.253112	0.477227	-6.06
266169_at	putative protease inhibitor ;supported b	---	AT2G38900	-1.09	-0.13	-1.25	0.253107	0.477227	-6.06
264683_at	unknown protein similar to putative inos	FRA3	AT1G65580	-1.08	-0.12	-1.25	0.253137	0.477234	-6.06
253793_at	myosin heavy chain - like protein (fragn	XIH	AT4G28710	1.09	0.12	1.25	0.25321	0.477268	-6.06
264061_at	putative cyclin-dependent kinase regula	CKS2	AT2G27970	-1.24	-0.31	-1.25	0.253177	0.477268	-6.06
252605_s_a	sulfotransferase-like protein FLAVONO	---	AT3G45070 /	-1.08	-0.12	-1.25	0.253218	0.477268	-6.06
260909_at	hypothetical protein predicted by genem	---	AT1G02670	1.12	0.16	1.25	0.253266	0.477320	-6.06
251602_at	Expressed protein ; supported by full-ler	---	AT3G57785	-1.10	-0.14	-1.25	0.253338	0.477415	-6.06
249647_at	putative protein hypothetical proteins - A	---	AT5G37040	1.14	0.18	1.25	0.253375	0.477445	-6.06
255571_at	hypothetical protein ; supported by cDN	---	AT4G01220	-1.18	-0.24	-1.25	0.253472	0.477484	-6.06
257775_at	short-chain alcohol dehydrogenase, put	---	AT3G29260	1.11	0.15	1.25	0.253479	0.477484	-6.06
250070_at	phosphoribosylanthranilate transferase-	---	AT5G17980	1.19	0.25	1.25	0.253431	0.477484	-6.06

260272_at	F-box protein family, AtFBL14 contains	---	AT1G80570	-1.15	-0.20	-1.25	0.253473	0.477484	-6.06
261720_at	hypothetical protein similar to hypothetic	HDA08	AT1G08460	-1.19	-0.25	-1.25	0.253511	0.477505	-6.06
262364_at	disease resistance protein, putative sim	---	AT1G72860	1.09	0.13	1.25	0.253614	0.477659	-6.06
245584_at	amine oxidase like protein	ATAO1	AT4G14940	1.08	0.12	1.25	0.253731	0.477763	-6.06
262614_at	putative pattern formation protein EMB3	GN	AT1G13980	-1.18	-0.24	-1.25	0.253725	0.477763	-6.06
256721_at	hypothetical protein predicted by genefi	WAVE1	AT2G34150	1.13	0.17	1.25	0.253714	0.477763	-6.06
251314_at	putative protein several hypothetical pro	---	AT3G61180	-1.08	-0.11	-1.25	0.253774	0.477803	-6.06
260579_at	putative cytochrome c oxidase Vc subur	---	AT2G47380	1.11	0.15	1.25	0.253845	0.477898	-6.06
264229_at	unknown protein	---	AT1G67480	1.17	0.23	1.25	0.253879	0.477923	-6.06
251323_at	delta-8 sphingolipid desaturase ;suppor	---	AT3G61580	1.12	0.16	1.25	0.253929	0.477965	-6.06
259511_at	unknown protein contains similarity to c	ATCCS	AT1G12520	1.36	0.45	1.25	0.253955	0.477965	-6.06
257605_at	hypothetical protein predicted by genem	---	AT3G13840	1.08	0.11	1.25	0.253965	0.477965	-6.06
250334_at	NADH dehydrogenase (ubiquinone) ;su	---	AT5G11770	1.10	0.14	1.25	0.254004	0.478000	-6.06
263663_at	putative malate dehydrogenase similar t	---	AT1G04410	1.10	0.14	1.25	0.254035	0.478019	-6.06
251547_at	putative protein predicted proteins, Arat	---	AT3G58860	-1.11	-0.15	-1.25	0.254075	0.478055	-6.06
251548_at	putative protein predicted protein, Arabi	---	---	1.13	0.18	1.25	0.254133	0.478125	-6.06
264919_at	hypothetical protein contains similarity to	---	AT1G60540	1.10	0.14	1.25	0.2542	0.478211	-6.06
251704_at	putative protein unknown protein 110K5	---	AT3G56360	-1.28	-0.35	-1.25	0.254278	0.478318	-6.06
260204_at	hypothetical protein predicted by gensca	---	AT1G52900	1.10	0.14	1.25	0.25434	0.478395	-6.06
254316_at	putative protein glycine-rich cell wall pro	---	---	-1.11	-0.15	-1.25	0.254438	0.478540	-6.06
248415_at	unknown protein	---	AT5G51620	-1.09	-0.13	-1.25	0.254523	0.478659	-6.06
247787_at	putative protein various predicted protei	---	AT5G58640	-1.09	-0.13	-1.24	0.25479	0.478965	-6.06
267215_at	hypothetical protein	---	AT2G02630	1.08	0.11	1.25	0.254734	0.478965	-6.06
260697_at	unknown protein	---	AT1G32530	1.16	0.22	1.24	0.254751	0.478965	-6.06
257728_at	hypothetical protein predicted by genem	---	AT3G18295	1.13	0.18	1.25	0.254708	0.478965	-6.06
260270_at	putative disease resistance protein simil	---	AT1G63730	-1.10	-0.14	-1.24	0.25479	0.478965	-6.06
257593_at	phosphatidylinositol transfer protein, pu	---	AT3G24840	1.09	0.13	1.24	0.254842	0.479023	-6.06
262495_at	unknown protein Contains similarity to g	---	AT1G21780	1.15	0.21	1.24	0.254897	0.479047	-6.06
252314_at	hypothetical protein	---	AT3G49400	-1.11	-0.15	-1.24	0.254889	0.479047	-6.06
258614_at	putative S-adenosylmethionine:2-demet	---	AT3G02770	1.19	0.25	1.24	0.254969	0.479143	-6.06
256412_at	hypothetical protein predicted by genem	ELO1	AT3G11220	-1.11	-0.15	-1.24	0.255013	0.479186	-6.06
249969_at	putative protein glycine-rich protein GR	---	AT5G19090	1.20	0.27	1.24	0.255062	0.479239	-6.06
263490_at	F-box protein ORE9, AtFBL7 identical t	MAX2	AT2G42620	-1.21	-0.28	-1.24	0.255101	0.479273	-6.06
245685_at	Expressed protein ; supported by cDNA	E2F1	AT5G22220	1.09	0.12	1.24	0.255125	0.479279	-6.06
260256_at	putative type II intron maturase contains	---	AT1G74350	1.12	0.16	1.24	0.255396	0.479747	-6.06

249919_at	putative protein predicted protein, Arabi	---	AT5G19250	1.12	0.16	1.24	0.255416	0.479747	-6.06
246205_at	hypothetical protein ; supported by cDNA	---	AT4G36970	-1.21	-0.27	-1.24	0.255617	0.480030	-6.06
258593_at	unknown protein	---	AT3G04480	1.16	0.22	1.24	0.25563	0.480030	-6.06
256036_at	fructose-2,6-bisphosphatase, putative s	F2KP	AT1G07110	-1.11	-0.15	-1.24	0.255629	0.480030	-6.06
256155_at	MYB-family transcription factor, putative	MYB83	AT3G08500	1.09	0.12	1.24	0.255689	0.480102	-6.06
250246_at	polyamine oxidase	ATPAO1	AT5G13700	1.08	0.12	1.24	0.25578	0.480193	-6.07
262286_at	Expressed protein ; supported by full-ler	---	AT1G68585	-1.23	-0.30	-1.24	0.255774	0.480193	-6.07
252750_at	putative protein hypothetical protein q3(	---	AT3G43420	-1.08	-0.11	-1.24	0.255841	0.480269	-6.07
249961_at	putative protein predicted proteins, Arat	---	AT5G18770	-1.12	-0.16	-1.24	0.255927	0.480390	-6.07
259716_at	unknown protein	---	AT1G60995 /	-1.14	-0.19	-1.24	0.256015	0.480516	-6.07
257065_at	diacylglycerol pyrophosphate phosphat	---	AT3G18220	1.16	0.22	1.24	0.25606	0.480560	-6.07
261799_at	unknown protein contains similarity to co	---	AT1G30473	1.15	0.20	1.24	0.256141	0.480673	-6.07
250108_at	homeobox-leucine zipper protein HAT7	ATHB-3	AT5G15150	1.13	0.18	1.24	0.256183	0.480712	-6.07
256286_at	unknown protein	---	AT3G12180	-1.11	-0.15	-1.24	0.256283	0.480859	-6.07
254989_at	retrotransposon like protein copia-like r	---	---	1.12	0.16	1.24	0.256313	0.480877	-6.07
252210_at	DNA binding protein	OBP1	AT3G50410	1.17	0.23	1.24	0.256383	0.480969	-6.07
253159_at	HMG delta protein ;supported by full-ler	HMGB5	AT4G35570	-1.09	-0.13	-1.24	0.256466	0.481086	-6.07
260259_at	unknown protein similar to unknown pro	---	AT1G74300	1.10	0.14	1.24	0.256505	0.481119	-6.07
250518_at	Expressed protein ; supported by cDNA	---	AT5G08139	-1.09	-0.12	-1.24	0.256538	0.481119	-6.07
263330_at	putative leucine-rich repeat disease resi	---	AT2G15320	-1.23	-0.30	-1.24	0.256548	0.481119	-6.07
258821_at	putative wound-induced basic protein s	---	AT3G07230	-1.13	-0.18	-1.24	0.256635	0.481243	-6.07
263347_at	putative U4/U6 small nuclear ribonucleo	---	AT2G05720	1.14	0.19	1.24	0.256723	0.481296	-6.07
246814_at	acyl carrier protein precursor - like acyl	ACP5	AT5G27200	1.09	0.13	1.24	0.256721	0.481296	-6.07
248408_at	ripening-related protein-like	---	AT5G51520	1.09	0.12	1.24	0.256726	0.481296	-6.07
246131_at	MOLYBDOPTERIN BIOSYNTHESIS CN	B73	AT5G20990	1.09	0.12	1.24	0.256945	0.481649	-6.07
249788_at	putative protein contains similarity to unl	ATXR6	AT5G24330	1.16	0.21	1.24	0.256978	0.481649	-6.07
264457_at	puative glucosyl transferase similar to in	---	AT1G10400	-1.11	-0.15	-1.24	0.256976	0.481649	-6.07
262444_at	hypothetical protein similar to putative e	---	AT1G47480	1.20	0.27	1.24	0.257002	0.481655	-6.07
264653_at	unknown protein Contains similarity to F	AMI1	AT1G08980	-1.15	-0.21	-1.24	0.257039	0.481684	-6.07
255244_at	putative protein various hypothetical pro	---	AT4G05620	1.10	0.14	1.24	0.25716	0.481871	-6.07
251891_at	aintegumaenta-like protein ovule develo	WRI1	AT3G54320	-1.09	-0.12	-1.24	0.257184	0.481876	-6.07
258086_at	dihydrolipoamide S-acetyltransferase id	LTA2	AT3G25860	-1.13	-0.17	-1.24	0.257262	0.481984	-6.07
252304_at	hypothetical protein	---	AT3G49230	1.08	0.11	1.24	0.257285	0.481987	-6.07
254403_at	subtilisin-like serine protease contains s	---	AT4G21323	1.08	0.11	1.24	0.257334	0.482039	-6.07
259271_at	Expressed protein ; supported by full-ler	---	AT3G01170	1.12	0.16	1.24	0.257398	0.482118	-6.07

267323_at	unknown protein	---	AT2G19340	1.10	0.14	1.24	0.257484	0.482241	-6.07
251041_at	ubiquitin-protein ligase E3-alpha -like p	PRT6	AT5G02310	1.15	0.20	1.24	0.257523	0.482275	-6.07
245980_at	putative protein ;supported by full-lengt	---	AT5G13140	1.96	0.97	1.24	0.257581	0.482343	-6.07
250033_at	eukaryotic cap-binding protein (gb|AAC1	NCBP	AT5G18110	1.09	0.13	1.24	0.257664	0.482459	-6.07
253126_at	putative protein probable membrane pr	---	AT4G36050	-1.19	-0.25	-1.24	0.257721	0.482489	-6.07
260743_at	unknown protein	---	AT1G15030	1.21	0.28	1.24	0.257722	0.482489	-6.07
259265_at	hypothetical protein predicted by gensca	---	AT3G01250	1.09	0.12	1.24	0.25779	0.482537	-6.07
250432_at	putative protein various predicted prote	---	AT5G10420	-1.10	-0.13	-1.24	0.257785	0.482537	-6.07
251178_at	cytokinin oxidase -like protein cytokinin	CKX6	AT3G63440	1.25	0.32	1.24	0.257847	0.482564	-6.07
266363_at	hypothetical protein predicted by gensca	---	AT2G41250	-1.20	-0.26	-1.24	0.257841	0.482564	-6.07
256997_at	subtilisin-like serine protease, putative	---	AT3G14067	-1.17	-0.23	-1.24	0.257899	0.482621	-6.07
264565_at	hypothetical protein Similar to hypotheti	---	AT1G05280	1.14	0.18	1.24	0.257995	0.482761	-6.07
267218_at	Expressed protein ; supported by full-ler	---	AT2G02515	1.10	0.14	1.24	0.258076	0.482873	-6.07
263089_at	putative retroelement pol polyprotein	---	---	1.13	0.18	1.24	0.258128	0.482932	-6.07
261863_at	unknown protein ; supported by cDNA: g	---	AT1G50630	1.14	0.18	1.24	0.258153	0.482938	-6.07
263103_at	putative Ta11-like non-LTR retroelemen	---	---	1.11	0.14	1.23	0.258287	0.483150	-6.07
255842_at	putative serine carboxypeptidase II	scpl46	AT2G33530	1.27	0.35	1.23	0.258375	0.483240	-6.07
267301_at	ubiquitin activating enzyme 1 (UBA1) id	ATUBA1	AT2G30110	-1.10	-0.14	-1.23	0.258378	0.483240	-6.07
261849_at	pectin methylesterase, putative similar t	---	AT1G11370	-1.11	-0.16	-1.23	0.258459	0.483352	-6.07
259606_at	hypothetical protein predicted by genem	MAP65-8	AT1G27920	-1.09	-0.12	-1.23	0.25858	0.483540	-6.07
265298_s_a	putative retroelement pol polyprotein co	---	---	-1.09	-0.12	-1.23	0.258672	0.483672	-6.07
263434_at	putative homeodomain transcription fact	PRS	AT2G28610	-1.09	-0.12	-1.23	0.258716	0.483715	-6.07
249227_at	peroxidase (emb|CAA66960.1)	---	AT5G42180	1.10	0.14	1.23	0.258811	0.483772	-6.08
248098_at	unknown protein ; supported by cDNA:	---	AT5G55290	-1.10	-0.14	-1.23	0.258804	0.483772	-6.08
265311_at	hypothetical protein predicted by gensca	---	AT2G20250	-1.18	-0.24	-1.23	0.258794	0.483772	-6.08
250069_at	disease resistance protein-like	---	AT5G17970	1.10	0.14	1.23	0.258835	0.483778	-6.08
259743_at	hypothetical protein predicted by genefir	---	AT1G71140	1.47	0.56	1.23	0.25894	0.483935	-6.08
255878_at	putative bZIP transcription factor contair	---	AT2G40620	-1.16	-0.22	-1.23	0.259078	0.484153	-6.08
257263_at	unknown protein ;supported by full-leng	---	AT3G22070	1.19	0.25	1.23	0.259183	0.484233	-6.08
260158_at	unknown protein	---	AT1G79910	1.11	0.15	1.23	0.259203	0.484233	-6.08
246628_at	signal recognition particle 54 kDa prote	---	AT1G48900	-1.08	-0.11	-1.23	0.259206	0.484233	-6.08
257342_at	pseudogene, putative polyprotein simila	---	---	1.17	0.23	1.23	0.259166	0.484233	-6.08
251771_at	putative protein cellulose synthase (cel	CSLA14	AT3G56000	1.11	0.15	1.23	0.259318	0.484244	-6.08
257750_at	unknown protein ;supported by full-leng	---	AT3G18800	1.12	0.17	1.23	0.259312	0.484244	-6.08
256007_at	allinase, putative similar to allinase GI:1	SAMC2	AT1G34065	-1.14	-0.19	-1.23	0.259255	0.484244	-6.08

248845_at	disease resistance protein-like	---	AT5G46470	-1.13	-0.18	-1.23	0.259276	0.484244	-6.08
249844_at	putative protein similar to unknown prote	---	AT5G23590	-1.12	-0.16	-1.23	0.259284	0.484244	-6.08
247945_at	putative protein contains similarity to unl	---	AT5G57150	-1.34	-0.42	-1.23	0.259375	0.484311	-6.08
266897_at	remorin identical to GB:M25268, a non-	---	AT2G45820	-1.18	-0.24	-1.23	0.259526	0.484553	-6.08
256998_at	hypothetical protein predicted by genem	---	AT3G14180	1.13	0.18	1.23	0.259624	0.484578	-6.08
261831_at	ADP-ribosylation factor, putative similar	ATARFA1I	AT1G10630	1.15	0.21	1.23	0.259591	0.484578	-6.08
266870_at	putative heterogeneous nuclear ribonuc	---	AT2G44710	-1.16	-0.22	-1.23	0.259626	0.484578	-6.08
265456_at	Expressed protein ; supported by full-ler	SDH4	AT2G46505	1.09	0.13	1.23	0.259645	0.484578	-6.08
253064_at	bZIP transcription factor - like protein b	AtbZIP7	AT4G37730	1.11	0.15	1.23	0.259635	0.484578	-6.08
249679_at	unknown protein	---	AT5G35980	-1.08	-0.10	-1.23	0.259706	0.484597	-6.08
253676_at	cytidine deaminase - like protein cytidin	---	AT4G29570	1.13	0.17	1.23	0.259713	0.484597	-6.08
256709_at	hypothetical protein predicted by genem	---	---	-1.09	-0.13	-1.23	0.259741	0.484597	-6.08
265882_at	putative copper amine oxidase	---	AT2G42490	1.16	0.21	1.23	0.259729	0.484597	-6.08
264386_at	putative pyrophosphate-fructose-6-phos	---	AT1G12000	1.22	0.29	1.23	0.259791	0.484652	-6.08
246827_at	copper binding - like protein mavicyanin	---	AT5G26330	-1.12	-0.16	-1.23	0.259842	0.484708	-6.08
267224_at	hypothetical protein predicted by gensca	---	AT2G43990	-1.13	-0.17	-1.23	0.259883	0.484744	-6.08
262379_at	hypothetical protein predicted by gensca	---	AT1G73020	1.09	0.13	1.23	0.260069	0.485050	-6.08
254625_at	Expressed protein ; supported by full-ler	SNI1	AT4G18470	1.12	0.16	1.23	0.26011	0.485088	-6.08
252417_at	putative calcium-binding protein calcium	---	AT3G47480	1.64	0.71	1.23	0.260371	0.485534	-6.08
255320_at	putative transposon protein	---	---	1.08	0.11	1.23	0.260421	0.485548	-6.08
250605_at	glycine/proline-rich protein flagelliform s	---	AT5G07570	1.11	0.16	1.23	0.26042	0.485548	-6.08
256448_s_a	unknown protein	MED21	AT4G04780 /	1.10	0.14	1.23	0.260464	0.485589	-6.08
264756_at	receptor protein kinase (IRK1), putative	---	AT1G61370	1.44	0.53	1.23	0.260613	0.485668	-6.08
251220_at	cytochrome c oxidase subunit 5c-like pr	---	AT3G62400	1.15	0.20	1.23	0.260634	0.485668	-6.08
264550_at	hypothetical protein predicted by gensca	---	AT1G09450	1.17	0.23	1.23	0.260621	0.485668	-6.08
257999_at	hypothetical protein similar to hypothetic	---	AT3G27540	1.20	0.27	1.23	0.260599	0.485668	-6.08
250596_at	putative protein contains similarity to unl	---	AT5G07780	1.16	0.21	1.23	0.260632	0.485668	-6.08
253389_at	hypothetical protein ;supported by full-le	---	AT4G32680	-1.09	-0.12	-1.23	0.260567	0.485668	-6.08
264856_at	3-hydroxy-3-methylglutaryl-coenzyme A	HMG2	AT2G17370	1.14	0.19	1.23	0.260677	0.485699	-6.08
253634_at	putative protein ENOD20 gene product	---	AT4G30590	1.08	0.11	1.23	0.260693	0.485699	-6.08
255696_at	putative nucleotide sugar epimerase	GAE3	AT4G00110	-1.11	-0.15	-1.23	0.260865	0.485814	-6.08
257668_at	sugar transporter, putative similar to GE	---	AT3G20460	1.15	0.21	1.23	0.260827	0.485814	-6.08
248462_at	nucleotide-binding protein ; supported b	NBP35	AT5G50960	-1.12	-0.16	-1.23	0.260788	0.485814	-6.08
262772_at	puative calcium-transporting ATPase sir	ACA.I	AT1G13210	1.22	0.29	1.23	0.260883	0.485814	-6.08
264721_at	hypothetical protein predicted by gensca	---	AT1G23000	1.10	0.14	1.23	0.260829	0.485814	-6.08

259663_at	hypothetical protein predicted by genem	PRA7	AT1G55190	1.12	0.17	1.23	0.260862	0.485814	-6.08
258218_at	methyltransferase, putative similar to m	XPL1	AT3G17998 /	-1.16	-0.21	-1.23	0.26099	0.485904	-6.08
251216_at	putative protein hypothetical protein a, t	---	---	1.09	0.13	1.23	0.261038	0.485904	-6.08
253355_at	putative protein	---	AT4G33380	-1.09	-0.12	-1.23	0.261021	0.485904	-6.08
257585_at	hypothetical protein predicted by genem	---	AT3G12420	1.11	0.15	1.23	0.261003	0.485904	-6.08
252547_at	putative protein many predicted protein	---	AT3G45840	-1.12	-0.17	-1.23	0.261025	0.485904	-6.08
249996_at	glutaredoxin -like protein glutaredoxin,	---	AT5G18600	1.22	0.29	1.23	0.261077	0.485905	-6.08
251992_at	putative protein myosin heavy chain, Er	---	AT3G53350	-1.14	-0.20	-1.23	0.261098	0.485905	-6.08
256218_at	hypothetical protein predicted by genem	---	AT1G56270	1.13	0.17	1.23	0.261102	0.485905	-6.08
246865_s_a	eukaryotic translation initiation factor - I	TIF3B1	AT5G25780 /	-1.08	-0.11	-1.23	0.261188	0.485975	-6.08
256704_at	deacetylvindoline 4-O-acetyltransferase	---	AT3G30280	1.09	0.13	1.23	0.261189	0.485975	-6.08
246471_s_a	putative protein predicted proteins, Arat	---	AT5G17100 /	-1.09	-0.12	-1.23	0.261204	0.485975	-6.08
247223_at	MADS box transcription factor-like	MAF4	AT5G65070	1.08	0.11	1.23	0.261261	0.486002	-6.08
255131_at	putative protein hypothetical protein ssr	---	AT4G08280	-1.10	-0.14	-1.23	0.261253	0.486002	-6.08
261853_at	unknown protein	---	AT1G50660	-1.14	-0.19	-1.23	0.261303	0.486042	-6.08
253497_at	putative protein microtubule-associated	---	AT4G31880	-1.12	-0.16	-1.23	0.261344	0.486077	-6.08
261516_at	hypoxanthine ribosyl transferase, putati	---	AT1G71750	-1.09	-0.13	-1.23	0.261386	0.486077	-6.08
256355_at	hypothetical protein predicted by genem	---	AT1G55040	-1.12	-0.16	-1.23	0.261383	0.486077	-6.08
257952_at	putative peroxidase almost identical to G	---	AT3G21770	1.16	0.21	1.23	0.261635	0.486500	-6.08
258672_at	hypothetical protein	---	AT3G08570	-1.12	-0.16	-1.23	0.2617	0.486582	-6.08
248458_at	putative protein contains similarity to unl	EYE	AT5G51430	-1.10	-0.13	-1.22	0.261776	0.486683	-6.08
256099_at	cytochrome P450, putative similar to cy	CYP78A5	AT1G13710	-1.16	-0.22	-1.22	0.26182	0.486685	-6.08
249781_at	unknown protein	---	AT5G24250	1.12	0.17	1.22	0.261814	0.486685	-6.08
262459_at	hypothetical protein similar to hypothetic	---	AT1G50400	1.14	0.19	1.22	0.262009	0.486996	-6.09
253953_at	putative protein extensin precursor - tor	---	AT4G26750	1.17	0.22	1.22	0.262044	0.487023	-6.09
251934_at	putative protein delta-latroinsectotoxin p	---	AT3G54070	1.12	0.17	1.22	0.262083	0.487054	-6.09
265816_s_a	putative elongation factor beta-1 ;supp	---	AT1G30230 /	-1.14	-0.19	-1.22	0.262213	0.487257	-6.09
264380_at	unknown protein predicted by genscan a	---	AT2G25190	1.08	0.11	1.22	0.262273	0.487329	-6.09
246833_at	putative protein	---	AT5G26620	-1.08	-0.11	-1.22	0.262374	0.487478	-6.09
246863_at	nodulin - like protein early nodulin N93,	---	AT5G25940	1.23	0.30	1.22	0.262522	0.487712	-6.09
260064_at	ethylene-insensitive3-like3 (EIL3) identi	EIL3	AT1G73730	1.14	0.19	1.22	0.262649	0.487907	-6.09
264316_at	unknown protein ; supported by cDNA: g	ENT1,AT	AT1G70330	1.13	0.17	1.22	0.262731	0.488020	-6.09
252327_at	MTN3-like protein MtN3 gene product -	---	AT3G48740	-1.16	-0.21	-1.22	0.262786	0.488083	-6.09
250776_at	monooxygenase ;supported by full-leng	---	AT5G05320	1.09	0.12	1.22	0.262837	0.488137	-6.09
245433_at	hypothetical protein	---	AT4G17140	1.10	0.14	1.22	0.262871	0.488162	-6.09

246126_at	putative protein predicted protein, Oryz	ATNUDX1	AT5G20070	-1.22	-0.29	-1.22	0.262973	0.488271	-6.09
247877_at	putative protein contains similarity to an	XBAT32	AT5G57740	1.18	0.24	1.22	0.262962	0.488271	-6.09
251429_at	dynamin-like protein 4 (ADL4) ; support	ADL1E	AT3G60190	-1.11	-0.15	-1.22	0.263107	0.488480	-6.09
261467_at	unknown protein	VOZ1	AT1G28520	-1.16	-0.21	-1.22	0.263143	0.488484	-6.09
263615_at	putative MYB family transcription factor	MYB100	AT2G25230	-1.08	-0.11	-1.22	0.263152	0.488484	-6.09
261854_at	unknown protein	---	AT1G50670	1.08	0.11	1.22	0.26323	0.488518	-6.09
265976_at	putative Athila retroelement ORF1 prote	---	---	-1.10	-0.14	-1.22	0.263217	0.488518	-6.09
256339_at	hypothetical protein	---	AT1G72080	1.10	0.13	1.22	0.263235	0.488518	-6.09
261740_at	hypothetical protein similar to unknown	---	AT1G47740	-1.15	-0.20	-1.22	0.263387	0.488742	-6.09
249446_at	receptor protein kinase -like protein pro	---	AT5G39390	1.10	0.13	1.22	0.263398	0.488742	-6.09
259201_at	hypothetical protein predicted using gen	---	AT3G09080	1.15	0.20	1.22	0.263438	0.488777	-6.09
246149_at	peroxidase ATP N ;supported by full-ler	---	AT5G19890	-1.68	-0.75	-1.22	0.263468	0.488792	-6.09
249794_at	putative protein contains similarity to un	AtCXE18	AT5G23530	1.08	0.12	1.22	0.263627	0.488912	-6.09
247398_at	putative protein predicted protein, Arab	---	AT5G62950	-1.12	-0.16	-1.22	0.263583	0.488912	-6.09
248411_at	unknown protein	---	AT5G51580	1.09	0.12	1.22	0.263633	0.488912	-6.09
249060_at	putative protein similar to unknown prot	VPS2.2	AT5G44560	-1.09	-0.12	-1.22	0.263652	0.488912	-6.09
256066_at	hypothetical protein similar to hypothetic	---	AT1G06980	-1.32	-0.40	-1.22	0.263569	0.488912	-6.09
263460_at	putative acetolactate synthase	---	AT2G31810	1.14	0.19	1.22	0.263661	0.488912	-6.09
267347_at	hypothetical protein predicted by genefir	---	AT2G39950	-1.09	-0.13	-1.22	0.263724	0.488989	-6.09
262097_at	hypothetical protein predicted by genem	---	AT1G55990	1.10	0.14	1.22	0.263767	0.488996	-6.09
258769_at	putative alpha-hydroxynitrile lyase simila	MES17	AT3G10870	-1.18	-0.24	-1.22	0.26377	0.488996	-6.09
254640_at	ion transporter - like protein integral me	NRAMP5	AT4G18790	1.10	0.14	1.22	0.26388	0.489119	-6.09
265224_at	putative pectinesterase	---	AT2G36710	-1.10	-0.14	-1.22	0.263865	0.489119	-6.09
245032_at	En/Spm-like transposon protein related	---	---	1.16	0.21	1.22	0.263943	0.489157	-6.09
266507_at	unknown protein EST matches on the r	---	AT2G47860	1.09	0.13	1.22	0.263938	0.489157	-6.09
255058_s_a	putative protein various hypothetical pro	---	---	1.08	0.11	1.22	0.263974	0.489175	-6.09
245012_at	NADH dehydrogenase D3	---	---	-1.14	-0.18	-1.22	0.264119	0.489403	-6.09
252209_at	putative protein RXF26, Arabidopsis tha	---	AT3G50400	1.20	0.26	1.22	0.264207	0.489522	-6.09
252730_at	putative protein	---	AT3G43110	1.14	0.20	1.22	0.264226	0.489522	-6.09
261169_at	sucrose-phosphate synthase, putative s	ATSPS3F	AT1G04920	1.11	0.15	1.22	0.264316	0.489610	-6.09
260169_at	hypothetical protein predicted by genet	FUT13	AT1G71990	-1.19	-0.26	-1.22	0.264311	0.489610	-6.09
247149_at	unknown protein ;supported by full-leng	---	AT5G65660	-1.23	-0.30	-1.22	0.264436	0.489791	-6.09
254872_at	putative protein several hypothetical pro	---	AT4G11560	-1.09	-0.13	-1.22	0.264696	0.490234	-6.09
247689_at	putative protein protein tyrosine phosph	---	AT5G59770	-1.14	-0.19	-1.22	0.264737	0.490250	-6.09
259820_at	subtilisin-like serine protease contains s	---	AT1G66210	1.11	0.15	1.22	0.264748	0.490250	-6.09

255400_at	hypothetical protein	---	---	1.11	0.15	1.22	0.26482	0.490270	-6.09
246112_at	putative protein predicted proteins - Aral	---	AT5G20200	1.12	0.17	1.22	0.264876	0.490270	-6.09
248474_at	pyruvate dehydrogenase E1 componen	MAB1	AT5G50850	1.12	0.17	1.22	0.264887	0.490270	-6.09
264148_at	NAM (no apical meristem)-like protein,	ANAC003	AT1G02220	2.25	1.17	1.22	0.264845	0.490270	-6.09
262696_at	hypothetical protein	---	AT1G75870	-1.10	-0.14	-1.22	0.264861	0.490270	-6.09
263501_s_a	hypothetical protein	---	AT2G07673	-1.11	-0.15	-1.22	0.264781	0.490270	-6.09
253811_at	hypothetical protein ;supported by full-le	ULT1	AT4G28190	1.22	0.28	1.22	0.264992	0.490348	-6.09
265955_at	putative ABC transporter	PDR5	AT2G37280	1.10	0.14	1.22	0.264994	0.490348	-6.09
262936_at	hypothetical protein similar to putative N	ATCHX2	AT1G79400	-1.14	-0.19	-1.22	0.26496	0.490348	-6.09
261734_at	hypothetical protein similar to hypothetic	---	AT1G47790	1.09	0.13	1.22	0.265054	0.490418	-6.10
245908_at	laccase-like protein laccase - Acer pseu	LAC14	AT5G09360	1.17	0.22	1.22	0.265108	0.490462	-6.10
257237_at	DNA nick sensor, putative contains Pfa	---	AT3G14890	-1.29	-0.37	-1.22	0.265134	0.490462	-6.10
246689_at	putative protein predicted proteins - Aral	---	---	-1.08	-0.11	-1.22	0.265142	0.490462	-6.10
255989_at	putative protein	---	AT5G35069	1.12	0.17	1.22	0.26517	0.490475	-6.10
255466_at	putative protein similar to A. thaliana pr	---	AT4G03000	-1.11	-0.15	-1.21	0.265338	0.490744	-6.10
260857_at	unknown protein contains Pfam profile:F	LYM1	AT1G21880	-1.26	-0.33	-1.21	0.26538	0.490778	-6.10
253397_at	putative protein kinase protein kinase T	---	AT4G32710	-1.09	-0.12	-1.21	0.265481	0.490778	-6.10
264775_at	putative endo-1,4-beta-D-glucanase sin	CEL5	AT1G22880	-1.13	-0.17	-1.21	0.265417	0.490778	-6.10
257524_at	hypothetical protein similar to putative p	DEL3	AT3G01330	1.11	0.15	1.21	0.265456	0.490778	-6.10
257106_at	unknown protein	---	AT3G29060	1.09	0.12	1.21	0.265474	0.490778	-6.10
248290_at	Ca2+-transporting ATPase-like protein	---	AT5G53010	1.11	0.16	1.21	0.265504	0.490778	-6.10
265944_at	putative SET-domain transcriptional reg	ASHR2	AT2G19640	1.12	0.17	1.21	0.265506	0.490778	-6.10
245835_at	hypothetical protein similar to putative tr	---	AT1G42190	1.09	0.13	1.21	0.265553	0.490825	-6.10
265730_at	60S ribosomal protein L27	---	AT2G32220	-1.37	-0.45	-1.21	0.265618	0.490904	-6.10
260939_at	hypothetical protein contains similarity to	---	AT1G45180	1.28	0.36	1.21	0.265668	0.490918	-6.10
248851_s_a	disease resistance protein-like ; suppor	---	AT5G46260 /	-1.11	-0.15	-1.21	0.265657	0.490918	-6.10
246132_at	Rad51-like protein ; supported by cDNA	ATRAD51	AT5G20850	1.08	0.11	1.21	0.265712	0.490959	-6.10
260521_at	putative villin 2	VLN2	AT2G41740	1.16	0.22	1.21	0.265811	0.490996	-6.10
255423_at	putative calmodulin	---	AT4G03290	1.09	0.13	1.21	0.265801	0.490996	-6.10
256966_at	pollen specific protein, putative similar t	sks13	AT3G13400	1.09	0.12	1.21	0.26581	0.490996	-6.10
265552_at	putative plasma membrane proton ATPa	AHA6	AT2G07560	1.10	0.13	1.21	0.265818	0.490996	-6.10
253520_at	hypothetical protein ;supported by full-le	---	AT4G31410	-1.09	-0.12	-1.21	0.265885	0.491041	-6.10
246677_at	putative protein predicted proteins - Aral	---	---	1.11	0.15	1.21	0.265877	0.491041	-6.10
264428_at	hypothetical protein predicted by genem	---	AT1G61790	1.16	0.22	1.21	0.266034	0.491276	-6.10
258198_at	putative transcription factor similar to tra	NF-YA6	AT3G14020	-1.12	-0.16	-1.21	0.266161	0.491471	-6.10

248261_at	putative protein similar to unknown prote	PDV1	AT5G53280	-1.10	-0.13	-1.21	0.266221	0.491542	-6.10
262791_at	unknown protein EST gb|F13926 comes	---	AT1G10830	-1.12	-0.17	-1.21	0.266267	0.491586	-6.10
258669_at	hypothetical protein predicted by gensca	---	AT3G08800	-1.09	-0.12	-1.21	0.266369	0.491655	-6.10
248992_at	disease resistance protein RPS4	---	AT5G45230	1.10	0.14	1.21	0.26633	0.491655	-6.10
262845_at	unknown protein ; supported by cDNA: g	---	AT1G14740	1.20	0.27	1.21	0.266361	0.491655	-6.10
251310_at	homeobox protein Anthocyaninless2 AI	HDG1	AT3G61150	-1.13	-0.18	-1.21	0.266413	0.491666	-6.10
254992_at	putative transcriptional regulator	SPT16	AT4G10710	-1.14	-0.19	-1.21	0.266418	0.491666	-6.10
247867_at	SNF1 related protein kinase-like protein	CIPK21	AT5G57630	-1.18	-0.24	-1.21	0.2665	0.491777	-6.10
266426_x_a	hypothetical protein predicted by gensca	---	AT2G07140	-1.19	-0.25	-1.21	0.266578	0.491881	-6.10
250734_at	putative protein similar to unknown prote	---	AT5G06270	1.28	0.36	1.21	0.266602	0.491887	-6.10
251275_at	putative protein anthranilate phosphorib	---	AT3G61720	1.16	0.22	1.21	0.266653	0.491917	-6.10
259230_at	unknown protein ; supported by cDNA:	OBE1	AT3G07780	1.13	0.18	1.21	0.266661	0.491917	-6.10
261979_at	nitrate reductase, putative similar to nitr	NIA2	AT1G37130	1.18	0.24	1.21	0.266751	0.492041	-6.10
254708_at	ubiquitin-specific protease 20 (UBP20),	UBP20	AT4G17895	1.10	0.13	1.21	0.266841	0.492062	-6.10
264883_s_a	secretory carrier membrane protein iden	---	AT1G11180 /	1.10	0.13	1.21	0.266812	0.492062	-6.10
248331_at	putative protein contains similarity to 40	---	AT5G52650	-1.18	-0.24	-1.21	0.266809	0.492062	-6.10
264877_at	putative obtusifoliol 14-alpha demethyla	CYP51G2	AT2G17330	1.08	0.11	1.21	0.266848	0.492062	-6.10
248155_at	putative protein 3 (2'), 5'-bisphosphate	AHL	AT5G54390	-1.12	-0.17	-1.21	0.266951	0.492211	-6.10
246309_at	putative transmembrane protein G1p Br	ATG1	AT3G51790	-1.25	-0.33	-1.21	0.266977	0.492220	-6.10
266475_at	putative lipase	---	AT2G31100	1.10	0.13	1.21	0.267008	0.492238	-6.10
250422_at	putative protein KIAA0255 gene, Homo	---	AT5G10840	1.17	0.23	1.21	0.267036	0.492250	-6.10
247755_at	subtilisin-like serine protease contains s	ATSBT4.1	AT5G59090	-1.09	-0.12	-1.21	0.267059	0.492251	-6.10
248599_at	putative protein contains similarity to unl	---	AT5G49380	1.17	0.22	1.21	0.267167	0.492410	-6.10
254394_at	subtilisin-like serine protease contains s	---	AT4G21630	1.08	0.11	1.21	0.267249	0.492446	-6.10
262842_at	xyloglucan endo-transglycosylase, puta	XTR2	AT1G14720	-1.22	-0.29	-1.21	0.26724	0.492446	-6.10
251889_at	putative protein probable lectin 2 precu	---	AT3G54080	-1.22	-0.29	-1.21	0.267251	0.492446	-6.10
250642_at	receptor-like protein kinase several rece	ERL2	AT5G07180	-1.08	-0.12	-1.21	0.267309	0.492513	-6.10
265316_at	unknown protein	---	AT2G20400	-1.15	-0.21	-1.21	0.267375	0.492595	-6.10
257001_at	Sm protein, putative similar to GB:AAB	---	AT3G14080	1.10	0.14	1.21	0.267417	0.492632	-6.10
267486_at	putative protein kinase contains a protei	APK2B	AT2G02800	1.16	0.21	1.21	0.267515	0.492712	-6.10
261890_at	hypothetical protein predicted by genem	---	AT1G80970	1.19	0.25	1.21	0.267525	0.492712	-6.10
254113_at	hypothetical protein	---	AT4G24900	-1.10	-0.14	-1.21	0.26752	0.492712	-6.10
264598_at	putative dimethylaniline monooxygenase	---	AT1G04610	1.09	0.12	1.21	0.267563	0.492743	-6.10
246968_at	RING finger-like protein RING-H2 finge	---	AT5G24870	1.14	0.19	1.21	0.267594	0.492758	-6.10
263070_at	unknown protein	---	AT2G17600	1.10	0.13	1.21	0.267618	0.492758	-6.10

266328_at	unknown protein ; supported by full-leng	---	AT2G01600	1.08	0.11	1.21	0.267691	0.492758	-6.10
256911_at	glutamine:fructose-6-phosphate amidot	---	AT3G24090	1.40	0.49	1.21	0.267649	0.492758	-6.10
256963_at	lysyl-tRNA synthetase, putative similar t	OVA5	AT3G13490	-1.15	-0.20	-1.21	0.267701	0.492758	-6.10
245292_at	Expressed protein ; supported by cDNA	---	AT4G15093	1.13	0.18	1.21	0.267681	0.492758	-6.10
248037_at	sexual differentiation process protein ISI	OPT1	AT5G55930	1.26	0.33	1.21	0.267762	0.492772	-6.10
257861_at	putative transporter similar to SV2 relate	---	AT3G13050	1.12	0.17	1.21	0.267773	0.492772	-6.10
256409_at	hypothetical protein	---	AT1G66620	-1.12	-0.16	-1.21	0.267766	0.492772	-6.10
248529_at	protein kinase ;supported by full-length c	---	AT5G50000	-1.15	-0.20	-1.21	0.267832	0.492801	-6.10
253859_at	Expressed protein ; supported by full-ler	---	AT4G27657	1.90	0.92	1.21	0.267828	0.492801	-6.10
248791_at	palmitoyl-protein thioesterase precursor	---	AT5G47350	1.08	0.11	1.21	0.267888	0.492863	-6.10
260176_at	unknown protein similar to Pi starvation-	---	AT1G71950	-1.11	-0.15	-1.21	0.268002	0.492994	-6.10
256900_at	pectate lyase, putative similar to pectat	---	AT3G24670	1.12	0.16	1.21	0.268002	0.492994	-6.10
264671_at	unknown protein ; supported by full-leng	---	AT1G09920	1.11	0.16	1.21	0.26803	0.493006	-6.10
249907_at	putative protein DNA repair protein RAD	RAD5	AT5G22750	-1.09	-0.13	-1.21	0.26808	0.493058	-6.10
245902_at	putative protein Scythe protein, Xenopu	---	AT5G11080	1.15	0.21	1.21	0.268324	0.493466	-6.11
257972_at	putative protein kinase, ATN1 almost id	ATN1	AT3G27560	1.11	0.15	1.21	0.268444	0.493648	-6.11
263077_at	putative mitotic control protein dis3 ; su	EMB2763	AT2G17510	-1.08	-0.12	-1.21	0.268475	0.493666	-6.11
260923_at	glycine-rich RNA-binding protein grp1a,	---	AT1G21570	-1.11	-0.15	-1.21	0.268516	0.493700	-6.11
260080_at	putative RNA-binding protein contains P	APUM7	AT1G78160	1.08	0.11	1.21	0.268573	0.493766	-6.11
260963_at	hypothetical protein predicted by genem	---	AT1G44990	-1.10	-0.14	-1.21	0.268618	0.493808	-6.11
261298_at	cytochrome c oxidase assembly protein	---	AT1G48510	-1.09	-0.13	-1.21	0.268673	0.493869	-6.11
255011_at	cytochrome c several plant cytochrome	CYTC-2	AT4G10040	1.37	0.45	1.21	0.268735	0.493943	-6.11
257990_at	putative myc-like DNA-binding protein si	---	AT3G19860	-1.14	-0.19	-1.21	0.268806	0.494035	-6.11
255268_at	putative protein ubiquitin, Tetrahymena	---	AT4G05230	1.11	0.15	1.20	0.268867	0.494068	-6.11
257768_at	RING zinc finger protein, putative conta	---	AT3G23060	1.13	0.18	1.21	0.268853	0.494068	-6.11
247509_at	heat shock factor 6	HSFB2A	AT5G62020	1.12	0.16	1.20	0.268968	0.494212	-6.11
249233_at	putative protein contains similarity to glu	---	AT5G42150	-1.31	-0.39	-1.20	0.2691	0.494336	-6.11
251465_at	transporter-like protein UDP-galactose t	UTR6	AT3G59360	1.08	0.11	1.20	0.26906	0.494336	-6.11
250376_at	putative protein	---	AT5G11550	1.18	0.24	1.20	0.269097	0.494336	-6.11
261662_at	MAP kinase kinase 5, putative similar to	ATMKK7	AT1G18350	1.09	0.13	1.20	0.269132	0.494354	-6.11
265849_at	hypothetical protein predicted by gensca	---	AT2G35736	1.15	0.20	1.20	0.269279	0.494386	-6.11
251539_at	serine/threonine-specific protein kinase	---	AT3G58690	-1.13	-0.18	-1.20	0.269268	0.494386	-6.11
257968_at	hypothetical protein predicted by genem	---	AT3G27550	-1.16	-0.21	-1.20	0.269252	0.494386	-6.11
246610_at	putative protein	---	AT5G35400	-1.10	-0.14	-1.20	0.269224	0.494386	-6.11
246713_at	mRNA capping enzyme - like capping e	---	AT5G28210	1.12	0.17	1.20	0.269239	0.494386	-6.11

245636_at	hypothetical protein similar to hypothetic	---	AT1G25240	-1.13	-0.18	-1.20	0.269279	0.494386	-6.11
245356_at	adenosylhomocysteinase ;supported by	MEE58	AT4G13940	1.15	0.21	1.20	0.269361	0.494496	-6.11
250366_at	putative protein predicted proteins in ca	---	AT5G11420	-1.83	-0.87	-1.20	0.269427	0.494578	-6.11
266526_at	putative tetracycline transporter protein	---	AT2G16980	1.11	0.15	1.20	0.269509	0.494688	-6.11
247883_at	unknown protein	---	AT5G57790	1.15	0.20	1.20	0.269727	0.495049	-6.11
251601_at	Expressed protein ; supported by full-ler	---	AT3G57800	-1.17	-0.23	-1.20	0.269961	0.495279	-6.11
262989_at	F28C11.5 similar to INNER NO OUTEF	INO	AT1G23420	1.12	0.16	1.20	0.269921	0.495279	-6.11
259260_at	unknown protein similar to unknown pro	---	AT3G11370	1.11	0.15	1.20	0.269912	0.495279	-6.11
250331_at	putative protein self-incompatibility prot	---	AT5G11820	1.11	0.15	1.20	0.269957	0.495279	-6.11
251852_at	putative protein	---	AT3G54750	-1.15	-0.20	-1.20	0.269876	0.495279	-6.11
264667_s_a	hypothetical protein identical to hypothe	ZW18	AT1G09980 /	-1.09	-0.13	-1.20	0.270148	0.495582	-6.11
265309_at	putative myosin heavy chain	XIG	AT2G20290	-1.15	-0.21	-1.20	0.270202	0.495643	-6.11
253784_at	putative protein WREBP-1, Nicotiana ta	PHR1	AT4G28610	-1.11	-0.15	-1.20	0.270293	0.495769	-6.11
248154_at	putative protein strong similarity to unkn	---	AT5G54400	1.44	0.52	1.20	0.270338	0.495812	-6.11
251570_at	putative protein several hypothetical pro	---	AT3G58300	1.11	0.15	1.20	0.27037	0.495830	-6.11
261162_at	hypothetical protein predicted by gensca	---	AT1G34440	1.12	0.16	1.20	0.270523	0.496072	-6.11
250857_at	unknown protein	---	AT5G04790	-1.15	-0.20	-1.20	0.270659	0.496281	-6.11
256305_at	glutathione S-conjugate transporting AT	MRP1	AT1G30400	1.15	0.21	1.20	0.270786	0.496400	-6.11
247544_at	putative protein ;supported by full-lengt	---	AT5G61670	-1.14	-0.19	-1.20	0.270748	0.496400	-6.11
264278_at	myrosinase binding protein, putative sir	---	AT1G60130	-1.09	-0.12	-1.20	0.270789	0.496400	-6.11
245189_at	F12A21.18 hypothetical protein	---	AT1G67670	1.08	0.11	1.20	0.27083	0.496434	-6.11
255480_at	Expressed protein ; supported by full-ler	---	AT4G02485	-1.09	-0.12	-1.20	0.270857	0.496443	-6.11
250948_at	putative protein	---	AT5G03490	1.17	0.23	1.20	0.270903	0.496488	-6.11
250416_at	putative protein predicted proteins, Arat	---	AT5G11220	1.10	0.14	1.20	0.27109	0.496774	-6.11
246787_s_a	cdc20-like protein putative cdc20 protei	---	AT5G27570 /	1.08	0.12	1.20	0.271102	0.496774	-6.11
265683_at	putative auxin-regulated protein	---	AT2G24400	-1.11	-0.15	-1.20	0.271143	0.496809	-6.11
251955_at	putative protein predicted proteins, Arat	---	AT3G53680	1.10	0.14	1.20	0.271203	0.496878	-6.11
260592_at	cellulose synthase catalytic subunit, put	CSLE1	AT1G55850	-1.13	-0.18	-1.20	0.271234	0.496896	-6.11
257584_at	hypothetical protein similar to putative n	---	---	-1.16	-0.21	-1.20	0.271281	0.496942	-6.11
254888_at	putative protein predicted protein, Arabi	---	AT4G11780	-1.10	-0.13	-1.20	0.271306	0.496948	-6.11
263473_at	putative glucosyltransferase ; supporte	UGT74D1	AT2G31750	-1.30	-0.38	-1.20	0.271331	0.496954	-6.11
254382_at	hypothetical protein	---	AT4G21890	1.15	0.20	1.20	0.271686	0.497446	-6.12
257860_at	Expressed protein ; supported by cDNA	---	AT3G13062	-1.16	-0.21	-1.20	0.271682	0.497446	-6.12
260455_at	hypothetical protein predicted by gensca	---	AT1G72500	-1.27	-0.35	-1.20	0.271697	0.497446	-6.12
251994_at	protein kinase - like protein kinase, Arat	KIPK	AT3G52890	-1.20	-0.27	-1.20	0.271709	0.497446	-6.12

257617_at	hypothetical protein	---	AT3G26550	1.09	0.13	1.20	0.271645	0.497446	-6.12
255865_at	unknown protein	---	AT2G30330	-1.08	-0.11	-1.20	0.271743	0.497469	-6.12
264737_at	unknown protein	---	AT1G62210	1.14	0.19	1.20	0.271928	0.497767	-6.12
251983_at	putative protein MtN21, Medicago trunc	---	AT3G53210	-1.15	-0.20	-1.20	0.272012	0.497840	-6.12
253499_at	putative protein zinc-finger helicase, Hc	---	AT4G31900	1.09	0.13	1.20	0.272006	0.497840	-6.12
261585_at	NAC domain protein, putative similar to	ANAC001	AT1G01010	1.17	0.23	1.20	0.272136	0.497974	-6.12
245699_at	putative protein ;supported by full-length	---	AT5G04250	1.19	0.25	1.20	0.272113	0.497974	-6.12
257800_at	unknown protein ;supported by full-leng	---	AT3G15900	1.13	0.17	1.20	0.27215	0.497974	-6.12
248323_at	unknown protein	---	AT5G52770	1.08	0.11	1.20	0.272241	0.498101	-6.12
247783_at	light harvesting pigment - like protein LI	---	AT5G58800	1.21	0.27	1.20	0.272406	0.498362	-6.12
257558_s_a	hypothetical protein contains Pfam profil	---	AT3G22000 /	-1.09	-0.13	-1.19	0.272505	0.498504	-6.12
266168_at	putative protease inhibitor ;supported b	---	AT2G38870	1.35	0.43	1.19	0.272948	0.499203	-6.12
252604_at	high-affinity nitrate transporter - like pro	NRT2.6	AT3G45060	1.37	0.45	1.19	0.272942	0.499203	-6.12
253512_at	putative protein protein phosphatase 2C	WIN2	AT4G31750	1.10	0.14	1.19	0.272953	0.499203	-6.12
255592_s_a	hypothetical protein	---	AT2G34280 /	-1.11	-0.16	-1.19	0.273062	0.499363	-6.12
247408_at	ZAP - like protein nuclear protein ZAP,	---	AT5G62760	-1.08	-0.11	-1.19	0.273095	0.499383	-6.12
250756_at	putative protein strong similarity to unkn	ROPGEF5	AT5G05940	1.10	0.14	1.19	0.273311	0.499719	-6.12
246464_at	quinone oxidoreductase -like protein pr	---	AT5G16980	1.10	0.13	1.19	0.273323	0.499719	-6.12
258594_at	hypothetical protein predicted by gensca	---	AT3G04490	-1.10	-0.14	-1.19	0.27353	0.500058	-6.12
265932_at	hypothetical protein predicted by grail	LBD8	AT2G19510	1.08	0.11	1.19	0.273577	0.500104	-6.12
250374_at	putative protein	EMF1	AT5G11530	1.19	0.25	1.19	0.273778	0.500432	-6.12
257296_at	hypothetical protein predicted by genem	---	AT3G28020	1.10	0.14	1.19	0.273841	0.500506	-6.12
264368_at	hypothetical protein Contains similarity	---	AT1G03280	-1.10	-0.13	-1.19	0.273896	0.500545	-6.12
248313_at	putative protein contains similarity to GT	---	AT5G52580	-1.08	-0.11	-1.19	0.273906	0.500545	-6.12
254768_at	hypothetical protein	---	AT4G13320	1.11	0.15	1.19	0.273973	0.500609	-6.12
260779_at	splicing factor, putative similar to humal	---	AT1G14650	-1.10	-0.14	-1.19	0.273985	0.500609	-6.12
250544_at	syntaxin-like protein syntaxin-related pr	SYP132	AT5G08080	-1.12	-0.17	-1.19	0.274029	0.500649	-6.12
254935_at	putative disease resistance protein simi	---	AT4G10780	1.12	0.16	1.19	0.274094	0.500728	-6.12
260461_at	membrane protein PTM1 precursor isolc	---	AT1G10980	-1.11	-0.15	-1.19	0.274139	0.500770	-6.12
245379_at	heat shock transcription factor HSF1	HSF1	AT4G17750	-1.12	-0.17	-1.19	0.274164	0.500776	-6.12
245371_at	hypothetical protein ;supported by full-le	---	AT4G15750	-1.11	-0.16	-1.19	0.274208	0.500816	-6.12
262806_at	putative pyrophosphate-dependent phos	---	AT1G20950	-1.16	-0.22	-1.19	0.274389	0.501105	-6.12
258110_at	putative cytochrome P450 similar to GB	CYP72A7	AT3G14610	1.13	0.17	1.19	0.274434	0.501116	-6.12
245785_at	cellulose synthase catalytic subunit, pu	ATCSLD6	AT1G32180	1.10	0.14	1.19	0.274458	0.501116	-6.12
256222_at	hypothetical protein predicted by genem	---	AT1G56210	-1.16	-0.21	-1.19	0.274482	0.501116	-6.12

255395_at	hypothetical protein	---	---	-1.09	-0.12	-1.19	0.274469	0.501116	-6.12
247564_at	RNA helicase - like protein RNA helicas	---	AT5G61140	-1.11	-0.15	-1.19	0.274639	0.501285	-6.12
258854_at	putative UDP-glucosyl transferase simil	---	AT3G02100	-1.11	-0.15	-1.19	0.274646	0.501285	-6.12
260113_at	hypothetical protein predicted by gensca	---	AT1G63300	1.08	0.11	1.19	0.274613	0.501285	-6.12
264369_at	Ste-20 related kinase SPAK, putative si	---	AT1G70430	1.10	0.14	1.19	0.274663	0.501285	-6.12
251940_at	putative protein lysine decarboxylase (E	---	AT3G53450	1.10	0.13	1.19	0.274739	0.501384	-6.13
258425_at	unknown protein	---	AT3G16760	-1.08	-0.11	-1.19	0.274846	0.501499	-6.13
248133_at	unknown protein	---	AT5G54850	1.15	0.20	1.19	0.274826	0.501499	-6.13
262854_at	unknown protein	---	AT1G20870	1.10	0.14	1.19	0.274892	0.501543	-6.13
258519_at	unknown protein	---	AT3G06760	1.13	0.17	1.19	0.274938	0.501571	-6.13
246882_at	putative protein predicted proteins, Hon	---	AT5G26180	-1.09	-0.12	-1.19	0.274952	0.501571	-6.13
260791_at	lipase-like protein similar to lipase GB:A	---	AT1G06250	1.10	0.13	1.19	0.275019	0.501655	-6.13
250100_at	Expressed protein ; supported by cDNA	GLN1;4	AT5G16570	1.30	0.38	1.19	0.275158	0.501867	-6.13
260252_at	putative mitochondrial carrier protein sin	---	AT1G74240	-1.14	-0.19	-1.19	0.275303	0.502092	-6.13
267345_at	unknown protein ; supported by cDNA:	---	AT2G44240	1.34	0.42	1.19	0.275332	0.502104	-6.13
253754_at	glycine-rich protein like glycine-rich prot	---	AT4G29020	1.40	0.49	1.19	0.275536	0.502406	-6.13
252390_at	Expressed protein ; supported by cDNA	---	AT3G47836	-1.11	-0.15	-1.19	0.275541	0.502406	-6.13
261896_at	mRNA export protein, putative similar to	---	AT1G80670	-1.12	-0.17	-1.19	0.275588	0.502418	-6.13
254242_at	serine /threonine kinase - like protein se	---	AT4G23200	1.36	0.45	1.19	0.275592	0.502418	-6.13
245060_at	GDP-mannose pyrophosphorylase upo	CYT1	AT2G39770	1.08	0.12	1.19	0.275634	0.502441	-6.13
248340_at	putative protein similar to unknown prote	---	AT5G52180	-1.10	-0.14	-1.19	0.275671	0.502441	-6.13
251114_at	transcription factor GT-3a	---	AT5G01380	1.40	0.49	1.19	0.275659	0.502441	-6.13
251322_at	cysteine synthase AtcysC1 ;supported b	CYSC1	AT3G61440	-1.26	-0.34	-1.19	0.275703	0.502460	-6.13
248864_at	bHLH protein-like	---	AT5G46760	-1.08	-0.11	-1.19	0.275764	0.502531	-6.13
247614_at	putative protein	---	AT5G60240	1.09	0.12	1.19	0.275856	0.502659	-6.13
257050_at	putative protein phosphatase type 2C si	---	AT3G15260	-1.13	-0.18	-1.19	0.275932	0.502710	-6.13
254913_at	putative protein beta-transducin repeats	---	AT4G11270	-1.09	-0.13	-1.19	0.275918	0.502710	-6.13
255079_s_a	14-3-3 protein GF14chi (grf1) identical t	GF14 PHI	AT1G35160 /	1.08	0.12	1.19	0.275951	0.502710	-6.13
257362_at	hypothetical protein predicted by genefir	---	AT2G45840	1.08	0.11	1.19	0.275977	0.502719	-6.13
252293_at	4-coumarate-CoA ligase -like protein 4-	---	AT3G48990	1.09	0.13	1.19	0.276138	0.502877	-6.13
257863_at	hypothetical protein similar to GRAB1 pr	anac057	AT3G17730	1.08	0.11	1.19	0.276141	0.502877	-6.13
262178_at	membrane protein, putative similar to m	KOM	AT1G77860	1.14	0.19	1.18	0.276176	0.502877	-6.13
263423_at	hypothetical protein predicted by gensca	---	AT2G31700	1.09	0.13	1.18	0.27623	0.502877	-6.13
259669_at	short chain alcohol dehydrogenase, put	ABA2	AT1G52340	-1.12	-0.17	-1.18	0.276183	0.502877	-6.13
246372_at	hypothetical protein predicted by genem	---	AT1G51900	1.09	0.13	1.18	0.276241	0.502877	-6.13

261665_at	beta-glucan-elicitor receptor, putative si	---	AT1G18310	-1.09	-0.13	-1.18	0.276207	0.502877	-6.13
265607_at	hypothetical protein predicted by gensca	---	AT2G25370	1.09	0.12	1.19	0.276167	0.502877	-6.13
264912_at	auxin-induced protein, putative similar t	---	AT1G60750	1.10	0.14	1.18	0.276281	0.502911	-6.13
266585_at	putative retroelement pol polyprotein	---	---	1.12	0.16	1.18	0.276315	0.502931	-6.13
252656_at	hypothetical protein	---	AT3G44770	1.14	0.18	1.18	0.276416	0.503076	-6.13
257916_at	unknown protein similar to hypothetical	---	AT3G23210	-1.16	-0.22	-1.18	0.276447	0.503092	-6.13
261030_at	unknown protein contains similarity to nu	---	AT1G17410	-1.12	-0.16	-1.18	0.276497	0.503143	-6.13
255825_at	Expressed protein ; supported by full-ler	---	AT2G40475	1.16	0.21	1.18	0.276594	0.503280	-6.13
250923_at	putative protein ; supported by full-lengt	CDC25	AT5G03455	1.12	0.17	1.18	0.276758	0.503537	-6.13
266266_at	putative enolase (2-phospho-D-glycerate	---	AT2G29560	-1.12	-0.16	-1.18	0.276834	0.503612	-6.13
264995_at	mutator-like transposase, putative simil	---	---	1.13	0.18	1.18	0.276843	0.503612	-6.13
249629_at	kinesin -like protein Krm protein, L.japo	---	AT5G37590	-1.14	-0.19	-1.18	0.27688	0.503639	-6.13
261192_at	NAM protein, putative similar to NAM pr	ANAC13	AT1G32870	-1.14	-0.19	-1.18	0.276928	0.503645	-6.13
264151_at	hypothetical protein predicted by gene	---	AT1G02070	1.11	0.14	1.18	0.276922	0.503645	-6.13
263707_at	hypothetical protein Similar to gi|157382	---	AT1G09300	-1.15	-0.21	-1.18	0.277039	0.503807	-6.13
263834_at	hypothetical protein	---	AT2G40316	-1.11	-0.15	-1.18	0.277109	0.503855	-6.13
250587_at	putative protein contains similarity to RI	---	AT5G07640	1.09	0.13	1.18	0.277093	0.503855	-6.13
257805_at	sugar transport, putative similar to D-XY	ATPLT5	AT3G18830	1.21	0.28	1.18	0.277207	0.503898	-6.13
257056_at	unknown protein similar to hypothetical	---	AT3G15350	1.10	0.14	1.18	0.27726	0.503898	-6.13
263254_x_a	hypothetical protein similar to hypothetic	---	---	-1.14	-0.19	-1.18	0.277265	0.503898	-6.13
247501_at	putative protein predicted proteins, Ara	---	AT5G61920	-1.08	-0.11	-1.18	0.277254	0.503898	-6.13
249738_at	60s acidic ribosomal protein P1	---	AT5G24510	1.08	0.11	1.18	0.277288	0.503898	-6.13
248697_at	putative protein contains similarity to acy	---	AT5G48370	-1.19	-0.25	-1.18	0.277287	0.503898	-6.13
246643_s_a	putative protein various predicted prote	---	---	-1.09	-0.12	-1.18	0.277253	0.503898	-6.13
252573_at	zinc finger protein zinc finger protein ID	---	AT3G45260	-1.10	-0.14	-1.18	0.277377	0.503941	-6.13
260671_at	unknown protein ;supported by full-lengt	---	AT1G19310	-1.12	-0.16	-1.18	0.277367	0.503941	-6.13
253450_at	putative protein MUS308 gene, Drosop	---	AT4G32700	-1.08	-0.12	-1.18	0.277352	0.503941	-6.13
244922_s_a	hypothetical protein	---	AT2G07674	-1.12	-0.17	-1.18	0.277441	0.503976	-6.13
252749_at	putative protein several hypothetical pro	---	---	1.10	0.13	1.18	0.277429	0.503976	-6.13
253961_at	putative protein SPF1 protein, Ipomoea	WRKY34	AT4G26440	1.09	0.12	1.18	0.277485	0.504017	-6.13
246179_at	putative protein hypothetical protein F2	---	AT5G28440	1.13	0.18	1.18	0.277539	0.504075	-6.13
250448_at	putative protein lignostilbene-alpha,beta	---	AT5G10820	1.18	0.24	1.18	0.277741	0.504401	-6.13
256681_at	unknown protein ; supported by cDNA: g	SPP2	AT3G52340	-1.33	-0.41	-1.18	0.277789	0.504423	-6.13
266389_s_a	unknown protein	---	AT2G31580 /	1.09	0.12	1.18	0.277797	0.504423	-6.13
265478_at	unknown protein ;supported by full-leng	MEE14	AT2G15890	-1.09	-0.13	-1.18	0.277905	0.504578	-6.13

264035_at	hypothetical protein predicted by genefi	---	AT2G03630	-1.11	-0.16	-1.18	0.277938	0.504598	-6.13
263038_at	conserved hypothetical protein protein p	---	AT1G23270	1.09	0.13	1.18	0.278081	0.504817	-6.14
266161_at	hypothetical protein	ATCHX7	AT2G28170	1.13	0.18	1.18	0.278164	0.504848	-6.14
254443_at	putative protein (fragment) BRCA1-ass	BRCA1	AT4G21070	1.09	0.13	1.18	0.278148	0.504848	-6.14
255559_at	putative NAK-like ser/thr protein kinase	---	AT4G02010	-1.13	-0.17	-1.18	0.278153	0.504848	-6.14
249358_at	sucrose cleavage protein -like sucrose	---	AT5G40510	1.11	0.15	1.18	0.27821	0.504891	-6.14
254818_at	pEARLI 1-like protein Arabidopsis thalia	---	AT4G12470	-1.49	-0.57	-1.18	0.278352	0.505087	-6.14
248652_at	putative protein contains similarity to ph	SHV2	AT5G49270	-1.16	-0.21	-1.18	0.278362	0.505087	-6.14
248591_at	xylulose kinase ; supported by cDNA: g	---	AT5G49650	1.11	0.15	1.18	0.278423	0.505157	-6.14
261975_at	unknown protein	---	AT1G64640	1.33	0.41	1.18	0.278469	0.505200	-6.14
260233_at	putative cytochrome P450 similar to cyt	CYP98A9	AT1G74550	1.17	0.22	1.18	0.278511	0.505235	-6.14
267423_at	putative potassium transporter	KUP11	AT2G35060	-1.18	-0.24	-1.18	0.278563	0.505290	-6.14
267523_at	unknown protein	---	AT2G30600	-1.11	-0.15	-1.18	0.278595	0.505308	-6.14
249574_at	putative protein embryonic abundant pr	PDLP7	AT5G37660	1.10	0.14	1.18	0.278718	0.505359	-6.14
263167_at	unknown protein Belongs to PF|01121	---	AT1G03030	-1.12	-0.16	-1.18	0.278678	0.505359	-6.14
260528_at	putative WRKY-type DNA binding protei	WRKY23	AT2G47260	1.25	0.33	1.18	0.278756	0.505359	-6.14
260797_at	neoxanthin cleavage enzyme, putative	NCED9	AT1G78390	1.11	0.15	1.18	0.278694	0.505359	-6.14
249352_at	putative transcription factor MYB22 ; su	MYB22	AT5G40430	-1.08	-0.11	-1.18	0.278669	0.505359	-6.14
261590_at	hypothetical protein predicted by genem	ROPGEF2	AT1G01700	-1.09	-0.12	-1.18	0.278749	0.505359	-6.14
260889_at	hypothetical protein predicted by genem	---	AT1G29120	-1.09	-0.12	-1.18	0.278825	0.505443	-6.14
254414_at	hypothetical protein	HSA32	AT4G21320	1.12	0.17	1.18	0.27885	0.505448	-6.14
260360_at	chorismate mutase, putative contains P	CM3	AT1G69370	-1.14	-0.19	-1.18	0.278909	0.505476	-6.14
258273_at	unknown protein ;supported by full-leng	GRX4	AT3G15660	-1.08	-0.11	-1.18	0.278896	0.505476	-6.14
264630_at	hypothetical protein predicted by genem	FAS1	AT1G65470	1.12	0.17	1.18	0.278994	0.505589	-6.14
266467_at	Not56-like protein ; supported by cDNA	ALG3	AT2G47760	1.11	0.15	1.18	0.279085	0.505674	-6.14
250844_at	putative protein ;supported by full-lengt	SIM	AT5G04470	-1.22	-0.29	-1.18	0.27907	0.505674	-6.14
250967_at	putative protein In2, Zea mays, EMBL:X	---	AT5G02790	1.14	0.19	1.18	0.279195	0.505833	-6.14
261883_at	protein kinase, putative similar to recep	---	AT1G80870	-1.11	-0.14	-1.18	0.279265	0.505862	-6.14
262320_at	hypothetical protein predicted by gensca	---	AT1G27550	-1.10	-0.13	-1.18	0.2793	0.505862	-6.14
248013_at	putative protein contains similarity to ca	ACA8	AT5G56330	1.14	0.19	1.18	0.279246	0.505862	-6.14
245086_at	putative translation initiation factor	---	AT2G39820	-1.09	-0.13	-1.18	0.279297	0.505862	-6.14
266446_at	hypothetical protein predicted by gensca	---	AT2G43310	-1.09	-0.12	-1.18	0.279342	0.505898	-6.14
251170_at	ATMRK1 ;supported by full-length cDN	ATMRK1	AT3G63260	1.08	0.11	1.18	0.279471	0.506093	-6.14
265811_at	unknown protein possibly related to thyr	EDA2	AT2G18080	1.09	0.13	1.18	0.279506	0.506115	-6.14
256378_at	receptor protein kinase, putative contai	---	AT1G66830	-1.09	-0.12	-1.18	0.279541	0.506139	-6.14

256047_at	hypothetical protein predicted by genem	---	AT1G07060	1.12	0.16	1.18	0.279597	0.506199	-6.14
259766_at	unknown protein ;supported by full-lengt	---	AT1G64360	-1.19	-0.25	-1.18	0.279719	0.506364	-6.14
259960_at	cell division control protein, putative sim	---	AT1G53710	1.13	0.17	1.18	0.279732	0.506364	-6.14
259072_at	unknown protein similar to unknown pro	FLA18	AT3G11700	1.14	0.19	1.18	0.279814	0.506472	-6.14
253584_at	putative protein several hypothetical pro	---	AT4G30700	-1.09	-0.13	-1.17	0.27994	0.506660	-6.14
252423_at	putative protein putative hydrolyse - Ara	---	AT3G47590	1.09	0.13	1.17	0.280041	0.506687	-6.14
260848_at	pectinesterase, putative similar to pecti	sks8	AT1G21850	1.14	0.18	1.17	0.280019	0.506687	-6.14
254544_at	putative chitinase chitinase (EC 3.2.1.1	---	AT4G19820	1.12	0.16	1.17	0.280044	0.506687	-6.14
261354_at	unknown protein ; supported by cDNA: g	atnudt3	AT1G79690	1.10	0.14	1.17	0.28004	0.506687	-6.14
261138_at	hypothetical protein contains Pfam profil	---	AT1G19710	-1.11	-0.15	-1.17	0.28008	0.506712	-6.14
248260_at	putative protein similar to unknown prote	---	AT5G53240	1.09	0.13	1.17	0.280105	0.506716	-6.14
256019_at	cytochrome P-450, putative similar to cy	---	AT1G58260 /	-1.09	-0.13	-1.17	0.280179	0.506811	-6.14
250601_at	putative protein contains similarity to He	---	AT5G07810	1.08	0.12	1.17	0.280392	0.507156	-6.14
251409_at	Expressed protein ; supported by full-ler	---	AT3G60245	-1.26	-0.34	-1.17	0.280471	0.507219	-6.14
250204_at	leucine zipper protein-like	ATEXO70(	AT5G13990	-1.11	-0.15	-1.17	0.280454	0.507219	-6.14
253622_at	cyclic nucleotide and calmodulin-regula	ATCNGC9	AT4G30560	1.10	0.13	1.17	0.280506	0.507241	-6.14
260545_at	putative glutathione peroxidase ;suppor	ATGPX3	AT2G43350	-1.11	-0.14	-1.17	0.280536	0.507255	-6.14
248891_at	MCM3 homolog (emb|CAA03887.1)	MCM3	AT5G46280	-1.45	-0.53	-1.17	0.280588	0.507309	-6.14
248119_at	serine/threonine-specific protein kinase-	---	AT5G54590	1.13	0.18	1.17	0.280786	0.507627	-6.14
251562_at	putative protein hypothetical protein T2	---	AT3G57890	-1.09	-0.13	-1.17	0.280813	0.507636	-6.14
252748_at	putative protein putative proteins - Arabi	---	---	-1.09	-0.12	-1.17	0.281048	0.508020	-6.14
250346_at	lysine decarboxylase - like protein lysin	---	AT5G11950	1.29	0.37	1.17	0.281114	0.508099	-6.14
267113_at	hypothetical protein predicted by gensca	---	AT2G14850	1.08	0.12	1.17	0.281285	0.508327	-6.14
258077_at	unknown protein ;supported by full-leng	---	AT3G26110	1.12	0.16	1.17	0.281282	0.508327	-6.14
255166_at	putative protein putative centromeric pr	---	---	1.09	0.12	1.17	0.281328	0.508365	-6.14
254091_at	hypothetical protein	---	AT4G25070	1.18	0.24	1.17	0.281423	0.508461	-6.15
249305_at	putative protein strong similarity to unkn	---	AT5G41490	1.11	0.16	1.17	0.281426	0.508461	-6.15
248779_at	acetoacyl-CoA-thiolase ;supported by fu	---	AT5G47720	-1.18	-0.23	-1.17	0.281473	0.508506	-6.15
263656_at	putative auxin-induced protein AUX2-11	SHY2	AT1G04240	-1.61	-0.68	-1.17	0.281606	0.508586	-6.15
255964_at	hypothetical protein predicted by genem	ZYP1b	AT1G22275	-1.09	-0.13	-1.17	0.281597	0.508586	-6.15
249616_s_a	contains similarity to DnaJ protein	---	AT5G37440 /	-1.09	-0.12	-1.17	0.281586	0.508586	-6.15
261497_x_a	hypothetical protein contains similarity to	AGL59	AT1G28460	-1.10	-0.14	-1.17	0.281575	0.508586	-6.15
249635_at	putative glucan synthase glucan synthas	ATGSL09	AT5G36870	1.10	0.14	1.17	0.281684	0.508657	-6.15
262082_s_a	wall-associated kinase 2, putative simila	---	AT1G56120 /	1.29	0.37	1.17	0.28169	0.508657	-6.15
263359_at	putative lysosomal acid lipase	ATLIP1	AT2G15230	-1.12	-0.16	-1.17	0.281752	0.508728	-6.15

247044_at	MAP protein kinase ; supported by cDN	MAPKKK5	AT5G66850	1.13	0.18	1.17	0.2818	0.508774	-6.15
253718_at	serine/threonine-specific receptor prote	---	AT4G29450	1.11	0.15	1.17	0.281929	0.508968	-6.15
245315_at	proteasome chain protein ; supported by	PBD2	AT4G14800	-1.09	-0.12	-1.17	0.281964	0.508973	-6.15
260320_at	hypothetical protein similar to putative p	---	AT1G63930	1.14	0.19	1.17	0.281979	0.508973	-6.15
247909_at	unknown protein ; supported by full-leng	---	AT5G57370	-1.11	-0.15	-1.17	0.282009	0.508973	-6.15
251156_at	putative protein ZCF61, Arabidopsis tha	EDL3	AT3G63060	1.12	0.17	1.17	0.282022	0.508973	-6.15
246494_at	putative protein putative cellulose synth	CSLA11	AT5G16190	1.11	0.15	1.17	0.28205	0.508984	-6.15
246754_at	transcription factor - like protein Hap5a	NF-YC8	AT5G27910	1.13	0.18	1.17	0.282142	0.509110	-6.15
264319_at	subtilisin-like serine protease, putative	SDD1	AT1G04110	1.12	0.16	1.17	0.282241	0.509128	-6.15
264535_at	Phosphatidylinositol Transfer Protein, p	---	AT1G55690	1.27	0.35	1.17	0.282219	0.509128	-6.15
257229_at	putative calmodulin-binding protein cont	IQD26	AT3G16490	1.13	0.17	1.17	0.282181	0.509128	-6.15
257434_at	hypothetical protein predicted by gensca	---	AT2G21740	1.08	0.11	1.17	0.282207	0.509128	-6.15
248522_at	predicted protein	---	AT5G50565 /	-1.09	-0.12	-1.17	0.282372	0.509323	-6.15
246014_at	putative protein	---	AT5G10680	1.10	0.13	1.17	0.282461	0.509324	-6.15
267402_at	putative SF16 protein {Helianthus annu	IQD6	AT2G26180	1.14	0.19	1.17	0.282421	0.509324	-6.15
260150_at	putative oxidoreductase similar to gibbe	---	AT1G52820	1.11	0.15	1.17	0.282452	0.509324	-6.15
263972_at	unknown protein	---	AT2G42760	-1.37	-0.45	-1.17	0.282405	0.509324	-6.15
248535_at	putative protein contains similarity to GT	---	AT5G50120	1.12	0.17	1.17	0.282557	0.509456	-6.15
264478_at	hypothetical protein predicted by gensca	---	AT1G77270	1.09	0.12	1.17	0.282594	0.509483	-6.15
253176_at	putative protein Human (H326) mRNA,	---	AT4G35140	-1.15	-0.21	-1.17	0.282739	0.509671	-6.15
246185_at	5-methyltetrahydropteroyltriglutamate-h	ATMS3	AT5G20980	-1.08	-0.11	-1.17	0.282744	0.509671	-6.15
256806_at	CCAAT-binding factor B chain, putative	NF-YA9	AT3G20910	-1.11	-0.15	-1.17	0.282832	0.509790	-6.15
248991_at	putative protein contains similarity to dis	---	AT5G45220	1.15	0.21	1.17	0.283052	0.510147	-6.15
254719_at	putative protein beta 1,3-glucanase, Tri	---	AT4G13600	1.11	0.15	1.17	0.283148	0.510279	-6.15
253778_at	heat-shock protein heat-shock protein h	---	AT4G28480	-1.12	-0.16	-1.17	0.283232	0.510350	-6.15
257847_at	hypothetical protein predicted by genefir	---	AT3G13020	1.10	0.14	1.17	0.283218	0.510350	-6.15
246212_at	putative protein ; supported by cDNA: gi	SPT	AT4G36930	-1.33	-0.41	-1.17	0.283329	0.510451	-6.15
257332_at	hypothetical protein	---	---	1.13	0.18	1.17	0.283333	0.510451	-6.15
247244_at	putative protein similar to unknown prote	---	AT5G64710	-1.09	-0.12	-1.17	0.283453	0.510628	-6.15
253935_at	putative aspartate-tRNA ligase aspartat	---	AT4G26870	-1.25	-0.32	-1.17	0.28352	0.510698	-6.15
256059_at	hypothetical protein contains similarity to	---	AT1G06990	-1.12	-0.16	-1.17	0.283537	0.510698	-6.15
250940_at	putative protein	---	AT5G03310	-1.08	-0.12	-1.17	0.283573	0.510722	-6.15
256717_at	hypothetical protein predicted by gensca	---	AT2G34110	1.11	0.15	1.17	0.283619	0.510725	-6.15
247192_at	histone H3 (sp|P05203) ; supported by	---	AT5G65360	-1.68	-0.75	-1.17	0.283598	0.510725	-6.15
251619_at	putative protein hypothetical protein At2	---	AT3G58050	-1.07	-0.10	-1.16	0.283809	0.511027	-6.15

253165_at	putative protein predicted protein, Arabi	---	AT4G35320	1.23	0.30	1.16	0.283904	0.511051	-6.15
264379_at	hypothetical protein predicted by grail	---	AT2G25200	-1.20	-0.26	-1.16	0.28398	0.511051	-6.15
254340_at	putative protein hypothetical protein HY	---	AT4G22120	1.24	0.31	1.16	0.283953	0.511051	-6.15
258492_at	unknown protein	---	AT3G02390	-1.09	-0.12	-1.16	0.283968	0.511051	-6.15
260188_at	Mutator-like transposase similar to mudr	---	---	1.08	0.11	1.16	0.283851	0.511051	-6.15
262446_at	hypothetical protein predicted by gensca	---	AT1G49310	-1.27	-0.34	-1.16	0.283904	0.511051	-6.15
252076_at	LS1-like protein AT-LS1 product - Arabi	---	AT3G51660	1.29	0.37	1.16	0.283976	0.511051	-6.15
250430_at	putative protein	---	AT5G10460	1.08	0.11	1.16	0.284009	0.511063	-6.15
248885_at	putative protein similar to unknown prote	---	AT5G46150	-1.09	-0.13	-1.16	0.284088	0.511165	-6.15
265635_at	hypothetical protein predicted by gensca	---	AT2G25360	1.08	0.11	1.16	0.284181	0.511293	-6.15
253582_at	Expressed protein ;supported by cDNA:	---	AT4G30670	-1.15	-0.20	-1.16	0.284335	0.511529	-6.15
255920_at	putative protein	---	AT5G28590	1.12	0.17	1.16	0.284397	0.511601	-6.15
249764_at	septum site-determining MinD (dbj|BAA	MIND	AT5G24020	-1.13	-0.17	-1.16	0.284484	0.511676	-6.15
248178_at	root cap protein 2-like protein	---	AT5G54370	1.13	0.18	1.16	0.284472	0.511676	-6.15
255802_s_a	putative protein RING-H2 finger protein	---	AT4G10150 /	-1.08	-0.12	-1.16	0.284513	0.511688	-6.15
245510_at	hypothetical protein	---	AT4G15740	1.16	0.21	1.16	0.284617	0.511835	-6.15
250814_at	E2, ubiquitin-conjugating enzyme, putat	UBC22	AT5G05080	-1.11	-0.15	-1.16	0.284663	0.511877	-6.15
256237_at	leucine rich repeat protein, putative con	DRT100	AT3G12610	2.57	1.36	1.16	0.284715	0.511931	-6.15
263164_at	putative glutamate/aspartate-binding pe	---	AT1G03070	-1.10	-0.14	-1.16	0.284786	0.511978	-6.15
250064_at	disease resistance protein - like downy	DAR4	AT5G17890	-1.13	-0.18	-1.16	0.28477	0.511978	-6.15
255703_at	putative chalcone synthase similar to pla	---	AT4G00040	-1.16	-0.21	-1.16	0.284861	0.512031	-6.16
265562_at	hypothetical protein predicted by gensca	---	AT2G05500	1.07	0.10	1.16	0.284855	0.512031	-6.16
246694_at	putative protein	---	---	1.09	0.13	1.16	0.285029	0.512294	-6.16
247470_at	putative protein various predicted prote	---	AT5G62220	1.34	0.42	1.16	0.285078	0.512301	-6.16
262740_at	lipase, putative contains Pfam profile: P	---	AT1G28590	-1.10	-0.13	-1.16	0.285076	0.512301	-6.16
264046_at	putative non-LTR retroelement reverse t	---	AT2G22440	1.10	0.13	1.16	0.285252	0.512573	-6.16
257539_at	hypothetical protein predicted by genem	---	AT3G29150	1.09	0.12	1.16	0.285334	0.512680	-6.16
265823_at	hypothetical protein predicted by gensca	---	AT2G35760	-1.10	-0.13	-1.16	0.285369	0.512702	-6.16
257602_at	hydrolase, putative similar to Metal Dep	---	AT3G13800	1.10	0.13	1.16	0.28547	0.512843	-6.16
246590_at	cyclic nucleotide and calmodulin-regula	CNGC18	AT5G14870	1.08	0.11	1.16	0.285507	0.512869	-6.16
265669_at	unknown protein ;supported by full-leng	---	AT2G32040	-1.17	-0.22	-1.16	0.285599	0.512993	-6.16
245161_at	putative myrosinase binding protein	NSP2	AT2G33070	-1.12	-0.17	-1.16	0.285793	0.513084	-6.16
253361_at	putative protein various predicted protei	---	AT4G33100	1.18	0.23	1.16	0.285733	0.513084	-6.16
266978_at	putative disease resistance response pr	---	AT2G39430	1.10	0.13	1.16	0.285675	0.513084	-6.16
259074_at	putative protein kinase contains Pfam pr	RPK2	AT3G02130	-1.15	-0.21	-1.16	0.285817	0.513084	-6.16

253797_at	putative protein 55.11 protein homolog,	RPN1B	AT4G28470	-1.07	-0.10	-1.16	0.285851	0.513084	-6.16
265957_at	hypothetical protein predicted by gensca	---	AT2G37300	1.07	0.10	1.16	0.285831	0.513084	-6.16
254285_at	putative cdc2 kinase homolog cdc2 kina	---	AT4G22940	-1.12	-0.17	-1.16	0.28584	0.513084	-6.16
253086_at	hypothetical protein	---	AT4G36370	1.08	0.11	1.16	0.285822	0.513084	-6.16
246386_at	beta-galactosidase, putative similar to b	BGAL16	AT1G77410	1.12	0.17	1.16	0.285772	0.513084	-6.16
256180_at	light repressible receptor protein kinase	---	AT1G51810	1.07	0.10	1.16	0.285909	0.513148	-6.16
249917_at	putative protein strong similarity to unkn	---	AT5G22460	1.58	0.66	1.16	0.285944	0.513169	-6.16
266258_at	60S acidic ribosomal protein P2 ;suppo	---	AT2G27720	-1.18	-0.24	-1.16	0.285999	0.513227	-6.16
247466_at	putative protein predicted proteins, Arat	---	AT5G62090	-1.15	-0.20	-1.16	0.286053	0.513284	-6.16
255077_at	putative protein	---	AT4G09150	-1.16	-0.21	-1.16	0.286216	0.513497	-6.16
249608_at	multispanning membrane protein - like	---	AT5G37310	-1.11	-0.15	-1.16	0.286195	0.513497	-6.16
245604_at	hypothetical protein	---	AT4G14290	-1.11	-0.14	-1.16	0.286293	0.513553	-6.16
260997_at	zinc-finger protein (ZPT4-4), putative si	---	AT1G26610	-1.08	-0.11	-1.16	0.28629	0.513553	-6.16
261601_at	ARP protein, putative similar to ARP pr	NQR	AT1G49670	1.09	0.12	1.16	0.286332	0.513562	-6.16
265488_at	hypothetical protein predicted by gensca	---	AT2G15610	1.10	0.14	1.16	0.286343	0.513562	-6.16
261754_at	alpha-amylase, putative similar to alpha	AMY2	AT1G76130	1.28	0.36	1.16	0.286539	0.513874	-6.16
256342_at	unknown protein ; supported by full-leng	---	AT1G72020	1.10	0.13	1.16	0.286573	0.513894	-6.16
250833_at	myotubularin - like protein myotubularin	---	AT5G04540	1.09	0.13	1.16	0.286606	0.513912	-6.16
262950_at	transcription initiation factor, putative si	---	AT1G75510	1.08	0.11	1.16	0.286797	0.514214	-6.16
265297_at	putative disease resistance protein cont	---	AT2G14080	1.08	0.12	1.16	0.286832	0.514238	-6.16
258239_at	putative chlorophyll A-B binding protein	LHCB2.3	AT3G27690	-1.55	-0.63	-1.16	0.286861	0.514249	-6.16
250900_at	putative protein ; supported by cDNA: g	ATB' ALPH	AT5G03470	-1.13	-0.18	-1.16	0.286895	0.514269	-6.16
245504_at	glutaredoxin	---	AT4G15660	-1.17	-0.22	-1.16	0.287242	0.514811	-6.16
248451_at	putative protein similar to unknown prote	---	AT5G51180	1.08	0.11	1.16	0.287229	0.514811	-6.16
251362_at	DEAD box RNA helicase RH12	---	AT3G61240	-1.10	-0.14	-1.16	0.287283	0.514843	-6.16
251820_at	putative protein In2-1 protein, Zea mays	GSTL2	AT3G55040	-1.21	-0.28	-1.16	0.287335	0.514897	-6.16
248486_at	respiratory burst oxidase protein	RHD2	AT5G51060	1.08	0.11	1.16	0.287369	0.514916	-6.16
265362_at	putative retroelement pol polyprotein	---	---	-1.09	-0.12	-1.16	0.287413	0.514955	-6.16
249173_at	unknown protein	---	AT5G43000	1.12	0.17	1.15	0.287517	0.515100	-6.16
252527_at	dTDP-glucose 4-6-dehydratases-like pr	UXS5	AT3G46440	1.12	0.16	1.15	0.287801	0.515528	-6.16
256498_at	hypothetical protein	---	---	-1.09	-0.12	-1.15	0.287799	0.515528	-6.16
257553_at	unknown protein contains Pfam profile:	TPR2	AT3G16830	-1.16	-0.21	-1.15	0.287835	0.515549	-6.16
267364_at	unknown protein ;supported by full-leng	ELF4	AT2G40080	-1.12	-0.16	-1.15	0.287936	0.515690	-6.16
257175_s_a	cyclopropane-fatty-acyl-phospholipid sy	---	AT3G23470 /	-1.10	-0.14	-1.15	0.288087	0.515779	-6.16
256455_at	unknown protein ;supported by full-lengt	---	AT1G75190	-1.09	-0.13	-1.15	0.288058	0.515779	-6.16

265899_s_a	SKP1/ASK1 (At3), putative similar to fir	ASK4	AT1G20140 /	-1.11	-0.14	-1.15	0.28805	0.515779	-6.16
263424_at	putative RING zinc finger protein	---	AT2G31510	-1.10	-0.13	-1.15	0.288099	0.515779	-6.16
246360_at	hypothetical protein	---	---	1.09	0.13	1.15	0.288051	0.515779	-6.16
265535_at	hypothetical protein predicted by gensc	---	AT2G15900	1.09	0.12	1.15	0.288188	0.515857	-6.16
259640_at	beta-glucosidase, putative identical to C	BGLU18	AT1G52400	-1.23	-0.30	-1.15	0.288171	0.515857	-6.16
267630_at	unknown protein predicted by genefinde	---	AT2G42130	-1.12	-0.17	-1.15	0.288362	0.516128	-6.17
253209_at	putative protein membrane-associated	---	AT4G34830	-1.13	-0.17	-1.15	0.288452	0.516248	-6.17
261469_at	unknown protein	AtRLP4	AT1G28340	-1.09	-0.13	-1.15	0.288504	0.516299	-6.17
246380_at	cytochrome P450, putative similar to cy	CYP96A15	AT1G57750	1.14	0.19	1.15	0.288525	0.516299	-6.17
264846_at	senescence-associated protein contains	---	AT2G17850	1.10	0.13	1.15	0.288687	0.516548	-6.17
252695_s_a	hypothetical protein predicted proteins,	---	---	-1.07	-0.10	-1.15	0.288717	0.516561	-6.17
255781_at	unknown protein	---	AT1G19880	1.09	0.12	1.15	0.288896	0.516840	-6.17
251115_at	putative protein symplekin - Homo sapi	ESP4	AT5G01400	1.10	0.13	1.15	0.288957	0.516869	-6.17
267466_at	putative GDSL-motif lipase/hydrolase si	---	AT2G19010	-1.09	-0.12	-1.15	0.288957	0.516869	-6.17
253591_at	putative protein hypothetical protein, Sc	MUS81	AT4G30870	-1.14	-0.19	-1.15	0.28905	0.516994	-6.17
253206_at	putative squalene synthase non-conser	SQS1	AT4G34640	1.10	0.14	1.15	0.289087	0.517021	-6.17
263500_s_a	hypothetical protein	---	AT2G07672	-1.11	-0.15	-1.15	0.289128	0.517052	-6.17
250766_at	putative protein similar to unknown prote	---	AT5G05550	1.11	0.15	1.15	0.289304	0.517292	-6.17
256868_at	eukaryotic translation initiation factor 4E	EIF4B1	AT3G26400	1.17	0.23	1.15	0.289307	0.517292	-6.17
256959_at	methyltransferase, putative	---	AT3G13440	-1.08	-0.11	-1.15	0.28938	0.517382	-6.17
253259_at	putative protein ethylene-responsive ele	RRTF1	AT4G34410	1.33	0.41	1.15	0.289421	0.517414	-6.17
266558_at	putative polygalacturonase	---	AT2G23900	-1.09	-0.12	-1.15	0.289456	0.517436	-6.17
266838_at	similar to jasmonate-inducible proteins f	---	AT2G25980	1.10	0.13	1.15	0.289516	0.517463	-6.17
249390_at	60S RIBOSOMAL PROTEIN L5 -like 60	---	AT5G40130	-1.08	-0.12	-1.15	0.289509	0.517463	-6.17
251346_at	putative protein hypothetical protein F14	---	AT3G60980	1.09	0.13	1.15	0.2896	0.517573	-6.17
251320_at	3-methyl-2-oxobutanoate hydroxy-meth	PANB2	AT3G61530	1.08	0.12	1.15	0.289679	0.517674	-6.17
253950_at	putative dihydrolipoamide succinyltrans	---	AT4G26910	1.17	0.23	1.15	0.289749	0.517688	-6.17
255415_at	hypothetical protein	---	AT4G03160	-1.07	-0.10	-1.15	0.289722	0.517688	-6.17
267546_at	putative disease resistance protein	AtRLP23	AT2G32680	1.57	0.65	1.15	0.289756	0.517688	-6.17
254062_at	putative protein zinc finger protein ZNF	---	AT4G25380	1.38	0.46	1.15	0.289862	0.517838	-6.17
266070_at	hypothetical protein predicted by gensca	EXLB3	AT2G18660	2.69	1.43	1.15	0.289908	0.517880	-6.17
257639_at	hypothetical protein	---	AT3G25720	1.10	0.14	1.15	0.289993	0.517950	-6.17
260724_at	unknown protein ;supported by full-lengt	---	AT1G48140	1.09	0.13	1.15	0.289988	0.517950	-6.17
253839_at	putative protein prolactin-induced T cell	---	AT4G27890	1.11	0.15	1.15	0.290025	0.517967	-6.17
252537_at	putative transporter protein peptide tran	---	AT3G45710	1.10	0.14	1.15	0.290158	0.518042	-6.17

247331_at	putative protein contains similarity to AT	FP3	AT5G63530	1.20	0.26	1.15	0.290123	0.518042	-6.17
265322_at	hypothetical protein predicted by gensca	---	AT2G18270	-1.08	-0.11	-1.15	0.290093	0.518042	-6.17
259369_s_a	hypothetical protein similar to putative C	---	AT1G69150 /	1.09	0.13	1.15	0.290158	0.518042	-6.17
264805_at	unknown protein similar to putative DNA	ATRX	AT1G08600	-1.10	-0.14	-1.15	0.290519	0.518613	-6.17
259088_at	unknown protein, contains TNFR/NGFF	---	AT3G04970	-1.15	-0.20	-1.15	0.290524	0.518613	-6.17
252526_at	putative protein ethylene-forming enzyn	---	AT3G46480	1.12	0.16	1.15	0.290605	0.518719	-6.17
257628_at	cytochrome P450, putative contains Pfa	CYP71B26	AT3G26290	-1.22	-0.29	-1.15	0.290877	0.518739	-6.17
246188_at	putative protein	---	AT5G21050	1.08	0.11	1.15	0.29079	0.518739	-6.17
264692_at	DNA binding protein MybSt1, putative s	---	AT1G70000	-1.12	-0.16	-1.15	0.290916	0.518739	-6.17
252241_at	putative protein CND41, chloroplast nuc	---	AT3G50050	1.10	0.13	1.15	0.290935	0.518739	-6.17
246135_at	putative protein non-consensus donor s	---	AT5G20885	-1.20	-0.26	-1.15	0.290772	0.518739	-6.17
249462_at	putative protein predicted proteins, Ara	EMB2744	AT5G39680	-1.10	-0.14	-1.15	0.290777	0.518739	-6.17
253862_at	NOZZLE/SPOROCYTELESS ; support	SPL	AT4G27330	1.13	0.17	1.15	0.290799	0.518739	-6.17
263728_at	gamma-adaptin, putative similar to gam	---	AT1G60070	-1.10	-0.14	-1.15	0.290854	0.518739	-6.17
247683_at	serine/threonine-specific protein kinase	---	AT5G59660	1.11	0.15	1.15	0.290865	0.518739	-6.17
246225_at	putative protein ;supported by full-length	LEJ2	AT4G36910	-1.12	-0.17	-1.15	0.29069	0.518739	-6.17
261172_at	hypothetical protein predicted by genem	---	AT1G04840	-1.11	-0.14	-1.15	0.290792	0.518739	-6.17
267283_at	Mutator-like transposase similar to MUR	---	---	-1.07	-0.10	-1.15	0.290763	0.518739	-6.17
258195_at	myb protein(myb26) contains myb DNA	ATMYB26	AT3G13890	-1.10	-0.14	-1.15	0.290811	0.518739	-6.17
246248_at	hypothetical protein	---	AT4G36560	-1.08	-0.11	-1.15	0.290927	0.518739	-6.17
249659_s_a	putative protein similar to unknown prote	---	AT5G36710 /	1.13	0.18	1.15	0.290991	0.518758	-6.17
255772_at	calmodulin, putative similar to calmodul	---	AT1G18530	-1.10	-0.14	-1.15	0.29097	0.518758	-6.17
258718_at	unknown protein ; supported by cDNA:	---	AT3G09760	-1.10	-0.14	-1.15	0.291026	0.518780	-6.17
246601_at	copper amine oxidase, putative similar	---	AT1G31710	1.89	0.92	1.15	0.291093	0.518859	-6.17
247997_at	putative protein contains similarity to act	ATARP8	AT5G56180	1.11	0.15	1.15	0.291148	0.518915	-6.17
250317_at	tubulin beta-6 chain (sp|P29514) ; supp	TUB6	AT5G12250	-1.31	-0.39	-1.14	0.291326	0.519193	-6.17
261108_at	1-aminocyclopropane-1-carboxylate sy	ACS10	AT1G62960	-1.12	-0.17	-1.14	0.291403	0.519208	-6.17
249860_at	prolylcarboxypeptidase-like protein ;sup	---	AT5G22860	1.69	0.76	1.14	0.291358	0.519208	-6.17
265516_at	putative Athila retroelement ORF1 prote	---	---	-1.10	-0.13	-1.14	0.291396	0.519208	-6.17
259898_at	hypothetical protein predicted by genefi	---	AT1G71200	1.09	0.13	1.14	0.291466	0.519281	-6.17
261792_at	cinnamoyl CoA reductase, puitative sim	CCR1	AT1G15950	1.11	0.15	1.14	0.291531	0.519355	-6.17
257448_s_a	putative protein various predicted protei	---	AT2G11620 /	1.09	0.13	1.14	0.291577	0.519396	-6.17
249289_at	N-hydroxycinnamoyl/benzoyltransferase	---	AT5G41040	1.45	0.53	1.14	0.291727	0.519622	-6.17
254731_at	hypothetical protein	---	AT4G13750	-1.11	-0.15	-1.14	0.291758	0.519637	-6.17
267500_s_a	putative cytochrome P450	CYP704A1	AT2G44890 /	-1.16	-0.22	-1.14	0.291864	0.519730	-6.18

247811_at	leucine zipper-containing protein leucin	ATEXO70I	AT5G58430	1.24	0.32	1.14	0.291878	0.519730	-6.18
261514_at	hypothetical protein predicted by genem	---	AT1G71870	-1.14	-0.19	-1.14	0.29184	0.519730	-6.17
258946_at	hypothetical protein predicted by gensca	---	AT3G10650	-1.12	-0.16	-1.14	0.292144	0.519920	-6.18
266053_at	unknown protein	---	AT2G40730	1.10	0.14	1.14	0.292139	0.519920	-6.18
251965_at	putative protein variety of predicted pro	---	AT3G53360	-1.10	-0.14	-1.14	0.292059	0.519920	-6.18
257901_at	hypothetical protein predicted by gensca	---	---	1.09	0.13	1.14	0.292083	0.519920	-6.18
255031_at	putative proteins various hypothetical pr	---	AT4G09490	1.12	0.17	1.14	0.292111	0.519920	-6.18
245163_at	putative flavin-containing monooxygena	---	AT2G33230	1.12	0.16	1.14	0.292133	0.519920	-6.18
248166_at	putative protein contains similarity to pre	---	AT5G54520	-1.08	-0.11	-1.14	0.292102	0.519920	-6.18
248302_at	putative protein similar to unknown prote	---	AT5G53160	-1.14	-0.18	-1.14	0.292218	0.520010	-6.18
246721_at	putative protein glycine-rich protein, Ph	---	---	-1.08	-0.11	-1.14	0.292241	0.520010	-6.18
262001_at	myrosinase binding protein, putative sir	---	AT1G33790	-1.11	-0.15	-1.14	0.29237	0.520186	-6.18
252869_at	putative protein	---	AT4G39930	1.09	0.13	1.14	0.292385	0.520186	-6.18
249933_at	rac GTPase activating protein	---	AT5G22400	-1.08	-0.12	-1.14	0.292455	0.520223	-6.18
256509_at	NADPH oxidoreductase, putative simila	---	AT1G75300	-1.18	-0.24	-1.14	0.292474	0.520223	-6.18
265663_at	unknown protein predicted by genscan;	---	AT2G24290	-1.11	-0.15	-1.14	0.292442	0.520223	-6.18
259590_at	hypothetical protein contains similarity to	---	AT1G28160	1.10	0.14	1.14	0.292543	0.520305	-6.18
254520_at	potassium transporter-like protein putat	---	AT4G19960	1.14	0.18	1.14	0.292746	0.520608	-6.18
254885_at	putative protein various predicted prote	---	AT4G11745	1.12	0.17	1.14	0.292759	0.520608	-6.18
263776_s_a	putative cyclic nucleotide-regulated ion (	ATCNGC3	AT2G46430 /	1.50	0.59	1.14	0.29279	0.520623	-6.18
245857_at	putative protein various predicted prote	---	---	1.13	0.17	1.14	0.292821	0.520636	-6.18
247670_at	putative protein predicted proteins, C.el	---	AT5G60190	-1.13	-0.17	-1.14	0.293095	0.521083	-6.18
246855_at	putative protein various predicted prote	---	AT5G26280	1.28	0.36	1.14	0.293263	0.521341	-6.18
247707_at	scarecrow-like 11 - like scarecrow-like 1	---	AT5G59450	1.47	0.56	1.14	0.293331	0.521422	-6.18
262121_at	endo-1,4-beta-glucanase precursor, pu	ATCEL2	AT1G02800	1.12	0.16	1.14	0.293362	0.521433	-6.18
251448_at	allyl alcohol dehydrogenase-like protein	---	AT3G59845	1.09	0.12	1.14	0.293383	0.521433	-6.18
250806_at	putative protein similar to unknown prote	---	AT5G05070	1.09	0.12	1.14	0.293492	0.521545	-6.18
260330_at	putative RING zinc finger protein contai	---	AT1G80400	-1.09	-0.13	-1.14	0.293482	0.521545	-6.18
262192_at	hypothetical protein predicted by genem	---	AT1G77830	-1.08	-0.11	-1.14	0.293517	0.521549	-6.18
252678_s_a	nitrilase 2 ;supported by full-length cDN	NIT2	AT3G44300 /	1.09	0.12	1.14	0.293591	0.521558	-6.18
251237_at	bZIP transcription factor-like protein DN	CPuORF3	AT3G62420 /	1.10	0.13	1.14	0.293576	0.521558	-6.18
251329_at	putative protein hypothetical protein F1	SYP73	AT3G61450	1.13	0.18	1.14	0.293589	0.521558	-6.18
255888_at	hypothetical protein contains similarity to	---	AT1G20300	-1.28	-0.36	-1.14	0.293627	0.521581	-6.18
245451_at	disease resistance RPP5 like protein	SNC1	AT4G16890	-1.08	-0.11	-1.14	0.293768	0.521791	-6.18
261839_at	unknown protein	---	AT1G16040	-1.10	-0.14	-1.14	0.29384	0.521797	-6.18

245635_at	zinc finger protein ID1, putative similar t	AtIDD16	AT1G25250	1.08	0.11	1.14	0.293836	0.521797	-6.18
259687_at	unknown protein	---	AT1G63110	-1.12	-0.17	-1.14	0.293804	0.521797	-6.18
249749_at	unknown protein	BIN4	AT5G24630	1.11	0.15	1.14	0.293922	0.521903	-6.18
250681_at	unknown protein	---	AT5G06590	-1.08	-0.11	-1.14	0.293961	0.521931	-6.18
266472_at	unknown protein	---	AT2G31150	-1.08	-0.11	-1.14	0.294012	0.521981	-6.18
264008_at	unknown protein	---	AT2G21120	1.13	0.17	1.14	0.294085	0.522070	-6.18
248741_at	putative protein similar to unknown prote	SLY2	AT5G48170	-1.15	-0.20	-1.14	0.294247	0.522317	-6.18
246637_at	putative protein polymorphic membrane	---	AT5G34870	1.10	0.14	1.14	0.29428	0.522335	-6.18
261777_at	hypothetical protein predicted by genem	---	AT1G76210	1.09	0.13	1.14	0.29433	0.522344	-6.18
257018_at	unknown protein	---	AT3G19630	-1.10	-0.14	-1.14	0.294345	0.522344	-6.18
265623_at	hypothetical protein predicted by genefir	---	AT2G27270	-1.11	-0.15	-1.14	0.294354	0.522344	-6.18
267646_at	putative phosphate transporter	PHT5	AT2G32830	1.15	0.20	1.14	0.294472	0.522514	-6.18
264953_at	alcohol dehydrogenase identical to alcol	ADH1	AT1G77120	-1.13	-0.18	-1.14	0.294515	0.522548	-6.18
266740_at	hypothetical protein predicted by genefir	---	AT2G46840	1.10	0.13	1.14	0.294584	0.522630	-6.18
250808_at	putative protein contains similarity to unl	ATG18E	AT5G05150	1.12	0.16	1.14	0.294649	0.522642	-6.18
262463_at	hexose transporter, putative similar to h	STP9	AT1G50310	1.18	0.24	1.14	0.294657	0.522642	-6.18
255949_at	hypothetical protein predicted by genem	---	AT1G22080	1.07	0.10	1.14	0.294659	0.522642	-6.18
254897_at	serine/threonine kinase-like protein rec	---	AT4G11470	1.31	0.39	1.14	0.29474	0.522704	-6.18
245577_at	kinase like protein	---	AT4G14780	-1.11	-0.15	-1.14	0.29473	0.522704	-6.18
255189_at	hypothetical protein	---	AT4G07350	1.08	0.12	1.14	0.294811	0.522789	-6.18
257058_at	Expressed protein ; supported by cDNA	COX17	AT3G15352	1.41	0.50	1.14	0.294845	0.522809	-6.18
262144_at	hypothetical protein predicted by genem	---	AT1G52620	1.09	0.12	1.14	0.29508	0.523185	-6.18
255263_at	4-coumarate--CoA ligase - like protein 4	---	AT4G05160	1.08	0.11	1.14	0.29513	0.523233	-6.18
250830_at	putative protein similar to unknown prote	---	AT5G04910	1.13	0.17	1.14	0.295154	0.523235	-6.18
255986_x_a	putative protein predicted proteins, Arat	---	---	1.07	0.10	1.13	0.295254	0.523371	-6.18
257502_at	unknown protein	---	AT1G78110	1.21	0.28	1.13	0.295277	0.523372	-6.18
254082_at	glutamine cyclotransferase precursor -	QC	AT4G25720	1.21	0.27	1.13	0.295303	0.523377	-6.18
264894_at	unknown protein Location of EST gb|AA	---	AT1G23040	1.11	0.16	1.13	0.295356	0.523430	-6.18
262389_at	hypothetical protein contains similarity to	---	AT1G49270	1.09	0.13	1.13	0.29548	0.523610	-6.19
248826_at	casein kinase II beta chain ; supported b	CKB1	AT5G47080	-1.12	-0.17	-1.13	0.295601	0.523743	-6.19
246320_at	unknown protein	---	AT1G16560	1.15	0.20	1.13	0.29558	0.523743	-6.19
266400_at	methylenetetrahydrofolate dehydrogena	---	AT2G38660	1.08	0.11	1.13	0.295707	0.523849	-6.19
262393_at	hypothetical protein contains similarity to	---	AT1G49490	-1.10	-0.13	-1.13	0.2957	0.523849	-6.19
258523_at	pectin methylesterase, putative similar t	---	AT3G06830	1.07	0.10	1.13	0.295819	0.524006	-6.19
246766_at	hypothetical protein	---	AT5G27340	1.15	0.20	1.13	0.295882	0.524077	-6.19

266125_at	putative GATA-type zinc finger transcrip	---	AT2G45050	1.12	0.16	1.13	0.296006	0.524256	-6.19
253964_at	putative protein qkI-7, Mus musculus	---	AT4G26480	-1.09	-0.13	-1.13	0.296067	0.524324	-6.19
254470_at	putative protein other hypothetical prote	---	---	1.12	0.17	1.13	0.296093	0.524328	-6.19
266561_at	unknown protein	---	AT2G23960	1.08	0.11	1.13	0.29645	0.524694	-6.19
264599_at	putative myosin heavy chain similar to G	XIA	AT1G04600	-1.09	-0.12	-1.13	0.29646	0.524694	-6.19
250889_at	putative protein exostose-related protei	---	AT5G04500	1.09	0.13	1.13	0.296422	0.524694	-6.19
263402_at	hypothetical protein similar to hypothetic	---	AT2G04050	1.42	0.51	1.13	0.296329	0.524694	-6.19
261010_at	hypothetical protein predicted by genem	---	AT1G26350	-1.09	-0.13	-1.13	0.296403	0.524694	-6.19
245815_at	unknown protein	---	AT1G26090	-1.11	-0.15	-1.13	0.296387	0.524694	-6.19
246276_at	Cu2+-transporting ATPase-like protein	HMA1	AT4G37270	-1.08	-0.12	-1.13	0.296415	0.524694	-6.19
264025_at	AUX1-like amino acid permease ; supp	---	AT2G21050	1.36	0.45	1.13	0.296521	0.524762	-6.19
251554_at	putative protein predicted protein, Arabi	---	AT3G58670	1.11	0.15	1.13	0.296556	0.524783	-6.19
255349_at	hypothetical protein	---	AT4G03830	-1.07	-0.10	-1.13	0.296642	0.524893	-6.19
253314_at	hypothetical protein	---	AT4G33890	-1.08	-0.11	-1.13	0.296701	0.524917	-6.19
253368_at	myosin - like protein unconventional my	XI-I	AT4G33200	-1.09	-0.13	-1.13	0.296682	0.524917	-6.19
267610_at	K+ transporter, AKT1 identical to GB:U	AKT1	AT2G26650	-1.27	-0.35	-1.13	0.296725	0.524919	-6.19
257497_at	hypothetical protein predicted by genem	---	AT1G51430	-1.15	-0.21	-1.13	0.296865	0.525126	-6.19
252741_at	putative protein predicted protein, Arabi	---	AT3G43280	-1.08	-0.12	-1.13	0.296961	0.525219	-6.19
257258_at	hypothetical protein contains Pfam profil	---	AT3G22040	-1.14	-0.19	-1.13	0.296964	0.525219	-6.19
261586_at	hypothetical protein predicted by genen	---	AT1G01640	-1.22	-0.29	-1.13	0.297119	0.525452	-6.19
249324_at	cytochrome c1 precursor ; supported by	---	AT5G40810	-1.08	-0.11	-1.13	0.29726	0.525620	-6.19
254920_at	putative protein 24 kDa seed maturation	BTI2	AT4G11220	-1.11	-0.15	-1.13	0.297256	0.525620	-6.19
260344_at	polyneuridine aldehyde esterase, putati	MES15	AT1G69240	1.10	0.14	1.13	0.297289	0.525631	-6.19
258632_s_a	putative MAP3K epsilon protein kinase	MAPKKK7	AT3G07980 /	-1.13	-0.18	-1.13	0.297429	0.525798	-6.19
254986_at	putative protein SF16 protein -Helianthu	IQD16	AT4G10640	1.07	0.10	1.13	0.297412	0.525798	-6.19
256580_s_a	hypothetical protein	---	AT3G28810 /	1.08	0.11	1.13	0.297481	0.525848	-6.19
247363_at	unknown protein	---	AT5G63200	-1.10	-0.13	-1.13	0.297568	0.525960	-6.19
257909_at	Expressed protein ; supported by full-ler	---	AT3G25480	-1.12	-0.17	-1.13	0.297631	0.526032	-6.19
253072_at	putative protein ;supported by full-lengt	---	AT4G37830	1.08	0.11	1.13	0.297764	0.526063	-6.19
266569_at	unknown protein	---	AT2G24080	1.08	0.12	1.13	0.297737	0.526063	-6.19
266248_at	hypothetical protein predicted by gensca	---	AT2G27650	1.07	0.10	1.13	0.297748	0.526063	-6.19
260307_at	unknown protein similar to unknown pro	---	AT1G70620	-1.07	-0.10	-1.13	0.2977	0.526063	-6.19
266564_at	putative serine carboxypeptidase II	scpl22	AT2G24000	1.13	0.17	1.13	0.297701	0.526063	-6.19
260954_at	glyoxalase II isozyme, putative similar t	GLX2-4	AT1G06130	-1.11	-0.15	-1.13	0.297927	0.526269	-6.19
248989_at	disease resistance protein RPS4	---	AT5G45200	-1.11	-0.15	-1.13	0.297925	0.526269	-6.19

265540_at	Mutator-like transposase similar to MUF	---	---	1.08	0.11	1.13	0.297985	0.526291	-6.19
264426_at	hypothetical protein similar to hypothetic	---	AT1G61760	-1.11	-0.15	-1.13	0.297963	0.526291	-6.19
264333_at	hypothetical protein similar to putative T	AtTLP4	AT1G61940	1.08	0.12	1.13	0.298042	0.526350	-6.19
259384_at	putative lectin contains Pfam profile: PF	---	AT3G16450	1.12	0.16	1.13	0.29809	0.526393	-6.19
260057_at	putative protein phosphatase 2C similar	---	AT1G78200	1.08	0.12	1.13	0.298165	0.526404	-6.19
256705_at	cytochrome P450, putative similar to GI	CYP702A8	AT3G30290	-1.11	-0.15	-1.13	0.298165	0.526404	-6.19
252696_at	hypothetical protein predicted transpos	---	---	1.08	0.10	1.13	0.298143	0.526404	-6.19
249833_at	putative protein contains similarity to unl	---	AT5G23430	1.12	0.16	1.13	0.298205	0.526435	-6.19
247267_at	40S ribosomal protein S28 (sp|P34789)	RPS28	AT5G64140	-1.21	-0.28	-1.13	0.298404	0.526704	-6.19
259142_at	unknown protein similar to ankyrin like p	---	AT3G10200	1.10	0.14	1.13	0.298398	0.526704	-6.19
261064_at	unknown protein	ftsh10	AT1G07510	-1.12	-0.16	-1.13	0.298441	0.526729	-6.19
262080_at	unknown protein ; supported by cDNA: g	CW14	AT1G59650	1.13	0.17	1.13	0.298585	0.526901	-6.19
267195_at	putative protein kinase contains a protei	---	AT2G30940	1.13	0.18	1.13	0.298564	0.526901	-6.19
251411_at	regulatory subunit of protein kinase CK2	CKB3	AT3G60250	-1.10	-0.14	-1.13	0.298684	0.527035	-6.19
253211_at	amidase - like protein amidase, Bacillus	---	AT4G34880	1.08	0.12	1.13	0.29872	0.527057	-6.19
249576_at	putative protein predicted protein, Arabi	---	AT5G37690	-1.08	-0.11	-1.13	0.298755	0.527079	-6.19
246774_at	polygalacturonase-like protein polygala	---	AT5G27530	1.09	0.13	1.13	0.298822	0.527132	-6.19
251040_at	ribonuclease II-like protein ribonuclease	EMB2730	AT5G02250	-1.16	-0.21	-1.13	0.298831	0.527132	-6.19
264833_at	putative protein phosphatase similar to (	---	AT1G03590	1.16	0.21	1.13	0.298917	0.527243	-6.19
264726_at	Expressed protein ; supported by full-ler	---	AT1G22985	1.12	0.17	1.13	0.299097	0.527489	-6.19
264240_at	protein kinase, putative Simisimilar to p	---	AT1G54820	-1.44	-0.53	-1.13	0.299103	0.527489	-6.19
266394_at	Ras-related GTP-binding protein (ARA-4	ARA4	AT2G43130	-1.10	-0.13	-1.12	0.299144	0.527520	-6.20
262783_at	receptor-kinase isolog	---	AT1G10850	-1.21	-0.27	-1.12	0.29941	0.527948	-6.20
246281_at	hypothetical protein	NAPRT1	AT4G36940	-1.15	-0.20	-1.12	0.299507	0.528078	-6.20
248569_at	receptor protein kinase-like	---	AT5G49770	-1.11	-0.15	-1.12	0.299654	0.528297	-6.20
267287_at	putative pectinesterase	sks16	AT2G23630	1.08	0.11	1.12	0.299755	0.528399	-6.20
253899_at	putative protein protein disulfide-isomer	ATPDIL5-4	AT4G27080	1.10	0.14	1.12	0.299793	0.528399	-6.20
253110_at	hypothetical protein	---	AT4G35930	1.14	0.19	1.12	0.299805	0.528399	-6.20
258481_at	putative phosphatidate phosphohydrolas	LPP3	AT3G02600	-1.13	-0.17	-1.12	0.299798	0.528399	-6.20
264853_at	putative ligand-gated ion channel protei	GLR2	AT2G17260 /	-1.11	-0.15	-1.12	0.299832	0.528401	-6.20
264074_at	putative retroelement pol polyprotein rel	---	---	-1.09	-0.13	-1.12	0.299852	0.528401	-6.20
257353_at	hypothetical protein predicted by gensca	NPY4	AT2G23050	1.09	0.13	1.12	0.299978	0.528582	-6.20
250478_at	non-phototropic hypocotyl 3-like protein	DOT3	AT5G10250	-1.12	-0.16	-1.12	0.300026	0.528586	-6.20
259925_at	thaumatin-like protein similar to thaumat	PR5	AT1G75040	2.71	1.44	1.12	0.300005	0.528586	-6.20
265766_at	unknown protein	---	AT2G48080	1.13	0.17	1.12	0.300121	0.528615	-6.20

260637_at	ACC oxidase, putative similar to ACC o	ACO2	AT1G62380	1.31	0.39	1.12	0.30007	0.528615	-6.20
249445_at	putative protein predicted protein, Arabi	---	AT5G39380	-1.11	-0.15	-1.12	0.300108	0.528615	-6.20
265191_at	hypothetical protein Similar to Saccharo	---	AT1G05120	-1.09	-0.13	-1.12	0.300136	0.528615	-6.20
264891_at	putative pectinesterase similar to GB:A	---	AT1G23200	-1.15	-0.21	-1.12	0.300254	0.528783	-6.20
246861_at	putative protein phytochrome-associate	IAA28	AT5G25890	1.10	0.13	1.12	0.300303	0.528793	-6.20
247532_at	putative protein disease resistance prot	---	AT5G61560	1.30	0.38	1.12	0.300329	0.528793	-6.20
258129_at	hypothetical protein predicted by genem	ROPGEF8	AT3G24620	-1.10	-0.13	-1.12	0.300324	0.528793	-6.20
261568_at	DNA-binding protein, putative similar to	NGA3	AT1G01030	1.10	0.13	1.12	0.300413	0.528900	-6.20
253968_at	putative calcineurin B-like protein calcir	CBL7	AT4G26560	1.09	0.12	1.12	0.300597	0.529183	-6.20
263130_at	hypothetical protein predicted by gensca	POLD3	AT1G78650	-1.18	-0.24	-1.12	0.300663	0.529257	-6.20
261020_at	hypothetical protein similar to reticuline	---	AT1G26390	1.28	0.36	1.12	0.300769	0.529281	-6.20
248108_at	molybdopterin synthase sulphurylase (g	CNX5	AT5G55130	1.10	0.14	1.12	0.300756	0.529281	-6.20
262182_at	hypothetical protein predicted by genem	---	AT1G77890	1.09	0.12	1.12	0.300708	0.529281	-6.20
252801_at	putative protein various predicted Helic	---	---	1.08	0.12	1.12	0.300732	0.529281	-6.20
258279_at	putative self-incompatibility protein simi	---	AT3G26870	-1.07	-0.10	-1.12	0.300947	0.529553	-6.20
259668_at	hypothetical protein predicted by genem	---	AT1G52390	1.09	0.12	1.12	0.301002	0.529609	-6.20
251393_at	putative protein symbiosis-related prote	ATG8G	AT3G60640	-1.14	-0.19	-1.12	0.30106	0.529670	-6.20
259102_at	unknown protein similar to hin1 GB:CAA	NHL1	AT3G11660	-1.11	-0.16	-1.12	0.301102	0.529704	-6.20
253171_at	putative protein ;supported by full-lengt	---	AT4G35040	-1.11	-0.15	-1.12	0.30113	0.529711	-6.20
247243_at	nodulin-like protein	---	AT5G64700	1.16	0.21	1.12	0.301197	0.529788	-6.20
252254_at	hypothetical protein ; supported by cDN	DMS3	AT3G49250	-1.08	-0.11	-1.12	0.301292	0.529890	-6.20
253026_at	hypothetical protein	---	AT4G38120	1.14	0.18	1.12	0.301301	0.529890	-6.20
264796_at	unknown protein similar to ESTs gb|T20	ZIGA4	AT1G08680	-1.09	-0.13	-1.12	0.301419	0.530033	-6.20
251894_at	putative protein predicted proteins, Ara	---	AT3G54380	1.11	0.15	1.12	0.301429	0.530033	-6.20
262971_at	receptor-like protein kinase, putative re	---	AT1G75640	1.13	0.18	1.12	0.3015	0.530118	-6.20
266868_at	hypothetical protein predicted by gensca	---	AT2G44630	-1.09	-0.12	-1.12	0.301616	0.530235	-6.20
253201_at	putative ribosomal protein S16 ribosom	SSR16	AT4G34620	-1.09	-0.13	-1.12	0.30159	0.530235	-6.20
264732_at	serpin, putative similar to serpin GI:119	---	AT1G62160	1.08	0.10	1.12	0.301636	0.530235	-6.20
267564_at	putative protein kinase contains a protei	---	AT2G30740	1.11	0.14	1.12	0.301763	0.530416	-6.20
252655_at	hypothetical protein with predicted heme	---	AT3G44760	1.08	0.11	1.12	0.301786	0.530416	-6.20
248468_at	UDP-glucose:protein transglucosylase;	RGP4	AT5G50750	1.11	0.15	1.12	0.301904	0.530513	-6.20
253073_at	cytochrome P450 monooxygenase - lik	CYP81F4	AT4G37410	1.11	0.15	1.12	0.301937	0.530513	-6.20
252035_at	beta-ketoacyl-CoA synthase like protein	KCS15	AT3G52160	1.11	0.15	1.12	0.301953	0.530513	-6.20
267485_at	putative MYB family transcription factor	MYB88	AT2G02820	-1.12	-0.16	-1.12	0.301942	0.530513	-6.20
267105_at	hypothetical protein predicted by gensca	---	AT2G14760	1.12	0.17	1.12	0.301958	0.530513	-6.20

249033_at	putative protein contains similarity to dis	---	AT5G44920	1.10	0.13	1.12	0.302016	0.530563	-6.20
248993_at	putative protein contains similarity to dis	---	AT5G45240	1.09	0.13	1.12	0.302032	0.530563	-6.20
264552_at	hypothetical protein predicted by gensca	---	AT1G09470	-1.15	-0.20	-1.12	0.30212	0.530675	-6.20
266628_at	unknown protein	---	AT2G35330	1.08	0.11	1.12	0.302152	0.530691	-6.20
252014_at	putative protein predicted proteins, Aral	---	AT3G52870	1.31	0.39	1.12	0.302198	0.530731	-6.20
247268_at	putative protein contains similarity to no	---	AT5G64080	1.12	0.17	1.12	0.302231	0.530749	-6.20
256434_at	putative 60S ribosomal protein L37a sim	---	AT3G10950	-1.08	-0.11	-1.12	0.302353	0.530921	-6.20
262174_at	putative GDP-mannose pyrophosphoryl	---	AT1G74910	1.13	0.17	1.12	0.302395	0.530955	-6.20
251073_at	putative protein hypothetical proteins - A	---	AT5G01750	-1.07	-0.10	-1.12	0.302606	0.531283	-6.20
258836_at	hypothetical protein predicted using gen	---	AT3G07210	-1.14	-0.18	-1.12	0.302691	0.531351	-6.20
257387_s_a	putative receptor-like protein kinase	---	AT2G14440 /	-1.11	-0.15	-1.12	0.302684	0.531351	-6.20
254495_at	hypothetical protein	EMB1895	AT4G20060	-1.15	-0.20	-1.12	0.302737	0.531391	-6.20
255532_at	hypothetical protein similar to orf at end	---	AT4G02170	1.13	0.18	1.12	0.302782	0.531401	-6.20
265982_at	putative retroelement pol polyprotein	---	---	1.08	0.11	1.12	0.302789	0.531401	-6.20
252352_at	Expressed protein ; supported by full-ler	---	AT3G48185	-1.12	-0.17	-1.12	0.302863	0.531449	-6.21
259467_at	hypothetical protein predicted by genem	---	AT1G19060	1.07	0.10	1.12	0.302858	0.531449	-6.21
250229_at	putative protein contains similarity to na	NACA3	AT5G13850	-1.16	-0.22	-1.12	0.302989	0.531547	-6.21
252788_at	putative protein several hypothetical pro	---	---	1.09	0.12	1.12	0.302977	0.531547	-6.21
255606_at	hypothetical protein similar to T3F17.5,	---	AT4G01110	-1.13	-0.17	-1.12	0.302957	0.531547	-6.21
262513_at	unknown protein ; supported by cDNA: g	---	AT1G34270	-1.10	-0.13	-1.12	0.303046	0.531607	-6.21
257933_at	aminoalcoholphosphotransferase, putat	AAPT2	AT3G25585	-1.16	-0.22	-1.11	0.303098	0.531607	-6.21
264344_at	putative aspartic proteinase similar to G	---	AT1G11910	1.07	0.10	1.11	0.303186	0.531607	-6.21
258311_at	transport inhibitor response 1 (TIR1), pu	AFB2	AT3G26810	1.10	0.13	1.11	0.30314	0.531607	-6.21
265079_at	hypothetical protein contains similarity to	---	AT1G55460	-1.08	-0.11	-1.11	0.303184	0.531607	-6.21
254024_at	putative pathogenesis-related protein g	---	AT4G25780	-1.16	-0.21	-1.11	0.303112	0.531607	-6.21
254468_at	UDP-glucose 4-epimerase - like protein	---	AT4G20460	1.09	0.13	1.11	0.303123	0.531607	-6.21
253878_at	trehalose-6-phosphate synthase - like p	TPS4	AT4G27550	1.08	0.11	1.11	0.303334	0.531825	-6.21
255561_at	putative hexose transporter similar to pla	---	AT4G02050	1.15	0.20	1.11	0.303409	0.531875	-6.21
260053_at	hypothetical protein similar to unknown	---	AT1G78120	-1.12	-0.16	-1.11	0.303407	0.531875	-6.21
264623_at	putative NPK1-related protein kinase 2 S	ANP1	AT1G09000	1.08	0.11	1.11	0.303501	0.531939	-6.21
245995_at	putative protein various predicted prote	---	---	1.13	0.18	1.11	0.303539	0.531939	-6.21
263399_at	unknown protein ; supported by full-leng	---	AT2G31490	-1.09	-0.13	-1.11	0.303525	0.531939	-6.21
259315_at	unknown protein	AtRP2	AT3G01200	-1.08	-0.11	-1.11	0.303531	0.531939	-6.21
247292_at	unknown protein	---	AT5G64490	-1.10	-0.14	-1.11	0.303772	0.532307	-6.21
260242_at	putative transcription factor similar to bH	EGL3	AT1G63650	1.09	0.13	1.11	0.303883	0.532461	-6.21

262567_at	hypothetical protein contains similarity to	---	AT1G34300	1.15	0.21	1.11	0.304067	0.532564	-6.21
246772_at	putative protein unknown protein T12H1	---	AT5G27490	-1.19	-0.25	-1.11	0.30404	0.532564	-6.21
266448_s_a	unknown protein ;supported by full-leng	---	AT2G43210	-1.09	-0.12	-1.11	0.304098	0.532564	-6.21
255142_at	stromal ascorbate peroxidase ; support	SAPX	AT4G08390	1.41	0.49	1.11	0.304082	0.532564	-6.21
266067_s_a	hypothetical protein predicted by gensca	---	AT2G18810 /	-1.07	-0.10	-1.11	0.304106	0.532564	-6.21
258028_at	hypothetical protein	---	AT3G27473	1.07	0.09	1.11	0.304027	0.532564	-6.21
254372_at	putative protein predicted proteins, Arat	---	AT4G21620	1.19	0.25	1.11	0.304096	0.532564	-6.21
245552_at	cytochrome P450 like protein	CYP705A3	AT4G15360	1.09	0.12	1.11	0.304147	0.532595	-6.21
265176_at	OBP32pep protein, putative identical to	---	AT1G23520	1.09	0.12	1.11	0.304248	0.532731	-6.21
265124_at	hypothetical protein similar to putative C	---	AT1G55430	-1.11	-0.15	-1.11	0.304411	0.532977	-6.21
258357_at	putative leucine-rich repeat transmembr	SRF7	AT3G14350	1.17	0.23	1.11	0.304532	0.533017	-6.21
253186_at	putative protein predicted proteins, Arat	---	AT4G35270	-1.14	-0.18	-1.11	0.304507	0.533017	-6.21
257532_at	hypothetical protein similar to hypothetic	---	AT3G04700	1.39	0.48	1.11	0.304574	0.533017	-6.21
262924_s_a	vacuolar ATP synthase, putative similar	AVA-P4	AT1G19910 /	-1.11	-0.15	-1.11	0.304539	0.533017	-6.21
245226_at	gene_id:K17E7.15~unknown protein	---	AT3G29970	1.51	0.60	1.11	0.304566	0.533017	-6.21
257208_at	hypothetical protein predicted by gensca	---	AT3G14910	-1.14	-0.18	-1.11	0.304525	0.533017	-6.21
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J0442	---	---	1.17	0.22	1.11	0.304673	0.533149	-6.21
257552_at	cellulase, putative contains Pfam profile	---	AT3G26130	1.08	0.11	1.11	0.304721	0.533191	-6.21
260659_s_a	hypothetical protein predicted by genem	---	AT1G19460 /	-1.07	-0.10	-1.11	0.304783	0.533259	-6.21
251581_at	putative protein CARBON CATABOLIT	---	AT3G58560	-1.11	-0.15	-1.11	0.304845	0.533326	-6.21
260175_at	neutral invertase, putative similar to neu	---	AT1G72000	-1.08	-0.11	-1.11	0.304901	0.533383	-6.21
253905_s_a	putative protein retrotransposon Opie-2	---	---	-1.07	-0.10	-1.11	0.304962	0.533403	-6.21
249480_s_a	protein kinase - like protein receptor-like	---	AT5G38990 /	1.24	0.31	1.11	0.304982	0.533403	-6.21
254838_at	hypothetical protein	---	AT4G12380	-1.12	-0.17	-1.11	0.304941	0.533403	-6.21
249753_at	putative protein similar to unknown prote	---	AT5G24610	1.07	0.10	1.11	0.305158	0.533629	-6.21
263563_at	putative retroelement pol polyprotein	---	---	1.09	0.13	1.11	0.305139	0.533629	-6.21
250207_at	chalcone synthase (naringenin-chalcone	TT4	AT5G13930	-1.30	-0.38	-1.11	0.305344	0.533912	-6.21
251709_at	response regulator-like protein respons	ARR17	AT3G56380	-1.07	-0.10	-1.11	0.305404	0.533978	-6.21
248787_at	putative protein similar to unknown prote	---	AT5G47420	1.14	0.19	1.11	0.305451	0.534002	-6.21
260478_at	DnaJ isolog	---	AT1G11040	1.08	0.12	1.11	0.305465	0.534002	-6.21
246614_at	serine/threonine protein kinase SOS2 (g	SOS2	AT5G35410	-1.09	-0.12	-1.11	0.305684	0.534058	-6.21
260823_at	hypothetical protein predicted by genen	DRIP1	AT1G06770	-1.09	-0.12	-1.11	0.305602	0.534058	-6.21
254616_at	shaggy-like protein kinase etha (EC 2.7.	BIN2	AT4G18710	-1.09	-0.12	-1.11	0.305672	0.534058	-6.21
267030_at	unknown protein	SCAR2	AT2G38440	-1.08	-0.12	-1.11	0.305643	0.534058	-6.21
262141_s_a	hypothetical protein predicted by genem	---	AT1G52440 /	-1.07	-0.10	-1.11	0.305668	0.534058	-6.21

265743_s_a	En/Spm-like transposon protein related	---	---	1.08	0.11	1.11	0.305551	0.534058	-6.21
251674_at	hypothetical protein	---	AT3G57250	1.09	0.13	1.11	0.30568	0.534058	-6.21
245566_at	disease resistance RPS2 like protein	---	AT4G14610	1.10	0.13	1.11	0.305612	0.534058	-6.21
255946_at	glycine hydroxymethyltransferase, puta	SHM6	AT1G22020	1.07	0.10	1.11	0.305745	0.534072	-6.21
248627_at	putative protein similar to unknown prote	---	AT5G48950	1.12	0.17	1.11	0.305763	0.534072	-6.21
254507_at	Glu-rich protein mature-parasite-infecte	---	AT4G20160	-1.08	-0.11	-1.11	0.305752	0.534072	-6.21
247897_at	unknown protein ;supported by full-leng	TET15	AT5G57810	1.09	0.12	1.11	0.305952	0.534362	-6.21
257784_at	geranylgeranylated protein, putative sin	MUB4	AT3G26980	1.31	0.39	1.11	0.306029	0.534415	-6.21
259740_at	phytochrome, putative similar to GI:296	---	AT1G64300	-1.14	-0.19	-1.11	0.306019	0.534415	-6.21
248000_at	WD-repeat protein-like ;supported by fu	---	AT5G56190	1.10	0.14	1.11	0.306084	0.534469	-6.21
256927_at	unknown protein	---	AT3G22550	-1.08	-0.12	-1.11	0.306109	0.534472	-6.21
256162_at	hypothetical protein similar to hypothetic	---	AT1G55390	1.08	0.11	1.11	0.306133	0.534473	-6.21
255761_at	hypothetical protein predicted by gensca	---	AT1G16770	1.09	0.13	1.11	0.306162	0.534483	-6.21
264916_at	ATP citrate-lyase, putative similar to AT	ACLA-2	AT1G60810	-1.13	-0.18	-1.11	0.306187	0.534485	-6.21
260578_at	unknown protein predicted by genscan	---	AT2G47350	-1.09	-0.12	-1.11	0.30628	0.534607	-6.21
251104_at	F-box protein family, AtFBL3 contains s	---	AT5G01720	1.12	0.17	1.11	0.306343	0.534676	-6.21
254268_at	putative protein FAF1, Mus musculus, F	---	AT4G23040	1.11	0.15	1.11	0.306386	0.534711	-6.21
247702_at	putative protein ;supported by full-lengt	---	AT5G59500	-1.10	-0.14	-1.11	0.306487	0.534845	-6.21
260838_at	hypothetical protein predicted by genem	---	AT1G43680	1.08	0.11	1.11	0.306552	0.534917	-6.21
256652_at	hypothetical protein similar to putative a	LPAT5	AT3G18850	1.25	0.32	1.11	0.306606	0.534971	-6.22
264187_at	unknown protein ;supported by full-lengt	---	AT1G54860	1.07	0.10	1.11	0.306652	0.534971	-6.22
257796_at	hypothetical protein predicted by genem	---	AT3G15930	-1.10	-0.14	-1.11	0.306637	0.534971	-6.22
254601_at	putative protein DNA (cytosine-5-)-meth	CMT2	AT4G19020	-1.14	-0.19	-1.11	0.306736	0.535035	-6.22
257681_at	hypothetical protein predicted by genem	---	AT3G13370	-1.07	-0.10	-1.11	0.306724	0.535035	-6.22
256427_at	hypothetical protein predicted by gensca	LBD21	AT3G11090	-1.19	-0.25	-1.11	0.306817	0.535135	-6.22
259153_at	unknown protein ;supported by full-leng	---	AT3G10250	-1.11	-0.15	-1.11	0.306874	0.535194	-6.22
248294_at	RNA-binding protein-like	---	AT5G53060	-1.10	-0.14	-1.11	0.306942	0.535271	-6.22
252647_at	protein-tyrosine-phosphatase-like prote	---	AT3G44620	-1.15	-0.21	-1.11	0.307013	0.535312	-6.22
263607_at	unknown protein predicted by genscan a	---	AT2G16270	1.13	0.17	1.11	0.307011	0.535312	-6.22
246506_at	putative protein hypothetical protein T2	---	AT5G16110	1.12	0.16	1.11	0.307053	0.535341	-6.22
247657_at	Expressed protein ; supported by full-ler	---	AT5G59845	1.11	0.15	1.11	0.307084	0.535355	-6.22
258938_at	germin-like protein similar to germin type	---	AT3G10080	1.48	0.57	1.10	0.307151	0.535431	-6.22
264266_at	putative protein phosphatase 2C similar	---	AT1G09160	-1.13	-0.18	-1.10	0.307294	0.535639	-6.22
267489_s_a	putative DNA2-NAM7 helicase family pr	---	AT2G19120 /	-1.14	-0.19	-1.10	0.307507	0.535869	-6.22
260952_at	hypothetical protein predicted by genem	---	AT1G06140	-1.13	-0.18	-1.10	0.307537	0.535869	-6.22

247273_at	unknown protein	CPuORF4	AT5G64340 /	-1.15	-0.21	-1.10	0.307494	0.535869	-6.22
261320_at	unknown protein ; supported by cDNA: g	---	AT1G53120	-1.08	-0.11	-1.10	0.307543	0.535869	-6.22
261288_at	hypothetical protein predicted by genem	---	AT1G37010	-1.10	-0.13	-1.10	0.307475	0.535869	-6.22
266859_at	putative MADS-box protein	AGL41	AT2G26880	1.11	0.15	1.10	0.307599	0.535885	-6.22
265443_at	beta-expansin ;supported by full-length	ATEXPB1	AT2G20750	1.13	0.17	1.10	0.307586	0.535885	-6.22
249681_s_a	putative protein strong similarity to unkn	---	---	1.12	0.17	1.10	0.307634	0.535905	-6.22
251494_at	protein kinase-like protein Pto kinase in	---	AT3G59350	1.23	0.30	1.10	0.307659	0.535907	-6.22
246971_at	Protein phosphatase 2C-like protein pro	---	AT5G24940	1.08	0.12	1.10	0.307709	0.535953	-6.22
258201_at	hypothetical protein predicted by gensca	---	AT3G13910	1.19	0.25	1.10	0.307872	0.536165	-6.22
254865_s_a	putative protein, fragment other predicte	---	AT4G05350 /	1.08	0.11	1.10	0.307912	0.536165	-6.22
248752_at	unknown protein	---	AT5G47600	1.08	0.12	1.10	0.307879	0.536165	-6.22
247671_at	putative protein slow myosin heavy cha	---	AT5G60210	-1.07	-0.10	-1.10	0.307933	0.536165	-6.22
246254_at	MAP kinase like protein	ATMPK14	AT4G36450	1.17	0.22	1.10	0.307948	0.536165	-6.22
256358_at	unknown protein	---	AT1G66470	-1.11	-0.15	-1.10	0.30804	0.536283	-6.22
259610_at	bZIP protein, putative similar to GI:6008	---	AT1G52320	-1.08	-0.11	-1.10	0.308094	0.536337	-6.22
261791_at	unknown protein ; supported by full-leng	---	AT1G16170	-1.23	-0.30	-1.10	0.308256	0.536578	-6.22
255506_at	predicted glycosyl transferase similar to	GATL6	AT4G02130	-1.20	-0.26	-1.10	0.308317	0.536644	-6.22
263832_at	putative polygalacturonase	---	AT2G40310	1.07	0.10	1.10	0.308403	0.536752	-6.22
253416_at	pyruvate decarboxylase-1 (Pdc1)	---	AT4G33070	1.13	0.17	1.10	0.308433	0.536763	-6.22
261355_at	putative malate oxidoreductase similar t	ATNADP-M	AT1G79750	1.11	0.15	1.10	0.308487	0.536816	-6.22
260367_at	unknown protein ;supported by full-leng	---	AT1G69760	-1.28	-0.36	-1.10	0.308528	0.536848	-6.22
256839_at	calmodulin, putative similar to calmodul	---	AT3G22930	1.11	0.15	1.10	0.308625	0.536853	-6.22
252519_at	hypothetical protein	---	AT3G46360	-1.09	-0.13	-1.10	0.308598	0.536853	-6.22
264525_at	unknown protein Highly Similar to branc	ATBCAT-1	AT1G10060	-1.39	-0.48	-1.10	0.308607	0.536853	-6.22
249696_at	copia-like retrotransposable element	---	---	-1.08	-0.11	-1.10	0.308618	0.536853	-6.22
253496_at	glutathione peroxidase - like protein glu	ATGPX7	AT4G31870	1.31	0.39	1.10	0.308775	0.536924	-6.22
255221_at	putative protein various predicted protei	---	AT4G05150	-1.10	-0.14	-1.10	0.308784	0.536924	-6.22
251226_at	proline-rich protein proline-rich protein p	PRP3	AT3G62680	1.10	0.13	1.10	0.308759	0.536924	-6.22
264603_at	hypothetical protein predicted by gensca	---	AT1G04670	1.07	0.10	1.10	0.308783	0.536924	-6.22
248206_at	unknown protein	---	AT5G54350	1.11	0.15	1.10	0.308764	0.536924	-6.22
248746_at	NADH dehydrogenase 10.5K chain-like	---	AT5G47890	-1.16	-0.21	-1.10	0.308822	0.536946	-6.22
257682_at	hypothetical protein predicted by genem	---	AT3G13240	-1.07	-0.10	-1.10	0.308844	0.536946	-6.22
259888_at	hypothetical protein similar to nodule inc	---	AT1G76350	-1.26	-0.33	-1.10	0.308885	0.536976	-6.22
250000_at	putative protein PGPD14 - Petunia x hy	---	AT5G18650	-1.13	-0.17	-1.10	0.308926	0.537006	-6.22
255441_at	putative cullin-like 1 protein similar to O.	ATCUL1	AT4G02570	1.09	0.12	1.10	0.308998	0.537050	-6.22

261571_at	hypothetical protein predicted by genem	---	AT1G01150	1.08	0.12	1.10	0.308993	0.537050	-6.22
255593_at	hypothetical protein	---	AT4G01650	-1.09	-0.13	-1.10	0.309036	0.537076	-6.22
262314_at	unknown protein contains similarity to zi	---	AT1G70810	1.11	0.15	1.10	0.309071	0.537095	-6.22
250001_at	tub family-like protein tubby-like protein	AtTLP11	AT5G18680	-1.15	-0.20	-1.10	0.309125	0.537148	-6.22
251222_at	putative membrane protein clone:2-72.	---	AT3G62580	-1.16	-0.22	-1.10	0.309253	0.537272	-6.22
266455_at	putative bHLH transcription factor	---	AT2G22760	1.23	0.30	1.10	0.309256	0.537272	-6.22
263642_at	putative fimbrin	---	AT2G04750	-1.08	-0.12	-1.10	0.309267	0.537272	-6.22
249613_at	putative protein mDj10, Mus musculus,	---	AT5G37380	-1.12	-0.16	-1.10	0.309364	0.537399	-6.22
252157_at	hypothetical protein	---	AT3G50430	-1.09	-0.12	-1.10	0.309528	0.537643	-6.22
263825_at	putative laccase (diphenol oxidase)	LAC5	AT2G40370	1.22	0.29	1.10	0.309573	0.537680	-6.22
263664_at	putative auxin-induced protein, IAA17/A	AXR3	AT1G04250	-1.27	-0.34	-1.10	0.309648	0.537720	-6.22
256435_at	putative leucoanthocyanidin dioxygenas	---	AT3G11180	1.10	0.13	1.10	0.30969	0.537720	-6.22
266665_at	unknown protein	---	AT2G29790	1.10	0.14	1.10	0.309641	0.537720	-6.22
255569_at	putative CAAX prenyl protease ; suppo	ATSTE24	AT4G01320	-1.08	-0.11	-1.10	0.309672	0.537720	-6.22
246012_at	Pspzf zinc finger protein - like DNA bin	---	AT5G10650	-1.14	-0.19	-1.10	0.309792	0.537857	-6.22
253641_at	hypothetical protein ;supported by full-le	---	AT4G29980	1.11	0.15	1.10	0.309858	0.537893	-6.22
249548_at	lipid transfer - like protein lipid transfer	---	AT5G38170	-1.09	-0.12	-1.10	0.30986	0.537893	-6.22
260798_at	unknown protein contains similarity to a	---	AT1G78280	1.15	0.20	1.10	0.309885	0.537896	-6.22
260048_at	unknown protein contains Pfam profile:	---	AT1G73750	1.36	0.45	1.10	0.309929	0.537931	-6.22
255345_at	putative aspartic protease ; supported b	---	AT4G04460	1.37	0.46	1.10	0.310012	0.538033	-6.22
245423_at	putative protein	---	AT4G17483	1.11	0.15	1.10	0.310082	0.538113	-6.22
247651_at	histone H2A - like protein histone H2A,	HTA6	AT5G59870	-1.43	-0.51	-1.10	0.310261	0.538384	-6.22
257140_at	MYB family transcription factor (hsr1), p	MYB30	AT3G28910	1.21	0.28	1.10	0.3103	0.538410	-6.22
258535_at	unknown protein ; supported by cDNA:	---	AT3G06750	-1.18	-0.24	-1.10	0.310364	0.538429	-6.22
250744_at	putative protein strong similarity to unkn	---	AT5G05840	1.11	0.15	1.10	0.310375	0.538429	-6.22
248209_at	flavonol 3-O-glucosyltransferase-like pro	---	AT5G53990	1.13	0.17	1.10	0.310382	0.538429	-6.22
253755_at	26S proteasome subunit 4-like protein	RPT2a	AT4G29040	-1.09	-0.13	-1.10	0.310494	0.538510	-6.23
264294_at	hypothetical protein similar to heat shoc	---	AT1G78750	-1.09	-0.13	-1.10	0.31051	0.538510	-6.23
261031_at	hypothetical protein predicted by genem	---	AT1G17360	-1.19	-0.25	-1.10	0.310501	0.538510	-6.23
256213_at	protein kinase, putative contains Pfam	---	AT1G50990	1.10	0.14	1.10	0.310523	0.538510	-6.23
258464_at	kinesin-like protein similar to KLP2 prote	POK1	AT3G17360	1.07	0.10	1.10	0.310599	0.538602	-6.23
265060_at	HD-Zip protein, putative similar to HD-Z	ATHB-15	AT1G52150	-1.22	-0.29	-1.10	0.310628	0.538611	-6.23
261613_at	abscisic acid responsive elements-bindi	ABF1	AT1G49720	-1.15	-0.20	-1.10	0.310845	0.538946	-6.23
250952_at	putative protein	ATIREG2	AT5G03570	1.12	0.16	1.10	0.310895	0.538963	-6.23
262874_at	hypothetical protein predicted by genem	---	AT1G65020	-1.11	-0.16	-1.10	0.310902	0.538963	-6.23

251696_at	putative protein	---	---	1.11	0.15	1.10	0.310979	0.539051	-6.23
247832_at	putative protein predicted proteins, Aral	EOL2	AT5G58550	-1.10	-0.14	-1.10	0.311	0.539051	-6.23
266206_at	unknown protein ; supported by full-leng	---	AT2G27730	1.12	0.17	1.10	0.311099	0.539145	-6.23
248365_at	putative protein strong similarity to unkn	---	AT5G52500	1.09	0.13	1.10	0.311101	0.539145	-6.23
246987_at	myb-related protein, 33.3K (pir |S71284	MYBR1	AT5G67300	1.18	0.24	1.09	0.311279	0.539412	-6.23
264528_at	hypothetical protein similar to Human XE	---	AT1G30810	1.07	0.10	1.09	0.311412	0.539600	-6.23
246995_at	formin-like protein	---	AT5G67470	-1.16	-0.21	-1.09	0.31155	0.539800	-6.23
263033_s_a	unknown protein ; supported by full-leng	---	AT1G23950 /	-1.15	-0.20	-1.09	0.311618	0.539868	-6.23
260554_at	putative zinc protease member of insulin	---	AT2G41790	1.08	0.10	1.09	0.311637	0.539868	-6.23
258240_at	oleosin isoform identical to oleosin isofo	OLEO4	AT3G27660	1.10	0.14	1.09	0.31172	0.539888	-6.23
253528_s_a	putative protein bcop gene product - Dr	---	AT4G31480 /	-1.08	-0.11	-1.09	0.311692	0.539888	-6.23
245652_at	F-box protein family, putative	---	AT4G13960	1.10	0.14	1.09	0.311707	0.539888	-6.23
249854_at	putative protein contains similarity to ser	---	AT5G22960	-1.11	-0.15	-1.09	0.311829	0.540036	-6.23
262276_at	hypothetical protein predicted by genem	---	AT1G68700	1.09	0.13	1.09	0.311901	0.540120	-6.23
264256_at	putative importin alpha similar to GB:AA	IMPA-4	AT1G09270	1.08	0.11	1.09	0.312093	0.540411	-6.23
261608_at	unknown protein similar to putative este	---	AT1G49650	-1.10	-0.14	-1.09	0.312266	0.540647	-6.23
259655_at	unknown protein	---	AT1G55210	1.31	0.39	1.09	0.312276	0.540647	-6.23
253518_at	hypothetical protein	---	AT4G31400	-1.11	-0.15	-1.09	0.312435	0.540880	-6.23
251938_at	60S RIBOSOMAL PROTEIN L12 -like 6	---	AT3G53430	-1.12	-0.17	-1.09	0.312501	0.540954	-6.23
262331_at	unknown protein	---	AT1G64050	-1.07	-0.10	-1.09	0.312579	0.541047	-6.23
252192_at	CASEIN KINASE II, ALPHA CHAIN 2 (	CKA2	AT3G50000	1.08	0.11	1.09	0.31262	0.541077	-6.23
264041_at	MADS-box protein (AGL3) ; supported	טפס-04	AT2G03710	-1.20	-0.27	-1.09	0.312713	0.541198	-6.23
256376_s_a	unknown protein	PXMT1	AT1G66690 /	1.32	0.40	1.09	0.312774	0.541262	-6.23
252026_at	serine protein kinase - like serine protei	SRPK4	AT3G53030	-1.09	-0.13	-1.09	0.312901	0.541434	-6.23
245172_at	hypothetical protein predicted by gensca	---	AT2G47540	1.07	0.10	1.09	0.312921	0.541434	-6.23
245999_at	putative protein predicted protein, Arabi	COPT5	AT5G20650	-1.08	-0.11	-1.09	0.313071	0.541612	-6.23
256882_at	RNA-binding protein, putative similar to	---	AT3G26420 /	-1.12	-0.16	-1.09	0.313059	0.541612	-6.23
266433_at	unknown protein	---	AT2G07110	1.08	0.11	1.09	0.313221	0.541830	-6.23
264909_at	unknown protein	---	AT2G17300	-1.09	-0.13	-1.09	0.313259	0.541855	-6.23
258987_at	putative SCO1 protein similar to SCO1	---	AT3G08950	-1.19	-0.26	-1.09	0.313366	0.541957	-6.23
258004_at	unknown protein similar to putative trans	MYB110	AT3G29020	1.09	0.13	1.09	0.313346	0.541957	-6.23
264530_at	hypothetical protein	---	AT1G30780	1.11	0.15	1.09	0.313459	0.542077	-6.23
261666_at	hypothetical protein contains similarity to	---	AT1G18440	1.12	0.16	1.09	0.313556	0.542204	-6.23
255173_at	putative transposon protein similar to A	---	---	1.10	0.14	1.09	0.313615	0.542265	-6.23
249154_at	Nicotiana EREBP-3 like	---	AT5G43410	1.45	0.54	1.09	0.313694	0.542360	-6.23

262916_at	glutathione S-transferase, putative simi	ATGSTU1	AT1G59700	-1.16	-0.21	-1.09	0.313764	0.542440	-6.23
250254_at	24-sterol C-methyltransferase ; support	SMT1	AT5G13710	1.14	0.18	1.09	0.313792	0.542448	-6.23
258628_at	unknown protein	---	AT3G02890	-1.19	-0.25	-1.09	0.313864	0.542532	-6.23
250696_at	putative protein similar to unknown prote	---	AT5G06790	-1.07	-0.09	-1.09	0.313894	0.542542	-6.23
262337_at	hypothetical protein similar to hypothetic	---	AT1G64260	-1.11	-0.15	-1.09	0.313952	0.542602	-6.23
264017_s_a	putative ER lumen protein retaining rece	---	AT2G21190 /	1.08	0.12	1.09	0.313999	0.542641	-6.23
252580_at	putative protein putative proteins - Arabi	---	AT3G45490	1.08	0.11	1.09	0.314031	0.542655	-6.23
247360_at	cytochrome P450-like protein ;supporte	CYP94B1	AT5G63450	1.29	0.37	1.09	0.314137	0.542726	-6.23
260941_at	peroxidase, putative similar to peroxida	---	AT1G44970	1.14	0.19	1.09	0.314199	0.542726	-6.23
251250_at	putative protein pectin methylesterase -	---	AT3G62180	1.12	0.16	1.09	0.314178	0.542726	-6.23
254477_at	zinc-finger protein Lsd1 ;supported by f	---	AT4G20380	1.12	0.16	1.09	0.314106	0.542726	-6.23
249175_at	COP8 (constitutive photomorphogenic) I	COP8	AT5G42970	-1.08	-0.11	-1.09	0.314144	0.542726	-6.23
257898_s_a	hypothetical protein predicted by gensca	---	---	-1.07	-0.10	-1.09	0.314215	0.542726	-6.23
249058_at	disease resistance protein-like	TAO1	AT5G44510	1.10	0.14	1.09	0.314338	0.542898	-6.24
248221_at	vacuolar sorting protein-like; embryoger	VPS26A	AT5G53530	-1.07	-0.10	-1.09	0.31441	0.542980	-6.24
264335_s_a	hypothetical protein contains similarity t	UPL1	AT1G55860 /	-1.07	-0.10	-1.09	0.314517	0.543125	-6.24
248366_at	SCARECROW transcriptional regulator-	---	AT5G52510	-1.11	-0.15	-1.09	0.314802	0.543461	-6.24
258959_at	putative amino acid transporter similar t	CAT7	AT3G10600	1.09	0.12	1.09	0.314807	0.543461	-6.24
248186_at	unknown protein ;supported by full-leng	---	AT5G53880	-1.41	-0.50	-1.09	0.314761	0.543461	-6.24
257559_at	hypothetical protein contains Pfam profil	---	AT3G22050	1.09	0.13	1.09	0.314765	0.543461	-6.24
262870_at	alcohol dehydrogenase, putative simila	---	AT1G64710	-1.36	-0.45	-1.09	0.314836	0.543470	-6.24
247301_at	DNA topoisomerase III	---	AT5G63920	1.14	0.19	1.09	0.314885	0.543513	-6.24
257970_at	putative sucrose cleavage protein simila	---	AT3G27570	-1.10	-0.14	-1.09	0.315071	0.543752	-6.24
249663_s_a	unknown protein	---	---	1.11	0.15	1.09	0.315066	0.543752	-6.24
253721_at	hypothetical protein ;supported by full-le	---	AT4G29250	1.12	0.16	1.09	0.315193	0.543881	-6.24
250310_at	unknown protein	---	AT5G12230	1.12	0.16	1.09	0.31517	0.543881	-6.24
262077_at	dynamin-like protein similar to dynamin	ADL3	AT1G59610	-1.08	-0.11	-1.09	0.315224	0.543892	-6.24
256086_at	hypothetical protein predicted by genem	---	AT1G20770	-1.09	-0.13	-1.08	0.31526	0.543914	-6.24
245185_at	F12A21.11 similar to T-Complex protein	---	AT1G67760	-1.12	-0.16	-1.08	0.31531	0.543958	-6.24
260599_at	cytochrome P450, putative similar to SF	CYP708A1	AT1G55940	-1.07	-0.10	-1.08	0.315342	0.543972	-6.24
248393_at	putative protein contains similarity to un	ATBAG1	AT5G52060	1.16	0.21	1.08	0.315436	0.543985	-6.24
267628_at	unknown protein similar to GP|2262147	---	AT2G42280	1.10	0.14	1.08	0.315445	0.543985	-6.24
253149_at	NAD+ dependent isocitrate dehydroger	---	AT4G35650	-1.09	-0.13	-1.08	0.315441	0.543985	-6.24
248277_at	ABC transporter-like protein	---	AT5G52860	1.11	0.15	1.08	0.31544	0.543985	-6.24
261009_at	hypothetical protein similar to putative a	MES13	AT1G26360	1.10	0.14	1.08	0.315529	0.544089	-6.24

254100_at	hypothetical protein ;supported by full-le	---	AT4G25020	-1.18	-0.23	-1.08	0.315563	0.544107	-6.24
250270_at	putative protein FL10, EGF responsive	---	AT5G12980	-1.11	-0.15	-1.08	0.315623	0.544169	-6.24
254448_at	fatty acid hydroxylase - like protein fatty	FAH2	AT4G20870	1.29	0.36	1.08	0.315649	0.544173	-6.24
254956_at	putative protein various predicted prote	---	AT4G10850	1.08	0.11	1.08	0.315685	0.544194	-6.24
255439_at	putative phospho-ser/thr phosphatase s	BSL1	AT4G03080	-1.08	-0.12	-1.08	0.315859	0.544453	-6.24
257778_at	hypothetical protein predicted by gensca	---	---	1.10	0.14	1.08	0.3159	0.544483	-6.24
245396_at	hypothetical protein ;supported by full-le	---	AT4G14870	-1.16	-0.21	-1.08	0.316024	0.544620	-6.24
246668_at	putative protein	---	---	1.08	0.11	1.08	0.316051	0.544620	-6.24
259228_at	unknown protein similar to hypothetical	---	AT3G07720	-1.11	-0.15	-1.08	0.316028	0.544620	-6.24
266739_at	unknown protein predicted by genscan	---	AT2G46730	-1.09	-0.12	-1.08	0.316162	0.544769	-6.24
256229_at	unknown protein	MSL3	AT1G58200	1.12	0.17	1.08	0.316296	0.544960	-6.24
250421_at	putative protein	OCP3	AT5G11270	-1.12	-0.16	-1.08	0.316455	0.545156	-6.24
245491_at	hypothetical protein	LDL3	---	1.11	0.15	1.08	0.316458	0.545156	-6.24
247527_at	leucine-rich receptor-like protein kinase	---	AT5G61480	1.14	0.19	1.08	0.316486	0.545164	-6.24
256063_at	Expressed protein ; supported by full-ler	STN1	AT1G07130	-1.10	-0.13	-1.08	0.31676	0.545470	-6.24
245971_at	putative protein ; supported by cDNA: g	NPH4	AT5G20730	1.09	0.12	1.08	0.316754	0.545470	-6.24
259555_at	hypothetical protein	---	---	1.08	0.11	1.08	0.316709	0.545470	-6.24
265232_s_a	hypothetical protein	---	AT2G07715	-1.10	-0.14	-1.08	0.316725	0.545470	-6.24
247800_at	Expressed protein ; supported by full-ler	---	AT5G58570	-1.41	-0.50	-1.08	0.316805	0.545484	-6.24
263745_at	hypothetical protein predicted by genefir	CHR34	AT2G21450	-1.08	-0.11	-1.08	0.316816	0.545484	-6.24
264432_at	hypothetical protein similar to hypothetic	---	AT1G61710	-1.08	-0.12	-1.08	0.31693	0.545639	-6.24
256820_at	far-red impaired response protein, puta	FHY3	AT3G22170	-1.08	-0.11	-1.08	0.317025	0.545651	-6.24
255803_at	putative protein vesicle-associated mer	---	AT4G10170	-1.08	-0.11	-1.08	0.317057	0.545651	-6.24
251832_at	putative protein tomato leucine zipper-c	ATEXO70I	AT3G55150	1.27	0.34	1.08	0.317039	0.545651	-6.24
262694_at	unknown protein	---	AT1G62790	1.21	0.27	1.08	0.317035	0.545651	-6.24
260043_at	hypothetical protein predicted by genem	---	---	-1.11	-0.15	-1.08	0.317032	0.545651	-6.24
262206_at	putative ubiquinol-cytochrome c reducta	---	AT2G01090	-1.11	-0.15	-1.08	0.317111	0.545662	-6.24
256298_at	DNA-binding protein contains Pfam prof	AGL94	AT1G69540	1.09	0.12	1.08	0.317092	0.545662	-6.24
263950_at	hypothetical protein predicted by genefir	HVA22J	AT2G36020	1.07	0.10	1.08	0.317138	0.545669	-6.24
252842_at	putative protein hypothetical proteins - A	---	---	-1.10	-0.14	-1.08	0.317191	0.545718	-6.24
259493_at	unknown protein	---	AT1G15840	-1.09	-0.13	-1.08	0.317257	0.545790	-6.24
246745_at	60S ribosomal protein L22 - like riboson	---	AT5G27770	-1.17	-0.22	-1.08	0.31736	0.545879	-6.24
249669_at	putative protein similar to unknown prote	---	---	-1.08	-0.11	-1.08	0.317398	0.545879	-6.24
245265_at	hypothetical protein ; supported by cDN/	ACD6	AT4G14400	1.73	0.79	1.08	0.317404	0.545879	-6.24
255144_at	putative protein predicted proteins - Ara	---	---	-1.07	-0.10	-1.08	0.317399	0.545879	-6.24

250321_at	zinc finger transcription factor -like prote	---	AT5G12850	1.09	0.13	1.08	0.31746	0.545899	-6.24
260826_at	hypothetical protein predicted by genem	---	AT1G06710	-1.09	-0.12	-1.08	0.317464	0.545899	-6.24
261920_at	isocitrate dehydrogenase, putative simi	---	AT1G65930	1.10	0.13	1.08	0.317495	0.545911	-6.24
247759_at	copper transport protein - like ;supporte	COPT3	AT5G59040	1.08	0.11	1.08	0.317542	0.545952	-6.24
252895_at	hypothetical protein	---	AT4G39450	-1.08	-0.11	-1.08	0.317736	0.546244	-6.24
258258_at	transcriptional regulator (FUSCA3) iden	FUS3	AT3G26790	-1.08	-0.11	-1.08	0.31777	0.546261	-6.24
259783_at	auxin-induced protein, putative similar t	SAUR68	AT1G29510	1.50	0.59	1.08	0.317952	0.546327	-6.24
265803_at	hypothetical protein predicted by gensca	---	AT2G18115	1.12	0.16	1.08	0.317913	0.546327	-6.24
247084_at	NAM (no apical meristem)-like protein	NAC105	AT5G66300	1.08	0.12	1.08	0.317937	0.546327	-6.24
245135_at	putative non-LTR retroelement reverse t	---	---	1.10	0.14	1.08	0.317951	0.546327	-6.24
246928_at	putative protein Scythe protein - Xenop	---	AT5G25270	1.08	0.11	1.08	0.31795	0.546327	-6.24
245431_at	hypothetical protein	---	AT4G17080	-1.09	-0.12	-1.08	0.317914	0.546327	-6.24
260634_at	initiation factor isozyme 4F p82 subunit	---	AT1G62410	1.09	0.13	1.08	0.318037	0.546391	-6.24
262475_at	hypothetical protein predicted by genem	---	AT1G50340	1.10	0.14	1.08	0.318037	0.546391	-6.24
253448_at	putative protein mRNA for KIAA0079 ge	---	AT4G32640	1.08	0.10	1.08	0.318196	0.546622	-6.24
259204_s_a	hypothetical protein predicted by gensc	---	---	1.08	0.11	1.08	0.318444	0.546966	-6.25
264536_at	hypothetical protein predicted by genem	PRA1.G1	AT1G55640	1.14	0.19	1.08	0.318438	0.546966	-6.25
247579_at	cytochrome P450 - like protein cytochro	CYP89A3	AT5G61320	-1.08	-0.11	-1.08	0.318501	0.547022	-6.25
247992_at	unknown protein	---	AT5G56520	-1.09	-0.12	-1.08	0.318557	0.547077	-6.25
264196_at	putative RING zinc finger protein Contai	---	AT1G22670	1.08	0.11	1.08	0.318678	0.547244	-6.25
259112_at	putative 60S ribosomal protein L22 sim	---	AT3G05560	-1.19	-0.25	-1.08	0.318713	0.547262	-6.25
260572_at	putative molybdopterin synthase large s	---	AT2G43760	1.08	0.11	1.08	0.318788	0.547290	-6.25
246939_at	AP2 domain containing protein AP2 dor	SHN2	AT5G25390	1.09	0.13	1.08	0.3188	0.547290	-6.25
262034_at	hypothetical protein predicted by genem	---	---	1.08	0.12	1.08	0.318798	0.547290	-6.25
260162_at	unknown protein	GC5	AT1G79830	-1.07	-0.10	-1.08	0.318847	0.547329	-6.25
257927_at	ethylene response factor 1 (ERF1) ident	ERF1	AT3G23240	1.94	0.95	1.08	0.318887	0.547353	-6.25
265466_at	putative CCAAT-box binding trancription	NF-YB8	AT2G37060	1.12	0.16	1.08	0.318909	0.547353	-6.25
258406_at	hypothetical protein similar to hypothetic	ATRBL14	AT3G17611	1.07	0.10	1.08	0.318953	0.547387	-6.25
245468_at	pectinesterase like protein	---	AT4G15980	1.08	0.11	1.08	0.319031	0.547426	-6.25
260469_at	BRCA1-associated RING domain protei	AGD4	AT1G10870	-1.11	-0.16	-1.08	0.319067	0.547426	-6.25
263088_at	putative replication protein A1	---	---	-1.08	-0.11	-1.08	0.319096	0.547426	-6.25
249196_at	unknown protein supported by full-lengt	---	AT5G42560	1.09	0.12	1.08	0.319076	0.547426	-6.25
248348_at	putative protein similar to unknown prote	---	AT5G52190	-1.09	-0.12	-1.08	0.319059	0.547426	-6.25
265414_at	nodulin-like protein	---	AT2G16660	-1.26	-0.33	-1.08	0.319209	0.547537	-6.25
245127_at	putative Na+/Ca2+ antiporter ; supporte	ATMHX	AT2G47600	1.17	0.23	1.08	0.319187	0.547537	-6.25

247616_at	putative protein various predicted prote	---	AT5G60260	1.09	0.12	1.08	0.319258	0.547581	-6.25
251388_at	putative protein protein regulating cytok	MAP65-4	AT3G60840	1.10	0.14	1.08	0.319287	0.547589	-6.25
246255_at	transcription initiation factor like protein	ATPBRP	AT4G36650	-1.10	-0.13	-1.08	0.319369	0.547689	-6.25
259719_at	unknown protein contains gamma-thioni	LCR66	AT1G61070	1.08	0.11	1.07	0.319414	0.547724	-6.25
256054_at	unknown protein	---	AT1G07120	-1.07	-0.09	-1.07	0.319641	0.548074	-6.25
247732_at	putative protein various predicted prote	---	AT5G59600	-1.07	-0.10	-1.07	0.319692	0.548097	-6.25
258932_at	hypothetical protein predicted by gensca	PAP16	AT3G10150	-1.08	-0.12	-1.07	0.319703	0.548097	-6.25
247012_at	putative protein contains similarity to MY	TRB2	AT5G67580	-1.09	-0.13	-1.07	0.319798	0.548219	-6.25
246088_at	putative protein	---	AT5G20600	-1.13	-0.17	-1.07	0.319915	0.548378	-6.25
263806_at	hypothetical protein predicted by genefir	---	AT2G04305	1.21	0.28	1.07	0.320006	0.548477	-6.25
259698_at	hypothetical protein similar to hypotheti	---	AT1G68930	-1.11	-0.15	-1.07	0.320021	0.548477	-6.25
254462_at	putative protein ;supported by full-lengt	---	AT4G20150	1.07	0.10	1.07	0.320053	0.548490	-6.25
264456_at	unknown protein similar to T cell recept	---	AT1G10390	-1.09	-0.12	-1.07	0.320094	0.548520	-6.25
245842_at	proline-rich protein, putative similar to p	RXF26	AT1G58430	1.08	0.11	1.07	0.320203	0.548665	-6.25
265130_at	unknown protein similar to ESTs gb|T76	---	AT1G30890	1.07	0.09	1.07	0.320339	0.548856	-6.25
257485_at	hypothetical protein contains Pfam profil	---	AT1G63580	1.19	0.26	1.07	0.320507	0.549103	-6.25
265069_at	awaiting functional assignment similar to	---	AT1G55545	1.09	0.12	1.07	0.320557	0.549124	-6.25
252651_at	putative protein several hypothetical pro	---	AT3G44700	1.10	0.14	1.07	0.320567	0.549124	-6.25
255293_at	putative zinc finger protein	---	AT4G04730	-1.09	-0.13	-1.07	0.320656	0.549235	-6.25
262324_at	hypothetical protein similar to hypothetic	ATCHX16	AT1G64170	-1.55	-0.63	-1.07	0.320781	0.549367	-6.25
256834_at	cyclophilin, putative similar to cyclophili	---	AT3G22920	1.08	0.11	1.07	0.320761	0.549367	-6.25
265510_at	putative microtubule-associated protein	ATG8D	AT2G05630	-1.09	-0.12	-1.07	0.320899	0.549527	-6.25
245132_at	hypothetical protein predicted by genefir	---	AT2G45320	-1.14	-0.18	-1.07	0.321081	0.549759	-6.25
262365_at	disease resistance protein, putative sim	---	AT1G72870	1.11	0.15	1.07	0.321082	0.549759	-6.25
261735_at	hypothetical protein similar to hypothetic	---	AT1G47765	-1.09	-0.13	-1.07	0.321182	0.549889	-6.25
266405_at	hypothetical protein predicted by gensca	---	AT2G38580	1.17	0.22	1.07	0.321229	0.549924	-6.25
261897_at	hypothetical protein predicted by genem	---	AT1G80950	1.10	0.13	1.07	0.321251	0.549924	-6.25
245511_at	hypothetical protein	---	AT4G15755	1.07	0.10	1.07	0.321359	0.550037	-6.25
252783_at	putative protein predicted proteins, Arat	---	---	1.08	0.11	1.07	0.321365	0.550037	-6.25
257197_at	selenium binding protein, putative simil	SBP3	AT3G23800	-1.08	-0.11	-1.07	0.321397	0.550050	-6.25
246000_at	putative protein predicted proteins, Arat	---	AT5G20820	1.17	0.23	1.07	0.321498	0.550181	-6.25
263631_at	unknown protein ; supported by full-leng	---	AT2G04900	1.08	0.11	1.07	0.321552	0.550191	-6.25
253741_at	putative protein various hypothetical and	---	AT4G28890	-1.08	-0.10	-1.07	0.321534	0.550191	-6.25
251356_at	putative protein hypothetical proteins - A	AtPP2-A13	AT3G61060	-1.11	-0.15	-1.07	0.321594	0.550213	-6.25
265449_at	putative arginine/serine-rich splicing fact	---	AT2G46610	-1.14	-0.19	-1.07	0.321613	0.550213	-6.25

261818_at	similar to hypethetical 62.8 KD protein i	---	AT1G11390	1.10	0.13	1.07	0.321685	0.550295	-6.25
249578_at	putative protein predicted protein, Arabi	---	AT5G37730	-1.07	-0.10	-1.07	0.32174	0.550348	-6.25
251423_at	regulatory protein - like regulatory prote	CYCP3;2	AT3G60550	1.11	0.15	1.07	0.321872	0.550533	-6.25
247706_at	putative ripening-related protein - like pu	---	AT5G59480	1.22	0.29	1.07	0.321923	0.550565	-6.25
260083_at	putative elicitor-responsive gene similar	---	AT1G63220	1.34	0.42	1.07	0.321939	0.550565	-6.25
259405_at	Expressed protein ; supported by cDNA	---	AT1G17744	1.14	0.18	1.07	0.321964	0.550566	-6.25
249682_at	putative protein similar to unknown prote	---	AT5G36080	1.08	0.11	1.07	0.322075	0.550715	-6.25
261935_at	phosphoribosylanthranilate transferase	---	AT1G22610	1.08	0.11	1.07	0.322146	0.550794	-6.25
266032_x_a	putative replication protein A1	---	---	1.09	0.13	1.07	0.322191	0.550831	-6.25
263782_at	hypothetical protein predicted by genefir	---	AT2G46380	1.10	0.13	1.07	0.322244	0.550880	-6.25
262647_at	putative growth regulator protein similar	---	AT1G14020	1.13	0.18	1.07	0.322321	0.550969	-6.26
253675_at	hypothetical protein	---	AT4G29560	-1.08	-0.11	-1.07	0.322404	0.551071	-6.26
248146_at	translation initiation factor-like protein	---	AT5G54940	-1.09	-0.12	-1.07	0.322674	0.551408	-6.26
247306_at	ser/thr protein phosphatase catalytic sub	PP7	AT5G63870	-1.11	-0.15	-1.07	0.322635	0.551408	-6.26
266040_at	hypothetical protein	---	AT2G07738	1.07	0.10	1.07	0.32267	0.551408	-6.26
259339_at	putative adenylylsulfate kinase similar to	---	AT3G03900	1.12	0.16	1.07	0.322772	0.551534	-6.26
246279_at	homeodomain protein	ATHB40	AT4G36740	1.12	0.17	1.07	0.322981	0.551834	-6.26
257767_at	hypothetical protein predicted by genem	---	AT3G23040	-1.11	-0.15	-1.07	0.322996	0.551834	-6.26
259692_at	unknown protein	---	AT1G63080	-1.09	-0.12	-1.07	0.323138	0.552036	-6.26
266485_at	putative phospholipase ;supported by fu	---	AT2G47630	1.21	0.28	1.07	0.323406	0.552452	-6.26
263210_at	Expressed protein ; supported by cDNA	---	AT1G10585	2.13	1.09	1.07	0.323432	0.552456	-6.26
261528_at	pectate lyase, putative similar to pectat	AT59	AT1G14420	1.09	0.13	1.07	0.32347	0.552479	-6.26
261058_at	histone, putative similar to histone H3 C	HTR12	AT1G01370	1.08	0.10	1.07	0.323525	0.552490	-6.26
248973_at	disease resistance protein-like	TTR1	AT5G45050	1.07	0.10	1.07	0.323511	0.552490	-6.26
255932_at	mutator-like transposase, putative simil	---	---	1.09	0.12	1.07	0.323554	0.552497	-6.26
255255_at	coded for by A. thaliana cDNA T44741	---	AT4G05070	-1.15	-0.21	-1.06	0.323716	0.552707	-6.26
247537_s_a	ABC transport protein - like ABC transp	ATH15	AT5G61690 /	-1.09	-0.12	-1.06	0.323725	0.552707	-6.26
248690_at	acetyl-CoA C-acetyltransferase ; suppo	ACAT2	AT5G48230	1.07	0.10	1.06	0.323765	0.552734	-6.26
264220_at	unknown protein similar to putative actin	ARPC3	AT1G60430	1.08	0.11	1.06	0.323798	0.552748	-6.26
259599_at	serine carboxypeptidase II, putative sim	SCPL45	AT1G28110	1.32	0.40	1.06	0.323867	0.552826	-6.26
265785_at	hypothetical protein predicted by gensca	---	AT2G07290	1.07	0.10	1.06	0.323921	0.552876	-6.26
257977_at	hypothetical protein predicted by genem	---	AT3G20850	1.09	0.12	1.06	0.324019	0.553003	-6.26
266942_at	putative ATP binding protein	TXND9	AT2G18990	-1.15	-0.20	-1.06	0.324119	0.553008	-6.26
265084_at	hypothetical protein contains Cys3His zi	SOM	AT1G03790	1.09	0.12	1.06	0.324058	0.553008	-6.26
260847_s_a	alanine aminotransferase, putative simi	AlaAT1	AT1G17290 /	1.09	0.12	1.06	0.324077	0.553008	-6.26

254324_at	putative protein various predicted prote	---	AT4G22640	1.11	0.15	1.06	0.324096	0.553008	-6.26
259255_at	putative glycerol-3-phosphate dehydrog	---	AT3G07690	1.17	0.23	1.06	0.324182	0.553074	-6.26
264704_at	unknown protein similar to putative glyc	LGT8	AT1G70090	1.15	0.21	1.06	0.324334	0.553281	-6.26
262601_at	hypothetical protein similar to GB:P4996	ATHSRP5	AT1G15310	1.12	0.17	1.06	0.324352	0.553281	-6.26
266890_at	acyl carrier protein identical to GB:L235	MTACP-1	AT2G44620	1.11	0.15	1.06	0.324565	0.553603	-6.26
260608_at	putative polygalacturonase	---	AT2G43870	1.99	0.99	1.06	0.3246	0.553621	-6.26
250237_at	putative protein strong similarity to unkn	---	AT5G13560	1.11	0.15	1.06	0.324684	0.553639	-6.26
262672_at	RNA pseudouridylate synthase, putativ	---	AT1G76050	-1.09	-0.12	-1.06	0.324644	0.553639	-6.26
259212_at	hypothetical protein predicted by genefi	---	AT3G09180	-1.10	-0.13	-1.06	0.324682	0.553639	-6.26
267510_at	unknown protein ; supported by full-leng	SAP18	AT2G45640	-1.12	-0.16	-1.06	0.324747	0.553706	-6.26
266670_at	putative flavonol 3-O-glucosyltransferas	UGT71C2	AT2G29740	-1.11	-0.15	-1.06	0.32479	0.553738	-6.26
264474_s_a	ribulose-bisphosphate carboxylase sma	RBCS1A	AT1G06820 /	1.07	0.10	1.06	0.324893	0.553873	-6.26
251521_at	putative protein receptor kinase homolo	ACR4	AT3G59420	-1.11	-0.15	-1.06	0.32494	0.553911	-6.26
258498_at	unknown protein similar to pollen coat p	---	AT3G02480	1.21	0.28	1.06	0.325095	0.554050	-6.26
256032_at	polyprotein, putative similar to polyprote	---	---	1.06	0.09	1.06	0.325052	0.554050	-6.26
261733_at	clathrin coat assembly protein AP17, pu	---	AT1G47830	-1.08	-0.11	-1.06	0.325071	0.554050	-6.26
257826_at	RING zinc finger protein, putative conta	---	AT3G26730	-1.08	-0.12	-1.06	0.325237	0.554162	-6.26
251816_at	Expressed protein ; supported by cDNA	TON1B	AT3G55005	-1.12	-0.17	-1.06	0.325196	0.554162	-6.26
257785_at	geranylgeranylated protein, putative sin	MUB4	AT3G26980	1.34	0.42	1.06	0.325299	0.554162	-6.26
265804_at	putative peptide methionine sulfoxide re	---	AT2G18030	-1.07	-0.10	-1.06	0.325321	0.554162	-6.26
266343_at	putative non-LTR retroelement reverse t	---	---	1.10	0.14	1.06	0.325265	0.554162	-6.26
246707_at	putative protein	---	---	-1.09	-0.12	-1.06	0.32533	0.554162	-6.26
257040_at	unknown protein ; supported by cDNA:	SCO2	AT3G19220	-1.14	-0.19	-1.06	0.325328	0.554162	-6.26
256605_at	hypothetical protein predicted by gensca	---	AT3G32940	-1.10	-0.13	-1.06	0.325444	0.554314	-6.26
263924_at	enolase (2-phospho-D-glycerate hydroy	LOS2	AT2G36530	1.21	0.27	1.06	0.325501	0.554370	-6.26
252466_x_a	putative protein several hypothetical pro	---	---	1.09	0.12	1.06	0.325527	0.554373	-6.26
262234_at	putative G protein coupled receptor iden	GCR1	AT1G48270	1.13	0.18	1.06	0.325582	0.554426	-6.26
250360_at	putative protein probable serine/threoni	---	AT5G11360	1.09	0.12	1.06	0.325846	0.554791	-6.26
263266_at	hypothetical protein predicted by gensca	---	AT2G16520	1.08	0.12	1.06	0.325839	0.554791	-6.26
266024_at	En/Spm-like transposon protein related	---	---	-1.08	-0.11	-1.06	0.325896	0.554835	-6.26
258082_at	Expressed protein ; supported by full-ler	CLE27	AT3G25905	-1.18	-0.24	-1.06	0.326103	0.555133	-6.26
255790_at	hypothetical protein predicted by genefi	---	AT2G33560	1.09	0.13	1.06	0.326119	0.555133	-6.26
251372_at	putative protein ;supported by full-lengt	---	AT3G60520	-1.11	-0.16	-1.06	0.326273	0.555234	-6.26
257274_at	geranylgeranyl pyrophosphate syntheta	---	AT3G14510	1.10	0.13	1.06	0.326328	0.555234	-6.26
245935_at	hypothetical protein	---	AT5G19840	-1.08	-0.11	-1.06	0.326299	0.555234	-6.26

247100_at	selenium-binding protein-like	---	AT5G66520	-1.09	-0.13	-1.06	0.326269	0.555234	-6.26
262042_at	polygalacturonase, putative similar to p	---	AT1G80140	-1.09	-0.13	-1.06	0.326349	0.555234	-6.26
253371_at	putative protein FAB1 protein, Sacchar	---	AT4G33240	1.10	0.14	1.06	0.326339	0.555234	-6.26
245261_at	Expressed protein ; supported by cDNA	---	AT4G14385	-1.08	-0.11	-1.06	0.326285	0.555234	-6.26
251387_at	putative protein	---	AT3G60810	-1.15	-0.20	-1.06	0.326465	0.555391	-6.27
255984_at	inositol polyphosphate 5-phosphatase I	IP5PI	AT1G34120	-1.09	-0.12	-1.06	0.326498	0.555404	-6.27
253394_at	putative protein predicted protein, Syne	VTE1	AT4G32770	-1.17	-0.23	-1.06	0.326535	0.555426	-6.27
248104_at	S-adenosyl-L-methionine:salicylic acid c	IAMT1	AT5G55250	-1.23	-0.29	-1.06	0.326799	0.555813	-6.27
245901_at	HOMEOBOX PROTEIN KNOTTED-1 LI	KNAT4	AT5G11060	-1.14	-0.19	-1.06	0.326811	0.555813	-6.27
253875_at	putative protein ENOD20 gene, Medica	---	AT4G27520	-1.19	-0.25	-1.06	0.326984	0.555816	-6.27
262065_at	hypothetical protein predicted by genem	---	AT1G56180	-1.16	-0.21	-1.06	0.326983	0.555816	-6.27
265074_at	hypothetical protein ; supported by cDN	emb1011	AT1G55540	-1.10	-0.14	-1.06	0.326876	0.555816	-6.27
266180_at	putative PHD-type zinc finger protein ;s	AL6	AT2G02470	-1.12	-0.16	-1.06	0.32689	0.555816	-6.27
263318_at	Expressed protein ; supported by full-ler	AtGDU4	AT2G24762	-1.45	-0.54	-1.06	0.326936	0.555816	-6.27
249183_at	E2, ubiquitin-conjugating enzyme 18 (U	UBC18	AT5G42990	-1.08	-0.11	-1.06	0.326845	0.555816	-6.27
264617_at	unknown protein	---	AT2G17660	1.18	0.24	1.06	0.326939	0.555816	-6.27
264476_at	hypothetical protein contains similarity t	PGSIP2	AT1G77130	-1.10	-0.14	-1.06	0.327178	0.556034	-6.27
251201_at	putative protein predicted protein, Arabi	---	AT3G63020	1.07	0.10	1.06	0.327184	0.556034	-6.27
255848_at	hypothetical protein predicted by gensca	---	AT2G33640	1.09	0.13	1.06	0.327209	0.556034	-6.27
251343_at	phosphatidate cytidylyltransferase - like	---	AT3G60620	-1.17	-0.22	-1.06	0.327188	0.556034	-6.27
258112_at	putative cytochrome P450 similar to GB	CYP72A1(	AT3G14640	-1.09	-0.13	-1.06	0.327332	0.556200	-6.27
257825_at	protein kinase, putative contains Pfam p	---	AT3G26700	1.09	0.13	1.06	0.327377	0.556229	-6.27
260088_at	tonoplast intrinsic protein, alpha (alpha-	TIP3;1	AT1G73190	1.10	0.14	1.06	0.327399	0.556229	-6.27
250379_at	transcription factor like protein transcrip	TINY2	AT5G11590	-1.08	-0.11	-1.06	0.327482	0.556229	-6.27
254267_at	dihydroorotase ; supported by cDNA: gi	PYR4	AT4G22930	-1.10	-0.13	-1.06	0.327495	0.556229	-6.27
265424_at	putative sugar transporter	---	AT2G20780	1.10	0.13	1.06	0.327429	0.556229	-6.27
258307_x_a	hypothetical protein predicted by genen	---	---	1.09	0.12	1.06	0.327473	0.556229	-6.27
266829_at	hypothetical protein predicted by gensca	---	AT2G22940	1.07	0.10	1.06	0.327543	0.556270	-6.27
257752_at	hypothetical protein predicted by gensca	---	AT3G18720	-1.09	-0.13	-1.06	0.327594	0.556314	-6.27
254691_at	hypothetical protein ; supported by full-l	---	AT4G17840	1.15	0.20	1.06	0.327764	0.556562	-6.27
252621_at	putative protein Ac-like transposases	---	---	-1.09	-0.12	-1.06	0.327802	0.556585	-6.27
257309_at	hypothetical protein predicted by genem	---	AT3G28150	-1.07	-0.09	-1.05	0.327847	0.556620	-6.27
248111_at	wax synthase-like protein	---	AT5G55330	1.08	0.11	1.05	0.328072	0.556960	-6.27
251897_at	RING finger - like protein DNA-binding	---	AT3G54360	-1.11	-0.15	-1.05	0.3281	0.556967	-6.27
264194_at	putative wall-associated kinase contains	---	AT1G22720	1.09	0.12	1.05	0.328277	0.557225	-6.27

250590_at	exonuclease-like protein	---	AT5G07710	-1.08	-0.11	-1.05	0.328362	0.557261	-6.27
255015_at	putative protein m6A methyltransferase	EMB1691	AT4G09980	-1.14	-0.19	-1.05	0.328336	0.557261	-6.27
255404_at	predicted protein	---	AT4G03153	1.09	0.12	1.05	0.328371	0.557261	-6.27
261178_at	synaptobrevin 7B, putative similar to GI	ATVAMP7	AT1G04760	-1.08	-0.10	-1.05	0.328562	0.557503	-6.27
258978_at	unknown protein ; supported by cDNA:	---	AT3G09320	-1.08	-0.11	-1.05	0.328541	0.557503	-6.27
246043_at	putative protein predicted protein, Arabi	---	AT5G19380	-1.17	-0.23	-1.05	0.328727	0.557741	-6.27
251851_at	structural maintenance of chromosome	TTN8	AT3G54670	-1.09	-0.13	-1.05	0.328777	0.557785	-6.27
254065_at	gibberellin 20-oxidase - Arabidopsis thal	GA20OX1	AT4G25420	1.24	0.31	1.05	0.328838	0.557845	-6.27
253280_at	poly(A)-binding protein non-consensus	PAB2	AT4G34110	-1.08	-0.11	-1.05	0.328931	0.557921	-6.27
264569_at	unknown protein EST gb|ATTS1136 cor	---	---	1.08	0.11	1.05	0.32893	0.557921	-6.27
251266_at	putative protein hypothetical protein At2	---	AT3G62320	1.10	0.14	1.05	0.328973	0.557950	-6.27
261699_at	hypothetical protein identical to hypothe	---	AT1G32660	1.10	0.13	1.05	0.328998	0.557951	-6.27
257059_at	unknown protein ; supported by cDNA:	---	AT3G15280	-1.08	-0.11	-1.05	0.329158	0.558139	-6.27
262265_at	hypothetical protein predicted by gensca	---	---	1.12	0.17	1.05	0.329137	0.558139	-6.27
254107_at	putative protein putative glycerol-3-phos	---	AT4G25220	1.11	0.15	1.05	0.329227	0.558179	-6.27
260090_at	putative serine carboxypeptidase simila	scpl4	AT1G73310	-1.07	-0.10	-1.05	0.32923	0.558179	-6.27
257430_at	hypothetical protein similar to hypothetic	---	AT2G28580	1.11	0.15	1.05	0.329373	0.558379	-6.27
265144_at	putative serine/threonine protein kinase	---	AT1G51170	-1.12	-0.17	-1.05	0.329552	0.558641	-6.27
252233_at	AtMYB84 ;supported by full-length cDN	MYB84	AT3G49690	-1.10	-0.13	-1.05	0.329637	0.558745	-6.27
260371_at	unknown protein ; supported by cDNA:	---	AT1G69690	-1.24	-0.32	-1.05	0.329664	0.558748	-6.27
267542_at	hypothetical protein predicted by genefir	---	AT2G32740	1.08	0.11	1.05	0.329714	0.558791	-6.27
266667_at	hypothetical protein predicted by gensca	---	AT2G29770	1.07	0.10	1.05	0.329801	0.558896	-6.27
249382_at	putative protein predicted proteins, Arat	---	AT5G40050	1.07	0.10	1.05	0.329825	0.558896	-6.27
245702_at	calcium lipid binding protein - like GC do	SYTC	AT5G04220	-1.13	-0.18	-1.05	0.329928	0.558918	-6.27
260008_at	putative RING zinc finger protein contai	---	AT1G68070	-1.08	-0.11	-1.05	0.329892	0.558918	-6.27
252381_s_a	ABC-type transport protein-like protein	ABCA4	AT3G47750 /	-1.10	-0.13	-1.05	0.329936	0.558918	-6.27
247714_at	wuschel protein - like wuschel protein, /	WOX2	AT5G59340	1.16	0.21	1.05	0.329874	0.558918	-6.27
250228_at	cell cycle switch protein	FZR3	AT5G13840	1.10	0.14	1.05	0.329977	0.558946	-6.27
247978_at	60S ribosomal protein L31 ;supported b	---	AT5G56710	-1.22	-0.29	-1.05	0.330117	0.559142	-6.27
250570_at	putative protein hypothetical bacterial pr	EMB1873	AT5G08170	-1.12	-0.16	-1.05	0.330281	0.559337	-6.27
245663_at	steroid sulfotransferase, putative simila	---	AT1G28170	1.08	0.11	1.05	0.330261	0.559337	-6.27
260114_at	AIG1-like protein similar to AIG1 protein	---	AT1G33880	1.08	0.11	1.05	0.330344	0.559402	-6.27
254694_at	putative protein	---	AT4G17900	1.12	0.17	1.05	0.330418	0.559485	-6.27
263852_at	putative mutT domain protein	ATNUDT6	AT2G04450	1.53	0.62	1.05	0.330476	0.559520	-6.27
266020_at	hypothetical protein	SDG11	AT2G05900	1.11	0.15	1.05	0.330487	0.559520	-6.27

251390_at	guanine nucleotide exchange factor - lik	---	AT3G60860	1.10	0.13	1.05	0.330559	0.559601	-6.28
266516_at	putative glutaredoxin ;supported by full-	---	AT2G47880	1.23	0.30	1.05	0.330617	0.559616	-6.28
262758_at	hypothetical protein predicted by genem	---	AT1G10780	-1.09	-0.13	-1.05	0.330602	0.559616	-6.28
252628_at	putative protein	---	AT3G44960	-1.07	-0.10	-1.05	0.330665	0.559654	-6.28
248922_at	putative protein contains similarity to hol	WOX8	AT5G45980	1.08	0.10	1.05	0.330695	0.559665	-6.28
264430_at	cineole synthase, putative similar to 1,8	TPS14	AT1G61680	-1.08	-0.11	-1.05	0.33079	0.559701	-6.28
256851_at	hypothetical protein predicted by genem	---	AT3G27930	1.07	0.10	1.05	0.330781	0.559701	-6.28
255922_at	trehalose-6-phosphate phosphatase, pu	---	AT1G22210	1.08	0.11	1.05	0.330787	0.559701	-6.28
249080_at	putative protein strong similarity to unkn	SUVR2	AT5G43990	1.12	0.16	1.05	0.330925	0.559887	-6.28
265123_at	hypothetical protein similar to putative C	---	AT1G55440	1.07	0.10	1.05	0.33128	0.559995	-6.28
259570_at	hypothetical protein	COR47	AT1G20440	1.18	0.23	1.05	0.331241	0.559995	-6.28
245081_at	unknown protein overlap with T20D16.8	---	---	1.14	0.19	1.05	0.331171	0.559995	-6.28
265291_at	unknown protein predicted by genscan;	---	AT2G22720	1.09	0.13	1.05	0.331227	0.559995	-6.28
259709_at	Expressed protein ; supported by full-ler	---	AT1G77655	1.10	0.14	1.05	0.331283	0.559995	-6.28
245591_at	hypothetical protein	---	AT4G14530	1.07	0.09	1.05	0.331057	0.559995	-6.28
262321_at	hypothetical protein predicted by gensca	---	AT1G27570	1.08	0.12	1.05	0.331252	0.559995	-6.28
260725_at	Expressed protein ; supported by full-ler	---	AT1G48170	1.09	0.12	1.05	0.33105	0.559995	-6.28
247869_at	CCHH finger protein 2-like protein (pir||S	ZFP2	AT5G57520	1.06	0.09	1.05	0.331113	0.559995	-6.28
245028_at	unknown protein	---	AT2G26570	1.13	0.17	1.05	0.331164	0.559995	-6.28
249495_at	germin - like protein GLP6 exon 2 interr	GLP6	AT5G39100	1.10	0.14	1.05	0.331282	0.559995	-6.28
245222_at	contains similarity to En/Spm transposol	---	---	-1.07	-0.10	-1.05	0.331123	0.559995	-6.28
266310_at	putative PCI domain protein proteasom	FUS12	AT2G26990	-1.09	-0.13	-1.05	0.331431	0.560202	-6.28
259267_at	unknown protein ;supported by full-leng	---	AT3G01130	-1.08	-0.11	-1.05	0.33149	0.560261	-6.28
252969_at	putative protein vsf-1 protein, Lycopersi	---	AT4G38900	-1.08	-0.11	-1.05	0.331565	0.560347	-6.28
259020_at	unknown protein ; supported by cDNA:	---	AT3G07470	-1.11	-0.15	-1.05	0.331726	0.560536	-6.28
253599_at	putative protein ash1 protein, Drosophil	SDG4	AT4G30860	1.13	0.18	1.05	0.331719	0.560536	-6.28
263622_at	hypothetical protein predicted by gensca	---	AT2G04870	-1.08	-0.12	-1.05	0.331774	0.560575	-6.28
245873_at	bHLH transcription factor GBOF-1, puta	CIB5	AT1G26260	-1.11	-0.15	-1.05	0.331807	0.560590	-6.28
247763_at	RNA polymerase II	NRPB7	AT5G59180	-1.09	-0.12	-1.05	0.331892	0.560691	-6.28
259710_at	putative aminotransferase similar to kyr	---	AT1G77670	-1.25	-0.32	-1.05	0.331976	0.560792	-6.28
261130_at	unknown protein ; supported by cDNA: g	PRMT10	AT1G04870	-1.17	-0.23	-1.05	0.332037	0.560821	-6.28
252973_s_a	peptidylprolyl isomerase ROC1 ;suppor	ROC1	AT4G38740	-1.13	-0.18	-1.05	0.332043	0.560821	-6.28
AFFX-Athal-	Arabidopsis thaliana /REF=M64116 /DE	GAPC1	---	1.18	0.24	1.05	0.332072	0.560830	-6.28
250537_at	Expressed protein ; supported by full-ler	---	AT5G08565	1.15	0.20	1.04	0.332131	0.560846	-6.28
258500_at	S-adenosylmethionine decarboxylase id	CPuORF9	AT3G02468 /	1.09	0.12	1.04	0.332129	0.560846	-6.28

252894_at	hypothetical protein	---	AT4G39440	-1.10	-0.14	-1.04	0.33221	0.560897	-6.28
263827_at	unknown protein	---	AT2G40420	1.15	0.20	1.04	0.332201	0.560897	-6.28
247366_at	putative protein contains similarity to zin	---	AT5G63260	1.11	0.14	1.04	0.332241	0.560908	-6.28
255847_at	putative thioredoxin	ACHT3	AT2G33270	1.07	0.10	1.04	0.332345	0.561042	-6.28
258529_at	hypothetical protein predicted by genen	---	AT3G06740	-1.12	-0.17	-1.04	0.332541	0.561330	-6.28
253367_at	hypothetical protein	---	AT4G33180	-1.15	-0.20	-1.04	0.3327	0.561432	-6.28
249378_at	putative protein microtubule-associated	---	AT5G40450	-1.13	-0.18	-1.04	0.332647	0.561432	-6.28
257979_at	unknown protein	---	AT3G20730	-1.09	-0.12	-1.04	0.332659	0.561432	-6.28
253681_at	cytidine deaminase 3 (CDA3)	---	AT4G29630	1.09	0.12	1.04	0.332677	0.561432	-6.28
250662_at	steroid sulfotransferase-like protein ;su	ST2A	AT5G07010	1.21	0.28	1.04	0.332748	0.561462	-6.28
264144_at	latex-abundant protein, putative similar	AtMC6	AT1G79320	1.08	0.11	1.04	0.332766	0.561462	-6.28
254611_at	Expressed protein ; supported by full-ler	---	AT4G19095	1.08	0.11	1.04	0.332797	0.561471	-6.28
247511_at	Fdr1 Cen - like protein Fdr1, Oryza sati	---	AT5G62040	1.10	0.14	1.04	0.332908	0.561576	-6.28
247353_at	alcohol dehydrogenase-like protein ;sup	---	AT5G63620	1.11	0.15	1.04	0.332906	0.561576	-6.28
266649_at	putative aquaporin (tonoplast intrinsic pr	TIP4;1	AT2G25810	-1.08	-0.11	-1.04	0.332967	0.561618	-6.28
255773_at	flavonol 4'-sulfotransferase, putative sir	SOT17	AT1G18590	-1.28	-0.36	-1.04	0.332982	0.561618	-6.28
263521_at	hypothetical protein predicted by gensca	---	AT2G24960	-1.12	-0.17	-1.04	0.333022	0.561632	-6.28
265279_at	hypothetical protein predicted by gensca	---	AT2G28460	1.13	0.18	1.04	0.33304	0.561632	-6.28
258562_at	unknown protein ;supported by full-leng	---	AT3G05980	1.07	0.10	1.04	0.33309	0.561635	-6.28
254627_at	Expressed protein ; supported by full-ler	---	AT4G18395	-1.08	-0.10	-1.04	0.333086	0.561635	-6.28
262013_s_a	mudrA-like protein similar to Mu transpo	---	---	-1.11	-0.15	-1.04	0.333144	0.561683	-6.28
250291_at	aspartate kinase ;supported by full-leng	AK-LYS1	AT5G13280	1.14	0.18	1.04	0.333181	0.561688	-6.28
251311_at	FUSCA PROTEIN FUS6 ; supported by	FUS6	AT3G61140	-1.08	-0.11	-1.04	0.333218	0.561688	-6.28
246466_at	sugar transporter - like protein D-XYLO	---	AT5G17010	-1.13	-0.18	-1.04	0.333234	0.561688	-6.28
245651_s_a	F5A9.18 unknown protein; similar to ES	---	AT1G24793 /	1.12	0.17	1.04	0.333245	0.561688	-6.28
264656_at	unknown protein Contains similarity to B	---	AT1G09010	-1.08	-0.11	-1.04	0.333301	0.561740	-6.28
251341_at	ribosomal protein S13 -like AtRPS13A r	---	AT3G60770	-1.18	-0.24	-1.04	0.33341	0.561758	-6.28
255233_at	putative protein ADRENODOXIN PREC	MFDX1	AT4G05450	-1.09	-0.13	-1.04	0.333368	0.561758	-6.28
247757_at	putative protein	---	AT5G59105 /	1.07	0.10	1.04	0.333405	0.561758	-6.28
255182_at	hypothetical protein	---	---	1.08	0.11	1.04	0.333351	0.561758	-6.28
266782_at	putative ligand-gated ion channel protei	ATGLR2.7	AT2G29120	1.08	0.11	1.04	0.333467	0.561813	-6.28
256010_at	auxin response factor, putative similar t	ARF19	AT1G19220	-1.10	-0.13	-1.04	0.333501	0.561828	-6.28
248085_at	putative protein similar to unknown prote	SVL1	AT5G55480	1.19	0.25	1.04	0.333526	0.561829	-6.28
244976_at	cytochrome B6	---	---	-1.08	-0.11	-1.04	0.333586	0.561888	-6.28
254825_at	putative protein Pad-1, Neurospora cra	---	AT4G12640	-1.12	-0.17	-1.04	0.333617	0.561899	-6.28

264423_at	hypothetical protein predicted by genem	---	AT1G61690	1.10	0.14	1.04	0.333698	0.561994	-6.28
246218_at	RUB1-conjugating enzyme RCE1, puta	RCE1	AT4G36800	-1.13	-0.18	-1.04	0.333875	0.562250	-6.28
265142_at	unknown protein	DABB1	AT1G51360	1.08	0.11	1.04	0.333904	0.562258	-6.28
252176_at	protein kinase ATN1 -like protein protei	---	AT3G50720	1.10	0.14	1.04	0.334022	0.562390	-6.28
264769_at	hypothetical protein predicted by genem	---	AT1G61350	1.20	0.26	1.04	0.334032	0.562390	-6.28
257651_at	polygalacturonase, putative similar to e	---	AT3G16850	-1.18	-0.24	-1.04	0.334107	0.562476	-6.28
254595_at	floral homeotic protein agamous (AGAM	AG	AT4G18960	1.07	0.10	1.04	0.334267	0.562704	-6.28
257498_at	hypothetical protein predicted by genem	---	AT1G69660	1.08	0.12	1.04	0.334329	0.562732	-6.28
259341_at	unknown protein similar to hypothetical	ATBPM4	AT3G03740	1.08	0.11	1.04	0.334333	0.562732	-6.28
263372_at	60S ribosomal protein L14 ;supported b	---	AT2G20450	-1.20	-0.26	-1.04	0.334561	0.563073	-6.28
263548_at	glycine-rich RNA binding protein 7 Alter	CCR2	AT2G21660 /	-1.09	-0.13	-1.04	0.334639	0.563163	-6.28
250713_at	putative protein similar to unknown prote	---	AT5G06130	-1.10	-0.13	-1.04	0.334756	0.563319	-6.29
245725_at	sucrose synthase, putative similar to su	SUS6	AT1G73370	1.19	0.26	1.04	0.334793	0.563340	-6.29
267206_at	putative dioxygenase	---	AT2G30830	1.08	0.12	1.04	0.334836	0.563370	-6.29
250890_at	3-oxoacyl-[acyl-carrier-protein] synthas	---	AT5G04520	1.08	0.11	1.04	0.334868	0.563382	-6.29
261693_at	hypothetical protein similar to hypothetic	DCP1	AT1G08370	-1.07	-0.10	-1.04	0.334902	0.563399	-6.29
265588_at	putative pathogenesis-related protein	---	AT2G19970	1.37	0.45	1.04	0.33504	0.563589	-6.29
253532_at	putative protein centromere protein E, H	---	AT4G31570	-1.08	-0.11	-1.04	0.335067	0.563592	-6.29
256373_at	hypothetical protein	SGA2	AT1G66740	1.11	0.16	1.04	0.335142	0.563678	-6.29
259659_at	hypothetical protein contains similarity to	---	AT1G55170	1.12	0.17	1.04	0.335287	0.563800	-6.29
245286_at	cytosolic O-acetylserine(thiol)lyase (EC	OASA1	AT4G14880	1.09	0.12	1.04	0.335289	0.563800	-6.29
246104_at	DNA-binding protein - like DNA-binding	WRKY74	AT5G28650	1.07	0.10	1.04	0.335263	0.563800	-6.29
247761_at	phosphoprotein phosphatase 1 catalytic	TOPP2	AT5G59160	1.09	0.12	1.04	0.335376	0.563904	-6.29
259936_at	putative UDP-glucose:glycoprotein gluc	EBS1	AT1G71220	-1.08	-0.11	-1.04	0.335447	0.563937	-6.29
246167_at	putative protein	---	---	1.10	0.14	1.04	0.335422	0.563937	-6.29
252435_at	putative protein several hypothetical pro	---	---	1.10	0.13	1.04	0.33547	0.563937	-6.29
258271_at	hypothetical protein predicted by genem	---	AT3G15605	1.09	0.13	1.04	0.335612	0.564112	-6.29
258793_at	hypothetical protein supported by full-ler	---	AT3G04780	1.08	0.12	1.04	0.335623	0.564112	-6.29
260509_at	natural resistance-associated macropha	NRAMP2	AT1G47240	1.07	0.09	1.04	0.335775	0.564316	-6.29
257148_at	cytochrome c, putative similar to cytoch	---	AT3G27240	1.15	0.20	1.04	0.335794	0.564316	-6.29
251782_at	beta-N-acetylhexosaminidase -like prote	HEXO1	AT3G55260	1.13	0.17	1.04	0.335866	0.564396	-6.29
260201_at	F12A21.27 hypothetical protein;supporte	---	AT1G67600	1.19	0.25	1.04	0.335931	0.564463	-6.29
259060_at	hypothetical protein predicted by gensca	---	AT3G07400	-1.12	-0.16	-1.04	0.336039	0.564603	-6.29
267418_at	putative RING zinc finger protein	---	AT2G35000	1.10	0.14	1.04	0.336076	0.564624	-6.29
260194_at	hypothetical protein similar to hypothetic	---	AT1G67530	-1.17	-0.22	-1.04	0.336323	0.564956	-6.29

261680_at	hypothetical protein similar to hypothetic	---	AT1G47350	-1.07	-0.09	-1.04	0.336313	0.564956	-6.29
263185_at	transport protein, putative similar to trar	---	AT1G05520	1.07	0.10	1.04	0.336401	0.565045	-6.29
259390_at	hypothetical protein predicted by genem	---	AT1G06340	1.09	0.12	1.03	0.336492	0.565156	-6.29
262790_at	putative translation initiation factor simila	TIF3H1	AT1G10840	-1.06	-0.09	-1.03	0.336535	0.565186	-6.29
260944_at	beta-galactosidase, putative similar to b	BGAL5	AT1G45130	1.65	0.73	1.03	0.336658	0.565345	-6.29
254614_at	putatative protein various predicted pro	---	AT4G19191	-1.11	-0.16	-1.03	0.336679	0.565345	-6.29
255114_at	putative protein various putative reverse	---	---	-1.13	-0.17	-1.03	0.336792	0.565492	-6.29
265646_at	putative lipase	---	AT2G27360	-1.09	-0.13	-1.03	0.336889	0.565614	-6.29
261939_at	cytochrome c oxidase subunit, putative	COX6B	AT1G22450	1.12	0.16	1.03	0.337031	0.565810	-6.29
262600_at	unknown protein ESTs gb|H37032, gb|I	MBD10	AT1G15340	-1.12	-0.17	-1.03	0.337186	0.565947	-6.29
260212_at	hypothetical protein predicted by gensca	---	AT1G74480	1.07	0.10	1.03	0.337145	0.565947	-6.29
251515_at	putative protein several hypothetical pro	---	AT3G59270	-1.06	-0.09	-1.03	0.33718	0.565947	-6.29
246697_at	putative protein	---	AT5G29210	-1.09	-0.13	-1.03	0.337354	0.566146	-6.29
262404_at	transposon-like ORF, putative similar to	---	---	1.08	0.12	1.03	0.337336	0.566146	-6.29
265348_at	putative RNA-binding protein	---	AT2G22600	-1.09	-0.13	-1.03	0.337516	0.566376	-6.29
248565_at	putative protein similar to unknown prote	---	AT5G49710	1.12	0.17	1.03	0.337571	0.566426	-6.29
260800_at	unknown protein	TSD2	AT1G78240	1.13	0.17	1.03	0.337624	0.566431	-6.29
247424_at	LIM7 - like protein LIM7, Lilium longiflor	AtVEX1	AT5G62850	-1.09	-0.12	-1.03	0.337616	0.566431	-6.29
259944_at	hypothetical protein predicted by gensca	---	AT1G71470	1.08	0.11	1.03	0.337788	0.566587	-6.29
255721_at	unknown protein ;supported by full-lengt	---	AT1G31940	-1.07	-0.10	-1.03	0.337747	0.566587	-6.29
263505_s_a	hypothetical protein	---	AT2G07678	-1.18	-0.23	-1.03	0.337791	0.566587	-6.29
264767_at	hypothetical protein similar to putative s	SD1-29	AT1G61380	1.24	0.31	1.03	0.337935	0.566786	-6.29
258393_at	unknown protein similar to unknown pro	---	AT3G15480	-1.14	-0.19	-1.03	0.338111	0.566844	-6.29
258832_at	putative protein kinase similar to APK1A	---	AT3G07070	1.09	0.13	1.03	0.338118	0.566844	-6.29
252197_at	receptor protein kinase -like protein rec	---	AT3G50230	1.07	0.10	1.03	0.33807	0.566844	-6.29
251354_at	putative protein hypothetical protein T1	---	AT3G61090	1.07	0.10	1.03	0.338053	0.566844	-6.29
257347_at	pseudogene, gene_id:K17E7.6	---	---	1.07	0.10	1.03	0.338063	0.566844	-6.29
259021_at	hypothetical protein predicted by genefir	---	AT3G07540	-1.17	-0.22	-1.03	0.338053	0.566844	-6.29
246342_at	putative protein male sterility protein 2 -	FAR6	AT3G56700	1.07	0.10	1.03	0.338154	0.566862	-6.29
265610_at	unknown protein ;supported by full-leng	---	AT2G25430	1.07	0.10	1.03	0.338489	0.566965	-6.29
248311_at	beta-carotene hydroxylase	BETA-OH/	AT5G52570	1.15	0.20	1.03	0.338431	0.566965	-6.29
255232_at	putative protein phosphatidylinositol-3,4	AGD13	AT4G05330	-1.12	-0.16	-1.03	0.338302	0.566965	-6.29
264568_at	putative O-GlcNAc transferase similar to	---	AT1G05150	-1.11	-0.15	-1.03	0.338451	0.566965	-6.29
258829_at	putative Sec24-like COPII protein simila	---	AT3G07100	1.07	0.09	1.03	0.338349	0.566965	-6.29
261368_at	protein kinase, putative similar to many	---	AT1G53070	1.12	0.16	1.03	0.33842	0.566965	-6.29

266287_at	putative tropinone reductase	---	AT2G29150	1.10	0.14	1.03	0.338419	0.566965	-6.29
252227_at	putative protein various predicted prote	---	AT3G49900	1.08	0.11	1.03	0.338467	0.566965	-6.29
258058_at	unknown protein	---	AT3G28980	-1.09	-0.12	-1.03	0.338358	0.566965	-6.29
253328_at	putative protein ABC-type transport pro	ATNAP13	AT4G33460	-1.08	-0.12	-1.03	0.338401	0.566965	-6.29
260354_at	unknown protein ;supported by full-leng	---	AT1G69330	-1.13	-0.18	-1.03	0.338426	0.566965	-6.29
250337_at	putative protein SF21 protein, Helianthu	---	AT5G11790	-1.31	-0.39	-1.03	0.338598	0.567107	-6.29
266016_at	putative RING zinc finger protein ; supp	---	AT2G18670 /	-1.09	-0.13	-1.03	0.338828	0.567246	-6.29
250659_at	MtN21 nodulin protein-like	---	AT5G07050	1.10	0.14	1.03	0.338844	0.567246	-6.29
257028_at	hypothetical protein predicted by genen	---	AT3G19230	1.15	0.21	1.03	0.338712	0.567246	-6.29
259503_at	unknown protein ; supported by cDNA: g	---	AT1G15870	-1.12	-0.17	-1.03	0.338856	0.567246	-6.29
265775_at	Mutator-like transposase similar to MUF	---	---	1.13	0.18	1.03	0.338835	0.567246	-6.29
267022_at	hypothetical protein predicted by gensca	---	AT2G34230	1.07	0.09	1.03	0.338792	0.567246	-6.29
265065_at	putative phytochelatin synthase	ATPCS2	AT1G03980	1.08	0.10	1.03	0.338803	0.567246	-6.29
263025_at	reverse transcriptase, putative similar to	---	---	-1.09	-0.12	-1.03	0.338892	0.567265	-6.29
258468_at	unknown protein predicted by genscan+	---	AT3G06070	-1.23	-0.29	-1.03	0.339185	0.567626	-6.30
247790_at	putative PRL1 associated protein ;supp	---	AT5G58720	1.09	0.13	1.03	0.339199	0.567626	-6.30
253187_at	putative zinc-finger protein PEThy;ZPT4	---	AT4G35280	-1.07	-0.10	-1.03	0.339282	0.567626	-6.30
247892_at	putative protein contains similarity to DN	---	AT5G57970	1.15	0.20	1.03	0.339266	0.567626	-6.30
255101_at	putative lipid transfer protein similar to F	---	AT4G08670	1.11	0.15	1.03	0.339245	0.567626	-6.30
257415_at	hypothetical protein similar to hypothetic	---	AT1G70040	1.09	0.13	1.03	0.339247	0.567626	-6.30
254027_at	putative mitochondrial protein Homo sa	---	AT4G25835	1.14	0.19	1.03	0.339213	0.567626	-6.30
251261_at	putative protein polygalacturonase - Ly	---	AT3G62110	-1.20	-0.26	-1.03	0.339478	0.567913	-6.30
263202_at	putative inositol 1,4,5-trisphosphate 5-p	5PTASE13	AT1G05630	1.22	0.29	1.03	0.339541	0.567977	-6.30
258032_at	hypothetical protein predicted by genem	---	AT3G21170	1.12	0.17	1.03	0.339579	0.567998	-6.30
250423_s_a	cytochrome P450 - like protein cytochro	CYP81K2	AT5G10600 /	1.08	0.10	1.03	0.33971	0.568175	-6.30
253470_s_a	putative protein dnaK-type molecular ch	SDH3-2	AT4G32210 /	-1.08	-0.11	-1.03	0.339734	0.568175	-6.30
255385_at	putative hydrolase	---	AT4G03610	-1.11	-0.15	-1.03	0.339787	0.568222	-6.30
266530_at	bHLH transcription factor	AMS	AT2G16910	1.07	0.09	1.03	0.339832	0.568255	-6.30
252673_at	CCR4-associated factor 1-like protein C	---	AT3G44240	1.08	0.12	1.03	0.339933	0.568302	-6.30
256689_at	hypothetical protein predicted by genem	---	AT3G32150	1.08	0.11	1.03	0.339937	0.568302	-6.30
262515_at	unknown protein ; supported by cDNA: g	---	AT1G34200	1.13	0.18	1.03	0.339903	0.568302	-6.30
257152_at	Expressed protein ; supported by full-ler	PUX1	AT3G27310	-1.07	-0.10	-1.03	0.339959	0.568302	-6.30
256879_at	unknown protein similar to auxin-indepe	---	AT3G26370	-1.07	-0.09	-1.03	0.340006	0.568338	-6.30
267216_at	hypothetical protein	---	AT2G02620	-1.08	-0.12	-1.03	0.340078	0.568417	-6.30
250475_at	sulfate transporter ; supported by cDNA	SULTR2;1	AT5G10180	-1.23	-0.30	-1.03	0.340158	0.568509	-6.30

267437_at	hypothetical protein predicted by genefir	---	AT2G19200	-1.08	-0.11	-1.03	0.34023	0.568587	-6.30
248681_at	pectate lyase non-consensus AG donor	---	AT5G48900	1.95	0.96	1.03	0.34035	0.568746	-6.30
247242_at	unknown protein	---	AT5G64690	1.07	0.10	1.03	0.340376	0.568748	-6.30
266082_at	hypothetical protein predicted by gensca	---	AT2G37830	-1.12	-0.17	-1.03	0.340414	0.568770	-6.30
245925_at	bZIP transcription factor family protein s	BZO2H3	AT5G28770	1.12	0.17	1.03	0.340514	0.568896	-6.30
260738_at	hypothetical protein predicted by genem	---	AT1G14990	-1.08	-0.11	-1.03	0.340569	0.568946	-6.30
249500_at	expansin-like protein expansin - Prunus	ATEXPA2	AT5G39260	1.13	0.18	1.03	0.34061	0.568973	-6.30
245610_at	hypothetical protein	---	AT4G14380	1.09	0.12	1.03	0.340666	0.569024	-6.30
262686_at	proteasome regulatory subunit S3, puta	---	AT1G75990	1.10	0.13	1.03	0.340739	0.569104	-6.30
247203_at	unknown protein ; supported by cDNA:	---	AT5G65180	-1.08	-0.11	-1.02	0.340926	0.569375	-6.30
247675_at	putative protein large number of predict	---	AT5G59940	1.11	0.16	1.02	0.340983	0.569428	-6.30
265821_at	putative homeodomain transcription fac	WUS	AT2G17950	-1.13	-0.17	-1.02	0.341036	0.569475	-6.30
264612_at	unknown protein similar to GB:AAC3746	---	AT1G04560	-1.11	-0.16	-1.02	0.341195	0.569699	-6.30
257404_at	hypothetical protein predicted by gensca	SUVR1	AT1G04050	1.09	0.12	1.02	0.341381	0.569969	-6.30
265250_at	putative receptor protein kinase similar t	BRL2	AT2G01950	-1.13	-0.18	-1.02	0.341435	0.570017	-6.30
262669_at	hypothetical protein	---	AT1G62850	-1.08	-0.12	-1.02	0.341604	0.570257	-6.30
267604_at	hypothetical protein predicted by genefir	ZFN2	AT2G32930	1.18	0.24	1.02	0.341708	0.570389	-6.30
249286_at	transcription factor-like protein	---	AT5G41580	-1.09	-0.12	-1.02	0.341814	0.570440	-6.30
255445_at	hypothetical protein	---	AT4G02740	1.10	0.13	1.02	0.341791	0.570440	-6.30
265757_x_a	putative PttA2-like transposon protein re	---	---	-1.11	-0.15	-1.02	0.341781	0.570440	-6.30
245879_at	putative subunit of TOC complex chlorc	ATTOC64-	AT5G09420	-1.24	-0.31	-1.02	0.34185	0.570458	-6.30
259425_at	4,5 PIP kinase, putative similar to 4,5 P	PIPK11	AT1G01460	-1.08	-0.11	-1.02	0.341883	0.570473	-6.30
250881_at	putative protein	---	AT5G04080	-1.13	-0.17	-1.02	0.342073	0.570706	-6.30
265209_at	putative DNA binding protein with home	ATHB22	AT2G36610	1.07	0.09	1.02	0.342055	0.570706	-6.30
259877_at	unknown protein C-terminal portion simi	SDG26	AT1G76710	-1.11	-0.15	-1.02	0.342205	0.570884	-6.30
250347_at	putative protein	---	AT5G11960	1.08	0.11	1.02	0.342353	0.571006	-6.30
248658_at	chromosome condensation protein	ATSMC3	AT5G48600	1.08	0.11	1.02	0.342329	0.571006	-6.30
246876_at	putative protein various predicted lysine	---	AT5G26140	-1.08	-0.11	-1.02	0.342328	0.571006	-6.30
263430_at	unknown protein ;supported by full-leng	---	AT2G22270	-1.10	-0.14	-1.02	0.34239	0.571025	-6.30
246432_at	RGA-like protein putative member of th	RGL3	AT5G17490	1.16	0.21	1.02	0.342648	0.571413	-6.30
248996_at	unknown protein	RRS1	AT5G45260	-1.14	-0.19	-1.02	0.342691	0.571433	-6.30
245487_at	phytochrome D	PHYD	AT4G16250	-1.10	-0.14	-1.02	0.342709	0.571433	-6.30
263241_at	arginine decarboxylase identical to GP:1	ADC1	AT2G16500	1.30	0.37	1.02	0.342785	0.571517	-6.30
256111_at	unknown protein	---	AT1G16820	-1.10	-0.14	-1.02	0.342993	0.571823	-6.30
254190_at	Expressed protein ; supported by full-ler	---	AT4G23885	1.14	0.19	1.02	0.343279	0.572215	-6.30

265494_at	putative calmodulin-like protein	---	AT2G15680	-1.11	-0.16	-1.02	0.343278	0.572215	-6.30
245829_at	hypothetical protein predicted by genem	---	AT1G57780	-1.09	-0.12	-1.02	0.343362	0.572312	-6.30
263944_at	hypothetical protein predicted by genefi	---	---	1.07	0.10	1.02	0.343448	0.572413	-6.31
253413_at	putative protein Fe(II) transport protein,	ZIP9	AT4G33020	1.06	0.09	1.02	0.343475	0.572416	-6.31
259452_at	En/Spm-like transposon protein, putativ	---	---	1.09	0.12	1.02	0.343518	0.572446	-6.31
255065_s_a	putative arginase similar to arginases (F	---	AT4G08870 /	-1.33	-0.41	-1.02	0.343553	0.572462	-6.31
261533_at	hypothetical protein predicted by genem	---	AT1G71690	-1.11	-0.15	-1.02	0.343581	0.572468	-6.31
265500_at	putative non-LTR retroelement reverse t	---	---	1.14	0.19	1.02	0.343789	0.572712	-6.31
245907_at	ubiquitin-like protein ubiquitins - differen	---	AT5G09340	-1.07	-0.09	-1.02	0.34377	0.572712	-6.31
259902_at	disease resistance protein, putative sim	AtRLP13	AT1G74170	1.20	0.26	1.02	0.343803	0.572712	-6.31
252856_at	putative protein ; supported by cDNA: gi	---	AT4G39690	-1.07	-0.10	-1.02	0.343828	0.572712	-6.31
253316_s_a	putative protein hyphally regulated prot	---	AT4G33930 /	-1.14	-0.19	-1.02	0.34388	0.572757	-6.31
263353_at	hypothetical protein predicted by gensca	---	AT2G22070	-1.09	-0.12	-1.02	0.344042	0.572942	-6.31
259101_at	hypothetical protein predicted by gensca	---	AT3G11640	1.07	0.10	1.02	0.344029	0.572942	-6.31
267545_at	unknown protein	GRP23	AT2G32690	-1.12	-0.17	-1.02	0.344109	0.573012	-6.31
263889_at	putative ABC transporter	ATNAP12	AT2G37010	1.09	0.13	1.02	0.344236	0.573056	-6.31
267636_at	hypothetical protein predicted by gensca	---	AT2G42110	1.07	0.10	1.02	0.344208	0.573056	-6.31
252714_x_a	putative protein p97 homologous protei	---	AT3G43880	-1.07	-0.09	-1.02	0.344162	0.573056	-6.31
260084_at	chromatin structure regulator, putative s	---	AT1G63210	1.10	0.13	1.02	0.344221	0.573056	-6.31
248490_at	putative protein similar to unknown prote	---	AT5G50940	-1.23	-0.30	-1.02	0.344272	0.573075	-6.31
266354_at	putative homeodomain transcription fact	PFS2	AT2G01500	1.08	0.12	1.02	0.344378	0.573139	-6.31
258476_at	hypothetical protein predicted by genefi	---	AT3G02400	-1.12	-0.16	-1.02	0.344346	0.573139	-6.31
255371_at	putative RPP1-like disease resistance p	---	AT4G04110	1.08	0.10	1.02	0.344386	0.573139	-6.31
259159_at	unknown protein contains Pfam profile:F	ACBP4	AT3G05420	1.12	0.16	1.02	0.344422	0.573158	-6.31
266693_at	unknown protein predicted by genscan;s	MIOX2	AT2G19800	1.55	0.63	1.02	0.344477	0.573208	-6.31
262750_at	unknown protein ; supported by cDNA: g	---	AT1G28710	-1.10	-0.13	-1.02	0.344577	0.573332	-6.31
267472_at	putative basic blue protein (plantacyanin	ARPN	AT2G02850	-1.09	-0.13	-1.02	0.344644	0.573359	-6.31
245102_at	putative non-LTR retroelement reverse t	---	---	-1.13	-0.17	-1.02	0.344636	0.573359	-6.31
250300_at	putative protein various predicted prote	---	AT5G11890	-1.13	-0.18	-1.02	0.344834	0.573612	-6.31
248385_at	putative protein contains similarity to DN	---	AT5G51910	1.11	0.14	1.02	0.344846	0.573612	-6.31
267439_at	putative GDSL-motif lipase/hydrolase si	---	AT2G19060	1.09	0.13	1.02	0.344934	0.573675	-6.31
261542_at	unknown protein contains Pfam profile:	---	AT1G63560	1.10	0.13	1.02	0.344918	0.573675	-6.31
263237_at	hypothetical protein contains similarity to	---	AT1G10610	-1.15	-0.20	-1.02	0.344989	0.573723	-6.31
266901_at	hypothetical protein predicted by gensca	JAZ7	AT2G34600	1.28	0.35	1.02	0.345127	0.573793	-6.31
256270_at	unknown protein ; supported by cDNA: g	---	AT3G12300	1.09	0.12	1.02	0.345156	0.573793	-6.31

248782_at	palmitoyl-protein thioesterase precursor	---	AT5G47340	-1.08	-0.12	-1.02	0.34506	0.573793	-6.31
258693_at	unknown protein	---	AT3G08650	1.07	0.10	1.02	0.345136	0.573793	-6.31
256234_at	50S ribosomal protein L10, putative sim	---	AT3G12370	-1.08	-0.11	-1.02	0.345149	0.573793	-6.31
256794_at	ribosomal protein L27, putative similar t	---	AT3G22230	-1.20	-0.27	-1.01	0.345341	0.574058	-6.31
249431_at	polygalacturonase-like protein polygala	---	AT5G39910	1.13	0.18	1.01	0.345386	0.574091	-6.31
256988_s_a	adenosine triphosphatase, putative sim	---	AT3G28710 /	1.07	0.10	1.01	0.34546	0.574128	-6.31
251982_at	pectate lyase -like protein pectate lyase	---	AT3G53190	1.13	0.17	1.01	0.345455	0.574128	-6.31
262422_at	hypothetical protein similar to hypothetic	---	AT1G23440	1.10	0.14	1.01	0.345484	0.574128	-6.31
263046_at	unknown protein ; supported by cDNA:	GRP3S	AT2G05380	1.18	0.23	1.01	0.345559	0.574212	-6.31
266019_at	putative calmodulin-binding protein ; su	---	AT2G18750	-1.07	-0.10	-1.01	0.345624	0.574278	-6.31
254513_at	cytochrome p450 like protein cytochrom	CYP71A27	AT4G20240	1.07	0.10	1.01	0.345657	0.574291	-6.31
249356_at	putative protein predicted proteins, Arat	---	AT5G40520	-1.15	-0.20	-1.01	0.3457	0.574320	-6.31
246730_at	40S ribosomal protein S19 - like 40S rib	---	AT5G28060	-1.16	-0.21	-1.01	0.345894	0.574558	-6.31
256443_at	hypothetical protein similar to hypothetic	---	AT3G10960	1.16	0.22	1.01	0.345889	0.574558	-6.31
260819_at	b-Zip DNA binding protein, putative sim	AtbZIP52	AT1G06850	1.17	0.22	1.01	0.345953	0.574587	-6.31
265344_at	unknown protein predicted by genefinde	---	AT2G22660	-1.12	-0.17	-1.01	0.345992	0.574587	-6.31
267285_at	unknown protein	---	AT2G23690	1.16	0.21	1.01	0.346037	0.574587	-6.31
262391_at	geranyl geranyl pyrophosphate synthas	GGPS6	AT1G49530	-1.09	-0.12	-1.01	0.345962	0.574587	-6.31
251540_at	citrate synthase -like protein citrate syn	CSY1	AT3G58740	1.07	0.09	1.01	0.34603	0.574587	-6.31
252624_at	Expressed protein ; supported by full-ler	PSK1	AT3G44735	-1.20	-0.26	-1.01	0.346066	0.574593	-6.31
255754_at	auxin-induced protein, putative similar t	---	AT1G43040	1.06	0.09	1.01	0.346125	0.574649	-6.31
249416_at	putative protein DNA DAMAGE-RESPO	---	AT5G39570	-1.09	-0.12	-1.01	0.346269	0.574847	-6.31
256452_at	hypothetical protein predicted by genem	AtHB33	AT1G75240	1.33	0.41	1.01	0.346397	0.574885	-6.31
246896_at	extensin - like protein Pex1 extensin-lik	---	AT5G25550	1.10	0.13	1.01	0.346387	0.574885	-6.31
257412_at	unknown protein	---	AT1G22980	-1.08	-0.12	-1.01	0.346418	0.574885	-6.31
253318_at	extensin-like protein extensin-like prote	---	AT4G33970	-1.07	-0.10	-1.01	0.346333	0.574885	-6.31
265977_at	putative retroelement pol polyprotein	---	---	-1.07	-0.10	-1.01	0.346365	0.574885	-6.31
262073_at	unknown protein ;supported by full-lengt	ZCW32	AT1G59640	-1.17	-0.23	-1.01	0.34679	0.575460	-6.31
265952_at	unknown protein supported by cDNA: gi	---	AT2G37478 /	-1.08	-0.12	-1.01	0.34684	0.575479	-6.31
257649_at	predicted protein	ARR1	AT3G16857	1.08	0.11	1.01	0.346893	0.575479	-6.31
251799_at	putative protein P59 PROTEIN (HSP B	---	AT3G55520	-1.11	-0.16	-1.01	0.346902	0.575479	-6.31
258564_at	poly(A) polymerase, putative similar to	---	AT3G06560	-1.08	-0.11	-1.01	0.346874	0.575479	-6.31
266379_at	1,4-beta-xylan endohydrolase	---	AT2G14690	1.09	0.12	1.01	0.34694	0.575500	-6.31
263849_at	putative retroelement pol polyprotein	---	---	-1.11	-0.14	-1.01	0.346999	0.575556	-6.31
257281_s_a	hypothetical protein predicted by gensca	---	AT3G29680 /	1.10	0.14	1.01	0.347037	0.575577	-6.31

249326_at	unknown protein ; supported by cDNA:	SYN2	AT5G40840	-1.09	-0.12	-1.01	0.347103	0.575612	-6.31
261917_at	hypothetical protein similar to TMV resis	---	AT1G65920	-1.19	-0.25	-1.01	0.34713	0.575612	-6.31
256632_at	hypothetical protein	---	AT3G28330	1.10	0.14	1.01	0.347134	0.575612	-6.31
266989_at	putative myrosinase-binding protein ;su	JAL23	AT2G39330	-1.59	-0.67	-1.01	0.347193	0.575627	-6.31
264762_at	receptor kinase, putative similar to rece	---	AT1G61460	1.10	0.13	1.01	0.34719	0.575627	-6.31
250324_at	putative protein nitrilase/Fhit protein, Ca	---	AT5G12040	-1.10	-0.14	-1.01	0.347245	0.575671	-6.31
253786_at	receptor protein kinase-like protein rece	---	AT4G28650	1.09	0.12	1.01	0.347343	0.575728	-6.31
256993_at	unknown protein ; supported by cDNA:	---	AT3G28670	-1.07	-0.10	-1.01	0.347355	0.575728	-6.31
266515_at	putative tubby protein	AtTLP3	AT2G47900	-1.12	-0.16	-1.01	0.347345	0.575728	-6.31
247858_at	similar to unknown protein (pir||T34863)	TTL	AT5G58220	1.09	0.13	1.01	0.34745	0.575844	-6.31
249381_at	acidic ribosomal protein P2 -like acidic r	---	AT5G40040	1.10	0.14	1.01	0.347538	0.575947	-6.31
263681_at	hypothetical protein predicted by gensca	ORC6	AT1G26840	-1.12	-0.17	-1.01	0.3477	0.576174	-6.31
252454_at	putative protein various predicted prote	---	AT3G47130	-1.07	-0.09	-1.01	0.34773	0.576182	-6.31
267455_at	hypothetical protein predicted by gensc	---	AT2G33760	-1.11	-0.15	-1.01	0.347892	0.576330	-6.32
248702_at	unknown protein	---	AT5G48420	-1.07	-0.10	-1.01	0.347895	0.576330	-6.32
265177_at	OBP32pep protein, putative identical to	---	AT1G23640	1.07	0.10	1.01	0.347847	0.576330	-6.31
251533_at	putative protein several hypothetical pro	ATRBL15	AT3G58460	1.07	0.10	1.01	0.347948	0.576375	-6.32
257191_at	Expressed protein ; supported by full-ler	---	AT3G13175	-1.10	-0.13	-1.01	0.348004	0.576427	-6.32
248457_at	putative protein contains similarity to wa	---	AT5G51420	1.12	0.16	1.01	0.348054	0.576460	-6.32
255085_at	putative protein several hypothetical pro	---	---	-1.08	-0.12	-1.01	0.348075	0.576460	-6.32
255470_at	hypothetical protein	---	AT4G03040	1.09	0.13	1.01	0.348338	0.576813	-6.32
267053_s_a	peroxidase	---	AT2G38380 /	1.19	0.25	1.01	0.348322	0.576813	-6.32
252833_at	Expressed protein ; supported by cDNA	AGP3	AT4G40090	-1.08	-0.10	-1.01	0.348457	0.576958	-6.32
253540_at	putative protein various predicted prote	---	AT4G31615	-1.08	-0.11	-1.01	0.348477	0.576958	-6.32
245170_at	60S ribosomal protein L18, 5'partial No	---	AT2G47570	1.09	0.12	1.01	0.348543	0.577025	-6.32
248279_at	putative protein similar to unknown prote	ATIM	AT5G52910	-1.20	-0.26	-1.01	0.348583	0.577051	-6.32
253940_at	putative protein other Arabidopsis hypot	---	AT4G26950	-1.10	-0.14	-1.01	0.348621	0.577071	-6.32
246216_at	cytochrome P450 like protein ; supporte	ROT3	AT4G36380	-1.12	-0.17	-1.01	0.348668	0.577107	-6.32
261855_at	unknown protein	---	AT1G50510	-1.11	-0.14	-1.01	0.348748	0.577198	-6.32
257980_at	hypothetical protein predicted by genem	---	AT3G20760	-1.08	-0.12	-1.01	0.348809	0.577258	-6.32
254855_s_a	putative protein other predicted proteins	---	AT4G12140 /	1.10	0.14	1.01	0.348929	0.577413	-6.32
246913_at	GATA transcription factor - like GATA t	---	AT5G25830	-1.11	-0.15	-1.01	0.348978	0.577454	-6.32
258830_at	unknown protein	---	AT3G07090	1.18	0.24	1.01	0.349033	0.577502	-6.32
248562_at	putative protein strong similarity to unkn	---	AT5G49680	1.20	0.27	1.01	0.349127	0.577616	-6.32
257984_at	putative cell differentiation protein simil	---	AT3G20800	1.11	0.16	1.01	0.349209	0.577626	-6.32

252146_at	putative protein steroid sulfotransferase	---	AT3G51210	1.07	0.09	1.01	0.349181	0.577626	-6.32
251335_at	1-aminocyclopropane-1-carboxylate oxi	---	AT3G61400	1.13	0.18	1.01	0.349187	0.577626	-6.32
248144_at	glucose-6-phosphate/phosphate translo	GPT1	AT5G54800	1.10	0.14	1.01	0.349296	0.577728	-6.32
251009_at	putative protein predicted proteins, Arat	---	AT5G02640	1.19	0.25	1.01	0.349396	0.577851	-6.32
261461_at	hypothetical protein predicted by genem	---	AT1G07860	1.10	0.13	1.01	0.349434	0.577872	-6.32
254620_at	pollen-specific protein - like 18.3K prote	---	AT4G18590	-1.09	-0.12	-1.01	0.34949	0.577880	-6.32
266151_x_a	En/Spm transposon protein (mosaic-like	---	---	1.08	0.12	1.01	0.349515	0.577880	-6.32
248925_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G45910	1.11	0.14	1.01	0.34948	0.577880	-6.32
255418_at	predicted protein of unknown function	---	AT4G03200	-1.11	-0.15	-1.01	0.349576	0.577940	-6.32
252691_at	kinesin -like protein KLP2 protein, Xenc	---	AT3G44050	-1.07	-0.10	-1.00	0.349699	0.578101	-6.32
266831_at	putative squalene epoxidase	SQE2	AT2G22830	-1.27	-0.35	-1.00	0.349926	0.578198	-6.32
256413_at	hypothetical protein predicted by genem	---	AT3G11100	1.09	0.12	1.00	0.349904	0.578198	-6.32
251862_at	putative protein arm repeat containing p	PUB14	AT3G54850	1.08	0.11	1.00	0.349814	0.578198	-6.32
267158_at	putative expansin	EXP3	AT2G37640	1.52	0.60	1.00	0.349951	0.578198	-6.32
256216_at	calreticulin (crt1) identical to calreticulin	CRT1	AT1G56340 /	1.18	0.24	1.00	0.349983	0.578198	-6.32
266233_at	putative phloem-specific lectin	AtPP2-B8	AT2G02340	1.07	0.10	1.00	0.350008	0.578198	-6.32
258102_at	unknown protein contains Pfam profile:	---	AT3G23600	1.11	0.15	1.00	0.349874	0.578198	-6.32
246873_at	putative protein	---	AT5G26100	-1.08	-0.11	-1.00	0.350003	0.578198	-6.32
245664_at	hypothetical protein predicted by genem	---	AT1G28327	1.07	0.10	1.00	0.350011	0.578198	-6.32
263187_at	athila ORF 1, putative similar to Athila C	---	---	-1.06	-0.09	-1.00	0.349825	0.578198	-6.32
258394_at	unknown protein ;supported by full-leng	---	AT3G15530	1.17	0.23	1.00	0.350069	0.578252	-6.32
254876_at	putative phosphoribosylanthranilate trar	---	AT4G11610	1.11	0.15	1.00	0.350135	0.578319	-6.32
248312_at	unknown protein	---	AT5G52580	1.09	0.13	1.00	0.350201	0.578343	-6.32
248788_at	DNA-binding protein-like	---	AT5G47430	1.07	0.10	1.00	0.350175	0.578343	-6.32
263361_at	putative senescence-associated protein	TET13	AT2G03840	-1.08	-0.12	-1.00	0.35033	0.578448	-6.32
258346_at	hypothetical protein predicted by genem	---	AT3G22690	-1.09	-0.13	-1.00	0.350317	0.578448	-6.32
250620_at	embryo-specific protein 3 (ATS3) ; supp	ATS3	AT5G07190	1.08	0.11	1.00	0.35034	0.578448	-6.32
257527_at	hypothetical protein similar to hypotheti	---	AT3G01880	1.08	0.11	1.00	0.350463	0.578609	-6.32
260263_at	hypothetical protein predicted by genefir	JAG	AT1G68480	-1.07	-0.09	-1.00	0.350518	0.578657	-6.32
264949_at	unknown protein contains similarity to M	MAF1	AT1G77080	-1.07	-0.10	-1.00	0.350545	0.578660	-6.32
250045_at	putative protein mRNA (orf04), Arabido	---	AT5G17700	1.13	0.18	1.00	0.350667	0.578819	-6.32
248626_at	receptor protein kinase-like protein	---	AT5G48940	-1.08	-0.11	-1.00	0.350717	0.578861	-6.32
250658_at	C3HC4-type RING zinc finger protein-lik	---	AT5G07040	1.10	0.13	1.00	0.350803	0.578938	-6.32
265518_at	hypothetical protein predicted by gensca	---	AT2G06040	-1.13	-0.18	-1.00	0.350814	0.578938	-6.32
260255_at	putative protein kinase similar to p58 pr	---	AT1G74330	1.16	0.21	1.00	0.351094	0.579357	-6.32

258668_at	hypothetical protein predicted by gensca	---	AT3G08780	1.08	0.11	1.00	0.35112	0.579359	-6.32
266463_at	hypothetical protein predicted by genefir	---	AT2G47840	-1.09	-0.13	-1.00	0.351222	0.579485	-6.32
259855_at	putative asparaginyl-tRNA synthetase si	---	AT1G68420	-1.08	-0.11	-1.00	0.351307	0.579582	-6.32
256982_at	unknown protein	ECT2	AT3G13460	1.08	0.11	1.00	0.351387	0.579674	-6.32
248722_at	pyrophosphate-fructose-6-phosphate 1-	PFK2	AT5G47810	-1.06	-0.09	-1.00	0.351487	0.579795	-6.32
267335_s_a	putative beta-1,3-glucanase	---	AT1G64760 /	-1.14	-0.19	-1.00	0.351534	0.579831	-6.32
258509_at	protein kinase, putative similar to SERI	---	AT3G06620	-1.14	-0.19	-1.00	0.351562	0.579833	-6.32
260495_at	unknown protein similar to T11A07.10	---	AT2G41810	1.12	0.16	1.00	0.351586	0.579833	-6.32
246986_at	receptor-like protein kinase ;supported	RLK	AT5G67280	-1.28	-0.36	-1.00	0.351616	0.579841	-6.32
245084_at	putative MYB family transcription factor	AtMYB70	AT2G23290	-1.15	-0.20	-1.00	0.351793	0.579850	-6.32
251431_at	protein synthesis initiation factor - like e	EIF4G	AT3G60240	-1.07	-0.10	-1.00	0.351819	0.579850	-6.32
256533_at	unknown protein	---	AT1G33250	-1.12	-0.16	-1.00	0.351744	0.579850	-6.32
250226_at	putative protein contains similarity to N-a	---	AT5G13780	-1.09	-0.13	-1.00	0.351768	0.579850	-6.32
254842_at	putative protein other hypothetical prote	---	AT4G11950	1.10	0.14	1.00	0.351776	0.579850	-6.32
253091_at	cytochrome p450 - like protein cytochro	CYP81D2	AT4G37360	1.08	0.11	1.00	0.351788	0.579850	-6.32
252839_at	putative protein PIF1 protein - Caenorh	---	---	1.12	0.16	1.00	0.351825	0.579850	-6.32
260657_at	wall-associated kinase 2, putative simila	---	AT1G19390	1.09	0.13	1.00	0.35172	0.579850	-6.32
249540_at	4-coumarate--CoA ligase -like protein 4	---	AT5G38120	1.18	0.24	1.00	0.351858	0.579863	-6.32
245500_at	reverse transcriptase like protein	---	---	1.08	0.10	1.00	0.351935	0.579883	-6.32
246655_at	hypothetical protein	---	AT5G35230	1.08	0.11	1.00	0.351928	0.579883	-6.32
257297_at	unknown protein contains Pfam profiles	---	AT3G28040	-1.22	-0.28	-1.00	0.351972	0.579883	-6.32
247772_at	putative protein various predicted prote	---	AT5G58610	1.10	0.13	1.00	0.351955	0.579883	-6.32
255259_at	coded for by A. thaliana cDNA W43435	NDB2	AT4G05020	1.43	0.51	1.00	0.352152	0.580096	-6.32
252285_at	calmodulin-binding heat-shock - like pro	---	AT3G49050	-1.08	-0.12	-1.00	0.352144	0.580096	-6.32
249882_at	putative protein contains similarity to C2	---	AT5G22890	-1.07	-0.10	-1.00	0.352182	0.580104	-6.32
263020_at	unknown protein	---	AT1G23880	1.08	0.11	1.00	0.352249	0.580171	-6.32
250849_at	putative protein NAC2, Arabidopsis tha	NAC2	AT5G04410	-1.08	-0.11	-1.00	0.352399	0.580377	-6.33
266517_at	glycine decarboxylase complex H-protei	---	AT2G35120	-1.20	-0.26	-1.00	0.3525	0.580501	-6.33
257630_at	cytochrome P450, putative similar to cy	CYP71B16	AT3G26150	1.07	0.10	1.00	0.352542	0.580529	-6.33
267275_at	putative Na H antiporter	ATCHX13	AT2G30240	1.11	0.15	1.00	0.352755	0.580837	-6.33
246849_at	putative protein various predicted prote	---	AT5G26850	1.20	0.26	1.00	0.352809	0.580885	-6.33
252622_at	cysteine proteinase AALP, putative sim	---	AT3G45310	-1.09	-0.13	-1.00	0.352976	0.581036	-6.33
245844_at	hypothetical protein predicted by genem	---	AT1G26170	-1.08	-0.12	-1.00	0.352976	0.581036	-6.33
259726_at	Expressed protein ; supported by full-ler	SCRL6	AT1G60985	-1.07	-0.10	-1.00	0.352977	0.581036	-6.33
250928_at	putative protein	EIN2	AT5G03280	-1.08	-0.11	-1.00	0.353217	0.581389	-6.33

255771_at	hypothetical protein contains similarity to	---	AT1G18550	-1.08	-0.12	-1.00	0.353244	0.581390	-6.33
250773_at	putative protein similar to unknown prote	---	AT5G05430	-1.14	-0.19	-1.00	0.353358	0.581536	-6.33
256225_at	unknown protein ; supported by full-leng	---	AT1G56220	-1.12	-0.16	-1.00	0.353415	0.581589	-6.33
252595_at	putative transporter protein peptide tran	---	AT3G45690	1.09	0.12	1.00	0.353535	0.581669	-6.33
257798_at	unknown protein	NAI2	AT3G15950	1.12	0.16	1.00	0.353521	0.581669	-6.33
258722_at	putative pathogenesis-related protein si	---	AT3G09590	1.08	0.11	1.00	0.35354	0.581669	-6.33
257242_at	9-cis-epoxycarotenoid dioxygenase, pu	NCED6	AT3G24220	-1.08	-0.11	-1.00	0.353577	0.581688	-6.33
247161_at	putative protein similar to unknown prote	---	AT5G65810	1.11	0.14	1.00	0.353695	0.581839	-6.33
255357_at	putative pectinesterase	---	AT4G03930	-1.07	-0.10	-1.00	0.353747	0.581861	-6.33
256136_s_a	lectin receptor kinase, putative similar t	---	AT1G48720	-1.07	-0.09	-1.00	0.353759	0.581861	-6.33
252805_at	putative protein	---	AT3G42380	1.07	0.10	1.00	0.353872	0.581963	-6.33
251404_at	putative protein	---	AT3G60310	-1.09	-0.12	-1.00	0.353871	0.581963	-6.33
266980_at	60S ribosomal protein L35 ;supported b	---	AT2G39390	-1.16	-0.22	-1.00	0.354001	0.582132	-6.33
253767_at	12S cruciferin seed storage protein	CRU3	AT4G28520	1.08	0.11	1.00	0.354056	0.582181	-6.33
247000_at	casein kinase II alpha subunit ; support	CKA1	AT5G67380	1.10	0.14	1.00	0.354092	0.582186	-6.33
245097_at	Expressed protein ; supported by full-ler	---	AT2G40935	-1.07	-0.09	-1.00	0.35411	0.582186	-6.33
254426_at	putative protein predicted protein, Arabi	---	AT4G21240	1.08	0.11	1.00	0.354143	0.582199	-6.33
249924_at	kinase associated protein phosphatase	KAPP	AT5G19280	-1.10	-0.14	-0.99	0.354182	0.582220	-6.33
263926_at	hypothetical protein predicted by gensca	ATEME1A	AT2G21800	1.09	0.13	0.99	0.354312	0.582347	-6.33
259155_at	transcription initiation factor IIB (TFIIB) i	---	AT3G10330	-1.10	-0.14	-0.99	0.354361	0.582347	-6.33
257303_at	hypothetical protein predicted by gensca	---	AT3G30230	-1.08	-0.11	-0.99	0.354352	0.582347	-6.33
255453_at	hypothetical protein similar to A. thalian	---	AT4G02900	-1.11	-0.15	-0.99	0.354342	0.582347	-6.33
255505_at	SAR1/GTP-binding secretory factor ;su	ATSAR2	AT4G02080	-1.08	-0.11	-0.99	0.354399	0.582367	-6.33
254146_at	endo-1,4-beta-glucanase like protein er	ATGH9A3	AT4G24260	1.10	0.14	0.99	0.354483	0.582463	-6.33
267263_at	similar to late embryogenesis abundant	---	AT2G23110	1.46	0.55	0.99	0.354518	0.582480	-6.33
261983_at	protein kinase, putative similar to cdc2-	---	AT1G33770	1.14	0.19	0.99	0.354595	0.582564	-6.33
260557_at	putative endochitinase	---	AT2G43610	1.06	0.09	0.99	0.354662	0.582565	-6.33
255898_at	hypothetical protein similar to hypothetic	---	AT1G17930	-1.08	-0.11	-0.99	0.354646	0.582565	-6.33
253705_at	hexokinase ; supported by cDNA: gi_85	HXK1	AT4G29130	1.13	0.17	0.99	0.354672	0.582565	-6.33
249590_at	putative protein SIAH1, Brassica napus	---	AT5G37870	-1.07	-0.10	-0.99	0.354707	0.582579	-6.33
258328_at	putative zinc finger protein similar to aut	---	AT3G16090	1.06	0.09	0.99	0.354886	0.582832	-6.33
256388_at	unknown protein	---	AT3G06180	-1.09	-0.12	-0.99	0.354935	0.582870	-6.33
264710_at	putative phytochelatin synthetase simila	COBL6	AT1G09790	-1.08	-0.11	-0.99	0.354973	0.582891	-6.33
245983_at	5-formyltetrahydrofolate cyclo-ligase-lik	5-FCL	AT5G13050	-1.08	-0.11	-0.99	0.355341	0.583242	-6.33
255695_at	putative protein	UNE11	AT4G00080	1.07	0.10	0.99	0.355315	0.583242	-6.33

256910_at	hypothetical protein	---	AT3G24080	-1.10	-0.14	-0.99	0.355258	0.583242	-6.33
258339_at	putative dynein light chain protein simila	---	AT3G16120	1.07	0.09	0.99	0.355294	0.583242	-6.33
260953_at	transcriptional activator RF2a, putative	---	AT1G06070	-1.09	-0.12	-0.99	0.355323	0.583242	-6.33
249203_at	cytochrome P450	CYP71A16	AT5G42590	1.09	0.12	0.99	0.355296	0.583242	-6.33
263096_at	class 1 non-symbiotic hemoglobin (AHB	AHB1	AT2G16060	1.22	0.29	0.99	0.355401	0.583300	-6.33
262412_at	14-3-3 protein GF14omicron (grf11) sim	GRF11	AT1G34760	-1.10	-0.14	-0.99	0.355459	0.583354	-6.33
257627_at	cytochrome P450, putative contains Pfa	CYP71B25	AT3G26270	-1.09	-0.12	-0.99	0.355532	0.583430	-6.33
257684_s_a	unknown protein contains Pfam profile:	VCS	AT3G13290 /	-1.10	-0.13	-0.99	0.3556	0.583500	-6.33
262882_at	cytochrome p450, putative similar to cy	CYP89A2	AT1G64900	1.26	0.33	0.99	0.355746	0.583698	-6.33
259435_at	hypothetical protein similar to putative p	---	AT1G01450	1.07	0.10	0.99	0.355799	0.583743	-6.33
261437_at	hypothetical protein predicted by gensca	RAD51D	AT1G07745	-1.09	-0.12	-0.99	0.355838	0.583765	-6.33
250014_at	anthranilate phosphoribosyltransferase	TRP1	AT5G17990	1.32	0.40	0.99	0.355917	0.583852	-6.33
251605_at	receptor-like protein kinase several rece	---	AT3G57830	1.10	0.13	0.99	0.35597	0.583897	-6.33
259843_at	hypothetical protein predicted by genem	---	AT1G73570	-1.11	-0.16	-0.99	0.355997	0.583900	-6.33
251882_at	peptide transport - like protein peptide t	PTR1	AT3G54140	1.10	0.13	0.99	0.356053	0.583927	-6.33
247669_at	putative protein transcriptional represso	---	AT5G60170	-1.11	-0.15	-0.99	0.356065	0.583927	-6.33
267230_at	unknown protein	ARL	AT2G44080	1.51	0.60	0.99	0.356191	0.584092	-6.33
258737_at	unknown protein similar to unknown pro	---	AT3G05940	-1.08	-0.10	-0.99	0.356299	0.584185	-6.33
261410_at	metallothionein-like protein identical to S	MT1C	AT1G07610	1.27	0.35	0.99	0.356295	0.584185	-6.33
246574_at	copper amine oxidase, putative similar t	---	AT1G31670	1.16	0.22	0.99	0.35642	0.584257	-6.33
259236_at	unknown protein ; supported by full-leng	---	AT3G11530	-1.07	-0.10	-0.99	0.356409	0.584257	-6.33
265156_at	hypothetical protein predicted by gensca	---	AT1G31000	-1.09	-0.12	-0.99	0.356394	0.584257	-6.33
257246_at	pectinesterase, putative contains Pfam	---	AT3G24130	1.08	0.11	0.99	0.356506	0.584357	-6.33
258597_x_a	hypothetical protein predicted by genem	---	AT3G04390	1.07	0.10	0.99	0.356561	0.584404	-6.33
256189_at	hypothetical protein predicted by genem	---	AT1G30140	-1.07	-0.10	-0.99	0.35672	0.584623	-6.33
251977_at	putative protein auxin-induced protein 6	---	AT3G53250	-1.07	-0.10	-0.99	0.356745	0.584623	-6.33
249409_at	putative protein KED, Nicotiana tabacu	---	AT5G40340	-1.27	-0.35	-0.99	0.356915	0.584817	-6.33
261567_at	Expressed protein ; supported by cDNA	---	AT1G33055	1.25	0.32	0.99	0.356892	0.584817	-6.33
266512_at	unknown protein	---	AT2G47690	-1.07	-0.09	-0.99	0.356958	0.584845	-6.33
250990_at	serine/threonine-specific protein kinase	NAK	AT5G02290	1.16	0.22	0.99	0.357026	0.584914	-6.34
264489_at	putative squamosa-promoter binding pro	---	AT1G27370	-1.17	-0.23	-0.99	0.357126	0.585035	-6.34
265555_at	putative Mutator-like transposase relate	---	---	-1.06	-0.08	-0.99	0.357166	0.585060	-6.34
252992_at	putative protein phosphatase-2c protein	---	AT4G38520	1.13	0.17	0.99	0.357303	0.585241	-6.34
251920_at	uracil phosphoribosyltransferase-like pr	---	AT3G53900	-1.18	-0.24	-0.99	0.357375	0.585276	-6.34
248750_at	putative protein similar to unknown prote	---	AT5G47530	1.13	0.18	0.99	0.357369	0.585276	-6.34

264391_at	pectate lyase-like protein Similar to style	---	AT1G11920	1.08	0.11	0.99	0.357416	0.585301	-6.34
245820_at	allyl alcohol dehydrogenase, putative si	---	AT1G26320	1.08	0.11	0.99	0.357502	0.585399	-6.34
264404_at	putative cytochrome P450	CYP82F1	AT2G25160	1.10	0.14	0.99	0.357541	0.585422	-6.34
256726_at	unknown protein	---	AT3G52210	1.11	0.16	0.99	0.357706	0.585649	-6.34
267334_at	hypothetical protein predicted by gensca	---	AT2G19420	1.09	0.12	0.99	0.357822	0.585798	-6.34
247499_at	predicted protein	---	AT5G61865	-1.08	-0.11	-0.99	0.357855	0.585810	-6.34
247293_at	putative protein similar to unknown prote	---	AT5G64510	1.31	0.38	0.99	0.357917	0.585869	-6.34
248482_at	unknown protein	---	AT5G50970	-1.07	-0.10	-0.99	0.358082	0.586097	-6.34
265303_at	hypothetical protein	---	---	1.08	0.11	0.99	0.358215	0.586272	-6.34
256610_at	hypothetical protein predicted by genem	---	AT3G30845	-1.07	-0.09	-0.99	0.358309	0.586385	-6.34
266640_at	Expressed protein ; supported by full-ler	---	AT2G35585	1.10	0.14	0.99	0.358364	0.586433	-6.34
257732_at	unknown protein contains Pfam profile:	AtCASP	AT3G18480	-1.08	-0.11	-0.99	0.358433	0.586503	-6.34
247838_at	ubiquitin-specific protease 23 (UBP23),	UBP23	AT5G57990	-1.15	-0.20	-0.99	0.358483	0.586535	-6.34
253488_at	putative protein reproductive meristem	REM1	AT4G31610	1.10	0.14	0.99	0.358504	0.586535	-6.34
257794_at	hypothetical protein predicted by gensca	---	AT3G27050	-1.11	-0.15	-0.99	0.358534	0.586543	-6.34
263623_at	hypothetical protein predicted by gensca	---	AT2G04860	-1.07	-0.09	-0.99	0.358617	0.586594	-6.34
253141_at	putative protein hypothetical protein F2	---	AT4G35430 /	-1.09	-0.13	-0.99	0.358602	0.586594	-6.34
256861_at	beta-amylase, putative similar to beta-a	BAM1	AT3G23920	1.16	0.21	0.98	0.358864	0.586882	-6.34
257958_at	unknown protein similar to disease resis	---	AT3G25510	1.09	0.13	0.98	0.358888	0.586882	-6.34
256903_at	hypothetical protein	---	AT3G23960	1.08	0.11	0.98	0.358826	0.586882	-6.34
255193_at	score=10.1, E=1.2, N=1 contains simila	VFB3	AT4G07400	-1.09	-0.12	-0.98	0.358922	0.586882	-6.34
261545_at	unknown protein	---	AT1G63530	1.08	0.12	0.98	0.358919	0.586882	-6.34
254449_at	putative protein predicted protein, Caer	HEN1	AT4G20910	-1.11	-0.15	-0.98	0.358997	0.586963	-6.34
259797_at	unknown protein	---	---	-1.10	-0.14	-0.98	0.359037	0.586986	-6.34
261687_at	hypothetical protein predicted by genem	---	AT1G47280	1.08	0.11	0.98	0.359116	0.587031	-6.34
264558_at	putative protein kinase Similar to cdc2 p	---	AT1G09600	1.07	0.10	0.98	0.359111	0.587031	-6.34
255122_at	putative athila-like protein	---	---	-1.11	-0.15	-0.98	0.359142	0.587032	-6.34
257227_at	monodehydroascorbate reductase simila	MDAR4	AT3G27820	-1.09	-0.12	-0.98	0.359208	0.587056	-6.34
252836_at	putative protein predicted polyproteins -	---	---	1.07	0.10	0.98	0.35919	0.587056	-6.34
259440_at	hypothetical protein predicted by genem	BPS1	AT1G01550	1.08	0.11	0.98	0.359371	0.587140	-6.34
255460_at	hypothetical protein similar to A. thaliana	---	AT4G02800	1.07	0.10	0.98	0.359372	0.587140	-6.34
248200_at	O-methyltransferase ;supported by full-	ATOMT1	AT5G54160	1.24	0.31	0.98	0.359296	0.587140	-6.34
263313_at	14-3-3 protein (grf15), putative contains	---	AT2G10450	1.08	0.12	0.98	0.359388	0.587140	-6.34
267631_at	hypothetical protein predicted by genefir	---	AT2G42150	-1.07	-0.10	-0.98	0.359325	0.587140	-6.34
251590_at	pollen-specific protein BAN102-like prot	AGP23	AT3G57690	1.12	0.16	0.98	0.359432	0.587169	-6.34

263368_at	putative protein kinase contains a protei	---	AT2G20470	1.10	0.14	0.98	0.359493	0.587227	-6.34
256439_at	putative [Mn] superoxide dismutase sim	MSD1	AT3G10920	-1.10	-0.13	-0.98	0.359553	0.587284	-6.34
253877_at	Expressed protein ; supported by cDNA	---	AT4G27435	-1.18	-0.24	-0.98	0.359597	0.587313	-6.34
246068_at	putative protein ribosomal protein S8 -	---	AT5G20290	-1.16	-0.22	-0.98	0.35963	0.587324	-6.34
258383_at	hypothetical protein predicted by gensca	---	AT3G15440	-1.19	-0.25	-0.98	0.359722	0.587433	-6.34
261328_at	unknown protein	---	AT1G44835	-1.09	-0.12	-0.98	0.359832	0.587571	-6.34
251103_at	putative protein protein phosphatase ty	---	AT5G01700	1.11	0.15	0.98	0.359905	0.587647	-6.34
266268_at	unknown protein predicted by genefinde	---	AT2G29510	-1.07	-0.10	-0.98	0.359985	0.587735	-6.34
252480_at	putative protein methyl-CpG-binding pr	MBD5	AT3G46580	-1.07	-0.09	-0.98	0.360013	0.587740	-6.34
254836_at	flavonoid 3,5-hydroxylase like protein fl	CYP706A7	AT4G12330	1.07	0.09	0.98	0.360103	0.587844	-6.34
255901_at	GDP-L-fucose synthetase, putative sim	GER2	AT1G17890	1.13	0.18	0.98	0.360389	0.588101	-6.34
258569_at	ribosomal protein L17, putative similar t	emb2171	AT3G04400	-1.12	-0.17	-0.98	0.360375	0.588101	-6.34
256920_at	hypothetical protein predicted by genem	---	AT3G18980	1.07	0.10	0.98	0.360386	0.588101	-6.34
261645_at	hypothetical protein similar to hypothetic	---	---	-1.07	-0.10	-0.98	0.360336	0.588101	-6.34
246147_s_a	26S proteasome AAA-ATPase subunit	RPT6A	AT5G19990 /	1.09	0.12	0.98	0.360287	0.588101	-6.34
257408_at	unknown protein similar to A. thaliana pr	SON1	AT2G17310	1.09	0.13	0.98	0.360475	0.588199	-6.34
258003_at	expansin At-EXP5 identical to expansin	EXPA5	AT3G29030	1.31	0.39	0.98	0.360567	0.588265	-6.34
256765_at	aminotransferase, putative similar to an	POP2	AT3G22200	1.11	0.15	0.98	0.360542	0.588265	-6.34
267133_at	unknown protein	---	AT2G23440	1.09	0.12	0.98	0.360604	0.588283	-6.34
262858_at	major latex protein type3 identical to ma	---	AT1G14940	-1.08	-0.11	-0.98	0.360658	0.588286	-6.34
266855_at	unknown protein	---	AT2G26920	-1.09	-0.13	-0.98	0.360649	0.588286	-6.34
260569_at	putative signal recognition particle prote	---	AT2G43640	-1.09	-0.12	-0.98	0.360782	0.588448	-6.34
263641_at	putative non-LTR retroelement reverse t	---	---	-1.07	-0.10	-0.98	0.360838	0.588496	-6.34
245481_at	hypothetical protein	---	AT4G16170	-1.08	-0.11	-0.98	0.360941	0.588565	-6.34
266210_at	60S ribosomal protein L10A ; supported	PGY1	AT2G27530	-1.15	-0.20	-0.98	0.360957	0.588565	-6.34
245561_at	indole-3-acetate beta-glucosyltransferas	UGT84A4	AT4G15500	1.10	0.14	0.98	0.360924	0.588565	-6.34
258277_at	putative cytochrome P450 similar to cyt	PAD3	AT3G26830	1.77	0.82	0.98	0.361042	0.588662	-6.34
251758_at	transcription factor L2 ;supported by ful	---	AT3G55770	-1.09	-0.12	-0.98	0.361293	0.588729	-6.34
260248_at	heat shock protein 101 (HSP101) identi	ATHSP101	AT1G74310	1.17	0.23	0.98	0.361265	0.588729	-6.34
262149_at	hypothetical protein predicted by genem	---	AT1G52530	-1.11	-0.15	-0.98	0.361135	0.588729	-6.34
247020_at	putative protein strong similarity to unkn	---	AT5G67020	1.11	0.16	0.98	0.361225	0.588729	-6.34
258626_at	transfactor, putative similar to transfact	---	AT3G04450	-1.09	-0.13	-0.98	0.3613	0.588729	-6.34
256224_at	GTP-binding protein (SAR1B) identical t	ATSAR1B	AT1G56330	1.12	0.16	0.98	0.361198	0.588729	-6.34
247629_at	putative protein	SIZ1	AT5G60410	1.09	0.13	0.98	0.361205	0.588729	-6.34
249100_at	unknown protein	---	AT5G43560	1.08	0.12	0.98	0.361316	0.588729	-6.34

257355_at	hypothetical protein predicted by gensca	---	AT2G38150	1.08	0.11	0.98	0.361251	0.588729	-6.34
247538_at	ABC family transporter - like protein AB	ATH16	AT5G61700	1.06	0.09	0.98	0.361384	0.588798	-6.34
252440_at	aquaporin-like protein aquaporin - Vern	TIP5;1	AT3G47440	-1.07	-0.10	-0.98	0.361432	0.588834	-6.34
262835_at	Na+ H+ antiporter, putative similar to N	ATNHX8	AT1G14660	-1.08	-0.11	-0.98	0.361591	0.589051	-6.34
248256_at	developmental protein SINA (seven in a	---	AT5G53360	1.09	0.12	0.98	0.361674	0.589144	-6.34
267501_at	unknown protein	---	AT2G45540	1.10	0.14	0.98	0.361797	0.589260	-6.35
267479_at	hypothetical protein	---	AT2G02690	1.06	0.09	0.98	0.361774	0.589260	-6.35
260326_at	putative MYB family transcription factor	AtMYB103	AT1G63910	1.09	0.13	0.98	0.361897	0.589381	-6.35
264301_at	hypothetical protein contains similarity to	---	AT1G78780	1.22	0.29	0.98	0.362017	0.589491	-6.35
246290_at	calmodulin-3 ;supported by full-length c	CAM3	AT3G56800	1.07	0.10	0.98	0.362008	0.589491	-6.35
247083_at	unknown protein	---	AT5G66290	1.07	0.10	0.98	0.362044	0.589491	-6.35
261529_at	hypothetical protein contains similarity to	---	AT1G14430	-1.07	-0.10	-0.98	0.362068	0.589491	-6.35
255626_at	coded for by A. thaliana cDNA T20615	---	AT4G00780	-1.10	-0.13	-0.98	0.362174	0.589533	-6.35
258700_at	putative SF16 protein similar to SF16 pr	IQD1	AT3G09710	1.08	0.11	0.98	0.362197	0.589533	-6.35
262218_at	hypothetical protein contains similarity to	---	AT1G74770	1.12	0.17	0.98	0.362125	0.589533	-6.35
265031_at	serine/threonine protein kinase, putative	---	AT1G61590	1.07	0.09	0.98	0.362157	0.589533	-6.35
265173_at	unknown protein	---	AT1G23530	1.08	0.11	0.98	0.362288	0.589580	-6.35
247359_at	acyltransferase-like protein ;supported b	---	AT5G63560	1.10	0.14	0.98	0.362297	0.589580	-6.35
266789_at	unknown protein ; supported by full-leng	---	AT2G29020	-1.08	-0.11	-0.98	0.362303	0.589580	-6.35
261415_at	globulin-like protein similar to GB:75953	---	AT1G07750	-1.16	-0.22	-0.98	0.362421	0.589687	-6.35
246207_at	RNA-binding like protein non-consensus	---	AT4G36960	-1.08	-0.11	-0.98	0.362408	0.589687	-6.35
250136_at	putative protein de novo DNA methyltra	DRM1	AT5G15380	1.15	0.21	0.98	0.36258	0.589861	-6.35
259028_at	putative C2H2-type zinc finger protein p	TAC1	AT3G09290	1.09	0.13	0.98	0.362556	0.589861	-6.35
248526_at	putative protein contains similarity to AT	---	AT5G50740	1.12	0.16	0.98	0.362852	0.590174	-6.35
252506_at	putative protein UDP-galactose transpo	UTR5	AT3G46180	-1.09	-0.12	-0.98	0.362799	0.590174	-6.35
262410_at	MAGE protein, putative identical to GB:	---	AT1G34770	-1.14	-0.19	-0.98	0.362901	0.590174	-6.35
249542_at	putative protein transcription factor Hap	NF-YC12	AT5G38140	-1.11	-0.15	-0.98	0.362859	0.590174	-6.35
250775_at	putative protein contains similarity to en	---	AT5G05460	1.16	0.21	0.98	0.362897	0.590174	-6.35
249979_s_a	putative protein	---	AT5G18860 /	1.21	0.27	0.98	0.362955	0.590184	-6.35
257518_at	hypothetical protein	---	AT3G03880	-1.07	-0.09	-0.98	0.362959	0.590184	-6.35
255106_at	putative protein hypothetical proteins of	---	---	1.07	0.09	0.98	0.363087	0.590349	-6.35
266371_at	calmodulin-like protein identical to GB:X	---	AT2G41410	1.18	0.23	0.98	0.363171	0.590394	-6.35
256115_at	unknown protein ; supported by cDNA: g	---	AT1G16880	1.13	0.17	0.98	0.363159	0.590394	-6.35
252397_at	hypothetical protein	---	AT3G47980	1.12	0.17	0.98	0.363192	0.590394	-6.35
251272_at	homeobox-leucine zipper protein ATHB-	ATHB-12	AT3G61890	1.25	0.32	0.98	0.363248	0.590444	-6.35

247208_at	nodulin-like ;supported by full-length cD	---	AT5G64870	1.09	0.12	0.97	0.363427	0.590554	-6.35
256165_at	hypothetical protein predicted by genem	---	AT1G48780	-1.11	-0.15	-0.97	0.363471	0.590554	-6.35
265799_at	unknown protein ; supported by cDNA:	---	AT2G35680	-1.09	-0.12	-0.97	0.363445	0.590554	-6.35
255286_at	see T14P8.10 (GB:AF069298)	---	AT4G04650	1.12	0.16	0.97	0.36335	0.590554	-6.35
246023_at	ethylene-insensitive3-like2 (EIL2)	EIL2	AT5G21120	1.08	0.11	0.97	0.363471	0.590554	-6.35
251247_at	hypothetical protein	---	AT3G62140	-1.10	-0.14	-0.97	0.363446	0.590554	-6.35
262125_at	heat shock protein, putative similar to m	EDA1	AT1G59680	1.08	0.12	0.97	0.363555	0.590605	-6.35
263819_x_a	putative TNP2-like transposon protein re	---	---	1.06	0.09	0.97	0.363545	0.590605	-6.35
251267_at	putative protein hypothetical protein BA	---	AT3G62330	1.10	0.13	0.97	0.363658	0.590625	-6.35
254451_at	adrenodoxin - like protein adrenodoxin	---	AT4G21090	-1.06	-0.09	-0.97	0.363628	0.590625	-6.35
254361_at	Expressed protein ; supported by full-ler	---	AT4G22212	1.11	0.15	0.97	0.363642	0.590625	-6.35
247770_at	putative protein predicted proteins, Arat	---	AT5G58930	-1.22	-0.29	-0.97	0.36367	0.590625	-6.35
257181_at	hypothetical protein	---	AT3G13190	-1.10	-0.14	-0.97	0.363762	0.590731	-6.35
250657_at	steroid sulfotransferase-like protein	ST2B	AT5G07000	1.18	0.24	0.97	0.364053	0.591119	-6.35
249280_at	unknown protein	---	AT5G41940	1.11	0.14	0.97	0.364045	0.591119	-6.35
261065_at	hypothetical protein predicted by genem	---	AT1G07500	-1.11	-0.15	-0.97	0.364156	0.591131	-6.35
261841_at	BTG1 binding factor 1, putative similar t	---	AT1G15920	-1.08	-0.11	-0.97	0.364164	0.591131	-6.35
257015_at	hypothetical protein predicted by genem	---	AT3G28680	1.09	0.12	0.97	0.364095	0.591131	-6.35
257118_at	hypothetical protein	---	AT3G20180	-1.07	-0.10	-0.97	0.364155	0.591131	-6.35
247799_at	subtilisin-like serine protease contains s	---	AT5G58840	1.12	0.16	0.97	0.364191	0.591134	-6.35
258739_s_a	unknown protein similar to hypothetical p	---	AT1G54300 /	1.07	0.10	0.97	0.364291	0.591253	-6.35
252970_at	small auxin up RNA (SAUR-AC1) ;supp	SAUR15	AT4G38850	-1.14	-0.19	-0.97	0.364443	0.591415	-6.35
255350_at	putative transposon protein similar to de	---	---	-1.07	-0.10	-0.97	0.364438	0.591415	-6.35
266845_at	unknown protein	---	AT2G26110	1.14	0.19	0.97	0.364608	0.591558	-6.35
260589_at	hypothetical protein predicted by genem	---	AT1G53400	-1.07	-0.09	-0.97	0.364572	0.591558	-6.35
249294_at	unknown protein	---	AT5G41270	-1.13	-0.18	-0.97	0.364586	0.591558	-6.35
259771_at	unknown protein	---	AT1G29470	-1.12	-0.16	-0.97	0.364647	0.591579	-6.35
261369_at	protein kinase, putative similar to many	---	AT1G53060	1.11	0.15	0.97	0.364838	0.591846	-6.35
262044_s_a	hypothetical protein predicted by gensca	---	AT1G80210 /	-1.08	-0.11	-0.97	0.364924	0.591945	-6.35
261356_at	predicted protein	---	AT1G79660	-1.12	-0.16	-0.97	0.365162	0.592109	-6.35
249167_at	putative protein similar to unknown prote	---	AT5G42860	1.22	0.28	0.97	0.36521	0.592109	-6.35
254846_at	Expressed protein ; supported by full-ler	PLDGAMM	AT4G11830	1.10	0.14	0.97	0.365224	0.592109	-6.35
253431_at	putative protein predicted protein, Arabi	---	AT4G32440	1.09	0.12	0.97	0.365233	0.592109	-6.35
249836_at	unknown protein ;supported by full-leng	HMGB6	AT5G23420	-1.18	-0.24	-0.97	0.365079	0.592109	-6.35
246551_at	putative protein predicted proteins, Arat	---	AT5G15070	1.09	0.12	0.97	0.365121	0.592109	-6.35

252071_at	putative protein DNA helicase homolog	---	AT3G51690	1.06	0.09	0.97	0.365137	0.592109	-6.35
247828_at	putative protein KIAA0066, Homo sapie	---	AT5G58510	1.07	0.10	0.97	0.365095	0.592109	-6.35
266977_at	putative phospholipase	---	AT2G39420	-1.21	-0.28	-0.97	0.365334	0.592230	-6.35
253025_at	hypothetical protein	---	AT4G38120	-1.12	-0.17	-0.97	0.365561	0.592430	-6.35
252267_at	putative protein NITROGEN REGULAT	---	AT3G49640	-1.12	-0.16	-0.97	0.365541	0.592430	-6.35
262293_at	heat-shock protein 90, putative identica	---	AT1G27640	1.12	0.17	0.97	0.365529	0.592430	-6.35
261228_at	C-8,7 sterol isomerase identical to GB:A	HYD1	AT1G20050	-1.10	-0.14	-0.97	0.365522	0.592430	-6.35
260770_at	RING-H2 finger protein RHA3a, putativ	---	AT1G49200	-1.41	-0.49	-0.97	0.365734	0.592669	-6.35
250365_at	putative protein serine threonine tyrosin	---	AT5G11410	-1.14	-0.18	-0.97	0.365798	0.592730	-6.35
266547_at	similar to eyes absent protein ;supporte	ATEYA	AT2G35320	-1.07	-0.09	-0.97	0.365913	0.592874	-6.35
265157_at	putative reverse transcriptase similar to	---	---	-1.08	-0.11	-0.97	0.365976	0.592933	-6.35
259108_at	putative translationally controlled tumor	---	AT3G05540	1.07	0.10	0.97	0.366107	0.593103	-6.35
257365_x_a	putative antifungal protein	PDF1.2b	AT2G26020	-1.49	-0.58	-0.97	0.366173	0.593169	-6.35
249521_at	putative protein strong similarity to unkn	---	AT5G38690	-1.08	-0.11	-0.97	0.366251	0.593252	-6.35
252324_at	protein translocation complex sec61 ga	---	AT3G48570	1.09	0.12	0.97	0.366314	0.593311	-6.35
261575_at	hypothetical protein contains similarity t	---	AT1G01130	1.13	0.18	0.97	0.366339	0.593311	-6.35
260650_at	Expressed protein ; supported by full-ler	TOM2B	AT1G32370	1.07	0.10	0.97	0.366373	0.593323	-6.35
260476_at	unknown protein	---	AT1G11060	1.10	0.14	0.97	0.366514	0.593510	-6.36
246033_at	hydroxymethylbilane synthase ;support	HEMC	AT5G08280	-1.11	-0.16	-0.97	0.366574	0.593526	-6.36
254227_at	putative protein chS-Rex-b - Gallus gall	BTI1	AT4G23630	-1.12	-0.16	-0.97	0.366576	0.593526	-6.36
264385_at	unknown protein	---	AT1G12020	-1.13	-0.17	-0.97	0.366605	0.593530	-6.36
246312_at	G-protein, putative contains Pfam profil	XLG3	AT1G31930	1.20	0.26	0.97	0.366735	0.593700	-6.36
259056_at	hypothetical protein similar to Ku70-bind	---	AT3G03420	-1.10	-0.14	-0.97	0.366763	0.593703	-6.36
245544_at	UTP-glucose glucosyltransferase like pr	---	AT4G15270	1.09	0.12	0.97	0.366913	0.593863	-6.36
259195_at	hypothetical protein predicted by gensca	---	AT3G01730	1.09	0.12	0.97	0.366914	0.593863	-6.36
257716_at	hypothetical protein predicted by genem	---	AT3G18300	1.08	0.11	0.97	0.366999	0.593958	-6.36
257418_at	hypothetical protein predicted by genefir	---	AT1G30850	1.12	0.16	0.97	0.367127	0.594060	-6.36
258031_s_a	hypothetical protein similar to hypothetic	---	AT3G27480 /	-1.10	-0.14	-0.97	0.36714	0.594060	-6.36
245496_at	LET1 like protein	---	AT4G16440	-1.08	-0.11	-0.97	0.367099	0.594060	-6.36
255034_at	putative protein Phaseolus vulgaris cDN	---	---	1.07	0.10	0.97	0.367196	0.594067	-6.36
258561_at	putative hexose transporter similar to he	STP6	AT3G05960	-1.11	-0.15	-0.97	0.367177	0.594067	-6.36
267043_at	unknown protein	---	AT2G34330	-1.09	-0.12	-0.97	0.367231	0.594081	-6.36
245091_at	unknown protein	---	AT2G40910	1.08	0.12	0.97	0.36735	0.594133	-6.36
262915_at	response regulator 3 identical to respon	ARR3	AT1G59940	1.09	0.13	0.97	0.367367	0.594133	-6.36
247146_at	unknown protein	---	AT5G65610	-1.13	-0.18	-0.97	0.367315	0.594133	-6.36

255239_at	contains similarity to Arabidopsis thalian	---	---	1.06	0.08	0.97	0.367359	0.594133	-6.36
247966_at	putative protein contains similarity to unl	---	AT5G56610	1.08	0.11	0.97	0.367426	0.594186	-6.36
262796_at	cysteine proteinase XCP2 identical to pa	XCP2	AT1G20850	1.23	0.30	0.97	0.367472	0.594198	-6.36
264242_at	hypothetical protein predicted by genem	---	AT1G54640	-1.06	-0.09	-0.97	0.367486	0.594198	-6.36
251257_at	ADP-ribosylation factor-like protein ADF	ATARFA1I	AT3G62290	1.12	0.16	0.97	0.367535	0.594235	-6.36
258320_at	hypothetical protein predicted by genem	---	AT3G22710	1.07	0.10	0.97	0.367693	0.594339	-6.36
258695_at	putative ascorbate peroxidase strong sir	APX2	AT3G09640	1.10	0.13	0.97	0.367648	0.594339	-6.36
250319_at	putative protein strong similarity to unkn	---	AT5G12120	-1.06	-0.09	-0.97	0.367703	0.594339	-6.36
265665_at	cysteine proteinase contains similarity to	---	AT2G27420	-1.07	-0.10	-0.97	0.367687	0.594339	-6.36
245429_at	Bax inhibitor-1-like protein	---	AT4G17580	1.06	0.09	0.97	0.36784	0.594518	-6.36
263526_at	hypothetical protein predicted by gensca	---	AT2G24830	1.07	0.10	0.97	0.367873	0.594529	-6.36
264485_at	unknown protein ; supported by cDNA: g	---	AT1G77220	1.08	0.11	0.96	0.367957	0.594622	-6.36
265498_at	putative C2H2-type zinc finger protein lil	---	AT2G15740	-1.07	-0.09	-0.96	0.368342	0.595203	-6.36
255373_s_a	putative protein	---	---	1.09	0.12	0.96	0.36839	0.595239	-6.36
265463_at	unknown protein	IRX9	AT2G37090	1.13	0.18	0.96	0.368443	0.595282	-6.36
253098_at	cytochrome P450-like protein	CYP81D3	AT4G37340	1.09	0.13	0.96	0.368632	0.595545	-6.36
267208_at	putative shaggy-like protein kinase dzeta	ASKdZeta	AT2G30980	1.06	0.09	0.96	0.368673	0.595569	-6.36
251378_at	putative protein	---	AT3G60660	-1.08	-0.11	-0.96	0.368791	0.595717	-6.36
261783_at	vacuolar assembly protein vps41, putat	---	AT1G08190	-1.09	-0.13	-0.96	0.36885	0.595729	-6.36
252956_at	farnesylated protein (ATFP6) ; supporte	ATFP6	AT4G38580	-1.21	-0.28	-0.96	0.368845	0.595729	-6.36
249102_at	patatin-like protein	---	AT5G43590	1.06	0.09	0.96	0.368941	0.595832	-6.36
261067_at	lectin, putative contains Pfam profile: PI	---	AT1G07460	-1.08	-0.11	-0.96	0.368976	0.595847	-6.36
263422_s_a	putative ubiquitin-like protein ; supporte	---	AT2G17190 /	1.07	0.10	0.96	0.369039	0.595906	-6.36
263146_at	lipase, putative similar to lipase GI:1145	GLIP2	AT1G53940	1.09	0.13	0.96	0.369166	0.596069	-6.36
266326_at	putative cytochrome b5 ;supported by f	CB5-C	AT2G46650	-1.32	-0.40	-0.96	0.369205	0.596091	-6.36
246846_at	putative protein	---	AT5G26760	-1.07	-0.10	-0.96	0.369338	0.596163	-6.36
261710_at	hypothetical protein identical to hypothe	---	AT1G32730	-1.09	-0.13	-0.96	0.369352	0.596163	-6.36
258539_at	putative RNA-binding protein contains F	---	AT3G06970	1.07	0.10	0.96	0.369348	0.596163	-6.36
249370_at	zinc finger - like protein predicted protei	---	AT5G40710	-1.06	-0.08	-0.96	0.369355	0.596163	-6.36
249004_at	unknown protein	---	AT5G44570	1.10	0.14	0.96	0.369488	0.596336	-6.36
257895_at	dihydrolipoamide dehydrogenase, putat	LPD1	AT3G16950	-1.17	-0.22	-0.96	0.369669	0.596586	-6.36
249697_at	unknown protein	---	AT5G35510	-1.08	-0.11	-0.96	0.369715	0.596619	-6.36
246452_at	putative protein predicted proteins - Aral	BPA1	AT5G16840	-1.08	-0.11	-0.96	0.369762	0.596622	-6.36
257383_at	hypothetical protein predicted by gensca	---	AT2G19630	-1.07	-0.10	-0.96	0.36977	0.596622	-6.36
253898_s_a	tryptophan synthase beta-subunit (TSB2	TSB2	AT4G27070 /	1.26	0.33	0.96	0.369842	0.596697	-6.36

251728_at	cysteine-tRNA ligase-like protein severa	---	AT3G56300	-1.08	-0.11	-0.96	0.36995	0.596829	-6.36
251789_at	serine/threonine-specific protein kinase	---	AT3G55450	-1.10	-0.14	-0.96	0.370038	0.596857	-6.36
267600_at	mitochondrial F1-ATPase, gamma subu	---	AT2G33040	1.12	0.17	0.96	0.37002	0.596857	-6.36
266976_at	putative phospholipase	---	AT2G39410	1.13	0.17	0.96	0.370046	0.596857	-6.36
250765_at	unknown protein ;supported by full-leng	---	AT5G05930	1.12	0.16	0.96	0.370121	0.596936	-6.36
252662_at	putative protein Sec24A protein, Homo	CEF	AT3G44340	1.08	0.12	0.96	0.370261	0.597111	-6.36
245109_at	hypothetical protein predicted by genefi	---	AT2G41520	-1.09	-0.12	-0.96	0.370282	0.597111	-6.36
252664_at	putative protein several hypothetical pro	---	AT3G44080	-1.06	-0.09	-0.96	0.370311	0.597115	-6.36
263294_at	hypothetical protein predicted by genefi	---	---	-1.11	-0.14	-0.96	0.370386	0.597193	-6.36
247346_at	diacylglycerol kinase	ATDGK2	AT5G63770	1.12	0.17	0.96	0.370443	0.597244	-6.36
245965_at	pectin methylesterase-like protein pecti	---	AT5G19730	1.15	0.20	0.96	0.370469	0.597244	-6.36
260213_at	putative protein kinase similar to protein	---	AT1G74490	-1.07	-0.09	-0.96	0.370524	0.597290	-6.36
252202_at	anthranilate N-hydroxycinnamoyl/benzo	---	AT3G50300	1.08	0.11	0.96	0.370643	0.597439	-6.36
246931_at	putative protein apoptosis-related prote	---	AT5G25170	1.27	0.34	0.96	0.370688	0.597470	-6.36
245175_at	putative protein disulfide-isomerase	UNE5	AT2G47470	1.15	0.20	0.96	0.370754	0.597535	-6.36
263243_at	putative glyoxalase II	GLX2-5	AT2G31350	1.09	0.13	0.96	0.370865	0.597641	-6.36
253697_at	nucleotide pyrophosphatase -like protei	---	AT4G29700	1.51	0.59	0.96	0.370873	0.597641	-6.36
245851_at	putative protein HERC2 - Homo sapien	KEG	AT5G13530	-1.08	-0.11	-0.96	0.371097	0.597744	-6.36
256154_at	hypothetical protein predicted by genem	---	AT3G08490	1.09	0.13	0.96	0.371093	0.597744	-6.36
261764_at	receptor lectin kinase, putative similar t	---	AT1G15530	-1.09	-0.12	-0.96	0.37099	0.597744	-6.36
267225_at	hypothetical protein predicted by gensca	---	AT2G44000	1.08	0.11	0.96	0.37102	0.597744	-6.36
255738_at	hypothetical protein predicted by genem	---	AT1G25570	-1.07	-0.10	-0.96	0.37112	0.597744	-6.36
255655_at	contains similarity to gag proteins	---	AT4G00980	-1.14	-0.18	-0.96	0.371105	0.597744	-6.36
252452_at	receptor protein kinase - like protein pro	---	AT3G47110	1.06	0.09	0.96	0.371005	0.597744	-6.36
245302_at	Expressed protein ; supported by cDNA	KAN3	AT4G17695	-1.14	-0.19	-0.96	0.371151	0.597751	-6.36
249437_at	putative protein predicted proteins - Aral	---	AT5G39990	1.10	0.13	0.96	0.371177	0.597751	-6.36
251721_s_a	alpha-soluble NSF attachment protein ;	ALPHA-SN	AT3G56190 /	-1.09	-0.12	-0.96	0.371274	0.597865	-6.36
257421_at	hypothetical protein predicted by genefi	---	AT1G12030	-1.15	-0.20	-0.96	0.371313	0.597885	-6.36
257259_at	hypothetical protein predicted by genem	---	AT3G22090	1.06	0.09	0.96	0.37135	0.597903	-6.37
261850_at	hypothetical protein predicted by genem	---	AT1G50470	1.11	0.15	0.96	0.371413	0.597962	-6.37
249584_s_a	Membrane integral protein (MIP) -like P	NIP4;1	AT5G37810 /	1.09	0.13	0.96	0.371467	0.597970	-6.37
254055_at	hypothetical protein	---	AT4G25330	1.07	0.10	0.96	0.371497	0.597970	-6.37
260751_at	unknown protein	SCD1	AT1G49040	1.13	0.18	0.96	0.371487	0.597970	-6.37
252271_s_a	putative protein CGI-141 protein- Homo	---	AT3G49420 /	-1.07	-0.09	-0.96	0.371765	0.598276	-6.37
255256_at	see GB:AC003952 similar to a family of	---	AT4G05080	-1.10	-0.13	-0.96	0.371757	0.598276	-6.37

264494_at	hypothetical protein predicted by genefi	---	AT1G27461	1.12	0.16	0.96	0.371726	0.598276	-6.37
249689_at	putative protein similar to unknown prote	---	AT5G36190	-1.06	-0.09	-0.96	0.371807	0.598301	-6.37
250737_at	putative protein similar to unknown prote	---	AT5G06370	1.11	0.15	0.96	0.371921	0.598442	-6.37
257766_at	auxin-inducible gene (IAA2) identical to	IAA2	AT3G23030	-1.13	-0.18	-0.96	0.371949	0.598445	-6.37
264328_at	putative IAA1 protein Match to IAA10 pr	IAA10	AT1G04100	1.12	0.16	0.96	0.372085	0.598622	-6.37
266825_at	unknown protein	---	AT2G22890	1.17	0.22	0.96	0.372188	0.598676	-6.37
259217_at	unknown protein similar to F16N3.20 G	---	AT3G03620	-1.08	-0.11	-0.96	0.372197	0.598676	-6.37
257441_at	putative GDSL-motif lipase/hydrolase si	---	AT2G04020	-1.09	-0.13	-0.96	0.372189	0.598676	-6.37
253293_at	Expressed protein ; supported by cDNA	---	AT4G33905	1.13	0.17	0.96	0.37225	0.598718	-6.37
248650_at	putative protein similar to unknown prote	---	AT5G49250	-1.11	-0.15	-0.96	0.37235	0.598795	-6.37
261875_at	receptor-like protein kinase, putative sir	---	AT1G50610	-1.07	-0.10	-0.96	0.372326	0.598795	-6.37
264723_at	putative salt-inducible protein similar to	---	AT1G22960	-1.07	-0.10	-0.96	0.372399	0.598832	-6.37
255693_s_a	putative BRCA2 homolog	BRCA2(IV	AT4G00020 /	-1.08	-0.11	-0.95	0.372637	0.599156	-6.37
245847_at	MYB DNA-binding - like protein myb-rel	MYB64	AT5G11050	1.09	0.13	0.95	0.372653	0.599156	-6.37
265898_at	hypothetical protein predicted by gensca	---	AT2G25690	1.14	0.19	0.95	0.372682	0.599159	-6.37
264403_at	unknown protein similarity to HSR201 p	---	AT2G25150	-1.07	-0.10	-0.95	0.372753	0.599232	-6.37
259872_at	putative translation initiation factor IF-2 s	---	AT1G76810	-1.07	-0.10	-0.95	0.372922	0.599462	-6.37
245977_at	glucose-6-phosphate 1-dehydrogenase	G6PD2	AT5G13110	1.16	0.21	0.95	0.373054	0.599631	-6.37
259453_at	gibberelin 20-oxidase, putative, 5' partia	ATGA20O	AT1G44090	1.11	0.15	0.95	0.37309	0.599646	-6.37
261584_at	CAF protein identical to RNA helicase/R	DCL1	AT1G01040	-1.12	-0.16	-0.95	0.373206	0.599791	-6.37
260612_at	hypothetical protein similar to hypothetic	---	AT1G53360	-1.07	-0.09	-0.95	0.373327	0.599943	-6.37
267608_at	hypothetical protein predicted by gensca	---	AT2G26770	-1.08	-0.11	-0.95	0.373403	0.600022	-6.37
265337_at	putative ADP-ribosylation factor ;suppo	TTN5	AT2G18390	-1.12	-0.17	-0.95	0.373463	0.600042	-6.37
252153_at	putative protein several hypothetical pro	---	AT3G51360	1.10	0.14	0.95	0.373467	0.600042	-6.37
253746_at	putative protein hypothetical protein - A	---	AT4G29100	1.17	0.23	0.95	0.373634	0.600257	-6.37
263801_at	putative Athila retroelement ORF1 prote	---	---	-1.07	-0.10	-0.95	0.373654	0.600257	-6.37
245457_s_a	disease resistance RPP5 like protein	---	AT4G16940 /	1.08	0.11	0.95	0.373695	0.600280	-6.37
252574_at	receptor like protein kinase receptor like	---	AT3G45430	1.09	0.12	0.95	0.373815	0.600430	-6.37
260485_at	putative amp-binding protein similar to a	---	AT1G68270	-1.08	-0.11	-0.95	0.374007	0.600697	-6.37
250652_at	putative protein similar to unknown prote	FLA21	AT5G06920	1.08	0.11	0.95	0.374045	0.600715	-6.37
262929_at	hypothetical protein ;supported by full-le	---	AT1G65720	1.11	0.15	0.95	0.374297	0.601079	-6.37
260005_at	unknown protein ;supported by full-leng	---	AT1G67920	1.29	0.37	0.95	0.37441	0.601217	-6.37
246742_at	TOPP8 serine/threonine protein phosph	TOPP8	AT5G27840	1.06	0.08	0.95	0.374463	0.601260	-6.37
258140_at	Expressed protein ; supported by cDNA	ALDH2C4	AT3G24503	1.22	0.29	0.95	0.374632	0.601338	-6.37
251858_at	aquaporin MIP - like protein aquaporin	PIP2;5	AT3G54820	1.13	0.18	0.95	0.37459	0.601338	-6.37

255913_at	kinase, putative similar to leaf rust resis	---	AT1G66980	-1.06	-0.09	-0.95	0.374636	0.601338	-6.37
267487_at	putative non-LTR retroelement reverse t	---	---	1.09	0.12	0.95	0.374643	0.601338	-6.37
258408_at	unknown protein similar to putative Na+/	ATCHX19	AT3G17630	-1.07	-0.10	-0.95	0.374597	0.601338	-6.37
245280_at	Expressed protein ; supported by cDNA	VRN2	AT4G16845	-1.08	-0.11	-0.95	0.374712	0.601405	-6.37
253342_at	Expressed protein ; supported by cDNA	PAA1	AT4G33520	-1.19	-0.26	-0.95	0.374774	0.601463	-6.37
264964_at	hypothetical protein predicted by genem	---	AT1G60460	1.10	0.13	0.95	0.374807	0.601474	-6.37
253292_at	Expressed protein ; supported by full-ler	---	AT4G33985	1.12	0.17	0.95	0.374879	0.601547	-6.37
256313_s_a	RNA-binding protein, putative contains	APUM17	AT1G35850 /	-1.06	-0.09	-0.95	0.374906	0.601548	-6.37
248253_at	putative protein contains similarity to pa	CRF3	AT5G53290	1.07	0.10	0.95	0.374972	0.601586	-6.37
246006_at	putative protein DIM1 protein, Homo sa	YLS8	AT5G08290	-1.07	-0.10	-0.95	0.374982	0.601586	-6.37
254005_at	subtilisin-like serine protease contains s	UNE17	AT4G26330	-1.11	-0.15	-0.95	0.375047	0.601647	-6.37
254871_at	Srw1 -like protein WD repeat protein Sr	CCS52A2	AT4G11920	-1.06	-0.09	-0.95	0.375146	0.601763	-6.37
262856_at	unknown protein contains Pfam profile:	---	AT1G14910	-1.10	-0.13	-0.95	0.375338	0.601988	-6.37
258301_at	hypothetical protein predicted by genem	---	---	1.06	0.09	0.95	0.375338	0.601988	-6.37
248074_at	putative protein similar to unknown prote	FLA1	AT5G55730	1.24	0.31	0.95	0.37537	0.601997	-6.37
258968_at	hypothetical protein similar to hypothetic	---	AT3G10460	1.08	0.11	0.95	0.375429	0.602048	-6.37
254633_at	putative protein (fragment)	MRH1	AT4G18640	-1.13	-0.17	-0.95	0.375604	0.602118	-6.37
245480_at	transcription factor like protein	---	AT4G16150	-1.06	-0.09	-0.95	0.375595	0.602118	-6.37
265321_at	putative Tub family protein	AtTLP2	AT2G18280	1.07	0.09	0.95	0.375601	0.602118	-6.37
261713_at	protein kinase, putative identical to bHL	MYC2	AT1G32640	-1.14	-0.18	-0.95	0.375584	0.602118	-6.37
266965_at	nodulin-like protein	---	AT2G39510	1.08	0.11	0.95	0.375511	0.602118	-6.37
248966_at	unknown protein ;supported by full-lengt	---	AT5G45360	-1.08	-0.12	-0.95	0.375685	0.602163	-6.37
253304_at	putative protein ;supported by full-lengt	---	AT4G33640	1.09	0.12	0.95	0.375662	0.602163	-6.37
249045_at	berberine bridge enzyme-like protein	---	AT5G44380	1.30	0.38	0.95	0.375771	0.602216	-6.37
245406_at	GTP-binding RAB2A like protein	ATRABB1/	AT4G17160	1.07	0.09	0.95	0.375766	0.602216	-6.37
267042_at	putative non-LTR retroelement reverse t	---	AT2G34320	1.08	0.10	0.95	0.375883	0.602353	-6.37
247251_at	cellulose synthase catalytic subunit	CESA6	AT5G64740	-1.11	-0.16	-0.95	0.375975	0.602377	-6.37
265419_at	putative secretory carrier-associated me	---	AT2G20840	1.10	0.13	0.95	0.376004	0.602377	-6.37
262909_at	serine/threonine protein phosphatase ty	PP2A-1	AT1G59830	1.08	0.11	0.95	0.375994	0.602377	-6.37
256800_at	hypothetical protein predicted by genem	---	AT3G20900	1.09	0.12	0.95	0.375942	0.602377	-6.37
256948_at	unknown protein	---	AT3G18930	1.07	0.10	0.95	0.37606	0.602425	-6.37
250063_at	disease resistance protein - like disease	CSA1	AT5G17880	1.10	0.14	0.95	0.376136	0.602505	-6.37
254069_at	putative protein similarity to antisense b	ATNUDT1	AT4G25434	-1.11	-0.15	-0.95	0.37621	0.602553	-6.37
263506_s_a	hypothetical protein	---	---	1.10	0.13	0.95	0.376232	0.602553	-6.37
251715_at	putative protein putative WRKY-type DI	---	AT3G56390	-1.07	-0.09	-0.95	0.376246	0.602553	-6.37

254740_s_a	glycine hydroxymethyltransferase - like	---	AT2G42450 /	1.26	0.34	0.95	0.376305	0.602605	-6.38
266790_at	expansin AtEx6 identical to GB U30480	ATEXPA6	AT2G28950	1.43	0.51	0.95	0.376421	0.602665	-6.38
259795_at	hypothetical protein predicted by genem	---	AT1G64290	1.09	0.12	0.95	0.376419	0.602665	-6.38
254129_at	putative tRNA isopentenyltransferase tF	IPT4	AT4G24650	1.07	0.10	0.95	0.376377	0.602665	-6.38
249220_at	putative protein strong similarity to unkn	---	AT5G42420	1.09	0.12	0.95	0.376465	0.602693	-6.38
267118_at	hypothetical protein	---	AT2G32590	1.09	0.12	0.95	0.37653	0.602713	-6.38
265688_at	putative calmodulin-binding protein	---	AT2G24300	-1.06	-0.08	-0.95	0.376505	0.602713	-6.38
251649_at	Ca2+-transporting ATPase-like protein	ACA11	AT3G57330	1.14	0.19	0.95	0.376598	0.602778	-6.38
245693_at	thioredoxin - like protein	WCRKC2	AT5G04260	1.09	0.12	0.95	0.376699	0.602807	-6.38
263839_at	putative cis-Golgi SNARE protein ;supp	MEMB11	AT2G36900	-1.12	-0.17	-0.95	0.376656	0.602807	-6.38
265764_at	hypothetical protein predicted by gensca	---	AT2G48060	-1.09	-0.13	-0.95	0.376678	0.602807	-6.38
250864_at	putative protein predicted proteins, Aral	---	AT5G03870	1.08	0.12	0.95	0.376722	0.602807	-6.38
256210_at	hypothetical protein	---	AT1G50950	-1.25	-0.32	-0.95	0.376755	0.602819	-6.38
257295_at	serine/threonine protein kinase, putative	GPK1	AT3G17420	1.14	0.19	0.95	0.37681	0.602864	-6.38
249012_at	flavonoid 3,5-hydroxylase-like; cytochro	CYP706A3	AT5G44620	1.08	0.11	0.95	0.376855	0.602895	-6.38
265963_s_a	40S ribosomal protein S5 identical to GF	ATRPS5B	AT2G37270 /	-1.16	-0.22	-0.95	0.376909	0.602938	-6.38
253960_at	putative protein various predicted prote	GAMT1	AT4G26420	1.09	0.13	0.95	0.376988	0.603023	-6.38
255736_at	unknown protein contains similarity to pe	---	AT1G25380	1.08	0.11	0.95	0.377064	0.603102	-6.38
246582_at	hypothetical protein predicted by genem	---	AT1G31750	-1.19	-0.25	-0.95	0.377113	0.603138	-6.38
250926_at	Expressed protein ; supported by full-ler	---	AT5G03555	-1.18	-0.24	-0.95	0.377168	0.603184	-6.38
258872_at	hypothetical protein similar to L1 specifi	HDG8	AT3G03260	1.12	0.16	0.95	0.37722	0.603224	-6.38
251159_at	hypothetical protein	---	AT3G63230	-1.11	-0.15	-0.94	0.377425	0.603510	-6.38
249191_at	putative protein similar to unknown prote	---	AT5G42760	-1.11	-0.14	-0.94	0.377658	0.603839	-6.38
267482_s_a	unknown protein	---	AT2G02770 /	-1.21	-0.28	-0.94	0.377773	0.603981	-6.38
248602_s_a	MADS-box protein-like	---	AT5G38620 /	1.06	0.09	0.94	0.377813	0.604002	-6.38
252488_at	glucuronosyl transferase-like protein glu	---	AT3G46700	-1.07	-0.10	-0.94	0.377895	0.604049	-6.38
249976_at	Serine/arginine rich protein - like Serine	SCL28	AT5G18810	1.08	0.11	0.94	0.377892	0.604049	-6.38
248086_at	putative protein similar to unknown prote	GEX1	AT5G55490	1.06	0.09	0.94	0.378101	0.604336	-6.38
259671_at	protein kinase, putative similar to GI:75	---	AT1G52290	1.20	0.26	0.94	0.378187	0.604390	-6.38
249133_at	putative protein strong similarity to unkn	TAF4	AT5G43130	1.06	0.09	0.94	0.378168	0.604390	-6.38
260875_at	hypothetical protein predicted by genem	SKP2A	AT1G21410	1.16	0.22	0.94	0.37829	0.604470	-6.38
248488_at	putative protein contains similarity to RN	---	AT5G51080	-1.08	-0.11	-0.94	0.378264	0.604470	-6.38
244994_at	NADH dehydrogenase ND5	---	---	-1.10	-0.13	-0.94	0.378393	0.604591	-6.38
255066_at	F-box protein family, AtFBW2 contains	---	AT4G08980	-1.07	-0.09	-0.94	0.378484	0.604695	-6.38
256577_at	unknown protein	---	AT3G28220	-1.33	-0.41	-0.94	0.37852	0.604710	-6.38

264003_at	Expressed protein ; supported by full-ler	GEM	AT2G22475	1.10	0.14	0.94	0.378628	0.604714	-6.38
257460_at	auxin induced protein, putative similar t	---	AT1G75580	1.07	0.10	0.94	0.378708	0.604714	-6.38
257841_at	nitrate transporter, putative similar to ni	---	AT3G25260	1.07	0.10	0.94	0.378651	0.604714	-6.38
260508_at	Unknown protein ; supported by cDNA:	GAMMA C	AT1G47260	1.07	0.10	0.94	0.378674	0.604714	-6.38
260118_s_a	hypothetical protein predicted by gensca	---	AT1G33940 /	-1.10	-0.14	-0.94	0.378629	0.604714	-6.38
267407_at	unknown protein	MEE27	AT2G34880	1.08	0.11	0.94	0.378641	0.604714	-6.38
262191_at	hypothetical protein contains similarity to	---	---	1.08	0.11	0.94	0.378703	0.604714	-6.38
259757_at	putative thioredoxin similar to protein dis	ATPDIL1-2	AT1G77510	1.28	0.36	0.94	0.378813	0.604838	-6.38
246402_at	jasmonate inducible protein, putative si	---	AT1G57570	1.07	0.09	0.94	0.378871	0.604862	-6.38
250592_at	putative protein contains similarity to unl	---	AT5G07740	1.09	0.13	0.94	0.378881	0.604862	-6.38
254454_at	hypothetical protein	EMB2271	AT4G21130	-1.08	-0.11	-0.94	0.378939	0.604912	-6.38
262074_at	glutathione S-transferase, putative simi	ATGSTU1	AT1G59670	-1.14	-0.19	-0.94	0.379126	0.605139	-6.38
253383_at	putative protein ;supported by full-lengt	---	AT4G32900	-1.12	-0.16	-0.94	0.379184	0.605139	-6.38
245192_at	F12A21.9 hypothetical protein	---	AT1G67780	-1.07	-0.09	-0.94	0.379187	0.605139	-6.38
256381_at	lipid transfer protein, putative contains	---	AT1G66850	-1.09	-0.12	-0.94	0.379136	0.605139	-6.38
257116_at	arginine methyltransferase, putative sim	PRMT6	AT3G20020	-1.09	-0.12	-0.94	0.379244	0.605187	-6.38
252152_at	putative protein several hypothetical pro	---	AT3G51350	1.07	0.10	0.94	0.379332	0.605287	-6.38
244945_at	cytochrome c biogenesis orf206	---	---	-1.10	-0.14	-0.94	0.379406	0.605362	-6.38
250242_at	putative protein similar to unknown prote	---	AT5G13620	1.07	0.10	0.94	0.3795	0.605439	-6.38
259972_at	unknown protein N-term similar to N-ter	CUC3	AT1G76420	1.13	0.17	0.94	0.379508	0.605439	-6.38
249791_at	amino acid transporter ; supported by c	AAP7	AT5G23810	-1.13	-0.18	-0.94	0.379564	0.605444	-6.38
245447_at	triacylglycerol lipase like protein	---	AT4G16820	1.27	0.34	0.94	0.379546	0.605444	-6.38
246540_at	nitrilase associated protein-like nitrilase	SP1L4	AT5G15600	-1.11	-0.16	-0.94	0.379593	0.605449	-6.38
250132_at	putative protein similar to unknown prote	KAN	AT5G16560	-1.16	-0.21	-0.94	0.379689	0.605501	-6.38
261779_at	hypothetical protein predicted by genem	---	AT1G76230	-1.06	-0.09	-0.94	0.379705	0.605501	-6.38
263816_at	putative CCHC-type zinc finger protein c	---	---	1.09	0.13	0.94	0.379663	0.605501	-6.38
252636_at	putative protein triacylglycerol lipase, P	---	AT3G44510	1.08	0.11	0.94	0.379795	0.605601	-6.38
259802_at	thionin identical to GI:1181531 from [Ar	THI2.1	AT1G72260	-1.58	-0.66	-0.94	0.379833	0.605620	-6.38
245930_at	transcriptional co-activator-like protein p	---	AT5G09240	-1.13	-0.18	-0.94	0.379973	0.605682	-6.38
262096_at	NAC1 identical to NAC1 GB:AAF21437	NAC1	AT1G56010	1.18	0.24	0.94	0.379978	0.605682	-6.38
253750_at	putative transcription factor leghemoglo	---	AT4G29000	1.11	0.15	0.94	0.379942	0.605682	-6.38
263026_at	hypothetical protein predicted by genem	---	AT1G24000	1.07	0.10	0.94	0.379922	0.605682	-6.38
256350_at	hypothetical protein contains similarity to	PGSIP4	AT1G54940	1.07	0.09	0.94	0.380135	0.605890	-6.38
259114_at	26S proteasome AAA-ATPase subunit R	RPT5A	AT3G05530	-1.07	-0.10	-0.94	0.380265	0.606020	-6.38
256547_at	receptor-like serine/threonine kinase, p	---	AT3G14840	1.17	0.22	0.94	0.38027	0.606020	-6.38

266731_at	unknown protein	---	AT2G03260	1.07	0.09	0.94	0.380322	0.606059	-6.38
250026_at	putative protein similar to unknown prote	---	AT5G18090	1.09	0.12	0.94	0.380656	0.606450	-6.38
248193_at	homogentisate 1,2-dioxygenase ;suppo	HGO	AT5G54080	1.15	0.21	0.94	0.38065	0.606450	-6.38
263162_at	hypothetical protein predicted by genem	---	AT1G54150	-1.07	-0.09	-0.94	0.380673	0.606450	-6.38
256977_at	hypothetical protein predicted by genen	---	---	-1.08	-0.11	-0.94	0.380653	0.606450	-6.38
263060_s_a	hypothetical protein	---	AT2G07679 /	-1.11	-0.16	-0.94	0.381049	0.607007	-6.38
267627_at	putative ATP-dependent RNA helicase	---	AT2G42270	-1.15	-0.20	-0.94	0.38134	0.607404	-6.39
265654_s_a	En/Spm-like transposon protein related	---	---	1.07	0.09	0.94	0.381351	0.607404	-6.39
264785_at	putative non-LTR retroelement reverse t	---	---	1.08	0.11	0.94	0.381437	0.607497	-6.39
264112_at	putative 1,3-beta-D-glucan synthase	CALS5	AT2G13680	1.09	0.12	0.94	0.381826	0.607863	-6.39
261436_at	protein kinase, putative (fragment) simil	---	AT1G07870	1.12	0.16	0.94	0.381806	0.607863	-6.39
253677_at	cytidine deaminase - like protein cytidin	---	AT4G29580	1.09	0.13	0.94	0.381795	0.607863	-6.39
245950_at	putative protein predicted protein, D. m	---	AT5G19570	-1.12	-0.17	-0.94	0.381738	0.607863	-6.39
250536_at	Expressed protein ; supported by full-ler	---	AT5G08535	-1.09	-0.12	-0.94	0.381816	0.607863	-6.39
248481_at	putative protein similar to unknown prote	---	AT5G50930	1.09	0.12	0.94	0.381779	0.607863	-6.39
263246_at	hypothetical protein predicted by gensca	---	AT2G31460	1.09	0.13	0.94	0.38187	0.607890	-6.39
258008_at	putative late embryogenesis abundant p	---	AT3G19430	1.08	0.10	0.94	0.381949	0.607931	-6.39
265684_at	unknown protein	---	AT2G24410	-1.06	-0.08	-0.94	0.381948	0.607931	-6.39
262152_s_a	hypothetical protein predicted by genem	---	AT1G52430 /	-1.07	-0.10	-0.94	0.381991	0.607955	-6.39
252105_at	protein phosphatase 2C-like protein pro	---	AT3G51470	-1.10	-0.13	-0.94	0.382036	0.607984	-6.39
248539_at	ribitol dehydrogenase-like ; supported b	---	AT5G50130	-1.10	-0.13	-0.94	0.382078	0.608009	-6.39
250711_at	cell division related protein-like	---	AT5G06110	-1.08	-0.11	-0.93	0.382196	0.608069	-6.39
249165_at	putative protein similar to unknown prote	ATIPK1	AT5G42810	-1.12	-0.16	-0.93	0.382191	0.608069	-6.39
245245_at	delta-aminolevulinic acid dehydratase (	hemb2	AT1G44318	-1.08	-0.11	-0.93	0.382195	0.608069	-6.39
265310_at	hypothetical protein predicted by genefir	---	AT2G20280	-1.07	-0.10	-0.93	0.38231	0.608109	-6.39
249591_at	putative protein predicted protein, Arabi	---	---	1.06	0.09	0.93	0.382322	0.608109	-6.39
258261_at	putative RING zinc finger protein contai	---	AT3G15740	1.14	0.19	0.93	0.382264	0.608109	-6.39
259539_at	axi 1 protein, putative similar to axi 1 pr	---	AT1G20550	-1.09	-0.12	-0.93	0.382354	0.608109	-6.39
248214_at	putative protein similar to unknown prote	---	AT5G53670	1.11	0.16	0.93	0.382333	0.608109	-6.39
259397_at	hypothetical protein predicted by genem	---	AT1G17680	-1.07	-0.10	-0.93	0.382421	0.608173	-6.39
256715_at	hypothetical protein predicted by genefi	MEE18	AT2G34090	1.12	0.16	0.93	0.38256	0.608309	-6.39
253991_at	putative nucleic acid binding protein sin	PEP	AT4G26000	-1.08	-0.11	-0.93	0.382544	0.608309	-6.39
253813_at	putative protein hypothetical protein - A	---	AT4G28150	1.08	0.12	0.93	0.382715	0.608471	-6.39
259510_at	hypothetical protein predicted by gensca	---	AT1G43970	1.06	0.08	0.93	0.382707	0.608471	-6.39
252803_at	putative protein various predicted prote	---	---	-1.09	-0.12	-0.93	0.382798	0.608561	-6.39

250894_s_a	putative protein proline-rich protein APC	---	AT5G03810 /	1.08	0.12	0.93	0.383063	0.608904	-6.39
265482_at	hypothetical protein contains a domain r	---	AT2G15780	1.78	0.83	0.93	0.383068	0.608904	-6.39
261179_at	unknown protein	---	AT1G04985	-1.09	-0.12	-0.93	0.38313	0.608919	-6.39
251990_at	putative protein MICRONUCLEAR LINK	---	AT3G53320	-1.12	-0.16	-0.93	0.383112	0.608919	-6.39
246488_at	steroid 5alpha-reductase-like protein st	---	AT5G16010	-1.15	-0.20	-0.93	0.383228	0.609031	-6.39
267478_at	hypothetical protein predicted by genscа	---	AT2G02700	1.06	0.09	0.93	0.383279	0.609070	-6.39
255674_at	probable plasma membrane intrinsic pro	PIP1;4	AT4G00430	-1.16	-0.21	-0.93	0.383383	0.609153	-6.39
245946_at	putative protein glyoxal oxidase precurs	---	AT5G19580	-1.10	-0.14	-0.93	0.383385	0.609153	-6.39
253109_at	putative protein predicted protein A_TM	MCA1	AT4G35920	-1.15	-0.20	-0.93	0.383564	0.609317	-6.39
254579_at	hypothetical protein ;supported by full-le	---	AT4G19400	-1.09	-0.13	-0.93	0.383576	0.609317	-6.39
265288_at	putative glutaredoxin ;supported by full-	---	AT2G20270	-1.10	-0.14	-0.93	0.383608	0.609317	-6.39
246737_at	putative protein	---	AT5G27710	-1.15	-0.20	-0.93	0.383578	0.609317	-6.39
247111_at	unknown protein	---	AT5G65880	-1.13	-0.17	-0.93	0.383621	0.609317	-6.39
265390_at	unknown protein ; supported by full-leng	---	AT2G20820	1.07	0.10	0.93	0.383934	0.609772	-6.39
250755_at	DnaJ-like protein ; supported by cDNA:	---	AT5G05750	1.10	0.13	0.93	0.383991	0.609819	-6.39
265251_at	unknown protein predicted by genscan	TET14	AT2G01960	1.08	0.11	0.93	0.38415	0.609987	-6.39
255022_at	NAM/NAP like protein nap gene, Arabid	ANAC070	AT4G10350	1.07	0.10	0.93	0.384124	0.609987	-6.39
267341_at	hypothetical protein predicted by genscа	---	AT2G44200	-1.11	-0.15	-0.93	0.384201	0.610026	-6.39
253819_at	receptor protein kinase like protein lecti	---	AT4G28350	1.46	0.55	0.93	0.38439	0.610283	-6.39
252347_at	ribosomal protein L13 homolog ribosom	---	AT3G48130	1.08	0.12	0.93	0.384454	0.610343	-6.39
252733_at	putative protein INDOLE-3-ACETIC AC	---	AT3G43120	-1.08	-0.10	-0.93	0.384499	0.610370	-6.39
266864_at	putative hydroxymethylglutaryl-CoA lyas	---	AT2G26800	1.10	0.14	0.93	0.384548	0.610406	-6.39
250457_at	splicing factor-like protein ; supported b	---	AT5G09880	-1.08	-0.11	-0.93	0.384659	0.610540	-6.39
264582_at	putative ovule-specific homeotic protein	HDG2	AT1G05230	-1.08	-0.11	-0.93	0.384695	0.610555	-6.39
262528_at	H+-transporting ATPase AHA10 Identica	AHA10	AT1G17260	1.10	0.13	0.93	0.384729	0.610566	-6.39
250393_at	serine/threonine protein phosphatase -l	---	AT5G10900	-1.08	-0.11	-0.93	0.384859	0.610730	-6.39
252614_at	serpin-like protein serpin - Hordeum vul	---	AT3G45220	1.06	0.08	0.93	0.385148	0.611146	-6.39
257944_at	SKP1/ASK1 (At9), putative similar to SK	ASK9	AT3G21850	1.07	0.10	0.93	0.385269	0.611295	-6.39
255352_at	putative transposon protein similar to att	---	---	-1.08	-0.11	-0.93	0.385418	0.611448	-6.39
257346_at	pseudogene, putative retroelement pol	---	---	-1.08	-0.11	-0.93	0.385412	0.611448	-6.39
252255_at	pectinesterase - like protein pectinester	---	AT3G49220	-1.19	-0.26	-0.93	0.38559	0.611634	-6.39
265981_s_a	putative replication protein A1	---	---	1.10	0.14	0.93	0.385584	0.611634	-6.39
255654_at	Similar to receptor kinase	---	AT4G00970	1.26	0.33	0.93	0.385654	0.611652	-6.39
245239_at	putative homeodomain-protein similarity	FWA	AT4G25530	-1.08	-0.11	-0.93	0.385652	0.611652	-6.39
251831_at	pectate lyase -like protein pectate lyase	---	AT3G55140	-1.06	-0.08	-0.93	0.385942	0.611797	-6.39

258289_at	hypothetical protein predicted by genem	---	AT3G23450	-1.07	-0.09	-0.93	0.385948	0.611797	-6.39
255185_at	hypothetical protein	---	AT4G07740	1.08	0.11	0.93	0.385961	0.611797	-6.39
248020_at	putative protein strong similarity to unkn	---	AT5G56490	1.06	0.09	0.93	0.385872	0.611797	-6.39
246156_at	putative protein predicted proteins from	---	AT5G20090	1.09	0.12	0.93	0.385888	0.611797	-6.39
263984_at	hypothetical protein predicted by gensca	---	AT2G42670	-1.08	-0.11	-0.93	0.3858	0.611797	-6.39
246357_x_a	hypothetical protein	---	---	-1.08	-0.11	-0.93	0.385789	0.611797	-6.39
248161_at	unknown protein	---	AT5G54480	1.08	0.11	0.93	0.385873	0.611797	-6.39
247094_at	GDP-D-mannose 4,6-dehydratase; GM	GMD1	AT5G66280	1.08	0.11	0.93	0.386179	0.611992	-6.39
255145_at	hypothetical protein	---	---	1.09	0.12	0.93	0.386191	0.611992	-6.39
264416_at	hypothetical protein similar to putative c	---	AT1G43140	-1.08	-0.11	-0.93	0.38615	0.611992	-6.39
248995_at	disease resistance protein-like	RRS1	AT5G45260	-1.07	-0.10	-0.93	0.386174	0.611992	-6.39
249155_at	unknown protein	---	AT5G43480	1.06	0.08	0.93	0.386457	0.612371	-6.39
245703_at	S-adenosyl-L-methionine:salicylic acid c	---	AT5G04380	-1.07	-0.10	-0.93	0.386519	0.612427	-6.40
262902_x_a	hypothetical protein similar to putative M	---	AT1G59930	-1.13	-0.18	-0.93	0.386628	0.612557	-6.40
267593_at	similar to disease resistance protein (Cf-	AtRLP25	AT2G33030	1.07	0.09	0.93	0.38678	0.612755	-6.40
259180_at	unknown protein	---	AT3G01680	1.23	0.30	0.92	0.386974	0.612896	-6.40
264200_at	putative invertase Similar to LIM17 gene	---	AT1G22650	1.13	0.17	0.92	0.386983	0.612896	-6.40
247691_at	heat shock protein 18 ;supported by full	HSP18.2	AT5G59720	1.08	0.11	0.93	0.386905	0.612896	-6.40
258190_at	hypothetical protein predicted by genem	---	AT3G29080	1.07	0.10	0.92	0.387057	0.612896	-6.40
246616_at	aspartyl protease-like	---	AT5G36260	1.13	0.17	0.92	0.387014	0.612896	-6.40
257013_at	hypothetical protein contains Pfam profil	---	AT3G26920 /	1.08	0.11	0.93	0.386923	0.612896	-6.40
245220_at	hypothetical protein contains similarity to	---	AT1G59171	-1.06	-0.09	-0.92	0.387045	0.612896	-6.40
246889_at	putative protein various predicted prote	---	AT5G25470	1.09	0.13	0.92	0.387173	0.613020	-6.40
253611_at	RNase L inhibitor-like protein ribonuclea	NAP15	AT4G30300	1.08	0.11	0.92	0.387189	0.613020	-6.40
247134_at	putative protein similar to unknown prote	---	AT5G66230	1.07	0.10	0.92	0.387287	0.613107	-6.40
259423_at	unknown protein similar to putative MYB	---	AT1G13880	-1.11	-0.15	-0.92	0.387351	0.613107	-6.40
255851_at	hypothetical protein predicted by genem	---	AT1G67040	-1.09	-0.13	-0.92	0.387334	0.613107	-6.40
263982_at	hypothetical protein predicted by genefir	---	AT2G42860	1.10	0.13	0.92	0.387325	0.613107	-6.40
260336_at	putative protease IV similar to protease	SPPA	AT1G73990	-1.09	-0.13	-0.92	0.387505	0.613308	-6.40
264526_at	putative calcium ATPase very similar to	ECA3	AT1G10130	-1.09	-0.12	-0.92	0.387598	0.613412	-6.40
266077_at	putative non-LTR retroelement reverse t	---	---	1.08	0.11	0.92	0.38766	0.613467	-6.40
259127_at	putative translation initiation factor EIF-2	---	AT3G02270	1.09	0.12	0.92	0.387926	0.613846	-6.40
245689_at	phosphoglycerate mutase - like protein	---	AT5G04120	1.08	0.11	0.92	0.388001	0.613922	-6.40
250823_at	putative protein similar to unknown prote	---	AT5G05180	-1.08	-0.11	-0.92	0.388272	0.614147	-6.40
248509_at	Expressed protein ; supported by full-ler	---	AT5G50335	2.04	1.03	0.92	0.388278	0.614147	-6.40

249609_at	putative protein predicted proteins, Arat	---	---	-1.07	-0.10	-0.92	0.388201	0.614147	-6.40
254899_at	serine/threonine kinase-like protein rec	---	AT4G11490	1.10	0.14	0.92	0.388256	0.614147	-6.40
252189_at	cyclin D3-like protein Nicotiana tabacun	CYCD3;3	AT3G50070	-1.12	-0.17	-0.92	0.388183	0.614147	-6.40
257549_at	hypothetical protein predicted by genen	agl103	AT3G18650	1.10	0.13	0.92	0.388428	0.614342	-6.40
248198_at	putative protein contains similarity to WI	---	AT5G54200	1.16	0.22	0.92	0.388652	0.614516	-6.40
266749_at	putative protein kinase contains a protei	---	AT2G47060	1.17	0.22	0.92	0.388695	0.614516	-6.40
251160_at	inositol-1,4,5-trisphosphate 5-Phosphat	---	AT3G63240	1.08	0.11	0.92	0.388673	0.614516	-6.40
263459_at	ankyrin-like protein	---	AT2G31820	1.12	0.16	0.92	0.3887	0.614516	-6.40
258065_at	putative pyruvate kinase similar to PYR	---	AT3G25960	1.09	0.12	0.92	0.388649	0.614516	-6.40
266176_at	lectin-like protein	AtPP2-B2	AT2G02250	1.10	0.14	0.92	0.388601	0.614516	-6.40
246292_at	putative protein hnRNP A/B related pro	UBA2A	AT3G56860	-1.09	-0.12	-0.92	0.388853	0.614716	-6.40
259377_at	putative poly(A) binding protein similar t	PAB6	AT3G16380	1.10	0.14	0.92	0.38895	0.614826	-6.40
256961_at	transcription initiation factor TFIID-1 (TA	TBP1	AT3G13445	-1.08	-0.11	-0.92	0.389065	0.614885	-6.40
250947_at	putative protein	---	AT5G03450	-1.10	-0.14	-0.92	0.389063	0.614885	-6.40
260392_at	putative enolase similar to ENOLASE (2	---	AT1G74030	1.48	0.56	0.92	0.389121	0.614885	-6.40
258010_at	unknown protein similar to receptor-like	---	AT3G19300	-1.07	-0.10	-0.92	0.389122	0.614885	-6.40
256601_s_a	At14a-1 protein identical to At14a prote	AT14A	AT3G28290 /	-1.07	-0.10	-0.92	0.389103	0.614885	-6.40
246634_at	epsilon-adaptin, putative similar to epsi	---	AT1G31730	1.07	0.10	0.92	0.389166	0.614912	-6.40
265921_at	putative C2H2-type zinc finger protein li	---	AT2G18490	-1.07	-0.10	-0.92	0.389207	0.614925	-6.40
253055_at	putative protein cyclin delta-1, Arabidop	CYCD5;1	AT4G37630	-1.11	-0.15	-0.92	0.389228	0.614925	-6.40
262673_at	unknown protein	EMB1793	AT1G76060	-1.08	-0.11	-0.92	0.389275	0.614956	-6.40
255502_at	contains similarity to a protein kinase d	---	AT4G02410	1.34	0.42	0.92	0.389329	0.614957	-6.40
259589_at	unknown protein	---	AT1G28135	-1.09	-0.13	-0.92	0.389328	0.614957	-6.40
255704_at	putative proline-rich protein ;supported	---	AT4G00170	-1.06	-0.09	-0.92	0.389392	0.614971	-6.40
262016_at	unknown protein	---	---	1.06	0.08	0.92	0.389375	0.614971	-6.40
247281_at	immunophilin (gb|AAB57847.1) ;suppor	FKBP12	AT5G64350	-1.07	-0.09	-0.92	0.389545	0.615043	-6.40
261998_at	putative gag-pol polyprotein similar to g	---	---	1.08	0.11	0.92	0.3895	0.615043	-6.40
257121_at	hypothetical protein similar to auxin-indu	---	AT3G20220	-1.08	-0.11	-0.92	0.389533	0.615043	-6.40
250436_at	RNA binding protein - like rna binding p	---	AT5G10350	-1.08	-0.12	-0.92	0.389465	0.615043	-6.40
253774_at	NAM / CUC2 -like protein No apical me	anac074	AT4G28530	1.14	0.18	0.92	0.389612	0.615107	-6.40
255643_at	hypothetical protein	---	AT4G00840	-1.07	-0.10	-0.92	0.3898	0.615360	-6.40
251647_at	protein kinase - like protein wall-associa	---	AT3G57770	1.09	0.12	0.92	0.38984	0.615381	-6.40
252669_at	putative protein hypothetical protein F2	---	AT3G44100	-1.07	-0.10	-0.92	0.389881	0.615403	-6.40
256768_at	hypothetical protein predicted by genen	LDL2	AT3G13682	-1.06	-0.09	-0.92	0.389999	0.615546	-6.40
263245_at	hypothetical protein predicted by gensca	---	AT2G31470	-1.06	-0.09	-0.92	0.390037	0.615564	-6.40

262757_at	putative Na/H antiporter similar to gi|483	ATCHX1	AT1G16380	-1.08	-0.11	-0.92	0.390082	0.615593	-6.40
250930_at	putative protein P58 protein, Bos primig	ATP58IPK	AT5G03160	1.18	0.24	0.92	0.390145	0.615648	-6.40
265234_at	hypothetical protein	---	AT2G07721	-1.09	-0.12	-0.92	0.390243	0.615761	-6.40
247591_at	high-affinity nitrate transporter ACH1 - I	NRT2.4	AT5G60770	1.07	0.10	0.92	0.390316	0.615834	-6.40
255602_at	Expressed protein ; supported by full-ler	---	AT4G01026	-1.09	-0.12	-0.92	0.390395	0.615915	-6.40
257453_at	hypothetical protein predicted by gensca	---	AT1G65130	-1.09	-0.12	-0.92	0.390449	0.615959	-6.40
253734_at	putative serine/threonine-specific recep	---	AT4G29180	-1.08	-0.11	-0.92	0.390535	0.616051	-6.40
262831_at	cytochrome B561, putative similar to cy	---	AT1G14730	1.14	0.19	0.92	0.390655	0.616197	-6.40
257955_at	unknown protein ; supported by cDNA:	---	AT3G21810	1.16	0.22	0.92	0.390855	0.616428	-6.40
246712_at	putative protein various predicted prote	---	---	1.06	0.08	0.92	0.390837	0.616428	-6.40
266886_at	Expressed protein ; supported by full-ler	---	AT2G44745	1.09	0.12	0.92	0.3909	0.616454	-6.40
251020_at	ABC transporter -like protein NBD-like p	NAP9	AT5G02270	1.21	0.28	0.92	0.390925	0.616454	-6.40
266937_at	hypothetical protein predicted by genefir	---	AT2G18930	-1.08	-0.11	-0.92	0.39098	0.616459	-6.40
266069_at	putative RING zinc finger protein	MEE16	AT2G18650	-1.14	-0.19	-0.92	0.390982	0.616459	-6.40
245470_at	retrotransposon like protein	---	---	1.09	0.13	0.92	0.391064	0.616544	-6.40
254822_at	polyubiquitin-like protein polyubiquitin 6	UPL5	AT4G12570	-1.07	-0.10	-0.92	0.39112	0.616591	-6.40
250078_at	putative protein	ORC3	AT5G16690	-1.09	-0.12	-0.92	0.39116	0.616611	-6.40
252295_at	signal recognition particle subunit 9 - lik	---	AT3G49100	-1.11	-0.15	-0.92	0.391243	0.616657	-6.40
248069_at	unknown protein	---	AT5G55650	1.08	0.11	0.92	0.391224	0.616657	-6.40
254916_at	putative protein hypothetical protein F1	---	AT4G11340	1.08	0.11	0.92	0.391352	0.616785	-6.40
266193_at	unknown protein	---	AT2G39080	1.09	0.12	0.92	0.391439	0.616881	-6.40
253296_at	putative protein inositol 1,3,4-trisphosph	---	AT4G33770	1.07	0.10	0.92	0.391477	0.616898	-6.40
247155_at	2-oxoglutarate dehydrogenase, E1 com	---	AT5G65750	1.11	0.16	0.92	0.391694	0.617112	-6.40
245587_at	putative protein	---	AT4G15020	-1.14	-0.19	-0.92	0.391669	0.617112	-6.40
263081_at	putative homeodomain transcription fact	BLH5	AT2G27220	1.06	0.08	0.92	0.39169	0.617112	-6.40
260684_at	transcription factor, putative similar to G	NF-YA8	AT1G17590	1.11	0.15	0.92	0.391788	0.617217	-6.41
263609_at	putative LRR receptor protein kinase	---	AT2G16250	-1.07	-0.10	-0.91	0.391909	0.617280	-6.41
248833_at	Bax inhibitor-1 like ;supported by full-le	ATBI1	AT5G47120	1.09	0.13	0.91	0.391876	0.617280	-6.41
265790_at	putative amino acid or GABA permease	BAT1	AT2G01170	-1.11	-0.15	-0.91	0.391905	0.617280	-6.41
252211_at	putative protein predicted proteins, Aral	---	AT3G50220	1.07	0.10	0.91	0.392044	0.617385	-6.41
255548_at	putative CHP-rich zinc finger protein sim	---	AT4G01930	1.06	0.08	0.91	0.392016	0.617385	-6.41
262447_at	hypothetical protein contains similarity to	---	AT1G49250	1.07	0.10	0.91	0.392057	0.617385	-6.41
256825_at	unknown protein similar to cell wall-plas	CWLP	AT3G22120	1.79	0.84	0.91	0.392097	0.617405	-6.41
260231_at	putative RING zinc finger protein contai	---	AT1G74410	-1.10	-0.14	-0.91	0.39213	0.617414	-6.41
256184_at	epsilon subunit of mitochondrial F1-ATP	---	AT1G51650	1.11	0.15	0.91	0.392174	0.617442	-6.41

249983_at	putative protein S-receptor kinase PK3	---	AT5G18470	1.62	0.69	0.91	0.392333	0.617610	-6.41
254983_at	putative protein other hypothetical prote	MEE53	AT4G10560	-1.07	-0.09	-0.91	0.392362	0.617610	-6.41
258790_at	putative RNA-binding protein similar put	FLK	AT3G04610	-1.06	-0.08	-0.91	0.392361	0.617610	-6.41
266436_at	putative clathrin binding protein (epsin)	---	AT2G43160	1.14	0.19	0.91	0.392415	0.617650	-6.41
256327_at	unknown protein ;supported by full-lengt	GAUT9	AT3G02350	-1.10	-0.13	-0.91	0.392457	0.617673	-6.41
263467_at	unknown protein	---	AT2G31730	1.17	0.23	0.91	0.392583	0.617787	-6.41
266583_at	Expressed protein ; supported by cDNA	---	AT2G46220	-1.11	-0.15	-0.91	0.392581	0.617787	-6.41
257292_s_a	hypothetical protein contains Pfam profil	---	---	1.06	0.08	0.91	0.392723	0.617965	-6.41
263112_at	unknown protein Strong similarity to gi|2	---	AT1G03080	-1.08	-0.12	-0.91	0.392915	0.618224	-6.41
267081_at	putative phosphatidylinositol-4-phospha	PIP5K5	AT2G41210	1.07	0.10	0.91	0.392992	0.618302	-6.41
263001_at	hypothetical protein contains similarity t	TAF6B4	AT1G54360	1.14	0.19	0.91	0.393036	0.618329	-6.41
265987_at	unknown protein	---	AT2G24240	1.12	0.17	0.91	0.393137	0.618405	-6.41
266909_at	hypothetical protein predicted by gensca	BRM	AT2G46020	1.09	0.13	0.91	0.393139	0.618405	-6.41
245403_at	putative protein	---	AT4G17590	-1.07	-0.09	-0.91	0.393201	0.618446	-6.41
261393_at	NAM (no apical meristem)-like protein (	SMB	AT1G79580	1.07	0.09	0.91	0.393219	0.618446	-6.41
246646_at	putative protein ;supported by full-lengt	---	AT5G35090	-1.08	-0.11	-0.91	0.393293	0.618519	-6.41
258477_at	hypothetical protein predicted by genefi	NBS1	AT3G02680	-1.06	-0.09	-0.91	0.393378	0.618611	-6.41
261326_s_a	aminoacylase, putative similar to amino	---	AT1G44180 /	-1.12	-0.16	-0.91	0.393601	0.618876	-6.41
249539_at	putative protein AtPP - Brassica napus,	---	AT5G38100	1.09	0.13	0.91	0.393593	0.618876	-6.41
265729_at	putative glucan synthase	ATGSL03	AT2G31960	-1.10	-0.14	-0.91	0.393778	0.619070	-6.41
263598_at	putative xyloglucan-specific glucanase i	EXGT-A3	AT2G01850	-1.08	-0.11	-0.91	0.393756	0.619070	-6.41
252089_at	putative protein	---	AT3G52110	1.11	0.15	0.91	0.393852	0.619137	-6.41
256736_at	terpene synthase, putative similar to ter	---	AT3G29410	1.07	0.10	0.91	0.393876	0.619137	-6.41
251776_at	eukaryotic translation initiation factor 6	emb1624	AT3G55620	-1.10	-0.14	-0.91	0.393913	0.619153	-6.41
261103_s_a	O-methyltransferase 1, putative similar	---	AT1G62900 /	1.08	0.11	0.91	0.394014	0.619270	-6.41
263976_at	unknown protein	---	AT2G42700	-1.09	-0.12	-0.91	0.394064	0.619306	-6.41
255712_at	hypothetical protein similar to A. thaliana	---	AT4G00280	-1.07	-0.10	-0.91	0.394124	0.619357	-6.41
251474_at	putative protein diphthamide synthesis	---	AT3G59630	-1.08	-0.11	-0.91	0.39428	0.619560	-6.41
263264_at	histone H2A ; supported by full-length c	HTA8	AT2G38810	-1.14	-0.18	-0.91	0.394389	0.619660	-6.41
266902_at	hypothetical protein predicted by gensca	---	AT2G34580	1.07	0.09	0.91	0.394406	0.619660	-6.41
249897_at	putative protein strong similarity to unkn	---	AT5G22550	1.08	0.10	0.91	0.394425	0.619660	-6.41
263100_at	hypothetical protein predicted by gensca	AtPOT1a	AT2G05210	-1.11	-0.14	-0.91	0.394534	0.619756	-6.41
262660_at	putative protein kinase	VIK	AT1G14000	1.08	0.11	0.91	0.394557	0.619756	-6.41
249549_at	lipid transfer - like protein lipid transfer l	---	AT5G38180	1.08	0.11	0.91	0.394568	0.619756	-6.41
251043_s_a	putative protein various predicted prote	---	AT5G02330 /	-1.08	-0.11	-0.91	0.394676	0.619883	-6.41

255172_x_a	putative transposon protein similar to A	---	---	1.10	0.14	0.91	0.394737	0.619936	-6.41
259210_at	hypothetical protein nearly identical to h	HY2	AT3G09150	-1.10	-0.14	-0.91	0.39505	0.620299	-6.41
257599_at	60S ribosomal protein, putative similar t	---	AT3G24830	-1.17	-0.23	-0.91	0.395102	0.620299	-6.41
267274_at	putative mitochondrial carrier protein ;s	---	AT2G30160	-1.11	-0.15	-0.91	0.395104	0.620299	-6.41
260975_at	receptor-like serine/threonine kinase, p	---	AT1G53430	1.21	0.28	0.91	0.395064	0.620299	-6.41
258627_at	unknown protein similar to peroxisomal	PEX12	AT3G04460	1.10	0.13	0.91	0.394996	0.620299	-6.41
253551_at	Expressed protein ; supported by cDNA	---	AT4G30996	1.08	0.12	0.91	0.395231	0.620456	-6.41
263939_at	hypothetical protein predicted by genefi	ATTIM44-2	AT2G36070	-1.07	-0.10	-0.91	0.395309	0.620536	-6.41
263331_at	unknown protein ; supported by cDNA:	---	AT2G15270	-1.07	-0.10	-0.91	0.395455	0.620722	-6.41
248031_at	unknown protein ; supported by cDNA:	---	AT5G55640	-1.06	-0.08	-0.91	0.395745	0.621134	-6.41
245872_at	hypothetical protein contains similarity t	---	AT1G26300	1.08	0.11	0.91	0.39579	0.621163	-6.41
258145_at	integral membrane protein, putative sim	---	AT3G18200	-1.09	-0.12	-0.91	0.395845	0.621205	-6.41
252773_at	putative protein predicted proteins, Aral	---	---	1.06	0.09	0.91	0.395873	0.621206	-6.41
256534_at	unknown protein	---	AT1G33270	-1.07	-0.10	-0.91	0.395982	0.621206	-6.41
249846_at	cation-transporting ATPase	---	AT5G23630	-1.06	-0.09	-0.91	0.395977	0.621206	-6.41
258785_at	unknown protein	---	---	-1.09	-0.13	-0.91	0.395966	0.621206	-6.41
266138_at	unknown protein ; supported by full-leng	---	AT2G28060	-1.08	-0.11	-0.91	0.395969	0.621206	-6.41
249732_at	6-phosphogluconolactonase-like protein	---	AT5G24420	-1.73	-0.79	-0.91	0.396171	0.621247	-6.41
256970_at	ABC transporter, putative similar to ATF	---	AT3G21090	-1.08	-0.11	-0.91	0.396159	0.621247	-6.41
249284_at	unknown protein ;supported by full-leng	---	AT5G41810	-1.08	-0.11	-0.91	0.396114	0.621247	-6.41
249620_at	putative protein predicted proteins, Aral	---	AT5G37520	1.07	0.09	0.91	0.396114	0.621247	-6.41
263682_at	hypothetical protein similar to reverse tra	AT5G4959	---	-1.06	-0.09	-0.91	0.396167	0.621247	-6.41
247590_at	putative protein predicted proteins, Aral	---	AT5G60720	1.08	0.12	0.91	0.396105	0.621247	-6.41
267473_at	hypothetical protein predicted by genefi	---	AT2G02750	-1.08	-0.10	-0.91	0.396359	0.621499	-6.41
248772_at	photoreceptor-interacting protein-like	---	AT5G47800	-1.17	-0.23	-0.91	0.396399	0.621520	-6.41
258679_at	putative 2,3-bisphosphoglycerate-indep	---	AT3G08590	1.15	0.21	0.91	0.396707	0.621709	-6.41
258045_at	ubiquitin-specific protease 7 (UBP7), pu	UBP7	AT3G21280	-1.08	-0.11	-0.90	0.396711	0.621709	-6.41
245475_at	hypothetical protein	---	AT4G16080	1.07	0.10	0.91	0.396674	0.621709	-6.41
253832_at	Expressed protein ; supported by full-len	---	AT4G27654	1.23	0.30	0.91	0.396553	0.621709	-6.41
255102_s_a	putative MuDR-A-like transposon protein	---	---	-1.08	-0.12	-0.91	0.396698	0.621709	-6.41
257664_at	hypothetical protein predicted by genem	EMB2743	AT3G20400	1.10	0.13	0.91	0.396697	0.621709	-6.41
263051_s_a	En/Spm-like transposon protein related	---	---	1.07	0.10	0.91	0.39658	0.621709	-6.41
261470_at	ethylene-responsive element binding fa	ERF11	AT1G28370	1.41	0.49	0.90	0.396779	0.621771	-6.41
252125_at	putative protein hypothetical protein T1	RTH	AT3G51040	-1.08	-0.11	-0.90	0.396805	0.621771	-6.41
267163_at	unknown protein	---	AT2G37520	1.10	0.14	0.90	0.396915	0.621816	-6.41

255192_at	hypothetical protein	---	AT4G07380	-1.07	-0.10	-0.90	0.396916	0.621816	-6.41
257284_at	TNP1-like protein similar to TNP1 protei	---	---	1.05	0.08	0.90	0.396875	0.621816	-6.41
248801_at	homeobox-leucine zipper protein-like ; s	HAT2	AT5G47370	-1.24	-0.31	-0.90	0.39702	0.621938	-6.41
249811_at	unknown protein ;supported by full-leng	---	AT5G23760	-1.06	-0.09	-0.90	0.39709	0.622005	-6.42
255061_at	putative protein disulfide isomerase	ATAPRL6	AT4G08930	-1.06	-0.09	-0.90	0.397132	0.622027	-6.42
264065_at	hypothetical protein predicted by gensca	---	AT2G27900	1.08	0.11	0.90	0.397367	0.622130	-6.42
262067_at	hypothetical protein predicted by gensca	---	AT1G80060	1.09	0.13	0.90	0.397454	0.622130	-6.42
261761_at	hypothetical protein predicted by genem	CENP-C	AT1G15660	-1.07	-0.10	-0.90	0.397525	0.622130	-6.42
254290_at	hypothetical protein	---	AT4G23000	-1.11	-0.15	-0.90	0.397503	0.622130	-6.42
249911_at	glucosyltransferase-like protein ; suppo	CSLA02	AT5G22740	-1.30	-0.38	-0.90	0.397296	0.622130	-6.42
261598_at	unknown protein contains similarity to ex	---	AT1G49750	1.38	0.47	0.90	0.397342	0.622130	-6.42
246458_at	putative protein various predicted prote	---	AT5G16860	-1.09	-0.12	-0.90	0.397309	0.622130	-6.42
264073_at	putative replication protein A1	---	---	-1.08	-0.11	-0.90	0.397503	0.622130	-6.42
244907_at	hypothetical protein	---	---	-1.06	-0.09	-0.90	0.397234	0.622130	-6.42
248413_at	putative protein strong similarity to unkn	PLE	AT5G51600	-1.08	-0.10	-0.90	0.39749	0.622130	-6.42
261275_at	Mlo protein, putative similar to GB:Z838	MLO14	AT1G26700	1.06	0.09	0.90	0.397496	0.622130	-6.42
256101_at	hypothetical protein predicted by gensca	---	AT1G13760	1.07	0.10	0.90	0.397358	0.622130	-6.42
266144_at	hypothetical protein	---	AT2G12170	-1.07	-0.10	-0.90	0.397562	0.622145	-6.42
255780_at	hypothetical protein contains Pfam profi	GAUT11	AT1G18580	1.09	0.12	0.90	0.397723	0.622354	-6.42
259292_at	unknown protein	---	AT3G11560	-1.08	-0.11	-0.90	0.398033	0.622711	-6.42
254945_at	putative RING finger protein ring finger	---	AT4G10940	1.09	0.13	0.90	0.397989	0.622711	-6.42
256821_at	hypothetical protein predicted by genen	---	AT3G22180	-1.12	-0.16	-0.90	0.39802	0.622711	-6.42
249121_at	aluminum-induced protein-like ; suppor	---	AT5G43830	1.08	0.11	0.90	0.398188	0.622912	-6.42
264861_at	putative glucosidase similar to a-glucos	---	AT1G24320	1.06	0.09	0.90	0.398401	0.623201	-6.42
248916_at	receptor protein kinase-like protein pred	---	AT5G45840	-1.19	-0.25	-0.90	0.398459	0.623226	-6.42
258537_at	putative disease resistance protein simil	---	AT3G04210	1.32	0.40	0.90	0.398471	0.623226	-6.42
254138_at	hypothetical protein	---	AT4G24950	1.07	0.10	0.90	0.398545	0.623269	-6.42
259697_at	putative DNA-binding protein similar to	---	AT1G68920	1.07	0.10	0.90	0.398553	0.623269	-6.42
262708_at	UV-sensitive rad23, putative similar to U	---	AT1G16190	-1.06	-0.09	-0.90	0.398663	0.623397	-6.42
246627_s_a	5-enolpyruvylshikimate-3-phosphate (E	---	AT1G48860 /	1.20	0.27	0.90	0.398746	0.623474	-6.42
265210_at	60S ribosomal protein L24 ;supported b	RPL24A	AT2G36620	-1.26	-0.33	-0.90	0.398767	0.623474	-6.42
260601_at	Expressed protein ; supported by cDNA	ZIP11	AT1G55910	1.14	0.18	0.90	0.398811	0.623491	-6.42
258600_at	putative protein kinase contains Pfam pr	---	AT3G02810	-1.07	-0.10	-0.90	0.398832	0.623491	-6.42
251946_at	putative protein predicted proteins, Arat	---	AT3G53540	-1.30	-0.38	-0.90	0.398965	0.623613	-6.42
266900_at	hypothetical protein predicted by gensca	---	AT2G34610	1.06	0.08	0.90	0.398959	0.623613	-6.42

265437_at	hypothetical protein predicted by gensca	MCM10	AT2G20980	1.08	0.11	0.90	0.399023	0.623661	-6.42
249662_s_a	putative protein hypothetical proteins - A	---	AT5G36680 /	1.06	0.08	0.90	0.399074	0.623699	-6.42
246413_at	unknown protein	---	AT1G77310	-1.08	-0.11	-0.90	0.399212	0.623828	-6.42
250434_at	histone H3 - like protein histone H3, Ara	---	AT5G10390	-1.37	-0.45	-0.90	0.399188	0.623828	-6.42
259895_at	unknown protein ;supported by full-lengt	PFI	AT1G71440	-1.07	-0.09	-0.90	0.399273	0.623880	-6.42
255846_at	putative SWI/SNF complex subunit SW1	ATSWI3B	AT2G33610	-1.10	-0.13	-0.90	0.399299	0.623880	-6.42
254154_at	hypothetical protein	---	AT4G24460	-1.10	-0.14	-0.90	0.39934	0.623901	-6.42
253799_at	putative DNA-binding protein AP2 doma	---	AT4G28140	1.53	0.61	0.90	0.399443	0.623975	-6.42
262138_at	NBS/LRR disease resistance protein, p	---	AT1G52660	-1.09	-0.12	-0.90	0.399423	0.623975	-6.42
261950_at	zinc finger protein, putative similar to D	---	AT1G64620	1.12	0.16	0.90	0.399574	0.624138	-6.42
247052_at	homeodomain transcription factor-like	HB53	AT5G66700	1.08	0.11	0.90	0.399721	0.624325	-6.42
265275_at	En/Spm-like transposon protein related	---	AT2G28440	1.14	0.18	0.90	0.399808	0.624399	-6.42
258344_at	hypothetical protein similar to hypothetic	CEG	AT3G22650	1.07	0.10	0.90	0.399824	0.624399	-6.42
259132_at	putative auxin-independent growth prom	---	AT3G02250	-1.11	-0.15	-0.90	0.399901	0.624434	-6.42
247928_at	villin	---	AT5G57320	-1.09	-0.12	-0.90	0.399883	0.624434	-6.42
261926_at	unknown protein	PATL2	AT1G22530	-1.09	-0.12	-0.90	0.399976	0.624462	-6.42
249099_at	putative protein similar to unknown prote	---	AT5G43550	-1.06	-0.08	-0.90	0.400001	0.624462	-6.42
252935_at	dnaJ-like protein CAJ1 protein, Saccha	---	AT4G39150	1.07	0.09	0.90	0.399949	0.624462	-6.42
256987_at	hypothetical protein predicted by genem	---	AT3G28560	1.07	0.09	0.90	0.400179	0.624686	-6.42
255900_at	hypothetical protein predicted by genem	---	AT1G17830 /	1.23	0.29	0.90	0.400199	0.624686	-6.42
265595_at	26S proteasome subunit 4 ;supported b	---	AT2G20140	-1.09	-0.12	-0.90	0.400307	0.624770	-6.42
265874_at	hypothetical protein predicted by genefir	---	AT2G01640	-1.09	-0.12	-0.90	0.400305	0.624770	-6.42
245942_at	putative protein transcription regulator,	---	AT5G19490	-1.06	-0.08	-0.90	0.400562	0.625125	-6.42
260471_at	hypothetical protein predicted by genefir	---	AT1G11070	1.06	0.09	0.90	0.400644	0.625209	-6.42
250840_at	putative protein predicted protein, Arabi	---	---	-1.10	-0.14	-0.90	0.400706	0.625264	-6.42
249692_s_a	putative protein strong similarity to unkn	---	AT5G36670 /	1.09	0.12	0.90	0.40074	0.625273	-6.42
266479_at	unknown protein ; supported by cDNA:	LSH3	AT2G31160	1.28	0.36	0.90	0.400804	0.625331	-6.42
255739_at	unknown protein similar to hypothetical	ANAC008	AT1G25580	1.10	0.14	0.90	0.40088	0.625387	-6.42
253624_at	putative protein 2-acylglycerophosphoe	ATS2	AT4G30580	-1.10	-0.13	-0.90	0.400895	0.625387	-6.42
245077_at	hypothetical protein predicted by gensca	---	AT2G23160	1.11	0.14	0.90	0.40093	0.625399	-6.42
257012_at	RNA-binding protein, putative similar to	TEL1	AT3G26120	1.07	0.09	0.90	0.400997	0.625419	-6.42
259078_at	unknown protein predicted by genefinde	HST	AT3G05040	-1.07	-0.09	-0.90	0.400973	0.625419	-6.42
260713_at	disease resistance protein RPP1-WsA,	---	AT1G17615	1.06	0.09	0.90	0.401074	0.625496	-6.42
258648_at	putative auxin-independent growth prom	---	AT3G07900	-1.13	-0.17	-0.90	0.401109	0.625508	-6.42
246519_at	proline-rich protein other proline-rich pro	---	AT3G23750 /	1.48	0.56	0.90	0.401288	0.625744	-6.42

263084_at	hypothetical protein predicted by gensca	---	AT2G27180	1.07	0.10	0.90	0.401367	0.625825	-6.42
255490_at	putative protein lysosomal trafficking re	---	AT4G02660	-1.07	-0.10	-0.90	0.40142	0.625863	-6.42
247072_at	putative protein similar to unknown prote	---	AT5G66490	-1.12	-0.16	-0.90	0.401539	0.625919	-6.42
253385_at	putative protein predicted protein, Caen	---	AT4G32930	-1.07	-0.09	-0.90	0.401513	0.625919	-6.42
258430_at	phospholipase D, putative similar to ph	PLDP1	AT3G16785	1.06	0.09	0.90	0.401536	0.625919	-6.42
251064_at	putative zinc finger protein several zinc f	---	AT5G01860	1.08	0.11	0.90	0.401565	0.625919	-6.42
258847_at	unknown protein ; supported by full-leng	---	AT3G03100	-1.06	-0.09	-0.89	0.401824	0.626194	-6.42
251778_at	putative protein various predicted prote	ROPGEF6	AT3G55660	1.09	0.12	0.89	0.401816	0.626194	-6.42
250313_at	Rab geranylgeranyltransferase, beta su	---	AT5G12210	-1.09	-0.13	-0.89	0.401789	0.626194	-6.42
262735_at	hypothetical protein	---	AT1G28630	1.07	0.10	0.89	0.401928	0.626270	-6.42
259529_at	hypothetical protein	---	AT1G12400	1.07	0.10	0.89	0.401906	0.626270	-6.42
261976_at	hypothetical protein predicted by genem	---	---	-1.08	-0.11	-0.89	0.401978	0.626306	-6.42
259488_at	hypothetical protein preedicted by gener	---	AT1G15780	-1.10	-0.13	-0.89	0.402038	0.626357	-6.42
251751_at	putative protein predicted proteins, Arat	---	AT3G55720	1.06	0.08	0.89	0.402112	0.626429	-6.42
261223_at	hypothetical protein predicted by genem	HVA22H	AT1G19950	1.06	0.08	0.89	0.402224	0.626488	-6.42
262838_at	major latex protein, putative similar to m	---	AT1G14960	1.08	0.11	0.89	0.40225	0.626488	-6.42
259167_at	putative oleosin similar to oleosin GB:AA	---	AT3G01570	-1.06	-0.09	-0.89	0.402247	0.626488	-6.42
257758_at	eukaryotic translation elongation factor	---	AT3G22980	1.08	0.12	0.89	0.402259	0.626488	-6.42
249789_at	putative protein similar to unknown prote	---	AT5G24340	-1.09	-0.12	-0.89	0.402343	0.626574	-6.42
262033_at	terminal ear1, putative similar to termina	MCT1	AT1G37140	1.08	0.11	0.89	0.402371	0.626576	-6.42
252954_at	putative thaumatin-like protein thaumati	---	AT4G38660	1.29	0.36	0.89	0.402549	0.626725	-6.43
253541_at	putative protein various predicted prote	---	AT4G31630	1.06	0.09	0.89	0.402517	0.626725	-6.43
260378_at	putative actin similar to actin GB:CAB55	ATARP4A	AT1G73910	1.06	0.08	0.89	0.402524	0.626725	-6.43
265017_at	unknown protein similar to EST emb|Z3	---	AT1G24390	1.08	0.11	0.89	0.402638	0.626820	-6.43
248683_at	putative protein similar to unknown prote	---	AT5G48490	1.26	0.34	0.89	0.40291	0.626987	-6.43
246451_at	Inositol 1,3,4-Trisphosphate 5/6 kinase	---	AT5G16760	1.06	0.08	0.89	0.402802	0.626987	-6.43
255824_at	hypothetical protein predicted by genefir	---	AT2G40530	-1.24	-0.31	-0.89	0.402854	0.626987	-6.43
266242_at	hypothetical protein predicted by gensca	---	AT2G27790	-1.07	-0.10	-0.89	0.402893	0.626987	-6.43
253250_at	hypothetical protein	---	AT4G34690	-1.06	-0.08	-0.89	0.402814	0.626987	-6.43
260054_at	putative transporter contains Pfam profil	UNE2	AT1G78130	-1.13	-0.18	-0.89	0.402879	0.626987	-6.43
265565_at	putative retroelement pol polyprotein	---	---	1.07	0.10	0.89	0.402956	0.627017	-6.43
250107_at	ids-4 protein - like ids-4 protein, Hordeu	SPX4	AT5G15330	-1.11	-0.15	-0.89	0.403015	0.627065	-6.43
248827_at	calcium sensor protein, calcineurin-like	CBL9	AT5G47100	-1.12	-0.16	-0.89	0.40307	0.627076	-6.43
249338_at	putative protein similar to unknown prote	anac095	AT5G41090	1.06	0.08	0.89	0.403077	0.627076	-6.43
245236_at	putative DNA mismatch repair protein s	MSH3	AT4G25540	-1.06	-0.09	-0.89	0.403319	0.627410	-6.43

256507_at	hypothetical protein predicted by genem	---	AT1G75150	1.09	0.12	0.89	0.403357	0.627426	-6.43
263496_at	unknown protein ; supported by full-leng	---	AT2G42570	1.10	0.14	0.89	0.40341	0.627466	-6.43
245217_at	retroelement pol polyprotein, putative	---	---	1.10	0.14	0.89	0.403456	0.627494	-6.43
262867_at	hypothetical protein predicted by gensca	---	AT1G64960	1.08	0.11	0.89	0.403633	0.627550	-6.43
257449_at	hypothetical protein predicted by gensca	---	AT2G31420	1.08	0.11	0.89	0.403648	0.627550	-6.43
246589_at	glucosyltransferase -like protein glucosy	---	AT5G14860	1.07	0.10	0.89	0.403742	0.627550	-6.43
262813_at	unknown protein strong similarity to gi|3	---	AT1G11670	1.23	0.30	0.89	0.4037	0.627550	-6.43
267349_at	60S acidic ribosomal protein P0	---	AT2G40010	-1.06	-0.09	-0.89	0.403762	0.627550	-6.43
262069_at	hypothetical protein similar to SNF4-kina	---	AT1G80090	-1.08	-0.12	-0.89	0.403587	0.627550	-6.43
263512_at	hypothetical protein predicted by genefir	---	---	-1.07	-0.09	-0.89	0.403767	0.627550	-6.43
263234_at	hypothetical protein predicted by genefir	---	AT1G10417	-1.07	-0.09	-0.89	0.403765	0.627550	-6.43
261358_s_a	hypothetical protein predicted by gensca	---	AT1G41920 /	1.07	0.10	0.89	0.403739	0.627550	-6.43
261486_at	nucleic acid binding protein (alfin-1), pu	AL7	AT1G14510	-1.08	-0.11	-0.89	0.403626	0.627550	-6.43
267109_at	hypothetical protein predicted by gensca	---	AT2G14810	1.08	0.12	0.89	0.403931	0.627720	-6.43
255351_x_a	putative transposon protein similar to atl	---	---	1.08	0.11	0.89	0.403913	0.627720	-6.43
261785_at	hypothetical protein contains similarity to	---	AT1G08230	-1.07	-0.09	-0.89	0.404001	0.627744	-6.43
255199_at	coded for by A. thaliana cDNA N64969	---	AT4G07390	-1.07	-0.09	-0.89	0.404029	0.627744	-6.43
258428_at	unknown protein	---	AT3G16610	-1.07	-0.10	-0.89	0.404027	0.627744	-6.43
266854_at	putative C2H2-type zinc finger protein lik	---	AT2G26940	1.10	0.13	0.89	0.404195	0.627831	-6.43
252765_at	putative protein hypothetical proteins - A	---	AT3G42800	-1.14	-0.19	-0.89	0.404129	0.627831	-6.43
249796_at	26S proteasome, non-ATPase regulato	---	AT5G23540	1.07	0.10	0.89	0.404173	0.627831	-6.43
260661_at	hypothetical protein predicted by gensca	---	AT1G19500	1.09	0.12	0.89	0.404155	0.627831	-6.43
265735_at	putative aldolase ;supported by full-leng	---	AT2G01140	1.11	0.15	0.89	0.404296	0.627858	-6.43
255228_at	F-box protein family, AtFBL21 contains	---	AT4G05470	-1.07	-0.09	-0.89	0.404241	0.627858	-6.43
259263_at	putative UDP-glucose 6-dehydrogenase	---	AT3G01010	1.07	0.10	0.89	0.404292	0.627858	-6.43
264688_at	hypothetical protein similar to LG27/30-l	---	AT1G09890	1.11	0.15	0.89	0.404327	0.627865	-6.43
262926_s_a	receptor kinase, putative similar to rece	ARK1	AT1G65790 /	1.22	0.28	0.89	0.404398	0.627889	-6.43
250815_s_a	putative protein similar to unknown prote	---	AT5G05040 /	1.10	0.13	0.89	0.404372	0.627889	-6.43
260865_at	reverse transcriptase, putative similar to	---	AT1G43760	-1.08	-0.11	-0.89	0.404436	0.627905	-6.43
256332_at	trihelix DNA-binding protein (GT2) ident	GT2	AT1G76890	1.18	0.24	0.89	0.404488	0.627943	-6.43
246560_at	putative protein hypothetical protein F1C	---	AT5G15560	1.07	0.10	0.89	0.404606	0.627998	-6.43
251777_s_a	pyruvate kinase - like protein pyruvate k	---	AT3G55650 /	-1.08	-0.11	-0.89	0.404558	0.627998	-6.43
257523_at	hypothetical protein similar to putative b	---	AT3G01620	1.07	0.10	0.89	0.404584	0.627998	-6.43
253035_at	glycosyltransferase like protein alpha-1	CGL1	AT4G38240	1.07	0.09	0.89	0.404844	0.628325	-6.43
253096_at	cytochrome P450-like protein	CYP81D4	AT4G37330	-1.08	-0.11	-0.89	0.404971	0.628440	-6.43

250042_at	putative protein non-consensus GC dor	---	AT5G18420	1.07	0.10	0.89	0.404973	0.628440	-6.43
249985_at	Ser/Thr specific protein kinase - like pro	---	AT5G18500	1.09	0.13	0.89	0.405052	0.628444	-6.43
266931_at	putative non-LTR retroelement reverse t	---	---	-1.07	-0.10	-0.89	0.405058	0.628444	-6.43
252078_at	putative protein brassinosteroid-insensi	IMK2	AT3G51740	-1.06	-0.08	-0.89	0.40503	0.628444	-6.43
253794_at	putative protein dimethylaniline monoox	---	AT4G28720	-1.22	-0.29	-0.89	0.405167	0.628516	-6.43
253402_at	HD-zip transcription factor (athb-8)	ATHB-8	AT4G32880	1.12	0.17	0.89	0.405188	0.628516	-6.43
267015_at	unknown protein	---	AT2G39340	-1.09	-0.12	-0.89	0.405143	0.628516	-6.43
245516_at	hypothetical protein	---	AT4G15820	-1.09	-0.13	-0.89	0.405469	0.628757	-6.43
266465_at	putative auxin-responsive protein ; supp	GH3.9	AT2G47750	1.08	0.11	0.89	0.405435	0.628757	-6.43
255711_at	putative WD repeat membrane protein ;	---	AT4G00090	-1.09	-0.12	-0.89	0.40541	0.628757	-6.43
251767_at	putative protein U4/U6 small nuclear rib	---	AT3G55930	-1.06	-0.08	-0.89	0.405384	0.628757	-6.43
261441_at	NAM protein, putative similar to NAM p	ANAC010	AT1G28470	1.13	0.18	0.89	0.405481	0.628757	-6.43
252777_at	hypothetical protein	---	AT3G42970	1.07	0.10	0.89	0.405524	0.628782	-6.43
262392_at	hypothetical protein predicted by gensca	---	AT1G49520	-1.11	-0.15	-0.89	0.405653	0.628938	-6.43
254494_at	putative protein C65DMY30S	QRT3	AT4G20050	1.06	0.09	0.89	0.40571	0.628984	-6.43
261253_at	unknown protein ;supported by full-lengt	---	AT1G05840	-1.11	-0.15	-0.89	0.405872	0.629193	-6.43
256788_at	cytochrome P450, putative similar to cy	CYP90D1	AT3G13730	-1.33	-0.41	-0.89	0.405905	0.629201	-6.43
248143_at	putative protein similar to unknown prote	---	AT5G55040	-1.07	-0.10	-0.89	0.405999	0.629305	-6.43
262827_at	putative cytochrome P450 monooxygen	CYP71B29	AT1G13100	1.15	0.21	0.89	0.406035	0.629317	-6.43
259147_at	putative RNA binding protein similar to F	APUM4	AT3G10360	1.13	0.17	0.89	0.406076	0.629339	-6.43
255335_at	putative transposon protein	---	---	-1.07	-0.10	-0.89	0.406114	0.629354	-6.43
246318_at	putative protein predicted protein BAA8	---	AT3G56740	1.09	0.12	0.89	0.406454	0.629837	-6.43
249214_at	beta-1,3-glucanase-like protein	---	AT5G42720	-1.15	-0.20	-0.89	0.406528	0.629893	-6.43
261599_at	hypothetical protein similar to hypothetic	---	AT1G49700	1.08	0.11	0.89	0.406545	0.629893	-6.43
264356_at	putative DNA repair protein Strong simil	UVH6	AT1G03190	-1.07	-0.10	-0.88	0.406758	0.630180	-6.43
267123_at	putative acetone-cyanohydrin lyase	MES7	AT2G23560	1.14	0.19	0.88	0.40687	0.630233	-6.43
257456_at	unknown protein predicted by genscan	SRS4	AT2G18120	1.08	0.11	0.88	0.406837	0.630233	-6.43
265609_at	hypothetical protein predicted by gensca	---	AT2G25420	-1.12	-0.16	-0.88	0.406875	0.630233	-6.43
264684_at	unknown protein	HEXO3	AT1G65590	-1.15	-0.20	-0.88	0.407159	0.630399	-6.43
267267_at	putative cytochrome P450	CYP71B9	AT2G02580	1.07	0.10	0.88	0.407023	0.630399	-6.43
258835_at	putative RNA-binding protein contains F	---	AT3G07250	1.08	0.11	0.88	0.407103	0.630399	-6.43
266613_at	similar to gibberellin-regulated proteins	---	AT2G14900	1.93	0.95	0.88	0.407107	0.630399	-6.43
249725_at	unknown protein	---	AT5G35470	-1.07	-0.09	-0.88	0.407175	0.630399	-6.43
252648_at	disease resistance protein homolog dis	---	AT3G44630	1.07	0.10	0.88	0.407164	0.630399	-6.43
249621_at	putative protein predicted proteins, Arat	---	AT5G37530	-1.08	-0.11	-0.88	0.407076	0.630399	-6.43

257645_at	unknown protein ;supported by full-leng	---	AT3G25790	1.09	0.13	0.88	0.4073	0.630549	-6.43
245661_at	purine permease, putative similar to pu	ATPUP3	AT1G28220	1.08	0.11	0.88	0.407344	0.630575	-6.43
265151_at	hypothetical protein similar to hypothetic	---	AT1G51340	-1.09	-0.13	-0.88	0.40747	0.630697	-6.43
263698_at	hypothetical protein similar to a multituc	---	---	1.09	0.13	0.88	0.407478	0.630697	-6.43
267260_at	putative proline-rich protein ; supported	AGP17	AT2G23130	-1.20	-0.27	-0.88	0.407656	0.630825	-6.43
266939_at	plasma membrane proton ATPase (PM	AHA1	AT2G18960	1.06	0.08	0.88	0.407699	0.630825	-6.43
253392_at	potassium channel protein AtKC potass	ATKC1	AT4G32650	1.26	0.33	0.88	0.407684	0.630825	-6.43
253735_at	putative protein SNF7 protein - Sacchar	SNF7.1	AT4G29160	-1.07	-0.10	-0.88	0.407659	0.630825	-6.43
265862_at	putative S-locus glycoprotein	---	AT2G01780	-1.08	-0.11	-0.88	0.407685	0.630825	-6.43
262310_at	unknown protein contains similarity to m	MLP31	AT1G70840	-1.07	-0.10	-0.88	0.407761	0.630878	-6.43
265150_at	unknown protein ; supported by cDNA:	---	AT1G51200	-1.09	-0.13	-0.88	0.408083	0.630991	-6.44
248427_at	subtilisin-like serine protease similar to s	ATSBT1.3	AT5G51750	1.10	0.13	0.88	0.407938	0.630991	-6.43
252099_at	putative protein senescence-associated	---	AT3G51250	1.09	0.12	0.88	0.408044	0.630991	-6.43
261026_at	hypothetical protein predicted by genem	---	AT1G01240	-1.09	-0.13	-0.88	0.407959	0.630991	-6.43
251763_at	MYB transcription factor - like protein R	MYB109	AT3G55730	1.09	0.12	0.88	0.408062	0.630991	-6.43
246935_at	leucine-rich repeats containing protein g	EBF2	AT5G25350	1.13	0.17	0.88	0.407994	0.630991	-6.43
266491_at	putative retroelement pol polyprotein	---	---	-1.07	-0.09	-0.88	0.407932	0.630991	-6.43
259844_at	lipid transfer protein, putative similar to	---	AT1G73560	-1.07	-0.10	-0.88	0.40808	0.630991	-6.44
252568_at	receptor-like protein kinase receptor like	---	AT3G45410	-1.12	-0.16	-0.88	0.407981	0.630991	-6.43
249530_at	putative protein asparaginyl-tRNA synth	---	AT5G38750	-1.06	-0.09	-0.88	0.408336	0.631239	-6.44
265202_at	unknown protein	AT2G3681	---	-1.08	-0.11	-0.88	0.408301	0.631239	-6.44
261705_at	hypothetical protein predicted by genem	---	AT1G32670	1.07	0.10	0.88	0.40833	0.631239	-6.44
251284_at	hypothetical protein	---	AT3G61840	-1.10	-0.14	-0.88	0.408354	0.631239	-6.44
248729_at	cycloartenol synthase	THAS1	AT5G48010	1.06	0.08	0.88	0.408386	0.631245	-6.44
250171_at	prohibitin - like protein prohibitin, Arabic	ATPHB5	AT5G14300	-1.07	-0.10	-0.88	0.408477	0.631344	-6.44
257213_at	mitochondrial NAD-dependent malate d	---	AT3G15020	1.13	0.18	0.88	0.408522	0.631369	-6.44
248343_at	putative protein contains similarity to my	AtMYB19	AT5G52260	1.06	0.08	0.88	0.408624	0.631484	-6.44
250167_at	myb-related protein - like myb-related p	ATMYB16	AT5G15310	-1.11	-0.15	-0.88	0.408738	0.631533	-6.44
254323_at	putative protein auxin-induced protein 1	---	AT4G22620	1.18	0.24	0.88	0.408714	0.631533	-6.44
246377_at	low-temperature-specific protein, putati	---	AT1G57550	-1.12	-0.16	-0.88	0.408694	0.631533	-6.44
245114_at	transcription factor IIB (TFIIB) identical t	TFIIB	AT2G41630	-1.13	-0.17	-0.88	0.40878	0.631554	-6.44
260038_at	Expressed protein ; supported by full-ler	---	AT1G68875	1.06	0.09	0.88	0.408936	0.631753	-6.44
253248_at	Putative S-phase-specific ribosomal pro	---	AT4G34670	-1.19	-0.26	-0.88	0.409018	0.631837	-6.44
256559_at	Athila ORF 1, putative similar to Athila (	---	---	-1.07	-0.09	-0.88	0.409099	0.631918	-6.44
263713_at	Expressed protein ; supported by full-ler	---	AT2G20595	1.08	0.11	0.88	0.409149	0.631953	-6.44

262961_at	exonuclease, putative similar to 5'-3' ex	XRN4	AT1G54490	1.07	0.10	0.88	0.409183	0.631964	-6.44
265572_at	putative carbonic anhydrase	ATACA2	AT2G28210	1.55	0.64	0.88	0.409293	0.632090	-6.44
252077_at	putative protein several putative myosin	---	AT3G51720	1.09	0.12	0.88	0.409391	0.632199	-6.44
256023_at	hypothetical protein predicted by genem	ZW2	AT1G58330	1.09	0.12	0.88	0.409606	0.632208	-6.44
255275_at	putative protein various ubiquitin-like pre	---	AT4G05310	-1.05	-0.08	-0.88	0.409539	0.632208	-6.44
252046_at	putative protein extensin -Nicotiana tab	---	AT3G52460	1.08	0.11	0.88	0.409454	0.632208	-6.44
266644_at	unknown protein ;supported by full-leng	---	AT2G29660	-1.09	-0.13	-0.88	0.409619	0.632208	-6.44
254621_at	gene 11-1 protein - like gene 11-1 prote	WAVE5	AT4G18600	-1.07	-0.10	-0.88	0.409608	0.632208	-6.44
262041_at	HPt phosphotransmitter, putative simila	AHP6	AT1G80100	1.09	0.12	0.88	0.409538	0.632208	-6.44
253179_at	putative protein various predicted prote	---	AT4G35200	-1.06	-0.08	-0.88	0.40961	0.632208	-6.44
255347_at	putative retrotransposon protein	---	---	-1.06	-0.09	-0.88	0.409469	0.632208	-6.44
253583_at	translation initiation factor-like protein tr	---	AT4G30680	-1.09	-0.13	-0.88	0.409674	0.632218	-6.44
260295_at	putative aminopeptidase similar to amin	---	AT1G63770	-1.09	-0.12	-0.88	0.40968	0.632218	-6.44
251597_at	protein kinase - like protein wall-associa	---	AT3G57750	1.17	0.22	0.88	0.409735	0.632259	-6.44
264672_at	hypothetical protein predicted by gensca	---	AT1G09750	1.81	0.85	0.88	0.410043	0.632359	-6.44
252451_at	hypothetical protein	---	AT3G47100	1.06	0.09	0.88	0.410006	0.632359	-6.44
253924_at	putative protein other hypothetical prote	COBL11	AT4G27110	1.08	0.11	0.88	0.410044	0.632359	-6.44
262997_at	disease resistance protein, putative sim	RPP27	AT1G54470	1.06	0.09	0.88	0.40998	0.632359	-6.44
250419_at	RPP1 disease resistance protein - like	---	AT5G11250	1.10	0.14	0.88	0.409978	0.632359	-6.44
256734_at	unknown protein	RIK	AT3G29390	1.07	0.09	0.88	0.409828	0.632359	-6.44
267403_at	MADS-box protein (AGL33)	AGL33	AT2G26320	-1.05	-0.08	-0.88	0.409984	0.632359	-6.44
266387_at	hypothetical protein predicted by gensca	---	AT2G32360	-1.07	-0.10	-0.88	0.409907	0.632359	-6.44
245450_at	disease resistance RPP5 like protein (fr	---	AT4G16880	-1.07	-0.10	-0.88	0.410049	0.632359	-6.44
245760_s_a	receptor serine/threonine kinase PR5K,	---	AT1G66910 /	1.18	0.24	0.88	0.410195	0.632366	-6.44
246148_at	glycine-rich RNA-binding protein - like g	---	AT5G19960	-1.08	-0.11	-0.88	0.41015	0.632366	-6.44
248057_at	putative protein strong similarity to unkn	---	AT5G55520	1.06	0.09	0.88	0.410116	0.632366	-6.44
249832_at	disease resistance protein-like	---	AT5G23400	1.09	0.12	0.88	0.410164	0.632366	-6.44
253106_at	putative protein predicted proteins, Aral	---	AT4G35870	-1.07	-0.10	-0.88	0.41018	0.632366	-6.44
259518_at	hypothetical protein ; supported by cDN/	OPCL1	AT1G20510	-1.22	-0.28	-0.88	0.41022	0.632366	-6.44
260515_at	ATP-dependent transmembrane transp	---	AT1G51460	1.08	0.11	0.88	0.410267	0.632395	-6.44
250949_at	putative protein	---	AT5G03510	1.06	0.09	0.88	0.410348	0.632477	-6.44
245070_at	metallothionein-like protein identical to a	---	AT2G23240	-1.10	-0.13	-0.88	0.410414	0.632537	-6.44
254096_at	acid phosphatase - like protein acid pho	---	AT4G25150	-1.08	-0.11	-0.88	0.410487	0.632574	-6.44
252185_at	putative protein	---	AT3G50780	1.10	0.13	0.88	0.410494	0.632574	-6.44
261690_at	branched-chain amino acid aminotrans	---	AT1G50090	1.07	0.10	0.88	0.410546	0.632612	-6.44

253406_at	putative protein GATA transcription fact	---	AT4G32890	-1.14	-0.19	-0.88	0.41058	0.632622	-6.44
251617_at	putative protein hypothetical protein T2	---	AT3G58000	-1.07	-0.09	-0.88	0.410696	0.632758	-6.44
264100_at	lupeol synthase identical to lupeol synth	LUP1	AT1G78970	1.25	0.33	0.88	0.410848	0.632948	-6.44
259948_at	unknown protein similar to LIGATIN GB	---	AT1G71350	-1.11	-0.15	-0.88	0.410875	0.632948	-6.44
250651_at	cytochrome P450	CYP93D1	AT5G06900	1.06	0.08	0.88	0.411047	0.633149	-6.44
264640_at	pollen allergen, putative similar to polle	ATEXPB2	AT1G65680	1.11	0.16	0.88	0.411061	0.633149	-6.44
261008_at	hypothetical protein contains similarity t	---	AT1G26370	-1.09	-0.13	-0.88	0.411331	0.633394	-6.44
260397_at	hypothetical protein predicted by genefi	---	AT1G69680	1.07	0.10	0.88	0.411266	0.633394	-6.44
259168_at	unknown protein similar to hypothetical	---	AT3G03570	1.08	0.11	0.88	0.411284	0.633394	-6.44
255282_at	putative polyprotein	---	---	1.06	0.09	0.88	0.411317	0.633394	-6.44
248401_at	putative protein similar to unknown prot	HCF208	AT5G52110	-1.15	-0.20	-0.88	0.41146	0.633549	-6.44
251650_at	hypothetical protein	---	AT3G57360	-1.10	-0.14	-0.88	0.411631	0.633680	-6.44
251450_at	squamosa promoter binding protein-like	SPL12	AT3G60030	-1.08	-0.12	-0.88	0.411673	0.633680	-6.44
247606_at	RNA helicase	---	AT5G61000	-1.22	-0.29	-0.88	0.411616	0.633680	-6.44
259920_at	putative phenylalanyl-tRNA synthetase	---	AT1G72550	-1.07	-0.10	-0.88	0.411683	0.633680	-6.44
258137_at	Expressed protein ; supported by cDNA	UBC37	AT3G24515	-1.06	-0.09	-0.88	0.411683	0.633680	-6.44
255955_at	hypothetical protein predicted by gensca	---	AT1G22030	-1.13	-0.18	-0.87	0.411759	0.633754	-6.44
264171_at	hypothetical protein predicted by gensca	---	AT1G02100	-1.09	-0.12	-0.87	0.411945	0.633996	-6.44
266632_at	putative serpin	---	AT2G35570	1.07	0.10	0.87	0.412007	0.634050	-6.44
263466_at	hypothetical protein predicted by gensca	---	AT2G31740	-1.06	-0.09	-0.87	0.412141	0.634084	-6.44
252360_at	putative protein predicted protein, Arabi	---	AT3G48480	-1.09	-0.12	-0.87	0.412105	0.634084	-6.44
257614_at	putative non-LTR retroelement reverse t	---	---	-1.08	-0.12	-0.87	0.412138	0.634084	-6.44
252846_at	putative protein several pectin methyles	---	AT3G42160	-1.06	-0.08	-0.87	0.412112	0.634084	-6.44
262147_at	phospholipase D1, putative similar to pl	PLDALPHA	AT1G52570	1.07	0.09	0.87	0.412238	0.634190	-6.44
250767_at	putative protein contains similarity to un	ATNFXL2	AT5G05660	1.06	0.09	0.87	0.412295	0.634236	-6.44
256815_at	unknown protein contains Pfam profile:	---	AT3G21380	1.07	0.10	0.87	0.41244	0.634415	-6.44
249593_at	putative protein SIAH1 protein, Brassica	---	AT5G37900	-1.07	-0.10	-0.87	0.412473	0.634425	-6.44
263885_at	unknown protein	---	AT2G36940	1.07	0.09	0.87	0.412605	0.634584	-6.44
265624_at	CLAVATA3 CLE family of proteins; ligan	CLV3	AT2G27250	-1.08	-0.11	-0.87	0.412718	0.634715	-6.44
252207_at	putative protein mRNA of unknown fun	---	AT3G50370	-1.07	-0.10	-0.87	0.41318	0.635212	-6.44
261612_at	fucosyltransferase c3 protein, putative s	FUT12	AT1G49710	-1.07	-0.09	-0.87	0.413125	0.635212	-6.44
253602_s_a	leucyl aminopeptidase - like protein leu	---	AT4G30910 /	1.06	0.09	0.87	0.41311	0.635212	-6.44
258267_at	putative delta 9 desaturase similar to de	---	AT3G15870	-1.06	-0.08	-0.87	0.413154	0.635212	-6.44
257359_x_a	putative protein kinase contains a protei	---	AT2G34290	-1.06	-0.09	-0.87	0.413133	0.635212	-6.44
253490_at	methyltransferase - like protein methylt	---	AT4G31790	-1.15	-0.20	-0.87	0.41324	0.635218	-6.44

250391_at	putative protein predicted proteins, Arat	---	---	-1.08	-0.11	-0.87	0.413222	0.635218	-6.44
256669_s_a	hypothetical protein similar to hypothetic	---	AT3G32200 /	1.08	0.12	0.87	0.413351	0.635347	-6.44
245196_at	F12A21.12 similar to pectate lyase like	---	AT1G67750	1.18	0.24	0.87	0.413434	0.635431	-6.44
249708_at	unknown protein	---	AT5G35660	-1.14	-0.19	-0.87	0.413564	0.635588	-6.44
259613_at	hypothetical protein predicted by genem	---	AT1G48010	1.06	0.09	0.87	0.413647	0.635673	-6.44
265951_at	hypothetical protein predicted by genefir	OFP7	AT2G18500	1.12	0.17	0.87	0.413745	0.635781	-6.45
259676_at	hypothetical protein similar to putative S	---	AT1G77730	1.07	0.10	0.87	0.413793	0.635812	-6.45
254225_at	putative major latex protein major latex	---	AT4G23670	-1.36	-0.44	-0.87	0.413826	0.635819	-6.45
249376_at	Expressed protein ; supported by full-ler	---	AT5G40645	1.06	0.08	0.87	0.413855	0.635820	-6.45
265902_at	hypothetical protein predicted by genscа	---	AT2G25590	1.07	0.10	0.87	0.413926	0.635887	-6.45
249361_at	protein kinase - like protein protein kina	---	AT5G40540	1.15	0.21	0.87	0.414025	0.635954	-6.45
264140_at	proteasome alpha subunit, putative sim	---	AT1G79210	-1.07	-0.09	-0.87	0.414023	0.635954	-6.45
266877_at	putative glucanase	AtGH9B12	AT2G44570	1.07	0.10	0.87	0.414091	0.636012	-6.45
262710_at	unknown protein ESTs gb|T04357 and g	---	AT1G16210	-1.06	-0.09	-0.87	0.414229	0.636144	-6.45
245319_at	Expressed protein ; supported by full-ler	---	AT4G16146	-1.13	-0.18	-0.87	0.414232	0.636144	-6.45
255451_at	putative protein similar to T5J8.17	---	AT4G02860	1.09	0.12	0.87	0.414437	0.636244	-6.45
256242_at	actin-like protein contains Pfam profile: I	ATARP5	AT3G12380	-1.09	-0.13	-0.87	0.414384	0.636244	-6.45
263408_at	predicted protein	---	AT2G04060	1.06	0.09	0.87	0.414368	0.636244	-6.45
264609_at	unknown protein ;supported by full-leng	---	AT1G04530	-1.14	-0.19	-0.87	0.414414	0.636244	-6.45
249904_at	unknown protein	---	AT5G22700	-1.07	-0.10	-0.87	0.414437	0.636244	-6.45
246042_at	cinnamyl-alcohol dehydrogenase - like	---	AT5G19440	1.17	0.23	0.87	0.41454	0.636360	-6.45
256028_at	poly(A)-binding protein, putative similar	PAB1	AT1G34140	1.10	0.13	0.87	0.414608	0.636420	-6.45
251596_at	1-acylcerol-3-phosphate acyltransferas	LPAT2	AT3G57650	1.06	0.08	0.87	0.414733	0.636570	-6.45
267491_at	unknown protein predicted by genscan	---	---	1.09	0.13	0.87	0.414807	0.636641	-6.45
261965_at	athila ORF 1, putative similar to athila C	---	---	1.05	0.08	0.87	0.414845	0.636656	-6.45
252442_at	dUTP pyrophosphatase-like protein dU	---	AT3G46940	-1.14	-0.19	-0.87	0.415018	0.636878	-6.45
251141_at	Expressed protein ; supported by full-ler	---	AT5G01075	-1.14	-0.19	-0.87	0.415078	0.636928	-6.45
257544_at	putative DNA-binding protein similar to C	---	AT3G20880	1.09	0.12	0.87	0.415192	0.637060	-6.45
262768_at	putative beta-1,4-N-acetylglucosaminylt	---	AT1G12990	1.17	0.23	0.87	0.415262	0.637124	-6.45
255504_at	drought-induced-19-like 1 similar to dro	---	AT4G02200	1.26	0.33	0.87	0.415478	0.637412	-6.45
265962_at	nodulin-like protein ;supported by full-le	---	AT2G37460	-1.21	-0.27	-0.87	0.415558	0.637493	-6.45
253256_at	putative protein endothelin converting e	---	AT4G34360	1.09	0.13	0.87	0.41559	0.637500	-6.45
253500_at	predicted protein RegA gene, Dictyoste	ARR10	AT4G31920	-1.11	-0.15	-0.87	0.415634	0.637523	-6.45
248853_at	protein kinase-like protein	BSK2	AT5G46570	-1.09	-0.13	-0.87	0.415687	0.637562	-6.45
260013_at	putative annexin similar to annexin p33	ANN5	AT1G68090	1.06	0.08	0.87	0.41576	0.637631	-6.45

246981_at	unknown protein	---	AT5G04840	-1.10	-0.14	-0.87	0.415795	0.637642	-6.45
250143_at	ADP-ribosylation factor - like protein AD	ATARFA1I	AT5G14670	-1.07	-0.10	-0.87	0.415855	0.637657	-6.45
260577_at	hypothetical protein predicted by genefir	---	AT2G47340	1.07	0.10	0.87	0.415868	0.637657	-6.45
259864_at	hypothetical protein predicted by gensca	---	AT1G72800	1.13	0.18	0.87	0.415889	0.637657	-6.45
255159_at	putative polyprotein	---	---	1.09	0.13	0.87	0.416002	0.637788	-6.45
249397_at	putative protein MtN21, Medicago trunc	---	AT5G40230	1.10	0.14	0.87	0.416046	0.637812	-6.45
254820_s_a	pEARLI 1-like protein Arabidopsis thalia	---	AT4G12510 /	1.17	0.22	0.87	0.416247	0.637926	-6.45
256671_at	unknown protein	IQD3	AT3G52290	-1.11	-0.15	-0.87	0.416291	0.637926	-6.45
253700_at	threonine synthase	MTO2	AT4G29840	-1.11	-0.15	-0.87	0.416316	0.637926	-6.45
251254_at	putative protein anion exchanger 3, car	---	AT3G62270	1.09	0.12	0.87	0.41629	0.637926	-6.45
245656_at	hypothetical protein predicted by genem	---	AT1G56620	1.07	0.10	0.87	0.416217	0.637926	-6.45
256001_at	unknown protein contains similarity to a	---	AT1G29850	-1.10	-0.14	-0.87	0.416281	0.637926	-6.45
264237_at	hypothetical protein predicted by genem	---	AT1G54700	-1.06	-0.08	-0.87	0.416309	0.637926	-6.45
259992_at	putative heat shock transcription factor	HSFA8	AT1G67970	1.12	0.17	0.87	0.416376	0.637945	-6.45
255223_at	putative protein predicted proteins, Ara	---	AT4G05370	1.06	0.08	0.87	0.416385	0.637945	-6.45
259788_at	lipase/hydrolase, putative contains Pfar	---	AT1G29670	1.33	0.41	0.87	0.416414	0.637948	-6.45
246275_at	putative protein ; supported by full-lengt	BEE2	AT4G36540	1.42	0.51	0.87	0.416582	0.637986	-6.45
252998_at	probable H+-transporting ATPase H+-tr	---	AT4G38510	1.08	0.11	0.87	0.41649	0.637986	-6.45
254789_at	blue copper-binding protein, 15K (lamin	---	AT4G12880	1.50	0.59	0.87	0.416575	0.637986	-6.45
266251_s_a	unknown protein	---	AT2G18320 /	-1.06	-0.08	-0.87	0.416607	0.637986	-6.45
252653_at	putative kinesin-like protein similar to 4	---	AT3G44730	1.08	0.11	0.87	0.416604	0.637986	-6.45
267306_at	Ran binding protein (AtRanBP1b) identi	---	AT2G30060	-1.07	-0.10	-0.87	0.416569	0.637986	-6.45
254236_at	putative protein VSG expression site-as	---	AT4G23840	-1.07	-0.09	-0.87	0.41666	0.638025	-6.45
263499_at	unknown protein ; supported by cDNA:	TTL3	AT2G42580	1.12	0.17	0.87	0.416706	0.638053	-6.45
253466_at	homeodomain containing protein 1 ; su	KNAT5	AT4G32040	1.08	0.12	0.87	0.416784	0.638129	-6.45
262295_at	putative U2 snRNP auxiliary factor Stro	ATU2AF35	AT1G27650	-1.09	-0.13	-0.86	0.416888	0.638202	-6.45
261291_at	hypothetical protein predicted by genem	---	AT1G36970	1.11	0.16	0.86	0.416885	0.638202	-6.45
253476_at	S-receptor kinase -like protein serine/th	SD2-5	AT4G32300	1.15	0.20	0.86	0.416982	0.638284	-6.45
246719_at	homology to many predicted putative re	---	---	1.06	0.08	0.86	0.416997	0.638284	-6.45
AFFX-r2-At-	Arabidopsis thaliana /REF=U84969 /DE	---	---	1.06	0.09	0.86	0.417077	0.638321	-6.45
257245_at	hypothetical protein contains Pfam prof	---	AT3G24110	1.09	0.12	0.86	0.417058	0.638321	-6.45
256707_at	hypothetical protein predicted by genem	---	---	-1.06	-0.08	-0.86	0.417421	0.638723	-6.45
251127_at	putative protein predicted protein, Arabi	---	AT5G01080	1.08	0.11	0.86	0.417401	0.638723	-6.45
264139_at	hypothetical protein contains similarity to	---	AT1G78940	-1.07	-0.10	-0.86	0.417424	0.638723	-6.45
245607_at	kinesin like protein	---	AT4G14330	1.07	0.10	0.86	0.417456	0.638729	-6.45

265622_at	unknown protein	---	AT2G27280	1.06	0.08	0.86	0.417529	0.638798	-6.45
251012_at	putative protein ;supported by full-lengt	---	AT5G02580	1.44	0.53	0.86	0.417607	0.638875	-6.45
251717_at	putative protein EXOENZYMES REGU	LAF3	AT3G55850	1.10	0.13	0.86	0.417679	0.638942	-6.45
263457_at	unknown protein	SR1	AT2G22300	1.16	0.22	0.86	0.41779	0.639068	-6.45
251714_at	putative protein leucine-rich receptor-lik	---	AT3G56370	1.18	0.24	0.86	0.417901	0.639159	-6.45
256832_at	meiotic recombination protein (AtDMC1	DMC1	AT3G22880	1.12	0.16	0.86	0.417905	0.639159	-6.45
266955_at	mitochondrial ribosomal protein S14	RPS14	AT2G34520	-1.08	-0.12	-0.86	0.417945	0.639177	-6.45
262746_at	Expressed protein ; supported by full-ler	ATNUDX1	AT1G28960	1.06	0.08	0.86	0.418078	0.639338	-6.45
250252_at	transporter-like protein ;supported by ful	ZIFL1	AT5G13750	1.27	0.35	0.86	0.418142	0.639349	-6.45
258666_at	hypothetical protein	KOB1	AT3G08550	-1.07	-0.09	-0.86	0.418137	0.639349	-6.45
258297_at	Expressed protein ; supported by full-ler	---	AT3G23325	-1.08	-0.11	-0.86	0.418239	0.639383	-6.45
262460_s_a	fructokinase, putative similar to fructoki	---	AT1G06030 /	1.06	0.09	0.86	0.418248	0.639383	-6.45
254446_at	tubulin beta-9 chain ;supported by full-l	TUB9	AT4G20890	-1.06	-0.09	-0.86	0.41824	0.639383	-6.45
255086_at	putative protein chromosome I BAC F1	---	AT4G09300	1.08	0.11	0.86	0.418279	0.639388	-6.45
267331_at	putative salt-inducible protein	---	AT2G19280	-1.09	-0.12	-0.86	0.418316	0.639402	-6.45
266837_x_a	unknown protein	---	AT2G25990	-1.06	-0.09	-0.86	0.418544	0.639707	-6.45
266114_at	hypothetical protein predicted by gensca	---	AT2G02150	-1.06	-0.08	-0.86	0.418645	0.639818	-6.45
249018_at	CHP-rich zinc finger protein-like	---	AT5G44770	1.11	0.15	0.86	0.418746	0.639929	-6.45
247402_at	putative protein predicted proteins, Cae	---	AT5G62750	1.06	0.09	0.86	0.418816	0.639995	-6.45
266428_at	putative protein kinase contains a protei	---	AT2G07180	1.09	0.12	0.86	0.418846	0.639997	-6.45
266438_at	putative carboxyphosphonoenolpyruvate	---	AT2G43180	-1.09	-0.12	-0.86	0.418987	0.640091	-6.45
264519_at	putative reverse transcriptase similar to	---	AT1G10000	1.09	0.12	0.86	0.419054	0.640091	-6.45
245087_at	hypothetical protein predicted by gensca	DAR2	AT2G39830	-1.11	-0.15	-0.86	0.418945	0.640091	-6.45
264801_at	hypothetical protein gene overlaps Sp6	emb2411	AT1G08840	1.07	0.10	0.86	0.419038	0.640091	-6.45
246802_at	kinesin-like heavy chain non-consensus	ATK4	AT5G27000	-1.09	-0.12	-0.86	0.419075	0.640091	-6.45
256469_at	zinc-finger protein, putative similar to G	LOL1	AT1G32540	-1.12	-0.17	-0.86	0.418996	0.640091	-6.45
259635_at	purple acid phosphatase, putative simil	PAP6	AT1G56360	1.08	0.11	0.86	0.419193	0.640227	-6.45
252138_at	peroxidase-like protein peroxidase ATP	---	AT3G50990	-1.09	-0.12	-0.86	0.419251	0.640273	-6.45
260700_at	hypothetical protein identical to hypothe	---	AT1G32260	-1.08	-0.11	-0.86	0.419357	0.640392	-6.45
263561_at	unknown protein	---	AT2G15360	1.05	0.07	0.86	0.419679	0.640841	-6.46
258704_at	putative protein kinase similar to Pto kin	CCR1	AT3G09780	1.10	0.14	0.86	0.419709	0.640844	-6.46
259725_at	Expressed protein ; supported by full-ler	---	AT1G61065	-1.12	-0.16	-0.86	0.419754	0.640869	-6.46
247794_at	phosphoinositide specific phospholipase	PLC1	AT5G58670	-1.09	-0.12	-0.86	0.419818	0.640924	-6.46
262944_at	phosphoglycerate kinase, putative simil	PGK	AT1G79550	1.10	0.14	0.86	0.419908	0.641019	-6.46
258215_at	phosphoprotein phosphatase, putative	atToc64-III	AT3G17970	-1.11	-0.15	-0.86	0.419954	0.641046	-6.46

265980_at	hypothetical protein predicted by genefir	---	---	1.08	0.10	0.86	0.419983	0.641046	-6.46
254397_at	gibberellin 3 beta-hydroxylase - like pro	GA3OX3	AT4G21690	1.13	0.18	0.86	0.42001	0.641046	-6.46
250835_at	putative protein various predicted prote	DME	AT5G04560	1.08	0.12	0.86	0.420074	0.641100	-6.46
259929_at	transcription factor, putative similar to S	---	AT1G34360	-1.08	-0.11	-0.86	0.420177	0.641215	-6.46
AFFX-r2-At-	Arabidopsis thaliana /REF=M64116 /DE	---	---	1.15	0.20	0.86	0.420268	0.641254	-6.46
266545_at	hypothetical protein predicted by genefir	---	AT2G35290	1.14	0.19	0.86	0.420262	0.641254	-6.46
250151_at	high affinity nitrate transporter - like pro	ATNRT2.7	AT5G14570	-1.14	-0.19	-0.86	0.420287	0.641254	-6.46
267261_at	unknown protein ;supported by full-leng	---	AT2G23120	1.14	0.19	0.86	0.420476	0.641500	-6.46
259821_at	subtilisin-like serine protease contains s	---	AT1G66220	-1.09	-0.13	-0.86	0.420553	0.641521	-6.46
256051_at	hypothetical protein similar to putative N	CHX14	AT1G06970	1.09	0.12	0.86	0.420575	0.641521	-6.46
248332_at	heat-shock protein ; supported by cDNA	ATHSP90.	AT5G52640	1.34	0.42	0.86	0.420529	0.641521	-6.46
256699_at	hypothetical protein predicted by genem	---	AT3G20690	-1.08	-0.12	-0.86	0.420608	0.641530	-6.46
258552_at	putative pectate lyase similar to pectate	---	AT3G07010	1.49	0.58	0.86	0.420654	0.641557	-6.46
245055_at	hypothetical protein predicted by gensca	---	AT2G26470	-1.08	-0.12	-0.86	0.420801	0.641738	-6.46
255891_at	hypothetical protein predicted by gensca	EGY3	AT1G17870	-1.08	-0.12	-0.86	0.420888	0.641799	-6.46
259546_at	unknown protein	---	AT1G35350	-1.19	-0.25	-0.86	0.420926	0.641799	-6.46
257538_at	hypothetical protein predicted by genem	---	AT3G16160	1.06	0.09	0.86	0.4209	0.641799	-6.46
251733_at	copper homeostasis factor ;supported b	CCH	AT3G56240	-1.08	-0.11	-0.86	0.421114	0.641938	-6.46
247118_at	uridylyl transferases-like ; supported by	ACR1	AT5G65890	1.12	0.16	0.86	0.421157	0.641938	-6.46
261736_at	hypothetical protein simlar to hypothetic	---	AT1G47810	1.07	0.09	0.86	0.421147	0.641938	-6.46
254109_at	Pollen-specific protein precursor like Pc	SKS1	AT4G25240	-1.06	-0.09	-0.86	0.421066	0.641938	-6.46
257049_at	hypothetical protein predicted by gensca	---	AT3G15250	1.09	0.13	0.86	0.421122	0.641938	-6.46
263002_at	hypothetical protein predicted by genem	---	AT1G54200	-1.17	-0.23	-0.86	0.42121	0.641975	-6.46
262088_at	unknown protein	---	AT1G56020	1.07	0.09	0.86	0.421302	0.642073	-6.46
260828_at	unknown protein	---	AT1G06750	-1.07	-0.09	-0.86	0.421334	0.642079	-6.46
252249_at	putative protein heat shock protein 108	---	AT3G49770	1.08	0.12	0.86	0.421494	0.642280	-6.46
264873_at	putative indole-3-acetate beta-glucosyltr	UGT74B1	AT1G24100	-1.21	-0.28	-0.86	0.421526	0.642285	-6.46
254722_at	putative protein predicted protein, Arabi	---	AT4G13530	1.13	0.18	0.86	0.421559	0.642292	-6.46
258994_at	unknown protein similar to putative guar	RAPTOR1	AT3G08850	-1.06	-0.09	-0.86	0.421624	0.642306	-6.46
249263_at	putative protein contains similarity to unl	---	AT5G41730	1.06	0.09	0.86	0.421606	0.642306	-6.46
258781_at	hypothetical protein predicted by gensca	---	AT3G11740	1.06	0.08	0.86	0.421685	0.642318	-6.46
255432_at	SYR1-like syntaxin ;supported by full-le	SYP123	AT4G03330	1.07	0.09	0.86	0.421689	0.642318	-6.46
247900_at	60S acidic ribosomal protein P3 ; suppo	---	AT5G57290	-1.15	-0.20	-0.86	0.421902	0.642471	-6.46
252551_at	phospholipase - like protein cytosolic ph	---	AT3G45880	-1.10	-0.13	-0.86	0.421862	0.642471	-6.46
262562_at	hypothetical protein predicted by genem	---	AT1G34220	-1.06	-0.08	-0.86	0.421862	0.642471	-6.46

250578_at	proanthranilate N-benzoyltransferase -l	---	AT5G07850	-1.06	-0.09	-0.86	0.4219	0.642471	-6.46
257084_at	unknown protein	---	AT3G20620	-1.11	-0.15	-0.85	0.421954	0.642507	-6.46
248430_at	putative protein similar to unknown prote	---	AT5G51800	-1.08	-0.10	-0.85	0.422001	0.642537	-6.46
252757_at	putative protein several hypothetical pro	---	---	1.08	0.11	0.85	0.422044	0.642559	-6.46
261822_at	unknown protein ;supported by full-lengt	---	AT1G11380	-1.14	-0.19	-0.85	0.422074	0.642562	-6.46
246825_at	putative protein various predicted prote	---	AT5G26260	1.06	0.08	0.85	0.422102	0.642562	-6.46
261110_at	E2, ubiquitin-conjugating enzyme 16 (U	UBC16	AT1G75440	1.10	0.14	0.85	0.422363	0.642873	-6.46
258799_at	putative 40S ribosomal protein identical	RPSAb	AT3G04770	-1.10	-0.14	-0.85	0.42235	0.642873	-6.46
252243_at	putative protein some putative proteins -	---	AT3G50120	-1.16	-0.21	-0.85	0.422473	0.642998	-6.46
262718_at	hypothetical protein similar to putative n	---	---	1.07	0.10	0.85	0.42261	0.643121	-6.46
252027_at	Spot 3 protein and vacuolar sorting rece	VSR1	AT3G52850	1.06	0.09	0.85	0.422589	0.643121	-6.46
249070_at	cellulose synthase catalytic subunit-like	CESA4	AT5G44030	1.09	0.12	0.85	0.422729	0.643240	-6.46
258970_at	putative serine carboxypeptidase precur	scpl49	AT3G10410	-1.10	-0.13	-0.85	0.422773	0.643240	-6.46
257852_at	unknown protein	---	AT3G12950	1.09	0.12	0.85	0.422765	0.643240	-6.46
255454_at	hypothetical protein	---	AT4G02910	1.06	0.09	0.85	0.422885	0.643368	-6.46
256464_at	late-embryogenesis abundant protein, p	---	AT1G32560	1.20	0.27	0.85	0.422914	0.643369	-6.46
253604_at	hypothetical protein	---	AT4G30970	1.06	0.08	0.85	0.423054	0.643539	-6.46
247613_at	xABC transporter - like protein breast c	---	AT5G60740	1.08	0.12	0.85	0.423199	0.643716	-6.46
251707_at	protein kinase C inhibitor-like protein pr	---	AT3G56490	1.08	0.10	0.85	0.423353	0.643826	-6.46
267242_at	hypothetical protein predicted by grail	---	AT2G02670	-1.07	-0.10	-0.85	0.423356	0.643826	-6.46
259828_at	RING-H2 zinc finger protein ATL3, puta	---	AT1G72220	1.09	0.12	0.85	0.423337	0.643826	-6.46
262606_at	hypothetical protein predicted by gensca	---	AT1G15190	1.09	0.12	0.85	0.42351	0.644018	-6.46
267464_at	putative pectinesterase	---	AT2G19150	1.07	0.10	0.85	0.423575	0.644073	-6.46
253105_at	putative protein zinc finger protein, Arat	---	AT4G35840	-1.11	-0.15	-0.85	0.423667	0.644170	-6.46
254954_at	hypothetical protein ;supported by full-le	---	AT4G10910	-1.21	-0.27	-0.85	0.423855	0.644370	-6.46
267316_at	homeodomain transcription factor (ATHI	PHB	AT2G34710	-1.13	-0.17	-0.85	0.423854	0.644370	-6.46
254993_at	putative protein kinase	---	AT4G10730	1.06	0.09	0.85	0.423951	0.644431	-6.46
248284_at	Expressed protein ; supported by full-ler	---	AT5G52975	-1.09	-0.12	-0.85	0.423945	0.644431	-6.46
267151_at	aspartate aminotransferase (AAT1) iden	ASP1	AT2G30970	1.10	0.14	0.85	0.423997	0.644457	-6.46
261727_at	S-adenosyl-methionine-sterol-C-methyl	SMT3	AT1G76090	1.14	0.19	0.85	0.424107	0.644538	-6.46
255553_at	predicted protein of unknown function ;s	---	AT4G01960	1.10	0.14	0.85	0.424105	0.644538	-6.46
260362_at	putative protein kinase similar to C-term	---	AT1G70530	1.17	0.23	0.85	0.424152	0.644548	-6.46
249260_at	Pto kinase interactor 1-like protein	---	AT5G41680	1.07	0.10	0.85	0.42417	0.644548	-6.46
264570_at	unknown protein Similar to Caenorhabd	---	AT1G05350	1.08	0.11	0.85	0.424224	0.644588	-6.46
251365_at	putative DNA-binding protein At2g3362	---	AT3G61310	-1.09	-0.13	-0.85	0.424294	0.644646	-6.46

257082_at	hypothetical protein	COBL10	AT3G20580	1.06	0.09	0.85	0.424347	0.644646	-6.46
260121_at	AIG1-like protein similar to AIG1 protein	---	AT1G33910	1.06	0.08	0.85	0.424332	0.644646	-6.46
245381_at	MYB transcription factor like protein	MYB39	AT4G17785	1.06	0.09	0.85	0.424456	0.644768	-6.46
265370_s_a	unknown protein related to GB:AAD153	---	AT3G30415	1.06	0.09	0.85	0.424582	0.644917	-6.46
247576_at	putative protein predicted protein, Arabi	---	AT5G61280	-1.06	-0.08	-0.85	0.42467	0.645008	-6.46
261624_at	nucleotide sugar epimerase, putative si	GAE2	AT1G02000	1.13	0.18	0.85	0.424744	0.645018	-6.46
259389_at	hypothetical protein predicted by genem	---	AT1G06320	1.06	0.09	0.85	0.424798	0.645018	-6.46
251610_at	putative protein hypothetical protein T2	---	AT3G57930	-1.23	-0.30	-0.85	0.424841	0.645018	-6.46
256523_at	unknown protein ;supported by full-lengt	---	AT1G66070	-1.08	-0.11	-0.85	0.424808	0.645018	-6.46
249535_at	transporter -like protein N system amino	---	AT5G38820	-1.09	-0.12	-0.85	0.424847	0.645018	-6.46
254548_at	putative protein various predicted prote	---	AT4G19865	-1.13	-0.18	-0.85	0.424746	0.645018	-6.46
259720_at	hypothetical protein predicted by genefir	---	AT1G61080	1.08	0.11	0.85	0.424945	0.645081	-6.46
264136_at	leucine-rich repeat transmembrane prot	SRF5	AT1G78980	1.10	0.14	0.85	0.424942	0.645081	-6.46
255027_at	hypothetical protein F21E10.5 Arabidop	---	AT4G09880	1.07	0.10	0.85	0.425046	0.645192	-6.46
246529_at	serine/threonine-specific protein kinase-	---	AT5G15730	1.17	0.22	0.85	0.425099	0.645229	-6.46
259530_at	hypothetical protein	---	AT1G12450	1.14	0.19	0.85	0.425156	0.645273	-6.46
264577_at	putative peroxidase Strong similarity to A	RCI3	AT1G05260	-1.06	-0.08	-0.85	0.425219	0.645285	-6.46
245258_at	lupeol synthase like protein ; supported	ATPEN1	AT4G15340	1.07	0.10	0.85	0.42522	0.645285	-6.46
266594_at	hypothetical protein	---	AT2G46190	1.05	0.07	0.85	0.425298	0.645360	-6.46
259808_at	hypothetical protein contains Pfam profil	---	AT1G49790	1.06	0.08	0.85	0.425648	0.645848	-6.47
250410_at	putative protein putative ATP/GTP-bind	---	AT5G11010	-1.11	-0.15	-0.85	0.425697	0.645879	-6.47
264497_at	hypothetical protein predicted by gensca	ATPUP4	AT1G30840	1.10	0.14	0.85	0.425866	0.646093	-6.47
252629_at	cytochrome P450 - like protein cytochro	---	AT3G44970	-1.06	-0.08	-0.85	0.425984	0.646228	-6.47
259653_at	unknown protein	---	AT1G55240	1.06	0.08	0.85	0.426034	0.646261	-6.47
267633_at	hypothetical protein predicted by genefir	---	AT2G42180	1.06	0.08	0.85	0.426154	0.646400	-6.47
248351_at	unknown protein ; supported by cDNA:	---	AT5G52200	1.12	0.16	0.85	0.426207	0.646439	-6.47
257492_at	hypothetical protein contains similarity to	ARR19	AT1G49190	-1.05	-0.08	-0.85	0.42631	0.646531	-6.47
252240_at	putative protein several hypothetical pro	---	AT3G50010	-1.08	-0.11	-0.85	0.426325	0.646531	-6.47
260302_at	putative sulfate transporter contains Pfa	---	AT1G80310 /	1.09	0.13	0.85	0.426391	0.646545	-6.47
263653_at	putative ethylene receptor (ERS2) EST	ERS2	AT1G04310	1.09	0.12	0.85	0.426381	0.646545	-6.47
253277_at	cinnamyl alcohol dehydrogenase - like	ATCAD5	AT4G34230	1.10	0.14	0.85	0.426425	0.646554	-6.47
258842_at	unknown protein similar to putative ATP	CLPS3	AT3G04680	-1.09	-0.13	-0.85	0.42654	0.646643	-6.47
258801_at	unknown protein predicted by genscan,	---	AT3G04560	1.05	0.08	0.85	0.426534	0.646643	-6.47
258893_at	putative disease resistance protein simil	AtRLP33	AT3G05660	-1.27	-0.35	-0.85	0.42662	0.646720	-6.47
266692_at	Ac-like transposase related to Ac Ds tra	---	AT2G19960	-1.07	-0.09	-0.85	0.426756	0.646884	-6.47

246508_at	sugar transporter-like protein putative s	PGLCT	AT5G16150	1.09	0.12	0.85	0.426987	0.647191	-6.47
259760_at	hypothetical protein similar to GB:AAD4	---	AT1G77580	-1.06	-0.08	-0.84	0.427148	0.647349	-6.47
254036_at	putative peroxidase peroxidase (EC 1.1	---	AT4G25980	-1.07	-0.09	-0.84	0.427134	0.647349	-6.47
245477_at	hypothetical protein	ARR2	AT4G16110	1.07	0.10	0.84	0.427282	0.647380	-6.47
263821_s_a	40S ribosomal protein S16 Same as GB	---	AT2G09990 /	-1.10	-0.14	-0.84	0.427229	0.647380	-6.47
259184_at	unknown protein ;supported by full-leng	---	AT3G01520	-1.07	-0.10	-0.84	0.427231	0.647380	-6.47
249046_at	berberine bridge enzyme	---	AT5G44400	-1.15	-0.20	-0.84	0.427281	0.647380	-6.47
253894_at	NWMU2 - 2S albumin 2 precursor	---	AT4G27150	-1.06	-0.09	-0.84	0.427319	0.647393	-6.47
249859_at	serine protein kinase-like protein ;suppo	---	AT5G22840 /	-1.13	-0.18	-0.84	0.427435	0.647483	-6.47
260571_at	MAP kinase (ATMPK6) identical to GB:(	ATMPK6	AT2G43790	1.06	0.09	0.84	0.42741	0.647483	-6.47
265131_at	putative polygalacuronase isoenzyme 1	JP630	AT1G23760	1.17	0.23	0.84	0.427518	0.647565	-6.47
252995_at	hypothetical protein ;supported by full-le	---	AT4G38370	-1.09	-0.12	-0.84	0.427577	0.647568	-6.47
254015_at	putative beta-galactosidase beta-galact	BGAL12	AT4G26140	-1.11	-0.15	-0.84	0.427554	0.647568	-6.47
256544_at	Mlo-like protein similar to Mlo [Hordeum	MLO9	AT1G42560	1.08	0.11	0.84	0.427855	0.647947	-6.47
252800_at	putative protein	---	---	-1.07	-0.09	-0.84	0.428062	0.648217	-6.47
255057_at	hypothetical protein	---	AT4G09840	-1.06	-0.08	-0.84	0.428097	0.648227	-6.47
245191_at	F12A21.10 similar to terminal ear1 gb|A	TEL2	AT1G67770	1.11	0.15	0.84	0.428247	0.648318	-6.47
265264_at	hypothetical protein predicted by gensca	---	AT2G42930	1.06	0.09	0.84	0.428195	0.648318	-6.47
250583_at	zinc finger transcription factor ; support	PEI1	AT5G07500	1.06	0.09	0.84	0.428299	0.648318	-6.47
262573_at	hypothetical protein Similar to gi|437740	PDF1A	AT1G15390	1.08	0.11	0.84	0.428238	0.648318	-6.47
260516_at	unknown protein	---	AT1G51450	-1.08	-0.11	-0.84	0.428296	0.648318	-6.47
265378_at	putative GATA-type zinc finger transcrip	---	AT2G18380	1.07	0.09	0.84	0.428378	0.648394	-6.47
263826_at	hypothetical protein predicted by gensca	---	AT2G40410	1.10	0.13	0.84	0.428512	0.648533	-6.47
259313_at	hypothetical protein predicted by gensca	---	AT3G05090	-1.08	-0.11	-0.84	0.428526	0.648533	-6.47
248946_at	putative protein similar to unknown prote	---	AT5G45530	1.06	0.09	0.84	0.428623	0.648636	-6.47
249168_at	putative protein strong similarity to unkn	---	AT5G42870	1.08	0.11	0.84	0.428662	0.648652	-6.47
265396_at	predicted protein	---	AT2G21040	-1.10	-0.14	-0.84	0.428835	0.648742	-6.47
252640_at	acyl CoA reductase -like protein acyl C	FAR8	AT3G44560	-1.06	-0.09	-0.84	0.428821	0.648742	-6.47
247264_at	putative protein contains similarity to NA	XND1	AT5G64530	1.17	0.23	0.84	0.428833	0.648742	-6.47
260093_at	putative serine carboxypeptidase simila	scpl6	AT1G73270	1.06	0.09	0.84	0.428813	0.648742	-6.47
246682_at	putative protein EXOSTOSIN-1 (PUTA	XGD1	AT5G33290	1.08	0.11	0.84	0.428974	0.648892	-6.47
261730_s_a	mutator-like transposase, putative simil	---	---	-1.07	-0.10	-0.84	0.428992	0.648892	-6.47
250068_at	CHP-rich zinc finger protein-like	---	AT5G17960	1.08	0.12	0.84	0.429071	0.648970	-6.47
253286_at	hypothetical protein	FUC95A	AT4G34260	1.31	0.39	0.84	0.429258	0.649179	-6.47
259234_at	unknown protein similar to unknown pro	---	AT3G11620	1.07	0.10	0.84	0.429281	0.649179	-6.47

266652_at	unknown protein	---	AT2G25760	-1.06	-0.09	-0.84	0.429323	0.649179	-6.47
263670_at	hypothetical protein predicted by gensca	---	AT2G04840	-1.06	-0.09	-0.84	0.429311	0.649179	-6.47
265765_at	hypothetical protein predicted by gensca	---	AT2G48060	-1.08	-0.10	-0.84	0.429401	0.649254	-6.47
246642_s_a	putative protein predicted proteins, Arat	---	---	1.05	0.08	0.84	0.429525	0.649398	-6.47
260510_at	hypothetical protein predicted by genem	---	AT1G51580	-1.12	-0.17	-0.84	0.429726	0.649635	-6.47
260917_at	unknown protein similar to hypothetical p	---	AT1G02700	1.08	0.11	0.84	0.429739	0.649635	-6.47
266356_at	putative uclacyanin I identical to GP:U76	UCC1	AT2G32300	1.06	0.08	0.84	0.429794	0.649676	-6.47
265940_at	putative nucleosome assembly protein	NAP1;2	AT2G19480	-1.07	-0.10	-0.84	0.429836	0.649696	-6.47
248553_at	putative protein strong similarity to unkn	---	AT5G50170	1.15	0.20	0.84	0.429908	0.649761	-6.47
256329_at	unknown protein	SEC5A	AT1G76850	1.05	0.08	0.84	0.43006	0.649949	-6.47
260665_at	unknown protein ;supported by full-lengt	---	AT1G19360	1.07	0.10	0.84	0.430161	0.650058	-6.47
260550_at	putative sterol dehydrogenase ; suppor	---	AT2G43420	1.10	0.14	0.84	0.430239	0.650089	-6.47
252755_at	putative protein hypothetical proteins - A	---	---	-1.07	-0.10	-0.84	0.430239	0.650089	-6.47
252019_at	late embryogenesis abundant protein -	---	AT3G53040	1.05	0.08	0.84	0.430274	0.650100	-6.47
259015_at	unknown protein similar to hypothetical p	---	AT3G07350	1.19	0.25	0.84	0.430354	0.650105	-6.47
246686_at	putative protein predicted proteins - Arat	---	---	1.09	0.13	0.84	0.430357	0.650105	-6.47
265830_at	putative helicase	---	---	1.09	0.12	0.84	0.430363	0.650105	-6.47
264016_at	putative auxin-regulated protein	---	AT2G21220	1.07	0.10	0.84	0.430431	0.650122	-6.47
266625_at	putative peroxidase	---	AT2G35380	1.07	0.10	0.84	0.430418	0.650122	-6.47
256419_at	RNA-binding protein similar to GI:82925	---	AT1G33470	-1.08	-0.11	-0.84	0.430474	0.650122	-6.47
252229_at	putative protein lea32, Arabidopsis thali	---	AT3G49890	-1.09	-0.12	-0.84	0.430489	0.650122	-6.47
252713_at	calmodulin 7 ; supported by full-length c	CAM7	AT3G43810	1.07	0.10	0.84	0.43064	0.650308	-6.47
261125_at	zinc finger protein 2, putative similar to	---	AT1G04990	1.13	0.18	0.84	0.430797	0.650501	-6.47
246443_at	hypothetical protein ;supported by full-le	---	AT5G17620	-1.08	-0.11	-0.84	0.430841	0.650525	-6.47
256952_at	mannosidase, putative similar to manno	---	AT3G21160	-1.08	-0.12	-0.84	0.430911	0.650588	-6.47
265970_at	Mutator-like transposase similar to MUF	---	---	1.06	0.08	0.84	0.431021	0.650711	-6.47
249541_at	anthranilate N-benzoyltransferase -like	---	AT5G38130	-1.07	-0.10	-0.84	0.431077	0.650753	-6.47
249069_at	unknown protein	---	AT5G44010	-1.16	-0.21	-0.84	0.431133	0.650794	-6.47
266513_at	unknown protein	---	AT2G47700	1.09	0.12	0.84	0.431263	0.650890	-6.47
265137_at	F-box protein family, AtFBX10 contains	---	AT1G51290	1.07	0.10	0.84	0.431283	0.650890	-6.47
265406_at	En/Spm-like transposon protein related	---	---	1.05	0.07	0.84	0.431251	0.650890	-6.47
256420_at	unknown protein	---	AT1G33475 /	1.09	0.12	0.84	0.431428	0.651025	-6.47
265644_at	hypothetical protein predicted by genefir	ATEPR1	AT2G27380	1.06	0.09	0.84	0.431429	0.651025	-6.47
264663_at	unknown protein Similar to A. thaliana r	LRR XI-23	AT1G09970	1.22	0.29	0.84	0.431502	0.651092	-6.48
259486_at	embryo abundance protein (EMB20), p	---	AT1G15710	-1.08	-0.11	-0.84	0.431629	0.651197	-6.48

252807_at	putative replication protein various pred	---	---	-1.05	-0.07	-0.84	0.431612	0.651197	-6.48
251195_at	glutaredoxin -like protein glutaredoxin, (	---	AT3G62930	-1.12	-0.17	-0.84	0.431702	0.651265	-6.48
265231_s_a	hypothetical protein	---	AT2G07713	1.07	0.09	0.84	0.431777	0.651268	-6.48
266346_at	putative homeodomain transcription fact	ATHB17	AT2G01430	1.09	0.12	0.84	0.43179	0.651268	-6.48
256120_at	hypothetical protein contains similarity to	---	AT1G18130	1.06	0.08	0.84	0.431749	0.651268	-6.48
256893_x_a	unknown protein	---	---	-1.06	-0.08	-0.84	0.431864	0.651337	-6.48
263357_s_a	Mutator-like transposase similar to MUF	---	---	-1.06	-0.08	-0.84	0.431906	0.651357	-6.48
253222_at	chalcone synthase - like protein chalcor	---	AT4G34850	-1.05	-0.08	-0.84	0.431969	0.651409	-6.48
262301_at	ripening-induced protein, putative simila	---	AT1G70880	1.07	0.10	0.84	0.432001	0.651414	-6.48
263741_at	hypothetical protein predicted by gensca	---	AT2G20620	-1.09	-0.12	-0.84	0.432052	0.651448	-6.48
249013_at	receptor-like protein kinase	GSO2	AT5G44700	-1.05	-0.08	-0.84	0.432228	0.651671	-6.48
250304_at	elongation factor 1B alpha-subunit (emb	---	AT5G12110	-1.23	-0.30	-0.84	0.432332	0.651784	-6.48
259846_at	peptide transporter PTR2-B, putative si	---	AT1G72140	1.08	0.11	0.83	0.432478	0.651875	-6.48
245458_at	kinase like protein	---	AT4G16970	1.07	0.10	0.83	0.432474	0.651875	-6.48
248215_at	putative protein contains similarity to RN	---	AT5G53680	1.10	0.14	0.83	0.432451	0.651875	-6.48
245698_at	phosphate/phosphoenolpyruvate translo	---	AT5G04160	1.12	0.17	0.83	0.432598	0.652013	-6.48
267447_at	putative GTP-binding protein	ArRABA1h	AT2G33870	1.06	0.08	0.83	0.432743	0.652188	-6.48
266865_at	omega-3 fatty acid desaturase identical	FAD3	AT2G29980	1.76	0.81	0.83	0.432812	0.652193	-6.48
251927_at	hypothetical protein ER6 protein - Lycor	---	AT3G53990	1.06	0.09	0.83	0.432991	0.652193	-6.48
252096_at	hypothetical protein ; supported by cDN	---	AT3G51180	-1.12	-0.17	-0.83	0.433004	0.652193	-6.48
260346_at	hypothetical protein predicted by genem	CLE10	AT1G69320 /	1.08	0.11	0.83	0.432931	0.652193	-6.48
256123_at	hypothetical protein predicted by gensca	GC2	AT1G18190	1.05	0.08	0.83	0.432982	0.652193	-6.48
245234_at	myb-like protein similarity to ATMYB4 -	AtMYB18	AT4G25560	1.08	0.11	0.83	0.432879	0.652193	-6.48
249296_at	kinesin-like protein	---	AT5G41310	1.08	0.11	0.83	0.432954	0.652193	-6.48
258795_at	hypothetical protein similar to putative D	---	AT3G04570	1.08	0.12	0.83	0.432846	0.652193	-6.48
251896_at	putative protein predicted proteins, Arat	---	AT3G54390	-1.09	-0.12	-0.83	0.432887	0.652193	-6.48
263369_at	unknown protein	---	AT2G20480	-1.06	-0.08	-0.83	0.433133	0.652259	-6.48
260003_at	unknown protein ;supported by full-leng	IAR1	AT1G68100	1.06	0.08	0.83	0.433119	0.652259	-6.48
249182_at	putative protein similar to unknown prote	---	AT5G42960	1.06	0.09	0.83	0.433126	0.652259	-6.48
250995_at	dnaK-type molecular chaperone hsc70.1	HSC70-1	AT5G02500	-1.10	-0.14	-0.83	0.433231	0.652363	-6.48
259832_at	transfactor, putative similar to GI:45196	---	AT1G69580	-1.19	-0.25	-0.83	0.433286	0.652403	-6.48
261768_at	gibberellin 3 beta-hydroxylase, putative	GA3OX1	AT1G15550	1.08	0.11	0.83	0.433344	0.652404	-6.48
264401_at	dihydroflavonol 4-reductase, putative si	BAN	AT1G61720	1.05	0.08	0.83	0.433329	0.652404	-6.48
261656_at	unknown protein similar to kinesin-like p	ARK2	AT1G01950	1.19	0.25	0.83	0.433459	0.652459	-6.48
247861_at	strong similarity to unknown protein (gb|	---	AT5G58160	1.08	0.12	0.83	0.433466	0.652459	-6.48

253007_at	putative protein hypothetical protein HI(	---	AT4G38090	-1.08	-0.12	-0.83	0.433436	0.652459	-6.48
253780_at	protein phosphatase 2C-like protein pro	---	AT4G28400	-1.16	-0.22	-0.83	0.433536	0.652520	-6.48
259330_at	hypothetical protein gene model predicte	---	AT3G16270	1.08	0.11	0.83	0.433586	0.652554	-6.48
248766_at	putative protein strong similarity to unkn	---	AT5G47580	-1.15	-0.20	-0.83	0.433637	0.652586	-6.48
251720_at	putative protein	---	AT3G56160	-1.14	-0.19	-0.83	0.433946	0.653009	-6.48
245716_at	Expressed protein ; supported by cDNA	NDC1	AT5G08740	-1.12	-0.17	-0.83	0.434112	0.653172	-6.48
249660_at	putative protein similar to unknown prote	---	AT5G36720 /	-1.09	-0.13	-0.83	0.434099	0.653172	-6.48
245154_at	putative protein similarity to predicted pr	---	AT5G12460	1.07	0.10	0.83	0.434194	0.653253	-6.48
253865_at	putative RING zinc finger protein Arabic	---	AT4G27470	-1.11	-0.15	-0.83	0.434268	0.653321	-6.48
266626_at	hypothetical protein predicted by gensca	---	AT2G35360	-1.10	-0.13	-0.83	0.43432	0.653326	-6.48
262318_at	putative hypersensitivity-related protein	---	AT1G27620	1.07	0.10	0.83	0.434329	0.653326	-6.48
252119_at	thioredoxin h ;supported by full-length c	ATTRX1	AT3G51030	1.13	0.18	0.83	0.434396	0.653380	-6.48
248184_at	CHP-rich zinc finger protein-like	---	AT5G54050	-1.06	-0.08	-0.83	0.434443	0.653380	-6.48
260016_at	Athila ORF 1, putative simlar to GI:8065	---	---	-1.06	-0.08	-0.83	0.434451	0.653380	-6.48
262240_at	Pto kinase interactor 1, putative similar	---	AT1G48220	1.07	0.10	0.83	0.434654	0.653644	-6.48
266586_s_a	putative protein	---	---	1.05	0.07	0.83	0.434758	0.653757	-6.48
249863_at	putative protein contains similarity to unl	VPS24.1	AT5G22950	1.05	0.07	0.83	0.434931	0.653974	-6.48
258777_at	hypothetical protein predicted by gensca	---	AT3G11850	-1.09	-0.13	-0.83	0.435077	0.654106	-6.48
264768_at	hypothetical protein similar to putative d	---	AT1G61410	-1.07	-0.09	-0.83	0.435065	0.654106	-6.48
248404_at	trehalose-6-phosphate phosphatase ; su	ATTPPA	AT5G51460	-1.15	-0.21	-0.83	0.435173	0.654113	-6.48
263918_at	putative proline transporter ;supported l	ProT3	AT2G36590	-1.28	-0.35	-0.83	0.435165	0.654113	-6.48
264001_at	putative peroxidase ;supported by full-le	---	AT2G22420	-1.14	-0.19	-0.83	0.435123	0.654113	-6.48
258248_at	hypothetical protein predicted by genem	---	AT3G29140	-1.11	-0.14	-0.83	0.435196	0.654113	-6.48
264616_at	unknown protein	---	AT2G17740	1.47	0.56	0.83	0.435305	0.654234	-6.48
263710_at	unknown protein ;supported by full-leng	---	AT1G09330	1.07	0.10	0.83	0.435347	0.654253	-6.48
251757_at	Ca-dependent solute carrier - like prote	---	AT3G55640	-1.11	-0.15	-0.83	0.435423	0.654325	-6.48
245728_at	steroid 22-alpha-hydroxylase, putative s	---	AT1G73340	1.08	0.12	0.83	0.435453	0.654326	-6.48
255708_at	predicted protein	---	AT4G00232	1.07	0.10	0.83	0.435525	0.654392	-6.48
246731_at	putative protein RING finger rngB prote	ACBP5	AT5G27630	1.07	0.10	0.83	0.435619	0.654491	-6.48
267344_at	hypothetical protein predicted by genefir	---	AT2G44230	-1.16	-0.22	-0.83	0.435669	0.654522	-6.48
266689_at	hypothetical protein predicted by gensca	---	AT2G19930	1.12	0.17	0.83	0.435813	0.654695	-6.48
262908_at	pyruvate dehydrogenase e1 alpha subu	AT-E1 ALF	AT1G59900	-1.06	-0.09	-0.83	0.435877	0.654705	-6.48
267387_at	hypothetical protein predicted by gensca	---	AT2G44440	-1.05	-0.08	-0.83	0.435854	0.654705	-6.48
254304_at	hypothetical protein ; supported by cDN	---	AT4G22270	-1.08	-0.12	-0.83	0.436053	0.654927	-6.48
253902_at	NWMU4 - 2S albumin 4 precursor ; sup	---	AT4G27170	1.06	0.08	0.83	0.436176	0.655063	-6.48

265125_at	hypothetical protein similar to putative C	---	AT1G55410	1.05	0.08	0.83	0.436202	0.655063	-6.48
265141_at	hypothetical protein predicted by gensca	---	AT1G51350	1.07	0.10	0.83	0.436307	0.655083	-6.48
254235_at	putative Ap2 domain protein DNA-bindi	CRF2	AT4G23750	-1.06	-0.09	-0.83	0.436329	0.655083	-6.48
253347_at	putative protein	---	AT4G33610	-1.06	-0.09	-0.83	0.436329	0.655083	-6.48
267183_at	hypothetical protein predicted by gensca	---	AT2G44020	-1.07	-0.09	-0.83	0.43627	0.655083	-6.48
259611_at	GTP-binding protein RAB7D, putative s	AtRABG3c	AT1G52280	-1.08	-0.11	-0.83	0.436519	0.655316	-6.48
260501_at	unknown protein ; supported by cDNA:	---	AT2G41770	1.10	0.13	0.83	0.43655	0.655316	-6.48
257569_at	hypothetical protein	---	AT3G26350	-1.10	-0.13	-0.83	0.436571	0.655316	-6.48
253107_at	putative protein predicted proteins, Arat	---	AT4G35880	1.09	0.12	0.83	0.436632	0.655365	-6.48
267241_at	hypothetical protein predicted by gensca	---	AT2G02490 /	1.06	0.08	0.83	0.43674	0.655440	-6.48
252589_s_a	putative protein different transporter pro	NAXT1	AT3G45650 /	1.19	0.25	0.83	0.43673	0.655440	-6.48
248257_at	putative protein similar to unknown prote	---	AT5G53410	-1.09	-0.13	-0.83	0.436782	0.655460	-6.48
266785_at	putative receptor-like protein kinase	---	AT2G28970	1.07	0.10	0.83	0.436956	0.655678	-6.48
252980_at	putative protein Human multiple exosto	---	AT4G38040	1.06	0.08	0.83	0.437286	0.655837	-6.48
265425_at	hypothetical protein	GCL2	AT2G20770	1.09	0.12	0.83	0.437253	0.655837	-6.48
249543_at	Expressed protein ; supported by full-ler	---	---	-1.08	-0.10	-0.83	0.43726	0.655837	-6.48
246915_at	malate dehydrogenase - like protein ma	ATNADP-M	AT5G25880	-1.13	-0.17	-0.83	0.437147	0.655837	-6.48
254351_at	putative protein probable membrane pr	SOBER1	AT4G22300	1.08	0.11	0.83	0.43725	0.655837	-6.48
259542_at	Expressed protein ; supported by full-ler	---	AT1G20575	-1.07	-0.09	-0.83	0.437191	0.655837	-6.48
246186_at	PINHEAD - like protein PINHEAD, Arab	---	AT5G21030	-1.10	-0.14	-0.83	0.437303	0.655837	-6.48
266975_at	hypothetical protein predicted by grail	ATEXO70I	AT2G39380	1.16	0.22	0.83	0.437256	0.655837	-6.48
254511_at	hypothetical protein	---	AT4G20220	1.07	0.09	0.83	0.43732	0.655837	-6.48
262638_at	oxidoreductase, putative contains Pfam	---	AT1G06650	-1.06	-0.09	-0.83	0.437396	0.655852	-6.48
258624_at	unknown protein ; supported by cDNA:	---	AT3G02950	-1.08	-0.11	-0.83	0.437417	0.655852	-6.48
263723_at	putative Ta11-like non-LTR retroelemen	---	AT2G13500	1.06	0.09	0.83	0.437394	0.655852	-6.48
255334_at	putative transposon protein	---	---	1.05	0.07	0.82	0.437648	0.656156	-6.49
262173_at	betaine aldehyde dehydrogenase, puta	ALDH10A8	AT1G74920	-1.07	-0.10	-0.82	0.437781	0.656268	-6.49
246354_at	hypothetical protein	---	AT1G38950	1.07	0.10	0.82	0.437759	0.656268	-6.49
252135_at	putative cold acclimation protein cold a	COR413-P	AT3G50830	-1.10	-0.13	-0.82	0.437877	0.656370	-6.49
259270_at	putative porin similar to outer mitochond	VDAC1	AT3G01280	1.08	0.11	0.82	0.438022	0.656544	-6.49
266195_at	putative RING zinc finger protein	---	AT2G39100	1.06	0.09	0.82	0.43806	0.656557	-6.49
257104_at	ER lumen retaining receptor (HDEL rec	---	AT3G25040	-1.07	-0.09	-0.82	0.438239	0.656783	-6.49
254331_s_a	cytochrome P450 - like protein flavonoi	CYP706A2	AT4G22690 /	1.21	0.27	0.82	0.438531	0.657177	-6.49
259372_at	homeotic protein boi1AP1, putative sim	AP1	AT1G69120	1.07	0.09	0.82	0.438596	0.657231	-6.49
245531_at	hydroxynitrile lyase like protein	scpl30	AT4G15100	1.10	0.14	0.82	0.438627	0.657234	-6.49

250012_x_a	auxin-induced protein-like	---	AT5G18060	-1.42	-0.51	-0.82	0.43883	0.657496	-6.49
257438_at	hypothetical protein similarity to plant lip	---	AT2G15325	1.06	0.08	0.82	0.439037	0.657736	-6.49
263892_at	putative MYB family transcription factor	RAX2	AT2G36890	1.05	0.07	0.82	0.439048	0.657736	-6.49
250712_at	human RAN binding protein 16-like	---	AT5G06120	-1.08	-0.10	-0.82	0.439116	0.657795	-6.49
256354_at	dormancy related protein, putative simil	---	AT1G54870	-1.09	-0.12	-0.82	0.439187	0.657857	-6.49
250932_s_a	putative protein MED7, Homo sapiens,	---	AT5G03220 /	-1.06	-0.09	-0.82	0.439253	0.657885	-6.49
248076_at	unknown protein	---	AT5G55750	1.06	0.08	0.82	0.439263	0.657885	-6.49
260669_at	hypothetical protein predicted by genem	---	AT1G19340	-1.07	-0.10	-0.82	0.439328	0.657940	-6.49
266559_at	unknown protein	---	AT2G23920	1.07	0.10	0.82	0.439372	0.657962	-6.49
246594_at	pyrroline-5-carboxylate reductase ;supp	P5CR	AT5G14800	-1.09	-0.12	-0.82	0.439454	0.657980	-6.49
265779_at	unknown protein	---	AT2G07360	1.11	0.15	0.82	0.439428	0.657980	-6.49
253409_at	putative protein	---	AT4G32960	-1.06	-0.08	-0.82	0.43947	0.657980	-6.49
248477_at	putative protein similar to unknown prote	---	AT5G50900	1.09	0.12	0.82	0.43952	0.658011	-6.49
261028_at	hypothetical protein predicted by genem	---	AT1G26620	-1.07	-0.09	-0.82	0.439634	0.658109	-6.49
255235_at	contains similarity to transposases	---	---	1.09	0.12	0.82	0.439643	0.658109	-6.49
265447_at	putative laccase (diphenol oxidase)	LAC6	AT2G46570	1.09	0.12	0.82	0.439776	0.658221	-6.49
245410_at	putative protein	ATMAP70	AT4G17220	1.06	0.09	0.82	0.439769	0.658221	-6.49
254349_at	hypothetical protein	---	AT4G22250	-1.08	-0.11	-0.82	0.43983	0.658259	-6.49
259790_s_a	auxin-induced protein, putative similar t	---	AT1G29430 /	1.23	0.30	0.82	0.439976	0.658434	-6.49
245927_at	sterol glucosyltransferase - like protein	---	AT5G24750	1.05	0.07	0.82	0.440433	0.658989	-6.49
257522_at	Yippee-like protein similar to Yippee put	---	AT3G08990	1.06	0.08	0.82	0.440409	0.658989	-6.49
263213_at	unknown protein Strong similarity to gi|2	---	AT1G30560	1.08	0.11	0.82	0.440429	0.658989	-6.49
264524_at	tat-binding protein, putative Highly Simi	ATBCAT-2	AT1G10070	1.32	0.40	0.82	0.440464	0.658992	-6.49
258536_at	Rab escort protein, putative similar to c	---	AT3G06540	1.08	0.11	0.82	0.440595	0.659110	-6.49
253989_at	uncharacterized protein ;supported by f	---	AT4G26130	-1.11	-0.15	-0.82	0.440601	0.659110	-6.49
256710_at	hypothetical protein predicted by genem	---	AT3G30350	1.12	0.16	0.82	0.440653	0.659145	-6.49
247092_at	putative protein contains similarity to pe	ATFOLT1	AT5G66380	1.08	0.11	0.82	0.440728	0.659171	-6.49
263993_at	hypothetical protein predicted by gensca	---	---	1.07	0.10	0.82	0.440727	0.659171	-6.49
263224_at	putative GTP-binding protein Similar to	---	AT1G30580	-1.09	-0.13	-0.82	0.440833	0.659180	-6.49
264203_at	putative 40S ribosomal protein S18 Ma	PFL	AT1G22780	-1.15	-0.21	-0.82	0.440809	0.659180	-6.49
259850_at	hypothetical protein predicted by genem	---	AT1G72240	-1.10	-0.13	-0.82	0.440768	0.659180	-6.49
261182_at	hypothetical protein predicted by genem	---	AT1G34575	-1.06	-0.08	-0.82	0.44085	0.659180	-6.49
261836_at	hypothetical protein contains similarity t	WAKL7	AT1G16090	1.28	0.36	0.82	0.440886	0.659190	-6.49
266046_at	hypothetical protein	---	AT2G07728	-1.09	-0.12	-0.82	0.441066	0.659417	-6.49
246577_at	MADS box transcription factor, putative	AGL92	AT1G31640	-1.06	-0.09	-0.82	0.441284	0.659698	-6.49

259208_at	hypothetical protein similar to GB:AAD4	---	AT3G09060	-1.07	-0.09	-0.82	0.441328	0.659721	-6.49
262530_at	putative receptor protein kinase Approxi	AtRLP2	AT1G17240	-1.08	-0.11	-0.82	0.441504	0.659942	-6.49
267254_at	putative protein kinase contains a protei	SNRK2.9	AT2G23030	1.23	0.30	0.82	0.441553	0.659971	-6.49
254833_s_a	copper amine oxidase like protein (frag	---	AT4G12280 /	-1.06	-0.08	-0.82	0.441652	0.660033	-6.49
250935_at	polyubiquitin (UBQ3) identical to GI:928	UBQ3	AT5G03240	-1.12	-0.16	-0.82	0.441635	0.660033	-6.49
246425_at	cellulose synthase catalytic subunit (IRX	IRX3	AT5G17420	-1.16	-0.21	-0.82	0.441867	0.660312	-6.49
266295_at	tubulin beta-7 chain identical to GB:M84	TUB7	AT2G29550	1.14	0.19	0.82	0.441962	0.660410	-6.49
248335_at	putative protein strong similarity to unkn	---	AT5G52450	1.12	0.16	0.82	0.442038	0.660463	-6.49
250785_at	unknown protein	---	AT5G05510	1.09	0.13	0.82	0.442056	0.660463	-6.49
258242_at	hypothetical protein predicted by genem	---	AT3G27640	-1.06	-0.09	-0.82	0.442087	0.660467	-6.49
261479_at	unknown protein ;supported by full-lengt	IQD28	AT1G14380	-1.10	-0.14	-0.82	0.442182	0.660565	-6.49
252169_at	putative protein several bacterial phosph	---	AT3G50520	1.11	0.15	0.82	0.442222	0.660582	-6.49
264162_at	acyl carrier protein, putative similar to a	mtACP2	AT1G65290	-1.08	-0.11	-0.82	0.442421	0.660836	-6.49
252569_at	receptor-like protein kinase receptor like	---	AT3G45420	-1.07	-0.10	-0.82	0.442457	0.660847	-6.49
261299_at	unknown protein	---	AT1G48550	-1.09	-0.12	-0.82	0.442521	0.660898	-6.49
265512_at	hypothetical protein predicted by gensca	---	AT2G05590	-1.09	-0.12	-0.82	0.442581	0.660901	-6.49
255533_at	putative CHP-rich zinc finger protein sim	---	AT4G02180	-1.06	-0.08	-0.82	0.442562	0.660901	-6.49
253453_at	protein phosphatase 2C - like protein pr	---	AT4G31860	1.06	0.08	0.82	0.442683	0.660975	-6.49
265227_s_a	hypothetical protein	---	AT2G07695	1.08	0.11	0.82	0.442746	0.660975	-6.49
247615_at	putative protein various predicted prote	---	AT5G60250	-1.06	-0.08	-0.82	0.442737	0.660975	-6.49
266729_at	50S ribosomal protein L7/L12	---	AT2G03130	-1.07	-0.09	-0.82	0.44274	0.660975	-6.49
258699_at	unknown protein	---	AT3G09470	-1.08	-0.11	-0.82	0.442793	0.661002	-6.49
264944_at	hypothetical protein similar to hypothetic	---	AT1G76940	1.10	0.13	0.82	0.44286	0.661058	-6.49
265281_at	unknown protein ; supported by full-leng	---	AT2G28370	1.08	0.11	0.82	0.442927	0.661109	-6.49
267049_at	putative transcription elongation factor	---	AT2G34210	1.13	0.17	0.82	0.442952	0.661109	-6.49
265001_at	hypothetical protein contains similarity to	---	AT1G67350	1.06	0.09	0.81	0.443121	0.661229	-6.49
253287_at	putative protein dJ69E11.3, Homo sapie	---	AT4G34270	1.06	0.08	0.81	0.443161	0.661229	-6.49
257316_at	hypothetical protein predicted by genem	---	---	1.06	0.08	0.81	0.443177	0.661229	-6.49
262895_at	hypothetical protein predicted by genem	---	AT1G59800	1.08	0.11	0.81	0.443103	0.661229	-6.49
251236_at	putative protein hypothetical proteins - A	---	AT3G62380	-1.05	-0.07	-0.81	0.443115	0.661229	-6.49
262968_at	hypothetical protein predicted by genem	---	AT1G75720	1.07	0.09	0.81	0.443345	0.661337	-6.49
258462_at	unknown protein	---	AT3G17350	1.16	0.22	0.81	0.443298	0.661337	-6.49
257859_at	Expressed protein ; supported by full-ler	---	AT3G12955	1.08	0.10	0.81	0.443366	0.661337	-6.49
255169_x_a	hypothetical protein	---	AT4G07940	-1.06	-0.09	-0.81	0.443331	0.661337	-6.49
253954_at	putative aconitase Pumpkin mRNA for a	---	AT4G26970	1.11	0.15	0.81	0.443508	0.661361	-6.49

249327_at	anion channel protein (gb|AAC05742.1)	ATCLC-A	AT5G40890	1.15	0.20	0.81	0.443553	0.661361	-6.49
250980_at	putative protein	---	AT5G03130	-1.16	-0.21	-0.81	0.443536	0.661361	-6.49
250491_at	putative protein predicted proteins, Aral	---	AT5G09780	-1.10	-0.14	-0.81	0.443446	0.661361	-6.49
255514_s_a	hypothetical protein similar to MNA5.4 s	AGL78	AT5G65330	-1.07	-0.10	-0.81	0.443551	0.661361	-6.49
255854_at	unknown protein ;supported by full-lengt	---	AT1G67050	-1.19	-0.25	-0.81	0.443556	0.661361	-6.49
251801_at	cytosolic triosephosphatisomerase ;sup	TPI	AT3G55440	-1.05	-0.07	-0.81	0.443647	0.661431	-6.49
263339_at	Mutator-like transposase similar to MUF	---	---	-1.05	-0.07	-0.81	0.443689	0.661431	-6.49
248902_at	unknown protein	---	AT5G46440	1.07	0.09	0.81	0.443668	0.661431	-6.49
251673_at	beta-1,3-glucanase	BG3	AT3G57240	1.86	0.90	0.81	0.44385	0.661591	-6.49
254792_at	putative protein nucleoid DNA-binding p	---	AT4G12920	1.07	0.09	0.81	0.443855	0.661591	-6.49
257729_at	histone deacetylase, putative contains I	HDA15	AT3G18520	-1.10	-0.14	-0.81	0.44392	0.661622	-6.49
249706_at	histone deacetylase	HDA7	AT5G35600	-1.06	-0.09	-0.81	0.443934	0.661622	-6.49
259190_at	unknown protein est hit, predicted by ge	TPLATE	AT3G01780	-1.09	-0.13	-0.81	0.444021	0.661665	-6.50
263835_at	putative eukaryotic translation initiation	---	AT2G40290	-1.06	-0.09	-0.81	0.444021	0.661665	-6.50
255314_at	putative transposon protein	---	---	-1.08	-0.11	-0.81	0.44408	0.661710	-6.50
251219_at	putative protein several hypothetical pro	---	AT3G62390	-1.14	-0.18	-0.81	0.444211	0.661811	-6.50
245763_at	transposon protein, putative similar to E	---	AT1G27850	1.06	0.08	0.81	0.444253	0.661811	-6.50
255399_at	hypothetical protein	---	---	-1.08	-0.11	-0.81	0.444255	0.661811	-6.50
254799_at	putative protein various predicted protei	---	AT4G13060	-1.07	-0.10	-0.81	0.444263	0.661811	-6.50
254000_at	galactinol synthase WSI76 protein indu	AtGolS6	AT4G26250	-1.05	-0.07	-0.81	0.444308	0.661834	-6.50
250950_at	putative protein	ATEXO70A	AT5G03540 /	1.08	0.12	0.81	0.4446	0.662225	-6.50
262574_at	unknown protein ESTs gb|R30529, gb|Z	---	AT1G15230	-1.12	-0.16	-0.81	0.444952	0.662597	-6.50
247663_at	putative protein predicted proteins, Aral	APUM18	AT5G60110	-1.06	-0.08	-0.81	0.444965	0.662597	-6.50
247087_at	putative protein contains similarity to elic	---	AT5G66330	1.13	0.17	0.81	0.444911	0.662597	-6.50
266220_at	putative dTDP-glucose 4-6-dehydratase	---	AT2G28755	1.08	0.12	0.81	0.444905	0.662597	-6.50
263945_at	hypothetical protein predicted by genefir	---	AT2G36030	1.09	0.12	0.81	0.445042	0.662668	-6.50
260689_at	hypothetical protein predicted by genem	---	AT1G32290	1.08	0.12	0.81	0.445103	0.662716	-6.50
255230_at	ferredoxin--NADP+ reductase - like pro	ATRFNR1	AT4G05390	1.26	0.33	0.81	0.445363	0.662838	-6.50
258814_at	putative short-chain type dehydrogenas	---	AT3G03980	-1.08	-0.11	-0.81	0.445304	0.662838	-6.50
250986_at	putative protein	---	AT5G02850	1.06	0.09	0.81	0.445389	0.662838	-6.50
265347_at	similar to mammalian MHC III region pro	SUVH6	AT2G22740	-1.05	-0.07	-0.81	0.445384	0.662838	-6.50
256697_at	hypothetical protein contains similarity to	AtOCT4	AT3G20660	1.15	0.20	0.81	0.445308	0.662838	-6.50
253687_at	putative protein ;supported by full-lengt	---	AT4G29520	1.35	0.43	0.81	0.445327	0.662838	-6.50
245596_at	hypothetical protein	AtPRD1	AT4G14180	-1.07	-0.09	-0.81	0.445276	0.662838	-6.50
251453_at	putative protein hypothetical protein At2	---	AT3G60070	1.07	0.10	0.81	0.44549	0.662902	-6.50

263854_at	putative mutT domain protein	atnudt5	AT2G04430	-1.06	-0.09	-0.81	0.445465	0.662902	-6.50
256114_at	unknown protein ; supported by cDNA: g	---	AT1G16850	-1.23	-0.30	-0.81	0.445674	0.663003	-6.50
261633_at	hypothetical protein predicted by genem	---	AT1G49930	-1.06	-0.09	-0.81	0.445658	0.663003	-6.50
262905_at	thioredoxin, putative similar to thioredox	ATH7	AT1G59730	1.05	0.08	0.81	0.445637	0.663003	-6.50
256555_at	hypothetical protein similar to putative a	---	---	1.06	0.08	0.81	0.445674	0.663003	-6.50
254525_at	putative protein predicted protein, Arabi	---	AT4G19580	-1.07	-0.10	-0.81	0.445723	0.663033	-6.50
245053_at	putative pectinesterase	---	AT2G26450	1.09	0.13	0.81	0.44583	0.663119	-6.50
250333_at	membrane translocase - like protein inn	TIM17-3	AT5G11690	-1.13	-0.18	-0.81	0.445839	0.663119	-6.50
247713_at	putative protein nonspecific lipid-transfe	---	AT5G59330	1.07	0.09	0.81	0.445928	0.663192	-6.50
248118_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G55050	1.38	0.46	0.81	0.445965	0.663192	-6.50
247204_at	GTP binding protein-like	AtRABH1a	AT5G64990	1.07	0.10	0.81	0.445976	0.663192	-6.50
264511_at	putative galactinol synthase similar to G	AtGolS3	AT1G09350	-1.24	-0.31	-0.81	0.446066	0.663283	-6.50
261547_at	protein kinase, putative contains Pfam p	---	AT1G63500	-1.07	-0.10	-0.81	0.446105	0.663297	-6.50
253842_at	putative protein putative proteins from A	---	AT4G27860	-1.21	-0.27	-0.81	0.446322	0.663561	-6.50
264269_at	hypothetical protein predicted by genem	---	AT1G60240	1.08	0.11	0.81	0.44634	0.663561	-6.50
250316_at	cystatin (emb|CAA03929.1) ; supported	ATCYS1	AT5G12140	1.06	0.09	0.81	0.446388	0.663588	-6.50
251339_at	putative protein various predicted prote	---	AT3G60780	-1.09	-0.12	-0.81	0.446472	0.663671	-6.50
250693_at	ubiquitin-specific protease 12 (UBP12)	UBP12	AT5G06600	1.06	0.08	0.81	0.446562	0.663761	-6.50
253407_at	putative protein	---	AT4G32920	1.07	0.10	0.81	0.446687	0.663903	-6.50
246969_at	glutamic acid-rich protein other glutamic	---	AT5G24880	1.07	0.10	0.81	0.44678	0.663999	-6.50
261080_at	proliferating cellular nuclear antigen ider	PCNA1	AT1G07370	-1.29	-0.37	-0.81	0.446832	0.664033	-6.50
258707_at	putative histone H2B similar to histone H	---	AT3G09480	1.09	0.12	0.81	0.446934	0.664098	-6.50
265958_at	putative adenylate kinase ;supported by	ADK	AT2G37250	1.12	0.16	0.81	0.446978	0.664098	-6.50
255253_at	contains similarity to S. cerevisiae vacu	VPS28-2	AT4G05000	-1.06	-0.09	-0.81	0.446992	0.664098	-6.50
263005_at	hypothetical protein predicted by genem	---	AT1G54540	-1.12	-0.16	-0.81	0.446991	0.664098	-6.50
263320_at	putative galactinol synthase ;supported	AtGolS1	AT2G47180	1.23	0.30	0.81	0.447074	0.664176	-6.50
265306_at	unknown protein	---	AT2G20320	1.10	0.14	0.81	0.447215	0.664299	-6.50
260891_at	cysteine protease contains similarity to c	---	AT1G29080	1.07	0.10	0.81	0.447193	0.664299	-6.50
252150_at	vacuolar sorting protein 35 homolog va	VPS35C	AT3G51310	1.06	0.08	0.81	0.447299	0.664380	-6.50
264540_at	hypothetical protein predicted by genem	---	AT1G55630	-1.07	-0.10	-0.81	0.447421	0.664475	-6.50
260854_at	CCAAT-box binding factor HAP3 homo	LEC1	AT1G21970	-1.09	-0.13	-0.81	0.447417	0.664475	-6.50
257531_at	putative RNA-binding protein contains R	---	AT3G07250	1.06	0.08	0.81	0.447472	0.664508	-6.50
263342_at	putative helicase	---	---	1.05	0.07	0.81	0.447592	0.664643	-6.50
249372_at	glucose-6-phosphate dehydrogenase	G6PD6	AT5G40760	1.13	0.18	0.81	0.447658	0.664698	-6.50
245042_at	hypothetical protein predicted by genefir	HEMD	AT2G26540	-1.12	-0.17	-0.81	0.447721	0.664723	-6.50

265052_at	caffeic acid O-methyltransferase, putati	---	AT1G51990	1.06	0.08	0.81	0.447792	0.664723	-6.50
261789_at	40S ribosomal protein S12, putative sin	---	AT1G15930	-1.15	-0.20	-0.81	0.447761	0.664723	-6.50
266200_at	hypothetical protein predicted by gensca	---	AT2G38920	1.11	0.15	0.81	0.44777	0.664723	-6.50
262529_at	putative receptor protein kinase Approxi	AtRLP3	AT1G17250	1.08	0.12	0.81	0.447911	0.664857	-6.50
258100_at	unknown protein	---	AT3G23550	-1.38	-0.47	-0.81	0.44802	0.664908	-6.50
258596_at	unknown protein	LSH2	AT3G04510	1.08	0.11	0.81	0.448062	0.664908	-6.50
253111_at	putative protein glutamic acid-rich prote	---	AT4G35940	1.09	0.13	0.81	0.447981	0.664908	-6.50
254735_at	putative disease resistance protein Cf-4	AtRLP47	AT4G13810	1.08	0.10	0.81	0.448039	0.664908	-6.50
254369_at	putative protein	---	AT4G21720	1.09	0.13	0.81	0.448138	0.664977	-6.50
245044_at	unknown protein Alternative splice forms	---	AT2G26500	-1.05	-0.07	-0.81	0.448273	0.665135	-6.50
250085_at	unknown protein	---	AT5G17250	-1.09	-0.12	-0.80	0.448351	0.665206	-6.50
266175_at	NAM (no apical meristem)-like protein	ANAC035	AT2G02450	1.06	0.09	0.80	0.448398	0.665234	-6.50
253291_at	Expressed protein ; supported by full-ler	---	AT4G33865	-1.09	-0.13	-0.80	0.448435	0.665244	-6.50
264009_at	putative disease resistance response pr	---	AT2G21110	1.06	0.09	0.80	0.448473	0.665257	-6.50
263665_at	putative putative 60S ribosomal protein	---	AT1G04480	-1.12	-0.17	-0.80	0.448514	0.665262	-6.50
251752_at	proline transporter 2	PROT2	AT3G55740	1.11	0.15	0.80	0.448534	0.665262	-6.50
261416_at	ribosomal protein S15 identical to GB:A	RPS15A	AT1G07770	-1.14	-0.19	-0.80	0.448572	0.665275	-6.50
255804_at	putative protein IB1C3-1 protein, Arabic	---	AT4G10220	1.08	0.11	0.80	0.44868	0.665377	-6.50
250467_at	trehalose-6-phosphate phosphatase -lik	---	AT5G10100	1.06	0.09	0.80	0.448728	0.665377	-6.50
249308_at	unknown protein ; supported by cDNA:	---	AT5G41350	-1.06	-0.08	-0.80	0.448716	0.665377	-6.50
259325_at	unknown protein	---	AT3G05320	1.48	0.57	0.80	0.448896	0.665582	-6.50
259420_at	hypothetical protein similar to putative p	---	AT1G13900	-1.05	-0.07	-0.80	0.448929	0.665587	-6.50
261882_at	GTP-binding protein, putative similar to	PDE318	AT1G80770	-1.07	-0.09	-0.80	0.448965	0.665598	-6.50
267567_at	putative cytochrome P450	CYP71A13	AT2G30770	1.75	0.81	0.80	0.449069	0.665629	-6.50
263194_at	AP2 domain transcription factor, putativ	---	AT1G36060	-1.10	-0.14	-0.80	0.449062	0.665629	-6.50
265534_at	En/Spm-like transposon protein related	---	---	-1.05	-0.07	-0.80	0.449073	0.665629	-6.50
250654_at	receptor protein kinase-like protein	---	AT5G06940	1.07	0.10	0.80	0.449117	0.665650	-6.50
257262_at	zinc finger protein, putative contains Pfa	---	AT3G21890	-1.13	-0.18	-0.80	0.449234	0.665750	-6.50
263461_at	putative protein kinase contains a protei	---	AT2G31800	-1.08	-0.11	-0.80	0.449242	0.665750	-6.50
262333_at	hypothetical protein similar to putative s	---	AT1G64020	-1.07	-0.10	-0.80	0.449292	0.665780	-6.50
245973_at	putative protein predicted proteins, Ara	---	---	1.05	0.07	0.80	0.449361	0.665838	-6.50
261534_at	unknown protein ;supported by full-leng	PEX11C	AT1G01820	-1.06	-0.08	-0.80	0.449502	0.665912	-6.50
258426_at	hypothetical protein predicted by genefir	PLDP1	AT3G16785	1.06	0.09	0.80	0.449527	0.665912	-6.50
245211_at	putative protein similarity to sec10, Dro	SEC10	AT5G12370	-1.05	-0.07	-0.80	0.449472	0.665912	-6.50
245586_at	hypothetical protein	---	AT4G14980	1.06	0.09	0.80	0.449508	0.665912	-6.50

260337_at	unknown protein	WRKY57	AT1G69310	-1.08	-0.11	-0.80	0.449806	0.666152	-6.50
249278_at	putative protein strong similarity to unkn	---	AT5G41900	1.54	0.62	0.80	0.449739	0.666152	-6.50
245537_at	hypothetical protein	---	AT4G15200	1.06	0.08	0.80	0.449777	0.666152	-6.50
264880_at	hypothetical protein contains similarity to	---	AT1G61210	1.08	0.11	0.80	0.449781	0.666152	-6.50
249146_at	putative protein contains similarity to CC	---	AT5G43310	-1.06	-0.09	-0.80	0.44992	0.666278	-6.50
260059_at	trehalose-6-phosphate phosphatase (A	ATTPPB	AT1G78090	1.12	0.16	0.80	0.450052	0.666431	-6.50
249180_at	26S proteasome AAA-ATPase subunit F	RPT4A	AT5G43010	-1.09	-0.12	-0.80	0.450083	0.666433	-6.50
259454_at	unknown protein similar to hypothetical	---	AT1G44050	1.07	0.10	0.80	0.450163	0.666508	-6.50
247801_at	putative protein ; supported by full-lengt	---	AT5G58560	-1.07	-0.09	-0.80	0.450303	0.666615	-6.50
262476_at	phosphoprotein phosphatase identical to	---	AT1G50370	1.06	0.09	0.80	0.450323	0.666615	-6.50
262200_at	unknown protein similar to membrane pr	---	AT2G01070	-1.08	-0.12	-0.80	0.450276	0.666615	-6.50
264233_at	ribosomal protein, putative similar to rib	---	AT1G67430	-1.14	-0.19	-0.80	0.450393	0.666641	-6.51
250841_at	putative protein CGI-01 protein, Homo s	---	AT5G04610	-1.12	-0.16	-0.80	0.450399	0.666641	-6.51
251594_at	putative protein DOC4, Mus musculus,	---	AT3G57630	1.22	0.29	0.80	0.450506	0.666755	-6.51
257151_at	blue copper protein, putative similar to	---	AT3G27200	1.08	0.12	0.80	0.450589	0.666836	-6.51
261941_at	hypothetical protein contains similarity to	---	AT1G22490	-1.16	-0.22	-0.80	0.450647	0.666878	-6.51
246784_at	signal peptidase ; supported by cDNA:	---	AT5G27430	-1.06	-0.08	-0.80	0.450779	0.667031	-6.51
249508_at	unknown protein	---	AT5G38380	-1.06	-0.09	-0.80	0.450848	0.667089	-6.51
264145_at	latex-abundant protein, putative similar	AtMC7	AT1G79310	-1.05	-0.07	-0.80	0.45088	0.667093	-6.51
262227_s_a	26S proteasome ATPase subunit, putat	---	AT1G53750 /	1.06	0.08	0.80	0.450947	0.667149	-6.51
261226_at	expansin S2 precursor, putative similar	ATEXPA1	AT1G20190	1.52	0.60	0.80	0.450989	0.667168	-6.51
255231_at	F-box protein family, AtFBL20 contains	---	AT4G05460	-1.06	-0.08	-0.80	0.451094	0.667280	-6.51
250754_at	arginine-tRNA-protein transferase 1 hon	ATE1	AT5G05700	1.06	0.09	0.80	0.451158	0.667317	-6.51
266408_at	putative retroelement pol polyprotein	---	---	1.08	0.11	0.80	0.451207	0.667317	-6.51
252262_at	putative protein several hypothetical pro	---	AT3G49510	1.05	0.08	0.80	0.451191	0.667317	-6.51
255499_at	putative WD-repeat protein similar to C	---	AT4G02730	1.06	0.08	0.80	0.451253	0.667342	-6.51
254523_at	putative protein hypothetical protein, Ar	FRS1	AT4G19990	1.10	0.14	0.80	0.451376	0.667467	-6.51
266123_at	unknown protein identical to GB:AAB82	---	AT2G45180	-1.05	-0.07	-0.80	0.451396	0.667467	-6.51
263842_at	Expressed protein ; supported by full-ler	---	AT2G36835	-1.10	-0.14	-0.80	0.451661	0.667645	-6.51
246119_at	ankyrin-repeat protein patsas protein -	TIP1	AT5G20350	-1.08	-0.11	-0.80	0.451663	0.667645	-6.51
262386_at	hypothetical protein predicted by gensca	---	AT1G49370	1.09	0.12	0.80	0.451663	0.667645	-6.51
251482_s_a	receptor lectin kinase 3	---	AT3G59740 /	1.07	0.10	0.80	0.451582	0.667645	-6.51
248876_at	putative protein similar to unknown prote	---	---	1.05	0.07	0.80	0.451652	0.667645	-6.51
263431_at	unknown protein ;supported by full-leng	---	AT2G22170	1.51	0.59	0.80	0.451883	0.667770	-6.51
258011_at	putative homeobox protein, HAT3.1 sim	HAT3.1	AT3G19510	-1.09	-0.12	-0.80	0.45192	0.667770	-6.51

245681_at	alkaline/neutral invertase, putative simil	---	AT1G56560	-1.06	-0.08	-0.80	0.451982	0.667770	-6.51
261074_at	hypothetical protein predicted by genem	---	AT1G07290	-1.06	-0.09	-0.80	0.451955	0.667770	-6.51
249825_at	putative protein similar to unknown prote	---	AT5G23390	-1.06	-0.09	-0.80	0.451946	0.667770	-6.51
246271_at	photosystem II oxygen-evolving comple	---	AT4G37230	1.07	0.09	0.80	0.451944	0.667770	-6.51
247778_at	wounding stress induced protein - like v	---	AT5G58750	-1.05	-0.08	-0.80	0.451827	0.667770	-6.51
263966_s_a	putative TNP2-like transposon protein re	---	---	-1.07	-0.09	-0.80	0.451929	0.667770	-6.51
257619_at	unknown protein	ICK3	AT3G24810	-1.08	-0.11	-0.80	0.452225	0.668048	-6.51
262261_at	CLE17, putative CLAVATA3/ESR-Relat	CLE17	AT1G70895	1.08	0.11	0.80	0.452287	0.668048	-6.51
265515_at	hypothetical protein predicted by gensca	---	---	-1.06	-0.09	-0.80	0.452258	0.668048	-6.51
248696_at	putative protein similar to unknown prote	---	AT5G48360	-1.07	-0.09	-0.80	0.452247	0.668048	-6.51
249861_at	Expressed protein ; supported by full-ler	---	AT5G22875	-1.07	-0.10	-0.80	0.452328	0.668065	-6.51
249428_at	putative protein predicted protein K5K1	---	AT5G39870	1.05	0.07	0.80	0.452475	0.668240	-6.51
263079_at	putative retroelement pol polyprotein	---	---	1.06	0.08	0.80	0.452545	0.668300	-6.51
259131_at	unknown protein similar to hypothetical	SP1L3	AT3G02180	1.06	0.09	0.80	0.452698	0.668403	-6.51
260066_at	putative lipase/acylhydrolase contains P	---	AT1G73610	1.16	0.22	0.80	0.452703	0.668403	-6.51
263507_s_a	hypothetical protein	---	---	-1.09	-0.13	-0.80	0.45267	0.668403	-6.51
262284_at	hypothetical protein predicted by genem	---	AT1G68670	-1.10	-0.14	-0.80	0.452823	0.668493	-6.51
257256_at	hypothetical protein contains Pfam profil	---	AT3G21970	1.05	0.07	0.80	0.4528	0.668493	-6.51
246526_at	putative protein RXF26 - Arabidopsis th	GLIP7	AT5G15720	1.06	0.08	0.80	0.45297	0.668667	-6.51
AFFX-Athal-	Arabidopsis thaliana /REF=U84969 /DE	---	---	1.05	0.07	0.80	0.453047	0.668695	-6.51
260205_at	hypothetical protein predicted by genefir	TIFY7	AT1G70700	-1.17	-0.22	-0.80	0.453023	0.668695	-6.51
256934_at	unknown protein contains Pfam profile:F	---	AT3G22530	1.08	0.11	0.80	0.453106	0.668739	-6.51
251069_at	(1-4)-beta-mannan endohydrolase-like	---	AT5G01930	-1.15	-0.21	-0.80	0.453171	0.668791	-6.51
254712_at	hypothetical protein	---	AT4G18080	-1.05	-0.07	-0.80	0.453206	0.668800	-6.51
255519_at	hypothetical protein	---	AT4G02310	-1.05	-0.07	-0.80	0.453313	0.668914	-6.51
260262_at	hypothetical protein similar to hypotheti	---	AT1G68470	1.17	0.23	0.79	0.453751	0.669123	-6.51
255882_x_a	hypothetical protein contains similarity to	---	AT1G20280	1.07	0.10	0.80	0.453696	0.669123	-6.51
257432_at	unknown protein	---	AT2G21850	1.08	0.11	0.80	0.453665	0.669123	-6.51
257683_at	hypothetical protein predicted by genem	---	AT3G13280	1.06	0.09	0.80	0.453669	0.669123	-6.51
252264_at	putative protein hypothetical protein - S	---	AT3G49590	1.06	0.09	0.79	0.453822	0.669123	-6.51
261308_at	protein kinase, putative contains similar	RKL1	AT1G48480	1.29	0.37	0.80	0.45355	0.669123	-6.51
265532_at	hypothetical protein predicted by gensca	---	---	1.07	0.10	0.79	0.453836	0.669123	-6.51
246129_at	putative protein predicted protein, Arabi	---	---	1.05	0.07	0.79	0.453754	0.669123	-6.51
259865_at	putative casein kinase I similar to casein	CKL2	AT1G72710	-1.09	-0.12	-0.80	0.453731	0.669123	-6.51
254199_at	putative protein Ste-20 related kinase S	---	AT4G24100	-1.07	-0.09	-0.79	0.453786	0.669123	-6.51

261636_at	branched-chain amino acid aminotrans	---	AT1G50110	-1.07	-0.10	-0.79	0.453762	0.669123	-6.51
266676_s_a	hypothetical protein predicted by grail	---	AT2G29605 /	-1.06	-0.09	-0.79	0.453806	0.669123	-6.51
267555_at	Expressed protein ; supported by full-ler	SUMO5	AT2G32765	1.07	0.10	0.80	0.453691	0.669123	-6.51
260229_at	putative RING zinc finger protein contai	---	AT1G74370	-1.08	-0.12	-0.79	0.453867	0.669125	-6.51
253200_at	vacuolar H+-transporting ATPase 16K c	AVA-P1	AT4G34720	-1.08	-0.11	-0.79	0.453963	0.669223	-6.51
253763_at	xyloglucan endotransglycosylase - like	---	AT4G28850	1.06	0.08	0.79	0.454026	0.669236	-6.51
AFFX-r2-At-	Arabidopsis thaliana /REF=U37281 /DE	---	---	-1.05	-0.08	-0.79	0.454034	0.669236	-6.51
253169_at	putative protein various predicted prote	---	AT4G35120	1.07	0.10	0.79	0.454059	0.669236	-6.51
247166_at	unknown protein	---	AT5G65840	-1.13	-0.18	-0.79	0.454251	0.669272	-6.51
255591_at	putative expansin	ATEXPA1	AT4G01630	1.07	0.09	0.79	0.454289	0.669272	-6.51
259395_at	GTP-binding protein(RAB11D), putative	ARA-2	AT1G06400	-1.06	-0.09	-0.79	0.454152	0.669272	-6.51
261144_s_a	unknown protein ;supported by full-lengt	---	AT1G19660 /	-1.07	-0.09	-0.79	0.454142	0.669272	-6.51
248954_at	unknown protein ; supported by cDNA:	---	AT5G45420	1.06	0.08	0.79	0.454245	0.669272	-6.51
245131_s_a	unknown protein	emb1067	AT2G45330 /	1.05	0.07	0.79	0.454279	0.669272	-6.51
249275_at	polygalacturonase-like protein	---	AT5G41870	-1.07	-0.10	-0.79	0.454237	0.669272	-6.51
246310_at	sulfate transporter ATST1 ; supported b	SULTR3;1	AT3G51895	-1.11	-0.15	-0.79	0.454425	0.669429	-6.51
258213_at	hypothetical protein predicted by genem	---	AT3G17950	-1.10	-0.14	-0.79	0.454482	0.669470	-6.51
248841_at	ubiquitin-specific protease 21 (UBP21) i	UBP21	AT5G46740	1.10	0.14	0.79	0.454535	0.669504	-6.51
245713_at	S-adenosyl-L-methionine:salicylic acid c	NAMT1	AT5G04370	1.09	0.13	0.79	0.4549	0.669955	-6.51
261466_at	hypothetical protein predicted by genem	---	AT1G07690	1.09	0.12	0.79	0.454873	0.669955	-6.51
250414_at	putative protein Glr5, Arabidopsis thalia	GLR2.6	AT5G11180	1.06	0.08	0.79	0.455083	0.670022	-6.51
248635_at	unknown protein	---	AT5G49050	1.06	0.09	0.79	0.455073	0.670022	-6.51
264649_at	hypothetical protein Similar to Vicia sativ	---	AT1G09060	-1.08	-0.11	-0.79	0.455151	0.670022	-6.51
260011_at	hypothetical protein similar to hypotheti	---	AT1G68110	1.08	0.11	0.79	0.454979	0.670022	-6.51
263830_at	hypothetical protein predicted by genefir	---	AT2G40260	-1.06	-0.09	-0.79	0.455017	0.670022	-6.51
256684_at	geranylgeranyl pyrophosphate synthase	---	AT3G32040	1.09	0.12	0.79	0.455131	0.670022	-6.51
267272_at	hypothetical protein predicted by gensca	---	---	-1.06	-0.08	-0.79	0.455128	0.670022	-6.51
264539_at	hypothetical protein predicted by genem	---	AT1G55590	-1.07	-0.10	-0.79	0.455258	0.670093	-6.51
257158_at	3-hydroxyisobutyryl-coenzyme A hydrol	---	AT3G24360	-1.08	-0.11	-0.79	0.455231	0.670093	-6.51
264032_at	unknown protein	GEK1	AT2G03800	1.07	0.10	0.79	0.455294	0.670104	-6.51
249813_at	acyltransferase ; supported by full-lengt	EMB3009	AT5G23940	-1.05	-0.07	-0.79	0.45534	0.670128	-6.51
255413_at	putative alcohol dehydrogenase similar	---	AT4G03140	1.07	0.10	0.79	0.455506	0.670329	-6.51
248892_at	unknown protein	---	AT5G46300	1.06	0.08	0.79	0.455581	0.670396	-6.51
249451_s_a	hypothetical protein	---	AT5G39480 /	1.05	0.07	0.79	0.455621	0.670412	-6.51
250051_at	MYB56 R2R3-MYB factor family membe	AtMYB56	AT5G17800	1.09	0.12	0.79	0.455832	0.670679	-6.51

249745_at	phloem-specific lectin-like protein	AtPP2-B12	AT5G24560	1.08	0.11	0.79	0.45596	0.670823	-6.51
247535_at	transcriptional activator - like protein D1	---	AT5G61620	1.09	0.13	0.79	0.45606	0.670928	-6.51
258030_at	hypothetical protein predicted by genem	---	AT3G27590	1.08	0.11	0.79	0.456161	0.671033	-6.51
246436_at	putative protein cisplatin resistance-ass	---	AT5G17440	-1.06	-0.08	-0.79	0.456286	0.671172	-6.51
255659_at	Expressed protein ; supported by full-ler	---	AT4G00895	1.14	0.19	0.79	0.456343	0.671172	-6.51
263812_at	putative replication protein A1	---	---	-1.05	-0.07	-0.79	0.456344	0.671172	-6.51
255689_at	hypothetical protein	---	AT4G00670	1.05	0.07	0.79	0.456469	0.671313	-6.51
249553_at	receptor serine/threonine protein kinase	---	AT5G38260	1.09	0.13	0.79	0.456533	0.671364	-6.51
265026_at	putative 3-oxoacyl [acyl-carrier protein]	---	AT1G24360	-1.10	-0.14	-0.79	0.456761	0.671655	-6.51
267544_at	putative cytochrome b5	CB5-B	AT2G32720	1.18	0.23	0.79	0.456853	0.671660	-6.51
259969_at	putative pyrophosphate-dependent phos	---	AT1G76550	1.15	0.20	0.79	0.456839	0.671660	-6.51
264492_at	unknown protein similar to unknown pro	---	AT1G27430	-1.05	-0.07	-0.79	0.456852	0.671660	-6.51
257688_at	Snf2-related CBP activator protein, puta	PIE1	AT3G12810	1.05	0.07	0.79	0.456919	0.671715	-6.51
265254_at	unknown protein ; supported by cDNA:	DRB2	AT2G28380	-1.07	-0.09	-0.79	0.457077	0.671730	-6.52
256836_at	pyruvate kinase, putative similar to pyru	PKP-ALPH	AT3G22960	-1.08	-0.11	-0.79	0.457023	0.671730	-6.52
264275_at	hypothetical protein predicted by gensca	anac024	AT1G60350	-1.05	-0.07	-0.79	0.456995	0.671730	-6.52
259243_at	unknown protein similar to unknown pro	---	AT3G07565	1.05	0.08	0.79	0.457072	0.671730	-6.52
265064_at	hypothetical protein contains similarity to	ENT7	AT1G61630	1.10	0.14	0.79	0.457073	0.671730	-6.52
261297_at	hypothetical protein predicted by genem	JAZ4	AT1G48500	-1.05	-0.08	-0.79	0.457315	0.672037	-6.52
250367_s_a	DEAD BOX RNA helicase RH15 ; supp	---	AT5G11170 /	-1.07	-0.09	-0.79	0.457384	0.672095	-6.52
258540_at	hypothetical protein predicted by gensca	---	AT3G06990	1.06	0.09	0.79	0.457421	0.672106	-6.52
254939_at	putative protein predicted proteins, Arat	---	AT4G10800	-1.10	-0.14	-0.79	0.457478	0.672147	-6.52
264315_at	aromatic rich glycoprotein, putative sim	---	AT1G70370	-1.25	-0.32	-0.79	0.457683	0.672404	-6.52
257513_s_a	hypothetical protein	---	AT1G12340 /	-1.07	-0.10	-0.79	0.457824	0.672568	-6.52
266381_at	putative sucrose-proton symporter	ATSUC8	AT2G14670	1.06	0.08	0.79	0.457984	0.672760	-6.52
248819_at	putative protein contains similarity to S-r	---	AT5G47050	1.12	0.16	0.79	0.458142	0.672949	-6.52
256663_at	unknown protein ;supported by full-lengt	---	AT3G12050	-1.11	-0.15	-0.79	0.458257	0.673037	-6.52
252354_at	betaine aldehyde dehydrogenase-like p	ALDH10A9	AT3G48170	1.06	0.08	0.79	0.458261	0.673037	-6.52
253998_at	putative peroxidase peroxidase ATP13a	---	AT4G26010	1.05	0.07	0.79	0.458389	0.673182	-6.52
244914_at	hypothetical protein	---	---	1.06	0.09	0.79	0.458469	0.673256	-6.52
255197_x_a	contains similarity to Oryza sativa replica	---	---	1.07	0.10	0.79	0.458581	0.673333	-6.52
252393_at	putative protein predicted proteins, Arat	---	AT3G47910	-1.07	-0.10	-0.79	0.458573	0.673333	-6.52
259607_at	P-glycoprotein, putative similar to P-gly	PGP13	AT1G27940	1.05	0.07	0.79	0.458698	0.673461	-6.52
254761_at	Expressed protein ; supported by full-ler	CLE44	AT4G13195	1.10	0.13	0.79	0.45915	0.673851	-6.52
264370_at	hybrid proline-rich protein, putative simi	---	AT1G12100	1.07	0.09	0.79	0.45909	0.673851	-6.52

253408_at	putative protein phosphoprotein phosph	---	AT4G32950	-1.05	-0.08	-0.79	0.459073	0.673851	-6.52
262560_at	hypothetical protein predicted by gensca	---	AT1G34280	-1.07	-0.10	-0.79	0.459005	0.673851	-6.52
245984_at	putative protein predicted proteins - Aral	---	AT5G13090	1.07	0.09	0.79	0.45917	0.673851	-6.52
255965_at	14-3-3 protein (grf14), putative similar t	---	AT1G22290	1.06	0.08	0.79	0.459139	0.673851	-6.52
263071_at	putative retroelement pol polyprotein	---	---	1.06	0.08	0.79	0.45908	0.673851	-6.52
263336_x_a	hypothetical protein predicted by gensca	---	---	-1.06	-0.08	-0.78	0.459441	0.674206	-6.52
255366_x_a	putative transposon protein	---	---	1.07	0.09	0.78	0.459516	0.674229	-6.52
257117_at	geranyl geranyl pyrophosphate synthas	---	AT3G20160	-1.06	-0.08	-0.78	0.459516	0.674229	-6.52
256666_at	histone H2A, putative similar to histone	HTA13	AT3G20670	1.15	0.20	0.78	0.459571	0.674241	-6.52
252448_at	beta-D-glucan exohydrolase - like prote	---	AT3G47050	-1.07	-0.09	-0.78	0.459583	0.674241	-6.52
265710_at	unknown protein	---	AT2G03370	1.06	0.08	0.78	0.459718	0.674364	-6.52
259509_at	mutator-like transposase, putative simil	---	---	1.06	0.08	0.78	0.459726	0.674364	-6.52
260687_at	inner mitochondrial membrane protein,	ATTIM23-1	AT1G17530	-1.10	-0.14	-0.78	0.460017	0.674443	-6.52
266223_at	putative thaumatin ;supported by full-le	---	AT2G28790	1.26	0.33	0.78	0.459973	0.674443	-6.52
255624_at	MAP kinase 4 (MPK4) ;supported by fu	ATMPK4	AT4G01370	1.08	0.12	0.78	0.459863	0.674443	-6.52
255915_at	putative protein	---	AT5G28620	1.06	0.09	0.78	0.459904	0.674443	-6.52
260142_at	unknown protein ; supported by cDNA:	---	AT1G71900	-1.08	-0.11	-0.78	0.459901	0.674443	-6.52
265379_at	similar to late embryogenesis abundant	---	AT2G18340	1.06	0.08	0.78	0.459904	0.674443	-6.52
252722_at	putative protein hypothetical protein F1	---	---	1.05	0.07	0.78	0.459991	0.674443	-6.52
258579_s_a	germin-like protein contains Pfam profile	---	AT3G04180 /	1.05	0.07	0.78	0.459966	0.674443	-6.52
267563_at	putative protein kinase contains a protei	---	AT2G30730	1.06	0.09	0.78	0.460053	0.674452	-6.52
261235_x_a	hypothetical protein predicted by genem	---	---	-1.06	-0.08	-0.78	0.46021	0.674466	-6.52
249597_at	putative protein probable quinone oxido	---	AT5G37960	1.05	0.07	0.78	0.460154	0.674466	-6.52
254782_at	putative calmodulin calmodulin - Chlam	UNE14	AT4G12860	1.07	0.10	0.78	0.460196	0.674466	-6.52
266043_at	hypothetical protein	---	AT2G07724	-1.08	-0.12	-0.78	0.460134	0.674466	-6.52
255354_at	putative transposon protein	---	---	-1.05	-0.07	-0.78	0.460112	0.674466	-6.52
266063_at	putative SNF2/RAD54 family DNA repai	CHR8	AT2G18760	-1.06	-0.09	-0.78	0.460283	0.674530	-6.52
265781_at	putative Athila retroelement ORF1 prote	---	---	1.06	0.08	0.78	0.46035	0.674584	-6.52
257435_at	putative RSZp22 splicing factor	---	AT2G24590	-1.09	-0.12	-0.78	0.460425	0.674619	-6.52
264632_at	DegP protease contains similarity to De	DegP4	AT1G65640	-1.05	-0.07	-0.78	0.460432	0.674619	-6.52
246959_at	unknown protein	---	AT5G24690	-1.14	-0.18	-0.78	0.460513	0.674650	-6.52
248994_at	disease resistance protein-like	RPS4	AT5G45250	-1.08	-0.12	-0.78	0.460496	0.674650	-6.52
245958_at	GNOM-like protein pattern-formation (G	---	AT5G19610	1.06	0.08	0.78	0.460581	0.674707	-6.52
245856_at	putative protein predicted proteins, Aral	---	---	1.09	0.12	0.78	0.460702	0.674840	-6.52
251571_at	putative protein several hypothetical pro	---	AT3G58330	1.06	0.08	0.78	0.460744	0.674858	-6.52

255168_at	putative protein hypothetical protein T2	---	---	1.07	0.10	0.78	0.460899	0.674998	-6.52
253844_at	hypothetical protein	---	AT4G27930	1.07	0.10	0.78	0.460882	0.674998	-6.52
257563_at	hypothetical protein predicted by genem	---	AT3G19610	1.05	0.07	0.78	0.46099	0.675088	-6.52
258738_at	hypothetical protein similar to hypothetic	---	AT3G05750	-1.08	-0.11	-0.78	0.461131	0.675252	-6.52
258651_at	putative phosphatidylinositol-4-phospha	PIP5K9	AT3G09920	1.08	0.11	0.78	0.461211	0.675316	-6.52
248316_at	putative protein similar to unknown prote	---	AT5G52670	1.09	0.12	0.78	0.461234	0.675316	-6.52
256759_at	hypothetical protein predicted by genem	---	AT3G25640	-1.09	-0.12	-0.78	0.461319	0.675397	-6.52
267234_x_a	putative protein kinase contains a protei	---	AT2G43930	1.07	0.09	0.78	0.461379	0.675441	-6.52
259940_at	hypothetical protein	---	AT1G71290	1.05	0.07	0.78	0.461442	0.675491	-6.52
266028_at	hypothetical protein predicted by gensca	---	AT2G06000	-1.09	-0.13	-0.78	0.461583	0.675570	-6.52
266744_at	putative nucleoside triphosphatase ; su	---	AT2G02970	1.05	0.07	0.78	0.461704	0.675570	-6.52
267173_at	origin recognition complex protein identi	ORC2	AT2G37560	1.11	0.15	0.78	0.46166	0.675570	-6.52
250296_at	heat shock protein 17.6-II ;supported by	HSP17.6II	AT5G12020	1.15	0.21	0.78	0.461689	0.675570	-6.52
248319_at	unknown protein	---	AT5G52710	1.06	0.08	0.78	0.461578	0.675570	-6.52
251016_at	pathogenesis related protein - like path	---	AT5G02730	1.11	0.15	0.78	0.461648	0.675570	-6.52
249413_at	ras - related GTP binding protein - like	AtRABG1	AT5G39620	1.06	0.08	0.78	0.461618	0.675570	-6.52
251824_at	ABC transporter - like protein ATP-bind	---	AT3G55090	1.07	0.09	0.78	0.461982	0.675934	-6.52
244956_s_a	hypothetical protein	---	---	-1.07	-0.10	-0.78	0.462102	0.676066	-6.52
260966_at	NBS/LRR disease resistance protein, p	RPS5	AT1G12220	1.07	0.09	0.78	0.462254	0.676201	-6.52
262720_s_a	hypothetical protein similar to hypothetic	---	AT1G43600 /	1.05	0.08	0.78	0.462243	0.676201	-6.52
253045_at	Expressed protein ; supported by full-ler	---	AT4G37445	1.11	0.15	0.78	0.46244	0.676343	-6.52
260138_at	calmodulin-4 identical to GB:Q03510 fr	CAM4	AT1G66410	-1.08	-0.11	-0.78	0.462424	0.676343	-6.52
262817_at	putative reticuline oxidase strong similar	---	AT1G11770	1.07	0.10	0.78	0.462418	0.676343	-6.52
257868_at	unknown protein	RIN4	AT3G25070	-1.09	-0.12	-0.78	0.462594	0.676525	-6.52
245572_at	hypothetical protein	PPD2	AT4G14720	-1.11	-0.16	-0.78	0.462739	0.676608	-6.52
262949_at	pectinesterase, putative similar to pecti	sks18	AT1G75790	1.06	0.09	0.78	0.462725	0.676608	-6.52
248263_at	pectinesterase ; supported by cDNA: gi	PMEPCRF	AT5G53370	1.14	0.18	0.78	0.462737	0.676608	-6.52
255157_at	hypothetical protein	---	---	1.05	0.07	0.78	0.462921	0.676831	-6.52
254325_at	putative protein various predicted prote	---	AT4G22650	1.09	0.13	0.78	0.463016	0.676926	-6.52
266133_at	putative C2H2-type zinc finger protein	---	AT2G45120	-1.06	-0.08	-0.78	0.463073	0.676966	-6.52
267132_at	unknown protein	NAPRT2	AT2G23420	1.12	0.17	0.78	0.463107	0.676972	-6.52
254144_at	putative protein	---	AT4G24690	-1.07	-0.09	-0.78	0.463156	0.676997	-6.52
246178_s_a	putative protein predicted proteins - Ara	---	---	1.08	0.11	0.78	0.463184	0.676997	-6.52
258869_at	hypothetical protein similar to xylose tra	AtVGT1	AT3G03090	-1.08	-0.11	-0.78	0.463278	0.677075	-6.52
257014_at	hypothetical protein predicted by gensca	---	AT3G26930	-1.08	-0.12	-0.78	0.463296	0.677075	-6.52

249090_at	Expressed protein ; supported by cDNA	---	AT5G43745	1.09	0.13	0.78	0.463571	0.677240	-6.52
257550_at	hypothetical protein similar to GB:AAD0	---	AT3G18460	1.08	0.11	0.78	0.463582	0.677240	-6.52
257238_at	unknown protein ; supported by cDNA:	---	AT3G17430	-1.09	-0.12	-0.78	0.463587	0.677240	-6.52
253339_at	metal-transporting P-type ATPase ; sup	PAA1	AT4G33520	1.10	0.14	0.78	0.463524	0.677240	-6.52
249728_at	GTPase activator-like protein of Rab-like	---	AT5G24390	1.07	0.10	0.78	0.463518	0.677240	-6.52
246635_at	hypothetical protein predicted by genem	---	AT1G31720	-1.10	-0.13	-0.78	0.463535	0.677240	-6.52
258270_at	putative lysophospholipase similar to lys	---	AT3G15650	1.15	0.21	0.78	0.463665	0.677309	-6.52
264341_at	hypothetical protein predicted by gensca	---	AT1G70270	1.05	0.07	0.78	0.463694	0.677309	-6.52
257673_at	unknown protein similar to GB:BAA879	---	AT3G20370	1.08	0.11	0.78	0.463762	0.677365	-6.53
257239_at	unknown protein	---	AT3G24100	-1.07	-0.09	-0.78	0.463814	0.677367	-6.53
253904_at	NWMU1 - 2S albumin 1 precursor ; sup	---	AT4G27140	1.06	0.08	0.78	0.463823	0.677367	-6.53
256690_at	hypothetical protein predicted by gensca	---	AT3G32160	1.08	0.11	0.78	0.463882	0.677411	-6.53
256846_at	pectin methylesterase, putative similar t	---	AT3G27980	-1.05	-0.07	-0.78	0.464	0.677540	-6.53
264214_s_a	MADS-box transcription factor, putative	AGL38	AT1G65300 /	1.06	0.08	0.78	0.464213	0.677804	-6.53
255012_at	putative protein ;supported by full-lengt	---	AT4G10030	-1.11	-0.16	-0.78	0.464241	0.677804	-6.53
267626_at	putative cytochrome P450	CYP712A1	AT2G42250	1.11	0.14	0.78	0.4643	0.677847	-6.53
252761_at	putative protein several hypothetical pro	---	AT3G42770	1.10	0.14	0.78	0.464354	0.677883	-6.53
265727_at	putative DNA topoisomerase III beta	---	AT2G32000	-1.06	-0.09	-0.78	0.464398	0.677903	-6.53
252860_at	putative protein bZIP protein, Arabidops	---	AT4G39790	1.05	0.07	0.78	0.464569	0.678084	-6.53
258846_at	unknown protein ; supported by full-leng	---	AT3G03070	1.06	0.08	0.78	0.464581	0.678084	-6.53
248719_at	respiratory burst oxidase protein ; supp	RBOHD	AT5G47910	1.24	0.31	0.78	0.464668	0.678168	-6.53
254692_at	putative protein predicted protein, Arabi	---	AT4G17860	1.06	0.09	0.77	0.464824	0.678265	-6.53
256450_at	NADPH oxidoreductase, putative simila	---	AT1G75290	1.06	0.08	0.77	0.464795	0.678265	-6.53
257899_at	P-glycoprotein, putative similar to P-gly	---	AT3G28345	-1.06	-0.08	-0.77	0.464773	0.678265	-6.53
254220_at	putative protein Arabidopsis hypothetica	---	AT4G23780	1.06	0.08	0.77	0.464928	0.678374	-6.53
249545_at	putative transmembrane protein putativ	---	AT5G38030	-1.05	-0.08	-0.77	0.465066	0.678532	-6.53
247246_at	invertase inhibitor homolog (emb|CAA73	C/VIF2	AT5G64620	1.12	0.16	0.77	0.465178	0.678542	-6.53
247881_at	putative protein similar to unknown prote	---	AT5G57700	1.16	0.22	0.77	0.465126	0.678542	-6.53
260837_at	fructose 1,6-bisphosphatase, putative s	---	AT1G43670	-1.12	-0.17	-0.77	0.465183	0.678542	-6.53
251628_at	translation initiation factor 3 -like protein	EIF3E	AT3G57290	-1.07	-0.10	-0.77	0.465207	0.678542	-6.53
266762_at	putative alcohol dehydrogenase	---	AT2G47120	-1.06	-0.08	-0.77	0.465222	0.678542	-6.53
263135_at	flavanone 3-hydroxylase, putative simila	---	AT1G78550	-1.08	-0.11	-0.77	0.465278	0.678580	-6.53
263578_at	F-box protein family, AtFBL10 contains	---	AT2G17020	1.06	0.08	0.77	0.465363	0.678661	-6.53
246302_at	Ca2+/H+-exchanging protein-like Arabid	CAX3	AT3G51860	1.22	0.29	0.77	0.465574	0.678925	-6.53
258446_at	hypothetical protein predicted by genma	---	AT3G22430	-1.06	-0.08	-0.77	0.465728	0.679106	-6.53

265820_at	hypothetical protein predicted by gensca	---	AT2G17940	-1.08	-0.11	-0.77	0.465924	0.679349	-6.53
249353_at	oleosin ; supported by cDNA: gi_72525	OLEO2	AT5G40420	-1.08	-0.11	-0.77	0.466006	0.679425	-6.53
249270_at	putative protein similar to unknown prote	---	AT5G41780	-1.05	-0.07	-0.77	0.466145	0.679583	-6.53
252208_at	putative protein hypothetical protein KIA	---	AT3G50380	-1.10	-0.13	-0.77	0.466192	0.679609	-6.53
263227_at	Expressed protein ; supported by cDNA	---	AT1G30750	1.07	0.10	0.77	0.466272	0.679651	-6.53
250855_at	putative protein predicted proteins, Arat	---	AT5G04730	1.06	0.09	0.77	0.466281	0.679651	-6.53
261991_at	hypothetical protein predicted by genem	---	AT1G33700	-1.08	-0.11	-0.77	0.466326	0.679674	-6.53
264064_at	hypothetical protein predicted by gensca	---	AT2G27900	-1.06	-0.08	-0.77	0.466526	0.679847	-6.53
253472_at	hypothetical protein	---	AT4G32230	1.06	0.09	0.77	0.466534	0.679847	-6.53
266524_at	putative importin, beta subunit	---	AT2G16960	1.07	0.09	0.77	0.46651	0.679847	-6.53
249723_at	putative protein similar to unknown prote	---	AT5G35430	-1.05	-0.07	-0.77	0.4667	0.680045	-6.53
245244_at	IAA-amino acid hydrolase, putative sim	ILL6	AT1G44350	1.10	0.14	0.77	0.46681	0.680075	-6.53
256615_at	hypothetical protein predicted by genem	---	AT3G22250	1.08	0.11	0.77	0.466789	0.680075	-6.53
254949_at	hypothetical protein	---	AT4G11020	1.06	0.09	0.77	0.466764	0.680075	-6.53
260002_at	putative ABC transporter similar to ABC	ATNAP3	AT1G67940	1.11	0.15	0.77	0.467058	0.680350	-6.53
255091_at	putative protein various predicted protei	---	---	1.05	0.07	0.77	0.467055	0.680350	-6.53
263881_at	unknown protein ; supported by cDNA:	---	AT2G21820	-1.06	-0.09	-0.77	0.467101	0.680369	-6.53
259346_at	putative glutamate dehydrogenase simil	GDH3	AT3G03910	1.06	0.08	0.77	0.467177	0.680392	-6.53
247229_at	putative protein contains similarity to tet	---	AT5G65160	1.10	0.13	0.77	0.467155	0.680392	-6.53
248205_at	cotton fiber expressed protein 1-like pro	---	AT5G54300	-1.21	-0.28	-0.77	0.467393	0.680543	-6.53
251300_at	hypothetical protein ;supported by full-le	---	AT3G61980	1.09	0.12	0.77	0.4674	0.680543	-6.53
266041_s_a	hypothetical protein	---	---	-1.06	-0.09	-0.77	0.467329	0.680543	-6.53
245617_at	hypothetical protein	---	AT4G14490	-1.05	-0.07	-0.77	0.467392	0.680543	-6.53
257923_at	hypothetical protein predicted by gensca	---	AT3G23160	1.18	0.24	0.77	0.467498	0.680643	-6.53
245969_at	putative protein nuclear gene for chloro	---	AT5G19830	-1.12	-0.16	-0.77	0.467717	0.680918	-6.53
247129_at	alpha-mannosidase	---	AT5G66150	1.10	0.14	0.77	0.467864	0.681089	-6.53
253704_at	X-Pro dipeptidase - like protein (fragme	---	AT4G29490	-1.07	-0.09	-0.77	0.467972	0.681144	-6.53
263742_at	predicted protein	---	AT2G20625	1.06	0.08	0.77	0.467992	0.681144	-6.53
260353_at	putative nitrilase-associated protein simi	SP1L2	AT1G69230	-1.07	-0.10	-0.77	0.467937	0.681144	-6.53
247514_at	peptide methionine sulfoxide reductase	PMSR1	AT5G61640	-1.08	-0.11	-0.77	0.468031	0.681158	-6.53
253616_at	blight-associated protein homolog bligh	EXLB2	AT4G30380	1.05	0.08	0.77	0.468084	0.681191	-6.53
260526_at	putative WD-40 repeat protein	---	AT2G47410	-1.06	-0.08	-0.77	0.468297	0.681458	-6.53
265066_at	unknown protein location of ESTs est V	FLA9	AT1G03870	-1.11	-0.15	-0.77	0.46838	0.681491	-6.53
260666_at	unknown protein ;supported by full-lengt	PARVUS	AT1G19300	-1.17	-0.22	-0.77	0.468365	0.681491	-6.53
260552_at	putative glyoxalase II ; supported by cD	GLX2-1	AT2G43430	-1.05	-0.07	-0.77	0.468608	0.681772	-6.53

266505_at	unknown protein	---	AT2G47830	1.06	0.08	0.77	0.468632	0.681772	-6.53
252030_at	hypothetical protein predicted proteins,	---	AT3G52690	1.05	0.07	0.77	0.468748	0.681897	-6.53
254919_at	RING-H2 finger protein RHA1b ;suppor	RHA1B	AT4G11360	1.11	0.15	0.77	0.468869	0.681986	-6.53
253102_at	Expressed protein ; supported by full-ler	---	AT4G36105	1.09	0.13	0.77	0.468852	0.681986	-6.53
257528_at	hypothetical protein predicted by genefir	---	AT3G02125	1.06	0.08	0.77	0.468991	0.682120	-6.53
246938_at	cyclin 3a	CYCA2;1	AT5G25380	1.07	0.10	0.77	0.469052	0.682165	-6.53
260716_at	peroxiredoxin identical to SP:O04005 fr	ATPER1	AT1G48130	1.08	0.11	0.77	0.469092	0.682179	-6.53
261856_at	hypothetical protein	---	AT1G50530	-1.07	-0.10	-0.77	0.469186	0.682272	-6.53
249872_at	unknown protein	---	AT5G23130	1.20	0.27	0.77	0.469253	0.682283	-6.53
252461_at	putative protein predicted protein, Arabi	---	---	1.07	0.10	0.77	0.469239	0.682283	-6.53
254979_at	subtilisin-like serine protease contains s	---	AT4G10550	-1.06	-0.09	-0.77	0.469319	0.682336	-6.53
246729_at	putative protein	---	AT5G28070	-1.06	-0.08	-0.77	0.469425	0.682447	-6.53
261267_at	unknown protein ;supported by full-lengt	---	AT1G26750	1.07	0.10	0.77	0.469584	0.682634	-6.53
253068_at	putative protein Kaposi's sarcoma-asso	---	AT4G37820	-1.06	-0.09	-0.77	0.469633	0.682661	-6.53
259186_at	unknown protein similar to possible apo	---	AT3G01590	-1.07	-0.10	-0.77	0.469729	0.682758	-6.53
261427_at	protein kinase, putative similar to CRK1	IBS1	AT1G18670	1.12	0.17	0.77	0.469777	0.682785	-6.53
256424_at	unknown protein ;supported by full-lengt	---	AT1G33490	1.06	0.09	0.77	0.469816	0.682797	-6.53
247234_at	putative protein similar to unknown prote	---	AT5G64980	-1.06	-0.08	-0.77	0.469891	0.682863	-6.53
264349_at	putative Proline synthetase associated p	---	AT1G11930	1.05	0.07	0.76	0.470301	0.683354	-6.53
259798_at	hypothetical protein predicted by genem	---	AT1G64310	1.08	0.12	0.76	0.470298	0.683354	-6.53
252024_at	monodehydroascorbate reductase (NA	ATMDAR1	AT3G52880	-1.08	-0.11	-0.76	0.470319	0.683354	-6.53
261688_at	unknown protein contains similarity to pr	---	AT1G47380	1.20	0.26	0.76	0.470419	0.683456	-6.53
250517_at	serine-type carboxypeptidase II-like pro	scpl35	AT5G08260	1.18	0.24	0.76	0.470649	0.683746	-6.54
246804_at	putative protein	---	---	1.05	0.08	0.76	0.470737	0.683830	-6.54
255787_at	putative cinnamoyl-CoA reductase highl	---	AT2G33590	-1.09	-0.12	-0.76	0.470881	0.683997	-6.54
252309_at	cysteine protease contains similarity to c	---	AT3G49340	-1.06	-0.09	-0.76	0.470943	0.684043	-6.54
255030_at	putative protein retrovirus-related polypr	---	---	1.06	0.09	0.76	0.471076	0.684193	-6.54
264982_at	hypothetical protein predicted by gensca	---	AT1G27220	1.07	0.10	0.76	0.471129	0.684225	-6.54
258546_at	hypothetical protein predicted by gensca	emb1974	AT3G07060	1.06	0.09	0.76	0.471219	0.684313	-6.54
254336_at	aspartic proteinase like protein oryzasir	---	AT4G22050	1.08	0.11	0.76	0.471306	0.684396	-6.54
267641_at	Argonaute (AGO1)-like protein	AGO6	AT2G32940	1.05	0.07	0.76	0.471444	0.684488	-6.54
263988_at	floral homeodomain transcription factor	SHP2	AT2G42830	-1.06	-0.08	-0.76	0.471489	0.684488	-6.54
253015_at	hypothetical protein	---	AT4G37950	-1.06	-0.09	-0.76	0.471467	0.684488	-6.54
265341_at	hypothetical protein predicted by gensca	---	AT2G18360	1.09	0.12	0.76	0.471438	0.684488	-6.54
245915_s_a	tubulin alpha-5 chain-like protein tubulir	TUA3	AT5G19770 /	-1.06	-0.09	-0.76	0.471765	0.684713	-6.54

264297_at	hypothetical protein similar to hypothetic	---	AT1G78710	1.05	0.07	0.76	0.471725	0.684713	-6.54
265401_at	hypothetical protein predicted by gensca	---	AT2G10970	1.06	0.08	0.76	0.471709	0.684713	-6.54
257695_at	hypothetical protein contains Pfam profil	HUA1	AT3G12680	-1.07	-0.09	-0.76	0.47176	0.684713	-6.54
251490_at	putative protein	---	AT3G59490	1.08	0.11	0.76	0.471864	0.684814	-6.54
248730_at	putative protein similar to unknown prote	---	AT5G48050	1.08	0.11	0.76	0.471901	0.684824	-6.54
255909_at	cdc2+/CDC28-related protein kinase, p	CDKD1;3	AT1G18040	-1.10	-0.14	-0.76	0.472003	0.684928	-6.54
248521_s_a	nodulin-like protein ; supported by cDNA	---	AT5G50520 /	1.06	0.09	0.76	0.472151	0.685012	-6.54
257358_at	unknown protein predicted by genscan	---	AT2G40990	1.10	0.13	0.76	0.472112	0.685012	-6.54
266610_at	Ac-like transposase related to Ac/Ds tra	---	---	-1.05	-0.07	-0.76	0.472133	0.685012	-6.54
248865_at	putative protein similar to unknown prote	---	AT5G46790	1.08	0.12	0.76	0.472409	0.685343	-6.54
250992_at	expansin precursor - like protein expan	ATEXPA9	AT5G02260	1.16	0.22	0.76	0.472439	0.685343	-6.54
263075_at	hypothetical protein predicted by genefi	---	AT2G17570	1.09	0.13	0.76	0.472576	0.685498	-6.54
262225_at	pectinesterase, putative similar to pecti	ATPME1	AT1G53840	1.14	0.19	0.76	0.472671	0.685593	-6.54
253830_at	Expressed protein ; supported by full-ler	---	AT4G27652	1.30	0.38	0.76	0.472964	0.685974	-6.54
261428_at	isochorismate synthase, putative simila	ICS2	AT1G18870	1.10	0.14	0.76	0.473127	0.686166	-6.54
255531_at	hypothetical protein similar to orf on MA	---	AT4G02160	-1.06	-0.09	-0.76	0.473177	0.686195	-6.54
251722_at	putative protein neuronal glutamine trar	---	AT3G56200	-1.12	-0.16	-0.76	0.473338	0.686385	-6.54
252584_at	putative protein several hypothetical pro	---	AT3G45560	1.06	0.08	0.76	0.473424	0.686466	-6.54
259647_at	acetyl-CoA synthetase, putative similar	---	AT1G55325	-1.07	-0.10	-0.76	0.473456	0.686469	-6.54
263913_at	putative receptor-like protein kinase	---	AT2G36570	1.11	0.15	0.76	0.473522	0.686481	-6.54
245804_at	hypothetical protein predicted by genem	---	AT1G46696	1.05	0.07	0.76	0.473525	0.686481	-6.54
247151_at	unknown protein ;supported by full-leng	bHLH093	AT5G65640	1.11	0.15	0.76	0.473571	0.686505	-6.54
257143_at	cytochrome P450, putative contains Pfa	CYP705A2	AT3G20110	-1.07	-0.10	-0.76	0.473634	0.686509	-6.54
256847_at	early nodule-specific protein, putative s	---	AT3G27950	1.06	0.09	0.76	0.47362	0.686509	-6.54
254269_at	putative serine/threonine kinase MAP3k	---	AT4G23050	1.08	0.11	0.76	0.473779	0.686631	-6.54
252631_s_a	putative protein predicted proteins, Aral	---	---	-1.05	-0.07	-0.76	0.473775	0.686631	-6.54
258479_at	hypothetical protein predicted by genscа	---	AT3G02440	1.06	0.09	0.76	0.474061	0.686935	-6.54
255905_at	tonoplast intrinsic protein, putative simil	BETA-TIP	AT1G17810	-1.11	-0.15	-0.76	0.474078	0.686935	-6.54
265055_at	hypothetical protein similar to hypothetic	---	---	1.06	0.09	0.76	0.474041	0.686935	-6.54
261489_at	hypothetical protein contains similarity to	---	AT1G14450	-1.05	-0.07	-0.76	0.474125	0.686959	-6.54
245562_at	OBP33pep like protein contains non_co	---	AT4G15520	-1.08	-0.11	-0.76	0.474266	0.687075	-6.54
257770_at	unknown protein ;supported by full-leng	LFR	AT3G22990	-1.07	-0.09	-0.76	0.47425	0.687075	-6.54
263319_at	putative anion exchange protein identica	BOR1	AT2G47160	1.13	0.17	0.76	0.474401	0.687228	-6.54
267620_at	putative beta-1,3-glucanase	---	AT2G39640	1.06	0.08	0.76	0.474462	0.687251	-6.54
258348_at	unknown protein ;supported by full-leng	---	AT3G17710	1.06	0.09	0.76	0.474485	0.687251	-6.54

246788_at	putative protein hypothetical proteins - /	AGL89	AT5G27580	-1.05	-0.08	-0.76	0.474507	0.687251	-6.54
261227_at	proteasome regulatory subunit S3, puta	EMB2719	AT1G20200	-1.05	-0.08	-0.76	0.474746	0.687553	-6.54
250453_at	putative protein predicted protein, Bacil	---	AT5G10620	1.08	0.11	0.76	0.474788	0.687570	-6.54
252610_x_a	putative protein putative MuDR protein	---	---	1.05	0.07	0.76	0.474844	0.687608	-6.54
258017_at	unknown protein	---	AT3G19370	-1.12	-0.17	-0.76	0.474937	0.687608	-6.54
262697_at	beta-glucosidase, putative similar to be	ATA27	AT1G75940	1.06	0.08	0.76	0.474878	0.687608	-6.54
248642_at	putative protein similar to unknown prote	---	AT5G49120	-1.06	-0.09	-0.76	0.474919	0.687608	-6.54
250778_at	unknown protein ;supported by full-lengt	---	AT5G05500	1.06	0.09	0.76	0.474965	0.687608	-6.54
256685_at	hypothetical protein predicted by genem	---	AT3G32100	1.07	0.09	0.76	0.475092	0.687749	-6.54
259279_at	putative cystathionine gamma-synthase	MTO1	AT3G01120	-1.06	-0.08	-0.76	0.475217	0.687885	-6.54
245724_at	hypothetical protein predicted by genem	---	AT1G73390	1.11	0.15	0.76	0.475324	0.687997	-6.54
263303_at	unknown protein ;supported by full-leng	---	AT2G15240	-1.07	-0.10	-0.76	0.475356	0.687999	-6.54
266511_at	putative ATP-dependent RNA helicase /	---	AT2G47680	-1.08	-0.11	-0.76	0.475439	0.688042	-6.54
263955_at	putative E2F5 family transcription factor	E2F3	AT2G36010	1.10	0.13	0.76	0.475446	0.688042	-6.54
255461_at	ent-kaurene synthetase A - like protein	GA1	AT4G02780	1.07	0.09	0.76	0.475522	0.688085	-6.54
250456_at	26S proteasome p55 protein-like ; supp	EMB2107	AT5G09900	-1.09	-0.12	-0.76	0.475566	0.688085	-6.54
248233_at	F-box protein family, AtFBL13 contains	---	AT5G53840	-1.06	-0.09	-0.76	0.475564	0.688085	-6.54
250643_at	putative protein similar to unknown prote	---	AT5G06780	-1.05	-0.08	-0.76	0.475662	0.688180	-6.54
264719_at	receptor-like kinase, putative similar to	---	AT1G70110	1.09	0.13	0.76	0.475709	0.688205	-6.54
253121_at	putative protein predicted protein, Caen	---	AT4G35890	-1.05	-0.07	-0.75	0.475884	0.688283	-6.54
264626_at	unknown protein	AS2	AT1G65620	-1.10	-0.14	-0.75	0.47588	0.688283	-6.54
266011_at	unknown protein	---	AT2G37440	1.06	0.09	0.75	0.475852	0.688283	-6.54
254843_at	putative protein TAK1 binding protein -	---	AT4G11860	-1.05	-0.07	-0.75	0.475877	0.688283	-6.54
256137_at	auxin-regulated protein, putative similar	---	AT1G48690	-1.05	-0.07	-0.75	0.475963	0.688353	-6.54
248210_at	ethylene-forming-enzyme-like dioxygena	---	AT5G54000	1.06	0.08	0.75	0.476196	0.688648	-6.54
245149_at	putative SWI/SNF family transcription ac	ATSWI3A	AT2G47620	-1.07	-0.09	-0.75	0.476279	0.688723	-6.54
247947_at	auxin transport protein EIR1 (gb|AAC39	EIR1	AT5G57090	1.08	0.11	0.75	0.476311	0.688726	-6.54
257720_at	hypothetical protein similar to GB:AAD0	---	AT3G18450	1.07	0.10	0.75	0.476382	0.688786	-6.54
259022_at	putative asparaginyl-tRNA synthetase (	NS2	AT3G07420	1.10	0.14	0.75	0.476597	0.688790	-6.54
263208_at	zinc finger protein 5, ZFP5 possible tran	ZFP5	AT1G10480	1.08	0.11	0.75	0.476579	0.688790	-6.54
251269_at	putative protein Pm5 protein - Homo sa	---	AT3G62360	-1.08	-0.11	-0.75	0.476574	0.688790	-6.54
251135_at	putative protein proteophosphoglycan p	---	AT5G01280	-1.06	-0.08	-0.75	0.476496	0.688790	-6.54
261619_x_a	hypothetical protein	---	---	1.06	0.08	0.75	0.476543	0.688790	-6.54
253059_s_a	putative protein other predicted proteins	HHP5	AT4G37680 /	-1.11	-0.14	-0.75	0.476502	0.688790	-6.54
257496_s_a	hypothetical protein predicted by grail	---	AT2G43730 /	-1.08	-0.11	-0.75	0.476424	0.688790	-6.54

261246_at	unknown protein	SYTB	AT1G20080	1.06	0.09	0.75	0.476652	0.688827	-6.54
261213_at	unknown protein ; supported by cDNA: g	---	AT1G12970	-1.06	-0.08	-0.75	0.476714	0.688872	-6.54
251147_at	kinesin heavy chain - like protein kinesi	---	AT3G63480	1.06	0.09	0.75	0.47689	0.689083	-6.54
263541_at	unknown protein ; supported by full-leng	---	AT2G24860	1.06	0.08	0.75	0.477019	0.689095	-6.54
255104_at	Expressed protein ; supported by full-ler	SAH7	AT4G08685	-1.24	-0.31	-0.75	0.476989	0.689095	-6.54
258630_at	putative CCHC-type zinc finger protein	---	AT3G02820	1.10	0.13	0.75	0.476937	0.689095	-6.54
260942_s_a	hypothetical protein contains similarity to	---	AT1G45190 /	-1.06	-0.09	-0.75	0.477016	0.689095	-6.54
245513_at	SYBL1 like protein	ATVAMP7	AT4G15780	-1.12	-0.16	-0.75	0.477061	0.689112	-6.54
250812_at	putative protein similar to unknown prote	---	AT5G04900	-1.06	-0.08	-0.75	0.477114	0.689144	-6.54
248100_at	beta-1,3-glucanase-like protein ;suppo	---	AT5G55180	-1.20	-0.26	-0.75	0.477318	0.689396	-6.54
264364_at	unknown protein Similar to gb|U85207 s	---	AT1G03330	-1.05	-0.08	-0.75	0.477429	0.689424	-6.54
254887_at	putative protein various predicted prote	---	AT4G11770	1.07	0.09	0.75	0.477371	0.689424	-6.54
266584_s_a	putative steroid sulfotransferase	ST4C	AT1G13430 /	-1.05	-0.07	-0.75	0.477424	0.689424	-6.54
266736_at	putative cytochrome P450 ; supported b	CYP709B1	AT2G46960	1.05	0.08	0.75	0.477543	0.689546	-6.54
263147_at	polyubiquitin, putative similar to polyubi	---	AT1G53980	-1.05	-0.07	-0.75	0.477602	0.689587	-6.54
245174_at	putative kinesin heavy chain	---	AT2G47500	-1.12	-0.16	-0.75	0.477686	0.689665	-6.55
255937_at	transcriptional activator CBF1, putative	DDF1	AT1G12610	1.13	0.18	0.75	0.477772	0.689746	-6.55
247138_at	3-dehydroquinate synthase-like protein	---	AT5G66120	1.10	0.13	0.75	0.477835	0.689792	-6.55
266166_at	putative glucosyltransferase ; supported	---	AT2G28080	1.09	0.13	0.75	0.478053	0.689843	-6.55
260123_at	AIG1-like protein similar to AIG1 protein	---	AT1G33890	-1.06	-0.08	-0.75	0.478021	0.689843	-6.55
265324_at	hypothetical protein predicted by genefin	ATCOAD	AT2G18250	-1.07	-0.10	-0.75	0.477969	0.689843	-6.55
251591_at	carboxyl terminal protease - like protein	---	AT3G57680	1.12	0.16	0.75	0.477933	0.689843	-6.55
246054_at	putative protein predicted proteins, Aral	---	AT5G08360	1.06	0.08	0.75	0.478045	0.689843	-6.55
261866_at	scarecrow-like 3 identical to GB:AAD24	SCL3	AT1G50420	-1.27	-0.35	-0.75	0.478081	0.689843	-6.55
261330_at	transcription factor, putative similar to G	MCM2	AT1G44900	-1.24	-0.31	-0.75	0.477948	0.689843	-6.55
250240_at	unknown protein	---	AT5G13590	-1.10	-0.13	-0.75	0.478115	0.689848	-6.55
262923_at	Dhp1-like protein similar to Dhp1 protein	XRN3	AT1G75660	1.06	0.08	0.75	0.478151	0.689856	-6.55
256338_at	hypothetical protein similar to seed matu	---	AT1G72100	1.06	0.09	0.75	0.478326	0.689977	-6.55
249517_at	putative protein similar to unknown prote	---	AT5G38580	1.05	0.07	0.75	0.478321	0.689977	-6.55
263436_at	hypothetical protein	---	AT2G28690	1.07	0.09	0.75	0.478277	0.689977	-6.55
258118_at	unknown protein	---	AT3G14710	1.08	0.11	0.75	0.47838	0.690012	-6.55
261895_at	metal ion transporter identical to GB:AA	NRAMP1	AT1G80830	1.16	0.21	0.75	0.478461	0.690075	-6.55
259557_at	hypothetical protein	WAK4	AT1G21210	-1.05	-0.08	-0.75	0.478484	0.690075	-6.55
256324_at	MATE efflux family protein, putative cor	---	AT1G66760	1.28	0.36	0.75	0.478598	0.690196	-6.55
254765_at	hypothetical protein	---	AT4G13270	-1.07	-0.10	-0.75	0.478633	0.690202	-6.55

252280_at	SF16 -like protein SF16 protein, pollen	iqd21	AT3G49260	1.17	0.22	0.75	0.478709	0.690241	-6.55
262986_at	unknown protein similar to hypothetical	---	AT1G23390	-1.12	-0.17	-0.75	0.478721	0.690241	-6.55
254666_at	translation initiation factor eIF-2 gamma	---	AT4G18330	1.05	0.07	0.75	0.478843	0.690330	-6.55
245343_at	hypothetical protein ;supported by full-le	---	AT4G15830	1.05	0.07	0.75	0.478873	0.690330	-6.55
247581_at	receptor-like protein kinase precursor -	---	AT5G61350	-1.05	-0.08	-0.75	0.478866	0.690330	-6.55
253050_at	putative protein probable arabinogalact	AGP18	AT4G37450	1.21	0.28	0.75	0.479006	0.690479	-6.55
248960_at	subtilisin-like protease	---	AT5G45640	-1.09	-0.12	-0.75	0.479116	0.690594	-6.55
255312_at	putative transposon protein	---	---	-1.06	-0.08	-0.75	0.479186	0.690650	-6.55
255150_at	putative xylan endohydrolase	---	AT4G08160	1.11	0.15	0.75	0.479228	0.690667	-6.55
260497_at	40S ribosomal protein S2 ;supported by	---	AT2G41840	-1.14	-0.19	-0.75	0.479299	0.690686	-6.55
247756_at	subtilisin-like serine protease contains s	---	AT5G59100	1.06	0.08	0.75	0.479302	0.690686	-6.55
246887_at	hexose transporter - like protein hexose	---	AT5G26250	-1.06	-0.09	-0.75	0.479405	0.690755	-6.55
262863_at	rhamnosyltransferase, putative similar t	---	AT1G64910	1.06	0.09	0.75	0.47941	0.690755	-6.55
265460_at	putative caltractin ;supported by full-len	---	AT2G46600	-1.11	-0.15	-0.75	0.479448	0.690767	-6.55
245988_at	putative protein predicted protein, Plasr	---	AT5G20610	-1.08	-0.12	-0.75	0.4796	0.690941	-6.55
263127_at	hypothetical protein predicted by genem	MSL6	AT1G78610	1.07	0.10	0.75	0.479819	0.691140	-6.55
249991_at	zinc finger -like protein zinc finger prote	---	AT5G18550	1.06	0.08	0.75	0.479779	0.691140	-6.55
248869_at	putative protein contains similarity to RN	---	AT5G46840	-1.11	-0.15	-0.75	0.479859	0.691140	-6.55
253231_at	Nonclathrin coat protein gamma - like p	---	AT4G34450	1.07	0.09	0.75	0.479849	0.691140	-6.55
260494_at	putative receptor-like protein kinase	---	AT2G41820	-1.08	-0.11	-0.75	0.479897	0.691152	-6.55
256869_at	nodulin, putative similar to nodulin GB:A	---	AT3G26420 /	-1.09	-0.13	-0.75	0.480079	0.691239	-6.55
248657_at	peptidylprolyl isomerase	ROF2	AT5G48570	-1.47	-0.56	-0.75	0.48005	0.691239	-6.55
255911_at	receptor-like kinase, putative similar to	---	AT1G66930	-1.05	-0.07	-0.75	0.48006	0.691239	-6.55
265302_at	Mutator-like transposase similar to MUF	---	---	1.05	0.07	0.75	0.480074	0.691239	-6.55
251316_s_a	putative protein putative protein BcDNA	---	AT3G61480 /	-1.06	-0.09	-0.75	0.480113	0.691244	-6.55
251473_at	putative protein myrosinase-binding pro	---	AT3G59610	1.09	0.12	0.75	0.480167	0.691278	-6.55
267582_at	putative protein kinase contains a protei	---	AT2G41970	1.06	0.08	0.75	0.480227	0.691278	-6.55
250076_at	putative protein; similar to unknown prot	---	AT5G16660	-1.07	-0.10	-0.75	0.480214	0.691278	-6.55
259813_at	glutathione S-transferase, putative simi	ATGSTF1	AT1G49860	-1.06	-0.09	-0.75	0.480415	0.691348	-6.55
247245_at	putative protein similar to unknown prote	---	AT5G64720	-1.05	-0.08	-0.75	0.480373	0.691348	-6.55
252321_at	hypothetical protein ;supported by full-le	---	AT3G48510	-1.07	-0.09	-0.75	0.480384	0.691348	-6.55
255873_at	hypothetical protein predicted by gensca	LBD13	AT2G30340	1.06	0.09	0.75	0.480335	0.691348	-6.55
246013_at	vacuolar calcium binding protein - like v	---	AT5G10660	1.05	0.08	0.75	0.480433	0.691348	-6.55
254288_at	putative protein Human mRNA for KIAA	AESP	AT4G22970	1.05	0.07	0.75	0.480458	0.691348	-6.55
248383_at	putative protein contains similarity to cyt	---	AT5G51900	1.06	0.08	0.75	0.480696	0.691646	-6.55

250609_at	peptide methionine sulfoxide reductase	PMSR3	AT5G07470	-1.05	-0.08	-0.75	0.480827	0.691791	-6.55
263348_at	cytoplasmic aconitate hydratase	---	AT2G05710	1.09	0.12	0.75	0.480952	0.691880	-6.55
257637_at	terpene synthase-related protein contair	---	AT3G25810	1.05	0.07	0.75	0.481047	0.691880	-6.55
263406_at	subtilisin-like serine protease AIR3 alm	AIR3	AT2G04160	-1.18	-0.24	-0.75	0.481045	0.691880	-6.55
258843_at	putative protein kinase similar to hypoth	---	AT3G04690	1.06	0.08	0.75	0.48107	0.691880	-6.55
265211_at	late embryogenesis abundant protein (A	ATECP63	AT2G36640	-1.05	-0.07	-0.75	0.480953	0.691880	-6.55
249246_at	unknown protein	---	AT5G42290	-1.05	-0.08	-0.75	0.481042	0.691880	-6.55
264642_at	putative CCAAT-binding transcription fa	NF-YB4	AT1G09030	1.06	0.09	0.75	0.48111	0.691893	-6.55
251732_at	putative protein prenylated Rab accept	PRA1.B1	AT3G56110	1.05	0.08	0.75	0.481153	0.691912	-6.55
267560_at	putative cytochrome P450	CYP76C3	AT2G45580	1.07	0.09	0.75	0.481246	0.692001	-6.55
264079_at	putative seed storage protein (vicilin-like	---	AT2G28490	1.06	0.08	0.74	0.481515	0.692311	-6.55
248740_at	putative protein contains similarity to bZ	---	AT5G48130	1.08	0.11	0.74	0.481552	0.692311	-6.55
261523_at	protein tyrosine phosphatase identical t	PTP1	AT1G71860	1.06	0.08	0.74	0.481524	0.692311	-6.55
252524_at	putative protein mitochondrial ATP SYN	---	AT3G46430	-1.07	-0.10	-0.74	0.481637	0.692333	-6.55
255129_at	nodulin-like protein nodulin gene MtN21	---	AT4G08290	1.16	0.21	0.74	0.481671	0.692333	-6.55
253217_at	actin depolymerizing factor - like protein	ADF9	AT4G34970	-1.15	-0.20	-0.74	0.481601	0.692333	-6.55
265194_at	1-aminocyclopropane-1-carboxylate ox	EFE	AT1G05010	1.15	0.20	0.74	0.481689	0.692333	-6.55
265277_at	unknown protein ;supported by full-leng	---	AT2G28410	-1.18	-0.24	-0.74	0.481824	0.692484	-6.55
266214_at	putative retroelement integrase	---	---	1.05	0.07	0.74	0.481861	0.692493	-6.55
259980_at	unknown protein ;supported by full-leng	---	AT1G76520	1.13	0.18	0.74	0.481933	0.692525	-6.55
249130_at	putative protein contains similarity to chl	---	AT5G43100	-1.05	-0.07	-0.74	0.481968	0.692525	-6.55
258056_at	hypothetical protein similar to GB:AAD1	---	AT3G29010	1.08	0.12	0.74	0.481975	0.692525	-6.55
264248_at	hypothetical protein predicted by gensca	---	AT1G78700	1.09	0.12	0.74	0.482086	0.692641	-6.55
248245_at	MtN3 protein-like	---	AT5G53190	1.07	0.10	0.74	0.482156	0.692698	-6.55
259487_at	hypothetical protein contains similarity t	TRFL5	AT1G15720	1.05	0.07	0.74	0.482244	0.692742	-6.55
245643_at	myb-related transcription factor (cpm7),	MYB116	AT1G25340	1.06	0.08	0.74	0.482247	0.692742	-6.55
266609_at	unknown protein ; supported by cDNA:	SRO1	AT2G35510	-1.09	-0.12	-0.74	0.482414	0.692856	-6.55
266573_at	unknown protein	---	AT2G23860	1.08	0.12	0.74	0.482425	0.692856	-6.55
247710_at	receptor-like protein kinase receptor-lik	---	AT5G59260	1.05	0.07	0.74	0.482439	0.692856	-6.55
259809_at	hypothetical protein predicted by genem	---	AT1G49800	1.09	0.13	0.74	0.482448	0.692856	-6.55
260304_at	unknown protein identical to most of OB	---	AT1G70480	1.10	0.14	0.74	0.482627	0.693052	-6.55
253936_at	STIG1 like protein STIG1 protein - com	---	AT4G26880	1.06	0.08	0.74	0.482675	0.693052	-6.55
259547_at	gypsy/Ty3 element polyprotein, putative	---	---	1.06	0.08	0.74	0.482653	0.693052	-6.55
261092_at	unknown protein	---	AT1G62870	1.05	0.07	0.74	0.482743	0.693062	-6.55
259894_at	hypothetical protein predicted by gensca	---	AT1G71430	1.07	0.10	0.74	0.482737	0.693062	-6.55

250343_at	putative protein density regulated prote	---	AT5G11900	-1.06	-0.08	-0.74	0.482854	0.693178	-6.55
257420_at	hypothetical protein predicted by genem	---	AT1G77250	-1.07	-0.10	-0.74	0.482991	0.693288	-6.55
252660_at	putative protein	---	AT3G44440	-1.05	-0.07	-0.74	0.482971	0.693288	-6.55
264210_at	putative myb-related transcription factor	MYB3	AT1G22640	-1.09	-0.13	-0.74	0.48322	0.693572	-6.55
255580_at	putative water channel protein	TIP1;3	AT4G01470	1.08	0.11	0.74	0.483409	0.693776	-6.55
263012_at	homeotic protein, putative similar to hor	KNAT6	AT1G23380	-1.05	-0.07	-0.74	0.483423	0.693776	-6.55
261562_at	actin depolymerizing factor, putative sir	ADF11	AT1G01750	1.08	0.11	0.74	0.483488	0.693826	-6.55
248059_at	putative protein similar to unknown prote	TRN1	AT5G55540	-1.12	-0.16	-0.74	0.48362	0.693840	-6.55
250568_at	putative protein several putative ATP-de	---	AT5G08110	-1.06	-0.09	-0.74	0.483564	0.693840	-6.55
246875_at	pathogenesis-related protein - like path	---	AT5G26130	1.06	0.08	0.74	0.48361	0.693840	-6.55
250638_at	glycine-rich protein atGRP-6	GRP16	AT5G07540	-1.08	-0.10	-0.74	0.483544	0.693840	-6.55
251878_at	putative protein predicted protein, Arabi	---	AT3G54310	-1.05	-0.07	-0.74	0.483729	0.693954	-6.55
262204_at	unknown protein ; supported by full-leng	---	AT2G01100	1.06	0.08	0.74	0.484126	0.694480	-6.55
257137_at	P-glycoprotein, putative similar to P-gly	ABCB19	AT3G28860	-1.23	-0.29	-0.74	0.484506	0.694662	-6.55
260553_at	unknown protein similar to T11A07.9	---	AT2G41800	1.06	0.08	0.74	0.484494	0.694662	-6.55
250661_at	nucleoid DNA-binding-like protein ;supp	---	AT5G07030	-1.43	-0.51	-0.74	0.484446	0.694662	-6.55
260894_at	hypothetical protein contains similarity to	---	AT1G29220	-1.06	-0.08	-0.74	0.484527	0.694662	-6.55
262323_at	6-phosphogluconate dehydrogenase, p	---	AT1G64190	1.05	0.07	0.74	0.484463	0.694662	-6.55
254437_s_a	putative protein	---	AT3G06433	-1.10	-0.14	-0.74	0.484476	0.694662	-6.55
248317_at	unknown protein	---	AT5G52680	1.06	0.08	0.74	0.484426	0.694662	-6.55
257090_at	protein kinase, putative contains Pfam p	---	AT3G20530	-1.06	-0.09	-0.74	0.48433	0.694662	-6.55
265527_at	putative Athila retroelement ORF1 prote	---	---	-1.05	-0.07	-0.74	0.48441	0.694662	-6.55
254895_at	hypothetical protein	---	AT4G11870	-1.08	-0.11	-0.74	0.484561	0.694667	-6.55
258043_at	unknown protein ; supported by cDNA:	---	AT3G21290	-1.05	-0.07	-0.74	0.484661	0.694766	-6.55
251561_at	E2 ubiquitin-conjugating-like enzyme Ah	SCE1	AT3G57870	-1.05	-0.07	-0.74	0.484765	0.694871	-6.55
261901_at	J8-like protein similar to DnaJ homologu	J8	AT1G80920	1.06	0.09	0.74	0.48494	0.695069	-6.56
256651_at	hypothetical protein predicted by genem	---	AT3G18840	1.07	0.10	0.74	0.484986	0.695069	-6.56
264495_at	hypothetical protein predicted by genscar	RIC2	AT1G27380	-1.06	-0.08	-0.74	0.484995	0.695069	-6.56
254104_at	putative protein predicted protein, Arabi	---	AT4G25040	1.07	0.10	0.74	0.485045	0.695099	-6.56
252485_at	disease resistance protein RPP13-like p	RPP13	AT3G46530	-1.06	-0.09	-0.74	0.485254	0.695310	-6.56
261797_at	cation-chloride co-transporter, putative	---	AT1G30455	-1.06	-0.09	-0.74	0.485253	0.695310	-6.56
262037_at	hypothetical protein predicted by genem	---	---	1.06	0.08	0.74	0.485334	0.695381	-6.56
254039_at	putative protein Human GS1 (protein of	GPP1	AT4G25840	-1.08	-0.11	-0.74	0.485388	0.695415	-6.56
257655_at	unknown protein contains Pfam profiles	---	AT3G13350	-1.13	-0.18	-0.74	0.485444	0.695451	-6.56
249538_at	kanadaptin - like protein unnamed ORF	---	AT5G38840	-1.06	-0.08	-0.74	0.485494	0.695480	-6.56

246923_at	putative multispanning membrane prote	---	AT5G25100	-1.07	-0.10	-0.74	0.485639	0.695643	-6.56
264282_at	hypothetical protein similar to hypothetic	---	AT1G61840	1.06	0.09	0.74	0.48573	0.695709	-6.56
261096_at	4-coumarate:coenzyme A ligase, putati	ACOS5	AT1G62940	1.06	0.09	0.74	0.485746	0.695709	-6.56
244905_at	hypothetical protein	---	---	-1.06	-0.08	-0.74	0.485822	0.695774	-6.56
258407_at	unknown protein similar to unknown pro	---	AT3G17620	1.09	0.13	0.74	0.485927	0.695882	-6.56
267536_at	phospholipase D ; supported by cDNA:	PLDBETA	AT2G42010	1.07	0.10	0.74	0.485965	0.695892	-6.56
253651_at	putative protein nucleoid DNA-binding p	---	AT4G30030	1.07	0.10	0.74	0.486185	0.696120	-6.56
262403_s_a	mutator-like transposase, putative simil	---	---	-1.05	-0.07	-0.74	0.486175	0.696120	-6.56
246269_at	putative protein	---	AT4G37110	-1.13	-0.18	-0.74	0.486225	0.696133	-6.56
264097_s_a	NADH dehydrogenase, putative similar	---	AT1G16700 /	1.06	0.08	0.74	0.486268	0.696151	-6.56
252974_at	putative protein ; supported by cDNA: g	MTN1	AT4G38800	1.06	0.08	0.74	0.486394	0.696183	-6.56
251716_at	anthranilate synthase alpha-1 chain - lik	---	AT3G55870	-1.06	-0.08	-0.74	0.486406	0.696183	-6.56
265237_s_a	hypothetical protein	---	AT2G07706	1.06	0.09	0.74	0.486412	0.696183	-6.56
245717_at	Expressed protein ; supported by cDNA	---	AT5G33390	-1.06	-0.09	-0.74	0.486386	0.696183	-6.56
254553_at	TMV resistance protein N - like TMV res	---	AT4G19530	-1.12	-0.16	-0.74	0.486488	0.696248	-6.56
262692_at	hypothetical protein predicted by genem	---	---	1.06	0.09	0.74	0.48669	0.696493	-6.56
266540_at	hypothetical protein predicted by gensca	---	AT2G35310	1.06	0.08	0.74	0.486764	0.696522	-6.56
262438_at	hypothetical protein identical to hypothe	---	AT1G47410	-1.12	-0.16	-0.74	0.486771	0.696522	-6.56
250396_at	zinc finger -like protein CCHH finger pro	---	AT5G10970	1.15	0.20	0.74	0.48682	0.696548	-6.56
251304_at	putative protein several O-methyltransfe	---	AT3G61990	1.22	0.29	0.74	0.487016	0.696785	-6.56
246609_at	putative receptor-like protein kinase rec	---	AT5G35390	-1.05	-0.07	-0.73	0.487272	0.697107	-6.56
254845_at	hydroxymethylglutaryl-CoA synthase ;s	MVA1	AT4G11820	1.08	0.11	0.73	0.487316	0.697121	-6.56
253419_at	putative protein predicted proteins, Aral	---	AT4G32780	-1.07	-0.10	-0.73	0.487374	0.697121	-6.56
259353_at	putative branched-chain amino acid ami	---	AT3G05190	-1.05	-0.07	-0.73	0.487364	0.697121	-6.56
266262_at	hypothetical protein predicted by gensca	---	AT2G27590	-1.11	-0.15	-0.73	0.487419	0.697142	-6.56
249212_at	putative protein strong similarity to unkn	---	AT5G42690	1.06	0.09	0.73	0.487494	0.697196	-6.56
261047_at	hypothetical protein predicted by genem	APUM22	AT1G01410	1.11	0.15	0.73	0.487518	0.697196	-6.56
262511_at	syntaxin-related protein At-SYR1, putat	SYP125	AT1G11250	1.08	0.11	0.73	0.487551	0.697201	-6.56
245554_at	cytochrome P450 like protein	CYP705A4	AT4G15380	1.05	0.07	0.73	0.487603	0.697231	-6.56
266418_at	putative annexin ;supported by full-leng	ANNAT4	AT2G38750	-1.19	-0.25	-0.73	0.487679	0.697264	-6.56
265507_s_a	Ac-like transposase related to Ac/Ds tra	---	---	-1.06	-0.08	-0.73	0.487688	0.697264	-6.56
250747_at	glucuronosyl transferase-like protein	---	AT5G05900	1.05	0.07	0.73	0.487916	0.697547	-6.56
246227_at	hypothetical protein	---	AT4G36510	-1.07	-0.10	-0.73	0.487961	0.697568	-6.56
266434_s_a	unknown protein	---	AT2G07120 /	1.05	0.07	0.73	0.488051	0.697652	-6.56
266170_at	unknown protein ;supported by full-leng	---	AT2G39050	1.11	0.16	0.73	0.488097	0.697675	-6.56

250973_at	60S ribosomal protein - like 60S roibos	---	AT5G02870	-1.11	-0.16	-0.73	0.488197	0.697774	-6.56
264961_at	unknown protein contains similarity to g	PRAF1	AT1G76950	1.13	0.17	0.73	0.488281	0.697851	-6.56
257426_at	hypothetical protein contains similarity t	---	AT1G54850	-1.08	-0.11	-0.73	0.488456	0.697924	-6.56
245903_at	CLB1 - like protein CLB1 protein, Lycop	SYTD	AT5G11100	1.06	0.09	0.73	0.488372	0.697924	-6.56
247195_at	putative protein contains similarity to rec	---	AT5G65500	1.07	0.10	0.73	0.488486	0.697924	-6.56
257917_at	ethylene responsive element binding pr	---	AT3G23220	1.05	0.07	0.73	0.488461	0.697924	-6.56
263257_at	putative DNA polymerase Beta similar t	---	AT1G10520	-1.08	-0.12	-0.73	0.488458	0.697924	-6.56
265608_at	hypothetical protein predicted by gensca	---	AT2G25380	1.05	0.07	0.73	0.488558	0.697984	-6.56
260512_at	unknown protein	---	AT1G51520	-1.08	-0.11	-0.73	0.488683	0.698119	-6.56
251937_at	putative protein predicted protein, Arabi	CPuORF4	AT3G53400 /	-1.21	-0.27	-0.73	0.488736	0.698151	-6.56
258745_at	unknown protein ; supported by full-leng	---	AT3G05920	-1.06	-0.09	-0.73	0.488849	0.698181	-6.56
248262_at	Avr9 elicitor response protein-like ; sup	---	AT5G53340	1.08	0.11	0.73	0.488828	0.698181	-6.56
259549_at	unknown protein ;supported by full-lengt	---	AT1G35290	1.06	0.08	0.73	0.488793	0.698181	-6.56
249631_at	sen1-like protein SEN1 - Saccharomyce	---	AT5G37160	1.06	0.08	0.73	0.488887	0.698192	-6.56
251162_at	putative protein hypothetical proteins - A	---	AT3G63300	-1.06	-0.08	-0.73	0.489077	0.698288	-6.56
263523_at	hypothetical protein predicted by gensca	---	---	-1.05	-0.08	-0.73	0.489052	0.698288	-6.56
245922_at	putative protein predicted proteins, Arat	---	AT5G28810	-1.06	-0.09	-0.73	0.489076	0.698288	-6.56
248632_at	unknown protein	SLD5	AT5G49010	-1.13	-0.18	-0.73	0.48899	0.698288	-6.56
264265_at	unknown protein ; supported by cDNA:	---	AT1G09280	-1.08	-0.11	-0.73	0.489186	0.698399	-6.56
254906_at	putative disease resistance response p	---	AT4G11180	-1.06	-0.08	-0.73	0.489492	0.698750	-6.56
251671_at	putative protein hypothetical protein T5	---	AT3G57210	1.06	0.08	0.73	0.48949	0.698750	-6.56
251463_at	hypothetical protein	---	AT3G59800	1.06	0.09	0.73	0.489694	0.698994	-6.56
260721_at	hypothetical protein predicted by genem	---	AT1G48060	-1.06	-0.08	-0.73	0.489776	0.699066	-6.56
257924_at	unknown protein	---	AT3G23190	1.08	0.12	0.73	0.489922	0.699232	-6.56
264581_at	hypothetical protein predicted by genefir	---	AT1G05210	1.13	0.18	0.73	0.490195	0.699519	-6.56
265883_at	unknown protein	---	AT2G42310	1.06	0.08	0.73	0.490241	0.699519	-6.56
264940_at	galactinol synthase, putative similar to g	AtGolS4	AT1G60470	1.21	0.27	0.73	0.490246	0.699519	-6.56
252339_at	hypothetical protein	---	AT3G48900	1.05	0.07	0.73	0.490217	0.699519	-6.56
250942_at	putative protein	---	AT5G03350	1.65	0.73	0.73	0.490302	0.699555	-6.56
256294_at	unknown protein	---	AT1G69450	1.07	0.10	0.73	0.490347	0.699575	-6.56
248561_at	unknown protein	---	AT5G49680	1.08	0.11	0.73	0.490437	0.699661	-6.56
255063_at	putative transposon protein similar to ma	---	---	-1.05	-0.06	-0.73	0.490583	0.699825	-6.56
247873_at	diacylglycerol kinase-like protein	---	AT5G57690	1.05	0.08	0.73	0.490638	0.699859	-6.56
264759_at	receptor protein kinase (IRK1), putative	---	AT1G61480	-1.06	-0.09	-0.73	0.4907	0.699904	-6.56
261929_at	hypothetical protein similar to axi 1-like p	---	AT1G22460	1.07	0.10	0.73	0.490826	0.700040	-6.56

266664_at	hypothetical protein predicted by grail	---	AT2G29800	-1.06	-0.08	-0.73	0.490948	0.700126	-6.56
252021_at	putative protein predicted protein, Arabi	---	AT3G53070	-1.07	-0.10	-0.73	0.49092	0.700126	-6.56
259667_at	unknown protein ; supported by cDNA: g	---	AT1G55270	-1.07	-0.10	-0.73	0.491007	0.700166	-6.56
265506_at	putative non-LTR retroelement reverse t	---	---	1.07	0.10	0.73	0.491115	0.700230	-6.56
246467_at	UDP glucose:flavonoid 3-o-glucosyltran	---	AT5G17040	1.09	0.13	0.73	0.491143	0.700230	-6.56
250219_at	putative protein similar to unknown prote	MPL1	AT5G14180	-1.15	-0.20	-0.73	0.491119	0.700230	-6.56
249052_at	antifungal protein-like (PDF1.2)	PDF1.2	AT5G44420	-1.29	-0.37	-0.73	0.491189	0.700251	-6.56
251847_at	tryptophan synthase alpha chain ; suppo	TSA1	AT3G54640	1.29	0.37	0.73	0.491382	0.700425	-6.56
256732_at	hypothetical protein predicted by genem	---	---	1.05	0.07	0.73	0.491362	0.700425	-6.56
252577_at	putative protein putative proteins - Arabi	---	AT3G45460	1.05	0.07	0.73	0.491403	0.700425	-6.56
258753_at	hypothetical protein predicted by genscа	ATEXO70I	AT3G09530	1.05	0.06	0.73	0.4917	0.700673	-6.56
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=gb:J044	---	---	1.13	0.18	0.73	0.491611	0.700673	-6.56
257692_at	hypothetical protein contains similarity to	---	AT3G12840	1.05	0.08	0.73	0.491693	0.700673	-6.56
265367_at	hypothetical protein predicted by genscа	---	---	-1.05	-0.07	-0.73	0.49168	0.700673	-6.56
257754_at	GTP binding protein, putative similar to	ATRAB7B	AT3G18820	-1.05	-0.08	-0.73	0.491738	0.700684	-6.56
265265_at	unknown protein	---	AT2G42900	1.09	0.12	0.73	0.492026	0.700992	-6.56
250411_at	putative protein	---	AT5G11120	-1.06	-0.08	-0.73	0.492047	0.700992	-6.56
262416_at	flavonol synthase, putative similar to fla	---	AT1G49390	1.05	0.08	0.73	0.491993	0.700992	-6.56
254170_at	LG27/30-like gene LG27/30 gene - Ara	---	AT4G24430	1.05	0.07	0.73	0.492116	0.701025	-6.56
267527_at	unknown protein	---	AT2G45610	-1.07	-0.10	-0.73	0.492131	0.701025	-6.56
257328_s_a	hypothetical protein	---	---	1.08	0.11	0.73	0.492204	0.701085	-6.56
258831_at	putative integral membrane protein cont	---	AT3G07080	-1.05	-0.07	-0.73	0.492237	0.701088	-6.56
264817_at	hypothetical protein similar to membrane	---	AT1G03540	1.05	0.07	0.73	0.49237	0.701221	-6.57
263281_at	putative glycine-rich RNA-binding protei	---	AT2G14160	1.06	0.08	0.73	0.492392	0.701221	-6.57
253870_at	putative protein	---	AT4G27530	1.06	0.09	0.73	0.492454	0.701266	-6.57
246449_at	hypothetical protein	---	AT5G16810	-1.07	-0.09	-0.73	0.492525	0.701269	-6.57
263575_at	hypothetical protein similar to hypothetic	---	AT2G17070	-1.05	-0.08	-0.73	0.492521	0.701269	-6.57
255513_at	PROLIFERA similar to S. cerevisiae MC	PRL	AT4G02060	-1.27	-0.35	-0.73	0.492548	0.701269	-6.57
255762_at	unknown protein contains Pfam profile:	HAC12	AT1G16710	-1.06	-0.08	-0.73	0.492608	0.701309	-6.57
260948_at	delta 9 desaturase, putative similar to d	---	AT1G06100	1.07	0.09	0.73	0.492675	0.701361	-6.57
261451_at	unknown protein	---	AT1G21060	-1.19	-0.25	-0.72	0.493035	0.701653	-6.57
261409_at	zinc finger protein OBP2 identical to GB	OBP2	AT1G07640	-1.06	-0.09	-0.72	0.49297	0.701653	-6.57
253603_at	putative protein SP8 binding protein, Cu	WRKY32	AT4G30935	-1.05	-0.07	-0.72	0.493064	0.701653	-6.57
248056_at	unknown protein ; supported by cDNA:	XYLT	AT5G55500	1.04	0.06	0.72	0.492982	0.701653	-6.57
267217_at	hypothetical protein	---	AT2G02610	1.05	0.07	0.72	0.492992	0.701653	-6.57

258754_at	hypothetical protein similar to hypothetic	---	AT3G11920	1.06	0.09	0.72	0.493029	0.701653	-6.57
256962_at	glucan endo-1,3-beta-glucosidase prec	---	AT3G13560	-1.17	-0.22	-0.72	0.493212	0.701819	-6.57
252852_at	hypothetical protein ;supported by full-le	---	AT4G39900	1.13	0.18	0.72	0.493267	0.701854	-6.57
253627_at	low temperature and salt responsive pr	---	AT4G30650	-1.40	-0.49	-0.72	0.493365	0.701950	-6.57
257349_at	unknown protein	---	AT2G30630	1.06	0.08	0.72	0.493425	0.701991	-6.57
261594_at	DNA-binding factor, putative similar to (	AT-GTL1	AT1G33240	-1.07	-0.09	-0.72	0.493624	0.702231	-6.57
260030_at	putative bZIP transcription factor similar	AtbZIP	AT1G68880	1.06	0.08	0.72	0.493775	0.702401	-6.57
248211_at	flavonol 3-O-glucosyltransferase-like pro	---	AT5G54010	1.04	0.06	0.72	0.493816	0.702415	-6.57
263456_at	unknown protein	---	AT2G22125	1.08	0.11	0.72	0.494126	0.702463	-6.57
267602_at	unknown protein ; supported by cDNA:	---	AT2G32970	1.08	0.11	0.72	0.49395	0.702463	-6.57
250564_at	putative protein sigma factor F inhibitor	---	AT5G08060	1.05	0.07	0.72	0.494057	0.702463	-6.57
245270_at	tubulin alpha-6 chain (TUA6) ; supporte	TUA6	AT4G14960	1.12	0.16	0.72	0.494072	0.702463	-6.57
248364_at	fibrillarin 3 (AtFib3) similar to fibrillarin 1	---	AT5G52490	1.05	0.07	0.72	0.494104	0.702463	-6.57
256157_at	longevity assurance protein, putative si	LAG13	AT1G13580	1.08	0.11	0.72	0.494071	0.702463	-6.57
248435_at	oleosin-like	OLEO3	AT5G51210	1.07	0.10	0.72	0.494069	0.702463	-6.57
258306_at	putative transcription factor similar to G/	ATBZIP42	AT3G30530	1.05	0.06	0.72	0.494026	0.702463	-6.57
253104_at	thaumatin-like protein thaumatin-like pr	---	AT4G36010	-1.22	-0.29	-0.72	0.493993	0.702463	-6.57
259438_at	unknown protein similar to putative dehy	AN	AT1G01510	-1.09	-0.12	-0.72	0.494168	0.702478	-6.57
248742_at	unknown protein	---	AT5G48200	-1.07	-0.09	-0.72	0.49448	0.702878	-6.57
263901_at	unknown protein ;supported by full-leng	---	AT2G36320	-1.08	-0.12	-0.72	0.494561	0.702949	-6.57
260758_at	endo-beta-1,4-glucanase, putative simi	AtGH9C1	AT1G48930	1.08	0.11	0.72	0.494668	0.703058	-6.57
266380_at	unknown protein	MEE13	AT2G14680	-1.06	-0.09	-0.72	0.494772	0.703162	-6.57
263738_at	hypothetical protein predicted by genem	---	AT1G60060	1.17	0.23	0.72	0.494834	0.703206	-6.57
258016_at	hypothetical protein similar to poly(A)-bi	MPC	AT3G19350	1.06	0.08	0.72	0.494916	0.703279	-6.57
262211_at	AP2 domain containing protein, putative	ORA47	AT1G74930	1.24	0.31	0.72	0.494958	0.703294	-6.57
248354_at	putative protein contains similarity to un	---	AT5G52330	1.06	0.08	0.72	0.494991	0.703298	-6.57
265197_at	putative glucosyl transferase	UGT73C1	AT2G36750	1.05	0.07	0.72	0.495098	0.703363	-6.57
265808_at	hypothetical protein predicted by gensca	---	AT2G17960	1.06	0.08	0.72	0.495091	0.703363	-6.57
260010_at	putative trehalose-6-phosphate synthas	ATTPS6	AT1G68020	1.10	0.13	0.72	0.495146	0.703387	-6.57
245430_at	hypothetical protein	FIP2	AT4G17060	-1.05	-0.06	-0.72	0.495435	0.703754	-6.57
250974_at	meiosis specific - like protein Spo11, M	RHL2	AT5G02820	-1.13	-0.18	-0.72	0.495506	0.703811	-6.57
250939_at	putative protein various predicted prote	iqd2	AT5G03040	1.10	0.13	0.72	0.495563	0.703848	-6.57
249493_at	acyltransferase -like protein Anthocyani	---	AT5G39080	1.10	0.14	0.72	0.495729	0.703943	-6.57
261151_at	sec14 cytosolic factor, putative similar t	---	AT1G19650	-1.06	-0.08	-0.72	0.495754	0.703943	-6.57
253345_at	putative protein	BCA5	AT4G33580	1.08	0.11	0.72	0.495683	0.703943	-6.57

249053_at	berberine bridge enzyme-like protein	---	AT5G44440	1.07	0.10	0.72	0.495745	0.703943	-6.57
253760_at	putative protein (fragment) predicted pr	AT4G2881	---	1.07	0.10	0.72	0.495842	0.704024	-6.57
265315_at	hypothetical protein predicted by genefir	CLASP	AT2G20190	-1.06	-0.08	-0.72	0.496093	0.704040	-6.57
257973_at	unknown protein	---	AT3G20720	1.07	0.10	0.72	0.4959	0.704040	-6.57
259815_at	hypothetical protein predicted by genem	---	AT1G49870	-1.06	-0.08	-0.72	0.496031	0.704040	-6.57
262294_at	hypothetical protein identical to hypothe	---	AT1G27610	1.06	0.08	0.72	0.495993	0.704040	-6.57
262269_at	hypothetical protein predicted by genem	---	---	1.05	0.07	0.72	0.495998	0.704040	-6.57
259890_at	inner mitochondrial membrane protein ic	ATTIM23-2	AT1G72750	1.11	0.14	0.72	0.496131	0.704040	-6.57
258210_at	Eukaryotic initiation factor 4A, putative	EIF4A1	AT3G13920	-1.06	-0.08	-0.72	0.496123	0.704040	-6.57
267003_at	hypothetical protein predicted by genefir	---	AT2G34340	1.06	0.08	0.72	0.496076	0.704040	-6.57
249520_at	putative protein similar to unknown prote	---	AT5G38670	1.05	0.07	0.72	0.496099	0.704040	-6.57
251307_at	putative protein ;supported by full-lengt	---	AT3G61200	1.07	0.10	0.72	0.496289	0.704221	-6.57
260667_at	very-long-chain fatty acid condensing e	KCS4	AT1G19440	1.05	0.08	0.72	0.496499	0.704321	-6.57
246838_at	flap endonuclease - like protein OsFEN	---	AT5G26680	-1.06	-0.08	-0.72	0.496531	0.704321	-6.57
259408_at	protein phosphatase 2A 65 kDa regulat	PP2AA2	AT3G25800	-1.05	-0.07	-0.72	0.496439	0.704321	-6.57
252685_at	disease resistence - like protein RPP1-	---	AT3G44410	1.11	0.15	0.72	0.496576	0.704321	-6.57
252933_at	putative receptor-like protein kinase rec	---	AT4G39110	-1.07	-0.10	-0.72	0.496422	0.704321	-6.57
251426_at	URIDYLATE KINASE-like protein URID	---	AT3G60180	-1.06	-0.09	-0.72	0.496458	0.704321	-6.57
252893_at	hypothetical protein	---	AT4G39420	1.04	0.06	0.72	0.496556	0.704321	-6.57
254246_at	protein kinase - like protein receptor kin	EMB1290	AT4G23250	1.05	0.07	0.72	0.496632	0.704357	-6.57
246741_at	glycine rich protein - like glycine rich pr	emb1644	AT5G27720	1.07	0.10	0.72	0.496737	0.704462	-6.57
250450_at	putative transcription factor MYB92 ; su	ATMYB92	AT5G10280	1.04	0.06	0.72	0.496773	0.704469	-6.57
248011_at	S-adenosyl-L-methionine:salicylic acid c	GAMT2	AT5G56300	-1.05	-0.07	-0.72	0.496812	0.704481	-6.57
249225_at	TMV resistance protein-like	---	AT5G42140	1.09	0.13	0.72	0.49689	0.704504	-6.57
258629_at	stelar K+ outward rectifying channel (SK	SKOR	AT3G02850	-1.05	-0.07	-0.72	0.496871	0.704504	-6.57
255378_at	putative glucan synthase component si	ATGSL05	AT4G03550	1.05	0.08	0.72	0.497214	0.704844	-6.57
251582_at	putative protein CARBON CATABOLIT	---	AT3G58580	1.06	0.08	0.72	0.497222	0.704844	-6.57
249819_at	unknown protein	---	AT5G23640	-1.05	-0.07	-0.72	0.497192	0.704844	-6.57
249930_at	synaptobrevin-like protein	ATVAMP7	AT5G22360	-1.06	-0.08	-0.72	0.497413	0.705071	-6.57
259245_at	unknown protein predicted by genefind	---	AT3G07660	-1.07	-0.10	-0.72	0.497648	0.705360	-6.57
267524_at	unknown protein	---	AT2G30600	-1.09	-0.12	-0.72	0.497788	0.705426	-6.57
265373_at	putative replication protein A1	RPA1A	AT2G06510	-1.11	-0.16	-0.72	0.497726	0.705426	-6.57
250770_at	laccase (diphenol oxidase)	LAC12	AT5G05390	1.08	0.12	0.72	0.497772	0.705426	-6.57
251598_at	AP2 transcription factor - like protein va	---	AT3G57600	1.05	0.07	0.72	0.497867	0.705465	-6.57
247634_at	late embryonic abundant protein - like l	---	AT5G60520	1.05	0.07	0.72	0.497903	0.705465	-6.57

254866_at	putative protein other predicted proteins	---	AT4G12220	-1.05	-0.06	-0.72	0.497908	0.705465	-6.57
265372_at	Ac-like transposase related to Ac/Ds tra	---	AT2G06500	1.07	0.09	0.72	0.498041	0.705609	-6.57
246640_x_a	putative protein predicted proteins, Aral	---	---	1.06	0.08	0.72	0.498138	0.705703	-6.57
252514_at	GTP-binding protein ara-3 ; supported b	ATRAB8A	AT3G46060	-1.05	-0.07	-0.72	0.498253	0.705778	-6.57
266339_s_a	hypothetical protein predicted by genscа	---	AT2G01360 /	1.06	0.09	0.72	0.498247	0.705778	-6.57
246685_at	putative protein nucleoid DNA-binding p	---	AT5G33350	1.11	0.15	0.72	0.498577	0.706194	-6.57
259985_at	unknown protein ; supported by cDNA:	---	AT1G76620	1.06	0.08	0.71	0.498695	0.706286	-6.57
255107_at	hypothetical protein	---	AT4G08730	1.07	0.10	0.71	0.498704	0.706286	-6.57
264085_at	putative glutamyl tRNA reductase	HEMA3	AT2G31250	1.05	0.07	0.71	0.498833	0.706381	-6.57
265392_at	lipoic acid synthase (LIP1) ; supported l	LIP1	AT2G20860	-1.05	-0.07	-0.71	0.498833	0.706381	-6.57
246477_at	putative transcription factor (MYB9)	AtMYB9	AT5G16770	1.11	0.15	0.71	0.498868	0.706387	-6.57
257103_at	hypothetical protein contains Pfam profil	---	AT3G25060	-1.07	-0.09	-0.71	0.49894	0.706401	-6.57
256901_at	hypothetical protein contains similarity to	---	---	1.04	0.06	0.71	0.498915	0.706401	-6.57
263971_at	hypothetical protein predicted by genefir	AtRLP29	AT2G42800	1.07	0.10	0.71	0.499312	0.706861	-6.57
245979_at	putative protein leucine zipper-containir	ATEXO70(	AT5G13150	1.05	0.07	0.71	0.499327	0.706861	-6.57
257265_at	PHD-finger protein, putative contains P	---	AT3G14980	-1.06	-0.09	-0.71	0.499542	0.707121	-6.57
253344_at	putative protein predicted protein, Arabi	---	AT4G33550	1.12	0.16	0.71	0.499682	0.707275	-6.57
265767_at	putative exonuclease contains zinc-finge	REF4	AT2G48110	1.07	0.09	0.71	0.499765	0.707350	-6.57
265405_at	putative protein kinase contains a protei	---	AT2G16750	-1.11	-0.15	-0.71	0.499907	0.707468	-6.57
246285_at	putative protein	---	AT4G36980	-1.05	-0.07	-0.71	0.499911	0.707468	-6.57
267034_at	unknown protein ;supported by full-leng	---	AT2G38310	-1.19	-0.25	-0.71	0.49996	0.707494	-6.58
249648_at	putative protein hypothetical protein T2	---	AT5G37050	-1.08	-0.12	-0.71	0.500106	0.707657	-6.58
255735_at	transmembrane protein, putative similar	---	AT1G25520	-1.11	-0.15	-0.71	0.500164	0.707660	-6.58
252387_at	aldose 1-epimerase - like protein aldose	---	AT3G47800	1.08	0.12	0.71	0.500171	0.707660	-6.58
247749_at	myb-related protein - like myb-related p	MYB119	AT5G58850	1.07	0.10	0.71	0.500325	0.707791	-6.58
254017_at	putative transcription factor	---	AT4G26170	1.04	0.06	0.71	0.500295	0.707791	-6.58
247186_at	putative protein contains similarity to au	---	AT5G65470	1.10	0.14	0.71	0.500395	0.707791	-6.58
248058_at	putative protein similar to unknown prote	---	AT5G55530	1.06	0.09	0.71	0.500417	0.707791	-6.58
261753_at	unknown protein	---	AT1G76340	1.07	0.09	0.71	0.500419	0.707791	-6.58
245609_at	disease resistance N like protein	---	AT4G14368 /	1.07	0.09	0.71	0.500536	0.707913	-6.58
257737_at	uridine kinase/uracil phosphoribosyl tra	---	AT3G27440	-1.06	-0.08	-0.71	0.500616	0.707982	-6.58
265848_at	putative sugar transporter	INT3	AT2G35740	1.09	0.12	0.71	0.500728	0.708009	-6.58
260306_at	hypothetical protein predicted by genscа	EDA24	AT1G70540	1.06	0.09	0.71	0.500715	0.708009	-6.58
264398_at	unknown protein similar to hypothetical p	---	AT1G61730	-1.06	-0.08	-0.71	0.500703	0.708009	-6.58
248862_at	unknown protein	---	AT5G46730	-1.09	-0.12	-0.71	0.500884	0.708015	-6.58

AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=gb:J044	---	---	1.14	0.19	0.71	0.500887	0.708015	-6.58
253487_at	ribosomal protein S6 - like ribosomal pr	RPS6	AT4G31700	-1.16	-0.21	-0.71	0.500875	0.708015	-6.58
251060_at	putative protein serine/threonine protein	ATSR1	AT5G01820	1.25	0.32	0.71	0.500786	0.708015	-6.58
265241_at	hypothetical protein	---	---	-1.07	-0.10	-0.71	0.500852	0.708015	-6.58
250618_at	putative protein hypothetical proteins - A	ATBAG3	AT5G07220	-1.05	-0.08	-0.71	0.501011	0.708016	-6.58
250764_at	putative protein similar to unknown prote	---	AT5G05960	1.54	0.62	0.71	0.501012	0.708016	-6.58
251944_at	ABC transporter -like protein breast can	---	AT3G53510	1.08	0.11	0.71	0.501004	0.708016	-6.58
261600_x_a	hypothetical protein similar to hypothetic	---	AT1G49680 /	-1.05	-0.07	-0.71	0.500967	0.708016	-6.58
253730_at	putative protein hypothetical protein T2	---	AT4G29480	1.10	0.14	0.71	0.50105	0.708022	-6.58
260506_at	Cyclin, putative similar to GB:CAB7726	CYCA3;2	AT1G47210	1.12	0.16	0.71	0.50108	0.708022	-6.58
264499_at	Expressed protein ; supported by full-len	---	AT1G30795	1.07	0.09	0.71	0.501109	0.708022	-6.58
257269_at	unknown protein contains Pfam profile:	NPSN13	AT3G17440	1.09	0.12	0.71	0.501314	0.708267	-6.58
252087_at	putative protein putative Na+/H+-excha	chx28	AT3G52080	-1.05	-0.07	-0.71	0.501354	0.708279	-6.58
267422_at	putative protein kinase contains a protei	---	AT2G35050	-1.05	-0.07	-0.71	0.501385	0.708279	-6.58
260708_at	expressed protein ; supported by full-len	---	AT1G32310	-1.07	-0.09	-0.71	0.501426	0.708294	-6.58
247122_at	putative protein non-consensus AT don	ATSAC1B	AT5G66020	1.08	0.11	0.71	0.501618	0.708521	-6.58
264908_at	unknown protein	---	AT2G17440	1.06	0.08	0.71	0.501701	0.708551	-6.58
260077_at	thaumatin-like protein contains Pfam pro	---	AT1G73620	-1.07	-0.10	-0.71	0.501685	0.708551	-6.58
252897_at	cytochrome P450 - like protein cytochro	CYP96A9	AT4G39480 /	-1.06	-0.08	-0.71	0.501804	0.708652	-6.58
265926_at	RUB1-conjugating enzyme, putative sim	---	AT2G18600	-1.09	-0.12	-0.71	0.501862	0.708691	-6.58
257081_at	RING zinc finger protein contains Pfam	---	AT3G30460	-1.05	-0.08	-0.71	0.502068	0.708762	-6.58
264707_at	unknown protein	---	AT1G09730	-1.05	-0.08	-0.71	0.501964	0.708762	-6.58
245533_at	putative phosphocholine cytidylyltransfe	CCT2	AT4G15130	-1.15	-0.21	-0.71	0.501977	0.708762	-6.58
254540_s_a	putative protein chitinase / lysozyme P2	---	AT4G19770 /	-1.05	-0.07	-0.71	0.502068	0.708762	-6.58
265783_at	putative Athila retroelement ORF1 prote	---	---	1.07	0.09	0.71	0.502025	0.708762	-6.58
266367_s_a	unknown protein	---	AT2G41390 /	1.05	0.07	0.71	0.502107	0.708773	-6.58
247856_at	receptor-like protein kinase	---	AT5G58300	-1.08	-0.11	-0.71	0.502226	0.708898	-6.58
257851_at	unknown protein	---	AT3G12940	-1.06	-0.08	-0.71	0.502313	0.708976	-6.58
254484_at	hypothetical protein	---	AT4G20760	-1.05	-0.08	-0.71	0.502446	0.709093	-6.58
262006_at	hypothetical protein predicted by gensca	---	AT1G64570	-1.06	-0.08	-0.71	0.502458	0.709093	-6.58
253910_at	putative receptor like kinase receptor-lik	---	AT4G27290	-1.05	-0.07	-0.71	0.50269	0.709376	-6.58
248744_at	putative protein contains similarity to CC	---	AT5G48250	-1.08	-0.11	-0.71	0.50283	0.709502	-6.58
245386_at	hypothetical protein ;supported by full-le	RALFL32	AT4G14010	1.14	0.19	0.71	0.502863	0.709502	-6.58
260643_at	hypothetical protein contains similarity to	---	AT1G53270	1.05	0.08	0.71	0.502873	0.709502	-6.58
255139_s_a	extensin-like protein hydroxyproline-rich	---	AT4G08400 /	1.05	0.07	0.71	0.502953	0.709571	-6.58

245650_at	F5A9.20 similar to S-adenosyl-L-methio	---	AT1G24735	-1.06	-0.09	-0.71	0.503089	0.709676	-6.58
263468_at	hypothetical protein predicted by gensca	---	AT2G31930	-1.07	-0.09	-0.71	0.503067	0.709676	-6.58
253148_at	cyclin 2b protein	CYCB2;2	AT4G35620	1.07	0.09	0.71	0.503231	0.709832	-6.58
255325_at	putative membrane trafficking factor ;su	PUX4	AT4G04210	-1.06	-0.08	-0.71	0.503341	0.709856	-6.58
255491_at	putative zinc finger protein similar to po	AtIDD12	AT4G02670	1.05	0.07	0.71	0.50332	0.709856	-6.58
262079_at	unknown protein ; supported by cDNA: g	ZCW7	AT1G59600	-1.09	-0.12	-0.71	0.503315	0.709856	-6.58
255198_at	contains similarity to an Arabidopsis tha	---	---	-1.05	-0.07	-0.71	0.503424	0.709929	-6.58
257054_at	Expressed protein ; supported by full-ler	MT3	AT3G15353	-1.04	-0.06	-0.71	0.503459	0.709935	-6.58
249601_at	quinone oxidoreductase -like protein pr	---	AT5G37980	-1.08	-0.11	-0.71	0.50383	0.710322	-6.58
256488_at	hypothetical protein	NFD4	AT1G31470	1.06	0.08	0.71	0.503858	0.710322	-6.58
267468_at	unknown protein ; supported by cDNA:	---	AT2G30530	1.07	0.09	0.71	0.503782	0.710322	-6.58
260296_at	putative disease resistance protein simil	---	AT1G63750	1.21	0.28	0.71	0.503829	0.710322	-6.58
261812_at	hypothetical protein contains similarity t	---	AT1G08270	1.05	0.07	0.71	0.503946	0.710394	-6.58
251434_at	polygalacturonase-like protein polygala	---	AT3G59850	1.06	0.08	0.71	0.504003	0.710394	-6.58
257136_at	hypothetical protein predicted by gensca	ASML2	AT3G12890	-1.06	-0.08	-0.71	0.503982	0.710394	-6.58
267009_at	unknown protein	---	AT2G39260	-1.05	-0.07	-0.71	0.504068	0.710442	-6.58
258770_at	hypothetical protein	---	AT3G10830	1.05	0.07	0.71	0.504118	0.710469	-6.58
264044_at	putative pyrophosphate--fructose-6-pho	PFK5	AT2G22480	1.06	0.08	0.71	0.504195	0.710490	-6.58
258926_s_a	unknown protein N-terminus similar to u	anac052	AT3G10480 /	1.08	0.11	0.71	0.504173	0.710490	-6.58
254016_at	putative transcription factor Arabidopsis	CGA1	AT4G26150	1.11	0.15	0.71	0.504311	0.710521	-6.58
260342_at	hypothetical protein predicted by genem	---	AT1G69280	-1.07	-0.09	-0.71	0.5043	0.710521	-6.58
251418_at	putative protein prib5, Ribes nigrum, EM	---	AT3G60440	1.10	0.14	0.71	0.504305	0.710521	-6.58
252431_at	putative protein	MAG2	AT3G47700	1.09	0.13	0.71	0.504438	0.710656	-6.58
257858_at	hypothetical protein predicted by genefir	---	AT3G12920	1.11	0.15	0.70	0.504611	0.710820	-6.58
254211_at	phosphatase like protein phosphoprotei	SGT1A	AT4G23570	-1.10	-0.13	-0.70	0.504617	0.710820	-6.58
248926_at	Ole e I (main olive allergen)-like protein	---	AT5G45880	-1.11	-0.15	-0.70	0.50472	0.710921	-6.58
266066_at	putative xyloglucan endo-transglycosyla	XTH21	AT2G18800	1.08	0.11	0.70	0.504924	0.711060	-6.58
266250_at	putative reverse transcriptase	---	---	1.06	0.08	0.70	0.504943	0.711060	-6.58
248188_at	putative protein contains similarity to he	HSFA9	AT5G54070	-1.05	-0.06	-0.70	0.504852	0.711060	-6.58
257231_at	DegP protease contains similarity to De	DEGP12	AT3G16550	1.05	0.07	0.70	0.504886	0.711060	-6.58
250442_at	putative protein hypothetical bacterial pr	MSL2	AT5G10490	1.06	0.08	0.70	0.505055	0.711174	-6.58
259545_at	hypothetical protein ; supported by cDN	AAE1	AT1G20560	-1.06	-0.08	-0.70	0.505142	0.711248	-6.58
244913_at	hypothetical protein	---	---	1.06	0.08	0.70	0.505214	0.711248	-6.58
258740_at	Lon protease, putative similar to Lon pr	LON3	AT3G05780	1.08	0.11	0.70	0.505232	0.711248	-6.58
246648_at	putative protein predicted proteins from	---	---	1.06	0.08	0.70	0.505214	0.711248	-6.58

260210_at	putative xyloglucan fucosyltransferase s	FUT3	AT1G74420	1.07	0.10	0.70	0.505424	0.711474	-6.58
245978_at	putative protein MORC microrchidia - H	---	AT5G13130	1.06	0.09	0.70	0.505553	0.711568	-6.58
266866_at	putative ABC transporter	PDR3	AT2G29940	-1.10	-0.14	-0.70	0.505538	0.711568	-6.58
252704_at	putative protein KIAA0161 gene, Homo	---	AT3G43750	-1.06	-0.08	-0.70	0.505601	0.711592	-6.58
258220_at	DnaJ, putative similar to DnaJ GB:BAA	---	AT3G17830	-1.08	-0.11	-0.70	0.505703	0.711691	-6.58
256904_at	unknown protein	---	AT3G23980	-1.05	-0.07	-0.70	0.5059	0.711837	-6.58
266999_at	putative HMG protein ; supported by full	---	AT2G34450	-1.08	-0.11	-0.70	0.505874	0.711837	-6.58
256292_at	unknown protein	---	AT1G69430	-1.07	-0.09	-0.70	0.505854	0.711837	-6.58
265801_at	fertilization-independent seed 2 protein	FIS2	AT2G35670	1.06	0.08	0.70	0.506059	0.711972	-6.58
253100_at	cytochrome P450 monooxygenase -like	CYP81F3	AT4G37400	-1.19	-0.26	-0.70	0.506042	0.711972	-6.58
256923_at	hypothetical protein	---	AT3G29635	-1.07	-0.10	-0.70	0.506126	0.712023	-6.58
260395_at	homeobox gene 13 protein identical to h	ATHB13	AT1G69780	1.14	0.18	0.70	0.50622	0.712111	-6.58
266404_at	hypothetical protein predicted by genefir	---	AT2G38590	-1.05	-0.07	-0.70	0.50633	0.712222	-6.58
252882_at	Expressed protein ; supported by full-ler	---	AT4G39675	1.04	0.06	0.70	0.506491	0.712317	-6.58
254570_s_a	puatative protein various predicted prot	---	AT4G19250 /	-1.06	-0.09	-0.70	0.506444	0.712317	-6.58
261943_at	plasma membrane ATPase, putative sir	AHA9	AT1G80660	1.06	0.08	0.70	0.506486	0.712317	-6.58
250490_at	pectin methylesterase - like protein pec	---	AT5G09760	1.13	0.18	0.70	0.506605	0.712395	-6.58
250892_at	putative protein beta-(1-3)-glucosyl tran	ATCSLA09	AT5G03760	1.46	0.55	0.70	0.506609	0.712395	-6.58
249281_at	GTPase activator protein of Rab-like sm	---	AT2G36460 /	1.06	0.08	0.70	0.506649	0.712406	-6.58
266411_at	putative peptidyl-prolyl cis-trans isomera	---	AT2G38730	-1.08	-0.10	-0.70	0.50675	0.712505	-6.58
266885_at	putative small GTP-binding protein cont	RAB6A	AT2G44610	-1.07	-0.09	-0.70	0.507107	0.712919	-6.58
264764_at	receptor kinase, putative similar to rece	---	AT1G61440	1.05	0.07	0.70	0.507095	0.712919	-6.58
258358_at	unknown protein similar to unknown pro	---	AT3G14380	1.06	0.08	0.70	0.507348	0.713214	-6.58
258903_at	hypothetical protein similar to zinc finge	---	AT3G06410	-1.09	-0.12	-0.70	0.507678	0.713634	-6.58
265018_s_a	hypothetical protein predicted by gensca	---	AT2G13770	1.05	0.08	0.70	0.507727	0.713658	-6.58
254459_at	gibberellin 20-oxidase - like protein gibl	GA2OX8	AT4G21200	-1.05	-0.07	-0.70	0.507853	0.713791	-6.59
266568_at	unknown protein	---	AT2G24070	1.05	0.07	0.70	0.507949	0.713839	-6.59
244903_at	hypothetical protein	---	---	-1.16	-0.21	-0.70	0.507921	0.713839	-6.59
256691_at	hypothetical protein predicted by genem	---	---	1.05	0.06	0.70	0.508132	0.713985	-6.59
254337_at	putative protein hypothetical protein dl4	---	AT4G22060	1.06	0.08	0.70	0.508147	0.713985	-6.59
263744_at	Mutator-like transposase similar to MUF	---	AT2G21420	1.06	0.08	0.70	0.50811	0.713985	-6.59
264402_at	HSP100/ClpB, putative similar to HSP1	CLPB4	AT2G25140	-1.12	-0.16	-0.70	0.508224	0.714049	-6.59
254713_at	hypothetical protein	---	AT4G18090	1.08	0.11	0.70	0.508457	0.714333	-6.59
247496_at	putative protein predicted proteins, Ara	GUT1	AT5G61840	-1.05	-0.07	-0.70	0.508633	0.714536	-6.59
262330_at	disease resistance protein, putative sim	RLM1	AT1G64070	1.06	0.09	0.70	0.509088	0.715102	-6.59

250169_at	putative protein many predicted protein	---	AT5G15340	-1.09	-0.13	-0.70	0.509098	0.715102	-6.59
264541_at	hypothetical protein predicted by genem	---	AT1G55660	1.07	0.10	0.70	0.509244	0.715218	-6.59
256316_at	hypothetical protein	---	AT1G35890	1.05	0.07	0.70	0.509232	0.715218	-6.59
260710_at	protein phosphatase 2C, putative simila	---	AT1G17545	1.05	0.07	0.70	0.509307	0.715263	-6.59
258971_at	unknown protein similar to uridylyl trans	ACR6	AT3G01990	1.15	0.20	0.70	0.50947	0.715403	-6.59
247750_at	protein kinase 6 - like protein kinase 6,	---	AT5G58950	1.06	0.08	0.70	0.50944	0.715403	-6.59
245059_at	unknown protein ;supported by full-leng	RHC2A	AT2G39720	1.05	0.07	0.70	0.509519	0.715427	-6.59
262285_at	hypothetical protein predicted by genem	---	AT1G68680	1.05	0.08	0.70	0.509551	0.715429	-6.59
250397_at	histon H3 protein HISTONE H3.2, MIN	---	AT5G10980	-1.04	-0.06	-0.70	0.509686	0.715575	-6.59
267549_at	hypothetical protein predicted by gensca	---	AT2G32640	-1.17	-0.22	-0.70	0.509719	0.715577	-6.59
248498_at	selenium-binding protein-like	---	AT5G50390	-1.06	-0.08	-0.70	0.509846	0.715672	-6.59
256202_s_a	hypothetical protein	---	AT1G48150 /	-1.05	-0.07	-0.70	0.509849	0.715672	-6.59
260061_at	cell division protein kinase similar to cell	CDKD1;1	AT1G73690	1.09	0.12	0.70	0.51005	0.715909	-6.59
265005_at	Expressed protein ; supported by full-ler	---	AT1G61667	-1.10	-0.14	-0.70	0.510147	0.715913	-6.59
263150_at	heat-shock protein, putative similar to h	---	AT1G54050	-1.12	-0.16	-0.70	0.510144	0.715913	-6.59
259504_at	inorganic pyrophosphatase, putative sir	AVP1	AT1G15690	1.07	0.10	0.70	0.51013	0.715913	-6.59
252597_at	putative protein several hypothetical pro	---	---	-1.07	-0.10	-0.70	0.510321	0.716113	-6.59
250431_at	cyclin protein - like cyclin D2.1 protein,	CYCD4;2	AT5G10440	1.05	0.08	0.69	0.510492	0.716233	-6.59
262934_s_a	hypothetical protein contains similarity to	---	AT1G16270 /	1.08	0.11	0.69	0.510523	0.716233	-6.59
249695_at	putative protein similar to unknown prote	---	---	-1.05	-0.07	-0.69	0.510595	0.716233	-6.59
249573_at	ubiquitin-like protein (UBQ9), putative s	UBQ9	AT5G37640	-1.05	-0.07	-0.69	0.510573	0.716233	-6.59
247236_at	putative protein similar to unknown prote	---	AT5G64590	-1.06	-0.08	-0.69	0.510587	0.716233	-6.59
245990_at	putative protein predicted proteins, Aral	---	AT5G20640	1.08	0.11	0.69	0.510473	0.716233	-6.59
252840_at	putative protein various predicted helica	---	---	1.05	0.07	0.69	0.510686	0.716312	-6.59
251625_at	beta-1,3-glucanase 2 (BG2) (PR-2) ;su	BGL2	AT3G57260	2.00	1.00	0.69	0.510714	0.716312	-6.59
258310_at	unknown protein	ICE1	AT3G26744	-1.06	-0.09	-0.69	0.510759	0.716331	-6.59
264110_at	unknown protein	---	---	-1.04	-0.06	-0.69	0.510804	0.716351	-6.59
255050_at	putative protein hypothetical protein F1	---	---	-1.07	-0.10	-0.69	0.510883	0.716417	-6.59
247636_at	putative protein predicted proteins from	---	AT5G60570	1.06	0.08	0.69	0.511002	0.716461	-6.59
247874_at	101 kDa heat shock protein; HSP101-lik	---	AT5G57710	1.09	0.12	0.69	0.511008	0.716461	-6.59
256581_at	hypothetical protein	---	AT3G28830	1.04	0.06	0.69	0.511005	0.716461	-6.59
255732_at	fatty acid condensing enzyme CUT1, p	KCS5	AT1G25450 /	1.16	0.22	0.69	0.511256	0.716579	-6.59
249971_at	dermal glycoprotein - like dermal glycop	---	AT5G19110	1.10	0.14	0.69	0.511249	0.716579	-6.59
253032_at	guanine nucleotide-exchange protein -li	---	AT4G38200	-1.05	-0.07	-0.69	0.511343	0.716579	-6.59
251586_at	zinc finger-like protein several zinc finge	GIS	AT3G58070	-1.08	-0.11	-0.69	0.511226	0.716579	-6.59

259018_at	unknown protein similar to unknown pro	AIR12	AT3G07390	1.20	0.26	0.69	0.511143	0.716579	-6.59
260035_at	peroxidase ATP23a identical to peroxida	---	AT1G68850	1.10	0.14	0.69	0.511213	0.716579	-6.59
264010_at	putative disease resistance response pr	---	AT2G21100	-1.09	-0.13	-0.69	0.511344	0.716579	-6.59
256670_at	Athila ORF 1, putative similar to Athila (	---	---	-1.05	-0.07	-0.69	0.511283	0.716579	-6.59
252764_at	nucleic acid binding protein-like nucleic	AL3	AT3G42790	-1.06	-0.08	-0.69	0.511393	0.716604	-6.59
264978_at	unknown protein contains Pfam profile:F	---	AT1G27120	1.11	0.16	0.69	0.511454	0.716646	-6.59
260985_at	dTDP-D-glucose 4,6-dehydratase, puta	MUM4	AT1G53500	1.06	0.09	0.69	0.51159	0.716709	-6.59
245800_at	heat shock transcription factor, putative	HSFB4	AT1G46264	1.05	0.08	0.69	0.511556	0.716709	-6.59
261484_at	E2, ubiquitin-conjugating enzyme 1 (UB	UBC1	AT1G14400	-1.05	-0.07	-0.69	0.511594	0.716709	-6.59
264792_at	hypothetical protein similar to hypothetic	---	AT1G08620	-1.05	-0.08	-0.69	0.511635	0.716723	-6.59
252875_at	GTP-binding protein GB3 ;supported by	RABA4B	AT4G39990	-1.05	-0.07	-0.69	0.511714	0.716745	-6.59
252371_at	putative protein finger protein SIG1, Sa	---	AT3G48070	-1.06	-0.09	-0.69	0.511702	0.716745	-6.59
245630_at	hypothetical protein similar to putative s	---	AT1G25360	-1.06	-0.08	-0.69	0.511901	0.716963	-6.59
249414_at	putative transcription factor MYB89 ; su	MYB89	AT5G39700	-1.06	-0.08	-0.69	0.511981	0.717031	-6.59
247569_at	Cf-5 disease resistance protein - like H	---	AT5G61240	1.08	0.12	0.69	0.512036	0.717033	-6.59
253930_at	embryo-specific protein 1 (ATS1)	ATS1	AT4G26740	1.06	0.08	0.69	0.512045	0.717033	-6.59
264780_at	putative protein kinase similar to MAP3k	EDR1	AT1G08720	-1.07	-0.10	-0.69	0.512238	0.717259	-6.59
246830_at	chaperonin gamma chain - like protein	---	AT5G26360	-1.11	-0.15	-0.69	0.512369	0.717382	-6.59
267079_at	hypothetical protein predicted by gensca	---	AT2G41200	-1.05	-0.07	-0.69	0.512389	0.717382	-6.59
252909_at	putative protein	---	AT4G39680	-1.05	-0.07	-0.69	0.5127	0.717774	-6.59
255923_at	hypothetical protein contains Pfam profil	---	AT1G22180	1.16	0.22	0.69	0.512804	0.717875	-6.59
264564_at	hypothetical protein predicted by gensca	---	AT1G05290	-1.04	-0.06	-0.69	0.512879	0.717937	-6.59
258244_at	unknown protein ; supported by cDNA:	---	AT3G27770	-1.05	-0.07	-0.69	0.512996	0.717968	-6.59
254266_at	protein kinase - like protein serine threo	CRK5	AT4G23130	1.19	0.25	0.69	0.512969	0.717968	-6.59
265159_at	unknown protein similar to EST gb|T432	---	AT1G31060	1.07	0.09	0.69	0.512986	0.717968	-6.59
264166_at	unknown protein ; supported by cDNA: g	---	AT1G65370	1.06	0.08	0.69	0.513034	0.717977	-6.59
267457_at	putative proline-rich protein	AGP30	AT2G33790	-1.06	-0.08	-0.69	0.51315	0.718096	-6.59
258910_at	putative RNA helicase similar to RNA h	---	AT3G06480	-1.05	-0.07	-0.69	0.513276	0.718228	-6.59
247893_at	RNA polymerase I, II and III 24.3 kDa s	RPB5C	AT5G57980	1.07	0.10	0.69	0.513391	0.718344	-6.59
257876_at	hypothetical protein predicted by genem	---	AT3G17130	1.11	0.15	0.69	0.513499	0.718437	-6.59
260759_at	hypothetical protein contains similarity t	---	AT1G49180	-1.10	-0.14	-0.69	0.513521	0.718437	-6.59
250477_at	putative protein CIS,CIS-MUCONATE	---	AT5G10190	-1.05	-0.07	-0.69	0.5136	0.718504	-6.59
249709_at	putative protein similar to unknown prote	iqd33	AT5G35670	-1.07	-0.10	-0.69	0.513664	0.718550	-6.59
265359_at	putative MYB family transcription factor	MYB7	AT2G16720	-1.16	-0.22	-0.69	0.513851	0.718723	-6.59
265407_at	F-box protein family, AtFBX8 contains F	---	AT2G16810	1.09	0.12	0.69	0.513841	0.718723	-6.59

262641_at	unknown protein ;supported by full-lengt	---	AT1G62730	-1.04	-0.06	-0.69	0.513942	0.718727	-6.59
258345_at	unknown protein	---	AT3G22845	1.05	0.07	0.69	0.513957	0.718727	-6.59
254441_at	prolamin box binding protein - like PBF	---	AT4G21050	1.05	0.07	0.69	0.51398	0.718727	-6.59
258117_at	hypothetical protein predicted by gensca	---	AT3G14700	1.05	0.07	0.69	0.513931	0.718727	-6.59
260149_at	putative oxidoreductase similar to adver	---	AT1G52810	-1.13	-0.18	-0.69	0.514046	0.718776	-6.59
265061_at	hypothetical protein contains similarity t	---	AT1G61640	-1.14	-0.19	-0.69	0.514201	0.718894	-6.59
247848_at	resistance protein - like disease resista	---	AT5G58120	-1.07	-0.10	-0.69	0.514225	0.718894	-6.59
251045_s_a	putative protein various predicted prote	---	AT2G13910 /	1.04	0.06	0.69	0.514189	0.718894	-6.59
260291_at	putative protein kinase similar to MAP3K	YDA	AT1G63700	1.04	0.06	0.69	0.514453	0.719032	-6.59
247250_at	FAS2 (dbj|BAA77766.1) ; supported by	FAS2	AT5G64630	1.09	0.13	0.69	0.514473	0.719032	-6.59
264198_at	unknown protein ESTs gb|Z34075, gb|Z	---	AT1G22800	-1.08	-0.11	-0.69	0.514369	0.719032	-6.59
261391_at	hypothetical protein similar to hypothetic	---	AT1G35030	1.06	0.09	0.69	0.514481	0.719032	-6.59
253708_at	gamma-glutamyltransferase-like protein	GGT4	AT4G29210	-1.13	-0.18	-0.69	0.514401	0.719032	-6.59
261432_at	hypothetical protein predicted by genem	---	AT1G07680	1.05	0.07	0.69	0.514597	0.719150	-6.59
248080_at	wax synthase-like protein	---	AT5G55380	1.07	0.10	0.69	0.514742	0.719175	-6.59
255653_at	Similar to receptor kinase	---	AT4G00960	-1.05	-0.07	-0.69	0.514672	0.719175	-6.59
247180_at	histone H3	---	AT5G65350 /	-1.05	-0.07	-0.69	0.514716	0.719175	-6.59
249444_at	putative protein S-locus-specific glycop	---	AT5G39370	-1.05	-0.07	-0.69	0.514709	0.719175	-6.59
251749_at	putative protein predicted proteins, Arat	---	AT3G55690	1.05	0.07	0.69	0.514944	0.719414	-6.59
262357_at	jacalin, putative similar to jacalin GI:289	---	AT1G73040	-1.19	-0.25	-0.69	0.515008	0.719424	-6.59
262115_at	Expressed protein ; supported by full-ler	---	AT1G02813	-1.06	-0.08	-0.69	0.515015	0.719424	-6.59
257622_at	hypothetical protein contains Pfam prof	---	AT3G20280	-1.08	-0.11	-0.69	0.515079	0.719470	-6.59
248267_at	NADH-dependent glutamate synthase	GLT1	AT5G53460	-1.09	-0.12	-0.69	0.515164	0.719545	-6.59
258936_s_a	hypothetical protein similar to hypotheti	---	---	1.05	0.07	0.69	0.515306	0.719700	-6.59
250212_at	putative protein contains similarity to SE	SUVH4	AT5G13960	1.06	0.08	0.69	0.515405	0.719793	-6.59
248342_at	unknown protein	MBD13	AT5G52230	-1.05	-0.07	-0.69	0.515666	0.720114	-6.59
248734_at	putative protein similar to unknown prote	ELP1	AT5G48090	-1.08	-0.11	-0.69	0.515719	0.720145	-6.59
250390_at	separation anxiety protein - like separat	---	AT5G11340	-1.04	-0.06	-0.69	0.515833	0.720215	-6.60
248389_at	AP2 domain transcription factor-like prot	CBF4	AT5G51990	-1.06	-0.08	-0.69	0.515813	0.720215	-6.60
261025_at	Expressed protein ; supported by full-ler	---	AT1G01225	1.11	0.15	0.69	0.515874	0.720228	-6.60
262268_at	hypothetical protein predicted by genem	---	---	-1.04	-0.06	-0.69	0.516029	0.720401	-6.60
250611_at	gibberellin 20-oxidase	GA20OX3	AT5G07200	-1.10	-0.13	-0.69	0.516074	0.720419	-6.60
246549_at	putative protein predicted proteins, Arat	---	AT5G15050	-1.11	-0.15	-0.69	0.516202	0.720509	-6.60
249369_at	putative protein Kelch motif containing	---	AT5G40680	1.05	0.08	0.69	0.516171	0.720509	-6.60
266802_at	Expressed protein ; supported by cDNA	---	AT2G22900	-1.27	-0.34	-0.68	0.51643	0.720749	-6.60

266493_at	Mutator-like transposase similar to MUF	---	---	1.05	0.07	0.68	0.516541	0.720749	-6.60
249142_at	putative protein similar to unknown prote	---	AT5G43230	1.06	0.09	0.68	0.516506	0.720749	-6.60
255126_at	putative protein hypothetical protein ssr	---	AT4G08270	1.05	0.07	0.68	0.516546	0.720749	-6.60
248662_at	unknown protein	---	AT5G48690	1.06	0.08	0.68	0.516554	0.720749	-6.60
257479_at	hypothetical protein contains similarity to	WAKL4	AT1G16150	1.09	0.13	0.68	0.516563	0.720749	-6.60
250777_at	putative protein similar to unknown prote	---	AT5G05440	1.25	0.33	0.68	0.516722	0.720880	-6.60
265872_at	unknown protein ;supported by full-leng	atnudt17	AT2G01670	1.08	0.12	0.68	0.516707	0.720880	-6.60
250899_at	putative protein ; supported by cDNA: g	---	AT5G03340	1.08	0.11	0.68	0.516815	0.720880	-6.60
256574_at	hypothetical protein similar to callose sy	---	AT3G14780	1.10	0.14	0.68	0.516799	0.720880	-6.60
263153_s_a	myrosinase-associated protein, putative	---	AT1G54000 /	1.14	0.18	0.68	0.516779	0.720880	-6.60
258891_at	unknown protein	EMB2016	AT3G05680	-1.05	-0.07	-0.68	0.516878	0.720923	-6.60
264262_at	Expressed protein ; supported by full-ler	---	AT1G09200	-1.27	-0.35	-0.68	0.516909	0.720923	-6.60
254106_at	geranylgeranylated protein ATGP4 ; su	ATGP4	AT4G24990	1.07	0.09	0.68	0.517059	0.721047	-6.60
266765_at	putative inorganic pyrophosphatase	AtPPa3	AT2G46860	-1.05	-0.07	-0.68	0.517061	0.721047	-6.60
264650_at	putative transcription factor Similar to Sc	NF-YC9	AT1G08970	-1.06	-0.08	-0.68	0.517098	0.721054	-6.60
254302_at	hypothetical protein	---	AT4G22800	-1.04	-0.06	-0.68	0.517391	0.721418	-6.60
244963_at	PSII cytochrome b559	---	---	-1.04	-0.06	-0.68	0.517451	0.721458	-6.60
252579_at	putative protein hypothetical protein At2	---	AT3G45510	-1.05	-0.07	-0.68	0.517516	0.721505	-6.60
249627_at	NADH dehydrogenase (ubiquinone) (E(	EMB1467	AT5G37510	1.07	0.10	0.68	0.51756	0.721522	-6.60
262195_at	allergen, putative similar to allergen (Ol	---	AT1G78040	1.13	0.18	0.68	0.51766	0.721550	-6.60
247064_at	putative protein contains similarity to dis	---	AT5G66890	1.10	0.14	0.68	0.517636	0.721550	-6.60
253914_at	putative protein late embryogenesis abu	---	AT4G27400	1.08	0.12	0.68	0.517675	0.721550	-6.60
250273_at	pre-mRNA splicing factor ATP-depende	EMB3011	AT5G13010	-1.05	-0.07	-0.68	0.517842	0.721739	-6.60
255442_at	predicted NADH dehydrogenase 24 kD	---	AT4G02580	1.05	0.07	0.68	0.517955	0.721852	-6.60
255164_at	hypothetical protein	---	---	1.05	0.07	0.68	0.518067	0.721964	-6.60
252408_at	putative transcription factor MYB94 ; su	ATMYB94	AT3G47600	1.05	0.07	0.68	0.518153	0.722040	-6.60
245608_at	protein kinase	---	AT4G14350	1.08	0.11	0.68	0.518342	0.722074	-6.60
247784_at	subtilisin-like serine protease contains s	---	AT5G58810	-1.05	-0.07	-0.68	0.518384	0.722074	-6.60
247503_at	GCN4-complementing protein - like GC	AGD1	AT5G61980	1.06	0.09	0.68	0.518399	0.722074	-6.60
251462_at	mitogen-activated protein kinase-like pr	ATMPK10	AT3G59790	1.07	0.10	0.68	0.518272	0.722074	-6.60
265655_at	unknown protein contains weak PHD zir	---	AT2G13920	-1.06	-0.08	-0.68	0.518294	0.722074	-6.60
266734_at	hypothetical protein predicted by genefir	---	AT2G46900	1.07	0.09	0.68	0.518364	0.722074	-6.60
264387_at	putative growth regulator protein contair	---	AT1G11990	-1.06	-0.08	-0.68	0.518377	0.722074	-6.60
259993_at	unknown protein	---	AT1G67960	1.06	0.09	0.68	0.518439	0.722086	-6.60
251967_at	putative protein DMR-N9 PROTEIN, Mu	---	AT3G53390	1.05	0.07	0.68	0.518571	0.722124	-6.60

257515_at	zinc finger protein, putative similar to zi	DOT5	AT1G13290	1.05	0.07	0.68	0.518733	0.722124	-6.60
249822_at	unknown protein	---	AT5G23710	-1.06	-0.08	-0.68	0.518703	0.722124	-6.60
259745_at	unknown protein	SAG18	AT1G71190	1.06	0.08	0.68	0.51869	0.722124	-6.60
258469_at	unknown protein contains Pfam profile:	PRXIIF	AT3G06050	1.05	0.07	0.68	0.518573	0.722124	-6.60
252201_at	putative protein anthranilate N-hydroxy	---	AT3G50295	1.05	0.07	0.68	0.518733	0.722124	-6.60
248280_at	putative protein similar to unknown prote	---	AT5G52950	1.06	0.08	0.68	0.518719	0.722124	-6.60
254569_s_a	hypothetical protein	---	---	1.05	0.07	0.68	0.518633	0.722124	-6.60
265208_at	putative giberellin beta-hydroxylase con	---	AT2G36690	1.16	0.22	0.68	0.518752	0.722124	-6.60
261658_at	hypothetical protein predicted by genem	---	AT1G50040	1.17	0.22	0.68	0.519032	0.722288	-6.60
259950_at	hypothetical protein predicted by genefi	---	AT1G71410	1.06	0.09	0.68	0.518925	0.722288	-6.60
253861_at	putative protein MSP1 protein, Sacchar	---	AT4G27680	1.05	0.08	0.68	0.519145	0.722288	-6.60
261039_at	Expressed protein ; supported by full-ler	ELF4-L4	AT1G17455	-1.09	-0.12	-0.68	0.519002	0.722288	-6.60
260675_at	unknown protein ; supported by cDNA: g	---	AT1G19430	-1.07	-0.10	-0.68	0.519012	0.722288	-6.60
248055_at	serine/threonine-specific kinase like prot	---	AT5G55830	1.06	0.08	0.68	0.518963	0.722288	-6.60
257762_at	hypothetical protein	XRCC4	AT3G23100	-1.05	-0.08	-0.68	0.519154	0.722288	-6.60
251253_at	putative zinc-finger protein zinc-finger p	---	AT3G62240	1.09	0.13	0.68	0.519098	0.722288	-6.60
259187_at	putative transcription factor similar to my	AtMYB57	AT3G01530	-1.07	-0.10	-0.68	0.519086	0.722288	-6.60
257029_at	dem-like protein similar to dem GB:CA	---	AT3G19240	-1.06	-0.08	-0.68	0.519294	0.722439	-6.60
254973_at	putative retrotransposon Oryza australi	---	---	1.06	0.09	0.68	0.519337	0.722454	-6.60
261404_at	alpha galactosyltransferase, putative si	---	AT1G18690	-1.10	-0.14	-0.68	0.5194	0.722498	-6.60
263531_s_a	hypothetical protein predicted by gensca	---	AT2G25020 /	1.05	0.07	0.68	0.519468	0.722548	-6.60
260451_at	putative AP2 domain transcription factor	---	AT1G72360	-1.22	-0.28	-0.68	0.519629	0.722684	-6.60
256370_at	MATE efflux family protein, putative cor	---	AT1G66780	1.05	0.08	0.68	0.519606	0.722684	-6.60
249678_at	protein kinase-like	---	AT5G35980	1.04	0.06	0.68	0.519698	0.722702	-6.60
262025_at	growth regulator, putative similar to axi	---	AT1G35510	-1.06	-0.09	-0.68	0.519737	0.722702	-6.60
257169_at	Expressed protein ; supported by full-ler	AtSec20	AT3G24315	-1.06	-0.09	-0.68	0.519726	0.722702	-6.60
260982_at	chalcone isomerase, putative similar to	---	AT1G53520	1.19	0.25	0.68	0.520037	0.722895	-6.60
262407_at	hypothetical protein predicted by genem	---	AT1G34630	1.10	0.14	0.68	0.519995	0.722895	-6.60
264779_at	putative thioredoxin similar to ESTs gb	ACHT4	AT1G08570	1.13	0.18	0.68	0.520043	0.722895	-6.60
254217_at	putative protein other hypothetical prote	---	AT4G23720	1.05	0.06	0.68	0.520009	0.722895	-6.60
258958_at	vacuolar membrane ATPase subunit G	VMA10	AT3G01390	1.08	0.11	0.68	0.520117	0.722895	-6.60
249564_at	unknown protein	---	AT5G38400	-1.06	-0.09	-0.68	0.520152	0.722895	-6.60
253226_at	beta-galactosidase - like protein beta-D	BGAL11	AT4G35010	-1.05	-0.07	-0.68	0.519981	0.722895	-6.60
260817_at	unknown protein	---	AT1G06900	-1.06	-0.08	-0.68	0.520161	0.722895	-6.60
256714_at	cysteine proteinase contains similarity to	---	AT2G34080	1.06	0.09	0.68	0.520102	0.722895	-6.60

264588_at	unknown protein contains similarity to C	---	AT2G17730	1.12	0.17	0.68	0.520207	0.722915	-6.60
267572_at	3-hydroxyisobutyryl-coenzyme A hydrola	---	AT2G30660	1.06	0.08	0.68	0.520265	0.722951	-6.60
251692_s_a	serine carboxypeptidase-like protein ca	---	AT3G52020 /	-1.05	-0.07	-0.68	0.52037	0.723052	-6.60
250413_at	adenine phosphoribosyltransferase - lik	APT5	AT5G11160	1.08	0.12	0.68	0.520611	0.723322	-6.60
248796_at	VAMP (vesicle-associated membrane pr	---	AT5G47180	-1.09	-0.13	-0.68	0.520627	0.723322	-6.60
262894_at	disease resistance protein, putative sim	---	AT1G59780	-1.06	-0.09	-0.68	0.520777	0.723487	-6.60
265032_at	ribosomal protein identical to ribosomal	RPL3B	AT1G61580	-1.13	-0.17	-0.68	0.520821	0.723504	-6.60
256972_at	unknown protein	---	AT3G21140	-1.06	-0.08	-0.68	0.52105	0.723734	-6.60
251006_at	putative protein predicted proteins, Arat	---	AT5G02600	-1.06	-0.09	-0.68	0.52102	0.723734	-6.60
255083_s_a	hypothetical protein	---	---	1.07	0.09	0.68	0.521108	0.723771	-6.60
254196_at	putative protein	---	AT4G24030	1.07	0.10	0.68	0.521495	0.724263	-6.60
249051_at	berberine bridge enzyme-like protein ; s	---	AT5G44390	-1.07	-0.10	-0.68	0.521758	0.724571	-6.60
260318_at	hypothetical protein predicted by genefir	---	AT1G63960	1.07	0.09	0.68	0.521873	0.724571	-6.60
245653_at	heat shock transcription factor like prote	FBD1	AT4G13985	1.06	0.08	0.68	0.521875	0.724571	-6.60
249848_at	putative protein similar to unknown prote	NIC3	AT5G23220	-1.06	-0.08	-0.68	0.521869	0.724571	-6.60
245526_at	putative protein	NRPD4	AT4G15950	1.05	0.06	0.68	0.521805	0.724571	-6.60
251113_at	hypothetical protein	---	AT5G01370	1.07	0.09	0.68	0.522008	0.724711	-6.60
245938_at	putative protein protein phosphatase-1	---	AT5G19680	-1.08	-0.11	-0.68	0.522072	0.724711	-6.60
253082_at	putative glycine-rich cell wall protein gly	---	AT4G36230	-1.10	-0.14	-0.68	0.522071	0.724711	-6.60
252779_at	putative protein	---	AT3G42990	1.05	0.07	0.67	0.522222	0.724832	-6.60
248384_at	mandelonitrile lyase-like protein	---	AT5G51930	1.05	0.07	0.67	0.522199	0.724832	-6.60
259887_at	putative protein kinase similar to protein	---	AT1G76360	-1.06	-0.08	-0.67	0.522384	0.724996	-6.60
252212_at	protein kinase -like protein NTPK1 prote	MAPKKK2	AT3G50310	1.14	0.19	0.67	0.522468	0.724996	-6.60
264354_s_a	unknown protein similar to Lambda-PRL	---	AT1G03200 /	-1.06	-0.08	-0.67	0.522457	0.724996	-6.60
259567_at	hypothetical protein	---	AT1G20500	-1.06	-0.09	-0.67	0.522459	0.724996	-6.60
258189_at	unknown protein ;supported by full-leng	JAZ3	AT3G17860	-1.11	-0.15	-0.67	0.522509	0.725010	-6.60
245370_at	Expressed protein ; supported by full-ler	---	AT4G16840	1.11	0.15	0.67	0.522562	0.725039	-6.60
265886_at	putative protein phosphatase 2C ; supp	---	AT2G25610 /	-1.12	-0.16	-0.67	0.522602	0.725051	-6.60
261500_at	hypothetical protein predicted by genem	---	AT1G28400	1.15	0.20	0.67	0.522924	0.725454	-6.60
259988_at	Athila ORF 1, putative simlar to GI:8065	---	---	-1.04	-0.06	-0.67	0.523021	0.725499	-6.60
250797_at	unknown protein	---	AT5G05310	1.06	0.09	0.67	0.523013	0.725499	-6.60
266531_at	putative plasma membrane intrinsic pro	---	AT2G16835	1.04	0.06	0.67	0.5231	0.725521	-6.60
264595_at	putative vesicle-associated membrane	VAMP721	AT1G04750	-1.08	-0.11	-0.67	0.523095	0.725521	-6.60
251646_at	putative protein	---	AT3G57780	1.21	0.28	0.67	0.52335	0.725824	-6.60
263508_s_a	hypothetical protein	---	---	-1.07	-0.10	-0.67	0.523576	0.726057	-6.60

265568_s_a	hypothetical protein predicted by gensca	---	---	-1.07	-0.10	-0.67	0.523582	0.726057	-6.60
249455_s_a	putative protein predicted proteins, Aral	---	AT1G50870 /	1.05	0.07	0.67	0.523628	0.726077	-6.60
251480_at	putative protein inducible carbonyl redu	---	AT3G59710	1.07	0.10	0.67	0.523894	0.726357	-6.60
254918_at	putative protein phosphatase like protei	SGT1B	AT4G11260	1.06	0.08	0.67	0.523871	0.726357	-6.60
257883_at	calmodulin-binding protein, putative cor	---	AT3G16940	-1.07	-0.10	-0.67	0.523965	0.726411	-6.60
255120_x_a	putative transposon protein similar to ma	---	---	1.05	0.07	0.67	0.524034	0.726462	-6.60
256596_at	hypothetical protein predicted by genem	---	AT3G28540	-1.11	-0.15	-0.67	0.524269	0.726567	-6.61
263269_at	En/Spm-like transposon protein related	---	---	-1.05	-0.07	-0.67	0.524255	0.726567	-6.61
257836_at	hypothetical protein	---	---	-1.05	-0.07	-0.67	0.524184	0.726567	-6.61
251618_at	putative protein unknown protein At2g4	---	AT3G58020	-1.09	-0.12	-0.67	0.524212	0.726567	-6.61
266681_at	copia-like retroelement pol polyprotein	---	---	1.04	0.06	0.67	0.524265	0.726567	-6.61
254674_at	EREBP - like protein EREBP-1 (Ethyler	---	AT4G18450	-1.04	-0.06	-0.67	0.524654	0.727013	-6.61
265201_at	unknown protein	---	AT2G36810	-1.04	-0.06	-0.67	0.524652	0.727013	-6.61
245021_at	PSII component	---	---	-1.07	-0.10	-0.67	0.524713	0.727050	-6.61
263219_at	putative serine proteinase Strong simila	---	AT1G30600	1.08	0.11	0.67	0.524859	0.727164	-6.61
249213_at	unknown protein	---	AT5G42700	-1.05	-0.07	-0.67	0.524838	0.727164	-6.61
250617_at	Mei2-like protein Mei2-like protein - Ara	AML4	AT5G07290	1.06	0.09	0.67	0.524989	0.727300	-6.61
254081_at	putative protein various predicted prote	---	AT4G25660	1.07	0.09	0.67	0.525158	0.727402	-6.61
264876_at	hypothetical protein	---	AT2G17410	-1.06	-0.08	-0.67	0.525153	0.727402	-6.61
259011_s_a	unknown protein similar to putative prote	---	AT3G07380 /	1.06	0.08	0.67	0.525137	0.727402	-6.61
262752_at	putative mitotic cyclin similar to gb|D896	CYCB3;1	AT1G16330	1.07	0.09	0.67	0.525206	0.727425	-6.61
245085_at	putative poly(A) binding protein ; suppo	PAB4	AT2G23350	1.07	0.10	0.67	0.525298	0.727507	-6.61
248018_at	putative protein strong similarity to unkn	---	AT5G56470	1.06	0.09	0.67	0.525356	0.727543	-6.61
265086_at	hypothetical protein contains Zinc finge	RING1B	AT1G03770	1.08	0.11	0.67	0.525516	0.727677	-6.61
250534_at	NADH dehydrogenase ;supported by fu	CI51	AT5G08530	-1.05	-0.07	-0.67	0.525496	0.727677	-6.61
267459_at	unknown protein ;supported by full-leng	---	AT2G33850	-1.05	-0.07	-0.67	0.525604	0.727754	-6.61
261963_at	hypothetical protein predicted by genem	---	---	-1.06	-0.09	-0.67	0.525688	0.727783	-6.61
260870_at	GTP-binding protein(RAB1Y), putative	ATRAB18	AT1G43890	1.06	0.09	0.67	0.525673	0.727783	-6.61
246419_at	UDP glucose:flavonoid 3-o-glucosyltran	UGT78D3	AT5G17030	-1.05	-0.07	-0.67	0.525832	0.727805	-6.61
256738_at	geranylgeranyl pyrophosphate synthase	---	AT3G29430	-1.06	-0.08	-0.67	0.525803	0.727805	-6.61
257842_at	P-glycoprotein, putative similar to P-gly	PGP18	AT3G28390	1.05	0.07	0.67	0.525815	0.727805	-6.61
265320_at	unknown protein predicted by genscan	---	AT2G18320	-1.05	-0.08	-0.67	0.525822	0.727805	-6.61
260610_at	putative SF16 protein {Helianthus annu	IQD14	AT2G43680	-1.09	-0.13	-0.67	0.525954	0.727930	-6.61
250558_at	flavonoid 3-hydroxylase - like protein fla	TT7	AT5G07990	-1.06	-0.09	-0.67	0.526296	0.728359	-6.61
245934_at	putative protein NAC1 - Medicago trunc	anac082	AT5G09330	1.07	0.10	0.67	0.526371	0.728397	-6.61

249251_at	putative protein similar to unknown prote	---	AT5G42000	1.07	0.10	0.67	0.52644	0.728397	-6.61
263201_at	putative ADP-glucose pyrophosphoryla	APS2	AT1G05610	1.06	0.08	0.67	0.526451	0.728397	-6.61
258841_at	hypothetical protein similar to hypothetic	---	AT3G04660	-1.05	-0.07	-0.67	0.526425	0.728397	-6.61
264813_at	putative Ca2+-dependent ser/thr protein	CPK16	AT2G17890	1.07	0.10	0.67	0.526552	0.728448	-6.61
253299_at	hypothetical protein ;supported by full-le	---	AT4G33800	-1.06	-0.09	-0.67	0.526527	0.728448	-6.61
263589_at	hypothetical protein predicted by gensca	---	AT2G25280	-1.05	-0.06	-0.67	0.526669	0.728545	-6.61
250924_at	putative protein ;supported by full-lengt	---	AT5G03440	-1.06	-0.08	-0.67	0.526686	0.728545	-6.61
263920_at	unknown protein ;supported by full-leng	---	AT2G36410	1.07	0.10	0.67	0.526967	0.728889	-6.61
255039_at	calmodulin-domain protein kinase CDPK	CPK4	AT4G09570	1.06	0.09	0.67	0.527114	0.729049	-6.61
253613_at	PR-1-like protein gene PR-1 protein - M	---	AT4G30320	-1.06	-0.09	-0.67	0.52719	0.729109	-6.61
266311_at	hypothetical protein predicted by gensca	---	AT2G27130	-1.18	-0.24	-0.67	0.5273	0.729181	-6.61
248610_at	SRP54 (signal recognition particle 54 KI	---	AT5G49500	-1.05	-0.07	-0.67	0.527306	0.729181	-6.61
252142_at	putative protein hypothetical protein F1	---	AT3G51120	-1.07	-0.09	-0.67	0.527373	0.729230	-6.61
256228_at	phosphoglycerate kinase, putative simil	---	AT1G56190	-1.07	-0.10	-0.67	0.527544	0.729414	-6.61
259638_at	coatomer complex subunit, putative sim	---	AT1G52360	1.06	0.09	0.67	0.52757	0.729414	-6.61
266873_at	putative PREG1-like negative regulator	CYCP4;1	AT2G44740	-1.21	-0.27	-0.67	0.527777	0.729523	-6.61
258972_at	hypothetical protein predicted by gensca	---	AT3G01920	-1.09	-0.12	-0.67	0.527774	0.729523	-6.61
266788_at	putative receptor-like protein kinase	---	AT2G29000	-1.04	-0.06	-0.67	0.527721	0.729523	-6.61
264814_at	putative SET-domain transcriptional reg	SDG37	AT2G17900	-1.08	-0.11	-0.67	0.527688	0.729523	-6.61
249380_at	glutaredoxin -like protein glutaredoxin,	---	AT5G40370	1.05	0.07	0.67	0.528079	0.729896	-6.61
252238_at	peroxidase ATP21a	---	AT3G49960	1.06	0.08	0.67	0.528142	0.729940	-6.61
254444_at	putative protein riboflavin biosynthesis	---	AT4G20960	-1.10	-0.14	-0.66	0.528286	0.730094	-6.61
249039_at	late embryogenesis abundant protein-lik	---	AT5G44310	1.06	0.08	0.66	0.528353	0.730143	-6.61
267229_s_a	putative translation initiation factor eIF-2	---	AT2G44070 /	1.11	0.16	0.66	0.528407	0.730174	-6.61
254962_at	putative glucanase endo-beta-1,4-D-glu	AtGH9C3	AT4G11050	-1.06	-0.08	-0.66	0.528441	0.730175	-6.61
246029_at	leucine-rich repeat protein ; supported b	---	AT5G21090	1.05	0.07	0.66	0.528499	0.730211	-6.61
259403_at	unknown protein ; supported by full-leng	PGDH	AT1G17745	1.24	0.31	0.66	0.52855	0.730238	-6.61
257930_at	hypothetical protein	---	AT3G17010	-1.07	-0.10	-0.66	0.528587	0.730244	-6.61
255392_at	hypothetical protein	---	---	1.04	0.06	0.66	0.528651	0.730289	-6.61
262787_at	putative clathrin-coat assembly protein s	---	AT1G10730	1.09	0.12	0.66	0.528829	0.730446	-6.61
262363_at	disease resistance protein, putative sim	---	AT1G72850	-1.05	-0.07	-0.66	0.528822	0.730446	-6.61
258897_at	unknown protein	---	AT3G05730	-1.44	-0.52	-0.66	0.529203	0.730741	-6.61
255832_at	hypothetical protein predicted by genefi	---	AT2G33360	1.08	0.10	0.66	0.529192	0.730741	-6.61
262605_at	hypothetical protein Strong similarity to	---	AT1G15170	1.19	0.25	0.66	0.529148	0.730741	-6.61
259622_at	hypothetical protein predicted by gensca	---	AT1G43010	-1.05	-0.07	-0.66	0.52918	0.730741	-6.61

247179_at	putative protein contains similarity to bH	---	AT5G65320	-1.05	-0.07	-0.66	0.529147	0.730741	-6.61
246953_at	unknown protein ;supported by full-leng	VPS60.2	AT5G04850	-1.05	-0.07	-0.66	0.529245	0.730755	-6.61
248495_at	putative protein strong similarity to unkn	---	AT5G50780	-1.06	-0.09	-0.66	0.52928	0.730760	-6.61
257878_at	hypothetical protein predicted by genem	---	AT3G17150	1.05	0.08	0.66	0.529406	0.730845	-6.61
264608_at	putative acetyl-CoA acyltransferase Stro	PKT4	AT1G04710	-1.05	-0.08	-0.66	0.529374	0.730845	-6.61
254578_at	putative pectinacetylesterase protein pe	---	AT4G19400 /	-1.09	-0.12	-0.66	0.529474	0.730894	-6.61
259537_at	hypothetical protein ; supported by cDN/	PHR1	AT1G12370	-1.07	-0.09	-0.66	0.52965	0.731093	-6.61
257444_at	hypothetical protein predicted by gensca	---	AT2G12550	-1.07	-0.09	-0.66	0.529717	0.731135	-6.61
256791_at	hypothetical protein predicted by gensca	---	---	-1.07	-0.10	-0.66	0.529745	0.731135	-6.61
248846_at	putative protein similar to unknown prote	---	AT5G46500	1.05	0.07	0.66	0.529795	0.731161	-6.61
247078_at	unknown protein ; supported by cDNA:	---	AT5G66000	-1.06	-0.08	-0.66	0.529829	0.731163	-6.61
267319_at	ABC transporter (AtMRP2) identical to C	ATMRP2	AT2G34660	1.08	0.11	0.66	0.529967	0.731310	-6.61
255608_at	hypothetical protein	---	AT4G01140	-1.07	-0.10	-0.66	0.53002	0.731339	-6.61
263767_at	putative retroelement pol polyprotein	---	---	1.04	0.06	0.66	0.530075	0.731370	-6.61
260723_at	unknown protein	---	AT1G48070	1.05	0.07	0.66	0.530126	0.731391	-6.61
256203_at	hypothetical protein	---	AT1G50800	-1.06	-0.08	-0.66	0.530155	0.731391	-6.61
250541_at	putative proline-rich protein surface pro	---	AT5G09520	1.10	0.14	0.66	0.530334	0.731595	-6.61
254087_at	brefeldin A-sensitive Golgi protein - like	---	AT4G24840	1.04	0.06	0.66	0.530508	0.731721	-6.61
261731_s_a	hypothetical protein similar to hypothetic	---	AT1G47780 /	1.04	0.06	0.66	0.530506	0.731721	-6.61
258343_at	unknown protein similar to hypothetical	---	AT3G22810	-1.06	-0.08	-0.66	0.530521	0.731721	-6.61
265638_at	similar to PIG-L	---	AT2G27340	-1.05	-0.07	-0.66	0.530624	0.731818	-6.61
246211_at	G-box-binding factor 1 ; supported by cD	GBF1	AT4G36730	1.11	0.15	0.66	0.530722	0.731909	-6.61
262508_at	serine/threonine kinase, putative simila	---	AT1G11300	1.13	0.18	0.66	0.53085	0.732042	-6.61
254572_at	putative protein predicted protein MTCY	---	AT4G19380	-1.05	-0.07	-0.66	0.530929	0.732062	-6.61
253327_at	putative transcription factor	MYB69	AT4G33450	1.07	0.10	0.66	0.530908	0.732062	-6.61
256886_at	hypothetical protein contains Pfam profil	---	AT3G15130	-1.04	-0.06	-0.66	0.531015	0.732135	-6.61
267294_at	hypothetical protein predicted by gensca	YCF37	AT2G23670	-1.08	-0.11	-0.66	0.53105	0.732139	-6.61
251263_at	putative protein DNAJ PROTEIN - Syne	---	AT3G62190	-1.05	-0.08	-0.66	0.531122	0.732194	-6.61
248157_at	putative protein similar to unknown prote	---	AT5G54420	1.05	0.07	0.66	0.531183	0.732235	-6.61
256333_at	Sm-like protein contains Pfam profile: PI	---	AT1G76860	-1.09	-0.12	-0.66	0.531585	0.732744	-6.61
261366_at	unknown protein	---	AT1G53100	1.15	0.20	0.66	0.531889	0.732844	-6.61
257060_at	unknown protein	---	AT3G18230	-1.06	-0.08	-0.66	0.531793	0.732844	-6.61
254819_at	pEARLI 1-like protein Arabidopsis thalia	---	AT4G12500	1.42	0.51	0.66	0.531978	0.732844	-6.61
267094_at	putative diphenol oxidase ; supported b	IRX12	AT2G38080	1.20	0.26	0.66	0.531755	0.732844	-6.61
256108_at	hypothetical protein predicted by genem	---	AT1G16940	1.08	0.11	0.66	0.531717	0.732844	-6.61

259128_at	unknown protein similar to pushover GB	BIG	AT3G02260	-1.08	-0.12	-0.66	0.531943	0.732844	-6.61
259383_at	putative lectin contains Pfam profile: PF	JR1	AT3G16470	-1.28	-0.35	-0.66	0.531968	0.732844	-6.61
247066_at	DNA binding protein-like	---	AT5G66940	1.04	0.06	0.66	0.531966	0.732844	-6.61
250488_at	beta-glucosidase - like protein beta-glu	---	AT5G09700	1.05	0.07	0.66	0.531731	0.732844	-6.61
248667_at	putative protein contains similarity to sm	---	AT5G48710	1.04	0.06	0.66	0.531833	0.732844	-6.61
264291_at	hypothetical protein contains similarity to	---	AT1G78800	1.06	0.08	0.66	0.53205	0.732898	-6.61
265537_at	putative retroelement pol polyprotein co	---	---	1.06	0.09	0.66	0.532126	0.732914	-6.61
257503_at	DAG-like protein similar to DAG protein	---	AT1G72530	1.07	0.10	0.66	0.532125	0.732914	-6.61
263251_at	unknown protein ; supported by cDNA:	---	AT2G31410	-1.11	-0.15	-0.66	0.53222	0.732917	-6.61
251013_at	putative protein various predicted prote	---	AT5G02540	-1.36	-0.44	-0.66	0.532265	0.732917	-6.61
267270_at	hypothetical protein predicted by gensca	---	AT2G02550	1.07	0.10	0.66	0.53225	0.732917	-6.61
256390_at	putative MAP kinase similar to MAP kina	ATMKK8	AT3G06230	1.05	0.07	0.66	0.532289	0.732917	-6.61
246393_at	phosphoglycerate kinase, putative simil	---	AT1G58150	-1.06	-0.08	-0.66	0.532231	0.732917	-6.61
265807_at	unknown protein	---	AT2G17990	1.06	0.08	0.66	0.532359	0.732969	-6.61
260195_at	hypothetical protein predicted by gensca	---	AT1G67540	1.05	0.08	0.66	0.532537	0.733126	-6.61
245846_at	P-type transporting ATPase, putative si	---	AT1G26130	-1.07	-0.10	-0.66	0.532522	0.733126	-6.61
262888_at	RNA-directed RNA polymerase, putativ	RDR1	AT1G14790	-1.14	-0.18	-0.66	0.532621	0.733167	-6.62
257221_at	MYB family transcription factor (GL1) id	ATMYB0	AT3G27920	1.07	0.10	0.66	0.532631	0.733167	-6.62
251121_at	putative protein ; supported by cDNA: g	AGG1	AT3G63420	1.08	0.11	0.66	0.532688	0.733202	-6.62
259554_at	hypothetical protein	---	---	-1.07	-0.10	-0.66	0.532802	0.733255	-6.62
267144_at	unknown protein	GPAT6	AT2G38110	1.13	0.18	0.66	0.532916	0.733255	-6.62
263206_at	unknown protein similar to ESTs gb|T4	---	AT1G10590	1.04	0.06	0.66	0.53286	0.733255	-6.62
251347_at	putative protein ferritin 1 precursor - Ara	---	AT3G61010	1.09	0.13	0.66	0.532913	0.733255	-6.62
248089_at	salt stress inducible small GTP binding p	AtRAN4	AT5G55080	1.06	0.08	0.66	0.53292	0.733255	-6.62
245445_at	apetala2 domain TINY like protein	---	AT4G16750	-1.14	-0.19	-0.66	0.532763	0.733255	-6.62
262010_at	hypothetical protein predicted by genem	---	---	1.06	0.08	0.66	0.533035	0.733369	-6.62
260258_at	putative ribosomal protein similar to ribo	---	AT1G74270	-1.08	-0.10	-0.66	0.533262	0.733417	-6.62
257735_at	pectate lyase, putative similar to pectat	---	AT3G27400	1.10	0.13	0.66	0.533226	0.733417	-6.62
263603_at	hypothetical protein	---	AT2G16340	1.07	0.09	0.66	0.533348	0.733417	-6.62
265146_at	putative glucosyl transferase	---	AT1G51210	1.11	0.14	0.66	0.53327	0.733417	-6.62
249557_at	receptor serine/threonine kinase PR5K	PR5K	AT5G38280	1.10	0.14	0.66	0.533298	0.733417	-6.62
260842_at	19S proteosome subunit 9, putative sim	ATS9	AT1G29150	-1.06	-0.08	-0.66	0.533153	0.733417	-6.62
245916_at	putative protein	---	AT5G28720	1.06	0.08	0.66	0.53334	0.733417	-6.62
257034_at	hypothetical protein predicted by gensca	---	AT3G19184	-1.05	-0.06	-0.66	0.533359	0.733417	-6.62
258784_at	unknown protein	---	AT3G11770	-1.09	-0.13	-0.66	0.533105	0.733417	-6.62

263956_at	putative homeodomain transcription fact	BLH1	AT2G35940	1.10	0.14	0.66	0.533431	0.733458	-6.62
246975_at	putative protein hypothetical proteins - A	---	AT5G24890	-1.07	-0.10	-0.66	0.533454	0.733458	-6.62
251991_at	transcription factor NF-Y, CCAAT-bindi	NF-YB10	AT3G53340	-1.07	-0.10	-0.66	0.53352	0.733506	-6.62
266217_at	unknown protein	AT2G2883	---	1.05	0.07	0.66	0.533566	0.733525	-6.62
250822_at	unknown protein	---	AT5G05230	-1.05	-0.07	-0.66	0.533781	0.733776	-6.62
244967_at	PSI J protein	---	---	1.11	0.16	0.66	0.534126	0.734206	-6.62
248969_at	unknown protein ; supported by cDNA:	---	AT5G45310	-1.12	-0.17	-0.65	0.534242	0.734272	-6.62
253615_at	cyclic nucleotide and calmodulin-regula	CNGC17	AT4G30360	-1.08	-0.11	-0.65	0.534244	0.734272	-6.62
261543_at	unknown protein contains Pfam profile:	---	AT1G63550	1.07	0.09	0.65	0.534271	0.734272	-6.62
257398_at	hypothetical protein predicted by genefi	---	AT2G01990	-1.04	-0.06	-0.65	0.534375	0.734371	-6.62
265827_at	hypothetical protein predicted by genefi	VOZ2	AT2G42400	1.04	0.06	0.65	0.534452	0.734433	-6.62
258194_at	unknown protein ; supported by full-leng	---	AT3G29170	1.07	0.10	0.65	0.534667	0.734684	-6.62
264986_at	glutathione transferase, putative similar	ATGSTU1	AT1G27130	-1.23	-0.30	-0.65	0.534782	0.734798	-6.62
257286_s_a	transposase, putative similar to transpo	---	AT1G19260 /	1.06	0.08	0.65	0.535036	0.735102	-6.62
251028_at	putative protein putative hydrolase At2g	---	AT5G02230	1.06	0.09	0.65	0.535084	0.735124	-6.62
252160_at	proline-rich protein	---	AT3G50570	1.07	0.10	0.65	0.535179	0.735211	-6.62
246550_at	putative protein predicted protein, Arabi	---	AT5G14920	1.23	0.30	0.65	0.535253	0.735268	-6.62
261155_at	unknown protein ;supported by full-lengt	---	AT1G04960	1.06	0.09	0.65	0.535535	0.735567	-6.62
248513_at	unknown protein	---	AT5G50500	-1.04	-0.06	-0.65	0.535525	0.735567	-6.62
260733_at	RNA-binding protein, putative similar to	---	AT1G17640	1.07	0.09	0.65	0.535721	0.735650	-6.62
267111_s_a	hypothetical protein predicted by gensca	---	---	1.07	0.09	0.65	0.535699	0.735650	-6.62
267420_at	hypothetical protein predicted by grail	---	AT2G35030	-1.11	-0.15	-0.65	0.535725	0.735650	-6.62
245777_at	unknown protein contains similarity to di	atnudt21	AT1G73540	1.26	0.34	0.65	0.535659	0.735650	-6.62
266474_at	hypothetical protein predicted by grail	---	AT2G31110	-1.17	-0.23	-0.65	0.535795	0.735661	-6.62
252768_at	putative protein hypothetical proteins - A	---	---	-1.05	-0.06	-0.65	0.535797	0.735661	-6.62
255845_at	putative cinnamoyl-CoA reductase highl	---	AT2G33600	-1.09	-0.12	-0.65	0.535848	0.735686	-6.62
261684_at	hypothetical protein predicted by genem	---	AT1G47400	-1.20	-0.26	-0.65	0.535894	0.735705	-6.62
263186_at	lectin receptor kinase, putative similar t	---	---	1.08	0.10	0.65	0.535983	0.735739	-6.62
244991_s_a	NADH dehydrogenase ND2	---	---	-1.05	-0.07	-0.65	0.535975	0.735739	-6.62
266959_at	putative DNA replication licensing facto	MCM5	AT2G07690	-1.18	-0.24	-0.65	0.536152	0.735926	-6.62
252709_at	putative protein predicted proteins, Arat	---	AT3G43840	1.04	0.06	0.65	0.536373	0.736186	-6.62
246751_at	pectin methyl-esterase - like protein pe	---	AT5G27870	-1.04	-0.06	-0.65	0.536595	0.736446	-6.62
257339_s_a	ATP synthase subunit 9	---	AT2G07671	1.09	0.12	0.65	0.536781	0.736532	-6.62
258874_at	hypothetical protein similar to unknown	---	AT3G03230	1.07	0.09	0.65	0.536787	0.736532	-6.62
254912_at	respiratory burst oxidase homolog F - li	---	AT4G11230	1.05	0.07	0.65	0.536716	0.736532	-6.62

266350_at	putative protein transport protein SEC1	STL2P	AT2G01470	-1.08	-0.10	-0.65	0.536754	0.736532	-6.62
256211_at	gibberellin 20-oxidase, putative similar	GA2OX7	AT1G50960	-1.04	-0.06	-0.65	0.536882	0.736574	-6.62
246665_s_a	putative protein predicted proteins - Aral	---	---	1.06	0.08	0.65	0.536871	0.736574	-6.62
261862_at	DNA-binding protein, putative similar to	---	AT1G50410	-1.07	-0.10	-0.65	0.537028	0.736686	-6.62
252403_at	hypothetical protein	---	AT3G48080	1.04	0.06	0.65	0.537016	0.736686	-6.62
247016_at	putative protein contains similarity to sig	---	AT5G66970	1.06	0.08	0.65	0.537163	0.736819	-6.62
250501_at	carboxypeptidase - like protein GC don	SCPL19	AT5G09640	-1.05	-0.07	-0.65	0.537222	0.736819	-6.62
248601_at	putative protein contains similarity to unl	---	AT5G49400	1.04	0.06	0.65	0.537213	0.736819	-6.62
261726_at	putative auxin-independent growth prom	---	AT1G76270	-1.09	-0.13	-0.65	0.537283	0.736858	-6.62
266850_at	unknown protein	---	AT2G26850	1.05	0.06	0.65	0.537356	0.736914	-6.62
259461_at	unknown protein	---	AT1G18900	1.09	0.12	0.65	0.537389	0.736915	-6.62
252657_at	hypothetical protein	---	AT3G44780	1.04	0.06	0.65	0.537479	0.736949	-6.62
257371_at	putative CCAAT-box binding trancription	NF-YB5	AT2G47810	1.06	0.09	0.65	0.537447	0.736949	-6.62
254166_at	HSP90-like protein HSP90 homolog - C	SHD	AT4G24190	1.17	0.23	0.65	0.537531	0.736977	-6.62
251809_at	putative protein predicted proteins, Aral	---	AT3G55600	-1.06	-0.08	-0.65	0.537614	0.737047	-6.62
252778_at	putative protein replication protein A 51	---	---	-1.05	-0.07	-0.65	0.537668	0.737070	-6.62
259189_at	unknown protein	AGP11	AT3G01700	-1.07	-0.09	-0.65	0.537696	0.737070	-6.62
248685_at	putative protein similar to unknown prote	---	AT5G48500	-1.08	-0.12	-0.65	0.537817	0.737192	-6.62
253120_at	putative protein phospholipase D, Arabi	PLDDELTA	AT4G35790	-1.07	-0.10	-0.65	0.5379	0.737199	-6.62
249656_at	putative protein hypothetical proteins - d	---	AT5G37130	-1.04	-0.06	-0.65	0.537878	0.737199	-6.62
260050_at	hypothetical protein predicted by genem	AGL64	AT1G29960 /	1.06	0.08	0.65	0.537919	0.737199	-6.62
252772_at	hypothetical protein	---	---	1.05	0.07	0.65	0.537979	0.737237	-6.62
264747_at	unknown protein	---	AT1G70150	-1.07	-0.10	-0.65	0.538201	0.737497	-6.62
249684_s_a	cytochrome P450-like	---	AT5G36110 /	-1.05	-0.07	-0.65	0.538311	0.737590	-6.62
265249_at	putative C2H2-type zinc finger protein li	SGR5	AT2G01940	-1.14	-0.19	-0.65	0.538334	0.737590	-6.62
256884_at	hypothetical protein contains Pfam profil	---	AT3G15200	-1.09	-0.12	-0.65	0.538532	0.737816	-6.62
250955_at	putative protein various predicted prote	CPUORF4	AT5G03190	-1.22	-0.29	-0.65	0.538642	0.737924	-6.62
264293_at	cell division cycle protein, putative simil	APC6	AT1G78770	-1.05	-0.06	-0.65	0.538809	0.738066	-6.62
257867_at	unknown protein	---	AT3G17780	1.06	0.09	0.65	0.53881	0.738066	-6.62
262992_at	hypothetical protein predicted by genem	ATG12A	AT1G54210	-1.07	-0.10	-0.65	0.538953	0.738084	-6.62
256835_at	ATP sulfurylase, putative similar to ATP	APS1	AT3G22890	-1.11	-0.15	-0.65	0.5389	0.738084	-6.62
266639_at	defender against cell death protein iden	DAD2	AT2G35520	-1.05	-0.07	-0.65	0.538908	0.738084	-6.62
257277_at	disease resistance protein, putative sim	---	AT3G14470	1.06	0.09	0.65	0.53895	0.738084	-6.62
252667_at	protein kinase-like protein MSTK2S kina	NEK6	AT3G44200	1.07	0.10	0.65	0.539099	0.738195	-6.62
260122_at	AIG1-like protein similar to AIG1 protein	---	AT1G33900	-1.06	-0.09	-0.65	0.539098	0.738195	-6.62

248376_at	unknown protein ; supported by full-leng	---	AT5G51880	1.05	0.07	0.65	0.539246	0.738219	-6.62
251698_at	putative protein	---	AT3G56610	1.04	0.06	0.65	0.539232	0.738219	-6.62
265421_s_a	predicted protein	---	AT2G20616 /	-1.05	-0.08	-0.65	0.539202	0.738219	-6.62
259731_at	unknown protein similar to unknown pro	---	AT1G77460	1.12	0.17	0.65	0.539217	0.738219	-6.62
266115_at	protease inhibitor II ;supported by full-le	LCR72	AT2G02140	1.09	0.13	0.65	0.539281	0.738222	-6.62
260372_at	unknown protein contains a region simil	---	AT1G73980	1.05	0.07	0.65	0.539532	0.738336	-6.62
248476_at	putative protein similar to unknown prote	---	AT5G50890	-1.12	-0.16	-0.65	0.539456	0.738336	-6.62
253671_at	serine threonine-specific receptor protei	---	AT4G29990	-1.07	-0.10	-0.65	0.539416	0.738336	-6.62
255090_at	putative protein disease resistance prot	---	AT4G09360	-1.05	-0.08	-0.65	0.539505	0.738336	-6.62
252703_at	leucine-rich repeat protein LRP -like leu	---	AT3G43740	-1.05	-0.07	-0.65	0.539472	0.738336	-6.62
262054_s_a	putative heat-shock protein contains Pf	---	AT1G79920 /	1.07	0.10	0.65	0.539558	0.738336	-6.62
265204_at	hypothetical protein predicted by gensca	---	AT2G36650	1.04	0.06	0.65	0.539663	0.738435	-6.62
245791_at	defender against cell death protein, put	ATDAD1	AT1G32210	1.06	0.08	0.65	0.539771	0.738539	-6.62
261421_at	hypothetical protein similar to unknown	IQD30	AT1G18840	1.13	0.18	0.65	0.53994	0.738641	-6.62
245478_at	galactokinase like protein	ARA1	AT4G16130	1.13	0.17	0.65	0.539952	0.738641	-6.62
261623_at	hypothetical protein similar to reticuline	ATSEC1A	AT1G01980	1.05	0.08	0.65	0.539902	0.738641	-6.62
262012_s_a	integral membrane protein, putative sim	---	AT1G35625 /	-1.05	-0.07	-0.65	0.539976	0.738641	-6.62
263190_at	mutator-like transposase, putative simil	---	---	1.04	0.06	0.65	0.540018	0.738655	-6.62
263968_s_a	PttA-like transposon protein no ATG ide	---	---	1.06	0.08	0.65	0.540197	0.738856	-6.62
249037_at	putative protein contains similarity to su	FLA13	AT5G44130	1.19	0.26	0.65	0.540247	0.738879	-6.62
249959_at	NADH:ubiquinone oxidoreductase - like	---	AT5G18800	1.07	0.09	0.64	0.54043	0.739009	-6.62
256971_at	unknown protein contains Pfam profile:F	---	AT3G21100	1.07	0.10	0.64	0.540471	0.739009	-6.62
266651_at	putative casein kinase I	---	AT2G25760	-1.06	-0.08	-0.64	0.54043	0.739009	-6.62
264629_at	hypothetical protein similar to hypothetic	---	AT1G65540	1.06	0.09	0.64	0.540447	0.739009	-6.62
259220_at	expressed protein predicted by genefin	---	AT3G03550	-1.06	-0.09	-0.64	0.54051	0.739018	-6.62
260060_at	feebly-like protein similar to feebly prote	---	AT1G73680	1.07	0.09	0.64	0.540712	0.739114	-6.62
257123_at	hypothetical protein	---	AT3G20030	1.04	0.06	0.64	0.540805	0.739114	-6.62
249871_at	putative protein similar to unknown prote	---	AT5G23110	1.08	0.11	0.64	0.540807	0.739114	-6.62
245223_at	gene_id:K17E7.5~unknown protein	---	AT3G29791	-1.05	-0.07	-0.64	0.54072	0.739114	-6.62
260742_at	putative glycerol kinase identical to SP:	IAA34	AT1G15050	1.05	0.06	0.64	0.54066	0.739114	-6.62
245448_at	disease resistance RPP5 like protein	RPP4	AT4G16860	-1.06	-0.08	-0.64	0.5408	0.739114	-6.62
263285_at	unknown protein	DOT1	AT2G36120	-1.10	-0.14	-0.64	0.540663	0.739114	-6.62
244906_at	hypothetical protein	---	ATMG00690	-1.05	-0.07	-0.64	0.540886	0.739135	-6.62
265542_at	putative SNF2 subfamily transcription re	SYD	AT2G28290	1.04	0.06	0.64	0.540887	0.739135	-6.62
251481_at	receptor lectin kinase-like protein (fragr	---	AT3G59730	1.04	0.06	0.64	0.540978	0.739215	-6.62

253442_at	H+-transporting ATPase - like protein H	---	AT4G32530	1.05	0.07	0.64	0.541018	0.739225	-6.62
260864_at	hypothetical protein predicted by gensca	---	---	-1.06	-0.08	-0.64	0.541133	0.739338	-6.62
250982_at	putative protein zinc finger protein, Arat	JKD	AT5G03150	1.09	0.13	0.64	0.541197	0.739381	-6.62
252585_s_a	putative protein UbcH 7-binding protein	---	AT3G45570 /	1.04	0.06	0.64	0.541575	0.739809	-6.63
257936_at	hypothetical protein contains similarity to	---	---	-1.06	-0.09	-0.64	0.541554	0.739809	-6.63
251380_at	putative protein	---	AT3G60700	1.05	0.07	0.64	0.541815	0.740074	-6.63
260561_at	putative endochitinase	---	AT2G43580	1.07	0.09	0.64	0.541834	0.740074	-6.63
260744_at	hypothetical protein predicted by genem	---	AT1G15010	1.26	0.33	0.64	0.54189	0.740106	-6.63
265408_at	Mutator-like transposase similar to MUF	---	---	1.04	0.06	0.64	0.541954	0.740149	-6.63
266035_at	enoyl-ACP reductase (enr-A)	MOD1	AT2G05990	1.11	0.15	0.64	0.542039	0.740221	-6.63
248463_at	putative protein contains similarity to unl	---	AT5G51130	-1.13	-0.17	-0.64	0.542488	0.740627	-6.63
249645_at	thionin Thi2.2 ;supported by full-length c	THI2.2	AT5G36910	1.07	0.10	0.64	0.542398	0.740627	-6.63
263777_at	putative cyclic nucleotide-regulated ion c	ATCNGC1	AT2G46450	-1.23	-0.29	-0.64	0.542499	0.740627	-6.63
262788_at	unknown protein ESTs gb|T75618 and g	---	AT1G10690	1.07	0.10	0.64	0.542448	0.740627	-6.63
256798_at	uracil-DNA glycosylase, putative similar	---	AT3G18630	1.07	0.10	0.64	0.542465	0.740627	-6.63
251017_at	protein phosphatase - like protein prote	---	AT5G02760	-1.36	-0.44	-0.64	0.542631	0.740737	-6.63
256770_at	hypothetical protein predicted by genen	---	AT3G13700 /	1.07	0.10	0.64	0.542742	0.740737	-6.63
260940_at	26S proteasome regulatory particle tripl	---	AT1G45000	-1.06	-0.09	-0.64	0.542701	0.740737	-6.63
258321_at	early light-induced protein identical to ea	ELIP1	AT3G22840	1.06	0.08	0.64	0.542644	0.740737	-6.63
263068_at	putative poly(A) polymerase	---	AT2G17580	-1.06	-0.09	-0.64	0.542722	0.740737	-6.63
260737_at	receptor-like serine threonine kinase, p	---	AT1G17540	-1.06	-0.09	-0.64	0.542774	0.740737	-6.63
250667_at	40S ribosomal protein S4 ;supported by	---	AT5G07090	-1.11	-0.15	-0.64	0.542956	0.740940	-6.63
264556_at	putative transcription factor contains My	MYB61	AT1G09540	-1.04	-0.06	-0.64	0.54312	0.741107	-6.63
252817_at	putative protein hypothetical proteins - A	---	---	1.06	0.09	0.64	0.543175	0.741107	-6.63
248218_at	unknown protein ;supported by full-lengt	---	AT5G53710	-1.07	-0.10	-0.64	0.543159	0.741107	-6.63
250055_at	NADH-cytochrome b5 reductase ;suppo	ATCBR	AT5G17770	1.13	0.18	0.64	0.543349	0.741182	-6.63
261621_at	hypothetical protein similar to guanine n	EDA10	AT1G01960	-1.05	-0.07	-0.64	0.54336	0.741182	-6.63
260534_at	hypothetical protein predicted by grail	---	---	-1.05	-0.07	-0.64	0.543347	0.741182	-6.63
258634_at	putative RNA-binding protein contains R	---	AT3G08000	-1.10	-0.14	-0.64	0.543327	0.741182	-6.63
265502_at	putative poly(A) binding protein	---	AT2G15500	-1.06	-0.09	-0.64	0.543489	0.741225	-6.63
263107_at	putative cytochrome P450	CYP705A6	AT2G05180	-1.05	-0.06	-0.64	0.543438	0.741225	-6.63
245936_at	putative protein predicted proteins - diffe	---	AT5G19850	1.07	0.10	0.64	0.54346	0.741225	-6.63
254914_at	peroxidase ATP19a	---	AT4G11290	-1.26	-0.34	-0.64	0.54358	0.741257	-6.63
257287_at	hypothetical protein predicted by genem	---	---	-1.04	-0.06	-0.64	0.5436	0.741257	-6.63
258108_at	unknown protein contains Pfam profile:	---	AT3G23570	-1.16	-0.21	-0.64	0.54361	0.741257	-6.63

261986_s_a	cytochrome P450, putative similar to CY	CYP76C5	AT1G33720 /	1.15	0.20	0.64	0.543673	0.741298	-6.63
262119_s_a	glutathione S-transferase, putative simi	ATGSTF6	AT1G02920 /	1.19	0.25	0.64	0.54384	0.741349	-6.63
263138_at	hypothetical protein predicted by genem	---	AT1G65090	1.04	0.06	0.64	0.543813	0.741349	-6.63
260396_at	putative heme oxygenase similar to hem	ho3	AT1G69720	1.09	0.13	0.64	0.543792	0.741349	-6.63
265561_s_a	putative glycine-rich protein	---	AT1G47480 /	-1.07	-0.10	-0.64	0.543781	0.741349	-6.63
255542_at	hypothetical protein	---	AT4G01860	-1.06	-0.09	-0.64	0.544168	0.741708	-6.63
255756_at	endo-beta-1,4-D-glucanase, putative si	AtGH9B5	AT1G19940	1.06	0.08	0.64	0.544152	0.741708	-6.63
264422_at	unknown protein similar to unknown pro	LCV2	AT1G43130	-1.05	-0.08	-0.64	0.544306	0.741851	-6.63
256167_at	hypothetical protein similar to putative re	---	---	1.05	0.07	0.64	0.544501	0.742028	-6.63
261993_at	unknown protein	---	AT1G33860	1.05	0.07	0.64	0.544484	0.742028	-6.63
245539_at	ABC transporter homolog	PDR2	AT4G15230	-1.07	-0.09	-0.64	0.54455	0.742050	-6.63
247562_at	putative protein	---	AT5G61120	-1.04	-0.06	-0.64	0.544661	0.742158	-6.63
265445_at	60S ribosomal protein L12 ;supported b	---	AT2G37190	-1.15	-0.20	-0.64	0.544756	0.742243	-6.63
251091_at	pyridoxine biosynthesis protein - like pyr	RSR4	AT5G01410	-1.13	-0.17	-0.64	0.544829	0.742297	-6.63
263890_at	putative auxin-induced protein	---	AT2G37030	-1.07	-0.10	-0.64	0.544864	0.742301	-6.63
258107_at	unknown protein ; supported by cDNA:	ALF5	AT3G23560	1.05	0.07	0.64	0.544909	0.742318	-6.63
261580_at	unknown protein ;supported by full-lengt	IQD18	AT1G01110	1.08	0.11	0.64	0.545022	0.742427	-6.63
245399_at	membrane channel like protein ;support	TIP2;2	AT4G17340	-1.10	-0.14	-0.64	0.545211	0.742510	-6.63
248760_at	unknown protein ;supported by full-leng	---	AT5G47570	-1.07	-0.10	-0.64	0.545188	0.742510	-6.63
264413_s_a	hypothetical protein similar to hypothetic	---	---	1.07	0.09	0.64	0.545212	0.742510	-6.63
249878_at	TATA-binding protein-associated phosp	NF-YB13	AT5G23090	-1.07	-0.09	-0.64	0.545133	0.742510	-6.63
250607_at	putative protein mammalian inositol hex	IPK2a	AT5G07370	-1.04	-0.06	-0.64	0.54533	0.742625	-6.63
264152_at	Mago Nashi-like protein similar to Mago	MAGO	AT1G02140	-1.05	-0.08	-0.64	0.545591	0.742777	-6.63
259615_at	dessication-related protein, putative sim	---	AT1G47980	1.06	0.09	0.64	0.545576	0.742777	-6.63
263043_at	conserved hypothetical protein predicted	---	AT1G23350	-1.06	-0.09	-0.64	0.54548	0.742777	-6.63
253661_at	putative protein bZIP protein - Arabidop	---	AT4G30130	-1.05	-0.08	-0.64	0.545556	0.742777	-6.63
253018_at	putative protein Zn finger protein BBF2a	---	AT4G38000	-1.05	-0.07	-0.64	0.545604	0.742777	-6.63
251903_at	putative protein 24 kDa seed maturation	---	AT3G54120	1.13	0.18	0.64	0.545717	0.742887	-6.63
256588_at	unknown protein	---	AT3G28790	1.06	0.08	0.64	0.545762	0.742903	-6.63
250635_at	glycine-rich protein glycine-rich protein	GRP14	AT5G07510	-1.06	-0.08	-0.64	0.545825	0.742945	-6.63
248776_at	unknown protein	---	AT5G47900	-1.05	-0.07	-0.64	0.545931	0.743000	-6.63
246853_at	putative protein	---	AT5G26890	-1.05	-0.07	-0.64	0.545899	0.743000	-6.63
253290_at	putative protein predicted protein F10M	---	AT4G34330	1.05	0.07	0.64	0.546	0.743034	-6.63
267281_at	putative protein kinase contains a protei	---	AT2G19400	-1.07	-0.09	-0.64	0.546021	0.743034	-6.63
251718_at	putative protein hypothetical proteins - A	MRLK	AT3G56100	1.07	0.09	0.64	0.546084	0.743075	-6.63

246358_x_a	hypothetical protein	---	AT2G06570	-1.05	-0.08	-0.64	0.546161	0.743137	-6.63
257611_at	unknown protein	---	AT3G26580	1.07	0.10	0.64	0.546232	0.743189	-6.63
252462_at	putative protein various predicted gene	---	AT3G47250	-1.05	-0.07	-0.64	0.546296	0.743231	-6.63
262665_at	xyloglucan fucosyltransferase, putative	FUT7	AT1G14070	-1.15	-0.20	-0.63	0.546436	0.743244	-6.63
249255_at	Na+/H+ antiporter-like protein	CHX18	AT5G41610	-1.06	-0.09	-0.63	0.54643	0.743244	-6.63
264714_at	receptor-like protein kinase, putative sir	---	AT1G69990	1.06	0.08	0.64	0.546391	0.743244	-6.63
266013_s_a	hypothetical protein	---	AT2G07702	1.05	0.07	0.64	0.54634	0.743244	-6.63
262205_at	hypothetical protein predicted by genefir	---	AT2G01080	-1.05	-0.08	-0.63	0.546469	0.743245	-6.63
257047_at	hypothetical protein predicted by genem	---	AT3G19570	1.08	0.10	0.63	0.546681	0.743343	-6.63
262223_at	hypothetical protein predicted by genem	---	AT1G74680	-1.09	-0.12	-0.63	0.546633	0.743343	-6.63
258844_at	hypothetical protein predicted by gensca	SWP	AT3G04740	-1.05	-0.06	-0.63	0.546704	0.743343	-6.63
250556_at	diacylglycerol kinase (ATDGK1) ; suppo	DGK1	AT5G07920	-1.11	-0.16	-0.63	0.546701	0.743343	-6.63
248550_at	putative protein similar to unknown prote	QS	AT5G50210	1.09	0.12	0.63	0.546698	0.743343	-6.63
254216_at	V-ATPase subunit G (vag2 gene)	VAG2	AT4G23710	1.10	0.14	0.63	0.546744	0.743353	-6.63
257885_at	S1 self-incompatibility protein, putative	---	AT3G16970	1.05	0.07	0.63	0.546842	0.743386	-6.63
263602_at	40S ribosomal protein S25	---	AT2G16360	-1.05	-0.07	-0.63	0.546866	0.743386	-6.63
250793_at	leucoanthocyanidin dioxygenase-like pr	---	AT5G05600	-1.14	-0.19	-0.63	0.546812	0.743386	-6.63
249207_at	C2H2-type zinc finger protein-like	---	AT5G42640	1.05	0.07	0.63	0.546912	0.743404	-6.63
254476_at	putative protein gamma-SNAP protein,	GSNAP	AT4G20410	-1.05	-0.07	-0.63	0.547158	0.743625	-6.63
258504_at	putative sterol-C5-desaturase identical t	---	AT3G02590	1.04	0.06	0.63	0.547186	0.743625	-6.63
259373_at	hypothetical protein predicted by genem	---	AT1G69160	-1.14	-0.18	-0.63	0.547205	0.743625	-6.63
258367_at	putative protein kinase similar to protein	WAG2	AT3G14370	1.05	0.08	0.63	0.547144	0.743625	-6.63
248296_at	protochlorophyllide reductase; oxidoredu	---	AT5G53090	-1.07	-0.09	-0.63	0.547286	0.743691	-6.63
265915_at	En/Spm-like transposon protein related	---	---	-1.04	-0.06	-0.63	0.547322	0.743696	-6.63
265252_at	putative Na+/H+ antiporter	SOS1	AT2G01980	-1.04	-0.06	-0.63	0.5476	0.743896	-6.63
247968_at	40S ribosomal protein S30 homolog (em	---	AT5G56670	-1.12	-0.16	-0.63	0.547599	0.743896	-6.63
252190_at	putative protein various predicted gene	---	AT3G50170	-1.05	-0.07	-0.63	0.547525	0.743896	-6.63
264342_at	unknown protein ; supported by full-leng	---	AT1G12080	-1.25	-0.33	-0.63	0.547564	0.743896	-6.63
246765_at	glutamic acid-rich protein hypothetical p	---	AT5G27330	-1.06	-0.08	-0.63	0.547774	0.744000	-6.63
253658_at	cadmium-transporting ATPase-like prot	HMA3	AT4G30120	-1.05	-0.07	-0.63	0.547756	0.744000	-6.63
264488_s_a	unknown protein similar to EST gb|AA65	---	AT1G27330 /	1.09	0.12	0.63	0.547736	0.744000	-6.63
259552_at	hypothetical protein	---	AT1G21320	1.06	0.08	0.63	0.547842	0.744048	-6.63
250639_at	oleosin-like protein oleosin - Brassica n	GRP20	AT5G07560	1.06	0.08	0.63	0.547923	0.744090	-6.63
265180_at	putative OBP32pep protein ;supported	---	AT1G23590	1.04	0.05	0.63	0.547939	0.744090	-6.63
262833_at	cyclin, putative contains Pfam profile: P	SDS	AT1G14750	-1.04	-0.06	-0.63	0.548087	0.744247	-6.63

257200_at	hypothetical protein predicted by genem	---	---	-1.04	-0.06	-0.63	0.548252	0.744427	-6.63
256623_at	myosin identical to myosin GB:CAB618	ATM1	AT3G19960	-1.06	-0.08	-0.63	0.548317	0.744471	-6.63
259810_at	Na+/H+ antiporter, putative similar to pr	ATNHD2	AT1G49810	1.04	0.06	0.63	0.548362	0.744487	-6.63
253244_at	putative protein SEC14 protein, Saccha	COW1	AT4G34580	1.07	0.10	0.63	0.54842	0.744522	-6.63
247473_at	putative protein AT-hook protein 2, Ara	---	AT5G62260	1.07	0.10	0.63	0.548583	0.744654	-6.63
249605_at	putative protein predicted protein, Arabi	---	AT5G37240	-1.06	-0.08	-0.63	0.548577	0.744654	-6.63
245696_at	phytochrome kinase substrate 1 - like pr	PKS4	AT5G04190	-1.16	-0.22	-0.63	0.548695	0.744762	-6.63
250261_at	peptide transporter - like protein peptide	---	AT5G13400	1.11	0.16	0.63	0.548777	0.744830	-6.63
248999_at	putative protein contains similarity to he	---	AT5G44970	1.05	0.06	0.63	0.548842	0.744873	-6.63
251381_at	secretory protein - like 33 kDa secretory	PDLP8	AT3G60720 /	-1.10	-0.14	-0.63	0.548955	0.744982	-6.63
263021_at	hypothetical protein predicted by genem	---	AT1G23910	1.04	0.06	0.63	0.549014	0.745018	-6.63
253623_at	GDP-mannose pyrophosphorylase like	---	AT4G30570	-1.05	-0.07	-0.63	0.549208	0.745237	-6.63
252545_at	putative protein	---	AT3G45820	1.06	0.08	0.63	0.549458	0.745532	-6.63
252666_at	putative protein hypothetical proteins - A	---	AT3G44180	1.06	0.08	0.63	0.549664	0.745767	-6.63
266830_at	1-aminocyclopropane-1-carboxylate syn	ACS4	AT2G22810	1.22	0.28	0.63	0.549704	0.745777	-6.63
255180_at	putative polyprotein	---	---	1.04	0.06	0.63	0.549778	0.745834	-6.63
245692_at	myc - like protein	BHLH101	AT5G04150	-1.07	-0.10	-0.63	0.549826	0.745835	-6.63
256809_at	hypothetical protein predicted by genem	ALY3	AT3G21430	1.06	0.09	0.63	0.549845	0.745835	-6.63
249468_at	putative protein predicted proteins, Arat	---	AT5G39650	-1.04	-0.06	-0.63	0.549916	0.745887	-6.63
256764_at	hypothetical protein predicted by gensca	---	AT3G29310	-1.07	-0.09	-0.63	0.549955	0.745888	-6.63
249865_at	unknown protein ; supported by cDNA:	---	AT5G22820	1.07	0.09	0.63	0.549982	0.745888	-6.63
246890_at	Expressed protein ; supported by cDNA	---	AT5G25410	1.06	0.08	0.63	0.55009	0.745946	-6.63
248618_at	myb-related transcription factor	AtMYB78	AT5G49620	1.06	0.08	0.63	0.550072	0.745946	-6.63
249297_at	unknown protein	---	AT5G41320	1.05	0.06	0.63	0.550287	0.746168	-6.63
260547_at	putative trypsin inhibitor ;supported by f	---	AT2G43550	-1.19	-0.26	-0.63	0.550423	0.746256	-6.64
261221_at	hypothetical protein predicted by genem	---	AT1G19960	1.42	0.50	0.63	0.550438	0.746256	-6.64
265691_at	unknown protein predicted by genscan	---	AT2G24330	-1.08	-0.11	-0.63	0.550482	0.746256	-6.64
263997_at	hypothetical protein predicted by genefir	---	AT2G22520	-1.04	-0.06	-0.63	0.550465	0.746256	-6.64
267594_at	hypothetical protein predicted by genefir	---	AT2G33000	1.05	0.07	0.63	0.550698	0.746504	-6.64
267063_at	hypothetical protein predicted by genefir	---	AT2G41120	1.07	0.10	0.63	0.550911	0.746623	-6.64
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J0442	---	---	1.14	0.19	0.63	0.550897	0.746623	-6.64
247582_at	putative protein various predicted prote	---	AT5G60760	1.06	0.08	0.63	0.550862	0.746623	-6.64
266879_at	putative phragmoplastin	ADL1D	AT2G44590	1.06	0.08	0.63	0.550917	0.746623	-6.64
249870_at	unknown protein	TGH	AT5G23080	-1.13	-0.17	-0.63	0.551062	0.746775	-6.64
258015_at	unknown protein	---	AT3G19340	-1.06	-0.08	-0.63	0.551202	0.746921	-6.64

246017_at	putative protein predicted proteins from	---	AT5G10730	-1.05	-0.06	-0.63	0.551285	0.746989	-6.64
251244_at	pectinacetylesterase precursor-like prot	---	AT3G62060	-1.06	-0.08	-0.63	0.551334	0.746998	-6.64
258288_at	unknown protein	LSH4	---	1.11	0.15	0.63	0.551357	0.746998	-6.64
259614_at	dioxygenase, putative similar to dioxyge	ATGA2OX	AT1G47990	1.05	0.08	0.63	0.551499	0.747146	-6.64
266618_at	unknown protein	---	AT2G35480	1.13	0.17	0.63	0.551577	0.747207	-6.64
257376_at	hypothetical protein predicted by gensca	---	AT2G32350	1.05	0.07	0.63	0.551647	0.747257	-6.64
264972_at	meiotic asynaptic mutant asy1, putative	ASY1	AT1G67370	-1.08	-0.11	-0.63	0.551703	0.747289	-6.64
261471_at	hypothetical protein contains similarity t	---	AT1G14460	1.09	0.12	0.63	0.551786	0.747357	-6.64
264943_at	hypothetical protein predicted by genem	---	AT1G76910	1.06	0.09	0.63	0.552035	0.747606	-6.64
265769_at	unknown protein weak similarity to prote	---	AT2G48090	1.06	0.08	0.63	0.552027	0.747606	-6.64
259197_at	putative peroxidase similar to peroxidas	---	AT3G03670	1.20	0.27	0.63	0.552142	0.747706	-6.64
263989_at	putative MAP kinase ; supported by cD	ATMPK20	AT2G42880	-1.08	-0.11	-0.63	0.552358	0.747865	-6.64
248390_at	importin alpha subunit	IMPA-8	AT5G52000	1.04	0.06	0.63	0.552344	0.747865	-6.64
249477_s_a	germin - like protein probable germin ty	---	AT5G38930 /	-1.04	-0.06	-0.63	0.552357	0.747865	-6.64
264825_at	hypothetical protein predicted by gensca	---	AT1G03720	-1.06	-0.08	-0.63	0.552443	0.747935	-6.64
266150_s_a	hypothetical protein	---	AT2G12290 /	-1.16	-0.21	-0.63	0.552543	0.747999	-6.64
249523_at	cytochrome b-561 (gb|AAD45585.1) ;su	ACYB-1	AT5G38630	1.05	0.07	0.63	0.552564	0.747999	-6.64
260277_at	hypothetical protein predicted by gensca	---	AT1G80520	1.11	0.15	0.62	0.552588	0.747999	-6.64
266087_at	putative alcohol dehydrogenase	---	AT2G37790	-1.06	-0.09	-0.62	0.552652	0.748006	-6.64
250043_at	putative protein proline-rich protein AP0	---	AT5G18430	1.06	0.09	0.62	0.552659	0.748006	-6.64
257643_at	AP2 domain transcription factor contain	---	AT3G25730	1.14	0.19	0.62	0.552712	0.748034	-6.64
260000_at	unknown protein similar to C-terminal h	ATMAP70	AT1G68060	-1.07	-0.09	-0.62	0.552888	0.748228	-6.64
250514_at	GDP dissociation inhibitor GDP dissoci	---	AT5G09550	1.05	0.07	0.62	0.552946	0.748262	-6.64
257086_at	hypothetical protein predicted by genem	---	AT3G20490	1.08	0.11	0.62	0.553022	0.748276	-6.64
257450_at	unknown protein similar to gb|AAD1447	---	AT1G10530	1.06	0.09	0.62	0.552999	0.748276	-6.64
266602_at	hypothetical protein predicted by gensca	---	AT2G46050	-1.04	-0.05	-0.62	0.553115	0.748357	-6.64
264399_at	postsynaptic protein CRIPT, putative si	---	AT1G61780	-1.04	-0.05	-0.62	0.553467	0.748522	-6.64
247914_at	xyloglucan endotransglycosylase	---	AT5G57540	1.06	0.08	0.62	0.553386	0.748522	-6.64
247211_at	unknown protein ; supported by full-leng	---	AT5G64880	-1.10	-0.13	-0.62	0.55343	0.748522	-6.64
253787_at	serine/threonine kinase-like protein rec	---	AT4G28670	1.05	0.07	0.62	0.553289	0.748522	-6.64
249802_at	putative protein similar to unknown prote	---	AT5G23770	-1.04	-0.06	-0.62	0.553382	0.748522	-6.64
256026_at	auxin response factor 1, putative simila	---	AT1G34170	1.05	0.06	0.62	0.553448	0.748522	-6.64
265758_at	hypothetical protein similar to myosin-lik	---	---	-1.04	-0.06	-0.62	0.553372	0.748522	-6.64
253088_at	ferulate-5-hydroxylase (FAH1) ; suppor	FAH1	AT4G36220	1.12	0.16	0.62	0.553568	0.748615	-6.64
263765_at	putative phosphatidylinositol phophatidy	SFH3	AT2G21540	1.17	0.23	0.62	0.553716	0.748760	-6.64

252994_at	putative protein gene PC326 protein - n	---	AT4G38480	1.13	0.17	0.62	0.553773	0.748760	-6.64
248588_at	unknown protein ; supported by cDNA:	---	AT5G49540	1.05	0.07	0.62	0.553754	0.748760	-6.64
253962_at	hypothetical protein	---	AT4G26460	1.05	0.07	0.62	0.553882	0.748862	-6.64
245928_s_a	vegetative storage protein Vsp1 ;suppo	VSP1	AT5G24770 /	-1.39	-0.48	-0.62	0.553974	0.748890	-6.64
245590_at	hypothetical protein	---	AT4G15060	1.05	0.07	0.62	0.553939	0.748890	-6.64
249044_at	Na+-dependent inorganic phosphate co	PHT4;6	AT5G44370	1.07	0.10	0.62	0.554001	0.748890	-6.64
252311_at	calcium dependent protein kinase - like	---	AT3G49370	1.12	0.17	0.62	0.554094	0.748971	-6.64
245461_at	hypothetical protein	---	AT4G17000	-1.05	-0.07	-0.62	0.554131	0.748977	-6.64
264829_at	hypothetical protein predicted by gensca	ANAC006	AT1G03490	-1.04	-0.06	-0.62	0.554324	0.749149	-6.64
262689_at	unknown protein	ANAC026	AT1G62700	1.05	0.07	0.62	0.554307	0.749149	-6.64
253362_s_a	putative protein cyclopropane-fatty-acyl	---	AT4G33110 /	1.07	0.10	0.62	0.554572	0.749174	-6.64
258532_at	ribosomal protein L29, putative similar t	---	AT3G06700	-1.13	-0.18	-0.62	0.554529	0.749174	-6.64
248972_at	putative protein similar to unknown prote	ATDSS1(V	AT5G45010	1.09	0.12	0.62	0.554434	0.749174	-6.64
247633_at	putative zinc finger protein finger protei	---	AT5G60470	1.08	0.12	0.62	0.55446	0.749174	-6.64
258204_at	hypothetical protein predicted by genem	AtGRF5	AT3G13960	-1.06	-0.09	-0.62	0.554573	0.749174	-6.64
265490_s_a	putative polygalacturonase	---	AT2G15450 /	-1.05	-0.07	-0.62	0.554551	0.749174	-6.64
263652_at	unknown protein EST gb|H76414 comes	---	AT1G04330	-1.04	-0.06	-0.62	0.554554	0.749174	-6.64
254303_at	predicted protein	---	AT4G22830	1.05	0.07	0.62	0.554656	0.749223	-6.64
251829_at	putative protein KIAA0882 protein, Hom	---	AT3G55020	-1.12	-0.16	-0.62	0.554674	0.749223	-6.64
265717_at	unknown protein ;supported by full-leng	---	AT2G03510	1.07	0.09	0.62	0.554792	0.749337	-6.64
262302_at	hypothetical protein predicted by genem	---	AT1G70910	-1.06	-0.08	-0.62	0.554832	0.749347	-6.64
260246_at	hypothetical protein similar to GB:AAD2	---	AT1G74220	1.05	0.07	0.62	0.554892	0.749383	-6.64
264182_at	MADS-box protein, putative similar to M	AGL23	AT1G65360	-1.05	-0.06	-0.62	0.554943	0.749406	-6.64
247362_at	putative protein strong similarity to unkn	ATPAP29	AT5G63140	-1.09	-0.13	-0.62	0.554974	0.749406	-6.64
251264_at	multifunctional aminoacyl-tRNA ligase-l	---	AT3G62120	-1.05	-0.06	-0.62	0.555072	0.749494	-6.64
249488_at	putative protein putative transposase T/	---	---	1.05	0.06	0.62	0.555151	0.749556	-6.64
262083_at	hypothetical protein predicted by genem	---	AT1G56100	-1.05	-0.07	-0.62	0.555267	0.749583	-6.64
258007_at	putative tyrosine phosphatase similar to	ATPEN2	AT3G19420	-1.07	-0.10	-0.62	0.55529	0.749583	-6.64
262186_at	hypothetical protein	---	AT1G77960	-1.11	-0.15	-0.62	0.555303	0.749583	-6.64
259427_at	MADS-box transcription factor, putative	AGL28	AT1G01530	1.05	0.06	0.62	0.555288	0.749583	-6.64
264858_at	hypothetical protein	SNL3	AT1G24190	1.05	0.08	0.62	0.555414	0.749670	-6.64
257030_at	unknown protein	---	---	1.05	0.07	0.62	0.555466	0.749670	-6.64
255868_at	putative MYB family transcription factor	---	AT2G30380	1.06	0.08	0.62	0.555448	0.749670	-6.64
247803_at	similar to unknown protein (gb|AAF6313	---	AT5G58340	1.04	0.05	0.62	0.555592	0.749796	-6.64
254995_at	putative protein	---	AT4G10370	1.06	0.08	0.62	0.555648	0.749814	-6.64

251687_at	quinone reductase-like protein zeta-cry	---	AT3G56460	-1.05	-0.06	-0.62	0.555671	0.749814	-6.64
260349_at	mitotic checkpoint protein, putative simi	---	AT1G69400	-1.06	-0.08	-0.62	0.555782	0.749846	-6.64
253846_at	putative protein MSP1, Saccharomyces	---	AT4G28000	1.04	0.06	0.62	0.555793	0.749846	-6.64
259095_at	acyl carrier protein 1 precursor (ACP) id	ACP1	AT3G05020	1.13	0.17	0.62	0.55577	0.749846	-6.64
264122_at	GTP-binding protein, ara-5 ras homolog	ARA-5	AT1G02130	-1.04	-0.05	-0.62	0.5559	0.749909	-6.64
259241_at	unknown protein similar to unknown pro	---	AT3G33530	-1.04	-0.06	-0.62	0.555971	0.749909	-6.64
265835_at	putative retroelement pol polyprotein	---	---	1.06	0.09	0.62	0.555961	0.749909	-6.64
250206_at	mitochondrial phosphate translocator	---	AT5G14040	1.10	0.13	0.62	0.555953	0.749909	-6.64
262585_at	hypothetical protein Is a member of the	BOR4	AT1G15460	1.07	0.10	0.62	0.556029	0.749942	-6.64
260971_at	hypothetical protein predicted by genem	---	AT1G53620	1.05	0.07	0.62	0.556105	0.749956	-6.64
265240_s_a	hypothetical protein	---	AT2G07691	-1.06	-0.08	-0.62	0.556091	0.749956	-6.64
252686_at	putative protein predicted protein, Arabi	---	---	-1.04	-0.06	-0.62	0.556159	0.749984	-6.64
265015_at	putative Ta11-1 reverse transcriptase si	---	---	1.04	0.06	0.62	0.556241	0.750050	-6.64
247764_at	subtilisin-like serine protease contains s	---	AT5G59190	-1.05	-0.07	-0.62	0.556282	0.750061	-6.64
264311_at	hypothetical protein similar to hypothetic	---	AT1G70400	-1.04	-0.06	-0.62	0.556431	0.750218	-6.64
252492_at	chloroplast import-associated channel p	TOC75-III	AT3G46740	-1.06	-0.08	-0.62	0.556553	0.750338	-6.64
256599_at	hypothetical protein predicted by gensca	---	AT3G14760	-1.05	-0.07	-0.62	0.556776	0.750554	-6.64
265905_at	putative transcription elongation factor S	---	AT2G25640	1.04	0.06	0.62	0.556779	0.750554	-6.64
250934_at	DNAJ protein - like DNAJ domain-conta	---	AT5G03030	1.08	0.12	0.62	0.557131	0.750940	-6.64
266385_at	pathogenesis-related PR-1-like protein i	PR1	AT2G14610	1.96	0.97	0.62	0.557104	0.750940	-6.64
249491_at	germin - like protein germin-like protein	---	AT5G39130	-1.05	-0.07	-0.62	0.557279	0.751095	-6.64
254514_at	hypothetical protein	---	AT4G20250	-1.06	-0.09	-0.62	0.557319	0.751105	-6.64
256687_x_a	hypothetical protein predicted by genem	---	AT3G32120	1.05	0.07	0.62	0.557364	0.751120	-6.64
257293_at	unknown protein similar to symbiosis-rel	APG8H	AT3G15580	-1.07	-0.10	-0.62	0.557567	0.751173	-6.64
265774_at	hypothetical protein predicted by gensca	---	AT2G07240	1.07	0.10	0.62	0.557628	0.751173	-6.64
252787_at	putative protein several En/Spm-like tra	---	---	1.04	0.05	0.62	0.557623	0.751173	-6.64
254209_at	Expressed protein ; supported by cDNA	---	AT4G23490	-1.08	-0.12	-0.62	0.557619	0.751173	-6.64
258199_at	unknown protein	---	AT3G14030	1.05	0.07	0.62	0.557497	0.751173	-6.64
258441_at	hypothetical protein predicted by genma	AT3G1726	---	1.05	0.07	0.62	0.557472	0.751173	-6.64
263833_at	hypothetical protein	---	AT2G40316	-1.04	-0.06	-0.62	0.557633	0.751173	-6.64
260955_at	unknown protein contains similarity to U	---	AT1G06000	1.12	0.16	0.62	0.557757	0.751207	-6.64
252999_at	putative protein other Arabidopsis hypot	---	AT4G38500	-1.05	-0.07	-0.62	0.557736	0.751207	-6.64
251001_at	putative protein	---	AT5G02670	-1.07	-0.09	-0.62	0.557716	0.751207	-6.64
262799_at	hypothetical protein predicted by gensca	---	AT1G20970	1.08	0.12	0.62	0.557916	0.751334	-6.64
245366_at	Expressed protein ; supported by full-ler	AtMAPR4	AT4G14965	-1.04	-0.06	-0.62	0.557999	0.751334	-6.64

265806_at	putative auxin-regulated protein	---	AT2G18010	1.16	0.22	0.62	0.558016	0.751334	-6.64
257822_at	rotamase FKBP (ROF1) identical to rota	ROF1	AT3G25230	-1.13	-0.18	-0.62	0.557932	0.751334	-6.64
248091_at	putative protein strong similarity to unkn	VTC5	AT5G55120	1.16	0.21	0.62	0.557965	0.751334	-6.64
264643_at	unknown protein	PGSIP5	AT1G08990	1.04	0.06	0.62	0.558116	0.751379	-6.64
257529_at	hypothetical protein predicted by gensca	---	AT3G03290	1.05	0.07	0.62	0.55809	0.751379	-6.64
252682_at	putative protein AtOXA1, Arabidopsis th	---	AT3G44370	1.06	0.09	0.62	0.558236	0.751453	-6.64
263329_at	hypothetical protein contains C3HC4 zin	---	AT2G15260	-1.05	-0.07	-0.62	0.558231	0.751453	-6.64
261858_at	Expressed protein ; supported by full-ler	---	AT1G50570	-1.04	-0.06	-0.62	0.55835	0.751473	-6.64
266911_at	putative protein kinase contains a protei	---	AT2G45910	-1.07	-0.09	-0.62	0.558337	0.751473	-6.64
257572_at	hypothetical protein predicted by genem	---	AT3G16880	1.06	0.08	0.62	0.558309	0.751473	-6.64
249632_at	caffeic acid O-methyltransferase-like pr	---	AT5G37170	1.04	0.06	0.62	0.558483	0.751479	-6.64
265642_at	putative nitrilase ;supported by full-leng	NLP1	AT2G27450	1.07	0.09	0.62	0.558519	0.751479	-6.64
246105_at	putative protein predicted helicase prote	---	---	1.04	0.05	0.62	0.558503	0.751479	-6.64
251808_at	AP3-complex beta-3A adaptin subunit-l	---	AT3G55480	1.06	0.08	0.62	0.558496	0.751479	-6.64
263362_at	putative selenium-binding protein	---	AT2G03880	-1.04	-0.06	-0.62	0.558468	0.751479	-6.64
252837_at	putative protein hypothetical proteins - A	---	---	1.04	0.06	0.62	0.558612	0.751560	-6.64
255130_at	hypothetical protein ; supported by full-l	---	AT4G08240	1.06	0.08	0.62	0.55866	0.751580	-6.64
260892_at	cysteine proteinase contains similarity to	---	AT1G29110	1.06	0.08	0.61	0.558901	0.751815	-6.64
248038_at	unknown protein	---	AT5G55980	-1.05	-0.06	-0.61	0.558897	0.751815	-6.64
266804_at	cyclophilin identical to GB:AF020433; p	CYP5	AT2G29960	-1.05	-0.08	-0.61	0.559105	0.751821	-6.64
265122_at	similar to flavin-binding monooxygenase	FMO GS-(	AT1G62540	-1.04	-0.06	-0.61	0.559133	0.751821	-6.64
267401_at	unknown protein	---	AT2G26210	-1.05	-0.07	-0.61	0.558994	0.751821	-6.64
245864_at	hypothetical protein predicted by genem	---	AT1G58070	1.09	0.12	0.61	0.559136	0.751821	-6.64
245098_at	ethylene response sensor (ERS) identic	ERS1	AT2G40940	1.12	0.16	0.61	0.559009	0.751821	-6.64
261677_at	unknown protein ;supported by full-lengt	---	AT1G18470	-1.08	-0.11	-0.61	0.559075	0.751821	-6.64
250370_at	putative protein putative transcription el	---	AT5G11430	1.04	0.06	0.61	0.559116	0.751821	-6.64
262137_at	transcription factor, putative similar to tr	---	AT1G77920	1.05	0.07	0.61	0.559237	0.751851	-6.64
258608_at	unknown protein ;supported by full-leng	---	AT3G03020	-1.10	-0.14	-0.61	0.559269	0.751851	-6.64
258331_at	putative coatomer complex subunit simil	---	AT3G15980	-1.06	-0.08	-0.61	0.55929	0.751851	-6.64
249599_at	putative protein AtPP protein, Brassica	---	AT5G37990	-1.06	-0.08	-0.61	0.559263	0.751851	-6.64
254734_at	methionyl-tRNA synthetase - like protei	---	AT4G13780	-1.05	-0.08	-0.61	0.55968	0.752327	-6.65
264418_at	nuclear ribonucleoprotein, putative simi	---	AT1G43190	-1.07	-0.10	-0.61	0.55971	0.752327	-6.65
261186_at	hypothetical protein predicted by genem	---	---	-1.04	-0.06	-0.61	0.559839	0.752456	-6.65
253837_at	putative proline-rich protein extensin - V	---	AT4G27850	1.05	0.07	0.61	0.559903	0.752498	-6.65
249461_at	putative protein predicted proteins, Arat	---	AT5G39640	1.05	0.07	0.61	0.55995	0.752516	-6.65

251675_at	helicase-like protein DNA helicase YGL	INO80	AT3G57300	-1.04	-0.06	-0.61	0.560082	0.752650	-6.65
250355_at	putative protein predicted protein, Arabi	---	AT5G11700	-1.06	-0.08	-0.61	0.560424	0.752931	-6.65
247791_at	cyclophilin ROC7 ;supported by full-len	ROC7	AT5G58710	1.07	0.10	0.61	0.560412	0.752931	-6.65
260658_at	hypothetical protein predicted by genem	---	AT1G19410	1.06	0.08	0.61	0.560376	0.752931	-6.65
247758_at	subtilisin-like serine protease contains s	ATSBT4.1	AT5G59120	1.06	0.09	0.61	0.560357	0.752931	-6.65
249217_at	ubiquitin-like protein ; supported by cDN	UBL5	AT5G42300	1.04	0.06	0.61	0.560571	0.753033	-6.65
249531_at	putative protein predicted protein, Arabi	AtGDU7	AT5G38770	1.05	0.07	0.61	0.560632	0.753033	-6.65
256318_s_a	hypothetical protein	---	---	-1.04	-0.06	-0.61	0.56055	0.753033	-6.65
263022_s_a	gamma-adaptin, putative similar to gam	---	AT1G23900 /	1.07	0.10	0.61	0.560615	0.753033	-6.65
253625_at	signal recognition particle receptor-like	---	AT4G30600	1.04	0.06	0.61	0.560724	0.753112	-6.65
260590_at	phosphoenolpyruvate carboxylase 1, pu	ATPPC1	AT1G53310	1.07	0.09	0.61	0.561042	0.753451	-6.65
254762_at	Expressed protein ; supported by full-ler	---	AT4G13230	-1.05	-0.07	-0.61	0.561023	0.753451	-6.65
264783_at	putative calcium-dependent protein kina	PPCK1	AT1G08650	-1.11	-0.15	-0.61	0.561243	0.753592	-6.65
258575_at	putative O-linked GlcNAc transferase sir	SEC	AT3G04240	1.05	0.07	0.61	0.561306	0.753592	-6.65
265098_at	unknown protein	---	AT1G04010	-1.11	-0.15	-0.61	0.561302	0.753592	-6.65
255741_at	tRNA isopentenyl transferase, putative	ATIPT6	AT1G25410	-1.05	-0.07	-0.61	0.561312	0.753592	-6.65
256804_at	hypothetical protein predicted by genem	---	AT3G20920	1.04	0.05	0.61	0.561304	0.753592	-6.65
249460_at	v-SNARE - like protein v-SNARE AtVTI	---	AT5G39630	-1.05	-0.07	-0.61	0.56136	0.753613	-6.65
262512_at	Expressed protein ; supported by full-ler	---	AT1G17145	1.12	0.16	0.61	0.561453	0.753693	-6.65
251177_at	cyclophylin -like protein CDC28/cdc2-lik	---	AT3G63400	1.06	0.09	0.61	0.561627	0.753882	-6.65
250083_at	glutathione S-transferase-like protein ; s	ATGSTF12	AT5G17220	-1.06	-0.08	-0.61	0.561686	0.753917	-6.65
264962_at	auxin transport protein EIR1, putative s	PIN6	AT1G77110	1.07	0.09	0.61	0.561745	0.753952	-6.65
252162_at	hypothetical protein	---	AT3G50590	1.08	0.12	0.61	0.561835	0.753974	-6.65
253177_s_a	O-methyltransferase - like protein caffei	---	AT4G35150 /	-1.08	-0.11	-0.61	0.561861	0.753974	-6.65
263308_at	hypothetical protein predicted by gensca	---	---	1.04	0.06	0.61	0.561831	0.753974	-6.65
246920_at	phytocyanin-related protein-like phytocy	---	AT5G25090	1.04	0.06	0.61	0.561976	0.754083	-6.65
246076_at	sucrose-phosphate synthase-like protei	ATSPS1F	AT5G20280	-1.05	-0.07	-0.61	0.562062	0.754110	-6.65
255014_at	MADS-box protein AGL11 ; supported b	STK	AT4G09960	1.04	0.06	0.61	0.562057	0.754110	-6.65
259451_at	synaptosomal associated protein (SNA	SNAP30	AT1G13890	1.04	0.06	0.61	0.562681	0.754897	-6.65
246776_at	kinesin-like protein kinesin-like heavy c	---	AT5G27550	1.07	0.10	0.61	0.562934	0.754970	-6.65
249340_at	putative protein contains similarity to my	---	AT5G41140	1.06	0.08	0.61	0.562927	0.754970	-6.65
263445_at	unknown protein	---	AT2G31590	1.04	0.06	0.61	0.562922	0.754970	-6.65
247304_at	amino acid transporter AAP4 (pir||S511	AAP4	AT5G63850	1.08	0.11	0.61	0.562908	0.754970	-6.65
258703_at	unknown protein	---	AT3G09750	-1.06	-0.08	-0.61	0.562931	0.754970	-6.65
251700_at	putative protein exocyst complex protei	---	AT3G56640	-1.09	-0.12	-0.61	0.562849	0.754970	-6.65

260843_at	unknown protein similar to hypothetical	---	AT1G29060	-1.04	-0.05	-0.61	0.562986	0.754995	-6.65
262795_at	hypothetical protein predicted by gensca	---	AT1G13130	1.07	0.10	0.61	0.563333	0.755416	-6.65
265246_at	putative pectinesterase	ATPMEPC	AT2G43050	1.06	0.08	0.61	0.563498	0.755593	-6.65
255983_at	polyneuridine aldehyde esterase, putati	MES14	AT1G33990	1.05	0.07	0.61	0.56361	0.755668	-6.65
246195_at	E2, ubiquitin-conjugating enzyme 17 (U	UBC17	AT4G36410	1.22	0.29	0.61	0.56362	0.755668	-6.65
264180_at	hypothetical protein contains similarity t	---	AT1G02190	1.05	0.07	0.61	0.563742	0.755787	-6.65
262312_at	hypothetical protein similar to putative ri	MLP28	AT1G70830	1.51	0.59	0.61	0.563891	0.755942	-6.65
254812_at	nucleotide sugar epimerase -like protei	GAE5	AT4G12250	1.12	0.17	0.61	0.563959	0.755988	-6.65
245726_at	homeobox protein, putative similar to h	HDG11	AT1G73360	-1.05	-0.07	-0.61	0.564018	0.756024	-6.65
253736_at	Proline-rich APG - like protein proline-ri	---	AT4G28780	1.08	0.12	0.61	0.564103	0.756093	-6.65
257981_at	ethylene-insensitive 3 (EIN3) identical t	EIN3	AT3G20770	-1.05	-0.07	-0.61	0.564141	0.756100	-6.65
266520_at	cyclic nucleotide and calmodulin-regulat	ATCNGC6	AT2G23980	1.06	0.08	0.61	0.56425	0.756108	-6.65
248388_at	putative protein contains similarity to my	---	AT5G51980	1.06	0.08	0.61	0.56428	0.756108	-6.65
260111_at	hypothetical protein similar to unknown	---	AT1G63320	-1.04	-0.06	-0.61	0.564248	0.756108	-6.65
261379_at	unknown protein similar to YGL010w-lik	---	AT1G18720	-1.04	-0.06	-0.61	0.564181	0.756108	-6.65
263769_at	5S ribosomal RNA	---	---	1.06	0.08	0.61	0.564416	0.756246	-6.65
261859_at	E2, ubiquitin-conjugating enzyme, puta	UBC20	AT1G50490	-1.06	-0.09	-0.61	0.56448	0.756288	-6.65
248917_at	putative protein similar to unknown prote	---	AT5G45850	-1.04	-0.05	-0.61	0.564519	0.756295	-6.65
257052_at	putative 3-hydroxybutyryl-CoA dehydrog	---	AT3G15290	-1.05	-0.06	-0.61	0.564656	0.756434	-6.65
262210_at	hypothetical protein predicted by gensca	IQD31	AT1G74690	-1.12	-0.16	-0.61	0.564722	0.756461	-6.65
258420_at	putative RNA polymerase similar to RN	---	AT3G16680	1.04	0.06	0.61	0.564743	0.756461	-6.65
261964_at	hypothetical protein similar to envelope-	---	---	1.04	0.05	0.61	0.564778	0.756464	-6.65
263188_at	hypothetical protein predicted by gensca	---	AT1G36095	1.05	0.07	0.61	0.564839	0.756501	-6.65
262253_s_a	unknown protein contains similarity to tra	---	AT1G53880 /	-1.05	-0.08	-0.60	0.565034	0.756629	-6.65
254809_at	putative protein auxin-induced protein 1	---	AT4G12410	-1.07	-0.10	-0.61	0.565008	0.756629	-6.65
245735_at	myb-like transcription factor, putative si	MYB54	AT1G73410	1.04	0.05	0.61	0.565008	0.756629	-6.65
265375_at	unknown protein ;supported by full-leng	VPS2.1	AT2G06530	1.06	0.09	0.60	0.565107	0.756682	-6.65
263156_at	myrosinase-associated protein, putative	---	AT1G54030	-1.10	-0.14	-0.60	0.56519	0.756749	-6.65
267632_at	hypothetical protein predicted by gensca	---	AT2G42160	-1.07	-0.10	-0.60	0.565302	0.756811	-6.65
251213_at	putative protein hypothetical proteins - A	---	---	-1.05	-0.06	-0.60	0.565302	0.756811	-6.65
265754_x_a	En/Spm transposon protein (mosaic-like	---	---	1.04	0.06	0.60	0.565479	0.757003	-6.65
257709_at	unknown protein similar to negative regu	---	AT3G27325	-1.07	-0.10	-0.60	0.565515	0.757007	-6.65
257105_at	unknown protein	---	AT3G15300	1.08	0.11	0.60	0.565575	0.757042	-6.65
249664_at	putative protein histone stem-loop bindi	---	AT5G36722 /	-1.05	-0.07	-0.60	0.565695	0.757160	-6.65
261595_at	hypothetical protein predicted by gensca	---	AT1G33070	1.04	0.06	0.60	0.565754	0.757193	-6.65

258941_at	putative monodehydroascorbate reducta	MDHAR	AT3G09940	1.44	0.53	0.60	0.565887	0.757328	-6.65
255863_s_a	putative GDSL-motif lipase/hydrolase si	---	AT2G30220 /	1.04	0.06	0.60	0.56598	0.757362	-6.65
246172_s_a	fragment of 1-aminocyclopropane-1-car	ACS1	AT3G61510 /	1.07	0.09	0.60	0.565951	0.757362	-6.65
251580_at	putative protein ethylene-responsive pr	---	AT3G58450	1.07	0.10	0.60	0.566075	0.757445	-6.65
246883_at	putative protein many predicted protein	---	AT5G26190	1.04	0.06	0.60	0.566215	0.757569	-6.65
254587_at	resistance protein RPP5 - like downy m	---	AT4G19520	1.06	0.08	0.60	0.566267	0.757569	-6.65
257419_at	hypothetical protein predicted by gensca	---	AT1G30800	-1.04	-0.06	-0.60	0.566248	0.757569	-6.65
253346_at	hypothetical protein	---	AT4G33600	1.05	0.06	0.60	0.566319	0.757595	-6.65
267236_at	GDP dissociation inhibitor identical to G	ATGDI1	AT2G44100	1.05	0.07	0.60	0.566482	0.757696	-6.65
248682_at	cytochrome b5 (dbj|BAA74840.1) ; supp	CB5-D	AT5G48810	-1.05	-0.07	-0.60	0.566528	0.757696	-6.65
246970_at	cytochrome P450-like protein fatty acid	CYP714A2	AT5G24900	1.08	0.11	0.60	0.566447	0.757696	-6.65
258885_at	putative uridylate kinase similar to uridy	---	AT3G10030	-1.04	-0.06	-0.60	0.566501	0.757696	-6.65
249206_at	putative protein similar to unknown prote	ATS	AT5G42630	-1.06	-0.09	-0.60	0.566596	0.757742	-6.65
267175_s_a	actin 3 identical to GB:U29480;supporte	ACT1	AT2G37620 /	1.07	0.10	0.60	0.5667	0.757836	-6.65
250962_at	putative protein various predicted prote	---	AT5G02990	-1.05	-0.07	-0.60	0.566754	0.757865	-6.65
263121_at	receptor protein kinase, putative similar	---	AT1G78530	1.06	0.08	0.60	0.566985	0.758130	-6.65
249161_at	20S proteasome subunit PAF1 (gb|AAC	PAF1	AT5G42790	-1.04	-0.05	-0.60	0.567048	0.758169	-6.65
264412_at	hypothetical protein similar to putative tr	---	AT1G43260	1.04	0.06	0.60	0.56717	0.758243	-6.65
260218_at	putative RING zinc finger protein contai	---	AT1G74620	1.04	0.05	0.60	0.567164	0.758243	-6.65
248646_at	unknown protein ;supported by full-leng	---	AT5G49100	-1.10	-0.14	-0.60	0.567276	0.758341	-6.65
248544_at	putative protein contains similarity to L-i	PIMT2	AT5G50240	-1.09	-0.13	-0.60	0.567326	0.758363	-6.65
251676_at	hypothetical protein	---	AT3G57320	-1.07	-0.10	-0.60	0.567431	0.758459	-6.65
263853_at	putative mutT domain protein	---	AT2G04440	1.07	0.10	0.60	0.567494	0.758499	-6.65
266212_at	putative retroelement pol polyprotein	---	---	-1.06	-0.09	-0.60	0.567532	0.758505	-6.65
257793_at	unknown protein ;supported by full-leng	---	AT3G26960	-1.21	-0.28	-0.60	0.567756	0.758760	-6.65
249363_at	DegP protease contains similarity to De	DegP13	AT5G40560	1.04	0.06	0.60	0.567974	0.759006	-6.65
261491_at	hypothetical protein contains similarity t	FLP	AT1G14350	1.14	0.19	0.60	0.568018	0.759021	-6.65
259053_at	unknown protein similar to hypothetical	---	AT3G03320	1.05	0.07	0.60	0.568096	0.759037	-6.65
245128_at	unknown protein similar to gi2344899|A	---	AT2G45380	-1.05	-0.08	-0.60	0.568075	0.759037	-6.65
246785_at	glutathione synthetase gsh2 non-conse	GSH2	AT5G27380	-1.10	-0.14	-0.60	0.568227	0.759044	-6.65
261171_at	unknown protein	---	AT1G04880	1.05	0.07	0.60	0.568187	0.759044	-6.65
247868_at	Myb-related transcription factor-like prot	MYB36	AT5G57620	-1.05	-0.07	-0.60	0.568268	0.759044	-6.65
249394_at	putative protein predicted protein, Arabi	---	AT5G40180	-1.04	-0.05	-0.60	0.568225	0.759044	-6.65
246465_at	quinone oxidoreductase - like protein pr	---	AT5G17000	1.09	0.12	0.60	0.568244	0.759044	-6.65
257417_at	hypothetical protein predicted by gensca	---	AT1G10110	1.05	0.07	0.60	0.56851	0.759323	-6.65

251979_at	caffeic acid O-methyltransferase - like p	LUT1	AT3G53130 /	-1.05	-0.07	-0.60	0.568563	0.759349	-6.65
247490_at	LFY floral meristem identity control prote	LFY	AT5G61850	1.04	0.06	0.60	0.568603	0.759359	-6.65
257983_at	unknown protein	---	AT3G20790	-1.14	-0.18	-0.60	0.568861	0.759441	-6.65
260715_at	hypothetical protein predicted by genem	---	AT1G48200	1.09	0.13	0.60	0.568867	0.759441	-6.65
266468_at	unknown protein ; supported by cDNA: g	---	AT2G47960	-1.06	-0.08	-0.60	0.568918	0.759441	-6.65
266759_at	unknown protein predicted by genefinde	---	AT2G46915	1.05	0.07	0.60	0.568765	0.759441	-6.65
249923_at	conglutin gamma - like protein conglutin	---	AT5G19120	1.10	0.13	0.60	0.568841	0.759441	-6.65
253723_at	extensin-like protein ;supported by full-l	---	AT4G29240	1.05	0.07	0.60	0.568932	0.759441	-6.65
255921_at	hypothetical protein contains Pfam profil	APUM8	AT1G22240	1.05	0.07	0.60	0.568789	0.759441	-6.65
245110_at	hypothetical protein predicted by genefir	---	AT2G41550	-1.04	-0.06	-0.60	0.568914	0.759441	-6.65
253732_at	putative protein several hypothetical pro	---	AT4G29140	-1.05	-0.07	-0.60	0.569084	0.759512	-6.65
258039_at	unknown protein ;supported by full-leng	---	AT3G21200	-1.05	-0.07	-0.60	0.569072	0.759512	-6.65
262187_at	hypothetical protein	---	AT1G77960	-1.04	-0.06	-0.60	0.569075	0.759512	-6.65
250178_at	putative protein various unknown or pre	---	AT5G14430	-1.04	-0.06	-0.60	0.569279	0.759682	-6.66
257416_at	unknown protein	---	AT2G17750	1.06	0.08	0.60	0.569312	0.759682	-6.66
256382_at	unknown protein ;supported by full-lengt	---	AT1G66860	-1.13	-0.18	-0.60	0.569249	0.759682	-6.66
259177_at	hypothetical protein similar to putative p	---	AT3G01630	1.04	0.06	0.60	0.5698	0.760288	-6.66
263823_s_a	AP2 domain transcription factor	---	AT2G40340 /	-1.11	-0.15	-0.60	0.570113	0.760509	-6.66
252276_at	hypothetical protein ; supported by cDN	---	AT3G49490	1.06	0.08	0.60	0.570105	0.760509	-6.66
252359_at	putative protein predicted proteins, Aral	---	AT3G48440	1.07	0.09	0.60	0.570409	0.760509	-6.66
259799_at	drought induced protein, putative simila	---	AT1G72290	1.04	0.06	0.60	0.570064	0.760509	-6.66
252101_at	rac-like GTP binding protein Arac11 ; su	ROP1	AT3G51300	1.05	0.07	0.60	0.570466	0.760509	-6.66
266440_at	unknown protein	---	AT2G43235 /	1.05	0.07	0.60	0.570396	0.760509	-6.66
250964_at	putative protein various predicted prote	---	AT5G03010	1.06	0.08	0.60	0.570565	0.760509	-6.66
256449_at	mutator transposase MUDRA, putative	---	---	1.05	0.07	0.60	0.570516	0.760509	-6.66
258073_at	putative auxin-resistance protein, AXR1	---	AT3G25880	-1.05	-0.06	-0.60	0.570173	0.760509	-6.66
262998_at	hypothetical protein predicted by genem	---	AT1G54280	1.04	0.05	0.60	0.570327	0.760509	-6.66
247639_s_a	undecaprenyl diphosphate synthase un	---	AT5G60500 /	1.04	0.05	0.60	0.570354	0.760509	-6.66
248870_at	putative protein similar to unknown prote	---	AT5G46710	1.17	0.23	0.60	0.570151	0.760509	-6.66
264039_at	putative cold-regulated protein ;support	---	AT2G03740	-1.05	-0.06	-0.60	0.570501	0.760509	-6.66
248582_at	heat shock protein 70 (gb|AAF27639.1)	CPHSC70	AT5G49910	1.09	0.12	0.60	0.570315	0.760509	-6.66
251543_at	putative protein	---	AT3G58770	1.05	0.07	0.60	0.570271	0.760509	-6.66
259964_at	glutathione transferase, putative similar	ATGSTU2	AT1G53680	1.05	0.06	0.60	0.570525	0.760509	-6.66
260280_at	unknown protein contains AP2 DNA-bin	---	AT1G80580	-1.08	-0.11	-0.60	0.57011	0.760509	-6.66
245571_at	light induced protein like	---	AT4G14695	-1.06	-0.09	-0.60	0.57056	0.760509	-6.66

262478_at	hypothetical protein similar to hypothetic	---	AT1G11170	-1.05	-0.07	-0.60	0.570646	0.760572	-6.66
254771_at	hypothetical protein	MEE56	AT4G13380	1.05	0.06	0.60	0.570839	0.760785	-6.66
254590_at	hypothetical protein	---	AT4G18860	1.04	0.06	0.60	0.570949	0.760888	-6.66
261327_at	transcription factor, putative contains A	---	AT1G44830	1.31	0.39	0.60	0.571172	0.761139	-6.66
254773_at	putative protein Cyclic beta-1-3-glucan	ATCSLA15	AT4G13410	-1.13	-0.18	-0.59	0.571343	0.761261	-6.66
265107_s_a	similar to glucose 1-dehydrogenase (AB	---	AT1G62610 /	1.05	0.07	0.60	0.571296	0.761261	-6.66
250276_at	putative protein mRNA, Moritella marina	---	AT5G13030	-1.05	-0.07	-0.59	0.571363	0.761261	-6.66
260117_at	AIG1-like protein similar to AIG1 protein	---	AT1G33950	-1.04	-0.05	-0.59	0.571492	0.761389	-6.66
253460_at	hypothetical protein	---	AT4G32130	1.06	0.08	0.59	0.571714	0.761439	-6.66
262500_at	unknown protein Contains PF|00646 F-	FBP7	AT1G21760	-1.05	-0.06	-0.59	0.571664	0.761439	-6.66
255152_at	Rab-like protein Rab11 protein - Arabid	---	AT4G08190	-1.04	-0.05	-0.59	0.571634	0.761439	-6.66
257873_at	P-glycoprotein, putative similar to P-gly	PGP17	AT3G28380	1.06	0.08	0.59	0.571666	0.761439	-6.66
248314_at	putative protein similar to unknown prote	---	AT5G52620	-1.04	-0.06	-0.59	0.571592	0.761439	-6.66
256931_at	LEA protein, putative similar to LEA pro	---	AT3G22490	1.04	0.06	0.59	0.57173	0.761439	-6.66
256946_at	hypothetical protein contains Pfam profil	HAF2	AT3G19040	1.08	0.11	0.59	0.571815	0.761507	-6.66
250093_at	hypothetical protein	---	AT5G17370	-1.04	-0.06	-0.59	0.571892	0.761565	-6.66
251589_at	putative protein SINA2p zinc finger prot	SINAT2	AT3G58040	-1.05	-0.07	-0.59	0.571963	0.761615	-6.66
266622_at	hypothetical protein predicted by gensca	---	AT2G35430	-1.06	-0.08	-0.59	0.57201	0.761634	-6.66
253353_at	pathogenesis-related protein - like path	---	AT4G33730	-1.04	-0.06	-0.59	0.572213	0.761816	-6.66
266483_at	unknown protein ;supported by full-leng	CRR6	AT2G47910	1.06	0.08	0.59	0.572236	0.761816	-6.66
247019_at	AP2 domain transcription factor-like	---	AT5G67010	1.05	0.07	0.59	0.572268	0.761816	-6.66
263784_at	Expressed protein ; supported by full-ler	---	AT2G46375	1.05	0.07	0.59	0.57228	0.761816	-6.66
249108_at	steroid sulfotransferase-like	---	AT5G43690	-1.04	-0.05	-0.59	0.572338	0.761848	-6.66
246698_at	putative protein	---	---	1.04	0.06	0.59	0.572517	0.762042	-6.66
249893_at	Expressed protein ; supported by full-ler	---	AT5G22555	-1.05	-0.07	-0.59	0.572563	0.762059	-6.66
250858_at	I-box binding factor - like protein I-box b	---	AT5G04760	1.07	0.10	0.59	0.572691	0.762140	-6.66
262785_at	putative carboxyl-terminal peptidase sim	---	AT1G10750	1.08	0.11	0.59	0.572665	0.762140	-6.66
265138_at	hypothetical protein predicted by gensca	---	AT1G51300	-1.07	-0.09	-0.59	0.572726	0.762143	-6.66
256404_at	unknown protein similar to far-red impair	FRS7	AT3G06250	-1.07	-0.09	-0.59	0.57285	0.762263	-6.66
266793_at	homeotic protein AGL30	AGL30	AT2G03060	-1.09	-0.12	-0.59	0.572906	0.762292	-6.66
250102_at	receptor-like protein kinase	LRR1	AT5G16590	1.06	0.08	0.59	0.573051	0.762441	-6.66
261643_at	hypothetical protein similar to hypothetic	TAF4B	AT1G27720	1.07	0.09	0.59	0.573143	0.762520	-6.66
245503_at	kinase like protein	---	AT4G15650	-1.04	-0.06	-0.59	0.573212	0.762564	-6.66
245570_at	heat shock protein 101 (HSP101),putat	CLPB2	AT4G14670	-1.05	-0.07	-0.59	0.573243	0.762564	-6.66
249509_at	strong similarity to unknown protein (gb|	---	AT5G38390	-1.04	-0.05	-0.59	0.573483	0.762838	-6.66

255483_at	putative glycosyltransferase similar to A	XT2	AT4G02500	-1.07	-0.10	-0.59	0.573685	0.763063	-6.66
252132_at	putative LEA protein Picea glauca late e	---	AT3G50790	-1.10	-0.14	-0.59	0.573763	0.763121	-6.66
263074_at	putative HMG protein ;supported by full	HMGB4	AT2G17560	-1.06	-0.08	-0.59	0.573824	0.763158	-6.66
264464_at	putative heat-shock protein similar to GE	---	AT1G10350	-1.05	-0.08	-0.59	0.57391	0.763183	-6.66
264215_at	cytochrome P450, putative similar to cy	CYP96A3	AT1G65340	1.04	0.06	0.59	0.573891	0.763183	-6.66
252756_s_a	putative protein hypothetical proteins - A	---	AT1G58520 /	-1.05	-0.06	-0.59	0.57404	0.763312	-6.66
267513_at	unknown protein ; supported by cDNA:	---	AT2G45620	-1.05	-0.07	-0.59	0.574131	0.763348	-6.66
249011_at	putative protein strong similarity to unkn	---	AT5G44670	-1.12	-0.16	-0.59	0.574201	0.763348	-6.66
254396_at	peptide transporter - like protein peptide	---	AT4G21680	-1.28	-0.35	-0.59	0.574187	0.763348	-6.66
248909_at	serine threonine protein kinase ; suppor	CIPK19	AT5G45810	1.07	0.09	0.59	0.574173	0.763348	-6.66
254359_at	putative protein hypothetical protein YM	---	AT4G22360	-1.05	-0.07	-0.59	0.574315	0.763455	-6.66
245337_at	Expressed protein ; supported by full-ler	---	AT4G16566	-1.04	-0.06	-0.59	0.574482	0.763632	-6.66
252809_at	putative protein various predicted prote	---	---	-1.04	-0.06	-0.59	0.574588	0.763729	-6.66
248725_at	acetyl-CoA:benzylalcohol acetyltranfera	---	AT5G47980	1.05	0.07	0.59	0.57474	0.763886	-6.66
253066_at	1-aminocyclopropane-1-carboxylate sy	ACS8	AT4G37770	1.23	0.30	0.59	0.574775	0.763889	-6.66
267481_at	putative receptor-like protein kinase	---	AT2G02780	1.13	0.17	0.59	0.574856	0.763952	-6.66
258727_at	ethylene-responsive protein, putative si	---	AT3G11930	1.06	0.08	0.59	0.575002	0.764031	-6.66
247167_at	unknown protein	---	AT5G65850	-1.06	-0.08	-0.59	0.574988	0.764031	-6.66
261807_at	Expressed protein ; supported by full-ler	---	AT1G30515	-1.04	-0.06	-0.59	0.575016	0.764031	-6.66
249765_at	putative protein contains similarity to un	SLAH3	AT5G24030	1.17	0.22	0.59	0.575124	0.764088	-6.66
245419_at	putative protein	MSH4	AT4G17380	-1.04	-0.06	-0.59	0.575126	0.764088	-6.66
258488_at	unknown protein ;supported by full-leng	---	AT3G02420	-1.05	-0.07	-0.59	0.575217	0.764127	-6.66
260662_at	2-hydroxyisoflavone reductase, putative	---	AT1G19540	1.06	0.08	0.59	0.575223	0.764127	-6.66
264973_at	nitrate transporter, putative nitrate trans	---	AT1G27040	1.06	0.08	0.59	0.575288	0.764170	-6.66
267252_at	hypothetical protein predicted by gensca	---	AT2G23100	1.05	0.07	0.59	0.575416	0.764295	-6.66
257271_at	Expressed protein ; supported by full-ler	---	AT3G28007	-1.16	-0.22	-0.59	0.575539	0.764369	-6.66
260901_at	flavin-containing monooxygenases, put	YUC11	AT1G21430	-1.06	-0.09	-0.59	0.575524	0.764369	-6.66
256400_at	putative RING zinc finger protein contai	---	AT3G06140	-1.06	-0.09	-0.59	0.575594	0.764382	-6.66
252930_at	putative endo-1,4-beta-glucanase endo	AtGH9B18	AT4G39010	1.06	0.08	0.59	0.575615	0.764382	-6.66
245811_at	hypothetical protein similar to putative re	---	---	1.05	0.07	0.59	0.57569	0.764437	-6.66
265631_at	putative helicase	---	---	1.04	0.05	0.59	0.57577	0.764498	-6.66
256694_at	hypothetical protein predicted genscan+	---	---	1.05	0.07	0.59	0.575849	0.764524	-6.66
252556_at	putative protein step II splicing factor hS	---	AT3G45950	-1.04	-0.05	-0.59	0.575881	0.764524	-6.66
248875_at	disease resistance protein-like	---	AT5G46470	1.08	0.11	0.59	0.57589	0.764524	-6.66
266546_at	putative AT-hook DNA-binding protein	---	AT2G35270	1.04	0.06	0.59	0.576158	0.764775	-6.66

260702_at	calmodulin, putative similar to calmodul	---	AT1G32250	1.05	0.06	0.59	0.57618	0.764775	-6.66
247767_at	putative protein various predicted prote	AGL82	AT5G58890	1.04	0.06	0.59	0.576135	0.764775	-6.66
246545_at	pectate lyase -like protein pectate lyase	---	AT5G15110	1.04	0.06	0.59	0.576242	0.764813	-6.66
255333_at	putative polyprotein	---	---	1.04	0.06	0.59	0.576303	0.764850	-6.66
249374_at	20S proteasome beta subunit PBB2 ;su	PBB2	AT5G40580	-1.05	-0.07	-0.59	0.576443	0.764991	-6.66
258237_at	myb protein identical to ATMYB3 GB:BA	ATMYB21	AT3G27810	-1.04	-0.06	-0.59	0.576621	0.765183	-6.66
259469_at	hypothetical protein predicted by gensca	---	AT1G19100	1.04	0.06	0.59	0.576719	0.765224	-6.66
264496_at	putative polyprotein similar to GB:AAC0	---	---	1.06	0.08	0.59	0.576696	0.765224	-6.66
256802_at	cytochrome P450, putative similar to cy	CYP705A3	AT3G20950	1.04	0.06	0.59	0.576892	0.765408	-6.66
251907_at	putative protein 85p protein - Medicago	---	AT3G53760	-1.09	-0.12	-0.59	0.576927	0.765411	-6.66
255665_at	hypothetical protein	CRP	AT4G00450	-1.04	-0.06	-0.59	0.57716	0.765617	-6.66
247910_at	putative protein similar to unknown prote	---	AT5G57410	1.06	0.09	0.59	0.577183	0.765617	-6.66
252872_at	putative serine/threonine protein kinase	SNRK2.7	AT4G40010	1.04	0.06	0.59	0.577164	0.765617	-6.66
250160_at	putative protein various predicted prote	ATHB30	AT5G15210	-1.12	-0.16	-0.59	0.577243	0.765626	-6.66
249547_at	lipid transfer - like protein P48h-10 prot	---	AT5G38160	1.06	0.09	0.59	0.577257	0.765626	-6.66
263312_at	putative replication protein A1	---	---	-1.05	-0.06	-0.59	0.577371	0.765732	-6.66
257953_at	predicted protein supported by full-lengt	PEX22	AT3G21865	-1.08	-0.11	-0.59	0.577496	0.765854	-6.66
250077_at	putative protein	---	AT5G16680	-1.04	-0.06	-0.59	0.577597	0.765943	-6.66
AFFX-Athal-	Arabidopsis thaliana /REF=M64116 /DE	GAPC1	---	1.07	0.09	0.58	0.577673	0.765999	-6.66
265616_at	hypothetical protein predicted by genefi	---	AT2G25500	1.04	0.05	0.58	0.577858	0.766200	-6.66
257813_at	Cdc45-like protein similar to Cdc45 GB	CDC45	AT3G25100	1.04	0.06	0.58	0.577941	0.766265	-6.66
252127_at	putative protein ATP binding protein - H	PLP3a	AT3G50960	-1.07	-0.09	-0.58	0.577983	0.766277	-6.66
252938_at	hypothetical protein	---	AT4G39190	-1.15	-0.21	-0.58	0.578101	0.766325	-6.66
252957_at	glycine-rich protein 2 (GRP2) ; supporte	GRP2	AT4G38680	-1.10	-0.13	-0.58	0.578096	0.766325	-6.66
248444_at	putative protein similar to unknown prote	---	---	1.04	0.06	0.58	0.57812	0.766325	-6.66
261825_at	endo-xyloglucan transferase, putative s	---	AT1G11545	1.31	0.39	0.58	0.578192	0.766375	-6.66
264925_at	hypothetical protein contains similarity t	---	AT1G60670	-1.05	-0.08	-0.58	0.578226	0.766376	-6.66
253357_at	Dem -like protein Dem (defective embry	---	AT4G33400	-1.05	-0.07	-0.58	0.578271	0.766391	-6.66
261778_at	hypothetical protein predicted by genem	---	AT1G76220	-1.04	-0.05	-0.58	0.578404	0.766523	-6.66
246658_at	putative protein predicted proteins, Aral	---	---	1.04	0.06	0.58	0.578448	0.766537	-6.66
252834_at	putative protein RING-H2 zinc finger pr	---	AT4G40070	-1.10	-0.14	-0.58	0.578554	0.766588	-6.66
251549_at	putative protein predicted proteins, Aral	---	AT3G58890	-1.04	-0.06	-0.58	0.578526	0.766588	-6.66
263297_at	putative ADP-ribosylation factor ; suppo	ATARFB1A	AT2G15310	1.08	0.11	0.58	0.578814	0.766666	-6.66
266925_at	unknown protein ;supported by full-leng	PEX11D	AT2G45740	-1.04	-0.06	-0.58	0.578811	0.766666	-6.66
263813_s_a	putative TNP1-like transposon protein re	---	---	-1.05	-0.06	-0.58	0.578805	0.766666	-6.66

248593_at	pectin methylesterase ;supported by ful	---	AT5G49180	1.07	0.09	0.58	0.578731	0.766666	-6.66
249555_at	putative protein predicted protein, rice;s	---	AT5G38300	-1.05	-0.07	-0.58	0.578679	0.766666	-6.66
262406_at	myb-related protein, putative similar to	AtMYB93	AT1G34670	1.06	0.08	0.58	0.578722	0.766666	-6.66
265877_at	unknown protein ; supported by cDNA:	BZIP34	AT2G42380	1.09	0.12	0.58	0.579096	0.766950	-6.66
246431_at	calcium-binding protein calcium binding	APC1	AT5G17480	-1.04	-0.05	-0.58	0.579065	0.766950	-6.66
258305_at	hypothetical protein predicted by gensca	---	---	1.03	0.05	0.58	0.579218	0.767067	-6.67
258061_at	unknown protein ; supported by cDNA:	---	AT3G25910	1.05	0.07	0.58	0.57928	0.767105	-6.67
247994_at	RNA-binding protein-like	---	AT5G56140	-1.06	-0.08	-0.58	0.579601	0.767485	-6.67
263317_s_a	similar to mammalian MHC III region pro	SUVH7	AT1G17770 /	1.07	0.10	0.58	0.579717	0.767594	-6.67
251231_at	Glutathione transferase III-like protein (	ATGSTF1	AT3G62760	1.05	0.06	0.58	0.579897	0.767788	-6.67
264730_at	hypothetical protein similar to putative re	---	AT1G62085	-1.05	-0.07	-0.58	0.579933	0.767791	-6.67
263671_at	hypothetical protein predicted by gensca	---	AT2G04830	1.04	0.06	0.58	0.580081	0.767853	-6.67
250956_at	putative protein	---	AT5G03210	1.07	0.10	0.58	0.580049	0.767853	-6.67
259115_at	hypothetical protein predicted by gensca	---	AT3G01360	-1.06	-0.08	-0.58	0.580029	0.767853	-6.67
251534_at	ATP-dependent RNA helicase-like prot	---	AT3G58510	1.08	0.11	0.58	0.580127	0.767869	-6.67
247522_at	putative protein ; supported by cDNA: g	---	AT5G61340	-1.06	-0.09	-0.58	0.58016	0.767869	-6.67
262769_at	actin-like protein strong similarity to gb|U	DIS1	AT1G13180	1.06	0.08	0.58	0.580426	0.767905	-6.67
257368_at	hypothetical protein predicted by gensca	---	AT2G29860	-1.04	-0.06	-0.58	0.580457	0.767905	-6.67
264451_s_a	putative lectin receptor kinase very simil	---	---	1.05	0.07	0.58	0.580491	0.767905	-6.67
256562_at	Ty1/Copia-type retroelement polyprotein	---	---	-1.04	-0.06	-0.58	0.58049	0.767905	-6.67
263695_at	putative phosphoribosylglycinamide for	---	AT1G31220	-1.05	-0.06	-0.58	0.580372	0.767905	-6.67
264610_at	Expressed protein ; supported by full-ler	---	AT1G04645	-1.05	-0.07	-0.58	0.580244	0.767905	-6.67
261966_x_a	hypothetical protein similar to putative tr	---	---	-1.04	-0.06	-0.58	0.580295	0.767905	-6.67
245772_at	hypothetical protein similar to putative h	---	AT1G30300	1.08	0.11	0.58	0.580343	0.767905	-6.67
246381_at	hypothetical protein	---	---	-1.08	-0.11	-0.58	0.5804	0.767905	-6.67
259593_at	nuclear transport factor 2, putative simil	NTF2B	AT1G27970	1.04	0.05	0.58	0.58064	0.768058	-6.67
246921_at	putative protein small unique nuclear re	---	AT5G25080	-1.07	-0.10	-0.58	0.580771	0.768106	-6.67
266362_at	unknown protein	---	AT2G32430	1.06	0.08	0.58	0.580739	0.768106	-6.67
250200_at	peroxidase ATP20a (emb|CAA67338.1)	---	AT5G14130	1.06	0.08	0.58	0.580777	0.768106	-6.67
259166_at	unknown protein ; supported by cDNA:	---	AT3G01670	1.15	0.21	0.58	0.580867	0.768107	-6.67
245781_at	S-ribonuclease binding protein SBP1, p	SBP1	AT1G45976	1.06	0.08	0.58	0.58085	0.768107	-6.67
258550_at	putative mudrA protein similar to mudrA	---	---	-1.05	-0.07	-0.58	0.580941	0.768107	-6.67
259812_at	unknown protein	---	AT1G49840	1.07	0.10	0.58	0.58098	0.768107	-6.67
253016_at	putative protein partial LG127/30 gene	---	AT4G37950	-1.04	-0.05	-0.58	0.58089	0.768107	-6.67
250509_at	cytochrome P450	CYP78A7	AT5G09970	1.06	0.08	0.58	0.580958	0.768107	-6.67

263376_at	putative surface protein ; supported by	FLA6	AT2G20520	1.04	0.05	0.58	0.581073	0.768186	-6.67
266030_x_a	hypothetical protein predicted by gensca	---	---	1.05	0.08	0.58	0.581126	0.768211	-6.67
266708_at	putative chloroplast nucleoid DNA bindi	---	AT2G03200	1.07	0.09	0.58	0.581419	0.768553	-6.67
247028_at	DNA polymerase alpha 1	ICU2	AT5G67100	1.11	0.15	0.58	0.581458	0.768561	-6.67
250235_s_a	ubiquinol--cytochrome-c reductase - like	---	AT5G13430 /	1.04	0.06	0.58	0.581681	0.768811	-6.67
245593_at	IAA7 like protein	IAA14	AT4G14550	1.13	0.17	0.58	0.581837	0.768973	-6.67
266459_at	unknown protein supported by full-lengt	---	AT2G47970	1.05	0.07	0.58	0.581932	0.769054	-6.67
245345_at	proteinase like protein ;supported by full	---	AT4G16640	-1.04	-0.06	-0.58	0.582224	0.769395	-6.67
260533_at	putative U1 small nuclear ribonucleopro	---	AT2G43370	1.04	0.06	0.58	0.582583	0.769825	-6.67
256116_at	unknown protein contains similarity to m	CPuORF5	AT1G16858 /	1.05	0.08	0.58	0.582727	0.769845	-6.67
262493_at	auxilin-like protein similar to GB:CAB40	---	AT1G21660	1.04	0.06	0.58	0.582793	0.769845	-6.67
246573_at	copper amine oxidase, putative similar t	---	AT1G31690	1.07	0.09	0.58	0.582852	0.769845	-6.67
253792_at	ammonium transporter - like protein am	AMT1;4	AT4G28700	1.06	0.08	0.58	0.582706	0.769845	-6.67
261365_at	proton pump interactor, putative similar	---	AT1G53110	1.13	0.18	0.58	0.582868	0.769845	-6.67
265772_at	putative protein kinase contains a protei	RKF3	AT2G48010	1.06	0.09	0.58	0.582832	0.769845	-6.67
249041_at	male sterility MS5; pollenless3	---	AT5G44330	-1.05	-0.07	-0.58	0.582832	0.769845	-6.67
252838_at	hypothetical protein	---	---	1.04	0.05	0.58	0.58273	0.769845	-6.67
247666_at	putative protein various predicted prote	---	AT5G60140	-1.04	-0.05	-0.58	0.582961	0.769923	-6.67
256391_at	hypothetical protein predicted by gensca	---	AT3G06090	1.04	0.05	0.58	0.583057	0.770005	-6.67
251477_at	putative protein	---	AT3G59680	1.04	0.06	0.58	0.583317	0.770259	-6.67
245871_at	hypothetical protein predicted by genem	---	AT1G26290	1.06	0.09	0.58	0.5833	0.770259	-6.67
248501_at	golgi SNARE protein	MEMB12	AT5G50440	1.06	0.08	0.58	0.583395	0.770318	-6.67
249359_at	putative protein unnamed ORF, Homo s	---	AT5G40470	-1.06	-0.08	-0.58	0.583484	0.770346	-6.67
253071_at	putative protein various predicted protei	---	AT4G37880	1.05	0.06	0.58	0.583464	0.770346	-6.67
259474_at	unknown protein ;supported by full-lengt	---	AT1G19130	1.12	0.16	0.58	0.583615	0.770475	-6.67
249926_at	E1, ubiquitin-like activating enzyme EC	ECR1	AT5G19180	-1.06	-0.08	-0.58	0.583714	0.770560	-6.67
255570_at	putative carrier protein similar to mitoch	ADNT1	AT4G01100	1.05	0.07	0.58	0.583856	0.770704	-6.67
265430_at	hypothetical protein predicted by genefir	---	AT2G20700	1.08	0.11	0.57	0.584076	0.770949	-6.67
252148_at	MS5-like protein	---	AT3G51280	1.05	0.07	0.57	0.584282	0.771147	-6.67
266663_at	putative receptor-like protein kinase ; su	---	AT2G25790	-1.07	-0.10	-0.57	0.584294	0.771147	-6.67
264324_at	myosin heavy chain MYA2 Strong simila	XIB	AT1G04160	-1.09	-0.13	-0.57	0.584334	0.771156	-6.67
246679_at	putative protein replication protein A1 -	---	---	-1.04	-0.06	-0.57	0.584491	0.771318	-6.67
245268_at	hypothetical protein ; supported by cDN	PRMT7	AT4G16570	1.09	0.12	0.57	0.584754	0.771487	-6.67
263063_s_a	putative peroxidase	---	AT2G18140 /	1.08	0.11	0.57	0.584711	0.771487	-6.67
263740_at	hypothetical protein predicted by gensca	RALFL14	AT2G20660	-1.06	-0.08	-0.57	0.584722	0.771487	-6.67

260417_at	putative chromomethylase similar to chr	CMT3	AT1G69770	1.10	0.14	0.57	0.58468	0.771487	-6.67
249082_at	legumin-like protein	CRA1	AT5G44120	1.04	0.06	0.57	0.584797	0.771499	-6.67
256040_at	hypothetical protein similar to putative C	---	AT1G07270	1.04	0.06	0.57	0.584849	0.771523	-6.67
266647_at	hypothetical protein predicted by grail	---	AT2G25870	-1.06	-0.09	-0.57	0.585029	0.771671	-6.67
254772_at	extensin-like protein extensin class 1 pr	---	AT4G13390	-1.03	-0.05	-0.57	0.585001	0.771671	-6.67
259648_at	hypothetical protein predicted by genem	---	---	-1.04	-0.05	-0.57	0.585118	0.771692	-6.67
256025_at	xylan endohydrolase, putative similar to	RXF12	AT1G58370	1.08	0.11	0.57	0.585118	0.771692	-6.67
257167_at	hypothetical protein predicted by genen	chr40	AT3G24340	-1.04	-0.06	-0.57	0.585146	0.771692	-6.67
254817_at	putative SWH1 protein SWH1 protein -	ORP2B	AT4G12460	-1.05	-0.07	-0.57	0.585332	0.771892	-6.67
261219_at	hypothetical protein predicted by genem	---	AT1G19980	1.05	0.08	0.57	0.585414	0.771941	-6.67
250466_at	putative protein TETRATRICOPEPTIDE	---	AT5G10090	1.04	0.06	0.57	0.585437	0.771941	-6.67
248429_at	putative protein contains similarity to pro	---	AT5G51770	1.10	0.14	0.57	0.585602	0.772114	-6.67
252593_at	putative protein tRNA intron endonuclea	ATSEN1	AT3G45590	-1.06	-0.08	-0.57	0.585732	0.772197	-6.67
250060_at	chromo domain protein polycomb-like p	TFL2	AT5G17690	-1.06	-0.08	-0.57	0.585731	0.772197	-6.67
262871_at	hypothetical protein predicted by genem	---	AT1G65010	1.15	0.20	0.57	0.58597	0.772358	-6.67
257171_at	unknown protein ; supported by full-leng	---	AT3G23760	-1.05	-0.07	-0.57	0.58599	0.772358	-6.67
265564_s_a	hypothetical protein predicted by gensca	---	---	1.05	0.07	0.57	0.585928	0.772358	-6.67
257307_at	myb-like transcription factor, putative co	MYB121	AT3G30210	-1.06	-0.09	-0.57	0.58591	0.772358	-6.67
267615_at	putative phytocyanin	---	AT2G26720	-1.07	-0.09	-0.57	0.58609	0.772446	-6.67
246864_at	cytochrome P450 GA3 ; supported by cI	GA3	AT5G25900	-1.09	-0.13	-0.57	0.586176	0.772505	-6.67
255171_at	hypothetical protein	---	AT4G07990	1.04	0.06	0.57	0.586236	0.772505	-6.67
246706_at	putative protein predicted proteins, Arat	---	---	1.08	0.11	0.57	0.586225	0.772505	-6.67
245972_at	putative protein predicted proteins, Arat	---	AT5G20680	-1.06	-0.08	-0.57	0.586409	0.772652	-6.67
262194_at	hypothetical protein similar to putative c	---	AT1G77930	-1.07	-0.10	-0.57	0.58645	0.772652	-6.67
253727_at	profilin 2 ; supported by full-length cDN	PFN2	AT4G29350	-1.05	-0.07	-0.57	0.586437	0.772652	-6.67
253957_at	putative protein ; supported by cDNA: g	AGP13	AT4G26320	-1.07	-0.10	-0.57	0.586625	0.772782	-6.67
264033_at	hypothetical protein predicted by gensca	---	AT2G03580	-1.05	-0.08	-0.57	0.586684	0.772782	-6.67
255448_at	hypothetical protein	---	AT4G02810	1.06	0.08	0.57	0.586612	0.772782	-6.67
261631_at	unknown protein contains similarity to pu	---	AT1G49940	-1.04	-0.06	-0.57	0.586671	0.772782	-6.67
257115_at	kinesin-like protein contains Pfam profile	---	AT3G20150	1.05	0.07	0.57	0.586839	0.772844	-6.67
257551_at	hypothetical protein contains similarity to	---	---	1.05	0.07	0.57	0.586897	0.772844	-6.67
245384_at	glycoprotein homolog ;supported by full-	---	AT4G16790	1.08	0.11	0.57	0.58678	0.772844	-6.67
255220_at	polyubiquitin (UBQ10) identical to GI:87	UBQ10	AT4G05320	-1.05	-0.08	-0.57	0.586901	0.772844	-6.67
254964_at	98b like protein 98b - Daucus carota (ca	---	AT4G11080	1.06	0.08	0.57	0.5868	0.772844	-6.67
257506_at	auxin-induced protein, putative similar t	---	AT1G29440	1.18	0.24	0.57	0.586951	0.772866	-6.67

264189_s_a	hypothetical protein similar to acyl-carrie	ACP3	AT1G54580 /	-1.06	-0.09	-0.57	0.587014	0.772904	-6.67
258845_at	unknown protein ; supported by full-leng	---	AT3G03150	-1.05	-0.07	-0.57	0.587176	0.773039	-6.67
259986_at	thaumatin-like protein similar to thaumat	---	AT1G75050	1.05	0.07	0.57	0.587185	0.773039	-6.67
262127_at	hypothetical protein predicted by genem	---	AT1G52550	-1.06	-0.09	-0.57	0.58738	0.773163	-6.67
258131_at	protein kinase, putative similar to GB:B/	---	AT3G24540	1.06	0.09	0.57	0.587348	0.773163	-6.67
248780_at	4-nitrophenylphosphatase-like protein ;s	ATPGLP2	AT5G47760	1.05	0.07	0.57	0.587333	0.773163	-6.67
253285_at	fatty acid elongase - like protein fatty ac	KCS16	AT4G34250	-1.09	-0.13	-0.57	0.587439	0.773196	-6.67
247471_at	putative protein receptor-like protein kir	ERL1	AT5G62230	1.05	0.07	0.57	0.587619	0.773315	-6.67
261668_at	2-isopropylmalate synthase, putative si	MAML-4	AT1G18500	-1.06	-0.08	-0.57	0.587631	0.773315	-6.67
248866_s_a	putative protein contains similarity to ca	---	AT5G46810 /	-1.04	-0.06	-0.57	0.587617	0.773315	-6.67
245036_at	putative SF16 protein {Helianthus annu	Iqd4	AT2G26410	1.04	0.06	0.57	0.588084	0.773419	-6.67
257468_at	hypothetical protein contains similarity to	---	AT1G47470	1.04	0.05	0.57	0.587901	0.773419	-6.67
246525_at	CONSTANS ;supported by full-length c	CO	AT5G15840	-1.05	-0.07	-0.57	0.588001	0.773419	-6.67
263113_at	unknown protein Belongs to PF|00583 A	---	AT1G03150	-1.04	-0.05	-0.57	0.588006	0.773419	-6.67
267253_at	putative serine carboxypeptidase I	---	AT2G22960	-1.04	-0.05	-0.57	0.588057	0.773419	-6.67
257472_at	hypothetical protein predicted by genem	---	AT1G56040	1.04	0.06	0.57	0.587792	0.773419	-6.67
262274_at	deaminase, putative similar to cytidine/(	TADA	AT1G68720	-1.04	-0.06	-0.57	0.587937	0.773419	-6.67
266612_at	22 kDa peroxisomal membrane protein	---	AT2G14860	-1.04	-0.06	-0.57	0.588038	0.773419	-6.67
260611_at	putative beta-1,3-glucanase, C terminal	---	AT2G43670	-1.06	-0.08	-0.57	0.587785	0.773419	-6.67
252989_at	putative pectinesterase pectinesterase	sks9	AT4G38420	-1.20	-0.27	-0.57	0.588003	0.773419	-6.67
260836_at	hypothetical protein predicted by gensca	---	---	-1.04	-0.05	-0.57	0.588058	0.773419	-6.67
250443_at	Pto kinase interactor - like protein Pto k	RBK1	AT5G10520	-1.24	-0.31	-0.57	0.588123	0.773426	-6.67
266682_at	putative disease resistance protein	---	AT2G19780	-1.08	-0.12	-0.57	0.588186	0.773465	-6.67
254807_at	putative protein	---	AT4G12700	1.06	0.09	0.57	0.588283	0.773549	-6.67
266619_at	similar to harpin-induced protein hin1 fro	---	AT2G35460	-1.06	-0.08	-0.57	0.588345	0.773585	-6.67
253379_at	putative protein glycogenin glucosyltran	PGSIP3	AT4G33330	-1.04	-0.06	-0.57	0.588432	0.773655	-6.67
258589_at	putative GDSL-motif lipase/acylhydrolas	LTL1	AT3G04290	-1.05	-0.08	-0.57	0.588603	0.773835	-6.67
248244_at	heat shock transcription factor HSF30-li	---	AT5G53640	-1.05	-0.07	-0.57	0.58873	0.773957	-6.67
253788_at	aromatic amino-acid decarboxylase - lik	---	AT4G28680	1.05	0.07	0.57	0.58885	0.774070	-6.67
252857_at	putative protein various predicted prote	---	AT4G39756	1.04	0.06	0.57	0.588919	0.774116	-6.67
258142_at	unknown protein	---	AT3G18120	1.05	0.08	0.57	0.588999	0.774177	-6.67
252215_at	kinesin -like protein KINESIN-LIKE PRO	KICP-02	AT3G50240	-1.14	-0.19	-0.57	0.589065	0.774219	-6.67
263898_at	SKP1 interacting partner 6 (SKIP6), put	SKIP6	AT2G21950	-1.05	-0.07	-0.57	0.589247	0.774414	-6.67
253199_at	clathrin assembly protein AP19 homolog	---	AT4G35410	-1.10	-0.14	-0.57	0.589327	0.774474	-6.67
260009_at	unknown protein ;supported by full-leng	---	AT1G67950	-1.07	-0.10	-0.57	0.589394	0.774478	-6.68

265222_at	putative endosomal protein ; supported	---	AT2G01970	1.04	0.05	0.57	0.58948	0.774478	-6.68
246301_at	calcium-dependent protein kinase	CPK13	AT3G51850	-1.04	-0.06	-0.57	0.589636	0.774478	-6.68
266203_at	putative phloem-specific lectin	AtPP2-B1	AT2G02230	-1.12	-0.16	-0.57	0.589604	0.774478	-6.68
256896_at	hypothetical protein predicted by genem	---	AT3G24630	1.09	0.13	0.57	0.589633	0.774478	-6.68
265995_at	hypothetical protein predicted by gensca	---	AT2G24140	1.04	0.06	0.57	0.589533	0.774478	-6.68
249392_at	peroxidase ATP26a	---	AT5G40150	-1.05	-0.07	-0.57	0.589544	0.774478	-6.68
257493_at	unknown protein	---	AT1G48180	1.07	0.10	0.57	0.58963	0.774478	-6.68
245203_at	hypothetical protein similar to protein pr	---	---	1.04	0.05	0.57	0.589604	0.774478	-6.68
265206_at	putative protease belongs to eukaryotic	---	AT2G36670	1.05	0.08	0.57	0.589992	0.774526	-6.68
263171_at	unknown protein	CCX4	AT1G54115	1.05	0.07	0.57	0.589833	0.774526	-6.68
250929_at	putative protein ; supported by cDNA: g	---	AT5G03290	1.07	0.10	0.57	0.589991	0.774526	-6.68
250519_at	GDSL-motif lipase/acylhydrolase-like pr	---	AT5G08460	1.05	0.07	0.57	0.590046	0.774526	-6.68
249366_at	dihydroxyacetone 3-phosphate reductas	---	AT5G40610	-1.13	-0.18	-0.57	0.589917	0.774526	-6.68
259151_at	kinesin-like protein similar to carboxy-te	---	AT3G10310	-1.06	-0.08	-0.57	0.589707	0.774526	-6.68
250640_at	putative protein protein kinase Xa21 - C	---	AT5G07150	1.09	0.12	0.57	0.589902	0.774526	-6.68
256571_at	hypothetical protein predicted by gensca	---	AT3G30730	1.04	0.05	0.57	0.590017	0.774526	-6.68
254366_s_a	LTR retrotransposon like protein retrovi	---	---	-1.04	-0.06	-0.57	0.589777	0.774526	-6.68
255097_at	predicted transposon protein similar to	---	---	1.06	0.08	0.57	0.589851	0.774526	-6.68
264252_at	putative GTP-binding protein, SAR1B s	ATSARA1	AT1G09180	-1.05	-0.06	-0.57	0.589961	0.774526	-6.68
245900_at	putative protein predicted proteins, Ara	---	AT5G11040	-1.05	-0.08	-0.57	0.590182	0.774660	-6.68
266508_at	hypothetical protein predicted by genefi	---	AT2G47920	1.06	0.08	0.57	0.590242	0.774695	-6.68
256801_at	cytochrome P450, putative similar to cy	CYP705A3	AT3G20940	1.04	0.06	0.56	0.590415	0.774877	-6.68
245865_at	hypothetical protein contains similarity t	---	AT1G58025	1.04	0.06	0.56	0.590609	0.775088	-6.68
251234_s_a	putative dTDP-glucose 4-6-dehydratase	UXS4	AT2G47650 /	-1.07	-0.10	-0.56	0.590721	0.775145	-6.68
266029_at	putative serine carboxypeptidase II	scpl38	AT2G05850	1.05	0.07	0.56	0.590704	0.775145	-6.68
245892_at	putative lipid transfer protein lipid transf	---	AT5G09370	1.07	0.09	0.56	0.590836	0.775235	-6.68
266301_at	putative MYB family transcription factor	AtMYB81	AT2G26960	1.07	0.09	0.56	0.590858	0.775235	-6.68
252539_at	putative protein	---	AT3G45730	1.06	0.08	0.56	0.591001	0.775379	-6.68
252085_s_a	serine-type carboxypeptidase like prote	scpl37	AT3G52000 /	-1.04	-0.05	-0.56	0.591044	0.775390	-6.68
257305_at	hypothetical protein predicted by genem	---	---	-1.05	-0.08	-0.56	0.591268	0.775639	-6.68
264267_at	hypothetical protein contains similarity t	---	AT1G60200	-1.05	-0.07	-0.56	0.591343	0.775693	-6.68
249957_at	putative protein predicted proteins, Ara	---	AT5G18900	1.06	0.08	0.56	0.591512	0.775852	-6.68
249172_at	putative protein similar to unknown prote	---	AT5G42950	1.05	0.07	0.56	0.59154	0.775852	-6.68
264247_at	potassium transporter, putative similar t	---	AT1G60160	1.10	0.14	0.56	0.591566	0.775852	-6.68
253449_at	putative protein hypothetical protein yjb	---	AT4G32700	1.04	0.06	0.56	0.591745	0.776042	-6.68

255369_at	putative NifU-like metallocluster assemb	ISU3	AT4G04080	1.05	0.07	0.56	0.591942	0.776255	-6.68
249383_at	putative protein putative DNA-binding p	PRE1	AT5G39860	-1.08	-0.12	-0.56	0.592308	0.776513	-6.68
250524_at	putative protein contains similarity to I-b	---	AT5G08520	-1.04	-0.06	-0.56	0.592287	0.776513	-6.68
255266_at	receptor protein kinase - like protein rec	---	AT4G05200	-1.05	-0.07	-0.56	0.592251	0.776513	-6.68
262798_at	putative SPL1-related protein similar to	SPL14	AT1G20980	-1.05	-0.07	-0.56	0.592214	0.776513	-6.68
260314_at	unknown protein similar to putative prote	---	AT1G63830	1.08	0.11	0.56	0.592282	0.776513	-6.68
265748_at	putative Athila retroelement ORF1 prote	---	---	-1.05	-0.06	-0.56	0.592509	0.776687	-6.68
267139_s_a	hypothetical protein predicted by genefir	---	AT2G38195 /	-1.04	-0.05	-0.56	0.592475	0.776687	-6.68
249960_at	squamosa promoter binding protein-like	SPL7	AT5G18830	-1.05	-0.06	-0.56	0.592602	0.776716	-6.68
256817_at	F-box protein family, AtFBW1 contains	---	AT3G21410	-1.05	-0.07	-0.56	0.592626	0.776716	-6.68
263811_at	putative acyl-CoA synthetase ; supporte	---	AT2G04350	-1.05	-0.07	-0.56	0.592633	0.776716	-6.68
246711_at	putative protein	---	AT5G28190	-1.04	-0.06	-0.56	0.592703	0.776763	-6.68
267145_at	putative acetyltransferase	ATMAK3	AT2G38130	-1.05	-0.07	-0.56	0.592759	0.776792	-6.68
262349_at	unknown protein ;supported by full-leng	---	AT2G48130	1.07	0.09	0.56	0.592845	0.776860	-6.68
245808_at	RNA binding protein identical to RNA bi	ATRBP1	AT1G58470	-1.06	-0.08	-0.56	0.592901	0.776888	-6.68
263613_at	unknown protein	---	AT2G25250	1.10	0.13	0.56	0.593045	0.776950	-6.68
258212_at	unknown protein contains Pfam profile:F	---	AT3G17920	-1.04	-0.05	-0.56	0.593042	0.776950	-6.68
255998_at	hypothetical protein contains similarity t	---	AT1G29780	-1.04	-0.06	-0.56	0.59305	0.776950	-6.68
246990_at	subtilisin-like serine protease ARA12 alr	ARA12	AT5G67360	-1.08	-0.11	-0.56	0.59312	0.776974	-6.68
254006_at	putative protein various predicted prote	---	AT4G26340	1.04	0.06	0.56	0.593137	0.776974	-6.68
252095_at	epoxide hydrolase-like protein epoxide	---	AT3G51000	1.06	0.08	0.56	0.593333	0.777172	-6.68
254044_at	putative xyloglucan endo-1,4-beta-D-glu	XTR9	AT4G25820	1.04	0.06	0.56	0.593356	0.777172	-6.68
259352_at	unknown protein	---	AT3G05170	1.08	0.11	0.56	0.593395	0.777178	-6.68
257886_at	pectinesterase, putative similar to pecti	---	AT3G17060	1.05	0.07	0.56	0.593447	0.777202	-6.68
254362_at	Expressed protein ; supported by full-ler	---	AT4G22160	1.06	0.09	0.56	0.593608	0.777368	-6.68
253556_at	serine/threonine-specific protein kinase	---	AT4G31100	1.04	0.05	0.56	0.593723	0.777475	-6.68
253090_at	beta-galactosidase like protein ; support	BGAL3	AT4G36360	1.21	0.27	0.56	0.594022	0.777495	-6.68
257962_at	hypothetical protein predicted by gensca	---	AT3G19790	1.08	0.11	0.56	0.593823	0.777495	-6.68
246351_at	unknown protein contains similarity to b	---	AT1G16570	-1.04	-0.06	-0.56	0.594008	0.777495	-6.68
249272_at	geranylgeranyl transferase alpha subun	---	AT5G41820	1.07	0.10	0.56	0.594114	0.777495	-6.68
251239_at	putative protein several hypothetical pro	---	AT3G62440	1.06	0.09	0.56	0.59386	0.777495	-6.68
254364_at	glycine-rich protein glycine-rich cell wal	---	AT4G22020	-1.05	-0.08	-0.56	0.594077	0.777495	-6.68
255405_s_a	hypothetical protein similar to A. thaliana	---	AT4G03440 /	-1.06	-0.08	-0.56	0.594074	0.777495	-6.68
249447_at	PTEN -like protein PTEN/MMAC1, Ratt	PTEN1	AT5G39400	1.07	0.10	0.56	0.593968	0.777495	-6.68
255212_at	putative athila transposon protein	---	---	1.04	0.05	0.56	0.593985	0.777495	-6.68

257595_at	hypothetical protein predicted by gensca	---	AT3G24750	1.04	0.06	0.56	0.59394	0.777495	-6.68
256508_at	unknown protein	---	AT1G75140	-1.04	-0.06	-0.56	0.594113	0.777495	-6.68
264305_at	Expressed protein ; supported by full-ler	LSH7	AT1G78815	-1.04	-0.06	-0.56	0.594247	0.777595	-6.68
255316_at	putative protein	---	---	1.04	0.06	0.56	0.594259	0.777595	-6.68
247808_at	contains similarity to unknown protein (g	ECT10	AT5G58190	1.04	0.05	0.56	0.594306	0.777613	-6.68
258352_at	putative auxin-induced protein similar to	IAA31	AT3G17600	-1.06	-0.08	-0.56	0.594343	0.777617	-6.68
250512_at	Expressed protein ; supported by full-ler	---	AT5G09995	1.05	0.07	0.56	0.594527	0.777724	-6.68
264234_at	hypothetical protein contains similarity t	---	AT1G54720	-1.04	-0.05	-0.56	0.594492	0.777724	-6.68
262359_at	disease resistance protein, putative sim	---	AT1G73060 /	1.05	0.07	0.56	0.594513	0.777724	-6.68
246717_at	putative protein	---	AT5G28920	-1.04	-0.06	-0.56	0.594644	0.777832	-6.68
262836_at	hypothetical protein predicted by genem	---	AT1G14680	1.04	0.05	0.56	0.594719	0.777885	-6.68
256551_at	unknown protein	---	---	-1.05	-0.07	-0.56	0.594805	0.777953	-6.68
246755_at	F-box protein family contains similarity t	---	AT5G27920	1.10	0.14	0.56	0.594906	0.778041	-6.68
254584_at	putative protein probable membrane pr	VPS54	AT4G19490	1.04	0.06	0.56	0.595165	0.778246	-6.68
248137_at	putative protein contains similarity to cyt	---	AT5G54950	1.05	0.06	0.56	0.595118	0.778246	-6.68
255377_at	hypothetical protein	---	AT4G03500	1.05	0.07	0.56	0.595162	0.778246	-6.68
264109_at	unknown protein	---	AT2G13720	1.04	0.06	0.56	0.5952	0.778246	-6.68
246427_at	ADP/ATP translocase-like protein adp/a	ER-ANT1	AT5G17400	1.05	0.08	0.56	0.595294	0.778325	-6.68
248326_at	Notchless protein homolog	---	AT5G52820	-1.06	-0.08	-0.56	0.595636	0.778504	-6.68
254179_at	putative protein various predicted prote	---	AT4G23910	-1.07	-0.09	-0.56	0.595498	0.778504	-6.68
247404_at	permease 1 - like protein permease 1, c	---	AT5G62890	-1.10	-0.14	-0.56	0.595612	0.778504	-6.68
267251_at	putative casein kinase II catalytic (alpha	---	AT2G23070	1.04	0.06	0.56	0.595596	0.778504	-6.68
248456_at	putative protein similar to unknown prote	---	AT5G51380	-1.03	-0.05	-0.56	0.595508	0.778504	-6.68
245179_at	putative protein similarity to predicted p	---	AT5G12400	1.05	0.07	0.56	0.595539	0.778504	-6.68
246067_at	membrane transporter - like protein whi	---	AT5G19410	-1.04	-0.06	-0.56	0.595686	0.778526	-6.68
253810_at	putative NADH dehydrogenase NADH d	NDB1	AT4G28220	-1.12	-0.16	-0.56	0.59583	0.778668	-6.68
253781_at	putative protein predicted protein, Arabi	---	AT4G28580	1.04	0.06	0.56	0.595892	0.778705	-6.68
246835_at	putative protein putative APC11 anapha	---	AT5G26640	1.05	0.08	0.56	0.596001	0.778803	-6.68
260844_at	peroxisomal targeting signal type 2 rece	PEX7	AT1G29260	-1.04	-0.06	-0.56	0.596078	0.778821	-6.68
253514_at	putative protein DNA-binding protein AB	---	AT4G31805	-1.04	-0.05	-0.56	0.596083	0.778821	-6.68
263465_at	hypothetical protein predicted by gensca	---	AT2G31940	1.06	0.08	0.56	0.596652	0.779519	-6.68
261459_at	O-methyltransferase, putative similar to	---	AT1G21100	-1.26	-0.33	-0.56	0.596728	0.779565	-6.68
259961_at	auxin-induced protein kinase, putative s	WAG1	AT1G53700	1.05	0.07	0.56	0.596755	0.779565	-6.68
260422_at	hypothetical protein predicted by genem	---	AT1G69630	1.04	0.06	0.55	0.596867	0.779667	-6.68
261306_at	regulatory protein HAL3B similar to GB:A	---	AT1G48610	1.05	0.06	0.55	0.596952	0.779733	-6.68

253210_at	putative protein predicted protein, Arabi	MTN2	AT4G34840	-1.05	-0.07	-0.55	0.596996	0.779742	-6.68
267276_at	hypothetical protein predicted by genscа	ASL5	AT2G30130	1.04	0.06	0.55	0.597027	0.779742	-6.68
262649_at	unknown protein contains similarity to xe	---	AT1G14040	1.13	0.17	0.55	0.597116	0.779814	-6.68
251693_at	putative protein several hypothetical pro	---	AT3G56550	1.05	0.07	0.55	0.597174	0.779844	-6.68
260312_at	putative disease resistance protein simil	---	AT1G63880	-1.06	-0.08	-0.55	0.597208	0.779844	-6.68
254400_at	kinesin-related protein katA ; supported	ATK1	AT4G21270	-1.04	-0.05	-0.55	0.597418	0.780029	-6.68
250099_at	unknown protein ; supported by cDNA:	---	AT5G17300	1.06	0.08	0.55	0.59741	0.780029	-6.68
253955_at	putative DNA binding protein DNA bind	ATRBP45(	AT4G27000	-1.07	-0.10	-0.55	0.597569	0.780181	-6.68
262644_at	beta-VPE nearly identical to beta-VPE G	BETA-VPE	AT1G62710	1.05	0.07	0.55	0.597682	0.780194	-6.68
264263_at	Expressed protein ; supported by full-ler	AtPP2-B15	AT1G09155	-1.04	-0.06	-0.55	0.597654	0.780194	-6.68
260105_at	hypothetical protein predicted by genscа	---	---	-1.04	-0.06	-0.55	0.597668	0.780194	-6.68
256272_at	unknown protein	---	AT3G12100	1.04	0.06	0.55	0.59782	0.780330	-6.68
255156_at	putative athila transposon protein	---	---	1.03	0.05	0.55	0.597872	0.780354	-6.68
261574_at	cytochrome P450, putative similar to cy	CYP78A8	AT1G01190	1.10	0.13	0.55	0.597922	0.780357	-6.68
259024_at	hypothetical protein predicted by genem	---	---	1.06	0.08	0.55	0.597977	0.780357	-6.68
263616_at	unknown protein	---	AT2G04680	1.05	0.07	0.55	0.597959	0.780357	-6.68
264498_at	Expressed protein ; supported by full-ler	DIS2	AT1G30825	1.05	0.07	0.55	0.598055	0.780360	-6.68
245960_at	subtilisin-like protein subtilisin/kexin iso	S1P	AT5G19660	1.03	0.05	0.55	0.598082	0.780360	-6.68
248511_at	Expressed protein ; supported by cDNA	CPI1	AT5G50375	-1.08	-0.11	-0.55	0.598036	0.780360	-6.68
258200_at	putative ATPase similar to ATPase II GE	---	AT3G13900	1.05	0.08	0.55	0.598165	0.780424	-6.68
245205_at	putative protein similarity to splicing fac	---	AT5G12280	1.06	0.09	0.55	0.598236	0.780472	-6.68
267128_at	putative acetone-cyanohydrin lyase	MES1	AT2G23620	-1.05	-0.08	-0.55	0.598511	0.780562	-6.68
265135_at	unknown protein similar to unknown pro	---	AT1G51270	1.05	0.06	0.55	0.598447	0.780562	-6.68
256403_at	unknown protein similar to SPOP (novel	BPM2	AT3G06190	-1.04	-0.06	-0.55	0.598483	0.780562	-6.68
264631_at	DegP protease contains similarity to De	DegP3	AT1G65630	-1.05	-0.07	-0.55	0.598448	0.780562	-6.68
253180_at	putative protein various predicted prote	---	AT4G35210	-1.04	-0.06	-0.55	0.598471	0.780562	-6.68
249714_at	unknown protein	---	---	-1.06	-0.08	-0.55	0.598469	0.780562	-6.68
266936_at	hypothetical protein predicted by genefir	---	AT2G18920	1.04	0.05	0.55	0.598637	0.780637	-6.68
250281_at	putative protein prdeicted proteins, Sch	---	AT5G13240	-1.06	-0.09	-0.55	0.598603	0.780637	-6.68
260527_at	unknown protein ;supported by full-leng	---	AT2G47270	1.17	0.23	0.55	0.598761	0.780709	-6.68
246394_at	myrosinase binding protein, putative sir	---	AT1G58160	1.04	0.05	0.55	0.598736	0.780709	-6.68
260969_at	beta-fructosidase identical to beta-fructo	ATBETAFI	AT1G12240	-1.11	-0.15	-0.55	0.598803	0.780720	-6.68
257166_at	hypothetical protein similar to putative N	---	AT3G24710	1.04	0.06	0.55	0.59896	0.780880	-6.68
252903_at	putative protein various predicted prote	---	AT4G39570	-1.08	-0.11	-0.55	0.599089	0.781003	-6.68
258997_at	hypothetical protein similar to unknown	---	AT3G01810	-1.08	-0.11	-0.55	0.599267	0.781042	-6.68

259124_at	floral homeotic protein AGL4 identical t	ספט-02	AT3G02310	1.04	0.05	0.55	0.599218	0.781042	-6.68
267249_at	hypothetical protein predicted by gensca	---	AT2G23040	-1.04	-0.06	-0.55	0.599249	0.781042	-6.68
259623_at	hypothetical protein predicted by genem	---	AT1G42700	-1.06	-0.08	-0.55	0.599289	0.781042	-6.68
255971_at	transposon related protein similar to retr	---	---	-1.04	-0.05	-0.55	0.599242	0.781042	-6.68
266403_at	putative acid phosphatase contains met	---	AT2G38600	-1.05	-0.07	-0.55	0.599439	0.781192	-6.68
248431_at	auxin-responsive GH3-like protein	---	AT5G51470	-1.05	-0.06	-0.55	0.59952	0.781208	-6.68
250976_at	putative protein various predicted prote	---	AT5G03060	-1.04	-0.06	-0.55	0.599519	0.781208	-6.68
261538_at	unknown protein ; supported by cDNA: g	---	AT1G01830	-1.10	-0.13	-0.55	0.599719	0.781411	-6.68
265747_s_a	hypothetical protein predicted by genefir	---	AT2G06570 /	-1.05	-0.07	-0.55	0.599744	0.781411	-6.68
264272_at	hypothetical protein contains similarity to	ANAC023	AT1G60280	1.04	0.05	0.55	0.599804	0.781444	-6.68
246411_at	hypothetical protein contains similarity to	---	AT1G57770	-1.10	-0.14	-0.55	0.600059	0.781687	-6.69
254237_at	cysteine proteinase contains similarity t	---	AT4G23520	-1.04	-0.05	-0.55	0.600041	0.781687	-6.69
249290_at	putative protein strong similarity to unkn	---	AT5G41060	1.08	0.11	0.55	0.60011	0.781709	-6.69
255007_at	putative oxidoreductase 11beta-hydroxy	AtHSD5	AT4G10020	-1.04	-0.06	-0.55	0.600224	0.781813	-6.69
259381_s_a	putative lectin contains Pfam profile: PF	NSP1	AT3G16390 /	-1.20	-0.27	-0.55	0.60032	0.781871	-6.69
267495_at	myb-like protein isolog	ETC2	AT2G30420	-1.09	-0.13	-0.55	0.600337	0.781871	-6.69
261050_at	transcription factor MYC7E, putative sir	---	AT1G01260	-1.07	-0.10	-0.55	0.600612	0.782184	-6.69
251614_at	hypothetical protein	---	AT3G57970	1.05	0.08	0.55	0.60082	0.782302	-6.69
255867_at	hypothetical protein predicted by gensca	---	AT2G30370	1.04	0.06	0.55	0.600773	0.782302	-6.69
267020_at	hypothetical protein predicted by gensca	---	AT2G39320	-1.05	-0.07	-0.55	0.600874	0.782302	-6.69
257810_at	TOM20, putative similar to TOM20 GB:	TOM20-1	AT3G27070	-1.05	-0.06	-0.55	0.60074	0.782302	-6.69
260514_at	hypothetical protein predicted by genem	---	AT1G51480	1.04	0.06	0.55	0.600856	0.782302	-6.69
251735_at	putative protein ferritin 2 precursor - Vig	ATFER3	AT3G56090	1.11	0.15	0.55	0.600978	0.782348	-6.69
246456_at	telomerase reverse transcriptase ; supp	ATTERT	AT5G16850	1.04	0.06	0.55	0.60097	0.782348	-6.69
262999_at	NAM protein, putative similar to NAM p	ANAC020	AT1G54330	-1.06	-0.09	-0.55	0.601079	0.782391	-6.69
249667_at	unknown protein	---	---	1.04	0.05	0.55	0.601077	0.782391	-6.69
263525_at	putative MADS-box protein	AGL61	AT2G24840	1.06	0.08	0.55	0.601238	0.782553	-6.69
250091_at	unknown protein	---	AT5G17340	1.04	0.05	0.55	0.601531	0.782860	-6.69
249852_at	monosaccharide transporter	STP11	AT5G23270	1.05	0.07	0.55	0.601571	0.782860	-6.69
245887_at	putative protein CD2 cytoplasmic doma	---	AT5G09390	-1.03	-0.05	-0.55	0.601577	0.782860	-6.69
255049_at	gibberellin-regulated protein GASA2 pre	GASA2	AT4G09610	-1.04	-0.05	-0.55	0.601779	0.783078	-6.69
251324_at	plasma membrane intrinsic protein 1a ;	PIP1A	AT3G61430	-1.05	-0.08	-0.55	0.601925	0.783179	-6.69
262219_at	hypothetical protein predicted by genem	---	AT1G74750	1.07	0.10	0.55	0.601919	0.783179	-6.69
261187_at	beta-1,3-glucanase precursor, putative	---	AT1G32860	-1.08	-0.11	-0.55	0.602183	0.783305	-6.69
264681_s_a	permease 1-like protein permease 1 - M	---	AT1G65550 /	1.05	0.08	0.55	0.602088	0.783305	-6.69

263580_at	hypothetical protein similar to hypothetic	---	AT2G17140	1.05	0.07	0.55	0.602194	0.783305	-6.69
257760_s_a	putative AC-like transposase similar to	---	---	1.04	0.06	0.55	0.602158	0.783305	-6.69
258119_at	putative MAP kinase similar to GB:AAD	MPK19	AT3G14720	-1.05	-0.07	-0.55	0.602094	0.783305	-6.69
245996_at	putative protein predicted non-LTR reve	---	---	-1.04	-0.06	-0.55	0.602326	0.783430	-6.69
251171_at	putative protein several hypothetical pro	---	AT3G63220	1.04	0.05	0.55	0.602358	0.783430	-6.69
257881_at	putative serine carboxypeptidase II simil	scpl33	AT3G17180	-1.06	-0.08	-0.55	0.602568	0.783435	-6.69
247049_at	putative protein similar to unknown prote	---	AT5G66440	1.22	0.28	0.55	0.60256	0.783435	-6.69
259398_at	hypothetical protein predicted by genem	PRA1.F1	AT1G17700	1.14	0.19	0.55	0.602415	0.783435	-6.69
266121_at	unknown protein ; supported by cDNA:	---	AT2G02160	-1.06	-0.08	-0.55	0.602549	0.783435	-6.69
254934_at	putative Ap2 domain protein DNA-bindi	CRF1	AT4G11140	-1.05	-0.07	-0.55	0.602531	0.783435	-6.69
259636_at	RNA pseudouridylate synthase, putativ	---	AT1G56345	-1.09	-0.13	-0.55	0.602484	0.783435	-6.69
252369_at	putative protein deoxycytidylate deamin	---	AT3G48540	1.04	0.06	0.55	0.602618	0.783455	-6.69
253845_at	putative protein myosin heavy chain chi	---	AT4G27980	1.03	0.05	0.55	0.60278	0.783576	-6.69
246166_at	putative protein	---	---	-1.05	-0.06	-0.55	0.602772	0.783576	-6.69
247079_at	Expressed protein ; supported by cDNA	AKRP	AT5G66055	-1.07	-0.09	-0.55	0.602838	0.783607	-6.69
248070_at	putative protein similar to unknown prote	---	AT5G55660	1.04	0.06	0.55	0.602914	0.783617	-6.69
246810_at	putative protein many predicted protein	---	---	1.04	0.06	0.55	0.602889	0.783617	-6.69
261007_at	hypothetical protein similar to reticuline	---	AT1G26400	-1.03	-0.05	-0.55	0.603199	0.783942	-6.69
246388_at	hypothetical protein predicted by gensca	---	AT1G77405	1.06	0.08	0.55	0.603248	0.783961	-6.69
260994_at	hypothetical protein contains similarity to	---	AT1G12130	-1.05	-0.07	-0.55	0.603335	0.784029	-6.69
250748_at	AtPH1-like protein ;supported by full-ler	---	AT5G05710	1.05	0.07	0.54	0.603513	0.784216	-6.69
252889_at	hypothetical protein	---	AT4G39380	1.05	0.08	0.54	0.603687	0.784398	-6.69
263120_at	cytochrome P450, putative similar to cy	CYP708A3	AT1G78490	1.28	0.35	0.54	0.603909	0.784508	-6.69
246047_at	putative protein predicted proteins, Arat	---	---	1.04	0.06	0.54	0.603811	0.784508	-6.69
267625_at	putative RNA-binding protein	---	AT2G42240	-1.04	-0.06	-0.54	0.603873	0.784508	-6.69
247915_at	putative protein similar to unknown prote	---	AT5G57570	-1.04	-0.06	-0.54	0.6039	0.784508	-6.69
255390_at	hypothetical protein similar to A. thalian	---	---	1.04	0.06	0.54	0.603971	0.784543	-6.69
249724_at	disease resistance protein	---	AT5G35450	1.03	0.05	0.54	0.604067	0.784623	-6.69
260418_s_a	hypothetical protein predicted by genefir	COX19-1	AT1G66590 /	-1.11	-0.15	-0.54	0.604118	0.784645	-6.69
258276_at	putative signal peptidase 21kDa subunit	---	AT3G15710	-1.05	-0.08	-0.54	0.604169	0.784664	-6.69
255876_at	hypothetical protein	---	AT2G40480	-1.10	-0.13	-0.54	0.604201	0.784664	-6.69
264124_at	hypothetical protein predicted by genem	ATOCT2	AT1G79360	1.05	0.07	0.54	0.604294	0.784739	-6.69
251242_at	ARGININE/SERINE-RICH SPLICING FA	RSP31	AT3G61860	-1.04	-0.06	-0.54	0.604694	0.784991	-6.69
254023_at	putative protein hypothetical protein T2	---	AT4G25770	-1.05	-0.07	-0.54	0.604606	0.784991	-6.69
246907_at	AtBgamma - like protein B' regulatory s	---	AT5G25510	-1.05	-0.08	-0.54	0.604548	0.784991	-6.69

245454_at	disease resistance RPP5 like protein	---	AT4G16920	1.04	0.05	0.54	0.604685	0.784991	-6.69
252830_at	putative protein 70K peroxisomal memb	PXA1	AT4G39850	-1.04	-0.05	-0.54	0.604692	0.784991	-6.69
257255_at	hypothetical protein contains Pfam profil	---	AT3G21960	-1.04	-0.06	-0.54	0.604627	0.784991	-6.69
259492_at	hypothetical protein predicted by genem	---	AT1G15830	-1.07	-0.10	-0.54	0.604845	0.785008	-6.69
246760_at	putative protein predicted proteins, Cae	---	AT5G27970	1.04	0.06	0.54	0.604879	0.785008	-6.69
266068_at	putative geranylgeranyl pyrophosphate s	GGPS4	AT2G18640	-1.05	-0.07	-0.54	0.604856	0.785008	-6.69
257098_at	hypothetical protein	---	---	-1.04	-0.06	-0.54	0.604746	0.785008	-6.69
261237_at	hypothetical protein contains similarity to	---	AT1G32980	1.04	0.06	0.54	0.6048	0.785008	-6.69
249887_at	putative protein similar to unknown prote	---	AT5G22310	1.14	0.19	0.54	0.605209	0.785391	-6.69
255229_at	F-box protein family, AtFBL22 contains	---	AT4G05490	1.03	0.05	0.54	0.605272	0.785428	-6.69
251863_at	kinesin-like protein kinesin, Syncephala	MRH2	AT3G54870	1.04	0.05	0.54	0.605334	0.785464	-6.69
267143_at	putative peptide/amino acid transporter	---	AT2G38100	-1.05	-0.06	-0.54	0.605383	0.785483	-6.69
258222_at	putative zinc finger protein contains Pfar	---	AT3G15680	-1.09	-0.12	-0.54	0.605493	0.785546	-6.69
261374_at	hypothetical protein contains thioredoxin	---	AT1G52990	-1.04	-0.05	-0.54	0.605501	0.785546	-6.69
267575_at	unknown protein predicted by genscan;	---	AT2G30690	1.05	0.06	0.54	0.605589	0.785616	-6.69
257326_s_a	hypothetical protein	---	---	-1.05	-0.07	-0.54	0.605754	0.785741	-6.69
264646_at	hypothetical protein Similar to Homo cop	BON3	AT1G08860	1.04	0.06	0.54	0.605749	0.785741	-6.69
246583_at	protein kinase -like protein Ste-20 relate	---	AT5G14720	-1.05	-0.08	-0.54	0.605814	0.785773	-6.69
252248_at	putative protein resistance gene Hcr2-5	AtRLP44	AT3G49750	-1.08	-0.11	-0.54	0.605871	0.785803	-6.69
265531_at	hypothetical protein predicted by genscar	AtGRF6	AT2G06200	1.04	0.06	0.54	0.605936	0.785843	-6.69
253483_at	putative protein anthranilate N-hydroxyc	---	AT4G31910	1.08	0.11	0.54	0.606009	0.785893	-6.69
266167_at	unknown protein ;supported by full-leng	YLS5	AT2G38860	1.16	0.21	0.54	0.606131	0.786007	-6.69
261539_at	hypothetical protein predicted by genem	---	AT1G01840	-1.05	-0.07	-0.54	0.606363	0.786184	-6.69
245541_at	hypothetical protein	---	AT4G15240	-1.07	-0.09	-0.54	0.606372	0.786184	-6.69
266373_x_a	putative retroelement pol polyprotein	---	---	1.05	0.07	0.54	0.606364	0.786184	-6.69
255285_at	putative protein A. thaliana hypothetical	---	AT4G04630	-1.15	-0.20	-0.54	0.60662	0.786462	-6.69
260563_at	putative glucosyltransferase	UGT74F1	AT2G43840	-1.05	-0.07	-0.54	0.606972	0.786794	-6.69
265351_at	putative MADS-box protein AGL17	AGL17	AT2G22630	1.05	0.07	0.54	0.607015	0.786794	-6.69
256463_s_a	unknown protein	---	---	1.04	0.06	0.54	0.606936	0.786794	-6.69
252427_at	hypothetical protein	---	AT3G47640	1.09	0.13	0.54	0.606998	0.786794	-6.69
253333_at	2-dehydro-3-deoxyphosphoheptonate al	DHS2	AT4G33510	1.05	0.06	0.54	0.607155	0.786810	-6.69
251563_at	anthranilate phosphoribosyltransferase-	---	AT3G57880	1.08	0.11	0.54	0.60707	0.786810	-6.69
251775_s_a	delta-1-pyrroline-5-carboxylate syntheta	P5CS1	AT2G39800 /	1.10	0.14	0.54	0.607142	0.786810	-6.69
250759_at	unknown protein	---	AT5G06020	-1.04	-0.05	-0.54	0.607165	0.786810	-6.69
260750_at	light repressible receptor protein kinase	---	AT1G49100	-1.04	-0.06	-0.54	0.607299	0.786895	-6.69

256830_at	eukaryotic translation initiation factor 3	TIF3C2	AT3G22860	1.05	0.07	0.54	0.6073	0.786895	-6.69
264555_at	hypothetical protein predicted by gensca	---	AT1G09360	1.04	0.06	0.54	0.607391	0.786969	-6.69
258641_at	unknown protein ;supported by full-leng	---	AT3G08030	1.16	0.22	0.54	0.60753	0.787077	-6.69
255940_at	prolyl endopeptidase, putative similar to	---	AT1G20380	-1.04	-0.05	-0.54	0.607544	0.787077	-6.69
255207_at	Expressed protein ; supported by full-ler	---	AT4G07515	1.03	0.05	0.54	0.607703	0.787239	-6.69
258517_at	galactose kinase identical to GB:AAB94	GALK	AT3G06580	1.05	0.06	0.54	0.608001	0.787537	-6.69
259558_at	hypothetical protein	WAK5	AT1G21230	-1.05	-0.07	-0.54	0.608002	0.787537	-6.69
258483_at	putative mannose-6-phosphate isomera	MEE31	AT3G02570	-1.07	-0.10	-0.54	0.608154	0.787547	-6.69
257285_at	unknown protein	---	AT3G29760	-1.06	-0.09	-0.54	0.608138	0.787547	-6.69
259042_at	RGA1-like protein similar to RGA1 prote	RGL2	AT3G03450	-1.07	-0.09	-0.54	0.608135	0.787547	-6.69
246663_at	putative protein	---	AT5G35300	1.04	0.06	0.54	0.608182	0.787547	-6.69
254676_at	putative protein Hypothetical protein YD	---	AT4G18460	1.05	0.08	0.54	0.608116	0.787547	-6.69
266213_s_a	Mutator-like transposase similar to MUF	---	---	1.04	0.06	0.54	0.608313	0.787671	-6.69
260863_at	hypothetical protein predicted by genem	---	---	1.07	0.09	0.54	0.608439	0.787789	-6.69
255191_at	may be a pseudogene	---	---	1.04	0.05	0.54	0.608507	0.787789	-6.69
261473_at	hypothetical protein similar to putative D	---	AT1G14490	-1.08	-0.11	-0.54	0.608501	0.787789	-6.69
255962_at	glycine-rich RNA-binding protein, putati	---	AT1G22330	1.17	0.23	0.54	0.608677	0.787886	-6.69
264255_at	putative SF2/ASF splicing modulator, S	---	AT1G09140	1.06	0.09	0.54	0.608721	0.787886	-6.69
246201_at	minor allergen ;supported by full-length	---	AT4G36750	-1.04	-0.05	-0.54	0.608661	0.787886	-6.69
267634_at	putative actin	---	AT2G42100	1.04	0.05	0.54	0.608709	0.787886	-6.69
254856_at	putative ribosomal protein (fragment) rib	---	AT4G12160	-1.04	-0.06	-0.54	0.60879	0.787931	-6.69
262367_at	hypothetical protein contains similarity to	VPS46.2	AT1G73030	-1.05	-0.08	-0.54	0.608828	0.787936	-6.69
252758_at	putative protein several hypothetical pro	---	---	1.05	0.07	0.54	0.608925	0.787972	-6.69
247396_at	putative protein predicted proteins, Ory	---	AT5G62930	1.04	0.05	0.54	0.608904	0.787972	-6.69
254456_at	putative protein ribophorin II precursor,	HAP6	AT4G21150	1.05	0.07	0.54	0.609062	0.788059	-6.69
254383_at	hypothetical protein	---	AT4G21950	-1.04	-0.06	-0.54	0.609043	0.788059	-6.69
252766_at	putative protein hypothetical proteins - A	---	---	1.06	0.08	0.54	0.609117	0.788086	-6.69
259912_at	hypothetical protein	iqd8	AT1G72670	1.05	0.07	0.54	0.609308	0.788285	-6.69
266027_at	En/Spm-like transposon protein related	---	---	1.04	0.05	0.54	0.60934	0.788285	-6.69
265022_at	putative agp1 similar to GB:CAA48293;s	BCP1	AT1G24520	1.06	0.08	0.54	0.609556	0.788520	-6.69
252932_at	putative proton pump vacuolar proton A	VHA-A3	AT4G39080	1.04	0.06	0.54	0.609674	0.788628	-6.69
262977_at	transcription factor, putative similar to D	---	AT1G75490	-1.05	-0.07	-0.54	0.609742	0.788670	-6.69
256138_at	Nt-gh3 deduced protein, putative simila	---	AT1G48670	-1.06	-0.08	-0.54	0.60978	0.788676	-6.69
252003_at	hypothetical protein emm32, Streptococ	ZPR3	AT3G52770	-1.04	-0.06	-0.54	0.609829	0.788695	-6.69
266953_at	hypothetical protein predicted by gensca	---	AT2G34540	1.04	0.06	0.53	0.609899	0.788700	-6.69

250052_at	putative protein predicted proteins, Arat	---	AT5G17830	-1.05	-0.07	-0.53	0.609919	0.788700	-6.69
265693_at	putative poly(A) binding protein	---	AT2G24350	-1.05	-0.07	-0.53	0.609938	0.788700	-6.69
256701_at	transcription initiation factor IIF, beta su	---	AT3G52270	-1.05	-0.07	-0.53	0.610015	0.788756	-6.69
252912_at	ribosomal protein S25 ribosomal protein	---	AT4G39200	-1.07	-0.10	-0.53	0.61006	0.788769	-6.69
265800_at	similar to ch-TOG protein from Homo sa	MOR1	AT2G35630	-1.05	-0.07	-0.53	0.610408	0.789174	-6.69
248116_at	putative protein contains similarity to MY	MYB120	AT5G55020	1.05	0.08	0.53	0.610599	0.789376	-6.69
255959_at	phosphatidylinositol-4-phosphate 5-kina	ATPIP5K1	AT1G21980	-1.16	-0.22	-0.53	0.610737	0.789422	-6.69
247045_at	putative protein similar to unknown prote	---	AT5G66930	-1.05	-0.08	-0.53	0.610822	0.789422	-6.69
266111_at	unknown protein	---	AT2G02060 /	-1.04	-0.06	-0.53	0.610842	0.789422	-6.69
267291_at	putative C2H2-type zinc finger protein lil	---	AT2G23740	1.08	0.11	0.53	0.610842	0.789422	-6.69
263094_at	hypothetical protein predicted by gensca	---	AT2G16020	-1.05	-0.06	-0.53	0.610826	0.789422	-6.69
245762_at	ATP-dependent DNA helicase RecQ, p	---	AT1G27880	1.03	0.05	0.53	0.610756	0.789422	-6.69
261359_at	hypothetical protein predicted by gensca	---	---	-1.04	-0.06	-0.53	0.610996	0.789577	-6.69
262587_at	unknown protein Contains PF|00561 alp	---	AT1G15490	1.08	0.11	0.53	0.611031	0.789578	-6.69
265397_at	hypothetical protein predicted by gensca	---	---	1.04	0.05	0.53	0.611631	0.790308	-6.70
250521_at	selenium-binding protein-like	---	AT5G08490	1.04	0.06	0.53	0.611729	0.790389	-6.70
262130_at	hypothetical protein predicted by genem	---	AT1G02890	-1.05	-0.07	-0.53	0.611841	0.790490	-6.70
259286_at	hypothetical protein similar to hypothetic	BSMT1	AT3G11480	-1.43	-0.51	-0.53	0.612443	0.790909	-6.70
264179_at	hypothetical protein predicted by genem	---	AT1G02180	1.07	0.10	0.53	0.61226	0.790909	-6.70
249637_at	hypothetical protein	---	AT5G36900	-1.04	-0.06	-0.53	0.612323	0.790909	-6.70
258732_at	putative alkaline/neutral invertase simila	---	AT3G05820	1.04	0.06	0.53	0.612357	0.790909	-6.70
AFFX-CreX-	Bacteriophage P1 /GEN=cre /DB_XREF	---	---	1.09	0.13	0.53	0.612398	0.790909	-6.70
265508_at	hypothetical protein predicted by gensca	---	AT2G15930	1.04	0.05	0.53	0.612431	0.790909	-6.70
247512_at	putative protein predicted protein, Arabi	---	AT5G61720	1.04	0.05	0.53	0.612348	0.790909	-6.70
251027_at	putative protein hypothetical protein F7/	---	AT5G02210	-1.03	-0.05	-0.53	0.612285	0.790909	-6.70
258158_at	acid phosphatase type 5 identical to GB	PAP17	AT3G17790	1.14	0.18	0.53	0.612507	0.790946	-6.70
259209_at	putative RNA-binding protein identical t	---	AT3G09160	1.03	0.05	0.53	0.612593	0.790974	-6.70
247067_at	putative protein strong similarity to unkn	---	AT5G66950	-1.06	-0.09	-0.53	0.612597	0.790974	-6.70
246941_at	putative protein several hypothetical pro	---	AT5G25415	1.04	0.06	0.53	0.612731	0.791025	-6.70
263611_at	hypothetical protein predicted by gensca	---	AT2G16450	1.04	0.05	0.53	0.612741	0.791025	-6.70
246812_at	putative protein predicted proteins, Arat	---	---	-1.04	-0.05	-0.53	0.612683	0.791025	-6.70
260690_at	RING finger protein, putative similar to (	NHL8	AT1G32340	1.03	0.05	0.53	0.612845	0.791091	-6.70
258442_at	hypothetical protein predicted by genem	---	AT3G01015	1.04	0.06	0.53	0.612861	0.791091	-6.70
263820_at	hypothetical protein predicted by gensca	---	---	-1.07	-0.09	-0.53	0.612983	0.791203	-6.70
250911_at	SERINE/THREONINE-PROTEIN KINAS	CTR1	AT5G03730	1.06	0.08	0.53	0.613169	0.791398	-6.70

251441_at	SKP1/ASK1 (At5), putative similar to SK	ASK5	AT3G60020	1.04	0.05	0.53	0.613283	0.791501	-6.70
252711_at	lipid-transfer protein-like protein nonspe	---	AT3G43720	1.15	0.21	0.53	0.613381	0.791582	-6.70
253034_at	calcium-dependent protein kinase -like	CPK26	AT4G38230	1.05	0.06	0.53	0.613472	0.791656	-6.70
248259_at	proline-rich cell wall protein-like ;suppor	---	AT5G53330	1.04	0.06	0.53	0.613543	0.791686	-6.70
256080_at	high mobility group protein (HMG1), put	---	AT1G20690	1.04	0.05	0.53	0.613565	0.791686	-6.70
248489_at	unknown protein	---	AT5G51090	1.04	0.05	0.53	0.613739	0.791820	-6.70
266427_at	hypothetical protein predicted by gensca	---	AT2G07170	1.05	0.07	0.53	0.613719	0.791820	-6.70
267350_at	putative DNA-directed RNA polymerase	NRPD1B	AT2G40030	1.05	0.07	0.53	0.613804	0.791845	-6.70
254202_at	putative protein hydroxymuconic semia	---	AT4G24140	1.07	0.10	0.53	0.613827	0.791845	-6.70
257442_at	legumin-like protein contains a 11-S pla	---	AT2G28680	1.06	0.09	0.53	0.613996	0.792017	-6.70
261795_at	unknown protein ; supported by cDNA: g	---	AT1G16010	-1.04	-0.05	-0.53	0.614037	0.792025	-6.70
267092_at	unknown protein ;supported by full-leng	AUX1	AT2G38120	1.10	0.14	0.53	0.614097	0.792054	-6.70
260926_at	unknown protein	GLTP2	AT1G21360	1.04	0.06	0.53	0.614128	0.792054	-6.70
247824_at	putative protein Na+/H+-exchanging pr	CHX25	AT5G58460	-1.05	-0.07	-0.53	0.61427	0.792135	-6.70
252826_at	hypothetical protein ; supported by cDN	---	AT4G40050	-1.04	-0.06	-0.53	0.61433	0.792135	-6.70
257405_at	putative calmodulin similar to EST gb|AA	---	AT1G24620	-1.04	-0.05	-0.53	0.614299	0.792135	-6.70
252962_at	splicing factor - like protein splicing fact	---	AT4G38780	-1.05	-0.06	-0.53	0.614319	0.792135	-6.70
251014_at	putative protein fimbriae-associated pro	---	AT5G02520	-1.04	-0.05	-0.53	0.61444	0.792232	-6.70
255935_at	hypothetical protein contains Pfam profil	---	AT1G12700	-1.05	-0.07	-0.53	0.614521	0.792292	-6.70
259007_at	putative MYB family transcription factor	MYB3R-3	AT3G09370	-1.06	-0.08	-0.53	0.614593	0.792325	-6.70
247719_at	Expressed protein ; supported by full-ler	---	AT5G59305	-1.05	-0.06	-0.53	0.614616	0.792325	-6.70
260452_at	putative SRF-type transcription factor co	---	AT1G72350	1.07	0.09	0.53	0.614671	0.792350	-6.70
252744_at	putative protein hypothetical protein At2	---	AT3G43310	-1.04	-0.06	-0.53	0.614709	0.792354	-6.70
250698_at	putative protein similar to unknown prote	---	AT5G06810	-1.04	-0.05	-0.53	0.614784	0.792407	-6.70
257302_at	hypothetical protein predicted by genem	---	AT3G30220	1.04	0.05	0.53	0.614882	0.792444	-6.70
263358_x_a	hypothetical protein similar to hypothetic	---	---	1.04	0.06	0.53	0.614864	0.792444	-6.70
261956_at	oxidoreductase, putative similar to PRO	---	AT1G64590	1.08	0.11	0.53	0.615013	0.792552	-6.70
256465_at	hypothetical protein predicted by gensca	---	AT1G32570	-1.06	-0.09	-0.53	0.615035	0.792552	-6.70
264473_at	hypothetical protein predicted by genem	---	AT1G67180	1.08	0.12	0.53	0.61508	0.792565	-6.70
245402_at	putative protein	---	AT4G17585	-1.05	-0.07	-0.53	0.615137	0.792593	-6.70
265543_at	unknown protein	---	AT2G28270	-1.03	-0.05	-0.53	0.615202	0.792611	-6.70
247113_at	unknown protein ;supported by full-lengt	---	AT5G65960	1.04	0.06	0.53	0.615255	0.792611	-6.70
261121_at	hypothetical protein predicted by genem	---	AT1G75340	-1.03	-0.05	-0.53	0.615237	0.792611	-6.70
258859_at	Expressed protein ; supported by full-ler	---	AT3G02120	1.03	0.05	0.53	0.615407	0.792639	-6.70
263905_at	putative beta-fructofuranosidase (inverta	AtcwINV4	AT2G36190	1.06	0.09	0.53	0.615364	0.792639	-6.70

262628_at	glucan synthase, putative similar to glu	ATGSL07	AT1G06490	-1.06	-0.08	-0.53	0.615402	0.792639	-6.70
263139_at	hypothetical protein similar to hypothetic	---	AT1G65110	1.03	0.05	0.53	0.615416	0.792639	-6.70
256918_s_a	hypothetical protein similar to hypothetic	---	AT3G18960 /	1.06	0.08	0.53	0.615606	0.792727	-6.70
246534_at	putative protein several hypothetical pro	---	AT5G15890	1.06	0.08	0.53	0.615558	0.792727	-6.70
254338_s_a	pectate lyase like protein pectate lyase,	---	AT4G22080 /	1.03	0.05	0.53	0.615537	0.792727	-6.70
255313_at	putative transposon protein	---	---	-1.05	-0.06	-0.53	0.615623	0.792727	-6.70
256371_at	hypothetical protein	---	AT1G66770	1.04	0.06	0.53	0.615698	0.792779	-6.70
258503_at	unknown protein	---	AT3G02500	1.05	0.07	0.53	0.615779	0.792839	-6.70
259941_s_a	putative DEAD/DEAH box helicase cont	---	AT1G71280 /	1.04	0.06	0.53	0.615877	0.792886	-6.70
245046_at	putative membrane transporter ; suppo	PDE135	AT2G26510	1.05	0.06	0.53	0.615886	0.792886	-6.70
265095_at	putative cruciferin 12S seed storage pr	CRU2	AT1G03880	1.04	0.06	0.53	0.615995	0.792982	-6.70
252335_at	putative protein putative protein - Arabi	---	AT3G48860	1.05	0.07	0.53	0.616088	0.793057	-6.70
246720_at	putative protein predicted proteins, Ara	---	AT5G28950	-1.03	-0.04	-0.53	0.616129	0.793065	-6.70
246924_at	putative protein KIAA0332 - Homo sapi	---	AT5G25060	1.03	0.05	0.53	0.61626	0.793189	-6.70
245883_at	ribosomal protein S15-like ribosomal pr	---	AT5G09500	1.04	0.05	0.53	0.616316	0.793216	-6.70
262045_at	hypothetical protein predicted by genem	---	AT1G80240 /	-1.07	-0.10	-0.52	0.616441	0.793333	-6.70
256153_at	ubiquitin-like (UBQ12), putative similar	UBQ12	AT1G55060	-1.05	-0.07	-0.52	0.61649	0.793351	-6.70
254343_at	PRH26 protein ;supported by full-length	אפר-03	AT4G21990	-1.14	-0.19	-0.52	0.61668	0.793451	-6.70
251366_at	putative protein several hypothetical pro	---	AT3G61340	1.04	0.06	0.52	0.616707	0.793451	-6.70
258581_at	hypothetical protein predicted by gensca	---	AT3G04160	-1.04	-0.06	-0.52	0.616685	0.793451	-6.70
258290_at	hypothetical protein predicted by genem	---	AT3G23460	-1.03	-0.05	-0.52	0.616644	0.793451	-6.70
247459_at	putative protein embryo-specific protein	---	AT5G62200	-1.04	-0.06	-0.52	0.616811	0.793540	-6.70
246385_at	mitotic cyclin a2-type, putative similar to	CYCA1;2	AT1G77390	1.11	0.15	0.52	0.617029	0.793776	-6.70
264306_at	unknown protein predicted by genemark	---	AT1G78890	1.05	0.07	0.52	0.617081	0.793798	-6.70
263743_at	coatomer alpha subunit	---	AT2G21390	-1.04	-0.05	-0.52	0.61712	0.793803	-6.70
265914_at	En/Spm-like transposon protein related	---	---	1.03	0.05	0.52	0.617306	0.793975	-6.70
256278_at	unknown protein ; supported by full-leng	---	AT3G12130	-1.04	-0.05	-0.52	0.617375	0.793975	-6.70
254542_s_a	putative LTR retrotransposon Brassica	---	---	-1.03	-0.05	-0.52	0.617376	0.793975	-6.70
266605_at	putative SNF2 subfamily transcriptional	BRM	AT2G46020	-1.04	-0.06	-0.52	0.617393	0.793975	-6.70
266055_at	hypothetical protein predicted by gensca	---	AT2G40650	1.05	0.07	0.52	0.617539	0.794118	-6.70
257204_at	Expressed protein ; supported by full-ler	RALFL24	AT3G23805	1.12	0.16	0.52	0.617633	0.794174	-6.70
257210_at	hypothetical protein	TTL2	AT3G14950	1.03	0.05	0.52	0.617679	0.794174	-6.70
258749_at	hypothetical protein predicted by gensca	---	AT3G05760	1.05	0.07	0.52	0.617687	0.794174	-6.70
265983_at	putative homeodomain transcription fact	HB-2	AT2G18550	-1.04	-0.05	-0.52	0.617756	0.794191	-6.70
263429_at	putative aspartate aminotransferase ;su	AAT	AT2G22250	1.15	0.21	0.52	0.617805	0.794191	-6.70

246277_at	hypothetical protein	---	AT4G36460	-1.05	-0.07	-0.52	0.617793	0.794191	-6.70
263045_at	hypothetical protein predicted by gensca	---	AT2G05370	1.04	0.06	0.52	0.617893	0.794205	-6.70
252306_at	hypothetical protein	---	AT3G49270	1.03	0.05	0.52	0.61803	0.794205	-6.70
261217_at	hypothetical protein contains similarity t	UBP11	AT1G32850	1.03	0.05	0.52	0.617973	0.794205	-6.70
254518_at	downy mildew resistance-like protein d	---	AT4G19910	1.04	0.06	0.52	0.617934	0.794205	-6.70
265840_at	hypothetical protein predicted by gensca	---	AT2G14530	-1.05	-0.08	-0.52	0.618025	0.794205	-6.70
246570_at	putative protein nonmuscle myosin hea	---	AT5G14990	1.04	0.06	0.52	0.61806	0.794205	-6.70
256895_at	zinc-finger protein, putative almost iden	---	---	1.04	0.06	0.52	0.617989	0.794205	-6.70
258568_at	unknown protein contains Pfam profile:F	---	AT3G04470	-1.04	-0.06	-0.52	0.618458	0.794441	-6.70
245040_at	hypothetical protein predicted by genefi	---	AT2G26520	1.05	0.07	0.52	0.618462	0.794441	-6.70
256626_at	hypothetical protein, 5' partial	---	AT3G20015	-1.11	-0.15	-0.52	0.618468	0.794441	-6.70
259991_at	putative S-adenosyl-L-methionine:salicy	---	AT1G68040	1.04	0.06	0.52	0.618439	0.794441	-6.70
249665_at	unknown protein	---	AT5G35830	-1.05	-0.07	-0.52	0.618487	0.794441	-6.70
265117_at	putative proline-rich cell wall protein (pi	---	AT1G62500	1.06	0.09	0.52	0.618306	0.794441	-6.70
256554_at	hypothetical protein similar to putative g	---	---	-1.06	-0.08	-0.52	0.61836	0.794441	-6.70
248281_at	unknown protein	---	AT5G52980	1.04	0.05	0.52	0.618622	0.794525	-6.70
248370_at	homeodomain transcription factor-like	HDG7	AT5G52170	-1.05	-0.08	-0.52	0.618601	0.794525	-6.70
251724_at	putative protein	---	AT3G56250	-1.04	-0.06	-0.52	0.618687	0.794564	-6.70
247181_at	putative protein similar to unknown prote	---	AT5G65370	1.04	0.06	0.52	0.618739	0.794586	-6.70
263485_at	putative villin ; supported by cDNA: gi_3	VLN1	AT2G29890	1.04	0.06	0.52	0.618905	0.794710	-6.70
265294_at	Mutator-like transposase similar to MUF	---	---	1.05	0.07	0.52	0.618898	0.794710	-6.70
254600_at	4-coumarate-CoA ligase - like 4-couma	---	AT4G19010	-1.08	-0.10	-0.52	0.619085	0.794896	-6.70
267207_at	putative dioxygenase	---	AT2G30840	1.11	0.15	0.52	0.619261	0.794917	-6.70
256259_at	hypothetical protein predicted by genem	---	AT3G12460	1.06	0.08	0.52	0.619275	0.794917	-6.70
252258_at	putative protein several hypothetical pro	---	AT3G49450	1.05	0.07	0.52	0.619265	0.794917	-6.70
251238_at	putative protein several hypothetical pro	---	AT3G62430	-1.05	-0.07	-0.52	0.619266	0.794917	-6.70
262009_at	hypothetical protein predicted by genem	---	AT1G35610	1.05	0.07	0.52	0.619237	0.794917	-6.70
248781_at	putative protein similar to unknown prote	---	AT5G47870	1.10	0.13	0.52	0.619331	0.794943	-6.70
250569_at	myc-like protein myc-like regulatory R g	BIM1	AT5G08130	1.08	0.12	0.52	0.619374	0.794954	-6.70
260692_at	hypothetical protein predicted by genem	---	AT1G32430	1.04	0.06	0.52	0.619449	0.794973	-6.70
246475_at	putative protein IFA-binding protein - Ar	---	AT5G16720	-1.06	-0.08	-0.52	0.619459	0.794973	-6.70
257471_at	G-box binding factor, putative similar to	ATBZIP4	AT1G59530	-1.03	-0.05	-0.52	0.619512	0.794997	-6.70
255840_at	unknown protein	---	AT2G33520	-1.06	-0.09	-0.52	0.619642	0.795043	-6.70
250945_at	putative protein	---	AT5G03400	-1.04	-0.06	-0.52	0.619653	0.795043	-6.70
266777_at	putative AAA-type ATPase	ftsh3	AT2G29080	-1.04	-0.05	-0.52	0.619608	0.795043	-6.70

250878_at	maturase -like protein gene cob intron 3	---	AT5G04050	-1.07	-0.10	-0.52	0.619691	0.795048	-6.70
258621_at	zinc finger protein 1 (zfn1) identical to zi	ZFN1	AT3G02830	-1.04	-0.06	-0.52	0.62006	0.795297	-6.70
259378_at	unknown protein supported by full-lengt	---	AT3G16310	-1.09	-0.13	-0.52	0.619997	0.795297	-6.70
262657_at	ribonuclease contains similarity to RNas	---	AT1G14210	1.10	0.14	0.52	0.620047	0.795297	-6.70
264988_at	glutathione transferase, putative similar	ATGSTU1	AT1G27140	-1.06	-0.08	-0.52	0.619998	0.795297	-6.70
262332_at	hypothetical protein similar to putative s	---	AT1G64030	1.04	0.06	0.52	0.619962	0.795297	-6.70
249638_at	acetyl-CoA synthetase ; supported by c	---	AT5G36880	1.11	0.15	0.52	0.620214	0.795451	-6.70
252401_at	putative protein predicted proteins, Aral	---	AT3G48030	1.05	0.07	0.52	0.620283	0.795494	-6.70
258368_at	subtilisin-like serine protease contains s	---	AT3G14240	-1.10	-0.13	-0.52	0.620402	0.795498	-6.70
249145_at	enoyl CoA hydratase-like protein	ATDCI1	AT5G43280	1.04	0.05	0.52	0.620433	0.795498	-6.70
246116_at	putative protein predicted proteins - Aral	---	AT5G20310	1.05	0.07	0.52	0.62044	0.795498	-6.70
260831_at	glutaredoxin, putative similar to glutared	---	AT1G06830	-1.25	-0.33	-0.52	0.62046	0.795498	-6.70
253182_at	putative protein ctf, Mycobacterium lepr	---	AT4G35190	1.08	0.10	0.52	0.620372	0.795498	-6.70
248045_at	HEAT SHOCK PROTEIN 81-2 (HSP81-	HSP81-2	AT5G56030	1.11	0.15	0.52	0.620513	0.795520	-6.70
254293_at	putative protein SF16 protein, Helianthu	IQD22	AT4G23060	1.08	0.12	0.52	0.620613	0.795588	-6.70
246624_at	flavin-containing monooxygenase, puta	YUC10	AT1G48910	-1.04	-0.06	-0.52	0.620635	0.795588	-6.70
257715_at	putative zinc transporter identical to put	ZIP1	AT3G12750	-1.08	-0.12	-0.52	0.620749	0.795689	-6.70
263903_at	putative touch-induced calmodulin	---	AT2G36180	1.04	0.05	0.52	0.620861	0.795788	-6.70
263092_at	hypothetical protein predicted by gensca	---	AT2G16210	-1.04	-0.05	-0.52	0.620916	0.795813	-6.70
246675_at	putative protein	---	AT5G30420	-1.04	-0.06	-0.52	0.620984	0.795856	-6.70
250624_at	putative protein	---	AT5G07330	1.04	0.06	0.52	0.621035	0.795877	-6.70
262087_at	hypothetical protein predicted by genem	---	AT1G56030	1.04	0.06	0.52	0.621135	0.795960	-6.70
248979_at	putative protein contains similarity to dis	AtPP2-A6	AT5G45080	-1.05	-0.06	-0.52	0.621287	0.796066	-6.70
261503_at	hypothetical protein predicted by genen	---	AT1G71691	1.05	0.07	0.52	0.621261	0.796066	-6.70
264325_at	putative phosphoribosylanthranilate tran	---	AT1G04150	1.05	0.08	0.52	0.62143	0.796102	-6.70
256003_at	Ta11 non-LTR retroelement protein, pu	---	AT3G31430	1.05	0.07	0.52	0.62149	0.796102	-6.70
261703_at	OsNAC7 protein, putative similar to Osl	ANAC012	AT1G32770	1.04	0.05	0.52	0.621364	0.796102	-6.70
260803_at	glutathione transferase, putative similar	ATGSTU2	AT1G78340	-1.04	-0.05	-0.52	0.621471	0.796102	-6.70
257490_x_a	Myb homolog (CPC), putative similar to	ETC1	AT1G01380	-1.03	-0.04	-0.52	0.621434	0.796102	-6.70
248703_at	dermal glycoprotein precursor, extracel	---	AT5G48430	1.36	0.45	0.52	0.62161	0.796211	-6.70
266661_at	TINY-like AP2 domain transcription facto	---	AT2G25820	1.05	0.07	0.52	0.621757	0.796310	-6.70
248643_at	putative protein strong similarity to unkn	---	AT5G49130	-1.04	-0.06	-0.52	0.621772	0.796310	-6.70
259886_at	putative protein kinase similar to protein	---	AT1G76370	-1.04	-0.05	-0.52	0.621809	0.796310	-6.70
253678_at	cytidine deaminase 7	---	AT4G29600	-1.04	-0.05	-0.52	0.621827	0.796310	-6.70
263115_at	Expressed protein ; supported by cDNA	---	AT1G03055	-1.08	-0.11	-0.52	0.621913	0.796332	-6.70

253008_at	expansin -like protein expansin (GhEX1	ATEXPA2(	AT4G38210	1.06	0.09	0.52	0.621914	0.796332	-6.70
256470_at	hypothetical protein predicted by genem	---	AT1G42570	-1.04	-0.05	-0.52	0.622015	0.796417	-6.70
246670_at	putative protein	---	AT5G30520	-1.05	-0.08	-0.52	0.622304	0.796742	-6.70
263316_s_a	putative ligand-gated ion channel protei	ATGLR2.3	AT2G24710 /	1.04	0.06	0.52	0.622359	0.796767	-6.70
263774_at	unknown protein ; supported by cDNA:	---	AT2G40280	-1.04	-0.06	-0.52	0.622478	0.796875	-6.70
257576_at	hypothetical protein predicted by genem	---	AT3G28280	1.04	0.06	0.52	0.622515	0.796878	-6.70
254119_at	putative pectate lyase pectate lyase, M	---	AT4G24780	1.18	0.24	0.52	0.622691	0.797059	-6.71
264823_at	putative serine/threonine protein phosph	BSU1	AT1G03445	1.06	0.08	0.52	0.622751	0.797090	-6.71
247552_at	phytochelatin synthetase - like protein p	COB	AT5G60920	-1.07	-0.10	-0.52	0.622928	0.797185	-6.71
249306_at	RING zinc finger protein-like ;supported	---	AT5G41400	1.11	0.15	0.51	0.62314	0.797185	-6.71
251351_s_a	CaLB protein	NTMC2T4	AT3G60950 /	-1.04	-0.06	-0.51	0.623049	0.797185	-6.71
244957_at	hypothetical protein	AT2G0783	---	-1.04	-0.06	-0.52	0.623016	0.797185	-6.71
245232_at	actin depolymerizing factor-like protein	ADF7	AT4G25590	-1.04	-0.06	-0.51	0.623094	0.797185	-6.71
260282_at	putative N-terminal acetyltransferase sir	EMB2753	AT1G80410	-1.04	-0.06	-0.51	0.623126	0.797185	-6.71
266128_at	hypothetical protein predicted by gensca	EMB2766	---	-1.04	-0.06	-0.51	0.623071	0.797185	-6.71
263817_at	hypothetical protein predicted by gensca	---	---	1.05	0.07	0.51	0.623109	0.797185	-6.71
264414_s_a	putative protein several hypothetical pro	---	---	-1.07	-0.10	-0.52	0.622931	0.797185	-6.71
258427_at	putative DNA-binding protein similar to	---	AT3G16600	1.03	0.05	0.51	0.623253	0.797265	-6.71
245753_at	hypothetical protein similar to putative re	---	---	1.04	0.05	0.51	0.623272	0.797265	-6.71
248718_at	farnesyl diphosphate synthase precurso	FPS1	AT5G47770	1.07	0.10	0.51	0.623386	0.797321	-6.71
260447_at	hypothetical protein similar to N-term of	---	AT1G72410	1.04	0.05	0.51	0.623358	0.797321	-6.71
261980_at	hypothetical protein predicted by genem	---	AT1G33820	1.03	0.05	0.51	0.623555	0.797493	-6.71
252106_at	putative glutamate receptor putative glu	ATGLR3.6	AT3G51480	1.06	0.08	0.51	0.623649	0.797503	-6.71
250915_at	homeodomain -like protein homeodoma	HB51	AT5G03790	1.07	0.10	0.51	0.623667	0.797503	-6.71
262023_at	hypothetical protein predicted by genem	---	AT1G35500	-1.04	-0.06	-0.51	0.623668	0.797503	-6.71
262063_at	unknown protein identical to unknown p	---	AT1G80000	1.05	0.07	0.51	0.623739	0.797549	-6.71
264181_at	ubiquitin, putative similar to ubiquitin GI	UBQ13	AT1G65350	-1.03	-0.05	-0.51	0.623801	0.797584	-6.71
256243_at	basic chitinase identical to basic chitina	ATHCHIB	AT3G12500	-1.15	-0.21	-0.51	0.623843	0.797593	-6.71
246065_at	calcium-dependent protein kinase - like	CPK34	AT5G19360	-1.04	-0.06	-0.51	0.623935	0.797622	-6.71
246004_at	germin-like protein ; supported by cDNA	GER3	AT5G20630	1.46	0.55	0.51	0.623931	0.797622	-6.71
246193_at	Expressed protein ; supported by full-ler	---	---	-1.04	-0.06	-0.51	0.623991	0.797648	-6.71
261751_at	chloroplast drought-induced stress prot	CDSP32	AT1G76080	-1.03	-0.05	-0.51	0.624066	0.797699	-6.71
245708_at	pectate lyase-like protein	---	AT5G04310	1.05	0.07	0.51	0.624343	0.797715	-6.71
263385_at	ABA-regulated gene (ATEM6) ; support	GEA6	AT2G40170	-1.05	-0.07	-0.51	0.624498	0.797715	-6.71
255252_at	contains similarity to Gossypium hirsutu	---	AT4G04990	1.04	0.06	0.51	0.62447	0.797715	-6.71

253653_at	hypothetical protein	---	AT4G30050	1.04	0.06	0.51	0.624305	0.797715	-6.71
264992_at	integral membrane protein, putative sim	---	AT1G67300	-1.05	-0.07	-0.51	0.624399	0.797715	-6.71
267222_at	putative polygalacturonase	---	AT2G43880	-1.04	-0.05	-0.51	0.62436	0.797715	-6.71
259040_at	putative glutathione transferase similar t	ATGSTU8	AT3G09270	1.22	0.29	0.51	0.624151	0.797715	-6.71
258304_at	hypothetical protein predicted by genem	---	---	-1.03	-0.05	-0.51	0.624406	0.797715	-6.71
263576_at	hypothetical protein similar to hypothetic	---	AT2G17080	1.03	0.05	0.51	0.62446	0.797715	-6.71
255450_at	putative protein similar to T5J8.18	---	AT4G02850	-1.04	-0.06	-0.51	0.62434	0.797715	-6.71
263908_at	hypothetical protein predicted by genefir	---	AT2G36480	-1.04	-0.06	-0.51	0.624145	0.797715	-6.71
263198_at	lipase, putative similar to lipase GI:1145	GLIP3	AT1G53990	1.06	0.08	0.51	0.624368	0.797715	-6.71
250591_at	alpha galactosyltransferase protein	---	AT5G07720	-1.05	-0.07	-0.51	0.624774	0.797906	-6.71
252528_at	E2, ubiquitin-conjugating enzyme 13 (U	UBC13	AT3G46460	-1.04	-0.05	-0.51	0.624768	0.797906	-6.71
254929_at	putative protein mitochondrial carrier pr	---	AT4G11440	1.04	0.06	0.51	0.624704	0.797906	-6.71
256037_at	hypothetical protein predicted by genem	---	AT1G19160	-1.05	-0.07	-0.51	0.624787	0.797906	-6.71
248179_at	receptor-protein kinase-like protein	THE1	AT5G54380	-1.10	-0.14	-0.51	0.624867	0.797912	-6.71
261251_at	hypothetical protein predicted by genem	---	AT1G05920	1.06	0.09	0.51	0.624897	0.797912	-6.71
265113_at	hypothetical protein	---	---	1.04	0.06	0.51	0.62484	0.797912	-6.71
263662_at	ankyrin-like protein EST gb|ATTS0956 c	---	AT1G04430	1.07	0.10	0.51	0.625003	0.798002	-6.71
245751_s_a	hypothetical protein contains similarity to	---	AT1G25682 /	1.08	0.11	0.51	0.625091	0.798071	-6.71
256476_at	TNP2-like transposon protein similar to (	---	---	1.04	0.05	0.51	0.625136	0.798083	-6.71
247983_at	pyrophosphate-dependent phosphofruct	PFK7	AT5G56630	1.12	0.16	0.51	0.62531	0.798127	-6.71
251332_at	putative protein putative protein At2g46	---	AT3G61670	1.06	0.09	0.51	0.625311	0.798127	-6.71
255835_at	unknown protein	---	AT2G33420	1.04	0.06	0.51	0.625258	0.798127	-6.71
249820_at	putative protein contains similarity to I-b	---	AT5G23650	-1.07	-0.10	-0.51	0.625215	0.798127	-6.71
253554_at	putative protein predicted protein, Caen	---	AT4G30940	-1.06	-0.09	-0.51	0.625345	0.798127	-6.71
257947_at	putative isocitrate lyase similar to GB:P2	ICL	AT3G21720	-1.05	-0.08	-0.51	0.625668	0.798494	-6.71
263684_at	hypothetical protein predicted by gensca	---	AT1G26900	-1.04	-0.06	-0.51	0.625802	0.798530	-6.71
249218_at	pitrilysin	---	AT5G42390	-1.06	-0.08	-0.51	0.625893	0.798530	-6.71
256743_at	Expressed protein ; supported by full-ler	---	AT3G29370	1.12	0.17	0.51	0.62585	0.798530	-6.71
262642_at	hypothetical protein predicted by genem	---	AT1G62690	1.04	0.06	0.51	0.625816	0.798530	-6.71
249853_at	farnesyl cysteine carboxyl methyltransfe	ATSTE14A	AT5G23320	-1.04	-0.06	-0.51	0.625906	0.798530	-6.71
248830_at	putative protein contains similarity to SE	---	AT5G47150	1.04	0.06	0.51	0.625772	0.798530	-6.71
253131_at	homeodomain - like protein several hom	WOX13	AT4G35550	-1.05	-0.07	-0.51	0.626033	0.798603	-6.71
254978_at	subtilisin-like serine protease contains s	---	AT4G10540	1.03	0.05	0.51	0.626012	0.798603	-6.71
248534_at	putative protein contains similarity to pol	---	AT5G50030	1.04	0.06	0.51	0.626231	0.798810	-6.71
263608_at	putative glycine-rich RNA-binding protei	---	---	-1.05	-0.07	-0.51	0.626282	0.798831	-6.71

253508_at	putative protein various predicted prote	---	AT4G31680	-1.04	-0.06	-0.51	0.62636	0.798886	-6.71
248723_at	acetyl-CoA:benzylalcohol acetyltranfera	---	AT5G47950	1.04	0.06	0.51	0.626464	0.798974	-6.71
246546_at	voltage-dependent anion-selective chan	VDAC3	AT5G15090	-1.06	-0.08	-0.51	0.62663	0.799060	-6.71
266603_at	hypothetical protein predicted by gensca	---	AT2G46040	1.04	0.06	0.51	0.626591	0.799060	-6.71
254941_s_a	putative protein various reverse transcri	---	---	1.04	0.06	0.51	0.626637	0.799060	-6.71
250922_at	Expressed protein ; supported by full-ler	---	AT5G03345	-1.04	-0.06	-0.51	0.626712	0.799067	-6.71
249768_at	receptor-like protein kinase	---	AT5G24100	1.05	0.07	0.51	0.626685	0.799067	-6.71
253918_at	putative protein ; supported by full-leng	PHOS34	AT4G27320	1.04	0.06	0.51	0.626789	0.799075	-6.71
255033_at	putative protein phosphonopyruvate de	---	AT4G09520	-1.05	-0.07	-0.51	0.626775	0.799075	-6.71
253163_at	putative protein E1B 19K/Bcl-2-interact	---	AT4G35750	-1.06	-0.08	-0.51	0.627073	0.799393	-6.71
249292_at	repair endonuclease (gb|AAF01274.1)	UVH1	AT5G41150	1.04	0.05	0.51	0.627174	0.799463	-6.71
256351_at	NPK1-related protein kinase, putative s	ANP2	AT1G54960	-1.04	-0.05	-0.51	0.627199	0.799463	-6.71
245075_at	putative cytochrome P450	CYP96A1	AT2G23180	-1.04	-0.06	-0.51	0.627385	0.799567	-6.71
250799_at	putative protein strong similarity to unkn	---	AT5G05350	-1.04	-0.06	-0.51	0.62737	0.799567	-6.71
250979_at	putative protein	---	AT5G03090	-1.06	-0.08	-0.51	0.627317	0.799567	-6.71
264235_at	myosin, putative similar to myosin GI:43	XIE	AT1G54560	1.05	0.07	0.51	0.6275	0.799599	-6.71
250047_at	BCS1 - like protein h-bcs1, Homo sapie	---	AT5G17730	1.05	0.07	0.51	0.627503	0.799599	-6.71
261035_at	hypothetical protein contains Pfam profil	---	---	-1.03	-0.05	-0.51	0.627515	0.799599	-6.71
246259_at	amino acid permease, putative contains	---	AT1G31830	-1.05	-0.07	-0.51	0.627625	0.799649	-6.71
265813_at	putative NAM (no apical meristem)-like	VND1	AT2G18060	-1.04	-0.05	-0.51	0.627605	0.799649	-6.71
260085_at	putative D-ribulose-5-phosphate similar	---	AT1G63290	1.04	0.05	0.51	0.627764	0.799732	-6.71
245904_at	sucrose-phosphate synthase -like prote	ATSPS2F	AT5G11110	-1.05	-0.07	-0.51	0.627795	0.799732	-6.71
256087_at	hypothetical protein predicted by gensca	---	AT1G20800	1.04	0.06	0.51	0.627794	0.799732	-6.71
249602_at	porin -like protein porin, Prunus armenia	---	AT5G37610	1.04	0.06	0.51	0.627985	0.799929	-6.71
249653_at	putative protein REPLICATION PROTE	---	---	1.04	0.05	0.51	0.628226	0.800191	-6.71
261024_at	hypothetical protein predicted by genem	---	AT1G12190	1.04	0.05	0.51	0.628265	0.800197	-6.71
251229_at	beta-glucosidase-like protein several be	BGLU7	AT3G62740	-1.04	-0.05	-0.51	0.628421	0.800339	-6.71
247559_at	histone deacetylase - like GR AF-1 spe	HDA18	AT5G61070	1.04	0.05	0.51	0.628447	0.800339	-6.71
249533_at	putative protein predicted protein, Arabi	---	AT5G38790	1.04	0.06	0.51	0.628532	0.800341	-6.71
249650_at	Expressed protein ; supported by cDNA	SEF	AT5G37055	1.05	0.07	0.51	0.628576	0.800341	-6.71
259473_at	hypothetical protein predicted by gensca	---	AT1G19025	1.05	0.07	0.51	0.628582	0.800341	-6.71
256201_at	hypothetical protein predicted by gensca	---	AT1G58230	-1.04	-0.06	-0.51	0.628589	0.800341	-6.71
265599_at	unknown protein	AT2G1425	---	1.04	0.06	0.51	0.628705	0.800346	-6.71
252612_at	hypothetical protein	---	AT3G45160	1.23	0.30	0.51	0.628733	0.800346	-6.71
263651_at	unknown protein Similar to Nicotiana les	---	AT1G04340	1.05	0.08	0.51	0.62867	0.800346	-6.71

249415_at	promoter-binding protein like ascorbate	CDF2	AT5G39660	-1.07	-0.10	-0.51	0.628707	0.800346	-6.71
245555_at	HSR201 like protein	---	AT4G15390	-1.04	-0.06	-0.51	0.628782	0.800364	-6.71
250162_at	FtsH protease, putative similar to FtsH-	FTSH6	AT5G15250	-1.03	-0.05	-0.51	0.628864	0.800423	-6.71
263481_at	predicted protein	---	AT2G04025	1.03	0.05	0.51	0.62906	0.800628	-6.71
261140_at	unknown protein	---	AT1G19680	-1.05	-0.06	-0.51	0.629204	0.800767	-6.71
265357_at	E2, ubiquitin-conjugating enzyme, putat	UBC29	AT2G16740	-1.06	-0.08	-0.51	0.62941	0.800912	-6.71
252594_at	putative transporter protein peptide tran	---	AT3G45680	1.07	0.10	0.51	0.629423	0.800912	-6.71
251344_at	putative protein beige-like protein (CDC4	---	AT3G60920	-1.04	-0.06	-0.51	0.629402	0.800912	-6.71
259854_at	RING-H2 zinc finger protein ATL3, puta	---	AT1G72200	1.06	0.08	0.51	0.629514	0.800982	-6.71
262868_at	unknown protein	---	AT1G64980	1.07	0.09	0.50	0.629713	0.801147	-6.71
246392_at	hypothetical protein predicted by genem	---	AT1G58120 /	-1.03	-0.05	-0.50	0.629697	0.801147	-6.71
258688_at	putative eukaryotic translation initiation f	---	AT3G07920	-1.03	-0.05	-0.50	0.629775	0.801173	-6.71
250731_at	putative protein contains similarity to MA	AGL96	AT5G06500	1.04	0.05	0.50	0.629804	0.801173	-6.71
256641_at	hypothetical protein similar to putative re	---	---	1.05	0.07	0.50	0.629894	0.801198	-6.71
245162_at	putative myosin heavy chain	XID	AT2G33240	1.07	0.10	0.50	0.62988	0.801198	-6.71
257321_at	hypothetical protein	---	---	1.08	0.12	0.50	0.629988	0.801273	-6.71
248324_at	putative protein similar to unknown prote	---	AT5G52790	-1.05	-0.07	-0.50	0.630096	0.801365	-6.71
265652_x_a	hypothetical protein predicted by gensca	---	---	-1.05	-0.07	-0.50	0.630156	0.801397	-6.71
245335_at	pore protein homolog ;supported by full-	ATOEP16-	AT4G16160	1.05	0.07	0.50	0.630235	0.801453	-6.71
248929_at	myrosinase-binding protein-like; jasmon	---	AT5G46000	-1.04	-0.06	-0.50	0.630285	0.801472	-6.71
254254_at	hypothetical protein	---	AT4G23330	-1.05	-0.07	-0.50	0.63034	0.801497	-6.71
252236_at	zinc-finger-like protein Cys2/His2-type z	---	AT3G49930	-1.04	-0.06	-0.50	0.630409	0.801541	-6.71
265134_at	putative acyl-CoA : 1-acylglycerol-3-pho	LPAT3	AT1G51260	1.06	0.08	0.50	0.630497	0.801608	-6.71
264052_at	putative cytochrome P450	CYP79B3	AT2G22330	1.08	0.12	0.50	0.630544	0.801622	-6.71
264283_at	hypothetical protein contains similarity to	---	AT1G61850	1.04	0.06	0.50	0.630736	0.801752	-6.71
254517_at	putative protein conserved hypothetical	---	AT4G20310	-1.04	-0.06	-0.50	0.630751	0.801752	-6.71
261382_at	hypothetical protein contains similarity to	CVP2	AT1G05470	1.05	0.07	0.50	0.630724	0.801752	-6.71
251249_at	putative protein 10-deacetylbaccatin III-	---	AT3G62160	1.04	0.06	0.50	0.630895	0.801890	-6.71
256151_at	multispanning membrane protein, putat	---	AT1G55130	-1.06	-0.08	-0.50	0.631187	0.802057	-6.71
263056_at	Mutator-like transposase similar to MUF	---	---	1.03	0.04	0.50	0.631138	0.802057	-6.71
265554_at	hypothetical protein predicted by gensca	---	AT2G07505	1.03	0.05	0.50	0.631273	0.802057	-6.71
259728_at	putative coatomer zeta subunit similar to	---	AT1G60970	1.04	0.05	0.50	0.631247	0.802057	-6.71
251377_at	putative protein	---	AT3G60650	-1.04	-0.05	-0.50	0.631114	0.802057	-6.71
247662_at	protein kinase - like protein kinase 1, P	---	AT5G60090	1.06	0.08	0.50	0.631086	0.802057	-6.71
245658_at	hypothetical protein predicted by genem	RALFL4	AT1G28270	-1.04	-0.05	-0.50	0.631235	0.802057	-6.71

258293_at	unknown protein	PHO1	AT3G23430	1.17	0.22	0.50	0.631458	0.802248	-6.71
252402_s_a	putative protein predicted proteins, Arat	---	AT3G48050 /	-1.04	-0.05	-0.50	0.631501	0.802258	-6.71
253900_at	translation initiation factor ; supported b	---	AT4G27130	-1.04	-0.06	-0.50	0.631688	0.802451	-6.71
267395_at	unknown protein	---	AT2G44250	1.03	0.05	0.50	0.631739	0.802471	-6.71
245145_at	putative dihydrodipicolinate synthase ;s	DHDPS2	AT2G45440	-1.07	-0.10	-0.50	0.63197	0.802541	-6.71
246537_at	putative protein protochlorophyllide redu	---	AT5G15940	-1.04	-0.06	-0.50	0.631842	0.802541	-6.71
264544_s_a	unknown protein	---	AT1G55790 /	-1.04	-0.05	-0.50	0.63191	0.802541	-6.71
248705_at	putative protein similar to unknown prote	---	AT5G48520	-1.05	-0.08	-0.50	0.631885	0.802541	-6.71
263029_at	unknown protein	---	AT1G24050	-1.03	-0.04	-0.50	0.631944	0.802541	-6.71
253142_at	putative protein methyl-directed mismat	MLH3	AT4G35520	-1.04	-0.05	-0.50	0.632055	0.802604	-6.71
260222_at	putative alpha galactosyltransferase sim	XXT5	AT1G74380	1.08	0.11	0.50	0.632188	0.802692	-6.71
267211_at	Expressed protein ; supported by full-ler	---	AT2G44065	1.03	0.05	0.50	0.63223	0.802692	-6.71
265645_at	unknown protein	---	AT2G27370	1.04	0.05	0.50	0.632219	0.802692	-6.71
262698_at	AMP-binding protein, putative contains	---	AT1G75960	-1.10	-0.14	-0.50	0.632376	0.802792	-6.71
250870_at	hypothetical protein	---	AT5G03920	-1.04	-0.06	-0.50	0.632414	0.802792	-6.71
258084_at	putative B regulatory subunit of protein p	---	AT3G26020	1.06	0.09	0.50	0.63239	0.802792	-6.71
265866_at	unknown protein ;supported by full-leng	---	AT2G01710	-1.05	-0.06	-0.50	0.632486	0.802838	-6.71
262677_at	unknown protein	---	AT1G75860	-1.08	-0.10	-0.50	0.632792	0.803137	-6.71
264600_at	hypothetical protein predicted by gensca	---	AT1G04730	1.06	0.09	0.50	0.632767	0.803137	-6.71
249737_at	putative protein similar to unknown prote	---	AT5G24480	1.04	0.06	0.50	0.63288	0.803164	-6.71
267137_at	hypothetical protein predicted by gensca	ACPT	AT2G23410	-1.04	-0.05	-0.50	0.632883	0.803164	-6.71
261537_at	carbonyl reductase, putative similar to c	---	AT1G01800	-1.03	-0.05	-0.50	0.633071	0.803358	-6.71
245742_at	aldehyde dehydrogenase, putative simi	ALDH3H1	AT1G44170	1.07	0.09	0.50	0.633209	0.803443	-6.71
247894_at	putative protein similar to unknown prote	CPL4	AT5G58000 /	-1.07	-0.10	-0.50	0.633178	0.803443	-6.71
262153_at	unknown protein	---	AT1G52710	-1.03	-0.05	-0.50	0.633414	0.803658	-6.71
262756_at	putative transport protein may be a mem	אוק-06	AT1G16370	-1.15	-0.20	-0.50	0.633637	0.803897	-6.71
266946_at	putative protein kinase contains a protei	---	AT2G18890	1.05	0.07	0.50	0.633841	0.804111	-6.71
254787_at	putative protein hypothetical proteins Ar	---	AT4G12690	-1.07	-0.10	-0.50	0.633913	0.804158	-6.71
252365_at	Expressed protein ; supported by full-ler	---	AT3G48350	-1.10	-0.14	-0.50	0.634083	0.804299	-6.71
260905_at	hypothetical protein predicted by genem	---	AT1G02710	-1.03	-0.04	-0.50	0.634095	0.804299	-6.71
248123_at	putative protein similar to unknown prote	---	AT5G54720	1.04	0.05	0.50	0.634139	0.804310	-6.71
256506_at	unknown protein	---	AT1G75160	1.05	0.07	0.50	0.634228	0.804333	-6.71
255254_at	hypothetical protein	---	AT4G05030	1.05	0.08	0.50	0.634224	0.804333	-6.71
251420_at	transcription factor - like protein transcr	---	AT3G60490	-1.06	-0.08	-0.50	0.634357	0.804408	-6.71
266383_at	putative pathogenesis related-1 (PR1) p	ATPRB1	AT2G14580	-1.06	-0.09	-0.50	0.634338	0.804408	-6.71

258337_at	hypothetical protein predicted by genem	---	AT3G16040	1.06	0.08	0.50	0.634426	0.804451	-6.71
264706_at	hypothetical protein predicted by gensca	---	AT1G09720	-1.03	-0.04	-0.50	0.634489	0.804485	-6.71
263173_at	hypothetical protein predicted by genem	BRX-LIKE	AT1G54180	1.04	0.05	0.50	0.634622	0.804521	-6.71
255852_at	unknown protein	SVL2	AT1G66970	1.12	0.16	0.50	0.634622	0.804521	-6.71
258895_at	putative epoxide hydrolase similar to ep	---	AT3G05600	-1.03	-0.05	-0.50	0.634623	0.804521	-6.71
266721_at	unknown protein	FT1	AT2G03220	1.06	0.08	0.50	0.634796	0.804607	-6.72
265198_at	putative glucosyl transferase	UGT73C2	AT2G36760	-1.03	-0.05	-0.50	0.63473	0.804607	-6.72
246324_at	arginine/serine-rich protein, putative sin	SR45	AT1G16610	-1.04	-0.05	-0.50	0.634768	0.804607	-6.72
265881_at	hypothetical protein predicted by gensca	---	AT2G42480	1.04	0.06	0.50	0.635214	0.804957	-6.72
247227_at	putative protein contains similarity to AP	---	AT5G65130	1.04	0.05	0.50	0.635168	0.804957	-6.72
265223_at	putative pectinesterase	---	AT2G36700	1.03	0.04	0.50	0.635214	0.804957	-6.72
261385_at	lipid-transfer protein, putative similar to	---	AT1G05450	1.03	0.05	0.50	0.635157	0.804957	-6.72
266915_at	hypothetical protein predicted by gensca	---	AT2G45870	-1.04	-0.05	-0.50	0.63526	0.804970	-6.72
256850_at	hypothetical protein similar to hypothetic	---	---	-1.03	-0.04	-0.50	0.635307	0.804986	-6.72
262277_at	transmembrane protein, putative similar	---	AT1G68650	1.09	0.13	0.50	0.635355	0.805001	-6.72
249438_at	putative protein BCS1 nuclear gene enc	AATP1	AT5G40010	-1.05	-0.07	-0.50	0.635451	0.805078	-6.72
255489_at	predicted protein destination factor simi	---	AT4G02650 /	1.05	0.08	0.50	0.635502	0.805098	-6.72
267332_at	hypothetical protein predicted by gensca	---	AT2G19290	-1.03	-0.04	-0.50	0.635564	0.805133	-6.72
248644_at	disease resistance protein-like	---	AT5G49140	1.03	0.05	0.50	0.635843	0.805441	-6.72
265590_at	SKP1/ASK1 (At17), putative similar to S	MEO	AT2G20160	1.04	0.05	0.50	0.636065	0.805596	-6.72
261671_at	hypothetical protein similar to hypothetic	---	AT1G18340	-1.07	-0.10	-0.50	0.63603	0.805596	-6.72
262255_at	hypothetical protein similar to hypothetic	---	AT1G53790	1.03	0.05	0.50	0.636071	0.805596	-6.72
263865_at	putative ABC transporter related to mult	ABCB1	AT2G36910	-1.06	-0.08	-0.50	0.636112	0.805602	-6.72
263513_at	unknown protein	---	AT2G12400	-1.07	-0.10	-0.50	0.636195	0.805664	-6.72
263775_at	putative MYB family transcription factor	CPC	AT2G46410	-1.04	-0.06	-0.50	0.636268	0.805711	-6.72
245668_at	dormancy-associated protein, putative s	DYL1	AT1G28330	-1.05	-0.08	-0.49	0.636398	0.805830	-6.72
248572_at	unknown protein	---	AT5G49800	1.04	0.06	0.49	0.636446	0.805846	-6.72
248441_at	putative protein contains similarity to rec	---	AT5G51270	-1.03	-0.04	-0.49	0.636657	0.806069	-6.72
258143_at	hypothetical protein	---	AT3G18170	1.06	0.09	0.49	0.636814	0.806162	-6.72
263381_at	putative MADS-box protein	AGL48	AT2G40210	1.04	0.05	0.49	0.636836	0.806162	-6.72
246647_at	putative protein predicted proteins from	---	---	-1.03	-0.05	-0.49	0.636779	0.806162	-6.72
255299_at	putative adenosine deaminase similar to	---	AT4G04880	1.04	0.06	0.49	0.636994	0.806296	-6.72
266597_at	putative WRKY-type DNA binding protei	WRKY43	AT2G46130	-1.03	-0.05	-0.49	0.637013	0.806296	-6.72
263625_at	F-box protein family, AtFBX9 contains F	---	AT2G04920	1.04	0.05	0.49	0.637186	0.806441	-6.72
261573_at	hypothetical protein identical to hyotheti	---	AT1G01180	-1.04	-0.05	-0.49	0.637198	0.806441	-6.72

249276_at	DNA polymerase alpha subunit IV (prim	POLA3	AT5G41880	-1.20	-0.26	-0.49	0.637324	0.806555	-6.72
AFFX-Athal-	Arabidopsis thaliana /REF=U37281.1 /D	---	---	-1.05	-0.07	-0.49	0.637679	0.806870	-6.72
257921_at	hypothetical protein contains Pfam prof	---	AT3G23270	1.03	0.05	0.49	0.637669	0.806870	-6.72
261188_at	hypothetical protein contains similarity t	---	---	-1.04	-0.06	-0.49	0.637643	0.806870	-6.72
252794_at	putative protein predicted proteins, Ara	---	---	-1.03	-0.05	-0.49	0.637826	0.806967	-6.72
264081_at	putative RING zinc finger transcription n	---	AT2G28540	-1.05	-0.07	-0.49	0.637807	0.806967	-6.72
251960_at	GTPase AtRAB8 ;supported by full-leng	HEMB1	AT1G69740 /	1.04	0.06	0.49	0.637963	0.807095	-6.72
259585_at	hypothetical protein contains similarity t	---	AT1G28090	-1.04	-0.05	-0.49	0.638015	0.807117	-6.72
264089_at	actin depolymerizing factor 6 ;supporte	ADF6	AT2G31200	-1.06	-0.08	-0.49	0.638095	0.807173	-6.72
252137_at	dehydrin-like protein dehydrin Xero2 - /	XERO1	AT3G50980	1.05	0.07	0.49	0.638148	0.807196	-6.72
264898_at	Unknown protein ; supported by full-leng	---	AT1G23205	-1.06	-0.09	-0.49	0.638265	0.807298	-6.72
255768_at	Expressed protein ; supported by full-ler	---	AT1G16705	-1.04	-0.05	-0.49	0.638426	0.807458	-6.72
264517_at	hypothetical protein predicted by gensca	---	AT1G10120	-1.05	-0.08	-0.49	0.638548	0.807522	-6.72
267465_at	subtilisin-like serine protease contains s	SLP3	AT2G19170	-1.10	-0.14	-0.49	0.638539	0.807522	-6.72
248412_at	putative protein contains similarity to DN	---	AT5G51590	1.04	0.06	0.49	0.638616	0.807563	-6.72
250307_at	putative protein similar to unknown prote	---	AT5G12170	1.07	0.10	0.49	0.638714	0.807643	-6.72
267108_at	hypothetical protein predicted by gensca	---	AT2G14830	1.03	0.05	0.49	0.638833	0.807749	-6.72
264482_at	sugar carrier protein, putative similar to	---	AT1G77210	1.10	0.14	0.49	0.638985	0.807895	-6.72
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J0442	---	---	1.08	0.11	0.49	0.639179	0.807951	-6.72
259029_at	putative oxysterol-binding protein simila	ORP3B	AT3G09300	1.05	0.07	0.49	0.639159	0.807951	-6.72
251781_at	P-glycoprotein - like P-glycoprotein (pm	PGP20	AT3G55320	1.04	0.06	0.49	0.639237	0.807951	-6.72
251102_at	putative transporter protein Na+/H+ anti	CHX27	AT5G01690	1.06	0.09	0.49	0.639094	0.807951	-6.72
261635_at	tubulin alpha-6 chain, putative identical	---	AT1G50020	1.05	0.07	0.49	0.639115	0.807951	-6.72
245062_at	hypothetical protein predicted by gensca	BPM3	AT2G39760	1.03	0.05	0.49	0.639241	0.807951	-6.72
255394_at	hypothetical protein similar to A. thalian	---	---	1.04	0.06	0.49	0.639424	0.808054	-6.72
256208_at	hypothetical protein predicted by genem	---	AT1G50930	1.03	0.04	0.49	0.639429	0.808054	-6.72
266669_at	putative flavonol 3-O-glucosyltransferas	UGT71C1	AT2G29750	-1.05	-0.07	-0.49	0.639369	0.808054	-6.72
261150_at	floral nectary-specific protein, putative s	JMT	AT1G19640	-1.15	-0.20	-0.49	0.639485	0.808080	-6.72
245564_at	hypothetical protein	emb2739	AT4G14590	1.04	0.06	0.49	0.639735	0.808351	-6.72
254728_at	hypothetical protein	---	AT4G13690	1.04	0.05	0.49	0.639811	0.808402	-6.72
265399_at	hypothetical protein predicted by gensca	---	AT2G11010	1.08	0.12	0.49	0.639911	0.808485	-6.72
266920_at	hypothetical protein predicted by gensca	---	AT2G45750	1.05	0.06	0.49	0.639956	0.808496	-6.72
260251_at	putative heat shock protein similar to GE	---	AT1G74250	-1.06	-0.08	-0.49	0.640096	0.808628	-6.72
248139_at	putative protein similar to unknown prote	---	AT5G54970	-1.30	-0.38	-0.49	0.640304	0.808847	-6.72
259374_at	putative AP2 domain transcription factor	---	AT3G16280	1.05	0.08	0.49	0.640351	0.808861	-6.72

252102_at	dehydrin Xero2 ; supported by cDNA: g	LTI30	AT3G50970	-1.13	-0.17	-0.49	0.640444	0.808909	-6.72
262405_at	hypothetical protein contains similarity t	HDG10	AT1G34650	-1.04	-0.06	-0.49	0.64046	0.808909	-6.72
248689_at	SCARECROW gene regulator-like ; sup	PAT1	AT5G48150	1.05	0.07	0.49	0.640664	0.808988	-6.72
262061_at	hypothetical protein contains similarity t	ATPP2-B1	AT1G80110	-1.04	-0.06	-0.49	0.640642	0.808988	-6.72
266809_at	unknown protein ; supported by cDNA:	---	AT2G29970	-1.08	-0.11	-0.49	0.640653	0.808988	-6.72
254071_at	hypothetical protein	---	AT4G25510	1.03	0.05	0.49	0.64058	0.808988	-6.72
259572_at	hypothetical protein	---	AT1G20400	1.05	0.06	0.49	0.640717	0.809010	-6.72
246084_at	putative protein predicted proteins, Aral	ATBRXL4	AT5G20540	1.04	0.06	0.49	0.640975	0.809291	-6.72
250049_at	putative protein predicted proteins, Aral	---	AT5G17780	1.04	0.06	0.49	0.641068	0.809363	-6.72
249766_at	peroxidase-like protein	---	AT5G24070	1.04	0.06	0.49	0.641238	0.809533	-6.72
258983_at	putative aminotransferase similar to bet	---	AT3G08860	1.13	0.18	0.49	0.641328	0.809602	-6.72
248168_at	beta-glucosidase	BGLU41	AT5G54570	1.04	0.06	0.49	0.641382	0.809625	-6.72
248208_at	unknown protein	ATHB52	AT5G53980	1.06	0.08	0.49	0.641445	0.809660	-6.72
250354_at	putative protein predicted proteins, Dros	---	AT5G11640	-1.04	-0.06	-0.49	0.641543	0.809738	-6.72
250215_at	putative protein similar to unknown prote	---	AT5G14080	-1.04	-0.05	-0.49	0.641736	0.809892	-6.72
247109_at	putative protein similar to unknown prote	ATPSK5	AT5G65870	-1.09	-0.12	-0.49	0.641727	0.809892	-6.72
258417_at	Expressed protein ; supported by cDNA	---	AT3G17365	-1.05	-0.07	-0.49	0.641942	0.810018	-6.72
254056_at	putative protein Group I Pectinesterase	---	AT4G25250	-1.04	-0.06	-0.49	0.641933	0.810018	-6.72
260504_at	Cyclin similar to GB:CAB77269 from [Pi	CYCA3;3	AT1G47220	1.04	0.06	0.49	0.641892	0.810018	-6.72
253869_at	hypothetical protein	---	AT4G27510	-1.05	-0.07	-0.49	0.64203	0.810084	-6.72
250507_at	putative protein similar to unknown prote	---	AT5G09940	1.04	0.05	0.49	0.642083	0.810106	-6.72
266409_at	hypothetical protein predicted by grail	---	AT2G38510	-1.05	-0.06	-0.49	0.64223	0.810247	-6.72
255358_at	hypothetical protein	---	AT4G03940	-1.03	-0.05	-0.49	0.642284	0.810270	-6.72
267390_at	putative beta-glucosidase	BGLU29	AT2G44470	1.04	0.05	0.49	0.642331	0.810284	-6.72
260413_at	hypothetical protein predicted by genefir	---	AT1G69800	-1.05	-0.08	-0.49	0.642502	0.810410	-6.72
264579_at	Expressed protein ; supported by full-ler	---	AT1G05205	1.06	0.08	0.49	0.642483	0.810410	-6.72
262399_at	unknown protein ;supported by full-lengt	---	AT1G49500	-1.06	-0.08	-0.49	0.642593	0.810481	-6.72
265578_at	unknown protein	---	AT2G20100	-1.05	-0.07	-0.49	0.642724	0.810602	-6.72
252302_at	putative protein hypothetical protein Rv	---	AT3G49190	1.03	0.05	0.49	0.642857	0.810711	-6.72
251077_at	putative protein COP1-interacting prote	---	AT5G01980	-1.03	-0.04	-0.49	0.642918	0.810711	-6.72
248062_at	unknown protein ;supported by full-leng	---	AT5G55450	1.39	0.47	0.49	0.642916	0.810711	-6.72
250184_at	putative protein various predicted prote	---	AT5G14240	1.04	0.05	0.49	0.643045	0.810827	-6.72
250201_at	ankyrin - like protein 270 kDa ankyrin G	---	AT5G14230	1.10	0.14	0.48	0.643108	0.810862	-6.72
246361_s_a	hypothetical protein	---	---	-1.03	-0.05	-0.48	0.643168	0.810892	-6.72
249512_at	DNA repair protein RAD23 homolog ;su	---	AT5G38470	-1.03	-0.04	-0.48	0.643268	0.810933	-6.72

252841_at	putative protein replication protein A 51	---	---	-1.05	-0.07	-0.48	0.643271	0.810933	-6.72
256486_at	chloroplast nucleoid DNA binding prote	---	AT1G31450	1.04	0.06	0.48	0.643326	0.810957	-6.72
260911_at	hypothetical protein predicted by genem	---	AT1G02490	-1.04	-0.05	-0.48	0.643389	0.810992	-6.72
265041_at	unknown protein Contains similarity to h	TOM22-I	AT1G04070	-1.06	-0.09	-0.48	0.643734	0.811379	-6.72
266674_at	hypothetical protein predicted by gensca	---	AT2G29620	-1.03	-0.05	-0.48	0.643768	0.811379	-6.72
253125_at	DnaJ-like protein DnaJ-like protein, Pha	---	AT4G36040	-1.05	-0.07	-0.48	0.643854	0.811444	-6.72
250771_at	NBS/LRR disease resistance protein	---	AT5G05400	-1.04	-0.05	-0.48	0.643945	0.811468	-6.72
265300_at	unknown protein contains weak PHD zir	---	AT2G13950	-1.05	-0.07	-0.48	0.643919	0.811468	-6.72
256860_at	hypothetical protein similar to acetyl-CoA	---	AT3G23840	-1.04	-0.06	-0.48	0.644061	0.811477	-6.72
256197_at	hypothetical protein	---	---	-1.06	-0.08	-0.48	0.64404	0.811477	-6.72
256084_at	hypothetical protein predicted by gensca	---	AT1G20750	1.05	0.06	0.48	0.644095	0.811477	-6.72
245839_at	disease resistance protein, putative sim	---	AT1G58390	1.03	0.05	0.48	0.644044	0.811477	-6.72
255969_at	Expressed protein ; supported by full-ler	---	AT1G22330	1.08	0.11	0.48	0.644201	0.811567	-6.72
260305_at	putative ADP-ribosylation factor 1 nearly	ARFA1D	AT1G70490	-1.05	-0.07	-0.48	0.644257	0.811592	-6.72
261499_at	cytochrome P450 (CYP93A1), putative	CYP705A2	AT1G28430	1.04	0.06	0.48	0.644548	0.811687	-6.72
255777_at	glycine-rich RNA-binding protein, putati	GR-RBP6	AT1G18630	-1.05	-0.07	-0.48	0.644465	0.811687	-6.72
248480_at	ATP-dependent Clp protease ATP-bindi	CLPC1	AT5G50920	-1.04	-0.05	-0.48	0.64462	0.811687	-6.72
261766_at	auxin-induced protein IAA5, putative sir	IAA5	AT1G15580	-1.12	-0.16	-0.48	0.644688	0.811687	-6.72
266577_at	predicted protein	---	AT2G23945	-1.04	-0.06	-0.48	0.644538	0.811687	-6.72
252266_at	putative protein ethylene-forming enzyn	---	AT3G49630	1.06	0.08	0.48	0.64453	0.811687	-6.72
246618_at	putative protein similar to unknown prote	---	AT5G36280	1.03	0.05	0.48	0.644502	0.811687	-6.72
258411_at	hypothetical protein predicted by genma	---	AT3G17280	-1.04	-0.05	-0.48	0.64468	0.811687	-6.72
249556_at	Expressed protein ; supported by full-ler	---	AT5G38195	-1.04	-0.05	-0.48	0.644593	0.811687	-6.72
252881_at	putative protein predicted proteins, Arat	---	AT4G39610	1.06	0.08	0.48	0.644481	0.811687	-6.72
253427_at	putative protein phosphate/phosphoenc	---	AT4G32390	-1.04	-0.05	-0.48	0.64475	0.811721	-6.72
248497_at	putative protein strong similarity to unkn	ATEXO70I	AT5G50380	1.06	0.09	0.48	0.644845	0.811750	-6.72
259206_at	hypothetical protein similar to putative p	---	AT3G09040	1.05	0.07	0.48	0.644829	0.811750	-6.72
255388_at	hypothetical protein similar to A. thalian	---	---	-1.03	-0.05	-0.48	0.645091	0.812015	-6.72
246680_at	putative protein predicted proteins - Arat	---	---	1.04	0.06	0.48	0.645163	0.812061	-6.72
249851_at	MADS-box transcription factor-like prote	TT16	AT5G23260	1.03	0.04	0.48	0.645237	0.812110	-6.72
256550_at	En/Spm-like transposon protein, putativ	---	---	1.03	0.05	0.48	0.645313	0.812160	-6.72
256639_at	hypothetical protein predicted by genem	---	---	1.05	0.07	0.48	0.645387	0.812208	-6.72
252231_at	hypothetical protein ;supported by full-le	---	AT3G49720	1.05	0.07	0.48	0.645434	0.812223	-6.72
250154_at	putative aldose 1-epimerase - like prote	---	AT5G15140	-1.03	-0.04	-0.48	0.645864	0.812629	-6.72
255625_at	GBF2, G-box binding factor ;supported	GBF2	AT4G01120	-1.06	-0.09	-0.48	0.645839	0.812629	-6.72

254902_at	putative protein several hypothetical pro	---	AT4G11550	-1.04	-0.05	-0.48	0.645843	0.812629	-6.72
259897_at	putative beta-glucanase similar to beta-g	ATCEL3	AT1G71380	1.04	0.05	0.48	0.646063	0.812835	-6.72
266419_at	putative annexin ;supported by full-leng	ANNAT3	AT2G38760	-1.06	-0.08	-0.48	0.646279	0.813016	-6.72
248097_at	protein phosphatase X isoform 2 (gb|AA	PPX2	AT5G55260	1.05	0.07	0.48	0.646349	0.813016	-6.72
259282_at	unknown protein similar to unknown pro	GPAT5	AT3G11430	1.05	0.07	0.48	0.646331	0.813016	-6.72
245646_x_a	F5A9.9 hypothetical protein	---	AT1G24851 /	1.03	0.05	0.48	0.646339	0.813016	-6.72
253729_at	beta-1,3-glucanase-like protein beta-1,3	---	AT4G29360	1.05	0.07	0.48	0.646486	0.813143	-6.72
250579_at	putative protein terminal ear1, Zea may	MCT2	AT5G07930	-1.04	-0.05	-0.48	0.646646	0.813299	-6.72
264751_at	putative superoxide-generating NADPH	FRO3	AT1G23020	1.13	0.18	0.48	0.64671	0.813332	-6.72
246567_at	alpha-mannosidase -like protein manno	GMII	AT5G14950	-1.03	-0.05	-0.48	0.646743	0.813332	-6.72
250760_at	unknown protein	---	AT5G06040	-1.04	-0.05	-0.48	0.647055	0.813643	-6.72
245739_at	mitotic cyclin a2-type, putative similar to	CYCA1;1	AT1G44110	1.03	0.05	0.48	0.647062	0.813643	-6.72
258820_at	putative tryptophanyl-tRNA synthetase s	---	AT3G04600	1.03	0.05	0.48	0.647108	0.813656	-6.72
258988_at	unknown protein similar to unknown pro	---	AT3G08890	1.04	0.06	0.48	0.647365	0.813853	-6.73
254481_at	hypothetical protein ; supported by cDN	---	AT4G20480	-1.06	-0.08	-0.48	0.647443	0.813853	-6.73
249497_at	putative protein predicted proteins - diffe	---	AT5G39220	1.05	0.06	0.48	0.647394	0.813853	-6.73
256073_at	terminal Flower 1 (TFL1), putative simil	E12A11	AT1G18100	1.04	0.06	0.48	0.647306	0.813853	-6.73
246715_at	putative protein glucose-6-phosphate/p	---	AT5G28230	1.05	0.07	0.48	0.647409	0.813853	-6.73
259413_at	hypothetical protein contains similarity to	---	AT1G02320	-1.04	-0.05	-0.48	0.647532	0.813920	-6.73
263516_at	AtRer1B ;supported by full-length cDNA	ATRER1B	AT2G21600	-1.04	-0.06	-0.48	0.647605	0.813922	-6.73
259885_at	hypothetical protein contains Pfam profil	---	AT1G76380	-1.06	-0.08	-0.48	0.647595	0.813922	-6.73
245634_at	MtN21 nodulin protein, putative similar t	---	AT1G25270	-1.04	-0.06	-0.48	0.647658	0.813944	-6.73
267318_at	fatty acid hydroxylase (FAH1) identical t	FAH1	AT2G34770	-1.04	-0.06	-0.48	0.647831	0.813973	-6.73
257991_at	unknown protein	---	AT3G19870	-1.05	-0.07	-0.48	0.64786	0.813973	-6.73
261198_at	nitrate transporter, putative similar to G	ATNRT2.5	AT1G12940	1.03	0.05	0.48	0.647821	0.813973	-6.73
263998_at	unknown protein	---	AT2G22510	1.09	0.12	0.48	0.647726	0.813973	-6.73
255529_at	CTP synthase - like protein	---	AT4G02120	1.04	0.06	0.48	0.647826	0.813973	-6.73
262102_at	hypothetical protein contains similarity to	CUL2	AT1G02980	1.03	0.05	0.48	0.647946	0.814013	-6.73
254539_s_a	chitinase - like protein chitinase / lysozy	---	AT4G19750 /	-1.03	-0.05	-0.48	0.647963	0.814013	-6.73
257484_at	unknown protein	---	AT1G01650	-1.03	-0.05	-0.48	0.64802	0.814021	-6.73
256935_at	unknown protein ;supported by full-leng	---	AT3G22570	1.03	0.05	0.48	0.648077	0.814021	-6.73
245884_at	branched-chain alpha keto-acid dehydr	---	AT5G09300	1.06	0.08	0.48	0.648072	0.814021	-6.73
245529_at	SEN1 like protein	MAA3	AT4G15570	-1.07	-0.10	-0.48	0.648251	0.814196	-6.73
252385_at	putative protein Vps29, Schizosaccharo	MAG1	AT3G47810	-1.03	-0.05	-0.48	0.648334	0.814255	-6.73
262972_at	unknown protein	---	AT1G75620	-1.04	-0.06	-0.48	0.6484	0.814293	-6.73

258512_at	beta-glucosidase, putative similar to be	---	AT3G06510 /	-1.03	-0.04	-0.48	0.648712	0.814301	-6.73
254923_at	protein phosphatase type 1 PP1BG ;su	TOPP7	AT4G11240	-1.05	-0.07	-0.48	0.648679	0.814301	-6.73
253297_at	beta-xylan endohydrolase -like protein (	---	AT4G33810	-1.04	-0.05	-0.48	0.64855	0.814301	-6.73
247981_at	putative protein similar to unknown prote	MIOX5	AT5G56640	1.03	0.05	0.48	0.648673	0.814301	-6.73
261780_at	cyclin, putative similar to B-like cyclin G	CYCB2;4	AT1G76310	1.04	0.06	0.48	0.648942	0.814301	-6.73
257020_at	mitotic checkpoint protein, putative simi	---	AT3G19590	-1.04	-0.06	-0.48	0.648766	0.814301	-6.73
251989_at	RNA helicase -like protein RNA helicas	LOS4	AT3G53110	-1.04	-0.06	-0.48	0.648886	0.814301	-6.73
263161_at	myrosinase-associated protein, putative	---	AT1G54020	-1.43	-0.51	-0.48	0.648772	0.814301	-6.73
261510_at	hypothetical protein predicted by gensca	---	AT1G71760	-1.04	-0.05	-0.48	0.648934	0.814301	-6.73
248407_at	pectinesterase	---	AT5G51500	-1.04	-0.05	-0.48	0.648534	0.814301	-6.73
266726_at	SKP1/ASK1 (At19), putative similar to S	ASK19	AT2G03160	-1.05	-0.08	-0.48	0.648895	0.814301	-6.73
266919_at	hypothetical protein predicted by gensca	AT2G4578	---	1.03	0.05	0.48	0.648904	0.814301	-6.73
252820_at	plasma membrane H+-ATPase-like pro	AHA8	AT3G42640	-1.06	-0.09	-0.48	0.648878	0.814301	-6.73
255002_at	AIG1-like protein AIG1 - Arabidopsis tha	---	AT4G09940	-1.04	-0.06	-0.48	0.648675	0.814301	-6.73
257386_at	hypothetical protein predicted by gensca	---	AT2G42440	1.03	0.04	0.48	0.648553	0.814301	-6.73
265843_at	putative acyl-CoA oxidase possibly a pe	ACX5	AT2G35690	-1.04	-0.06	-0.48	0.649158	0.814528	-6.73
248142_at	putative protein similar to unknown prote	---	AT5G55040	-1.03	-0.05	-0.48	0.649207	0.814545	-6.73
267543_at	26S proteasome regulatory subunit	---	AT2G32730	-1.03	-0.04	-0.48	0.649343	0.814566	-6.73
244955_at	hypothetical protein	---	---	1.06	0.08	0.48	0.649302	0.814566	-6.73
248293_at	unknown protein	---	AT5G53050	-1.06	-0.09	-0.48	0.649367	0.814566	-6.73
262683_at	anter-specific proline-rich -like protein (A	---	AT1G75920	1.03	0.05	0.48	0.649355	0.814566	-6.73
255162_at	putative transposon protein	---	---	1.03	0.04	0.48	0.649591	0.814802	-6.73
246071_at	ids4-like protein ids-4 protein - Hordeun	SPX1	AT5G20150	-1.11	-0.15	-0.48	0.649647	0.814827	-6.73
254655_s_a	ribosomal protein L32 -like protein ribos	---	AT4G18100 /	-1.07	-0.09	-0.48	0.649763	0.814838	-6.73
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J0442	---	---	1.11	0.15	0.48	0.649752	0.814838	-6.73
246353_s_a	hypothetical protein	---	---	-1.03	-0.05	-0.48	0.64973	0.814838	-6.73
261392_at	hypothetical protein predicted by genem	---	AT1G79780	1.03	0.05	0.47	0.650102	0.814877	-6.73
258141_at	hypothetical protein	HON4	AT3G18035	-1.05	-0.07	-0.47	0.650085	0.814877	-6.73
255916_at	putative protein	---	AT5G28550	-1.05	-0.06	-0.47	0.649832	0.814877	-6.73
257336_at	hypothetical protein	---	---	-1.03	-0.05	-0.47	0.650109	0.814877	-6.73
254030_at	putative acidic ribosomal protein acidic	---	AT4G25890	-1.10	-0.14	-0.47	0.650108	0.814877	-6.73
250633_at	peptide methionine sulfoxide reductase	PMSR2	AT5G07460	1.13	0.18	0.47	0.650151	0.814877	-6.73
260990_at	hypothetical protein predicted by genem	---	AT1G12180	-1.05	-0.07	-0.47	0.650149	0.814877	-6.73
264532_at	seed imbibition protein, putative similar	AtSIP1	AT1G55740	-1.04	-0.05	-0.47	0.650103	0.814877	-6.73
245819_at	cauliflower identical to CAULIFLOWER	CAL	AT1G26310	1.04	0.05	0.47	0.650148	0.814877	-6.73

246709_s_a	putative protein many predicted protein	---	AT5G28160 /	1.03	0.04	0.47	0.650103	0.814877	-6.73
259276_at	putative peroxidase very similar to perox	---	AT3G01190	1.03	0.05	0.47	0.650256	0.814964	-6.73
267449_at	hypothetical protein predicted by gensca	---	AT2G33690	-1.03	-0.04	-0.47	0.650319	0.814998	-6.73
265285_at	hypothetical protein predicted by gensca	---	AT2G20410	1.05	0.06	0.47	0.6504	0.815009	-6.73
267417_at	putative RING zinc finger protein	---	AT2G34990	1.03	0.05	0.47	0.650394	0.815009	-6.73
260655_at	pathogenesis-related protein 5 precurso	---	AT1G19320	-1.08	-0.11	-0.47	0.650828	0.815250	-6.73
247810_at	26S proteasome AAA-ATPase subunit F	RPT3	AT5G58290	1.04	0.05	0.47	0.650877	0.815250	-6.73
266770_at	putative expansin Experimental evidenc	ATEXPA1	AT2G03090	1.06	0.09	0.47	0.650851	0.815250	-6.73
260965_s_a	hypothetical protein predicted by genem	---	---	1.03	0.05	0.47	0.650839	0.815250	-6.73
256280_at	unknown protein	---	AT3G12590	1.04	0.06	0.47	0.650807	0.815250	-6.73
250205_at	unknown protein	---	AT5G14020	1.04	0.05	0.47	0.650784	0.815250	-6.73
254596_at	putative protein proline-rich protein AP(	---	AT4G18975	-1.04	-0.05	-0.47	0.650872	0.815250	-6.73
261312_at	putative NPK1-related protein kinase 2 p	---	AT1G05790	1.04	0.06	0.47	0.65081	0.815250	-6.73
253694_at	Expressed protein ; supported by full-ler	---	AT4G29735	-1.04	-0.06	-0.47	0.65107	0.815402	-6.73
253454_at	Expressed protein ; supported by cDNA	---	AT4G31875	1.07	0.09	0.47	0.651059	0.815402	-6.73
256614_at	hypothetical protein predicted by genem	---	AT3G29300	1.04	0.05	0.47	0.651202	0.815450	-6.73
253771_at	hypothetical protein ;supported by full-le	---	AT4G28430	-1.04	-0.06	-0.47	0.651194	0.815450	-6.73
248345_at	unknown protein	SHOC1	AT5G52290	1.03	0.05	0.47	0.651216	0.815450	-6.73
258214_at	amidase, putative similar to amidase G	atToc64-III	AT3G17970	-1.07	-0.10	-0.47	0.651397	0.815543	-6.73
259002_at	putative glutaredoxin similar to glutaredo	ROXY1	AT3G02000	-1.06	-0.08	-0.47	0.651394	0.815543	-6.73
265459_at	unknown protein ; supported by full-leng	---	AT2G46540	1.03	0.05	0.47	0.65138	0.815543	-6.73
252213_at	flavonol synthase - like protein SRG1 p	---	AT3G50210	1.05	0.07	0.47	0.651561	0.815613	-6.73
264343_at	unknown protein ; supported by full-leng	---	AT1G11850	1.06	0.09	0.47	0.651558	0.815613	-6.73
256783_at	casein kinase, putative similar to casein	---	AT3G13670	1.03	0.04	0.47	0.651533	0.815613	-6.73
260091_at	putative serine carboxypeptidase simila	scpl5	AT1G73290	-1.04	-0.05	-0.47	0.651683	0.815722	-6.73
248548_at	transmembrane transport protein-like	---	AT5G50300	1.03	0.05	0.47	0.651922	0.815752	-6.73
256748_x_a	En/Spm transposon protein, putative sir	---	---	-1.04	-0.06	-0.47	0.651794	0.815752	-6.73
256206_at	hypothetical protein predicted by genem	---	AT1G50910	1.05	0.08	0.47	0.651863	0.815752	-6.73
252804_at	putative protein	---	---	1.03	0.04	0.47	0.651781	0.815752	-6.73
261937_at	peptide transporter, putative similar to p	---	AT1G22570	-1.09	-0.13	-0.47	0.651908	0.815752	-6.73
256693_at	hypothetical protein predicted by genem	---	---	1.03	0.05	0.47	0.651894	0.815752	-6.73
265700_at	putative MYB family transcription factor	---	AT2G03470	1.03	0.04	0.47	0.651989	0.815791	-6.73
254007_s_a	putative protein RNA-directed DNA poly	---	AT1G60720	1.03	0.05	0.47	0.652094	0.815878	-6.73
251529_at	ATP-dependent RNA helicase-like prote	---	AT3G58570	1.04	0.05	0.47	0.652379	0.816190	-6.73
264481_at	transcription factor TINY, putative simila	---	AT1G77200	-1.04	-0.06	-0.47	0.652725	0.816578	-6.73

245782_at	60S ribosomal protein (fragment), putat	---	AT1G35200	-1.05	-0.07	-0.47	0.652933	0.816792	-6.73
252816_at	putative protein several putative protein	---	AT3G42550	1.03	0.04	0.47	0.653019	0.816855	-6.73
252554_s_a	protein kinase - like receptor-like protei	MEE39	AT3G45920 /	-1.03	-0.05	-0.47	0.653061	0.816863	-6.73
250157_at	prx10 peroxidase - like protein prx10 pe	---	AT5G15180	1.04	0.05	0.47	0.653164	0.816903	-6.73
258221_at	Snf1-related protein kinase KIN11 (AKIN	AKIN11	AT3G29160	-1.07	-0.10	-0.47	0.653128	0.816903	-6.73
251557_at	v-ATPase subunit D (vATPD) ; supporte	---	AT3G58730	-1.04	-0.05	-0.47	0.653235	0.816946	-6.73
264104_at	En/Spm-like transposon protein related	---	---	-1.04	-0.06	-0.47	0.653469	0.817194	-6.73
257330_at	hypothetical protein	---	---	-1.04	-0.05	-0.47	0.653546	0.817246	-6.73
247752_at	putative protein	---	AT5G59060	1.03	0.04	0.47	0.653589	0.817255	-6.73
251294_at	zinc transporter-like protein zinc transp	MTPA1	AT3G61940	-1.04	-0.05	-0.47	0.65382	0.817498	-6.73
254334_at	predicted protein	---	AT4G22760	-1.04	-0.06	-0.47	0.653888	0.817540	-6.73
258094_at	putative cytochrome P450 similar to GB	CYP72A15	AT3G14690	1.04	0.06	0.47	0.653959	0.817583	-6.73
247058_at	dolichyl-di-phosphooligosaccharide-prot	DGL1	AT5G66680	-1.04	-0.06	-0.47	0.65402	0.817614	-6.73
246562_at	putative protein unknown protein F14P1	LNG1	AT5G15580	1.24	0.31	0.47	0.654168	0.817755	-6.73
258721_at	unknown protein similar to hypothetical	---	AT3G09560	-1.06	-0.08	-0.47	0.654269	0.817798	-6.73
252641_at	putative protein predicted protein, Arabi	---	AT3G44570	1.04	0.05	0.47	0.654274	0.817798	-6.73
265289_at	unknown protein predicted by genscan;s	---	AT2G22690	1.03	0.04	0.47	0.654369	0.817871	-6.73
255672_at	hypothetical protein ; supported by cDN	EDA8	AT4G00310	1.04	0.06	0.47	0.654677	0.818212	-6.73
263337_at	hypothetical protein predicted by gensca	---	---	-1.03	-0.04	-0.47	0.654803	0.818218	-6.73
252069_s_a	putative protein putative protein T18N14	---	AT3G51640 /	-1.04	-0.05	-0.47	0.654825	0.818218	-6.73
247430_at	putative protein contains similarity to DN	---	AT5G62610	1.04	0.06	0.47	0.654728	0.818218	-6.73
265196_at	hypothetical protein predicted by gensca	SWC2	AT2G36740	-1.05	-0.07	-0.47	0.654811	0.818218	-6.73
245603_at	hypothetical protein	---	AT4G14280	1.04	0.06	0.47	0.654953	0.818332	-6.73
257782_at	hypothetical protein predicted by genem	---	AT3G27120 /	1.04	0.06	0.47	0.655209	0.818473	-6.73
249205_at	cycloartenol synthase	MRN1	AT5G42600	-1.07	-0.09	-0.47	0.655148	0.818473	-6.73
263323_at	putative receptor-like protein kinase	---	AT2G04300	-1.04	-0.05	-0.47	0.655183	0.818473	-6.73
259926_at	putative DNA-3-methyladenine glycosyla	---	AT1G75090	-1.03	-0.04	-0.47	0.655167	0.818473	-6.73
265230_s_a	hypothetical protein	---	AT2G07707	-1.05	-0.08	-0.47	0.655271	0.818486	-6.73
259396_at	shaggy-like kinase, putative similar to P	GSK1	AT1G06390	-1.03	-0.05	-0.47	0.655414	0.818486	-6.73
266738_at	unknown protein predicted by genefinde	---	AT2G47010	1.06	0.08	0.47	0.655296	0.818486	-6.73
251535_at	hypothetical protein ;supported by full-le	---	AT3G58540	1.06	0.08	0.47	0.655513	0.818486	-6.73
247103_at	putative protein similar to unknown prote	DAR7	AT5G66610	1.04	0.05	0.47	0.655578	0.818486	-6.73
266186_at	unknown protein	AERO2	AT2G38960	-1.03	-0.04	-0.47	0.65553	0.818486	-6.73
263535_at	hypothetical protein predicted by gensca	---	AT2G24970	-1.05	-0.06	-0.47	0.655346	0.818486	-6.73
263524_x_a	hypothetical protein predicted by gensca	---	---	-1.05	-0.07	-0.47	0.655518	0.818486	-6.73

255311_at	putative protein	---	---	-1.03	-0.05	-0.47	0.655518	0.818486	-6.73
267149_s_a	Mutator-like transposase similar to MUF	---	---	-1.05	-0.07	-0.47	0.655562	0.818486	-6.73
252180_at	putative protein cyclin-dependent kinas	KRP2	AT3G50630	1.06	0.08	0.47	0.655723	0.818596	-6.73
258779_at	putative protein kinase contains Pfam pr	---	AT3G11870	-1.03	-0.04	-0.47	0.65581	0.818596	-6.73
248822_at	peroxidase ;supported by full-length cD	---	AT5G47000	1.03	0.05	0.47	0.655794	0.818596	-6.73
256867_at	hypothetical protein predicted by genem	---	AT3G26390	1.03	0.05	0.47	0.655772	0.818596	-6.73
247521_at	putative protein ATP/GTP nucleotide-bi	---	AT5G61450	-1.04	-0.06	-0.47	0.655875	0.818633	-6.73
261137_at	auxin-induced protein, putative similar t	---	AT1G19830	1.03	0.05	0.47	0.655951	0.818683	-6.73
259932_at	zinc finger protein, putative similar to G	STOP1	AT1G34370	1.04	0.06	0.47	0.656337	0.818795	-6.73
250627_at	putative amidase	---	AT5G07360	1.04	0.06	0.47	0.656304	0.818795	-6.73
260389_at	Expressed protein ; supported by full-ler	---	AT1G74055	1.06	0.08	0.47	0.656116	0.818795	-6.73
248957_at	26S proteasome subunit-like protein	---	AT5G45620	1.04	0.05	0.47	0.656364	0.818795	-6.73
264397_at	hypothetical protein	---	AT1G11820	1.05	0.08	0.47	0.656136	0.818795	-6.73
256176_at	hypothetical protein predicted by genem	ATEXO70(	AT1G51640	1.03	0.05	0.47	0.656307	0.818795	-6.73
265364_at	putative retroelement pol polyprotein	---	---	1.03	0.05	0.47	0.656333	0.818795	-6.73
266191_at	putative peroxidase	---	AT2G39040	1.04	0.06	0.47	0.656249	0.818795	-6.73
255722_at	hypothetical protein	---	AT3G29570	-1.04	-0.06	-0.47	0.656205	0.818795	-6.73
247282_at	putative protein strong similarity to unkn	AtMC3	AT5G64240	1.04	0.06	0.47	0.65647	0.818879	-6.73
247259_at	CPR5 protein, putative Constitutive exp	CPR5	AT5G64930	-1.05	-0.08	-0.46	0.656691	0.818879	-6.73
251280_at	putative protein beta-1,3-glucanase pre	---	AT3G61810	-1.04	-0.05	-0.46	0.656719	0.818879	-6.73
265557_at	unknown protein	---	---	1.04	0.06	0.46	0.656667	0.818879	-6.73
251458_at	putative protein several retrotransposon	---	---	1.04	0.05	0.47	0.656591	0.818879	-6.73
266107_at	hypothetical protein predicted by gensca	---	AT2G37910	1.06	0.08	0.47	0.656566	0.818879	-6.73
255391_at	hypothetical protein similar to T6P5.7, (	---	---	-1.03	-0.04	-0.47	0.656577	0.818879	-6.73
254714_at	myb-like protein snapdragon myb prote	AtMYB79	AT4G13480	1.03	0.05	0.46	0.656684	0.818879	-6.73
256808_at	unknown protein	ALY3	AT3G21430	1.03	0.04	0.46	0.657053	0.818966	-6.73
249589_at	pyridoxal kinase -like protein pyridoxal I	SOS4	AT5G37850	1.03	0.04	0.46	0.656856	0.818966	-6.73
249955_at	sugar transporter - like protein probable	---	AT5G18840	1.10	0.13	0.46	0.656939	0.818966	-6.73
258473_s_a	putative stearoyl-acyl carrier protein des	---	AT3G02610 /	-1.06	-0.08	-0.46	0.657094	0.818966	-6.73
250597_at	NAM (no apical meristem)-like protein ;	ANAC080	AT5G07680	-1.08	-0.11	-0.46	0.656956	0.818966	-6.73
256552_at	hypothetical protein predicted by genem	---	AT3G31350	1.04	0.06	0.46	0.657017	0.818966	-6.73
266654_at	putative oleosin protein	---	AT2G25890	1.05	0.07	0.46	0.657079	0.818966	-6.73
254379_at	putative protein calmodulin-binding prot	---	AT4G21820	-1.03	-0.04	-0.46	0.657111	0.818966	-6.73
246530_at	Expressed protein ; supported by full-ler	---	AT5G15725	-1.03	-0.05	-0.46	0.657089	0.818966	-6.73
263672_at	putative retroelement pol polyprotein	---	---	1.03	0.05	0.46	0.65721	0.819043	-6.73

254663_at	potassium channel protein KAT2	KAT2	AT4G18290	1.05	0.07	0.46	0.657418	0.819258	-6.73
250656_at	putative protein contains similarity to unl	---	AT5G06970	-1.05	-0.08	-0.46	0.657568	0.819356	-6.73
255919_at	putative protein	---	---	1.04	0.05	0.46	0.657537	0.819356	-6.73
258387_at	hypothetical protein predicted by gensca	---	AT3G15550	1.04	0.06	0.46	0.657699	0.819475	-6.73
253230_at	putative protein ; supported by full-leng	---	AT4G34700	1.04	0.05	0.46	0.657748	0.819491	-6.73
266921_at	putative cytochrome P450	CYP86A8	AT2G45970	1.11	0.15	0.46	0.658008	0.819593	-6.73
256360_at	hypothetical protein	---	AT1G66440	-1.05	-0.07	-0.46	0.65787	0.819593	-6.73
248400_at	putative protein contains similarity to AP	---	AT5G52020	-1.05	-0.07	-0.46	0.658111	0.819593	-6.73
257165_at	beta-1,3-glucanase, putative similar to I	---	AT3G24330	-1.05	-0.08	-0.46	0.658042	0.819593	-6.73
254156_at	Rab geranylgeranyl transferase like pro	---	AT4G24490	-1.05	-0.07	-0.46	0.658116	0.819593	-6.73
262765_at	putative cytochrome P450 monooxygen	CYP86C4	AT1G13150	1.04	0.06	0.46	0.658037	0.819593	-6.73
263640_at	hypothetical protein predicted by gensca	---	AT2G25270	-1.04	-0.05	-0.46	0.658118	0.819593	-6.73
251988_at	CYTOCHROME P450-like protein CYT	CYP71B31	AT3G53300	1.03	0.04	0.46	0.658021	0.819593	-6.73
258547_at	unknown protein	---	AT3G06895	-1.03	-0.04	-0.46	0.658181	0.819627	-6.73
251338_at	putative protein VAP27, Nicotiana plum	VAP	AT3G60600 /	1.03	0.05	0.46	0.658333	0.819637	-6.73
250445_at	nucleoid DNA-binding protein cnd41 - li	---	AT5G10760	1.30	0.37	0.46	0.658293	0.819637	-6.73
258802_at	unknown protein predicted by genscan,	---	AT3G04650	-1.05	-0.07	-0.46	0.658257	0.819637	-6.73
259939_s_a	ARE1-like protein similar to ARE1 GB:C	---	AT1G71270 /	1.05	0.07	0.46	0.658332	0.819637	-6.73
257128_at	cytochrome P450, putative contains Pfa	CYP705A1	AT3G20080	-1.05	-0.07	-0.46	0.658488	0.819785	-6.73
261478_at	unknown protein	MIOX1	AT1G14520	1.06	0.08	0.46	0.658588	0.819866	-6.73
253766_at	putative protein ;supported by full-lengt	---	AT4G28770	-1.04	-0.05	-0.46	0.658657	0.819894	-6.73
251067_at	hypothetical protein	---	AT5G01910	-1.06	-0.08	-0.46	0.658683	0.819894	-6.73
258867_at	hypothetical protein predicted by genefir	---	AT3G03130	-1.04	-0.05	-0.46	0.658762	0.819948	-6.73
245411_at	hypothetical protein	---	AT4G17240	-1.07	-0.09	-0.46	0.65903	0.820102	-6.73
262994_at	hypothetical protein predicted by gensca	---	AT1G54420	-1.03	-0.04	-0.46	0.659012	0.820102	-6.73
248903_at	3-oxoacyl-[acyl-carrier-protein] synthase	KAS I	AT5G46290	1.07	0.10	0.46	0.658951	0.820102	-6.73
246942_at	anion exchanger-like protein chloride-bi	---	AT5G25430	-1.04	-0.06	-0.46	0.658967	0.820102	-6.73
262497_at	putative 20S proteasome beta subunit F	PBC1	AT1G21720	-1.04	-0.05	-0.46	0.659098	0.820142	-6.73
252692_at	cysteine proteinase contains similarity t	---	AT3G43960	1.09	0.13	0.46	0.659205	0.820231	-6.73
259023_at	unknown protein ; supported by cDNA:	---	AT3G07510	-1.06	-0.09	-0.46	0.659242	0.820232	-6.73
260853_at	hypothetical protein predicted by genem	---	AT1G21950	-1.06	-0.08	-0.46	0.659537	0.820554	-6.73
244941_at	hypothetical protein	---	---	-1.04	-0.06	-0.46	0.659624	0.820617	-6.73
258450_at	hypothetical protein predicted by gensc	---	---	1.04	0.05	0.46	0.659662	0.820620	-6.73
259713_at	unknown protein similar to phosphate tr	---	AT1G77610	-1.05	-0.08	-0.46	0.659732	0.820662	-6.73
266833_at	hypothetical protein predicted by gensca	---	---	-1.03	-0.04	-0.46	0.659894	0.820774	-6.73

256515_at	terpene synthase, putative contains Pfa	---	AT1G66020	-1.04	-0.05	-0.46	0.659892	0.820774	-6.73
247299_at	putative protein contains similarity to PH	---	AT5G63900	-1.03	-0.05	-0.46	0.660182	0.821087	-6.73
267354_at	putative MYB family transcription factor	MYB25	AT2G39880	1.06	0.08	0.46	0.660325	0.821098	-6.73
262808_at	Avr9 elicitor response-like protein strong	---	AT1G11730	-1.04	-0.05	-0.46	0.660334	0.821098	-6.73
252518_at	receptor-like protein kinase homolog lig	---	AT3G46350	-1.04	-0.05	-0.46	0.660316	0.821098	-6.73
252926_at	H+-transporting ATPase 16K chain P2,	ATVHA-C3	AT4G38920	1.04	0.06	0.46	0.660232	0.821098	-6.73
260810_s_a	retroelement protein, putative similar to	---	---	1.04	0.05	0.46	0.660558	0.821331	-6.74
259839_at	peptide transporter, putative similar to p	---	AT1G52190	-1.22	-0.29	-0.46	0.660833	0.821629	-6.74
264966_at	hypothetical protein predicted by genem	---	AT1G60570	1.05	0.07	0.46	0.661023	0.821820	-6.74
267566_at	unknown protein predicted by genscan	---	AT2G30760	1.03	0.04	0.46	0.66116	0.821856	-6.74
249935_at	acyl CoA reductase-like protein	FAR7	AT5G22420	1.03	0.05	0.46	0.661139	0.821856	-6.74
264425_at	serine/threonine protein kinase, putative	---	AT1G61750	-1.03	-0.05	-0.46	0.66115	0.821856	-6.74
253215_at	putative protein AT.I.24-7, Arabidopsis	---	AT4G34950	-1.10	-0.14	-0.46	0.661354	0.822016	-6.74
256127_at	small GTP-binding protein (RAB11F), p	AtRABA6b	AT1G18200	1.04	0.06	0.46	0.661384	0.822016	-6.74
248150_at	kinesin-like protein ; supported by cDNA	ATK3	AT5G54670	1.09	0.13	0.46	0.661396	0.822016	-6.74
256021_at	unknown protein contains Pfam profile:	ZW9	AT1G58270	1.06	0.08	0.46	0.661541	0.822089	-6.74
248623_at	putative protein similar to unknown prote	---	AT5G49170	1.13	0.18	0.46	0.661635	0.822089	-6.74
262289_at	unknown protein identical to unknown p	---	AT1G70770	1.03	0.05	0.46	0.66161	0.822089	-6.74
260072_at	unknown protein supported by cDNA: C	---	AT1G73650	1.04	0.06	0.46	0.661568	0.822089	-6.74
260811_s_a	hypothetical protein predicted by genem	---	---	-1.03	-0.04	-0.46	0.661543	0.822089	-6.74
253720_at	acid phosphatase-like protein acid pho	---	AT4G29270	-1.03	-0.05	-0.46	0.661782	0.822227	-6.74
257504_at	dynein light chain, putative similar to dy	ROPGEF1	AT1G52240	1.08	0.11	0.46	0.661855	0.822234	-6.74
266199_at	putative calcium-dependent protein kina	CPK20	AT2G38910	-1.03	-0.05	-0.46	0.661896	0.822234	-6.74
247003_at	putative protein similar to unknown prote	---	AT5G67550	1.05	0.07	0.46	0.661874	0.822234	-6.74
265170_at	putative carbonic anhydrase	BCA3	AT1G23730	-1.23	-0.30	-0.46	0.661933	0.822235	-6.74
245549_at	cellulose synthase like protein	ATCSLB06	AT4G15320	-1.04	-0.05	-0.46	0.662013	0.822290	-6.74
266891_at	putative GTP-binding protein ; supporte	ARAC9	AT2G44690	1.04	0.06	0.46	0.662101	0.822309	-6.74
265217_s_a	unknown protein ESTs gb|H76594 and g	---	AT1G05090 /	-1.05	-0.08	-0.46	0.66207	0.822309	-6.74
245313_at	UFD1 like protein ; supported by full-len	---	AT4G15420	1.04	0.06	0.46	0.662151	0.822326	-6.74
265786_at	putative replication protein A1	---	---	-1.03	-0.04	-0.46	0.662311	0.822435	-6.74
246299_at	embryonic abundant protein AtEm1	EM1	AT3G51810	-1.03	-0.04	-0.46	0.662309	0.822435	-6.74
265579_at	hypothetical protein predicted by gensca	---	AT2G20070	1.04	0.05	0.46	0.662354	0.822443	-6.74
255818_at	hypothetical protein predicted by genefir	---	AT2G33570	1.11	0.15	0.46	0.662487	0.822475	-6.74
254205_at	putative protein kinesin heavy chain -St	---	AT4G24170	1.04	0.06	0.46	0.662467	0.822475	-6.74
253712_at	putative protein putative NADH oxidore	DER1	AT4G29330	-1.04	-0.06	-0.46	0.662421	0.822475	-6.74

255834_at	putative RNA-binding protein	---	AT2G33410	-1.03	-0.04	-0.46	0.662594	0.822533	-6.74
262008_s_a	CACTA-element, putative similar to TNI	---	---	-1.05	-0.06	-0.46	0.662606	0.822533	-6.74
251071_at	putative protein receptor protein kinases	---	AT5G01950	1.06	0.09	0.46	0.662793	0.822720	-6.74
253848_at	putative protein regulator protein, Pseu	---	AT4G28020	-1.05	-0.07	-0.46	0.662834	0.822726	-6.74
251449_at	Rab GDP dissociation inhibitor ; suppor	ATGDI2	AT3G59920	1.05	0.07	0.46	0.662943	0.822817	-6.74
256353_at	unknown protein ; supported by full-leng	---	AT1G55000	-1.04	-0.05	-0.46	0.66302	0.822868	-6.74
247513_at	quinone oxidoreductase - like protein q	---	AT5G61510	1.05	0.07	0.46	0.663108	0.822933	-6.74
260319_at	hypothetical protein predicted by genefi	---	AT1G63950	1.05	0.06	0.46	0.663181	0.822978	-6.74
258438_at	hypothetical protein predicted by gensca	---	AT3G17230	1.03	0.04	0.46	0.663308	0.823091	-6.74
254123_at	Bnm1 like protein pollen-specific protei	APPB1	AT4G24640	-1.04	-0.05	-0.45	0.66348	0.823259	-6.74
261765_at	cyclin, putative similar to cyclin GI:5621	CYCA2;3	AT1G15570	1.04	0.06	0.45	0.663544	0.823294	-6.74
246338_s_a	putative protein putative integral membr	ATCHX10	AT3G44920 /	-1.03	-0.04	-0.45	0.663596	0.823314	-6.74
250561_at	glycerophosphodiester phosphodiestera	---	AT5G08030	-1.05	-0.06	-0.45	0.663708	0.823318	-6.74
261493_at	DNA-binding protein p24, putative simil	WHY1	AT1G14410	-1.06	-0.08	-0.45	0.663702	0.823318	-6.74
254169_at	putative protein ; supported by cDNA: g	---	AT4G24290	-1.05	-0.07	-0.45	0.66367	0.823318	-6.74
247412_at	unknown protein	---	AT5G63010	1.04	0.06	0.45	0.663751	0.823327	-6.74
253880_at	Expressed protein ;supported by cDNA:	---	AT4G27590	1.04	0.06	0.45	0.663848	0.823403	-6.74
247674_at	putative protein large number of predict	---	AT5G59930	1.05	0.07	0.45	0.663928	0.823457	-6.74
267408_at	putative CTP synthase	---	AT2G34890	-1.03	-0.05	-0.45	0.664088	0.823610	-6.74
266943_at	putative reverse transcriptase	---	---	1.05	0.08	0.45	0.664211	0.823718	-6.74
257257_at	hypothetical protein contains Pfam profil	---	AT3G22020	1.03	0.04	0.45	0.664398	0.823905	-6.74
252877_at	hypothetical protein supported by full-ler	---	AT4G39630	-1.04	-0.06	-0.45	0.664441	0.823915	-6.74
249526_at	putative protein contains similarity to pro	---	AT5G38560	1.05	0.07	0.45	0.664536	0.823987	-6.74
254637_at	putative protein KIAA0244 gene, Homo	---	AT4G18720	-1.04	-0.05	-0.45	0.664625	0.824053	-6.74
261426_at	unknown protein contains similarity to D	---	AT1G18680	1.03	0.05	0.45	0.66467	0.824063	-6.74
251047_at	putative protein mature-parasite-infecte	---	AT5G02390	1.04	0.06	0.45	0.664746	0.824114	-6.74
250103_at	transcription factor (gb|AAD53095.1) ; s	MYB43	AT5G16600	1.04	0.05	0.45	0.664813	0.824151	-6.74
252746_at	sucrose synthase -like protein SUCROS	SUS4	AT3G43190	-1.04	-0.05	-0.45	0.664971	0.824268	-6.74
261683_at	hypothetical protein similar to hypothetic	---	AT1G47300	-1.03	-0.05	-0.45	0.66498	0.824268	-6.74
254313_at	extensin like protein extensin like protei	---	AT4G22460	-1.04	-0.06	-0.45	0.665108	0.824383	-6.74
251292_at	putative protein hypothetical protein F1	---	AT3G61920	1.05	0.07	0.45	0.665305	0.824582	-6.74
249178_at	putative protein similar to unknown prote	SCP2	AT5G42890	1.03	0.05	0.45	0.665499	0.824778	-6.74
256421_at	hypothetical protein predicted by genem	---	AT1G33500	1.03	0.05	0.45	0.665542	0.824787	-6.74
252581_at	hypothetical protein	---	AT3G45500	1.04	0.06	0.45	0.665615	0.824797	-6.74
265904_at	putative beta-glucosidase	BGLU14	AT2G25630	1.04	0.05	0.45	0.665623	0.824797	-6.74

256367_at	C-x8-C-x5-C-x3-H type Zinc finger prote	---	AT1G66810	1.04	0.06	0.45	0.665965	0.824898	-6.74
262434_at	lysine and histidine specific transporter,	---	AT1G47670	-1.07	-0.10	-0.45	0.665994	0.824898	-6.74
262110_at	SF2/ASF-like splicing modulator Srp30,	SR1	AT1G02840	-1.05	-0.06	-0.45	0.665902	0.824898	-6.74
251491_at	fructokinase-like protein fructokinase - l	---	AT3G59480	1.05	0.08	0.45	0.665819	0.824898	-6.74
246684_at	putative protein nucleoid DNA-binding p	CDR1	AT5G33340	1.05	0.07	0.45	0.665749	0.824898	-6.74
246102_at	putative protein various predicted prote	---	AT5G32590	-1.03	-0.05	-0.45	0.66588	0.824898	-6.74
263992_at	putative retroelement pol polyprotein	---	---	1.03	0.05	0.45	0.665934	0.824898	-6.74
252489_at	disease resistance protein RPP8-like pr	---	AT3G46710	1.04	0.06	0.45	0.665869	0.824898	-6.74
262051_at	putative coatomer protein complex, sub	---	AT1G79990	1.04	0.06	0.45	0.666124	0.824925	-6.74
262889_at	hypothetical protein	---	AT1G14800	1.05	0.07	0.45	0.666121	0.824925	-6.74
258522_at	hypothetical protein predicted by genem	---	AT3G06660	1.06	0.08	0.45	0.666064	0.824925	-6.74
266060_at	unknown protein unusual splice site at s	---	AT2G18630	1.05	0.07	0.45	0.666252	0.825038	-6.74
263204_at	hypothetical protein contains similarity to	chr31	AT1G05490	-1.03	-0.04	-0.45	0.66632	0.825078	-6.74
252279_at	1-aminocyclopropane-1-carboxylate syn	ACS9	AT3G49700	1.04	0.06	0.45	0.666532	0.825295	-6.74
250118_at	putative protein similar to unknown prote	---	AT5G16460	1.04	0.05	0.45	0.666653	0.825348	-6.74
261714_at	hypothetical protein similar to hypothetic	TET16	AT1G18510	1.05	0.07	0.45	0.666622	0.825348	-6.74
254583_at	hypothetical protein	---	AT4G19480	-1.04	-0.05	-0.45	0.666683	0.825348	-6.74
247135_at	auxin-induced protein-like	---	AT5G66260	1.03	0.04	0.45	0.66679	0.825436	-6.74
251412_at	RING-H2 zinc finger protein ATL4 ; sup	ATL4	AT3G60220	1.09	0.12	0.45	0.666862	0.825480	-6.74
260920_at	amp-binding protein, putative similar to	---	AT1G21530	-1.03	-0.04	-0.45	0.666941	0.825534	-6.74
257099_s_a	disease resistance protein, putative, 3'	---	AT3G24982 /	1.03	0.04	0.45	0.667081	0.825616	-6.74
245177_at	annexin-like protein genmodel supporte	---	AT5G12380	1.04	0.05	0.45	0.66706	0.825616	-6.74
260131_at	unknown protein contains Pfam profile:	---	AT1G66310	-1.04	-0.05	-0.45	0.667161	0.825671	-6.74
251468_at	epsin-like protein Af10-protein - Avena	---	AT3G59290	-1.04	-0.05	-0.45	0.667206	0.825682	-6.74
253789_at	putative protein predicted proteins, Arat	---	AT4G28570	1.05	0.06	0.45	0.667348	0.825752	-6.74
249704_at	Myb-related transcription factor LBM2-lil	TT2	AT5G35550	1.05	0.07	0.45	0.667371	0.825752	-6.74
254748_at	unknown protein	---	---	-1.03	-0.05	-0.45	0.667334	0.825752	-6.74
255177_at	strong similarity to 1-aminocyclopropane	ACS11	AT4G08040	1.12	0.16	0.45	0.667467	0.825785	-6.74
266498_at	1-aminocyclopropane-1-carboxylate oxi	---	AT2G06960	1.03	0.05	0.45	0.66747	0.825785	-6.74
266851_at	similar to avrRpt2-induced protein 1	ATPP2-A3	AT2G26820	1.03	0.04	0.45	0.667638	0.825813	-6.74
256951_at	hypothetical protein predicted by genem	---	AT3G19085	-1.03	-0.04	-0.45	0.667605	0.825813	-6.74
263315_at	Expressed protein ; supported by full-ler	---	AT2G05755	1.03	0.04	0.45	0.667551	0.825813	-6.74
266307_at	putative cytochrome P450	CYP705A8	AT2G27000	-1.04	-0.06	-0.45	0.667608	0.825813	-6.74
248344_at	hyaluronan mediated motility receptor-lil	---	AT5G52280	-1.07	-0.10	-0.45	0.667709	0.825856	-6.74
265666_at	putative rac GTPase activating protein	---	AT2G27440	-1.03	-0.04	-0.45	0.66782	0.825949	-6.74

262913_at	NADPH-dependent codeinone reductas	---	AT1G59960	-1.10	-0.14	-0.45	0.667892	0.825993	-6.74
248609_at	unknown protein ; supported by cDNA:	---	AT5G49440	1.04	0.06	0.45	0.667952	0.826022	-6.74
258533_at	hypothetical protein	---	AT3G06670	1.04	0.06	0.45	0.668045	0.826092	-6.74
247647_at	respiratory burst oxidase protein - like r	---	AT5G60010	-1.04	-0.05	-0.45	0.668123	0.826144	-6.74
257993_at	hypothetical protein similar to hypothetic	---	AT3G19890	-1.03	-0.05	-0.45	0.668301	0.826320	-6.74
245944_at	putative protein various predicted prote	MSL9	AT5G19520	1.04	0.05	0.45	0.668348	0.826333	-6.74
264448_at	putative sensory transduction histidine k	AHK3	AT1G27320	1.03	0.04	0.45	0.668597	0.826596	-6.74
247534_at	pyrophosphate-dependent phosphofruc	PFK4	AT5G61580	-1.03	-0.04	-0.45	0.668643	0.826608	-6.74
249915_at	putative protein similar to unknown prote	---	AT5G22870	1.03	0.05	0.45	0.668773	0.826634	-6.74
246298_at	putative protein sequence in GenBank A	ETO1	AT3G51770	-1.03	-0.05	-0.45	0.668766	0.826634	-6.74
252522_at	hypothetical protein	---	AT1G32337 /	1.03	0.05	0.45	0.668766	0.826634	-6.74
258111_at	putative cytochrome P450 similar to GB	CYP72A9	AT3G14630	-1.05	-0.07	-0.45	0.668828	0.826658	-6.74
260240_at	putative tRNA isopentenyl transferase s	ATIPT1	AT1G68460	-1.03	-0.05	-0.45	0.668894	0.826695	-6.74
257938_at	cell elongation protein, Dwarf1 identical	DWF1	AT3G19820	1.17	0.22	0.45	0.668966	0.826738	-6.74
249733_at	6-phosphogluconolactonase-like protein	emb2024	AT5G24400	1.04	0.05	0.45	0.669019	0.826738	-6.74
259620_s_a	Tam3-like transposon protein similar to	---	---	1.05	0.08	0.45	0.669038	0.826738	-6.74
264075_at	envelope-like protein identical to GB:AA	---	---	1.05	0.07	0.45	0.669245	0.826950	-6.74
267157_at	putative MYB family transcription factor	AS1	AT2G37630	1.06	0.08	0.45	0.669381	0.826966	-6.74
262355_at	unknown protein	---	AT1G72820	-1.05	-0.07	-0.45	0.66939	0.826966	-6.74
260181_at	endo-1,4-beta-glucanase identical to er	ATGH9B1	AT1G70710	-1.09	-0.12	-0.45	0.669391	0.826966	-6.74
247798_at	subtilisin-like serine protease contains s	---	AT5G58830	-1.03	-0.04	-0.45	0.669403	0.826966	-6.74
251435_at	putative protein hypothetical proteins - A	---	---	-1.03	-0.05	-0.45	0.669456	0.826986	-6.74
265282_at	unknown protein	---	AT2G20380	-1.04	-0.05	-0.45	0.669628	0.827153	-6.74
258170_at	unknown protein similar to senescence-	---	AT3G21600	-1.09	-0.12	-0.45	0.669664	0.827153	-6.74
246740_at	putative protein	---	AT5G27810	1.03	0.04	0.45	0.669789	0.827218	-6.74
254180_at	putative protein hin1 protein homolog, C	---	AT4G23930	-1.06	-0.09	-0.45	0.669778	0.827218	-6.74
263850_at	hypothetical protein predicted by genefir	---	AT2G04480	1.06	0.08	0.45	0.669901	0.827311	-6.74
256217_at	hypothetical protein predicted by genem	---	AT1G56320	1.07	0.10	0.45	0.669995	0.827383	-6.74
260198_at	F12A21.23 hypothetical protein	---	AT1G67635	1.03	0.04	0.45	0.670131	0.827506	-6.74
264274_at	disease resistance protein RPS4, putat	---	AT1G60320	1.04	0.05	0.45	0.670243	0.827534	-6.74
254644_at	CLE2, putative CLAVATA3/ESR-Relate	CLE2	AT4G18510	1.04	0.06	0.44	0.670312	0.827534	-6.74
255765_at	protein kinase, putative contains Pfam p	---	AT1G16760	-1.03	-0.04	-0.44	0.670285	0.827534	-6.74
256031_at	choline kinase (GmCK2p), putative sim	---	AT1G34100	-1.03	-0.05	-0.44	0.670336	0.827534	-6.74
262423_at	hypothetical protein predicted by gensca	---	AT1G23450	-1.03	-0.05	-0.45	0.670223	0.827534	-6.74
253462_at	synaptobrevin-like protein synaptobrevi	ATVAMP7	AT4G32150	-1.04	-0.06	-0.44	0.670601	0.827719	-6.74

249127_at	actin-like protein ; supported by cDNA:	ATARP9	AT5G43500	-1.04	-0.06	-0.44	0.67063	0.827719	-6.74
258711_at	ubiquitin-like protein (UBQ8) identical to	UBQ8	AT3G09790	-1.04	-0.05	-0.44	0.670598	0.827719	-6.74
261200_at	60S ribosomal protein L27a, putative si	---	AT1G12960	1.04	0.05	0.44	0.670547	0.827719	-6.74
265695_at	putative replication protein A1 ;supporte	RPA2	AT2G24490	-1.10	-0.14	-0.44	0.670696	0.827755	-6.74
264715_at	hypothetical protein contains similarity to	---	AT1G70180	-1.04	-0.05	-0.44	0.670794	0.827832	-6.74
264431_at	RNA polymerase II subunit (hsRPB10),	---	AT1G61700	-1.04	-0.06	-0.44	0.670889	0.827904	-6.74
259432_at	myb-related protein, putative similar to	---	AT1G01520	1.05	0.07	0.44	0.671021	0.828022	-6.74
248907_at	putative protein contains similarity to unl	---	AT5G46340	-1.03	-0.05	-0.44	0.67128	0.828055	-6.74
255952_at	MADS-box protein (ZAP1), putative sim	AGL104	AT1G22130	-1.03	-0.04	-0.44	0.671189	0.828055	-6.74
258948_at	putative sulfite oxidase similar to sulfite	SOX	AT3G01910	1.03	0.04	0.44	0.671246	0.828055	-6.74
263407_at	bZIP protein (AtbZIP48) to be published	AtbZIP48	AT2G04038	-1.03	-0.05	-0.44	0.671202	0.828055	-6.74
252645_at	bZIP transcription factor -like protein Dc	DPBF2	AT3G44460	1.04	0.05	0.44	0.671122	0.828055	-6.74
259779_s_a	hypothetical protein predicted by genem	---	AT1G29620 /	-1.04	-0.05	-0.44	0.671302	0.828055	-6.74
260376_at	putative cytochrome P-450 similar to cyt	CYP78A10	AT1G74110	-1.03	-0.05	-0.44	0.671263	0.828055	-6.74
257817_at	putative RNA-binding protein contains R	---	AT3G25150	1.04	0.05	0.44	0.671383	0.828073	-6.74
260387_at	putative flavonol sulfotransferase similar	SOT16	AT1G74100	1.09	0.13	0.44	0.671425	0.828073	-6.74
261811_at	DNA polymerase epsilon catalytic subu	TIL1	AT1G08260	-1.05	-0.08	-0.44	0.671415	0.828073	-6.74
262280_at	unknown protein	---	AT1G68580	1.07	0.10	0.44	0.67171	0.828272	-6.74
247403_at	putative protein hypersensitive-induced	---	AT5G62740	1.04	0.05	0.44	0.671872	0.828272	-6.74
262260_at	major latex protein (MLP149), putative s	MLP34	AT1G70850	1.05	0.07	0.44	0.67168	0.828272	-6.74
253103_at	putative auxin-induced protein high sim	---	AT4G36110	1.19	0.25	0.44	0.671913	0.828272	-6.74
250687_at	putative protein similar to unknown prote	---	AT5G06660	1.03	0.04	0.44	0.671894	0.828272	-6.74
262556_at	hypothetical protein	---	AT1G31370	-1.03	-0.05	-0.44	0.671832	0.828272	-6.74
262723_at	hypothetical protein predicted by genem	---	AT1G43630	1.05	0.07	0.44	0.671882	0.828272	-6.74
267324_at	hypothetical protein predicted by gensca	---	AT2G19360	1.03	0.04	0.44	0.671806	0.828272	-6.74
260906_at	hypothetical protein predicted by genem	---	AT1G02540	-1.03	-0.05	-0.44	0.671767	0.828272	-6.74
258670_at	unknown protein	---	AT3G08810	-1.04	-0.06	-0.44	0.671954	0.828278	-6.74
246208_at	hypothetical protein ; supported by cDN	SFH12	AT4G36490	1.04	0.05	0.44	0.672053	0.828354	-6.74
254858_at	putative protein other predicted proteins	---	AT4G12070	1.04	0.05	0.44	0.672244	0.828545	-6.74
253756_at	Cdk-activating kinase CAK1At ; support	CAK1AT	AT4G28980	1.03	0.04	0.44	0.672348	0.828629	-6.74
252356_at	putative protein various predicted protei	---	---	1.05	0.07	0.44	0.672413	0.828664	-6.74
263175_at	hypothetical protein similar to unknown	---	AT1G05510	1.03	0.04	0.44	0.672472	0.828692	-6.74
254282_at	hypothetical protein	---	AT4G22860	-1.03	-0.05	-0.44	0.672799	0.828960	-6.74
263462_at	similar to Ariadne protein from Drosophi	ARI11	AT2G31780	1.03	0.05	0.44	0.672796	0.828960	-6.74
265358_at	putative HesB-like protein ; supported b	---	AT2G16710	1.05	0.07	0.44	0.672798	0.828960	-6.74

246066_at	putative protein predicted proteins, Hon	SMG7	AT5G19400	1.04	0.06	0.44	0.672891	0.828984	-6.74
262443_at	Expressed protein ; supported by full-ler	---	AT1G47655	1.05	0.07	0.44	0.672882	0.828984	-6.74
260208_s_a	unknown protein similar to Ca+2-binding	---	AT1G70670 /	1.07	0.10	0.44	0.673097	0.829188	-6.74
247269_at	alternative oxidase 2 (sp|O22049)	AOX2	AT5G64210	1.03	0.05	0.44	0.673166	0.829188	-6.74
259777_at	zinc finger protein, putative similar to G	---	AT1G29570	1.03	0.05	0.44	0.673164	0.829188	-6.74
261364_at	dynamin-like protein similar to GB:U255	---	AT1G53140	1.04	0.06	0.44	0.673373	0.829225	-6.74
250615_at	putative protein ankyrins - different spec	---	AT5G07270	-1.04	-0.06	-0.44	0.67332	0.829225	-6.74
260850_at	glucose 6 phosphate/phosphate translo	---	AT1G21870	-1.04	-0.06	-0.44	0.673354	0.829225	-6.74
254139_at	hypothetical protein	---	AT4G24600	1.04	0.06	0.44	0.673269	0.829225	-6.74
261878_at	cytochrome P450, putative similar to CY	CYP705A2	AT1G50560	1.03	0.05	0.44	0.673378	0.829225	-6.74
245684_at	Expressed protein ; supported by cDNA	RHF2A	AT5G22000	1.03	0.05	0.44	0.673467	0.829249	-6.74
263549_at	unknown protein	MEE3	AT2G21650	-1.16	-0.21	-0.44	0.673469	0.829249	-6.74
256969_at	unknown protein	---	AT3G21080	1.13	0.18	0.44	0.673539	0.829289	-6.74
264744_at	hypothetical protein predicted by genem	---	AT1G62050	1.07	0.09	0.44	0.673681	0.829420	-6.74
260104_x_a	hypothetical protein predicted by genem	---	AT1G35410	1.04	0.06	0.44	0.67372	0.829423	-6.74
AFFX-BioDr	E. coli /GEN=bioD /DB_XREF=gb:J0442	---	---	1.09	0.12	0.44	0.673813	0.829426	-6.74
247411_at	putative protein contains similarity to unl	---	AT5G63000	-1.04	-0.06	-0.44	0.673826	0.829426	-6.74
265420_s_a	hypothetical protein predicted by genscar	BRX	AT1G31880 /	1.05	0.07	0.44	0.673831	0.829426	-6.74
250746_at	glucuronosyl transferase-like protein	---	AT5G05880	1.03	0.04	0.44	0.673953	0.829503	-6.74
257425_at	hypothetical protein similar to heat shoc	---	AT1G60400	1.05	0.07	0.44	0.673966	0.829503	-6.74
249109_at	auxin-induced protein AUX2-11 (sp P33	ATAUX2-1	AT5G43700	-1.13	-0.18	-0.44	0.674278	0.829707	-6.75
264088_at	unknown protein	emb1381	AT2G31340	-1.04	-0.05	-0.44	0.674232	0.829707	-6.75
258763_s_a	putative beta-mannan endohydrolase sil	---	AT3G10900 /	1.03	0.04	0.44	0.674175	0.829707	-6.74
257354_x_a	hypothetical protein predicted by genefir	---	---	-1.04	-0.06	-0.44	0.674256	0.829707	-6.75
254174_at	putative protein various predicted protei	YSL1	AT4G24120	-1.06	-0.08	-0.44	0.674413	0.829714	-6.75
249174_at	putative protein similar to unknown prote	---	AT5G42900	-1.07	-0.09	-0.44	0.67437	0.829714	-6.75
256773_at	hypothetical protein predicted by genem	---	AT3G13630	-1.04	-0.05	-0.44	0.674328	0.829714	-6.75
259336_at	hypothetical protein C-term portion simil	SDG20	AT3G03750	1.06	0.08	0.44	0.674567	0.829714	-6.75
248439_at	putative protein similar to unknown prote	---	AT5G51250	-1.03	-0.05	-0.44	0.674506	0.829714	-6.75
265133_s_a	unknown protein similar to hypothetical	---	AT1G51240 /	-1.03	-0.04	-0.44	0.674574	0.829714	-6.75
247451_at	MYB99 ; supported by cDNA: gi_15375	ATMYB99	AT5G62320	1.04	0.06	0.44	0.674534	0.829714	-6.75
248090_at	putative protein contains similarity to NP	MAPKKK1	AT5G55090	1.03	0.04	0.44	0.674508	0.829714	-6.75
252191_at	putative protein various predicted gene	---	AT3G50180	1.04	0.06	0.44	0.674669	0.829768	-6.75
265936_at	putative potassium/proton antiporter	ATKEA4	AT2G19600	-1.04	-0.06	-0.44	0.674691	0.829768	-6.75
255463_at	putative polyprotein of LTR transposon	---	---	1.04	0.05	0.44	0.674764	0.829799	-6.75

251607_at	hypothetical protein	---	AT3G57850	1.03	0.05	0.44	0.674789	0.829799	-6.75
261597_at	hypothetical protein predicted by genem	PUB26	AT1G49780	-1.14	-0.19	-0.44	0.67485	0.829829	-6.75
259772_at	hypothetical protein predicted by genem	---	AT1G29480	1.03	0.04	0.44	0.674945	0.829901	-6.75
245278_at	syntaxin ; supported by cDNA: gi_21493	SYP23	AT4G17730	-1.05	-0.07	-0.44	0.675071	0.830011	-6.75
252484_at	glucuronosyl transferase-like protein glu	---	AT3G46690	1.04	0.06	0.44	0.675334	0.830166	-6.75
249716_at	sterile apetala (emb|CAA11128.1)	SAP	AT5G35770	-1.04	-0.05	-0.44	0.675343	0.830166	-6.75
248109_at	DNA topoisomerase I	TOP1BET	AT5G55310	1.03	0.05	0.44	0.675335	0.830166	-6.75
253128_at	Calcium-dependent serine/threonine pr	CPK18	AT4G36070	1.03	0.04	0.44	0.675237	0.830166	-6.75
256944_at	unknown protein similar to unknown pro	VRN1	AT3G18990	1.05	0.07	0.44	0.675504	0.830305	-6.75
259375_at	putative APG protein similar to anter-spe	---	AT3G16370	1.39	0.47	0.44	0.675622	0.830305	-6.75
262262_at	unknown protein identical to unknown pi	---	AT1G70780 /	1.06	0.08	0.44	0.675634	0.830305	-6.75
257261_s_a	hypothetical protein contains Pfam profil	---	AT3G21920 /	1.03	0.04	0.44	0.675599	0.830305	-6.75
263192_at	hypothetical protein putative acetyl-CoA	ACC1	AT1G36160	-1.05	-0.07	-0.44	0.675638	0.830305	-6.75
250710_at	MYB family transcription factor-like	MYB33	AT5G06100	-1.03	-0.05	-0.44	0.675705	0.830343	-6.75
262400_at	unknown protein ; supported by cDNA: g	RTV1	AT1G49480	-1.03	-0.04	-0.44	0.675762	0.830369	-6.75
246220_at	putative protein ; supported by cDNA: gi	---	AT4G37210	-1.03	-0.05	-0.44	0.67583	0.830407	-6.75
259674_at	thaumatin-like protein similar to thaumat	---	AT1G77700	1.04	0.06	0.44	0.675891	0.830423	-6.75
245056_at	putative glucosyltransferase	UGT76D1	AT2G26480	1.05	0.07	0.44	0.67594	0.830423	-6.75
267443_at	hypothetical protein predicted by genefin	---	AT2G19000	1.03	0.04	0.44	0.675952	0.830423	-6.75
256128_at	laccase, putative similar to high-pI lacca	LAC1	AT1G18140	-1.04	-0.05	-0.44	0.676057	0.830507	-6.75
264060_at	hypothetical protein predicted by gensca	---	AT2G27980	1.03	0.04	0.44	0.676162	0.830591	-6.75
265333_at	hypothetical protein predicted by gensca	AtHB24	AT2G18350	-1.05	-0.07	-0.44	0.676203	0.830597	-6.75
247729_at	1-aminocyclopropane-1-carboxylate oxi	---	AT5G59530	1.07	0.10	0.44	0.676474	0.830622	-6.75
262891_at	ent-kaurene synthase, putative similar t	GA2	AT1G79460	1.06	0.08	0.44	0.676368	0.830622	-6.75
267311_at	hypothetical protein	---	AT2G34670	1.03	0.04	0.44	0.676493	0.830622	-6.75
261809_at	rac GTPase activating protein, putative	---	AT1G08340	1.05	0.07	0.44	0.676514	0.830622	-6.75
250632_at	putative protein cyclin 2 - Trypanosoma	CYCP4;3	AT5G07450	1.04	0.06	0.44	0.676301	0.830622	-6.75
251913_at	putative protein several malat dehydrog	---	AT3G53910	1.03	0.05	0.44	0.676292	0.830622	-6.75
255393_at	hypothetical protein	---	---	-1.03	-0.04	-0.44	0.676497	0.830622	-6.75
263007_at	hypothetical protein contains similarity to	---	AT1G54260	-1.03	-0.05	-0.44	0.676461	0.830622	-6.75
265228_s_a	hypothetical protein	---	AT2G07698	-1.04	-0.06	-0.44	0.676609	0.830693	-6.75
253550_at	putative protein kinase serine/threonine	SIP3	AT4G30960	1.06	0.09	0.44	0.67683	0.830920	-6.75
261011_at	cytochrome b5 similar to cytochrome b5	CB5-A	AT1G26340	1.04	0.06	0.44	0.676942	0.831013	-6.75
250483_at	alpha-hydroxynitrile lyase-like protein a	MES5	AT5G10300	1.05	0.07	0.44	0.677113	0.831177	-6.75
256570_at	unknown protein ; supported by cDNA:	---	AT3G19540	1.03	0.04	0.43	0.677318	0.831178	-6.75

250298_at	putative protein NLI-interacting factor is	---	AT5G11860	-1.04	-0.05	-0.43	0.677368	0.831178	-6.75
251317_at	putative protein polygalacturonase - Ze	---	AT3G61490	-1.06	-0.08	-0.43	0.677304	0.831178	-6.75
246109_at	hypothetical protein (fragment?)	---	AT5G20120	-1.04	-0.06	-0.43	0.677282	0.831178	-6.75
262356_at	hypothetical protein predicted by genem	---	AT1G73000	1.03	0.05	0.43	0.677294	0.831178	-6.75
253501_at	predicted protein predicted protein on B	HSL1	AT4G32010	1.04	0.05	0.43	0.677298	0.831178	-6.75
254828_at	putative cell wall-plasma membrane dis	AIR1	AT4G12550	1.03	0.05	0.43	0.677334	0.831178	-6.75
256974_at	unknown protein similar to putative retro	---	---	-1.03	-0.04	-0.43	0.677477	0.831250	-6.75
265802_at	predicted protein	---	AT2G35733	-1.04	-0.06	-0.43	0.677499	0.831250	-6.75
261115_at	hypothetical protein predicted by genem	---	AT1G75360	1.03	0.04	0.43	0.677684	0.831432	-6.75
263884_at	hypothetical protein predicted by gensca	---	AT2G36920	1.03	0.04	0.43	0.677792	0.831519	-6.75
246613_at	acetyl-CoA carboxylase ;supported by f	CAC2	AT5G35360	-1.05	-0.06	-0.43	0.678042	0.831695	-6.75
267416_at	putative phosphatidylinositol-glycan syn	SETH1	AT2G34980	1.03	0.05	0.43	0.678045	0.831695	-6.75
254152_at	hypothetical protein	---	AT4G24410	-1.03	-0.04	-0.43	0.678037	0.831695	-6.75
254859_at	putative protein Arabidopsis thaliana Cl	---	AT4G12060	-1.05	-0.06	-0.43	0.678225	0.831696	-6.75
256067_at	unknown protein ;supported by full-lengt	---	AT1G07170	-1.05	-0.07	-0.43	0.678228	0.831696	-6.75
261583_at	pyruvate dehydrogenase E1 alpha subu	PDH-E1 A	AT1G01090	1.03	0.05	0.43	0.67813	0.831696	-6.75
259032_at	hypothetical protein similar to hypotheti	---	AT3G09380	1.03	0.04	0.43	0.678149	0.831696	-6.75
248949_at	putative protein strong similarity to unkn	---	AT5G45570	-1.03	-0.04	-0.43	0.678176	0.831696	-6.75
254987_s_a	hypothetical protein	---	AT4G10660 /	-1.03	-0.04	-0.43	0.678266	0.831698	-6.75
265097_at	unknown protein	BARD1	AT1G04020	1.06	0.08	0.43	0.678427	0.831822	-6.75
265108_s_a	similar to flavin-binding monooxygenas	---	AT1G62620 /	1.04	0.06	0.43	0.678513	0.831822	-6.75
248598_at	putative protein contains similarity to unl	---	AT5G49370	1.04	0.06	0.43	0.678511	0.831822	-6.75
247196_at	putative protein similar to unknown prote	AIL7	AT5G65510	1.03	0.04	0.43	0.67848	0.831822	-6.75
255642_at	hypothetical protein	iqd17	AT4G00820	-1.06	-0.09	-0.43	0.678632	0.831923	-6.75
246263_at	unknown protein	---	AT1G31780	-1.05	-0.06	-0.43	0.67882	0.832083	-6.75
258798_at	hypothetical protein predicted by genem	---	AT3G04540	1.04	0.05	0.43	0.678901	0.832083	-6.75
256182_at	Expressed protein ; supported by full-ler	SYP81	AT1G51740	-1.05	-0.07	-0.43	0.678908	0.832083	-6.75
254538_at	putative protein chitinase / lysozyme PZ	---	AT4G19740	-1.03	-0.04	-0.43	0.678896	0.832083	-6.75
245807_at	AP2 domain containing protein RAP2.1	RAP2.1	AT1G46768	-1.08	-0.11	-0.43	0.679058	0.832222	-6.75
262685_at	unknown protein ; supported by cDNA: g	---	AT1G76010	-1.05	-0.07	-0.43	0.679302	0.832297	-6.75
256841_x_a	hypothetical protein predicted by genem	---	---	-1.06	-0.08	-0.43	0.679294	0.832297	-6.75
252753_at	hypothetical protein	---	AT3G43500	1.04	0.05	0.43	0.679215	0.832297	-6.75
246032_s_a	putative protein	---	---	1.04	0.05	0.43	0.67918	0.832297	-6.75
263011_at	conserved hypothetical protein protein s	---	AT1G23250	-1.03	-0.05	-0.43	0.679277	0.832297	-6.75
250612_s_a	putative protein ARR2 protein - Arabido	ARR13	AT2G27070 /	1.05	0.07	0.43	0.679389	0.832360	-6.75

249722_at	putative protein similar to unknown prote	---	AT5G35430	-1.03	-0.04	-0.43	0.679648	0.832632	-6.75
252028_at	hypothetical protein	---	AT3G52640	-1.06	-0.08	-0.43	0.679979	0.832992	-6.75
250233_at	putative protein weak homology with pr	IQD11	AT5G13460	1.13	0.17	0.43	0.680034	0.833015	-6.75
247733_at	putative protein heat shock protein 40 D	---	AT5G59610	-1.05	-0.08	-0.43	0.680083	0.833030	-6.75
255167_at	putative protein hypothetical protein T2	---	---	1.03	0.04	0.43	0.680125	0.833037	-6.75
260021_at	unknown protein	---	AT1G30010	-1.06	-0.09	-0.43	0.680229	0.833120	-6.75
257808_at	unknown protein, putative contains Pfa	---	AT3G26935	1.03	0.05	0.43	0.680277	0.833134	-6.75
259450_at	hypothetical protein predicted by genem	DRL1	AT1G13870	1.04	0.06	0.43	0.680543	0.833414	-6.75
255751_at	terpene synthase family protein, putativ	---	AT1G31950	1.04	0.06	0.43	0.680639	0.833488	-6.75
247097_at	mannan endo-1,4-beta-mannosidase	---	AT5G66460	1.05	0.07	0.43	0.680718	0.833540	-6.75
250904_at	subtilisin-like serine protease contains s	---	AT5G03620	-1.03	-0.04	-0.43	0.680823	0.833579	-6.75
254183_at	putative protein predicted protein, Arabi	---	AT4G23960	-1.04	-0.05	-0.43	0.680793	0.833579	-6.75
248432_at	putative protein similar to unknown prote	---	AT5G51390	1.08	0.11	0.43	0.681042	0.833802	-6.75
255616_at	hypothetical protein	---	AT4G01290	-1.05	-0.08	-0.43	0.681147	0.833885	-6.75
253094_at	putative protein DnaJ-like protein, Phas	---	AT4G37480	-1.03	-0.04	-0.43	0.681263	0.833983	-6.75
257488_s_a	putative RING-finger protein	---	AT1G36950 /	1.03	0.04	0.43	0.681337	0.834029	-6.75
260448_at	hypothetical protein predicted by gensca	---	AT1G72410	1.04	0.05	0.43	0.681497	0.834059	-6.75
255903_at	myb-like protein, putative similar to myb	MYB52	AT1G17950	-1.03	-0.04	-0.43	0.681467	0.834059	-6.75
248873_at	disease resistance protein-like	---	AT5G46450	-1.11	-0.15	-0.43	0.681437	0.834059	-6.75
254173_at	putative protein Kaposi's sarcoma-asso	REN1	AT4G24580	-1.03	-0.04	-0.43	0.681508	0.834059	-6.75
252399_at	putative cyclic nucleotide-gated channe	CNGC16	AT3G48010	1.03	0.04	0.43	0.68169	0.834224	-6.75
247165_at	transcription factor-like protein ; suppor	MYB68	AT5G65790	1.03	0.04	0.43	0.681716	0.834224	-6.75
250387_at	putative protein predicted proteins, Arat	---	AT5G11290	1.03	0.04	0.43	0.681783	0.834262	-6.75
254197_at	trehalase - like protein trehalase 1 GMT	TRE1	AT4G24040	-1.05	-0.08	-0.43	0.681863	0.834315	-6.75
252313_at	RNA-binding - like protein RNA-binding	CID10	AT3G49390	1.06	0.09	0.43	0.681913	0.834332	-6.75
265242_at	hypothetical protein	---	AT2G07705	-1.06	-0.09	-0.43	0.682084	0.834496	-6.75
248829_at	putative protein contains similarity to Ba	---	AT5G47130	-1.05	-0.08	-0.43	0.682124	0.834499	-6.75
251975_at	CDC48 - like protein transitional endopl	---	AT3G53230	1.11	0.16	0.43	0.682352	0.834734	-6.75
254974_at	putative flavanone 3-beta-hydroxylase r	---	AT4G10490	1.03	0.04	0.43	0.682426	0.834780	-6.75
251632_at	hypothetical protein	---	AT3G57440	-1.04	-0.06	-0.43	0.682494	0.834818	-6.75
252582_at	putative protein several hypothetical pro	---	AT3G45530	1.03	0.05	0.43	0.682619	0.834926	-6.75
246902_at	putative protein	---	AT5G25640	-1.03	-0.04	-0.43	0.682757	0.835050	-6.75
247253_at	beta-1,3-glucanase	---	AT5G64790	1.11	0.15	0.43	0.682802	0.835060	-6.75
255017_at	hypothetical protein ;supported by full-le	CNX7	AT4G10100	-1.04	-0.05	-0.43	0.682856	0.835082	-6.75
257226_at	hypothetical protein predicted by genem	---	AT3G27880	1.09	0.13	0.43	0.683159	0.835176	-6.75

252592_at	mitogen-activated protein kinase 3 ; sup	NAXT1	AT3G45640 /	1.10	0.14	0.43	0.683227	0.835176	-6.75
249492_at	germin-like protein (GLP2a) copy1	GER2	AT5G39130 /	-1.03	-0.04	-0.43	0.683252	0.835176	-6.75
265994_at	putative multispanning membrane prote	---	AT2G24170	-1.08	-0.11	-0.43	0.683269	0.835176	-6.75
257560_at	galactosyltransferase, putative contains	---	AT3G14960	1.03	0.04	0.43	0.682979	0.835176	-6.75
253887_at	putative protein isp4 protein, Schizosac	OPT6	AT4G27730	-1.09	-0.12	-0.43	0.683184	0.835176	-6.75
265856_at	hypothetical protein predicted by genefi	LBD16	AT2G42430	-1.05	-0.07	-0.43	0.683271	0.835176	-6.75
264036_at	hypothetical protein similar to hypothetic	---	AT2G03810	1.05	0.07	0.43	0.683076	0.835176	-6.75
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_XREF	---	---	1.06	0.08	0.43	0.683299	0.835176	-6.75
265890_s_a	En/Spm-like transposon protein related	---	---	1.03	0.04	0.43	0.683226	0.835176	-6.75
254660_at	receptor serine/threonine kinase-like pr	---	AT4G18250	1.06	0.08	0.43	0.683498	0.835215	-6.75
267228_at	putative polygalacturonase	---	AT2G43890	1.03	0.04	0.43	0.6834	0.835215	-6.75
262709_at	unknown protein ESTs gb|F15498, gb|H	SYP51	AT1G16240	1.04	0.06	0.43	0.683459	0.835215	-6.75
252576_s_a	clpC-like protein AtClpC - Arabidopsis t	---	AT3G45450 /	1.06	0.08	0.43	0.683514	0.835215	-6.75
252159_at	hypothetical protein	---	AT3G50540	1.03	0.05	0.43	0.683457	0.835215	-6.75
256939_at	multicatalytic endopeptidase complex, p	PBD1	AT3G22630	-1.05	-0.07	-0.43	0.6836	0.835275	-6.75
254996_at	putative protein kinase CLV1 receptor k	---	AT4G10390	-1.04	-0.06	-0.43	0.683705	0.835359	-6.75
265380_at	putative retroelement pol polyprotein	---	---	1.03	0.05	0.43	0.683768	0.835391	-6.75
259391_s_a	delta 9 desaturase, putative similar to d	---	AT1G06350 /	1.03	0.05	0.43	0.683869	0.835469	-6.75
246221_at	step II splicing factor - like protein ; supp	SMP2	AT4G37120	1.04	0.05	0.43	0.683953	0.835482	-6.75
256642_at	hypothetical protein similar to hypothetic	---	AT3G32280	1.03	0.04	0.43	0.683927	0.835482	-6.75
249114_at	putative protein similar to unknown prote	---	---	1.04	0.06	0.43	0.683994	0.835488	-6.75
257633_at	hypothetical protein	CYP86C2	AT3G26125	-1.03	-0.04	-0.43	0.684035	0.835493	-6.75
260609_at	putative receptor protein kinase	---	AT2G43690	1.03	0.05	0.42	0.684128	0.835563	-6.75
260490_at	ATP-dependent transmembrane transp	CER5	AT1G51500	1.07	0.10	0.42	0.684492	0.835786	-6.75
259822_at	myb-related transcription factor, putativ	MYB20	AT1G66230	1.07	0.10	0.42	0.684531	0.835786	-6.75
255271_at	putative protein (ubiquitin like) to various	---	AT4G05260	1.04	0.05	0.42	0.684387	0.835786	-6.75
251761_at	glucuronosyl transferase - like protein g	---	AT3G55700	-1.05	-0.07	-0.42	0.684436	0.835786	-6.75
248893_at	unknown protein	---	AT5G46310	1.04	0.06	0.42	0.684382	0.835786	-6.75
253931_at	putative CDP-diacylglycerol synthetase	---	AT4G26770	1.04	0.05	0.42	0.68453	0.835786	-6.75
246724_at	putative protein CDPK substrate protein	---	AT5G29000	-1.04	-0.06	-0.42	0.68484	0.835849	-6.75
257905_at	unknown protein	---	---	-1.04	-0.05	-0.42	0.6848	0.835849	-6.75
246424_at	Exportin1 (XPO1) protein ; supported b	XPO1A	AT5G17020	-1.04	-0.06	-0.42	0.684814	0.835849	-6.75
261868_s_a	hypothetical protein contains similarity to	---	AT1G11450 /	1.02	0.04	0.42	0.684673	0.835849	-6.75
258096_at	hypothetical protein similar to putative p	---	AT3G23650	-1.04	-0.05	-0.42	0.684839	0.835849	-6.75
261504_at	MADS-box protein identical to GB:AAC	AGL12	AT1G71692	-1.04	-0.06	-0.42	0.684697	0.835849	-6.75

254279_at	Expressed protein ; supported by full-ler	---	AT4G22750	1.04	0.05	0.42	0.684781	0.835849	-6.75
254380_at	putative protein	---	AT4G21865	1.12	0.16	0.42	0.684959	0.835951	-6.75
248514_s_a	unknown protein	---	AT5G50510 /	-1.03	-0.04	-0.42	0.685004	0.835960	-6.75
255612_at	hypothetical protein	---	AT4G01240	1.05	0.06	0.42	0.685058	0.835978	-6.75
248571_at	putative protein similar to unknown prote	---	---	-1.03	-0.04	-0.42	0.685091	0.835978	-6.75
258251_at	unknown protein ; supported by full-leng	---	AT3G15810	-1.04	-0.05	-0.42	0.685241	0.836116	-6.75
263102_at	unknown protein	---	AT2G05270	-1.03	-0.04	-0.42	0.685347	0.836201	-6.75
252676_at	putative protein	---	AT3G44280	-1.03	-0.04	-0.42	0.685432	0.836259	-6.75
259304_at	putative nucleotide repair protein similar	ERCC1	AT3G05210	-1.03	-0.05	-0.42	0.685515	0.836271	-6.75
262814_at	putative heat-shock protein strong simila	---	AT1G11660	-1.03	-0.04	-0.42	0.685491	0.836271	-6.75
266263_at	putative flavonol sulfotransferase	---	AT2G27570	1.03	0.05	0.42	0.685667	0.836342	-6.75
259494_at	mitotic checkpoint protein, putative simi	---	AT1G15850	-1.04	-0.06	-0.42	0.685645	0.836342	-6.75
263346_at	En/Spm-like transposon protein related	---	---	1.03	0.05	0.42	0.685683	0.836342	-6.75
252384_at	ABC-type transport protein-like protein ,	ATH7	AT3G47790	-1.03	-0.04	-0.42	0.685759	0.836389	-6.75
261383_at	hypothetical protein predicted by genem	---	AT1G05380	-1.04	-0.05	-0.42	0.685929	0.836553	-6.75
255218_at	putative athila transposon protein	---	---	1.03	0.04	0.42	0.686111	0.836729	-6.75
248754_at	putative protein contains similarity to CC	NF-YB6	AT5G47670	1.03	0.04	0.42	0.686162	0.836747	-6.75
249776_at	unknown protein	---	AT5G24170	-1.05	-0.07	-0.42	0.686241	0.836799	-6.75
247124_at	prolyl 4-hydroxylase, alpha subunit-like	---	AT5G66060	1.03	0.04	0.42	0.68629	0.836814	-6.75
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gb:J0442	---	---	1.11	0.14	0.42	0.686334	0.836823	-6.75
257900_at	hypothetical protein predicted by genem	---	AT3G28420	1.03	0.04	0.42	0.686439	0.836870	-6.75
259457_at	auxin response factor 1, putative simila	ARF23	AT1G43950	1.03	0.04	0.42	0.686446	0.836870	-6.75
247820_at	serine/threonine protein kinase ; suppor	SIP1	AT5G58380	1.05	0.06	0.42	0.686628	0.837032	-6.75
253261_at	putative protein mRNA, partial cds, Sch	CHB3	AT4G34430	-1.04	-0.05	-0.42	0.686652	0.837032	-6.75
260136_at	hypothetical protein predicted by genem	---	AT1G66360	-1.03	-0.05	-0.42	0.686885	0.837270	-6.75
246048_at	putative protein	---	---	-1.04	-0.05	-0.42	0.68708	0.837464	-6.75
258445_at	putative lipoxygenase similar to lipoxyge	LOX5	AT3G22400	-1.06	-0.08	-0.42	0.687278	0.837660	-6.75
261343_s_a	putative protein hypothetical proteins - d	---	---	1.03	0.04	0.42	0.6875	0.837805	-6.75
254223_at	putative protein Pennisetum ciliare poss	---	AT4G23730	-1.03	-0.04	-0.42	0.687507	0.837805	-6.75
249170_at	abscisic acid responsive elements-bindi	---	AT5G42910	1.03	0.04	0.42	0.687497	0.837805	-6.75
256187_at	55 kDa B regulatory subunit of phospha	ATB ALPH	AT1G51690	1.04	0.06	0.42	0.687655	0.837940	-6.75
249760_at	(+)-delta-cadinene synthase (d-cadinene	TPS21	AT5G23960	1.03	0.04	0.42	0.6877	0.837951	-6.75
267191_at	similar to Mlo proteins from H. vulgare ;	MLO15	AT2G44110	1.05	0.07	0.42	0.687763	0.837983	-6.75
254060_at	putative protein polytropic murine leuka	SHB1	AT4G25350	1.06	0.09	0.42	0.688036	0.838270	-6.75
263189_at	hypothetical protein similar to hypothetic	---	AT1G36100	1.03	0.04	0.42	0.688101	0.838305	-6.75

252847_at	putative transposase hypothetical prote	---	AT3G42170	-1.04	-0.05	-0.42	0.688206	0.838388	-6.75
261697_at	hypothetical protein identical to hypothe	---	AT1G32610	-1.06	-0.08	-0.42	0.688254	0.838402	-6.75
246063_at	putative protein predicted proteins, Aral	---	AT5G19340	1.03	0.04	0.42	0.688524	0.838665	-6.75
253164_at	Expressed protein ; supported by full-ler	---	AT4G35725	1.03	0.05	0.42	0.688544	0.838665	-6.75
263751_at	putative kinesin heavy chain	---	AT2G21300	1.06	0.08	0.42	0.68945	0.839724	-6.76
247384_at	protein kinase ; supported by cDNA: gi_	---	AT5G63370	1.06	0.08	0.42	0.689546	0.839797	-6.76
257913_at	unknown protein ; supported by cDNA:	LAG1	AT3G25540	1.04	0.05	0.42	0.689672	0.839890	-6.76
252791_at	transposase - like protein putative trans	---	---	1.03	0.04	0.42	0.689697	0.839890	-6.76
259125_at	unknown protein Pfam HMM hit: Regula	---	AT3G02300	-1.03	-0.04	-0.42	0.68979	0.839959	-6.76
259706_at	unknown protein similar to GB:AAD4143	---	AT1G77540	1.04	0.05	0.42	0.689875	0.840017	-6.76
266918_at	putative LIM-domain protein	---	AT2G45800	1.03	0.04	0.42	0.690019	0.840058	-6.76
261442_at	Expressed protein ; supported by full-ler	---	AT1G28375	-1.03	-0.05	-0.42	0.689951	0.840058	-6.76
256423_at	serine carboxypeptidase, putative simila	scpl18	AT1G33540	1.03	0.04	0.42	0.68999	0.840058	-6.76
261870_at	nuclear transport factor 2, putative simil	NTL	AT1G11570	1.04	0.05	0.42	0.69006	0.840063	-6.76
258591_at	hypothetical protein ; supported by full-l	---	AT3G04360	1.03	0.04	0.42	0.690192	0.840179	-6.76
255429_at	hypothetical protein	---	AT4G03410	1.05	0.06	0.42	0.690338	0.840313	-6.76
249525_at	putative protein similar to unknown prote	---	AT5G38650	-1.03	-0.04	-0.42	0.690445	0.840329	-6.76
265155_at	putative major latex protein type 1 simil	---	AT1G30990	1.03	0.05	0.42	0.690473	0.840329	-6.76
255648_at	coded for by A. thaliana cDNA T20730	---	AT4G00910	-1.03	-0.04	-0.42	0.690499	0.840329	-6.76
252870_at	adenosine-5-phosphosulfate-kinase	AKN2	AT4G39940	-1.13	-0.18	-0.42	0.690444	0.840329	-6.76
246235_at	putative protein	---	AT4G36830	-1.04	-0.06	-0.42	0.690555	0.840352	-6.76
250455_at	unknown protein ; supported by full-leng	PROPEP4	AT5G09980	-1.05	-0.07	-0.42	0.69068	0.840459	-6.76
257142_at	cytochrome P450, putative contains Pfa	CYP705A1	AT3G20090	1.05	0.06	0.42	0.690901	0.840639	-6.76
259744_at	putative ketoacyl-CoA synthase similar t	KCS7	AT1G71160	-1.03	-0.04	-0.42	0.690892	0.840639	-6.76
266124_at	putative PREG1-like negative regulator	cycp3;1	AT2G45080	1.04	0.05	0.42	0.690975	0.840683	-6.76
259774_at	plasma membrane associated protein,	---	AT1G29520	1.05	0.07	0.41	0.691179	0.840798	-6.76
257791_at	unknown protein contains Pfam profile:F	---	AT3G27110	1.05	0.06	0.41	0.691149	0.840798	-6.76
262828_at	major latex protein type1 identical to ma	---	AT1G14950	1.06	0.08	0.41	0.691169	0.840798	-6.76
249755_at	unknown protein ;supported by full-leng	---	AT5G24580	1.11	0.15	0.41	0.691358	0.840824	-6.76
264486_at	hypothetical protein contains similarity to	---	AT1G77180	-1.04	-0.06	-0.41	0.691394	0.840824	-6.76
258176_at	B regulatory subunit of PP2A, putative s	---	AT3G21650	-1.06	-0.09	-0.41	0.691259	0.840824	-6.76
265068_at	hypothetical protein Similar to Kinesin pl	---	AT1G55550	-1.03	-0.04	-0.41	0.691373	0.840824	-6.76
252251_at	hypothetical protein	---	AT3G49820	1.03	0.04	0.41	0.691276	0.840824	-6.76
248368_at	mandelonitrile lyase-like protein ; suppo	---	AT5G51950	-1.03	-0.04	-0.41	0.691422	0.840824	-6.76
255376_x_a	putative athila-like protein	---	---	1.05	0.07	0.41	0.691485	0.840855	-6.76

250116_at	putative protein similar to unknown prote	---	AT5G16430	1.04	0.06	0.41	0.691643	0.841001	-6.76
252553_at	putative protein	---	AT3G45910	-1.03	-0.05	-0.41	0.691678	0.841001	-6.76
252368_at	cytochrome P450-like protein cytochror	CYP94B3	AT3G48520	1.08	0.12	0.41	0.69173	0.841019	-6.76
251658_at	putative protein strictosidine synthase (E	---	AT3G57020	-1.08	-0.11	-0.41	0.691939	0.841223	-6.76
254957_at	putative protein ; supported by full-leng	---	AT4G10970	-1.04	-0.05	-0.41	0.691972	0.841223	-6.76
267235_at	unknown protein	---	AT2G43945	-1.03	-0.04	-0.41	0.692033	0.841254	-6.76
267171_at	putative DOF zinc finger protein	DOF2.4	AT2G37590	-1.04	-0.06	-0.41	0.692107	0.841298	-6.76
260115_at	AIG1-like protein similar to AIG1 protein	---	AT1G33870	1.04	0.06	0.41	0.692144	0.841298	-6.76
265651_at	hypothetical protein predicted by gensca	---	AT2G13900	-1.03	-0.04	-0.41	0.692246	0.841378	-6.76
252372_at	aldehyde dehydrogenase (NAD+)-like p	ALDH2B4	AT3G48000	1.05	0.07	0.41	0.692314	0.841398	-6.76
249429_at	putative protein	---	AT5G39880	-1.03	-0.04	-0.41	0.692337	0.841398	-6.76
263967_at	En/Spm-like transposon protein	---	---	-1.03	-0.04	-0.41	0.692381	0.841406	-6.76
250572_at	putative protein	MIR834A	---	-1.05	-0.06	-0.41	0.692616	0.841558	-6.76
265971_at	putative retroelement pol polyprotein	---	---	-1.03	-0.04	-0.41	0.692571	0.841558	-6.76
248963_at	unknown protein	---	AT5G45700	-1.04	-0.05	-0.41	0.69261	0.841558	-6.76
260154_at	putative histone H2A similar to histone H	HTA9	AT1G52740	-1.05	-0.07	-0.41	0.692785	0.841718	-6.76
249083_at	prohibitin non-consensus TT acceptor s	ATPHB7	AT5G44140	-1.03	-0.05	-0.41	0.692912	0.841829	-6.76
261332_s_a	hypothetical protein contains similarity to	---	---	-1.03	-0.04	-0.41	0.69301	0.841903	-6.76
251306_at	putative DNA-binding protein DNA-bind	---	AT3G61260	-1.04	-0.06	-0.41	0.693127	0.841954	-6.76
261215_at	subtilase, putative similar to subtilase G	---	AT1G32970	1.03	0.04	0.41	0.693099	0.841954	-6.76
259916_at	hypothetical protein predicted by genefir	---	AT1G72600	1.03	0.04	0.41	0.693189	0.841985	-6.76
261091_at	protein kinase, putative contains Pfam p	---	AT1G07550	1.03	0.05	0.41	0.69324	0.842003	-6.76
263781_at	hypothetical protein predicted by genefir	---	AT2G46360	1.03	0.04	0.41	0.693348	0.842044	-6.76
260144_at	putative ABC transporter similar to breas	---	AT1G71960	-1.04	-0.06	-0.41	0.693318	0.842044	-6.76
250357_at	putative protein various predicted prote	---	AT5G11730	-1.04	-0.05	-0.41	0.693402	0.842065	-6.76
262148_at	chloroplast-localized small heat shock p	---	AT1G52560	-1.07	-0.10	-0.41	0.693489	0.842125	-6.76
257077_at	PR-1 protein, putative similar to PR-1a	---	AT3G19690	-1.05	-0.07	-0.41	0.693649	0.842275	-6.76
251949_at	receptor protein kinase -like protein CLV	---	AT3G53590	1.04	0.06	0.41	0.693792	0.842297	-6.76
255222_at	putative protein Mitochondrial ATPase (	---	AT4G05340	1.03	0.04	0.41	0.693787	0.842297	-6.76
250048_s_a	BCS1 - like protein h-bcs1, Homo sapie	---	AT5G17740 /	1.03	0.05	0.41	0.693815	0.842297	-6.76
250405_at	ubiquitin-specific protease 22 (UBP22)	UBP22	AT5G10790	-1.05	-0.07	-0.41	0.693809	0.842297	-6.76
264974_at	unknown protein contains Pfam proifle:F	ATHB54	AT1G27050	-1.04	-0.05	-0.41	0.693898	0.842353	-6.76
259010_at	unknown protein contains helix-loop-hel	---	AT3G07340	1.06	0.08	0.41	0.693955	0.842378	-6.76
265412_at	putative chloroplast outer membrane pro	TOC132	AT2G16640	-1.03	-0.04	-0.41	0.694039	0.842411	-6.76
246106_at	receptor-like protein kinase precursor -	---	AT5G28680	1.02	0.03	0.41	0.694074	0.842411	-6.76

256097_at	unknown protein	---	AT1G13670	1.03	0.04	0.41	0.694093	0.842411	-6.76
254851_at	putative disease resistance protein (TM	---	AT4G12010	-1.06	-0.09	-0.41	0.694313	0.842632	-6.76
250461_at	hypothetical protein	---	AT5G10010	1.04	0.06	0.41	0.694464	0.842683	-6.76
263952_s_a	unknown protein ;supported by full-leng	---	AT2G35810 /	-1.03	-0.05	-0.41	0.694502	0.842683	-6.76
263752_at	putative retroelement pol polyprotein	---	---	-1.04	-0.06	-0.41	0.694498	0.842683	-6.76
248617_at	putative protein similar to unknown prote	---	AT5G49590	1.03	0.04	0.41	0.694443	0.842683	-6.76
255560_at	hypothetical protein similar to C. elegan	---	AT4G02030	-1.03	-0.04	-0.41	0.694724	0.842908	-6.76
255980_at	hypothetical protein ;supported by full-le	---	AT1G33970	-1.04	-0.05	-0.41	0.694768	0.842916	-6.76
258443_at	unknown protein	---	AT3G22290	1.04	0.05	0.41	0.694814	0.842926	-6.76
261400_at	protein phosphatase-2C, putative simila	---	AT1G79630	-1.05	-0.07	-0.41	0.694854	0.842930	-6.76
248306_at	unknown protein ; supported by cDNA:	WRKY27	AT5G52830	1.05	0.08	0.41	0.695039	0.843110	-6.76
250684_at	zinc finger-like protein	GIS2	AT5G06650	1.03	0.05	0.41	0.695277	0.843264	-6.76
262917_at	hypothetical protein contains similarity to	---	AT1G64800	-1.04	-0.06	-0.41	0.695261	0.843264	-6.76
251750_at	glucuronosyl transferase - like protein g	---	AT3G55710	-1.05	-0.07	-0.41	0.69521	0.843264	-6.76
254428_at	putative protein Human mRNA for KIAA	ZAC	AT4G21160	1.03	0.05	0.41	0.69533	0.843283	-6.76
261073_at	hypothetical protein predicted by genem	---	AT1G07300	1.03	0.05	0.41	0.69539	0.843311	-6.76
264051_at	hypothetical protein predicted by gensca	---	AT2G22340	-1.03	-0.05	-0.41	0.69543	0.843315	-6.76
264977_at	unknown protein	---	AT1G27090	-1.06	-0.08	-0.41	0.69561	0.843334	-6.76
260419_at	putative protein kinase contains Pfam pr	---	AT1G69730	1.09	0.12	0.41	0.695488	0.843334	-6.76
248250_at	cyclic nucleotide-regulated ion channel (	CNGC1	AT5G53130	-1.07	-0.10	-0.41	0.695529	0.843334	-6.76
260621_at	carbonic anhydrase, putative	ACA5	AT1G08065	-1.03	-0.05	-0.41	0.69563	0.843334	-6.76
247631_at	putative MADS box protein various prec	AGL62	AT5G60440	1.03	0.04	0.41	0.695602	0.843334	-6.76
249277_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G41890	1.09	0.13	0.41	0.69573	0.843409	-6.76
261922_at	amp-binding protein, putative similar to	AAE12	AT1G65890	1.05	0.07	0.41	0.695931	0.843503	-6.76
264594_at	hypothetical protein ; supported by cDN/	ATSERAT	AT2G17640	1.03	0.05	0.41	0.695863	0.843503	-6.76
251615_at	putative protein hypothetical protein T2	---	AT3G57980	1.05	0.07	0.41	0.695967	0.843503	-6.76
245394_at	hypothetical protein ;supported by full-le	---	AT4G16450	1.04	0.06	0.41	0.695992	0.843503	-6.76
256475_s_a	myosin heavy chain ATM2, putative sim	---	AT1G42680 /	1.03	0.05	0.41	0.695916	0.843503	-6.76
260459_at	hypothetical protein predicted by gensca	---	AT1G68240	1.03	0.05	0.41	0.696041	0.843515	-6.76
264734_at	hypothetical protein predicted by genem	SLAH1	AT1G62280	1.03	0.04	0.41	0.696075	0.843515	-6.76
258217_at	unknown protein contains Pfam profile P	XPL1	AT3G17998 /	1.06	0.08	0.41	0.696142	0.843551	-6.76
251443_at	putative protein unknown protein At2g4	---	AT3G59940	1.06	0.09	0.41	0.696381	0.843626	-6.76
265836_at	Mutator-like transposase similar to MUF	---	---	1.03	0.05	0.41	0.696347	0.843626	-6.76
248438_at	putative protein contains similarity to fer	EMF2	AT5G51230	1.05	0.07	0.41	0.696374	0.843626	-6.76
259264_at	putative aldose 1-epimerase shows simi	---	AT3G01260	1.04	0.06	0.41	0.696389	0.843626	-6.76

246022_at	putative protein predicted protein - Arab	---	AT5G21110	-1.03	-0.04	-0.41	0.696276	0.843626	-6.76
249071_at	putative protein similar to unknown prote	---	AT5G44050	-1.08	-0.12	-0.41	0.696978	0.843659	-6.76
250314_at	putative protein contains similarity to RN	---	AT5G12190	-1.03	-0.04	-0.41	0.696703	0.843659	-6.76
266246_at	putative cytochrome P450	CYP94C1	AT2G27690	1.11	0.14	0.41	0.696953	0.843659	-6.76
264852_at	similar to Mlo proteins from H. vulgare ;	MLO8	AT2G17480	-1.08	-0.12	-0.41	0.697008	0.843659	-6.76
253838_at	putative zinc finger protein zinc finger p	---	AT4G27880	1.05	0.07	0.41	0.696799	0.843659	-6.76
261249_at	hypothetical protein predicted by genem	---	AT1G05880	1.03	0.05	0.41	0.696587	0.843659	-6.76
258330_at	unknown protein	ROPGEF1	AT3G16130	1.03	0.05	0.41	0.696916	0.843659	-6.76
247730_at	glucuronosyl transferase - like protein g	UGT76E1	AT5G59580	1.06	0.08	0.41	0.696618	0.843659	-6.76
264826_at	putative 1-aminocyclopropane-1-carbox	2A6	AT1G03410	-1.04	-0.06	-0.41	0.696999	0.843659	-6.76
260287_at	unknown protein contains two Kelch mo	---	AT1G80440	-1.06	-0.08	-0.41	0.69694	0.843659	-6.76
266232_at	putative phloem-specific lectin	AtPP2-B6	AT2G02310	1.03	0.04	0.41	0.696943	0.843659	-6.76
254070_at	hypothetical protein	---	AT4G25430	1.05	0.07	0.41	0.696812	0.843659	-6.76
266502_at	hypothetical protein predicted by gensca	---	AT2G47720 /	-1.03	-0.04	-0.41	0.696625	0.843659	-6.76
263454_at	putative cysteine proteinase	---	AT2G22160	-1.03	-0.05	-0.41	0.696722	0.843659	-6.76
246806_at	putative cdc20 protein	---	AT5G27080	-1.03	-0.05	-0.41	0.696483	0.843659	-6.76
249657_at	sen1-like protein SEN1 - Saccharomyce	---	AT5G37140	-1.03	-0.04	-0.41	0.696971	0.843659	-6.76
255148_at	putative mitogen-activated protein kinas	MAPKKK1	AT4G08470	1.08	0.11	0.41	0.697246	0.843902	-6.76
249711_at	putative protein contains similarity to tra	---	AT5G35680	-1.04	-0.06	-0.41	0.697393	0.843990	-6.76
257514_at	hypothetical protein similar to putative re	---	---	-1.05	-0.07	-0.41	0.697362	0.843990	-6.76
247354_at	flavonol synthase ;supported by full-len	FLS3	AT5G63590	1.03	0.04	0.41	0.697606	0.844186	-6.76
252966_at	putative protein various predicted prote	---	AT4G38870	1.04	0.05	0.41	0.697628	0.844186	-6.76
247884_at	lipid transfer protein; glossy1 homolog	CER3	AT5G57800	-1.09	-0.12	-0.41	0.697735	0.844245	-6.76
265143_at	unknown protein	NFU5	AT1G51390	-1.04	-0.05	-0.41	0.697751	0.844245	-6.76
255879_at	receptor-like kinase, putative similar to	---	AT1G67000	1.08	0.11	0.41	0.697876	0.844261	-6.76
251893_at	putative protein	---	AT3G54380	1.03	0.04	0.41	0.697846	0.844261	-6.76
250086_at	NAM (no apical meristem)-like protein	anac086	AT5G17260	-1.04	-0.05	-0.41	0.697837	0.844261	-6.76
263335_x_a	hypothetical protein	---	---	1.03	0.04	0.41	0.697936	0.844289	-6.76
265768_at	putative sugar transporter ;supported by	---	AT2G48020	-1.03	-0.04	-0.40	0.698629	0.844710	-6.76
266382_at	hypothetical protein predicted by gensca	---	---	1.03	0.04	0.40	0.698608	0.844710	-6.76
252221_at	RuvB DNA helicase - like protein DNA h	---	AT3G49830	1.03	0.05	0.40	0.6985	0.844710	-6.76
248978_at	putative protein contains similarity to dis	AtPP2-A8	AT5G45070	1.04	0.06	0.40	0.698654	0.844710	-6.76
258268_at	putative WD-repeat protein contains Pfa	WSIP2	AT3G15880	-1.05	-0.07	-0.40	0.698558	0.844710	-6.76
252500_at	proteinase inhibitor-like protein endopep	---	AT3G46860	-1.03	-0.04	-0.40	0.698424	0.844710	-6.76
251568_at	putative protein several hypothetical pro	---	AT3G58280	1.04	0.05	0.40	0.698418	0.844710	-6.76

254165_at	putative protein hypothetical protein - C	---	AT4G24330	-1.05	-0.07	-0.40	0.698375	0.844710	-6.76
258826_at	putative glucan synthase similar to gluca	ATGSL10	AT3G07160	1.03	0.04	0.40	0.698432	0.844710	-6.76
246241_at	patatin-like protein	PLP4	AT4G37050	-1.04	-0.06	-0.40	0.698637	0.844710	-6.76
260311_at	hypothetical protein predicted by gensca	---	AT1G70570	1.03	0.04	0.40	0.698955	0.844822	-6.76
253468_at	putative protein predicted gene T10G3.	---	AT4G32160	1.04	0.06	0.40	0.698974	0.844822	-6.76
257986_at	Expressed protein ; supported by full-ler	AGP40	AT3G20865	1.05	0.07	0.40	0.699078	0.844822	-6.76
263087_s_a	putative sugar transporter	---	AT2G16120 /	1.03	0.05	0.40	0.69906	0.844822	-6.76
260809_at	hypothetical protein predicted by genem	---	AT1G43730	-1.03	-0.04	-0.40	0.698891	0.844822	-6.76
248496_at	MtN3-like protein ;supported by full-leng	---	AT5G50790	1.04	0.06	0.40	0.699049	0.844822	-6.76
255539_at	putative actin polymerization factor simi	CRK	AT4G01710	-1.03	-0.05	-0.40	0.69904	0.844822	-6.76
258870_at	putative NADP-dependent oxidoreducta	---	AT3G03080	1.03	0.05	0.40	0.69908	0.844822	-6.76
255800_at	putative protein transposase, Ipomoea	---	AT4G10200	1.03	0.04	0.40	0.699004	0.844822	-6.76
255417_at	F-box protein GRR1-like protein 1, AtFE	GRH1	AT4G03190	1.13	0.18	0.40	0.69933	0.844901	-6.76
259998_at	hypothetical protein similar to unknown	BPC3	AT1G68120	1.05	0.07	0.40	0.699287	0.844901	-6.76
256320_at	DnaJ protein, putative contains Pfam pr	---	AT3G12170	1.04	0.05	0.40	0.699268	0.844901	-6.76
256985_at	myb-related protein 5 identical to GB:S	ATMYB5	AT3G13540	1.04	0.06	0.40	0.699254	0.844901	-6.76
262973_at	histone H3, putative similar to HISTONI	---	AT1G75600	-1.03	-0.04	-0.40	0.699313	0.844901	-6.76
261107_at	unknown protein ; supported by cDNA: g	---	AT1G63010	-1.03	-0.04	-0.40	0.699426	0.844971	-6.76
259807_at	hypothetical protein predicted by gensca	---	AT1G47920	1.03	0.04	0.40	0.699586	0.845120	-6.76
251131_at	laccase - like protein laccase precursor	LAC10	AT5G01190	1.03	0.04	0.40	0.699712	0.845227	-6.76
246288_at	unknown protein	---	AT1G31850	-1.04	-0.06	-0.40	0.699905	0.845371	-6.76
258686_at	putative polygalacturonase similar to pc	---	AT3G07840	-1.03	-0.04	-0.40	0.699869	0.845371	-6.76
249680_s_a	putative protein strong similarity to unkn	---	AT3G61730 /	1.02	0.03	0.40	0.700026	0.845427	-6.76
257161_at	hypothetical protein predicted by gensca	SMAP2	AT3G24280	-1.03	-0.04	-0.40	0.69999	0.845427	-6.76
259573_at	hypothetical protein	---	---	1.03	0.04	0.40	0.700088	0.845458	-6.76
251773_at	putative protein HSPC058, Homo sapie	---	AT3G55960	-1.05	-0.08	-0.40	0.700307	0.845513	-6.76
253937_at	putative NPK1-related protein kinase N	MAPKKK1	AT4G26890	-1.06	-0.08	-0.40	0.700319	0.845513	-6.76
261587_at	hypothetical protein predicted by genem	---	AT1G01660	-1.03	-0.04	-0.40	0.700176	0.845513	-6.76
266008_at	hypothetical protein predicted by gensca	---	AT2G37390	1.04	0.05	0.40	0.700269	0.845513	-6.76
247341_at	unknown protein	---	AT5G63720	-1.03	-0.04	-0.40	0.700252	0.845513	-6.76
267488_at	putative cadmium-transporting ATPase	HMA4	AT2G19110	-1.05	-0.07	-0.40	0.700419	0.845589	-6.76
259608_at	unknown protein	ECT9	AT1G27960	-1.04	-0.05	-0.40	0.700593	0.845755	-6.76
262761_at	unknown protein ESTs gb|AA395702, g	---	AT1G10720	1.05	0.07	0.40	0.700729	0.845873	-6.76
258070_at	hypothetical protein predicted by genem	---	AT3G26040	-1.04	-0.06	-0.40	0.70084	0.845963	-6.76
260928_at	hypothetical protein similar to putative g	GATL5	AT1G02720	1.03	0.05	0.40	0.701278	0.846367	-6.76

261914_at	dirigent protein, putative similar to dirige	---	AT1G65870	-1.05	-0.07	-0.40	0.701265	0.846367	-6.76
254824_s_a	origin recognition complex subunit 1 -lik	ORC1B	AT4G12620 /	-1.05	-0.06	-0.40	0.701286	0.846367	-6.76
266163_at	hypothetical protein predicted by gensca	---	AT2G28130	1.05	0.07	0.40	0.701418	0.846470	-6.76
252054_at	hypothetical protein ;supported by full-le	OFP18	AT3G52540	1.04	0.05	0.40	0.701446	0.846470	-6.76
263341_at	hypothetical protein predicted by gensca	---	---	1.03	0.05	0.40	0.701575	0.846581	-6.76
263055_at	unknown protein	---	---	-1.03	-0.04	-0.40	0.701633	0.846607	-6.76
256807_at	unknown protein contains Pfam profile:	NFU4	AT3G20970	1.03	0.05	0.40	0.701834	0.846757	-6.76
257067_at	unknown protein contains Pfam profile:	CYP77A5F	AT3G18270	-1.04	-0.05	-0.40	0.701943	0.846757	-6.76
259678_at	putative 30S ribosomal protein S13 sim	---	AT1G77750	-1.05	-0.07	-0.40	0.701935	0.846757	-6.76
263855_at	putative non-LTR retrolelement reverse	---	AT2G04420	1.03	0.05	0.40	0.701891	0.846757	-6.76
265452_at	putative bHLH transcription factor	ATAIB	AT2G46510	-1.11	-0.15	-0.40	0.701806	0.846757	-6.76
259433_at	hypothetical protein predicted by gensca	---	AT1G01570	1.04	0.05	0.40	0.702127	0.846933	-6.76
266954_at	hypothetical protein predicted by genefir	---	AT2G34530	-1.03	-0.04	-0.40	0.702191	0.846966	-6.76
247197_at	receptor-like protein kinase	---	AT5G65240	-1.08	-0.11	-0.40	0.702418	0.847018	-6.76
257571_at	hypothetical protein predicted by genen	---	AT3G16870	-1.06	-0.09	-0.40	0.70242	0.847018	-6.76
257037_at	nuclear acid binding protein, putative si	ATRBP47B	AT3G19130	1.06	0.09	0.40	0.702377	0.847018	-6.76
255769_at	hypothetical protein predicted by genem	---	AT1G18610	-1.03	-0.04	-0.40	0.702366	0.847018	-6.76
266377_at	Mutator-like transposase similar to MUF	---	---	1.02	0.03	0.40	0.702359	0.847018	-6.76
263841_at	putative xyloglucan endo-transglycosyla	---	AT2G36870	1.25	0.32	0.40	0.702548	0.847109	-6.76
256058_at	UDP-glucose glucosyltransferase, puta	UGT71C5	AT1G07240	-1.04	-0.06	-0.40	0.702569	0.847109	-6.76
249939_at	unknown protein ;supported by full-leng	---	AT5G22430	1.04	0.06	0.40	0.702628	0.847135	-6.76
245080_at	putative receptor-like protein kinase	---	AT2G23300	-1.05	-0.06	-0.40	0.702809	0.847308	-6.76
251635_at	endo-polygalacturonase	ADPG1	AT3G57510	1.04	0.06	0.40	0.702953	0.847437	-6.76
267598_at	hypothetical protein predicted by genefir	---	AT2G33010	1.04	0.06	0.40	0.702991	0.847438	-6.76
248217_at	cytochrome b5 (dbj|BAA74839.1) ;supp	CB5-E	AT5G53560	1.04	0.06	0.40	0.703158	0.847551	-6.76
266456_at	putative bHLH transcription factor	NAI1	AT2G22770	-1.04	-0.05	-0.40	0.703235	0.847551	-6.76
245294_at	casein kinase I ; supported by cDNA: gi_	CKI1	AT4G14340	-1.03	-0.05	-0.40	0.703253	0.847551	-6.76
262358_at	mandelonitrile lyase, putative similar to	---	AT1G73050	1.04	0.05	0.40	0.703165	0.847551	-6.76
262256_at	hypothetical protein similar to putative re	---	---	1.04	0.05	0.40	0.70327	0.847551	-6.76
247257_at	proteasome regulatory subunit-like ; su	RPN5B	AT5G64760	-1.07	-0.10	-0.40	0.703312	0.847556	-6.76
265556_at	putative Athila retroelement ORF1-like p	---	---	1.03	0.05	0.40	0.703701	0.847980	-6.76
267551_at	ubiquitin-specific protease 1 (UBP1), pu	UBP1	AT2G32780	-1.04	-0.06	-0.40	0.703801	0.848056	-6.76
259730_at	unknown protein similar to hypothetical	---	AT1G77660	1.09	0.12	0.40	0.704029	0.848067	-6.76
252312_at	hypothetical protein SF16 protein, Helia	iqd15	AT3G49380	-1.04	-0.05	-0.40	0.703983	0.848067	-6.76
257797_at	hypothetical protein contains Pfam profil	---	AT3G15940	1.04	0.05	0.40	0.70391	0.848067	-6.76

261101_at	transcription factor DREB1A, putative s	ddf2	AT1G63030	1.04	0.06	0.40	0.70392	0.848067	-6.76
254512_at	terpene cyclase like protein vetispiradie	---	AT4G20230	-1.03	-0.05	-0.40	0.704052	0.848067	-6.76
253374_at	hypothetical protein ; supported by cDN	---	AT4G33140	1.03	0.04	0.40	0.703982	0.848067	-6.76
253185_at	putative protein bZIP protein - Arabidop	---	AT4G35240	-1.04	-0.06	-0.40	0.70407	0.848067	-6.76
264724_at	putative JUN kinase activator protein si	CSN5A	AT1G22920	-1.03	-0.04	-0.40	0.704109	0.848068	-6.76
256716_at	hypothetical protein predicted by genefi	---	AT2G34100	1.03	0.05	0.40	0.704159	0.848085	-6.76
253085_s_a	putative protein hypothetical protein, Ar	---	AT4G36270 /	-1.05	-0.07	-0.40	0.704278	0.848155	-6.76
249837_at	Expressed protein ; supported by full-ler	---	AT5G23480	1.03	0.05	0.40	0.704293	0.848155	-6.76
249432_at	putative ATP/GTP-binding protein putat	CLPS5	AT5G39930	-1.03	-0.04	-0.40	0.704386	0.848202	-6.77
266313_at	putative protein kinase contains a protei	CIPK3	AT2G26980	1.06	0.08	0.40	0.704405	0.848202	-6.77
251661_at	putative protein NODULIN-26 - Glycine	SIP2;1	AT3G56950	1.04	0.06	0.40	0.70492	0.848429	-6.77
257093_at	hypothetical protein ;supported by full-le	---	AT3G20570	1.06	0.08	0.40	0.704921	0.848429	-6.77
262487_at	unknown protein ESTs gb|T42839 and g	---	AT1G21610	-1.02	-0.03	-0.40	0.704896	0.848429	-6.77
267469_at	unknown protein ; supported by cDNA:	WRKY21	AT2G30590	1.04	0.05	0.40	0.704895	0.848429	-6.77
246323_at	hypothetical protein predicted by genem	---	AT1G16690	1.04	0.05	0.40	0.704874	0.848429	-6.77
255930_at	hypothetical protein predicted by gensca	---	AT1G12660	1.03	0.04	0.40	0.704703	0.848429	-6.77
252029_s_a	putative RNA binding protein heteroger	---	AT3G52660 /	-1.03	-0.04	-0.40	0.704644	0.848429	-6.77
259464_at	hypothetical protein predicted by genem	---	AT1G18990	-1.03	-0.04	-0.40	0.704929	0.848429	-6.77
263747_at	putative ubiquitin activating enzyme	SAE2	AT2G21470	1.03	0.04	0.40	0.70481	0.848429	-6.77
260366_at	putative protein kinase similar to C-term	---	AT1G70460	-1.03	-0.04	-0.40	0.704967	0.848430	-6.77
246150_at	putative protein predicted proteins from	---	AT5G19930	1.06	0.08	0.40	0.705057	0.848494	-6.77
249956_at	putative protein CGI-66 protein, Homo s	---	AT5G18940	1.03	0.04	0.39	0.705339	0.848744	-6.77
259833_at	MYB-family transcription factor, putative	MYB105	AT1G69560	-1.03	-0.04	-0.39	0.705316	0.848744	-6.77
263480_at	putative root iron transporter protein	ZIP7	AT2G04032	-1.04	-0.05	-0.39	0.70559	0.848815	-6.77
245320_at	Expressed protein ; supported by full-ler	---	AT4G16444	-1.03	-0.04	-0.39	0.705543	0.848815	-6.77
252538_at	putative transporter protein peptide tran	---	AT3G45720	1.03	0.04	0.39	0.705453	0.848815	-6.77
260691_s_a	hypothetical protein predicted by genem	---	---	1.03	0.05	0.39	0.705499	0.848815	-6.77
261915_at	amp-binding protein, putative similar to	BZO1	AT1G65880	-1.02	-0.04	-0.39	0.705595	0.848815	-6.77
267203_at	hypothetical protein predicted by genefir	---	AT2G31035	1.02	0.03	0.39	0.705621	0.848815	-6.77
265889_at	hypothetical protein predicted by genefir	---	AT2G15130	1.04	0.05	0.39	0.705752	0.848837	-6.77
247700_at	RNA-binding protein - like cold-inducible	---	AT5G59860	-1.02	-0.04	-0.39	0.705683	0.848837	-6.77
264453_at	putative GTP-binding protein similar to	---	AT1G10300	-1.02	-0.04	-0.39	0.705716	0.848837	-6.77
246615_at	putative protein similar to unknown prote	---	---	1.03	0.05	0.39	0.705857	0.848919	-6.77
248460_at	Expressed protein ; supported by full-ler	---	AT5G50915	1.12	0.16	0.39	0.706057	0.849115	-6.77
264668_at	putative 2,3-bisphosphoglycerate-indep	---	AT1G09780	1.04	0.06	0.39	0.706137	0.849166	-6.77

245948_at	putative protein ;supported by full-lengt	---	AT5G19540	-1.05	-0.07	-0.39	0.7062	0.849197	-6.77
254224_at	calcium-dependent protein kinase (CDP	CDPK6	AT4G23650	1.03	0.04	0.39	0.706297	0.849224	-6.77
260866_at	polyprotein, putative similar to polyprote	---	---	-1.03	-0.05	-0.39	0.706278	0.849224	-6.77
253288_at	hypothetical protein	---	AT4G34310	1.03	0.05	0.39	0.706466	0.849383	-6.77
253650_at	EST GB:N37377 spans last intron and 3	---	AT4G30020	-1.19	-0.26	-0.39	0.706528	0.849413	-6.77
262542_at	hypothetical protein similar to NAM-like	anac016	AT1G34180	-1.06	-0.08	-0.39	0.706641	0.849447	-6.77
251085_at	putative protein insulinase - Homo sapi	---	AT5G01440	1.03	0.05	0.39	0.706668	0.849447	-6.77
245779_at	hypothetical protein predicted by genem	---	AT1G73510	-1.03	-0.04	-0.39	0.706629	0.849447	-6.77
250619_at	A9 ;supported by full-length cDNA: Cer	---	AT5G07230	1.02	0.03	0.39	0.706713	0.849456	-6.77
251747_at	putative protein various predicted prote	---	AT3G55670	1.03	0.04	0.39	0.706906	0.849643	-6.77
247693_at	putative protein leucine zipper-containir	ATEXO70I	AT5G59730	1.10	0.14	0.39	0.707009	0.849722	-6.77
248858_at	AP47 50p (gb|AAB88283.1) ; supported	---	AT5G46630	1.03	0.05	0.39	0.707072	0.849753	-6.77
254186_at	putative protein cellulose synthase cata	CSLG1	AT4G24010	1.03	0.05	0.39	0.70713	0.849777	-6.77
251754_at	beta-1,3-glucanase - like protein beta-1	---	AT3G55780	-1.04	-0.05	-0.39	0.70739	0.850045	-6.77
256481_at	elicitor response protein, putative simila	---	AT1G33430	-1.03	-0.04	-0.39	0.70747	0.850096	-6.77
250585_at	putative protein contains similarity to rec	---	AT5G07620	1.07	0.10	0.39	0.707517	0.850109	-6.77
258272_at	unknown protein similar to serine/threor	---	AT3G15610	-1.05	-0.06	-0.39	0.707762	0.850358	-6.77
260680_s_a	GATA transcription factor 3, putative sir	---	AT1G08000 /	1.03	0.04	0.39	0.707821	0.850385	-6.77
264058_at	F-box protein family, AtFBX7 contains F	---	AT2G03560	1.03	0.04	0.39	0.707927	0.850467	-6.77
246016_at	histidine kinase - like protein sensory tr	AHK5	AT5G10720	1.04	0.05	0.39	0.708096	0.850625	-6.77
254090_at	MtN3 - like protein MtN3 (induced durin	---	AT4G25010	1.04	0.05	0.39	0.708381	0.850883	-6.77
253800_at	putative protein probable cell wall prote	---	AT4G28160	-1.04	-0.05	-0.39	0.708385	0.850883	-6.77
249176_at	thioredoxin (clone GIF1) (pir||S58118) ;	ATTRX3	AT5G42980	1.03	0.04	0.39	0.708534	0.850893	-6.77
253191_at	cysteine protease XCP1 identical to pap	XCP1	AT4G35350	1.11	0.16	0.39	0.708499	0.850893	-6.77
266006_at	putative ABC transporter	---	AT2G37360	-1.04	-0.06	-0.39	0.708549	0.850893	-6.77
253031_at	putative protein cellulose synthase - Po	CSLD4	AT4G38190	-1.03	-0.05	-0.39	0.708585	0.850893	-6.77
265604_s_a	hypothetical protein predicted by gensca	---	---	-1.03	-0.05	-0.39	0.70857	0.850893	-6.77
265600_at	hypothetical protein predicted by gensca	---	---	-1.03	-0.04	-0.39	0.708617	0.850893	-6.77
246672_at	putative protein	---	---	1.03	0.04	0.39	0.708694	0.850940	-6.77
248621_at	putative protein similar to unknown prote	---	AT5G49350	-1.03	-0.05	-0.39	0.708869	0.851106	-6.77
251498_at	putative protein hypothetical proteins - A	---	AT3G59070	-1.04	-0.05	-0.39	0.709113	0.851309	-6.77
245801_at	hypothetical protein similar to hypothetic	---	AT1G46912	1.03	0.04	0.39	0.709088	0.851309	-6.77
266160_at	hypothetical protein	ATCHX8	AT2G28180	1.04	0.06	0.39	0.709356	0.851556	-6.77
258515_at	ATP citrate lyase, putative similar to AT	ACLB-1	AT3G06650	1.03	0.04	0.39	0.709451	0.851580	-6.77
248114_at	wax synthase-like protein	---	AT5G55370	1.03	0.05	0.39	0.70943	0.851580	-6.77

258578_at	germin-like protein contains Pfam profile	---	AT3G04200	1.05	0.07	0.39	0.70962	0.851693	-6.77
251978_at	CYTOCHROME P450 - like protein CY	CYP71B30	AT3G53290	1.04	0.05	0.39	0.709586	0.851693	-6.77
266538_at	hypothetical protein predicted by gensca	---	AT2G35230	-1.03	-0.04	-0.39	0.70966	0.851697	-6.77
261729_s_a	hexokinase, putative similar to hexokina	HXK3	AT1G47840	1.02	0.04	0.39	0.709707	0.851708	-6.77
249499_at	hypothetical protein	---	AT5G39250	1.03	0.04	0.39	0.709811	0.851744	-6.77
246739_at	putative protein predicted protein, Arabi	---	AT5G27800	-1.03	-0.04	-0.39	0.709789	0.851744	-6.77
267100_at	unknown protein	---	AT2G41470	1.03	0.04	0.39	0.709931	0.851809	-6.77
256349_at	late embryogenesis protein, putative sir	---	AT1G54890	1.31	0.39	0.39	0.709954	0.851809	-6.77
266386_at	putative homeodomain transcription fact	HDG3	AT2G32370	1.04	0.05	0.39	0.709978	0.851809	-6.77
249617_at	receptor protein kinase-like protein	---	AT5G37450	1.04	0.06	0.39	0.710117	0.851886	-6.77
263232_at	putative light repressible receptor prote	---	AT1G05700	-1.03	-0.04	-0.39	0.710095	0.851886	-6.77
248022_at	putative protein contains similarity to RN	APUM12	AT5G56510	1.02	0.04	0.39	0.710523	0.852290	-6.77
262266_at	mudrA-like protein similar to mudrA GB:	---	---	-1.03	-0.05	-0.39	0.710566	0.852290	-6.77
262053_at	putative DnaJ protein contains Pfam pr	ATERDJ2A	AT1G79940	1.04	0.05	0.39	0.710559	0.852290	-6.77
261737_at	hypothetical protein similar to putative d	---	AT1G47885	1.03	0.05	0.39	0.710656	0.852354	-6.77
257910_at	hypothetical protein similar to hypothetic	---	AT3G25580	1.04	0.05	0.39	0.710807	0.852490	-6.77
246056_at	katanin p80 subunit - like protein katani	---	AT5G08390	1.04	0.05	0.39	0.710919	0.852525	-6.77
253129_at	glycine-rich protein glycine-rich protein	CSDP1	AT4G36020	-1.05	-0.06	-0.39	0.710936	0.852525	-6.77
255661_at	hypothetical protein	ULP1B	AT4G00690	1.03	0.04	0.39	0.710948	0.852525	-6.77
245890_at	ribosomal protein S15-like ribosomal pr	---	AT5G09490	-1.02	-0.03	-0.39	0.711187	0.852712	-6.77
252495_at	putative protein hypothetical proteins - A	---	AT3G46770	1.03	0.05	0.39	0.711154	0.852712	-6.77
245920_at	putative protein	---	---	-1.02	-0.03	-0.39	0.711216	0.852712	-6.77
262834_at	hypothetical protein predicted by gensca	MAP65-7	AT1G14690	-1.03	-0.04	-0.39	0.71133	0.852760	-6.77
249661_x_a	putative protein similar to unknown prote	---	---	-1.04	-0.05	-0.39	0.711331	0.852760	-6.77
252066_at	receptor-protein kinase-like protein rece	FER	AT3G51550	1.05	0.07	0.39	0.711515	0.852853	-6.77
264154_at	unknown protein	---	AT1G65430	-1.03	-0.04	-0.39	0.711696	0.852853	-6.77
266222_at	hypothetical protein predicted by gensca	---	AT2G28780	1.03	0.04	0.39	0.711566	0.852853	-6.77
245160_at	putative leucine-rich repeat disease resi	AtRLP28	AT2G33080	1.03	0.04	0.39	0.711587	0.852853	-6.77
259356_at	unknown protein	---	AT3G05250	-1.03	-0.04	-0.39	0.711572	0.852853	-6.77
245894_at	putative protein ; supported by full-leng	---	AT5G09310	1.03	0.04	0.39	0.711607	0.852853	-6.77
246556_at	putative protein hypothetical protein T4	---	AT5G15480	1.04	0.05	0.39	0.711693	0.852853	-6.77
260755_at	hypothetical protein predicted by genem	---	AT1G48980	-1.03	-0.04	-0.39	0.711708	0.852853	-6.77
258236_at	hypothetical protein predicted by genem	---	AT3G27800	-1.03	-0.04	-0.39	0.711845	0.852972	-6.77
249806_at	putative protein contains similarity to un	---	AT5G23850	-1.07	-0.09	-0.39	0.711947	0.853050	-6.77
264461_s_a	hypothetical protein	---	AT1G10190 /	1.02	0.03	0.39	0.711999	0.853068	-6.77

265049_at	jasmonate inducible protein, putative si	---	AT1G52060	-1.03	-0.04	-0.39	0.712082	0.853122	-6.77
267115_s_a	putative cellulose synthase	ATCSLB04	AT2G32530 /	1.07	0.10	0.38	0.712204	0.853178	-6.77
245125_at	putative histidine kinase identical to GB:	CKI1	AT2G47430	1.03	0.05	0.38	0.7122	0.853178	-6.77
258543_at	unknown protein	---	AT3G06870	-1.04	-0.05	-0.38	0.712296	0.853200	-6.77
261316_at	MAP kinase BnMAP4K alpha1, putative	ATMAP4K	AT1G53165	1.03	0.04	0.38	0.712274	0.853200	-6.77
262793_at	putative cytochrome P450 monooxyger	CYP71B7	AT1G13110	-1.08	-0.10	-0.38	0.712364	0.853236	-6.77
264241_at	hypothetical protein contains similarity to	---	AT1G54840	-1.02	-0.03	-0.38	0.71243	0.853271	-6.77
263211_at	germin-like oxalate oxidase similar to ES	GLP7	AT1G10460	-1.04	-0.06	-0.38	0.712479	0.853284	-6.77
258000_at	AIG2-like protein similar to AIG2 protein	---	AT3G28940	-1.06	-0.08	-0.38	0.712763	0.853430	-6.77
260518_at	cinnamyl alcohol dehydrogenase, putat	---	AT1G51410	1.03	0.04	0.38	0.712788	0.853430	-6.77
246645_at	putative protein ;supported by full-lengt	---	AT5G35080	1.04	0.05	0.38	0.712785	0.853430	-6.77
257391_at	hypothetical protein predicted by gensca	---	AT2G32050	1.02	0.04	0.38	0.712737	0.853430	-6.77
266764_at	putative pectinesterase ;supported by f	---	AT2G47050	1.03	0.05	0.38	0.712672	0.853430	-6.77
256337_at	unknown protein	---	AT1G72060	1.09	0.13	0.38	0.71305	0.853449	-6.77
247368_at	putative protein contains similarity to kin	---	AT5G63320	1.04	0.05	0.38	0.713051	0.853449	-6.77
261276_at	v-SNARE protein AtVTI1b, putative sim	VTI1B	AT1G26670	-1.04	-0.06	-0.38	0.712931	0.853449	-6.77
245455_at	disease resistance RPP5 like protein (fra	---	AT4G16930	1.03	0.04	0.38	0.713066	0.853449	-6.77
267394_s_a	putative cellulase	AtGH9B9	AT2G44540 /	1.03	0.05	0.38	0.712917	0.853449	-6.77
254378_at	putative protein NADH oxidoreductase	DER2.1	AT4G21810	-1.06	-0.08	-0.38	0.712846	0.853449	-6.77
250553_at	putative protein PTD008, Homo sapien	---	AT5G07960	1.04	0.05	0.38	0.713053	0.853449	-6.77
255743_at	unknown protein ; supported by cDNA: g	---	AT1G25375	-1.03	-0.04	-0.38	0.713158	0.853480	-6.77
254194_at	auxin response factor 9 (ARF9) ; suppo	ARF9	AT4G23980	1.05	0.07	0.38	0.713167	0.853480	-6.77
265128_at	hypothetical protein predicted by gensca	---	AT1G30860	1.04	0.06	0.38	0.713278	0.853569	-6.77
260034_at	putative DNA-binding protein Pfam HMM	---	AT1G68810	-1.09	-0.13	-0.38	0.713631	0.853638	-6.77
252315_at	putative protein PrMC3 - Pinus radiata,	CXE12	AT3G48690	1.04	0.05	0.38	0.713495	0.853638	-6.77
260482_at	endomembrane protein EMP70 precuso	---	AT1G10950	-1.03	-0.04	-0.38	0.713533	0.853638	-6.77
249184_at	receptor kinase-like protein	---	AT5G43020	-1.05	-0.07	-0.38	0.713636	0.853638	-6.77
265110_at	hypothetical protein predicted by gensca	---	AT1G62490	-1.04	-0.06	-0.38	0.713491	0.853638	-6.77
245823_at	hypothetical protein predicted by genem	---	AT1G57906	1.03	0.05	0.38	0.713535	0.853638	-6.77
248016_at	putative protein similar to unknown prote	---	AT5G56380	-1.04	-0.06	-0.38	0.713592	0.853638	-6.77
252047_at	putative protein heat shock protein - Gly	---	AT3G52490	1.04	0.05	0.38	0.71361	0.853638	-6.77
255431_at	putative C-type U1 snRNP similar to U1	---	AT4G03120	-1.02	-0.03	-0.38	0.71384	0.853838	-6.77
248469_at	putative protein similar to unknown prote	anac097	AT5G50820	1.04	0.06	0.38	0.713992	0.853952	-6.77
246164_at	putative protein predicted proteins, Ara	---	---	1.03	0.04	0.38	0.71401	0.853952	-6.77
264742_at	hypothetical protein similar to hypothetic	---	AT1G62130	-1.04	-0.05	-0.38	0.714285	0.854236	-6.77

247533_at	putative protein kinase-like transmembr	---	AT5G61570	-1.08	-0.11	-0.38	0.714421	0.854354	-6.77
247260_at	putative protein contains similarity to unl	---	AT5G64500	-1.04	-0.06	-0.38	0.714769	0.854725	-6.77
262156_at	hypothetical protein contains similarity to	---	AT1G52680	1.03	0.05	0.38	0.714968	0.854836	-6.77
262241_at	hypothetical protein predicted by genem	---	AT1G48390	-1.02	-0.04	-0.38	0.71499	0.854836	-6.77
250117_at	isopentenyl pyrophosphate:dimethyllally	IPP1	AT5G16440	1.05	0.07	0.38	0.714997	0.854836	-6.77
257440_at	unknown protein	---	AT2G24880	-1.03	-0.04	-0.38	0.715012	0.854836	-6.77
257740_at	hypothetical protein predicted by genen	---	AT3G27330	1.02	0.03	0.38	0.715054	0.854842	-6.77
256117_at	unknown protein ; supported by cDNA: g	---	AT1G16840	-1.03	-0.04	-0.38	0.715166	0.854894	-6.77
245218_s_a	viral resistance protein, putative, 5' part	---	AT1G58848 /	-1.03	-0.04	-0.38	0.715173	0.854894	-6.77
263441_at	putative kinesin-like spindle protein	---	AT2G28620	1.03	0.04	0.38	0.715263	0.854957	-6.77
261691_at	branched-chain amino acid aminotrans	---	AT1G50060	-1.03	-0.04	-0.38	0.715426	0.855107	-6.77
261910_at	zinc finger protein identical to GB:AAA8	ZFP1	AT1G80730	-1.03	-0.04	-0.38	0.715532	0.855189	-6.77
263476_at	putative poly(ADP-ribose) glycohydrolas	TEJ	AT2G31870	-1.03	-0.04	-0.38	0.715764	0.855398	-6.77
246688_at	putative protein predicted proteins - Aral	---	---	1.03	0.04	0.38	0.715782	0.855398	-6.77
257340_at	pseudogene, retroelement pol polyprote	---	---	-1.03	-0.05	-0.38	0.71587	0.855459	-6.77
264309_at	coatomer alpha subunit, putative simila	---	AT1G62020	-1.03	-0.04	-0.38	0.715971	0.855534	-6.77
247927_at	unknown protein	---	AT5G57310	1.03	0.04	0.38	0.716021	0.855550	-6.77
255855_at	ABC transporter, putative similar to ABC	PDR11	AT1G66950	-1.04	-0.06	-0.38	0.716144	0.855607	-6.77
266187_at	putative retroelement pol polyprotein	---	AT2G38970	1.05	0.07	0.38	0.71611	0.855607	-6.77
261712_at	alcohol dehydrogenase, putative simila	---	AT1G32780	1.03	0.05	0.38	0.716392	0.855858	-6.77
262637_at	oxidoreductase, putative contains Pfam	---	AT1G06640	-1.15	-0.20	-0.38	0.716491	0.855932	-6.77
266365_at	ferredoxin-dependent glutamate synthas	GLU2	AT2G41220	1.04	0.06	0.38	0.716875	0.856265	-6.77
257889_at	S1 self-incompatibility protein, putative	---	AT3G17080	-1.04	-0.05	-0.38	0.716872	0.856265	-6.77
251682_s_a	hypothetical protein	---	AT3G57110 /	-1.04	-0.05	-0.38	0.71689	0.856265	-6.77
248574_at	putative protein strong similarity to unkn	---	AT5G49830	1.03	0.04	0.38	0.71692	0.856265	-6.77
249771_at	receptor-like protein kinase ; supported	---	AT5G24080	1.05	0.07	0.38	0.716966	0.856275	-6.77
260707_s_a	Expressed protein ; supported by full-ler	---	AT1G32410	1.04	0.06	0.38	0.717129	0.856425	-6.77
260829_s_a	chloroplast thylakoidal processing pepti	---	AT1G06870 /	1.04	0.06	0.38	0.717232	0.856503	-6.77
261324_at	unknown protein	---	AT1G44770	1.04	0.06	0.38	0.717436	0.856567	-6.77
257146_at	unknown protein contains Pfam profile:F	GTE8	AT3G27260	-1.02	-0.03	-0.38	0.717341	0.856567	-6.77
250913_at	3-deoxy-D-manno-octulosonic acid tran	---	AT5G03770	-1.03	-0.04	-0.38	0.717391	0.856567	-6.77
251779_at	putative protein various predicted prote	---	---	1.03	0.04	0.38	0.717434	0.856567	-6.77
253350_at	hypothetical protein	---	AT4G33690	-1.03	-0.04	-0.38	0.717525	0.856628	-6.77
264271_at	beta-glucosidase, putative similar to be	BGLU6	AT1G60270	1.06	0.08	0.38	0.71776	0.856733	-6.77
267461_at	putative auxin-regulated protein ;suppo	---	AT2G33830	-1.04	-0.05	-0.38	0.717701	0.856733	-6.77

255715_s_a	hypothetical protein	---	AT4G00320 /	-1.03	-0.04	-0.38	0.717763	0.856733	-6.77
267245_at	hypothetical protein	---	AT2G02640	-1.03	-0.04	-0.38	0.71767	0.856733	-6.77
266344_at	hypothetical protein predicted by gensca	---	AT2G01580	-1.03	-0.04	-0.38	0.717877	0.856824	-6.77
258419_at	unknown protein	---	AT3G16670	1.14	0.19	0.38	0.718042	0.856976	-6.77
255076_at	putative protein RING-H2 zinc finger pr	---	AT4G09130	1.03	0.04	0.38	0.718321	0.857265	-6.77
249884_at	Na+/H+ antiporter-like protein	CHX9	AT5G22910	-1.03	-0.04	-0.38	0.718434	0.857324	-6.77
264997_at	hypothetical protein contains similarity t	HAC2	AT1G67220	1.04	0.05	0.38	0.718481	0.857324	-6.77
250610_at	glycine-rich protein PUTG1 ;supported	GRP19	AT5G07550	1.05	0.07	0.38	0.71851	0.857324	-6.77
252005_at	purple acid phosphatase-like protein pu	PAP21	AT3G52810	1.04	0.06	0.38	0.718521	0.857324	-6.77
248212_at	CHP-rich zinc finger protein-like	---	AT5G54020	-1.03	-0.05	-0.38	0.71858	0.857349	-6.77
257288_at	anthocyanin 5-aromatic acyltransferase	---	AT3G29670	1.03	0.04	0.38	0.718659	0.857354	-6.77
253946_at	putative APG protein proline-rich protei	---	AT4G26790	1.05	0.07	0.38	0.718634	0.857354	-6.77
256718_at	hypothetical protein predicted by gensca	---	AT2G34120	1.03	0.04	0.38	0.718775	0.857447	-6.77
260244_at	putative choline kinase similar to GB:AA	---	AT1G74320	1.03	0.04	0.38	0.718957	0.857485	-6.77
252715_x_a	putative protein predicted protein, Arabi	---	AT3G43900	1.03	0.05	0.38	0.718874	0.857485	-6.77
263394_at	hypothetical protein predicted by genefi	---	---	1.03	0.04	0.38	0.718898	0.857485	-6.77
264034_s_a	unknown protein	ATUPS1	AT2G03590 /	1.03	0.04	0.38	0.718951	0.857485	-6.77
245391_at	symbiosis-related like protein ;supporte	ATG8F	AT4G16520	1.05	0.06	0.38	0.719037	0.857536	-6.77
254489_at	putative protein berberine bridge enzym	---	AT4G20800	1.03	0.04	0.37	0.719202	0.857688	-6.77
262743_at	unknown protein similar to unknown pro	---	AT1G29020	1.03	0.05	0.37	0.719393	0.857866	-6.77
259157_at	hypothetical protein predicted by genem	---	AT3G05440	1.02	0.03	0.37	0.719426	0.857866	-6.77
257240_at	monooxygenase, putatve contains Pfar	---	AT3G24200	1.03	0.04	0.37	0.719592	0.858018	-6.77
257997_at	hypothetical protein similar to hypothetic	---	AT3G27500	1.03	0.04	0.37	0.719692	0.858093	-6.77
256352_at	proline-rich protein, putative similar to p	ATPRP1	AT1G54970	-1.04	-0.05	-0.37	0.71973	0.858093	-6.77
266544_at	similar to late embryogenesis abundant	---	AT2G35300	1.03	0.04	0.37	0.719829	0.858122	-6.77
264207_at	unknown protein strong similarity to hyp	---	AT1G22750	-1.04	-0.06	-0.37	0.71982	0.858122	-6.77
245880_at	putative hydrolase EtbD1 - Rhodococcu	---	AT5G09430	-1.04	-0.06	-0.37	0.719926	0.858193	-6.77
256991_at	unknown protein	---	AT3G28600	-1.03	-0.04	-0.37	0.720046	0.858275	-6.77
252600_at	putative protein unknown protein CGI-1	VPS24.2	AT3G45000	-1.04	-0.05	-0.37	0.720071	0.858275	-6.77
252438_at	putative protein riboflavin biosynthesis p	---	AT3G47390	-1.02	-0.04	-0.37	0.720145	0.858316	-6.77
263262_at	unknown protein	---	AT2G38830	-1.03	-0.04	-0.37	0.720181	0.858316	-6.77
262027_at	DNA-binding protein, putative similar to	HOS10	AT1G35515	1.06	0.08	0.37	0.720228	0.858328	-6.77
246705_x_a	putative protein predicted resistance pr	---	---	1.03	0.04	0.37	0.720442	0.858538	-6.77
257500_s_a	putative serine carboxypeptidase simila	scpl2	AT1G73300 /	1.02	0.03	0.37	0.720486	0.858546	-6.77
261876_at	pirin-like protein similar to pirin GB:AAF	---	AT1G50590	-1.08	-0.11	-0.37	0.720576	0.858608	-6.77

246978_at	cytochrome P450-like protein fatty acid	CYP714A1	AT5G24910	-1.05	-0.07	-0.37	0.720951	0.859010	-6.78
265861_at	hypothetical protein predicted by gensca	---	AT2G01790	1.03	0.04	0.37	0.72104	0.859045	-6.78
255914_at	hypothetical protein predicted by genem	---	AT1G20290	1.04	0.05	0.37	0.721216	0.859045	-6.78
254536_at	putative protein chitinase / lysozyme PZ	---	AT4G19720	-1.03	-0.04	-0.37	0.721235	0.859045	-6.78
265633_at	F-box protein family, AtFBL6 contains s	EBF1	AT2G25490	1.04	0.05	0.37	0.721173	0.859045	-6.78
255726_at	lysine and histidine specific transporter,	---	AT1G25530	1.11	0.15	0.37	0.72112	0.859045	-6.78
265514_s_a	Mutator-like transposase similar to MUF	---	---	-1.03	-0.04	-0.37	0.721244	0.859045	-6.78
255383_at	hypothetical protein	---	AT4G03570	1.02	0.03	0.37	0.721153	0.859045	-6.78
247999_at	E2, ubiquitin-conjugating enzyme, putat	UBC30	AT5G56150	1.03	0.04	0.37	0.721539	0.859094	-6.78
252343_at	putative protein hypothetical protein F1	---	AT3G48610	-1.10	-0.14	-0.37	0.721555	0.859094	-6.78
260888_at	hypothetical protein similar to allergen G	---	AT1G29140	1.03	0.04	0.37	0.721474	0.859094	-6.78
261104_at	unknown protein	---	AT1G62910	1.03	0.05	0.37	0.721649	0.859094	-6.78
261884_at	myrosinase precursor, putative	---	AT1G80910	-1.03	-0.05	-0.37	0.721605	0.859094	-6.78
263116_s_a	unknown protein Similar to gb|U51990 p	---	AT1G03140 /	1.03	0.05	0.37	0.721682	0.859094	-6.78
262849_at	unknown protein ; supported by cDNA: g	---	AT1G14710	1.08	0.11	0.37	0.72156	0.859094	-6.78
254690_at	N-acetylornithine deacetylase-like prote	---	AT4G17830	1.02	0.03	0.37	0.7217	0.859094	-6.78
265014_at	hypothetical protein similar to deacetylv	---	AT1G24430	1.04	0.06	0.37	0.721545	0.859094	-6.78
250594_at	putative protein contains similarity to unl	---	AT5G07760	-1.03	-0.04	-0.37	0.72162	0.859094	-6.78
257669_at	DNA mismatch repair protein, putative c	MSH5	AT3G20475	-1.03	-0.04	-0.37	0.721582	0.859094	-6.78
266841_at	putative heat shock transcription factor	ATHSFA2	AT2G26150	-1.05	-0.07	-0.37	0.721978	0.859380	-6.78
265756_at	putative bZIP transcription factor similar	---	AT2G13150	-1.02	-0.03	-0.37	0.722099	0.859481	-6.78
267386_at	unknown protein	---	AT2G44430	-1.05	-0.06	-0.37	0.722197	0.859552	-6.78
262322_at	hypothetical protein similar to hypothetic	---	AT1G27590	-1.04	-0.05	-0.37	0.72232	0.859653	-6.78
248268_at	importin beta	---	AT5G53480	-1.04	-0.05	-0.37	0.722506	0.859655	-6.78
254283_s_a	anthocyanidin synthase - like protein pu	---	AT4G22870 /	-1.04	-0.06	-0.37	0.722499	0.859655	-6.78
266872_at	unknown protein	---	AT2G44730	1.03	0.05	0.37	0.722455	0.859655	-6.78
258349_at	Expressed protein ; supported by full-ler	HYH	AT3G17609	-1.07	-0.10	-0.37	0.722548	0.859655	-6.78
257696_at	protein kinase, putative similar to protei	AGC1.5	AT3G12690	-1.05	-0.06	-0.37	0.722536	0.859655	-6.78
249226_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G42170	-1.03	-0.04	-0.37	0.722481	0.859655	-6.78
246891_at	putative protein various predicted prote	---	AT5G25490	-1.02	-0.04	-0.37	0.722659	0.859733	-6.78
246710_at	putative protein predicted proteins, Aral	---	---	1.02	0.03	0.37	0.722688	0.859733	-6.78
254585_at	resistence protein - like downy mildew r	---	AT4G19500	-1.03	-0.04	-0.37	0.72276	0.859773	-6.78
262190_at	unknown protein	---	AT1G78030	-1.04	-0.06	-0.37	0.722838	0.859821	-6.78
264138_at	beta-Amyrin Synthase, putative similar	---	AT1G78950	-1.03	-0.05	-0.37	0.723397	0.860217	-6.78
257915_at	superman protein identical to superman	SUP	AT3G23130	1.03	0.05	0.37	0.723348	0.860217	-6.78

256082_at	hypothetical protein predicted by gensca	---	AT1G20720	1.05	0.08	0.37	0.723313	0.860217	-6.78
266750_s_a	putative pectinesterase	VGDH1	AT2G47030 /	-1.03	-0.04	-0.37	0.72336	0.860217	-6.78
246983_at	receptor protein kinase-like protein ; su	---	AT5G67200	-1.04	-0.06	-0.37	0.723256	0.860217	-6.78
266443_at	putative myb-related transcription factor	---	AT2G43270	-1.02	-0.04	-0.37	0.723225	0.860217	-6.78
252795_at	putative protein predicted proteins, Aral	---	---	1.03	0.04	0.37	0.723834	0.860692	-6.78
265386_at	unknown protein ;supported by full-leng	---	AT2G20930	-1.03	-0.04	-0.37	0.723926	0.860757	-6.78
258013_at	unknown protein	---	AT3G19320	1.04	0.05	0.37	0.723991	0.860759	-6.78
247961_at	putative protein similar to unknown prote	---	AT5G56570	-1.03	-0.04	-0.37	0.724004	0.860759	-6.78
265308_at	putative protein kinase contains a protei	ALE2	AT2G20300	1.02	0.03	0.37	0.724134	0.860869	-6.78
264417_at	hypothetical protein contains similarity to	---	---	-1.05	-0.06	-0.37	0.724279	0.860997	-6.78
250209_at	putative protein similar to unknown prote	---	AT5G14030	-1.04	-0.05	-0.37	0.724363	0.861051	-6.78
267589_at	hypothetical protein	---	---	1.02	0.03	0.37	0.72446	0.861122	-6.78
260092_at	putative serine carboxypeptidase simila	scpl3	AT1G73280	1.03	0.04	0.37	0.724615	0.861127	-6.78
246811_at	putative protein	---	AT5G27170	-1.03	-0.04	-0.37	0.724595	0.861127	-6.78
245210_at	putative protein similarity to UVB-resista	---	AT5G12350	-1.03	-0.04	-0.37	0.724509	0.861127	-6.78
255361_at	hypothetical protein	---	---	1.02	0.03	0.37	0.724541	0.861127	-6.78
265489_at	hypothetical protein predicted by gensca	---	AT2G15640	-1.04	-0.06	-0.37	0.724996	0.861535	-6.78
265906_at	hypothetical protein predicted by gensca	---	AT2G25565	1.03	0.04	0.37	0.725283	0.861765	-6.78
265395_at	putative LRR receptor protein kinase ; s	SRF1	AT2G20850	-1.04	-0.06	-0.37	0.725303	0.861765	-6.78
249812_at	putative protein similar to unknown prote	---	AT5G23830	1.04	0.06	0.37	0.725247	0.861765	-6.78
249131_at	putative protein contains similarity to RN	APUM14	AT5G43110	-1.02	-0.04	-0.37	0.725347	0.861772	-6.78
248712_at	unknown protein	---	AT5G48280	-1.03	-0.04	-0.37	0.725691	0.862136	-6.78
258840_at	unknown protein similar to unknown pro	---	AT3G04620	-1.02	-0.03	-0.37	0.725745	0.862156	-6.78
253938_at	putative homeodomain protein homeod	---	AT4G26920	-1.03	-0.05	-0.37	0.725948	0.862351	-6.78
258565_at	unknown protein ; supported by cDNA:	---	AT3G04350	1.05	0.06	0.37	0.726035	0.862373	-6.78
245858_at	CER1-like protein CER1-like, A.thaliana	---	AT5G28280	-1.03	-0.05	-0.37	0.726042	0.862373	-6.78
255443_at	sulfate transporter protein similar to sulf	SULTR3;2	AT4G02700	-1.03	-0.05	-0.36	0.72641	0.862462	-6.78
259513_at	hypothetical protein ; supported by cDN	ARK3	AT1G12430	-1.03	-0.04	-0.36	0.72635	0.862462	-6.78
248246_at	putative protein contains similarity to MY	TRY	AT5G53200	1.03	0.05	0.37	0.726278	0.862462	-6.78
246626_at	hypothetical protein contains similarity to	---	AT1G48870	-1.04	-0.06	-0.36	0.726338	0.862462	-6.78
254499_at	putative protein probable membrane pr	---	AT4G20100	1.03	0.04	0.36	0.72633	0.862462	-6.78
253134_at	putative protein procollagen-proline dio	---	AT4G35820	1.03	0.04	0.36	0.72636	0.862462	-6.78
260845_at	transcription factor, putative similar to tr	---	AT1G17310	-1.03	-0.04	-0.37	0.726288	0.862462	-6.78
264934_at	hypothetical protein predicted by gensca	---	AT1G61090	-1.03	-0.04	-0.36	0.726419	0.862462	-6.78
267453_at	putative homeodomain transcription fact	HB-3	AT2G33880	-1.04	-0.06	-0.36	0.726551	0.862498	-6.78

260934_at	hypothetical protein predicted by genem	---	AT1G45100	-1.02	-0.03	-0.36	0.726557	0.862498	-6.78
259459_at	En/Spm-like transposon protein, putativ	---	---	-1.03	-0.04	-0.36	0.726563	0.862498	-6.78
247399_at	putative protein similar to unknown prote	---	AT5G62960	1.06	0.08	0.36	0.726772	0.862567	-6.78
247599_at	putative protein	---	AT5G60880	-1.06	-0.08	-0.36	0.726693	0.862567	-6.78
264393_at	unknown protein Contains similarity to h	---	AT1G11880	-1.03	-0.04	-0.36	0.726754	0.862567	-6.78
264596_at	unknown protein similar to polygalacturo	---	AT1G04625	1.04	0.05	0.36	0.726768	0.862567	-6.78
263018_at	putative non-LTR retroelement reverse t	---	---	-1.02	-0.03	-0.36	0.726854	0.862619	-6.78
260919_at	hypothetical protein predicted by genem	---	AT1G21520 /	1.12	0.16	0.36	0.72699	0.862730	-6.78
246414_at	hypothetical protein similar to hypothetic	---	AT1G77340	1.03	0.04	0.36	0.727061	0.862730	-6.78
261548_at	DNA-binding protein, putative contains	---	AT1G63480	1.04	0.05	0.36	0.727035	0.862730	-6.78
261342_at	putative replication protein similar to rep	---	AT1G52950	1.02	0.04	0.36	0.72711	0.862743	-6.78
260140_at	Myb-related transcription factor, putativ	MYB90	AT1G66390	-1.03	-0.05	-0.36	0.727175	0.862775	-6.78
263919_at	unknown protein ;supported by full-leng	---	AT2G36470	-1.10	-0.14	-0.36	0.727314	0.862851	-6.78
248003_at	putative protein contains similarity to un	---	AT5G56220	-1.11	-0.15	-0.36	0.727283	0.862851	-6.78
245626_at	unknown protein ;supported by full-lengt	---	AT1G56700	1.04	0.06	0.36	0.727414	0.862880	-6.78
245553_at	lupeol synthase like protein	BARS1	AT4G15370	-1.02	-0.03	-0.36	0.727405	0.862880	-6.78
254985_x_a	putative reverse-transcriptase -like prot	---	---	-1.04	-0.05	-0.36	0.727538	0.862981	-6.78
245089_at	putative transketolase precursor ; supp	---	AT2G45290	1.15	0.20	0.36	0.727601	0.863012	-6.78
248197_at	NADPH:protochlorophyllide oxidoreduct	PORA	AT5G54190	1.03	0.04	0.36	0.727855	0.863179	-6.78
260574_at	hypothetical protein predicted by genefir	---	AT2G47300	-1.03	-0.05	-0.36	0.727788	0.863179	-6.78
256477_at	unknown protein	---	---	-1.03	-0.04	-0.36	0.727855	0.863179	-6.78
257511_at	hypothetical protein	---	AT1G43000	1.03	0.04	0.36	0.72798	0.863282	-6.78
256132_at	hypothetical protein similar to hypothetic	---	AT1G13610	-1.03	-0.04	-0.36	0.728344	0.863598	-6.78
262091_at	Myb-family transcription factor, putative	MYB72	AT1G56160	-1.03	-0.04	-0.36	0.728337	0.863598	-6.78
257183_at	ABC transporter contains Pfam profile: F	---	AT3G13220	-1.03	-0.04	-0.36	0.728398	0.863598	-6.78
261214_at	Mutator-like protein similar to many prec	---	---	-1.04	-0.05	-0.36	0.728389	0.863598	-6.78
246541_at	ubiquitin-fusion degradation protein-like	---	AT5G15400	1.03	0.04	0.36	0.728507	0.863682	-6.78
257704_at	myb-related transcription factor, putativ	ATMYB67	AT3G12720	1.02	0.03	0.36	0.72857	0.863712	-6.78
256950_at	hypothetical protein similar to hypothetic	---	AT3G19080	-1.06	-0.08	-0.36	0.728693	0.863813	-6.78
266351_at	unknown protein ;supported by full-leng	---	AT2G01490	-1.03	-0.05	-0.36	0.728841	0.863898	-6.78
246222_at	TINY-like protein ; supported by cDNA: (	RAP2.10	AT4G36900	1.06	0.09	0.36	0.728837	0.863898	-6.78
255307_at	hypothetical protein similar to A. thalian	RIC10	AT4G04900	1.03	0.05	0.36	0.728968	0.864004	-6.78
262767_at	putative oxysterol-binding protein simila	ORP1D	AT1G13170	1.06	0.09	0.36	0.729021	0.864023	-6.78
253498_at	putative protein various predicted protei	---	AT4G31890	1.06	0.09	0.36	0.729195	0.864184	-6.78
263925_at	putative glycine-rich RNA binding protei	---	AT2G21690	-1.02	-0.03	-0.36	0.729307	0.864271	-6.78

252114_at	mucin -like protein hemomucin, Drosop	---	AT3G51450	-1.09	-0.13	-0.36	0.729365	0.864295	-6.78
253826_s_a	E2, ubiquitin-conjugating enzyme 9 (UB	UBC9	AT4G27960 /	1.02	0.03	0.36	0.729479	0.864367	-6.78
251587_at	hypothetical protein	---	AT3G58080	-1.05	-0.07	-0.36	0.729502	0.864367	-6.78
266843_at	hypothetical protein predicted by gensca	---	AT2G26135	1.03	0.04	0.36	0.729573	0.864407	-6.78
251928_at	putative protein hypothetical protein At2	---	AT3G53980	1.09	0.13	0.36	0.729714	0.864529	-6.78
251881_at	DIPHOSPHOMEVALONATE DECARB	---	AT3G54250	1.06	0.08	0.36	0.730015	0.864841	-6.78
267573_at	putative tropinone reductase	---	AT2G30670	1.02	0.03	0.36	0.730114	0.864895	-6.78
263479_x_a	hypothetical protein predicted by gensca	---	---	1.03	0.04	0.36	0.730137	0.864895	-6.78
250447_at	putative protein KIAA0332 gene, Homo	---	AT5G10800	1.03	0.04	0.36	0.730246	0.864980	-6.78
246107_at	putative protein various predicted prote	---	---	1.03	0.04	0.36	0.730352	0.865060	-6.78
267121_at	putative GDSL-motif lipase/hydrolase si	---	AT2G23540	1.06	0.08	0.36	0.730393	0.865064	-6.78
265025_at	Expressed protein ; supported by full-ler	---	AT1G24575	1.03	0.05	0.36	0.730842	0.865550	-6.78
263006_at	hypothetical protein contains similarity t	---	AT1G54240	-1.03	-0.04	-0.36	0.730971	0.865658	-6.78
264606_at	unknown protein ;supported by full-leng	---	AT1G04660	1.04	0.06	0.36	0.731065	0.865694	-6.78
256810_at	adenyl cyclase, putative similar to aden	---	AT3G21465	-1.03	-0.05	-0.36	0.731141	0.865694	-6.78
245535_at	cell wall protein like	---	AT4G15160	1.03	0.05	0.36	0.731109	0.865694	-6.78
255972_at	hypothetical protein similar to hypothetic	---	---	-1.02	-0.03	-0.36	0.731153	0.865694	-6.78
263290_at	unknown protein	---	AT2G10930	-1.02	-0.03	-0.36	0.7312	0.865705	-6.78
256786_at	unknown protein ;supported by full-leng	---	AT3G13740	-1.04	-0.05	-0.36	0.731289	0.865720	-6.78
265167_at	putative OBP32pep protein	---	AT1G23680	-1.03	-0.04	-0.36	0.731256	0.865720	-6.78
264288_at	Expressed protein ; supported by full-ler	---	AT1G62045	1.03	0.04	0.36	0.731455	0.865872	-6.78
262353_at	hypothetical protein similar to hypothetic	---	AT1G64210	-1.02	-0.03	-0.36	0.731528	0.865894	-6.78
255396_at	hypothetical protein	---	---	1.03	0.04	0.36	0.731617	0.865894	-6.78
252308_at	putative protein sugar transporter 2, Dr	---	AT3G49310	1.03	0.04	0.36	0.731582	0.865894	-6.78
261916_at	jasmonic acid, putative similar to jasmo	anac028	AT1G65910	1.03	0.05	0.36	0.731626	0.865894	-6.78
258388_at	putative expansin S2 precursor similar t	ATEXPA1	AT3G15370	-1.02	-0.03	-0.36	0.731705	0.865943	-6.78
264822_at	putative ribonucleoprotein	---	AT1G03457	1.05	0.08	0.36	0.731807	0.865975	-6.78
258605_at	phi-1-like protein similar to phi-1 (phosp	EXL6	AT3G02970	1.03	0.05	0.36	0.7318	0.865975	-6.78
264501_at	putative lipase Similar to nodulins and l	---	AT1G09390	-1.08	-0.12	-0.36	0.732015	0.866176	-6.78
254429_at	Expressed protein ; supported by full-ler	---	AT4G21105	1.03	0.04	0.36	0.732081	0.866209	-6.78
252571_at	putative protein syntaxin 8 - Homo sapi	SYP72	AT3G45280	-1.03	-0.05	-0.36	0.732133	0.866225	-6.78
263240_s_a	unknown protein ; supported by cDNA:	---	AT1G72590 /	1.04	0.06	0.36	0.732173	0.866227	-6.78
245859_at	serine (threonine) protein kinase - like s	ATNEK3	AT5G28290	1.05	0.07	0.36	0.732466	0.866427	-6.78
264405_at	putative mitogen-activated protein kinas	ATMPK1	AT1G10210	-1.06	-0.08	-0.36	0.732494	0.866427	-6.78
247039_at	putative protein contains similarity to AP	ATEB1C	AT5G67270	-1.04	-0.06	-0.36	0.732413	0.866427	-6.78

248356_at	putative protein strong similarity to unkn	ATEXO70A	AT5G52350	-1.02	-0.03	-0.36	0.732424	0.866427	-6.78
255950_at	hypothetical protein predicted by genem	---	AT1G22110	1.04	0.05	0.36	0.732544	0.866441	-6.78
260161_at	hypothetical protein similar to putative p	ROPGEF1	AT1G79860	1.02	0.03	0.36	0.73274	0.866629	-6.78
254802_at	endoxyloglucan transferase-like protein	---	AT4G13090	-1.04	-0.05	-0.36	0.732792	0.866645	-6.78
249157_at	unknown protein	---	AT5G43510 /	1.02	0.03	0.36	0.732972	0.866813	-6.78
264352_at	unknown protein Strong similarity to gi|2	---	AT1G03270	1.05	0.07	0.36	0.733143	0.866970	-6.78
248988_at	putative protein contains similarity to cyc	---	AT5G45190	-1.03	-0.04	-0.36	0.733312	0.867035	-6.78
253436_at	ubiquinol-cytochrome c reductase - like	---	AT4G32470	1.03	0.04	0.36	0.7333	0.867035	-6.78
254519_at	putative protein W15DMY30S	---	AT4G19940	-1.04	-0.06	-0.36	0.733272	0.867035	-6.78
251999_at	hypothetical protein teichoic acid biosyr	---	AT3G52700	1.03	0.04	0.36	0.733351	0.867036	-6.78
246175_s_a	putative protein hypothetical protein F1	---	AT5G28320 /	-1.03	-0.04	-0.35	0.733516	0.867141	-6.78
264066_at	Argonaute (AGO1)-like protein	AGO5	AT2G27880	1.03	0.04	0.35	0.733505	0.867141	-6.78
264901_at	putative sulphate transporter protein str	AST91	AT1G23090	1.09	0.13	0.35	0.733688	0.867300	-6.78
265878_at	putative SUPERMAN-like C2H2 zinc fin	ZFP11	AT2G42410	-1.02	-0.03	-0.35	0.733993	0.867536	-6.78
267071_at	unknown protein	---	AT2G40980	-1.03	-0.04	-0.35	0.734002	0.867536	-6.78
245157_at	putative polygalacturonase	---	AT2G33160	1.02	0.04	0.35	0.73394	0.867536	-6.78
267611_at	unknown protein	SPX2	AT2G26660	1.05	0.07	0.35	0.734429	0.867823	-6.78
256543_at	unknown protein supported by full-lengt	---	AT1G42480	-1.03	-0.05	-0.35	0.734358	0.867823	-6.78
265019_at	putative myosin heavy chain similar to E	---	AT1G24560	1.02	0.03	0.35	0.734473	0.867823	-6.78
247711_at	receptor-like protein kinase receptor-lik	---	AT5G59270	-1.03	-0.04	-0.35	0.734475	0.867823	-6.78
248141_at	unknown protein	---	AT5G55010	-1.03	-0.04	-0.35	0.734444	0.867823	-6.78
245737_at	hypothetical protein similar to putative h	---	AT1G44160	-1.04	-0.06	-0.35	0.734511	0.867823	-6.78
255476_at	hypothetical protein similar to reverse tr	---	---	1.03	0.05	0.35	0.734422	0.867823	-6.78
254496_at	hyuC-like protein 5-substituted hydanto	ATAAH	AT4G20070	-1.08	-0.11	-0.35	0.734699	0.868000	-6.78
263365_at	putative heat shock protein	---	AT2G20550	-1.05	-0.06	-0.35	0.73484	0.868123	-6.78
262258_at	20S proteasome subunit PAE1 identical	PAE1	AT1G53850	-1.03	-0.05	-0.35	0.734881	0.868126	-6.78
260126_at	putative hydroxymethyltransferase simil	SHM7	AT1G36370	-1.05	-0.06	-0.35	0.735118	0.868136	-6.78
254873_at	putative protein a 162 kDa component	EIF3A	AT4G11420	-1.03	-0.04	-0.35	0.73527	0.868136	-6.78
255242_at	putative protein putative retrotransposo	---	---	1.03	0.04	0.35	0.735229	0.868136	-6.78
249038_at	putative protein contains similarity to unl	RING1A	AT5G44280	1.03	0.04	0.35	0.73501	0.868136	-6.78
260957_at	delta 9 desaturase identical to delta 9 de	ADS1	AT1G06080	1.05	0.07	0.35	0.735247	0.868136	-6.78
252865_at	Expressed protein ; supported by full-ler	---	AT4G39753	-1.04	-0.06	-0.35	0.735029	0.868136	-6.78
264518_at	unknown protein	---	AT1G09980	-1.04	-0.06	-0.35	0.735161	0.868136	-6.78
262015_at	hypothetical protein predicted by genem	---	---	-1.03	-0.04	-0.35	0.73493	0.868136	-6.78
254534_at	putative Fe(II) transport protein Fe(II) tr	IRT2	AT4G19680	1.02	0.03	0.35	0.735157	0.868136	-6.78

262036_at	ATP-dependent RNA helicase, putative	---	AT1G35530	1.04	0.06	0.35	0.735173	0.868136	-6.78
267376_at	putative receptor-like protein kinase, EF	ER	AT2G26330	1.12	0.16	0.35	0.735454	0.868270	-6.78
252340_at	myb-like protein	AtMYB45	AT3G48920	1.05	0.06	0.35	0.73546	0.868270	-6.78
248848_at	disease resistance protein-like	---	AT5G46520	1.02	0.03	0.35	0.735649	0.868449	-6.78
246170_at	putative protein various predicted prote	---	AT5G32450	-1.03	-0.05	-0.35	0.735815	0.868533	-6.78
246287_at	unknown protein	---	AT1G31870	-1.03	-0.04	-0.35	0.735765	0.868533	-6.78
252767_at	ring-box protein-like ring-box protein 1 -	---	AT3G42830	1.03	0.04	0.35	0.735874	0.868533	-6.78
250032_at	glutamate dehydrogenase (EC 1.4.1.-) 1	GDH1	AT5G18170	1.09	0.13	0.35	0.735859	0.868533	-6.78
267170_at	putative RING zinc finger protein	---	AT2G37585	-1.05	-0.07	-0.35	0.735975	0.868608	-6.78
267138_s_a	similar to SOR1 from the fungus Cercos	PDX1.1	AT2G38210 /	-1.07	-0.09	-0.35	0.736125	0.868740	-6.78
251998_at	putative protein KIAA0010 protein, Hom	UPL7	AT3G53090	-1.03	-0.04	-0.35	0.736221	0.868805	-6.78
247462_at	A9 protein precursor - like A9 protein pr	---	AT5G62080	1.03	0.05	0.35	0.736256	0.868805	-6.78
257982_at	unknown protein similar to TYPE II DNA	ATTOP6B	AT3G20780	1.04	0.05	0.35	0.736688	0.869125	-6.78
255710_at	predicted protein of unknown function ;	---	AT4G00030 /	1.05	0.07	0.35	0.736591	0.869125	-6.78
264907_at	unknown protein similar to S.pombe pro	---	AT2G17280	1.08	0.11	0.35	0.736698	0.869125	-6.78
250275_at	putative protein mRNA, Moritella marina	---	AT5G13030	1.04	0.05	0.35	0.736646	0.869125	-6.78
264028_at	putative nitrilase-associated protein Alte	SPR1	AT2G03680	1.05	0.07	0.35	0.736718	0.869125	-6.78
265257_at	succinyl-CoA ligase beta subunit ;suppo	---	AT2G20420	1.06	0.08	0.35	0.736865	0.869254	-6.78
256921_at	unknown protein ;supported by full-leng	---	AT3G18940	-1.03	-0.04	-0.35	0.736958	0.869254	-6.78
267012_at	similar to latex allergen from Hevea bras	PLP6	AT2G39220	1.08	0.11	0.35	0.736941	0.869254	-6.78
253030_at	hypothetical protein	FRS5	AT4G38180	-1.02	-0.03	-0.35	0.73698	0.869254	-6.78
267190_at	putative N-myristoyltransferase ; suppo	NMT2	AT2G44170	-1.03	-0.04	-0.35	0.737066	0.869311	-6.78
263960_at	putative kinesin-related cytokinesis prot	---	AT2G36200	-1.03	-0.04	-0.35	0.737145	0.869359	-6.78
253434_at	potassium channel - protein	AKT5	AT4G32500	-1.03	-0.04	-0.35	0.737262	0.869414	-6.78
256519_at	hypothetical protein predicted by gensca	---	AT1G66110	1.04	0.06	0.35	0.737268	0.869414	-6.78
255527_at	putative protein	---	AT4G02360	1.11	0.15	0.35	0.737323	0.869434	-6.78
253570_at	hypothetical protein	---	AT4G31260	1.03	0.05	0.35	0.73741	0.869492	-6.78
261247_at	hypothetical protein predicted by genem	---	AT1G20070	-1.12	-0.16	-0.35	0.737798	0.869608	-6.78
256160_at	pyruvate dehydrogenase E1 beta subu	PDH-E1 B	AT1G30120	-1.04	-0.06	-0.35	0.737688	0.869608	-6.78
264332_at	hypothetical protein predicted by genem	---	AT1G61920	1.03	0.04	0.35	0.737961	0.869608	-6.78
255082_at	putative protein polyphosphoinositide b	---	AT4G09160	1.03	0.04	0.35	0.738179	0.869608	-6.78
258894_at	putative disease resistance protein simil	AtRLP32	AT3G05650	-1.07	-0.09	-0.35	0.738126	0.869608	-6.78
254240_at	Expressed protein ; supported by full-ler	SP1L5	AT4G23496	1.03	0.04	0.35	0.737912	0.869608	-6.78
248520_at	11-beta-hydroxysteroid dehydrogenase-	AtHSD1	AT5G50600 /	-1.04	-0.06	-0.35	0.737827	0.869608	-6.78
246750_at	putative protein predicted proteins, Dro	AT5G2786	---	1.05	0.07	0.35	0.737815	0.869608	-6.78

258858_at	putative 40S ribosomal protein S19 simi	---	AT3G02080	-1.05	-0.07	-0.35	0.737787	0.869608	-6.78
258326_at	unknown protein similar to putative DNA	SOL1	AT3G22760	1.04	0.06	0.35	0.738114	0.869608	-6.78
259949_at	hypothetical protein predicted by gensca	---	AT1G71420	-1.03	-0.04	-0.35	0.738191	0.869608	-6.78
259061_at	putative GTP-binding protein similar to	AtRABA5b	AT3G07410	1.06	0.08	0.35	0.738309	0.869608	-6.78
256692_at	hypothetical protein predicted by genem	---	AT3G32050	-1.02	-0.03	-0.35	0.737655	0.869608	-6.78
261430_at	hypothetical protein predicted by genem	---	AT1G18830	-1.04	-0.05	-0.35	0.738277	0.869608	-6.78
259785_at	unknown protein ;supported by full-lengt	---	AT1G29490	-1.03	-0.05	-0.35	0.738093	0.869608	-6.78
248033_s_a	putative protein similar to unknown prote	---	AT5G54330 /	1.03	0.04	0.35	0.737708	0.869608	-6.78
267050_at	putative RNA-binding protein ; supporte	---	AT2G41060	1.03	0.04	0.35	0.737956	0.869608	-6.78
266840_at	hypothetical protein predicted by gensca	---	AT2G26160	1.02	0.03	0.35	0.737619	0.869608	-6.78
267052_at	unknown protein	---	AT2G38410	1.03	0.04	0.35	0.738167	0.869608	-6.78
263059_at	putative non-LTR retrolelement reverse	---	---	-1.03	-0.04	-0.35	0.738237	0.869608	-6.78
256527_at	thionin, putative similar to thionin [Arabi	---	AT1G66100	-1.04	-0.06	-0.35	0.738211	0.869608	-6.78
259468_at	unknown protein	TTN10	AT1G19080 /	1.03	0.05	0.35	0.738443	0.869721	-6.78
266753_at	auxin-induced protein (IAA20) identical t	IAA20	AT2G46990	1.03	0.04	0.35	0.738517	0.869763	-6.78
263386_at	unknown protein ; supported by cDNA:	---	AT2G40150	1.06	0.08	0.35	0.73872	0.869826	-6.79
263133_at	hypothetical protein predicted by genem	---	AT1G78450	1.12	0.16	0.35	0.738648	0.869826	-6.79
253510_at	hypothetical protein	GDU1	AT4G31730	-1.06	-0.09	-0.35	0.738622	0.869826	-6.78
249387_at	putative protein predicted proteins, Arat	---	AT5G40070	-1.04	-0.05	-0.35	0.738723	0.869826	-6.79
260368_at	AtHVA22c identical to AtHVA22c GB:AF	ATHVA22(	AT1G69700	-1.09	-0.13	-0.35	0.738896	0.869983	-6.79
246535_at	putative protein several hypothetical pro	---	AT5G15900	1.04	0.06	0.35	0.738949	0.869983	-6.79
249623_at	putative protein Ariadne-2 protein (ARI2	---	AT5G37560	1.02	0.03	0.35	0.73897	0.869983	-6.79
259289_at	hypothetical protein predicted by gensca	---	AT3G11350	1.03	0.04	0.35	0.739012	0.869987	-6.79
260869_at	stearoyl acyl carrier protein desaturase.	---	AT1G43800	-1.02	-0.03	-0.35	0.73907	0.870010	-6.79
255929_at	hypothetical protein predicted by genem	---	AT1G12650	-1.03	-0.05	-0.35	0.739176	0.870069	-6.79
259994_at	putative C2H2-type zinc finger protein c	AtIDD14	AT1G68130 /	-1.04	-0.06	-0.35	0.739272	0.870069	-6.79
247539_at	putative protein predicted protein, Arabi	---	AT5G61710	-1.02	-0.03	-0.35	0.739229	0.870069	-6.79
253927_at	putative protein	---	AT4G26710	1.03	0.05	0.35	0.739257	0.870069	-6.79
250476_at	MADS box protein FLOWERING LOCU	FLC	AT5G10140	-1.03	-0.04	-0.35	0.739313	0.870071	-6.79
265050_at	jasmonate inducible protein, putative si	---	AT1G52070	1.02	0.04	0.35	0.739446	0.870129	-6.79
261760_at	hypothetical protein similar to putative R	---	AT1G15600	1.04	0.05	0.35	0.739561	0.870129	-6.79
262643_at	unknown protein ;supported by full-lengt	---	AT1G62770	1.05	0.07	0.35	0.73957	0.870129	-6.79
250637_at	glycine-rich protein atGRP-7	GRP17	AT5G07530	1.03	0.04	0.35	0.739449	0.870129	-6.79
255382_at	putative pre-mRNA splicing factor simila	EMB2770	AT4G03430	1.02	0.03	0.35	0.739577	0.870129	-6.79
258280_at	putative self-incompatibility protein simi	---	AT3G26880	-1.02	-0.03	-0.35	0.739591	0.870129	-6.79

245483_at	cysteine proteinase contains similarity to	---	AT4G16190	-1.02	-0.04	-0.35	0.73983	0.870186	-6.79
266713_at	unknown protein	---	AT2G46760	-1.03	-0.04	-0.35	0.739804	0.870186	-6.79
259415_at	hypothetical protein contains similarity to	---	AT1G02330	-1.04	-0.05	-0.35	0.739782	0.870186	-6.79
261331_at	hypothetical protein predicted by genem	---	---	-1.03	-0.04	-0.35	0.73972	0.870186	-6.79
258942_at	unknown protein predicted by genscan,	---	AT3G09960	-1.03	-0.04	-0.35	0.739684	0.870186	-6.79
260524_at	unknown protein	---	AT2G47230	1.03	0.04	0.35	0.739911	0.870192	-6.79
247957_at	protein phosphatase 2C ABI2 (PP2C) (s	ABI2	AT5G57050	1.05	0.07	0.35	0.739881	0.870192	-6.79
257594_at	unknown protein	---	AT3G24740	-1.03	-0.05	-0.35	0.740004	0.870217	-6.79
253356_at	putative protein myosin II heavy chain -	---	AT4G33390	1.03	0.04	0.35	0.740009	0.870217	-6.79
264976_at	peptide transporter, putative similar to p	NRT1.6	AT1G27080	1.03	0.05	0.35	0.740089	0.870266	-6.79
262872_at	hypothetical protein predicted by genem	---	AT1G64690	1.04	0.06	0.35	0.740223	0.870292	-6.79
260698_at	unknown protein contains similarity to L-	---	AT1G32300	1.02	0.03	0.35	0.740225	0.870292	-6.79
257480_at	hypothetical protein similar to putative R	---	AT1G15640	1.05	0.08	0.35	0.740182	0.870292	-6.79
259686_at	transcription factor SCARECROW, puta	---	AT1G63100	-1.04	-0.06	-0.35	0.740439	0.870481	-6.79
261454_at	hypothetical protein predicted by genem	---	AT1G21090	-1.03	-0.04	-0.35	0.740462	0.870481	-6.79
255477_at	coded for by A. thaliana cDNA R64991	---	AT4G02370	1.04	0.05	0.35	0.740528	0.870514	-6.79
262559_at	unknown protein similar to hypothetical	---	AT1G31300	-1.03	-0.04	-0.35	0.740587	0.870538	-6.79
265692_at	hypothetical protein predicted by gensca	---	AT2G24340	1.03	0.04	0.34	0.740636	0.870551	-6.79
246933_at	ZFP3 zinc finger protein ; supported by	ZFP3	AT5G25160	1.02	0.03	0.34	0.740706	0.870588	-6.79
254801_at	endoxyloglucan transferase-like protein	---	AT4G13080	-1.02	-0.03	-0.34	0.74083	0.870682	-6.79
255202_at	putative polyprotein	---	---	1.03	0.04	0.34	0.740862	0.870682	-6.79
264786_at	putative Ta11-like non-LTR retroelemen	---	AT2G17920	-1.03	-0.04	-0.34	0.740949	0.870739	-6.79
256731_at	hypothetical protein contains Pfam profil	---	AT3G30340	1.03	0.04	0.34	0.741035	0.870751	-6.79
250468_at	transcription factor TEIL/ethylene-insen	---	AT5G10120	1.02	0.03	0.34	0.741024	0.870751	-6.79
254492_at	endomembrane-associated protein ; su	PCAP1	AT4G20260	-1.03	-0.04	-0.34	0.741098	0.870779	-6.79
266201_at	similar to MtN3 protein ;supported by fu	---	AT2G39060	1.03	0.04	0.34	0.741177	0.870828	-6.79
252811_at	putative protein several hypothetical pro	---	---	1.03	0.04	0.34	0.741247	0.870865	-6.79
247036_at	putative protein contains similarity to MA	---	AT5G67130	-1.04	-0.06	-0.34	0.741317	0.870902	-6.79
247358_at	flavonol synthase	FLS2	AT5G63580	-1.03	-0.05	-0.34	0.741395	0.870904	-6.79
266178_at	putative phloem-specific lectin	AtPP2-B4	AT2G02280	1.03	0.04	0.34	0.741363	0.870904	-6.79
251303_at	NAM-like protein no apical meristem (N	ANAC066	AT3G61910	-1.02	-0.03	-0.34	0.741682	0.871132	-6.79
263293_x_a	hypothetical protein similar to hypothetic	---	---	1.02	0.03	0.34	0.741734	0.871132	-6.79
248930_at	unknown protein	---	AT5G46010	1.03	0.04	0.34	0.741742	0.871132	-6.79
257491_at	hypothetical protein predicted by genen	---	AT1G06170	-1.02	-0.03	-0.34	0.741725	0.871132	-6.79
257880_at	AMP-binding protein, putative contains	AAE7	AT3G16910	1.05	0.07	0.34	0.741786	0.871139	-6.79

262803_at	unknown protein Location of ESTs 152	---	AT1G21000	-1.05	-0.07	-0.34	0.741986	0.871195	-6.79
264378_at	hypothetical protein predicted by gensca	---	AT2G25220	-1.08	-0.11	-0.34	0.741985	0.871195	-6.79
259093_at	unknown protein similar to putative prote	---	AT3G04860	1.06	0.08	0.34	0.741901	0.871195	-6.79
246330_at	aldehyde oxidase ; supported by cDNA	AAO2	AT3G43600	-1.07	-0.10	-0.34	0.741964	0.871195	-6.79
246125_at	Expressed protein ; supported by full-ler	---	AT5G19875	-1.09	-0.13	-0.34	0.742246	0.871411	-6.79
262271_x_a	hypothetical protein predicted by genem	---	---	1.05	0.07	0.34	0.742226	0.871411	-6.79
265473_at	Expressed protein ; supported by full-ler	LCR10	AT2G15535	1.03	0.04	0.34	0.742302	0.871431	-6.79
250010_at	AP2-domain DNA-binding protein -like I	---	AT5G18450	-1.04	-0.05	-0.34	0.742359	0.871454	-6.79
260193_at	putative amino acid permease similar to	---	AT1G67640	1.04	0.05	0.34	0.742469	0.871537	-6.79
262969_at	unknown protein	---	AT1G75710	-1.04	-0.05	-0.34	0.742634	0.871642	-6.79
265485_at	putative Ta11-like non-LTR retroelemen	---	---	1.04	0.06	0.34	0.742619	0.871642	-6.79
263159_at	RSH3 (RelA/SpoT homolog) identical to	RSH3	AT1G54130	-1.04	-0.05	-0.34	0.742791	0.871781	-6.79
256411_at	ATP-dependent Clp protease proteolytic	CLPP3	AT1G66670	-1.05	-0.06	-0.34	0.742857	0.871801	-6.79
266571_at	unknown protein	---	AT2G23830	1.06	0.08	0.34	0.742922	0.871801	-6.79
265812_at	hypothetical protein predicted by gensca	---	AT2G18070	1.03	0.05	0.34	0.74291	0.871801	-6.79
245822_at	unknown protein ; supported by cDNA: g	---	AT1G26110	-1.03	-0.05	-0.34	0.743807	0.871944	-6.79
258184_at	two-component phosphorelay mediator	AHP1	AT3G21510	1.04	0.05	0.34	0.743614	0.871944	-6.79
254573_at	putative pectinacetylesterase pectinace	---	AT4G19420	1.06	0.08	0.34	0.743765	0.871944	-6.79
251194_at	putative protein	---	AT3G62920	1.05	0.06	0.34	0.74381	0.871944	-6.79
255525_at	coded for by A. thaliana cDNA T04215 s	---	AT4G02340	1.03	0.04	0.34	0.743509	0.871944	-6.79
250183_at	putative protein various predicted prote	---	AT5G14510	1.04	0.06	0.34	0.743574	0.871944	-6.79
256302_at	Expressed protein ; supported by full-ler	---	AT1G69526	1.03	0.05	0.34	0.743671	0.871944	-6.79
246992_at	N-acetyltransferase hookless1-like prote	---	AT5G67430	1.03	0.04	0.34	0.743699	0.871944	-6.79
247941_at	putative protein strong similarity to unkn	---	AT5G57200	-1.02	-0.03	-0.34	0.743242	0.871944	-6.79
247635_at	serine/threonine-protein kinase - like pr	GRIK2	AT5G60548 /	1.02	0.03	0.34	0.743595	0.871944	-6.79
252471_at	phosphoprotein phosphatase ;supporte	TOPP5	AT3G46820	-1.03	-0.04	-0.34	0.743761	0.871944	-6.79
262250_at	Expressed protein predicted by genscan	---	AT1G48280	-1.10	-0.13	-0.34	0.743797	0.871944	-6.79
250037_at	disease resistance protein -like disease	---	AT5G18350	1.04	0.05	0.34	0.743126	0.871944	-6.79
265493_at	unknown protein predicted by genscan	---	AT2G15670	-1.03	-0.04	-0.34	0.743279	0.871944	-6.79
265603_at	hypothetical protein predicted by gensca	---	---	1.03	0.04	0.34	0.743286	0.871944	-6.79
247472_at	cytokinesis regulating protein - like PR	MAP65-9	AT5G62250	-1.02	-0.03	-0.34	0.743593	0.871944	-6.79
261706_at	hypothetical protein similar to hypothetic	---	---	1.02	0.03	0.34	0.743802	0.871944	-6.79
252560_at	histone H2B -like protein histone H2B1,	HTB11	AT3G46030	-1.02	-0.03	-0.34	0.743526	0.871944	-6.79
266023_at	copia-like retroelement pol polyprotein	---	---	1.03	0.04	0.34	0.743279	0.871944	-6.79
258513_at	protein kinase, putative contains Pfam	---	AT3G06630	-1.02	-0.03	-0.34	0.743242	0.871944	-6.79

245778_at	RNA-binding glycine-rich protein, putati	---	AT1G73530	1.04	0.06	0.34	0.743902	0.872009	-6.79
251126_at	putative protein various predicted prote	---	AT5G01070	1.02	0.04	0.34	0.744298	0.872128	-6.79
253731_at	acid phosphatase-like protein acid pho	---	AT4G29260	-1.02	-0.03	-0.34	0.744136	0.872128	-6.79
249717_at	unknown protein ;supported by full-leng	---	AT5G35730	1.03	0.04	0.34	0.744236	0.872128	-6.79
256359_at	protein kinase, putative contains Pfam	---	AT1G66460	-1.02	-0.03	-0.34	0.744244	0.872128	-6.79
245452_at	retrotransposon like protein	---	---	-1.02	-0.03	-0.34	0.74425	0.872128	-6.79
256618_at	hypothetical protein	VRN5	AT3G24440	1.06	0.09	0.34	0.744253	0.872128	-6.79
252007_at	hypothetical protein MobA, Pseudomon	---	AT3G52830	1.03	0.05	0.34	0.74431	0.872128	-6.79
250872_at	putative protein SF16 protein, common	IQD12	AT5G03960	-1.03	-0.04	-0.34	0.744198	0.872128	-6.79
255190_x_a	may be a pseudogene similar to a famil	---	---	-1.02	-0.03	-0.34	0.744477	0.872244	-6.79
257186_at	hypothetical protein predicted by genem	---	AT3G13130	-1.03	-0.05	-0.34	0.744486	0.872244	-6.79
259565_at	hypothetical protein	---	AT1G20530	-1.02	-0.03	-0.34	0.744552	0.872277	-6.79
244990_s_a	hypothetical protein	---	---	-1.06	-0.09	-0.34	0.744779	0.872498	-6.79
250046_at	putative protein predicted proteins, Ara	---	AT5G17720	1.03	0.04	0.34	0.744819	0.872500	-6.79
266849_at	putative vacuolar processing enzyme id	ALPHA-VP	AT2G25940	-1.03	-0.04	-0.34	0.744857	0.872500	-6.79
251101_at	putative transporter protein Na+/H+ anti	CHX26	AT5G01680	1.02	0.03	0.34	0.745024	0.872651	-6.79
257736_at	hypothetical protein predicted by genem	---	AT3G27410	1.03	0.04	0.34	0.745107	0.872703	-6.79
246678_at	putative protein predicted replication A1	---	---	-1.03	-0.04	-0.34	0.745186	0.872751	-6.79
251973_at	nodulin / glutamate-ammonia ligase - lik	---	AT3G53180	-1.05	-0.07	-0.34	0.745583	0.872900	-6.79
260087_at	hypothetical protein predicted by gensca	---	AT1G73200	1.04	0.05	0.34	0.745573	0.872900	-6.79
262715_at	putative myb-related transcription factor	MYB58	AT1G16490	-1.02	-0.03	-0.34	0.745521	0.872900	-6.79
252891_at	putative WRKY DNA-binding protein DN	WRKY13	AT4G39410	-1.04	-0.05	-0.34	0.745459	0.872900	-6.79
258047_at	putative 4-coumarate:CoA ligase 2 almo	4CL2	AT3G21240	1.11	0.15	0.34	0.74562	0.872900	-6.79
251279_at	hypothetical protein	---	AT3G61800	1.05	0.06	0.34	0.745573	0.872900	-6.79
257961_at	unknown protein	---	AT3G19780	-1.03	-0.04	-0.34	0.74546	0.872900	-6.79
248872_at	Expressed protein ; supported by full-ler	MSP2	AT5G46795	-1.03	-0.04	-0.34	0.745554	0.872900	-6.79
249532_at	AtPP - like protein AtPP protein, Brassi	---	AT5G38780	1.06	0.09	0.34	0.745695	0.872943	-6.79
246284_at	putative protein	---	AT4G36780	-1.03	-0.04	-0.34	0.746201	0.873397	-6.79
255770_at	hypothetical protein predicted by gensca	---	AT1G18560	1.03	0.04	0.34	0.74645	0.873397	-6.79
247630_at	putative protein	SIZ1	AT5G60410	1.03	0.04	0.34	0.746375	0.873397	-6.79
254053_s_a	SRG1-like protein strong homology to S	---	AT4G25300 /	1.05	0.07	0.34	0.746519	0.873397	-6.79
261072_at	hexose transporter, putative similar to C	ATSTP2	AT1G07340	1.03	0.05	0.34	0.746341	0.873397	-6.79
262179_at	hypothetical protein predicted by genem	AGL66	AT1G77980	1.03	0.05	0.34	0.746479	0.873397	-6.79
250230_at	putative protein similar to unknown prote	---	AT5G13900	1.05	0.07	0.34	0.746371	0.873397	-6.79
256312_x_a	hypothetical protein	---	AT1G35820	1.02	0.03	0.34	0.746504	0.873397	-6.79

266143_at	Expressed protein ; supported by cDNA	---	AT2G38905	1.03	0.05	0.34	0.746232	0.873397	-6.79
266935_at	F-box protein LKP2/ADO2, AtFBX2c ide	LKP2	AT2G18915	1.03	0.04	0.34	0.746542	0.873397	-6.79
262702_at	putative protein phosphatase 2C similar	---	AT1G16220	1.03	0.04	0.34	0.746477	0.873397	-6.79
249683_x_a	putative protein similar to unknown prote	---	---	-1.03	-0.04	-0.34	0.746301	0.873397	-6.79
267607_s_a	epoxide hydrolase (ATsEH) identical to	ATSEH	AT2G26740 /	-1.05	-0.07	-0.34	0.746721	0.873517	-6.79
254177_at	putative protein gene T22C1.1, Caenor	---	AT4G23860	-1.04	-0.05	-0.34	0.746709	0.873517	-6.79
251909_at	putative protein initiator-binding protein	TRFL4	AT3G53790	-1.03	-0.04	-0.34	0.746775	0.873536	-6.79
258347_at	unknown protein identical to LEA-like pr	---	AT3G17520	-1.03	-0.04	-0.34	0.746905	0.873598	-6.79
263874_at	putative ATP synthase ;supported by fu	---	AT2G21870	1.04	0.05	0.34	0.74689	0.873598	-6.79
261311_at	disease resistance protein RTM1, putat	---	AT1G05770	1.04	0.06	0.34	0.747108	0.873612	-6.79
262196_at	ubiquitin-fusion protein, putative similar	MUB5	AT1G77870	-1.06	-0.08	-0.34	0.74704	0.873612	-6.79
265910_at	putative vacuolar ATP synthase proteoli	---	AT2G25610	-1.03	-0.04	-0.34	0.747115	0.873612	-6.79
261185_at	cytochrome p450, putative similar to GE	CYP94D1	AT1G34540	-1.02	-0.04	-0.34	0.74704	0.873612	-6.79
257195_at	hypothetical protein predicted by genem	---	AT3G23680	1.03	0.04	0.34	0.747119	0.873612	-6.79
253000_at	putative protein other predicted proteins	---	AT4G38360	1.03	0.05	0.34	0.747147	0.873612	-6.79
247436_at	dehydrogenase ; supported by cDNA: g	ALDH12A1	AT5G62530	-1.04	-0.05	-0.34	0.747502	0.873822	-6.79
245522_at	hypothetical protein	---	AT4G15890	1.02	0.04	0.34	0.74748	0.873822	-6.79
266430_at	unknown protein	---	AT2G07200	1.02	0.03	0.34	0.747391	0.873822	-6.79
249079_at	putative protein contains similarity to unl	---	AT5G43930	-1.04	-0.05	-0.34	0.747518	0.873822	-6.79
261894_at	unknown protein ;supported by full-lengt	MGT1	AT1G80900	1.03	0.04	0.34	0.747442	0.873822	-6.79
257495_at	unknown protein	ATPDIL5-1	AT1G07960	1.03	0.04	0.33	0.74789	0.873906	-6.79
259051_at	unknown protein similar to CGI-86 prote	---	AT3G03330	-1.03	-0.04	-0.33	0.74796	0.873906	-6.79
254850_at	putative protein predicted proteins Arabi	---	AT4G12000	-1.04	-0.06	-0.34	0.747737	0.873906	-6.79
250972_at	putative protein various Myb related pro	LCL1	AT5G02840	1.04	0.06	0.33	0.748095	0.873906	-6.79
264808_at	unknown protein similar to EST gb|H372	PRA1.E	AT1G08770	1.03	0.04	0.34	0.74779	0.873906	-6.79
259045_at	calmodulin-like protein similar to calmo	---	AT3G03410	-1.03	-0.04	-0.33	0.747847	0.873906	-6.79
263008_at	unknown protein	RPP27	AT1G54470	1.02	0.03	0.33	0.748066	0.873906	-6.79
AFFX-Athal-	Arabidopsis thaliana /REF=U84969 /DE	---	---	1.03	0.04	0.34	0.747723	0.873906	-6.79
246531_at	MADS box protein AGL2 ; supported by	ספט-01	AT5G15800	1.03	0.05	0.33	0.748165	0.873906	-6.79
264159_at	unknown protein ;supported by full-lengt	---	AT1G65270	-1.02	-0.03	-0.33	0.748022	0.873906	-6.79
250722_at	unknown protein ;supported by full-leng	---	AT5G06190	1.04	0.06	0.34	0.747691	0.873906	-6.79
250888_at	putative protein trichohyalin, Oryctolagu	---	AT5G04460	-1.04	-0.06	-0.33	0.747876	0.873906	-6.79
246726_at	putative protein predicted protein, Arabi	---	AT5G29050	-1.02	-0.03	-0.33	0.748017	0.873906	-6.79
265591_at	hypothetical protein predicted by gensca	---	AT2G20150	1.04	0.05	0.33	0.74815	0.873906	-6.79
259829_at	oligopeptide transporter, putative simila	---	---	-1.03	-0.05	-0.33	0.747942	0.873906	-6.79

250428_at	putative protein phosphatase protein ty	PAS2	AT5G10480	1.05	0.07	0.33	0.748378	0.874065	-6.79
256474_at	unknown protein	---	---	1.03	0.05	0.33	0.748339	0.874065	-6.79
265099_at	unknown protein Location of EST 248L	---	AT1G03990	1.07	0.10	0.33	0.748491	0.874108	-6.79
265168_at	putative Ser/Thr protein kinase	---	AT1G23700	1.03	0.04	0.33	0.748464	0.874108	-6.79
250717_at	putative protein similar to unknown prote	---	AT5G06200	1.04	0.05	0.33	0.748731	0.874343	-6.79
251424_at	putative protein 04.05.01.01	---	AT3G60560	1.02	0.03	0.33	0.748835	0.874421	-6.79
257877_at	hypothetical protein	---	AT3G17140	1.03	0.04	0.33	0.749001	0.874569	-6.79
246409_at	CRK1 protein, putative similar to CRK1	---	AT1G57700	-1.04	-0.05	-0.33	0.749302	0.874876	-6.79
262650_at	lipoamide dehydrogenase, putative	---	AT1G14090	1.02	0.03	0.33	0.749346	0.874882	-6.79
252997_at	putative pollen allergen pollen allergen	ATEXLA2	AT4G38400	-1.08	-0.10	-0.33	0.749435	0.874899	-6.79
255640_at	hypothetical protein	---	AT4G00800	1.04	0.05	0.33	0.749436	0.874899	-6.79
263969_at	putative VSF-1-like b-ZIP transcription fa	UNE4	AT2G12940	-1.03	-0.04	-0.33	0.749592	0.875035	-6.79
254381_at	putative protein membrane-associated	---	AT4G21880	1.03	0.05	0.33	0.749652	0.875061	-6.79
266958_at	putative trans-prenyltransferase	GPS1	AT2G34630	-1.04	-0.05	-0.33	0.74978	0.875165	-6.79
265409_at	unknown protein	PIP2;8	AT2G16830 /	-1.03	-0.04	-0.33	0.749874	0.875230	-6.79
256141_at	lysine and histidine specific transporter,	---	AT1G48640	-1.02	-0.03	-0.33	0.749979	0.875263	-6.79
258361_at	unknown protein similar to hypothetical	---	AT3G14270	1.05	0.07	0.33	0.74997	0.875263	-6.79
251403_at	putative protein RING finger protein AO	---	AT3G60300	-1.04	-0.05	-0.33	0.750125	0.875345	-6.79
257589_at	hypothetical protein predicted by gensca	---	AT1G55050	-1.03	-0.05	-0.33	0.750088	0.875345	-6.79
262654_at	putative mandelonitrile lyase similar to	---	AT1G14180	1.04	0.05	0.33	0.750169	0.875351	-6.79
255766_at	unknown protein ;supported by full-lengt	---	AT1G16750	-1.03	-0.05	-0.33	0.750295	0.875440	-6.79
260782_at	unknown protein ; supported by cDNA: g	---	AT1G14570	-1.02	-0.03	-0.33	0.750323	0.875440	-6.79
261293_at	unknown protein ; supported by cDNA: g	---	AT1G36980	-1.02	-0.03	-0.33	0.750424	0.875514	-6.79
262442_at	unknown protein identical to hypothetica	---	AT1G47420	-1.02	-0.03	-0.33	0.750719	0.875813	-6.79
248377_at	unknown protein ; supported by full-leng	---	AT5G51720	-1.06	-0.08	-0.33	0.7508	0.875818	-6.79
257454_at	hypothetical protein predicted by genem	---	AT1G65170	1.03	0.05	0.33	0.750798	0.875818	-6.79
260012_at	Expressed protein ; supported by cDNA	---	AT1G67865	-1.05	-0.07	-0.33	0.751189	0.875909	-6.79
253684_at	nucleotide pyrophosphatase - like protei	---	AT4G29690	1.03	0.04	0.33	0.751054	0.875909	-6.79
260851_at	nodulin-like protein similar to MtN21 GE	---	AT1G21890	1.03	0.04	0.33	0.751332	0.875909	-6.79
252016_at	putative protein predicted protein, Arabi	---	AT3G52950	-1.03	-0.04	-0.33	0.751082	0.875909	-6.79
253354_at	putative protein RNA helicase DBP2 - S	---	AT4G33370	-1.05	-0.07	-0.33	0.751195	0.875909	-6.79
250269_at	anthranilate phosphoribosyltransferase	---	AT5G12970	-1.03	-0.04	-0.33	0.750953	0.875909	-6.79
265698_at	hypothetical protein predicted by gensca	---	AT2G32160	-1.03	-0.04	-0.33	0.751327	0.875909	-6.79
253680_at	cytidine deaminase 2 (CDA2)	---	AT4G29620	1.02	0.03	0.33	0.75123	0.875909	-6.79
254465_at	tapetum-specific A3 like protein Arabido	---	AT4G20420	-1.03	-0.04	-0.33	0.751229	0.875909	-6.79

252812_at	putative protein hypothetical proteins - A	---	---	-1.02	-0.03	-0.33	0.75106	0.875909	-6.79
255006_at	putative protein kinase M.sativa mRNA	---	AT4G10010	-1.02	-0.03	-0.33	0.751335	0.875909	-6.79
248604_at	protein kinase	---	AT5G49470	-1.05	-0.06	-0.33	0.751338	0.875909	-6.79
257565_at	hypothetical protein predicted by genem	---	AT3G28620	-1.02	-0.03	-0.33	0.751494	0.875956	-6.79
267432_at	putative UDP-N-acetylglucosamine pyro	---	AT2G35020	1.04	0.06	0.33	0.751459	0.875956	-6.79
257462_at	hypothetical protein	---	AT1G65740	-1.03	-0.04	-0.33	0.751432	0.875956	-6.79
249132_at	putative protein contains similarity to unl	---	AT5G43120	-1.03	-0.04	-0.33	0.751541	0.875965	-6.79
246587_at	putative protein predicted proteins, Aral	---	---	1.03	0.04	0.33	0.751587	0.875974	-6.79
262624_at	CCR4-associated factor, putative simila	---	AT1G06450	1.03	0.04	0.33	0.75166	0.875991	-6.79
258080_at	unknown protein ;supported by full-leng	---	AT3G25930	1.02	0.03	0.33	0.751678	0.875991	-6.79
247933_at	putative protein non-consensus CG dor	---	AT5G56980	1.07	0.10	0.33	0.751897	0.876198	-6.79
249232_at	dynamin-like protein (pir||S59558) ;supp	ADL1	AT5G42080	1.04	0.05	0.33	0.75197	0.876198	-6.79
245722_at	unknown protein	---	AT1G73430	-1.04	-0.05	-0.33	0.751968	0.876198	-6.79
258238_at	unknown protein	RST1	AT3G27670	-1.02	-0.03	-0.33	0.752061	0.876258	-6.79
263614_at	putative serpin	---	AT2G25240	1.03	0.05	0.33	0.75224	0.876422	-6.79
245953_at	myrosinase - binding protein - like prob	---	AT5G28520	1.04	0.05	0.33	0.752295	0.876442	-6.79
248484_at	carbonyl reductase-like protein	---	AT5G51030	-1.02	-0.03	-0.33	0.752406	0.876526	-6.79
264323_at	putative dimethylaniline monooxygenase	---	AT1G04180	1.10	0.14	0.33	0.752541	0.876594	-6.79
256287_at	hypothetical protein	---	AT3G12190	1.02	0.04	0.33	0.752536	0.876594	-6.79
262656_at	unknown protein location of EST TAT5A	---	AT1G14200	1.03	0.04	0.33	0.752702	0.876736	-6.79
251487_at	cysteine synthase	OASC	AT3G59760	-1.05	-0.08	-0.33	0.752881	0.876766	-6.79
263928_at	hypothetical protein predicted by gensca	---	AT2G36330	-1.04	-0.06	-0.33	0.752878	0.876766	-6.79
252284_at	putative protein various predicted prote	---	AT3G49020	1.03	0.04	0.33	0.752848	0.876766	-6.79
262076_at	hypothetical protein identical to GB:Q39	ATMPK2	AT1G59580	-1.03	-0.05	-0.33	0.752818	0.876766	-6.79
247587_at	putative protein predicted proteins, C.el	---	AT5G60620	1.03	0.04	0.33	0.752962	0.876815	-6.79
264449_at	hypothetical protein predicted by gensca	NPGR1	AT1G27460	1.05	0.07	0.33	0.753121	0.876912	-6.79
246495_at	putative protein hypothetical protein T2	---	AT5G16200	-1.09	-0.13	-0.33	0.753109	0.876912	-6.79
266904_at	putative pyruvate dehydrogenase E1 be	---	AT2G34590	1.05	0.07	0.33	0.75323	0.876983	-6.79
AFFX-TrpnX	B. subtilis /GEN=trpD, trpC /DB_XREF=	---	---	1.02	0.03	0.33	0.75326	0.876983	-6.79
257946_at	hypothetical protein predicted by genem	---	AT3G21710	-1.03	-0.04	-0.33	0.753332	0.876989	-6.79
260492_at	putative polygalacturonase	PGAZAT	AT2G41850	1.04	0.05	0.33	0.753418	0.876989	-6.79
255815_at	histone H3, putative similar to histone H	MGH3	AT1G19890	1.03	0.04	0.33	0.753408	0.876989	-6.79
261157_at	peroxidase ATP13a, putative similar to	---	AT1G34510	-1.02	-0.03	-0.33	0.753389	0.876989	-6.79
267119_at	putative cellulose synthase	ATCSLB0	AT2G32610	1.02	0.03	0.33	0.753556	0.876998	-6.79
263309_at	putative replication protein A1	---	---	-1.04	-0.05	-0.33	0.75358	0.876998	-6.79

256139_at	Nt-gh3 deduced protein, putative simila	---	AT1G48660	-1.03	-0.04	-0.33	0.753563	0.876998	-6.79
257604_s_a	hypothetical protein predicted by genem	---	AT1G11810 /	-1.02	-0.04	-0.33	0.753571	0.876998	-6.79
255755_s_a	polygalacturonase, putative similar to p	---	AT1G43050 /	-1.03	-0.04	-0.33	0.75364	0.877023	-6.79
259355_at	hypothetical protein predicted by genefi	---	AT3G05240	-1.03	-0.04	-0.33	0.753682	0.877027	-6.79
260597_at	hypothetical protein predicted by genem	---	AT1G55915	-1.04	-0.06	-0.33	0.75378	0.877036	-6.79
255912_at	2,3-oxidosqualene-triterpenoid cyclase,	---	AT1G66960	-1.03	-0.05	-0.33	0.753841	0.877036	-6.79
263017_at	putative cyclin 2	CYCB2;1	AT2G17620	-1.02	-0.03	-0.33	0.753844	0.877036	-6.79
245030_at	putative polygalacturonase	---	AT2G26620	1.02	0.03	0.33	0.753833	0.877036	-6.79
256347_at	unknown protein similar to putative dise	---	---	1.03	0.04	0.33	0.753898	0.877054	-6.79
245184_at	F12A21.8 hypothetical protein	---	AT1G67790	-1.03	-0.04	-0.33	0.753963	0.877078	-6.79
256357_at	hypothetical protein	---	AT1G66490	-1.02	-0.03	-0.33	0.753995	0.877078	-6.79
254881_at	hypothetical protein	---	AT4G11700	1.02	0.03	0.33	0.754132	0.877155	-6.79
247825_at	RNA/ssDNA-binding protein - like RNA/	TAF15b	AT5G58470	1.03	0.04	0.33	0.754138	0.877155	-6.79
251565_at	putative protein several hypothetical pro	LBD29	AT3G58190	1.02	0.03	0.33	0.754196	0.877178	-6.79
258363_at	putative pectin methylesterase similar to	ATPMEPC	AT3G14300	1.03	0.04	0.33	0.75445	0.877428	-6.79
252798_at	putative protein	---	AT3G42310	-1.02	-0.03	-0.33	0.75461	0.877569	-6.79
259624_at	hypothetical protein similar to unknown	---	AT1G43020	1.03	0.04	0.33	0.754665	0.877589	-6.79
263795_at	putative cyclic nucleotide-regulated ion	ATCNGC1	AT2G24610	1.03	0.04	0.33	0.754807	0.877710	-6.79
255471_at	putative oxidoreductase similar to A. tha	AOP3	AT4G03050	-1.03	-0.04	-0.33	0.754896	0.877723	-6.79
245469_at	reverse transcriptase like protein	---	---	1.02	0.03	0.33	0.754872	0.877723	-6.79
249371_at	hypothetical protein	---	AT5G40750	1.02	0.03	0.32	0.755078	0.877845	-6.79
247116_at	Mlo protein-like ; supported by cDNA: gi	MLO10	AT5G65970	1.03	0.04	0.32	0.755051	0.877845	-6.79
263551_at	hypothetical protein contains NLS (PS50	---	AT2G17110	-1.06	-0.08	-0.32	0.755248	0.877954	-6.79
249655_at	putative helicase PIF1 protein - Caenor	---	---	-1.02	-0.03	-0.32	0.755234	0.877954	-6.79
253494_at	putative protein	---	AT4G31830	-1.03	-0.04	-0.32	0.755539	0.878157	-6.79
248078_at	putative protein contains similarity to CH	---	AT5G55780	1.02	0.03	0.32	0.755501	0.878157	-6.79
249504_at	disease resistance protein - like disease	---	AT5G38850	-1.05	-0.08	-0.32	0.755525	0.878157	-6.79
256104_at	trehalose-6-phosphate synthase, putati	ATTPS2	AT1G16980	-1.02	-0.03	-0.32	0.755658	0.878172	-6.79
248428_at	protein phosphatase-2C; PP2C-like prot	AHG1	AT5G51760	1.02	0.03	0.32	0.755667	0.878172	-6.79
254946_at	putative protein proline-rich protein, Bra	---	AT4G10950	-1.03	-0.04	-0.32	0.7556	0.878172	-6.79
254425_at	putative membrane associated protein	---	AT4G21450	-1.02	-0.03	-0.32	0.75588	0.878196	-6.79
267456_at	E2, ubiquitin-conjugating enzyme, puta	PHO2	AT2G33770	-1.06	-0.08	-0.32	0.755822	0.878196	-6.79
250155_at	putative protein predicted proteins, Aral	---	AT5G15160	-1.07	-0.09	-0.32	0.755821	0.878196	-6.79
246169_at	putative protein predicted protein, Haen	---	AT5G32470	-1.03	-0.04	-0.32	0.75584	0.878196	-6.79
252674_at	cytochrome P450-like protein CYTOCH	CYP71B38	AT3G44250	1.02	0.03	0.32	0.755848	0.878196	-6.79

255778_at	3-phosphoserine phosphatase identical	PSP	AT1G18640	1.02	0.03	0.32	0.755939	0.878220	-6.79
244930_at	hypothetical protein	---	AT2G07809	1.02	0.03	0.32	0.756032	0.878264	-6.79
261128_at	ubiquitin-specific protease 2 (UBP2) ide	UBP2	AT1G04860	-1.03	-0.04	-0.32	0.756083	0.878264	-6.79
255493_at	putative glutamate-/aspartate-binding p	---	AT4G02690	-1.02	-0.03	-0.32	0.756092	0.878264	-6.79
258433_at	translationally controlled tumor protein-li	TCTP	AT3G16640	1.03	0.04	0.32	0.756442	0.878541	-6.79
253155_at	putative protein predicted protein, Arabi	---	AT4G35720	-1.03	-0.04	-0.32	0.756522	0.878541	-6.79
264888_at	hypothetical protein	---	AT1G23070	-1.03	-0.04	-0.32	0.756524	0.878541	-6.79
266754_at	hypothetical protein	---	AT2G46980	-1.03	-0.05	-0.32	0.756371	0.878541	-6.79
252721_at	putative protein predicted proteins, Arat	---	AT3G43990	1.04	0.05	0.32	0.756497	0.878541	-6.79
AFFX-TrpnX	B. subtilis /GEN=trpC, trpF /DB_XREF=	---	---	-1.02	-0.03	-0.32	0.756629	0.878574	-6.79
250082_at	polygalacturonase-like protein	---	AT5G17200	1.03	0.05	0.32	0.756598	0.878574	-6.79
254840_at	hypothetical protein	---	AT4G11930	-1.04	-0.05	-0.32	0.756669	0.878575	-6.79
245334_at	Expressed protein ; supported by full-ler	RALFL33	AT4G15800	-1.06	-0.08	-0.32	0.756734	0.878607	-6.79
259516_at	hypothetical protein ; supported by cDN/	ERD10	AT1G20450	-1.05	-0.08	-0.32	0.75695	0.878726	-6.79
255934_at	cytochrome P450, putative similar to cy	CYP87A2	AT1G12740	1.02	0.03	0.32	0.756911	0.878726	-6.79
262725_at	hypothetical protein predicted by genem	---	AT1G43580	1.05	0.07	0.32	0.756952	0.878726	-6.79
254434_at	ethylene-regulated transcript 2 (ERT2)	---	AT4G20880	-1.02	-0.03	-0.32	0.757282	0.878973	-6.79
253769_at	putative protein (fragment) protein kinas	RIC7	AT4G28560	-1.03	-0.05	-0.32	0.757235	0.878973	-6.79
256994_s_a	limonene cyclase, putative similar to lim	ATTPS-CI	AT3G25820 /	-1.02	-0.03	-0.32	0.757549	0.878973	-6.79
264410_s_a	hypothetical protein predicted by genem	---	---	1.02	0.03	0.32	0.757407	0.878973	-6.79
266372_at	putative two-component response regu	ATRR3	AT2G41310	1.03	0.04	0.32	0.757567	0.878973	-6.79
265524_at	hypothetical protein	---	---	-1.02	-0.03	-0.32	0.757479	0.878973	-6.79
254472_at	putative protein predicted proteins, Arat	---	---	-1.02	-0.03	-0.32	0.757589	0.878973	-6.79
253023_at	hypothetical protein	---	AT4G38070	1.04	0.05	0.32	0.757587	0.878973	-6.79
265549_at	hypothetical protein predicted by gensca	---	---	-1.03	-0.04	-0.32	0.757459	0.878973	-6.79
261759_at	hypothetical protein similar to putative R	---	AT1G15590	1.03	0.04	0.32	0.757429	0.878973	-6.79
252726_at	putative protein predicted proteins, Arat	---	---	1.04	0.05	0.32	0.757247	0.878973	-6.79
245412_at	hypothetical protein	---	AT4G17280	-1.04	-0.06	-0.32	0.757785	0.879101	-6.79
260615_at	mitochondrial NAD-dependent malate d	---	AT1G53240	-1.05	-0.08	-0.32	0.757815	0.879101	-6.79
246256_at	glucosyltransferase-like protein	---	AT4G36770	1.04	0.06	0.32	0.757739	0.879101	-6.79
256620_at	disease resistance protein, putative sim	---	AT3G24480	1.05	0.07	0.32	0.757901	0.879156	-6.79
261546_at	hypothetical protein	---	AT1G63520	-1.02	-0.04	-0.32	0.757939	0.879156	-6.79
252330_at	hypothetical protein	---	AT3G48770	1.04	0.05	0.32	0.758041	0.879184	-6.80
266341_at	hypothetical protein predicted by gensca	---	AT2G01510	-1.03	-0.04	-0.32	0.758028	0.879184	-6.80
262439_at	hypothetical protein identical to hypothe	---	AT1G47730	1.02	0.03	0.32	0.758195	0.879228	-6.80

249673_at	cytochrome P450-like	CYP79A4F	AT5G35920	1.02	0.03	0.32	0.758174	0.879228	-6.80
254884_at	H+-transporting ATPase - like protein H	---	AT4G11730	1.02	0.03	0.32	0.758127	0.879228	-6.80
254758_at	putative protein dimethylaniline monoox	YUC2	AT4G13260	1.05	0.07	0.32	0.75827	0.879271	-6.80
257244_at	receptor kinase, putative similar to CLV	---	AT3G24240	1.05	0.07	0.32	0.758373	0.879345	-6.80
260976_at	hypothetical protein	CID8	AT1G53650	1.04	0.05	0.32	0.758516	0.879401	-6.80
AFFX-BioC-	E. coli /GEN=bioC /DB_XREF=gb:J0442	---	---	1.05	0.07	0.32	0.758536	0.879401	-6.80
260321_at	putative RING zinc finger protein Pfam	---	AT1G63900	-1.03	-0.04	-0.32	0.758502	0.879401	-6.80
262445_at	Expressed protein ; supported by full-ler	---	AT1G47485	-1.03	-0.04	-0.32	0.75861	0.879434	-6.80
254097_at	putative Ser/Thr protein kinase serine/t	---	AT4G25160	-1.02	-0.03	-0.32	0.758797	0.879434	-6.80
249514_at	14-3-3 protein GF14psi (grf3/RCI1) ider	GRF3	AT5G38480	-1.03	-0.04	-0.32	0.758689	0.879434	-6.80
258234_at	hypothetical protein similar to myb-relate	MYB118	AT3G27785	-1.02	-0.03	-0.32	0.758783	0.879434	-6.80
262011_at	hypothetical protein predicted by genem	---	AT1G35614	1.03	0.05	0.32	0.758751	0.879434	-6.80
247969_at	putative protein similar to unknown prote	---	AT5G56700	-1.04	-0.06	-0.32	0.758684	0.879434	-6.80
249506_at	putative protein	---	AT5G38880	-1.03	-0.04	-0.32	0.759005	0.879587	-6.80
257436_s_a	hypothetical protein predicted by genefir	---	AT2G24650 /	-1.03	-0.05	-0.32	0.758967	0.879587	-6.80
254677_at	chloroplast protein cs/ch-42	---	AT4G18490	-1.03	-0.04	-0.32	0.759136	0.879694	-6.80
259412_at	DNA binding protein GT-1, putative sim	---	AT1G13450	-1.03	-0.04	-0.32	0.759348	0.879761	-6.80
262739_at	lipase, putative contains Pfam profile: P	---	AT1G28650	1.05	0.07	0.32	0.759312	0.879761	-6.80
247343_at	unknown protein	---	AT5G63740	-1.02	-0.03	-0.32	0.759343	0.879761	-6.80
252670_at	dnaJ protein homolog atj3 ;supported b	ATJ3	AT3G44110	-1.03	-0.04	-0.32	0.759297	0.879761	-6.80
260365_at	hypothetical protein predicted by genefir	---	AT1G70630	1.03	0.04	0.32	0.759598	0.879843	-6.80
250479_at	GTP-binding protein GTP-binding prote	AtRABH1e	AT5G10260	1.03	0.04	0.32	0.759697	0.879843	-6.80
252268_at	kinesin-like protein several kinesin-like p	---	AT3G49650	-1.04	-0.05	-0.32	0.759714	0.879843	-6.80
264740_at	unknown protein	---	AT1G62070	1.03	0.04	0.32	0.759614	0.879843	-6.80
263974_at	hypothetical protein predicted by grail	---	AT2G42720	1.03	0.04	0.32	0.759705	0.879843	-6.80
262519_at	putative ribokinase Except for first 69 a	---	AT1G17160	-1.04	-0.06	-0.32	0.759727	0.879843	-6.80
256702_at	unknown protein contains Pfam profile:	---	AT3G30380	1.04	0.06	0.32	0.759727	0.879843	-6.80
258839_at	unknown protein ; supported by cDNA:	---	AT3G07170	-1.02	-0.03	-0.32	0.759625	0.879843	-6.80
245787_at	unknown protein	---	AT1G32130	1.03	0.04	0.32	0.759822	0.879907	-6.80
264304_at	Expressed protein ; supported by full-ler	---	AT1G78895	1.03	0.05	0.32	0.759903	0.879956	-6.80
255816_at	unknown protein ;supported by full-leng	GLTP1	AT2G33470	1.02	0.03	0.32	0.760132	0.880046	-6.80
263470_at	putative unconventional myosin	XIF	AT2G31900	1.02	0.03	0.32	0.760047	0.880046	-6.80
249962_at	pectin methyl esterase -like protein pec	---	AT5G18990	1.04	0.06	0.32	0.760079	0.880046	-6.80
263657_at	putative casein kinase I similar to GB:C/	CKL13	AT1G04440	1.05	0.07	0.32	0.760135	0.880046	-6.80
263977_at	hypothetical protein predicted by gensca	---	AT2G42660	-1.03	-0.05	-0.32	0.760189	0.880064	-6.80

259054_at	putative hypersensitivity-related gene si	CHAT	AT3G03480	-1.15	-0.20	-0.32	0.760248	0.880088	-6.80
249501_s_a	expansin-like protein expansin - Prunus	ATEXP26	AT5G39270 /	-1.02	-0.03	-0.32	0.760297	0.880100	-6.80
265598_at	putative protein phosphatase 2C	---	AT2G14270	1.03	0.04	0.32	0.760375	0.880146	-6.80
253995_at	Col-0 casein kinase I-like protein ; supp	CK1	AT4G26100	1.03	0.05	0.32	0.760425	0.880149	-6.80
267243_at	hypothetical protein predicted by gensca	---	AT2G02660	-1.02	-0.03	-0.32	0.760455	0.880149	-6.80
248360_at	putative protein contains similarity to un	---	AT5G52430	1.04	0.05	0.32	0.760764	0.880373	-6.80
266994_at	MADS-box protein (AGL29)	AGL29	AT2G34440	-1.03	-0.04	-0.32	0.760746	0.880373	-6.80
246718_at	putative protein various predicted prote	---	---	-1.03	-0.04	-0.32	0.760715	0.880373	-6.80
255895_at	12-oxophytodienoate reductase, putativ	---	AT1G17990 /	1.09	0.13	0.32	0.760817	0.880390	-6.80
258092_at	Expressed protein ; supported by full-ler	---	AT3G14595	-1.04	-0.06	-0.32	0.760942	0.880490	-6.80
256679_at	putative protein similar to ATP synthase	ATPQ	AT3G52300	1.03	0.04	0.32	0.761107	0.880561	-6.80
253084_at	putative protein lateral root primordia (L	STY2	AT4G36260	1.04	0.06	0.32	0.761197	0.880561	-6.80
250708_at	Expressed protein ; supported by full-ler	RBE	AT5G06070	1.02	0.03	0.32	0.761095	0.880561	-6.80
265111_at	similar to 14KD proline-rich protein DC2	---	AT1G62510	-1.14	-0.19	-0.32	0.76117	0.880561	-6.80
259722_at	putative DNA helicase similar to ATP-DE	ATRECQ4	AT1G60930	1.02	0.03	0.32	0.761192	0.880561	-6.80
256532_at	PPR-repeat protein, putative contains n	---	AT1G33350	-1.04	-0.06	-0.32	0.761358	0.880591	-6.80
260473_at	hypothetical protein predicted by genefir	---	AT1G10880	1.03	0.04	0.32	0.761377	0.880591	-6.80
258619_at	isopentenyl diphosphate:dimethylallyl di	IPP2	AT3G02780	1.03	0.05	0.32	0.761303	0.880591	-6.80
254795_at	putative protein	---	AT4G12990	1.02	0.03	0.32	0.761272	0.880591	-6.80
263301_x_a	hypothetical protein predicted by genefir	---	---	-1.02	-0.04	-0.32	0.761646	0.880857	-6.80
257469_at	hypothetical protein predicted by genem	---	AT1G49290	-1.02	-0.03	-0.32	0.761731	0.880911	-6.80
251079_at	hypothetical protein	---	AT5G02000	-1.02	-0.03	-0.32	0.76198	0.881114	-6.80
248426_at	putative protein contains similarity to pe	---	AT5G51740	-1.02	-0.03	-0.32	0.761984	0.881114	-6.80
264126_at	hypothetical protein predicted by genem	NUA	AT1G79280	-1.02	-0.03	-0.32	0.762196	0.881182	-6.80
249804_at	galactinol synthase	AtGolS5	AT5G23790	1.02	0.03	0.32	0.762135	0.881182	-6.80
258135_at	Expressed protein ; supported by full-ler	---	AT3G24506	1.03	0.04	0.32	0.762231	0.881182	-6.80
260186_at	hypothetical protein predicted by genefir	---	AT1G36020	1.03	0.05	0.32	0.762236	0.881182	-6.80
254064_at	putative protein hypothetical protein - A	---	AT4G25410	-1.02	-0.03	-0.32	0.762165	0.881182	-6.80
263272_at	hypothetical protein predicted by gensca	---	---	-1.02	-0.03	-0.31	0.762356	0.881276	-6.80
246340_s_a	AtPP -like protein AtPP protein, Brassic	---	AT3G44860 /	-1.06	-0.08	-0.31	0.762462	0.881354	-6.80
267097_at	unknown protein predicted by genscan	---	AT2G41440	-1.02	-0.03	-0.31	0.762518	0.881374	-6.80
266688_at	hypothetical protein	---	AT2G19660	-1.02	-0.03	-0.31	0.762641	0.881427	-6.80
248699_at	putative protein similar to unknown prote	ATZIP4	AT5G48390	1.03	0.05	0.31	0.76263	0.881427	-6.80
252219_at	putative protein some putative proteins -	---	AT3G50160	-1.03	-0.04	-0.31	0.762719	0.881427	-6.80
250129_at	S-adenosylmethionine:2-demethylmena	---	AT5G16450	1.03	0.04	0.31	0.762711	0.881427	-6.80

259058_at	putative cytochrome P450 similar to cyt	CYP89A9	AT3G03470	1.06	0.08	0.31	0.762759	0.881429	-6.80
257160_at	hypothetical protein predicted by genem	---	---	-1.04	-0.05	-0.31	0.762855	0.881451	-6.80
252361_at	hypothetical protein	---	AT3G48490	1.05	0.08	0.31	0.762855	0.881451	-6.80
262154_at	unknown protein contains similarity to ly	---	AT1G52700	1.04	0.06	0.31	0.763298	0.881714	-6.80
266607_at	hypothetical protein predicted by genefi	---	AT2G46300	1.03	0.04	0.31	0.763496	0.881714	-6.80
263093_at	putative replication protein A1	---	---	1.02	0.03	0.31	0.763221	0.881714	-6.80
247684_at	serine/threonine-specific protein kinase	---	AT5G59670	1.16	0.22	0.31	0.763481	0.881714	-6.80
252936_at	putative protein transcription initiation fa	---	AT4G39160	-1.04	-0.06	-0.31	0.763191	0.881714	-6.80
261371_at	ubiquitin-conjugating enzyme, putative	UBC26	AT1G53020	1.02	0.03	0.31	0.76358	0.881714	-6.80
247121_at	putative protein contains similarity to rib	---	AT5G66010	1.03	0.04	0.31	0.763585	0.881714	-6.80
247991_at	expansin ;supported by full-length cDN	ATEXPA1	AT5G56320	1.02	0.03	0.31	0.763565	0.881714	-6.80
245212_at	hypothetical protein predicted by gensca	AT1G4422	---	-1.04	-0.05	-0.31	0.76351	0.881714	-6.80
258506_at	hypothetical protein predicted by genem	---	AT3G06520	1.04	0.05	0.31	0.763456	0.881714	-6.80
255938_at	hypothetical protein contains Pfam profi	---	AT1G12620	-1.03	-0.05	-0.31	0.763313	0.881714	-6.80
253595_at	putative protein M1 protein, Streptococ	---	AT4G30830	-1.02	-0.03	-0.31	0.76334	0.881714	-6.80
250344_at	glutaredoxin - like protein glutaredoxin,	---	AT5G11930	1.05	0.07	0.31	0.76315	0.881714	-6.80
257574_at	hypothetical protein predicted by genem	---	AT3G20710	1.03	0.04	0.31	0.763668	0.881765	-6.80
254482_at	TWIN SISTER OF FT (TSF) terminal flo	TSF	AT4G20370	1.03	0.04	0.31	0.764033	0.881964	-6.80
246369_at	light repressible receptor protein kinase	---	AT1G51910	1.03	0.04	0.31	0.763986	0.881964	-6.80
262615_at	initiation factor 5A-4 identical to initiatior	ELF5A-1	AT1G13950	1.03	0.04	0.31	0.763909	0.881964	-6.80
263568_at	hypothetical protein predicted by gensca	---	AT2G27160	-1.03	-0.05	-0.31	0.764021	0.881964	-6.80
264149_at	NAM (no apical meristem)-like protein,	anac005	AT1G02250	1.02	0.03	0.31	0.763987	0.881964	-6.80
256395_at	putative helix-loop-helix DNA-binding pr	MUTE	AT3G06120	1.03	0.04	0.31	0.764128	0.882028	-6.80
249023_at	putative protein strong similarity to unkn	---	AT5G44850	1.06	0.08	0.31	0.76433	0.882172	-6.80
259575_at	unknown protein	---	AT1G35320	-1.02	-0.03	-0.31	0.764323	0.882172	-6.80
253198_at	putative protein various predicted protei	---	AT4G35360	1.03	0.04	0.31	0.764434	0.882207	-6.80
255750_at	hypothetical protein predicted by genem	---	AT1G31960	-1.02	-0.03	-0.31	0.764437	0.882207	-6.80
262674_at	anter-specific proline-rich -like protein (A	EXL4	AT1G75910	-1.03	-0.04	-0.31	0.76458	0.882326	-6.80
259773_at	auxin-induced protein, putative similar t	---	AT1G29500	1.09	0.13	0.31	0.764692	0.882346	-6.80
255184_at	putative athila transposon protein	---	---	-1.02	-0.03	-0.31	0.764713	0.882346	-6.80
251921_at	40S ribosomal protein S21 homolog rib	---	AT3G53890	-1.06	-0.09	-0.31	0.764662	0.882346	-6.80
252503_at	putative protein hypothetical protein F1	---	AT3G46910	1.03	0.04	0.31	0.764859	0.882413	-6.80
260192_at	putative DNA polymerase alpha subunit	POLA2	AT1G67630	-1.07	-0.10	-0.31	0.764916	0.882413	-6.80
249373_at	putative protein vanilloid receptor gene	---	AT5G40670	-1.03	-0.04	-0.31	0.764856	0.882413	-6.80
262167_at	putative RING zinc finger protein contai	---	AT1G74990	1.03	0.04	0.31	0.764925	0.882413	-6.80

246979_s_a	putative protein hypothetical proteins - A	---	AT5G24990 /	-1.03	-0.05	-0.31	0.765048	0.882509	-6.80
263591_at	unknown protein	ATMAP65	AT2G01910	-1.09	-0.12	-0.31	0.765187	0.882581	-6.80
259310_s_a	Expressed protein ; supported by cDNA	---	AT3G05160 /	1.03	0.04	0.31	0.765171	0.882581	-6.80
258418_at	unknown protein	---	AT3G16660	1.09	0.13	0.31	0.76527	0.882631	-6.80
267480_at	putative retroelement pol polyprotein	---	---	-1.02	-0.03	-0.31	0.765321	0.882646	-6.80
267038_at	expressed protein supported by cDNA: (	---	AT2G38480	1.06	0.09	0.31	0.765647	0.882854	-6.80
245975_at	putative protein CGI-107 protein - Hom	---	AT5G13070	-1.03	-0.04	-0.31	0.765581	0.882854	-6.80
262983_at	hypothetical protein similar to unknown	---	AT1G54550	1.03	0.04	0.31	0.765646	0.882854	-6.80
246683_at	putative protein chromokinesin KIF4 - H	---	AT5G33300	-1.03	-0.04	-0.31	0.765656	0.882854	-6.80
265486_at	unknown protein predicted by genscan	---	AT2G15560	1.03	0.04	0.31	0.765702	0.882863	-6.80
255826_at	putative uroporphyrinogen decarboxylas	HEME2	AT2G40490	-1.03	-0.04	-0.31	0.765991	0.882897	-6.80
248807_at	pectin methylesterase-like	---	AT5G47500	1.02	0.03	0.31	0.766028	0.882897	-6.80
248673_at	putative protein contains similarity to dis	---	AT5G48780	-1.02	-0.03	-0.31	0.765888	0.882897	-6.80
254882_s_a	putative protein various predicted rever	---	---	1.02	0.03	0.31	0.766081	0.882897	-6.80
258169_at	hypothetical protein	---	AT3G21590	1.03	0.04	0.31	0.766046	0.882897	-6.80
262311_at	homeodomain leucine zipper protein, p	ATHB18	AT1G70920	1.03	0.04	0.31	0.765986	0.882897	-6.80
253363_at	hypothetical protein	---	AT4G33130	1.03	0.04	0.31	0.766062	0.882897	-6.80
246314_at	promoter-binding factor-like protein Dc3	AREB3	AT3G56850	-1.03	-0.04	-0.31	0.766045	0.882897	-6.80
250378_at	putative oligopeptide transporter protein	---	AT5G11570	-1.03	-0.04	-0.31	0.765966	0.882897	-6.80
250641_at	putative bZIP protein bZIP protein HY5	---	AT5G07160	-1.03	-0.04	-0.31	0.766123	0.882902	-6.80
263273_x_a	En/Spm-like transposon protein related	---	---	1.02	0.03	0.31	0.766181	0.882924	-6.80
259323_at	unknown protein	---	AT3G05280	1.02	0.03	0.31	0.766335	0.883011	-6.80
245378_at	GLABRA2 like protein	HDG4	AT4G17710	1.02	0.03	0.31	0.766371	0.883011	-6.80
258834_at	GTP cyclohydrolase I similar to GTP cyc	---	AT3G07270	1.03	0.04	0.31	0.766373	0.883011	-6.80
255153_at	putative protein several hypothetical pro	---	AT4G08210	-1.03	-0.04	-0.31	0.766582	0.883074	-6.80
254868_at	copper amine oxidase like protein (frag	---	AT4G12270	-1.03	-0.04	-0.31	0.766545	0.883074	-6.80
265829_at	unknown protein	---	AT2G14490	-1.02	-0.03	-0.31	0.766621	0.883074	-6.80
264955_at	F-box protein family, AtFBX3 contains s	---	AT1G76920	-1.03	-0.05	-0.31	0.766483	0.883074	-6.80
250902_at	putative protein predicted proteins, Ara	---	AT5G03590	1.03	0.04	0.31	0.766614	0.883074	-6.80
258448_at	unknown protein	---	AT3G22290	-1.02	-0.03	-0.31	0.766789	0.883081	-6.80
248818_at	Lon protease homolog 1 precursor ident	LON2	AT5G47040	-1.03	-0.05	-0.31	0.76684	0.883081	-6.80
248396_at	unknown protein	---	AT5G52130	-1.03	-0.04	-0.31	0.766808	0.883081	-6.80
255731_at	phosphoprotein phosphatase 2A, regula	RCN1	AT1G25490	-1.02	-0.03	-0.31	0.76692	0.883081	-6.80
261805_at	hypothetical protein almost identical to h	---	AT1G30540	1.03	0.04	0.31	0.766698	0.883081	-6.80
247739_at	40S ribosomal protein S8 - like 40S ribo	---	AT5G59240	-1.03	-0.05	-0.31	0.766794	0.883081	-6.80

264348_at	putative NPK1-related protein kinase 2 s	NRT1.1	AT1G12110	-1.15	-0.20	-0.31	0.766908	0.883081	-6.80
256362_at	hypothetical protein	---	AT1G66450	1.03	0.04	0.31	0.766937	0.883081	-6.80
249000_at	putative protein contains similarity to he	---	AT5G44980	-1.03	-0.04	-0.31	0.767081	0.883202	-6.80
253162_at	phosphoserine aminotransferase ;supp	PSAT	AT4G35630	1.10	0.13	0.31	0.767259	0.883318	-6.80
248645_at	unknown protein	GEX2	AT5G49150	1.03	0.04	0.31	0.76724	0.883318	-6.80
263258_at	putative permease similar to putative pe	---	AT1G10540	1.04	0.05	0.31	0.767337	0.883364	-6.80
253370_at	pectinesterase - like protein pectin meth	---	AT4G33230	-1.03	-0.05	-0.31	0.7674	0.883391	-6.80
263109_at	hypothetical protein similar to putative C	---	AT1G65180	-1.03	-0.04	-0.31	0.767452	0.883406	-6.80
245546_at	cellulose synthase like protein	ATCSLB0	AT4G15290	1.04	0.06	0.31	0.767551	0.883475	-6.80
265046_s_a	mutator-like transposase, putative simil	---	---	1.02	0.03	0.31	0.767712	0.883616	-6.80
264798_at	putative myosin MYA1, class V (Z2838	XIC	AT1G08730	1.02	0.03	0.31	0.767872	0.883756	-6.80
252424_at	putative protein activating signal cointe	---	AT3G47610	-1.03	-0.05	-0.31	0.768093	0.883921	-6.80
245585_at	hypothetical	---	AT4G14970	-1.02	-0.04	-0.31	0.768064	0.883921	-6.80
245159_at	putative cellulose synthase	ATCSLD1	AT2G33100	-1.03	-0.04	-0.31	0.768215	0.884017	-6.80
258590_at	putative response regulator protein (rec	ARR22	AT3G04280	-1.02	-0.03	-0.31	0.768453	0.884246	-6.80
265833_at	Mutator-like transposase similar to MUF	---	---	1.02	0.03	0.31	0.768575	0.884342	-6.80
267164_at	CER1-like protein may be involved in wa	---	AT2G37700	1.02	0.03	0.31	0.768684	0.884422	-6.80
252171_at	hypothetical protein ; supported by cDN	---	AT3G50590	1.02	0.03	0.31	0.768734	0.884430	-6.80
267424_at	hypothetical protein predicted by gensca	---	AT2G34800	1.02	0.03	0.31	0.768768	0.884430	-6.80
264914_at	clathrin adaptor medium chain protein M	HAP13	AT1G60780	1.03	0.04	0.31	0.768857	0.884488	-6.80
259977_at	unknown protein ;supported by full-leng	---	AT1G76590	-1.07	-0.09	-0.31	0.769024	0.884636	-6.80
260930_at	GTP-binding protein Sar1, putative simi	---	AT1G02620	-1.05	-0.07	-0.31	0.7692	0.884652	-6.80
267125_at	putative acetone-cyanohydrin lyase	MES4	AT2G23580	-1.02	-0.03	-0.31	0.769326	0.884652	-6.80
254149_at	putative protein hypothetical protein - A	---	AT4G24300	1.03	0.05	0.31	0.769338	0.884652	-6.80
256563_at	unknown protein	RALFL27	AT3G29780	1.03	0.04	0.31	0.769145	0.884652	-6.80
258019_at	hypothetical protein predicted by genem	---	AT3G19470	-1.02	-0.03	-0.31	0.769341	0.884652	-6.80
248641_at	unknown protein	---	AT5G49110	-1.03	-0.04	-0.31	0.769186	0.884652	-6.80
254172_at	clathrin coat assembly like protein clath	---	AT4G24550	1.02	0.03	0.31	0.769372	0.884652	-6.80
265520_at	hypothetical protein predicted by gensca	---	AT2G06020	-1.03	-0.05	-0.31	0.769387	0.884652	-6.80
263489_at	putative inositol polyphosphate 5'-phosp	---	AT2G31830	-1.03	-0.04	-0.31	0.769115	0.884652	-6.80
251168_at	putative protein several hypothetical pro	---	AT3G63370	1.03	0.04	0.30	0.769622	0.884833	-6.80
259836_at	unknown protein	ROPGEF1	AT1G52240	-1.02	-0.03	-0.30	0.769602	0.884833	-6.80
254766_at	putative protein predicted protein, Arabi	TPS12	AT4G13280	1.02	0.03	0.30	0.769798	0.884991	-6.80
256980_at	hypothetical protein contains Pfam profi	DRB3	AT3G26932	1.03	0.05	0.30	0.769926	0.885048	-6.80
255109_s_a	hypothetical protein	---	AT4G08760	1.02	0.03	0.30	0.769915	0.885048	-6.80

265593_s_a	unknown protein ;supported by full-leng	LCV1	AT2G20120 /	1.02	0.03	0.30	0.770131	0.885115	-6.80
264163_at	Expressed protein ; supported by full-ler	---	AT1G65445	1.03	0.04	0.30	0.770088	0.885115	-6.80
245224_at	gene_id:K17E7.8~unknown protein	---	AT3G29796	-1.02	-0.03	-0.30	0.770086	0.885115	-6.80
245619_at	hypothetical protein	---	AT4G13990	-1.04	-0.05	-0.30	0.770151	0.885115	-6.80
252444_at	putative protein Na+-dependent inorgar	PHT4;3	AT3G46980	-1.02	-0.03	-0.30	0.770179	0.885115	-6.80
252332_at	putative protein	---	AT3G48810	1.03	0.05	0.30	0.770366	0.885287	-6.80
267539_at	putative RING zinc finger protein ; supp	---	AT2G42030	-1.03	-0.04	-0.30	0.770612	0.885480	-6.80
267024_s_a	putative aquaporin (plasma membrane i	NIP2;1	AT2G29870 /	-1.03	-0.04	-0.30	0.770603	0.885480	-6.80
250072_at	putative protein similar to unknown prote	---	AT5G17210	1.04	0.05	0.30	0.770713	0.885548	-6.80
264444_at	putative squamosa-promoter binding pro	---	AT1G27360	-1.02	-0.03	-0.30	0.770749	0.885548	-6.80
253906_at	putative protein disease resistance prot	---	AT4G27220	-1.03	-0.05	-0.30	0.770801	0.885563	-6.80
260644_at	hypothetical protein contains similarity to	---	AT1G53290	-1.03	-0.04	-0.30	0.771152	0.885878	-6.80
262471_at	hypothetical protein similar to hypothetic	---	AT1G50140	1.03	0.04	0.30	0.771131	0.885878	-6.80
266746_s_a	putative glutathione S-transferase ;supp	ATGSTF3	AT2G02930 /	1.11	0.15	0.30	0.771391	0.885910	-6.80
267614_at	putative cytochrome P450	BAS1	AT2G26710	-1.08	-0.11	-0.30	0.77129	0.885910	-6.80
261953_at	UDP-galactose 4-epimerase, putative s	RHD1	AT1G64440	-1.05	-0.07	-0.30	0.771426	0.885910	-6.80
248600_at	putative protein contains similarity to unl	---	AT5G49390	1.03	0.04	0.30	0.771353	0.885910	-6.80
254769_at	hypothetical protein	---	AT4G13330	1.05	0.07	0.30	0.77142	0.885910	-6.80
261468_s_a	hypothetical protein predicted by genem	---	AT1G27860 /	-1.03	-0.04	-0.30	0.771389	0.885910	-6.80
255099_at	hypothetical protein	---	---	1.02	0.03	0.30	0.771452	0.885910	-6.80
266312_at	20S proteasome subunit C8 (PAG1/PR(	PAG1	AT2G27020	-1.03	-0.04	-0.30	0.771578	0.885957	-6.80
266165_at	putative copper/zinc superoxide dismuta	CSD2	AT2G28190	1.13	0.18	0.30	0.771601	0.885957	-6.80
255048_at	gibberellin-regulated protein GASA3 pre	GASA3	AT4G09600	-1.02	-0.03	-0.30	0.77161	0.885957	-6.80
256842_at	hypothetical protein predicted by genem	---	---	1.02	0.03	0.30	0.771878	0.886175	-6.80
254001_at	putative protein PRE87 mRNA, Pinus ra	MIOX4	AT4G26260	1.08	0.11	0.30	0.771862	0.886175	-6.80
265047_at	hypothetical protein similar to unknown	IQD27	AT1G51960	1.03	0.04	0.30	0.772077	0.886315	-6.80
261258_at	unknown protein	---	AT1G26640	-1.03	-0.04	-0.30	0.772057	0.886315	-6.80
254085_at	abscisic acid-induced - like protein abs	HVA22D	AT4G24960	-1.05	-0.07	-0.30	0.772228	0.886443	-6.80
259498_at	unknown protein similar to putative cis-(	GOS11	AT1G15880	1.02	0.03	0.30	0.772366	0.886537	-6.80
264409_s_a	hypothetical protein similar to hypothetic	---	---	-1.03	-0.04	-0.30	0.772387	0.886537	-6.80
251651_at	putative protein transcription initiation fa	---	AT3G57370	-1.02	-0.03	-0.30	0.772539	0.886545	-6.80
259269_at	putative pectate lyase similar to pectate	---	AT3G01270	-1.03	-0.04	-0.30	0.772637	0.886545	-6.80
256416_at	ferritin subunit, putative similar to ferritir	ATFER2	AT3G11050	1.03	0.04	0.30	0.772659	0.886545	-6.80
257455_s_a	hypothetical protein	---	AT1G27870 /	-1.02	-0.03	-0.30	0.772553	0.886545	-6.80
265035_at	hypothetical protein contains Pfam profi	---	AT1G61620	-1.03	-0.04	-0.30	0.772537	0.886545	-6.80

255201_at	putative transposon protein	---	---	1.02	0.03	0.30	0.772608	0.886545	-6.80
254672_at	hypothetical protein	---	---	-1.03	-0.04	-0.30	0.772666	0.886545	-6.80
262857_at	major latex homologue type2 identical to	---	AT1G14930	-1.02	-0.03	-0.30	0.77275	0.886597	-6.80
254586_at	TMV resistance protein N-like TMV resi	---	AT4G19510	1.03	0.04	0.30	0.772796	0.886605	-6.80
259068_at	unknown protein	PEX13	AT3G07560	-1.03	-0.04	-0.30	0.77291	0.886646	-6.80
256467_at	copia-type polyprotein, putative similar t	---	---	-1.02	-0.03	-0.30	0.772874	0.886646	-6.80
254811_at	putative protein 2-hydroxy-6-oxohepta-2	---	AT4G12230	-1.03	-0.04	-0.30	0.773024	0.886649	-6.80
263645_at	putative GTP-binding protein	---	AT2G04720	1.02	0.03	0.30	0.773068	0.886649	-6.80
248113_at	wax synthase-like protein	---	AT5G55360	-1.03	-0.04	-0.30	0.773067	0.886649	-6.80
245959_at	peptide transport protein-like peptide tra	---	AT5G19640	-1.02	-0.04	-0.30	0.772999	0.886649	-6.80
267321_at	hypothetical protein predicted by genefir	---	AT2G19320	1.03	0.04	0.30	0.773132	0.886678	-6.80
262142_at	hypothetical protein predicted by genem	---	AT1G52640	-1.03	-0.04	-0.30	0.773246	0.886764	-6.80
252476_at	glucosyltransferase-like protein UDP-gl	---	AT3G46650	-1.03	-0.04	-0.30	0.773539	0.887056	-6.80
266257_at	putative chorismate mutase/prephenate	PD1	AT2G27820	1.03	0.05	0.30	0.773776	0.887238	-6.80
263964_at	putative CCHC-type zinc finger protein c	---	AT2G12880	-1.03	-0.04	-0.30	0.773741	0.887238	-6.80
261232_at	unknown protein ; supported by cDNA: g	---	AT1G20220	1.02	0.03	0.30	0.773907	0.887299	-6.80
265839_at	putative serpin	---	AT2G14540	1.02	0.04	0.30	0.773946	0.887299	-6.80
250389_at	putative protein probable flavin-containi	YUC4	AT5G11320	1.02	0.03	0.30	0.773943	0.887299	-6.80
264141_at	hypothetical protein predicted by genem	---	AT1G79090	-1.02	-0.03	-0.30	0.774008	0.887326	-6.80
264281_at	hypothetical protein similar to putative C	---	AT1G61830	1.03	0.04	0.30	0.774084	0.887369	-6.80
251401_at	stellacyanin (uclacyanin 3) - like protein	---	AT3G60270	1.03	0.04	0.30	0.774293	0.887518	-6.80
259145_at	hypothetical protein predicted by gensca	---	AT3G10180	-1.02	-0.03	-0.30	0.774271	0.887518	-6.80
262307_at	heat shock protein DnaJ, putative simila	---	AT1G71000	1.03	0.05	0.30	0.77439	0.887585	-6.80
261774_at	unknown protein	---	AT1G76260	1.04	0.06	0.30	0.774501	0.887668	-6.80
248101_at	chaperone GrpE-like protein ;supported	---	AT5G55200	1.06	0.08	0.30	0.77455	0.887680	-6.80
254971_at	major intrinsic protein (MIP) - like nodul	NIP5;1	AT4G10380	1.04	0.05	0.30	0.774594	0.887685	-6.80
254756_at	putative protein late embryogenesis abu	EDA21	AT4G13235	-1.02	-0.03	-0.30	0.774671	0.887729	-6.80
250851_at	putative protein rngB protein, Dictyostel	---	AT5G04420	-1.03	-0.04	-0.30	0.774896	0.887943	-6.80
248974_at	disease resistance protein-like	---	AT5G45060	-1.02	-0.03	-0.30	0.775091	0.888090	-6.80
257896_at	basic chitinase, putative similar to basic	---	AT3G16920	1.09	0.12	0.30	0.775103	0.888090	-6.80
263530_at	HSP100/ClpB, putative similar to HSP1	---	AT2G25030 /	1.02	0.03	0.30	0.77521	0.888124	-6.80
248443_at	gibberellin 20-oxidase-like protein	---	AT5G51310	-1.02	-0.03	-0.30	0.775179	0.888124	-6.80
249483_at	Expressed protein ; supported by cDNA	---	AT5G38895	1.03	0.04	0.30	0.775317	0.888201	-6.80
259858_at	putative receptor kinase similar to recep	---	AT1G68400	1.05	0.06	0.30	0.775578	0.888366	-6.80
258961_at	hypothetical protein similar to myb-relat	---	AT3G10580	-1.02	-0.03	-0.30	0.775511	0.888366	-6.80

264559_at	unknown protein similar to hypothetical	---	AT1G09610	-1.02	-0.03	-0.30	0.775573	0.888366	-6.80
256566_at	hypothetical protein	---	AT3G19530	1.02	0.03	0.30	0.775754	0.888524	-6.80
256335_at	hypothetical protein predicted by genem	---	AT1G72110	1.03	0.04	0.30	0.7758	0.888532	-6.80
257439_at	hypothetical protein similar to hypothetic	---	AT2G17000	1.02	0.03	0.30	0.775897	0.888598	-6.80
259025_at	hypothetical protein predicted by genem	---	---	-1.03	-0.04	-0.30	0.776157	0.888792	-6.80
263214_at	hypothetical protein predicted by gensca	---	AT1G30660	-1.03	-0.04	-0.30	0.776106	0.888792	-6.80
249649_at	putative transporter protein Na+ H+-exc	CHX24	AT5G37060	-1.02	-0.03	-0.30	0.776183	0.888792	-6.80
260124_at	E2, ubiquitin-conjugating enzyme, putat	UBC31	AT1G36340	1.02	0.03	0.30	0.776223	0.888794	-6.80
265550_at	hypothetical protein predicted by gensca	---	---	1.02	0.03	0.30	0.776339	0.888853	-6.80
249503_at	expansin-like protein expansin - Prunus	ATEXPA24	AT5G39310	1.02	0.03	0.30	0.776353	0.888853	-6.80
250138_at	DRH1 DEAD box protein - like DRH1 D	---	AT5G14610	1.02	0.03	0.30	0.776459	0.888885	-6.80
255381_at	RMA1 RING zinc finger protein identical	RMA1	AT4G03510	-1.05	-0.07	-0.30	0.77642	0.888885	-6.80
259246_s_a	hypothetical protein predicted by gensca	---	AT3G07730 /	-1.03	-0.04	-0.30	0.776567	0.888902	-6.80
265504_at	putative Ta11-like non-LTR retroelemen	---	---	-1.02	-0.04	-0.30	0.776541	0.888902	-6.80
252831_at	2-dehydro-3-deoxyphosphoheptonate al	DHS1	AT4G39980	1.07	0.10	0.30	0.776591	0.888902	-6.80
257215_at	RING zinc finger protein, putative conta	---	AT3G15070	1.02	0.03	0.29	0.776936	0.889252	-6.80
264990_at	unknown protein supported by cDNA: C	---	AT1G27210	1.05	0.07	0.29	0.776992	0.889272	-6.80
267135_at	cyclin-dependent kinase inhibitor protein	ICK1	AT2G23430	-1.05	-0.07	-0.29	0.777104	0.889355	-6.80
264127_at	serine/threonine protein kinase, putative	AGC1.7	AT1G79250	-1.02	-0.03	-0.29	0.777388	0.889520	-6.80
253269_at	hypothetical protein	---	AT4G34140	1.02	0.03	0.29	0.777307	0.889520	-6.80
255364_s_a	putative fibrillin ; supported by full-lengt	---	AT4G04020 /	1.03	0.04	0.29	0.777404	0.889520	-6.80
258748_at	germin-like protein similar to germin pre	GLP8	AT3G05930	1.03	0.04	0.29	0.7774	0.889520	-6.80
264510_at	putative phytochrome-associated protei	PIF3	AT1G09530	-1.04	-0.06	-0.29	0.777548	0.889640	-6.80
262531_at	putative leucine-rich receptor protein kin	---	AT1G17230 /	1.03	0.05	0.29	0.777867	0.889670	-6.80
246859_at	putative protein various predicted prote	---	AT5G25950	-1.02	-0.03	-0.29	0.777837	0.889670	-6.80
246687_at	putative protein proline-rich protein APC	---	AT5G33370	1.03	0.04	0.29	0.777884	0.889670	-6.80
257564_at	unknown protein	---	AT3G28610	-1.03	-0.05	-0.29	0.777663	0.889670	-6.80
245490_at	hypothetical protein	LDL3	AT4G16310	1.03	0.04	0.29	0.777886	0.889670	-6.80
264892_at	GH3-like auxin-regulated protein highly	---	AT1G23160	1.02	0.03	0.29	0.777831	0.889670	-6.80
247413_at	NBS/LRR disease resistance protein	---	AT5G63020	1.03	0.04	0.29	0.777861	0.889670	-6.80
255217_s_a	hypothetical protein	---	---	-1.03	-0.05	-0.29	0.777832	0.889670	-6.80
262781_s_a	proteasome epsilon chain precursor ide	PBE1	AT1G13060 /	1.03	0.04	0.29	0.778062	0.889827	-6.80
257547_at	hypothetical protein predicted by gensca	---	AT3G13000	-1.07	-0.09	-0.29	0.778108	0.889835	-6.80
252072_at	putative protein protein kinase PK1, rec	---	AT3G51710	1.02	0.03	0.29	0.778165	0.889855	-6.80
267339_at	unknown protein ; supported by cDNA:	---	AT2G39870	1.04	0.06	0.29	0.778287	0.889950	-6.80

261203_at	Expressed protein ; supported by full-ler	---	AT1G12845	1.10	0.13	0.29	0.778342	0.889969	-6.80
253309_at	male sterility 2-like protein male sterility	CER4	AT4G33790	-1.05	-0.07	-0.29	0.778576	0.890102	-6.80
257975_at	unknown protein similar to GB:AAD3063	---	AT3G20830	-1.04	-0.05	-0.29	0.778548	0.890102	-6.80
266369_at	hypothetical protein predicted by gensca	BOP2	AT2G41370	1.03	0.05	0.29	0.7785	0.890102	-6.80
262057_at	unknown protein ;supported by full-lengt	---	AT1G80040	-1.02	-0.03	-0.29	0.77862	0.890108	-6.80
252224_at	putative protein various ADP-RIBOSYLA	ATARLA1E	AT3G49860	1.03	0.04	0.29	0.778774	0.890239	-6.80
253504_at	hypothetical protein	---	AT4G31960	1.02	0.02	0.29	0.778832	0.890262	-6.80
253376_at	hypothetical protein Arabidopsis thalian	---	AT4G33290	1.02	0.03	0.29	0.77892	0.890317	-6.80
259784_at	auxin-induced protein, putative similar t	---	AT1G29450	-1.05	-0.07	-0.29	0.778999	0.890318	-6.80
252052_at	beta-fructofuranosidase	AtcwINV2	AT3G52600	1.02	0.03	0.29	0.778973	0.890318	-6.80
249111_at	unknown protein	---	AT5G43770	1.02	0.03	0.29	0.779184	0.890485	-6.81
254925_at	beta-adaptin - like protein beta-adaptin	---	AT4G11380	1.03	0.04	0.29	0.77939	0.890519	-6.81
247530_at	glycosylasparaginase - like protein glyc	---	AT5G61540	-1.03	-0.05	-0.29	0.779409	0.890519	-6.81
251748_at	putative protein predicted protein, Arabi	---	AT3G55680	1.03	0.04	0.29	0.779253	0.890519	-6.81
256635_at	hypothetical protein predicted by gensca	---	AT3G28260	-1.02	-0.03	-0.29	0.779354	0.890519	-6.81
255024_at	hypothetical protein	---	AT4G09860	1.02	0.03	0.29	0.779294	0.890519	-6.81
261531_at	RB-binding protein -like similar to retinol	---	AT1G63490	1.03	0.05	0.29	0.779517	0.890553	-6.81
255075_at	putative protein RING-H2 zinc finger pr	---	AT4G09110	-1.02	-0.03	-0.29	0.779506	0.890553	-6.81
247804_at	strong similarity to unknown protein (pir|	SVL5	AT5G58170	1.02	0.03	0.29	0.779606	0.890611	-6.81
253717_at	putative protein putative suppressor pro	---	AT4G29440	1.02	0.03	0.29	0.779763	0.890611	-6.81
255056_at	putative protein helix-loop-helix protein	TT8	AT4G09820	-1.02	-0.03	-0.29	0.779707	0.890611	-6.81
246903_at	putative protein	---	AT5G25750	1.03	0.04	0.29	0.779738	0.890611	-6.81
263877_at	hypothetical protein predicted by genefir	---	AT2G21780	-1.02	-0.03	-0.29	0.779657	0.890611	-6.81
261051_at	cytochrome P450, putative similar to cy	CYP703A2	AT1G01280	1.02	0.03	0.29	0.780172	0.891034	-6.81
252911_at	cytochrome P450 -like protein cytochro	CYP96A12	AT4G39510	-1.07	-0.09	-0.29	0.78033	0.891170	-6.81
246851_at	putative protein various predicted prote	AGL26	AT5G26870	1.02	0.03	0.29	0.780375	0.891176	-6.81
259462_at	hypothetical protein contains similarity to	---	AT1G18940	1.03	0.05	0.29	0.780623	0.891329	-6.81
252914_at	putative protein dehydrin, Glycine max,	---	AT4G39130	1.03	0.04	0.29	0.780558	0.891329	-6.81
258746_at	germin-like protein similar to germin pre	---	AT3G05950	-1.02	-0.04	-0.29	0.780626	0.891329	-6.81
263207_at	putative endoxyloglucan transferase sim	XTH33	AT1G10550	-1.10	-0.14	-0.29	0.780933	0.891635	-6.81
247369_at	unknown protein	---	AT5G63340	1.03	0.04	0.29	0.780977	0.891641	-6.81
255370_at	putative protein	---	---	-1.02	-0.03	-0.29	0.781079	0.891713	-6.81
246093_at	ethylene-forming-enzyme-like dioxygen	---	AT5G20550	1.02	0.03	0.29	0.781133	0.891729	-6.81
257566_x_a	hypothetical protein predicted by genem	---	---	1.02	0.03	0.29	0.781191	0.891751	-6.81
263086_at	putative non-LTR retrolelement reverse	---	AT2G16110	-1.02	-0.03	-0.29	0.781299	0.891785	-6.81

246695_at	putative protein	---	---	1.03	0.04	0.29	0.781295	0.891785	-6.81
247344_at	ARI-like RING zinc finger protein-like	---	AT5G63750	-1.03	-0.04	-0.29	0.781363	0.891813	-6.81
248656_at	fimbrin 2 (gb|AAB97844.1) ; supported	---	AT5G48460	-1.07	-0.10	-0.29	0.781502	0.891872	-6.81
257072_at	myrosinase-associated protein, putative	---	AT3G14220	-1.05	-0.06	-0.29	0.781571	0.891872	-6.81
266322_at	putative auxin-regulated protein	---	AT2G46690	1.05	0.07	0.29	0.781569	0.891872	-6.81
264755_at	receptor kinase, putative similar to rece	---	AT1G61390	-1.02	-0.03	-0.29	0.781489	0.891872	-6.81
249248_at	unknown protein	---	AT5G42320	1.03	0.04	0.29	0.781631	0.891896	-6.81
255806_at	fructokinase - like protein fructokinase,	---	AT4G10260	1.02	0.02	0.29	0.781718	0.891951	-6.81
251166_at	heat shock transcription factor-like prot	AT-HSFA7	AT3G63350	1.02	0.03	0.29	0.781827	0.892030	-6.81
247596_at	putative protein predicted protein, Dros	---	AT5G60840	-1.04	-0.06	-0.29	0.781906	0.892053	-6.81
257872_at	P-glycoprotein, putative similar to P-gly	PGP16	AT3G28360	-1.02	-0.03	-0.29	0.781925	0.892053	-6.81
260347_at	DHHC-type zinc finger protein, putative	---	AT1G69420	-1.04	-0.05	-0.29	0.782172	0.892188	-6.81
246473_at	putative protein cathepsin L-like cystein	---	AT5G17140	1.02	0.04	0.29	0.782224	0.892188	-6.81
247887_at	unknown protein	---	AT5G57880	1.02	0.03	0.29	0.782239	0.892188	-6.81
263453_at	hypothetical protein predicted by genefi	---	AT2G22180	-1.02	-0.03	-0.29	0.782205	0.892188	-6.81
264040_at	putative uridylyl transferase ; supported	ACR5	AT2G03730	1.02	0.03	0.29	0.782113	0.892188	-6.81
265745_at	hypothetical protein predicted by gensca	---	---	1.02	0.03	0.29	0.782422	0.892308	-6.81
256549_at	hypothetical protein predicted by genem	---	---	-1.02	-0.03	-0.29	0.78242	0.892308	-6.81
251406_at	putative protein various predicted prote	---	AT3G60260	1.04	0.06	0.29	0.782702	0.892570	-6.81
254319_at	putative protein predicted proteins, Aral	---	AT4G22560	-1.03	-0.05	-0.29	0.78273	0.892570	-6.81
266179_at	putative phloem-specific lectin	AtPP2-B5	AT2G02300	1.02	0.03	0.29	0.782781	0.892583	-6.81
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB_XREF	---	---	1.04	0.06	0.29	0.782821	0.892584	-6.81
253418_at	putative protein tom-1B protein, Gallus	---	AT4G32760	-1.02	-0.03	-0.29	0.782875	0.892595	-6.81
254717_at	histone H2A.F/Z - like protein histone H	HTA4	AT4G13570	-1.03	-0.04	-0.29	0.782908	0.892595	-6.81
253749_at	phytochrome-associated protein PAP2 ;	PAP2	AT4G29080	1.12	0.17	0.29	0.783031	0.892689	-6.81
263191_at	polyprotein, putative similar to polyprote	---	---	1.03	0.04	0.29	0.783114	0.892739	-6.81
254754_at	pectate lyase like protein pectate lyase	---	AT4G13210	1.02	0.03	0.29	0.783163	0.892751	-6.81
254508_at	putative protein gene F4P9.34 chromos	---	AT4G20170	-1.03	-0.04	-0.29	0.783415	0.892784	-6.81
263941_at	unknown protein	---	---	-1.03	-0.04	-0.29	0.783261	0.892784	-6.81
261835_at	hypothetical protein contains similarity t	---	AT1G16040	-1.02	-0.03	-0.29	0.783466	0.892784	-6.81
252140_at	putative protein several hypothetical pro	---	AT3G51070	-1.02	-0.03	-0.29	0.783335	0.892784	-6.81
266085_at	hypothetical protein	---	AT2G37800	1.03	0.04	0.29	0.783428	0.892784	-6.81
266392_at	late embryogenesis abundant M10 prote	M10	AT2G41280	1.02	0.03	0.29	0.783411	0.892784	-6.81
266706_at	hypothetical protein predicted by gensca	---	AT2G03320	-1.02	-0.03	-0.29	0.783415	0.892784	-6.81
261274_at	myb-related protein, putative similar to	MYB117	AT1G26780	1.02	0.03	0.29	0.783591	0.892882	-6.81

252609_at	putative protein	---	AT3G45110	-1.02	-0.03	-0.29	0.783689	0.892949	-6.81
254488_at	putative protein receptor-like protein kir	---	AT4G20790	-1.02	-0.02	-0.29	0.783928	0.893177	-6.81
252059_at	E2, ubiquitin-conjugating enzyme, putat	UEV1D-4	AT3G52560	1.02	0.03	0.29	0.78414	0.893196	-6.81
258294_at	hypothetical protein predicted by genem	---	AT3G23350	1.02	0.03	0.29	0.784109	0.893196	-6.81
262974_at	hypothetical protein predicted by genem	---	AT1G75550	-1.02	-0.03	-0.29	0.784053	0.893196	-6.81
258572_at	hypothetical protein	---	AT3G04270	-1.02	-0.03	-0.29	0.784152	0.893196	-6.81
245931_at	major pollen allergen-like protein pollen	---	AT5G09280	-1.03	-0.04	-0.29	0.78418	0.893196	-6.81
252705_at	putative protein predicted proteins, Aral	---	---	1.03	0.04	0.29	0.784149	0.893196	-6.81
246667_at	putative protein hypothetical proteins - A	---	---	-1.02	-0.03	-0.28	0.784278	0.893264	-6.81
249330_at	putative protein similar to unknown prote	---	AT5G40970	1.02	0.03	0.28	0.784361	0.893268	-6.81
246491_at	hypothetical protein	---	AT5G16100	1.02	0.03	0.28	0.78434	0.893268	-6.81
251436_at	putative protein hypothetical protein At2	ARGOS	AT3G59900	1.11	0.16	0.28	0.784549	0.893438	-6.81
255611_at	hypothetical protein	---	AT4G01210	1.02	0.03	0.28	0.784708	0.893557	-6.81
252349_at	cell division cycle protein 23 homolog c	APC8	AT3G48150	-1.04	-0.05	-0.28	0.784771	0.893557	-6.81
250044_at	disease resistance protein RPP1-WsB -	---	AT5G17680	-1.03	-0.05	-0.28	0.784764	0.893557	-6.81
251555_at	shatterproof 1 (SHP1)/ agamous -like 1	SHP1	AT3G58780	1.02	0.03	0.28	0.78505	0.893786	-6.81
251197_at	glutaredoxin -like protein glutaredoxin, c	---	AT3G62960	-1.05	-0.07	-0.28	0.785017	0.893786	-6.81
255402_at	Expressed protein	hemf2	AT4G03205	-1.05	-0.07	-0.28	0.785177	0.893885	-6.81
256747_at	unknown protein similar to CW14 GB:BA	---	AT3G29180	-1.03	-0.04	-0.28	0.785341	0.893890	-6.81
259327_at	putative lectin contains Pfam profile: PF	---	AT3G16460	-1.10	-0.14	-0.28	0.785368	0.893890	-6.81
245688_at	prolin-rich protein, putative similar to pr	AGP31	AT1G28290	1.13	0.17	0.28	0.785279	0.893890	-6.81
252598_at	putative protein putative proteins AT4g0	---	---	1.02	0.02	0.28	0.785377	0.893890	-6.81
256758_at	hypothetical protein similar to Athila retr	---	---	1.02	0.04	0.28	0.785325	0.893890	-6.81
247742_at	random slug protein - like random slug	---	AT5G58980	-1.03	-0.04	-0.28	0.785441	0.893918	-6.81
258486_at	putative 40S ribosomal protein similar to	---	AT3G02560	-1.06	-0.08	-0.28	0.785549	0.893997	-6.81
251382_at	pectinesterase - like protein pectinester	---	AT3G60730	1.02	0.03	0.28	0.785834	0.894276	-6.81
257400_s_a	hypothetical protein	---	AT1G23810 /	-1.02	-0.03	-0.28	0.785886	0.894290	-6.81
267239_at	unknown protein	---	AT2G02510	1.02	0.03	0.28	0.786024	0.894336	-6.81
267618_at	putative cyclin ; supported by cDNA: gi_	CYCB1;4	AT2G26760	-1.03	-0.04	-0.28	0.785985	0.894336	-6.81
251075_at	putative protein leucine-rich receptor-lik	---	AT5G01890	1.05	0.07	0.28	0.786043	0.894336	-6.81
259968_at	unknown protein	---	AT1G76530	1.02	0.03	0.28	0.786107	0.894364	-6.81
265621_at	NAM (no apical meristem)-like protein	NTL8	AT2G27300	1.02	0.03	0.28	0.786177	0.894377	-6.81
245241_at	hypothetical protein contains similarity to	---	AT1G44478	-1.02	-0.03	-0.28	0.786198	0.894377	-6.81
244958_at	hypothetical protein	---	---	-1.02	-0.03	-0.28	0.786236	0.894377	-6.81
250134_at	Expressed protein ; supported by cDNA	---	---	-1.03	-0.04	-0.28	0.786346	0.894455	-6.81

249452_at	Sec7/gnom -like protein GNOM, Arabid	---	AT5G39500	-1.02	-0.03	-0.28	0.786383	0.894455	-6.81
261352_at	DNA repair protein RAD23, putative sin	RAD23	AT1G79650	-1.02	-0.03	-0.28	0.786535	0.894538	-6.81
253982_at	calcineurin B-like protein 3 ;supported b	ATCBL3	AT4G26570	1.04	0.05	0.28	0.786534	0.894538	-6.81
253709_at	pyrophosphate-dependent phosphofruc	PFK1	AT4G29220	-1.03	-0.04	-0.28	0.786622	0.894548	-6.81
254471_s_a	putative protein parts of other proteins c	---	---	1.02	0.03	0.28	0.78659	0.894548	-6.81
256303_at	disease resistance protein, putative sim	---	AT1G69550	-1.03	-0.04	-0.28	0.786686	0.894576	-6.81
264844_at	putative glycosylation enzyme ; support	---	AT1G03520	-1.03	-0.04	-0.28	0.786797	0.894590	-6.81
265513_at	hypothetical protein	---	---	1.02	0.03	0.28	0.786738	0.894590	-6.81
264358_at	hypothetical protein predicted by genefi	---	AT1G03180	-1.03	-0.04	-0.28	0.786815	0.894590	-6.81
245624_at	glucosyltransferase like protein	---	AT4G14090	1.03	0.04	0.28	0.787017	0.894715	-6.81
267176_at	putative zinc finger protein	---	AT2G37730	-1.02	-0.03	-0.28	0.787005	0.894715	-6.81
255295_at	putative sugar transporter	---	AT4G04760	1.02	0.03	0.28	0.787043	0.894715	-6.81
258658_at	putative adenosine kinase similar to ade	ADK1	AT3G09820	1.05	0.07	0.28	0.787143	0.894784	-6.81
256317_at	hypothetical protein predicted by genem	---	AT1G35900	-1.04	-0.05	-0.28	0.78726	0.894872	-6.81
259437_at	protein serine/threonine kinase, putative	---	AT1G01540	-1.04	-0.06	-0.28	0.787711	0.894914	-6.81
266453_at	putative protein kinase contains a protei	---	AT2G43230	1.02	0.03	0.28	0.787401	0.894914	-6.81
248043_s_a	heat shock protein (emb|CAA72514.1)	---	AT5G56000 /	-1.04	-0.06	-0.28	0.787634	0.894914	-6.81
255059_at	putative protein downy mildew resistan	---	AT4G09420	-1.05	-0.08	-0.28	0.787692	0.894914	-6.81
251504_at	putative protein putative multidrug efflu	TT12	AT3G59030	-1.02	-0.04	-0.28	0.78772	0.894914	-6.81
250328_at	putative protein	---	AT5G11780	1.03	0.04	0.28	0.787657	0.894914	-6.81
262548_at	unknown protein contains similarity to ar	AGO2	AT1G31280	-1.03	-0.04	-0.28	0.787563	0.894914	-6.81
249110_at	disease resistance protein	---	AT5G43730	-1.02	-0.03	-0.28	0.787729	0.894914	-6.81
265140_at	F-box protein family, AtFBX11 contains	---	AT1G51320	1.02	0.03	0.28	0.787541	0.894914	-6.81
252793_at	hypothetical protein	---	---	1.02	0.02	0.28	0.787665	0.894914	-6.81
255123_at	putative lipid transfer protein	---	AT4G08530	-1.02	-0.03	-0.28	0.787602	0.894914	-6.81
251846_at	histone H2A.F/Z ;supported by full-leng	HTA11	AT3G54560	-1.07	-0.10	-0.28	0.78779	0.894940	-6.81
255397_at	putative transposon protein	---	---	1.03	0.04	0.28	0.787972	0.895102	-6.81
245560_at	indole-3-acetate beta-glucosyltransferas	UGT84A1	AT4G15480	1.03	0.04	0.28	0.788113	0.895166	-6.81
257906_at	ribosomal protein, putative similar to 60	ATL5	AT3G25520	-1.06	-0.08	-0.28	0.788127	0.895166	-6.81
255398_at	hypothetical protein	---	AT4G03740	-1.02	-0.03	-0.28	0.788147	0.895166	-6.81
257610_at	zinc finger protein, putative similar to fir	AtIDD11	AT3G13810	-1.05	-0.08	-0.28	0.78822	0.895172	-6.81
266912_at	hypothetical protein predicted by genefi	---	AT2G45900	-1.08	-0.12	-0.28	0.788231	0.895172	-6.81
249030_at	putative protein similar to unknown prote	---	---	-1.02	-0.03	-0.28	0.788394	0.895313	-6.81
267182_at	unknown protein	---	AT2G23360	1.03	0.04	0.28	0.788706	0.895590	-6.81
253639_at	putative protein component of aniline di	---	AT4G30550	-1.03	-0.05	-0.28	0.788716	0.895590	-6.81

248661_at	putative protein contains similarity to MA	AGL80	AT5G48670	1.04	0.05	0.28	0.788843	0.895689	-6.81
265083_at	hypothetical protein predicted by genefir	---	AT1G03820	1.05	0.07	0.28	0.788945	0.895716	-6.81
246652_at	extensin -like protein extensin, soybean	---	AT5G35190	1.02	0.03	0.28	0.788943	0.895716	-6.81
255563_at	putative CHP-rich zinc finger protein sir	---	AT4G01740	-1.02	-0.03	-0.28	0.789023	0.895716	-6.81
AFFX-CreX-	Bacteriophage P1 /GEN=cre /DB_XREF	---	---	1.05	0.07	0.28	0.788986	0.895716	-6.81
252196_at	putative protein predicted protein, Arabi	---	AT3G50200	1.03	0.04	0.28	0.789085	0.895742	-6.81
251952_at	histone H2B - like protein histone H2B-	---	AT3G53650	1.02	0.03	0.28	0.789137	0.895755	-6.81
262527_at	SRG1-like protein Strong homology to S	---	AT1G17010	-1.02	-0.03	-0.28	0.789277	0.895870	-6.81
256456_at	unknown protein ; supported by full-leng	---	AT1G75180	1.04	0.06	0.28	0.789439	0.895876	-6.81
254294_at	putative membrane protein membrane I	ATRBL7	AT4G23070	1.04	0.06	0.28	0.789362	0.895876	-6.81
249686_at	putative protein contains similarity to cyt	CYP716A2	AT5G36140	1.02	0.02	0.28	0.789374	0.895876	-6.81
251953_at	putative protein predicted protein, Arabi	CPuORF5	AT3G53668 /	-1.03	-0.04	-0.28	0.789436	0.895876	-6.81
267605_at	putative protein disulfide isomerase ; su	ATPDIL2-3	AT2G32920	-1.03	-0.04	-0.28	0.789592	0.895940	-6.81
262300_at	ripening-induced protein, putative simila	---	AT1G70870	-1.02	-0.03	-0.28	0.789645	0.895940	-6.81
254829_at	AIR1A-like protein putative cell wall-pla	---	AT4G12530	-1.02	-0.03	-0.28	0.789731	0.895940	-6.81
251180_at	putative protein hypothetical protein (T3	---	AT3G62640	-1.04	-0.05	-0.28	0.789536	0.895940	-6.81
258603_at	putative heat shock transcription factor s	ATHSFA1I	AT3G02990	-1.03	-0.04	-0.28	0.789656	0.895940	-6.81
247646_at	putative protein various predicted prote	---	AT5G59990	1.02	0.03	0.28	0.789704	0.895940	-6.81
266522_at	putative ubiquitin-conjugating enzyme	UBC23	AT2G16920	-1.02	-0.03	-0.28	0.79003	0.896055	-6.81
256496_at	hypothetical protein similar to hypothetic	---	AT1G31510	1.02	0.03	0.28	0.790021	0.896055	-6.81
256567_at	amino acid permease, putative contains	---	AT3G19553	1.02	0.03	0.28	0.789938	0.896055	-6.81
254609_at	Expressed protein ; supported by full-ler	---	AT4G18970	1.06	0.08	0.28	0.790068	0.896055	-6.81
255179_at	putative transposon protein	---	---	-1.02	-0.02	-0.28	0.790064	0.896055	-6.81
256949_at	hypothetical protein predicted by genem	---	AT3G19070	-1.02	-0.03	-0.28	0.789931	0.896055	-6.81
261999_at	hypothetical protein predicted by genem	---	AT1G33800	-1.03	-0.04	-0.28	0.790198	0.896056	-6.81
257804_at	protein kinase, putative similar to soma	---	AT3G18810	1.02	0.03	0.28	0.790227	0.896056	-6.81
250551_at	SNAP25 - like protein SNAP25A protein	SNAP29	AT5G07880	1.02	0.03	0.28	0.790173	0.896056	-6.81
247377_at	pectate lyase ; supported by cDNA: gi_	---	AT5G63180	1.18	0.24	0.28	0.79021	0.896056	-6.81
255992_at	unknown protein	---	AT1G29790	-1.03	-0.04	-0.28	0.790281	0.896073	-6.81
262700_at	unknown protein	---	AT1G76020	-1.03	-0.04	-0.28	0.790408	0.896129	-6.81
259693_at	hypothetical protein predicted by genem	---	AT1G63060	-1.03	-0.04	-0.28	0.790385	0.896129	-6.81
265428_at	hypothetical protein predicted by grail	---	AT2G20720	1.05	0.07	0.28	0.790489	0.896176	-6.81
253057_at	putative protein amino-acid N-acetyltran	---	AT4G37670	1.06	0.09	0.28	0.790545	0.896194	-6.81
263936_at	putative ATP-dependent RNA helicase A	---	AT2G35920	-1.03	-0.04	-0.28	0.790632	0.896249	-6.81
250943_at	putative protein	---	AT5G03360	1.02	0.03	0.28	0.790759	0.896348	-6.81

262812_at	hypothetical protein predicted by gensca	---	AT1G11690	-1.02	-0.02	-0.28	0.790836	0.896390	-6.81
247005_at	adenylylsulfate kinase-like protein ;supp	---	AT5G67520	-1.03	-0.04	-0.28	0.791025	0.896525	-6.81
253069_at	hexokinase - like protein hexokinase, A	HKL3	AT4G37840	1.02	0.03	0.28	0.791033	0.896525	-6.81
257252_at	glutathione reductase, cytosolic identica	ATGR1	AT3G24170	-1.04	-0.06	-0.28	0.791148	0.896566	-6.81
260503_at	proteasome, 30 kda subunit (ec 3.4.99.	PAF2	AT1G47250	-1.02	-0.03	-0.28	0.791109	0.896566	-6.81
260580_at	unknown protein	---	AT2G47390	-1.02	-0.03	-0.28	0.791306	0.896567	-6.81
263685_at	unknown protein similar to cell differenti	ATCUL3	AT1G26830	-1.02	-0.03	-0.28	0.791292	0.896567	-6.81
248714_at	polygalacturonase ;supported by full-ler	---	AT5G48140	1.02	0.03	0.28	0.791301	0.896567	-6.81
252307_at	putative protein SAE1-S9-protein, Bras	---	---	-1.02	-0.03	-0.28	0.791267	0.896567	-6.81
255594_at	putative ABC transporter	ATABC1	AT4G01660	-1.02	-0.03	-0.28	0.791484	0.896680	-6.81
261723_at	unknown protein ; supported by full-leng	---	AT1G76200	1.02	0.03	0.28	0.791477	0.896680	-6.81
255683_at	putative malate oxidoreductase	---	AT4G00570	1.03	0.04	0.27	0.791604	0.896771	-6.81
249817_at	putative protein similar to unknown prote	---	AT5G23820	1.12	0.17	0.27	0.791807	0.896956	-6.81
250248_at	transporter-like protein	ZIF1	AT5G13740	1.05	0.07	0.27	0.792305	0.896969	-6.81
261279_at	class I chitinase, putative similar to GB:	POM1	AT1G05850	1.11	0.15	0.27	0.792031	0.896969	-6.81
253562_at	putative protein ;supported by full-lengt	---	AT4G31130	1.02	0.03	0.27	0.792407	0.896969	-6.81
250011_at	putative protein crp1 protein, maize, PIR	---	AT5G18475	-1.02	-0.03	-0.27	0.792389	0.896969	-6.81
266192_at	unknown protein	---	AT2G39080	1.02	0.03	0.27	0.791865	0.896969	-6.81
260410_at	putative peptide transporter similar to pe	---	AT1G69870	1.04	0.06	0.27	0.792196	0.896969	-6.81
248353_at	cytochrome P450	CYP96A4	AT5G52320	-1.02	-0.03	-0.27	0.792266	0.896969	-6.81
261462_at	hypothetical protein predicted by gensca	---	AT1G07850	-1.03	-0.04	-0.27	0.792104	0.896969	-6.81
266755_at	putative alcohol dehydrogenase	---	AT2G47150	-1.02	-0.04	-0.27	0.792322	0.896969	-6.81
248724_at	putative protein strong similarity to unkn	---	AT5G47970	1.04	0.05	0.27	0.792365	0.896969	-6.81
257364_at	hypothetical protein predicted by gensca	---	AT2G45940	1.02	0.03	0.27	0.792061	0.896969	-6.81
257507_at	zinc finger protein, putative similar to G	---	AT1G29600	1.02	0.02	0.27	0.791897	0.896969	-6.81
246690_at	hypothetical protein	---	---	-1.02	-0.03	-0.27	0.791981	0.896969	-6.81
249522_at	putative protein similar to unknown prote	---	AT5G38700	1.02	0.03	0.27	0.792261	0.896969	-6.81
245099_at	unknown protein ; supported by cDNA:	RHC1A	AT2G40830	1.03	0.05	0.27	0.791959	0.896969	-6.81
256592_at	hypothetical protein predicted by genem	---	---	1.02	0.03	0.27	0.79246	0.896983	-6.81
249505_at	putative protein	---	---	-1.05	-0.06	-0.27	0.792726	0.897240	-6.81
264395_at	putative GDP-dissociation inhibitor Cont	---	AT1G12070	-1.03	-0.04	-0.27	0.792816	0.897253	-6.81
263571_at	putative disease resistance protein iden	---	AT2G17050	-1.02	-0.02	-0.27	0.792795	0.897253	-6.81
246918_at	putative protein hypothetical protein F1	---	AT5G25340	1.03	0.04	0.27	0.793123	0.897518	-6.81
261770_at	prolyl endopeptidase, putative similar to	---	AT1G76140	1.02	0.03	0.27	0.793129	0.897518	-6.81
245534_at	hypothetical protein	---	AT4G15150	1.02	0.03	0.27	0.793183	0.897535	-6.81

246691_at	putative protein predicted proteins - Aral	---	---	1.02	0.03	0.27	0.793264	0.897537	-6.81
264366_at	unknown protein EST gb|N96383 comes	---	AT1G03250	-1.03	-0.04	-0.27	0.793231	0.897537	-6.81
249245_at	putative protein contains similarity to CH	---	AT5G42280	1.03	0.04	0.27	0.793409	0.897657	-6.81
259495_at	NBS/LRR disease resistance protein, p	---	AT1G15890	-1.03	-0.04	-0.27	0.793594	0.897822	-6.81
255613_at	putative RING zinc finger protein	---	AT4G01270	1.03	0.04	0.27	0.793695	0.897860	-6.81
259100_at	DNA-damage-repair/toleration protein D	DRT102	AT3G04880	1.02	0.03	0.27	0.793707	0.897860	-6.81
245146_at	putative cis-Golgi SNARE protein ; supp	GOS12	AT2G45200	-1.02	-0.03	-0.27	0.793765	0.897881	-6.81
264546_at	Expressed protein ; supported by cDNA	---	AT1G55805	1.04	0.06	0.27	0.793841	0.897923	-6.81
267460_at	putative squamosa-promoter binding pro	SPL3	AT2G33810	1.08	0.11	0.27	0.793889	0.897932	-6.81
264155_at	unknown protein	GTB1	AT1G65440	-1.03	-0.04	-0.27	0.794241	0.898286	-6.81
262490_at	hypothetical protein predicted by gensca	UREF	AT1G21840	1.03	0.04	0.27	0.79445	0.898409	-6.81
251248_at	P-glycoprotein-like proetin P-glycoprote	PGP21	AT3G62150	1.10	0.14	0.27	0.794504	0.898409	-6.81
263789_at	putative GDSL-motif lipase/hydrolase si	---	AT2G24560	1.03	0.04	0.27	0.794495	0.898409	-6.81
260646_at	hypothetical protein similar to CHP-rich	---	AT1G53340	1.03	0.05	0.27	0.794507	0.898409	-6.81
259379_at	putative MYB family transcription factor	---	AT3G16350	-1.05	-0.07	-0.27	0.794621	0.898449	-6.81
256859_at	hypothetical protein	---	AT3G22940	-1.03	-0.04	-0.27	0.794591	0.898449	-6.81
262022_at	hypothetical protein predicted by genem	---	AT1G35490	-1.03	-0.04	-0.27	0.794839	0.898651	-6.81
256444_at	hypothetical protein predicted by genem	---	AT3G11060	1.02	0.03	0.27	0.795113	0.898761	-6.81
266164_at	putative salt-inducible protein	---	AT2G28050	1.04	0.05	0.27	0.795173	0.898761	-6.81
248274_at	isp4 protein	ATOPT9	AT5G53510	1.02	0.03	0.27	0.79515	0.898761	-6.81
261977_at	hypothetical protein contains similarity t	---	---	1.02	0.03	0.27	0.795063	0.898761	-6.81
260776_at	zinc finger protein, putative similar to zi	---	AT1G14580	-1.05	-0.07	-0.27	0.795052	0.898761	-6.81
247626_at	receptor like protein kinase receptor like	---	AT5G60300 /	1.07	0.10	0.27	0.795039	0.898761	-6.81
265934_at	unknown protein	EER5	AT2G19560	-1.02	-0.03	-0.27	0.795403	0.898977	-6.81
252414_at	putative protein sn-glycerol-3-phosphat	---	AT3G47420	-1.03	-0.05	-0.27	0.795592	0.899146	-6.81
264083_at	ethylene reponse factor-like AP2 domai	ATERF15	AT2G31230	1.08	0.11	0.27	0.795811	0.899259	-6.81
251214_at	putative protein hypothetical proteins - A	---	AT3G62500	1.02	0.03	0.27	0.795805	0.899259	-6.81
261921_at	hypothetical protein predicted by genem	---	AT1G65900	-1.04	-0.06	-0.27	0.795804	0.899259	-6.81
267438_at	putative GDSL-motif lipase/hydrolase si	---	AT2G19050	-1.03	-0.05	-0.27	0.795905	0.899321	-6.81
257575_at	hypothetical protein similar to hypothetic	---	---	1.02	0.03	0.27	0.79601	0.899395	-6.81
261801_at	hypothetical protein similar to hypothetic	AAE14	AT1G30520	-1.03	-0.04	-0.27	0.796146	0.899504	-6.81
252044_at	outer envelope membrane protein-like p	OEP7	AT3G52420	-1.02	-0.03	-0.27	0.796204	0.899525	-6.81
258659_at	B' regulatory subunit of PP2A (AtB'beta	ATB' BETA	AT3G09880	-1.02	-0.03	-0.27	0.796315	0.899606	-6.81
261148_at	unknown protein ; supported by full-leng	GAMMA C	AT1G19580	1.02	0.03	0.27	0.796553	0.899830	-6.81
264020_at	putative signal sequence receptor, alph	---	AT2G21160	-1.03	-0.04	-0.27	0.796644	0.899889	-6.81

257384_at	unknown protein	---	AT2G15110	-1.02	-0.03	-0.27	0.796746	0.899959	-6.81
250805_at	unknown protein	---	AT5G05050	-1.02	-0.03	-0.27	0.797028	0.900099	-6.81
253580_at	putative protein RING-H2 finger protein	---	AT4G30400	-1.05	-0.07	-0.27	0.797006	0.900099	-6.81
256295_at	hypothetical protein	---	AT1G69470	1.02	0.03	0.27	0.796969	0.900099	-6.81
259866_at	putative calmodulin similar to calmodulin	---	AT1G76640	1.07	0.09	0.27	0.796911	0.900099	-6.81
245748_at	unknown protein contains similarity to pl	---	AT1G51140	1.04	0.06	0.27	0.797093	0.900128	-6.81
255408_at	hypothetical protein similar to A. thalian	---	AT4G03490	1.04	0.05	0.27	0.797291	0.900307	-6.81
266228_at	unknown protein ; supported by full-leng	CXIP4	AT2G28910	-1.03	-0.04	-0.27	0.797379	0.900354	-6.81
255206_at	putative transposon protein	---	---	-1.02	-0.02	-0.27	0.797451	0.900354	-6.81
266810_at	hypothetical protein predicted by gensca	---	AT2G44880	1.02	0.03	0.27	0.797417	0.900354	-6.81
267177_at	Expressed protein ; supported by full-ler	---	AT2G37580	1.04	0.05	0.27	0.79753	0.900355	-6.81
261264_at	hypothetical protein predicted by genem	---	AT1G26710	1.03	0.04	0.27	0.797504	0.900355	-6.81
251235_at	putative protein lysophospholipase hom	---	AT3G62860	-1.04	-0.05	-0.27	0.797593	0.900363	-6.81
252432_at	hypothetical protein	---	AT3G47675 /	1.02	0.02	0.27	0.797617	0.900363	-6.81
259811_at	hypothetical protein predicted by genem	---	AT1G49830	-1.02	-0.03	-0.27	0.797956	0.900659	-6.81
247852_at	ATGP1 ; supported by cDNA: gi_13358	YKT61	AT5G58060	-1.02	-0.03	-0.27	0.797958	0.900659	-6.81
246333_at	proteinkinase AtPP -like protein AtPP p	---	AT3G44840	1.02	0.03	0.27	0.798086	0.900759	-6.81
245434_at	hypothetical protein	---	AT4G17140	-1.02	-0.03	-0.27	0.79814	0.900775	-6.81
267051_at	hypothetical protein predicted by genefin	---	AT2G38500	-1.03	-0.04	-0.27	0.798296	0.900818	-6.81
259544_at	hypothetical protein ; supported by full-le	CAT3	AT1G20620	1.02	0.03	0.27	0.798293	0.900818	-6.81
254653_at	polygalacturonase-like protein exopolyg	---	AT4G18180	-1.02	-0.02	-0.27	0.798239	0.900818	-6.81
259031_at	putative transcription factor similar to ge	---	AT3G09360	-1.03	-0.04	-0.27	0.798503	0.901007	-6.81
261234_x_a	hypothetical protein predicted by genem	---	---	-1.02	-0.03	-0.27	0.798663	0.901101	-6.81
261738_s_a	hypothetical protein identical to hypothe	---	AT1G47813 /	-1.03	-0.05	-0.27	0.798665	0.901101	-6.81
253990_at	putative thioredoxin thioredoxin - Lilium	ACHT1	AT4G26160	-1.04	-0.05	-0.27	0.798815	0.901225	-6.81
264021_at	putative auxin-regulated protein ;suppo	---	AT2G21200	1.05	0.07	0.27	0.798921	0.901300	-6.81
267240_at	hypothetical protein predicted by gensca	---	AT2G02680	1.02	0.03	0.26	0.798986	0.901328	-6.81
249999_at	triacylglycerol lipase-like protein triacylg	---	AT5G18640	-1.04	-0.06	-0.26	0.799206	0.901399	-6.81
265950_s_a	putative protein kinase contains a protei	---	AT2G18530 /	-1.02	-0.03	-0.26	0.799184	0.901399	-6.81
249562_at	disease resistance protein-like	---	AT5G38350	-1.02	-0.03	-0.26	0.7991	0.901399	-6.81
256245_at	heat shock protein 70 identical to heat s	HSP70	AT3G12580	-1.09	-0.13	-0.26	0.799127	0.901399	-6.81
246602_at	copper amine oxidase, putative similar t	---	AT1G31710	-1.04	-0.06	-0.26	0.799302	0.901418	-6.81
258913_at	unknown protein similar to putative Anio	---	AT3G06450	1.03	0.04	0.26	0.799265	0.901418	-6.81
245589_at	subtilisin-like serine protease contains s	---	AT4G15040	-1.03	-0.04	-0.26	0.799348	0.901426	-6.81
255133_at	putative protein (fragment) glutamine-ri	---	AT4G08320	-1.02	-0.03	-0.26	0.799753	0.901456	-6.81

247147_at	putative protein contains similarity to RI	GTE7	AT5G65630	1.03	0.04	0.26	0.799654	0.901456	-6.81
262409_at	hypothetical protein predicted by genem	---	---	1.03	0.04	0.26	0.799889	0.901456	-6.81
256462_at	hypothetical protein predicted by genem	---	AT1G36230	1.02	0.03	0.26	0.79943	0.901456	-6.81
261184_at	pol polyprotein, putative similar to many	---	---	1.02	0.04	0.26	0.799866	0.901456	-6.81
266423_at	putative DNA-directed RNA polymerase	RPB5D	AT2G41340	-1.03	-0.04	-0.26	0.799852	0.901456	-6.81
259107_at	hypothetical protein predicted by genem	---	AT3G05460	1.02	0.03	0.26	0.799612	0.901456	-6.81
246857_at	putative protein	---	AT5G25920	1.02	0.03	0.26	0.7996	0.901456	-6.81
264043_at	putative cyclin D	CYCD2;1	AT2G22490	-1.02	-0.03	-0.26	0.799826	0.901456	-6.81
264622_at	putative vacuolar sorting protein 35	VPS35A	AT2G17790	-1.02	-0.03	-0.26	0.799844	0.901456	-6.81
250260_at	putative protein contains similarity to un	---	AT5G13810	-1.02	-0.03	-0.26	0.799594	0.901456	-6.81
263244_at	hypothetical protein predicted by gensca	---	AT2G31480	-1.02	-0.03	-0.26	0.799858	0.901456	-6.81
251947_at	putative protein various predicted prote	---	AT3G53550	-1.02	-0.02	-0.26	0.799868	0.901456	-6.81
245005_at	ribosomal protein S14	---	---	-1.04	-0.05	-0.26	0.800025	0.901520	-6.81
256864_at	topoisomerase II identical to topoisome	TOPII	AT3G23890	1.03	0.04	0.26	0.800008	0.901520	-6.81
266714_at	NAM (no apical meristem)-like protein	EMB2301	AT2G46770	-1.02	-0.03	-0.26	0.800096	0.901531	-6.81
259261_at	unknown protein similar to unknown pro	---	AT3G11390	-1.02	-0.04	-0.26	0.800114	0.901531	-6.81
245514_at	OEP8 like protein	---	AT4G15810	1.03	0.05	0.26	0.800168	0.901547	-6.81
265973_at	putative non-LTR retroelement reverse t	---	---	-1.02	-0.02	-0.26	0.800405	0.901681	-6.81
247228_at	trehalose-6-phosphate phosphatase	---	AT5G65140	1.07	0.10	0.26	0.800384	0.901681	-6.81
248778_at	unknown protein	---	AT5G47940	-1.02	-0.03	-0.26	0.800351	0.901681	-6.81
253152_at	putative protein predicted proteins, Ara	---	AT4G35690	-1.03	-0.04	-0.26	0.800537	0.901785	-6.81
249823_s_a	putative protein contains similarity to AB	---	AT5G23350 /	-1.03	-0.04	-0.26	0.80063	0.901846	-6.81
256196_at	hypothetical protein predicted by genem	---	---	1.02	0.03	0.26	0.800828	0.902024	-6.81
262820_at	putative obtusifoliol 14-alpha demethyla	CYP51G1	AT1G11680	-1.02	-0.03	-0.26	0.801045	0.902094	-6.81
266249_at	hypothetical protein predicted by gensca	---	AT2G27630	-1.02	-0.03	-0.26	0.801078	0.902094	-6.81
245912_at	putative protein sulfate transporter ATS	SULTR3;5	AT5G19600	1.06	0.08	0.26	0.801013	0.902094	-6.81
263169_at	hypothetical protein similar to unknown	---	AT1G03010	1.03	0.04	0.26	0.801028	0.902094	-6.81
246805_at	putative protein various predicted trans	AGL101	AT5G27050	-1.02	-0.03	-0.26	0.801088	0.902094	-6.81
247703_at	putative protein predicted proteins, Hon	SRR1	AT5G59560	1.02	0.03	0.26	0.801146	0.902115	-6.81
262150_at	hypothetical protein contains similarity t	FRS6	AT1G52520	-1.02	-0.03	-0.26	0.801257	0.902196	-6.81
258828_at	putative purple acid phosphatase simila	PAP15	AT3G07130	1.02	0.03	0.26	0.80145	0.902368	-6.81
263675_x_a	En/Spm-like transposon protein related	---	---	1.03	0.04	0.26	0.801594	0.902486	-6.81
251286_at	putative protein Bcl-2-interacting protei	---	AT3G61710	-1.02	-0.03	-0.26	0.801696	0.902555	-6.81
252634_x_a	putative protein predicted proteins, Ara	---	---	1.02	0.03	0.26	0.801939	0.902785	-6.81
259048_at	DegP protease contains similarity to deg	DegP7	AT3G03380	-1.02	-0.03	-0.26	0.802021	0.902789	-6.81

263540_at	unknown protein	---	AT2G24780	-1.02	-0.03	-0.26	0.802011	0.902789	-6.81
249273_at	unknown protein	---	AT5G41850	1.03	0.04	0.26	0.802068	0.902797	-6.81
255137_at	extensin-like protein extensin precursor	---	AT4G08370	-1.02	-0.03	-0.26	0.802217	0.902919	-6.81
259786_at	lipase/hydrolase, putative contains Pfar	---	AT1G29660	1.20	0.26	0.26	0.802381	0.902977	-6.81
259702_at	putative endo-1,3-beta-glucanase simila	---	AT1G77780	-1.02	-0.03	-0.26	0.80237	0.902977	-6.81
261679_at	polyprotein, putative similar to polyprote	---	---	-1.02	-0.02	-0.26	0.802386	0.902977	-6.81
251395_at	unknown protein ;supported by full-leng	FLA8	AT2G45470	1.16	0.21	0.26	0.802476	0.902986	-6.81
257027_at	DNA repair protein, putative similar to R	ATRAD54	AT3G19210	1.02	0.03	0.26	0.802638	0.902986	-6.81
254510_at	cadinene synthase like protein (+)-delta	---	AT4G20210	1.03	0.04	0.26	0.802667	0.902986	-6.81
262043_at	unknown protein	PSF1	AT1G80190	-1.03	-0.04	-0.26	0.802504	0.902986	-6.81
266038_at	putative ABC transporter	ATMRP11	AT2G07680	-1.04	-0.05	-0.26	0.802632	0.902986	-6.81
265793_at	unknown protein	---	AT2G01220	1.03	0.04	0.26	0.802695	0.902986	-6.81
257738_at	40S ribosomal subunit protein S21, puta	---	AT3G27450	-1.02	-0.02	-0.26	0.802711	0.902986	-6.81
263280_x_a	hypothetical protein predicted by genscа	---	---	1.02	0.03	0.26	0.802702	0.902986	-6.81
267348_at	unknown protein	---	AT2G39960	1.02	0.03	0.26	0.802789	0.903029	-6.81
251905_at	putative protein zinc finger protein GCS	GAPB	AT1G42970 /	1.02	0.03	0.26	0.802866	0.903071	-6.81
249855_at	unknown protein	---	AT5G22970	1.02	0.03	0.26	0.802989	0.903076	-6.82
262792_at	hypothetical protein predicted by genem	---	AT1G10710	1.02	0.03	0.26	0.802981	0.903076	-6.82
262002_at	hypothetical protein predicted by genem	---	AT1G64450	-1.02	-0.02	-0.26	0.802978	0.903076	-6.82
247062_at	putative protein similar to unknown prote	---	AT5G66810	-1.04	-0.06	-0.26	0.803145	0.903164	-6.82
245538_at	p140mDia like protein	---	AT4G15200	-1.02	-0.03	-0.26	0.803147	0.903164	-6.82
257155_at	hypothetical protein predicted by genscа	---	AT3G27290	1.03	0.04	0.26	0.80345	0.903352	-6.82
254864_at	putative reverse transcriptase other puta	---	---	1.02	0.02	0.26	0.803473	0.903352	-6.82
245353_at	hypothetical protein ;supported by full-le	---	AT4G16000	1.04	0.06	0.26	0.803445	0.903352	-6.82
249569_at	putative protein Pit1 - Arabidopsis thalia	---	AT5G38070	1.03	0.04	0.26	0.803434	0.903352	-6.82
266974_at	unknown protein	---	AT2G39370	1.02	0.02	0.26	0.803528	0.903370	-6.82
251513_at	pirin-like protein pirin - Lycopersicon es	PRN	AT3G59220	1.08	0.11	0.26	0.803632	0.903443	-6.82
258340_at	hypothetical protein predicted by genscа	---	AT3G22770	1.02	0.02	0.26	0.803678	0.903449	-6.82
248394_at	unknown protein	---	AT5G52070	-1.02	-0.03	-0.26	0.804118	0.903706	-6.82
260249_s_a	unknown protein similar to unknown pro	---	AT1G74280 /	-1.03	-0.04	-0.26	0.804183	0.903706	-6.82
253753_at	glycine-rich protein like glycine-rich prot	---	AT4G29030	-1.02	-0.03	-0.26	0.804011	0.903706	-6.82
259781_at	reverse transcriptase, putative similar to	---	---	-1.02	-0.03	-0.26	0.804093	0.903706	-6.82
264459_at	putative reverse transcriptase similar to	---	---	1.03	0.05	0.26	0.804057	0.903706	-6.82
255315_at	hypothetical protein	---	---	1.02	0.03	0.26	0.804071	0.903706	-6.82
264812_at	putative thaumatin-like pathogenesis-rel	---	AT2G17860	-1.02	-0.03	-0.26	0.804177	0.903706	-6.82

248808_at	putative protein contains similarity to ph	---	AT5G47510	1.02	0.02	0.26	0.804227	0.903711	-6.82
264647_at	putative respiratory burst oxidase protei	ATRBOHB	AT1G09090	-1.02	-0.03	-0.26	0.804268	0.903712	-6.82
255336_at	putative transposon protein	---	---	-1.02	-0.02	-0.26	0.804451	0.903873	-6.82
247516_at	germin-like protein - like germin-like pro	---	AT5G61750	1.02	0.03	0.26	0.804622	0.903887	-6.82
260825_at	hypothetical protein predicted by genem	---	AT1G06810	1.02	0.03	0.26	0.804518	0.903887	-6.82
246869_at	putative protein various predicted prote	---	---	1.02	0.03	0.26	0.804596	0.903887	-6.82
251836_at	lipase -like protein monoglyceride lipas	---	AT3G55190	1.02	0.02	0.26	0.804603	0.903887	-6.82
256956_at	expressed protein supported by cDNA:	---	AT3G13410	-1.02	-0.03	-0.26	0.80468	0.903908	-6.82
244918_at	hypothetical protein	AT2G0774	---	-1.02	-0.03	-0.26	0.80478	0.903975	-6.82
259787_at	auxin-induced protein, putative similar t	---	AT1G29460	-1.07	-0.09	-0.26	0.80491	0.904078	-6.82
265009_at	putative protein kinase similar to GB:AA	---	AT1G24650	1.02	0.03	0.26	0.804974	0.904104	-6.82
260196_at	hypothetical protein similar to hypothetic	---	AT1G67570	-1.02	-0.02	-0.26	0.805074	0.904172	-6.82
246619_at	transmembrane protein FT27/PFT27-like	---	AT5G36290	1.02	0.02	0.26	0.805234	0.904234	-6.82
259456_s_a	unknown protein similar to putative non-	---	---	1.02	0.03	0.26	0.805248	0.904234	-6.82
248406_at	pectinesterase	---	AT5G51490	1.03	0.04	0.26	0.805218	0.904234	-6.82
245828_at	transcription factor, putative similar to tr	VIM1	AT1G57820	-1.02	-0.03	-0.26	0.805337	0.904289	-6.82
265343_at	unknown protein ; supported by full-leng	NIC1	AT2G22570	1.04	0.05	0.26	0.805527	0.904413	-6.82
248837_at	putative protein similar to unknown prote	---	AT5G47260	1.02	0.02	0.26	0.805515	0.904413	-6.82
250603_at	putative protein mature parasite-infecte	---	AT5G07820	1.02	0.03	0.26	0.805638	0.904494	-6.82
252164_at	hypothetical protein nodH - Rhizobium s	---	AT3G50620	-1.05	-0.06	-0.26	0.805738	0.904509	-6.82
253033_at	putative protein aminoacylase I - Sus s	---	AT4G38220	-1.02	-0.03	-0.26	0.805859	0.904509	-6.82
262734_at	lipase, putative similar to lipase GB:AA	---	AT1G28640	1.02	0.03	0.26	0.805766	0.904509	-6.82
261877_at	putative indole-3-acetate beta-glucosyltr	---	AT1G50580	-1.02	-0.03	-0.26	0.805779	0.904509	-6.82
256389_at	hypothetical protein predicted by genefir	---	AT3G06220	-1.02	-0.03	-0.26	0.80589	0.904509	-6.82
258898_at	putative DNA helicase	RECQI1	AT3G05740	-1.04	-0.05	-0.26	0.805884	0.904509	-6.82
257070_at	hypothetical protein predicted by genem	---	AT3G28190	-1.02	-0.03	-0.26	0.80609	0.904690	-6.82
251466_at	putative protein hypothetical protein SP	---	AT3G59340	-1.02	-0.03	-0.26	0.806167	0.904731	-6.82
253348_at	putative protein SMT4 protein - Saccha	---	AT4G33620	-1.02	-0.02	-0.26	0.806237	0.904765	-6.82
264339_at	trehalose-6-phosphate synthase, putati	TPS8	AT1G70290	-1.03	-0.05	-0.25	0.806639	0.904886	-6.82
259055_at	unknown protein ;supported by full-leng	UNE6	AT3G03340	-1.02	-0.03	-0.25	0.806662	0.904886	-6.82
263058_at	putative non-LTR retrolelement reverse	---	---	-1.02	-0.03	-0.25	0.806623	0.904886	-6.82
266496_at	putative zinc finger protein	---	---	1.02	0.03	0.25	0.806545	0.904886	-6.82
266209_at	similar to terminal flower ; supported by	ATC	AT2G27550	1.03	0.05	0.25	0.806639	0.904886	-6.82
259780_at	exonuclease, putative similar to GI:488	---	AT1G29630	1.02	0.03	0.25	0.806415	0.904886	-6.82
246215_at	putative cytoskeletal protein ; supported	---	AT4G37180	-1.05	-0.07	-0.25	0.806554	0.904886	-6.82

266173_at	unknown protein	---	AT2G02410	-1.02	-0.03	-0.25	0.806448	0.904886	-6.82
254473_s_a	putative protein kinase like proteins, Ara	---	AT4G20520 /	-1.02	-0.03	-0.25	0.806744	0.904934	-6.82
266860_at	putative phospholipase C	---	AT2G26870	1.04	0.06	0.25	0.806927	0.905095	-6.82
251917_at	putative protein	---	AT3G53970	-1.02	-0.03	-0.25	0.807072	0.905112	-6.82
258508_at	protein kinase, putative similar to SERI	---	AT3G06640	1.02	0.02	0.25	0.807099	0.905112	-6.82
263439_at	hypothetical protein predicted by gensca	ATEXO70I	AT2G28650	-1.02	-0.03	-0.25	0.807101	0.905112	-6.82
265350_at	unknown protein predicted by genscan	---	AT2G22620	1.02	0.03	0.25	0.807094	0.905112	-6.82
254791_at	SERINE CARBOXYPEPTIDASE I PRE	scpl20	AT4G12910	-1.02	-0.03	-0.25	0.807186	0.905163	-6.82
262774_at	chloroplast nucleoid DNA binding prote	---	AT1G13230	-1.02	-0.02	-0.25	0.807309	0.905256	-6.82
245821_at	hypothetical protein similar to putative u	---	AT1G26270	1.03	0.04	0.25	0.807392	0.905260	-6.82
265393_at	unknown protein ; supported by cDNA:	---	AT2G20830	-1.04	-0.05	-0.25	0.80739	0.905260	-6.82
266108_at	putative peptide/amino acid transporter	---	AT2G37900	1.02	0.03	0.25	0.807591	0.905382	-6.82
266960_at	putative retroelement pol polyprotein	---	---	1.02	0.03	0.25	0.807713	0.905382	-6.82
264641_at	ATP-dependent Clp protease proteolyti	---	AT1G09130	-1.02	-0.03	-0.25	0.807666	0.905382	-6.82
248066_at	putative protein contains similarity to pe	QRT1	AT5G55590	1.02	0.03	0.25	0.807739	0.905382	-6.82
261097_at	protein kinase, putative contains protein	---	AT1G62950	1.03	0.04	0.25	0.807676	0.905382	-6.82
250749_at	26S proteasome regulatory subunit S12	RPN8A	AT5G05780	-1.02	-0.02	-0.25	0.807733	0.905382	-6.82
267601_at	hypothetical protein predicted by genefi	---	AT2G32980	-1.02	-0.03	-0.25	0.807942	0.905476	-6.82
249303_at	putative protein strong similarity to unkn	---	AT5G41460	1.03	0.05	0.25	0.807874	0.905476	-6.82
252370_at	putative protein	---	AT3G48600	-1.04	-0.05	-0.25	0.807932	0.905476	-6.82
258472_at	unknown protein identical to unknown p	---	AT3G06080	-1.03	-0.05	-0.25	0.808028	0.905528	-6.82
255421_at	putative protein phosphatase regulatory	---	AT4G03260	-1.02	-0.03	-0.25	0.808073	0.905534	-6.82
265481_at	unknown protein ; supported by cDNA:	---	AT2G15960	-1.02	-0.03	-0.25	0.808137	0.905561	-6.82
261380_at	hypothetical protein predicted by genem	---	AT1G05400	1.03	0.04	0.25	0.808223	0.905613	-6.82
261945_at	unknown protein	---	AT1G64530	1.04	0.05	0.25	0.808266	0.905616	-6.82
245906_at	putative protein ;supported by full-lengt	---	AT5G11070	1.05	0.07	0.25	0.808373	0.905692	-6.82
262214_at	germin subunit, putative similar to germ	---	AT1G74820	1.02	0.03	0.25	0.80853	0.905824	-6.82
246384_at	glutaredoxin, putative similar to glutare	---	AT1G77370	-1.02	-0.03	-0.25	0.808616	0.905835	-6.82
249135_at	putative protein similar to unknown prot	---	AT5G43160	-1.04	-0.06	-0.25	0.808675	0.905835	-6.82
246470_at	putative protein predicted proteins, from	---	AT5G17080	-1.02	-0.03	-0.25	0.808699	0.905835	-6.82
261477_at	unknown protein	---	AT1G14310	-1.03	-0.04	-0.25	0.808687	0.905835	-6.82
255727_at	hypothetical protein similar to unknown	---	AT1G25510	1.02	0.03	0.25	0.808785	0.905848	-6.82
253649_at	putative protein predicted protein, Arabi	---	AT4G29790	-1.04	-0.05	-0.25	0.80879	0.905848	-6.82
250023_at	beta-1,3-glucanase-like protein	---	AT5G18220	-1.02	-0.03	-0.25	0.809141	0.906196	-6.82
246608_at	putative protein various predicted prote	---	AT5G35380	1.02	0.03	0.25	0.809281	0.906220	-6.82

255713_s_a	predicted protein	---	AT4G00234 /	-1.02	-0.02	-0.25	0.809243	0.906220	-6.82
263586_at	unknown protein predicted by genscan;(	---	AT2G25350	-1.03	-0.04	-0.25	0.809265	0.906220	-6.82
255195_at	may be a pseudogene	---	---	1.02	0.03	0.25	0.809391	0.906299	-6.82
253891_at	putative protein ;supported by full-lengt	---	AT4G27720	1.04	0.06	0.25	0.809576	0.906410	-6.82
261313_at	hypothetical protein predicted by gensca	---	AT1G52970	1.02	0.02	0.25	0.80961	0.906410	-6.82
246273_at	globulin-like protein	---	AT4G36700	-1.02	-0.03	-0.25	0.809559	0.906410	-6.82
245700_at	carbonate dehydratase - like protein ;su	ACA3	AT5G04180	-1.02	-0.03	-0.25	0.809953	0.906750	-6.82
260988_at	MAP3K alpha protein kinase, putative s	MAP3KA	AT1G53570	1.03	0.04	0.25	0.810051	0.906815	-6.82
264994_at	hypothetical protein contains similarity t	---	AT1G67270	-1.02	-0.03	-0.25	0.810265	0.907011	-6.82
248840_at	unknown protein ; supported by cDNA:	---	AT5G46770	1.02	0.03	0.25	0.810438	0.907159	-6.82
252388_at	putative protein ;supported by full-lengt	---	AT3G47850	1.02	0.03	0.25	0.810483	0.907165	-6.82
262236_at	hypothetical protein similar to hypothetic	---	AT1G48330	1.04	0.06	0.25	0.810539	0.907184	-6.82
247314_at	3(2),5-bisphosphate nucleotidase (emb	SAL2	AT5G64000	-1.06	-0.08	-0.25	0.810824	0.907369	-6.82
257392_at	hypothetical protein	FLA3	AT2G24450	-1.02	-0.03	-0.25	0.810794	0.907369	-6.82
259446_at	hypothetical protein contains similarity t	---	AT1G02410	-1.03	-0.04	-0.25	0.810824	0.907369	-6.82
250847_at	putative protein predicted protein, Arabi	---	AT5G04480	-1.04	-0.06	-0.25	0.810951	0.907377	-6.82
251210_at	hypothetical protein ;supported by full-le	---	AT3G62810	1.02	0.03	0.25	0.810945	0.907377	-6.82
248156_at	unknown protein	---	AT5G54410	-1.02	-0.02	-0.25	0.810937	0.907377	-6.82
265984_at	putative limonene cyclase	TPS10	AT2G24210	-1.02	-0.03	-0.25	0.811095	0.907392	-6.82
253873_at	hypothetical protein ;supported by full-le	PRA1.H	AT4G27540	-1.02	-0.03	-0.25	0.811139	0.907392	-6.82
246247_at	putative protein	---	AT4G36640	1.06	0.09	0.25	0.811004	0.907392	-6.82
259183_at	hypothetical protein similar to putative p	---	AT3G01580	-1.03	-0.04	-0.25	0.811163	0.907392	-6.82
255757_at	putative protein	ROPGEF3	AT4G00460	-1.02	-0.03	-0.25	0.81115	0.907392	-6.82
258931_at	hypothetical protein similar to hypotheti	DML2	AT3G10010	1.03	0.05	0.25	0.81125	0.907423	-6.82
248266_at	putative protein similar to unknown prote	---	AT5G53440	1.02	0.02	0.25	0.81131	0.907423	-6.82
253014_at	MADS-box protein AGL17 -like protein	AGL21	AT4G37940	1.02	0.02	0.25	0.811283	0.907423	-6.82
259532_at	hypothetical protein	---	AT1G12470	1.02	0.02	0.25	0.811456	0.907453	-6.82
254702_at	putative protein predicted protein, Arabi	---	AT4G17940	-1.02	-0.03	-0.25	0.811387	0.907453	-6.82
245495_at	hypothetical protein	---	AT4G16400	-1.02	-0.02	-0.25	0.811445	0.907453	-6.82
264116_at	putative poly (ADP-ribose) polymerase	PARP2	AT2G31320	-1.04	-0.05	-0.25	0.811507	0.907462	-6.82
255954_at	hypothetical protein predicted by genem	emb2204	AT1G22090	1.02	0.03	0.25	0.811544	0.907462	-6.82
257234_at	hypothetical protein predicted by genem	---	AT3G14880	1.03	0.04	0.25	0.811606	0.907487	-6.82
255238_at	see GB:AL022580)	---	---	-1.01	-0.02	-0.25	0.811746	0.907599	-6.82
256447_at	nitrate transporter NTL1, putative simila	---	AT1G33440	1.02	0.04	0.25	0.811822	0.907639	-6.82
258002_at	AIG2-like protein similar to AIG2 protein	AIG2	AT3G28930	-1.10	-0.14	-0.25	0.811879	0.907658	-6.82

247906_at	putative protein similar to unknown prote	IAA33	AT5G57420	-1.03	-0.04	-0.25	0.811936	0.907678	-6.82
265938_at	putative SF21 protein {Helianthus annu	---	AT2G19620	1.06	0.08	0.25	0.811987	0.907691	-6.82
265290_at	putative anthocyanidin-3-glucoside rham	---	AT2G22590	1.02	0.03	0.25	0.812027	0.907691	-6.82
258631_at	putative polygalacturonase similar to po	QRT2	AT3G07970	1.06	0.09	0.25	0.812174	0.907726	-6.82
263349_at	putative chromodomain-helicase-DNA-b	CHR5	AT2G13370	1.03	0.04	0.25	0.812172	0.907726	-6.82
263447_s_a	putative PHD-type zinc finger protein	ATX2	AT1G05830 /	-1.04	-0.06	-0.25	0.812178	0.907726	-6.82
244946_at	hypothetical protein	---	---	1.02	0.02	0.25	0.812222	0.907731	-6.82
256277_at	omega-6 fatty acid desaturase, endopla	FAD2	AT3G12120	-1.03	-0.05	-0.25	0.812335	0.907768	-6.82
257992_at	hypothetical protein similar to hypothetic	---	AT3G19880	1.03	0.04	0.25	0.812316	0.907768	-6.82
260918_at	hypothetical protein predicted by genem	---	AT1G21510	-1.02	-0.03	-0.25	0.812491	0.907853	-6.82
267045_at	putative protein kinase contains a protei	CIPK13	AT2G34180	1.02	0.03	0.25	0.812469	0.907853	-6.82
266650_at	unknown protein	---	AT2G25800	-1.02	-0.04	-0.25	0.812571	0.907898	-6.82
246579_at	hypothetical protein predicted by genem	---	AT1G31620	1.02	0.03	0.25	0.812671	0.907921	-6.82
250919_at	putative protein myosin heavy chain, G	---	AT5G03660	1.02	0.03	0.25	0.812639	0.907921	-6.82
266412_at	hypothetical protein predicted by gensca	MAP65-5	AT2G38720	-1.02	-0.03	-0.25	0.812825	0.908049	-6.82
262565_at	hypothetical protein predicted by gensca	---	AT1G34320	1.02	0.03	0.25	0.81301	0.908177	-6.82
251827_at	chalcone isomerase ;supported by full-l	TT5	AT3G55120	-1.03	-0.04	-0.25	0.813056	0.908177	-6.82
259205_at	hypothetical protein similar to putative p	---	AT3G09030	-1.02	-0.03	-0.25	0.813059	0.908177	-6.82
264098_at	hypothetical protein predicted by genem	---	AT1G79260	-1.03	-0.05	-0.25	0.813173	0.908260	-6.82
263536_at	putative WRKY-type DNA binding protei	WRKY60	AT2G25000	1.05	0.07	0.25	0.81328	0.908334	-6.82
252188_at	putative clathrin coat assembly protein	---	AT3G50860	-1.03	-0.05	-0.24	0.813779	0.908803	-6.82
262390_at	hypothetical protein predicted by gensca	---	AT1G49260	-1.02	-0.03	-0.24	0.813775	0.908803	-6.82
252242_at	F-box protein family, AtFBL16 contains	VFB2	AT3G50080	-1.02	-0.03	-0.24	0.813909	0.908872	-6.82
260184_s_a	putative protein predicted proteins, Arat	---	---	1.02	0.02	0.24	0.813921	0.908872	-6.82
255188_at	contains similarity to Xenopus laevis rep	---	---	1.02	0.02	0.24	0.813966	0.908878	-6.82
260795_at	CLE3, putative CLAVATA3/ESR-Relate	CLE3	AT1G06225	-1.02	-0.03	-0.24	0.814106	0.908945	-6.82
265148_at	unknown protein	---	AT1G51160	1.02	0.03	0.24	0.814086	0.908945	-6.82
259680_at	putative AUX1-like permease similar to	LAX3	AT1G77690	1.09	0.13	0.24	0.814223	0.909031	-6.82
253711_at	hypothetical protein	DER1	---	1.02	0.03	0.24	0.814336	0.909113	-6.82
263619_at	putative GDP-mannose pyrophosphory	---	AT2G04650	1.02	0.03	0.24	0.814498	0.909116	-6.82
259904_at	hypothetical protein predicted by genem	---	AT1G74150	1.02	0.03	0.24	0.814453	0.909116	-6.82
247484_at	putative protein predicted proteins, Plas	---	AT5G62110	-1.02	-0.03	-0.24	0.814497	0.909116	-6.82
261657_at	pathogenesis-related protein 1b precurs	---	AT1G50050	1.02	0.03	0.24	0.814401	0.909116	-6.82
248054_at	unknown protein	---	AT5G55820	1.03	0.04	0.24	0.814595	0.909136	-6.82
253311_s_a	putative protein xylan endohydrolase is	---	AT4G33830 /	1.02	0.02	0.24	0.814565	0.909136	-6.82

251018_at	60S ribosomal protein - like 60S riboso	---	AT5G02450	1.03	0.04	0.24	0.814652	0.909155	-6.82
248159_at	unknown protein	---	AT5G54460	1.02	0.02	0.24	0.814734	0.909202	-6.82
257481_at	hypothetical protein identical to hypothe	ALMT1	AT1G08430	1.02	0.03	0.24	0.814859	0.909297	-6.82
256672_at	ABC transporter, putative contains Pfar	---	AT3G52310	1.02	0.04	0.24	0.81503	0.909443	-6.82
255856_at	unknown protein identical to unknown p	---	AT1G66940	1.08	0.12	0.24	0.815159	0.909543	-6.82
244910_s_a	hypothetical protein	---	---	-1.02	-0.03	-0.24	0.815341	0.909701	-6.82
249598_at	putative protein AtPP protein, Brassica	---	AT5G37970	-1.02	-0.03	-0.24	0.815402	0.909725	-6.82
259319_at	Snf1-related protein kinase KIN10 (AKI	AKIN10	AT3G01090	-1.02	-0.02	-0.24	0.815501	0.909746	-6.82
256739_s_a	hypothetical protein similar to putative re	---	---	-1.01	-0.02	-0.24	0.815462	0.909746	-6.82
265928_at	Ac-like transposase related to Ac/Ds tra	---	---	1.02	0.03	0.24	0.815633	0.909760	-6.82
246337_at	putative protein putative integral membr	CHX12	AT3G44910	-1.03	-0.04	-0.24	0.815586	0.909760	-6.82
253805_at	putative protein	---	AT4G28260	1.02	0.03	0.24	0.815617	0.909760	-6.82
254221_at	putative polygalacturonase polygalactu	---	AT4G23820	-1.08	-0.11	-0.24	0.815673	0.909760	-6.82
253127_at	putative Myc-type transcription factor m	---	AT4G36060	1.02	0.02	0.24	0.815845	0.909908	-6.82
263042_at	conserved hypothetical protein protein p	---	AT1G23340	1.02	0.03	0.24	0.815929	0.909957	-6.82
266861_at	putative choline kinase ;supported by fu	emb1187	AT2G26830	-1.02	-0.03	-0.24	0.816002	0.909994	-6.82
245306_at	Expressed protein ; supported by full-ler	ELIP2	AT4G14690	1.02	0.03	0.24	0.816089	0.910011	-6.82
248363_at	nodulin-like protein	---	AT5G52480	1.02	0.02	0.24	0.816137	0.910011	-6.82
249003_at	putative protein contains similarity to sm	---	AT5G44500	-1.02	-0.03	-0.24	0.816103	0.910011	-6.82
267585_s_a	putative actin	ACT9	AT2G42090	1.02	0.03	0.24	0.816435	0.910165	-6.82
258278_at	putative self-incompatibility protein simi	---	AT3G26860	1.02	0.03	0.24	0.816408	0.910165	-6.82
267537_at	putative guanylate kinase ; supported b	GK-1	AT2G41880	-1.06	-0.08	-0.24	0.816399	0.910165	-6.82
251765_at	putative protein	---	---	1.02	0.03	0.24	0.816325	0.910165	-6.82
248355_at	putative protein strong similarity to unkn	ATEXO70A	AT5G52340	1.02	0.02	0.24	0.816504	0.910197	-6.82
246999_at	photoreceptor-interacting protein-like ; s	NPY3	AT5G67440	-1.04	-0.05	-0.24	0.816629	0.910292	-6.82
258791_at	hevein-like protein precursor (PR-4) ide	PR4	AT3G04720	1.05	0.08	0.24	0.816846	0.910345	-6.82
252198_x_a	putative protein predicted protein, Arabi	---	AT3G50250	1.03	0.04	0.24	0.816853	0.910345	-6.82
258886_at	putative importin alpha similar to GB:AA	IMPA-7	AT3G05720	1.02	0.03	0.24	0.816803	0.910345	-6.82
250790_at	putative protein similar to unknown prote	---	AT5G05640	1.03	0.04	0.24	0.816768	0.910345	-6.82
256537_at	unknown protein	---	AT1G33340	-1.05	-0.07	-0.24	0.816876	0.910345	-6.82
261004_at	hypothetical protein similar to putative b	---	AT1G26450	1.03	0.04	0.24	0.81708	0.910443	-6.82
259382_s_a	jasmonate inducible protein isolog ;sup	JAL31	AT3G16420 /	-1.10	-0.14	-0.24	0.817061	0.910443	-6.82
259223_at	hypothetical protein	WOX11	AT3G03660	-1.02	-0.03	-0.24	0.817084	0.910443	-6.82
250839_at	MADS-box protein - like SLM3 MADS-b	AGL99	AT5G04640	1.02	0.02	0.24	0.817204	0.910532	-6.82
260964_at	E2, ubiquitin-conjugating enzyme 15 (U	ATUBC2-1	AT1G45050	1.02	0.02	0.24	0.817443	0.910755	-6.82

251802_at	E2, ubiquitin-conjugating enzyme 14 (U	UBC14	AT3G55380	1.02	0.02	0.24	0.817514	0.910763	-6.82
263983_at	unknown protein ;supported by full-leng	---	AT2G42780	1.02	0.02	0.24	0.81757	0.910763	-6.82
248374_at	MADS box transcription factor-like	AGL71	AT5G51870	-1.02	-0.02	-0.24	0.817548	0.910763	-6.82
257568_s_a	hypothetical protein	---	AT3G23950 /	-1.02	-0.04	-0.24	0.817643	0.910800	-6.82
252983_at	cinnamyl-alcohol dehydrogenase ELI3-1	ELI3-1	AT4G37980	1.04	0.05	0.24	0.817724	0.910800	-6.82
264618_at	hypothetical protein predicted by genefi	---	AT2G17680	1.02	0.03	0.24	0.817718	0.910800	-6.82
265398_at	unknown protein	ATMAK10	AT2G11000	-1.02	-0.03	-0.24	0.817865	0.910914	-6.82
266103_at	putative VAMP-associated protein ;sup	PVA12	AT2G45140	1.02	0.03	0.24	0.81817	0.911162	-6.82
247365_at	putative protein similar to unknown prote	---	AT5G63220	1.02	0.03	0.24	0.818146	0.911162	-6.82
263897_at	putative shikimate kinase precursor	---	AT2G21940	1.03	0.05	0.24	0.818238	0.911162	-6.82
249448_at	cdc2-like protein	cdc2cAt	AT5G39420	-1.03	-0.04	-0.24	0.818248	0.911162	-6.82
265261_at	putative APG isolog protein	---	AT2G42990	1.06	0.09	0.24	0.818437	0.911327	-6.82
249707_at	putative protein similar to unknown prote	---	AT5G35640	-1.03	-0.04	-0.24	0.818522	0.911333	-6.82
259758_s_a	putative caffeic acid 3-O-methyltransfera	---	AT1G77520 /	-1.02	-0.03	-0.24	0.8185	0.911333	-6.82
264998_at	unknown protein similar to hypothetical	---	AT1G67330	-1.07	-0.10	-0.24	0.818702	0.911445	-6.82
266698_at	copia-like retroelement pol polyprotein ;	SNF7.2	AT2G19830	1.02	0.03	0.24	0.818696	0.911445	-6.82
259233_at	hypothetical protein	---	AT3G11380	1.01	0.02	0.24	0.818869	0.911585	-6.82
246639_x_a	adenylate kinase -like protein predicted	---	---	1.02	0.03	0.24	0.818908	0.911585	-6.82
251026_at	hypothetical protein	FHL	AT5G02200	1.08	0.10	0.24	0.819084	0.911653	-6.82
252490_at	glucuronosyl transferase-like protein glu	---	AT3G46720	1.02	0.03	0.24	0.819099	0.911653	-6.82
257971_at	unknown protein similar to hypothetical	GC6	AT3G27530	1.03	0.04	0.24	0.819129	0.911653	-6.82
260197_at	F12A21.25 hypothetical protein	---	AT1G67623	-1.02	-0.03	-0.24	0.81902	0.911653	-6.82
264030_at	putative steroid sulfotransferase	---	AT2G03770	-1.02	-0.03	-0.24	0.819598	0.912005	-6.82
247840_at	putative protein protein x 0001, Homo s	---	AT5G58020	-1.02	-0.02	-0.24	0.819564	0.912005	-6.82
246592_at	putative protein predicted protein, Arabi	---	AT5G14890	1.02	0.03	0.24	0.819605	0.912005	-6.82
253324_at	Expressed protein ; supported by full-ler	---	AT4G33940	1.02	0.03	0.24	0.819602	0.912005	-6.82
245895_at	SIR2-family protein sirtuin type 4 (SIRT	SRT2	AT5G09230	1.02	0.03	0.24	0.819656	0.912018	-6.82
252849_at	Histon H3 ;supported by full-length cDN	---	AT4G40040	1.02	0.03	0.24	0.81971	0.912033	-6.82
264827_at	hypothetical protein similar to anthranila	---	AT1G03390	-1.02	-0.02	-0.24	0.819831	0.912123	-6.82
254699_at	putative protein predicted protein, Arabi	---	AT4G17990	1.02	0.03	0.24	0.819943	0.912203	-6.82
252529_at	putative protein several oxidases, main	---	AT3G46490	1.06	0.08	0.24	0.820076	0.912307	-6.82
254883_at	putative protein histidine-rich glycoprote	HAP2	AT4G11720	1.02	0.03	0.24	0.820127	0.912318	-6.82
266477_at	CLE4 CLAVATA3/ESR-Related 4 (CLE4	CLE6	AT2G31085	1.02	0.03	0.24	0.820271	0.912434	-6.82
250921_at	Expressed protein ; supported by full-ler	---	AT5G03460	1.03	0.04	0.24	0.820681	0.912812	-6.82
246049_at	putative protein predicted proteins, Arat	---	---	-1.02	-0.03	-0.24	0.820691	0.912812	-6.82

247839_at	eukaryotic initiation factor 4, eIF4-like p	---	AT5G57870	1.03	0.04	0.24	0.82084	0.912914	-6.82
257976_at	putative transcription factor contains AF	PLT1	AT3G20840	1.02	0.03	0.24	0.820862	0.912914	-6.82
262869_s_a	putative protein predicted protein, Caen	GTG1	AT1G64990 /	-1.02	-0.03	-0.24	0.820922	0.912936	-6.82
265625_at	hypothetical protein predicted by gensca	---	AT2G27240	1.02	0.03	0.24	0.820979	0.912955	-6.82
251912_at	protein kinase-like protein wall-associat	---	AT3G53840	-1.02	-0.03	-0.24	0.821057	0.912997	-6.82
263554_at	putative Ta11-like non-LTR retroelemen	---	---	-1.03	-0.05	-0.24	0.821156	0.913063	-6.82
247682_at	serine/threonine-specific protein kinase	---	AT5G59650	1.02	0.03	0.23	0.821312	0.913192	-6.82
254296_at	hypothetical protein	---	AT4G23090	1.02	0.03	0.23	0.821411	0.913257	-6.82
249992_at	AP2 domain -like protein AP2/EREBP-l	PUCHI	AT5G18560	1.02	0.03	0.23	0.821555	0.913309	-6.82
245588_at	putative protein	---	AT4G15030	1.03	0.04	0.23	0.821578	0.913309	-6.82
262545_at	prolin rich protein, putative similar to pr	---	AT1G31250	-1.02	-0.03	-0.23	0.821526	0.913309	-6.82
253713_at	putative protein several hypothetical pro	---	AT4G29370	-1.02	-0.02	-0.23	0.821634	0.913327	-6.82
251273_at	serine/threonine-protein kinase-like pro	---	AT3G61960	-1.03	-0.04	-0.23	0.822381	0.913757	-6.82
248341_at	unknown protein	---	AT5G52220	1.02	0.04	0.23	0.822301	0.913757	-6.82
266281_at	putative protein kinase contains a protei	---	AT2G29250	-1.02	-0.03	-0.23	0.822311	0.913757	-6.82
248375_at	potassium/proton antiporter-like protein	KEA5	AT5G51710	-1.02	-0.02	-0.23	0.822325	0.913757	-6.82
263464_at	putative ARI-like RING zinc finger protei	---	AT2G31760	-1.02	-0.03	-0.23	0.822359	0.913757	-6.82
259266_at	hypothetical protein predicted by gensca	---	AT3G01240	-1.02	-0.02	-0.23	0.822102	0.913757	-6.82
247920_at	putative protein contains similarity to un	---	AT5G57670	1.02	0.03	0.23	0.822227	0.913757	-6.82
251572_at	pelota-like protein pelota PEL1 - Arabid	---	AT3G58390	1.02	0.03	0.23	0.822351	0.913757	-6.82
249646_at	SEN1-like protein SEN1 - Saccharomyc	---	AT5G37030	1.02	0.02	0.23	0.822316	0.913757	-6.82
247107_at	senescence-associated protein almost id	STR16	AT5G66040	1.03	0.04	0.23	0.822684	0.913781	-6.82
255060_at	putative protein TMV resistance protein	---	AT4G09430	1.02	0.03	0.23	0.82252	0.913781	-6.82
245715_s_a	Expressed protein ; supported by cDNA	---	AT5G08670 /	1.02	0.03	0.23	0.822759	0.913781	-6.82
244989_s_a	hypothetical protein	---	---	1.03	0.04	0.23	0.822575	0.913781	-6.82
247054_at	zinc finger protein	---	AT5G66730	1.02	0.03	0.23	0.822733	0.913781	-6.82
251433_at	putative protein SERINE/THREONINE-	---	AT3G59830	1.01	0.02	0.23	0.822764	0.913781	-6.82
251363_at	putative transcription factor (MYB17)	AtMYB17	AT3G61250	-1.03	-0.04	-0.23	0.822693	0.913781	-6.82
261830_at	protein kinase, putative similar to protei	---	AT1G10620	1.02	0.03	0.23	0.822724	0.913781	-6.82
256925_at	hypothetical protein predicted by genem	---	---	1.02	0.02	0.23	0.822491	0.913781	-6.82
263310_s_a	hypothetical protein	---	---	-1.02	-0.02	-0.23	0.822987	0.913984	-6.82
257173_at	S-adenosyl-L-homocysteinas, putative	SAHH2	AT3G23810	1.07	0.10	0.23	0.823125	0.914093	-6.82
251871_at	hypothetical protein	---	AT3G54520	1.01	0.02	0.23	0.823259	0.914192	-6.82
249880_at	putative protein similar to unknown prote	---	AT5G23180	1.02	0.03	0.23	0.823315	0.914192	-6.82
263617_at	putative retroelement pol polyprotein	---	---	1.02	0.03	0.23	0.823334	0.914192	-6.82

257113_at	cytochrome P450, putative contains Pfa	CYP705A2	AT3G20130	1.04	0.06	0.23	0.823681	0.914489	-6.82
262815_at	putative cytochrome P450 strong similar	CYP71A18	AT1G11610	-1.04	-0.05	-0.23	0.823646	0.914489	-6.82
266259_at	unknown protein ;supported by full-leng	---	AT2G27830	-1.02	-0.03	-0.23	0.824262	0.914536	-6.82
259174_at	hypothetical protein similar to putative g	UNE7	AT3G03690	1.01	0.02	0.23	0.824378	0.914536	-6.82
265702_at	putative purple acid phosphatase contai	PAP9	AT2G03450	1.02	0.03	0.23	0.823783	0.914536	-6.82
255511_at	Expressed protein ; supported by cDNA	PIT1	AT4G02075	1.04	0.06	0.23	0.824443	0.914536	-6.82
247896_at	26S proteasome regulatory subunit p27	---	AT5G57950	-1.02	-0.02	-0.23	0.823944	0.914536	-6.82
248305_at	putative protein similar to unknown prote	ATUSP	AT5G52560	-1.02	-0.03	-0.23	0.824202	0.914536	-6.82
261397_at	hexose transporter, putative similar to h	SGB1	AT1G79820	1.03	0.05	0.23	0.824486	0.914536	-6.82
251648_at	protein kinase - like protein S-receptor k	---	AT3G57720	1.02	0.03	0.23	0.824066	0.914536	-6.82
264886_at	S-linalool synthase, putative similar to S	TPS04	AT1G61120	1.15	0.20	0.23	0.824031	0.914536	-6.82
247905_at	unknown protein	---	AT5G57400	-1.01	-0.02	-0.23	0.824225	0.914536	-6.82
255178_at	may be a pseudogene	---	---	-1.02	-0.02	-0.23	0.824299	0.914536	-6.82
253660_at	putative protein proline-rich protein AP0	---	AT4G30140	1.02	0.02	0.23	0.824256	0.914536	-6.82
255996_s_a	receptor-like serine threonine kinase, p	---	AT1G29730 /	-1.02	-0.03	-0.23	0.824017	0.914536	-6.82
261997_at	hypothetical protein similar C-term of ga	---	---	1.02	0.02	0.23	0.823925	0.914536	-6.82
260116_at	AIG1 identical to AIG1 (exhibits RPS2-	AIG1	AT1G33960	-1.02	-0.02	-0.23	0.824009	0.914536	-6.82
264068_at	putative homeodomain transcription fact	BLH8	AT2G27990	-1.04	-0.05	-0.23	0.824466	0.914536	-6.82
246813_at	putative protein various predicted prote	---	---	1.02	0.02	0.23	0.824456	0.914536	-6.82
247589_at	REVOLUTA or interfascicular fiberless 1	REV	AT5G60690	-1.02	-0.03	-0.23	0.824037	0.914536	-6.82
257920_at	hypothetical protein predicted by genem	---	AT3G23260	1.02	0.02	0.23	0.824265	0.914536	-6.82
244909_at	hypothetical protein	---	---	1.02	0.03	0.23	0.824633	0.914610	-6.82
260067_at	putative lipid transfer protein similar to li	---	AT1G73780	1.02	0.03	0.23	0.824601	0.914610	-6.82
263389_at	putative retroelement pol polyprotein	---	---	1.02	0.02	0.23	0.824701	0.914641	-6.82
253022_at	putative protein	---	AT4G38060	1.04	0.05	0.23	0.824845	0.914742	-6.82
257640_at	hypothetical protein	---	AT3G25750	-1.02	-0.03	-0.23	0.824872	0.914742	-6.82
245413_at	asparagine--tRNA ligase	NS1	AT4G17300	1.02	0.03	0.23	0.824936	0.914768	-6.82
252186_at	putative protein	---	AT3G50810	-1.02	-0.03	-0.23	0.825006	0.914802	-6.82
254816_at	putative adenine phosphoribosyltransfe	APT4	AT4G12440	1.01	0.02	0.23	0.825379	0.915082	-6.82
255300_at	putative phosphatidylglycerotransferase	CLS	AT4G04870	-1.03	-0.04	-0.23	0.825307	0.915082	-6.82
249596_s_a	glucuronosyl transferase-like protein glu	---	AT5G37950 /	1.03	0.04	0.23	0.825352	0.915082	-6.82
256471_at	hypothetical protein predicted by genem	---	---	-1.02	-0.02	-0.23	0.82542	0.915083	-6.82
255368_at	hypothetical protein	---	---	-1.02	-0.02	-0.23	0.825498	0.915125	-6.82
255386_at	hypothetical protein	---	AT4G03620	-1.02	-0.02	-0.23	0.825618	0.915213	-6.82
251898_at	floral homeotic protein APETALA3 (AP3	AP3	AT3G54340	-1.01	-0.02	-0.23	0.825716	0.915278	-6.82

263340_at	hypothetical protein predicted by gensca	---	---	-1.02	-0.02	-0.23	0.825767	0.915290	-6.82
246644_at	putative protein	---	AT5G35100	1.03	0.04	0.23	0.825922	0.915333	-6.82
262730_at	putative transport protein may be a mem	ATOCT3	AT1G16390	-1.02	-0.03	-0.23	0.826008	0.915333	-6.82
245111_at	putative Ta11-like non-LTR retroelemen	---	---	-1.02	-0.03	-0.23	0.826123	0.915333	-6.82
256322_at	unknown protein ; supported by cDNA: g	AXR4	AT1G54990	-1.04	-0.05	-0.23	0.826167	0.915333	-6.82
252008_at	hypothetical protein ; supported by cDN	---	AT3G52610	-1.02	-0.03	-0.23	0.825992	0.915333	-6.82
266244_at	unknown protein	---	AT2G27740	1.05	0.07	0.23	0.826102	0.915333	-6.82
263141_at	hypothetical protein similar to unknown	---	AT1G65210	1.02	0.02	0.23	0.825939	0.915333	-6.82
262541_at	hypothetical protein contains similarity to	---	---	-1.01	-0.02	-0.23	0.825849	0.915333	-6.82
257579_at	hypothetical protein predicted by genefir	---	AT3G11000	-1.02	-0.03	-0.23	0.826152	0.915333	-6.82
260991_at	hypothetical protein predicted by genem	---	AT1G12160	1.02	0.02	0.23	0.826227	0.915355	-6.82
261181_at	monosaccharide transporter, putative s	---	AT1G34580	1.02	0.03	0.23	0.82639	0.915415	-6.82
252544_at	respiratory burst oxidase - like protein (	---	AT3G45810	1.02	0.03	0.23	0.826402	0.915415	-6.82
248581_at	putative protein strong similarity to unkn	---	AT5G49900	1.03	0.04	0.23	0.826346	0.915415	-6.82
267091_at	Expressed protein ; supported by full-ler	---	AT2G38185	-1.03	-0.04	-0.23	0.826615	0.915607	-6.82
262329_at	hypothetical protein similar to hypothetic	---	AT1G64090	-1.02	-0.02	-0.23	0.826685	0.915640	-6.82
249702_at	axi 1 (auxin-independent growth promot	---	AT5G35570	1.05	0.07	0.23	0.826892	0.915736	-6.82
261120_at	homeodomain protein BELL1, putative	BLH3	AT1G75410	-1.03	-0.04	-0.23	0.826858	0.915736	-6.82
257853_at	hypothetical protein predicted by genefi	---	AT3G12960	-1.02	-0.03	-0.23	0.826819	0.915736	-6.82
249419_s_a	putative protein MADS-box protein 2, L	AGL98	AT5G39750 /	1.02	0.02	0.23	0.827042	0.915858	-6.82
251350_at	cytochrome P450 monooxygenase-like	CYP76C7	AT3G61040	-1.03	-0.04	-0.23	0.827224	0.916014	-6.82
250239_at	ABC transporter-like protein	---	AT5G13580	-1.03	-0.04	-0.23	0.827285	0.916038	-6.82
252819_at	putative protein several hypothetical pro	---	---	-1.01	-0.02	-0.23	0.82752	0.916198	-6.82
251106_at	putative protein peroxisomal Ca-depen	---	AT5G01500	1.07	0.09	0.23	0.827551	0.916198	-6.82
248660_at	RNA-binding protein-like	---	AT5G48650	1.02	0.03	0.23	0.827513	0.916198	-6.82
266735_at	putative pectinesterase ; supported by	---	AT2G46930	1.02	0.03	0.23	0.827892	0.916442	-6.82
247859_at	unknown protein	---	AT5G58410	-1.01	-0.02	-0.23	0.827829	0.916442	-6.82
249640_at	cationic amino acid transporter -like pro	CAT3	AT5G36940	1.03	0.04	0.23	0.827873	0.916442	-6.82
262372_at	hypothetical protein predicted by genefir	---	AT1G73130	1.03	0.04	0.23	0.828045	0.916450	-6.82
248027_at	outward rectifying potassium channel K	ATKCO1	AT5G55630	-1.02	-0.03	-0.23	0.828099	0.916450	-6.82
259695_at	hypothetical protein predicted by genem	---	AT1G63170	1.02	0.03	0.23	0.828083	0.916450	-6.82
252642_at	putative protein predicted protein, Arab	---	AT3G44580	-1.01	-0.02	-0.23	0.828003	0.916450	-6.82
254823_at	putative protein predicted protein	---	AT4G12580	1.01	0.02	0.23	0.828008	0.916450	-6.82
263062_at	putative phosphatidylinositol/phophatidy	---	AT2G18180	-1.02	-0.03	-0.23	0.828181	0.916496	-6.82
267576_at	putative Mutator-like transposase	---	---	-1.02	-0.03	-0.23	0.82828	0.916561	-6.82

266949_s_a	unknown protein ;supported by full-lengt	---	AT2G18840 /	1.02	0.03	0.23	0.828323	0.916564	-6.82
253934_at	putative beta-1,3-glucanase beta-1,3-gl	---	AT4G26830	1.02	0.02	0.23	0.828478	0.916646	-6.82
254439_s_a	carbonic anhydrase -like protein carbon	ACA6	AT4G20990 /	1.01	0.02	0.23	0.828462	0.916646	-6.82
248017_at	protein kinase-like protein	---	AT5G56460	1.03	0.04	0.23	0.828562	0.916695	-6.82
258024_at	hypothetical protein predicted by genem	---	AT3G19360	-1.04	-0.05	-0.22	0.828683	0.916784	-6.82
262488_at	unknown protein EST gb|AA586241 con	---	AT1G21830	-1.04	-0.05	-0.22	0.829041	0.917080	-6.82
265023_at	unknown protein weak similarity to C3H(	---	AT1G24440	-1.02	-0.04	-0.22	0.829067	0.917080	-6.82
256749_at	hypothetical protein similar to putative re	---	---	1.02	0.02	0.22	0.829111	0.917080	-6.82
267522_at	hypothetical protein predicted by gensca	---	AT2G30430	1.02	0.03	0.22	0.829073	0.917080	-6.82
245921_at	putative protein predicted protein, Arabi	---	AT5G28800	-1.01	-0.02	-0.22	0.829183	0.917115	-6.82
266895_at	hypothetical protein predicted by gensca	---	AT2G26040	-1.02	-0.02	-0.22	0.829259	0.917155	-6.82
258018_at	hypothetical protein predicted by gensca	---	AT3G19500	-1.02	-0.04	-0.22	0.829331	0.917190	-6.82
248587_at	Expressed protein ; supported by full-ler	---	AT5G49550	-1.02	-0.03	-0.22	0.829596	0.917438	-6.82
257675_at	ethylene responsive element binding fa	ERF7	AT3G20310	-1.02	-0.03	-0.22	0.829685	0.917493	-6.82
257278_at	hypothetical protein predicted by genem	---	AT3G14480	1.02	0.03	0.22	0.830059	0.917861	-6.82
245465_at	cellulose synthase like protein	ATCSLA01	AT4G16590	1.07	0.10	0.22	0.830232	0.918009	-6.82
253853_at	putative diacylglycerol kinase (fragment	---	AT4G28130	1.02	0.02	0.22	0.830531	0.918294	-6.83
252216_at	putative protein several hypothetical pro	---	AT3G50420	-1.02	-0.03	-0.22	0.830644	0.918375	-6.83
255281_at	contains similarity to glucan synthases	GSL1	AT4G04970	-1.01	-0.02	-0.22	0.830895	0.918608	-6.83
262980_at	endo-beta-1,4-glucanase, putative simil	AtGH9B7	AT1G75680	1.08	0.11	0.22	0.830978	0.918655	-6.83
253207_at	putative protein small auxin up-regulate	---	AT4G34770	-1.05	-0.07	-0.22	0.831203	0.918770	-6.83
247110_at	putative protein contains similarity to rec	---	AT5G65830	1.03	0.04	0.22	0.831179	0.918770	-6.83
258652_at	putative Ras-like GTP-binding protein c	ATRABC2	AT3G09910	1.03	0.05	0.22	0.831168	0.918770	-6.83
260463_at	DNA helicase isolog	RECQ4A	AT1G10930	-1.01	-0.02	-0.22	0.831335	0.918827	-6.83
261174_at	26S proteasome regulatory subunit, put	---	AT1G04810	-1.02	-0.03	-0.22	0.831296	0.918827	-6.83
266969_at	similar to gibberellin-regulated proteins	---	AT2G39540	-1.02	-0.03	-0.22	0.831394	0.918848	-6.83
245181_at	putative protein similarity to various prec	---	AT5G12420	-1.05	-0.07	-0.22	0.83147	0.918887	-6.83
245559_at	glycine-rich protein like	---	AT4G15460	1.02	0.02	0.22	0.831922	0.919313	-6.83
253214_at	putative protein karyopherin alpha 1, D	ARO1	AT4G34940	1.02	0.02	0.22	0.831936	0.919313	-6.83
267552_at	putative purple acid phosphatase precu	PAP13	AT2G32770	1.02	0.02	0.22	0.832015	0.919356	-6.83
263768_x_a	putative Athila retroelement ORF1 prote	---	---	1.01	0.02	0.22	0.832083	0.919387	-6.83
248240_at	CUC2 (dbj|BAA19529.1)	CUC2	AT5G53950	1.02	0.02	0.22	0.832457	0.919755	-6.83
256260_at	hypothetical protein	---	AT3G12440	-1.01	-0.02	-0.22	0.832546	0.919809	-6.83
245962_at	putative protein predicted proteins - Ara	---	AT5G19700	-1.02	-0.03	-0.22	0.832674	0.919861	-6.83
267373_at	unknown protein	CID7	AT2G26280	1.02	0.03	0.22	0.832646	0.919861	-6.83

260517_at	unknown protein	SPP1	AT1G51420	1.01	0.02	0.22	0.832881	0.920045	-6.83
257542_at	hypothetical protein predicted by genem	---	AT3G26050	1.01	0.02	0.22	0.832981	0.920067	-6.83
266827_at	putative serine carboxypeptidase I	SCPL12	AT2G22920	1.02	0.02	0.22	0.832944	0.920067	-6.83
265329_at	putative succinate dehydrogenase flavo	SDH1-2	AT2G18450	1.02	0.03	0.22	0.833046	0.920094	-6.83
261016_at	beta-glucosidase, putative similar to be	BGLU40	AT1G26560	1.06	0.09	0.22	0.833283	0.920203	-6.83
256226_at	unknown protein ; supported by cDNA: g	ATDI19	AT1G56280	-1.02	-0.03	-0.22	0.833196	0.920203	-6.83
261959_s_a	polyprotein, putative similar to polyprote	---	---	1.02	0.03	0.22	0.833377	0.920203	-6.83
261517_at	unknown protein ; supported by full-leng	---	AT1G71780	-1.02	-0.03	-0.22	0.833387	0.920203	-6.83
246291_at	hypothetical protein ; supported by full-l	---	AT3G56820	-1.02	-0.03	-0.22	0.833363	0.920203	-6.83
262551_at	putative heat shock transcription factor s	RUB1	AT1G31340	-1.02	-0.03	-0.22	0.833363	0.920203	-6.83
248887_at	Expressed protein ; supported by full-ler	---	AT5G46115	1.02	0.03	0.22	0.833456	0.920234	-6.83
257314_at	integral membrane protein, putative cor	---	AT3G26590	-1.04	-0.06	-0.22	0.833541	0.920243	-6.83
251694_s_a	putative protein NAM (no apical meriste	anac063	AT3G55210 /	1.01	0.02	0.22	0.833544	0.920243	-6.83
261527_at	hypothetical protein similar to putative re	---	AT1G14390	-1.02	-0.03	-0.22	0.833774	0.920452	-6.83
267192_at	hypothetical protein predicted by grail	---	AT2G30890	-1.02	-0.03	-0.22	0.834068	0.920509	-6.83
253807_at	putative GPI-anchored protein GPI-anc	---	AT4G28280	-1.02	-0.03	-0.22	0.834006	0.920509	-6.83
252407_at	chloroplast NAD-dependent malate deh	MDH	AT3G47520	1.02	0.03	0.22	0.833944	0.920509	-6.83
262675_at	anter-specific proline-rich -like protein (A	EXL6	AT1G75930	1.02	0.03	0.22	0.833892	0.920509	-6.83
251509_at	pectinesterase precursor-like protein pe	---	AT3G59010	-1.05	-0.07	-0.22	0.834036	0.920509	-6.83
261978_at	Athila retroelment ORF 1, putative simil	---	---	1.01	0.02	0.22	0.833998	0.920509	-6.83
255944_at	putative protein	---	---	1.02	0.03	0.22	0.834196	0.920607	-6.83
245670_at	mitochondrial protein (AtJ1), putative si	ATJ1	AT1G28210	-1.03	-0.05	-0.22	0.834239	0.920609	-6.83
251719_at	putative protein PUTATIVE PROTEIN A	---	AT3G56140	1.02	0.03	0.22	0.83433	0.920621	-6.83
265509_at	putative retroelement pol polyprotein co	---	---	-1.02	-0.03	-0.22	0.834312	0.920621	-6.83
245453_at	disease resistance RPP5 like protein	---	AT4G16900	1.02	0.02	0.22	0.834474	0.920690	-6.83
266025_at	putative retroelement pol polyprotein	---	---	-1.02	-0.02	-0.22	0.83444	0.920690	-6.83
252165_at	hypothetical protein ;supported by full-le	---	AT3G50550	-1.02	-0.03	-0.22	0.834644	0.920834	-6.83
262824_at	putative DNA binding protein similar to	RBP45B	AT1G11650	-1.01	-0.02	-0.22	0.834722	0.920874	-6.83
248041_at	unknown protein ;supported by full-leng	emb2731	AT5G55940	1.01	0.02	0.22	0.834836	0.920956	-6.83
259146_at	putative glycerol-3-phosphate dehydrog	SDP6	AT3G10370	1.02	0.03	0.22	0.834984	0.921030	-6.83
249005_at	terpene cyclase/synthase	---	AT5G44630	1.01	0.02	0.22	0.834965	0.921030	-6.83
245551_at	cytochrome P450 like protein	CYP705A2	AT4G15350	-1.01	-0.02	-0.22	0.835061	0.921071	-6.83
249932_at	unknown protein	---	AT5G22390	1.05	0.07	0.22	0.835299	0.921260	-6.83
252505_at	dehydrogenase -like protein alcohol del	---	AT3G46170	1.02	0.03	0.22	0.835314	0.921260	-6.83
265363_at	hypothetical protein predicted by gensca	---	---	1.01	0.02	0.22	0.835379	0.921288	-6.83

247423_at	putative protein predicted proteins, Aral	---	AT5G62830	1.01	0.02	0.22	0.83556	0.921369	-6.83
263498_at	unknown protein ; supported by cDNA:	LSH10	AT2G42610	1.09	0.12	0.22	0.835573	0.921369	-6.83
263915_at	hypothetical protein predicted by gensca	---	AT2G36430	1.05	0.07	0.22	0.835502	0.921369	-6.83
267484_at	E2, ubiquitin-conjugating enzyme 2 (UB	ATUBC2	AT2G02760	1.02	0.02	0.22	0.835743	0.921511	-6.83
245786_at	G-Box binding protein, putative similar t	---	AT1G32150	-1.01	-0.02	-0.22	0.835833	0.921521	-6.83
263940_at	putative calcium-dependent protein kina	CPK25	AT2G35890	-1.01	-0.02	-0.22	0.835823	0.921521	-6.83
249761_at	acetyl-CoA:benzylalcohol acetyltranfera	---	AT5G23970	-1.02	-0.03	-0.22	0.83588	0.921529	-6.83
254207_at	putative protein Dof zinc finger protein -	---	AT4G24060	1.02	0.03	0.21	0.83615	0.921571	-6.83
254222_at	hypothetical protein	---	AT4G23840	-1.02	-0.03	-0.22	0.836031	0.921571	-6.83
264302_at	ATPase 70 kDa subunit, putative simila	VHA-A	AT1G78900	-1.02	-0.03	-0.22	0.836111	0.921571	-6.83
251560_at	squamosa promoter-binding protein hor	SPL15	AT3G57920	1.02	0.03	0.21	0.836161	0.921571	-6.83
257739_at	unknown protein	---	AT3G27470	1.02	0.03	0.22	0.835978	0.921571	-6.83
247974_at	putative protein contains similarity to tra	---	AT5G56780	1.02	0.02	0.22	0.836136	0.921571	-6.83
246184_at	beta-D-glucan exohydrolase - like prote	---	AT5G20950	-1.03	-0.04	-0.21	0.836269	0.921645	-6.83
252259_at	putative protein acidic ribosomal protein	---	AT3G49460	-1.03	-0.04	-0.21	0.836382	0.921726	-6.83
248359_at	unknown protein	---	AT5G52410	-1.02	-0.03	-0.21	0.836722	0.921878	-6.83
249643_at	putative transposase putative transposa	---	---	1.02	0.03	0.21	0.836702	0.921878	-6.83
251569_at	putative protein several hypothetical pro	---	AT3G58290	-1.02	-0.03	-0.21	0.836653	0.921878	-6.83
250499_at	beta-xylosidase - like protein beta-xylos	BXL3	AT5G09730	-1.02	-0.02	-0.21	0.836689	0.921878	-6.83
261079_s_a	transcription factor IIA large subunit sim	---	AT1G07470 /	-1.02	-0.02	-0.21	0.836659	0.921878	-6.83
246823_at	putative protein	---	AT5G26970	-1.01	-0.02	-0.21	0.836882	0.921938	-6.83
258465_at	unknown protein	PMEI2	AT3G17220	1.02	0.03	0.21	0.836871	0.921938	-6.83
257467_at	hypothetical protein similar to hypothetic	LBD4	AT1G31320	-1.03	-0.04	-0.21	0.836898	0.921938	-6.83
246242_at	putative protein	---	AT4G36600	-1.02	-0.04	-0.21	0.83708	0.921960	-6.83
253006_at	putative amino acid transport protein ar	---	AT4G38250	1.02	0.03	0.21	0.837055	0.921960	-6.83
245923_at	putative protein predicted proteins, Aral	---	AT5G28820	-1.02	-0.03	-0.21	0.837052	0.921960	-6.83
252810_at	putative protein several hypothetical pro	---	---	1.02	0.03	0.21	0.837057	0.921960	-6.83
260402_at	putative gamma-glutamyltransferase (li	GGT3	AT1G69820	1.02	0.03	0.21	0.837157	0.922001	-6.83
252203_at	hypothetical protein	---	AT3G50320	-1.02	-0.02	-0.21	0.837565	0.922368	-6.83
246497_at	putative protein hypothetical proteins - A	---	AT5G16220	-1.03	-0.05	-0.21	0.837572	0.922368	-6.83
258877_at	putative expansin precursor similar to ex	ATEXPA1	AT3G03220	1.04	0.06	0.21	0.837674	0.922436	-6.83
247845_at	beta-1,3 glucanase - like protein beta-1	---	AT5G58090	1.02	0.02	0.21	0.837916	0.922555	-6.83
257312_at	Expressed protein ; supported by full-ler	AT3G2659	---	1.02	0.02	0.21	0.837909	0.922555	-6.83
248125_at	2S storage protein-like	---	AT5G54740	1.02	0.03	0.21	0.837944	0.922555	-6.83
264029_at	unknown protein	MRH6	AT2G03720	1.02	0.02	0.21	0.837944	0.922555	-6.83

255146_at	putative protein disease resistance prot	---	AT4G08450	-1.01	-0.02	-0.21	0.837993	0.922564	-6.83
260722_at	protein phosphatase-2C, putative simila	---	AT1G48040	-1.03	-0.04	-0.21	0.838082	0.922618	-6.83
266525_at	putative tetracycline transporter protein	MEE15	AT2G16970	1.02	0.03	0.21	0.838352	0.922871	-6.83
246346_at	hypothetical protein	---	AT3G56810	-1.03	-0.04	-0.21	0.838479	0.922966	-6.83
248923_at	putative protein similar to unknown prote	atnudt11	AT5G45940	1.02	0.03	0.21	0.838558	0.923009	-6.83
256326_at	RING zinc-finger protein, putative conta	---	AT3G02340	-1.02	-0.03	-0.21	0.838646	0.923017	-6.83
262019_s_a	hypothetical protein predicted by gensca	---	---	1.02	0.02	0.21	0.83863	0.923017	-6.83
259995_at	putative golgi transport complex protein	---	AT1G67930	1.02	0.03	0.21	0.838692	0.923020	-6.83
256175_at	unknown protein	---	AT1G51670	-1.02	-0.02	-0.21	0.83873	0.923020	-6.83
255579_at	putative bHLH DNA-binding protein	---	AT4G01460	1.04	0.05	0.21	0.83888	0.923129	-6.83
252719_at	putative protein predicted protein, Arabi	---	AT3G43950	1.02	0.02	0.21	0.83891	0.923129	-6.83
256346_s_a	unknown protein	---	AT2G15040	-1.01	-0.02	-0.21	0.839033	0.923220	-6.83
247975_at	putative protein similar to unknown prote	---	AT5G56800	1.01	0.02	0.21	0.839184	0.923341	-6.83
258322_at	putative selenocysteine methyltransfera	HMT3	AT3G22740	-1.05	-0.08	-0.21	0.839285	0.923408	-6.83
259769_at	RNA-binding protein MEI2, putative sim	AML5	AT1G29400	1.03	0.04	0.21	0.839411	0.923502	-6.83
260393_at	putative lipase similar to lipase GB:CAA	---	AT1G73920	1.02	0.03	0.21	0.839632	0.923656	-6.83
255874_at	hypothetical protein predicted by gensca	ETG1	AT2G40550	-1.05	-0.08	-0.21	0.839606	0.923656	-6.83
251308_at	putative protein several hypothetical pro	GAUT1	AT3G61130	1.02	0.02	0.21	0.839944	0.923955	-6.83
264346_at	putative amino-cyclopropane-carboxylic	---	AT1G12010	-1.02	-0.02	-0.21	0.84005	0.924027	-6.83
245425_at	carboxyl-terminal proteinase like protein	UCH3	AT4G17510	-1.01	-0.02	-0.21	0.840177	0.924039	-6.83
266473_at	unknown protein	---	AT2G31110	1.05	0.07	0.21	0.840149	0.924039	-6.83
264697_at	cyclin, putative similar to cyclin D GI:36	CYCD1;1	AT1G70210	1.08	0.11	0.21	0.840207	0.924039	-6.83
260382_at	unknown protein	---	AT1G73850	-1.02	-0.03	-0.21	0.840224	0.924039	-6.83
267603_at	unknown protein ; supported by cDNA:	ATZW10	AT2G32900	1.02	0.03	0.21	0.840279	0.924056	-6.83
258246_s_a	hypothetical protein similar to putative tr	---	---	1.01	0.02	0.21	0.840408	0.924153	-6.83
259588_at	unknown protein ;supported by full-lengt	---	AT1G27930	-1.01	-0.02	-0.21	0.840547	0.924262	-6.83
246363_at	hypothetical protein	---	AT1G40390	-1.02	-0.03	-0.21	0.840803	0.924498	-6.83
247872_at	putative protein similar to unknown prote	---	AT5G57670	1.02	0.03	0.21	0.840883	0.924542	-6.83
252260_at	putative protein several hypothetical pro	---	AT3G49480	1.02	0.03	0.21	0.841016	0.924554	-6.83
260960_at	calcium-binding protein, putative similar	---	AT1G05990	-1.02	-0.03	-0.21	0.840988	0.924554	-6.83
263815_at	hypothetical protein predicted by gensca	---	AT2G10020	1.03	0.04	0.21	0.840976	0.924554	-6.83
261717_at	helix-loop-helix protein homolog, putativ	BEE1	AT1G18400	1.06	0.09	0.21	0.84127	0.924566	-6.83
254960_at	predicted protein	---	AT4G10845	1.02	0.03	0.21	0.841083	0.924566	-6.83
255748_at	hypothetical protein predicted by genem	---	AT1G32000	1.01	0.02	0.21	0.84127	0.924566	-6.83
250997_at	putative protein histone H2B-2, tomato,	---	AT5G02570	1.02	0.02	0.21	0.841119	0.924566	-6.83

249349_at	putative transcription factor MYB24 ; su	MYB24	AT5G40350	-1.02	-0.02	-0.21	0.841181	0.924566	-6.83
250451_at	cdc2-like protein kinase cdc2-like protei	CDKC;1	AT5G10270	1.02	0.03	0.21	0.841269	0.924566	-6.83
245466_at	glucosyltransferase like protein	---	AT4G16600	1.02	0.03	0.21	0.841694	0.924988	-6.83
261904_at	unknown protein contains similarity to a	---	AT1G65040	-1.01	-0.02	-0.21	0.841787	0.925045	-6.83
264114_at	hypothetical protein predicted by gensca	CDT1A	AT2G31270	1.04	0.05	0.21	0.841883	0.925106	-6.83
263917_at	putative AP2 domain transcription factor	HRD	AT2G36450	1.02	0.03	0.21	0.841929	0.925112	-6.83
264863_at	putative peroxidase similar to peroxidas	---	AT1G24110	1.02	0.03	0.21	0.842006	0.925152	-6.83
267425_at	putative berberine bridge enzyme	---	AT2G34810	1.05	0.07	0.21	0.842163	0.925280	-6.83
258771_at	unknown protein ;supported by full-leng	---	AT3G10770	-1.02	-0.02	-0.21	0.842258	0.925282	-6.83
250573_at	putative protein	---	AT5G08220 /	-1.02	-0.03	-0.21	0.842287	0.925282	-6.83
254367_at	hypothetical protein	---	AT4G21700	1.02	0.03	0.21	0.842246	0.925282	-6.83
257039_at	tRNA isopentenyl transferase, putative	ATIPT8	AT3G19160	1.02	0.03	0.21	0.842374	0.925333	-6.83
261363_at	pectinesterase, putative similar to GB:Z	SKS6	AT1G41830	1.11	0.15	0.21	0.842574	0.925352	-6.83
264644_at	hypothetical protein Similar to Caenorha	CAX11	AT1G08960	-1.02	-0.03	-0.21	0.842553	0.925352	-6.83
256348_at	hypothetical protein predicted by genem	---	AT1G54880	-1.02	-0.02	-0.21	0.842527	0.925352	-6.83
256646_at	hypothetical protein predicted by genem	---	AT3G13590	1.02	0.03	0.21	0.842593	0.925352	-6.83
262384_at	disease resistance protein, putative sim	---	AT1G72950	-1.02	-0.03	-0.21	0.842574	0.925352	-6.83
255322_at	putative protein	---	---	-1.01	-0.02	-0.21	0.842729	0.925421	-6.83
255425_s_a	putative protein	---	AT4G02950 /	1.02	0.03	0.21	0.842737	0.925421	-6.83
257477_at	unknown protein	---	AT1G10660	-1.02	-0.03	-0.21	0.842783	0.925427	-6.83
248716_at	unknown protein ;supported by full-leng	---	AT5G48210	-1.02	-0.03	-0.21	0.842946	0.925516	-6.83
254774_at	hypothetical protein	---	AT4G13440	1.03	0.04	0.21	0.84293	0.925516	-6.83
252868_at	putative protein tubulin-folding cofactor	POR	AT4G39920	1.01	0.02	0.21	0.843128	0.925672	-6.83
262904_at	chaperone, putative similar to chaperon	---	AT1G59725	1.02	0.03	0.21	0.8435	0.926035	-6.83
251631_at	putative protein several hypothetical pro	---	AT3G57430	1.02	0.03	0.21	0.8436	0.926101	-6.83
265042_at	unknown protein Similar to acid phosph	---	AT1G04040	-1.05	-0.07	-0.20	0.843721	0.926140	-6.83
251105_at	putative protein unknown protein At2g3	ATSCAR4	AT5G01730	1.04	0.05	0.20	0.843734	0.926140	-6.83
260152_at	putative IAA6 protein similar to IAA6 pro	IAA6	AT1G52830	-1.04	-0.05	-0.20	0.843757	0.926140	-6.83
261961_at	hypothetical protein predicted by genem	---	AT1G36510	-1.02	-0.03	-0.20	0.843867	0.926215	-6.83
254678_at	hypothetical protein	---	AT4G18500	-1.02	-0.02	-0.20	0.843959	0.926272	-6.83
259621_at	unknown protein	---	AT1G42710	1.01	0.02	0.20	0.844178	0.926467	-6.83
258381_at	kinesin-like protein similar to mitotic cen	KINESIN-1	AT3G16630	-1.02	-0.03	-0.20	0.844308	0.926517	-6.83
266710_at	putative Ser/Thr protein kinase	---	AT2G46850	1.02	0.02	0.20	0.844345	0.926517	-6.83
260778_at	splicing factor, putative similar to huma	---	AT1G14640	1.02	0.03	0.20	0.844328	0.926517	-6.83
248213_at	putative protein similar to unknown prote	AtGRF7	AT5G53660	-1.02	-0.02	-0.20	0.844458	0.926597	-6.83

249129_at	cyclin A-type	CYCA3;1	AT5G43080	1.02	0.02	0.20	0.844896	0.927033	-6.83
253320_at	putative protein ThiJ protein, Escherich	---	AT4G34020	-1.02	-0.02	-0.20	0.845142	0.927213	-6.83
250059_at	peroxidase ATP13a ; supported by full-	---	AT5G17820	1.02	0.02	0.20	0.845134	0.927213	-6.83
263174_at	jasmonate inducible protein, putative si	ESP	AT1G54040	-1.04	-0.06	-0.20	0.845286	0.927327	-6.83
257718_at	organ separation protein, putative simil	anac058	AT3G18400	1.02	0.03	0.20	0.845424	0.927388	-6.83
252155_at	putative protein	---	AT3G50920	1.02	0.03	0.20	0.845411	0.927388	-6.83
264824_at	unknown protein similar to gb|T45484,	2A6	---	-1.03	-0.04	-0.20	0.845526	0.927411	-6.83
266134_s_a	putative beta-expansin	---	AT1G65680 /	-1.02	-0.02	-0.20	0.845503	0.927411	-6.83
256163_at	terpene cyclase, putative similar to terp	---	AT1G48820	-1.01	-0.02	-0.20	0.845707	0.927565	-6.83
260856_at	TINY-like protein similar to TINY GB:CA	---	AT1G21910	1.07	0.10	0.20	0.845809	0.927633	-6.83
260767_s_a	unknown protein ; supported by full-leng	---	AT1G49140 /	1.02	0.02	0.20	0.846037	0.927838	-6.83
252616_at	serine threonine-protein kinase-like pro	GRIK1	AT3G45240 /	-1.02	-0.03	-0.20	0.846211	0.927985	-6.83
258371_at	hypothetical protein contains similarity t	---	AT3G14410	1.02	0.03	0.20	0.846255	0.927988	-6.83
265423_at	unknown protein	---	AT2G20790	1.03	0.04	0.20	0.846455	0.928163	-6.83
253515_at	auxin induced like-protein auxin-induce	---	AT4G31320	1.02	0.03	0.20	0.846622	0.928261	-6.83
258767_at	putative (1-4)-beta-mannan endohydrola	---	AT3G10890	1.01	0.02	0.20	0.846626	0.928261	-6.83
256085_at	hypothetical protein predicted by gensca	---	AT1G20760	-1.01	-0.02	-0.20	0.84667	0.928264	-6.83
247010_at	60S ribosomal protein L26 ;supported b	---	AT5G67510	1.04	0.06	0.20	0.846794	0.928355	-6.83
260074_at	putative ras-related GTP-binding protein	AtRABA6a	AT1G73640	1.02	0.02	0.20	0.846901	0.928428	-6.83
246676_at	putative protein	---	---	1.01	0.02	0.20	0.846977	0.928457	-6.83
252049_at	putative protein putative and hypothetica	---	AT3G52510	-1.02	-0.02	-0.20	0.847009	0.928457	-6.83
267450_at	hypothetical protein predicted by gensca	---	AT2G33720	1.02	0.03	0.20	0.847108	0.928486	-6.83
254406_at	putative transposable element reverse t	---	---	-1.01	-0.02	-0.20	0.847117	0.928486	-6.83
266871_at	unknown protein	---	AT2G44710	-1.01	-0.02	-0.20	0.84718	0.928511	-6.83
266722_at	unknown protein	FUT2	AT2G03210	-1.02	-0.02	-0.20	0.847316	0.928526	-6.83
249402_at	Expressed protein ; supported by full-ler	---	AT5G40155	1.02	0.02	0.20	0.847289	0.928526	-6.83
260456_at	hypothetical protein	---	AT1G72490	1.02	0.03	0.20	0.847291	0.928526	-6.83
245336_at	Expressed protein ; supported by full-ler	---	AT4G16515	1.07	0.10	0.20	0.847491	0.928674	-6.83
257845_at	unknown protein GC donor splice site at	---	AT3G28430	1.02	0.02	0.20	0.847544	0.928687	-6.83
266888_s_a	putative thiamin pyrophosphokinase ; s	TPK1	AT1G02880 /	-1.02	-0.02	-0.20	0.849139	0.929107	-6.83
253302_at	Expressed protein ; supported by full-ler	---	AT4G33660	-1.02	-0.03	-0.20	0.848596	0.929107	-6.83
264157_at	xyloglucan endotransglycosylase, putat	XTH17	AT1G65310	-1.03	-0.04	-0.20	0.848917	0.929107	-6.83
247517_at	100 kDa coactivator - like protein 100 k	---	AT5G61780	-1.02	-0.03	-0.20	0.848617	0.929107	-6.83
251623_at	MADS transcription factor-like protein a	AGL18	AT3G57390	1.01	0.02	0.20	0.848806	0.929107	-6.83
259496_at	hypothetical protein predicted by gensca	---	AT1G15900	1.02	0.02	0.20	0.848937	0.929107	-6.83

259407_at	protein phosphatase 2A regulatory subu	PP2AA3	AT1G13320	1.01	0.02	0.20	0.849081	0.929107	-6.83
255813_at	hypothetical protein contains Pfam prof	---	AT1G19930	1.02	0.02	0.20	0.848468	0.929107	-6.83
258583_at	putative SRF-type transcription factor co	AGL57	AT3G04100	-1.01	-0.02	-0.20	0.848703	0.929107	-6.83
256955_at	L-ascorbate oxidase precursor, putative	sks11	AT3G13390	1.02	0.03	0.20	0.849017	0.929107	-6.83
266680_s_a	hypothetical protein predicted by genefir	---	AT2G19850 /	1.01	0.02	0.20	0.848276	0.929107	-6.83
264090_at	cytochrome P-450, putative similar to cy	CYP79C1	AT1G79370	-1.02	-0.02	-0.20	0.848935	0.929107	-6.83
255849_at	hypothetical protein predicted by genefir	---	AT2G33320	-1.01	-0.02	-0.20	0.848435	0.929107	-6.83
245945_at	putative protein various predicted prote	ROPGEF1	AT5G19560	1.01	0.02	0.20	0.848118	0.929107	-6.83
263271_s_a	hypothetical protein predicted by gensca	---	---	-1.01	-0.02	-0.20	0.848049	0.929107	-6.83
249328_at	AtRAD3 (dbj|BAA92828.1) ; supported	ATR	AT5G40820	-1.02	-0.03	-0.20	0.849033	0.929107	-6.83
245855_at	sulfate transporter ; supported by cDNA	SULTR4;1	AT5G13550	1.02	0.03	0.20	0.848468	0.929107	-6.83
252781_at	polygalacturonase -like protein polygala	---	AT3G42950	1.02	0.02	0.20	0.848353	0.929107	-6.83
263183_at	putative glucan synthase Highly similar t	CALS1	AT1G05570	1.05	0.07	0.20	0.849135	0.929107	-6.83
259651_at	unknown protein	---	AT1G55280	-1.04	-0.05	-0.20	0.848567	0.929107	-6.83
AFFX-TrpnX	B. subtilis /GEN=trpE, trpD /DB_XREF=	---	---	1.02	0.02	0.20	0.849149	0.929107	-6.83
262105_at	pectin esterase, putative similar to pect	---	AT1G02810	1.02	0.03	0.20	0.848458	0.929107	-6.83
249883_at	Na+/H+ antiporter-like protein	CHX3	AT5G22900	1.01	0.02	0.20	0.848072	0.929107	-6.83
246836_s_a	putative protein MADS box protein AGL	---	AT5G26650 /	1.01	0.02	0.20	0.848995	0.929107	-6.83
246629_at	unknown protein similar to hypothetical	---	AT1G50750	1.02	0.03	0.20	0.84797	0.929107	-6.83
260711_at	myosin, putative similar to myosin GI:43	MYA1	AT1G17580	1.02	0.03	0.20	0.848894	0.929107	-6.83
265004_at	polyprotein, putative similar to polyprote	---	---	-1.02	-0.03	-0.20	0.848594	0.929107	-6.83
260180_at	E2, ubiquitin-conjugating enzyme, putat	MMZ2	AT1G70660	-1.02	-0.03	-0.20	0.848617	0.929107	-6.83
251165_at	putative protein different MAP kinases	---	AT3G63330	1.02	0.03	0.20	0.848253	0.929107	-6.83
251202_at	putative protein predicted protein, C.ele	---	AT3G63040	-1.01	-0.02	-0.20	0.848642	0.929107	-6.83
247888_at	phytocyanin/early nodulin-like protein	---	AT5G57920	-1.02	-0.02	-0.20	0.849203	0.929121	-6.83
260879_at	hypothetical protein predicted by genem	---	AT1G21480	1.02	0.02	0.20	0.849351	0.929150	-6.83
262514_at	NAM(no apical meristem) protein, putat	anac017	AT1G34190	1.01	0.02	0.20	0.849308	0.929150	-6.83
251123_at	putative protein predicted proteins, Ara	---	AT5G01030	1.01	0.02	0.20	0.849348	0.929150	-6.83
250983_at	putative protein In2, Zea mays, EMBL:X	---	AT5G02780	1.06	0.09	0.20	0.849787	0.929508	-6.83
246919_at	putative protein hypothetical protein - R	---	AT5G25460	1.13	0.17	0.20	0.849842	0.929508	-6.83
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J0442	---	---	-1.03	-0.04	-0.20	0.849831	0.929508	-6.83
252079_at	MAP kinase ; supported by cDNA: gi_1	CPuORF4	AT3G51630 /	-1.01	-0.02	-0.20	0.84972	0.929508	-6.83
261758_at	hypothetical protein contains similarity to	ADT6	AT1G08250	1.03	0.04	0.20	0.849944	0.929514	-6.83
252718_at	putative protein predicted proteins, Ara	---	AT3G43940	1.02	0.02	0.20	0.849992	0.929514	-6.83
254114_at	putative protein (fragment) MtN21 gene	---	AT4G24980	1.02	0.03	0.20	0.850092	0.929514	-6.83

253587_at	hypothetical protein	---	AT4G30770	-1.02	-0.02	-0.20	0.850009	0.929514	-6.83
253439_at	dimethylaniline monooxygenase - like p	YUC1	AT4G32540	1.02	0.02	0.20	0.850078	0.929514	-6.83
246991_at	peroxidase (emb|CAA66967.1)	---	AT5G67400	1.02	0.02	0.20	0.850051	0.929514	-6.83
252843_at	glycine-rich protein other glycine-rich pr	---	AT3G42130	1.02	0.03	0.20	0.850137	0.929519	-6.83
248847_at	disease resistance protein-like	---	AT5G46510	1.01	0.02	0.20	0.850233	0.929580	-6.83
263872_at	putative cellulose synthase catalytic sub	CESA9	AT2G21770	-1.02	-0.03	-0.20	0.850524	0.929853	-6.83
249818_at	Expressed protein ; supported by cDNA	TUB8	AT5G23860	1.03	0.04	0.20	0.851071	0.929868	-6.83
252110_at	disease resistance-like protein TMV res	---	AT3G51560	-1.01	-0.02	-0.20	0.851014	0.929868	-6.83
262472_at	hypothetical protein similar to putative n	---	AT1G50160	1.01	0.02	0.20	0.85106	0.929868	-6.83
267342_at	putative heme A:farnesyltransferase ; s	COX10	AT2G44520	1.02	0.03	0.20	0.851036	0.929868	-6.83
264503_at	hypothetical protein Similar to Arabidop	---	AT1G09410	-1.01	-0.02	-0.20	0.851017	0.929868	-6.83
256795_at	20S proteasome subunit PAC1 identica	PAC1	AT3G22110	-1.01	-0.02	-0.20	0.850907	0.929868	-6.83
254497_at	Phosphoribosylanthranilate transferase	---	AT4G20080	-1.02	-0.03	-0.20	0.850743	0.929868	-6.83
248077_at	putative protein contains similarity to CH	---	AT5G55770	1.01	0.02	0.20	0.850754	0.929868	-6.83
256375_at	unknown protein	---	AT1G66720	1.01	0.02	0.20	0.85104	0.929868	-6.83
AFFX-Athal	Arabidopsis thaliana /REF=U37281.1 /D	---	---	-1.01	-0.02	-0.20	0.850945	0.929868	-6.83
261642_at	ADP-glucose pyrophosphorylase, putat	APL2	AT1G27680	1.02	0.03	0.20	0.850862	0.929868	-6.83
249614_at	putative protein predicted proteins, Ara	WSD1	AT5G37300	-1.01	-0.02	-0.20	0.850847	0.929868	-6.83
255054_s_a	cellulase-like protein cellulase (EC 3.2.	AtGH9B15	AT4G09740 /	-1.02	-0.02	-0.20	0.850584	0.929868	-6.83
245548_at	cytochrome P450 like protein	CYP702A3	AT4G15310	1.01	0.02	0.20	0.851108	0.929868	-6.83
257806_at	hypothetical protein predicted by gensca	---	AT3G18670	1.02	0.02	0.19	0.851229	0.929955	-6.83
261852_at	unknown protein ;supported by full-lengt	---	AT1G50440	1.01	0.02	0.19	0.85128	0.929966	-6.83
260587_at	unknown protein ; supported by cDNA: g	---	AT1G53210	-1.02	-0.02	-0.19	0.851426	0.930061	-6.83
262691_at	TPR-repeat protein contains multiple TP	---	AT1G62740	-1.02	-0.03	-0.19	0.851448	0.930061	-6.83
251527_at	putative protein hypothetical protein A_	---	AT3G58650	-1.01	-0.02	-0.19	0.85159	0.930127	-6.83
255158_s_a	hypothetical protein	---	---	1.01	0.02	0.19	0.85156	0.930127	-6.83
257017_at	beta-xylosidase, putative similar to beta	---	AT3G19620	1.01	0.02	0.19	0.851837	0.930353	-6.83
245606_at	hypothetical protein	---	AT4G14310	1.02	0.02	0.19	0.851928	0.930406	-6.83
245230_at	hypothetical protein Contains Zinc finge	---	AT4G25610	-1.02	-0.03	-0.19	0.852203	0.930662	-6.83
253075_at	putative disease resistance protein TMV	---	AT4G36150	-1.01	-0.02	-0.19	0.852597	0.930767	-6.83
253241_at	fatty acid elongase 1	KCS18	AT4G34520	1.02	0.03	0.19	0.852586	0.930767	-6.83
262676_at	SKP1/ASK1 (At1) identical to Skp1a GI	SKP1	AT1G75950	1.01	0.02	0.19	0.852561	0.930767	-6.83
252244_at	putative protein some putative proteins -	---	AT3G50130	1.02	0.03	0.19	0.852504	0.930767	-6.83
252955_at	multiubiquitin chain binding protein (MBI	RPN10	AT4G38630	-1.01	-0.02	-0.19	0.852469	0.930767	-6.83
247796_at	Expressed protein ;supported by cDNA:	---	AT5G58782	-1.02	-0.02	-0.19	0.852613	0.930767	-6.83

264225_at	hypothetical protein predicted by genem	---	AT1G67420	1.02	0.04	0.19	0.852625	0.930767	-6.83
265667_at	putative CCAAT-binding transcription fa	NF-YB11	AT2G27470	1.01	0.02	0.19	0.85239	0.930767	-6.83
255111_at	peroxidase C2 precursor like protein pe	---	AT4G08780	-1.12	-0.16	-0.19	0.852692	0.930795	-6.83
255016_at	sucrose-phosphate synthase - like prot	ATSPS4F	AT4G10120	-1.02	-0.03	-0.19	0.852799	0.930868	-6.83
253884_at	heat shock protein 21	HSP21	AT4G27670	1.02	0.03	0.19	0.852946	0.930984	-6.83
246034_at	putative protein FH protein interacting p	---	AT5G08350	1.03	0.04	0.19	0.853052	0.931035	-6.83
257068_at	non-LTR reverse transcriptase, putative	---	---	-1.01	-0.02	-0.19	0.853093	0.931035	-6.83
261555_s_a	hypothetical protein predicted by gensca	---	AT1G63230 /	1.01	0.02	0.19	0.853116	0.931035	-6.83
266984_at	unknown protein ; supported by cDNA:	---	AT2G39570	1.03	0.04	0.19	0.853241	0.931083	-6.83
253645_at	putative protein G protein beta subunit-	VIP3	AT4G29830	-1.01	-0.02	-0.19	0.853214	0.931083	-6.83
249254_at	unknown protein	---	AT5G42110	1.02	0.02	0.19	0.853387	0.931153	-6.83
249603_at	putative protein predicted proteins, Ara	---	AT5G37210	1.01	0.02	0.19	0.853365	0.931153	-6.83
252517_at	receptor-like protein kinase homolog lig	---	AT3G46340	1.02	0.02	0.19	0.853483	0.931214	-6.83
256673_at	unknown protein	FLA15	AT3G52370	1.06	0.09	0.19	0.853692	0.931224	-6.83
246630_at	hypothetical protein predicted by genem	---	AT1G50730	-1.03	-0.04	-0.19	0.853697	0.931224	-6.83
253965_at	hypothetical protein	---	AT4G26490	-1.02	-0.03	-0.19	0.853536	0.931224	-6.83
256330_at	hypothetical protein predicted by genem	---	AT1G76870	1.02	0.03	0.19	0.853602	0.931224	-6.83
265789_at	putative receptor-like protein kinase	---	AT2G01210	1.02	0.02	0.19	0.85365	0.931224	-6.83
259869_at	putative heat shock protein predicted by	---	AT1G76770	-1.02	-0.02	-0.19	0.853752	0.931240	-6.83
260632_at	homeobox protein, putative similar to h	STM	AT1G62360	1.02	0.02	0.19	0.853928	0.931307	-6.83
260748_at	RING-H2 finger protein RHA3a, putativ	---	AT1G49210	1.06	0.08	0.19	0.853936	0.931307	-6.83
245344_at	F-box protein family, AtFBL4 contains s	---	AT4G15475	1.02	0.03	0.19	0.8539	0.931307	-6.83
260560_at	putative endochitinase	---	AT2G43590	-1.03	-0.04	-0.19	0.854093	0.931388	-6.83
252396_at	hypothetical protein	---	AT3G47980	1.01	0.02	0.19	0.854069	0.931388	-6.83
244915_s_a	hypothetical protein	---	---	-1.01	-0.02	-0.19	0.854188	0.931404	-6.83
245369_at	Expressed protein ; supported by full-ler	---	AT4G15975	1.03	0.04	0.19	0.85415	0.931404	-6.83
260756_at	hypothetical protein contains similarity t	---	AT1G48970	1.01	0.02	0.19	0.854339	0.931480	-6.83
254554_at	hypothetical protein	---	AT4G19550	1.02	0.02	0.19	0.854307	0.931480	-6.83
263328_at	hypothetical protein similar to hypothetic	---	AT2G15280	-1.02	-0.03	-0.19	0.854636	0.931758	-6.83
265497_at	putative non-LTR retroelement reverse t	---	---	1.04	0.05	0.19	0.854833	0.931928	-6.83
252301_at	putative protein various predicted prote	EMB2261	---	1.02	0.03	0.19	0.85491	0.931968	-6.83
258146_at	putative WD-repeat protein (WDR1-like	---	AT3G18060	-1.02	-0.02	-0.19	0.854985	0.932006	-6.83
262317_at	unknown protein ;supported by full-leng	EDA4	AT2G48140	-1.03	-0.04	-0.19	0.85507	0.932053	-6.83
245435_at	hypothetical protein	AT4G1714	---	-1.01	-0.02	-0.19	0.85525	0.932205	-6.83
247162_at	xyloglucan endo-transglycosylase-like p	---	AT5G65730	1.04	0.06	0.19	0.855458	0.932211	-6.83

250165_at	putative protein many predicted protein	---	AT5G15290	-1.01	-0.02	-0.19	0.85543	0.932211	-6.83
260281_at	unknown protein	---	AT1G80500	1.02	0.02	0.19	0.855412	0.932211	-6.83
256750_at	unknown protein contains Pfam profile:	---	AT3G27150	-1.02	-0.03	-0.19	0.855512	0.932211	-6.83
256924_at	Anthocyanin 5-aromatic acyltransferase	AT5MAT	AT3G29590	-1.02	-0.02	-0.19	0.855506	0.932211	-6.83
252237_at	putative protein lateral suppressor prote	---	AT3G49950	1.02	0.03	0.19	0.855582	0.932211	-6.83
251844_at	putative protein retinoblastoma-associa	---	AT3G54630	1.02	0.02	0.19	0.855447	0.932211	-6.83
262267_at	hypothetical protein predicted by gensca	---	---	-1.01	-0.02	-0.19	0.855556	0.932211	-6.83
253405_at	transcription factor TINY homolog trans	---	AT4G32800	1.03	0.04	0.19	0.855881	0.932268	-6.83
258356_at	unknown protein	---	AT3G14340	-1.02	-0.03	-0.19	0.855954	0.932268	-6.83
267186_at	unknown protein ; supported by cDNA:	---	AT2G44090	1.01	0.02	0.19	0.855823	0.932268	-6.83
258175_at	FKBP-type peptidyl-prolyl cis-trans ison	TWD1	AT3G21640	-1.02	-0.02	-0.19	0.855962	0.932268	-6.83
248361_at	putative protein similar to unknown prote	EDA41	AT5G52460	1.02	0.02	0.19	0.855776	0.932268	-6.83
246533_at	putative protein	---	AT5G15880	-1.02	-0.03	-0.19	0.855957	0.932268	-6.83
258618_at	Expressed protein ; supported by cDNA	GASA5	AT3G02885	1.02	0.03	0.19	0.855825	0.932268	-6.83
247953_at	cytochrome P450	CYP71B1(	AT5G57260	-1.01	-0.02	-0.19	0.855768	0.932268	-6.83
247248_at	putative protein contains similarity to unl	---	AT5G64560	1.03	0.04	0.19	0.856044	0.932269	-6.83
255545_at	putative polygalacturonidase similar to	---	AT4G01890	1.01	0.02	0.19	0.85604	0.932269	-6.83
258059_at	NAM-like protein (No Apical Meristem)	ATNAC3	AT3G29035	1.02	0.03	0.19	0.856175	0.932281	-6.83
246176_at	putative protein DYNAMIN-LIKE PROT	---	AT5G28410	1.01	0.02	0.19	0.85613	0.932281	-6.83
260432_at	putative DNA binding protein similar to D	WRKY9	AT1G68150	1.02	0.03	0.19	0.856178	0.932281	-6.83
263837_at	unknown protein	---	AT2G04500	1.01	0.02	0.19	0.856307	0.932377	-6.83
266432_s_a	putative gag-protease polyprotein	---	---	1.01	0.02	0.19	0.856352	0.932381	-6.83
265888_at	putative cleavage and polyadenylation s	RIE1	AT2G01735	1.01	0.02	0.19	0.856399	0.932388	-6.83
248838_at	carnitine/acylcarnitine translocase-like p	BOU	AT5G46800	-1.03	-0.04	-0.19	0.856746	0.932461	-6.83
259801_at	blue copper protein, putative similar to (	---	AT1G72230	1.04	0.05	0.19	0.856664	0.932461	-6.83
262829_at	auxin-independent growth promoter, pu	---	AT1G14970	-1.03	-0.04	-0.19	0.856698	0.932461	-6.83
261399_at	receptor protein kinase, putative similar	---	AT1G79620	1.02	0.03	0.19	0.85661	0.932461	-6.83
260063_at	unknown protein contains Pfam profile:	---	AT1G73720	-1.02	-0.02	-0.19	0.856741	0.932461	-6.83
259005_at	unknown protein similar to nodule-speci	---	AT3G01930	1.02	0.03	0.19	0.856752	0.932461	-6.83
263176_at	UDP-glucose:indole-3-acetate beta-D-g	UGT75B2	AT1G05530	-1.01	-0.02	-0.19	0.856634	0.932461	-6.83
251828_at	putative protein unnamed sequence, H	---	AT3G55070	-1.02	-0.02	-0.19	0.856877	0.932463	-6.83
255374_at	hypothetical protein	---	---	1.01	0.02	0.19	0.856869	0.932463	-6.83
253123_at	thaumatin-like protein thaumatin-like pr	---	AT4G36000	-1.02	-0.03	-0.19	0.856831	0.932463	-6.83
260701_at	heat shock transcription factor HSF8, p	ATHSFA1I	AT1G32330	1.02	0.03	0.19	0.857057	0.932481	-6.83
252776_at	putative protein predicted proteins, Ara	---	AT3G42940	-1.02	-0.02	-0.19	0.857047	0.932481	-6.83

261994_at	hypothetical protein contains similarity to	---	AT1G33640	1.01	0.02	0.19	0.856988	0.932481	-6.83
259049_at	unknown protein	---	AT3G03370	-1.02	-0.03	-0.19	0.856938	0.932481	-6.83
260645_at	hypothetical protein predicted by genem	TTL1	AT1G53300	-1.03	-0.04	-0.19	0.857455	0.932736	-6.83
245909_at	putative protein DNA-directed RNA poly	---	AT5G09380	-1.02	-0.03	-0.19	0.85743	0.932736	-6.83
259857_at	hypothetical protein predicted by genefir	---	AT1G68430	1.02	0.02	0.19	0.857409	0.932736	-6.83
264493_at	unknown protein similar to multiple exos	GUT2	AT1G27440	-1.03	-0.04	-0.19	0.857354	0.932736	-6.83
255565_at	putative CHP-rich zinc finger protein sir	---	AT4G01760	1.01	0.02	0.19	0.857633	0.932885	-6.83
262655_s_a	putative mandelonitrile lyase similar to r	---	AT1G14185 /	-1.01	-0.02	-0.19	0.857716	0.932931	-6.83
253748_at	putative protein RNA-binding protein Ev	---	AT4G28990	1.02	0.03	0.19	0.857832	0.933001	-6.83
257201_at	unknown protein	---	AT3G23740	-1.02	-0.02	-0.19	0.857862	0.933001	-6.83
245568_at	hypothetical protein	---	AT4G14650	-1.02	-0.03	-0.19	0.857974	0.933078	-6.83
263028_at	protein kinase, putative similar to PROT	---	AT1G24030	-1.02	-0.03	-0.19	0.858061	0.933078	-6.83
254354_at	hypothetical protein	---	AT4G22370	1.01	0.02	0.19	0.8581	0.933078	-6.83
265517_at	putative S1 self-incompatibility protein	---	AT2G06090	1.01	0.02	0.19	0.858205	0.933078	-6.83
250560_at	replication factor A - like protein replicat	RPA70B	AT5G08020	1.03	0.04	0.19	0.858219	0.933078	-6.83
256004_at	retroelement pol polyprotein, putative	---	---	-1.01	-0.02	-0.19	0.858069	0.933078	-6.83
261641_at	hypothetical protein similar to hypothetic	---	AT1G27670	1.03	0.04	0.19	0.858145	0.933078	-6.83
246735_at	histone H2A-like protein histone H2A - l	HTA7	AT5G27670	-1.02	-0.02	-0.19	0.858421	0.933119	-6.83
255181_at	predicted protein of unknown function	---	---	1.02	0.02	0.19	0.858385	0.933119	-6.83
245580_at	hypothetical protein	---	AT4G14820	-1.02	-0.03	-0.19	0.85839	0.933119	-6.83
260265_at	hypothetical protein similar to hypothetic	LBD42	AT1G68510	-1.02	-0.03	-0.19	0.858353	0.933119	-6.83
249587_at	putative protein copper homeostasis fac	---	AT5G37860	-1.01	-0.02	-0.19	0.858578	0.933246	-6.83
264896_at	Hypothetical protein similar to endo-1,4	AtGH9B6	AT1G23210	1.01	0.02	0.19	0.858649	0.933279	-6.83
264567_s_a	putative peroxidase ATP12a Strong sim	---	AT1G05240 /	-1.02	-0.02	-0.18	0.85871	0.933300	-6.83
254143_at	putative protein histidine-rich calcium-b	---	AT4G24680	1.01	0.02	0.18	0.85882	0.933375	-6.83
249559_at	putative protein	---	AT5G38320	1.02	0.03	0.18	0.858939	0.933416	-6.83
245214_at	F12A21.1 hypothetical protein	---	AT1G67855	1.01	0.02	0.18	0.858931	0.933416	-6.83
247190_at	D-type cyclin (emb|CAB41347.1) ;supp	CYCD4;1	AT5G65420	1.02	0.02	0.18	0.859069	0.933513	-6.83
267201_at	putative protein kinase contains a protei	---	AT2G31010	-1.03	-0.04	-0.18	0.859369	0.933757	-6.83
256660_at	hypothetical protein similar to hypothetic	---	AT3G12060	1.02	0.02	0.18	0.859376	0.933757	-6.83
248987_at	dimethylaniline monooxygenase (N-oxid	---	AT5G45180	1.01	0.02	0.18	0.859545	0.933897	-6.83
245816_at	hypothetical protein similar to hypothetic	---	AT1G26210	-1.03	-0.05	-0.18	0.85972	0.933997	-6.83
245073_at	putative glucosyltransferase	---	AT2G23210	-1.01	-0.02	-0.18	0.859708	0.933997	-6.83
246671_at	putative protein	---	---	1.01	0.02	0.18	0.859834	0.934077	-6.83
255175_at	putative glucosyltransferase ;supported	ATCSLC1	AT4G07960	-1.02	-0.02	-0.18	0.859945	0.934152	-6.83

264480_at	hypothetical protein predicted by genem	EFS	AT1G77300	1.02	0.02	0.18	0.86008	0.934187	-6.83
246100_at	putative protein predicted protein, Arabi	---	---	-1.01	-0.02	-0.18	0.860029	0.934187	-6.83
261329_at	hypothetical protein predicted by genem	---	AT1G44890	1.02	0.02	0.18	0.860099	0.934187	-6.83
247379_at	unknown protein	---	---	-1.02	-0.03	-0.18	0.860168	0.934198	-6.83
250152_at	putative protein predicted proteins, Arat	---	AT5G15120	1.01	0.02	0.18	0.860194	0.934198	-6.83
247035_at	putative protein similar to unknown prote	ALC	AT5G67110	1.01	0.02	0.18	0.860232	0.934198	-6.83
261272_at	Expressed protein ; supported by cDNA	---	AT1G26665	-1.03	-0.04	-0.18	0.860274	0.934199	-6.83
266971_at	unknown protein	---	AT2G39580	1.03	0.04	0.18	0.860403	0.934257	-6.83
263370_at	hypothetical protein predicted by gensca	---	AT2G20500	1.03	0.04	0.18	0.860451	0.934257	-6.83
252050_at	hypothetical protein	---	AT3G52550	1.02	0.03	0.18	0.860433	0.934257	-6.83
266875_at	putative flavonol synthase	---	AT2G44800	1.02	0.02	0.18	0.860603	0.934363	-6.83
265360_s_a	putative Athila retroelement ORF1 prote	---	---	-1.01	-0.02	-0.18	0.860629	0.934363	-6.83
255831_at	hypothetical protein predicted by gensca	---	AT2G33350	-1.01	-0.02	-0.18	0.860793	0.934496	-6.83
258772_at	putative ubiquinol-cytochrome C reducta	---	AT3G10860	-1.02	-0.03	-0.18	0.86113	0.934796	-6.83
245139_at	putative AT-hook DNA-binding protein h	---	AT2G45430	-1.01	-0.02	-0.18	0.861234	0.934796	-6.83
255875_s_a	putative protein kinase contains a protei	---	AT2G40500 /	-1.02	-0.02	-0.18	0.861206	0.934796	-6.83
245482_at	hypothetical protein	---	AT4G16180	-1.02	-0.03	-0.18	0.861161	0.934796	-6.83
263050_at	unknown protein ; supported by cDNA:	ATVPS11	AT2G05170	-1.01	-0.02	-0.18	0.861316	0.934841	-6.83
245186_at	F12A21.15 hypothetical protein	ARR11	AT1G67710	1.03	0.05	0.18	0.861601	0.935017	-6.83
249736_at	unknown protein	---	AT5G24460	-1.01	-0.02	-0.18	0.861553	0.935017	-6.83
264132_at	hypothetical protein predicted by genem	---	AT1G79100	-1.02	-0.03	-0.18	0.861579	0.935017	-6.83
256572_at	40S RIBOSOMAL PROTEIN S25, puta	---	AT3G30740	1.01	0.02	0.18	0.861682	0.935060	-6.83
254041_at	Expressed protein ; supported by full-ler	---	AT4G25830	-1.05	-0.07	-0.18	0.862123	0.935417	-6.83
251609_at	putative protein hypothetical protein T2	---	AT3G57900	-1.01	-0.02	-0.18	0.862122	0.935417	-6.83
245360_at	naringenin 3-dioxygenase like protein ;s	---	AT4G16330	-1.01	-0.02	-0.18	0.862134	0.935417	-6.83
267391_at	putative beta-glucosidase	BGLU17	AT2G44480	1.02	0.03	0.18	0.862184	0.935427	-6.83
266858_at	unknown protein	GRV2	AT2G26890	-1.01	-0.02	-0.18	0.862353	0.935432	-6.83
257470_at	hypothetical protein predicted by genem	---	AT1G53770	-1.02	-0.03	-0.18	0.862342	0.935432	-6.83
252111_at	propable disease resistance protein dis	---	AT3G51570	1.02	0.03	0.18	0.862273	0.935432	-6.83
257603_at	unknown protein	---	AT3G13820	1.01	0.02	0.18	0.862289	0.935432	-6.83
262670_s_a	transposase [Escherichia coli] must be c	---	---	-1.01	-0.02	-0.18	0.862704	0.935719	-6.83
250677_at	putative protein similar to unknown prote	---	AT5G06520	-1.01	-0.02	-0.18	0.86268	0.935719	-6.83
255119_at	hypothetical protein	---	---	1.01	0.02	0.18	0.86274	0.935719	-6.83
259249_at	hypothetical protein predicted by genefin	---	AT3G07790	-1.02	-0.03	-0.18	0.862806	0.935746	-6.83
258612_at	putative replication factor A similar to re	---	AT3G02920	1.01	0.02	0.18	0.862983	0.935893	-6.83

264562_at	hypothetical protein predicted by genem	---	AT1G55760	-1.03	-0.04	-0.18	0.863114	0.935914	-6.83
250850_at	putative protein ; supported by cDNA: g	---	AT5G04550	-1.02	-0.03	-0.18	0.863125	0.935914	-6.83
251567_at	putative protein several hypothetical pro	---	AT3G58230	1.02	0.02	0.18	0.86307	0.935914	-6.83
245140_at	unknown protein predicted by genefinde	LBD18	AT2G45420	1.01	0.02	0.18	0.863324	0.936085	-6.83
254037_at	hypothetical protein hypothetical protein	ATGDU2	AT4G25760	-1.01	-0.02	-0.18	0.863519	0.936136	-6.84
267366_at	unknown protein ;supported by full-leng	---	AT2G44310 /	-1.01	-0.02	-0.18	0.863459	0.936136	-6.83
252617_at	n-acetylglucosaminyl-phosphatidylinosi	SETH2	AT3G45100	1.01	0.02	0.18	0.863535	0.936136	-6.84
245527_at	putative epoxide hydrolase	---	AT4G15955	1.02	0.03	0.18	0.8635	0.936136	-6.84
263069_at	unknown protein	---	AT2G17590	1.03	0.04	0.18	0.863692	0.936176	-6.84
247879_at	unknown protein	---	AT5G57770	-1.01	-0.02	-0.18	0.863695	0.936176	-6.84
254930_at	putative protein hypothetical protein - A	---	AT4G11450	1.03	0.04	0.18	0.863678	0.936176	-6.84
261757_at	hypothetical protein similar to putative p	---	AT1G08210	1.02	0.03	0.18	0.863749	0.936190	-6.84
258644_at	putative RNA-binding protein contains R	---	AT3G07810	-1.01	-0.02	-0.18	0.863801	0.936202	-6.84
267326_at	putative RNA-binding protein	---	AT2G19380	1.02	0.02	0.18	0.863893	0.936257	-6.84
259806_at	mysoin-like protein similar to GI:235122	---	AT1G47900	1.02	0.03	0.18	0.863988	0.936315	-6.84
267250_at	similar to hookless1 (HLS1)	---	AT2G23060	1.01	0.02	0.18	0.864055	0.936318	-6.84
257996_at	unknown protein	---	AT3G19950	-1.01	-0.02	-0.18	0.864073	0.936318	-6.84
259388_at	steroid sulfotransferase, putative simila	ST4B	AT1G13420	1.01	0.02	0.18	0.864199	0.936322	-6.84
262146_at	membrane protein, putative similar to m	ATRBL5	AT1G52580	1.03	0.04	0.18	0.864199	0.936322	-6.84
263091_at	unknown protein	---	AT2G16200	1.01	0.02	0.18	0.864163	0.936322	-6.84
257233_at	hypothetical protein similar to SF16 prot	IQD10	AT3G15050	1.01	0.02	0.18	0.864279	0.936364	-6.84
266659_at	putative poly(A) polymerase ; supporte	---	AT2G25850	-1.01	-0.02	-0.18	0.864322	0.936366	-6.84
266444_at	putative extensin	---	AT2G43150	1.02	0.03	0.18	0.864453	0.936463	-6.84
263726_at	putative ABC transporter ;supported by	---	AT2G13610	1.06	0.09	0.18	0.864774	0.936767	-6.84
264957_at	F-box protein family, AtFBL5 contains s	SKP2B	AT1G77000	-1.03	-0.04	-0.18	0.864973	0.936893	-6.84
261848_at	pectin methylesterase, putative similar t	---	AT1G11590	1.02	0.02	0.18	0.864951	0.936893	-6.84
256361_at	formyl transferase, putative contains Pf	pde194	AT1G66520	-1.02	-0.03	-0.18	0.865124	0.936999	-6.84
249671_at	putative protein similar to unknown prote	LBD35	AT5G35900	1.01	0.02	0.18	0.865153	0.936999	-6.84
255241_at	putative protein hypothetical protein T5	---	---	-1.01	-0.02	-0.18	0.865317	0.937133	-6.84
252638_at	acyl CoA reductase - protein acyl CoA r	FAR4	AT3G44540	1.02	0.02	0.18	0.865373	0.937149	-6.84
266961_at	Athila retroelement ORF1-like protein	---	---	-1.02	-0.02	-0.18	0.865437	0.937174	-6.84
251402_at	SRG1 - like protein SRG1 protein, Arab	---	AT3G60290	-1.04	-0.05	-0.18	0.865547	0.937248	-6.84
250487_at	putative protein MRS2 protein, Sacchar	---	AT5G09690	1.02	0.03	0.18	0.865668	0.937334	-6.84
261689_at	hypothetical protein contains similarity t	---	AT1G50140	-1.02	-0.03	-0.18	0.86596	0.937561	-6.84
262554_at	hypothetical protein similar to hypothetic	---	AT1G31380	1.01	0.02	0.18	0.865945	0.937561	-6.84

262927_at	hypothetical protein shares similarity to (	---	AT1G65810	-1.01	-0.02	-0.18	0.866059	0.937624	-6.84
264802_at	putative syntaxin-related protein (U3945	SYP111	AT1G08560	-1.03	-0.04	-0.17	0.86631	0.937841	-6.84
246662_at	putative protein	---	AT5G35290	1.01	0.02	0.17	0.866341	0.937841	-6.84
248904_at	Expressed protein ; supported by full-ler	---	AT5G46295	-1.01	-0.02	-0.17	0.866439	0.937902	-6.84
249968_at	putative protein predicted proteins, Aral	---	AT5G19070	1.03	0.04	0.17	0.866679	0.938086	-6.84
266333_at	putative ubiquitin activating enzyme	AXL	AT2G32410	-1.02	-0.02	-0.17	0.866691	0.938086	-6.84
256133_at	hypothetical protein predicted by genem	---	AT1G13570	1.02	0.04	0.17	0.866761	0.938111	-6.84
257335_at	hypothetical protein	---	---	1.01	0.02	0.17	0.866867	0.938111	-6.84
250140_at	putative protein	DRM2	AT5G14620	1.02	0.03	0.17	0.86681	0.938111	-6.84
261142_at	cyclic nucleotide and calmodulin-regula	ATCNGC8	AT1G19780	1.01	0.02	0.17	0.866878	0.938111	-6.84
265491_s_a	putative retroelement pol polyprotein	---	---	1.01	0.02	0.17	0.867012	0.938210	-6.84
259752_at	spore coat protein-like protein similar to	LPR2	AT1G71040	-1.02	-0.03	-0.17	0.867198	0.938331	-6.84
255669_at	predicted protein	MBD3	AT4G00416	1.01	0.02	0.17	0.867205	0.938331	-6.84
264521_at	unknown protein Location of EST gb|T4	---	AT1G10020	1.03	0.05	0.17	0.867389	0.938370	-6.84
258496_at	putative plant adhesion molecule similar	---	AT3G02460	-1.02	-0.03	-0.17	0.867333	0.938370	-6.84
249953_at	FAR1 - like protein far-red impaired res	FRS12	AT5G18960	-1.02	-0.02	-0.17	0.867406	0.938370	-6.84
250474_at	annexin -like protein annexin (AnnAt2),	ANNAT7	AT5G10230	1.01	0.02	0.17	0.867327	0.938370	-6.84
253559_at	1,3-beta-glucanase - like protein 1,3-be	---	AT4G31140	1.01	0.02	0.17	0.867549	0.938470	-6.84
259281_at	putative Myb-related transcription factor	MYB106	AT3G01140	-1.02	-0.02	-0.17	0.86762	0.938470	-6.84
254909_at	putative disease resistance response p	---	AT4G11210	-1.02	-0.02	-0.17	0.867622	0.938470	-6.84
262848_at	unknown protein ; supported by cDNA: g	BPC2	AT1G14685	-1.01	-0.02	-0.17	0.867778	0.938556	-6.84
251746_at	mandelonitrile lyase-like protein ADHES	---	AT3G56060	-1.02	-0.02	-0.17	0.867783	0.938556	-6.84
261541_at	unknown protein contains Pfam profile:	---	AT1G63600	-1.01	-0.02	-0.17	0.867835	0.938567	-6.84
254399_at	G10 - like protein Maternal G10 like pro	---	AT4G21110	1.01	0.02	0.17	0.867924	0.938618	-6.84
266807_at	hypothetical protein	---	AT2G29920	1.02	0.02	0.17	0.868495	0.938969	-6.84
252206_at	centrin	ATCEN2	AT3G50360	-1.01	-0.02	-0.17	0.868486	0.938969	-6.84
248802_at	Expressed protein ; supported by cDNA	---	AT5G47435	1.01	0.02	0.17	0.868468	0.938969	-6.84
246472_at	putative protein predicted protein, Arabi	---	AT5G17130	1.01	0.02	0.17	0.868341	0.938969	-6.84
248183_at	CHP-rich zinc finger protein-like	---	AT5G54040	-1.01	-0.02	-0.17	0.868428	0.938969	-6.84
252782_at	putative protein predicted proteins, Aral	---	---	1.01	0.02	0.17	0.868447	0.938969	-6.84
254339_at	glucosidase like protein furostanol glyc	BGLU3	AT4G22100	-1.01	-0.02	-0.17	0.868616	0.939011	-6.84
265538_at	unknown protein predicted by genscan a	---	AT2G15860	-1.02	-0.03	-0.17	0.868591	0.939011	-6.84
246217_at	APETALA2 protein ; supported by cDNA	AP2	AT4G36920	-1.03	-0.04	-0.17	0.868706	0.939063	-6.84
253685_at	putative protein nucleotide pyrophospha	---	AT4G29710	-1.01	-0.02	-0.17	0.869184	0.939536	-6.84
256598_at	cytochrome P450 homolog, putative sir	BR6OX2	AT3G30180	1.02	0.03	0.17	0.869342	0.939567	-6.84

255677_at	putative calmodulin-binding heat shock	---	AT4G00500	-1.02	-0.03	-0.17	0.869464	0.939567	-6.84
247254_at	CLE21, putative CLAVATA3/ESR-Rela	CLE21	AT5G64800	-1.03	-0.04	-0.17	0.869501	0.939567	-6.84
264050_at	putative non-LTR retroelement reverse t	---	---	-1.02	-0.03	-0.17	0.86946	0.939567	-6.84
265885_at	hypothetical protein predicted by genefi	---	AT2G42330	1.02	0.03	0.17	0.869417	0.939567	-6.84
247219_at	COP1-interacting protein CIP8 ; suppor	CIP8	AT5G64920	-1.01	-0.02	-0.17	0.869362	0.939567	-6.84
261045_at	pathogenesis related protein, putative s	---	AT1G01310	-1.01	-0.02	-0.17	0.869368	0.939567	-6.84
249902_at	unknown protein	---	AT5G22680	-1.02	-0.03	-0.17	0.869793	0.939837	-6.84
265352_at	cytosolic cyclophilin (ROC3) ;supported	ROC3	AT2G16600	-1.01	-0.02	-0.17	0.86998	0.939909	-6.84
247143_at	unknown protein	---	AT5G65580	-1.02	-0.03	-0.17	0.869983	0.939909	-6.84
247678_at	putative zinc transporter ZIP2 - like Z25	ZIP2	AT5G59520	1.03	0.04	0.17	0.869914	0.939909	-6.84
255584_at	putative reverse transcriptase-like protei	---	---	-1.01	-0.02	-0.17	0.87011	0.939997	-6.84
263395_at	putative mitochondrial inner membrane	ATTIM44-1	AT2G20500 /	-1.01	-0.02	-0.17	0.870146	0.939997	-6.84
256658_at	unknown protein	---	AT3G12010 /	1.01	0.02	0.17	0.870211	0.940022	-6.84
253051_at	cyclin cyc1 ; supported by cDNA: gi_16	CYCB1;1	AT4G37490	1.02	0.03	0.17	0.870311	0.940086	-6.84
264446_at	putative nuclear transport factor similar	NTF2A	AT1G27310	-1.01	-0.02	-0.17	0.870593	0.940346	-6.84
251974_at	myb protein(MYB27) contains myb DNA	AtMYB27	AT3G53200	-1.01	-0.02	-0.17	0.87069	0.940367	-6.84
256975_at	unknown protein similar to putative retro	---	AT3G21000	1.02	0.02	0.17	0.870695	0.940367	-6.84
262335_at	hypothetical protein predicted by genem	SPO11-2	AT1G63990	1.01	0.01	0.17	0.870949	0.940508	-6.84
248745_at	unknown protein	---	AT5G48250	-1.02	-0.02	-0.17	0.870894	0.940508	-6.84
258595_at	unknown protein contains Pfam profile:F	---	AT3G04500	-1.01	-0.02	-0.17	0.870925	0.940508	-6.84
254315_at	putative glycine-rich protein glycine-rich	---	---	-1.02	-0.03	-0.17	0.871033	0.940554	-6.84
264576_at	unknown protein Similar to Arabidopsis	---	AT1G05360	1.01	0.02	0.17	0.871124	0.940563	-6.84
261082_at	unknown protein ; supported by cDNA: g	---	AT1G07360	-1.01	-0.01	-0.17	0.871095	0.940563	-6.84
246940_at	expressed protein glucose-6-phosphate	---	AT5G25400	1.01	0.02	0.17	0.871201	0.940593	-6.84
256557_at	hypothetical protein similar to hypothetic	---	---	-1.01	-0.02	-0.17	0.871259	0.940593	-6.84
255124_at	putative self-incompatability RNA-bindin	APUM15	AT4G08560	1.02	0.03	0.17	0.871276	0.940593	-6.84
256092_at	Expressed protein ; supported by full-ler	HMGB3	AT1G20696	-1.01	-0.02	-0.17	0.871497	0.940775	-6.84
252141_at	putative protein	---	AT3G51100	1.01	0.02	0.17	0.871526	0.940775	-6.84
266153_at	hypothetical protein	---	---	1.01	0.02	0.17	0.871706	0.940924	-6.84
264872_at	putative floral homeotic protein, AGL9 s	ʊɔo-03	AT1G24260	1.02	0.03	0.17	0.871859	0.941045	-6.84
259917_at	hypothetical protein predicted by gensca	---	AT1G72580	1.01	0.02	0.17	0.871987	0.941052	-6.84
254793_at	hypothetical protein	---	AT4G12930	-1.01	-0.02	-0.17	0.871989	0.941052	-6.84
260187_at	hypothetical protein	LBD5	AT1G36000	-1.01	-0.02	-0.17	0.871942	0.941052	-6.84
246659_at	putative protein predicted proteins Arabi	---	---	1.01	0.02	0.17	0.872075	0.941100	-6.84
AFFX-r2-At-	/FEATURE=cds-2 /GENE= /LABEL= /PI	---	---	1.01	0.02	0.17	0.872139	0.941124	-6.84

262770_at	hypothetical protein predicted by gensca	---	AT1G13190	-1.02	-0.03	-0.17	0.872287	0.941151	-6.84
252128_at	transcription factor-like protein Arabidop	MNP	AT3G50870	-1.01	-0.02	-0.17	0.87228	0.941151	-6.84
263916_at	hypothetical protein predicted by gensca	---	AT2G36440	-1.01	-0.02	-0.17	0.872282	0.941151	-6.84
254274_at	putative DNA binding protein DNA-bind	---	AT4G22770	1.02	0.03	0.17	0.872468	0.941301	-6.84
255958_at	high affinity sulphate transporter, putati	SULTR1;3	AT1G22150	-1.02	-0.02	-0.17	0.872733	0.941543	-6.84
258808_at	putative pyruvate kinase similar to pyru	---	AT3G04050	-1.01	-0.02	-0.17	0.872793	0.941563	-6.84
265548_s_a	putative helicase	---	---	1.01	0.01	0.17	0.872891	0.941624	-6.84
254701_at	putative protein predicted protein, Arabi	---	AT4G18030	-1.02	-0.04	-0.17	0.873437	0.941688	-6.84
252663_at	putative protein several hypothetical pro	---	AT3G44070	1.01	0.02	0.17	0.873512	0.941688	-6.84
261560_at	acyl CoA thioesterase, putative similar t	---	AT1G01710	-1.01	-0.02	-0.17	0.87332	0.941688	-6.84
262887_at	hypothetical protein	---	AT1G14780	1.04	0.06	0.17	0.873619	0.941688	-6.84
252947_at	putative protein ubiquitin fusion degrada	KAK	AT4G38600	-1.01	-0.02	-0.17	0.873456	0.941688	-6.84
246660_at	putative protein predicted protein, Arabi	---	AT5G35180	-1.01	-0.02	-0.17	0.87315	0.941688	-6.84
257922_at	ethylene receptor, putative (ETR2) simi	ETR2	AT3G23150	1.03	0.04	0.17	0.873652	0.941688	-6.84
254915_s_a	cysteine proteinase contains similarity t	---	AT4G11310 /	1.06	0.09	0.17	0.873227	0.941688	-6.84
258083_at	Expressed protein ; supported by full-ler	---	AT3G25855	1.01	0.02	0.17	0.873353	0.941688	-6.84
246382_at	hypothetical protein	---	---	-1.02	-0.02	-0.17	0.873573	0.941688	-6.84
262427_s_a	thioglucosidase, putative similar to thiog	BGLU34	AT1G47600 /	1.01	0.02	0.17	0.873375	0.941688	-6.84
254130_at	MADS-box protein AGL24 ; supported b	AGL24	AT4G24540	1.02	0.03	0.17	0.8731	0.941688	-6.84
265213_at	clathrin protein family Similar to clathrin	---	AT1G05020	1.02	0.03	0.17	0.873294	0.941688	-6.84
255897_at	mutator-like transposase, putative simil	---	---	1.01	0.01	0.17	0.873458	0.941688	-6.84
266678_at	hypothetical protein predicted by grail	---	AT2G25870	1.01	0.02	0.17	0.873435	0.941688	-6.84
257586_at	hypothetical protein predicted by genem	---	AT1G50760	1.01	0.02	0.17	0.873302	0.941688	-6.84
262707_at	hypothetical protein	---	AT1G16290	1.02	0.02	0.17	0.873584	0.941688	-6.84
255363_x_a	hypothetical protein	---	---	-1.02	-0.03	-0.17	0.873764	0.941764	-6.84
257884_at	hypothetical protein predicted by genem	---	AT3G16960	1.01	0.02	0.16	0.873809	0.941768	-6.84
258423_at	hypothetical protein predicted by genefir	---	AT3G16730	-1.01	-0.02	-0.16	0.874222	0.942086	-6.84
251049_at	putative protein rab11 binding protein, E	---	AT5G02430	1.01	0.02	0.16	0.874269	0.942086	-6.84
261847_at	hypothetical protein predicted by genem	---	AT1G11560	-1.02	-0.02	-0.16	0.874234	0.942086	-6.84
249561_at	disease resistance - like protein disease	---	AT5G38340	-1.01	-0.02	-0.16	0.87426	0.942086	-6.84
248425_at	ACC synthase; 1-aminocyclopropane-1-	ACS12	AT5G51690	1.02	0.02	0.16	0.874349	0.942128	-6.84
254968_at	putative protein various predicted prote	---	AT4G10420	-1.01	-0.02	-0.16	0.874421	0.942161	-6.84
247378_at	ATP-dependent RNA helicase-like prote	---	AT5G63120	-1.02	-0.03	-0.16	0.874493	0.942194	-6.84
254805_at	pEARLI 1 ; supported by cDNA: gi_871	pEARLI 1	AT4G12480	-1.08	-0.12	-0.16	0.874796	0.942459	-6.84
261512_at	actin capping protein beta-2, putative si	---	AT1G71790	-1.02	-0.03	-0.16	0.874822	0.942459	-6.84

262893_at	hypothetical protein contains similarity to	---	AT1G59790	-1.01	-0.02	-0.16	0.874945	0.942502	-6.84
260340_at	putative dihydropterin pyrophosphokinas	---	AT1G69190	1.01	0.02	0.16	0.874943	0.942502	-6.84
264699_at	unknown protein ;supported by full-lengt	---	AT1G69980 /	-1.01	-0.02	-0.16	0.875019	0.942504	-6.84
262550_at	hypothetical protein similar to hypothetic	---	AT1G31310	1.01	0.02	0.16	0.875111	0.942504	-6.84
258969_at	hypothetical protein predicted by gensc	---	AT3G10680	1.01	0.02	0.16	0.875082	0.942504	-6.84
251460_at	hypothetical protein	SAC9	AT3G59770	1.01	0.02	0.16	0.875099	0.942504	-6.84
252874_at	putative protein ipiB1 gene, Phytophth	---	---	-1.01	-0.02	-0.16	0.875159	0.942511	-6.84
250175_at	putative protein CGI-67, Homo sapiens	---	AT5G14390	-1.02	-0.03	-0.16	0.87528	0.942596	-6.84
265978_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.16	0.87533	0.942606	-6.84
259918_at	putative AP2 domain transcription factor	---	AT1G72570	1.01	0.02	0.16	0.875534	0.942781	-6.84
247982_at	serine O-acetyltransferase (EC 2.3.1.30	ATSERAT	AT5G56760	1.01	0.02	0.16	0.875815	0.942950	-6.84
255226_at	UV-damaged DNA binding factor - like	DDB1A	AT4G05420	1.01	0.02	0.16	0.875812	0.942950	-6.84
258757_at	putative RING zinc finger protein contai	---	AT3G10910 /	-1.02	-0.03	-0.16	0.875757	0.942950	-6.84
250392_at	putative protein multifunctional aminoac	---	AT5G10880	1.01	0.02	0.16	0.875861	0.942955	-6.84
261434_at	receptor-like serine/threonine kinase, p	---	AT1G07650	1.02	0.03	0.16	0.876095	0.943080	-6.84
256995_at	protein kinase, putative contains similar	---	AT3G25840	-1.01	-0.02	-0.16	0.876142	0.943080	-6.84
255149_at	KNAT1 homeobox-like protein	KNAT1	AT4G08150	-1.01	-0.02	-0.16	0.876107	0.943080	-6.84
249798_at	putative protein contains similarity to ph	---	AT5G23730	1.01	0.02	0.16	0.876143	0.943080	-6.84
266157_at	unknown protein	ATFUC1	AT2G28100	-1.01	-0.01	-0.16	0.87643	0.943306	-6.84
245676_at	nodule-specific protein, putative similar	---	AT1G56670	1.01	0.02	0.16	0.876514	0.943306	-6.84
263909_at	hypothetical protein predicted by genscan	DML1	AT2G36490	-1.02	-0.03	-0.16	0.876512	0.943306	-6.84
249980_at	putative protein	---	AT5G18870	1.01	0.02	0.16	0.876518	0.943306	-6.84
256737_at	farnesyltranstransferase, putative (fragr	---	AT3G29420	-1.01	-0.02	-0.16	0.876592	0.943337	-6.84
256029_at	integral membrane protein, putative sim	STT3B	AT1G34130	-1.03	-0.04	-0.16	0.876643	0.943337	-6.84
255375_at	putative athila-like protein	---	---	-1.01	-0.02	-0.16	0.87667	0.943337	-6.84
263930_at	hypothetical protein predicted by genscan	---	AT2G36300	1.01	0.02	0.16	0.876823	0.943448	-6.84
252469_at	protein kinase - like protein Raf protein	---	AT3G46920	1.02	0.02	0.16	0.87725	0.943448	-6.84
259823_at	beta-1,3-glucanase precursor, putative	---	AT1G66250	-1.02	-0.02	-0.16	0.877365	0.943448	-6.84
253135_at	cytoplasmatic aconitate hydratase (citra	---	AT4G35830	-1.02	-0.03	-0.16	0.876977	0.943448	-6.84
257135_at	hypothetical protein similar to oxidoredu	---	AT3G12900	1.02	0.02	0.16	0.877542	0.943448	-6.84
261114_at	bZIP transcription factor ATB2, putative	AtbZIP44	AT1G75388 /	1.08	0.11	0.16	0.87696	0.943448	-6.84
257101_at	disease resistance protein, putative sim	AtRLP42	AT3G25020	1.01	0.02	0.16	0.877532	0.943448	-6.84
256608_at	hypothetical protein predicted by genem	---	AT3G30840	1.01	0.01	0.16	0.877016	0.943448	-6.84
255001_at	AIG1-like protein AIG1 - Arabidopsis tha	---	AT4G09930	1.02	0.02	0.16	0.877218	0.943448	-6.84
256501_at	hypothetical protein predicted by genem	---	AT1G36756	-1.01	-0.02	-0.16	0.877433	0.943448	-6.84

244947_at	hypothetical protein	---	---	-1.02	-0.02	-0.16	0.877547	0.943448	-6.84
253380_at	hypothetical protein hypothetical protein	PGSIP3	AT4G33330	1.01	0.02	0.16	0.8775	0.943448	-6.84
257298_at	hypothetical protein predicted by genem	---	AT3G28155	-1.02	-0.02	-0.16	0.877055	0.943448	-6.84
254988_at	putative protein Ran GTPase activator	GTC2	AT4G10670	-1.01	-0.02	-0.16	0.876875	0.943448	-6.84
260540_at	hypothetical protein predicted by genefi	---	AT2G43500	-1.01	-0.02	-0.16	0.877128	0.943448	-6.84
260159_at	putative helicase similar to helicase GB:	---	AT1G79890	-1.01	-0.02	-0.16	0.87756	0.943448	-6.84
265427_at	unknown protein	---	AT2G20740	-1.02	-0.02	-0.16	0.877296	0.943448	-6.84
262510_at	hypothetical protein similar to hypothetic	---	AT1G11270	-1.01	-0.02	-0.16	0.877541	0.943448	-6.84
255204_at	putative myosin-like protein	---	---	1.02	0.02	0.16	0.877066	0.943448	-6.84
260788_at	cysteine proteinase contains similarity t	---	AT1G06260	-1.01	-0.02	-0.16	0.8777	0.943554	-6.84
265404_at	putative beta-galactosidase	BGAL13	AT2G16730	1.02	0.03	0.16	0.877745	0.943558	-6.84
263677_at	unknown protein	PDLP2	AT1G04520	1.01	0.02	0.16	0.877844	0.943620	-6.84
265834_at	hypothetical protein predicted by gensca	---	AT2G14410	1.01	0.01	0.16	0.878014	0.943715	-6.84
263818_at	putative retroelement pol polyprotein ap	---	---	-1.01	-0.01	-0.16	0.877978	0.943715	-6.84
258231_at	hypothetical protein contains Pfam profil	RCK	AT3G27730	-1.01	-0.02	-0.16	0.878086	0.943747	-6.84
247090_at	putative protein similar to unknown prote	---	AT5G66370	-1.01	-0.02	-0.16	0.878179	0.943758	-6.84
263023_at	unknown protein	---	AT1G23960	1.03	0.04	0.16	0.878169	0.943758	-6.84
245827_at	disease resistance protein RPS4, putat	---	AT1G57830	1.01	0.02	0.16	0.878304	0.943835	-6.84
260018_at	hypothetical protein predicted by genem	---	AT1G41820	-1.01	-0.02	-0.16	0.878333	0.943835	-6.84
256472_at	unknown protein	---	---	-1.02	-0.02	-0.16	0.87839	0.943851	-6.84
255675_at	MYC1 transcription factor	ATMYC1	AT4G00480	1.01	0.02	0.16	0.878432	0.943853	-6.84
266914_at	putative beta-amylase	BAM7	AT2G45880	-1.02	-0.03	-0.16	0.878665	0.944058	-6.84
248148_at	putative protein similar to unknown prote	---	AT5G54930	1.02	0.03	0.16	0.878783	0.944076	-6.84
253822_at	hypothetical protein	---	AT4G28410	-1.01	-0.02	-0.16	0.878888	0.944076	-6.84
253888_at	hypothetical protein	ISI1	AT4G27750	-1.01	-0.02	-0.16	0.87885	0.944076	-6.84
261260_at	hypothetical protein predicted by genem	---	AT1G26680	1.01	0.02	0.16	0.878828	0.944076	-6.84
246783_at	sugar transporter-like protein putative s	SFP2	AT5G27360	1.04	0.06	0.16	0.878747	0.944076	-6.84
260747_at	unknown protein ; supported by cDNA: g	---	AT1G78420	1.01	0.02	0.16	0.879015	0.944167	-6.84
251899_at	nucleoid DNA-binding - like protein nuc	---	AT3G54400	1.06	0.09	0.16	0.879069	0.944181	-6.84
245869_at	hypothetical protein predicted by genem	---	AT1G26330	-1.01	-0.02	-0.16	0.879908	0.944590	-6.84
250469_at	pollen allergen -like protein SAH7 prote	---	AT5G10130	-1.02	-0.02	-0.16	0.879953	0.944590	-6.84
250933_at	arabinogalactan protein - like arabinoga	FLA11	AT5G03170	-1.03	-0.04	-0.16	0.879778	0.944590	-6.84
247878_at	unknown protein	---	AT5G57760	-1.11	-0.15	-0.16	0.880072	0.944590	-6.84
249756_at	Expressed protein ; supported by full-ler	---	AT5G24313	1.01	0.02	0.16	0.8797	0.944590	-6.84
261593_at	unknown protein	---	AT1G33170	-1.08	-0.10	-0.16	0.879953	0.944590	-6.84

246077_at	putative protein XNP-1, Caenorhabditis	CHR42	AT5G20420	-1.02	-0.03	-0.16	0.880066	0.944590	-6.84
266375_at	En/Spm-like transposon protein related	---	---	1.01	0.02	0.16	0.880023	0.944590	-6.84
263860_at	hypothetical protein predicted by genscа	---	---	1.01	0.02	0.16	0.879748	0.944590	-6.84
257711_at	20S proteasome beta subunit (PBB1) ic	PBB1	AT3G27430	1.01	0.02	0.16	0.879919	0.944590	-6.84
255105_at	putative sulfate transporter ; supported	SULTR1;1	AT4G08620	-1.01	-0.02	-0.16	0.87963	0.944590	-6.84
265992_at	putative receptor-like protein kinase	---	AT2G24130	-1.01	-0.02	-0.16	0.879617	0.944590	-6.84
259679_at	putative protein kinase Pfam HMM hit: I	---	AT1G77720	1.01	0.01	0.16	0.879725	0.944590	-6.84
257508_at	bZIP transcription factor, putative conta	---	AT1G64320	-1.01	-0.02	-0.16	0.879965	0.944590	-6.84
246605_at	putative protein predicted proteins, Ara	---	---	1.01	0.02	0.16	0.879905	0.944590	-6.84
253041_at	phosphoenolpyruvate carboxykinase (A	PCK1	AT4G37870	1.02	0.04	0.16	0.880123	0.944601	-6.84
267514_at	putative glycerate dehydrogenase ; sup	---	AT2G45630	1.03	0.05	0.16	0.880185	0.944623	-6.84
247226_at	putative protein contains similarity to tra	---	AT5G65100	-1.01	-0.01	-0.16	0.880263	0.944662	-6.84
260925_at	DNA-binding protein, putative contains	---	AT1G21340	-1.01	-0.02	-0.16	0.880595	0.944885	-6.84
265640_at	putative cysteine proteinase	---	AT2G27395	-1.01	-0.01	-0.16	0.88058	0.944885	-6.84
263119_at	hypothetical protein predicted by genefi	---	AT1G03110	-1.02	-0.03	-0.16	0.880538	0.944885	-6.84
251817_at	small GTP-binding protein - like (fragme	ARA6	AT3G54840	-1.01	-0.02	-0.16	0.880645	0.944895	-6.84
251966_at	receptor lectin kinase -like protein recep	---	AT3G53380	1.02	0.02	0.16	0.88069	0.944899	-6.84
264284_at	protein kinase, putative similar to protei	---	AT1G61860	1.01	0.02	0.16	0.880771	0.944941	-6.84
261055_at	chloroplast nucleoid DNA binding prote	---	AT1G01300	1.01	0.02	0.16	0.88091	0.945046	-6.84
245229_at	putative protein contains EST gb:T4504	---	AT4G25620	-1.02	-0.03	-0.16	0.880993	0.945079	-6.84
246096_at	beta-1,3-glucanase bg4 ;supported by	BETAG4	AT5G20330	-1.01	-0.02	-0.16	0.881024	0.945079	-6.84
259660_at	unknown protein ; supported by full-leng	---	AT1G55260	1.05	0.07	0.16	0.881186	0.945152	-6.84
260640_at	viral resistance protein, putative similar	---	AT1G53350	-1.03	-0.04	-0.16	0.881216	0.945152	-6.84
253944_at	SNF8 like protein SNF8 protein - yeast,	VPS22	AT4G27040	1.01	0.02	0.16	0.881193	0.945152	-6.84
263124_at	beta-Amyrin Synthase, putative similar	---	AT1G78480	-1.02	-0.02	-0.16	0.881282	0.945178	-6.84
252020_at	SKP1/ASK1 (At6), putative similar to SI	ASK6	AT3G53060	1.01	0.01	0.15	0.881469	0.945334	-6.84
245393_at	beta-1,3-glucanase class I precursor ;s	---	AT4G16260	1.03	0.04	0.15	0.881902	0.945754	-6.84
250172_at	putative protein	---	AT5G14330	-1.02	-0.02	-0.15	0.882004	0.945774	-6.84
254695_at	putative protein predicted protein, Sacc	ATL4H	AT4G17905 /	1.01	0.02	0.15	0.881966	0.945774	-6.84
256283_at	hypothetical protein	---	AT3G12540	1.01	0.02	0.15	0.882095	0.945827	-6.84
259990_s_a	F-box protein FKF1/ADO3, AtFBX2a id	FKF1	AT1G68050 /	-1.02	-0.03	-0.15	0.882304	0.945962	-6.84
267006_at	putative membrane transporter ; suppo	---	AT2G34190	1.01	0.02	0.15	0.882281	0.945962	-6.84
257832_at	light regulated protein, putative similar t	CCL	AT3G26740	1.01	0.02	0.15	0.882375	0.945994	-6.84
259742_at	putative proline-rich APG protein similar	GLIP6	AT1G71120	1.02	0.03	0.15	0.882433	0.946012	-6.84
256377_at	hypothetical protein	---	AT1G66650	-1.01	-0.01	-0.15	0.882553	0.946096	-6.84

253579_at	SERINE CARBOXYPEPTIDASE II-like	BRS1	AT4G30610	-1.03	-0.04	-0.15	0.882714	0.946215	-6.84
256776_at	multispanning membrane protein, putat	---	AT3G13772	1.01	0.02	0.15	0.882747	0.946215	-6.84
265942_at	putative casein kinase I ;supported by f	ckl5	AT2G19470	-1.01	-0.02	-0.15	0.882806	0.946234	-6.84
259767_s_a	unknown protein	---	AT1G29350 /	1.01	0.02	0.15	0.882852	0.946239	-6.84
245614_at	retrovirus-related like polyprotein	---	---	-1.01	-0.02	-0.15	0.882922	0.946269	-6.84
261502_at	hypothetical protein predicted by genem	AtHB31	AT1G14440	-1.02	-0.03	-0.15	0.882968	0.946274	-6.84
260604_at	polyphosphoinositide binding protein, p	---	AT1G55840	-1.02	-0.02	-0.15	0.883023	0.946289	-6.84
248859_at	putative protein contains similarity to CH	---	AT5G46660	-1.01	-0.02	-0.15	0.883113	0.946302	-6.84
247661_at	protein kinase - like protein kinase 1, P	---	AT5G60080	-1.01	-0.02	-0.15	0.883118	0.946302	-6.84
246367_at	light repressible receptor protein kinase	---	AT1G51880	1.01	0.02	0.15	0.883282	0.946311	-6.84
249061_at	putative protein similar to unknown prote	---	AT5G44550	-1.01	-0.02	-0.15	0.883249	0.946311	-6.84
246168_at	meristem protein - like reproductive me	---	AT5G32460	-1.02	-0.03	-0.15	0.883293	0.946311	-6.84
256811_at	serine/threonine-specific protein kinase	---	AT3G21340	1.01	0.02	0.15	0.883231	0.946311	-6.84
266358_at	hypothetical protein predicted by gensca	---	AT2G32280	1.03	0.04	0.15	0.883362	0.946341	-6.84
265832_at	putative replication protein A1	---	---	-1.01	-0.02	-0.15	0.883458	0.946400	-6.84
245675_at	hypothetical protein similar to putative re	---	---	-1.02	-0.02	-0.15	0.883554	0.946428	-6.84
261000_at	hypothetical protein predicted by genem	---	AT1G26540	1.01	0.02	0.15	0.883568	0.946428	-6.84
248420_at	receptor-like protein kinase ;supported	---	AT5G51560	-1.03	-0.05	-0.15	0.883812	0.946560	-6.84
246035_at	succinyl-CoA-ligase alpha subunit ;supp	---	AT5G08300	-1.03	-0.04	-0.15	0.883857	0.946560	-6.84
247416_at	40S ribosomal protein S15-like protein	---	AT5G63070	1.01	0.02	0.15	0.883818	0.946560	-6.84
246542_at	transcriptional regulatory - like protein t	SNL2	AT5G15020	1.02	0.02	0.15	0.883773	0.946560	-6.84
265089_at	hypothetical protein similar to hypothetic	SUVR1	AT1G04050	-1.01	-0.02	-0.15	0.883907	0.946569	-6.84
252937_at	SEC14 - like protein phosphatidylinosito	SEC14	AT4G39180	-1.01	-0.02	-0.15	0.884132	0.946583	-6.84
255353_at	putative transposon protein similar to Mu	---	---	-1.01	-0.01	-0.15	0.884115	0.946583	-6.84
266627_at	putative pre-mRNA splicing factor RNA	MEE29	AT2G35340	1.01	0.02	0.15	0.884018	0.946583	-6.84
260322_at	unknown protein	---	AT1G63900	-1.01	-0.02	-0.15	0.884169	0.946583	-6.84
253154_at	putative protein predicted protein, Arabi	---	AT4G35710	-1.01	-0.02	-0.15	0.884161	0.946583	-6.84
246336_at	putative protein putative integral membr	ATCHX4	AT3G44900	-1.01	-0.02	-0.15	0.883974	0.946583	-6.84
247224_at	MADS box transcription factor-like prote	MAF5	AT5G65080	1.02	0.03	0.15	0.884308	0.946673	-6.84
263446_at	putative SET-domain transcriptional reg	ATX1	AT2G31650	-1.01	-0.02	-0.15	0.884336	0.946673	-6.84
250811_at	cysteine proteinase inhibitor-like protein	---	AT5G05110	-1.02	-0.03	-0.15	0.884397	0.946693	-6.84
266988_at	putative myrosinase-binding protein ;su	JAL22	AT2G39310	1.02	0.03	0.15	0.884584	0.946768	-6.84
246764_s_a	putative protein At2g27780 and At2g13	---	AT2G13640 /	1.01	0.01	0.15	0.884627	0.946768	-6.84
246801_at	threonyl-tRNA synthetase ; supported b	---	AT5G26830	1.01	0.02	0.15	0.884633	0.946768	-6.84
261321_at	hypothetical protein predicted by genem	---	AT1G44740	-1.01	-0.02	-0.15	0.884525	0.946768	-6.84

259574_at	hypothetical protein	MLP168	AT1G35310	-1.01	-0.01	-0.15	0.884773	0.946874	-6.84
245401_at	hypothetical protein ;supported by full-le	---	AT4G17670	1.03	0.05	0.15	0.884841	0.946902	-6.84
266846_at	unknown protein	---	AT2G25970	1.01	0.02	0.15	0.884991	0.947018	-6.84
267370_at	unknown protein ;supported by full-leng	---	AT2G44525	1.01	0.01	0.15	0.885109	0.947051	-6.84
251129_at	putative protein predicted protein, Arabi	---	AT5G01150	1.01	0.02	0.15	0.885224	0.947051	-6.84
266159_at	putative chloroplast nucleoid DNA bindir	---	AT2G28030	1.01	0.01	0.15	0.88508	0.947051	-6.84
261283_s_a	hypothetical protein predicted by gensca	---	---	-1.01	-0.01	-0.15	0.885229	0.947051	-6.84
260720_at	hypothetical protein predicted by gensca	---	AT1G48095	1.01	0.02	0.15	0.88515	0.947051	-6.84
257849_at	unknown protein	ECT5	AT3G13060	-1.02	-0.02	-0.15	0.885358	0.947053	-6.84
256790_at	ARR1 protein, putative similar to ARR1	ARR1	AT3G16857	1.01	0.02	0.15	0.885397	0.947053	-6.84
248479_at	unknown protein	---	AT5G50910	1.01	0.01	0.15	0.885366	0.947053	-6.84
263343_at	putative replication protein A1	---	---	-1.01	-0.01	-0.15	0.885366	0.947053	-6.84
248612_at	putative protein contains similarity to unl	---	AT5G49530	1.02	0.03	0.15	0.885561	0.947105	-6.84
256688_at	non-LTR reverse transcriptase, putative	---	AT3G32130	-1.01	-0.01	-0.15	0.885612	0.947105	-6.84
260699_at	MAP kinase, putative similar to MAP kir	ATMKK10	AT1G32320	-1.01	-0.02	-0.15	0.885559	0.947105	-6.84
259317_at	hypothetical protein identical to hypothe	HYP1	AT3G01100	1.01	0.02	0.15	0.885592	0.947105	-6.84
253322_at	putative protein ;supported by full-lengt	---	AT4G33980	1.02	0.02	0.15	0.885696	0.947150	-6.84
267104_at	ERD15 protein identical to GB D30719;	ERD15	AT2G41430	-1.01	-0.02	-0.15	0.885743	0.947157	-6.84
247048_at	photoreceptor-interacting protein-like ; s	---	AT5G66560	1.03	0.04	0.15	0.885976	0.947228	-6.84
250101_at	putative protein contains similarity to bet	BGLU2	AT5G16580	1.02	0.03	0.15	0.885942	0.947228	-6.84
266982_at	unknown protein ; supported by cDNA:	---	AT2G39500	1.02	0.02	0.15	0.88589	0.947228	-6.84
256634_s_a	hypothetical protein predicted by gensca	---	---	1.01	0.01	0.15	0.88592	0.947228	-6.84
254436_at	putative protein receptor kinase-like pro	---	AT4G20940	-1.01	-0.01	-0.15	0.886058	0.947260	-6.84
265924_at	putative geranylgeranyl pyrophosphate s	---	AT2G18620	-1.01	-0.01	-0.15	0.886089	0.947260	-6.84
254725_at	putative protein various predicted prote	---	AT4G13650	-1.01	-0.02	-0.15	0.886184	0.947318	-6.84
257714_at	histone H3, putative similar to histone H	---	AT3G27360	-1.01	-0.02	-0.15	0.886299	0.947352	-6.84
246723_at	putative protein various predicted prote	---	AT5G29030	-1.01	-0.02	-0.15	0.886277	0.947352	-6.84
255261_s_a	putative protein equilibrative nucleoside	FUR1	AT4G05110 /	1.03	0.05	0.15	0.886898	0.947802	-6.84
258906_at	unknown protein similar to C-terminal h	ATTLP9	AT3G06380	-1.01	-0.02	-0.15	0.8868	0.947802	-6.84
245310_at	hypothetical protein ;supported by full-le	RALFL31	AT4G13950	1.03	0.04	0.15	0.88696	0.947802	-6.84
244954_s_a	hypothetical protein	---	AT2G07732	-1.02	-0.04	-0.15	0.887006	0.947802	-6.84
248577_at	myrosinase binding protein-like ; suppor	---	AT5G49870	1.01	0.01	0.15	0.887089	0.947802	-6.84
251872_at	putative protein predicted protein Arabid	---	AT3G54570	-1.01	-0.02	-0.15	0.886883	0.947802	-6.84
262101_at	hypothetical protein identical to hypothe	---	AT1G59535	1.01	0.01	0.15	0.886981	0.947802	-6.84
267282_at	unknown protein ; supported by cDNA:	---	AT2G19390	-1.01	-0.02	-0.15	0.887091	0.947802	-6.84

248416_at	putative protein disease resistance prote	---	AT5G51630	-1.01	-0.02	-0.15	0.887094	0.947802	-6.84
263522_at	hypothetical protein	---	AT2G24950	-1.01	-0.01	-0.15	0.887204	0.947875	-6.84
266026_at	putative non-LTR retroelement reverse t	---	---	1.01	0.02	0.15	0.887277	0.947909	-6.84
256174_at	NADP-specific glutatamate dehydrogen	---	AT1G51720	1.01	0.02	0.15	0.887376	0.947926	-6.84
256556_at	mutator-like transposase, putative simil	---	---	1.01	0.01	0.15	0.887345	0.947926	-6.84
254927_at	putative protein hypothetical protein - A	---	AT4G11400	-1.01	-0.02	-0.15	0.887431	0.947940	-6.84
245754_at	hypothetical protein predicted by genem	---	AT1G35183	1.01	0.01	0.15	0.887571	0.948045	-6.84
254115_at	putative protein binding protein HPV16	---	AT4G24710	1.01	0.02	0.15	0.887736	0.948146	-6.84
265239_s_a	hypothetical protein	---	AT2G07692	1.01	0.02	0.15	0.887749	0.948146	-6.84
258062_at	unknown protein ; supported by cDNA:	---	AT3G26000	-1.02	-0.02	-0.15	0.887824	0.948182	-6.84
257757_at	hypothetical protein predicted by gensca	PGSIP1	AT3G18660	-1.01	-0.02	-0.15	0.888013	0.948295	-6.84
256005_at	hypothetical protein similar to putative re	---	---	1.01	0.02	0.15	0.887992	0.948295	-6.84
251190_at	RING-H2 zinc finger protein ATL5 ; sup	ATL5	AT3G62690	1.02	0.03	0.15	0.888063	0.948304	-6.84
248288_at	unknown protein ; supported by cDNA:	---	AT5G52840	1.01	0.02	0.15	0.88811	0.948309	-6.84
248191_at	putative protein similar to unknown prote	---	AT5G54130	1.01	0.02	0.15	0.888261	0.948337	-6.84
253895_at	NWMU3 - 2S albumin 3 precursor	AT2S3	AT4G27160	1.01	0.01	0.15	0.888201	0.948337	-6.84
265526_x_a	putative Athila retroelement ORF1 prote	---	---	-1.01	-0.01	-0.15	0.88824	0.948337	-6.84
257212_at	zinc-binding dehydrogenase, putative c	---	AT3G15090	-1.02	-0.02	-0.15	0.888383	0.948379	-6.84
253656_at	putative protein hypothetical protein - A	emb1353	AT4G30090	-1.01	-0.01	-0.15	0.888346	0.948379	-6.84
258470_at	Expressed protein ; supported by full-ler	---	AT3G06035	1.06	0.08	0.15	0.888752	0.948445	-6.84
261094_at	hypothetical protein predicted by genem	---	AT1G62920	-1.02	-0.02	-0.15	0.888571	0.948445	-6.84
260513_at	cyanogenic beta-glucosidase, putative	BGLU36	AT1G51490	1.01	0.02	0.15	0.888777	0.948445	-6.84
262334_at	hypothetical protein similar to putative s	---	AT1G64010	-1.01	-0.02	-0.15	0.888668	0.948445	-6.84
262212_at	response regulator 7, putative similar to	ARR15	AT1G74890	-1.02	-0.02	-0.15	0.888721	0.948445	-6.84
256258_at	unknown protein	NF-YC11	AT3G12480	1.01	0.01	0.15	0.888727	0.948445	-6.84
254589_at	hypothetical protein	---	AT4G18850	-1.01	-0.02	-0.15	0.888701	0.948445	-6.84
267117_at	unknown protein	---	AT2G32560	-1.01	-0.01	-0.15	0.888721	0.948445	-6.84
265000_at	hypothetical protein predicted by genem	---	AT1G67410	1.01	0.02	0.14	0.888977	0.948570	-6.84
246123_at	beta-1,3-glucanase-like protein beta-1,3	---	AT5G20390	1.01	0.01	0.14	0.888966	0.948570	-6.84
266773_at	hypothetical protein predicted by gensca	---	AT2G29040	1.01	0.02	0.14	0.889099	0.948655	-6.84
249274_at	unknown protein	---	AT5G41860	1.02	0.02	0.14	0.889625	0.949172	-6.84
258098_at	hypothetical protein similar to kinesin lik	KINESIN-1	AT3G23670	1.02	0.02	0.14	0.889695	0.949202	-6.84
246837_at	pectin acetylesterase precursor - like pr	---	AT5G26670	1.02	0.03	0.14	0.889851	0.949280	-6.84
262264_at	Niemann-Pick C disease protein-like pro	---	AT1G42470	1.03	0.04	0.14	0.889828	0.949280	-6.84
259915_at	unknown protein	---	AT1G72790	-1.03	-0.04	-0.14	0.890019	0.949318	-6.84

255833_at	unknown protein	---	AT2G33390	1.01	0.02	0.14	0.890027	0.949318	-6.84
267328_at	putative receptor-like protein kinase	---	AT2G19230	1.01	0.02	0.14	0.890053	0.949318	-6.84
253744_s_a	putative protein hypothetical protein F2	---	---	-1.01	-0.01	-0.14	0.889959	0.949318	-6.84
252296_at	putative protein GMFP7 isoprenylated p	---	AT3G48970	-1.02	-0.03	-0.14	0.890213	0.949428	-6.84
259500_at	unknown protein ; supported by cDNA: g	---	AT1G15740	1.02	0.02	0.14	0.890281	0.949428	-6.84
252668_at	hypothetical protein	---	AT3G44210	1.01	0.01	0.14	0.890254	0.949428	-6.84
263226_at	unknown protein Contains the PF|0065	---	AT1G30690	-1.01	-0.01	-0.14	0.890375	0.949439	-6.84
252699_at	hypothetical protein predicted proteins,	---	---	-1.02	-0.03	-0.14	0.890375	0.949439	-6.84
264290_at	hypothetical protein predicted by genem	---	AT1G78810	-1.02	-0.02	-0.14	0.890429	0.949453	-6.84
259729_at	hypothetical protein predicted by genefi	---	AT1G77640	1.03	0.05	0.14	0.890502	0.949486	-6.84
261605_at	CDPK-related protein kinase, putative s	---	AT1G49580	-1.01	-0.02	-0.14	0.890645	0.949580	-6.84
263604_s_a	putative replication protein A1	---	---	-1.01	-0.01	-0.14	0.890673	0.949580	-6.84
262243_at	hypothetical protein predicted by genem	---	---	1.01	0.02	0.14	0.890811	0.949682	-6.84
259579_at	P-glycoprotein, putative similar to P-gly	PGP14	AT1G28010	-1.04	-0.06	-0.14	0.890856	0.949685	-6.84
248706_at	unknown protein	---	AT5G48530	-1.01	-0.02	-0.14	0.89092	0.949710	-6.84
247317_at	putative protein contains similarity to NA	anac103	AT5G64060	-1.01	-0.02	-0.14	0.891105	0.949862	-6.84
266194_at	unknown protein	---	AT2G39090	1.01	0.01	0.14	0.891212	0.949926	-6.84
255469_at	predicted OR23 protein of unknown func	---	AT4G03030	1.01	0.02	0.14	0.891248	0.949926	-6.84
263463_at	putative ARI-like RING zinc finger protei	---	AT2G31770	-1.01	-0.01	-0.14	0.891486	0.950135	-6.84
257835_at	cytochrome P450 monooxygenase, put	CYP82G1	AT3G25180	1.04	0.05	0.14	0.891653	0.950180	-6.84
267529_at	putative protein kinase contains a protei	AtAUR3	AT2G45490	1.01	0.02	0.14	0.891613	0.950180	-6.84
252523_at	putative protein light repressible recept	---	AT3G46400	-1.01	-0.02	-0.14	0.891612	0.950180	-6.84
267429_at	putative UDP-galactose-4-epimerase	MEE25	AT2G34850	1.02	0.02	0.14	0.89175	0.950184	-6.84
263585_at	60S ribosomal protein L39	---	AT2G25210	-1.03	-0.04	-0.14	0.891782	0.950184	-6.84
256150_at	beta-fructofuranosidase identical to beta	ATFRUCT	AT1G55120	1.03	0.04	0.14	0.891751	0.950184	-6.84
263572_at	putative disease resistance protein simil	---	AT2G17060	1.01	0.01	0.14	0.89195	0.950186	-6.84
255503_at	contains similarity to a protein kinase d	---	AT4G02420	1.04	0.06	0.14	0.89193	0.950186	-6.84
245507_at	hypothetical protein	---	AT4G15710	1.02	0.02	0.14	0.891945	0.950186	-6.84
257306_at	hypothetical protein contains regions si	---	AT3G30200	1.01	0.01	0.14	0.891933	0.950186	-6.84
258602_at	putative protein phosphatase-2C (PP2C	---	AT3G02750	1.01	0.01	0.14	0.892169	0.950286	-6.84
265368_at	hypothetical protein identical to hypothe	---	AT2G13350	1.02	0.02	0.14	0.892166	0.950286	-6.84
246797_at	putative protein ;supported by full-lengt	---	AT5G26790	-1.01	-0.01	-0.14	0.892149	0.950286	-6.84
254415_at	subtilisin-like serine protease contains s	ATSBT3.1	AT4G21326	-1.01	-0.01	-0.14	0.892229	0.950306	-6.84
253254_at	predicted protein	SQS2	AT4G34650	1.02	0.03	0.14	0.892401	0.950445	-6.84
258227_at	6-4 photolyase (UVR3) identical to 6-4	UVR3	AT3G15620	-1.04	-0.06	-0.14	0.892594	0.950577	-6.84

248654_at	importin alpha	IMPA-5	AT5G49310	1.01	0.02	0.14	0.892609	0.950577	-6.84
267187_s_a	putative methylenetetrahydrofolate redu	MTHFR2	AT2G44160 /	-1.02	-0.02	-0.14	0.892684	0.950613	-6.84
264935_at	hypothetical protein predicted by genem	---	AT1G61150	1.02	0.02	0.14	0.892745	0.950634	-6.84
257875_at	hypothetical protein	---	AT3G17120	-1.01	-0.02	-0.14	0.892791	0.950636	-6.84
260763_at	RING-H2 finger protein RHA3a, putativ	---	AT1G49220	1.01	0.01	0.14	0.892831	0.950636	-6.84
260071_at	putative proline-rich protein precursor si	ESP1	AT1G73840	-1.01	-0.01	-0.14	0.892895	0.950660	-6.84
247388_s_a	transcription factor Hap5a-like protein	NF-YC1	AT3G48590 /	-1.02	-0.03	-0.14	0.893026	0.950666	-6.84
252263_at	putative protein several hypothetical pro	---	AT3G49520	-1.01	-0.02	-0.14	0.892994	0.950666	-6.84
247397_at	Dof zinc finger protein - like Dof zinc fin	---	AT5G62940	1.02	0.03	0.14	0.89296	0.950666	-6.84
258374_at	hypothetical protein predicted by gensca	---	AT3G14360	1.02	0.03	0.14	0.893211	0.950819	-6.84
261199_at	unknown protein	---	AT1G12950	-1.01	-0.01	-0.14	0.893267	0.950834	-6.84
266894_at	hypothetical protein predicted by gensca	---	AT2G26050	1.01	0.01	0.14	0.893565	0.950974	-6.84
259256_at	putative coated vesicle membrane prote	---	AT3G07680	1.01	0.02	0.14	0.893607	0.950974	-6.84
261059_at	transcription factor TINY, putative simila	---	AT1G01250	1.02	0.02	0.14	0.893441	0.950974	-6.84
249449_at	unknown protein	---	AT5G39430	-1.01	-0.01	-0.14	0.893532	0.950974	-6.84
245849_at	leukotriene-A4 hydrolase-like protein le	---	AT5G13520	-1.02	-0.03	-0.14	0.893649	0.950974	-6.84
260483_at	Barley Mlo protein isolog ; supported by	MLO4	AT1G11000	1.02	0.02	0.14	0.893645	0.950974	-6.84
246894_at	heat-shock protein - like heat-shock pro	---	AT5G25530	-1.02	-0.03	-0.14	0.893704	0.950980	-6.84
250295_at	putative protein	NEF1	AT5G13390	-1.01	-0.02	-0.14	0.893738	0.950980	-6.84
249544_at	anti-silencing factor 1-like protein S-locu	ASF1B	AT5G38110	1.02	0.02	0.14	0.893881	0.951088	-6.84
262582_at	hypothetical protein Is a member of the	---	AT1G15410	1.03	0.04	0.14	0.89418	0.951362	-6.84
262437_at	hypothetical protein	---	---	-1.01	-0.02	-0.14	0.894396	0.951547	-6.84
260370_at	putative aminolevulinate dehydratase si	HEMB1	AT1G69740	-1.01	-0.02	-0.14	0.894588	0.951593	-6.84
246115_at	putative protein chloroplast outer envel	---	AT5G20300	1.01	0.02	0.14	0.894606	0.951593	-6.84
262578_at	hypothetical protein Similar to gi|22113 /	---	---	-1.01	-0.02	-0.14	0.894564	0.951593	-6.84
267041_at	unknown protein	---	AT2G34315	-1.01	-0.01	-0.14	0.894497	0.951593	-6.84
251856_at	Peptidase - like protein ileal peptidase,	AMP1	AT3G54720	1.02	0.03	0.14	0.894742	0.951649	-6.84
257557_at	terpene synthase-related protein, putati	---	AT3G14490	-1.01	-0.02	-0.14	0.894728	0.951649	-6.84
264950_at	peroxidase, putative similar to peroxida	---	AT1G77100	-1.01	-0.02	-0.14	0.89482	0.951687	-6.84
250050_at	putative protein predicted protein, Arabi	VAR3	AT5G17790	1.01	0.02	0.14	0.894943	0.951730	-6.84
264842_at	hypothetical protein predicted by gensca	---	AT1G03700	1.01	0.01	0.14	0.894903	0.951730	-6.84
255828_at	hypothetical protein predicted by genefi	---	AT2G40630	-1.01	-0.01	-0.14	0.895028	0.951776	-6.84
265705_at	unknown protein related to MO25 (mous	---	AT2G03410	1.03	0.04	0.14	0.895083	0.951790	-6.84
263487_at	hypothetical protein predicted by genefi	---	AT2G31850	-1.01	-0.01	-0.14	0.895145	0.951811	-6.84
258647_at	unknown protein ; supported by cDNA:	---	AT3G07870	1.01	0.02	0.14	0.895515	0.951814	-6.84

248008_at	transcription factor NtWRKY4-like ; supp	WRKY2	AT5G56270	-1.02	-0.02	-0.14	0.895547	0.951814	-6.84
267070_at	putative DnaJ protein	---	AT2G41000	-1.02	-0.02	-0.14	0.8954	0.951814	-6.84
246749_at	putative protein ; supported by cDNA: g	---	AT5G27830	1.02	0.02	0.14	0.895235	0.951814	-6.84
255262_at	putative protein equilibrative nucleoside	---	AT4G05140	1.01	0.01	0.14	0.895571	0.951814	-6.84
249921_at	reverse-transcriptase - like protein predi	---	AT5G19270	-1.01	-0.01	-0.14	0.895607	0.951814	-6.84
267264_at	putative serine carboxypeptidase II ; su	SCPL11	AT2G22970	-1.03	-0.04	-0.14	0.895332	0.951814	-6.84
256947_at	hypothetical protein contains Pfam profi	POK2	AT3G19050	-1.01	-0.01	-0.14	0.895555	0.951814	-6.84
257089_at	hypothetical protein	SVL3	AT3G20520	1.01	0.02	0.14	0.895438	0.951814	-6.84
256719_at	En/Spm-like transposon protein related	---	---	1.01	0.02	0.14	0.895295	0.951814	-6.84
250241_at	photoreceptor-interacting protein-like; n	---	AT5G13600	1.01	0.02	0.14	0.895328	0.951814	-6.84
260325_at	putative monodehydroascorbate reducta	MDAR6	AT1G63940	-1.01	-0.02	-0.14	0.896045	0.952107	-6.84
247433_at	E2, ubiquitin-conjugating enzyme 3 (UB	UBC3	AT5G62540	-1.02	-0.02	-0.14	0.896011	0.952107	-6.84
245208_at	lateral root primordia (LRP1)	LRP1	AT5G12330	-1.01	-0.02	-0.14	0.89605	0.952107	-6.84
257464_at	hypothetical protein predicted by gensca	---	AT1G20940	1.01	0.01	0.14	0.896043	0.952107	-6.84
257110_x_a	hypothetical protein	---	---	-1.01	-0.02	-0.14	0.896205	0.952140	-6.84
265560_at	putative glycine-rich protein	GRP-3	AT2G05520	1.01	0.01	0.14	0.896191	0.952140	-6.84
267521_at	hypothetical protein predicted by genfin	---	AT2G30480	1.01	0.02	0.14	0.896172	0.952140	-6.84
260624_at	high-affinity nitrate transporter ACH2 id	NRT2.2	AT1G08100	-1.02	-0.02	-0.14	0.896249	0.952142	-6.84
245834_at	transposon protein, putative similar to E	---	---	-1.01	-0.01	-0.14	0.896338	0.952148	-6.84
256492_at	hypothetical protein contains similarity t	---	AT1G31490	-1.01	-0.02	-0.14	0.896311	0.952148	-6.84
262185_at	MADS box transcription factor, putative	AGL67	AT1G77950	1.01	0.01	0.14	0.896439	0.952166	-6.84
257134_at	hypothetical protein similar to oxidoredu	---	AT3G12870	1.01	0.02	0.14	0.896414	0.952166	-6.84
254631_at	putative protein predicted proteins, Ara	LSH9	AT4G18610	-1.02	-0.03	-0.13	0.896569	0.952174	-6.84
255141_at	putative protein several hypothetical pro	---	---	-1.01	-0.01	-0.14	0.896514	0.952174	-6.84
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gb:J044	---	---	1.03	0.04	0.13	0.896571	0.952174	-6.84
259595_at	CONSTANS family zinc finger protein,	---	AT1G28050	-1.02	-0.02	-0.13	0.896782	0.952292	-6.84
256282_at	unknown protein	---	AT3G12550	-1.01	-0.02	-0.13	0.896808	0.952292	-6.84
260859_at	serine carboxypeptidase II, putative sim	scpl44	AT1G43780	1.01	0.02	0.13	0.896728	0.952292	-6.84
261630_at	hypothetical protein predicted by genem	---	AT1G50080	-1.01	-0.01	-0.13	0.896969	0.952419	-6.84
259560_at	hypothetical protein	WAK2	AT1G21270	-1.03	-0.05	-0.13	0.897208	0.952577	-6.84
247950_at	unknown protein	---	AT5G57230	-1.01	-0.01	-0.13	0.897243	0.952577	-6.84
255205_at	putative transposon protein	---	---	-1.01	-0.01	-0.13	0.897214	0.952577	-6.84
267458_at	similar to Mlo proteins from H. vulgare ;	MLO5	AT2G33670	-1.01	-0.02	-0.13	0.897449	0.952659	-6.84
267307_at	putative laccase	LAC3	AT2G30210	1.01	0.02	0.13	0.897371	0.952659	-6.84
255746_at	heat shock transcription factor, putative	---	AT1G32020	-1.01	-0.01	-0.13	0.897487	0.952659	-6.84

258440_at	putative protein phosphatase similar to p	---	AT3G17250	-1.01	-0.02	-0.13	0.897454	0.952659	-6.84
247728_at	putative protein	---	---	1.01	0.02	0.13	0.897567	0.952699	-6.84
254061_at	putative protein several hypothetical pro	---	AT4G25360	-1.01	-0.02	-0.13	0.897667	0.952716	-6.84
257781_at	spastin protein, putative similar to spast	---	AT3G27120	-1.01	-0.01	-0.13	0.897645	0.952716	-6.84
261678_at	disease resistance protein, putative sim	---	AT1G47370	-1.01	-0.02	-0.13	0.897939	0.952928	-6.84
246725_at	putative protein various predicted prote	---	AT5G29040	1.02	0.02	0.13	0.89795	0.952928	-6.84
257693_at	hypothetical protein predicted by genem	---	AT3G12850	1.02	0.03	0.13	0.898102	0.953045	-6.84
257114_at	cytochrome P450, putative contains Pfa	CYP705A2	AT3G20140	1.01	0.02	0.13	0.898163	0.953066	-6.84
254550_at	Fe(II) transport protein ;supported by fu	IRT1	AT4G19690	-1.01	-0.01	-0.13	0.898206	0.953067	-6.84
257403_at	hypothetical protein similar to hypothetic	---	AT1G62520	1.01	0.02	0.13	0.898385	0.953083	-6.84
253882_at	pelota (PEL1)	PEL1	AT4G27650	-1.01	-0.02	-0.13	0.898332	0.953083	-6.84
253568_at	putative protein receptor-like kinase, Pe	---	AT4G31230	1.01	0.02	0.13	0.898272	0.953083	-6.84
256953_at	flavonol 3-O-Glucosyltransferase, putat	---	AT3G29630	1.01	0.02	0.13	0.898388	0.953083	-6.84
264389_at	unknown protein similar to hypothetical p	---	AT1G11960	1.02	0.03	0.13	0.898493	0.953150	-6.84
245695_at	rec - like protein	---	AT5G04270	-1.01	-0.02	-0.13	0.898767	0.953396	-6.84
251772_at	cyclophilin-like protein ROC7, cyclophili	---	AT3G55920	1.01	0.02	0.13	0.898972	0.953408	-6.84
258889_at	putative pectinesterase similar to pectin	---	AT3G05610	-1.01	-0.02	-0.13	0.898978	0.953408	-6.84
247479_at	NAC - like protein OsNAC7, Oryza sativ	ANAC101	AT5G62380	1.01	0.01	0.13	0.898982	0.953408	-6.84
248899_at	carboxy-terminal proteinase D1-like prot	---	AT5G46390	-1.01	-0.02	-0.13	0.898869	0.953408	-6.84
259508_at	hypothetical protein predicted by genem	---	---	-1.02	-0.02	-0.13	0.898988	0.953408	-6.84
248255_at	ATP-dependent Clp protease ATP-bindi	CLPX	AT5G53350	-1.01	-0.02	-0.13	0.899043	0.953423	-6.84
248789_at	putative protein strong similarity to unkn	---	AT5G47440	-1.02	-0.02	-0.13	0.899124	0.953464	-6.84
253507_at	serine threonine protein kinase like prot	---	AT4G32000	-1.02	-0.02	-0.13	0.899208	0.953509	-6.84
249235_at	beta-1,3-glucanase-like protein ;suppo	BG_PPAP	AT5G42100	1.01	0.01	0.13	0.899467	0.953675	-6.84
258471_at	NPK1-related protein kinase 3 identical	ANP3	AT3G06030	-1.01	-0.02	-0.13	0.899421	0.953675	-6.84
254344_at	alcohol dehydrogenase like protein prot	---	AT4G22110	-1.02	-0.02	-0.13	0.899499	0.953675	-6.84
249117_at	heat shock transcription factor-like prote	AT-HSFA6	AT5G43840	-1.01	-0.01	-0.13	0.899532	0.953675	-6.84
259837_at	aquaporin, putative similar to delta tono	---	AT1G52180	-1.02	-0.02	-0.13	0.899794	0.953907	-6.84
248811_at	putative protein contains similarity to ER	---	AT5G47310	-1.01	-0.02	-0.13	0.899834	0.953907	-6.84
246516_at	putative protein auxin-independent grov	---	AT5G15740	-1.04	-0.05	-0.13	0.899878	0.953909	-6.84
255209_at	see GB:AF077408	---	---	-1.01	-0.02	-0.13	0.899985	0.953978	-6.84
259531_at	hypothetical protein	---	AT1G12460	1.02	0.02	0.13	0.900209	0.954021	-6.84
259294_at	hypothetical protein predicted by genscar	ATN	AT3G05330	-1.02	-0.02	-0.13	0.900185	0.954021	-6.84
264590_at	unknown protein ;supported by full-leng	---	AT2G17710	-1.05	-0.07	-0.13	0.900074	0.954021	-6.84
259328_at	putative lectin contains Pfam profile: PF	ATMLP-30	AT3G16440	1.01	0.02	0.13	0.900234	0.954021	-6.84

257282_at	TNP2-like transposon protein, putative	---	---	-1.01	-0.02	-0.13	0.900141	0.954021	-6.84
252702_at	putative protein predicted proteins, Arat	---	---	1.01	0.01	0.13	0.9003	0.954046	-6.84
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=gb:J0442	---	---	-1.02	-0.04	-0.13	0.900423	0.954088	-6.84
249043_at	berberine bridge enzyme	---	AT5G44360	1.01	0.01	0.13	0.900407	0.954088	-6.84
262716_at	multicatalytic endopeptidase identical to	PAB1	AT1G16470	-1.01	-0.02	-0.13	0.900592	0.954223	-6.84
247995_at	putative protein contains similarity to ph	---	AT5G56160	-1.01	-0.02	-0.13	0.900687	0.954279	-6.84
258130_at	unknown protein	---	AT3G24510	-1.01	-0.01	-0.13	0.900768	0.954320	-6.84
255822_at	putative expansin ;supported by full-len	ATEXPA8	AT2G40610	1.09	0.12	0.13	0.900865	0.954379	-6.84
251908_at	putative protein late embryogenis abun	---	AT3G53770	1.01	0.02	0.13	0.900965	0.954423	-6.84
257361_at	putative Ta11-like non-LTR retroelemen	---	---	1.01	0.02	0.13	0.90099	0.954423	-6.84
263004_at	hypothetical protein contains similarity to	ATNEK1	AT1G54510	-1.01	-0.02	-0.13	0.901277	0.954431	-6.84
252194_at	putative tyrosine phosphatase phospha	ATPEN3	AT3G50110	-1.01	-0.02	-0.13	0.901291	0.954431	-6.84
246039_at	putative protein serine-arginine-rich spli	---	AT5G19480	-1.01	-0.01	-0.13	0.901141	0.954431	-6.84
258224_at	LEA76 homologue type2 identical to LE	---	AT3G15670	-1.01	-0.01	-0.13	0.901209	0.954431	-6.84
252739_at	putative protein mRNA, Homo sapiens,	---	AT3G43250	-1.01	-0.01	-0.13	0.901222	0.954431	-6.84
257520_at	hypothetical protein	---	AT3G07710	-1.01	-0.02	-0.13	0.901098	0.954431	-6.84
248545_at	cysteine proteinase similar to cysteine e	---	AT5G50260	1.01	0.01	0.13	0.901234	0.954431	-6.84
246504_at	hypothetical protein ;supported by full-le	---	AT5G16160	1.01	0.01	0.13	0.901396	0.954498	-6.84
258765_at	putative pectinesterase contains similari	---	AT3G10710	1.01	0.01	0.13	0.901564	0.954626	-6.84
260910_at	importin alpha, putative similar to impor	IMPA-6	AT1G02690	-1.02	-0.02	-0.13	0.901642	0.954626	-6.84
253883_at	hypothetical protein	---	AT4G27660	1.01	0.02	0.13	0.901643	0.954626	-6.84
249094_at	dimethylaniline monooxygenase-like	YUC5	AT5G43890	-1.01	-0.02	-0.13	0.901766	0.954659	-6.84
263324_at	hypothetical protein predicted by gensca	---	AT2G04220	-1.01	-0.01	-0.13	0.9018	0.954659	-6.84
265436_at	putative retroelement pol polyprotein	---	---	1.01	0.01	0.13	0.901717	0.954659	-6.84
266142_at	unknown protein ; supported by cDNA:	---	AT2G39030	-1.06	-0.08	-0.13	0.901937	0.954761	-6.84
247361_at	unknown protein ;supported by full-leng	---	AT5G63480	-1.01	-0.02	-0.13	0.902142	0.954912	-6.84
266047_at	unknown protein	---	AT2G40800	-1.01	-0.02	-0.13	0.902164	0.954912	-6.84
264129_at	hypothetical protein predicted by genem	---	AT1G79170	-1.01	-0.02	-0.13	0.902221	0.954928	-6.84
263673_at	unknown protein	---	AT2G04800	-1.02	-0.02	-0.13	0.902336	0.955006	-6.84
261936_at	seed maturation protein PM27, putative	---	AT1G22600	1.01	0.02	0.13	0.902439	0.955070	-6.84
245812_at	hypothetical protein predicted by genem	---	---	-1.01	-0.01	-0.13	0.902607	0.955204	-6.84
255917_at	putative protein	---	AT5G28560	1.01	0.01	0.13	0.902729	0.955289	-6.84
250629_at	respiratory burst oxidase protein A	ATRBOHA	AT5G07390	1.01	0.02	0.13	0.90278	0.955299	-6.84
248084_at	sodium proton exchanger	NHX3	AT5G55470	-1.01	-0.02	-0.13	0.902936	0.955420	-6.84
266695_at	putative CCCH-type zinc finger protein	---	AT2G19810	-1.02	-0.03	-0.13	0.902997	0.955439	-6.84

260703_at	syntaxin, putative similar to syntaxin GE	ATSYP24	AT1G32270	-1.01	-0.01	-0.13	0.90306	0.955461	-6.84
256093_at	predicted protein ; supported by cDNA: (	---	AT1G20823	1.03	0.05	0.13	0.903144	0.955498	-6.84
259393_at	trehalose-6-phosphate synthase, putati	ATTPS7	AT1G06410	1.01	0.02	0.13	0.903234	0.955498	-6.84
253312_s_a	putative protein (1,4)-beta-xylan endohy	---	AT4G33850 /	1.01	0.01	0.13	0.903247	0.955498	-6.84
258325_at	putative heat shock protein similar to pu	HSFA6B	AT3G22830	1.01	0.01	0.13	0.903262	0.955498	-6.84
266245_at	putative translation initiation factor IF2	---	AT2G27700	1.01	0.01	0.13	0.903336	0.955532	-6.84
257743_at	unknown protein	---	AT3G27390	1.01	0.02	0.13	0.903549	0.955536	-6.84
265630_at	unknown protein similar to ovarian tumo	---	AT2G27350	1.01	0.01	0.13	0.903428	0.955536	-6.84
260230_at	putative DNA-binding protein contains P	---	AT1G74500	1.01	0.01	0.13	0.903431	0.955536	-6.84
255658_at	hypothetical protein ;supported by full-le	---	AT4G00770	1.01	0.02	0.13	0.903508	0.955536	-6.84
249029_at	disease resistance protein-like	---	AT5G44870	1.01	0.01	0.13	0.903469	0.955536	-6.84
263587_at	putative synaptobrevin	ATVAMP7	AT2G25340	1.01	0.02	0.13	0.903596	0.955541	-6.84
267141_at	putative MYB family transcription factor	---	AT2G38090	-1.01	-0.02	-0.13	0.903845	0.955726	-6.84
257341_at	pseudogene, Mutator-like transposase	---	---	1.01	0.01	0.13	0.903855	0.955726	-6.84
261772_at	hypothetical protein predicted by genem	---	AT1G76240	-1.02	-0.03	-0.13	0.903999	0.955789	-6.84
256942_at	hypothetical protein similar to unknown	LSH4	AT3G23290	1.03	0.04	0.13	0.90404	0.955789	-6.84
259963_at	phosphate/phosphoenolpyruvate transl	---	AT1G53660	-1.01	-0.01	-0.13	0.903959	0.955789	-6.84
257942_at	SKP1/ASK1 (At8), putative similar to SI	ASK8	AT3G21830	-1.01	-0.02	-0.12	0.904201	0.955915	-6.84
247765_at	cytochrome P450 CYP86A1	CYP86A1	AT5G58860	1.02	0.03	0.12	0.904441	0.956125	-6.84
254794_at	putative protein	---	AT4G12970	1.04	0.05	0.12	0.904495	0.956138	-6.84
248717_at	Expressed protein ; supported by full-ler	---	AT5G48175	-1.01	-0.01	-0.12	0.904634	0.956239	-6.84
265355_at	hypothetical protein predicted by genefir	---	AT2G16760	1.02	0.02	0.12	0.90487	0.956432	-6.84
253146_at	putative protein predicted protein, Arabi	---	AT4G35590	1.01	0.01	0.12	0.9049	0.956432	-6.84
248525_s_a	unknown protein	---	AT5G50610 /	1.01	0.01	0.12	0.905033	0.956529	-6.84
261940_at	hypothetical protein predicted by genem	---	AT1G22520	1.01	0.02	0.12	0.905121	0.956577	-6.84
253253_at	putative protein auxin-regulated gene, \	---	AT4G34750	1.01	0.01	0.12	0.905479	0.956646	-6.84
253274_at	Phosphoglycerate dehydrogenase - like	EDA9	AT4G34200	1.06	0.08	0.12	0.90547	0.956646	-6.84
255005_at	putative protein putative proteins Arabid	---	AT4G09990	-1.01	-0.02	-0.12	0.905361	0.956646	-6.84
260773_at	gibberellin 2- oxidase identical to gibber	ATGA2OX	AT1G78440	-1.01	-0.02	-0.12	0.905234	0.956646	-6.84
263620_at	hypothetical protein predicted by gensca	---	---	1.01	0.01	0.12	0.905338	0.956646	-6.84
251613_at	hypothetical protein	---	AT3G57960	-1.01	-0.02	-0.12	0.905303	0.956646	-6.84
250081_at	unknown protein	---	AT5G17180	1.01	0.01	0.12	0.905441	0.956646	-6.84
263649_at	putative 1-aminocyclopropane-1-carbox	---	AT1G04380	-1.01	-0.01	-0.12	0.905586	0.956706	-6.84
250802_at	pectinesterase	---	AT5G04970	-1.01	-0.01	-0.12	0.90562	0.956706	-6.84
266701_at	profilin 1 ; supported by cDNA: gi_1353	PRF1	AT2G19760	1.01	0.01	0.12	0.905759	0.956808	-6.84

250630_at	hypothetical protein	---	AT5G07400	-1.01	-0.02	-0.12	0.905927	0.956942	-6.84
261202_at	flower pigmentation protein ATAN11 ide	ATAN11	AT1G12910	1.01	0.01	0.12	0.905984	0.956957	-6.84
250437_at	AtAGP4 ; supported by cDNA: gi_1392(	AGP4	AT5G10430	1.04	0.06	0.12	0.906248	0.956971	-6.84
257625_at	cytochrome P450, putative contains Pfa	CYP71B24	AT3G26230	-1.05	-0.07	-0.12	0.906116	0.956971	-6.84
262249_at	root hairless 1 (RHL1) similar to root hai	RHL1	AT1G48380	1.01	0.02	0.12	0.906163	0.956971	-6.84
248897_at	KCO-like protein 3 (emb|CAB40380.1)	KCO3	AT5G46360	-1.01	-0.02	-0.12	0.906226	0.956971	-6.84
246571_at	putative protein	---	AT5G15000	-1.01	-0.01	-0.12	0.90614	0.956971	-6.84
265054_x_a	mutator-like transposase, putative simil	---	---	1.01	0.02	0.12	0.906179	0.956971	-6.84
256778_at	nucleosome assembly protein, putative	NAP1;4	AT3G13782	1.01	0.01	0.12	0.906292	0.956972	-6.84
262064_at	elongation factor, putative similar to EL(	LOS1	AT1G56070	-1.01	-0.02	-0.12	0.906346	0.956979	-6.84
247998_at	unknown protein	---	AT5G56200	-1.02	-0.02	-0.12	0.906382	0.956979	-6.84
264002_at	putative DnaJ protein ;supported by full	---	AT2G22360	-1.01	-0.02	-0.12	0.906441	0.956997	-6.84
266230_at	hypothetical protein predicted by gensca	---	AT2G28830	-1.02	-0.03	-0.12	0.906561	0.957075	-6.84
257703_at	unknown protein ; supported by full-leng	---	AT3G12640	-1.01	-0.01	-0.12	0.906641	0.957075	-6.84
246620_at	cytochrome P450 ; supported by cDNA	CYP81D1	AT5G36220	-1.02	-0.03	-0.12	0.906639	0.957075	-6.84
256368_at	cinnamyl alcohol dehydrogenase, putat	---	AT1G66800	1.01	0.01	0.12	0.906865	0.957268	-6.84
250294_at	auxin reponsive - like protein Nt-gh3 de	---	AT5G13380	1.01	0.01	0.12	0.907041	0.957409	-6.84
255979_at	hypothetical protein	UPF3	AT1G33980	-1.01	-0.01	-0.12	0.907151	0.957481	-6.84
257390_x_a	hypothetical protein predicted by gensca	---	---	-1.01	-0.02	-0.12	0.907251	0.957522	-6.84
252987_at	putative growth regulator protein auxin-	---	AT4G38390	-1.01	-0.02	-0.12	0.907335	0.957522	-6.84
257710_at	unknown protein ;supported by full-leng	---	AT3G27350	1.01	0.01	0.12	0.907398	0.957522	-6.84
255160_at	putative pathogenesis-related protein	---	AT4G07820	1.01	0.01	0.12	0.907389	0.957522	-6.84
256604_at	hypothetical protein predicted by genem	---	---	-1.01	-0.01	-0.12	0.907401	0.957522	-6.84
252729_at	putative protein replication protein A1, X	---	---	-1.01	-0.01	-0.12	0.907603	0.957692	-6.84
265469_at	unknown protein predicted by genscan	---	AT2G37160	-1.01	-0.01	-0.12	0.907868	0.957797	-6.84
265762_at	hypothetical protein	---	AT2G01240	-1.01	-0.02	-0.12	0.907912	0.957797	-6.84
254151_at	F-box protein family, AtFBX14 similar to	---	AT4G24390	1.01	0.01	0.12	0.907884	0.957797	-6.84
253315_at	putative protein various predicted prote	---	AT4G33900	-1.01	-0.01	-0.12	0.907788	0.957797	-6.84
250142_at	polygalacturonase - like protein polygal	---	AT5G14650	-1.02	-0.03	-0.12	0.90777	0.957797	-6.84
258633_at	putative serine carboxypeptidase II simil	SCPL27	AT3G07990	-1.02	-0.03	-0.12	0.908158	0.957997	-6.84
264881_s_a	lysine and histidine specific transporter,	---	AT1G61270 /	-1.01	-0.01	-0.12	0.908186	0.957997	-6.84
257057_at	hypothetical protein predicted by gensca	---	---	-1.01	-0.01	-0.12	0.908365	0.958053	-6.84
246315_at	hypothetical protein	---	AT3G56870	-1.02	-0.02	-0.12	0.908286	0.958053	-6.84
255970_s_a	hypothetical protein predicted by genesc	---	---	-1.01	-0.01	-0.12	0.908356	0.958053	-6.84
265533_at	putative replication protein A1	---	---	1.01	0.01	0.12	0.908457	0.958105	-6.84

248506_at	adenylate kinase ;supported by full-leng	---	AT5G50370	-1.03	-0.04	-0.12	0.908697	0.958314	-6.85
247585_at	putative protein predicted proteins, Arat	---	AT5G60680	1.01	0.02	0.12	0.908869	0.958363	-6.85
265838_at	putative spliceosome associated protein	---	AT2G14550	-1.01	-0.01	-0.12	0.90882	0.958363	-6.85
250282_at	putative protein predicted protein, Arabi	---	AT5G13260	1.01	0.02	0.12	0.908859	0.958363	-6.85
255246_at	putative protein hypothetical protein F14	---	---	1.01	0.02	0.12	0.909053	0.958512	-6.85
262424_at	hypothetical protein predicted by genem	---	AT1G47680	-1.01	-0.01	-0.12	0.9091	0.958518	-6.85
246569_at	lysophospholipase -like protein lysopho	---	AT5G14980	1.01	0.01	0.12	0.909156	0.958532	-6.85
252167_at	putative protein steroid dehydrogenase	---	AT3G50560	1.01	0.02	0.12	0.909434	0.958780	-6.85
260858_at	hypothetical protein predicted by genem	---	AT1G43770	-1.01	-0.01	-0.12	0.90962	0.958780	-6.85
257820_at	immunophilin (FKBP15-1) identical to in	FKBP15-1	AT3G25220	1.01	0.02	0.12	0.909608	0.958780	-6.85
246599_at	putative protein ATP-dependent RNA h	---	AT5G14900	1.01	0.01	0.12	0.909633	0.958780	-6.85
255196_x_a	see GB:AF058826	---	---	1.01	0.01	0.12	0.909627	0.958780	-6.85
251384_at	putative protein	---	AT3G60760	-1.01	-0.01	-0.12	0.909643	0.958780	-6.85
246137_at	putative protein predicted proteins, Arat	LSH1	AT5G28490	1.02	0.04	0.12	0.90969	0.958785	-6.85
247731_at	glucuronosyl transferase - like protein g	UGT76E2	AT5G59590	1.01	0.01	0.12	0.909756	0.958810	-6.85
260284_at	unknown protein ; supported by full-leng	---	AT1G80380	-1.01	-0.01	-0.12	0.909839	0.958854	-6.85
246793_at	putative protein seven transmembrane	---	AT5G27210	1.01	0.01	0.12	0.909952	0.958884	-6.85
256761_at	hypothetical protein predicted by gensca	---	AT3G25670	1.01	0.02	0.12	0.909921	0.958884	-6.85
245253_at	hydroperoxide lyase (HPOL) like protein	HPL1	AT4G15440	-1.05	-0.07	-0.12	0.910092	0.958906	-6.85
260472_at	hypothetical protein predicted by genefir	---	AT1G10990	-1.06	-0.08	-0.12	0.910099	0.958906	-6.85
256941_at	hypothetical protein	---	---	-1.01	-0.02	-0.12	0.910056	0.958906	-6.85
257811_at	nitrate transporter, putative similar to ni	---	AT3G25280	1.01	0.01	0.12	0.910147	0.958913	-6.85
253818_at	hypothetical protein	---	AT4G28330	-1.01	-0.02	-0.12	0.910203	0.958927	-6.85
245648_at	F5A9.12 hypothetical protein	---	---	-1.01	-0.01	-0.12	0.9105	0.959196	-6.85
256386_at	cytochrome P450, putative contains Pfa	---	AT1G66540	1.01	0.01	0.12	0.910557	0.959211	-6.85
260970_at	unknown protein	---	AT1G53640	1.01	0.02	0.12	0.91068	0.959297	-6.85
250807_at	helicase-like transcription factor-like pro	---	AT5G05130	-1.01	-0.02	-0.12	0.910732	0.959307	-6.85
248727_at	cytochrome P450	CYP705A5	AT5G47990	1.01	0.01	0.12	0.910862	0.959355	-6.85
245282_at	hypothetical protein ; supported by cDNA	---	AT4G14990	-1.01	-0.02	-0.12	0.910836	0.959355	-6.85
258878_at	hypothetical protein predicted by gensca	---	AT3G03170	1.01	0.01	0.12	0.910975	0.959430	-6.85
249772_at	unknown protein	---	AT5G24130	1.02	0.02	0.12	0.911027	0.959441	-6.85
263894_at	putative cytochrome P450	CYP96A5	AT2G21910	1.01	0.01	0.12	0.911105	0.959472	-6.85
261456_at	hypothetical protein predicted by genem	---	AT1G21050	1.05	0.06	0.12	0.911141	0.959472	-6.85
254391_at	putative bifunctional nuclease bifunctior	ENDO3	AT4G21590	1.01	0.01	0.12	0.911445	0.959582	-6.85
259136_at	unknown protein	---	AT3G05470	1.01	0.02	0.12	0.911427	0.959582	-6.85

245489_at	FCA gamma protein	FCA	AT4G16280	1.01	0.01	0.12	0.911456	0.959582	-6.85
248763_at	putative protein similar to unknown prote	---	AT5G47550	-1.07	-0.10	-0.12	0.91144	0.959582	-6.85
255422_at	putative D-type cyclin	CYCD6;1	AT4G03270	1.01	0.01	0.12	0.911291	0.959582	-6.85
265171_at	hypothetical protein	---	AT1G23790	-1.01	-0.01	-0.12	0.911549	0.959636	-6.85
258541_at	hypothetical protein	---	AT3G07000	1.01	0.01	0.12	0.911635	0.959656	-6.85
254733_at	putative polygalacturonase polygalactu	---	AT4G13760	-1.01	-0.01	-0.12	0.911652	0.959656	-6.85
259386_at	hypothetical protein contains similarity t	NUB	AT1G13400	1.01	0.01	0.12	0.911702	0.959664	-6.85
245659_at	hypothetical protein predicted by genem	---	AT1G28260	-1.02	-0.02	-0.11	0.911847	0.959773	-6.85
257790_at	gda-1, putative similar to gda-1 GB:CA	---	AT3G27090	-1.01	-0.02	-0.11	0.912048	0.959940	-6.85
261290_at	hypothetical protein predicted by genem	---	AT1G36990	1.01	0.02	0.11	0.912211	0.959978	-6.85
265181_at	putative OBP32pep protein ;supported	---	AT1G23510	-1.01	-0.02	-0.11	0.912161	0.959978	-6.85
247622_at	putative protein	---	AT5G60350	1.01	0.01	0.11	0.912169	0.959978	-6.85
255110_at	peroxidase C2 precursor like protein pe	---	AT4G08770	1.05	0.07	0.11	0.912325	0.960010	-6.85
257446_at	hypothetical protein predicted by gensca	---	AT2G10440	-1.01	-0.01	-0.11	0.912305	0.960010	-6.85
258265_at	putative beta-1,3-glucanase precursor s	---	AT3G15800	-1.01	-0.01	-0.11	0.912435	0.960081	-6.85
258127_at	unknown protein	---	AT3G24570	1.01	0.01	0.11	0.91256	0.960124	-6.85
262898_at	hypothetical protein predicted by genem	---	AT1G59850	1.01	0.01	0.11	0.912527	0.960124	-6.85
263807_at	putative indole-3-glycerol phosphate syr	---	AT2G04400	1.04	0.06	0.11	0.912637	0.960160	-6.85
254327_at	RCc3- like protein RCc3 protein, Oryza	---	AT4G22490	-1.02	-0.03	-0.11	0.912782	0.960231	-6.85
265972_at	putative retroelement pol polyprotein	---	---	1.01	0.01	0.11	0.912788	0.960231	-6.85
246657_at	putative protein predicted proteins, Ara	---	---	-1.01	-0.01	-0.11	0.912918	0.960324	-6.85
267169_at	putative oxidoreductase	---	AT2G37540	-1.02	-0.03	-0.11	0.913023	0.960390	-6.85
248110_at	wax synthase-like protein	---	AT5G55320	1.01	0.01	0.11	0.91312	0.960447	-6.85
266956_at	unknown protein	---	AT2G34510	1.02	0.03	0.11	0.913224	0.960474	-6.85
253563_at	putative protein predicted protein, Schiz	---	AT4G31150	-1.01	-0.02	-0.11	0.91323	0.960474	-6.85
255121_at	putative mitogen-activated protein kinas	MAPKKK9	AT4G08480	-1.01	-0.02	-0.11	0.913349	0.960511	-6.85
265525_at	putative Ty3-gypsy-like retroelement pol	---	---	1.01	0.01	0.11	0.913325	0.960511	-6.85
258040_at	unknown protein ;supported by full-leng	---	AT3G21190	-1.05	-0.07	-0.11	0.913479	0.960604	-6.85
245520_at	delta-cadinene synthase like protein	ATTS1	AT4G15870	1.01	0.01	0.11	0.913636	0.960610	-6.85
256445_at	hypothetical protein predicted by genem	---	AT3G11160	-1.01	-0.01	-0.11	0.913692	0.960610	-6.85
265763_at	unknown protein	---	AT2G48060	-1.01	-0.01	-0.11	0.913569	0.960610	-6.85
261123_at	hypothetical protein predicted by gensca	---	AT1G62860	1.01	0.02	0.11	0.913696	0.960610	-6.85
245837_at	peptidylprolyl isomerase, putative simila	---	AT1G58450	1.01	0.01	0.11	0.913693	0.960610	-6.85
263256_at	unknown protein similar to ESTs gb|H36	ATCPISCA	AT1G10500	-1.01	-0.02	-0.11	0.913904	0.960785	-6.85
246233_at	putative protein	---	AT4G36550	1.02	0.03	0.11	0.914036	0.960802	-6.85

263596_at	putative inositol polyphosphate-5-phosp	---	AT2G01900	1.01	0.01	0.11	0.914046	0.960802	-6.85
267039_at	hypothetical protein predicted by genefir	---	AT2G34270	-1.01	-0.01	-0.11	0.913999	0.960802	-6.85
256848_at	hypothetical protein similar to hypothetic	---	AT3G27960	1.03	0.04	0.11	0.914362	0.960830	-6.85
265661_at	putative protein kinase contains a protei	---	AT2G24360	1.01	0.01	0.11	0.914634	0.960830	-6.85
264253_at	putative kinesin similar to GB:AAB6106(	---	AT1G09170	1.01	0.02	0.11	0.914747	0.960830	-6.85
266388_at	hypothetical protein predicted by gensca	---	AT2G32340	-1.01	-0.02	-0.11	0.914698	0.960830	-6.85
264585_at	auxin-resistance protein AXR1 E1 ubiqu	AXR1	AT1G05180	-1.01	-0.01	-0.11	0.914164	0.960830	-6.85
251167_at	putative protein proteinase inhibitor - O	---	AT3G63360	1.01	0.01	0.11	0.914283	0.960830	-6.85
246157_at	cytochrome-b5 reductase - like protein	---	AT5G20080	-1.01	-0.02	-0.11	0.914608	0.960830	-6.85
249163_at	glucose-6-phosphate isomerase, cytos	---	AT5G42740	-1.01	-0.02	-0.11	0.914523	0.960830	-6.85
252727_s_a	putative protein predicted proteins, Ara	---	---	1.01	0.01	0.11	0.914169	0.960830	-6.85
258115_at	hypothetical protein predicted by gescar	---	AT3G14670	-1.01	-0.01	-0.11	0.914745	0.960830	-6.85
250631_at	pectin methyl-esterase-like protein pect	---	AT5G07430	1.01	0.01	0.11	0.914603	0.960830	-6.85
261360_at	hypothetical protein predicted by gensca	---	---	1.01	0.01	0.11	0.914493	0.960830	-6.85
255174_at	putative Athila-like protein	---	---	1.01	0.01	0.11	0.914319	0.960830	-6.85
263527_at	putative thaumatin-like pathogenesis-rel	---	AT2G24810	-1.01	-0.02	-0.11	0.914465	0.960830	-6.85
254094_at	putative protein ATP-dependent DNA h	---	AT4G25120	-1.01	-0.02	-0.11	0.914302	0.960830	-6.85
261918_at	hypothetical protein	---	AT1G65940	-1.01	-0.01	-0.11	0.91447	0.960830	-6.85
256640_at	hypothetical protein predicted by genem	---	AT3G32260	1.01	0.01	0.11	0.914812	0.960854	-6.85
265553_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.11	0.914921	0.960924	-6.85
254786_at	putative protein gamma-interferon-indu	---	AT4G12890	1.01	0.01	0.11	0.915012	0.960931	-6.85
252341_at	remorin -like protein remorin, Solanum	---	AT3G48940	-1.01	-0.01	-0.11	0.914993	0.960931	-6.85
265126_s_a	hypothetical protein similar to hypothetic	---	AT1G55380 /	1.01	0.01	0.11	0.915131	0.961012	-6.85
266655_at	putative protein kinase contains a protei	AtAUR2	AT2G25880	-1.01	-0.02	-0.11	0.915238	0.961080	-6.85
253375_at	hypothetical protein	---	AT4G33280	1.01	0.01	0.11	0.915331	0.961089	-6.85
263078_at	hypothetical protein predicted by genefir	---	AT2G05350	-1.01	-0.01	-0.11	0.915295	0.961089	-6.85
263600_at	hypothetical protein predicted by gensca	DRD1	AT2G16390	-1.01	-0.01	-0.11	0.915415	0.961134	-6.85
257157_at	syntaxin-like protein similar to syntaxin	SYP32	AT3G24350	1.01	0.02	0.11	0.915568	0.961249	-6.85
253759_at	AIM1 protein ; supported by cDNA: gi_1	AIM1	AT4G29010	-1.01	-0.01	-0.11	0.915813	0.961452	-6.85
254516_at	putative protein	---	AT4G20290	1.01	0.01	0.11	0.915845	0.961452	-6.85
249016_at	putative protein contains similarity to DN	REV1	AT5G44750	-1.01	-0.02	-0.11	0.915913	0.961479	-6.85
265755_at	En/Spm transposon hypothetical protein	---	---	1.01	0.01	0.11	0.915957	0.961481	-6.85
257122_at	RNA-binding protein, putative contains	APUM5	AT3G20250	1.01	0.02	0.11	0.91671	0.961493	-6.85
259257_at	unknown protein ;supported by full-leng	---	AT3G07760	-1.01	-0.01	-0.11	0.916147	0.961493	-6.85
255724_at	hypothetical protein	BRCA2(IV	AT4G00020	-1.01	-0.01	-0.11	0.916625	0.961493	-6.85

261606_at	peroxidase, putative similar to peroxida	---	AT1G49570	-1.01	-0.02	-0.11	0.916183	0.961493	-6.85
263067_at	hypothetical protein predicted by gensca	---	AT2G17550	1.02	0.02	0.11	0.916485	0.961493	-6.85
261460_at	MAP kinase, putative similar to GB:CAE	ATMPK13	AT1G07880	-1.01	-0.01	-0.11	0.916828	0.961493	-6.85
254681_at	putative protein HYA22 protein, Homo s	---	AT4G18140	-1.01	-0.02	-0.11	0.916472	0.961493	-6.85
250927_at	lysine decarboxylase - like protein lysin	---	AT5G03270	-1.01	-0.02	-0.11	0.916748	0.961493	-6.85
252177_at	protein kinase ATN1 - like protein prote	---	AT3G50730	-1.01	-0.01	-0.11	0.916426	0.961493	-6.85
251271_at	hypothetical protein ; supported by full-le	---	AT3G62050	-1.01	-0.02	-0.11	0.916794	0.961493	-6.85
251312_at	MADS-box protein AGL13 ; supported b	AGL13	AT3G61120	1.01	0.01	0.11	0.916527	0.961493	-6.85
257476_at	unknown protein	---	AT1G80960	-1.01	-0.01	-0.11	0.916537	0.961493	-6.85
267019_at	hypothetical protein predicted by gensca	---	AT2G39130	-1.01	-0.01	-0.11	0.916884	0.961493	-6.85
249688_at	putative protein tyrosine aminotransfera	---	AT5G36160	-1.01	-0.02	-0.11	0.916127	0.961493	-6.85
256565_at	hypothetical protein	AT3G1951	---	-1.01	-0.01	-0.11	0.916133	0.961493	-6.85
251164_s_a	putative protein protein phosphatase 2C	---	AT3G63320 /	1.01	0.01	0.11	0.916367	0.961493	-6.85
256345_at	hypothetical protein similar to hypothetic	---	AT1G55030	1.01	0.01	0.11	0.916642	0.961493	-6.85
250901_at	putative protein ; supported by cDNA: g	RABC2A	AT5G03530	1.03	0.04	0.11	0.916775	0.961493	-6.85
245741_at	hypothetical protein similar to unknown p	---	AT1G44120	1.01	0.01	0.11	0.9163	0.961493	-6.85
263437_at	putative disease resistance response pr	---	AT2G28670	1.01	0.01	0.11	0.916205	0.961493	-6.85
265487_at	hypothetical protein	---	---	1.01	0.01	0.11	0.916796	0.961493	-6.85
252074_at	putative protein DNA helicase homolog	---	AT3G51700	-1.01	-0.01	-0.11	0.916896	0.961493	-6.85
254002_at	steroid sulfotransferase - like protein ste	---	AT4G26280	1.01	0.01	0.11	0.917101	0.961564	-6.85
263296_at	unknown protein	---	AT2G38800	1.02	0.03	0.11	0.917086	0.961564	-6.85
247321_s_a	phosphatidylinositol 4-kinase (emb|CAB	PI-4KBETA	AT5G09350 /	-1.01	-0.02	-0.11	0.917121	0.961564	-6.85
245826_at	disease resistance protein RPS4, putat	---	AT1G57850	-1.01	-0.01	-0.11	0.917138	0.961564	-6.85
260285_at	putative 3-isopropylmalate dehydrogena	---	AT1G80560	1.01	0.02	0.11	0.917174	0.961564	-6.85
267609_at	unknown protein similar to GP|522127|g	---	AT2G26780	1.01	0.01	0.11	0.917317	0.961587	-6.85
266933_at	putative Ta11-like non-LTR retroelemen	---	AT2G07760	1.01	0.02	0.11	0.917398	0.961587	-6.85
261509_at	hypothetical protein predicted by genem	---	AT1G71740	-1.01	-0.02	-0.11	0.917331	0.961587	-6.85
249017_at	C2 domain-containing protein-like	---	AT5G44760	-1.01	-0.02	-0.11	0.917407	0.961587	-6.85
248321_at	putative protein similar to unknown prote	---	AT5G52740	1.01	0.01	0.11	0.917332	0.961587	-6.85
264420_at	hypothetical protein predicted by genem	---	AT1G43320	-1.01	-0.01	-0.11	0.917798	0.961953	-6.85
247120_at	amino acid transporter protein-like	---	AT5G65990	-1.01	-0.01	-0.11	0.917993	0.962024	-6.85
248325_at	unknown protein	---	AT5G52800	1.01	0.01	0.11	0.917965	0.962024	-6.85
247088_at	unknown protein	---	AT5G66340	-1.01	-0.01	-0.11	0.917966	0.962024	-6.85
251246_at	auxin-induced protein homolog auxin-in	IAA30	AT3G62100	1.01	0.01	0.11	0.918085	0.962077	-6.85
262713_at	unknown protein	---	AT1G16520	1.02	0.02	0.11	0.918219	0.962172	-6.85

256586_at	hypothetical protein	---	AT3G28770	1.01	0.01	0.11	0.918289	0.962202	-6.85
249803_at	putative protein similar to unknown prote	---	AT5G23780	-1.01	-0.01	-0.11	0.918414	0.962289	-6.85
255752_at	secretory carrier membrane protein, pu	---	AT1G32050	-1.01	-0.02	-0.11	0.91869	0.962534	-6.85
263393_at	hypothetical protein similar to hypothetic	---	---	-1.01	-0.01	-0.11	0.918824	0.962585	-6.85
257815_at	unknown protein	---	AT3G25130	-1.01	-0.01	-0.11	0.918801	0.962585	-6.85
250375_at	putative protein L-gulono-gamma-lactor	---	AT5G11540	-1.01	-0.01	-0.11	0.91907	0.962755	-6.85
254046_at	hypothetical protein	---	AT4G26020	1.01	0.01	0.11	0.919032	0.962755	-6.85
248117_at	FH protein interacting protein FIP2 (gb|A	FIP2	AT5G55000	-1.01	-0.02	-0.11	0.919225	0.962784	-6.85
245677_at	hypothetical protein predicted by genem	---	AT1G56660	1.01	0.01	0.11	0.919191	0.962784	-6.85
255893_at	threonyl-tRNA synthetase, putative sim	---	AT1G17960	1.02	0.02	0.11	0.919163	0.962784	-6.85
257598_at	PRT1 identical to GB:CAA11891 from [	PRT1	AT3G24800	-1.01	-0.02	-0.11	0.919364	0.962833	-6.85
266548_at	unknown protein ;supported by full-leng	RPA	AT2G35210	1.01	0.02	0.11	0.919344	0.962833	-6.85
255096_at	hypothetical protein similar to T21B4.5,	---	---	-1.01	-0.01	-0.10	0.919458	0.962833	-6.85
253036_at	putative protein other predicted proteins	---	AT4G38340	1.01	0.01	0.10	0.919482	0.962833	-6.85
260839_at	unknown protein	---	AT1G43690	-1.01	-0.01	-0.11	0.919412	0.962833	-6.85
261826_at	pectin methylesterase, putative similar t	PMEPCRA	AT1G11580	1.02	0.03	0.10	0.919634	0.962948	-6.85
248423_at	putative protein contains similarity to unl	---	AT5G51670	1.01	0.02	0.10	0.919835	0.963070	-6.85
246229_at	pectinesterase like protein	sks15	AT4G37160	-1.01	-0.01	-0.10	0.919805	0.963070	-6.85
258165_at	unknown protein ; supported by cDNA:	---	AT3G17900	-1.01	-0.01	-0.10	0.919934	0.963085	-6.85
265997_at	Expressed protein ; supported by cDNA	---	AT2G24250	-1.01	-0.01	-0.10	0.919903	0.963085	-6.85
255348_at	hypothetical protein	---	AT4G03820	-1.01	-0.01	-0.10	0.920102	0.963216	-6.85
251053_at	Ca2+/H+ exchanger-like protein Ca2+/H	CAX4	AT5G01490	-1.02	-0.02	-0.10	0.920245	0.963322	-6.85
265842_at	putative AP2 domain transcription factor	ERF38	AT2G35700	1.02	0.03	0.10	0.920386	0.963337	-6.85
263990_at	putative phosphoprotein phosphatase ;	PP5.2	AT2G42810	-1.01	-0.01	-0.10	0.920361	0.963337	-6.85
266769_s_a	putative reverse transcriptase	---	---	-1.01	-0.01	-0.10	0.920316	0.963337	-6.85
253457_at	putative protein C56A3.6,Caenorhabdit	---	AT4G32060	1.01	0.01	0.10	0.920585	0.963457	-6.85
256124_at	hypothetical protein predicted by gensca	ATPUP9	AT1G18220	1.01	0.01	0.10	0.920547	0.963457	-6.85
253426_at	putative protein polygalacturonase (EC	---	AT4G32375	-1.01	-0.01	-0.10	0.920684	0.963517	-6.85
254896_at	MADS-box protein AGL14	AGL14	AT4G11880	-1.01	-0.01	-0.10	0.920753	0.963544	-6.85
267643_at	hypothetical protein predicted by genefir	RALFL17	AT2G32890	-1.01	-0.01	-0.10	0.920823	0.963573	-6.85
265286_at	putative NADH-ubiquinone oxireductase	---	AT2G20360	-1.01	-0.01	-0.10	0.920959	0.963671	-6.85
253471_at	hypothetical protein	---	---	1.01	0.01	0.10	0.921074	0.963748	-6.85
245542_at	CONSTANS like protein	---	AT4G15250	-1.01	-0.01	-0.10	0.921279	0.963917	-6.85
259306_at	unknown protein ;supported by full-leng	PNC1	AT3G05290	1.01	0.01	0.10	0.921544	0.964151	-6.85
245896_at	putative transcriptional co-activator (KIW	KIWI	AT5G09250	1.01	0.02	0.10	0.921715	0.964286	-6.85

257062_at	zinc finger protein, putative contains Pf	EMB2454	AT3G18290	1.02	0.03	0.10	0.922018	0.964302	-6.85
254615_at	RNase L inhibitor-like protein RNase L	RLI2	AT4G19210	-1.01	-0.01	-0.10	0.921857	0.964302	-6.85
262394_at	unknown protein	emb1273	AT1G49510	1.01	0.02	0.10	0.921875	0.964302	-6.85
257396_at	predicted protein	EPF1	AT2G20875	-1.01	-0.01	-0.10	0.922027	0.964302	-6.85
257380_at	hypothetical protein predicted by genefi	---	AT2G28090	1.01	0.01	0.10	0.921948	0.964302	-6.85
247986_at	unknown protein	---	AT5G56880	1.01	0.01	0.10	0.921889	0.964302	-6.85
252530_at	putative protein several oxidases, main	---	AT3G46500	1.01	0.01	0.10	0.921993	0.964302	-6.85
262458_at	serine/threonine kinase, putative simila	---	AT1G11280	-1.01	-0.01	-0.10	0.922152	0.964389	-6.85
257731_at	unknown protein similar to CALCINEUF	---	AT3G18430	1.01	0.01	0.10	0.922291	0.964490	-6.85
259962_at	RNA polymerase II, putative similar to C	---	AT1G53690	1.01	0.01	0.10	0.922384	0.964543	-6.85
254297_at	hypothetical protein	---	AT4G23110	1.01	0.01	0.10	0.922441	0.964559	-6.85
259103_at	unknown protein ; supported by cDNA:	---	AT3G11690	-1.02	-0.03	-0.10	0.922487	0.964563	-6.85
252780_at	alcohol dehydrogenase (ATA1) ;suppor	ATA1	AT3G42960	1.01	0.02	0.10	0.922634	0.964672	-6.85
246816_at	putative protein	---	AT5G27230	1.01	0.01	0.10	0.922724	0.964722	-6.85
260752_at	unknown protein contains similarity to fla	---	AT1G49030	-1.01	-0.01	-0.10	0.922774	0.964729	-6.85
252380_at	ABC-type transport protein-like protein	ATH2	AT3G47740	-1.01	-0.01	-0.10	0.922838	0.964739	-6.85
262470_at	disease resistance protein, putative sim	---	AT1G50180	-1.01	-0.01	-0.10	0.922867	0.964739	-6.85
259046_at	calmodulin-like protein similar to calmo	---	AT3G03400	1.01	0.01	0.10	0.922934	0.964765	-6.85
265063_at	receptor kinase, putative similar to rece	---	AT1G61500	1.01	0.01	0.10	0.923019	0.964809	-6.85
256594_at	hypothetical protein similar to putative A	---	AT3G28520	-1.01	-0.01	-0.10	0.923065	0.964813	-6.85
266304_at	hypothetical protein	---	AT2G27090	1.01	0.01	0.10	0.923375	0.964953	-6.85
263965_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.10	0.923348	0.964953	-6.85
262516_at	putative glutathione transferase One of	ATGSTU2	AT1G17190	1.01	0.01	0.10	0.923298	0.964953	-6.85
265587_at	putative pathogenesis-related protein	---	AT2G19980	1.01	0.01	0.10	0.923356	0.964953	-6.85
253511_at	putative protein Sly1 protein, rat, PIR2:	---	AT4G31740	-1.01	-0.01	-0.10	0.92341	0.964953	-6.85
247712_at	E2, ubiquitin-conjugating enzyme 7 (UB	UBC7	AT5G59300	-1.01	-0.01	-0.10	0.92348	0.964982	-6.85
245259_at	kinesin like protein ; supported by cDNA	PAKRP1	AT4G14150	-1.01	-0.01	-0.10	0.923536	0.964995	-6.85
246937_at	phospholipase D1-like protein phospho	PLDALPH/	AT5G25370	-1.01	-0.01	-0.10	0.923581	0.964998	-6.85
246638_at	putative protein predicted proteins, Ara	---	---	1.01	0.01	0.10	0.923813	0.965164	-6.85
262679_at	unknown protein ; supported by cDNA: g	LCR67	AT1G75830	-1.01	-0.01	-0.10	0.923824	0.965164	-6.85
248928_at	Rac-like gtp binding protein ARAC2 (sp	ARAC2	AT5G45970	-1.01	-0.01	-0.10	0.92389	0.965189	-6.85
260507_at	unknown protein contains similarity to M	WPP2	AT1G47200	1.01	0.02	0.10	0.923945	0.965202	-6.85
267498_at	unknown protein	---	AT2G45720	-1.01	-0.02	-0.10	0.924016	0.965214	-6.85
265163_at	putative OBP32pep protein	---	AT1G23580	-1.01	-0.01	-0.10	0.92406	0.965214	-6.85
260310_at	hypothetical protein predicted by gensca	---	AT1G70590	1.01	0.01	0.10	0.924083	0.965214	-6.85

249773_at	squalene monooxygenase 2 (squalene	SQP2	AT5G24140	-1.01	-0.01	-0.10	0.924171	0.965261	-6.85
263144_at	unknown protein similar to putative auxi	---	AT1G54070	1.01	0.01	0.10	0.924296	0.965348	-6.85
247023_at	putative protein similar to unknown prote	HEC1	AT5G67060	1.01	0.02	0.10	0.924456	0.965382	-6.85
260625_at	storage protein, putative similar to GB:(	MOM	AT1G08060	1.01	0.01	0.10	0.924426	0.965382	-6.85
254808_at	adenine DNA glycosylase like protein A	---	AT4G12740	1.01	0.01	0.10	0.924453	0.965382	-6.85
256212_at	hypothetical protein	---	AT1G50970	1.01	0.01	0.10	0.924604	0.965460	-6.85
256460_at	60S ribosomal protein L30, putative sim	---	AT1G36240	1.01	0.01	0.10	0.924615	0.965460	-6.85
253855_at	senescence-associated protein -like se	TET7	AT4G28050	1.02	0.03	0.10	0.924726	0.965495	-6.85
260873_at	hypothetical protein predicted by gensca	---	AT1G21580	1.01	0.01	0.10	0.924967	0.965495	-6.85
257949_at	putative UDP-glucose glucosyltransfera	UGT71B1	AT3G21750	1.01	0.02	0.10	0.925152	0.965495	-6.85
264470_at	cytochrome P450, putative similar to cy	CYP735A2	AT1G67110	1.01	0.01	0.10	0.924901	0.965495	-6.85
248229_at	caffeic acid 3-O-methyltransferase-like p	---	AT5G53810	1.01	0.01	0.10	0.924796	0.965495	-6.85
253533_at	putative protein cellulose synthase, Agr	ATCSLC5	AT4G31590	1.03	0.04	0.10	0.924966	0.965495	-6.85
247960_at	N-myristoyl transferase ;supported by f	NMT1	AT5G57020	1.01	0.01	0.10	0.925251	0.965495	-6.85
251188_at	putative protein DESSICATION-RELAT	---	AT3G62730	-1.01	-0.01	-0.10	0.924836	0.965495	-6.85
249050_at	cyclin-dependent protein kinase-like pro	---	AT5G44290	-1.01	-0.01	-0.10	0.925237	0.965495	-6.85
AFFX-BioC-	E. coli /GEN=bioC /DB_XREF=gb:J044	---	---	1.02	0.03	0.10	0.925242	0.965495	-6.85
245937_at	putative protein 22kDa peroxisomal me	---	AT5G19750	1.01	0.02	0.10	0.924976	0.965495	-6.85
248471_at	unknown protein	---	AT5G50840	-1.01	-0.01	-0.10	0.925137	0.965495	-6.85
250372_at	putative protein various predicted prote	---	AT5G11460	1.01	0.01	0.10	0.925114	0.965495	-6.85
258944_at	hypothetical protein similar to hypothetic	FLD	AT3G10390	-1.01	-0.01	-0.10	0.925083	0.965495	-6.85
263458_at	putative GTP-binding protein	ATRABH1	AT2G22290	-1.01	-0.01	-0.10	0.925283	0.965495	-6.85
265467_at	putative receptor-like protein kinase	---	AT2G37050	1.01	0.02	0.10	0.92635	0.965538	-6.85
246994_at	putative protein similar to unknown prote	---	AT5G67460	1.02	0.03	0.10	0.926314	0.965538	-6.85
250506_at	ABC transporter, ATP-binding protein-li	GCN2	AT5G09930	-1.01	-0.01	-0.10	0.926383	0.965538	-6.85
261156_s_a	hypothetical protein predicted by genem	---	AT1G34490 /	-1.01	-0.01	-0.10	0.925971	0.965538	-6.85
263753_at	putative dehydrin ;supported by full-leng	LEA	AT2G21490	1.01	0.01	0.10	0.925515	0.965538	-6.85
248052_at	putative protein contains similarity to CH	---	AT5G55800	1.01	0.01	0.10	0.926297	0.965538	-6.85
247337_at	putative protein similar to unknown prote	PDF2.5	AT5G63660	-1.01	-0.01	-0.10	0.925816	0.965538	-6.85
252499_s_a	subtilisin-like serine protease contains s	---	AT3G46840 /	1.01	0.01	0.10	0.925505	0.965538	-6.85
264905_at	putative Mlo protein	MLO7	AT2G17430	1.01	0.01	0.10	0.925785	0.965538	-6.85
253225_at	Rho1Ps homolog Rac-like protein ; sup	ARAC3	AT4G35020	1.01	0.01	0.10	0.925844	0.965538	-6.85
259851_at	kinesin, putative	---	AT1G72250	1.01	0.01	0.10	0.926157	0.965538	-6.85
256695_at	unknown protein	---	AT3G32090	1.01	0.01	0.10	0.9263	0.965538	-6.85
250096_at	putative protein similar to unknown prote	---	AT5G17190	-1.01	-0.01	-0.10	0.925922	0.965538	-6.85

262388_at	unknown protein	---	AT1G49320	1.01	0.01	0.10	0.925889	0.965538	-6.85
255265_at	kinesin - like protein kinesin like protein	ATK5	AT4G05190	-1.01	-0.01	-0.10	0.925703	0.965538	-6.85
266457_at	putative glyoxysomal malate dehydroge	PMDH1	AT2G22780	1.01	0.01	0.10	0.925634	0.965538	-6.85
262429_at	polyprotein, putative similar to polyprote	---	---	-1.01	-0.01	-0.10	0.925862	0.965538	-6.85
264334_at	calcium-dependent protein kinase, puta	CPK19	AT1G61950	1.01	0.01	0.10	0.925383	0.965538	-6.85
251452_at	putative protein male sterility protein 2 -	---	AT3G60060	1.01	0.01	0.10	0.925892	0.965538	-6.85
257554_at	synaptobrevin, putative similar to SYNA	VAMP728	AT3G24890	1.01	0.01	0.10	0.925937	0.965538	-6.85
257974_at	unknown protein similar to NA-DAMAGE	---	AT3G20820	-1.02	-0.04	-0.10	0.926206	0.965538	-6.85
255367_at	putative transposon protein	---	---	1.01	0.01	0.10	0.926305	0.965538	-6.85
262979_s_a	unknown protein similar to histone H3.2	---	AT1G13370 /	-1.01	-0.01	-0.10	0.926246	0.965538	-6.85
261813_at	hypothetical protein contains similarity t	---	AT1G08280	-1.01	-0.02	-0.10	0.925882	0.965538	-6.85
249412_at	putative protein predicted proteins, Arat	---	AT5G40410	1.01	0.01	0.10	0.926344	0.965538	-6.85
247315_at	unknown protein	---	AT5G64010	-1.01	-0.01	-0.10	0.92663	0.965654	-6.85
249615_x_a	contains similarity to unknown protein (p	AGL105	AT5G37420	1.01	0.01	0.10	0.926586	0.965654	-6.85
263229_s_a	putative polygalacturonase similar to GE	---	AT1G05650 /	-1.01	-0.01	-0.10	0.926569	0.965654	-6.85
260511_at	anthranilate phosphoribosyltransferase	---	AT1G51570	-1.01	-0.02	-0.10	0.926664	0.965654	-6.85
250820_at	receptor-like protein kinase	---	AT5G05160	-1.01	-0.01	-0.10	0.927002	0.965698	-6.85
248194_at	Expressed protein ; supported by full-ler	---	AT5G54095	-1.01	-0.01	-0.10	0.926769	0.965698	-6.85
267360_at	unknown protein ;supported by full-leng	---	AT2G40060	1.01	0.01	0.10	0.926794	0.965698	-6.85
247370_at	putative protein similar to unknown prote	---	AT5G63320	1.01	0.02	0.10	0.927041	0.965698	-6.85
254311_at	hypothetical protein	---	AT4G22440	-1.01	-0.01	-0.10	0.926992	0.965698	-6.85
261158_at	hypothetical protein predicted by genem	---	AT1G34500	1.01	0.01	0.10	0.927045	0.965698	-6.85
248825_at	ATP synthase delta chain, mitochondria	---	AT5G47030	1.01	0.01	0.10	0.927022	0.965698	-6.85
267221_at	similar to prokaryotic DNA polymerase I	STI	AT2G02480	1.01	0.01	0.10	0.927032	0.965698	-6.85
256888_at	hypothetical protein predicted by genem	---	AT3G15160	1.01	0.01	0.09	0.92725	0.965867	-6.85
248842_at	unknown protein	---	AT5G46850	-1.01	-0.01	-0.09	0.927304	0.965880	-6.85
259324_at	unknown protein	MIRO3	AT3G05310	1.01	0.01	0.09	0.92738	0.965915	-6.85
250263_at	putative protein	---	AT5G13470	1.01	0.01	0.09	0.927593	0.965916	-6.85
246972_s_a	cytochrome P-450-like protein cytochro	CYP71A14	AT5G24950 /	-1.02	-0.02	-0.09	0.927558	0.965916	-6.85
257273_at	hypothetical protein contains Pfam profil	UVH3	AT3G28030	1.01	0.01	0.09	0.927493	0.965916	-6.85
261637_at	DNA-binding protein PcMYB1, putative	TRB1	AT1G49950	1.01	0.01	0.09	0.927581	0.965916	-6.85
266940_at	unknown protein	---	AT2G18970	1.01	0.01	0.09	0.927563	0.965916	-6.85
266136_at	unknown protein ;supported by full-leng	---	AT2G45060	-1.01	-0.01	-0.09	0.927832	0.966121	-6.85
253798_at	predicted protein CUC2 (involved in org	ANAC073	AT4G28500	-1.01	-0.01	-0.09	0.927881	0.966128	-6.85
251677_at	putative protein hypothetical protein At2	BHLH039	AT3G56980	1.02	0.03	0.09	0.927964	0.966170	-6.85

247644_s_a	translation elongation factor eEF-1 alpha	---	AT1G07920 /	1.01	0.01	0.09	0.928243	0.966259	-6.85
267595_at	putative glucanse	AtGH9B8	AT2G32990	-1.05	-0.07	-0.09	0.928162	0.966259	-6.85
254618_at	cellulose synthase - like protein cellulos	IRX1	AT4G18780	-1.01	-0.02	-0.09	0.928171	0.966259	-6.85
248711_at	putative protein similar to unknown prote	---	AT5G48270	-1.01	-0.01	-0.09	0.928261	0.966259	-6.85
252333_at	putative protein N-terminus: several pre	---	AT3G48830	1.01	0.01	0.09	0.928201	0.966259	-6.85
265160_at	unknown protein similar to EST gb|AA39	---	AT1G31050	1.01	0.01	0.09	0.928313	0.966269	-6.85
255289_at	score=11/3, E=0.23, N=1 contains F-bo	---	AT4G04690	-1.01	-0.01	-0.09	0.928677	0.966472	-6.85
244904_at	hypothetical protein	---	---	-1.01	-0.02	-0.09	0.928629	0.966472	-6.85
259905_s_a	hypothetical protein predicted by genem	---	AT1G74130 /	-1.01	-0.01	-0.09	0.928587	0.966472	-6.85
257428_at	hypothetical protein predicted by genem	---	AT1G78990	-1.01	-0.01	-0.09	0.928656	0.966472	-6.85
262123_at	hypothetical protein predicted by gensca	---	AT1G59630	1.01	0.01	0.09	0.928851	0.966608	-6.85
263970_at	putative cytochrome P450	CYP718	AT2G42850	1.01	0.01	0.09	0.929044	0.966765	-6.85
262661_s_a	hypothetical protein	---	AT1G14230 /	1.03	0.04	0.09	0.929206	0.966882	-6.85
261603_at	DNA binding protein ACBF, putative sir	ATRBP47A	AT1G49600	1.02	0.02	0.09	0.929241	0.966882	-6.85
244908_at	hypothetical protein	---	---	-1.01	-0.02	-0.09	0.929403	0.967007	-6.85
247189_at	unknown protein ;supported by full-leng	AGP7	AT5G65390	-1.02	-0.03	-0.09	0.929498	0.967061	-6.85
254709_at	Expressed protein ; supported by cDNA	AGD8	AT4G17890	1.01	0.01	0.09	0.929625	0.967150	-6.85
253227_at	protein kinase - like leucine rich repeat	---	AT4G35030	1.01	0.01	0.09	0.929804	0.967291	-6.85
250916_at	monodehydroascorbate reductase (NAI	ATMDAR2	AT5G03630	1.02	0.03	0.09	0.930041	0.967494	-6.85
247483_at	aldose reductase-like protein	---	AT5G62420	-1.01	-0.01	-0.09	0.93019	0.967560	-6.85
249105_at	40S ribosomal protein S15	---	AT5G43640	-1.01	-0.01	-0.09	0.930183	0.967560	-6.85
248803_at	selenium-binding protein-like	---	AT5G47460	-1.01	-0.01	-0.09	0.930344	0.967676	-6.85
251608_at	putative protein hypothetical protein At	UVI4-LIKE	AT3G57860	-1.01	-0.01	-0.09	0.93046	0.967753	-6.85
251215_at	putative protein region within disulfide-i	---	AT3G62510	1.01	0.01	0.09	0.930567	0.967821	-6.85
266591_at	expressed protein supported by cDNA:	ABIL1	AT2G46225	-1.01	-0.02	-0.09	0.930616	0.967827	-6.85
263076_at	putative protein kinase/endoribonucleas	IRE1A	AT2G17520	1.01	0.01	0.09	0.930757	0.967873	-6.85
245964_at	putative protein C-terminus of glutamine	---	AT5G19720	-1.01	-0.01	-0.09	0.930734	0.967873	-6.85
267571_at	3-hydroxyisobutyryl-coenzyme A hydrola	---	AT2G30650	-1.01	-0.01	-0.09	0.930867	0.967873	-6.85
250364_at	putative protein serine threonine tyrosin	---	AT5G11400	1.01	0.01	0.09	0.930873	0.967873	-6.85
248350_at	putative protein similar to unknown prote	---	AT5G52160	1.01	0.01	0.09	0.930824	0.967873	-6.85
250003_at	hypothetical protein predicted proteins -	---	AT5G18710	-1.01	-0.01	-0.09	0.930985	0.967946	-6.85
250539_at	WD-repeat protein-like ; supported by c	---	AT5G08560	-1.01	-0.01	-0.09	0.931039	0.967958	-6.85
266420_at	putative RNA-binding protein ; supporte	---	AT2G38610	-1.01	-0.01	-0.09	0.931083	0.967960	-6.85
259086_at	hypothetical protein predicted by genefin	---	AT3G04990	1.01	0.01	0.09	0.931143	0.967978	-6.85
256662_at	male sterility protein 2 (MS2) nearly ider	MS2	AT3G11980	-1.01	-0.01	-0.09	0.931268	0.968064	-6.85

263702_at	hypothetical protein identical to hypothe	---	AT1G31240	1.01	0.01	0.09	0.931329	0.968083	-6.85
248647_at	sucrose synthase	SUS2	AT5G49190	1.01	0.01	0.09	0.931407	0.968105	-6.85
262540_at	hypothetical protein predicted by genem	---	AT1G34260	1.01	0.02	0.09	0.931435	0.968105	-6.85
254900_at	hypothetical protein	RALFL28	AT4G11510	-1.01	-0.01	-0.09	0.931571	0.968203	-6.85
254048_at	putative protein various predicted prote	---	AT4G25680	-1.01	-0.02	-0.09	0.931732	0.968326	-6.85
254875_at	putative protein various predicted prote	---	AT4G11590	-1.01	-0.01	-0.09	0.931795	0.968347	-6.85
259718_at	unknown protein	VIP5	AT1G61040	-1.01	-0.01	-0.09	0.932043	0.968404	-6.85
261068_at	tropinone reductase-I, putative similar t	---	AT1G07450	1.01	0.01	0.09	0.932208	0.968404	-6.85
261873_at	serine/threonine kinase, putative simila	SD1-13	AT1G11350	-1.01	-0.02	-0.09	0.932295	0.968404	-6.85
257424_at	hypothetical protein predicted by genem	---	AT1G78840	1.01	0.01	0.09	0.931944	0.968404	-6.85
262242_at	hypothetical protein predicted by genem	---	AT1G48360	-1.01	-0.01	-0.09	0.932231	0.968404	-6.85
262035_at	polyprotein, putative similar to polyprote	---	---	1.01	0.01	0.09	0.932317	0.968404	-6.85
260147_at	putative oxidoreductase similar to adve	---	AT1G52790	1.01	0.01	0.09	0.932254	0.968404	-6.85
249471_at	putative protein predicted proteins, Arat	EDL2	AT5G39360	1.01	0.01	0.09	0.932232	0.968404	-6.85
261880_at	unknown protein	HIT1	AT1G50500	-1.01	-0.01	-0.09	0.932186	0.968404	-6.85
251081_at	putative protein kinase wall-associated	---	AT5G02070	1.01	0.01	0.09	0.932081	0.968404	-6.85
247395_at	putative protein predicted proteins, Arat	---	AT5G62910	-1.01	-0.01	-0.09	0.93216	0.968404	-6.85
248755_at	putative protein strong similarity to unkn	---	AT5G47690	-1.01	-0.01	-0.09	0.932364	0.968409	-6.85
245407_at	GTP-binding RAB2A like protein	RABB1C	AT4G17170	1.01	0.01	0.09	0.932564	0.968491	-6.85
247697_at	subtilisin-like protease - like protein sub	SBT5.4	AT5G59810	1.01	0.01	0.09	0.932571	0.968491	-6.85
253699_at	putative protein patatin-like protein, Sor	PLP8	AT4G29800	-1.01	-0.01	-0.09	0.932547	0.968491	-6.85
254841_at	putative protein predicted proteins Arabi	---	AT4G11940	-1.01	-0.01	-0.09	0.932698	0.968579	-6.85
263569_at	putative chromosome associated protein	TTN7	AT2G27170	-1.01	-0.02	-0.09	0.932787	0.968628	-6.85
261702_at	unknown protein similar to hypothetical p	---	AT1G32760	-1.01	-0.01	-0.09	0.932849	0.968648	-6.85
264338_at	potassium transporter, putative similar t	KUP6	AT1G70300	-1.01	-0.02	-0.09	0.933302	0.968677	-6.85
256263_at	5,10-methylenetetrahydrofolate dehydro	---	AT3G12290	1.01	0.01	0.09	0.933294	0.968677	-6.85
251550_at	putative protein proline-rich protein A41	---	AT3G58800	-1.01	-0.01	-0.09	0.933104	0.968677	-6.85
258660_at	hypothetical protein predicted by gensca	---	AT3G09850	-1.01	-0.01	-0.09	0.933141	0.968677	-6.85
248300_at	PP2A regulatory subunit ;supported by	TAP46	AT5G53000	1.01	0.01	0.09	0.933196	0.968677	-6.85
255297_x_a	hypothetical protein	---	---	1.01	0.01	0.09	0.933083	0.968677	-6.85
249442_at	putative protein ; supported by cDNA: g	---	AT5G39590	-1.02	-0.02	-0.09	0.933026	0.968677	-6.85
262387_s_a	hypothetical protein contains similarity to	---	AT1G49340 /	-1.01	-0.01	-0.09	0.933009	0.968677	-6.85
255758_at	hypothetical protein predicted by genem	---	AT1G16800	1.01	0.01	0.09	0.933269	0.968677	-6.85
249759_at	putative protein contains similarity to int	YSL2	AT5G24380	-1.01	-0.01	-0.09	0.932989	0.968677	-6.85
265127_at	hypothetical protein similar to pollen spe	sks14	AT1G55560	-1.01	-0.01	-0.09	0.933448	0.968741	-6.85

260559_at	putative polygalacturonase	---	AT2G43860	-1.01	-0.01	-0.09	0.933427	0.968741	-6.85
254084_at	ubiquitin activating enzyme - like protei	SAE1A	AT4G24940	1.01	0.02	0.09	0.933541	0.968777	-6.85
267047_at	putative selenium-binding protein	---	AT2G34370	-1.01	-0.01	-0.09	0.933568	0.968777	-6.85
256209_at	electron transport flavoprotein, putative	ETFALPHA	AT1G50940	-1.01	-0.01	-0.09	0.933791	0.968921	-6.85
247971_at	zinc protease PQQL-like protein	---	AT5G56730	1.01	0.01	0.09	0.933754	0.968921	-6.85
246078_s_a	putative protein probable mitosis and m	---	AT5G20430 /	-1.01	-0.02	-0.09	0.933869	0.968957	-6.85
252143_at	putative protein centromere protein E -	---	AT3G51150	1.01	0.01	0.09	0.934027	0.969077	-6.85
251968_at	putative protein proline-rich protein, Ra	---	AT3G53100	-1.01	-0.01	-0.09	0.934092	0.969100	-6.85
247153_at	receptor protein kinase-like protein	BAM1	AT5G65700	1.01	0.02	0.09	0.934137	0.969103	-6.85
253673_at	putative protein putative phosphatase, (	---	AT4G29530	1.01	0.01	0.09	0.934262	0.969153	-6.85
267156_at	hypothetical protein predicted by gensca	---	AT2G37610	1.01	0.01	0.09	0.934434	0.969153	-6.85
262976_at	unknown protein	SRS5	AT1G75520	-1.01	-0.01	-0.09	0.93444	0.969153	-6.85
257929_at	RNA Polymerase II subunit 14.5 kD, pu	NRPB9A	AT3G16980	1.01	0.01	0.09	0.934349	0.969153	-6.85
263991_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.09	0.934407	0.969153	-6.85
254729_at	putative protein purple acid phosphatas	PAP23	AT4G13700	1.01	0.01	0.09	0.934322	0.969153	-6.85
253851_at	putative transcription factor MYB41	AtMYB41	AT4G28110	1.01	0.01	0.09	0.934592	0.969225	-6.85
262564_at	anionic peroxidase, putative similar to a	---	AT1G34330	1.01	0.01	0.09	0.934595	0.969225	-6.85
257251_at	type 1 membrane protein, putative iden	PMP	AT3G24160	-1.01	-0.01	-0.09	0.934649	0.969237	-6.85
264981_at	valyl- tRNA synthetase, putative similar	---	AT1G27160	-1.01	-0.01	-0.08	0.934951	0.969507	-6.85
251397_at	putative protein cim1 protein, Glycine m	ATEXPB5	AT3G60570	-1.01	-0.01	-0.08	0.935282	0.969629	-6.85
263111_s_a	hypothetical protein contains similarity t	---	AT1G65190 /	-1.01	-0.01	-0.08	0.935211	0.969629	-6.85
257329_at	hypothetical protein	---	---	-1.01	-0.02	-0.08	0.935223	0.969629	-6.85
250369_at	cyclin 3b ; supported by cDNA: gi_6008	CYC3B	AT5G11300	-1.01	-0.01	-0.08	0.935269	0.969629	-6.85
256495_at	hypothetical protein contains similarity t	---	AT1G31530	1.01	0.01	0.08	0.935164	0.969629	-6.85
245318_at	Expressed protein ; supported by full-ler	---	AT4G16980	-1.04	-0.06	-0.08	0.935513	0.969649	-6.85
258233_at	hypothetical protein contains similarity t	MYB118	AT3G27785	-1.01	-0.01	-0.08	0.935501	0.969649	-6.85
260520_at	mannosyl-oligosaccharide alpha-1,2-ma	---	AT1G51590	1.01	0.01	0.08	0.935398	0.969649	-6.85
259634_at	hypothetical protein	---	AT1G56380	1.01	0.01	0.08	0.93537	0.969649	-6.85
263338_at	hypothetical protein predicted by gensca	---	---	1.01	0.01	0.08	0.935445	0.969649	-6.85
254924_at	MAP kinase (ATMPK5) possible interna	ATMPK5	AT4G11330	-1.01	-0.02	-0.08	0.935657	0.969753	-6.85
254047_at	hypothetical protein	---	AT4G26040	1.01	0.01	0.08	0.935773	0.969765	-6.85
257821_at	Expressed protein ; supported by full-ler	RALFL26	AT3G25170	1.01	0.01	0.08	0.935796	0.969765	-6.85
261967_at	En/Spm-like transposon protein, putativ	---	---	-1.01	-0.01	-0.08	0.935739	0.969765	-6.85
254333_at	predicted protein predicted protein ERG	SMO1-3	AT4G22753	1.02	0.03	0.08	0.936006	0.969768	-6.85
261832_at	S-ribonuclease binding protein SBP1, p	---	AT1G10650	-1.01	-0.02	-0.08	0.936138	0.969768	-6.85

261971_at	type 2 peroxiredoxin, putative similar to	---	AT1G65990	1.01	0.01	0.08	0.936222	0.969768	-6.85
255877_at	putative PTR2 family peptide transporte	---	AT2G40460	-1.02	-0.03	-0.08	0.935979	0.969768	-6.85
266317_at	calmodulin identical to GB:L18912; supp	CAM5	AT2G27030	-1.01	-0.01	-0.08	0.936224	0.969768	-6.85
257043_at	receptor-like protein kinase, putative sir	IKU2	AT3G19700	1.01	0.01	0.08	0.936079	0.969768	-6.85
252599_at	receptor-like protein kinase receptor like	---	AT3G45390	1.01	0.01	0.08	0.936169	0.969768	-6.85
252088_at	putative protein	---	AT3G52100 /	1.01	0.01	0.08	0.935882	0.969768	-6.85
259522_at	hypothetical protein	---	AT1G12490	-1.01	-0.01	-0.08	0.93617	0.969768	-6.85
260202_at	hypothetical protein predicted by gensca	---	---	-1.01	-0.01	-0.08	0.936026	0.969768	-6.85
248536_at	ankyrin-like protein	---	AT5G50140	-1.01	-0.01	-0.08	0.936364	0.969869	-6.85
247603_at	microtubule-associated motor - like mic	---	AT5G60930	1.01	0.01	0.08	0.93655	0.970018	-6.85
266997_at	hypothetical protein predicted by genefir	---	AT2G34410	1.01	0.02	0.08	0.936663	0.970091	-6.85
264479_at	hypothetical protein similar to receptor-li	---	AT1G77280	1.01	0.01	0.08	0.936936	0.970097	-6.85
247442_s_a	tubulin beta-2/beta-3 chain (sp|P29512)	TUB2	AT5G62690 /	-1.01	-0.02	-0.08	0.936766	0.970097	-6.85
249622_at	putative protein	---	AT5G37550	-1.01	-0.01	-0.08	0.937292	0.970097	-6.85
262282_at	hypothetical protein predicted by gensca	---	AT1G68610	-1.01	-0.01	-0.08	0.937253	0.970097	-6.85
256636_at	S-locus related protein SLR1 homolog (	---	AT3G12000	-1.01	-0.01	-0.08	0.937009	0.970097	-6.85
258341_at	unknown protein similar to centromere p	---	AT3G22790	-1.02	-0.03	-0.08	0.93701	0.970097	-6.85
259064_at	putative calmodulin similar to calmoduli	AGD11	AT3G07490	-1.01	-0.01	-0.08	0.937307	0.970097	-6.85
251708_at	Expressed protein ; supported by cDNA	---	AT3G56580	1.01	0.01	0.08	0.937227	0.970097	-6.85
255684_at	putative glycosylasparaginase	---	AT4G00590	1.01	0.01	0.08	0.936739	0.970097	-6.85
265851_at	hypothetical protein predicted by gensca	---	AT2G42340	1.01	0.01	0.08	0.937131	0.970097	-6.85
252732_at	putative protein predicted proteins, Ara	---	---	-1.01	-0.01	-0.08	0.937123	0.970097	-6.85
251517_at	putative protein hypothetical protein F1	---	AT3G59370	1.00	0.01	0.08	0.937274	0.970097	-6.85
262553_at	hypothetical protein similar to hypothetic	RECQL2	AT1G31360	-1.01	-0.01	-0.08	0.937056	0.970097	-6.85
250675_at	putative protein contains similarity to unl	---	AT5G06260	1.01	0.01	0.08	0.93713	0.970097	-6.85
264312_at	putative protein kinase similar to protein	---	AT1G70450	-1.01	-0.01	-0.08	0.937189	0.970097	-6.85
251062_at	putative protein putative proteins - Arabi	OFP1	AT5G01840	1.01	0.01	0.08	0.937372	0.970120	-6.85
257360_at	unknown protein	---	AT2G39240	-1.01	-0.01	-0.08	0.93747	0.970178	-6.85
257445_x_a	hypothetical protein predicted by gensca	---	---	1.01	0.01	0.08	0.9377	0.970240	-6.85
258208_at	putative acetyltransferase similar to dihy	---	AT3G13930	1.01	0.01	0.08	0.937599	0.970240	-6.85
259853_at	leucine-rich receptor-like protein kinase	---	AT1G72300	-1.01	-0.01	-0.08	0.937679	0.970240	-6.85
249215_at	dihydroflavonol 4-reductase	DFR	AT5G42800	1.01	0.01	0.08	0.937616	0.970240	-6.85
248216_at	unknown protein	---	AT5G53690	-1.01	-0.01	-0.08	0.937811	0.970310	-6.85
255517_at	putative endo-1,4-beta glucanase simila	AtGH9B13	AT4G02290	-1.01	-0.01	-0.08	0.937857	0.970314	-6.85
261302_at	hypothetical protein predicted by genem	---	AT1G48580	-1.01	-0.01	-0.08	0.937931	0.970347	-6.85

259089_at	hypothetical protein similar to GB:CAB3	---	AT3G04960	-1.01	-0.01	-0.08	0.93805	0.970426	-6.85
249536_at	pollen coat -like protein pollen coat prot	---	AT5G38760	1.01	0.01	0.08	0.938099	0.970433	-6.85
258370_at	Expressed protein ; supported by full-ler	---	AT3G14395	1.01	0.01	0.08	0.938169	0.970434	-6.85
248570_at	receptor protein kinase-like	---	AT5G49780	1.01	0.01	0.08	0.938185	0.970434	-6.85
253378_at	hypothetical protein	---	AT4G33310	-1.01	-0.01	-0.08	0.938252	0.970459	-6.85
248219_at	unknown protein ; supported by full-leng	---	AT5G53650	1.00	0.01	0.08	0.938603	0.970471	-6.85
259371_at	unknown protein ;supported by full-lengt	---	AT1G69080	1.02	0.03	0.08	0.938378	0.970471	-6.85
265986_at	putative receptor-like protein kinase	---	AT2G24230	1.01	0.01	0.08	0.938441	0.970471	-6.85
265933_at	putative esterase contains esterase/lipa	---	AT2G19550	1.01	0.01	0.08	0.938401	0.970471	-6.85
246430_at	calmodulin-like protein calmodulin-relat	---	AT5G17470	1.01	0.01	0.08	0.938604	0.970471	-6.85
251405_at	plasma membrane H+-ATPase - like pl	AHA7	AT3G60330	-1.01	-0.01	-0.08	0.938555	0.970471	-6.85
255215_at	putative athila transposon protein	---	---	-1.00	-0.01	-0.08	0.938569	0.970471	-6.85
257243_at	pectate lyase, putative similar to GB:AA	---	AT3G24230	1.00	0.01	0.08	0.938401	0.970471	-6.85
267122_at	putative acetone-cyanohydrin lyase	MES6	AT2G23550	-1.01	-0.01	-0.08	0.938755	0.970583	-6.85
259332_at	putative auxin-induced protein similar to	---	AT3G03830	-1.01	-0.01	-0.08	0.938806	0.970591	-6.85
260860_at	hypothetical protein predicted by genem	---	AT1G43810	1.01	0.01	0.08	0.93889	0.970592	-6.85
262106_at	hypothetical protein similar to Wee1-like	WEE1	AT1G02970	1.01	0.01	0.08	0.938891	0.970592	-6.85
250584_at	WD-repeat protein-like	---	AT5G07590	-1.01	-0.01	-0.08	0.939126	0.970611	-6.85
247965_at	putative protein similar to unknown prot	AGP14	AT5G56540	-1.01	-0.01	-0.08	0.93901	0.970611	-6.85
257301_at	hypothetical protein predicted by genem	---	---	-1.01	-0.01	-0.08	0.939191	0.970611	-6.85
258623_at	unknown protein ; supported by cDNA:	---	AT3G02790	-1.01	-0.02	-0.08	0.939208	0.970611	-6.85
254950_at	putative protein ;supported by full-lengt	---	AT4G10810	1.01	0.01	0.08	0.939068	0.970611	-6.85
261908_at	stig1-like protein similar to Stig1 GB:AA	---	AT1G50650	-1.01	-0.01	-0.08	0.939187	0.970611	-6.85
248318_at	unknown protein	---	AT5G52690	1.01	0.01	0.08	0.939135	0.970611	-6.85
250577_at	putative protein densin-180, Rattus nor	---	AT5G07910	1.01	0.01	0.08	0.939306	0.970625	-6.85
254775_at	hypothetical protein	---	AT4G13450	-1.00	-0.01	-0.08	0.9393	0.970625	-6.85
245637_at	hypothetical protein similar to putative p	---	AT1G25230	-1.02	-0.03	-0.08	0.939351	0.970627	-6.85
249367_at	putative protein predicted protein, Arabi	---	AT5G40630	1.01	0.01	0.08	0.939394	0.970628	-6.85
263612_at	putative CDC21 protein	MCM4	AT2G16440	1.02	0.03	0.08	0.939473	0.970662	-6.85
258303_at	hypothetical protein predicted by genem	---	---	1.01	0.01	0.08	0.939512	0.970662	-6.85
263197_at	polyubiquitin, putative similar to polyubi	---	AT1G53930	1.01	0.01	0.08	0.939822	0.970866	-6.85
266694_at	putative clathrin assembly protein ;supp	---	AT2G19790	-1.01	-0.01	-0.08	0.939783	0.970866	-6.85
256517_at	PHD-finger protein, putative contains P	MMD1	AT1G66170	-1.01	-0.01	-0.08	0.939838	0.970866	-6.85
253070_at	putative protein symbiotic ammonium tr	---	AT4G37850	1.01	0.01	0.08	0.93999	0.970980	-6.85
256083_at	hypothetical protein predicted by gensca	---	AT1G20730	1.01	0.01	0.08	0.940061	0.971009	-6.85

247169_at	unknown protein	---	AT5G65520	-1.01	-0.01	-0.08	0.940439	0.971355	-6.85
246203_at	putative protein ; supported by full-lengt	---	AT4G36610	-1.01	-0.02	-0.08	0.940585	0.971463	-6.85
252275_at	ubiquitin-specific protease 26 (UBP26)	UBP26	AT3G49600	-1.01	-0.01	-0.08	0.940782	0.971622	-6.85
254033_at	V-ATPase G-subunit like protein G sub	VATG3	AT4G25950	1.00	0.01	0.08	0.940824	0.971622	-6.85
257279_at	unknown protein ;supported by full-leng	---	AT3G14430	1.01	0.01	0.08	0.940991	0.971749	-6.85
253776_at	ADP,ATP carrier-like protein ADP,ATP	AAC3	AT4G28390	-1.01	-0.01	-0.08	0.941095	0.971813	-6.85
245071_at	putative vetispiradiene synthase	---	AT2G23230	1.01	0.01	0.08	0.941366	0.972049	-6.85
255634_at	hypothetical protein ; supported by cDN	FRI	AT4G00650	1.00	0.01	0.08	0.941621	0.972269	-6.85
249611_at	putative protein unnamed ORF, Homo s	ATSRL1	AT5G37370	1.01	0.01	0.08	0.941809	0.972418	-6.85
255632_at	putative actin-depolymerizing factor ;su	ADF8	AT4G00680	-1.00	-0.01	-0.08	0.941882	0.972425	-6.85
246468_at	UDP glucose:flavonoid 3-o-glucosyltran	UGT78D2	AT5G17050	-1.01	-0.02	-0.08	0.941901	0.972425	-6.85
248794_at	ethylene responsive element binding fac	ERF2	AT5G47220	1.03	0.04	0.08	0.941973	0.972455	-6.85
246868_at	protein phosphatase - like protein phos	---	AT5G26010	1.01	0.01	0.08	0.942088	0.972530	-6.85
262742_at	GTP-binding protein, putative similar to	AtRABA1i	AT1G28550	1.01	0.01	0.08	0.942213	0.972536	-6.85
249243_s_a	beta-glucosidase	BGLU13	AT5G42260 /	-1.01	-0.01	-0.08	0.942219	0.972536	-6.85
249169_at	putative protein strong similarity to unkn	---	AT5G42880	-1.01	-0.01	-0.08	0.942222	0.972536	-6.85
267297_at	putative RING zinc finger protein ;supp	---	AT2G23780	1.01	0.01	0.08	0.942366	0.972597	-6.85
254718_at	putative protein disease resistance resp	---	AT4G13580	1.01	0.01	0.08	0.942358	0.972597	-6.85
260924_at	hypothetical protein similar to Pto kinase	---	AT1G21590	1.01	0.01	0.07	0.942796	0.972997	-6.85
249943_at	putative protein similar to unknown prote	---	AT5G22280	-1.01	-0.02	-0.07	0.942887	0.973047	-6.85
256629_at	serine/threonine protein phosphatase, p	ATFYPP3	AT3G19980	-1.01	-0.01	-0.07	0.943104	0.973138	-6.85
250308_at	calcium-dependent protein kinase	CPK17	AT5G12180	-1.01	-0.01	-0.07	0.943069	0.973138	-6.85
249668_at	putative protein similar to unknown prote	---	AT5G35870	1.01	0.01	0.07	0.943092	0.973138	-6.85
259331_at	putative auxin-induced protein similar to	---	AT3G03840	-1.01	-0.01	-0.07	0.943383	0.973339	-6.85
251035_at	Expressed protein ; supported by full-ler	---	AT5G02220	-1.01	-0.01	-0.07	0.943375	0.973339	-6.85
244952_at	hypothetical protein	---	---	-1.01	-0.01	-0.07	0.943546	0.973463	-6.85
255681_at	predicted protein of unknown function	DGD2	AT4G00550	1.01	0.01	0.07	0.943737	0.973615	-6.85
252081_at	putative heat shock transcription factor	HSFA7A	AT3G51910	1.01	0.02	0.07	0.943779	0.973615	-6.85
255861_at	putative vacuolar sorting receptor	---	AT2G30290	-1.00	-0.01	-0.07	0.943825	0.973618	-6.85
264537_at	receptor kinase, putative similar to CLV	BRL1	AT1G55610	1.01	0.01	0.07	0.943952	0.973705	-6.85
256725_at	hypothetical protein predicted by genefi	---	AT2G34070	-1.01	-0.02	-0.07	0.944468	0.973882	-6.85
259756_at	unknown protein ; supported by cDNA:	---	AT1G71080	1.01	0.01	0.07	0.94433	0.973882	-6.85
260544_at	unknown protein predicted by genscan a	---	AT2G43540	1.01	0.01	0.07	0.944541	0.973882	-6.85
264884_at	unknown protein ;supported by full-lengt	---	AT1G61170	1.01	0.02	0.07	0.944593	0.973882	-6.85
252567_at	zinc finger -like protein zinc finger prote	---	AT3G46070	1.01	0.01	0.07	0.944566	0.973882	-6.85

248912_at	GDSL-motif lipase/hydrolase-like protein	---	AT5G45670	1.01	0.01	0.07	0.944404	0.973882	-6.85
257904_at	myb transcription factor, putative simila	TDF1	AT3G28470	-1.00	-0.01	-0.07	0.944484	0.973882	-6.85
258266_at	hypothetical protein predicted by genem	---	AT3G15860	-1.01	-0.01	-0.07	0.944441	0.973882	-6.85
255306_at	putative calcium dependent protein kina	CPK23	AT4G04740	-1.01	-0.01	-0.07	0.944407	0.973882	-6.85
267154_at	glutathione S-transferase identical to GE	GSTF10	AT2G30870	-1.02	-0.03	-0.07	0.944289	0.973882	-6.85
262543_at	Expressed protein ; supported by full-ler	---	AT1G34245	1.01	0.01	0.07	0.944413	0.973882	-6.85
253263_at	abscisic acid responsive elements-bindi	ABF3	AT4G34000	1.01	0.02	0.07	0.944731	0.973937	-6.85
254547_at	putative protein	---	AT4G19860	1.01	0.01	0.07	0.944723	0.973937	-6.85
246692_at	putative protein predicted protein, Arabi	---	---	-1.01	-0.01	-0.07	0.944979	0.974148	-6.85
266657_at	unknown protein ;supported by full-leng	---	AT2G25910	-1.00	-0.01	-0.07	0.945228	0.974360	-6.85
246595_at	formate dehydrogenase (FDH) ;support	FDH	AT5G14780	-1.01	-0.01	-0.07	0.945343	0.974392	-6.85
254479_at	putative protein hypothetical protein - C	---	AT4G20350	-1.01	-0.01	-0.07	0.945312	0.974392	-6.85
260433_at	MtN21-like protein similar to MtN21 GB:	---	AT1G68170	-1.01	-0.01	-0.07	0.945428	0.974411	-6.85
259362_s_a	serin threonin-kinase, putative similar to	---	AT1G13350 /	1.01	0.01	0.07	0.94547	0.974411	-6.85
264634_at	cytochrome P450, putative	CYP702A1	AT1G65670	1.00	0.01	0.07	0.945491	0.974411	-6.85
266730_at	putative RNA-binding protein	---	AT2G03110	1.01	0.01	0.07	0.945548	0.974427	-6.85
253300_at	carbonate dehydratase - like protein ca	BCA5	AT4G33580	1.01	0.01	0.07	0.945713	0.974489	-6.85
245850_at	ankyrin-repeat containing protein ankyri	KEG	AT5G13530	-1.01	-0.01	-0.07	0.945865	0.974489	-6.85
249031_at	putative protein contains similarity to dis	---	AT5G44900	1.01	0.01	0.07	0.945722	0.974489	-6.85
254099_at	protein-methionine-S-oxide reductase ;;	---	AT4G25130	-1.01	-0.01	-0.07	0.945836	0.974489	-6.85
250908_at	GT2 -like protein GT2, Arabidopsis thal	PTL	AT5G03680	-1.01	-0.01	-0.07	0.945824	0.974489	-6.85
257548_s_a	hypothetical protein	LBD23	AT3G26620 /	1.00	0.01	0.07	0.945823	0.974489	-6.85
253974_at	receptor protein kinase - like protein Cf-	---	AT4G26540	-1.01	-0.02	-0.07	0.946322	0.974787	-6.85
247477_at	putative protein 21K protein precursor,	---	AT5G62340	-1.01	-0.01	-0.07	0.946368	0.974787	-6.85
265925_at	hypothetical protein predicted by gensca	---	AT2G18610	1.01	0.01	0.07	0.946345	0.974787	-6.85
254880_at	putative protein Crp1, Zea mays, AF07	---	AT4G11690	-1.01	-0.01	-0.07	0.946276	0.974787	-6.85
247911_at	putative protein contains similarity to DN	XRCC3	AT5G57450	1.01	0.01	0.07	0.946364	0.974787	-6.85
257577_at	hypothetical protein predicted by genem	---	---	-1.01	-0.01	-0.07	0.94652	0.974900	-6.85
255324_s_a	putative reverse transcriptase	---	---	-1.00	-0.01	-0.07	0.94659	0.974928	-6.85
264682_at	polygalacturonase, putative similar to p	---	AT1G65570	-1.00	-0.01	-0.07	0.946844	0.974969	-6.85
250709_at	putative protein similar to unknown prote	LBD33	AT5G06080	1.01	0.01	0.07	0.946687	0.974969	-6.85
260998_at	CAF protein similar to C2H2 zinc finger	---	AT1G26590	1.01	0.01	0.07	0.946744	0.974969	-6.85
247200_at	unknown protein ;supported by full-leng	---	AT5G65120	1.01	0.01	0.07	0.946809	0.974969	-6.85
255237_at	hypothetical protein	---	---	1.00	0.01	0.07	0.946838	0.974969	-6.85
257814_at	acyl-(acyl carrier protein) thioesterase i	AtFaTA	AT3G25110	1.01	0.02	0.07	0.947084	0.975128	-6.85

256418_at	hypothetical protein	---	AT3G06160	1.00	0.01	0.07	0.94706	0.975128	-6.85
246177_at	putative protein predicted proteins - Aral	---	AT5G28420	-1.00	-0.01	-0.07	0.947272	0.975233	-6.85
266786_at	putative non-LTR retroelement reverse t	---	---	1.00	0.01	0.07	0.947234	0.975233	-6.85
261076_at	unknown protein ;supported by full-lengt	SMO2-1	AT1G07420	-1.00	-0.01	-0.07	0.947487	0.975410	-6.85
249022_s_a	polygalacturonase-like protein	---	AT5G44830 /	1.01	0.01	0.07	0.947618	0.975502	-6.85
266273_at	putative zinc transporter	MTPB1	AT2G29410	1.02	0.03	0.07	0.947678	0.975516	-6.85
254940_at	putative protein predicted proteins, Aral	---	AT4G10820	1.01	0.01	0.07	0.94776	0.975516	-6.85
254191_at	hypothetical protein ;supported by full-le	---	AT4G23900	1.01	0.01	0.07	0.947753	0.975516	-6.85
254738_at	RNA-binding protein like	AT4G1386	---	-1.01	-0.01	-0.07	0.948036	0.975589	-6.85
252540_at	putative protein CDP-alcohol phosphati	---	AT3G45740	1.01	0.01	0.07	0.948014	0.975589	-6.85
245970_at	beta-galactosidase ; supported by cDNA	BGAL7	AT5G20710	-1.01	-0.01	-0.07	0.947879	0.975589	-6.85
257397_at	hypothetical protein predicted by genscal	RIC6	AT2G20430	1.01	0.01	0.07	0.947955	0.975589	-6.85
252493_at	hypothetical protein	---	AT3G46750	1.01	0.01	0.07	0.948045	0.975589	-6.85
262681_at	anter-specific proline-rich -like protein (A	---	AT1G75890	1.00	0.01	0.07	0.94823	0.975712	-6.85
264784_s_a	unknown protein similar to Arabidopsis	---	AT2G17830 /	-1.01	-0.01	-0.07	0.948251	0.975712	-6.85
260041_at	unknown protein similar to hypothetical p	---	AT1G68780	-1.01	-0.01	-0.07	0.948537	0.975963	-6.85
249885_at	putative protein strong similarity to unkn	F8H	AT5G22940	1.01	0.01	0.07	0.948664	0.975967	-6.85
258401_at	unknown protein ; supported by cDNA:	---	AT3G15430	1.01	0.01	0.07	0.948619	0.975967	-6.85
266947_at	hypothetical protein predicted by genscal	---	AT2G18830	-1.01	-0.01	-0.07	0.948669	0.975967	-6.85
248252_at	putative protein similar to unknown prote	AGP22	AT5G53250	1.02	0.02	0.07	0.948778	0.976035	-6.85
266565_at	putative serine carboxypeptidase II	scpl23	AT2G24010	1.01	0.01	0.07	0.948886	0.976095	-6.85
254632_at	putative protein predicted protein, Arabi	---	AT4G18630	1.01	0.01	0.07	0.948921	0.976095	-6.85
261829_at	P-glycoprotein, putative similar to P-gly	PGP10	AT1G10680	-1.01	-0.01	-0.07	0.94916	0.976120	-6.85
255475_at	contains a short region of similarity to ar	---	AT4G02480	1.01	0.01	0.07	0.94915	0.976120	-6.85
261054_at	hypothetical protein predicted by genem	---	AT1G01320	1.01	0.01	0.07	0.949103	0.976120	-6.85
252892_at	hypothetical protein	---	AT4G39420	1.00	0.01	0.07	0.949072	0.976120	-6.85
264125_at	hypothetical protein predicted by genem	EMB1135	AT1G79350	-1.01	-0.01	-0.07	0.949142	0.976120	-6.85
247724_at	putative protein predicted protein, Arabi	MBD6	AT5G59380	-1.00	-0.01	-0.07	0.949389	0.976311	-6.85
265106_s_a	putative membrane-associated salt-indu	---	AT1G62590 /	1.00	0.01	0.07	0.949469	0.976349	-6.85
256171_s_a	hypothetical protein similar to reverse tra	---	---	-1.01	-0.01	-0.07	0.949535	0.976350	-6.85
254568_x_a	hypothtetical protein	---	---	1.01	0.01	0.07	0.949555	0.976350	-6.85
256261_at	ras-related GTP-binding protein contains	RABA4D	AT3G12160	1.01	0.01	0.07	0.949665	0.976375	-6.85
246355_at	hypothetical protein	---	---	1.01	0.02	0.07	0.949629	0.976375	-6.85
246037_at	putative protein predicted chromosome	---	AT5G19420	-1.01	-0.01	-0.07	0.949873	0.976545	-6.85
257769_at	indoleacetic acid (IAA)-inducible gene (	IAA7	AT3G23050	-1.03	-0.05	-0.07	0.949983	0.976588	-6.85

245647_at	F5A9.22 hypothetical protein	---	AT1G24706	1.00	0.01	0.07	0.95	0.976588	-6.85
258955_s_a	unknown protein ;supported by full-leng	---	AT3G01450 /	-1.01	-0.01	-0.07	0.950045	0.976590	-6.85
246128_at	putative protein predicted proteins, Arat	---	---	1.01	0.01	0.06	0.950093	0.976595	-6.85
257133_at	hypothetical protein predicted by genem	---	AT3G17190	1.00	0.01	0.06	0.950149	0.976609	-6.85
261490_at	tumor suppressor, putative similar to tu	SAC52	AT1G14320	1.01	0.01	0.06	0.950246	0.976620	-6.85
266869_at	putative glucosyltransferase	---	AT2G44660	1.01	0.01	0.06	0.950222	0.976620	-6.85
250666_at	SPF1-like protein SPF1 protein - Ipomo	WRKY26	AT5G07100	1.01	0.02	0.06	0.950345	0.976678	-6.85
248516_at	unknown protein	---	AT5G50540 /	-1.01	-0.01	-0.06	0.950492	0.976785	-6.85
261334_at	unknown protein	---	AT1G44960	1.01	0.01	0.06	0.950784	0.977041	-6.85
251962_at	plasma membrane intrinsic protein 2a ;F	PIP2A	AT3G53420	-1.01	-0.01	-0.06	0.950926	0.977062	-6.85
256546_at	hypothetical protein contains similarity to	---	AT3G14820	1.00	0.01	0.06	0.950853	0.977062	-6.85
256039_at	hypothetical protein contains similarity to	---	AT1G19190	-1.01	-0.01	-0.06	0.950932	0.977062	-6.85
247917_at	putative protein similar to unknown prote	BIO1	AT5G57590	-1.00	-0.01	-0.06	0.951092	0.977182	-6.85
257096_at	hypothetical protein	---	AT3G30820	-1.00	-0.01	-0.06	0.951212	0.977238	-6.85
265919_at	putative retroelement pol polyprotein	---	---	-1.01	-0.01	-0.06	0.951276	0.977238	-6.85
249675_at	putative protein myrosinase-binding prot	---	AT5G35940	1.00	0.01	0.06	0.951263	0.977238	-6.85
248638_at	fatty acid elongase; beta-ketoacyl-CoA s	KCS21	AT5G49070	-1.00	-0.01	-0.06	0.9514	0.977322	-6.85
260630_at	subtilisin-like serine protease contains s	ALE1	AT1G62340	1.01	0.01	0.06	0.951651	0.977498	-6.85
247336_at	putative protein similar to unknown prote	---	AT5G63640	1.01	0.01	0.06	0.951657	0.977498	-6.85
255697_at	hypothetical protein	---	AT4G00130	-1.01	-0.01	-0.06	0.951776	0.977576	-6.85
254908_at	putative protein other hypothetical prote	---	---	1.01	0.01	0.06	0.951924	0.977684	-6.85
256915_at	unknown protein	---	AT3G23900	-1.01	-0.01	-0.06	0.951975	0.977692	-6.85
260108_at	hypothetical protein similar to putative s	---	AT1G63280	1.01	0.01	0.06	0.9521	0.977764	-6.85
255858_at	zinc finger protein (ZFP6) identical to zir	ZFP6	AT1G67030	-1.01	-0.01	-0.06	0.95213	0.977764	-6.85
265371_at	putative PttA-like transposon protein rela	---	---	-1.00	-0.01	-0.06	0.952431	0.978028	-6.85
250819_at	putative protein strong similarity to unkn	---	AT5G05100	1.01	0.01	0.06	0.952517	0.978073	-6.85
252512_at	receptor protein kinase -like receptor-lik	---	AT3G46290	1.00	0.01	0.06	0.952751	0.978101	-6.85
260247_at	putative disease resistance protein simil	AtRLP16	AT1G74200	-1.00	-0.01	-0.06	0.952776	0.978101	-6.85
262017_at	elongation factor, putative similar to EL	---	AT1G35550	-1.01	-0.01	-0.06	0.952905	0.978101	-6.85
266923_at	unknown protein ;supported by full-leng	---	AT2G45980	1.00	0.01	0.06	0.952769	0.978101	-6.85
265996_at	putative leucine aminopeptidase identica	---	AT2G24200	-1.01	-0.02	-0.06	0.952802	0.978101	-6.85
250782_at	SYN1 splice variant 1 (gb AAF08981.1)	SYN1	AT5G05490	-1.01	-0.01	-0.06	0.952737	0.978101	-6.85
254478_at	putative protein TRANSCRIPTION INIT	---	AT4G20330	-1.01	-0.01	-0.06	0.95293	0.978101	-6.85
262103_at	glutathione S-transferase, putative simi	GSTF5	AT1G02940	1.01	0.01	0.06	0.952665	0.978101	-6.85
255274_at	putative protein various predicted prote	---	---	1.01	0.01	0.06	0.95291	0.978101	-6.85

260727_at	polygalacturonase PG1, putative simila	---	AT1G48100	-1.01	-0.01	-0.06	0.953064	0.978113	-6.85
266783_at	putative laccase (diphenol oxidase)	LAC2	AT2G29130	1.01	0.01	0.06	0.953035	0.978113	-6.85
261340_at	hypothetical protein predicted by genem	APUM9	AT1G35730	1.01	0.01	0.06	0.953071	0.978113	-6.85
254854_at	putative protein hypothetical protein SP	---	AT4G12130	-1.01	-0.01	-0.06	0.95318	0.978137	-6.85
247290_at	putative protein similar to unknown prote	---	AT5G64450	1.01	0.01	0.06	0.953159	0.978137	-6.85
263661_at	unknown protein EST gb|T45093 comes	---	AT1G04290	1.01	0.01	0.06	0.953269	0.978184	-6.85
251805_at	putative protein RING-H2 finger protein	SDIR1	AT3G55530	1.00	0.01	0.06	0.953442	0.978186	-6.85
252158_at	CDPK-related protein kinase	CRK	AT3G50530	-1.01	-0.01	-0.06	0.953337	0.978186	-6.85
246416_at	putative protein predicted proteins, Arat	---	AT5G16920	1.00	0.01	0.06	0.953397	0.978186	-6.85
256814_at	beta-glucosidase, putative similar to be	BGLU19	AT3G21370	1.01	0.01	0.06	0.953433	0.978186	-6.85
264560_at	hypothetical protein predicted by genem	---	AT1G55820	-1.00	-0.01	-0.06	0.95355	0.978253	-6.85
245190_at	F12A21.16 hypothetical protein	---	AT1G67690	-1.01	-0.01	-0.06	0.953629	0.978290	-6.85
252447_at	beta-D-glucan exohydrolase - like prote	---	AT3G47040	-1.00	-0.01	-0.06	0.95373	0.978350	-6.85
263562_at	hypothetical protein predicted by gensca	---	AT2G15420	-1.00	-0.01	-0.06	0.953773	0.978350	-6.85
252149_at	putative protein hypothetical protein T7	---	AT3G51290	1.00	0.01	0.06	0.954037	0.978577	-6.85
245305_at	Expressed protein ; supported by full-ler	---	AT4G17215	-1.02	-0.02	-0.06	0.954333	0.978827	-6.85
257943_at	SKP1/ASK1 (At7), putative similar to SK	ASK7	AT3G21840	-1.01	-0.01	-0.06	0.954368	0.978827	-6.85
245436_at	membrane protein homolog	---	AT4G16620	1.00	0.01	0.06	0.954508	0.978884	-6.85
253534_at	cytochrome P450 monooxygenase ;sup	CYP83B1	AT4G31500	-1.01	-0.02	-0.06	0.9545	0.978884	-6.85
245691_at	zinc finger protein - like	ELF6	AT5G04240	1.01	0.01	0.06	0.954814	0.979108	-6.85
247356_at	beta-galactosidase (emb|CAB64742.1)	MUM2	AT5G63800	-1.01	-0.01	-0.06	0.954856	0.979108	-6.85
250425_at	lectin-like protein kinase - like lectin-like	---	AT5G10530	1.00	0.01	0.06	0.954806	0.979108	-6.85
264960_at	hypothetical protein contains similarity to	ATEXT4	AT1G76930	1.02	0.03	0.06	0.955016	0.979229	-6.85
244950_at	cytochrome c oxidase subunit 2	---	---	-1.01	-0.01	-0.06	0.955135	0.979232	-6.85
259782_at	unknown protein	---	AT1G29680	1.00	0.01	0.06	0.9552	0.979232	-6.85
259366_at	allene oxide cyclase, putative similar to	AOC4	AT1G13280	1.01	0.01	0.06	0.955065	0.979232	-6.85
259559_at	hypothetical protein	WAK3	AT1G21240	-1.01	-0.01	-0.06	0.955235	0.979232	-6.85
259299_at	unknown protein	---	AT3G05080	1.01	0.01	0.06	0.95519	0.979232	-6.85
267427_at	putative WRKY-type DNA binding protei	WRKY35	AT2G34830	-1.00	-0.01	-0.06	0.955278	0.979233	-6.85
253024_at	putative protein	---	AT4G38080	-1.02	-0.03	-0.06	0.95537	0.979283	-6.85
267351_at	unknown protein	NRPD1B	AT2G40030	1.00	0.01	0.06	0.955463	0.979331	-6.85
257394_at	hypothetical protein predicted by gensca	---	---	-1.01	-0.01	-0.06	0.955502	0.979331	-6.85
257156_at	hypothetical protein predicted by genem	---	AT3G24260	1.00	0.01	0.06	0.95565	0.979394	-6.85
254555_at	putative protein curved DNA-binding pr	---	AT4G19570	-1.00	-0.01	-0.06	0.955634	0.979394	-6.85
255943_at	UDP-glucose glucosyltransferase, puta	AtUGT85A	AT1G22370	1.01	0.02	0.06	0.955834	0.979417	-6.85

267541_at	hypothetical protein predicted by genefir	---	AT2G32750	1.01	0.01	0.06	0.955844	0.979417	-6.85
252988_at	putative cold-regulated protein cold-reg	---	AT4G38410	1.01	0.01	0.06	0.955818	0.979417	-6.85
263627_at	Expressed protein ; supported by full-ler	---	AT2G04675	1.01	0.01	0.06	0.955755	0.979417	-6.85
263438_at	unknown protein	---	AT2G28660	1.01	0.01	0.06	0.955977	0.979510	-6.85
264733_at	phloem serpin-1, putative similar to phl	---	AT1G62170	1.00	0.01	0.06	0.956308	0.979804	-6.85
262602_at	unknown protein ESTs gb|AA650895, g	---	AT1G15270	1.00	0.01	0.06	0.956551	0.980010	-6.85
254942_at	putative protein predicted proteins, Ara	---	AT4G10880	-1.00	0.00	-0.06	0.956737	0.980156	-6.85
257159_at	protein kinase, putative similar to protei	---	AT3G24400	1.01	0.01	0.06	0.956888	0.980245	-6.85
252728_at	putative protein various predicted prote	---	---	-1.00	-0.01	-0.06	0.956909	0.980245	-6.85
244919_at	cytochrome c biogenesis orf203 Protein	---	AT2G07768 /	-1.00	-0.01	-0.06	0.957123	0.980375	-6.85
248182_at	putative protein contains similarity to CH	---	AT5G54030	-1.00	-0.01	-0.06	0.957118	0.980375	-6.85
252532_at	glucosidase-like protein GLUCAN END	---	AT3G46570	-1.01	-0.01	-0.06	0.957249	0.980460	-6.85
246151_at	putative protein predicted proteins from	---	AT5G19950	-1.00	-0.01	-0.06	0.9575	0.980629	-6.85
244987_s_a	ribosomal protein L2	---	---	1.00	0.00	0.06	0.957462	0.980629	-6.85
258177_at	ubiquitin-regulatory protein, putative co	---	AT3G21660	1.00	0.01	0.06	0.957654	0.980743	-6.85
265376_at	hypothetical protein predicted by genefir	---	AT2G05810	1.00	0.01	0.05	0.957747	0.980795	-6.85
250963_at	putative protein various predicted prote	---	AT5G03000	1.01	0.01	0.05	0.957793	0.980797	-6.85
247515_at	ABC family transporter - like protein AB	ATH14	AT5G61740	-1.00	0.00	-0.05	0.957933	0.980842	-6.85
260977_at	hypothetical protein predicted by genem	---	AT1G53420	-1.00	-0.01	-0.05	0.957952	0.980842	-6.85
263041_at	putative alliinase similar to alliinase GB:	TAR1	AT1G23320	-1.00	-0.01	-0.05	0.957966	0.980842	-6.85
255633_at	Expressed protein ; supported by full-ler	---	AT4G00585	1.00	0.01	0.05	0.958034	0.980868	-6.85
254341_at	serine/threonine protein kinase like prot	SRF8	AT4G22130	-1.01	-0.02	-0.05	0.958304	0.981062	-6.85
254009_at	pyruvate kinase like protein pyruvate ki	---	AT4G26390	-1.01	-0.01	-0.05	0.958468	0.981062	-6.85
246834_at	putative protein homeotic protein boi1A	---	AT5G26630	-1.00	-0.01	-0.05	0.958405	0.981062	-6.85
264991_s_a	putative protein hypothetical proteins - A	---	AT1G67400 /	1.01	0.01	0.05	0.958431	0.981062	-6.85
265749_at	putative retroelement pol polyprotein	---	---	1.00	0.01	0.05	0.958483	0.981062	-6.85
249937_at	putative protein seed maturation protein	---	AT5G22470	1.01	0.01	0.05	0.958462	0.981062	-6.85
265080_at	overlap with bases 100,099-109,160 of	sks12	AT1G55570	1.01	0.01	0.05	0.958524	0.981062	-6.85
260449_at	unknown protein	---	AT1G72390	1.00	0.00	0.05	0.958828	0.981106	-6.85
255200_at	hypothetical protein	---	---	-1.00	-0.01	-0.05	0.958763	0.981106	-6.85
265687_s_a	hypothetical protein predicted by gensca	---	AT2G24470 /	-1.00	-0.01	-0.05	0.958811	0.981106	-6.85
257069_at	hypothetical protein predicted by gensca	---	AT3G28170	-1.00	-0.01	-0.05	0.958863	0.981106	-6.85
252144_at	ribosomal protein L8 homolog ribosoma	---	AT3G51190	1.00	0.01	0.05	0.958801	0.981106	-6.85
262546_at	iron-regulated transporter protein, putat	ZIP10	AT1G31260	1.01	0.01	0.05	0.958655	0.981106	-6.85
265365_at	En/Spm-like transposon protein related	---	---	-1.00	-0.01	-0.05	0.958868	0.981106	-6.85

260435_at	putative transcription factor similar to Cp	MYB62	AT1G68320	-1.01	-0.01	-0.05	0.959017	0.981179	-6.85
266691_at	hypothetical protein predicted by gensca	---	AT2G19890	-1.00	-0.01	-0.05	0.959026	0.981179	-6.85
249300_at	putative protein similar to unknown prote	---	AT5G41380	1.00	0.01	0.05	0.959139	0.981251	-6.85
251125_at	putative protein - kinase protein kinase	---	AT5G01060	-1.00	-0.01	-0.05	0.959263	0.981334	-6.85
248519_at	11-beta-hydroxysteroid dehydrogenase-	AtHSD7	AT5G50590 /	-1.00	-0.01	-0.05	0.959333	0.981361	-6.85
252763_at	Expressed protein ; supported by cDNA	---	AT3G42725	1.00	0.01	0.05	0.959892	0.981889	-6.85
253764_s_a	protein kinase - like protein ADK1 prote	ckl4	AT4G28860 /	1.00	0.01	0.05	0.959947	0.981901	-6.85
249997_at	chromatin remodelling complex ATPase	CHR17	AT5G18620	-1.00	-0.01	-0.05	0.960003	0.981914	-6.85
254777_at	putative protein hypothetical protein - A	---	AT4G12960	1.01	0.01	0.05	0.960111	0.981981	-6.85
253262_at	putative serine threonine protein kinase	---	AT4G34440	-1.00	-0.01	-0.05	0.960233	0.982061	-6.85
246633_at	hypothetical protein ; supported by cDN	---	AT1G29720	1.01	0.02	0.05	0.960388	0.982082	-6.85
257184_at	ABC transporter, putative similar to AtM	ATMRP8	AT3G13090	-1.00	-0.01	-0.05	0.960385	0.982082	-6.85
250271_at	putative protein predicted protein, Arabi	CLE40	AT5G12990	-1.00	-0.01	-0.05	0.960362	0.982082	-6.85
254031_at	putative protein other hypothetical prote	---	AT4G25920	1.00	0.01	0.05	0.960426	0.982082	-6.85
252525_at	putative protein hypothetical proteins	---	AT3G46450	-1.00	-0.01	-0.05	0.960523	0.982094	-6.85
263546_at	putative dihydrofolate reductase-thymidy	---	AT2G21550	1.01	0.01	0.05	0.960492	0.982094	-6.85
259506_at	protein phosphatase type 2C, putative s	---	AT1G43900	1.00	0.01	0.05	0.960626	0.982156	-6.85
247546_at	Expressed protein ; supported by full-ler	---	AT5G61605	1.00	0.01	0.05	0.960679	0.982165	-6.85
253435_at	adenylate translocator (brittle-1) - like p	SHS1	AT4G32400	-1.01	-0.01	-0.05	0.960787	0.982231	-6.85
250567_at	hypothetical protein	---	AT5G08090	-1.00	-0.01	-0.05	0.960959	0.982364	-6.85
258912_at	unknown protein similar to hypothetical	---	AT3G06460	1.01	0.01	0.05	0.961092	0.982412	-6.85
259394_at	hypothetical protein predicted by genem	---	AT1G06420	1.00	0.00	0.05	0.961064	0.982412	-6.85
246753_at	putative protein	---	---	1.00	0.01	0.05	0.961138	0.982414	-6.85
264102_at	hypothetical protein predicted by genem	ECT8	AT1G79270	1.01	0.01	0.05	0.961428	0.982535	-6.85
266378_at	hypothetical protein predicted by genefir	---	AT2G14700	-1.00	-0.01	-0.05	0.96138	0.982535	-6.85
265528_at	hypothetical protein predicted by gensca	---	---	-1.00	0.00	-0.05	0.961395	0.982535	-6.85
249507_at	similar to unknown protein (pir||T02618)	---	AT5G38370	-1.00	0.00	-0.05	0.96142	0.982535	-6.85
263756_at	putative ubiquitin fusion-degradation pro	---	AT2G21270	1.00	0.00	0.05	0.961515	0.982547	-6.85
245264_at	Expressed protein ; supported by cDNA	---	AT4G17245	-1.01	-0.02	-0.05	0.961569	0.982547	-6.85
245523_at	drought-induced protein like	ATDI21	AT4G15910	1.01	0.01	0.05	0.961568	0.982547	-6.85
252051_at	putative protein similarity hypothetical p	---	AT3G52570	1.00	0.01	0.05	0.961782	0.982720	-6.85
250853_s_a	putative protein prtedicted prteins, Arab	---	AT5G04680 /	1.00	0.00	0.05	0.961906	0.982803	-6.85
252717_at	putative protein predicted proteins, Aral	---	AT3G43930	-1.01	-0.01	-0.05	0.961964	0.982818	-6.85
245267_at	major latex protein like ; supported by cl	---	AT4G14060	1.00	0.01	0.05	0.962283	0.983100	-6.85
267098_at	hypothetical protein predicted by gensca	---	AT2G41451	1.00	0.01	0.05	0.962595	0.983374	-6.85

258865_at	NAM-like protein (no apical meristem)	anac045	AT3G03200	1.00	0.00	0.05	0.962658	0.983395	-6.85
257409_at	unknown protein predicted by genscan	---	AT2G17470	-1.00	-0.01	-0.05	0.962706	0.983400	-6.85
260170_at	putative sucrose transport protein simila	SUC5	AT1G71890	-1.01	-0.01	-0.05	0.962774	0.983425	-6.85
265468_at	hypothetical protein predicted by genefir	---	AT2G37210	1.00	0.01	0.05	0.962989	0.983558	-6.85
247567_at	putative protein various predicted prote	---	AT5G61190	-1.01	-0.01	-0.05	0.96299	0.983558	-6.85
248367_at	actin depolymerizing factor-like ;suppor	ADF10	AT5G52360	-1.00	-0.01	-0.05	0.963114	0.983596	-6.85
250804_at	putative protein contains similarity to ca	---	AT5G05030	-1.00	-0.01	-0.05	0.963096	0.983596	-6.85
257912_at	formin-like protein AHF1 identical to forr	AFH1	AT3G25500	1.01	0.01	0.05	0.963536	0.983851	-6.85
258751_at	low temperature and salt responsive pro	RCI2B	AT3G05890	1.01	0.02	0.05	0.963442	0.983851	-6.85
267310_at	unknown protein	AIR9	AT2G34680	1.01	0.01	0.05	0.963508	0.983851	-6.85
267463_at	Expressed protein ; supported by full-ler	---	AT2G33845	-1.01	-0.01	-0.05	0.963458	0.983851	-6.85
246625_at	hypothetical protein predicted by gensca	---	AT1G48880	-1.00	-0.01	-0.05	0.963595	0.983868	-6.85
259825_at	RNA and export factor binding protein,	---	AT1G66260	1.00	0.01	0.05	0.963719	0.983906	-6.85
246120_at	tetratricopeptide repeat protein tetratric	---	AT5G20360	1.00	0.01	0.05	0.963691	0.983906	-6.85
246136_at	peptide transporter - like protein peptide	---	AT5G28470	-1.00	-0.01	-0.05	0.963782	0.983925	-6.85
265334_at	putative lipid transfer protein ; supporte	---	AT2G18370	-1.01	-0.01	-0.05	0.963824	0.983925	-6.85
257427_at	hypothetical protein predicted by genem	---	AT1G79060	1.01	0.01	0.05	0.963928	0.983988	-6.85
256638_at	RNA-binding protein, putative similar to	---	AT3G19090	1.01	0.01	0.05	0.964114	0.984114	-6.85
267570_at	putative RNA helicase A identical to GE	HVT1	AT2G30800	1.00	0.01	0.05	0.964139	0.984114	-6.85
253247_at	Homeodomain - like protein similaritry t	BLH6	AT4G34610	-1.01	-0.01	-0.05	0.964292	0.984193	-6.85
256659_at	unknown protein similar to putative kine	---	AT3G12020	-1.00	-0.01	-0.05	0.964329	0.984193	-6.85
254322_at	hypothetical protein	---	AT4G22600	1.01	0.01	0.05	0.964389	0.984193	-6.85
249364_at	putative protein predicted protein, Arabi	---	AT5G40590	-1.00	-0.01	-0.05	0.964385	0.984193	-6.85
245153_at	putative protein similarity to predicted p	---	AT5G12450	-1.00	0.00	-0.05	0.964446	0.984207	-6.85
264450_s_a	unknown protein similar to hypothetical	SNL6	AT1G10250 /	1.01	0.01	0.05	0.964746	0.984470	-6.85
252145_at	putative protein several putative protein	---	AT3G51200	-1.00	0.00	-0.05	0.964945	0.984629	-6.85
254329_at	putative protein oxysterol-binding prote	ORP2A	AT4G22540	1.00	0.01	0.05	0.965331	0.984660	-6.85
249063_at	NBD-like protein (gb|AAD20643.1) ;sup	POP1	AT5G44110	-1.01	-0.01	-0.05	0.965399	0.984660	-6.85
262978_at	tubulin beta-1 chain identical to GB:P12	TUB1	AT1G75780	1.02	0.03	0.05	0.965293	0.984660	-6.85
265791_at	putative transcription factor	MEE65	AT2G01280	-1.00	-0.01	-0.05	0.965286	0.984660	-6.85
247650_at	putative protein ;supported by full-lengt	---	AT5G59960	1.01	0.01	0.05	0.965367	0.984660	-6.85
253707_at	hypothetical protein	---	AT4G29200	-1.00	0.00	-0.05	0.965284	0.984660	-6.85
245090_at	putative integral membrane protein nodu	---	AT2G40900	-1.01	-0.01	-0.05	0.965067	0.984660	-6.85
265165_at	putative OBP32pep protein	---	AT1G23610	1.00	0.00	0.05	0.965121	0.984660	-6.85
261716_at	kinesin-related protein, putative similar	---	AT1G18410	1.00	0.00	0.05	0.965407	0.984660	-6.85

260861_at	hypothetical protein predicted by genem	---	---	-1.00	-0.01	-0.05	0.965115	0.984660	-6.85
259741_at	unknown protein	---	AT1G71020	-1.01	-0.01	-0.04	0.96556	0.984672	-6.85
245963_at	putative protein HPt phosphotransmitte	---	AT5G19710	1.00	0.00	0.04	0.965592	0.984672	-6.85
264150_at	unknown protein similar to FUS5 protei	FUS5	AT1G02090	1.00	0.00	0.04	0.965568	0.984672	-6.85
255213_at	putative athila transposon protein	---	---	-1.00	0.00	-0.04	0.965571	0.984672	-6.85
253056_at	SHORT-ROOT (SHR)	SHR	AT4G37650	-1.01	-0.01	-0.04	0.965742	0.984782	-6.85
259523_at	hypothetical protein	---	AT1G12500	-1.01	-0.01	-0.04	0.965802	0.984799	-6.85
260279_at	putative DNA repair protein similar to D	---	AT1G80420	1.00	0.01	0.04	0.965849	0.984803	-6.85
250589_at	transcription factor (gb|AAD53097.1) ; s	MYB76	AT5G07700	1.01	0.01	0.04	0.965895	0.984805	-6.85
247751_at	putative protein	---	AT5G59050	-1.01	-0.01	-0.04	0.965959	0.984827	-6.85
257995_at	putative monosaccharide transport prot	---	AT3G19940	-1.00	-0.01	-0.04	0.966222	0.985051	-6.85
264797_at	unknown protein similar to ESTs gb|T22	---	AT1G08710	1.00	0.01	0.04	0.966325	0.985051	-6.85
266697_at	profilin 4 ; supported by full-length cDN	PRF5	AT2G19770	1.00	0.01	0.04	0.966363	0.985051	-6.85
247322_at	unknown protein	---	AT5G64090	-1.00	0.00	-0.04	0.966338	0.985051	-6.85
263814_at	putative TNP2-like transposon protein re	---	---	-1.00	0.00	-0.04	0.966395	0.985051	-6.85
266470_at	putative non-LTR retroelement reverse t	---	---	-1.01	-0.01	-0.04	0.966452	0.985066	-6.85
256030_at	hypothetical protein contains similarity t	---	AT1G34110	1.00	0.01	0.04	0.966532	0.985102	-6.85
245274_at	ankyrin like protein ; supported by cDNA	---	AT4G14360	1.00	0.01	0.04	0.967037	0.985153	-6.85
263509_s_a	hypothetical protein	---	AT2G07687	1.01	0.01	0.04	0.966678	0.985153	-6.85
254213_at	tyrosine transaminase like protein tyros	---	AT4G23590	-1.00	0.00	-0.04	0.967004	0.985153	-6.85
257378_s_a	hypothetical protein predicted by gensca	---	AT2G02290 /	-1.00	-0.01	-0.04	0.966976	0.985153	-6.85
AFFX-BioDr	E. coli /GEN=bioD /DB_XREF=gb:J0442	---	---	-1.01	-0.01	-0.04	0.966936	0.985153	-6.85
248083_at	unknown protein	---	AT5G55420	-1.01	-0.02	-0.04	0.967057	0.985153	-6.85
255663_at	hypothetical protein	---	AT4G00420	-1.00	-0.01	-0.04	0.966787	0.985153	-6.85
250606_s_a	pectin methyl-esterase-like protein pect	PPME1	AT1G69940 /	-1.00	0.00	-0.04	0.967028	0.985153	-6.85
255251_at	see GB:U95973 similar to a family of Ar	---	AT4G04980	1.00	0.00	0.04	0.966936	0.985153	-6.85
256393_at	hypothetical protein	---	AT3G06280	1.00	0.00	0.04	0.966709	0.985153	-6.85
254392_at	endonuclease, putative ; supported by t	ENDO5	AT4G21600	-1.00	0.00	-0.04	0.966948	0.985153	-6.85
261989_at	disease resistance protein, putative sim	---	AT1G33670	1.00	0.01	0.04	0.967134	0.985188	-6.85
250781_at	DREB2A (dbj|BAA33794.1) ; supported	DREB2A	AT5G05410	1.01	0.01	0.04	0.967195	0.985206	-6.85
259268_at	putative lamin similar to blue copper-bin	---	AT3G01070	1.00	0.00	0.04	0.967251	0.985219	-6.85
247686_at	receptor-like protein kinase precursor -	---	AT5G59700	-1.01	-0.01	-0.04	0.967422	0.985305	-6.85
248596_at	putative protein contains similarity to my	AtMYB111	AT5G49330	-1.01	-0.01	-0.04	0.967421	0.985305	-6.85
256849_at	hypothetical protein similar to hypothetic	---	---	-1.00	-0.01	-0.04	0.967627	0.985470	-6.85
256214_x_a	hypothetical protein predicted by genem	---	AT1G51000	1.00	0.00	0.04	0.967737	0.985532	-6.85

266677_at	hypothetical protein predicted by gensca	---	AT2G29820	-1.00	-0.01	-0.04	0.967774	0.985532	-6.85
261549_at	DNA-binding protein, putative contains	---	AT1G63470	1.00	0.01	0.04	0.967825	0.985539	-6.85
257570_at	dirigent protein, putative similar to dirige	---	AT3G13662	1.00	0.00	0.04	0.967964	0.985625	-6.85
245889_at	PEE-rich protein ;supported by full-leng	---	AT5G09480	1.01	0.01	0.04	0.967995	0.985625	-6.85
259827_at	hypothetical protein	---	AT1G72270	-1.00	0.00	-0.04	0.968122	0.985710	-6.85
247797_at	predicted protein	---	AT5G58780	1.00	0.01	0.04	0.968203	0.985739	-6.85
258022_at	hypothetical protein predicted by genem	---	AT3G19460	-1.00	0.00	-0.04	0.968237	0.985739	-6.85
253606_at	putative protein component of aniline di	---	AT4G30530	1.01	0.01	0.04	0.968298	0.985757	-6.85
245836_at	hypothetical protein similar to hypothetic	---	---	1.00	0.00	0.04	0.968461	0.985879	-6.85
250318_at	dihydropyrimidinase ; supported by cDN	---	AT5G12200	-1.00	-0.01	-0.04	0.968589	0.985913	-6.85
245069_at	putative glucosyltransferase	UGT84B2	AT2G23250	1.00	0.00	0.04	0.968621	0.985913	-6.85
264174_s_a	hypothetical protein	ANAC004	AT1G02230	-1.00	-0.01	-0.04	0.968624	0.985913	-6.85
265416_at	unknown protein ; supported by full-leng	---	AT2G37120	-1.01	-0.01	-0.04	0.968688	0.985934	-6.85
252063_at	lipid transfer protein-like protein lipid tra	LTP12	AT3G51590	-1.00	0.00	-0.04	0.968966	0.986158	-6.85
250145_at	putative protein predicted protein, Arabi	---	AT5G14690	-1.00	-0.01	-0.04	0.968995	0.986158	-6.85
252620_at	hypothetical protein	---	---	1.00	0.00	0.04	0.969105	0.986227	-6.85
250714_at	sorting nexin-like protein	SNX1	AT5G06140	1.00	0.01	0.04	0.969271	0.986228	-6.85
253824_at	putative protein protein kinase LePK7, I	MTM1	AT4G27940	1.01	0.02	0.04	0.969323	0.986228	-6.85
257626_s_a	hypothetical protein	---	AT3G26240 /	-1.00	0.00	-0.04	0.969292	0.986228	-6.85
249758_at	putative protein similar to unknown prote	---	AT5G24350	1.00	0.01	0.04	0.969214	0.986228	-6.85
245440_at	RNA helicase	---	AT4G16680	-1.00	0.00	-0.04	0.969317	0.986228	-6.85
255705_at	hypothetical protein ;supported by full-le	---	AT4G00160	-1.00	0.00	-0.04	0.969383	0.986246	-6.85
245133_at	putative nucleotide sugar epimerase	GAE4	AT2G45310	1.01	0.01	0.04	0.969497	0.986274	-6.85
246395_at	dirigent protein, putative similar to dirige	---	AT1G58170	-1.00	0.00	-0.04	0.969495	0.986274	-6.85
256426_at	hypothetical protein predicted by gensca	---	AT1G33420	1.01	0.01	0.04	0.969557	0.986291	-6.85
249734_at	putative protein strong similarity to unkn	IRE1-1	AT5G24360	1.00	0.00	0.04	0.969718	0.986357	-6.85
262128_at	late embryogenesis-abundant protein, p	---	AT1G52690	1.02	0.03	0.04	0.969795	0.986357	-6.85
266174_at	hypothetical protein predicted by gensca	---	AT2G02440	-1.00	0.00	-0.04	0.969678	0.986357	-6.85
262975_at	zinc finger protein, putative similar to zi	STH2	AT1G75540	1.00	0.01	0.04	0.969795	0.986357	-6.85
251620_at	putative protein hypothetical protein F1	---	AT3G58060	-1.00	-0.01	-0.04	0.969858	0.986377	-6.85
254704_at	putative protein predicted protein, Arabi	APRR2	AT4G18020	-1.00	0.00	-0.04	0.970055	0.986489	-6.85
254528_at	hypothetical protein	---	AT4G19620	-1.00	0.00	-0.04	0.97003	0.986489	-6.85
259629_at	disease resistance protein contains dom	WRR4	AT1G56510	1.00	0.01	0.04	0.970228	0.986544	-6.85
252896_at	cytochrome P450 - like protein cytochro	CYP96A9	AT4G39480	1.00	0.00	0.04	0.970219	0.986544	-6.85
266724_at	hypothetical protein predicted by gensca	---	AT2G03180	1.00	0.00	0.04	0.970238	0.986544	-6.85

248504_at	transcription factor Hap5a-like	NF-YC6	AT5G50480	-1.00	-0.01	-0.04	0.970385	0.986552	-6.85
262568_at	hypothetical protein contains similarity t	AtRLP5	AT1G34290	-1.00	0.00	-0.04	0.970506	0.986552	-6.85
246734_at	putative protein WRN (Werner syndrom	RECQSIM	AT5G27680	1.00	0.00	0.04	0.970415	0.986552	-6.85
256665_at	hypothetical protein predicted by genem	---	AT3G20700	1.00	0.01	0.04	0.970464	0.986552	-6.85
249634_at	putative protein several hypothetical pro	---	---	-1.00	0.00	-0.04	0.970415	0.986552	-6.85
265410_at	putative protein kinase contains a protei	---	AT2G16620	1.00	0.00	0.04	0.970432	0.986552	-6.85
254474_at	putative protein predicted proteins, Ara	---	AT4G20390	-1.00	-0.01	-0.04	0.970678	0.986577	-6.85
247381_at	auxin-independent growth promoter-like	---	AT5G63390	1.00	0.00	0.04	0.970646	0.986577	-6.85
255649_at	contains region of similarity to mouse m	---	AT4G00920	1.00	0.00	0.04	0.970604	0.986577	-6.85
258178_at	hypothetical protein predicted by genem	---	AT3G21680	1.00	0.00	0.04	0.970703	0.986577	-6.85
252265_at	putative protein SRG1 protein - Arabido	DIN11	AT3G49620	-1.01	-0.02	-0.04	0.970925	0.986680	-6.85
260565_at	unknown protein predicted by genefinde	---	AT2G43800	-1.01	-0.01	-0.04	0.970934	0.986680	-6.85
255210_at	may be a pseudogene	---	---	1.00	0.00	0.04	0.970864	0.986680	-6.85
249032_at	putative protein contains similarity to dis	---	AT5G44910	1.01	0.02	0.04	0.971025	0.986728	-6.85
257620_at	hypothetical protein predicted by genem	---	AT3G24850	1.00	0.00	0.04	0.971156	0.986817	-6.85
251368_at	putative protein hypothetical protein At2	---	AT3G61380	-1.01	-0.01	-0.04	0.971244	0.986818	-6.85
244942_at	hypothetical protein	---	---	-1.00	0.00	-0.04	0.971212	0.986818	-6.85
250834_at	putative protein various predicted prote	DME	AT5G04560	-1.00	-0.01	-0.04	0.971361	0.986889	-6.85
259845_at	auxin transporter splice variant b, putati	PIN1	AT1G73590	-1.00	-0.01	-0.04	0.971433	0.986889	-6.85
251410_at	uclacyanin 3 ; supported by cDNA: gi_1	UCC3	AT3G60280	1.00	0.00	0.04	0.971443	0.986889	-6.85
248254_at	receptor protein kinase-like protein	---	AT5G53320	1.00	0.01	0.04	0.971538	0.986942	-6.85
250220_at	receptor protein kinase-like protein	---	AT5G14210	-1.01	-0.01	-0.04	0.971727	0.986958	-6.85
265937_at	putative RING zinc finger protein	---	AT2G19610	1.00	0.00	0.04	0.971643	0.986958	-6.85
261066_at	hypothetical protein predicted by genem	---	AT1G07485	1.00	0.00	0.04	0.971711	0.986958	-6.85
264695_at	lipid transfer protein, putative similar to	---	AT1G70250	1.00	0.01	0.04	0.971659	0.986958	-6.85
260130_s_a	beta-glucosidase, putative similar to GE	BGLU21	AT1G66270 /	-1.00	0.00	-0.04	0.971785	0.986973	-6.85
248867_at	bHLH transcription factor	---	AT5G46830	-1.00	0.00	-0.04	0.971874	0.987019	-6.85
256630_at	unknown protein	---	AT3G28230	-1.00	0.00	-0.04	0.972029	0.987107	-6.85
245380_at	hypothetical protein	---	AT4G17760	-1.00	-0.01	-0.04	0.972047	0.987107	-6.85
262611_at	Expressed protein ; supported by full-ler	---	AT1G14060	1.00	0.01	0.04	0.972106	0.987122	-6.85
252623_at	hypothetical protein	---	AT3G45320	-1.00	0.00	-0.04	0.97225	0.987181	-6.85
266042_s_a	hypothetical protein	---	AT2G07734	1.00	0.01	0.04	0.972226	0.987181	-6.85
249219_at	putative protein contains similarity to SE	SDG25	AT5G42400	-1.00	0.00	-0.04	0.972469	0.987315	-6.85
248546_at	putative protein similar to unknown prote	---	AT5G50270	-1.00	0.00	-0.04	0.972458	0.987315	-6.85
245072_s_a	putative cytochrome P450	CYP81D7	AT2G23190 /	1.00	0.00	0.04	0.972532	0.987336	-6.85

248485_at	calcium-binding transporter-like protein	---	AT5G51050	-1.00	-0.01	-0.04	0.972628	0.987336	-6.85
250500_at	periaxin - like protein periaxin, Rattus n	---	AT5G09530	-1.03	-0.04	-0.04	0.972596	0.987336	-6.85
257304_at	hypothetical protein predicted by gensca	---	---	1.00	0.00	0.04	0.972663	0.987336	-6.85
247588_at	protein disulfide isomerase precursor -	ATPDIL1-4	AT5G60640	-1.00	0.00	-0.04	0.972731	0.987344	-6.85
252708_at	putative protein amine oxidase, Canava	---	AT3G43820	-1.00	0.00	-0.04	0.972757	0.987344	-6.85
250356_at	clathrin binding protein - like Af10-prote	---	AT5G11710	-1.00	0.00	-0.04	0.972839	0.987384	-6.85
258756_at	hypothetical protein similar to hypothetic	---	AT3G11960	-1.00	0.00	-0.04	0.973041	0.987544	-6.85
265523_at	putative Ty3-gypsy-like retroelement pol	---	---	-1.00	0.00	-0.03	0.973164	0.987625	-6.85
260458_at	unknown protein	---	AT1G68250	-1.00	0.00	-0.03	0.973411	0.987832	-6.85
254683_at	hypothetical protein ;supported by full-le	---	AT4G13800	-1.00	0.00	-0.03	0.973493	0.987872	-6.85
253482_at	Expressed protein ; supported by cDNA	---	AT4G31985	1.01	0.01	0.03	0.973674	0.987879	-6.85
260151_at	unknown protein ;supported by full-leng	---	AT1G52910	1.01	0.01	0.03	0.973659	0.987879	-6.85
257162_s_a	ammonium transporter, putative similar	AMT1;3	AT3G24290 /	-1.00	0.00	-0.03	0.973667	0.987879	-6.85
253194_s_a	hypothetical protein	---	---	1.00	0.00	0.03	0.973653	0.987879	-6.85
263947_at	unknown protein ;supported by full-leng	---	AT2G35820	1.00	0.01	0.03	0.974073	0.988152	-6.85
262339_at	WRKY DNA binding protein, putative si	WRKY56	AT1G64000	-1.00	0.00	-0.03	0.974034	0.988152	-6.85
245655_at	hypothetical protein predicted by genem	---	AT1G56530	1.00	0.00	0.03	0.974053	0.988152	-6.85
264836_at	unknown protein similar to hypothetical	---	AT1G03610	-1.00	-0.01	-0.03	0.974419	0.988415	-6.85
257588_x_a	En/Spm-like transposon protein, putativ	---	---	1.00	0.01	0.03	0.974392	0.988415	-6.85
248405_at	putative protein pectinesterase-like; stro	SKS2	AT5G51480	-1.01	-0.02	-0.03	0.974592	0.988415	-6.85
257276_at	disease resistance protein, putative sim	---	AT3G14460	1.00	0.00	0.03	0.974472	0.988415	-6.85
246974_at	putative protein	---	AT5G24980	1.00	0.00	0.03	0.97457	0.988415	-6.85
265891_at	putative thionin	---	AT2G15010	-1.00	0.00	-0.03	0.97454	0.988415	-6.85
265573_at	putative zinc-finger protein similar to zin	---	AT2G28200	1.01	0.01	0.03	0.97467	0.988451	-6.85
253313_at	putative peroxidase peroxidase ATP12a	---	AT4G33870	1.00	0.00	0.03	0.974745	0.988452	-6.85
248888_at	potassium channel protein KAT1 (pir||S3	KAT1	AT5G46240	-1.01	-0.01	-0.03	0.974903	0.988452	-6.85
266492_at	putative protein kinase contains a protei	---	AT2G07020	1.00	0.00	0.03	0.974808	0.988452	-6.85
263450_at	putative calcium-dependent protein kina	CPK24	AT2G31500	-1.00	0.00	-0.03	0.974932	0.988452	-6.85
245860_at	putative protein predicted proteins, Ara	---	AT5G28310	-1.00	0.00	-0.03	0.974817	0.988452	-6.85
253145_at	hypothetical protein	---	AT4G35560	1.00	0.01	0.03	0.974915	0.988452	-6.85
254176_at	hypothetical protein hypothetical protein	---	AT4G24200	-1.00	0.00	-0.03	0.975084	0.988519	-6.85
266549_at	Expressed protein ; supported by full-ler	EXL1	AT2G35150	1.00	0.00	0.03	0.975061	0.988519	-6.85
261721_at	unknown protein ; supported by cDNA: g	---	AT1G08480	-1.00	0.00	-0.03	0.975146	0.988538	-6.85
248131_at	unknown protein	---	AT5G54830	1.01	0.01	0.03	0.975353	0.988703	-6.85
246578_at	MADS-box protein, putative similar to M	AGL86	AT1G31630	1.00	0.00	0.03	0.975398	0.988705	-6.85

262326_at	hypothetical protein similar to putative d	---	AT1G64140 /	-1.00	0.00	-0.03	0.975724	0.988769	-6.85
257087_at	purple acid phosphatase, putative simil	PAP18	AT3G20500	-1.00	0.00	-0.03	0.975593	0.988769	-6.85
246025_at	zwille/pinhead-like protein GERp95 - Ra	---	AT5G21150	1.00	0.00	0.03	0.975789	0.988769	-6.85
253831_at	Expressed protein ; supported by full-ler	---	AT4G27580	1.00	0.00	0.03	0.97553	0.988769	-6.85
263896_at	hypothetical protein predicted by gensca	---	AT2G21930	1.00	0.00	0.03	0.975626	0.988769	-6.85
248751_at	putative protein similar to unknown prote	---	AT5G47540	1.00	0.00	0.03	0.975732	0.988769	-6.85
246187_at	putative protein	AT5G2102	---	-1.00	0.00	-0.03	0.975863	0.988769	-6.85
246588_at	putative protein predicted protein, Arabi	---	AT3G06433 /	1.00	0.00	0.03	0.975777	0.988769	-6.85
252687_at	putative protein predicted protein, Arabi	---	---	1.00	0.00	0.03	0.975861	0.988769	-6.85
262995_s_a	hypothetical protein predicted by genem	---	---	-1.00	0.00	-0.03	0.975895	0.988769	-6.85
259834_at	H-protein promoter binding factor-2b nea	---	AT1G69570	-1.00	-0.01	-0.03	0.97603	0.988775	-6.85
266088_at	hypothetical protein predicted by gensca	---	AT2G37780	1.00	0.00	0.03	0.975983	0.988775	-6.85
265448_at	putative DOF zinc finger protein	DAG2	AT2G46590	-1.00	0.00	-0.03	0.97601	0.988775	-6.85
259119_at	transport protein SEC13, putative simila	---	AT3G01340	1.00	0.00	0.03	0.976287	0.988963	-6.85
253491_at	RNA lariat debranching enzyme - like p	---	AT4G31770	-1.00	-0.01	-0.03	0.976303	0.988963	-6.85
249750_at	unknown protein ;supported by full-leng	---	AT5G24570	1.00	0.01	0.03	0.976483	0.989102	-6.85
248067_at	unknown protein	---	AT5G55600	-1.00	0.00	-0.03	0.976678	0.989135	-6.85
259930_at	hypothetical protein predicted by genem	---	AT1G34355	1.00	0.00	0.03	0.976584	0.989135	-6.85
247391_at	unknown protein	---	AT5G63540	-1.00	0.00	-0.03	0.976686	0.989135	-6.85
257230_at	DegP protease contains similarity to De	DegP11	AT3G16540	-1.00	0.00	-0.03	0.976689	0.989135	-6.85
251566_at	putative protein several hypothetical pro	---	AT3G58210	1.00	0.00	0.03	0.976759	0.989162	-6.85
252649_at	putative protein histone deacetylase 1 -	HDA9	AT3G44680	1.00	0.00	0.03	0.976853	0.989212	-6.85
254671_at	MuDR transposable element - like prote	---	---	1.00	0.00	0.03	0.976987	0.989261	-6.85
257192_at	unknown protein ;supported by full-leng	EMB2769	AT3G13200	-1.00	0.00	-0.03	0.976974	0.989261	-6.85
251093_at	putative protein several hypothetical pro	---	AT5G01360	1.00	0.01	0.03	0.97707	0.989300	-6.85
252762_at	putative protein hypothetical protein MZ	---	AT3G42780	-1.00	0.00	-0.03	0.977364	0.989473	-6.85
256166_at	hypothetical protein	---	AT1G36920	-1.00	0.00	-0.03	0.977386	0.989473	-6.85
251737_at	40S ribosomal protein S26 homolog sev	---	AT3G56340	1.01	0.01	0.03	0.977393	0.989473	-6.85
260052_at	14-3-3 protein (grf13), putative contains	GRF13	AT1G78220	1.00	0.00	0.03	0.977414	0.989473	-6.85
254332_at	leucine rich repeat receptor kinase-like	---	AT4G22730	-1.00	0.00	-0.03	0.977611	0.989542	-6.85
260705_at	unknown protein ;supported by full-lengt	TOM2A	AT1G32400	-1.00	0.00	-0.03	0.97757	0.989542	-6.85
249654_at	putative protein hypothetical proteins - A	---	---	1.00	0.00	0.03	0.977578	0.989542	-6.85
265238_s_a	hypothetical protein	---	AT2G07696	-1.00	0.00	-0.03	0.977664	0.989551	-6.85
256954_at	E2, ubiquitin-conjugating enzyme, putat	FUS9	AT3G13550	1.00	0.00	0.03	0.977809	0.989609	-6.85
262032_at	biotin holocarboxylase synthetase, puta	HCS2	AT1G37150	1.00	0.00	0.03	0.97778	0.989609	-6.85

262426_s_a	cytochrome P450, putative similar to cy	---	AT1G47625 /	-1.00	0.00	-0.03	0.977953	0.989712	-6.85
265243_at	hypothetical protein predicted by gensca	NPG1	AT2G43040	1.00	0.00	0.03	0.978187	0.989905	-6.85
249249_at	unknown protein	---	AT5G42330	-1.00	0.00	-0.03	0.978273	0.989921	-6.85
264080_at	putative vacuolar proton-ATPase subun	VHA-A1	AT2G28520	-1.00	0.00	-0.03	0.978334	0.989921	-6.85
256558_at	hypothetical protein predicted by genem	---	---	-1.00	0.00	-0.03	0.978333	0.989921	-6.85
249006_at	putative protein similar to unknown prote	---	AT5G44650 /	-1.00	0.00	-0.03	0.978407	0.989947	-6.85
251223_at	putative transcription factor MYB11	ATMYB11	AT3G62610	1.00	0.00	0.03	0.978446	0.989947	-6.85
260119_at	AIG1-like protein similar to AIG1 protein	---	AT1G33930	-1.00	0.00	-0.03	0.978533	0.989952	-6.85
265312_at	unknown protein	---	AT2G20240	1.00	0.01	0.03	0.978625	0.989952	-6.85
260647_at	hypothetical protein predicted by genem	---	AT1G08030	1.00	0.00	0.03	0.978649	0.989952	-6.85
248733_at	unknown protein	ELP1	---	-1.00	0.00	-0.03	0.978668	0.989952	-6.85
261345_at	hypothetical protein predicted by genefir	DTA4	AT1G79760	1.00	0.00	0.03	0.978547	0.989952	-6.85
263195_at	non-specific lipid transfer protein, putati	---	AT1G36150	-1.00	0.00	-0.03	0.978789	0.989986	-6.85
253151_at	putative polygalacturonase polygalactu	---	AT4G35670	1.00	0.00	0.03	0.978762	0.989986	-6.85
255966_at	14-3-3 protein GF14epsilon (grf10) ider	GRF10	AT1G22300	-1.00	0.00	-0.03	0.97892	0.990075	-6.85
248072_at	unknown protein	---	AT5G55680	-1.00	0.00	-0.03	0.979034	0.990147	-6.85
257941_at	putative UDP-glucose glucosyltransfera	UGT71B8	AT3G21800	-1.00	0.00	-0.03	0.979098	0.990167	-6.85
248982_at	chloroplast nucleoid DNA-binding protei	---	AT5G45120	1.00	0.00	0.03	0.979375	0.990403	-6.85
250690_at	ABC transporter-like protein ; supported	---	AT5G06530	-1.00	0.00	-0.03	0.979428	0.990413	-6.85
251811_at	APETALA2 - like protein APETALA2, A	SMZ	AT3G54990	1.00	0.00	0.03	0.979482	0.990424	-6.85
260761_at	hypothetical protein predicted by genem	---	AT1G49150	1.00	0.00	0.03	0.979595	0.990494	-6.85
258308_at	putative reverse transcriptase similar to	---	---	-1.00	-0.01	-0.03	0.97964	0.990496	-6.85
248677_at	unknown protein	---	AT5G48860	-1.00	0.00	-0.03	0.979765	0.990520	-6.85
263721_at	hypothetical protein predicted by gensca	---	AT2G13630	1.00	0.00	0.03	0.979781	0.990520	-6.85
249857_at	C2H2-type zinc finger protein-like	---	AT5G22990	-1.00	0.00	-0.03	0.979795	0.990520	-6.85
261250_at	unknown protein	---	AT1G05890	-1.00	0.00	-0.03	0.980264	0.990907	-6.85
249153_s_a	putative protein strong similarity to unkn	---	AT5G43390 /	1.00	0.00	0.03	0.980229	0.990907	-6.85
253896_at	putative protein NBS/LRR disease resis	---	AT4G27190	1.00	0.00	0.03	0.980354	0.990912	-6.85
261261_at	putative aldehyde oxidase	---	AT1G26730	1.01	0.01	0.03	0.980356	0.990912	-6.85
263694_at	putative reverse transcriptase strong sin	---	---	1.00	0.00	0.03	0.980407	0.990920	-6.85
266776_at	putative ubiquitin fusion-degradation pro	---	AT2G29070	1.00	0.00	0.03	0.980634	0.990959	-6.85
256538_x_a	hypothetical protein predicted by genem	---	---	1.00	0.00	0.03	0.980594	0.990959	-6.85
253702_at	Ca2+-transporting ATPase - like protein	ACA10	AT4G29900	-1.00	0.00	-0.03	0.980606	0.990959	-6.85
266305_at	putative DNA polymerase epsilon catalyt	TIL2	AT2G27120	-1.00	0.00	-0.03	0.980678	0.990959	-6.85
255747_s_a	hypothetical protein predicted by genem	---	AT1G32010 /	1.00	0.00	0.03	0.980706	0.990959	-6.85

264411_at	mutator-like transposase, putative simil	---	---	1.00	0.00	0.03	0.980548	0.990959	-6.85
244928_s_a	hypothetical protein	---	AT2G07716	1.00	0.00	0.02	0.980785	0.990995	-6.85
266424_at	unknown protein	---	AT2G41330	1.00	0.00	0.02	0.981022	0.991172	-6.85
257322_at	hypothetical protein	AT2G0766	---	-1.00	0.00	-0.02	0.981058	0.991172	-6.85
247481_at	putative protein predicted protein, Arabi	---	AT5G62400	-1.00	0.00	-0.02	0.981091	0.991172	-6.85
262278_at	transcription factor PERIANTHIA identic	PAN	AT1G68640	1.00	0.00	0.02	0.98118	0.991187	-6.85
265792_at	predicted by genscan and genefinder	---	AT2G01390	-1.00	0.00	-0.02	0.981236	0.991187	-6.85
255528_at	hypothetical protein	---	AT4G02090	1.00	0.00	0.02	0.981236	0.991187	-6.85
256135_at	hypothetical protein predicted by genem	---	AT1G48730	-1.00	0.00	-0.02	0.981428	0.991205	-6.85
262139_at	mutator-like transposase, putative simil	AT1G5261	---	-1.00	0.00	-0.02	0.981411	0.991205	-6.85
258639_at	polygalacturonase (PGA3) identical to p	---	AT3G07820	-1.00	0.00	-0.02	0.981357	0.991205	-6.85
262608_at	dioxygenase-like protein very similar to	---	AT1G14120	-1.00	0.00	-0.02	0.981338	0.991205	-6.85
267033_at	unknown protein ;supported by full-leng	---	AT2G38450	-1.00	0.00	-0.02	0.981481	0.991215	-6.85
245752_at	hypothetical protein similar to Ac-like tra	---	AT1G35150	1.00	0.00	0.02	0.981659	0.991351	-6.85
256789_at	seven in absentia-like protein similar to	---	AT3G13672	-1.00	-0.01	-0.02	0.981777	0.991407	-6.85
261709_at	RNA-binding protein, putative similar to	CID11	AT1G32790	-1.00	0.00	-0.02	0.981801	0.991407	-6.85
259923_at	putative protein kinase contains Pfam pr	---	AT1G72760	1.00	0.00	0.02	0.981849	0.991411	-6.85
245257_at	calmodulin ; supported by cDNA: gi_582	CAM8	AT4G14640	1.00	0.00	0.02	0.98197	0.991470	-6.85
245221_s_a	polyprotein, putative similar to polyprote	---	---	-1.00	0.00	-0.02	0.981995	0.991470	-6.85
245207_at	RING finger-like protein similarity to pre	---	AT5G12310	1.00	0.00	0.02	0.982092	0.991525	-6.85
266593_at	hypothetical protein predicted by gensca	---	AT2G46200	1.00	0.00	0.02	0.982193	0.991583	-6.85
251039_at	putative protein hypothetical protein T6	---	AT5G02020	-1.00	-0.01	-0.02	0.982406	0.991618	-6.85
250332_at	putative protein predicted proteins, Arat	---	AT5G11680	-1.00	0.00	-0.02	0.982419	0.991618	-6.85
256079_at	hypothetical protein predicted by gensca	---	AT1G20680	-1.00	0.00	-0.02	0.9823	0.991618	-6.85
264287_at	hypothetical protein similar to hypothetic	---	AT1G61930	-1.00	0.00	-0.02	0.982446	0.991618	-6.85
248372_at	putative protein similar to unknown prote	---	AT5G51850	1.00	0.00	0.02	0.982385	0.991618	-6.85
264184_at	early nodule-specific protein, putative s	---	AT1G54790	1.00	0.00	0.02	0.982641	0.991772	-6.85
248264_at	putative protein similar to unknown prote	---	AT5G53310	-1.00	0.00	-0.02	0.982693	0.991781	-6.85
257112_at	cytochrome P450, putative contains Pfa	CYP705A2	AT3G20120	-1.00	0.00	-0.02	0.982946	0.991948	-6.85
258702_at	hypothetical protein predicted by genefir	---	AT3G09730	-1.00	0.00	-0.02	0.98293	0.991948	-6.85
261802_at	hypothetical protein similar to hypothetic	---	AT1G30550	-1.00	0.00	-0.02	0.983047	0.992006	-6.85
246181_at	pectinesterase - like protein probable pe	---	AT5G20860	-1.00	0.00	-0.02	0.98311	0.992025	-6.85
262081_at	kinesin motor protein (kin2), putative sir	ZCF125	AT1G59540	1.00	0.00	0.02	0.983197	0.992069	-6.85
257080_at	unknown protein	---	AT3G15240	1.00	0.00	0.02	0.983777	0.992094	-6.85
247875_at	putative protein similar to unknown prote	---	AT5G57720	1.00	0.00	0.02	0.983605	0.992094	-6.85

260191_at	putative protein kinase Pfam HMM hit: E	---	AT1G67580	-1.00	0.00	-0.02	0.983508	0.992094	-6.85
245424_at	putative protein	---	AT4G17505	-1.00	0.00	-0.02	0.983665	0.992094	-6.85
257091_at	DNA polymerase, putative C-term simil	POLGAMM	AT3G20540	1.00	0.00	0.02	0.983608	0.992094	-6.85
255125_at	putative protein SCARECROW - Arabid	---	AT4G08250	-1.00	0.00	-0.02	0.983787	0.992094	-6.85
254124_at	hypothetical protein ; supported by cDN	---	AT4G24500	-1.00	0.00	-0.02	0.983296	0.992094	-6.85
266393_at	late embryogenesis abundant M17 prote	M17	AT2G41260	-1.00	0.00	-0.02	0.983695	0.992094	-6.85
252684_at	disease resistence - like protein RPP1-	---	AT3G44400	-1.00	0.00	-0.02	0.983353	0.992094	-6.85
261647_at	hypothetical protein similar to hypothetic	---	AT1G27740	-1.00	0.00	-0.02	0.983775	0.992094	-6.85
248301_at	DnaJ protein-like	---	AT5G53150	1.00	0.00	0.02	0.983414	0.992094	-6.85
255187_s_a	putative transposon protein	---	---	1.00	0.00	0.02	0.983349	0.992094	-6.85
265081_at	hypothetical protein contains Zinc finge	MGP	AT1G03840	-1.00	0.00	-0.02	0.983628	0.992094	-6.85
247114_at	unknown protein ; supported by cDNA:	---	AT5G65910	-1.00	0.00	-0.02	0.983937	0.992202	-6.85
257494_at	hypothetical protein predicted by genem	---	AT1G32375	1.00	0.00	0.02	0.984159	0.992341	-6.85
267280_at	diacylglycerol O-acyltransferase ; suppo	TAG1	AT2G19450	-1.00	0.00	-0.02	0.984177	0.992341	-6.85
264062_at	unknown protein	---	AT2G27950	1.00	0.00	0.02	0.984206	0.992341	-6.85
251736_at	putative protein acetyl-CoA carboxylase	---	AT3G56130	1.00	0.00	0.02	0.984251	0.992343	-6.85
257290_at	hypothetical protein predicted by gensca	---	AT3G15550	-1.00	0.00	-0.02	0.984362	0.992367	-6.85
249892_at	unknown protein	---	AT5G22600	-1.00	0.00	-0.02	0.98436	0.992367	-6.85
265822_at	putative SEC1 family transport protein s	ATSLY1	AT2G17980	-1.00	0.00	-0.02	0.98442	0.992381	-6.85
245079_at	putative retroelement pol polyprotein	---	---	-1.00	0.00	-0.02	0.984474	0.992391	-6.85
249262_at	putative protein similar to unknown prote	---	AT5G41720	1.00	0.00	0.02	0.984517	0.992391	-6.85
253529_at	putative protein hypothetical protein - A	---	AT4G31520	1.00	0.00	0.02	0.984576	0.992407	-6.85
247595_at	ring finger protein - like ring finger prote	---	AT5G60820	1.00	0.00	0.02	0.984785	0.992575	-6.85
258429_at	putative GTP-binding protein similar to C	TOC120	AT3G16620	-1.00	0.00	-0.02	0.984903	0.992605	-6.85
257429_at	putative RING zinc finger protein	---	AT2G27940	1.00	0.00	0.02	0.984869	0.992605	-6.85
265689_at	hypothetical protein predicted by gensca	---	AT2G24310	-1.00	0.00	-0.02	0.985073	0.992646	-6.85
262435_at	cytochrome P450, putative similar to cy	CYP96A8	AT1G47620	1.00	0.00	0.02	0.985054	0.992646	-6.85
249179_at	Expressed protein ; supported by full-ler	---	AT5G42955	-1.00	0.00	-0.02	0.985019	0.992646	-6.85
249642_at	putative protein	---	AT5G36960	1.00	0.00	0.02	0.985198	0.992727	-6.85
251577_at	putative protein several hypothetical pro	---	AT3G58350	-1.00	0.00	-0.02	0.985247	0.992732	-6.85
247070_at	Expressed protein ; supported by full-ler	---	AT5G66815	-1.00	0.00	-0.02	0.985381	0.992780	-6.85
251373_at	GATA transcription factor 4 ; supported	---	AT3G60530	1.01	0.01	0.02	0.985372	0.992780	-6.85
258116_at	hypothetical protein similar to terpene sy	---	AT3G14520	1.00	0.00	0.02	0.985534	0.992867	-6.85
257048_at	hypothetical protein predicted by genem	---	AT3G19740	-1.00	0.00	-0.02	0.985554	0.992867	-6.85
248812_at	palmitoyl-protein thioesterase precursor	---	AT5G47330	-1.01	-0.01	-0.02	0.985695	0.992877	-6.85

251489_at	putative protein putative proteins - Arabi	---	AT3G59460	-1.00	0.00	-0.02	0.985678	0.992877	-6.85
248671_at	putative protein strong similarity to unkn	---	AT5G48750	1.00	0.00	0.02	0.985662	0.992877	-6.85
264439_at	adenine phosphoribosyltransferase 1, A	APT1	AT1G27450	1.00	0.00	0.02	0.986098	0.993239	-6.85
250497_at	putative protein predicted proteins, Arat	---	AT5G09630	-1.00	0.00	-0.02	0.986254	0.993265	-6.85
247276_at	putative protein contains similarity to RN	HEN4	AT5G64390	1.00	0.00	0.02	0.986179	0.993265	-6.85
245997_at	putative protein saur1 protein, Zea may	---	AT5G20810	-1.00	0.00	-0.02	0.986218	0.993265	-6.85
258122_at	hypothetical protein contains similarity t	ATGSL04	AT3G14570	1.00	0.00	0.02	0.986382	0.993303	-6.85
257223_at	50S ribosomal protein L12-B identical t	RPL12-B	AT3G27840	1.00	0.00	0.02	0.986423	0.993303	-6.85
257543_at	hypothetical protein predicted by genem	---	AT3G28960	1.00	0.00	0.02	0.986343	0.993303	-6.85
256668_at	hypothetical protein similar to hypothetic	---	AT3G32190	1.00	0.00	0.02	0.986551	0.993345	-6.85
256871_at	WD-repeat protein, putative contains Pf	---	AT3G26480	1.00	0.00	0.02	0.986535	0.993345	-6.85
256894_at	PREG-like protein, putative similar to P	CYCP2;1	AT3G21870	1.00	0.00	0.02	0.986719	0.993445	-6.85
263397_s_a	putative GDSL-motif lipase/hydrolase si	---	AT2G31540 /	1.00	0.00	0.02	0.986907	0.993445	-6.85
249560_at	putative protein	LCR80	AT5G38330	1.00	0.00	0.02	0.986955	0.993445	-6.85
257581_s_a	RAV-like DNA-binding protein, putative	---	AT1G50680 /	1.00	0.00	0.02	0.986948	0.993445	-6.85
265744_at	putative CENP-B/ARS binding protein-li	---	---	-1.00	0.00	-0.02	0.986907	0.993445	-6.85
255407_at	hypothetical protein similar to A. thalian	---	AT4G03480	1.00	0.00	0.02	0.98686	0.993445	-6.85
245805_at	hypothetical protein predicted by genem	---	AT1G46336	-1.00	0.00	-0.02	0.986761	0.993445	-6.85
253352_at	pathogenesis-related protein 1 precurs	---	AT4G33710	1.00	0.00	0.02	0.987098	0.993525	-6.85
248844_s_a	extA (emb CAA47807.1)	---	AT5G46890 /	-1.00	0.00	-0.02	0.987123	0.993525	-6.85
263985_at	unknown protein ;supported by full-leng	---	AT2G42750	1.00	0.00	0.02	0.987382	0.993699	-6.85
257591_at	leucine-rich repeat disease resistance p	AtRLP39	AT3G24900	-1.00	0.00	-0.02	0.987355	0.993699	-6.85
249565_at	contains similarity to S1 self-incompatibi	---	AT5G38440	-1.00	0.00	-0.02	0.98752	0.993794	-6.85
261263_at	H-protein promoter binding factor-2b, p	---	AT1G26790	1.00	0.00	0.02	0.987579	0.993809	-6.85
260146_at	putative non-phototropic hypocotyl simil	---	AT1G52770	1.00	0.00	0.02	0.987734	0.993878	-6.85
254435_at	putative protein	MS5	AT4G20900	-1.00	0.00	-0.02	0.987732	0.993878	-6.85
251070_at	translation initiation factor eIF-2 beta ch	---	AT5G01940	-1.00	0.00	-0.02	0.987781	0.993881	-6.85
267198_at	putative gibberellin-regulated protein	---	AT2G30810	1.00	0.00	0.02	0.987831	0.993888	-6.85
255631_at	hypothetical protein	BSK3	AT4G00710	1.00	0.00	0.02	0.987912	0.993902	-6.85
250648_at	late embryogenesis abundant protein LE	---	AT5G06760	1.00	0.00	0.02	0.987932	0.993902	-6.85
246961_at	unknown protein	---	AT5G24710	-1.00	0.00	-0.02	0.988037	0.993963	-6.85
263065_at	MAP kinase (ATMPK7) identical to GB:(	ATMPK7	AT2G18170	1.00	0.00	0.02	0.988257	0.994117	-6.85
263095_at	Ac-like transposase related to Ac/Ds tra	---	AT2G16040	1.00	0.00	0.02	0.988277	0.994117	-6.85
255052_at	rab7 -like protein rab7 protein -Vigna ac	ATRABG3	AT4G09720	1.00	0.00	0.01	0.98851	0.994264	-6.85
264729_at	putative metal-binding protein highly sim	---	AT1G22990	1.00	0.00	0.01	0.988504	0.994264	-6.85

248276_at	EspB-like protein	YSL3	AT5G53550	-1.00	0.00	-0.01	0.988595	0.994305	-6.85
258415_at	putative s-adenosylmethionine syntheta	MTO3	AT3G17390	1.00	0.00	0.01	0.9887	0.994367	-6.85
267087_at	putative MYB family transcription factor	MYB101	AT2G32460	1.00	0.00	0.01	0.988792	0.994416	-6.85
249840_at	unknown protein ; supported by cDNA:	ATLCBK1	AT5G23450	1.00	0.00	0.01	0.988972	0.994553	-6.85
255620_at	putative copper-containing glycoprotein	---	AT4G01380	-1.00	0.00	-0.01	0.989259	0.994798	-6.85
253825_at	Expressed protein ; supported by full-ler	---	AT4G28025	1.00	0.00	0.01	0.989406	0.994865	-6.85
267613_at	putative second messenger-dependent	PID2	AT2G26700	-1.00	0.00	-0.01	0.989414	0.994865	-6.85
254239_at	water channel - like protein plasma mer	PIP1;5	AT4G23400	1.00	0.00	0.01	0.989725	0.995091	-6.85
256774_at	hypothetical protein predicted by genem	---	AT3G13760	1.00	0.00	0.01	0.989717	0.995091	-6.85
245669_at	hypothetical protein contains similarity t	LEC2	AT1G28300	1.00	0.00	0.01	0.989818	0.995125	-6.85
249384_at	putative protein hypothetical protein F8	---	AT5G39890	-1.00	0.00	-0.01	0.989847	0.995125	-6.85
257457_at	hypothetical protein predicted by genefi	---	AT2G05430	1.00	0.00	0.01	0.989962	0.995198	-6.85
259525_at	hypothetical protein	ATEXPA7	AT1G12560	1.00	0.00	0.01	0.990054	0.995246	-6.85
254533_at	putative protein ARI protein - Drosophil	---	AT4G19670	1.00	0.00	0.01	0.990102	0.995251	-6.85
265782_at	putative two-component response regul	---	AT2G07440	-1.00	0.00	-0.01	0.990159	0.995264	-6.85
256824_at	hypothetical protein predicted by genem	AT3G2212	---	1.00	0.00	0.01	0.990232	0.995294	-6.85
253513_at	peroxidase - like protein peroxidase, Sp	---	AT4G31760	-1.00	0.00	-0.01	0.990295	0.995313	-6.85
248379_at	RAR1 (gb|AAF18433.1) non-consensus	PBS2	AT5G51700	1.00	0.00	0.01	0.990466	0.995353	-6.85
252792_at	hypothetical protein	---	---	1.00	0.00	0.01	0.990385	0.995353	-6.85
249261_at	putative protein similar to unknown prote	---	---	1.00	0.00	0.01	0.990431	0.995353	-6.85
247334_at	cdc2-like protein kinase-like protein sup	CDKE;1	AT5G63610	-1.00	0.00	-0.01	0.990706	0.995419	-6.85
267587_at	unknown protein	---	AT2G42080	1.00	0.00	0.01	0.990689	0.995419	-6.85
260962_at	pectin methylesterase, putative similar t	PME7	AT1G44980	1.00	0.00	0.01	0.990685	0.995419	-6.85
248251_at	unknown protein	---	AT5G53220	-1.00	0.00	-0.01	0.990626	0.995419	-6.85
258318_at	unknown protein	---	AT3G22680	-1.00	0.00	-0.01	0.990823	0.995493	-6.85
250119_at	putative protein similar to unknown prote	---	AT5G16470	-1.00	0.00	-0.01	0.991093	0.995514	-6.85
264712_at	unknown protein	ECT11	AT1G09810	-1.00	0.00	-0.01	0.991063	0.995514	-6.85
245540_at	ABC transporter like protein	PDR2	AT4G15230	-1.00	0.00	-0.01	0.990909	0.995514	-6.85
264945_at	MADS-box protein (MADS2), putative s	MAF1	AT1G77080	-1.00	0.00	-0.01	0.991214	0.995514	-6.85
249476_at	germin - like protein probable germin ty	---	AT5G38910	-1.00	0.00	-0.01	0.991305	0.995514	-6.85
257837_at	hypothetical protein predicted by genem	---	AT3G25200	1.00	0.00	0.01	0.991129	0.995514	-6.85
255671_at	Expressed protein ; supported by full-ler	---	AT4G00355	1.00	0.00	0.01	0.991211	0.995514	-6.85
245667_at	FH protein interacting protein FIP1 ident	FIP1	AT1G28200	-1.00	0.00	-0.01	0.991225	0.995514	-6.85
251510_at	putative protein several hypothetical pro	---	AT3G59170	1.00	0.00	0.01	0.991279	0.995514	-6.85
259556_at	hypothetical protein	---	---	-1.00	0.00	-0.01	0.991294	0.995514	-6.85

265558_at	putative non-LTR retroelement reverse t	---	---	1.00	0.00	0.01	0.991324	0.995514	-6.85
266848_at	unknown protein ;supported by full-leng	---	AT2G25950	-1.00	0.00	-0.01	0.991632	0.995697	-6.85
247638_at	arabinogalactan protein - like arabinoga	FLA12	AT5G60490	-1.00	0.00	-0.01	0.991637	0.995697	-6.85
248543_at	putative protein similar to unknown prote	---	AT5G50230	-1.00	0.00	-0.01	0.991561	0.995697	-6.85
251731_at	manganese superoxide dismutase-like	---	AT3G56350	1.00	0.00	0.01	0.9917	0.995710	-6.85
266966_at	hypothetical protein predicted by gensca	---	AT2G39520	-1.00	0.00	-0.01	0.991737	0.995710	-6.85
252689_at	putative protein predicted proteins, Arat	---	AT3G44030	-1.00	0.00	-0.01	0.992108	0.996038	-6.85
246963_at	putative protein nucleoid DNA-binding p	---	AT5G24820	-1.00	0.00	-0.01	0.992276	0.996119	-6.85
258967_at	hypothetical protein predicted by gensc	---	AT3G10470	1.00	0.00	0.01	0.992237	0.996119	-6.85
262652_at	hypothetical protein One of a cluster of	FUT9	AT1G14110	-1.00	0.00	-0.01	0.99242	0.996219	-6.85
255276_at	putative fatty acid desaturase similar to	DES-1-LIK	AT4G04930	-1.00	0.00	-0.01	0.992738	0.996401	-6.85
266236_at	putative glutathione S-transferase	ATGSTZ2	AT2G02380	-1.00	0.00	-0.01	0.992775	0.996401	-6.85
265672_at	putative cysteine proteinase inhibitor B (	---	AT2G31980	-1.00	0.00	-0.01	0.992696	0.996401	-6.85
254407_at	receptor kinase - like protein receptor-li	---	AT4G21370	-1.00	0.00	-0.01	0.992733	0.996401	-6.85
249496_s_a	putative protein predicted proteins - Arat	---	AT5G39140 /	1.00	0.00	0.01	0.99299	0.996573	-6.85
252789_s_a	hypothetical protein ; supported by full-l	---	AT1G21930 /	-1.00	0.00	-0.01	0.993145	0.996641	-6.85
266118_at	protease inhibitor II ; supported by cDN	LCR68	AT2G02130	1.00	0.00	0.01	0.993139	0.996641	-6.85
266145_at	putative TNP2-like transposon protein	---	---	-1.00	0.00	-0.01	0.993264	0.996716	-6.85
260765_at	actin 8 almost identical to actin 8 GI:166	ACT8	AT1G49240	-1.00	0.00	-0.01	0.993351	0.996760	-6.85
253459_at	hypothetical protein	---	AT4G32080	-1.00	0.00	-0.01	0.993449	0.996814	-6.85
264958_at	unknown protein ; supported by cDNA: g	---	AT1G76960	1.00	0.00	0.01	0.993598	0.996920	-6.85
267531_at	putative calcium-dependent protein kina	CPK14	AT2G41860	-1.00	0.00	-0.01	0.993767	0.997045	-6.85
255428_at	putative LRR receptor-like protein kinas	SRF3	AT4G03390	-1.00	0.00	-0.01	0.993857	0.997091	-6.85
264969_at	hypothetical protein contains similarity to	---	AT1G67320	-1.00	0.00	-0.01	0.993921	0.997113	-6.85
253642_at	hypothetical protein ;supported by full-le	---	AT4G29960	1.00	0.00	0.01	0.99409	0.997238	-6.85
253196_at	NAD+ dependent isocitrate dehydrogen	IDH1	AT4G35260	1.00	0.00	0.01	0.994155	0.997259	-6.85
263921_at	putative fructose bisphosphate aldolase	---	AT2G36460	-1.00	0.00	-0.01	0.994273	0.997334	-6.85
245324_at	lactate dehydrogenase (LDH1) ;support	---	AT4G17260	1.00	0.00	0.01	0.994575	0.997505	-6.85
253817_at	hypothetical protein ;supported by full-le	---	AT4G28310	1.00	0.00	0.01	0.994494	0.997505	-6.85
248670_at	receptor protein kinase-like protein	---	AT5G48740	-1.00	0.00	-0.01	0.994562	0.997505	-6.85
246714_at	putative protein predicted proteins, Arat	---	AT5G28220	-1.00	0.00	-0.01	0.994757	0.997644	-6.85
263592_at	putative non-LTR retroelement reverse t	---	---	1.00	0.00	0.01	0.994846	0.997645	-6.85
255308_at	putative component of vesicle-mediated	NSF	AT4G04910	-1.00	0.00	-0.01	0.994803	0.997645	-6.85
246426_at	ovule development protein aintegument	BBM	AT5G17430	-1.00	0.00	-0.01	0.995071	0.997699	-6.85
254886_at	putative protein bp4A protein, Brassica	LCR17	AT4G11760	-1.00	0.00	-0.01	0.995045	0.997699	-6.85

246664_at	putative protein predicted proteins - Aral	---	---	1.00	0.00	0.01	0.995075	0.997699	-6.85
251553_at	DNA-binding WRKY - like protein AR41	WRKY69	AT3G58710	1.00	0.00	0.01	0.99496	0.997699	-6.85
258649_at	putative transitional endoplasmic reticul	CDC48	AT3G09840	-1.00	0.00	-0.01	0.995343	0.997862	-6.85
267058_at	putative protein kinase contains a protei	MAPKKK1	AT2G32510	1.00	0.00	0.01	0.995393	0.997862	-6.85
256926_at	hypothetical protein predicted by genem	---	AT3G22540	1.00	0.00	0.01	0.995293	0.997862	-6.85
259203_at	hypothetical protein predicted by genefir	---	AT3G09130	1.00	0.00	0.01	0.995413	0.997862	-6.85
249551_at	putative protein predicted proteins, Aral	---	AT5G38220	1.00	0.00	0.01	0.995671	0.998043	-6.85
257283_at	hypothetical protein predicted by genem	---	AT3G29750	-1.00	0.00	-0.01	0.99574	0.998043	-6.85
262020_at	polyprotein, putative similar to gag-pol p	---	---	-1.00	0.00	-0.01	0.995768	0.998043	-6.85
245519_at	retrotransposon like protein	---	---	-1.00	0.00	-0.01	0.995725	0.998043	-6.85
252498_at	putative protein several hypothetical pro	---	AT3G46810	1.00	0.00	0.01	0.995849	0.998080	-6.85
250424_at	bromodomain protein - like bromodoma	GTE2	AT5G10550	-1.00	0.00	-0.01	0.996026	0.998214	-6.85
266205_s_a	putative dTDP-glucose 4-6-dehydratase	AXS2	AT1G08200 /	-1.00	0.00	-0.01	0.996075	0.998219	-6.85
258362_at	unknown protein	---	AT3G14280	1.00	0.00	0.00	0.996279	0.998336	-6.85
251440_at	SKP1/ASK1 (At13), putative similar to S	ASK13	AT3G60010	-1.00	0.00	0.00	0.996252	0.998336	-6.85
256027_at	putative protein	---	AT1G34160	1.00	0.00	0.00	0.996335	0.998348	-6.85
246482_at	plant adhesion molecule 1 (PAM1) ;sup	PAM1	AT5G15930	1.00	0.00	0.00	0.996732	0.998443	-6.85
248185_at	flavonol 3-O-glucosyltransferase-like	UF3GT	AT5G54060	-1.00	0.00	0.00	0.996779	0.998443	-6.85
258980_at	putative reversibly glycosylatable polype	RGP3	AT3G08900	1.00	0.00	0.00	0.996525	0.998443	-6.85
259465_at	hypothetical protein similar to putative n	---	AT1G19025	-1.00	0.00	0.00	0.996622	0.998443	-6.85
258558_at	hypothetical protein predicted by genefir	---	AT3G06000	-1.00	0.00	0.00	0.996685	0.998443	-6.85
250368_at	putative protein ; supported by cDNA: g	---	AT5G11280	1.00	0.00	0.00	0.996603	0.998443	-6.85
253228_at	putative protein ;supported by full-lengt	---	AT4G34630	1.00	0.00	0.00	0.996749	0.998443	-6.85
254581_at	putative protein membrane-associated	---	AT4G19440	1.00	0.00	0.00	0.996627	0.998443	-6.85
261305_at	glutamine synthetase, putative similar t	GLN1;5	AT1G48470	1.00	0.00	0.00	0.997097	0.998717	-6.85
248919_at	putative protein contains similarity to iso	---	AT5G45920	-1.00	0.00	0.00	0.997367	0.998827	-6.85
249056_at	putative protein similar to unknown prote	---	AT5G44470	-1.00	0.00	0.00	0.997382	0.998827	-6.85
266390_at	hypothetical protein predicted by gensca	---	AT2G32310	1.00	0.00	0.00	0.997343	0.998827	-6.85
253521_at	multicatalytic endopeptidase complex, p	PBA1	AT4G31300	1.00	0.00	0.00	0.997253	0.998827	-6.85
262759_at	unknown protein	---	AT1G10800	-1.00	0.00	0.00	0.997438	0.998839	-6.85
263886_at	hypothetical protein predicted by gensca	TKI1	AT2G36960	1.00	0.00	0.00	0.997488	0.998846	-6.85
263690_at	putative DNA-binding protein Similar to	AtHB23	AT1G26960	-1.00	0.00	0.00	0.997795	0.999106	-6.85
248653_at	disease resistance protein-like	---	AT5G49290	-1.00	0.00	0.00	0.997879	0.999106	-6.85
267155_at	CLE7, putative CLAVATA3/ESR-relate	---	AT2G30925	1.00	0.00	0.00	0.997861	0.999106	-6.85
257379_x_a	Mutator-like transposase similar to MUF	---	---	1.00	0.00	0.00	0.997936	0.999119	-6.85

249194_at	kinesin heavy chain-like protein	---	AT5G42490	1.00	0.00	0.00	0.997981	0.999120	-6.85
248297_at	protochlorophyllide reductase; oxidoredu	---	AT5G53100	-1.00	0.00	0.00	0.998362	0.999383	-6.85
253077_at	hypothetical protein	---	AT4G36170	1.00	0.00	0.00	0.998329	0.999383	-6.85
264720_at	hypothetical protein similar to vetispiradi	---	AT1G70080	1.00	0.00	0.00	0.998376	0.999383	-6.85
256408_at	hypothetical protein	---	AT1G66610	-1.00	0.00	0.00	0.998525	0.999489	-6.85
260880_at	hypothetical protein similar to unknown p	---	AT1G21380	-1.00	0.00	0.00	0.998733	0.999491	-6.85
256703_at	MADS-box transcription factor similar to	AGL79	AT3G30260	-1.00	0.00	0.00	0.998699	0.999491	-6.85
248220_at	26S proteasome regulatory particle chai	---	AT5G53540	-1.00	0.00	0.00	0.998775	0.999491	-6.85
249881_at	cytochrome P450-like protein	CYP86B1	AT5G23190	1.00	0.00	0.00	0.998653	0.999491	-6.85
254567_s_a	hypothetical protein	---	AT4G19260 /	1.00	0.00	0.00	0.998702	0.999491	-6.85
250628_at	hypothetical protein	---	AT5G07380	-1.00	0.00	0.00	0.99879	0.999491	-6.85
247069_at	pectinesterase like protein ;supported b	sks17	AT5G66920	1.00	0.00	0.00	0.999066	0.999526	-6.85
262217_at	hypothetical protein predicted by genem	---	AT1G74770	1.00	0.00	0.00	0.999076	0.999526	-6.85
259314_at	putative glucose and ribitol dehydrogena	---	AT3G05260	1.00	0.00	0.00	0.999087	0.999526	-6.85
253978_at	putative protein probable kinesin - Arab	---	AT4G26660	-1.00	0.00	0.00	0.998969	0.999526	-6.85
250699_at	receptor-like protein kinase	SRF2	AT5G06820	-1.00	0.00	0.00	0.999046	0.999526	-6.85
264771_at	phosphomethylpyrimidine kinase proba	TH1	AT1G22940	1.00	0.00	0.00	0.998961	0.999526	-6.85
263354_at	hypothetical protein predicted by grail	---	AT2G22060	-1.00	0.00	0.00	0.999182	0.999576	-6.85
257597_at	protein kinase, putative similar to protei	---	AT3G24790	-1.00	0.00	0.00	0.999263	0.999613	-6.85
251044_at	putative protein various predicted prote	---	AT5G02350	1.00	0.00	0.00	0.999397	0.999704	-6.85
251923_at	reductase-like protein abscisic acid acti	---	AT3G53880	-1.00	0.00	0.00	0.99956	0.999823	-6.85
260437_at	hypothetical protein predicted by gensca	---	AT1G68380	1.00	0.00	0.00	0.999675	0.999839	-6.85
252735_at	putative protein predicted proteins, Arat	---	AT3G43170	1.00	0.00	0.00	0.999708	0.999839	-6.85
261520_at	unknown protein ; supported by cDNA: g	SEC6	AT1G71820	-1.00	0.00	0.00	0.999695	0.999839	-6.85
257452_at	hypothetical protein predicted by gensca	---	AT1G05740	1.00	0.00	0.00	0.999835	0.999922	-6.85
253690_at	putative protein various predicted prote	---	AT4G29550	-1.00	0.00	0.00	0.999941	0.999945	-6.85
266637_at	hypothetical protein ;supported by full-le	BRXL1	AT2G35600	1.00	0.00	0.00	0.999945	0.999945	-6.85

	Interaction:(mut.72- mut.0) - (wt.72 - wt.0)									
	Description	Gene Symb	AGI	FC	logFC	t	P.Value	adj.P.Val	B	
264415_at	AP2 domain containing protein,	RAP2.6	AT1G43160	31.40	4.97	24.33	8.22E-08	0.0018758	6.89	FALSE
257774_at	short-chain alcohol dehydrogena	---	AT3G29250	16.85	4.07	19.92	3.11E-07	0.0035452	6.28	FALSE
252118_at	putative protein various predicte	---	AT3G51400	-4.43	-2.15	-17.03	8.77E-07	0.0066673	5.69	FALSE
251142_at	Expressed protein ; supported by	---	AT5G01015	6.84	2.77	15.98	1.34E-06	0.0076141	5.43	TRUE
263180_at	unknown protein ;supported by f	URH2	AT1G05620	5.88	2.56	14.83	2.17E-06	0.0099118	5.11	FALSE
248701_at	ligand-gated ion channel protein-	GLR1.3	AT5G48410	4.38	2.13	12.66	6.09E-06	0.0199696	4.37	TRUE
266967_at	unknown protein	---	AT2G39530	3.30	1.72	12.65	6.13E-06	0.0199696	4.36	FALSE
256964_at	unknown protein ;supported by f	AGP12	AT3G13520	3.99	1.99	11.22	1.33E-05	0.0220421	3.75	TRUE
259942_at	unknown protein	ATWHY2	AT1G71260	-2.66	-1.41	-11.25	1.31E-05	0.0220421	3.76	TRUE
247030_at	putative protein similar to unknov	---	AT5G67210	2.98	1.58	12.09	8.24E-06	0.0220421	4.13	TRUE
260235_at	putative SET protein, phospatas	NRP1	AT1G74560	-2.93	-1.55	-11.33	1.25E-05	0.0220421	3.80	TRUE
248753_at	acyl carrier protein-like	mtACP3	AT5G47630	-3.21	-1.68	-10.92	1.58E-05	0.0220421	3.61	TRUE
266117_at	hypothetical protein ; supported	---	AT2G02170	-2.93	-1.55	-10.56	1.97E-05	0.0220421	3.42	FALSE
251642_at	imbibition protein homolog proba	AtSIP2	AT3G57520	3.65	1.87	10.62	1.90E-05	0.0220421	3.45	FALSE
264107_s_a	putative receptor-like protein kina	SERK5	AT2G13790 ///	3.78	1.92	10.73	1.77E-05	0.0220421	3.51	FALSE
248700_at	ligand-gated ion channel protein-	ATGLR1.2	AT5G48400	4.09	2.03	10.62	1.90E-05	0.0220421	3.45	FALSE
264160_at	hypothetical protein predicted by	---	AT1G65450	-4.16	-2.06	-10.66	1.85E-05	0.0220421	3.48	FALSE
252097_at	putative protein hypothetical prot	---	AT3G51090	2.94	1.56	10.68	1.83E-05	0.0220421	3.49	FALSE
253101_at	cytochrome P450 monooxygenas	CYP91A2	AT4G37430	11.53	3.53	11.18	1.36E-05	0.0220421	3.73	FALSE
248918_at	senescence-specific cysteine pro	SAG12	AT5G45890	4.85	2.28	10.51	2.03E-05	0.0220421	3.40	FALSE
264614_s_a	putative aldehyde oxidase simila	---	AT1G02590 ///	3.45	1.79	10.74	1.77E-05	0.0220421	3.51	FALSE
266247_at	hypothetical protein predicted by	---	AT2G27660	4.44	2.15	10.42	2.14E-05	0.0221827	3.35	FALSE
259150_at	unknown protein similar to unkno	---	AT3G10320	2.63	1.40	9.27	4.49E-05	0.023529	2.71	TRUE
267256_s_a	putative serine carboxypeptidase	scpl10	AT2G23000 ///	3.84	1.94	9.39	4.13E-05	0.023529	2.78	TRUE
262811_at	unknown protein ESTs gb|R6538	---	AT1G11700	-3.29	-1.72	-9.90	2.96E-05	0.023529	3.07	TRUE
255604_at	hypothetical protein	---	AT4G01080	5.10	2.35	9.25	4.54E-05	0.023529	2.70	TRUE
249970_at	dermal glycoprotein precursor -l	---	AT5G19100	7.08	2.82	9.43	4.03E-05	0.023529	2.80	FALSE
263786_at	putative auxin-responsive protein	JAR1	AT2G46370	2.35	1.23	10.15	2.53E-05	0.023529	3.21	FALSE
250484_at	asparagine synthetase ASN3 ; s	ASN3	AT5G10240	-2.87	-1.52	-9.66	3.45E-05	0.023529	2.94	TRUE
249115_at	PINHEAD (gb|AAD40098.1); tran	ZLL	AT5G43810	-2.42	-1.28	-9.34	4.28E-05	0.023529	2.75	TRUE
259272_at	unknown protein similar to hypotl	---	AT3G01290	3.70	1.89	9.58	3.65E-05	0.023529	2.89	FALSE
261335_at	nodulin protein, putative similar t	---	AT1G44800	2.29	1.19	9.32	4.35E-05	0.023529	2.74	FALSE
256436_at	hypothetical protein predicted by	---	AT3G11150	2.95	1.56	9.33	4.33E-05	0.023529	2.74	FALSE

264053_at	hypothetical protein predicted by	---	AT2G22560	4.06	2.02	9.31	4.38E-05	0.023529	2.73	FALSE
260408_at	putative thioredoxin similar to thi	ATH8	AT1G69880	3.85	1.95	9.98	2.81E-05	0.023529	3.12	FALSE
264685_at	endo-1,4-beta-glucanase, putati	KOR2	AT1G65610	3.31	1.73	9.59	3.62E-05	0.023529	2.90	FALSE
249527_at	proline oxidase, mitochondrial pr	---	AT5G38710	5.22	2.38	9.75	3.26E-05	0.023529	2.99	FALSE
244997_at	RNA polymerase beta' subunit-2	---	---	-3.15	-1.66	-9.69	3.40E-05	0.023529	2.95	FALSE
258259_s_a	unknown protein ; supported by	---	AT3G26820 ///	2.99	1.58	9.32	4.35E-05	0.023529	2.74	FALSE
247723_at	protein phosphatase 2C - like AB	---	AT5G59220	8.55	3.10	9.85	3.06E-05	0.023529	3.05	FALSE
248353_at	cytochrome P450	CYP96A4	AT5G52320	2.64	1.40	9.52	3.80E-05	0.023529	2.86	FALSE
255074_at	putative protein RING-H2 zinc fi	---	AT4G09100	3.16	1.66	9.84	3.08E-05	0.023529	3.04	FALSE
259418_at	unknown protein ; supported by c	GPAT2	AT1G02390	4.42	2.14	10.04	2.71E-05	0.023529	3.15	FALSE
258167_at	UDP-glucose:indole-3-acetate b	UGT84A2	AT3G21560	8.52	3.09	9.93	2.91E-05	0.023529	3.09	FALSE
261819_at	receptor-like kinase, putative sin	---	AT1G11410	-2.71	-1.44	-9.18	4.77E-05	0.0236309	2.66	TRUE
254612_at	putative protein hypothetical pro	---	AT4G19100	-2.35	-1.23	-9.20	4.70E-05	0.0236309	2.67	FALSE
245130_at	putative receptor-like protein kina	---	AT2G45340	-2.41	-1.27	-9.11	5.00E-05	0.0242557	2.61	FALSE
256466_at	plastid protein, putative similar to	---	AT1G32580	-2.33	-1.22	-9.06	5.18E-05	0.0246272	2.58	TRUE
245367_at	Expressed protein ; supported by	NRPB9B	AT4G16265	-2.88	-1.52	-8.98	5.47E-05	0.0248348	2.53	FALSE
267134_at	putative protein kinase contains a	---	AT2G23450	2.14	1.10	8.96	5.55E-05	0.0248348	2.52	FALSE
267496_at	putative lipase ; supported by fu	---	AT2G30550	3.99	2.00	8.97	5.54E-05	0.0248348	2.52	FALSE
257765_at	hypothetical protein contains Pfa	---	AT3G23020	-2.40	-1.26	-8.80	6.22E-05	0.0255363	2.41	TRUE
256818_at	hypothetical protein contains Pfa	---	AT3G21420	2.43	1.28	8.80	6.23E-05	0.0255363	2.41	FALSE
265945_at	putative cytokinin oxidase ; supp	CKX2	AT2G19500	2.58	1.37	8.75	6.46E-05	0.0255363	2.38	FALSE
250975_at	putative protein	---	AT5G03050	-3.40	-1.77	-8.84	6.05E-05	0.0255363	2.44	FALSE
264458_at	unknown protein similar to ESTs	---	AT1G10410	2.65	1.41	8.78	6.30E-05	0.0255363	2.40	FALSE
267266_at	putative metal ion transporter (NI	NRAMP3	AT2G23150	2.60	1.38	8.74	6.49E-05	0.0255363	2.38	FALSE
257363_at	hypothetical protein predicted by	BAP2	AT2G45760	3.80	1.92	8.76	6.42E-05	0.0255363	2.39	FALSE
256771_at	unknown protein	---	AT3G13700 ///	-2.38	-1.25	-8.71	6.62E-05	0.0255863	2.36	FALSE
262653_at	dioxygenase-like protein very sir	---	AT1G14130	2.25	1.17	8.68	6.80E-05	0.0258651	2.33	FALSE
264239_at	hypothetical protein predicted by	---	AT1G54770	-2.31	-1.21	-8.59	7.26E-05	0.0262334	2.27	TRUE
252921_at	putative protein DNA damage-in	EDS5	AT4G39030	8.80	3.14	8.61	7.13E-05	0.0262334	2.29	FALSE
246214_at	heat shock transcription factor HS	HSF4	AT4G36988 ///	3.80	1.92	8.57	7.36E-05	0.0262334	2.26	FALSE
261373_at	CMP-KDO synthetase, putative	---	AT1G53000	-2.49	-1.32	-8.59	7.22E-05	0.0262334	2.28	FALSE
261951_at	hypothetical protein predicted by	---	AT1G64490	-2.63	-1.40	-8.44	8.05E-05	0.0282335	2.18	FALSE
249839_at	Expressed protein ; supported by	---	AT5G23405	-2.86	-1.52	-8.38	8.46E-05	0.0283625	2.13	TRUE
258616_at	putative protein kinase contains	---	AT3G02880	3.34	1.74	8.42	8.22E-05	0.0283625	2.16	TRUE
253277_at	cinnamyl alcohol dehydrogenase	ATCAD5	AT4G34230	3.89	1.96	8.38	8.45E-05	0.0283625	2.13	FALSE

251472_at	putative protein nodule inceptior	---	AT3G59580	-2.40	-1.26	-8.29	9.06E-05	0.029945	2.07	TRUE
266712_at	unknown protein	---	AT2G46750	3.06	1.61	8.03	0.00011	0.0308938	1.89	TRUE
250646_at	peroxidase (emb|CAA68212.1) ;	---	AT5G06720	3.66	1.87	8.18	9.79E-05	0.0308938	2.00	TRUE
251096_at	receptor like protein kinase rece	LECRKA4.2	AT5G01550	4.96	2.31	8.11	0.0001032	0.0308938	1.95	TRUE
263412_at	putative histone H2B ;supported	---	AT2G28720	-2.41	-1.27	-7.92	0.0001199	0.0308938	1.81	TRUE
255264_at	putative protein ethylene respon	---	AT4G05170	2.65	1.41	7.81	0.00013	0.0308938	1.73	FALSE
249540_at	4-coumarate--CoA ligase -like pr	---	AT5G38120	6.76	2.76	8.04	0.0001088	0.0308938	1.90	TRUE
260605_at	hypothetical protein predicted by	---	AT2G43780	-2.36	-1.24	-8.00	0.0001124	0.0308938	1.87	FALSE
263679_at	RNA helicase, putative similar to	---	AT1G59990	-3.00	-1.58	-7.97	0.0001153	0.0308938	1.84	TRUE
248878_at	50S ribosomal protein L14	---	AT5G46160	-2.29	-1.20	-7.85	0.0001267	0.0308938	1.76	FALSE
266419_at	putative annexin ;supported by f	ANNAT3	AT2G38760	3.63	1.86	7.85	0.0001264	0.0308938	1.76	TRUE
247247_at	50S ribosomal protein L17 ;supp	---	AT5G64650	-2.29	-1.19	-7.94	0.000118	0.0308938	1.82	TRUE
245710_at	ferulate-5-hydroxylase	---	AT5G04330	3.48	1.80	7.89	0.0001223	0.0308938	1.79	TRUE
250126_at	ubiquitin C-terminal hydrolase-lik	UCH1	AT5G16310	-2.88	-1.52	-7.87	0.0001246	0.0308938	1.77	TRUE
260897_at	ER lumen protein retaining recep	ERD2	AT1G29330	2.48	1.31	8.10	0.0001039	0.0308938	1.94	TRUE
259347_at	putative GAR1 protein similar to	---	AT3G03920	-2.35	-1.23	-7.99	0.0001132	0.0308938	1.86	TRUE
267562_at	unknown protein similar to hypot	---	AT2G39670	-2.28	-1.19	-8.01	0.0001114	0.0308938	1.88	FALSE
263863_at	3-oxoacyl carrier protein synthas	---	AT2G04540	-2.03	-1.02	-7.82	0.0001297	0.0308938	1.73	FALSE
257756_at	uridylate kinase, putative similar	---	AT3G18680	-2.83	-1.50	-8.12	0.0001026	0.0308938	1.95	FALSE
262648_at	putative ribulose-1,5 bisphospha	---	AT1G14030	-2.35	-1.23	-7.84	0.0001274	0.0308938	1.75	FALSE
251706_at	nodulin-like protein MtN21 - Mec	---	AT3G56620	2.86	1.52	7.92	0.0001195	0.0308938	1.81	FALSE
257824_at	unknown protein ; supported by	---	AT3G25290	5.98	2.58	8.12	0.0001029	0.0308938	1.95	FALSE
259399_at	hypothetical protein similar to put	---	AT1G17710	3.20	1.68	7.83	0.0001284	0.0308938	1.74	FALSE
266098_at	hypothetical protein predicted by	---	AT2G37870	3.56	1.83	7.85	0.0001264	0.0308938	1.76	FALSE
260023_at	unknown protein	ATGA2OX2	AT1G30040	4.66	2.22	7.98	0.0001138	0.0308938	1.86	FALSE
252543_at	nonphototropic hypocotyl 1 ; sup	PHOT1	AT3G45780	-2.14	-1.10	-7.93	0.0001188	0.0308938	1.82	FALSE
248927_at	ubiquitin activating enzyme E1-lik	APG7	AT5G45900	2.72	1.45	8.03	0.0001102	0.0308938	1.89	FALSE
252511_at	putative protein serine/threonine	---	AT3G46280	11.14	3.48	8.06	0.0001072	0.0308938	1.91	FALSE
260391_at	putative strictosidine synthase ex	SS2	AT1G74020	2.90	1.54	7.80	0.0001318	0.0309893	1.72	TRUE
265305_at	putative tyrosine decarboxylase	---	AT2G20340	3.00	1.58	7.57	0.0001575	0.0320122	1.55	TRUE
264271_at	beta-glucosidase, putative simila	BGLU6	AT1G60270	4.68	2.23	7.58	0.0001569	0.0320122	1.55	TRUE
250180_at	early nodule-specific protein - lik	---	AT5G14450	-2.38	-1.25	-7.70	0.0001427	0.0320122	1.64	TRUE
250194_at	putative protein various predicte	---	AT5G14550	-2.34	-1.23	-7.67	0.0001461	0.0320122	1.62	TRUE
266264_at	Expressed protein ; supported by	---	AT2G27775	-2.19	-1.13	-7.55	0.0001602	0.0320122	1.53	TRUE
246057_at	putative protein predicted protei	---	AT5G08400	-2.19	-1.13	-7.54	0.0001611	0.0320122	1.53	FALSE

263483_at	putative heat shock protein ; sup	CR88	AT2G04030	-2.47	-1.31	-7.63	0.0001503	0.0320122	1.60	TRUE
266841_at	putative heat shock transcription	ATHSFA2	AT2G26150	4.16	2.05	7.64	0.0001489	0.0320122	1.60	TRUE
248362_at	fibrillarin 1 (AtFib1) identical to fit	FIB1	AT5G52470	-2.27	-1.19	-7.66	0.0001471	0.0320122	1.62	TRUE
266551_at	unknown protein ; supported by	---	AT2G35260	-1.91	-0.94	-7.56	0.0001588	0.0320122	1.54	FALSE
266957_at	unknown protein	PTAC12	AT2G34640	-2.78	-1.48	-7.64	0.0001497	0.0320122	1.60	TRUE
251355_at	putative protein hypothetical pro	---	AT3G61100	-2.98	-1.58	-7.52	0.0001649	0.0320122	1.51	TRUE
262937_at	FtsH protease, putative contains	FTSH12	AT1G79560	-2.13	-1.09	-7.63	0.0001509	0.0320122	1.59	FALSE
261112_at	unknown protein	---	AT1G75420	-2.73	-1.45	-7.63	0.0001507	0.0320122	1.59	FALSE
252374_at	response reactor 2 (ATRR2) ; su	ARR5	AT3G48100	4.43	2.15	7.52	0.0001649	0.0320122	1.51	FALSE
247718_at	nonspecific lipid-transfer protein	LTP4	AT5G59310	-3.24	-1.69	-7.63	0.0001501	0.0320122	1.60	FALSE
258534_at	thioredoxin, putative similar to th	---	AT3G06730	-2.19	-1.13	-7.51	0.0001654	0.0320122	1.50	FALSE
255521_at	putative sucrose synthetase sim	SUS3	AT4G02280	3.97	1.99	7.52	0.0001645	0.0320122	1.51	FALSE
259596_at	auxin-regulated GH3 protein, pu	GH3.17	AT1G28130	6.80	2.76	7.51	0.0001656	0.0320122	1.50	FALSE
248563_at	anthocyanidin-3-glucoside rhamn	---	AT5G49690	4.13	2.05	7.67	0.0001462	0.0320122	1.62	FALSE
256024_at	unknown protein contains Pfam p	ZF14	AT1G58340	9.28	3.21	7.61	0.0001529	0.0320122	1.58	FALSE
266570_at	putative chloroplast ribosomal pr	---	AT2G24090	-2.19	-1.13	-7.50	0.0001676	0.0321305	1.49	FALSE
245275_at	beta-amylase ; supported by cDN	BAM5	AT4G15210	7.47	2.90	7.28	0.0001994	0.0322043	1.33	TRUE
245362_at	homeobox-leucine zipper protein	HAT1	AT4G17460	-3.27	-1.71	-7.38	0.0001848	0.0322043	1.40	TRUE
263184_at	UDP-glucose:indole-3-acetate b	UGT75B1	AT1G05560	3.45	1.79	7.44	0.000176	0.0322043	1.44	TRUE
253558_at	kinase binding protein - like Skb	SKB1	AT4G31120	-2.54	-1.35	-7.31	0.0001944	0.0322043	1.35	FALSE
266197_at	hypothetical protein predicted by	---	AT2G39120	-2.20	-1.14	-7.32	0.0001931	0.0322043	1.36	TRUE
256595_x_a	hypothetical protein	---	AT3G28530	-2.65	-1.40	-7.36	0.0001873	0.0322043	1.39	TRUE
245569_at	RNA polymerase II fifth largest su	NRPE7	AT4G14660	-1.97	-0.98	-7.34	0.0001908	0.0322043	1.37	FALSE
263049_at	unknown protein ;supported by f	---	AT2G05260	2.33	1.22	7.35	0.0001895	0.0322043	1.37	TRUE
262947_at	unknown protein ;supported by fu	GASA1	AT1G75750	-1.92	-0.94	-7.39	0.0001822	0.0322043	1.41	FALSE
250787_at	meiotic check point regulator-like	EMB2771	AT5G05560	-2.15	-1.10	-7.37	0.0001858	0.0322043	1.39	FALSE
267553_s_a	hypothetical protein predicted by	---	AT2G32180 ///	-3.48	-1.80	-7.26	0.0002033	0.0322043	1.31	FALSE
255623_at	putative L5 ribosomal protein ;su	---	AT4G01310	-2.16	-1.11	-7.28	0.0001996	0.0322043	1.32	FALSE
245010_at	NADH dehydrogenase subunit	---	---	-2.63	-1.39	-7.40	0.0001815	0.0322043	1.42	FALSE
246001_at	putative protein predicted protein	---	AT5G20790	5.82	2.54	7.35	0.0001891	0.0322043	1.38	FALSE
258586_s_a	putative trypsin inhibitor similar to	---	AT3G04320 ///	7.96	2.99	7.28	0.0002006	0.0322043	1.32	FALSE
261551_at	ATP dependent copper transpor	HMA5	AT1G63440	2.22	1.15	7.30	0.0001976	0.0322043	1.33	FALSE
250158_at	putative protein	---	AT5G15190	4.25	2.09	7.30	0.0001975	0.0322043	1.33	FALSE
257632_at	cytochrome P450, putative simil	CYP71B21	AT3G26190	4.77	2.25	7.28	0.0001999	0.0322043	1.32	FALSE
255436_at	Expressed protein ; supported by	---	AT4G03150	-1.91	-0.94	-7.41	0.0001792	0.0322043	1.43	FALSE

251155_at	putative protein outer envelope r	---	AT3G63160	-2.05	-1.04	-7.45	0.0001742	0.0322043	1.45	FALSE
245027_at	heme oxygenase 2 (HO2)	HO2	AT2G26550	-2.27	-1.18	-7.45	0.0001744	0.0322043	1.45	FALSE
250580_at	glutamate dehydrogenase 2 ; su	GDH2	AT5G07440	7.01	2.81	7.48	0.0001698	0.0322043	1.48	FALSE
249193_at	putative protein similar to unknov	ARC6	AT5G42480	-1.93	-0.95	-7.26	0.0002026	0.0322043	1.31	FALSE
245784_at	hypothetical protein similar to hyp	---	AT1G32190	-2.46	-1.30	-7.40	0.0001818	0.0322043	1.41	FALSE
262925_at	hypothetical protein	YSL7	AT1G65730	2.47	1.30	7.40	0.0001813	0.0322043	1.42	FALSE
254453_at	amino acid transport protein AAT	AAT1	AT4G21120	3.61	1.85	7.25	0.0002051	0.0322709	1.30	TRUE
247386_at	putative protein similar to unknov	emb2746	AT5G63420	-2.15	-1.10	-7.20	0.0002133	0.0325207	1.26	TRUE
259759_at	hypothetical protein similar to GI	---	AT1G77550	-2.25	-1.17	-7.19	0.000216	0.0325207	1.25	TRUE
263674_at	hypothetical protein predicted by	---	AT2G04790	-2.40	-1.26	-7.18	0.0002167	0.0325207	1.25	FALSE
256274_at	GTPase, putative contains Pfam	emb2738	AT3G12080	-2.10	-1.07	-7.20	0.0002147	0.0325207	1.25	FALSE
253635_at	putative protein hypothetical pro	---	AT4G30620	-2.05	-1.04	-7.19	0.0002149	0.0325207	1.25	FALSE
253791_at	early auxin-inducible protein 11 (	IAA11	AT4G28640	-2.82	-1.49	-7.19	0.0002165	0.0325207	1.25	FALSE
253630_at	putative protein putative ATPase	---	AT4G30490	2.82	1.50	7.20	0.0002146	0.0325207	1.25	FALSE
261772_at	hypothetical protein predicted by	---	AT1G76240	4.94	2.31	7.17	0.0002189	0.0325407	1.24	TRUE
259443_at	chitinase, putative similar to chit	---	AT1G02360	6.40	2.68	7.17	0.0002197	0.0325407	1.23	FALSE
267308_at	putative malonyl-CoA:Acyl carrie	---	AT2G30200	-2.57	-1.36	-7.14	0.0002242	0.0329903	1.21	FALSE
254773_at	putative protein Cyclic beta-1-3-	ATCSLA15	AT4G13410	8.05	3.01	7.09	0.0002354	0.0334062	1.17	FALSE
245108_at	putative cytokinin oxidase	CKX1	AT2G41510	-2.13	-1.09	-7.09	0.0002351	0.0334062	1.17	TRUE
256894_at	PREG-like protein, putative simi	CYCP2;1	AT3G21870	-1.93	-0.95	-7.11	0.0002315	0.0334062	1.18	FALSE
251834_at	ribosomal protein L35 -like variou	---	AT3G55170	-2.15	-1.11	-7.08	0.0002358	0.0334062	1.16	FALSE
245525_at	dynein light chain like protein	---	AT4G15930	-1.86	-0.90	-7.12	0.000229	0.0334062	1.19	FALSE
252409_at	putative protein bundle sheath d	---	AT3G47650	-2.26	-1.18	-7.11	0.0002301	0.0334062	1.19	FALSE
250441_at	oligopeptidase A - like protein ol	---	AT5G10540	-1.92	-0.94	-7.07	0.0002387	0.0336037	1.15	FALSE
252058_at	putative protein hin1 protein -Nic	---	AT3G52470	3.69	1.88	7.05	0.0002433	0.0340531	1.13	TRUE
245008_at	hypothetical protein	---	---	-2.02	-1.01	-7.03	0.000247	0.034143	1.12	TRUE
248798_at	putative protein contains similarit	---	AT5G47190	-2.31	-1.21	-7.03	0.0002462	0.034143	1.12	FALSE
260364_at	putative alliinase similar to aliinas	TAA1	AT1G70560	-3.15	-1.65	-7.02	0.0002497	0.0342582	1.11	TRUE
265895_at	unknown protein ;supported by f	---	AT2G15000	-2.42	-1.28	-7.01	0.0002514	0.0342582	1.10	FALSE
246366_at	light repressible receptor protein	---	AT1G51850	3.03	1.60	7.01	0.0002523	0.0342582	1.10	FALSE
252355_at	putative protein various predicte	---	AT3G48250	-2.15	-1.11	-6.95	0.0002643	0.0346297	1.05	FALSE
254133_at	putative protein various predicted	---	AT4G24810	-1.95	-0.96	-6.95	0.0002657	0.0346297	1.05	FALSE
261931_at	alcohol dehydrogenase ADH, pu	---	AT1G22430	-1.99	-0.99	-6.97	0.0002599	0.0346297	1.07	FALSE
265776_at	hypothetical protein predicted by	---	AT2G07340	-1.99	-0.99	-6.95	0.0002638	0.0346297	1.05	FALSE
254350_at	putative protein hypothetical pro	---	AT4G22280	-1.91	-0.93	-6.98	0.0002588	0.0346297	1.07	FALSE

257670_at	unknown protein	---	AT3G20340	6.07	2.60	6.97	0.0002599	0.0346297	1.07	FALSE
266684_at	40S ribosomal protein S15A	rps15ab	AT2G19720	-1.95	-0.97	-6.96	0.0002624	0.0346297	1.06	FALSE
251011_at	putative protein histone H2A, ga	HTA12	AT5G02560	-2.01	-1.00	-6.92	0.0002712	0.034944	1.03	FALSE
247826_at	beta 1-3 glucanase - like protein	---	AT5G58480	-2.19	-1.13	-6.92	0.0002705	0.034944	1.03	FALSE
251959_at	putative protein KIAA0544 prote	---	AT3G53410	-2.08	-1.06	-6.89	0.0002784	0.0349814	1.00	FALSE
250969_at	putative protein ;supported by fu	---	AT5G02740	-2.07	-1.05	-6.89	0.0002788	0.0349814	1.00	FALSE
267435_at	30S ribosomal protein S5 ; supp	---	AT2G33800	-1.99	-0.99	-6.91	0.0002745	0.0349814	1.02	FALSE
259863_at	hypothetical protein ;supported b	ELF4-L2	AT1G72630	-2.09	-1.06	-6.89	0.0002791	0.0349814	1.00	FALSE
261525_at	hypothetical protein predicted by	---	AT1G14330	2.79	1.48	6.90	0.0002771	0.0349814	1.01	FALSE
251172_at	putative protein chloroplast ribos	RRF	AT3G63190	-2.06	-1.04	-6.88	0.0002821	0.0349869	0.99	FALSE
259133_at	sugar transporter, putative simila	---	AT3G05400	5.23	2.39	6.88	0.0002822	0.0349869	0.99	FALSE
257193_at	Expressed protein ; supported by	---	AT3G13160	-1.96	-0.97	-6.87	0.000284	0.035015	0.98	TRUE
260496_at	putative ABC transporter	---	AT2G41700	-1.91	-0.93	-6.85	0.0002879	0.0352607	0.97	TRUE
260100_at	Expressed protein ; supported by	BNS	AT1G73177	-1.93	-0.95	-6.85	0.0002891	0.0352607	0.97	FALSE
258365_s_a	putative diaminopimelate decarb	---	AT3G14390 /	-2.32	-1.21	-6.84	0.0002911	0.0353083	0.96	FALSE
246272_at	hydroxynitrile lyase like protein	MES9	AT4G37150	8.82	3.14	6.83	0.0002934	0.0353083	0.95	FALSE
254724_at	putative protein IFA-binding prot	---	AT4G13630	2.47	1.30	6.83	0.0002941	0.0353083	0.95	FALSE
255360_at	putative protein ;supported by fu	---	AT4G03960	-2.15	-1.11	-6.81	0.0002995	0.0353219	0.93	TRUE
249026_at	Expressed protein ; supported by	OSB3	AT5G44785	-2.68	-1.42	-6.81	0.0002996	0.0353219	0.93	FALSE
255583_at	hypothetical protein similar to C.	ARV2	AT4G01510	-2.36	-1.24	-6.80	0.000302	0.0353219	0.92	FALSE
256215_at	unknown protein ;supported by fu	---	AT1G50900	-2.26	-1.17	-6.80	0.0003012	0.0353219	0.93	FALSE
255332_at	predicted protein of unknown fun	---	AT4G04340	-1.93	-0.95	-6.80	0.0003012	0.0353219	0.93	FALSE
251336_at	putative protein hypothetical pro	BAP1	AT3G61190	5.34	2.42	6.79	0.0003037	0.0353434	0.92	TRUE
246003_at	chloroplast Cpn21 protein ; supp	CPN20	AT5G20720	-2.34	-1.23	-6.78	0.0003082	0.035691	0.90	FALSE
260390_at	unknown protein ; supported by	---	AT1G73940	-2.35	-1.23	-6.76	0.0003112	0.035846	0.89	TRUE
258815_at	putative short-chain type dehydr	---	AT3G04000	4.03	2.01	6.76	0.0003135	0.0358467	0.89	TRUE
248298_at	putative protein similar to unknov	---	AT5G53110	3.54	1.82	6.75	0.0003143	0.0358467	0.88	FALSE
263902_at	phosphoribosylformimino-5-amin	APG10	AT2G36230	-2.09	-1.06	-6.75	0.0003165	0.0359174	0.88	FALSE
251083_at	hypothetical protein ; supported	---	AT5G01590	-2.19	-1.13	-6.74	0.0003188	0.0360047	0.87	FALSE
250327_at	putative serine rich protein predi	---	AT5G12050	-9.15	-3.19	-6.71	0.0003254	0.0361998	0.85	TRUE
255948_at	hypothetical protein predicted by	---	AT1G22060	-1.88	-0.91	-6.72	0.0003235	0.0361998	0.86	FALSE
252377_at	putative peptide transporter pep	---	AT3G47960	2.67	1.42	6.67	0.0003372	0.0361998	0.82	FALSE
257530_at	unknown protein	---	AT3G03040	-2.04	-1.03	-6.70	0.0003296	0.0361998	0.84	FALSE
256050_at	leucine zipper protein, putative s	ATEXO70B	AT1G07000	2.17	1.12	6.67	0.000338	0.0361998	0.81	FALSE
254502_at	hypothetical protein	PTAC14	AT4G20130	-2.47	-1.30	-6.68	0.0003341	0.0361998	0.82	FALSE

247862_at	similar to unknown protein (sp|P7	---	AT5G58250	-2.12	-1.08	-6.68	0.0003362	0.0361998	0.82	FALSE
248285_at	putative protein similar to unknov	---	AT5G52960	-1.77	-0.83	-6.68	0.000336	0.0361998	0.82	FALSE
253251_at	putative protein similarity predict	---	AT4G34730	-2.92	-1.54	-6.69	0.0003313	0.0361998	0.83	FALSE
247340_at	unknown protein	---	AT5G63700	-1.94	-0.96	-6.72	0.0003238	0.0361998	0.86	FALSE
259658_at	hypothetical protein predicted by	NDF5	AT1G55370	-3.04	-1.60	-6.68	0.0003357	0.0361998	0.82	FALSE
249123_at	beta-ketoacyl-CoA synthase ; su	KCS20	AT5G43760	1.77	0.83	6.56	0.0003728	0.0363303	0.72	TRUE
245060_at	GDP-mannose pyrophosphoryl	CYT1	AT2G39770	1.89	0.92	6.61	0.000356	0.0363303	0.76	TRUE
246809_s_a	SAR DNA-binding protein - like S	---	AT5G27120 /	-1.79	-0.84	-6.62	0.0003551	0.0363303	0.76	TRUE
249090_at	Expressed protein ; supported by	---	AT5G43745	2.91	1.54	6.59	0.000364	0.0363303	0.74	TRUE
257164_at	mismatch binding protein, putati	MSH1	AT3G24320	-2.16	-1.11	-6.60	0.00036	0.0363303	0.75	TRUE
265511_at	putative glycine-rich protein ; su	---	AT2G05540	-3.03	-1.60	-6.56	0.000375	0.0363303	0.71	TRUE
252362_at	hypothetical protein	PDE312	AT3G48500	-3.51	-1.81	-6.59	0.0003624	0.0363303	0.74	FALSE
266466_at	hypothetical protein The first 3 ex	---	AT2G47790	-2.07	-1.05	-6.61	0.0003579	0.0363303	0.76	TRUE
254026_at	putative calmodulin-binding prot	---	AT4G25800	-1.82	-0.87	-6.55	0.0003775	0.0363303	0.70	FALSE
249315_at	unknown protein	---	AT5G41190	-1.91	-0.94	-6.61	0.0003582	0.0363303	0.76	FALSE
261044_at	molybdopterin biosynthesis CNX	CNX3	AT1G01290	-2.24	-1.16	-6.65	0.0003446	0.0363303	0.79	TRUE
257891_at	hypothetical protein predicted by	RFC3	AT3G17170	-3.26	-1.70	-6.60	0.000359	0.0363303	0.75	TRUE
255572_at	hypothetical protein ; supported	---	AT4G01050	-1.79	-0.84	-6.63	0.0003505	0.0363303	0.78	FALSE
260343_at	fructokinase (Frk1), putative sim	---	AT1G69200	-2.89	-1.53	-6.58	0.0003654	0.0363303	0.74	FALSE
266280_at	putative tropinone reductase	---	AT2G29260	-1.83	-0.87	-6.62	0.0003547	0.0363303	0.77	FALSE
266889_at	hypothetical protein predicted by	---	AT2G44640	-2.27	-1.18	-6.59	0.0003651	0.0363303	0.74	FALSE
267388_at	putative beta-glucosidase	BGLU15	AT2G44450	4.37	2.13	6.64	0.0003469	0.0363303	0.79	FALSE
266279_at	putative tropinone reductase	---	AT2G29290	-2.65	-1.41	-6.58	0.0003666	0.0363303	0.73	FALSE
263226_at	unknown protein Contains the P	---	AT1G30690	-1.83	-0.87	-6.57	0.0003696	0.0363303	0.73	FALSE
252084_at	wax synthase-like protein wax s	AtSAT1	AT3G51970	2.55	1.35	6.66	0.0003411	0.0363303	0.80	FALSE
254011_at	putative protein transcription ter	---	AT4G26370	-2.28	-1.19	-6.65	0.0003436	0.0363303	0.80	FALSE
247059_at	UTP-glucose glucosyltransferase	UGT72E2	AT5G66690	2.04	1.03	6.56	0.0003726	0.0363303	0.72	FALSE
245209_at	putative protein similarity to prec	---	AT5G12340	13.80	3.79	6.56	0.0003748	0.0363303	0.71	FALSE
257773_at	hypothetical protein predicted by	---	AT3G29185	-2.21	-1.14	-6.55	0.0003768	0.0363303	0.71	FALSE
251447_at	U6 snRNA-associated Sm-like p	---	AT3G59810	-1.83	-0.87	-6.53	0.0003852	0.0369151	0.69	FALSE
248173_at	putative protein contains similarit	---	AT5G54580	-2.00	-1.00	-6.51	0.0003908	0.0373	0.67	FALSE
261242_at	subtilisin-like serine protease cor	SBT3.3	AT1G32960	3.63	1.86	6.50	0.0003955	0.037573	0.66	TRUE
263236_at	putative response regulator 3 sir	ARR4	AT1G10470	3.46	1.79	6.49	0.0003974	0.037573	0.65	TRUE
259705_at	GRAB1-like protein similar to GF	anac032	AT1G77450	3.50	1.81	6.49	0.0003986	0.037573	0.65	FALSE
258957_at	feebly-like protein contains simila	DOX1	AT3G01420	2.87	1.52	6.46	0.0004072	0.037663	0.63	TRUE

253273_at	putative protein hypothetical pro	---	AT4G34180	1.90	0.93	6.34	0.0004584	0.037663	0.51	TRUE
264195_at	putative gibberellin-regulated pro	---	AT1G22690	-3.53	-1.82	-6.29	0.0004786	0.037663	0.47	FALSE
246603_at	copper amine oxidase, putative	---	AT1G31690	2.82	1.49	6.38	0.00044	0.037663	0.55	TRUE
255825_at	Expressed protein ; supported by	---	AT2G40475	3.04	1.60	6.33	0.0004619	0.037663	0.51	TRUE
261872_s_a	hypthetical protein contains simil	---	AT1G11520 /	-2.16	-1.11	-6.42	0.0004245	0.037663	0.59	TRUE
251278_at	putative protein hypothetical pro	emb1703	AT3G61780	-2.31	-1.21	-6.46	0.0004104	0.037663	0.62	TRUE
263371_at	unknown protein ;supported by f	NOP10	AT2G20490	-2.49	-1.32	-6.39	0.0004357	0.037663	0.56	TRUE
260595_at	unknown protein	---	AT1G55890	-2.28	-1.19	-6.35	0.0004525	0.037663	0.53	FALSE
247776_at	phosphoinositide-specific phosp	PLC4	AT5G58700	2.47	1.30	6.33	0.0004601	0.037663	0.51	FALSE
261102_at	unknown protein	---	AT1G62880	-1.91	-0.93	-6.38	0.0004382	0.037663	0.56	FALSE
246478_at	putative protein several hypothet	---	AT5G15980	-1.95	-0.96	-6.30	0.000474	0.037663	0.48	FALSE
258120_at	hypothetical protein predicted by	---	AT3G14730	-1.85	-0.89	-6.35	0.0004521	0.037663	0.53	FALSE
264047_at	hypothetical protein predicted by	---	AT2G22410	-2.02	-1.02	-6.32	0.0004668	0.037663	0.50	TRUE
260292_at	putative UDP-N-acetylmuramoyl	MURE	AT1G63680	-1.74	-0.80	-6.32	0.0004642	0.037663	0.50	FALSE
255819_s_a	40S ribosomal protein S26	---	AT2G40510 /	-2.02	-1.01	-6.29	0.0004784	0.037663	0.47	FALSE
259945_at	unknown protein	---	AT1G71460	-2.30	-1.20	-6.41	0.0004292	0.037663	0.58	FALSE
253703_at	putative protein origin recognitio	ORC5	AT4G29910	-2.16	-1.11	-6.33	0.0004601	0.037663	0.51	FALSE
246494_at	putative protein putative cellulos	CSLA11	AT5G16190	2.26	1.18	6.37	0.0004456	0.037663	0.54	FALSE
259138_s_a	putative DNA gyrase subunit B s	---	AT3G10270 /	-2.13	-1.09	-6.36	0.0004481	0.037663	0.54	FALSE
245886_at	ribosomal protein S15-like ribos	---	AT5G09510	-1.83	-0.87	-6.46	0.0004107	0.037663	0.62	FALSE
261824_at	DAG protein, putative similar to	---	AT1G11430	-1.83	-0.87	-6.30	0.000476	0.037663	0.48	FALSE
261119_at	chloroplast 50S ribosomal protei	emb2184	AT1G75350	-1.71	-0.77	-6.47	0.0004061	0.037663	0.63	FALSE
253020_at	hypothetical protein	---	AT4G38020	-2.57	-1.36	-6.31	0.0004706	0.037663	0.49	FALSE
251762_at	sedoheptulose-bisphosphatase p	SBPASE	AT3G55800	-2.13	-1.09	-6.43	0.0004221	0.037663	0.59	FALSE
257280_at	9-cis-epoxycarotenoid dioxygena	NCED3	AT3G14440	3.40	1.77	6.39	0.0004359	0.037663	0.56	FALSE
262616_at	oxidoreductase, putative contain	---	AT1G06620	4.14	2.05	6.31	0.000469	0.037663	0.49	FALSE
253632_at	senescence-associated protein	TET9	AT4G30430	1.75	0.81	6.40	0.0004305	0.037663	0.58	FALSE
255458_at	small nuclear riboprotein Sm-D1	---	AT4G02840	-1.88	-0.91	-6.43	0.00042	0.037663	0.60	FALSE
245198_at	Expressed protein ; supported by	---	AT1G67700	-2.01	-1.01	-6.41	0.0004291	0.037663	0.58	FALSE
266832_at	putative protein kinase contains a	MAPKKK14	AT2G30040	3.12	1.64	6.33	0.0004625	0.037663	0.50	FALSE
252922_at	putative protein	---	AT4G39040	-2.04	-1.03	-6.44	0.0004181	0.037663	0.60	FALSE
254126_at	RNA-binding protein RNP-T prec	RBP31	AT4G24770	-2.14	-1.10	-6.44	0.0004161	0.037663	0.61	FALSE
262745_at	lipase, putative contains Pfam p	---	AT1G28600	2.52	1.33	6.41	0.0004262	0.037663	0.59	FALSE
267425_at	putative berberine bridge enzyme	---	AT2G34810	9.18	3.20	6.31	0.0004706	0.037663	0.49	FALSE
260793_at	unknown protein ;supported by fu	---	AT1G06190	-2.07	-1.05	-6.44	0.0004153	0.037663	0.61	FALSE

262671_at	calcium-dependent protein kinas	CPK29	AT1G76040	2.62	1.39	6.41	0.0004265	0.037663	0.58	FALSE
262738_at	hypothetical protein	---	AT1G28530	-2.45	-1.29	-6.47	0.0004042	0.037663	0.64	FALSE
257903_at	unknown protein	---	AT3G28460	-2.00	-1.00	-6.41	0.0004277	0.037663	0.58	FALSE
247786_at	putative protein various predicte	PMR5	AT5G58600	-1.89	-0.92	-6.43	0.0004206	0.037663	0.60	FALSE
245705_at	zinc finger transcription factor-lik	---	AT5G04390	1.91	0.93	6.36	0.0004495	0.037663	0.53	FALSE
263014_at	unknown protein similar to hypot	CAF2	AT1G23400	-2.05	-1.04	-6.29	0.0004788	0.037663	0.47	FALSE
253802_at	putative protein	---	AT4G28180	-2.03	-1.02	-6.37	0.0004431	0.037663	0.55	FALSE
251839_at	putative protein patatin, Solanun	PLA IIIA	AT3G54950	3.23	1.69	6.31	0.0004677	0.037663	0.49	FALSE
251241_s_a	putative protein hypothetical prot	---	AT3G62460 ///	-2.74	-1.45	-6.40	0.0004338	0.037663	0.57	FALSE
246518_at	acetyltransferase-like protein Gl	AtGNA1	AT5G15770	-1.98	-0.98	-6.32	0.0004659	0.037663	0.50	FALSE
259526_at	hypothetical protein	---	AT1G12570	-4.44	-2.15	-6.30	0.0004733	0.037663	0.48	FALSE
259038_at	unknown protein predicted by ge	PTAC13	AT3G09210	-2.10	-1.07	-6.33	0.0004602	0.037663	0.51	FALSE
255462_at	hypothetical protein similar to A.	---	AT4G02940	3.59	1.84	6.28	0.0004815	0.0377403	0.46	TRUE
245592_at	CCAAT-binding transcription fact	NF-YB3	AT4G14540	-2.70	-1.43	-6.28	0.0004842	0.0377935	0.46	FALSE
248552_at	RNA-binding protein-like ; suppo	---	AT5G50250	-2.03	-1.02	-6.27	0.0004855	0.0377935	0.46	FALSE
254452_at	UV-damaged DNA-binding prote	DDB1B	AT4G21100	-2.48	-1.31	-6.26	0.0004921	0.0378806	0.44	FALSE
246947_at	cytochrome P450-like protein CY	CYP71B11	AT5G25120	-1.94	-0.96	-6.26	0.0004913	0.0378806	0.44	FALSE
251372_at	putative protein ;supported by fu	---	AT3G60520	-2.46	-1.30	-6.26	0.000492	0.0378806	0.44	FALSE
256607_at	unknown protein ; supported by	---	AT3G32930	-1.86	-0.89	-6.26	0.0004938	0.0378806	0.44	FALSE
251934_at	putative protein delta-latroinsect	---	AT3G54070	-2.32	-1.21	-6.25	0.0004949	0.0378806	0.44	FALSE
260438_at	putative bifunctional nuclease sir	ENDO 2	AT1G68290	5.92	2.57	6.22	0.0005105	0.0381991	0.41	FALSE
264657_at	putative 26S protease regulatory	RPT5B	AT1G09100	-1.95	-0.96	-6.21	0.0005162	0.0381991	0.40	TRUE
263929_at	hypothetical protein predicted by	URH1	AT2G36310	2.19	1.13	6.21	0.0005172	0.0381991	0.39	FALSE
245141_at	putative flavonol reductase	BEN1	AT2G45400	2.23	1.16	6.22	0.0005116	0.0381991	0.40	TRUE
262618_at	unknown protein	---	AT1G06560	-1.79	-0.84	-6.22	0.0005085	0.0381991	0.41	TRUE
264099_at	replicase, putative similar to repl	---	AT1G79050	-2.09	-1.06	-6.24	0.0005032	0.0381991	0.42	TRUE
251256_at	putative protein hypothetical prot	---	AT3G62300	-2.42	-1.27	-6.21	0.0005166	0.0381991	0.39	TRUE
247312_at	putative protein strong similarity t	---	AT5G63970	2.37	1.24	6.24	0.0005032	0.0381991	0.42	FALSE
264523_at	unknown protein Location of EST	ERG28	AT1G10030	-1.86	-0.90	-6.20	0.0005208	0.0381991	0.39	FALSE
246568_at	E2F transcription factor -like pro	DEL2	AT5G14960	-2.32	-1.22	-6.22	0.0005126	0.0381991	0.40	FALSE
246997_at	putative protein similar to unknov	---	AT5G67390	-2.83	-1.50	-6.20	0.0005197	0.0381991	0.39	FALSE
254347_at	putative protein DNA-binding pro	WRKY31	AT4G22070	2.34	1.22	6.21	0.0005134	0.0381991	0.40	FALSE
252562_s_a	Histone H4 - like protein histone	---	AT3G45930 ///	-2.05	-1.04	-6.20	0.0005189	0.0381991	0.39	FALSE
267356_at	putative isoamylase	ISA1	AT2G39930	-2.05	-1.03	-6.19	0.0005247	0.0383574	0.38	FALSE
248984_at	DNA-directed RNA polymerase s	NRPC2	AT5G45140	-2.42	-1.27	-6.17	0.0005338	0.0383996	0.36	FALSE

255749_at	p68 RNA helicase, putative simi	STRS1	AT1G31970	-1.97	-0.98	-6.17	0.0005336	0.0383996	0.36	FALSE
266903_at	hypothetical protein predicted by	MEE21	AT2G34570	-1.85	-0.89	-6.17	0.0005353	0.0383996	0.36	FALSE
264360_at	putative isoamylase Similar to gi	DBE1	AT1G03310	-2.38	-1.25	-6.17	0.000535	0.0383996	0.36	FALSE
264201_at	unknown protein ;supported by fu	---	AT1G22630	-2.94	-1.56	-6.18	0.000531	0.0383996	0.37	FALSE
256499_at	unknown protein	---	AT1G36640	3.71	1.89	6.18	0.0005321	0.0383996	0.37	FALSE
256356_s_a	hypothetical protein	---	AT1G66500 ///	2.15	1.10	6.16	0.0005396	0.0385854	0.35	FALSE
245388_at	hypothetical protein ;supported b	---	AT4G16410	-1.83	-0.87	-6.14	0.0005494	0.038918	0.33	FALSE
264619_at	putative chloroplast nucleoid DN/	---	AT2G17760	2.16	1.11	6.15	0.0005478	0.038918	0.34	FALSE
263937_at	putative RING zinc finger protein	---	AT2G35910	2.09	1.06	6.15	0.0005474	0.038918	0.34	FALSE
248315_at	selenium-binding protein-like	MEF1	AT5G52630	-2.06	-1.04	-6.13	0.0005549	0.0389454	0.32	TRUE
250613_at	putative protein SF16 protein, p	IQD24	AT5G07240	-2.33	-1.22	-6.13	0.000554	0.0389454	0.33	FALSE
244993_s_a	hypothetical protein	---	---	-2.37	-1.25	-6.14	0.0005517	0.0389454	0.33	FALSE
266132_at	hypothetical protein predicted by	SPX3	AT2G45130	4.69	2.23	6.12	0.0005593	0.039074	0.32	TRUE
257225_s_a	50S ribosomal protein L12-C ide	RPL12-C	AT3G27830 ///	-1.88	-0.91	-6.12	0.0005619	0.039074	0.31	FALSE
245642_at	Expressed protein ; supported by	---	AT1G25275	1.77	0.82	6.12	0.0005604	0.039074	0.31	FALSE
252123_at	flavanone 3-hydroxylase (FH3) ;	F3H	AT3G51240	1.90	0.93	6.08	0.0005823	0.0391237	0.28	FALSE
256661_at	hypothetical protein similar to put	---	AT3G11964	-1.91	-0.93	-6.11	0.0005683	0.0391237	0.30	TRUE
264605_at	putative auxin-induced protein, I	IAA12	AT1G04550	-2.05	-1.04	-6.09	0.0005778	0.0391237	0.28	TRUE
256002_at	carbamoylphosphate synthetase	CARB	AT1G29900	-2.05	-1.04	-6.11	0.0005666	0.0391237	0.30	FALSE
249330_at	putative protein similar to unknov	---	AT5G40970	-2.02	-1.01	-6.09	0.000579	0.0391237	0.28	FALSE
256383_at	hypothetical protein ; supported b	---	AT1G66820	-2.22	-1.15	-6.10	0.0005715	0.0391237	0.29	FALSE
252559_at	RNA binding protein -like COLD	---	AT3G46020	-1.77	-0.82	-6.09	0.0005751	0.0391237	0.29	FALSE
245738_at	nucellin, putative similar to nuce	---	AT1G44130	3.19	1.67	6.08	0.0005809	0.0391237	0.28	FALSE
259087_at	hypothetical protein, contains Dr	---	AT3G04980	-1.73	-0.79	-6.08	0.0005832	0.0391237	0.27	FALSE
259996_at	hypothetical protein predicted by	---	AT1G67910	-2.49	-1.32	-6.10	0.0005713	0.0391237	0.30	FALSE
245357_at	putative protein ;supported by ful	---	AT4G17560	-2.53	-1.34	-6.10	0.0005714	0.0391237	0.29	FALSE
256829_at	unknown protein similar to alumi	---	AT3G22850	3.20	1.68	6.08	0.0005818	0.0391237	0.28	FALSE
259793_at	AP2-containing DNA-binding pro	---	AT1G64380	7.05	2.82	6.07	0.0005892	0.0393827	0.26	TRUE
247891_at	GTP binding protein-like	---	AT5G57960	-1.96	-0.97	-6.06	0.0005922	0.0393827	0.26	FALSE
254181_at	FtsH protease, putative contains	---	AT4G23940	-1.79	-0.84	-6.06	0.0005918	0.0393827	0.26	FALSE
245845_at	Pto kinase interactor, putative si	PERK10	AT1G26150	-1.96	-0.97	-6.06	0.0005951	0.0394631	0.25	FALSE
253203_at	arginine decarboxylase SPE2 ; s	ADC2	AT4G34710	6.86	2.78	6.02	0.0006182	0.0395319	0.22	TRUE
250598_at	transcription factor-like protein ;	ATMYB29	AT5G07690	2.91	1.54	6.02	0.000615	0.0395319	0.22	FALSE
259515_at	hypothetical protein ; supported b	---	AT1G20430	-1.78	-0.83	-6.01	0.0006224	0.0395319	0.21	FALSE
252942_at	putative protein ;supported by fu	---	AT4G39300	-2.17	-1.12	-6.00	0.000632	0.0395319	0.19	TRUE

257697_at	hypothetical protein predicted by	---	AT3G12700	2.86	1.52	6.05	0.0006014	0.0395319	0.24	TRUE
265946_s_a	putative WD-40 repeat protein, M	FVE	AT2G19520 ///	-1.83	-0.87	-6.01	0.0006259	0.0395319	0.20	FALSE
262307_at	heat shock protein DnaJ, putativ	---	AT1G71000	2.50	1.32	6.04	0.0006051	0.0395319	0.24	TRUE
259285_at	hypothetical protein similar to put	---	AT3G11460	-1.91	-0.94	-6.03	0.0006095	0.0395319	0.23	FALSE
258245_at	hypothetical protein	---	AT3G29075	1.98	0.98	6.05	0.0006026	0.0395319	0.24	FALSE
246943_at	putative protein kinase serine/th	---	AT5G25440	2.99	1.58	6.00	0.0006294	0.0395319	0.20	FALSE
264849_at	putative ribosomal protein S4 cor	---	AT2G17360	-2.27	-1.18	-6.02	0.0006171	0.0395319	0.22	FALSE
267088_at	30S ribosomal protein S31 ;supp	PSRP4	AT2G38140	-2.38	-1.25	-5.99	0.0006344	0.0395319	0.19	FALSE
252015_at	putative protein growth-regulatin	AtGRF4	AT3G52910	-1.69	-0.76	-5.99	0.0006378	0.0395319	0.19	FALSE
245347_at	ferredoxin ;supported by full-leng	---	AT4G14890	-2.47	-1.30	-6.01	0.0006245	0.0395319	0.21	FALSE
253696_at	cytokinin oxidase - like protein c	CKX4	AT4G29740	5.51	2.46	6.05	0.0005992	0.0395319	0.25	FALSE
246746_at	putative protein predicted protei	---	AT5G27820	-2.17	-1.12	-6.00	0.0006282	0.0395319	0.20	FALSE
245769_at	hypothetical protein similar to put	INT2	AT1G30220	1.81	0.86	6.01	0.0006226	0.0395319	0.21	FALSE
258920_at	class 2 non-symbiotic hemoglobi	---	AT1G04380 ///	-4.09	-2.03	-6.00	0.0006272	0.0395319	0.20	FALSE
247943_at	light-inducible protein ATLS1-like	---	AT5G57170	-3.28	-1.71	-5.99	0.0006372	0.0395319	0.19	FALSE
266747_at	predicted by genefinder and gen	---	AT2G02870	2.24	1.17	5.99	0.0006342	0.0395319	0.19	FALSE
266685_at	hypothetical protein	---	AT2G19710	1.99	0.99	6.01	0.0006258	0.0395319	0.20	FALSE
251021_at	thaumatin-like protein thaumatin	---	AT5G02140	-3.55	-1.83	-6.02	0.0006156	0.0395319	0.22	FALSE
251497_at	putative protein phytochrome-as	PIL6	AT3G59060	-2.10	-1.07	-6.02	0.000619	0.0395319	0.22	FALSE
260943_at	thioredoxin, putative similar to th	ATTRX5	AT1G45145	2.74	1.45	5.99	0.0006341	0.0395319	0.19	FALSE
262970_at	unknown protein	---	AT1G75690	-1.96	-0.97	-5.94	0.0006655	0.0395798	0.14	TRUE
264313_at	carbonic anhydrase, putative sir	BCA4	AT1G70410	-1.73	-0.79	-5.93	0.0006715	0.0395798	0.13	TRUE
245502_at	hypothetical protein	---	AT4G15640	-2.31	-1.21	-5.94	0.0006656	0.0395798	0.14	FALSE
260294_at	GMP synthase similar to GMP sy	---	AT1G63660	-1.85	-0.88	-5.97	0.0006467	0.0395798	0.17	FALSE
255132_at	inositol 1,3,4-trisphosphate 5/6-k	---	AT4G08170	2.30	1.20	5.96	0.0006526	0.0395798	0.16	TRUE
256253_at	60S acidic ribosomal protein, pu	---	AT3G11250	-2.09	-1.06	-5.97	0.0006503	0.0395798	0.17	TRUE
263636_at	unknown protein ; supported by	---	AT2G11910	-2.08	-1.06	-5.94	0.0006648	0.0395798	0.14	FALSE
265118_at	beta-fructosidase nearly identica	---	AT1G62660	3.12	1.64	5.94	0.0006692	0.0395798	0.14	FALSE
260873_at	hypothetical protein predicted by	---	AT1G21580	1.73	0.79	5.95	0.000658	0.0395798	0.15	FALSE
261190_at	ribosomal protein L11, putative s	PRPL11	AT1G32990	-2.04	-1.03	-5.94	0.0006649	0.0395798	0.14	FALSE
265724_at	hypothetical protein predicted by	OFP16	AT2G32100	-2.81	-1.49	-5.95	0.000659	0.0395798	0.15	FALSE
252056_at	ubiquitin extension protein (UBQ	UBQ1	AT3G52590	-1.89	-0.92	-5.94	0.0006699	0.0395798	0.14	FALSE
249900_at	unknown protein	emb1211	AT5G22640	-1.89	-0.92	-5.94	0.0006703	0.0395798	0.14	FALSE
249993_at	GTP-binding protein obg -like G	---	AT5G18570	-1.70	-0.77	-5.95	0.0006611	0.0395798	0.15	FALSE
250243_at	cobalamin biosynthesis protein	GUN5	AT5G13630	-2.55	-1.35	-5.96	0.0006563	0.0395798	0.16	FALSE

260167_at	hypothetical protein predicted by	---	AT1G71970	-2.19	-1.13	-5.98	0.000645	0.0395798	0.17	FALSE
265338_at	putative ribosomal protein L6 ; s	---	AT2G18400	-1.96	-0.97	-5.96	0.0006535	0.0395798	0.16	FALSE
251063_at	protein kinase ATN1-like protein	---	AT5G01850	1.95	0.96	5.97	0.0006475	0.0395798	0.17	FALSE
258475_at	putative tyrosyl-tRNA synthetase	emb2768	AT3G02660	-1.85	-0.89	-5.98	0.0006451	0.0395798	0.17	FALSE
259422_at	unknown protein	---	AT1G13810	-2.69	-1.43	-5.92	0.0006809	0.0398244	0.12	FALSE
258281_at	putative shikimate kinase similar	---	AT3G26900	-1.68	-0.75	-5.92	0.0006785	0.0398244	0.12	FALSE
260047_at	putative UDP-N-acetylglucosami	---	AT1G73740	1.92	0.94	5.92	0.0006794	0.0398244	0.12	FALSE
263375_s_a	putative prohibitin ;supported by	ATPHB6	AT2G20530 /	-2.16	-1.11	-5.90	0.0006912	0.0402213	0.11	TRUE
256706_at	auxin-independent growth prom	---	AT3G30300	-2.05	-1.03	-5.90	0.0006909	0.0402213	0.11	FALSE
263737_at	unknown protein ;supported by fu	---	AT1G60010	-2.23	-1.16	-5.89	0.0006974	0.0404766	0.10	FALSE
260693_at	peptide transporter PTR2-B, put	NRT1.5	AT1G32450	5.65	2.50	5.88	0.0007104	0.0405331	0.08	FALSE
255668_s_a	predicted protein ; supported by	---	AT4G00238 /	-2.32	-1.22	-5.87	0.0007146	0.0405331	0.07	TRUE
255788_at	auxin regulated protein (IAA13) (	IAA13	AT2G33310	-2.49	-1.31	-5.87	0.0007161	0.0405331	0.07	FALSE
256336_at	unknown protein	---	AT1G72030	-2.40	-1.26	-5.88	0.0007065	0.0405331	0.08	FALSE
253812_at	putative wound induced protein	---	AT4G28240	-2.19	-1.13	-5.89	0.0007028	0.0405331	0.09	FALSE
253669_at	dihydropteroate synthase-like pr	---	AT4G30000	-1.85	-0.89	-5.87	0.0007136	0.0405331	0.07	FALSE
262170_at	hypothetical protein predicted by	---	AT1G74940	-2.77	-1.47	-5.88	0.0007086	0.0405331	0.08	FALSE
248248_at	spermidine synthase ;supported	SPDS3	AT5G53120	3.22	1.69	5.87	0.0007119	0.0405331	0.08	FALSE
261886_s_a	hypothetical protein predicted by	---	AT1G80700 /	-1.70	-0.76	-5.89	0.0007009	0.0405331	0.09	FALSE
245743_at	hypothetical protein contains sim	---	AT1G51080	-2.58	-1.37	-5.88	0.0007081	0.0405331	0.08	FALSE
260581_at	MYB transcription factor (Atmyb2	MYB2	AT2G47190	2.63	1.39	5.85	0.0007276	0.0408154	0.05	TRUE
257608_at	chaperonin, putative similar to C	HSP60-3A	AT3G13860	-1.96	-0.97	-5.85	0.0007257	0.0408154	0.06	TRUE
254928_at	putative protein hypothetical pro	---	AT4G11410	-1.97	-0.98	-5.85	0.0007283	0.0408154	0.05	FALSE
245354_at	Lil3 protein ;supported by full-len	LIL3:1	AT4G17600	-2.16	-1.11	-5.85	0.0007253	0.0408154	0.06	FALSE
254398_at	photosystem II oxygen-evolving	PSBQA	AT4G21280	-2.03	-1.02	-5.84	0.0007337	0.0408181	0.05	FALSE
265571_s_a	unknown protein	---	AT2G28020 /	-1.83	-0.87	-5.84	0.0007328	0.0408181	0.05	FALSE
267385_at	unknown protein highly similar to	---	AT2G44380	3.14	1.65	5.85	0.0007314	0.0408181	0.05	FALSE
249975_s_a	ribosomal protein L33 - like ribos	---	AT3G06320 /	-3.22	-1.69	-5.84	0.0007391	0.0408823	0.04	TRUE
253860_at	hypothetical protein ;supported b	---	AT4G27700	-1.83	-0.87	-5.83	0.0007402	0.0408823	0.04	FALSE
246620_at	cytochrome P450 ; supported by	CYP81D1	AT5G36220	3.37	1.75	5.83	0.0007402	0.0408823	0.04	FALSE
261768_at	gibberellin 3 beta-hydroxylase, p	GA3OX1	AT1G15550	-2.18	-1.12	-5.81	0.0007592	0.0411669	0.01	TRUE
250196_at	polynucleotide phosphorylase	---	AT5G14580	-2.22	-1.15	-5.79	0.0007703	0.0411669	0.00	FALSE
255795_at	putative calcium-binding EF-han	RD20	AT2G33380	5.03	2.33	5.81	0.0007562	0.0411669	0.02	FALSE
256932_at	unknown protein	---	AT3G22520	-1.84	-0.88	-5.80	0.000766	0.0411669	0.00	FALSE
264031_at	unknown protein	---	AT2G03780	-2.19	-1.13	-5.80	0.0007676	0.0411669	0.00	FALSE

249067_at	putative protein similar to unknov	---	AT5G43960	-1.93	-0.95	-5.82	0.000753	0.0411669	0.02	FALSE
264351_at	unknown protein Contains simila	---	AT1G03370	1.99	0.99	5.80	0.0007649	0.0411669	0.00	FALSE
262622_at	hypothetical protein predicted by	---	AT1G06510	-1.80	-0.85	-5.81	0.0007583	0.0411669	0.01	FALSE
263864_at	hypothetical protein predicted by	CPZ	AT2G04530	-1.99	-0.99	-5.80	0.0007654	0.0411669	0.00	FALSE
256170_at	receptor protein kinase, putative	---	AT1G51790	3.09	1.63	5.82	0.0007526	0.0411669	0.02	FALSE
260567_at	putative glucosyltransferase ;su	UGT74F2	AT2G43820	2.81	1.49	5.80	0.0007651	0.0411669	0.00	FALSE
251914_at	putative protein serine/threonine	---	AT3G53930	1.92	0.94	5.79	0.0007706	0.0411669	0.00	FALSE
263363_at	putative cold-regulated protein ;s	---	AT2G03850	6.88	2.78	5.81	0.0007611	0.0411669	0.01	FALSE
266575_at	putative chloroplast initiation fact	---	AT2G24060	-2.05	-1.04	-5.81	0.0007589	0.0411669	0.01	FALSE
263488_at	hypothetical protein predicted by	---	AT2G31840	-2.39	-1.26	-5.79	0.0007739	0.0412422	-0.01	FALSE
264111_at	hypothetical protein predicted by	---	AT2G13690	-1.75	-0.81	-5.78	0.0007837	0.0416698	-0.02	FALSE
247258_at	expressed protein similar to unkr	---	AT5G64816	-2.13	-1.09	-5.77	0.0007916	0.0418076	-0.03	FALSE
244996_at	ribosomal protein S2	---	---	-2.08	-1.06	-5.77	0.0007889	0.0418076	-0.03	FALSE
265583_at	unknown protein	---	AT2G20010	1.72	0.78	5.77	0.0007918	0.0418076	-0.03	FALSE
255978_at	hypothetical protein	---	AT1G34010	-1.79	-0.84	-5.76	0.0007937	0.0418136	-0.03	FALSE
262733_s_a	lipase identical to lipase GB:AAA	---	AT1G28660 ///	-2.13	-1.09	-5.76	0.0007962	0.0418331	-0.04	TRUE
248906_at	putative protein similar to unknov	---	AT5G46420	-1.87	-0.91	-5.76	0.0007978	0.0418331	-0.04	FALSE
245797_at	defective chloroplasts and leave	---	AT1G45230	-1.62	-0.69	-5.75	0.000801	0.0419042	-0.04	FALSE
250884_at	signal recognition particle 54CP (	CPSRP54	AT5G03940	-1.81	-0.86	-5.75	0.0008053	0.0420331	-0.05	FALSE
263471_at	hypothetical protein predicted by	RAP	AT2G31890	-2.06	-1.04	-5.74	0.0008084	0.0421016	-0.05	FALSE
256401_at	putative guanylate kinase similar	---	AT3G06200	-1.63	-0.71	-5.73	0.0008232	0.0421033	-0.07	FALSE
263142_at	unknown protein	---	AT1G65230	-2.02	-1.02	-5.73	0.0008182	0.0421033	-0.06	FALSE
251935_at	fructokinase - like protein fructok	---	AT3G54090	-2.58	-1.37	-5.73	0.0008185	0.0421033	-0.06	TRUE
257940_at	putative UDP-glucose glucosyltra	---	AT3G21790	2.22	1.15	5.73	0.0008216	0.0421033	-0.07	FALSE
266598_at	3-methyl-2-oxobutanoate hydrox	KPHMT1	AT2G46110	-2.30	-1.20	-5.73	0.0008211	0.0421033	-0.07	FALSE
262879_at	plastid RNA polymerase sigma-s	SIGA	AT1G64860	-2.04	-1.03	-5.74	0.0008128	0.0421033	-0.06	FALSE
261443_at	glutaredoxin, putative similar to (	GRX480	AT1G28480	7.20	2.85	5.74	0.0008145	0.0421033	-0.06	FALSE
255657_at	acidic ribosomal protein p1 simila	---	AT4G00810	-2.10	-1.07	-5.73	0.0008232	0.0421033	-0.07	FALSE
257064_at	hypothetical protein predicted by	---	AT3G18260	2.23	1.16	5.72	0.0008293	0.042226	-0.08	FALSE
251780_s_a	beta-ketoacyl-ACP reductase - l	---	AT3G55290 ///	3.00	1.58	5.72	0.000828	0.042226	-0.08	FALSE
259172_at	O-acetylserine (thiol) lyase identi	CS26	AT3G03630	-3.63	-1.86	-5.71	0.0008335	0.0423426	-0.08	FALSE
251536_at	ketol-acid reductoisomerase ; su	---	AT3G58610	-1.99	-0.99	-5.71	0.0008409	0.0424443	-0.09	FALSE
248387_at	unknown protein	---	AT5G51960	-2.12	-1.08	-5.71	0.0008411	0.0424443	-0.09	FALSE
247618_at	receptor like protein kinase rece	---	AT5G60280	2.00	1.00	5.71	0.0008401	0.0424443	-0.09	FALSE
248075_at	selenium-binding protein-like	CRR21	AT5G55740	-2.74	-1.45	-5.70	0.0008438	0.0424881	-0.09	FALSE

251804_at	beta-1,3-glucanase - like protein	---	AT3G55430	2.51	1.33	5.70	0.0008464	0.0425241	-0.10	FALSE
261078_at	unknown protein identical to SP:(	RPL4	AT1G07320	-1.89	-0.92	-5.69	0.000855	0.0428644	-0.11	FALSE
258554_at	putative DEAD/DEAH box helica	---	AT3G06980	-1.79	-0.84	-5.68	0.0008633	0.0431826	-0.12	FALSE
250415_at	putative protein GLUR3 ligand-g	GLR2.5	AT5G11210	7.61	2.93	5.63	0.0009078	0.0433465	-0.17	TRUE
250529_at	RNA helicase-like protein	---	AT5G08610	-2.47	-1.31	-5.67	0.0008695	0.0433465	-0.13	TRUE
266643_s_a	putative flavonol 3-O-glucosyltra	---	AT2G29710 /.	2.32	1.22	5.66	0.0008806	0.0433465	-0.14	TRUE
260020_at	hydrophilic protein, putative simi	PDF6	AT1G29990	-1.70	-0.76	-5.65	0.0008919	0.0433465	-0.15	FALSE
261954_at	plastid ribosomal protein S6, put	---	AT1G64510	-1.90	-0.93	-5.63	0.0009108	0.0433465	-0.17	FALSE
255446_at	hypothetical protein similar to A.	---	AT4G02750	-2.02	-1.01	-5.65	0.0008916	0.0433465	-0.15	FALSE
249641_at	DegP protease contains similarity	DegP10	AT5G36950	-2.02	-1.01	-5.65	0.0008862	0.0433465	-0.14	FALSE
250733_at	2-cys peroxiredoxin-like protein	2-Cys Prx B	AT5G06290	-2.16	-1.11	-5.64	0.0008996	0.0433465	-0.16	FALSE
250718_at	unknown protein	emb2735	AT5G06240	-1.88	-0.91	-5.64	0.0008988	0.0433465	-0.16	FALSE
258538_at	putative tRNA pseudouridine syn	---	AT3G06950	-1.81	-0.86	-5.67	0.0008729	0.0433465	-0.13	FALSE
256062_at	unknown protein ;supported by fu	LSH6	AT1G07090	-1.77	-0.82	-5.65	0.0008848	0.0433465	-0.14	FALSE
258355_at	hypothetical protein predicted by	---	AT3G14330	-2.52	-1.34	-5.63	0.0009028	0.0433465	-0.16	FALSE
251360_at	putative protein embryonic abun	---	AT3G61210	-1.83	-0.87	-5.63	0.000908	0.0433465	-0.17	FALSE
259738_at	predicted protein	---	AT1G64355	-1.95	-0.96	-5.66	0.0008822	0.0433465	-0.14	FALSE
262933_at	polyamine oxidase, putative sim	ATPAO4	AT1G65840	2.88	1.53	5.66	0.000877	0.0433465	-0.13	FALSE
254645_at	putative protein	---	AT4G18520	-2.01	-1.00	-5.64	0.0008991	0.0433465	-0.16	FALSE
257848_at	hypothetical protein predicted by	---	AT3G13030	-2.19	-1.13	-5.64	0.0009025	0.0433465	-0.16	FALSE
258557_at	hypothetical protein similar to re	---	AT3G05990	1.84	0.88	5.66	0.0008765	0.0433465	-0.13	FALSE
251031_at	one helix protein (OHP) ;suppor	OHP	AT5G02120	-2.05	-1.04	-5.64	0.0009021	0.0433465	-0.16	FALSE
259370_at	hypothetical protein predicted by	---	AT1G69050	2.18	1.12	5.66	0.0008798	0.0433465	-0.14	FALSE
257911_at	hypothetical protein contains sim	GLYR1	AT3G25530	-1.70	-0.77	-5.65	0.0008869	0.0433465	-0.14	FALSE
264839_at	putative protochlorophyllide redu	POR C	AT1G03630	-2.50	-1.32	-5.63	0.0009056	0.0433465	-0.17	FALSE
256698_at	unknown protein	---	AT3G20680	-2.14	-1.10	-5.62	0.0009122	0.0433465	-0.17	FALSE
253722_at	putative protein zinc finger trans	---	AT4G29190	-2.15	-1.11	-5.63	0.0009109	0.0433465	-0.17	FALSE
248422_at	putative protein strong similarity t	YLS7	AT5G51640	1.63	0.71	5.62	0.0009155	0.0434132	-0.18	FALSE
262754_at	putative inosine-5-monophospha	---	AT1G16350	-2.08	-1.06	-5.62	0.0009199	0.0434412	-0.18	TRUE
245840_at	hypothetical protein predicted by	---	AT1G58420	4.66	2.22	5.62	0.0009195	0.0434412	-0.18	FALSE
247586_at	mipC protein - like (aquaporin) n	PIP2;4	AT5G60660	1.89	0.92	5.61	0.0009223	0.0434671	-0.18	FALSE
244978_at	RNA polymerase alpha subunit	---	---	-1.79	-0.84	-5.60	0.0009341	0.0438423	-0.20	FALSE
267548_at	putative disease resistance prote	AtRLP22	AT2G32660	6.39	2.68	5.60	0.0009323	0.0438423	-0.20	FALSE
259253_at	hypothetical protein predicted by	---	AT3G07640	-1.65	-0.72	-5.60	0.0009366	0.0438695	-0.20	FALSE
253996_at	nucleosome assembly protein I-li	NAP1;1	AT4G26110	-2.04	-1.03	-5.59	0.0009403	0.0439505	-0.20	TRUE

265139_at	unknown protein	---	AT1G51310	-2.11	-1.08	-5.58	0.0009513	0.0441453	-0.22	TRUE
254503_at	hypothetical protein ;supported b	PTAC9	AT4G20010	-1.98	-0.98	-5.59	0.0009482	0.0441453	-0.21	FALSE
245249_at	acyl-CoA oxidase like protein ; su	ACX1	AT4G16760	2.46	1.30	5.58	0.0009508	0.0441453	-0.22	FALSE
247563_at	putative protein various predicte	PDCB1	AT5G61130	-2.32	-1.21	-5.58	0.0009522	0.0441453	-0.22	FALSE
251892_at	putative protein	WRI1	AT3G54320	-2.42	-1.28	-5.57	0.0009663	0.044351	-0.23	FALSE
251853_at	putative protein various Arabidop	---	AT3G54790	-1.78	-0.84	-5.57	0.0009643	0.044351	-0.23	FALSE
253440_at	putative protein ;supported by ful	TIFY8	AT4G32570	-1.62	-0.70	-5.57	0.000964	0.044351	-0.23	FALSE
264702_at	hypothetical protein contains sim	---	AT1G70190	-2.01	-1.01	-5.57	0.0009629	0.044351	-0.23	FALSE
258027_at	hypothetical protein predicted by	---	AT3G19515	-1.88	-0.91	-5.57	0.0009659	0.044351	-0.23	FALSE
253021_at	putative protein permease 1 - M	---	AT4G38050	-2.00	-1.00	-5.56	0.0009735	0.0445881	-0.24	FALSE
253358_at	gamma-VPE (vacuolar processin	GAMMA-VP	AT4G32940	-1.84	-0.88	-5.53	0.0009994	0.0446321	-0.27	FALSE
260089_at	putative ATPase contains Pfam p	---	AT1G73170	-1.67	-0.74	-5.53	0.0010011	0.0446321	-0.27	TRUE
246316_at	putative protein predicted protein	---	AT3G56890	-1.63	-0.71	-5.55	0.0009864	0.0446321	-0.25	FALSE
247748_at	putative protein ;supported by fu	---	AT5G58920	-1.89	-0.92	-5.56	0.0009781	0.0446321	-0.24	FALSE
249230_at	putative protein similar to unknov	---	AT5G42070	-2.18	-1.12	-5.55	0.0009875	0.0446321	-0.25	FALSE
253264_at	protein kinase - like protein prote	OST1	AT4G33950	-1.70	-0.77	-5.54	0.0009969	0.0446321	-0.26	FALSE
258805_at	putative beta-1,3-glucanase sim	---	AT3G04010	2.53	1.34	5.54	0.0009963	0.0446321	-0.26	FALSE
248449_at	putative protein similar to unknov	---	AT5G51110	-1.72	-0.78	-5.55	0.0009865	0.0446321	-0.25	FALSE
262483_at	putative translation initiation fact	FUG1	AT1G17220	-1.77	-0.83	-5.53	0.0010018	0.0446321	-0.27	FALSE
258424_at	hypothetical protein predicted by	---	AT3G16750	-2.02	-1.02	-5.55	0.0009817	0.0446321	-0.25	FALSE
267226_at	unknown protein	---	AT2G44010	4.33	2.11	5.53	0.000999	0.0446321	-0.26	FALSE
253981_at	putative protein ;supported by ful	---	AT4G26670	-1.77	-0.83	-5.54	0.0009968	0.0446321	-0.26	FALSE
267586_at	hypothetical protein predicted by	---	AT2G41950	-2.34	-1.22	-5.54	0.0009938	0.0446321	-0.26	FALSE
264575_at	putative chloroplast 50S riboson	emb2394	AT1G05190	-1.88	-0.91	-5.55	0.0009849	0.0446321	-0.25	FALSE
248035_at	sucrose cleavage protein-like ;su	---	AT5G55900	-1.80	-0.85	-5.53	0.0010056	0.044711	-0.27	FALSE
256873_at	cytochrome P450, putative conta	CYP71B34	AT3G26300 ///	-1.96	-0.97	-5.53	0.001009	0.0447774	-0.27	FALSE
245323_at	cysteine proteinase inhibitor like	---	AT4G16500	2.20	1.14	5.50	0.0010337	0.0455153	-0.30	TRUE
264689_at	hypothetical protein predicted by	---	AT1G09900	-2.47	-1.31	-5.50	0.0010396	0.0455153	-0.31	TRUE
253004_at	putative protein	---	AT4G38280 ///	-2.38	-1.25	-5.50	0.0010349	0.0455153	-0.30	TRUE
245747_at	hypothetical protein predicted by	---	AT1G51100	-2.39	-1.26	-5.50	0.0010387	0.0455153	-0.30	FALSE
258643_at	unknown protein ;supported by f	ATAB2	AT3G08010	-1.69	-0.75	-5.50	0.0010364	0.0455153	-0.30	FALSE
264186_at	hypothetical protein predicted by	---	AT1G54570	5.07	2.34	5.50	0.0010344	0.0455153	-0.30	FALSE
266293_at	putative tropinone reductase ;su	---	AT2G29360	-1.77	-0.83	-5.50	0.0010323	0.0455153	-0.30	FALSE
253973_at	Expressed protein ; supported by	---	AT4G26555	-1.60	-0.68	-5.49	0.0010438	0.0455589	-0.31	FALSE
254187_at	putative protein hypothetical pro	---	AT4G23890	-1.70	-0.76	-5.49	0.0010446	0.0455589	-0.31	FALSE

252688_at	putative protein	---	AT3G44020	-1.99	-0.99	-5.49	0.0010485	0.0456411	-0.31	FALSE
257451_at	hypothetical protein predicted by	BT3	AT1G05690	-1.89	-0.92	-5.48	0.0010515	0.0456863	-0.32	FALSE
261746_at	unknown protein ;supported by fu	PSAO	AT1G08380	-1.71	-0.77	-5.48	0.0010579	0.0458778	-0.32	FALSE
245106_at	unknown protein	---	AT2G41650	-2.09	-1.07	-5.47	0.001064	0.0460131	-0.33	TRUE
265873_at	putative beta-1,3-glucanase ;su	---	AT2G01630	-2.09	-1.07	-5.47	0.001066	0.0460131	-0.33	FALSE
245492_at	putative protein	SPK1	AT4G16340	-1.89	-0.92	-5.47	0.0010671	0.0460131	-0.33	FALSE
265965_at	putative glutamate/ornithine acet	---	AT2G37500	-1.92	-0.94	-5.47	0.0010721	0.0461424	-0.34	FALSE
249876_at	putative protein similar to unknov	CaS	AT5G23060	-2.13	-1.09	-5.46	0.001078	0.0463077	-0.34	FALSE
256070_at	hypothetical protein predicted by	---	AT1G13730	-1.77	-0.83	-5.46	0.0010814	0.0463201	-0.34	FALSE
255720_at	phosphoribulokinase precursor ic	PRK	AT1G32060	-1.91	-0.93	-5.46	0.0010824	0.0463201	-0.35	FALSE
252677_at	nitrilase 3 ;supported by full-leng	NIT3	AT3G44320	3.00	1.58	5.45	0.0010894	0.0465358	-0.35	TRUE
258079_at	hypothetical protein predicted by	---	AT3G25940	-1.86	-0.90	-5.45	0.0010949	0.0466828	-0.36	FALSE
260683_at	ribosomal protein, putative simila	HLL	AT1G17560	-1.89	-0.92	-5.44	0.0011069	0.0471045	-0.37	FALSE
259838_at	unknown protein ;supported by fu	---	AT1G52220	-1.70	-0.77	-5.43	0.0011111	0.0471087	-0.37	FALSE
264289_at	hypothetical protein similar to hyp	---	AT1G61890	4.98	2.32	5.43	0.00111	0.0471087	-0.37	FALSE
255440_at	predicted protein of unknown fun	---	AT4G02530	-2.06	-1.04	-5.43	0.0011165	0.047163	-0.38	FALSE
253856_at	hypothetical protein ;supported b	---	AT4G28100	-1.67	-0.74	-5.43	0.0011147	0.047163	-0.38	FALSE
265722_at	putative chlorophyll a/b binding p	LHCB4.3	AT2G40100	2.84	1.51	5.42	0.0011231	0.047334	-0.38	TRUE
258292_at	hypothetical protein predicted by	---	AT3G23330	-2.07	-1.05	-5.42	0.0011247	0.047334	-0.38	FALSE
256603_at	unknown protein similar to At14a	---	AT3G28270	4.24	2.08	5.42	0.0011286	0.0474094	-0.39	FALSE
253028_at	putative protein	pde191	AT4G38160	-1.84	-0.88	-5.41	0.0011307	0.0474105	-0.39	FALSE
246701_at	cysteine synthase ;supported by	CYSD2	AT5G28020	-2.06	-1.04	-5.41	0.0011339	0.047459	-0.39	FALSE
248510_at	Expressed protein ; supported by	---	---	-1.65	-0.72	-5.41	0.0011372	0.047509	-0.40	FALSE
244926_s_a	maturase	---	AT2G07711 ///	2.09	1.07	5.40	0.0011426	0.0475834	-0.40	TRUE
251151_at	hypothetical protein ; supported b	---	AT3G63170	-2.08	-1.06	-5.40	0.0011436	0.0475834	-0.40	FALSE
258573_at	hypothetical protein contains Pfa	PTAC3	AT3G04260	-1.67	-0.74	-5.40	0.0011453	0.0475834	-0.40	FALSE
250139_at	putative protein de novo DNA m	DRM2	AT5G14620	-1.62	-0.69	-5.40	0.00115	0.0475899	-0.41	FALSE
245338_at	Expressed protein ; supported by	---	AT4G16442	-2.28	-1.19	-5.40	0.0011496	0.0475899	-0.41	FALSE
250821_at	putative protein similar to unknov	---	AT5G05190	2.01	1.00	5.40	0.0011517	0.0475899	-0.41	FALSE
267068_at	unknown protein	---	AT2G41020	-2.10	-1.07	-5.39	0.001154	0.0475988	-0.41	FALSE
256981_at	brassinosteroid receptor kinase,	BRL3	AT3G13380	2.71	1.44	5.35	0.0012093	0.047715	-0.46	TRUE
262946_at	hypothetical protein predicted by	---	AT1G79390	-1.85	-0.89	-5.37	0.0011894	0.047715	-0.44	TRUE
262957_s_a	RNA polymerase II subunit, puta	NRPB8A	AT1G54250 ///	-1.58	-0.66	-5.35	0.0012155	0.047715	-0.46	FALSE
262402_at	unknown protein ; supported by c	TOM6	AT1G49410	-2.20	-1.14	-5.34	0.0012216	0.047715	-0.47	FALSE
265483_at	hypothetical protein ; supported b	SQN	AT2G15790	-2.39	-1.26	-5.35	0.0012125	0.047715	-0.46	TRUE

260989_at	unknown protein ; supported by	---	AT1G53450	-2.23	-1.16	-5.36	0.0012004	0.047715	-0.45	TRUE
267174_at	60S ribosomal protein L36 ;supp	---	AT2G37600	-3.01	-1.59	-5.39	0.001164	0.047715	-0.42	TRUE
255046_at	H+-transporting ATP synthase-li	ATPD	AT4G09650	-2.00	-1.00	-5.38	0.0011748	0.047715	-0.43	FALSE
258993_at	putative chlorophyll a/b-binding	LHCB4.2	AT3G08940	-2.02	-1.02	-5.37	0.0011877	0.047715	-0.44	FALSE
255028_at	putative protein Arabidopsis thal	PMP	AT3G24160 /	-3.60	-1.85	-5.38	0.0011778	0.047715	-0.43	TRUE
249015_at	Dreg-2 like protein	---	AT5G44730	-1.85	-0.89	-5.34	0.0012176	0.047715	-0.46	FALSE
245933_at	putative protein KIAA1521 - Hor	VPS9B	AT5G09320	-1.71	-0.77	-5.37	0.0011864	0.047715	-0.44	FALSE
260548_at	biotin synthase (Bio B) ;supporte	BIO2	AT2G43360	-2.64	-1.40	-5.37	0.0011889	0.047715	-0.44	FALSE
264045_at	putative GTP cyclohydrolase	---	AT2G22450	-1.75	-0.81	-5.36	0.0011949	0.047715	-0.45	FALSE
261578_at	acidic ribosomal protein, putative	---	AT1G01100	-2.22	-1.15	-5.36	0.001201	0.047715	-0.45	FALSE
262699_at	unknown protein	---	AT1G75980	-1.86	-0.90	-5.37	0.0011817	0.047715	-0.43	FALSE
253547_at	chloroplast omega-6 fatty acid de	FAD6	AT4G30950	-1.80	-0.85	-5.36	0.0011908	0.047715	-0.44	FALSE
254262_at	putative protein annexin VII, Dic	---	AT4G23470	2.13	1.09	5.34	0.0012177	0.047715	-0.46	FALSE
260799_at	UDP-glucose glucosyltransferas	AtUGT85A4	AT1G78270	-2.05	-1.03	-5.37	0.0011897	0.047715	-0.44	FALSE
247158_at	branched-chain amino acid amin	ATBCAT-5	AT5G65780	-1.74	-0.80	-5.34	0.0012209	0.047715	-0.47	FALSE
265943_at	putative cytidine deaminase ;sup	CDA1	AT2G19570	3.61	1.85	5.38	0.0011703	0.047715	-0.42	FALSE
250563_at	putative protein predicted protei	---	AT5G08050	-2.49	-1.32	-5.35	0.0012111	0.047715	-0.46	FALSE
252350_at	ataxia-telangiectasia mutated pr	ATM	AT3G48190	-1.68	-0.75	-5.36	0.0011999	0.047715	-0.45	FALSE
266799_at	unknown protein	ATPSK2	AT2G22860	3.26	1.70	5.35	0.0012144	0.047715	-0.46	FALSE
264185_at	unknown protein ;supported by fu	---	AT1G54780	-1.78	-0.83	-5.37	0.0011844	0.047715	-0.44	FALSE
258730_at	putative GTP-binding protein (AT	ATFP8	AT3G11730	-1.59	-0.66	-5.36	0.0012019	0.047715	-0.45	FALSE
264543_at	hypothetical protein predicted by	---	AT1G55780	2.14	1.10	5.38	0.0011681	0.047715	-0.42	FALSE
266929_at	putative AT-hook DNA-binding pr	---	AT2G45850	-1.84	-0.88	-5.37	0.0011802	0.047715	-0.43	FALSE
258162_at	dehydrogenase, putative similar	---	AT3G17810	2.32	1.21	5.39	0.0011659	0.047715	-0.42	FALSE
248094_at	trigger factor-like protein	---	AT5G55220	-2.23	-1.16	-5.35	0.0012034	0.047715	-0.45	FALSE
253122_at	hypothetical protein	---	AT4G35987	-1.90	-0.93	-5.35	0.0012136	0.047715	-0.46	FALSE
252291_s_a	peroxidase ;supported by full-ler	PRXCB	AT3G49110 /	3.15	1.66	5.34	0.0012269	0.0478383	-0.47	TRUE
256134_at	aminoalcoholphosphotransferase	AAPT1	AT1G13560	-1.72	-0.78	-5.33	0.0012296	0.0478634	-0.47	FALSE
252274_at	branched-chain-amino-acid tran	BCAT3	AT3G49680	-1.79	-0.84	-5.33	0.001237	0.0480696	-0.48	FALSE
260806_at	RNA recognition motif-containing	---	AT1G78260	1.62	0.70	5.31	0.0012548	0.0486769	-0.50	FALSE
258975_at	putative WRKY-like transcription	WRKY45	AT3G01970	2.03	1.02	5.31	0.0012629	0.048907	-0.50	TRUE
253879_s_a	UDP rhamnose--anthocyanidin-3	---	AT4G27560 /	3.53	1.82	5.30	0.0012683	0.0489517	-0.51	TRUE
257131_at	mitochondrial carrier protein, put	---	AT3G20240	-1.68	-0.75	-5.30	0.0012682	0.0489517	-0.51	FALSE
261086_at	hypothetical protein predicted by	TRFL3	AT1G17460	-1.69	-0.76	-5.30	0.0012748	0.0490676	-0.51	TRUE
253308_at	putative protein aminotransferas	AGD2	AT4G33680	-1.74	-0.80	-5.30	0.0012756	0.0490676	-0.51	FALSE

259417_at	unknown protein contains similar	HFR1	AT1G02340	-2.72	-1.44	-5.30	0.0012794	0.0491303	-0.51	FALSE
247440_at	peptide transporter	---	AT5G62680	1.74	0.80	5.29	0.0012843	0.0491717	-0.52	TRUE
250283_at	putative protein many hypothetic	---	AT5G13270	-1.89	-0.92	-5.29	0.001287	0.0491717	-0.52	FALSE
251712_at	putative protein non-consensus	---	AT3G56120	-1.65	-0.72	-5.29	0.0012856	0.0491717	-0.52	FALSE
264280_at	beta-glucosidase, putative simila	BGLU46	AT1G61820	3.61	1.85	5.26	0.0013352	0.0492107	-0.56	TRUE
251519_at	putative protein hypothetical pro	GUN4	AT3G59400	-2.19	-1.13	-5.25	0.0013504	0.0492107	-0.57	TRUE
249354_at	nuclear pore protein -like nuclea	EMB3012	AT5G40480	-2.46	-1.30	-5.26	0.0013291	0.0492107	-0.55	TRUE
258453_at	RNA polymerase I, II and III 24.3	NRPB5	AT3G22320	-1.66	-0.73	-5.27	0.0013117	0.0492107	-0.54	FALSE
253585_at	putative protein hypothetical pro	---	AT4G30720	-1.73	-0.79	-5.26	0.0013271	0.0492107	-0.55	FALSE
259344_at	putative polynucleotide phospho	RIF10	AT3G03710	-2.05	-1.04	-5.27	0.0013186	0.0492107	-0.55	TRUE
251427_at	beta-glucosidase-like protein sev	BGLU16	AT3G60130	2.36	1.24	5.25	0.0013426	0.0492107	-0.56	FALSE
256741_at	hypothetical protein predicted by	---	AT3G29375	-2.37	-1.25	-5.26	0.0013319	0.0492107	-0.56	TRUE
248093_at	putative protein similar to unknov	---	AT5G55210	-1.98	-0.98	-5.27	0.0013156	0.0492107	-0.54	FALSE
260981_at	hypothetical protein predicted by	---	AT1G53460	-2.06	-1.04	-5.26	0.0013286	0.0492107	-0.55	FALSE
255070_at	isoamylase-like protein probable	ISA3	AT4G09020	-1.71	-0.77	-5.26	0.0013353	0.0492107	-0.56	FALSE
245195_at	F12A21.13 putative photosysten	PSBY	AT1G67740	-1.78	-0.83	-5.26	0.0013353	0.0492107	-0.56	FALSE
248491_at	unknown protein ;supported by f	---	AT5G51010	-2.35	-1.23	-5.26	0.0013328	0.0492107	-0.56	FALSE
258776_at	putative T-complex protein 1, ET	---	AT3G11830	-1.98	-0.99	-5.27	0.0013094	0.0492107	-0.54	FALSE
260420_at	unknown protein	---	AT1G69610	1.82	0.87	5.27	0.0013186	0.0492107	-0.55	FALSE
252181_at	Expressed protein ; supported by	---	AT3G50685	-1.75	-0.81	-5.25	0.0013404	0.0492107	-0.56	FALSE
254796_at	putative protein protein kinase h	---	AT4G13000	2.01	1.01	5.28	0.0012953	0.0492107	-0.53	FALSE
247376_at	nucleotide diphosphate kinase la	NDPK2	AT5G63310	-1.70	-0.77	-5.24	0.0013505	0.0492107	-0.57	FALSE
247899_at	Expressed protein ; supported by	---	AT5G57345	-2.06	-1.04	-5.25	0.0013448	0.0492107	-0.57	FALSE
265274_at	putative RNA methyltransferase	---	AT2G28450	-2.03	-1.02	-5.25	0.0013473	0.0492107	-0.57	FALSE
255154_at	putative protein several hypothet	---	---	-1.63	-0.70	-5.28	0.0012954	0.0492107	-0.53	FALSE
252862_at	putative L-ascorbate oxidase L-a	---	AT4G39830	4.96	2.31	5.26	0.0013272	0.0492107	-0.55	FALSE
265335_at	Expressed protein ; supported by	---	AT2G18245	-1.59	-0.67	-5.25	0.0013381	0.0492107	-0.56	FALSE
248105_at	cell division protein FtsZ chloropl	FTSZ1-1	AT5G55280	-2.22	-1.15	-5.27	0.0013169	0.0492107	-0.54	FALSE
246492_at	CRS2-like protein CRS2 - Zea m	---	AT5G16140	-2.37	-1.25	-5.25	0.001349	0.0492107	-0.57	FALSE
262878_at	hypothetical protein predicted by	NDF2	AT1G64770	-2.01	-1.01	-5.28	0.0013053	0.0492107	-0.54	FALSE
246799_at	putative protein various predicted	---	AT5G26940	2.25	1.17	5.26	0.0013263	0.0492107	-0.55	FALSE
244992_s_a	ribosomal protein S7	---	---	-1.91	-0.93	-5.27	0.0013118	0.0492107	-0.54	FALSE
259751_at	putative transcription factor simila	MYBL2	AT1G71030	-1.84	-0.88	-5.28	0.0012965	0.0492107	-0.53	FALSE
251008_at	putative protein ;supported by ful	---	AT5G02710	-2.03	-1.02	-5.24	0.0013573	0.0492985	-0.57	FALSE
258917_at	unknown protein C-terminal porti	---	AT3G10630	-1.57	-0.65	-5.24	0.001356	0.0492985	-0.57	FALSE

250213_at	H-protein promoter binding factor	TBP1	AT5G13820	2.32	1.22	5.23	0.001366	0.0493022	-0.58	TRUE
255685_s_a	putative tetrahydrofolate synthas	---	AT4G00600 ///	-2.60	-1.38	-5.23	0.0013654	0.0493022	-0.58	TRUE
265021_at	unknown protein ;supported by f	---	AT1G24610	-1.63	-0.70	-5.24	0.0013647	0.0493022	-0.58	FALSE
261957_at	methionine/cystathionine gamma	ATMGL	AT1G64660	3.48	1.80	5.24	0.0013635	0.0493022	-0.58	FALSE
246152_at	IPP transferase - like protein tRN	IPT9	AT5G20040	-1.77	-0.82	-5.23	0.0013699	0.0493083	-0.58	FALSE
245016_at	carboxytransferase beta subunit	---	---	-1.72	-0.79	-5.23	0.0013705	0.0493083	-0.58	FALSE
259984_at	putative RNA-binding protein co	---	AT1G76460	-1.95	-0.97	-5.22	0.0013843	0.0496469	-0.59	FALSE
253485_at	Expressed protein ; supported by	WRKY18	AT4G31800	3.68	1.88	5.22	0.0013837	0.0496469	-0.59	FALSE
265330_at	unknown protein	GUT15	---	-1.94	-0.96	-5.21	0.0013989	0.0499678	-0.61	FALSE
250813_at	GTP-binding protein (gb|AAD092	TOC34	AT5G05000	-2.04	-1.03	-5.21	0.0013993	0.0499678	-0.61	FALSE
261189_at	hypothetical protein contains sim	NACA5	AT1G33040	-1.85	-0.89	-5.21	0.0013998	0.0499678	-0.61	FALSE
262931_at	small nuclear ribonucleoprotein,	---	AT1G65700	-1.84	-0.88	-5.21	0.0014055	0.0500187	-0.61	FALSE
263114_at	putative photosystem I reaction	PSAD-2	AT1G03130	-1.87	-0.91	-5.21	0.0014083	0.0500187	-0.61	FALSE
248547_at	putative protein contains similarit	EMB1006	AT5G50280	-2.65	-1.41	-5.20	0.00141	0.0500187	-0.61	FALSE
248541_at	protein kinase ATN1-like protein	---	AT5G50180	-2.26	-1.18	-5.21	0.0014088	0.0500187	-0.61	FALSE
250257_at	putative protein similar to unknov	---	AT5G13770	-1.99	-0.99	-5.20	0.0014134	0.0500605	-0.62	FALSE
253609_at	H+-transporting ATPase type 2,	AHA2	AT4G30190	2.00	1.00	5.20	0.0014167	0.0501002	-0.62	FALSE
265828_at	hypothetical protein predicted by	---	AT2G14520	-1.69	-0.76	-5.20	0.0014221	0.0501493	-0.62	FALSE
255041_at	putative protein hypothetical pro	---	AT4G09620	-2.03	-1.02	-5.20	0.0014225	0.0501493	-0.62	FALSE
258526_at	DAG protein, putative similar to	---	AT3G06790	-1.83	-0.87	-5.19	0.0014287	0.0501566	-0.63	FALSE
266948_at	unknown protein	---	AT2G18850	-2.77	-1.47	-5.19	0.0014293	0.0501566	-0.63	FALSE
260457_at	unknown protein	---	AT1G72480	-1.80	-0.85	-5.19	0.001425	0.0501566	-0.62	FALSE
267220_at	putative sugar nucleotide phosph	ISPD	AT2G02500	-2.03	-1.02	-5.19	0.001437	0.0502709	-0.63	TRUE
248624_at	unknown protein ; supported by	---	AT5G48790	-1.73	-0.79	-5.19	0.0014391	0.0502709	-0.63	FALSE
262501_at	putative replication factor Simila	emb1968	AT1G21690	-1.95	-0.96	-5.19	0.0014369	0.0502709	-0.63	FALSE
263680_at	unknown protein	---	AT1G26930	1.59	0.67	5.17	0.0014561	0.050428	-0.65	TRUE
267162_s_a	putative phosphoribosylaminoimi	---	AT2G05140 ///	-2.46	-1.30	-5.17	0.0014606	0.050428	-0.65	TRUE
255977_at	ribosomal protein S18, putative	---	AT1G34030	-2.21	-1.14	-5.17	0.0014558	0.050428	-0.65	FALSE
251883_at	ribosomal protein L17 -like prote	---	AT3G54210	-1.78	-0.83	-5.18	0.0014494	0.050428	-0.64	FALSE
250444_at	beta-xylosidase - like protein bet	---	AT5G10560	-1.87	-0.91	-5.18	0.0014498	0.050428	-0.64	FALSE
251766_at	putative protein PA26, p53 regul	---	AT3G55890 ///	1.79	0.84	5.17	0.001462	0.050428	-0.65	FALSE
247903_at	unknown protein ; supported by	---	AT5G57340	-2.13	-1.09	-5.17	0.0014635	0.050428	-0.65	FALSE
264199_at	unknown protein contains simila	---	AT1G22700	-1.92	-0.94	-5.17	0.0014622	0.050428	-0.65	FALSE
247201_at	50S ribosomal protein L29 ; sup	---	AT5G65220	-2.05	-1.04	-5.17	0.0014571	0.050428	-0.65	FALSE
263676_at	putative RNA-binding protein Ide	CRB	AT1G09340	-2.22	-1.15	-5.17	0.0014697	0.050494	-0.66	TRUE

267606_at	putative beta-ketoacyl-CoA synth	KCS11	AT2G26640	-1.67	-0.74	-5.16	0.0014765	0.050494	-0.66	FALSE
261540_at	unknown protein	---	AT1G63610	-1.92	-0.94	-5.16	0.0014736	0.050494	-0.66	FALSE
254597_at	hypothetical protein	---	AT4G18980	2.40	1.26	5.16	0.0014723	0.050494	-0.66	FALSE
254271_at	serine/threonine kinase - like pro	---	AT4G23150	3.76	1.91	5.16	0.0014744	0.050494	-0.66	FALSE
253172_at	putative protein ;supported by ful	---	AT4G35060	5.03	2.33	5.16	0.0014799	0.0505335	-0.66	FALSE
261300_at	hypothetical protein predicted by	---	AT1G48560	-1.93	-0.95	-5.15	0.0014866	0.0505366	-0.67	FALSE
261903_at	chromomethylase identical to GE	CMT1	AT1G80740	1.62	0.70	5.16	0.0014852	0.0505366	-0.67	FALSE
261482_at	unknown protein ;supported by fu	THH1	AT1G14530	1.83	0.87	5.16	0.0014852	0.0505366	-0.67	FALSE
253140_at	RING-H2 finger protein RHA3b ;	RHA3B	AT4G35480	2.07	1.05	5.15	0.0015014	0.0509639	-0.68	FALSE
257937_at	hypothetical protein predicted by	---	AT3G19810	-1.63	-0.71	-5.14	0.0015051	0.0510137	-0.68	FALSE
252093_at	putative protein predicted protei	---	AT3G51500	-1.86	-0.89	-5.14	0.0015134	0.0510614	-0.69	FALSE
255799_at	Deetiolated1 (DET1) light signal	DET1	AT4G10180	-1.86	-0.90	-5.14	0.0015098	0.0510614	-0.68	FALSE
264254_at	unknown protein	---	AT1G09150	-1.60	-0.68	-5.14	0.0015155	0.0510614	-0.69	FALSE
260531_at	putative acyl-CoA synthetase ; s	CER8	AT2G47240	-2.21	-1.14	-5.14	0.0015126	0.0510614	-0.68	FALSE
265594_at	50S ribosomal protein L4 ;suppo	---	AT2G20060	-2.57	-1.36	-5.13	0.0015283	0.0512037	-0.70	FALSE
263621_at	putative DNA-directed RNA polyr	NRPB6B	AT2G04630	-1.84	-0.88	-5.13	0.001528	0.0512037	-0.70	FALSE
251744_at	putative protein CHLOROPLAST	---	AT3G56010	-2.04	-1.03	-5.13	0.0015238	0.0512037	-0.69	FALSE
249691_at	translation releasing factor RF-2	HCF109	AT5G36170	-1.61	-0.69	-5.13	0.0015287	0.0512037	-0.70	FALSE
257856_at	hypothetical protein predicted by	---	AT3G12930	-1.62	-0.69	-5.13	0.001532	0.0512381	-0.70	FALSE
247304_at	amino acid transporter AAP4 (pir	AAP4	AT5G63850	2.44	1.28	5.12	0.0015353	0.0512751	-0.70	FALSE
247208_at	nodulin-like ;supported by full-le	---	AT5G64870	1.90	0.92	5.12	0.0015411	0.0513933	-0.70	FALSE
245682_at	Expressed protein ; supported by	---	AT5G08750	1.81	0.86	5.12	0.001545	0.0514485	-0.71	FALSE
245317_at	hypothetical protein ; supported b	---	AT4G15610	1.82	0.86	5.10	0.0015727	0.0515418	-0.72	TRUE
248704_at	putative protein pectinesterase-li	sks3	AT5G48450	2.20	1.14	5.11	0.0015603	0.0515418	-0.72	TRUE
248039_at	putative protein similar to unknov	---	AT5G55950	1.61	0.69	5.11	0.0015519	0.0515418	-0.71	FALSE
263156_at	myrosinase-associated protein,	---	AT1G54030	3.20	1.68	5.11	0.0015524	0.0515418	-0.71	TRUE
249827_at	unknown protein ;supported by f	---	AT5G23330	-1.98	-0.99	-5.11	0.0015644	0.0515418	-0.72	FALSE
253903_at	kinesin-related protein katB ; su	ATK2	AT4G27180	-1.55	-0.64	-5.11	0.001561	0.0515418	-0.72	FALSE
264442_at	hypothetical protein similar to lec	---	AT1G27480	-2.51	-1.33	-5.11	0.0015672	0.0515418	-0.72	FALSE
249138_at	putative protein contains similarit	WPP1	AT5G43070	1.74	0.80	5.10	0.001571	0.0515418	-0.72	FALSE
253216_at	cyclophilin - like protein cyclophi	---	AT4G34960	-1.99	-0.99	-5.11	0.0015641	0.0515418	-0.72	FALSE
253607_at	small nuclear ribonucleoprotein	---	AT4G30330	-2.19	-1.13	-5.11	0.0015634	0.0515418	-0.72	FALSE
246454_at	Expressed protein ; supported by	DHAR3	AT5G16710	-1.77	-0.82	-5.10	0.0015719	0.0515418	-0.72	FALSE
249433_at	putative protein hypothetical pro	---	AT5G39940	-2.23	-1.16	-5.10	0.0015796	0.0515452	-0.73	TRUE
266705_at	40S ribosomal protein S30 ; sup	---	AT2G19750	-2.40	-1.26	-5.10	0.0015756	0.0515452	-0.73	FALSE

258324_at	putative DNA binding protein ide	TSO1	AT3G22780	-1.64	-0.72	-5.10	0.0015784	0.0515452	-0.73	FALSE
249377_at	putative protein predicted protei	---	AT5G40690	2.92	1.55	5.10	0.0015819	0.051547	-0.73	TRUE
254779_at	hypothetical protein	---	AT4G12760	-1.66	-0.73	-5.09	0.0015872	0.0515719	-0.73	FALSE
259625_at	glyceraldehyde-3-phosphate de	GAPB	AT1G42970	-2.06	-1.04	-5.09	0.0015869	0.0515719	-0.73	FALSE
252179_at	putative protein UDP-glucose:(g	GATL2	AT3G50760	2.41	1.27	5.09	0.0015896	0.0515781	-0.74	FALSE
264613_at	lipoyltransferase identical to GB:	LIP2	AT1G04640	-1.83	-0.88	-5.09	0.0015924	0.0515962	-0.74	FALSE
249335_at	putative protein contains similarit	NRPB12	AT5G41010	-1.78	-0.83	-5.09	0.0016006	0.0517864	-0.74	TRUE
252183_at	UTP-glucose glucosyltransferas	UGT72E1	AT3G50740	-2.09	-1.07	-5.08	0.001619	0.0519057	-0.75	TRUE
245152_at	putative mitochondrial carrier pro	---	AT2G47490	1.79	0.84	5.08	0.0016133	0.0519057	-0.75	FALSE
257587_at	3'-5' exonuclease, putative conta	---	AT1G56310	-1.69	-0.76	-5.08	0.0016113	0.0519057	-0.75	FALSE
250523_at	putative protein strong similarity t	---	AT5G08510	-1.59	-0.67	-5.07	0.0016246	0.0519057	-0.76	FALSE
251066_at	putative protein RING-H2 finger	---	AT5G01880	-2.59	-1.37	-5.07	0.0016248	0.0519057	-0.76	FALSE
248107_at	small Ras-like GTP-binding prote	RAN3	AT5G55190	-1.62	-0.69	-5.08	0.0016118	0.0519057	-0.75	FALSE
255636_at	homeodomain protein AHDP ; s	ANL2	AT4G00730	-1.97	-0.98	-5.07	0.0016241	0.0519057	-0.76	FALSE
253768_at	putative protein	---	AT4G28550	2.45	1.29	5.08	0.0016172	0.0519057	-0.75	FALSE
250879_at	putative protein various predicte	---	AT5G04060	-2.13	-1.09	-5.08	0.0016185	0.0519057	-0.75	FALSE
246371_at	unknown protein contains similar	---	AT1G51940	-1.88	-0.91	-5.07	0.0016325	0.0519598	-0.76	TRUE
257635_at	cytochrome P450 monooxygena	CYP71B4	AT3G26280	-2.01	-1.01	-5.06	0.0016415	0.0519598	-0.77	FALSE
252548_at	kinesin-related protein - like kine	---	AT3G45850	-1.89	-0.92	-5.06	0.0016392	0.0519598	-0.77	FALSE
251240_at	putative protein	---	AT3G62450	-1.67	-0.74	-5.06	0.0016424	0.0519598	-0.77	FALSE
267210_at	dihydroxypolyprenylbenzoate me	ATCOQ3	AT2G30920	-1.56	-0.64	-5.07	0.0016291	0.0519598	-0.76	FALSE
253283_at	hypothetical protein ; supported	---	AT4G34090	-2.29	-1.20	-5.07	0.0016376	0.0519598	-0.77	FALSE
259207_at	unknown protein	---	AT3G09050	-2.05	-1.03	-5.07	0.0016339	0.0519598	-0.76	FALSE
261728_at	pectinesterase, putative similar t	sks5	AT1G76160	2.66	1.41	5.05	0.0016718	0.0520284	-0.79	TRUE
263851_at	putative retroelement pol polypro	---	---	4.54	2.18	5.05	0.0016641	0.0520284	-0.78	TRUE
266589_at	hypothetical protein predicted by	---	AT2G46250	-2.19	-1.13	-5.05	0.0016715	0.0520284	-0.79	TRUE
246249_at	salt-inducible like protein	---	AT4G36680	-2.05	-1.03	-5.05	0.0016719	0.0520284	-0.79	FALSE
266482_at	putative small nuclear ribonucleo	---	AT2G47640	-2.08	-1.06	-5.05	0.0016565	0.0520284	-0.78	FALSE
247446_at	unknown protein ; supported by	---	AT5G62650	-1.64	-0.71	-5.06	0.0016538	0.0520284	-0.78	FALSE
253537_at	putative protein ; supported by f	HCF153	AT4G31560	-1.85	-0.89	-5.05	0.0016688	0.0520284	-0.78	FALSE
250174_at	agp6	AGP6	AT5G14380	1.66	0.73	5.05	0.0016659	0.0520284	-0.78	FALSE
258911_at	unknown protein similar to hypot	---	AT3G06470	1.86	0.89	5.05	0.0016672	0.0520284	-0.78	FALSE
250058_at	plastid-specific ribosomal protei	PSRP6	AT5G17870	-2.04	-1.03	-5.05	0.0016633	0.0520284	-0.78	FALSE
253795_at	tyrosine transaminase-like prote	---	AT4G28420	1.85	0.89	5.06	0.0016501	0.0520284	-0.77	FALSE
256796_at	hypothetical protein predicted by	---	AT3G22210	-2.69	-1.43	-5.05	0.0016643	0.0520284	-0.78	FALSE

262996_at	hypothetical protein predicted by	---	AT1G54440	-1.75	-0.81	-5.04	0.0016801	0.0521297	-0.79	TRUE
247187_at	putative protein similar to unknov	---	AT5G65490	-1.74	-0.80	-5.04	0.0016809	0.0521297	-0.79	FALSE
250938_at	putative protein various predicte	---	AT5G03180	-2.21	-1.15	-5.04	0.001682	0.0521297	-0.79	TRUE
256672_at	ABC transporter, putative contai	---	AT3G52310	2.06	1.04	5.04	0.0016875	0.0521505	-0.80	TRUE
247572_at	putative protein ; supported by fu	---	AT5G61220	-1.66	-0.73	-5.04	0.0016899	0.0521505	-0.80	FALSE
248403_at	arginine-aspartate-rich RNA bind	---	AT5G51410	-1.78	-0.83	-5.04	0.001689	0.0521505	-0.80	FALSE
249162_at	Expressed protein ; supported by	---	AT5G42765	-2.20	-1.14	-5.03	0.0016919	0.0521505	-0.80	FALSE
256309_at	photosystem I subunit X precurso	PSAK	AT1G30380	-1.67	-0.74	-5.03	0.0016981	0.0522717	-0.80	FALSE
264317_at	spermidine synthase, putative si	SPDS2	AT1G70310	-1.77	-0.82	-5.03	0.0017016	0.0523091	-0.80	FALSE
263711_at	putative protein phosphatase 2C	---	AT2G20630	1.78	0.83	5.02	0.001715	0.0523602	-0.81	TRUE
248709_at	unknown protein ;supported by f	---	AT5G48470	-2.70	-1.43	-5.02	0.0017158	0.0523602	-0.81	TRUE
249318_at	uridine kinase-like protein	AtUK/UPRT	AT5G40870	-1.76	-0.82	-5.03	0.0017101	0.0523602	-0.81	FALSE
260465_at	membrane-associated salt-induc	---	AT1G10910	-1.54	-0.62	-5.03	0.0017057	0.0523602	-0.81	FALSE
255718_at	unknown protein ;supported by fu	ATNSI	AT1G32070	-1.79	-0.84	-5.02	0.0017105	0.0523602	-0.81	FALSE
258149_at	hypothetical protein contains Pfa	EMB1270	AT3G18110	-1.99	-0.99	-5.02	0.001717	0.0523602	-0.81	FALSE
248854_at	putative protein contains similarit	---	AT5G46580	-1.95	-0.97	-5.02	0.0017198	0.0523756	-0.82	FALSE
246457_at	WD40-repeat protein transducin	TOZ	AT5G16750	-1.81	-0.86	-5.01	0.0017303	0.0526171	-0.82	TRUE
252036_at	putative protein ;supported by fu	---	AT3G52070	-2.08	-1.06	-5.01	0.0017324	0.0526171	-0.82	FALSE
252032_at	putative protein RNA-binding pro	---	AT3G52150	-1.62	-0.70	-5.01	0.0017355	0.052642	-0.82	FALSE
256746_at	alpha-glucan phosphorylase, pu	---	AT3G29320	-2.31	-1.21	-5.01	0.0017454	0.0528715	-0.83	FALSE
265521_at	hypothetical protein predicted by	ORG4	AT2G06010	-1.96	-0.97	-5.00	0.0017531	0.0529631	-0.83	FALSE
253438_at	glycine hydroxymethyltransferas	SHM3	AT4G32520	-2.11	-1.07	-5.00	0.0017515	0.0529631	-0.83	FALSE
260250_at	putative phosphoribosylformylgly	PUR4	AT1G74260	-1.98	-0.98	-5.00	0.0017565	0.0529982	-0.84	TRUE
265584_at	unknown protein	PIL5	AT2G20180	-1.64	-0.71	-5.00	0.0017621	0.0530969	-0.84	FALSE
265247_at	50S ribosomal protein L3 ;suppo	---	AT2G43030	-1.67	-0.74	-4.99	0.0017714	0.0533053	-0.85	FALSE
247360_at	cytochrome P450-like protein ;su	CYP94B1	AT5G63450	5.27	2.40	4.99	0.0017765	0.0533183	-0.85	TRUE
254955_at	putative protein RNA polymeras	KELP	AT4G10920	-1.68	-0.75	-4.99	0.0017744	0.0533183	-0.85	FALSE
266641_at	Expressed protein ; supported by	---	AT2G35605	-1.78	-0.83	-4.99	0.0017806	0.0533722	-0.85	FALSE
247297_at	peroxidase ATP3a (emb|CAA67	---	AT5G64100	4.67	2.22	4.98	0.0017867	0.0534844	-0.85	FALSE
250168_at	putative protein predicted protei	---	AT5G15320	-1.71	-0.77	-4.98	0.0017905	0.0535278	-0.86	FALSE
266127_s_a	putative mitochondrial translation	---	AT1G45332 /	-2.21	-1.14	-4.98	0.0017975	0.0535974	-0.86	FALSE
251518_at	putative protein protein CG1564	---	AT3G59390	-1.80	-0.84	-4.98	0.0017967	0.0535974	-0.86	FALSE
248933_at	putative protein contains similarit	---	AT5G46070	-1.70	-0.77	-4.98	0.0018003	0.0536107	-0.86	TRUE
258253_at	putative short chain alcohol dehy	---	AT3G26760	-1.67	-0.74	-4.98	0.0018032	0.0536251	-0.86	FALSE
250217_at	nodulin-like protein	---	AT5G14120	2.16	1.11	4.97	0.0018147	0.0537058	-0.87	TRUE

259952_at	putative disease resistance prote	AtRLP12	AT1G71400	2.87	1.52	4.97	0.0018123	0.0537058	-0.87	FALSE
248910_at	serine threonine protein kinase ;	CIPK20	AT5G45820	-2.79	-1.48	-4.97	0.0018153	0.0537058	-0.87	FALSE
247788_at	putative protein carbohydrate kir	---	AT5G58730	2.49	1.32	4.97	0.0018125	0.0537058	-0.87	FALSE
266259_at	unknown protein ;supported by f	---	AT2G27830	-1.74	-0.80	-4.97	0.001823	0.0537096	-0.87	TRUE
250495_at	ribsomal protein - like chloroplas	---	AT5G09770	-2.03	-1.02	-4.97	0.0018218	0.0537096	-0.87	TRUE
264487_at	vacuolar protein sorting homolog	VPS45	AT1G77140	1.62	0.70	4.96	0.0018343	0.0537096	-0.88	FALSE
254943_at	putative protein predicted protei	---	AT4G10890	-1.73	-0.79	-4.96	0.0018339	0.0537096	-0.88	FALSE
250723_at	lysine decarboxylase-like protein	---	AT5G06300	-2.18	-1.13	-4.96	0.0018326	0.0537096	-0.88	FALSE
251321_at	RING finger protein ;supported b	BRH1	AT3G61460	-2.45	-1.29	-4.96	0.0018294	0.0537096	-0.88	FALSE
249906_at	unknown protein	---	AT5G22730	-1.61	-0.69	-4.96	0.001834	0.0537096	-0.88	FALSE
250751_at	glucuronosyl transferase-like pro	---	AT5G05890	-1.89	-0.92	-4.96	0.0018271	0.0537096	-0.88	FALSE
253163_at	putative protein E1B 19K/Bcl-2-i	---	AT4G35750	-2.24	-1.17	-4.96	0.0018402	0.0538059	-0.88	TRUE
247406_at	response regulator 6 (ARR6) ; s	ARR6	AT5G62920	4.23	2.08	4.95	0.0018517	0.0538059	-0.89	FALSE
253668_at	snRNP Sm protein F - like Sm p	RUXF	AT4G30220	-1.91	-0.94	-4.95	0.0018515	0.0538059	-0.89	FALSE
254524_at	hypothetical protein	---	AT4G20000	7.15	2.84	4.96	0.0018441	0.0538059	-0.89	FALSE
265795_at	putative serine carboxypeptidase	scpl26	AT2G35780	-1.82	-0.86	-4.95	0.0018496	0.0538059	-0.89	FALSE
255331_at	hypothetical protein ; supported	---	AT4G04330	-1.78	-0.84	-4.96	0.001846	0.0538059	-0.89	FALSE
260431_at	putative zinc finger protein simila	---	AT1G68190	-1.56	-0.64	-4.95	0.0018594	0.0538228	-0.89	TRUE
255603_at	hypothetical protein	---	AT4G01040	-1.63	-0.71	-4.95	0.0018567	0.0538228	-0.89	FALSE
249690_at	acyl-peptide hydrolase-like	---	AT5G36210	-1.70	-0.77	-4.95	0.0018578	0.0538228	-0.89	FALSE
257650_at	protein phosphatase, putative si	---	AT3G16800	-2.13	-1.09	-4.93	0.0019021	0.0539151	-0.92	TRUE
254638_at	hypothetical protein	---	AT4G18740	-2.37	-1.24	-4.93	0.0018888	0.0539151	-0.91	TRUE
262314_at	unknown protein contains similar	---	AT1G70810	1.93	0.95	4.92	0.0019269	0.0539151	-0.93	TRUE
249971_at	dermal glycoprotein - like derma	---	AT5G19110	2.57	1.36	4.92	0.0019207	0.0539151	-0.93	TRUE
264811_at	hypothetical protein predicted by	---	AT1G08640	-1.60	-0.68	-4.93	0.0018892	0.0539151	-0.91	FALSE
266072_at	putative trehalose-6-phosphate s	ATTPS11	AT2G18700	2.62	1.39	4.94	0.0018859	0.0539151	-0.91	FALSE
266951_at	putative salt-inducible protein ; s	---	AT2G18940	-1.60	-0.67	-4.92	0.0019112	0.0539151	-0.92	FALSE
256480_at	unknown protein	SAR1	AT1G33410	-1.98	-0.98	-4.92	0.0019156	0.0539151	-0.93	FALSE
253538_at	putative protein ribosomal protei	---	AT4G31460	-1.61	-0.69	-4.92	0.0019259	0.0539151	-0.93	FALSE
261803_at	transcription factor, putative sim	NF-YA7	AT1G30500	-2.19	-1.13	-4.92	0.0019227	0.0539151	-0.93	TRUE
250148_at	putative protein various predicte	---	AT5G14530	-1.84	-0.88	-4.92	0.0019245	0.0539151	-0.93	FALSE
258800_at	unknown protein predicted by ge	---	AT3G04550	-1.90	-0.93	-4.91	0.0019298	0.0539151	-0.93	FALSE
264188_at	histone H2A, putative similar to I	GAMMA-H2	AT1G54690	-3.19	-1.67	-4.93	0.0019007	0.0539151	-0.92	TRUE
256648_at	ribosomal protein, putative simila	---	AT3G13580	-2.20	-1.14	-4.94	0.0018814	0.0539151	-0.91	FALSE
258747_at	unknown protein ; supported by	---	AT3G05810	-2.14	-1.10	-4.92	0.0019115	0.0539151	-0.92	FALSE

256753_at	unknown protein contains Pfam p	GHS1	AT3G27160	-1.99	-0.99	-4.93	0.0018888	0.0539151	-0.91	FALSE
255117_s_a	putative protein various hypothet	ATPUP13	AT4G08700 ///	-1.56	-0.64	-4.94	0.0018855	0.0539151	-0.91	FALSE
246294_at	ribosomal protein, chloroplast rib	PSRP5	AT3G56910	-1.68	-0.74	-4.92	0.0019084	0.0539151	-0.92	FALSE
259583_at	hypothetical protein	---	AT1G28070	-1.89	-0.92	-4.93	0.0018963	0.0539151	-0.92	FALSE
260051_at	hypothetical protein	---	AT1G78210	3.41	1.77	4.94	0.0018724	0.0539151	-0.90	FALSE
265464_at	putative myosin heavy chain	---	AT2G37080	-1.58	-0.66	-4.94	0.0018802	0.0539151	-0.91	FALSE
249424_s_a	hypothetical protein ; supported	---	AT5G39800 ///	-1.88	-0.91	-4.92	0.0019253	0.0539151	-0.93	FALSE
257644_at	unknown protein ;supported by f	AOC3	AT3G25780	9.38	3.23	4.93	0.0018915	0.0539151	-0.91	FALSE
246673_at	ribosomal protein S1 ;supported	RPS1	AT5G30510	-1.66	-0.73	-4.94	0.00187	0.0539151	-0.90	FALSE
254108_at	putative protein	RIN2	AT4G25230	1.90	0.92	4.94	0.0018754	0.0539151	-0.90	FALSE
255798_at	unknown protein predicted by ge	---	AT2G33255	-1.82	-0.87	-4.92	0.0019199	0.0539151	-0.93	FALSE
259442_at	(1-4)-beta-mannan endohydrola	---	AT1G02310	2.66	1.41	4.92	0.0019102	0.0539151	-0.92	FALSE
255342_at	putative receptor-like protein kina	---	AT4G04510	1.91	0.93	4.93	0.0018931	0.0539151	-0.91	FALSE
263442_at	hypothetical protein	---	AT2G28605	-1.62	-0.70	-4.91	0.0019311	0.0539151	-0.93	FALSE
265287_at	putative photosystem I reaction c	PSAE-2	AT2G20260	-1.55	-0.63	-4.91	0.0019392	0.0540759	-0.94	FALSE
248589_at	von Hippel-Lindau binding protei	PDF3	AT5G49510	-1.65	-0.72	-4.91	0.0019449	0.0541672	-0.94	FALSE
259884_at	hypothetical protein predicted by	---	AT1G76390	1.65	0.72	4.91	0.0019475	0.0541722	-0.94	FALSE
248942_at	putative protein similar to unknov	---	AT5G45480	1.88	0.91	4.90	0.0019641	0.0541722	-0.95	FALSE
260938_at	hypothetical protein contains sim	---	AT1G45170	-1.95	-0.96	-4.90	0.0019634	0.0541722	-0.95	FALSE
244979_at	ribosomal protein S11	---	---	-1.55	-0.63	-4.90	0.001959	0.0541722	-0.95	FALSE
248792_at	ras-related small GTP-binding pr	ATRAB1A	AT5G47200	1.79	0.84	4.90	0.0019627	0.0541722	-0.95	FALSE
246779_at	putative protein peroxisomal inte	PNC2	AT5G27520	2.82	1.49	4.90	0.0019509	0.0541722	-0.94	FALSE
259351_at	putative sugar transporter simila	---	AT3G05150	1.71	0.78	4.90	0.0019528	0.0541722	-0.94	FALSE
263846_at	putative RNA polymerase sigma-	SIGF	AT2G36990	-2.26	-1.18	-4.90	0.0019597	0.0541722	-0.95	FALSE
262751_at	hypothetical protein predicted by	---	AT1G16310	-1.63	-0.71	-4.89	0.0019738	0.0542278	-0.96	FALSE
246480_at	TCP-1 chaperonin-like protein t-	---	AT5G16070	-2.12	-1.08	-4.89	0.0019756	0.0542278	-0.96	FALSE
264163_at	Expressed protein ; supported by	---	AT1G65445	-1.89	-0.92	-4.90	0.0019695	0.0542278	-0.95	FALSE
265570_at	unknown protein	---	AT2G28310	-2.00	-1.00	-4.89	0.0019733	0.0542278	-0.96	FALSE
253674_at	UDP-N-acetylglucosamine O-ac	---	AT4G29540	-1.73	-0.79	-4.89	0.0019782	0.054235	-0.96	FALSE
265024_at	Expressed protein ; supported by	---	AT1G24600	3.24	1.69	4.89	0.0019813	0.0542532	-0.96	FALSE
259591_at	unknown protein ;supported by fu	---	AT1G28150	-1.52	-0.61	-4.88	0.0020049	0.0547691	-0.97	FALSE
248828_at	Lil3 protein	---	AT5G47110	-1.59	-0.67	-4.88	0.0020034	0.0547691	-0.97	FALSE
267419_at	putative thioredoxin	ATO1	AT2G35010	-1.76	-0.82	-4.87	0.0020184	0.0548744	-0.98	FALSE
250353_at	putative protein predicted protei	---	AT5G11630	-1.87	-0.91	-4.88	0.002013	0.0548744	-0.98	FALSE
266700_at	60S ribosomal protein L31 ; sup	---	AT2G19740	-2.16	-1.11	-4.88	0.0020166	0.0548744	-0.98	FALSE

259235_at	hypothetical protein predicted by	---	AT3G11600	3.81	1.93	4.88	0.0020156	0.0548744	-0.98	FALSE
255870_at	hypothetical protein predicted by	---	AT2G30280	-1.68	-0.75	-4.87	0.0020291	0.0551005	-0.98	FALSE
248634_at	isoleucyl-tRNA synthetase	OVA2	AT5G49030	-2.01	-1.01	-4.87	0.0020353	0.0552019	-0.99	FALSE
266170_at	unknown protein ;supported by f	---	AT2G39050	2.77	1.47	4.86	0.0020393	0.0552444	-0.99	FALSE
254763_at	ribosomal protein L13a like prote	---	AT4G13170	-2.02	-1.01	-4.86	0.002056	0.055566	-1.00	FALSE
245049_at	ribosomal protein S16	---	---	-2.39	-1.26	-4.86	0.0020537	0.055566	-1.00	FALSE
248921_at	GDSL-motif lipase/hydrolase-like	---	AT5G45950	4.33	2.11	4.85	0.0020689	0.055769	-1.00	TRUE
254147_at	putative protein similarity Humar	---	AT4G24270	-2.43	-1.28	-4.85	0.0020692	0.055769	-1.00	TRUE
245377_at	hypothetical protein	---	AT4G17700	1.73	0.79	4.85	0.0020709	0.055769	-1.00	FALSE
258531_at	importin alpha identical to GB:A/	IMPA-1	AT3G06720	-1.61	-0.69	-4.85	0.0020794	0.0559333	-1.01	TRUE
251305_at	peptidylprolyl isomerase ROC4	ROC4	AT3G62030	-2.34	-1.23	-4.84	0.0020872	0.0559461	-1.01	TRUE
251936_at	putative protein crp1 protein, Ze	MEE40	AT3G53700	-1.98	-0.98	-4.85	0.0020828	0.0559461	-1.01	FALSE
264177_at	hypothetical protein contains Pfa	---	AT1G02150	-1.70	-0.77	-4.84	0.0020856	0.0559461	-1.01	FALSE
248855_at	NAM-like	anac096	AT5G46590	2.70	1.44	4.84	0.0020939	0.0560588	-1.02	FALSE
261572_at	unknown protein	---	AT1G01170	-1.90	-0.92	-4.84	0.0020994	0.0561399	-1.02	FALSE
262598_at	unknown protein EST gb|N65467	---	AT1G15260	-2.28	-1.19	-4.84	0.0021019	0.0561406	-1.02	FALSE
259955_s_a	unknown protein ;supported by f	BZR1	AT1G19350 ///	-1.82	-0.86	-4.84	0.002106	0.0561839	-1.02	FALSE
253857_at	putative protein hypothetical chl	---	AT4G27990	-1.76	-0.81	-4.83	0.0021085	0.0561854	-1.02	FALSE
256468_at	ferredoxin, putative similar to GE	---	AT1G32550	-1.90	-0.92	-4.83	0.0021132	0.0562444	-1.03	FALSE
264192_at	hypothetical protein predicted by	ATATG18H	AT1G54710	1.55	0.63	4.83	0.0021225	0.0563604	-1.03	FALSE
248149_at	Expressed protein ; supported by	---	AT5G54855	-1.63	-0.71	-4.83	0.002122	0.0563604	-1.03	FALSE
248785_at	unknown protein	---	AT5G47400	-1.55	-0.63	-4.83	0.0021262	0.0563939	-1.03	FALSE
255294_at	putative sugar transporter	---	AT4G04750	-1.75	-0.81	-4.83	0.0021305	0.0564415	-1.03	FALSE
246074_at	hypothetical protein ; supported	---	AT5G20130	-1.65	-0.72	-4.82	0.0021341	0.056471	-1.04	FALSE
264580_at	unknown protein EST gb|ATTS0	---	AT1G05340	3.31	1.73	4.82	0.0021373	0.0564914	-1.04	FALSE
247198_at	unknown protein	---	AT5G65290	1.65	0.72	4.82	0.0021424	0.0565601	-1.04	FALSE
265876_at	putative receptor-like protein kina	---	AT2G42290	-1.63	-0.70	-4.82	0.0021491	0.056671	-1.04	FALSE
247745_at	copper transport protein	COPT1	AT5G59030	-1.56	-0.64	-4.82	0.0021526	0.0566992	-1.04	FALSE
245011_at	photosystem II G protein	---	---	-1.73	-0.79	-4.81	0.0021587	0.056771	-1.05	TRUE
262354_at	H+-transporting ATPase protein	VHA-E3	AT1G64200	3.46	1.79	4.81	0.0021653	0.056771	-1.05	TRUE
246479_at	hypothetical protein	---	AT5G16060	-1.74	-0.80	-4.81	0.0021699	0.056771	-1.05	FALSE
263696_at	putative aspartate kinase-homos	AK-HSDH I	AT1G31230	-2.42	-1.28	-4.81	0.0021688	0.056771	-1.05	FALSE
245020_at	cytochrome f	---	---	-1.73	-0.79	-4.81	0.0021703	0.056771	-1.05	FALSE
256343_at	unknown protein ; supported by	---	AT1G72090	-1.88	-0.91	-4.81	0.0021623	0.056771	-1.05	FALSE
267079_at	hypothetical protein predicted by	---	AT2G41200	-1.60	-0.67	-4.81	0.0021731	0.056779	-1.05	FALSE

261927_at	RING-H2 zinc finger protein ATL	---	AT1G22500	-3.48	-1.80	-4.80	0.0021894	0.0568802	-1.06	TRUE
267051_at	hypothetical protein predicted by	---	AT2G38500	2.18	1.13	4.80	0.0021892	0.0568802	-1.06	FALSE
262029_at	50S ribosomal protein L21 chlorc	---	AT1G35680	-2.04	-1.03	-4.80	0.0021847	0.0568802	-1.06	FALSE
257890_s_a	putative protein peroxidase - Ly	---	AT3G17070 ///	2.10	1.07	4.80	0.0021832	0.0568802	-1.06	FALSE
263963_at	putative DNA-binding protein RA	---	AT2G36080	2.26	1.18	4.80	0.0021822	0.0568802	-1.06	FALSE
257949_at	putative UDP-glucose glucosyltra	UGT71B1	AT3G21750	2.22	1.15	4.80	0.0021924	0.0568924	-1.06	FALSE
257299_at	unknown protein ;supported by f	---	AT3G28050	-1.84	-0.88	-4.80	0.0021977	0.0569014	-1.07	TRUE
255118_at	nitrilase 1 like protein nitrilase 1	---	AT4G08790	-1.90	-0.92	-4.80	0.0021973	0.0569014	-1.07	FALSE
249014_at	putative protein similar to unknov	---	AT5G44710	-1.96	-0.97	-4.79	0.0022056	0.0570407	-1.07	FALSE
263532_s_a	putative protein RIO1 protein, Sa	---	AT2G24990 ///	-2.12	-1.08	-4.79	0.0022185	0.0570504	-1.08	TRUE
259160_at	unknown protein	---	AT3G05410	-1.82	-0.86	-4.79	0.0022091	0.0570504	-1.07	FALSE
250724_at	harpin-induced protein-like	---	AT5G06330	2.46	1.30	4.79	0.0022177	0.0570504	-1.07	FALSE
265353_at	unknown protein ;supported by f	---	AT2G16800	-1.57	-0.65	-4.79	0.0022148	0.0570504	-1.07	FALSE
254727_at	hypothetical protein	PTAC5	AT4G13670	-1.55	-0.63	-4.79	0.0022169	0.0570504	-1.07	FALSE
254228_at	putative protein ; supported by fu	---	AT4G23620	-1.70	-0.77	-4.79	0.0022224	0.0570866	-1.08	FALSE
251184_at	small nuclear ribonucleoprotein-	---	AT3G62840	-1.54	-0.62	-4.78	0.0022399	0.0573628	-1.09	FALSE
260648_at	unknown protein	---	AT1G08050	2.60	1.38	4.78	0.0022361	0.0573628	-1.08	FALSE
266608_at	hypothetical protein predicted by	---	AT2G35500	-2.07	-1.05	-4.78	0.0022407	0.0573628	-1.09	FALSE
251039_at	putative protein hypothetical pro	---	AT5G02020	-3.73	-1.90	-4.78	0.002244	0.0573818	-1.09	FALSE
261696_at	unknown protein similar to hypotl	---	AT1G08470	-2.30	-1.20	-4.78	0.0022492	0.057452	-1.09	FALSE
261428_at	isochorismate synthase, putative	ICS2	AT1G18870	2.42	1.28	4.78	0.0022546	0.0574596	-1.09	FALSE
261107_at	unknown protein ; supported by c	---	AT1G63010	1.65	0.73	4.78	0.0022539	0.0574596	-1.09	FALSE
262600_at	unknown protein ESTs gb|H370	MBD10	AT1G15340	-2.15	-1.11	-4.77	0.0022605	0.0575228	-1.09	FALSE
259491_at	chlorophyll binding protein, puta	LHCB6	AT1G15820	-1.82	-0.87	-4.77	0.0022632	0.0575228	-1.10	FALSE
266648_at	putative trytophanyl-tRNA synthe	OVA4	AT2G25840	-1.63	-0.71	-4.77	0.0022646	0.0575228	-1.10	FALSE
258712_s_a	putative 40S ribosomal protein S	---	AT3G09680 ///	-1.97	-0.98	-4.77	0.0022677	0.0575386	-1.10	FALSE
258090_at	putative 60S ribosomal protein L	---	AT3G14600	-2.11	-1.07	-4.77	0.0022715	0.0575692	-1.10	FALSE
258585_at	unknown protein C-term similar t	emb2458	AT3G04340	-1.68	-0.75	-4.77	0.0022742	0.0575738	-1.10	FALSE
261942_at	unknown protein similar to putati	AGL87	AT1G22590	-2.85	-1.51	-4.77	0.0022791	0.057634	-1.10	FALSE
267147_at	putative anthocyanidin synthase	---	AT2G38240	9.88	3.30	4.76	0.0022876	0.0577255	-1.11	TRUE
244998_at	RNA polymerase beta' subunit-1	---	---	-2.08	-1.05	-4.76	0.0022878	0.0577255	-1.11	FALSE
253386_at	sulfolipid biosynthesis protein SQ	SQD1	AT4G33030	-2.14	-1.10	-4.76	0.0022952	0.0577782	-1.11	FALSE
258553_at	hypothetical protein ; supported	PDE320	AT3G06960	-1.62	-0.70	-4.76	0.0023037	0.0577782	-1.11	FALSE
261588_at	hypothetical protein predicted by	---	AT1G01670	-1.54	-0.62	-4.75	0.0023121	0.0577782	-1.12	FALSE
255857_at	unknown protein ;supported by fu	ABA4	AT1G67080	-1.57	-0.65	-4.75	0.0023124	0.0577782	-1.12	FALSE

266192_at	unknown protein	---	AT2G39080	-1.56	-0.65	-4.76	0.0023039	0.0577782	-1.11	FALSE
246159_at	Expressed protein ; supported by	---	AT5G20935	-2.75	-1.46	-4.76	0.0022998	0.0577782	-1.11	FALSE
259701_at	unknown protein similar to GB:A	---	AT1G77770	1.96	0.97	4.75	0.0023126	0.0577782	-1.12	FALSE
265059_at	unknown protein ; supported by	AR791	AT1G52080	2.08	1.06	4.76	0.0022924	0.0577782	-1.11	FALSE
266018_at	putative preprotein translocase	SCY1	AT2G18710	-1.60	-0.68	-4.76	0.0023052	0.0577782	-1.11	FALSE
248299_at	unknown protein ;supported by	---	AT5G53080	-1.72	-0.78	-4.74	0.0023342	0.0580751	-1.13	FALSE
245422_at	putative protein	---	AT4G17470	5.92	2.57	4.74	0.0023424	0.0580751	-1.13	FALSE
249268_at	Expressed protein ; supported by	---	AT5G41685	-1.62	-0.70	-4.75	0.0023276	0.0580751	-1.12	FALSE
250190_at	ribosomal protein precursor - lik	---	AT5G14320	-1.65	-0.72	-4.74	0.0023364	0.0580751	-1.13	FALSE
245348_at	trehalose-6-phosphate synthase	ATTPS5	AT4G17770	-2.14	-1.10	-4.74	0.0023326	0.0580751	-1.13	FALSE
254376_at	putative protein ; supported by	TOM1	AT4G21790	1.52	0.61	4.74	0.0023417	0.0580751	-1.13	FALSE
262823_at	ATP-dependent Clp protease pro	CLPP6	AT1G11750	-1.68	-0.75	-4.74	0.0023406	0.0580751	-1.13	FALSE
258995_at	putative ribosomal protein L13 si	---	AT3G01790	-2.18	-1.13	-4.74	0.0023475	0.0581399	-1.13	FALSE
264514_at	putative cinnamyl alcohol dehyd	---	AT1G09500	15.14	3.92	4.72	0.0023953	0.0581903	-1.15	TRUE
265326_at	unknown protein predicted by ge	---	AT2G18220	-2.10	-1.07	-4.72	0.0023907	0.0581903	-1.15	TRUE
256890_at	glycine-rich RNA binding protein	GRP4	AT3G23830	-3.24	-1.70	-4.73	0.0023849	0.0581903	-1.15	FALSE
248515_at	putative protein strong similarity	---	AT5G50530 ///	1.83	0.87	4.73	0.0023636	0.0581903	-1.14	FALSE
260805_at	glutathione transferase, putative	ATGSTU23	AT1G78320	-1.57	-0.65	-4.73	0.0023784	0.0581903	-1.15	FALSE
258333_at	myosin heavy chain-like protein	MFP1	AT3G16000	-1.72	-0.78	-4.72	0.0023883	0.0581903	-1.15	FALSE
252566_at	cytoplasmic ribosomal protein S	RPS15AD	AT3G46040	-2.02	-1.01	-4.74	0.0023562	0.0581903	-1.14	FALSE
245852_at	ribosomal protein L10-like ribos	---	AT5G13510	-1.94	-0.96	-4.73	0.0023838	0.0581903	-1.15	FALSE
252759_at	putative protein hypothetical prot	---	AT3G42630	-1.52	-0.61	-4.73	0.0023766	0.0581903	-1.15	FALSE
258366_at	DNA-binding protein contains AF	RAP2.2	AT3G14230	-1.79	-0.84	-4.72	0.0023909	0.0581903	-1.15	FALSE
248230_at	putative protein similar to unknov	---	AT5G53830	2.92	1.55	4.72	0.0023946	0.0581903	-1.15	FALSE
246154_at	putative protein predicted protei	---	AT5G19940	-1.69	-0.76	-4.72	0.0023955	0.0581903	-1.15	FALSE
262398_at	hypothetical protein predicted by	---	AT1G49350	-1.55	-0.63	-4.73	0.002372	0.0581903	-1.14	FALSE
251970_at	glucosyltransferase - like protein	UGT73D1	AT3G53150	2.54	1.34	4.73	0.0023676	0.0581903	-1.14	FALSE
247673_at	tRNA intron endonuclease - like	SEN2	AT5G60230	-1.53	-0.61	-4.73	0.0023633	0.0581903	-1.14	FALSE
260220_at	putative MYB family transcription	MYB31	AT1G74650	-2.23	-1.16	-4.73	0.002378	0.0581903	-1.15	FALSE
267637_at	unknown protein predicted by ge	---	AT2G42190	-2.26	-1.18	-4.73	0.0023854	0.0581903	-1.15	FALSE
250727_at	putative protein similar to unknov	---	AT5G06430	-1.61	-0.68	-4.73	0.0023839	0.0581903	-1.15	FALSE
254620_at	pollen-specific protein - like 18.3	---	AT4G18590	-1.74	-0.80	-4.72	0.0024004	0.0582485	-1.16	FALSE
248678_at	U6 snRNA-associated Sm-like pr	SAD1	AT5G48870	-1.77	-0.83	-4.72	0.0024043	0.0582797	-1.16	FALSE
266141_at	protease inhibitor II contains a ga	PDF2.1	AT2G02120	1.60	0.68	4.71	0.0024155	0.0584361	-1.16	FALSE
248459_at	putative protein similar to unknov	CRL	AT5G51020	-1.70	-0.77	-4.71	0.0024158	0.0584361	-1.16	FALSE

247193_at	putative protein strong similarity t	---	AT5G65380	2.09	1.06	4.71	0.0024191	0.058452	-1.16	FALSE
264953_at	alcohol dehydrogenase identical	ADH1	AT1G77120	2.06	1.04	4.71	0.0024256	0.0584958	-1.17	TRUE
263432_at	putative beta-hydroxyacyl-ACP d	---	AT2G22230	-1.99	-1.00	-4.71	0.002426	0.0584958	-1.17	FALSE
260412_at	putative alpha-amylase similar to	AMY3	AT1G69830	-1.54	-0.62	-4.71	0.0024336	0.0585549	-1.17	FALSE
250532_at	putative protein similar to unknov	---	AT5G08540	-1.87	-0.90	-4.71	0.0024395	0.0585549	-1.17	FALSE
260264_at	hypothetical protein predicted by	---	AT1G68500	-2.13	-1.09	-4.71	0.0024338	0.0585549	-1.17	FALSE
265034_at	unknown protein ;supported by fu	---	AT1G61660	1.82	0.86	4.70	0.0024413	0.0585549	-1.17	FALSE
258599_at	L-allo-threonine aldolase, putativ	THA2	AT3G04520	2.38	1.25	4.71	0.0024389	0.0585549	-1.17	FALSE
250784_at	unknown protein ; supported by c	---	AT5G05480	-1.91	-0.94	-4.70	0.0024471	0.0586336	-1.18	FALSE
251995_at	nuclear envelope membrane pro	FK	AT3G52940	-1.59	-0.67	-4.70	0.0024524	0.058637	-1.18	FALSE
244935_at	NADH dehydrogenase subunit	---	---	-1.64	-0.72	-4.70	0.0024515	0.058637	-1.18	FALSE
259300_at	hypothetical protein predicted by	---	AT3G05100	-1.67	-0.74	-4.70	0.002458	0.0586471	-1.18	FALSE
249234_at	putative protein similar to unknov	---	AT5G42200	-2.66	-1.41	-4.70	0.0024575	0.0586471	-1.18	FALSE
260718_at	unknown protein	ECT7	AT1G48110	1.50	0.58	4.69	0.0024696	0.0588618	-1.18	FALSE
246083_at	zinc finger protein - like probable	AL5	AT5G20510	-1.62	-0.70	-4.69	0.002492	0.0590195	-1.19	FALSE
250735_at	putative protein similar to unknov	---	AT5G06280	-1.71	-0.77	-4.69	0.0024943	0.0590195	-1.20	FALSE
249222_at	putative protein similar to unknov	---	AT5G42450	-1.53	-0.61	-4.69	0.0024931	0.0590195	-1.19	FALSE
255887_at	hypothetical protein contains Pfa	---	AT1G20370	-1.58	-0.66	-4.69	0.0024935	0.0590195	-1.19	FALSE
261037_at	lipoxygenase identical to GB:CAI	LOX3	AT1G17420	12.07	3.59	4.69	0.0024934	0.0590195	-1.19	FALSE
265663_at	unknown protein predicted by ge	---	AT2G24290	-1.82	-0.86	-4.69	0.0024929	0.0590195	-1.19	FALSE
264648_at	putative luminal binding protein S	BIP3	AT1G09080	2.00	1.00	4.69	0.0024805	0.0590195	-1.19	FALSE
260236_at	geranylgeranyl reductase identic	---	AT1G74470	-1.55	-0.63	-4.68	0.0024991	0.0590719	-1.20	FALSE
246824_at	drought-induced protein - like no	---	AT5G26990	1.59	0.67	4.68	0.0025188	0.0592319	-1.21	FALSE
253782_at	hypothetical protein	---	AT4G28590	-1.54	-0.63	-4.68	0.0025142	0.0592319	-1.20	FALSE
255447_at	hypothetical protein similar to A.	---	AT4G02790	-2.67	-1.42	-4.68	0.0025166	0.0592319	-1.20	FALSE
262000_at	Expressed protein ; supported by	---	AT1G33810	-1.84	-0.88	-4.68	0.0025142	0.0592319	-1.20	FALSE
266863_at	putative ripening-associated prot	ATCDPMEI	AT2G26930	-1.63	-0.71	-4.68	0.0025188	0.0592319	-1.21	FALSE
252319_at	putative protein putative protein	---	AT3G48710	-2.10	-1.07	-4.67	0.0025313	0.0592519	-1.21	TRUE
245248_at	Expressed protein ; supported by	ATB' GAMM	AT4G15415	-1.47	-0.56	-4.67	0.0025266	0.0592519	-1.21	FALSE
259871_at	nodulin-like protein similar to noc	---	AT1G76800	-3.55	-1.83	-4.67	0.0025314	0.0592519	-1.21	FALSE
256943_at	hypothetical protein similar to hyp	---	AT3G18910	-1.60	-0.67	-4.68	0.0025224	0.0592519	-1.21	FALSE
248595_at	drought-induced protein Di19-like	HRB1	AT5G49230	-1.75	-0.80	-4.67	0.0025327	0.0592519	-1.21	FALSE
250856_at	putative protein salt-inducible pr	---	AT5G04810	-1.94	-0.95	-4.67	0.0025465	0.0593918	-1.22	FALSE
249470_at	putative protein predicted protei	---	AT5G39350	-1.89	-0.92	-4.67	0.0025458	0.0593918	-1.22	FALSE
246237_at	putative protein	---	AT4G36390	-1.82	-0.86	-4.67	0.0025441	0.0593918	-1.22	FALSE

259889_at	predicted protein ; supported by	---	AT1G76405	-2.13	-1.09	-4.66	0.0025546	0.0595213	-1.22	FALSE
265569_at	unknown protein ;supported by f	PGR5	AT2G05620	-1.71	-0.77	-4.66	0.0025602	0.0595905	-1.22	FALSE
261161_at	hypothetical protein contains Pfa	---	AT1G34420	2.52	1.33	4.66	0.0025634	0.0596025	-1.22	FALSE
256600_at	hypothetical protein predicted by	---	AT3G14850	5.98	2.58	4.66	0.0025716	0.0597345	-1.23	FALSE
245565_at	hypothetical protein	---	AT4G14605	-1.75	-0.81	-4.65	0.0025909	0.0600583	-1.23	FALSE
262283_at	unknown protein ;supported by fu	---	AT1G68590	-2.02	-1.01	-4.65	0.0025896	0.0600583	-1.23	FALSE
265258_at	hypothetical protein predicted by	---	AT2G20390	-1.55	-0.63	-4.65	0.0025942	0.0600659	-1.24	FALSE
250937_at	putative protein various predicte	---	AT5G03230	-2.50	-1.32	-4.65	0.0025964	0.0600659	-1.24	FALSE
261435_at	GTP-binding protein, putative sir	---	AT1G07615 /	-2.45	-1.29	-4.65	0.0026009	0.0600917	-1.24	FALSE
262346_at	unknown protein similar to hypotl	---	AT1G63980	-2.03	-1.02	-4.65	0.0026038	0.0600917	-1.24	FALSE
249779_at	putative protein similar to unknov	---	AT5G24230	1.61	0.68	4.65	0.0026055	0.0600917	-1.24	FALSE
250287_at	putative protein AP2 domain cor	Rap2.6L	AT5G13330	2.23	1.16	4.64	0.0026202	0.0601245	-1.25	TRUE
266579_at	putative small nuclear ribonucleo	SNRNP-G	AT2G23930	-1.91	-0.94	-4.64	0.0026188	0.0601245	-1.24	TRUE
265314_at	hypothetical protein predicted by	---	AT2G20210	-1.77	-0.82	-4.64	0.0026277	0.0601245	-1.25	FALSE
251206_at	putative protein various predicte	---	AT3G63090	-2.22	-1.15	-4.64	0.002628	0.0601245	-1.25	FALSE
262062_s_a	hypothetical protein	emb1427	AT1G20570 /	-1.72	-0.78	-4.64	0.0026235	0.0601245	-1.25	FALSE
252975_s_a	putative protein other predicted p	ROPGEF1	AT4G38430	-1.63	-0.70	-4.64	0.0026196	0.0601245	-1.25	FALSE
260068_at	putative calmodulin-binding prote	---	AT1G73805	5.23	2.39	4.64	0.0026224	0.0601245	-1.25	FALSE
257763_s_a	disease resistance protein, puta	AtRLP37	AT3G23110 /	4.86	2.28	4.64	0.0026151	0.0601245	-1.24	FALSE
253381_at	Tic22 -like protein strong homol	---	AT4G33350	-1.80	-0.85	-4.64	0.0026363	0.0602538	-1.25	FALSE
256249_at	26S proteasome regulatory subu	MEE34	AT3G11270	-1.72	-0.78	-4.63	0.0026471	0.0603815	-1.26	FALSE
254910_at	translation initiation factor IF-1, p	---	AT4G11175	-1.58	-0.66	-4.63	0.0026449	0.0603815	-1.26	FALSE
254952_at	UDP-galactose 4-epimerase - lik	UGE5	AT4G10955 /	1.84	0.88	4.63	0.0026622	0.0604478	-1.26	FALSE
251664_at	leucine zipper-containing protein	CRD1	AT3G56940	-1.83	-0.87	-4.63	0.0026602	0.0604478	-1.26	FALSE
254931_at	serine/threonine kinase-like prot	---	AT4G11460	-2.01	-1.01	-4.63	0.0026633	0.0604478	-1.26	FALSE
264926_at	cytochrome b5, putative similar t	CB5LP	AT1G60660	-1.69	-0.76	-4.63	0.002661	0.0604478	-1.26	FALSE
258173_at	putative protein kinase similar to	CERK1	AT3G21630	1.70	0.76	4.63	0.0026621	0.0604478	-1.26	FALSE
261071_at	unknown protein	---	AT1G07380	-1.90	-0.93	-4.63	0.0026676	0.0604848	-1.26	TRUE
261769_at	plastocyanin identical to plastocy	PETE1	AT1G76100	-1.89	-0.92	-4.62	0.0026907	0.0605088	-1.27	TRUE
256675_at	putative protein DNA-binding pro	---	AT3G52170	-2.74	-1.45	-4.62	0.0026856	0.0605088	-1.27	FALSE
266152_s_a	hypothetical protein predicted by	---	AT2G12050 /	1.58	0.66	4.62	0.0026925	0.0605088	-1.27	FALSE
251576_at	putative protein several hypothet	---	AT3G58200	-1.62	-0.69	-4.62	0.0026837	0.0605088	-1.27	FALSE
249331_at	50S ribosomal protein L27 ;supp	RPL27	AT5G40950	-1.71	-0.77	-4.62	0.0026843	0.0605088	-1.27	FALSE
263735_s_a	hypothetical protein predicted by	AGL50	AT1G59810 /	1.56	0.64	4.62	0.0026884	0.0605088	-1.27	FALSE
256143_at	40S ribosomal protein S7 homol	---	AT1G48830	-1.96	-0.97	-4.62	0.0026876	0.0605088	-1.27	FALSE

250061_at	chloroplast GrpE protein ; suppo	EMB1241	AT5G17710	-1.89	-0.92	-4.63	0.0026725	0.0605088	-1.27	FALSE
267014_at	unknown protein	---	AT2G39170	-1.50	-0.58	-4.62	0.0026883	0.0605088	-1.27	FALSE
259846_at	peptide transporter PTR2-B, put	---	AT1G72140	1.79	0.84	4.62	0.0027002	0.0605108	-1.28	FALSE
248409_at	putative protein contains similarit	LPA2	AT5G51540 /	-1.89	-0.92	-4.62	0.0027006	0.0605108	-1.28	FALSE
253866_at	putative protein various putative	---	AT4G27480	1.81	0.86	4.62	0.0026977	0.0605108	-1.28	FALSE
248920_at	magnesium chelatase subunit of	CHLI2	AT5G45930	-1.74	-0.80	-4.61	0.0027056	0.060564	-1.28	FALSE
259551_at	hypothetical protein	---	AT1G21190	-1.65	-0.73	-4.60	0.0027366	0.060572	-1.29	FALSE
259746_at	hypothetical protein predicted by	---	AT1G71060	-2.08	-1.05	-4.60	0.0027555	0.060572	-1.30	FALSE
252886_at	cellulose synthase catalytic subu	CESA2	AT4G39350	-1.80	-0.85	-4.60	0.0027487	0.060572	-1.29	FALSE
266916_at	hypothetical protein predicted by	---	AT2G45860	-2.26	-1.18	-4.60	0.002737	0.060572	-1.29	FALSE
262136_at	auxin response factor, putative s	ARF17	AT1G77850	-1.63	-0.70	-4.61	0.0027096	0.060572	-1.28	FALSE
252055_at	putative ribosomal protein S14 r	---	AT3G52580	-1.91	-0.94	-4.61	0.0027287	0.060572	-1.29	FALSE
247815_at	ribosomal protein S4 - like ribos	---	AT5G58420	-2.19	-1.13	-4.61	0.0027336	0.060572	-1.29	FALSE
265336_at	hypothetical protein predicted by	APC10	AT2G18290	-1.61	-0.69	-4.60	0.0027377	0.060572	-1.29	FALSE
246240_at	nucleoporin-like protein	---	AT4G37130	-1.52	-0.60	-4.61	0.0027177	0.060572	-1.28	FALSE
252282_at	6-phosphogluconolactonase - lik	---	AT3G49360	-1.58	-0.66	-4.60	0.0027502	0.060572	-1.30	FALSE
255880_at	hypothetical protein predicted by	---	AT1G67060	1.61	0.69	4.61	0.0027284	0.060572	-1.29	FALSE
264870_at	hypothetical protein ;supported b	---	AT1G24210	-1.77	-0.83	-4.60	0.002738	0.060572	-1.29	FALSE
253257_at	extra-large G-protein - like extra	XLG2	AT4G34390	1.87	0.90	4.60	0.0027352	0.060572	-1.29	FALSE
249282_at	CMP-sialic acid transporter-like p	---	AT5G41760	-2.01	-1.01	-4.60	0.002752	0.060572	-1.30	FALSE
246768_at	putative protein hypothetical prot	---	AT5G27400	-1.48	-0.57	-4.60	0.002751	0.060572	-1.30	FALSE
257036_at	hypothetical protein predicted by	---	AT3G19120	-1.60	-0.68	-4.60	0.0027564	0.060572	-1.30	FALSE
263715_at	unknown protein ; supported by	GPRI1	AT2G20570	-1.68	-0.74	-4.61	0.0027272	0.060572	-1.29	FALSE
245924_at	Tha4 protein - like Tha4 protein,	---	AT5G28750	-1.57	-0.65	-4.60	0.0027554	0.060572	-1.30	FALSE
248770_at	unknown protein	---	AT5G47740	1.91	0.93	4.60	0.0027456	0.060572	-1.29	FALSE
267596_s_a	putative leucine-rich repeat disea	AtRLP26	AT2G33050 /	-3.82	-1.93	-4.60	0.0027645	0.0606252	-1.30	TRUE
258285_at	photosystem I subunit VI precurs	PSAH-1	AT3G16140	-1.56	-0.64	-4.59	0.0027668	0.0606252	-1.30	FALSE
256181_at	light repressible receptor protein	---	AT1G51820	5.31	2.41	4.60	0.0027619	0.0606252	-1.30	FALSE
264257_at	unknown protein	---	AT1G09230	-1.84	-0.88	-4.59	0.0027721	0.0606254	-1.30	TRUE
252325_at	acetolactate synthase ; supporte	CSR1	AT3G48560	-1.52	-0.60	-4.59	0.0027711	0.0606254	-1.30	FALSE
249472_at	hypothetical protein ;supported b	CRR7	AT5G39210	-2.51	-1.33	-4.59	0.0027756	0.0606442	-1.30	FALSE
255628_at	coded for by A. thaliana cDNA T4	GIF3	AT4G00850	-1.69	-0.76	-4.59	0.0027813	0.0607102	-1.31	FALSE
245761_at	hypothetical protein predicted by	---	AT1G66890	-1.69	-0.76	-4.59	0.0027955	0.0609606	-1.31	FALSE
253790_at	photosystem II protein W - like p	PSB28	AT4G28660	-2.43	-1.28	-4.58	0.0028129	0.0612827	-1.32	FALSE
257699_at	phosphoglycerate kinase, putati	PGK1	AT3G12780	-1.88	-0.91	-4.58	0.0028223	0.0614281	-1.32	FALSE

259105_at	stress related protein, putative s	---	AT3G05500	2.06	1.04	4.57	0.0028398	0.0614685	-1.33	FALSE
249047_at	berberine bridge enzyme-like pro	---	AT5G44410	-1.76	-0.81	-4.57	0.0028414	0.0614685	-1.33	FALSE
254269_at	putative serine/threonine kinase	---	AT4G23050	1.86	0.90	4.57	0.0028352	0.0614685	-1.33	FALSE
255457_at	putative photosystem I reaction	PSAD-1	AT4G02770	-1.52	-0.60	-4.58	0.0028292	0.0614685	-1.32	FALSE
261481_at	nucleoside triphosphatase, puta	---	AT1G14260	1.96	0.97	4.57	0.0028439	0.0614685	-1.33	FALSE
266896_at	putative ATP-dependent RNA he	---	AT2G45810	-1.53	-0.61	-4.57	0.0028457	0.0614685	-1.33	FALSE
246982_s_a	unknown protein	---	AT2G10560 ///	2.91	1.54	4.57	0.0028322	0.0614685	-1.33	FALSE
257253_at	unknown protein ; supported by	---	AT3G24190	-1.75	-0.81	-4.57	0.0028335	0.0614685	-1.33	FALSE
255627_at	Expressed protein ; supported by	---	AT4G00955	1.57	0.65	4.56	0.0028685	0.061549	-1.34	FALSE
247320_at	photosystem I reaction centre su	PSAN	AT5G64040	-1.65	-0.72	-4.57	0.0028633	0.061549	-1.34	FALSE
264390_at	putative DNA-binding protein Co	---	AT1G11950	-1.87	-0.90	-4.56	0.0028673	0.061549	-1.34	FALSE
256678_at	RNA-binding protein (cp33) iden	CP33	AT3G52380	-1.74	-0.80	-4.56	0.0028753	0.061549	-1.34	FALSE
260635_at	unknown protein	---	AT1G62420 ///	1.94	0.96	4.57	0.0028583	0.061549	-1.33	FALSE
252984_at	cinnamyl-alcohol dehydrogenase	ELI3-2	AT4G37990	5.11	2.35	4.56	0.0028685	0.061549	-1.34	FALSE
251230_at	beta-glucosidase-like protein sev	BGLU8	AT3G62750	-1.55	-0.63	-4.56	0.0028764	0.061549	-1.34	FALSE
253054_at	probable N-acetyltransferase hoo	HLS1	AT4G37580	-1.63	-0.71	-4.57	0.0028532	0.061549	-1.33	FALSE
249929_at	unknown protein	---	AT5G22340	-1.86	-0.90	-4.56	0.0028744	0.061549	-1.34	FALSE
259962_at	RNA polymerase II, putative sim	---	AT1G53690	-1.75	-0.81	-4.56	0.0028705	0.061549	-1.34	FALSE
265961_at	unknown protein ;supported by f	---	AT2G37400	-2.25	-1.17	-4.56	0.0028792	0.0615515	-1.34	TRUE
266271_at	putative glutathione S-transferas	ATGSTU6	AT2G29440	5.91	2.56	4.56	0.0028843	0.061587	-1.34	FALSE
245255_at	COP9 protein ; supported by cDN	COP9	AT4G14110	-1.70	-0.77	-4.56	0.0028863	0.061587	-1.34	FALSE
255660_at	Expressed protein ; supported by	---	AT4G00755	-1.79	-0.84	-4.56	0.0028928	0.0616109	-1.35	FALSE
257132_at	hypothetical protein predicted by	---	AT3G20230	-1.65	-0.72	-4.56	0.0028906	0.0616109	-1.35	FALSE
251185_at	60S RIBOSOMAL PROTEIN L7	---	AT3G62870	-1.98	-0.98	-4.56	0.002896	0.0616211	-1.35	FALSE
255886_at	plastocyanin, putative similar to	DRT112	AT1G20340	-1.60	-0.68	-4.55	0.0029016	0.0616828	-1.35	FALSE
253188_at	putative sugar transporter protei	TMT2	AT4G35300	-1.74	-0.80	-4.55	0.0029053	0.0617048	-1.35	FALSE
261750_at	hypothetical protein contains sim	---	AT1G76120	-1.87	-0.90	-4.55	0.0029135	0.0618036	-1.35	TRUE
254639_at	putative protein various predicte	DOT4	AT4G18750	-1.73	-0.79	-4.55	0.0029175	0.0618036	-1.36	FALSE
259303_at	hypothetical protein predicted by	---	AT3G05130	-1.46	-0.55	-4.55	0.0029181	0.0618036	-1.36	FALSE
250268_s_a	putative protein putative secrete	---	AT5G12950 ///	-2.04	-1.03	-4.55	0.0029249	0.0618313	-1.36	FALSE
267177_at	Expressed protein ; supported by	---	AT2G37580	2.37	1.25	4.55	0.0029238	0.0618313	-1.36	FALSE
253620_at	receptor-like kinase homolog so	---	AT4G30520	-1.75	-0.81	-4.54	0.0029309	0.061901	-1.36	FALSE
266716_at	unknown protein ;supported by f	PSI-P	AT2G46820	-1.71	-0.77	-4.54	0.002941	0.0619672	-1.36	FALSE
250966_at	putative protein various predicte	---	AT5G02910	-1.86	-0.90	-4.54	0.0029422	0.0619672	-1.36	FALSE
265679_at	putative myosin heavy chain ; su	---	AT2G32235 ///	1.73	0.79	4.54	0.0029406	0.0619672	-1.36	FALSE

256855_at	30S ribosomal protein S20 conta	---	AT3G15190	-1.88	-0.91	-4.53	0.0029666	0.0620478	-1.37	TRUE
250545_at	serine/threonine protein kinase ;	ATPK3	AT5G08160	1.58	0.66	4.54	0.0029628	0.0620478	-1.37	TRUE
248065_at	putative protein similar to unknov	---	AT5G55580	-2.00	-1.00	-4.53	0.0029755	0.0620478	-1.38	TRUE
249264_s_a	disease resistance protein-like	---	AT5G41740 ///	2.59	1.38	4.54	0.0029618	0.0620478	-1.37	TRUE
249210_at	unknown protein	---	AT5G42670	-1.56	-0.64	-4.53	0.002968	0.0620478	-1.37	FALSE
262112_at	unknown protein ;supported by fu	---	AT1G02870	-2.00	-1.00	-4.53	0.002985	0.0620478	-1.38	FALSE
250256_at	GTP-binding protein typA (tyrosir	---	AT5G13650	-1.63	-0.70	-4.53	0.0029653	0.0620478	-1.37	FALSE
252948_at	putative protein NLS receptor - (	KAK	AT4G38600	1.74	0.80	4.53	0.0029842	0.0620478	-1.38	FALSE
264717_at	hypothetical protein predicted by	ATFH8	AT1G70140	2.82	1.50	4.53	0.0029868	0.0620478	-1.38	FALSE
254280_at	Expressed protein ; supported by	SMO1-2	AT4G22756	-2.17	-1.12	-4.53	0.0029731	0.0620478	-1.37	FALSE
247034_at	cyclin D3-like protein ;supported	CYCD3;2	AT5G67260	-2.07	-1.05	-4.53	0.0029736	0.0620478	-1.38	FALSE
254244_at	putative protein S-receptor kinas	---	AT4G23230	1.82	0.86	4.53	0.0029799	0.0620478	-1.38	FALSE
246631_at	unknown protein ; supported by f	---	AT1G50740	1.61	0.68	4.54	0.0029588	0.0620478	-1.37	FALSE
266022_at	subtilisin-like serine protease, pu	---	AT2G05920	-2.21	-1.14	-4.54	0.0029565	0.0620478	-1.37	FALSE
247389_at	putative protein strong similarity t	---	AT5G63490	2.05	1.04	4.53	0.0029853	0.0620478	-1.38	FALSE
253980_at	sucrase-like protein sucrose clea	---	AT4G26620	-2.32	-1.21	-4.53	0.0029962	0.0621492	-1.38	TRUE
267102_at	putative small nuclear ribonucleo	LIS	AT2G41500	-1.74	-0.80	-4.53	0.0029971	0.0621492	-1.38	FALSE
246596_at	CARBONIC ANHYDRASE 2 ; su	CA2	AT5G14740	-1.64	-0.71	-4.52	0.0030183	0.0621494	-1.39	TRUE
265147_at	hypothetical protein	---	AT1G51380	-2.13	-1.09	-4.52	0.0030152	0.0621494	-1.39	TRUE
255278_at	putative WD-repeat membrane p	---	AT4G04940	-2.24	-1.17	-4.52	0.0030019	0.0621494	-1.38	TRUE
255465_at	hypothetical protein similar to A.	---	AT4G02990	-1.86	-0.90	-4.52	0.0030251	0.0621494	-1.39	TRUE
245926_at	VPS13 - like protein VPS13, Sac	---	AT5G24740	-1.69	-0.76	-4.52	0.0030271	0.0621494	-1.39	FALSE
261230_at	beta tubulin 1, putative similar to	TUB5	AT1G20010	-1.60	-0.68	-4.52	0.0030221	0.0621494	-1.39	FALSE
248163_at	auxin-responsive-like protein ; su	DFL1	AT5G54510	11.34	3.50	4.52	0.0030244	0.0621494	-1.39	TRUE
261923_at	UDP-glucose glucosyltransferas	AtUGT85A3	AT1G22380	1.77	0.83	4.52	0.0030058	0.0621494	-1.39	FALSE
246954_at	unknown protein ; supported by	---	AT5G04830	1.55	0.63	4.52	0.0030133	0.0621494	-1.39	FALSE
266052_at	putative WRKY-type DNA bindin	WRKY55	AT2G40740	2.62	1.39	4.52	0.0030237	0.0621494	-1.39	FALSE
251019_at	putative protein predicted protei	---	AT5G02420	1.74	0.80	4.52	0.0030131	0.0621494	-1.39	FALSE
262930_at	hypothetical protein similar to hir	---	AT1G65690	2.79	1.48	4.51	0.0030366	0.0622878	-1.40	TRUE
247139_at	unknown protein ;supported by f	---	AT5G66090	-1.70	-0.76	-4.51	0.0030418	0.0623399	-1.40	FALSE
257294_at	non-phototropic hypocotyl protei	---	AT3G15570	-2.25	-1.17	-4.51	0.0030469	0.0623676	-1.40	FALSE
257236_at	hypothetical protein	---	AT3G15095	-1.93	-0.95	-4.51	0.0030487	0.0623676	-1.40	FALSE
260968_at	hypothetical protein predicted by	---	AT1G12250	-1.82	-0.86	-4.51	0.0030602	0.0624581	-1.40	FALSE
258853_at	unknown protein similar to GB:A/	---	AT3G06440	-1.63	-0.71	-4.51	0.0030613	0.0624581	-1.40	FALSE
251815_at	putative protein thioredoxin-like	CXIP1	AT3G54900	-1.82	-0.87	-4.51	0.0030611	0.0624581	-1.40	FALSE

245616_at	kinase like protein	---	AT4G14480	-2.63	-1.40	-4.50	0.0030704	0.0625875	-1.41	FALSE
246261_at	unknown protein	---	AT1G31810	-1.72	-0.78	-4.50	0.0030752	0.0626306	-1.41	FALSE
245311_at	ribosomal protein ; supported by	---	AT4G14320	-2.20	-1.14	-4.50	0.0030809	0.0626898	-1.41	FALSE
266707_at	hypothetical protein predicted by	---	AT2G03310	-1.61	-0.69	-4.50	0.0030924	0.0628673	-1.42	FALSE
247027_at	subtilisin-like serine protease cor	---	AT5G67090	1.53	0.61	4.50	0.0031038	0.0629294	-1.42	FALSE
253410_at	putative protein various predicte	---	AT4G32970	-1.95	-0.96	-4.49	0.0031095	0.0629294	-1.42	TRUE
261337_at	unknown protein ; supported by	---	AT1G44810	-2.52	-1.33	-4.49	0.0031081	0.0629294	-1.42	TRUE
258426_at	hypothetical protein predicted by	PLDP1	AT3G16785	1.64	0.72	4.50	0.0031053	0.0629294	-1.42	FALSE
255789_at	60S ribosomal protein L23 ;supp	---	AT2G33370	-3.67	-1.88	-4.49	0.0031147	0.0629294	-1.42	FALSE
253971_at	fructose-bisphosphate aldolase	---	AT4G26530	-2.97	-1.57	-4.49	0.0031129	0.0629294	-1.42	FALSE
262340_at	Expressed protein ; supported by	ANAC027	AT1G64100 /	-1.59	-0.67	-4.50	0.0031001	0.0629294	-1.42	FALSE
252983_at	cinnamyl-alcohol dehydrogenase	ELI3-1	AT4G37980	2.51	1.33	4.49	0.0031227	0.0630336	-1.43	FALSE
254790_at	probable photosystem I chain XI	PSAL	AT4G12800	-1.57	-0.65	-4.49	0.0031294	0.0631022	-1.43	FALSE
261165_at	dihydrolipoamide S-acetyltransfe	EMB3003	AT1G34430	-1.68	-0.74	-4.49	0.0031316	0.0631022	-1.43	FALSE
266509_at	DegP2 protease identical to Deg	DEGP2	AT2G47940	-1.77	-0.83	-4.49	0.0031404	0.063223	-1.43	FALSE
254515_at	CLV1 receptor kinase like protei	BAM3	AT4G20270	-1.62	-0.70	-4.48	0.003153	0.0634207	-1.44	FALSE
258474_at	hypothetical protein predicted by	---	AT3G02650	-2.17	-1.12	-4.48	0.0031639	0.063528	-1.44	FALSE
251525_at	putative protein several hypothet	---	AT3G59000	-1.78	-0.83	-4.48	0.0031613	0.063528	-1.44	FALSE
266822_at	60S ribosomal protein L30 ;supp	---	AT2G44860	-2.09	-1.07	-4.48	0.0031769	0.0635819	-1.44	TRUE
249977_at	chaperonin 60 alpha chain - like	EMB3007	AT5G18820	-1.99	-0.99	-4.48	0.0031755	0.0635819	-1.44	TRUE
265680_at	putative hydrolase ; supported b	---	AT2G32150	2.46	1.30	4.48	0.0031731	0.0635819	-1.44	FALSE
259194_at	RNA helicase, DRH1 identical to	DRH1	AT3G01540	1.51	0.59	4.48	0.0031777	0.0635819	-1.44	FALSE
250383_at	putative GTP-binding protein GT	---	AT5G11480	-2.08	-1.06	-4.47	0.0031809	0.0635893	-1.44	FALSE
265865_at	hypothetical protein predicted by	---	AT2G01740	-1.53	-0.62	-4.47	0.0031955	0.0636089	-1.45	FALSE
253001_at	Expressed protein ; supported by	---	AT4G38490	-1.49	-0.57	-4.47	0.0031986	0.0636089	-1.45	FALSE
260651_at	hypothetical protein predicted by	---	AT1G32460	1.61	0.69	4.47	0.0032014	0.0636089	-1.45	FALSE
246576_at	hypothetical protein predicted by	ROPGEF14	AT1G31650	-1.51	-0.60	-4.47	0.0031971	0.0636089	-1.45	FALSE
249710_at	glutamate-ammonia ligase (EC	GS2	AT5G35630	-1.70	-0.76	-4.47	0.0031999	0.0636089	-1.45	FALSE
255733_at	unknown protein similar to unkno	---	AT1G25400	2.36	1.24	4.47	0.0031854	0.0636089	-1.45	FALSE
250994_at	dnaK-type molecular chaperone	---	AT5G02490	4.17	2.06	4.47	0.0031921	0.0636089	-1.45	FALSE
258317_at	hypothetical protein predicted by	---	AT3G22670	-1.60	-0.68	-4.47	0.0032058	0.0636423	-1.45	FALSE
247800_at	Expressed protein ; supported by	---	AT5G58570	-7.57	-2.92	-4.47	0.0032142	0.0636676	-1.45	FALSE
250483_at	alpha-hydroxynitrile lyase-like pr	MES5	AT5G10300	2.03	1.02	4.46	0.0032183	0.0636676	-1.46	FALSE
246387_at	hypothetical protein predicted by	---	AT1G77400	-1.96	-0.97	-4.47	0.0032128	0.0636676	-1.45	FALSE
266004_at	unknown protein predicted by ge	ALS3	AT2G37330	-1.51	-0.60	-4.46	0.0032174	0.0636676	-1.46	FALSE

265660_at	putative disease resistance prote	AtRLP21	AT2G25470	2.10	1.07	4.46	0.0032288	0.0638208	-1.46	FALSE
248219_at	unknown protein ; supported by	---	AT5G53650	-1.46	-0.54	-4.46	0.0032344	0.0638757	-1.46	FALSE
260498_at	putative AP2 domain transcriptio	---	AT2G41710	-1.87	-0.91	-4.45	0.0032586	0.0640955	-1.47	FALSE
251018_at	60S ribosomal protein - like 60S	---	AT5G02450	-2.08	-1.05	-4.45	0.0032625	0.0640955	-1.47	FALSE
245486_x_a	glycine-rich protein homolog	---	AT4G16240	1.65	0.72	4.45	0.0032605	0.0640955	-1.47	FALSE
266587_at	unknown protein ; supported by	---	AT2G14880	-1.78	-0.83	-4.45	0.0032586	0.0640955	-1.47	FALSE
264133_at	hypothetical protein predicted by	---	AT1G79080	-1.67	-0.74	-4.45	0.0032575	0.0640955	-1.47	FALSE
251885_at	fructose-bisphosphatase precurs	---	AT3G54050	-2.25	-1.17	-4.46	0.0032498	0.0640955	-1.47	FALSE
265699_at	putative esterase (contains an es	---	AT2G03550	-1.68	-0.75	-4.45	0.0032652	0.0640955	-1.47	FALSE
263491_at	phosphoenolpyruvate carboxylas	ATPPC2	AT2G42600	-1.75	-0.81	-4.45	0.0032689	0.0641133	-1.47	FALSE
252602_at	putative protein KIAA1094 prote	---	AT3G45040	1.76	0.81	4.45	0.0032799	0.0642739	-1.48	FALSE
250981_at	receptor like protein kinase rece	---	AT5G03140	-2.02	-1.01	-4.45	0.0032912	0.0643849	-1.48	FALSE
254710_at	multidrug resistance protein/P-g	PGP9	AT4G18050	2.37	1.25	4.45	0.0032894	0.0643849	-1.48	FALSE
253999_at	1-aminocyclopropane-1-carboxy	ACS7	AT4G26200	2.95	1.56	4.44	0.0032948	0.0643993	-1.48	FALSE
246339_at	RP19 gene for chloroplast riboso	RPL9	AT3G44890	-1.71	-0.78	-4.44	0.0032977	0.0644012	-1.48	FALSE
255872_at	putative protein kinase contains a	SIP4	AT2G30360	3.62	1.86	4.44	0.0033062	0.0644568	-1.48	FALSE
255706_at	putative ribosomal protein S13 si	ATRPS13A	AT4G00100	-2.16	-1.11	-4.44	0.0033062	0.0644568	-1.48	FALSE
263448_at	putative importin (nuclear transpo	SAD2	AT2G31660	-1.82	-0.86	-4.44	0.0033129	0.0645332	-1.49	FALSE
267184_at	unknown protein ; supported by	ASHH3	AT2G44150	-1.59	-0.67	-4.44	0.0033184	0.0645844	-1.49	FALSE
253268_s_a	glucosyltransferase -like protein	UGT73B2	AT4G34131 /.	2.54	1.35	4.44	0.003325	0.064658	-1.49	TRUE
264436_at	putative glutathione S-transferas	ERD9	AT1G10370	6.56	2.71	4.44	0.0033294	0.0646886	-1.49	TRUE
259232_at	unknown protein similar to hypot	---	AT3G11420	2.24	1.16	4.43	0.0033391	0.0648085	-1.49	TRUE
245244_at	IAA-amino acid hydrolase, putat	ILL6	AT1G44350	2.18	1.12	4.43	0.0033413	0.0648085	-1.49	TRUE
261090_at	protein kinase, putative contains	---	AT1G07560	1.79	0.84	4.43	0.0033511	0.0649439	-1.50	FALSE
262235_at	ribosomal protein L18, putative s	---	AT1G48350	-2.11	-1.08	-4.43	0.0033649	0.0649848	-1.50	TRUE
246988_at	putative protein strong similarity t	---	AT5G67340	3.51	1.81	4.42	0.0033772	0.0649848	-1.51	TRUE
255482_at	putative chloroplast outer envelo	TOC159	AT4G02510	-1.60	-0.68	-4.42	0.0033789	0.0649848	-1.51	FALSE
260165_at	30S ribosomal protein S17, chlo	RPS17	AT1G79850	-2.00	-1.00	-4.43	0.0033666	0.0649848	-1.50	FALSE
264383_at	putative glutathione peroxidase	ATGPX1	AT2G25080	-1.87	-0.90	-4.42	0.0033714	0.0649848	-1.50	FALSE
262753_at	putative 3-deoxy-D-manno-2-oct	ATKDSA2	AT1G16340	-1.62	-0.69	-4.42	0.0033769	0.0649848	-1.51	FALSE
245150_at	photolyase/blue-light receptor (P	PHR2	AT2G47590	-1.79	-0.84	-4.43	0.0033575	0.0649848	-1.50	FALSE
255047_at	AX110P -like protein AX110P -D	---	AT4G09670	-1.64	-0.72	-4.42	0.0033784	0.0649848	-1.51	FALSE
265618_at	hypothetical protein predicted by	---	AT2G25460	1.72	0.79	4.43	0.003364	0.0649848	-1.50	FALSE
265826_at	hypothetical protein predicted by	---	AT2G35795	-1.54	-0.62	-4.42	0.0033963	0.0651552	-1.51	FALSE
254750_at	putative protein	---	AT4G13150	-1.88	-0.91	-4.42	0.0033942	0.0651552	-1.51	FALSE

251496_at	putative protein crp1 protein, inv	---	AT3G59040	-1.57	-0.65	-4.42	0.0033907	0.0651552	-1.51	FALSE
246302_at	Ca2+/H+-exchanging protein-like	CAX3	AT3G51860	-4.95	-2.31	-4.42	0.003404	0.0651942	-1.51	TRUE
249235_at	beta-1,3-glucanase-like protein	BG_PPAP	AT5G42100	-1.45	-0.54	-4.42	0.0034025	0.0651942	-1.51	FALSE
261415_at	globulin-like protein similar to GB	---	AT1G07750	2.60	1.38	4.41	0.003413	0.0653108	-1.52	TRUE
259789_at	Expressed protein ; supported by	COR414-TI	AT1G29395	-1.74	-0.80	-4.41	0.0034163	0.0653184	-1.52	FALSE
254189_at	putative protein cellulose syntha	CSLG2	AT4G24000	4.20	2.07	4.41	0.0034264	0.0654579	-1.52	TRUE
260095_at	putative transcription factor BTF	---	AT1G73230	-2.11	-1.08	-4.41	0.0034304	0.0654799	-1.52	FALSE
261307_at	unknown protein similar to Glu-tF	GATB	AT1G48520	-1.59	-0.67	-4.41	0.0034379	0.0655163	-1.52	FALSE
251612_at	putative protein hypothetical pro	---	AT3G57950	1.67	0.74	4.41	0.0034381	0.0655163	-1.52	FALSE
246050_s_a	protein phosphatase 2A regulato	---	AT5G28850 /A	-1.49	-0.58	-4.41	0.0034428	0.0655516	-1.53	FALSE
250406_at	enhancer of rudimentary ; suppo	ER	AT5G10810	-2.04	-1.03	-4.40	0.0034507	0.0656474	-1.53	FALSE
257071_at	unknown protein ; supported by	ATCSLC04	AT3G28180	2.17	1.12	4.40	0.0034774	0.0658854	-1.54	TRUE
246623_at	nuM1 protein, putative similar to	ATNUC-L1	AT1G48920	-1.96	-0.97	-4.40	0.0034777	0.0658854	-1.54	TRUE
251997_at	60S ribosomal protein - like 60S	STV1	AT3G53020	-1.98	-0.98	-4.40	0.0034745	0.0658854	-1.53	FALSE
248231_at	putative protein contains similarit	---	AT5G53770	-1.73	-0.79	-4.40	0.00347	0.0658854	-1.53	FALSE
253095_at	putative protein ribonuclease III,	---	AT4G37510	-1.67	-0.74	-4.40	0.003469	0.0658854	-1.53	FALSE
263200_at	hypothetical protein predicted by	---	AT1G05600	-1.95	-0.96	-4.40	0.0034814	0.0659001	-1.54	FALSE
248952_at	putative protein similar to unknov	---	AT5G45410	1.75	0.80	4.39	0.0034977	0.0661	-1.54	FALSE
250080_at	translocon Tic40-like protein ; su	TIC40	AT5G16620	-1.51	-0.59	-4.39	0.0034958	0.0661	-1.54	FALSE
262412_at	14-3-3 protein GF14omicron (grf	GRF11	AT1G34760	-1.80	-0.85	-4.39	0.0035042	0.0661671	-1.54	FALSE
265704_at	hypothetical protein predicted by	---	AT2G03420	-2.06	-1.04	-4.39	0.0035165	0.0663455	-1.55	FALSE
250238_at	unknown protein	DCP2	AT5G13570	-1.60	-0.67	-4.39	0.0035222	0.0663975	-1.55	FALSE
257300_at	unknown protein ; supported by	---	AT3G28080	-2.46	-1.30	-4.39	0.0035255	0.0664054	-1.55	TRUE
261762_at	hypothetical protein predicted by	---	AT1G15510	-2.60	-1.38	-4.39	0.0035285	0.0664062	-1.55	TRUE
266682_at	putative disease resistance prote	---	AT2G19780	2.41	1.27	4.38	0.0035646	0.0664593	-1.56	TRUE
253740_at	Expressed protein ; supported by	---	AT4G28706	-1.80	-0.84	-4.38	0.0035607	0.0664593	-1.56	TRUE
260898_at	plastid ribosomal protein L34 pre	---	AT1G29070	-1.94	-0.95	-4.37	0.0035815	0.0664593	-1.57	TRUE
263122_at	prenyltransferase, putative simil	SPS1	AT1G78510	-1.82	-0.86	-4.38	0.0035525	0.0664593	-1.56	TRUE
264120_at	latex-abundant protein, putative	AtMC4	AT1G79340	1.51	0.59	4.38	0.0035395	0.0664593	-1.55	FALSE
245893_at	hypothetical protein ;supported b	---	AT5G09270	-1.62	-0.69	-4.38	0.0035417	0.0664593	-1.55	FALSE
257141_at	60S ribosomal protein L34, puta	---	AT3G28900	-2.51	-1.33	-4.37	0.0035779	0.0664593	-1.56	TRUE
248971_at	putative protein contains similarit	---	AT5G45000	2.20	1.14	4.37	0.0035768	0.0664593	-1.56	FALSE
263667_at	putative 40S ribosomal protein S	RPS15	AT1G04270	-1.94	-0.95	-4.38	0.0035524	0.0664593	-1.56	FALSE
253089_at	putative protein hypothetical pro	---	AT4G36290	-1.53	-0.62	-4.37	0.0035866	0.0664593	-1.57	FALSE
265777_at	hypothetical protein predicted by	---	AT2G07340	-1.56	-0.64	-4.38	0.0035687	0.0664593	-1.56	FALSE

246528_at	putative mitochondrial carrier pr	---	AT5G15640	2.36	1.24	4.37	0.003584	0.0664593	-1.57	FALSE
265186_at	Expressed protein ; supported by	---	AT1G23560	1.90	0.93	4.38	0.0035598	0.0664593	-1.56	FALSE
265819_at	Expressed protein ; supported by	---	AT2G17972	-1.78	-0.83	-4.38	0.0035464	0.0664593	-1.56	FALSE
250005_at	putative protein predicted protei	---	AT5G18760	-1.55	-0.63	-4.37	0.003575	0.0664593	-1.56	FALSE
246927_s_a	nodulin - like protein nodulin, Gl	---	AT5G25250 ///	2.35	1.23	4.37	0.0035811	0.0664593	-1.57	FALSE
263044_at	spore germination protein c2 sim	---	AT1G23360	-1.66	-0.73	-4.38	0.0035654	0.0664593	-1.56	FALSE
259499_at	PRLI-interacting factor L, putativ	---	AT1G15730	-1.88	-0.91	-4.37	0.0035773	0.0664593	-1.56	FALSE
257185_at	ABC transporter, putative similar	ATMRP7	AT3G13100	2.38	1.25	4.38	0.0035365	0.0664593	-1.55	FALSE
261651_at	unknown protein similar to unkno	SAT32	AT1G27760	2.66	1.41	4.37	0.0035897	0.0664612	-1.57	FALSE
246548_at	putative protein ;supported by fu	---	AT5G14910	-1.70	-0.76	-4.37	0.003593	0.0664697	-1.57	FALSE
252365_at	Expressed protein ; supported by	---	AT3G48350	3.34	1.74	4.37	0.0036105	0.0666558	-1.57	TRUE
259543_at	hypothetical protein ; supported b	---	AT1G20580	-1.76	-0.81	-4.37	0.0036109	0.0666558	-1.57	FALSE
264893_at	unknown protein similar to unkno	---	AT1G23140	1.86	0.90	4.37	0.0036119	0.0666558	-1.57	FALSE
249404_at	ankyrin repeat protein EMB506 ;	EMB506	AT5G40160	-1.94	-0.95	-4.36	0.0036244	0.0668326	-1.58	FALSE
250538_at	RNA helicase (emb|CAA09212.1	STRS2	AT5G08620	-2.29	-1.19	-4.36	0.0036389	0.0668976	-1.58	FALSE
245017_at	PSI I protein	---	---	-1.75	-0.80	-4.36	0.0036402	0.0668976	-1.58	FALSE
248235_at	unknown protein ;supported by fu	emb2737	AT5G53860	-1.50	-0.58	-4.36	0.0036426	0.0668976	-1.58	FALSE
266120_at	putative C2H2-type zinc finger pr	AtIDD5	AT2G02070	-1.70	-0.77	-4.36	0.0036338	0.0668976	-1.58	FALSE
264800_at	hypothetical protein similar to IFA	---	AT1G08800	1.83	0.87	4.36	0.0036355	0.0668976	-1.58	FALSE
254101_at	alpha-amylase - like protein alph	AMY1	AT4G25000	4.42	2.14	4.36	0.0036491	0.0669103	-1.59	TRUE
262505_at	unknown protein ESTs gb|N960	---	AT1G21680	-1.75	-0.81	-4.36	0.0036464	0.0669103	-1.58	FALSE
261034_s_a	hypothetical protein predicted by	---	AT1G17450 ///	-1.93	-0.95	-4.35	0.0036619	0.0670375	-1.59	FALSE
248956_at	unknown protein	---	AT5G45610	-1.66	-0.73	-4.35	0.003661	0.0670375	-1.59	FALSE
256979_at	Expressed protein ; supported by	PSBTN	AT3G09550 ///	-1.72	-0.78	-4.35	0.0036809	0.0672232	-1.59	FALSE
257044_at	hypothetical protein predicted by	ARC5	AT3G19720	-1.83	-0.87	-4.35	0.0036784	0.0672232	-1.59	FALSE
247131_at	ferredoxin-NADP+ reductase	FNR1	AT5G66190	-1.55	-0.64	-4.35	0.0036761	0.0672232	-1.59	FALSE
267509_at	MADS-box protein (AGL20) ; su	AGL20	AT2G45660	-2.05	-1.04	-4.35	0.0036898	0.0673322	-1.60	FALSE
255000_at	S18.A ribosomal protein ;suppor	RPS18C	AT4G09800	-2.10	-1.07	-4.35	0.0036945	0.0673485	-1.60	FALSE
260672_at	Expressed protein ; supported by	---	AT1G19480	-1.57	-0.65	-4.35	0.0036966	0.0673485	-1.60	FALSE
255365_at	putative phosphofructokinase be	MEE51	AT4G04040	-1.57	-0.65	-4.34	0.0037125	0.0673687	-1.60	FALSE
254038_at	nitrogen fixation like protein nitro	NFU3	AT4G25910	-1.54	-0.63	-4.34	0.0037097	0.0673687	-1.60	FALSE
252693_s_a	ribosomal protein S29 - like ribos	---	AT3G43980 ///	-1.59	-0.67	-4.34	0.0037099	0.0673687	-1.60	FALSE
261694_at	60S ribosomal protein L10A, put	---	AT1G08360	-2.02	-1.01	-4.34	0.0037112	0.0673687	-1.60	FALSE
250385_at	aspartate aminotransferase (Asp	ASP3	AT5G11520	2.61	1.39	4.34	0.0037067	0.0673687	-1.60	FALSE
264222_at	hypothetical protein predicted by	---	AT1G60230	-1.61	-0.69	-4.34	0.0037186	0.067425	-1.60	FALSE

259541_at	protein kinase, putative similar t	---	AT1G20650	-2.24	-1.16	-4.34	0.0037306	0.0675888	-1.61	FALSE
250454_at	unknown protein ; supported by	---	AT5G09830	-1.45	-0.53	-4.34	0.0037479	0.0677953	-1.61	FALSE
262380_at	threonine synthase, putative sim	---	AT1G72810	-1.73	-0.79	-4.34	0.0037451	0.0677953	-1.61	FALSE
252529_at	putative protein several oxidase	---	AT3G46490	4.29	2.10	4.33	0.003754	0.0677972	-1.61	TRUE
254623_at	protein ch-42 precursor, chlorop	CHLI1	AT4G18480	-1.96	-0.97	-4.33	0.0037514	0.0677972	-1.61	FALSE
252410_at	putative protein br-1 protein (NI	NOA1	AT3G47450	-1.84	-0.88	-4.33	0.0037621	0.0678902	-1.62	FALSE
261804_at	UDP glucose:flavonoid 3-o-gluc	UGT78D1	AT1G30530	2.13	1.09	4.33	0.0037799	0.0681572	-1.62	FALSE
244995_at	ATPase a subunit	---	---	-2.55	-1.35	-4.32	0.0037947	0.0683158	-1.63	TRUE
260283_at	hypothetical protein predicted by	PTAC17	AT1G80480	-1.47	-0.56	-4.33	0.0037919	0.0683158	-1.62	FALSE
267005_at	unknown protein ; supported by	---	AT2G34460	-1.63	-0.70	-4.32	0.0038018	0.0683363	-1.63	TRUE
254680_at	phytochrome E	PHYE	AT4G18130	-1.89	-0.92	-4.32	0.0038007	0.0683363	-1.63	FALSE
253758_at	Expressed protein ;supported by	emb2726	AT4G29060	-1.80	-0.85	-4.32	0.0038138	0.0684989	-1.63	FALSE
250823_at	putative protein similar to unknov	---	AT5G05180	-1.63	-0.71	-4.32	0.0038192	0.0685418	-1.63	FALSE
262852_at	hypothetical protein predicted by	---	AT1G20910	-1.59	-0.67	-4.32	0.0038302	0.0686313	-1.63	FALSE
249726_at	unknown protein	---	AT5G35480	-2.41	-1.27	-4.32	0.0038299	0.0686313	-1.63	FALSE
247933_at	putative protein non-consensus	---	AT5G56980	3.61	1.85	4.31	0.0038393	0.0687127	-1.64	FALSE
247216_at	4-alpha-glucanotransferase ; su	DPE1	AT5G64860	-1.95	-0.96	-4.31	0.0038408	0.0687127	-1.64	FALSE
257636_at	cytochrome P450, putative conta	CYP71B22	AT3G26200	3.20	1.68	4.31	0.0038481	0.0687143	-1.64	TRUE
245465_at	cellulose synthase like protein	ATCSLA01	AT4G16590	6.78	2.76	4.31	0.0038508	0.0687143	-1.64	FALSE
253762_at	putative protein conserved hypo	---	AT4G28830	-1.65	-0.72	-4.31	0.0038491	0.0687143	-1.64	FALSE
249910_at	chorismate mutase/prephenate d	ADT5	AT5G22630	4.29	2.10	4.31	0.0038529	0.0687143	-1.64	FALSE
247889_at	putative protein similar to unknov	APO2	AT5G57930	-1.65	-0.72	-4.31	0.0038574	0.0687409	-1.64	FALSE
253009_at	glycine hydroxymethyltransferas	SHM1	AT4G37930	-1.94	-0.96	-4.31	0.0038783	0.0690593	-1.65	FALSE
251130_at	oligopeptide transporter - like pr	PTR5	AT5G01180	1.53	0.61	4.30	0.0038881	0.0691024	-1.65	FALSE
251461_at	putative protein	---	AT3G59780	-1.84	-0.88	-4.30	0.0038874	0.0691024	-1.65	FALSE
259357_at	unknown protein ;supported by fu	---	AT1G13380	-1.78	-0.83	-4.30	0.0038899	0.0691024	-1.65	FALSE
251181_at	putative protein pectinesterase h	---	AT3G62820	1.88	0.91	4.30	0.003895	0.0691399	-1.65	FALSE
249842_at	putative protein contains similarit	---	AT5G23550	-1.55	-0.63	-4.30	0.0039206	0.0694867	-1.66	FALSE
259749_at	putative ribose 5-phosphate isom	RSW10	AT1G71100	2.75	1.46	4.30	0.0039186	0.0694867	-1.66	FALSE
251186_at	putative protein unknown protein	---	AT3G62790	-1.46	-0.55	-4.30	0.0039282	0.0695672	-1.66	FALSE
245158_at	hypothetical protein predicted by	RALFL18	AT2G33130	2.02	1.01	4.29	0.0039335	0.0696074	-1.66	FALSE
260682_at	hypothetical protein predicted by	---	AT1G17510	-1.61	-0.69	-4.29	0.003949	0.0697191	-1.67	FALSE
255902_at	transcription factor, putative sim	---	AT1G17880	-1.60	-0.68	-4.29	0.0039464	0.0697191	-1.67	FALSE
266867_at	putative signal recognition particl	CPFTSY	AT2G45770	-1.64	-0.71	-4.29	0.003945	0.0697191	-1.67	FALSE
258059_at	NAM-like protein (No Apical Mer	ATNAC3	AT3G29035	-2.17	-1.12	-4.29	0.003961	0.0698361	-1.67	TRUE

263320_at	putative galactinol synthase ;sup	AtGolS1	AT2G47180	4.84	2.27	4.29	0.0039618	0.0698361	-1.67	TRUE
264471_at	hypothetical protein predicted by	---	AT1G67120	-2.40	-1.27	-4.29	0.0039679	0.0698443	-1.67	TRUE
262610_at	putative mitochondrial uncoupling	---	AT1G14140	-1.46	-0.54	-4.29	0.0039697	0.0698443	-1.67	FALSE
250371_at	putative protein 23 kDa polypept	---	AT5G11450	-1.77	-0.82	-4.29	0.0039714	0.0698443	-1.67	FALSE
256512_at	Expressed protein ; supported by	---	AT1G33265	-1.79	-0.84	-4.29	0.0039781	0.0699073	-1.67	FALSE
254732_at	hypothetical protein	---	AT4G13750	-2.03	-1.02	-4.28	0.003984	0.0699371	-1.68	FALSE
265575_at	proline iminopeptidase identical t	PIP	AT2G14260	-1.56	-0.64	-4.28	0.0039906	0.0699371	-1.68	FALSE
248174_at	50S ribosomal protein L24, chlor	---	AT5G54600	-1.63	-0.71	-4.28	0.0039875	0.0699371	-1.68	FALSE
259841_at	unknown protein ; supported by f	---	AT1G52200	1.90	0.93	4.28	0.003992	0.0699371	-1.68	FALSE
260843_at	unknown protein similar to hypotl	---	AT1G29060	-1.45	-0.54	-4.28	0.0039968	0.0699672	-1.68	FALSE
248605_at	putative protein similar to unknov	---	AT5G49410	-2.20	-1.13	-4.28	0.0040075	0.0699734	-1.68	FALSE
245775_at	serine/threonine kinase, putative	CIPK23	AT1G30270	1.62	0.70	4.28	0.0040112	0.0699734	-1.68	FALSE
248713_at	putative protein contains similarit	NSP5	AT5G48180	2.94	1.55	4.28	0.0040016	0.0699734	-1.68	FALSE
259564_at	hypothetical protein	---	AT1G20540	-1.51	-0.60	-4.28	0.0040137	0.0699734	-1.68	FALSE
262411_at	hypothetical protein predicted by	---	AT1G34640	-1.67	-0.74	-4.28	0.0040063	0.0699734	-1.68	FALSE
245201_at	F12A21.3 unknown protein; sim	CSK	AT1G67840	-1.68	-0.75	-4.28	0.0040156	0.0699734	-1.68	FALSE
253484_at	Transcription factor II homolog ;	TAFII15	AT4G31720	-1.50	-0.58	-4.28	0.0040188	0.0699765	-1.68	FALSE
248338_at	HCF106 (gb|AAD32652.1) ; sup	HCF106	AT5G52440	-1.76	-0.82	-4.28	0.0040229	0.0699933	-1.69	FALSE
252723_at	hypothetical protein ; supported	---	AT3G43520	-1.49	-0.58	-4.27	0.0040273	0.0700166	-1.69	FALSE
246831_at	hexose transporter - like protein	MSS1	AT5G26340	2.32	1.21	4.27	0.0040419	0.0701105	-1.69	TRUE
260922_at	hypothetical protein predicted by	---	AT1G21560	-1.60	-0.68	-4.27	0.0040413	0.0701105	-1.69	FALSE
261646_at	putative lipase similar to hypothe	---	AT1G27690	-1.64	-0.71	-4.27	0.0040377	0.0701105	-1.69	FALSE
265726_at	putative inositol polyphosphate 5	---	AT2G32010	-1.99	-0.99	-4.27	0.004058	0.0702513	-1.69	FALSE
266881_at	putative casein kinase II beta sut	CKB4	AT2G44680	-1.62	-0.69	-4.27	0.0040582	0.0702513	-1.69	FALSE
245273_at	hypothetical protein ; supported b	---	AT4G14950	1.77	0.82	4.27	0.0040592	0.0702513	-1.69	FALSE
251916_at	transporter-like protein oligopept	---	AT3G53960	2.10	1.07	4.27	0.0040637	0.0702757	-1.70	FALSE
264205_at	hypothetical protein identical to h	---	AT1G22790	-1.52	-0.60	-4.27	0.0040709	0.0703461	-1.70	FALSE
251699_at	cytochrome P450-like protein cy	CYP94D2	AT3G56630	-1.66	-0.73	-4.26	0.0040782	0.0703637	-1.70	TRUE
249307_s_a	DNA excision repair cross-compl	XPB1	AT5G41360 /.	-1.63	-0.70	-4.26	0.0040825	0.0703637	-1.70	FALSE
257407_at	unknown protein	---	AT1G27100	1.59	0.67	4.26	0.004077	0.0703637	-1.70	FALSE
245003_at	PSII 43 KDa protein	---	---	-1.66	-0.73	-4.26	0.0040842	0.0703637	-1.70	FALSE
262942_at	hypothetical protein similar to un	ALIS5	AT1G79450	3.43	1.78	4.26	0.0041052	0.0703823	-1.71	FALSE
257007_at	Expressed protein ; supported by	---	AT3G14205	1.50	0.59	4.26	0.0041059	0.0703823	-1.71	FALSE
266554_s_a	eukaryotic translation initiation fa	---	AT2G46280 /.	-1.83	-0.87	-4.26	0.0041073	0.0703823	-1.71	FALSE
266703_at	unknown protein predicted by ge	---	AT2G19880	2.09	1.06	4.26	0.00411	0.0703823	-1.71	FALSE

248749_at	eukaryotic release factor 1 homo	ERF1-1	AT5G47880	1.51	0.60	4.26	0.0040932	0.0703823	-1.70	FALSE
263134_at	dTDP-glucose 4,6-dehydratase,	RHM1	AT1G78570	2.00	1.00	4.26	0.0040934	0.0703823	-1.70	FALSE
245009_at	ribosomal protein S4	---	---	-1.48	-0.56	-4.26	0.0041024	0.0703823	-1.71	FALSE
255151_at	putative protein oxysterol-bindin	ORP1C	AT4G08180	1.43	0.52	4.26	0.0041071	0.0703823	-1.71	FALSE
253912_at	putative protein met-10+ protein	---	AT4G27340	-1.77	-0.82	-4.25	0.0041288	0.0704931	-1.71	FALSE
260764_at	unknown protein	---	AT1G48950	-1.80	-0.85	-4.26	0.0041198	0.0704931	-1.71	FALSE
261713_at	protein kinase, putative identical	MYC2	AT1G32640	2.24	1.16	4.25	0.0041265	0.0704931	-1.71	FALSE
266400_at	methylenetetrahydrofolate dehyd	---	AT2G38660	1.49	0.58	4.25	0.0041261	0.0704931	-1.71	FALSE
253659_at	hypothetical protein	---	AT4G30150	-1.63	-0.70	-4.25	0.0041386	0.0705548	-1.71	FALSE
261614_at	poly(A)-binding protein, putative	PAB8	AT1G49760	-1.95	-0.97	-4.25	0.0041362	0.0705548	-1.71	FALSE
267078_at	unknown protein ;supported by f	---	AT2G40960	-1.61	-0.69	-4.25	0.0041542	0.0706353	-1.72	TRUE
249443_at	putative protein ; supported by c	---	AT5G39600	-1.90	-0.93	-4.25	0.00415	0.0706353	-1.72	FALSE
266767_at	Expressed protein ; supported by	---	AT2G46910	-1.88	-0.91	-4.25	0.0041557	0.0706353	-1.72	FALSE
253181_at	amino acid permease - like prote	LHT7	AT4G35180	7.83	2.97	4.25	0.0041539	0.0706353	-1.72	FALSE
249826_at	iron superoxide dismutase 3 (gb|	FSD3	AT5G23310	-1.97	-0.98	-4.25	0.0041648	0.0706837	-1.72	FALSE
250057_at	putative protein ; supported by fu	---	AT5G17840	-1.51	-0.59	-4.25	0.0041637	0.0706837	-1.72	FALSE
249786_at	putative protein strong similarity t	ABIL3	AT5G24310	-2.52	-1.33	-4.24	0.004177	0.0708378	-1.72	FALSE
266521_at	unknown protein ; supported by	---	AT2G24020	-1.52	-0.61	-4.24	0.0041812	0.0708562	-1.72	FALSE
255543_at	predicted protein of unknown fun	---	AT4G01870	3.77	1.92	4.24	0.0041915	0.0709389	-1.73	TRUE
247866_at	endoxyloglucan transferase (gb|A	XTR3	AT5G57550	4.78	2.26	4.24	0.0041923	0.0709389	-1.73	FALSE
245161_at	putative myrosinase binding prot	NSP2	AT2G33070	1.81	0.86	4.24	0.0042073	0.0711397	-1.73	FALSE
267497_at	putative glutaredoxin ;supported	---	AT2G30540	2.76	1.46	4.24	0.0042197	0.0712979	-1.73	TRUE
246060_at	rev interacting protein mis3 - like	---	AT5G08420	-1.49	-0.57	-4.24	0.0042241	0.0713194	-1.74	FALSE
265472_at	putative RING-H2 zinc finger pro	---	AT2G15580	-1.79	-0.84	-4.23	0.0042506	0.0715542	-1.74	FALSE
246453_at	syntaxin homologue ;supported	SYP21	AT5G16830	1.68	0.75	4.23	0.0042429	0.0715542	-1.74	FALSE
261582_at	unknown protein ; supported by c	GIF2	AT1G01160	-1.56	-0.64	-4.23	0.0042447	0.0715542	-1.74	FALSE
256659_at	unknown protein similar to putativ	---	AT3G12020	-1.64	-0.71	-4.23	0.0042486	0.0715542	-1.74	FALSE
255670_at	Expressed protein ; supported by	RHB1A	AT4G00335	-1.49	-0.58	-4.23	0.0042575	0.0715643	-1.74	FALSE
245183_at	putative protein similarity to pred	---	AT5G12440	-1.89	-0.92	-4.23	0.0042553	0.0715643	-1.74	FALSE
255600_s_a	putative protein predicted protein	---	AT4G01020 ///	-1.50	-0.58	-4.23	0.0042711	0.0715827	-1.75	FALSE
256542_at	unknown protein	PMI1	AT1G42550	-1.85	-0.89	-4.23	0.0042701	0.0715827	-1.75	FALSE
263209_at	Expressed protein ; supported by	---	AT1G10522	-2.59	-1.37	-4.23	0.0042694	0.0715827	-1.75	FALSE
266275_at	putative tropinone reductase	---	AT2G29370	-1.81	-0.85	-4.23	0.0042668	0.0715827	-1.75	FALSE
245987_at	NAM-like protein hypothetical pr	ANAC083	AT5G13180	1.69	0.76	4.22	0.0042844	0.0717055	-1.75	TRUE
250013_at	putative protein similar to unknov	---	AT5G18040	-1.55	-0.63	-4.22	0.0042854	0.0717055	-1.75	FALSE

257831_at	unknown protein ;supported by f	CCB1	AT3G26710	-1.77	-0.82	-4.22	0.0042879	0.0717055	-1.75	FALSE
261934_at	UDP-glucose glucosyltransferas	UGT85A1	AT1G22400	4.12	2.04	4.22	0.0042968	0.0718017	-1.75	FALSE
264835_at	unknown protein similar to unkno	---	AT1G03550	-1.44	-0.53	-4.22	0.0043094	0.0718587	-1.76	FALSE
263906_at	plastid division protein (FtsZ) ide	FTSZ2-1	AT2G36250	-1.71	-0.78	-4.22	0.0043096	0.0718587	-1.76	FALSE
260248_at	heat shock protein 101 (HSP101	ATHSP101	AT1G74310	2.63	1.40	4.22	0.0043035	0.0718587	-1.75	FALSE
248680_at	pantoate-beta-alanine ligase ;su	PANC	AT5G48840	-1.71	-0.77	-4.22	0.0043148	0.0718917	-1.76	FALSE
259835_at	unknown protein	TRZ3	AT1G52160	-1.57	-0.65	-4.21	0.004333	0.0720901	-1.76	FALSE
256130_at	unknown protein contains Pfam p	---	AT1G18170	-1.75	-0.80	-4.21	0.0043311	0.0720901	-1.76	FALSE
245138_at	unknown protein predicted by ge	AFO	AT2G45190	-2.21	-1.15	-4.21	0.0043469	0.0722695	-1.76	FALSE
265374_at	hypothetical protein ;supported b	PSBX	AT2G06520	-1.49	-0.58	-4.21	0.0043522	0.072305	-1.77	FALSE
250137_at	rRNA methylase - like protein rR	---	AT5G15390	-1.62	-0.70	-4.21	0.004367	0.0724976	-1.77	FALSE
247449_at	putative protein swelling-induce	---	AT5G62290	-2.30	-1.20	-4.20	0.0043805	0.0726688	-1.77	TRUE
245745_at	unknown protein contains similar	---	AT1G51110	-2.04	-1.03	-4.20	0.0043992	0.0728435	-1.78	FALSE
260403_at	hypothetical protein predicted by	WRKY36	AT1G69810	1.51	0.59	4.20	0.0044024	0.0728435	-1.78	FALSE
254535_at	aspartate kinase-homoserine de	AK-HSDH I	AT4G19710	-1.52	-0.61	-4.20	0.0044038	0.0728435	-1.78	FALSE
248124_at	putative protein contains similarit	ATG18F	AT5G54730	1.68	0.74	4.20	0.0044035	0.0728435	-1.78	FALSE
245137_at	unknown protein	---	AT2G45460	-1.87	-0.91	-4.20	0.004412	0.0729083	-1.78	FALSE
265760_at	unknown protein	---	AT2G01220	-1.63	-0.71	-4.20	0.0044173	0.0729083	-1.78	FALSE
245730_at	unknown protein ;supported by fu	---	AT1G73470	-1.55	-0.63	-4.20	0.0044161	0.0729083	-1.78	FALSE
246188_at	putative protein	---	AT5G21050	1.47	0.56	4.20	0.0044244	0.0729725	-1.78	FALSE
255960_at	unknown protein ; supported by c	---	AT1G22140	-1.84	-0.88	-4.19	0.004435	0.0730027	-1.79	FALSE
249128_at	1-aminocyclopropane-1-carboxyl	---	AT5G43440	-1.58	-0.66	-4.19	0.0044388	0.0730027	-1.79	FALSE
251833_at	putative protein various predicted	---	AT3G55160	-1.56	-0.64	-4.19	0.0044483	0.0730027	-1.79	FALSE
257374_at	hypothetical protein predicted by	---	AT2G43280	-1.94	-0.95	-4.19	0.0044458	0.0730027	-1.79	FALSE
248558_at	permease	---	AT5G49990	-2.15	-1.10	-4.19	0.0044487	0.0730027	-1.79	FALSE
256438_s_a	ribosomal protein L41 identical to	---	AT2G40205 ///	-2.82	-1.50	-4.19	0.0044333	0.0730027	-1.79	FALSE
263543_at	putative pectinesterase	PE11	AT2G21610	1.50	0.58	4.19	0.0044449	0.0730027	-1.79	FALSE
255650_s_a	hypothetical protein	CIP4.1	AT4G00930 ///	-1.75	-0.80	-4.19	0.0044592	0.0730182	-1.79	FALSE
253336_at	putative protein Caenorhabditis	EIF3K	AT4G33250	-1.67	-0.74	-4.19	0.0044577	0.0730182	-1.79	FALSE
258610_at	IAA-amino acid hydrolase (ILR1)	ILR1	AT3G02875	2.35	1.23	4.19	0.0044548	0.0730182	-1.79	FALSE
252269_at	putative protein ;supported by fu	LSU1	AT3G49580	-3.82	-1.93	-4.19	0.0044643	0.0730498	-1.79	FALSE
248850_at	putative protein contains similarit	---	AT5G46550	-1.64	-0.71	-4.19	0.0044694	0.0730798	-1.79	FALSE
256107_at	hypothetical protein predicted by	---	AT1G16830	-1.51	-0.60	-4.18	0.0044892	0.0731934	-1.80	FALSE
262607_at	unknown protein ;supported by fu	---	AT1G13990	1.81	0.85	4.18	0.0044881	0.0731934	-1.80	FALSE
255844_at	putative protein kinase contains a	---	AT2G33580	2.81	1.49	4.18	0.0044875	0.0731934	-1.80	FALSE

256813_at	unknown protein	---	AT3G21360	-1.64	-0.71	-4.19	0.0044829	0.0731934	-1.80	FALSE
262345_at	hypothetical protein similar to hyp	---	AT1G64180	-1.67	-0.74	-4.18	0.0044927	0.0731986	-1.80	FALSE
266699_at	putative ribosomal protein L28 ;	---	AT2G19730	-2.15	-1.11	-4.18	0.0045082	0.0733463	-1.80	FALSE
259050_at	hypothetical protein similar to GB	---	AT3G03356 ///	1.44	0.52	4.18	0.0045063	0.0733463	-1.80	FALSE
249071_at	putative protein similar to unknov	---	AT5G44050	3.26	1.70	4.18	0.0045158	0.0733642	-1.80	TRUE
248102_at	putative protein contains similarit	---	AT5G55140	-1.94	-0.96	-4.18	0.0045254	0.0733642	-1.81	FALSE
246322_at	S-locus protein, putative similar	---	AT1G16680	-1.55	-0.63	-4.18	0.004517	0.0733642	-1.80	FALSE
262839_at	PhD-finger protein, putative cont	---	AT1G14770	-2.27	-1.18	-4.18	0.004525	0.0733642	-1.81	FALSE
263494_at	14-3-3 protein GF14mu (grf9) id	GRF9	AT2G42590	-1.51	-0.60	-4.18	0.0045237	0.0733642	-1.81	FALSE
244974_at	PSII low MW protein	---	---	-1.60	-0.68	-4.18	0.0045321	0.0734209	-1.81	FALSE
248418_at	cleavage and polyadenylation sp	CPSF160	AT5G51660	-1.65	-0.72	-4.18	0.0045396	0.0734387	-1.81	FALSE
267140_at	putative GT-1-like transcription fa	---	AT2G38250	2.36	1.24	4.18	0.0045393	0.0734387	-1.81	FALSE
259690_at	replication factor, putative simila	---	AT1G63160	-2.13	-1.09	-4.17	0.0045728	0.0735066	-1.82	TRUE
246681_at	chloride channel-like protein chl	---	AT5G33280	-1.50	-0.58	-4.17	0.0045521	0.0735066	-1.81	FALSE
247156_at	lysosomal Pro-X carboxypeptidas	---	AT5G65760	-1.62	-0.70	-4.17	0.0045722	0.0735066	-1.82	FALSE
265119_at	flavin-containing monooxygenas	FMO GS-O	AT1G62570	2.76	1.47	4.17	0.0045726	0.0735066	-1.82	FALSE
257600_at	hypothetical protein predicted by	CLE41	AT3G24770	1.79	0.84	4.17	0.0045641	0.0735066	-1.82	FALSE
250264_at	glucosyltransferase -like protein	---	AT5G12890	1.43	0.52	4.17	0.0045511	0.0735066	-1.81	FALSE
263515_at	unknown protein	---	AT2G21640	5.10	2.35	4.17	0.0045713	0.0735066	-1.82	FALSE
255068_at	Arabidopsis thaliana flavin-type	CRY1	AT4G08920	-1.45	-0.54	-4.17	0.0045602	0.0735066	-1.81	FALSE
258263_at	unknown protein	---	AT3G15780	-2.31	-1.21	-4.17	0.004557	0.0735066	-1.81	FALSE
266938_at	hypothetical protein predicted by	HPT1	AT2G18950	1.79	0.84	4.16	0.0046041	0.0737945	-1.82	TRUE
265931_at	unknown protein ;supported by f	---	AT2G18520	-1.85	-0.88	-4.16	0.0046069	0.0737945	-1.82	FALSE
248287_at	putative protein similar to unknov	---	AT5G52970	-1.98	-0.99	-4.16	0.0046067	0.0737945	-1.82	FALSE
252199_at	anthranilate N-hydroxycinnamoy	---	AT3G50270	-1.73	-0.79	-4.16	0.0045993	0.0737945	-1.82	FALSE
257642_at	putative HLH DNA-binding protei	BHLH32	AT3G25710	-1.80	-0.85	-4.16	0.0046067	0.0737945	-1.82	FALSE
260430_at	putative zinc finger protein simila	---	AT1G68200	1.49	0.58	4.16	0.0046129	0.0738092	-1.83	FALSE
265582_at	putative RING zinc finger protein	---	AT2G20030	1.74	0.80	4.16	0.0046143	0.0738092	-1.83	FALSE
267378_at	hypothetical protein	---	AT2G26200	-1.48	-0.57	-4.16	0.0046223	0.0738801	-1.83	FALSE
250716_at	sucrose transporter protein	ATSUC9	AT5G06170	1.54	0.62	4.16	0.0046284	0.0738801	-1.83	FALSE
251057_at	putative protein alkB protein - Es	---	AT5G01780	-1.44	-0.52	-4.16	0.0046281	0.0738801	-1.83	FALSE
261479_at	unknown protein ;supported by fu	IQD28	AT1G14380	-2.05	-1.04	-4.16	0.0046385	0.0739888	-1.83	FALSE
248607_at	NaCl-inducible Ca2+-binding pro	ATCP1	AT5G49480	3.39	1.76	4.16	0.0046445	0.0739956	-1.83	TRUE
264052_at	putative cytochrome P450	CYP79B3	AT2G22330	2.55	1.35	4.16	0.0046454	0.0739956	-1.83	TRUE
266207_at	unknown protein ; supported by	---	AT2G27680	-1.84	-0.88	-4.15	0.0046547	0.0740914	-1.84	FALSE

265484_at	unknown protein ; supported by	OTP51	AT2G15820	-1.64	-0.71	-4.15	0.0046699	0.0741029	-1.84	FALSE
249283_at	amino acid permease-like protein	---	AT5G41800	1.95	0.96	4.15	0.0046745	0.0741029	-1.84	FALSE
266661_at	TINY-like AP2 domain transcripti	---	AT2G25820	1.73	0.79	4.15	0.0046766	0.0741029	-1.84	FALSE
249594_at	putative protein SIAH1 protein, E	---	AT5G37910	1.53	0.61	4.15	0.0046726	0.0741029	-1.84	FALSE
260065_at	putative RING zinc finger protein	---	AT1G73760	1.67	0.74	4.15	0.0046771	0.0741029	-1.84	FALSE
246832_at	putative protein isopenicillin N e	---	AT5G26600	1.70	0.77	4.15	0.0046652	0.0741029	-1.84	FALSE
264202_at	TINY-like transcription factor Cor	---	AT1G22810	4.37	2.13	4.15	0.0046814	0.0741029	-1.84	FALSE
248633_at	arginine methyltransferase-like p	PRMT4A	AT5G49020	-1.65	-0.73	-4.15	0.0046785	0.0741029	-1.84	FALSE
267338_at	26S proteasome regulatory subu	EIF2	AT2G39990	-1.72	-0.78	-4.15	0.0046975	0.0741114	-1.84	FALSE
264270_at	beta-glucosidase, putative simila	---	---	1.50	0.58	4.15	0.0046936	0.0741114	-1.84	FALSE
247844_at	ARR2 - like protein ARR2 protei	ARR18	AT5G58080	1.51	0.59	4.15	0.0046971	0.0741114	-1.84	FALSE
251289_at	auxin response factor-like protei	ARF18	AT3G61830	-1.83	-0.87	-4.15	0.0047014	0.0741114	-1.85	FALSE
246517_at	ribosomal protein 3 precursor-lik	---	AT5G15760	-1.73	-0.79	-4.15	0.0046917	0.0741114	-1.84	FALSE
248738_at	unknown protein ;supported by f	---	AT5G48020	1.60	0.68	4.15	0.0046987	0.0741114	-1.84	FALSE
260160_at	putative RNA-binding protein co	---	AT1G79880	-1.55	-0.63	-4.15	0.0047052	0.0741194	-1.85	FALSE
245701_at	ferredoxin-dependent glutamate	GLU1	AT5G04140	-1.98	-0.99	-4.14	0.0047118	0.0741724	-1.85	FALSE
261771_at	hypothetical protein contains sim	---	AT1G76150	1.43	0.52	4.14	0.0047202	0.0742537	-1.85	FALSE
260486_at	F-box protein ZEITLUPE/FKF/LK	---	AT1G51550	-1.62	-0.69	-4.14	0.0047386	0.0743885	-1.85	FALSE
267462_at	Expressed protein ; supported by	---	AT2G33735	-2.36	-1.24	-4.14	0.004737	0.0743885	-1.85	FALSE
251770_at	leucoanthocyanidin dioxygenase	---	AT3G55970	9.29	3.22	4.14	0.004734	0.0743885	-1.85	FALSE
260157_at	unknown protein ; supported by	---	AT1G52930	-2.83	-1.50	-4.14	0.0047487	0.0744318	-1.86	FALSE
253715_at	RIBOSOMAL PROTEIN S30 ho	---	AT4G29390	-1.67	-0.74	-4.14	0.0047633	0.0744318	-1.86	FALSE
249224_at	mitochondrial carrier protein-like	---	AT5G42130	-1.47	-0.56	-4.13	0.0047739	0.0744318	-1.86	FALSE
260137_at	unknown protein ;supported by fu	---	AT1G66330	-2.00	-1.00	-4.13	0.0047709	0.0744318	-1.86	FALSE
253827_at	Expressed protein ; supported by	---	AT4G28085	4.06	2.02	4.14	0.0047665	0.0744318	-1.86	FALSE
261828_at	unknown protein ; supported by c	---	AT1G11360	-1.55	-0.63	-4.14	0.0047472	0.0744318	-1.86	FALSE
258109_at	hypothetical protein contains Pfa	HGL1	AT3G23640	-1.62	-0.69	-4.14	0.0047639	0.0744318	-1.86	FALSE
249795_at	40S ribosomal protein S11 ;supp	RPS11-BE	AT5G23740	-2.44	-1.29	-4.14	0.0047664	0.0744318	-1.86	FALSE
248538_at	putative protein contains similarit	---	AT5G50110	-1.85	-0.89	-4.13	0.0047688	0.0744318	-1.86	FALSE
254647_at	hypothetical protein	---	AT4G18540	1.44	0.53	4.13	0.0047702	0.0744318	-1.86	FALSE
262448_at	En/Spm-like transposon protein,	---	AT1G49450	1.61	0.69	4.13	0.0047782	0.0744474	-1.86	FALSE
259192_at	unknown protein ;supported by f	---	AT3G01740	-1.75	-0.80	-4.13	0.0047946	0.0745269	-1.87	FALSE
247746_at	uncoupling protein AtUCP2 ;sup	ATUCP2	AT5G58970	-1.88	-0.91	-4.13	0.0047928	0.0745269	-1.87	FALSE
263882_at	putative ribonucleoside-diphosph	RNR1	AT2G21790	-3.04	-1.60	-4.13	0.0047964	0.0745269	-1.87	FALSE
261902_at	unknown protein ; supported by f	PLMT	AT1G80860	-1.54	-0.62	-4.13	0.0047961	0.0745269	-1.87	FALSE

246736_at	putative protein hypothetical pro	---	AT5G27560	-1.64	-0.72	-4.13	0.0048013	0.0745526	-1.87	FALSE
247098_at	GTP-binding protein-like	---	AT5G66470	-2.12	-1.08	-4.13	0.0048168	0.0747426	-1.87	FALSE
256797_at	DEAD box helicase protein, puta	---	AT3G18600	-2.08	-1.06	-4.12	0.0048274	0.0747623	-1.87	FALSE
245052_at	putative pectinesterase	---	AT2G26440	1.81	0.86	4.13	0.0048228	0.0747623	-1.87	FALSE
250426_at	ovule development protein - like	AIL6	AT5G10510	1.51	0.60	4.12	0.0048279	0.0747623	-1.87	FALSE
246145_at	peroxidase peroxidase, Lycoper	---	AT5G19880	3.74	1.90	4.12	0.0048407	0.0749087	-1.88	FALSE
259840_at	photosystem I subunit VI precurs	PSAH2	AT1G52230	-1.79	-0.84	-4.12	0.0048448	0.0749219	-1.88	FALSE
250125_at	biotin carboxyl carrier protein of a	CAC1	AT5G16390	-1.61	-0.68	-4.12	0.0048581	0.0749484	-1.88	TRUE
249120_at	unknown protein ;supported by f	---	AT5G43750	-1.60	-0.68	-4.12	0.0048615	0.0749484	-1.88	TRUE
247311_at	DNA polymerase III catalytic sub	EMB2780	AT5G63960	-1.64	-0.71	-4.12	0.0048629	0.0749484	-1.88	FALSE
250429_at	putative protein TH65 protein, A	---	AT5G10470	-1.60	-0.68	-4.12	0.0048605	0.0749484	-1.88	FALSE
260106_at	unknown protein ;supported by fu	---	AT1G35420	-1.61	-0.68	-4.12	0.0048507	0.0749484	-1.88	FALSE
246052_at	putative protein predicted protei	---	AT5G08310	-1.80	-0.85	-4.11	0.0048901	0.0751739	-1.89	FALSE
250555_at	putative protein ferredoxin (2Fe-	---	AT5G07950	-1.95	-0.96	-4.11	0.0048908	0.0751739	-1.89	FALSE
258132_at	protein kinase, putative similar t	ATPERK1	AT3G24550	1.98	0.99	4.11	0.0048871	0.0751739	-1.89	FALSE
246738_at	replication factor C - like replicat	EMB2775	AT5G27740	-1.58	-0.66	-4.12	0.0048844	0.0751739	-1.88	FALSE
254198_at	hypothetical protein	---	AT4G24090	-1.65	-0.72	-4.11	0.0048968	0.0752164	-1.89	FALSE
266616_at	putative CDC6 protein ; supporte	CDC6	AT2G29680	-1.54	-0.62	-4.11	0.0049052	0.0752941	-1.89	FALSE
245774_at	hypothetical protein contains sim	TCP24	AT1G30210	-1.53	-0.61	-4.11	0.0049115	0.0753408	-1.89	FALSE
246340_s_a	AtPP -like protein AtPP protein,	---	AT3G44860 ///	2.73	1.45	4.11	0.0049159	0.0753579	-1.89	FALSE
261118_at	protease, putative similar to SP:	---	AT1G75460	-1.61	-0.68	-4.11	0.0049222	0.0754038	-1.89	FALSE
262259_s_a	hypothetical protein predicted by	---	AT1G53870 ///	-2.09	-1.06	-4.11	0.0049267	0.0754215	-1.89	FALSE
255219_at	hypothetical protein	---	AT4G07720	1.51	0.59	4.11	0.0049309	0.0754355	-1.89	FALSE
245256_at	Expressed protein ; supported by	FAR1	AT4G15090	-1.70	-0.77	-4.11	0.004939	0.0755091	-1.90	FALSE
261851_at	hexokinase, putative similar to c	HKL1	AT1G50460	2.43	1.28	4.10	0.0049548	0.0755369	-1.90	TRUE
262172_at	ribosomal protein S9, putative si	RPS9	AT1G74970	-1.58	-0.66	-4.10	0.0049538	0.0755369	-1.90	FALSE
256876_at	hypothetical protein predicted by	---	AT3G26360	-1.42	-0.50	-4.10	0.0049574	0.0755369	-1.90	FALSE
254605_at	protein kinase - like protein prote	---	AT4G18950	3.08	1.62	4.10	0.0049561	0.0755369	-1.90	FALSE
250603_at	putative protein mature parasite-	---	AT5G07820	-1.64	-0.71	-4.10	0.0049559	0.0755369	-1.90	FALSE
261077_at	protein phosphatase 2C, putativ	---	AT1G07430	2.09	1.06	4.10	0.0049648	0.0755982	-1.90	FALSE
261664_s_a	hypothetical protein contains sim	---	AT1G18320 ///	-1.97	-0.98	-4.10	0.004981	0.0756943	-1.90	TRUE
257199_at	Tic22, putative similar to Tic22 C	---	AT3G23710	-1.70	-0.77	-4.10	0.0049805	0.0756943	-1.90	FALSE
261638_at	Expressed protein ; supported by	---	AT1G49975	-2.55	-1.35	-4.10	0.0049771	0.0756943	-1.90	FALSE
248340_at	putative protein similar to unknov	---	AT5G52180	-1.58	-0.66	-4.10	0.0049854	0.0757046	-1.91	FALSE
264698_at	unknown protein	---	AT1G70200	-1.57	-0.65	-4.10	0.0049883	0.0757046	-1.91	FALSE

259477_at	unknown protein ;supported by fu	---	AT1G19120	-1.50	-0.58	-4.10	0.0049954	0.0757608	-1.91	FALSE
256204_at	DNA polymerase A family protei	POLGAMM	AT1G50840	-1.81	-0.86	-4.09	0.0050076	0.0758122	-1.91	TRUE
248473_at	small zinc finger-like protein ;sup	TIM8	AT5G50810	-1.77	-0.83	-4.10	0.0050058	0.0758122	-1.91	FALSE
259566_at	hypothetical protein	---	AT1G20520	1.48	0.56	4.09	0.0050087	0.0758122	-1.91	FALSE
256094_at	hypothetical protein predicted by	SAUL1	AT1G20780	1.59	0.67	4.09	0.0050161	0.07584	-1.91	FALSE
253329_at	hypothetical protein	---	AT4G33480	-1.50	-0.58	-4.09	0.0050172	0.07584	-1.91	FALSE
246260_at	amino acid permease, putative c	---	AT1G31820	-1.89	-0.92	-4.09	0.005031	0.0758641	-1.92	FALSE
264806_at	hypothetical protein predicted by	---	AT1G08610	-2.49	-1.32	-4.09	0.0050284	0.0758641	-1.91	FALSE
260383_s_a	putative 60S ribosomal protein L(	---	AT1G74050 ///	-1.91	-0.93	-4.09	0.0050321	0.0758641	-1.92	FALSE
254977_s_a	subtilisin-like serine protease cor	---	AT4G10520 ///	1.43	0.52	4.09	0.005029	0.0758641	-1.91	FALSE
253920_at	histone H2A- like protein histone	HTA2	AT4G27230	-2.01	-1.01	-4.09	0.0050366	0.0758823	-1.92	FALSE
262369_at	hypothetical protein predicted by	---	AT1G73010	7.27	2.86	4.09	0.005058	0.0758957	-1.92	TRUE
250753_at	glucuronosyl transferase-like pro	UGT76C2	AT5G05860	1.83	0.87	4.09	0.0050514	0.0758957	-1.92	FALSE
263332_at	putative snRNP splicing factor ;s	---	AT2G03870	-1.53	-0.61	-4.09	0.0050608	0.0758957	-1.92	FALSE
261414_at	Expressed protein ; supported by	---	AT1G07795	1.98	0.99	4.09	0.005057	0.0758957	-1.92	FALSE
263845_at	phenylalanine ammonia lyase (P	pal1	AT2G37040	4.99	2.32	4.09	0.0050557	0.0758957	-1.92	FALSE
251956_at	RNA-binding protein cp29 protein	CP29	AT3G53460	-1.58	-0.66	-4.09	0.0050601	0.0758957	-1.92	FALSE
255456_at	hypothetical protein ;supported b	---	AT4G02920	-1.58	-0.66	-4.09	0.0050494	0.0758957	-1.92	FALSE
247549_at	putative transcription factor MYB	MYB28	AT5G61420	-2.13	-1.09	-4.08	0.0050739	0.0760414	-1.92	FALSE
264516_at	unknown protein	---	AT1G10090	1.54	0.62	4.08	0.0050901	0.0760533	-1.93	TRUE
245093_at	hypothetical protein predicted by	---	AT2G40815 ///	-1.60	-0.67	-4.08	0.0050913	0.0760533	-1.93	FALSE
246019_at	putative protein predicted protein	---	AT5G10690	-1.82	-0.86	-4.08	0.0050849	0.0760533	-1.93	FALSE
245867_at	ATP phosphoribosyl transferase	ATATP-PR1	AT1G58080	-1.66	-0.73	-4.08	0.0050815	0.0760533	-1.93	FALSE
254413_at	myb-related protein M4 ;support	ATMYB102	AT4G21440	2.14	1.10	4.08	0.005078	0.0760533	-1.92	FALSE
249552_s_a	receptor serine/threonine protein	---	AT5G38240 ///	2.32	1.21	4.08	0.0051261	0.0761001	-1.93	TRUE
258009_at	unknown protein	---	AT3G19440	-1.44	-0.53	-4.08	0.005129	0.0761001	-1.94	FALSE
247529_at	monosaccharide transporter STP	---	AT5G61520	-1.59	-0.67	-4.08	0.0050995	0.0761001	-1.93	TRUE
252508_at	putative protein tRNA nucleotidy	---	AT3G46210	-2.11	-1.07	-4.08	0.0051032	0.0761001	-1.93	TRUE
257056_at	unknown protein similar to hypot	---	AT3G15350	1.62	0.69	4.08	0.0051296	0.0761001	-1.94	FALSE
258461_at	hypothetical protein predicted by	---	AT3G17340	1.49	0.57	4.08	0.0051096	0.0761001	-1.93	FALSE
258192_at	putative terpene synthase-relate	---	AT3G29110	1.47	0.55	4.08	0.0051129	0.0761001	-1.93	FALSE
258329_at	putative protein disulfide isomera	ATPDIL1-6	AT3G16110	-1.57	-0.65	-4.08	0.0051226	0.0761001	-1.93	FALSE
266924_at	unknown protein ;supported by f	---	AT2G45730	-1.76	-0.81	-4.08	0.0051215	0.0761001	-1.93	FALSE
245061_at	hypothetical protein ;supported b	RCA	AT2G39730	-1.47	-0.56	-4.07	0.0051312	0.0761001	-1.94	FALSE
266078_at	putative two-component respons	ARR16	AT2G40670	1.56	0.64	4.08	0.0051179	0.0761001	-1.93	FALSE

252122_at	putative protein hypothetical pro	---	AT3G51140	-1.64	-0.71	-4.07	0.0051393	0.0761715	-1.94	FALSE
247571_at	snap25a ;supported by full-lengt	SNAP33	AT5G61210	1.49	0.57	4.07	0.0051525	0.0763176	-1.94	FALSE
249945_at	60S ribosomal protein L10A ; su	---	AT5G22440	-2.77	-1.47	-4.07	0.0051563	0.0763242	-1.94	FALSE
259791_at	unknown protein ; supported by	---	AT1G29700	-2.31	-1.21	-4.07	0.0051874	0.0763635	-1.95	TRUE
261166_s_a	Expressed protein ; supported by	---	AT1G34570 /	-1.85	-0.89	-4.06	0.0052201	0.0763635	-1.95	TRUE
252941_at	phenylalanyl-trna synthetase - li	---	AT4G39280	-1.49	-0.58	-4.06	0.005221	0.0763635	-1.95	FALSE
261973_at	hypothetical protein predicted by	---	AT1G64610	2.00	1.00	4.07	0.0051829	0.0763635	-1.95	FALSE
248242_at	aldo/keto reductase-like protein	---	AT5G53580	-1.80	-0.85	-4.06	0.005218	0.0763635	-1.95	FALSE
263638_at	unknown protein	---	AT2G25310	-1.45	-0.54	-4.07	0.0051636	0.0763635	-1.94	FALSE
260598_at	unknown protein	---	AT1G55930	-1.96	-0.97	-4.07	0.0051677	0.0763635	-1.94	FALSE
254752_at	putative protein IFA-binding prot	---	AT4G13160	-1.61	-0.69	-4.06	0.0052105	0.0763635	-1.95	FALSE
249342_at	putative protein ATP12 protein p	---	AT5G40660	-1.66	-0.74	-4.06	0.0052195	0.0763635	-1.95	FALSE
263181_at	unknown protein ;supported by f	---	AT1G05720	-1.51	-0.59	-4.07	0.0051846	0.0763635	-1.95	FALSE
245952_at	putative protein predicted protei	---	AT5G28500	-1.78	-0.83	-4.07	0.005187	0.0763635	-1.95	FALSE
262086_at	GTP-binding protein, putative si	---	AT1G56050	-1.75	-0.80	-4.06	0.0051973	0.0763635	-1.95	FALSE
261815_at	leucine zipper protein, putative s	---	AT1G08320	1.80	0.85	4.07	0.0051765	0.0763635	-1.94	FALSE
265581_at	putative cAMP-dependent protei	---	AT2G20050	-1.53	-0.61	-4.06	0.0052226	0.0763635	-1.95	FALSE
250016_at	Cu/Zn superoxide dismutase-like	CSD3	AT5G18100	-1.62	-0.69	-4.06	0.0052122	0.0763635	-1.95	FALSE
257180_at	sun protein (fmu protein), putativ	---	AT3G13180	-1.78	-0.83	-4.06	0.0052052	0.0763635	-1.95	FALSE
267233_s_a	unknown protein	---	AT2G43910 /	-1.98	-0.98	-4.06	0.0052163	0.0763635	-1.95	FALSE
252646_at	protein kinase-like protein protei	---	AT3G44610	-1.51	-0.60	-4.06	0.0052175	0.0763635	-1.95	FALSE
267374_at	putative uricase subunit similar to	---	AT2G26230	1.47	0.56	4.06	0.0052153	0.0763635	-1.95	FALSE
247072_at	putative protein similar to unknov	---	AT5G66490	-2.03	-1.02	-4.06	0.0052405	0.0764321	-1.96	TRUE
255481_at	T14P8.6 ; supported by cDNA: g	PMS1	AT4G02460	-1.82	-0.86	-4.06	0.0052507	0.0764321	-1.96	TRUE
249257_at	unknown protein	---	AT5G41640	1.42	0.51	4.06	0.0052465	0.0764321	-1.96	FALSE
249829_at	c-myc binding protein MM-1-like	PDF5	AT5G23290	-1.57	-0.65	-4.06	0.0052488	0.0764321	-1.96	FALSE
254167_at	serine/threonine kinase-like prot	CIPK8	AT4G24400	1.66	0.73	4.06	0.0052506	0.0764321	-1.96	FALSE
251941_at	putative protein ribosomal protei	---	AT3G53470	-1.58	-0.66	-4.06	0.0052491	0.0764321	-1.96	FALSE
251349_s_a	putative protein several hypothet	---	AT3G11030 /	-1.87	-0.90	-4.06	0.0052348	0.0764321	-1.96	FALSE
265383_at	putative WD-40 repeat protein, M	MSI2	AT2G16780	-1.92	-0.94	-4.05	0.0052608	0.0765305	-1.96	FALSE
250156_at	putative protein predicted protei	---	AT5G15170	-1.48	-0.56	-4.05	0.0052836	0.076812	-1.97	FALSE
251929_at	sigma factor SigC ; supported by	SIGC	AT3G53920	-1.56	-0.64	-4.05	0.0052876	0.0768224	-1.97	FALSE
255647_at	Ca2+-transporting ATPase - like	ECA2	AT4G00900	1.76	0.82	4.05	0.0052972	0.0768592	-1.97	TRUE
250382_at	putative protein rjs protein, Mus	---	AT5G11580	-1.43	-0.52	-4.05	0.005303	0.0768592	-1.97	FALSE
259708_at	lysophospholipase isolog, putati	---	AT1G77420	1.81	0.86	4.05	0.0053037	0.0768592	-1.97	FALSE

253335_at	putative protein YHR077c (NMD	---	AT4G33500	-1.65	-0.73	-4.05	0.0053013	0.0768592	-1.97	FALSE
261838_at	heat shock protein hsp70, putati	Hsp70b	AT1G16030	-1.58	-0.66	-4.05	0.0053173	0.076874	-1.97	FALSE
254045_at	pumilio-like protein abdominal s	APUM6	AT4G25880	-1.51	-0.60	-4.05	0.0053127	0.076874	-1.97	FALSE
250669_at	polygalacturonase inhibiting prot	PGIP2	AT5G06870	3.89	1.96	4.05	0.0053204	0.076874	-1.97	FALSE
247696_at	MYB27 protein - like MYB27 pro	MYB59	AT5G59780	-2.90	-1.54	-4.05	0.0053194	0.076874	-1.97	FALSE
258979_at	heat-shock protein (At-hsc70-3) i	---	AT3G09440	2.49	1.32	4.05	0.0053215	0.076874	-1.97	FALSE
265415_at	unknown protein ;supported by f	PSB29	AT2G20890	-1.64	-0.71	-4.04	0.0053292	0.0769359	-1.97	FALSE
262400_at	unknown protein ; supported by	RTV1	AT1G49480	-1.44	-0.53	-4.04	0.0053707	0.0774857	-1.98	FALSE
245982_at	senescence-associated protein (	SAG29	AT5G13170	9.60	3.26	4.04	0.0053795	0.0775637	-1.98	FALSE
263866_at	putative farnesylated protein ;su	---	AT2G36950	2.09	1.07	4.03	0.0053946	0.0775858	-1.99	TRUE
261891_at	transcriptional regulator, putative	---	AT1G80790	-1.46	-0.54	-4.03	0.0054004	0.0775858	-1.99	FALSE
246400_at	hypothetical protein contains sim	---	AT1G57540	-1.48	-0.57	-4.03	0.0054007	0.0775858	-1.99	FALSE
252823_at	Expressed protein ; supported by	---	AT4G40045	-1.60	-0.68	-4.03	0.0054029	0.0775858	-1.99	FALSE
255018_at	hypothetical protein ; supported	---	AT4G10090	-1.81	-0.86	-4.03	0.0053908	0.0775858	-1.99	FALSE
249231_at	putative protein similar to unknov	ABIL4	AT5G42030	-1.65	-0.72	-4.03	0.0053911	0.0775858	-1.99	FALSE
253295_at	putative aspartate--tRNA ligase	---	AT4G33760	-1.99	-1.00	-4.03	0.0054048	0.0775858	-1.99	FALSE
261788_at	unknown protein ;supported by fu	NDF1	AT1G15980	-2.37	-1.25	-4.03	0.0054255	0.0777676	-1.99	TRUE
249466_at	ribosomal protein L5 - like ribosc	RPL5B	AT5G39740	-2.07	-1.05	-4.03	0.0054228	0.0777676	-1.99	FALSE
264508_at	putative phytochrome A similar to	PHYA	AT1G09570	-2.20	-1.14	-4.03	0.0054277	0.0777676	-1.99	FALSE
264115_at	hypothetical protein	---	AT2G31290	-1.74	-0.80	-4.03	0.0054322	0.0777837	-1.99	FALSE
262599_at	unknown protein ESTs gb|R651	---	AT1G15350	-1.56	-0.64	-4.03	0.0054379	0.0778159	-2.00	FALSE
267175_s_a	actin 3 identical to GB:U29480;su	ACT1	AT2G37620 //	1.91	0.94	4.03	0.0054547	0.0780075	-2.00	TRUE
249821_at	putative protein contains similarit	---	AT5G23690	-2.21	-1.14	-4.02	0.0054584	0.078011	-2.00	TRUE
249847_at	serine carboxypeptidase II-like pr	SCPL34	AT5G23210	-2.03	-1.02	-4.02	0.0054653	0.0780123	-2.00	TRUE
250672_at	DnaJ homologue (gb|AAB91418	ATJ6	AT5G06910	-1.44	-0.53	-4.02	0.0054644	0.0780123	-2.00	FALSE
250510_at	15.9 kDa subunit of RNA polyme	NRPB4	AT5G09920	-1.52	-0.60	-4.02	0.0054692	0.0780195	-2.00	FALSE
248968_at	pectin acetylesterase ;supported	---	AT5G45280	2.54	1.34	4.02	0.0055072	0.0780532	-2.01	TRUE
263131_at	ribosomal protein L13, putative s	emb1473	AT1G78630	-1.57	-0.65	-4.02	0.0054964	0.0780532	-2.01	TRUE
256617_at	unknown protein ; supported by	---	AT3G22240	3.12	1.64	4.02	0.0054803	0.0780532	-2.00	TRUE
252619_at	putative protein several hypothet	---	AT3G45210	-2.36	-1.24	-4.02	0.0055127	0.0780532	-2.01	TRUE
256337_at	unknown protein	---	AT1G72060	-3.80	-1.93	-4.02	0.0055125	0.0780532	-2.01	FALSE
267096_at	unknown protein ; supported by	---	AT2G38180	-2.41	-1.27	-4.02	0.0054861	0.0780532	-2.00	FALSE
258051_at	hypothetical protein predicted by	TRZ4	AT3G16260	-1.82	-0.86	-4.02	0.0054877	0.0780532	-2.00	FALSE
260328_at	putative aspartate aminotransfer	---	AT1G80360	1.45	0.54	4.02	0.0054856	0.0780532	-2.00	FALSE
247128_at	atfp6-like protein	---	AT5G66110	-1.90	-0.92	-4.02	0.0055071	0.0780532	-2.01	FALSE

262911_s_a	heat shock protein, putative simi	---	AT1G07400 /.	4.62	2.21	4.02	0.0055051	0.0780532	-2.01	FALSE
251599_at	adenylosuccinate synthetase ;su	ADSS	AT3G57610	-1.61	-0.69	-4.02	0.0054932	0.0780532	-2.01	FALSE
263750_at	unknown protein	---	AT2G21530	-1.82	-0.87	-4.02	0.0054996	0.0780532	-2.01	FALSE
255719_at	unknown protein ;supported by fu	---	AT1G32080	-2.72	-1.44	-4.01	0.0055248	0.0780955	-2.01	TRUE
250087_at	putative protein contains similarit	---	AT5G17270	-2.20	-1.14	-4.02	0.0055223	0.0780955	-2.01	FALSE
254004_at	arginyl-tRNA synthetase	emb1027	AT4G26300	-1.41	-0.50	-4.01	0.0055259	0.0780955	-2.01	FALSE
255850_at	putative chloroplast 50S ribosom	---	AT2G33450	-1.69	-0.76	-4.01	0.0055366	0.0781536	-2.01	TRUE
248768_at	60S acidic ribosomal protein P1-	---	AT5G47700	-2.16	-1.11	-4.01	0.0055369	0.0781536	-2.01	FALSE
264938_at	unknown protein contains similar	---	AT1G60610	1.59	0.67	4.01	0.0055707	0.0785548	-2.02	FALSE
264340_at	unknown protein similar to hypot	---	AT1G70280	-1.70	-0.77	-4.01	0.0055736	0.0785548	-2.02	FALSE
244965_at	hypothetical protein	---	---	-1.94	-0.95	-4.01	0.0055756	0.0785548	-2.02	FALSE
264959_at	hypothetical protein predicted by	---	AT1G77090	-1.68	-0.75	-4.01	0.0055832	0.0785641	-2.02	FALSE
260384_at	putative 2-isopropylmalate synth	IMS1	AT1G74040	-1.57	-0.65	-4.01	0.0055826	0.0785641	-2.02	FALSE
260946_at	hypothetical protein predicted by	---	AT1G06010	-1.69	-0.75	-4.00	0.005593	0.0786058	-2.02	FALSE
265670_s_a	unknown protein ;supported by f	---	AT2G32190 /.	4.10	2.04	4.01	0.0055899	0.0786058	-2.02	FALSE
247982_at	serine O-acetyltransferase (EC 2	ATSERAT1	AT5G56760	1.61	0.69	4.00	0.0056153	0.0786145	-2.03	TRUE
260268_at	unknown protein ;supported by f	---	AT1G68490	-1.52	-0.60	-4.00	0.0056212	0.0786145	-2.03	FALSE
265446_at	unknown protein ;supported by f	---	AT2G37110	1.59	0.67	4.00	0.0056126	0.0786145	-2.03	FALSE
264173_at	unknown protein	---	AT1G02160	-1.52	-0.61	-4.00	0.0056064	0.0786145	-2.03	FALSE
257003_at	unknown protein ;supported by f	FLU	AT3G14110	-1.91	-0.93	-4.00	0.0056021	0.0786145	-2.03	FALSE
253731_at	acid phosphatase-like protein a	---	AT4G29260	-1.47	-0.55	-4.00	0.0056057	0.0786145	-2.03	FALSE
253534_at	cytochrome P450 monooxygena	CYP83B1	AT4G31500	2.90	1.54	4.00	0.0056094	0.0786145	-2.03	FALSE
263537_at	CONSTANS-like B-box zinc finge	COL3	AT2G24790	-1.53	-0.61	-4.00	0.0056179	0.0786145	-2.03	FALSE
248765_at	MutT domain protein-like ; suppo	ATNUDT2	AT5G47650	-1.50	-0.58	-4.00	0.0056348	0.0787553	-2.03	FALSE
259981_at	unknown protein ; supported by	---	AT1G76450	-1.71	-0.78	-4.00	0.0056404	0.0787861	-2.03	FALSE
247493_at	copine - like protein copine I, Ho	BON1	AT5G61900	2.41	1.27	4.00	0.0056547	0.0789379	-2.04	FALSE
248493_at	putative protein contains similarit	FSD2	AT5G51100	-1.64	-0.72	-3.99	0.0056817	0.079266	-2.04	FALSE
248981_at	regulatory protein NPR1-like; tra	NPR3	AT5G45110	1.58	0.66	3.99	0.005693	0.0793755	-2.04	FALSE
253612_at	putative protein D-ribulokinase -	---	AT4G30310	-1.52	-0.60	-3.99	0.005707	0.0795213	-2.04	FALSE
255128_at	putative protein glutamic acid-ric	---	AT4G08310	-1.77	-0.83	-3.99	0.0057146	0.0795784	-2.05	FALSE
254527_at	putative protein KIAA0682 prote	---	AT4G19610	-1.43	-0.52	-3.99	0.0057298	0.079644	-2.05	FALSE
250891_at	fatty acid elongase - like protein	KCS19	AT5G04530	1.74	0.80	3.99	0.0057253	0.079644	-2.05	FALSE
256043_at	hypothetical protein contains Pfa	---	AT1G07210	-1.96	-0.97	-3.99	0.0057285	0.079644	-2.05	FALSE
246463_at	quinone oxidoreductase -like pro	AT-AER	AT5G16970	1.99	0.99	3.98	0.0057428	0.0796728	-2.05	TRUE
258193_at	putative pectinesterase similar to	PME31	AT3G29090	-1.48	-0.57	-3.98	0.005737	0.0796728	-2.05	FALSE

262433_s_a	DNA binding protein, putative sir	ATRBP47C	AT1G47490 /.	-1.50	-0.58	-3.98	0.0057493	0.0796728	-2.05	FALSE
266299_at	glutathione S-transferase identic	ATGSTU5	AT2G29450	2.62	1.39	3.98	0.0057471	0.0796728	-2.05	FALSE
249579_at	ADP-ribosylation factor - like pro	ATARLA1A	AT5G37680	-1.56	-0.65	-3.98	0.0057437	0.0796728	-2.05	FALSE
253952_at	ubiquitin-like protein ubiquitin-lik	SUMO1	AT4G26840	-1.55	-0.63	-3.98	0.0057567	0.079703	-2.05	FALSE
255791_at	plastid protein identical to GB:Z8	DAL1	AT2G33430	-1.86	-0.89	-3.98	0.0057585	0.079703	-2.05	FALSE
261922_at	amp-binding protein, putative sir	AAE12	AT1G65890	1.87	0.90	3.98	0.0057639	0.0797304	-2.06	FALSE
251285_at	putative protein several hypothet	---	AT3G61770	-1.56	-0.64	-3.98	0.0057729	0.0797478	-2.06	FALSE
245387_at	nuclear RNA binding protein A-lik	---	AT4G17520	-1.80	-0.85	-3.98	0.0057757	0.0797478	-2.06	FALSE
266696_at	copia-like retroelement pol polyp	---	AT2G19680	-1.71	-0.77	-3.98	0.0057705	0.0797478	-2.06	FALSE
260592_at	cellulose synthase catalytic subu	CSLE1	AT1G55850	-1.79	-0.84	-3.98	0.0057925	0.0798674	-2.06	TRUE
248095_at	putative protein strong similarity t	ATMAP65-1	AT5G55230	-1.84	-0.88	-3.97	0.0058471	0.0798674	-2.07	TRUE
254215_at	putative Na+/H+-exchanging pro	ATCHX17	AT4G23700	6.27	2.65	3.98	0.0057976	0.0798674	-2.06	FALSE
246808_at	putative protein many predicted	---	AT5G27110	-1.55	-0.63	-3.98	0.0058008	0.0798674	-2.06	FALSE
260407_at	putative protein kinase Pfam HM	---	AT1G69910	1.46	0.55	3.97	0.0058373	0.0798674	-2.07	FALSE
266108_at	putative peptide/amino acid trans	---	AT2G37900	1.71	0.77	3.97	0.0058092	0.0798674	-2.06	FALSE
261909_at	hypothetical protein predicted by	SAR3	AT1G80680	-1.74	-0.80	-3.97	0.0058481	0.0798674	-2.07	FALSE
249817_at	putative protein similar to unknov	---	AT5G23820	10.63	3.41	3.97	0.0058229	0.0798674	-2.07	TRUE
248386_at	DNA-directed RNA polymerase I	NRPB6A	AT5G51940	-1.60	-0.68	-3.97	0.0058553	0.0798674	-2.07	FALSE
246976_s_a	putative protein UBIQUINONE B	---	AT5G24810	2.05	1.04	3.97	0.0058323	0.0798674	-2.07	FALSE
255695_at	putative protein	UNE11	AT4G00080	1.50	0.58	3.98	0.0057928	0.0798674	-2.06	FALSE
267093_at	high affinity Ca2+ antiporter iden	CAX1	AT2G38170	-2.10	-1.07	-3.97	0.0058349	0.0798674	-2.07	FALSE
261378_at	calcium-dependent protein kinas	ATCDPK1	AT1G18890	2.02	1.02	3.97	0.0058196	0.0798674	-2.07	FALSE
251119_at	putative protein nifR3 protein, A	---	AT3G63510	-1.89	-0.92	-3.97	0.0058083	0.0798674	-2.06	FALSE
252228_at	porin - like protein porin, Mesem	VDAC5	AT3G49920	-1.47	-0.56	-3.97	0.0058214	0.0798674	-2.07	FALSE
245350_at	nuclear antigen homolog ;suppor	---	AT4G16830	-1.66	-0.73	-3.97	0.0058359	0.0798674	-2.07	FALSE
253473_at	putative protein mixed-lineage p	---	AT4G32250	2.37	1.24	3.97	0.0058534	0.0798674	-2.07	FALSE
259856_at	unknown protein ;supported by f	---	AT1G68440	2.97	1.57	3.97	0.0058325	0.0798674	-2.07	FALSE
250843_at	putative RNA-binding protein as	BTR1L	AT5G04430	-1.49	-0.58	-3.97	0.0058119	0.0798674	-2.06	FALSE
245501_at	hypothetical protein	---	AT4G15620	2.80	1.48	3.97	0.0058558	0.0798674	-2.07	FALSE
251425_at	putative protein chloroplast Cpn	---	AT3G60210	-1.63	-0.70	-3.97	0.0058579	0.0798674	-2.07	FALSE
260069_at	unknown protein	---	AT1G73820	-1.53	-0.62	-3.97	0.0058676	0.0798722	-2.07	FALSE
253208_at	putative protein	---	AT4G34830	-1.52	-0.60	-3.97	0.0058624	0.0798722	-2.07	FALSE
263693_at	hypothetical protein predicted by	ATPP2-A9	AT1G31200	-3.10	-1.63	-3.97	0.0058719	0.0798722	-2.07	FALSE
253773_s_a	Expressed protein ; supported by	---	AT1G52370 /.	-1.70	-0.77	-3.97	0.0058722	0.0798722	-2.07	FALSE
246191_at	T-complex protein 1, beta subur	---	AT5G20890	-1.73	-0.79	-3.96	0.0058873	0.0799342	-2.08	FALSE

249510_at	putative protein similar to unknov	---	AT5G38510	-1.60	-0.68	-3.96	0.005886	0.0799342	-2.08	FALSE
261106_at	homeodomain-containing protei	KNAT7	AT1G62990	1.49	0.57	3.96	0.0058844	0.0799342	-2.08	FALSE
256536_at	peptide chain release factor, put	---	AT1G33330	-1.51	-0.60	-3.96	0.0059038	0.0801105	-2.08	FALSE
246747_at	ribosomal protein S21 - like ribo	---	AT5G27700	-1.93	-0.95	-3.96	0.005913	0.0801394	-2.08	FALSE
249346_at	amino acid permease	LTH1	AT5G40780	1.75	0.81	3.96	0.0059119	0.0801394	-2.08	FALSE
253942_at	putative protein	---	AT4G27010	-2.08	-1.06	-3.96	0.005918	0.0801599	-2.08	TRUE
260215_at	unknown protein	---	AT1G74530	-1.57	-0.65	-3.96	0.0059277	0.0801958	-2.08	FALSE
248500_at	unknown protein	---	AT5G50410	-1.70	-0.77	-3.96	0.0059263	0.0801958	-2.08	FALSE
245793_at	unknown protein ;supported by fu	---	AT1G32220	-2.55	-1.35	-3.96	0.0059381	0.080243	-2.09	FALSE
259643_at	putative menaquinone biosynthe	---	AT1G68890	1.48	0.56	3.95	0.005954	0.080243	-2.09	FALSE
259505_at	hypothetical protein contains sim	---	AT1G15810	-1.80	-0.85	-3.95	0.0059693	0.080243	-2.09	FALSE
246432_at	RGA-like protein putative memb	RGL3	AT5G17490	2.21	1.14	3.96	0.0059401	0.080243	-2.09	TRUE
263098_at	Expressed protein ; supported by	---	AT2G16005	1.48	0.57	3.95	0.0059518	0.080243	-2.09	FALSE
253561_at	aspartate--tRNA ligase - like pro	---	AT4G31180	-1.50	-0.58	-3.95	0.005964	0.080243	-2.09	FALSE
264913_at	hypothetical protein predicted by	---	AT1G60770	-2.13	-1.09	-3.95	0.0059566	0.080243	-2.09	FALSE
254980_at	putative ribosomal protein L9, cy	---	AT4G10450	-2.57	-1.36	-3.95	0.0059528	0.080243	-2.09	FALSE
259937_s_a	putative ABC transporter contain	ATNAP5	AT1G71330 ///	1.58	0.66	3.95	0.005958	0.080243	-2.09	FALSE
266182_at	hypothetical protein predicted by	---	AT2G02370	1.82	0.86	3.95	0.0059645	0.080243	-2.09	FALSE
267202_s_a	putative oxysterol-binding protei	ORP1A	AT2G31020 ///	2.12	1.09	3.95	0.0059699	0.080243	-2.09	FALSE
257805_at	sugar transport, putative similar	ATPLT5	AT3G18830	2.47	1.31	3.95	0.0059811	0.0802578	-2.09	TRUE
250562_at	putative protein	TOM5	AT5G08040	-1.70	-0.77	-3.95	0.0059815	0.0802578	-2.09	FALSE
255782_at	transcription factor identical to tra	MP	AT1G19850	2.49	1.32	3.95	0.005975	0.0802578	-2.09	FALSE
251740_at	peptidylprolyl isomerase	ROC2	AT3G56070	-2.48	-1.31	-3.95	0.0059946	0.0803858	-2.10	TRUE
253344_at	putative protein predicted protei	---	AT4G33550	2.41	1.27	3.95	0.0059986	0.0803919	-2.10	FALSE
265228_s_a	hypothetical protein	---	AT2G07698	1.72	0.79	3.95	0.0060027	0.0804004	-2.10	TRUE
263953_at	hypothetical protein predicted by	OFP15	AT2G36050	-2.33	-1.22	-3.95	0.0060131	0.080435	-2.10	TRUE
246020_at	putative protein ; supported by c	---	AT5G10710	-1.55	-0.63	-3.94	0.0060332	0.080435	-2.10	FALSE
258937_at	putative ribosomal protein S28 si	---	AT3G10090	-2.02	-1.02	-3.94	0.0060247	0.080435	-2.10	TRUE
266348_at	putative MAP kinase	ATMPK17	AT2G01450	1.77	0.83	3.95	0.0060216	0.080435	-2.10	FALSE
259225_at	putative small nuclear ribonucleo	---	AT3G07590	-3.14	-1.65	-3.94	0.0060387	0.080435	-2.10	TRUE
258742_at	hypothetical protein predicted by	---	AT3G05800	2.40	1.26	3.94	0.0060285	0.080435	-2.10	FALSE
266578_at	putative cinnamoyl CoA reductas	---	AT2G23910	1.71	0.77	3.95	0.0060153	0.080435	-2.10	FALSE
253058_at	ribosomal - like protein ribosoma	---	AT4G37660	-1.94	-0.96	-3.94	0.0060413	0.080435	-2.10	FALSE
252991_at	protein kinase like protein protei	---	AT4G38470	4.29	2.10	3.94	0.0060441	0.080435	-2.10	FALSE
262830_at	purple acid phosphatase, putativ	PAP3	AT1G14700	-2.06	-1.04	-3.94	0.0060366	0.080435	-2.10	FALSE

258674_at	putative elongation factor P (EF-	---	AT3G08740	-2.05	-1.03	-3.94	0.0060406	0.080435	-2.10	FALSE
251652_at	putative protein hypothetical pro	---	AT3G57380	2.02	1.01	3.94	0.0060502	0.0804692	-2.10	FALSE
256266_at	unknown protein ; supported by c	---	AT3G12320	-2.42	-1.27	-3.94	0.0060575	0.0805199	-2.11	FALSE
261362_s_a	ribosomal protein identical to GB	---	AT1G41880 /	-2.16	-1.11	-3.94	0.0060648	0.0805221	-2.11	FALSE
248399_at	putative protein strong similarity t	---	AT5G52010	-1.51	-0.60	-3.94	0.0060626	0.0805221	-2.11	FALSE
246030_at	Expressed protein genomic sequ	---	AT5G21105	1.56	0.64	3.94	0.0060734	0.0805898	-2.11	FALSE
256129_at	calcium-binding protein, putative	---	AT1G18210	2.23	1.15	3.94	0.0060867	0.0807198	-2.11	FALSE
267406_at	unknown protein	MEE22	AT2G34780	-1.69	-0.75	-3.93	0.0061065	0.0808101	-2.11	FALSE
266274_at	putative protein phosphatase 2C	---	AT2G29380	1.55	0.63	3.93	0.0061077	0.0808101	-2.11	FALSE
259036_at	putative laccase similar to laccas	LAC7	AT3G09220	1.47	0.55	3.93	0.006102	0.0808101	-2.11	FALSE
261033_at	unknown protein ;supported by fu	JAZ5	AT1G17380	5.47	2.45	3.93	0.0061057	0.0808101	-2.11	FALSE
267044_at	nodulin-like protein	---	AT2G34357	-2.19	-1.13	-3.93	0.0061193	0.0809047	-2.12	FALSE
245932_at	3'(2'),5'-bisphosphate nucleotida	---	AT5G09290	2.72	1.44	3.93	0.0061219	0.0809047	-2.12	FALSE
256892_at	hypothetical protein contains sim	---	AT3G19000	-2.22	-1.15	-3.93	0.0061339	0.0809964	-2.12	FALSE
261979_at	nitrate reductase, putative simila	NIA2	AT1G37130	-2.18	-1.12	-3.93	0.0061377	0.0809964	-2.12	FALSE
263356_at	putative RNA-binding protein ; s	UBA1A	AT2G22090	1.47	0.55	3.93	0.0061395	0.0809964	-2.12	FALSE
261418_at	mitochondrial ribosomal protein,	---	AT1G07830	-1.96	-0.97	-3.93	0.0061543	0.0810977	-2.12	FALSE
260209_at	putative AP2 domain transcriptio	CPuORF53	AT1G68550 /	-1.64	-0.72	-3.93	0.0061509	0.0810977	-2.12	FALSE
266188_at	unknown protein	---	AT2G39000	-1.66	-0.73	-3.93	0.0061725	0.081196	-2.13	FALSE
245949_at	elongation factor 1B alpha-subur	---	AT5G19510	-1.78	-0.83	-3.93	0.0061676	0.081196	-2.12	FALSE
254447_at	berberine bridge enzyme - like pr	---	AT4G20860	4.89	2.29	3.93	0.0061711	0.081196	-2.13	FALSE
261535_at	Expressed protein ; supported by	---	AT1G01725	-1.72	-0.78	-3.92	0.0062106	0.0814265	-2.13	FALSE
252246_at	putative protein various predicted	---	AT3G49725 /	-1.60	-0.68	-3.92	0.0062114	0.0814265	-2.13	FALSE
247705_at	putative protein ;supported by fu	---	AT5G59460	-1.54	-0.63	-3.92	0.0062087	0.0814265	-2.13	FALSE
257863_at	hypothetical protein similar to GF	anac057	AT3G17730	1.43	0.51	3.92	0.0062084	0.0814265	-2.13	FALSE
248044_at	putative protein similar to unknov	---	AT5G56020	-1.55	-0.63	-3.92	0.0061936	0.0814265	-2.13	FALSE
250516_at	putative protein predicted protei	---	AT5G09620	1.55	0.63	3.92	0.0062052	0.0814265	-2.13	FALSE
249843_at	putative protein similar to unknov	SGS3	AT5G23570	-1.94	-0.96	-3.92	0.0062203	0.0814501	-2.13	TRUE
258966_at	putative DNA gyrase subunit A s	---	AT3G10690	-2.28	-1.19	-3.92	0.0062177	0.0814501	-2.13	FALSE
245329_at	Expressed protein ; supported by	---	AT4G14365	3.15	1.65	3.92	0.0062275	0.0814973	-2.13	FALSE
262288_at	unknown protein identical to resi	CRR23	AT1G70760	-3.12	-1.64	-3.91	0.0062591	0.0815425	-2.14	TRUE
253549_at	Expressed protein ; supported by	NFD1	AT4G30930	-2.09	-1.06	-3.91	0.0062566	0.0815425	-2.14	TRUE
266563_at	nodulin-like protein	---	AT2G23990	1.53	0.61	3.92	0.0062476	0.0815425	-2.14	FALSE
250757_at	tetrahydrofolylpolyglutamate synt	ATDFB	AT5G05980	-1.57	-0.65	-3.92	0.0062375	0.0815425	-2.14	FALSE
262964_at	hypothetical protein predicted by	---	AT1G54380	-1.95	-0.97	-3.92	0.0062477	0.0815425	-2.14	FALSE

264728_at	unknown protein location of EST	---	AT1G22850	-1.69	-0.75	-3.91	0.0062551	0.0815425	-2.14	FALSE
259927_at	unknown protein ; supported by	JAC1	AT1G75100	-2.07	-1.05	-3.92	0.0062454	0.0815425	-2.14	FALSE
251848_at	Expressed protein ; supported by	BZIP25	AT3G54620	1.59	0.67	3.91	0.0062596	0.0815425	-2.14	FALSE
248442_at	DEAD-box protein abstrakt	---	AT5G51280	-1.70	-0.76	-3.91	0.0062643	0.081558	-2.14	FALSE
248757_at	putative protein contains similarit	---	AT5G47680	-1.47	-0.56	-3.91	0.0062865	0.0817069	-2.14	FALSE
253190_at	UDP-galactose transporter - like	---	AT4G35335	-1.58	-0.66	-3.91	0.0062846	0.0817069	-2.14	FALSE
267365_at	putative phosphoribosyl pyropho	---	AT2G44530	-1.42	-0.51	-3.91	0.0062824	0.0817069	-2.14	FALSE
249997_at	chromatin remodelling complex	CHR17	AT5G18620	-1.64	-0.72	-3.91	0.0062927	0.0817412	-2.15	FALSE
264922_s_a	U2 snRNP auxiliary factor, large	---	AT1G60830 /	-1.45	-0.54	-3.91	0.0063054	0.081838	-2.15	TRUE
260525_at	putative pre-mRNA splicing facto	---	AT2G47250	-1.48	-0.57	-3.91	0.0063074	0.081838	-2.15	FALSE
248797_at	putative protein similar to unknov	---	AT5G47210	-1.66	-0.73	-3.91	0.0063315	0.0818713	-2.15	FALSE
250526_at	pyruvate kinase	---	AT5G08570	-1.54	-0.62	-3.91	0.0063196	0.0818713	-2.15	FALSE
261351_at	hypothetical protein predicted by	---	AT1G79790	-1.63	-0.70	-3.91	0.006317	0.0818713	-2.15	FALSE
246450_at	Heat Shock Factor 3	HSF3	AT5G16820	-1.48	-0.57	-3.91	0.0063282	0.0818713	-2.15	FALSE
245024_at	ATPase alpha subunit	---	---	-1.46	-0.54	-3.91	0.0063261	0.0818713	-2.15	FALSE
266154_at	putative cytochrome p450	---	AT2G12190	1.93	0.95	3.91	0.0063261	0.0818713	-2.15	FALSE
247609_at	cleavage stimulation factor 50K	---	AT5G60940	-1.55	-0.63	-3.90	0.0063378	0.0819061	-2.15	FALSE
251157_at	mRNA binding protein precursor	CSP41A	AT3G63140	-1.90	-0.93	-3.90	0.0063507	0.0819133	-2.15	TRUE
266410_at	unknown protein	EMB2765	AT2G38770	-1.49	-0.58	-3.90	0.0063506	0.0819133	-2.15	FALSE
250832_at	nicotianamine synthase (dbj|BAA	NAS1	AT5G04950	-5.43	-2.44	-3.90	0.0063588	0.0819133	-2.16	TRUE
250634_at	putative protein 2-oxoglutarate-d	---	AT5G07480	1.49	0.57	3.90	0.0063599	0.0819133	-2.16	FALSE
251810_at	putative protein predicted pectat	---	AT3G55250	-1.77	-0.82	-3.90	0.0063598	0.0819133	-2.16	FALSE
263072_at	putative protein kinase contains a	---	AT2G17530	1.52	0.61	3.90	0.0063487	0.0819133	-2.15	FALSE
253803_at	putative protein hypothetical pro	---	AT4G28200	-1.52	-0.61	-3.90	0.0063647	0.0819292	-2.16	FALSE
266461_at	glutathione S-transferase (GST6	ATGSTF8	AT2G47730	2.19	1.13	3.90	0.0063766	0.0820272	-2.16	FALSE
265076_at	Rubisco subunit binding-protein I	CPN60B	AT1G55490	-2.23	-1.16	-3.90	0.0063802	0.0820272	-2.16	FALSE
254355_at	Ribosomal protein L7Ae - like NI	---	AT4G22380	-2.01	-1.00	-3.90	0.0063831	0.0820272	-2.16	FALSE
246317_at	putative protein unnamed ORF -	---	AT3G56900	-1.92	-0.94	-3.90	0.006403	0.0821901	-2.16	FALSE
252064_at	putative protein various predicte	---	AT3G51520	-1.52	-0.61	-3.90	0.0064007	0.0821901	-2.16	FALSE
258093_at	unknown protein ; supported by	---	AT3G14750	-1.69	-0.76	-3.89	0.0064315	0.0824635	-2.17	FALSE
249036_at	nuclear cap-binding protein; CBI	CBP20	AT5G44200	-1.65	-0.73	-3.89	0.0064313	0.0824635	-2.17	FALSE
266284_at	putative pumilio/Mpt5 family RNA	APUM2	AT2G29190	-1.61	-0.69	-3.89	0.0064599	0.0825492	-2.17	FALSE
250625_at	calnexin homolog	---	AT5G07340	-1.88	-0.91	-3.89	0.0064577	0.0825492	-2.17	FALSE
265998_at	putative NADP-dependent glycer	ALDH11A3	AT2G24270	-1.60	-0.68	-3.89	0.0064466	0.0825492	-2.17	FALSE
254617_s_a	ribosomal protein L11, cytosolic	RPL16B	AT4G18730 /	-1.98	-0.99	-3.89	0.0064519	0.0825492	-2.17	FALSE

245096_at	putative cysteine proteinase inhit	ATCYSA	AT2G40880	-1.63	-0.70	-3.89	0.0064538	0.0825492	-2.17	FALSE
255809_at	putative protein predicted protei	---	AT4G10300	-1.66	-0.73	-3.89	0.0064507	0.0825492	-2.17	FALSE
258850_at	putative cellulose synthase catal	CSLD3	AT3G03050	1.58	0.66	3.89	0.0064693	0.0826232	-2.17	TRUE
252542_at	nuclear receptor binding factor-l	---	AT3G45770	-1.45	-0.54	-3.89	0.0064744	0.0826424	-2.17	FALSE
267178_at	unknown protein ; supported by	---	AT2G37750	5.75	2.52	3.88	0.0065237	0.0826867	-2.18	TRUE
265270_at	putative ribose phosphate pyroph	---	AT2G42910	-1.52	-0.61	-3.89	0.0064912	0.0826867	-2.18	FALSE
261826_at	pectin methylesterase, putative	PMEPCRA	AT1G11580	2.65	1.40	3.89	0.0064876	0.0826867	-2.18	FALSE
251551_at	transcriptional coactivator - like	MBF1B	AT3G58680	-1.40	-0.49	-3.88	0.0065304	0.0826867	-2.18	FALSE
259193_at	putative thylakoid lumen rotamas	CYP38	AT3G01480	-1.89	-0.92	-3.88	0.0065273	0.0826867	-2.18	FALSE
246015_at	putative protein predicted protei	---	AT5G10700	-1.51	-0.59	-3.88	0.0064965	0.0826867	-2.18	FALSE
245532_at	cytochrome P450 like protein	CYP97B3	AT4G15110	-1.40	-0.49	-3.88	0.0065064	0.0826867	-2.18	FALSE
255487_at	tryptophan synthase alpha 1-like	---	AT4G02610	-1.63	-0.70	-3.88	0.0065235	0.0826867	-2.18	FALSE
248223_at	unknown protein ; supported by	---	AT5G53620	-1.40	-0.49	-3.88	0.0065101	0.0826867	-2.18	FALSE
255549_at	predicted protein of unknown fun	GPAT3	AT4G01950	8.34	3.06	3.88	0.0065006	0.0826867	-2.18	FALSE
249456_at	unknown protein ;supported by f	---	AT5G39410	-1.60	-0.67	-3.88	0.0065323	0.0826867	-2.18	FALSE
252827_at	cytochrome P450 - like protein c	CYP79B2	AT4G39950	6.61	2.72	3.88	0.006508	0.0826867	-2.18	FALSE
265345_at	copia-like retroelement pol polyp	---	AT2G22680	1.52	0.61	3.88	0.0065156	0.0826867	-2.18	FALSE
252189_at	cyclin D3-like protein Nicotiana t	CYCD3;3	AT3G50070	-1.98	-0.98	-3.89	0.0064926	0.0826867	-2.18	FALSE
253266_s_a	putative protein predicted protei	---	AT2G45260 ///	-1.67	-0.74	-3.88	0.0065316	0.0826867	-2.18	FALSE
251152_at	RAN GTPase activating protein 1	RANGAP1	AT3G63130	-1.97	-0.98	-3.88	0.0065377	0.0827092	-2.18	FALSE
264375_at	putative protein kinase contains a	CIPK16	AT2G25090	3.55	1.83	3.88	0.0065572	0.0829106	-2.19	FALSE
259536_s_a	putative protein hypothetical prot	ATCOAB	AT1G12350 ///	-1.41	-0.50	-3.88	0.006573	0.0830636	-2.19	FALSE
253505_at	Cytochrome P450-like protein fla	CYP82C2	AT4G31970	1.82	0.86	3.87	0.0065884	0.0831665	-2.19	TRUE
252353_at	putative protein KIAA0226 gene	---	AT3G48200	-1.57	-0.65	-3.87	0.0065872	0.0831665	-2.19	FALSE
255617_at	putative protein kinase	---	AT4G01330	-1.74	-0.80	-3.87	0.0065963	0.0832101	-2.19	TRUE
249441_at	avirulence induced gene (AIG) -	---	AT5G39730	1.75	0.81	3.87	0.0065992	0.0832101	-2.19	FALSE
256285_at	hypothetical protein predicted by	---	AT3G12510	1.90	0.92	3.87	0.0066043	0.0832289	-2.20	FALSE
263104_at	unknown protein	---	AT2G05120	-1.62	-0.69	-3.87	0.0066164	0.0833353	-2.20	TRUE
258687_at	unknown protein	---	AT3G07860	-1.84	-0.88	-3.87	0.0066484	0.0833696	-2.20	TRUE
256229_at	unknown protein	MSL3	AT1G58200	1.80	0.85	3.87	0.0066303	0.0833696	-2.20	TRUE
266635_at	unknown protein ;supported by f	---	AT2G35470	-1.73	-0.79	-3.87	0.0066284	0.0833696	-2.20	FALSE
266534_at	putative splicing factor ;supporte	---	AT2G16940	-1.46	-0.55	-3.87	0.0066434	0.0833696	-2.20	FALSE
250895_at	RIBOSOMAL PROTEIN S28- lik	---	AT5G03850	-2.01	-1.00	-3.87	0.0066397	0.0833696	-2.20	FALSE
263400_s_a	40S ribosomal protein; contains (	---	AT2G31610 ///	-1.68	-0.75	-3.87	0.0066373	0.0833696	-2.20	FALSE
261674_at	unknown protein	---	AT1G18270	2.18	1.12	3.87	0.0066249	0.0833696	-2.20	FALSE

254029_at	putative protein other hypothetica	---	AT4G25870	-1.63	-0.71	-3.87	0.0066479	0.0833696	-2.20	FALSE
251198_at	putative protein PGP237-11, Pe	---	AT3G62970	-1.50	-0.59	-3.87	0.0066592	0.0834598	-2.20	FALSE
258334_at	hypothetical protein predicted by	---	AT3G16010	-1.56	-0.64	-3.86	0.0066792	0.0836642	-2.21	FALSE
250657_at	steroid sulfotransferase-like prote	ST2B	AT5G07000	2.53	1.34	3.86	0.0066834	0.0836707	-2.21	TRUE
264790_at	putative histidine kinase histidine	ATHK1	AT2G17820	-1.71	-0.77	-3.86	0.0066886	0.0836901	-2.21	FALSE
260774_at	serine-threonine protein kinase,	---	AT1G78290	-3.30	-1.72	-3.86	0.006717	0.0839532	-2.21	TRUE
255420_at	putative frataxin-like protein simil	FH	AT4G03240	-1.45	-0.53	-3.86	0.0067138	0.0839532	-2.21	FALSE
249253_at	putative protein similar to unknov	---	AT5G42060	-1.63	-0.70	-3.85	0.0067629	0.0843178	-2.22	TRUE
256792_at	hypothetical protein predicted by	---	AT3G22150	-2.63	-1.39	-3.85	0.0067643	0.0843178	-2.22	FALSE
264128_at	unknown protein	---	AT1G79190	-1.52	-0.61	-3.85	0.0067619	0.0843178	-2.22	FALSE
266535_s_a	50S ribosomal protein L27 ;supp	---	AT2G16930 ///	-1.77	-0.82	-3.85	0.0067646	0.0843178	-2.22	FALSE
258607_at	thioredoxin f1 identical to thiored	TRXF1	AT3G02730	-1.75	-0.81	-3.85	0.0067529	0.0843178	-2.22	FALSE
263048_s_a	unknown protein ;supported by f	---	AT2G05310 ///	-1.66	-0.74	-3.85	0.0067684	0.0843191	-2.22	FALSE
256191_at	unknown protein similar to hypot	---	AT1G30130	1.61	0.69	3.85	0.00678	0.0844169	-2.22	FALSE
264069_at	putative rubisco subunit binding-p	CPN60A	AT2G28000	-1.98	-0.99	-3.85	0.0067911	0.0844448	-2.22	FALSE
258128_at	chloroplast thylakoidal processin	PLSP1	AT3G24590	-1.71	-0.78	-3.85	0.0068005	0.0844448	-2.23	FALSE
264900_at	putative auxin transport protein s	PIN7	AT1G23080	-2.04	-1.03	-3.85	0.0067931	0.0844448	-2.22	FALSE
264121_at	putative GTP-binding protein Ca	TOC33	AT1G02280	-1.66	-0.73	-3.85	0.0068007	0.0844448	-2.23	FALSE
250129_at	S-adenosylmethionine:2-demeth	---	AT5G16450	1.62	0.69	3.85	0.0067945	0.0844448	-2.22	FALSE
253218_at	subtilisin-like serine protease sir	SLP2	AT4G34980	-2.37	-1.24	-3.85	0.0068054	0.0844567	-2.23	FALSE
250703_at	putative protein similar to unknov	---	AT5G06360	-1.75	-0.80	-3.85	0.006816	0.0845419	-2.23	FALSE
249658_s_a	N-glyceraldehyde-2-phosphotran	---	AT5G36700 ///	-1.86	-0.90	-3.84	0.0068527	0.0848584	-2.23	FALSE
258283_at	hypothetical protein predicted by	---	AT3G26750	-1.56	-0.64	-3.84	0.006846	0.0848584	-2.23	FALSE
260046_at	Expressed protein ; supported by	---	AT1G73805	6.10	2.61	3.84	0.0068494	0.0848584	-2.23	FALSE
256874_at	cytochrome P450, putative conta	CYP71B36	AT3G26320	-1.63	-0.70	-3.84	0.0068626	0.0849358	-2.23	FALSE
245830_at	hypothetical protein predicted by	---	AT1G57790	-1.48	-0.56	-3.84	0.0068684	0.0849617	-2.24	FALSE
258126_at	hypothetical protein predicted by	---	AT3G24490	-1.61	-0.69	-3.84	0.0068769	0.0850201	-2.24	FALSE
263875_at	unknown protein ;supported by f	סעס-02	AT2G21970	-1.97	-0.98	-3.84	0.0068986	0.0851061	-2.24	TRUE
260678_at	hypothetical protein predicted by	---	AT1G07970	-1.41	-0.50	-3.84	0.0068988	0.0851061	-2.24	FALSE
245117_at	putative Ca2+-ATPase ; support	ACA4	AT2G41560	-1.86	-0.90	-3.84	0.0068887	0.0851061	-2.24	FALSE
247795_at	putative protein zinc finger trans	---	AT5G58620	1.64	0.71	3.84	0.0068932	0.0851061	-2.24	FALSE
257016_at	protein kinase, putative similar t	---	AT3G28690	-1.62	-0.70	-3.84	0.0069054	0.0851413	-2.24	FALSE
252289_at	putative protein pre-mRNA splic	---	AT3G49130	1.95	0.96	3.83	0.006921	0.0852886	-2.24	FALSE
257846_at	unknown protein	---	AT3G12910	5.45	2.45	3.83	0.0069346	0.0854093	-2.25	FALSE
260986_at	glyoxalase II, putative similar to	GLY3	AT1G53580	2.07	1.05	3.83	0.0069428	0.0854648	-2.25	FALSE

260824_at	unknown protein	---	AT1G06720	-2.36	-1.24	-3.83	0.0069508	0.0854938	-2.25	TRUE
267442_at	unknown protein ;supported by f	---	AT2G19080	-1.46	-0.55	-3.83	0.0069527	0.0854938	-2.25	FALSE
250394_at	putative protein yllC, Enterococc	---	AT5G10910	-1.68	-0.75	-3.83	0.0069665	0.0856172	-2.25	FALSE
261141_at	unknown protein contains Pfam p	---	AT1G19740	-1.63	-0.70	-3.83	0.0069733	0.0856544	-2.25	FALSE
248103_at	ubiquitin-like protein SMT3-like ;	SUMO2	AT5G55160	-1.92	-0.94	-3.83	0.0069829	0.0856813	-2.25	FALSE
266033_at	putative translation initiation facto	---	AT2G05830	-1.73	-0.79	-3.83	0.006983	0.0856813	-2.25	FALSE
264679_s_a	putative 60S ribosomal protein L	---	AT1G09590 ///	-2.10	-1.07	-3.82	0.0070101	0.0857637	-2.26	FALSE
253495_at	putative protein crp1 protein, Ze	PGR3	AT4G31850	-1.92	-0.94	-3.82	0.007016	0.0857637	-2.26	FALSE
259043_at	unknown protein similar to putativ	---	AT3G03440	1.98	0.99	3.82	0.007016	0.0857637	-2.26	FALSE
247987_at	putative protein similar to unknov	---	AT5G56900	-1.59	-0.67	-3.82	0.0070119	0.0857637	-2.26	FALSE
252004_at	purple acid phosphatase-like pro	PAP20	AT3G52780	2.53	1.34	3.83	0.0069975	0.0857637	-2.25	FALSE
261087_at	hypothetical protein similar to unl	---	AT1G17350	-1.97	-0.98	-3.82	0.0070125	0.0857637	-2.26	FALSE
258935_at	unknown protein predicted by ge	---	AT3G10120	-2.20	-1.13	-3.83	0.0069939	0.0857637	-2.25	FALSE
246282_at	ATPase-like protein	---	AT4G36580	-2.05	-1.04	-3.82	0.0070351	0.0859054	-2.26	FALSE
262456_at	glucose transporter almost identi	STP1	AT1G11260	2.29	1.20	3.82	0.0070334	0.0859054	-2.26	TRUE
255764_at	unknown protein	HCF173	AT1G16720	-1.72	-0.78	-3.82	0.0070541	0.0859883	-2.26	FALSE
249672_at	nucleolar protein-like	---	AT5G35910	-1.72	-0.78	-3.82	0.0070486	0.0859883	-2.26	FALSE
261742_at	hypothetical protein predicted by	---	AT1G08390	-1.47	-0.55	-3.82	0.0070683	0.0859883	-2.26	FALSE
253138_at	ribosomal protein L11 homolog s	MRPL11	AT4G35490	-1.46	-0.55	-3.82	0.0070661	0.0859883	-2.26	FALSE
251958_at	putative protein predicted protei	---	AT3G53560	-2.25	-1.17	-3.82	0.007063	0.0859883	-2.26	FALSE
258710_s_a	putative coatomer zeta subunit (z	---	AT3G09800 ///	-1.47	-0.56	-3.82	0.0070681	0.0859883	-2.26	FALSE
258107_at	unknown protein ; supported by	ALF5	AT3G23560	1.53	0.61	3.82	0.0070605	0.0859883	-2.26	FALSE
253947_at	putative protein hypothetical pro	MAP65-2	AT4G26760	-1.64	-0.71	-3.82	0.0070866	0.0861186	-2.27	FALSE
253458_at	putative protein predicted protei	---	AT4G32070	2.02	1.02	3.82	0.0070854	0.0861186	-2.27	FALSE
249140_at	F-box protein family, AtFBX6 co	---	AT5G43190	1.83	0.87	3.81	0.0071058	0.0861322	-2.27	FALSE
251943_at	splicing factor - like protein splic	RSZ32	AT3G53500	-1.42	-0.50	-3.81	0.0071034	0.0861322	-2.27	FALSE
250905_at	protein kinase -like protein prote	---	AT5G03640	-1.44	-0.52	-3.81	0.0071066	0.0861322	-2.27	FALSE
247643_at	auxin response factor 4 ; suppor	ARF4	AT5G60450	-1.99	-0.99	-3.81	0.0070975	0.0861322	-2.27	FALSE
262099_s_a	auxin-regulated protein GH3, pu	GH3.4	AT1G59500 ///	10.92	3.45	3.81	0.0070935	0.0861322	-2.27	FALSE
249685_at	putative protein similar to unknov	CCB3	AT5G36120	-1.45	-0.54	-3.81	0.007122	0.0862273	-2.27	FALSE
265966_at	putative RNA-binding protein ; s	---	AT2G37220	-1.75	-0.80	-3.81	0.0071183	0.0862273	-2.27	FALSE
256091_at	Expressed protein ; supported by	HMGB2	AT1G20693	-1.54	-0.63	-3.81	0.0071261	0.0862274	-2.27	TRUE
247342_at	ARI-like RING zinc finger protein	---	AT5G63730	1.51	0.59	3.81	0.0071333	0.0862274	-2.27	FALSE
260653_at	pyruvate kinase, plastid isozyme	PKp3	AT1G32440	-1.58	-0.66	-3.81	0.0071308	0.0862274	-2.27	FALSE
246509_at	valine--tRNA ligase-like protein s	EMB2247	AT5G16715	-2.05	-1.04	-3.81	0.0071414	0.0862794	-2.28	FALSE

253710_at	putative protein hypothetical pro	anac075	AT4G29230	1.70	0.76	3.81	0.0071506	0.0863442	-2.28	FALSE
266184_s_a	phosphate transporter (AtPT2) id	ATPT2	AT2G38940 /	2.51	1.33	3.81	0.0071667	0.0864018	-2.28	TRUE
249247_at	maize crp1 protein-like	---	AT5G42310	-1.73	-0.79	-3.81	0.0071645	0.0864018	-2.28	FALSE
267430_at	unknown protein	EDA3	AT2G34860	-1.91	-0.93	-3.81	0.0071642	0.0864018	-2.28	FALSE
245612_at	carnitine racemase like protein	HCD1	AT4G14440	3.99	2.00	3.80	0.0071847	0.0865536	-2.28	FALSE
251288_at	exonuclease RRP41 ; supported	RRP41	AT3G61620	-1.82	-0.86	-3.80	0.0071869	0.0865536	-2.28	FALSE
255691_at	hypothetical protein	ANTR2	AT4G00370	-1.62	-0.69	-3.80	0.0071957	0.086609	-2.28	FALSE
251787_at	2-oxoglutarate dehydrogenase,	---	AT3G55410	1.66	0.73	3.80	0.0071991	0.086609	-2.28	FALSE
258313_at	unknown protein contains RanBF	---	AT3G15970	-1.47	-0.55	-3.80	0.007229	0.0868319	-2.29	FALSE
253119_at	Expressed protein ; supported by	---	AT4G35980	-1.48	-0.56	-3.80	0.0072274	0.0868319	-2.29	FALSE
251573_at	phenylalanine-tRNA synthetase-	---	AT3G58140	-1.57	-0.65	-3.80	0.0072261	0.0868319	-2.29	FALSE
246076_at	sucrose-phosphate synthase-like	ATSPS1F	AT5G20280	-1.57	-0.65	-3.80	0.0072417	0.0868523	-2.29	FALSE
250546_at	nhp2-like protein high mobility gr	---	AT5G08180	-2.39	-1.25	-3.80	0.0072364	0.0868523	-2.29	TRUE
250306_at	putative protein similar to unknov	---	AT5G12170	1.91	0.94	3.80	0.0072497	0.0868523	-2.29	FALSE
246313_at	PPR-repeat protein, putative cor	---	AT1G31920	-2.63	-1.40	-3.80	0.0072478	0.0868523	-2.29	FALSE
253234_at	Expressed protein ; supported by	---	AT4G34265	-1.55	-0.64	-3.80	0.0072491	0.0868523	-2.29	FALSE
256986_at	unknown protein	---	AT3G28700	-1.83	-0.87	-3.80	0.0072609	0.0869399	-2.29	FALSE
262591_at	hypothetical protein Similar to gb	CCMH	AT1G15220	-1.48	-0.57	-3.79	0.0072797	0.0871198	-2.30	FALSE
247063_at	unknown protein	---	AT5G66820	-1.92	-0.94	-3.79	0.0072855	0.0871438	-2.30	TRUE
253562_at	putative protein ;supported by fu	---	AT4G31130	-1.42	-0.50	-3.79	0.0073146	0.0871559	-2.30	FALSE
249700_at	40S ribosomal protein S3 ; supp	---	AT5G35530	-1.75	-0.81	-3.79	0.007293	0.0871559	-2.30	FALSE
251357_at	ribosomal protein S27 ; supporte	ARS27A	AT3G61110	-2.18	-1.13	-3.79	0.0073118	0.0871559	-2.30	FALSE
255839_at	putative CONSTANS-like B-box	---	AT2G33500	-1.45	-0.54	-3.79	0.0073118	0.0871559	-2.30	FALSE
252671_at	putative protein dehydrogenases	---	AT3G44190	1.74	0.80	3.79	0.0073171	0.0871559	-2.30	FALSE
255290_at	coded for by A. thaliana cDNA A	ATPC1	AT4G04640	-1.39	-0.47	-3.79	0.0073066	0.0871559	-2.30	FALSE
260972_at	hypothetical protein contains sim	---	AT1G53530	-1.53	-0.61	-3.79	0.0072957	0.0871559	-2.30	FALSE
258782_at	putative dihydroneopterin aldolas	---	AT3G11750	-1.78	-0.83	-3.79	0.0073046	0.0871559	-2.30	FALSE
264361_at	unknown protein Strong similarity	---	AT1G03300	-1.55	-0.63	-3.79	0.0073386	0.0873663	-2.30	FALSE
260780_at	valyl-tRNA synthetase, putative	TWN2	AT1G14610	-1.44	-0.52	-3.79	0.007353	0.0874031	-2.31	FALSE
247073_at	33 kDa polypeptide of oxygen-ev	PSBO1	AT5G66570	-1.44	-0.52	-3.79	0.0073484	0.0874031	-2.30	FALSE
251486_at	60S RIBOSOMAL PROTEIN L3	---	AT3G59540	-2.00	-1.00	-3.79	0.0073532	0.0874031	-2.31	FALSE
266261_at	putative zinc finger protein ;supp	---	AT2G27580	1.40	0.49	3.79	0.0073574	0.0874071	-2.31	FALSE
250350_at	putative protein predicted protei	---	AT5G12010	2.42	1.27	3.79	0.0073671	0.0874771	-2.31	FALSE
245018_at	hypothetical protein	---	---	-1.44	-0.53	-3.78	0.0073927	0.0875839	-2.31	TRUE
250485_at	Expressed protein ; supported by	PROPEP5	AT5G09990	-2.15	-1.11	-3.78	0.0074022	0.0875839	-2.31	TRUE

265101_at	unknown protein similar to ESTs	---	AT1G30880	-2.05	-1.03	-3.78	0.0073869	0.0875839	-2.31	TRUE
250440_at	40S ribsomal protein S6 ; suppo	EMB3010	AT5G10360	-1.84	-0.88	-3.78	0.007392	0.0875839	-2.31	TRUE
249192_at	brain and reproductive organ-exp	---	AT5G42470	-1.41	-0.49	-3.78	0.0074024	0.0875839	-2.31	FALSE
245124_at	small nuclear ribonucleoprotein U	U1A	AT2G47580	-1.56	-0.64	-3.78	0.007403	0.0875839	-2.31	FALSE
266319_s_a	putative beta-ketoacyl-CoA synth	KCS13	AT2G46720 ///	-1.97	-0.98	-3.78	0.0073872	0.0875839	-2.31	FALSE
265707_at	unknown protein	---	AT2G03390	-1.65	-0.73	-3.78	0.0074105	0.0876271	-2.31	FALSE
258524_at	acetyl-coA dehydrogenase, puta	IBR3	AT3G06810	1.63	0.70	3.78	0.0074196	0.0876896	-2.31	FALSE
258161_at	hypothetical protein predicted by	---	AT3G17930	-1.61	-0.68	-3.78	0.0074295	0.0877491	-2.32	FALSE
262632_at	23 kDa polypeptide of oxygen-ev	PSBP-1	AT1G06680	-1.52	-0.61	-3.78	0.0074323	0.0877491	-2.32	FALSE
253294_at	hypothetical protein	---	AT4G33740	-1.55	-0.64	-3.78	0.007448	0.0877907	-2.32	FALSE
267099_at	DNA-(apurinic or apyrimidinic site	ARP	AT2G41460	-1.98	-0.99	-3.78	0.0074437	0.0877907	-2.32	TRUE
261761_at	hypothetical protein predicted by	CENP-C	AT1G15660	-1.50	-0.58	-3.78	0.0074512	0.0877907	-2.32	FALSE
261457_at	Expressed protein ; supported by	---	AT1G21065 ///	-1.58	-0.66	-3.78	0.0074512	0.0877907	-2.32	FALSE
264746_at	unknown protein similar to putativ	WRKY6	AT1G62300	3.40	1.76	3.77	0.0074982	0.0879035	-2.33	TRUE
246173_s_a	putative protein hypothetical pro	---	AT3G61520 ///	-1.83	-0.87	-3.77	0.0074914	0.0879035	-2.32	TRUE
265172_at	putative spermidine synthase	SPDS1	AT1G23820	-1.44	-0.52	-3.77	0.0074803	0.0879035	-2.32	FALSE
252245_at	putative protein various predicte	---	AT3G49710	-2.05	-1.04	-3.77	0.007482	0.0879035	-2.32	FALSE
254438_at	translation initiation factor eIF3 -	---	AT4G20980	-1.70	-0.77	-3.77	0.0075165	0.0879035	-2.33	FALSE
252878_at	mitochondrial carrier - like protei	SAMC1	AT4G39460	-1.54	-0.62	-3.77	0.0075186	0.0879035	-2.33	FALSE
250305_at	putative protein contains similarit	---	AT5G12150	-1.69	-0.76	-3.77	0.0074903	0.0879035	-2.32	FALSE
258405_at	unknown protein almost identica	BSH	AT3G17590	-1.87	-0.90	-3.77	0.0075124	0.0879035	-2.33	FALSE
259090_at	putative ribosomal protein s19 or	---	AT3G04920	-2.09	-1.06	-3.77	0.0075171	0.0879035	-2.33	FALSE
261100_at	RNA polymerase IIA large subur	NRPD1A	AT1G63020	1.55	0.63	3.77	0.0074767	0.0879035	-2.32	FALSE
249152_s_a	inorganic phosphate transporter	APT1	AT5G43350 ///	1.92	0.94	3.77	0.0075141	0.0879035	-2.33	FALSE
264381_at	putative ribonuclease large subu	---	AT2G25100	-1.92	-0.94	-3.77	0.007483	0.0879035	-2.32	FALSE
255587_at	putative inorganic phosphatase	AtPPa5	AT4G01480	1.78	0.83	3.77	0.0074987	0.0879035	-2.33	FALSE
251108_at	putative protein several hypothet	---	AT5G01620	-1.91	-0.94	-3.77	0.0075115	0.0879035	-2.33	FALSE
267363_at	putative peroxisomal membrane	---	AT2G39970	1.51	0.59	3.77	0.0074751	0.0879035	-2.32	FALSE
264475_s_a	hypothetical protein predicted by	---	AT1G77150 ///	-1.72	-0.78	-3.77	0.0075277	0.0879642	-2.33	FALSE
259403_at	unknown protein ; supported by f	PGDH	AT1G17745	5.59	2.48	3.77	0.0075402	0.0879752	-2.33	TRUE
247833_at	putative protein	---	AT5G58575	-1.44	-0.53	-3.77	0.0075398	0.0879752	-2.33	FALSE
255957_at	unknown protein ;supported by fu	---	AT1G22160	-3.06	-1.61	-3.77	0.0075378	0.0879752	-2.33	TRUE
251895_at	class IV chitinase (CHIV)	ATEP3	AT3G54420	3.14	1.65	3.77	0.0075536	0.0880871	-2.33	FALSE
253988_at	putative protein elongation facto	---	AT4G26310	-1.48	-0.56	-3.76	0.0075702	0.088235	-2.34	FALSE
252305_at	putative protein CRP1 protein, Z	emb1796	AT3G49240	-1.88	-0.91	-3.76	0.0075781	0.0882368	-2.34	TRUE

254480_at	translation elongation factor EF-	ATRABE1B	AT4G20360	-1.60	-0.68	-3.76	0.0075778	0.0882368	-2.34	FALSE
255279_at	putative thioredoxin ; supported	---	AT4G04950	-1.97	-0.98	-3.76	0.0075882	0.0883092	-2.34	FALSE
264072_at	hypothetical protein	---	---	-1.46	-0.55	-3.76	0.0076296	0.0884983	-2.34	FALSE
247648_at	laccase - like protein laccase LA	LAC17	AT5G60020	-1.62	-0.70	-3.76	0.0076222	0.0884983	-2.34	FALSE
265225_at	putative PHD-type zinc finger pro	---	AT2G36720	-1.52	-0.60	-3.76	0.0076102	0.0884983	-2.34	FALSE
261305_at	glutamine synthetase, putative s	GLN1;5	AT1G48470	-1.42	-0.50	-3.76	0.0076238	0.0884983	-2.34	FALSE
250885_at	ABC transporter -like protein AB	ATH12	AT5G03910	-1.48	-0.57	-3.76	0.0076201	0.0884983	-2.34	FALSE
264000_at	putative mitochondrial dicarboxyl	UCP5	AT2G22500	4.95	2.31	3.76	0.0076316	0.0884983	-2.34	FALSE
251334_at	putative protein several hypothet	---	AT3G61390	1.70	0.77	3.76	0.0076283	0.0884983	-2.34	FALSE
264571_at	hypothetical protein predicted by	---	AT1G05330	1.41	0.49	3.76	0.0076411	0.088562	-2.35	FALSE
255786_at	unknown protein contains similar	ATCLH1	AT1G19670	2.88	1.53	3.76	0.0076448	0.088562	-2.35	FALSE
254669_at	HhoA protease precursor, putati	DEG5	AT4G18370	-1.79	-0.84	-3.75	0.0076616	0.0886259	-2.35	FALSE
259129_at	unknown protein predicted by ge	PTF1	AT3G02150	2.68	1.42	3.75	0.0076624	0.0886259	-2.35	FALSE
250498_at	microbody NAD-dependent mala	PMDH2	AT5G09660	-1.98	-0.98	-3.75	0.0076656	0.0886259	-2.35	FALSE
266887_at	unknown protein ; supported by	CHL-CPN1	AT2G44650	-1.68	-0.74	-3.75	0.0076698	0.0886259	-2.35	FALSE
250177_at	putative protein copine I, Homo	RGLG2	AT5G14420	1.63	0.71	3.75	0.0076667	0.0886259	-2.35	FALSE
266442_at	hypothetical protein	---	AT2G43260	-1.39	-0.48	-3.75	0.0076878	0.0887893	-2.35	FALSE
251414_at	hypothetical protein	---	AT3G60370	-1.71	-0.77	-3.75	0.0077025	0.0888686	-2.35	FALSE
253738_at	photosystem I subunit PSI-E - lik	PSAE-1	AT4G28750	-1.38	-0.47	-3.75	0.0076995	0.0888686	-2.35	FALSE
250122_at	unknown protein	---	AT5G16520	-1.57	-0.65	-3.75	0.0077085	0.0888931	-2.35	FALSE
259198_at	hypothetical protein similar to F1	---	AT3G03610	1.56	0.64	3.75	0.0077193	0.0889284	-2.36	FALSE
267188_at	6,7-dimethyl-8-ribityllumazine sy	COS1	AT2G44050 /	-1.52	-0.61	-3.75	0.0077186	0.0889284	-2.36	FALSE
260629_at	unknown protein	---	AT1G62330	-1.63	-0.71	-3.75	0.0077345	0.0890581	-2.36	FALSE
254730_at	putative protein GTPase activati	---	AT4G13730	-1.44	-0.53	-3.75	0.00774	0.0890766	-2.36	FALSE
257807_at	glyceraldehyde 3-phosphate del	GAPA	AT3G26650	-1.46	-0.54	-3.75	0.0077442	0.0890796	-2.36	FALSE
262629_at	heat shock protein, putative con	ACD32.1	AT1G06460	-1.46	-0.55	-3.74	0.0077592	0.0892075	-2.36	FALSE
251207_at	putative protein ;supported by fu	---	AT3G63050	2.21	1.14	3.74	0.007776	0.0893557	-2.36	FALSE
267123_at	putative acetone-cyanohydrin lya	MES7	AT2G23560	2.18	1.12	3.74	0.0077874	0.0894417	-2.36	TRUE
262175_at	unknown protein ; supported by c	NDH-O	AT1G74880	-1.78	-0.83	-3.74	0.0078033	0.0895339	-2.37	FALSE
263701_at	putative protein kinase C inhibito	---	AT1G31160	-1.43	-0.52	-3.74	0.0078021	0.0895339	-2.37	FALSE
250728_at	putative protein similar to unknov	---	AT5G06440	-1.63	-0.71	-3.74	0.0078285	0.0897784	-2.37	FALSE
248026_at	putative protein similar to unknov	---	AT5G55710	-1.60	-0.68	-3.74	0.0078371	0.0898309	-2.37	FALSE
248347_at	putative protein contains similarit	---	AT5G52250	1.43	0.51	3.74	0.007842	0.089842	-2.37	FALSE
254784_at	growth factor like protein antiser	NUDT7	AT4G12720	2.75	1.46	3.74	0.0078469	0.0898536	-2.37	FALSE
254117_at	putative protein	---	AT4G24750	-1.77	-0.83	-3.73	0.0078606	0.0899203	-2.37	FALSE

248566_s_a	FRO2-like protein; NADPH oxida	ATFRO7	AT5G49730 /.	-2.24	-1.16	-3.73	0.0078582	0.0899203	-2.37	FALSE
256178_s_a	auxin conjugate hydrolase (ILL5)	ILL5	AT1G51760 /.	4.19	2.07	3.73	0.0078665	0.0899423	-2.38	FALSE
265453_at	putative cellular apoptosis susce	---	AT2G46520	1.66	0.73	3.73	0.0078917	0.09004	-2.38	FALSE
262859_at	hypothetical protein predicted by	---	AT1G64790	-1.54	-0.62	-3.73	0.0078841	0.09004	-2.38	FALSE
266126_at	putative metalloproteinase ; sup	---	AT2G45040	2.04	1.03	3.73	0.0078948	0.09004	-2.38	FALSE
254839_at	stress-induced protein sti1 -like	---	AT4G12400	2.87	1.52	3.73	0.0078846	0.09004	-2.38	FALSE
266258_at	60S acidic ribosomal protein P2	---	AT2G27720	-2.11	-1.08	-3.73	0.0078891	0.09004	-2.38	FALSE
266051_at	rhodanese-like family protein	---	AT2G40760	-1.82	-0.86	-3.73	0.0079261	0.0903515	-2.38	FALSE
251760_at	Expressed protein ; supported by	---	AT3G55605	-2.18	-1.13	-3.73	0.0079533	0.0905662	-2.39	TRUE
257964_at	hypothetical protein similar to hy	---	AT3G19850	-1.98	-0.98	-3.72	0.0079608	0.0905662	-2.39	FALSE
265728_at	hypothetical protein predicted by	---	AT2G31990	1.78	0.83	3.72	0.0079586	0.0905662	-2.39	FALSE
265461_at	unknown protein similarity to ubi	---	AT2G46500	1.52	0.60	3.72	0.0079588	0.0905662	-2.39	FALSE
264299_s_a	hypothetical protein predicted by	---	AT1G78850 /.	2.71	1.44	3.72	0.0079689	0.0906139	-2.39	TRUE
264652_at	putative sugar transport protein,	---	AT1G08920	2.92	1.55	3.72	0.0079769	0.0906594	-2.39	FALSE
246045_at	putative protein predicted protei	---	AT5G19430	-1.73	-0.79	-3.72	0.0079996	0.0906913	-2.39	FALSE
257987_at	fertilization-independent endospe	FIE	AT3G20740	-1.49	-0.57	-3.72	0.0079911	0.0906913	-2.39	FALSE
246099_at	blue copper binding protein ;sup	ATBCB	AT5G20230	2.18	1.12	3.72	0.0079989	0.0906913	-2.39	FALSE
251774_at	nematode resistance protein-like	---	AT3G55840	4.87	2.28	3.72	0.0079984	0.0906913	-2.39	FALSE
264867_at	unknown protein	FH4	AT1G24150	2.74	1.45	3.72	0.0079885	0.0906913	-2.39	FALSE
255071_at	putative protein putative chlorop	---	AT4G09040	-1.57	-0.65	-3.72	0.0080061	0.0907199	-2.39	FALSE
246856_at	nucleic acid binding protein - like	AL4	AT5G26210	-1.42	-0.50	-3.72	0.0080272	0.0909135	-2.40	FALSE
265712_s_a	unknown protein	---	AT2G03330 /.	-1.52	-0.60	-3.72	0.0080523	0.0909721	-2.40	FALSE
256255_at	MYB-family transcription factor,	---	AT3G11280	-1.39	-0.48	-3.72	0.0080499	0.0909721	-2.40	FALSE
265960_at	putative histone H2B ;supported	---	AT2G37470	-2.21	-1.15	-3.72	0.0080518	0.0909721	-2.40	FALSE
256784_at	hypothetical protein predicted by	---	AT3G13674	-1.46	-0.55	-3.72	0.0080507	0.0909721	-2.40	FALSE
251193_at	translation releasing factor RF-1	APG3	AT3G62910	-1.86	-0.89	-3.72	0.0080457	0.0909721	-2.40	FALSE
247177_at	unknown protein ; supported by	---	AT5G65300	3.72	1.90	3.71	0.0080604	0.0910184	-2.40	FALSE
261150_at	floral nectary-specific protein, pu	JMT	AT1G19640	4.47	2.16	3.71	0.0080714	0.0910973	-2.40	TRUE
259013_at	unknown protein similar to putati	emb1990	AT3G07430	-1.50	-0.59	-3.71	0.008093	0.0912515	-2.40	FALSE
250462_at	receptor protein kinase -like(frag	---	AT5G10020	-1.38	-0.47	-3.71	0.0080893	0.0912515	-2.40	FALSE
254105_at	magnesium-protoporphyrin IX m	CHLM	AT4G25080	-1.59	-0.67	-3.71	0.0081024	0.091281	-2.41	FALSE
254938_at	putative oligopeptide transporter	OPT7	AT4G10770	-1.49	-0.57	-3.71	0.0081036	0.091281	-2.41	FALSE
266821_at	putative ethylene response elem	ERF13	AT2G44840	8.74	3.13	3.70	0.0081709	0.0919931	-2.41	FALSE
260203_at	NAM-like protein similar to NAM	ANAC019	AT1G52890	2.15	1.10	3.70	0.0081885	0.0921454	-2.42	TRUE
248507_at	putative protein strong similarity	---	AT5G50420	-1.67	-0.74	-3.70	0.0082105	0.0921454	-2.42	FALSE

251798_at	putative RNA binding protein Se	SCL30	AT3G55460	-1.49	-0.58	-3.70	0.008214	0.0921454	-2.42	FALSE
263053_at	similar to glucose inhibited divisio	---	AT2G13440	-1.54	-0.62	-3.70	0.0082085	0.0921454	-2.42	FALSE
246440_at	glycine/proline-rich protein glycir	---	AT5G17650	2.40	1.26	3.70	0.0082004	0.0921454	-2.42	FALSE
255035_at	putative protein	---	AT4G09550	-1.82	-0.87	-3.70	0.0082028	0.0921454	-2.42	FALSE
260369_at	60S ribosomal protein L34, puta	RPL34	AT1G69620	-1.81	-0.86	-3.70	0.0082089	0.0921454	-2.42	FALSE
248140_at	putative protein similar to unknov	---	AT5G54980	-1.53	-0.61	-3.70	0.0082167	0.0921454	-2.42	FALSE
245314_at	Expressed protein ; supported by	---	AT4G16745	1.54	0.62	3.70	0.0082229	0.0921695	-2.42	FALSE
260733_at	RNA-binding protein, putative sir	---	AT1G17640	-1.66	-0.73	-3.70	0.0082403	0.0922402	-2.42	FALSE
252504_at	telomere repeat-binding protein	TRFL1	AT3G46590	-1.49	-0.58	-3.70	0.0082414	0.0922402	-2.42	FALSE
254877_at	putative protein threonine dehyd	ATSR	AT4G11640	-1.58	-0.66	-3.70	0.0082355	0.0922402	-2.42	FALSE
256397_at	putative dual-specificity protein p	MKP2	AT3G06110	-1.48	-0.56	-3.70	0.0082542	0.0923381	-2.42	FALSE
248771_at	unknown protein	---	AT5G47790	-1.64	-0.71	-3.69	0.0082662	0.0924275	-2.43	FALSE
257207_at	hypothetical protein predicted by	---	AT3G14900	-1.63	-0.70	-3.69	0.0082855	0.0924915	-2.43	FALSE
260245_at	putative RNA-binding protein sim	GR-RBP5	AT1G74230	-1.42	-0.51	-3.69	0.0082922	0.0924915	-2.43	FALSE
253842_at	putative protein putative proteins	---	AT4G27860	3.38	1.76	3.69	0.0082888	0.0924915	-2.43	FALSE
249473_at	His-Asp Phosphotransfer Signal	AHP3	AT5G39340	-1.57	-0.65	-3.69	0.0082903	0.0924915	-2.43	FALSE
256156_at	phosphoinositide specific phosph	ATPLC2	AT3G08510	-1.49	-0.58	-3.69	0.0082832	0.0924915	-2.43	FALSE
259141_at	putative cytoskeleton-associated	---	AT3G10220	-1.52	-0.60	-3.69	0.0083018	0.0925528	-2.43	FALSE
246621_at	putative protein strong similarity t	---	AT5G36230	-1.37	-0.46	-3.69	0.0083084	0.0925818	-2.43	FALSE
258485_at	putative stearoyl-acyl carrier prot	---	AT3G02630	-1.37	-0.45	-3.69	0.0083591	0.0928796	-2.44	FALSE
267429_at	putative UDP-galactose-4-epime	MEE25	AT2G34850	1.86	0.89	3.69	0.0083676	0.0928796	-2.44	FALSE
264908_at	unknown protein	---	AT2G17440	-1.51	-0.60	-3.69	0.0083664	0.0928796	-2.44	FALSE
257726_at	hypothetical protein predicted by	---	AT3G18360	1.48	0.56	3.69	0.0083393	0.0928796	-2.44	FALSE
245134_s_a	unknown protein	---	AT2G45250 ///	-1.52	-0.60	-3.69	0.0083577	0.0928796	-2.44	FALSE
258989_at	rhodanese-like family protein con	---	AT3G08920	-1.61	-0.69	-3.69	0.0083677	0.0928796	-2.44	FALSE
261138_at	hypothetical protein contains Pfa	---	AT1G19710	-1.57	-0.65	-3.69	0.0083495	0.0928796	-2.44	FALSE
255302_at	putative protein similar to transcr	ATMSRB5	AT4G04830	-1.82	-0.86	-3.69	0.0083538	0.0928796	-2.44	FALSE
266993_at	nodulin-like protein ; supported b	---	AT2G39210	2.14	1.10	3.68	0.0084026	0.0929897	-2.44	TRUE
253917_at	hypothetical protein ;supported b	---	AT4G27380	-1.87	-0.90	-3.68	0.0083991	0.0929897	-2.44	TRUE
251961_at	inorganic pyrophosphatase -like	AtPPa4	AT3G53620	2.19	1.13	3.68	0.0083931	0.0929897	-2.44	FALSE
265678_at	putative RAD50 DNA repair prote	RAD50	AT2G31970	-1.95	-0.96	-3.68	0.0084062	0.0929897	-2.44	FALSE
259340_at	hypothetical protein predicted us	PYK10	AT3G03870 ///	-1.61	-0.69	-3.68	0.0084028	0.0929897	-2.44	TRUE
256649_at	serine/arginine-rich protein, puta	SCL30A	AT3G13570	-1.71	-0.78	-3.68	0.0083843	0.0929897	-2.44	FALSE
245817_at	hypothetical protein similar to un	---	AT1G26160	-1.42	-0.51	-3.68	0.008386	0.0929897	-2.44	FALSE
246521_at	N2,N2-dimethylguanine tRNA m	---	AT5G15810	-1.71	-0.77	-3.68	0.008431	0.0931291	-2.45	FALSE

267017_at	unknown protein	SVR1	AT2G39140	-2.51	-1.33	-3.68	0.0084273	0.0931291	-2.45	FALSE
245029_at	hypothetical protein predicted by	YAB5	AT2G26580	-2.69	-1.43	-3.68	0.008425	0.0931291	-2.45	FALSE
250554_at	unknown protein ;supported by f	---	AT5G07900	-1.52	-0.61	-3.68	0.0084428	0.0931684	-2.45	FALSE
255026_at	hypothetical protein	MES12	AT4G09900	-2.24	-1.16	-3.68	0.0084425	0.0931684	-2.45	FALSE
267089_at	unknown protein	---	AT2G38300	-1.74	-0.80	-3.68	0.0084482	0.0931834	-2.45	FALSE
249139_at	Cys2/His2-type zinc finger protei	AZF3	AT5G43170	2.51	1.33	3.68	0.0084636	0.0933077	-2.45	FALSE
258086_at	dihydrolipoamide S-acetyltransfe	LTA2	AT3G25860	-1.64	-0.72	-3.67	0.0085059	0.0937292	-2.46	FALSE
261474_at	anionic peroxidase, putative sim	---	AT1G14540	11.15	3.48	3.67	0.0085123	0.093755	-2.46	FALSE
255644_at	coded for by A. thaliana cDNA T4	---	AT4G00870	-1.47	-0.56	-3.67	0.0085328	0.0938446	-2.46	FALSE
248330_at	putative protein contains similarit	---	AT5G52810	2.26	1.17	3.67	0.0085248	0.0938446	-2.46	FALSE
262784_at	unknown protein strong similarity	SEX1	AT1G10760	-1.93	-0.95	-3.67	0.00853	0.0938446	-2.46	FALSE
265634_at	hypothetical protein predicted by	---	AT2G25530	1.53	0.61	3.67	0.0085461	0.0939459	-2.46	FALSE
267344_at	hypothetical protein predicted by	---	AT2G44230	2.57	1.36	3.67	0.0085551	0.0939534	-2.46	TRUE
259226_at	unknown protein similar to hypot	---	AT3G07700	1.70	0.77	3.67	0.008551	0.0939534	-2.46	FALSE
253672_at	mRNA cleavage factor subunit -	CFIM-25	AT4G29820	-1.69	-0.76	-3.67	0.00856	0.0939552	-2.46	TRUE
257517_at	unknown protein	---	AT3G16330	4.29	2.10	3.67	0.0085635	0.0939552	-2.46	FALSE
257932_at	unknown protein contains Pfam p	HCF107	AT3G17040	-1.61	-0.68	-3.67	0.0085889	0.0940113	-2.47	FALSE
259152_at	hypothetical protein similar to put	---	AT3G10210	-1.39	-0.47	-3.66	0.0086057	0.0940113	-2.47	FALSE
256014_at	hypothetical protein predicted by	---	AT1G19200	3.47	1.79	3.66	0.008592	0.0940113	-2.47	FALSE
253282_at	putative protein hypothetical pro	LEJ1	AT4G34120	1.40	0.49	3.67	0.0085806	0.0940113	-2.46	FALSE
266439_s_a	hypothetical protein predicted by	---	AT2G43200	-1.52	-0.61	-3.66	0.0085954	0.0940113	-2.47	FALSE
262287_at	unknown protein ;supported by fu	---	AT1G68660	-1.57	-0.65	-3.66	0.0085954	0.0940113	-2.47	FALSE
257127_at	hypothetical protein predicted by	TTN9	AT3G20070	-1.64	-0.72	-3.66	0.0086011	0.0940113	-2.47	FALSE
251140_at	lectin - like protein lectin precurs	---	AT5G01090	-1.56	-0.64	-3.66	0.0086018	0.0940113	-2.47	FALSE
260772_at	unknown protein contains similar	---	AT1G49050	1.65	0.72	3.67	0.0085869	0.0940113	-2.47	FALSE
266561_at	unknown protein	---	AT2G23960	1.42	0.51	3.66	0.0086187	0.0941084	-2.47	FALSE
267436_at	putative receptor-like protein kina	FRK1	AT2G19190	3.98	1.99	3.66	0.0086432	0.0941212	-2.47	TRUE
247575_at	RNA-binding protein - like RNA-	GR-RBP3	AT5G61030	-1.74	-0.80	-3.66	0.008645	0.0941212	-2.47	TRUE
261576_at	unknown protein ;supported by fu	---	AT1G01070	-2.61	-1.38	-3.66	0.0086288	0.0941212	-2.47	TRUE
259782_at	unknown protein	---	AT1G29680	1.41	0.50	3.66	0.0086455	0.0941212	-2.47	FALSE
250817_at	SET-domain protein-like ; suppo	SUVH1	AT5G04940	-1.48	-0.57	-3.66	0.0086349	0.0941212	-2.47	FALSE
246879_at	endopeptidase - like protein O-s	---	AT5G26110	-1.52	-0.60	-3.66	0.0086487	0.0941212	-2.47	FALSE
252068_at	mucin -like protein hemomucin,	---	AT3G51440	3.11	1.64	3.66	0.0086331	0.0941212	-2.47	FALSE
261420_at	fatty acid elongase 3-ketoacyl-C	KCS3	AT1G07720	2.47	1.31	3.66	0.0086617	0.0941816	-2.47	TRUE
249938_at	Ruv DNA-helicase-like protein ;s	RIN1	AT5G22330	-1.47	-0.56	-3.66	0.0086626	0.0941816	-2.47	FALSE

248747_at	ribosomal protein S27 ;supported	---	AT5G47930	-1.78	-0.83	-3.66	0.0086838	0.0943229	-2.48	FALSE
262370_at	hypothetical protein predicted by	---	AT1G73090	-1.75	-0.81	-3.66	0.0086803	0.0943229	-2.48	FALSE
267591_at	Expressed protein ; supported by	RTFL8	AT2G39705	-3.24	-1.69	-3.65	0.0087062	0.0944759	-2.48	FALSE
254905_at	RPP1-WsA-like disease resistar	---	AT4G11170	3.97	1.99	3.65	0.0087039	0.0944759	-2.48	FALSE
258037_at	putative 4-coumarate:CoA ligase	4CL5	AT3G21230	9.06	3.18	3.65	0.0087112	0.0944853	-2.48	FALSE
256870_at	cytochrome P450, putative conta	CYP71B34	AT3G26300	-2.17	-1.12	-3.65	0.0087396	0.0947482	-2.48	FALSE
245712_at	pullulanase-like protein (starch d	ATLDA	AT5G04360	-1.47	-0.55	-3.65	0.0087501	0.0948171	-2.48	FALSE
262168_at	unknown protein ;supported by fu	---	AT1G74730	-1.53	-0.61	-3.65	0.0087578	0.0948557	-2.49	FALSE
262464_at	hypothetical protein contains sim	---	AT1G50280	-2.11	-1.08	-3.65	0.0087691	0.0949325	-2.49	FALSE
259392_at	hypothetical protein similar to hyp	---	AT1G06380	-1.44	-0.53	-3.65	0.0087971	0.0950344	-2.49	FALSE
258656_at	putative Ras-like GTP-binding pr	ATRABE1E	AT3G09900	-1.80	-0.85	-3.64	0.0088285	0.0950344	-2.49	FALSE
247015_at	protease-like	---	AT5G66960	-1.73	-0.79	-3.65	0.0088064	0.0950344	-2.49	FALSE
253867_at	putative protein tRNA nucleotidy	---	AT4G27490	-1.98	-0.99	-3.65	0.0087974	0.0950344	-2.49	FALSE
259816_at	RING-H2 finger protein RHY1a i	---	AT1G49850	-1.52	-0.61	-3.64	0.0088261	0.0950344	-2.49	FALSE
260404_at	unknown protein similar to activa	---	---	-1.98	-0.99	-3.65	0.0087907	0.0950344	-2.49	FALSE
258866_at	unknown protein	---	AT3G03180	-1.43	-0.52	-3.65	0.0088036	0.0950344	-2.49	FALSE
253233_at	putative protein various predicted	---	AT4G34290	-2.00	-1.00	-3.64	0.0088183	0.0950344	-2.49	FALSE
244986_at	ribosomal protein S19	---	---	-1.94	-0.96	-3.65	0.0088135	0.0950344	-2.49	FALSE
265674_at	unknown protein ; supported by	---	AT2G32190	3.73	1.90	3.64	0.0088273	0.0950344	-2.49	FALSE
261629_at	unknown protein	---	AT1G49980	-1.45	-0.54	-3.65	0.0088067	0.0950344	-2.49	FALSE
248705_at	putative protein similar to unknov	---	AT5G48520	-1.72	-0.78	-3.65	0.0088104	0.0950344	-2.49	FALSE
260895_at	unknown protein similar to unkno	---	AT1G29250	-2.26	-1.18	-3.64	0.008845	0.0951677	-2.50	FALSE
249727_at	putative protein similar to unknov	MRU1	AT5G35490	-1.44	-0.52	-3.64	0.0088718	0.095199	-2.50	FALSE
265596_at	hypothetical protein predicted by	CAF1	AT2G20020	-2.37	-1.25	-3.64	0.0088679	0.095199	-2.50	FALSE
245400_at	ATP-dependent Clp protease pr	---	AT4G17040	-1.67	-0.74	-3.64	0.008873	0.095199	-2.50	FALSE
250616_at	receptor-like protein kinase-like	EMS1	AT5G07280	1.62	0.69	3.64	0.008866	0.095199	-2.50	FALSE
248238_at	putative protein similar to unknov	---	AT5G53900	-1.79	-0.84	-3.64	0.0088655	0.095199	-2.50	FALSE
248698_at	receptor-like protein kinase ; sup	---	AT5G48380	1.98	0.99	3.64	0.0088534	0.095199	-2.50	FALSE
261620_s_a	ribosomal protein L9, putative si	PGY2	AT1G33120 ///	-1.74	-0.80	-3.64	0.0088801	0.0952303	-2.50	FALSE
248603_at	WD-40 repeat protein-like	---	AT5G49430	-1.41	-0.50	-3.64	0.0088891	0.0952654	-2.50	FALSE
267446_s_a	putative tyrosyl-tRNA synthetase	---	AT1G28350 ///	-1.44	-0.53	-3.64	0.0088917	0.0952654	-2.50	FALSE
267452_at	auxin response transcription fact	ETT	AT2G33860	-1.55	-0.64	-3.64	0.0088997	0.0953058	-2.50	FALSE
263778_at	putative cytochrome oxidase biog	OXA1L	AT2G46470	-1.57	-0.66	-3.64	0.0089096	0.0953679	-2.50	FALSE
248739_at	DnaJ protein-like ;supported by	GFA2	AT5G48030	-1.44	-0.53	-3.63	0.0089371	0.0954672	-2.51	TRUE
251583_at	putative protein several hypothet	---	AT3G58590	-1.83	-0.87	-3.63	0.0089327	0.0954672	-2.51	TRUE

256207_at	GTP-binding protein, putative si	---	AT1G50920	-1.71	-0.77	-3.63	0.0089408	0.0954672	-2.51	FALSE
245512_at	hypothetical protein	---	AT4G15770	-1.92	-0.94	-3.64	0.0089253	0.0954672	-2.50	TRUE
258934_at	putative RecA protein similar to F	RECA3	AT3G10140	-1.57	-0.65	-3.64	0.0089279	0.0954672	-2.51	FALSE
264330_at	multi-drug resistance protein Stro	ATMRP5	AT1G04120	1.49	0.57	3.63	0.008946	0.0954672	-2.51	FALSE
251785_at	ABC transporter - like protein br	ATWBC19	AT3G55130	2.44	1.28	3.63	0.0089482	0.0954672	-2.51	FALSE
252468_at	starch phosphorylase H (cytosol	PHS2	AT3G46970	-1.73	-0.79	-3.63	0.008962	0.0955254	-2.51	FALSE
262727_at	thaumatin, putative contains Pfa	---	AT1G75800	-1.46	-0.54	-3.63	0.0089596	0.0955254	-2.51	FALSE
267211_at	Expressed protein ; supported by	---	AT2G44065	-1.40	-0.48	-3.63	0.0089762	0.0955535	-2.51	FALSE
260044_at	Expressed protein ; supported by	---	AT1G73655	-1.51	-0.59	-3.63	0.0089814	0.0955535	-2.51	FALSE
255595_at	putative chitinase similar to pear	---	AT4G01700	4.23	2.08	3.63	0.0089721	0.0955535	-2.51	FALSE
254321_at	trehalose-6-phosphate phospha	CPuORF27	AT4G22590 /	2.08	1.06	3.63	0.0089775	0.0955535	-2.51	FALSE
249393_at	disease resistance - like protein	AtRLP54	AT5G40170	2.29	1.20	3.63	0.0089894	0.0955692	-2.51	FALSE
254933_at	putative RNA-directed RNA poly	RDR2	AT4G11130	-1.63	-0.71	-3.63	0.0089913	0.0955692	-2.51	FALSE
246564_at	putative protein hypothetical pro	---	AT5G15610	-1.40	-0.49	-3.63	0.0090001	0.0955732	-2.51	FALSE
256837_at	hypothetical protein similar to DN	NRPD7	AT3G22900	-2.04	-1.03	-3.63	0.0089975	0.0955732	-2.51	FALSE
251260_at	putative protein ISOPENICILLIN	---	AT3G62130	-1.96	-0.97	-3.63	0.0090093	0.0956268	-2.51	FALSE
247600_at	Myb transcription factor homolog	MYB34	AT5G60890	2.94	1.56	3.63	0.0090181	0.0956762	-2.52	TRUE
258087_at	putative peroxiredoxin similar to	ATPRX Q	AT3G26060	-1.87	-0.90	-3.62	0.0090618	0.0956977	-2.52	TRUE
264960_at	hypothetical protein contains sim	ATEXT4	AT1G76930	-7.26	-2.86	-3.63	0.0090446	0.0956977	-2.52	TRUE
245479_at	extensin like protein	---	AT4G16140	1.53	0.61	3.62	0.0090621	0.0956977	-2.52	FALSE
254664_at	initiation factor-2Bepsilon-like pr	---	AT4G18300	-1.58	-0.66	-3.63	0.009039	0.0956977	-2.52	FALSE
256677_at	unknown protein contains Pfam	PHF1	AT3G52190	1.59	0.67	3.62	0.009051	0.0956977	-2.52	FALSE
249742_at	putative protein contains similarit	---	AT5G24490	-1.64	-0.71	-3.62	0.0090608	0.0956977	-2.52	FALSE
267584_at	putative protein kinase contains a	---	AT2G41930	1.50	0.59	3.62	0.0090515	0.0956977	-2.52	FALSE
246727_at	major latex protein homolog - lik	---	AT5G28010	-1.72	-0.78	-3.63	0.0090434	0.0956977	-2.52	FALSE
245621_at	AMP-binding protein	AAE15	AT4G14070	-1.83	-0.87	-3.62	0.0090592	0.0956977	-2.52	FALSE
252116_at	putative protein ;supported by fu	---	AT3G51510	-1.63	-0.70	-3.63	0.009031	0.0956977	-2.52	FALSE
250189_at	putative protein ;supported by fu	---	AT5G14410	-1.97	-0.98	-3.62	0.0090675	0.0957097	-2.52	FALSE
266267_at	putative glutathione S-transferas	ATGSTU4	AT2G29460	7.48	2.90	3.62	0.0090904	0.0958924	-2.52	TRUE
250671_at	transcription factor HBP-1b homo	AHBP-1B	AT5G06950	-1.45	-0.54	-3.62	0.0090974	0.0958924	-2.52	FALSE
255936_at	calcium dependent protein kinas	---	AT1G12680 /	-1.49	-0.57	-3.62	0.0090944	0.0958924	-2.52	FALSE
251701_at	putative protein hypothetical pro	---	AT3G56650	-1.55	-0.63	-3.62	0.0091123	0.0959045	-2.53	TRUE
251637_at	hypothetical protein	---	AT3G57570	-1.56	-0.64	-3.62	0.0091271	0.0959045	-2.53	TRUE
264467_at	unknown protein similar to EST g	---	AT1G10140	1.56	0.64	3.62	0.009128	0.0959045	-2.53	FALSE
265805_s_a	60S ribosomal protein L2	EMB2296	AT2G18020 /	-1.78	-0.83	-3.62	0.0091215	0.0959045	-2.53	FALSE

256613_at	hypothetical protein predicted by	emb2076	AT3G29290	-1.69	-0.76	-3.62	0.0091262	0.0959045	-2.53	FALSE
260017_at	hypothetical protein predicted by	---	---	1.94	0.96	3.62	0.0091128	0.0959045	-2.53	FALSE
252404_at	glycine--tRNA ligase precursor,	EDD1	AT3G48110	-1.48	-0.57	-3.62	0.0091085	0.0959045	-2.53	FALSE
254598_at	xyloglucan endo-transglycosylas	---	AT4G18990	2.42	1.28	3.61	0.0091689	0.0959989	-2.53	FALSE
253422_at	putative protein ;supported by fu	---	AT4G32240	-1.54	-0.62	-3.62	0.0091604	0.0959989	-2.53	FALSE
247497_at	Peter Pan - like protein Peter Pa	PPAN	AT5G61770	-1.86	-0.90	-3.61	0.0091782	0.0959989	-2.53	TRUE
264322_at	unknown protein Contains simila	---	AT1G04190	-1.59	-0.67	-3.62	0.0091632	0.0959989	-2.53	FALSE
249607_at	putative protein RING-H2 finger	---	AT5G37280	1.45	0.54	3.61	0.0091931	0.0959989	-2.54	FALSE
252173_at	scarecrow-like 7 (SCL7)	---	AT3G50650	2.13	1.09	3.61	0.0091834	0.0959989	-2.53	FALSE
265200_s_a	putative glucosyl transferase an	UGT73C6	AT2G36790 /	2.94	1.56	3.61	0.0091856	0.0959989	-2.53	FALSE
255435_at	putative component of cytochrom	PETC	AT4G03280	-1.54	-0.62	-3.61	0.0091835	0.0959989	-2.53	FALSE
246197_at	caltractin-like protein ;supported	CEN2	AT4G37010	3.78	1.92	3.61	0.0091779	0.0959989	-2.53	FALSE
265104_at	unknown protein 3'-end of protei	ATO2	AT1G31020	-1.51	-0.60	-3.61	0.0091932	0.0959989	-2.54	FALSE
265880_at	unknown protein	---	AT2G42300	-1.83	-0.87	-3.61	0.009189	0.0959989	-2.53	FALSE
249563_at	similar to unknown protein (pir |T	---	AT5G38360	-1.47	-0.55	-3.62	0.009153	0.0959989	-2.53	FALSE
246228_at	peroxidase like protein	---	AT4G36430	4.99	2.32	3.61	0.0091959	0.0959989	-2.54	FALSE
264930_at	receptor-like kinase, putative sir	NIK3	AT1G60800	-1.71	-0.77	-3.61	0.0091674	0.0959989	-2.53	FALSE
259732_at	putative replication factor C simil	---	AT1G77470	-1.55	-0.63	-3.61	0.0092078	0.0960793	-2.54	FALSE
261122_at	ornithine carbamoyltransferase p	OTC	AT1G75330	-1.76	-0.81	-3.61	0.0092205	0.0961686	-2.54	FALSE
262401_at	small GTP-binding protein, putat	RABG3E	AT1G49300	-1.39	-0.48	-3.61	0.0092262	0.0961837	-2.54	FALSE
261268_at	unknown protein similar to 50S ri	---	AT1G26740	-1.60	-0.68	-3.61	0.0092329	0.096209	-2.54	FALSE
263605_at	hypothetical protein predicted by	---	AT2G16485	-1.65	-0.72	-3.61	0.0092452	0.0962665	-2.54	FALSE
255021_at	hypothetical protein	---	AT4G10330	-1.51	-0.59	-3.61	0.0092468	0.0962665	-2.54	FALSE
265908_at	contains similarity to S. cerevisia	---	AT4G00270	-1.82	-0.87	-3.61	0.009269	0.0964535	-2.54	FALSE
260877_at	unknown protein ; supported by f	---	AT1G21500	-1.81	-0.86	-3.60	0.0092995	0.0966108	-2.55	TRUE
267492_at	histone H1 ;supported by full-leng	---	AT2G30620	-1.73	-0.79	-3.60	0.0092947	0.0966108	-2.55	FALSE
264485_at	unknown protein ; supported by c	---	AT1G77220	1.48	0.57	3.60	0.0092901	0.0966108	-2.55	FALSE
253806_at	putative protein Arabidopsis thal	---	AT4G28270	-1.66	-0.73	-3.60	0.0093011	0.0966108	-2.55	FALSE
258138_at	Expressed protein GC donor spli	MSH7	AT3G24495	-1.42	-0.50	-3.60	0.0093059	0.0966173	-2.55	FALSE
264384_at	putative chromodomain-helicase	PKL	AT2G25170	-1.40	-0.48	-3.60	0.009327	0.0967923	-2.55	FALSE
261043_at	hypothetical protein similar to un	---	AT1G01220	-1.64	-0.71	-3.60	0.0093514	0.0970012	-2.55	FALSE
260602_at	serine acetyltransferase identica	ATSERAT2	AT1G55920	1.58	0.66	3.59	0.009408	0.0971209	-2.56	TRUE
250300_at	putative protein various predicte	---	AT5G11890	-1.85	-0.88	-3.60	0.0093722	0.0971209	-2.56	TRUE
248326_at	Notchless protein homolog	---	AT5G52820	-1.70	-0.77	-3.59	0.0094157	0.0971209	-2.56	TRUE
265605_at	putative cellulose synthase catal	CESA10	AT2G25540	1.36	0.45	3.60	0.0093925	0.0971209	-2.56	FALSE

263039_at	mak16-like protein-related simila	---	AT1G23280	-1.81	-0.86	-3.59	0.0094132	0.0971209	-2.56	TRUE
263843_at	translin-like protein ; supported b	---	AT2G37020	-1.47	-0.56	-3.60	0.0093794	0.0971209	-2.56	FALSE
256284_at	unknown protein	PSF2	AT3G12530	-1.87	-0.90	-3.59	0.0094193	0.0971209	-2.56	FALSE
244940_at	ribosomal protein S12 (trans-spli	---	---	-1.65	-0.72	-3.60	0.0093793	0.0971209	-2.56	FALSE
248913_at	unknown protein ;supported by f	---	AT5G45760	-1.48	-0.57	-3.59	0.009427	0.0971209	-2.56	FALSE
265073_at	unknown protein similar to putati	---	AT1G55480	-2.16	-1.11	-3.59	0.0094295	0.0971209	-2.56	FALSE
261933_at	3-deoxy-D-arabino-heptulosonat	---	AT1G22410	2.31	1.21	3.59	0.0094351	0.0971209	-2.56	FALSE
256996_at	unknown protein similar to unkno	---	AT3G25850	1.39	0.48	3.60	0.0093984	0.0971209	-2.56	FALSE
261681_at	hypothetical protein similar to hy	---	AT1G47340	-1.93	-0.95	-3.60	0.0093872	0.0971209	-2.56	FALSE
263172_at	hypothetical protein predicted by	CID3	AT1G54170	1.37	0.45	3.60	0.0093843	0.0971209	-2.56	FALSE
260014_at	hydroxypyruvate reductase (HPR	HPR	AT1G68010	-1.60	-0.68	-3.59	0.0094353	0.0971209	-2.56	FALSE
254982_at	putative protein ; supported by c	---	AT4G10470	-1.63	-0.70	-3.60	0.0094053	0.0971209	-2.56	FALSE
261616_at	NAC domain containing protein,	ANAC014	AT1G33060	-1.35	-0.44	-3.60	0.0093965	0.0971209	-2.56	FALSE
245358_at	PRL1 protein ;supported by full-le	PRL1	AT4G15900	-1.60	-0.67	-3.59	0.0094555	0.0972843	-2.56	FALSE
266964_at	putative ABC transporter related	PGP6	AT2G39480	1.36	0.45	3.59	0.0094702	0.0973692	-2.57	FALSE
264573_at	putative pectin methylesterase S	---	AT1G05310	-1.71	-0.78	-3.59	0.0094723	0.0973692	-2.57	FALSE
245392_at	glutaredoxin ;supported by full-le	---	AT4G15680	-4.75	-2.25	-3.59	0.0094906	0.0975141	-2.57	FALSE
267533_at	unknown protein ;supported by f	ATNUDX23	AT2G42070	-1.54	-0.62	-3.59	0.0095259	0.0977886	-2.57	FALSE
262248_at	hypothetical protein predicted by	YSL8	AT1G48370	2.17	1.12	3.59	0.0095236	0.0977886	-2.57	FALSE
247819_at	MAP kinase ; supported by cDNA	WNK4	AT5G58350	1.83	0.87	3.58	0.0095371	0.0978596	-2.57	TRUE
266663_at	putative receptor-like protein kina	---	AT2G25790	-1.86	-0.90	-3.58	0.0095607	0.0980573	-2.58	FALSE
258403_at	hypothetical protein predicted by	---	AT3G15380	-1.48	-0.56	-3.58	0.0095826	0.0982374	-2.58	FALSE
263637_at	hypothetical protein predicted by	---	AT2G11890	-1.44	-0.53	-3.58	0.0095967	0.0982494	-2.58	FALSE
247004_at	putative protein similar to unknov	DG1	AT5G67570	-1.55	-0.63	-3.58	0.0095962	0.0982494	-2.58	FALSE
246901_at	putative protein Leaf protein, Ph	---	AT5G25630	-1.47	-0.55	-3.58	0.0095923	0.0982494	-2.58	FALSE
266874_at	unknown protein	---	AT2G44760	-1.39	-0.48	-3.58	0.0096084	0.0983258	-2.58	FALSE
261839_at	unknown protein	---	AT1G16040	-1.55	-0.64	-3.58	0.0096197	0.0983532	-2.58	FALSE
251852_at	putative protein	---	AT3G54750	-1.80	-0.85	-3.58	0.0096177	0.0983532	-2.58	FALSE
263286_at	40S ribosomal protein S14 ;supp	---	AT2G36160	-1.87	-0.90	-3.58	0.0096297	0.0984108	-2.58	FALSE
254948_at	putative protein various predicte	---	AT4G11000	1.56	0.64	3.58	0.0096366	0.0984374	-2.58	FALSE
250679_at	putative protein contains similarit	---	AT5G06550	-1.85	-0.89	-3.58	0.0096458	0.0984869	-2.58	TRUE
246602_at	copper amine oxidase, putative	---	AT1G31710	2.19	1.13	3.57	0.0096557	0.0984906	-2.59	FALSE
259587_at	unknown protein ;supported by fu	---	AT1G28120	-1.52	-0.61	-3.57	0.0096591	0.0984906	-2.59	FALSE
248091_at	putative protein strong similarity t	VTC5	AT5G55120	3.27	1.71	3.57	0.0096548	0.0984906	-2.59	FALSE
267072_at	unknown protein	---	AT2G41170	1.65	0.72	3.57	0.0096822	0.0986379	-2.59	FALSE

248900_at	putative protein strong similarity	PRP39-2	AT5G46400	-1.79	-0.84	-3.57	0.0096787	0.0986379	-2.59	FALSE
254431_at	reticuline oxidase - like protein r	---	AT4G20840	-1.96	-0.97	-3.57	0.0096869	0.098642	-2.59	FALSE
246730_at	40S ribosomal protein S19 - like	---	AT5G28060	-2.08	-1.06	-3.57	0.0096952	0.0986822	-2.59	FALSE
247173_at	poly(A)-binding protein II-like ; s	---	AT5G65260	-1.61	-0.68	-3.57	0.0097012	0.0986996	-2.59	FALSE
259819_at	unknown protein ; supported by	ATMTK	AT1G49820	-1.38	-0.47	-3.57	0.0097212	0.0988428	-2.59	FALSE
247239_at	pectin methylesterase-like protei	---	AT5G64640	-1.55	-0.63	-3.57	0.0097239	0.0988428	-2.59	FALSE
255403_at	putative GH3-like protein similar	DFL2	AT4G03400	-1.68	-0.75	-3.57	0.0097337	0.0988535	-2.59	FALSE
259113_at	hypothetical protein predicted by	---	AT3G05510	-1.58	-0.66	-3.57	0.0097334	0.0988535	-2.59	FALSE
247333_at	1-aminocyclopropane-1-carboxyl	FLS5	AT5G63600	2.43	1.28	3.57	0.0097411	0.0988854	-2.59	FALSE
265149_at	unknown protein ; supported by f	---	AT1G51400	-1.57	-0.65	-3.57	0.0097545	0.0989354	-2.60	FALSE
253545_at	AIG2-like protein AIG2 protein, A	---	AT4G31310	-1.70	-0.77	-3.57	0.0097634	0.0989354	-2.60	FALSE
260172_s_a	putative histidinol-phosphate ami	---	AT1G71920 /	-1.72	-0.78	-3.57	0.0097587	0.0989354	-2.60	FALSE
247390_at	putative protein similar to unknov	---	AT5G63520	-1.42	-0.51	-3.57	0.00976	0.0989354	-2.60	FALSE
250721_at	putative protein contains similarit	---	AT5G06210	-1.45	-0.53	-3.57	0.0097689	0.0989475	-2.60	FALSE
265920_s_a	unknown protein	---	AT2G15120 /	2.76	1.46	3.57	0.0097792	0.0990074	-2.60	TRUE
247094_at	GDP-D-mannose 4,6-dehydrata	GMD1	AT5G66280	1.51	0.60	3.56	0.0097934	0.0991073	-2.60	FALSE
264100_at	lupeol synthase identical to lupeo	LUP1	AT1G78970	3.67	1.87	3.56	0.0098011	0.0991411	-2.60	FALSE
262991_at	hypothetical protein predicted by	BRX-LIKE3	AT1G54180	1.39	0.47	3.56	0.0098126	0.0992135	-2.60	FALSE
264134_at	unknown protein contains similar	---	AT1G79070	-1.38	-0.46	-3.56	0.0098218	0.0992188	-2.60	FALSE
266636_at	glycine decarboxylase complex H	GDCH	AT2G35370	-1.57	-0.65	-3.56	0.009821	0.0992188	-2.60	FALSE
264586_at	putative cytochrome P450 Simila	CYP88A3	AT1G05160	-1.51	-0.60	-3.56	0.009841	0.0993242	-2.61	FALSE
264761_at	hypothetical protein predicted by	---	AT1G61280	-1.44	-0.53	-3.56	0.0098379	0.0993242	-2.60	FALSE
246789_at	long-chain-fatty-acid--CoA ligase	LACS7	AT5G27600	1.44	0.53	3.56	0.0098538	0.0993512	-2.61	FALSE
251771_at	putative protein cellulose syntha	CSLA14	AT3G56000	1.55	0.63	3.56	0.0098567	0.0993512	-2.61	FALSE
253573_at	putative protein BEM46 PROTE	---	AT4G31020	1.59	0.67	3.56	0.0098509	0.0993512	-2.61	FALSE
249994_at	putative protein cell polarity prot	---	AT5G18590	-1.53	-0.61	-3.56	0.0098663	0.0993596	-2.61	FALSE
255778_at	3-phosphoserine phosphatase id	PSP	AT1G18640	-1.39	-0.47	-3.56	0.009862	0.0993596	-2.61	FALSE
255136_s_a	putative protein chromatin struct	---	AT4G08350 /	-1.58	-0.66	-3.56	0.0098836	0.0994904	-2.61	FALSE
261406_at	unknown protein contains similar	NRP2	AT1G18800	-1.88	-0.91	-3.55	0.0099098	0.0996544	-2.61	FALSE
256269_at	transcription factor HBP-1B-like r	TGA6	AT3G12250	-1.44	-0.52	-3.55	0.0099168	0.0996544	-2.61	FALSE
261296_at	unknown protein	---	AT1G48460	-2.12	-1.08	-3.55	0.0099469	0.0996544	-2.62	TRUE
265739_at	unknown protein ; supported by	AtQSOX2	AT2G01270	-1.37	-0.45	-3.55	0.0099219	0.0996544	-2.61	FALSE
247694_at	GTP cyclohydrolase II / 3,4-dihy	---	AT5G59750	-1.53	-0.62	-3.55	0.0099161	0.0996544	-2.61	FALSE
264022_at	Expressed protein ; supported by	---	AT2G21185	-1.69	-0.76	-3.55	0.009948	0.0996544	-2.62	FALSE
256957_at	hypothetical protein predicted by	---	AT3G13420	1.50	0.58	3.55	0.0099445	0.0996544	-2.62	FALSE

267237_s_a	unknown protein ;supported by f	---	AT2G44040 /.	-2.42	-1.28	-3.55	0.0099331	0.0996544	-2.61	FALSE
259140_at	lycopene beta cyclase identical t	LYC	AT3G10230	-1.43	-0.51	-3.55	0.0099376	0.0996544	-2.62	FALSE
261408_s_a	histone H4 identical to GB:M366	---	AT1G07660 /.	-1.74	-0.80	-3.55	0.0099397	0.0996544	-2.62	FALSE
260959_at	unknown protein ;supported by fu	---	AT1G06050	1.49	0.57	3.55	0.0099398	0.0996544	-2.62	FALSE
252593_at	putative protein tRNA intron end	ATSEN1	AT3G45590	-1.64	-0.72	-3.55	0.0099595	0.0997258	-2.62	TRUE
245019_at	hypothetical protein	---	---	-1.38	-0.46	-3.55	0.0099703	0.0997904	-2.62	FALSE
260500_at	Expressed protein ; supported by	---	AT2G41705	-1.41	-0.49	-3.55	0.0099748	0.0997917	-2.62	TRUE
261439_at	Expressed protein ; supported by	---	AT1G28395	-2.18	-1.12	-3.55	0.0099919	0.0999193	-2.62	TRUE
263351_at	hypothetical protein predicted by	---	AT2G22120	-1.37	-0.45	-3.55	0.009998	0.0999357	-2.62	FALSE
259237_at	putative 2-cys peroxiredoxin BAS	---	AT3G11630	-1.76	-0.81	-3.55	0.0100082	0.0999757	-2.62	TRUE
254218_at	putative receptor kinase recepto	---	AT4G23740	-1.53	-0.61	-3.55	0.0100107	0.0999757	-2.62	FALSE
263064_at	putative bZIP transcription factor	CPuORF1	AT2G18160 /.	-1.77	-0.82	-3.55	0.0100267	0.1000914	-2.62	FALSE
246503_at	40S ribosomal protein S7-like 40	---	AT5G16130	-2.19	-1.13	-3.55	0.0100364	0.1001391	-2.63	FALSE
249265_at	E2, ubiquitin-conjugating enzym	---	AT5G41080 /.	-1.38	-0.46	-3.54	0.0100403	0.1001391	-2.63	FALSE
253837_at	putative proline-rich protein exte	---	AT4G27850	1.45	0.53	3.54	0.0100642	0.1001532	-2.63	FALSE
253726_at	ribosomal protein S15a homolog	rps15ae	AT4G29430	-2.38	-1.25	-3.54	0.0100521	0.1001532	-2.63	FALSE
251446_at	Expressed protein ; supported by	---	AT3G59840	-1.42	-0.50	-3.54	0.0100683	0.1001532	-2.63	FALSE
259123_at	unknown protein	---	AT3G02200	-1.44	-0.52	-3.54	0.010068	0.1001532	-2.63	FALSE
260414_at	nitrate transporter (NTL1) identic	ATNRT1:2	AT1G69850	-1.58	-0.66	-3.54	0.0100724	0.1001532	-2.63	FALSE
260538_at	60S ribosomal protein L38	---	AT2G43460	-1.84	-0.88	-3.54	0.0100632	0.1001532	-2.63	FALSE
255257_at	score=526.5, E=1.9e-154, N=3	UBQ11	AT4G05050	1.40	0.49	3.54	0.0100475	0.1001532	-2.63	FALSE
266557_at	unknown protein ; supported by	---	AT2G46080	1.35	0.44	3.54	0.010098	0.100199	-2.63	FALSE
258804_at	hypothetical protein similar to hyp	---	AT3G04760	-1.74	-0.80	-3.54	0.0101122	0.100199	-2.63	FALSE
254013_at	putative leucine-rich-repeat prot	---	AT4G26050	1.82	0.87	3.54	0.0100867	0.100199	-2.63	FALSE
264549_at	putative ser/thr protein kinase sir	---	AT1G09440	-1.45	-0.54	-3.54	0.0100955	0.100199	-2.63	FALSE
251666_at	CYSTATHIONINE BETA-LYASE	CBL	AT3G57050	-1.69	-0.76	-3.54	0.010101	0.100199	-2.63	FALSE
267384_at	unknown protein highly similar to	---	AT2G44370	4.67	2.22	3.54	0.0100849	0.100199	-2.63	FALSE
245426_at	hypothetical protein	---	AT4G17540	-1.61	-0.69	-3.54	0.0101098	0.100199	-2.63	FALSE
264161_at	antigen receptor, putative simila	---	AT1G65420	-1.51	-0.59	-3.54	0.0101094	0.100199	-2.63	FALSE
260955_at	unknown protein contains similar	---	AT1G06000	2.46	1.30	3.54	0.0101391	0.1004109	-2.64	FALSE
264105_x_a	hypothetical protein	---	AT2G13760	1.57	0.65	3.54	0.0101423	0.1004109	-2.64	FALSE
250663_at	putative protein prenylated rab a	PRA1.B6	AT5G07110	1.46	0.55	3.54	0.0101515	0.1004203	-2.64	FALSE
266331_at	putative RGA1, giberellin repsor	RGA1	AT2G01570	-1.63	-0.71	-3.54	0.0101521	0.1004203	-2.64	FALSE
262229_at	unknown protein ; supported by c	---	AT1G68620	3.03	1.60	3.54	0.0101592	0.1004466	-2.64	TRUE
250920_at	putative protein ;supported by fu	---	AT5G03390	2.05	1.04	3.53	0.0101905	0.1006287	-2.64	FALSE

263593_at	hypothetical protein predicted by	EMB975	AT2G01860	-1.64	-0.71	-3.53	0.0101821	0.1006287	-2.64	FALSE
245998_at	sucrose-UDP glucosyltransferase	SUS1	AT5G20830	2.26	1.17	3.53	0.0101908	0.1006287	-2.64	FALSE
247741_at	putative protein predicted protei	GIL1	AT5G58960	-2.14	-1.10	-3.53	0.0102001	0.1006765	-2.64	FALSE
249383_at	putative protein putative DNA-bi	PRE1	AT5G39860	2.04	1.03	3.53	0.0102114	0.1006963	-2.64	TRUE
260179_at	unknown protein similar to hypot	HWI1	AT1G70690	2.43	1.28	3.53	0.0102297	0.1006963	-2.65	TRUE
253005_at	hypothetical protein ;supported b	---	AT4G38100	-1.88	-0.91	-3.53	0.0102208	0.1006963	-2.64	FALSE
267181_at	putative alcohol dehydrogenase	---	AT2G37760	2.15	1.10	3.53	0.0102075	0.1006963	-2.64	FALSE
258725_at	putative RNA helicase similar to	---	AT3G09620	1.42	0.51	3.53	0.010229	0.1006963	-2.65	FALSE
251149_at	putative protein CGI-77 protein,	---	AT3G62940	-1.36	-0.45	-3.53	0.010233	0.1006963	-2.65	FALSE
262373_at	hypothetical protein predicted by	---	AT1G73120	-2.45	-1.29	-3.53	0.0102321	0.1006963	-2.65	FALSE
261952_at	unknown protein	---	AT1G64430	-1.37	-0.45	-3.53	0.0102492	0.1007604	-2.65	FALSE
262853_at	unknown protein Location of ES	---	AT1G20890	-1.52	-0.60	-3.53	0.0102527	0.1007604	-2.65	FALSE
258493_at	Expressed protein ; supported by	---	AT3G02555	-1.53	-0.61	-3.53	0.0102487	0.1007604	-2.65	FALSE
247316_at	ankyrin-like protein	---	AT5G64030	-1.45	-0.54	-3.53	0.0102616	0.1007876	-2.65	FALSE
249816_at	cleavage and polyadenylation sp	CPSF100	AT5G23880	-1.72	-0.78	-3.53	0.010267	0.1007876	-2.65	FALSE
253708_at	gamma-glutamyltransferase-like	GGT4	AT4G29210	2.47	1.30	3.53	0.0102688	0.1007876	-2.65	FALSE
246148_at	glycine-rich RNA-binding protein	---	AT5G19960	-1.57	-0.65	-3.52	0.010306	0.1009716	-2.65	FALSE
260055_at	unknown protein similar to putati	---	AT1G78150	-1.43	-0.51	-3.52	0.0103055	0.1009716	-2.65	FALSE
263958_at	putative salt-inducible protein	---	AT2G36240	-1.37	-0.45	-3.53	0.0102969	0.1009716	-2.65	FALSE
250301_at	putative protein predicted protei	---	AT5G11970	1.77	0.82	3.53	0.010304	0.1009716	-2.65	FALSE
253398_at	putative protein retinal pigment r	CCD8	AT4G32810	2.64	1.40	3.52	0.0103096	0.1009716	-2.65	FALSE
256405_at	calcium-dependent protein kinas	CPK33	AT1G50700	-1.43	-0.52	-3.52	0.0103156	0.1009863	-2.65	FALSE
254415_at	subtilisin-like serine protease cor	ATSBT3.12	AT4G21326	1.39	0.48	3.52	0.0103276	0.1010611	-2.65	FALSE
247101_at	apospory-associated protein C-li	---	AT5G66530	-1.70	-0.77	-3.52	0.0103377	0.1010945	-2.66	FALSE
245372_at	ribosomal protein ;supported by t	---	AT4G15000	-2.18	-1.13	-3.52	0.0103488	0.1010945	-2.66	FALSE
258646_at	MATE efflux family protein, puta	FRD3	AT3G08040	1.44	0.52	3.52	0.0103461	0.1010945	-2.66	FALSE
259947_at	putative protein kinase similar to	---	AT1G71530	1.61	0.69	3.52	0.0103411	0.1010945	-2.66	FALSE
247347_at	putative protein similar to unknov	SHA1	AT5G63780	-2.62	-1.39	-3.52	0.0103551	0.1011133	-2.66	FALSE
255116_at	receptor protein kinase-like prote	---	AT4G08850	1.76	0.81	3.52	0.0103668	0.1011401	-2.66	FALSE
256573_at	hypothetical protein predicted by	---	AT3G14860	-1.48	-0.56	-3.52	0.0103648	0.1011401	-2.66	FALSE
246327_at	receptor-like serine/threonine kir	---	AT1G16670	1.66	0.73	3.52	0.0103743	0.1011709	-2.66	FALSE
253897_at	putative protein	---	AT4G27120	-1.45	-0.53	-3.52	0.0103956	0.1012489	-2.66	FALSE
266119_at	protease inhibitor II identical to C	LCR69	AT2G02100	4.21	2.07	3.52	0.010398	0.1012489	-2.66	FALSE
253647_at	putative protein KIAA0210 gene	---	AT4G29950	1.60	0.68	3.52	0.0103882	0.1012489	-2.66	FALSE
246915_at	malate dehydrogenase - like pro	ATNADP-M	AT5G25880	-2.05	-1.04	-3.52	0.0104001	0.1012489	-2.66	FALSE

256676_at	putative protein ;supported by fu	SEX4	AT3G52180	-1.90	-0.93	-3.52	0.0104071	0.1012738	-2.66	FALSE
265088_at	hypothetical protein similar to DN	SWI2	AT1G03750	-1.38	-0.46	-3.52	0.0104403	0.1015106	-2.67	FALSE
249256_at	putative protein strong similarity t	---	AT5G41620	-1.74	-0.80	-3.52	0.0104364	0.1015106	-2.67	FALSE
258254_at	unknown protein contains Pfam p	---	AT3G26780 ///	-1.71	-0.78	-3.51	0.0104532	0.1015921	-2.67	FALSE
250513_at	protein kinase ;supported by full	---	AT5G09890	1.48	0.56	3.51	0.0104755	0.1017227	-2.67	TRUE
253175_at	WD-40 repeat protein (MSI3) ; s	MSI3	AT4G35050	-1.98	-0.99	-3.51	0.0104743	0.1017227	-2.67	FALSE
263298_at	unknown protein ; supported by	TIC21	AT2G15290	-1.41	-0.50	-3.51	0.0104895	0.1017717	-2.67	FALSE
252412_at	Expressed protein ; supported by	---	AT3G47295	-2.02	-1.01	-3.51	0.0104861	0.1017717	-2.67	FALSE
265947_at	putative WD-40 repeat protein ;	---	AT2G19540	-1.93	-0.95	-3.51	0.0105115	0.1019421	-2.67	FALSE
251411_at	regulatory subunit of protein kina	CKB3	AT3G60250	-1.54	-0.62	-3.51	0.0105302	0.1020799	-2.67	FALSE
251340_at	actin - like protein actin 3, Drosc	ATARP7	AT3G60830	-1.48	-0.56	-3.51	0.0105394	0.1021259	-2.68	FALSE
266100_at	similar to axi 1 protein from Nicot	---	AT2G37980	1.99	0.99	3.51	0.0105612	0.1022034	-2.68	FALSE
256045_at	MAP3K gamma protein kinase,	MAPKKK13	AT1G07150	1.55	0.63	3.51	0.0105759	0.1022034	-2.68	FALSE
264832_at	unknown unknown	---	AT1G03660	1.71	0.77	3.51	0.0105533	0.1022034	-2.68	FALSE
251118_at	putative chloroplast inner envelo	APG1	AT3G63410	-1.68	-0.75	-3.51	0.0105695	0.1022034	-2.68	FALSE
267517_at	unknown protein	RPT2	AT2G30520	-1.57	-0.65	-3.50	0.0105788	0.1022034	-2.68	FALSE
253301_at	pathogenesis-related protein 1 p	---	AT4G33720	3.21	1.68	3.51	0.0105701	0.1022034	-2.68	FALSE
266226_at	histone H4 identical to GB:M171	HIS4	AT2G28740	-1.91	-0.94	-3.51	0.010567	0.1022034	-2.68	FALSE
247261_at	ZW10-like protein ; supported by	---	AT5G64460	-1.46	-0.55	-3.50	0.0105909	0.1022186	-2.68	FALSE
256789_at	seven in absentia-like protein sin	---	AT3G13672	-2.31	-1.21	-3.50	0.0105987	0.1022186	-2.68	TRUE
255557_at	hypothetical protein ; supported	---	AT4G01990	-1.88	-0.91	-3.50	0.0106039	0.1022186	-2.68	FALSE
261387_at	hypothetical protein predicted by	---	AT1G05410	-2.00	-1.00	-3.50	0.0106117	0.1022186	-2.68	FALSE
248800_at	40S ribosomal protein S19 ; sup	RPS19	AT5G47320	-1.50	-0.58	-3.50	0.0105942	0.1022186	-2.68	FALSE
247330_at	putative protein contains similarit	GAMMA CA	AT5G63510	-1.38	-0.47	-3.50	0.0106088	0.1022186	-2.68	FALSE
256514_at	oxidoreductase, putative contain	---	AT1G66130	-1.91	-0.94	-3.50	0.0105987	0.1022186	-2.68	FALSE
246193_at	Expressed protein ; supported by	---	---	-1.47	-0.55	-3.50	0.0106193	0.1022484	-2.68	FALSE
258025_at	putative D-3-phosphoglycerate d	---	AT3G19480	-1.97	-0.98	-3.50	0.010637	0.1023755	-2.69	FALSE
266671_at	anthranilate synthase, alpha sub	ASA2	AT2G29690	-1.54	-0.62	-3.50	0.0106789	0.1027116	-2.69	FALSE
246296_at	putative protein hypothetical pro	---	AT3G56750	-1.43	-0.52	-3.50	0.0106848	0.1027116	-2.69	FALSE
254416_at	receptor-like serine/threonine pro	ARK3	AT4G21380	3.63	1.86	3.50	0.0106854	0.1027116	-2.69	FALSE
264438_at	putative 60S ribosomal protein L	---	AT1G27400	-1.99	-0.99	-3.50	0.0106983	0.1027917	-2.69	FALSE
261124_at	hypothetical protein predicted by	---	AT1G04900	-1.47	-0.56	-3.50	0.0107095	0.1028564	-2.69	FALSE
262482_at	SRG1-like protein Strong homol	SRG1	AT1G17020	3.98	1.99	3.50	0.0107146	0.1028618	-2.69	TRUE
262347_at	unknown protein similar to hypot	---	AT1G64110	1.55	0.64	3.49	0.0107197	0.1028677	-2.69	FALSE
250978_at	putative protein contains transm	---	AT5G03080	1.38	0.46	3.49	0.0107521	0.1028747	-2.70	FALSE

248492_at	putative protein similar to unknov	---	AT5G51040	1.41	0.50	3.49	0.0107343	0.1028747	-2.69	FALSE
256836_at	pyruvate kinase, putative similar	PKP-ALPH/	AT3G22960	-1.64	-0.71	-3.49	0.0107321	0.1028747	-2.69	FALSE
254810_at	putative protein pectinesterase -	PME1	AT4G12390	-2.50	-1.32	-3.49	0.0107518	0.1028747	-2.70	FALSE
262092_at	unknown protein	---	AT1G56150	-3.38	-1.76	-3.49	0.0107338	0.1028747	-2.69	FALSE
245364_at	hypothetical protein ;supported b	---	AT4G15790	-1.63	-0.70	-3.49	0.0107489	0.1028747	-2.70	FALSE
250020_at	putative protein contains similarit	---	AT5G18180	1.59	0.67	3.49	0.0107506	0.1028747	-2.70	FALSE
265869_at	putative two-component respons	ARR14	AT2G01760	-1.68	-0.75	-3.49	0.0107565	0.1028747	-2.70	FALSE
260041_at	unknown protein similar to hypotl	---	AT1G68780	-1.57	-0.65	-3.49	0.0107681	0.1028994	-2.70	FALSE
252463_at	putative protein ;supported by fu	---	AT3G47070	-2.20	-1.14	-3.49	0.0107665	0.1028994	-2.70	FALSE
259761_at	putative acyl-CoA synthetase sin	LACS9	AT1G77590	1.80	0.85	3.49	0.0107802	0.1029715	-2.70	FALSE
265182_at	putative auxin-induced protein ;s	---	AT1G23740	-1.77	-0.82	-3.49	0.0107888	0.1030107	-2.70	FALSE
267559_at	putative cytochrome P450	CYP76C2	AT2G45570	5.70	2.51	3.49	0.0108294	0.1030173	-2.70	TRUE
258114_at	putative cytochrome P450 simila	CYP72A13	AT3G14660	-1.47	-0.56	-3.49	0.0108408	0.1030173	-2.70	FALSE
254357_at	nifU-like protein nifU protein hon	ISU1	AT4G22220	-1.35	-0.43	-3.49	0.0108437	0.1030173	-2.70	FALSE
262117_at	ribosomal protein L19, putative s	emb2386	AT1G02780	-1.64	-0.72	-3.49	0.0108219	0.1030173	-2.70	FALSE
249040_at	eukaryotic translation initiation fa	---	AT5G44320	-1.50	-0.59	-3.49	0.0108189	0.1030173	-2.70	FALSE
263326_at	unknown protein ; supported by	---	AT2G04280	-1.79	-0.84	-3.49	0.0107999	0.1030173	-2.70	FALSE
251552_at	ribosomal protein L11 -like ribos	---	AT3G58700	-2.07	-1.05	-3.49	0.0108061	0.1030173	-2.70	FALSE
263716_at	26S proteasome regulatory subu	RPN1A	AT2G20580	-1.38	-0.46	-3.49	0.0108402	0.1030173	-2.70	FALSE
261669_at	unknown protein similar to hypotl	---	AT1G18490	-1.35	-0.43	-3.49	0.0108194	0.1030173	-2.70	FALSE
254686_at	putative protein putative oncoge	---	AT4G13720	-1.55	-0.63	-3.49	0.0108368	0.1030173	-2.70	FALSE
249284_at	unknown protein ;supported by f	---	AT5G41810	1.53	0.61	3.49	0.010824	0.1030173	-2.70	FALSE
255088_at	putative protein heat shock prote	---	AT4G09350	-1.93	-0.95	-3.49	0.0108128	0.1030173	-2.70	FALSE
253974_at	receptor protein kinase - like pro	---	AT4G26540	2.16	1.11	3.48	0.0108661	0.1031869	-2.71	TRUE
261644_s_a	hypothetical protein contains sim	ATCSA-1	AT1G19750 /,	-1.54	-0.62	-3.48	0.0108754	0.1032246	-2.71	FALSE
250996_at	putative protein BcDNA.LD2479	---	AT5G02530	-1.44	-0.52	-3.48	0.0108791	0.1032246	-2.71	FALSE
248134_at	putative protein contains similarit	---	AT5G54860	2.10	1.07	3.48	0.0108957	0.1033391	-2.71	FALSE
256106_at	unknown protein	---	AT1G16870	-1.44	-0.52	-3.48	0.0109066	0.103357	-2.71	FALSE
263582_at	unknown protein similar to hypotl	LYM2	AT2G17120	1.88	0.91	3.48	0.0109044	0.103357	-2.71	FALSE
245269_at	hypothetical protein ; supported b	---	AT4G14500	1.52	0.60	3.48	0.0109205	0.1033597	-2.71	FALSE
251416_at	putative protein various predicte	---	AT3G60400	-1.44	-0.53	-3.48	0.0109175	0.1033597	-2.71	FALSE
252418_at	hypothetical protein	---	AT3G47490	-1.64	-0.72	-3.48	0.0109125	0.1033597	-2.71	FALSE
252136_at	calmodulin-like protein flagellar c	---	AT3G50770	-8.51	-3.09	-3.48	0.0109361	0.1033787	-2.71	TRUE
258218_at	methyltransferase, putative simil	XPL1	AT3G17998 /,	-1.81	-0.85	-3.48	0.0109288	0.1033787	-2.71	FALSE
251669_at	putative protein hypothetical pro	---	AT3G57180	-2.24	-1.17	-3.48	0.0109331	0.1033787	-2.71	FALSE

259121_at	unknown protein	---	AT3G02220	-1.66	-0.73	-3.48	0.0109551	0.1034601	-2.72	FALSE
255328_at	putative leucyl tRNA synthetase	EMB2369	AT4G04350	-1.70	-0.77	-3.48	0.0109535	0.1034601	-2.72	FALSE
257717_at	unknown protein	EMB1865	AT3G18390	-1.64	-0.71	-3.48	0.0109583	0.1034601	-2.72	FALSE
245342_at	ribosomal protein ;supported by f	---	AT4G16720	-1.78	-0.83	-3.48	0.0109638	0.103469	-2.72	FALSE
250463_at	transcription factor OBF4	TGA4	AT5G10030	-1.58	-0.66	-3.48	0.0109717	0.1035011	-2.72	FALSE
261350_at	hypothetical protein predicted by	---	AT1G79770	-1.84	-0.88	-3.48	0.0109827	0.103562	-2.72	FALSE
262231_at	putative receptor protein similar	---	AT1G68740	-2.56	-1.36	-3.48	0.010989	0.1035777	-2.72	TRUE
252002_at	hypothetical protein YIP1 protein	---	AT3G52760	-1.45	-0.54	-3.47	0.0110061	0.103696	-2.72	FALSE
266490_at	unknown protein	---	AT2G07000	-1.61	-0.69	-3.47	0.0110343	0.1037475	-2.72	FALSE
247972_at	histone acetyltransferase HAT B	HAG2	AT5G56740	-1.74	-0.79	-3.47	0.011018	0.1037475	-2.72	FALSE
258726_at	Expressed protein ; supported by	---	AT3G11745	-1.42	-0.51	-3.47	0.0110329	0.1037475	-2.72	FALSE
256530_at	unknown protein	---	AT1G33290	-1.48	-0.56	-3.47	0.0110246	0.1037475	-2.72	FALSE
249459_at	peroxidase ATP24a	---	AT5G39580	8.91	3.15	3.47	0.0110308	0.1037475	-2.72	FALSE
253557_at	putative protein wall-associated	---	AT4G31110 /	-1.39	-0.47	-3.47	0.0110659	0.1040025	-2.73	FALSE
251985_at	thioredoxin -like protein cop c2,	---	AT3G53220	-1.62	-0.69	-3.47	0.0110754	0.1040484	-2.73	FALSE
253291_at	Expressed protein ; supported by	---	AT4G33865	-1.72	-0.78	-3.47	0.0110866	0.1041109	-2.73	FALSE
265815_at	predicted protein	---	AT2G17975	-1.34	-0.43	-3.47	0.0110914	0.1041127	-2.73	FALSE
253197_at	putative protein Cyanophora par	---	AT4G35250	-1.78	-0.83	-3.47	0.0111341	0.1042564	-2.73	TRUE
248962_at	putative protein contains similarit	FKBP13	AT5G45680	-1.93	-0.94	-3.47	0.0111182	0.1042564	-2.73	TRUE
260696_at	unknown protein	---	AT1G32520	-1.52	-0.60	-3.47	0.01113	0.1042564	-2.73	TRUE
256071_at	ubiquitin, putative similar to ubiq	---	AT1G13640	-1.82	-0.87	-3.47	0.0111337	0.1042564	-2.73	FALSE
261145_at	thioredoxin identical to GB:CAA	ATTRX4	AT1G19730	-1.49	-0.57	-3.47	0.0111201	0.1042564	-2.73	FALSE
259914_at	hypothetical protein predicted by	---	AT1G72640	-1.64	-0.71	-3.47	0.0111341	0.1042564	-2.73	FALSE
247212_at	putative protein similar to unknov	---	AT5G65040	1.40	0.49	3.47	0.0111393	0.1042627	-2.73	FALSE
257061_at	hypothetical protein predicted by	---	AT3G18250	2.03	1.02	3.46	0.0111571	0.1043513	-2.73	TRUE
265999_at	unknown protein ; supported by	---	AT2G24100	1.70	0.77	3.46	0.0111579	0.1043513	-2.73	FALSE
246301_at	calcium-dependent protein kinas	CPK13	AT3G51850	-1.44	-0.53	-3.46	0.0111716	0.1044364	-2.74	FALSE
252422_at	putative protein PIT1 - Arabidop	---	AT3G47550	1.79	0.84	3.46	0.0111974	0.1046344	-2.74	FALSE
263566_at	hypothetical protein predicted by	---	AT2G15340	1.56	0.64	3.46	0.0112024	0.1046381	-2.74	FALSE
252946_at	Expressed protein ; supported by	---	AT4G39235	-1.88	-0.91	-3.46	0.0112364	0.1048376	-2.74	TRUE
254831_at	Ribosomal protein L7Ae -like var	---	AT4G12600	-2.35	-1.23	-3.46	0.0112513	0.1048376	-2.74	FALSE
266003_at	hypothetical protein predicted by	---	AT2G37320	-1.71	-0.77	-3.46	0.0112389	0.1048376	-2.74	FALSE
246929_at	putative protein ; supported by ft	---	AT5G25210	-1.69	-0.76	-3.46	0.011247	0.1048376	-2.74	FALSE
266447_at	putative calcium binding protein ;	MSS3	AT2G43290	2.83	1.50	3.46	0.0112484	0.1048376	-2.74	FALSE
254687_at	cytochrome P450 monooxygena	CYP83A1	AT4G13770 /	-1.80	-0.85	-3.46	0.0112483	0.1048376	-2.74	FALSE

257149_at	prohibitin, putative similar to pro	ATPHB4	AT3G27280	-2.26	-1.18	-3.46	0.0112753	0.10489	-2.75	FALSE
260523_at	putative salt-inducible protein	EMB2654	AT2G41720	-1.76	-0.81	-3.46	0.0112724	0.10489	-2.74	FALSE
258502_at	unknown protein	---	AT3G02490	-1.97	-0.98	-3.46	0.0112621	0.10489	-2.74	FALSE
257401_at	hypothetical protein identical to h	SRO2	AT1G23550	1.66	0.73	3.46	0.011268	0.10489	-2.74	FALSE
255500_at	NAD+ ADP-ribosyltransferase	APP	AT4G02390	-1.65	-0.73	-3.46	0.0112852	0.1049392	-2.75	FALSE
267110_at	hypothetical protein predicted by	---	AT2G14800	-1.62	-0.70	-3.46	0.0112956	0.1049933	-2.75	FALSE
261955_at	proteasome regulatory subunit,	RPN12a	AT1G64520	-1.40	-0.48	-3.45	0.0113007	0.1049978	-2.75	FALSE
264864_at	hypothetical protein predicted by	---	AT1G24310	-1.89	-0.92	-3.45	0.0113102	0.1050006	-2.75	FALSE
260276_at	unknown protein	---	AT1G80450	2.54	1.35	3.45	0.0113102	0.1050006	-2.75	FALSE
264584_at	unknown protein Similar to Syne	---	AT1G05140	-1.55	-0.63	-3.45	0.0113202	0.1050501	-2.75	FALSE
258495_at	unknown protein ;supported by f	---	AT3G02690	-1.43	-0.51	-3.45	0.0113288	0.1050872	-2.75	FALSE
261317_at	cytochrome C oxidase assembly	---	AT1G53030	-1.48	-0.57	-3.45	0.011356	0.1051683	-2.75	TRUE
252929_at	putative fructose-bisphosphate a	---	AT4G38970	-1.46	-0.55	-3.45	0.0113549	0.1051683	-2.75	FALSE
252912_at	ribosomal protein S25 ribosoma	---	AT4G39200	-1.85	-0.89	-3.45	0.0113531	0.1051683	-2.75	FALSE
260904_at	unknown protein	NIMIN1	AT1G02450	4.09	2.03	3.45	0.0113546	0.1051683	-2.75	FALSE
260754_at	unknown protein	---	AT1G49000	2.53	1.34	3.45	0.0113776	0.1052563	-2.75	TRUE
247375_at	Expressed protein ; supported by	---	AT5G63135	-1.35	-0.43	-3.45	0.011382	0.1052563	-2.75	FALSE
252596_at	receptor-like protein kinase rece	---	AT3G45330	1.40	0.48	3.45	0.0113885	0.1052563	-2.76	FALSE
263529_at	ADP-ribosylation factor 3	ARF3	AT2G24765	-1.42	-0.51	-3.45	0.0113755	0.1052563	-2.75	FALSE
258314_at	putative RAS-related GTP-bindin	ATRABG3C	AT3G16100	-1.52	-0.60	-3.45	0.0113851	0.1052563	-2.76	FALSE
248334_s_a	unknown protein ; supported by	---	AT5G52370 /.	-2.00	-1.00	-3.45	0.0113958	0.1052805	-2.76	FALSE
250691_at	glycolate oxidase subunit D-like;	---	AT5G06580	-1.37	-0.45	-3.45	0.0114106	0.105332	-2.76	FALSE
251900_at	putative protein lateral root prim	SRS6	AT3G54430	-1.63	-0.71	-3.45	0.0114089	0.105332	-2.76	FALSE
250207_at	chalcone synthase (naringenin-c	TT4	AT5G13930	3.18	1.67	3.45	0.0114377	0.1054066	-2.76	FALSE
260815_at	chloroplast inner envelope prote	TIC110	AT1G06950	-1.92	-0.94	-3.45	0.0114344	0.1054066	-2.76	TRUE
257802_at	unknown protein	---	AT3G18770	-1.67	-0.74	-3.45	0.0114455	0.1054066	-2.76	FALSE
263539_at	putative tyrosine aminotransferas	TAT3	AT2G24850	12.15	3.60	3.45	0.0114391	0.1054066	-2.76	FALSE
253783_at	putative protein predicted protei	NPGR2	AT4G28600	1.52	0.60	3.45	0.0114464	0.1054066	-2.76	FALSE
246538_at	40S RIBOSOMAL PROTEIN S1	---	AT5G15520	-1.91	-0.93	-3.45	0.0114321	0.1054066	-2.76	FALSE
251200_at	putative protein PrMC3, Pinus ra	GID1B	AT3G63010	1.67	0.74	3.44	0.0114864	0.1055191	-2.76	TRUE
262488_at	unknown protein EST gb|AA586	---	AT1G21830	-2.15	-1.11	-3.44	0.0114765	0.1055191	-2.76	TRUE
246435_at	hypothetical protein ; supported	---	AT5G17460	-1.38	-0.47	-3.44	0.0114823	0.1055191	-2.76	FALSE
246758_at	60S ribosomal protein - like 60S	---	AT5G27850	-2.01	-1.01	-3.44	0.0114684	0.1055191	-2.76	FALSE
262166_at	myb-related transcription activat	---	AT1G74840	-1.66	-0.73	-3.44	0.0114784	0.1055191	-2.76	FALSE
253417_at	putative protein	PC-MYB1	AT4G32730	1.46	0.55	3.44	0.0114785	0.1055191	-2.76	FALSE

246252_s_a	patatin-like protein ;supported by	PLP1	AT4G37060 /.	1.37	0.46	3.44	0.0115113	0.1057059	-2.77	FALSE
263703_at	unknown protein ;supported by f	SRX	AT1G31170	-1.57	-0.65	-3.44	0.0115351	0.1058819	-2.77	FALSE
260613_at	unknown protein	---	AT1G53380	-1.51	-0.60	-3.44	0.0115403	0.1058866	-2.77	FALSE
250678_at	selenium-binding protein-like	---	AT5G06540	-1.40	-0.48	-3.44	0.0115607	0.1059166	-2.77	FALSE
255488_at	putative serine/threonine protein	---	AT4G02630	-1.67	-0.74	-3.44	0.0115548	0.1059166	-2.77	FALSE
254668_at	neoxanthin cleavage enzyme - li	NCED2	AT4G18350	1.63	0.70	3.44	0.0115539	0.1059166	-2.77	FALSE
245408_at	putative protein	---	AT4G17180	-1.59	-0.67	-3.44	0.0115621	0.1059166	-2.77	FALSE
247222_at	ABC transporter protein 1-like ; s	ATGCN5	AT5G64840	-1.91	-0.94	-3.44	0.0115695	0.105942	-2.77	FALSE
256257_at	arginine-tRNA-protein transferas	ATE2	AT3G11240	-1.41	-0.49	-3.44	0.0115817	0.1060109	-2.77	FALSE
265948_at	1-aminocyclopropane-1-carboxyl	ACO1	AT2G19590	1.52	0.61	3.44	0.0115883	0.1060283	-2.77	FALSE
253871_at	protochlorophyllide reductase pre	PORB	AT4G27440	-1.82	-0.87	-3.43	0.0116023	0.1061144	-2.77	TRUE
246792_at	putative protein predicted protei	---	AT5G27290	-2.32	-1.22	-3.43	0.0116091	0.1061338	-2.78	TRUE
252901_at	putative protein various predicte	---	AT4G39550	-1.43	-0.52	-3.43	0.0116259	0.1061641	-2.78	FALSE
264845_at	putative thioredoxin-m similar to	ATHM1	AT1G03680	-1.53	-0.61	-3.43	0.0116264	0.1061641	-2.78	FALSE
245961_at	putative protein predicted protein	---	AT5G19670	-1.58	-0.66	-3.43	0.01162	0.1061641	-2.78	FALSE
248132_at	SGP1 monomeric G-protein (eml	SGP1	AT5G54840	1.81	0.86	3.43	0.0116579	0.1063668	-2.78	FALSE
266796_at	predicted by genscan	---	AT2G02880	-1.47	-0.55	-3.43	0.0116546	0.1063668	-2.78	FALSE
256991_at	unknown protein	---	AT3G28600	1.40	0.48	3.43	0.0116762	0.1064058	-2.78	FALSE
250791_at	nucleic acid binding protein-like	AL1	AT5G05610	-1.43	-0.52	-3.43	0.011667	0.1064058	-2.78	FALSE
248823_s_a	unknown protein ;supported by f	---	AT5G46950 /.	17.17	4.10	3.43	0.011672	0.1064058	-2.78	FALSE
254650_at	hypothetical protein	---	---	1.40	0.48	3.43	0.0116971	0.1064909	-2.78	FALSE
259528_at	hypothetical protein	---	AT1G12330	-1.78	-0.83	-3.43	0.0117042	0.1064909	-2.78	FALSE
259883_at	putative ribophorin I (dolichyl-dip	---	AT1G76400	-1.61	-0.68	-3.43	0.011692	0.1064909	-2.78	FALSE
266285_at	unknown protein	---	AT2G29180	-2.15	-1.10	-3.43	0.0117023	0.1064909	-2.78	FALSE
252147_at	putative protein several hypothet	---	AT3G51270	-1.80	-0.85	-3.43	0.0117176	0.1065305	-2.78	FALSE
251662_at	putative protein DNA-DIRECTEI	NRPE5	AT3G57080	-1.62	-0.70	-3.43	0.0117179	0.1065305	-2.78	FALSE
263876_at	putative RAS superfamily GTP-b	ATRAB7A	AT2G21880	1.72	0.78	3.43	0.0117494	0.1066719	-2.79	TRUE
247453_at	putative protein similar to unknov	---	AT5G62440	-1.65	-0.73	-3.42	0.0117594	0.1066719	-2.79	TRUE
251015_at	putative protein predicted protei	---	AT5G02480	-1.41	-0.49	-3.43	0.0117487	0.1066719	-2.79	TRUE
263934_at	hypothetical protein predicted by	EDA12	AT2G35950	-1.36	-0.45	-3.42	0.0117719	0.1066719	-2.79	FALSE
265332_at	hypothetical protein predicted by	---	AT2G18410	-1.59	-0.67	-3.42	0.0117763	0.1066719	-2.79	FALSE
253589_at	puative protein membrane-asso	---	AT4G30825	-1.73	-0.79	-3.42	0.0117676	0.1066719	-2.79	FALSE
257190_at	30S ribosomal protein S10, puta	---	AT3G13120	-1.82	-0.87	-3.42	0.0117619	0.1066719	-2.79	FALSE
254247_at	putative protein receptor protein	---	AT4G23260	2.25	1.17	3.43	0.0117453	0.1066719	-2.79	FALSE
255622_at	putative flavonol glucosyltransfe	GT72B1	AT4G01070	1.65	0.72	3.42	0.0117802	0.1066719	-2.79	FALSE

265226_at	unknown protein ; supported by	---	AT2G28430	-1.38	-0.47	-3.42	0.0117702	0.1066719	-2.79	FALSE
253684_at	nucleotide pyrophosphatase - lik	---	AT4G29690	1.54	0.63	3.42	0.0117891	0.1067097	-2.79	FALSE
264056_at	putative DOF zinc finger protein	---	AT2G28510	1.72	0.79	3.42	0.011797	0.1067388	-2.79	FALSE
249815_at	60S ribosomal protein L13 ; sup	---	AT5G23900	-1.81	-0.86	-3.42	0.0118221	0.106924	-2.79	FALSE
248283_at	pyruvate kinase ;supported by fu	PKP-BETA	AT5G52920	-1.98	-0.99	-3.42	0.0118284	0.1069388	-2.79	FALSE
266074_at	putative small nuclear ribonucleo	---	AT2G18740	-1.88	-0.91	-3.42	0.0118434	0.1069861	-2.80	FALSE
251295_at	putative protein several O-methy	---	AT3G62000	-1.68	-0.75	-3.42	0.0118477	0.1069861	-2.80	FALSE
254682_at	putative protein WERBP-1 - Nic	UNE16	AT4G13640	-1.54	-0.62	-3.42	0.0118456	0.1069861	-2.80	FALSE
247089_at	dimethyladenosine transferase-li	---	AT5G66360	-1.54	-0.62	-3.42	0.0118645	0.107095	-2.80	FALSE
262415_at	40S ribosomal protein S17, puta	emb1129	AT1G49400	-1.63	-0.70	-3.42	0.011874	0.1071382	-2.80	FALSE
245297_at	hypothetical protein ; supported b	---	AT4G16510	-1.57	-0.65	-3.42	0.0118875	0.1072177	-2.80	FALSE
262620_at	hypothetical protein predicted by	---	AT1G06540	1.40	0.48	3.42	0.0119103	0.1072534	-2.80	FALSE
252724_at	putative protein hypothetical pro	---	AT3G43540	-1.60	-0.67	-3.42	0.0119099	0.1072534	-2.80	FALSE
261888_at	ribosomal protein, putative simil	---	AT1G80800	-1.53	-0.62	-3.42	0.0119044	0.1072534	-2.80	FALSE
254742_at	putative protein various predicte	IIL1	AT4G13430	-1.36	-0.45	-3.42	0.0118996	0.1072534	-2.80	FALSE
255760_at	vacuolar-type H+-translocating i	---	AT1G16780	-1.48	-0.56	-3.41	0.0119178	0.1072786	-2.80	FALSE
248162_at	1,4-benzoquinone reductase-like	FQR1	AT5G54500	1.94	0.96	3.41	0.0119248	0.1072996	-2.80	TRUE
263948_at	similar to harpin-induced protein	YLS9	AT2G35980	3.03	1.60	3.41	0.0119369	0.1073243	-2.80	TRUE
257660_at	unknown protein ; supported by	WIP3	AT3G13360	-1.37	-0.46	-3.41	0.0119341	0.1073243	-2.80	FALSE
246429_at	farnesylated protein ATFP6-like	---	AT5G17450	2.71	1.44	3.41	0.0119456	0.1073596	-2.80	FALSE
264712_at	unknown protein	ECT11	AT1G09810	-1.69	-0.76	-3.41	0.0119895	0.1073757	-2.81	FALSE
256268_at	retinoblastoma-related protein, p	RBR1	AT3G12280	-1.65	-0.72	-3.41	0.0119781	0.1073757	-2.81	FALSE
247709_at	D-xylose-H+ symporter - like pro	---	AT5G59250	-1.61	-0.69	-3.41	0.0119881	0.1073757	-2.81	FALSE
251327_at	prolyl aminopeptidase-like prote	---	AT3G61540	-1.36	-0.44	-3.41	0.0119897	0.1073757	-2.81	FALSE
249092_at	putative protein similar to unknov	---	AT5G43710	-1.54	-0.63	-3.41	0.0119552	0.1073757	-2.81	FALSE
262003_at	unknown protein	---	AT1G64460	1.49	0.57	3.41	0.0119592	0.1073757	-2.81	FALSE
263003_at	protein phosphatase 2A 72 kDa	---	AT1G54450	1.37	0.46	3.41	0.0119645	0.1073757	-2.81	FALSE
252659_at	putative protein	---	AT3G44430	-1.54	-0.63	-3.41	0.0119867	0.1073757	-2.81	FALSE
252964_at	receptor-like protein kinase - like	---	AT4G38830	1.46	0.54	3.41	0.0119737	0.1073757	-2.81	FALSE
257288_at	anthocyanin 5-aromatic acyltran	---	AT3G29670	1.44	0.53	3.40	0.0120778	0.1078329	-2.82	FALSE
261532_at	amino acid permease, putative s	---	AT1G71680	1.42	0.51	3.40	0.0120733	0.1078329	-2.82	FALSE
249076_at	putative protein similar to unknov	TOM22-V	AT5G43970	-1.71	-0.78	-3.40	0.0120786	0.1078329	-2.82	FALSE
255961_at	UDP-glucose glucosyltransferas	AtUGT85A7	AT1G22340	1.97	0.97	3.40	0.0120752	0.1078329	-2.82	FALSE
254501_at	hypothetical protein	PTAC14	AT4G20130	-1.93	-0.95	-3.41	0.0120576	0.1078329	-2.81	FALSE
254917_at	putative protein various hypothet	---	AT4G11350	1.85	0.89	3.41	0.0120646	0.1078329	-2.81	FALSE

264525_at	unknown protein Highly Similar t	ATBCAT-1	AT1G10060	-4.28	-2.10	-3.41	0.0120532	0.1078329	-2.81	FALSE
251120_at	chloroplast ribosomal L1 - like pr	---	AT3G63490	-1.63	-0.70	-3.40	0.0120768	0.1078329	-2.82	FALSE
258655_at	putative isocitrate dehydrogenas	---	AT3G09810	1.72	0.79	3.40	0.0120891	0.1078844	-2.82	FALSE
254229_at	hypothetical protein ; supported	---	AT4G23610	3.45	1.79	3.40	0.0121109	0.1079944	-2.82	TRUE
253388_at	putative protein ; supported by c	---	AT4G32910	-1.77	-0.82	-3.40	0.0121066	0.1079944	-2.82	FALSE
264862_at	hypothetical protein predicted by	---	AT1G24330	1.79	0.84	3.40	0.0121179	0.1080144	-2.82	FALSE
264183_at	unknown protein	CLV2	AT1G65380	-1.53	-0.61	-3.40	0.0121312	0.1080905	-2.82	FALSE
262247_at	unknown protein contains similar	D-CDES	AT1G48420	-1.45	-0.54	-3.40	0.012138	0.1081094	-2.82	FALSE
260686_at	unknown protein ; supported by c	---	AT1G17620	2.32	1.21	3.40	0.0121847	0.1081677	-2.82	TRUE
249065_at	putative protein similar to unknov	---	AT5G44260	-2.09	-1.06	-3.40	0.0122211	0.1081677	-2.83	TRUE
265909_at	unknown protein ;supported by f	---	AT2G25720	-1.51	-0.60	-3.40	0.0122156	0.1081677	-2.83	FALSE
255317_at	putative vesicle transfer ATPase	---	AT4G04180	-1.99	-0.99	-3.40	0.0122208	0.1081677	-2.83	TRUE
266104_at	putative phosphatidate cytidylyltr	---	AT2G45150	-1.52	-0.61	-3.40	0.0122238	0.1081677	-2.83	FALSE
246573_at	copper amine oxidase, putative	---	AT1G31690	1.70	0.77	3.40	0.0122015	0.1081677	-2.83	FALSE
246842_at	Expressed protein ; supported by	---	AT5G26731	1.95	0.97	3.40	0.0121635	0.1081677	-2.82	FALSE
264293_at	cell division cycle protein, putativ	APC6	AT1G78770	-1.39	-0.47	-3.40	0.012202	0.1081677	-2.83	FALSE
260937_at	hypothetical protein contains sim	---	AT1G45160	1.36	0.45	3.40	0.012154	0.1081677	-2.82	FALSE
263633_at	putative SCARECROW gene reg	SCL21	AT2G04890	-1.60	-0.68	-3.40	0.0122127	0.1081677	-2.83	FALSE
251415_at	putative protein	---	AT3G60380	-1.44	-0.52	-3.40	0.0121747	0.1081677	-2.82	FALSE
262180_at	phosphoglycerate mutase, putat	PGM	AT1G78050	1.42	0.51	3.40	0.0121638	0.1081677	-2.82	FALSE
245545_at	UTP-glucose glucosyltransferase	UGT71B5	AT4G15280	1.63	0.70	3.40	0.0122252	0.1081677	-2.83	FALSE
266277_at	putative tropinone reductase	---	AT2G29310	-1.53	-0.61	-3.40	0.0122174	0.1081677	-2.83	FALSE
256654_at	ribosomal protein, putative simila	---	AT3G18880	-1.77	-0.82	-3.40	0.012196	0.1081677	-2.83	FALSE
246547_at	seed maturation -like protein see	---	AT5G14970	-1.69	-0.76	-3.40	0.0121654	0.1081677	-2.82	FALSE
245261_at	Expressed protein ; supported by	---	AT4G14385	-1.43	-0.51	-3.40	0.0121784	0.1081677	-2.82	FALSE
247100_at	selenium-binding protein-like	---	AT5G66520	-1.50	-0.58	-3.39	0.0122323	0.1081887	-2.83	FALSE
261422_at	unknown protein	NDF6	AT1G18730	-1.59	-0.67	-3.39	0.0122399	0.1082137	-2.83	FALSE
251141_at	Expressed protein ; supported by	---	AT5G01075	2.07	1.05	3.39	0.0122447	0.1082149	-2.83	TRUE
255967_at	protein phosphatase type 2C, pu	---	AT1G22280	1.60	0.68	3.39	0.0122567	0.1082789	-2.83	FALSE
261552_at	receptor protein kinase, putative	---	AT1G63430	-1.52	-0.61	-3.39	0.0122701	0.1083546	-2.83	FALSE
251794_at	mannose-1-phosphate guanylylt	---	AT3G55590	1.40	0.49	3.39	0.0122868	0.1084606	-2.83	FALSE
256887_at	hypothetical protein predicted by	---	AT3G15150	-1.54	-0.63	-3.39	0.012298	0.1084757	-2.83	FALSE
258174_at	hypothetical protein contains Pfa	---	AT3G21470	-1.49	-0.58	-3.39	0.0122968	0.1084757	-2.83	FALSE
248663_at	putative protein strong similarity t	---	AT5G48590	-1.36	-0.44	-3.39	0.0123075	0.1085172	-2.83	FALSE
261098_at	unknown protein	---	AT1G62970	-1.46	-0.54	-3.39	0.0123139	0.1085321	-2.84	FALSE

256593_at	hypothetical protein similar to put	---	AT3G28510	2.88	1.53	3.39	0.0123189	0.108534	-2.84	FALSE
267033_at	unknown protein ;supported by f	---	AT2G38450	-1.36	-0.44	-3.39	0.0123462	0.1086869	-2.84	FALSE
252281_at	putative protein various predicted	---	AT3G49320	-1.69	-0.76	-3.39	0.0123546	0.1086869	-2.84	FALSE
255510_at	polycomb group - like protein sir	SWN	AT4G02020	-1.68	-0.75	-3.39	0.0123649	0.1086869	-2.84	FALSE
251755_at	putative protein predicted protei	---	AT3G55790	1.86	0.89	3.39	0.0123644	0.1086869	-2.84	FALSE
249310_at	putative protein contains similarit	---	AT5G41520	-1.53	-0.61	-3.39	0.0123484	0.1086869	-2.84	FALSE
248380_at	phosphoglucomutase (emb|CAB	PGM	AT5G51820	-2.15	-1.11	-3.39	0.0123575	0.1086869	-2.84	FALSE
266813_at	unknown protein	---	AT2G44920	-1.60	-0.68	-3.39	0.0123806	0.1087831	-2.84	FALSE
262580_at	hypothetical protein Similar to gb	---	AT1G15330	-1.71	-0.77	-3.39	0.0123869	0.1087969	-2.84	FALSE
252475_s_a	putative protein several hypothet	PCL1	AT3G46640 ///	1.62	0.69	3.38	0.0123987	0.1088581	-2.84	FALSE
265301_s_a	putative MYB family transcription	---	AT2G13960 ///	-1.49	-0.57	-3.38	0.0124255	0.1089762	-2.84	FALSE
252606_at	carboxypeptidase precursor-like	scpl48	AT3G45010	2.71	1.44	3.38	0.0124182	0.1089762	-2.84	FALSE
253665_at	hypothetical protein	---	AT4G30230	1.98	0.99	3.38	0.0124264	0.1089762	-2.84	FALSE
261270_at	initiation factor 5A-4, putative sir	FBR12	AT1G26630	-1.40	-0.49	-3.38	0.0124447	0.1090946	-2.85	FALSE
254504_at	putative protein RNPL, Homo sa	---	AT4G20030	-1.86	-0.90	-3.38	0.0124579	0.1091681	-2.85	FALSE
248331_at	putative protein contains similarit	---	AT5G52650	-1.95	-0.96	-3.38	0.0124635	0.109175	-2.85	FALSE
262351_at	beta-galactosidase (BGAL), puta	BGAL17	AT1G72990	-1.37	-0.45	-3.38	0.0124758	0.1092409	-2.85	FALSE
256723_at	unknown protein ;supported by f	---	AT2G34160	-1.36	-0.45	-3.38	0.0125007	0.109249	-2.85	FALSE
264286_at	unknown protein ;supported by fu	PPR336	AT1G61870	-1.96	-0.97	-3.38	0.0124886	0.109249	-2.85	FALSE
247168_at	putative protein contains similarit	---	AT5G65860	-1.60	-0.68	-3.38	0.0124937	0.109249	-2.85	FALSE
250186_at	putative protein apospory-assoc	---	AT5G14500	-1.60	-0.68	-3.38	0.0124962	0.109249	-2.85	FALSE
249799_at	serine palmitoyltransferase ; sup	LCB2	AT5G23670	-1.37	-0.45	-3.38	0.0124891	0.109249	-2.85	FALSE
256645_at	hypothetical protein predicted by	---	AT3G24250	1.38	0.47	3.38	0.0125185	0.1093418	-2.85	FALSE
261795_at	unknown protein ; supported by c	---	AT1G16010	1.39	0.47	3.38	0.0125209	0.1093418	-2.85	FALSE
261187_at	beta-1,3-glucanase precursor, p	---	AT1G32860	1.92	0.94	3.38	0.0125332	0.1093785	-2.85	FALSE
264336_at	hypothetical protein contains sim	---	AT1G70360	-1.55	-0.64	-3.38	0.0125347	0.1093785	-2.85	FALSE
251686_at	putative protein hypothetical prot	ATATG18D	AT3G56440	1.42	0.50	3.38	0.0125401	0.109384	-2.85	FALSE
255224_at	putative protein hypothetical pro	---	AT4G05400	-1.61	-0.69	-3.37	0.01257	0.1095919	-2.86	FALSE
253701_at	choline monooxygenase - like pr	---	AT4G29890	-1.64	-0.71	-3.37	0.0125735	0.1095919	-2.86	FALSE
262068_at	splicing factor Prp8, putative sim	SUS2	AT1G80070	-1.72	-0.78	-3.37	0.0126061	0.1096785	-2.86	FALSE
263255_at	unknown protein similar to stero	---	AT1G10490	-1.69	-0.76	-3.37	0.0126166	0.1096785	-2.86	FALSE
254711_at	putative protein	---	AT4G18060	-1.53	-0.62	-3.37	0.0126019	0.1096785	-2.86	FALSE
257786_at	hypothetical protein predicted by	---	AT3G26990	-1.68	-0.75	-3.37	0.0126078	0.1096785	-2.86	FALSE
257522_at	Yippee-like protein similar to Yip	---	AT3G08990	1.39	0.47	3.37	0.0126171	0.1096785	-2.86	FALSE
259924_at	putative DNA-binding protein sim	---	AT1G72740	-1.53	-0.61	-3.37	0.0125975	0.1096785	-2.86	FALSE

255793_at	Expressed protein ; supported by	---	AT2G33250	-1.60	-0.68	-3.37	0.0126106	0.1096785	-2.86	FALSE
249188_at	N-hydroxycinnamoyl benzoyltran	---	AT5G42830	2.70	1.43	3.37	0.0126316	0.1097622	-2.86	TRUE
264705_at	putative leucyl-tRNA synthetase	---	AT1G09620	-1.53	-0.62	-3.37	0.0126459	0.1097753	-2.86	FALSE
267525_at	putative glycine-rich protein	---	AT2G30560	1.35	0.43	3.37	0.0126475	0.1097753	-2.86	FALSE
247007_at	porin-like protein ;supported by f	VDAC2	AT5G67500	1.60	0.68	3.37	0.0126469	0.1097753	-2.86	FALSE
251951_s_a	putative protein predicted protei	---	AT1G55710 /	-1.48	-0.56	-3.37	0.0126572	0.1097774	-2.86	FALSE
247284_at	Isp4-like protein ; supported by f	OPT4	AT5G64410	2.37	1.25	3.37	0.0126704	0.1097774	-2.86	FALSE
249948_at	eIF-4AII - like protein EUKARYO	---	AT5G19210	-1.65	-0.72	-3.37	0.012674	0.1097774	-2.87	FALSE
260484_at	putative zinc finger protein simila	---	AT1G68360	1.50	0.59	3.37	0.0126665	0.1097774	-2.86	FALSE
265193_at	unknown protein ESTs gb|T1440	---	AT1G05070	-1.42	-0.51	-3.37	0.0126758	0.1097774	-2.87	FALSE
253606_at	putative protein component of ar	---	AT4G30530	2.21	1.14	3.37	0.0126766	0.1097774	-2.87	FALSE
266977_at	putative phospholipase	---	AT2G39420	2.58	1.37	3.37	0.0126999	0.1098182	-2.87	TRUE
257835_at	cytochrome P450 monooxygena	CYP82G1	AT3G25180	3.26	1.70	3.37	0.0127025	0.1098182	-2.87	FALSE
264279_s_a	glycoprotein(EP1), putative simil	---	AT1G78820 /	1.69	0.76	3.37	0.0126963	0.1098182	-2.87	FALSE
267289_at	putative protein kinase contains a	---	AT2G23770	1.39	0.47	3.37	0.012693	0.1098182	-2.87	FALSE
261405_at	unknown protein ;supported by fu	---	AT1G18740	2.18	1.12	3.37	0.0127054	0.1098182	-2.87	FALSE
258085_at	unknown protein ; supported by	---	AT3G26100	1.55	0.63	3.37	0.0127273	0.1099494	-2.87	FALSE
258006_at	cysteine proteinase non-consen	---	AT3G19400	-1.69	-0.76	-3.36	0.0127302	0.1099494	-2.87	FALSE
253492_at	enoyl-CoA hydratase - like prote	---	AT4G31810	-2.56	-1.36	-3.36	0.0127408	0.1099717	-2.87	TRUE
260324_at	unknown protein similar to hypot	ISPF	AT1G63970	-1.61	-0.69	-3.36	0.0127424	0.1099717	-2.87	FALSE
261900_at	unknown protein ;supported by fu	---	AT1G80940	-1.46	-0.54	-3.36	0.0127681	0.1100911	-2.87	FALSE
259928_at	DNA polymerase type I, putative	---	AT1G34380	-1.91	-0.94	-3.36	0.012767	0.1100911	-2.87	FALSE
259381_s_a	putative lectin contains Pfam pro	NSP1	AT3G16390 /	4.91	2.29	3.36	0.0127708	0.1100911	-2.87	FALSE
246442_at	hypothetical protein ;supported b	---	AT5G17610	-1.40	-0.48	-3.36	0.0127909	0.1101812	-2.87	FALSE
265027_at	putative ribonuclease III similar to	NFD2	AT1G24450	-1.64	-0.71	-3.36	0.0127893	0.1101812	-2.87	FALSE
257580_at	hypothetical protein	---	AT3G06210	-1.50	-0.59	-3.36	0.012804	0.110211	-2.88	FALSE
247326_at	peroxidase ATP3a homolog ;sup	---	AT5G64110	5.04	2.33	3.36	0.0127999	0.110211	-2.88	FALSE
265953_at	unknown protein	---	AT2G37478 /	-1.43	-0.51	-3.36	0.0128348	0.1104346	-2.88	FALSE
263912_at	starch branching enzyme II	SBE2.1	AT2G36390	-1.64	-0.72	-3.36	0.0128555	0.1105712	-2.88	FALSE
251502_at	putative protein several hypothet	---	AT3G59130	1.40	0.48	3.36	0.0128723	0.1105962	-2.88	FALSE
254564_at	neoxanthin cleavage enzyme-lik	NCED4	AT4G19170	-1.90	-0.92	-3.36	0.0128827	0.1105962	-2.88	FALSE
254865_s_a	putative protein, fragment other	---	AT4G05350 /	1.40	0.48	3.36	0.012876	0.1105962	-2.88	FALSE
254148_at	hsp 70-like protein heat shock 7	cpHsc70-1	AT4G24280	-1.46	-0.55	-3.36	0.0128798	0.1105962	-2.88	FALSE
261754_at	alpha-amylase, putative similar t	AMY2	AT1G76130	2.75	1.46	3.36	0.0128732	0.1105962	-2.88	FALSE
253553_at	putative protein LipB gene, Proc	---	AT4G31050	-1.52	-0.60	-3.36	0.0128994	0.1106979	-2.88	FALSE

253490_at	methyltransferase - like protein r	---	AT4G31790	-2.14	-1.10	-3.35	0.0129063	0.1107154	-2.88	TRUE
254889_at	osmotin precursor ;supported by	ATOSM34	AT4G11650	-1.89	-0.92	-3.35	0.0129295	0.1107541	-2.89	TRUE
257685_at	unknown protein	---	AT3G12770	-1.57	-0.65	-3.35	0.0129836	0.1107541	-2.89	FALSE
262313_at	unknown protein ;supported by fu	---	AT1G70900	-1.74	-0.80	-3.35	0.0129432	0.1107541	-2.89	FALSE
252925_at	ES43 like protein ES43 protein -	SHL1	AT4G39100	-1.61	-0.69	-3.35	0.0129691	0.1107541	-2.89	FALSE
246965_at	methyltransferase-like protein m	---	AT5G24840	-1.83	-0.88	-3.35	0.0129525	0.1107541	-2.89	FALSE
264678_at	putative U2 small nuclear ribonu	U2A'	AT1G09760	-1.47	-0.56	-3.35	0.0129708	0.1107541	-2.89	FALSE
246904_at	DNA methyltransferase PMT1 -	DNMT2	AT5G25480	-1.55	-0.63	-3.35	0.0129533	0.1107541	-2.89	FALSE
258849_at	putative UDP-glucose pyrophosp	UGP	AT3G03250	-1.63	-0.71	-3.35	0.012978	0.1107541	-2.89	FALSE
258514_at	unknown protein ; supported by	---	AT3G06610	-1.40	-0.49	-3.35	0.0129226	0.1107541	-2.88	FALSE
266780_at	putative ligand-gated ion channe	ATGLR2.8	AT2G29110	1.82	0.87	3.35	0.0129624	0.1107541	-2.89	FALSE
246110_at	putative protein predicted protein	---	AT5G20140	-1.83	-0.87	-3.35	0.0129395	0.1107541	-2.89	FALSE
254158_at	putative protein dihydrofolate re	---	AT4G24380	5.00	2.32	3.35	0.0129813	0.1107541	-2.89	FALSE
248339_at	prolyl tRNA synthetase	OVA6	AT5G52520	-1.50	-0.58	-3.35	0.012973	0.1107541	-2.89	FALSE
260872_at	hypothetical protein predicted by	---	AT1G21350	-1.78	-0.83	-3.35	0.0129686	0.1107541	-2.89	FALSE
263763_at	Expressed protein ; supported by	---	AT2G21385	-2.00	-1.00	-3.35	0.0129711	0.1107541	-2.89	FALSE
255248_at	Oxygen-evolving enhancer prote	PSBQ-2	AT4G05180	-1.34	-0.42	-3.35	0.0129981	0.1108362	-2.89	FALSE
248508_at	histone acetyltransferase ;suppo	ELO3	AT5G50320	-1.66	-0.73	-3.35	0.013006	0.110862	-2.89	FALSE
258673_at	unknown protein	---	AT3G08620	-1.73	-0.79	-3.35	0.0130171	0.11088	-2.89	TRUE
260275_at	hypothetical protein predicted by	---	AT1G80610	1.45	0.53	3.35	0.0130178	0.11088	-2.89	FALSE
247357_at	receptor-like protein kinase ; sup	---	AT5G63710	-1.48	-0.56	-3.35	0.0130505	0.1111168	-2.90	FALSE
258297_at	Expressed protein ; supported by	---	AT3G23325	-1.50	-0.58	-3.35	0.0130674	0.1111775	-2.90	FALSE
266297_at	putative proliferating cell nuclear	PCNA2	AT2G29570	-3.74	-1.90	-3.35	0.0130723	0.1111775	-2.90	FALSE
253654_at	putative protein several hypothet	---	AT4G30060	2.28	1.19	3.35	0.013065	0.1111775	-2.90	FALSE
261852_at	unknown protein ;supported by fu	---	AT1G50440	1.37	0.45	3.34	0.0130781	0.1111862	-2.90	FALSE
254821_at	hypothetical protein	---	AT4G12540	1.40	0.49	3.34	0.013099	0.1113224	-2.90	FALSE
258640_at	hypothetical protein predicted by	---	AT3G07930	-1.61	-0.68	-3.34	0.013108	0.1113567	-2.90	FALSE
260127_at	hypothetical protein similar to hy	---	AT1G36320	-1.71	-0.77	-3.34	0.0131319	0.1113782	-2.90	FALSE
265090_at	putative protein phosphatase 2A	---	AT1G03960	-1.46	-0.55	-3.34	0.0131341	0.1113782	-2.90	FALSE
247507_at	putative protein predicted protein	APO3	AT5G61930	-2.12	-1.08	-3.34	0.013131	0.1113782	-2.90	FALSE
247505_at	signal recognition particle - like p	---	AT5G61970	-1.36	-0.44	-3.34	0.0131246	0.1113782	-2.90	FALSE
262104_at	hypothetical protein predicted by	LPA1	AT1G02910	-1.46	-0.55	-3.34	0.0131349	0.1113782	-2.90	FALSE
253173_at	putative protein pEARLI 4, Arabi	---	AT4G35110	3.06	1.62	3.34	0.0131547	0.1115042	-2.90	FALSE
259297_at	putative disease resistance prote	AtRLP30	AT3G05360	2.64	1.40	3.34	0.0131613	0.1115193	-2.90	TRUE
260427_at	hypothetical protein predicted by	---	AT1G72430	-2.52	-1.34	-3.34	0.013169	0.1115428	-2.90	FALSE

263168_at	putative glutaredoxin Strong simi	---	AT1G03020	-3.41	-1.77	-3.34	0.0132161	0.1119006	-2.91	FALSE
258338_at	putative L-asparaginase similar t	---	AT3G16150	1.96	0.97	3.34	0.0132414	0.1119478	-2.91	FALSE
251634_at	putative protein putative zinc fin	---	AT3G57480	1.48	0.56	3.34	0.013235	0.1119478	-2.91	FALSE
252632_s_a	disease resistance protein -like	RPP1	AT3G44480 /	1.50	0.59	3.34	0.0132379	0.1119478	-2.91	FALSE
249007_at	unknown protein ;supported by f	---	AT5G44650	-1.90	-0.92	-3.34	0.0132361	0.1119478	-2.91	FALSE
254670_at	teosinte branched1 - like protein	---	AT4G18390	-1.91	-0.93	-3.33	0.0132516	0.1119926	-2.91	FALSE
259380_at	putative ABC transporter similar	PDR1	AT3G16340	1.59	0.66	3.33	0.0132783	0.1119953	-2.91	FALSE
251451_s_a	putative protein several hypothet	---	AT3G60040 /	-1.48	-0.56	-3.33	0.0132737	0.1119953	-2.91	FALSE
260223_at	putative exonuclease contains P	---	AT1G74390	-1.45	-0.53	-3.33	0.0132646	0.1119953	-2.91	FALSE
254835_s_a	flavonoid 3,5-hydroxylase -like p	CYP706A5	AT4G12310 /	-2.09	-1.07	-3.33	0.0132813	0.1119953	-2.91	FALSE
245065_at	unknown protein ; supported by	---	AT2G39750	-1.37	-0.45	-3.33	0.0132569	0.1119953	-2.91	FALSE
267382_at	unknown protein	---	AT2G44300	1.82	0.86	3.33	0.0132752	0.1119953	-2.91	FALSE
257799_at	protein kinase, putative similar t	---	AT3G15890	-1.48	-0.56	-3.33	0.0133067	0.1120435	-2.91	FALSE
258134_at	rubisco expression protein, puta	---	AT3G24530	1.71	0.77	3.33	0.0133031	0.1120435	-2.91	FALSE
247455_at	MYB96 transcription factor-like p	MYB96	AT5G62470	1.91	0.93	3.33	0.0132933	0.1120435	-2.91	FALSE
251325_s_a	Lhca2 protein ;supported by full-	LHCA2	AT3G61470 /	-1.33	-0.41	-3.33	0.013297	0.1120435	-2.91	FALSE
262910_at	unknown protein ;supported by fu	---	AT1G59710	1.68	0.75	3.33	0.013325	0.1121566	-2.92	TRUE
258241_at	hypothetical protein similar to hy	LBD25	AT3G27650	1.68	0.75	3.33	0.0133307	0.1121628	-2.92	FALSE
255801_at	putative protein heat shock prote	---	AT4G10130	-1.39	-0.47	-3.33	0.0133425	0.1122209	-2.92	FALSE
247074_at	putative protein contains similarit	---	AT5G66590	-1.70	-0.77	-3.33	0.01335	0.1122421	-2.92	TRUE
255714_at	contains weak similarity to S. cer	---	AT4G00300	1.53	0.61	3.33	0.0133803	0.1123846	-2.92	TRUE
262756_at	putative transport protein may be	אוק-06	AT1G16370	3.80	1.93	3.33	0.0133817	0.1123846	-2.92	TRUE
265985_at	hypothetical protein predicted by	ATPUP5	AT2G24220	-1.39	-0.48	-3.33	0.0133781	0.1123846	-2.92	FALSE
247277_at	putative protein similar to unknov	---	AT5G64420	-1.47	-0.56	-3.33	0.0133923	0.1123861	-2.92	FALSE
264748_at	hypothetical protein predicted by	EMB25	AT1G70070	-1.37	-0.45	-3.33	0.0133981	0.1123861	-2.92	FALSE
256779_at	beta-fructofuranosidase, putative	AtcwINV5	AT3G13784	1.34	0.43	3.33	0.0134016	0.1123861	-2.92	FALSE
260260_at	putative reductase similar to cin	---	AT1G68540	-1.64	-0.72	-3.33	0.013389	0.1123861	-2.92	FALSE
258542_at	unknown protein	---	AT3G07030	-1.56	-0.64	-3.33	0.0134284	0.1125415	-2.92	FALSE
256251_at	hypothetical protein predicted by	---	AT3G11330	1.63	0.71	3.32	0.01343	0.1125415	-2.92	FALSE
257218_at	unknown protein similar to DAG	---	AT3G15000	-1.42	-0.50	-3.32	0.0134549	0.1125894	-2.93	FALSE
246700_at	cysteine synthase - like cysteine	---	AT5G28030	-2.14	-1.10	-3.32	0.0134604	0.1125894	-2.93	FALSE
266847_at	hypothetical protein predicted by	emb1345	AT2G26060	-1.59	-0.67	-3.32	0.0134505	0.1125894	-2.93	FALSE
249001_at	putative protein strong similarity t	---	AT5G44990	3.39	1.76	3.32	0.0134558	0.1125894	-2.93	FALSE
253779_at	receptor-like protein kinase 5 pre	HAE	AT4G28490	2.26	1.17	3.32	0.0134546	0.1125894	-2.93	FALSE
252707_at	transporter-like protein multidrug	ZIFL2	AT3G43790	-1.59	-0.67	-3.32	0.0134812	0.1127221	-2.93	FALSE

250589_at	transcription factor (gb|AAD5309	MYB76	AT5G07700	2.84	1.50	3.32	0.0134967	0.1128101	-2.93	TRUE
266484_at	putative putative sister-chromatic	SCC3	AT2G47980	-1.48	-0.57	-3.32	0.0135159	0.1129292	-2.93	FALSE
253220_s_a	putative protein phospholipase C	---	AT4G34920 /	1.69	0.75	3.32	0.0135245	0.1129601	-2.93	FALSE
267090_at	unknown protein ; supported by	CXIP2	AT2G38270	-1.36	-0.45	-3.32	0.0135415	0.1130351	-2.93	FALSE
263564_s_a	DNA-directed RNA polymerase	NRPB3	AT2G15400 /	-1.47	-0.55	-3.32	0.0135434	0.1130351	-2.93	FALSE
248037_at	sexual differentiation process pro	OPT1	AT5G55930	2.46	1.30	3.32	0.0135569	0.1131062	-2.93	FALSE
247628_at	putative protein	---	AT5G60400	-1.68	-0.75	-3.32	0.0135821	0.1132753	-2.94	FALSE
252239_at	putative protein putative protein	---	AT3G49990	-1.88	-0.91	-3.32	0.0135931	0.1133253	-2.94	FALSE
251391_at	putative protein weak homology	---	AT3G60910	-1.56	-0.65	-3.32	0.0136088	0.1133735	-2.94	FALSE
266235_at	putative phloem-specific lectin	AtPP2-B10	AT2G02360	1.66	0.73	3.32	0.0136077	0.1133735	-2.94	FALSE
247635_at	serine/threonine-protein kinase -	GRIK2	AT5G60548 /	1.37	0.46	3.31	0.0136158	0.1133908	-2.94	FALSE
247747_at	putative protein predicted protei	---	AT5G59000	-1.66	-0.73	-3.31	0.0136229	0.1134079	-2.94	FALSE
265403_at	putative Ta11-like non-LTR retro	---	---	1.51	0.60	3.31	0.0136312	0.1134358	-2.94	FALSE
262207_at	hypothetical protein predicted by	PTAC2	AT1G74850	-1.61	-0.69	-3.31	0.0136448	0.1134663	-2.94	FALSE
245668_at	dormancy-associated protein, pu	DYL1	AT1G28330	-1.65	-0.72	-3.31	0.0136443	0.1134663	-2.94	FALSE
258284_at	putative ribosomal protein similar	---	AT3G16080	-2.27	-1.18	-3.31	0.0136551	0.1135102	-2.94	FALSE
252853_at	hypothetical protein ; supported b	---	AT4G39710	-2.37	-1.24	-3.31	0.0136655	0.1135555	-2.94	FALSE
259817_at	hypothetical protein predicted by	---	AT1G49880	-1.46	-0.54	-3.31	0.0136722	0.1135698	-2.94	FALSE
250272_at	callose synthase catalytic subun	ATGSL12	AT5G13000	-1.59	-0.67	-3.31	0.0136825	0.1136137	-2.94	FALSE
254116_at	hypothetical protein	---	AT4G24730	1.41	0.50	3.31	0.0137019	0.1137143	-2.94	FALSE
261278_at	hypothetical protein predicted by	DGL	AT1G05800	1.41	0.50	3.31	0.0137045	0.1137143	-2.95	FALSE
265884_at	unknown protein	---	AT2G42320	-1.60	-0.68	-3.31	0.0137221	0.1137643	-2.95	TRUE
250676_at	harpin-induced protein-like ; sup	NHL3	AT5G06320	1.90	0.92	3.31	0.0137255	0.1137643	-2.95	FALSE
250582_at	transcription factor-like protein e	---	AT5G07580	-2.11	-1.08	-3.31	0.0137175	0.1137643	-2.95	FALSE
248721_at	putative protein strong similarity t	GAUT4	AT5G47780	-1.33	-0.41	-3.31	0.0137451	0.1137916	-2.95	TRUE
245795_at	unknown protein contains similar	---	AT1G32160	-1.41	-0.49	-3.31	0.0137345	0.1137916	-2.95	FALSE
250286_at	auxin-responsive - like protein N	PBS3	AT5G13320	8.89	3.15	3.31	0.0137411	0.1137916	-2.95	FALSE
256319_at	trehalose-phosphatase, putative	---	AT1G35910	3.20	1.68	3.31	0.0137488	0.1137916	-2.95	FALSE
267278_at	unknown protein ; supported by	---	AT2G19350	-1.32	-0.40	-3.31	0.0137644	0.1138379	-2.95	FALSE
245438_at	growth regulator like protein	---	AT4G16650	-1.43	-0.52	-3.31	0.01376	0.1138379	-2.95	FALSE
267580_at	unknown protein	---	AT2G41990	1.55	0.63	3.31	0.013773	0.1138548	-2.95	FALSE
261204_s_a	Eukaryotic peptide chain release	ERF1-2	AT1G12920 /	-1.33	-0.42	-3.31	0.0137764	0.1138548	-2.95	FALSE
250288_at	auxin-responsive - like protein N	---	AT5G13350	1.49	0.57	3.31	0.0137867	0.1138991	-2.95	FALSE
266246_at	putative cytochrome P450	CYP94C1	AT2G27690	3.16	1.66	3.30	0.0138266	0.1139578	-2.95	FALSE
258716_at	unknown protein similar to a regi	---	AT3G09700	-1.83	-0.87	-3.30	0.0138157	0.1139578	-2.95	FALSE

257004_s_a	glycolate oxidase, putative simila	---	AT3G14130 /.	-1.38	-0.47	-3.30	0.0138298	0.1139578	-2.95	FALSE
256720_at	putative DOF zinc finger protein	---	AT2G34140	2.14	1.10	3.30	0.0138077	0.1139578	-2.95	FALSE
267213_at	60S ribosomal protein L7 ;suppo	---	AT2G44120	-2.07	-1.05	-3.30	0.0138318	0.1139578	-2.95	FALSE
247842_at	SPP30 - like protein SPP30, Sol	---	AT5G58030	-1.37	-0.46	-3.30	0.0137999	0.1139578	-2.95	FALSE
250719_at	putative protein contains similarit	---	AT5G06250	1.55	0.63	3.30	0.0138388	0.1139578	-2.96	FALSE
256812_at	hypothetical protein contains sim	---	AT3G21350	-1.39	-0.48	-3.30	0.013809	0.1139578	-2.95	FALSE
259017_at	unknown protein ; supported by	---	AT3G07310	-1.48	-0.57	-3.30	0.0138369	0.1139578	-2.96	FALSE
250159_at	40S ribosomal protein - like 40S	---	AT5G15200	-1.76	-0.82	-3.30	0.0138523	0.1140282	-2.96	FALSE
260133_at	ethylene-response protein, ETR	ETR1	AT1G66340	1.36	0.44	3.30	0.0138651	0.1140919	-2.96	FALSE
259179_at	hypothetical protein similar to put	---	AT3G01660	-1.64	-0.71	-3.30	0.0138751	0.1141327	-2.96	FALSE
251987_at	CYTOCHROME P450 71B5 ; su	CYP71B5	AT3G53280	-1.54	-0.62	-3.30	0.0138854	0.1141357	-2.96	TRUE
250482_at	putative protein	---	AT5G10320	-1.59	-0.67	-3.30	0.013883	0.1141357	-2.96	FALSE
262569_at	hypothetical protein Strong simila	---	AT1G15180	-1.82	-0.87	-3.30	0.0138968	0.114187	-2.96	FALSE
255547_at	putative CHP-rich zinc finger pro	---	AT4G01920	1.69	0.76	3.30	0.0139017	0.114187	-2.96	FALSE
265216_at	putative NPK1-related MAP kina	MAPKKK18	AT1G05100	1.90	0.93	3.30	0.0139124	0.1142339	-2.96	FALSE
266353_at	unknown protein ;supported by f	MLP328	AT2G01520	1.89	0.92	3.30	0.013924	0.114288	-2.96	FALSE
260082_at	putative mitochondrial carrier pro	---	AT1G78180	-1.61	-0.69	-3.30	0.0139344	0.1142911	-2.96	FALSE
246781_at	sugar transporter-like protein pu	SFP1	AT5G27350	2.29	1.20	3.30	0.0139301	0.1142911	-2.96	FALSE
267612_at	putative nitrate transporter	---	AT2G26690	2.91	1.54	3.30	0.013943	0.1143208	-2.96	FALSE
260199_at	unknown protein similar to putati	---	AT1G67590	-1.39	-0.48	-3.30	0.0139506	0.1143414	-2.96	FALSE
248955_at	putative protein contains similarit	GAS41	AT5G45600	-1.41	-0.49	-3.30	0.0139676	0.1143484	-2.96	FALSE
256065_at	ribosomal protein, putative simila	---	AT1G07070	-2.11	-1.08	-3.30	0.0139686	0.1143484	-2.96	FALSE
262270_x_a	polyprotein, putative similar to p	---	---	1.34	0.42	3.30	0.0139613	0.1143484	-2.96	FALSE
256735_at	hypothetical protein predicted by	ATEXO70E	AT3G29400	1.56	0.65	3.30	0.0139715	0.1143484	-2.96	FALSE
250704_at	Expressed protein ; supported by	---	AT5G06265	-1.59	-0.67	-3.29	0.0139894	0.1144134	-2.97	FALSE
245050_at	PSII K protein	---	---	-1.33	-0.41	-3.29	0.0139891	0.1144134	-2.97	FALSE
246445_at	glucose 6 phosphate/phosphate	---	AT5G17630	-1.53	-0.62	-3.29	0.014002	0.1144755	-2.97	FALSE
264563_s_a	unknown protein	---	AT1G55750 /.	-1.50	-0.58	-3.29	0.0140091	0.1144924	-2.97	FALSE
250504_at	putative protein similar to unknov	---	AT5G09840	-1.59	-0.67	-3.29	0.0140161	0.1145082	-2.97	FALSE
265154_at	putative GTP-binding protein, EI	---	AT1G30960	-2.06	-1.04	-3.29	0.014026	0.1145481	-2.97	FALSE
251972_at	nodulin / glutamate-ammonia lig	---	AT3G53170	-1.50	-0.58	-3.29	0.0140353	0.1145832	-2.97	FALSE
251267_at	putative protein hypothetical pro	---	AT3G62330	1.55	0.63	3.29	0.0140467	0.1146355	-2.97	TRUE
254466_at	subtilisin-like serine protease cor	---	AT4G20430	-1.66	-0.73	-3.29	0.0140551	0.1146624	-2.97	FALSE
246370_at	hypothetical protein predicted by	---	AT1G51920	4.84	2.27	3.29	0.0140948	0.1148612	-2.97	TRUE
250409_at	putative protein 110K5.11, unkn	---	AT5G10860	-1.45	-0.53	-3.29	0.0140947	0.1148612	-2.97	FALSE

254032_at	predicted protein destination fac	---	AT4G25940	1.62	0.70	3.29	0.0141002	0.1148612	-2.97	FALSE
257168_at	mrp protein, putative similar to n	HCF101	AT3G24430	-2.27	-1.18	-3.29	0.0141046	0.1148612	-2.97	FALSE
253451_at	putative myb-protein transformin	PC-MYB1	AT4G32730	1.42	0.51	3.29	0.0140981	0.1148612	-2.97	FALSE
257540_at	hypothetical protein	---	AT3G21520	1.50	0.59	3.29	0.014112	0.1148801	-2.98	FALSE
250335_at	lysophospholipase - like protein	---	AT5G11650	1.88	0.91	3.29	0.0141171	0.1148807	-2.98	FALSE
254892_at	putative protein other hypothetica	---	AT4G11800	1.54	0.62	3.29	0.01413	0.1149452	-2.98	FALSE
254250_at	serine/threonine kinase - like pro	---	AT4G23290	-2.14	-1.10	-3.29	0.0141439	0.1149535	-2.98	TRUE
249979_s_a	putative protein	---	AT5G18860 /.	2.46	1.30	3.29	0.0141427	0.1149535	-2.98	FALSE
258327_at	unknown protein contains similar	PAP85	AT3G22640	1.37	0.46	3.29	0.0141546	0.1149535	-2.98	FALSE
260387_at	putative flavonol sulfotransferase	SOT16	AT1G74100	2.49	1.32	3.29	0.0141541	0.1149535	-2.98	FALSE
261748_at	hypothetical protein predicted by	---	AT1G76070	3.70	1.89	3.29	0.0141563	0.1149535	-2.98	FALSE
265657_at	unknown protein ; supported by	---	AT2G13840	-1.50	-0.58	-3.28	0.0141715	0.1150364	-2.98	FALSE
262943_at	inosine-5'-monophosphate dehy	---	AT1G79470	-1.43	-0.51	-3.28	0.0141837	0.1150943	-2.98	FALSE
266418_at	putative annexin ;supported by f	ANNAT4	AT2G38750	3.04	1.60	3.28	0.0141947	0.1151122	-2.98	FALSE
254830_at	putative protein predicted protei	---	AT4G12590	-1.34	-0.42	-3.28	0.014196	0.1151122	-2.98	FALSE
262667_at	amine oxidase, putative similar t	---	AT1G62810	-1.78	-0.83	-3.28	0.0142069	0.1151597	-2.98	FALSE
259642_at	hypothetical protein predicted by	---	AT1G69030	1.76	0.81	3.28	0.0142402	0.1153889	-2.98	TRUE
263517_at	unknown protein ;supported by f	RD2	AT2G21620	1.77	0.82	3.28	0.0142478	0.1154093	-2.99	TRUE
255910_at	unknown protein contains similar	---	AT1G18030	-1.45	-0.53	-3.28	0.014264	0.1154995	-2.99	FALSE
247441_at	receptor - like protein kinase - lik	---	AT5G62710	-1.51	-0.59	-3.28	0.0142778	0.1155702	-2.99	FALSE
249925_at	putative protein predicted protei	---	AT5G19150	-1.70	-0.76	-3.28	0.0143119	0.1158047	-2.99	FALSE
266417_at	putative non-green plastid inner e	---	AT2G38550	-1.57	-0.65	-3.28	0.0143293	0.1159047	-2.99	FALSE
256458_at	integral membrane protein, puta	---	AT1G75220	1.87	0.90	3.28	0.0143475	0.1160109	-2.99	TRUE
251783_at	ribosomal L23a - like protein vari	RPL23AB	AT3G55280	-2.22	-1.15	-3.27	0.0143648	0.1161098	-2.99	FALSE
260410_at	putative peptide transporter simil	---	AT1G69870	2.09	1.07	3.27	0.0143818	0.1162056	-2.99	FALSE
256978_at	phosphoribosyamidoimidazole-s	PUR7	AT3G21110	-2.04	-1.03	-3.27	0.0144012	0.1162562	-3.00	FALSE
257406_at	hypothetical protein predicted by	---	AT1G27060	-1.58	-0.66	-3.27	0.0144033	0.1162562	-3.00	FALSE
257713_at	succinate dehydrogenase iron-p	SDH2-1	AT3G27380	1.87	0.91	3.27	0.0143959	0.1162562	-3.00	FALSE
261984_at	TINY-like protein similar to TINY	---	AT1G33760	1.61	0.69	3.27	0.014412	0.1162853	-3.00	TRUE
247743_at	protein kinase - like serine/threo	---	AT5G59010	-1.58	-0.66	-3.27	0.0144384	0.1164564	-3.00	FALSE
265388_s_a	unknown protein ;supported by f	---	AT2G20990 /.	-1.42	-0.50	-3.27	0.0144594	0.1165851	-3.00	FALSE
256052_at	spliceosomal protein (U2B), puta	---	AT1G06960	-1.47	-0.56	-3.27	0.0144761	0.1166785	-3.00	FALSE
266668_at	hypothetical protein predicted by	---	AT2G29760	-2.11	-1.08	-3.27	0.0144937	0.1167452	-3.00	FALSE
258511_at	unknown protein ;supported by f	---	AT3G06590	-1.55	-0.63	-3.27	0.0144946	0.1167452	-3.00	FALSE
259444_at	hypothetical protein predicted by	---	AT1G02370	-2.33	-1.22	-3.27	0.0145243	0.1168479	-3.00	FALSE

264258_at	hypothetical protein predicted by	---	AT1G09220	-1.48	-0.57	-3.27	0.0145279	0.1168479	-3.00	FALSE
255585_at	putative NAM-like protein	anac069	AT4G01550	-1.79	-0.84	-3.27	0.0145236	0.1168479	-3.00	FALSE
256459_at	acetyl-CoA carboxylase, putative	ACC2	AT1G36180	-1.59	-0.67	-3.27	0.0145163	0.1168479	-3.00	FALSE
246134_at	protein kinase tousled ; supporte	TSL	AT5G20930	-1.58	-0.66	-3.27	0.0145416	0.1168762	-3.01	FALSE
246699_at	putative protein predicted protei	---	AT5G27990	-1.70	-0.77	-3.27	0.0145413	0.1168762	-3.01	FALSE
251483_at	putative protein hypothetical pro	---	AT3G59650	-1.53	-0.61	-3.27	0.0145519	0.1169176	-3.01	FALSE
245277_at	glucosyltransferase like protein ;	IAGLU	AT4G15550	2.13	1.09	3.26	0.0145631	0.1169204	-3.01	TRUE
266732_at	unknown protein	---	AT2G03240	1.73	0.79	3.26	0.0145641	0.1169204	-3.01	TRUE
259287_at	putative rac GTPase activating p	---	AT3G11490	-1.55	-0.64	-3.26	0.0145676	0.1169204	-3.01	FALSE
262687_at	PPR-repeat protein contains mul	---	AT1G62670	-1.36	-0.44	-3.26	0.0145977	0.1171208	-3.01	FALSE
257637_at	terpene synthase-related protein	---	AT3G25810	1.36	0.44	3.26	0.0146146	0.1171962	-3.01	FALSE
246888_at	putative protein	---	AT5G26270	1.36	0.44	3.26	0.0146174	0.1171962	-3.01	FALSE
246554_at	HSP100/ClpB, putative similar to	CLPB3	AT5G15450	-1.50	-0.59	-3.26	0.0146334	0.1172835	-3.01	FALSE
267481_at	putative receptor-like protein kina	---	AT2G02780	2.54	1.34	3.26	0.0146498	0.1173322	-3.01	TRUE
260620_at	unknown protein	---	AT1G08070	-1.44	-0.53	-3.26	0.0146467	0.1173322	-3.01	FALSE
258921_at	unknown protein N-terminus simi	anac053	AT3G10500	1.62	0.69	3.26	0.0146913	0.117557	-3.02	TRUE
266450_s_a	hypothetical protein predicted by	---	AT2G43190	-1.66	-0.73	-3.26	0.0146832	0.117557	-3.02	FALSE
256805_at	unknown protein contains simila	---	AT3G20930	-2.18	-1.13	-3.26	0.0146933	0.117557	-3.02	FALSE
254628_at	Expressed protein ; supported by	---	AT4G18593	-1.34	-0.42	-3.26	0.0147039	0.1175999	-3.02	FALSE
250662_at	steroid sulfotransferase-like prote	ST2A	AT5G07010	2.32	1.22	3.26	0.0147187	0.117663	-3.02	TRUE
251986_at	putative protein various predicte	---	AT3G53310	-2.23	-1.16	-3.26	0.0147221	0.117663	-3.02	FALSE
252441_at	putative protein ; supported by c	PTAC16	AT3G46780	-1.77	-0.82	-3.26	0.0147413	0.1177753	-3.02	TRUE
260144_at	putative ABC transporter similar	---	AT1G71960	1.63	0.70	3.25	0.0147572	0.1178615	-3.02	FALSE
261336_at	unknown protein ;supported by fu	---	AT1G44790	1.76	0.82	3.25	0.0147946	0.1180777	-3.02	FALSE
246231_at	putative protein	---	AT4G37080	-1.65	-0.72	-3.25	0.0147899	0.1180777	-3.02	FALSE
263410_at	predicted protein ;supported by fu	---	AT2G04039	-1.86	-0.89	-3.25	0.0148919	0.1180868	-3.03	TRUE
260607_at	putative receptor protein kinase	---	AT2G43700	-1.62	-0.70	-3.25	0.0148512	0.1180868	-3.03	FALSE
265984_at	putative limonene cyclase	TPS10	AT2G24210	1.41	0.50	3.25	0.0148865	0.1180868	-3.03	FALSE
258651_at	putative phosphatidylinositol-4-ph	PIP5K9	AT3G09920	1.54	0.62	3.25	0.0149045	0.1180868	-3.03	FALSE
245144_at	putative methionine aminopeptid	MAP1A	AT2G45240	-1.48	-0.56	-3.25	0.0148408	0.1180868	-3.03	FALSE
250826_at	unknown protein ; supported by c	---	AT5G05220	1.48	0.56	3.25	0.0148256	0.1180868	-3.03	FALSE
251537_at	putative protein several hypothet	---	AT3G58470	-1.94	-0.95	-3.25	0.0148491	0.1180868	-3.03	FALSE
266158_at	putative ABC transporter	---	AT2G28070	-1.67	-0.74	-3.25	0.0149009	0.1180868	-3.03	FALSE
253881_at	putative protein Ran_GTP bindi	---	AT4G27640	-1.41	-0.49	-3.25	0.0148824	0.1180868	-3.03	FALSE
265602_at	putative retroelement pol polypro	---	---	1.51	0.60	3.25	0.0148281	0.1180868	-3.03	FALSE

252456_at	hypersensitivity-related protein-li	---	AT3G47170	1.46	0.55	3.25	0.0148655	0.1180868	-3.03	FALSE
246352_at	hypothetical protein	---	---	1.34	0.42	3.25	0.0148067	0.1180868	-3.02	FALSE
246246_at	putative protein	---	AT4G37170	-1.59	-0.67	-3.25	0.0148092	0.1180868	-3.02	FALSE
245057_at	En/Spm-like transposon protein r	---	AT2G26490	1.32	0.40	3.25	0.0148334	0.1180868	-3.03	FALSE
258406_at	hypothetical protein similar to hy	ATRBL14	AT3G17611	1.33	0.41	3.25	0.0148906	0.1180868	-3.03	FALSE
248568_at	receptor protein kinase-like	---	AT5G49760	1.54	0.63	3.25	0.014886	0.1180868	-3.03	FALSE
265262_at	putative chloroplast nucleoid DN	---	AT2G42980	1.59	0.67	3.25	0.0148593	0.1180868	-3.03	FALSE
253124_at	putative protein unknown protein	ARO3	AT4G36030	2.91	1.54	3.25	0.0149037	0.1180868	-3.03	FALSE
255134_at	putative protein	---	AT4G08330	-1.49	-0.57	-3.25	0.0148387	0.1180868	-3.03	FALSE
265268_at	putative protein kinase contains a	---	AT2G42960	-1.45	-0.53	-3.25	0.0148524	0.1180868	-3.03	FALSE
260993_at	hypothetical protein predicted by	FMO GS-O	AT1G12140	1.34	0.42	3.25	0.0148673	0.1180868	-3.03	FALSE
255601_at	putative protein (fragment) vario	---	AT4G01030	-1.50	-0.59	-3.25	0.0149211	0.1181774	-3.03	FALSE
259671_at	protein kinase, putative similar t	---	AT1G52290	2.39	1.26	3.24	0.0149572	0.1183261	-3.03	TRUE
251713_at	putative protein several hypothet	---	AT3G56080	-1.62	-0.69	-3.25	0.0149505	0.1183261	-3.03	FALSE
262952_at	hypothetical protein predicted by	---	AT1G75770	-1.56	-0.64	-3.24	0.0149606	0.1183261	-3.04	FALSE
262507_at	receptor-like protein kinase, puta	---	AT1G11330	1.57	0.65	3.24	0.0149581	0.1183261	-3.03	FALSE
266718_at	putative zinc transporter ;suppor	ZAT	AT2G46800	1.46	0.54	3.24	0.0149667	0.1183325	-3.04	FALSE
260238_at	AtHVA22a identical to AtHVA22	ATHVA22A	AT1G74520	-1.59	-0.67	-3.24	0.0149735	0.1183454	-3.04	FALSE
258373_at	20S proteasome subunit PAE2 id	PAE2	AT3G14290	-1.43	-0.51	-3.24	0.0149854	0.118399	-3.04	FALSE
248303_at	FtsH protease, putative similar t	FTSH11	AT5G53170	-1.46	-0.54	-3.24	0.0149957	0.1184387	-3.04	FALSE
261948_at	unknown protein ;supported by fu	---	AT1G64680	-1.93	-0.94	-3.24	0.0150161	0.1185589	-3.04	FALSE
248594_at	unknown protein ; supported by	---	AT5G49210	-1.75	-0.81	-3.24	0.0150338	0.1186581	-3.04	FALSE
253567_at	protein kinase-like protein serine	---	AT4G31230	1.62	0.70	3.24	0.0150613	0.1188334	-3.04	FALSE
247775_at	phosphoinositide-specific phosp	PLC5	AT5G58690	1.91	0.93	3.24	0.0150768	0.1189151	-3.04	FALSE
260814_at	histidine decarboxylase, putative	emb1075	AT1G43710	-1.41	-0.50	-3.24	0.0151017	0.1190698	-3.04	FALSE
254945_at	putative RING finger protein ring	---	AT4G10940	1.56	0.64	3.24	0.0151282	0.1191695	-3.05	FALSE
259849_at	phosphoglycerate dehydrogenas	---	AT1G72190	-1.35	-0.43	-3.24	0.0151244	0.1191695	-3.05	FALSE
258715_at	putative 60S ribosomal protein L	---	AT3G09630	-1.70	-0.77	-3.24	0.01513	0.1191695	-3.05	FALSE
247401_at	1-deoxy-D-xylulose 5-phosphate	DXR	AT5G62790	-1.75	-0.81	-3.23	0.0151608	0.1193711	-3.05	FALSE
262134_at	sulfate transporter, putative simi	AST56	AT1G77990	-2.03	-1.02	-3.23	0.0151665	0.1193744	-3.05	FALSE
257951_at	putative SGP1 monomeric G-pro	SGP2	AT3G21700	2.41	1.27	3.23	0.0151807	0.119445	-3.05	TRUE
251144_at	anthranilate N-benzoyltransferas	---	AT5G01210	2.07	1.05	3.23	0.0152053	0.1195979	-3.05	FALSE
255716_at	coded for by A. thaliana cDNA R	CRCK2	AT4G00330	1.32	0.40	3.23	0.0152327	0.1197303	-3.05	FALSE
254427_at	putative protein predicted protein	emb1417	AT4G21190	-1.88	-0.91	-3.23	0.0152295	0.1197303	-3.05	FALSE
249454_at	expressed protein predicted prot	---	AT5G39520	-3.47	-1.79	-3.23	0.0153273	0.1198019	-3.06	TRUE

255078_at	putative protein ascorbate perox	APX4	AT4G09010	-1.68	-0.75	-3.23	0.0153	0.1198019	-3.06	TRUE
264512_at	Expressed protein ; supported by	---	AT1G09575	1.50	0.59	3.23	0.0153144	0.1198019	-3.06	TRUE
254999_at	putative protein ; supported by fu	---	AT4G09830	-1.62	-0.69	-3.23	0.0153225	0.1198019	-3.06	TRUE
254778_at	putative protein	---	AT4G12750	-1.59	-0.67	-3.23	0.0153491	0.1198019	-3.06	FALSE
256279_at	protein phosphatase 2C, putativ	---	AT3G12620	1.32	0.40	3.23	0.0152721	0.1198019	-3.06	FALSE
262967_at	hypothetical protein predicted by	---	AT1G75730	-1.48	-0.56	-3.23	0.0153521	0.1198019	-3.06	FALSE
260786_s_a	unknown protein similar to Crypto	MEE5	AT1G06220 ///	-1.56	-0.64	-3.23	0.0152607	0.1198019	-3.06	FALSE
257315_at	proline oxidase, mitochondrial pr	ERD5	AT3G30775	3.84	1.94	3.23	0.0153218	0.1198019	-3.06	TRUE
263333_at	unknown protein ; supported by	---	AT2G03890	-1.66	-0.73	-3.23	0.0153482	0.1198019	-3.06	FALSE
251392_at	dihydrodipicolinate synthase pre	DHDPS1	AT3G60880	-1.41	-0.49	-3.23	0.015345	0.1198019	-3.06	FALSE
255384_at	hypothetical protein	---	AT4G03580	1.35	0.43	3.23	0.0152913	0.1198019	-3.06	FALSE
251258_at	PECTINESTERASE-like protein	VGDH2	AT3G62170	1.53	0.61	3.23	0.0153265	0.1198019	-3.06	FALSE
259006_at	putative 60S acidic ribosomal pro	---	AT3G09200	-1.85	-0.89	-3.23	0.0153254	0.1198019	-3.06	FALSE
263248_at	putative endonuclease ;supporte	ATNTH1	AT2G31450	-1.42	-0.50	-3.23	0.0153368	0.1198019	-3.06	FALSE
265736_at	putative ribosomal protein L7 ;su	---	AT2G01250	-2.06	-1.05	-3.23	0.015347	0.1198019	-3.06	FALSE
245321_at	Expressed protein ; supported by	---	AT4G15545	-1.36	-0.44	-3.23	0.0152979	0.1198019	-3.06	FALSE
252041_at	DNA-directed RNA polymerase I	NRPB11	AT3G52090	-1.45	-0.53	-3.23	0.0152951	0.1198019	-3.06	FALSE
258955_s_a	unknown protein ;supported by f	---	AT3G01450 ///	-1.62	-0.69	-3.23	0.0153135	0.1198019	-3.06	FALSE
250644_at	protein phosphatase 2C-like ;su	---	AT5G06750	1.77	0.83	3.23	0.0152883	0.1198019	-3.06	FALSE
252982_at	Histone deacetylase ; supported	HD1	AT4G38130	-1.44	-0.53	-3.23	0.0152583	0.1198019	-3.06	FALSE
253764_s_a	protein kinase - like protein ADK	ckl4	AT4G28860 ///	-1.55	-0.63	-3.23	0.0153576	0.1198037	-3.06	FALSE
253249_at	GATA transcription factor 3	---	AT4G34680	-1.62	-0.70	-3.22	0.0153718	0.1198739	-3.06	TRUE
260915_at	hypothetical protein similar to hyp	---	AT1G02660	2.37	1.24	3.22	0.0154378	0.1201421	-3.07	TRUE
259724_at	putative serine/threonine-protein	SNRK2.10	AT1G60940	-1.62	-0.69	-3.22	0.0154364	0.1201421	-3.07	FALSE
250857_at	unknown protein	---	AT5G04790	-1.69	-0.76	-3.22	0.0154263	0.1201421	-3.07	FALSE
253097_at	cytochrome P450-like protein	CYP81D5	AT4G37320	2.69	1.43	3.22	0.0154337	0.1201421	-3.07	FALSE
249918_at	putative protein predicted protei	---	AT5G19240	3.16	1.66	3.22	0.0154231	0.1201421	-3.07	FALSE
266672_at	putative Na+-dependent inorgani	PHT4;1	AT2G29650	-1.42	-0.50	-3.22	0.0154374	0.1201421	-3.07	FALSE
254208_at	Expressed protein ; supported by	---	AT4G24175	-1.51	-0.59	-3.22	0.0154806	0.1203928	-3.07	FALSE
253012_at	putative protein Caenorhabditis	---	AT4G37900	1.45	0.54	3.22	0.0154774	0.1203928	-3.07	FALSE
253338_at	somatic embryogenesis recepto	BAK1	AT4G33430	1.45	0.54	3.22	0.0154914	0.1203948	-3.07	FALSE
266582_at	unknown protein ; supported by	---	AT2G46090	-1.57	-0.65	-3.22	0.0154913	0.1203948	-3.07	FALSE
262159_at	hypothetical protein predicted by	---	AT1G52720	2.34	1.23	3.22	0.0155293	0.1206481	-3.07	FALSE
264670_s_a	unknown protein Similar to elong	---	AT1G09640 ///	-1.55	-0.63	-3.22	0.0155347	0.1206495	-3.07	FALSE
266237_at	DNA-directed RNA polymerase	ATRPC14	AT2G29540	-1.80	-0.85	-3.22	0.0155454	0.1206908	-3.07	FALSE

260886_at	hypothetical protein contains sim	---	AT1G29200	1.36	0.44	3.22	0.0155597	0.1207614	-3.08	FALSE
248969_at	unknown protein ; supported by	---	AT5G45310	-2.22	-1.15	-3.21	0.015579	0.1208695	-3.08	FALSE
253815_at	putative beta-expansin/allergen	ATEXPB3	AT4G28250	1.74	0.80	3.21	0.0155893	0.1208725	-3.08	FALSE
261085_at	hypothetical protein similar to hy	IQD7	AT1G17480	1.39	0.47	3.21	0.01559	0.1208725	-3.08	FALSE
266166_at	putative glucosyltransferase ; su	---	AT2G28080	1.71	0.77	3.21	0.0156144	0.1210209	-3.08	TRUE
264928_at	auxin-induced protein, putative s	ATB2	AT1G60710	1.44	0.53	3.21	0.0156376	0.1211599	-3.08	FALSE
258518_at	unknown protein ; supported by	---	AT3G06570	-1.36	-0.45	-3.21	0.0156778	0.1214296	-3.08	FALSE
250796_at	putative protein similar to unknov	---	AT5G05300	5.36	2.42	3.21	0.0156858	0.1214506	-3.08	FALSE
257063_s_a	unknown protein ;supported by f	---	AT3G18240 /,	-1.36	-0.44	-3.21	0.0157038	0.1215489	-3.08	FALSE
248579_at	mitotic checkpoint protein-like	---	AT5G49880	-1.69	-0.76	-3.21	0.0157116	0.1215678	-3.09	FALSE
266142_at	unknown protein ; supported by	---	AT2G39030	6.99	2.80	3.21	0.0157373	0.1217253	-3.09	FALSE
262024_at	protein disulfide isomerase, puta	ATPDIL5-2	AT1G35620	-1.56	-0.64	-3.21	0.0157641	0.121789	-3.09	FALSE
247457_at	putative protein various predicte	---	AT5G62170	1.38	0.46	3.21	0.015763	0.121789	-3.09	FALSE
254755_at	hypothetical protein	---	AT4G13220	-1.50	-0.59	-3.21	0.0157701	0.121789	-3.09	FALSE
263873_at	unknown protein predicted by ge	---	AT2G21860	-1.57	-0.65	-3.21	0.0157722	0.121789	-3.09	FALSE
261887_at	CCR4-associated factor, putativ	---	AT1G80780	-1.35	-0.43	-3.21	0.0157668	0.121789	-3.09	FALSE
261672_at	unknown protein contains similar	ATARP4	AT1G18450	-1.63	-0.71	-3.20	0.0157956	0.1219282	-3.09	FALSE
258386_at	hypothetical protein predicted by	---	AT3G15520	-1.70	-0.76	-3.20	0.0158471	0.1219543	-3.09	TRUE
251265_at	ATP-dependent RNA helicase-li	---	AT3G62310	-1.61	-0.69	-3.20	0.0158323	0.1219543	-3.09	FALSE
264327_at	putative translation initiation fact	EIF2 GAMM	AT1G04170	-1.39	-0.48	-3.20	0.0158336	0.1219543	-3.09	FALSE
265887_at	biotin holocarboxylase synthetas	HCS1	AT2G25710	-1.55	-0.63	-3.20	0.0158155	0.1219543	-3.09	FALSE
262532_at	hypothetical protein predicted by	---	AT1G17210	-1.44	-0.52	-3.20	0.0158464	0.1219543	-3.09	FALSE
252001_at	plastid division protein FtsZ-like	FTSZ2-2	AT3G52750	-2.01	-1.01	-3.20	0.0158115	0.1219543	-3.09	FALSE
250848_at	3-phosphoinositide-dependent pr	PDK1	AT5G04510	-1.47	-0.55	-3.20	0.0158384	0.1219543	-3.09	FALSE
250633_at	peptide methionine sulfoxide red	PMSR2	AT5G07460	3.18	1.67	3.20	0.0158264	0.1219543	-3.09	FALSE
254857_at	putative protein acetylcholine re	SEC1B	AT4G12120	1.50	0.59	3.20	0.0158351	0.1219543	-3.09	FALSE
257707_at	hypothetical protein predicted by	---	AT3G12650	-1.39	-0.48	-3.20	0.0158605	0.122016	-3.09	FALSE
253063_at	plasma membrane-type calcium	ACA2	AT4G37640	1.92	0.94	3.20	0.0158681	0.1220331	-3.10	FALSE
250673_at	serine threonine protein kinase-l	CIPK2	AT5G07070	1.64	0.72	3.20	0.0159075	0.1222133	-3.10	FALSE
264140_at	proteasome alpha subunit, putat	---	AT1G79210	-1.39	-0.47	-3.20	0.0159015	0.1222133	-3.10	FALSE
266883_at	putative triacylglycerol lipase	DAD1	AT2G44810	1.42	0.50	3.20	0.0159075	0.1222133	-3.10	FALSE
248820_at	putative protein similar to unknov	---	AT5G47060	-1.63	-0.71	-3.20	0.0159158	0.1222358	-3.10	TRUE
253998_at	putative peroxidase peroxidase	---	AT4G26010	1.35	0.43	3.20	0.0159565	0.1225068	-3.10	FALSE
251919_at	putative protein Hsp70 binding p	---	AT3G53800	-1.76	-0.82	-3.20	0.0159622	0.1225092	-3.10	FALSE
250045_at	putative protein mRNA (orf04), A	---	AT5G17700	1.77	0.82	3.20	0.0159777	0.122582	-3.10	FALSE

258113_at	putative cytochrome P450 simila	CYP72A11	AT3G14650	-1.81	-0.86	-3.20	0.0159869	0.122582	-3.10	FALSE
259447_s_a	ADP-ribosylation factor, putative	ATARFD1A	AT1G02430 /	1.42	0.51	3.20	0.0159878	0.122582	-3.10	FALSE
255866_at	hypothetical protein predicted by	---	AT2G30350	-1.47	-0.56	-3.20	0.0159971	0.1226123	-3.10	FALSE
249304_at	folylpolyglutamate synthase-like	GLA1	AT5G41480	-1.62	-0.70	-3.19	0.0160065	0.1226432	-3.10	FALSE
247942_at	putative protein similar to unknov	---	AT5G57120	-1.69	-0.75	-3.19	0.0160243	0.1227382	-3.11	FALSE
257779_at	protein kinase, putative similar t	CDG1	AT3G26940	1.31	0.39	3.19	0.0160429	0.1228395	-3.11	FALSE
251621_at	protein kinase - like protein wall-	---	AT3G57700	1.93	0.95	3.19	0.0161042	0.1228864	-3.11	TRUE
247818_at	contains similarity to GTP-bindin	---	AT5G58370	-1.43	-0.52	-3.19	0.0161249	0.1228864	-3.11	FALSE
262595_at	putative ethylene responsive ele	SHN1	AT1G15360	1.44	0.53	3.19	0.0160623	0.1228864	-3.11	FALSE
262714_s_a	unknown protein similar to gb|AJ	---	AT1G07950 /	-1.39	-0.48	-3.19	0.0161514	0.1228864	-3.11	FALSE
249694_at	glucose-6-phosphate dehydroge	G6PD1	AT5G35790	-1.34	-0.42	-3.19	0.0161141	0.1228864	-3.11	FALSE
245560_at	indole-3-acetate beta-glucosyltra	UGT84A1	AT4G15480	1.53	0.61	3.19	0.0160923	0.1228864	-3.11	FALSE
254675_at	RNA helicase - like protein Cdc2	---	AT4G18465	-1.76	-0.81	-3.19	0.016066	0.1228864	-3.11	FALSE
250906_at	1,4-alpha-glucan branching enzy	SBE2.2	AT5G03650	-1.48	-0.57	-3.19	0.0161496	0.1228864	-3.11	FALSE
261213_at	unknown protein ; supported by c	---	AT1G12970	-1.42	-0.51	-3.19	0.0160681	0.1228864	-3.11	FALSE
258152_at	chaperonin subunit, putative sim	---	AT3G18190	-1.51	-0.59	-3.19	0.0161463	0.1228864	-3.11	FALSE
266202_at	putative cinnamoyl-CoA reductas	---	AT2G02400	-1.38	-0.47	-3.19	0.0161451	0.1228864	-3.11	FALSE
256055_at	mitochondrial carrier protein, put	---	AT1G07030	1.39	0.48	3.19	0.0161415	0.1228864	-3.11	FALSE
255019_at	putative protein IB1C3-1 protein	---	AT4G10210	1.39	0.48	3.19	0.0161122	0.1228864	-3.11	FALSE
262275_at	ATPase, putative similar to chro	---	AT1G68710	1.49	0.58	3.19	0.0160807	0.1228864	-3.11	FALSE
256681_at	unknown protein ; supported by c	SPP2	AT3G52340	-2.97	-1.57	-3.19	0.0161331	0.1228864	-3.11	FALSE
258900_at	putative 60S ribosomal protein L	RPL18	AT3G05590	-1.91	-0.94	-3.19	0.0161082	0.1228864	-3.11	FALSE
250262_at	putative protein peptidyl-prolyl ci	---	AT5G13410	-1.89	-0.92	-3.19	0.0161046	0.1228864	-3.11	FALSE
255881_at	phosphomannose isomerase, pu	DIN9	AT1G67070	3.04	1.60	3.19	0.0161332	0.1228864	-3.11	FALSE
250014_at	anthranilate phosphoribosyltrans	TRP1	AT5G17990	3.57	1.83	3.19	0.016111	0.1228864	-3.11	FALSE
257680_at	aspartate carbamoyltransferase	---	AT3G20330	-1.61	-0.68	-3.19	0.0161616	0.1229227	-3.11	FALSE
251926_at	60S RIBOSOMAL PROTEIN L3	---	AT3G53740	-1.97	-0.98	-3.19	0.0161839	0.1230517	-3.12	FALSE
244936_at	NADH dehydrogenase ND1	---	---	-1.42	-0.50	-3.19	0.0162072	0.1231348	-3.12	FALSE
260537_at	hypothetical protein predicted by	---	AT2G43450	1.33	0.41	3.19	0.0162004	0.1231348	-3.12	FALSE
259280_at	putative polypyrimidine tract-bin	PTB1	AT3G01150	-1.34	-0.43	-3.19	0.016211	0.1231348	-3.12	FALSE
247731_at	glucuronosyl transferase - like p	UGT76E2	AT5G59590	1.42	0.51	3.19	0.0162165	0.1231353	-3.12	FALSE
261982_at	hypothetical protein predicted by	---	AT1G33780	-1.38	-0.46	-3.18	0.016224	0.123151	-3.12	FALSE
261821_at	thioredoxin h, putative similar to	ATCXXS1	AT1G11530	-1.46	-0.54	-3.18	0.0162921	0.1235035	-3.12	FALSE
256250_at	integral membrane protein, puta	---	AT3G11320	1.62	0.69	3.18	0.0162835	0.1235035	-3.12	FALSE
245985_at	peptidylprolyl isomerase-like pro	---	AT5G13120	-1.57	-0.65	-3.18	0.0162858	0.1235035	-3.12	FALSE

267629_at	putative DNA polymerase delta s	POLD2	AT2G42120	-1.64	-0.71	-3.18	0.0162868	0.1235035	-3.12	FALSE
254040_at	possible apospory-associated lik	---	AT4G25900	1.82	0.87	3.18	0.0163201	0.1235929	-3.12	TRUE
258141_at	hypothetical protein	HON4	AT3G18035	-1.58	-0.66	-3.18	0.0163128	0.1235929	-3.12	FALSE
262454_at	bifunctional nuclease bfn1 almos	BFN1	AT1G11190	6.00	2.58	3.18	0.0163199	0.1235929	-3.12	FALSE
261725_at	small nuclear ribonucleoprotein,	SmD3	AT1G76300	-1.64	-0.71	-3.18	0.0163438	0.1237313	-3.13	FALSE
262094_at	SAR DNA binding protein, putati	NOP56	AT1G56110	-2.19	-1.13	-3.18	0.0163854	0.1238522	-3.13	FALSE
261524_at	hypothetical protein predicted by	---	AT1G14300	-1.50	-0.58	-3.18	0.0164005	0.1238522	-3.13	FALSE
256113_at	unknown protein ;supported by fu	---	AT1G16810	-1.50	-0.58	-3.18	0.0163749	0.1238522	-3.13	FALSE
258555_at	fatty acid multifunctional protein (	MFP2	AT3G06860	1.50	0.58	3.18	0.0163721	0.1238522	-3.13	FALSE
250559_at	putative protein condensin subu	---	AT5G08010	-1.51	-0.60	-3.18	0.0163955	0.1238522	-3.13	FALSE
261163_x_a	auxin response factor, putative s	ARF21	AT1G34410	1.33	0.41	3.18	0.0163872	0.1238522	-3.13	FALSE
258466_at	hypothetical protein contains sim	---	AT3G06040	-1.52	-0.60	-3.18	0.0164037	0.1238522	-3.13	FALSE
254958_at	nucleoside diphosphate kinase 3	NDPK3	AT4G11010	-1.65	-0.72	-3.18	0.016381	0.1238522	-3.13	FALSE
257907_at	hemolysin, putative similar to he	---	AT3G25470	-1.32	-0.40	-3.18	0.0164086	0.1238522	-3.13	FALSE
262706_at	putative ATP-dependent RNA he	---	AT1G16280	-1.62	-0.70	-3.18	0.0164265	0.1239161	-3.13	FALSE
265295_at	putative DNA replication licensin	MCM9	AT2G14050	-1.54	-0.62	-3.18	0.0164291	0.1239161	-3.13	FALSE
257205_at	putative glucosyltransferase sim	UGT88A1	AT3G16520	-1.41	-0.50	-3.18	0.0164334	0.1239161	-3.13	FALSE
250515_at	putative protein	---	AT5G09570	1.30	0.38	3.17	0.0164472	0.1239789	-3.13	FALSE
245976_at	WRKY-like protein WRKY DNA	WRKY75	AT5G13080	4.85	2.28	3.17	0.0164796	0.124059	-3.13	TRUE
267545_at	unknown protein	GRP23	AT2G32690	1.67	0.74	3.17	0.016474	0.124059	-3.13	FALSE
250246_at	polyamine oxidase	ATPAO1	AT5G13700	1.34	0.43	3.17	0.0164651	0.124059	-3.13	FALSE
263034_at	pollen allergen-like protein simila	MLP423	AT1G24020	2.06	1.04	3.17	0.0164794	0.124059	-3.13	FALSE
252081_at	putative heat shock transcription	HSFA7A	AT3G51910	-2.26	-1.18	-3.17	0.016486	0.1240668	-3.13	FALSE
246348_at	putative protein putative glycerol-	---	AT3G56840	-1.30	-0.38	-3.17	0.0165427	0.1244521	-3.14	FALSE
256863_at	CCHC-type zinc finger protein, p	---	AT3G24070	-1.35	-0.43	-3.17	0.0165647	0.1245769	-3.14	FALSE
262419_at	hypothetical protein identical to h	---	AT1G50380	-1.63	-0.70	-3.17	0.0165719	0.1245895	-3.14	FALSE
247528_at	MIM protein ; supported by cDN	MIM	AT5G61460	-1.51	-0.59	-3.17	0.0165872	0.1246633	-3.14	FALSE
264285_at	symbiosis-related protein, putati	ATG8C	AT1G62040	-1.47	-0.56	-3.17	0.0166263	0.1249101	-3.14	FALSE
246379_s_a	60S ribosomal protein L21, puta	---	AT1G57660 ///	-1.75	-0.80	-3.17	0.0166309	0.1249101	-3.14	FALSE
245671_at	purine permease identical to puri	PUP1	AT1G28230	1.40	0.48	3.16	0.0166658	0.1250728	-3.15	TRUE
256398_at	putative major intrinsic protein co	NIP7;1	AT3G06100	1.33	0.41	3.17	0.0166608	0.1250728	-3.15	FALSE
266816_at	unknown protein identical to GB:	---	AT2G44970	1.37	0.45	3.16	0.0166691	0.1250728	-3.15	FALSE
267082_at	CPDK-related protein kinase CD	CRK1	AT2G41140	-1.37	-0.46	-3.16	0.0167046	0.1251338	-3.15	TRUE
247132_at	putative protein strong similarity t	ARO2	AT5G66200	1.62	0.70	3.16	0.0167058	0.1251338	-3.15	TRUE
260290_at	hypothetical protein predicted by	---	AT1G80510	1.45	0.54	3.16	0.0167092	0.1251338	-3.15	FALSE

264987_at	unknown protein ; supported by c	---	AT1G27030	-2.22	-1.15	-3.16	0.0167014	0.1251338	-3.15	FALSE
261369_at	protein kinase, putative similar t	---	AT1G53060	1.59	0.67	3.16	0.0167101	0.1251338	-3.15	FALSE
263378_at	protein phosphatase 2C (AthPP2	ATHPP2C5	AT2G40180	1.73	0.79	3.16	0.016695	0.1251338	-3.15	FALSE
263761_at	putative fructose bisphosphate a	---	AT2G21330	-1.64	-0.71	-3.16	0.0167222	0.1251408	-3.15	FALSE
254721_at	hypothetical protein ;supported b	SMAP1	AT4G13520	-1.45	-0.53	-3.16	0.016717	0.1251408	-3.15	FALSE
264227_at	hypothetical protein contains sim	ATREV3	AT1G67500	-1.43	-0.51	-3.16	0.0167275	0.1251408	-3.15	FALSE
244970_at	ribosomal protein L20	---	---	-1.91	-0.94	-3.16	0.0167332	0.125142	-3.15	FALSE
253396_at	putative protein RNA-binding pro	AtLa1	AT4G32720	-1.42	-0.51	-3.16	0.0167462	0.1251987	-3.15	FALSE
265615_at	putative dioxygenase ; supporte	---	AT2G25450	1.52	0.60	3.16	0.0167601	0.1252615	-3.15	FALSE
256407_at	sucrose-proton symporter, putat	ATSUC7	AT1G66570	3.52	1.81	3.16	0.0167832	0.1252948	-3.15	TRUE
259077_s_a	reversibly glycosylated polypepti	RGP1	AT3G02230 /	2.00	1.00	3.16	0.0167788	0.1252948	-3.15	FALSE
258945_at	calmodulin-domain protein kinas	CPK2	AT3G10660	1.34	0.42	3.16	0.0167733	0.1252948	-3.15	FALSE
266981_at	60S ribosomal protein L23A iden	RPL23AA	AT2G39460	-2.07	-1.05	-3.16	0.0167865	0.1252948	-3.15	FALSE
258696_at	hypothetical protein predicted by	HCF152	AT3G09650	-1.78	-0.83	-3.16	0.0168183	0.125491	-3.15	TRUE
258525_at	hypothetical protein predicted by	IBR3	AT3G06810	1.65	0.72	3.16	0.0168326	0.1255563	-3.16	FALSE
256860_at	hypothetical protein similar to ac	---	AT3G23840	1.44	0.53	3.16	0.0168416	0.1255826	-3.16	FALSE
247487_at	putative protein predicted protei	---	AT5G62150	4.79	2.26	3.16	0.0168636	0.1256084	-3.16	TRUE
262161_at	signal peptidase subunit, putativ	---	AT1G52600	-1.39	-0.47	-3.16	0.0168643	0.1256084	-3.16	FALSE
251784_at	putative protein photosystem II c	PPL1	AT3G55330	-1.81	-0.85	-3.16	0.016874	0.1256084	-3.16	FALSE
256023_at	hypothetical protein predicted by	ZW2	AT1G58330	1.52	0.61	3.16	0.016876	0.1256084	-3.16	FALSE
263755_at	unknown protein ;supported by f	---	AT2G21340	-1.61	-0.69	-3.16	0.0168781	0.1256084	-3.16	FALSE
261151_at	sec14 cytosolic factor, putative s	---	AT1G19650	1.44	0.52	3.16	0.0168733	0.1256084	-3.16	FALSE
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gi	---	---	2.05	1.04	3.15	0.0169008	0.1257332	-3.16	FALSE
262988_at	putative alanine aminotra	GGT1	AT1G23310	-1.37	-0.46	-3.15	0.0169059	0.1257332	-3.16	FALSE
261108_at	1-aminocyclopropane-1-carboxy	ACS10	AT1G62960	-1.57	-0.65	-3.15	0.0169148	0.125758	-3.16	FALSE
252644_at	putative protein KIAA0073, Hom	CYP71	AT3G44600	-1.54	-0.62	-3.15	0.0169345	0.1257818	-3.16	FALSE
245425_at	carboxyl-terminal proteinase like	UCH3	AT4G17510	-1.30	-0.38	-3.15	0.0169308	0.1257818	-3.16	FALSE
267083_at	calmodulin-like protein identical t	TCH3	AT2G41100	2.13	1.09	3.15	0.0169313	0.1257818	-3.16	FALSE
266349_at	unknown protein predicted by ge	---	AT2G01460	1.45	0.53	3.15	0.0169404	0.1257849	-3.16	FALSE
251741_at	putative protein predicted protei	UGP3	AT3G56040	-2.10	-1.07	-3.15	0.0169594	0.1258845	-3.16	FALSE
247345_at	putative protein contains similarit	---	AT5G63760	-1.51	-0.60	-3.15	0.0169768	0.125891	-3.16	FALSE
245639_at	unknown protein contains similar	---	AT1G25260	-1.90	-0.93	-3.15	0.016973	0.125891	-3.16	FALSE
247726_at	telomere repeat-binding protein	TRP1	AT5G59430	1.57	0.65	3.15	0.0169686	0.125891	-3.16	FALSE
247123_at	unknown protein	---	AT5G66050	1.69	0.75	3.15	0.0169932	0.1259305	-3.17	TRUE
247558_at	histone deacetylase - like histon	HDA05	AT5G61060	-1.43	-0.52	-3.15	0.01699	0.1259305	-3.17	FALSE

245732_at	unknown protein contains similar	---	AT1G73440	-1.41	-0.50	-3.15	0.0170008	0.1259309	-3.17	FALSE
250527_at	serine/threonine-protein kinase	SNRK2.1	AT5G08590	-1.37	-0.45	-3.15	0.0170098	0.1259309	-3.17	FALSE
253966_at	fructose-bisphosphate aldolase	---	AT4G26520	-1.61	-0.68	-3.15	0.0170048	0.1259309	-3.17	FALSE
246368_at	light repressible receptor protein	---	AT1G51890	3.12	1.64	3.15	0.0170395	0.1259876	-3.17	TRUE
252625_at	putative histone deacetylase sim	HDA3	AT3G44750	-2.69	-1.43	-3.15	0.0170291	0.1259876	-3.17	FALSE
264026_at	glycine-rich protein (AtGRP2) Sa	ATGRP2B	AT2G21060	1.95	0.96	3.15	0.0170375	0.1259876	-3.17	FALSE
247813_at	NADP-dependent malate dehydr	---	AT5G58330	-1.43	-0.52	-3.15	0.0170375	0.1259876	-3.17	FALSE
267064_at	calmodulin (cam2)	CAM2	AT2G41110	2.05	1.04	3.15	0.0170478	0.1260078	-3.17	TRUE
260271_at	unknown protein similar to unkno	---	AT1G63690	-1.40	-0.48	-3.15	0.0170705	0.1260533	-3.17	FALSE
259717_at	putative cleavage and polyadeny	CPSF73-I	AT1G61010	-1.51	-0.59	-3.15	0.0170642	0.1260533	-3.17	FALSE
260535_at	hypothetical protein predicted by	---	AT2G43390	1.34	0.42	3.15	0.0170672	0.1260533	-3.17	FALSE
253808_at	predicted proline-rich protein hy	---	AT4G28300	1.57	0.65	3.15	0.0170775	0.126064	-3.17	FALSE
248555_at	DNA repair protein-like	---	AT5G50340	-1.45	-0.53	-3.15	0.0170924	0.1261334	-3.17	FALSE
246952_at	putative protein similar to unknov	OFP13	AT5G04820	-1.56	-0.64	-3.15	0.0171096	0.1261787	-3.17	TRUE
254972_at	putative protein more than 10 pu	---	AT4G10440	1.46	0.55	3.15	0.0171065	0.1261787	-3.17	FALSE
265697_at	hypothetical protein predicted by	---	AT2G32170	-1.39	-0.48	-3.14	0.017174	0.1266121	-3.18	FALSE
247450_at	ripening-related protein - like rip	---	AT5G62350	-1.57	-0.65	-3.14	0.0171889	0.1266811	-3.18	FALSE
249792_at	putative protein contains similarit	PHS1	AT5G23720	-1.38	-0.47	-3.14	0.0171987	0.1267123	-3.18	FALSE
264820_at	putative coproporphyrinogen III c	LIN2	AT1G03475	-1.32	-0.40	-3.14	0.0172187	0.1268191	-3.18	FALSE
265132_at	unknown protein ; supported by	---	AT1G23830	1.96	0.97	3.14	0.0172254	0.1268272	-3.18	FALSE
259677_at	putative phosphatidylinositol-4-pl	---	AT1G77740	1.60	0.68	3.14	0.0172399	0.126849	-3.18	FALSE
258896_at	putative syntaxin protein, AtSNA	SYP43	AT3G05710	1.46	0.55	3.14	0.0172361	0.126849	-3.18	FALSE
263085_at	hypothetical protein predicted by	ARI12	AT2G16090	-1.60	-0.68	-3.14	0.017245	0.126849	-3.18	FALSE
258377_at	hypothetical protein contains sim	CNGC19	AT3G17690	1.47	0.55	3.14	0.0172558	0.1268878	-3.18	FALSE
258483_at	putative mannose-6-phosphate is	MEE31	AT3G02570	1.72	0.79	3.14	0.0173029	0.1270006	-3.18	TRUE
246295_at	calmodulin-binding protein ; sup	CIP111	AT3G56690	-1.60	-0.68	-3.14	0.0172928	0.1270006	-3.18	TRUE
265100_at	hypothetical protein predicted by	OSB4	AT1G31010	-1.67	-0.74	-3.14	0.0172959	0.1270006	-3.18	FALSE
263810_at	putative translation initiation facto	---	AT2G04520	-1.35	-0.43	-3.14	0.0173082	0.1270006	-3.18	FALSE
262005_at	ABC transporter protein, putative	ATGCN3	AT1G64550	-1.64	-0.72	-3.14	0.0172951	0.1270006	-3.18	FALSE
261670_at	hypothetical protein contains sim	TET11	AT1G18520	1.34	0.42	3.14	0.0172776	0.1270006	-3.18	FALSE
245556_at	HSR201 like protein	---	AT4G15400	1.34	0.42	3.14	0.0173102	0.1270006	-3.18	FALSE
261354_at	unknown protein ; supported by c	atnudt3	AT1G79690	1.43	0.51	3.14	0.017351	0.1272214	-3.19	FALSE
266227_at	unknown protein ;supported by f	---	AT2G28870	-1.33	-0.41	-3.14	0.0173514	0.1272214	-3.19	FALSE
247279_at	arabinogalactan-protein (gb|AAC	AGP1	AT5G64310	4.16	2.06	3.13	0.0173654	0.1272831	-3.19	FALSE
250284_at	protein kinase precursor - like re	CRN	AT5G13290	-1.71	-0.78	-3.13	0.0173729	0.1272972	-3.19	FALSE

253706_at	putative protein D-threonine deh	---	AT4G29120	-1.40	-0.49	-3.13	0.0173956	0.1274223	-3.19	FALSE
247836_at	putative protein similar to unknov	---	AT5G57860	-1.50	-0.58	-3.13	0.0174301	0.1274612	-3.19	TRUE
247325_at	putative protein contains similarit	SC35	AT5G64200	-1.38	-0.46	-3.13	0.0174512	0.1274612	-3.19	FALSE
255607_at	putative acetyltransferase simila	---	AT4G01130	-1.85	-0.88	-3.13	0.0174392	0.1274612	-3.19	FALSE
264214_s_a	MADS-box transcription factor, p	AGL38	AT1G65300 /	1.38	0.46	3.13	0.0174189	0.1274612	-3.19	FALSE
253858_at	carbohydrate kinase - like protei	---	AT4G27600	-1.37	-0.45	-3.13	0.0174266	0.1274612	-3.19	FALSE
265969_at	En/Spm-like transposon protein r	---	---	1.42	0.50	3.13	0.0174504	0.1274612	-3.19	FALSE
250198_at	expressed protein contains simil	NAP14	AT5G14100	-1.73	-0.79	-3.13	0.0174138	0.1274612	-3.19	FALSE
253284_at	putative protein hydroxyproline-r	---	AT4G34150	2.12	1.09	3.13	0.0174366	0.1274612	-3.19	FALSE
245281_at	DEF (CLA1) protein ; supported l	CLA1	AT4G15560	-1.50	-0.59	-3.13	0.0174476	0.1274612	-3.19	FALSE
257172_at	hypothetical protein predicted by	---	AT3G23700	-1.57	-0.65	-3.13	0.0174584	0.1274729	-3.19	FALSE
263766_at	hypothetical protein predicted by	---	AT2G21440	-1.60	-0.68	-3.13	0.0174676	0.1274994	-3.19	FALSE
258880_at	hypothetical protein similar to sy	ATG8H	AT3G06420	2.25	1.17	3.13	0.0174755	0.1275164	-3.19	FALSE
253969_at	putative protein hypothetical pro	CSN6B	AT4G26430	-1.86	-0.89	-3.13	0.0174887	0.1275719	-3.19	FALSE
256612_at	hypothetical protein predicted by	---	AT3G29280	-1.52	-0.61	-3.13	0.017503	0.1276354	-3.20	FALSE
260273_at	unknown protein	---	AT1G80550	-1.52	-0.61	-3.13	0.0175311	0.1277583	-3.20	FALSE
266265_at	putative tropinone reductase ; su	---	AT2G29340	1.77	0.82	3.13	0.0175257	0.1277583	-3.20	FALSE
256936_at	prefoldin-like protein similar to p	PDF2	AT3G22480	-1.42	-0.51	-3.13	0.017547	0.1278336	-3.20	FALSE
255662_at	putative protein	GPAT8	AT4G00400	2.06	1.04	3.13	0.0175765	0.1278442	-3.20	TRUE
252277_at	alpha NAC-like protein Nascent	NACA2	AT3G49470	-1.32	-0.40	-3.13	0.0175574	0.1278442	-3.20	FALSE
257352_at	putative RING3 protein	IMB1	AT2G34900	-1.53	-0.61	-3.13	0.0175666	0.1278442	-3.20	FALSE
259466_at	response regulator 5, putative si	ARR7	AT1G19050	3.74	1.90	3.13	0.0175602	0.1278442	-3.20	FALSE
260617_at	Expressed protein ; supported by	---	AT1G53345	-1.51	-0.60	-3.13	0.0175747	0.1278442	-3.20	FALSE
258175_at	FKBP-type peptidyl-prolyl cis-tra	TWD1	AT3G21640	-1.42	-0.51	-3.13	0.0175822	0.1278452	-3.20	FALSE
246892_at	putative protein predicted protei	---	AT5G25500	-1.45	-0.54	-3.12	0.0176022	0.1279495	-3.20	FALSE
267499_at	hypothetical protein predicted by	---	AT2G45500	1.44	0.53	3.12	0.0176203	0.1280404	-3.20	FALSE
257125_at	t-complex polypeptide 1 homolog	ATTCP-1	AT3G20050	-1.52	-0.60	-3.12	0.0176348	0.128105	-3.20	FALSE
254593_s_a	putative protein IEF SSP 9502, l	---	AT4G18900 /	-1.52	-0.61	-3.12	0.0176446	0.1281351	-3.20	TRUE
251753_at	putative protein predicted protei	---	AT3G55760	-2.37	-1.24	-3.12	0.0176539	0.1281625	-3.20	FALSE
251882_at	peptide transport - like protein p	PTR1	AT3G54140	1.52	0.60	3.12	0.0176616	0.1281773	-3.20	FALSE
264318_at	putative beta-ketoacyl-CoA synth	KCS2	AT1G04220	-2.02	-1.01	-3.12	0.0177144	0.1284378	-3.21	TRUE
250987_at	putative protein crp1 protein, Ze	---	AT5G02860	-1.49	-0.58	-3.12	0.0177105	0.1284378	-3.21	TRUE
254320_at	putative protein various predicte	---	AT4G22580	-1.35	-0.44	-3.12	0.0177129	0.1284378	-3.21	FALSE
252716_at	putative protein CAF protein, Ara	DCL3	AT3G43920	-1.54	-0.62	-3.12	0.0177209	0.1284443	-3.21	FALSE
263127_at	hypothetical protein predicted by	MSL6	AT1G78610	1.51	0.59	3.12	0.0177437	0.128508	-3.21	TRUE

247932_at	putative protein similar to unknov	---	AT5G56920	1.34	0.42	3.12	0.0177432	0.128508	-3.21	FALSE
267578_at	Expressed protein ; supported by	---	AT2G30695	-1.97	-0.98	-3.12	0.0177466	0.128508	-3.21	FALSE
253849_at	putative protein 150-kD protein,	---	AT4G28080	-1.39	-0.47	-3.12	0.0177811	0.1285942	-3.21	FALSE
260261_at	unknown protein	---	AT1G68450	3.83	1.94	3.12	0.0177789	0.1285942	-3.21	FALSE
266256_at	60S acidic ribosomal protein P2	---	AT2G27710	-1.90	-0.93	-3.12	0.0177787	0.1285942	-3.21	FALSE
258247_at	hypothetical protein predicted by	---	AT3G29130	-1.29	-0.37	-3.12	0.0177744	0.1285942	-3.21	FALSE
262736_at	lipase, putative contains Pfam p	---	AT1G28570	-1.39	-0.48	-3.12	0.0177885	0.1286072	-3.21	FALSE
257442_at	legumin-like protein contains a 1	---	AT2G28680	1.66	0.73	3.12	0.0178027	0.1286648	-3.21	FALSE
262368_at	unknown protein ;supported by fu	---	AT1G73060 /	-1.78	-0.83	-3.12	0.0178077	0.1286648	-3.21	FALSE
258927_at	putative folylpolyglutamate synth	DFC	AT3G10160	-1.41	-0.49	-3.12	0.0178153	0.1286787	-3.21	FALSE
253443_at	putative protein beta transducin-	LUG	AT4G32551	-1.30	-0.38	-3.12	0.0178284	0.1286919	-3.21	FALSE
267061_at	unknown protein ;supported by f	---	AT2G32480	-1.41	-0.49	-3.12	0.0178265	0.1286919	-3.21	FALSE
250071_at	putative protein similar to unknov	---	AT5G18000	1.34	0.42	3.11	0.0178434	0.1287595	-3.22	FALSE
252770_at	putative protein cellular nucleic a	---	AT3G42860	-1.48	-0.57	-3.11	0.0178617	0.128769	-3.22	FALSE
260356_at	unknown protein ; supported by	ATMINE1	AT1G69390	-1.41	-0.50	-3.11	0.0178585	0.128769	-3.22	FALSE
256958_at	unknown protein contains Pfam	---	AT3G13430	1.77	0.83	3.11	0.0178599	0.128769	-3.22	FALSE
260731_at	P-type ATPase, putative similar	---	AT1G17500	1.50	0.59	3.11	0.0178679	0.1287733	-3.22	FALSE
266884_at	phytocyanin identical to GB:U904	UCC2	AT2G44790	2.69	1.43	3.11	0.0179006	0.1288055	-3.22	TRUE
245790_at	glycerol-3-phosphate acyltransfe	ATS1	AT1G32200	-1.51	-0.59	-3.11	0.017879	0.1288055	-3.22	FALSE
256060_at	hypothetical protein contains sim	---	AT1G07050	1.74	0.80	3.11	0.0178964	0.1288055	-3.22	FALSE
260931_at	hypothetical protein predicted by	---	AT1G02550	1.53	0.61	3.11	0.0178948	0.1288055	-3.22	FALSE
251984_at	phenylalanine ammonia-lyase ;s	PAL2	AT3G53260	4.09	2.03	3.11	0.0178941	0.1288055	-3.22	FALSE
253060_at	putative protein predicted protei	---	AT4G37710	2.36	1.24	3.11	0.017914	0.1288609	-3.22	FALSE
265649_at	putative ferredoxin ; supported b	ATFD3	AT2G27510	1.96	0.97	3.11	0.0179555	0.1290106	-3.22	TRUE
267519_at	putative VP1/ABI3 family regulat	HSI2	AT2G30470	1.64	0.71	3.11	0.0179574	0.1290106	-3.22	FALSE
263031_at	glucosyltransferase, putative sim	ATCSLA10	AT1G24070	5.05	2.34	3.11	0.0179488	0.1290106	-3.22	FALSE
253697_at	nucleotide pyrophosphatase -like	---	AT4G29700	6.60	2.72	3.11	0.0179474	0.1290106	-3.22	FALSE
254493_at	DAG-like protein DAG precursor	---	AT4G20020	-1.86	-0.90	-3.11	0.0180116	0.1290495	-3.22	FALSE
266932_s_a	putative RNA helicase	---	AT1G63250 /	-1.76	-0.82	-3.11	0.0180428	0.1290495	-3.23	FALSE
251117_at	putative protein predicted protei	---	AT3G63390	-1.54	-0.62	-3.11	0.0180236	0.1290495	-3.23	FALSE
259768_at	expressed protein supported by c	COR314-TI	AT1G29390	-1.31	-0.39	-3.11	0.0179876	0.1290495	-3.22	FALSE
262539_at	unknown protein Location of est	---	AT1G17200	-1.67	-0.74	-3.11	0.01799	0.1290495	-3.22	FALSE
245794_at	endoxyloglucan transferase, put	XTR4	AT1G32170	1.57	0.65	3.11	0.018036	0.1290495	-3.23	FALSE
258270_at	putative lysophospholipase simila	---	AT3G15650	2.24	1.17	3.11	0.0180317	0.1290495	-3.23	FALSE
267218_at	Expressed protein ; supported by	---	AT2G02515	1.40	0.49	3.11	0.0180546	0.1290495	-3.23	FALSE

255227_at	D123 -like protein protein D123,	EDA35	AT4G05440	-1.58	-0.66	-3.11	0.0180467	0.1290495	-3.23	FALSE
262594_at	putative 60s ribosomal protein L3	---	AT1G15250	-2.62	-1.39	-3.11	0.0180565	0.1290495	-3.23	FALSE
246103_at	putative protein	AN3	AT5G28640	1.31	0.39	3.11	0.0180179	0.1290495	-3.23	FALSE
248329_at	putative protein similar to unknov	---	AT5G52780	-1.66	-0.73	-3.11	0.0180647	0.1290495	-3.23	FALSE
265664_at	unknown protein predicted by ge	---	AT2G24420	-1.50	-0.59	-3.11	0.0180402	0.1290495	-3.23	FALSE
254318_at	putative protein embryo-abunda	---	AT4G22530	3.69	1.88	3.11	0.0180374	0.1290495	-3.23	FALSE
265641_at	putative RNA-binding glycine rich	---	AT2G27330	-1.49	-0.58	-3.11	0.0179771	0.1290495	-3.22	FALSE
266634_at	putative G-box binding bZIP tran	---	AT2G35530	1.38	0.46	3.11	0.01798	0.1290495	-3.22	FALSE
265643_at	hypothetical protein predicted by	---	AT2G27390 /	1.96	0.97	3.11	0.0180174	0.1290495	-3.23	FALSE
258577_at	putative disease resistance prote	---	AT3G04220	2.14	1.10	3.11	0.0180642	0.1290495	-3.23	FALSE
248505_at	putative protein similar to unknov	---	AT5G50360	1.53	0.61	3.11	0.0180709	0.1290536	-3.23	FALSE
250028_at	putative protein similar to unknov	---	AT5G18130	-1.42	-0.50	-3.10	0.0181224	0.1292598	-3.23	FALSE
259859_at	putative protein phosphatase sim	---	AT1G68410	2.40	1.26	3.10	0.0181066	0.1292598	-3.23	FALSE
246702_at	putative cytidine deaminase - lik	---	AT5G28050	2.65	1.41	3.10	0.01812	0.1292598	-3.23	FALSE
250599_at	unknown protein ; supported by	---	AT5G07730	1.62	0.69	3.10	0.0181165	0.1292598	-3.23	FALSE
259668_at	hypothetical protein predicted by	---	AT1G52390	1.40	0.49	3.10	0.0181401	0.1293455	-3.23	FALSE
250133_at	thioredoxin f2 (gb|AAD35004.1)	TRXF2	AT5G16400	-1.90	-0.93	-3.10	0.018155	0.1294112	-3.23	FALSE
258380_at	PP1/PP2A phosphatases pleiotro	---	AT3G16650	-1.45	-0.54	-3.10	0.0181675	0.1294191	-3.23	FALSE
245094_at	4-alpha-glucanotransferase	DPE2	AT2G40840	-1.56	-0.65	-3.10	0.0181666	0.1294191	-3.23	FALSE
254389_s_a	putative protein various predicted	---	AT4G21903 /	2.37	1.25	3.10	0.0181916	0.1294784	-3.23	FALSE
255803_at	putative protein vesicle-associat	---	AT4G10170	-1.38	-0.46	-3.10	0.0181928	0.1294784	-3.23	FALSE
251179_at	putative protein ABP130 protein	---	AT3G63460	1.32	0.40	3.10	0.0181892	0.1294784	-3.23	FALSE
261314_at	putative GTP-binding protein sim	---	AT1G52980	-1.69	-0.75	-3.10	0.0182142	0.1295901	-3.24	FALSE
257275_at	RNA-binding protein, putative co	CID9	AT3G14450	-1.86	-0.89	-3.10	0.0182266	0.1296382	-3.24	FALSE
253901_at	ribosomal protein L14 -like prote	---	AT4G27090	-1.78	-0.83	-3.10	0.0182415	0.1297032	-3.24	FALSE
263212_at	unknown protein similar to ribonu	emb2004	AT1G10510	-1.42	-0.50	-3.10	0.0182499	0.1297224	-3.24	FALSE
253921_at	glutamine amidotransferase/cycl	AT-HF	AT4G26900	-1.48	-0.56	-3.10	0.0182648	0.1297883	-3.24	FALSE
253872_at	putative protein Arabidopsis thal	RD26	AT4G27410	1.75	0.81	3.10	0.0182796	0.1298195	-3.24	FALSE
255838_at	unknown protein	---	AT2G33490	1.39	0.47	3.10	0.0182806	0.1298195	-3.24	FALSE
253605_at	putative protein probable membr	---	AT4G30990	-1.62	-0.70	-3.10	0.0182942	0.1298357	-3.24	TRUE
261338_at	hypothetical protein predicted by	---	AT1G44920	-1.52	-0.60	-3.10	0.0182932	0.1298357	-3.24	FALSE
248548_at	transmembrane transport protein	---	AT5G50300	1.36	0.44	3.10	0.0183054	0.1298745	-3.24	FALSE
245875_at	hypothetical protein predicted by	---	AT1G26240	1.52	0.61	3.10	0.0183254	0.1299757	-3.24	FALSE
258243_at	carbamoyl phosphate synthetase	CARA	AT3G27740	-1.69	-0.76	-3.10	0.0183332	0.129991	-3.24	FALSE
249905_at	unknown protein	---	AT5G22710	-1.41	-0.50	-3.09	0.0183734	0.130235	-3.25	FALSE

251243_at	putative protein hypothetical pro	---	AT3G61870	-1.64	-0.71	-3.09	0.0183968	0.1302481	-3.25	FALSE
246086_at	beta-1,3-glucanase - like protein	---	AT5G20560	1.35	0.43	3.09	0.018398	0.1302481	-3.25	FALSE
255480_at	Expressed protein ; supported by	---	AT4G02485	-1.37	-0.45	-3.09	0.018388	0.1302481	-3.25	FALSE
246031_at	putative protein KIAA0731 - Hor	---	AT5G21160	-1.48	-0.57	-3.09	0.0183856	0.1302481	-3.25	FALSE
254052_at	UMP/CMP kinase like protein UI	---	AT4G25280	-1.50	-0.59	-3.09	0.018412	0.1303068	-3.25	FALSE
264158_at	hypothetical protein contains sim	PTAC4	AT1G65260	-1.53	-0.62	-3.09	0.0184364	0.130435	-3.25	FALSE
252358_at	putative protein cfxY protein, Alc	---	AT3G48425	-1.37	-0.46	-3.09	0.0184416	0.130435	-3.25	FALSE
256076_at	unknown protein ; supported by c	---	AT1G18060	-1.78	-0.83	-3.09	0.0184731	0.1304958	-3.25	TRUE
255429_at	hypothetical protein	---	AT4G03410	1.60	0.68	3.09	0.0184713	0.1304958	-3.25	FALSE
252318_at	glutamate-1-semialdehyde amino	GSA2	AT3G48730	-1.74	-0.80	-3.09	0.0184631	0.1304958	-3.25	FALSE
260406_at	putative glutathione transferase s	ATGSTU12	AT1G69920	9.94	3.31	3.09	0.0184667	0.1304958	-3.25	FALSE
253115_at	putative protein ;supported by fu	---	AT4G35910	-1.38	-0.47	-3.09	0.01848	0.1305045	-3.25	FALSE
258409_at	hypothetical protein similar to GE	---	AT3G17640	-1.96	-0.97	-3.09	0.0185049	0.1305995	-3.25	FALSE
249312_at	disease resistance protein-like	---	AT5G41550	1.57	0.65	3.09	0.0185026	0.1305995	-3.25	FALSE
247241_at	unknown protein	---	AT5G64680	-1.90	-0.93	-3.09	0.0185505	0.1308404	-3.25	FALSE
252297_at	cytosolic ribosomal protein S11	EMB1080	AT3G48930	-1.97	-0.98	-3.09	0.0185491	0.1308404	-3.25	FALSE
254543_at	putative chitinase chitinase (EC	---	AT4G19810	3.20	1.68	3.09	0.0185573	0.1308476	-3.26	FALSE
265857_s_a	serine threonine protein phospha	PP2A-4	AT2G42500 /,	-1.46	-0.55	-3.09	0.0185741	0.1309259	-3.26	FALSE
246420_at	putative protein various predicted	---	AT5G16870	-1.53	-0.61	-3.08	0.0185947	0.1309311	-3.26	FALSE
264527_at	putative reticuline oxidase-like p	---	AT1G30760	2.19	1.13	3.08	0.0185978	0.1309311	-3.26	FALSE
247629_at	putative protein	SIZ1	AT5G60410	1.48	0.57	3.09	0.0185862	0.1309311	-3.26	FALSE
250540_at	unknown protein ; supported by	---	AT5G08580	-1.63	-0.71	-3.08	0.0185947	0.1309311	-3.26	FALSE
261062_at	transcription factor scarecrow-lik	SCL14	AT1G07530	-1.40	-0.49	-3.08	0.0186102	0.130978	-3.26	FALSE
259860_at	putative protein kinase similar to	---	AT1G80640	-1.64	-0.72	-3.08	0.0186438	0.131133	-3.26	FALSE
254576_at	putative protein ;supported by fu	EMB3006	AT4G19350	-1.38	-0.46	-3.08	0.0186422	0.131133	-3.26	FALSE
256235_at	cysteine proteinase inhibitor, put	ATCYSB	AT3G12490	1.32	0.40	3.08	0.0186633	0.1312296	-3.26	FALSE
266857_at	putative Na+ dependent ileal bile	---	AT2G26900	-1.39	-0.47	-3.08	0.0186787	0.1312977	-3.26	FALSE
248232_at	putative protein contains similarit	MLO11	AT5G53760	1.55	0.63	3.08	0.0186947	0.1313495	-3.26	FALSE
247692_s_a	histone H4 - like protein histone	---	AT5G59690 /,	-2.02	-1.01	-3.08	0.0187033	0.1313495	-3.26	FALSE
247302_at	unknown protein ;supported by f	VPS20.1	AT5G63880	1.39	0.48	3.08	0.0187023	0.1313495	-3.26	FALSE
265694_at	hypothetical protein predicted by	---	AT2G24440	-1.47	-0.55	-3.08	0.0187326	0.1315145	-3.26	FALSE
251013_at	putative protein various predicte	---	AT5G02540	-7.62	-2.93	-3.08	0.0187458	0.1315263	-3.27	FALSE
251061_at	putative protein hypothetical pro	---	AT5G01830	2.36	1.24	3.08	0.0187405	0.1315263	-3.27	FALSE
257919_at	myb-related transcription factor,	MYB15	AT3G23250	6.59	2.72	3.08	0.01876	0.1315851	-3.27	FALSE
260177_at	hypothetical protein predicted by	---	AT1G70650	-1.73	-0.79	-3.08	0.0187715	0.1316257	-3.27	FALSE

262890_at	nucleoporin, putative similar to n	NUP155	AT1G14850	-1.70	-0.77	-3.08	0.0187882	0.1316857	-3.27	FALSE
252202_at	anthranilate N-hydroxycinnamoy	---	AT3G50300	1.41	0.49	3.08	0.0187916	0.1316857	-3.27	FALSE
264023_at	Expressed protein ; supported by	---	AT2G21195	-1.82	-0.86	-3.08	0.0187981	0.1316905	-3.27	FALSE
261488_at	Expressed protein ; supported by	---	AT1G14345	-1.54	-0.62	-3.08	0.0188049	0.1316978	-3.27	FALSE
266986_at	putative dolichyl-phosphate beta-	---	AT2G39630	-1.34	-0.43	-3.08	0.0188356	0.1317326	-3.27	FALSE
254263_at	Expressed protein ; supported by	---	AT4G23493	-1.38	-0.46	-3.08	0.0188276	0.1317326	-3.27	FALSE
245734_at	lysophospholipase homolog, put	---	AT1G73480	1.84	0.88	3.08	0.0188387	0.1317326	-3.27	FALSE
252972_at	auxin-induced protein - like auxi	---	AT4G38840	-2.32	-1.22	-3.08	0.0188224	0.1317326	-3.27	FALSE
257672_at	unknown protein ;supported by f	---	AT3G20300	-1.88	-0.91	-3.08	0.0188221	0.1317326	-3.27	FALSE
246206_at	Expressed protein ; supported by	ATPBRP	---	1.38	0.46	3.07	0.0188586	0.1317593	-3.27	FALSE
258296_at	putative ribosomal protein similar	---	AT3G23390	-2.17	-1.12	-3.07	0.0188657	0.1317593	-3.27	FALSE
252039_at	Expressed protein ; supported by	---	AT3G52155	-1.50	-0.58	-3.07	0.018854	0.1317593	-3.27	FALSE
254901_at	serine/threonine kinase-like prot	---	AT4G11530	1.41	0.50	3.07	0.0188611	0.1317593	-3.27	FALSE
250887_at	putative protein	---	---	-1.46	-0.54	-3.07	0.0188962	0.131892	-3.27	FALSE
247278_at	fructose-bisphosphatase-like pro	---	AT5G64380	-1.52	-0.61	-3.07	0.0188916	0.131892	-3.27	FALSE
261319_at	phytochrome A supressor spa1,	SPA4	AT1G53090	-1.29	-0.37	-3.07	0.0189117	0.1319561	-3.27	FALSE
261333_at	hypothetical protein predicted by	---	AT1G44910	-1.68	-0.75	-3.07	0.018917	0.1319561	-3.27	FALSE
250110_at	putative protein many predicted	---	AT5G15350	2.36	1.24	3.07	0.0189254	0.1319745	-3.28	TRUE
251025_at	putative protein CND41, chlorop	PCS1	AT5G02190	1.57	0.65	3.07	0.0189327	0.1319851	-3.28	FALSE
248578_at	putative protein contains similarit	emb1879	AT5G49820	-1.60	-0.68	-3.07	0.0189604	0.1321377	-3.28	FALSE
261206_at	heat shock factor protein hsf8, p	---	AT1G12800	-1.54	-0.62	-3.07	0.0189686	0.1321548	-3.28	FALSE
255176_s_a	putative DNA-directed RNA poly	---	AT1G01210 /A	-1.40	-0.48	-3.07	0.0190092	0.1322757	-3.28	FALSE
257000_at	hypothetical protein predicted by	---	AT3G14120	-1.73	-0.79	-3.07	0.0189983	0.1322757	-3.28	FALSE
260564_at	putative small nuclear ribonucleo	---	AT2G43810	-1.49	-0.58	-3.07	0.0189927	0.1322757	-3.28	FALSE
261724_at	Expressed protein ; supported by	---	AT1G76185	-1.40	-0.48	-3.07	0.0190083	0.1322757	-3.28	FALSE
251678_at	putative protein conserved hypo	EDA7	AT3G56990	-1.36	-0.45	-3.07	0.0190334	0.1324038	-3.28	FALSE
261060_at	unknown protein	---	AT1G17340	1.52	0.60	3.07	0.0190541	0.1324972	-3.28	FALSE
249190_at	unknown protein ;supported by f	BKI1	AT5G42750	-1.47	-0.55	-3.07	0.0190584	0.1324972	-3.28	FALSE
260008_at	putative RING zinc finger protein	---	AT1G68070	-1.37	-0.45	-3.07	0.0190692	0.1325314	-3.28	FALSE
256147_at	hypothetical protein predicted by	---	AT1G55080	1.55	0.63	3.07	0.0190861	0.1326084	-3.28	FALSE
259611_at	GTP-binding protein RAB7D, pu	AtRABG3d	AT1G52280	1.47	0.55	3.06	0.0191649	0.1326396	-3.29	TRUE
251143_at	putative protein SqdX protein, S	SQD2	AT5G01220	-1.98	-0.99	-3.06	0.0191286	0.1326396	-3.29	TRUE
253679_at	cytidine deaminase 6 (CDA6)	---	AT4G29610	2.32	1.21	3.06	0.0191599	0.1326396	-3.29	TRUE
258260_at	unknown protein ; supported by	---	AT3G26850	-1.36	-0.44	-3.06	0.0191662	0.1326396	-3.29	FALSE
255434_at	predicted protein of unknown fun	---	AT4G03180	-1.42	-0.51	-3.06	0.0191575	0.1326396	-3.29	FALSE

258322_at	putative selenocysteine methyltra	HMT3	AT3G22740	2.98	1.57	3.06	0.019134	0.1326396	-3.29	FALSE
257855_at	hypothetical protein predicted by	---	AT3G13040	-1.39	-0.48	-3.06	0.0191587	0.1326396	-3.29	FALSE
247194_at	putative protein similar to unknov	---	AT5G65480	-1.68	-0.75	-3.06	0.0191126	0.1326396	-3.29	FALSE
246909_at	putative protein predicted protei	---	AT5G25770	2.32	1.22	3.06	0.0191131	0.1326396	-3.29	FALSE
259326_at	putative mitochondrial processing	MPPalpha	AT3G16480	-1.36	-0.44	-3.07	0.0190975	0.1326396	-3.28	FALSE
244966_at	cytochrome b6-f complex, subur	---	---	-1.68	-0.75	-3.06	0.0191576	0.1326396	-3.29	FALSE
258068_at	putative DNA-binding protein, G	---	AT3G25990	1.38	0.47	3.06	0.0191629	0.1326396	-3.29	FALSE
248450_at	putative protein contains similarit	---	AT5G51290	1.47	0.55	3.06	0.0191437	0.1326396	-3.29	FALSE
251173_at	putative protein hypothetical pro	---	AT3G63270	-1.33	-0.41	-3.06	0.0191721	0.1326401	-3.29	FALSE
256655_at	hypothetical protein predicted by	---	AT3G18890	-1.72	-0.78	-3.06	0.0192259	0.132691	-3.29	TRUE
256745_at	UDP-glucose dehydrogenase, p	---	AT3G29360	1.52	0.61	3.06	0.0192217	0.132691	-3.29	TRUE
252633_x_a	putative protein HISTONE DEA(	hda17	AT3G44490 ///	-1.31	-0.39	-3.06	0.0192133	0.132691	-3.29	FALSE
258810_at	hypothetical protein similar to hyp	---	AT3G03970	1.47	0.56	3.06	0.0192132	0.132691	-3.29	FALSE
264996_at	nuclear matrix constituent protei	LINC1	AT1G67230	1.50	0.59	3.06	0.0191953	0.132691	-3.29	FALSE
262157_at	unknown protein contains similar	---	AT1G52670	-1.45	-0.54	-3.06	0.019201	0.132691	-3.29	FALSE
245866_s_a	unknown protein	---	AT1G57980 ///	4.11	2.04	3.06	0.0192174	0.132691	-3.29	FALSE
254997_s_a	putative protein various predicte	---	AT4G09920 ///	-1.37	-0.45	-3.06	0.0192028	0.132691	-3.29	FALSE
245004_at	hypothetical protein	---	---	-1.58	-0.66	-3.06	0.0192348	0.1327123	-3.29	FALSE
260783_at	ethylene response factor, putativ	ORA59	AT1G06160	-2.91	-1.54	-3.06	0.0192581	0.1328111	-3.29	TRUE
254975_at	putative Fe(II)/ascorbate oxidase	---	AT4G10500	20.53	4.36	3.06	0.0192608	0.1328111	-3.29	FALSE
267337_at	putative anthocyanin 5-aromatic	---	AT2G39980	1.70	0.77	3.06	0.0192777	0.1328876	-3.29	FALSE
254353_s_a	putative protein probable membr	---	AT4G22285 ///	-1.62	-0.70	-3.06	0.0192987	0.1329517	-3.30	FALSE
266320_at	hypothetical protein predicted by	---	AT2G46640	1.80	0.85	3.06	0.0192967	0.1329517	-3.30	FALSE
249886_at	unknown protein ; supported by	---	AT5G22320	-1.70	-0.77	-3.06	0.0193071	0.1329694	-3.30	TRUE
252198_x_a	putative protein predicted protei	---	AT3G50250	1.69	0.76	3.06	0.0193191	0.1330123	-3.30	FALSE
253452_at	hypothetical protein ; supported b	---	AT4G31930	-1.40	-0.48	-3.06	0.0193281	0.1330336	-3.30	FALSE
258786_at	putative syntaxin contains Pfam	SYP121	AT3G11820	2.17	1.12	3.06	0.0193345	0.1330379	-3.30	FALSE
263133_at	hypothetical protein predicted by	---	AT1G78450	3.91	1.97	3.06	0.0193487	0.1330954	-3.30	FALSE
256509_at	NADPH oxidoreductase, putativ	---	AT1G75300	1.90	0.92	3.06	0.0193565	0.1331091	-3.30	FALSE
262780_at	putative cytochrome P450 monc	CYP71B28	AT1G13090	-1.58	-0.66	-3.06	0.0193627	0.1331114	-3.30	TRUE
255231_at	F-box protein family, AtFBL20 c	---	AT4G05460	-1.36	-0.45	-3.05	0.0193911	0.1332271	-3.30	FALSE
266950_at	expressed protein supported by f	---	AT2G18910	-1.70	-0.76	-3.05	0.0193912	0.1332271	-3.30	FALSE
248985_at	GTP-binding protein-like; root ha	---	AT5G45160	-1.36	-0.44	-3.05	0.0193991	0.1332394	-3.30	FALSE
262728_at	receptor kinase (CLV1) identical	CLV1	AT1G75820	-1.88	-0.91	-3.05	0.0194047	0.1332394	-3.30	FALSE
247335_at	RNA helicase	---	AT5G63630	-1.42	-0.51	-3.05	0.0194145	0.1332664	-3.30	FALSE

259295_at	hypothetical protein predicted by	---	AT3G05340	-1.55	-0.63	-3.05	0.0194296	0.1332898	-3.30	FALSE
252561_at	histone H2B ;supported by full-le	HTB9	AT3G45980	-1.65	-0.72	-3.05	0.0194275	0.1332898	-3.30	FALSE
251139_at	cell division - like protein JM23 p	---	AT5G01230	-1.53	-0.61	-3.05	0.0194489	0.1332934	-3.30	FALSE
266054_at	hypothetical protein predicted by	---	AT2G40640	-1.55	-0.63	-3.05	0.0194535	0.1332934	-3.30	FALSE
257759_at	hypothetical protein	---	AT3G23070	-1.70	-0.77	-3.05	0.0194415	0.1332934	-3.30	FALSE
250763_at	short chain alcohol dehydrogena	---	AT5G06060	-1.48	-0.57	-3.05	0.0194484	0.1332934	-3.30	FALSE
260771_at	serine/threonine protein kinase,	WNK7	AT1G49160	1.88	0.91	3.05	0.0194684	0.1333554	-3.30	FALSE
264651_at	putative histone H2A Strong sim	H2AXA	AT1G08880	-1.82	-0.87	-3.05	0.0195027	0.1335505	-3.31	FALSE
261259_at	unknown protein	---	AT1G26660	-1.44	-0.52	-3.05	0.01952	0.1335607	-3.31	FALSE
260145_at	putative G protein-coupled recep	GPCR	AT1G52920	-1.31	-0.39	-3.05	0.0195218	0.1335607	-3.31	FALSE
248611_at	putative protein contains similarit	WRKY48	AT5G49520	3.03	1.60	3.05	0.0195186	0.1335607	-3.31	FALSE
260542_at	putative FKBP type peptidyl-proly	---	AT2G43560	-1.84	-0.88	-3.05	0.0195718	0.1335885	-3.31	TRUE
262151_at	hypothetical protein predicted by	---	AT1G52510	-1.98	-0.99	-3.05	0.0195605	0.1335885	-3.31	TRUE
264335_s_a	hypothetical protein contains sim	UPL1	AT1G55860 ///	-1.32	-0.40	-3.05	0.0195643	0.1335885	-3.31	FALSE
255081_at	MLH1 protein ; supported by cD	MLH1	AT4G09140	-1.84	-0.88	-3.05	0.0195945	0.1335885	-3.31	TRUE
246817_at	putative protein various predicte	---	AT5G27240	-1.47	-0.55	-3.05	0.0195926	0.1335885	-3.31	FALSE
254663_at	potassium channel protein KAT2	KAT2	AT4G18290	1.62	0.70	3.05	0.0195369	0.1335885	-3.31	FALSE
252680_at	putative protein predicted protei	---	AT3G44330	-1.32	-0.40	-3.05	0.0195636	0.1335885	-3.31	FALSE
253945_at	putative protein gene F23F1.15	---	AT4G27050	-1.32	-0.40	-3.05	0.0195934	0.1335885	-3.31	FALSE
266340_at	similar to axi 1 protein from Nicot	---	AT2G01480	1.32	0.40	3.05	0.0195961	0.1335885	-3.31	FALSE
262084_at	hypothetical protein predicted by	---	AT1G56080	1.47	0.56	3.05	0.0195851	0.1335885	-3.31	FALSE
250342_at	putative protein predicted protei	---	AT5G11870	1.61	0.69	3.05	0.0195499	0.1335885	-3.31	FALSE
249159_at	Nicotiana lesion-inducing like ; s	---	AT5G43460	-1.62	-0.70	-3.05	0.0195598	0.1335885	-3.31	FALSE
251242_at	ARGININE/SERINE-RICH SPLIC	RSP31	AT3G61860	-1.36	-0.44	-3.05	0.0196167	0.1336091	-3.31	FALSE
262163_at	ribosomal protein L30, putative s	---	AT1G77940	-2.19	-1.13	-3.05	0.0196111	0.1336091	-3.31	FALSE
251739_at	putative protein protein of unkno	CAN	AT3G56170	1.60	0.68	3.05	0.0196154	0.1336091	-3.31	FALSE
259085_at	unknown protein similar to GB:C/	---	AT3G05000	-1.42	-0.50	-3.05	0.0196263	0.1336348	-3.31	FALSE
266556_at	hypothetical protein predicted by	---	AT2G46230	-1.50	-0.59	-3.04	0.0196563	0.1337991	-3.31	FALSE
259097_at	unknown protein similar to GB:A/	---	AT3G04830	-1.36	-0.44	-3.04	0.0196883	0.1339768	-3.32	FALSE
246098_at	ethylene-forming-enzyme-like di	---	AT5G20400	-1.77	-0.82	-3.04	0.0196998	0.134015	-3.32	TRUE
261195_at	transport inhibitor response 1 (T	AFB3	AT1G12820	-1.42	-0.51	-3.04	0.0197136	0.1340177	-3.32	FALSE
262060_at	polygalacturonase, putative simi	---	AT1G80170	-1.43	-0.52	-3.04	0.0197178	0.1340177	-3.32	FALSE
266795_at	unknown protein	---	AT2G03070	-1.49	-0.58	-3.04	0.0197151	0.1340177	-3.32	FALSE
257369_at	hypothetical protein predicted by	BPC7	AT2G35550	-1.45	-0.54	-3.04	0.0197356	0.1340586	-3.32	FALSE
250403_at	argininosuccinate lyase (AtArgH)	---	AT5G10920	-1.91	-0.94	-3.04	0.0197306	0.1340586	-3.32	FALSE

249678_at	protein kinase-like	---	AT5G35980	1.31	0.39	3.04	0.019751	0.1340834	-3.32	FALSE
249841_at	unknown protein	---	AT5G23520	1.41	0.50	3.04	0.0197467	0.1340834	-3.32	FALSE
252130_at	putative protein 1 photosystem I	PSBO2	AT3G50820	-1.42	-0.50	-3.04	0.0198279	0.1343356	-3.32	FALSE
253814_at	putative protein ;supported by fu	---	AT4G28290	1.71	0.78	3.04	0.0198038	0.1343356	-3.32	FALSE
262098_at	transcription factor, putative sim	NF-YC2	AT1G56170	-1.57	-0.65	-3.04	0.0198141	0.1343356	-3.32	FALSE
250794_at	putative protein contains similarit	---	AT5G05270	1.38	0.47	3.04	0.0197994	0.1343356	-3.32	FALSE
262586_at	hypothetical protein predicted by	---	AT1G15480	-1.80	-0.85	-3.04	0.0198194	0.1343356	-3.32	FALSE
255877_at	putative PTR2 family peptide tran	---	AT2G40460	2.55	1.35	3.04	0.0198247	0.1343356	-3.32	FALSE
246364_at	hypothetical protein	---	---	1.34	0.43	3.04	0.0198353	0.1343356	-3.32	FALSE
263192_at	hypothetical protein putative ace	ACC1	AT1G36160	-1.67	-0.74	-3.04	0.0198323	0.1343356	-3.32	FALSE
252031_at	putative protein 150-kD protein c	---	AT3G52140	-1.38	-0.46	-3.04	0.019868	0.1344285	-3.32	FALSE
249741_at	putative protein contains similarit	APRR5	AT5G24470	-1.30	-0.38	-3.04	0.0198784	0.1344285	-3.33	FALSE
265530_at	12-oxophytodienoate-10,11-redu	OPR3	AT2G06050	2.56	1.36	3.04	0.0198622	0.1344285	-3.32	FALSE
262570_at	unknown protein EST gb|H77143	---	AT1G15200	-1.41	-0.50	-3.04	0.0198765	0.1344285	-3.33	FALSE
259231_at	protein phosphatase 2C (PP2C)	PP2CA	AT3G11410	1.88	0.91	3.04	0.0198704	0.1344285	-3.32	FALSE
267305_at	high affinity K+ transporter (AtKU	ATKT1	AT2G30070	-1.95	-0.96	-3.04	0.0198901	0.1344671	-3.33	FALSE
253863_at	putative protein D.melanogaster	---	AT4G27420	1.49	0.57	3.04	0.0199049	0.1345275	-3.33	FALSE
249066_at	WD-repeat protein-like	---	AT5G43920	-1.32	-0.40	-3.03	0.0199137	0.1345338	-3.33	FALSE
256520_at	hypothetical protein	CYP96A14	AT1G66030	1.38	0.47	3.03	0.0199235	0.1345338	-3.33	FALSE
245567_at	germin precursor oxalate oxidase	GLP9	AT4G14630	4.23	2.08	3.03	0.0199194	0.1345338	-3.33	FALSE
253193_at	putative protein SEC7 protein, S	---	AT4G35380	1.63	0.70	3.03	0.0199605	0.1347437	-3.33	FALSE
251819_at	phosphatidylglycerophosphate s	PGPS2	AT3G55030	-1.43	-0.51	-3.03	0.0199688	0.13476	-3.33	FALSE
264906_at	putative mitochondrial phosphate	---	AT2G17270	-1.61	-0.69	-3.03	0.0199799	0.1347946	-3.33	FALSE
255340_at	putative receptor-like protein kina	---	AT4G04490	3.52	1.82	3.03	0.0200166	0.1348434	-3.33	TRUE
254298_at	putative protein ;supported by fu	PGR5-LIKE	AT4G22890	-1.57	-0.65	-3.03	0.0200111	0.1348434	-3.33	FALSE
267007_at	60S ribosomal protein L18A ; sup	---	AT2G34480	-1.77	-0.83	-3.03	0.0200159	0.1348434	-3.33	FALSE
248889_at	unknown protein ;supported by fu	---	AT5G46230	1.79	0.84	3.03	0.0199961	0.1348434	-3.33	FALSE
249034_at	putative protein contains similarit	NUC	AT5G44160	-1.45	-0.53	-3.03	0.0200151	0.1348434	-3.33	FALSE
266298_at	unknown protein ;supported by f	---	AT2G29590	-1.50	-0.58	-3.03	0.0200405	0.1349235	-3.33	FALSE
260360_at	chorismate mutase, putative cor	CM3	AT1G69370	1.61	0.69	3.03	0.0200362	0.1349235	-3.33	FALSE
248773_at	kinesin-like protein	FRA1	AT5G47820	-1.54	-0.63	-3.03	0.0200463	0.1349235	-3.33	FALSE
261445_at	unknown protein ; supported by c	NSL1	AT1G28380	2.26	1.18	3.03	0.0200612	0.134984	-3.33	FALSE
259535_at	hypothetical protein	---	AT1G12280	-1.66	-0.73	-3.03	0.0200995	0.1350821	-3.34	FALSE
259176_at	putative cell division control prot	CDC48C	AT3G01610	-1.43	-0.51	-3.03	0.0200992	0.1350821	-3.34	FALSE
253544_at	hypothetical protein	---	AT4G31280	1.34	0.42	3.03	0.0200866	0.1350821	-3.34	FALSE

259094_at	putative cysteine synthase simila	CYSD1	AT3G04940	-1.67	-0.74	-3.03	0.020093	0.1350821	-3.34	FALSE
256756_at	ATPase II, putative similar to GE	---	AT3G25610	2.23	1.16	3.03	0.0201251	0.1352146	-3.34	FALSE
266839_at	unknown protein	ELF3	AT2G25930	-1.36	-0.44	-3.03	0.0201486	0.1352221	-3.34	FALSE
257876_at	hypothetical protein predicted by	---	AT3G17130	1.90	0.93	3.03	0.0201502	0.1352221	-3.34	FALSE
258482_at	putative chaperonin similar to cha	---	AT3G02530	-1.50	-0.58	-3.03	0.0201618	0.1352221	-3.34	FALSE
260929_at	transcription factor TFIID, putativ	TAF13	AT1G02680	-1.66	-0.73	-3.03	0.0201401	0.1352221	-3.34	FALSE
252129_at	putative protein hypothetical pro	AtHB28	AT3G50890	1.46	0.54	3.03	0.0201611	0.1352221	-3.34	FALSE
259173_at	beta-glucosidase identical to beta	BGLU25	AT3G03640	-1.87	-0.90	-3.03	0.0201566	0.1352221	-3.34	FALSE
258823_at	putative RING zinc finger protein	---	AT3G07200	-1.57	-0.65	-3.03	0.0201722	0.1352519	-3.34	FALSE
267393_at	similar to axi 1 protein from Nicot	---	AT2G44500	1.87	0.91	3.03	0.020189	0.135325	-3.34	FALSE
264999_at	hypothetical protein contains sim	---	AT1G67310	-1.37	-0.46	-3.02	0.0202314	0.1354103	-3.34	FALSE
245006_at	PSI P700 apoprotein A2	---	---	-1.29	-0.37	-3.02	0.0202255	0.1354103	-3.34	FALSE
249064_at	putative protein contains similarit	---	AT5G44250	-1.33	-0.41	-3.02	0.0202221	0.1354103	-3.34	FALSE
245188_at	F12A21.19 unknown protein; si	---	AT1G67660	-1.43	-0.52	-3.02	0.020214	0.1354103	-3.34	FALSE
261577_at	ribonucleoprotein, putative simila	---	AT1G01080	-1.64	-0.71	-3.02	0.0202287	0.1354103	-3.34	FALSE
246307_at	putative nuclear DNA-binding pro	ATG2	AT3G51800	-1.69	-0.76	-3.02	0.0202694	0.135625	-3.35	FALSE
254820_s_a	pEARLI 1-like protein Arabidops	---	AT4G12510 //	2.13	1.09	3.02	0.0202834	0.1356785	-3.35	FALSE
259251_at	unknown protein identical to resi	---	AT3G07600	2.81	1.49	3.02	0.0202905	0.1356865	-3.35	FALSE
260359_at	hypothetical protein predicted by	---	AT1G69210	-1.59	-0.67	-3.02	0.0203122	0.1357518	-3.35	FALSE
262668_at	flavin-containing amine oxidase c	LDL1	AT1G62830	-1.42	-0.51	-3.02	0.0203095	0.1357518	-3.35	FALSE
250604_at	putative protein heparanase pre	PIP1B	AT2G45960 //	-1.70	-0.76	-3.02	0.020333	0.1358114	-3.35	FALSE
255138_at	extensin-like protein extensin cla	---	AT4G08380	1.35	0.43	3.02	0.0203281	0.1358114	-3.35	FALSE
257687_at	hypothetical protein predicted by	SDRB	AT3G12800	1.40	0.49	3.02	0.0203668	0.1359633	-3.35	FALSE
259027_at	hypothetical protein predicted by	---	AT3G09280	1.31	0.39	3.02	0.0203677	0.1359633	-3.35	FALSE
262177_at	isochorismate synthase (icsI) ide	EDS16	AT1G74710	2.82	1.50	3.02	0.0203817	0.1360171	-3.35	FALSE
265318_at	putative D-amino acid dehydroge	---	AT2G22650	-1.62	-0.70	-3.02	0.0203925	0.1360493	-3.35	FALSE
253633_at	putative protein tetratricopeptide	---	AT4G30480	-1.49	-0.57	-3.02	0.0204102	0.1361276	-3.35	FALSE
247434_at	Expressed protein ; supported by	---	AT5G62575	-1.35	-0.43	-3.02	0.020426	0.1361933	-3.35	FALSE
260405_at	putative glutathione transferase s	ATGSTU11	AT1G69930	8.65	3.11	3.01	0.0204808	0.1362202	-3.36	TRUE
252990_at	putative protein	---	AT4G38440	-2.01	-1.01	-3.02	0.0204471	0.1362202	-3.35	TRUE
258861_at	putative helicase similar to C-terr	---	AT3G02060	-1.61	-0.69	-3.01	0.020488	0.1362202	-3.36	FALSE
249427_at	40S ribosomal protein S9-like 40	---	AT5G39850	-2.50	-1.32	-3.01	0.0204892	0.1362202	-3.36	FALSE
247053_at	protein kinase ATN1-like protein	---	AT5G66710	1.31	0.39	3.01	0.0204898	0.1362202	-3.36	FALSE
266093_at	unknown protein ;supported by f	---	AT2G37990	-1.67	-0.74	-3.01	0.0204778	0.1362202	-3.36	FALSE
258830_at	unknown protein	---	AT3G07090	2.00	1.00	3.02	0.020465	0.1362202	-3.35	FALSE

249489_at	acyltransferase -like protein ant	---	AT5G39090	1.54	0.62	3.02	0.0204696	0.1362202	-3.36	FALSE
267247_at	hypothetical protein predicted by	---	AT2G30170	-1.49	-0.58	-3.01	0.0204815	0.1362202	-3.36	FALSE
254072_at	putative protein ClpC protease -	---	AT4G25370	-1.45	-0.53	-3.01	0.0204789	0.1362202	-3.36	FALSE
265573_at	putative zinc-finger protein simila	---	AT2G28200	-2.04	-1.03	-3.01	0.0205673	0.1362984	-3.36	TRUE
263411_at	putative C2H2-type zinc finger pr	---	AT2G28710	1.93	0.95	3.01	0.0205173	0.1362984	-3.36	TRUE
258939_at	unknown protein predicted by ge	---	AT3G10020	2.01	1.01	3.01	0.0205491	0.1362984	-3.36	FALSE
252915_at	EF-Hand containing protein -like	---	AT4G38810	1.53	0.61	3.01	0.0205597	0.1362984	-3.36	FALSE
248720_at	protein kinase (EC 2.7.1.37) 5 (p	D6PKL2	AT5G47750	-1.39	-0.47	-3.01	0.0205494	0.1362984	-3.36	FALSE
249790_at	putative protein similar to unknov	---	AT5G24290	4.02	2.01	3.01	0.0205428	0.1362984	-3.36	FALSE
251146_at	neoxanthin cleavage enzyme nc	CCD1	AT3G63520	-1.60	-0.68	-3.01	0.0205525	0.1362984	-3.36	FALSE
254050_s_a	hypothetical protein ; supported	---	AT4G25670 ///	1.40	0.48	3.01	0.0205317	0.1362984	-3.36	FALSE
259770_s_a	phosphoribosylanthranilate isom	PAI3	AT1G07780 ///	-1.72	-0.78	-3.01	0.020544	0.1362984	-3.36	FALSE
254760_at	putative protein hypothetical pro	---	AT4G13200	-1.36	-0.45	-3.01	0.0205608	0.1362984	-3.36	FALSE
257615_at	unknown protein	---	AT3G26510	-1.65	-0.72	-3.01	0.0205635	0.1362984	-3.36	FALSE
255830_at	putative PRP19-like spliceosoma	---	AT2G33340	-1.91	-0.93	-3.01	0.0205797	0.1363414	-3.36	TRUE
253445_at	putative protein pAFD103 mRNA	---	AT4G32605 ///	-1.47	-0.55	-3.01	0.020609	0.1364959	-3.36	FALSE
251353_at	putative protein hypothetical pro	---	AT3G61080	-1.55	-0.63	-3.01	0.0206331	0.1365935	-3.36	FALSE
254463_at	putative protein transcription init	TAF11	AT4G20280	-1.50	-0.58	-3.01	0.0206357	0.1365935	-3.36	FALSE
245986_at	protein kinase-like protein kinas	PBS1	AT5G13160	1.33	0.41	3.01	0.0206623	0.1367148	-3.36	FALSE
259896_at	unknown protein ;supported by fu	---	AT1G71500	-1.45	-0.53	-3.01	0.0206661	0.1367148	-3.36	FALSE
267200_at	hypothetical protein predicted by	---	AT2G31010	1.48	0.57	3.01	0.0206999	0.1368592	-3.37	TRUE
262493_at	auxilin-like protein similar to GB	---	AT1G21660	1.38	0.46	3.01	0.0206944	0.1368592	-3.37	FALSE
263161_at	myrosinase-associated protein,	---	AT1G54020	23.65	4.56	3.01	0.0207084	0.1368757	-3.37	FALSE
257578_x_a	unknown protein similar to hypot	---	AT3G30160	1.34	0.42	3.01	0.0207146	0.1368774	-3.37	FALSE
258203_at	hypothetical protein predicted by	---	AT3G13950	4.94	2.30	3.01	0.0207502	0.1369771	-3.37	TRUE
266728_at	similar to late embryogenesis ab	---	AT2G03140	-1.39	-0.48	-3.00	0.0207597	0.1369771	-3.37	FALSE
251209_at	putative protein several hypothet	---	AT3G62890	-1.52	-0.61	-3.00	0.0207575	0.1369771	-3.37	FALSE
260494_at	putative receptor-like protein kina	---	AT2G41820	-1.52	-0.60	-3.01	0.0207464	0.1369771	-3.37	FALSE
256244_at	sulphate transporter, putative sir	SULTR4;2	AT3G12520	-1.36	-0.45	-3.01	0.0207432	0.1369771	-3.37	FALSE
263000_at	hypothetical protein similar to hyp	---	AT1G54350	-1.46	-0.54	-3.00	0.0208097	0.137267	-3.37	FALSE
252126_at	putative disease resistance prote	---	AT3G50950	1.62	0.70	3.00	0.020816	0.1372688	-3.37	FALSE
256186_at	4-coumarate:CoA ligase 1 identic	4CL1	AT1G51680	2.36	1.24	3.00	0.0208454	0.1374001	-3.37	TRUE
255939_at	hypothetical protein predicted by	---	AT1G12730	-1.64	-0.72	-3.00	0.020848	0.1374001	-3.37	FALSE
267286_at	putative seed maturation protein	---	AT2G23640	1.33	0.41	3.00	0.0208675	0.1374617	-3.37	FALSE
254356_at	hypothetical protein ;supported b	---	AT4G22190	-1.51	-0.60	-3.00	0.0208693	0.1374617	-3.37	FALSE

259862_at	hypothetical protein ;supported b	TRFL6	AT1G72650	-1.51	-0.60	-3.00	0.0208951	0.1375122	-3.38	TRUE
261792_at	cinnamoyl CoA reductase, puta	CCR1	AT1G15950	1.49	0.57	3.00	0.0208925	0.1375122	-3.38	FALSE
264191_at	integral membrane protein, puta	---	AT1G54730	-1.70	-0.77	-3.00	0.0208938	0.1375122	-3.38	FALSE
253401_at	putative protein hypothetical pro	---	AT4G32870	7.55	2.92	3.00	0.0209181	0.1376236	-3.38	FALSE
252924_at	putative zinc finger protein salt-t	---	AT4G39070	-2.40	-1.26	-3.00	0.0209449	0.137721	-3.38	FALSE
247913_at	unknown protein	---	AT5G57510	6.44	2.69	3.00	0.0209406	0.137721	-3.38	FALSE
263419_at	putative protein kinase contains a	---	AT2G17220	1.64	0.72	3.00	0.0209513	0.1377233	-3.38	FALSE
260386_at	putative strictosidine synthase si	---	AT1G74010	3.30	1.72	3.00	0.0210325	0.1377272	-3.38	TRUE
247213_at	unknown protein ; supported by	PROPEP1	AT5G64900	3.17	1.66	3.00	0.020984	0.1377272	-3.38	TRUE
246308_at	chlorophyll synthetase ; support	G4	AT3G51820	-1.53	-0.61	-3.00	0.02096	0.1377272	-3.38	FALSE
256324_at	MATE efflux family protein, puta	---	AT1G66760	4.05	2.02	3.00	0.0210162	0.1377272	-3.38	FALSE
252426_at	putative protein proline transpor	---	AT3G47630	-1.48	-0.57	-3.00	0.021018	0.1377272	-3.38	FALSE
255688_at	putative RNA helicase similar to	---	AT4G00660	-1.39	-0.47	-3.00	0.0209937	0.1377272	-3.38	FALSE
246199_at	putative protein ;supported by ful	---	AT4G36530	-1.67	-0.74	-3.00	0.0209825	0.1377272	-3.38	FALSE
253657_at	cadmium-transporting ATPase-li	HMA2	AT4G30110	-2.41	-1.27	-3.00	0.0210318	0.1377272	-3.38	TRUE
246075_at	monogalactosyldiacylglycerol syr	MGD2	AT5G20410	-2.78	-1.47	-3.00	0.020984	0.1377272	-3.38	FALSE
248786_at	unknown protein	---	AT5G47410	-1.82	-0.86	-3.00	0.0210365	0.1377272	-3.38	FALSE
257463_at	phosphatidylinositol/phosphatidy	---	AT1G14820	-1.53	-0.62	-3.00	0.0210304	0.1377272	-3.38	FALSE
257999_at	hypothetical protein similar to hy	---	AT3G27540	1.90	0.92	3.00	0.0209697	0.1377272	-3.38	FALSE
263644_at	hypothetical protein predicted by	---	AT2G04730	1.41	0.49	3.00	0.021034	0.1377272	-3.38	FALSE
249126_at	Expressed protein ; supported by	TOPP6	AT5G43380	2.12	1.08	3.00	0.0210362	0.1377272	-3.38	FALSE
250244_at	putative protein similar to unknov	ABO1	AT5G13680	-1.77	-0.83	-2.99	0.0210514	0.1377856	-3.38	TRUE
267312_at	unknown protein	---	AT2G34750	-1.57	-0.65	-2.99	0.0210728	0.1378857	-3.38	FALSE
255062_at	hypothetical protein	---	AT4G08940	-1.50	-0.58	-2.99	0.0211048	0.1380558	-3.39	FALSE
257857_s_a	unknown protein contains an RN	RRP45a	AT3G12990 /	-1.68	-0.75	-2.99	0.0211238	0.138101	-3.39	FALSE
250494_at	embryogenic callus protein - like	HAM2	AT5G09740	-1.52	-0.60	-2.99	0.0211217	0.138101	-3.39	FALSE
245015_at	large subunit of riblose-1,5-bisph	---	---	-1.75	-0.81	-2.99	0.0211334	0.1381241	-3.39	FALSE
266758_at	unknown protein	POL	AT2G46920	-1.45	-0.53	-2.99	0.0211407	0.1381287	-3.39	FALSE
248532_at	Expressed protein ; supported by	NFU2	AT5G49940	-1.49	-0.58	-2.99	0.0211462	0.1381287	-3.39	FALSE
257809_at	ribonucleotide reductase small s	TSO2	AT3G27060	-1.64	-0.71	-2.99	0.0211534	0.1381363	-3.39	FALSE
260570_at	stearoyl-ACP desaturase ; supp	SSI2	AT2G43710	-1.66	-0.73	-2.99	0.0211764	0.1382469	-3.39	FALSE
265398_at	unknown protein	ATMAK10	AT2G11000	-1.41	-0.49	-2.99	0.0212064	0.1384029	-3.39	FALSE
267494_at	TCP1-chaperonin cofactor A isol	KIS	AT2G30410	-1.41	-0.50	-2.99	0.0212251	0.1384855	-3.39	FALSE
264831_at	hypothetical protein predicted by	---	AT1G03687	-1.42	-0.50	-2.99	0.0212415	0.1385529	-3.39	FALSE
249628_at	putative protein tropomyosin ger	---	AT5G37590	-1.51	-0.60	-2.99	0.0212545	0.1385976	-3.39	FALSE

249748_at	thaumatin-like protein	---	AT5G24620	1.44	0.52	2.99	0.0212859	0.1387627	-3.40	FALSE
264014_at	putative auxin-regulated protein	---	AT2G21210	-2.98	-1.57	-2.99	0.0212968	0.1387943	-3.40	TRUE
250222_at	putative protein similar to unknov	---	AT5G14050	-1.75	-0.80	-2.99	0.0213097	0.1388388	-3.40	FALSE
259130_at	putative ribosomal protein L39 si	---	AT3G02190	-1.46	-0.55	-2.99	0.0213209	0.1388717	-3.40	FALSE
260969_at	beta-fructosidase identical to bet	ATBETAFR	AT1G12240	2.18	1.12	2.99	0.0213324	0.1389072	-3.40	FALSE
264209_at	RAS-related protein, RAB7 iden	RABG3B	AT1G22740	-1.50	-0.59	-2.98	0.0213487	0.1389343	-3.40	TRUE
263380_at	hypothetical protein	---	AT2G40200	1.38	0.47	2.98	0.0213464	0.1389343	-3.40	FALSE
247464_at	putative protein various predicte	IQD23	AT5G62070	1.78	0.83	2.98	0.0213635	0.1389427	-3.40	FALSE
267515_at	putative PCF2-like DNA binding	---	AT2G45680	1.51	0.59	2.98	0.0213683	0.1389427	-3.40	FALSE
265026_at	putative 3-oxoacyl [acyl-carrier p	---	AT1G24360	-1.65	-0.72	-2.98	0.0213584	0.1389427	-3.40	FALSE
249403_at	putative protein intracellular prot	---	AT5G40270	-1.54	-0.62	-2.98	0.0213962	0.1390847	-3.40	FALSE
251722_at	putative protein neuronal glutam	---	AT3G56200	1.86	0.90	2.98	0.0214217	0.1392065	-3.40	FALSE
267048_at	hypothetical protein predicted by	---	AT2G34200	-1.58	-0.66	-2.98	0.0214272	0.1392065	-3.40	FALSE
267172_at	unknown protein ;supported by f	---	AT2G37660	-1.54	-0.62	-2.98	0.0214978	0.1396254	-3.41	FALSE
245025_at	ATPase I subunit	---	---	-1.28	-0.36	-2.98	0.0215419	0.139872	-3.41	TRUE
264142_at	hypothetical protein predicted by	---	AT1G78930	-1.64	-0.72	-2.98	0.0215491	0.1398791	-3.41	TRUE
256781_at	dirigent protein, putative similar	---	AT3G13650	11.89	3.57	2.98	0.0215618	0.139922	-3.41	FALSE
256725_at	hypothetical protein predicted by	---	AT2G34070	2.09	1.07	2.98	0.0216064	0.1401714	-3.41	TRUE
260768_at	Expressed protein ; supported by	---	AT1G49245	-1.41	-0.49	-2.98	0.0216215	0.1401897	-3.41	FALSE
263736_at	nucleic acid-binding protein, put	---	AT1G60000	-1.62	-0.70	-2.98	0.0216205	0.1401897	-3.41	FALSE
263585_at	60S ribosomal protein L39	---	AT2G25210	-2.09	-1.06	-2.98	0.0216279	0.1401913	-3.41	FALSE
249137_at	putative protein contains similarit	---	AT5G43140	-1.71	-0.78	-2.98	0.0216348	0.140196	-3.41	FALSE
263624_at	putative ferredoxin-thioredoxin re	---	AT2G04700	-1.52	-0.61	-2.97	0.0216601	0.1403198	-3.41	FALSE
257724_at	hypothetical protein predicted by	---	AT3G18510	-1.48	-0.56	-2.97	0.0216695	0.1403413	-3.41	FALSE
256173_at	unknown protein	---	AT1G51730	-1.34	-0.42	-2.97	0.0216987	0.1404626	-3.41	FALSE
252131_at	BCS1 protein-like protein Homo	BCS1	AT3G50930	4.94	2.30	2.97	0.0217006	0.1404626	-3.41	FALSE
266079_at	unknown protein	LCD1	AT2G37860	-1.52	-0.60	-2.97	0.0217072	0.1404655	-3.41	FALSE
257108_x_a	hypothetical protein	---	---	1.33	0.41	2.97	0.0217144	0.1404726	-3.42	FALSE
249434_at	putative protein GTP-binding pro	---	AT5G39960	-1.59	-0.67	-2.97	0.0217247	0.1404739	-3.42	FALSE
250667_at	40S ribosomal protein S4 ;suppo	---	AT5G07090	-2.02	-1.01	-2.97	0.021727	0.1404739	-3.42	FALSE
249103_at	N-carbamyl-L-amino acid amidoh	UAH	AT5G43600	-1.42	-0.51	-2.97	0.021766	0.1406864	-3.42	FALSE
261628_at	hypothetical protein predicted by	---	AT1G50000	-1.34	-0.42	-2.97	0.0217818	0.1407484	-3.42	FALSE
265816_s_a	putative elongation factor beta-1	---	AT1G30230 /	-1.57	-0.65	-2.97	0.0217953	0.1407963	-3.42	FALSE
251800_at	putative protein various predicted	RBL	AT3G55510	-1.98	-0.99	-2.97	0.0218391	0.1410361	-3.42	TRUE
259305_at	unknown protein ;supported by f	---	AT3G05070	-1.40	-0.49	-2.97	0.0218448	0.1410361	-3.42	FALSE

267526_at	photosystem II reaction center 6.	PSBW	AT2G30570	-1.29	-0.37	-2.97	0.0218673	0.1411015	-3.42	FALSE
247174_at	unknown protein ; supported by	---	AT5G65250	-1.36	-0.44	-2.97	0.0218668	0.1411015	-3.42	FALSE
255438_at	putative oxidoreductase	AOP1	AT4G03070	-2.14	-1.10	-2.97	0.0218748	0.1411097	-3.42	FALSE
262914_at	auxin response factor 1 identical	ARF1	AT1G59750	-1.42	-0.51	-2.97	0.0218966	0.1411972	-3.42	FALSE
259627_at	unknown protein ; supported by	---	AT1G42960	-1.45	-0.54	-2.97	0.0219007	0.1411972	-3.42	FALSE
253061_at	putative protein SPOP, Homo sa	BT5	AT4G37610	1.85	0.88	2.97	0.0219243	0.1412314	-3.43	FALSE
250875_at	putative protein fimbriae-associa	---	AT5G04020	2.35	1.23	2.96	0.0219432	0.1412314	-3.43	FALSE
262208_at	hypothetical protein predicted by	---	AT1G74800	-1.48	-0.56	-2.96	0.0219432	0.1412314	-3.43	FALSE
264766_at	receptor kinase, putative similar	---	AT1G61420	2.12	1.08	2.97	0.0219265	0.1412314	-3.43	FALSE
253113_at	putative protein physical impeda	---	AT4G35985	-1.79	-0.84	-2.97	0.0219353	0.1412314	-3.43	FALSE
252187_at	putative protein UV inducible pro	---	AT3G50850	1.47	0.56	2.97	0.0219315	0.1412314	-3.43	FALSE
262803_at	unknown protein Location of ES	---	AT1G21000	-1.75	-0.80	-2.96	0.0219899	0.1414642	-3.43	TRUE
252366_at	Expressed protein ; supported by	---	AT3G48420	-2.19	-1.13	-2.96	0.0219918	0.1414642	-3.43	TRUE
257525_at	hypothetical protein predicted by	---	AT3G04900	1.46	0.55	2.96	0.0219988	0.1414697	-3.43	FALSE
249899_at	putative protein similar to unknov	---	AT5G22620	-1.83	-0.88	-2.96	0.0220293	0.1415205	-3.43	FALSE
245417_at	phosphoribosylglycinamide formy	---	AT4G17360	-1.71	-0.78	-2.96	0.0220377	0.1415205	-3.43	FALSE
248967_at	unknown protein ;supported by fu	---	AT5G45350	1.53	0.61	2.96	0.0220337	0.1415205	-3.43	FALSE
247963_at	beta-1,3-glucanase-like protein	---	AT5G56590	-1.37	-0.45	-2.96	0.0220315	0.1415205	-3.43	FALSE
250040_at	putative protein predicted protei	---	AT5G18390	-1.34	-0.42	-2.96	0.022025	0.1415205	-3.43	FALSE
256041_at	unknown protein	---	AT1G07230	-1.55	-0.63	-2.96	0.0220725	0.1416923	-3.43	FALSE
264855_at	3-hydroxy-3-methylglutaryl-coen	HSK	AT2G17265	-1.35	-0.44	-2.96	0.0220817	0.1416923	-3.43	FALSE
261379_at	unknown protein similar to YGL0	---	AT1G18720	1.34	0.42	2.96	0.0220831	0.1416923	-3.43	FALSE
257024_at	CDPK-related kinase identical to	---	AT3G19100	1.63	0.70	2.96	0.0221163	0.1417855	-3.43	FALSE
248070_at	putative protein similar to unknov	---	AT5G55660	1.37	0.46	2.96	0.0221047	0.1417855	-3.43	FALSE
264662_at	putative sucrose/H+ symporter s	SUT4	AT1G09960	1.61	0.69	2.96	0.0221107	0.1417855	-3.43	FALSE
259776_s_a	eukaryotic translation initiation fa	---	AT1G29550 /.	-1.39	-0.47	-2.96	0.0221311	0.1418406	-3.43	FALSE
264054_at	unknown protein	SVP	AT2G22540	-1.47	-0.55	-2.96	0.0221589	0.1418591	-3.44	FALSE
257816_at	glycosyl transferase, putative co	QUA1	AT3G25140	-1.44	-0.53	-2.96	0.022151	0.1418591	-3.44	FALSE
255982_at	hypothetical protein contains sim	OHP2	AT1G34000	-1.37	-0.45	-2.96	0.0221553	0.1418591	-3.44	FALSE
246326_at	unknown protein ; supported by	REV7	AT1G16590	-1.35	-0.43	-2.96	0.0221524	0.1418591	-3.44	FALSE
255776_at	60S ribosomal protein L6, putati	---	AT1G18540	-2.13	-1.09	-2.96	0.0221666	0.1418689	-3.44	FALSE
263808_at	hypothetical protein predicted by	---	AT2G04340	-1.39	-0.47	-2.96	0.0221752	0.1418841	-3.44	FALSE
249916_at	histone H2B like protein (emb|CA	HTB2	AT5G22880	-1.71	-0.77	-2.96	0.0222159	0.1421043	-3.44	FALSE
248292_at	putative protein similar to unknov	---	AT5G53030	-1.67	-0.74	-2.96	0.0222292	0.1421495	-3.44	FALSE
256432_at	hypothetical protein similar to hy	---	AT3G10990	1.33	0.41	2.95	0.022249	0.1422362	-3.44	FALSE

246266_at	30S ribosomal protein S11, puta	NFD3	AT1G31817	-1.60	-0.67	-2.95	0.0222864	0.1424358	-3.44	FALSE
255988_at	putative protein	---	---	1.38	0.47	2.95	0.0223035	0.1424652	-3.44	FALSE
253854_at	putative protein zinc-finger prote	---	AT4G27900	-2.49	-1.32	-2.95	0.0223004	0.1424652	-3.44	FALSE
261197_at	putative calcium-binding protein	GAPA-2	AT1G12900	-1.45	-0.53	-2.95	0.0223102	0.1424679	-3.44	FALSE
244916_at	hypothetical protein	ORF187	ATMG00880	1.35	0.44	2.95	0.0223385	0.1425687	-3.44	FALSE
266568_at	unknown protein	---	AT2G24070	1.33	0.42	2.95	0.0223367	0.1425687	-3.44	FALSE
245168_at	3-ketoacyl-CoA thiolase ;suppor	PKT3	AT2G33150	1.51	0.59	2.95	0.022351	0.1426088	-3.44	FALSE
265444_s_a	aquaporin (plasma membrane in	RD28	AT2G37170 /	1.97	0.98	2.95	0.0223733	0.1426556	-3.45	TRUE
266329_at	unknown protein ; supported by	CRR3	AT2G01590	-1.97	-0.98	-2.95	0.0223771	0.1426556	-3.45	FALSE
252134_at	putative protein ; supported by c	---	AT3G50910	2.28	1.19	2.95	0.0223665	0.1426556	-3.45	FALSE
245315_at	proteasome chain protein ; suppo	PBD2	AT4G14800	-1.34	-0.42	-2.95	0.0223898	0.1426966	-3.45	FALSE
253312_s_a	putative protein (1,4)-beta-xylan	---	AT4G33850 /	1.38	0.46	2.95	0.0224068	0.142765	-3.45	FALSE
266168_at	putative protease inhibitor ;supp	---	AT2G38870	-2.82	-1.50	-2.95	0.0224209	0.142815	-3.45	TRUE
259733_at	nucellin-like protein similar to nuc	---	AT1G77480	-1.75	-0.81	-2.95	0.0224288	0.1428258	-3.45	FALSE
259919_at	putative exportin, tRNA (nuclear	PSD	AT1G72560	-1.57	-0.66	-2.95	0.0224397	0.1428552	-3.45	FALSE
263773_at	putative xylulose kinase	---	AT2G21370	-1.57	-0.65	-2.95	0.0224471	0.1428622	-3.45	FALSE
264509_at	unknown protein Location of EST	---	AT1G09520	-1.43	-0.51	-2.95	0.0224732	0.1429885	-3.45	FALSE
261579_at	soluble inorganic pyrophosphata	AtPPa1	AT1G01050	-1.32	-0.40	-2.95	0.0225112	0.1431903	-3.45	FALSE
262592_at	unknown protein ESTs gb|H3729	---	AT1G15400	-1.60	-0.68	-2.95	0.0225214	0.1432156	-3.45	TRUE
248307_at	selenium-binding protein-like	---	AT5G52850	-1.46	-0.54	-2.95	0.0225385	0.1432226	-3.45	FALSE
250752_at	cytochrome P450 90A1 (sp|Q425	CPD	AT5G05690	-1.51	-0.59	-2.95	0.0225414	0.1432226	-3.45	FALSE
265162_at	hypothetical protein predicted by	---	AT1G30910	-1.44	-0.53	-2.95	0.0225337	0.1432226	-3.45	FALSE
253923_at	hypothetical protein Arabidopsis	TOR1	AT4G27060	-1.40	-0.49	-2.94	0.0225697	0.1433628	-3.45	FALSE
263599_at	putative histidine kinase ; suppo	WOL	AT2G01830	1.69	0.76	2.94	0.0225821	0.1433818	-3.46	TRUE
251513_at	pirin-like protein pirin - Lycopers	PRN	AT3G59220	3.35	1.74	2.94	0.0225853	0.1433818	-3.46	FALSE
255567_at	hypothetical protein ; supported	---	AT4G01150	-1.40	-0.48	-2.94	0.0226356	0.1436549	-3.46	FALSE
252665_at	valine-rich protein	---	AT3G44140	1.45	0.54	2.94	0.0226413	0.1436549	-3.46	FALSE
255045_at	putative protein hypothetical pro	---	AT4G09690	1.44	0.52	2.94	0.0226598	0.1436549	-3.46	FALSE
250266_at	histone H3 -like protein histone	---	AT5G12910	1.44	0.52	2.94	0.0226575	0.1436549	-3.46	FALSE
249405_at	beta subunit of protein farnesyl tr	ERA1	AT5G40280	-1.36	-0.44	-2.94	0.0226557	0.1436549	-3.46	FALSE
258459_at	hypothetical protein predicted by	---	---	1.41	0.50	2.94	0.0226671	0.1436611	-3.46	FALSE
257211_at	exonuclease, putative contains	---	AT3G15080	-1.56	-0.64	-2.94	0.0227093	0.1437701	-3.46	TRUE
259655_at	unknown protein	---	AT1G55210	2.82	1.50	2.94	0.0227114	0.1437701	-3.46	FALSE
262039_at	adenine phosphoribosyltransfera	APT2	AT1G80050	1.56	0.64	2.94	0.0227116	0.1437701	-3.46	FALSE
261424_at	unknown protein	---	AT1G18700	-1.30	-0.38	-2.94	0.0227158	0.1437701	-3.46	FALSE

250245_at	alpha-N-acetylglucosaminidase	---	AT5G13690	-1.50	-0.59	-2.94	0.022692	0.1437701	-3.46	FALSE
249195_s_a	disease resistance response pro	---	AT5G42500 /	1.66	0.74	2.94	0.0227476	0.1439317	-3.46	FALSE
249197_at	putative protein contains similarit	CML37	AT5G42380	9.55	3.26	2.94	0.0227658	0.1439823	-3.46	FALSE
254419_at	NADH dehydrogenase like prote	NDB3	AT4G21490	1.31	0.39	2.94	0.0227683	0.1439823	-3.46	FALSE
246775_at	putative protein GTP-binding pro	MIRO1	AT5G27540	-1.32	-0.40	-2.94	0.0228039	0.1441678	-3.47	FALSE
256794_at	ribosomal protein L27, putative s	---	AT3G22230	-2.13	-1.09	-2.94	0.0228263	0.1442457	-3.47	FALSE
261454_at	hypothetical protein predicted by	---	AT1G21090	-1.42	-0.51	-2.94	0.0228289	0.1442457	-3.47	FALSE
246820_at	putative protein predicted protei	---	AT5G26910	-1.31	-0.39	-2.94	0.0228671	0.1443325	-3.47	TRUE
255904_at	lemir (miraculin), putative similar	---	AT1G17860	1.54	0.62	2.93	0.0228869	0.1443325	-3.47	TRUE
251233_at	putative protein hypothetical pro	DRB4	AT3G62800	-1.39	-0.48	-2.93	0.0228869	0.1443325	-3.47	FALSE
251627_at	glucan endo-1,3-beta-D-glucosid	BG1	AT3G57270	1.41	0.50	2.93	0.0228735	0.1443325	-3.47	FALSE
250742_at	putative protein similar to unknov	---	AT5G05800	-1.44	-0.52	-2.94	0.0228614	0.1443325	-3.47	FALSE
250114_s_a	AMP-binding protein	AAE5	AT5G16340 /	1.71	0.77	2.93	0.0228801	0.1443325	-3.47	FALSE
266452_at	hypothetical protein predicted by	---	AT2G43320	1.67	0.74	2.94	0.022849	0.1443325	-3.47	FALSE
261911_at	ribosomal protein L7, putative si	---	AT1G80750	-1.92	-0.94	-2.93	0.0229107	0.1444425	-3.47	FALSE
254363_at	pectinesterase like protein pecti	sks4	AT4G22010	1.74	0.80	2.93	0.0229324	0.1444995	-3.47	TRUE
259286_at	hypothetical protein similar to hy	BSMT1	AT3G11480	16.00	4.00	2.93	0.0229277	0.1444995	-3.47	FALSE
261023_at	unknown protein similar to unkno	---	AT1G12200	1.48	0.57	2.93	0.0229406	0.1445112	-3.47	TRUE
247218_at	asparagine synthetase (gb|AAC7	ASN2	AT5G65010	-3.58	-1.84	-2.93	0.0229579	0.1445402	-3.47	FALSE
264941_at	auxin-induced protein, putative s	---	AT1G60680	1.80	0.84	2.93	0.0229557	0.1445402	-3.47	FALSE
249834_at	putative protein contains similarit	FTRA1	AT5G23440	-1.56	-0.64	-2.93	0.0229801	0.1446399	-3.47	FALSE
254469_at	hypothetical protein	---	AT4G20470	1.37	0.45	2.93	0.0229909	0.1446682	-3.47	FALSE
253137_at	protein kinase - like protein prote	---	AT4G35500	1.54	0.62	2.93	0.0230124	0.1446838	-3.47	FALSE
248688_at	indole-3-glycerol phosphate synt	---	AT5G48220	-1.57	-0.65	-2.93	0.0230025	0.1446838	-3.47	FALSE
252858_at	puative protein various predicted	---	AT4G39770	-1.46	-0.54	-2.93	0.0230063	0.1446838	-3.47	FALSE
255310_at	Expressed protein ; supported by	ATALN	AT4G04955	-2.28	-1.19	-2.93	0.0230277	0.1447399	-3.48	FALSE
245415_at	G2484-1 protein	ATG2484-1	AT4G17330	-1.33	-0.41	-2.93	0.02306	0.1449033	-3.48	FALSE
260464_at	disease resistance protein RPM1	LOV1	AT1G10920	1.34	0.42	2.93	0.0230895	0.1450486	-3.48	FALSE
247511_at	Fdr1 Cen - like protein Fdr1, Ory	---	AT5G62040	1.46	0.54	2.93	0.0231023	0.1450889	-3.48	FALSE
263177_at	hypothetical protein predicted by	---	AT1G05540	-1.37	-0.46	-2.93	0.0231137	0.1451206	-3.48	FALSE
246594_at	pyrroline-5-carboxylate reductase	P5CR	AT5G14800	-1.52	-0.60	-2.93	0.0231466	0.1452677	-3.48	FALSE
258396_at	unknown protein similar to unkno	---	AT3G15460	-1.91	-0.93	-2.93	0.0231498	0.1452677	-3.48	FALSE
263228_at	putative reticuline oxidase-like p	---	AT1G30700	1.91	0.94	2.92	0.0232267	0.1453901	-3.48	TRUE
254073_at	splicing factor At-SRp40 contain	RSP35	AT4G25500	-1.42	-0.51	-2.92	0.0232256	0.1453901	-3.48	FALSE
250741_at	putative protein contains similarit	---	AT5G05790	-1.95	-0.97	-2.92	0.0232016	0.1453901	-3.48	FALSE

261846_at	hypothetical protein similar to hyp	---	AT1G11540	1.43	0.52	2.92	0.0232072	0.1453901	-3.48	FALSE
247959_at	unknown protein	---	AT5G57080	-1.59	-0.67	-2.92	0.0231977	0.1453901	-3.48	FALSE
245562_at	OBP33pep like protein contains r	---	AT4G15520	-1.53	-0.61	-2.92	0.0231908	0.1453901	-3.48	FALSE
263413_at	unknown protein ;supported by f	BPC4	AT2G21240	-1.46	-0.54	-2.92	0.0232007	0.1453901	-3.48	FALSE
265259_at	putative WD-40 repeat protein si	---	AT2G20330	-1.42	-0.51	-2.92	0.0232135	0.1453901	-3.48	FALSE
248836_at	NBS/LRR disease resistance pro	---	AT5G47260	1.53	0.61	2.92	0.0232238	0.1453901	-3.48	FALSE
266621_at	unknown protein	---	AT2G35450	-1.71	-0.77	-2.92	0.0232928	0.1457635	-3.49	FALSE
258104_at	hypothetical protein predicted by	---	AT3G23620	-1.72	-0.78	-2.92	0.0233217	0.1459048	-3.49	FALSE
259204_s_a	hypothetical protein predicted by	---	---	1.35	0.44	2.92	0.0233836	0.1462101	-3.49	FALSE
254049_at	putative ribosomal protein S10 4	---	AT4G25740	-1.87	-0.90	-2.92	0.0233898	0.1462101	-3.49	FALSE
264376_at	putative protein phosphatase 2C	---	AT2G25070	-1.58	-0.66	-2.92	0.0233806	0.1462101	-3.49	FALSE
248243_at	unknown protein	CPuORF50	AT5G53588 /	1.31	0.39	2.92	0.0234165	0.1463373	-3.49	FALSE
250862_s_a	40S ribosomal protein S17 -like	---	AT2G04390 /	-1.76	-0.82	-2.92	0.0234388	0.1464362	-3.49	FALSE
253761_at	putative protein thyroid receptor	---	AT4G28820	-1.46	-0.55	-2.92	0.0234913	0.1467239	-3.50	FALSE
265037_at	putative prohibitin 2 B-cell recept	ATPHB2	AT1G03860	-1.47	-0.56	-2.92	0.0234995	0.1467353	-3.50	FALSE
255053_at	putative protein RNA helicase -M	---	AT4G09730	-2.29	-1.19	-2.91	0.0235259	0.1468599	-3.50	FALSE
263979_at	En/Spm-like transposon protein r	PDF1	AT2G42840	1.60	0.68	2.91	0.0235354	0.1468789	-3.50	FALSE
257771_at	SNF1 related protein kinase (ATS	CIPK7	AT3G23000	-2.80	-1.48	-2.91	0.023556	0.1469673	-3.50	TRUE
258456_at	putative protein kinase similar to	WNK2	AT3G22420	-2.45	-1.29	-2.91	0.0236065	0.147242	-3.50	FALSE
259082_at	unknown protein similar to hypot	---	AT3G04820	-1.74	-0.80	-2.91	0.0236951	0.1474758	-3.50	FALSE
246850_at	Lon protease homolog 2 precurs	LON1	AT5G26860	-2.05	-1.04	-2.91	0.0237119	0.1474758	-3.50	FALSE
246614_at	serine/threonine protein kinase S	SOS2	AT5G35410	-1.37	-0.45	-2.91	0.0237078	0.1474758	-3.50	FALSE
249167_at	putative protein similar to unknov	---	AT5G42860	2.30	1.20	2.91	0.0237216	0.1474758	-3.51	TRUE
249164_at	U2 snRNP auxiliary factor, small	U2AF35B	AT5G42820	-1.47	-0.55	-2.91	0.0236771	0.1474758	-3.50	FALSE
250449_at	embryonic abundant protein -like	---	AT5G10830	2.05	1.04	2.91	0.0237172	0.1474758	-3.50	FALSE
247703_at	putative protein predicted protei	SRR1	AT5G59560	-1.44	-0.52	-2.91	0.0237011	0.1474758	-3.50	FALSE
258709_at	putative 60S ribosomal protein L	---	AT3G09500	-1.93	-0.95	-2.91	0.0236907	0.1474758	-3.50	FALSE
258949_at	unknown protein	ATCFM2	AT3G01370	-1.55	-0.63	-2.91	0.0237099	0.1474758	-3.50	FALSE
257969_at	hypothetical protein predicted by	---	AT3G27520	-1.77	-0.82	-2.91	0.0236924	0.1474758	-3.50	FALSE
254937_at	putative aldolase similar to 2,4-d	---	AT4G10750	-1.34	-0.42	-2.91	0.023693	0.1474758	-3.50	FALSE
253465_at	putative protein ATAC98, Arabid	---	AT4G32120	-1.52	-0.61	-2.91	0.0236585	0.1474758	-3.50	FALSE
266210_at	60S ribosomal protein L10A ; su	PGY1	AT2G27530	-1.80	-0.85	-2.91	0.0237546	0.147641	-3.51	FALSE
245605_at	ribonucleoprotein like protein	---	AT4G14300	-1.31	-0.38	-2.91	0.0238022	0.1478565	-3.51	FALSE
266487_at	hypothetical protein predicted by	---	AT2G47660	1.28	0.36	2.91	0.0237984	0.1478565	-3.51	FALSE
267309_at	Expressed protein ; supported by	---	AT2G19385	-1.63	-0.70	-2.91	0.0238113	0.1478723	-3.51	FALSE

254649_at	pherophorin - like protein pherop	---	AT4G18570	-1.44	-0.52	-2.91	0.02384	0.1479734	-3.51	FALSE
266037_at	putative protein kinase contains a	---	AT2G05940	2.77	1.47	2.91	0.0238405	0.1479734	-3.51	FALSE
247821_at	WD-40 repeat protein MSI1 (sp|C	MSI1	AT5G58230	-1.43	-0.52	-2.90	0.0238767	0.1481172	-3.51	FALSE
252953_at	putative phosphatidylinositol syn	PIS2	AT4G38570	-1.38	-0.46	-2.90	0.0238717	0.1481172	-3.51	FALSE
259795_at	hypothetical protein predicted by	---	AT1G64290	1.44	0.52	2.90	0.0238908	0.1481243	-3.51	FALSE
246993_at	Cys2/His2-type zinc finger protei	AZF1	AT5G67450	3.01	1.59	2.90	0.0238887	0.1481243	-3.51	FALSE
251175_at	homocysteine S-methyltransfera	HMT2	AT3G63250	-1.39	-0.47	-2.90	0.0239172	0.1482479	-3.51	FALSE
259550_at	hypothetical protein ;supported b	AGP5	AT1G35230	3.71	1.89	2.90	0.0239603	0.1484742	-3.52	FALSE
259517_at	hypothetical protein ; supported b	CAT1	AT1G20630	1.67	0.74	2.90	0.0239861	0.1485534	-3.52	FALSE
259727_at	ferrodoxin precursor identical to I	FED A	AT1G60950	-1.33	-0.41	-2.90	0.0239796	0.1485534	-3.52	FALSE
251107_at	putative protein several hypothet	---	AT5G01610	1.48	0.57	2.90	0.0239953	0.1485702	-3.52	FALSE
263428_at	ubiquitin-specific protease 4 (UB	ATUBP4	AT2G22310	-1.42	-0.51	-2.90	0.0240034	0.14858	-3.52	FALSE
250825_at	putative protein similar to unknov	---	AT5G05210	-1.37	-0.45	-2.90	0.0240685	0.148648	-3.52	FALSE
262637_at	oxidoreductase, putative contair	---	AT1G06640	4.63	2.21	2.90	0.0241467	0.148648	-3.52	TRUE
248938_at	receptor-like protein kinase	---	AT5G45780	-1.33	-0.42	-2.90	0.0241216	0.148648	-3.52	FALSE
264828_at	hypothetical protein predicted by	ATATG18G	AT1G03380	-1.58	-0.66	-2.90	0.0241458	0.148648	-3.52	FALSE
255087_at	putative protein proteins of this b	---	AT4G09340	-1.33	-0.42	-2.90	0.0240934	0.148648	-3.52	FALSE
260912_at	ATP-dependent Clp protease pro	CLPP5	AT1G02560	-1.35	-0.43	-2.90	0.0240618	0.148648	-3.52	FALSE
264946_at	hypothetical protein predicted by	---	AT1G77010	-1.48	-0.57	-2.90	0.0240939	0.148648	-3.52	FALSE
251007_at	ribosomal protein L35 - like ribos	---	AT5G02610	-1.48	-0.57	-2.90	0.0241418	0.148648	-3.52	FALSE
263143_at	hypothetical protein Contains PF	---	AT1G03100	-1.45	-0.53	-2.90	0.024068	0.148648	-3.52	FALSE
258963_at	putative myotubularin similar to r	---	AT3G10550	1.43	0.52	2.90	0.0240547	0.148648	-3.52	FALSE
251538_at	putative protein PBK1 protein, H	---	AT3G58660	-1.72	-0.78	-2.90	0.0240305	0.148648	-3.52	FALSE
252107_at	sugar transporter-like protein su	TMT3	AT3G51490	1.57	0.65	2.90	0.0240989	0.148648	-3.52	FALSE
260497_at	40S ribosomal protein S2 ;suppo	---	AT2G41840	-2.04	-1.03	-2.90	0.0241512	0.148648	-3.52	FALSE
266604_at	E2, ubiquitin-conjugating enzym	UBC6	AT2G46030	1.85	0.89	2.90	0.0240585	0.148648	-3.52	FALSE
246944_at	ubiquinol--cytochrome-c reducta	---	AT5G25450	1.41	0.50	2.90	0.0241217	0.148648	-3.52	FALSE
255080_at	arabinogalactan-protein homolo	AGP10	AT4G09030	1.78	0.83	2.90	0.0241274	0.148648	-3.52	FALSE
265441_at	unknown protein ;supported by f	---	AT2G20870	1.55	0.63	2.90	0.0241086	0.148648	-3.52	FALSE
255055_at	hypothetical protein	---	AT4G09810	-1.54	-0.62	-2.90	0.0241309	0.148648	-3.52	FALSE
247931_at	putative protein similar to unknov	---	AT5G57040	-1.50	-0.58	-2.90	0.0240675	0.148648	-3.52	FALSE
252364_at	hypothetical protein ;supported b	---	AT3G48450	3.27	1.71	2.90	0.0240715	0.148648	-3.52	FALSE
255025_at	putative host response protein p	MES12	AT4G09900	-1.77	-0.82	-2.90	0.0241127	0.148648	-3.52	FALSE
258647_at	unknown protein ; supported by	---	AT3G07870	-1.42	-0.50	-2.90	0.0241651	0.1486933	-3.52	FALSE
262802_at	putative cell division control prot	CDKB2;2	AT1G20930	1.30	0.38	2.90	0.0241791	0.148739	-3.52	FALSE

248127_at	transport protein particle compon	---	AT5G54750	-1.34	-0.42	-2.89	0.0241886	0.1487577	-3.52	FALSE
259250_at	unknown protein	---	AT3G07580	1.67	0.74	2.89	0.0242134	0.1488697	-3.53	FALSE
266530_at	bHLH transcription factor	AMS	AT2G16910	1.29	0.37	2.89	0.0242205	0.1488736	-3.53	FALSE
266361_at	putative O-GlcNAc transferase	---	AT2G32450	-1.89	-0.92	-2.89	0.0242604	0.1490786	-3.53	FALSE
266181_at	putative glutathione S-transferas	ATGSTZ1	AT2G02390	1.49	0.58	2.89	0.0242686	0.1490887	-3.53	FALSE
250358_at	putative protein gibberellin-respo	AGP15	AT5G11740	1.54	0.62	2.89	0.0242942	0.1492057	-3.53	TRUE
252156_at	BCS1 protein-like protein BCS1	---	AT3G50940	-1.50	-0.59	-2.89	0.0243101	0.1492633	-3.53	FALSE
267534_at	putative CCCH-type zinc finger p	---	AT2G41900	-1.35	-0.44	-2.89	0.0243368	0.1493389	-3.53	TRUE
255089_at	nucleoside-diphosphate kinase ;	NDPK1	AT4G09320	-1.61	-0.69	-2.89	0.024343	0.1493389	-3.53	FALSE
267035_at	putative beta-alanine-pyruvate a	AGT3	AT2G38400	2.68	1.42	2.89	0.0243578	0.1493389	-3.53	FALSE
249966_at	putative protein COLD-INDUCIB	---	AT5G19030	-1.87	-0.90	-2.89	0.0243555	0.1493389	-3.53	FALSE
265237_s_a	hypothetical protein	---	AT2G07706	1.42	0.50	2.89	0.0243617	0.1493389	-3.53	FALSE
255554_at	Expressed protein ; supported by	---	AT4G01897	-1.38	-0.46	-2.89	0.0243598	0.1493389	-3.53	FALSE
252294_at	60S ribosomal protein L13, BBC	ATBBC1	AT3G49010	-2.21	-1.14	-2.89	0.0243762	0.1493876	-3.53	FALSE
262164_at	unknown protein ; supported by c	---	AT1G78070	-1.55	-0.63	-2.89	0.0243931	0.1494512	-3.53	FALSE
249242_at	alcohol dehydrogenase	---	AT5G42250	1.48	0.57	2.89	0.0244085	0.1494655	-3.53	FALSE
247522_at	putative protein ; supported by c	---	AT5G61340	-1.54	-0.62	-2.89	0.0244072	0.1494655	-3.53	FALSE
246543_at	putative protein	---	AT5G15060	1.29	0.37	2.89	0.0244271	0.1494986	-3.53	FALSE
257332_at	hypothetical protein	---	---	1.54	0.63	2.89	0.0244206	0.1494986	-3.53	FALSE
264675_at	putative phosphoribosylglycinam	---	AT1G09830	-1.35	-0.44	-2.89	0.0244439	0.1495617	-3.54	FALSE
263597_at	hypothetical protein predicted by	---	AT2G01870	-2.27	-1.18	-2.89	0.024458	0.1495677	-3.54	FALSE
246329_at	putative protein gamma-tubulin i	---	AT3G43610	-1.44	-0.52	-2.89	0.0244534	0.1495677	-3.54	FALSE
245723_at	hypothetical protein predicted by	---	AT1G73400	-1.52	-0.61	-2.89	0.0244695	0.1495977	-3.54	FALSE
258507_at	neutral invertase, putative simila	---	AT3G06500	2.16	1.11	2.89	0.0244785	0.1496124	-3.54	FALSE
253925_at	putative protein ; supported by cI	SHV3	AT4G26690	1.87	0.90	2.89	0.0244906	0.1496465	-3.54	TRUE
262379_at	hypothetical protein predicted by	---	AT1G73020	1.34	0.42	2.89	0.0244995	0.1496606	-3.54	FALSE
251993_at	peroxiredoxin - like protein perox	---	AT3G52960	-1.47	-0.56	-2.89	0.0245176	0.1496747	-3.54	TRUE
256583_at	hypothetical protein	---	AT3G28850	2.15	1.11	2.88	0.024528	0.1496747	-3.54	TRUE
264920_at	hypothetical protein contains sim	ECHID	AT1G60550	-1.45	-0.54	-2.88	0.0245272	0.1496747	-3.54	FALSE
264722_at	unknown protein location of EST	---	AT1G22970	-1.54	-0.62	-2.89	0.0245137	0.1496747	-3.54	FALSE
248199_at	membrane related protein-like ;s	---	AT5G54170	2.04	1.03	2.88	0.0245356	0.1496759	-3.54	FALSE
258729_at	putative amino acid transporter p	ANT1	AT3G11900	1.33	0.42	2.88	0.0245413	0.1496759	-3.54	FALSE
245276_at	DNA-binding homeotic protein At	ATHB-2	AT4G16780	-1.48	-0.56	-2.88	0.0245686	0.1496819	-3.54	TRUE
251611_at	putative protein several hypothet	---	AT3G57940	-1.58	-0.66	-2.88	0.0245617	0.1496819	-3.54	FALSE
245180_at	putative protein similarity to prote	---	AT5G12410	-1.64	-0.71	-2.88	0.024558	0.1496819	-3.54	TRUE

254562_at	cytochrome P450 cytochrome P	CYP707A1	AT4G19230	2.17	1.12	2.88	0.0245656	0.1496819	-3.54	FALSE
250993_at	putative protein HSPC172, Hom	---	AT5G02280	-1.42	-0.51	-2.88	0.0245844	0.1497385	-3.54	FALSE
253733_at	hypothetical protein	ATMND1	AT4G29170	-1.46	-0.55	-2.88	0.0246064	0.1498321	-3.54	FALSE
247400_at	putative protein ;supported by fu	---	AT5G62840	-1.58	-0.66	-2.88	0.0246164	0.1498532	-3.54	FALSE
262636_at	DEIH-box RNA/DNA helicase ide	NIH	AT1G06670	-1.46	-0.55	-2.88	0.0246361	0.1499329	-3.54	TRUE
249801_at	calcium-dependent protein kinas	CDPK9	AT5G23580	1.39	0.48	2.88	0.0246439	0.1499407	-3.54	FALSE
262496_at	unknown protein ; supported by f	---	AT1G21790	-1.86	-0.89	-2.88	0.0246771	0.1499572	-3.55	TRUE
250769_at	putative protein similar to unknov	---	AT5G05680	-1.80	-0.85	-2.88	0.0246957	0.1499572	-3.55	TRUE
251098_at	light-inducible protein ATLS1	---	AT5G01650	-1.30	-0.38	-2.88	0.0246721	0.1499572	-3.55	FALSE
254640_at	ion transporter - like protein inte	NRAMP5	AT4G18790	1.38	0.46	2.88	0.0246992	0.1499572	-3.55	FALSE
267126_s_a	putative acetone-cyanohydrin lya	ACL	AT2G23590 //	-1.70	-0.76	-2.88	0.0246601	0.1499572	-3.54	FALSE
257270_at	unknown protein ; supported by	---	AT3G28140	-1.31	-0.39	-2.88	0.0246973	0.1499572	-3.55	FALSE
262954_at	rubredoxin, putative similar to ru	---	AT1G54500	-1.51	-0.59	-2.88	0.0246657	0.1499572	-3.54	FALSE
258984_at	putative DnaJ protein Pfam HMM	ATERDJ3A	AT3G08970	1.48	0.56	2.88	0.0246851	0.1499572	-3.55	FALSE
260978_at	17.6 kDa heat shock protein (AA	---	AT1G53540	2.16	1.11	2.88	0.02474	0.150126	-3.55	TRUE
249828_at	succinyl-CoA synthetase, alpha	---	AT5G23250	-1.49	-0.58	-2.88	0.0247402	0.150126	-3.55	FALSE
248759_at	putative protein similar to unknov	---	AT5G47610	-2.13	-1.09	-2.88	0.024781	0.1502537	-3.55	FALSE
253797_at	putative protein 55.11 protein ho	RPN1B	AT4G28470	-1.28	-0.36	-2.88	0.0247687	0.1502537	-3.55	FALSE
245914_at	putative protein outer membrane	OEP80	AT5G19620	-1.42	-0.50	-2.88	0.0247749	0.1502537	-3.55	FALSE
245999_at	putative protein predicted protei	COPT5	AT5G20650	-1.33	-0.41	-2.88	0.0247965	0.1503076	-3.55	FALSE
256220_at	unknown protein	---	AT1G56230	-1.51	-0.59	-2.88	0.0248338	0.1503343	-3.55	FALSE
260689_at	hypothetical protein predicted by	---	AT1G32290	1.50	0.59	2.88	0.0248098	0.1503343	-3.55	FALSE
244933_at	NADH dehydrogenase ND4L	---	---	-1.41	-0.50	-2.88	0.024827	0.1503343	-3.55	FALSE
245613_at	hypothetical protein	---	AT4G14450 //	5.65	2.50	2.88	0.0248338	0.1503343	-3.55	FALSE
262984_at	hypothetical protein predicted by	---	AT1G54460	1.83	0.88	2.88	0.0248248	0.1503343	-3.55	FALSE
247355_at	unknown protein ; supported by	SPT42	AT5G63670	-1.35	-0.43	-2.88	0.0248601	0.1504536	-3.55	FALSE
266370_at	hypothetical protein predicted by	---	AT2G41350	-1.30	-0.38	-2.87	0.0248806	0.150458	-3.55	FALSE
252904_at	putative protein crp1 protein, Ze	EMB2453	AT4G39620	-1.43	-0.52	-2.87	0.0248703	0.150458	-3.55	FALSE
250738_at	anthranilate synthase componen	ASA1	AT5G05730	2.80	1.48	2.87	0.0248758	0.150458	-3.55	FALSE
259429_at	cytochrome P450, putative simil	CYP86A4	AT1G01600	-3.51	-1.81	-2.87	0.0248942	0.1505002	-3.55	FALSE
254759_at	short-chain alcohol dehydrogena	---	AT4G13180	1.65	0.72	2.87	0.0249051	0.1505051	-3.55	TRUE
253368_at	myosin - like protein unconventi	XI-I	AT4G33200	-1.38	-0.46	-2.87	0.0249082	0.1505051	-3.55	FALSE
260316_at	hypothetical protein similar to hy	---	AT1G63810	-1.51	-0.59	-2.87	0.0249264	0.1505751	-3.56	FALSE
257194_at	serine acetyltransferase (Sat-1)	ATSERAT2	AT3G13110	1.41	0.50	2.87	0.0249432	0.150607	-3.56	TRUE
247608_at	replication protein A1 - like prob	---	AT5G60990	-1.49	-0.57	-2.87	0.0249713	0.150607	-3.56	FALSE

248427_at	subtilisin-like serine protease sim	ATSBT1.3	AT5G51750	1.54	0.62	2.87	0.024961	0.150607	-3.56	FALSE
250886_at	putative protein	---	AT5G04440	-1.43	-0.52	-2.87	0.0249674	0.150607	-3.56	FALSE
246268_at	cytochrome P450, putative conta	CYP97A3	AT1G31800	-1.51	-0.60	-2.87	0.024958	0.150607	-3.56	FALSE
261596_at	hypothetical protein predicted by	---	AT1G33080	-1.41	-0.49	-2.87	0.024959	0.150607	-3.56	FALSE
248167_at	putative protein similar to unknov	---	AT5G54530	-1.57	-0.65	-2.87	0.0250046	0.1507344	-3.56	FALSE
245355_at	60S ribosomal protein L15 homo	---	AT4G17390	-2.05	-1.04	-2.87	0.0250056	0.1507344	-3.56	FALSE
261722_at	acyl-(acyl carrier protein) thioest	FATB	AT1G08510	1.32	0.41	2.87	0.0250363	0.1507926	-3.56	TRUE
257456_at	unknown protein predicted by ge	SRS4	AT2G18120	1.40	0.49	2.87	0.0250355	0.1507926	-3.56	FALSE
262631_at	hypothetical protein predicted by	---	AT1G06500	-1.36	-0.44	-2.87	0.0250417	0.1507926	-3.56	FALSE
256494_at	hypothetical protein predicted by	---	AT1G31520	1.34	0.42	2.87	0.0250409	0.1507926	-3.56	FALSE
254213_at	tyrosine transaminase like prote	---	AT4G23590	1.36	0.44	2.87	0.0250567	0.150814	-3.56	FALSE
254505_at	Expressed protein ; supported by	---	AT4G19985	-1.61	-0.68	-2.87	0.0250585	0.150814	-3.56	FALSE
263729_at	hypothetical protein predicted by	---	AT1G60080	-1.29	-0.37	-2.87	0.0250899	0.1509229	-3.56	FALSE
259288_at	putative small nuclear ribonucleo	---	AT3G11500	-1.40	-0.49	-2.87	0.0250848	0.1509229	-3.56	FALSE
266761_at	putative alcohol dehydrogenase	---	AT2G47130	2.21	1.14	2.87	0.0250967	0.1509243	-3.56	FALSE
263035_at	splicing factor, putative similar to	RSZP21	AT1G23860	-1.53	-0.61	-2.87	0.0251433	0.150941	-3.56	FALSE
250688_at	transcription factor-like protein ;s	NF-YA10	AT5G06510	-1.34	-0.42	-2.87	0.0251458	0.150941	-3.56	FALSE
258457_at	Expressed protein ; supported by	IGPD	AT3G22425	-1.53	-0.62	-2.87	0.0251085	0.150941	-3.56	FALSE
252601_s_a	40S ribsomomal protein 40S ribs	---	AT3G45030 ///	-1.84	-0.88	-2.87	0.0251289	0.150941	-3.56	FALSE
254716_at	putative protein LEA protein , Ci	UNE15	AT4G13560	-1.62	-0.69	-2.87	0.0251269	0.150941	-3.56	FALSE
259683_at	unknown protein	---	AT1G63050	-1.69	-0.76	-2.87	0.0251142	0.150941	-3.56	FALSE
253785_s_a	ABC transporter - like protein AB	ATM2	AT4G28620 ///	-1.38	-0.47	-2.87	0.0251439	0.150941	-3.56	FALSE
266005_at	unknown protein	RSZ33	AT2G37340	-1.54	-0.62	-2.87	0.0251792	0.1510968	-3.57	TRUE
257198_at	DNA-binding protein, putative sir	---	AT3G23690	-1.46	-0.55	-2.87	0.025185	0.1510968	-3.57	FALSE
257888_at	seed maturation protein, putative	---	AT3G16990	1.77	0.82	2.87	0.0252014	0.1511158	-3.57	FALSE
245623_s_a	hypothetical protein	---	AT4G14096 ///	-1.35	-0.43	-2.87	0.0251983	0.1511158	-3.57	FALSE
265340_at	putative AAA-type ATPase simila	---	AT2G18330	-1.82	-0.86	-2.86	0.0252258	0.1512221	-3.57	FALSE
254002_at	steroid sulfotransferase - like pro	---	AT4G26280	1.29	0.37	2.86	0.0252412	0.1512746	-3.57	FALSE
263712_at	Expressed protein ; supported by	NFD6	AT2G20585	-1.62	-0.69	-2.86	0.0252947	0.1513912	-3.57	FALSE
265539_at	unknown protein	---	AT2G15830	-2.30	-1.20	-2.86	0.0252907	0.1513912	-3.57	FALSE
245841_s_a	ribosomal protein S2, putative sir	XW6	AT1G58380 ///	-1.69	-0.75	-2.86	0.0252965	0.1513912	-3.57	FALSE
246443_at	hypothetical protein ;supported b	---	AT5G17620	-1.44	-0.52	-2.86	0.0252706	0.1513912	-3.57	FALSE
247812_at	peroxidase ;supported by full-len	---	AT5G58390	2.68	1.42	2.86	0.025298	0.1513912	-3.57	FALSE
262813_at	unknown protein strong similarity	---	AT1G11670	2.58	1.37	2.86	0.0253004	0.1513912	-3.57	FALSE
248402_at	dihydrodipicolinate reductase-like	crr1	AT5G52100	-1.73	-0.79	-2.86	0.0253138	0.1513915	-3.57	TRUE

255426_at	putative protein	---	AT4G03370	1.37	0.45	2.86	0.025309	0.1513915	-3.57	FALSE
261536_at	K Efflux antiporter KEA1 identica	KEA1	AT1G01790	-1.55	-0.63	-2.86	0.0253372	0.151492	-3.57	FALSE
261567_at	Expressed protein ; supported by	---	AT1G33055	-2.47	-1.31	-2.86	0.025346	0.1515045	-3.57	FALSE
266002_at	hypothetical protein predicted by	---	AT2G37310	-1.39	-0.47	-2.86	0.0253533	0.1515084	-3.57	TRUE
250522_at	cleft lip and palate associated tra	---	AT5G08500	-1.35	-0.43	-2.86	0.0253604	0.1515112	-3.57	FALSE
247081_at	AtRAD17 (dbj|BAA90479.1) ; su	ATRAD17	AT5G66130	-1.46	-0.55	-2.86	0.0253761	0.1515654	-3.57	FALSE
252479_at	small zinc finger-like protein TIM9	TIM9	AT3G46560	-1.60	-0.68	-2.86	0.0254022	0.1516352	-3.57	FALSE
265675_at	70kD heat shock protein ;suppor	HSP70T-2	AT2G32120	-1.56	-0.64	-2.86	0.0254033	0.1516352	-3.57	FALSE
250584_at	WD-repeat protein-like	---	AT5G07590	-1.46	-0.54	-2.86	0.0254143	0.1516352	-3.58	FALSE
253048_at	formamidase - like protein forma	---	AT4G37560	-2.42	-1.28	-2.86	0.0254081	0.1516352	-3.57	FALSE
261715_at	hypothetical protein similar to hy	---	AT1G18485	-1.39	-0.47	-2.86	0.0254678	0.1519141	-3.58	FALSE
252310_at	GTPase activating -like protein (	---	AT3G49350	1.88	0.91	2.86	0.0254766	0.1519272	-3.58	FALSE
266283_at	putative proline-rich protein	---	AT2G29210	-1.41	-0.50	-2.86	0.0255126	0.1519827	-3.58	FALSE
259191_at	unknown protein	---	AT3G01720	1.49	0.58	2.86	0.0255112	0.1519827	-3.58	FALSE
266560_at	putative LRR receptor protein kin	---	AT2G23950	-1.48	-0.57	-2.86	0.0255025	0.1519827	-3.58	FALSE
247468_at	ARF1-binding protein ; supporte	ARF2	AT5G62000	-1.41	-0.50	-2.86	0.0255044	0.1519827	-3.58	FALSE
245758_at	unknown protein contains similar	KAN2	AT1G32240	-1.67	-0.74	-2.86	0.0255664	0.1522299	-3.58	FALSE
265854_at	hypothetical protein predicted by	---	AT2G42370	-1.33	-0.41	-2.85	0.0255741	0.1522299	-3.58	FALSE
261429_at	hypothetical protein contains sim	WRKY61	AT1G18860	1.37	0.46	2.86	0.0255676	0.1522299	-3.58	FALSE
255907_at	homeobox protein, putative simi	HDG12	AT1G17920	1.33	0.41	2.85	0.0256363	0.1525607	-3.58	FALSE
250279_at	ABA-responsive protein - like AB	---	AT5G13200	1.70	0.77	2.85	0.0256628	0.1526781	-3.59	FALSE
257060_at	unknown protein	---	AT3G18230	-1.41	-0.49	-2.85	0.0256832	0.1527601	-3.59	FALSE
256914_at	hypothetical protein	---	AT3G23880	-1.68	-0.75	-2.85	0.0257065	0.1528587	-3.59	FALSE
250621_at	membrane protein membrane pr	ATRBL3	AT5G07250	-1.40	-0.49	-2.85	0.0257235	0.1529198	-3.59	FALSE
248282_at	unknown protein ;supported by f	---	AT5G52900	-2.98	-1.58	-2.85	0.0257422	0.1529909	-3.59	FALSE
261303_at	unknown protein contains DNA-b	HON5	AT1G48620	-1.29	-0.37	-2.85	0.0257799	0.1531425	-3.59	FALSE
256013_at	unknown protein	DA1	AT1G19270	1.51	0.59	2.85	0.0257811	0.1531425	-3.59	FALSE
247779_at	putative protein damage-specific	DDB2	AT5G58760	-1.48	-0.56	-2.85	0.0258293	0.1533487	-3.59	FALSE
258899_at	Expressed protein ; supported by	---	AT3G05675	-1.49	-0.57	-2.85	0.0258258	0.1533487	-3.59	FALSE
253776_at	ADP,ATP carrier-like protein AD	AAC3	AT4G28390	-1.66	-0.73	-2.85	0.0258714	0.1534926	-3.59	TRUE
258999_at	putative D-ribulose-5-phosphate	---	AT3G01850	-1.38	-0.46	-2.85	0.0258737	0.1534926	-3.59	FALSE
264018_at	putative triosephosphate isomera	TIM	AT2G21170	-1.37	-0.45	-2.85	0.0258703	0.1534926	-3.59	FALSE
258213_at	hypothetical protein predicted by	---	AT3G17950	-1.64	-0.71	-2.85	0.0258814	0.1534982	-3.59	FALSE
246916_at	disease resistance protein - like	AtRLP52	AT5G25910	1.31	0.38	2.85	0.0259028	0.1535055	-3.59	FALSE
264965_at	hypothetical protein predicted by	---	AT1G60560	-1.49	-0.57	-2.85	0.0259011	0.1535055	-3.59	FALSE

258286_at	kinesin-like protein similar to kine	---	AT3G16060	-1.43	-0.52	-2.85	0.0258934	0.1535055	-3.59	FALSE
252065_at	putative protein ;supported by fu	---	AT3G51610	-1.47	-0.56	-2.85	0.0259134	0.1535287	-3.59	FALSE
267620_at	putative beta-1,3-glucanase	---	AT2G39640	1.34	0.42	2.84	0.025943	0.1536641	-3.60	FALSE
259908_at	RNA polymerase subunit identica	ATRPAC42	AT1G60850	-1.57	-0.65	-2.84	0.0259965	0.1539118	-3.60	FALSE
249898_at	alkaline/neutral invertase ; supp	---	AT5G22510	-1.58	-0.66	-2.84	0.0260041	0.1539118	-3.60	FALSE
248726_at	RAS superfamily GTP-binding pr	ATRABA4C	AT5G47960	4.26	2.09	2.84	0.0260051	0.1539118	-3.60	FALSE
262794_at	unknown protein EST gb|N3787(	emb1745	AT1G13120	-1.39	-0.48	-2.84	0.0260196	0.1539383	-3.60	FALSE
259935_at	putative GDSL-motif lipase/acylh	---	AT1G71250	1.44	0.53	2.84	0.0260231	0.1539383	-3.60	FALSE
256763_at	unknown protein	COBL8	AT3G16860	2.79	1.48	2.84	0.0260356	0.1539724	-3.60	FALSE
261618_at	unknown protein	---	AT1G33110	2.04	1.03	2.84	0.02613	0.1543803	-3.60	TRUE
249204_at	unknown protein ;supported by f	---	AT5G42570	1.36	0.44	2.84	0.0261375	0.1543803	-3.60	FALSE
253276_at	caffeoyl-CoA O-methyltransferas	---	AT4G34050	1.62	0.70	2.84	0.0261131	0.1543803	-3.60	FALSE
266495_at	cycloartenol synthase identical to	CAS1	AT2G07050	-1.43	-0.51	-2.84	0.02613	0.1543803	-3.60	FALSE
250685_at	kinesin heavy chain-like protein	---	AT5G06670	-1.27	-0.35	-2.84	0.0261384	0.1543803	-3.60	FALSE
264677_at	hypothetical protein predicted by	HYL1	AT1G09700	-1.28	-0.36	-2.84	0.0261512	0.1544163	-3.60	FALSE
255535_at	putative RNaseP-associated pro	---	AT4G01790	-1.59	-0.67	-2.84	0.0261675	0.1544722	-3.60	FALSE
267503_at	unknown protein ; supported by	---	AT2G45600	-1.71	-0.77	-2.84	0.0261856	0.1545392	-3.61	TRUE
258569_at	ribosomal protein L17, putative s	emb2171	AT3G04400	-1.60	-0.68	-2.84	0.0261952	0.1545555	-3.61	FALSE
246061_at	RAN GTPase activating protein 2	RANGAP2	AT5G19320	-1.28	-0.35	-2.84	0.0262228	0.1546783	-3.61	FALSE
250464_at	hypothetical protein	---	AT5G10040	1.28	0.35	2.84	0.0262438	0.1547623	-3.61	FALSE
254102_at	acyl carrier - like protein acyl car	ACP4	AT4G25050	-1.46	-0.55	-2.84	0.0262677	0.1548231	-3.61	FALSE
262431_at	trypsin inhibitor 2, putative simila	---	AT1G47540	1.35	0.43	2.84	0.0262622	0.1548231	-3.61	FALSE
256394_at	unknown protein contains non-co	---	AT3G06290	-1.34	-0.43	-2.83	0.0263072	0.1550014	-3.61	FALSE
249020_at	helicase-like protein	CHR4	AT5G44800	-1.44	-0.52	-2.83	0.0263115	0.1550014	-3.61	FALSE
252931_at	putative ubiquitin-dependent pro	---	AT4G38930	1.37	0.46	2.83	0.026324	0.1550349	-3.61	FALSE
259005_at	unknown protein similar to nodul	---	AT3G01930	1.53	0.62	2.83	0.0263341	0.1550546	-3.61	FALSE
260125_at	putative heat shock protein simila	---	AT1G36390	-1.57	-0.65	-2.83	0.0263469	0.1550897	-3.61	FALSE
251259_at	putative protein phosphoprotein	---	AT3G62260	1.69	0.76	2.83	0.026382	0.155096	-3.61	TRUE
253683_at	cytidine deaminase 4 (CDA4)	---	AT4G29650	1.36	0.44	2.83	0.0263767	0.155096	-3.61	FALSE
245289_at	Expressed protein ; supported by	---	AT4G15470	1.29	0.37	2.83	0.0263752	0.155096	-3.61	FALSE
253463_at	Expressed protein ; supported by	---	AT4G32105	1.37	0.45	2.83	0.0263598	0.155096	-3.61	FALSE
257647_at	Expressed protein ; supported by	---	AT3G25805	-1.78	-0.83	-2.83	0.02637	0.155096	-3.61	FALSE
262603_at	hypothetical protein Is a membe	---	AT1G15380	-2.15	-1.10	-2.83	0.0264244	0.1552655	-3.61	TRUE
258947_at	hypothetical protein similar to cal	---	AT3G01830	5.60	2.48	2.83	0.026424	0.1552655	-3.61	FALSE
266962_at	hypothetical protein predicted by	---	AT2G39435 ///	1.38	0.47	2.83	0.0264408	0.1553221	-3.62	TRUE

259242_at	putative actin similar to actin 1 G	ATARP6	AT3G33520	-1.34	-0.42	-2.83	0.0264504	0.1553383	-3.62	FALSE
266272_at	hypothetical protein predicted by	---	AT2G29600	1.39	0.47	2.83	0.0264617	0.1553646	-3.62	FALSE
264882_at	NAM protein, putative similar to	anac025	AT1G61110	1.34	0.42	2.83	0.0264768	0.1553865	-3.62	FALSE
267588_at	unknown protein	---	AT2G42060	1.32	0.40	2.83	0.0264791	0.1553865	-3.62	FALSE
251790_at	elicitor responsive/phloem -like p	---	AT3G55470	1.44	0.53	2.83	0.0265029	0.1554063	-3.62	TRUE
263868_at	hypothetical protein predicted by	---	AT2G36840	-1.42	-0.51	-2.83	0.0265025	0.1554063	-3.62	FALSE
249746_at	NAC2-like protein	TIP	AT5G24590	1.45	0.53	2.83	0.0264899	0.1554063	-3.62	FALSE
263957_at	unknown protein ; supported by	---	AT2G35880	-1.33	-0.41	-2.83	0.0265167	0.1554474	-3.62	TRUE
248098_at	unknown protein ; supported by	---	AT5G55290	-1.37	-0.46	-2.83	0.0265322	0.1554982	-3.62	FALSE
246912_at	putative protein various predicte	---	AT5G25820	2.28	1.19	2.83	0.0265396	0.1555018	-3.62	FALSE
247280_at	phi-1-like protein ;supported by t	EXL2	AT5G64260	1.98	0.99	2.83	0.0265707	0.1555109	-3.62	FALSE
261896_at	mRNA export protein, putative s	---	AT1G80670	-1.47	-0.56	-2.83	0.0265558	0.1555109	-3.62	FALSE
259012_at	hypothetical protein similar to hyp	PUB9	AT3G07360	-1.53	-0.62	-2.83	0.0265484	0.1555109	-3.62	FALSE
260642_at	plastid protein, putative similar to	---	AT1G53260	1.60	0.67	2.83	0.0265752	0.1555109	-3.62	FALSE
254826_at	putative protein predicted protein	---	AT4G12640	-1.47	-0.55	-2.83	0.0265626	0.1555109	-3.62	FALSE
262155_at	glycosyl transferase, putative sim	---	AT1G52420	-1.44	-0.53	-2.83	0.0265896	0.1555552	-3.62	FALSE
252092_at	mucin-like protein hemomucin, D	SSL4	AT3G51420	-1.75	-0.80	-2.83	0.0266113	0.1556417	-3.62	FALSE
252905_at	putative protein predicted protein	---	AT4G39720	1.50	0.58	2.83	0.0266212	0.1556599	-3.62	FALSE
255656_at	putative protein (fragment) DNA	---	AT4G00990	-1.43	-0.52	-2.83	0.0266409	0.1557351	-3.62	FALSE
264364_at	unknown protein Similar to gb|U8	---	AT1G03330	-1.32	-0.40	-2.83	0.0266563	0.1557456	-3.62	FALSE
262892_at	succinic semialdehyde dehydrog	ALDH5F1	AT1G79440	-1.34	-0.42	-2.83	0.0266502	0.1557456	-3.62	FALSE
258067_at	putative mitotic checkpoint prote	---	AT3G25980	1.36	0.44	2.83	0.0266676	0.1557716	-3.62	FALSE
251983_at	putative protein MtN21, Medicag	---	AT3G53210	-1.60	-0.68	-2.82	0.0266887	0.1558152	-3.62	FALSE
255029_x_a	hypothetical protein	---	AT4G09470	1.29	0.36	2.82	0.0266856	0.1558152	-3.62	FALSE
264636_at	hypothetical protein predicted by	---	AT1G65490	2.02	1.01	2.82	0.0267184	0.1559484	-3.63	FALSE
253043_at	putative protein predicted protein	LBD39	AT4G37540	-1.85	-0.89	-2.82	0.0267291	0.1559711	-3.63	FALSE
267635_at	rhodanese-like family protein ;su	---	AT2G42220	-1.73	-0.79	-2.82	0.0267422	0.1560078	-3.63	TRUE
245332_at	isomerase like protein ;supported	---	AT4G15940	1.28	0.35	2.82	0.026753	0.1560306	-3.63	FALSE
251500_at	receptor-like protein kinase rece	---	AT3G59110	-1.35	-0.44	-2.82	0.026764	0.1560546	-3.63	FALSE
252698_at	amine oxidase -like protein amin	---	AT3G43670	-1.47	-0.56	-2.82	0.0267708	0.1560546	-3.63	FALSE
250961_at	putative protein various predicte	---	AT5G02980	1.37	0.46	2.82	0.0267964	0.1561242	-3.63	FALSE
267380_at	putative thromboxane-A synthas	CYP711A1	AT2G26170	2.02	1.01	2.82	0.0267905	0.1561242	-3.63	FALSE
255759_at	hypothetical protein predicted by	---	AT1G16790	-1.39	-0.48	-2.82	0.0268183	0.1562115	-3.63	FALSE
249558_at	hypothetical protein	---	AT5G38310	3.07	1.62	2.82	0.0268458	0.1563323	-3.63	FALSE
264394_at	aminomethyltransferase-like pre	---	AT1G11860	-1.64	-0.71	-2.82	0.02686	0.1563748	-3.63	FALSE

253224_at	invertase - like protein mRNA, L	---	AT4G34860	-1.64	-0.72	-2.82	0.0268697	0.1563915	-3.63	TRUE
245127_at	putative Na+/Ca2+ antiporter ; s	ATMHX	AT2G47600	1.80	0.84	2.82	0.0268836	0.1564101	-3.63	FALSE
267018_at	unknown protein	SVR1	AT2G39140	-1.67	-0.74	-2.82	0.0268866	0.1564101	-3.63	FALSE
248582_at	heat shock protein 70 (gb|AAF27	CPHSC70-1	AT5G49910	1.77	0.82	2.82	0.0269047	0.156475	-3.63	FALSE
245476_at	hypothetical protein	---	AT4G16090	1.39	0.48	2.82	0.0269196	0.1564821	-3.63	FALSE
263366_at	unknown protein	---	AT2G20440	1.41	0.50	2.82	0.0269189	0.1564821	-3.63	FALSE
256199_at	unknown protein	SAB	AT1G58250	-1.51	-0.59	-2.82	0.0269288	0.156496	-3.63	FALSE
247902_at	plasma membrane ATPase 3 (pr	AHA3	AT5G57350	-1.45	-0.54	-2.82	0.0269466	0.1565595	-3.63	FALSE
256293_at	pinhead-like protein similar to pir	AGO7	AT1G69440	-1.62	-0.69	-2.82	0.0269729	0.1566692	-3.64	TRUE
249677_at	DNA helicase-like	---	AT5G35970	-1.78	-0.84	-2.82	0.0270342	0.1566692	-3.64	FALSE
261069_at	small G protein, putative similar	ATRABA2B	AT1G07410	1.30	0.37	2.82	0.0270327	0.1566692	-3.64	FALSE
260664_at	myb-related protein, putative sin	ATRL5	AT1G19510	-1.96	-0.97	-2.82	0.0270134	0.1566692	-3.64	TRUE
251578_at	putative protein contains alterna	---	AT3G58180	-1.35	-0.44	-2.82	0.0269824	0.1566692	-3.64	FALSE
AFFX-r2-At-	/FEATURE=cds-2 /GENE= /LAB	---	---	1.38	0.47	2.82	0.0270142	0.1566692	-3.64	FALSE
246826_at	UTP-glucose glucosyltransferas	UGT72E3	AT5G26310	1.36	0.44	2.82	0.0270205	0.1566692	-3.64	FALSE
254027_at	putative mitochondrial protein H	---	AT4G25835	-1.67	-0.74	-2.82	0.0270165	0.1566692	-3.64	FALSE
246406_at	disease resistance protein RPP1	---	AT1G57650	1.27	0.34	2.82	0.0269905	0.1566692	-3.64	FALSE
259219_at	hypothetical protein predicted by	---	AT3G03560	1.63	0.71	2.82	0.0270219	0.1566692	-3.64	FALSE
253201_at	putative ribosomal protein S16 r	SSR16	AT4G34620	-1.37	-0.45	-2.82	0.0270463	0.1566993	-3.64	FALSE
245122_at	putative dimethyladenosine trans	---	AT2G47420	-1.42	-0.50	-2.81	0.0270703	0.1567865	-3.64	FALSE
266576_at	hypothetical protein predicted by	---	AT2G23940	-1.37	-0.45	-2.81	0.0270751	0.1567865	-3.64	FALSE
259593_at	nuclear transport factor 2, putati	NTF2B	AT1G27970	-1.29	-0.37	-2.81	0.0270847	0.1568026	-3.64	FALSE
254738_at	RNA-binding protein like	AT4G13860	---	1.40	0.48	2.81	0.0271015	0.1568602	-3.64	FALSE
254798_at	oleoyl-[acyl-carrier-protein] hydr	---	AT4G13050	-1.75	-0.80	-2.81	0.0271265	0.1569483	-3.64	FALSE
261003_at	hypothetical protein predicted by	---	AT1G26500	-1.46	-0.55	-2.81	0.0271305	0.1569483	-3.64	FALSE
250428_at	putative protein phosphatase pr	PAS2	AT5G10480	-1.78	-0.83	-2.81	0.0271453	0.1569826	-3.64	FALSE
261626_at	unknown protein ; supported by c	---	AT1G01990	-1.46	-0.55	-2.81	0.0271502	0.1569826	-3.64	FALSE
264094_at	unknown protein ;supported by fu	---	AT1G79200	-1.42	-0.50	-2.81	0.0271697	0.1570557	-3.64	FALSE
265476_at	putative thioredoxin M ; supporte	ATHM3	AT2G15570	-1.31	-0.39	-2.81	0.027178	0.1570634	-3.64	FALSE
264770_at	unknown protein similar to unkno	---	AT1G23030	1.97	0.98	2.81	0.0271854	0.1570637	-3.64	TRUE
263899_at	hypothetical protein predicted by	EMB2219	AT2G21710	-1.48	-0.56	-2.81	0.0271918	0.1570637	-3.64	FALSE
266290_at	putative glutathione S-transferas	ATGSTU1	AT2G29490	5.66	2.50	2.81	0.0272	0.1570712	-3.64	TRUE
257744_at	hypothetical protein contains Pfa	---	AT3G29230	-1.48	-0.57	-2.81	0.027214	0.1571124	-3.64	FALSE
254219_at	putative protein	---	AT4G23760	-1.37	-0.46	-2.81	0.0272217	0.1571172	-3.64	FALSE
251444_at	putative protein ETHIONINE AM	MAP2B	AT3G59990	-1.32	-0.40	-2.81	0.0272426	0.1571581	-3.65	FALSE

266778_at	putative cytochrome P450	CYP707A2	AT2G29090	-1.46	-0.55	-2.81	0.0272425	0.1571581	-3.65	FALSE
252178_at	putative protein various predicted	---	AT3G50750	-2.15	-1.10	-2.81	0.0272498	0.1571601	-3.65	TRUE
248950_at	ATP-dependent Clp protease pro	CLPP4	AT5G45390	-1.44	-0.53	-2.81	0.0272654	0.1572102	-3.65	FALSE
254137_at	hypothetical protein	---	AT4G24930	-1.76	-0.82	-2.81	0.027276	0.1572314	-3.65	TRUE
247176_at	acyl-CoA oxidase (gb|AAC13497	ACX2	AT5G65110	1.65	0.72	2.81	0.0273029	0.15729	-3.65	FALSE
267246_at	putative WRKY-type DNA bindin	WRKY25	AT2G30250	1.84	0.88	2.81	0.0273331	0.15729	-3.65	FALSE
252235_at	60S RIBOSOMAL PROTEIN - li	---	AT3G49910	-1.84	-0.88	-2.81	0.0273343	0.15729	-3.65	FALSE
253943_at	putative protein gene F19K23.1	---	AT4G27030	-2.45	-1.29	-2.81	0.0273013	0.15729	-3.65	FALSE
254008_at	hypothetical protein various pre	---	AT4G26380	1.38	0.46	2.81	0.0273191	0.15729	-3.65	FALSE
245284_at	phytoene dehydrogenase precur	PDS3	AT4G14210	-1.59	-0.67	-2.81	0.0273197	0.15729	-3.65	FALSE
267196_at	FtsH protease (VAR2) identical t	VAR2	AT2G30950	-1.38	-0.46	-2.81	0.0273344	0.15729	-3.65	FALSE
259735_at	Expressed protein ; supported by	---	AT1G64405	-1.72	-0.78	-2.81	0.0273512	0.1573314	-3.65	FALSE
257516_at	unknown protein	ACR4	AT1G69040	-1.66	-0.73	-2.81	0.0273692	0.1573314	-3.65	FALSE
246611_at	putative protein predicted protei	MBD02	AT5G35330	-1.75	-0.81	-2.81	0.0273685	0.1573314	-3.65	FALSE
251870_at	putative protein Various predicte	---	AT3G54510	1.34	0.42	2.81	0.027356	0.1573314	-3.65	FALSE
250808_at	putative protein contains similarit	ATG18E	AT5G05150	1.47	0.55	2.81	0.0273853	0.1573447	-3.65	FALSE
258034_at	hypothetical protein predicted by	---	AT3G21300	-2.15	-1.10	-2.81	0.0273796	0.1573447	-3.65	FALSE
264259_at	hypothetical protein This gene is	---	AT1G09290	-1.63	-0.70	-2.81	0.0274028	0.1574055	-3.65	FALSE
251467_at	putative protein putative proteins	---	AT3G59470	-1.47	-0.56	-2.81	0.0274152	0.1574151	-3.65	FALSE
265673_at	unknown protein ;supported by f	---	AT2G32090	-1.50	-0.58	-2.81	0.0274182	0.1574151	-3.65	FALSE
251743_at	Yippee-like protein Yippee prote	---	AT3G55890	2.02	1.02	2.80	0.0274687	0.1576652	-3.65	TRUE
252223_at	MYB -like protein DNA-binding p	TRB3	AT3G49850	-1.61	-0.68	-2.80	0.0275134	0.1578024	-3.66	FALSE
250531_at	GTP-binding protein LepA homol	---	AT5G08650	-1.62	-0.70	-2.80	0.0275099	0.1578024	-3.66	FALSE
247939_at	putative protein contains similarit	ATLIG4	AT5G57160	-1.36	-0.44	-2.80	0.0275032	0.1578024	-3.66	FALSE
258780_at	putative ubiquitin carboxyl-termir	UBP13	AT3G11910	-1.28	-0.36	-2.80	0.0275407	0.1579192	-3.66	FALSE
248197_at	NADPH:protochlorophyllide oxid	PORA	AT5G54190	1.36	0.45	2.80	0.027555	0.1579614	-3.66	FALSE
259034_at	putative pectinacetylesterase sim	---	AT3G09410	-1.65	-0.72	-2.80	0.0275816	0.1580548	-3.66	TRUE
252496_at	putative protein several hypothet	CRR2	AT3G46790	-1.64	-0.72	-2.80	0.0275861	0.1580548	-3.66	FALSE
266673_at	putative thiamin biosynthesis pro	THIC	AT2G29630	-1.68	-0.75	-2.80	0.027592	0.1580548	-3.66	FALSE
252789_s_a	hypothetical protein ; supported	---	AT1G21930 //	-1.31	-0.39	-2.80	0.0276265	0.1581331	-3.66	FALSE
257698_at	regulatory protein of P-starvation	---	AT3G12730	-1.38	-0.47	-2.80	0.0276228	0.1581331	-3.66	FALSE
259092_at	putative zeta-carotene desaturas	ZDS	AT3G04870	-1.28	-0.36	-2.80	0.0276211	0.1581331	-3.66	FALSE
253319_at	putative protein various predicte	EMB2758	AT4G33990	-1.63	-0.71	-2.80	0.0276499	0.1581981	-3.66	FALSE
258413_at	unknown protein ;supported by f	---	AT3G17300	-1.44	-0.53	-2.80	0.0276517	0.1581981	-3.66	FALSE
267448_at	putative protein phosphatase 2C	---	AT2G33700	1.29	0.37	2.80	0.0276699	0.1582626	-3.66	FALSE

249845_at	putative protein similar to unknov	---	AT5G23610	-1.34	-0.42	-2.80	0.0276963	0.1583736	-3.66	FALSE
258682_at	putative ribosomal-protein S6 ki	S6K2	AT3G08720	2.25	1.17	2.80	0.0277104	0.1584143	-3.66	FALSE
244983_at	ribosomal protein L16	---	---	-1.79	-0.84	-2.80	0.0277398	0.1584238	-3.66	TRUE
246977_at	putative protein CONSTANS-like	COL4	AT5G24930	-1.31	-0.39	-2.80	0.0277234	0.1584238	-3.66	FALSE
246748_at	putative protein predicted protei	---	AT5G27730	-1.38	-0.46	-2.80	0.0277383	0.1584238	-3.66	FALSE
254236_at	putative protein VSG expressior	---	AT4G23840	-1.35	-0.43	-2.80	0.0277315	0.1584238	-3.66	FALSE
251888_at	putative protein GTP-binding reg	---	AT3G54190	-1.31	-0.39	-2.80	0.027758	0.158488	-3.66	FALSE
249901_at	histone deacetylase-like protein	HD2B	AT5G22650	-1.57	-0.65	-2.80	0.0277822	0.1585864	-3.67	FALSE
251593_at	DNA-directed RNA polymerase	NRPA1	AT3G57660	-1.70	-0.77	-2.79	0.0278442	0.1587022	-3.67	TRUE
267205_at	unknown protein	---	AT2G30820	1.40	0.49	2.79	0.0278243	0.1587022	-3.67	FALSE
254890_at	phospholipid hydroperoxide gluta	ATGPX6	AT4G11600	1.38	0.47	2.80	0.0278095	0.1587022	-3.67	FALSE
263322_at	putative ribonuclease E	RNEE/G	AT2G04270	-1.68	-0.75	-2.79	0.0278364	0.1587022	-3.67	FALSE
264572_at	unknown protein ESTs gb|AA04	---	AT1G05320	-1.41	-0.49	-2.79	0.027821	0.1587022	-3.67	FALSE
254255_at	serine/threonine kinase - like pro	---	AT4G23220	2.37	1.25	2.79	0.0278439	0.1587022	-3.67	FALSE
245063_at	Expressed protein ; supported by	---	AT2G39795	-2.11	-1.08	-2.79	0.0278731	0.1587606	-3.67	FALSE
246524_at	Carboxylesterase-like protein ste	ATPCME	AT5G15860	-1.60	-0.67	-2.79	0.027887	0.1587606	-3.67	FALSE
262764_at	putative cytochrome P450 mono	CYP86C3	AT1G13140	1.35	0.43	2.79	0.0278637	0.1587606	-3.67	FALSE
264408_at	hypothetical protein predicted by	FRS11	AT1G10240	-1.35	-0.43	-2.79	0.0278892	0.1587606	-3.67	FALSE
251082_at	chlorophyll a/b-binding protein C	---	AT5G01530	-1.27	-0.34	-2.79	0.0278871	0.1587606	-3.67	FALSE
254079_at	putative protein pmt2 methyltran	---	AT4G25730	-1.82	-0.87	-2.79	0.0279325	0.1588324	-3.67	TRUE
250075_at	putative protein	---	AT5G17670	-1.78	-0.83	-2.79	0.0279367	0.1588324	-3.67	FALSE
250292_at	putative protein predicted protei	JAZ10	AT5G13220	4.23	2.08	2.79	0.0279141	0.1588324	-3.67	FALSE
248155_at	putative protein 3 (2'), 5'-bisphos	AHL	AT5G54390	1.46	0.55	2.79	0.0279354	0.1588324	-3.67	FALSE
247348_at	beta-galactosidase (emb CAB64	BGAL10	AT5G63810	-1.48	-0.57	-2.79	0.0279252	0.1588324	-3.67	FALSE
254758_at	putative protein dimethylaniline r	YUC2	AT4G13260	1.88	0.91	2.79	0.0279482	0.1588582	-3.67	FALSE
261592_at	double-stranded RNA-specific e	---	AT1G01760	1.41	0.49	2.79	0.0279809	0.1590045	-3.67	FALSE
265096_at	unknown protein Location of ES	---	AT1G04030	-1.43	-0.51	-2.79	0.0280161	0.1591651	-3.67	FALSE
250622_at	putative transcription factor AP2	---	AT5G07310	1.32	0.41	2.79	0.0280465	0.1592118	-3.67	FALSE
267031_at	hypothetical protein predicted by	---	AT2G38420	-1.33	-0.42	-2.79	0.0280455	0.1592118	-3.67	FALSE
247378_at	ATP-dependent RNA helicase-lik	---	AT5G63120	1.54	0.62	2.79	0.0280453	0.1592118	-3.67	FALSE
246007_at	Expressed protein ; supported by	FTRA2	AT5G08410	-1.45	-0.54	-2.79	0.0280523	0.1592118	-3.68	FALSE
247584_at	60S ribosomal protein L12 - like	---	AT5G60670	-2.17	-1.12	-2.79	0.0280886	0.1592993	-3.68	FALSE
264967_at	unknown protein ;supported by fu	---	AT1G67250	-1.31	-0.39	-2.79	0.028083	0.1592993	-3.68	FALSE
257879_at	unknown protein	---	AT3G17160	-1.69	-0.76	-2.79	0.0280778	0.1592993	-3.68	FALSE
258701_at	putative RNA helicase similar to	---	AT3G09720	-1.72	-0.78	-2.79	0.028128	0.1594435	-3.68	TRUE

250089_at	homeobox protein	HDG9	AT5G17320	1.45	0.54	2.79	0.0281221	0.1594435	-3.68	FALSE
249187_at	cysteine proteinase RD21A simi	---	AT5G43060	2.16	1.11	2.79	0.0281523	0.1595416	-3.68	FALSE
259000_at	hypothetical protein predicted by	---	AT3G01860	-1.97	-0.98	-2.79	0.0281812	0.1596657	-3.68	FALSE
262953_at	hypothetical protein predicted by	---	AT1G75670	-1.73	-0.79	-2.79	0.0282006	0.1597358	-3.68	FALSE
249269_at	cell cycle control crn (crooked ne	---	AT5G41770	-1.52	-0.60	-2.78	0.0282219	0.1598169	-3.68	FALSE
245246_at	hypothetical protein predicted by	---	AT1G44224	1.32	0.41	2.78	0.0282404	0.1598817	-3.68	FALSE
245383_at	SUPERMAN like protein	---	AT4G17810	-1.78	-0.83	-2.78	0.0282567	0.1599344	-3.68	FALSE
262985_s_a	60s ribosomal protein l27a. simila	RPL27AB	AT1G23290 /	-1.70	-0.77	-2.78	0.0282799	0.1600258	-3.68	FALSE
259754_at	hypothetical protein predicted by	---	AT1G71090	-1.41	-0.49	-2.78	0.0282989	0.1600935	-3.68	FALSE
259001_at	hypothetical protein predicted by	---	AT3G01960	-2.37	-1.24	-2.78	0.0283124	0.1601304	-3.68	FALSE
265492_at	hypothetical protein	AGL95	AT2G15660	1.36	0.44	2.78	0.0283311	0.1601965	-3.69	FALSE
247612_at	ATPase - like protein ATPase, S	---	AT5G60730	-1.40	-0.48	-2.78	0.028431	0.1604827	-3.69	FALSE
258544_at	disease resistance gene (RPM1)	RPM1	AT3G07040	1.76	0.81	2.78	0.0283973	0.1604827	-3.69	FALSE
264101_at	unknown protein similar to putati	HAC1	AT1G79000	-1.45	-0.54	-2.78	0.0284038	0.1604827	-3.69	FALSE
246800_at	glycine hydroxymethyltransferas	SHM2	AT5G26780	-1.48	-0.56	-2.78	0.0284269	0.1604827	-3.69	FALSE
255783_at	hypothetical protein contains Pfa	iqd32	AT1G19870	-1.60	-0.67	-2.78	0.0283985	0.1604827	-3.69	FALSE
253832_at	Expressed protein ; supported by	---	AT4G27654	2.50	1.32	2.78	0.028424	0.1604827	-3.69	FALSE
250458_s_a	ACTIN 2/7 (sp|P53492) ; suppor	ACT7	AT5G09810	-1.28	-0.36	-2.78	0.0284211	0.1604827	-3.69	FALSE
264466_at	Expressed protein ; supported by	---	AT1G10380	-1.95	-0.97	-2.78	0.0284395	0.1604912	-3.69	FALSE
266463_at	hypothetical protein predicted by	---	AT2G47840	-1.42	-0.51	-2.78	0.02845	0.1605106	-3.69	FALSE
258811_at	unknown protein similar to putati	---	AT3G03990	1.64	0.72	2.78	0.0284703	0.1605259	-3.69	TRUE
249365_at	putative protein predicted protei	---	AT5G40600	-1.36	-0.44	-2.78	0.028463	0.1605259	-3.69	FALSE
259922_at	protein phosphatase 2C (AtP2C	HAB1	AT1G72770	1.62	0.70	2.78	0.0284738	0.1605259	-3.69	FALSE
257333_at	cytochrome c oxidase subunit 1	---	---	1.88	0.91	2.78	0.0284941	0.160537	-3.69	TRUE
245597_at	salt-inducible protein homolog	---	AT4G14190	-1.36	-0.44	-2.78	0.028511	0.160537	-3.69	FALSE
265384_at	unknown protein ;supported by f	---	AT2G20760	1.29	0.36	2.78	0.0284863	0.160537	-3.69	FALSE
259349_at	unknown protein ; supported by	ATAPRL5	AT3G03860	-1.32	-0.40	-2.78	0.0285045	0.160537	-3.69	FALSE
249446_at	receptor protein kinase -like prot	---	AT5G39390	1.34	0.42	2.78	0.0285044	0.160537	-3.69	FALSE
256568_at	hypothetical protein ;supported b	---	AT3G19520	-1.34	-0.43	-2.78	0.0285357	0.1606368	-3.69	FALSE
260029_at	endoplasmic reticulum alpha-ma	---	AT1G30000	1.32	0.40	2.78	0.0285734	0.1607299	-3.69	FALSE
263289_at	ubiquitin extension protein (UBQ	---	AT2G36170	-1.79	-0.84	-2.78	0.0285654	0.1607299	-3.69	FALSE
259607_at	P-glycoprotein, putative similar t	PGP13	AT1G27940	-1.28	-0.36	-2.78	0.028572	0.1607299	-3.69	FALSE
260822_at	RNA polymerase, putative simila	---	AT1G06790	-1.35	-0.44	-2.78	0.0285834	0.1607462	-3.69	FALSE
258359_s_a	putative glycolate oxidase similar	---	AT3G14415 /	-1.48	-0.56	-2.78	0.0285929	0.1607602	-3.69	FALSE
251657_at	putative protein MULTICOPY SU	---	AT3G57000	-1.70	-0.76	-2.77	0.0286151	0.1608453	-3.70	FALSE

251478_at	putative protein SF16 protein, pc	IQD13	AT3G59690	1.31	0.39	2.77	0.0286343	0.1608884	-3.70	FALSE
264818_at	hypothetical protein similar to hy	NAF1	AT1G03530	-1.99	-0.99	-2.77	0.0286369	0.1608884	-3.70	FALSE
259775_at	hypothetical protein predicted by	---	AT1G29530	-1.71	-0.78	-2.77	0.0286446	0.1608921	-3.70	FALSE
260575_at	hypothetical protein predicted by	---	AT2G47300	-1.38	-0.47	-2.77	0.0286848	0.1610786	-3.70	FALSE
245635_at	zinc finger protein ID1, putative s	AtIDD16	AT1G25250	1.29	0.37	2.77	0.028723	0.1611741	-3.70	FALSE
257279_at	unknown protein ;supported by f	---	AT3G14430	-1.37	-0.45	-2.77	0.028723	0.1611741	-3.70	FALSE
251204_at	putative protein HMW prekininog	AT3G63095	---	1.39	0.48	2.77	0.0287131	0.1611741	-3.70	FALSE
256017_at	unknown protein ;supported by fu	JAZ1	AT1G19180	2.71	1.44	2.77	0.0287302	0.1611748	-3.70	FALSE
251161_at	putative protein hypothetical pro	---	AT3G63290	-1.40	-0.48	-2.77	0.0287456	0.1612214	-3.70	FALSE
251255_at	putative protein early nodule-spe	---	AT3G62280	1.30	0.38	2.77	0.0287892	0.1613599	-3.70	FALSE
250214_at	endoxyloglucan transferase (dbj	EXGT-A4	AT5G13870	-1.45	-0.54	-2.77	0.0287915	0.1613599	-3.70	FALSE
255364_s_a	putative fibrillin ; supported by fu	---	AT4G04020 /	1.50	0.59	2.77	0.0287856	0.1613599	-3.70	FALSE
258454_at	putative 40S ribosomal protein S	RPS10	AT3G22300	-1.56	-0.64	-2.77	0.0288006	0.1613712	-3.70	FALSE
258041_at	Expressed protein ; supported by	ZML1	AT3G21175	-1.39	-0.47	-2.77	0.0288371	0.1614571	-3.70	FALSE
258981_at	hypothetical protein predicted by	---	AT3G08880	-1.30	-0.38	-2.77	0.028835	0.1614571	-3.70	FALSE
250359_at	putative protein predicted protei	---	AT5G11350	-1.33	-0.41	-2.77	0.0288535	0.1614571	-3.70	FALSE
259792_at	unknown protein ; supported by c	CAD1	AT1G29690	2.47	1.31	2.77	0.0288494	0.1614571	-3.70	FALSE
251315_at	putative protein protein kinase h	---	AT3G61410	1.44	0.52	2.77	0.0288394	0.1614571	-3.70	FALSE
251846_at	histone H2A.F/Z ;supported by f	HTA11	AT3G54560	-2.70	-1.43	-2.77	0.0288584	0.1614571	-3.70	FALSE
264169_at	hypothetical protein predicted by	---	AT1G02020	-1.26	-0.33	-2.77	0.0288941	0.161594	-3.71	FALSE
260979_at	MAP kinase ATMPK9, putative s	ATMPK18	AT1G53510	-1.34	-0.42	-2.77	0.0288971	0.161594	-3.71	FALSE
251174_at	putative protein latex protein alle	PLP9	AT3G63200	1.91	0.93	2.77	0.0289056	0.1616022	-3.71	TRUE
247372_at	unknown protein ;supported by f	---	AT5G63280	-1.62	-0.70	-2.77	0.028961	0.161872	-3.71	FALSE
254852_at	putative disease resistance prot	WRKY19	AT4G12020	1.28	0.36	2.77	0.0289931	0.1620119	-3.71	FALSE
250234_at	transaldolase - like protein trans	---	AT5G13420	1.57	0.65	2.77	0.0290092	0.1620623	-3.71	FALSE
258076_at	50S ribosomal protein L15, chlo	RPL15	AT3G25920	-1.57	-0.65	-2.76	0.029024	0.1620643	-3.71	TRUE
258559_at	putative transcriptional regulator	ATCHR12	AT3G06010	-1.48	-0.56	-2.76	0.0290257	0.1620643	-3.71	TRUE
263914_at	unknown protein	AtGRF3	AT2G36400	-1.76	-0.81	-2.76	0.0290309	0.1620643	-3.71	FALSE
265235_s_a	hypothetical protein	---	AT2G07719	1.41	0.49	2.76	0.029044	0.1620978	-3.71	FALSE
265129_at	putative zinc finger protein simila	SUF4	AT1G30970	1.39	0.47	2.76	0.0290586	0.1621385	-3.71	FALSE
266402_at	hypothetical protein predicted by	---	AT2G38780	-1.66	-0.73	-2.76	0.0290655	0.1621385	-3.71	FALSE
262225_at	pectinesterase, putative similar t	ATPME1	AT1G53840	1.95	0.97	2.76	0.0290838	0.1621522	-3.71	TRUE
266240_at	putative RNA-binding protein ; s	---	AT2G29580	-1.27	-0.35	-2.76	0.0290833	0.1621522	-3.71	FALSE
262640_at	hypothetical protein	---	AT1G62760	11.48	3.52	2.76	0.0290893	0.1621522	-3.71	FALSE
261747_at	unknown protein similar to putati	---	AT1G08350	-1.51	-0.59	-2.76	0.029114	0.1621663	-3.71	FALSE

256435_at	putative leucoanthocyanidin diox	---	AT3G11180	1.38	0.47	2.76	0.0291159	0.1621663	-3.71	FALSE
262820_at	putative obtusifoliol 14-alpha de	CYP51G1	AT1G11680	-1.36	-0.44	-2.76	0.0291129	0.1621663	-3.71	FALSE
264793_at	unknown protein similar to beta-	---	AT1G08660	-1.58	-0.66	-2.76	0.0291203	0.1621663	-3.71	FALSE
254911_at	putative protein ;supported by fu	---	AT4G11100	-1.34	-0.42	-2.76	0.0291542	0.1622271	-3.71	FALSE
262721_at	thioredoxin, putative similar to th	Aty2	AT1G43560	-1.46	-0.54	-2.76	0.0291584	0.1622271	-3.71	FALSE
265863_at	putative membrane protein	VIT1	AT2G01770	1.49	0.58	2.76	0.0291596	0.1622271	-3.71	FALSE
249606_at	putative protein DNA-binding pr	RVE2	AT5G37260	1.38	0.47	2.76	0.0291553	0.1622271	-3.71	FALSE
265036_at	unknown protein Contains simila	PRP39	AT1G04080	-1.32	-0.40	-2.76	0.0291772	0.1622852	-3.71	FALSE
255556_at	putative NifU-like metallocluster	NFU1	AT4G01940	-1.50	-0.58	-2.76	0.0291859	0.1622943	-3.72	FALSE
260380_at	hypothetical protein predicted by	---	AT1G73870	-1.90	-0.92	-2.76	0.0291979	0.1623211	-3.72	FALSE
257828_at	unknown protein	---	AT3G26670	1.75	0.81	2.76	0.0292086	0.162341	-3.72	FALSE
253992_at	putative protein ;supported by fu	---	AT4G26060	1.39	0.48	2.76	0.0292366	0.1623779	-3.72	FALSE
266662_at	hypothetical protein predicted by	---	AT2G25830	-1.51	-0.59	-2.76	0.029225	0.1623779	-3.72	FALSE
252121_at	GDP-D-mannose-4,6-dehydrata	MUR1	AT3G51160	1.86	0.90	2.76	0.0292338	0.1623779	-3.72	FALSE
249757_at	Expressed protein ; supported by	---	AT5G24316	1.42	0.51	2.76	0.0292955	0.1626658	-3.72	FALSE
264838_at	putative AHP2 similar to GB:BAA	AHP5	AT1G03430	-1.27	-0.34	-2.76	0.0293068	0.162689	-3.72	FALSE
257509_at	unknown protein	---	AT1G63190	-1.40	-0.48	-2.76	0.0293374	0.1627961	-3.72	FALSE
246040_at	peptidyl-prolyl cis-trans isomeras	---	AT5G19370	-1.36	-0.44	-2.76	0.0293404	0.1627961	-3.72	FALSE
257659_at	Expressed protein ; supported by	---	AT3G13226	-1.30	-0.38	-2.76	0.029369	0.1629152	-3.72	FALSE
250837_at	8-amino-7-oxononanoate syntha	ATBIOF	AT5G04620	-1.50	-0.58	-2.76	0.0294119	0.1631137	-3.72	FALSE
259734_at	unknown protein similar to GB:A	---	AT1G77500	2.01	1.01	2.76	0.0294273	0.163159	-3.72	FALSE
245882_at	mitochondrial carrier-like protein	DIC3	AT5G09470	1.43	0.51	2.75	0.0294348	0.1631613	-3.72	FALSE
252459_s_a	1-phosphatidylinositol-4,5-bisph	PLC9	AT3G47220 /	1.31	0.39	2.75	0.0294819	0.1633031	-3.73	FALSE
256503_at	myb-related protein similar to GI:	ATRL6	AT1G75250	-3.17	-1.66	-2.75	0.0294713	0.1633031	-3.73	FALSE
259258_at	putative ribulose-1,5-bisphospha	---	AT3G07670	-1.72	-0.78	-2.75	0.02948	0.1633031	-3.73	FALSE
244901_at	hypothetical protein	---	ATMG00640	1.42	0.50	2.75	0.0295314	0.1634105	-3.73	TRUE
264476_at	hypothetical protein contains sim	PGSIP2	AT1G77130	-1.43	-0.52	-2.75	0.0295307	0.1634105	-3.73	FALSE
257395_at	putative salt-inducible protein	---	AT2G15630	-1.52	-0.60	-2.75	0.0295185	0.1634105	-3.73	FALSE
261036_at	developmentally regulated GTP-	ATDRG1	AT1G17470	-1.31	-0.39	-2.75	0.0295635	0.1634105	-3.73	FALSE
253695_at	arginine methyltransferase (pam	PRMT11	AT4G29510	-1.57	-0.65	-2.75	0.0295658	0.1634105	-3.73	FALSE
262046_at	hypothetical protein predicted by	OFP14	AT1G79960	1.48	0.57	2.75	0.0295524	0.1634105	-3.73	FALSE
264421_at	ribosomal protein identical to ribo	ARP1	AT1G43170	-1.57	-0.65	-2.75	0.0295514	0.1634105	-3.73	FALSE
266252_at	hypothetical protein predicted by	---	AT2G27520	1.37	0.46	2.75	0.0295615	0.1634105	-3.73	FALSE
256576_at	zinc finger protein (PMZ), putativ	PMZ	AT3G28210	2.80	1.48	2.75	0.029516	0.1634105	-3.73	FALSE
248795_at	Myb-related transcription activato	---	AT5G47390	-1.30	-0.38	-2.75	0.0296032	0.1634193	-3.73	FALSE

251854_at	putative protein various predicte	---	AT3G54800	1.33	0.42	2.75	0.0295801	0.1634193	-3.73	FALSE
249396_at	DegP protease contains similarity	DegP9	AT5G40200	-1.31	-0.39	-2.75	0.0295964	0.1634193	-3.73	FALSE
245456_at	disease resistance RPP5 like pro	RPP5	AT4G16950	1.46	0.54	2.75	0.0295874	0.1634193	-3.73	FALSE
246439_at	RING-H2 zinc finger protein-like	---	AT5G17600	-2.38	-1.25	-2.75	0.0296013	0.1634193	-3.73	FALSE
252430_at	CHLOROPHYLL A-B BINDING	LHCA4	AT3G47470	-1.46	-0.55	-2.75	0.029639	0.1635774	-3.73	FALSE
252996_s_a	geranylgeranyl pyrophosphate sy	GGR	AT4G38460	1.42	0.51	2.75	0.0297026	0.1638887	-3.73	FALSE
246555_at	putative protein 68 kDa protein -	GAUT14	AT5G15470	1.61	0.69	2.75	0.0297187	0.1639145	-3.73	FALSE
255540_at	putative SecA-type chloroplast pr	---	AT4G01800	-1.58	-0.66	-2.75	0.0297216	0.1639145	-3.73	FALSE
250665_at	unknown protein ;supported by f	---	AT5G06980	-1.49	-0.57	-2.75	0.0298105	0.1642457	-3.74	TRUE
257074_at	unknown protein	---	AT3G19660	1.89	0.92	2.75	0.0298069	0.1642457	-3.74	TRUE
265814_at	hypothetical protein similar to hy	---	AT2G17930	-1.37	-0.45	-2.75	0.0298018	0.1642457	-3.74	FALSE
245047_at	PSII 32 KDa protein	---	---	-1.34	-0.42	-2.75	0.0297926	0.1642457	-3.74	FALSE
255495_at	predicted protein of unknown fur	---	AT4G02720	-1.36	-0.45	-2.75	0.0298381	0.1643584	-3.74	FALSE
260442_at	unknown protein ; supported by	---	AT1G68220	-1.49	-0.58	-2.74	0.029861	0.1644448	-3.74	FALSE
253572_at	hypothetical protein	---	AT4G31010	-1.39	-0.48	-2.74	0.029888	0.1645535	-3.74	FALSE
251616_at	putative protein	---	AT3G57990	-1.30	-0.38	-2.74	0.0299244	0.164714	-3.74	FALSE
247607_at	putative protein various predicte	---	AT5G60960	-1.79	-0.84	-2.74	0.0299597	0.1648289	-3.74	FALSE
245227_s_a	gunknown protein contains non-c	---	AT1G08410	-1.61	-0.69	-2.74	0.0299531	0.1648289	-3.74	FALSE
258447_at	hypothetical protein predicted by	---	AT3G22450	-1.31	-0.39	-2.74	0.0299907	0.1649598	-3.74	FALSE
253951_at	putative Proline synthetase assc	---	AT4G26860	-1.62	-0.70	-2.74	0.0300024	0.1649842	-3.74	FALSE
247465_at	RNA helicase ; supported by cDN	PRH75	AT5G62190	-1.69	-0.76	-2.74	0.0300157	0.1650174	-3.74	FALSE
261604_at	unknown protein contains similar	---	AT1G49590	-1.42	-0.51	-2.74	0.0300237	0.1650217	-3.74	FALSE
252464_at	RNA-binding protein-like protein	---	AT3G47160	-1.51	-0.59	-2.74	0.0300751	0.1651204	-3.75	FALSE
246818_at	putative protein crp1, Zea mays,	EMB976	AT5G27270	-1.90	-0.92	-2.74	0.0300778	0.1651204	-3.75	FALSE
253317_at	putative protein	---	AT4G33960	-2.05	-1.04	-2.74	0.0300503	0.1651204	-3.74	FALSE
259612_at	60S ribosomal protein L37, puta	---	AT1G52300	-1.90	-0.92	-2.74	0.0300752	0.1651204	-3.75	FALSE
247901_at	ubiquinone/menaquinone biosyn	---	AT5G57300	-1.34	-0.42	-2.74	0.0300609	0.1651204	-3.75	FALSE
261277_at	hypothetical protein predicted by	---	AT1G20230	-1.44	-0.53	-2.74	0.0301039	0.1651955	-3.75	FALSE
260874_at	hypothetical protein predicted by	emb2170	AT1G21390	1.44	0.53	2.74	0.030106	0.1651955	-3.75	FALSE
258953_at	hypothetical protein predicted by	---	AT3G01430	1.44	0.53	2.74	0.0301219	0.1652032	-3.75	TRUE
261928_at	uclacyanin II, putative similar to	---	AT1G22480	1.58	0.66	2.74	0.0301178	0.1652032	-3.75	FALSE
263722_at	putative vanadate resistance pro	GONST1	AT2G13650	1.38	0.46	2.74	0.0301729	0.1654434	-3.75	FALSE
245076_at	unknown protein	GH3.3	AT2G23170	6.40	2.68	2.74	0.0301826	0.1654568	-3.75	FALSE
251228_at	beta-D-glucan exohydrolase-like	---	AT3G62710	1.34	0.42	2.74	0.0301926	0.1654715	-3.75	FALSE
259411_at	hypothetical protein contains Pfa	---	AT1G13410	-1.36	-0.44	-2.74	0.0302077	0.165475	-3.75	FALSE

251187_at	putative protein putative proteins	AtATG18a	AT3G62770	1.28	0.36	2.74	0.0302067	0.165475	-3.75	FALSE
251531_at	putative protein hypothetical pro	---	AT3G58550	1.41	0.49	2.74	0.0302173	0.165488	-3.75	FALSE
264048_at	unknown protein	---	AT2G22400	-1.57	-0.65	-2.74	0.0302347	0.1655034	-3.75	FALSE
266131_at	putative SCARECROW gene reg	---	AT2G45160	-1.60	-0.68	-2.74	0.0302311	0.1655034	-3.75	FALSE
252163_at	hypothetical protein	---	AT3G50610	1.37	0.46	2.74	0.0302598	0.1656011	-3.75	FALSE
251195_at	glutaredoxin -like protein glutare	---	AT3G62930	-1.70	-0.77	-2.74	0.030268	0.1656065	-3.75	FALSE
261607_at	unknown protein similar to putati	AtCXE5	AT1G49660	-2.24	-1.16	-2.73	0.0302766	0.1656135	-3.75	FALSE
245946_at	putative protein glyoxal oxidase	---	AT5G19580	1.48	0.57	2.73	0.0303189	0.1657657	-3.75	FALSE
254643_at	putative protein DNA polymeras	---	AT4G18820	-1.38	-0.47	-2.73	0.0303183	0.1657657	-3.75	FALSE
266254_at	putative membrane transporter	NAT12	AT2G27810	-1.50	-0.58	-2.73	0.0303598	0.1659497	-3.76	TRUE
254996_at	putative protein kinase CLV1 rec	---	AT4G10390	1.49	0.57	2.73	0.0303703	0.165967	-3.76	FALSE
247249_at	putative protein similar to unknov	---	AT5G64670	-1.55	-0.63	-2.73	0.0304109	0.1661493	-3.76	FALSE
246868_at	protein phosphatase - like protei	---	AT5G26010	1.34	0.42	2.73	0.0304226	0.1661622	-3.76	FALSE
256823_at	hypothetical protein predicted by	---	AT3G22220	-1.42	-0.50	-2.73	0.0304279	0.1661622	-3.76	FALSE
255305_at	putative ABC transporter similar	ATABC1	AT4G04770	-1.50	-0.59	-2.73	0.0304572	0.1662824	-3.76	TRUE
247492_at	putative protein AP2 domain cor	---	AT5G61890	2.36	1.24	2.73	0.0304891	0.1664169	-3.76	FALSE
247698_at	putative protein predicted protei	---	AT5G59830	-1.41	-0.49	-2.73	0.0305218	0.1664758	-3.76	FALSE
256246_at	betaine aldehyde dehydrogenas	ALDH22a1	AT3G66658	-1.49	-0.58	-2.73	0.0305205	0.1664758	-3.76	FALSE
249395_at	putative protein	---	AT5G40190	-1.30	-0.37	-2.73	0.0305108	0.1664758	-3.76	FALSE
266084_at	hypothetical protein predicted by	---	AT2G37810	1.49	0.57	2.73	0.0305442	0.1665584	-3.76	FALSE
262941_at	hypothetical protein predicted by	EMB2217	AT1G79490	-1.58	-0.66	-2.73	0.0305609	0.1666095	-3.76	FALSE
265896_at	unknown protein	emb2410	AT2G25660	-1.37	-0.46	-2.73	0.0305826	0.1666878	-3.76	FALSE
266801_at	putative nucleotide-binding prote	EMB2001	AT2G22870	-1.87	-0.90	-2.73	0.0306047	0.166692	-3.76	FALSE
245341_at	Expressed protein ; supported by	---	AT4G16447	-2.31	-1.21	-2.73	0.0306053	0.166692	-3.76	FALSE
246247_at	putative protein	---	AT4G36640	2.61	1.38	2.73	0.0305983	0.166692	-3.76	FALSE
258775_at	hydroxyacylglutathione hydrolas	GLY2	AT3G10850	-1.36	-0.44	-2.73	0.0306149	0.1667047	-3.76	FALSE
256644_at	unknown protein similar to hypot	---	---	1.33	0.41	2.73	0.0306247	0.1667184	-3.76	FALSE
265188_at	putative aldehyde dehydrogenas	ALDH2B7	AT1G23800	1.51	0.59	2.73	0.0306555	0.1668116	-3.76	FALSE
247598_at	UVB-resistance protein UVR8 -	---	AT5G60870	-1.37	-0.45	-2.73	0.0306565	0.1668116	-3.76	FALSE
253479_at	ferredoxin-NADP+ reductase - li	---	AT4G32360	-1.31	-0.39	-2.73	0.03069	0.1668749	-3.77	FALSE
256587_at	histone-H4-like protein similar to	---	AT3G28780	1.39	0.47	2.73	0.0306878	0.1668749	-3.77	FALSE
246498_at	stearoyl-acyl carrier protein desa	---	AT5G16230	2.14	1.10	2.73	0.0306844	0.1668749	-3.77	FALSE
264122_at	GTP-binding protein, ara-5 ras h	ARA-5	AT1G02130	-1.26	-0.33	-2.72	0.0307369	0.1670524	-3.77	FALSE
265798_at	unknown protein ; supported by c	---	AT2G35790	-1.60	-0.68	-2.72	0.0307501	0.1670524	-3.77	FALSE
267206_at	putative dioxygenase	---	AT2G30830	1.35	0.43	2.72	0.0307398	0.1670524	-3.77	FALSE

248253_at	putative protein contains similarit	CRF3	AT5G53290	1.33	0.41	2.72	0.030752	0.1670524	-3.77	FALSE
265025_at	Expressed protein ; supported by	---	AT1G24575	-1.40	-0.49	-2.72	0.0307704	0.1670955	-3.77	TRUE
266371_at	calmodulin-like protein identical t	---	AT2G41410	-1.89	-0.92	-2.72	0.0307904	0.1670955	-3.77	FALSE
249295_at	putative protein contains similarit	---	AT5G41280	1.29	0.37	2.72	0.0307963	0.1670955	-3.77	FALSE
267504_at	unknown protein ;supported by f	---	AT2G45530	-1.46	-0.55	-2.72	0.0307966	0.1670955	-3.77	FALSE
261617_s_a	hypothetical protein predicted by	---	AT1G33090 /.	1.30	0.38	2.72	0.0307952	0.1670955	-3.77	FALSE
257220_at	MYB family transcription factor (	ATMYB21	AT3G27810	1.44	0.53	2.72	0.0308192	0.1671785	-3.77	FALSE
262397_at	hypothetical protein predicted by	---	AT1G49380	-1.70	-0.76	-2.72	0.0308453	0.1672805	-3.77	FALSE
258269_at	putative acetyl-CoA carboxylase	---	AT3G15690	-1.34	-0.42	-2.72	0.0308586	0.1673126	-3.77	FALSE
250465_at	putative protein various predicted	---	AT5G10070	-1.28	-0.36	-2.72	0.0308684	0.167326	-3.77	FALSE
259910_at	putative P-type transporting ATP	---	AT1G72700	1.83	0.87	2.72	0.0308769	0.1673326	-3.77	FALSE
255411_at	putative ribonucleoprotein simila	---	AT4G03110	1.43	0.52	2.72	0.0309433	0.1673471	-3.77	TRUE
264615_at	unknown protein ; supported by	---	AT1G04590	-1.64	-0.71	-2.72	0.0308951	0.1673471	-3.77	FALSE
254483_at	putative protein CRP1, Zea may	---	AT4G20740	-1.53	-0.61	-2.72	0.0309334	0.1673471	-3.77	FALSE
247989_at	pyruvate kinase ;supported by fu	---	AT5G56350	1.55	0.63	2.72	0.03094	0.1673471	-3.77	FALSE
264365_s_a	unknown protein Strong similarit	---	AT1G03220 /.	2.19	1.13	2.72	0.0309258	0.1673471	-3.77	FALSE
267262_at	putative serine carboxypeptidase	SNG1	AT2G22990	-1.56	-0.65	-2.72	0.0308911	0.1673471	-3.77	FALSE
253504_at	hypothetical protein	---	AT4G31960	1.25	0.32	2.72	0.0309113	0.1673471	-3.77	FALSE
266719_at	MYB-related transcription factor (	CCA1	AT2G46830	-1.48	-0.56	-2.72	0.0309387	0.1673471	-3.77	FALSE
245287_at	imidazoleglycerol-phosphate deh	---	AT4G14910	-1.55	-0.63	-2.72	0.0309456	0.1673471	-3.77	FALSE
245121_at	60S ribosomal protein L7A ;supp	---	AT2G47610	-1.82	-0.86	-2.72	0.0309962	0.1675412	-3.78	FALSE
251396_at	transketolase - like protein trans	---	AT3G60750	-1.33	-0.41	-2.72	0.0309936	0.1675412	-3.78	FALSE
266185_at	unknown protein	---	AT2G38950	-1.32	-0.40	-2.72	0.0310289	0.1676781	-3.78	FALSE
253796_at	hypothetical protein	---	AT4G28460	5.02	2.33	2.72	0.0310453	0.167727	-3.78	FALSE
256889_at	PHD-finger protein, putative con	ING1	AT3G24010	-1.29	-0.37	-2.72	0.0310664	0.1677386	-3.78	FALSE
265394_at	predicted protein ; supported by	---	AT2G20725	-1.43	-0.52	-2.72	0.0310603	0.1677386	-3.78	FALSE
245494_at	salt-inducible protein homolog	---	AT4G16390	-1.40	-0.49	-2.72	0.031074	0.1677386	-3.78	FALSE
265658_at	putative aspartate aminotransfer	ALD1	AT2G13810	3.48	1.80	2.72	0.0310769	0.1677386	-3.78	FALSE
265008_at	Mlo protein, putative similar to M	MLO6	AT1G61560	3.11	1.64	2.72	0.0310951	0.1677578	-3.78	FALSE
250128_at	zinc finger protein 3 (gb|AAD278	ZFN3	AT5G16540	-1.61	-0.69	-2.72	0.0310938	0.1677578	-3.78	FALSE
266471_at	putative GTP-binding protein	---	AT2G31060	-1.66	-0.73	-2.72	0.0311312	0.167873	-3.78	TRUE
247398_at	putative protein predicted protei	---	AT5G62950	-1.43	-0.52	-2.72	0.0311312	0.167873	-3.78	FALSE
250249_at	putative protein similar to unknov	---	AT5G13760	1.42	0.51	2.71	0.0311841	0.1681185	-3.78	FALSE
266225_at	putative membrane channel prot	ATOEP16-1	AT2G28900	-2.13	-1.09	-2.71	0.0312295	0.1682839	-3.78	FALSE
250433_at	histone H3 - like protein histone	---	AT5G10400	-1.42	-0.51	-2.71	0.0312251	0.1682839	-3.78	FALSE

260480_at	Ser/Thr kinase ;supported by ful	SNRK2.4	AT1G10940	-1.27	-0.35	-2.71	0.0312437	0.1683207	-3.78	FALSE
267300_at	putative glucosyltransferase	---	AT2G30140	1.32	0.40	2.71	0.0312593	0.1683251	-3.78	FALSE
260190_at	putative lipoxygenase similar to 1	---	AT1G67560	1.69	0.76	2.71	0.0312572	0.1683251	-3.78	FALSE
246344_at	putative protein predicted protein	---	AT3G56730	-1.79	-0.84	-2.71	0.0312753	0.1683712	-3.79	FALSE
260365_at	hypothetical protein predicted by	---	AT1G70630	1.37	0.45	2.71	0.0313017	0.1684738	-3.79	FALSE
248975_at	unknown protein ; supported by	---	AT5G45040	-1.37	-0.45	-2.71	0.0313313	0.1685534	-3.79	FALSE
263352_at	En/Spm-like transposon protein r	---	AT2G22080	-1.59	-0.67	-2.71	0.0313276	0.1685534	-3.79	FALSE
265647_at	hypothetical protein predicted by	---	AT2G27410	1.35	0.43	2.71	0.0313428	0.1685678	-3.79	FALSE
248249_at	protein phosphatase 2C-like ; su	---	AT5G53140	-1.34	-0.43	-2.71	0.0313487	0.1685678	-3.79	FALSE
251541_at	citrate synthase -like protein citr	CSY2	AT3G58750	1.53	0.61	2.71	0.0313741	0.1686643	-3.79	FALSE
247554_at	putative protein leucine zipper-c	ATEXO70E	AT5G61010	2.26	1.18	2.71	0.0313861	0.1686892	-3.79	FALSE
251868_at	RNA polymerase 24kDa subunit	RPB5E	AT3G54490	1.38	0.47	2.71	0.0314066	0.1687597	-3.79	FALSE
248581_at	putative protein strong similarity t	---	AT5G49900	1.56	0.64	2.71	0.0314227	0.1688061	-3.79	FALSE
260128_at	hypothetical protein similar to Ym	---	AT1G36310	-1.39	-0.47	-2.71	0.0314336	0.1688252	-3.79	FALSE
260892_at	cysteine proteinase contains sim	---	AT1G29110	1.40	0.49	2.71	0.0314655	0.1688772	-3.79	FALSE
258521_at	ribosomal protein L29, putative s	---	AT3G06680	-2.14	-1.10	-2.71	0.0314559	0.1688772	-3.79	FALSE
261448_at	tonoplast intrinsic protein, alpha	---	AT1G21140	1.64	0.71	2.71	0.0314608	0.1688772	-3.79	FALSE
266091_at	hypothetical protein predicted by	emb1513	AT2G37920	-1.45	-0.54	-2.71	0.0314765	0.1688965	-3.79	FALSE
246829_at	putative protein pyruvate water d	ATGWD3	AT5G26570	-1.32	-0.40	-2.71	0.0314849	0.1689017	-3.79	FALSE
250423_s_a	cytochrome P450 - like protein c	CYP81K2	AT5G10600 ///	1.31	0.39	2.71	0.0315525	0.1691452	-3.79	FALSE
246895_at	putative protein predicted protein	CID6	AT5G25540	1.33	0.41	2.71	0.0315413	0.1691452	-3.79	FALSE
252654_at	similar to glycyl tRNA synthetase	---	AT3G44740	-1.29	-0.37	-2.71	0.0315512	0.1691452	-3.79	FALSE
257573_at	putative SF16 protein {Helianthus	iqd9	AT2G33990	-1.56	-0.65	-2.71	0.0315746	0.1692237	-3.79	FALSE
253092_at	putative protein various predicte	---	AT4G37380	-1.70	-0.77	-2.70	0.0316122	0.1692765	-3.80	FALSE
249200_at	5-3 exoribonuclease 2 ; supporte	XRN2	AT5G42540	-1.47	-0.56	-2.70	0.0316215	0.1692765	-3.80	FALSE
252510_at	putative protein serine/threonine	---	AT3G46270	1.35	0.43	2.70	0.0316195	0.1692765	-3.80	FALSE
265386_at	unknown protein ;supported by f	---	AT2G20930	-1.32	-0.40	-2.70	0.0315946	0.1692765	-3.80	FALSE
263099_at	putative non-LTR retroelement re	---	---	1.50	0.58	2.70	0.0316173	0.1692765	-3.80	FALSE
255580_at	putative water channel protein	TIP1;3	AT4G01470	1.46	0.54	2.70	0.0316419	0.169346	-3.80	FALSE
260062_at	hypothetical protein contains Pfa	---	AT1G73710	-1.44	-0.53	-2.70	0.0316879	0.1693959	-3.80	TRUE
260638_at	unknown protein similar to putati	---	AT1G62390	-1.68	-0.75	-2.70	0.0316718	0.1693959	-3.80	FALSE
258211_at	hypothetical protein predicted by	---	AT3G17890	-1.51	-0.59	-2.70	0.0316884	0.1693959	-3.80	FALSE
250412_at	putative protein synaptobrevin-li	ATVAMP71	AT5G11150	-1.48	-0.57	-2.70	0.0316866	0.1693959	-3.80	FALSE
259149_at	putative phenylalanine ammonia-	PAL4	AT3G10340	4.00	2.00	2.70	0.0316735	0.1693959	-3.80	FALSE
253222_at	chalcone synthase - like protein	---	AT4G34850	1.27	0.35	2.70	0.0317375	0.1694714	-3.80	FALSE

257827_at	unknown protein contains Pfam p	---	AT3G26630	-1.68	-0.75	-2.70	0.0317315	0.1694714	-3.80	FALSE
250459_at	unknown protein ; supported by	---	AT5G09860	-1.37	-0.45	-2.70	0.0317444	0.1694714	-3.80	FALSE
258863_at	unknown protein similar to RNA I	DCL2	AT3G03300	-1.67	-0.74	-2.70	0.031736	0.1694714	-3.80	FALSE
260639_at	hypothetical protein predicted by	---	AT1G53180	2.14	1.10	2.70	0.0317444	0.1694714	-3.80	FALSE
256159_at	Expressed protein ; supported by	JAZ8	AT1G30135	3.97	1.99	2.70	0.0317471	0.1694714	-3.80	FALSE
254035_at	putative phosphatidylserine deca	PSD3	AT4G25970 /	-1.35	-0.43	-2.70	0.0318396	0.1696873	-3.80	FALSE
261507_at	RIBOSOMAL PROTEIN, putativ	---	AT1G71720	-1.34	-0.42	-2.70	0.0318364	0.1696873	-3.80	FALSE
262645_at	unknown protein similar to elong	SCO1	AT1G62750	-1.48	-0.56	-2.70	0.0318386	0.1696873	-3.80	FALSE
246522_at	bZIP DNA-binding protein-like p	AtbZIP3	AT5G15830	-2.22	-1.15	-2.70	0.0318145	0.1696873	-3.80	FALSE
246345_at	calcium-dependent protein kinas	---	AT3G56760	-1.47	-0.56	-2.70	0.0318203	0.1696873	-3.80	FALSE
252200_at	anthranilate N-hydroxycinnamoy	---	AT3G50280	2.51	1.32	2.70	0.031827	0.1696873	-3.80	FALSE
252534_at	Myb DNA binding protein -like M	MYB111	AT3G46130	-1.33	-0.42	-2.70	0.0318258	0.1696873	-3.80	FALSE
261879_at	cytochrome P450, putative simil	CYP705A2	AT1G50520	1.31	0.39	2.70	0.0318732	0.1698264	-3.80	FALSE
259014_at	putative glucan endo-1-3-beta-gl	---	AT3G07320	1.62	0.69	2.70	0.0318873	0.1698367	-3.80	TRUE
261609_at	unknown protein similar to MAP3	---	AT1G49740	1.64	0.72	2.70	0.03189	0.1698367	-3.80	FALSE
259763_at	unknown protein similar to GB:A/	---	AT1G77630	-1.60	-0.68	-2.70	0.0319291	0.1700051	-3.81	FALSE
251074_at	putative protein hypothetical pro	---	AT5G01800	1.42	0.51	2.70	0.0319442	0.170046	-3.81	FALSE
253248_at	Putative S-phase-specific riboson	---	AT4G34670	-2.16	-1.11	-2.70	0.0319689	0.1701376	-3.81	FALSE
250202_at	putative protein similar to unknov	---	AT5G13970	-1.41	-0.50	-2.70	0.0319857	0.1701878	-3.81	FALSE
251033_at	hypothetical protein ;supported b	---	AT5G01960	1.27	0.34	2.70	0.0319989	0.1702181	-3.81	FALSE
257840_at	protein kinase, putative contains	AGC2-1	AT3G25250	4.61	2.20	2.70	0.0320247	0.1703156	-3.81	FALSE
246095_at	homeotic gene regulator - like pr	---	AT5G19310	-1.63	-0.71	-2.69	0.0320519	0.1704204	-3.81	FALSE
254956_at	putative protein various predicte	---	AT4G10850	1.30	0.38	2.69	0.0320616	0.1704292	-3.81	FALSE
262558_at	Expressed protein ; supported by	---	AT1G31335	-1.40	-0.48	-2.69	0.0320759	0.1704292	-3.81	FALSE
264878_at	unknown protein	---	AT2G17410	-1.29	-0.37	-2.69	0.0320756	0.1704292	-3.81	FALSE
263288_at	cyclophilin-like protein ;supporte	---	AT2G36130	-1.44	-0.53	-2.69	0.0321085	0.1705623	-3.81	FALSE
259334_at	unknown protein similar to hect d	---	AT3G03790	1.57	0.65	2.69	0.0321353	0.1706651	-3.81	FALSE
247886_at	branched-chain amino acid amin	---	AT5G57850	-1.54	-0.62	-2.69	0.0321566	0.1706915	-3.81	FALSE
246026_at	putative protein predicted protein	---	AT5G21070	-1.35	-0.43	-2.69	0.0321627	0.1706915	-3.81	FALSE
250146_at	putative protein polypeptide defo	PDF1B	AT5G14660	-1.66	-0.73	-2.69	0.0321586	0.1706915	-3.81	FALSE
256852_at	unknown protein contains Pfam p	ATRANGAI	AT3G18610	-1.54	-0.62	-2.69	0.0321956	0.1707132	-3.81	TRUE
258160_at	glutamine synthetase, putative s	GLN1.3	AT3G17820	1.72	0.78	2.69	0.0321864	0.1707132	-3.81	FALSE
263975_at	hypothetical protein predicted by	---	AT2G42710	-1.39	-0.48	-2.69	0.0321954	0.1707132	-3.81	FALSE
253624_at	putative protein 2-acylglycerophi	ATS2	AT4G30580	-1.47	-0.56	-2.69	0.0321968	0.1707132	-3.81	FALSE
261893_at	unknown protein ;supported by fu	---	AT1G80690	1.35	0.44	2.69	0.0322314	0.170729	-3.82	FALSE

262055_at	unknown protein ; supported by f	---	AT1G79970	1.31	0.39	2.69	0.0322447	0.170729	-3.82	FALSE
247339_at	unknown protein	---	AT5G63690	-1.44	-0.52	-2.69	0.0322258	0.170729	-3.82	FALSE
264013_at	unknown protein	FIO1	AT2G21070	-1.27	-0.34	-2.69	0.0322333	0.170729	-3.82	FALSE
250170_at	putative protein ribulose-1,5-bisp	---	AT5G14260	-1.41	-0.49	-2.69	0.0322441	0.170729	-3.82	FALSE
267077_at	unknown protein similar to cytosk	---	AT2G40970	-1.51	-0.59	-2.69	0.0322314	0.170729	-3.82	FALSE
253387_at	P-Protein - like protein P-Protein	AtGLDP1	AT4G33010	-1.92	-0.94	-2.69	0.0322672	0.1708086	-3.82	FALSE
251658_at	putative protein strictosidine synt	---	AT3G57020	2.07	1.05	2.69	0.032352	0.171181	-3.82	TRUE
252509_at	putative protein serine/threonine	---	AT3G46240	1.27	0.34	2.69	0.0323525	0.171181	-3.82	FALSE
246830_at	chaperonin gamma chain - like p	---	AT5G26360	-1.76	-0.82	-2.69	0.0323632	0.1711813	-3.82	TRUE
245644_at	unknown protein similar to putati	---	AT1G25320	-1.43	-0.51	-2.69	0.0323901	0.1711813	-3.82	FALSE
246910_at	exonuclease - like protein ribonu	---	AT5G25800	-1.59	-0.67	-2.69	0.0323753	0.1711813	-3.82	FALSE
257533_at	putative alpha/beta hydrolase co	---	AT3G10840	-1.71	-0.77	-2.69	0.0323855	0.1711813	-3.82	FALSE
262286_at	Expressed protein ; supported by	---	AT1G68585	-1.89	-0.92	-2.69	0.032375	0.1711813	-3.82	FALSE
254606_at	nodulin-26 - like protein major in	NLM1	AT4G19030	1.29	0.37	2.69	0.0324131	0.1712634	-3.82	FALSE
253366_at	putative protein predicted protei	---	AT4G33180	1.49	0.57	2.69	0.0324447	0.1713905	-3.82	FALSE
262800_at	putative ATP-dependent RNA he	emb1507	AT1G20960	-1.37	-0.46	-2.69	0.0324668	0.1714674	-3.82	FALSE
248045_at	HEAT SHOCK PROTEIN 81-2 (H	HSP81-2	AT5G56030	2.18	1.12	2.68	0.0325077	0.1716438	-3.82	FALSE
256919_at	hypothetical protein predicted by	---	AT3G18970	-1.40	-0.48	-2.68	0.03254	0.1717262	-3.82	FALSE
251132_at	putative protein Myb-related tran	---	AT5G01200	-1.52	-0.60	-2.68	0.0325421	0.1717262	-3.83	FALSE
261652_at	dimethyladenosine transferase,	PFC1	AT1G01860	-1.40	-0.49	-2.68	0.0325459	0.1717262	-3.83	FALSE
267268_at	hypothetical protein predicted by	---	AT2G02570	-1.36	-0.45	-2.68	0.0326079	0.1718636	-3.83	FALSE
250854_at	aspartyl aminopeptidase -like pr	---	AT5G04710	-1.45	-0.54	-2.68	0.0325821	0.1718636	-3.83	FALSE
248649_at	putative protein contains similarit	APRR4	AT5G49240	1.40	0.48	2.68	0.032609	0.1718636	-3.83	FALSE
248030_at	transcription regulator Sir2-like p	SRT1	AT5G55760	-1.52	-0.61	-2.68	0.0326096	0.1718636	-3.83	FALSE
265840_at	hypothetical protein predicted by	---	AT2G14530	-1.46	-0.55	-2.68	0.0325898	0.1718636	-3.83	FALSE
258350_at	unknown protein similar to serine	CIPK1	AT3G17510	1.91	0.93	2.68	0.0326184	0.1718702	-3.83	FALSE
247106_at	WD repeat protein-like ;supporte	---	AT5G66240	-1.39	-0.47	-2.68	0.0326456	0.1719669	-3.83	FALSE
254063_at	receptor kinase-like protein rece	---	AT4G25390	1.92	0.94	2.68	0.0326518	0.1719669	-3.83	FALSE
255699_at	putative pectinesterase	PME38	AT4G00190	1.30	0.38	2.68	0.0326802	0.1719771	-3.83	FALSE
255890_at	rhodanese-like family protein pre	---	AT1G17850	-1.69	-0.76	-2.68	0.0326727	0.1719771	-3.83	FALSE
250130_at	amylogenin; reversibly glycosylat	---	AT5G16510	1.51	0.60	2.68	0.0326839	0.1719771	-3.83	FALSE
247150_at	putative protein similar to unknov	---	AT5G65650	-1.45	-0.54	-2.68	0.0326792	0.1719771	-3.83	FALSE
254368_at	DNA-directed RNA polymerase (	NRPB2	AT4G21710	-1.33	-0.41	-2.68	0.0327084	0.1720659	-3.83	FALSE
246460_at	cellulose synthase catalytic subu	CSLD2	AT5G16910	1.66	0.73	2.68	0.0327495	0.1722426	-3.83	FALSE
259660_at	unknown protein ; supported by f	---	AT1G55260	3.07	1.62	2.68	0.032793	0.1722597	-3.83	TRUE

260129_at	hypothetical protein similar to var	---	AT1G36380	-1.31	-0.39	-2.68	0.0327889	0.1722597	-3.83	FALSE
245303_at	hypothetical protein ; supported b	---	AT4G17010	-1.31	-0.39	-2.68	0.0327765	0.1722597	-3.83	FALSE
262285_at	hypothetical protein predicted by	---	AT1G68680	-1.33	-0.42	-2.68	0.0327942	0.1722597	-3.83	FALSE
265169_x_a	unknown protein	---	AT1G23720	1.36	0.45	2.68	0.0328008	0.1722597	-3.83	FALSE
266878_at	putative RING zinc finger protein	---	AT2G44580	1.36	0.44	2.68	0.0328056	0.1722597	-3.83	FALSE
251302_at	RAV-like protein DNA-binding pr	NGA2	AT3G61970	-1.26	-0.34	-2.68	0.0327896	0.1722597	-3.83	FALSE
248172_at	unknown protein ;supported by f	---	AT5G54660	-1.74	-0.80	-2.68	0.0328518	0.1724506	-3.83	TRUE
264042_at	putative steroid sulfotransferase	ST	AT2G03760	4.00	2.00	2.68	0.0328571	0.1724506	-3.83	FALSE
265029_at	zinc finger protein 7, ZFP7 ; sup	ZFP7	AT1G24625	-1.53	-0.61	-2.68	0.0328811	0.1725368	-3.84	FALSE
255817_at	unknown protein ;supported by f	PDLP3	AT2G33330	-1.86	-0.90	-2.68	0.0329199	0.1726305	-3.84	TRUE
248531_at	putative protein contains similarit	---	AT5G49950	1.37	0.45	2.68	0.0329216	0.1726305	-3.84	FALSE
264970_at	glyoxalase I, putative similar to g	---	AT1G67280	-1.32	-0.40	-2.68	0.0329082	0.1726305	-3.84	FALSE
256145_at	lipid transfer protein, putative sir	---	AT1G48750	2.09	1.06	2.68	0.0329513	0.1726687	-3.84	TRUE
253171_at	putative protein ;supported by fu	---	AT4G35040	-1.41	-0.50	-2.68	0.0329516	0.1726687	-3.84	FALSE
246803_at	tSNARE AtTLG2a ; supported b	SYP41	AT5G26980	-1.33	-0.41	-2.68	0.0329451	0.1726687	-3.84	FALSE
256489_at	unknown protein	---	AT1G31550	1.27	0.35	2.67	0.0329973	0.1728409	-3.84	FALSE
254121_at	putative protein putative protein	---	AT4G24760	-1.73	-0.79	-2.67	0.0329997	0.1728409	-3.84	FALSE
263558_at	putative phosphatidylinositol/pho	---	AT2G16380	-1.52	-0.60	-2.67	0.0330523	0.1730771	-3.84	FALSE
247816_at	similar to unknown protein (pir||S	---	AT5G58260	-1.99	-0.99	-2.67	0.0330605	0.1730804	-3.84	TRUE
254012_at	putative ribosomal protein riboso	---	AT4G26230	-1.81	-0.85	-2.67	0.0330787	0.1731358	-3.84	FALSE
255291_at	putative calcium dependent prote	CPK27	AT4G04700	1.40	0.48	2.67	0.0330919	0.1731651	-3.84	FALSE
255095_at	MEKK1/MAP kinase kinase kinas	MEKK1	AT4G08500	1.58	0.66	2.67	0.033104	0.1731887	-3.84	FALSE
252608_at	putative protein 2-phosphoglyce	---	AT3G45090	1.40	0.48	2.67	0.0331205	0.1732354	-3.84	FALSE
258693_at	unknown protein	---	AT3G08650	1.29	0.37	2.67	0.0331578	0.1733905	-3.84	FALSE
265903_at	putative potassium transporter/ch	SPIK	AT2G25600	1.31	0.39	2.67	0.0331861	0.1734987	-3.84	FALSE
250798_at	peroxidase	---	AT5G05340	6.16	2.62	2.67	0.0332415	0.1735853	-3.85	FALSE
247706_at	putative ripening-related protein	---	AT5G59480	2.04	1.03	2.67	0.0332407	0.1735853	-3.85	FALSE
266241_s_a	hypothetical protein predicted by	---	AT2G27800 /	-1.39	-0.48	-2.67	0.0332172	0.1735853	-3.85	FALSE
253582_at	Expressed protein ;supported by	---	AT4G30670	-1.56	-0.64	-2.67	0.0332555	0.1735853	-3.85	FALSE
263714_at	putative tyrosine aminotransferas	SUR1	AT2G20610	1.79	0.84	2.67	0.033252	0.1735853	-3.85	FALSE
256633_at	unknown protein	GATL10	AT3G28340	4.30	2.11	2.67	0.0332559	0.1735853	-3.85	FALSE
266811_at	unknown protein	---	AT2G44850	-1.33	-0.41	-2.67	0.0332341	0.1735853	-3.85	FALSE
257250_at	transfactor, putative similar to G	---	AT3G24120	-1.37	-0.45	-2.67	0.0333169	0.1738637	-3.85	FALSE
262162_at	unknown protein ;supported by fu	---	AT1G78020	-1.50	-0.58	-2.67	0.0333258	0.1738703	-3.85	TRUE
267644_s_a	unknown protein highly similar to	---	AT2G32870 /	-1.58	-0.66	-2.67	0.0333419	0.1739149	-3.85	FALSE

255829_at	putative potassium transporter ;	KT2	AT2G40540	-1.29	-0.36	-2.67	0.033354	0.1739378	-3.85	FALSE
263239_at	amidophosphoribosyltransferase	ATASE1	AT2G16570	1.39	0.47	2.67	0.0333616	0.1739378	-3.85	FALSE
260102_at	unknown protein	---	AT1G35470	-1.41	-0.50	-2.67	0.0333702	0.1739428	-3.85	FALSE
263973_at	60S ribosomal protein L11B	RPL16A	AT2G42740	-1.69	-0.76	-2.67	0.0333803	0.1739559	-3.85	FALSE
246572_at	putative protein predicted protei	---	AT5G15010	-1.37	-0.46	-2.67	0.0333959	0.1739785	-3.85	FALSE
259091_at	hypothetical protein predicted by	---	AT3G04890	-1.39	-0.47	-2.67	0.0333999	0.1739785	-3.85	FALSE
251469_at	putative protein strictosidine syn	---	AT3G59530	1.31	0.39	2.66	0.0334359	0.1741262	-3.85	FALSE
254076_at	putative protein immunophilin FK	---	AT4G25340	-1.75	-0.81	-2.66	0.033492	0.1741364	-3.85	TRUE
267506_at	unknown protein ;supported by f	---	AT2G45520	-1.31	-0.39	-2.66	0.033486	0.1741364	-3.85	FALSE
265092_at	hypothetical protein predicted by	---	AT1G03910	-1.29	-0.37	-2.66	0.0334708	0.1741364	-3.85	FALSE
263931_at	unknown protein ;supported by f	---	AT2G36220	2.18	1.12	2.66	0.0334648	0.1741364	-3.85	FALSE
257926_at	unknown protein contains Pfam p	---	AT3G23280	-1.27	-0.34	-2.66	0.0334955	0.1741364	-3.85	FALSE
259364_at	DNA-binding protein RAV1 identi	RAV1	AT1G13260	-1.42	-0.50	-2.66	0.0334989	0.1741364	-3.85	FALSE
265844_at	putative receptor-like protein kina	FEI2	AT2G35620	-1.55	-0.63	-2.66	0.0334785	0.1741364	-3.85	FALSE
256708_at	hypothetical protein predicted by	---	AT3G30320	1.30	0.38	2.66	0.0334478	0.1741364	-3.85	FALSE
253337_at	putative protein acetylpolyamine	hda14	AT4G33470	-1.67	-0.74	-2.66	0.0335119	0.1741425	-3.85	FALSE
249324_at	cytochrome c1 precursor ; suppo	---	AT5G40810	-1.28	-0.36	-2.66	0.033523	0.1741425	-3.85	FALSE
258661_at	unknown protein	---	AT3G02930	2.02	1.01	2.66	0.0335156	0.1741425	-3.85	FALSE
251942_at	ABC transporter - like protein PD	PDR9	AT3G53480	2.35	1.24	2.66	0.0335419	0.1742011	-3.86	FALSE
254111_at	putative protein acid phosphatas	PAP24	AT4G24890	1.59	0.67	2.66	0.0335645	0.1742785	-3.86	FALSE
253424_at	putative protein ; supported by cD	---	AT4G32330	-1.46	-0.54	-2.66	0.0336176	0.1745012	-3.86	TRUE
258560_at	hypothetical protein predicted by	---	AT3G06020	1.53	0.61	2.66	0.0336303	0.1745012	-3.86	FALSE
250626_at	putative protein p100 co-activato	---	AT5G07350	1.35	0.43	2.66	0.0336293	0.1745012	-3.86	FALSE
256089_at	hypothetical protein predicted by	---	AT1G20830	-1.58	-0.66	-2.66	0.0336703	0.1746005	-3.86	FALSE
254641_at	ras-like GTP-binding protein stro	ATRABA1D	AT4G18800	1.60	0.68	2.66	0.0336724	0.1746005	-3.86	FALSE
261416_at	ribosomal protein S15 identical t	RPS15A	AT1G07770	-1.83	-0.87	-2.66	0.0336572	0.1746005	-3.86	FALSE
256428_at	putative disease resistance prote	AtRLP35	AT3G11080	1.71	0.77	2.66	0.033697	0.1746088	-3.86	FALSE
248664_at	peptidyl-prolyl cis-trans isomeras	FKBP15-2	AT5G48580	-1.55	-0.64	-2.66	0.0336914	0.1746088	-3.86	FALSE
253816_at	hypothetical protein ;supported b	emb1923	AT4G28210	-1.43	-0.52	-2.66	0.0336951	0.1746088	-3.86	FALSE
261864_s_a	10-formyltetrahydrofolate synthet	THFS	AT1G50480 //	-1.38	-0.46	-2.66	0.0337295	0.1746474	-3.86	FALSE
246423_at	putative protein ribosomal protei	---	AT5G16950	-1.48	-0.57	-2.66	0.0337189	0.1746474	-3.86	FALSE
251725_at	putative protein	---	AT3G56260	1.62	0.69	2.66	0.033735	0.1746474	-3.86	FALSE
255449_at	hypothetical protein	---	AT4G02820	-1.51	-0.59	-2.66	0.0337289	0.1746474	-3.86	FALSE
260425_at	hypothetical protein similar to C0	EDA25	AT1G72440	-2.05	-1.03	-2.66	0.0337671	0.1746942	-3.86	TRUE
254323_at	putative protein auxin-induced p	---	AT4G22620	2.01	1.01	2.66	0.0337562	0.1746942	-3.86	FALSE

254532_at	putative protein regulatory prote	NPR4	AT4G19660	1.65	0.72	2.66	0.0337647	0.1746942	-3.86	FALSE
263221_at	UDP-galactose 4-epimerase-like	MUR4	AT1G30620	2.50	1.32	2.66	0.0338527	0.1750589	-3.86	FALSE
266789_at	unknown protein ; supported by	---	AT2G29020	-1.32	-0.40	-2.66	0.0338529	0.1750589	-3.86	FALSE
253520_at	hypothetical protein ;supported b	---	AT4G31410	-1.30	-0.37	-2.66	0.0339018	0.1752273	-3.87	FALSE
260443_at	Expressed protein ; supported by	---	AT1G68185	-1.27	-0.35	-2.66	0.0339085	0.1752273	-3.87	FALSE
250212_at	putative protein contains similarit	SUVH4	AT5G13960	-1.37	-0.45	-2.66	0.0339027	0.1752273	-3.87	FALSE
255394_at	hypothetical protein similar to A.	---	---	1.35	0.43	2.65	0.0339541	0.1752645	-3.87	FALSE
259363_at	methionine aminopeptidase I (M	MAP1C	AT1G13270	-1.38	-0.46	-2.65	0.0339405	0.1752645	-3.87	FALSE
258448_at	unknown protein	---	AT3G22290	1.29	0.36	2.65	0.0339359	0.1752645	-3.87	FALSE
256757_at	membrane transporter, putative	---	AT3G25620	1.36	0.45	2.65	0.0339336	0.1752645	-3.87	FALSE
257025_at	hypothetical protein predicted by	ATG2	AT3G19190	1.52	0.60	2.65	0.0339493	0.1752645	-3.87	FALSE
248685_at	putative protein similar to unknov	---	AT5G48500	-1.59	-0.67	-2.65	0.033997	0.1753666	-3.87	FALSE
263550_at	Expressed protein ; supported by	---	AT2G17033	-1.41	-0.50	-2.65	0.0339899	0.1753666	-3.87	FALSE
267421_at	putative phosphoribosylaminoimi	---	AT2G35040	-1.47	-0.55	-2.65	0.0339953	0.1753666	-3.87	FALSE
257239_at	unknown protein	---	AT3G24100	-1.37	-0.45	-2.65	0.0340336	0.1754345	-3.87	TRUE
260792_at	unknown protein ;supported by fu	---	AT1G06270	-1.38	-0.46	-2.65	0.0340351	0.1754345	-3.87	FALSE
251024_at	putative protein hypothetical prot	---	AT5G02180	1.44	0.53	2.65	0.0340267	0.1754345	-3.87	FALSE
255989_at	putative protein	---	AT5G35069	1.43	0.52	2.65	0.0340409	0.1754345	-3.87	FALSE
254575_at	putative protein various predicte	---	AT4G19460	2.13	1.09	2.65	0.0340676	0.1755327	-3.87	FALSE
254833_s_a	copper amine oxidase like prote	---	AT4G12280 /A	1.29	0.37	2.65	0.0340754	0.1755327	-3.87	TRUE
245905_at	putative protein predicted protei	---	AT5G11090	-1.37	-0.46	-2.65	0.0341012	0.1755865	-3.87	TRUE
245897_at	potassium transport protein-like s	KUP7	AT5G09400	1.51	0.60	2.65	0.0340999	0.1755865	-3.87	FALSE
262299_at	unknown protein Similar to gb|U	---	AT1G27520	-1.34	-0.42	-2.65	0.0341232	0.1756604	-3.87	FALSE
255260_at	score=63.7, E=3.9e-15, N=8 ; s	---	AT4G05040	-1.46	-0.55	-2.65	0.0341325	0.1756686	-3.87	FALSE
260545_at	putative glutathione peroxidase	ATGPX3	AT2G43350	-1.38	-0.46	-2.65	0.034166	0.1758011	-3.87	FALSE
251570_at	putative protein several hypothet	---	AT3G58300	1.37	0.45	2.65	0.0341805	0.1758362	-3.87	FALSE
252320_at	endoxyloglucan transferase-like	---	AT3G48580	2.07	1.05	2.65	0.0342466	0.176057	-3.88	TRUE
261591_at	protein kinase, putative similar t	---	AT1G01740	-1.50	-0.58	-2.65	0.0342384	0.176057	-3.88	FALSE
262502_at	unknown protein similar to hypot	PTAC6	AT1G21600	-1.34	-0.43	-2.65	0.0342393	0.176057	-3.88	FALSE
258766_at	galactokinase-like protein simila	---	AT3G10700	1.31	0.39	2.65	0.0342557	0.1760639	-3.88	FALSE
253524_at	predicted protein ; supported by	---	AT4G31430	-1.38	-0.46	-2.65	0.0342722	0.1760694	-3.88	FALSE
245327_at	hypothetical protein ; supported b	---	AT4G16850	-1.32	-0.40	-2.65	0.0342701	0.1760694	-3.88	FALSE
248683_at	putative protein similar to unknov	---	AT5G48490	-2.67	-1.42	-2.65	0.0343483	0.1761477	-3.88	TRUE
247735_at	thymidylate kinase - like protein	ZEU1	AT5G59440	-1.85	-0.89	-2.65	0.0343302	0.1761477	-3.88	TRUE
245991_at	24 kDa vacuolar protein - like 24	---	AT5G20660	-1.32	-0.40	-2.65	0.0343542	0.1761477	-3.88	FALSE

251814_at	chlorophyll a/b-binding protein ;	LHCA1	AT3G54890	-1.26	-0.33	-2.65	0.0343397	0.1761477	-3.88	FALSE
262552_at	hypothetical protein similar to hyp	---	AT1G31350	1.64	0.71	2.65	0.0343557	0.1761477	-3.88	FALSE
256667_at	hypothetical protein predicted by	---	AT3G32180	1.26	0.33	2.65	0.0343562	0.1761477	-3.88	FALSE
254560_at	kinase-like protein protein kinase	---	AT4G19110 ///	1.28	0.35	2.65	0.0343254	0.1761477	-3.88	FALSE
258182_at	1-D-deoxyxylulose 5-phosphate	DXPS1	AT3G21500	2.42	1.28	2.65	0.0343161	0.1761477	-3.88	FALSE
262408_at	protein phosphatase type 2C, pu	---	AT1G34750	2.02	1.02	2.65	0.0343569	0.1761477	-3.88	FALSE
262955_at	unknown protein ;supported by fu	---	AT1G54520	-1.43	-0.51	-2.65	0.0343664	0.1761566	-3.88	FALSE
247349_at	putative protein similar to unknov	---	AT5G63820	1.31	0.39	2.64	0.0344331	0.1764592	-3.88	FALSE
248369_at	arginine/serine-rich splicing facto	ATRSP41	AT5G52040	-1.48	-0.57	-2.64	0.034445	0.1764803	-3.88	FALSE
255821_at	putative initiator tRNA phosphorib	---	AT2G40570	-1.36	-0.44	-2.64	0.0344885	0.1765585	-3.88	FALSE
262992_at	hypothetical protein predicted by	ATG12A	AT1G54210	-1.51	-0.60	-2.64	0.0344828	0.1765585	-3.88	FALSE
250255_at	sigma-like factor (gb|AAC97954.	SIG4	AT5G13730	-1.84	-0.88	-2.64	0.0344912	0.1765585	-3.88	FALSE
249630_s_a	sen1-like protein SEN1 - Saccha	---	AT5G37150 ///	1.27	0.34	2.64	0.0344772	0.1765585	-3.88	FALSE
266097_at	unknown protein ; supported by	SOUL-1	AT2G37970	2.01	1.01	2.64	0.0345251	0.1765733	-3.88	FALSE
261483_at	hypothetical protein predicted by	---	AT1G14270	-1.39	-0.48	-2.64	0.0345109	0.1765733	-3.88	FALSE
254696_at	hypothetical protein	---	AT4G17930	1.29	0.37	2.64	0.0345231	0.1765733	-3.88	FALSE
257989_at	unknown protein ; supported by c	VPS9A	AT3G19770	1.37	0.45	2.64	0.0345095	0.1765733	-3.88	FALSE
245443_at	limonene cyclase like protein	---	AT4G16730	14.90	3.90	2.64	0.0345434	0.1766276	-3.89	FALSE
264664_at	putative elongation factor similar	---	AT1G09660	-1.56	-0.65	-2.64	0.0345691	0.1767194	-3.89	FALSE
266806_at	unknown protein ;supported by f	---	AT2G30000	-1.46	-0.54	-2.64	0.0345804	0.1767373	-3.89	FALSE
261841_at	BTG1 binding factor 1, putative s	---	AT1G15920	-1.33	-0.42	-2.64	0.034608	0.1768388	-3.89	FALSE
266289_at	putative C-4 sterol methyl oxidas	SMO2-2	AT2G29390	-1.33	-0.41	-2.64	0.0346297	0.1768706	-3.89	FALSE
262573_at	hypothetical protein Similar to gi|	PDF1A	AT1G15390	-1.42	-0.50	-2.64	0.0346249	0.1768706	-3.89	FALSE
254788_at	putative protein other predicted p	---	AT4G12790	1.30	0.38	2.64	0.0348142	0.1775175	-3.89	TRUE
257122_at	RNA-binding protein, putative co	APUM5	AT3G20250	-1.59	-0.67	-2.64	0.0348143	0.1775175	-3.89	FALSE
252114_at	mucin -like protein hemomucin,	---	AT3G51450	2.46	1.30	2.64	0.0347855	0.1775175	-3.89	FALSE
262295_at	putative U2 snRNP auxiliary fact	ATU2AF35/	AT1G27650	-1.46	-0.55	-2.64	0.0348134	0.1775175	-3.89	FALSE
265460_at	putative caltractin ;supported by	---	AT2G46600	-1.69	-0.75	-2.64	0.0347747	0.1775175	-3.89	FALSE
252449_at	FtsH protease, putative contains	ftsh7	AT3G47060	1.27	0.34	2.64	0.0348071	0.1775175	-3.89	FALSE
252751_at	putative protein RING-H2 zinc fi	---	AT3G43430	1.87	0.90	2.64	0.0348186	0.1775175	-3.89	FALSE
250017_at	unknown protein	---	AT5G18140	-1.64	-0.71	-2.64	0.0347979	0.1775175	-3.89	FALSE
252010_at	hypothetical protein ; supported b	---	AT3G52740	-1.48	-0.57	-2.64	0.0348315	0.1775433	-3.89	FALSE
252876_at	putative protein ;supported by fu	---	AT4G39970	-1.62	-0.70	-2.64	0.0348474	0.1775447	-3.89	TRUE
247385_at	putative protein similar to unknov	emb2746	AT5G63420	-1.53	-0.62	-2.64	0.0348643	0.1775447	-3.89	FALSE
259210_at	hypothetical protein nearly identi	HY2	AT3G09150	-1.49	-0.57	-2.64	0.0348641	0.1775447	-3.89	FALSE

253391_at	hypothetical protein ; supported	---	AT4G32590	-1.57	-0.65	-2.64	0.0348707	0.1775447	-3.89	FALSE
245863_s_a	hypothetical protein contains sim	---	AT1G58050 ///	-1.40	-0.49	-2.64	0.034851	0.1775447	-3.89	FALSE
264332_at	hypothetical protein predicted by	---	AT1G61920	1.32	0.40	2.64	0.0348816	0.1775605	-3.89	FALSE
251493_at	putative protein hypothetical pro	---	AT3G59300	1.44	0.52	2.63	0.0349325	0.1777009	-3.90	FALSE
265989_at	unknown protein	---	AT2G24260	1.32	0.40	2.63	0.0349305	0.1777009	-3.90	FALSE
246975_at	putative protein hypothetical prot	---	AT5G24890	-1.50	-0.58	-2.63	0.0349213	0.1777009	-3.90	FALSE
248941_s_a	putative protein similar to unknov	---	AT5G45460 ///	1.44	0.53	2.63	0.0349864	0.177918	-3.90	FALSE
248079_at	unknown protein	---	AT5G55790	-1.52	-0.60	-2.63	0.0349908	0.177918	-3.90	FALSE
264367_at	unknown protein ESTs gb|T212	---	AT1G03350	1.32	0.40	2.63	0.0350161	0.1779768	-3.90	FALSE
257083_s_a	non-race specific disease resista	---	AT3G20590 ///	1.73	0.79	2.63	0.035018	0.1779768	-3.90	FALSE
258050_at	unknown protein	---	AT3G16200	-1.42	-0.51	-2.63	0.0350323	0.17801	-3.90	FALSE
255614_at	putative myb-related DNA-bindin	---	AT4G01280	-1.31	-0.39	-2.63	0.0351141	0.1781333	-3.90	FALSE
265510_at	putative microtubule-associated	ATG8D	AT2G05630	-1.34	-0.42	-2.63	0.035085	0.1781333	-3.90	FALSE
260619_at	glyoxalase I, putative similar to (	---	AT1G08110	-1.47	-0.55	-2.63	0.0350865	0.1781333	-3.90	FALSE
260732_at	myb-related DNA-binding protei	---	AT1G17520	-1.31	-0.39	-2.63	0.0351154	0.1781333	-3.90	FALSE
260297_at	unknown protein contains Pfam p	---	AT1G80280	1.38	0.47	2.63	0.035119	0.1781333	-3.90	FALSE
246987_at	myb-related protein, 33.3K (pir |	MYBR1	AT5G67300	1.76	0.82	2.63	0.0351177	0.1781333	-3.90	FALSE
258479_at	hypothetical protein predicted by	---	AT3G02440	1.36	0.44	2.63	0.0350939	0.1781333	-3.90	FALSE
260677_at	translation elongation factor EF-	RNL	AT1G07910	-1.67	-0.74	-2.63	0.0350755	0.1781333	-3.90	FALSE
260841_at	Expressed protein ; supported by	---	AT1G29195	1.43	0.52	2.63	0.0351293	0.1781457	-3.90	FALSE
254546_at	lectin like protein lectin 2, phloer	PP2-A2	AT4G19850	-2.31	-1.21	-2.63	0.0351477	0.1781993	-3.90	TRUE
264952_at	Tub family protein, putative cont	AtTLP1	AT1G76900	1.29	0.37	2.63	0.0352016	0.1784329	-3.90	FALSE
249494_at	acyltransferase - like protein Ant	---	AT5G39050	2.05	1.04	2.63	0.0352597	0.1786877	-3.91	FALSE
264264_at	unknown protein ESTs gb|T046	---	AT1G09250	1.93	0.95	2.63	0.0353111	0.1788443	-3.91	TRUE
254432_at	reticuline oxidase -like protein re	---	AT4G20830 ///	2.67	1.42	2.63	0.0353141	0.1788443	-3.91	FALSE
251991_at	transcription factor NF-Y, CCAA	NF-YB10	AT3G53340	-1.46	-0.54	-2.63	0.0353063	0.1788443	-3.91	FALSE
261569_at	DNA-binding protein, putative si	LHY	AT1G01060	1.41	0.49	2.63	0.0353295	0.1788824	-3.91	FALSE
252701_at	hypothetical protein SPOP prote	ATBPM6	AT3G43700	-1.45	-0.53	-2.63	0.0353494	0.1789436	-3.91	FALSE
266296_at	putative glutathione S-transferas	ATGSTU7	AT2G29420	1.44	0.52	2.63	0.0353603	0.1789589	-3.91	TRUE
251791_at	expansin-like protein expansin A	ATEXPA16	AT3G55500	2.04	1.03	2.63	0.0353831	0.1790347	-3.91	TRUE
248043_s_a	heat shock protein (emb|CAA725	---	AT5G56000 ///	1.70	0.76	2.62	0.0354015	0.1790482	-3.91	FALSE
255518_at	putative pectinesterase similar to	---	AT4G02300	1.37	0.45	2.62	0.0353989	0.1790482	-3.91	FALSE
262244_at	serine threonine kinase, putative	CIPK17	AT1G48260	3.78	1.92	2.62	0.0354238	0.1791213	-3.91	FALSE
261565_at	beta-1,3-glucanase, putative sim	---	AT1G33220	1.26	0.34	2.62	0.0354456	0.1791918	-3.91	FALSE
263664_at	putative auxin-induced protein, I	AXR3	AT1G04250	2.21	1.15	2.62	0.0354624	0.1792372	-3.91	TRUE

256064_at	Expressed protein ; supported by	---	AT1G07020	1.34	0.42	2.62	0.0354809	0.1792908	-3.91	TRUE
266031_at	hypothetical protein predicted by	---	---	1.31	0.39	2.62	0.0355069	0.1793824	-3.91	FALSE
266808_at	Expressed protein ; supported by	---	AT2G29995	1.48	0.56	2.62	0.0355397	0.1794719	-3.91	FALSE
265619_at	hypothetical protein	---	AT2G27320	1.47	0.55	2.62	0.0355403	0.1794719	-3.91	FALSE
250381_at	putative protein various predicte	---	AT5G11610	-1.75	-0.81	-2.62	0.0355598	0.1794909	-3.91	FALSE
252552_at	putative protein	---	AT3G45900	-1.51	-0.60	-2.62	0.0355533	0.1794909	-3.91	FALSE
257461_at	hypothetical protein predicted by	ATPUP15	AT1G75470	1.27	0.34	2.62	0.0355937	0.1796222	-3.92	FALSE
257708_at	hypothetical protein predicted by	---	AT3G13330	1.33	0.42	2.62	0.0356019	0.1796237	-3.92	FALSE
249211_at	putative protein similar to unknov	---	AT5G42680	-1.89	-0.92	-2.62	0.0356273	0.1797122	-3.92	FALSE
254204_at	putative protein CGI-58 protein -	---	AT4G24160	1.91	0.93	2.62	0.0356603	0.1797992	-3.92	FALSE
253597_at	putative protein translation initiat	---	AT4G30690	-1.71	-0.77	-2.62	0.0356537	0.1797992	-3.92	FALSE
251089_at	heat shock protein 40-like heat s	---	AT5G01390	-1.32	-0.40	-2.62	0.0356694	0.1798055	-3.92	FALSE
258706_at	unknown protein similar to putati	---	AT3G09570	1.35	0.43	2.62	0.0356942	0.1798904	-3.92	FALSE
263949_at	E2, ubiquitin-conjugating enzym	MMZ3	AT2G36060	-1.28	-0.35	-2.62	0.0357026	0.1798933	-3.92	FALSE
246958_at	putative protein similar to unknov	---	AT5G24690	-1.50	-0.59	-2.62	0.0357246	0.1799314	-3.92	TRUE
249889_at	putative protein strong similarity t	---	AT5G22540	2.52	1.33	2.62	0.035726	0.1799314	-3.92	FALSE
246601_at	copper amine oxidase, putative	---	AT1G31710	7.81	2.97	2.62	0.0357635	0.1800423	-3.92	FALSE
247540_at	ethylene responsive element bir	---	AT5G61590	-1.99	-0.99	-2.62	0.0357638	0.1800423	-3.92	FALSE
251964_at	hypothetical protein ; supported	---	AT3G53370	1.61	0.69	2.62	0.0358369	0.1803307	-3.92	FALSE
252652_at	putative chloroplast prephenate d	ADT4	AT3G44720	2.96	1.57	2.62	0.0358346	0.1803307	-3.92	FALSE
256386_at	cytochrome P450, putative conta	---	AT1G66540	1.29	0.36	2.62	0.0358452	0.1803327	-3.92	FALSE
260984_at	Expressed protein ; supported by	---	AT1G53645	-1.75	-0.81	-2.61	0.0359537	0.1807589	-3.93	TRUE
261169_at	sucrose-phosphate synthase, pu	ATSPS3F	AT1G04920	1.38	0.46	2.61	0.0359481	0.1807589	-3.93	FALSE
245365_at	hypothetical protein ;supported b	---	AT4G17720	1.66	0.73	2.61	0.035947	0.1807589	-3.93	FALSE
265563_s_a	hypothetical protein predicted by	---	---	1.25	0.32	2.61	0.0359626	0.1807639	-3.93	FALSE
245711_at	putative c2h2 zinc finger transcri	ZAT6	AT5G04340	2.87	1.52	2.61	0.0359725	0.1807738	-3.93	TRUE
260565_at	unknown protein predicted by ge	---	AT2G43800	1.69	0.76	2.61	0.0359904	0.1808239	-3.93	FALSE
245037_at	putative phosphatidylinositol-4-pl	PIP5K3	AT2G26420	1.28	0.35	2.61	0.0360053	0.1808451	-3.93	FALSE
256627_at	unknown protein ; supported by	---	AT3G19970	3.41	1.77	2.61	0.0360104	0.1808451	-3.93	FALSE
260656_at	hypothetical protein predicted by	---	AT1G19380	3.08	1.62	2.61	0.0360432	0.1809436	-3.93	TRUE
253979_at	putative protein other putative pr	---	AT4G26680	-1.36	-0.44	-2.61	0.0360459	0.1809436	-3.93	FALSE
259808_at	hypothetical protein contains Pfa	---	AT1G49790	-1.28	-0.36	-2.61	0.0360552	0.1809501	-3.93	FALSE
261127_at	unknown protein ; supported by c	---	AT1G04790	-1.47	-0.56	-2.61	0.0360749	0.1810093	-3.93	FALSE
245674_at	chitinase, putative similar to chit	---	AT1G56680	1.30	0.38	2.61	0.0361407	0.1812898	-3.93	FALSE
264918_at	interferon-induced GTP-binding	---	AT1G60530	1.33	0.41	2.61	0.0361467	0.1812898	-3.93	FALSE

245064_at	Expressed protein ; supported by	---	AT2G39725	1.66	0.73	2.61	0.0361557	0.181295	-3.93	FALSE
260685_at	Expressed protein ; supported by	GLYR2	AT1G17650	-1.54	-0.62	-2.61	0.036176	0.181317	-3.93	TRUE
260726_at	signal recognition particle 19 kD	---	AT1G48160	-1.49	-0.58	-2.61	0.0361756	0.181317	-3.93	FALSE
248392_at	integral membrane protein-like	---	AT5G52050	4.66	2.22	2.61	0.036202	0.1814078	-3.93	FALSE
259161_at	carbonic anhydrase, chloroplast	CA1	AT3G01500	-2.25	-1.17	-2.61	0.036236	0.1814983	-3.93	TRUE
249426_at	putative RNA helicase putative A	---	AT5G39840	-1.99	-0.99	-2.61	0.0362338	0.1814983	-3.93	FALSE
259707_at	thylakoid-bound ascorbate perox	TAPX	AT1G77490	-1.54	-0.62	-2.61	0.0363301	0.1815947	-3.94	FALSE
263287_at	Expressed protein ; supported by	---	AT2G36145	-2.31	-1.21	-2.61	0.0362689	0.1815947	-3.93	TRUE
266017_at	unknown protein ; supported by	---	AT2G18690	2.30	1.20	2.61	0.0363409	0.1815947	-3.94	FALSE
252303_at	putative protein hypothetical pro	---	AT3G49210	1.31	0.39	2.61	0.0363253	0.1815947	-3.94	FALSE
248224_at	thylakoid lumenal 17.4 kD protei	---	AT5G53490	-1.53	-0.61	-2.61	0.0363428	0.1815947	-3.94	FALSE
265051_at	jasmonate inducible protein, put	---	AT1G52100	1.48	0.57	2.61	0.0363087	0.1815947	-3.94	FALSE
266794_at	hypothetical protein	---	AT2G02980	-1.31	-0.39	-2.61	0.0363308	0.1815947	-3.94	FALSE
250019_at	putative protein similar to unknov	---	AT5G18160	1.41	0.50	2.61	0.0362962	0.1815947	-3.93	FALSE
247960_at	N-myristoyl transferase ;support	NMT1	AT5G57020	-1.28	-0.36	-2.61	0.0362846	0.1815947	-3.93	FALSE
257055_at	Expressed protein ; supported by	---	AT3G15351	-1.33	-0.42	-2.61	0.0363218	0.1815947	-3.94	FALSE
261388_at	Expressed protein ; supported by	---	AT1G05385	-1.30	-0.38	-2.61	0.0362803	0.1815947	-3.93	FALSE
266036_s_a	20S proteasome subunit (PAA2)	PAA2	AT2G05840 /	-1.33	-0.41	-2.61	0.0363652	0.181627	-3.94	FALSE
247136_at	senescence-associated protein c	---	AT5G66170	3.27	1.71	2.61	0.036363	0.181627	-3.94	FALSE
263218_at	putative serine/threonine protein	---	AT1G30570	-1.48	-0.56	-2.61	0.0363951	0.1817367	-3.94	FALSE
246437_at	putative protein hypersensitivity-	---	AT5G17540	1.30	0.38	2.60	0.0364124	0.1817433	-3.94	FALSE
253506_at	putative protein EREBP-4 homo	---	AT4G31980	1.64	0.71	2.61	0.0364121	0.1817433	-3.94	FALSE
262962_at	NADP-isocitrate dehydrogenase	ICDH	AT1G54340	1.25	0.33	2.60	0.0364229	0.1817557	-3.94	FALSE
253775_at	putative protein T01B08.14 gene	---	AT4G28440	-1.28	-0.36	-2.60	0.0364687	0.1819448	-3.94	FALSE
262188_at	Avr9 elicitor response protein, p	---	AT1G77810	1.40	0.49	2.60	0.0365275	0.1821175	-3.94	FALSE
253144_at	putative protein transcription fac	---	AT4G35540	-1.32	-0.40	-2.60	0.0365249	0.1821175	-3.94	FALSE
264851_at	putative calmodulin-domain prot	CPK6	AT2G17290	1.73	0.79	2.60	0.0365353	0.1821175	-3.94	FALSE
257535_at	hypothetical protein predicted by	---	AT3G09490	1.86	0.90	2.60	0.036516	0.1821175	-3.94	FALSE
252120_at	putative protein lin-10 protein - F	---	AT3G51130	1.38	0.46	2.60	0.0365577	0.1821895	-3.94	FALSE
252329_at	putative protein several hypothet	---	AT3G48760	1.29	0.37	2.60	0.036586	0.1822907	-3.94	FALSE
258264_at	unknown protein	MBD11	AT3G15790	1.43	0.52	2.60	0.0366834	0.1823119	-3.95	TRUE
261857_at	hypothetical protein predicted by	---	AT1G50620	-1.95	-0.96	-2.60	0.0366875	0.1823119	-3.95	TRUE
256006_at	hypothetical protein	---	AT1G34070	1.30	0.37	2.60	0.0367158	0.1823119	-3.95	FALSE
250695_at	lectin-like protein kinase	---	AT5G06740	2.28	1.19	2.60	0.0367261	0.1823119	-3.95	FALSE
246245_at	putative protein	---	AT4G36440	-1.33	-0.42	-2.60	0.0366871	0.1823119	-3.95	FALSE

245306_at	Expressed protein ; supported by	ELIP2	AT4G14690	1.42	0.51	2.60	0.0366549	0.1823119	-3.94	FALSE
246745_at	60S ribosomal protein L22 - like	---	AT5G27770	-1.69	-0.76	-2.60	0.0366771	0.1823119	-3.95	FALSE
254894_at	putative phospholipase D-gamm	PLDGAMM	AT4G11840	1.56	0.64	2.60	0.0367223	0.1823119	-3.95	FALSE
258612_at	putative replication factor A simil	---	AT3G02920	-1.36	-0.44	-2.60	0.0367258	0.1823119	-3.95	FALSE
263946_at	hypothetical protein ;supported b	---	AT2G36000	-1.39	-0.47	-2.60	0.0366167	0.1823119	-3.94	FALSE
255250_at	MYB - like protein cM4 myb tran	AtMYB74	AT4G05100	3.08	1.62	2.60	0.0366165	0.1823119	-3.94	FALSE
253053_at	putative protein beta-ketoadipate	---	AT4G37470	-1.46	-0.55	-2.60	0.0366307	0.1823119	-3.94	FALSE
249219_at	putative protein contains similarit	SDG25	AT5G42400	1.43	0.51	2.60	0.0367034	0.1823119	-3.95	FALSE
251757_at	Ca-dependent solute carrier - lik	---	AT3G55640	1.56	0.64	2.60	0.0367056	0.1823119	-3.95	FALSE
251438_s_a	putative protein hypothetical pro	---	AT3G59930 /	4.65	2.22	2.60	0.0366116	0.1823119	-3.94	FALSE
247611_at	putative protein predicted protein	---	AT5G60710	-1.29	-0.36	-2.60	0.0366852	0.1823119	-3.95	FALSE
250210_at	putative protein similar to unknov	---	AT5G13890	-1.39	-0.47	-2.60	0.0366686	0.1823119	-3.95	FALSE
261758_at	hypothetical protein contains sim	ADT6	AT1G08250	1.62	0.70	2.60	0.0367799	0.182462	-3.95	TRUE
259278_at	hypothetical protein predicted by	---	AT3G01160	-1.40	-0.48	-2.60	0.0368284	0.182462	-3.95	FALSE
246235_at	putative protein	---	AT4G36830	1.42	0.51	2.60	0.036818	0.182462	-3.95	FALSE
258883_at	unknown protein predicted by ge	---	AT3G09970	-1.38	-0.47	-2.60	0.0367933	0.182462	-3.95	FALSE
258881_at	unknown protein ; supported by	---	AT3G06310	-1.36	-0.44	-2.60	0.0368071	0.182462	-3.95	FALSE
261970_at	glutamate decarboxylase (gad),	GAD2	AT1G65960	-1.50	-0.58	-2.60	0.0368262	0.182462	-3.95	FALSE
254791_at	SERINE CARBOXYPEPTIDASE	scpl20	AT4G12910	1.41	0.50	2.60	0.0367673	0.182462	-3.95	FALSE
253049_at	putative protein ; supported by cI	MEE59	AT4G37300	-1.88	-0.91	-2.60	0.036809	0.182462	-3.95	FALSE
263732_at	hypothetical protein predicted by	ARL2	AT1G59980	-1.37	-0.45	-2.60	0.0368164	0.182462	-3.95	FALSE
257948_at	hypothetical protein predicted by	APO4	AT3G21740	-1.37	-0.46	-2.60	0.0368662	0.1826096	-3.95	FALSE
261989_at	disease resistance protein, puta	---	AT1G33670	1.37	0.45	2.60	0.0368906	0.1826911	-3.95	FALSE
253693_at	Thioredoxin - like protein thioredo	ACHT2	AT4G29670	1.63	0.71	2.59	0.0369619	0.1830045	-3.95	FALSE
253916_at	hypothetical protein ;supported b	---	AT4G27240	-1.73	-0.79	-2.59	0.0369856	0.1830102	-3.95	FALSE
264810_at	putative GPI-anchor transamidas	---	AT1G08750	-1.39	-0.48	-2.59	0.0369871	0.1830102	-3.95	FALSE
249078_at	phytochelatin synthase (gb|AAD4	CAD1	AT5G44070	2.35	1.23	2.59	0.0369769	0.1830102	-3.95	FALSE
245713_at	S-adenosyl-L-methionine:salicylic	NAMT1	AT5G04370	1.51	0.60	2.59	0.0370173	0.1831195	-3.95	FALSE
245301_at	farnesyl-pyrophosphate syntheta	FPS2	AT4G17190	-1.80	-0.85	-2.59	0.0370439	0.1831752	-3.96	FALSE
266313_at	putative protein kinase contains a	CIPK3	AT2G26980	-1.70	-0.77	-2.59	0.0370446	0.1831752	-3.96	FALSE
245729_at	unknown protein	---	AT1G73490	-1.43	-0.51	-2.59	0.0370784	0.1833027	-3.96	FALSE
252218_at	putative protein some putative pr	---	AT3G50150	1.32	0.40	2.59	0.0371192	0.1834643	-3.96	FALSE
263054_at	putative cation transport protein	---	AT2G04620	-1.33	-0.41	-2.59	0.0371408	0.1835067	-3.96	FALSE
265385_at	putative diacylglycerol kinase ;su	---	AT2G20900	1.68	0.75	2.59	0.0371438	0.1835067	-3.96	FALSE
249285_at	unknown protein	---	AT5G41960	-1.42	-0.50	-2.59	0.037161	0.1835121	-3.96	FALSE

254626_at	hypothetical protein ; supported	---	AT4G18400	-1.39	-0.48	-2.59	0.0371572	0.1835121	-3.96	FALSE
249575_at	low-molecular-weight heat shocl	---	AT5G37670	-1.56	-0.64	-2.59	0.0372156	0.1835606	-3.96	TRUE
260606_at	putative splicing factor	---	AT2G43770	-1.56	-0.65	-2.59	0.0372191	0.1835606	-3.96	FALSE
257753_at	60S ribosomal protein, putative	---	AT3G18740	-1.56	-0.65	-2.59	0.0371891	0.1835606	-3.96	FALSE
264718_at	receptor-like kinase, putative sin	---	AT1G70130	1.28	0.35	2.59	0.0372049	0.1835606	-3.96	FALSE
260956_at	salt-tolerance protein identical to	STO	AT1G06040	-1.31	-0.39	-2.59	0.0371853	0.1835606	-3.96	FALSE
265944_at	putative SET-domain transcriptio	ASHR2	AT2G19640	1.41	0.50	2.59	0.0372139	0.1835606	-3.96	FALSE
264211_at	putative gigantea protein strong	GI	AT1G22770	-1.28	-0.35	-2.59	0.0372291	0.18357	-3.96	FALSE
245346_at	putative beta-amylase ;supporte	CT-BMY	AT4G17090	-1.43	-0.51	-2.59	0.037248	0.1836196	-3.96	FALSE
258156_at	unknown protein ; supported by	---	AT3G18050	-1.79	-0.84	-2.59	0.0372552	0.1836196	-3.96	FALSE
264589_at	hypothetical protein	---	AT2G17650	-1.45	-0.54	-2.59	0.0372767	0.1836859	-3.96	FALSE
249785_at	soluble starch synthase	SSI1	AT5G24300	-1.37	-0.45	-2.59	0.0372855	0.1836897	-3.96	FALSE
251969_at	Cytochrom P450 -like protein CY	LUT1	AT3G53130	-1.46	-0.54	-2.59	0.0372938	0.1836909	-3.96	FALSE
265831_at	unknown protein	---	AT2G14460	-1.93	-0.94	-2.59	0.0373595	0.1838156	-3.96	TRUE
259162_at	unknown protein similar to unkno	---	AT3G01640	1.42	0.51	2.59	0.0373585	0.1838156	-3.96	FALSE
252458_at	putative protein various predicte	---	AT3G47210	1.31	0.39	2.59	0.0373286	0.1838156	-3.96	FALSE
261353_at	hypothetical protein contains sim	---	AT1G79600	1.55	0.63	2.59	0.0373462	0.1838156	-3.96	FALSE
253663_at	putative villin	VLN4	AT4G30160	1.36	0.45	2.59	0.0373459	0.1838156	-3.96	FALSE
250833_at	myotubularin - like protein myotu	---	AT5G04540	1.32	0.40	2.59	0.0373836	0.1838949	-3.96	FALSE
253117_at	Expressed protein ; supported by	---	AT4G35905	-1.44	-0.53	-2.59	0.0374096	0.1839435	-3.97	FALSE
254642_at	putative protein hypothetical pro	---	AT4G18810	-1.68	-0.75	-2.59	0.0374041	0.1839435	-3.97	FALSE
252993_at	monooxygenase 2 (MO2)	---	AT4G38540	-1.83	-0.87	-2.59	0.0374329	0.1840183	-3.97	TRUE
263821_s_a	40S ribosomal protein S16 Same	---	AT2G09990 /	-1.53	-0.62	-2.58	0.0375017	0.1841908	-3.97	FALSE
249145_at	enoyl CoA hydratase-like protein	ATDCI1	AT5G43280	1.29	0.37	2.58	0.0374801	0.1841908	-3.97	FALSE
251475_at	putative protein other hypothetica	---	AT3G59660	1.64	0.71	2.58	0.037501	0.1841908	-3.97	FALSE
258623_at	unknown protein ; supported by	---	AT3G02790	-1.84	-0.88	-2.58	0.0375084	0.1841908	-3.97	FALSE
263250_at	putative fructokinase ; supporte	---	AT2G31390	1.87	0.90	2.58	0.0374869	0.1841908	-3.97	FALSE
256172_at	hypothetical protein	---	AT1G51745	1.30	0.37	2.58	0.0375317	0.1842657	-3.97	FALSE
248881_at	unknown protein ;supported by f	---	AT5G46020	-1.27	-0.35	-2.58	0.0375405	0.1842691	-3.97	FALSE
266516_at	putative glutaredoxin ;supported	---	AT2G47880	-2.05	-1.04	-2.58	0.0375689	0.1843687	-3.97	TRUE
257721_at	hypothetical protein predicted by	---	AT3G18310	-1.27	-0.34	-2.58	0.0376059	0.1845105	-3.97	FALSE
255093_s_a	putative microfibril-associated pr	---	AT4G08580 /	-1.28	-0.36	-2.58	0.0376163	0.1845219	-3.97	FALSE
247295_at	putative protein similar to unknov	---	AT5G64180	-1.36	-0.44	-2.58	0.0376311	0.1845445	-3.97	FALSE
260769_at	Expressed protein ; supported by	---	AT1G49010	-1.68	-0.75	-2.58	0.037637	0.1845445	-3.97	FALSE
252334_at	mitochondrial phosphate transpo	---	AT3G48850	3.81	1.93	2.58	0.0376599	0.1846169	-3.97	TRUE

245870_at	hypothetical protein similar to hyp	---	AT1G26300	1.31	0.39	2.58	0.0376919	0.1846942	-3.97	FALSE
259404_at	type 2A protein serine/threonine	ATB BETA	AT1G17720	1.25	0.32	2.58	0.0376894	0.1846942	-3.97	FALSE
262517_at	putative glutathione transferase S	ATGSTU25	AT1G17180	5.53	2.47	2.58	0.0377033	0.1847105	-3.97	FALSE
252413_at	40S ribosomal protein S20-like p	---	AT3G47370	-1.80	-0.85	-2.58	0.0377249	0.1847766	-3.97	FALSE
257875_at	hypothetical protein	---	AT3G17120	1.36	0.44	2.58	0.0377521	0.1848703	-3.97	FALSE
250181_at	tRNA synthase - like protein tRN	---	AT5G14460	-1.35	-0.43	-2.58	0.0377741	0.1849381	-3.97	FALSE
259302_at	unknown protein	GID1A	AT3G05120	-1.53	-0.61	-2.58	0.0377959	0.1850053	-3.98	FALSE
262033_at	terminal ear1, putative similar to	MCT1	AT1G37140	1.36	0.44	2.58	0.0378444	0.185203	-3.98	FALSE
259979_at	unknown protein ;supported by f	---	AT1G76600	1.92	0.94	2.58	0.0378978	0.185364	-3.98	TRUE
263525_at	putative MADS-box protein	AGL61	AT2G24840	1.44	0.52	2.58	0.0378937	0.185364	-3.98	FALSE
260789_s_a	acyl-CoA oxidase ACX3 identica	ACX3	AT1G06290 /	1.28	0.36	2.58	0.0379017	0.185364	-3.98	FALSE
267530_at	putative receptor-like protein kina	---	AT2G41890	-1.97	-0.98	-2.58	0.0379125	0.1853769	-3.98	FALSE
260291_at	putative protein kinase similar to	YDA	AT1G63700	1.26	0.33	2.58	0.0379306	0.1854259	-3.98	FALSE
254655_s_a	ribosomal protein L32 -like prote	---	AT4G18100 /	-1.63	-0.70	-2.57	0.0380186	0.1855381	-3.98	FALSE
257447_at	hypothetical protein predicted by	---	AT2G04230	-1.25	-0.32	-2.57	0.0380144	0.1855381	-3.98	FALSE
266073_at	putative signal recognition particl	---	AT2G18770	-1.33	-0.41	-2.58	0.0379976	0.1855381	-3.98	FALSE
251579_at	putative protein Bet1 homolog -	BS14A	AT3G58170	-1.31	-0.39	-2.58	0.0379869	0.1855381	-3.98	FALSE
259571_at	hypothetical protein	---	AT1G20410	-1.48	-0.57	-2.58	0.0380049	0.1855381	-3.98	FALSE
249150_at	inorganic phosphate transporter	PHT6	AT5G43340	1.30	0.37	2.58	0.037998	0.1855381	-3.98	FALSE
245788_at	hypothetical protein similar to hyp	---	AT1G32120 /	1.99	0.99	2.58	0.0379922	0.1855381	-3.98	FALSE
250801_at	pectinesterase	---	AT5G04960	-1.31	-0.38	-2.58	0.0379986	0.1855381	-3.98	FALSE
248170_at	ankyrin-repeat-containing protein	---	AT5G54620	1.48	0.56	2.57	0.0380353	0.1855798	-3.98	FALSE
258822_s_a	unknown protein contains Pfam p	---	AT3G07220 /	-1.65	-0.72	-2.57	0.0380444	0.1855845	-3.98	FALSE
264224_at	hypothetical protein predicted by	emb1688	AT1G67440	-1.38	-0.46	-2.57	0.038088	0.1857574	-3.98	FALSE
263416_at	hypothetical protein contains pro	---	AT2G17170	1.34	0.42	2.57	0.0380979	0.1857659	-3.98	FALSE
258675_at	putative nonspecific lipid-transfer	LTP6	AT3G08770	1.34	0.43	2.57	0.0381159	0.1858142	-3.98	FALSE
259293_at	putative DNA binding protein sim	---	AT3G11580	1.67	0.74	2.57	0.0381247	0.1858171	-3.98	FALSE
248762_at	Expressed protein ; supported by	---	AT5G47455	-1.62	-0.69	-2.57	0.0381736	0.1859852	-3.99	FALSE
258223_at	unknown protein ; supported by	PIFI	AT3G15840	-1.39	-0.47	-2.57	0.0381755	0.1859852	-3.99	FALSE
258683_at	putative protein kinase contains I	ATSIK	AT3G08760	1.69	0.76	2.57	0.0381864	0.1859989	-3.99	FALSE
259584_at	hypothetical protein predicted by	---	AT1G28080	1.29	0.36	2.57	0.0382344	0.186034	-3.99	FALSE
258452_at	alternative oxidase 1a precursor	AOX1A	AT3G22370	2.58	1.36	2.57	0.0382232	0.186034	-3.99	FALSE
266955_at	mitochondrial ribosomal protein S	RPS14	AT2G34520	-1.40	-0.49	-2.57	0.038232	0.186034	-3.99	FALSE
248868_at	putative protein similar to unknov	---	AT5G46780	1.92	0.94	2.57	0.0382338	0.186034	-3.99	FALSE
260207_at	putative phosphoglucomutase sir	---	AT1G70730	-1.49	-0.58	-2.57	0.0382073	0.186034	-3.99	FALSE

250424_at	bromodomain protein - like brom	GTE2	AT5G10550	1.28	0.36	2.57	0.0382497	0.1860509	-3.99	FALSE
257663_at	hypothetical protein predicted by	---	AT3G20260	-1.34	-0.42	-2.57	0.0382542	0.1860509	-3.99	FALSE
252437_at	putative protein pectinesterase h	---	AT3G47380	2.27	1.18	2.57	0.0382687	0.1860814	-3.99	FALSE
263082_at	putative nucleotide-binding prote	---	AT2G27200	1.26	0.33	2.57	0.0382786	0.1860899	-3.99	FALSE
260530_at	putative peptidyl-prolyl cis-trans i	---	AT2G47320	-1.29	-0.36	-2.57	0.0382936	0.1861234	-3.99	FALSE
262385_at	root hair defective, putative simil	---	AT1G72960	1.26	0.34	2.57	0.0383456	0.1862969	-3.99	FALSE
255539_at	putative actin polymerization fac	CRK	AT4G01710	-1.35	-0.44	-2.57	0.0383397	0.1862969	-3.99	FALSE
248748_at	putative protein contains similarit	AMK2	AT5G47840	-1.34	-0.43	-2.57	0.0383702	0.1863486	-3.99	FALSE
249355_at	hypothetical protein	---	AT5G40500	-1.31	-0.39	-2.57	0.0383726	0.1863486	-3.99	FALSE
251670_at	putative protein translation relea	---	AT3G57190	-1.44	-0.53	-2.57	0.0384065	0.1864337	-3.99	FALSE
251843_x_a	extensin precursor -like protein e	ATHRGP1	AT3G54590	1.74	0.80	2.57	0.0384027	0.1864337	-3.99	FALSE
250739_at	putative protein similar to unknov	EGY2	AT5G05740	-1.53	-0.62	-2.57	0.0384436	0.1865741	-3.99	FALSE
249406_at	putative protein MtN21, Medicag	---	AT5G40210	1.41	0.50	2.57	0.0384784	0.1867034	-3.99	FALSE
246949_at	cytochrome P450-like protein CY	CYP71B13	AT5G25140	-2.47	-1.30	-2.57	0.0384979	0.1867584	-3.99	TRUE
251059_at	serine/threonine protein kinase A	CIPK15	AT5G01810	2.21	1.15	2.57	0.0385191	0.1868215	-3.99	FALSE
248655_at	60S ribosomal protein L13a ;sup	---	AT5G48760	-1.50	-0.58	-2.56	0.0385715	0.186956	-4.00	FALSE
258818_at	putative ethylene receptor (EIN4	EIN4	AT3G04580	1.40	0.49	2.56	0.0385577	0.186956	-4.00	FALSE
266110_at	putative C2H2-type zinc finger pr	AtIDD4	AT2G02080	-1.36	-0.45	-2.56	0.0385704	0.186956	-4.00	FALSE
262701_at	hypothetical protein predicted by	---	AT1G16480	-1.40	-0.49	-2.56	0.0386952	0.1872859	-4.00	FALSE
246462_at	putative protein predicted protei	---	AT5G16940	-1.59	-0.67	-2.56	0.0386839	0.1872859	-4.00	FALSE
266675_s_a	hypothetical protein predicted by	---	AT2G29610 ///	1.25	0.32	2.56	0.0386825	0.1872859	-4.00	FALSE
252797_at	putative protein	---	---	1.49	0.58	2.56	0.0386491	0.1872859	-4.00	FALSE
267513_at	unknown protein ; supported by	---	AT2G45620	-1.35	-0.43	-2.56	0.0386569	0.1872859	-4.00	FALSE
256334_at	oligopeptide transporter, putative	---	AT1G72120 ///	1.52	0.60	2.56	0.0386955	0.1872859	-4.00	FALSE
252831_at	2-dehydro-3-deoxyphosphohepto	DHS1	AT4G39980	2.43	1.28	2.56	0.038697	0.1872859	-4.00	FALSE
259592_at	lipid transfer protein, putative co	LTPG1	AT1G27950	2.43	1.28	2.56	0.0387196	0.1873157	-4.00	TRUE
248549_at	putative protein contains similarit	---	AT5G50310	-1.32	-0.40	-2.56	0.0387167	0.1873157	-4.00	FALSE
257188_at	hypothetical protein contains Pfa	---	AT3G13150	-1.38	-0.47	-2.56	0.0387443	0.1873561	-4.00	FALSE
246956_at	unknown protein ; supported by	RTM2	AT5G04890	1.34	0.42	2.56	0.038741	0.1873561	-4.00	FALSE
251920_at	uracil phosphoribosyltransferase	---	AT3G53900	-1.86	-0.90	-2.56	0.038799	0.1873718	-4.00	TRUE
246196_at	hypothetical protein ;supported b	---	AT4G37090	-1.52	-0.60	-2.56	0.0387725	0.1873718	-4.00	FALSE
261286_at	unknown protein ; supported by c	---	AT1G35780	-1.45	-0.54	-2.56	0.0387892	0.1873718	-4.00	FALSE
246536_at	putative protein KIAA0594 - Hon	---	AT5G15920	-2.02	-1.02	-2.56	0.0387567	0.1873718	-4.00	FALSE
253296_at	putative protein inositol 1,3,4-tris	---	AT4G33770	1.31	0.39	2.56	0.0388051	0.1873718	-4.00	FALSE
266918_at	putative LIM-domain protein	---	AT2G45800	1.28	0.36	2.56	0.0388006	0.1873718	-4.00	FALSE

245768_at	hypothetical protein similar to put	---	AT1G33590	1.94	0.96	2.56	0.0387991	0.1873718	-4.00	FALSE
260228_at	putative cytochrome P450 simila	CYP98A8	AT1G74540	1.34	0.42	2.56	0.0388462	0.1875304	-4.00	FALSE
248241_at	unknown protein	---	AT5G53960	1.31	0.38	2.56	0.0388638	0.1875759	-4.00	FALSE
263502_s_a	hypothetical protein	---	AT2G07675	1.59	0.67	2.56	0.0388865	0.1876457	-4.00	FALSE
250893_at	putative protein predicted protein	EMB175	AT5G03795 /,	1.29	0.36	2.56	0.0389417	0.1878326	-4.01	FALSE
256422_at	unknown protein	MOS2	AT1G33520	-1.34	-0.42	-2.56	0.0389408	0.1878326	-4.01	FALSE
254200_at	putative protein predicted protein	---	AT4G24110	3.67	1.88	2.56	0.0389735	0.1879461	-4.01	FALSE
262362_at	disease resistance protein, puta	---	AT1G72840	-1.31	-0.39	-2.56	0.0390115	0.1880501	-4.01	FALSE
246743_at	putative protein predicted protein	---	AT5G27750	-1.38	-0.47	-2.56	0.0390094	0.1880501	-4.01	FALSE
261480_at	phytochrome kinase substrate 1	PKS2	AT1G14280	-2.92	-1.54	-2.56	0.0390247	0.1880736	-4.01	TRUE
251786_at	phosphatase - like protein DUAL	MKP1	AT3G55270	1.30	0.38	2.56	0.0390983	0.1881503	-4.01	FALSE
245428_at	putative protein	---	AT4G17570	-1.34	-0.42	-2.56	0.0390582	0.1881503	-4.01	FALSE
245773_at	hypothetical protein predicted by	---	AT1G30290	-1.34	-0.42	-2.56	0.0390614	0.1881503	-4.01	FALSE
256479_at	unknown protein	---	AT1G33400	-1.48	-0.56	-2.56	0.0390704	0.1881503	-4.01	FALSE
260189_at	putative urease similar to urease	URE	AT1G67550	-1.40	-0.49	-2.56	0.0390835	0.1881503	-4.01	FALSE
247469_at	Expressed protein ; supported by	AGL42	AT5G62165	-4.08	-2.03	-2.56	0.0390919	0.1881503	-4.01	FALSE
260357_at	unknown protein ;supported by fu	AFP1	AT1G69260	1.46	0.55	2.56	0.0390982	0.1881503	-4.01	FALSE
259346_at	putative glutamate dehydrogenas	GDH3	AT3G03910	1.29	0.36	2.55	0.0391379	0.1882697	-4.01	FALSE
260830_at	histone H1, putative similar to hi	---	AT1G06760	-1.66	-0.73	-2.55	0.0391514	0.1882697	-4.01	TRUE
252166_at	protein kinase SPK-2 ;supported	SNRK2.2	AT3G50500	-1.42	-0.51	-2.55	0.0391561	0.1882697	-4.01	FALSE
255728_at	unknown protein	---	AT1G25500	1.67	0.74	2.55	0.0391481	0.1882697	-4.01	FALSE
263137_at	gamma glutamyl hydrolase, puta	ATGGH1	AT1G78660	1.83	0.87	2.55	0.0391831	0.1883598	-4.01	FALSE
262189_at	GTPase, putative similar to GTP	---	AT1G78010	-1.34	-0.43	-2.55	0.0392039	0.1883934	-4.01	FALSE
260426_at	putative 40S ribosomal protein S	P40	AT1G72370	-1.71	-0.77	-2.55	0.0392066	0.1883934	-4.01	FALSE
251689_at	putative protein motif in hypothe	---	AT3G56500	2.75	1.46	2.55	0.0392276	0.1884496	-4.01	FALSE
260303_at	putative protein kinase similar to	---	AT1G70520	1.84	0.88	2.55	0.0392349	0.1884496	-4.01	FALSE
257022_at	zinc finger protein, putative simil	AZF2	AT3G19580	1.45	0.54	2.55	0.039279	0.18854	-4.01	TRUE
251830_at	phosphoribosylformylglycinamidi	PUR5	AT3G55010	-1.69	-0.75	-2.55	0.0392786	0.18854	-4.01	FALSE
255682_at	putative dTDP-6-deoxy-L-manno	---	AT4G00560	-1.34	-0.42	-2.55	0.0392857	0.18854	-4.01	FALSE
259577_at	unknown protein	---	AT1G35340	-1.45	-0.54	-2.55	0.0392867	0.18854	-4.01	FALSE
246926_at	putative protein	---	AT5G25240	-1.67	-0.74	-2.55	0.0393144	0.1886048	-4.01	TRUE
264505_at	putative nodulin protein, N21 Sir	---	AT1G09380	1.54	0.63	2.55	0.0393168	0.1886048	-4.02	FALSE
259967_at	putative DNA-binding protein cor	---	AT1G76510	-1.28	-0.36	-2.55	0.0393287	0.1886221	-4.02	FALSE
255113_at	putative protein various hypothe	---	---	1.31	0.39	2.55	0.0393541	0.1887043	-4.02	FALSE
245033_at	putative disease resistance prote	---	AT2G26380	1.31	0.39	2.55	0.0394139	0.188795	-4.02	FALSE

245101_at	putative cytochrome P450 ; supp	CYP98A3	AT2G40890	1.53	0.62	2.55	0.0394136	0.188795	-4.02	FALSE
260164_at	putative D-isomer specific 2-hydr	---	AT1G79870	-1.33	-0.41	-2.55	0.0393961	0.188795	-4.02	FALSE
254703_at	putative protein ; supported by fu	---	AT4G17960	-1.50	-0.58	-2.55	0.0394032	0.188795	-4.02	FALSE
265333_at	hypothetical protein predicted by	AtHB24	AT2G18350	1.46	0.55	2.55	0.0394144	0.188795	-4.02	FALSE
254991_at	putative protein conserved hypo	---	AT4G10620	-1.42	-0.50	-2.55	0.0394268	0.1888147	-4.02	FALSE
253692_at	putative protein Cs protein, Dros	ATPAO5	AT4G29720	-1.26	-0.34	-2.55	0.0394419	0.1888473	-4.02	FALSE
254963_at	putative protein single strand DN	MTSSB	AT4G11060	-1.38	-0.46	-2.55	0.0394567	0.1888789	-4.02	FALSE
255983_at	polyneuridine aldehyde esterase	MES14	AT1G33990	-1.33	-0.42	-2.55	0.0394796	0.1889093	-4.02	FALSE
256959_at	methyltransferase, putative	---	AT3G13440	-1.27	-0.34	-2.55	0.0394745	0.1889093	-4.02	FALSE
262783_at	receptor-kinase isolog	---	AT1G10850	-1.84	-0.88	-2.55	0.0395226	0.1890753	-4.02	FALSE
AFFX-DapX	B. subtilis /GEN=jojG /DB_XREF	---	---	-1.42	-0.50	-2.55	0.0395472	0.1891532	-4.02	FALSE
258136_at	hypothetical protein predicted by	RSY3	AT3G24560	-1.39	-0.47	-2.55	0.0395636	0.1891737	-4.02	FALSE
255040_at	putative protein hypothetical pro	---	AT4G09580	1.36	0.44	2.55	0.0395681	0.1891737	-4.02	FALSE
259540_at	nodule inception protein, putativ	---	AT1G20640	-1.65	-0.72	-2.55	0.0396006	0.1892894	-4.02	FALSE
250762_at	putative protein similar to unknov	---	AT5G05990	-1.88	-0.91	-2.55	0.0396228	0.1893559	-4.02	FALSE
250732_at	putative protein contains similarit	---	AT5G06480	-1.66	-0.73	-2.55	0.0396477	0.1894355	-4.02	FALSE
252450_s_a	receptor kinase-like protein rece	---	AT3G47090 //	1.79	0.84	2.54	0.039697	0.1896311	-4.02	FALSE
253530_at	putative protein hypothetical pro	---	AT4G31530	-1.69	-0.76	-2.54	0.039715	0.1896772	-4.03	FALSE
266725_at	SKP1/ASK1 (At14), putative sim	ASK14	AT2G03170	1.31	0.39	2.54	0.0397676	0.1898887	-4.03	FALSE
262498_at	8-oxoguanine DNA glycosylase-l	OGG1	AT1G21710	-1.36	-0.45	-2.54	0.0397843	0.1899287	-4.03	FALSE
266224_at	chloroplast membrane protein (A	ALB3	AT2G28800	-1.28	-0.35	-2.54	0.0397995	0.1899618	-4.03	FALSE
248804_at	nodulin-like protein	---	AT5G47470	1.35	0.43	2.54	0.0398336	0.1900577	-4.03	FALSE
253765_at	hypothetical protein ;supported b	---	AT4G28740	-1.70	-0.77	-2.54	0.0398363	0.1900577	-4.03	FALSE
267361_at	hypothetical protein predicted by	---	AT2G39920	-1.63	-0.70	-2.54	0.0398467	0.1900674	-4.03	FALSE
265474_at	Expressed protein ; supported by	---	AT2G15690	-1.63	-0.70	-2.54	0.0398638	0.1901093	-4.03	FALSE
264203_at	putative 40S ribosomal protein S	PFL	AT1G22780	-1.87	-0.90	-2.54	0.0399587	0.190522	-4.03	FALSE
248710_at	unknown protein ;supported by f	---	AT5G48480	-1.46	-0.54	-2.54	0.0399749	0.1905598	-4.03	TRUE
254333_at	predicted protein predicted prote	SMO1-3	AT4G22753	2.38	1.25	2.54	0.0400373	0.1908081	-4.03	FALSE
264228_at	hypothetical protein contains sim	GCS1	AT1G67490	-1.34	-0.42	-2.54	0.0400521	0.1908081	-4.03	FALSE
254487_at	calcium-binding protein - like cal	---	AT4G20780	2.99	1.58	2.54	0.0400484	0.1908081	-4.03	FALSE
258012_at	unknown protein similar to GB:C/	---	AT3G19310	1.25	0.33	2.54	0.0400663	0.1908357	-4.03	FALSE
249309_at	homeotic protein BEL1 homolog	BEL1	AT5G41410	-1.41	-0.49	-2.54	0.0401217	0.1909002	-4.04	TRUE
256110_at	Ser Thr protein kinase, putative	---	AT1G16900	-1.51	-0.59	-2.54	0.0400999	0.1909002	-4.03	FALSE
247410_at	putative protein similar to unknov	emb1692	AT5G62990	-1.72	-0.78	-2.54	0.0400931	0.1909002	-4.03	FALSE
246807_at	ion channel - like protein ligand (	GLR2.1	AT5G27100	1.50	0.59	2.54	0.0401194	0.1909002	-4.04	FALSE

252016_at	putative protein predicted protei	---	AT3G52950	1.33	0.41	2.54	0.0401204	0.1909002	-4.04	FALSE
253946_at	putative APG protein proline-rich	---	AT4G26790	1.57	0.65	2.54	0.0401444	0.1909685	-4.04	FALSE
260358_at	unknown protein ; supported by c	---	AT1G69340	-1.29	-0.36	-2.54	0.0401599	0.1910024	-4.04	FALSE
246860_at	putative protein various predicte	---	AT5G25840	-2.18	-1.12	-2.54	0.0402299	0.1912955	-4.04	FALSE
253160_at	putative protein predicted protei	---	AT4G35760	-1.56	-0.64	-2.54	0.040242	0.1913129	-4.04	FALSE
250941_at	putative protein	---	AT5G03320	1.43	0.52	2.53	0.0402557	0.1913383	-4.04	FALSE
259070_at	digalactosyldiacylglycerol syntha	DGD1	AT3G11670	-1.78	-0.83	-2.53	0.0403106	0.1915195	-4.04	FALSE
261084_at	tropinone reductase-I, putative s	---	AT1G07440	-1.62	-0.70	-2.53	0.0403088	0.1915195	-4.04	FALSE
255593_at	hypothetical protein	---	AT4G01650	-1.33	-0.41	-2.53	0.040337	0.1915397	-4.04	FALSE
259096_at	putative 40S ribosomal protein S	---	AT3G04840	-1.92	-0.94	-2.53	0.0403347	0.1915397	-4.04	FALSE
259320_at	putative DNA-binding protein sim	WRKY58	AT3G01080	2.32	1.21	2.53	0.0403401	0.1915397	-4.04	FALSE
246396_at	carbonic anhydrase, putative sir	BCA6	AT1G58180	1.55	0.64	2.53	0.040374	0.1916607	-4.04	FALSE
251068_at	putative protein several protein k	STN8	AT5G01920	-1.60	-0.68	-2.53	0.0403846	0.1916713	-4.04	FALSE
250009_at	putative protein nuclear FMRP ir	---	AT5G18440	-1.84	-0.88	-2.53	0.0404103	0.1916785	-4.04	TRUE
255701_at	predicted protein of unknown fun	JLO	AT4G00220	1.28	0.36	2.53	0.0404113	0.1916785	-4.04	FALSE
267490_at	putative receptor-like protein kina	---	AT2G19130	1.76	0.82	2.53	0.0404112	0.1916785	-4.04	FALSE
255309_at	hypothetical protein	SFR6	AT4G04920	1.27	0.35	2.53	0.0404423	0.1917857	-4.04	FALSE
252391_at	putative protein ; supported by c	---	AT3G47860	-1.41	-0.50	-2.53	0.0404829	0.1919382	-4.04	FALSE
245544_at	UTP-glucose glucosyltransferase	---	AT4G15270	1.37	0.46	2.53	0.0404925	0.1919437	-4.04	FALSE
245509_at	hypothetical protein	---	AT4G15730	-1.41	-0.49	-2.53	0.0405288	0.1920761	-4.05	FALSE
263678_at	hypothetical protein Similar to Ba	---	AT1G04420	-1.60	-0.68	-2.53	0.0405428	0.1921023	-4.05	FALSE
246984_at	cytochrome P450	CYP81G1	AT5G67310	2.76	1.47	2.53	0.0405514	0.1921031	-4.05	TRUE
250651_at	cytochrome P450	CYP93D1	AT5G06900	1.25	0.33	2.53	0.0405625	0.1921161	-4.05	FALSE
253682_at	cytidine deaminase 5 (CDA5)	---	AT4G29640	1.42	0.51	2.53	0.0405799	0.1921584	-4.05	FALSE
247491_at	putative protein supported by cD	---	AT5G61880	-1.76	-0.82	-2.53	0.0405887	0.1921602	-4.05	FALSE
251864_at	pectate lyase - like protein pecta	PMR6	AT3G54920	-1.43	-0.52	-2.53	0.0406193	0.1921854	-4.05	TRUE
247613_at	xABC transporter - like protein b	---	AT5G60740	1.40	0.49	2.53	0.0406085	0.1921854	-4.05	FALSE
254289_at	putative protein predicted protei	---	AT4G22980	3.38	1.76	2.53	0.0406167	0.1921854	-4.05	FALSE
250729_at	ubiquitin activating enzyme 2 (UE	UBA 2	AT5G06460	-1.33	-0.41	-2.53	0.0406953	0.1925049	-4.05	FALSE
265197_at	putative glucosyl transferase	UGT73C1	AT2G36750	1.26	0.33	2.53	0.0407105	0.1925372	-4.05	FALSE
249125_at	1-aminocyclopropane-1-carboxyl	---	AT5G43450	-1.58	-0.66	-2.53	0.0407256	0.1925687	-4.05	TRUE
248335_at	putative protein strong similarity t	---	AT5G52450	1.64	0.72	2.53	0.0407367	0.1925814	-4.05	TRUE
259982_at	putative RING zinc finger protein	ATL8	AT1G76410	2.24	1.16	2.53	0.0408183	0.1929268	-4.05	FALSE
247873_at	diacylglycerol kinase-like protein	---	AT5G57690	1.29	0.37	2.52	0.0408576	0.1930713	-4.05	FALSE
264948_at	RNA helicase, putative similar to	---	AT1G77030	1.30	0.38	2.52	0.0408658	0.1930713	-4.05	FALSE

247447_at	nitrate transporter NTL1 - like pr	---	AT5G62730	-2.02	-1.01	-2.52	0.0408849	0.1931217	-4.05	FALSE
261134_at	cytochrome P450, putative simil	CYP722A1	AT1G19630	1.31	0.39	2.52	0.0408976	0.1931416	-4.05	FALSE
266505_at	unknown protein	---	AT2G47830	1.31	0.38	2.52	0.0409208	0.193211	-4.06	FALSE
261752_at	putative AMP-binding protein cor	---	AT1G76290	1.34	0.42	2.52	0.0409494	0.1933062	-4.06	FALSE
267036_at	Expressed protein ; supported by	---	AT2G38465	-1.68	-0.75	-2.52	0.0410328	0.1935399	-4.06	FALSE
265445_at	60S ribosomal protein L12 ;supp	---	AT2G37190	-2.14	-1.10	-2.52	0.0410328	0.1935399	-4.06	FALSE
265711_at	unknown protein	---	AT2G03360	1.27	0.34	2.52	0.041018	0.1935399	-4.06	FALSE
248332_at	heat-shock protein ; supported b	ATHSP90.1	AT5G52640	3.33	1.74	2.52	0.0410148	0.1935399	-4.06	FALSE
249475_at	putative protein CGI-108 protein	---	AT5G38890	-1.46	-0.55	-2.52	0.0410806	0.1936592	-4.06	TRUE
245242_at	chlorophyll a oxygenase identica	CH1	AT1G44446	-1.46	-0.54	-2.52	0.0410698	0.1936592	-4.06	FALSE
265659_at	putative disease resistance prote	AtRLP20	AT2G25440	1.93	0.95	2.52	0.0411037	0.1936592	-4.06	FALSE
261732_at	hypothetical protein predicted by	---	AT1G47770	1.33	0.41	2.52	0.0410933	0.1936592	-4.06	FALSE
258943_at	hypothetical protein predicted by	---	AT3G10400	1.38	0.46	2.52	0.0411091	0.1936592	-4.06	FALSE
249347_at	putative protein similar to unknov	---	AT5G40830	-1.75	-0.81	-2.52	0.0410845	0.1936592	-4.06	FALSE
254095_at	oleosin, 18.5K	OLEO1	AT4G25140	1.33	0.41	2.52	0.0411791	0.193909	-4.06	FALSE
262956_at	eukaryotic translation initiation fa	EIF4A-2	AT1G54270	1.38	0.47	2.52	0.0411721	0.193909	-4.06	FALSE
247634_at	late embryonic abundant protein	---	AT5G60520	1.26	0.33	2.52	0.0412006	0.19393	-4.06	FALSE
248302_at	putative protein similar to unknov	---	AT5G53160	-1.49	-0.57	-2.52	0.0411958	0.19393	-4.06	FALSE
262452_at	hypothetical protein similar to hyp	---	AT1G11210	-1.33	-0.41	-2.52	0.0412431	0.1940101	-4.06	TRUE
262712_at	mercaptopyruvate sulfurtransfera	ATRDH2	AT1G16460	-1.39	-0.47	-2.52	0.0412386	0.1940101	-4.06	FALSE
248446_at	putative protein similar to unknov	---	AT5G51140	-1.31	-0.39	-2.52	0.0412332	0.1940101	-4.06	FALSE
245345_at	proteinase like protein ;supported	---	AT4G16640	1.29	0.37	2.52	0.0412754	0.1941219	-4.06	FALSE
259361_at	glyceraldehyde-3-phosphate del	GAPC2	AT1G13440	-1.37	-0.45	-2.52	0.0413131	0.1942286	-4.06	FALSE
264887_at	unknown protein similar to ripen	---	AT1G23120	1.55	0.63	2.52	0.0413447	0.1942286	-4.07	FALSE
262220_at	calcium-dependent protein kinas	CPK30	AT1G74740	1.29	0.36	2.52	0.0413172	0.1942286	-4.06	FALSE
248019_at	putative protein similar to unknov	---	AT5G56480	1.33	0.41	2.52	0.0413532	0.1942286	-4.07	FALSE
257274_at	geranylgeranyl pyrophosphate s	---	AT3G14510	1.37	0.45	2.52	0.0413439	0.1942286	-4.07	FALSE
246205_at	hypothetical protein ; supported b	---	AT4G36970	-1.72	-0.78	-2.52	0.0413577	0.1942286	-4.07	FALSE
252976_s_a	Phospholipase like protein Arabi	---	AT4G38550	1.67	0.74	2.52	0.0413359	0.1942286	-4.07	FALSE
263374_at	putative heat shock protein ;sup	---	AT2G20560	1.79	0.84	2.52	0.0413908	0.1943044	-4.07	FALSE
264869_at	hypothetical protein similar to hyp	---	AT1G24350	1.32	0.40	2.52	0.0413901	0.1943044	-4.07	FALSE
247310_at	putative protein contains similarit	CHR24	AT5G63950	-1.49	-0.57	-2.52	0.041409	0.1943095	-4.07	FALSE
253793_at	myosin heavy chain - like protein	XIH	AT4G28710	1.27	0.35	2.52	0.0414051	0.1943095	-4.07	FALSE
259109_at	putative serine threonine protein	---	AT3G05580	1.56	0.64	2.51	0.0414184	0.1943137	-4.07	FALSE
264923_s_a	peroxiredoxin, putative similar to	---	AT1G60740 ///	1.87	0.90	2.51	0.0414458	0.1943623	-4.07	TRUE

255131_at	putative protein hypothetical pro	---	AT4G08280	-1.31	-0.39	-2.51	0.0414448	0.1943623	-4.07	FALSE
249753_at	putative protein similar to unknov	---	AT5G24610	1.25	0.33	2.51	0.0414676	0.194396	-4.07	FALSE
264319_at	subtilisin-like serine protease, pu	SDD1	AT1G04110	1.40	0.49	2.51	0.0414956	0.194396	-4.07	FALSE
262866_at	cytochrome p450, putative simila	CYP89A6	AT1G64940	1.27	0.35	2.51	0.0414793	0.194396	-4.07	FALSE
251850_at	F-box protein family, AtFBL17 c	FBL17	AT3G54650	-1.51	-0.60	-2.51	0.0414943	0.194396	-4.07	FALSE
262897_at	hypothetical protein predicted by	CCB4	AT1G59840	-2.00	-1.00	-2.51	0.0414885	0.194396	-4.07	FALSE
247474_at	putative protein predicted protei	---	AT5G62280	-5.68	-2.51	-2.51	0.041535	0.194461	-4.07	FALSE
245034_at	putative serpin	---	AT2G26390	1.44	0.53	2.51	0.0415334	0.194461	-4.07	FALSE
248256_at	developmental protein SINA (sev	---	AT5G53360	1.36	0.44	2.51	0.0415252	0.194461	-4.07	FALSE
252013_at	putative protein	---	AT3G52860	-1.30	-0.38	-2.51	0.0415582	0.1945297	-4.07	FALSE
251561_at	E2 ubiquitin-conjugating-like enz	SCE1	AT3G57870	-1.28	-0.36	-2.51	0.0415827	0.1946044	-4.07	FALSE
250955_at	putative protein various predicte	CPUORF47	AT5G03190	2.97	1.57	2.51	0.0415917	0.1946064	-4.07	FALSE
265174_s_a	polygalacturonase, putative simi	---	AT1G23460 /.	-1.53	-0.61	-2.51	0.0416145	0.1946733	-4.07	FALSE
260109_at	hypothetical protein predicted by	TET10	AT1G63260	1.43	0.51	2.51	0.0416403	0.194714	-4.07	TRUE
256478_at	unknown protein	---	---	1.36	0.45	2.51	0.041638	0.194714	-4.07	FALSE
252043_at	putative protein mttC protein, Es	---	AT3G52390	-1.38	-0.46	-2.51	0.041651	0.1947242	-4.07	FALSE
256858_at	hypothetical protein predicted by	---	AT3G15140	-1.52	-0.61	-2.51	0.0416609	0.1947306	-4.07	FALSE
251371_at	putative protein CGI-94 protein,	EDA14	AT3G60360	-1.64	-0.71	-2.51	0.041725	0.1949901	-4.07	FALSE
263249_at	delta 9 desaturase ALMOST ider	ADS2	AT2G31360	-1.29	-0.36	-2.51	0.0417845	0.195121	-4.08	FALSE
248267_at	NADH-dependent glutamate syn	GLT1	AT5G53460	-1.52	-0.61	-2.51	0.0417957	0.195121	-4.08	FALSE
260801_at	hypothetical protein predicted by	---	AT1G78430	1.24	0.31	2.51	0.0417891	0.195121	-4.08	FALSE
260299_at	putative gibberellin 3 beta-hydrox	GA3OX4	AT1G80330	1.25	0.32	2.51	0.0417724	0.195121	-4.08	FALSE
246223_at	UDP-glucuronyltransferase-like p	IRX14	AT4G36890	-1.29	-0.36	-2.51	0.0417888	0.195121	-4.08	FALSE
253114_at	GTP-binding protein GB2 ;suppo	ATGB2	AT4G35860	1.38	0.47	2.51	0.0418345	0.195262	-4.08	FALSE
264076_at	unknown protein	---	AT2G28540	-1.25	-0.33	-2.51	0.0418669	0.1953731	-4.08	FALSE
264106_at	unknown protein	SERK4	AT2G13790	1.30	0.37	2.51	0.0419224	0.195592	-4.08	FALSE
259471_at	hypothetical protein contains sim	---	AT1G19040	1.25	0.32	2.51	0.0419312	0.1955933	-4.08	FALSE
248651_at	unknown protein	---	AT5G49260	1.28	0.35	2.51	0.041954	0.1956594	-4.08	FALSE
262118_at	beta-glucosidase, putative simila	BGLU11	AT1G02850	-2.49	-1.32	-2.51	0.0419656	0.1956736	-4.08	FALSE
246262_at	hypothetical protein	---	AT1G31790	-1.50	-0.58	-2.51	0.0419818	0.1957093	-4.08	FALSE
247504_at	putative protein various predicte	---	AT5G61990	-1.51	-0.59	-2.50	0.0420257	0.1958737	-4.08	FALSE
255249_at	3(2),5-BISPHOSPHATE NUCLE	---	AT4G05090	-1.59	-0.67	-2.50	0.0420678	0.1960299	-4.08	FALSE
245389_at	putative protein ;supported by ful	---	AT4G17480	1.42	0.50	2.50	0.0420987	0.1961337	-4.08	FALSE
259273_s_a	serine/threonine specific protein	---	AT3G01300 /.	-1.32	-0.40	-2.50	0.0421277	0.1961912	-4.08	FALSE
255120_x_a	putative transposon protein simila	---	---	1.27	0.35	2.50	0.0421282	0.1961912	-4.08	FALSE

246973_at	putative protein UBIQUINONE B	---	AT5G24970	-1.55	-0.63	-2.50	0.042164	0.1963177	-4.08	FALSE
250852_at	putative protein BRL protein, Ho	---	AT5G04670	-1.27	-0.34	-2.50	0.0421996	0.1964067	-4.09	FALSE
252920_at	putative endo-1,4-beta-glucanas	AtGH9B17	AT4G39000	1.38	0.46	2.50	0.0422003	0.1964067	-4.09	FALSE
250436_at	RNA binding protein - like rna bi	---	AT5G10350	-1.36	-0.44	-2.50	0.0422418	0.1965595	-4.09	FALSE
253052_at	cytochrome P450-like protein ; su	CYP81H1	AT4G37310	1.95	0.97	2.50	0.0422622	0.1965744	-4.09	TRUE
247267_at	40S ribosomal protein S28 (sp|P	RPS28	AT5G64140	-1.82	-0.86	-2.50	0.0422536	0.1965744	-4.09	FALSE
246033_at	hydroxymethylbilane synthase ;s	HEMC	AT5G08280	-1.49	-0.57	-2.50	0.0423013	0.1967162	-4.09	FALSE
246058_at	putative protein predicted protei	---	AT5G08430	-1.35	-0.44	-2.50	0.0423401	0.1967205	-4.09	FALSE
263995_at	putative MADS-box protein	SVP	AT2G22540	-1.41	-0.49	-2.50	0.0423199	0.1967205	-4.09	FALSE
252672_at	hypothetical protein	---	AT3G44230	1.27	0.34	2.50	0.042354	0.1967205	-4.09	FALSE
247871_at	xyloglucan endotransglycosylase	---	AT5G57530	1.27	0.34	2.50	0.0423323	0.1967205	-4.09	FALSE
260753_at	RING-H2 finger protein RHA3a,	---	AT1G49230	-2.01	-1.00	-2.50	0.0423391	0.1967205	-4.09	FALSE
265715_s_a	expressed protein non-consensu	---	AT1G13860 ///	-1.70	-0.76	-2.50	0.0423485	0.1967205	-4.09	FALSE
260566_at	cysteine synthase (cpACS1) ;su	OASB	AT2G43750	-1.41	-0.50	-2.50	0.0423687	0.1967489	-4.09	FALSE
245785_at	cellulose synthase catalytic subu	ATCSLD6	AT1G32180	1.33	0.41	2.50	0.0424247	0.1969286	-4.09	FALSE
263359_at	putative lysosomal acid lipase	ATLIP1	AT2G15230	-1.40	-0.48	-2.50	0.042422	0.1969286	-4.09	FALSE
254679_at	putative protein Mei2-like protei	AML3	AT4G18120	-1.34	-0.42	-2.50	0.0424643	0.1969943	-4.09	FALSE
266064_at	expressed protein	---	AT2G18780	-1.44	-0.53	-2.50	0.0424576	0.1969943	-4.09	FALSE
266893_at	hypothetical protein predicted by	RTE1	AT2G26070	-1.36	-0.44	-2.50	0.042482	0.1969943	-4.09	FALSE
257541_at	hypothetical protein predicted by	---	AT3G25950	1.95	0.96	2.50	0.0424803	0.1969943	-4.09	FALSE
259030_at	putative alpha-hemolysin similar	---	AT3G09310	-1.24	-0.31	-2.50	0.0424712	0.1969943	-4.09	FALSE
258907_at	putative sodium proton exchange	NHX4	AT3G06370	1.36	0.45	2.50	0.0424994	0.1970346	-4.09	FALSE
266743_at	ribonuclease, RNS1 identical to	RNS1	AT2G02990 ///	4.11	2.04	2.50	0.0425463	0.1972121	-4.09	FALSE
252843_at	glycine-rich protein other glycine-	---	AT3G42130	1.43	0.52	2.50	0.0426001	0.1974215	-4.10	FALSE
262396_at	unknown protein ;supported by fu	---	AT1G49470	-1.83	-0.87	-2.49	0.0426533	0.1976279	-4.10	TRUE
257459_at	unknown protein	---	AT1G24040	-1.33	-0.41	-2.49	0.0426874	0.1977401	-4.10	FALSE
256816_at	unknown protein	---	AT3G21400	-1.35	-0.44	-2.49	0.0426949	0.1977401	-4.10	FALSE
250161_at	putative protein amino acid trans	---	AT5G15240	1.65	0.72	2.49	0.0427307	0.1978215	-4.10	FALSE
266523_at	putative transportin	TRN1	AT2G16950	1.30	0.38	2.49	0.0427375	0.1978215	-4.10	FALSE
251697_at	putative protein hypothetical pro	---	AT3G56600	1.25	0.32	2.49	0.0427385	0.1978215	-4.10	FALSE
250881_at	putative protein	---	AT5G04080	-1.52	-0.60	-2.49	0.0427844	0.1979941	-4.10	FALSE
250289_at	putative protein ;supported by fu	---	AT5G13190	1.95	0.97	2.49	0.0428358	0.1981419	-4.10	FALSE
265672_at	putative cysteine proteinase inhib	---	AT2G31980	-2.99	-1.58	-2.49	0.0428418	0.1981419	-4.10	FALSE
250547_at	asparaginase ; supported by cD	---	AT5G08100	-1.34	-0.42	-2.49	0.0428424	0.1981419	-4.10	FALSE
253073_at	cytochrome P450 monooxygena	CYP81F4	AT4G37410	1.39	0.47	2.49	0.0428588	0.1981774	-4.10	FALSE

250112_at	low density lipoprotein B-like prot	---	AT5G16300	1.29	0.37	2.49	0.0428725	0.1982004	-4.10	FALSE
252866_at	putative protein	---	AT4G39840	2.18	1.12	2.49	0.0429408	0.1982909	-4.10	TRUE
248675_at	putative protein similar to unknov	ICK6	AT5G48820	1.59	0.67	2.49	0.0429441	0.1982909	-4.10	FALSE
248640_at	selenium-binding protein-like ; s	---	AT5G48910	-1.38	-0.46	-2.49	0.0429096	0.1982909	-4.10	FALSE
260963_at	hypothetical protein predicted by	---	AT1G44990	1.32	0.40	2.49	0.0429313	0.1982909	-4.10	FALSE
249797_at	putative protein contains similarit	---	AT5G23750	-1.45	-0.53	-2.49	0.0429217	0.1982909	-4.10	FALSE
252821_at	putative protein ;supported by fu	---	AT4G39860	-1.99	-0.99	-2.49	0.0429442	0.1982909	-4.10	FALSE
245595_at	hypothetical protein	---	AT4G14170	-1.28	-0.36	-2.49	0.0429902	0.1984633	-4.10	FALSE
259966_at	unknown protein	SOB3	AT1G76500	1.35	0.44	2.49	0.0430055	0.1984934	-4.10	FALSE
258868_at	putative exportin1 (XPO1) protei	XPO1B	AT3G03110	-1.36	-0.44	-2.49	0.0430727	0.1985936	-4.11	FALSE
248237_at	receptor protein kinase-like prote	---	AT5G53890	-1.42	-0.51	-2.49	0.0430684	0.1985936	-4.11	FALSE
245253_at	hydroperoxide lyase (HPOL) like	HPL1	AT4G15440	4.20	2.07	2.49	0.043041	0.1985936	-4.11	FALSE
246130_at	putative protein various predicte	---	---	1.52	0.60	2.49	0.0430596	0.1985936	-4.11	FALSE
244971_at	ATP-dependent protease subuni	---	---	-1.32	-0.40	-2.49	0.0430616	0.1985936	-4.11	FALSE
255899_at	zinc-finger protein (C-terminal),	---	AT1G17970	-1.55	-0.63	-2.49	0.0430794	0.1985936	-4.11	FALSE
244972_at	PSII 47KDa protein	---	---	-2.07	-1.05	-2.49	0.0430932	0.1986172	-4.11	FALSE
246476_at	putative protein predicted protein	---	AT5G16730	-1.50	-0.58	-2.49	0.0431282	0.1986979	-4.11	FALSE
245082_at	hypothetical protein predicted by	---	AT2G23270	6.10	2.61	2.49	0.0431234	0.1986979	-4.11	FALSE
266365_at	ferredoxin-dependent glutamate	GLU2	AT2G41220	-1.47	-0.56	-2.49	0.043169	0.1988055	-4.11	FALSE
266763_at	unknown protein	SPL1	AT2G47070	-1.39	-0.47	-2.49	0.0431604	0.1988055	-4.11	FALSE
245618_at	hypothetical protein	---	AT4G14510	-1.39	-0.48	-2.49	0.0432136	0.198929	-4.11	FALSE
245453_at	disease resistance RPP5 like pro	---	AT4G16900	1.32	0.40	2.49	0.0432078	0.198929	-4.11	FALSE
248613_at	phytoene dehydrogenase-like	---	AT5G49555	-1.48	-0.57	-2.49	0.0432219	0.198929	-4.11	FALSE
250388_at	putative protein various predicte	---	AT5G11310	-1.89	-0.92	-2.48	0.0432749	0.1990926	-4.11	FALSE
265963_s_a	40S ribosomal protein S5 identic	ATRPS5B	AT2G37270 /	-1.75	-0.81	-2.48	0.0432739	0.1990926	-4.11	FALSE
264377_at	similar to early nodulins	---	AT2G25060	1.27	0.35	2.48	0.0433564	0.1991797	-4.11	FALSE
250649_at	thioredoxin-like ; supported by c	WCRKC1	AT5G06690	-1.38	-0.47	-2.48	0.0433637	0.1991797	-4.11	FALSE
262455_at	Mlo protein, putative similar to M	MLO2	AT1G11310	1.49	0.57	2.48	0.0433244	0.1991797	-4.11	FALSE
247654_at	cytoplasmic ribosomal protein S	---	AT5G59850	-2.02	-1.01	-2.48	0.0433613	0.1991797	-4.11	FALSE
263804_at	putative protein kinase contains a	---	AT2G40270	1.42	0.51	2.48	0.0433267	0.1991797	-4.11	FALSE
266112_x_a	hypothetical protein predicted by	---	---	1.38	0.47	2.48	0.0433325	0.1991797	-4.11	FALSE
248181_at	cytochrome c biogenesis protein	---	AT5G54290	-1.48	-0.57	-2.48	0.0433555	0.1991797	-4.11	FALSE
247789_at	putative protein various predicte	---	AT5G58680	1.38	0.46	2.48	0.0433595	0.1991797	-4.11	FALSE
248227_at	ABA-inducible protein-like ;supp	---	AT5G53820	1.33	0.41	2.48	0.0433891	0.1992564	-4.11	FALSE
256482_at	protein kinase, putative contains	FEI1	AT1G31420	-1.32	-0.40	-2.48	0.0434112	0.1992775	-4.11	FALSE

257475_at	hypothetical protein predicted by	---	AT1G80880	-1.24	-0.32	-2.48	0.0434046	0.1992775	-4.11	FALSE
253850_at	pectinesterase like protein pecti	sks10	AT4G28090	1.42	0.51	2.48	0.0434256	0.1993034	-4.11	FALSE
264804_at	putative receptor kinase, CLV1 s	---	AT1G08590	1.40	0.48	2.48	0.0434562	0.1994036	-4.12	FALSE
255492_at	hypothetical protein similar to A.	EOL1	AT4G02680	-1.34	-0.42	-2.48	0.043472	0.1994361	-4.12	FALSE
267346_at	coronatine-insensitive 1 (COI1),	COI1	AT2G39940	-1.45	-0.54	-2.48	0.0434938	0.1994959	-4.12	FALSE
266617_at	unknown protein ; supported by	---	AT2G29670	-1.89	-0.92	-2.48	0.0435078	0.1995202	-4.12	FALSE
248313_at	putative protein contains similarit	---	AT5G52580	-1.26	-0.33	-2.48	0.0435299	0.1995811	-4.12	FALSE
246114_at	seed imbitition protein-like seed	DIN10	AT5G20250	1.61	0.69	2.48	0.0435821	0.1997321	-4.12	FALSE
247863_at	SKP1 interacting partner 1 (SKIP	---	AT5G57890 /	1.33	0.41	2.48	0.043589	0.1997321	-4.12	FALSE
257702_at	CTP-synthetase, putative simila	emb2742	AT3G12670	-1.39	-0.47	-2.48	0.0435806	0.1997321	-4.12	FALSE
256310_at	unknown protein ; supported by	ERD4	AT1G30360	-1.53	-0.61	-2.48	0.0436453	0.1997489	-4.12	TRUE
257051_at	squamosa promoter binding prot	SPL5	AT3G15270	2.38	1.25	2.48	0.0436123	0.1997489	-4.12	TRUE
252357_at	putative protein predicted protei	---	AT3G48410	-1.52	-0.60	-2.48	0.043614	0.1997489	-4.12	TRUE
265284_at	unknown protein ;supported by f	---	AT2G20230	-1.36	-0.44	-2.48	0.0436316	0.1997489	-4.12	FALSE
253202_at	Expressed protein ; supported by	---	AT4G34555	-1.77	-0.83	-2.48	0.0436393	0.1997489	-4.12	FALSE
246922_at	serine/threonine protein kinase-li	CIPK25	AT5G25110	-1.57	-0.65	-2.48	0.0436327	0.1997489	-4.12	FALSE
AFFX-r2-Bs	B. subtilis /GEN=pheB /DB_XRE	---	---	-1.61	-0.68	-2.48	0.0436594	0.1997734	-4.12	FALSE
258789_at	Mutator-like transposase similar	---	---	-1.33	-0.41	-2.48	0.0436755	0.1998071	-4.12	FALSE
245136_at	putative auxin-regulated protein	---	AT2G45210	2.02	1.02	2.48	0.0436926	0.1998454	-4.12	TRUE
246487_at	putative protein with poly glutam	---	AT5G16030	-1.72	-0.78	-2.48	0.0437344	0.199956	-4.12	TRUE
249591_at	putative protein predicted protei	---	---	1.26	0.34	2.48	0.0437332	0.199956	-4.12	FALSE
267130_at	hypothetical protein predicted by	---	AT2G23390	-1.49	-0.58	-2.48	0.043769	0.2000344	-4.12	FALSE
262075_at	hypothetical protein contains sim	ZCF61	AT1G59560	-1.54	-0.63	-2.48	0.0437665	0.2000344	-4.12	FALSE
249525_at	putative protein similar to unknov	---	AT5G38650	-1.29	-0.37	-2.48	0.0437789	0.2000394	-4.12	FALSE
262064_at	elongation factor, putative simila	LOS1	AT1G56070	-1.37	-0.46	-2.48	0.0438343	0.2001685	-4.12	FALSE
246632_at	hypothetical protein similar to put	---	AT1G29710	-1.35	-0.43	-2.47	0.0438749	0.2001685	-4.12	FALSE
248690_at	acetyl-CoA C-acetyltransferase	ACAT2	AT5G48230	-1.26	-0.34	-2.47	0.0438854	0.2001685	-4.12	FALSE
247172_at	anthocyanidin-3-glucoside rhamr	---	AT5G65550	1.29	0.37	2.48	0.0438178	0.2001685	-4.12	FALSE
247846_at	putative protein	---	AT5G58100	-1.32	-0.40	-2.47	0.0438622	0.2001685	-4.12	FALSE
254797_at	putative protein	---	AT4G13030	-1.61	-0.69	-2.47	0.0439124	0.2001685	-4.13	FALSE
257494_at	hypothetical protein predicted by	---	AT1G32375	1.25	0.33	2.47	0.0438909	0.2001685	-4.12	FALSE
257609_at	Expressed protein ; supported by	---	AT3G13845	-1.37	-0.46	-2.47	0.0439119	0.2001685	-4.13	FALSE
251367_at	SKP1 interacting partner 4 (SKIP	SKIP4	AT3G61350	-1.40	-0.48	-2.47	0.0438967	0.2001685	-4.13	FALSE
254104_at	putative protein predicted protei	---	AT4G25040	1.39	0.48	2.48	0.0438569	0.2001685	-4.12	FALSE
259548_at	hypothetical protein similar to rip	MLP165	AT1G35260	1.97	0.98	2.47	0.0438614	0.2001685	-4.12	FALSE

249586_at	putative protein predicted protei	---	AT5G37840	2.01	1.01	2.47	0.0438898	0.2001685	-4.12	FALSE
262132_at	ribosomal protein L22, putative s	---	AT1G02830	1.29	0.37	2.47	0.0439368	0.2002396	-4.13	FALSE
251041_at	ubiquitin-protein ligase E3-alpha	PRT6	AT5G02310	1.47	0.56	2.47	0.0439559	0.2002865	-4.13	FALSE
256717_at	hypothetical protein predicted by	---	AT2G34110	1.38	0.46	2.47	0.0439821	0.2003259	-4.13	FALSE
259076_at	hypothetical protein predicted by	TMAC2	AT3G02140	3.23	1.69	2.47	0.0439795	0.2003259	-4.13	FALSE
266302_at	ethylene-insensitive3-like1 (EIL1	EIL1	AT2G27050	-1.42	-0.50	-2.47	0.0440159	0.2003529	-4.13	FALSE
251476_at	putative protein hypothetical pro	---	AT3G59670	-1.60	-0.68	-2.47	0.0440007	0.2003529	-4.13	FALSE
249875_at	photosystem II stability/assembly	HCF136	AT5G23120	-1.57	-0.65	-2.47	0.0440232	0.2003529	-4.13	FALSE
249676_at	serine/threonine protein kinase-li	---	AT5G35960	1.37	0.46	2.47	0.0440087	0.2003529	-4.13	FALSE
247283_at	2-nitropropane dioxygenase-like	---	AT5G64250	1.35	0.44	2.47	0.0440367	0.2003743	-4.13	FALSE
245968_at	proline-rich protein extensins	---	AT5G19800 ///	1.40	0.49	2.47	0.0441186	0.2007073	-4.13	FALSE
254981_at	putative alpha NAC stong simila	---	AT4G10480	-1.63	-0.70	-2.47	0.0441299	0.2007186	-4.13	FALSE
258486_at	putative 40S ribosomal protein si	---	AT3G02560	-1.96	-0.97	-2.47	0.0441538	0.2007608	-4.13	FALSE
252520_at	receptor-like protein kinase hom	---	AT3G46370	-1.91	-0.93	-2.47	0.0441568	0.2007608	-4.13	FALSE
263325_at	putative RING zinc finger protein	XERICO	AT2G04240	-1.76	-0.82	-2.47	0.0442074	0.2009506	-4.13	FALSE
258592_at	hypothetical protein contains Pfa	---	AT3G04130	-1.36	-0.45	-2.47	0.0442328	0.2010263	-4.13	FALSE
266229_at	putative RING zinc finger ankyrin	---	AT2G28840	-1.29	-0.37	-2.47	0.0442931	0.2012588	-4.13	FALSE
263125_at	hypothetical protein predicted by	---	AT1G78470	1.31	0.39	2.47	0.0443016	0.2012588	-4.13	FALSE
245002_at	PSII D2 protein	---	---	-1.41	-0.50	-2.47	0.0443224	0.2012969	-4.13	FALSE
253743_at	putative protein vegetative stora	---	AT4G28940	1.23	0.30	2.47	0.0443277	0.2012969	-4.13	FALSE
263334_at	putative nonsense-mediated mR	---	AT2G03820	-1.32	-0.40	-2.47	0.0443405	0.2013149	-4.14	FALSE
253332_at	peroxidase ATP17a -like protein	---	AT4G33420	2.41	1.27	2.47	0.044368	0.2014	-4.14	FALSE
261817_at	hypothetical protein predicted by	---	AT1G08180	-1.84	-0.88	-2.47	0.0443898	0.2014187	-4.14	FALSE
264725_at	Expressed protein ; supported by	---	AT1G22885	1.76	0.82	2.47	0.0443843	0.2014187	-4.14	FALSE
267383_at	unknown protein	---	AT2G44360	1.25	0.32	2.47	0.0444182	0.2015075	-4.14	FALSE
253272_at	putative protein ;supported by fu	ספס-01	AT4G34190	-1.52	-0.60	-2.47	0.0444814	0.2017485	-4.14	FALSE
247205_at	unknown protein ;supported by f	PROPEP2	AT5G64890	3.92	1.97	2.47	0.044489	0.2017485	-4.14	FALSE
252575_at	receptor like protein kinase rece	---	AT3G45440	1.48	0.57	2.46	0.0445339	0.2017514	-4.14	FALSE
251170_at	ATMRK1 ;supported by full-leng	ATMRK1	AT3G63260	-1.25	-0.32	-2.46	0.0445197	0.2017514	-4.14	FALSE
251559_at	putative protein hypothetical pro	---	AT3G58010	-1.44	-0.53	-2.46	0.0445314	0.2017514	-4.14	FALSE
247853_at	non phototropic hypocotyl 1-like	PHOT2	AT5G58140	-1.36	-0.44	-2.46	0.0445128	0.2017514	-4.14	FALSE
249800_at	MtN3-like protein ; supported by	MTN3	AT5G23660	1.33	0.41	2.46	0.0445315	0.2017514	-4.14	FALSE
254936_at	predicted protein of unknown fun	---	AT4G10790	-1.25	-0.32	-2.46	0.0445931	0.2019794	-4.14	FALSE
254092_at	respiratory burst oxidase - like p	---	AT4G25090	1.24	0.31	2.46	0.0446235	0.2020771	-4.14	FALSE
259239_at	putative 40S ribosomal protein s	---	AT3G11510	-2.07	-1.05	-2.46	0.0446365	0.2020959	-4.14	FALSE

258154_at	unknown protein ; supported by	---	AT3G18210	-1.41	-0.49	-2.46	0.0446488	0.2021115	-4.14	FALSE
263369_at	unknown protein	---	AT2G20480	-1.26	-0.34	-2.46	0.0446586	0.2021157	-4.14	FALSE
258858_at	putative 40S ribosomal protein S	---	AT3G02080	-1.67	-0.74	-2.46	0.0446798	0.2021715	-4.14	FALSE
263594_at	putative purple acid phosphatase	PAP7	AT2G01880	1.89	0.92	2.46	0.0447147	0.202289	-4.14	FALSE
266109_at	putative mitochondrial carrier pro	---	AT2G37890	-1.72	-0.78	-2.46	0.0447735	0.2024751	-4.14	FALSE
262509_at	hypothetical protein similar to hy	CRR22	AT1G11290	-1.36	-0.45	-2.46	0.044773	0.2024751	-4.14	FALSE
254805_at	pEARLI 1 ; supported by cDNA:	pEARLI 1	AT4G12480	-5.48	-2.45	-2.46	0.0448787	0.2028702	-4.15	TRUE
255520_at	putative ribosomal protein L19 si	---	AT4G02230	-1.62	-0.69	-2.46	0.0448716	0.2028702	-4.15	FALSE
248585_at	unknown protein	---	AT5G49640	-1.32	-0.40	-2.46	0.0448975	0.2029148	-4.15	FALSE
251948_at	diaminopimelate epimerase - lik	---	AT3G53580	-1.37	-0.46	-2.46	0.0449082	0.2029231	-4.15	FALSE
256414_at	putative nucleic acid binding prot	AL2	AT3G11200	1.31	0.39	2.46	0.0449255	0.2029609	-4.15	FALSE
249777_at	putative protein similar to unknov	---	AT5G24210	1.45	0.54	2.46	0.0449667	0.2030667	-4.15	FALSE
261475_at	anionic peroxidase, putative sim	---	AT1G14550	1.59	0.67	2.46	0.044965	0.2030667	-4.15	FALSE
253975_at	putative protein proliferating-cell	---	AT4G26600	-1.91	-0.93	-2.46	0.0450025	0.2031504	-4.15	TRUE
247978_at	60S ribosomal protein L31 ;supp	---	AT5G56710	-1.95	-0.97	-2.46	0.045003	0.2031504	-4.15	FALSE
264686_at	shaggy-like protien kinase, kapp	ATSK41	AT1G09840	-1.25	-0.33	-2.46	0.0450147	0.203163	-4.15	FALSE
260985_at	dTDP-D-glucose 4,6-dehydratas	MUM4	AT1G53500	1.36	0.44	2.46	0.0450411	0.2032016	-4.15	TRUE
262228_at	protein kinase, putative similar t	---	AT1G68690	2.67	1.42	2.46	0.0450348	0.2032016	-4.15	FALSE
266930_at	hypothetical protein predicted by	---	AT2G45930	1.40	0.49	2.46	0.0450661	0.2032742	-4.15	FALSE
251880_at	hypothetical protein ;supported b	---	AT3G54290	-1.45	-0.54	-2.46	0.0450759	0.2032781	-4.15	FALSE
266310_at	putative PCI domain protein prot	FUS12	AT2G26990	-1.35	-0.43	-2.46	0.0451022	0.2033368	-4.15	FALSE
259335_s_a	unknown protein similar to unkno	---	AT3G03930 ///	-1.43	-0.51	-2.46	0.0451067	0.2033368	-4.15	FALSE
260757_at	phytocyanin, putative similar to p	---	AT1G48940	1.27	0.35	2.46	0.0451193	0.2033533	-4.15	FALSE
254673_at	membrane-bound small GTP-bir	AtRABA1e	AT4G18430	2.28	1.19	2.45	0.0451461	0.2034337	-4.15	TRUE
248023_at	ADP/ATP translocase-like protei	---	AT5G56450	-1.34	-0.42	-2.45	0.0451669	0.2034877	-4.15	FALSE
249375_at	putative protein predicted protei	AGP24	AT5G40730	1.33	0.41	2.45	0.0451856	0.2035316	-4.15	TRUE
264329_at	unknown protein Contains simila	---	AT1G04140	-1.28	-0.35	-2.45	0.0452173	0.2035542	-4.15	FALSE
259874_at	unknown protein	---	AT1G76660	-1.48	-0.57	-2.45	0.0452143	0.2035542	-4.15	FALSE
257897_at	HAL3A protein identical to GB:A	HAL3A	AT3G18030	-1.46	-0.55	-2.45	0.0452174	0.2035542	-4.15	FALSE
256511_at	RNA helicase, putative similar to	---	AT1G33390	-1.29	-0.37	-2.45	0.0452365	0.2036	-4.16	FALSE
257422_at	hypothetical protein Contains sim	---	AT1G11940	1.29	0.37	2.45	0.0452702	0.2037115	-4.16	FALSE
262044_s_a	hypothetical protein predicted by	---	AT1G80210 ///	-1.32	-0.40	-2.45	0.0453043	0.2037887	-4.16	FALSE
248668_at	putative protein similar to unknov	XRI1	AT5G48720	-1.60	-0.68	-2.45	0.0453052	0.2037887	-4.16	FALSE
249931_at	putative protein similar to unknov	QQT1	AT5G22370	-1.48	-0.57	-2.45	0.0453319	0.2038316	-4.16	FALSE
247966_at	putative protein contains similarit	---	AT5G56610	1.33	0.41	2.45	0.0453326	0.2038316	-4.16	FALSE

246243_at	trichohyalin like protein	---	AT4G36520	1.26	0.34	2.45	0.0453508	0.2038732	-4.16	FALSE
254610_at	putative protein predicted protei	---	AT4G18890	1.33	0.42	2.45	0.0453615	0.2038811	-4.16	FALSE
245500_at	reverse transcriptase like protein	---	---	1.29	0.36	2.45	0.045382	0.2039331	-4.16	FALSE
256728_at	glutamyl-tRNA amidotransferase	---	AT3G25660	-1.48	-0.57	-2.45	0.0454487	0.2040315	-4.16	FALSE
261500_at	hypothetical protein predicted by	---	AT1G28400	-2.07	-1.05	-2.45	0.0454171	0.2040315	-4.16	FALSE
249513_at	glucosyltransferase-like protein ;	---	AT5G38460	-1.31	-0.38	-2.45	0.0454427	0.2040315	-4.16	FALSE
254705_at	putative protein ; supported by c	---	AT4G17870	-1.56	-0.64	-2.45	0.0454295	0.2040315	-4.16	FALSE
248236_at	putative protein contains similarit	---	AT5G53870	3.55	1.83	2.45	0.045445	0.2040315	-4.16	FALSE
256922_at	hypothetical protein contains sin	---	AT3G19010	1.90	0.93	2.45	0.0454634	0.2040528	-4.16	FALSE
248639_at	anthranilate N-benzoyltransferas	HCT	AT5G48930	1.57	0.65	2.45	0.0454802	0.2040528	-4.16	FALSE
262513_at	unknown protein ; supported by c	---	AT1G34270	-1.34	-0.42	-2.45	0.0454796	0.2040528	-4.16	FALSE
248289_at	unknown protein ; supported by	---	AT5G52880	-1.29	-0.37	-2.45	0.0455024	0.2040896	-4.16	FALSE
254753_at	putative protein Pto kinase intera	---	AT4G13190	1.27	0.34	2.45	0.0455319	0.2040896	-4.16	FALSE
264860_at	hypothetical protein contains ATF	---	AT1G24290	-1.27	-0.34	-2.45	0.0455332	0.2040896	-4.16	FALSE
251097_at	receptor like protein kinase rece	LECRKA4.3	AT5G01560	2.97	1.57	2.45	0.0455303	0.2040896	-4.16	FALSE
266800_at	hypothetical protein predicted by	---	AT2G22880	6.85	2.78	2.45	0.0455138	0.2040896	-4.16	FALSE
251264_at	multifunctional aminoacyl-tRNA	---	AT3G62120	-1.28	-0.36	-2.45	0.0455424	0.2040908	-4.16	FALSE
264778_at	unknown protein similar to C-1 (H	AIP3	AT1G08780	-1.30	-0.38	-2.45	0.0455955	0.2042888	-4.16	FALSE
266514_at	putative zinc-finger protein (B-bo	---	AT2G47890	-1.47	-0.55	-2.45	0.0456066	0.2042981	-4.16	FALSE
250668_at	unknown protein ; supported by	---	AT5G07020	-1.46	-0.55	-2.45	0.0456194	0.2043153	-4.16	TRUE
263148_at	ubiquitin, putative similar to ubiq	---	AT1G53950	1.34	0.42	2.45	0.0456294	0.2043199	-4.16	FALSE
247592_at	high affinity nitrate transporter pr	NRT2.3	AT5G60780	1.27	0.35	2.45	0.0456495	0.2043699	-4.16	FALSE
256793_at	unknown protein ;supported by f	---	AT3G22160	1.90	0.93	2.45	0.0456787	0.2044605	-4.16	TRUE
259762_at	hypothetical protein predicted by	---	AT1G77600	-1.36	-0.44	-2.45	0.0456982	0.2045076	-4.17	FALSE
259880_at	hypothetical protein similar to hy	---	AT1G76730	-1.52	-0.60	-2.45	0.0457383	0.2046473	-4.17	FALSE
247566_at	40S ribsomal protein S19 - like 4	---	AT5G61170	-1.86	-0.90	-2.45	0.0457888	0.2048327	-4.17	FALSE
264531_at	hypothetical protein predicted by	---	AT1G30790	1.30	0.38	2.44	0.045802	0.2048516	-4.17	FALSE
246660_at	putative protein predicted protei	---	AT5G35180	1.32	0.40	2.44	0.0458424	0.2048717	-4.17	FALSE
258915_at	unknown protein similar to hypot	VPS60.1	AT3G10640	1.41	0.49	2.44	0.0458407	0.2048717	-4.17	FALSE
251261_at	putative protein polygalacturona	---	AT3G62110	-1.83	-0.87	-2.44	0.0458292	0.2048717	-4.17	FALSE
254746_at	putative protein hypothetical pro	---	AT4G12980	-1.71	-0.77	-2.44	0.0458273	0.2048717	-4.17	FALSE
266702_at	hexokinase (ATHXK2) ; support	HXK2	AT2G19860	-1.30	-0.38	-2.44	0.0458719	0.2049633	-4.17	FALSE
264621_at	putative protein kinase contains a	---	AT2G17700	-1.36	-0.44	-2.44	0.0459629	0.2050105	-4.17	FALSE
255586_at	hypothetical protein ;supported b	MEE49	AT4G01560	-1.61	-0.69	-2.44	0.0459312	0.2050105	-4.17	FALSE
264799_at	putative violaxanthin de-epoxidas	NPQ1	AT1G08550	-1.39	-0.48	-2.44	0.0459602	0.2050105	-4.17	FALSE

263570_at	aldehyde oxidase identical to GP	AAO3	AT2G27150	1.61	0.69	2.44	0.0459633	0.2050105	-4.17	FALSE
259419_at	acyl-CoA oxidase ACX3, putativ	ACX6	AT1G06310	1.30	0.38	2.44	0.0459161	0.2050105	-4.17	FALSE
247701_at	putative protein many predicted	---	AT5G59900	-1.29	-0.37	-2.44	0.0458969	0.2050105	-4.17	FALSE
258490_at	hypothetical protein predicted by	---	AT3G02670	1.30	0.38	2.44	0.0459622	0.2050105	-4.17	FALSE
267069_at	unknown protein	ATCAMBP2	AT2G41010	2.48	1.31	2.44	0.0459616	0.2050105	-4.17	FALSE
246218_at	RUB1-conjugating enzyme RCE	RCE1	AT4G36800	-1.50	-0.59	-2.44	0.0459181	0.2050105	-4.17	FALSE
257599_at	60S ribosomal protein, putative	---	AT3G24830	-1.83	-0.87	-2.44	0.0459766	0.2050295	-4.17	FALSE
251293_at	hypothetical protein	---	AT3G61930	5.72	2.52	2.44	0.046025	0.2051654	-4.17	FALSE
265030_at	receptor-like kinase, putative sin	---	AT1G61610	1.79	0.84	2.44	0.0460182	0.2051654	-4.17	FALSE
265847_at	unknown protein	---	AT2G35750	-1.28	-0.35	-2.44	0.0460397	0.2051907	-4.17	FALSE
263145_at	hypothetical protein predicted by	ATEXO70D	AT1G54090	1.45	0.53	2.44	0.0460508	0.2052002	-4.17	FALSE
257626_s_a	hypothetical protein	---	AT3G26240 /	-1.34	-0.42	-2.44	0.0460781	0.2052815	-4.17	FALSE
258699_at	unknown protein	---	AT3G09470	-1.36	-0.45	-2.44	0.0461028	0.2052849	-4.17	FALSE
252070_at	short-chain alcohol dehydrogena	---	AT3G51680	1.40	0.49	2.44	0.0461076	0.2052849	-4.17	FALSE
247170_at	putative protein contains similarit	---	AT5G65530	1.26	0.33	2.44	0.0461149	0.2052849	-4.17	FALSE
246636_at	acid phosphatase-like protein pu	PAP26	AT5G34850	1.46	0.55	2.44	0.0461028	0.2052849	-4.17	FALSE
245038_at	similar to latex allergen from Hev	PLA2A	AT2G26560	2.51	1.33	2.44	0.0461693	0.2053051	-4.18	TRUE
265475_at	ferredoxin--nitrite reductase ; su	NIR1	AT2G15620	-1.52	-0.60	-2.44	0.046181	0.2053051	-4.18	TRUE
258026_at	abscisic acid responsive element	ABF4	AT3G19290	-1.45	-0.53	-2.44	0.0461371	0.2053051	-4.17	FALSE
246591_at	putative cation transport protein	---	AT5G14880	-1.39	-0.48	-2.44	0.0461543	0.2053051	-4.18	FALSE
259834_at	H-protein promoter binding factor	---	AT1G69570	1.67	0.74	2.44	0.0461729	0.2053051	-4.18	FALSE
261808_at	DNA damage repair protein, put	DRT111	AT1G30480	-1.28	-0.36	-2.44	0.0461824	0.2053051	-4.18	FALSE
245113_at	hypothetical protein predicted by	MIZ1	AT2G41660	1.47	0.55	2.44	0.0461443	0.2053051	-4.17	FALSE
264455_at	hypothetical protein predicted by	---	AT1G10330	-1.38	-0.47	-2.44	0.0461958	0.2053246	-4.18	FALSE
255871_at	putative small nuclear ribonucleo	U2B"	AT2G30260	-1.35	-0.43	-2.44	0.0462156	0.2053729	-4.18	FALSE
256581_at	hypothetical protein	---	AT3G28830	1.24	0.31	2.44	0.0462463	0.2053999	-4.18	FALSE
259274_at	putative homeobox-leucine zipp	ATHB20	AT3G01220	1.29	0.36	2.44	0.0462488	0.2053999	-4.18	FALSE
257097_at	hypothetical protein predicted by	---	---	1.27	0.35	2.44	0.0462442	0.2053999	-4.18	FALSE
266520_at	cyclic nucleotide and calmodulin-	ATCNGC6	AT2G23980	-1.38	-0.46	-2.44	0.0462735	0.2054697	-4.18	FALSE
265206_at	putative protease belongs to euk	---	AT2G36670	-1.38	-0.47	-2.44	0.0463162	0.2054992	-4.18	FALSE
247408_at	ZAP - like protein nuclear protei	---	AT5G62760	1.25	0.33	2.44	0.0463144	0.2054992	-4.18	FALSE
267193_at	hypothetical protein predicted by	---	AT2G30900	1.31	0.39	2.44	0.0463099	0.2054992	-4.18	FALSE
259875_s_a	12-oxophytodienoate reductase (	OPR1	AT1G76680 /	2.25	1.17	2.44	0.0463069	0.2054992	-4.18	FALSE
249258_at	putative protein similar to unknov	---	AT5G41650	-1.26	-0.34	-2.44	0.0463403	0.2055662	-4.18	FALSE
262856_at	unknown protein contains Pfam p	---	AT1G14910	-1.39	-0.48	-2.44	0.0464136	0.2058115	-4.18	FALSE

262169_at	hypothetical protein predicted by	---	AT1G74860	-1.37	-0.45	-2.44	0.046412	0.2058115	-4.18	FALSE
248815_at	putative protein contains similarit	---	AT5G46920	-1.50	-0.59	-2.43	0.0464717	0.2058423	-4.18	FALSE
266253_at	unknown protein contains non-cc	HDT4	AT2G27840	-1.72	-0.79	-2.43	0.0464734	0.2058423	-4.18	TRUE
257009_at	unknown protein ; supported by	---	AT3G14160	-1.27	-0.35	-2.43	0.0464747	0.2058423	-4.18	FALSE
245155_at	putative protein similarity to prec	---	AT5G12470	-1.52	-0.61	-2.44	0.0464409	0.2058423	-4.18	FALSE
249546_at	putative protein chromosome se	PMI15	AT5G38150	-1.57	-0.65	-2.43	0.0464611	0.2058423	-4.18	FALSE
266737_at	putative alcohol dehydrogenase	---	AT2G47140	1.36	0.44	2.43	0.0464694	0.2058423	-4.18	FALSE
246070_at	ribosomal protein L7Ae-like NHF	---	AT5G20160	-1.53	-0.62	-2.43	0.0464843	0.2058448	-4.18	FALSE
253331_at	nucellin -like protein nucellin - H	---	AT4G33490	-1.50	-0.59	-2.43	0.046502	0.2058832	-4.18	FALSE
259514_at	hypothetical protein ; supported b	OZS1	AT1G12480	1.33	0.41	2.43	0.0465418	0.2060196	-4.18	FALSE
248158_at	unknown protein	---	AT5G54440	-1.25	-0.32	-2.43	0.0465629	0.2060727	-4.18	FALSE
255522_at	putative GTP pyrophosphokinas	RSH1	AT4G02260	-1.34	-0.42	-2.43	0.0465795	0.2061066	-4.18	FALSE
254665_at	beta-1,3-glucanase-like protein s	---	AT4G18340	1.65	0.72	2.43	0.0465905	0.206109	-4.18	TRUE
263700_at	unknown protein EST gb|Z33866	---	AT1G31150	-1.46	-0.54	-2.43	0.0465982	0.206109	-4.18	FALSE
258445_at	putative lipoxygenase similar to l	LOX5	AT3G22400	1.61	0.69	2.43	0.0466305	0.2061288	-4.19	TRUE
252615_at	serine/proline-rich protein	---	AT3G45230	-1.54	-0.63	-2.43	0.0466193	0.2061288	-4.19	FALSE
264638_at	flowering signals mediating prote	FT	AT1G65480	2.15	1.10	2.43	0.0466319	0.2061288	-4.19	FALSE
257393_at	unknown protein	---	AT2G20080	1.24	0.31	2.43	0.0466388	0.2061288	-4.19	FALSE
259426_at	hypothetical protein contains sim	LEA14	AT1G01470	1.36	0.44	2.43	0.046698	0.2063452	-4.19	TRUE
252217_at	putative protein some putative pr	---	AT3G50140	1.49	0.58	2.43	0.0467058	0.2063452	-4.19	FALSE
263295_at	putative MADS-box protein ANR	AGL44	AT2G14210	-1.26	-0.33	-2.43	0.04673	0.2063656	-4.19	FALSE
266909_at	hypothetical protein predicted by	BRM	AT2G46020	1.40	0.48	2.43	0.0467273	0.2063656	-4.19	FALSE
265273_at	unknown protein	---	AT2G28320	1.34	0.42	2.43	0.0467376	0.2063656	-4.19	FALSE
266149_x_a	En/Spm-like transposon protein r	---	---	1.31	0.39	2.43	0.0467792	0.2065091	-4.19	FALSE
255051_at	RNA-directed DNA polymerase	---	---	1.54	0.62	2.43	0.0468047	0.2065817	-4.19	FALSE
248398_at	sorbitol dehydrogenase-like prote	---	AT5G51970	-1.37	-0.46	-2.43	0.0468909	0.2069222	-4.19	FALSE
259213_at	putative receptor ser/thr protein k	---	AT3G09010	2.71	1.44	2.43	0.0469429	0.2070842	-4.19	TRUE
245263_at	PSII D1 protein processing enzyr	---	AT4G17740	-1.29	-0.36	-2.43	0.0469457	0.2070842	-4.19	FALSE
250867_at	putative protein predicted protei	---	AT5G03880	-1.51	-0.59	-2.43	0.0469834	0.2072103	-4.19	FALSE
265044_at	hypothetical protein Similar to hu	VPS2.3	AT1G03950	1.41	0.50	2.43	0.0470093	0.2072644	-4.19	FALSE
252474_at	putative protein several hypothet	---	AT3G46620	2.19	1.13	2.43	0.0470138	0.2072644	-4.19	FALSE
254566_at	hypothetical protein	---	AT4G19240	-1.42	-0.50	-2.43	0.0470545	0.2074036	-4.19	FALSE
266895_at	hypothetical protein predicted by	---	AT2G26040	1.29	0.37	2.43	0.0470848	0.2074438	-4.19	FALSE
265480_at	similar to cold acclimation protein	COR413-PI	AT2G15970	-1.60	-0.68	-2.43	0.047085	0.2074438	-4.19	FALSE
252057_at	putative protein ;supported by fu	---	AT3G52480	1.68	0.74	2.43	0.0470909	0.2074438	-4.20	FALSE

249291_at	glutathione transferase AtGST 1(	ATGSTT1	AT5G41210	-1.35	-0.43	-2.42	0.0471544	0.2076432	-4.20	FALSE
259965_at	transcriptional regulator, putative	MSRB1	AT1G53670	-1.40	-0.49	-2.42	0.0471455	0.2076432	-4.20	FALSE
264300_at	gamma glutamyl hydrolase, puta	ATGGH3	AT1G78670	-1.31	-0.38	-2.42	0.0471998	0.2077919	-4.20	TRUE
247178_at	Expressed protein ; supported by	---	AT5G65205	-1.89	-0.92	-2.42	0.0472064	0.2077919	-4.20	FALSE
261381_at	hypothetical protein predicted by	SDE3	AT1G05460	-1.26	-0.34	-2.42	0.0472468	0.2079297	-4.20	FALSE
264307_at	hypothetical protein contains sim	---	AT1G61900	-1.39	-0.47	-2.42	0.0472726	0.207949	-4.20	TRUE
251429_at	dynamin-like protein 4 (ADL4) ;	ADL1E	AT3G60190	-1.34	-0.42	-2.42	0.0472785	0.207949	-4.20	FALSE
264298_at	hypothetical protein contains sim	---	AT1G78690	-1.32	-0.40	-2.42	0.047275	0.207949	-4.20	FALSE
252103_at	putative protein various predicte	---	AT3G51410	-1.27	-0.35	-2.42	0.0472897	0.2079582	-4.20	FALSE
253359_at	putative protein kinase protein k	---	AT4G33080	-1.40	-0.48	-2.42	0.0473502	0.2081838	-4.20	FALSE
249134_at	unknown protein	---	AT5G43150	-1.62	-0.69	-2.42	0.0473604	0.2081885	-4.20	FALSE
246064_at	DNA binding protein ACBF - like	---	AT5G19350	-1.32	-0.40	-2.42	0.0474255	0.2082426	-4.20	FALSE
251598_at	AP2 transcription factor - like pr	---	AT3G57600	1.27	0.35	2.42	0.0474154	0.2082426	-4.20	FALSE
259578_at	unknown protein	---	AT1G27990	-1.54	-0.63	-2.42	0.0473954	0.2082426	-4.20	FALSE
267165_at	putative receptor-like protein kina	RLK	AT2G37710	1.97	0.98	2.42	0.0474033	0.2082426	-4.20	FALSE
267357_at	putative nematode-resistance pr	HSPRO2	AT2G40000	2.01	1.01	2.42	0.0474366	0.2082426	-4.20	FALSE
251484_at	putative protein putative protein	---	AT3G59640	1.26	0.34	2.42	0.0474135	0.2082426	-4.20	FALSE
248109_at	DNA topoisomerase I	TOP1BETA	AT5G55310	1.30	0.38	2.42	0.0474332	0.2082426	-4.20	FALSE
267057_at	hypothetical protein predicted by	---	AT2G32500	-1.96	-0.97	-2.42	0.0474574	0.208271	-4.20	TRUE
250914_at	myb -like protein telomeric DNA	TRFL10	AT5G03780	-1.36	-0.44	-2.42	0.0474613	0.208271	-4.20	FALSE
255884_at	hypothetical protein predicted by	---	AT1G20310	3.41	1.77	2.42	0.0474741	0.2082871	-4.20	FALSE
249743_at	beta-glucosidase	BGLU31	AT5G24540	4.78	2.26	2.42	0.047489	0.2083124	-4.20	FALSE
263545_at	unknown protein	---	AT2G21560	-1.94	-0.96	-2.42	0.0475495	0.2084257	-4.20	TRUE
249750_at	unknown protein ;supported by f	---	AT5G24570	-1.61	-0.68	-2.42	0.0475694	0.2084257	-4.21	FALSE
266552_at	unknown protein ; supported by (	AGP16	AT2G46330	1.50	0.58	2.42	0.0475659	0.2084257	-4.21	FALSE
248336_at	unknown protein ; supported by	---	AT5G52420	-1.57	-0.65	-2.42	0.0475697	0.2084257	-4.21	FALSE
266239_at	unknown protein ; supported by	---	AT2G29530	-1.81	-0.86	-2.42	0.0475466	0.2084257	-4.20	FALSE
250557_at	putative protein ankyrin, Rattus	CPuORF16	AT5G07840 /	-1.28	-0.35	-2.42	0.0475241	0.2084257	-4.20	FALSE
245831_at	unknown protein	---	AT1G48840	-1.34	-0.42	-2.42	0.0475958	0.20846	-4.21	FALSE
258499_at	putative RAD23 similar to RAD23	RAD23-3	AT3G02540	-1.32	-0.40	-2.42	0.0475946	0.20846	-4.21	FALSE
248880_at	putative protein contains similarit	---	AT5G46200	1.28	0.36	2.42	0.0476448	0.2086348	-4.21	FALSE
259682_at	transcription factor DREB1A, pu	---	AT1G63040	1.47	0.56	2.42	0.0476586	0.2086548	-4.21	FALSE
267040_at	unknown protein	---	AT2G34300	1.86	0.89	2.42	0.0477436	0.2088367	-4.21	TRUE
246858_at	receptor-like protein kinase - like	---	AT5G25930	2.48	1.31	2.42	0.0477334	0.2088367	-4.21	TRUE
260258_at	putative ribosomal protein similar	---	AT1G74270	-1.46	-0.54	-2.42	0.047738	0.2088367	-4.21	TRUE

256314_at	hypothetical protein	TOC75-I	AT1G35860	1.32	0.40	2.42	0.047755	0.2088367	-4.21	FALSE
252415_at	glutamine-dependent asparagine	ASN1	AT3G47340	6.26	2.65	2.42	0.0477479	0.2088367	-4.21	FALSE
262308_at	unknown protein	---	AT1G71010	1.38	0.46	2.42	0.0477365	0.2088367	-4.21	FALSE
250932_s_a	putative protein MED7, Homo sa	---	AT5G03220 /A	-1.29	-0.37	-2.42	0.0477694	0.2088595	-4.21	FALSE
261490_at	tumor suppressor, putative simil	SAC52	AT1G14320	-1.45	-0.54	-2.42	0.0478023	0.2089634	-4.21	FALSE
249769_at	sigma-like factor (emb CAA7721	SIGE	AT5G24120	-1.48	-0.56	-2.41	0.0478239	0.2090176	-4.21	FALSE
254014_at	NPR1 like protein regulatory pro	---	AT4G26120	1.95	0.96	2.41	0.0478405	0.2090275	-4.21	FALSE
249301_at	putative protein similar to unknov	---	AT5G41440	1.38	0.47	2.41	0.0478445	0.2090275	-4.21	FALSE
259519_at	hypothetical protein	---	AT1G12270	-1.41	-0.49	-2.41	0.0478757	0.2090859	-4.21	FALSE
260708_at	expressed protein ; supported by	---	AT1G32310	-1.36	-0.44	-2.41	0.0478762	0.2090859	-4.21	FALSE
247271_at	nuclear protein-like	---	AT5G64270	-1.37	-0.45	-2.41	0.0479	0.2091499	-4.21	FALSE
250004_at	putative protein predicted protein	---	AT5G18750	-1.44	-0.53	-2.41	0.0479564	0.2092058	-4.21	FALSE
247520_at	cytochrome c oxidase subunit - I	---	AT5G61310	-1.64	-0.72	-2.41	0.0479587	0.2092058	-4.21	FALSE
256909_at	hypothetical protein predicted by	---	AT3G24060	1.38	0.47	2.41	0.0479222	0.2092058	-4.21	FALSE
250095_at	phytoene synthase (gb|AAB6569	---	AT5G17230	-1.67	-0.74	-2.41	0.0479538	0.2092058	-4.21	FALSE
251889_at	putative protein probable lectin 2	---	AT3G54080	-1.75	-0.81	-2.41	0.0479363	0.2092058	-4.21	FALSE
259460_at	unknown protein ; supported by c	---	AT1G44000	-1.67	-0.74	-2.41	0.0480065	0.2093744	-4.21	FALSE
253121_at	putative protein predicted protei	---	AT4G35890	1.23	0.30	2.41	0.0480542	0.2095423	-4.22	FALSE
256286_at	unknown protein	---	AT3G12180	-1.34	-0.42	-2.41	0.0480809	0.2096044	-4.22	FALSE
265529_at	hypothetical protein predicted by	---	---	1.27	0.34	2.41	0.0480868	0.2096044	-4.22	FALSE
248914_at	Rab-type small GTP-binding prot	AtRABA1c	AT5G45750	1.59	0.67	2.41	0.0481169	0.209638	-4.22	TRUE
251759_at	tetrahydrofolylpolyglutamate syn	ATDFD	AT3G55630	-1.66	-0.73	-2.41	0.0481313	0.209638	-4.22	FALSE
245602_at	Expressed protein ;supported by	---	AT4G14270	-1.51	-0.60	-2.41	0.0481299	0.209638	-4.22	FALSE
259639_at	unknown protein ;supported by fu	---	AT1G52380	-1.35	-0.44	-2.41	0.0481086	0.209638	-4.22	FALSE
259372_at	homeotic protein boi1AP1, putat	AP1	AT1G69120	1.31	0.39	2.41	0.048147	0.2096664	-4.22	FALSE
261016_at	beta-glucosidase, putative simila	BGLU40	AT1G26560	2.66	1.41	2.41	0.0482	0.2098173	-4.22	TRUE
251095_at	putative protein hypothetical pro	---	AT5G01510	-1.47	-0.55	-2.41	0.0482	0.2098173	-4.22	FALSE
261002_at	hypothetical protein contains sim	---	AT1G26520	-1.31	-0.39	-2.41	0.0482191	0.2098394	-4.22	FALSE
258837_at	putative 60S ribosomal protein L	---	AT3G07110	-1.92	-0.94	-2.41	0.0482419	0.2098394	-4.22	FALSE
252465_x_a	putative protein several hypothet	---	---	1.30	0.38	2.41	0.0482401	0.2098394	-4.22	FALSE
261912_s_a	unknown protein	---	AT1G66000 /A	-1.37	-0.45	-2.41	0.0482367	0.2098394	-4.22	FALSE
262459_at	hypothetical protein similar to hyp	---	AT1G50400	1.44	0.53	2.41	0.0482835	0.2099401	-4.22	FALSE
258654_at	unknown protein	---	AT3G09860	-1.54	-0.62	-2.41	0.0482786	0.2099401	-4.22	FALSE
250149_at	cinnamoyl CoA reductase - like p	---	AT5G14700	3.98	1.99	2.41	0.0483058	0.2099973	-4.22	FALSE
249002_at	putative protein contains similarit	---	AT5G44520	-1.40	-0.49	-2.41	0.0483495	0.2101472	-4.22	FALSE

247720_at	dTDP-glucose 4-6-dehydratase	UXS3	AT5G59290	1.37	0.45	2.41	0.0483815	0.2102462	-4.22	FALSE
263727_at	putative cap-binding protein ; su	ABH1	AT2G13540	-1.41	-0.49	-2.41	0.0484328	0.2104284	-4.22	FALSE
263345_s_a	putative chlorophyll a/b binding p	LHCB2.1	AT2G05070 /.	-2.04	-1.03	-2.41	0.0484419	0.2104284	-4.22	FALSE
248669_at	putative protein contains similarit	---	AT5G48730	-1.50	-0.58	-2.41	0.0484575	0.2104563	-4.22	FALSE
256513_at	unknown protein similar to phosp	SGR2	AT1G31480	-1.29	-0.37	-2.41	0.0484873	0.2104746	-4.22	FALSE
260818_at	unknown protein	---	AT1G06890	-1.24	-0.31	-2.41	0.0484894	0.2104746	-4.22	FALSE
262085_at	hypothetical protein predicted by	---	AT1G56060	3.46	1.79	2.41	0.0484733	0.2104746	-4.22	FALSE
253602_s_a	leucyl aminopeptidase - like prot	---	AT4G30910 /.	-1.28	-0.35	-2.40	0.0485241	0.2105258	-4.22	FALSE
257367_at	hypothetical protein predicted by	---	AT2G25780	-1.33	-0.41	-2.40	0.0485141	0.2105258	-4.22	FALSE
245165_at	unknown protein predicted by ge	---	AT2G33180	-1.84	-0.88	-2.40	0.0485289	0.2105258	-4.22	FALSE
265425_at	hypothetical protein	GCL2	AT2G20770	1.40	0.49	2.40	0.0485724	0.2105942	-4.23	TRUE
263482_at	putative GDSL-motif lipase/hydro	---	AT2G03980	3.58	1.84	2.40	0.0485569	0.2105942	-4.23	TRUE
260321_at	putative RING zinc finger protein	---	AT1G63900	-1.30	-0.38	-2.40	0.0485714	0.2105942	-4.23	FALSE
252359_at	putative protein predicted protei	---	AT3G48440	1.43	0.52	2.40	0.0485914	0.2106317	-4.23	FALSE
245606_at	hypothetical protein	---	AT4G14310	1.34	0.42	2.40	0.0485995	0.2106317	-4.23	FALSE
250953_at	putative protein ;supported by fu	DPB	AT5G03415	-1.50	-0.59	-2.40	0.0486163	0.2106647	-4.23	FALSE
261556_s_a	unknown protein	---	AT1G62600 /.	1.43	0.51	2.40	0.0486304	0.2106854	-4.23	FALSE
257187_at	hypothetical protein predicted by	---	AT3G13140	1.30	0.38	2.40	0.0486463	0.2107146	-4.23	FALSE
260063_at	unknown protein contains Pfam	---	AT1G73720	-1.34	-0.42	-2.40	0.0486645	0.2107533	-4.23	FALSE
258235_at	alternative oxidase 1c precursor	AOX1C	AT3G27620	1.35	0.43	2.40	0.0486852	0.2107627	-4.23	FALSE
256331_at	GT-like trihelix DNA-binding prot	---	AT1G76880	-1.30	-0.37	-2.40	0.0486789	0.2107627	-4.23	FALSE
259318_at	unknown protein similar to HYP1	HYP1	AT3G01100	-1.41	-0.50	-2.40	0.0488102	0.2112638	-4.23	FALSE
256072_at	WD-40 repeat protein identical to	ATARCA	AT1G18080	-1.75	-0.81	-2.40	0.0488369	0.2113393	-4.23	FALSE
257988_at	unknown protein ; supported by	---	AT3G20870	-1.31	-0.39	-2.40	0.0488724	0.2114125	-4.23	FALSE
259490_at	hypothetical protein preedicted b	---	AT1G15800	1.31	0.39	2.40	0.0488696	0.2114125	-4.23	FALSE
246311_at	high mobility group protein 2-like	HMGB1	AT3G51880	-1.35	-0.43	-2.40	0.0489047	0.2114843	-4.23	FALSE
265897_at	hypothetical protein predicted by	MOT1	AT2G25680	1.58	0.66	2.40	0.0489154	0.2114843	-4.23	FALSE
258155_at	protein kinase C-receptor/G-prot	RACK1C_A	AT3G18130	-2.30	-1.20	-2.40	0.0489168	0.2114843	-4.23	FALSE
251938_at	60S RIBOSOMAL PROTEIN L1	---	AT3G53430	-1.43	-0.52	-2.40	0.0489332	0.2115151	-4.23	FALSE
266882_at	unknown protein ;supported by f	---	AT2G44670	-2.01	-1.01	-2.40	0.0489443	0.2115233	-4.23	FALSE
260760_at	hypothetical protein predicted by	---	AT1G49170	-1.41	-0.50	-2.40	0.0489648	0.2115716	-4.23	FALSE
257618_at	protein kinase, putative similar t	---	AT3G24715	1.24	0.31	2.40	0.048994	0.2116175	-4.23	FALSE
254804_at	putative protein putative oxidore	---	AT4G13010	-1.36	-0.44	-2.40	0.0489922	0.2116175	-4.23	FALSE
255401_at	hypothetical protein ;supported b	---	AT4G03600	-1.39	-0.48	-2.40	0.0490034	0.211618	-4.23	FALSE
253420_at	H+-transporting ATP synthase c	---	AT4G32260	-1.36	-0.45	-2.40	0.0490335	0.2117083	-4.24	FALSE

264154_at	unknown protein	---	AT1G65430	1.30	0.37	2.40	0.0490455	0.21172	-4.24	FALSE
263420_at	unknown protein ; supported by	---	AT2G17240	-1.28	-0.35	-2.40	0.049062	0.2117508	-4.24	FALSE
246286_at	unknown protein	---	AT1G31910	-1.28	-0.35	-2.40	0.0491205	0.2118944	-4.24	FALSE
255421_at	putative protein phosphatase reg	---	AT4G03260	1.35	0.43	2.40	0.0491231	0.2118944	-4.24	FALSE
254971_at	major intrinsic protein (MIP) - lik	NIP5;1	AT4G10380	1.54	0.62	2.40	0.0491164	0.2118944	-4.24	FALSE
267084_at	unknown protein ; supported by	---	AT2G41180	-2.80	-1.49	-2.40	0.0491978	0.2121765	-4.24	FALSE
256856_at	Expressed protein ; supported by	---	AT3G15110	-1.49	-0.58	-2.39	0.0492326	0.2122463	-4.24	FALSE
248977_at	putative protein strong similarity t	---	AT5G45020	-1.44	-0.52	-2.39	0.0492324	0.2122463	-4.24	FALSE
250323_at	putative protein hydroxyproline-r	---	AT5G12880	2.73	1.45	2.39	0.0492527	0.2122527	-4.24	FALSE
256680_at	unknown protein ; supported by f	---	AT3G52230	-1.48	-0.57	-2.39	0.0492434	0.2122527	-4.24	FALSE
257787_at	actin related protein, putative sir	ARP2	AT3G27000	-1.23	-0.30	-2.39	0.0492811	0.2122949	-4.24	FALSE
259062_at	unknown protein est hits to gens	---	AT3G07440	-1.47	-0.56	-2.39	0.0492805	0.2122949	-4.24	FALSE
249581_at	glutamate--ammonia ligase ; sup	GSR 1	AT5G37600	1.30	0.37	2.39	0.0492964	0.212321	-4.24	FALSE
258215_at	phosphoprotein phosphatase, pu	atToc64-III	AT3G17970	-1.49	-0.58	-2.39	0.0493299	0.2123373	-4.24	FALSE
265109_s_a	NBS/LRR disease resistance pr	---	AT1G62630 ///	-1.57	-0.65	-2.39	0.0493375	0.2123373	-4.24	FALSE
260118_s_a	hypothetical protein predicted by	---	AT1G33940 ///	-1.42	-0.51	-2.39	0.0493173	0.2123373	-4.24	FALSE
262485_at	kinesin-like protein Similar to gb|	---	AT1G21730	-1.26	-0.33	-2.39	0.04933	0.2123373	-4.24	FALSE
253581_at	stress responsive protein homol	---	AT4G30660	-1.81	-0.86	-2.39	0.0493718	0.212445	-4.24	FALSE
260948_at	delta 9 desaturase, putative sim	---	AT1G06100	1.35	0.43	2.39	0.0494092	0.2125656	-4.24	FALSE
262392_at	hypothetical protein predicted by	---	AT1G49520	1.48	0.57	2.39	0.0494783	0.2128038	-4.24	FALSE
265010_at	T-complex chaperonin protein ,	---	AT1G24510	-1.50	-0.59	-2.39	0.0494832	0.2128038	-4.24	FALSE
258046_at	MAP kinase kinase 5 identical to	MKK5	AT3G21220	1.32	0.40	2.39	0.0495572	0.2130181	-4.25	FALSE
264441_at	Expressed protein ; supported by	---	AT1G27435	-1.37	-0.46	-2.39	0.049561	0.2130181	-4.25	FALSE
261320_at	unknown protein ; supported by	---	AT1G53120	-1.27	-0.34	-2.39	0.0495603	0.2130181	-4.25	FALSE
266596_at	hypothetical protein predicted by	---	AT2G46150	1.98	0.98	2.39	0.0496275	0.2132637	-4.25	FALSE
260734_at	disease resistance protein RPP1	---	AT1G17600	1.39	0.48	2.39	0.0496579	0.2133539	-4.25	FALSE
250493_at	putative protein various predicte	---	AT5G09800	5.70	2.51	2.39	0.0497299	0.2136232	-4.25	FALSE
265120_at	3-ketoacyl-acyl carrier protein sy	KAS III	AT1G62640	-1.39	-0.48	-2.39	0.0497565	0.213697	-4.25	FALSE
265245_at	unknown protein	---	AT2G43060	-1.66	-0.73	-2.39	0.0497682	0.2137074	-4.25	FALSE
246253_at	myb-related protein	MYB73	AT4G37260	1.46	0.54	2.39	0.0497967	0.2137892	-4.25	TRUE
259881_at	Expressed protein ; supported by	---	AT1G76820	-1.50	-0.59	-2.39	0.0498316	0.2138711	-4.25	TRUE
261603_at	DNA binding protein ACBF, puta	ATRBP47A	AT1G49600	-1.73	-0.79	-2.39	0.049835	0.2138711	-4.25	FALSE
252806_at	putative protein	---	AT3G42390	1.30	0.38	2.39	0.0498439	0.2138711	-4.25	FALSE
245574_at	hypothetical protein	IQD19	AT4G14750	1.48	0.56	2.39	0.0498818	0.2139009	-4.25	FALSE
259670_at	protein kinase, putative similar t	---	AT1G52310	-1.38	-0.47	-2.39	0.0498977	0.2139009	-4.25	FALSE

255942_at	UDP-glucose glucosyltransferase	AtUGT85A2	AT1G22360	2.49	1.32	2.39	0.0498733	0.2139009	-4.25	FALSE
261241_at	subtilisin-like serine protease cor	---	AT1G32950	1.29	0.36	2.39	0.0498957	0.2139009	-4.25	FALSE
250290_at	putative protein ;supported by fu	---	AT5G13310	-1.27	-0.35	-2.39	0.0498741	0.2139009	-4.25	FALSE
250974_at	meiosis specific - like protein Sp	RHL2	AT5G02820	-1.79	-0.84	-2.39	0.0499119	0.2139215	-4.25	FALSE
251683_at	putative protein several hypothe	---	AT3G57120	1.79	0.84	2.38	0.0499607	0.2140568	-4.25	TRUE
265016_at	unknown protein similar to deac	---	AT1G24420	1.25	0.32	2.38	0.0499622	0.2140568	-4.25	FALSE
264645_at	unknown protein Similar to Sacc	---	AT1G08940	2.29	1.19	2.38	0.0499759	0.2140751	-4.25	TRUE
259673_at	putative phorbol ester / diacylgly	---	AT1G77800	-1.43	-0.52	-2.38	0.050023	0.2142366	-4.26	FALSE
245694_at	EF - hand Calcium binding protei	---	AT5G04170	1.28	0.36	2.38	0.0500437	0.2142849	-4.26	FALSE
260749_at	hypothetical protein predicted by	---	AT1G49110	1.36	0.44	2.38	0.0500571	0.2143024	-4.26	FALSE
266089_at	hypothetical protein predicted by	---	AT2G38010	1.72	0.78	2.38	0.0500813	0.2143654	-4.26	FALSE
260415_at	putative protein kinase similar to	---	AT1G69790	1.62	0.69	2.38	0.0501246	0.2144704	-4.26	FALSE
267512_at	hypothetical protein predicted by	SSE1	AT2G45690	-1.34	-0.42	-2.38	0.0501165	0.2144704	-4.26	FALSE
257793_at	unknown protein ;supported by f	---	AT3G26960	2.98	1.57	2.38	0.0502049	0.2146099	-4.26	TRUE
267056_at	hypothetical protein predicted by	---	AT2G32470	1.43	0.51	2.38	0.0501734	0.2146099	-4.26	FALSE
258625_at	hypothetical protein predicted by	PDLP4	AT3G04370	1.30	0.38	2.38	0.0501946	0.2146099	-4.26	FALSE
245474_at	hypothetical protein	---	AT4G16060	-1.38	-0.47	-2.38	0.0502136	0.2146099	-4.26	FALSE
256306_at	lipase, putative contains Pfam p	---	AT1G30370	6.81	2.77	2.38	0.0502085	0.2146099	-4.26	FALSE
263972_at	unknown protein	---	AT2G42760	2.47	1.30	2.38	0.0501804	0.2146099	-4.26	FALSE
266543_at	hypothetical protein predicted by	---	AT2G35075	-1.23	-0.30	-2.38	0.0502366	0.2146396	-4.26	FALSE
250509_at	cytochrome P450	CYP78A7	AT5G09970	-1.39	-0.48	-2.38	0.0502394	0.2146396	-4.26	FALSE
259512_at	hypothetical protein ; supported b	KEU	AT1G12360	1.25	0.32	2.38	0.0502516	0.2146516	-4.26	FALSE
249048_at	auxin-repressed protein-like ;sup	---	AT5G44300	1.31	0.39	2.38	0.050279	0.2147285	-4.26	FALSE
267055_at	unknown protein	PRA1.B4	AT2G38360	2.05	1.03	2.38	0.0502965	0.214746	-4.26	TRUE
256038_at	hypothetical protein similar to pol	---	AT1G19170	-1.37	-0.46	-2.38	0.050302	0.214746	-4.26	FALSE
246666_at	hypothetical protein	---	AT5G34830	1.24	0.31	2.38	0.050363	0.2149262	-4.26	FALSE
260849_at	pectinesterase, putative similar t	sks7	AT1G21860	1.25	0.32	2.38	0.0503566	0.2149262	-4.26	FALSE
253745_at	putative protein the C-terminus c	---	AT4G29090	1.29	0.37	2.38	0.0503879	0.214992	-4.26	FALSE
252824_at	histone H3.3 ; supported by cDN	---	AT4G40030	-1.34	-0.42	-2.38	0.050421	0.2150898	-4.26	TRUE
261049_at	hypothetical protein similar to hy	---	AT1G01430	-1.52	-0.61	-2.38	0.0504296	0.2150898	-4.26	FALSE
261487_at	hypothetical protein predicted by	---	AT1G14340	-1.29	-0.36	-2.38	0.0504933	0.2151199	-4.26	FALSE
255010_at	lipase-like protein monoglyceride	---	AT4G10050	-1.28	-0.35	-2.38	0.050466	0.2151199	-4.26	FALSE
258752_at	hypothetical protein predicted by	ATEXO70H	AT3G09520	1.74	0.80	2.38	0.050476	0.2151199	-4.26	FALSE
254043_at	putative protein ; supported by cI	CIL	AT4G25990	-2.29	-1.20	-2.38	0.0504792	0.2151199	-4.26	FALSE
254723_at	ammonium transport protein (AM	AMT1;1	AT4G13510	1.45	0.53	2.38	0.0504908	0.2151199	-4.26	FALSE

244968_at	ribosomal protein L33	---	---	-1.35	-0.43	-2.38	0.0504762	0.2151199	-4.26	FALSE
262348_at	unknown protein similar to transc	---	AT2G48160	-1.27	-0.34	-2.38	0.0505095	0.215149	-4.26	FALSE
267011_at	unknown protein	---	AT2G39230	-1.43	-0.52	-2.38	0.0505468	0.2151792	-4.27	FALSE
247287_at	unknown protein ; supported by	---	AT5G64230	1.66	0.73	2.38	0.0505536	0.2151792	-4.27	FALSE
259650_at	leucoanthocyanidin dioxygenase	---	AT1G55290	1.31	0.39	2.38	0.0505544	0.2151792	-4.27	FALSE
265227_s_a	hypothetical protein	---	AT2G07695	1.38	0.46	2.38	0.0505282	0.2151792	-4.27	FALSE
252902_at	putative protein various predicte	---	AT4G39560	-1.30	-0.38	-2.38	0.0505686	0.2151801	-4.27	FALSE
247443_at	putative protein predicted protei	---	AT5G62720	-1.51	-0.60	-2.38	0.0505735	0.2151801	-4.27	FALSE
259058_at	putative cytochrome P450 simila	CYP89A9	AT3G03470	-1.86	-0.89	-2.38	0.0506358	0.2153107	-4.27	TRUE
262056_at	Expressed protein ; supported by	---	AT1G80245	-1.33	-0.41	-2.37	0.0506638	0.2153107	-4.27	FALSE
251546_at	putative protein predicted protei	---	AT3G58830	-1.52	-0.61	-2.37	0.0506587	0.2153107	-4.27	FALSE
249035_at	putative protein contains similarit	GLK2	AT5G44190	-1.37	-0.46	-2.38	0.0506249	0.2153107	-4.27	FALSE
256241_at	nascent polypeptide associated	---	AT3G12390	-1.64	-0.71	-2.37	0.0506702	0.2153107	-4.27	FALSE
251326_at	putative protein stamina pistilloid	HWS	AT3G61590	-1.44	-0.52	-2.38	0.0506161	0.2153107	-4.27	FALSE
249199_at	putative protein similar to unknov	BPC6	AT5G42520	-1.31	-0.39	-2.37	0.0506587	0.2153107	-4.27	FALSE
247754_at	putative protein	---	AT5G59080	-1.94	-0.96	-2.37	0.05068	0.2153121	-4.27	FALSE
251752_at	proline transporter 2	PROT2	AT3G55740	1.54	0.62	2.37	0.0507144	0.2153995	-4.27	FALSE
245530_at	splicing factor like protein	---	---	1.35	0.44	2.37	0.0507195	0.2153995	-4.27	FALSE
251342_at	putative protein SAUR-AC1, Ara	---	AT3G60690	-1.45	-0.54	-2.37	0.0507373	0.2154124	-4.27	TRUE
250135_at	putative protein	---	AT5G15360	-1.31	-0.39	-2.37	0.050743	0.2154124	-4.27	FALSE
261784_at	hypothetical protein predicted by	---	AT1G08220	-1.29	-0.36	-2.37	0.0507508	0.2154124	-4.27	FALSE
254734_at	methionyl-tRNA synthetase - like	---	AT4G13780	-1.33	-0.42	-2.37	0.0507631	0.2154244	-4.27	FALSE
260770_at	RING-H2 finger protein RHA3a,	---	AT1G49200	-3.26	-1.70	-2.37	0.0507997	0.215493	-4.27	FALSE
247149_at	unknown protein ;supported by f	---	AT5G65660	-1.78	-0.83	-2.37	0.0508045	0.215493	-4.27	FALSE
255995_at	receptor-like serine/threonine kir	RKF1	AT1G29750	1.40	0.49	2.37	0.0508076	0.215493	-4.27	FALSE
263687_at	unknown protein ;supported by f	---	AT1G26940	-1.46	-0.55	-2.37	0.0508424	0.2156004	-4.27	FALSE
252934_at	Inositol monophosphatase - like	IMPL2	AT4G39120	-1.43	-0.51	-2.37	0.0509207	0.2158524	-4.27	FALSE
255004_at	putative protein	---	AT4G09970	-1.41	-0.50	-2.37	0.0509186	0.2158524	-4.27	FALSE
258642_at	unknown protein ;supported by f	---	AT3G07910	-1.27	-0.34	-2.37	0.0509602	0.2158591	-4.27	FALSE
254464_at	putative protein retinoblastoma b	---	AT4G20400	-1.46	-0.54	-2.37	0.0509324	0.2158591	-4.27	FALSE
246265_at	phosphoribosyl-ATP pyrophosph	AT-IE	AT1G31860	-1.78	-0.83	-2.37	0.050951	0.2158591	-4.27	FALSE
251640_at	putative protein ;supported by fu	---	AT3G57450	2.78	1.47	2.37	0.0509458	0.2158591	-4.27	FALSE
250049_at	putative protein predicted protei	---	AT5G17780	1.33	0.41	2.37	0.0510013	0.2159934	-4.27	FALSE
249933_at	rac GTPase activating protein	---	AT5G22400	1.27	0.34	2.37	0.0511033	0.2160377	-4.28	FALSE
253622_at	cyclic nucleotide and calmodulin	ATCNGC9	AT4G30560	1.30	0.37	2.37	0.051116	0.2160377	-4.28	FALSE

259277_at	putative glycogen synthase simil	AtSS2	AT3G01180	1.51	0.59	2.37	0.0510353	0.2160377	-4.27	FALSE
250027_at	putative protein similar to unknov	---	AT5G18250	-1.41	-0.49	-2.37	0.0511009	0.2160377	-4.28	FALSE
247670_at	putative protein predicted protei	---	AT5G60190	-1.42	-0.50	-2.37	0.0511144	0.2160377	-4.28	FALSE
254986_at	putative protein SF16 protein -H	IQD16	AT4G10640	1.24	0.31	2.37	0.0510728	0.2160377	-4.28	FALSE
248187_at	zinc-binding protein-like ; suppo	---	AT5G53940	-1.33	-0.41	-2.37	0.0511099	0.2160377	-4.28	FALSE
250341_at	MAP3K delta-1 protein kinase	---	AT5G11850	1.25	0.33	2.37	0.0510577	0.2160377	-4.28	FALSE
260163_at	putative carnitine/acylcarnitine tr	BAC2	AT1G79900	2.31	1.21	2.37	0.0510734	0.2160377	-4.28	FALSE
267410_at	hypothetical protein predicted by	EDA18	AT2G34920	-1.63	-0.70	-2.37	0.0510898	0.2160377	-4.28	FALSE
256700_at	pseudouridine synthase, putativ	---	AT3G52260	-1.28	-0.35	-2.37	0.0510881	0.2160377	-4.28	FALSE
262095_at	hypothetical protein predicted by	---	AT1G56090	-1.44	-0.52	-2.37	0.0511354	0.2160399	-4.28	FALSE
255280_at	score=179, E=5.7e-06, N=1)	---	AT4G04960	1.80	0.84	2.37	0.0511315	0.2160399	-4.28	FALSE
250278_at	2-oxoglutarate/malate translocat	DiT1	AT5G12860	-1.60	-0.68	-2.37	0.0511491	0.2160577	-4.28	FALSE
263922_s_a	putative pyruvate kinase ;suppo	---	AT2G36580 /	1.26	0.33	2.37	0.0512215	0.2162832	-4.28	FALSE
246651_at	adenylate kinase -like protein ac	---	AT5G35170	-1.45	-0.54	-2.37	0.0512186	0.2162832	-4.28	FALSE
254667_at	glycine-rich cell wall protein-like	---	AT4G18280	1.71	0.77	2.37	0.051276	0.2164735	-4.28	TRUE
254186_at	putative protein cellulose syntha	CSLG1	AT4G24010	1.32	0.40	2.37	0.0513238	0.2165951	-4.28	FALSE
265738_at	NADC homolog identical to GP|1	QPT	AT2G01350	1.33	0.41	2.37	0.0513162	0.2165951	-4.28	FALSE
253285_at	fatty acid elongase - like protein	KCS16	AT4G34250	1.68	0.75	2.37	0.0513387	0.2166178	-4.28	FALSE
251110_at	putative protein various alpha am	---	AT5G01260	-1.56	-0.64	-2.37	0.0513537	0.216641	-4.28	FALSE
258755_at	hypothetical protein identical to h	---	AT3G11945 /	-1.36	-0.44	-2.36	0.0513979	0.2167872	-4.28	FALSE
260399_at	putative lipoxygenase similar to l	---	AT1G72520	4.70	2.23	2.36	0.0514185	0.2168342	-4.28	FALSE
266155_at	cytochrome p450, putative simil	CYP89A5	AT1G64950 /	1.87	0.90	2.36	0.0514635	0.2169564	-4.28	TRUE
265867_at	unknown protein ;supported by f	MEE11	AT2G01620	-1.37	-0.46	-2.36	0.0514665	0.2169564	-4.28	FALSE
265913_at	Expressed protein ; supported by	---	AT2G25625	2.02	1.01	2.36	0.051548	0.2172599	-4.28	TRUE
266510_at	unknown protein	SWA1	AT2G47990	-1.75	-0.80	-2.36	0.0515754	0.2173352	-4.29	FALSE
258225_at	unknown protein ; supported by	---	AT3G15630	1.93	0.95	2.36	0.0515881	0.2173486	-4.29	TRUE
267371_at	Expressed protein ; supported by	---	AT2G44510	-1.53	-0.61	-2.36	0.0516558	0.2175936	-4.29	TRUE
252734_at	putative protein merozoite surfa	MEE38	AT3G43160	1.31	0.39	2.36	0.0516728	0.217625	-4.29	FALSE
255338_at	PEROXISOMAL MEMBRANE P	PMP22	AT4G04470	-1.26	-0.33	-2.36	0.05169	0.217657	-4.29	FALSE
255542_at	hypothetical protein	---	AT4G01860	-1.37	-0.45	-2.36	0.0517248	0.2177235	-4.29	FALSE
259665_at	unknown protein ; supported by	---	AT1G55160	-1.42	-0.50	-2.36	0.0517231	0.2177235	-4.29	FALSE
250543_at	DR1-like protein TATA-binding p	NF-YB12	AT5G08190	-1.31	-0.38	-2.36	0.051748	0.2177808	-4.29	FALSE
246662_at	putative protein	---	AT5G35290	1.30	0.38	2.36	0.0517809	0.2178792	-4.29	FALSE
264113_at	unknown protein	APG9	AT2G31260	1.37	0.45	2.36	0.0517954	0.2178999	-4.29	FALSE
249046_at	berberine bridge enzyme	---	AT5G44400	1.71	0.78	2.36	0.0518165	0.2179486	-4.29	FALSE

267470_at	cinnamate-4-hydroxylase molecu	C4H	AT2G30490	2.12	1.08	2.36	0.0518523	0.2180302	-4.29	FALSE
258671_at	putative vacuolar ATP synthase s	VHA-E2	AT3G08560	1.41	0.49	2.36	0.0518551	0.2180302	-4.29	FALSE
258764_at	putative pectinesterase contains	---	AT3G10720	1.80	0.85	2.36	0.0519	0.2180473	-4.29	TRUE
267411_at	putative disease resistance prote	---	AT2G34930	4.26	2.09	2.36	0.0518985	0.2180473	-4.29	FALSE
252298_at	putative protein various predicte	---	AT3G49060	1.27	0.34	2.36	0.0518786	0.2180473	-4.29	FALSE
264274_at	disease resistance protein RPS4	---	AT1G60320	1.30	0.38	2.36	0.0518844	0.2180473	-4.29	FALSE
267197_at	hypothetical protein predicted by	---	AT2G30960	-1.28	-0.36	-2.36	0.0519069	0.2180473	-4.29	FALSE
245036_at	putative SF16 protein {Helianthus	lqd4	AT2G26410	1.26	0.33	2.36	0.0519542	0.2181584	-4.29	FALSE
258321_at	early light-induced protein identic	ELIP1	AT3G22840	1.34	0.42	2.36	0.0519477	0.2181584	-4.29	FALSE
262772_at	puative calcium-transporting ATP	ACA.l	AT1G13210	1.72	0.78	2.36	0.051962	0.2181584	-4.29	FALSE
245981_at	putative protein ;supported by fu	---	AT5G13100	1.35	0.43	2.36	0.0519931	0.2181745	-4.29	FALSE
246957_at	unknown protein	---	AT5G24670	1.23	0.30	2.36	0.0519849	0.2181745	-4.29	FALSE
266772_s_a	predicted by genefinder	---	AT2G03020 ///	-1.52	-0.61	-2.36	0.0519946	0.2181745	-4.29	FALSE
260798_at	unknown protein contains similar	---	AT1G78280	1.54	0.62	2.36	0.052012	0.2182073	-4.29	FALSE
249891_at	unknown protein	---	AT5G22590	-1.21	-0.28	-2.36	0.0520485	0.2183205	-4.29	FALSE
251924_at	histone H4-like protein several hi	---	AT3G53730	-1.47	-0.56	-2.36	0.0520727	0.2183818	-4.29	FALSE
250536_at	Expressed protein ; supported by	---	AT5G08535	-1.35	-0.43	-2.36	0.052111	0.2184621	-4.30	FALSE
267379_at	unknown protein ; supported by	---	AT2G26340	-1.52	-0.61	-2.36	0.0521073	0.2184621	-4.30	FALSE
247910_at	putative protein similar to unknov	---	AT5G57410	-1.41	-0.49	-2.36	0.0521219	0.2184677	-4.30	FALSE
257689_at	myb-related protein, putative my	AtMYB10	AT3G12820	1.31	0.40	2.35	0.0521503	0.2185463	-4.30	FALSE
253183_at	putative protein predicted protei	---	AT4G35220	-1.26	-0.33	-2.35	0.0521684	0.2185821	-4.30	FALSE
256529_at	protein kinase, putative contains	---	AT1G33260	1.68	0.75	2.35	0.0522047	0.2186426	-4.30	TRUE
252923_at	kinesin like protein kinesin moto	---	AT4G39050	1.44	0.53	2.35	0.0522203	0.2186426	-4.30	FALSE
246418_at	quinone oxidoreductase -like pro	---	AT5G16960	1.40	0.48	2.35	0.0522252	0.2186426	-4.30	FALSE
262549_at	hypothetical protein similar to hyp	---	AT1G31290	1.27	0.35	2.35	0.0522308	0.2186426	-4.30	FALSE
260001_at	putative S-adenosyl-L-methionin	TSM1	AT1G67990	1.39	0.47	2.35	0.0522241	0.2186426	-4.30	FALSE
265671_at	40S ribosomal protein S12 ;supp	---	AT2G32060	-1.80	-0.85	-2.35	0.0522522	0.2186921	-4.30	FALSE
250390_at	separation anxiety protein - like	---	AT5G11340	-1.23	-0.30	-2.35	0.0523215	0.2187013	-4.30	FALSE
258432_at	unknown protein ;supported by f	RALFL23	AT3G16570	-1.57	-0.65	-2.35	0.0523129	0.2187013	-4.30	FALSE
246489_at	14-3-3 protein GF14upsilon (grf5	GRF5	AT5G16050	-1.33	-0.41	-2.35	0.0523098	0.2187013	-4.30	FALSE
257725_at	DNA mismatch repair protein MS	MSH2	AT3G18524	-1.45	-0.54	-2.35	0.0522907	0.2187013	-4.30	FALSE
259909_at	unknown protein ; supported by f	MEE9	AT1G60870	-1.28	-0.35	-2.35	0.0522943	0.2187013	-4.30	FALSE
247033_at	SKP1 interacting partner 2 (SKIP	SKIP2	AT5G67250	1.35	0.43	2.35	0.0522874	0.2187013	-4.30	FALSE
248628_at	putative protein contains similarit	---	AT5G48960	-1.32	-0.40	-2.35	0.0523098	0.2187013	-4.30	FALSE
258690_at	putative phosphatidylinositol-4-ph	---	AT3G07960	1.28	0.36	2.35	0.0523706	0.2188262	-4.30	FALSE

251138_at	putative protein various predicted	---	AT5G01160	-1.34	-0.42	-2.35	0.0523674	0.2188262	-4.30	FALSE
262360_at	receptor protein kinase, putative	---	AT1G73080 /	3.04	1.60	2.35	0.0523927	0.2188788	-4.30	FALSE
249360_at	putative protein KIAA0409 prote	---	AT5G40530	-1.30	-0.37	-2.35	0.0524175	0.2189424	-4.30	FALSE
266325_at	putative extensin	---	AT2G46630	2.43	1.28	2.35	0.0524921	0.2192136	-4.30	FALSE
248028_at	putative protein similar to unknov	---	AT5G55620	-1.94	-0.96	-2.35	0.0525081	0.2192402	-4.30	FALSE
265577_at	unknown protein	---	AT2G20100	-1.28	-0.35	-2.35	0.0525282	0.2192839	-4.30	FALSE
264190_at	heme activated protein, putative	NF-YC3	AT1G54830	-1.24	-0.31	-2.35	0.0525675	0.2193677	-4.30	FALSE
249861_at	Expressed protein ; supported by	---	AT5G22875	-1.35	-0.43	-2.35	0.0525583	0.2193677	-4.30	FALSE
267599_at	putative serine/threonine protein	---	AT2G32850	1.26	0.34	2.35	0.0526178	0.2195378	-4.31	FALSE
246484_at	UVB-resistance protein-like UVE	---	AT5G16040	-1.33	-0.42	-2.35	0.052641	0.219554	-4.31	FALSE
259377_at	putative poly(A) binding protein	PAB6	AT3G16380	1.41	0.50	2.35	0.0526354	0.219554	-4.31	FALSE
263618_at	hypothetical protein predicted by	APC2	AT2G04660	-1.39	-0.47	-2.35	0.0526591	0.2195893	-4.31	FALSE
248530_at	putative protein strong similarity	---	AT5G49945	-1.38	-0.46	-2.35	0.0526708	0.2195982	-4.31	FALSE
246870_at	ferrochelatase-I	FC1	AT5G26030	2.35	1.23	2.35	0.05273	0.2198049	-4.31	FALSE
255951_at	unknown protein contains similar	MUB6	AT1G22050	-1.38	-0.47	-2.35	0.0527616	0.2198962	-4.31	FALSE
247393_at	unknown protein	---	AT5G63130	3.19	1.67	2.35	0.0527971	0.2199054	-4.31	TRUE
247307_at	UVB-resistance protein UVR8 (g	---	AT5G21326 /	-1.28	-0.35	-2.35	0.0527853	0.2199054	-4.31	FALSE
249216_at	serine carboxypeptidase II-like ;	scpl42	AT5G42240	-1.69	-0.76	-2.35	0.0528024	0.2199054	-4.31	FALSE
259098_at	putative ribose 5-phosphate isor	---	AT3G04790	-1.54	-0.63	-2.35	0.0527847	0.2199054	-4.31	FALSE
251010_at	putative protein ;supported by fu	---	AT5G02550	1.41	0.49	2.35	0.0528213	0.219944	-4.31	FALSE
258505_at	hypothetical protein predicted by	---	AT3G06530	-2.15	-1.11	-2.35	0.0528694	0.2199535	-4.31	TRUE
250786_at	putative protein strong similarity	SDN2	AT5G05540	-1.44	-0.52	-2.35	0.0528718	0.2199535	-4.31	FALSE
252626_at	putative protein predicted protei	---	AT3G44940	1.41	0.49	2.35	0.052844	0.2199535	-4.31	FALSE
263794_at	similar to S-locus glycoproteins	---	AT2G24620	1.25	0.32	2.35	0.0528438	0.2199535	-4.31	FALSE
257078_at	putative MAP kinase very similar	---	AT3G15220	-1.29	-0.37	-2.35	0.0528571	0.2199535	-4.31	FALSE
256835_at	ATP sulfurylase, putative similar	APS1	AT3G22890	1.70	0.77	2.35	0.0528893	0.2199861	-4.31	FALSE
250108_at	homeobox-leucine zipper protein	ATHB-3	AT5G15150	1.40	0.48	2.34	0.0529436	0.2201721	-4.31	FALSE
260237_at	putative MYB family transcription	MYB95	AT1G74430	1.93	0.95	2.34	0.0529605	0.2202023	-4.31	FALSE
251052_at	DP-2 transcription factor - like tr	DPA	AT5G02470	-1.34	-0.42	-2.34	0.0529885	0.2202786	-4.31	FALSE
246108_at	putative protein retinal glutamic	---	AT5G28630	1.85	0.88	2.34	0.0530289	0.2203799	-4.31	FALSE
250265_at	putative protein predicted protei	---	AT5G12900	-1.48	-0.56	-2.34	0.0530322	0.2203799	-4.31	FALSE
258179_at	integral membrane protein, puta	---	AT3G21690	1.49	0.57	2.34	0.053059	0.2204107	-4.31	TRUE
248295_at	putative protein contains similarit	---	AT5G53070	-1.33	-0.41	-2.34	0.0530581	0.2204107	-4.31	FALSE
266566_at	unknown protein	---	AT2G24040	1.35	0.43	2.34	0.0531094	0.2205595	-4.31	FALSE
254388_at	Expressed protein ; supported by	MSRB2	AT4G21860	-1.30	-0.38	-2.34	0.0531141	0.2205595	-4.31	FALSE

266590_at	hypothetical protein predicted by	BAG6	AT2G46240	1.58	0.66	2.34	0.0531242	0.220561	-4.31	FALSE
261659_at	unknown protein contains similar	TOR	AT1G50030	-1.27	-0.35	-2.34	0.0532493	0.2210402	-4.32	FALSE
252292_at	RNA polymerase III subunit - like	---	AT3G49000	-1.34	-0.42	-2.34	0.0532897	0.2211462	-4.32	FALSE
257706_at	Expressed protein ; supported by	---	AT3G12685	-1.55	-0.63	-2.34	0.0532942	0.2211462	-4.32	FALSE
245690_at	phenylalanine ammonia-lyase PA	PAL3	AT5G04230	-1.64	-0.72	-2.34	0.0533136	0.2211863	-4.32	FALSE
249112_at	ATP sulfurylase precursor (gb|AA	APS4	AT5G43780	1.66	0.73	2.34	0.0533757	0.2214038	-4.32	FALSE
261346_at	putative aspartyl protease contai	---	AT1G79720	-1.32	-0.40	-2.34	0.0534543	0.2214299	-4.32	TRUE
267269_at	unknown protein	CAND1	AT2G02560	-1.33	-0.41	-2.34	0.0535082	0.2214299	-4.32	FALSE
263237_at	hypothetical protein contains sim	---	AT1G10610	-1.56	-0.64	-2.34	0.0534394	0.2214299	-4.32	FALSE
257553_at	unknown protein contains Pfam	TPR2	AT3G16830	-1.52	-0.61	-2.34	0.0535033	0.2214299	-4.32	FALSE
253828_at	putative protein predicted protei	SLAH2	AT4G27970	1.41	0.49	2.34	0.0534683	0.2214299	-4.32	FALSE
259974_at	putative phosphate transporter si	---	AT1G76430	1.39	0.47	2.34	0.053487	0.2214299	-4.32	FALSE
250232_at	unknown protein	---	AT5G13950	-1.28	-0.35	-2.34	0.0534424	0.2214299	-4.32	FALSE
255621_at	hypothetical protein	---	AT4G01390	-3.13	-1.64	-2.34	0.0534054	0.2214299	-4.32	FALSE
260394_at	putative transcription factor simil	MYB122	AT1G74080	3.74	1.90	2.34	0.0533935	0.2214299	-4.32	FALSE
249705_at	serine/threonine protein kinase-li	---	AT5G35580	1.50	0.58	2.34	0.0534442	0.2214299	-4.32	FALSE
248452_at	putative protein contains similarit	---	AT5G51300	-1.23	-0.30	-2.34	0.0534938	0.2214299	-4.32	FALSE
259037_at	hypothetical protein predicted by	---	AT3G09350	2.48	1.31	2.34	0.0534671	0.2214299	-4.32	FALSE
261640_at	permease, putative similar to pe	---	AT1G49960	1.35	0.43	2.34	0.0535003	0.2214299	-4.32	FALSE
263495_at	cold-regulated protein cor15b pre	COR15B	AT2G42530	-2.67	-1.42	-2.34	0.0535246	0.2214575	-4.32	FALSE
260663_at	hypothetical protein predicted by	NFD5	AT1G19520	-1.55	-0.63	-2.34	0.0535363	0.2214594	-4.32	FALSE
265797_at	Expressed protein ; supported by	---	AT2G35710	2.97	1.57	2.34	0.0535444	0.2214594	-4.32	FALSE
250380_at	putative protein	---	AT5G11600	-1.29	-0.37	-2.34	0.0535606	0.2214859	-4.32	FALSE
247338_at	pyruvate kinase	---	AT5G63680	1.30	0.37	2.34	0.0535758	0.2215086	-4.32	TRUE
251400_at	putative protein prib5, Ribes nigr	---	AT3G60420	2.99	1.58	2.34	0.0535986	0.2215627	-4.32	FALSE
262344_at	cytochrome b245 beta chain hor	ATRBOH F	AT1G64060	2.11	1.07	2.33	0.0537032	0.2219537	-4.33	FALSE
257764_at	disease resistance protein, puta	AtRLP36	AT3G23010	1.61	0.68	2.33	0.0537126	0.2219537	-4.33	FALSE
257489_at	hypothetical protein predicted by	---	AT1G07330	1.29	0.37	2.33	0.053727	0.221973	-4.33	FALSE
258549_at	putative arginine methyltransfera	PRMT4B	AT3G06930	-1.24	-0.31	-2.33	0.0537627	0.2219749	-4.33	FALSE
264168_at	unknown protein Similar to yeast	---	AT1G02080	-1.33	-0.41	-2.33	0.0537596	0.2219749	-4.33	FALSE
262279_at	hypothetical protein predicted by	---	AT1G68630	1.75	0.81	2.33	0.0537664	0.2219749	-4.33	FALSE
258645_s_a	exopolygalacturonase identical t	---	AT3G07850 ///	1.31	0.39	2.33	0.0537623	0.2219749	-4.33	FALSE
256061_at	unknown protein ;supported by fu	---	AT1G07040	1.55	0.63	2.33	0.0537808	0.2219943	-4.33	FALSE
254571_at	hypothetical protein	---	AT4G19370	2.83	1.50	2.33	0.0538094	0.222072	-4.33	FALSE
246613_at	acetyl-CoA carboxylase ;suppor	CAC2	AT5G35360	-1.40	-0.49	-2.33	0.0538254	0.2220978	-4.33	FALSE

263666_at	putative pre-mRNA splicing facto	---	AT1G04510	-1.46	-0.54	-2.33	0.0538491	0.2221156	-4.33	FALSE
264096_at	Expressed protein ; supported by	---	AT1G78995	-1.72	-0.78	-2.33	0.0538491	0.2221156	-4.33	FALSE
262625_at	hypothetical protein predicted by	---	AT1G06440	-1.25	-0.32	-2.33	0.0538604	0.2221217	-4.33	FALSE
267284_at	unknown protein predicted by ge	---	AT2G23700	1.40	0.49	2.33	0.053902	0.222253	-4.33	FALSE
248766_at	putative protein strong similarity t	---	AT5G47580	-1.74	-0.80	-2.33	0.0539348	0.2222734	-4.33	FALSE
254345_at	hypothetical protein ;supported b	---	AT4G22000	-1.52	-0.61	-2.33	0.0539459	0.2222734	-4.33	FALSE
259669_at	short chain alcohol dehydrogena	ABA2	AT1G52340	-1.38	-0.46	-2.33	0.0539445	0.2222734	-4.33	FALSE
256182_at	Expressed protein ; supported by	SYP81	AT1G51740	-1.41	-0.50	-2.33	0.0539412	0.2222734	-4.33	FALSE
262588_at	unknown protein Similar to gb|A	---	AT1G15130	1.31	0.39	2.33	0.0539742	0.2223098	-4.33	FALSE
AFFX-r2-At	Arabidopsis thaliana /REF=U37	---	---	-1.30	-0.38	-2.33	0.0539676	0.2223098	-4.33	FALSE
253594_at	Expressed protein ; supported by	---	AT4G30820	-1.36	-0.44	-2.33	0.0540011	0.2223803	-4.33	FALSE
252210_at	DNA binding protein	OBP1	AT3G50410	1.51	0.60	2.33	0.0540579	0.2225741	-4.33	FALSE
246754_at	transcription factor - like protein	NF-YC8	AT5G27910	1.42	0.51	2.33	0.0541024	0.222717	-4.33	FALSE
259389_at	hypothetical protein predicted by	---	AT1G06320	1.26	0.34	2.33	0.054161	0.2228378	-4.33	FALSE
246472_at	putative protein predicted protei	---	AT5G17130	1.24	0.31	2.33	0.0541574	0.2228378	-4.33	FALSE
248814_at	putative protein similar to unknov	---	AT5G46910	3.22	1.69	2.33	0.054154	0.2228378	-4.33	FALSE
259124_at	floral homeotic protein AGL4 ide	ספס-02	AT3G02310	1.23	0.30	2.33	0.0541737	0.2228498	-4.33	FALSE
255968_at	Expressed protein ; supported by	---	AT1G22270	-1.36	-0.44	-2.33	0.0542394	0.2230397	-4.34	FALSE
263583_at	putative NAD+ dependent isocitr	IDH2	AT2G17130	1.49	0.57	2.33	0.0542363	0.2230397	-4.34	FALSE
247206_at	putative protein similar to unknov	---	AT5G64950	-1.22	-0.28	-2.33	0.0542969	0.2232357	-4.34	FALSE
257795_at	hypothetical protein predicted by	---	AT3G15910	1.40	0.48	2.33	0.0544445	0.2237209	-4.34	FALSE
249171_at	putative protein contains similarit	---	AT5G42940	1.39	0.48	2.33	0.0544373	0.2237209	-4.34	FALSE
266945_at	hypothetical protein predicted by	VEL2	AT2G18880	1.26	0.34	2.32	0.0544541	0.2237209	-4.34	FALSE
265232_s_a	hypothetical protein	---	AT2G07715	1.35	0.43	2.32	0.0544514	0.2237209	-4.34	FALSE
262703_at	putative auxin-induced protein si	---	AT1G16510	-1.49	-0.58	-2.32	0.054475	0.2237259	-4.34	FALSE
247078_at	unknown protein ; supported by	---	AT5G66000	-1.33	-0.41	-2.32	0.0544693	0.2237259	-4.34	FALSE
250971_at	putative protein ABI3-interacting	PRR7	AT5G02810	-1.32	-0.40	-2.32	0.05449	0.2237473	-4.34	FALSE
262108_at	unknown protein similar to unkno	---	AT1G02740	-1.36	-0.45	-2.32	0.0545006	0.2237507	-4.34	FALSE
249537_at	cysteine-tRNA ligase -like protei	---	AT5G38830	1.40	0.49	2.32	0.0545249	0.2237701	-4.34	FALSE
256340_at	DnaJ protein, putative contains	---	AT1G72070	1.34	0.42	2.32	0.0545158	0.2237701	-4.34	FALSE
249519_at	putative protein similar to unknov	APE1	AT5G38660	-1.40	-0.49	-2.32	0.0545419	0.2237994	-4.34	FALSE
255020_at	isoleucine-tRNA ligase - like pro	---	AT4G10320	-1.22	-0.29	-2.32	0.0545627	0.2238446	-4.34	FALSE
251370_at	putative protein prib5, Ribes nig	---	AT3G60450	2.13	1.09	2.32	0.0545777	0.2238657	-4.34	FALSE
258390_at	unknown protein similar to leucin	---	AT3G15410	-1.29	-0.37	-2.32	0.0546067	0.223904	-4.34	FALSE
251383_at	beta-tubulin cofactor - like protei	TTN1	AT3G60740	-1.51	-0.60	-2.32	0.0546056	0.223904	-4.34	FALSE

265841_at	putative glycogenin	---	AT2G35710	3.44	1.78	2.32	0.0546254	0.2239408	-4.34	FALSE
250789_at	putative protein contains similarit	---	AT5G05630	-1.32	-0.40	-2.32	0.054644	0.2239767	-4.34	FALSE
256016_at	hypothetical protein predicted by	---	AT1G19240	-1.36	-0.44	-2.32	0.0547279	0.2241447	-4.34	FALSE
250803_at	putative protein contains similarit	---	AT5G04980	1.52	0.60	2.32	0.0547106	0.2241447	-4.34	FALSE
265767_at	putative exonuclease contains zi	REF4	AT2G48110	1.34	0.42	2.32	0.0547164	0.2241447	-4.34	FALSE
254736_at	putative disease resistance prot	---	AT4G13820	1.63	0.70	2.32	0.0547342	0.2241447	-4.34	FALSE
246656_at	hypothetical protein	---	---	1.33	0.42	2.32	0.0547306	0.2241447	-4.34	FALSE
253400_at	putative protein unknown protein	---	AT4G32860	1.26	0.33	2.32	0.0547833	0.2243056	-4.35	FALSE
257960_at	S-adenosylmethionine decarbox	---	AT3G25570 /	1.25	0.32	2.32	0.0548077	0.2243655	-4.35	FALSE
257628_at	cytochrome P450, putative conta	CYP71B26	AT3G26290	-1.77	-0.83	-2.32	0.0548318	0.2244239	-4.35	TRUE
264372_at	lactoylglutathione lyase-like prot	ATGLX1	AT1G11840	1.49	0.58	2.32	0.0549183	0.2247001	-4.35	TRUE
265614_at	Expressed protein ; supported by	---	AT2G25355	-1.41	-0.50	-2.32	0.054919	0.2247001	-4.35	FALSE
263603_at	hypothetical protein	---	AT2G16340	1.38	0.47	2.32	0.0549501	0.2247868	-4.35	FALSE
254125_at	putative alliin lyase alliin lyase (E	TAR2	AT4G24670	-1.72	-0.79	-2.32	0.0550102	0.2249923	-4.35	FALSE
263681_at	hypothetical protein predicted by	ORC6	AT1G26840	-1.45	-0.54	-2.32	0.0550429	0.2250453	-4.35	FALSE
251022_at	putative protein Hsp70 binding p	---	AT5G02150	-1.34	-0.42	-2.32	0.0550337	0.2250453	-4.35	FALSE
264242_at	hypothetical protein predicted by	---	AT1G54640	1.22	0.29	2.32	0.0550697	0.2251146	-4.35	FALSE
251262_at	hypothetical protein ; supported	---	AT3G62080	-1.51	-0.59	-2.32	0.055123	0.2252923	-4.35	FALSE
247456_at	iron-regulated transporter - like p	AtZIP12	AT5G62160	1.29	0.36	2.32	0.0551639	0.2253913	-4.35	FALSE
251643_at	guanylate kinase-like protein gu	AGK2	AT3G57550	1.88	0.91	2.32	0.055167	0.2253913	-4.35	FALSE
250006_at	putative protein 2'-hydroxyisofla	PCB2	AT5G18660	-2.01	-1.01	-2.32	0.0552318	0.2254318	-4.35	TRUE
264323_at	putative dimethylaniline monooxy	---	AT1G04180	2.55	1.35	2.31	0.055267	0.2254318	-4.35	FALSE
262310_at	unknown protein contains similar	MLP31	AT1G70840	1.31	0.38	2.32	0.0552323	0.2254318	-4.35	FALSE
245043_at	putative cyclin ;supported by full	RCY1	AT2G26430	-1.55	-0.64	-2.31	0.0552528	0.2254318	-4.35	FALSE
266913_at	hypothetical protein predicted by	ROPGEF4	AT2G45890	1.24	0.31	2.31	0.0552622	0.2254318	-4.35	FALSE
252583_at	putative protein several hypothet	---	AT3G45540	1.31	0.39	2.31	0.0552794	0.2254318	-4.35	FALSE
258133_at	ethylene-responsive transcriptio	MBF1C	AT3G24500	1.45	0.53	2.31	0.0552856	0.2254318	-4.35	FALSE
262233_at	hypothetical protein contains sim	CHR18	AT1G48310	-1.27	-0.35	-2.31	0.0552586	0.2254318	-4.35	FALSE
262377_at	rubisco activase, putative simila	---	AT1G73110	-1.64	-0.71	-2.31	0.0552715	0.2254318	-4.35	FALSE
250035_at	putative protein contains similarit	---	AT5G18230	-1.25	-0.32	-2.32	0.0552091	0.2254318	-4.35	FALSE
250407_at	chorismate mutase CM2 ; suppo	ATCM2	AT5G10870	-1.29	-0.37	-2.32	0.0552258	0.2254318	-4.35	FALSE
253948_at	Avr9 elicitor response like protei	---	AT4G26940	1.30	0.37	2.31	0.0553213	0.225537	-4.35	FALSE
249100_at	unknown protein	---	AT5G43560	1.31	0.39	2.31	0.0553373	0.2255619	-4.35	FALSE
265825_at	ubiquitin-like (UBQ7), putative si	UBQ7	AT2G35635	-1.32	-0.40	-2.31	0.0554045	0.225634	-4.36	FALSE
264848_at	unknown protein ;supported by f	---	AT2G17350	-1.24	-0.31	-2.31	0.0553966	0.225634	-4.36	FALSE

262908_at	pyruvate dehydrogenase e1 alpl	AT-E1 ALP	AT1G59900	-1.28	-0.35	-2.31	0.0554016	0.225634	-4.36	FALSE
261218_at	ferredoxin--NADP reductase pre	FNR2	AT1G20020	-1.53	-0.62	-2.31	0.055388	0.225634	-4.36	FALSE
253178_at	putative protein predicted protei	---	AT4G35170	1.36	0.44	2.31	0.0553896	0.225634	-4.36	FALSE
265991_at	chloroplast single subunit DNA-d	SCA3	AT2G24120	-1.59	-0.67	-2.31	0.055429	0.2256695	-4.36	TRUE
261014_at	unknown protein ;supported by fu	---	AT1G26460	-1.30	-0.38	-2.31	0.055433	0.2256695	-4.36	FALSE
253042_at	formamidase - like protein forma	---	AT4G37550	-1.56	-0.64	-2.31	0.0554845	0.2258186	-4.36	TRUE
257666_at	bactericidal permeability-increas	---	AT3G20270	1.55	0.64	2.31	0.0554894	0.2258186	-4.36	FALSE
263466_at	hypothetical protein predicted by	---	AT2G31740	-1.25	-0.33	-2.31	0.0555042	0.2258385	-4.36	FALSE
262526_at	putative prenyl transferase (prep	SPS2	AT1G17050	-2.02	-1.02	-2.31	0.0555161	0.2258466	-4.36	FALSE
261135_at	defensin AMP1, putative similar	PDF1.4	AT1G19610	-3.29	-1.72	-2.31	0.0555261	0.2258471	-4.36	TRUE
260058_at	unknown protein ; supported by	---	AT1G78100	-1.33	-0.41	-2.31	0.055546	0.2258473	-4.36	FALSE
260526_at	putative WD-40 repeat protein	---	AT2G47410	1.27	0.35	2.31	0.0555388	0.2258473	-4.36	FALSE
260266_at	putative B-box zinc finger protein	---	AT1G68520	-1.44	-0.52	-2.31	0.0556079	0.2260548	-4.36	FALSE
248597_at	DNA (cytosine-5)-methyltransfera	MET1	AT5G49160	-1.81	-0.86	-2.31	0.0556168	0.2260548	-4.36	FALSE
247577_at	putative protein flavin-containing	---	AT5G61290	-1.32	-0.40	-2.31	0.0556776	0.2262615	-4.36	FALSE
266917_at	unknown protein	DTA2	AT2G45830	-1.27	-0.34	-2.31	0.0556883	0.2262645	-4.36	FALSE
264833_at	putative protein phosphatase sim	---	AT1G03590	1.52	0.60	2.31	0.0557072	0.2263011	-4.36	TRUE
267185_at	unknown protein ; supported by	OEP37	AT2G43950	-1.33	-0.41	-2.31	0.0557438	0.2264097	-4.36	FALSE
260039_at	CLE12 CLAVATA3/ESR-Related	CLE12	AT1G68795	1.37	0.45	2.31	0.0557876	0.2265469	-4.36	FALSE
247364_at	putative protein similar to unknov	---	AT5G63200	-1.25	-0.33	-2.31	0.0558013	0.2265622	-4.36	FALSE
249298_at	putative protein similar to unknov	---	AT5G41330	1.29	0.36	2.31	0.0558329	0.2266506	-4.36	FALSE
250418_at	putative protein predicted protei	---	AT5G11240	-1.67	-0.74	-2.31	0.0558973	0.2266697	-4.36	FALSE
263759_at	hypothetical protein predicted by	---	AT2G21290	-1.31	-0.39	-2.31	0.0558959	0.2266697	-4.36	FALSE
258504_at	putative sterol-C5-desaturase ide	---	AT3G02590	1.23	0.30	2.31	0.0558804	0.2266697	-4.36	FALSE
261550_at	hypothetical protein	---	AT1G63450	1.28	0.36	2.31	0.0558789	0.2266697	-4.36	FALSE
257038_at	longevity factor-like protein simil	LOH2	AT3G19260	1.62	0.70	2.31	0.0558592	0.2266697	-4.36	FALSE
263032_at	unknown protein ;supported by fu	---	AT1G23850	1.87	0.90	2.31	0.055893	0.2266697	-4.36	FALSE
247865_at	Expressed protein ; supported by	---	AT5G57815	-1.27	-0.35	-2.31	0.0559121	0.2266895	-4.37	FALSE
258316_at	unknown protein	---	AT3G22660	-1.50	-0.59	-2.31	0.055931	0.2267258	-4.37	FALSE
257217_at	phosphoenolpyruvate carboxylas	ATPPC3	AT3G14940	-1.45	-0.53	-2.31	0.0559516	0.2267688	-4.37	FALSE
259112_at	putative 60S ribosomal protein L	---	AT3G05560	-1.70	-0.76	-2.31	0.0559759	0.2268274	-4.37	FALSE
247238_at	histone acetyltransferase	HAM1	AT5G64610	-1.24	-0.31	-2.31	0.0559932	0.226857	-4.37	FALSE
251807_at	methionyl-tRNA synthetase (Atcp	OVA1	AT3G55400	-1.39	-0.47	-2.31	0.0560386	0.2270007	-4.37	FALSE
260704_at	glycine cleavage system H prote	---	AT1G32470	-2.17	-1.12	-2.30	0.0560807	0.2271004	-4.37	TRUE
262232_at	unknown protein ; supported by	---	AT1G68600	1.51	0.59	2.30	0.0560831	0.2271004	-4.37	FALSE

253432_at	putative protein various predicted	---	AT4G32450	-1.25	-0.32	-2.30	0.0561029	0.2271399	-4.37	FALSE
259248_at	putative heat-shock protein simila	---	AT3G07770	-1.79	-0.84	-2.30	0.0561426	0.2272306	-4.37	TRUE
255692_at	putative protein	GPAT8	AT4G00400	2.32	1.22	2.30	0.0561605	0.2272306	-4.37	TRUE
260729_at	regulatory protein, putative conta	KU80	AT1G48050	-1.24	-0.31	-2.30	0.0561723	0.2272306	-4.37	FALSE
261798_at	hypothetical protein similar to hyp	CPSF30	AT1G30460	-1.34	-0.42	-2.30	0.056185	0.2272306	-4.37	FALSE
265370_s_a	unknown protein related to GB:A	---	AT3G30415	1.26	0.33	2.30	0.0561805	0.2272306	-4.37	FALSE
259521_at	ATP-dependent Clp protease pro	CLP2	AT1G12410	-1.37	-0.46	-2.30	0.056185	0.2272306	-4.37	FALSE
246347_at	putative protein probable chlorop	---	AT3G56830	-1.30	-0.38	-2.30	0.0562056	0.2272734	-4.37	FALSE
266213_s_a	Mutator-like transposase similar t	---	---	1.30	0.38	2.30	0.0562235	0.2273058	-4.37	FALSE
250957_at	photoreceptor-interacting protein	---	AT5G03250	-1.24	-0.31	-2.30	0.0562439	0.2273247	-4.37	FALSE
263798_at	putative ubiquitin carboxyl termin	UBP19	AT2G24640	1.25	0.32	2.30	0.0562482	0.2273247	-4.37	FALSE
263519_at	40S ribosomal protein S25 ; sup	---	AT2G21580	-1.65	-0.73	-2.30	0.0562813	0.2273378	-4.37	FALSE
247971_at	zinc protease PQQL-like protein	---	AT5G56730	-1.28	-0.36	-2.30	0.0562798	0.2273378	-4.37	FALSE
254861_at	putative protein zinc finger prote	---	AT4G12040	1.43	0.52	2.30	0.0562748	0.2273378	-4.37	FALSE
256238_at	unknown protein ; supported by f	ELC	AT3G12400	1.41	0.50	2.30	0.0563714	0.2276612	-4.37	FALSE
248997_at	beta-amylase-like	BMY2	AT5G45300	-1.46	-0.55	-2.30	0.0564118	0.2277781	-4.37	FALSE
260079_s_a	helix-loop-helix protein 1A, putat	---	AT1G35460 ///	-1.30	-0.38	-2.30	0.0564203	0.2277781	-4.37	FALSE
254418_at	glucose transporter glucose tran	---	AT4G21480	1.30	0.38	2.30	0.0564361	0.2278017	-4.37	FALSE
245363_at	hypothetical protein ;supported b	---	AT4G15120	2.38	1.25	2.30	0.0564569	0.227805	-4.37	FALSE
244938_at	ribosomal protein S15	---	---	-1.59	-0.67	-2.30	0.0564481	0.227805	-4.37	FALSE
253836_at	putative protein hypothetical pro	---	AT4G27840	-1.29	-0.37	-2.30	0.0564725	0.2278279	-4.38	FALSE
262887_at	hypothetical protein	---	AT1G14780	2.37	1.25	2.30	0.0565002	0.2278587	-4.38	FALSE
254700_at	hypothetical protein	---	AT4G18000	1.32	0.40	2.30	0.0564921	0.2278587	-4.38	FALSE
257755_at	unknown protein ; supported by	---	AT3G18760	-1.57	-0.65	-2.30	0.0565302	0.2278589	-4.38	FALSE
254658_at	putative protein predicted gene l	---	AT4G18230	-1.29	-0.37	-2.30	0.0565289	0.2278589	-4.38	FALSE
266886_at	Expressed protein ; supported by	---	AT2G44745	1.36	0.44	2.30	0.0565182	0.2278589	-4.38	FALSE
254020_at	beta-carotene hydroxylase ; sup	BETA-OHA	AT4G25700	2.42	1.28	2.30	0.0565661	0.2279632	-4.38	FALSE
251183_at	putative protein putative protein	---	AT3G62630	-2.25	-1.17	-2.30	0.0565909	0.2280231	-4.38	FALSE
265272_at	unknown protein	ARF10	AT2G28350	-1.46	-0.54	-2.30	0.0566211	0.2280397	-4.38	FALSE
252328_at	Expressed protein ; supported by	---	AT3G48570	1.28	0.36	2.30	0.0566246	0.2280397	-4.38	FALSE
255344_s_a	putative receptor-like protein kina	---	AT4G04540 ///	2.05	1.04	2.30	0.056625	0.2280397	-4.38	TRUE
252890_at	brassinosteroid insensitive 1 gen	BRI1	AT4G39400	-1.27	-0.35	-2.30	0.0566706	0.228183	-4.38	TRUE
255956_at	Expressed protein ; supported by	DD46	AT1G22015	1.33	0.41	2.30	0.05673	0.2283414	-4.38	FALSE
249600_s_a	oxidoreductase-like protein zeta	---	AT5G37940 ///	1.22	0.29	2.30	0.0567264	0.2283414	-4.38	FALSE
265002_at	putative lysine/histidine-specific	LHT2	AT1G24400	-1.47	-0.56	-2.30	0.0567801	0.2285028	-4.38	FALSE

263138_at	hypothetical protein predicted by	---	AT1G65090	1.24	0.31	2.30	0.0568379	0.228695	-4.38	FALSE
249944_at	NAM (no apical meristem)-like pr	anac089	AT5G22290	-1.89	-0.92	-2.30	0.0568551	0.2287238	-4.38	FALSE
258713_at	Expressed protein ; supported by	---	AT3G09735	-1.27	-0.34	-2.29	0.0568833	0.2287969	-4.38	FALSE
247243_at	nodulin-like protein	---	AT5G64700	1.53	0.61	2.29	0.0569042	0.2288408	-4.38	FALSE
245328_at	Expressed protein ; supported by	---	AT4G14465	1.28	0.36	2.29	0.0569508	0.2289877	-4.38	FALSE
248007_at	S-adenosylmethionine:2-demeth	---	AT5G56260	1.25	0.32	2.29	0.0569867	0.229092	-4.38	FALSE
255820_at	putative protein kinase contains a	---	AT2G40580	1.34	0.42	2.29	0.0570344	0.229243	-4.38	FALSE
259439_at	1-aminocyclopropane-1-carboxyl	ACS2	AT1G01480	3.97	1.99	2.29	0.0570725	0.2293385	-4.39	TRUE
249650_at	Expressed protein ; supported by	SEF	AT5G37055	-1.34	-0.43	-2.29	0.0570883	0.2293385	-4.39	FALSE
255638_at	predicted protein of unknown fun	---	AT4G00740	-1.41	-0.50	-2.29	0.0570867	0.2293385	-4.39	FALSE
267062_at	putative spliceosome associated	---	AT2G32600	-1.37	-0.45	-2.29	0.0571149	0.2293646	-4.39	FALSE
257935_at	unknown protein	---	AT3G25440	-1.29	-0.36	-2.29	0.0571093	0.2293646	-4.39	FALSE
253763_at	xyloglucan endotransglycosylas	---	AT4G28850	1.25	0.32	2.29	0.0571623	0.2294741	-4.39	FALSE
256935_at	unknown protein ;supported by f	---	AT3G22570	1.25	0.33	2.29	0.0571526	0.2294741	-4.39	FALSE
253293_at	Expressed protein ; supported by	---	AT4G33905	1.50	0.59	2.29	0.0572005	0.2295871	-4.39	FALSE
261796_at	non-phototropic hypocotyl, putat	---	AT1G30440	1.29	0.37	2.29	0.0572817	0.2296707	-4.39	TRUE
260148_at	putative oxidoreductase similar t	---	AT1G52800	-1.49	-0.57	-2.29	0.0572684	0.2296707	-4.39	FALSE
252378_at	receptor kinase-like protein prote	---	AT3G47570	1.50	0.59	2.29	0.0572666	0.2296707	-4.39	FALSE
260951_at	hypothetical protein similar to hy	---	AT1G06145 ///	-1.38	-0.47	-2.29	0.0572649	0.2296707	-4.39	FALSE
257260_at	hypothetical protein predicted by	---	AT3G22104	-1.44	-0.52	-2.29	0.0572814	0.2296707	-4.39	FALSE
246392_at	hypothetical protein predicted by	---	AT1G58120 ///	1.25	0.32	2.29	0.057241	0.2296707	-4.39	FALSE
244927_at	hypothetical protein	---	AT2G07776	1.39	0.47	2.29	0.0572923	0.2296725	-4.39	FALSE
264951_at	unknown protein contains similar	---	AT1G76970	1.23	0.30	2.29	0.057343	0.229674	-4.39	FALSE
252613_at	putative protein hypothetical pro	---	AT3G45190	-1.24	-0.31	-2.29	0.0573315	0.229674	-4.39	FALSE
255931_at	hypothetical protein similar to put	AtPP2-A12	AT1G12710	-1.55	-0.64	-2.29	0.0573254	0.229674	-4.39	FALSE
254688_at	DnaJ-like protein DnaJ-like prote	J20	AT4G13830	-1.29	-0.36	-2.29	0.0573384	0.229674	-4.39	FALSE
262017_at	elongation factor, putative simila	---	AT1G35550	-1.45	-0.54	-2.29	0.0573156	0.229674	-4.39	FALSE
260078_at	hypothetical protein predicted by	---	AT1G73790	-1.32	-0.40	-2.29	0.0573951	0.2298423	-4.39	FALSE
264357_at	hypothetical protein Similar to hy	ATRRP4	AT1G03360	-2.08	-1.05	-2.29	0.0574093	0.2298517	-4.39	FALSE
261946_at	unknown protein	---	AT1G64560	-1.38	-0.46	-2.29	0.0574176	0.2298517	-4.39	FALSE
256223_at	unknown protein ;supported by fu	emb1303	AT1G56200	-1.34	-0.42	-2.29	0.0574483	0.2298834	-4.39	FALSE
258918_at	putative cytochrome P450 simila	UNE9	AT3G10560	1.47	0.56	2.29	0.0574532	0.2298834	-4.39	FALSE
265952_at	unknown protein supported by cD	---	AT2G37478 ///	-1.29	-0.37	-2.29	0.0574557	0.2298834	-4.39	FALSE
245418_at	putative protein	---	AT4G17370	-1.42	-0.50	-2.29	0.057486	0.2299641	-4.39	FALSE
251837_s_a	spliceosomal - like protein splice	---	AT3G55200 ///	-1.36	-0.45	-2.29	0.0575011	0.2299843	-4.39	FALSE

248777_at	putative protein similar to unknov	---	AT5G47920	1.32	0.40	2.29	0.0575522	0.2301078	-4.39	FALSE
264155_at	unknown protein	GTB1	AT1G65440	1.45	0.54	2.29	0.0575503	0.2301078	-4.39	FALSE
256230_at	FKBP-type peptidyl-prolyl cis-tra	---	AT3G12340	-1.39	-0.47	-2.29	0.0575626	0.230109	-4.39	FALSE
252090_at	5B protein like protein cysteine-r	---	AT3G52130	1.27	0.34	2.29	0.0575835	0.2301524	-4.39	FALSE
253518_at	hypothetical protein	---	AT4G31400	-1.36	-0.44	-2.29	0.0575995	0.2301762	-4.39	FALSE
244950_at	cytochrome c oxidase subunit 2	---	---	1.51	0.60	2.29	0.0576307	0.2302602	-4.40	TRUE
246021_at	ascorbate oxidase-like protein a	---	AT5G21100	-1.51	-0.60	-2.29	0.0576603	0.2302978	-4.40	FALSE
249836_at	unknown protein ;supported by f	HMGB6	AT5G23420	-1.74	-0.80	-2.29	0.0576565	0.2302978	-4.40	FALSE
260178_at	hypothetical protein similar to unl	---	AT1G70720	1.30	0.38	2.28	0.0577256	0.2305185	-4.40	FALSE
248069_at	unknown protein	---	AT5G55650	1.31	0.39	2.28	0.0577371	0.230524	-4.40	FALSE
266979_at	unknown protein ;supported by f	PPL2	AT2G39470	-2.77	-1.47	-2.28	0.0578091	0.2306244	-4.40	TRUE
257794_at	hypothetical protein predicted by	---	AT3G27050	-1.40	-0.49	-2.28	0.057798	0.2306244	-4.40	FALSE
262912_at	oligopeptide transporter, putative	---	AT1G59740	2.54	1.34	2.28	0.0577871	0.2306244	-4.40	FALSE
259641_at	putative protease similar to prote	---	AT1G69020	-1.37	-0.45	-2.28	0.0578128	0.2306244	-4.40	FALSE
255773_at	flavonol 4'-sulfotransferase, puta	SOT17	AT1G18590	2.15	1.10	2.28	0.0577909	0.2306244	-4.40	FALSE
258922_at	putative 40S ribosomal protein S	---	AT3G10610	-1.93	-0.95	-2.28	0.0578375	0.2306825	-4.40	FALSE
254157_at	putative protein protein induced	VEP1	AT4G24220	1.31	0.39	2.28	0.0578536	0.2307066	-4.40	FALSE
253804_at	putative protein	---	AT4G28230	-1.34	-0.42	-2.28	0.0579146	0.2309093	-4.40	FALSE
257727_at	unknown protein	---	AT3G18380	-1.28	-0.36	-2.28	0.0579461	0.2309946	-4.40	FALSE
259116_at	putative peptide transporter simil	---	AT3G01350	-1.58	-0.66	-2.28	0.0579564	0.2309953	-4.40	FALSE
250578_at	proanthranilate N-benzoyltransfe	---	AT5G07850	-1.25	-0.32	-2.28	0.0579776	0.2310392	-4.40	FALSE
246390_at	1-aminocyclopropane-1-carboxy	---	AT1G77330	1.42	0.51	2.28	0.0579928	0.2310562	-4.40	FALSE
261932_at	hypothetical protein predicted by	---	AT1G22420	1.24	0.31	2.28	0.0580122	0.2310562	-4.40	FALSE
265071_at	transcription initiation factor TFIII	TBP2	AT1G55520	-1.30	-0.37	-2.28	0.0580119	0.2310562	-4.40	FALSE
249320_at	disease resistance protein-like n	---	AT5G40910	-1.47	-0.56	-2.28	0.058025	0.2310665	-4.40	FALSE
253754_at	glycine-rich protein like glycine-r	---	AT4G29020	2.51	1.33	2.28	0.0581002	0.2311644	-4.40	FALSE
245260_at	kinase like protein ; supported by	---	AT4G16360	-1.25	-0.32	-2.28	0.0580731	0.2311644	-4.40	FALSE
254184_at	hypothetical protein	---	AT4G23970	1.29	0.37	2.28	0.0580666	0.2311644	-4.40	FALSE
260168_at	unknown protein contains zinc fi	---	AT1G71980	-1.39	-0.48	-2.28	0.0580849	0.2311644	-4.40	FALSE
254337_at	putative protein hypothetical pro	---	AT4G22060	1.31	0.38	2.28	0.0580977	0.2311644	-4.40	FALSE
257746_at	chorismate mutase identical to cl	CM1	AT3G29200	1.26	0.33	2.28	0.0581563	0.2313287	-4.40	TRUE
255296_at	hypothetical protein	---	AT4G04790	-1.66	-0.73	-2.28	0.0581618	0.2313287	-4.40	FALSE
253911_at	putative receptor protein kinase	---	AT4G27300	-1.82	-0.87	-2.28	0.0582591	0.2315066	-4.41	TRUE
261547_at	protein kinase, putative contains	---	AT1G63500	1.30	0.38	2.28	0.0582656	0.2315066	-4.41	FALSE
259215_at	unknown protein largely predicte	DEX1	AT3G09090	-1.27	-0.34	-2.28	0.0582674	0.2315066	-4.41	FALSE

265007_s_a	Expressed protein ; supported by	RALFL8	AT1G61563 /.	1.22	0.28	2.28	0.0582377	0.2315066	-4.41	FALSE
265860_at	hypothetical protein predicted by	---	AT2G01810	1.25	0.32	2.28	0.0582197	0.2315066	-4.41	FALSE
252154_at	putative DNA-3-methyladenine g	---	AT3G50880	-1.43	-0.52	-2.28	0.0582334	0.2315066	-4.41	FALSE
246451_at	Inositol 1,3,4-Trisphosphate 5/6	---	AT5G16760	1.23	0.30	2.28	0.0582806	0.2315188	-4.41	FALSE
252182_at	U1 snRNP 70K protein ; support	U1-70K	AT3G50670	-1.28	-0.36	-2.28	0.0583714	0.2318392	-4.41	FALSE
248371_at	gibberellin 20-oxidase (emb|CAA	GA20OX2	AT5G51810	-1.92	-0.94	-2.28	0.0584119	0.2319595	-4.41	FALSE
258760_at	putative membrane protein simil	---	AT3G10780	1.63	0.70	2.28	0.0584246	0.2319694	-4.41	FALSE
260195_at	hypothetical protein predicted by	---	AT1G67540	1.30	0.37	2.28	0.0584731	0.2320981	-4.41	FALSE
261731_s_a	hypothetical protein similar to hy	---	AT1G47780 /.	1.24	0.31	2.28	0.0584773	0.2320981	-4.41	FALSE
256404_at	unknown protein similar to far-re	FRS7	AT3G06250	-1.42	-0.51	-2.28	0.0585023	0.2321568	-4.41	FALSE
259244_at	unknown protein similar to zinc fi	COL9	AT3G07650	1.78	0.83	2.27	0.0585978	0.2324549	-4.41	TRUE
267415_at	putative translation initiation fact	---	AT2G34970	-1.24	-0.31	-2.27	0.0585959	0.2324549	-4.41	FALSE
264635_at	unknown protein ;supported by fu	---	AT1G65500	2.05	1.04	2.27	0.0586344	0.2325596	-4.41	FALSE
260269_at	putative disease resistance prote	---	AT1G63740	1.37	0.45	2.27	0.0586447	0.23256	-4.41	FALSE
258787_at	hypothetical protein predicted by	PUB24	AT3G11840	3.31	1.73	2.27	0.0586578	0.2325717	-4.41	TRUE
252971_at	extensin - like protein proline-ric	PRP4	AT4G38770	5.24	2.39	2.27	0.0586735	0.2325936	-4.41	FALSE
263083_at	purple acid phosphatase precurs	PAP12	AT2G27190	-1.29	-0.37	-2.27	0.0587618	0.232701	-4.41	TRUE
253496_at	glutathione peroxidase - like pro	ATGPX7	AT4G31870	2.19	1.13	2.27	0.0587507	0.232701	-4.41	TRUE
260239_at	putative receptor protein kinase	---	AT1G74360	3.29	1.72	2.27	0.0587616	0.232701	-4.41	TRUE
257144_at	glucose-6-phosphate 1-dehydro	G6PD5	AT3G27300	-1.27	-0.35	-2.27	0.0587572	0.232701	-4.41	FALSE
264437_at	unknown protein EST gb|N65787	---	AT1G27510	-1.31	-0.39	-2.27	0.058747	0.232701	-4.41	FALSE
245129_at	hypothetical protein predicted by	CRR4	AT2G45350	-1.22	-0.29	-2.27	0.0587555	0.232701	-4.41	FALSE
264731_at	hypothetical protein predicted by	---	AT1G62150	-1.31	-0.39	-2.27	0.0588197	0.2328898	-4.42	FALSE
265013_at	unknown protein similar to EST g	---	AT1G24460	1.27	0.35	2.27	0.0588684	0.233042	-4.42	FALSE
251470_at	putative protein hypothetical pro	---	AT3G59570	1.37	0.46	2.27	0.0588931	0.2330589	-4.42	FALSE
257433_at	hypothetical protein predicted by	---	AT2G21990	-1.25	-0.32	-2.27	0.0588876	0.2330589	-4.42	FALSE
255507_at	AtKAP alpha similar to AtKAP, G	MOS6	AT4G02150	-1.23	-0.30	-2.27	0.0589078	0.2330765	-4.42	FALSE
260205_at	hypothetical protein predicted by	TIFY7	AT1G70700	1.86	0.90	2.27	0.0589409	0.2331583	-4.42	FALSE
249626_at	putative protein nucleoid DNA-b	---	AT5G37540	1.66	0.73	2.27	0.0589489	0.2331583	-4.42	FALSE
252018_at	putative protein various predicte	AtPP2-A15	AT3G53000	1.43	0.52	2.27	0.0590208	0.2333781	-4.42	FALSE
250696_at	putative protein similar to unknov	---	AT5G06790	-1.21	-0.27	-2.27	0.0590249	0.2333781	-4.42	FALSE
264566_at	hypothetical protein predicted by	---	AT1G05270	1.33	0.41	2.27	0.0590641	0.2334927	-4.42	FALSE
245810_at	axi 1 protein, putative similar to a	---	AT1G38065 /.	-1.32	-0.40	-2.27	0.0591005	0.2335958	-4.42	FALSE
266344_at	hypothetical protein predicted by	---	AT2G01580	1.27	0.34	2.27	0.0591401	0.2336915	-4.42	FALSE
247438_at	unknown protein ; supported by	---	AT5G62460	1.58	0.66	2.27	0.0591452	0.2336915	-4.42	FALSE

267225_at	hypothetical protein predicted by	---	AT2G44000	1.30	0.37	2.27	0.0591617	0.2337162	-4.42	FALSE
250827_at	cellulose synthase catalytic subu	CEV1	AT5G05170	-1.44	-0.52	-2.27	0.0592315	0.2337492	-4.42	TRUE
247215_at	Expressed protein ; supported by	PROPEP3	AT5G64905	4.27	2.09	2.27	0.0592314	0.2337492	-4.42	TRUE
247506_at	Mei2-like protein Mei2-like prote	AML1	AT5G61960	1.24	0.31	2.27	0.0592156	0.2337492	-4.42	FALSE
261148_at	unknown protein ; supported by f	GAMMA CA	AT1G19580	1.25	0.32	2.27	0.059185	0.2337492	-4.42	FALSE
267640_at	photomorphogenesis repressor (	COP1	AT2G32950	-1.39	-0.48	-2.27	0.0592175	0.2337492	-4.42	FALSE
256834_at	cyclophilin, putative similar to cy	---	AT3G22920	1.25	0.32	2.27	0.0591924	0.2337492	-4.42	FALSE
247721_at	elongin - like protein elongin C,	---	AT5G59140	-1.23	-0.30	-2.27	0.0592796	0.2337774	-4.42	FALSE
257350_x_a	hypothetical protein predicted by	RALFL12	AT2G19040	1.30	0.37	2.27	0.0592782	0.2337774	-4.42	FALSE
262612_at	unknown protein location of EST	---	AT1G14150	-1.92	-0.94	-2.27	0.0592694	0.2337774	-4.42	FALSE
257228_at	NADPH:quinone oxidoreductase	NQR	AT3G27890	1.26	0.34	2.27	0.059279	0.2337774	-4.42	FALSE
247831_at	putative protein serine/threonine	---	AT5G58540	1.58	0.66	2.27	0.0592932	0.2337905	-4.42	FALSE
263264_at	histone H2A ; supported by full-l	HTA8	AT2G38810	-1.57	-0.65	-2.27	0.0593757	0.2340754	-4.42	FALSE
258516_at	myb-related protein, putative sim	MYB108	AT3G06490	2.27	1.18	2.26	0.0593927	0.2341019	-4.42	FALSE
266360_at	Mutator-like transposase similar	FRS2	AT2G32250	1.72	0.78	2.26	0.0594539	0.2343027	-4.43	FALSE
250883_at	putative protein predicted protei	---	AT5G03970	-1.40	-0.49	-2.26	0.0595196	0.2343617	-4.43	TRUE
260781_at	decoy identical to GB:AAB51588	DECOY	AT1G14620	-2.13	-1.09	-2.26	0.0594997	0.2343617	-4.43	FALSE
253116_at	putative protein CRP1, Zea may	---	AT4G35850	-1.61	-0.68	-2.26	0.0595214	0.2343617	-4.43	FALSE
253584_at	putative protein several hypothet	---	AT4G30700	-1.28	-0.36	-2.26	0.0595305	0.2343617	-4.43	FALSE
258744_at	hypothetical protein similar to pl	---	AT3G05830	1.34	0.43	2.26	0.0595189	0.2343617	-4.43	FALSE
261282_at	hypothetical protein predicted by	APUM10	AT1G35750	-1.40	-0.48	-2.26	0.0595141	0.2343617	-4.43	FALSE
251150_at	putative protein Sb34 (PREG-lik	CYCP1;1	AT3G63120	-1.33	-0.41	-2.26	0.0595489	0.2343934	-4.43	TRUE
251028_at	putative protein putative hydrola	---	AT5G02230	1.34	0.43	2.26	0.0595722	0.2344404	-4.43	FALSE
265612_at	hypothetical protein predicted by	---	AT2G25390 /	-1.26	-0.34	-2.26	0.0596019	0.2344404	-4.43	FALSE
254258_at	hypothetical protein	TET5	AT4G23410	-1.36	-0.44	-2.26	0.0595991	0.2344404	-4.43	FALSE
262855_at	putative inorganic phosphate tran	---	AT1G20860	1.42	0.51	2.26	0.0595878	0.2344404	-4.43	FALSE
265723_at	putative disease resistance prote	---	AT2G32140	1.24	0.31	2.26	0.0596333	0.2345233	-4.43	FALSE
253614_at	putative protein heat shock prote	---	AT4G30350	1.57	0.65	2.26	0.0597036	0.2347517	-4.43	FALSE
262899_at	ABC transporter, putative simila	PEN3	AT1G59870	1.32	0.40	2.26	0.059712	0.2347517	-4.43	FALSE
256245_at	heat shock protein 70 identical to	HSP70	AT3G12580	2.94	1.56	2.26	0.0597517	0.2348675	-4.43	FALSE
266774_at	hypothetical protein predicted by	ATRBL1	AT2G29050	1.38	0.47	2.26	0.0597782	0.2349311	-4.43	FALSE
266583_at	Expressed protein ; supported by	---	AT2G46220	-1.43	-0.52	-2.26	0.0598548	0.2351511	-4.43	FALSE
245421_at	hypothetical protein	---	AT4G17430	-1.23	-0.30	-2.26	0.0598519	0.2351511	-4.43	FALSE
245759_at	hypothetical protein predicted by	---	AT1G66900	-1.39	-0.47	-2.26	0.0599206	0.2353691	-4.43	FALSE
255469_at	predicted OR23 protein of unkno	---	AT4G03030	-1.31	-0.39	-2.26	0.0599564	0.2354287	-4.43	FALSE

264696_at	unknown protein	---	AT1G70230	-1.86	-0.89	-2.26	0.0599491	0.2354287	-4.43	FALSE
267004_at	hypothetical protein predicted by	---	AT2G34260	-2.19	-1.13	-2.26	0.0600137	0.2356131	-4.43	TRUE
265601_at	hypothetical protein predicted by	---	AT2G14390	1.30	0.38	2.26	0.0600271	0.2356252	-4.44	FALSE
262533_at	hypothetical protein Pfam	---	AT1G17090	-1.31	-0.39	-2.26	0.0601027	0.2358812	-4.44	FALSE
256782_at	dirigent protein, putative similar	---	AT3G13660	1.23	0.30	2.26	0.0601324	0.2359572	-4.44	FALSE
252261_at	RNA-directed RNA polymerase F	RDR6	AT3G49500	-1.32	-0.40	-2.26	0.0601452	0.235967	-4.44	FALSE
265221_s_a	putative glutamate decarboxylas	GAD3	AT2G02000 /	2.59	1.37	2.26	0.0602076	0.2359981	-4.44	TRUE
250421_at	putative protein	OCP3	AT5G11270	-1.38	-0.46	-2.26	0.0602265	0.2359981	-4.44	FALSE
250083_at	glutathione S-transferase-like pro	ATGSTF12	AT5G17220	1.33	0.42	2.26	0.0602359	0.2359981	-4.44	FALSE
255837_at	unknown protein	RIC1	AT2G33460	1.29	0.36	2.26	0.0601971	0.2359981	-4.44	FALSE
256152_at	ethylene-responsive RNA helica	---	AT1G55150	-1.23	-0.30	-2.26	0.0601906	0.2359981	-4.44	FALSE
263225_at	putative DNA-binding protein sir	WRKY14	AT1G30650	1.33	0.41	2.26	0.0602058	0.2359981	-4.44	FALSE
252965_at	putative auxin-induced protein a	---	AT4G38860	-1.90	-0.93	-2.26	0.0602293	0.2359981	-4.44	FALSE
253728_at	putative protein unknown protein	---	AT4G29410	-1.51	-0.59	-2.26	0.0602131	0.2359981	-4.44	FALSE
245104_at	hypothetical protein predicted by	---	AT2G41600	-1.27	-0.35	-2.26	0.0602582	0.236008	-4.44	FALSE
250442_at	putative protein hypothetical bact	MSL2	AT5G10490	1.28	0.36	2.26	0.0602591	0.236008	-4.44	FALSE
246391_at	unknown protein ; supported by c	---	AT1G77350	-1.35	-0.43	-2.25	0.0602825	0.2360591	-4.44	FALSE
250666_at	SPF1-like protein SPF1 protein -	WRKY26	AT5G07100	-1.79	-0.84	-2.25	0.0603029	0.2360985	-4.44	FALSE
261793_at	unknown protein ; supported by c	---	AT1G16080	-1.79	-0.84	-2.25	0.0603146	0.2361038	-4.44	FALSE
247805_at	ATGP1-like protein	ATYKT62	AT5G58180	1.47	0.56	2.25	0.0603642	0.2362574	-4.44	FALSE
247050_at	At14a protein-like	---	AT5G66660	1.44	0.52	2.25	0.0603823	0.2362874	-4.44	FALSE
252102_at	dehydrin Xero2 ; supported by c	LTI30	AT3G50970	2.17	1.11	2.25	0.0604178	0.2362898	-4.44	TRUE
266076_at	ATP-dependent RNA helicase ic	---	AT2G40700	-1.60	-0.67	-2.25	0.0604311	0.2362898	-4.44	FALSE
250384_at	putative protein various predicte	---	AT5G11500	1.27	0.34	2.25	0.0604347	0.2362898	-4.44	FALSE
262487_at	unknown protein ESTs gb|T4283	---	AT1G21610	-1.21	-0.27	-2.25	0.0603953	0.2362898	-4.44	FALSE
249244_at	FtsH protease, putative similar t	VAR1	AT5G42270	-1.30	-0.38	-2.25	0.0604162	0.2362898	-4.44	FALSE
265033_at	PSI type III chlorophyll a/b-bindi	LHCA3	AT1G61520	-1.22	-0.28	-2.25	0.0604899	0.2364651	-4.44	FALSE
264782_at	putative transcription factor simil	MYB60	AT1G08810	-1.40	-0.48	-2.25	0.0605115	0.236509	-4.44	FALSE
249160_at	putative protein similar to unknov	---	AT5G42660	-1.26	-0.33	-2.25	0.0605363	0.2365654	-4.44	FALSE
247175_at	G protein-coupled receptor-like p	GCL1	AT5G65280	2.02	1.01	2.25	0.0605621	0.2366259	-4.44	TRUE
251407_at	Arm repeat containing protein - I	---	AT3G60350	-1.31	-0.39	-2.25	0.060581	0.2366593	-4.44	FALSE
252557_at	putative protein cim1 induced all	ATEXLA3	AT3G45960	1.26	0.34	2.25	0.0606138	0.2367468	-4.44	FALSE
255730_at	dihydroflavonol 4-reductase, put	---	AT1G25460	1.28	0.35	2.25	0.0606358	0.236792	-4.45	FALSE
250758_at	eukaryotic translation initiation fa	EIF3G2	AT5G06000	-1.44	-0.52	-2.25	0.0606485	0.2368013	-4.45	FALSE
252937_at	SEC14 - like protein phosphatidy	SEC14	AT4G39180	1.27	0.34	2.25	0.0607375	0.2370266	-4.45	FALSE

254666_at	translation initiation factor eIF-2	---	AT4G18330	1.22	0.29	2.25	0.0607478	0.2370266	-4.45	FALSE
262282_at	hypothetical protein predicted by	---	AT1G68610	1.34	0.42	2.25	0.0607367	0.2370266	-4.45	FALSE
263373_at	Expressed protein ; supported by	---	AT2G20515	-1.53	-0.62	-2.25	0.0607446	0.2370266	-4.45	FALSE
262327_at	hypothetical protein similar to hy	---	AT1G64130	1.28	0.36	2.25	0.0607836	0.2371257	-4.45	FALSE
254371_at	beta-glucosidase -like protein be	BGLU47	AT4G21760	1.26	0.33	2.25	0.0608274	0.237256	-4.45	FALSE
253767_at	12S cruciferin seed storage prote	CRU3	AT4G28520	1.29	0.36	2.25	0.060862	0.2373502	-4.45	FALSE
264781_at	putative plastid RNA polymerase	SIG2	AT1G08540	-1.41	-0.50	-2.25	0.0608751	0.2373609	-4.45	FALSE
259805_at	disease resistance protein, puta	AtRLP7	AT1G47890	1.44	0.52	2.25	0.0609078	0.2374478	-4.45	FALSE
265267_at	hypothetical protein predicted by	---	AT2G42920	-1.37	-0.46	-2.25	0.0609269	0.2374816	-4.45	FALSE
251103_at	putative protein protein phospha	---	AT5G01700	1.41	0.50	2.25	0.0609735	0.2376226	-4.45	FALSE
245528_at	pyruvate,orthophosphate dikinas	PPDK	AT4G15530	1.37	0.45	2.25	0.0610571	0.2379078	-4.45	TRUE
251122_at	protein kinase -like protein serin	---	AT5G01020	-1.44	-0.53	-2.25	0.061086	0.2379797	-4.45	FALSE
260746_at	glutathione transferase, putative	ATGSTU19	AT1G78380	1.30	0.38	2.25	0.0611202	0.2380724	-4.45	TRUE
255027_at	hypothetical protein F21E10.5 A	---	AT4G09880	1.30	0.38	2.24	0.0611555	0.2381692	-4.45	FALSE
247593_at	ABC transporter homolog PnAT	GCN1	AT5G60790	1.31	0.39	2.24	0.0611824	0.2381886	-4.45	FALSE
252590_at	putative protein kinase NPK1-re	---	AT3G45670	1.29	0.37	2.24	0.0611918	0.2381886	-4.45	FALSE
253087_at	purple acid phosphatase like pro	PAP25	AT4G36350	1.32	0.40	2.24	0.0611712	0.2381886	-4.45	FALSE
264130_at	hypothetical protein predicted by	---	AT1G79160	-1.37	-0.46	-2.24	0.0612087	0.2382137	-4.45	FALSE
259154_at	unknown protein similar to unkno	---	AT3G10260	1.28	0.36	2.24	0.0612334	0.2382693	-4.45	FALSE
247847_at	putative protein predicted protei	---	AT5G58110	-1.49	-0.58	-2.24	0.0612837	0.2384197	-4.46	FALSE
AFFX-BioC	E. coli /GEN=bioC /DB_XREF=g	---	---	1.61	0.68	2.24	0.061293	0.2384197	-4.46	FALSE
246267_at	Acyl CoA binding protein, putati	ACBP6	AT1G31812	-1.24	-0.31	-2.24	0.0613299	0.2385183	-4.46	FALSE
248775_at	receptor kinase-like protein	CCR4	AT5G47850	3.73	1.90	2.24	0.0613393	0.2385183	-4.46	FALSE
258250_at	putative delta 9 desaturase simil	FAD5	AT3G15850	-1.24	-0.31	-2.24	0.06148	0.2387939	-4.46	TRUE
258545_at	putative GTPase contains Pfam	---	AT3G07050	-1.53	-0.62	-2.24	0.0615008	0.2387939	-4.46	TRUE
262428_at	hypothetical protein predicted by	---	AT1G47570	-1.28	-0.35	-2.24	0.0615043	0.2387939	-4.46	FALSE
256484_at	PPR-repeat protein contains mul	---	AT1G31430	-1.32	-0.40	-2.24	0.0614989	0.2387939	-4.46	FALSE
249119_at	unknown protein ;supported by f	---	AT5G43720	-1.22	-0.29	-2.24	0.0614543	0.2387939	-4.46	FALSE
262583_at	putative phosphatidylserine synth	---	AT1G15110	1.39	0.48	2.24	0.061477	0.2387939	-4.46	FALSE
266623_at	unknown protein	---	AT2G35390	1.40	0.49	2.24	0.0614843	0.2387939	-4.46	FALSE
249379_at	putative protein predicted protei	---	AT5G40460	1.79	0.84	2.24	0.0614955	0.2387939	-4.46	FALSE
250324_at	putative protein nitrilase/Fhit pro	---	AT5G12040	-1.35	-0.43	-2.24	0.0614835	0.2387939	-4.46	FALSE
251225_at	putative protein glycosyl transfe	GATL7	AT3G62660	-1.44	-0.52	-2.24	0.0615403	0.2388521	-4.46	FALSE
256828_at	unknown protein	---	AT3G22968 /	-1.69	-0.75	-2.24	0.061531	0.2388521	-4.46	FALSE
257601_at	hypothetical protein predicted by	---	AT3G24820	-1.26	-0.33	-2.24	0.0615597	0.2388868	-4.46	FALSE

245780_at	unknown protein ;supported by fu	---	AT1G45688	1.34	0.42	2.24	0.0616172	0.2389881	-4.46	TRUE
263720_at	putative Na/H antiporter	ATCHX15	AT2G13620	1.25	0.32	2.24	0.0616016	0.2389881	-4.46	FALSE
253576_at	putative protein various predicte	---	AT4G31070	-1.24	-0.31	-2.24	0.06161	0.2389881	-4.46	FALSE
262341_at	E2, ubiquitin-conjugating enzym	UBC28	AT1G64230	-1.34	-0.43	-2.24	0.0616479	0.2390664	-4.46	FALSE
247602_at	S-receptor kinase homolog 2 pre	RLK1	AT5G60900	2.10	1.07	2.24	0.0616707	0.2391141	-4.46	FALSE
262059_at	DnaJ protein, putative similar to	---	AT1G80030	-1.43	-0.52	-2.24	0.0616857	0.2391317	-4.46	FALSE
247068_at	putative protein similar to unknov	---	AT5G66800	1.33	0.42	2.24	0.0617261	0.2391663	-4.46	FALSE
264213_at	hypothetical protein contains sim	ATPP2-A5	AT1G65390	3.66	1.87	2.24	0.0617136	0.2391663	-4.46	FALSE
252949_at	putative thaumatin-like protein th	---	AT4G38670	-1.62	-0.70	-2.24	0.0617166	0.2391663	-4.46	FALSE
257196_at	AMP-binding protein, putative si	---	AT3G23790	1.38	0.47	2.24	0.0617374	0.2391696	-4.46	TRUE
249866_at	2-isopropylmalate synthase-like;	MAM1	AT5G23010	-1.68	-0.75	-2.24	0.061807	0.2393359	-4.46	FALSE
263635_at	hypothetical protein predicted by	---	---	1.22	0.29	2.24	0.0618118	0.2393359	-4.46	FALSE
245579_at	hypothetical protein	---	AT4G14810	1.24	0.31	2.24	0.0618084	0.2393359	-4.46	FALSE
246068_at	putative protein ribosomal protei	---	AT5G20290	-1.63	-0.71	-2.24	0.0618289	0.2393612	-4.46	FALSE
248191_at	putative protein similar to unknov	---	AT5G54130	1.34	0.42	2.24	0.0618604	0.2394426	-4.46	FALSE
251645_at	putative protein polygalacturona	---	AT3G57790	-1.32	-0.40	-2.24	0.0618934	0.2395299	-4.47	FALSE
250041_at	putative protein p53 inducible pr	PIR121	AT5G18410	-1.22	-0.29	-2.24	0.0619088	0.2395487	-4.47	FALSE
258965_at	hypothetical protein similar to hy	---	AT3G10530	-1.65	-0.73	-2.24	0.0619384	0.2396227	-4.47	FALSE
266057_at	putative methionyl-tRNA syntheta	---	AT2G40660	-1.25	-0.32	-2.24	0.0619502	0.2396278	-4.47	FALSE
252516_at	histidyl-tRNA synthetase ; suppo	ATHRS1	AT3G46100	-1.32	-0.41	-2.24	0.0619641	0.2396406	-4.47	FALSE
247538_at	ABC family transporter - like pro	ATH16	AT5G61700	1.22	0.28	2.24	0.06202	0.2398161	-4.47	FALSE
259290_at	putative cyclin similar to cyclin cy	CYCB1;3	AT3G11520	1.43	0.52	2.24	0.0620316	0.2398205	-4.47	FALSE
253426_at	putative protein polygalacturona	---	AT4G32375	1.26	0.33	2.23	0.0620567	0.2398767	-4.47	FALSE
264694_at	receptor serine/threonine kinase	---	AT1G70250	1.23	0.30	2.23	0.0621002	0.2400042	-4.47	FALSE
262806_at	putative pyrophosphate-depende	---	AT1G20950	-1.49	-0.57	-2.23	0.0621709	0.2402295	-4.47	FALSE
249122_at	putative protein similar to unknov	ARD4	AT5G43850	-1.45	-0.53	-2.23	0.0621901	0.2402295	-4.47	FALSE
263305_at	unknown protein ;supported by f	BPC1	AT2G01930	-1.43	-0.52	-2.23	0.0621897	0.2402295	-4.47	FALSE
250461_at	hypothetical protein	---	AT5G10010	-1.38	-0.46	-2.23	0.0622212	0.2403092	-4.47	FALSE
261392_at	hypothetical protein predicted by	---	AT1G79780	1.25	0.32	2.23	0.0623386	0.2405906	-4.47	FALSE
260211_at	hypothetical protein similar to YG	---	AT1G74440	2.23	1.16	2.23	0.0623096	0.2405906	-4.47	FALSE
261057_at	hypothetical protein predicted by	---	AT1G01230	-1.29	-0.37	-2.23	0.062348	0.2405906	-4.47	FALSE
261126_at	TATA binding protein-associated	TAF6	AT1G04950	-1.25	-0.33	-2.23	0.0623495	0.2405906	-4.47	FALSE
257939_at	monosaccharide transport prote	STP4	AT3G19930	1.56	0.65	2.23	0.0623526	0.2405906	-4.47	FALSE
263493_at	putative ATP-dependent RNA he	---	AT2G42520	1.44	0.53	2.23	0.0623574	0.2405906	-4.47	FALSE
258353_s_a	unknown protein similar to GB:A/	YSL5	AT3G17650 /.	-1.41	-0.49	-2.23	0.0623862	0.2406611	-4.47	FALSE

247374_at	topoisomerase-like protein ;supp	---	AT5G63190	-1.48	-0.56	-2.23	0.0624045	0.2406909	-4.47	FALSE
261216_at	catechol O-methyltransferase, p	---	AT1G33030	2.27	1.18	2.23	0.0625307	0.2410425	-4.48	TRUE
266347_at	putative ATP-dependent DNA he	---	AT2G01440	-1.39	-0.48	-2.23	0.0625079	0.2410425	-4.47	FALSE
266614_at	unknown protein	---	AT2G14910	-1.32	-0.40	-2.23	0.0625441	0.2410425	-4.48	FALSE
252295_at	signal recognition particle subun	---	AT3G49100	-1.42	-0.51	-2.23	0.0625581	0.2410425	-4.48	FALSE
252747_at	putative protein retrotransposon	---	---	1.32	0.40	2.23	0.062559	0.2410425	-4.48	FALSE
254622_at	hypothetical protein contains sim	---	AT4G18375	-1.52	-0.60	-2.23	0.0625195	0.2410425	-4.48	FALSE
248629_at	mitochondrial carrier protein-like	---	AT5G48970	1.41	0.50	2.23	0.0625759	0.2410667	-4.48	FALSE
257291_at	DNA-binding protein, putative si	---	AT3G15590	-1.76	-0.82	-2.23	0.0626125	0.2411262	-4.48	FALSE
249479_at	germin - like protein probable ge	---	AT5G38960	1.38	0.46	2.23	0.0626109	0.2411262	-4.48	FALSE
254140_at	putative protein	---	AT4G24610	-1.45	-0.54	-2.23	0.062631	0.2411568	-4.48	FALSE
251283_at	seven in absentia-like protein SI	---	AT3G61790	-1.27	-0.35	-2.23	0.0626467	0.2411767	-4.48	FALSE
263708_at	unknown protein	---	AT1G09320	-1.28	-0.35	-2.23	0.062691	0.2412993	-4.48	FALSE
267396_at	hypothetical protein predicted by	---	AT2G44270	-1.36	-0.45	-2.23	0.0627209	0.2412993	-4.48	FALSE
264875_at	putative glucanase	AKR2B	AT2G17390	-1.21	-0.28	-2.23	0.0627116	0.2412993	-4.48	FALSE
260361_at	unknown protein ; supported by	---	AT1G69360	1.42	0.50	2.23	0.062704	0.2412993	-4.48	FALSE
246434_at	root cap 1 (RCP1) ;supported by	RCP1	AT5G17520	-1.40	-0.49	-2.23	0.0627362	0.2413175	-4.48	FALSE
260987_at	hypothetical protein predicted by	NTMC2T6.	AT1G53590	-1.37	-0.45	-2.23	0.0628076	0.2415505	-4.48	FALSE
263016_at	ubiquitin extension protein, puta	---	AT1G23410	-1.32	-0.40	-2.23	0.062818	0.2415505	-4.48	FALSE
249057_at	putative protein contains similarit	DUR	AT5G44480	2.41	1.27	2.23	0.0628641	0.2415941	-4.48	TRUE
248832_at	putative protein similar to unknov	---	AT5G47170	1.24	0.31	2.23	0.0628454	0.2415941	-4.48	FALSE
252477_at	glucosyltransferase-like protein	---	AT3G46680	1.41	0.49	2.23	0.0628716	0.2415941	-4.48	FALSE
250925_at	putative protein ; supported by fu	---	AT5G03370	-1.36	-0.44	-2.23	0.0628539	0.2415941	-4.48	FALSE
260243_at	hypothetical protein similar to put	---	AT1G63720	1.89	0.92	2.23	0.0629033	0.2416749	-4.48	FALSE
247155_at	2-oxoglutarate dehydrogenase,	---	AT5G65750	-1.45	-0.53	-2.22	0.0629825	0.241842	-4.48	TRUE
247936_at	lycopene epsilon cyclase ; supp	LUT2	AT5G57030	-1.44	-0.52	-2.22	0.0629724	0.241842	-4.48	FALSE
251955_at	putative protein predicted protei	---	AT3G53680	1.29	0.37	2.22	0.0629908	0.241842	-4.48	FALSE
255990_at	glycyl tRNA synthetase, putative	---	AT1G29870	1.30	0.37	2.22	0.0629687	0.241842	-4.48	FALSE
253384_at	Expressed protein ; supported by	---	AT4G32915	-1.34	-0.43	-2.22	0.0629998	0.241842	-4.48	FALSE
260288_at	nodulin-like protein similar to noc	---	AT1G80530	-1.47	-0.56	-2.22	0.0630142	0.2418565	-4.48	FALSE
254103_at	putative protein ;supported by fu	---	AT4G25030	1.90	0.93	2.22	0.0630423	0.2418831	-4.48	FALSE
261054_at	hypothetical protein predicted by	---	AT1G01320	1.62	0.70	2.22	0.0630337	0.2418831	-4.48	FALSE
252908_at	putative protein	---	AT4G39670	3.99	2.00	2.22	0.0630593	0.2419077	-4.48	TRUE
247516_at	germin-like protein - like germin-	---	AT5G61750	1.31	0.39	2.22	0.0631064	0.2420477	-4.48	FALSE
252293_at	4-coumarate-CoA ligase -like pr	---	AT3G48990	-1.26	-0.34	-2.22	0.0632149	0.2421418	-4.49	FALSE

248477_at	putative protein similar to unknov	---	AT5G50900	1.37	0.45	2.22	0.0632822	0.2421418	-4.49	FALSE
256365_at	arginyl-tRNA synthetase nearly id	---	AT1G66530	-1.51	-0.59	-2.22	0.0632542	0.2421418	-4.49	FALSE
263066_at	unknown protein	---	AT2G17540	-1.22	-0.29	-2.22	0.0631786	0.2421418	-4.49	FALSE
264314_at	unknown protein ; supported by c	---	AT1G70420	-1.52	-0.61	-2.22	0.0631993	0.2421418	-4.49	FALSE
260397_at	hypothetical protein predicted by	---	AT1G69680	1.29	0.37	2.22	0.0633045	0.2421418	-4.49	FALSE
250869_at	Terminal flower1 (TFL1) ; suppor	TFL1	AT5G03840	1.28	0.36	2.22	0.0632978	0.2421418	-4.49	FALSE
265454_at	putative ARF1 family auxin respo	ARF11	AT2G46530	-2.19	-1.13	-2.22	0.0632539	0.2421418	-4.49	FALSE
249604_x_a	putative protein RING-H2 finger	---	AT5G37230	1.30	0.38	2.22	0.0631969	0.2421418	-4.49	FALSE
246917_at	serine-rich protein ;supported by	---	AT5G25280	-1.63	-0.70	-2.22	0.0632694	0.2421418	-4.49	FALSE
246213_at	serine C-palmitoyltransferase like	ATLCB1	AT4G36480	1.37	0.45	2.22	0.0632145	0.2421418	-4.49	FALSE
255779_at	unknown protein similar to beta-	PDCB3	AT1G18650	-1.73	-0.79	-2.22	0.0632321	0.2421418	-4.49	FALSE
254185_at	cellulose synthase catalytic subu	CSLG3	AT4G23990	1.50	0.58	2.22	0.0631979	0.2421418	-4.49	FALSE
247984_s_a	IAA-amino acid hydrolase homol	ILL1	AT5G56650 /	-1.43	-0.52	-2.22	0.0632026	0.2421418	-4.49	FALSE
244961_at	hypothetical protein	---	---	-1.23	-0.30	-2.22	0.0633114	0.2421418	-4.49	FALSE
248511_at	Expressed protein ; supported by	CPI1	AT5G50375	-1.55	-0.63	-2.22	0.0632858	0.2421418	-4.49	FALSE
264752_at	unknown protein similar to Bacill	LPR1	AT1G23010	1.23	0.30	2.22	0.06327	0.2421418	-4.49	FALSE
256585_at	hypothetical protein	---	AT3G28760	-1.46	-0.55	-2.22	0.0633526	0.2421775	-4.49	TRUE
266894_at	hypothetical protein predicted by	---	AT2G26050	1.22	0.29	2.22	0.0633521	0.2421775	-4.49	FALSE
250898_at	putative protein ; supported by c	ADK2	AT5G03300	-1.37	-0.46	-2.22	0.0633386	0.2421775	-4.49	FALSE
255602_at	Expressed protein ; supported by	---	AT4G01026	-1.33	-0.42	-2.22	0.0633806	0.242244	-4.49	FALSE
247716_at	putative protein predicted protei	---	AT5G59350	-1.48	-0.57	-2.22	0.0634074	0.2423059	-4.49	FALSE
262775_at	unknown protein	---	AT1G13000	1.26	0.33	2.22	0.0634367	0.2423769	-4.49	FALSE
266338_at	putative ligand-gated ion channe	GLR5	AT2G32400	-1.37	-0.45	-2.22	0.0634617	0.2424296	-4.49	TRUE
260533_at	putative U1 small nuclear ribonu	---	AT2G43370	-1.25	-0.32	-2.22	0.0634719	0.2424296	-4.49	FALSE
250229_at	putative protein contains similarit	NACA3	AT5G13850	-1.53	-0.61	-2.22	0.0634823	0.2424296	-4.49	FALSE
255452_at	hypothetical protein similar to A.	---	AT4G02880	-1.25	-0.33	-2.22	0.0635181	0.2424557	-4.49	FALSE
265911_at	unknown protein ;supported by f	---	AT2G25670	-1.24	-0.31	-2.22	0.0635317	0.2424557	-4.49	FALSE
263665_at	putative putative 60S ribosomal p	---	AT1G04480	-1.58	-0.66	-2.22	0.0635078	0.2424557	-4.49	FALSE
262790_at	putative translation initiation fact	TIF3H1	AT1G10840	-1.20	-0.27	-2.22	0.0635273	0.2424557	-4.49	FALSE
264065_at	hypothetical protein predicted by	---	AT2G27900	1.31	0.39	2.22	0.0635541	0.2425005	-4.49	FALSE
249809_at	unknown protein	---	AT5G23910	1.24	0.31	2.22	0.063575	0.24254	-4.49	FALSE
254393_at	putative NADPH quinone oxidor	---	AT4G21580	1.28	0.35	2.22	0.0635901	0.242557	-4.49	FALSE
257792_at	TOM20, putative similar to TOM	TOM20-3	AT3G27080	-1.35	-0.43	-2.22	0.0636011	0.2425584	-4.49	FALSE
245292_at	Expressed protein ; supported by	---	AT4G15093	1.37	0.46	2.22	0.0636119	0.2425588	-4.49	FALSE
249127_at	actin-like protein ; supported by	ATARP9	AT5G43500	-1.34	-0.42	-2.22	0.0636254	0.2425699	-4.49	FALSE

265471_at	putative peroxidase ATP2a ;sup	---	AT2G37130	-1.86	-0.89	-2.22	0.063658	0.2425955	-4.49	TRUE
259186_at	unknown protein similar to possit	---	AT3G01590	-1.32	-0.40	-2.22	0.063664	0.2425955	-4.49	FALSE
262762_at	phosphoribosyl diphosphate synt	---	AT1G10700	2.79	1.48	2.22	0.0636631	0.2425955	-4.49	FALSE
265087_at	hypothetical protein predicted by	---	AT1G03760	-1.57	-0.65	-2.22	0.0637213	0.2427732	-4.49	FALSE
256652_at	hypothetical protein similar to put	LPAT5	AT3G18850	1.86	0.90	2.22	0.0637577	0.2428713	-4.49	FALSE
266147_at	putative C-1-tetrahydrofolate syn	---	AT2G12230	1.21	0.27	2.22	0.0637736	0.2428912	-4.49	FALSE
250314_at	putative protein contains similarit	---	AT5G12190	-1.24	-0.31	-2.22	0.0637962	0.2429348	-4.49	FALSE
256443_at	hypothetical protein similar to hyp	---	AT3G10960	1.60	0.68	2.22	0.0638063	0.2429348	-4.50	FALSE
258478_at	unknown protein	---	AT3G02710	-1.28	-0.36	-2.22	0.0638223	0.2429552	-4.50	FALSE
254529_at	ATP binding protein - like nuclec	INDL	AT4G19540	-1.25	-0.32	-2.21	0.0638818	0.2431408	-4.50	FALSE
257019_at	unknown protein	---	AT3G19640	-1.21	-0.28	-2.21	0.0639282	0.2431708	-4.50	FALSE
245714_at	RNA-binding protein-like	---	AT5G04280	-1.28	-0.36	-2.21	0.0639305	0.2431708	-4.50	FALSE
249288_at	unknown protein ;supported by f	---	AT5G41050	-2.14	-1.10	-2.21	0.0639323	0.2431708	-4.50	FALSE
251137_at	putative protein several hypothet	---	AT5G01300	-1.42	-0.51	-2.21	0.0639191	0.2431708	-4.50	FALSE
267215_at	hypothetical protein	---	AT2G02630	1.21	0.28	2.21	0.0639881	0.2433021	-4.50	FALSE
259238_at	putative eukaryotic translation ini	EIF3G1	AT3G11400	-1.28	-0.36	-2.21	0.0639843	0.2433021	-4.50	FALSE
250880_at	putative protein Ube-1a, Mus mu	---	AT5G04070	-1.23	-0.30	-2.21	0.0640045	0.2433237	-4.50	FALSE
264932_at	hypothetical protein similar to hyp	---	AT1G61240	-1.41	-0.50	-2.21	0.0640335	0.2433936	-4.50	FALSE
267368_at	citrate synthase similar to GB:X1	ATCS	AT2G44350	1.33	0.41	2.21	0.0640582	0.2434469	-4.50	FALSE
249008_at	putative protein contains similarit	---	AT5G44680	-1.55	-0.63	-2.21	0.0640759	0.2434737	-4.50	TRUE
253421_at	putative protein predicted protei	---	AT4G32340	-1.39	-0.47	-2.21	0.0641381	0.2436288	-4.50	FALSE
263404_s_a	hypothetical protein similar to hyp	---	AT2G04090 ///	2.27	1.18	2.21	0.0641298	0.2436288	-4.50	FALSE
264012_at	hypothetical protein predicted by	---	AT2G21080	1.36	0.45	2.21	0.0642546	0.2440233	-4.50	FALSE
246069_at	zinc finger protein ;supported by	---	AT5G20220	-1.53	-0.61	-2.21	0.0642634	0.2440233	-4.50	FALSE
265122_at	similar to flavin-binding monooxy	FMO GS-O	AT1G62540	1.22	0.28	2.21	0.0643023	0.2440898	-4.50	FALSE
249903_at	disease resistance protein-like	---	AT5G22690	2.19	1.13	2.21	0.0642946	0.2440898	-4.50	FALSE
261719_at	hypothetical protein similar to hyp	---	AT1G18390	2.16	1.11	2.21	0.0643451	0.244171	-4.50	FALSE
255512_at	Expressed protein ; supported by	SYP42	AT4G02195	-1.38	-0.47	-2.21	0.0643363	0.244171	-4.50	FALSE
255277_at	putative homeotic protein ; supp	PDF2	AT4G04890	-1.40	-0.49	-2.21	0.0643722	0.2442331	-4.50	FALSE
245572_at	hypothetical protein	PPD2	AT4G14720	-1.55	-0.63	-2.21	0.0644732	0.2445497	-4.51	FALSE
252861_at	hypothetical protein	---	AT4G39820	1.50	0.58	2.21	0.0644771	0.2445497	-4.51	FALSE
262236_at	hypothetical protein similar to hyp	---	AT1G48330	1.67	0.74	2.21	0.0645045	0.2445724	-4.51	FALSE
250575_at	putative protein	---	AT5G08240	1.56	0.64	2.21	0.0645017	0.2445724	-4.51	FALSE
266555_at	G-box binding bZIP transcription	GBF3	AT2G46270	1.79	0.84	2.21	0.0645321	0.2446364	-4.51	FALSE
265112_at	hypothetical protein predicted by	---	AT1G62530	1.22	0.29	2.21	0.0645902	0.2447754	-4.51	FALSE

258287_at	putative sulfate transporter simila	SULTR3;4	AT3G15990	1.96	0.97	2.21	0.0645814	0.2447754	-4.51	FALSE
250511_at	putative protein similar to unknov	---	AT5G09960	-1.29	-0.37	-2.21	0.0646187	0.2448426	-4.51	FALSE
264152_at	Mago Nashi-like protein similar t	MAGO	AT1G02140	-1.29	-0.37	-2.21	0.0647095	0.2451458	-4.51	FALSE
264063_at	unknown protein	---	AT2G27900	-1.27	-0.35	-2.21	0.0647288	0.2451785	-4.51	FALSE
249325_at	urophorphyrin III methylase (gb|A	UPM1	AT5G40850	-1.38	-0.47	-2.21	0.0647644	0.2452245	-4.51	FALSE
255066_at	F-box protein family, AtFBW2 co	---	AT4G08980	-1.24	-0.31	-2.21	0.0647732	0.2452245	-4.51	FALSE
247922_at	putative protein similar to unknov	---	AT5G57500	1.88	0.91	2.21	0.0647668	0.2452245	-4.51	FALSE
257730_at	unknown protein contains Pfam p	---	AT3G18420	-1.42	-0.51	-2.20	0.0648514	0.2453469	-4.51	FALSE
258151_at	beta-glucosidase, putative simila	BGLU44	AT3G18080	-1.63	-0.71	-2.20	0.0648332	0.2453469	-4.51	FALSE
260262_at	hypothetical protein similar to hy	---	AT1G68470	1.87	0.90	2.20	0.0648593	0.2453469	-4.51	FALSE
258697_at	putative minichromosome mainte	MCM8	AT3G09660	-1.34	-0.43	-2.20	0.0648461	0.2453469	-4.51	FALSE
262365_at	disease resistance protein, puta	---	AT1G72870	1.34	0.43	2.20	0.0648278	0.2453469	-4.51	FALSE
247760_at	subtilisin-like serine protease cor	---	AT5G59130	-2.78	-1.47	-2.20	0.0649081	0.2454906	-4.51	FALSE
245378_at	GLABRA2 like protein	HDG4	AT4G17710	1.24	0.31	2.20	0.0649546	0.2456258	-4.51	FALSE
264277_at	polygalacturonase isoenzyme 1	---	AT1G60390	1.30	0.38	2.20	0.0650097	0.2457934	-4.51	FALSE
247794_at	phosphoinositide specific phosph	PLC1	AT5G58670	1.37	0.45	2.20	0.0651331	0.2459753	-4.52	TRUE
252940_at	receptor protein kinase - like pro	---	AT4G39270	1.52	0.60	2.20	0.0650895	0.2459753	-4.51	TRUE
248767_at	putative protein contains similarit	---	AT5G47710	-1.33	-0.41	-2.20	0.0651287	0.2459753	-4.52	FALSE
258497_at	putative flowering-time gene CO	COL2	AT3G02380	-1.30	-0.38	-2.20	0.0650998	0.2459753	-4.51	FALSE
251035_at	Expressed protein ; supported by	---	AT5G02220	-1.46	-0.54	-2.20	0.0650723	0.2459753	-4.51	FALSE
260286_at	putative acetylornithine transami	WIN1	AT1G80600	-1.36	-0.45	-2.20	0.0651333	0.2459753	-4.52	FALSE
252394_at	heat shock protein-like protein h	---	AT3G47940	-1.41	-0.49	-2.20	0.0651317	0.2459753	-4.52	FALSE
249625_at	hypothetical protein ;supported b	---	AT5G37480	1.27	0.34	2.20	0.0651666	0.2460604	-4.52	FALSE
246446_at	putative protein hypothetical pro	---	AT5G17640	-1.37	-0.45	-2.20	0.0652011	0.2461398	-4.52	TRUE
263259_at	putative zinc-binding protein simi	PUB18	AT1G10560	1.59	0.67	2.20	0.0652416	0.2461398	-4.52	TRUE
252786_at	putative protein putative DNA-he	CHR38	AT3G42670	-1.61	-0.69	-2.20	0.0652317	0.2461398	-4.52	FALSE
258412_at	unknown protein similar to pop3	HS1	AT3G17210	-1.30	-0.38	-2.20	0.0652116	0.2461398	-4.52	FALSE
247324_at	putative protein strong similarity t	---	AT5G64190	2.56	1.36	2.20	0.0652241	0.2461398	-4.52	FALSE
247677_at	oxysterol-binding protein - like o	ORP3C	AT5G59420	1.24	0.31	2.20	0.0652672	0.2461956	-4.52	FALSE
264857_at	putative glycosyl transferase sim	LGT9	AT1G24170	1.46	0.54	2.20	0.0652825	0.2462125	-4.52	TRUE
264392_at	hypothetical protein Similar to sa	---	AT1G11900	-1.35	-0.44	-2.20	0.0653368	0.2463359	-4.52	FALSE
246780_at	seryl-tRNA synthetase ; support	---	AT5G27470	-1.29	-0.37	-2.20	0.065331	0.2463359	-4.52	FALSE
249767_at	acidic endochitinase (dbj|BAA21	---	AT5G24090	1.96	0.97	2.20	0.0653662	0.2463655	-4.52	FALSE
253227_at	protein kinase - like leucine rich	---	AT4G35030	-1.32	-0.40	-2.20	0.0653636	0.2463655	-4.52	FALSE
261987_at	hypothetical protein predicted by	---	AT1G33710	1.21	0.27	2.20	0.0653852	0.2463962	-4.52	FALSE

258049_at	hypothetical protein similar to CG	---	AT3G16220	1.23	0.30	2.20	0.0654084	0.2464431	-4.52	FALSE
248564_at	putative protein contains similarit	---	AT5G49700	1.42	0.50	2.20	0.0654563	0.2465828	-4.52	FALSE
248461_s_a	fumarate hydratase ; supported	FUM1	AT2G47510 /	1.33	0.42	2.20	0.0655546	0.2467042	-4.52	FALSE
261273_at	unknown protein ; supported by	---	AT1G26650	-1.47	-0.55	-2.20	0.0655705	0.2467042	-4.52	FALSE
249589_at	pyridoxal kinase -like protein pyr	SOS4	AT5G37850	-1.22	-0.29	-2.20	0.065526	0.2467042	-4.52	FALSE
245874_at	unknown protein	---	AT1G26250	1.30	0.38	2.20	0.065517	0.2467042	-4.52	FALSE
249401_at	putative protein LIM7, Lily, EMB	---	AT5G40260	1.24	0.31	2.20	0.06554	0.2467042	-4.52	FALSE
262614_at	putative pattern formation protein	GN	AT1G13980	-1.51	-0.60	-2.20	0.0655751	0.2467042	-4.52	FALSE
260790_at	hypothetical protein predicted by	---	AT1G06240	-1.49	-0.58	-2.20	0.0655271	0.2467042	-4.52	FALSE
249468_at	putative protein predicted protein	---	AT5G39650	-1.24	-0.31	-2.20	0.0655676	0.2467042	-4.52	FALSE
266113_x_a	hypothetical protein predicted by	---	---	1.34	0.42	2.20	0.0655898	0.246719	-4.52	FALSE
244984_at	ribosomal protein S3	---	---	-1.46	-0.54	-2.20	0.0656218	0.2467986	-4.52	FALSE
256980_at	hypothetical protein contains Pfa	DRB3	AT3G26932	-1.40	-0.48	-2.20	0.0656601	0.2469021	-4.52	FALSE
262200_at	unknown protein similar to memb	---	AT2G01070	-1.36	-0.45	-2.20	0.0657199	0.2470046	-4.52	FALSE
267536_at	phospholipase D ; supported by	PLDBETA1	AT2G42010	1.32	0.40	2.20	0.0657061	0.2470046	-4.52	FALSE
259714_at	putative gibberellin 20-oxidase si	ATGA20OX	AT1G60980	1.30	0.38	2.20	0.0657189	0.2470046	-4.52	FALSE
250571_at	hypothetical protein	---	AT5G08200	1.42	0.51	2.19	0.0657638	0.2470985	-4.52	FALSE
250056_at	putative protein predicted protein	---	AT5G17660	-1.73	-0.79	-2.19	0.0657665	0.2470985	-4.52	FALSE
257537_at	hypothetical protein predicted by	---	AT3G22350	1.38	0.47	2.19	0.0658108	0.2472125	-4.53	FALSE
264480_at	hypothetical protein predicted by	EFS	AT1G77300	1.30	0.37	2.19	0.0658186	0.2472125	-4.53	FALSE
247573_at	anthocyanin 5-aromatic acyltran	AACT1	AT5G61160	-3.90	-1.96	-2.19	0.0659185	0.2472216	-4.53	TRUE
258003_at	expansin At-EXP5 identical to ex	EXPA5	AT3G29030	2.34	1.22	2.19	0.0659043	0.2472216	-4.53	TRUE
246447_at	putative protein SART-1 protein	DOT2	AT5G16780	-1.32	-0.40	-2.19	0.0658837	0.2472216	-4.53	FALSE
245304_at	hypothetical protein ; supported b	---	AT4G15630	2.08	1.05	2.19	0.0658639	0.2472216	-4.53	FALSE
249612_at	putative protein CG14881, Dros	---	AT5G37290	-1.61	-0.69	-2.19	0.065895	0.2472216	-4.53	FALSE
246897_at	putative protein predicted protein	---	AT5G25560	1.34	0.42	2.19	0.0659132	0.2472216	-4.53	FALSE
257478_at	hypothetical protein similar to put	WAKL2	AT1G16130	1.77	0.82	2.19	0.0658521	0.2472216	-4.53	FALSE
256364_at	wrky-type DNA binding protein,	WRKY67	AT1G66550	1.32	0.40	2.19	0.0658915	0.2472216	-4.53	FALSE
256000_at	glycyl tRNA synthetase, putative	---	AT1G29880	-1.31	-0.39	-2.19	0.0658679	0.2472216	-4.53	FALSE
257892_at	unknown protein similar to ER6 p	---	AT3G17020	-1.28	-0.36	-2.19	0.0659527	0.2472815	-4.53	FALSE
254814_at	hypothetical protein ; supported	---	AT4G12340	-1.21	-0.28	-2.19	0.0659562	0.2472815	-4.53	FALSE
248147_at	putative protein contains similarit	ATRBP45A	AT5G54900	-1.29	-0.36	-2.19	0.0659701	0.247293	-4.53	FALSE
250701_at	bZIP transcription factor-like prot	---	AT5G06839	1.31	0.39	2.19	0.0659814	0.2472947	-4.53	FALSE
265714_at	putative integral membrane prote	ATUPS4	AT2G03520	1.23	0.30	2.19	0.0660835	0.2476366	-4.53	FALSE
262818_at	hypothetical protein predicted by	---	AT1G11755 /	-1.28	-0.35	-2.19	0.0661	0.2476578	-4.53	FALSE

256598_at	cytochrome P450 homolog, puta	BR6OX2	AT3G30180	1.44	0.52	2.19	0.0661309	0.2476924	-4.53	TRUE
259811_at	hypothetical protein predicted by	---	AT1G49830	1.28	0.35	2.19	0.0661266	0.2476924	-4.53	FALSE
260308_at	putative ABC transporter contain	ATTAP1	AT1G70610	1.65	0.72	2.19	0.066187	0.2478616	-4.53	FALSE
247291_at	unknown protein	---	AT5G64480	-1.29	-0.36	-2.19	0.0661987	0.247865	-4.53	FALSE
247717_at	nonspecific lipid-transfer protein	LTP3	AT5G59320	-1.75	-0.81	-2.19	0.0663766	0.2479303	-4.53	TRUE
251879_at	putative protein hin1 protein, Nic	---	AT3G54200	1.64	0.71	2.19	0.0664121	0.2479303	-4.53	FALSE
261844_at	hypothetical protein predicted by	---	AT1G15940	-1.53	-0.61	-2.19	0.0663654	0.2479303	-4.53	FALSE
245593_at	IAA7 like protein	IAA14	AT4G14550	1.89	0.92	2.19	0.0663476	0.2479303	-4.53	FALSE
249181_at	putative protein contains similarit	---	AT5G42920	-1.29	-0.37	-2.19	0.0664444	0.2479303	-4.53	FALSE
248111_at	wax synthase-like protein	---	AT5G55330	1.25	0.33	2.19	0.0662837	0.2479303	-4.53	FALSE
250386_at	MYB like protein MYB like protei	MYB3R-4	AT5G11510	1.35	0.44	2.19	0.0663691	0.2479303	-4.53	FALSE
267065_at	hypothetical protein predicted by	---	AT2G41080	-1.33	-0.41	-2.19	0.0663033	0.2479303	-4.53	FALSE
260141_at	gibberellin regulatory protein, pu	RGL1	AT1G66350	2.49	1.32	2.19	0.0662532	0.2479303	-4.53	FALSE
246407_at	disease resistance protein RPS4	---	AT1G57670	1.23	0.30	2.19	0.0663965	0.2479303	-4.53	FALSE
246319_at	putative protein HYPOTHETICA	---	AT3G56680	-1.26	-0.34	-2.19	0.0662273	0.2479303	-4.53	FALSE
249524_at	putative protein similar to unknov	---	AT5G38520	-1.49	-0.58	-2.19	0.0664244	0.2479303	-4.53	FALSE
261419_at	hypothetical protein predicted by	---	AT1G07840	-1.22	-0.29	-2.19	0.0663477	0.2479303	-4.53	FALSE
247610_at	putative protein predicted protei	---	AT5G60630	3.94	1.98	2.19	0.0663668	0.2479303	-4.53	FALSE
AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=gi	---	---	1.53	0.62	2.19	0.0664153	0.2479303	-4.53	FALSE
266061_at	putative translation initiation facto	---	AT2G18720	1.29	0.37	2.19	0.0664074	0.2479303	-4.53	FALSE
252175_at	zinc finger protein zinc finger pro	AtIDD2	AT3G50700	-1.22	-0.29	-2.19	0.0664369	0.2479303	-4.53	FALSE
263632_at	Expressed protein ; supported by	---	AT2G04795	-1.95	-0.96	-2.19	0.0664307	0.2479303	-4.53	FALSE
253588_at	putative protein	---	AT4G30790	1.31	0.39	2.19	0.066302	0.2479303	-4.53	FALSE
247047_at	putative protein contains similarit	---	AT5G66650	3.01	1.59	2.19	0.0663862	0.2479303	-4.53	FALSE
261280_at	hypothetical protein predicted by	---	AT1G05860	-1.42	-0.51	-2.19	0.0662535	0.2479303	-4.53	FALSE
262284_at	hypothetical protein predicted by	---	AT1G68670	-1.46	-0.54	-2.19	0.0664744	0.2480013	-4.54	FALSE
266620_at	unknown protein	---	AT2G35450	-1.34	-0.43	-2.19	0.0665069	0.2480821	-4.54	FALSE
256213_at	protein kinase, putative contains	---	AT1G50990	1.31	0.39	2.19	0.0665222	0.2480987	-4.54	FALSE
263010_at	T76725 come from this gene.	---	AT1G23330	1.25	0.32	2.19	0.0665921	0.2482692	-4.54	FALSE
259433_at	hypothetical protein predicted by	---	AT1G01570	1.33	0.41	2.19	0.0666074	0.2482692	-4.54	FALSE
247990_at	unknown protein ;supported by f	---	AT5G56360	-1.24	-0.32	-2.19	0.0666115	0.2482692	-4.54	FALSE
245654_at	disease resistance protein, puta	---	AT1G56540	1.29	0.37	2.19	0.0665808	0.2482692	-4.54	FALSE
248096_at	embryo-specific protein 1; Ca2+-	---	AT5G55240	1.27	0.34	2.19	0.066628	0.2482904	-4.54	FALSE
257860_at	Expressed protein ; supported by	---	AT3G13062	-1.46	-0.54	-2.19	0.0666531	0.2483433	-4.54	FALSE
249077_at	alcohol dehydrogenase (EC 1.1.	HOT5	AT5G43940	-1.30	-0.38	-2.19	0.0666823	0.2483711	-4.54	FALSE

248176_at	putative protein contains similarit	Fh5	AT5G54650	1.64	0.72	2.19	0.066676	0.2483711	-4.54	FALSE
256225_at	unknown protein ; supported by f	---	AT1G56220	-1.42	-0.51	-2.18	0.0667057	0.2483769	-4.54	FALSE
250448_at	putative protein lignostilbene-alp	---	AT5G10820	1.53	0.62	2.18	0.0667001	0.2483769	-4.54	FALSE
263824_at	putative WD-40 repeat protein	---	AT2G40360	-1.55	-0.63	-2.18	0.0667754	0.2485554	-4.54	TRUE
256042_at	hypothetical protein predicted by	---	AT1G07220	1.22	0.29	2.18	0.066772	0.2485554	-4.54	FALSE
246176_at	putative protein DYNAMIN-LIKE	---	AT5G28410	1.24	0.31	2.18	0.0668064	0.2486299	-4.54	FALSE
254921_at	putative protein hypothetical pro	---	AT4G11300	1.47	0.55	2.18	0.0668335	0.2486903	-4.54	FALSE
267199_at	hypothetical protein predicted by	---	AT2G30990	2.21	1.14	2.18	0.0668576	0.248725	-4.54	TRUE
263279_x_a	hypothetical protein predicted by	---	---	1.29	0.37	2.18	0.0668646	0.248725	-4.54	FALSE
253477_at	L-ascorbate peroxidase - like pro	APX6	AT4G32320	-1.58	-0.66	-2.18	0.0669109	0.2487753	-4.54	TRUE
246051_at	epimerase/dehydratase - like pr	GME	AT5G28840	-1.37	-0.45	-2.18	0.0669037	0.2487753	-4.54	FALSE
249124_at	disease resistance protein ; sup	---	AT5G43740	1.27	0.34	2.18	0.066907	0.2487753	-4.54	FALSE
262338_at	Expressed protein ; supported by	---	AT1G64185	-1.41	-0.50	-2.18	0.06696	0.2489175	-4.54	FALSE
265366_at	putative N-acetylglucosaminyltra	---	AT2G13290	-1.30	-0.37	-2.18	0.0670192	0.2490339	-4.54	FALSE
254145_at	hypothetical protein	---	AT4G24700	-1.70	-0.76	-2.18	0.0670568	0.2490339	-4.54	FALSE
247266_at	beta-xylosidase	XYL4	AT5G64570	1.54	0.62	2.18	0.0670347	0.2490339	-4.54	FALSE
264716_at	matrix metalloproteinase, putativ	MMP	AT1G70170	1.97	0.98	2.18	0.0670463	0.2490339	-4.54	FALSE
257079_at	unknown protein	---	AT3G15240	1.24	0.31	2.18	0.067016	0.2490339	-4.54	FALSE
246485_at	putative protein cell death assoc	AtCXE17	AT5G16080	2.71	1.44	2.18	0.067046	0.2490339	-4.54	FALSE
264019_at	cyclophilin (CYP2) Same as GB:	---	AT2G21130	-1.36	-0.44	-2.18	0.0670755	0.2490626	-4.54	FALSE
248518_at	putative protein similar to unknov	---	AT5G50560 ///	1.46	0.55	2.18	0.067114	0.2491651	-4.54	FALSE
263405_s_a	hypothetical protein similar to hyp	---	AT2G04066 ///	1.23	0.30	2.18	0.0671482	0.2492517	-4.55	FALSE
252226_at	putative protein transcribed gene	---	AT3G49880	-1.25	-0.32	-2.18	0.0671967	0.2493763	-4.55	FALSE
250185_at	putative protein esterase HDE, P	AtCXE16	AT5G14310	1.34	0.42	2.18	0.0672037	0.2493763	-4.55	FALSE
246552_at	putative protein	---	AT5G15420	-1.64	-0.71	-2.18	0.0672376	0.2494011	-4.55	FALSE
267026_at	DREB-like AP2 domain transcrip	---	AT2G38340	2.18	1.12	2.18	0.0672432	0.2494011	-4.55	FALSE
258398_at	thioredoxin m4 identical to GB:A	TRX-M4	AT3G15360	-1.24	-0.31	-2.18	0.0672268	0.2494011	-4.55	FALSE
266980_at	60S ribosomal protein L35 ;supp	---	AT2G39390	-1.59	-0.67	-2.18	0.067326	0.2496679	-4.55	FALSE
257838_at	hypothetical protein contains Pfa	---	AT3G25210	-1.25	-0.32	-2.18	0.0673494	0.2496733	-4.55	FALSE
245068_at	putative glucosyltransferase	UGT84B1	AT2G23260	1.29	0.36	2.18	0.0673407	0.2496733	-4.55	FALSE
262882_at	cytochrome p450, putative simil	CYP89A2	AT1G64900	2.03	1.02	2.18	0.0673961	0.2498059	-4.55	TRUE
257171_at	unknown protein ; supported by	---	AT3G23760	-1.32	-0.40	-2.18	0.0674129	0.2498276	-4.55	FALSE
257477_at	unknown protein	---	AT1G10660	-1.38	-0.47	-2.18	0.0674405	0.2498372	-4.55	FALSE
261253_at	unknown protein ;supported by fu	---	AT1G05840	-1.42	-0.51	-2.18	0.0674484	0.2498372	-4.55	FALSE
248164_at	putative protein similar to unknov	PBP1	AT5G54490	4.11	2.04	2.18	0.0674434	0.2498372	-4.55	FALSE

257914_at	Expressed protein ; supported by	---	AT3G25545	-1.34	-0.43	-2.18	0.0674878	0.2498617	-4.55	FALSE
250106_at	putative protein strong similarity t	---	AT5G16640	-1.26	-0.33	-2.18	0.0674782	0.2498617	-4.55	FALSE
264760_at	syntaxin-related protein Nt-syr1,	SYP124	AT1G61290	1.40	0.48	2.18	0.0674722	0.2498617	-4.55	FALSE
262844_at	unknown protein similar to pectin	---	AT1G14890	1.96	0.97	2.18	0.067509	0.2498992	-4.55	FALSE
259932_at	zinc finger protein, putative simil	STOP1	AT1G34370	-1.29	-0.37	-2.18	0.0675294	0.2499073	-4.55	FALSE
257147_at	unknown protein	---	AT3G27270	1.43	0.51	2.18	0.0675438	0.2499073	-4.55	FALSE
252442_at	dUTP pyrophosphatase-like prot	---	AT3G46940	-1.60	-0.68	-2.18	0.067544	0.2499073	-4.55	FALSE
253467_at	putative protein hypothetical pro	---	AT4G32140	1.32	0.40	2.18	0.0675787	0.2499952	-4.55	FALSE
254919_at	RING-H2 finger protein RHA1b ;	RHA1B	AT4G11360	-1.50	-0.58	-2.17	0.0677015	0.2503683	-4.55	TRUE
261301_at	hypothetical protein predicted by	---	AT1G48570	-1.79	-0.84	-2.17	0.0676908	0.2503683	-4.55	FALSE
258751_at	low temperature and salt respons	RCI2B	AT3G05890	-2.32	-1.21	-2.17	0.0677531	0.2504374	-4.55	TRUE
256180_at	light repressible receptor protein	---	AT1G51810	1.20	0.27	2.17	0.0677348	0.2504374	-4.55	FALSE
265804_at	putative peptide methionine sulfo	---	AT2G18030	-1.23	-0.30	-2.17	0.067746	0.2504374	-4.55	FALSE
247730_at	glucuronosyl transferase - like p	UGT76E1	AT5G59580	1.51	0.59	2.17	0.0678109	0.2506103	-4.55	FALSE
260890_at	cysteine proteinase contains sim	---	AT1G29090	1.43	0.51	2.17	0.067844	0.2506921	-4.56	FALSE
263691_at	60s ribosomal protein L34 identi	---	AT1G26880	-1.59	-0.67	-2.17	0.0678674	0.2507379	-4.56	FALSE
245995_at	putative protein various predicte	---	---	1.41	0.50	2.17	0.0678808	0.2507467	-4.56	FALSE
265974_at	unknown protein	---	---	1.52	0.60	2.17	0.0679061	0.2507995	-4.56	FALSE
257041_at	unknown protein	---	AT3G28550	1.40	0.48	2.17	0.0679789	0.2510277	-4.56	FALSE
248885_at	putative protein similar to unknov	---	AT5G46150	-1.26	-0.33	-2.17	0.0680397	0.2512117	-4.56	FALSE
256328_at	6-phosphogluconate dehydroge	---	AT3G02360	1.58	0.66	2.17	0.0680598	0.251245	-4.56	FALSE
260766_at	unknown protein similar to hypot	---	AT1G48960	1.29	0.37	2.17	0.0680961	0.2512907	-4.56	FALSE
258210_at	Eukaryotic initiation factor 4A, pu	EIF4A1	AT3G13920	-1.26	-0.34	-2.17	0.0680928	0.2512907	-4.56	FALSE
257066_at	lipid transfer protein, putative sir	---	AT3G18280	1.89	0.92	2.17	0.0681052	0.2512907	-4.56	FALSE
261695_at	Mg-chelatase, putative similar to	CHLD	AT1G08520	-1.33	-0.41	-2.17	0.0681181	0.2512977	-4.56	FALSE
250367_s_a	DEAD BOX RNA helicase RH15	---	AT5G11170 /.	-1.28	-0.36	-2.17	0.0682006	0.2515615	-4.56	FALSE
263844_at	unknown protein ; supported by	---	AT2G36930	-1.74	-0.80	-2.17	0.0682334	0.2515821	-4.56	FALSE
262209_at	hypothetical protein contains sim	---	AT1G74720	-1.34	-0.43	-2.17	0.068218	0.2515821	-4.56	FALSE
264070_at	putative cyclin-dependent kinase	CKS1	AT2G27960	-1.43	-0.52	-2.17	0.0682454	0.2515821	-4.56	FALSE
258985_at	hypothetical protein similar to hy	---	AT3G08960	1.24	0.31	2.17	0.0682585	0.2515821	-4.56	FALSE
265706_at	unknown protein	---	AT2G03390	-1.39	-0.47	-2.17	0.0682614	0.2515821	-4.56	FALSE
250542_at	hypothetical protein (fragment at	---	AT5G08270	-1.61	-0.68	-2.17	0.0682814	0.2516151	-4.56	FALSE
261019_at	unknown protein ; supported by c	---	AT1G26470	-1.30	-0.38	-2.17	0.0683119	0.2516382	-4.56	FALSE
254349_at	hypothetical protein	---	AT4G22250	-1.32	-0.40	-2.17	0.0683474	0.2516382	-4.56	FALSE
251823_at	putative protein	---	AT3G55080	-1.23	-0.30	-2.17	0.0683648	0.2516382	-4.56	FALSE

253507_at	serine threonine protein kinase l	---	AT4G32000	1.45	0.54	2.17	0.0683579	0.2516382	-4.56	FALSE
246782_at	putative protein PrMC3 - Pinus r	GID1C	AT5G27320	-1.64	-0.71	-2.17	0.0683315	0.2516382	-4.56	FALSE
256912_at	hypothetical protein predicted by	---	AT3G23850	1.28	0.35	2.17	0.0683235	0.2516382	-4.56	FALSE
249576_at	putative protein predicted protei	---	AT5G37690	-1.23	-0.30	-2.17	0.0683643	0.2516382	-4.56	FALSE
260600_at	hypothetical protein predicted by	---	AT1G55950	1.30	0.37	2.17	0.0684006	0.2517291	-4.56	FALSE
245776_at	hypothetical protein predicted by	---	AT1G30260	1.56	0.65	2.17	0.0684173	0.2517501	-4.56	FALSE
265082_at	hypothetical protein predicted by	---	AT1G03830	-1.27	-0.34	-2.17	0.0684344	0.2517723	-4.56	FALSE
267510_at	unknown protein ; supported by	SAP18	AT2G45640	-1.39	-0.47	-2.17	0.0684629	0.2518367	-4.56	FALSE
264708_at	putative ER6 protein similar to G	---	AT1G09740	1.40	0.49	2.17	0.068537	0.2520499	-4.57	TRUE
265039_at	unknown protein Location of ES	---	AT1G04000	1.26	0.34	2.17	0.0685528	0.2520499	-4.57	FALSE
257344_s_a	pseudogene, putative mutator-li	---	---	1.42	0.51	2.17	0.0685651	0.2520499	-4.57	FALSE
253147_at	protein kinase - like protein serir	CONNEXIN	AT4G35600	1.55	0.63	2.17	0.0685575	0.2520499	-4.57	FALSE
256944_at	unknown protein similar to unkno	VRN1	AT3G18990	-1.41	-0.50	-2.17	0.0685862	0.2520869	-4.57	FALSE
256440_at	unknown protein ;supported by f	---	AT3G10970	-1.26	-0.33	-2.17	0.0686627	0.2522768	-4.57	FALSE
246374_at	light repressible receptor protein	---	AT1G51840	1.21	0.28	2.16	0.0686796	0.2522768	-4.57	FALSE
247256_at	putative protein contains similarit	---	AT5G64730	-1.23	-0.30	-2.16	0.0687042	0.2522768	-4.57	FALSE
245142_at	putative O-sialoglycoprotein end	---	AT2G45270	-1.28	-0.36	-2.16	0.0686967	0.2522768	-4.57	FALSE
249736_at	unknown protein	---	AT5G24460	-1.21	-0.28	-2.16	0.0686921	0.2522768	-4.57	FALSE
264639_at	unknown protein similar to ubiqui	UCH2	AT1G65650	-1.34	-0.42	-2.17	0.0686597	0.2522768	-4.57	FALSE
265688_at	putative calmodulin-binding prote	---	AT2G24300	-1.21	-0.27	-2.16	0.0687168	0.2522823	-4.57	FALSE
249376_at	Expressed protein ; supported by	---	AT5G40645	1.21	0.27	2.16	0.0687493	0.2523205	-4.57	FALSE
255867_at	hypothetical protein predicted by	---	AT2G30370	1.25	0.32	2.16	0.068748	0.2523205	-4.57	FALSE
261899_at	cinnamoyl CoA reductase, putat	CCR2	AT1G80820	4.07	2.02	2.16	0.0687622	0.2523273	-4.57	FALSE
261859_at	E2, ubiquitin-conjugating enzym	UBC20	AT1G50490	-1.37	-0.45	-2.16	0.0688117	0.2524682	-4.57	FALSE
266768_s_a	ubiquitin extension protein (UBQ	UBQ6	AT2G47110 /,	-1.46	-0.54	-2.16	0.0688754	0.2526206	-4.57	FALSE
267466_at	putative GDSL-motif lipase/hydro	---	AT2G19010	-1.24	-0.31	-2.16	0.0688717	0.2526206	-4.57	FALSE
255598_at	putative protein similar to nucleol	---	AT4G00830	-1.37	-0.45	-2.16	0.0689075	0.2526979	-4.57	FALSE
252285_at	calmodulin-binding heat-shock -	---	AT3G49050	-1.28	-0.35	-2.16	0.0689304	0.2527412	-4.57	FALSE
250793_at	leucoanthocyanidin dioxygenase	---	AT5G05600	1.90	0.92	2.16	0.0689585	0.2528034	-4.57	FALSE
255527_at	putative protein	---	AT4G02360	2.54	1.34	2.16	0.0690076	0.2528642	-4.57	FALSE
259079_at	unknown protein	---	AT3G04950	-1.39	-0.48	-2.16	0.0690079	0.2528642	-4.57	FALSE
267474_at	hypothetical protein predicted by	WHY3	AT2G02740	-1.31	-0.39	-2.16	0.0690194	0.2528642	-4.57	FALSE
267223_at	hypothetical protein predicted by	AtITPK4	AT2G43980	1.30	0.37	2.16	0.0690085	0.2528642	-4.57	FALSE
260056_at	hypothetical protein predicted by	---	AT1G78140	-1.46	-0.55	-2.16	0.0690497	0.2529346	-4.57	FALSE
249039_at	late embryogenesis abundant pr	---	AT5G44310	1.31	0.39	2.16	0.0690643	0.2529476	-4.57	FALSE

266992_at	similar to Mlo proteins from H. vu	MLO12	AT2G39200	2.78	1.48	2.16	0.0690959	0.2530225	-4.57	FALSE
253664_at	NADPH-ferrihemoprotein reducta	ATR2	AT4G30210	2.10	1.07	2.16	0.0691278	0.2530628	-4.57	FALSE
247974_at	putative protein contains similarit	---	AT5G56780	-1.25	-0.32	-2.16	0.0691291	0.2530628	-4.57	FALSE
257150_at	unknown protein ;supported by f	---	AT3G27230	-1.36	-0.44	-2.16	0.0691633	0.2531475	-4.57	FALSE
256196_at	hypothetical protein predicted by	---	---	1.31	0.39	2.16	0.0691862	0.2531905	-4.57	FALSE
263783_at	putative WRKY-type DNA bindin	WRKY46	AT2G46400	2.81	1.49	2.16	0.0692327	0.2532795	-4.57	FALSE
260467_at	unknown protein	---	AT1G10890	1.22	0.29	2.16	0.0692301	0.2532795	-4.57	FALSE
258973_at	putative cytochrome P450 simila	CYP94B2	AT3G01900	1.30	0.38	2.16	0.0692732	0.2533057	-4.58	FALSE
256525_at	unknown protein ;supported by fu	---	AT1G66180	-1.65	-0.72	-2.16	0.0692709	0.2533057	-4.58	FALSE
250595_at	unknown protein	---	AT5G07770	1.47	0.55	2.16	0.0692522	0.2533057	-4.58	FALSE
262770_at	hypothetical protein predicted by	---	AT1G13190	1.47	0.55	2.16	0.0693059	0.2533392	-4.58	FALSE
264482_at	sugar carrier protein, putative si	---	AT1G77210	1.82	0.86	2.16	0.0692938	0.2533392	-4.58	FALSE
263650_at	hypothetical protein predicted by	---	AT1G04360	1.28	0.35	2.16	0.0693157	0.2533392	-4.58	FALSE
258956_at	hypothetical protein predicted by	---	AT3G01440	-2.07	-1.05	-2.16	0.0693731	0.2535086	-4.58	FALSE
256078_at	hypothetical protein predicted by	---	AT1G20670	1.28	0.36	2.16	0.0694407	0.2537149	-4.58	FALSE
246558_at	putative protein IDN3-B - Homo	EMB2773	AT5G15540	-1.34	-0.42	-2.16	0.0694925	0.2538636	-4.58	FALSE
246192_at	translation initiation factor eIF-2	EIF2 BETA	AT5G20920	-1.24	-0.31	-2.16	0.069509	0.2538832	-4.58	FALSE
262071_at	unknown protein ;supported by fu	CF9	AT1G59510	-1.32	-0.40	-2.16	0.0695279	0.2539117	-4.58	FALSE
259430_at	hypothetical protein similar to unl	GPAT4	AT1G01610	1.46	0.55	2.16	0.0696064	0.2541169	-4.58	TRUE
257658_at	unknown protein ; supported by	---	AT3G13230	-1.82	-0.86	-2.16	0.0696013	0.2541169	-4.58	TRUE
255511_at	Expressed protein ; supported by	PIT1	AT4G02075	-1.66	-0.73	-2.16	0.0696292	0.2541593	-4.58	FALSE
261160_at	hypothetical protein	---	AT1G34480	1.26	0.34	2.16	0.0696439	0.2541723	-4.58	FALSE
248528_at	putative protein similar to unknov	---	AT5G50760	4.28	2.10	2.15	0.0697039	0.2542387	-4.58	FALSE
256597_at	acidic ribosomal protein P2b (rp	---	AT3G28500	-1.82	-0.87	-2.15	0.0696845	0.2542387	-4.58	FALSE
245876_at	chaperonin precursor, putative s	---	AT1G26230	-1.55	-0.63	-2.15	0.0697096	0.2542387	-4.58	FALSE
249275_at	polygalacturonase-like protein	---	AT5G41870	-1.30	-0.38	-2.15	0.0697178	0.2542387	-4.58	FALSE
263833_at	hypothetical protein	---	AT2G40316	-1.24	-0.30	-2.15	0.0696797	0.2542387	-4.58	FALSE
248522_at	predicted protein	---	AT5G50565 /	-1.25	-0.32	-2.15	0.0697386	0.2542587	-4.58	FALSE
248476_at	putative protein similar to unknov	---	AT5G50890	1.69	0.76	2.15	0.0697456	0.2542587	-4.58	FALSE
257370_at	hypothetical protein predicted by	---	AT2G35080	1.28	0.36	2.15	0.0697623	0.2542791	-4.58	FALSE
256752_at	hypothetical protein predicted by	---	AT3G27180	-1.50	-0.59	-2.15	0.0698012	0.2543137	-4.58	FALSE
262441_at	hypothetical protein similar to hy	OSB1	AT1G47720	-1.33	-0.41	-2.15	0.0698053	0.2543137	-4.58	FALSE
266013_s_a	hypothetical protein	---	AT2G07702	1.25	0.33	2.15	0.0697887	0.2543137	-4.58	FALSE
262575_at	putative ABC transporter Similar	PDR7	AT1G15210	1.29	0.36	2.15	0.0698414	0.2543236	-4.58	FALSE
252844_at	putative protein several hypothet	---	AT3G42140	1.32	0.40	2.15	0.0698371	0.2543236	-4.58	FALSE

266518_at	hypothetical protein predicted by	---	AT2G35170	1.30	0.38	2.15	0.0698391	0.2543236	-4.58	FALSE
261006_at	unknown protein similar to reticul	---	AT1G26410	1.82	0.87	2.15	0.069892	0.2543522	-4.58	TRUE
260622_at	hypothetical protein predicted by	NF-YC10	AT1G07980	-1.25	-0.32	-2.15	0.0698692	0.2543522	-4.58	FALSE
256219_at	hypothetical protein predicted by	---	AT1G56260	-1.28	-0.36	-2.15	0.0698729	0.2543522	-4.58	FALSE
264607_at	putative K+ channel, beta subun	KAB1	AT1G04690	-1.21	-0.28	-2.15	0.0698939	0.2543522	-4.58	FALSE
256015_at	PSI type II chlorophyll a/b-bindir	LHCA6	AT1G19150	-2.73	-1.45	-2.15	0.0699164	0.2543935	-4.58	FALSE
246405_at	disease resistance protein RPP1	---	AT1G57630	3.53	1.82	2.15	0.0699595	0.2545099	-4.59	FALSE
252873_at	putative protein myosin heavy ch	---	AT4G40020	1.32	0.40	2.15	0.0699874	0.2545706	-4.59	FALSE
257414_at	hypothetical protein similar to hyp	---	AT1G62110	1.27	0.34	2.15	0.0700159	0.2546336	-4.59	FALSE
265299_at	putative retroelement pol polypro	---	---	1.43	0.51	2.15	0.0700398	0.25468	-4.59	FALSE
252214_at	putative protein EREBP-3 homo	CEJ1	AT3G50260	1.82	0.87	2.15	0.0700841	0.2547599	-4.59	TRUE
246269_at	putative protein	---	AT4G37110	-1.67	-0.74	-2.15	0.0700816	0.2547599	-4.59	FALSE
245368_at	hypothetical protein ; supported b	---	AT4G15510	-1.50	-0.58	-2.15	0.0701587	0.2549904	-4.59	FALSE
256767_at	hypothetical protein predicted by	---	AT3G13680	1.26	0.34	2.15	0.0702084	0.2550694	-4.59	FALSE
266046_at	hypothetical protein	---	AT2G07728	1.37	0.46	2.15	0.070214	0.2550694	-4.59	FALSE
259502_at	unknown protein ; supported by c	---	AT1G15670	1.68	0.74	2.15	0.0702107	0.2550694	-4.59	FALSE
249722_at	putative protein similar to unknov	---	AT5G35430	1.21	0.28	2.15	0.0702702	0.2552329	-4.59	FALSE
250151_at	high affinity nitrate transporter -	ATNRT2.7	AT5G14570	-1.58	-0.66	-2.15	0.0702865	0.2552516	-4.59	FALSE
264027_at	putative AAA-type ATPase simila	CDC48B	AT2G03670	-1.39	-0.47	-2.15	0.0703178	0.2552934	-4.59	FALSE
255268_at	putative protein ubiquitin, Tetrah	---	AT4G05230	1.31	0.39	2.15	0.0703316	0.2552934	-4.59	FALSE
255044_at	putative protein	---	AT4G09680	-1.30	-0.37	-2.15	0.0703233	0.2552934	-4.59	FALSE
262661_s_a	hypothetical protein	---	AT1G14230 ///	2.59	1.37	2.15	0.0704377	0.2553576	-4.59	TRUE
253949_at	grpE like protein ;supported by f	AR192	AT4G26780	-1.89	-0.92	-2.15	0.0704131	0.2553576	-4.59	TRUE
247525_at	pseudo-response regulator 1 ; s	TOC1	AT5G61380	1.21	0.28	2.15	0.0704501	0.2553576	-4.59	FALSE
247043_at	protein kinase, 41K (EC 2.7.1.-)	SNRK2.3	AT5G66880	-1.49	-0.57	-2.15	0.0703965	0.2553576	-4.59	FALSE
266876_at	hypothetical protein predicted by	---	AT2G44820	-1.30	-0.38	-2.15	0.070447	0.2553576	-4.59	FALSE
251653_at	putative protein regulatory prote	BOP1	AT3G57130	1.33	0.41	2.15	0.0704156	0.2553576	-4.59	FALSE
255318_at	hypothetical protein	---	AT4G04190	-1.32	-0.40	-2.15	0.0703893	0.2553576	-4.59	FALSE
259527_at	hypothetical protein	---	AT1G12600	1.21	0.28	2.15	0.0704612	0.2553576	-4.59	FALSE
248135_at	putative protein similar to unknov	---	AT5G54890	-1.38	-0.46	-2.15	0.0704333	0.2553576	-4.59	FALSE
247770_at	putative protein predicted protei	---	AT5G58930	-1.88	-0.91	-2.15	0.0704138	0.2553576	-4.59	FALSE
249954_at	putative protein ;supported by fu	---	AT5G18920	-1.20	-0.26	-2.15	0.0704885	0.2554052	-4.59	FALSE
248001_at	calcineurin B-like protein 2 (gb|A	CBL2	AT5G55990	-1.37	-0.45	-2.15	0.0704968	0.2554052	-4.59	FALSE
263877_at	hypothetical protein predicted by	---	AT2G21780	1.20	0.26	2.15	0.0705144	0.2554084	-4.59	FALSE
266803_at	putative protein kinase contains a	APK1B	AT2G28930	-1.76	-0.82	-2.15	0.07052	0.2554084	-4.59	FALSE

249759_at	putative protein contains similarit	YSL2	AT5G24380	1.43	0.52	2.15	0.0705489	0.2554724	-4.59	FALSE
248144_at	glucose-6-phosphate/phosphate	GPT1	AT5G54800	1.34	0.42	2.15	0.0705855	0.2555644	-4.59	FALSE
245473_at	hypothetical protein	---	AT4G16050	-1.23	-0.30	-2.14	0.070697	0.2558866	-4.60	FALSE
257088_at	unknown protein	---	AT3G20510	1.79	0.84	2.14	0.0706917	0.2558866	-4.60	FALSE
248049_at	putative protein contains similarit	COX15	AT5G56090	-1.71	-0.77	-2.14	0.0707295	0.2559637	-4.60	FALSE
251037_at	putative protein oxysterol-bindin	UNE18	AT5G02100	1.46	0.54	2.14	0.0708387	0.2560255	-4.60	FALSE
257843_at	hypothetical protein predicted by	---	---	1.23	0.30	2.14	0.0708054	0.2560255	-4.60	FALSE
250842_at	putative protein predicted protei	VTE5	AT5G04490	-1.39	-0.48	-2.14	0.0708458	0.2560255	-4.60	FALSE
257423_at	hypothetical protein predicted by	---	AT1G62010	-1.32	-0.40	-2.14	0.0708588	0.2560255	-4.60	FALSE
258430_at	phospholipase D, putative simila	PLDP1	AT3G16785	1.23	0.30	2.14	0.070856	0.2560255	-4.60	FALSE
266083_at	hypothetical protein predicted by	---	AT2G37820	1.21	0.27	2.14	0.0708515	0.2560255	-4.60	FALSE
252487_at	glucosyltransferase-like protein	UGT76E12	AT3G46660	3.02	1.59	2.14	0.070835	0.2560255	-4.60	FALSE
248314_at	putative protein similar to unknov	---	AT5G52620	-1.22	-0.29	-2.14	0.0708335	0.2560255	-4.60	FALSE
245798_at	hypothetical protein predicted by	---	AT1G45545	-1.21	-0.27	-2.14	0.0708527	0.2560255	-4.60	FALSE
251737_at	40S ribosomal protein S26 homo	---	AT3G56340	-1.72	-0.78	-2.14	0.0708555	0.2560255	-4.60	FALSE
253546_at	hypothetical protein ;supported b	---	AT4G31030 ///	-1.34	-0.42	-2.14	0.0708714	0.2560306	-4.60	FALSE
252083_at	putative protein hypothetical pro	---	AT3G51960	1.80	0.85	2.14	0.0708865	0.2560446	-4.60	FALSE
247849_at	putative protein fibrinogen-bindi	---	AT5G58130	-1.35	-0.44	-2.14	0.0709113	0.2560935	-4.60	FALSE
262393_at	hypothetical protein contains sim	---	AT1G49490	-1.28	-0.36	-2.14	0.0710322	0.2564894	-4.60	FALSE
266547_at	similar to eyes absent protein ;s	ATEYA	AT2G35320	-1.22	-0.29	-2.14	0.0710623	0.2565576	-4.60	FALSE
248882_at	cullin ;supported by full-length c	CUL4	AT5G46210	-1.23	-0.29	-2.14	0.0710928	0.2566273	-4.60	FALSE
248465_at	putative protein contains similarit	---	AT5G51200	-1.42	-0.51	-2.14	0.071105	0.2566304	-4.60	FALSE
255812_at	potassium uptake transporter - li	HKT1	AT4G10310	-1.54	-0.62	-2.14	0.0711326	0.2566897	-4.60	FALSE
266105_at	putative transport protein SEC61	SEC61 BE	AT2G45070	1.40	0.49	2.14	0.0711458	0.2566964	-4.60	FALSE
251116_at	serin carboxypeptidase - like pro	scpl40	AT3G63470	1.34	0.42	2.14	0.0711615	0.2567127	-4.60	FALSE
247152_at	oligopeptidase A ; supported by	---	AT5G65620	-1.23	-0.30	-2.14	0.0711848	0.2567561	-4.60	FALSE
259603_at	Expressed protein ; supported by	---	AT1G56500	-1.45	-0.54	-2.14	0.0712023	0.2567784	-4.60	FALSE
254932_at	putative translation elongation fa	---	AT4G11120	-1.46	-0.54	-2.14	0.0712612	0.2569502	-4.60	FALSE
263938_at	hypothetical protein predicted by	---	AT2G35900	-1.27	-0.34	-2.14	0.0713001	0.2570274	-4.60	FALSE
251703_at	putative protein hypothetical prot	---	AT3G56670	1.37	0.46	2.14	0.0713051	0.2570274	-4.60	FALSE
250936_at	putative protein ;supported by fu	---	AT5G03120	-1.63	-0.70	-2.14	0.0713325	0.257045	-4.60	TRUE
267538_at	putative DNA binding protein ; su	---	AT2G41870	-1.23	-0.29	-2.14	0.0713285	0.257045	-4.60	FALSE
247029_at	TINY-like protein	---	AT5G67190	1.38	0.46	2.14	0.0713955	0.2572314	-4.60	TRUE
255186_at	putative transposon protein simil	---	---	1.45	0.54	2.14	0.071436	0.2572967	-4.61	FALSE
257398_at	hypothetical protein predicted by	---	AT2G01990	-1.22	-0.29	-2.14	0.0714362	0.2572967	-4.61	FALSE

251595_at	putative protein galactose oxida	---	AT3G57620	1.28	0.36	2.14	0.0714684	0.2573719	-4.61	FALSE
267508_at	hypothetical protein predicted by	---	AT2G45700	-1.26	-0.33	-2.14	0.0715382	0.2575125	-4.61	FALSE
246867_at	putative protein various predicte	---	AT5G25990	-1.22	-0.29	-2.14	0.0715413	0.2575125	-4.61	FALSE
265588_at	putative pathogenesis-related pr	---	AT2G19970	2.48	1.31	2.14	0.071522	0.2575125	-4.61	FALSE
249423_at	Expressed protein ; supported by	---	AT5G39785	1.37	0.46	2.14	0.0715623	0.2575135	-4.61	FALSE
255908_s_a	unknown protein ;supported by fu	---	AT1G18000 /.	-1.28	-0.36	-2.14	0.0715642	0.2575135	-4.61	FALSE
252042_at	putative serine/threonine protein	---	AT3G51990	1.34	0.42	2.14	0.0716068	0.2576265	-4.61	FALSE
254275_at	HSP associated protein like p48	AtHip1	AT4G22670	-1.35	-0.43	-2.14	0.0716627	0.2577778	-4.61	FALSE
247263_at	putative protein similar to unknov	---	AT5G64470	-1.39	-0.47	-2.14	0.0716715	0.2577778	-4.61	FALSE
267621_at	unknown protein	---	---	-1.33	-0.42	-2.14	0.0716916	0.2578096	-4.61	FALSE
262619_at	3-hydroxyisobutyryl-coenzyme A	---	AT1G06550	2.11	1.08	2.14	0.0717059	0.2578203	-4.61	FALSE
254135_at	putative protein MSP1 protein, S	---	AT4G24860	1.29	0.36	2.13	0.071743	0.2579128	-4.61	FALSE
259799_at	drought induced protein, putative	---	AT1G72290	1.21	0.28	2.13	0.0717844	0.2579398	-4.61	FALSE
257345_s_a	pseudogene	---	---	1.22	0.29	2.13	0.0717627	0.2579398	-4.61	FALSE
248118_at	GDSL-motif lipase/hydrolase-like	---	AT5G55050	3.28	1.72	2.13	0.0717744	0.2579398	-4.61	FALSE
253340_s_a	WD-repeat protein -like protein V	CDC20.2	AT4G33260 /.	-1.26	-0.34	-2.13	0.0717957	0.2579398	-4.61	FALSE
252754_at	putative protein hypothetical pro	---	---	-1.52	-0.60	-2.13	0.0718538	0.258108	-4.61	FALSE
250809_at	putative protein contains similarit	---	AT5G05140	1.69	0.76	2.13	0.0718768	0.2581499	-4.61	FALSE
262729_at	rac-like GTP binding protein (AR	ARAC5	AT1G75840	-1.38	-0.47	-2.13	0.0719114	0.2582335	-4.61	TRUE
248695_at	putative protein similar to unknov	---	AT5G48350	1.41	0.50	2.13	0.0719793	0.2584366	-4.61	FALSE
253405_at	transcription factor TINY homolo	---	AT4G32800	1.56	0.64	2.13	0.0720164	0.2584528	-4.61	TRUE
246951_at	unknown protein	---	AT5G04880	-1.66	-0.73	-2.13	0.0720178	0.2584528	-4.61	TRUE
267136_at	putative GTP-binding protein (ex	XLG1	AT2G23460	-1.29	-0.36	-2.13	0.0720026	0.2584528	-4.61	FALSE
248394_at	unknown protein	---	AT5G52070	-1.25	-0.32	-2.13	0.0720962	0.2586934	-4.61	TRUE
257382_at	hypothetical protein predicted by	WRKY54	AT2G40750	5.23	2.39	2.13	0.0721285	0.2587686	-4.61	FALSE
251922_at	protein kinase -like protein prote	---	AT3G54030	1.60	0.68	2.13	0.0722609	0.2590807	-4.62	TRUE
266065_at	phytochrome B Identical to GB:X	PHYB	AT2G18790	-1.32	-0.40	-2.13	0.0722523	0.2590807	-4.62	FALSE
251270_at	putative protein	---	AT3G62370	1.44	0.52	2.13	0.0722609	0.2590807	-4.62	FALSE
264680_at	hypothetical protein predicted by	---	AT1G65510	1.68	0.74	2.13	0.0722546	0.2590807	-4.62	FALSE
245067_at	S-like ribonuclease RNS2 identi	RNS2	AT2G39780	1.29	0.37	2.13	0.072327	0.2592767	-4.62	FALSE
247235_at	putative protein contains similarit	---	AT5G64580	-1.54	-0.62	-2.13	0.0723487	0.2593139	-4.62	FALSE
263120_at	cytochrome P450, putative simil	CYP708A3	AT1G78490	3.84	1.94	2.13	0.0723717	0.2593147	-4.62	FALSE
256169_at	receptor protein kinase, putative	---	AT1G51800	2.90	1.54	2.13	0.0723642	0.2593147	-4.62	FALSE
249914_at	protease-like protein	---	AT5G22850	1.37	0.45	2.13	0.0724197	0.2594053	-4.62	FALSE
260434_at	hypothetical protein predicted by	---	AT1G68330	1.48	0.57	2.13	0.0724164	0.2594053	-4.62	FALSE

252863_at	myo-inositol-1-phosphate syntha	MIPS1	AT4G39800	-3.31	-1.73	-2.13	0.0724365	0.2594249	-4.62	FALSE
262919_at	unknown protein ; supported by	---	AT1G79380	1.39	0.48	2.13	0.072454	0.2594469	-4.62	FALSE
260965_s_a	hypothetical protein predicted by	---	---	1.22	0.29	2.13	0.0724805	0.2595008	-4.62	FALSE
247188_at	14-3-3 protein GF14kappa (grf8	GRF8	AT5G65430	-1.30	-0.38	-2.13	0.0725843	0.2598317	-4.62	FALSE
266456_at	putative bHLH transcription facto	NAI1	AT2G22770	1.30	0.38	2.13	0.0726256	0.2599389	-4.62	FALSE
265853_at	putative RING zinc finger protein	---	AT2G42360	2.22	1.15	2.13	0.0726512	0.2599577	-4.62	TRUE
266352_at	unknown protein	---	AT2G01610	2.04	1.03	2.13	0.0726537	0.2599577	-4.62	FALSE
249999_at	triacylglycerol lipase-like protein	---	AT5G18640	-1.57	-0.65	-2.12	0.0727813	0.2601694	-4.62	FALSE
254430_at	reticuline oxidase - like protein r	---	AT4G20820	-1.78	-0.83	-2.13	0.072744	0.2601694	-4.62	FALSE
247620_at	receptor like protein kinase rece	---	AT5G60310	1.29	0.37	2.12	0.0727753	0.2601694	-4.62	FALSE
260573_at	putative pectinesterase	---	AT2G47280	1.30	0.37	2.13	0.0727551	0.2601694	-4.62	FALSE
259316_at	unknown protein	---	AT3G01175	1.36	0.44	2.12	0.0727725	0.2601694	-4.62	FALSE
264956_at	unknown protein similar to putati	ACR3	AT1G76990	-1.93	-0.95	-2.13	0.0727295	0.2601694	-4.62	FALSE
262766_at	hypothetical protein predicted by	---	AT1G13160	-1.53	-0.62	-2.12	0.0727947	0.2601768	-4.62	FALSE
247099_at	putative protein contains similarit	---	AT5G66500	-1.32	-0.40	-2.12	0.0729093	0.2605187	-4.63	FALSE
267614_at	putative cytochrome P450	BAS1	AT2G26710	-2.12	-1.08	-2.12	0.0729257	0.2605187	-4.63	FALSE
256722_at	hypothetical protein predicted by	---	AT2G34050	-1.58	-0.66	-2.12	0.0729329	0.2605187	-4.63	FALSE
259920_at	putative phenylalanyl-tRNA synth	---	AT1G72550	-1.27	-0.34	-2.12	0.0729361	0.2605187	-4.63	FALSE
245696_at	phytochrome kinase substrate 1	PKS4	AT5G04190	-2.06	-1.05	-2.12	0.0729935	0.260683	-4.63	FALSE
258048_at	FtsH protease, putative contains	EMB2083	AT3G16290	-1.28	-0.36	-2.12	0.0730075	0.2606919	-4.63	FALSE
253994_at	protein phosphatase ABI1 ; supp	ABI1	AT4G26080	1.28	0.35	2.12	0.0730218	0.2607025	-4.63	TRUE
253608_at	xyloglucan endo-1,4-beta-D-gluc	XTH19	AT4G30290	-2.20	-1.14	-2.12	0.0731108	0.2609312	-4.63	FALSE
251356_at	putative protein hypothetical prot	AtPP2-A13	AT3G61060	-1.34	-0.42	-2.12	0.0730992	0.2609312	-4.63	FALSE
267464_at	putative pectinesterase	---	AT2G19150	1.28	0.36	2.12	0.0731202	0.2609312	-4.63	FALSE
256487_at	disease resistance gene, putativ	---	AT1G31540	1.39	0.47	2.12	0.0731621	0.2610398	-4.63	FALSE
251647_at	protein kinase - like protein wall-	---	AT3G57770	-1.33	-0.41	-2.12	0.0732284	0.2611317	-4.63	FALSE
261088_at	DNA-binding protein, putative si	---	AT1G07590	-1.33	-0.41	-2.12	0.073243	0.2611317	-4.63	FALSE
249028_at	DNA-damage-inducible protein P	POLH	AT5G44740	-1.36	-0.44	-2.12	0.0732451	0.2611317	-4.63	FALSE
257460_at	auxin induced protein, putative s	---	AT1G75580	1.25	0.33	2.12	0.0732177	0.2611317	-4.63	FALSE
251203_at	putative protein putative transcri	---	AT3G63070	1.23	0.30	2.12	0.0732432	0.2611317	-4.63	FALSE
260520_at	mannosyl-oligosaccharide alpha	---	AT1G51590	-1.29	-0.37	-2.12	0.0732612	0.2611482	-4.63	FALSE
253788_at	aromatic amino-acid decarboxyl	---	AT4G28680	1.31	0.39	2.12	0.0733023	0.261254	-4.63	FALSE
263542_at	putative protein transport protein	---	AT2G21630	-1.41	-0.49	-2.12	0.0733226	0.2612854	-4.63	FALSE
256622_at	unknown protein	AtHB34	AT3G28920	-1.22	-0.28	-2.12	0.0733411	0.2613104	-4.63	FALSE
254557_at	hypothetical protein ;supported b	---	AT4G19140	1.60	0.68	2.12	0.0733769	0.2613975	-4.63	FALSE

260585_at	unknown protein	EMB2777	AT2G43650	-1.65	-0.72	-2.12	0.0734057	0.2614155	-4.63	FALSE
259240_at	unknown protein ; supported by	---	AT3G11590	-1.39	-0.47	-2.12	0.0734156	0.2614155	-4.63	FALSE
266102_at	unknown protein	---	AT2G40720	-1.28	-0.35	-2.12	0.0734164	0.2614155	-4.63	FALSE
261271_at	Expressed protein ; supported by	---	AT1G26795	1.30	0.37	2.12	0.073457	0.2615192	-4.63	FALSE
256755_at	calmodulin, putative similar to G	---	AT3G25600	1.60	0.68	2.12	0.073524	0.261717	-4.63	FALSE
266368_at	putative embryo-abundant protei	---	AT2G41380	3.87	1.95	2.12	0.0735848	0.2618107	-4.63	TRUE
257050_at	putative protein phosphatase typ	---	AT3G15260	-1.36	-0.45	-2.12	0.0735806	0.2618107	-4.63	FALSE
250653_at	putative protein strong similarity t	---	AT5G06930	1.75	0.81	2.12	0.0735801	0.2618107	-4.63	FALSE
261147_at	unknown protein ;supported by fu	---	AT1G19690	-1.51	-0.60	-2.12	0.0736914	0.2621085	-4.64	FALSE
248278_at	putative protein similar to unknov	---	AT5G52890	-1.32	-0.40	-2.12	0.0736859	0.2621085	-4.64	FALSE
256009_at	AP2 domain transcription factor,	---	AT1G19210	2.39	1.26	2.12	0.0737126	0.262143	-4.64	FALSE
252272_at	receptor protein kinase - like pro	BAM2	AT3G49670	-1.67	-0.74	-2.11	0.0739525	0.2629551	-4.64	FALSE
254444_at	putative protein riboflavin biosyn	---	AT4G20960	-1.54	-0.63	-2.11	0.0739883	0.2629707	-4.64	FALSE
258332_at	putative transport protein similar	---	AT3G16180	-1.93	-0.95	-2.11	0.0739938	0.2629707	-4.64	FALSE
247755_at	subtilisin-like serine protease cor	ATSBT4.12	AT5G59090	-1.23	-0.30	-2.11	0.0740146	0.2629707	-4.64	FALSE
253543_at	hypothetical protein	---	AT4G31270	-1.26	-0.34	-2.11	0.0740121	0.2629707	-4.64	FALSE
257861_at	putative transporter similar to SV	---	AT3G13050	1.33	0.41	2.11	0.073987	0.2629707	-4.64	FALSE
250231_at	AP2/EREBP-like transcription fac	LEP	AT5G13910	1.24	0.31	2.11	0.0740338	0.2629982	-4.64	FALSE
246877_at	putative protein various predicte	---	AT5G26150	1.21	0.28	2.11	0.0740486	0.2630097	-4.64	FALSE
261341_s_a	putative purple acid phosphatase	PAP5	AT1G52940 ///	1.20	0.27	2.11	0.0741208	0.2632251	-4.64	FALSE
252113_at	putative protein predicted protei	---	AT3G51620	-1.23	-0.30	-2.11	0.0741924	0.263267	-4.64	FALSE
255037_at	DNA-binding protein ;supported	ATMYB6	AT4G09460	1.69	0.76	2.11	0.0742074	0.263267	-4.64	FALSE
258125_s_a	hypothetical protein contains Pfa	---	AT3G23510 ///	1.85	0.89	2.11	0.0741839	0.263267	-4.64	FALSE
258848_at	Expressed protein ; supported by	DCL2	AT3G03300 ///	-1.26	-0.33	-2.11	0.0741965	0.263267	-4.64	FALSE
249299_at	E2, ubiquitin-conjugating enzym	UBC4	AT5G41340	-1.34	-0.42	-2.11	0.0741989	0.263267	-4.64	FALSE
258838_at	unknown protein ; supported by	---	AT3G07140	-1.24	-0.31	-2.11	0.0742249	0.263267	-4.64	FALSE
254342_at	receptor like protein (fragment) I	---	AT4G22140	-1.22	-0.29	-2.11	0.0741823	0.263267	-4.64	FALSE
262420_at	hypothetical protein contains sim	TAF15	AT1G50300	-1.21	-0.27	-2.11	0.0742237	0.263267	-4.64	FALSE
266366_at	unknown protein	---	AT2G41420	1.35	0.43	2.11	0.0742593	0.2633417	-4.64	FALSE
256826_at	hypothetical protein predicted by	---	AT3G18540	1.21	0.28	2.11	0.0742766	0.2633417	-4.64	FALSE
253469_at	putative protein gene C42D8.3,	ATPANK2	AT4G32180	-1.27	-0.34	-2.11	0.0742806	0.2633417	-4.64	FALSE
251337_at	proteasome component C5 ;sup	PBF1	AT3G60820	-1.22	-0.28	-2.11	0.0743198	0.2634396	-4.64	FALSE
248659_at	cyclin C-like protein	---	AT5G48640	1.31	0.39	2.11	0.0743949	0.263665	-4.64	FALSE
266819_at	unknown protein ;supported by f	---	AT2G44870	-1.36	-0.45	-2.11	0.0744197	0.263712	-4.65	FALSE
256048_at	hypothetical protein contains sim	---	AT1G07025	1.25	0.32	2.11	0.0744611	0.2638177	-4.65	FALSE

259666_at	unknown protein ; supported by	SR33	AT1G55310	-1.26	-0.34	-2.11	0.0744882	0.2638317	-4.65	FALSE
245678_at	unknown protein	---	AT1G56610	-1.38	-0.47	-2.11	0.0744846	0.2638317	-4.65	FALSE
252077_at	putative protein several putative	---	AT3G51720	-1.33	-0.41	-2.11	0.0745422	0.2639409	-4.65	FALSE
264558_at	putative protein kinase Similar to	---	AT1G09600	1.23	0.30	2.11	0.0745371	0.2639409	-4.65	FALSE
256754_at	unknown protein	CHUP1	AT3G25690	-1.30	-0.38	-2.11	0.0745712	0.2640028	-4.65	FALSE
248020_at	putative protein strong similarity t	---	AT5G56490	1.22	0.29	2.11	0.0745992	0.2640608	-4.65	FALSE
267556_at	putative beta-galactosidase ; su	BGAL9	AT2G32810	-1.32	-0.40	-2.11	0.074637	0.2641185	-4.65	FALSE
255389_at	putative reverse transcriptase	---	---	-1.20	-0.27	-2.11	0.0746387	0.2641185	-4.65	FALSE
256824_at	hypothetical protein predicted by	AT3G2212	---	1.51	0.60	2.11	0.074722	0.2643725	-4.65	FALSE
251825_at	ABC transporter - like protein AT	---	AT3G55100	1.28	0.35	2.11	0.0747497	0.2644293	-4.65	FALSE
249860_at	prolylcarboxypeptidase-like prote	---	AT5G22860	3.91	1.97	2.11	0.0747683	0.2644543	-4.65	FALSE
247845_at	beta-1,3 glucanase - like protein	---	AT5G58090	-1.26	-0.33	-2.11	0.0748055	0.2644772	-4.65	FALSE
263196_at	hypothetical protein predicted by	---	AT1G36070	-1.47	-0.56	-2.11	0.0748096	0.2644772	-4.65	FALSE
246884_at	putative protein cation transport	---	AT5G26220	-1.63	-0.71	-2.11	0.0747867	0.2644772	-4.65	FALSE
259872_at	putative translation initiation facto	---	AT1G76810	-1.24	-0.31	-2.11	0.0748217	0.2644791	-4.65	FALSE
248027_at	outward rectifying potassium cha	ATKCO1	AT5G55630	-1.33	-0.41	-2.11	0.0748612	0.2645367	-4.65	FALSE
252502_at	copper transport protein - like pr	COPT2	AT3G46900	-1.98	-0.99	-2.11	0.0748594	0.2645367	-4.65	FALSE
259712_at	putative 20S proteasome beta su	PBC2	AT1G77440	-1.23	-0.30	-2.10	0.0749312	0.2647429	-4.65	FALSE
248746_at	NADH dehydrogenase 10.5K cha	---	AT5G47890	-1.48	-0.56	-2.10	0.0749503	0.2647694	-4.65	FALSE
253548_at	Expressed protein ; supported by	---	AT4G30993	-1.39	-0.48	-2.10	0.0750023	0.2649121	-4.65	FALSE
247414_at	unknown protein	EMB2759	AT5G63050	-1.34	-0.42	-2.10	0.075021	0.264937	-4.65	FALSE
246764_s_a	putative protein At2g27780 and	---	AT2G13640 /	1.22	0.29	2.10	0.0750415	0.2649686	-4.65	FALSE
262868_at	unknown protein	---	AT1G64980	1.46	0.54	2.10	0.0751362	0.2649832	-4.65	TRUE
251667_at	putative protein DYSKERIN (NU	NAP57	AT3G57150	-1.74	-0.80	-2.10	0.0751616	0.2649832	-4.65	FALSE
257607_at	hypothetical protein predicted by	---	AT3G13880	-1.21	-0.27	-2.10	0.075154	0.2649832	-4.65	FALSE
254207_at	putative protein Dof zinc finger p	---	AT4G24060	1.29	0.37	2.10	0.0751239	0.2649832	-4.65	FALSE
255731_at	phosphoprotein phosphatase 2A	RCN1	AT1G25490	-1.21	-0.27	-2.10	0.0750586	0.2649832	-4.65	FALSE
260027_at	unknown protein	CPuORF34	AT1G29950 /	-1.39	-0.47	-2.10	0.0751434	0.2649832	-4.65	FALSE
261323_at	hypothetical protein predicted by	---	AT1G44760	-1.48	-0.56	-2.10	0.0751425	0.2649832	-4.65	FALSE
263390_at	hypothetical protein similar to Ta	---	---	1.23	0.29	2.10	0.0750879	0.2649832	-4.65	FALSE
248440_at	acid phosphatase	---	AT5G51260	1.32	0.40	2.10	0.0751618	0.2649832	-4.65	FALSE
251245_at	putative protein phytochrome-as	PIL2	AT3G62090	-2.05	-1.04	-2.10	0.0751564	0.2649832	-4.65	FALSE
253236_at	putative protein ARI protein, Dro	ARI1	AT4G34370	-1.22	-0.29	-2.10	0.0752053	0.2650956	-4.66	FALSE
252595_at	putative transporter protein pept	---	AT3G45690	1.29	0.36	2.10	0.075229	0.2651382	-4.66	FALSE
249998_at	putative protein unnamed ORF,	FASS	AT5G18580	-1.25	-0.32	-2.10	0.0752436	0.2651485	-4.66	FALSE

252290_at	putative protein various predicte	---	AT3G49140	-1.32	-0.40	-2.10	0.0752659	0.2651863	-4.66	FALSE
251976_at	disease resistance - like protein	AtRLP45	AT3G53240	-1.32	-0.40	-2.10	0.0752831	0.2651928	-4.66	FALSE
246053_at	putative protein farnesyl cysteine	---	AT5G08340	-1.36	-0.45	-2.10	0.0753027	0.2651928	-4.66	FALSE
259748_at	putative dehydrogenase similar t	---	AT1G71180	-1.30	-0.38	-2.10	0.0753008	0.2651928	-4.66	FALSE
260688_at	hypothetical protein similar to del	---	AT1G17665	-1.29	-0.37	-2.10	0.0753396	0.265282	-4.66	TRUE
246024_at	putative protein predicted protein	---	AT5G21130	1.32	0.41	2.10	0.0753667	0.2653364	-4.66	FALSE
266941_at	peroxidase (ATP22a) identical to	---	AT2G18980	1.34	0.43	2.10	0.0754663	0.265646	-4.66	FALSE
252009_at	zinc finger - like protein zinc fing	---	AT3G52800	1.42	0.51	2.10	0.0754803	0.2656545	-4.66	FALSE
259458_at	glycine-rich protein, putative sim	---	AT1G44085	1.30	0.38	2.10	0.0755061	0.2656824	-4.66	FALSE
266162_at	putative bHLH transcription facto	FRU	AT2G28160	1.28	0.35	2.10	0.0755116	0.2656824	-4.66	FALSE
254681_at	putative protein HYA22 protein,	---	AT4G18140	1.46	0.55	2.10	0.0755248	0.265688	-4.66	FALSE
262884_at	membrane related protein CP5,	CP5	AT1G64720	-1.27	-0.34	-2.10	0.075593	0.265887	-4.66	FALSE
266991_at	putative CDP-diacylglycerol--glyc	PGP1	AT2G39290	-1.21	-0.27	-2.10	0.0756219	0.2659066	-4.66	FALSE
259199_at	putative signal peptidase similar	---	AT3G08980	-1.23	-0.30	-2.10	0.0756217	0.2659066	-4.66	FALSE
255785_at	sulfate adenylyltransferase identi	APS2	AT1G19920	-1.28	-0.36	-2.10	0.0756601	0.2659645	-4.66	FALSE
257139_at	disease resistance protein, puta	AtRLP43	AT3G28890	1.42	0.51	2.10	0.0756617	0.2659645	-4.66	FALSE
260004_at	unknown protein ;supported by f	---	AT1G67860	1.52	0.60	2.10	0.0757424	0.2660842	-4.66	FALSE
247822_at	putative protein sorting nexin 2,	SNX2a	AT5G58440	-1.32	-0.40	-2.10	0.0757321	0.2660842	-4.66	FALSE
250683_x_a	putative protein similar to unknov	---	AT5G06640	1.43	0.51	2.10	0.0757348	0.2660842	-4.66	FALSE
248104_at	S-adenosyl-L-methionine:salicyli	IAMT1	AT5G55250	-1.77	-0.83	-2.10	0.0757393	0.2660842	-4.66	FALSE
261751_at	chloroplast drought-induced stre	CDSP32	AT1G76080	1.20	0.26	2.10	0.0757747	0.2661566	-4.66	FALSE
251590_at	pollen-specific protein BAN102-l	AGP23	AT3G57690	1.40	0.48	2.10	0.0758461	0.2663664	-4.66	FALSE
255013_at	putative protein ;supported by fu	---	AT4G10000	-1.31	-0.39	-2.10	0.0758847	0.2664608	-4.66	FALSE
266129_at	hypothetical protein predicted by	CCD7	AT2G44990	2.13	1.09	2.10	0.0759208	0.2664646	-4.66	FALSE
267153_at	glutathione S-transferase identica	ATGSTF9	AT2G30860	1.40	0.48	2.10	0.0759156	0.2664646	-4.66	FALSE
264873_at	putative indole-3-acetate beta-glu	UGT74B1	AT1G24100	1.94	0.95	2.10	0.0759058	0.2664646	-4.66	FALSE
256799_at	unknown protein ; supported by	---	AT3G18560	1.79	0.84	2.10	0.0759531	0.2664959	-4.67	FALSE
256177_at	protein kinase, putative contains	---	AT1G51620	2.03	1.02	2.10	0.0759465	0.2664959	-4.66	FALSE
251845_at	Expressed protein ; supported by	ATGCN4	AT3G54540	-1.38	-0.46	-2.10	0.075968	0.2665074	-4.67	FALSE
247652_at	histone H2B - like protein histon	HTB4	AT5G59910	-1.34	-0.42	-2.09	0.0760177	0.2666304	-4.67	FALSE
256602_at	unknown protein	---	AT3G28310	1.37	0.46	2.09	0.0760265	0.2666304	-4.67	FALSE
248728_at	cytochrome P450-like protein	CYP708A2	AT5G48000	1.28	0.35	2.09	0.0760469	0.2666608	-4.67	FALSE
260706_at	oxidase, putative similar to oxida	AOX1D	AT1G32350	6.03	2.59	2.09	0.0761381	0.2668964	-4.67	TRUE
265356_at	putative TRAP protein	---	AT2G16595	-1.36	-0.44	-2.09	0.0761491	0.2668964	-4.67	FALSE
247623_at	receptor-like protein kinase rece	---	AT5G60320	1.25	0.32	2.09	0.0761486	0.2668964	-4.67	FALSE

266099_at	putative alpha-carboxyltransferas	CAC3	AT2G38040	-1.40	-0.49	-2.09	0.0761901	0.2669512	-4.67	FALSE
267476_at	putative pectate lyase	---	AT2G02720	1.25	0.32	2.09	0.0761999	0.2669512	-4.67	FALSE
250702_at	peroxidase ;supported by full-ler	---	AT5G06730	3.60	1.85	2.09	0.0761966	0.2669512	-4.67	FALSE
251646_at	putative protein	---	AT3G57780	2.32	1.22	2.09	0.0762733	0.2671263	-4.67	TRUE
258354_at	putative zinc finger protein simila	---	AT3G14320	1.22	0.29	2.09	0.0762618	0.2671263	-4.67	FALSE
249844_at	putative protein similar to unknov	---	AT5G23590	-1.30	-0.38	-2.09	0.0763106	0.267216	-4.67	FALSE
266908_at	putative protein kinase contains a	PID	AT2G34650	1.78	0.83	2.09	0.0763491	0.2673098	-4.67	FALSE
250309_at	putative protein similar to unknov	---	AT5G12220	-1.38	-0.47	-2.09	0.0763956	0.2674315	-4.67	FALSE
256967_at	hypothetical protein predicted by	---	AT3G21060	-1.30	-0.38	-2.09	0.0764266	0.267499	-4.67	FALSE
245861_at	GTL1 - like protein GTL1, Arabic	---	AT5G28300	-1.65	-0.72	-2.09	0.0764427	0.2675144	-4.67	FALSE
259384_at	putative lectin contains Pfam pro	---	AT3G16450	1.34	0.42	2.09	0.0764748	0.2675856	-4.67	FALSE
266562_at	unknown protein	---	AT2G23970	1.41	0.49	2.09	0.0765285	0.2677325	-4.67	FALSE
265668_at	putative alanine acetyl transferas	---	AT2G32020	2.34	1.22	2.09	0.0765583	0.2677956	-4.67	FALSE
255100_at	putative MuDR-like transposon p	---	---	-1.22	-0.29	-2.09	0.0766132	0.2679465	-4.67	FALSE
258199_at	unknown protein	---	AT3G14030	1.26	0.33	2.09	0.0767055	0.268228	-4.67	FALSE
254212_at	putative protein many putative p	---	AT4G23580	1.25	0.33	2.09	0.0767289	0.2682687	-4.67	FALSE
263077_at	putative mitotic control protein dis	EMB2763	AT2G17510	-1.22	-0.28	-2.09	0.0767814	0.2684114	-4.68	FALSE
250715_at	splicing factor 3a ; supported by	ATO	AT5G06160	-1.38	-0.47	-2.09	0.0768095	0.2684684	-4.68	FALSE
257780_at	hypothetical protein predicted by	---	AT3G27100	-1.32	-0.40	-2.09	0.0768685	0.2686129	-4.68	FALSE
261412_at	L-ascorbate peroxidase identica	APX1	AT1G07890	1.56	0.64	2.09	0.0768744	0.2686129	-4.68	FALSE
262065_at	hypothetical protein predicted by	---	AT1G56180	-1.50	-0.59	-2.09	0.0768954	0.2686451	-4.68	FALSE
251331_s_a	tubulin gamma-1 chain	TUBG1	AT3G61650 ///	-1.81	-0.86	-2.09	0.0769259	0.2687106	-4.68	FALSE
246153_s_a	RAN1 small Ras-like GTP-bindin	RAN-1	AT5G20010 ///	-1.49	-0.57	-2.09	0.0769804	0.2688186	-4.68	TRUE
252045_at	putative protein arm repeat cont	PUB22	AT3G52450	4.01	2.00	2.09	0.0769703	0.2688186	-4.68	FALSE
261539_at	hypothetical protein predicted by	---	AT1G01840	1.30	0.38	2.09	0.0770474	0.2689701	-4.68	FALSE
259720_at	hypothetical protein predicted by	---	AT1G61080	1.30	0.38	2.09	0.0770375	0.2689701	-4.68	FALSE
258232_at	unknown protein	---	AT3G27750	-1.42	-0.51	-2.09	0.0770681	0.2690013	-4.68	FALSE
263686_at	putative 60s ribosomal protein L	---	AT1G26910	-1.46	-0.54	-2.09	0.0771029	0.2690816	-4.68	FALSE
248620_at	putative protein similar to unknov	---	AT5G49320	1.26	0.33	2.09	0.0771228	0.2691097	-4.68	FALSE
253958_at	putative protein RING zinc finge	---	AT4G26400	1.29	0.36	2.08	0.0771496	0.2691231	-4.68	FALSE
245376_at	peroxidase like protein	---	AT4G17690	1.23	0.30	2.08	0.0771502	0.2691231	-4.68	FALSE
246257_at	splicing factor-like protein	ATU2AF65	AT4G36690	-1.26	-0.33	-2.08	0.0771625	0.2691249	-4.68	FALSE
249508_at	unknown protein	---	AT5G38380	-1.26	-0.33	-2.08	0.0772248	0.269301	-4.68	FALSE
265057_at	unknown protein ;supported by fu	---	AT1G52140	1.28	0.36	2.08	0.077348	0.2695277	-4.68	TRUE
250505_at	cellulose synthase catalytic subu	CESA5	AT5G09870	1.41	0.49	2.08	0.0773489	0.2695277	-4.68	TRUE

261765_at	cyclin, putative similar to cyclin C	CYCA2;3	AT1G15570	1.29	0.37	2.08	0.0773097	0.2695277	-4.68	FALSE
246674_at	bcnt-like protein ; supported by fu	---	AT5G30490	-1.26	-0.34	-2.08	0.077336	0.2695277	-4.68	FALSE
247001_at	natural resistance-associated ma	NRAMP4	AT5G67330	1.30	0.38	2.08	0.0773217	0.2695277	-4.68	FALSE
250831_at	unknown protein	---	AT5G04920	1.25	0.32	2.08	0.077374	0.2695739	-4.68	FALSE
267624_at	putative protein kinase	BIK1	AT2G39660	1.69	0.76	2.08	0.0774164	0.2696396	-4.68	FALSE
260833_at	lipase, putative similar to lipase	---	AT1G06800	1.75	0.81	2.08	0.0774165	0.2696396	-4.68	FALSE
262760_at	hypothetical protein contains sim	---	AT1G10770	-2.18	-1.12	-2.08	0.0774817	0.2697865	-4.68	FALSE
259976_at	hypothetical protein ;supported b	CP12-3	AT1G76560	1.52	0.60	2.08	0.0774845	0.2697865	-4.68	FALSE
255616_at	hypothetical protein	---	AT4G01290	1.44	0.52	2.08	0.0774941	0.2697865	-4.68	FALSE
245116_at	unknown protein ; supported by	---	AT2G41620	-1.63	-0.70	-2.08	0.0775366	0.2698932	-4.69	FALSE
260971_at	hypothetical protein predicted by	---	AT1G53620	1.25	0.32	2.08	0.077564	0.2699473	-4.69	FALSE
245312_at	Expressed protein ; supported by	---	AT4G14600	-1.35	-0.43	-2.08	0.0776178	0.2700932	-4.69	FALSE
264243_at	hypothetical protein predicted by	---	AT1G54650	-1.40	-0.48	-2.08	0.0776406	0.2701315	-4.69	FALSE
251448_at	allyl alcohol dehydrogenase-like	---	AT3G59845	1.24	0.31	2.08	0.0776795	0.2701433	-4.69	FALSE
260206_at	putative protein kinase contains l	---	AT1G70740	1.73	0.79	2.08	0.0776595	0.2701433	-4.69	FALSE
264911_at	auxin-induced protein, putative s	---	AT1G60690	-1.37	-0.45	-2.08	0.0776791	0.2701433	-4.69	FALSE
252112_at	putative protein merozoite surfac	---	AT3G51580	1.32	0.40	2.08	0.0776927	0.2701478	-4.69	FALSE
247935_at	30S ribosomal protein S16 ; sup	---	AT5G56940	-1.37	-0.46	-2.08	0.0777313	0.2702409	-4.69	FALSE
260446_at	unknown protein	---	AT1G72420	-1.29	-0.37	-2.08	0.0777691	0.2703312	-4.69	FALSE
249856_at	serine carboxypeptidase	scpl47	AT5G22980	1.43	0.52	2.08	0.0777921	0.2703699	-4.69	FALSE
255288_at	coded for by A. thaliana cDNA T4	---	AT4G04670	-1.44	-0.53	-2.08	0.0778119	0.2703975	-4.69	FALSE
261240_at	subtilisin-like serine protease cor	SBT3.5	AT1G32940	1.86	0.90	2.08	0.077897	0.2705698	-4.69	TRUE
245736_at	Dr4(protease inhibitor) identical t	ATDR4	AT1G73330	-1.72	-0.79	-2.08	0.0778939	0.2705698	-4.69	FALSE
255255_at	coded for by A. thaliana cDNA T4	---	AT4G05070	-1.49	-0.57	-2.08	0.0778852	0.2705698	-4.69	FALSE
254976_at	subtilisin-like serine protease cor	---	AT4G10510	1.25	0.32	2.08	0.0779333	0.2706545	-4.69	FALSE
245044_at	unknown protein Alternative splic	---	AT2G26500	-1.20	-0.27	-2.08	0.0779485	0.270666	-4.69	FALSE
247640_at	putative protein various predicte	---	AT5G60610	-1.26	-0.34	-2.08	0.077988	0.2707621	-4.69	FALSE
250694_at	putative protein contains similarit	HAT14	AT5G06710	-1.35	-0.43	-2.08	0.078013	0.2707834	-4.69	FALSE
265737_at	putative phosphatidic acid phosp	ATPAP1	AT2G01180	2.56	1.36	2.08	0.0780179	0.2707834	-4.69	FALSE
248869_at	putative protein contains similarit	---	AT5G46840	-1.51	-0.59	-2.08	0.0780941	0.2708777	-4.69	FALSE
262491_at	putative SecA-type chloroplast p	---	AT1G21650	-1.30	-0.37	-2.08	0.0781045	0.2708777	-4.69	FALSE
255466_at	putative protein similar to A. thal	---	AT4G03000	-1.28	-0.36	-2.08	0.0780986	0.2708777	-4.69	FALSE
259604_at	20S proteasome beta subunit (P	PBG1	AT1G56450	-1.25	-0.32	-2.08	0.0780707	0.2708777	-4.69	FALSE
262126_at	disease resistance protein, puta	CW9	AT1G59620	1.39	0.47	2.08	0.0780688	0.2708777	-4.69	FALSE
254482_at	TWIN SISTER OF FT (TSF) terr	TSF	AT4G20370	1.32	0.40	2.08	0.0781359	0.2709429	-4.69	FALSE

255974_at	hypothetical protein	---	---	1.31	0.39	2.08	0.078147	0.2709429	-4.69	FALSE
245091_at	unknown protein	---	AT2G40910	1.28	0.36	2.08	0.0782004	0.2710767	-4.69	FALSE
264980_at	receptor kinase, putative similar	---	AT1G27190	-1.32	-0.40	-2.08	0.0782094	0.2710767	-4.69	FALSE
251884_at	embryonic abundant protein -like	---	AT3G54150	3.12	1.64	2.08	0.0782379	0.2711344	-4.69	FALSE
263384_at	hypothetical protein predicted by	---	AT2G40130	1.30	0.38	2.07	0.0782686	0.2711996	-4.69	FALSE
267405_at	putative related to microbial diva	CUTA	AT2G33740	-1.23	-0.30	-2.07	0.0783064	0.2712895	-4.69	FALSE
251471_at	putative protein GTPASE-ACTIV	---	AT3G59570	1.29	0.36	2.07	0.0783273	0.2713207	-4.69	FALSE
257691_at	hypothetical protein predicted by	FLA14	AT3G12660	1.40	0.49	2.07	0.0783544	0.2713732	-4.70	FALSE
266866_at	putative ABC transporter	PDR3	AT2G29940	1.48	0.57	2.07	0.0783917	0.2714612	-4.70	FALSE
247351_at	putative protein contains similarit	ANAC102	AT5G63790	1.85	0.89	2.07	0.0784159	0.2715038	-4.70	TRUE
262202_at	TATC-like protein similar to GB:A	APG2	AT2G01110	-1.43	-0.51	-2.07	0.0784352	0.2715293	-4.70	FALSE
267333_at	putative WD-40 repeat protein co	---	AT2G19430	-1.23	-0.30	-2.07	0.0784604	0.2715755	-4.70	FALSE
266978_at	putative disease resistance respo	---	AT2G39430	1.26	0.34	2.07	0.0784997	0.2716703	-4.70	FALSE
253191_at	cysteine protease XCP1 identica	XCP1	AT4G35350	-2.25	-1.17	-2.07	0.0786218	0.2720514	-4.70	FALSE
261018_at	unknown protein contains similar	---	AT1G26550	-1.19	-0.26	-2.07	0.0786426	0.2720823	-4.70	FALSE
265682_at	similar to avrRpt2-induced protei	---	AT2G24390	-1.38	-0.46	-2.07	0.0786903	0.2721938	-4.70	FALSE
259552_at	hypothetical protein	---	AT1G21320	1.30	0.38	2.07	0.0787107	0.2721938	-4.70	FALSE
251442_at	putative protein multisynthetase	---	AT3G59980	-1.46	-0.54	-2.07	0.0787091	0.2721938	-4.70	FALSE
248082_at	fimbrin	---	AT5G55400	1.52	0.61	2.07	0.0787771	0.2722586	-4.70	TRUE
262518_at	putative glutathione transferase (	ATGSTU24	AT1G17170	6.34	2.66	2.07	0.078754	0.2722586	-4.70	TRUE
245888_at	putative protein DNA-binding pro	---	AT5G09450	-1.27	-0.35	-2.07	0.0787656	0.2722586	-4.70	FALSE
247232_at	ABC transporter-like	ATH13	AT5G64940	-1.36	-0.44	-2.07	0.0787665	0.2722586	-4.70	FALSE
256069_at	hypothetical protein predicted by	AFP2	AT1G13740	1.55	0.63	2.07	0.0787967	0.2722849	-4.70	FALSE
252663_at	putative protein several hypothet	---	AT3G44070	1.21	0.27	2.07	0.0789135	0.2725232	-4.70	FALSE
264955_at	F-box protein family, AtFBX3 co	---	AT1G76920	-1.35	-0.43	-2.07	0.0789064	0.2725232	-4.70	FALSE
256714_at	cysteine proteinase contains sim	---	AT2G34080	1.30	0.38	2.07	0.0789045	0.2725232	-4.70	FALSE
260821_at	unknown protein contains Pfam p	CRTISO	AT1G06820	-1.32	-0.40	-2.07	0.0789108	0.2725232	-4.70	FALSE
250215_at	putative protein similar to unknov	---	AT5G14080	-1.26	-0.33	-2.07	0.0789728	0.2726618	-4.70	FALSE
249514_at	14-3-3 protein GF14psi (grf3/RC	GRF3	AT5G38480	-1.29	-0.37	-2.07	0.0789775	0.2726618	-4.70	FALSE
262778_at	hypothetical protein predicted by	---	AT1G13050	-1.21	-0.28	-2.07	0.0790079	0.2726843	-4.70	FALSE
265488_at	hypothetical protein predicted by	---	AT2G15610	1.27	0.35	2.07	0.0790057	0.2726843	-4.70	FALSE
254226_at	putative disease resistance resp	---	AT4G23690	3.86	1.95	2.07	0.079028	0.2727124	-4.70	FALSE
263155_at	transcriptional activation factor T	TAFII21	AT1G54140	-1.30	-0.38	-2.07	0.0790685	0.272811	-4.70	FALSE
252611_at	oxidosqualene cyclase - like pro	LAS1	AT3G45130	1.79	0.84	2.07	0.0791608	0.2730813	-4.71	FALSE
265210_at	60S ribosomal protein L24 ;supp	RPL24A	AT2G36620	-2.09	-1.07	-2.07	0.0791828	0.2730813	-4.71	FALSE

245641_at	Expressed protein ; supported by	---	AT1G25370	2.57	1.36	2.07	0.0791753	0.2730813	-4.71	FALSE
264924_at	RNA polymerase subunit identica	ATRPAC43	AT1G60620	-1.23	-0.30	-2.07	0.0792287	0.2731386	-4.71	FALSE
250748_at	AtPH1-like protein ;supported by	---	AT5G05710	-1.31	-0.39	-2.07	0.0792372	0.2731386	-4.71	FALSE
259327_at	putative lectin contains Pfam pro	---	AT3G16460	2.75	1.46	2.07	0.0792621	0.2731386	-4.71	FALSE
266457_at	putative glyoxysomal malate deh	PMDH1	AT2G22780	1.25	0.33	2.07	0.0792564	0.2731386	-4.71	FALSE
254168_at	Mlo-like protein Mlo protein - Ho	MLO13	AT4G24250	-1.30	-0.38	-2.07	0.0792713	0.2731386	-4.71	FALSE
262635_at	4-hydroxyphenylpyruvate dioxyg	PDS1	AT1G06570	1.60	0.68	2.07	0.0792392	0.2731386	-4.71	FALSE
257638_at	terpene synthase-related protein	ATTPS-CIN	AT3G25820 /	1.24	0.31	2.07	0.079299	0.2731929	-4.71	FALSE
247183_at	putative protein strong similarity t	---	AT5G65440	-1.23	-0.30	-2.07	0.0793136	0.2732019	-4.71	TRUE
246759_at	putative protein kinesin heavy ch	---	AT5G27950	-1.38	-0.46	-2.07	0.0793361	0.2732382	-4.71	FALSE
255387_at	putative nodulin similar to M. tru	---	AT4G03630	1.35	0.43	2.06	0.0794046	0.2734328	-4.71	FALSE
249782_at	dipeptidyl peptidase IV-like prote	---	AT5G24260	1.27	0.34	2.06	0.0794289	0.2734339	-4.71	FALSE
257468_at	hypothetical protein contains sim	---	AT1G47470	1.21	0.28	2.06	0.0794173	0.2734339	-4.71	FALSE
260518_at	cinnamyl alcohol dehydrogenase	---	AT1G51410	1.22	0.29	2.06	0.0794717	0.2735236	-4.71	FALSE
264917_at	unknown protein contains Pfam p	---	AT1G60500	1.21	0.27	2.06	0.0794789	0.2735236	-4.71	FALSE
248085_at	putative protein similar to unknov	SVL1	AT5G55480	1.62	0.70	2.06	0.0795056	0.2735741	-4.71	TRUE
260925_at	DNA-binding protein, putative co	---	AT1G21340	1.29	0.37	2.06	0.0795519	0.2736923	-4.71	FALSE
263073_at	unknown protein ;supported by f	---	AT2G17500	6.13	2.62	2.06	0.0795821	0.2737549	-4.71	FALSE
266045_s_a	hypothetical protein	---	AT2G07727	1.38	0.46	2.06	0.0796095	0.2737664	-4.71	FALSE
260536_at	putative electron transfer flavopro	ETFQO	AT2G43400	1.51	0.60	2.06	0.079598	0.2737664	-4.71	FALSE
262471_at	hypothetical protein similar to hyp	---	AT1G50140	1.32	0.40	2.06	0.0796576	0.2738491	-4.71	FALSE
258677_at	putative ribosomal-protein S6 kin	PK1	AT3G08730	1.30	0.38	2.06	0.0796487	0.2738491	-4.71	FALSE
246008_at	putative protein predicted protein	---	AT5G08320	-1.32	-0.40	-2.06	0.0796962	0.2739405	-4.71	FALSE
262127_at	hypothetical protein predicted by	---	AT1G52550	-1.37	-0.46	-2.06	0.0797112	0.273951	-4.71	FALSE
258609_at	unknown protein ;supported by f	---	AT3G02910	-1.30	-0.38	-2.06	0.0797526	0.2740296	-4.71	FALSE
247056_at	SWI2/SNF2-like protein (gb|AAD	CHR1	AT5G66750	-1.26	-0.33	-2.06	0.079781	0.2740296	-4.71	FALSE
249129_at	cyclin A-type	CYCA3;1	AT5G43080	-1.28	-0.36	-2.06	0.0797647	0.2740296	-4.71	FALSE
251813_at	Expressed protein ; supported by	TON1A	AT3G55000	-1.34	-0.42	-2.06	0.0797821	0.2740296	-4.71	FALSE
255651_at	putative protein	---	AT4G00940	-1.27	-0.35	-2.06	0.0798166	0.2740655	-4.71	TRUE
258054_at	delta tonoplast integral protein (	DELTA-TIP	AT3G16240	4.42	2.14	2.06	0.0798128	0.2740655	-4.71	FALSE
260453_s_a	unknown protein	---	AT1G72510 /	-1.36	-0.45	-2.06	0.0798668	0.2741141	-4.71	FALSE
248205_at	cotton fiber expressed protein 1-	---	AT5G54300	2.08	1.06	2.06	0.0798499	0.2741141	-4.71	FALSE
247777_at	putative protein MNUDC protein	---	AT5G58740	-1.22	-0.29	-2.06	0.079859	0.2741141	-4.71	FALSE
258617_at	putative calmodulin similar to cal	---	AT3G03000	1.22	0.28	2.06	0.0798829	0.2741281	-4.71	FALSE
251751_at	putative protein predicted protein	---	AT3G55720	1.20	0.26	2.06	0.079933	0.2741818	-4.71	FALSE

266633_at	putative DnaJ protein	---	AT2G35540	-1.30	-0.38	-2.06	0.0799215	0.2741818	-4.71	FALSE
249751_at	putative protein similar to unknov	---	AT5G24650	-1.34	-0.43	-2.06	0.0799346	0.2741818	-4.71	FALSE
245744_at	unknown protein	---	AT1G51110	-1.85	-0.88	-2.06	0.079987	0.2743203	-4.72	TRUE
247992_at	unknown protein	---	AT5G56520	-1.25	-0.33	-2.06	0.0800091	0.2743548	-4.72	FALSE
263867_at	putative aquaporin (tonoplast intr	GAMMA-TI	AT2G36830	1.60	0.68	2.06	0.0800758	0.2743774	-4.72	TRUE
258180_at	unknown protein	---	AT3G21480	-1.48	-0.57	-2.06	0.0800659	0.2743774	-4.72	FALSE
245551_at	cytochrome P450 like protein	CYP705A2	AT4G15350	1.22	0.28	2.06	0.0800657	0.2743774	-4.72	FALSE
253080_at	hypothatical protein	---	---	-1.24	-0.31	-2.06	0.0800327	0.2743774	-4.72	FALSE
256843_at	hypothetical protein predicted by	---	---	1.25	0.33	2.06	0.0800495	0.2743774	-4.72	FALSE
253459_at	hypothetical protein	---	AT4G32080	1.21	0.27	2.06	0.0801119	0.2744596	-4.72	FALSE
261132_at	hypothetical protein predicted by	TGD1	AT1G19800	-1.25	-0.32	-2.06	0.0801434	0.2745264	-4.72	FALSE
262719_at	hypothetical protein predicted by	---	---	1.27	0.34	2.06	0.0801891	0.2746417	-4.72	FALSE
245842_at	proline-rich protein, putative sim	RXF26	AT1G58430	1.22	0.29	2.06	0.0802023	0.2746455	-4.72	FALSE
253393_at	Expressed protein ; supported by	GLB3	AT4G32690	-1.28	-0.36	-2.06	0.0802523	0.2747756	-4.72	TRUE
250477_at	putative protein CIS,CIS-MUCO	---	AT5G10190	-1.22	-0.29	-2.06	0.0802655	0.2747797	-4.72	FALSE
261357_at	hypothetical protein predicted by	---	---	1.22	0.28	2.06	0.0803066	0.2748379	-4.72	FALSE
254214_at	putative potassium transport pro	TRH1	AT4G23640	1.30	0.38	2.06	0.0802977	0.2748379	-4.72	FALSE
249201_at	putative protein similar to unknov	---	AT5G42370	-1.36	-0.44	-2.06	0.0803398	0.2749102	-4.72	TRUE
259493_at	unknown protein	---	AT1G15840	1.26	0.34	2.06	0.0803569	0.2749275	-4.72	FALSE
247292_at	unknown protein	---	AT5G64490	-1.29	-0.37	-2.06	0.0803728	0.2749406	-4.72	FALSE
260112_at	unknown protein similar to unkno	---	AT1G63310	-1.35	-0.43	-2.06	0.0804066	0.2750149	-4.72	FALSE
263438_at	unknown protein	---	AT2G28660	-1.35	-0.43	-2.06	0.0804355	0.2750725	-4.72	FALSE
258606_at	unknown protein ;supported by f	---	AT3G02840	4.93	2.30	2.06	0.0804622	0.2751227	-4.72	FALSE
266288_s_a	putative pumilio/Mpt5 family RNA	APUM1	AT2G29140 /.	-1.31	-0.39	-2.06	0.0805044	0.2751611	-4.72	TRUE
248165_at	putative protein similar to unknov	PHOS32	AT5G54430	-1.32	-0.40	-2.06	0.0805096	0.2751611	-4.72	FALSE
256384_at	hypothetical protein	---	AT1G66660	-1.30	-0.38	-2.06	0.0804942	0.2751611	-4.72	FALSE
256366_at	protein kinase, putative contains	---	AT1G66880	1.66	0.73	2.05	0.0806485	0.2754707	-4.72	TRUE
256505_at	unknown protein	---	AT1G75200	-1.38	-0.47	-2.05	0.0806423	0.2754707	-4.72	FALSE
256910_at	hypothetical protein	---	AT3G24080	1.33	0.41	2.05	0.080638	0.2754707	-4.72	FALSE
245850_at	ankyrin-repeat containing protein	KEG	AT5G13530	1.39	0.47	2.05	0.0806361	0.2754707	-4.72	FALSE
265576_at	unknown protein	CLASP	AT2G20190	-1.22	-0.29	-2.05	0.0806853	0.2755551	-4.72	FALSE
258812_at	unknown protein similar to GB:A/	ECT1	AT3G03950	-1.30	-0.38	-2.05	0.0807866	0.2756445	-4.72	TRUE
248364_at	fibrillarin 3 (AtFib3) similar to fibri	---	AT5G52490	1.22	0.29	2.05	0.0807743	0.2756445	-4.72	FALSE
253139_at	ankyrin repeat-containing protein	AKR2	AT4G35450	-1.22	-0.29	-2.05	0.0807897	0.2756445	-4.72	FALSE
248401_at	putative protein similar to unknov	HCF208	AT5G52110	-1.57	-0.65	-2.05	0.080741	0.2756445	-4.72	FALSE

255379_at	putative M-type thioredoxin simil	ATHM2	AT4G03520	-1.21	-0.27	-2.05	0.0807713	0.2756445	-4.72	FALSE
247111_at	unknown protein	---	AT5G65880	-1.45	-0.54	-2.05	0.0807402	0.2756445	-4.72	FALSE
253067_at	myb transcription factor - like pro	MYB87	AT4G37780	1.25	0.32	2.05	0.0807961	0.2756445	-4.72	FALSE
257798_at	unknown protein	NAI2	AT3G15950	1.38	0.46	2.05	0.0808876	0.2759155	-4.73	FALSE
266101_at	unknown protein ; supported by	---	AT2G37940	1.93	0.95	2.05	0.0809178	0.2759771	-4.73	FALSE
255859_at	putative protein embryonic abun	---	AT5G34930	1.44	0.53	2.05	0.0809604	0.2760121	-4.73	FALSE
254399_at	G10 - like protein Maternal G10	---	AT4G21110	-1.21	-0.28	-2.05	0.08096	0.2760121	-4.73	FALSE
259039_at	unknown protein ;supported by f	---	AT3G09250	-1.25	-0.32	-2.05	0.0809644	0.2760121	-4.73	FALSE
254985_x_a	putative reverse-transcriptase -li	---	---	1.34	0.43	2.05	0.0810116	0.2761318	-4.73	FALSE
267073_at	unknown protein	---	AT2G41160	1.35	0.43	2.05	0.0810292	0.2761508	-4.73	FALSE
264858_at	hypothetical protein	SNL3	AT1G24190	1.28	0.36	2.05	0.0810669	0.2761553	-4.73	FALSE
267451_at	putative AP2 domain transcriptio	---	AT2G33710	3.42	1.77	2.05	0.0810641	0.2761553	-4.73	FALSE
265091_s_a	hypothetical protein similar to An	---	AT1G03495 /.	1.35	0.44	2.05	0.0810569	0.2761553	-4.73	FALSE
251622_at	dnaJ-like protein DNAJ protein -	---	AT3G57340	-1.22	-0.29	-2.05	0.0811333	0.2763401	-4.73	FALSE
251749_at	putative protein predicted protei	---	AT3G55690	1.24	0.30	2.05	0.0811721	0.276431	-4.73	FALSE
253136_at	putative protein leucine-rich prot	---	AT4G35470	-1.28	-0.36	-2.05	0.0811961	0.2764699	-4.73	TRUE
258982_at	putative serine/threonine protein	---	AT3G08870	1.45	0.54	2.05	0.0812077	0.2764699	-4.73	TRUE
256154_at	hypothetical protein predicted by	---	AT3G08490	1.31	0.39	2.05	0.0812543	0.2765871	-4.73	FALSE
260823_at	hypothetical protein predicted by	DRIP1	AT1G06770	-1.25	-0.32	-2.05	0.0812989	0.2766551	-4.73	FALSE
258240_at	oleosin isoform identical to oleos	OLEO4	AT3G27660	1.28	0.36	2.05	0.0813214	0.2766551	-4.73	FALSE
248758_at	RNA-binding protein-like ;suppo	---	AT5G47620	-1.31	-0.39	-2.05	0.0813228	0.2766551	-4.73	FALSE
248145_at	unknown protein ;supported by f	---	AT5G54880	-1.29	-0.36	-2.05	0.0813179	0.2766551	-4.73	FALSE
266262_at	hypothetical protein predicted by	---	AT2G27590	-1.51	-0.59	-2.05	0.0813514	0.2767111	-4.73	FALSE
259520_at	hypothetical protein	---	AT1G12320	1.49	0.57	2.05	0.0814531	0.2770158	-4.73	TRUE
267315_at	putative CCAAT-binding transcri	NF-YA4	AT2G34720	-1.43	-0.52	-2.05	0.0814743	0.2770467	-4.73	FALSE
258395_at	putative jasmonic acid regulatory	ANAC055	AT3G15500	1.53	0.61	2.05	0.0815001	0.277093	-4.73	TRUE
265939_at	putative Ta11-like non-LTR retro	---	AT2G19650	-1.42	-0.51	-2.05	0.0815496	0.2771374	-4.73	FALSE
249770_at	unknown protein ;supported by fu	WRKY30	AT5G24110	3.74	1.90	2.05	0.0815316	0.2771374	-4.73	FALSE
255679_at	putative acetyl CoA thioesterase	---	AT4G00520	-1.37	-0.46	-2.05	0.0815469	0.2771374	-4.73	FALSE
246417_at	quinone oxidoreductase - like pr	---	AT5G16990	-1.40	-0.49	-2.05	0.0816317	0.2773751	-4.73	FALSE
266631_at	putative serpin	---	AT2G35570	1.20	0.26	2.05	0.0816515	0.2774009	-4.74	FALSE
260370_at	putative aminolevulinate dehydra	HEMB1	AT1G69740	-1.25	-0.32	-2.05	0.0816938	0.2774208	-4.74	FALSE
246190_at	hypothetical protein (fragment) ;s	ATBPM5	AT5G21010	-1.20	-0.27	-2.05	0.0816792	0.2774208	-4.74	FALSE
257839_at	hypothetical protein	---	AT3G25080	-1.22	-0.29	-2.05	0.0816826	0.2774208	-4.74	FALSE
258722_at	putative pathogenesis-related pr	---	AT3G09590	1.25	0.32	2.05	0.0817215	0.2774737	-4.74	FALSE

248559_at	unknown protein	---	AT5G50010 /.	1.27	0.34	2.04	0.0817405	0.2774969	-4.74	FALSE
265632_at	hypothetical protein predicted by	---	AT2G14290	3.67	1.88	2.04	0.0817635	0.2775334	-4.74	FALSE
264897_at	dynein light subunit lc6, flagellar	---	AT1G23220	-1.30	-0.38	-2.04	0.0818046	0.2776318	-4.74	FALSE
263150_at	heat-shock protein, putative sim	---	AT1G54050	1.59	0.67	2.04	0.0819073	0.277939	-4.74	FALSE
250144_at	putative protein various predicte	---	AT5G14680	-1.50	-0.58	-2.04	0.0819227	0.2779498	-4.74	FALSE
246985_at	putative protein contains similarit	---	AT5G67290	-1.28	-0.36	-2.04	0.0819643	0.2780447	-4.74	FALSE
245966_at	AP2 domain containing protein R	RAP2.11	AT5G19790	1.28	0.35	2.04	0.081975	0.2780447	-4.74	FALSE
256068_at	hypothetical protein contains sim	ATE1	AT1G13690	-1.24	-0.31	-2.04	0.0820241	0.278087	-4.74	FALSE
260334_at	homeotic protein (ATK1) identica	KNAT2	AT1G70510	1.22	0.29	2.04	0.082001	0.278087	-4.74	FALSE
257977_at	hypothetical protein predicted by	---	AT3G20850	1.25	0.32	2.04	0.0820231	0.278087	-4.74	FALSE
249421_at	DegP protease contains similarity	DEG8	AT5G39830	-1.29	-0.37	-2.04	0.0820516	0.2781391	-4.74	FALSE
254739_at	putative disease resistance prot	AtRLP48	AT4G13880	1.24	0.31	2.04	0.0820725	0.2781685	-4.74	FALSE
258929_at	unknown protein Pfam HMM hit:	---	AT3G10060	-1.85	-0.89	-2.04	0.0820996	0.2781965	-4.74	FALSE
248453_at	unknown protein	---	AT5G51340	-1.25	-0.32	-2.04	0.0821783	0.2781965	-4.74	FALSE
258358_at	unknown protein similar to unkno	---	AT3G14380	1.27	0.35	2.04	0.0821571	0.2781965	-4.74	FALSE
258570_at	phosphoenolpyruvate carboxyla	PPCK2	AT3G04530	1.33	0.41	2.04	0.082151	0.2781965	-4.74	FALSE
257854_at	putative CREB-binding protein si	HAC5	AT3G12980	1.26	0.33	2.04	0.0821537	0.2781965	-4.74	FALSE
255356_x_a	putative transposon protein	---	---	1.27	0.35	2.04	0.0821719	0.2781965	-4.74	FALSE
257351_at	putative mitochondrial carrier pro	MBAC1	AT2G33820	-1.34	-0.42	-2.04	0.0821651	0.2781965	-4.74	FALSE
245950_at	putative protein predicted protei	---	AT5G19570	-1.43	-0.52	-2.04	0.082176	0.2781965	-4.74	FALSE
263823_s_a	AP2 domain transcription factor	---	AT2G40340 /.	-1.65	-0.73	-2.04	0.0823011	0.2782362	-4.74	TRUE
261700_at	hypothetical protein similar to hy	---	AT1G32690	1.34	0.42	2.04	0.0822267	0.2782362	-4.74	FALSE
248189_at	DNA mismatch repair protein Mu	---	AT5G54090	-1.32	-0.40	-2.04	0.0822453	0.2782362	-4.74	FALSE
256611_at	unknown protein similar to putati	---	AT3G29270	-1.31	-0.39	-2.04	0.0823442	0.2782362	-4.74	FALSE
254728_at	hypothetical protein	---	AT4G13690	1.24	0.31	2.04	0.0823008	0.2782362	-4.74	FALSE
261971_at	type 2 peroxiredoxin, putative si	---	AT1G65990	1.32	0.40	2.04	0.0823399	0.2782362	-4.74	FALSE
248126_at	protein translation factor Sui1 ho	ROC5	AT4G34870 /.	-1.20	-0.26	-2.04	0.082373	0.2782362	-4.74	FALSE
264886_at	S-linalool synthase, putative sim	TPS04	AT1G61120	5.61	2.49	2.04	0.0823494	0.2782362	-4.74	FALSE
255846_at	putative SWI/SNF complex subu	ATSWI3B	AT2G33610	-1.35	-0.43	-2.04	0.0823375	0.2782362	-4.74	FALSE
245300_at	hypothetical protein ; supported b	CBL6	AT4G16350	1.22	0.28	2.04	0.0823445	0.2782362	-4.74	FALSE
263883_at	hypothetical protein predicted by	---	AT2G21830	-1.28	-0.35	-2.04	0.0822749	0.2782362	-4.74	FALSE
254783_at	hydrolase-like protein 2-hydroxy	---	AT4G12830	-1.70	-0.76	-2.04	0.0823646	0.2782362	-4.74	FALSE
251455_at	citrate synthase-like protein citra	CSY5	AT3G60100	1.21	0.28	2.04	0.082283	0.2782362	-4.74	FALSE
267353_at	En/Spm-like transposon protein r	---	AT2G40070	-1.34	-0.42	-2.04	0.0823122	0.2782362	-4.74	FALSE
265317_at	unknown protein	BRK1	AT2G22640	-1.25	-0.32	-2.04	0.0822674	0.2782362	-4.74	FALSE

259311_at	putative SAR DNA-binding protei	---	AT3G05060	-1.57	-0.65	-2.04	0.0824162	0.2783407	-4.74	TRUE
264046_at	putative non-LTR retroelement re	---	AT2G22440	1.26	0.33	2.04	0.0824748	0.2784976	-4.74	FALSE
266232_at	putative phloem-specific lectin	AtPP2-B6	AT2G02310	1.21	0.27	2.04	0.0825092	0.2785723	-4.75	FALSE
256785_at	unknown protein ;supported by f	PRA8	AT3G13720	1.39	0.47	2.04	0.0825782	0.2786459	-4.75	FALSE
256992_at	hypothetical protein predicted by	---	AT3G28630	1.27	0.35	2.04	0.0825704	0.2786459	-4.75	FALSE
246415_at	putative protein (fragment) predi	---	AT5G17160	1.43	0.52	2.04	0.0825439	0.2786459	-4.75	FALSE
262975_at	zinc finger protein, putative simil	STH2	AT1G75540	-1.38	-0.47	-2.04	0.0825798	0.2786459	-4.75	FALSE
AFFX-r2-Bs	B. subtilis /GEN=jojG /DB_XREF	---	---	-1.46	-0.55	-2.04	0.0825989	0.2786691	-4.75	FALSE
263451_at	putative triacylglycerol lipase	---	AT2G31690	1.20	0.26	2.04	0.0826161	0.2786858	-4.75	FALSE
247759_at	copper transport protein - like ;su	COPT3	AT5G59040	1.22	0.28	2.04	0.0826981	0.2788939	-4.75	FALSE
246113_at	putative protein predicted protein	---	---	1.23	0.30	2.04	0.0827023	0.2788939	-4.75	FALSE
266744_at	putative nucleoside triphosphatas	---	AT2G02970	1.21	0.27	2.04	0.082753	0.2789001	-4.75	FALSE
261718_at	wall-associated kinase, putative	---	AT1G18390	2.02	1.01	2.04	0.0827356	0.2789001	-4.75	FALSE
265803_at	hypothetical protein predicted by	---	AT2G18115	1.34	0.42	2.04	0.0827211	0.2789001	-4.75	FALSE
255472_at	82.09 and 30.80) similar to alterr	---	AT4G02430	-1.25	-0.32	-2.04	0.0827476	0.2789001	-4.75	FALSE
264556_at	putative transcription factor cont	MYB61	AT1G09540	-1.20	-0.27	-2.04	0.0827654	0.2789007	-4.75	FALSE
263144_at	unknown protein similar to putati	---	AT1G54070	1.31	0.39	2.04	0.0827809	0.2789116	-4.75	FALSE
267577_at	unknown protein ; supported by	---	AT2G30710	-1.20	-0.26	-2.04	0.0828231	0.2789716	-4.75	FALSE
244962_at	NADH dehydrogenase ND4	---	---	-1.19	-0.26	-2.04	0.0828192	0.2789716	-4.75	FALSE
259338_at	s-syntaxin-like protein similar to s	SYP131	AT3G03800	1.22	0.29	2.04	0.0828423	0.278995	-4.75	FALSE
246455_at	putative protein predicted protei	---	AT5G16790	-1.28	-0.36	-2.04	0.0829218	0.2792214	-4.75	FALSE
265779_at	unknown protein	---	AT2G07360	1.44	0.52	2.03	0.082989	0.2793775	-4.75	FALSE
246575_at	bystin, putative similar to bystin	---	AT1G31660	-1.46	-0.54	-2.03	0.0829926	0.2793775	-4.75	FALSE
266704_at	putative N-acetyl-gamma-glutam	---	AT2G19940	-1.32	-0.40	-2.03	0.0830106	0.2793968	-4.75	FALSE
252773_at	putative protein predicted protei	---	---	1.22	0.29	2.03	0.0830395	0.2794528	-4.75	FALSE
264210_at	putative myb-related transcriptio	MYB3	AT1G22640	-1.41	-0.50	-2.03	0.0830862	0.2795687	-4.75	FALSE
250094_at	2-hydroxyphytanoyl-CoA lyase-li	---	AT5G17380	1.78	0.84	2.03	0.0831092	0.2796049	-4.75	FALSE
257751_at	hypothetical protein predicted by	MKS1	AT3G18690	2.21	1.14	2.03	0.0831518	0.279707	-4.75	FALSE
257887_at	protein phosphatase-2c, putative	---	AT3G17090	-1.32	-0.40	-2.03	0.0832637	0.2798362	-4.75	FALSE
254315_at	putative glycine-rich protein glyc	---	---	1.39	0.47	2.03	0.0832385	0.2798362	-4.75	FALSE
249333_at	GDSL-motif lipase/hydrolase-like	GLIP1	AT5G40990	2.46	1.30	2.03	0.0832412	0.2798362	-4.75	FALSE
265236_s_a	hypothetical protein	---	AT2G07714	1.26	0.33	2.03	0.0832639	0.2798362	-4.75	FALSE
249764_at	septum site-determining MinD (d	MIND	AT5G24020	-1.34	-0.42	-2.03	0.0832466	0.2798362	-4.75	FALSE
263945_at	hypothetical protein predicted by	---	AT2G36030	1.35	0.43	2.03	0.083241	0.2798362	-4.75	FALSE
260331_at	hypothetical protein contains Pfa	---	AT1G80270	-2.67	-1.42	-2.03	0.0832994	0.2799144	-4.75	FALSE

265773_at	unknown protein ; supported by	RPH1	AT2G48070	-1.28	-0.36	-2.03	0.083312	0.2799156	-4.75	FALSE
252254_at	hypothetical protein ; supported	DMS3	AT3G49250	-1.22	-0.28	-2.03	0.0833374	0.2799597	-4.75	FALSE
258440_at	putative protein phosphatase sim	---	AT3G17250	1.26	0.34	2.03	0.0834014	0.2801336	-4.76	FALSE
262886_at	hypothetical protein	KNATM	AT1G14760	1.34	0.42	2.03	0.0834182	0.2801485	-4.76	FALSE
250197_at	isocitrate dehydrogenase - like p	---	AT5G14590	-1.22	-0.29	-2.03	0.0834852	0.2801933	-4.76	FALSE
249585_at	5-oxoprolinase -like protein 5-ox	OXP1	AT5G37830	-1.25	-0.32	-2.03	0.083461	0.2801933	-4.76	FALSE
247541_at	structural protein - like glycine-ri	---	AT5G61660	-1.31	-0.39	-2.03	0.083495	0.2801933	-4.76	FALSE
252034_at	putative protein ;supported by fu	---	AT3G52040	-1.56	-0.65	-2.03	0.0834642	0.2801933	-4.76	FALSE
265288_at	putative glutaredoxin ;supported	---	AT2G20270	-1.35	-0.44	-2.03	0.0835175	0.2801933	-4.76	FALSE
249293_at	protein kinase-like	---	AT5G41260	-1.33	-0.41	-2.03	0.0835047	0.2801933	-4.76	FALSE
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.44	-0.53	-2.03	0.0835175	0.2801933	-4.76	FALSE
247944_at	putative protein similar to unknov	---	AT5G57100	-1.31	-0.39	-2.03	0.083574	0.2802181	-4.76	FALSE
251530_at	putative protein several hypothet	---	AT3G58520	-1.38	-0.46	-2.03	0.0835724	0.2802181	-4.76	FALSE
248161_at	unknown protein	---	AT5G54480	1.27	0.35	2.03	0.0835676	0.2802181	-4.76	FALSE
250948_at	putative protein	---	AT5G03490	1.46	0.54	2.03	0.0835529	0.2802181	-4.76	FALSE
252854_at	ubiquitin-specific protease 27 (U	UBP27	AT4G39370	-1.21	-0.28	-2.03	0.0835973	0.280255	-4.76	FALSE
252383_at	ABC-type transport protein-like p	ATH6	AT3G47780	1.91	0.93	2.03	0.0836308	0.2803261	-4.76	FALSE
263893_at	putative WRKY-type DNA bindin	WRKY59	AT2G21900	1.36	0.45	2.03	0.0836951	0.2803354	-4.76	FALSE
264968_at	stress related protein, putative s	---	AT1G67360	1.73	0.79	2.03	0.0836867	0.2803354	-4.76	FALSE
261289_at	hypothetical protein predicted by	---	AT1G37000	-1.22	-0.29	-2.03	0.0836584	0.2803354	-4.76	FALSE
263170_at	putative peroxisome assembly fa	PEX6	AT1G03000	-1.19	-0.26	-2.03	0.0836895	0.2803354	-4.76	FALSE
251277_at	dynamin-like protein phragmopla	ADL1B	AT3G61760	1.19	0.26	2.03	0.0836603	0.2803354	-4.76	FALSE
262907_at	hypothetical protein predicted by	CRR28	AT1G59720	-1.27	-0.35	-2.03	0.0837708	0.280548	-4.76	FALSE
255107_at	hypothetical protein	---	AT4G08730	1.34	0.42	2.03	0.0838187	0.2806673	-4.76	FALSE
250022_at	Brn1-like protein	---	AT5G18210	-1.52	-0.60	-2.03	0.0838378	0.2806898	-4.76	FALSE
257487_at	hypothetical protein predicted by	---	AT1G71850	-1.54	-0.63	-2.03	0.0838754	0.2807695	-4.76	FALSE
256897_at	hypothetical protein predicted by	---	AT3G24640	1.21	0.28	2.03	0.0838862	0.2807695	-4.76	FALSE
259756_at	unknown protein ; supported by	---	AT1G71080	1.23	0.30	2.03	0.083901	0.2807779	-4.76	FALSE
254837_at	putative protein	---	AT4G12360	1.30	0.38	2.03	0.0839347	0.2808494	-4.76	FALSE
265810_at	unknown protein	---	AT2G18090	1.45	0.54	2.03	0.0839538	0.2808721	-4.76	FALSE
250226_at	putative protein contains similarit	---	AT5G13780	-1.30	-0.37	-2.03	0.084003	0.2809954	-4.76	FALSE
246559_at	putative protein YTM1 - Homo s	---	AT5G15550	-1.45	-0.54	-2.03	0.0840381	0.2810195	-4.76	FALSE
254656_at	putative protein ;supported by fu	---	AT4G18070	-1.39	-0.48	-2.03	0.0840471	0.2810195	-4.76	FALSE
262579_at	hypothetical protein predicted by	---	AT1G15320	-1.23	-0.29	-2.03	0.0840246	0.2810195	-4.76	FALSE
263478_at	putative receptor-like protein kina	---	AT2G31880	1.98	0.99	2.02	0.0841522	0.2813294	-4.76	FALSE

264472_at	hypothetical protein predicted by	SWEETIE	AT1G67140	-1.34	-0.42	-2.02	0.0841686	0.281343	-4.76	FALSE
248807_at	pectin methylesterase-like	---	AT5G47500	1.19	0.25	2.02	0.084206	0.2813856	-4.76	FALSE
267001_at	putative urease accessory protei	UREG	AT2G34470	-1.37	-0.45	-2.02	0.0841975	0.2813856	-4.76	FALSE
264542_at	hypothetical protein predicted by	---	AT1G55830	-1.21	-0.27	-2.02	0.0842468	0.2814808	-4.77	FALSE
249687_at	putative protein oxidosqualene c	ATPEN3	AT5G36150	1.24	0.31	2.02	0.0842591	0.2814808	-4.77	FALSE
258158_at	acid phosphatase type 5 identica	PAP17	AT3G17790	-1.99	-1.00	-2.02	0.0843467	0.2816582	-4.77	TRUE
260641_at	hypothetical protein predicted by	---	AT1G53200	-1.54	-0.62	-2.02	0.0843493	0.2816582	-4.77	FALSE
263685_at	unknown protein similar to cell di	ATCUL3	AT1G26830	-1.20	-0.27	-2.02	0.0843398	0.2816582	-4.77	FALSE
258455_at	unknown protein ;supported by f	---	AT3G22440	-1.40	-0.49	-2.02	0.0843939	0.2817659	-4.77	FALSE
263731_at	metalloproteinase, putative simil	---	AT1G59970	2.04	1.03	2.02	0.0844188	0.2818077	-4.77	FALSE
256192_at	diadenosine 5,5-P1,P4-tetrapho	ATNUDX25	AT1G30110	1.28	0.36	2.02	0.0844858	0.2819901	-4.77	FALSE
246527_at	ribosomal protein-like 40S RIBO	---	AT5G15750	-1.72	-0.78	-2.02	0.0845423	0.281993	-4.77	FALSE
246513_at	hypothetical protein	---	AT5G15680	-1.22	-0.29	-2.02	0.0845396	0.281993	-4.77	FALSE
248576_at	methionine S-methyltransferase	MMT	AT5G49810	-1.24	-0.32	-2.02	0.0845678	0.281993	-4.77	FALSE
251409_at	Expressed protein ; supported by	---	AT3G60245	-1.77	-0.82	-2.02	0.0845501	0.281993	-4.77	FALSE
250593_at	putative protein similar to unknov	---	AT5G07740	1.22	0.29	2.02	0.0845614	0.281993	-4.77	FALSE
260454_at	RING-H2 zinc finger protein (ATL	ATL3	AT1G72310	-1.61	-0.69	-2.02	0.0845732	0.281993	-4.77	FALSE
267471_at	putative ferrochelatase precusor	FC2	AT2G30390	-1.48	-0.57	-2.02	0.0845031	0.281993	-4.77	FALSE
256350_at	hypothetical protein contains sim	PGSIP4	AT1G54940	1.22	0.28	2.02	0.0846144	0.2820893	-4.77	FALSE
262366_at	disease resistance protein, puta	---	AT1G72890	1.80	0.84	2.02	0.0846328	0.2821095	-4.77	TRUE
257513_s_a	hypothetical protein	---	AT1G12340 /.	-1.27	-0.35	-2.02	0.0846566	0.2821474	-4.77	FALSE
250247_at	unknown protein	---	AT5G13720	-1.22	-0.29	-2.02	0.0846973	0.2822007	-4.77	FALSE
252017_at	cytochrome P450 - like protein c	CYP76G1	AT3G52970	1.28	0.35	2.02	0.0846902	0.2822007	-4.77	FALSE
254234_at	putative major latex protein majo	---	AT4G23680	-1.99	-0.99	-2.02	0.0847373	0.2822927	-4.77	TRUE
248843_at	homeobox protein	HB-7	AT5G46880	1.29	0.37	2.02	0.0847556	0.2823124	-4.77	FALSE
251858_at	aquaporin MIP - like protein aqu	PIP2;5	AT3G54820	1.46	0.55	2.02	0.0847824	0.2823444	-4.77	FALSE
255207_at	Expressed protein ; supported by	---	AT4G07515	1.19	0.25	2.02	0.08479	0.2823444	-4.77	FALSE
258887_at	putative phospholipase D similar	PLDP2	AT3G05630	1.40	0.48	2.02	0.0848289	0.2823691	-4.77	TRUE
263117_at	putative lipoamide dehydrogena	---	AT1G03040	-1.21	-0.27	-2.02	0.084812	0.2823691	-4.77	FALSE
253834_at	protein phosphatase homolog (P	---	AT4G27800	-1.30	-0.37	-2.02	0.0848345	0.2823691	-4.77	FALSE
253839_at	putative protein prolactin-induce	---	AT4G27890	1.29	0.37	2.02	0.0848493	0.2823771	-4.77	FALSE
255140_x_a	extensin-like protein hydroxypro	---	AT4G08410	1.44	0.52	2.02	0.0848766	0.2824267	-4.77	FALSE
248877_at	putative protein similar to unknov	---	AT5G46140	1.24	0.31	2.02	0.0849308	0.2825659	-4.77	FALSE
266818_at	unknown protein	HUB1	AT2G44950	-1.31	-0.39	-2.02	0.0849863	0.2827092	-4.77	FALSE
263372_at	60S ribosomal protein L14 ;supp	---	AT2G20450	-1.65	-0.72	-2.02	0.0850506	0.282882	-4.77	FALSE

257741_at	hypothetical protein predicted by	---	AT3G27340	-1.38	-0.47	-2.02	0.0850778	0.2828899	-4.77	FALSE
254794_at	putative protein	---	AT4G12970	-2.20	-1.14	-2.02	0.0850693	0.2828899	-4.77	FALSE
264753_at	receptor kinase, putative similar	---	AT1G61490	-1.20	-0.26	-2.02	0.0850934	0.2829005	-4.77	FALSE
264506_at	germin-like protein Identical to A	GLP5	AT1G09560	1.30	0.38	2.02	0.0851359	0.282901	-4.78	FALSE
254265_s_a	serine threonine kinase - like pro	CRK6	AT4G23140 /	2.35	1.23	2.02	0.0851351	0.282901	-4.78	FALSE
248000_at	WD-repeat protein-like ;supporte	---	AT5G56190	1.29	0.37	2.02	0.0851431	0.282901	-4.78	FALSE
259114_at	26S proteasome AAA-ATPase su	RPT5A	AT3G05530	-1.24	-0.31	-2.02	0.0851284	0.282901	-4.78	FALSE
254657_s_a	putative protein W15DMY32F, W	---	AT4G18210 /	1.58	0.66	2.02	0.0851689	0.2829454	-4.78	FALSE
250627_at	putative amidase	---	AT5G07360	-1.31	-0.39	-2.02	0.0852245	0.2830065	-4.78	FALSE
263440_at	unknown protein predicted by ge	ATEXO70H	AT2G28640	1.19	0.25	2.02	0.0852111	0.2830065	-4.78	FALSE
249987_at	putative protein predicted protei	---	AT5G18490	1.46	0.55	2.02	0.085216	0.2830065	-4.78	FALSE
257053_at	ethylene responsive element bin	ERF4	AT3G15210	2.16	1.11	2.02	0.0852393	0.2830143	-4.78	FALSE
265917_at	putative disease resistance prote	AtRLP19	AT2G15080	1.35	0.43	2.02	0.0853427	0.283124	-4.78	FALSE
255501_at	hypothetical protein	---	AT4G02400	-1.42	-0.51	-2.02	0.085355	0.283124	-4.78	FALSE
267585_s_a	putative actin	ACT9	AT2G42090	1.23	0.30	2.02	0.0853405	0.283124	-4.78	FALSE
250221_at	protoporphyrinogen oxidase - lik	HEMG2	AT5G14220	-1.43	-0.52	-2.02	0.0853222	0.283124	-4.78	FALSE
259428_at	MAP kinase, putative similar to M	ATMPK11	AT1G01560	3.26	1.71	2.02	0.0852897	0.283124	-4.78	FALSE
267274_at	putative mitochondrial carrier pro	---	AT2G30160	-1.37	-0.46	-2.02	0.0853592	0.283124	-4.78	FALSE
259365_at	unknown protein ; supported by c	---	AT1G13300	2.49	1.32	2.02	0.0853526	0.283124	-4.78	FALSE
258519_at	unknown protein	---	AT3G06760	1.33	0.41	2.01	0.0854242	0.2832572	-4.78	TRUE
262258_at	20S proteasome subunit PAE1 ic	PAE1	AT1G53850	-1.31	-0.39	-2.01	0.0854209	0.2832572	-4.78	FALSE
262489_at	unknown protein EST gb|T21171	---	AT1G21830	-1.37	-0.45	-2.01	0.0854951	0.2834097	-4.78	FALSE
255566_s_a	hypothetical protein	---	AT3G48670 /	-1.27	-0.35	-2.01	0.0854883	0.2834097	-4.78	FALSE
252874_at	putative protein ipiB1 gene, Phy	---	---	1.26	0.33	2.01	0.0855117	0.2834238	-4.78	FALSE
265067_at	hypothetical protein predicted by	---	AT1G03850	2.09	1.06	2.01	0.0855324	0.2834512	-4.78	TRUE
249530_at	putative protein asparaginyl-tRN	---	AT5G38750	1.21	0.27	2.01	0.0855708	0.2835371	-4.78	FALSE
252312_at	hypothetical protein SF16 protei	iqd15	AT3G49380	1.31	0.39	2.01	0.0855993	0.2835394	-4.78	FALSE
257178_at	hemolysin-like protein similar to h	---	AT3G13070	1.28	0.36	2.01	0.0856339	0.2835394	-4.78	FALSE
256252_at	glucosyl transferase, putative sir	---	AT3G11340	3.91	1.97	2.01	0.085651	0.2835394	-4.78	FALSE
248304_at	polypyrimidine tract-binding RNA	PTB2	AT5G53180	-1.21	-0.27	-2.01	0.0856098	0.2835394	-4.78	FALSE
265949_at	putative vicilin storage protein (gl	---	AT2G18540	-1.20	-0.26	-2.01	0.0856697	0.2835394	-4.78	FALSE
249698_at	unknown protein	MIS12	AT5G35520	-1.38	-0.47	-2.01	0.0856709	0.2835394	-4.78	FALSE
252344_s_a	putative protein	---	AT3G44160 /	-1.24	-0.31	-2.01	0.0855972	0.2835394	-4.78	FALSE
245041_at	AR781, similar to yeast pheromo	AR781	AT2G26530	2.95	1.56	2.01	0.0856691	0.2835394	-4.78	FALSE
264837_at	unknown protein similar to ESTs	---	AT1G03600	-1.50	-0.58	-2.01	0.0857074	0.2835694	-4.78	TRUE

266010_at	putative C2H2-type zinc finger pr	---	AT2G37430	4.91	2.30	2.01	0.0857173	0.2835694	-4.78	FALSE
254380_at	putative protein	---	AT4G21865	2.11	1.08	2.01	0.0857012	0.2835694	-4.78	FALSE
252022_at	fructose bisphosphate aldolase -	---	AT3G52930	1.41	0.49	2.01	0.0857664	0.2836907	-4.78	FALSE
251221_at	putative protein ER6 protein - Ly	---	AT3G62550	-1.26	-0.33	-2.01	0.085798	0.283713	-4.78	TRUE
266592_at	putative fatty acid desaturase/cyt	---	AT2G46210	1.24	0.31	2.01	0.0857874	0.283713	-4.78	FALSE
259879_at	putative calmodulin similar to cal	CML38	AT1G76650	2.80	1.48	2.01	0.0858108	0.2837143	-4.78	FALSE
260150_at	putative oxidoreductase similar to	---	AT1G52820	1.28	0.36	2.01	0.0858278	0.2837294	-4.78	FALSE
250714_at	sorting nexin-like protein	SNX1	AT5G06140	-1.29	-0.37	-2.01	0.0858528	0.2837709	-4.78	FALSE
264663_at	unknown protein Similar to A. th	LRR XI-23	AT1G09970	1.96	0.97	2.01	0.085875	0.283803	-4.78	FALSE
265907_at	unknown protein ;supported by f	---	AT2G25650	-1.30	-0.38	-2.01	0.0859651	0.2840595	-4.78	FALSE
247185_at	putative protein contains similarit	---	AT5G65460	-1.31	-0.39	-2.01	0.0859901	0.284101	-4.78	FALSE
261413_at	unknown protein ;supported by fu	PLL5	AT1G07630	1.73	0.79	2.01	0.0860584	0.2841581	-4.79	TRUE
260153_at	putative lipase similar to monogly	---	AT1G52760	1.57	0.65	2.01	0.0860315	0.2841581	-4.79	TRUE
249849_at	putative protein similar to unknov	NIC2	AT5G23230	-1.33	-0.41	-2.01	0.0860601	0.2841581	-4.79	FALSE
264927_at	phosphatidylinositol 3-kinase, pu	VPS34	AT1G60490	-1.19	-0.25	-2.01	0.0860523	0.2841581	-4.79	FALSE
250370_at	putative protein putative transcri	---	AT5G11430	1.20	0.26	2.01	0.0860696	0.2841581	-4.79	FALSE
259711_at	putative DNA-binding protein sir	---	AT1G77570	-1.69	-0.76	-2.01	0.0862247	0.2844742	-4.79	FALSE
258827_at	hypothetical protein predicted by	---	AT3G07150	-1.38	-0.46	-2.01	0.0861824	0.2844742	-4.79	FALSE
249682_at	putative protein similar to unknov	---	AT5G36080	1.21	0.28	2.01	0.0862277	0.2844742	-4.79	FALSE
265889_at	hypothetical protein predicted by	---	AT2G15130	1.30	0.37	2.01	0.0862258	0.2844742	-4.79	FALSE
266694_at	putative clathrin assembly protei	---	AT2G19790	-1.20	-0.26	-2.01	0.0862264	0.2844742	-4.79	FALSE
265328_at	unknown protein	---	AT2G18200	1.19	0.25	2.01	0.0862432	0.2844841	-4.79	FALSE
253105_at	putative protein zinc finger prote	---	AT4G35840	-1.40	-0.48	-2.01	0.0863892	0.2849245	-4.79	FALSE
265271_at	hypothetical protein predicted by	---	AT2G28360	-1.29	-0.37	-2.01	0.0864178	0.2849775	-4.79	FALSE
261159_s_a	cyclin, putative similar to GB:AA	CYCB1;5	AT1G34460 /A	-1.32	-0.40	-2.01	0.086469	0.285064	-4.79	FALSE
260045_at	putative MAP kinase similar to m	ATMPK15	AT1G73670	1.20	0.26	2.01	0.0864592	0.285064	-4.79	FALSE
247303_at	histidinol dehydrogenase ;suppo	ATHDH	AT5G63890	-1.37	-0.45	-2.01	0.0865231	0.2852011	-4.79	FALSE
251975_at	CDC48 - like protein transitional	---	AT3G53230	2.05	1.03	2.01	0.0865378	0.2852084	-4.79	FALSE
252639_at	acyl CoA reductase -like protein	FAR5	AT3G44550	-1.20	-0.26	-2.01	0.0865823	0.2853139	-4.79	FALSE
251292_at	putative protein hypothetical pro	---	AT3G61920	1.37	0.45	2.01	0.0866162	0.2853845	-4.79	FALSE
262680_at	anter-specific proline-rich -like pr	---	AT1G75880	-1.45	-0.54	-2.00	0.0866342	0.2854024	-4.79	FALSE
261701_at	hypothetical protein similar to hy	HAF01	AT1G32750	-1.19	-0.25	-2.00	0.0867076	0.2854793	-4.79	FALSE
248034_at	serine threonine-specific protein	D6PK	AT5G55910	-1.28	-0.36	-2.00	0.0866976	0.2854793	-4.79	FALSE
253694_at	Expressed protein ; supported by	---	AT4G29735	-1.28	-0.36	-2.00	0.0866802	0.2854793	-4.79	FALSE
248615_at	putative protein contains similarit	AtPNG1	AT5G49570	1.44	0.53	2.00	0.0866949	0.2854793	-4.79	FALSE

262571_at	hypothetical protein predicted by	---	AT1G15430	1.71	0.77	2.00	0.0867547	0.2855931	-4.79	FALSE
264424_at	unknown protein similar to hypot	---	AT1G61740	-1.33	-0.41	-2.00	0.0867854	0.285653	-4.79	TRUE
253955_at	putative DNA binding protein DN	ATRBP45C	AT4G27000	-1.41	-0.50	-2.00	0.0868044	0.2856743	-4.79	FALSE
258185_at	hypothetical protein similar to hyp	---	AT3G21580	-1.34	-0.42	-2.00	0.0868292	0.2857147	-4.79	FALSE
262154_at	unknown protein contains similar	---	AT1G52700	1.43	0.51	2.00	0.0868631	0.285785	-4.79	FALSE
247008_at	ADP-ribosylation factor-like prote	ATARLA1D	AT5G67560	-1.23	-0.30	-2.00	0.0869346	0.2859138	-4.80	FALSE
249729_at	6-phosphogluconolactonase-like	---	AT5G24410	1.27	0.34	2.00	0.086938	0.2859138	-4.80	FALSE
261281_at	hypothetical protein predicted by	---	AT1G35740	-1.21	-0.28	-2.00	0.0869398	0.2859138	-4.80	FALSE
244951_s_a	cytochrome c biogenesis orf452	---	AT2G07723	1.58	0.66	2.00	0.0869544	0.2859203	-4.80	FALSE
260323_at	putative U3 small nucleolar ribon	IMP4	AT1G63780	-1.56	-0.64	-2.00	0.0869757	0.2859492	-4.80	FALSE
259024_at	hypothetical protein predicted by	---	---	1.34	0.43	2.00	0.0870026	0.2859551	-4.80	FALSE
253959_at	putative protein	---	AT4G26410	-1.22	-0.29	-2.00	0.086994	0.2859551	-4.80	FALSE
249951_at	S-adenosyl-L-methionine decarb	BUD2	AT5G18930	-1.43	-0.51	-2.00	0.0870971	0.2862246	-4.80	FALSE
245816_at	hypothetical protein similar to hyp	---	AT1G26210	1.66	0.73	2.00	0.0871197	0.2862577	-4.80	TRUE
265438_at	hypothetical protein	---	AT2G20970	1.21	0.27	2.00	0.0871894	0.2862797	-4.80	FALSE
265195_at	hypothetical protein	---	AT2G36730	-1.22	-0.28	-2.00	0.0871764	0.2862797	-4.80	FALSE
245481_at	hypothetical protein	---	AT4G16170	-1.23	-0.30	-2.00	0.0871785	0.2862797	-4.80	FALSE
254907_at	putative disease resistance resp	---	AT4G11190	1.24	0.32	2.00	0.0872017	0.2862797	-4.80	FALSE
259654_at	hypothetical protein predicted by	---	AT1G55220	1.27	0.35	2.00	0.087143	0.2862797	-4.80	FALSE
AFFX-r2-Bs	B. subtilis /GEN=dapB, jojF /DB_	---	---	-1.51	-0.59	-2.00	0.0871618	0.2862797	-4.80	FALSE
248358_at	cytochrome P-450-like protein	CYP715A1	AT5G52400	1.70	0.76	2.00	0.0872549	0.2864131	-4.80	FALSE
256769_at	protein kinase, putative similar t	---	AT3G13690	-1.52	-0.60	-2.00	0.0872741	0.2864347	-4.80	FALSE
253041_at	phosphoenolpyruvate carboxykin	PCK1	AT4G37870	1.56	0.64	2.00	0.0873005	0.2864802	-4.80	FALSE
263344_at	unknown protein ;supported by f	---	AT2G04940	-1.34	-0.42	-2.00	0.0873215	0.286508	-4.80	FALSE
250141_at	protein kinase MSK-3 - like prote	SK13	AT5G14640	1.31	0.39	2.00	0.0873708	0.2866284	-4.80	FALSE
249101_at	unknown protein	---	AT5G43580	1.89	0.92	2.00	0.0874181	0.2867424	-4.80	TRUE
253099_s_a	peroxidase - like protein peroxid	---	AT4G37520 ///	1.30	0.38	2.00	0.0874833	0.2867914	-4.80	TRUE
261433_s_a	endoplasmic reticulum-type calci	---	AT1G07670 ///	1.20	0.26	2.00	0.0874691	0.2867914	-4.80	FALSE
248390_at	importin alpha subunit	IMPA-8	AT5G52000	1.19	0.25	2.00	0.0874828	0.2867914	-4.80	FALSE
251485_at	putative protein rad21 mitotic co	SYN3	AT3G59550	1.21	0.28	2.00	0.0874713	0.2867914	-4.80	FALSE
257900_at	hypothetical protein predicted by	---	AT3G28420	-1.22	-0.29	-2.00	0.0875091	0.2868128	-4.80	FALSE
258319_at	hypothetical protein similar to hyp	---	AT3G22700	1.23	0.29	2.00	0.087515	0.2868128	-4.80	FALSE
263319_at	putative anion exchange protein	BOR1	AT2G47160	1.57	0.65	2.00	0.0875418	0.2868577	-4.80	TRUE
263754_at	putative DnaJ protein ;supported	---	AT2G21510	1.74	0.80	2.00	0.0875538	0.2868577	-4.80	FALSE
251413_at	bZIP protein ; supported by cDN	---	AT3G60320	-1.32	-0.40	-2.00	0.0876047	0.2868595	-4.80	TRUE

247429_at	putative protein strong similarity t	---	AT5G62620	1.36	0.45	2.00	0.0876047	0.2868595	-4.80	FALSE
266401_s_a	putative cell division control prote	CDKB1;2	AT2G38620 /	1.21	0.27	2.00	0.087588	0.2868595	-4.80	FALSE
252326_at	putative protein ferripyochelin bi	GAMMA CA	AT3G48680	-1.27	-0.35	-2.00	0.0876016	0.2868595	-4.80	FALSE
245146_at	putative cis-Golgi SNARE protein	GOS12	AT2G45200	-1.28	-0.36	-2.00	0.0876231	0.2868787	-4.80	FALSE
256521_at	AMP-binding enzyme, putative c	---	AT1G66120	1.25	0.32	2.00	0.0876667	0.2869801	-4.80	FALSE
265708_at	unknown protein member of a la	---	AT2G03380	-1.23	-0.30	-2.00	0.0877191	0.2871106	-4.80	FALSE
265114_at	hypothetical protein contains sim	LRX2	AT1G62440	1.55	0.63	2.00	0.0878091	0.2873226	-4.81	FALSE
245919_at	putative protein various predicte	---	AT5G28780	1.20	0.26	2.00	0.0878038	0.2873226	-4.81	FALSE
266742_at	predicted by genefinder and gen	---	AT2G03050	-1.24	-0.31	-2.00	0.0878411	0.287386	-4.81	FALSE
257271_at	Expressed protein ; supported by	---	AT3G28007	2.05	1.03	1.99	0.0879347	0.2876508	-4.81	TRUE
252337_at	CELL DIVISION CONTROL PRO	CDC2	AT3G48750	-1.44	-0.53	-1.99	0.0879669	0.2876803	-4.81	FALSE
254720_at	DNA (cytosine-5-)-methyltransfe	MEE57	AT4G13610	1.27	0.35	1.99	0.0879754	0.2876803	-4.81	FALSE
247869_at	CCHH finger protein 2-like protei	ZFP2	AT5G57520	1.18	0.24	1.99	0.0879815	0.2876803	-4.81	FALSE
251341_at	ribosomal protein S13 -like AtRP	---	AT3G60770	-1.56	-0.64	-1.99	0.0880427	0.2878392	-4.81	FALSE
265681_at	putative protein kinase contains a	---	AT2G24370	1.22	0.28	1.99	0.0880914	0.2879434	-4.81	FALSE
261660_at	kinesin heavy chain isolog, puta	HIK	AT1G18370	1.22	0.28	1.99	0.0880998	0.2879434	-4.81	FALSE
256740_at	hypothetical protein predicted by	---	AT3G29330	-1.21	-0.28	-1.99	0.0881394	0.2880316	-4.81	FALSE
258824_at	unknown protein	---	AT3G07190	-1.35	-0.43	-1.99	0.0881578	0.2880504	-4.81	FALSE
250910_at	heat shock transcription factor -l	HSFA3	AT5G03720	-1.96	-0.97	-1.99	0.08827	0.2883757	-4.81	FALSE
254923_at	protein phosphatase type 1 PP1	TOPP7	AT4G11240	-1.33	-0.41	-1.99	0.0883211	0.2885012	-4.81	FALSE
254485_at	cell-cell signaling protein csgA -	---	AT4G20760	-1.35	-0.43	-1.99	0.0883996	0.2886597	-4.81	TRUE
253404_at	putative pyrophosphate--fructos	PFK6	AT4G32840	-1.31	-0.39	-1.99	0.0884076	0.2886597	-4.81	FALSE
266395_at	3-isopropylmalate dehydratase,	---	AT2G43100	-1.84	-0.88	-1.99	0.0883946	0.2886597	-4.81	FALSE
259764_at	transcription factor inhibitor I kap	NPR1	AT1G64280	1.42	0.50	1.99	0.0884254	0.2886767	-4.81	FALSE
262131_at	hypothetical protein predicted by	RALF1	AT1G02900	2.20	1.14	1.99	0.0884454	0.2887007	-4.81	FALSE
263705_at	unknown protein contains similar	IMPL1	AT1G31190	-1.36	-0.44	-1.99	0.0884709	0.2887424	-4.81	FALSE
253259_at	putative protein ethylene-respon	RRTF1	AT4G34410	2.01	1.01	1.99	0.0885279	0.2888871	-4.81	FALSE
251841_at	putative protein CRP1, Zea may	---	AT3G54980	-1.45	-0.54	-1.99	0.0886485	0.2890544	-4.81	FALSE
266804_at	cyclophilin identical to GB:AF02	CYP5	AT2G29960	-1.27	-0.35	-1.99	0.0886617	0.2890544	-4.81	FALSE
259139_at	hypothetical protein similar to F1	---	AT3G10240	1.24	0.31	1.99	0.0886544	0.2890544	-4.81	FALSE
251386_at	putative protein rec, Homo sapie	---	AT3G60800	1.20	0.26	1.99	0.0886378	0.2890544	-4.81	FALSE
258045_at	ubiquitin-specific protease 7 (UB	UBP7	AT3G21280	-1.27	-0.35	-1.99	0.0886679	0.2890544	-4.81	FALSE
252278_at	NAC2-like protein NAC2 - Arabi	anac062	AT3G49530	1.78	0.83	1.99	0.0886565	0.2890544	-4.81	FALSE
253389_at	hypothetical protein ;supported b	---	AT4G32680	-1.22	-0.28	-1.99	0.0886155	0.2890544	-4.81	FALSE
267214_at	unknown protein ; supported by	---	AT2G43970	-1.35	-0.43	-1.99	0.0886894	0.2890834	-4.81	FALSE

262542_at	hypothetical protein similar to NA	anac016	AT1G34180	-1.47	-0.56	-1.99	0.088706	0.2890961	-4.81	FALSE
248061_at	putative protein contains similarit	---	AT5G55340	1.20	0.26	1.99	0.0887505	0.2891998	-4.82	FALSE
256724_at	unknown protein ;supported by f	---	AT2G34040	-1.28	-0.35	-1.99	0.0887775	0.2892466	-4.82	FALSE
252893_at	hypothetical protein	---	AT4G39420	1.19	0.25	1.99	0.0887971	0.289269	-4.82	FALSE
245266_at	hypothetical protein ; supported b	---	AT4G17070	-1.47	-0.56	-1.99	0.0888649	0.2894073	-4.82	FALSE
257391_at	hypothetical protein predicted by	---	AT2G32050	1.19	0.26	1.99	0.0888607	0.2894073	-4.82	FALSE
266198_at	unknown protein predicted by ge	---	AT2G38890	1.25	0.32	1.99	0.0889386	0.2895233	-4.82	FALSE
245791_at	defender against cell death prot	ATDAD1	AT1G32210	-1.28	-0.36	-1.99	0.0889295	0.2895233	-4.82	FALSE
260652_at	putative MYB family transcriptior	---	AT1G32360	-1.22	-0.29	-1.99	0.0889316	0.2895233	-4.82	FALSE
258856_at	hypothetical protein predicted by	SRG3	AT3G02040	-1.66	-0.73	-1.99	0.0890051	0.2896206	-4.82	TRUE
251696_at	putative protein	---	---	1.31	0.39	1.99	0.0890066	0.2896206	-4.82	FALSE
246722_at	putative protein various predicte	---	---	1.32	0.40	1.99	0.0889988	0.2896206	-4.82	FALSE
258988_at	unknown protein similar to unkno	---	AT3G08890	-1.26	-0.33	-1.99	0.089135	0.2899467	-4.82	FALSE
246043_at	putative protein predicted protei	---	AT5G19380	1.53	0.61	1.99	0.0891449	0.2899467	-4.82	FALSE
263907_at	abscisic acid insensitive 5 (ABI5)	ABI5	AT2G36270	1.33	0.41	1.99	0.0891371	0.2899467	-4.82	FALSE
256628_at	membrane import protein, putati	TOM40	AT3G20000	-1.44	-0.52	-1.98	0.089223	0.2900766	-4.82	FALSE
254249_at	serine /threonine kinase - like pr	---	AT4G23280	1.80	0.85	1.98	0.0891999	0.2900766	-4.82	FALSE
248359_at	unknown protein	---	AT5G52410	1.29	0.37	1.98	0.0892104	0.2900766	-4.82	FALSE
252480_at	putative protein methyl-CpG-bin	MBD5	AT3G46580	-1.20	-0.26	-1.98	0.0892559	0.2901009	-4.82	FALSE
257758_at	eukaryotic translation elongation	---	AT3G22980	1.29	0.36	1.98	0.0892485	0.2901009	-4.82	FALSE
265656_at	putative nonspecific lipid-transfer	---	AT2G13820	-1.72	-0.78	-1.98	0.0894549	0.290255	-4.82	FALSE
255505_at	SAR1/GTP-binding secretory fac	ATSAR2	AT4G02080	-1.25	-0.32	-1.98	0.0894615	0.290255	-4.82	FALSE
247130_at	putative protein contains similarit	---	AT5G66180	-1.55	-0.63	-1.98	0.0893668	0.290255	-4.82	FALSE
260174_at	unknown protein ;supported by f	---	AT1G71940	1.23	0.30	1.98	0.0893331	0.290255	-4.82	FALSE
251456_at	beta-glucosidase-like protein sev	BGLU27	AT3G60120	6.79	2.76	1.98	0.0894427	0.290255	-4.82	FALSE
265465_at	hypothetical protein predicted by	---	AT2G37070	1.71	0.77	1.98	0.0893938	0.290255	-4.82	FALSE
258574_at	hypothetical protein	---	AT3G04250	1.25	0.32	1.98	0.089463	0.290255	-4.82	FALSE
245974_at	putative protein	---	---	1.43	0.51	1.98	0.0894588	0.290255	-4.82	FALSE
255987_s_a	putative protein predicted protei	---	AT5G35050	-1.21	-0.27	-1.98	0.0893847	0.290255	-4.82	FALSE
266335_at	putative cytochrome P450 ; supp	KAO2	AT2G32440	-1.48	-0.56	-1.98	0.0893424	0.290255	-4.82	FALSE
261295_at	unknown protein	---	AT1G48450	-1.21	-0.28	-1.98	0.0894645	0.290255	-4.82	FALSE
254446_at	tubulin beta-9 chain ;supported b	TUB9	AT4G20890	-1.22	-0.28	-1.98	0.0894688	0.290255	-4.82	FALSE
247272_at	GTP cyclohydrolase II; 3,4-dihyd	---	AT5G14040 /A	1.83	0.87	1.98	0.0893352	0.290255	-4.82	FALSE
245316_at	hypothetical protein ;supported b	---	AT4G14000	-1.27	-0.34	-1.98	0.089552	0.2904836	-4.82	FALSE
248221_at	vacuolar sorting protein-like; emb	VPS26A	AT5G53530	-1.20	-0.27	-1.98	0.0895729	0.2905103	-4.82	FALSE

264156_at	unknown protein	---	AT1G65280	-1.19	-0.25	-1.98	0.0895911	0.2905278	-4.82	FALSE
250034_at	apyrase (gb|AAF00612.1) ; supp	ATAPY2	AT5G18280	1.28	0.36	1.98	0.0896219	0.2905864	-4.82	FALSE
245472_at	hypothetical protein	---	AT4G16040	1.31	0.39	1.98	0.089636	0.290591	-4.82	FALSE
257402_at	hypothetical protein similar to put	---	AT1G23570	1.25	0.32	1.98	0.0896919	0.2907308	-4.83	FALSE
250776_at	monooxygenase ;supported by f	---	AT5G05320	-1.21	-0.28	-1.98	0.0897373	0.290836	-4.83	FALSE
256011_at	respiratory burst oxidase protein	---	AT1G19230	1.25	0.33	1.98	0.0897626	0.290836	-4.83	FALSE
262789_at	putative auxin-induced protein st	---	AT1G10810	1.22	0.29	1.98	0.0897534	0.290836	-4.83	FALSE
252273_at	putative WD-40 repeat - protein	---	AT3G49660	-1.27	-0.34	-1.98	0.0898031	0.2909258	-4.83	FALSE
257648_at	RNA helicase, putative similar to	---	AT3G16840	-1.49	-0.57	-1.98	0.0898395	0.2909612	-4.83	FALSE
264407_at	unknown protein similar to EST g	---	AT1G10180	-1.30	-0.38	-1.98	0.0898378	0.2909612	-4.83	FALSE
247486_at	putative protein	---	AT5G62140	-1.41	-0.50	-1.98	0.0898673	0.2910097	-4.83	FALSE
248586_at	putative protein similar to unknov	---	AT5G49610	-1.26	-0.34	-1.98	0.0899122	0.2911139	-4.83	FALSE
249778_at	Expressed protein ; supported by	---	AT5G24165	-1.23	-0.30	-1.98	0.089991	0.291121	-4.83	FALSE
257515_at	zinc finger protein, putative simil	DOT5	AT1G13290	1.23	0.30	1.98	0.0899551	0.291121	-4.83	FALSE
265730_at	60S ribosomal protein L27	---	AT2G32220	-2.06	-1.05	-1.98	0.0899647	0.291121	-4.83	TRUE
262312_at	hypothetical protein similar to put	MLP28	AT1G70830	6.67	2.74	1.98	0.0899333	0.291121	-4.83	FALSE
253702_at	Ca2+-transporting ATPase - like	ACA10	AT4G29900	-1.35	-0.43	-1.98	0.0899663	0.291121	-4.83	FALSE
257035_at	cytochrome P450, putative simil	CYP707A4	AT3G19270	1.29	0.36	1.98	0.0899808	0.291121	-4.83	FALSE
249430_at	GTP-binding protein-like GTP-bi	---	AT5G39900	-1.41	-0.49	-1.98	0.0900188	0.2911698	-4.83	FALSE
246885_at	putative protein predicted protei	---	AT5G26230	1.81	0.86	1.98	0.0900942	0.2913437	-4.83	FALSE
258825_at	unknown protein	---	AT3G07180	-1.22	-0.28	-1.98	0.0900981	0.2913437	-4.83	FALSE
257043_at	receptor-like protein kinase, puta	IKU2	AT3G19700	1.25	0.33	1.98	0.0901415	0.2914078	-4.83	FALSE
250076_at	putative protein; similar to unkno	---	AT5G16660	-1.29	-0.36	-1.98	0.0901435	0.2914078	-4.83	FALSE
267355_at	putative LIM-domain protein	---	AT2G39900	-1.36	-0.45	-1.98	0.0901825	0.2914706	-4.83	FALSE
245326_at	Expressed protein ; supported by	---	AT4G14100	-1.34	-0.42	-1.98	0.0901885	0.2914706	-4.83	FALSE
266468_at	unknown protein ; supported by c	---	AT2G47960	-1.29	-0.37	-1.98	0.0902238	0.2915435	-4.83	FALSE
261229_at	RAC-like GTP-binding protein AF	ROP2	AT1G20090	-1.20	-0.27	-1.98	0.0902485	0.2915818	-4.83	TRUE
261220_at	ER lumen protein-retaining recep	---	AT1G19970	1.67	0.74	1.98	0.0902733	0.2916208	-4.83	FALSE
257219_at	uroporphyrinogen decarboxylase	HEME1	AT3G14930	-1.38	-0.46	-1.98	0.090337	0.2916744	-4.83	TRUE
264251_at	hypothetical protein identical to G	---	AT1G09190	-1.36	-0.45	-1.98	0.0903304	0.2916744	-4.83	FALSE
265501_at	putative glucosyltransferase	UGT73B4	AT2G15490	1.90	0.92	1.98	0.0903163	0.2916744	-4.83	FALSE
259804_at	cytosolic factor, putative similar	---	AT1G72160	-1.51	-0.60	-1.98	0.0903411	0.2916744	-4.83	FALSE
248687_at	ADPG pyrophosphorylase small	ADG1	AT5G48300	-1.58	-0.66	-1.98	0.0904251	0.291748	-4.83	TRUE
263231_at	putative indole-3-acetate beta-glu	---	AT1G05680	7.14	2.84	1.98	0.0904038	0.291748	-4.83	TRUE
247080_at	20S proteasome subunit PAD2 (	PAD2	AT5G66140	-1.27	-0.34	-1.98	0.0903982	0.291748	-4.83	FALSE

263853_at	putative mutT domain protein	---	AT2G04440	1.39	0.47	1.98	0.0903862	0.291748	-4.83	FALSE
264391_at	pectate lyase-like protein Similar	---	AT1G11920	1.25	0.32	1.98	0.0904278	0.291748	-4.83	FALSE
259616_at	hypothetical protein contains sim	C/VIF1	AT1G47960	-1.44	-0.52	-1.97	0.0905332	0.2917993	-4.83	FALSE
261208_at	unknown protein ; supported by c	---	AT1G12930	-1.35	-0.43	-1.98	0.0904861	0.2917993	-4.83	FALSE
267550_at	putative protein kinase contains a	AP4.3A	AT2G32800	1.71	0.77	1.98	0.0904768	0.2917993	-4.83	TRUE
251866_at	putative protein MSP58 - nucleo	emb1967	AT3G54350	-1.21	-0.27	-1.97	0.0905267	0.2917993	-4.83	FALSE
247217_s_a	MADS box transcription factors-li	MAF3	AT5G65050 ///	1.19	0.25	1.97	0.0905113	0.2917993	-4.83	FALSE
259687_at	unknown protein	---	AT1G63110	-1.33	-0.41	-1.98	0.0904618	0.2917993	-4.83	FALSE
255147_at	hypothetical protein	---	AT4G08460	-1.26	-0.33	-1.97	0.0905095	0.2917993	-4.83	FALSE
247144_at	DOF zinc finger protein-like	---	AT5G65590	1.41	0.49	1.97	0.0905461	0.2917995	-4.83	FALSE
258357_at	putative leucine-rich repeat trans	SRF7	AT3G14350	1.49	0.58	1.97	0.0905704	0.2918366	-4.83	TRUE
261309_at	phosphoethanolamine N-methyl	CPuORF31	AT1G48598 ///	-1.47	-0.55	-1.97	0.0906438	0.2920317	-4.84	TRUE
257743_at	unknown protein	---	AT3G27390	-1.37	-0.45	-1.97	0.0906865	0.2920457	-4.84	FALSE
251711_at	phosphatidylinositol-4-phosphat	PIP5K4	AT3G56960	-1.33	-0.41	-1.97	0.0906752	0.2920457	-4.84	FALSE
250783_at	cytochrome P450 ; supported by	CYP79A2	AT5G05260	1.29	0.36	1.97	0.0906806	0.2920457	-4.84	FALSE
256921_at	unknown protein ;supported by f	---	AT3G18940	-1.27	-0.34	-1.97	0.090742	0.2921831	-4.84	FALSE
262777_at	hypothetical protein predicted by	---	AT1G13030	-1.42	-0.51	-1.97	0.0907647	0.2922036	-4.84	FALSE
248128_at	thiazole biosynthetic enzyme pre	THI1	AT5G54770	-1.33	-0.41	-1.97	0.090774	0.2922036	-4.84	FALSE
257518_at	hypothetical protein	---	AT3G03880	-1.20	-0.26	-1.97	0.0908057	0.2922342	-4.84	FALSE
263838_at	putative s-adenosylmethionine sy	MAT3	AT2G36880	1.75	0.81	1.97	0.0908091	0.2922342	-4.84	FALSE
250985_at	putative protein various predicte	---	AT5G02830	-1.22	-0.29	-1.97	0.0908469	0.2922487	-4.84	FALSE
266203_at	putative phloem-specific lectin	AtPP2-B1	AT2G02230	-1.75	-0.81	-1.97	0.0908649	0.2922487	-4.84	FALSE
256034_at	unknown protein ; supported by c	---	AT1G07080	-1.22	-0.29	-1.97	0.0908387	0.2922487	-4.84	FALSE
259171_at	hypothetical protein predicted by	---	AT3G03590	-1.27	-0.34	-1.97	0.0908579	0.2922487	-4.84	FALSE
253717_at	putative protein putative suppres	---	AT4G29440	1.24	0.31	1.97	0.0908953	0.2923046	-4.84	FALSE
248580_at	chloride channel (emb|CAA7031	CLC-C	AT5G49890	1.34	0.42	1.97	0.0909079	0.2923046	-4.84	FALSE
254326_at	putative protein AIR1, Arabidops	---	AT4G22610	1.27	0.34	1.97	0.0909671	0.2924538	-4.84	FALSE
247026_at	protein kinase-like protein	MAPKKK19	AT5G67080	3.35	1.74	1.97	0.0909849	0.2924697	-4.84	TRUE
261992_at	unknown protein	---	AT1G33680	-1.26	-0.33	-1.97	0.0910121	0.292516	-4.84	FALSE
264824_at	unknown protein similar to gb|T4	2A6	---	-1.44	-0.53	-1.97	0.0910834	0.2927039	-4.84	FALSE
247268_at	putative protein contains similarit	---	AT5G64080	1.33	0.41	1.97	0.0910969	0.2927059	-4.84	FALSE
253118_at	ras-related small GTP-binding p	ARAC6	AT4G35950	-1.33	-0.41	-1.97	0.0911126	0.2927153	-4.84	FALSE
264885_s_a	NBS/LRR disease resistance pr	---	AT1G61180 ///	-1.30	-0.38	-1.97	0.0911422	0.2927691	-4.84	FALSE
262182_at	hypothetical protein predicted by	---	AT1G77890	1.24	0.31	1.97	0.0911904	0.2928826	-4.84	FALSE
255491_at	putative zinc finger protein simila	AtIDD12	AT4G02670	1.19	0.26	1.97	0.0912213	0.2929407	-4.84	FALSE

262116_at	Expressed protein ; supported by	---	AT1G02816	1.60	0.68	1.97	0.0912538	0.2930039	-4.84	FALSE
247237_at	auxin-independent growth promo	---	AT5G64600	-1.29	-0.36	-1.97	0.0912876	0.293071	-4.84	FALSE
246510_at	cyclic nucleotide-gated cation ch	DND1	AT5G15410	-1.28	-0.36	-1.97	0.0913304	0.2931501	-4.84	TRUE
254559_at	putative protein glycine/proline-r	---	AT4G19200	1.39	0.48	1.97	0.0913415	0.2931501	-4.84	FALSE
248735_at	laccase (diphenol oxidase)	TT10	AT5G48100	1.23	0.30	1.97	0.0913604	0.2931501	-4.84	FALSE
251940_at	putative protein lysine decarboxy	---	AT3G53450	1.24	0.31	1.97	0.0913636	0.2931501	-4.84	FALSE
258257_at	putative short chain alcohol dehy	---	AT3G26770	1.20	0.27	1.97	0.0914014	0.2932301	-4.84	FALSE
252061_at	hypothetical protein phosphate a	---	AT3G52620	1.22	0.29	1.97	0.0914356	0.2932985	-4.84	FALSE
267547_at	putative synaptobrevin	ATVAMP72	AT2G32670	1.34	0.42	1.97	0.0914637	0.2933475	-4.84	FALSE
250345_at	subtilisin-like serine protease cor	---	AT5G11940	1.26	0.34	1.97	0.0915191	0.2934839	-4.84	FALSE
264700_at	hypothetical protein predicted by	---	AT1G70100	-1.31	-0.39	-1.97	0.0916054	0.2937194	-4.85	FALSE
253254_at	predicted protein	SQS2	AT4G34650	1.57	0.65	1.97	0.091635	0.2937318	-4.85	FALSE
258919_at	Expressed protein ; supported by	---	AT3G10525	-1.34	-0.42	-1.97	0.0916275	0.2937318	-4.85	FALSE
245442_at	hypothetical protein	---	AT4G16710	-1.21	-0.27	-1.97	0.0917172	0.2939539	-4.85	FALSE
244917_at	hypothetical protein	---	---	1.23	0.30	1.97	0.0917724	0.2940893	-4.85	FALSE
251499_at	putative protein putative callose	ATGSL11	AT3G59100	1.24	0.31	1.97	0.0918027	0.2941037	-4.85	FALSE
265269_at	hypothetical protein predicted by	---	AT2G42950	1.29	0.37	1.97	0.0917939	0.2941037	-4.85	FALSE
247300_at	unknown protein	FCLY	AT5G63910	-1.27	-0.34	-1.96	0.091847	0.2942046	-4.85	FALSE
249554_at	CRS2 -like protein CRS2, Zea m	---	AT5G38290	-1.72	-0.79	-1.96	0.0919015	0.2943377	-4.85	FALSE
259664_at	unknown protein ; supported by f	AGP21	AT1G55330	3.89	1.96	1.96	0.0919194	0.2943538	-4.85	TRUE
263435_at	putative ATP-dependent RNA he	---	AT2G28600	-1.50	-0.59	-1.96	0.0919466	0.2943996	-4.85	FALSE
262021_at	unknown protein	AT1G3554	---	-1.27	-0.35	-1.96	0.0919894	0.2944951	-4.85	FALSE
248691_at	putative protein strong similarity t	---	AT5G48310	1.24	0.30	1.96	0.092015	0.2945358	-4.85	FALSE
247597_at	GTP-binding protein - like GTP-l	AtRABA1f	AT5G60860	1.67	0.74	1.96	0.0921025	0.2946318	-4.85	TRUE
254360_at	CDP-diacylglycerol synthetase-l	---	AT4G22340	1.24	0.31	1.96	0.0921096	0.2946318	-4.85	FALSE
256881_at	hypothetical protein ; supported	---	AT3G26410	-1.24	-0.32	-1.96	0.0920975	0.2946318	-4.85	FALSE
245907_at	ubiquitin-like protein ubiquitins -	---	AT5G09340	-1.19	-0.25	-1.96	0.09206	0.2946318	-4.85	FALSE
255135_at	putative protein several hypothet	---	---	1.25	0.32	1.96	0.0920916	0.2946318	-4.85	FALSE
261583_at	pyruvate dehydrogenase E1 alph	PDH-E1 AL	AT1G01090	-1.24	-0.31	-1.96	0.0921279	0.294649	-4.85	FALSE
252304_at	hypothetical protein	---	AT3G49230	1.20	0.26	1.96	0.092148	0.2946721	-4.85	FALSE
254460_at	putative protein sigma70 operon	ATRP1	AT4G21210	-1.34	-0.42	-1.96	0.0922159	0.2948479	-4.85	FALSE
245686_at	Expressed protein ; supported by	J2	AT5G22060	1.58	0.66	1.96	0.0922369	0.2948737	-4.85	FALSE
252467_at	putative protein predicted protei	---	AT3G47080	1.34	0.42	1.96	0.0922753	0.294955	-4.85	FALSE
262193_at	eukaryotic initiation factor 5 (eIF	---	AT1G77840	1.37	0.46	1.96	0.0923309	0.2950501	-4.85	FALSE
256973_at	unknown protein similar to putati	---	AT3G20980	1.24	0.31	1.96	0.0923189	0.2950501	-4.85	FALSE

252661_at	putative protein	---	AT3G44450	-1.98	-0.99	-1.96	0.0923696	0.2951326	-4.85	FALSE
251605_at	receptor-like protein kinase seve	---	AT3G57830	1.30	0.38	1.96	0.092383	0.2951338	-4.85	FALSE
260894_at	hypothetical protein contains sim	---	AT1G29220	-1.22	-0.29	-1.96	0.0924098	0.2951782	-4.85	FALSE
259118_at	unknown protein similar to unkn	---	AT3G01310	-1.32	-0.40	-1.96	0.0924256	0.2951873	-4.85	FALSE
252813_at	putative protein several hypothet	---	---	1.23	0.29	1.96	0.0924642	0.2952693	-4.85	FALSE
264660_at	putative glutamyl-tRNA reductas	HEMA2	AT1G09940	1.84	0.88	1.96	0.0924914	0.2953147	-4.85	FALSE
251422_at	transport protein subunit - like S	---	AT3G60540	1.72	0.78	1.96	0.0925324	0.2954044	-4.86	FALSE
254299_at	hypothetical protein ;supported b	NYE1	AT4G22920	1.56	0.65	1.96	0.0925593	0.295421	-4.86	FALSE
267633_at	hypothetical protein predicted by	---	AT2G42180	1.20	0.26	1.96	0.0925635	0.295421	-4.86	FALSE
252482_at	glucosyltransferase-like protein	UGT76E11	AT3G46670	2.16	1.11	1.96	0.0926151	0.2955443	-4.86	FALSE
252958_at	putative transcription factor (MYB	MYB4	AT4G38620	1.80	0.85	1.96	0.0926445	0.2955969	-4.86	FALSE
263426_at	putative glutathione peroxidase	ATGPX2	AT2G31570	1.40	0.49	1.96	0.0926878	0.2956936	-4.86	FALSE
254684_at	glycine-rich RNA-binding protein	GR-RBP2	AT4G13850	-1.39	-0.48	-1.96	0.0927122	0.29573	-4.86	FALSE
258994_at	unknown protein similar to putati	RAPTOR1	AT3G08850	-1.22	-0.28	-1.96	0.0927372	0.2957685	-4.86	FALSE
261668_at	2-isopropylmalate synthase, put	MAML-4	AT1G18500	-1.30	-0.38	-1.96	0.0927584	0.2957945	-4.86	FALSE
262221_at	hypothetical protein predicted by	ARC3	AT1G75010	-1.34	-0.42	-1.96	0.0928291	0.2959429	-4.86	FALSE
261736_at	hypothetical protein simlar to hyp	---	AT1G47810	1.23	0.30	1.96	0.0928308	0.2959429	-4.86	FALSE
263108_at	hypothetical protein similar to put	---	AT1G65240	2.06	1.04	1.96	0.0928836	0.2960696	-4.86	FALSE
252968_at	putative protein unknown mRNA	---	AT4G38890	-1.39	-0.48	-1.96	0.0929528	0.2961545	-4.86	FALSE
261684_at	hypothetical protein predicted by	---	AT1G47400	2.17	1.12	1.96	0.0929751	0.2961545	-4.86	TRUE
265422_at	putative NADH-ubiquinone oxire	NDB4	AT2G20800	1.27	0.35	1.96	0.0929686	0.2961545	-4.86	FALSE
260335_at	putative strictosidine synthase si	SS3	AT1G74000	1.73	0.79	1.96	0.0929746	0.2961545	-4.86	FALSE
264890_at	unknown protein	---	AT1G23180	-1.36	-0.44	-1.96	0.0929469	0.2961545	-4.86	FALSE
245757_at	phosphate-induced (phi-1) prote	PHI-1	AT1G35140	3.20	1.68	1.96	0.0930372	0.2962583	-4.86	TRUE
263251_at	unknown protein ; supported by	---	AT2G31410	-1.56	-0.64	-1.96	0.0930579	0.2962583	-4.86	FALSE
254019_at	putative protein mature-parasite	---	AT4G26190	-1.18	-0.24	-1.96	0.0930491	0.2962583	-4.86	FALSE
255610_at	putative phosphatidylinositol kin	ATPIPK10	AT4G01190	1.23	0.30	1.96	0.0930641	0.2962583	-4.86	FALSE
265855_at	unknown protein ;supported by f	---	AT2G42390	-1.22	-0.28	-1.96	0.0930856	0.2962583	-4.86	FALSE
252906_at	putative gamma-glutamyltransfe	GGT1	AT4G39640	1.50	0.59	1.96	0.0930739	0.2962583	-4.86	FALSE
244985_at	ribosomal protein L22	---	---	-1.41	-0.50	-1.95	0.0931553	0.2964388	-4.86	FALSE
251148_at	hypothetical protein	TKL	AT3G63180	-1.24	-0.31	-1.95	0.0931967	0.296529	-4.86	FALSE
246398_at	auxin-induced basic helix-loop-h	---	AT1G58100	1.19	0.25	1.95	0.0932881	0.296737	-4.86	FALSE
251556_at	putative protein predicted protei	---	AT3G58840	-1.35	-0.44	-1.95	0.0932877	0.296737	-4.86	FALSE
247459_at	putative protein embryo-specific	---	AT5G62200	-1.25	-0.32	-1.95	0.0933724	0.2967891	-4.86	FALSE
254132_at	putative protein hypothetical pro	ATHB22	AT4G24660	-1.42	-0.50	-1.95	0.0933294	0.2967891	-4.86	FALSE

248998_at	unknown protein	---	AT5G45320	1.22	0.29	1.95	0.093414	0.2967891	-4.86	FALSE
246232_at	hypothetical protein	EMB2754	AT4G36630	-1.24	-0.31	-1.95	0.0933949	0.2967891	-4.86	FALSE
258404_at	ribosomal protein L3	RPL3P	AT3G17465	-1.31	-0.38	-1.95	0.0934323	0.2967891	-4.86	FALSE
249666_at	phytochrome C (sp|P14714)	PHYC	AT5G35840	-1.32	-0.40	-1.95	0.0933716	0.2967891	-4.86	FALSE
252252_at	putative protein GTP-binding pro	RID3	AT3G49180	-1.53	-0.62	-1.95	0.0934346	0.2967891	-4.86	FALSE
267016_at	hypothetical protein predicted by	---	AT2G39160 /	1.24	0.31	1.95	0.0934172	0.2967891	-4.86	FALSE
252675_at	putative protein hypothetical prot	---	---	1.23	0.30	1.95	0.0933472	0.2967891	-4.86	FALSE
250548_at	myosin heavy chain-like protein	MBP2C	AT5G08120	-1.26	-0.33	-1.95	0.0933852	0.2967891	-4.86	FALSE
252899_at	putative protein leaf protein, lpo	---	AT4G39530	-1.27	-0.34	-1.95	0.09346	0.2968285	-4.86	FALSE
259495_at	NBS/LRR disease resistance pr	---	AT1G15890	1.29	0.37	1.95	0.0934872	0.2968737	-4.87	FALSE
255947_at	hypothetical protein contains Pfa	---	AT1G22040	-1.24	-0.31	-1.95	0.0935187	0.2969322	-4.87	FALSE
251821_at	protein phosphatase 2C - like pr	---	AT3G55050	1.57	0.65	1.95	0.0936488	0.2972213	-4.87	FALSE
260553_at	unknown protein similar to T11A	---	AT2G41800	1.22	0.29	1.95	0.0936415	0.2972213	-4.87	FALSE
249747_at	putative protein similar to unknov	---	AT5G24600	1.29	0.37	1.95	0.0936376	0.2972213	-4.87	FALSE
261570_at	fatty acid elongase 3-ketoacyl-C	KCS1	AT1G01120	2.74	1.45	1.95	0.0937278	0.2973175	-4.87	TRUE
252286_at	putative protein	---	AT3G49070	1.18	0.24	1.95	0.0937442	0.2973175	-4.87	FALSE
252174_at	putative protein APRIL protein, H	---	AT3G50690	-1.20	-0.27	-1.95	0.0937528	0.2973175	-4.87	FALSE
261390_at	hypothetical protein similar to hy	---	AT1G35040	1.21	0.28	1.95	0.0937573	0.2973175	-4.87	FALSE
265457_at	unknown protein ; supported by	---	AT2G46550	-1.32	-0.40	-1.95	0.0937241	0.2973175	-4.87	FALSE
260411_at	hypothetical protein similar to GE	---	AT1G69890	1.62	0.69	1.95	0.0937165	0.2973175	-4.87	FALSE
260025_at	unknown protein ;supported by fu	---	AT1G30070	-1.43	-0.52	-1.95	0.0938023	0.2974186	-4.87	FALSE
260200_at	unknown protein ; supported by	---	AT1G67620	-1.26	-0.33	-1.95	0.0938175	0.2974256	-4.87	FALSE
254358_at	putative protein light induced pro	---	AT4G22310	-1.18	-0.24	-1.95	0.0938535	0.2974572	-4.87	FALSE
250503_at	putative protein similar to unknov	---	AT5G09820	-1.37	-0.46	-1.95	0.0938439	0.2974572	-4.87	FALSE
262058_at	Expressed protein ; supported by	---	AT1G79990	1.19	0.25	1.95	0.0939449	0.2974738	-4.87	FALSE
245543_at	glucosyltransferase	---	AT4G15260	1.29	0.37	1.95	0.0939027	0.2974738	-4.87	FALSE
245386_at	hypothetical protein ;supported b	RALFL32	AT4G14010	1.68	0.75	1.95	0.0939346	0.2974738	-4.87	FALSE
262974_at	hypothetical protein predicted by	---	AT1G75550	-1.24	-0.31	-1.95	0.093938	0.2974738	-4.87	FALSE
258758_at	putative RING zinc finger protein	---	AT3G10810	-1.40	-0.49	-1.95	0.0939494	0.2974738	-4.87	FALSE
255993_at	hypothetical protein contains sim	---	AT1G29770	1.21	0.27	1.95	0.0939124	0.2974738	-4.87	FALSE
245936_at	putative protein predicted protein	---	AT5G19850	1.33	0.41	1.95	0.0939501	0.2974738	-4.87	FALSE
264591_at	hypothetical protein contains sim	---	AT2G17670	-1.25	-0.32	-1.95	0.0940396	0.2975506	-4.87	FALSE
262066_at	hypothetical protein contains sim	---	AT1G79950	-1.51	-0.60	-1.95	0.0940358	0.2975506	-4.87	FALSE
265967_at	nodulin-like protein ; supported b	---	AT2G37450	-1.36	-0.44	-1.95	0.0940188	0.2975506	-4.87	FALSE
259956_at	unknown protein ;supported by f	RRA2	AT1G75110	-1.23	-0.30	-1.95	0.0940186	0.2975506	-4.87	FALSE

249316_s_a	glutathione transferase-like ;supp	ATGSTT2	AT5G41220 /	-1.25	-0.32	-1.95	0.0939888	0.2975506	-4.87	FALSE
256657_at	unknown protein contains similar	---	AT3G18860	-1.24	-0.31	-1.95	0.0940724	0.2976048	-4.87	FALSE
249380_at	glutaredoxin -like protein glutare	---	AT5G40370	1.21	0.28	1.95	0.0940828	0.2976048	-4.87	FALSE
252741_at	putative protein predicted protei	---	AT3G43280	-1.22	-0.29	-1.95	0.0941302	0.2977136	-4.87	FALSE
259368_at	aspartic protease, putative simila	---	AT1G69100	1.23	0.30	1.95	0.094164	0.297748	-4.87	FALSE
252736_at	kinesin -like protein kinesin-like	TES	AT3G43210	1.23	0.30	1.95	0.0941672	0.297748	-4.87	FALSE
253926_at	hnRNP-like protein ; supported b	---	AT4G26650	1.23	0.29	1.95	0.0941817	0.2977527	-4.87	TRUE
258171_at	unknown protein	---	AT3G21610	1.25	0.32	1.95	0.0942401	0.2977986	-4.87	FALSE
252445_at	beta-D-glucan exohydrolase - lik	---	AT3G47000	-1.25	-0.32	-1.95	0.0942485	0.2977986	-4.87	FALSE
251953_at	putative protein predicted protei	CPuORF51	AT3G53668 /	-1.29	-0.37	-1.95	0.0942128	0.2977986	-4.87	FALSE
262617_at	unknown protein	POR C	AT1G03630 /	-1.23	-0.30	-1.95	0.0942394	0.2977986	-4.87	FALSE
259435_at	hypothetical protein similar to put	---	AT1G01450	1.21	0.27	1.95	0.0942873	0.29788	-4.87	FALSE
256273_at	senescence-assocated protein,	TET6	AT3G12090	-1.29	-0.37	-1.95	0.0943599	0.2980547	-4.87	FALSE
246279_at	homeodomain protein	ATHB40	AT4G36740	1.35	0.43	1.95	0.0943688	0.2980547	-4.87	FALSE
267299_at	putative glucosyltransferase	---	AT2G30150	-1.33	-0.41	-1.95	0.0944312	0.2981562	-4.87	FALSE
250107_at	ids-4 protein - like ids-4 protein,	SPX4	AT5G15330	-1.38	-0.47	-1.95	0.0944401	0.2981562	-4.87	FALSE
266968_at	putative protein kinase contains a	---	AT2G39360	1.69	0.76	1.95	0.0944193	0.2981562	-4.87	FALSE
255433_at	putative xyloglucan endotransgly	XTH9	AT4G03210	-1.66	-0.73	-1.95	0.0944624	0.2981725	-4.88	TRUE
262072_at	hypothetical protein predicted by	ZCF37	AT1G59590	1.75	0.81	1.95	0.0944714	0.2981725	-4.88	FALSE
259099_at	unknown protein similar to GB:A	---	AT3G05010	-1.25	-0.33	-1.94	0.0945725	0.2984503	-4.88	FALSE
247037_at	putative protein similar to unknov	RALFL34	AT5G67070	2.95	1.56	1.94	0.0946366	0.29857	-4.88	TRUE
267231_at	putative inositol polyphosphate 5	---	AT2G43900	-1.25	-0.32	-1.94	0.0946344	0.29857	-4.88	FALSE
248457_at	putative protein contains similarit	---	AT5G51420	1.35	0.43	1.94	0.0946527	0.2985795	-4.88	FALSE
262807_at	unknown protein strong similarity	---	AT1G11740	1.33	0.41	1.94	0.0947091	0.2986812	-4.88	FALSE
249238_at	GAMM1 protein-like ; supported	---	AT5G41970	-1.24	-0.31	-1.94	0.0947112	0.2986812	-4.88	FALSE
266838_at	similar to jasmonate-inducible pr	---	AT2G25980	1.24	0.31	1.94	0.0947316	0.2987044	-4.88	FALSE
254870_at	KI domain interacting kinase 1 -l	---	AT4G11900	1.55	0.63	1.94	0.0947851	0.2988319	-4.88	FALSE
252053_at	syntaxin-like protein synt4 ;supp	SYP122	AT3G52400	2.02	1.02	1.94	0.0948035	0.2988486	-4.88	FALSE
262977_at	transcription factor, putative sim	---	AT1G75490	-1.29	-0.36	-1.94	0.0948171	0.29885	-4.88	FALSE
256589_at	cytochrome P450, putative conta	CYP81D1	AT3G28740	3.06	1.61	1.94	0.0948369	0.2988523	-4.88	TRUE
264217_at	hypothetical protein predicted by	---	AT1G60190	2.73	1.45	1.94	0.094844	0.2988523	-4.88	FALSE
247214_at	putative protein similar to unknov	---	AT5G64850	-1.78	-0.84	-1.94	0.0948823	0.2989231	-4.88	TRUE
260582_at	hypothetical protein predicted by	---	AT2G47200	1.28	0.35	1.94	0.0948927	0.2989231	-4.88	FALSE
262074_at	glutathione S-transferase, putati	ATGSTU15	AT1G59670	-1.48	-0.56	-1.94	0.0949878	0.2991814	-4.88	TRUE
267362_at	hypothetical protein predicted by	---	AT2G39910	-1.20	-0.27	-1.94	0.0950115	0.2992146	-4.88	FALSE

258551_at	hypothetical protein predicted by	---	AT3G06890	1.19	0.25	1.94	0.0950596	0.2993249	-4.88	FALSE
249862_at	PGPD14 protein ;supported by f	---	AT5G22920	1.60	0.68	1.94	0.0950971	0.2994018	-4.88	FALSE
260679_at	unknown protein	---	AT1G07990	-1.21	-0.28	-1.94	0.0951558	0.2995038	-4.88	FALSE
250973_at	60S ribosomal protein - like 60S	---	AT5G02870	-1.50	-0.59	-1.94	0.0951483	0.2995038	-4.88	FALSE
251214_at	putative protein hypothetical prot	---	AT3G62500	1.24	0.31	1.94	0.0952189	0.2996286	-4.88	FALSE
260513_at	cyanogenic beta-glucosidase, pu	BGLU36	AT1G51490	1.23	0.30	1.94	0.0952217	0.2996286	-4.88	FALSE
249798_at	putative protein contains similarit	---	AT5G23730	1.22	0.29	1.94	0.0952665	0.2997281	-4.88	FALSE
250147_at	putative protein predicted protei	---	AT5G14600	-1.40	-0.48	-1.94	0.095309	0.2997793	-4.88	FALSE
266615_s_a	putative monooxygenase ;suppo	CTF2A	AT2G29720 ///	2.19	1.13	1.94	0.0953069	0.2997793	-4.88	FALSE
245755_at	hypothetical protein predicted by	---	AT1G35210	3.71	1.89	1.94	0.0953234	0.299783	-4.88	FALSE
249807_at	pectinacetylesterase	---	AT5G23870	-1.38	-0.47	-1.94	0.0953957	0.2999277	-4.88	TRUE
259209_at	putative RNA-binding protein ide	---	AT3G09160	1.18	0.24	1.94	0.0953933	0.2999277	-4.88	FALSE
247248_at	putative protein contains similarit	---	AT5G64560	1.48	0.56	1.94	0.0954144	0.2999454	-4.88	FALSE
261496_at	ethylene responsive element bir	ERF12	AT1G28360	1.28	0.35	1.94	0.0954914	0.300146	-4.89	FALSE
250617_at	Mei2-like protein Mei2-like prote	AML4	AT5G07290	1.29	0.37	1.94	0.095514	0.3001755	-4.89	FALSE
264295_at	hypothetical protein predicted by	---	AT1G78740	1.19	0.25	1.94	0.095531	0.3001877	-4.89	FALSE
246343_at	putative protein	---	AT3G56720	-1.18	-0.23	-1.94	0.0956066	0.3003838	-4.89	FALSE
AFFX-r2-At-	Arabidopsis thaliana /REF=U849	---	---	1.18	0.24	1.94	0.0956543	0.3004508	-4.89	FALSE
261401_at	kinase, putative similar to Ste-20	---	AT1G79640	-1.33	-0.41	-1.94	0.0956509	0.3004508	-4.89	FALSE
260950_s_a	delta 9 desaturase, putative sim	---	AT1G06090 ///	1.29	0.37	1.94	0.0956773	0.3004818	-4.89	FALSE
248177_at	putative protein strong similarity t	---	AT5G54630	-1.22	-0.29	-1.94	0.0957267	0.3005955	-4.89	FALSE
259766_at	unknown protein ;supported by fu	---	AT1G64360	1.49	0.57	1.94	0.0957479	0.3006207	-4.89	TRUE
257372_at	hypothetical protein predicted by	---	AT2G43220	1.22	0.29	1.94	0.0957702	0.3006493	-4.89	FALSE
254080_at	fibrillarin 2 (AtFib2) identical to fit	FIB2	AT4G25630	-1.87	-0.90	-1.94	0.0958419	0.300772	-4.89	FALSE
261162_at	hypothetical protein predicted by	---	AT1G34440	1.29	0.37	1.94	0.0958448	0.300772	-4.89	FALSE
255333_at	putative polyprotein	---	---	1.21	0.28	1.94	0.0958488	0.300772	-4.89	FALSE
266942_at	putative ATP binding protein	TXND9	AT2G18990	-1.43	-0.51	-1.93	0.0959267	0.3009748	-4.89	FALSE
248010_at	peroxisomal targeting signal type	PEX5	AT5G56290	-1.21	-0.27	-1.93	0.0959732	0.3009965	-4.89	FALSE
253984_at	isp4 like protein isp4 protein -Sc	OPT5	AT4G26590	1.26	0.34	1.93	0.0959666	0.3009965	-4.89	FALSE
245894_at	putative protein ; supported by fu	---	AT5G09310	-1.21	-0.28	-1.93	0.0959719	0.3009965	-4.89	FALSE
253349_at	putative protein	---	---	-1.20	-0.27	-1.93	0.0960754	0.3012758	-4.89	FALSE
249337_at	putative protein contains similarit	---	AT5G41080	2.31	1.21	1.93	0.0961459	0.3014554	-4.89	FALSE
253886_at	cytochrome P450 - like protein c	CYP709B3	AT4G27710	-1.22	-0.29	-1.93	0.0962079	0.3015668	-4.89	FALSE
255763_at	hypothetical protein predicted by	---	AT1G16730	-1.30	-0.38	-1.93	0.0962006	0.3015668	-4.89	FALSE
252411_at	putative protein PMP31 protein -	PEX11B	AT3G47430	-1.58	-0.66	-1.93	0.0962263	0.301576	-4.89	TRUE

AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.48	-0.57	-1.93	0.0962373	0.301576	-4.89	FALSE
258166_at	WD-repeat protein, putative con	---	AT3G21540	-1.56	-0.64	-1.93	0.0963234	0.3017866	-4.89	FALSE
258460_at	unknown protein	ECT6	AT3G17330	-1.31	-0.39	-1.93	0.0963309	0.3017866	-4.89	FALSE
251654_at	putative protein several hypothet	SDP1-LIKE	AT3G57140	1.21	0.28	1.93	0.096379	0.3018959	-4.89	FALSE
251437_at	putative protein hypothetical pro	---	AT3G59910	-1.21	-0.27	-1.93	0.0963945	0.3018965	-4.89	FALSE
261633_at	hypothetical protein predicted by	---	AT1G49930	-1.22	-0.29	-1.93	0.0964057	0.3018965	-4.89	FALSE
263154_at	Expressed protein ; supported by	---	AT1G54110	-1.30	-0.38	-1.93	0.0964536	0.3020051	-4.89	FALSE
247645_at	late embryonic abundant protein	---	AT5G60530	1.23	0.30	1.93	0.0964694	0.3020131	-4.90	FALSE
246459_at	receptor protein kinase -like prot	---	AT5G16900	1.23	0.30	1.93	0.0965122	0.3021057	-4.90	FALSE
267224_at	hypothetical protein predicted by	---	AT2G43990	-1.30	-0.38	-1.93	0.0966049	0.3023127	-4.90	FALSE
252956_at	farnesylated protein (ATFP6) ; s	ATFP6	AT4G38580	-1.73	-0.79	-1.93	0.0966008	0.3023127	-4.90	FALSE
266868_at	hypothetical protein predicted by	---	AT2G44630	-1.23	-0.30	-1.93	0.0966272	0.302341	-4.90	FALSE
253757_at	rac GTP binding protein Arac7 ;	ROP9	AT4G28950	1.28	0.36	1.93	0.0967326	0.302422	-4.90	FALSE
255276_at	putative fatty acid desaturase si	DES-1-LIKE	AT4G04930	1.21	0.28	1.93	0.0967186	0.302422	-4.90	FALSE
256296_at	hypothetical protein	---	AT1G69480	1.21	0.28	1.93	0.0967273	0.302422	-4.90	FALSE
257327_at	hypothetical protein	---	---	1.46	0.55	1.93	0.0967017	0.302422	-4.90	FALSE
262329_at	hypothetical protein similar to hy	---	AT1G64090	-1.20	-0.27	-1.93	0.0966894	0.302422	-4.90	FALSE
249271_at	myosin heavy chain-like protein	CIP1	AT5G41790	-1.41	-0.50	-1.93	0.0967065	0.302422	-4.90	FALSE
255261_s_a	putative protein equilibrative nuc	FUR1	AT4G05110 /A	1.84	0.88	1.93	0.096769	0.3024942	-4.90	FALSE
258952_at	putative RNase H contains Pfam	---	AT3G01410	1.29	0.37	1.93	0.0967951	0.3025344	-4.90	FALSE
255923_at	hypothetical protein contains Pfa	---	AT1G22180	1.81	0.86	1.93	0.0968291	0.3025994	-4.90	TRUE
258637_at	putative RHO GDP-dissociation i	---	AT3G07880	-1.30	-0.38	-1.93	0.0968574	0.302645	-4.90	FALSE
267412_at	putative vacuolar sorting recepto	---	AT2G34940	1.95	0.96	1.93	0.0968703	0.302645	-4.90	FALSE
257086_at	hypothetical protein predicted by	---	AT3G20490	-1.38	-0.47	-1.93	0.0969033	0.3026652	-4.90	FALSE
252995_at	hypothetical protein ;supported b	---	AT4G38370	-1.31	-0.39	-1.93	0.0969013	0.3026652	-4.90	FALSE
263533_at	putative Rieske iron-sulfur protei	TIC55	AT2G24820	-1.18	-0.24	-1.93	0.0970062	0.3027097	-4.90	FALSE
257002_at	oligouridylate binding protein, pu	---	AT3G14100	-1.32	-0.40	-1.93	0.0969608	0.3027097	-4.90	FALSE
246921_at	putative protein small unique nu	---	AT5G25080	-1.39	-0.48	-1.93	0.0969823	0.3027097	-4.90	FALSE
254537_at	putative protein chitinase / lysoz	---	AT4G19730	1.26	0.34	1.93	0.0970295	0.3027097	-4.90	FALSE
249133_at	putative protein strong similarity	TAF4	AT5G43130	-1.19	-0.26	-1.93	0.0969714	0.3027097	-4.90	FALSE
246428_at	spindle pole body protein-like sp	---	AT5G17410	-1.31	-0.39	-1.93	0.0970078	0.3027097	-4.90	FALSE
263935_at	unknown protein	PUB23	AT2G35930	3.82	1.93	1.93	0.0969344	0.3027097	-4.90	FALSE
267142_at	putative ammonium transporter	ATAMT2	AT2G38290	1.52	0.60	1.93	0.097037	0.3027097	-4.90	FALSE
258784_at	unknown protein	---	AT3G11770	-1.45	-0.53	-1.93	0.0970131	0.3027097	-4.90	FALSE
266500_at	Expressed protein ; supported by	PLA2-ALPH	AT2G06925	-1.47	-0.56	-1.93	0.097052	0.3027153	-4.90	FALSE

254818_at	pEARLI 1-like protein Arabidops	---	AT4G12470	-2.51	-1.33	-1.93	0.0970894	0.302769	-4.90	FALSE
267288_at	similar to cold acclimation protein	---	AT2G23680	2.02	1.02	1.93	0.0970958	0.302769	-4.90	FALSE
252071_at	putative protein DNA helicase h	---	AT3G51690	1.18	0.24	1.93	0.0971561	0.3029157	-4.90	FALSE
246402_at	jasmonate inducible protein, put	---	AT1G57570	1.20	0.26	1.93	0.0972198	0.3030313	-4.90	FALSE
250868_at	malate synthase -like protein ma	MLS	AT5G03860	-1.39	-0.47	-1.93	0.0972103	0.3030313	-4.90	FALSE
266995_at	putative cytochrome P450	CYP710A1	AT2G34500	2.59	1.37	1.93	0.097263	0.3030833	-4.90	TRUE
247060_at	succinate dehydrogenase flavopr	SDH1-1	AT5G66760	1.95	0.96	1.93	0.0972533	0.3030833	-4.90	FALSE
256744_at	ATHP2, putative similar to ATHF	AHP2	AT3G29350	-1.29	-0.37	-1.92	0.0973326	0.3032173	-4.90	FALSE
253487_at	ribosomal protein S6 - like ribos	RPS6	AT4G31700	-1.76	-0.81	-1.92	0.0973232	0.3032173	-4.90	FALSE
266710_at	putative Ser/Thr protein kinase	---	AT2G46850	1.24	0.31	1.92	0.097355	0.3032455	-4.90	FALSE
245247_at	scarecrow-like 13 (SCL13) ; supp	SCL13	AT4G17230	1.82	0.87	1.92	0.0973996	0.303343	-4.90	FALSE
259644_at	unknown protein	---	AT1G68910	-1.30	-0.38	-1.92	0.0974237	0.3033767	-4.90	FALSE
258914_at	hypothetical protein predicted by	AGP27	AT3G06360	1.20	0.27	1.92	0.0974833	0.3035204	-4.91	FALSE
259307_at	unknown protein similar to MICR	---	AT3G05230	1.33	0.41	1.92	0.0974965	0.3035204	-4.91	FALSE
247825_at	RNA/ssDNA-binding protein - lik	TAF15b	AT5G58470	1.27	0.34	1.92	0.0975426	0.3036227	-4.91	FALSE
265916_at	hypothetical protein similar to En	---	---	1.23	0.30	1.92	0.0975891	0.3037038	-4.91	FALSE
245594_at	acylaminoacyl-peptidase like pro	---	AT4G14570	-1.39	-0.47	-1.92	0.0975953	0.3037038	-4.91	FALSE
249143_at	putative protein strong similarity t	---	AT5G43230	1.19	0.25	1.92	0.097674	0.3038537	-4.91	FALSE
263601_s_a	dihydrofolate reductase-thymidyl	THY-1	AT2G16370 ///	-1.33	-0.41	-1.92	0.0976834	0.3038537	-4.91	FALSE
265842_at	putative AP2 domain transcriptio	ERF38	AT2G35700	-1.61	-0.69	-1.92	0.09766	0.3038537	-4.91	FALSE
264356_at	putative DNA repair protein Stror	UVH6	AT1G03190	-1.23	-0.30	-1.92	0.0977702	0.3040559	-4.91	FALSE
266040_at	hypothetical protein	---	AT2G07738	1.20	0.26	1.92	0.0977751	0.3040559	-4.91	FALSE
253029_at	hypothetical protein	FRS9	AT4G38170	-1.59	-0.67	-1.92	0.0978082	0.3041175	-4.91	FALSE
258908_at	putative dehydroquinase shikima	MEE32	AT3G06350	1.37	0.45	1.92	0.0978408	0.3041774	-4.91	FALSE
259958_at	leucine-rich repeat transmembra	SRF6	AT1G53730	-1.26	-0.33	-1.92	0.0978806	0.3042594	-4.91	TRUE
265538_at	unknown protein predicted by ge	---	AT2G15860	-1.34	-0.42	-1.92	0.0979221	0.3042753	-4.91	FALSE
265628_at	hypothetical protein predicted by	---	AT2G27290	-1.45	-0.54	-1.92	0.0979164	0.3042753	-4.91	FALSE
266739_at	unknown protein predicted by ge	---	AT2G46730	-1.24	-0.31	-1.92	0.0979257	0.3042753	-4.91	FALSE
253090_at	beta-galactosidase like protein ;	BGAL3	AT4G36360	2.52	1.33	1.92	0.0979523	0.3043165	-4.91	FALSE
252167_at	putative protein steroid dehydro	---	AT3G50560	-1.28	-0.36	-1.92	0.0980344	0.3044841	-4.91	TRUE
266374_at	putative retroelement pol polypro	---	---	1.32	0.40	1.92	0.0980275	0.3044841	-4.91	FALSE
261756_at	Expressed protein ; supported by	---	AT1G08315	1.59	0.67	1.92	0.0980487	0.3044841	-4.91	FALSE
261344_at	hypothetical protein similar to hy	---	AT1G79710	1.23	0.30	1.92	0.0980596	0.3044841	-4.91	FALSE
257092_at	unknown protein	DDL	AT3G20550	-1.33	-0.41	-1.92	0.0980959	0.3045552	-4.91	FALSE
264341_at	hypothetical protein predicted by	---	AT1G70270	1.20	0.26	1.92	0.0981313	0.3045821	-4.91	FALSE

264265_at	unknown protein ; supported by	---	AT1G09280	-1.31	-0.39	-1.92	0.0981294	0.3045821	-4.91	FALSE
245211_at	putative protein similarity to sec1	SEC10	AT5G12370	-1.19	-0.25	-1.92	0.0982101	0.3047855	-4.91	FALSE
246332_at	putative protein phosphatidylcho	---	AT3G44830	1.31	0.39	1.92	0.0982467	0.3048575	-4.91	FALSE
246906_at	Expressed protein ; supported by	---	AT5G25475	-1.23	-0.30	-1.92	0.098274	0.3049007	-4.91	FALSE
253373_at	lysine-ketoglutarate reductase/sa	---	AT4G33150	1.87	0.90	1.92	0.098305	0.3049555	-4.91	TRUE
259802_at	thionin identical to GI:1181531 fr	THI2.1	AT1G72260	3.77	1.91	1.92	0.0983238	0.3049723	-4.91	FALSE
263260_at	putative protein-tyrosine phosph	OTS2	AT1G10570	-1.21	-0.28	-1.92	0.0983464	0.3050009	-4.91	FALSE
263496_at	unknown protein ; supported by	---	AT2G42570	-1.34	-0.42	-1.92	0.0983781	0.3050576	-4.91	FALSE
264294_at	hypothetical protein similar to hea	---	AT1G78750	-1.24	-0.31	-1.92	0.0983961	0.305072	-4.91	FALSE
253777_at	SOF1 protein-like protein SOF1 (	---	AT4G28450	-1.72	-0.78	-1.92	0.098431	0.3051041	-4.91	TRUE
245611_at	hypothetical protein	---	AT4G14390	1.38	0.46	1.92	0.0984464	0.3051041	-4.91	FALSE
263994_at	putative VSF-1-like b-ZIP transcr	---	AT2G12900	1.20	0.26	1.92	0.0984466	0.3051041	-4.91	FALSE
245333_at	Expressed protein ; supported by	---	AT4G14615	-1.18	-0.24	-1.92	0.0984616	0.3051092	-4.91	FALSE
256982_at	unknown protein	ECT2	AT3G13460	-1.24	-0.31	-1.92	0.0984768	0.3051148	-4.91	FALSE
251169_at	putative protein putative protein	MARD1	AT3G63210	-1.63	-0.70	-1.92	0.0985643	0.3051373	-4.92	TRUE
247108_at	ReMembR-H2 protein JR700 (gb	RMR1	AT5G66160	-1.28	-0.36	-1.92	0.0985149	0.3051373	-4.92	FALSE
260614_at	hypothetical protein contains Pfa	---	AT1G53390	1.20	0.26	1.92	0.098551	0.3051373	-4.92	FALSE
265323_at	putative syntaxin	SYP112	AT2G18260	-1.33	-0.41	-1.92	0.0985294	0.3051373	-4.92	FALSE
258369_at	putative pectin methylesterase si	ATPME3	AT3G14310	-1.28	-0.36	-1.92	0.0985425	0.3051373	-4.92	FALSE
258378_at	hypothetical protein contains sim	---	AT3G17490	1.21	0.28	1.92	0.0985096	0.3051373	-4.92	FALSE
255281_at	contains similarity to glucan synt	GSL1	AT4G04970	1.18	0.24	1.92	0.098583	0.3051538	-4.92	FALSE
267008_at	putative ABC transporter	---	AT2G39350	1.42	0.50	1.92	0.0986159	0.3052141	-4.92	TRUE
247855_at	similar to unknown protein (sp|P2	---	AT5G58210	-1.33	-0.41	-1.92	0.0986501	0.3052217	-4.92	FALSE
259441_at	cathepsin B-like cysteine protea	---	AT1G02300	-1.31	-0.39	-1.92	0.0986718	0.3052217	-4.92	FALSE
246655_at	hypothetical protein	---	AT5G35230	1.23	0.30	1.92	0.0986683	0.3052217	-4.92	FALSE
262477_at	hypothetical protein contains sim	---	AT1G11220	1.38	0.47	1.92	0.0986661	0.3052217	-4.92	FALSE
265858_at	putative ribophorin I	---	AT2G01720	-1.30	-0.38	-1.92	0.0986992	0.305265	-4.92	FALSE
263350_at	alanine-glyoxylate aminotransfer	AGT	AT2G13360	-1.40	-0.49	-1.91	0.0987227	0.3052963	-4.92	FALSE
259254_at	putative P-protein: chorismate m	ADT2	AT3G07630	-1.27	-0.35	-1.91	0.0987412	0.305312	-4.92	FALSE
266526_at	putative tetracycline transporter p	---	AT2G16980	1.27	0.34	1.91	0.0987797	0.3053896	-4.92	FALSE
248099_at	DNA topoisomerase I (sp P3018	TOP1ALPH	AT5G55300	-1.21	-0.27	-1.91	0.0988237	0.3054543	-4.92	FALSE
245283_at	Expressed protein ; supported by	AT-HSFA5	AT4G13980	1.26	0.33	1.91	0.0988274	0.3054543	-4.92	FALSE
251851_at	structural maintenance of chrom	TTN8	AT3G54670	-1.25	-0.32	-1.91	0.0988862	0.3055569	-4.92	FALSE
253626_at	F-box protein family, AtFBL19 co	---	AT4G30640	1.44	0.53	1.91	0.0988874	0.3055569	-4.92	FALSE
245855_at	sulfate transporter ; supported b	SULTR4;1	AT5G13550	1.37	0.45	1.91	0.0989041	0.305567	-4.92	FALSE

253482_at	Expressed protein ; supported by	---	AT4G31985	-1.74	-0.80	-1.91	0.0989332	0.30561	-4.92	FALSE
254385_s_a	putative protein CGI-131 protein	ATMSRB7	AT4G21830 /	5.93	2.57	1.91	0.0989447	0.30561	-4.92	FALSE
262350_at	putative glutathione peroxidase	ATGPX4	AT2G48150	1.23	0.29	1.91	0.0989843	0.3056907	-4.92	FALSE
258906_at	unknown protein similar to C-ter	ATTLP9	AT3G06380	-1.29	-0.36	-1.91	0.0990024	0.3057023	-4.92	FALSE
264907_at	unknown protein similar to S.pon	---	AT2G17280	1.82	0.87	1.91	0.0990221	0.3057023	-4.92	FALSE
259900_at	c-Jun coactivator-like protein (AJ	CSN5B	AT1G71230	-1.19	-0.25	-1.91	0.0990282	0.3057023	-4.92	FALSE
256584_at	unknown protein	---	AT3G28750	1.22	0.29	1.91	0.0990493	0.3057258	-4.92	FALSE
259373_at	hypothetical protein predicted by	---	AT1G69160	1.72	0.78	1.91	0.0991107	0.3058327	-4.92	FALSE
252775_s_a	putative protein various predicte	---	---	-1.23	-0.30	-1.91	0.0990997	0.3058327	-4.92	FALSE
261698_at	unknown protein identical to hyp	---	AT1G32630	-1.30	-0.38	-1.91	0.0991387	0.3058615	-4.92	FALSE
249116_at	putative protein similar to unknov	---	AT5G43820 /	-1.31	-0.39	-1.91	0.0991469	0.3058615	-4.92	FALSE
266779_at	putative ligand-gated ion channe	ATGLR2.9	AT2G29100	1.28	0.35	1.91	0.0991823	0.3059295	-4.92	FALSE
248676_at	putative protein similar to unknov	ATSDI1	AT5G48850	-2.18	-1.12	-1.91	0.0992326	0.3060108	-4.92	TRUE
256289_s_a	serine carboxypeptidase, putativ	scpl14	AT3G12230 /	1.71	0.78	1.91	0.0992355	0.3060108	-4.92	FALSE
256148_at	hypothetical protein similar to put	---	AT1G55090	-1.19	-0.25	-1.91	0.0992824	0.3061139	-4.92	FALSE
247489_at	carbonyl reductase - like protein	---	AT5G61830	-1.27	-0.34	-1.91	0.0993306	0.30618	-4.92	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U849	---	---	1.27	0.34	1.91	0.0993272	0.30618	-4.92	FALSE
251012_at	putative protein ;supported by fu	---	AT5G02580	-3.14	-1.65	-1.91	0.0993586	0.3062247	-4.92	FALSE
266852_at	hypothetical protein predicted by	---	AT2G26810	-1.23	-0.30	-1.91	0.0994302	0.3064042	-4.92	FALSE
258847_at	unknown protein ; supported by	---	AT3G03100	-1.20	-0.27	-1.91	0.0994841	0.3064047	-4.92	FALSE
265941_s_a	recA, putative similar to GB:CAA	---	AT2G19490 /	-1.42	-0.51	-1.91	0.0994758	0.3064047	-4.92	FALSE
262490_at	hypothetical protein predicted by	UREF	AT1G21840	-1.31	-0.38	-1.91	0.099448	0.3064047	-4.92	FALSE
248002_at	Expressed protein ; supported by	ATARP8	AT5G56180	1.35	0.43	1.91	0.099469	0.3064047	-4.92	FALSE
252673_at	CCR4-associated factor 1-like p	---	AT3G44240	1.24	0.30	1.91	0.0995189	0.3064704	-4.92	FALSE
259175_at	unknown protein	---	AT3G01560	-1.29	-0.37	-1.91	0.0995601	0.3065559	-4.93	FALSE
257124_at	hexokinase, putative similar to h	ATHXK4	AT3G20040	1.24	0.31	1.91	0.0996797	0.3068412	-4.93	FALSE
247500_at	putative protein B2 protein, Dau	---	AT5G61910	1.38	0.47	1.91	0.0996712	0.3068412	-4.93	FALSE
248201_at	putative protein similar to unknov	PTAC15	AT5G54180	-1.58	-0.66	-1.91	0.0996943	0.306845	-4.93	FALSE
244906_at	hypothetical protein	---	ATMG00690	1.23	0.30	1.91	0.0997956	0.307038	-4.93	FALSE
255058_s_a	putative protein various hypothe	---	---	1.19	0.25	1.91	0.0997737	0.307038	-4.93	FALSE
258163_at	aldose 1-epimerase, putative sir	---	AT3G17940	-1.23	-0.29	-1.91	0.0997974	0.307038	-4.93	FALSE
252073_at	hypothetical protein	---	AT3G51750	-2.32	-1.21	-1.91	0.0998176	0.3070585	-4.93	FALSE
263306_at	putative serine carboxypeptidase	SCPL43	AT2G12480	1.22	0.29	1.91	0.0999042	0.3072834	-4.93	FALSE
251163_at	putative protein S1R protein - H	---	AT3G63310	1.19	0.25	1.91	0.0999628	0.3074224	-4.93	FALSE
260416_at	putative cullin similar to cullin 3 C	CUL3B	AT1G69670	-1.23	-0.30	-1.91	0.0999798	0.3074331	-4.93	FALSE

251176_at	Ca2+-transporting ATPase -like	---	AT3G63380	2.21	1.14	1.91	0.1000448	0.3075503	-4.93	TRUE
253809_at	putative (1-4)-beta-mannan end	---	AT4G28320	-1.34	-0.43	-1.91	0.1000401	0.3075503	-4.93	FALSE
264150_at	unknown protein similar to FUS5	FUS5	AT1G02090	1.21	0.27	1.91	0.1000715	0.3075908	-4.93	FALSE
263047_at	putative phosphoserine aminotra	---	AT2G17630	-1.57	-0.65	-1.91	0.100115	0.3076	-4.93	FALSE
248204_at	myosin heavy chain	ATM2	AT5G54280	1.32	0.40	1.91	0.1001099	0.3076	-4.93	FALSE
260158_at	unknown protein	---	AT1G79910	1.26	0.33	1.91	0.1001054	0.3076	-4.93	FALSE
257994_at	unknown protein	---	AT3G19920	1.36	0.44	1.91	0.1001451	0.3076511	-4.93	FALSE
262230_at	alpha-xylosidase precursor ident	XYL1	AT1G68560	-1.65	-0.73	-1.90	0.1001785	0.3076709	-4.93	FALSE
249436_at	putative protein crp1 protein - Ze	---	AT5G39980	-1.40	-0.49	-1.90	0.1001651	0.3076709	-4.93	FALSE
244902_at	NADH dehydrogenase subunit 4	---	ATMG00650	1.27	0.35	1.90	0.1002885	0.3079672	-4.93	TRUE
262135_at	AP2 domain containing protein,	RAP2.4	AT1G78080	1.53	0.61	1.90	0.1003153	0.3080081	-4.93	FALSE
258736_at	unknown protein	---	AT3G05900	-1.41	-0.49	-1.90	0.1003437	0.3080124	-4.93	TRUE
250822_at	unknown protein	---	AT5G05230	-1.21	-0.27	-1.90	0.1003358	0.3080124	-4.93	FALSE
249009_at	unknown protein ; supported by	MAP18	AT5G44610	1.43	0.52	1.90	0.1003578	0.3080143	-4.93	FALSE
262860_at	unknown protein	APO1	AT1G64810	-1.32	-0.40	-1.90	0.1004211	0.3081671	-4.93	FALSE
255591_at	putative expansin	ATEXPA17	AT4G01630	1.24	0.32	1.90	0.1004401	0.3081839	-4.93	FALSE
248136_at	RNA helicase-like protein	---	AT5G54910	-1.48	-0.56	-1.90	0.1004779	0.3082582	-4.93	FALSE
267107_at	hypothetical protein predicted by	---	---	1.24	0.31	1.90	0.1005108	0.3083179	-4.93	FALSE
249089_at	ATPase, calcium-transporting	---	AT5G44240	1.18	0.24	1.90	0.1005336	0.3083462	-4.93	FALSE
252850_at	putative protein ;supported by fu	---	AT4G39880	-1.32	-0.40	-1.90	0.1005547	0.3083694	-4.93	FALSE
264656_at	unknown protein Contains simila	---	AT1G09010	-1.22	-0.29	-1.90	0.1005871	0.3084275	-4.93	FALSE
263658_at	unknown protein EST gb|T21788	---	AT1G04490	1.22	0.29	1.90	0.1006197	0.308486	-4.94	FALSE
266035_at	enoyl-ACP reductase (enr-A)	MOD1	AT2G05990	-1.53	-0.62	-1.90	0.1006542	0.3085503	-4.94	FALSE
250492_at	putative protein Requiem protein	ATXR5	AT5G09790	1.26	0.33	1.90	0.1006852	0.3086039	-4.94	FALSE
255891_at	hypothetical protein predicted by	EGY3	AT1G17870	1.29	0.37	1.90	0.1007438	0.308742	-4.94	FALSE
252133_at	hypothetical protein hypothetical	---	AT3G50900	2.01	1.00	1.90	0.1007863	0.3087891	-4.94	FALSE
253972_at	putative protein Uvi31, Schizosa	CPSUFE	AT4G26500	-1.17	-0.23	-1.90	0.1007761	0.3087891	-4.94	FALSE
255226_at	UV-damaged DNA binding facto	DDB1A	AT4G05420	-1.21	-0.28	-1.90	0.1008317	0.3088303	-4.94	FALSE
257869_at	ER lumen protein retaining rece	---	AT3G25160	1.20	0.26	1.90	0.1008295	0.3088303	-4.94	FALSE
264989_at	unknown protein ; supported by	---	AT1G27200	-1.36	-0.44	-1.90	0.1008403	0.3088303	-4.94	FALSE
258423_at	hypothetical protein predicted by	---	AT3G16730	-1.20	-0.26	-1.90	0.1008976	0.3088398	-4.94	FALSE
260284_at	unknown protein ; supported by	---	AT1G80380	-1.21	-0.28	-1.90	0.1008733	0.3088398	-4.94	FALSE
251875_at	putative protein various predicte	---	AT3G54270	1.30	0.38	1.90	0.1008962	0.3088398	-4.94	FALSE
247228_at	trehalose-6-phosphate phosphat	---	AT5G65140	2.00	1.00	1.90	0.1008712	0.3088398	-4.94	FALSE
251375_at	putative protein various predicte	---	AT3G60410	1.37	0.45	1.90	0.100933	0.3089066	-4.94	FALSE

260738_at	hypothetical protein predicted by	---	AT1G14990	-1.22	-0.29	-1.90	0.1009604	0.3089123	-4.94	FALSE
263787_at	unknown protein ; supported by	---	AT2G46420	-1.38	-0.46	-1.90	0.1009821	0.3089123	-4.94	FALSE
245789_at	hypothetical protein similar to hy	---	AT1G32090	1.55	0.63	1.90	0.100989	0.3089123	-4.94	FALSE
248964_at	cytochrome P450	CYP707A3	AT5G45340	1.86	0.90	1.90	0.1009787	0.3089123	-4.94	FALSE
244990_s_a	hypothetical protein	---	---	-1.63	-0.71	-1.90	0.101004	0.3089168	-4.94	FALSE
261287_at	hypothetical protein predicted by	---	AT1G37020	1.18	0.23	1.90	0.1010316	0.3089596	-4.94	FALSE
267273_at	putative non-LTR retroelement re	---	AT2G02520	1.19	0.25	1.90	0.1010483	0.3089693	-4.94	FALSE
253189_at	putative protein	---	AT4G35335	-1.40	-0.48	-1.90	0.1011982	0.3091131	-4.94	FALSE
259075_at	putative N2,N2-dimethylguanosi	---	AT3G02320	-1.26	-0.34	-1.90	0.1011622	0.3091131	-4.94	FALSE
260527_at	unknown protein ;supported by f	---	AT2G47270	-2.16	-1.11	-1.90	0.1012037	0.3091131	-4.94	FALSE
267322_at	putative leucine-rich-repeat prote	---	AT2G19330	1.20	0.27	1.90	0.1011343	0.3091131	-4.94	FALSE
256882_at	RNA-binding protein, putative si	---	AT3G26420 /	-1.32	-0.40	-1.90	0.1011877	0.3091131	-4.94	FALSE
259390_at	hypothetical protein predicted by	---	AT1G06340	1.24	0.32	1.90	0.1011914	0.3091131	-4.94	FALSE
246204_at	putative protein ; supported by cl	---	AT4G37020	-1.24	-0.32	-1.90	0.1011777	0.3091131	-4.94	FALSE
252345_at	hypothetical protein	---	AT3G48640	1.39	0.47	1.90	0.1011628	0.3091131	-4.94	FALSE
264609_at	unknown protein ;supported by f	---	AT1G04530	-1.50	-0.58	-1.90	0.1012276	0.3091447	-4.94	FALSE
265676_at	putative CCR4-associated factor	---	AT2G32070	-1.21	-0.28	-1.90	0.101246	0.3091595	-4.94	FALSE
254372_at	putative protein predicted protei	---	AT4G21620	-1.53	-0.61	-1.90	0.1012644	0.3091743	-4.94	FALSE
258150_at	hypothetical protein ;supported b	---	AT3G18160	-1.53	-0.62	-1.90	0.1013313	0.3093372	-4.94	FALSE
266771_s_a	unknown protein	---	AT2G03010 /	-1.22	-0.29	-1.90	0.1013723	0.3093384	-4.94	FALSE
258604_at	putative N-acetlytransferase cont	---	AT3G02980	-1.29	-0.37	-1.90	0.1013751	0.3093384	-4.94	FALSE
256096_at	unknown protein	---	AT1G13650	-1.62	-0.69	-1.90	0.101349	0.3093384	-4.94	FALSE
259084_at	putative inner mitochondrial mem	ATTIM23-3	AT3G04800	1.24	0.31	1.90	0.101386	0.3093384	-4.94	FALSE
249988_at	putative protein predicted protei	---	AT5G18310	1.32	0.40	1.90	0.1014515	0.3094142	-4.94	FALSE
255689_at	hypothetical protein	---	AT4G00670	1.19	0.25	1.90	0.101443	0.3094142	-4.94	FALSE
249227_at	peroxidase (emb|CAA66960.1)	---	AT5G42180	1.23	0.29	1.90	0.1014302	0.3094142	-4.94	FALSE
253919_at	putative protein ; supported by fu	---	AT4G27350	1.55	0.63	1.90	0.1014714	0.3094335	-4.94	FALSE
252649_at	putative protein histone deacety	HDA9	AT3G44680	-1.19	-0.25	-1.90	0.1016173	0.3097541	-4.94	FALSE
256815_at	unknown protein contains Pfam p	---	AT3G21380	1.23	0.29	1.90	0.1015945	0.3097541	-4.94	FALSE
258095_at	dual-specificity protein phosphat	---	AT3G23610	-1.28	-0.36	-1.90	0.101612	0.3097541	-4.94	FALSE
258936_s_a	hypothetical protein similar to hy	---	---	1.22	0.29	1.89	0.1016359	0.3097694	-4.94	FALSE
255734_at	hypothetical protein similar to put	---	AT1G25550	-1.36	-0.44	-1.89	0.1017075	0.3099066	-4.95	FALSE
266766_at	hypothetical protein predicted by	PAP14	AT2G46880	1.50	0.58	1.89	0.1017081	0.3099066	-4.95	FALSE
249635_at	putative glucan synthase glucan	ATGSL09	AT5G36870	1.25	0.32	1.89	0.1017572	0.3100151	-4.95	FALSE
250904_at	subtilisin-like serine protease cor	---	AT5G03620	1.21	0.28	1.89	0.1017774	0.3100351	-4.95	FALSE

259899_at	hypothetical protein predicted by	---	AT1G71210	-1.34	-0.42	-1.89	0.1018369	0.310098	-4.95	FALSE
249577_at	calmodulin-binding heat-shock p	---	AT5G37710	1.40	0.48	1.89	0.1018387	0.310098	-4.95	FALSE
248894_at	unknown protein	---	AT5G46320	1.25	0.33	1.89	0.1018388	0.310098	-4.95	FALSE
245645_at	F5A9.19 unknown protein; simila	ATMAP70-2	AT1G24764	-1.37	-0.46	-1.89	0.1018531	0.3101001	-4.95	FALSE
251124_s_a	laccase -like protein lac110 lacc	LAC8	AT5G01040 /	2.80	1.48	1.89	0.1018943	0.3101011	-4.95	FALSE
246310_at	sulfate transporter ATST1 ; supp	SULTR3;1	AT3G51895	1.43	0.52	1.89	0.1018928	0.3101011	-4.95	FALSE
257906_at	ribosomal protein, putative simila	ATL5	AT3G25520	-1.70	-0.77	-1.89	0.1018878	0.3101011	-4.95	FALSE
252336_at	putative protein N7 protein - Me	---	AT3G48880	1.21	0.28	1.89	0.1019858	0.3103384	-4.95	FALSE
264983_at	hypothetical protein predicted by	---	AT1G27240	1.22	0.28	1.89	0.1020103	0.3103478	-4.95	FALSE
253937_at	putative NPK1-related protein ki	MAPKKK16	AT4G26890	-1.45	-0.54	-1.89	0.1020161	0.3103478	-4.95	FALSE
247738_at	putative protein myosin heavy ch	---	AT5G59210	-1.27	-0.35	-1.89	0.1020676	0.3104629	-4.95	FALSE
266679_at	putative helicase ; supported by	---	AT2G03270	1.26	0.33	1.89	0.10215	0.3106721	-4.95	FALSE
248948_at	putative protein strong similarity t	---	AT5G45560	-1.36	-0.44	-1.89	0.1021786	0.3107179	-4.95	FALSE
245031_at	putative mitochondrial carrier pro	---	AT2G26360	-1.20	-0.26	-1.89	0.1022299	0.3108322	-4.95	FALSE
244928_s_a	hypothetical protein	---	AT2G07716	1.23	0.30	1.89	0.1022457	0.310839	-4.95	FALSE
245640_at	helix-loop-helix protein homolog	---	AT1G25330	1.23	0.30	1.89	0.1023277	0.3110467	-4.95	FALSE
257901_at	hypothetical protein predicted by	---	---	1.24	0.30	1.89	0.1023797	0.3111634	-4.95	FALSE
259383_at	putative lectin contains Pfam pro	JR1	AT3G16470	2.70	1.43	1.89	0.1024377	0.3112567	-4.95	FALSE
251217_at	Sar1-like GTP binding protein sr	---	AT3G62560	-1.26	-0.33	-1.89	0.1024287	0.3112567	-4.95	FALSE
245746_at	bHLH transcription factor, putati	---	AT1G51070	1.31	0.39	1.89	0.1024928	0.3113475	-4.95	FALSE
261789_at	40S ribosomal protein S12, puta	---	AT1G15930	-1.59	-0.67	-1.89	0.1024949	0.3113475	-4.95	FALSE
245083_at	putative integral membrane prote	ATRER1C1	AT2G23310	-1.25	-0.32	-1.89	0.1025823	0.3115717	-4.95	FALSE
256140_at	hypothetical protein contains sim	---	AT1G48650	-1.37	-0.46	-1.89	0.1026672	0.3117878	-4.95	FALSE
262290_at	Expressed protein ; supported by	---	AT1G70985	-1.37	-0.46	-1.89	0.1026963	0.3118347	-4.95	FALSE
263655_at	hypothetical protein predicted by	---	AT1G04500	1.23	0.30	1.89	0.1027391	0.3119231	-4.96	FALSE
249266_at	6-phosphogluconate dehydroger	---	AT5G41670	-1.34	-0.43	-1.89	0.1028046	0.311985	-4.96	FALSE
253953_at	putative protein extensin precurs	---	AT4G26750	1.40	0.49	1.89	0.1027962	0.311985	-4.96	FALSE
262376_at	unknown protein contains similar	HTH	AT1G72970	-1.22	-0.28	-1.89	0.1028163	0.311985	-4.96	FALSE
261231_at	unknown protein ; supported by	---	AT1G20110	1.19	0.25	1.89	0.1028278	0.311985	-4.96	FALSE
258071_s_a	unknown protein	---	AT3G26070 /	-1.37	-0.46	-1.89	0.1028276	0.311985	-4.96	FALSE
252300_at	pyruvate kinase -like protein vari	---	AT3G49160	1.49	0.58	1.89	0.1028558	0.3120284	-4.96	FALSE
247209_at	putative protein contains similarit	---	AT5G64830	-1.23	-0.29	-1.89	0.1028844	0.3120734	-4.96	FALSE
253876_at	COP1-interacting protein 7 (CIP7	CIP7	AT4G27430	-1.41	-0.49	-1.89	0.1029028	0.312088	-4.96	FALSE
264292_at	hypothetical protein predicted by	---	AT1G78790	-1.28	-0.36	-1.89	0.1029313	0.3121061	-4.96	FALSE
262399_at	unknown protein ;supported by fu	---	AT1G49500	-1.38	-0.46	-1.89	0.1029362	0.3121061	-4.96	FALSE

261136_at	ribokinase, putative similar to GI	---	AT1G19600	-1.21	-0.28	-1.89	0.1029861	0.3122158	-4.96	FALSE
258018_at	hypothetical protein predicted by	---	AT3G19500	1.34	0.42	1.89	0.1030415	0.3123424	-4.96	FALSE
255431_at	putative C-type U1 snRNP simila	---	AT4G03120	-1.18	-0.24	-1.89	0.1031033	0.3124882	-4.96	FALSE
260632_at	homeobox protein, putative simi	STM	AT1G62360	1.25	0.32	1.88	0.1032858	0.3129996	-4.96	FALSE
263284_at	unknown protein	---	AT2G36100	1.23	0.30	1.88	0.1033056	0.3130181	-4.96	FALSE
266020_at	hypothetical protein	SDG11	AT2G05900	1.30	0.38	1.88	0.1033656	0.3130349	-4.96	FALSE
262776_at	unknown protein EST gb|T22808	---	AT1G13020	1.29	0.37	1.88	0.1033543	0.3130349	-4.96	FALSE
265470_at	putative protein with C-terminal F	---	AT2G37150	1.29	0.37	1.88	0.103366	0.3130349	-4.96	FALSE
250705_at	diadenosine 5,5-P1,P4-tetrapho	ATNUDX27	AT5G06340	-1.29	-0.37	-1.88	0.1033436	0.3130349	-4.96	FALSE
266476_at	unknown protein ;supported by f	---	AT2G31090	1.33	0.42	1.88	0.1034259	0.3131747	-4.96	FALSE
255568_at	putative DNA-binding protein ; s	WRKY22	AT4G01250	2.11	1.08	1.88	0.1035015	0.3132357	-4.96	FALSE
265732_at	predicted by genscan and genefi	---	AT2G01300	3.37	1.75	1.88	0.1034662	0.3132357	-4.96	TRUE
248171_at	putative protein similar to unknov	ILR3	AT5G54680	-1.20	-0.26	-1.88	0.1035147	0.3132357	-4.96	FALSE
259137_at	unknown protein Pfam HMM hit:	---	AT3G10300	1.41	0.50	1.88	0.1034897	0.3132357	-4.96	FALSE
249942_at	Nitrilase 4 (sp|P46011) ; support	GAPB	AT1G42970 /	4.15	2.05	1.88	0.1034851	0.3132357	-4.96	FALSE
259289_at	hypothetical protein predicted by	---	AT3G11350	1.27	0.34	1.88	0.1035661	0.3133497	-4.96	FALSE
258202_at	unknown protein	---	AT3G13940	-1.43	-0.52	-1.88	0.1035962	0.3133991	-4.96	TRUE
262203_at	transfactor-like protein similar to	---	AT2G01060	-1.26	-0.33	-1.88	0.1036328	0.3134267	-4.96	FALSE
246762_at	cyclin H-like protein cycH (CAK	CYCH;1	AT5G27620	-1.40	-0.48	-1.88	0.1036279	0.3134267	-4.96	FALSE
246563_at	putative protein	---	AT5G15581	1.28	0.36	1.88	0.10372	0.3135017	-4.96	FALSE
250725_at	putative protein similar to unknov	---	AT5G06400	-1.28	-0.36	-1.88	0.1037263	0.3135017	-4.96	FALSE
245295_at	hypothetical protein ; supported b	---	AT4G16100	-1.29	-0.37	-1.88	0.1037187	0.3135017	-4.96	FALSE
249877_at	transcription factor-like protein (g	HUA2	AT5G23150	1.20	0.26	1.88	0.1037079	0.3135017	-4.96	FALSE
249341_at	salt-inducible protein-like	---	AT5G41170	1.46	0.54	1.88	0.1036732	0.3135017	-4.96	FALSE
258852_at	unknown protein similar to C-terr	AT-P4H-2	AT3G06300	1.36	0.45	1.88	0.1037433	0.3135115	-4.96	FALSE
265187_at	putative ADP-ribosylation factor	---	AT1G23490 /	1.17	0.23	1.88	0.1037642	0.313533	-4.96	FALSE
262467_at	hypothetical protein similar to hy	FU	AT1G50240	1.29	0.36	1.88	0.1037901	0.31357	-4.96	FALSE
257761_at	unknown protein	---	AT3G23090	1.50	0.58	1.88	0.1038213	0.313581	-4.96	FALSE
247594_at	putative protein farnesylated pro	---	AT5G60800	1.32	0.40	1.88	0.1038157	0.313581	-4.96	FALSE
257956_at	unknown protein	---	AT3G25400	-1.32	-0.40	-1.88	0.1038806	0.3137185	-4.97	FALSE
249385_at	thioredoxin ; supported by full-le	ATTRX2	AT5G39950	1.30	0.38	1.88	0.103911	0.3137688	-4.97	FALSE
248886_at	phosphate/triose-phosphate tran	APE2	AT5G46110	-1.25	-0.32	-1.88	0.1039664	0.3138224	-4.97	FALSE
247431_at	putative protein similar to unknov	SRO5	AT5G62520	1.61	0.69	1.88	0.10397	0.3138224	-4.97	FALSE
255630_at	putative phosphoribosylanthranila	---	AT4G00700	5.55	2.47	1.88	0.1039541	0.3138224	-4.97	FALSE
247032_at	putative protein strong similarity t	SDN3	AT5G67240	-1.22	-0.29	-1.88	0.1040358	0.3139793	-4.97	FALSE

250408_at	serine/threonine protein kinase -	CIPK5	AT5G10930	-1.46	-0.54	-1.88	0.1040892	0.3140991	-4.97	TRUE
263311_at	hypothetical protein predicted by	---	AT2G10340	1.27	0.34	1.88	0.1041099	0.3141201	-4.97	FALSE
263978_at	unknown protein ;supported by fu	MBF1A	AT2G42680	-1.21	-0.28	-1.88	0.1041481	0.3141498	-4.97	FALSE
245672_at	polygalacturonase, putative simi	---	AT1G56710	-1.33	-0.41	-1.88	0.1041477	0.3141498	-4.97	FALSE
259378_at	unknown protein supported by fu	---	AT3G16310	-1.56	-0.64	-1.88	0.1041611	0.3141498	-4.97	FALSE
252752_s_a	putative protein hypothetical pro	---	AT3G43470 /.	1.20	0.27	1.88	0.1042663	0.3144254	-4.97	FALSE
254609_at	Expressed protein ; supported by	---	AT4G18970	-1.74	-0.80	-1.88	0.1043058	0.3144278	-4.97	FALSE
246465_at	quinone oxidoreductase - like pr	---	AT5G17000	1.44	0.53	1.88	0.1043022	0.3144278	-4.97	FALSE
266399_at	putative phospholipid cytidylyltra	PECT1	AT2G38670	-1.29	-0.37	-1.88	0.1043084	0.3144278	-4.97	FALSE
261164_at	hypothetical protein ;supported b	---	AT1G34470	-1.25	-0.32	-1.88	0.1043499	0.3145113	-4.97	FALSE
265729_at	putative glucan synthase	ATGSL03	AT2G31960	-1.32	-0.40	-1.88	0.1044065	0.3146403	-4.97	FALSE
254819_at	pEARLI 1-like protein Arabidops	---	AT4G12500	-4.11	-2.04	-1.88	0.1044377	0.3146926	-4.97	FALSE
249867_at	2-isopropylmalate synthase-like p	IMS2	AT5G23020	-2.84	-1.51	-1.88	0.1045076	0.3148619	-4.97	FALSE
256899_at	putative kinase-like protein TMK	TMKL1	AT3G24660	-1.25	-0.32	-1.88	0.1045264	0.3148767	-4.97	FALSE
261196_at	unknown protein	SCRM2	AT1G12860	-1.53	-0.61	-1.88	0.1045511	0.3149096	-4.97	FALSE
250326_at	putative protein strong similarity t	MSL10	AT5G12080	-1.34	-0.42	-1.88	0.1046056	0.3149409	-4.97	FALSE
260210_at	putative xyloglucan fucosyltrans	FUT3	AT1G74420	1.31	0.39	1.87	0.1046263	0.3149409	-4.97	FALSE
264545_at	photosystem I subunit V precurs	PSAG	AT1G55670	-1.18	-0.24	-1.88	0.1045983	0.3149409	-4.97	FALSE
264371_at	pEARLI 1-like protein may be inc	ELP	AT1G12090	-1.52	-0.61	-1.87	0.1046305	0.3149409	-4.97	FALSE
246303_at	putative carrier protein peroxisor	---	AT3G51870	1.43	0.51	1.88	0.1045784	0.3149409	-4.97	FALSE
250944_at	putative protein	---	AT5G03380	2.14	1.10	1.87	0.1048289	0.3154131	-4.97	FALSE
266595_at	hypothetical protein predicted by	GC4	AT2G46180	-1.26	-0.33	-1.87	0.1048217	0.3154131	-4.97	FALSE
261491_at	hypothetical protein contains sim	FLP	AT1G14350	1.78	0.83	1.87	0.1048052	0.3154131	-4.97	FALSE
245431_at	hypothetical protein	---	AT4G17080	-1.23	-0.30	-1.87	0.1048661	0.3154836	-4.97	FALSE
247076_at	ferripyochelin-binding protein-like	GAMMA CA	AT5G66510	1.22	0.29	1.87	0.104908	0.3155678	-4.97	FALSE
261653_at	subtilisin-like serine protease, pu	SBTI1.1	AT1G01900	-1.70	-0.76	-1.87	0.1049434	0.3156096	-4.98	TRUE
245299_at	ras-related small GTP-binding pr	ATRAB1C	AT4G17530	1.33	0.41	1.87	0.1049495	0.3156096	-4.98	FALSE
244969_at	ribosomal protein S18	---	---	-1.61	-0.68	-1.87	0.1049821	0.3156658	-4.98	FALSE
251685_at	putative protein unknown protein	---	AT3G56430	-1.61	-0.69	-1.87	0.1050366	0.315788	-4.98	FALSE
263027_at	hypothetical protein predicted by	---	AT1G24010	1.19	0.25	1.87	0.1050861	0.3158536	-4.98	FALSE
258821_at	putative wound-induced basic pr	---	AT3G07230	-1.30	-0.38	-1.87	0.1050799	0.3158536	-4.98	FALSE
262343_at	phosphoprotein phosphatase 1 ic	TOPP3	AT1G64040	-1.21	-0.28	-1.87	0.1051434	0.3159426	-4.98	FALSE
265993_at	putative disease resistance prote	---	AT2G24160	2.96	1.57	1.87	0.1051374	0.3159426	-4.98	FALSE
248591_at	xylulose kinase ; supported by c	---	AT5G49650	1.27	0.34	1.87	0.1051618	0.3159563	-4.98	FALSE
260119_at	AIG1-like protein similar to AIG1	---	AT1G33930	1.22	0.29	1.87	0.1052272	0.3160921	-4.98	FALSE

247919_at	putative protein similar to unknov	---	AT5G57650	1.27	0.34	1.87	0.1052347	0.3160921	-4.98	FALSE
250845_at	rna binding protein - like rna bin	---	AT5G04600	-1.37	-0.45	-1.87	0.1052497	0.3160955	-4.98	FALSE
245804_at	hypothetical protein predicted by	---	AT1G46696	1.20	0.26	1.87	0.1052738	0.3161262	-4.98	FALSE
257990_at	putative myc-like DNA-binding pr	---	AT3G19860	-1.33	-0.42	-1.87	0.1052969	0.3161539	-4.98	FALSE
261622_at	hypothetical protein predicted by	---	AT1G01970	-1.25	-0.32	-1.87	0.1053341	0.3161824	-4.98	FALSE
251626_at	UDP-GlcNAc:dolichol phosphate	---	AT3G57220	-1.24	-0.31	-1.87	0.10533	0.3161824	-4.98	FALSE
259476_at	Myb-related transcription activat	---	AT1G19000	-1.32	-0.40	-1.87	0.10536	0.3162187	-4.98	FALSE
254182_at	putative protein various npredict	---	AT4G23950	-1.28	-0.36	-1.87	0.1053818	0.3162425	-4.98	FALSE
252985_at	putative protein Niemann-Pick C	---	AT4G38350	-1.23	-0.30	-1.87	0.1054029	0.3162641	-4.98	FALSE
260225_at	putative glutathione S-transferas	GSTU10	AT1G74590	2.53	1.34	1.87	0.1054332	0.3163134	-4.98	TRUE
253126_at	putative protein probable membr	---	AT4G36050	-1.45	-0.54	-1.87	0.1055349	0.3165771	-4.98	FALSE
252108_at	putative protein various predicte	---	AT3G51530	-1.23	-0.30	-1.87	0.1055664	0.3165881	-4.98	FALSE
248945_at	putative protein strong similarity t	---	AT5G45510	1.29	0.37	1.87	0.1055634	0.3165881	-4.98	FALSE
263799_at	unknown protein ; supported by	---	AT2G24550	1.38	0.46	1.87	0.1056569	0.3166929	-4.98	FALSE
263647_at	unknown protein	---	AT2G04690	-1.33	-0.41	-1.87	0.1056256	0.3166929	-4.98	FALSE
252725_at	putative protein mudrA transpos	---	---	1.22	0.28	1.87	0.1056548	0.3166929	-4.98	FALSE
252500_at	proteinase inhibitor-like protein e	---	AT3G46860	1.20	0.27	1.87	0.1056374	0.3166929	-4.98	FALSE
267298_at	putative homeodomain transcript	BLH4	AT2G23760	-1.35	-0.43	-1.87	0.1056838	0.3167319	-4.98	FALSE
246908_at	dehydration-induced protein RD2	RD22	AT5G25610	2.54	1.35	1.87	0.1057524	0.3168253	-4.98	FALSE
254708_at	ubiquitin-specific protease 20 (U	UBP20	AT4G17895	1.22	0.29	1.87	0.1057566	0.3168253	-4.98	FALSE
262948_at	DNA-binding protein similar to ce	---	AT1G75560	-1.24	-0.31	-1.87	0.1057447	0.3168253	-4.98	FALSE
257233_at	hypothetical protein similar to SF	IQD10	AT3G15050	1.22	0.28	1.87	0.1058413	0.3170181	-4.98	FALSE
260569_at	putative signal recognition partic	---	AT2G43640	-1.26	-0.34	-1.87	0.1058487	0.3170181	-4.98	FALSE
250722_at	unknown protein ;supported by f	---	AT5G06190	-1.41	-0.50	-1.87	0.1059102	0.3171606	-4.98	FALSE
258771_at	unknown protein ;supported by f	---	AT3G10770	-1.24	-0.31	-1.87	0.1059503	0.3171972	-4.98	FALSE
252977_at	Phospholipase like protein Arabi	---	AT4G38560	1.78	0.83	1.87	0.1059481	0.3171972	-4.98	FALSE
263639_at	unknown protein	---	AT2G25300	-1.26	-0.33	-1.87	0.1059808	0.3172052	-4.98	FALSE
257874_at	hypothetical protein	---	AT3G17110	1.26	0.33	1.87	0.1059685	0.3172052	-4.98	FALSE
246436_at	putative protein cisplatin resistar	---	AT5G17440	-1.20	-0.26	-1.87	0.1060066	0.3172409	-4.98	FALSE
256425_at	disease resistance protein, puta	ADR1	AT1G33560	1.35	0.43	1.87	0.1060764	0.3174081	-4.99	FALSE
255208_at	see GB:AL022580	---	---	1.23	0.30	1.87	0.1061203	0.3174978	-4.99	FALSE
253019_at	putative protein crp1-hcf111 alle	---	AT4G38010	-1.22	-0.29	-1.86	0.10618	0.3176348	-4.99	FALSE
266828_at	putative flavonol 3-O-glucosyltrar	---	AT2G22930	-1.19	-0.26	-1.86	0.1062541	0.3177731	-4.99	FALSE
247870_at	calmodulin-binding protein ; sup	---	AT5G57580	1.21	0.28	1.86	0.1062469	0.3177731	-4.99	FALSE
266541_at	unknown protein	GRL	AT2G35110	-1.29	-0.36	-1.86	0.1062829	0.3178177	-4.99	FALSE

257177_at	cyanate lyase (CYN) identical to	CYN	AT3G23490	-1.36	-0.45	-1.86	0.1062992	0.3178246	-4.99	FALSE
253516_at	hypothetical protein	---	AT4G31360	-1.39	-0.48	-1.86	0.1063307	0.3178774	-4.99	FALSE
266756_at	putative cytochrome P450	CYP709B2	AT2G46950	2.86	1.52	1.86	0.1063594	0.3179213	-4.99	FALSE
253578_at	putative protein diacylglycerol ki	ATDGK7	AT4G30340	1.37	0.46	1.86	0.1065016	0.3181827	-4.99	FALSE
254573_at	putative pectinacetylesterase pe	---	AT4G19420	-1.55	-0.63	-1.86	0.1065137	0.3181827	-4.99	FALSE
260961_at	unknown protein similar to hypot	---	AT1G05960	1.19	0.25	1.86	0.1065166	0.3181827	-4.99	FALSE
257100_at	disease resistance protein, puta	AtRLP41	AT3G25010	1.29	0.37	1.86	0.1065138	0.3181827	-4.99	FALSE
260511_at	anthranilate phosphoribosyltrans	---	AT1G51570	-1.35	-0.43	-1.86	0.1064851	0.3181827	-4.99	FALSE
261269_at	unknown protein ; supported by f	---	AT1G26690	1.28	0.35	1.86	0.1065862	0.3182802	-4.99	FALSE
264388_at	hypothetical protein contains sim	---	AT1G11970	1.28	0.36	1.86	0.1065911	0.3182802	-4.99	FALSE
247665_at	putative protein various predicte	---	AT5G60130	-1.19	-0.26	-1.86	0.106568	0.3182802	-4.99	FALSE
250303_at	putative protein similar to unknov	---	AT5G12100	-1.48	-0.56	-1.86	0.1066265	0.3183346	-4.99	FALSE
246791_at	putative protein predicted protei	---	AT5G27280	-1.27	-0.35	-1.86	0.1066372	0.3183346	-4.99	FALSE
254545_at	putative protein FKBP-type pept	---	AT4G19830	-1.44	-0.53	-1.86	0.1067106	0.3184285	-4.99	FALSE
245285_s_a	selenium-binding protein like ; su	SBP1	AT4G14030 /,	-1.21	-0.28	-1.86	0.1067084	0.3184285	-4.99	FALSE
259167_at	putative oleosin similar to oleosir	---	AT3G01570	-1.20	-0.27	-1.86	0.1066917	0.3184285	-4.99	FALSE
262521_at	unknown protein Location of est	---	AT1G17130	-1.24	-0.31	-1.86	0.1067487	0.3185006	-4.99	FALSE
262506_at	unknown protein Similar to gb|X8	NADK2	AT1G21640	-1.35	-0.44	-1.86	0.1068471	0.3187526	-4.99	FALSE
254179_at	putative protein various predicte	---	AT4G23910	-1.35	-0.43	-1.86	0.1068762	0.3187978	-4.99	FALSE
246814_at	acyl carrier protein precursor - li	ACP5	AT5G27200	1.20	0.27	1.86	0.1068928	0.3188057	-4.99	FALSE
266092_at	hypothetical protein predicted by	---	AT2G37880	1.24	0.31	1.86	0.1069888	0.3190501	-4.99	FALSE
246194_at	putative protein ;supported by ful	ACD2	AT4G37000	-1.32	-0.41	-1.86	0.1070315	0.3191359	-4.99	FALSE
265032_at	ribosomal protein identical to ribo	RPL3B	AT1G61580	-1.59	-0.67	-1.86	0.1071277	0.3192331	-4.99	TRUE
251379_at	putative protein various predicted	---	AT3G60680	1.43	0.52	1.86	0.1071147	0.3192331	-4.99	FALSE
249780_at	ubiquitin	---	AT5G24240	1.29	0.37	1.86	0.1070939	0.3192331	-4.99	FALSE
266626_at	hypothetical protein predicted by	---	AT2G35360	-1.34	-0.42	-1.86	0.1070919	0.3192331	-4.99	FALSE
252872_at	putative serine/threonine protein	SNRK2.7	AT4G40010	1.20	0.26	1.86	0.1071341	0.3192331	-4.99	FALSE
251849_at	Expressed protein ; supported by	HAG1	AT3G54610	-1.26	-0.34	-1.86	0.1071608	0.319271	-4.99	FALSE
255928_at	unknown protein	---	AT1G12640	1.39	0.47	1.86	0.1072515	0.319416	-5.00	FALSE
248635_at	unknown protein	---	AT5G49050	1.22	0.28	1.86	0.1072407	0.319416	-5.00	FALSE
262828_at	major latex protein type1 identica	---	AT1G14950	1.42	0.51	1.86	0.1072244	0.319416	-5.00	FALSE
255784_at	hypothetical protein predicted by	---	AT1G19860	-1.22	-0.29	-1.86	0.1073368	0.3195176	-5.00	FALSE
255667_at	phospholipase D, putative	PLDBETA2	AT4G00240	1.22	0.29	1.86	0.1073185	0.3195176	-5.00	FALSE
262795_at	hypothetical protein predicted by	---	AT1G13130	1.35	0.44	1.86	0.107311	0.3195176	-5.00	FALSE
265354_at	actin depolymerizing factor 5 ;su	ADF5	AT2G16700	1.61	0.69	1.86	0.1073417	0.3195176	-5.00	FALSE

254192_at	acyl-CoA synthetase - like prote	---	AT4G23850	1.24	0.31	1.86	0.1074269	0.3195649	-5.00	FALSE
253002_at	phosphoinositide-specific phosph	ATPLC1	AT4G38530	1.27	0.35	1.86	0.107406	0.3195649	-5.00	FALSE
248072_at	unknown protein	---	AT5G55680	1.25	0.32	1.86	0.107413	0.3195649	-5.00	FALSE
257748_at	hypothetical protein predicted by	PUB29	AT3G18710	3.86	1.95	1.86	0.1074035	0.3195649	-5.00	FALSE
260460_at	unknown protein	---	AT1G68230	-1.24	-0.31	-1.86	0.1074276	0.3195649	-5.00	FALSE
253698_at	nucleotide pyrophosphatase - lik	---	AT4G29680	-1.22	-0.29	-1.86	0.1074679	0.3195874	-5.00	FALSE
258596_at	unknown protein	LSH2	AT3G04510	1.27	0.35	1.86	0.1074772	0.3195874	-5.00	FALSE
266528_at	putative disease resistance prote	---	AT2G16870	1.19	0.25	1.86	0.1074683	0.3195874	-5.00	FALSE
254816_at	putative adenine phosphoribosy	APT4	AT4G12440	1.18	0.24	1.86	0.1075302	0.3196329	-5.00	FALSE
261693_at	hypothetical protein similar to hy	DCP1	AT1G08370	-1.19	-0.25	-1.86	0.1075217	0.3196329	-5.00	FALSE
258065_at	putative pyruvate kinase similar	---	AT3G25960	1.27	0.34	1.86	0.1075345	0.3196329	-5.00	FALSE
249775_at	squalene monooxygenase 1,2 (s	SQE6	AT5G24160	1.42	0.51	1.85	0.1076932	0.3199795	-5.00	FALSE
247381_at	auxin-independent growth promo	---	AT5G63390	1.24	0.31	1.86	0.1076701	0.3199795	-5.00	FALSE
254272_at	predicted protein hypothetical pr	---	AT4G22850	1.19	0.25	1.85	0.1076919	0.3199795	-5.00	FALSE
255161_at	putative reverse transcriptase	---	---	-1.22	-0.28	-1.85	0.1077299	0.3200052	-5.00	FALSE
265048_at	jasmonate inducible protein, pu	---	AT1G52050	1.28	0.36	1.85	0.1077244	0.3200052	-5.00	FALSE
247071_at	putative protein similar to unknov	DAR3	AT5G66640	1.98	0.99	1.85	0.1077679	0.3200522	-5.00	FALSE
245531_at	hydroxynitrile lyase like protein	scpl30	AT4G15100	1.35	0.43	1.85	0.1077738	0.3200522	-5.00	FALSE
265220_at	histidine transport protein (PTR2	PTR2	AT2G02040	1.19	0.26	1.85	0.1078798	0.3202835	-5.00	FALSE
244904_at	hypothetical protein	---	---	1.41	0.50	1.85	0.107873	0.3202835	-5.00	FALSE
260741_at	hypothetical protein contains Pfa	---	AT1G15040	5.50	2.46	1.85	0.107905	0.3203165	-5.00	FALSE
259864_at	hypothetical protein predicted by	---	AT1G72800	1.46	0.55	1.85	0.1079493	0.320323	-5.00	FALSE
257823_at	integral membrane protein, puta	---	AT3G25190	1.25	0.33	1.85	0.1079449	0.320323	-5.00	FALSE
249739_at	Ttg1 protein (emb CAB45372.1)	TTG1	AT5G24520	-1.20	-0.26	-1.85	0.1079254	0.320323	-5.00	FALSE
251971_at	glucosyltransferase - like protein	UGT73C7	AT3G53160	2.95	1.56	1.85	0.1081422	0.3208119	-5.00	FALSE
244946_at	hypothetical protein	---	---	1.19	0.26	1.85	0.1081395	0.3208119	-5.00	FALSE
266081_at	putative protein kinase contains a	---	AT2G37840	1.22	0.29	1.85	0.1082288	0.3209853	-5.00	FALSE
246422_at	ADP-ribosylation factor -like prot	ATARFB1B	AT5G17060	1.56	0.64	1.85	0.1082245	0.3209853	-5.00	FALSE
264400_at	glucose-6-phosphate/phosphate	GPT2	AT1G61800	3.42	1.77	1.85	0.1083288	0.3211879	-5.01	TRUE
267456_at	E2, ubiquitin-conjugating enzym	PHO2	AT2G33770	-1.59	-0.67	-1.85	0.1083568	0.3211879	-5.01	FALSE
265495_at	unknown protein predicted by ge	---	AT2G15695	-1.24	-0.31	-1.85	0.1083542	0.3211879	-5.01	FALSE
257679_at	glycine-rich protein, putative ide	GRP5	AT3G20470	1.95	0.97	1.85	0.1083675	0.3211879	-5.01	FALSE
262260_at	major latex protein (MLP149), pu	MLP34	AT1G70850	1.36	0.44	1.85	0.1083308	0.3211879	-5.01	FALSE
252913_at	AtRer1A ; supported by full-leng	ATRER1A	AT4G39220	1.23	0.29	1.85	0.1084272	0.3212102	-5.01	FALSE
256742_at	transcription initiation factor IIB,	---	AT3G29380	1.22	0.28	1.85	0.1084292	0.3212102	-5.01	FALSE

257042_s_a	hypothetical protein predicted by	---	AT3G28640 /.	-1.20	-0.27	-1.85	0.1084485	0.3212102	-5.01	FALSE
248630_at	putative protein strong similarity t	---	AT5G48990	-1.23	-0.30	-1.85	0.1084595	0.3212102	-5.01	FALSE
250700_at	CDK5 activator-binding protein-li	---	AT5G06830	-1.24	-0.31	-1.85	0.1084107	0.3212102	-5.01	FALSE
261773_at	hypothetical protein predicted by	---	AT1G76250	1.33	0.41	1.85	0.1084329	0.3212102	-5.01	FALSE
265276_at	hypothetical protein predicted by	---	AT2G28400	1.40	0.48	1.85	0.1085108	0.321237	-5.01	FALSE
253759_at	AIM1 protein ; supported by cDN	AIM1	AT4G29010	1.19	0.25	1.85	0.1084983	0.321237	-5.01	FALSE
259747_at	putative dehydrogenase similar t	---	AT1G71170	1.27	0.34	1.85	0.108509	0.321237	-5.01	FALSE
252176_at	protein kinase ATN1 -like protein	---	AT3G50720	1.28	0.35	1.85	0.108544	0.3212935	-5.01	FALSE
259861_at	unknown protein similar to ribosc	---	AT1G80620	-1.30	-0.38	-1.85	0.1085711	0.3213322	-5.01	FALSE
260097_at	putative transporter similar to org	AtOCT1	AT1G73220	3.38	1.76	1.85	0.1086103	0.3214064	-5.01	FALSE
250173_at	MYB40 - putative transcription fa	AtMYB40	AT5G14340	1.27	0.34	1.85	0.1087117	0.3214171	-5.01	FALSE
261860_at	scarecrow-like protein similar to S	SCL5	AT1G50600	-1.29	-0.36	-1.85	0.1086667	0.3214171	-5.01	FALSE
249908_at	putative protein similar to unknov	---	AT5G22760	-1.22	-0.28	-1.85	0.1087407	0.3214171	-5.01	FALSE
247651_at	histone H2A - like protein histon	HTA6	AT5G59870	-2.33	-1.22	-1.85	0.1087037	0.3214171	-5.01	FALSE
263423_at	hypothetical protein predicted by	---	AT2G31700	1.21	0.28	1.85	0.1086792	0.3214171	-5.01	FALSE
261056_at	hypothetical protein similar to hyp	---	AT1G01360	-1.35	-0.43	-1.85	0.1087082	0.3214171	-5.01	FALSE
255069_s_a	Met2-type cytosine DNA-methylt	---	AT4G08990 /.	-1.39	-0.48	-1.85	0.1086595	0.3214171	-5.01	FALSE
253643_at	hypothetical protein ;supported b	---	AT4G29780	2.12	1.08	1.85	0.1087365	0.3214171	-5.01	FALSE
256450_at	NADPH oxidoreductase, putative	---	AT1G75290	1.21	0.27	1.85	0.1087366	0.3214171	-5.01	FALSE
253705_at	hexokinase ; supported by cDNA	HXK1	AT4G29130	1.37	0.46	1.85	0.108813	0.3215474	-5.01	FALSE
267302_at	putative unknown protein, leucin	---	AT2G30100	-1.18	-0.24	-1.85	0.1088079	0.3215474	-5.01	FALSE
252406_at	putative protein pectinesterase -	---	AT3G47670	1.18	0.24	1.85	0.1089426	0.3218886	-5.01	FALSE
251746_at	mandelonitrile lyase-like protein /	---	AT3G56060	1.30	0.38	1.85	0.1090085	0.3220418	-5.01	FALSE
248946_at	putative protein similar to unknov	---	AT5G45530	1.20	0.26	1.85	0.1090993	0.3221273	-5.01	FALSE
263572_at	putative disease resistance prote	---	AT2G17060	1.20	0.27	1.85	0.1090939	0.3221273	-5.01	FALSE
260339_at	putative serine/threonine kinase	SIK1	AT1G69220	-1.35	-0.43	-1.85	0.1090854	0.3221273	-5.01	FALSE
254203_at	putative protein various predicte	AtGRF8	AT4G24150	-1.20	-0.26	-1.85	0.1091081	0.3221273	-5.01	FALSE
255569_at	putative CAAX prenyl protease ;	ATSTE24	AT4G01320	-1.21	-0.27	-1.85	0.1091066	0.3221273	-5.01	FALSE
250659_at	MtN21 nodulin protein-like	---	AT5G07050	1.28	0.36	1.85	0.1091309	0.3221529	-5.01	FALSE
248679_at	unknown protein ;supported by f	---	AT5G48830	-1.38	-0.46	-1.85	0.1091467	0.3221578	-5.01	FALSE
249400_at	putative protein MtN24 gene, Me	---	AT5G40300	-1.30	-0.38	-1.85	0.1092433	0.3223834	-5.01	FALSE
264003_at	Expressed protein ; supported by	GEM	AT2G22475	1.31	0.39	1.85	0.1092514	0.3223834	-5.01	FALSE
263770_at	Mutator-like transposase similar t	---	---	1.35	0.43	1.84	0.1093058	0.3225023	-5.01	FALSE
258374_at	hypothetical protein predicted by	---	AT3G14360	1.51	0.59	1.84	0.1093633	0.3226303	-5.01	FALSE
256872_at	non-phototropic hypocotyl, putat	---	AT3G26490	-1.23	-0.29	-1.84	0.1093822	0.3226442	-5.01	FALSE

248434_at	mitochondrial heat shock 22 kd p	---	AT5G51440	3.06	1.61	1.84	0.1094054	0.3226709	-5.01	FALSE
250607_at	putative protein mammalian inos	IPK2a	AT5G07370	-1.18	-0.23	-1.84	0.1094243	0.3226851	-5.01	FALSE
266989_at	putative myrosinase-binding prot	JAL23	AT2G39330	3.29	1.72	1.84	0.109474	0.3227899	-5.02	FALSE
257356_s_a	hypothetical protein predicted by	---	AT2G32490 ///	1.25	0.32	1.84	0.1094959	0.3228126	-5.02	FALSE
246574_at	copper amine oxidase, putative	---	AT1G31670	1.49	0.57	1.84	0.1095855	0.3230096	-5.02	FALSE
246063_at	putative protein predicted protei	---	AT5G19340	1.21	0.27	1.84	0.1095953	0.3230096	-5.02	FALSE
262906_at	unknown protein contains similar	---	AT1G59760	-1.31	-0.39	-1.84	0.1096052	0.3230096	-5.02	FALSE
259047_at	unknown protein	DegP7	AT3G03380	-1.18	-0.24	-1.84	0.1096355	0.3230571	-5.02	FALSE
249824_at	putative protein similar to unknov	---	AT5G23380	-1.22	-0.29	-1.84	0.1097069	0.323212	-5.02	FALSE
251085_at	putative protein insulinase - Hon	---	AT5G01440	1.24	0.31	1.84	0.1097164	0.323212	-5.02	FALSE
262862_at	hypothetical protein predicted by	---	AT1G64830	1.37	0.45	1.84	0.1097451	0.3232131	-5.02	FALSE
252104_at	putative protein KIAA0851 prote	RHD4	AT3G51460	1.29	0.37	1.84	0.1097376	0.3232131	-5.02	FALSE
267317_at	putative proline-rich glycoprotein	---	AT2G34700	1.22	0.29	1.84	0.1097927	0.3232517	-5.02	FALSE
265435_s_a	putative major intrinsic (channel)	---	AT1G31885 ///	1.30	0.38	1.84	0.109776	0.3232517	-5.02	FALSE
247119_at	ATP-dependent RNA helicase-lik	---	AT5G65900	-1.17	-0.23	-1.84	0.1098007	0.3232517	-5.02	FALSE
245181_at	putative protein similarity to vario	---	AT5G12420	-1.77	-0.82	-1.84	0.1098396	0.3232892	-5.02	FALSE
252014_at	putative protein predicted protei	---	AT3G52870	1.86	0.90	1.84	0.1098701	0.3232892	-5.02	FALSE
247614_at	putative protein	---	AT5G60240	1.20	0.26	1.84	0.1098425	0.3232892	-5.02	FALSE
266138_at	unknown protein ; supported by	---	AT2G28060	-1.25	-0.32	-1.84	0.1098695	0.3232892	-5.02	FALSE
262453_at	hypothetical protein predicted by	---	AT1G11240	-1.19	-0.25	-1.84	0.1098891	0.3233034	-5.02	FALSE
266928_at	putative phosphomannomutase	PMM	AT2G45790	-1.34	-0.42	-1.84	0.109918	0.3233465	-5.02	FALSE
262395_at	hypothetical protein similar to hyp	---	AT1G49540	-1.50	-0.58	-1.84	0.1100032	0.323519	-5.02	TRUE
265554_at	hypothetical protein predicted by	---	AT2G07505	1.19	0.25	1.84	0.1100192	0.323519	-5.02	FALSE
264925_at	hypothetical protein contains sim	---	AT1G60670	1.27	0.34	1.84	0.1100072	0.323519	-5.02	FALSE
258168_at	hypothetical protein predicted by	---	AT3G21570	1.19	0.25	1.84	0.1100344	0.323522	-5.02	FALSE
259753_at	putative isoprenylated protein sim	---	AT1G71050	1.37	0.45	1.84	0.1100817	0.3236195	-5.02	FALSE
255885_at	sterol-C-methyltransferase identi	SMT2	AT1G20330	1.23	0.30	1.84	0.1100992	0.3236227	-5.02	TRUE
245078_at	putative AP2 domain transcriptio	---	AT2G23340	1.78	0.83	1.84	0.1101112	0.3236227	-5.02	TRUE
257076_at	unknown protein	---	AT3G19680	-1.59	-0.67	-1.84	0.1101479	0.3236888	-5.02	TRUE
261109_at	cytokinin oxidase, putative simila	CKX5	AT1G75450	2.54	1.35	1.84	0.1102307	0.3238489	-5.02	TRUE
267557_at	unknown protein ; supported by	KRP4	AT2G32710	-1.30	-0.38	-1.84	0.1102197	0.3238489	-5.02	FALSE
256092_at	Expressed protein ; supported by	HMGB3	AT1G20696	-1.18	-0.24	-1.84	0.11025	0.3238638	-5.02	TRUE
261394_at	wall-associated kinase 2, putativ	---	AT1G79680	2.91	1.54	1.84	0.1102855	0.3239264	-5.02	TRUE
247771_at	Ran binding protein 1 homolog -	RANBP1	AT5G58590	-1.26	-0.34	-1.84	0.1103774	0.3241546	-5.02	FALSE
262847_at	unknown protein similar to myosi	ATMAP70-4	AT1G14840	-1.54	-0.63	-1.84	0.1104423	0.3243034	-5.02	FALSE

254872_at	putative protein several hypothet	---	AT4G11560	1.21	0.27	1.84	0.1104612	0.3243171	-5.02	FALSE
246566_at	oligopeptide transporter -like pro	---	AT5G14940	-1.48	-0.57	-1.84	0.1104987	0.3243514	-5.02	FALSE
263173_at	hypothetical protein predicted by	BRX-LIKE3	AT1G54180	1.20	0.26	1.84	0.1105013	0.3243514	-5.02	FALSE
264550_at	hypothetical protein predicted by	---	AT1G09450	1.40	0.49	1.84	0.1105862	0.324559	-5.02	FALSE
251318_at	putative protein putative protein /	GDAP1	AT3G61570	1.21	0.27	1.84	0.1106197	0.3245736	-5.02	FALSE
262666_at	xyloglucan fucosyltransferase, p	FUT6	AT1G14080	1.52	0.60	1.84	0.1106149	0.3245736	-5.02	FALSE
248533_at	putative protein contains similarit	---	AT5G50020	-1.34	-0.42	-1.84	0.110652	0.3246265	-5.03	FALSE
252515_at	heat shock protein 17 ; supporte	HSP17.4	AT3G46230	2.25	1.17	1.84	0.1106896	0.3246952	-5.03	TRUE
261602_at	hydrogenase protein, putative si	ATPREP2	AT1G49630	1.19	0.25	1.84	0.1107406	0.3248031	-5.03	FALSE
253688_at	putative protein ;supported by fu	---	AT4G29590	-1.36	-0.44	-1.83	0.1108699	0.32499	-5.03	TRUE
265011_at	putative chloroplast membrane p	ALB4	AT1G24490	-1.18	-0.24	-1.83	0.1109041	0.32499	-5.03	FALSE
263871_at	hypothetical protein predicted by	RKP	AT2G22010	1.28	0.35	1.83	0.1108846	0.32499	-5.03	FALSE
256879_at	unknown protein similar to auxin-	---	AT3G26370	-1.18	-0.24	-1.83	0.1108919	0.32499	-5.03	FALSE
260374_at	unknown protein	TAF2	AT1G73960	-1.22	-0.29	-1.83	0.1108816	0.32499	-5.03	FALSE
255997_s_a	photosystem II type I chlorophy	CAB3	AT1G29910 /	-1.36	-0.45	-1.83	0.1108467	0.32499	-5.03	FALSE
247020_at	putative protein strong similarity t	---	AT5G67020	1.33	0.42	1.84	0.1108303	0.32499	-5.03	FALSE
264276_at	hypothetical protein contains sim	---	AT1G60380	1.20	0.26	1.83	0.1109526	0.3250905	-5.03	FALSE
258884_at	threonine dehydratase/deamina	OMR1	AT3G10050	-1.48	-0.57	-1.83	0.1110193	0.325244	-5.03	FALSE
264268_at	hypothetical protein predicted by	ULP1D	AT1G60220	-1.20	-0.27	-1.83	0.1110482	0.3252869	-5.03	FALSE
256569_at	hypothetical protein ; supported	---	AT3G19550	-1.83	-0.87	-1.83	0.1110774	0.325289	-5.03	TRUE
256247_at	SRF-type transcription factor con	AGL91	AT3G66656	1.20	0.26	1.83	0.111064	0.325289	-5.03	FALSE
252263_at	putative protein several hypothet	---	AT3G49520	1.27	0.35	1.83	0.1111066	0.3253327	-5.03	FALSE
255874_at	hypothetical protein predicted by	ETG1	AT2G40550	-1.92	-0.94	-1.83	0.111147	0.3254091	-5.03	FALSE
250720_at	putative protein similar to unknov	---	AT5G06180	-1.35	-0.44	-1.83	0.1112338	0.325538	-5.03	FALSE
259609_at	myosin-like protein contains Pfa	TSA1	AT1G52410	2.53	1.34	1.83	0.1112139	0.325538	-5.03	FALSE
262306_s_a	asparaginyl-tRNA synthetase(S	SYNC3	AT1G70980 /	-1.30	-0.38	-1.83	0.1112332	0.325538	-5.03	FALSE
254634_at	putative protein transcription fac	---	AT4G18650	1.25	0.32	1.83	0.1112913	0.3256252	-5.03	FALSE
262140_at	hypothetical protein predicted by	---	AT1G52470	1.20	0.26	1.83	0.1113064	0.3256252	-5.03	FALSE
252637_at	WD repeat domain protein nucle	HIRA	AT3G44530	1.26	0.34	1.83	0.1112953	0.3256252	-5.03	FALSE
245007_at	PSI P700 apoprotein A1	---	---	-1.46	-0.54	-1.83	0.1113711	0.3257308	-5.03	TRUE
252162_at	hypothetical protein	---	AT3G50590	1.41	0.50	1.83	0.1113706	0.3257308	-5.03	FALSE
263222_at	putative protein kinase Strong sir	---	AT1G30640	1.38	0.46	1.83	0.1114489	0.325876	-5.03	FALSE
248990_at	disease resistance protein-like	---	AT5G45210	1.22	0.29	1.83	0.1114493	0.325876	-5.03	FALSE
264208_at	putative polyA-binding protein, F	PAB3	AT1G22760	1.40	0.48	1.83	0.1115748	0.3261593	-5.03	FALSE
262901_at	hypothetical protein predicted by	---	AT1G59910	1.66	0.73	1.83	0.1115619	0.3261593	-5.03	FALSE

251861_at	putative protein GATA transcript	BME3	AT3G54810	1.93	0.95	1.83	0.1115938	0.3261731	-5.03	TRUE
245056_at	putative glucosyltransferase	UGT76D1	AT2G26480	1.35	0.43	1.83	0.1116082	0.3261732	-5.03	FALSE
261522_at	RIBOSOMAL PROTEIN, putativ	---	AT1G71710	-1.52	-0.61	-1.83	0.1116821	0.3263475	-5.03	FALSE
246372_at	hypothetical protein predicted by	---	AT1G51900	1.22	0.29	1.83	0.1117374	0.3264673	-5.03	FALSE
261667_at	unknown protein similar to putati	---	AT1G18460	-1.34	-0.42	-1.83	0.1117848	0.326564	-5.03	FALSE
266294_at	putative small heat shock protein	---	AT2G29500	2.60	1.38	1.83	0.1118367	0.32659	-5.04	FALSE
263788_at	putative sarcosine oxidase	---	AT2G24580	1.40	0.49	1.83	0.1118191	0.32659	-5.04	FALSE
251439_at	putative protein unknown protein	---	AT3G59950	1.26	0.33	1.83	0.1118251	0.32659	-5.04	FALSE
260999_at	hypothetical protein similar to put	---	AT1G26580	-1.20	-0.26	-1.83	0.1119108	0.326681	-5.04	FALSE
247526_at	putative protein C2H2 zinc-finge	---	AT5G61470	1.21	0.28	1.83	0.1118882	0.326681	-5.04	FALSE
252236_at	zinc-finger-like protein Cys2/His	---	AT3G49930	-1.24	-0.30	-1.83	0.1118968	0.326681	-5.04	FALSE
263785_at	unknown protein ; supported by	---	AT2G46390	1.24	0.31	1.83	0.111988	0.3268544	-5.04	FALSE
258186_s_a	protein kinase, putative similar to	---	AT1G48490 ///	1.21	0.27	1.83	0.1119988	0.3268544	-5.04	FALSE
255805_at	zinc-finger - like protein zinc-fing	---	AT4G10240	1.23	0.30	1.83	0.1120281	0.3268981	-5.04	FALSE
246005_at	lipoic acid synthase - like protein	---	AT5G08415	-1.34	-0.43	-1.83	0.1120448	0.3269049	-5.04	FALSE
258467_at	unknown protein contains Pfam p	---	AT3G06060	1.27	0.34	1.83	0.1121579	0.3270676	-5.04	TRUE
255319_at	putative disease resistance prote	AtRLP46	AT4G04220	1.55	0.63	1.83	0.1121574	0.3270676	-5.04	FALSE
258582_at	germin-like protein contains Pfam	---	AT3G04150	1.17	0.23	1.83	0.1121412	0.3270676	-5.04	FALSE
261906_at	hypothetical protein predicted by	---	AT1G65080	-1.43	-0.51	-1.83	0.1121299	0.3270676	-5.04	FALSE
264164_at	Expressed protein ; supported by	---	AT1G65295	-1.28	-0.36	-1.83	0.1122304	0.327237	-5.04	FALSE
267477_at	putative receptor-like protein kina	PLPB	AT2G02710	1.49	0.58	1.83	0.1122525	0.3272598	-5.04	FALSE
264933_at	hypothetical protein predicted by	---	AT1G61160	1.25	0.33	1.83	0.1123253	0.3274301	-5.04	FALSE
255674_at	probable plasma membrane intri	PIP1;4	AT4G00430	1.49	0.58	1.83	0.1123767	0.3274678	-5.04	TRUE
263797_at	putative WRKY-type DNA bindin	WRKY17	AT2G24570	2.06	1.04	1.83	0.1123813	0.3274678	-5.04	FALSE
256609_at	hypothetical protein predicted by	---	---	1.19	0.26	1.83	0.1123653	0.3274678	-5.04	FALSE
247420_at	unknown protein	---	AT5G63100	-1.34	-0.42	-1.83	0.112422	0.3275446	-5.04	FALSE
265725_at	putative alanine acetyl transferas	---	AT2G32030	4.33	2.11	1.82	0.1124686	0.3276384	-5.04	FALSE
250749_at	26S proteasome regulatory subu	RPN8A	AT5G05780	-1.19	-0.25	-1.82	0.1124982	0.3276827	-5.04	FALSE
252571_at	putative protein syntaxin 8 - Hor	SYP72	AT3G45280	1.26	0.33	1.82	0.1125289	0.327713	-5.04	FALSE
247523_at	ribulose-5-phosphate-3-epimeras	RPE	AT5G61410	-1.27	-0.35	-1.82	0.1125373	0.327713	-5.04	FALSE
253564_at	protein kinase - like protein prote	---	AT4G31170	1.25	0.32	1.82	0.1126211	0.3278733	-5.04	FALSE
262463_at	hexose transporter, putative sim	STP9	AT1G50310	1.46	0.54	1.82	0.1126124	0.3278733	-5.04	FALSE
259990_s_a	F-box protein FKF1/ADO3, AtFB	FKF1	AT1G68050 ///	-1.38	-0.46	-1.82	0.1126717	0.3279398	-5.04	TRUE
263092_at	hypothetical protein predicted by	---	AT2G16210	1.19	0.26	1.82	0.1126727	0.3279398	-5.04	FALSE
263856_at	unknown protein	---	AT2G04410	-1.33	-0.41	-1.82	0.112692	0.3279515	-5.04	FALSE

267164_at	CER1-like protein may be involve	---	AT2G37700	1.22	0.29	1.82	0.1127153	0.3279515	-5.04	FALSE
250065_at	putative protein predicted protei	---	AT5G17910	1.34	0.42	1.82	0.1127198	0.3279515	-5.04	FALSE
261140_at	unknown protein	---	AT1G19680	1.25	0.33	1.82	0.1128199	0.3282007	-5.04	FALSE
263396_at	unknown protein ;supported by f	---	AT2G31710	-1.24	-0.32	-1.82	0.1129253	0.3284235	-5.04	FALSE
253511_at	putative protein Sly1 protein, rat	---	AT4G31740	1.21	0.28	1.82	0.1129233	0.3284235	-5.04	FALSE
261322_at	hypothetical protein predicted by	ATPUP11	AT1G44750	-1.25	-0.33	-1.82	0.1130037	0.3284423	-5.05	FALSE
261207_at	peroxisomal targeting signal type	---	AT1G12830	-1.38	-0.46	-1.82	0.1129504	0.3284423	-5.04	FALSE
247298_at	glucosidase II alpha subunit	RSW3	AT5G63840	-1.21	-0.28	-1.82	0.1129622	0.3284423	-5.04	FALSE
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=g	---	---	1.56	0.64	1.82	0.1129751	0.3284423	-5.04	FALSE
260796_at	glutathione transferase, putative	ATGSTU21	AT1G78360	1.31	0.39	1.82	0.1129969	0.3284423	-5.04	FALSE
263828_at	putative GDSL-motif lipase/hydro	---	AT2G40250	1.30	0.38	1.82	0.1130473	0.3285272	-5.05	FALSE
250079_at	putative protein similar to unknov	---	AT5G16650	1.27	0.35	1.82	0.1131009	0.3285573	-5.05	FALSE
262916_at	glutathione S-transferase, putati	ATGSTU16	AT1G59700	-1.41	-0.50	-1.82	0.1130728	0.3285573	-5.05	FALSE
265983_at	putative homeodomain transcript	HB-2	AT2G18550	1.20	0.27	1.82	0.1130975	0.3285573	-5.05	FALSE
249608_at	multispanning membrane protei	---	AT5G37310	-1.26	-0.33	-1.82	0.1131401	0.3285874	-5.05	FALSE
245390_at	putative protein ;supported by ful	---	AT4G17650	1.50	0.59	1.82	0.1131361	0.3285874	-5.05	FALSE
266731_at	unknown protein	---	AT2G03260	1.19	0.25	1.82	0.1131897	0.32866	-5.05	FALSE
249568_at	glucosyltransferase-like protein	---	AT5G38040	-1.27	-0.35	-1.82	0.1131939	0.32866	-5.05	FALSE
264990_at	unknown protein supported by c	---	AT1G27210	1.50	0.59	1.82	0.1132255	0.3286682	-5.05	TRUE
259481_at	germin, putative similar to germi	GLP4	AT1G18970	1.54	0.62	1.82	0.113216	0.3286682	-5.05	FALSE
257466_at	hypothetical protein predicted by	---	AT1G62840	1.70	0.76	1.82	0.1132801	0.3287428	-5.05	TRUE
257820_at	immunophilin (FKBP15-1) identi	FKBP15-1	AT3G25220	-1.27	-0.34	-1.82	0.1132676	0.3287428	-5.05	FALSE
252143_at	putative protein centromere prot	---	AT3G51150	1.22	0.28	1.82	0.1133331	0.3288306	-5.05	FALSE
251088_at	putative protein several hypothet	---	AT5G01480	1.36	0.45	1.82	0.1133392	0.3288306	-5.05	FALSE
251932_at	pasticcino 1 ; supported by cDN	PAS1	AT3G54010	-1.22	-0.28	-1.82	0.1133682	0.3288347	-5.05	FALSE
254093_at	putative protein extensin, Cathar	AtMC2	AT4G25110	1.74	0.80	1.82	0.1133694	0.3288347	-5.05	FALSE
251474_at	putative protein diphthamide syn	---	AT3G59630	1.23	0.30	1.82	0.1134118	0.3289159	-5.05	FALSE
260982_at	chalcone isomerase, putative sir	---	AT1G53520	-1.94	-0.96	-1.82	0.1135458	0.3292626	-5.05	TRUE
251540_at	citrate synthase -like protein citr	CSY1	AT3G58740	1.18	0.24	1.82	0.1136107	0.3293671	-5.05	FALSE
245451_at	disease resistance RPP5 like pro	SNC1	AT4G16890	-1.19	-0.25	-1.82	0.1136057	0.3293671	-5.05	FALSE
247192_at	histone H3 (sp|P05203) ; suppo	---	AT5G65360	-3.14	-1.65	-1.82	0.1136271	0.3293729	-5.05	FALSE
261526_at	protein kinase identical to protein	APK2A	AT1G14370	1.45	0.53	1.82	0.1136915	0.3294811	-5.05	TRUE
263347_at	putative U4/U6 small nuclear ribo	---	AT2G05720	1.31	0.39	1.82	0.1137336	0.3294811	-5.05	FALSE
264653_at	unknown protein Contains simila	AMI1	AT1G08980	-1.34	-0.43	-1.82	0.1137356	0.3294811	-5.05	FALSE
244988_s_a	ribosomal protein L23	---	---	-1.28	-0.36	-1.82	0.1137367	0.3294811	-5.05	FALSE

255625_at	GBF2, G-box binding factor ;su	GBF2	AT4G01120	-1.40	-0.48	-1.82	0.1137149	0.3294811	-5.05	FALSE
262835_at	Na+ H+ antiporter, putative simil	ATNHX8	AT1G14660	-1.22	-0.28	-1.82	0.113762	0.3295126	-5.05	FALSE
265015_at	putative Ta11-1 reverse transcrip	---	---	1.17	0.23	1.82	0.1138155	0.3295839	-5.05	FALSE
251232_at	shock protein SRC2-like shock p	---	AT3G62780	1.93	0.95	1.82	0.1138014	0.3295839	-5.05	FALSE
260492_at	putative polygalacturonase	PGAZAT	AT2G41850	1.34	0.42	1.82	0.1138468	0.3296327	-5.05	FALSE
247834_at	cinnamoyl-CoA reductase - like	---	AT5G58490	-1.20	-0.26	-1.82	0.1138916	0.3297205	-5.05	FALSE
256951_at	hypothetical protein predicted by	---	AT3G19085	1.18	0.23	1.82	0.1140538	0.3301481	-5.05	FALSE
244980_at	ribosomal protein L36	---	---	-1.23	-0.30	-1.81	0.1141094	0.3301638	-5.05	FALSE
260819_at	b-Zip DNA binding protein, putat	AtbZIP52	AT1G06850	1.48	0.56	1.81	0.1141605	0.3301638	-5.05	FALSE
260852_at	transmembrane protein, putative	---	AT1G21900	1.19	0.26	1.81	0.1141139	0.3301638	-5.05	FALSE
261904_at	unknown protein contains similar	---	AT1G65040	-1.19	-0.25	-1.81	0.1141016	0.3301638	-5.05	FALSE
261101_at	transcription factor DREB1A, pu	ddf2	AT1G63030	1.30	0.38	1.81	0.1141437	0.3301638	-5.05	FALSE
266317_at	calmodulin identical to GB:L1891	CAM5	AT2G27030	-1.22	-0.28	-1.81	0.1141281	0.3301638	-5.05	FALSE
248729_at	cycloartenol synthase	THAS1	AT5G48010	1.18	0.24	1.81	0.114149	0.3301638	-5.05	FALSE
245521_at	Expressed protein ;supported by	ESD4	AT4G15880	-1.21	-0.27	-1.81	0.1141896	0.3302061	-5.05	FALSE
250338_at	putative protein ; supported by c	---	AT5G11760	-1.20	-0.26	-1.81	0.1142102	0.3302192	-5.06	FALSE
257803_at	unknown protein	---	AT3G18790	-1.21	-0.27	-1.81	0.1142231	0.3302192	-5.06	FALSE
253094_at	putative protein DnaJ-like protei	---	AT4G37480	-1.18	-0.24	-1.81	0.1143427	0.3305229	-5.06	FALSE
262918_at	hypothetical protein predicted by	---	AT1G65000	-1.25	-0.32	-1.81	0.1144024	0.3306117	-5.06	FALSE
247102_at	putative protein similar to unknov	---	AT5G66550	-1.27	-0.34	-1.81	0.1143978	0.3306117	-5.06	FALSE
258282_at	unknown protein	---	AT3G26910	1.73	0.79	1.81	0.1145295	0.3307696	-5.06	TRUE
266270_at	putative glutathione S-transferas	ATGSTU3	AT2G29470	3.88	1.95	1.81	0.1144909	0.3307696	-5.06	TRUE
253932_at	putative protein other Arabidopsi	---	AT4G26800	-1.19	-0.25	-1.81	0.1145151	0.3307696	-5.06	FALSE
254990_at	RNA-binding protein ;supported	CID12	AT4G10610	-1.18	-0.24	-1.81	0.1145064	0.3307696	-5.06	FALSE
249186_at	CHP-rich zinc finger protein-like	---	AT5G43040	1.21	0.27	1.81	0.1145054	0.3307696	-5.06	FALSE
263469_at	putative Na+/H+ antiporter	ATCHX21	AT2G31910	1.21	0.28	1.81	0.114566	0.330833	-5.06	FALSE
263157_at	aldehyde dehydrogenase homol	ALDH7B4	AT1G54100	1.45	0.53	1.81	0.1145867	0.3308509	-5.06	FALSE
266359_at	putative phospholipid cytidylyltra	CCT1	AT2G32260	-1.21	-0.27	-1.81	0.114656	0.3309253	-5.06	FALSE
260448_at	hypothetical protein predicted by	---	AT1G72410	-1.25	-0.33	-1.81	0.1146345	0.3309253	-5.06	FALSE
262378_at	CCAAT-binding factor B subunit	NF-YA3	AT1G72830	1.33	0.41	1.81	0.1146416	0.3309253	-5.06	FALSE
254377_at	subtilisin proteinase - like subtilis	---	AT4G21650	2.83	1.50	1.81	0.1146883	0.3309767	-5.06	FALSE
261324_at	unknown protein	---	AT1G44770	-1.32	-0.40	-1.81	0.1147997	0.3312564	-5.06	FALSE
262758_at	hypothetical protein predicted by	---	AT1G10780	-1.24	-0.31	-1.81	0.1148199	0.3312727	-5.06	FALSE
259009_at	thioglucosidase 3D precursor ide	PYK10	AT3G09260	1.41	0.49	1.81	0.1148707	0.3313774	-5.06	FALSE
255341_at	putative receptor-like protein kina	---	AT4G04500	3.40	1.76	1.81	0.1149039	0.3314313	-5.06	FALSE

261686_at	unknown protein ;supported by fu	---	AT1G47310	-1.23	-0.29	-1.81	0.1149381	0.3314655	-5.06	FALSE
252501_at	hypothetical protein	---	AT3G46880	1.22	0.28	1.81	0.1149448	0.3314655	-5.06	FALSE
247908_at	GS1-like protein ;supported by fu	GS1	AT5G57440	-1.59	-0.67	-1.81	0.1149978	0.3315197	-5.06	TRUE
265136_at	hypothetical protein similar to dis	---	AT1G51270	1.17	0.22	1.81	0.1150348	0.3315197	-5.06	FALSE
256504_at	cytosolic IMP-GMP specific 5'-nu	---	AT1G75210	-1.23	-0.29	-1.81	0.1150363	0.3315197	-5.06	FALSE
248954_at	unknown protein ; supported by	---	AT5G45420	1.19	0.25	1.81	0.1150315	0.3315197	-5.06	FALSE
262160_at	hypothetical protein predicted by	---	AT1G52590	-1.46	-0.55	-1.81	0.1150301	0.3315197	-5.06	FALSE
261606_at	peroxidase, putative similar to p	---	AT1G49570	1.30	0.38	1.81	0.1151258	0.331652	-5.06	FALSE
251354_at	putative protein hypothetical pro	---	AT3G61090	1.19	0.25	1.81	0.1151084	0.331652	-5.06	FALSE
252679_at	CCR4-associated factor 1-like p	---	AT3G44260	2.86	1.52	1.81	0.1151167	0.331652	-5.06	FALSE
247685_at	serine/threonine-specific protein	---	AT5G59680	1.80	0.85	1.81	0.1151605	0.3317098	-5.06	FALSE
261055_at	chloroplast nucleoid DNA bindin	---	AT1G01300	-1.27	-0.34	-1.81	0.1152713	0.331987	-5.06	TRUE
258364_at	unknown protein	GLIP4	AT3G14225	1.51	0.59	1.81	0.1153145	0.3320695	-5.06	FALSE
260287_at	unknown protein contains two Ke	---	AT1G80440	-1.40	-0.49	-1.81	0.115355	0.3321443	-5.06	FALSE
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XRE	---	---	-1.71	-0.77	-1.81	0.1153823	0.332181	-5.06	FALSE
249096_at	putative protein similar to unknov	---	AT5G43910	1.47	0.56	1.81	0.1154332	0.3322857	-5.07	FALSE
253648_at	pathogenesis related homeodom	PRHA	AT4G29940	-1.19	-0.25	-1.81	0.1154783	0.3323736	-5.07	FALSE
266336_at	putative Fe(II) transporter identic	ZIP3	AT2G32270	1.29	0.37	1.81	0.1155159	0.3324398	-5.07	FALSE
256577_at	unknown protein	---	AT3G28220	2.17	1.12	1.81	0.115568	0.3325477	-5.07	FALSE
260593_at	poly(A)-specific ribonuclease, pu	AHG2	AT1G55870	-1.30	-0.38	-1.81	0.1156247	0.3326689	-5.07	FALSE
264975_at	hypothetical protein predicted by	---	AT1G27070	-1.23	-0.30	-1.81	0.1156424	0.3326779	-5.07	FALSE
251532_at	putative protein F-box protein Fb	---	AT3G58530	-1.22	-0.29	-1.81	0.1156904	0.332774	-5.07	FALSE
262273_at	hypothetical protein predicted by	---	AT1G68730	1.20	0.26	1.81	0.1157136	0.3327988	-5.07	FALSE
261623_at	hypothetical protein similar to ret	ATSEC1A	AT1G01980	1.23	0.30	1.81	0.1157504	0.33284	-5.07	FALSE
248875_at	disease resistance protein-like	---	AT5G46470	1.41	0.49	1.80	0.1157571	0.33284	-5.07	FALSE
254058_at	putative protein cylicin II - huma	---	AT4G25210	-1.27	-0.34	-1.80	0.1159025	0.3332161	-5.07	FALSE
253898_s_a	tryptophan synthase beta-subuni	TSB2	AT4G27070 //	1.85	0.89	1.80	0.1159551	0.3333253	-5.07	FALSE
251842_at	extensin precursor -like protein e	---	AT3G54580	1.65	0.73	1.80	0.1160496	0.3335549	-5.07	FALSE
249359_at	putative protein unnamed ORF,	---	AT5G40470	-1.28	-0.36	-1.80	0.1160977	0.333651	-5.07	FALSE
254153_at	putative protein hypothetical pro	PWD	AT4G24450	-1.49	-0.57	-1.80	0.116163	0.3337967	-5.07	FALSE
264929_at	auxin-induced protein, putative s	---	AT1G60730	2.44	1.29	1.80	0.1161925	0.3338393	-5.07	FALSE
248861_at	senescence-associated protein 5	TRN2	AT5G46700	1.94	0.95	1.80	0.1162142	0.3338598	-5.07	FALSE
265093_at	unknown protein similar to NBD-	---	AT1G03905	1.31	0.38	1.80	0.1162351	0.3338776	-5.07	FALSE
261986_s_a	cytochrome P450, putative simil	CYP76C5	AT1G33720 //	1.75	0.81	1.80	0.1163904	0.3342396	-5.07	TRUE
255221_at	putative protein various predicte	---	AT4G05150	-1.26	-0.33	-1.80	0.1163818	0.3342396	-5.07	FALSE

259021_at	hypothetical protein predicted by	---	AT3G07540	-1.47	-0.56	-1.80	0.1164679	0.33442	-5.07	FALSE
254409_at	serine/threonine protein kinase -	---	AT4G21400	1.97	0.98	1.80	0.116514	0.3345102	-5.07	FALSE
263926_at	hypothetical protein predicted by	ATEME1A	AT2G21800	1.26	0.33	1.80	0.1165319	0.3345196	-5.07	FALSE
263013_at	knotted-like homeobox protein, p	KNAT6	AT1G23380	1.26	0.34	1.80	0.1165921	0.3346503	-5.07	FALSE
256833_at	calmodulin-stimulated calcium-A	---	AT3G22910	2.22	1.15	1.80	0.1166462	0.3347634	-5.07	FALSE
245375_at	NAK like protein kinase	---	AT4G17660	1.24	0.31	1.80	0.1166819	0.3347713	-5.08	FALSE
265432_at	hypothetical protein predicted by	---	AT2G20650	1.27	0.34	1.80	0.116693	0.3347713	-5.08	FALSE
266553_at	unknown protein ; supported by	---	AT2G46170	1.27	0.35	1.80	0.1166741	0.3347713	-5.08	FALSE
248421_at	unknown protein ;supported by f	---	AT5G51510	-1.23	-0.30	-1.80	0.1167273	0.3348143	-5.08	FALSE
247968_at	40S ribosomal protein S30 homo	---	AT5G56670	-1.58	-0.66	-1.80	0.1167373	0.3348143	-5.08	FALSE
255848_at	hypothetical protein predicted by	---	AT2G33640	1.24	0.32	1.80	0.1168021	0.3349579	-5.08	FALSE
260916_at	predicted protein ; supported by	---	AT1G02475	-1.24	-0.31	-1.80	0.1168696	0.3351093	-5.08	FALSE
259308_at	putative nodulin similar to noduli	---	AT3G05180	-1.43	-0.51	-1.80	0.1169211	0.3352149	-5.08	FALSE
249148_at	unknown protein ; supported by	---	AT5G43260	1.41	0.50	1.80	0.1169563	0.3352736	-5.08	FALSE
246335_at	lethal leaf-spot 1 homolog Lls1	ACD1	AT3G44880	1.31	0.39	1.80	0.1170005	0.3353162	-5.08	FALSE
255707_at	predicted protein	MEE50	AT4G00231	-1.19	-0.25	-1.80	0.116998	0.3353162	-5.08	FALSE
251480_at	putative protein inducible carbor	---	AT3G59710	1.30	0.38	1.80	0.1170729	0.3354596	-5.08	FALSE
253475_at	putative protein predicted protei	---	AT4G32290	-1.48	-0.57	-1.80	0.11708	0.3354596	-5.08	FALSE
252796_at	putative protein predicted protei	---	---	1.34	0.42	1.80	0.1171574	0.3355972	-5.08	FALSE
249631_at	sen1-like protein SEN1 - Saccha	---	AT5G37160	1.22	0.29	1.80	0.1171449	0.3355972	-5.08	FALSE
245709_at	putative protein	---	AT5G04320	-1.30	-0.37	-1.80	0.1172143	0.3356435	-5.08	FALSE
260947_at	fructokinase, putative similar to f	---	AT1G06020	1.18	0.23	1.80	0.1172177	0.3356435	-5.08	FALSE
261239_at	Avr9 elicitor response protein, p	---	AT1G32930	1.20	0.26	1.80	0.1172016	0.3356435	-5.08	FALSE
247145_at	receptor protein kinase-like prote	---	AT5G65600	2.98	1.58	1.80	0.1173318	0.335928	-5.08	FALSE
265716_at	unknown protein ;supported by f	---	AT2G03350	-1.32	-0.40	-1.80	0.1174252	0.3360552	-5.08	TRUE
259081_at	putative sodium proton exchange	NHX2	AT3G05030	-1.28	-0.36	-1.80	0.1174352	0.3360552	-5.08	TRUE
261678_at	disease resistance protein, puta	---	AT1G47370	1.26	0.33	1.80	0.1173933	0.3360552	-5.08	FALSE
261173_at	hypothetical protein predicted by	---	AT1G04830	-1.22	-0.29	-1.80	0.1174294	0.3360552	-5.08	FALSE
256239_at	hypothetical protein predicted by	---	AT3G12470	1.25	0.32	1.79	0.1174843	0.3361538	-5.08	FALSE
247367_at	oxygen-independent coproporph	---	AT5G63290	-1.40	-0.48	-1.79	0.117506	0.3361735	-5.08	FALSE
266687_at	putative arginine N-methyltransfe	PRMT1A	AT2G19670	-1.46	-0.54	-1.79	0.1175665	0.3362624	-5.08	FALSE
246350_at	hypothetical protein predicted by	---	AT1G16650	1.27	0.34	1.79	0.1175591	0.3362624	-5.08	FALSE
250250_at	putative protein similar to unknov	---	AT5G13610	-1.24	-0.31	-1.79	0.1176188	0.3363277	-5.08	FALSE
257833_at	transcriptional regulator protein,	LWD2	AT3G26640	-1.19	-0.25	-1.79	0.1176093	0.3363277	-5.08	FALSE
257065_at	diacylglycerol pyrophosphate ph	---	AT3G18220	1.36	0.44	1.79	0.117748	0.3364019	-5.08	FALSE

246642_s_a	putative protein predicted protei	---	---	1.17	0.23	1.79	0.1177435	0.3364019	-5.08	FALSE
264212_at	putative tRNA adenylyltransferas	---	AT1G22660	-1.37	-0.45	-1.79	0.1176963	0.3364019	-5.08	FALSE
256067_at	unknown protein ;supported by fu	---	AT1G07170	-1.31	-0.39	-1.79	0.1177177	0.3364019	-5.08	FALSE
256497_at	ORF1, putative similar to ORF1	ECS1	AT1G31580	1.51	0.59	1.79	0.1177358	0.3364019	-5.08	FALSE
253288_at	hypothetical protein	---	AT4G34310	1.24	0.31	1.79	0.1176744	0.3364019	-5.08	FALSE
254924_at	MAP kinase (ATMPK5) possible	ATMPK5	AT4G11330	1.40	0.48	1.79	0.1177086	0.3364019	-5.08	FALSE
250863_at	F1F0-ATPase inhibitor - like pro	---	AT5G04750	1.18	0.24	1.79	0.1179516	0.3367911	-5.09	FALSE
266812_at	putative protein kinase contains a	---	AT2G44830	1.31	0.39	1.79	0.1179325	0.3367911	-5.09	FALSE
262121_at	endo-1,4-beta-glucanase precur	ATCEL2	AT1G02800	1.28	0.35	1.79	0.1179876	0.3367911	-5.09	FALSE
255588_at	hypothetical protein	---	AT4G01570	-1.35	-0.43	-1.79	0.1179709	0.3367911	-5.09	FALSE
245179_at	putative protein similarity to prec	---	AT5G12400	1.23	0.30	1.79	0.1179854	0.3367911	-5.09	FALSE
250117_at	isopentenyl pyrophosphate:dime	IPP1	AT5G16440	-1.38	-0.46	-1.79	0.1179748	0.3367911	-5.09	FALSE
250369_at	cyclin 3b ; supported by cDNA: g	CYC3B	AT5G11300	1.29	0.37	1.79	0.1179412	0.3367911	-5.09	FALSE
247328_at	unknown protein ;supported by f	---	AT5G64130	1.38	0.46	1.79	0.1180073	0.336805	-5.09	FALSE
260692_at	hypothetical protein predicted by	---	AT1G32430	1.21	0.28	1.79	0.118085	0.3368288	-5.09	FALSE
267285_at	unknown protein	---	AT2G23690	1.44	0.52	1.79	0.1180475	0.3368288	-5.09	FALSE
253739_at	putative protein predicted protein	---	AT4G28760	-1.29	-0.37	-1.79	0.118083	0.3368288	-5.09	FALSE
250224_at	putative protein similar to unknov	---	AT5G14150	1.31	0.39	1.79	0.1180916	0.3368288	-5.09	FALSE
260155_at	unknown protein	---	AT1G52870	-1.58	-0.66	-1.79	0.1181015	0.3368288	-5.09	FALSE
263210_at	Expressed protein ; supported by	---	AT1G10585	6.01	2.59	1.79	0.1181042	0.3368288	-5.09	FALSE
249596_s_a	glucuronosyl transferase-like pro	---	AT5G37950 //	1.39	0.47	1.79	0.1181221	0.3368377	-5.09	FALSE
254661_at	unknown protein multidrug resis	---	AT4G18260	-1.24	-0.32	-1.79	0.118157	0.3368953	-5.09	FALSE
262718_at	hypothetical protein similar to put	---	---	1.23	0.29	1.79	0.1182027	0.3369834	-5.09	FALSE
259063_at	putative 5B-anther specific protei	---	AT3G07450	1.17	0.23	1.79	0.1182536	0.3370441	-5.09	FALSE
265243_at	hypothetical protein predicted by	NPG1	AT2G43040	-1.24	-0.31	-1.79	0.118252	0.3370441	-5.09	FALSE
260939_at	hypothetical protein contains sim	---	AT1G45180	1.68	0.75	1.79	0.1183456	0.3372375	-5.09	TRUE
249582_at	calmodulin 1 (CAM1) ; supporte	CAM1	AT5G37780	-1.28	-0.35	-1.79	0.118351	0.3372375	-5.09	FALSE
259178_at	unknown protein similar to hypot	RGLG1	AT3G01650	1.30	0.38	1.79	0.118449	0.337317	-5.09	FALSE
247058_at	dolichyl-di-phosphooligosacchari	DGL1	AT5G66680	-1.26	-0.33	-1.79	0.1184328	0.337317	-5.09	FALSE
251511_at	putative protein several hypothet	---	AT3G59180	1.20	0.26	1.79	0.1184624	0.337317	-5.09	FALSE
246141_at	TipD - like WD repeat protein Tip	---	AT5G19920	-1.27	-0.35	-1.79	0.1184389	0.337317	-5.09	FALSE
267103_at	putative UDP-N-acetylglucosami	GPT	AT2G41490	1.22	0.29	1.79	0.1184676	0.337317	-5.09	FALSE
260135_at	calmodulin-related protein simila	---	AT1G66400	1.93	0.95	1.79	0.1184274	0.337317	-5.09	FALSE
251548_at	putative protein predicted protei	---	---	1.28	0.36	1.79	0.1184953	0.3373538	-5.09	FALSE
263166_at	putative protein destination facto	---	AT1G03050	1.18	0.24	1.79	0.1185341	0.3374221	-5.09	FALSE

262133_at	high affinity sulphate transporter	SULTR1;2	AT1G78000	-1.95	-0.97	-1.79	0.1185731	0.3374911	-5.09	FALSE
267350_at	putative DNA-directed RNA polyr	NRPD1B	AT2G40030	1.27	0.35	1.79	0.1186107	0.3375286	-5.09	FALSE
252818_at	putative protein several hypothet	---	---	1.26	0.33	1.79	0.1186159	0.3375286	-5.09	FALSE
267320_at	hypothetical protein predicted by	---	AT2G19300	1.23	0.30	1.79	0.1186355	0.3375423	-5.09	FALSE
256629_at	serine/threonine protein phospha	ATFYPP3	AT3G19980	-1.21	-0.28	-1.79	0.118651	0.3375441	-5.09	FALSE
255832_at	hypothetical protein predicted by	---	AT2G33360	-1.32	-0.40	-1.79	0.1186754	0.3375716	-5.09	FALSE
267179_at	putative ADP ribosylation factor 1	AGD7	AT2G37550	1.34	0.43	1.79	0.1187438	0.3375731	-5.09	FALSE
246925_at	cytochrome P450 71B1 - like pro	CYP71B14	AT5G25180	-1.21	-0.27	-1.79	0.1187185	0.3375731	-5.09	FALSE
246055_at	alpha-galactosidase - like protei	AtAGAL1	AT5G08380	-1.58	-0.66	-1.79	0.1187375	0.3375731	-5.09	FALSE
261950_at	zinc finger protein, putative simil	---	AT1G64620	1.37	0.45	1.79	0.11875	0.3375731	-5.09	FALSE
259148_at	putative ATPase similar to ATPa	---	AT3G10350	-1.28	-0.35	-1.79	0.1187398	0.3375731	-5.09	FALSE
247448_at	putative protein predicted protei	---	AT5G62770	1.98	0.99	1.79	0.1187648	0.3375731	-5.09	FALSE
264971_at	Expressed protein ; supported by	---	AT1G67210	-1.18	-0.23	-1.79	0.1187811	0.3375776	-5.09	FALSE
253364_at	F-box protein family, AtFBX13 c	---	AT4G33160	1.18	0.24	1.79	0.1187969	0.3375803	-5.09	FALSE
249087_at	DNA binding protein EREBP-3-lil	ERF9	AT5G44210	-1.38	-0.47	-1.79	0.1188128	0.3375836	-5.09	FALSE
253818_at	hypothetical protein	---	AT4G28330	1.30	0.38	1.79	0.1188417	0.3376236	-5.09	FALSE
248932_at	peptide transporter	PTR3	AT5G46050	2.12	1.08	1.79	0.1188632	0.3376425	-5.09	FALSE
260337_at	unknown protein	WRKY57	AT1G69310	-1.27	-0.34	-1.79	0.1189761	0.3379213	-5.09	FALSE
254671_at	MuDR transposable element - lil	---	---	1.21	0.27	1.79	0.1189929	0.3379267	-5.09	FALSE
246038_s_a	putative protein thiamin pyropho	atnudt20	AT5G19460 ///	1.31	0.39	1.79	0.1191084	0.3381855	-5.09	FALSE
255725_at	hypothetical protein similar to put	PFT1	AT1G25540	1.17	0.23	1.79	0.1191136	0.3381855	-5.09	FALSE
255139_s_a	extensin-like protein hydroxypro	---	AT4G08400 ///	1.18	0.24	1.78	0.119173	0.3383119	-5.09	FALSE
254054_at	putative protein DNA-binding pro	---	AT4G25320	-1.34	-0.42	-1.78	0.1192009	0.3383489	-5.10	FALSE
266268_at	unknown protein predicted by ge	---	AT2G29510	-1.20	-0.26	-1.78	0.1192691	0.3383741	-5.10	FALSE
249838_at	unknown protein ;supported by f	---	AT5G23460	-1.31	-0.39	-1.78	0.1192517	0.3383741	-5.10	FALSE
263292_at	putative Ta11-like non-LTR retro	---	---	1.22	0.29	1.78	0.1192682	0.3383741	-5.10	FALSE
248200_at	O-methyltransferase ;supported	ATOMT1	AT5G54160	1.75	0.81	1.78	0.1192646	0.3383741	-5.10	FALSE
245405_at	hypothetical protein	---	AT4G17150	-1.18	-0.24	-1.78	0.1193595	0.3385592	-5.10	FALSE
252392_s_a	putative protein various predicte	---	AT3G47890 ///	-1.31	-0.39	-1.78	0.1193937	0.3385592	-5.10	FALSE
267535_at	putative C2H2-type zinc finger pr	ZFP8	AT2G41940	-1.46	-0.55	-1.78	0.1193911	0.3385592	-5.10	FALSE
262821_at	unknown protein EST gb|F14156	---	AT1G11800	-1.16	-0.21	-1.78	0.1193689	0.3385592	-5.10	FALSE
253997_at	disease resistance protein RPS2	RPS2	AT4G26090	1.87	0.90	1.78	0.1194422	0.3386159	-5.10	FALSE
253983_at	putative protein SPF1 protein -lp	WRKY20	AT4G26640	-1.27	-0.34	-1.78	0.1194434	0.3386159	-5.10	FALSE
262584_at	hypothetical protein Strong simil	---	AT1G15440	-1.56	-0.65	-1.78	0.1194966	0.3387246	-5.10	FALSE
260134_at	Myb-related transcription factor,	MYB113	AT1G66370	1.29	0.37	1.78	0.1195389	0.3387603	-5.10	FALSE

248320_at	putative protein similar to unknov	---	AT5G52720	1.25	0.32	1.78	0.1195326	0.3387603	-5.10	FALSE
248424_at	unknown protein	---	AT5G51680	1.89	0.92	1.78	0.1195588	0.3387747	-5.10	FALSE
253527_at	pathogenesis-related protein hor	---	AT4G31470	1.23	0.30	1.78	0.1196038	0.33886	-5.10	FALSE
260249_s_a	unknown protein similar to unkno	---	AT1G74280 ///	-1.28	-0.36	-1.78	0.1196364	0.3388682	-5.10	FALSE
248152_at	DNA repair and meiosis protein M	MRE11	AT5G54260	-1.32	-0.41	-1.78	0.1196235	0.3388682	-5.10	FALSE
255878_at	putative bZIP transcription factor	---	AT2G40620	-1.36	-0.44	-1.78	0.1196789	0.3389044	-5.10	FALSE
252222_at	putative protein various predicte	---	AT3G49840 ///	1.52	0.61	1.78	0.1196646	0.3389044	-5.10	FALSE
266171_at	putative CCAAT-binding transcri	NF-YB1	AT2G38880	-1.29	-0.36	-1.78	0.1197344	0.3389774	-5.10	FALSE
248587_at	Expressed protein ; supported by	---	AT5G49550	-1.23	-0.30	-1.78	0.1197265	0.3389774	-5.10	FALSE
260719_at	unknown protein	---	AT1G48090	-1.29	-0.36	-1.78	0.1198258	0.339194	-5.10	FALSE
252373_at	disease resistance protein EDS1	EDS1	AT3G48090	1.87	0.91	1.78	0.1199232	0.3394279	-5.10	FALSE
259479_at	Expressed protein ; supported by	---	AT1G19020	2.35	1.23	1.78	0.1199789	0.339501	-5.10	FALSE
265848_at	putative sugar transporter	INT3	AT2G35740	1.36	0.44	1.78	0.1199778	0.339501	-5.10	FALSE
258302_at	hypothetical protein predicted by	---	---	1.19	0.25	1.78	0.1199962	0.3395081	-5.10	FALSE
245828_at	transcription factor, putative sim	VIM1	AT1G57820	-1.27	-0.34	-1.78	0.1200364	0.3395796	-5.10	FALSE
246821_at	calmodulin-binding - like protein	CBP60G	AT5G26920	2.19	1.13	1.78	0.1200702	0.3395911	-5.10	FALSE
257505_at	hypothetical protein	---	AT1G47940	1.17	0.22	1.78	0.1200569	0.3395911	-5.10	FALSE
266215_at	putative endoxyloglucan glycosyl	EXGT-A1	AT2G06850	1.85	0.89	1.78	0.1201283	0.339671	-5.10	TRUE
260900_s_a	branched-chain alpha keto-acid	---	AT1G21400 ///	1.47	0.56	1.78	0.1201232	0.339671	-5.10	TRUE
260551_at	putative trypsin inhibitor ; suppo	ATTI1	AT2G43510	-1.62	-0.69	-1.78	0.1201587	0.3397149	-5.10	TRUE
265610_at	unknown protein ;supported by f	---	AT2G25430	1.18	0.24	1.78	0.1202083	0.3397623	-5.10	TRUE
254765_at	hypothetical protein	---	AT4G13270	-1.25	-0.32	-1.78	0.1202202	0.3397623	-5.10	FALSE
251847_at	tryptophan synthase alpha chain	TSA1	AT3G54640	2.41	1.27	1.78	0.1202103	0.3397623	-5.10	FALSE
248365_at	putative protein strong similarity t	---	AT5G52500	1.23	0.30	1.78	0.1202567	0.3398236	-5.10	FALSE
251769_at	receptor kinase - like protein rec	CCR3	AT3G55950	2.91	1.54	1.78	0.1202875	0.3398684	-5.10	FALSE
247502_at	putative protein predicted protei	---	AT5G61940	-1.20	-0.27	-1.78	0.1203473	0.339886	-5.10	FALSE
247024_at	Expressed protein ; supported by	---	AT5G66985	1.28	0.35	1.78	0.1203591	0.339886	-5.10	FALSE
250500_at	periaxin - like protein periaxin, R	---	AT5G09530	-7.32	-2.87	-1.78	0.1203605	0.339886	-5.10	FALSE
264776_at	unknown protein location of EST	---	AT1G22860	-1.22	-0.29	-1.78	0.1203682	0.339886	-5.10	FALSE
246195_at	E2, ubiquitin-conjugating enzym	UBC17	AT4G36410	-2.27	-1.18	-1.78	0.1203392	0.339886	-5.10	FALSE
257449_at	hypothetical protein predicted by	---	AT2G31420	1.23	0.30	1.78	0.1204536	0.340085	-5.10	FALSE
266038_at	putative ABC transporter	ATMRP11	AT2G07680	-1.44	-0.53	-1.78	0.120485	0.3401315	-5.11	FALSE
253566_at	DNA topoisomerase like- protein	---	AT4G31210	-1.74	-0.80	-1.78	0.1205792	0.3403555	-5.11	FALSE
247940_at	phosphatidylserine decarboxylas	PSD2	AT5G57190	1.80	0.85	1.78	0.1206269	0.3404058	-5.11	FALSE
250430_at	putative protein	---	AT5G10460	-1.19	-0.25	-1.78	0.1206264	0.3404058	-5.11	FALSE

253831_at	Expressed protein ; supported by	---	AT4G27580	1.23	0.30	1.78	0.120646	0.3404175	-5.11	FALSE
250982_at	putative protein zinc finger prote	JKD	AT5G03150	1.42	0.51	1.78	0.1206966	0.3405181	-5.11	FALSE
262786_at	putative lipase similar to gb|X028	---	AT1G10740	-1.32	-0.40	-1.78	0.1208239	0.3407489	-5.11	FALSE
249223_at	receptor lectin kinase-like protein	---	AT5G42120	-1.25	-0.32	-1.78	0.1207967	0.3407489	-5.11	FALSE
249381_at	acidic ribosomal protein P2 -like	---	AT5G40040	1.27	0.35	1.78	0.1208381	0.3407489	-5.11	FALSE
253062_at	putative protein predicted protein	NPY5	AT4G37590	-1.70	-0.76	-1.78	0.1208105	0.3407489	-5.11	FALSE
256248_at	hypothetical protein	---	AT3G66652	-1.35	-0.43	-1.78	0.1208639	0.3407793	-5.11	FALSE
257062_at	zinc finger protein, putative cont	EMB2454	AT3G18290	1.56	0.65	1.77	0.1209364	0.3408995	-5.11	TRUE
258449_s_a	putative RNA helicase similar to	PMH1	AT3G22310 /	-1.35	-0.43	-1.77	0.1209356	0.3408995	-5.11	FALSE
252473_s_a	hypothetical protein several hypo	---	AT3G46610 /	-1.36	-0.44	-1.77	0.1211425	0.3414384	-5.11	FALSE
257094_at	hypothetical protein similar to tet	---	AT3G20480	-1.35	-0.43	-1.77	0.1212445	0.3416836	-5.11	FALSE
260142_at	unknown protein ; supported by	---	AT1G71900	-1.27	-0.34	-1.77	0.1212595	0.3416836	-5.11	FALSE
247430_at	putative protein contains similarit	---	AT5G62610	-1.27	-0.34	-1.77	0.1213078	0.3417776	-5.11	FALSE
265233_s_a	hypothetical protein	---	AT2G07718	1.23	0.30	1.77	0.1213388	0.3417805	-5.11	TRUE
255645_at	coded for by A. thaliana cDNA T4	---	AT4G00880	-1.39	-0.48	-1.77	0.121334	0.3417805	-5.11	FALSE
247925_at	TCH4 protein (gb|AAA92363.1)	TCH4	AT5G57560	2.34	1.23	1.77	0.1213882	0.3417882	-5.11	TRUE
248357_at	putative protein similar to unknov	---	AT5G52380	-1.49	-0.57	-1.77	0.1214165	0.3417882	-5.11	TRUE
261505_at	carboxypeptidase, putative simil	SOL1	AT1G71696	1.30	0.37	1.77	0.1213687	0.3417882	-5.11	FALSE
263304_at	hypothetical protein predicted by	---	AT2G01920	1.21	0.28	1.77	0.1214103	0.3417882	-5.11	FALSE
250486_at	putative protein predicted protein	---	AT5G09670 /	-1.23	-0.30	-1.77	0.1214145	0.3417882	-5.11	FALSE
255298_at	putative protein similar to transcr	ATMSRB6	AT4G04840	2.07	1.05	1.77	0.1215372	0.3418106	-5.11	TRUE
246011_at	putative protein auxin-induced b	---	AT5G08330	-1.51	-0.60	-1.77	0.1214993	0.3418106	-5.11	TRUE
252115_at	non-specific lipid transfer protein	LTP5	AT3G51600	-1.28	-0.35	-1.77	0.1214947	0.3418106	-5.11	FALSE
256367_at	C-x8-C-x5-C-x3-H type Zinc fing	---	AT1G66810	1.24	0.31	1.77	0.1215446	0.3418106	-5.11	FALSE
257012_at	RNA-binding protein, putative si	TEL1	AT3G26120	1.20	0.26	1.77	0.1215743	0.3418106	-5.11	FALSE
258318_at	unknown protein	---	AT3G22680	-1.42	-0.50	-1.77	0.1215375	0.3418106	-5.11	FALSE
251614_at	hypothetical protein	---	AT3G57970	1.27	0.35	1.77	0.1214564	0.3418106	-5.11	FALSE
259452_at	En/Spm-like transposon protein,	---	---	1.23	0.29	1.77	0.1215585	0.3418106	-5.11	FALSE
263858_at	hypothetical protein predicted by	---	AT2G04370	1.19	0.26	1.77	0.1215654	0.3418106	-5.11	FALSE
249618_at	putative protein predicted protein	---	AT5G37490	3.54	1.83	1.77	0.1215593	0.3418106	-5.11	FALSE
249648_at	putative protein hypothetical pro	---	AT5G37050	1.33	0.41	1.77	0.121675	0.3420516	-5.11	FALSE
263459_at	ankyrin-like protein	---	AT2G31820	1.36	0.44	1.77	0.1217074	0.3421005	-5.11	FALSE
248961_at	subtilisin-like protease	---	AT5G45650	-1.80	-0.85	-1.77	0.1217428	0.3421171	-5.11	FALSE
247808_at	contains similarity to unknown pr	ECT10	AT5G58190	1.19	0.25	1.77	0.1217433	0.3421171	-5.11	FALSE
262254_at	unknown protein similar to GDSL	GLIP5	AT1G53920	1.52	0.60	1.77	0.12188	0.3424566	-5.12	FALSE

265794_at	unknown protein	---	AT2G01310	-1.18	-0.24	-1.77	0.1218941	0.3424566	-5.12	FALSE
262375_at	unknown protein ; supported by	SUVH3	AT1G73100	-1.26	-0.34	-1.77	0.1220085	0.3426244	-5.12	FALSE
257059_at	unknown protein ; supported by	---	AT3G15280	1.20	0.26	1.77	0.1219976	0.3426244	-5.12	FALSE
254683_at	hypothetical protein ;supported b	---	AT4G13800	1.24	0.31	1.77	0.122014	0.3426244	-5.12	FALSE
249074_at	putative protein contains similarit	---	AT5G44080	-1.22	-0.29	-1.77	0.1219899	0.3426244	-5.12	FALSE
249228_at	SKP1/ASK1 (At2) identical to UI	ASK2	AT5G42190	-1.31	-0.39	-1.77	0.1220311	0.3426303	-5.12	FALSE
250980_at	putative protein	---	AT5G03130	-1.58	-0.66	-1.77	0.1220758	0.3427139	-5.12	FALSE
245624_at	glucosyltransferase like protein	---	AT4G14090	1.30	0.38	1.77	0.1221196	0.3427945	-5.12	FALSE
263434_at	putative homeodomain transcript	PRS	AT2G28610	-1.18	-0.24	-1.77	0.1221722	0.3429	-5.12	FALSE
252790_at	putative protein various predicte	---	---	1.19	0.25	1.77	0.1222033	0.3429451	-5.12	FALSE
257544_at	putative DNA-binding protein sim	---	AT3G20880	1.28	0.36	1.77	0.1222281	0.3429724	-5.12	FALSE
267458_at	similar to Mlo proteins from H. vu	MLO5	AT2G33670	1.29	0.36	1.77	0.1222534	0.3430011	-5.12	FALSE
267239_at	unknown protein	---	AT2G02510	-1.23	-0.30	-1.77	0.1222789	0.3430282	-5.12	FALSE
265957_at	hypothetical protein predicted by	---	AT2G37300	1.16	0.22	1.77	0.1223286	0.3430282	-5.12	FALSE
267392_at	putative beta-glucosidase	PEN2	AT2G44490	1.37	0.45	1.77	0.1222954	0.3430282	-5.12	FALSE
264868_at	unknown protein	---	AT1G24090	1.53	0.61	1.77	0.1223252	0.3430282	-5.12	FALSE
261501_at	wall-associated kinase 1, putativ	---	AT1G28390	1.33	0.42	1.77	0.1223382	0.3430282	-5.12	FALSE
255523_at	pectinesterase - like protein simil	---	AT4G02320	-1.22	-0.28	-1.77	0.1223791	0.3430584	-5.12	FALSE
249984_at	putative protein rsc43, Dictyoste	---	AT5G18400	1.49	0.57	1.77	0.122371	0.3430584	-5.12	FALSE
263848_at	putative reverse transcriptase	---	---	1.25	0.32	1.77	0.1224024	0.3430817	-5.12	FALSE
258001_at	AIG2-like protein similar to AIG2	---	AT3G28950	-1.21	-0.27	-1.77	0.1225523	0.3434595	-5.12	FALSE
253813_at	putative protein hypothetical pro	---	AT4G28150	-1.24	-0.31	-1.77	0.1225961	0.3435402	-5.12	FALSE
251060_at	putative protein serine/threonine	ATSR1	AT5G01820	2.19	1.13	1.76	0.1226802	0.3437336	-5.12	FALSE
251602_at	Expressed protein ; supported by	---	AT3G57785	-1.21	-0.28	-1.76	0.1227013	0.3437504	-5.12	FALSE
262965_at	hypothetical protein predicted by	---	AT1G54310	-1.32	-0.40	-1.76	0.1227349	0.3438023	-5.12	FALSE
251299_at	putative protein transcription fac	---	AT3G61950	-1.24	-0.31	-1.76	0.1227517	0.3438072	-5.12	FALSE
258681_at	unknown protein ; supported by	---	AT3G08610	-1.23	-0.30	-1.76	0.1228288	0.3439388	-5.12	FALSE
252076_at	LS1-like protein AT-LS1 product	---	AT3G51660	1.72	0.78	1.76	0.1228259	0.3439388	-5.12	FALSE
262850_at	signal response protein (GAI) ide	GAI	AT1G14920	-1.48	-0.57	-1.76	0.1228915	0.344072	-5.12	TRUE
259631_at	heat shock protein, putative simi	ERD2	AT1G56410	1.18	0.24	1.76	0.1229198	0.344109	-5.12	FALSE
245118_at	putative thioredoxin reductase T	NTRC	AT2G41680	-1.21	-0.27	-1.76	0.122962	0.3441623	-5.12	FALSE
258414_at	unknown protein ;supported by f	---	AT3G17380	-1.23	-0.30	-1.76	0.122969	0.3441623	-5.12	FALSE
261564_at	NAC domain protein, putative si	ATAF1	AT1G01720	1.33	0.41	1.76	0.1230265	0.3442388	-5.12	TRUE
264880_at	hypothetical protein contains sim	---	AT1G61210	1.26	0.34	1.76	0.123013	0.3442388	-5.12	FALSE
255883_at	unknown protein similar to putat	---	AT1G20270	-1.28	-0.35	-1.76	0.1230884	0.3442852	-5.13	FALSE

257739_at	unknown protein	---	AT3G27470	1.31	0.39	1.76	0.1230772	0.3442852	-5.13	FALSE
252428_at	putative protein rjs - Mus muscu	---	AT3G47660	1.25	0.32	1.76	0.1230593	0.3442852	-5.12	FALSE
262176_at	3-ketoacyl-ACP synthase, putati	FAB1	AT1G74960	-1.27	-0.34	-1.76	0.1231249	0.3443209	-5.13	FALSE
260844_at	peroxisomal targeting signal type	PEX7	AT1G29260	-1.20	-0.26	-1.76	0.1231313	0.3443209	-5.13	FALSE
265311_at	hypothetical protein predicted by	---	AT2G20250	-1.39	-0.48	-1.76	0.1231703	0.3443529	-5.13	FALSE
257510_at	unknown protein	---	AT1G55360	-1.72	-0.78	-1.76	0.123173	0.3443529	-5.13	FALSE
255133_at	putative protein (fragment) gluta	---	AT4G08320	-1.26	-0.33	-1.76	0.1232451	0.3444713	-5.13	FALSE
253325_at	Expressed protein ; supported by	---	AT4G33925	1.48	0.57	1.76	0.1232455	0.3444713	-5.13	FALSE
252540_at	putative protein CDP-alcohol ph	---	AT3G45740	1.20	0.27	1.76	0.1232954	0.3445685	-5.13	FALSE
260834_at	sugar kinase, putative similar to	---	AT1G06730	-1.28	-0.36	-1.76	0.1233529	0.3446869	-5.13	FALSE
247169_at	unknown protein	---	AT5G65520	-1.32	-0.40	-1.76	0.1233705	0.3446939	-5.13	FALSE
248764_at	putative protein contains similarit	NF-YB2	AT5G47640	-1.29	-0.36	-1.76	0.1233913	0.3447099	-5.13	FALSE
253481_at	aspartate aminotransferase ;su	ASP5	AT4G31990	-1.23	-0.29	-1.76	0.1235428	0.3450906	-5.13	FALSE
262659_at	putative nucleoside triphosphata	---	AT1G14240	1.22	0.29	1.76	0.12357	0.3451245	-5.13	FALSE
246483_at	receptor protein kinase-like prot	NIK1	AT5G16000	-1.59	-0.67	-1.76	0.1236384	0.3452732	-5.13	FALSE
257106_at	unknown protein	---	AT3G29060	1.19	0.25	1.76	0.1236799	0.345347	-5.13	FALSE
253666_at	xyloglucan endo-1,4-beta-D-gluc	MERI5B	AT4G30270	1.20	0.26	1.76	0.1237467	0.3454911	-5.13	FALSE
258547_at	unknown protein	---	AT3G06895	-1.18	-0.23	-1.76	0.1237621	0.3454917	-5.13	FALSE
250414_at	putative protein Glr5, Arabidopsi	GLR2.6	AT5G11180	1.19	0.25	1.76	0.1237985	0.3455512	-5.13	FALSE
261191_at	starch synthase, putative similar	---	AT1G32900	1.49	0.58	1.76	0.1238653	0.3456331	-5.13	TRUE
258047_at	putative 4-coumarate:CoA ligase	4CL2	AT3G21240	2.14	1.10	1.76	0.1238473	0.3456331	-5.13	FALSE
246610_at	putative protein	---	AT5G35400	-1.22	-0.28	-1.76	0.1238733	0.3456331	-5.13	FALSE
263950_at	hypothetical protein predicted by	HVA22J	AT2G36020	1.17	0.22	1.76	0.1239036	0.3456596	-5.13	FALSE
259906_at	unknown protein	---	AT1G74120	-1.19	-0.25	-1.76	0.1239131	0.3456596	-5.13	FALSE
260610_at	putative SF16 protein {Helianthus	IQD14	AT2G43680	-1.38	-0.47	-1.76	0.1239748	0.3457657	-5.13	FALSE
257362_at	hypothetical protein predicted by	---	AT2G45840	1.18	0.23	1.76	0.1239815	0.3457657	-5.13	FALSE
267270_at	hypothetical protein predicted by	---	AT2G02550	1.29	0.37	1.76	0.1241058	0.34607	-5.13	FALSE
257010_at	Expressed protein ; supported by	ATEXO70D	AT3G14090	1.36	0.45	1.76	0.1241674	0.3461388	-5.13	FALSE
246373_at	receptor-like protein kinase, puta	---	AT1G51860	1.36	0.44	1.76	0.1241665	0.3461388	-5.13	FALSE
266959_at	putative DNA replication licensin	MCM5	AT2G07690	-1.86	-0.90	-1.76	0.124176	0.3461388	-5.13	FALSE
245449_at	retrotransposon like protein	---	---	1.40	0.49	1.76	0.124227	0.3461964	-5.13	FALSE
263119_at	hypothetical protein predicted by	---	AT1G03110	-1.32	-0.40	-1.76	0.1242223	0.3461964	-5.13	FALSE
258184_at	two-component phosphorelay m	AHP1	AT3G21510	1.32	0.40	1.76	0.1242575	0.3462391	-5.13	FALSE
263297_at	putative ADP-ribosylation factor	ATARFB1A	AT2G15310	1.37	0.46	1.76	0.1243432	0.3464357	-5.13	TRUE
261544_at	unknown protein	---	AT1G63540	-1.31	-0.39	-1.76	0.124393	0.3464916	-5.14	FALSE

247699_at	GTP-binding protein ara-3 GTP-	---	AT5G59840	1.42	0.50	1.75	0.1244142	0.3464916	-5.14	FALSE
246684_at	putative protein nucleoid DNA-b	CDR1	AT5G33340	1.30	0.37	1.75	0.124424	0.3464916	-5.14	FALSE
251114_at	transcription factor GT-3a	---	AT5G01380	2.04	1.03	1.75	0.1244127	0.3464916	-5.14	FALSE
250952_at	putative protein	ATIREG2	AT5G03570	1.29	0.37	1.75	0.1244565	0.3465396	-5.14	FALSE
261377_at	unknown protein ;supported by fu	---	AT1G18850	-1.52	-0.61	-1.75	0.1244906	0.3465924	-5.14	FALSE
247164_at	NifS-like aminotranfserase ; sup	NFS1	AT5G65720	-1.23	-0.29	-1.75	0.1245246	0.3466023	-5.14	FALSE
259696_at	unknown protein ; supported by	---	AT1G63150	-1.22	-0.29	-1.75	0.1245206	0.3466023	-5.14	FALSE
258832_at	putative protein kinase similar to	---	AT3G07070	1.24	0.31	1.75	0.1245722	0.3466501	-5.14	FALSE
250740_at	t-SNARE SED5 (gb|AAC06291.1	SYP31	AT5G05760	1.18	0.24	1.75	0.1245719	0.3466501	-5.14	FALSE
252959_at	putative protein NADH dehydrog	---	AT4G38640	-1.22	-0.29	-1.75	0.1246256	0.3467511	-5.14	FALSE
252454_at	putative protein various predicte	---	AT3G47130	1.17	0.23	1.75	0.1246389	0.3467511	-5.14	FALSE
247851_at	outer membrane lipoprotein - lik	TIL	AT5G58070	-1.51	-0.60	-1.75	0.1246887	0.3468474	-5.14	FALSE
253993_at	mitogen activated protein kinase	MEK1	AT4G26070	1.45	0.54	1.75	0.1247414	0.3469095	-5.14	FALSE
256831_at	hypothetical protein	---	AT3G22870	1.22	0.29	1.75	0.1247286	0.3469095	-5.14	FALSE
256417_s_a	omega-3 fatty acid desaturase,	FAD7	AT3G11170 /	1.43	0.51	1.75	0.1249074	0.3472865	-5.14	TRUE
251129_at	putative protein predicted protei	---	AT5G01150	1.22	0.28	1.75	0.1249042	0.3472865	-5.14	FALSE
265627_at	Expressed protein ; supported by	---	AT2G27285	-1.24	-0.31	-1.75	0.125025	0.3475711	-5.14	FALSE
253644_at	putative protein predicted protei	---	AT4G29870	-1.32	-0.40	-1.75	0.1250708	0.347633	-5.14	FALSE
267616_at	unknown protein ;supported by f	---	AT2G26680	-1.24	-0.31	-1.75	0.1250778	0.347633	-5.14	FALSE
252470_at	protein kinase 6-like protein prot	---	AT3G46930	1.73	0.79	1.75	0.1251027	0.347656	-5.14	FALSE
245679_at	clathrin-associated protein, puta	---	AT1G56590	-1.24	-0.30	-1.75	0.1251165	0.347656	-5.14	FALSE
260816_at	hypothetical protein predicted by	---	AT1G06930	1.29	0.37	1.75	0.1251651	0.3477486	-5.14	FALSE
253646_at	MAP kinase kinase 2 ; supporte	ATMKK2	AT4G29810	1.39	0.48	1.75	0.1251852	0.3477622	-5.14	FALSE
258072_at	unknown protein	RGS1	AT3G26090	1.19	0.25	1.75	0.1252213	0.3477776	-5.14	FALSE
249311_at	disease resistance protein-like	---	AT5G41540	1.26	0.33	1.75	0.1252112	0.3477776	-5.14	FALSE
258778_s_a	hypothetical protein predicted by	---	AT3G11860 /	-1.26	-0.33	-1.75	0.1253178	0.347961	-5.14	FALSE
251127_at	putative protein predicted protei	---	AT5G01080	-1.25	-0.32	-1.75	0.1253136	0.347961	-5.14	FALSE
250569_at	myc-like protein myc-like regulat	BIM1	AT5G08130	1.47	0.56	1.75	0.1254739	0.3479705	-5.14	TRUE
258528_at	unknown protein contains Pfam p	---	AT3G06770	-1.60	-0.68	-1.75	0.1254129	0.3479705	-5.14	TRUE
248625_at	3-keto-acyl-CoA thiolase 2 (gb|A	PKT2	AT5G48880	1.50	0.58	1.75	0.1254211	0.3479705	-5.14	FALSE
245877_at	unknown protein	---	AT1G26220	-1.31	-0.39	-1.75	0.1255043	0.3479705	-5.14	FALSE
264470_at	cytochrome P450, putative simil	CYP735A2	AT1G67110	1.29	0.37	1.75	0.1254898	0.3479705	-5.14	FALSE
261925_at	oligopeptide transporter, putative	---	AT1G22540	-1.22	-0.28	-1.75	0.1254467	0.3479705	-5.14	FALSE
258976_at	putative dehydrogenase contain	---	AT3G01980	-1.19	-0.25	-1.75	0.1254947	0.3479705	-5.14	FALSE
260624_at	high-affinity nitrate transporter A	NRT2.2	AT1G08100	1.33	0.41	1.75	0.1254231	0.3479705	-5.14	FALSE

258798_at	hypothetical protein predicted by	---	AT3G04540	1.24	0.31	1.75	0.125504	0.3479705	-5.14	FALSE
258905_at	unknown protein similar to hypot	---	AT3G06390	1.39	0.48	1.75	0.1254429	0.3479705	-5.14	FALSE
254267_at	dihydroorotase ; supported by cl	PYR4	AT4G22930	-1.24	-0.31	-1.75	0.1254731	0.3479705	-5.14	FALSE
253000_at	putative protein other predicted p	---	AT4G38360	1.27	0.35	1.75	0.1254537	0.3479705	-5.14	FALSE
247025_at	zeaxanthin epoxidase precursor	ABA1	AT5G67030	-1.28	-0.36	-1.75	0.1255208	0.3479739	-5.14	FALSE
253271_s_a	SKP1/ASK1 (At11), putative sim	ASK12	AT4G34210 /	1.27	0.35	1.75	0.1255401	0.3479851	-5.14	FALSE
256772_at	galactosidase, putative similar to	BGAL1	AT3G13750	1.97	0.98	1.75	0.1257269	0.3482491	-5.14	FALSE
252287_at	30S ribosomal protein S9 -like si	---	AT3G49080	-1.37	-0.45	-1.75	0.1256853	0.3482491	-5.14	FALSE
247536_at	PREG-like - like protein PREG-l	CYCP4;2	AT5G61650	1.27	0.34	1.75	0.1256922	0.3482491	-5.14	FALSE
261432_at	hypothetical protein predicted by	---	AT1G07680	1.19	0.26	1.75	0.1256732	0.3482491	-5.14	FALSE
249095_at	myosin heavy chain MYA2 (pir||S	MYA2	AT5G43900	1.38	0.47	1.75	0.1257	0.3482491	-5.14	FALSE
255981_at	hypothetical protein ;supported b	---	AT1G34020	-1.26	-0.33	-1.75	0.1257229	0.3482491	-5.14	FALSE
248207_at	tyrosine aminotransferase	---	AT5G53970	1.79	0.84	1.75	0.125769	0.3483232	-5.15	FALSE
248959_at	putative protein similar to unknov	---	AT5G45630	1.69	0.75	1.75	0.125801	0.3483696	-5.15	FALSE
254813_at	putative transcription factor myb	MYB42	AT4G12350	1.18	0.24	1.75	0.1258209	0.3483825	-5.15	FALSE
259555_at	hypothetical protein	---	---	1.20	0.26	1.75	0.1258756	0.3484916	-5.15	FALSE
254613_at	ankyrin-like protein ankyrin 3, M	---	AT4G19150	-1.23	-0.30	-1.75	0.1259238	0.3485826	-5.15	FALSE
249818_at	Expressed protein ; supported by	TUB8	AT5G23860	1.44	0.53	1.75	0.125941	0.348588	-5.15	TRUE
248717_at	Expressed protein ; supported by	---	AT5G48175	1.17	0.23	1.75	0.1259944	0.3486513	-5.15	FALSE
261498_at	receptor kinase, putative similar	HSL1	AT1G28440	-1.29	-0.37	-1.75	0.1259864	0.3486513	-5.15	FALSE
266585_at	putative retroelement pol polypro	---	---	1.26	0.34	1.75	0.126017	0.3486714	-5.15	FALSE
257163_at	DNA-binding protein, putative si	MYB305	AT3G24310	1.21	0.28	1.75	0.1260365	0.348683	-5.15	FALSE
263509_s_a	hypothetical protein	---	AT2G07687	1.37	0.46	1.75	0.1260648	0.3487115	-5.15	TRUE
262473_at	chloroplast FtsH protease almos	FTSH1	AT1G50250	-1.29	-0.37	-1.75	0.1260773	0.3487115	-5.15	FALSE
258011_at	putative homeobox protein, HAT	HAT3.1	AT3G19510	-1.29	-0.37	-1.75	0.1261567	0.3487275	-5.15	FALSE
261511_at	polyadenylate-binding protein 5 i	PAB5	AT1G71770	1.24	0.31	1.75	0.1261176	0.3487275	-5.15	FALSE
257276_at	disease resistance protein, puta	---	AT3G14460	1.18	0.24	1.75	0.1261596	0.3487275	-5.15	FALSE
262693_at	unknown protein	---	AT1G62780	-1.52	-0.60	-1.75	0.1261102	0.3487275	-5.15	FALSE
255807_at	probable wound-induced protein	---	AT4G10270	-1.17	-0.22	-1.75	0.1261291	0.3487275	-5.15	FALSE
263536_at	putative WRKY-type DNA bindin	WRKY60	AT2G25000	-1.58	-0.66	-1.74	0.1262309	0.3488825	-5.15	TRUE
262582_at	hypothetical protein Is a member	---	AT1G15410	-1.72	-0.79	-1.74	0.1262624	0.3489273	-5.15	FALSE
255008_at	putative protein hypothetical pro	---	AT4G10060	1.22	0.29	1.74	0.1263195	0.3489752	-5.15	TRUE
263889_at	putative ABC transporter	ATNAP12	AT2G37010	1.25	0.32	1.74	0.126341	0.3489752	-5.15	FALSE
264350_at	putative seryl-tRNA synthetase s	SRS	AT1G11870	-1.35	-0.43	-1.74	0.1263339	0.3489752	-5.15	FALSE
262303_at	homeobox protein, putative simi	ATHB18	AT1G70920	1.39	0.47	1.74	0.1263237	0.3489752	-5.15	FALSE

261869_at	hypothetical protein predicted by	---	AT1G11470	1.24	0.31	1.74	0.1263623	0.3489919	-5.15	FALSE
265022_at	putative agp1 similar to GB:CAA	BCP1	AT1G24520	1.30	0.38	1.74	0.1263819	0.3490037	-5.15	FALSE
264233_at	ribosomal protein, putative simila	---	AT1G67430	-1.50	-0.59	-1.74	0.1264477	0.3491433	-5.15	FALSE
253309_at	male sterility 2-like protein male	CER4	AT4G33790	-1.54	-0.62	-1.74	0.1265105	0.3492727	-5.15	TRUE
255843_at	unknown protein	CPL3	AT2G33540	1.18	0.24	1.74	0.1265405	0.3492727	-5.15	FALSE
254754_at	pectate lyase like protein pectat	---	AT4G13210	1.18	0.24	1.74	0.126532	0.3492727	-5.15	FALSE
252574_at	receptor like protein kinase rece	---	AT3G45430	1.24	0.31	1.74	0.1266091	0.3494156	-5.15	FALSE
251876_at	TATA box binding protein (TBP)	RGD3	AT3G54280	-1.23	-0.29	-1.74	0.1266229	0.3494156	-5.15	FALSE
246682_at	putative protein EXOSTOSIN-1	XGD1	AT5G33290	1.26	0.33	1.74	0.1267092	0.3496114	-5.15	TRUE
248106_at	putative protein similar to unknov	---	AT5G55100	1.19	0.25	1.74	0.126751	0.3496845	-5.15	FALSE
252947_at	putative protein ubiquitin fusion	KAK	AT4G38600	-1.18	-0.23	-1.74	0.1267803	0.349723	-5.15	FALSE
254209_at	Expressed protein ; supported by	---	AT4G23490	-1.37	-0.46	-1.74	0.1269063	0.3500281	-5.15	FALSE
256298_at	DNA-binding protein contains Pfa	AGL94	AT1G69540	1.22	0.28	1.74	0.1269279	0.3500453	-5.15	FALSE
264587_at	putative ligand-gated ion channe	ATGLR3.4	AT1G05200	-1.93	-0.95	-1.74	0.126951	0.3500669	-5.15	FALSE
253046_at	cytochrome P450 - like protein c	CYP81D8	AT4G37370	2.22	1.15	1.74	0.127077	0.3503294	-5.15	TRUE
264655_at	unknown protein Similar to Glyci	SRC2	AT1G09070	1.52	0.60	1.74	0.1270678	0.3503294	-5.15	FALSE
257661_at	unknown protein contains Pfam	---	AT3G13340	-1.17	-0.22	-1.74	0.1271167	0.3503967	-5.16	FALSE
253736_at	Proline-rich APG - like protein pr	---	AT4G28780	-1.39	-0.48	-1.74	0.1273388	0.3504545	-5.16	TRUE
265768_at	putative sugar transporter ;supp	---	AT2G48020	1.20	0.26	1.74	0.1273653	0.3504545	-5.16	FALSE
259718_at	unknown protein	VIP5	AT1G61040	-1.17	-0.23	-1.74	0.1272482	0.3504545	-5.16	FALSE
261938_at	hypothetical protein predicted by	---	AT1G22510	1.49	0.57	1.74	0.1272398	0.3504545	-5.16	FALSE
250259_at	putative protein similar to unknov	---	AT5G13800	1.31	0.39	1.74	0.1272121	0.3504545	-5.16	FALSE
247917_at	putative protein similar to unknov	BIO1	AT5G57590	1.19	0.26	1.74	0.1272225	0.3504545	-5.16	FALSE
250637_at	glycine-rich protein atGRP-7	GRP17	AT5G07530	1.23	0.29	1.74	0.1273741	0.3504545	-5.16	FALSE
248849_at	multidrug resistance p-glycoprote	PGP7	AT5G46540	1.18	0.24	1.74	0.1272761	0.3504545	-5.16	FALSE
261308_at	protein kinase, putative contains	RKL1	AT1G48480	-2.22	-1.15	-1.74	0.1273835	0.3504545	-5.16	FALSE
255531_at	hypothetical protein similar to or	---	AT4G02160	1.22	0.29	1.74	0.1273604	0.3504545	-5.16	FALSE
265478_at	unknown protein ;supported by f	MEE14	AT2G15890	-1.20	-0.27	-1.74	0.1273716	0.3504545	-5.16	FALSE
259345_s_a	hypothetical protein predicted by	---	AT3G03700 ///	1.55	0.63	1.74	0.1273719	0.3504545	-5.16	FALSE
263800_at	hypothetical protein predicted by	---	AT2G24600	3.29	1.72	1.74	0.1273505	0.3504545	-5.16	FALSE
247125_at	putative protein contains similarit	---	AT5G66070	1.69	0.76	1.74	0.1272989	0.3504545	-5.16	FALSE
264750_at	hypothetical protein predicted by	---	AT1G22870	1.19	0.25	1.74	0.1271949	0.3504545	-5.16	FALSE
251529_at	ATP-dependent RNA helicase-li	---	AT3G58570	1.20	0.26	1.74	0.1272303	0.3504545	-5.16	FALSE
249928_at	CCR4-associated factor-like prot	---	AT5G22250	3.01	1.59	1.74	0.1274952	0.3506772	-5.16	TRUE
263045_at	hypothetical protein predicted by	---	AT2G05370	1.21	0.28	1.74	0.1274863	0.3506772	-5.16	FALSE

253753_at	glycine-rich protein like glycine-r	---	AT4G29030	1.23	0.30	1.74	0.1275456	0.3507676	-5.16	FALSE
247112_at	unknown protein	---	AT5G65950	-1.23	-0.30	-1.74	0.1275742	0.3507676	-5.16	FALSE
265648_at	putative beta-1,3-glucanase ;su	---	AT2G27500	1.56	0.64	1.74	0.1275601	0.3507676	-5.16	FALSE
257963_at	hypothetical protein predicted by	---	AT3G19840	-1.43	-0.52	-1.74	0.1276012	0.3507995	-5.16	FALSE
254704_at	putative protein predicted protei	APRR2	AT4G18020	1.24	0.31	1.74	0.1276653	0.3509333	-5.16	FALSE
267335_s_a	putative beta-1,3-glucanase	---	AT1G64760 ///	-1.37	-0.45	-1.74	0.1277114	0.3509755	-5.16	TRUE
260616_at	hypothetical protein contains Pfa	---	AT1G53280	-1.31	-0.39	-1.74	0.127709	0.3509755	-5.16	FALSE
258503_at	unknown protein	---	AT3G02500	1.27	0.35	1.74	0.1278081	0.3511568	-5.16	FALSE
264714_at	receptor-like protein kinase, puta	---	AT1G69990	1.24	0.31	1.74	0.1277992	0.3511568	-5.16	FALSE
257950_at	putative UDP-glucose glucosyltra	UGT71B6	AT3G21780	1.91	0.93	1.74	0.1278572	0.3512492	-5.16	FALSE
255509_at	hypothetical protein identical to T	---	AT4G02210	-1.36	-0.45	-1.74	0.1278849	0.3512832	-5.16	FALSE
253900_at	translation initiation factor ; supp	---	AT4G27130	-1.21	-0.28	-1.74	0.1280177	0.3515208	-5.16	FALSE
246549_at	putative protein predicted protei	---	AT5G15050	-1.47	-0.55	-1.74	0.1279921	0.3515208	-5.16	FALSE
255380_at	putative calcium channel ; suppo	ATTPC1	AT4G03560	-1.32	-0.40	-1.74	0.1280023	0.3515208	-5.16	FALSE
247876_at	unknown protein	---	AT5G57730	-1.19	-0.25	-1.73	0.1280685	0.3515848	-5.16	FALSE
265058_s_a	myrosinase-binding protein hom	MBP2	AT1G52030 ///	2.97	1.57	1.73	0.1280718	0.3515848	-5.16	FALSE
259933_at	Expressed protein ; supported by	---	AT1G34350	-1.29	-0.37	-1.73	0.1281113	0.3516509	-5.16	FALSE
265450_at	hypothetical protein predicted by	---	AT2G46620	1.37	0.46	1.73	0.1282034	0.3516947	-5.16	TRUE
253167_at	calmodulin-domain protein kinas	CPK5	AT4G35310	1.27	0.35	1.73	0.1281878	0.3516947	-5.16	FALSE
265914_at	En/Spm-like transposon protein r	---	---	1.17	0.23	1.73	0.1282043	0.3516947	-5.16	FALSE
247843_at	aluminium tolerance associated -	SVL4	AT5G58050	1.25	0.32	1.73	0.1281544	0.3516947	-5.16	FALSE
245463_at	allergen like protein	ATEXLB1	AT4G17030	-1.54	-0.62	-1.73	0.1281616	0.3516947	-5.16	FALSE
247641_at	imidazoleglycerol-phosphate syn	PDX2	AT5G60540	-1.23	-0.29	-1.73	0.1282715	0.3518367	-5.16	FALSE
252960_at	hypothetical protein	---	AT4G38750	-1.41	-0.50	-1.73	0.1283294	0.35185	-5.16	FALSE
265500_at	putative non-LTR retroelement re	---	---	1.37	0.45	1.73	0.128338	0.35185	-5.16	FALSE
248791_at	palmitoyl-protein thioesterase pre	---	AT5G47350	1.17	0.22	1.73	0.128369	0.35185	-5.16	FALSE
249644_at	putative serine-rich protein hypo	---	AT5G37010	1.26	0.34	1.73	0.1283651	0.35185	-5.16	FALSE
255806_at	fructokinase - like protein fructok	---	AT4G10260	1.16	0.21	1.73	0.1283526	0.35185	-5.16	FALSE
257366_s_a	unknown protein	---	AT2G03040 ///	1.22	0.29	1.73	0.1283234	0.35185	-5.16	FALSE
266303_at	putative receptor-like protein kina	---	AT2G27060	-1.43	-0.51	-1.73	0.1284423	0.3519834	-5.16	FALSE
265508_at	hypothetical protein predicted by	---	AT2G15930	1.17	0.23	1.73	0.1284485	0.3519834	-5.16	FALSE
261075_at	unknown protein	---	AT1G07280	-1.24	-0.31	-1.73	0.1284909	0.3520575	-5.17	FALSE
252368_at	cytochrome P450-like protein cy	CYP94B3	AT3G48520	1.60	0.68	1.73	0.1286	0.3521449	-5.17	FALSE
251004_at	putative protein predicted protei	---	AT5G02720	1.22	0.29	1.73	0.1285753	0.3521449	-5.17	FALSE
253107_at	putative protein predicted protei	---	AT4G35880	1.29	0.36	1.73	0.1285646	0.3521449	-5.17	FALSE

249457_s_a	zinc finger -like protein transcrip	VIM4	AT1G66040 /.	1.31	0.38	1.73	0.128593	0.3521449	-5.17	FALSE
265800_at	similar to ch-TOG protein from H	MOR1	AT2G35630	-1.23	-0.30	-1.73	0.1285874	0.3521449	-5.17	FALSE
250960_at	putative protein	---	AT5G02940	1.45	0.53	1.73	0.1286613	0.3522204	-5.17	TRUE
246565_at	biotin carboxyl carrier protein pre	BCCP2	AT5G15530	1.23	0.29	1.73	0.1286731	0.3522204	-5.17	FALSE
264546_at	Expressed protein ; supported by	---	AT1G55805	-1.45	-0.53	-1.73	0.1286739	0.3522204	-5.17	FALSE
251134_at	hypothetical protein RNA polyme	AtQSOX2	AT2G01270 /.	-1.22	-0.29	-1.73	0.1287977	0.3523917	-5.17	FALSE
247569_at	Cf-5 disease resistance protein -	---	AT5G61240	1.33	0.41	1.73	0.1287579	0.3523917	-5.17	FALSE
247519_at	NAM, no apical meristem, - like	ANAC100	AT5G61430	1.27	0.35	1.73	0.1287791	0.3523917	-5.17	FALSE
251806_at	zinc finger protein OBP3 ; suppo	OBP3	AT3G55370	1.19	0.25	1.73	0.1287983	0.3523917	-5.17	FALSE
249055_at	calmodulin-like protein	---	AT5G44460	1.17	0.23	1.73	0.1288424	0.3524701	-5.17	FALSE
263913_at	putative receptor-like protein kina	---	AT2G36570	1.39	0.47	1.73	0.1288756	0.3525185	-5.17	FALSE
261775_at	hypothetical protein predicted by	---	AT1G76280	-1.24	-0.31	-1.73	0.1289068	0.3525404	-5.17	FALSE
260329_at	putative cyclin similar to cyclin G	CYCA2;4	AT1G80370	1.25	0.32	1.73	0.1289145	0.3525404	-5.17	FALSE
246401_at	DNA-binding protein, putative sil	AtMYB50	AT1G57560	1.38	0.47	1.73	0.1289389	0.3525649	-5.17	FALSE
264454_at	unknown protein similar to U2 sn	---	AT1G10320	-1.25	-0.32	-1.73	0.1291056	0.3529785	-5.17	FALSE
248644_at	disease resistance protein-like	---	AT5G49140	1.17	0.22	1.73	0.1291408	0.3529901	-5.17	FALSE
264819_at	hypothetical protein similar to me	---	AT1G03510	-1.36	-0.45	-1.73	0.1291289	0.3529901	-5.17	FALSE
245399_at	membrane channel like protein ;s	TIP2;2	AT4G17340	-1.46	-0.54	-1.73	0.1291837	0.3530225	-5.17	TRUE
255680_at	hypothetical protein	---	AT4G00530	-1.28	-0.36	-1.73	0.1291741	0.3530225	-5.17	FALSE
251224_at	hypothetical protein	---	AT3G62620	-1.24	-0.31	-1.73	0.1292191	0.3530349	-5.17	FALSE
247956_at	cytokinin oxidase ; supported by	CKX3	AT5G56970	-1.21	-0.28	-1.73	0.1292064	0.3530349	-5.17	FALSE
264623_at	putative NPK1-related protein kir	ANP1	AT1G09000	1.18	0.24	1.73	0.129256	0.3530934	-5.17	FALSE
266717_at	Expressed protein ; supported by	---	AT2G46735	1.21	0.28	1.73	0.1293091	0.3531962	-5.17	FALSE
247488_at	putative protein MtN19, Medicag	---	AT5G61820	1.35	0.43	1.73	0.1293412	0.3532414	-5.17	TRUE
259539_at	axi 1 protein, putative similar to a	---	AT1G20550	-1.24	-0.32	-1.73	0.129361	0.3532533	-5.17	FALSE
264834_at	unknown protein similar to ESTs	---	AT1G03730	1.49	0.57	1.73	0.129482	0.3535415	-5.17	FALSE
265205_at	putative poly(A) binding protein	PAB7	AT2G36660	1.20	0.26	1.73	0.1295568	0.3535944	-5.17	FALSE
264452_at	unknown protein similar to salt-in	GRP23	AT1G10270	-1.79	-0.84	-1.73	0.1295383	0.3535944	-5.17	FALSE
253593_at	putative protein hypothetical pro	---	AT4G30760	-1.25	-0.32	-1.73	0.1295634	0.3535944	-5.17	FALSE
250098_at	putative protein ;supported by fu	---	AT5G17350	3.29	1.72	1.73	0.1295514	0.3535944	-5.17	FALSE
250312_at	unknown protein	---	AT5G12260	-1.25	-0.32	-1.73	0.1296074	0.3536722	-5.17	FALSE
260735_at	disease resistance protein, puta	---	AT1G17610	1.46	0.55	1.73	0.129697	0.3538743	-5.17	FALSE
250030_at	putative protein contains similarit	ATAPRL7	AT5G18120	-1.20	-0.26	-1.73	0.1297523	0.3539829	-5.17	FALSE
264538_at	hypothetical protein predicted by	WRKY10	AT1G55600	1.26	0.34	1.73	0.1298173	0.3540985	-5.17	FALSE
253821_at	extensin-like protein extensin-lik	---	AT4G28380	1.23	0.29	1.73	0.1298258	0.3540985	-5.17	FALSE

AFFX-BioB-	E. coli /GEN=bioB /DB_XREF=g	---	---	1.78	0.83	1.73	0.1298423	0.3541012	-5.17	FALSE
262198_at	pectin methylesterase (PMEU1)	ATPME2	AT1G53830	1.86	0.90	1.73	0.1298808	0.3541449	-5.18	FALSE
256690_at	hypothetical protein predicted by	---	AT3G32160	1.26	0.33	1.72	0.1299008	0.3541449	-5.18	FALSE
265589_at	hypothetical protein predicted by	---	AT2G20170	1.23	0.30	1.72	0.1299515	0.3541449	-5.18	FALSE
245633_at	unknown protein similar to putati	AtTLP10	AT1G25280	1.16	0.22	1.72	0.1299255	0.3541449	-5.18	FALSE
263203_at	hypothetical protein predicted by	chr31	AT1G05490	1.16	0.21	1.72	0.1299225	0.3541449	-5.18	FALSE
250140_at	putative protein	DRM2	AT5G14620	1.28	0.36	1.72	0.1299496	0.3541449	-5.18	FALSE
259482_at	receptor-like serine/threonine kir	RKF2	AT1G19090	1.23	0.29	1.72	0.1299826	0.3541875	-5.18	FALSE
258876_at	putative ADP-ribosylation factor s	ATARFB1C	AT3G03120	-1.18	-0.24	-1.72	0.1301981	0.3542274	-5.18	FALSE
249177_at	unknown protein ;supported by f	---	AT5G42850	1.21	0.27	1.72	0.1301453	0.3542274	-5.18	FALSE
247885_at	putative protein similar to unknov	---	AT5G57830	1.38	0.46	1.72	0.1302147	0.3542274	-5.18	FALSE
255474_at	coded for by A. thaliana cDNA T	---	AT4G02480	-1.22	-0.28	-1.72	0.1301344	0.3542274	-5.18	FALSE
265306_at	unknown protein	---	AT2G20320	1.34	0.42	1.72	0.1301028	0.3542274	-5.18	FALSE
247958_at	putative protein similar to unknov	---	AT5G57070	1.23	0.30	1.72	0.1301166	0.3542274	-5.18	FALSE
256144_at	guanine nucleotide-binding prote	RACK1B_A	AT1G48630	-1.75	-0.81	-1.72	0.1300486	0.3542274	-5.18	FALSE
266493_at	Mutator-like transposase similar	---	---	1.20	0.26	1.72	0.1302064	0.3542274	-5.18	FALSE
252676_at	putative protein	---	AT3G44280	-1.17	-0.22	-1.72	0.130032	0.3542274	-5.18	FALSE
247219_at	COP1-interacting protein CIP8 ;	CIP8	AT5G64920	-1.22	-0.29	-1.72	0.1301623	0.3542274	-5.18	FALSE
253541_at	putative protein various predicte	---	AT4G31630	1.19	0.25	1.72	0.1301997	0.3542274	-5.18	FALSE
267131_at	hypothetical protein predicted by	---	AT2G23400	-1.18	-0.23	-1.72	0.1301301	0.3542274	-5.18	FALSE
259233_at	hypothetical protein	---	AT3G11380	1.16	0.22	1.72	0.1300205	0.3542274	-5.18	FALSE
260903_at	polygalacturonase PG1, putative	---	AT1G02460	2.28	1.19	1.72	0.1301577	0.3542274	-5.18	FALSE
254162_at	transcription factor IIA small subu	---	AT4G24440	-1.30	-0.38	-1.72	0.1303026	0.3542477	-5.18	FALSE
254089_at	putative protein apoptosis gene	---	AT4G24800	-1.22	-0.29	-1.72	0.130343	0.3542477	-5.18	FALSE
256485_at	unknown protein	---	AT1G31440	-1.21	-0.27	-1.72	0.1302427	0.3542477	-5.18	FALSE
255121_at	putative mitogen-activated protei	MAPKKK9	AT4G08480	1.35	0.43	1.72	0.130393	0.3542477	-5.18	FALSE
266049_at	putative translation initiation facto	---	AT2G40780	-1.21	-0.27	-1.72	0.1303702	0.3542477	-5.18	FALSE
266531_at	putative plasma membrane intrir	---	AT2G16835	1.17	0.22	1.72	0.1303212	0.3542477	-5.18	FALSE
258367_at	putative protein kinase similar to	WAG2	AT3G14370	1.23	0.30	1.72	0.1302724	0.3542477	-5.18	FALSE
263401_at	hypothetical protein similar to hyp	---	AT2G04070	1.36	0.45	1.72	0.1303016	0.3542477	-5.18	FALSE
255811_at	heat shock protein 22.0 ; support	ATHSP22.0	AT4G10250	1.26	0.34	1.72	0.1303872	0.3542477	-5.18	FALSE
259885_at	hypothetical protein contains Pfa	---	AT1G76380	1.32	0.40	1.72	0.1303518	0.3542477	-5.18	FALSE
267145_at	putative acetyltransferase	ATMAK3	AT2G38130	-1.23	-0.30	-1.72	0.1302691	0.3542477	-5.18	FALSE
262555_at	hypothetical protein	---	AT1G31400	1.18	0.24	1.72	0.1304494	0.3543589	-5.18	FALSE
251040_at	ribonuclease II-like protein ribon	EMB2730	AT5G02250	-1.37	-0.46	-1.72	0.1305089	0.3544365	-5.18	FALSE

257723_at	hypothetical protein predicted by	---	AT3G18500	-1.29	-0.37	-1.72	0.1305091	0.3544365	-5.18	FALSE
266438_at	putative carboxyphosphonoenolp	---	AT2G43180	-1.28	-0.35	-1.72	0.1305344	0.3544631	-5.18	FALSE
255513_at	PROLIFERA similar to S. cerevis	PRL	AT4G02060	-2.24	-1.16	-1.72	0.1306061	0.3546155	-5.18	FALSE
267590_at	putative expansin ;supported by	ATEXPA4	AT2G39700	1.48	0.57	1.72	0.1306707	0.3547486	-5.18	FALSE
255468_at	putative WD-repeat protein simil	---	AT4G03020	-1.20	-0.26	-1.72	0.1307483	0.3548911	-5.18	FALSE
254264_at	putative protein various predicte	---	AT4G23510	1.20	0.26	1.72	0.1307543	0.3548911	-5.18	FALSE
255696_at	putative nucleotide sugar epimer	GAE3	AT4G00110	1.23	0.30	1.72	0.1307931	0.3549543	-5.18	FALSE
259882_at	unknown protein similar to hypot	---	AT1G76670	-1.23	-0.30	-1.72	0.1308641	0.3550623	-5.18	FALSE
246725_at	putative protein various predicte	---	AT5G29040	1.34	0.42	1.72	0.1308587	0.3550623	-5.18	FALSE
256962_at	glucan endo-1,3-beta-glucosidas	---	AT3G13560	-1.69	-0.75	-1.72	0.1308984	0.3551134	-5.18	FALSE
254075_at	DRE CRT-binding protein DREB	CBF2	AT4G25470	-1.40	-0.48	-1.72	0.1309218	0.3551235	-5.18	FALSE
258233_at	hypothetical protein contains sim	MYB118	AT3G27785	1.23	0.29	1.72	0.1309333	0.3551235	-5.18	FALSE
258601_at	putative histidyl tRNA synthetase	---	AT3G02760	-1.25	-0.32	-1.72	0.1309675	0.3551318	-5.18	FALSE
257834_at	alpha-mannosidase, putative sir	---	AT3G26720	-1.17	-0.22	-1.72	0.1309599	0.3551318	-5.18	FALSE
256901_at	hypothetical protein contains sim	---	---	1.16	0.21	1.72	0.131071	0.3553703	-5.18	FALSE
250104_at	unknown protein	---	AT5G16610	-1.31	-0.39	-1.72	0.1311386	0.355469	-5.18	FALSE
260935_at	hypothetical protein predicted by	---	AT1G45110	-1.28	-0.36	-1.72	0.1311385	0.355469	-5.18	FALSE
252943_at	cinnamyl-alcohol dehydrogenase	CAD9	AT4G39330	3.89	1.96	1.72	0.1311626	0.3554824	-5.18	FALSE
245120_at	hypothetical protein predicted by	HOS1	AT2G39810	-1.26	-0.34	-1.72	0.1311747	0.3554824	-5.18	FALSE
249720_at	fimbrin ; supported by cDNA: gi_	FIM2	AT5G35700	1.20	0.26	1.72	0.131243	0.3556252	-5.18	FALSE
253569_at	receptor kinase - like protein rec	---	AT4G31250	-1.27	-0.34	-1.72	0.1313166	0.355774	-5.19	FALSE
258082_at	Expressed protein ; supported by	CLE27	AT3G25905	-1.46	-0.54	-1.72	0.1313291	0.355774	-5.19	FALSE
259989_at	hypothetical protein predicted by	---	---	1.24	0.31	1.72	0.1314305	0.3558412	-5.19	FALSE
252907_at	putative gamma-glutamyltransfe	GGT2	AT4G39650	1.19	0.25	1.72	0.1314319	0.3558412	-5.19	FALSE
245902_at	putative protein Scythe protein,	---	AT5G11080	1.33	0.41	1.72	0.1313964	0.3558412	-5.19	FALSE
247957_at	protein phosphatase 2C ABI2 (P	ABI2	AT5G57050	1.44	0.53	1.72	0.1314246	0.3558412	-5.19	FALSE
253168_at	putative protein various predicte	---	AT4G35070	1.50	0.58	1.72	0.1313998	0.3558412	-5.19	FALSE
250903_at	putative protein coil protein PO2	---	AT5G03600	1.29	0.37	1.72	0.1314833	0.3559381	-5.19	FALSE
263224_at	putative GTP-binding protein Sim	---	AT1G30580	-1.30	-0.37	-1.72	0.1315303	0.3560231	-5.19	FALSE
263018_at	putative non-LTR retroelement re	---	---	1.16	0.22	1.72	0.1316612	0.356335	-5.19	FALSE
250999_at	putative protein predicted proyei	---	AT5G02630	1.30	0.38	1.72	0.1317226	0.3564102	-5.19	FALSE
267447_at	putative GTP-binding protein	ArRABA1h	AT2G33870	1.17	0.23	1.72	0.1317315	0.3564102	-5.19	FALSE
250475_at	sulfate transporter ; supported b	SULTR2;1	AT5G10180	1.64	0.71	1.72	0.1317358	0.3564102	-5.19	FALSE
263689_at	ribonuclease, RNS3 identical to	RNS3	AT1G26820	1.40	0.48	1.71	0.131802	0.3564625	-5.19	TRUE
248195_at	membrane associated protein ; s	ATMAMI	AT5G54110	1.27	0.34	1.72	0.131771	0.3564625	-5.19	FALSE

260033_at	putative mutT protein contains P	ATNUDX1	AT1G68760	-1.25	-0.32	-1.71	0.1317903	0.3564625	-5.19	FALSE
246774_at	polygalacturonase-like protein p	---	AT5G27530	1.21	0.28	1.71	0.1318559	0.356566	-5.19	FALSE
258816_at	putative T-complex protein 1, the	---	AT3G03960	-1.33	-0.41	-1.71	0.1319326	0.3567309	-5.19	FALSE
244981_at	ribosomal protein S8	---	---	-1.26	-0.33	-1.71	0.1319603	0.3567636	-5.19	TRUE
257073_at	hypothetical protein predicted by	---	AT3G19650	-1.28	-0.35	-1.71	0.1320055	0.3568434	-5.19	FALSE
252424_at	putative protein activating signal	---	AT3G47610	-1.29	-0.37	-1.71	0.1321148	0.3568851	-5.19	FALSE
250438_at	putative protein predicted protei	---	AT5G10580	1.18	0.24	1.71	0.1320958	0.3568851	-5.19	FALSE
256410_at	hypothetical protein	---	AT1G66630	1.15	0.21	1.71	0.132112	0.3568851	-5.19	FALSE
252079_at	MAP kinase ; supported by cDN	CPuORF44	AT3G51630 /	1.19	0.25	1.71	0.1320836	0.3568851	-5.19	FALSE
246703_at	mitogen activated protein kinase	WNK9	AT5G28080	-1.81	-0.86	-1.71	0.132082	0.3568851	-5.19	FALSE
257201_at	unknown protein	---	AT3G23740	-1.25	-0.32	-1.71	0.132107	0.3568851	-5.19	FALSE
262026_at	calcium-dependent protein kinas	ATCDPK2	AT1G35670	1.28	0.35	1.71	0.1322443	0.3569338	-5.19	TRUE
247918_at	putative protein contains similarit	---	AT5G57610	-1.28	-0.36	-1.71	0.1322893	0.3569338	-5.19	FALSE
257458_at	hypothetical protein predicted by	---	AT2G05400	1.17	0.22	1.71	0.1321755	0.3569338	-5.19	FALSE
246221_at	step II splicing factor - like protei	SMP2	AT4G37120	1.22	0.28	1.71	0.1322711	0.3569338	-5.19	FALSE
249542_at	putative protein transcription fac	NF-YC12	AT5G38140	-1.30	-0.38	-1.71	0.1322101	0.3569338	-5.19	FALSE
245984_at	putative protein predicted protein	---	AT5G13090	-1.22	-0.29	-1.71	0.132227	0.3569338	-5.19	FALSE
251234_s_a	putative dTDP-glucose 4-6-dehy	UXS4	AT2G47650 /	-1.33	-0.41	-1.71	0.1322771	0.3569338	-5.19	FALSE
257979_at	unknown protein	---	AT3G20730	1.21	0.28	1.71	0.1321571	0.3569338	-5.19	FALSE
256195_at	hypothetical protein predicted by	---	---	-1.16	-0.22	-1.71	0.1322671	0.3569338	-5.19	FALSE
266985_at	putative geranylgeranyl transfera	PGGT-I	AT2G39550	1.25	0.33	1.71	0.1322738	0.3569338	-5.19	FALSE
259719_at	unknown protein contains gamm	LCR66	AT1G61070	1.18	0.24	1.71	0.1323183	0.3569698	-5.19	FALSE
252918_at	putative protein	---	AT4G38980	-1.17	-0.22	-1.71	0.13234	0.3569861	-5.19	FALSE
250900_at	putative protein ; supported by c	ATB' ALPH	AT5G03470	-1.30	-0.38	-1.71	0.1324261	0.3571381	-5.19	FALSE
247285_at	putative protein similar to unknov	---	AT5G64400	1.19	0.26	1.71	0.1324276	0.3571381	-5.19	FALSE
260940_at	26S proteasome regulatory parti	---	AT1G45000	-1.25	-0.32	-1.71	0.132455	0.3571696	-5.19	FALSE
261996_at	AIG1-like protein similar to AIG1	---	AT1G33830	-1.17	-0.22	-1.71	0.1325802	0.357465	-5.19	FALSE
264585_at	auxin-resistance protein AXR1 E	AXR1	AT1G05180	-1.17	-0.22	-1.71	0.1326157	0.3574762	-5.19	FALSE
265469_at	unknown protein predicted by ge	---	AT2G37160	1.17	0.23	1.71	0.1326154	0.3574762	-5.19	FALSE
246042_at	cinnamyl-alcohol dehydrogenas	---	AT5G19440	1.55	0.63	1.71	0.1326854	0.3576219	-5.20	FALSE
265718_at	putative WRKY DNA-binding pro	WRKY3	AT2G03340	-1.23	-0.30	-1.71	0.1327517	0.3576456	-5.20	FALSE
264118_at	unknown protein	---	AT1G79150	-1.56	-0.64	-1.71	0.1327715	0.3576456	-5.20	TRUE
257075_at	unknown protein contains Pfam p	---	AT3G19670	-1.29	-0.37	-1.71	0.132788	0.3576456	-5.20	FALSE
257719_at	unknown protein	AtALMT9	AT3G18440	1.31	0.39	1.71	0.1327712	0.3576456	-5.20	FALSE
256641_at	hypothetical protein similar to put	---	---	1.26	0.34	1.71	0.1327372	0.3576456	-5.20	FALSE

259818_at	unknown protein ; supported by	---	AT1G49890	-1.32	-0.40	-1.71	0.1328196	0.3576456	-5.20	FALSE
266042_s_a	hypothetical protein	---	AT2G07734	1.35	0.43	1.71	0.1328178	0.3576456	-5.20	FALSE
264187_at	unknown protein ;supported by fu	---	AT1G54860	1.17	0.22	1.71	0.1327885	0.3576456	-5.20	FALSE
258229_at	unknown protein contains Pfam p	---	AT3G27700	-1.19	-0.25	-1.71	0.1328821	0.3577557	-5.20	FALSE
248225_at	unknown protein	---	AT5G53740	1.20	0.26	1.71	0.1328919	0.3577557	-5.20	FALSE
261398_at	hypothetical protein contains sim	NHX6	AT1G79610	1.22	0.28	1.71	0.1329627	0.3578631	-5.20	FALSE
259948_at	unknown protein similar to LIGA	---	AT1G71350	-1.34	-0.42	-1.71	0.1329992	0.3578631	-5.20	FALSE
255455_at	mitochondrial elongation factor T	---	AT4G02930	-1.49	-0.57	-1.71	0.1330102	0.3578631	-5.20	FALSE
258862_at	putative mitochondrial processing	MPPBETA	AT3G02090	1.22	0.28	1.71	0.1329818	0.3578631	-5.20	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U372	ACT7	---	-1.19	-0.26	-1.71	0.1329658	0.3578631	-5.20	FALSE
263136_at	trehalose-6-phosphate synthase	ATTPS1	AT1G78580	-1.22	-0.29	-1.71	0.1330335	0.3578667	-5.20	FALSE
251857_at	RNA binding protein - like SEB4	---	AT3G54770	1.21	0.28	1.71	0.133043	0.3578667	-5.20	FALSE
267115_s_a	putative cellulose synthase	ATCSLB04	AT2G32530 /	-1.57	-0.65	-1.71	0.1330806	0.3579259	-5.20	FALSE
265078_at	hypothetical protein contains sim	ECT4	AT1G55500	-1.45	-0.53	-1.71	0.1331369	0.3579852	-5.20	TRUE
263878_s_a	unknown protein	---	AT2G22040 /	-1.26	-0.33	-1.71	0.1331498	0.3579852	-5.20	FALSE
261059_at	transcription factor TINY, putativ	---	AT1G01250	1.31	0.38	1.71	0.1331276	0.3579852	-5.20	FALSE
261898_at	hypothetical protein predicted by	---	AT1G80720	-1.49	-0.58	-1.71	0.1332016	0.3579998	-5.20	FALSE
247560_at	putative protein predicted protei	---	AT5G61090	1.27	0.35	1.71	0.1331879	0.3579998	-5.20	FALSE
264055_at	putative protein kinase contains a	---	AT2G28590	-1.25	-0.32	-1.71	0.1332023	0.3579998	-5.20	FALSE
261017_at	UDP-glucose dehydrogenase, p	UGD1	AT1G26570	1.24	0.32	1.71	0.133232	0.3580227	-5.20	TRUE
255581_at	putative transposon protein simi	---	---	1.26	0.34	1.71	0.1332422	0.3580227	-5.20	FALSE
262624_at	CCR4-associated factor, putativ	---	AT1G06450	-1.24	-0.31	-1.71	0.1332588	0.3580252	-5.20	FALSE
256669_s_a	hypothetical protein similar to hyp	---	AT3G32200 /	1.25	0.32	1.71	0.1333553	0.3581098	-5.20	FALSE
248112_at	wax synthase-like protein	---	AT5G55350	1.27	0.35	1.71	0.1333505	0.3581098	-5.20	FALSE
251901_at	putative protein axi1 protein, Nic	---	AT3G54100	1.27	0.34	1.71	0.1333549	0.3581098	-5.20	FALSE
256267_at	unknown protein ; supported by	---	AT3G12260	-1.20	-0.27	-1.71	0.1333688	0.3581098	-5.20	FALSE
247921_at	CONSTANS-like B-box zinc finge	COL5	AT5G57660	-1.32	-0.40	-1.71	0.1333263	0.3581098	-5.20	FALSE
246767_at	putative protein CG6949 - Drosc	---	AT5G27395	-1.64	-0.72	-1.71	0.1334004	0.3581398	-5.20	FALSE
265050_at	jasmonate inducible protein, put	---	AT1G52070	1.19	0.25	1.71	0.1334114	0.3581398	-5.20	FALSE
247979_at	pollen specific protein SF21 ;sup	---	AT5G56750	1.25	0.33	1.71	0.1335039	0.3583459	-5.20	TRUE
245652_at	F-box protein family, putative	---	AT4G13960	1.24	0.31	1.71	0.1335225	0.3583537	-5.20	FALSE
246677_at	putative protein predicted protein	---	---	1.24	0.31	1.71	0.1335901	0.3584882	-5.20	FALSE
248891_at	MCM3 homolog (emb|CAA03887	MCM3	AT5G46280	-2.13	-1.09	-1.71	0.133604	0.3584882	-5.20	FALSE
263521_at	hypothetical protein predicted by	---	AT2G24960	-1.31	-0.39	-1.70	0.1337154	0.3587249	-5.20	TRUE
261845_at	metal ion transporter, putative si	NRAMP6	AT1G15960	-1.32	-0.40	-1.70	0.1337237	0.3587249	-5.20	FALSE

260309_at	putative alanine aminotransferas	AOAT2	AT1G70580	-1.29	-0.37	-1.70	0.13375	0.3587394	-5.20	FALSE
248348_at	putative protein similar to unknov	---	AT5G52190	-1.21	-0.27	-1.70	0.1337606	0.3587394	-5.20	FALSE
265070_at	branched-chain alpha-keto acid d	BCDH BET	AT1G55510	1.58	0.66	1.70	0.1337882	0.3587713	-5.20	FALSE
257686_at	unknown protein similar to unkno	SDRB	AT3G12800	1.24	0.31	1.70	0.1339588	0.358849	-5.20	TRUE
259653_at	unknown protein	---	AT1G55240	1.17	0.23	1.70	0.1338798	0.358849	-5.20	FALSE
257248_at	hypothetical protein predicted by	---	AT3G24150	-1.30	-0.38	-1.70	0.1338774	0.358849	-5.20	FALSE
252421_at	endochitinase-like protein BASI(	---	AT3G47540	2.92	1.55	1.70	0.1338895	0.358849	-5.20	FALSE
258806_at	unknown protein	---	AT3G04020	-1.40	-0.48	-1.70	0.1339078	0.358849	-5.20	FALSE
263377_at	AP2 domain transcription factor (	ABI4	AT2G40220	1.18	0.24	1.70	0.133939	0.358849	-5.20	FALSE
258903_at	hypothetical protein similar to zir	---	AT3G06410	-1.34	-0.42	-1.70	0.1338566	0.358849	-5.20	FALSE
248560_at	putative protein contains similarit	ATPPOX	AT5G49970	-1.28	-0.35	-1.70	0.1339546	0.358849	-5.20	FALSE
250487_at	putative protein MRS2 protein, S	---	AT5G09690	-1.28	-0.35	-1.70	0.1339252	0.358849	-5.20	FALSE
246507_at	lipase-like protein monoglyceride	---	AT5G16120	1.35	0.43	1.70	0.1339852	0.3588776	-5.20	FALSE
255524_at	hypothetical protein similar to pe	ATPMEPCI	AT4G02330	2.46	1.30	1.70	0.1340674	0.3590556	-5.20	FALSE
246146_at	receptor-like protein kinase - like	---	AT5G20050	1.30	0.37	1.70	0.1341108	0.3591297	-5.20	FALSE
260126_at	putative hydroxymethyltransferas	SHM7	AT1G36370	1.36	0.44	1.70	0.1341711	0.3592069	-5.21	FALSE
248923_at	putative protein similar to unknov	atnudt11	AT5G45940	-1.32	-0.40	-1.70	0.1341557	0.3592069	-5.21	FALSE
250191_at	kinase - like protein RING3 prote	ATBET9	AT5G14270	-1.23	-0.30	-1.70	0.1341932	0.3592239	-5.21	FALSE
253592_at	hypothetical protein ;supported b	---	AT4G30840	-1.19	-0.25	-1.70	0.1342598	0.3592758	-5.21	FALSE
246796_at	putative protein myosin heavy ch	---	AT5G26770	-1.30	-0.38	-1.70	0.1342568	0.3592758	-5.21	FALSE
258721_at	unknown protein similar to hypotl	---	AT3G09560	1.34	0.42	1.70	0.1342512	0.3592758	-5.21	FALSE
264520_at	putative amino acid permease G	AAP8	AT1G10010	1.36	0.44	1.70	0.1342935	0.3593208	-5.21	FALSE
254292_at	putative protein	---	AT4G23030	1.80	0.85	1.70	0.1343082	0.3593208	-5.21	FALSE
246449_at	hypothetical protein	---	AT5G16810	1.23	0.30	1.70	0.1344234	0.3595098	-5.21	TRUE
246776_at	kinesin-like protein kinesin-like h	---	AT5G27550	1.32	0.40	1.70	0.1344013	0.3595098	-5.21	FALSE
263610_at	putative beta-1,3-glucanase	---	AT2G16230	1.25	0.32	1.70	0.1344261	0.3595098	-5.21	FALSE
253017_at	cinnamyl alcohol dehydrogenase	CAD6	AT4G37970	1.18	0.23	1.70	0.1346254	0.3597436	-5.21	FALSE
258650_at	putative protein kinase similar to	---	AT3G09830	1.41	0.50	1.70	0.1346266	0.3597436	-5.21	FALSE
244914_at	hypothetical protein	---	---	1.21	0.27	1.70	0.134624	0.3597436	-5.21	FALSE
251358_at	shaggy-like kinase beta	---	AT3G61160	-1.56	-0.64	-1.70	0.1345854	0.3597436	-5.21	FALSE
246224_at	putative MADS-box protein ;supp	---	AT4G36590	1.29	0.37	1.70	0.1346191	0.3597436	-5.21	FALSE
263557_at	putative homeodomain transcript	BLH7	AT2G16400	-1.27	-0.35	-1.70	0.1346397	0.3597436	-5.21	FALSE
264043_at	putative cyclin D	CYCD2;1	AT2G22490	-1.18	-0.24	-1.70	0.1345494	0.3597436	-5.21	FALSE
259111_at	alpha subunit of F-actin capping	---	AT3G05520	-1.28	-0.36	-1.70	0.1345611	0.3597436	-5.21	FALSE
264337_at	hypothetical protein predicted by	---	AT1G70350	-1.21	-0.27	-1.70	0.1346556	0.359744	-5.21	FALSE

266792_at	putative sucrose/H+ symporter	SUT2	AT2G02860	1.57	0.65	1.70	0.1347118	0.359771	-5.21	FALSE
265506_at	putative non-LTR retroelement re	---	---	1.26	0.33	1.70	0.1347215	0.359771	-5.21	FALSE
267058_at	putative protein kinase contains a	MAPKKK17	AT2G32510	1.36	0.45	1.70	0.1346895	0.359771	-5.21	FALSE
250989_at	cytochrome P450 - like protein c	CYP96A13	AT5G02900	1.16	0.21	1.70	0.1347288	0.359771	-5.21	FALSE
246966_at	DNA photolyase - like protein DI	CRY3	AT5G24850	1.33	0.41	1.70	0.1347497	0.3597848	-5.21	FALSE
255292_s_a	putative calcium dependent prote	CPK22	AT4G04710 /.	-1.28	-0.36	-1.70	0.1347813	0.3598269	-5.21	FALSE
251062_at	putative protein putative proteins	OFP1	AT5G01840	1.22	0.29	1.70	0.1348563	0.3598588	-5.21	FALSE
260902_at	hypothetical protein similar to car	---	AT1G21440	-1.41	-0.49	-1.70	0.1348462	0.3598588	-5.21	FALSE
255082_at	putative protein polyphosphoino	---	AT4G09160	1.20	0.26	1.70	0.1348485	0.3598588	-5.21	FALSE
254475_at	putative snRNP protein small nu	smB	AT4G20440	-1.41	-0.50	-1.70	0.1348097	0.3598588	-5.21	FALSE
248835_at	NBS/LRR disease resistance pro	---	AT5G47250	-1.40	-0.49	-1.70	0.1349663	0.36011	-5.21	FALSE
246838_at	flap endonuclease - like protein	---	AT5G26680	-1.22	-0.28	-1.70	0.1349868	0.3601226	-5.21	FALSE
246097_at	putative protein CGI-45 protein -	HHP1	AT5G20270	1.65	0.72	1.70	0.13504	0.3601575	-5.21	TRUE
266330_at	unknown protein ; supported by	MLP329	AT2G01530	-1.35	-0.44	-1.70	0.1350192	0.3601575	-5.21	FALSE
250927_at	lysine decarboxylase - like prote	---	AT5G03270	1.28	0.35	1.70	0.1350472	0.3601575	-5.21	FALSE
259292_at	unknown protein	---	AT3G11560	-1.22	-0.29	-1.70	0.1350844	0.3602146	-5.21	FALSE
261709_at	RNA-binding protein, putative si	CID11	AT1G32790	-1.20	-0.26	-1.70	0.1351894	0.3603806	-5.21	FALSE
251369_at	putative protein ;supported by fu	---	AT3G60480	-1.24	-0.31	-1.70	0.1351941	0.3603806	-5.21	FALSE
256183_at	MAP kinase kinase 4 (ATMKK4)	MKK4	AT1G51660	1.66	0.73	1.70	0.1351904	0.3603806	-5.21	FALSE
252526_at	putative protein ethylene-forming	---	AT3G46480	1.27	0.34	1.70	0.1352417	0.3604233	-5.21	FALSE
256188_at	unknown protein similar to hypot	---	AT1G30160	1.45	0.54	1.70	0.1352299	0.3604233	-5.21	FALSE
264513_at	putative glucose-6-phosphate de	G6PD4	AT1G09420	-1.21	-0.28	-1.70	0.1352754	0.3604288	-5.21	TRUE
250768_at	signal recognition particle recept	---	AT5G05670	-1.30	-0.38	-1.70	0.1352744	0.3604288	-5.21	FALSE
256972_at	unknown protein	---	AT3G21140	-1.22	-0.28	-1.70	0.1353445	0.3605709	-5.21	FALSE
267595_at	putative glucanse	AtGH9B8	AT2G32990	3.67	1.88	1.70	0.1354144	0.3607149	-5.21	FALSE
251874_at	putative protein (fragment) ester	---	AT3G54240	1.28	0.36	1.70	0.1354432	0.3607349	-5.21	FALSE
263153_s_a	myrosinase-associated protein,	---	AT1G54000 /.	1.56	0.64	1.70	0.1354535	0.3607349	-5.21	FALSE
253143_at	putative protein	---	AT4G35530	-1.27	-0.34	-1.70	0.1354714	0.3607404	-5.21	FALSE
262038_at	invertase, putative similar to neu	CINV1	AT1G35580	1.37	0.46	1.70	0.1355102	0.3607594	-5.21	FALSE
256591_at	hypothetical protein	---	AT3G31910	1.16	0.21	1.70	0.13551	0.3607594	-5.21	FALSE
257313_at	gamma tonoplast intrinsic protein	TIP2	AT3G26520	1.27	0.35	1.70	0.1355638	0.3608602	-5.21	FALSE
250873_at	lipase -like protein lipase Arab-1	---	AT5G03980	1.22	0.29	1.70	0.1356114	0.3609446	-5.22	FALSE
246612_at	putative protein ;supported by fu	---	AT5G35320	-1.26	-0.33	-1.69	0.1357457	0.3612062	-5.22	FALSE
261310_at	hypothetical protein predicted by	PDE247	AT1G05750	-1.28	-0.35	-1.69	0.1357571	0.3612062	-5.22	FALSE
254030_at	putative acidic ribosomal protein	---	AT4G25890	-1.62	-0.70	-1.69	0.1357454	0.3612062	-5.22	FALSE

258458_at	Expressed protein ; supported by	---	AT3G22435	-1.34	-0.42	-1.69	0.1358222	0.3613371	-5.22	FALSE
245484_at	enoyl-CoA hydratase like protein	ECHIA	AT4G16210	1.21	0.27	1.69	0.1358777	0.3614426	-5.22	FALSE
260232_at	unknown protein contains Pfam p	---	AT1G74640	1.41	0.50	1.69	0.1359319	0.3615447	-5.22	FALSE
260373_at	unknown protein	---	AT1G73970	-1.21	-0.27	-1.69	0.135967	0.3615733	-5.22	FALSE
259360_at	hypothetical protein predicted by	---	AT1G13310	1.19	0.25	1.69	0.1359902	0.3615733	-5.22	FALSE
252376_at	L-galactono-1,4-lactone dehydro	ATGLDH	AT3G47930	-1.31	-0.39	-1.69	0.1359834	0.3615733	-5.22	FALSE
254751_at	hypothetical protein	---	AT4G13150	-1.19	-0.25	-1.69	0.1360779	0.3617643	-5.22	FALSE
258532_at	ribosomal protein L29, putative s	---	AT3G06700	-1.63	-0.70	-1.69	0.136133	0.3617956	-5.22	FALSE
255920_at	putative protein	---	AT5G28590	1.27	0.35	1.69	0.1361373	0.3617956	-5.22	FALSE
258089_at	hypothetical protein predicted by	---	AT3G14740	-1.46	-0.54	-1.69	0.1361236	0.3617956	-5.22	FALSE
256998_at	hypothetical protein predicted by	---	AT3G14180	1.27	0.35	1.69	0.136188	0.3618526	-5.22	FALSE
247967_at	putative protein similar to unknov	anac099	AT5G56620	1.16	0.22	1.69	0.1361905	0.3618526	-5.22	FALSE
258879_at	unknown protein ; supported by	---	AT3G03270	1.50	0.58	1.69	0.1362421	0.3619054	-5.22	TRUE
251388_at	putative protein protein regulatin	MAP65-4	AT3G60840	1.23	0.30	1.69	0.136229	0.3619054	-5.22	FALSE
248129_at	putative protein contains similarit	---	AT5G54780	1.24	0.31	1.69	0.1362773	0.3619569	-5.22	FALSE
261801_at	hypothetical protein similar to hyp	AAE14	AT1G30520	-1.30	-0.38	-1.69	0.1363398	0.3620359	-5.22	TRUE
262531_at	putative leucine-rich receptor pro	---	AT1G17230 //	1.30	0.38	1.69	0.1364023	0.3620359	-5.22	FALSE
264230_at	hypothetical protein predicted by	---	AT1G67460	1.20	0.26	1.69	0.1363864	0.3620359	-5.22	FALSE
257655_at	unknown protein contains Pfam	---	AT3G13350	-1.49	-0.57	-1.69	0.1363847	0.3620359	-5.22	FALSE
264665_at	unknown protein ESTs gb|H372	---	AT1G09660	-1.25	-0.33	-1.69	0.1363614	0.3620359	-5.22	FALSE
256044_at	protein phosphatase 2C, putativ	---	AT1G07160	2.85	1.51	1.69	0.1363742	0.3620359	-5.22	FALSE
259434_at	unknown protein	---	AT1G01490	-1.19	-0.25	-1.69	0.1364307	0.3620691	-5.22	FALSE
254817_at	putative SWH1 protein SWH1 pr	ORP2B	AT4G12460	-1.23	-0.29	-1.69	0.1365439	0.3622431	-5.22	FALSE
253212_s_a	xanthine dehydrogenase - like p	XDH1	AT4G34890 //	1.29	0.37	1.69	0.1365353	0.3622431	-5.22	FALSE
246288_at	unknown protein	---	AT1G31850	-1.29	-0.37	-1.69	0.1365419	0.3622431	-5.22	FALSE
248074_at	putative protein similar to unknov	FLA1	AT5G55730	1.71	0.77	1.69	0.1365781	0.3622917	-5.22	FALSE
255950_at	hypothetical protein predicted by	---	AT1G22110	1.29	0.37	1.69	0.1366423	0.3624197	-5.22	FALSE
264484_at	hypothetical protein similar to an	---	AT1G77260	1.19	0.25	1.69	0.1366839	0.3624647	-5.22	FALSE
247061_at	putative protein similar to unknov	---	AT5G66780	1.35	0.43	1.69	0.136691	0.3624647	-5.22	FALSE
261763_at	ABC transporter, putative simila	PDR12	AT1G15520	2.29	1.20	1.69	0.1367358	0.3624991	-5.22	TRUE
245590_at	hypothetical protein	---	AT4G15060	1.20	0.26	1.69	0.1367216	0.3624991	-5.22	FALSE
252808_at	putative protein various predicte	---	---	1.24	0.31	1.69	0.1367523	0.3625008	-5.22	FALSE
247688_at	putative protein predicted protei	---	AT5G59760	1.19	0.25	1.69	0.1367923	0.3625649	-5.22	FALSE
245123_at	unknown protein ; supported by	CAO	AT2G47450	-1.24	-0.31	-1.69	0.1368184	0.3625917	-5.22	FALSE
263760_at	unknown protein ; supported by	SULA	AT2G21280	-1.37	-0.46	-1.69	0.1368941	0.3627504	-5.22	FALSE

247476_at	putative protein	---	AT5G62330	1.20	0.26	1.69	0.1371483	0.3633276	-5.23	FALSE
250746_at	glucuronosyl transferase-like pro	---	AT5G05880	1.18	0.24	1.69	0.1371757	0.3633276	-5.23	FALSE
263839_at	putative cis-Golgi SNARE protein	MEMB11	AT2G36900	-1.33	-0.42	-1.69	0.1371555	0.3633276	-5.23	FALSE
267010_at	putative AP2 domain transcriptio	SNZ	AT2G39250	-1.27	-0.34	-1.69	0.1371626	0.3633276	-5.23	FALSE
266431_at	Mutator-like transposase similar	---	---	-1.20	-0.27	-1.69	0.1371966	0.3633407	-5.23	FALSE
253550_at	putative protein kinase serine/th	SIP3	AT4G30960	1.40	0.49	1.69	0.137268	0.3633611	-5.23	FALSE
253559_at	1,3-beta-glucanase - like protein	---	AT4G31140	-1.20	-0.26	-1.69	0.1372373	0.3633611	-5.23	FALSE
261170_at	growth regulator protein similar t	---	AT1G04910	-1.21	-0.28	-1.69	0.1372532	0.3633611	-5.23	FALSE
263327_at	putative receptor-like protein kina	---	AT2G15300	1.18	0.23	1.69	0.137265	0.3633611	-5.23	FALSE
257311_at	phosphate transporter, putative	PHT2;1	AT3G26570	-1.22	-0.29	-1.69	0.1372872	0.3633698	-5.23	FALSE
261372_at	zinc finger protein, putative simil	---	AT1G53010	1.24	0.31	1.69	0.1373586	0.3635036	-5.23	FALSE
264059_at	Expressed protein ; supported by	INH3	AT2G31305	-1.21	-0.28	-1.69	0.1373696	0.3635036	-5.23	FALSE
263271_s_a	hypothetical protein predicted by	---	---	-1.16	-0.21	-1.69	0.1374783	0.363749	-5.23	FALSE
260954_at	glyoxalase II isozyme, putative s	GLX2-4	AT1G06130	-1.25	-0.32	-1.69	0.1375503	0.3638972	-5.23	FALSE
255767_at	ribosomal protein L20, putative s	---	AT1G16740	-1.21	-0.27	-1.69	0.1375702	0.3639066	-5.23	FALSE
254970_at	chlorophyll a/b-binding protein -	LHCB5	AT4G10340	-1.20	-0.26	-1.68	0.1376017	0.3639066	-5.23	FALSE
262663_at	hypothetical protein identical to h	---	AT1G13940	-1.23	-0.30	-1.68	0.1375895	0.3639066	-5.23	FALSE
249467_at	NAM / CUC2 - like protein CUC2	ATNAC6	AT5G39610	-1.87	-0.90	-1.68	0.1377031	0.3640483	-5.23	TRUE
264553_s_a	putative cinnamyl alcohol dehyd	---	AT1G09480 ///	1.25	0.33	1.68	0.1376908	0.3640483	-5.23	FALSE
264673_at	Expressed protein ; supported by	ATATP-PR1	AT1G09795	-1.21	-0.28	-1.68	0.1377031	0.3640483	-5.23	FALSE
259354_at	unknown protein	---	AT3G05220	1.37	0.45	1.68	0.1377379	0.364098	-5.23	FALSE
266295_at	tubulin beta-7 chain identical to C	TUB7	AT2G29550	1.48	0.56	1.68	0.1377889	0.3641906	-5.23	TRUE
264936_at	hypothetical protein predicted by	EDA16	AT1G61140	1.18	0.24	1.68	0.1378434	0.3642553	-5.23	FALSE
266885_at	putative small GTP-binding prote	RAB6A	AT2G44610	-1.24	-0.31	-1.68	0.1378453	0.3642553	-5.23	FALSE
254387_at	putative protein CGI-131 protein	ATMSRB9	AT4G21850	3.43	1.78	1.68	0.1379032	0.3643661	-5.23	FALSE
267171_at	putative DOF zinc finger protein	DOF2.4	AT2G37590	1.27	0.34	1.68	0.1379401	0.3643792	-5.23	FALSE
247115_at	kinesin-like calmodulin-binding p	ZWI	AT5G65930	-1.26	-0.34	-1.68	0.1379362	0.3643792	-5.23	FALSE
264320_at	unknown protein	---	AT1G04090	1.16	0.22	1.68	0.1380879	0.3646851	-5.23	FALSE
261009_at	hypothetical protein similar to put	MES13	AT1G26360	1.24	0.31	1.68	0.1380742	0.3646851	-5.23	FALSE
246084_at	putative protein predicted protein	ATBRXL4	AT5G20540	1.22	0.29	1.68	0.1382034	0.3649479	-5.23	FALSE
252848_at	putative protein several hypothet	---	---	1.24	0.31	1.68	0.1383263	0.3651212	-5.23	FALSE
267244_at	putative reverse transcriptase	---	AT2G02650	1.19	0.25	1.68	0.1382891	0.3651212	-5.23	FALSE
247725_at	putative Rab5-interacting protein	---	AT5G59410	-1.35	-0.43	-1.68	0.1383491	0.3651212	-5.23	FALSE
245663_at	steroid sulfotransferase, putative	---	AT1G28170	1.19	0.26	1.68	0.1383471	0.3651212	-5.23	FALSE
253908_at	GH3 like protein GH3 protein, G	WES1	AT4G27260	2.31	1.21	1.68	0.1383086	0.3651212	-5.23	FALSE

259618_at	myb-related transcription factor (	MYB112	AT1G48000	1.31	0.40	1.68	0.1383851	0.3651741	-5.23	TRUE
260279_at	putative DNA repair protein simil	---	AT1G80420	-1.21	-0.27	-1.68	0.1384689	0.3653332	-5.23	FALSE
267444_at	hypothetical protein predicted by	---	AT2G19180	-1.30	-0.38	-1.68	0.1384825	0.3653332	-5.23	FALSE
261386_at	unknown protein ;supported by fu	---	AT1G05430	-1.24	-0.32	-1.68	0.1384935	0.3653332	-5.23	FALSE
261673_at	lipid transfer protein, putative sir	---	AT1G18280	2.13	1.09	1.68	0.1385126	0.3653414	-5.23	FALSE
262825_at	putative chloroplast prephenate d	ADT1	AT1G11790	1.40	0.49	1.68	0.1385317	0.3653497	-5.23	TRUE
248694_at	unknown protein	---	AT5G48340	-1.19	-0.26	-1.68	0.1386103	0.36543	-5.24	FALSE
256590_at	recombination signal sequence r	ATHMG	AT3G28730	-1.28	-0.36	-1.68	0.1386068	0.36543	-5.24	FALSE
253716_at	hypothetical protein	---	AT4G29420	-1.24	-0.31	-1.68	0.1385967	0.36543	-5.24	FALSE
254879_at	hypothetical protein	---	AT4G11670	1.22	0.28	1.68	0.1386536	0.3654909	-5.24	FALSE
267524_at	unknown protein	---	AT2G30600	1.33	0.41	1.68	0.1386654	0.3654909	-5.24	FALSE
259934_at	unknown protein	---	AT1G71340	-1.33	-0.41	-1.68	0.1387174	0.3655012	-5.24	FALSE
249699_at	putative protein similar to unknov	---	AT5G35540	1.16	0.21	1.68	0.1387166	0.3655012	-5.24	FALSE
259221_s_a	putative phospholipase similar to	NPC5	AT3G03530 ///	2.89	1.53	1.68	0.1386925	0.3655012	-5.24	FALSE
255242_at	putative protein putative retrotra	---	---	1.19	0.25	1.68	0.1387649	0.3655842	-5.24	FALSE
248433_at	putative protein strong similarity t	---	AT5G51400	1.19	0.25	1.68	0.1388232	0.3656468	-5.24	FALSE
249086_at	putative protein strong similarity t	---	AT5G44180	-1.21	-0.28	-1.68	0.1388368	0.3656468	-5.24	FALSE
249835_s_a	putative protein similar to unknov	---	AT5G23490 ///	1.46	0.55	1.68	0.1388231	0.3656468	-5.24	FALSE
265158_at	hypothetical protein predicted by	---	AT1G31040	1.17	0.23	1.68	0.1388876	0.3657383	-5.24	FALSE
265620_at	unknown protein	---	AT2G27310	1.81	0.86	1.68	0.1389583	0.3658728	-5.24	TRUE
245506_at	glutaredoxin homolog	---	AT4G15700	-1.53	-0.62	-1.68	0.1389707	0.3658728	-5.24	FALSE
245575_at	centromere protein homolog	---	AT4G14760	-1.20	-0.27	-1.68	0.1390959	0.3661178	-5.24	FALSE
266019_at	putative calmodulin-binding prote	---	AT2G18750	1.17	0.22	1.68	0.1390952	0.3661178	-5.24	FALSE
265449_at	putative arginine/serine-rich splic	---	AT2G46610	-1.33	-0.41	-1.68	0.1391262	0.3661554	-5.24	FALSE
253447_at	hypothetical protein	---	AT4G32630	1.17	0.22	1.68	0.1391453	0.3661634	-5.24	FALSE
256614_at	hypothetical protein predicted by	---	AT3G29300	1.20	0.26	1.68	0.1393157	0.366485	-5.24	FALSE
251034_at	putative protein ;supported by fu	PRA1.A1	AT5G02040	1.22	0.29	1.68	0.1392876	0.366485	-5.24	FALSE
250074_at	UDP-glucose pyrophosphorylase	---	AT5G17310	-1.31	-0.39	-1.68	0.1393156	0.366485	-5.24	FALSE
258809_at	NAM-like protein (no apical meris	anac047	AT3G04070	1.62	0.70	1.68	0.1393528	0.3665262	-5.24	TRUE
256315_at	hypothetical protein predicted by	---	AT1G35880	1.19	0.25	1.68	0.1393635	0.3665262	-5.24	FALSE
262263_at	auxin transport protein REH1, pu	PIN3	AT1G70940	-1.74	-0.80	-1.68	0.1393871	0.3665459	-5.24	TRUE
247704_at	Expressed protein ; supported by	RTFL5	AT5G59510	1.68	0.74	1.68	0.1394505	0.3666703	-5.24	FALSE
252069_s_a	putative protein putative protein	---	AT3G51640 ///	1.19	0.25	1.68	0.1394773	0.3666987	-5.24	FALSE
248674_at	non-phototropic hypocotyl-like pr	---	AT5G48800	-1.44	-0.52	-1.68	0.139528	0.3667746	-5.24	FALSE
255551_at	putative potassium channel ;sup	KCO5	AT4G01840	-1.17	-0.23	-1.68	0.1395544	0.3667746	-5.24	FALSE

261734_at	hypothetical protein similar to hyp	---	AT1G47790	1.19	0.25	1.68	0.1395459	0.3667746	-5.24	FALSE
258273_at	unknown protein ;supported by f	GRX4	AT3G15660	-1.16	-0.22	-1.67	0.1396061	0.3668284	-5.24	FALSE
255023_at	hypothetical protein	---	AT4G09850	1.22	0.28	1.67	0.1396071	0.3668284	-5.24	FALSE
265369_s_a	putative retroelement pol polypro	---	---	-1.19	-0.25	-1.67	0.1396596	0.3668676	-5.24	FALSE
264733_at	phloem serpin-1, putative similar	---	AT1G62170	1.17	0.23	1.67	0.1396702	0.3668676	-5.24	FALSE
253944_at	SNF8 like protein SNF8 protein	VPS22	AT4G27040	-1.21	-0.28	-1.67	0.1396554	0.3668676	-5.24	FALSE
258207_at	putative GTP pyrophosphokinase	RSH2	AT3G14050	1.49	0.57	1.67	0.139693	0.366885	-5.24	FALSE
247409_at	dihydroneopterin aldolase-like pr	---	AT5G62980	-1.34	-0.43	-1.67	0.1397215	0.3669176	-5.24	FALSE
259455_x_a	unknown protein	---	AT1G44030	1.28	0.35	1.67	0.1398593	0.3672374	-5.24	FALSE
254873_at	putative protein a 162 kDa comp	EIF3A	AT4G11420	-1.19	-0.25	-1.67	0.1398967	0.3672711	-5.24	FALSE
252603_at	putative protein	---	AT3G45050	-1.28	-0.35	-1.67	0.1399044	0.3672711	-5.24	FALSE
258140_at	Expressed protein ; supported by	ALDH2C4	AT3G24503	1.64	0.72	1.67	0.1399402	0.367323	-5.24	FALSE
257918_at	ethylene responsive element bin	---	AT3G23230	4.63	2.21	1.67	0.1399697	0.3673581	-5.24	FALSE
264659_at	unknown protein Similar to S. po	ATOPT2	AT1G09930	1.19	0.25	1.67	0.1399993	0.3673935	-5.24	FALSE
250935_at	polyubiquitin (UBQ3) identical to	UBQ3	AT5G03240	-1.38	-0.46	-1.67	0.1400647	0.3674804	-5.25	FALSE
265792_at	predicted by genscan and genefi	---	AT2G01390	1.23	0.30	1.67	0.1400528	0.3674804	-5.24	FALSE
256486_at	chloroplast nucleoid DNA bindin	---	AT1G31450	1.21	0.28	1.67	0.1400926	0.3675115	-5.25	FALSE
249927_at	Glucose-1-phosphate adenylyltra	APL1	AT5G19220	-1.37	-0.45	-1.67	0.1401691	0.3675426	-5.25	TRUE
262206_at	putative ubiquinol-cytochrome c	---	AT2G01090	-1.26	-0.33	-1.67	0.140177	0.3675426	-5.25	FALSE
248234_at	putative protein contains similarit	---	AT5G53850	-1.18	-0.24	-1.67	0.1401731	0.3675426	-5.25	FALSE
253455_at	putative protein	---	AT4G32020	1.40	0.49	1.67	0.1401375	0.3675426	-5.25	FALSE
262426_s_a	cytochrome P450, putative simil	---	AT1G47625 /A	-1.28	-0.36	-1.67	0.140185	0.3675426	-5.25	FALSE
265304_at	putative AP2 domain transcriptio	---	AT2G20350	1.17	0.23	1.67	0.1402259	0.3675652	-5.25	FALSE
260908_at	maternal embryogenesis control	MEA	AT1G02580	1.43	0.51	1.67	0.1402118	0.3675652	-5.25	FALSE
266211_at	putative retroelement pol polypro	---	---	1.20	0.27	1.67	0.1402642	0.367596	-5.25	FALSE
253852_at	putative protein diacylglycerol ki	---	AT4G28130	1.18	0.24	1.67	0.1402698	0.367596	-5.25	FALSE
246464_at	quinone oxidoreductase -like pro	---	AT5G16980	1.20	0.26	1.67	0.1403121	0.3676644	-5.25	FALSE
259485_at	ATP synthase gamma-subunit, p	ATPC2	AT1G15700	-1.52	-0.60	-1.67	0.1403542	0.3676902	-5.25	FALSE
249754_at	flavanone 3-hydroxylase-like pro	DMR6	AT5G24530	2.47	1.30	1.67	0.1403401	0.3676902	-5.25	FALSE
253238_at	putative protein (fragment)	---	AT4G34480	1.25	0.32	1.67	0.1404517	0.3678886	-5.25	FALSE
251545_at	zinc transporter -like protein zinc	MTPA2	AT3G58810	1.31	0.39	1.67	0.1404621	0.3678886	-5.25	FALSE
250192_at	pescadillo - like protein embryon	---	AT5G14520	-1.35	-0.43	-1.67	0.1404901	0.3679196	-5.25	FALSE
265392_at	lipoic acid synthase (LIP1) ; sup	LIP1	AT2G20860	-1.18	-0.24	-1.67	0.1405695	0.3680851	-5.25	FALSE
252443_at	putative helicase helicase SKI2V	---	AT3G46960	-1.24	-0.31	-1.67	0.1406115	0.368153	-5.25	FALSE
247281_at	immunophilin (gb|AAB57847.1)	FKBP12	AT5G64350	-1.18	-0.24	-1.67	0.140644	0.3681684	-5.25	FALSE

256928_at	unknown protein	---	AT3G22590	-1.21	-0.28	-1.67	0.1406806	0.3681684	-5.25	FALSE
252158_at	CDPK-related protein kinase	CRK	AT3G50530	-1.25	-0.32	-1.67	0.140682	0.3681684	-5.25	FALSE
250000_at	putative protein PGPD14 - Petu	---	AT5G18650	-1.29	-0.37	-1.67	0.1406565	0.3681684	-5.25	FALSE
263511_at	En/Spm-like transposon protein r	---	---	1.19	0.25	1.67	0.1407738	0.3683666	-5.25	FALSE
245702_at	calcium lipid binding protein - like	SYTC	AT5G04220	-1.32	-0.40	-1.67	0.140908	0.3685907	-5.25	TRUE
259218_at	hypothetical protein similar to pu	---	AT3G03580	-1.23	-0.30	-1.67	0.1409012	0.3685907	-5.25	FALSE
248934_at	serine/threonine protein kinase-li	---	AT5G46080	2.11	1.08	1.67	0.1408966	0.3685907	-5.25	FALSE
260522_x_a	hypothetical protein predicted by	---	AT2G41730	2.72	1.44	1.67	0.1409962	0.368737	-5.25	TRUE
261409_at	zinc finger protein OBP2 identica	OBP2	AT1G07640	-1.22	-0.29	-1.67	0.1409911	0.368737	-5.25	FALSE
251507_at	putative protein CND41, chlorop	---	AT3G59080	2.30	1.20	1.67	0.1410694	0.3688437	-5.25	FALSE
251275_at	putative protein anthranilate pho	---	AT3G61720	1.34	0.43	1.67	0.141057	0.3688437	-5.25	FALSE
260085_at	putative D-ribulose-5-phosphate	---	AT1G63290	-1.19	-0.25	-1.67	0.1412142	0.36918	-5.25	FALSE
251659_at	hypothetical protein ;supported b	BIGYIN	AT3G57090	1.22	0.28	1.67	0.1412441	0.3692159	-5.25	FALSE
265586_at	pathogenesis-related protein (PR	PR-1-LIKE	AT2G19990	1.26	0.34	1.67	0.1413032	0.3693281	-5.25	FALSE
253598_at	ribosomal protein S11 - like ribo	---	AT4G30800	-1.70	-0.77	-1.67	0.1413555	0.3693494	-5.25	FALSE
261235_x_a	hypothetical protein predicted by	---	---	1.18	0.23	1.67	0.1413568	0.3693494	-5.25	FALSE
261458_at	unknown protein contains DNA-J	---	AT1G21080	1.25	0.33	1.67	0.1413599	0.3693494	-5.25	FALSE
266478_at	putative cysteinyl-tRNA syntheta	SYCO ARA	AT2G31170	-1.35	-0.44	-1.67	0.1414029	0.3693963	-5.25	FALSE
266532_at	putative glucosyltransferase ;su	---	AT2G16890	2.61	1.38	1.67	0.1414103	0.3693963	-5.25	FALSE
266824_at	homeodomain transcription facto	HAT9	AT2G22800	-1.19	-0.25	-1.67	0.1415011	0.3694105	-5.25	FALSE
265346_at	hypothetical protein	---	---	1.20	0.26	1.67	0.1415291	0.3694105	-5.25	FALSE
258665_at	thioredoxin-like protein similar to	ATH9	AT3G08710	1.42	0.51	1.67	0.1414785	0.3694105	-5.25	FALSE
250687_at	putative protein similar to unknov	---	AT5G06660	-1.16	-0.22	-1.67	0.1415217	0.3694105	-5.25	FALSE
251250_at	putative protein pectin methyles	---	AT3G62180	1.28	0.36	1.67	0.1414555	0.3694105	-5.25	FALSE
267241_at	hypothetical protein predicted by	---	AT2G02490 /	1.17	0.23	1.67	0.1414533	0.3694105	-5.25	FALSE
264841_at	putative protein kinase similar to	---	AT1G03740	1.53	0.62	1.67	0.1415114	0.3694105	-5.25	FALSE
265709_at	hypothetical protein predicted by	---	---	1.68	0.75	1.66	0.1416177	0.3695994	-5.26	FALSE
253390_at	hypothetical protein ;supported b	---	AT4G32750	-1.29	-0.36	-1.66	0.1416638	0.3696776	-5.26	FALSE
247912_at	putative protein contains similarit	---	AT5G57480	1.49	0.58	1.66	0.1417286	0.3698043	-5.26	TRUE
253091_at	cytochrome p450 - like protein c	CYP81D2	AT4G37360	1.20	0.26	1.66	0.1418831	0.3701652	-5.26	FALSE
255924_at	unknown protein contains similar	---	AT1G22170	1.25	0.32	1.66	0.1419908	0.3703815	-5.26	FALSE
249276_at	DNA polymerase alpha subunit I	POLA3	AT5G41880	-2.40	-1.26	-1.66	0.1419985	0.3703815	-5.26	FALSE
245235_at	putative protein similarity to prec	---	AT4G25550	-1.21	-0.28	-1.66	0.1420366	0.3704386	-5.26	FALSE
250136_at	putative protein de novo DNA m	DRM1	AT5G15380	1.41	0.50	1.66	0.1420777	0.370461	-5.26	FALSE
259409_at	hypothetical protein contains sim	---	AT1G13330	-1.19	-0.25	-1.66	0.1420688	0.370461	-5.26	FALSE

263956_at	putative homeodomain transcript	BLH1	AT2G35940	1.40	0.49	1.66	0.142123	0.3705368	-5.26	FALSE
257775_at	short-chain alcohol dehydrogena	---	AT3G29260	1.22	0.29	1.66	0.1421639	0.3705586	-5.26	FALSE
257613_at	polygalacturonase, putative simi	---	AT3G26610	-1.19	-0.25	-1.66	0.1421532	0.3705586	-5.26	FALSE
250066_at	unknown protein	---	AT5G17930	-1.36	-0.45	-1.66	0.1422134	0.3705719	-5.26	FALSE
246441_at	putative protein ;supported by fu	---	AT5G17560	-1.19	-0.25	-1.66	0.1421872	0.3705719	-5.26	FALSE
260429_at	unknown protein ;supported by f	JAZ6	AT1G72450	1.58	0.66	1.66	0.1422177	0.3705719	-5.26	FALSE
260352_at	Expressed protein ; supported by	PDCB4	AT1G69295	1.20	0.26	1.66	0.1422464	0.3706041	-5.26	FALSE
256412_at	hypothetical protein predicted by	ELO1	AT3G11220	-1.22	-0.29	-1.66	0.142306	0.3706524	-5.26	FALSE
254619_at	myb - like protein transforming p	MYB98	AT4G18770	1.20	0.26	1.66	0.1423136	0.3706524	-5.26	FALSE
260970_at	unknown protein	---	AT1G53640	1.24	0.31	1.66	0.142305	0.3706524	-5.26	FALSE
258064_at	putative cytochrome P450 simila	CYP72A14	AT3G14680	-1.66	-0.73	-1.66	0.1424618	0.3706589	-5.26	FALSE
255494_at	predicted protein of unknown fur	---	AT4G02710	-1.19	-0.25	-1.66	0.1424624	0.3706589	-5.26	FALSE
251246_at	auxin-induced protein homolog a	IAA30	AT3G62100	-1.17	-0.22	-1.66	0.1423812	0.3706589	-5.26	FALSE
251023_at	putative protein amino acid trans	---	AT5G02170	-1.24	-0.31	-1.66	0.1424413	0.3706589	-5.26	FALSE
265541_at	hypothetical protein predicted by	SQN	---	1.18	0.24	1.66	0.1424028	0.3706589	-5.26	FALSE
260341_at	squamosa-promoter binding pro	---	AT1G69170	-1.30	-0.38	-1.66	0.1424182	0.3706589	-5.26	FALSE
266952_at	putative gibberellin 2-oxidase	ATGA2OX3	AT2G34555	1.23	0.30	1.66	0.1424589	0.3706589	-5.26	FALSE
254237_at	cysteine proteinase contains sim	---	AT4G23520	1.17	0.23	1.66	0.1424485	0.3706589	-5.26	FALSE
265250_at	putative receptor protein kinase s	BRL2	AT2G01950	-1.33	-0.41	-1.66	0.1424134	0.3706589	-5.26	FALSE
255259_at	coded for by A. thaliana cDNA W	NDB2	AT4G05020	2.31	1.21	1.66	0.1425328	0.3707999	-5.26	FALSE
265040_at	G-box binding factor, GBF4 Ider	GBF4	AT1G03970	-1.29	-0.37	-1.66	0.1425928	0.3708714	-5.26	FALSE
261236_at	importin alpha, putative similar t	---	AT1G32880	1.19	0.25	1.66	0.1425895	0.3708714	-5.26	FALSE
245722_at	unknown protein	---	AT1G73430	-1.29	-0.37	-1.66	0.1426611	0.3710068	-5.26	FALSE
255918_at	putative protein	---	---	1.17	0.23	1.66	0.1427301	0.3711016	-5.26	FALSE
251702_at	transcription factor-like protein n	BZIP49	AT3G56660	1.29	0.36	1.66	0.1427266	0.3711016	-5.26	FALSE
264743_at	receptor-like protein kinase, puta	---	AT1G62090	1.18	0.23	1.66	0.14275	0.371111	-5.26	FALSE
267532_at	unknown protein ;supported by f	---	AT2G42040	-1.38	-0.47	-1.66	0.1428392	0.3713004	-5.26	FALSE
249348_at	unknown protein	---	AT5G40860	1.25	0.32	1.66	0.1428639	0.3713224	-5.26	FALSE
259903_at	unknown protein	---	AT1G74160	-1.36	-0.45	-1.66	0.142909	0.3713972	-5.26	FALSE
247864_s_a	anthranilate synthase beta chain	---	AT1G24807 //	2.00	1.00	1.66	0.1429562	0.3714776	-5.26	FALSE
251254_at	putative protein anion exchange	---	AT3G62270	1.25	0.32	1.66	0.1430093	0.3715415	-5.26	FALSE
256819_at	unknown protein contains Pfam p	---	AT3G21390	-1.19	-0.25	-1.66	0.1430459	0.3715415	-5.26	FALSE
251330_at	putative protein putative protein A	---	AT3G61550	-1.31	-0.39	-1.66	0.1430348	0.3715415	-5.26	FALSE
265964_at	putative RNA-binding protein ; s	---	AT2G37510	-1.22	-0.28	-1.66	0.1430385	0.3715415	-5.26	FALSE
255143_at	putative protein several hypothet	---	AT4G08430	1.15	0.20	1.66	0.1430903	0.3716145	-5.26	FALSE

256056_at	hypothetical protein contains sim	---	AT1G07190	1.17	0.22	1.66	0.1431759	0.3717944	-5.27	FALSE
259126_at	putative NADPH-ferrihemoprotei	---	AT3G02280	-1.18	-0.23	-1.66	0.1432144	0.371852	-5.27	FALSE
254129_at	putative tRNA isopentenyltransfe	IPT4	AT4G24650	1.18	0.24	1.66	0.143294	0.371974	-5.27	FALSE
245942_at	putative protein transcription reg	---	AT5G19490	1.16	0.21	1.66	0.1432907	0.371974	-5.27	FALSE
263718_at	putative CCAAT-box binding tran	NF-YB7	AT2G13570	1.25	0.32	1.66	0.1433347	0.3720374	-5.27	FALSE
265006_at	unknown protein similar to small	TIM13	AT1G61570	-1.54	-0.62	-1.66	0.1433816	0.3721107	-5.27	FALSE
263300_at	Mutator-like transposase similar t	---	---	1.17	0.22	1.66	0.1433956	0.3721107	-5.27	FALSE
254969_at	hypothetical protein ;supported b	---	AT4G10360	1.19	0.25	1.66	0.1434198	0.3721289	-5.27	FALSE
252784_at	putative protein predicted protei	---	---	1.16	0.21	1.66	0.1434354	0.3721289	-5.27	FALSE
259438_at	unknown protein similar to putati	AN	AT1G01510	-1.32	-0.40	-1.66	0.1434515	0.3721289	-5.27	FALSE
245145_at	putative dihydrodipicolinate synth	DHDPS2	AT2G45440	-1.38	-0.46	-1.66	0.1435484	0.3722423	-5.27	FALSE
256885_at	chaperone-like ATPase contains	---	AT3G15120	-1.24	-0.31	-1.66	0.1435299	0.3722423	-5.27	FALSE
258796_at	unknown protein ;supported by f	WDL1	AT3G04630	-1.52	-0.60	-1.66	0.1435575	0.3722423	-5.27	FALSE
261318_at	Expressed protein ; supported by	---	AT1G53035	-2.21	-1.15	-1.66	0.1435605	0.3722423	-5.27	FALSE
258055_at	putative 2Fe-2S iron-sulfur cluste	NDF4	AT3G16250	-1.71	-0.78	-1.65	0.1436284	0.3722428	-5.27	TRUE
266206_at	unknown protein ; supported by	---	AT2G27730	1.28	0.35	1.65	0.1436423	0.3722428	-5.27	FALSE
265264_at	hypothetical protein predicted by	---	AT2G42930	1.18	0.24	1.65	0.1436353	0.3722428	-5.27	FALSE
251727_at	putative protein	---	AT3G56290	-1.53	-0.61	-1.66	0.1435776	0.3722428	-5.27	FALSE
246637_at	putative protein polymorphic me	---	AT5G34870	1.22	0.29	1.66	0.1436007	0.3722428	-5.27	FALSE
265190_at	unknown protein ; supported by	---	AT1G23780	-1.17	-0.23	-1.65	0.1436781	0.3722731	-5.27	FALSE
248915_at	putative protein strong similarity t	---	AT5G45690	1.23	0.30	1.65	0.143703	0.3722731	-5.27	FALSE
258451_at	alternative oxidase 1b precursor	AOX1B	AT3G22360	1.25	0.32	1.65	0.1436914	0.3722731	-5.27	FALSE
263242_at	unknown protein	---	AT2G31400	1.22	0.29	1.65	0.1439433	0.3726419	-5.27	FALSE
253847_at	putative protein CRP1, Zea may	---	AT4G28010	-1.19	-0.26	-1.65	0.1439418	0.3726419	-5.27	FALSE
246597_at	L-aspartate oxidase -like protein	AO	AT5G14760	1.84	0.88	1.65	0.1439191	0.3726419	-5.27	FALSE
266137_at	unknown protein ;supported by f	---	AT2G45010	1.20	0.26	1.65	0.1439383	0.3726419	-5.27	FALSE
245107_at	putative heat shock transcription	AT-HSFB3	AT2G41690	1.65	0.72	1.65	0.1438657	0.3726419	-5.27	FALSE
255541_s_a	P-glycoprotein-like protein pgp3 s	PGP5	AT4G01820 ///	-1.17	-0.23	-1.65	0.14393	0.3726419	-5.27	FALSE
247740_at	receptor-like protein kinase prec	CRCK1	AT5G58940	1.74	0.80	1.65	0.1439751	0.3726819	-5.27	FALSE
247394_at	putative protein predicted protei	---	AT5G62860	1.48	0.56	1.65	0.1440051	0.3727171	-5.27	FALSE
260073_at	putative protein kinase contains l	---	AT1G73660	-1.28	-0.35	-1.65	0.1440911	0.3728882	-5.27	FALSE
252444_at	putative protein Na+-dependent	PHT4;3	AT3G46980	-1.16	-0.21	-1.65	0.1441039	0.3728882	-5.27	FALSE
257849_at	unknown protein	ECT5	AT3G13060	-1.29	-0.36	-1.65	0.1441758	0.3729897	-5.27	FALSE
245409_at	putative protein	---	AT4G17200	1.15	0.20	1.65	0.1441595	0.3729897	-5.27	FALSE
251893_at	putative protein	---	AT3G54380	-1.19	-0.25	-1.65	0.1442843	0.3731094	-5.27	FALSE

245547_at	cytochrome P450 like protein	CYP702A2	AT4G15300	1.18	0.23	1.65	0.1443039	0.3731094	-5.27	FALSE
252760_x_a	putative protein several hypothet	---	---	1.18	0.24	1.65	0.1442534	0.3731094	-5.27	FALSE
264422_at	unknown protein similar to unkno	LCV2	AT1G43130	-1.22	-0.28	-1.65	0.1442948	0.3731094	-5.27	FALSE
264628_at	hypothetical protein contains sim	---	AT1G65540	1.16	0.21	1.65	0.1442658	0.3731094	-5.27	FALSE
251056_at	putative protein KIAA1303 prote	RAPTOR2	AT5G01770	1.27	0.34	1.65	0.1443443	0.3731718	-5.27	FALSE
259296_at	putative aminopeptidase similar t	---	AT3G05350	-1.25	-0.32	-1.65	0.1443904	0.3732062	-5.27	FALSE
249029_at	disease resistance protein-like	---	AT5G44870	1.20	0.27	1.65	0.1443787	0.3732062	-5.27	FALSE
246018_at	Expressed protein ; supported by	---	AT5G10695	1.82	0.86	1.65	0.1444085	0.3732107	-5.27	FALSE
250533_at	flavonol synthase (FLS) (sp|Q96	FLS	AT5G08640	1.18	0.24	1.65	0.1444401	0.3732501	-5.27	FALSE
247660_at	ankyrin-like protein ankyrin 3, M	---	AT5G60070	1.18	0.24	1.65	0.1444865	0.3733277	-5.27	FALSE
266627_at	putative pre-mRNA splicing facto	MEE29	AT2G35340	1.22	0.29	1.65	0.1445804	0.3734857	-5.27	FALSE
252870_at	adenosine-5-phosphosulfate-kina	AKN2	AT4G39940	1.98	0.98	1.65	0.1445758	0.3734857	-5.27	FALSE
255619_s_a	putative CHP-rich zinc finger pro	---	AT4G01350 /A	1.29	0.37	1.65	0.1446186	0.3734997	-5.27	FALSE
265296_at	hypothetical protein predicted by	---	AT2G14060	1.18	0.24	1.65	0.144612	0.3734997	-5.27	FALSE
259352_at	unknown protein	---	AT3G05170	1.39	0.48	1.65	0.1446735	0.3735626	-5.27	FALSE
260315_at	hypothetical protein similar to C-	---	AT1G63820	-1.19	-0.25	-1.65	0.1446757	0.3735626	-5.27	FALSE
257583_at	hypothetical protein	PMI2	AT1G66480	2.10	1.07	1.65	0.1447431	0.3736944	-5.28	FALSE
253011_at	putative protein retrotransposon	EDA40	AT4G37890	1.45	0.54	1.65	0.1447784	0.3737432	-5.28	FALSE
250670_at	polygalacturonase inhibiting prot	PGIP1	AT5G06860	1.72	0.78	1.65	0.144797	0.3737489	-5.28	FALSE
266453_at	putative protein kinase contains a	---	AT2G43230	1.17	0.22	1.65	0.1448721	0.3739006	-5.28	FALSE
253412_at	putative protein (fragment) calci	CBL10	AT4G33000	-1.26	-0.33	-1.65	0.1449989	0.3740232	-5.28	TRUE
266327_at	homeodomain transcription facto	ATHB-7	AT2G46680	1.48	0.57	1.65	0.1450016	0.3740232	-5.28	TRUE
257652_at	unknown protein contains Pfam p	APUM24	AT3G16810	-1.43	-0.51	-1.65	0.1449709	0.3740232	-5.28	FALSE
246426_at	ovule development protein ainte	BBM	AT5G17430	1.18	0.23	1.65	0.1449478	0.3740232	-5.28	FALSE
252539_at	putative protein	---	AT3G45730	-1.27	-0.35	-1.65	0.144972	0.3740232	-5.28	FALSE
257768_at	RING zinc finger protein, putativ	---	AT3G23060	1.27	0.34	1.65	0.145019	0.3740258	-5.28	FALSE
245610_at	hypothetical protein	---	AT4G14380	1.22	0.28	1.65	0.1450607	0.3740909	-5.28	FALSE
251365_at	putative DNA-binding protein At	---	AT3G61310	-1.27	-0.35	-1.65	0.1451301	0.3741854	-5.28	TRUE
255537_at	protoporphyrinogen oxidase ; su	PPOX	AT4G01690	-1.26	-0.34	-1.65	0.1451201	0.3741854	-5.28	FALSE
261885_at	unknown protein	---	AT1G80930	-1.24	-0.31	-1.65	0.145354	0.3747202	-5.28	FALSE
262238_at	hypothetical protein predicted by	---	AT1G48300	-1.36	-0.44	-1.65	0.1454012	0.3747997	-5.28	FALSE
248999_at	putative protein contains similarit	---	AT5G44970	1.18	0.24	1.65	0.145474	0.3749447	-5.28	FALSE
263645_at	putative GTP-binding protein	---	AT2G04720	1.16	0.21	1.65	0.1455149	0.375008	-5.28	FALSE
253645_at	putative protein G protein beta s	VIP3	AT4G29830	-1.19	-0.25	-1.65	0.1455907	0.3751608	-5.28	FALSE
244982_at	ribosomal protein L14	---	---	-1.24	-0.31	-1.65	0.1456588	0.375294	-5.28	TRUE

260259_at	unknown protein similar to unkno	---	AT1G74300	1.21	0.27	1.65	0.1456828	0.3753134	-5.28	FALSE
246961_at	unknown protein	---	AT5G24710	1.39	0.48	1.64	0.1457717	0.3754383	-5.28	FALSE
256965_at	branched chain alpha-keto acid	DIN4	AT3G13450	1.51	0.59	1.64	0.1457895	0.3754383	-5.28	FALSE
261502_at	hypothetical protein predicted by	AtHB31	AT1G14440	-1.44	-0.53	-1.64	0.1457971	0.3754383	-5.28	FALSE
253064_at	bZIP transcription factor - like pr	AtbZIP7	AT4G37730	1.21	0.28	1.64	0.1457612	0.3754383	-5.28	FALSE
253885_at	putative protein essential for em	VPS26B	AT4G27690	-1.26	-0.34	-1.64	0.1458168	0.3754465	-5.28	FALSE
245410_at	putative protein	ATMAP70-5	AT4G17220	1.18	0.24	1.64	0.145861	0.375518	-5.28	FALSE
251632_at	hypothetical protein	---	AT3G57440	1.26	0.33	1.64	0.1458884	0.3755462	-5.28	FALSE
254715_at	putative protein hypothetical pro	---	AT4G13550	-1.32	-0.40	-1.64	0.1459147	0.3755714	-5.28	FALSE
250029_at	galactose-1-phosphate uridyl tra	---	AT5G18200	-1.25	-0.32	-1.64	0.1460125	0.375731	-5.28	FALSE
245490_at	hypothetical protein	LDL3	AT4G16310	1.23	0.30	1.64	0.1460261	0.375731	-5.28	FALSE
263205_at	Ca2+-dependent lipid-binding pr	NTMC2T2.1	AT1G05500	-1.19	-0.25	-1.64	0.146001	0.375731	-5.28	FALSE
267628_at	unknown protein similar to GP|22	---	AT2G42280	-1.22	-0.29	-1.64	0.146145	0.3759521	-5.28	FALSE
247680_s_a	glycine-rich protein - like glycine	---	AT1G61210 ///	-1.20	-0.27	-1.64	0.1461411	0.3759521	-5.28	FALSE
248404_at	trehalose-6-phosphate phosphat	ATTPPA	AT5G51460	-1.49	-0.57	-1.64	0.1461883	0.376021	-5.28	TRUE
247422_at	putative protein	PEX14	AT5G62810	-1.19	-0.25	-1.64	0.1462229	0.3760678	-5.28	FALSE
248982_at	chloroplast nucleoid DNA-binding	---	AT5G45120	1.22	0.29	1.64	0.1462724	0.3761525	-5.28	FALSE
250706_at	deoxyhypusine synthase ;suppo	DHS	AT5G05920	-1.24	-0.31	-1.64	0.1464185	0.3764859	-5.29	FALSE
250329_at	putative potassium transport pro	KEA6	AT5G11800	1.21	0.28	1.64	0.1464411	0.3765016	-5.29	FALSE
249940_at	NAC-domain protein-like ;suppo	anac090	AT5G22380	1.22	0.28	1.64	0.1464923	0.3765906	-5.29	FALSE
249151_at	inorganic phosphate transporter	PHT3	AT5G43360	1.21	0.27	1.64	0.1465363	0.3766614	-5.29	FALSE
258008_at	putative late embryogenesis abu	---	AT3G19430	1.20	0.26	1.64	0.1465773	0.3767166	-5.29	FALSE
248503_at	putative protein contains similarit	NF-YC7	AT5G50470	1.36	0.44	1.64	0.1465908	0.3767166	-5.29	FALSE
260424_at	putative receptor-like protein kin	---	AT1G72460	1.19	0.26	1.64	0.1466696	0.3768766	-5.29	FALSE
260846_at	unknown protein	---	AT1G17300	1.21	0.27	1.64	0.1467133	0.3769465	-5.29	FALSE
249327_at	anion channel protein (gb|AAC05	ATCLC-A	AT5G40890	1.47	0.56	1.64	0.1467478	0.3769927	-5.29	FALSE
257052_at	putative 3-hydroxybutyryl-CoA de	---	AT3G15290	1.19	0.25	1.64	0.1468275	0.376998	-5.29	FALSE
261446_at	unknown protein	SEC5B	AT1G21170	1.28	0.36	1.64	0.1467947	0.376998	-5.29	FALSE
255766_at	unknown protein ;supported by fu	---	AT1G16750	-1.27	-0.35	-1.64	0.1468101	0.376998	-5.29	FALSE
263087_s_a	putative sugar transporter	---	AT2G16120 ///	1.21	0.27	1.64	0.1468491	0.376998	-5.29	FALSE
249907_at	putative protein DNA repair prote	RAD5	AT5G22750	-1.19	-0.25	-1.64	0.1468164	0.376998	-5.29	FALSE
248053_at	putative protein similar to unknov	AtNMNAT	AT5G55810	-1.22	-0.29	-1.64	0.1468375	0.376998	-5.29	FALSE
266999_at	putative HMG protein ; supported	---	AT2G34450	-1.29	-0.36	-1.64	0.1468806	0.3770364	-5.29	FALSE
265968_at	putative protein translocase ; su	ATTIM17-2	AT2G37410	-1.33	-0.42	-1.64	0.1469293	0.377119	-5.29	FALSE
259033_at	putative pectinacetylesterase sim	---	AT3G09405 ///	2.80	1.48	1.64	0.1469548	0.3771421	-5.29	TRUE

250396_at	zinc finger -like protein CCHH fir	---	AT5G10970	1.53	0.62	1.64	0.1470044	0.3771845	-5.29	FALSE
257909_at	Expressed protein ; supported by	---	AT3G25480	-1.27	-0.34	-1.64	0.1469928	0.3771845	-5.29	FALSE
264296_at	protein transport protein sec61 a	---	AT1G78720	1.33	0.41	1.64	0.1470363	0.3772239	-5.29	FALSE
254849_at	putative protein RNA splicing-rel	---	AT4G11970	-1.16	-0.22	-1.64	0.1471712	0.3775276	-5.29	FALSE
266606_at	putative AP2 domain transcriptio	CRF5	AT2G46310	1.40	0.48	1.64	0.1472039	0.3775689	-5.29	FALSE
252420_at	putative protein several hypothet	---	AT3G47530	-1.32	-0.41	-1.64	0.1472955	0.3777189	-5.29	FALSE
246640_x_a	putative protein predicted protei	---	---	1.21	0.27	1.64	0.1472926	0.3777189	-5.29	FALSE
266591_at	expressed protein supported by	ABIL1	AT2G46225	-1.35	-0.43	-1.64	0.1474176	0.3779046	-5.29	FALSE
253313_at	putative peroxidase peroxidase	---	AT4G33870	1.22	0.28	1.64	0.1474094	0.3779046	-5.29	FALSE
259826_at	arm repeat-containing protein, p	PUB17	AT1G29340	1.35	0.43	1.64	0.1473878	0.3779046	-5.29	FALSE
249149_at	casein kinase I ; supported by cD	ckl8	AT5G43320	1.16	0.21	1.64	0.1475128	0.3781063	-5.29	FALSE
263584_at	NAM (no apical meristem)-like pr	anac036	AT2G17040	-1.79	-0.84	-1.64	0.1475986	0.3782806	-5.29	FALSE
251226_at	proline-rich protein proline-rich p	PRP3	AT3G62680	1.22	0.28	1.64	0.147614	0.3782806	-5.29	FALSE
264661_at	hypothetical protein Similar to Ni	---	AT1G09950	1.39	0.48	1.64	0.1476855	0.3783802	-5.29	FALSE
250709_at	putative protein similar to unknov	LBD33	AT5G06080	1.20	0.26	1.64	0.147686	0.3783802	-5.29	FALSE
254844_at	hypothetical protein supported by	---	AT4G11790	-1.34	-0.43	-1.64	0.1477313	0.3784112	-5.29	FALSE
253185_at	putative protein bZIP protein - A	---	AT4G35240	-1.25	-0.32	-1.64	0.1477166	0.3784112	-5.29	FALSE
249497_at	putative protein predicted protein	---	AT5G39220	1.24	0.31	1.64	0.1477564	0.378433	-5.29	FALSE
260791_at	lipase-like protein similar to lipas	---	AT1G06250	1.20	0.26	1.63	0.1478329	0.3785863	-5.29	FALSE
258882_at	unknown protein ; supported by	---	AT3G06330	-1.22	-0.29	-1.63	0.1479015	0.3786769	-5.29	FALSE
259579_at	P-glycoprotein, putative similar t	PGP14	AT1G28010	-1.93	-0.95	-1.63	0.1478916	0.3786769	-5.29	FALSE
255017_at	hypothetical protein ;supported b	CNX7	AT4G10100	-1.21	-0.27	-1.63	0.148018	0.3789327	-5.30	FALSE
265770_at	Expressed protein ; supported by	---	AT2G48100	-1.26	-0.33	-1.63	0.1480594	0.3789961	-5.30	FALSE
251950_at	zinc finger - like protein Zat11 zi	---	AT3G53600	2.80	1.48	1.63	0.1481077	0.3790772	-5.30	FALSE
245680_at	hypothetical protein contains sim	---	AT1G56570	-1.20	-0.26	-1.63	0.1481475	0.3791366	-5.30	FALSE
262130_at	hypothetical protein predicted by	---	AT1G02890	1.22	0.29	1.63	0.1481683	0.3791472	-5.30	FALSE
255862_at	hypothetical protein predicted by	---	AT2G30300	1.20	0.27	1.63	0.1482017	0.3791902	-5.30	FALSE
246250_at	cysteine proteinase similar to cys	CP1	AT4G36880	2.62	1.39	1.63	0.1482308	0.3792221	-5.30	FALSE
258901_at	putative protein phosphatase-2C	---	AT3G05640	2.35	1.23	1.63	0.1483087	0.3793066	-5.30	TRUE
252737_at	putative protein KIAA0274 prote	---	AT3G43220	-1.18	-0.24	-1.63	0.148323	0.3793066	-5.30	FALSE
249322_at	protein import receptor TOM20,	TOM20-4	AT5G40930	1.17	0.23	1.63	0.148333	0.3793066	-5.30	FALSE
260110_at	hypothetical protein similar to NB	---	AT1G63350	1.17	0.23	1.63	0.1483019	0.3793066	-5.30	FALSE
267493_at	unknown protein	OFP2	AT2G30400	1.34	0.42	1.63	0.1483636	0.3793066	-5.30	FALSE
253199_at	clathrin assembly protein AP19 h	---	AT4G35410	-1.47	-0.56	-1.63	0.1483499	0.3793066	-5.30	FALSE
251865_at	protein phosphatase 2A regulato	---	AT3G54930	-1.17	-0.23	-1.63	0.1483919	0.3793366	-5.30	FALSE

260381_at	putative kinesin similar to kinesin	---	AT1G73860	1.23	0.30	1.63	0.148413	0.3793479	-5.30	FALSE
245921_at	putative protein predicted protei	---	AT5G28800	1.16	0.22	1.63	0.1484736	0.3794602	-5.30	FALSE
267573_at	putative tropinone reductase	---	AT2G30670	1.16	0.22	1.63	0.1484997	0.3794846	-5.30	FALSE
263061_at	putative AAA-type ATPase	---	AT2G18190	1.23	0.29	1.63	0.1485251	0.3795069	-5.30	FALSE
258615_at	putative aspartyl protease contai	---	AT3G02740	1.26	0.34	1.63	0.1485805	0.379575	-5.30	FALSE
251286_at	putative protein Bcl-2-interacting	---	AT3G61710	-1.18	-0.24	-1.63	0.148585	0.379575	-5.30	FALSE
263607_at	unknown protein predicted by ge	---	AT2G16270	-1.28	-0.36	-1.63	0.1486265	0.3796384	-5.30	FALSE
252180_at	putative protein cyclin-depender	KRP2	AT3G50630	1.33	0.41	1.63	0.1486837	0.3797077	-5.30	FALSE
247988_at	putative protein similar to unknov	---	AT5G56910	-1.33	-0.41	-1.63	0.1487021	0.3797077	-5.30	FALSE
261571_at	hypothetical protein predicted by	---	AT1G01150	1.18	0.24	1.63	0.1487036	0.3797077	-5.30	FALSE
262737_at	hypothetical protein	SRD2	AT1G28560	-1.24	-0.31	-1.63	0.148738	0.3797106	-5.30	FALSE
245204_at	1-AMINOCYCLOPROPANE-1-C	---	AT5G12270	1.32	0.40	1.63	0.1487293	0.3797106	-5.30	FALSE
252094_at	multicatalytic endopeptidase com	PAD1	AT3G51260	-1.32	-0.40	-1.63	0.1487611	0.379727	-5.30	FALSE
245262_at	predicted protein ; supported by (	---	AT4G16563	-1.38	-0.46	-1.63	0.1490125	0.3799861	-5.30	TRUE
256929_at	unknown protein	---	---	1.23	0.30	1.63	0.1489213	0.3799861	-5.30	FALSE
265397_at	hypothetical protein predicted by	---	---	1.18	0.23	1.63	0.1489625	0.3799861	-5.30	FALSE
261816_at	unknown protein	CHX6B	AT1G08135	1.19	0.25	1.63	0.1488811	0.3799861	-5.30	FALSE
266923_at	unknown protein ;supported by f	---	AT2G45980	-1.20	-0.27	-1.63	0.1489397	0.3799861	-5.30	FALSE
258069_at	hypothetical protein predicted by	---	AT3G26010	1.28	0.36	1.63	0.148994	0.3799861	-5.30	FALSE
250258_at	floral homeotic protein AGL15 (s	AGL15	AT5G13790	1.22	0.28	1.63	0.14901	0.3799861	-5.30	FALSE
260487_at	RNA-binding protein, putative si	Y14	AT1G51510	-1.19	-0.25	-1.63	0.1489459	0.3799861	-5.30	FALSE
256548_at	hypothetical protein contains sim	---	AT3G14770	2.66	1.41	1.63	0.1489893	0.3799861	-5.30	FALSE
245026_at	ATPase III subunit	---	---	-1.18	-0.24	-1.63	0.1490935	0.3800024	-5.30	TRUE
246354_at	hypothetical protein	---	AT1G38950	1.22	0.28	1.63	0.1491022	0.3800024	-5.30	FALSE
245126_at	putative MYB family transcription	MYB12	AT2G47460	1.18	0.24	1.63	0.1490507	0.3800024	-5.30	FALSE
248922_at	putative protein contains similarit	WOX8	AT5G45980	1.17	0.23	1.63	0.1490615	0.3800024	-5.30	FALSE
256232_at	unknown protein ; supported by f	FYD	AT3G12570	1.15	0.20	1.63	0.1490788	0.3800024	-5.30	FALSE
265179_at	unknown protein predicted by ge	---	AT1G23650	1.27	0.34	1.63	0.1491243	0.3800162	-5.30	FALSE
250586_at	putative protein similar to unknov	---	AT5G07630	-1.25	-0.32	-1.63	0.1492081	0.3801874	-5.30	FALSE
250119_at	putative protein similar to unknov	---	AT5G16470	-1.18	-0.24	-1.63	0.1494032	0.3802683	-5.30	FALSE
262741_at	hypothetical protein	---	AT1G28760	-1.18	-0.24	-1.63	0.1494066	0.3802683	-5.30	FALSE
255826_at	putative uroporphyrinogen decar	HEME2	AT2G40490	-1.21	-0.28	-1.63	0.1493708	0.3802683	-5.30	FALSE
250208_at	unknown protein ;supported by f	anac084	AT5G14000	1.73	0.79	1.63	0.1493384	0.3802683	-5.30	FALSE
247082_at	putative protein contains similarit	ATGRIP	AT5G66030	-1.22	-0.29	-1.63	0.1492668	0.3802683	-5.30	FALSE
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.41	-0.49	-1.63	0.1492755	0.3802683	-5.30	FALSE

250340_at	putative protein predicted protei	---	AT5G11840	-1.28	-0.36	-1.63	0.1493993	0.3802683	-5.30	FALSE
266515_at	putative tubby protein	AtTLP3	AT2G47900	-1.29	-0.37	-1.63	0.149366	0.3802683	-5.30	FALSE
266809_at	unknown protein ; supported by	---	AT2G29970	1.42	0.50	1.63	0.1493482	0.3802683	-5.30	FALSE
253223_at	L-ascorbate peroxidase ;support	APX3	AT4G35000	-1.18	-0.24	-1.63	0.1493589	0.3802683	-5.30	FALSE
257189_at	hypothetical protein	GIP1	AT3G13222	-1.17	-0.23	-1.63	0.1495003	0.3804644	-5.30	FALSE
252505_at	dehydrogenase -like protein alc	---	AT3G46170	1.22	0.29	1.63	0.1495248	0.3804843	-5.30	FALSE
248810_at	disease resistance protein-like	ADR1-L3	AT5G47280	1.17	0.23	1.63	0.1495769	0.3805319	-5.31	FALSE
249981_at	putative protein predicted protei	---	AT5G18510	1.26	0.33	1.63	0.1495667	0.3805319	-5.31	FALSE
246769_at	hypothetical protein	---	AT5G27440	-1.19	-0.25	-1.63	0.1495953	0.3805325	-5.31	FALSE
246704_at	putative protein	---	AT5G28090	1.20	0.26	1.63	0.1496105	0.3805325	-5.31	FALSE
260388_at	hypothetical protein predicted by	---	AT1G74070	-1.46	-0.54	-1.63	0.1496388	0.380562	-5.31	FALSE
264153_at	disease resistance protein RPS4	ATPP2-A5	AT1G65390	1.54	0.62	1.63	0.1496664	0.3805899	-5.31	FALSE
253385_at	putative protein predicted protei	---	AT4G32930	-1.18	-0.24	-1.63	0.1497242	0.3806945	-5.31	FALSE
267441_at	putative receptor-like protein kina	---	AT2G19210	1.17	0.23	1.62	0.1499308	0.3810422	-5.31	FALSE
255550_at	putative raffinose synthase or se	AtSTS	AT4G01970	1.17	0.23	1.63	0.1498938	0.3810422	-5.31	FALSE
247655_at	zinc finger protein Zat12 ;suppor	RHL41	AT5G59820	2.07	1.05	1.63	0.149907	0.3810422	-5.31	FALSE
253323_at	putative protein protein phospha	---	AT4G33920	1.63	0.70	1.62	0.1499446	0.3810422	-5.31	FALSE
267381_at	unknown protein ; supported by	---	AT2G26190	2.35	1.23	1.62	0.1499363	0.3810422	-5.31	FALSE
266318_at	Mutator-like transposase similar	FRS3	AT2G27110	-1.15	-0.20	-1.62	0.1499755	0.3810783	-5.31	FALSE
261708_at	unknown protein similar to hypot	---	AT1G32740	1.19	0.25	1.62	0.1500236	0.3811157	-5.31	TRUE
251994_at	protein kinase - like protein kina	KIPK	AT3G52890	-1.43	-0.51	-1.62	0.150015	0.3811157	-5.31	FALSE
258735_at	low temperature and salt respons	RCI2A	AT3G05880	1.36	0.44	1.62	0.1500838	0.3812262	-5.31	FALSE
264763_at	hypothetical protein contains sim	---	AT1G61450	1.16	0.22	1.62	0.1501181	0.3812709	-5.31	FALSE
267105_at	hypothetical protein predicted by	---	AT2G14760	1.27	0.34	1.62	0.1502079	0.3814054	-5.31	FALSE
263135_at	flavanone 3-hydroxylase, putativ	---	AT1G78550	-1.26	-0.34	-1.62	0.1502035	0.3814054	-5.31	FALSE
265293_at	hypothetical protein predicted by	---	---	1.21	0.28	1.62	0.1502212	0.3814054	-5.31	FALSE
251544_at	putative protein general stress p	GAUT15	AT3G58790	1.31	0.39	1.62	0.1505581	0.3815365	-5.31	TRUE
264773_at	putative disease resistance resp	---	AT1G22900	1.68	0.75	1.62	0.1504943	0.3815365	-5.31	TRUE
259675_at	unknown protein similar to hypot	---	AT1G77710	-1.19	-0.25	-1.62	0.1502923	0.3815365	-5.31	FALSE
246090_at	putative protein BEM46 bem1/bu	WAV2	AT5G20520	-1.41	-0.50	-1.62	0.1505153	0.3815365	-5.31	TRUE
247154_at	receptor protein kinase-like prote	HSL2	AT5G65710	-1.18	-0.24	-1.62	0.1505568	0.3815365	-5.31	FALSE
247110_at	putative protein contains similarit	---	AT5G65830	-1.29	-0.37	-1.62	0.1504183	0.3815365	-5.31	FALSE
252780_at	alcohol dehydrogenase (ATA1) ;	ATA1	AT3G42960	1.33	0.42	1.62	0.1504066	0.3815365	-5.31	FALSE
246511_at	UDP-glucose dehydrogenase-lik	---	AT5G15490	1.54	0.62	1.62	0.1505883	0.3815365	-5.31	FALSE
260748_at	RING-H2 finger protein RHA3a,	---	AT1G49210	-1.99	-0.99	-1.62	0.1503296	0.3815365	-5.31	FALSE

267594_at	hypothetical protein predicted by	---	AT2G33000	1.19	0.25	1.62	0.1505505	0.3815365	-5.31	FALSE
248760_at	unknown protein ;supported by f	---	AT5G47570	-1.28	-0.36	-1.62	0.150358	0.3815365	-5.31	FALSE
252787_at	putative protein several En/Spm-	---	---	1.15	0.20	1.62	0.1505879	0.3815365	-5.31	FALSE
258753_at	hypothetical protein predicted by	ATEXO70H	AT3G09530	1.15	0.20	1.62	0.1504966	0.3815365	-5.31	FALSE
248813_at	Expressed protein ; supported by	VAM3	AT5G46860	-1.30	-0.38	-1.62	0.1505625	0.3815365	-5.31	FALSE
251408_at	palmitoyl-protein thioesterase pr	---	AT3G60340	-1.26	-0.33	-1.62	0.1504131	0.3815365	-5.31	FALSE
247467_at	putative protein predicted protei	---	AT5G62130	-1.45	-0.54	-1.62	0.1503604	0.3815365	-5.31	FALSE
260779_at	splicing factor, putative similar to	---	AT1G14650	-1.21	-0.27	-1.62	0.1505948	0.3815365	-5.31	FALSE
246713_at	mRNA capping enzyme - like ca	---	AT5G28210	1.25	0.32	1.62	0.1505439	0.3815365	-5.31	FALSE
256476_at	TNP2-like transposon protein sim	---	---	1.18	0.24	1.62	0.1506074	0.3815365	-5.31	FALSE
252952_at	putative protein cylicin II - bovine	---	AT4G38710	1.28	0.35	1.62	0.1503778	0.3815365	-5.31	FALSE
263625_at	F-box protein family, AtFBX9 co	---	AT2G04920	1.18	0.24	1.62	0.150704	0.3817389	-5.31	FALSE
255723_at	hypothetical protein	AFP3	AT3G29575	1.57	0.65	1.62	0.1507384	0.3817836	-5.31	FALSE
262418_at	thioredoxin, putative similar to th	ATHX	AT1G50320	-1.32	-0.40	-1.62	0.1508362	0.381989	-5.31	FALSE
246071_at	ids4-like protein ids-4 protein - H	SPX1	AT5G20150	-1.64	-0.71	-1.62	0.1508697	0.3820313	-5.31	TRUE
258419_at	unknown protein	---	AT3G16670	-2.23	-1.16	-1.62	0.1509192	0.3821142	-5.31	FALSE
257317_at	hypothetical protein	AT2G0774	---	1.23	0.30	1.62	0.1510721	0.3824234	-5.31	FALSE
254588_at	putative protein hypothetical prot	---	AT4G18840	-1.19	-0.25	-1.62	0.1511031	0.3824234	-5.31	FALSE
262440_at	serpin, putative similar to serpin	---	AT1G47710	-1.31	-0.39	-1.62	0.1510946	0.3824234	-5.31	FALSE
258890_at	putative transcription factor simil	NF-YA2	AT3G05690	-1.37	-0.46	-1.62	0.1511084	0.3824234	-5.31	FALSE
264162_at	acyl carrier protein, putative sim	mtACP2	AT1G65290	-1.24	-0.31	-1.62	0.1511412	0.3824641	-5.31	FALSE
258400_at	unknown protein ; supported by	---	AT3G15470	-1.26	-0.34	-1.62	0.1511765	0.3825109	-5.32	FALSE
261806_at	ferrodoxin NADP oxidoreductase	ATRFNR2	AT1G30510	-1.42	-0.51	-1.62	0.1512117	0.3825398	-5.32	FALSE
264993_at	glyoxal oxidase (glx1), putative s	---	AT1G67290	1.38	0.46	1.62	0.1512382	0.3825398	-5.32	FALSE
256022_at	amino acid permease I identical t	AAP1	AT1G58360	1.62	0.70	1.62	0.1512382	0.3825398	-5.32	FALSE
250452_at	putative protein KIAA1038 prote	---	AT5G10630	-1.22	-0.29	-1.62	0.1512611	0.3825553	-5.32	FALSE
249924_at	kinase associated protein phospl	KAPP	AT5G19280	-1.26	-0.33	-1.62	0.151301	0.3825714	-5.32	FALSE
252981_at	putative protein gene T10 protei	---	AT4G38260	1.28	0.35	1.62	0.1512989	0.3825714	-5.32	FALSE
252255_at	pectinesterase - like protein pec	---	AT3G49220	1.55	0.63	1.62	0.151346	0.3825799	-5.32	TRUE
248845_at	disease resistance protein-like	---	AT5G46470	1.26	0.33	1.62	0.1513547	0.3825799	-5.32	FALSE
255414_at	hypothetical protein	---	AT4G03156	-1.16	-0.21	-1.62	0.151323	0.3825799	-5.32	FALSE
258153_at	Expressed protein ; supported by	MOS4	AT3G18165	-1.25	-0.32	-1.62	0.151483	0.3828618	-5.32	FALSE
261521_at	protein kinase, putative similar t	SERK1	AT1G71830	1.58	0.66	1.62	0.1515371	0.3829562	-5.32	FALSE
267108_at	hypothetical protein predicted by	---	AT2G14830	1.17	0.23	1.62	0.1516916	0.383304	-5.32	FALSE
265940_at	putative nucleosome assembly p	NAP1;2	AT2G19480	-1.20	-0.26	-1.62	0.1517196	0.3833282	-5.32	FALSE

261139_at	homeodomain protein, putative s	BEL10	AT1G19700	-1.18	-0.23	-1.62	0.1517348	0.3833282	-5.32	FALSE
245213_at	photosystem II 22kDa protein, p	NPQ4	AT1G44575	-1.61	-0.68	-1.62	0.1517845	0.3834113	-5.32	FALSE
259615_at	dessication-related protein, puta	---	AT1G47980	1.24	0.31	1.62	0.1518053	0.3834215	-5.32	FALSE
247319_at	glutamate-tRNA ligase ; supporte	ERS	AT5G64050	-1.21	-0.27	-1.62	0.1518558	0.3834561	-5.32	FALSE
259975_at	putative cinnamoyl-CoA reductas	---	AT1G76470	1.75	0.81	1.62	0.1518695	0.3834561	-5.32	FALSE
248991_at	putative protein contains similarit	---	AT5G45220	1.32	0.40	1.62	0.1518529	0.3834561	-5.32	FALSE
252446_at	beta-D-glucan exohydrolase - lik	---	AT3G47010	-1.17	-0.23	-1.62	0.1518948	0.3834777	-5.32	FALSE
262304_at	major latex protein (MLP149), pu	MLP43	AT1G70890	2.53	1.34	1.62	0.1519522	0.3835801	-5.32	FALSE
265391_at	Expressed protein ; supported by	GAUT10	AT2G20810	-1.16	-0.22	-1.62	0.1519898	0.3836325	-5.32	FALSE
252978_at	galactosidase like protein ss-1,4	BGAL14	AT4G38590	1.26	0.34	1.62	0.1520231	0.3836743	-5.32	FALSE
263706_s_a	3-methyladenine DNA glycosyla	---	AT1G31180 ///	-1.36	-0.44	-1.61	0.1520872	0.3837085	-5.32	TRUE
248980_at	putative protein similar to unknov	AtPP2-A7	AT5G45090	1.26	0.33	1.61	0.1520745	0.3837085	-5.32	FALSE
267291_at	putative C2H2-type zinc finger pr	---	AT2G23740	1.39	0.47	1.61	0.1520741	0.3837085	-5.32	FALSE
250912_at	histone deacetylase -like protein	HD2C	AT5G03740	-1.44	-0.52	-1.61	0.1521154	0.3837096	-5.32	FALSE
262672_at	RNA pseudouridylate synthase,	---	AT1G76050	-1.20	-0.26	-1.61	0.1521213	0.3837096	-5.32	FALSE
262364_at	disease resistance protein, puta	---	AT1G72860	1.17	0.23	1.61	0.1521719	0.383795	-5.32	FALSE
262711_at	hypothetical protein predicted by	---	AT1G16500	1.32	0.40	1.61	0.1521961	0.3838136	-5.32	FALSE
247637_at	putative protein gcpE protein, Cl	HDS	AT5G60600	-1.28	-0.35	-1.61	0.1522593	0.3839303	-5.32	FALSE
260580_at	unknown protein	---	AT2G47390	1.16	0.22	1.61	0.1523063	0.3840065	-5.32	FALSE
245200_at	F12A21.2 hypothetical protein; s	---	AT1G67850	1.43	0.51	1.61	0.1523967	0.3841919	-5.32	FALSE
248812_at	palmitoyl-protein thioesterase pre	---	AT5G47330	1.99	0.99	1.61	0.1524727	0.3843411	-5.32	TRUE
247362_at	putative protein strong similarity t	ATPAP29	AT5G63140	-1.39	-0.47	-1.61	0.1526048	0.3846316	-5.32	FALSE
266071_at	unknown protein	---	AT2G18670 ///	1.88	0.91	1.61	0.1527601	0.3847254	-5.32	TRUE
248951_at	putative protein similar to unknov	---	AT5G45550	1.25	0.32	1.61	0.1527102	0.3847254	-5.32	FALSE
253200_at	vacuolar H+-transporting ATPase	AVA-P1	AT4G34720	-1.25	-0.32	-1.61	0.1527287	0.3847254	-5.32	FALSE
249930_at	synaptobrevin-like protein	ATVAMP71	AT5G22360	-1.19	-0.25	-1.61	0.152704	0.3847254	-5.32	FALSE
266907_at	Expressed protein ; supported by	ATGA2OX3	---	1.24	0.31	1.61	0.1527032	0.3847254	-5.32	FALSE
265592_at	hypothetical protein predicted by	---	AT2G20110	-1.21	-0.28	-1.61	0.1527514	0.3847254	-5.32	FALSE
250788_at	putative protein similar to unknov	---	AT5G05570	-1.27	-0.34	-1.61	0.15266	0.3847254	-5.32	FALSE
247976_at	unknown protein	---	---	1.24	0.31	1.61	0.1528858	0.3849994	-5.33	FALSE
248058_at	putative protein similar to unknov	---	AT5G55530	-1.21	-0.28	-1.61	0.1529579	0.385011	-5.33	FALSE
254806_at	putative trehalose-6-phosphate p	---	AT4G12430 ///	-1.21	-0.27	-1.61	0.1529542	0.385011	-5.33	FALSE
246689_at	putative protein predicted protein	---	---	-1.15	-0.20	-1.61	0.1529346	0.385011	-5.33	FALSE
256902_s_a	HAPp48,5 protein identical to HA	---	AT3G23910 ///	-1.32	-0.41	-1.61	0.1529389	0.385011	-5.33	FALSE
248411_at	unknown protein	---	AT5G51580	1.17	0.22	1.61	0.1530033	0.3850827	-5.33	FALSE

246404_at	hypothetical protein contains sim	---	AT1G57600	-1.18	-0.23	-1.61	0.1530646	0.3851945	-5.33	FALSE
255792_at	AT-hook DNA-binding protein (A	---	AT2G33620	-1.26	-0.33	-1.61	0.1532294	0.3855667	-5.33	FALSE
256348_at	hypothetical protein predicted by	---	AT1G54880	1.20	0.26	1.61	0.1533502	0.3858283	-5.33	FALSE
251368_at	putative protein hypothetical pro	---	AT3G61380	1.36	0.45	1.61	0.1535603	0.3862714	-5.33	FALSE
261589_at	hypothetical protein predicted by	---	AT1G01690	1.25	0.32	1.61	0.153554	0.3862714	-5.33	FALSE
247428_at	unknown protein	---	AT5G62600	-1.16	-0.22	-1.61	0.1536627	0.3864439	-5.33	FALSE
249339_at	putative protein similar to unknov	---	AT5G41100	1.79	0.84	1.61	0.153659	0.3864439	-5.33	FALSE
245197_at	F12A21.7 hypothetical protein;su	---	AT1G67800	1.19	0.25	1.61	0.1537373	0.3865888	-5.33	FALSE
245928_s_a	vegetative storage protein Vsp1	VSP1	AT5G24770 ///	3.35	1.74	1.61	0.1538012	0.3866694	-5.33	FALSE
264465_at	SKP1/ASK1 (At18), putative sim	ASK18	AT1G10230	-1.16	-0.22	-1.61	0.1538032	0.3866694	-5.33	FALSE
248523_s_a	ubiquitin activating enzyme ;sup	SAE1B	AT5G50580 ///	-1.25	-0.32	-1.61	0.153822	0.3866739	-5.33	FALSE
259921_at	putative protein kinase similar to	---	AT1G72540	2.00	1.00	1.61	0.1538464	0.3866927	-5.33	FALSE
258117_at	hypothetical protein predicted by	---	AT3G14700	1.19	0.25	1.61	0.1539296	0.3868593	-5.33	FALSE
246111_at	putative protein	---	AT5G20170	-1.21	-0.27	-1.61	0.1539867	0.3869261	-5.33	FALSE
259504_at	inorganic pyrophosphatase, puta	AVP1	AT1G15690	-1.25	-0.32	-1.61	0.1539901	0.3869261	-5.33	FALSE
258539_at	putative RNA-binding protein co	---	AT3G06970	1.17	0.23	1.61	0.1540348	0.3869957	-5.33	FALSE
248937_at	putative protein contains similarit	AtRLP55	AT5G45770	1.30	0.38	1.61	0.1540821	0.3870719	-5.33	FALSE
254693_at	bHLH protein - like bHLH protein	---	AT4G17880	-1.76	-0.82	-1.61	0.1541382	0.3871702	-5.33	FALSE
253861_at	putative protein MSP1 protein, S	---	AT4G27680	1.19	0.25	1.60	0.1542736	0.3873869	-5.33	FALSE
252106_at	putative glutamate receptor puta	ATGLR3.6	AT3G51480	1.28	0.35	1.60	0.1542754	0.3873869	-5.33	FALSE
248590_at	receptor protein kinase	---	AT5G49660	-1.19	-0.25	-1.60	0.1542508	0.3873869	-5.33	FALSE
258807_at	transfactor-like similar to transfac	---	AT3G04030	1.36	0.45	1.60	0.1543095	0.3874298	-5.33	FALSE
266308_at	putative cytochrome P450	CYP705A9	AT2G27010	-1.23	-0.30	-1.60	0.1544404	0.3875031	-5.33	FALSE
248088_at	2-oxoglutarate dehydrogenase E	---	AT5G55070	1.30	0.37	1.60	0.154358	0.3875031	-5.33	FALSE
262574_at	unknown protein ESTs gb|R305	---	AT1G15230	-1.37	-0.45	-1.60	0.1544406	0.3875031	-5.33	FALSE
258416_at	hypothetical protein predicted by	---	AT3G17310	-1.21	-0.27	-1.60	0.1544386	0.3875031	-5.33	FALSE
262704_at	hypothetical protein predicted by	ASL9	AT1G16530	1.51	0.60	1.60	0.1544316	0.3875031	-5.33	FALSE
261469_at	unknown protein	AtRLP4	AT1G28340	-1.19	-0.25	-1.60	0.1543997	0.3875031	-5.33	FALSE
254915_s_a	cysteine proteinase contains sim	---	AT4G11310 ///	2.35	1.23	1.60	0.1544935	0.3875931	-5.33	FALSE
262356_at	hypothetical protein predicted by	---	AT1G73000	1.18	0.24	1.60	0.1545378	0.3876595	-5.34	FALSE
258335_at	unknown protein	---	AT3G16020	-1.16	-0.22	-1.60	0.154554	0.3876595	-5.34	FALSE
267027_at	hypothetical protein	---	AT2G38330	-1.28	-0.35	-1.60	0.1546259	0.3877974	-5.34	FALSE
260932_s_a	hypothetical protein contains sim	PGP12	AT1G02520 ///	1.97	0.98	1.60	0.1547907	0.3881679	-5.34	FALSE
247006_at	unknown protein ;supported by f	---	AT5G67490	1.14	0.19	1.60	0.154831	0.3882262	-5.34	FALSE
259174_at	hypothetical protein similar to pu	UNE7	AT3G03690	1.15	0.20	1.60	0.154871	0.3882841	-5.34	FALSE

246236_at	hypothetical protein	---	AT4G36470	1.23	0.30	1.60	0.1550042	0.3883267	-5.34	FALSE
245930_at	transcriptional co-activator-like p	---	AT5G09240	-1.34	-0.42	-1.60	0.1549643	0.3883267	-5.34	FALSE
249252_at	putative protein contains similarit	---	AT5G42010	1.87	0.90	1.60	0.1549997	0.3883267	-5.34	FALSE
263063_s_a	putative peroxidase	---	AT2G18140 ///	1.33	0.42	1.60	0.1550201	0.3883267	-5.34	FALSE
261264_at	hypothetical protein predicted by	---	AT1G26710	1.24	0.31	1.60	0.1550712	0.3883267	-5.34	FALSE
255991_at	unknown protein	---	AT1G29820	-1.36	-0.45	-1.60	0.1550753	0.3883267	-5.34	FALSE
249012_at	flavonoid 3,5-hydroxylase-like; c	CYP706A3	AT5G44620	1.20	0.26	1.60	0.1549665	0.3883267	-5.34	FALSE
255975_at	hypothetical protein	---	---	1.24	0.31	1.60	0.1550189	0.3883267	-5.34	FALSE
260173_at	NAM-like protein similar to NAM	VND7	AT1G71930	-1.22	-0.29	-1.60	0.1550671	0.3883267	-5.34	FALSE
260251_at	putative heat shock protein simila	---	AT1G74250	1.30	0.38	1.60	0.1550651	0.3883267	-5.34	FALSE
257862_s_a	unknown protein similar to N-terr	---	AT3G17720 ///	1.16	0.21	1.60	0.1549849	0.3883267	-5.34	FALSE
252044_at	outer envelope membrane prote	OEP7	AT3G52420	-1.17	-0.22	-1.60	0.155156	0.3883582	-5.34	FALSE
262730_at	putative transport protein may be	ATOCT3	AT1G16390	1.22	0.29	1.60	0.1551311	0.3883582	-5.34	FALSE
259704_at	putative 3'-5' exoribonuclease sir	---	AT1G77680	1.25	0.32	1.60	0.1551466	0.3883582	-5.34	FALSE
266435_s_a	hypothetical protein predicted by	---	AT2G07130 ///	-1.19	-0.26	-1.60	0.1551168	0.3883582	-5.34	FALSE
254382_at	hypothetical protein	---	AT4G21890	1.30	0.38	1.60	0.1551929	0.3883653	-5.34	FALSE
261249_at	hypothetical protein predicted by	---	AT1G05880	1.20	0.27	1.60	0.1551894	0.3883653	-5.34	FALSE
247057_at	SCARECROW gene regulator	---	AT5G66770	-1.63	-0.71	-1.60	0.1552329	0.3884229	-5.34	FALSE
250356_at	clathrin binding protein - like Af1	---	AT5G11710	1.15	0.20	1.60	0.1553451	0.3885633	-5.34	FALSE
253843_at	putative protein MLL protein, Ga	SDG16	AT4G27910	1.16	0.22	1.60	0.1553473	0.3885633	-5.34	FALSE
253275_at	Expressed protein ; supported by	---	AT4G34215	-1.22	-0.29	-1.60	0.1553455	0.3885633	-5.34	FALSE
252455_at	putative protein various predicte	---	AT3G47140	1.16	0.21	1.60	0.1553572	0.3885633	-5.34	FALSE
253862_at	NOZZLE/SPOROCYTELESS ; s	SPL	AT4G27330	1.27	0.34	1.60	0.1553958	0.3885747	-5.34	FALSE
246625_at	hypothetical protein predicted by	---	AT1G48880	1.20	0.26	1.60	0.1553863	0.3885747	-5.34	FALSE
257381_at	unknown protein	---	AT2G37950	-1.40	-0.48	-1.60	0.1554933	0.3886586	-5.34	FALSE
262880_at	hypothetical protein contains sim	---	AT1G64880	-1.58	-0.66	-1.60	0.1555146	0.3886586	-5.34	FALSE
255475_at	contains a short region of similar	---	AT4G02480	1.24	0.32	1.60	0.1554958	0.3886586	-5.34	FALSE
247412_at	unknown protein	---	AT5G63010	-1.22	-0.28	-1.60	0.1555138	0.3886586	-5.34	FALSE
256111_at	unknown protein	---	AT1G16820	-1.24	-0.31	-1.60	0.1554912	0.3886586	-5.34	FALSE
264325_at	putative phosphoribosylanthranila	---	AT1G04150	1.26	0.33	1.60	0.1555604	0.3886906	-5.34	FALSE
251464_at	farnesyltransferase subunit A (F	FTA	AT3G59380	-1.24	-0.31	-1.60	0.1555614	0.3886906	-5.34	FALSE
259236_at	unknown protein ; supported by	---	AT3G11530	-1.18	-0.24	-1.60	0.1555881	0.3887146	-5.34	FALSE
258477_at	hypothetical protein predicted by	NBS1	AT3G02680	-1.17	-0.22	-1.60	0.1556209	0.3887541	-5.34	FALSE
252146_at	putative protein steroid sulfotran	---	AT3G51210	1.15	0.21	1.60	0.1556953	0.3888973	-5.34	FALSE
248737_at	unknown protein	---	AT5G48120	-1.30	-0.38	-1.60	0.1557172	0.3889094	-5.34	FALSE

245359_at	carnitine racemase like protein ;s	IBR10	AT4G14430	1.40	0.48	1.60	0.1557971	0.3889811	-5.34	FALSE
264891_at	putative pectinesterase similar t	---	AT1G23200	1.34	0.42	1.60	0.1557842	0.3889811	-5.34	FALSE
266741_s_a	putative disease resistance prote	---	AT2G03030 /	1.16	0.22	1.60	0.1557874	0.3889811	-5.34	FALSE
262425_at	hypothetical protein predicted by	---	AT1G47660	1.18	0.24	1.60	0.1558416	0.3890496	-5.34	FALSE
250577_at	putative protein densin-180, Rat	---	AT5G07910	1.17	0.23	1.60	0.1559013	0.3891561	-5.34	FALSE
245112_at	glycerol-3-phosphate dehydroge	GPDHC1	AT2G41540	1.69	0.75	1.60	0.1559325	0.3891915	-5.34	FALSE
264255_at	putative SF2/ASF splicing modu	---	AT1G09140	1.28	0.36	1.60	0.1559755	0.3892134	-5.34	FALSE
AFFX-PheX	B. subtilis /GEN=pheA /DB_XRE	---	---	-1.41	-0.50	-1.60	0.1559656	0.3892134	-5.34	FALSE
250420_at	HY5(bZIP transcription factor fan	HY5	AT5G11260	1.24	0.31	1.60	0.1560065	0.3892188	-5.34	FALSE
249183_at	E2, ubiquitin-conjugating enzym	UBC18	AT5G42990	-1.17	-0.23	-1.60	0.1560117	0.3892188	-5.34	FALSE
245967_at	proline-rich protein extensins	---	AT5G19800	1.18	0.24	1.60	0.1560561	0.3892482	-5.34	FALSE
245885_at	putative protein phi-1 - Nicotiana	EXL4	AT5G09440	1.40	0.49	1.60	0.1560576	0.3892482	-5.34	FALSE
267500_s_a	putative cytochrome P450	CYP704A1	AT2G44890 /	-1.34	-0.43	-1.60	0.1561612	0.3894639	-5.34	FALSE
256773_at	hypothetical protein predicted by	---	AT3G13630	1.21	0.28	1.60	0.1562246	0.3894942	-5.34	FALSE
265075_at	hypothetical protein similar to em	---	AT1G55450	1.95	0.96	1.60	0.1562204	0.3894942	-5.34	FALSE
259961_at	auxin-induced protein kinase, pu	WAG1	AT1G53700	1.22	0.28	1.60	0.1562158	0.3894942	-5.34	FALSE
251690_at	putative protein TATA-binding pr	---	AT3G56510	-1.20	-0.26	-1.60	0.1562734	0.3895735	-5.35	FALSE
264221_s_a	unknown protein contains similar	emb1220	AT1G60170 /	-1.21	-0.27	-1.59	0.156473	0.3900282	-5.35	FALSE
253829_at	Medicago nodulin N21-like prote	---	AT4G28040	1.85	0.89	1.59	0.1565412	0.3901556	-5.35	TRUE
247009_at	unknown protein ;supported by f	---	AT5G67600	1.44	0.53	1.59	0.1567121	0.3904691	-5.35	FALSE
255669_at	predicted protein	MBD3	AT4G00416	1.15	0.20	1.59	0.1566895	0.3904691	-5.35	FALSE
254496_at	hyuC-like protein 5-substituted h	ATAAH	AT4G20070	-1.62	-0.69	-1.59	0.1567183	0.3904691	-5.35	FALSE
264410_s_a	hypothetical protein predicted by	---	---	-1.16	-0.21	-1.59	0.1567863	0.3905531	-5.35	FALSE
247681_at	serine/threonine-specific protein	---	---	1.27	0.34	1.59	0.1567797	0.3905531	-5.35	FALSE
246732_at	putative protein hypothetical pro	---	AT5G27650	-1.25	-0.32	-1.59	0.1568228	0.3906014	-5.35	FALSE
255194_at	score=37.6, E=2.9e-07, N=3	---	AT4G07410	-1.31	-0.39	-1.59	0.1568511	0.3906293	-5.35	FALSE
248931_at	peptide transporter	---	AT5G46040	1.15	0.21	1.59	0.1569323	0.3906617	-5.35	FALSE
262838_at	major latex protein, putative sim	---	AT1G14960	1.21	0.28	1.59	0.156929	0.3906617	-5.35	FALSE
263247_at	unknown protein	---	AT2G31440	-1.16	-0.22	-1.59	0.156926	0.3906617	-5.35	FALSE
259267_at	unknown protein ;supported by f	---	AT3G01130	-1.18	-0.24	-1.59	0.1569326	0.3906617	-5.35	FALSE
258621_at	zinc finger protein 1 (zfn1) identi	ZFN1	AT3G02830	1.18	0.24	1.59	0.1570541	0.3908788	-5.35	FALSE
256807_at	unknown protein contains Pfam p	NFU4	AT3G20970	-1.20	-0.26	-1.59	0.1570402	0.3908788	-5.35	FALSE
258379_at	putative decarboxilase similar to	---	AT3G16700	1.30	0.38	1.59	0.1570775	0.3908945	-5.35	FALSE
266862_at	putative MYB family transcription	AtMYB104	AT2G26950	1.16	0.21	1.59	0.1571519	0.3909199	-5.35	FALSE
265579_at	hypothetical protein predicted by	---	AT2G20070	1.19	0.25	1.59	0.1571563	0.3909199	-5.35	FALSE

248183_at	CHP-rich zinc finger protein-like	---	AT5G54040	1.16	0.21	1.59	0.1571343	0.3909199	-5.35	FALSE
252591_at	putative protein senescence-ass	TET3	AT3G45600	-1.38	-0.46	-1.59	0.1571383	0.3909199	-5.35	FALSE
255962_at	glycine-rich RNA-binding protein	---	AT1G22330	1.92	0.94	1.59	0.1571981	0.3909712	-5.35	TRUE
256572_at	40S RIBOSOMAL PROTEIN S2	---	AT3G30740	-1.18	-0.24	-1.59	0.1572112	0.3909712	-5.35	FALSE
249161_at	20S proteasome subunit PAF1 (g	PAF1	AT5G42790	-1.15	-0.20	-1.59	0.1573239	0.3910382	-5.35	FALSE
267166_at	unknown protein	---	AT2G37720	1.14	0.19	1.59	0.1572646	0.3910382	-5.35	FALSE
249732_at	6-phosphogluconolactonase-like	---	AT5G24420	3.92	1.97	1.59	0.1572913	0.3910382	-5.35	FALSE
253965_at	hypothetical protein	---	AT4G26490	-1.26	-0.34	-1.59	0.1573166	0.3910382	-5.35	FALSE
259999_at	hypothetical protein predicted by	---	AT1G68080	-1.30	-0.38	-1.59	0.1572965	0.3910382	-5.35	FALSE
259453_at	gibberelin 20-oxidase, putative,	ATGA20OX	AT1G44090	1.28	0.36	1.59	0.1573609	0.3910877	-5.35	FALSE
257893_at	E2, ubiquitin-conjugating enzym	UBC32	AT3G17000	1.35	0.43	1.59	0.1574122	0.3911724	-5.35	FALSE
256579_at	hypothetical protein	---	AT3G28720	-1.17	-0.23	-1.59	0.1574475	0.3912177	-5.35	FALSE
245508_at	hypothetical protein	---	AT4G15720	-1.15	-0.21	-1.59	0.1575295	0.3913489	-5.35	FALSE
258885_at	putative uridylate kinase similar	---	AT3G10030	-1.17	-0.23	-1.59	0.1575347	0.3913489	-5.35	FALSE
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.57	-0.65	-1.59	0.1576734	0.3916508	-5.35	FALSE
245557_at	phosphatase like protein	PUX5	AT4G15410	1.15	0.20	1.59	0.1577183	0.3916575	-5.35	FALSE
266519_at	unknown protein ; supported by	---	AT2G35155	-1.22	-0.29	-1.59	0.1577233	0.3916575	-5.35	FALSE
254256_at	serine/threonine kinase -like pro	CRK10	AT4G23180	1.34	0.42	1.59	0.1577276	0.3916575	-5.35	FALSE
264481_at	transcription factor TINY, putativ	---	AT1G77200	1.23	0.29	1.59	0.1577786	0.3917416	-5.35	FALSE
262726_at	hypothetical protein similar to put	AtTLP5	AT1G43640	1.24	0.31	1.59	0.1578481	0.3918462	-5.35	FALSE
264061_at	putative cyclin-dependent kinase	CKS2	AT2G27970	-1.47	-0.56	-1.59	0.1578551	0.3918462	-5.35	FALSE
251402_at	SRG1 - like protein SRG1 protei	---	AT3G60290	-1.56	-0.64	-1.59	0.1578911	0.3918929	-5.35	TRUE
251520_at	protein kinase like GCN2 - Sacc	---	AT3G59410	-1.17	-0.23	-1.59	0.1579429	0.3919789	-5.35	FALSE
244949_at	hypothetical protein	---	---	-1.21	-0.28	-1.59	0.1580245	0.3921388	-5.36	FALSE
264175_at	unknown protein Similar to rice c	---	AT1G02050	-1.25	-0.32	-1.59	0.1580526	0.3921657	-5.36	FALSE
253205_at	putative cyclase associated prot	ATCAP1	AT4G34490	1.39	0.47	1.59	0.1581275	0.3923089	-5.36	FALSE
263803_at	hypothetical protein predicted by	---	AT2G40440	1.18	0.23	1.59	0.1581541	0.3923321	-5.36	FALSE
247229_at	putative protein contains similarit	---	AT5G65160	1.31	0.39	1.59	0.1581769	0.3923462	-5.36	FALSE
261770_at	prolyl endopeptidase, putative si	---	AT1G76140	1.16	0.21	1.59	0.158272	0.3925394	-5.36	FALSE
266077_at	putative non-LTR retroelement re	---	---	1.21	0.28	1.59	0.158397	0.3927658	-5.36	FALSE
246158_at	Expressed protein ; supported by	---	AT5G19855	1.33	0.41	1.59	0.1583977	0.3927658	-5.36	FALSE
262682_at	anter-specific proline-rich -like pr	---	AT1G75900	1.81	0.86	1.59	0.158417	0.3927708	-5.36	TRUE
253258_at	putative protein NF-180, Petrom	---	AT4G34400	1.23	0.30	1.59	0.158448	0.392805	-5.36	FALSE
248151_at	Lhcb3 chlorophyll a/b binding pro	LHCB3	AT5G54270	-1.40	-0.49	-1.59	0.158496	0.3928812	-5.36	FALSE
261554_at	PPR-repeat protein contains mul	---	AT1G63400	-1.15	-0.20	-1.59	0.1585132	0.3928812	-5.36	FALSE

259436_at	hypothetical protein predicted by	---	AT1G01500	-1.19	-0.25	-1.59	0.1585829	0.3929434	-5.36	FALSE
264011_at	unknown protein	---	AT2G21090	-1.21	-0.28	-1.59	0.1586072	0.3929434	-5.36	FALSE
264981_at	valyl- tRNA synthetase, putative	---	AT1G27160	1.22	0.28	1.59	0.1585603	0.3929434	-5.36	FALSE
261897_at	hypothetical protein predicted by	---	AT1G80950	1.21	0.28	1.59	0.1585916	0.3929434	-5.36	FALSE
246935_at	leucine-rich repeats containing p	EBF2	AT5G25350	-1.36	-0.44	-1.59	0.1586259	0.3929471	-5.36	FALSE
262658_at	ribonuclease contains similarity t	---	AT1G14220	1.16	0.22	1.58	0.1588705	0.3935002	-5.36	FALSE
252197_at	receptor protein kinase -like prot	---	AT3G50230	1.16	0.21	1.58	0.1588837	0.3935002	-5.36	FALSE
261998_at	putative gag-pol polyprotein sim	---	---	1.20	0.26	1.58	0.1589374	0.3935906	-5.36	FALSE
247427_at	putative protein similar to unknov	---	AT5G62580	1.38	0.47	1.58	0.1590446	0.3937529	-5.36	TRUE
257376_at	hypothetical protein predicted by	---	AT2G32350	1.20	0.27	1.58	0.1591005	0.3937529	-5.36	FALSE
249372_at	glucose-6-phosphate dehydroge	G6PD6	AT5G40760	1.41	0.50	1.58	0.1591066	0.3937529	-5.36	FALSE
246091_at	putative protein various predicte	---	AT5G20590	-1.24	-0.31	-1.58	0.1590709	0.3937529	-5.36	FALSE
251501_at	putative protein several hypothet	---	AT3G59120	1.19	0.25	1.58	0.1590341	0.3937529	-5.36	FALSE
247171_at	unknown protein	---	AT5G65540	-1.17	-0.23	-1.58	0.1590887	0.3937529	-5.36	FALSE
251705_at	DNA-binding protein-like DNA-b	WRKY70	AT3G56400	3.62	1.86	1.58	0.1591316	0.3937721	-5.36	FALSE
247014_at	RuvB DNA helicase-like protein	---	AT5G67630	-1.44	-0.53	-1.58	0.159172	0.3937834	-5.36	FALSE
264557_at	putative pectinacetylesterase pr	---	AT1G09550	1.29	0.37	1.58	0.1591621	0.3937834	-5.36	FALSE
248272_at	Expressed protein ; supported by	---	AT5G53480	-1.27	-0.34	-1.58	0.1591879	0.3937834	-5.36	FALSE
249142_at	putative protein similar to unknov	---	AT5G43230	1.22	0.29	1.58	0.1592757	0.3938735	-5.36	FALSE
260586_at	unknown protein predicted by ge	---	AT2G43630	-1.21	-0.28	-1.58	0.1592934	0.3938735	-5.36	FALSE
246006_at	putative protein DIM1 protein, H	YLS8	AT5G08290	-1.18	-0.24	-1.58	0.1592607	0.3938735	-5.36	FALSE
257738_at	40S ribosomal subunit protein S	---	AT3G27450	-1.16	-0.21	-1.58	0.1592812	0.3938735	-5.36	FALSE
257174_at	uracil phosphoribosyltransferase	---	AT3G27190	-1.26	-0.34	-1.58	0.159331	0.3939236	-5.36	FALSE
255756_at	endo-beta-1,4-D-glucanase, put	AtGH9B5	AT1G19940	1.21	0.27	1.58	0.159385	0.3940144	-5.36	FALSE
247626_at	receptor like protein kinase rece	---	AT5G60300 /	1.73	0.79	1.58	0.1594088	0.3940307	-5.36	FALSE
255578_at	predicted protein of unknown fur	---	AT4G01450	-1.49	-0.57	-1.58	0.15947	0.3940964	-5.36	FALSE
256294_at	unknown protein	---	AT1G69450	1.23	0.30	1.58	0.1594625	0.3940964	-5.36	FALSE
250248_at	transporter-like protein	ZIF1	AT5G13740	1.48	0.57	1.58	0.159539	0.3941817	-5.36	TRUE
247148_at	auxin-induced protein IAA9 (pir ||	IAA9	AT5G65670	-1.32	-0.40	-1.58	0.1595319	0.3941817	-5.36	FALSE
249130_at	putative protein contains similarit	---	AT5G43100	-1.17	-0.22	-1.58	0.1595933	0.394273	-5.36	FALSE
253489_at	monogalactosyldiacylglycerol sy	MGD1	AT4G31780	1.30	0.38	1.58	0.1596803	0.3944452	-5.36	TRUE
259371_at	unknown protein ;supported by fu	---	AT1G69080	1.73	0.79	1.58	0.1597099	0.3944757	-5.36	FALSE
245308_at	putative protein ; supported by cI	---	AT4G17486	1.17	0.22	1.58	0.1597618	0.3945612	-5.37	FALSE
256125_at	pathogenesis-related group 5 pr	ATLP-1	AT1G18250	1.29	0.37	1.58	0.1598293	0.394685	-5.37	FALSE
261248_at	calreticulin, putative similar to G	---	AT1G20030	-1.59	-0.67	-1.58	0.1599225	0.3947926	-5.37	TRUE

258331_at	putative coatomer complex subu	---	AT3G15980	-1.23	-0.30	-1.58	0.1598945	0.3947926	-5.37	FALSE
249259_at	putative protein similar to unknov	---	AT5G41660	1.94	0.96	1.58	0.1599421	0.3947926	-5.37	FALSE
261489_at	hypothetical protein contains sim	---	AT1G14450	-1.15	-0.20	-1.58	0.1599378	0.3947926	-5.37	FALSE
249704_at	Myb-related transcription factor L	TT2	AT5G35550	1.26	0.34	1.58	0.1599698	0.3948184	-5.37	FALSE
251393_at	putative protein symbiosis-relate	ATG8G	AT3G60640	-1.30	-0.38	-1.58	0.1600372	0.3949195	-5.37	FALSE
266711_at	unknown protein	---	AT2G46740	1.18	0.23	1.58	0.1600454	0.3949195	-5.37	FALSE
252657_at	hypothetical protein	---	AT3G44780	1.15	0.21	1.58	0.1601929	0.3952407	-5.37	FALSE
254630_at	glycolate oxidase - like protein (S	---	AT4G18360	2.12	1.08	1.58	0.1602293	0.3952459	-5.37	TRUE
260848_at	pectinesterase, putative similar t	sks8	AT1G21850	1.27	0.35	1.58	0.1602297	0.3952459	-5.37	FALSE
266148_x_a	En/Spm-like transposon protein r	---	---	1.23	0.29	1.58	0.1602801	0.3952849	-5.37	FALSE
253192_at	putative protein nuclear phospho	---	AT4G35370	1.17	0.23	1.58	0.1602735	0.3952849	-5.37	FALSE
248925_at	GDSL-motif lipase/hydrolase-like	---	AT5G45910	1.25	0.32	1.58	0.1604043	0.3955483	-5.37	FALSE
255155_at	hypothetical protein	---	AT4G08230	1.23	0.30	1.58	0.1604253	0.3955573	-5.37	FALSE
257507_at	zinc finger protein, putative simil	---	AT1G29600	-1.15	-0.20	-1.58	0.1604434	0.3955592	-5.37	FALSE
264443_at	Expressed protein ; supported by	---	AT1G27385	-1.28	-0.35	-1.58	0.1604802	0.3956071	-5.37	FALSE
252030_at	hypothetical protein predicted pr	---	AT3G52690	1.16	0.21	1.58	0.1605309	0.3956467	-5.37	FALSE
248468_at	UDP-glucose:protein transglucos	RGP4	AT5G50750	1.23	0.30	1.58	0.1605254	0.3956467	-5.37	FALSE
256704_at	deacetylvindoline 4-O-acetyltran	---	AT3G30280	1.18	0.23	1.58	0.1605887	0.3956848	-5.37	FALSE
263490_at	F-box protein ORE9, AtFBL7 ide	MAX2	AT2G42620	-1.41	-0.50	-1.58	0.1605984	0.3956848	-5.37	FALSE
256299_at	expansin (At-EXP1) identical to e	ATEXPA1	AT1G69530	2.18	1.12	1.58	0.160576	0.3956848	-5.37	FALSE
262114_at	unknown protein contains similar	NLA	AT1G02860	1.38	0.47	1.58	0.1606161	0.3956857	-5.37	FALSE
246960_at	unknown protein	---	AT5G24710	1.18	0.24	1.58	0.1606442	0.3957002	-5.37	FALSE
265864_at	putative myosin heavy chain-like	ATMAP70-3	AT2G01750	-1.28	-0.36	-1.58	0.1606567	0.3957002	-5.37	FALSE
259343_s_a	putative methionine synthase sim	ATMS2	AT3G03780 ///	-1.32	-0.40	-1.58	0.1606813	0.3957181	-5.37	FALSE
263598_at	putative xyloglucan-specific gluca	EXGT-A3	AT2G01850	-1.21	-0.28	-1.58	0.1607094	0.3957446	-5.37	FALSE
261484_at	E2, ubiquitin-conjugating enzym	UBC1	AT1G14400	-1.18	-0.24	-1.58	0.1608311	0.3960015	-5.37	FALSE
256020_at	glutamyl-tRNA reductase, putati	HEMA1	AT1G58290	-1.31	-0.39	-1.58	0.1608699	0.3960541	-5.37	FALSE
245607_at	kinesin like protein	---	AT4G14330	1.20	0.26	1.58	0.1609166	0.3960837	-5.37	FALSE
255247_at	hypothetical protein	---	---	-1.15	-0.20	-1.58	0.1609111	0.3960837	-5.37	FALSE
261330_at	transcription factor, putative sim	MCM2	AT1G44900	-1.89	-0.92	-1.58	0.1609674	0.3961458	-5.37	FALSE
251907_at	putative protein 85p protein - Me	---	AT3G53760	-1.37	-0.46	-1.57	0.1609766	0.3961458	-5.37	FALSE
266652_at	unknown protein	---	AT2G25760	-1.17	-0.23	-1.57	0.161086	0.3963724	-5.37	FALSE
247265_at	putative protein strong similarity t	CPuORF22	AT5G64550 ///	-1.49	-0.57	-1.57	0.1611209	0.3964156	-5.37	FALSE
257788_at	unknown protein	TCP20	AT3G27010	1.26	0.33	1.57	0.1611844	0.396529	-5.37	FALSE
253320_at	putative protein ThiJ protein, Es	---	AT4G34020	-1.19	-0.25	-1.57	0.1612949	0.396758	-5.37	FALSE

247048_at	photoreceptor-interacting protein	---	AT5G66560	1.46	0.55	1.57	0.1613363	0.396817	-5.37	TRUE
247437_at	AtHVA22b-like protein ; supporte	HVA22B	AT5G62490	1.24	0.31	1.57	0.1613628	0.3968261	-5.37	FALSE
267296_at	hypothetical protein predicted by	LBD10	AT2G23660	1.19	0.25	1.57	0.1613748	0.3968261	-5.37	FALSE
267132_at	unknown protein	NAPRT2	AT2G23420	-1.39	-0.48	-1.57	0.1614756	0.3970312	-5.37	FALSE
255286_at	see T14P8.10 (GB:AF069298)	---	AT4G04650	1.29	0.37	1.57	0.1615101	0.3970732	-5.38	FALSE
266486_at	hypothetical protein predicted by	---	AT2G47950	2.34	1.23	1.57	0.1615807	0.397204	-5.38	FALSE
259256_at	putative coated vesicle membran	---	AT3G07680	-1.19	-0.25	-1.57	0.1616544	0.3973203	-5.38	FALSE
245631_at	tRNA-glutamine synthetase, put	OVA9	AT1G25350	-1.18	-0.23	-1.57	0.1616629	0.3973203	-5.38	FALSE
263415_at	hypothetical protein similar to GE	EMB2762	AT2G17250	-1.28	-0.36	-1.57	0.1618541	0.3977474	-5.38	FALSE
256842_at	hypothetical protein predicted by	---	---	1.18	0.24	1.57	0.1619103	0.3978204	-5.38	FALSE
258435_at	unknown protein ;supported by f	---	AT3G16740	-1.21	-0.28	-1.57	0.1619186	0.3978204	-5.38	FALSE
258201_at	hypothetical protein predicted by	---	AT3G13910	1.41	0.50	1.57	0.1619766	0.3979199	-5.38	FALSE
261787_at	hypothetical protein predicted by	---	AT1G16020	-1.20	-0.26	-1.57	0.1620055	0.397948	-5.38	FALSE
253628_at	xyloglucan endo-1,4-beta-D-gluc	XTH18	AT4G30280	3.53	1.82	1.57	0.162063	0.3979532	-5.38	FALSE
250480_at	protein serine/threonine kinase-l	---	AT5G10290	-1.59	-0.67	-1.57	0.1620545	0.3979532	-5.38	FALSE
255927_at	transcriptional activator CBF1, p	---	AT1G12630	1.37	0.45	1.57	0.162031	0.3979532	-5.38	FALSE
247589_at	REVOLUTA or interfascicular fibe	REV	AT5G60690	-1.22	-0.28	-1.57	0.1620774	0.3979532	-5.38	FALSE
257818_at	hypothetical protein predicted by	---	AT3G25120	-1.22	-0.29	-1.57	0.1621356	0.3980534	-5.38	FALSE
249118_at	putative protein similar to unknov	---	AT5G43870	-1.25	-0.32	-1.57	0.1621753	0.3981078	-5.38	TRUE
260667_at	very-long-chain fatty acid conde	KCS4	AT1G19440	1.18	0.23	1.57	0.1622225	0.3981656	-5.38	TRUE
251399_at	putative protein	---	AT3G60590	-1.23	-0.30	-1.57	0.1622337	0.3981656	-5.38	FALSE
250036_at	putative protein predicted protei	---	AT5G18340	-1.27	-0.34	-1.57	0.1623866	0.398498	-5.38	FALSE
262224_at	hypothetical protein contains Pfa	OTP43	AT1G74900	-1.16	-0.22	-1.57	0.1624424	0.3985492	-5.38	FALSE
261258_at	unknown protein	---	AT1G26640	-1.25	-0.32	-1.57	0.1624258	0.3985492	-5.38	FALSE
258591_at	hypothetical protein ; supported	---	AT3G04360	1.18	0.24	1.57	0.1624851	0.3986111	-5.38	FALSE
252314_at	hypothetical protein	---	AT3G49400	-1.21	-0.27	-1.57	0.1625665	0.3987606	-5.38	FALSE
250965_at	putative protein various predicte	---	AT5G03020	1.17	0.22	1.57	0.162581	0.3987606	-5.38	FALSE
263004_at	hypothetical protein contains sim	ATNEK1	AT1G54510	-1.22	-0.28	-1.57	0.1626274	0.3987662	-5.38	FALSE
254961_at	putative acyl-CoA synthetase ac	---	AT4G11030	1.20	0.26	1.57	0.1626358	0.3987662	-5.38	FALSE
251457_s_a	multi resistance protein homolog	ATMRP9	AT3G60160 //	1.19	0.25	1.57	0.1626229	0.3987662	-5.38	FALSE
262245_at	unknown protein	NPSN12	AT1G48240	-1.26	-0.33	-1.57	0.162674	0.3988098	-5.38	FALSE
256290_at	serine carboxypeptidase, putativ	scpl17	AT3G12203	-1.18	-0.23	-1.57	0.1626885	0.3988098	-5.38	FALSE
255244_at	putative protein various hypothet	---	AT4G05620	1.19	0.25	1.57	0.1627307	0.3988703	-5.38	FALSE
250836_at	putative protein various predicte	DME	AT5G04560	1.16	0.21	1.57	0.1627719	0.3989283	-5.38	FALSE
249334_at	putative protein strong similarity t	YSL4	AT5G41000	-1.30	-0.38	-1.57	0.1628658	0.3991156	-5.38	FALSE

251990_at	putative protein MICRONUCLEA	---	AT3G53320	-1.30	-0.38	-1.57	0.1629045	0.3991677	-5.38	FALSE
259108_at	putative translationally controlled	---	AT3G05540	1.17	0.23	1.57	0.1629397	0.399211	-5.38	FALSE
261981_at	unknown protein	---	AT1G33811	-1.77	-0.82	-1.57	0.1629675	0.3992362	-5.38	FALSE
249570_at	hypothetical protein	---	AT5G38080	1.23	0.30	1.57	0.1630706	0.3994029	-5.38	FALSE
245910_at	putative protein ER66 - Lycoper	EICBP.B	AT5G09410	-1.19	-0.25	-1.57	0.1630633	0.3994029	-5.38	FALSE
262530_at	putative receptor protein kinase A	AtRLP2	AT1G17240	-1.23	-0.30	-1.57	0.1631004	0.399433	-5.38	FALSE
260351_at	hypothetical protein predicated b	---	AT1G69380	-1.45	-0.54	-1.57	0.163144	0.399497	-5.38	FALSE
260156_at	NAM-like protein similar to NAM	NAM	AT1G52880	-1.36	-0.44	-1.57	0.1631766	0.3995028	-5.38	FALSE
256012_at	unknown protein similar to dimet	FMO1	AT1G19250	4.26	2.09	1.57	0.1631989	0.3995028	-5.38	FALSE
245035_at	unknown protein similar to GP|22	ATARD3	AT2G26400	1.53	0.62	1.57	0.1631985	0.3995028	-5.38	FALSE
253964_at	putative protein qkI-7, Mus musc	---	AT4G26480	1.19	0.25	1.56	0.1633703	0.3997399	-5.39	FALSE
266960_at	putative retroelement pol polypro	---	---	1.22	0.29	1.56	0.1633834	0.3997399	-5.39	FALSE
264642_at	putative CCAAT-binding transcri	NF-YB4	AT1G09030	1.19	0.25	1.56	0.1633531	0.3997399	-5.39	FALSE
266314_at	Argonaute (AGO1)-like protein ;	AGO4	AT2G27040	-1.27	-0.35	-1.56	0.163365	0.3997399	-5.39	FALSE
257006_at	hypothetical protein predicted by	---	AT3G14075	1.18	0.24	1.56	0.1633708	0.3997399	-5.39	FALSE
264071_at	putative carboxypeptidase ; supp	SCPL51	AT2G27920	-1.37	-0.46	-1.56	0.1634341	0.3998199	-5.39	FALSE
254847_at	putative phospholipase D-gamm	PLDGAMM	AT4G11850	1.56	0.64	1.56	0.1634512	0.3998199	-5.39	FALSE
250336_at	alpha-glucosidase 1 ; supported	---	AT5G11720	-1.24	-0.31	-1.56	0.1635381	0.3999468	-5.39	FALSE
262410_at	MAGE protein, putative identical	---	AT1G34770	-1.34	-0.42	-1.56	0.1635256	0.3999468	-5.39	FALSE
260666_at	unknown protein ;supported by fu	PARVUS	AT1G19300	1.56	0.64	1.56	0.1636462	0.4001253	-5.39	FALSE
264430_at	cineole synthase, putative simila	TPS14	AT1G61680	-1.18	-0.24	-1.56	0.1636419	0.4001253	-5.39	FALSE
267129_at	curly leaf protein (polycomb-grou	CLF	AT2G23380	1.17	0.23	1.56	0.1636845	0.4001492	-5.39	FALSE
245813_at	hypothetical protein contains sim	---	AT1G49920	1.28	0.36	1.56	0.163691	0.4001492	-5.39	FALSE
251750_at	glucuronosyl transferase - like p	---	AT3G55710	-1.28	-0.35	-1.56	0.1637258	0.4001914	-5.39	FALSE
265818_at	putative peptidyl-prolyl cis-trans i	PIN1AT	AT2G18040	-1.18	-0.24	-1.56	0.1637892	0.4003034	-5.39	FALSE
248217_at	cytochrome b5 (dbj|BAA74839.1	CB5-E	AT5G53560	-1.24	-0.31	-1.56	0.1639251	0.4004692	-5.39	FALSE
259700_at	unknown protein	---	AT1G68980	-1.14	-0.20	-1.56	0.1639273	0.4004692	-5.39	FALSE
257782_at	hypothetical protein predicted by	---	AT3G27120 /	1.20	0.27	1.56	0.1639166	0.4004692	-5.39	FALSE
266218_s_a	putative cytochrome P450	CYP710A4	AT2G28850 /	1.18	0.24	1.56	0.1639136	0.4004692	-5.39	FALSE
264359_at	hypothetical protein predicted by	---	AT1G03320	1.22	0.29	1.56	0.1639451	0.4004699	-5.39	FALSE
254401_at	putative protein various predicte	---	AT4G21300	-1.19	-0.25	-1.56	0.1640502	0.4005909	-5.39	FALSE
246493_at	putative protein hypothetical prot	CRS1	AT5G16180	-1.22	-0.29	-1.56	0.1640649	0.4005909	-5.39	FALSE
262993_at	hypothetical protein contains sim	---	AT1G54230	-1.17	-0.22	-1.56	0.1640618	0.4005909	-5.39	FALSE
245022_at	PSII L protein	---	---	-1.29	-0.37	-1.56	0.1640456	0.4005909	-5.39	FALSE
255359_at	putative glucose-6-phosphate/ph	---	AT4G03950	1.19	0.25	1.56	0.1641215	0.4006862	-5.39	FALSE

251192_at	alpha galactosyltransferase-like	XT1	AT3G62720	1.55	0.63	1.56	0.1643089	0.4007326	-5.39	TRUE
252213_at	flavonol synthase - like protein S	---	AT3G50210	-1.24	-0.31	-1.56	0.1642769	0.4007326	-5.39	FALSE
247882_at	Expressed protein ; supported by	---	AT5G57785	1.82	0.86	1.56	0.164355	0.4007326	-5.39	FALSE
266501_at	unknown protein ; supported by	HEN2	AT2G06990	-1.22	-0.29	-1.56	0.164219	0.4007326	-5.39	FALSE
267598_at	hypothetical protein predicted by	---	AT2G33010	1.24	0.31	1.56	0.1642326	0.4007326	-5.39	FALSE
260941_at	peroxidase, putative similar to p	---	AT1G44970	1.31	0.39	1.56	0.164206	0.4007326	-5.39	FALSE
252436_x_a	putative protein several hypothet	---	---	1.38	0.46	1.56	0.1643689	0.4007326	-5.39	FALSE
246604_at	putative protein	---	---	1.19	0.25	1.56	0.1643577	0.4007326	-5.39	FALSE
266529_at	putative salt-inducible protein	---	AT2G16880	-1.22	-0.29	-1.56	0.1641902	0.4007326	-5.39	FALSE
253374_at	hypothetical protein ; supported	---	AT4G33140	1.17	0.22	1.56	0.1643546	0.4007326	-5.39	FALSE
264039_at	putative cold-regulated protein ;s	---	AT2G03740	-1.18	-0.24	-1.56	0.1643592	0.4007326	-5.39	FALSE
253074_at	putative disease resistance prot	---	AT4G36140	-1.15	-0.21	-1.56	0.1643687	0.4007326	-5.39	FALSE
254860_at	putative C-4 sterol methyl oxidas	SMO1-1	AT4G12110	-1.23	-0.29	-1.56	0.1643153	0.4007326	-5.39	FALSE
245498_at	hypothetical protein	---	AT4G16470	-1.17	-0.22	-1.56	0.164388	0.4007364	-5.39	FALSE
247259_at	CPR5 protein, putative Constitut	CPR5	AT5G64930	-1.28	-0.36	-1.56	0.1645409	0.4009157	-5.39	FALSE
248884_at	putative protein similar to unknov	---	AT5G46030	-1.16	-0.21	-1.56	0.1645437	0.4009157	-5.39	FALSE
246270_at	putative protein	---	AT4G36500	1.88	0.91	1.56	0.1645592	0.4009157	-5.39	FALSE
266451_at	3-isopropylmalate dehydratase,	---	AT2G43090	-1.18	-0.24	-1.56	0.1645507	0.4009157	-5.39	FALSE
263118_at	putative 3-methylcrotonyl-CoA c	MCCA	AT1G03090	1.56	0.64	1.56	0.1645309	0.4009157	-5.39	FALSE
252124_at	hypothetical protein ;supported b	---	AT3G51010	-1.25	-0.32	-1.56	0.164567	0.4009157	-5.39	FALSE
261224_at	subtilisin-like serine protease sim	ATSBT5.2	AT1G20160	-1.60	-0.68	-1.56	0.1645964	0.4009444	-5.39	FALSE
266455_at	putative bHLH transcription facto	---	AT2G22760	1.51	0.59	1.56	0.1646356	0.4009972	-5.39	FALSE
264865_at	DNAJ-like heatshock protein sim	ARL1	AT1G24120	-1.16	-0.22	-1.56	0.1646891	0.4010417	-5.39	FALSE
263407_at	bZIP protein (AtbZIP48) to be pu	AtbZIP48	AT2G04038	1.18	0.24	1.56	0.1646755	0.4010417	-5.39	FALSE
251000_at	putative protein	---	AT5G02650	-1.21	-0.27	-1.56	0.1647289	0.401096	-5.39	FALSE
259102_at	unknown protein similar to hin1 C	NHL1	AT3G11660	1.24	0.31	1.56	0.1648502	0.4013484	-5.39	FALSE
258147_at	beta-glucosidase, putative simila	BGLU43	AT3G18070	-1.19	-0.26	-1.56	0.1648727	0.4013603	-5.39	FALSE
247270_at	ER66 protein-like	---	AT5G64220	1.17	0.23	1.56	0.1649125	0.4014145	-5.39	FALSE
256696_at	unknown protein	---	AT3G20650	-1.18	-0.24	-1.56	0.1649538	0.4014722	-5.39	FALSE
267023_at	putative protein transport protein	---	AT2G34250	1.24	0.31	1.56	0.1649847	0.4015045	-5.39	FALSE
264895_at	putative 10kd chaperonin strongl	---	AT1G23100	-1.54	-0.62	-1.56	0.1650062	0.401514	-5.39	TRUE
266782_at	putative ligand-gated ion channe	ATGLR2.7	AT2G29120	1.18	0.24	1.56	0.1651006	0.4016909	-5.39	FALSE
252919_at	putative endo-1,4-beta-glucanas	AtGH9B16	AT4G38990	1.26	0.34	1.56	0.1651141	0.4016909	-5.40	FALSE
259895_at	unknown protein ;supported by fu	PFI	AT1G71440	-1.17	-0.23	-1.56	0.1652054	0.4017022	-5.40	FALSE
258388_at	putative expansin S2 precursor s	ATEXPA12	AT3G15370	1.16	0.21	1.56	0.165184	0.4017022	-5.40	FALSE

265934_at	unknown protein	EER5	AT2G19560	-1.15	-0.21	-1.56	0.1651662	0.4017022	-5.40	FALSE
260584_at	putative beta-1,3-glucanase, C t	---	AT2G43660	1.17	0.23	1.56	0.1652069	0.4017022	-5.40	FALSE
252466_x_a	putative protein several hypothet	---	---	1.19	0.25	1.56	0.1651623	0.4017022	-5.40	FALSE
250209_at	putative protein similar to unknov	---	AT5G14030	-1.26	-0.33	-1.56	0.165244	0.4017496	-5.40	FALSE
266760_at	putative RAV-like B3 domain DN	NGA1	AT2G46870	-1.25	-0.33	-1.56	0.1653163	0.4018398	-5.40	FALSE
246183_at	beta-glucosidase - like protein b	---	AT5G20940	1.22	0.29	1.56	0.1653001	0.4018398	-5.40	FALSE
250451_at	cdc2-like protein kinase cdc2-lik	CDKC;1	AT5G10270	1.23	0.29	1.56	0.1654976	0.4022376	-5.40	FALSE
252249_at	putative protein heat shock prote	---	AT3G49770	1.23	0.30	1.56	0.1655161	0.4022397	-5.40	FALSE
264262_at	Expressed protein ; supported by	---	AT1G09200	-2.17	-1.12	-1.56	0.1655884	0.4023301	-5.40	FALSE
262374_s_a	flax rust resistance protein, puta	TIR	AT1G72910 /,	1.88	0.91	1.56	0.1655886	0.4023301	-5.40	FALSE
252215_at	kinesin -like protein KINESIN-LI	KICP-02	AT3G50240	-1.66	-0.73	-1.55	0.1657852	0.402765	-5.40	FALSE
262183_at	unknown protein	---	AT1G77890	1.18	0.24	1.55	0.1658133	0.4027903	-5.40	FALSE
246258_at	PPR-repeat protein, putative cor	---	AT1G31840	-1.18	-0.24	-1.55	0.1658821	0.4028715	-5.40	FALSE
247926_at	protein carboxyl methylase-like	---	AT5G57280	-1.45	-0.54	-1.55	0.1658693	0.4028715	-5.40	FALSE
255641_at	contains region of similarity to be	---	AT4G00800	1.20	0.26	1.55	0.1659473	0.40289	-5.40	FALSE
255526_at	hypothetical protein	---	AT4G02350	1.22	0.29	1.55	0.1659603	0.40289	-5.40	FALSE
253991_at	putative nucleic acid binding pro	PEP	AT4G26000	-1.19	-0.25	-1.55	0.1659407	0.40289	-5.40	FALSE
265638_at	similar to PIG-L	---	AT2G27340	-1.18	-0.24	-1.55	0.1659419	0.40289	-5.40	FALSE
254486_at	putative protein crp1 protein, Ze	---	AT4G20770	-1.22	-0.28	-1.55	0.1660341	0.4030262	-5.40	FALSE
264200_at	putative invertase Similar to LIM1	---	AT1G22650	1.33	0.42	1.55	0.166063	0.4030535	-5.40	FALSE
261782_at	unknown protein	---	AT1G76110	-1.25	-0.33	-1.55	0.166095	0.4030884	-5.40	FALSE
259912_at	hypothetical protein	iqd8	AT1G72670	1.24	0.31	1.55	0.1661831	0.4031398	-5.40	FALSE
263842_at	Expressed protein ; supported by	---	AT2G36835	-1.29	-0.37	-1.55	0.1661976	0.4031398	-5.40	FALSE
263164_at	putative glutamate/aspartate-bin	---	AT1G03070	1.19	0.26	1.55	0.1662003	0.4031398	-5.40	FALSE
256449_at	mutator transposase MUDRA, p	---	---	1.18	0.24	1.55	0.1661479	0.4031398	-5.40	FALSE
248015_at	putative protein similar to unknov	---	AT5G56370	1.19	0.25	1.55	0.1662046	0.4031398	-5.40	FALSE
255011_at	cytochrome c several plant cyto	CYTC-2	AT4G10040	1.77	0.83	1.55	0.1663769	0.4035148	-5.40	TRUE
256862_at	dihydroxyacid dehydratase, puta	---	AT3G23940	-1.52	-0.60	-1.55	0.1665446	0.4037927	-5.40	FALSE
265020_at	putative cytochrome P450 simila	CYP86C1	AT1G24540	1.16	0.22	1.55	0.1665414	0.4037927	-5.40	FALSE
258664_at	E2, ubiquitin-conjugating enzym	UBC12	AT3G08700	1.21	0.27	1.55	0.166541	0.4037927	-5.40	FALSE
246087_at	putative protein predicted protei	---	AT5G20580	-1.31	-0.39	-1.55	0.1666731	0.4040613	-5.40	FALSE
253909_at	putative protein LEDI-3 protein,	---	AT4G27270	1.23	0.30	1.55	0.1666947	0.4040708	-5.40	FALSE
258910_at	putative RNA helicase similar to	---	AT3G06480	-1.17	-0.23	-1.55	0.1668115	0.4041362	-5.40	FALSE
266781_at	putative protein kinase contains a	---	AT2G28940	-1.26	-0.34	-1.55	0.1667704	0.4041362	-5.40	FALSE
266201_at	similar to MtN3 protein ;supporte	---	AT2G39060	1.21	0.27	1.55	0.1668236	0.4041362	-5.40	FALSE

253830_at	Expressed protein ; supported by	---	AT4G27652	2.14	1.10	1.55	0.1667983	0.4041362	-5.40	FALSE
254629_at	Expressed protein ; supported by	---	AT4G18425	1.26	0.33	1.55	0.1668442	0.4041362	-5.40	FALSE
266266_at	putative enolase (2-phospho-D-g	---	AT2G29560	-1.23	-0.30	-1.55	0.1667601	0.4041362	-5.40	FALSE
246694_at	putative protein	---	---	1.19	0.25	1.55	0.1668457	0.4041362	-5.40	FALSE
251073_at	putative protein hypothetical prot	---	AT5G01750	1.15	0.20	1.55	0.1668673	0.4041457	-5.40	FALSE
248014_at	putative protein similar to unknov	---	AT5G56340	1.26	0.33	1.55	0.1669091	0.4041796	-5.40	FALSE
246788_at	putative protein hypothetical pro	AGL89	AT5G27580	1.16	0.22	1.55	0.1669168	0.4041796	-5.40	FALSE
247122_at	putative protein non-consensus	ATSAC1B	AT5G66020	1.27	0.35	1.55	0.1669407	0.4041945	-5.40	FALSE
255183_at	hypothetical protein	---	AT4G08140	1.22	0.29	1.55	0.1669675	0.4042167	-5.41	FALSE
247555_at	putative protein various predicted	ECT3	AT5G61020	-1.35	-0.43	-1.55	0.1670263	0.4042627	-5.41	FALSE
245799_at	disease resistance protein, puta	AtRLP6	AT1G45616	-1.18	-0.24	-1.55	0.1670397	0.4042627	-5.41	FALSE
247230_at	putative protein similar to unknov	---	AT5G65170	1.17	0.22	1.55	0.1670125	0.4042627	-5.41	FALSE
265780_at	Mutator-like transposase similar	---	---	1.19	0.25	1.55	0.1671477	0.404481	-5.41	FALSE
249528_at	putative protein predicted protei	---	AT5G38720	-1.33	-0.41	-1.55	0.1671892	0.4044956	-5.41	FALSE
253721_at	hypothetical protein ;supported b	---	AT4G29250	1.26	0.33	1.55	0.1671882	0.4044956	-5.41	FALSE
258860_at	putative potassium transporter si	KUP3	AT3G02050	-1.35	-0.43	-1.55	0.1672485	0.4045963	-5.41	FALSE
252481_at	putative protein DCL PROTEIN,	---	AT3G46630	-1.23	-0.29	-1.55	0.167336	0.404632	-5.41	FALSE
256433_at	unknown protein	SAG20	AT3G10985	1.29	0.37	1.55	0.1673271	0.404632	-5.41	FALSE
261436_at	protein kinase, putative (fragmer	---	AT1G07870	1.29	0.37	1.55	0.1673212	0.404632	-5.41	FALSE
256552_at	hypothetical protein predicted by	---	AT3G31350	1.22	0.29	1.55	0.1673519	0.404632	-5.41	FALSE
245173_at	putative AP2 domain transcriptio	---	AT2G47520	1.55	0.63	1.55	0.1673151	0.404632	-5.41	FALSE
253232_at	hypothetical protein ;supported b	TAF8	AT4G34340	1.21	0.27	1.55	0.1674196	0.4047526	-5.41	FALSE
252324_at	protein translocation complex se	---	AT3G48570	1.21	0.28	1.55	0.1674792	0.4048538	-5.41	FALSE
261201_at	unknown protein ;supported by fu	---	AT1G12850	-1.20	-0.26	-1.55	0.1676288	0.4050866	-5.41	FALSE
252764_at	nucleic acid binding protein-like	AL3	AT3G42790	-1.19	-0.25	-1.55	0.1675933	0.4050866	-5.41	FALSE
265689_at	hypothetical protein predicted by	---	AT2G24310	1.16	0.21	1.55	0.1676223	0.4050866	-5.41	FALSE
246162_at	actin interacting protein ; support	---	AT4G36400	1.25	0.33	1.55	0.1676583	0.4051062	-5.41	FALSE
251734_at	putative protein Centrosome- an	---	AT3G56270	-1.47	-0.55	-1.55	0.1676724	0.4051062	-5.41	FALSE
258583_at	putative SRF-type transcription fa	AGL57	AT3G04100	1.17	0.22	1.55	0.1677232	0.4051432	-5.41	FALSE
245896_at	putative transcriptional co-activat	KIWI	AT5G09250	-1.25	-0.32	-1.55	0.1677134	0.4051432	-5.41	FALSE
249572_at	chromosome condensation prote	EMB2656	AT5G37630	1.24	0.31	1.55	0.1677671	0.405195	-5.41	FALSE
245225_at	mitochondrial protein-like; contai	---	AT3G29800	1.26	0.34	1.55	0.1677802	0.405195	-5.41	FALSE
263857_at	unknown protein	---	AT2G04380	1.14	0.19	1.55	0.1678957	0.405431	-5.41	FALSE
248226_at	putative protein strong similarity t	---	AT5G53750	1.72	0.78	1.55	0.167933	0.4054782	-5.41	FALSE
245778_at	RNA-binding glycine-rich protein	---	AT1G73530	-1.29	-0.37	-1.54	0.1679839	0.4055152	-5.41	FALSE

252356_at	putative protein various predicted	---	---	1.26	0.33	1.54	0.1679679	0.4055152	-5.41	FALSE
255686_at	putative potassium/H+ antiporter	KEA2	AT4G00630	-1.24	-0.31	-1.54	0.168056	0.4055176	-5.41	FALSE
251319_at	putative protein POSSIBLE APC	---	AT3G61610	1.28	0.36	1.54	0.1680469	0.4055176	-5.41	FALSE
251641_at	protease-like protein INSULIN-D	---	AT3G57470	-1.29	-0.36	-1.54	0.1680221	0.4055176	-5.41	FALSE
251574_at	putative protein GLUCAN ENDC	PDCB5	AT3G58100	-1.22	-0.29	-1.54	0.1680044	0.4055176	-5.41	FALSE
259750_at	hypothetical protein predicted by	---	AT1G71130	-1.31	-0.39	-1.54	0.1680741	0.4055183	-5.41	FALSE
264794_at	hypothetical protein predicted by	---	AT1G08670	1.16	0.22	1.54	0.1681864	0.4057465	-5.41	FALSE
247924_at	Expressed protein	---	AT5G57655	1.45	0.54	1.54	0.1682052	0.4057488	-5.41	FALSE
256976_at	unknown protein similar to putati	---	---	-1.29	-0.37	-1.54	0.16834	0.406031	-5.41	FALSE
260413_at	hypothetical protein predicted by	---	AT1G69800	-1.27	-0.35	-1.54	0.1684727	0.4062843	-5.41	FALSE
260120_at	hypothetical protein	ATPP2-A4	AT1G33920	1.19	0.25	1.54	0.1685053	0.4062843	-5.41	FALSE
249463_s_a	putative protein predicted protei	anac064	AT3G56530 ///	1.20	0.26	1.54	0.1685163	0.4062843	-5.41	FALSE
246841_at	nectarin - like protein nectarin I p	---	AT5G26700	1.38	0.46	1.54	0.168501	0.4062843	-5.41	FALSE
245466_at	glucosyltransferase like protein	---	AT4G16600	1.24	0.31	1.54	0.1685631	0.4063426	-5.41	FALSE
257430_at	hypothetical protein similar to hyp	---	AT2G28580	1.24	0.31	1.54	0.168576	0.4063426	-5.41	FALSE
248730_at	putative protein similar to unknov	---	AT5G48050	1.25	0.32	1.54	0.168642	0.4064585	-5.41	FALSE
249895_at	male sterility 2-like protein (embl	FAR1	AT5G22500	1.82	0.87	1.54	0.168759	0.4066507	-5.41	TRUE
267359_at	hypothetical protein predicted by	---	AT2G40020	-1.26	-0.34	-1.54	0.1687752	0.4066507	-5.41	FALSE
263985_at	unknown protein ;supported by f	---	AT2G42750	1.33	0.42	1.54	0.168742	0.4066507	-5.41	FALSE
265185_at	OBP32pep protein, putative iden	---	AT1G23670	1.21	0.28	1.54	0.1688262	0.4067307	-5.42	FALSE
258256_at	unknown protein ; supported by	---	AT3G26890	-1.21	-0.27	-1.54	0.1688467	0.406737	-5.42	FALSE
246283_at	putative protein	---	AT4G36860	1.23	0.30	1.54	0.1689265	0.4068863	-5.42	FALSE
254134_at	argininosuccinate synthase -like	---	AT4G24830	1.38	0.46	1.54	0.168973	0.4069553	-5.42	FALSE
266055_at	hypothetical protein predicted by	---	AT2G40650	-1.22	-0.29	-1.54	0.1690575	0.4069746	-5.42	FALSE
265595_at	26S proteasome subunit 4 ;supp	---	AT2G20140	-1.23	-0.30	-1.54	0.1690201	0.4069746	-5.42	FALSE
245880_at	putative hydrolase EtbD1 - Rhoc	---	AT5G09430	1.25	0.33	1.54	0.1690702	0.4069746	-5.42	FALSE
244915_s_a	hypothetical protein	---	---	1.18	0.24	1.54	0.1690471	0.4069746	-5.42	FALSE
263646_at	Ac-like transposase related to Ac	---	---	-1.15	-0.20	-1.54	0.1690254	0.4069746	-5.42	FALSE
253638_at	cinnamoyl-CoA reductase - like	---	AT4G30470	1.62	0.70	1.54	0.1691567	0.4070969	-5.42	TRUE
252766_at	putative protein hypothetical prot	---	---	1.26	0.34	1.54	0.1691392	0.4070969	-5.42	FALSE
245352_at	indole-3-acetate beta-glucosyltra	UGT84A3	AT4G15490	1.36	0.44	1.54	0.1694645	0.4076226	-5.42	TRUE
253186_at	putative protein predicted protei	---	AT4G35270	-1.28	-0.36	-1.54	0.1694102	0.4076226	-5.42	FALSE
265319_at	auxin-regulated protein (IAA8) ;s	IAA8	AT2G22670	-1.43	-0.51	-1.54	0.1694417	0.4076226	-5.42	FALSE
256301_at	unknown protein ;supported by fu	---	AT1G69510	-1.19	-0.25	-1.54	0.169436	0.4076226	-5.42	FALSE
261827_at	unknown protein contains similar	---	AT1G11480	1.18	0.24	1.54	0.1694536	0.4076226	-5.42	FALSE

253976_at	putative protein kinase protein k	D6PKL1	AT4G26610	1.15	0.20	1.54	0.1695442	0.4076598	-5.42	TRUE
257046_at	ATPase, putative similar to spas	---	AT3G19740	-1.27	-0.34	-1.54	0.1695072	0.4076598	-5.42	FALSE
264624_at	zinc finger protein ATZF1, putati	ERD6	AT1G08930	1.28	0.35	1.54	0.1695365	0.4076598	-5.42	FALSE
266784_at	putative receptor-like protein kina	---	AT2G28960	1.15	0.20	1.54	0.1695515	0.4076598	-5.42	FALSE
253423_at	Expressed protein ; supported by	IAA29	AT4G32280	-2.38	-1.25	-1.54	0.1696901	0.4079502	-5.42	TRUE
263167_at	unknown protein Belongs to PF	---	AT1G03030	-1.22	-0.29	-1.54	0.1697509	0.4079545	-5.42	FALSE
248395_at	putative protein contains similarit	AtPP2-A14	AT5G52120	1.28	0.36	1.54	0.1697215	0.4079545	-5.42	FALSE
262596_at	putative phosphatidic acid phosp	LPP2	AT1G15080	-1.22	-0.28	-1.54	0.1697634	0.4079545	-5.42	FALSE
264758_at	late embryogenesis abundant pr	---	AT1G61340	2.34	1.23	1.54	0.1697544	0.4079545	-5.42	FALSE
255690_at	probable cytochrome P450	CYP86A2	AT4G00360	2.33	1.22	1.54	0.1698181	0.4079667	-5.42	TRUE
253868_at	proton pump interactor non-cons	PPI1	AT4G27500	1.21	0.28	1.54	0.1698094	0.4079667	-5.42	FALSE
266787_at	putative receptor-like protein kina	---	AT2G28990	1.16	0.21	1.54	0.1698222	0.4079667	-5.42	FALSE
253428_at	cellulose synthase catalytic subu	CESA1	AT4G32410	-1.27	-0.35	-1.54	0.1699504	0.4080789	-5.42	TRUE
248862_at	unknown protein	---	AT5G46730	1.30	0.38	1.54	0.1700252	0.4080789	-5.42	FALSE
258198_at	putative transcription factor simil	NF-YA6	AT3G14020	-1.22	-0.28	-1.54	0.1699142	0.4080789	-5.42	FALSE
263074_at	putative HMG protein ;supported	HMGB4	AT2G17560	-1.24	-0.31	-1.54	0.1700299	0.4080789	-5.42	FALSE
266475_at	putative lipase	---	AT2G31100	1.18	0.24	1.54	0.1700048	0.4080789	-5.42	FALSE
249033_at	putative protein contains similarit	---	AT5G44920	1.19	0.26	1.54	0.169979	0.4080789	-5.42	FALSE
254160_at	putative protein ;supported by fu	SLY1	AT4G24210	-1.25	-0.32	-1.54	0.1699726	0.4080789	-5.42	FALSE
252533_at	putative protein predicted protei	---	AT3G46110	1.64	0.72	1.54	0.1699264	0.4080789	-5.42	FALSE
245956_s_a	luminal binding protein ; support	BIP2	AT5G28540 /	1.73	0.79	1.54	0.1699139	0.4080789	-5.42	FALSE
260193_at	putative amino acid permease si	---	AT1G67640	1.26	0.33	1.54	0.1700891	0.4081372	-5.42	FALSE
247724_at	putative protein predicted protei	MBD6	AT5G59380	-1.17	-0.23	-1.54	0.17009	0.4081372	-5.42	FALSE
260676_at	integral membrane protein, puta	---	AT1G19450	-1.40	-0.49	-1.54	0.1701164	0.4081577	-5.42	TRUE
260491_at	hypothetical protein predicted by	---	AT1G51440	1.29	0.37	1.54	0.1701425	0.4081773	-5.42	FALSE
253878_at	trehalose-6-phosphate synthase	TPS4	AT4G27550	1.17	0.22	1.54	0.1701852	0.408194	-5.42	FALSE
245497_at	hypothetical protein	---	AT4G16460	1.21	0.27	1.54	0.1701702	0.408194	-5.42	FALSE
255371_at	putative RPP1-like disease resist	---	AT4G04110	1.17	0.22	1.54	0.1702217	0.4082386	-5.42	FALSE
266715_at	putative RNA-binding protein	---	AT2G46780	1.22	0.29	1.54	0.1702625	0.4082936	-5.42	FALSE
262305_at	hypothetical protein predicted by	---	AT1G70950	1.18	0.24	1.54	0.1702823	0.408298	-5.42	FALSE
255635_at	Shaggy related protein kinase te	ATSK32	AT4G00720	-1.21	-0.27	-1.54	0.1703266	0.4083522	-5.42	FALSE
264627_at	hypothetical protein similar to ca	ECI1	AT1G65520	1.21	0.28	1.54	0.1703407	0.4083522	-5.42	FALSE
246533_at	putative protein	---	AT5G15880	-1.26	-0.33	-1.53	0.170376	0.408394	-5.42	FALSE
263683_at	putative NAM protein similar to	FEZ	AT1G26870	1.19	0.25	1.53	0.1704002	0.4084091	-5.42	FALSE
265215_at	hypothetical protein predicted by	---	AT1G05040	1.15	0.20	1.53	0.1705337	0.4084715	-5.42	FALSE

255321_at	putative ES43-like protein	---	AT4G04260	-1.19	-0.26	-1.53	0.1704945	0.4084715	-5.42	FALSE
245807_at	AP2 domain containing protein R	RAP2.1	AT1G46768	-1.45	-0.54	-1.53	0.1704904	0.4084715	-5.42	FALSE
256217_at	hypothetical protein predicted by	---	AT1G56320	-1.40	-0.49	-1.53	0.1705192	0.4084715	-5.42	FALSE
255459_at	polyubiquitin (UBQ14) identical t	UBQ14	AT4G02890	1.18	0.24	1.53	0.1704507	0.4084715	-5.42	FALSE
245811_at	hypothetical protein similar to put	---	---	1.20	0.26	1.53	0.1705037	0.4084715	-5.42	FALSE
256453_at	GSH-dependent dehydroascorb	DHAR2	AT1G75270	1.42	0.51	1.53	0.1706843	0.4085987	-5.42	TRUE
266345_at	hypothetical protein predicted by	---	AT2G01410	1.17	0.23	1.53	0.1706441	0.4085987	-5.42	FALSE
267054_at	hypothetical protein	---	AT2G38370	-1.33	-0.41	-1.53	0.1706132	0.4085987	-5.42	FALSE
261476_at	hypothetical protein contains sim	---	AT1G14480	1.47	0.55	1.53	0.1706602	0.4085987	-5.42	FALSE
246330_at	aldehyde oxidase ; supported by	AAO2	AT3G43600	-1.52	-0.60	-1.53	0.1707122	0.4085987	-5.43	FALSE
258672_at	hypothetical protein	---	AT3G08570	-1.21	-0.28	-1.53	0.1706268	0.4085987	-5.42	FALSE
255738_at	hypothetical protein predicted by	---	AT1G25570	-1.17	-0.23	-1.53	0.1706953	0.4085987	-5.42	FALSE
256161_at	unknown protein ; supported by c	---	AT1G30090	1.19	0.26	1.53	0.170748	0.4086415	-5.43	FALSE
264283_at	hypothetical protein contains sim	---	AT1G61850	1.19	0.25	1.53	0.170804	0.4087326	-5.43	FALSE
260655_at	pathogenesis-related protein 5 p	---	AT1G19320	1.44	0.52	1.53	0.1708221	0.408733	-5.43	FALSE
255548_at	putative CHP-rich zinc finger pro	---	AT4G01930	1.15	0.20	1.53	0.1708714	0.4087673	-5.43	FALSE
250218_at	putative protein contains similarit	CHC1	AT5G14170	-1.26	-0.33	-1.53	0.1708902	0.4087673	-5.43	FALSE
260298_at	putative oxidoreductase contains	---	AT1G80320	1.16	0.21	1.53	0.1708738	0.4087673	-5.43	FALSE
247797_at	predicted protein	---	AT5G58780	1.22	0.29	1.53	0.1709191	0.4087937	-5.43	FALSE
266513_at	unknown protein	---	AT2G47700	1.24	0.32	1.53	0.171021	0.4088333	-5.43	FALSE
266396_at	unknown protein	---	AT2G38790	-1.29	-0.37	-1.53	0.1709681	0.4088333	-5.43	FALSE
247545_at	putative protein rhoGAP, Homo	---	AT5G61530	1.17	0.22	1.53	0.1710142	0.4088333	-5.43	FALSE
249831_at	putative protein contains similarit	---	AT5G23340	1.38	0.47	1.53	0.170999	0.4088333	-5.43	FALSE
266691_at	hypothetical protein predicted by	---	AT2G19890	-1.22	-0.28	-1.53	0.1710253	0.4088333	-5.43	FALSE
250471_at	myo-inositol-1-phosphate syntha	MIPS3	AT5G10170	-1.32	-0.40	-1.53	0.1711224	0.4089985	-5.43	FALSE
264931_at	polygalacturonase, putative simi	---	AT1G60590	1.19	0.26	1.53	0.1711303	0.4089985	-5.43	FALSE
256615_at	hypothetical protein predicted by	---	AT3G22250	1.25	0.32	1.53	0.1711653	0.4090394	-5.43	FALSE
AFFX-r2-At	Arabidopsis thaliana /REF=U84	---	---	1.17	0.22	1.53	0.1711899	0.4090553	-5.43	FALSE
254442_at	putative protein predicted protei	---	AT4G21060	-1.18	-0.24	-1.53	0.1712091	0.4090582	-5.43	FALSE
245972_at	putative protein predicted protei	---	AT5G20680	1.25	0.32	1.53	0.1712722	0.4091663	-5.43	FALSE
251196_at	glutaredoxin -like protein glutare	---	AT3G62950	-1.70	-0.77	-1.53	0.1714295	0.409294	-5.43	TRUE
250874_at	putative protein	---	AT5G04010	1.21	0.27	1.53	0.1713752	0.409294	-5.43	FALSE
261495_at	hypothetical protein predicted by	---	AT1G28410	-1.19	-0.26	-1.53	0.1714051	0.409294	-5.43	FALSE
247105_at	putative protein similar to unknov	DAR5	AT5G66630	1.26	0.34	1.53	0.1714334	0.409294	-5.43	FALSE
247160_at	putative protein contains similarit	---	AT5G65820	-1.17	-0.23	-1.53	0.1713646	0.409294	-5.43	FALSE

261707_at	unknown protein	---	AT1G32650	-1.17	-0.23	-1.53	0.1714129	0.409294	-5.43	FALSE
253229_at	putative protein ;supported by fu	---	AT4G34660	1.13	0.18	1.53	0.1714615	0.4093183	-5.43	FALSE
262805_at	putative DNA-binding protein sir	ESC	AT1G20900	1.18	0.24	1.53	0.1715136	0.4093998	-5.43	FALSE
257321_at	hypothetical protein	---	---	1.41	0.49	1.53	0.17156	0.4094652	-5.43	FALSE
262213_at	hypothetical protein predicted by	---	AT1G74870	1.26	0.33	1.53	0.1715769	0.4094652	-5.43	FALSE
253341_at	putative protein ; supported by c	---	AT4G33410	-1.20	-0.27	-1.53	0.1716944	0.4097027	-5.43	FALSE
251952_at	histone H2B - like protein histon	---	AT3G53650	-1.15	-0.20	-1.53	0.1718002	0.4099125	-5.43	FALSE
246865_s_a	eukaryotic translation initiation fa	TIF3B1	AT5G25780 /	-1.14	-0.19	-1.53	0.171851	0.4099566	-5.43	FALSE
257676_at	unknown protein ;supported by f	TGD2	AT3G20320	-1.19	-0.25	-1.53	0.1718547	0.4099566	-5.43	FALSE
256121_at	MAP kinase, putative similar to M	---	AT1G18160	-1.19	-0.25	-1.53	0.1719391	0.4101152	-5.43	FALSE
250877_at	putative protein predicted protei	SDP1	AT5G04040	1.28	0.35	1.53	0.1719674	0.4101398	-5.43	FALSE
258124_at	Expressed protein ; supported by	---	AT3G18215	-1.32	-0.40	-1.53	0.1720609	0.4103197	-5.43	FALSE
261299_at	unknown protein	---	AT1G48550	-1.25	-0.32	-1.53	0.172177	0.4105537	-5.43	FALSE
261639_at	tubulin alpha-2/alpha-4 chain, pu	TUA2	AT1G50010	1.69	0.76	1.53	0.1721962	0.4105567	-5.43	TRUE
254776_at	3-hydroxyisobutyryl-coenzyme A	---	AT4G13360	-1.14	-0.20	-1.53	0.1722425	0.4105793	-5.43	FALSE
247787_at	putative protein various predicted	---	AT5G58640	-1.16	-0.22	-1.53	0.1722517	0.4105793	-5.43	FALSE
262840_at	linker histone protein, putative c	HMGA	AT1G14900	-1.21	-0.28	-1.53	0.172298	0.4105793	-5.43	FALSE
257033_at	metalloprotease, putative similar	ATPREP1	AT3G19170	-1.42	-0.50	-1.53	0.1723137	0.4105793	-5.43	FALSE
261015_at	14-3-3 protein GF14iota (grf12) i	GRF12	AT1G26480	-1.18	-0.24	-1.53	0.1722792	0.4105793	-5.43	FALSE
260755_at	hypothetical protein predicted by	---	AT1G48980	-1.18	-0.24	-1.53	0.1722704	0.4105793	-5.43	FALSE
261966_x_a	hypothetical protein similar to put	---	---	-1.17	-0.23	-1.53	0.1723487	0.4106198	-5.43	FALSE
251251_at	serine/threonine protein kinase-l	---	AT3G62220	-1.21	-0.27	-1.53	0.1724811	0.4108924	-5.43	FALSE
256419_at	RNA-binding protein similar to G	---	AT1G33470	-1.21	-0.27	-1.53	0.1725262	0.4109569	-5.43	FALSE
266713_at	unknown protein	---	AT2G46760	1.18	0.24	1.53	0.1725589	0.4109918	-5.43	FALSE
261266_at	expansin 10 identical to GB:AAF	ATEXPA10	AT1G26770	1.28	0.35	1.53	0.1725781	0.4109946	-5.43	FALSE
247419_at	unknown protein	---	AT5G63080	-1.25	-0.32	-1.53	0.1726153	0.4110402	-5.44	FALSE
259379_at	putative MYB family transcription	---	AT3G16350	1.47	0.56	1.53	0.1727129	0.4112298	-5.44	FALSE
245660_at	unknown protein	---	AT1G28240	1.33	0.41	1.53	0.1727578	0.4112938	-5.44	FALSE
254563_at	putative protein several hypothet	ERD3	AT4G19120	-1.26	-0.34	-1.52	0.1728382	0.4113994	-5.44	TRUE
245432_at	putative serine protease-like prot	---	AT4G17100	-1.16	-0.21	-1.52	0.1728317	0.4113994	-5.44	FALSE
258576_at	putative 40S ribosomal protein S	---	AT3G04230	-1.27	-0.35	-1.52	0.1729486	0.4114044	-5.44	FALSE
251778_at	putative protein various predicte	ROPGEF6	AT3G55660	1.23	0.30	1.52	0.1728956	0.4114044	-5.44	FALSE
249544_at	anti-silencing factor 1-like protei	ASF1B	AT5G38110	-1.28	-0.36	-1.52	0.1728766	0.4114044	-5.44	FALSE
260887_at	ascorbate oxidase promoter-bin	---	AT1G29160	1.77	0.82	1.52	0.1729459	0.4114044	-5.44	FALSE
259831_at	hypothetical protein predicted by	ZFHD1	AT1G69600	1.17	0.23	1.52	0.1729192	0.4114044	-5.44	FALSE

252346_at	hypothetical protein	---	AT3G48650	1.15	0.21	1.52	0.1729104	0.4114044	-5.44	FALSE
253792_at	ammonium transporter - like pro	AMT1;4	AT4G28700	1.23	0.30	1.52	0.1729884	0.4114133	-5.44	FALSE
264092_at	photosystem II polypeptide, puta	PSBR	AT1G79040 /	-1.16	-0.22	-1.52	0.1729871	0.4114133	-5.44	FALSE
257975_at	unknown protein similar to GB:A/	---	AT3G20830	1.29	0.37	1.52	0.1731179	0.4116784	-5.44	FALSE
262082_s_a	wall-associated kinase 2, putativ	---	AT1G56120 /	1.61	0.68	1.52	0.1731585	0.411732	-5.44	FALSE
263911_at	hypothetical protein predicted by	---	AT2G36560	-1.16	-0.22	-1.52	0.1732055	0.4118009	-5.44	FALSE
257928_at	hypothetical protein contains Pfa	PPR40	AT3G16890	-1.14	-0.20	-1.52	0.1732597	0.4118868	-5.44	FALSE
258157_at	putative MYB family transcription	MYB4R1	AT3G18100	-1.30	-0.38	-1.52	0.1733063	0.4119117	-5.44	FALSE
AFFX-r2-Ec	E. coli /GEN=bioC /DB_XREF=g	---	---	1.48	0.56	1.52	0.173294	0.4119117	-5.44	FALSE
244934_at	NADH dehydrogenase ND6	---	---	-1.43	-0.52	-1.52	0.1733748	0.4120041	-5.44	TRUE
247383_at	putative protein contains similarit	---	AT5G63410	-1.38	-0.47	-1.52	0.1733813	0.4120041	-5.44	FALSE
257700_at	unknown protein similar to unkno	ALIS1	AT3G12740	1.22	0.29	1.52	0.1734738	0.412096	-5.44	FALSE
257310_at	ATP-dependent RNA helicase, p	---	AT3G26560	-1.21	-0.27	-1.52	0.1734387	0.412096	-5.44	FALSE
255700_at	putative transcription factor simil	---	AT4G00200	1.36	0.44	1.52	0.1734742	0.412096	-5.44	FALSE
253890_s_a	putative protein contains similarit	---	AT4G27585 /	1.50	0.59	1.52	0.1735238	0.4121281	-5.44	FALSE
255976_at	hypothetical protein predicted by	---	AT1G22010	1.17	0.23	1.52	0.1735143	0.4121281	-5.44	FALSE
258375_at	hypothetical protein predicted by	---	AT3G17470	-1.17	-0.22	-1.52	0.1736162	0.4121632	-5.44	FALSE
266738_at	unknown protein predicted by ge	---	AT2G47010	1.28	0.36	1.52	0.173647	0.4121632	-5.44	FALSE
256496_at	hypothetical protein similar to hy	---	AT1G31510	1.19	0.25	1.52	0.173576	0.4121632	-5.44	FALSE
245143_at	unknown protein ;supported by f	ZPR1	AT2G45450	1.44	0.53	1.52	0.1736262	0.4121632	-5.44	FALSE
257111_x_a	hypothetical protein	---	---	1.16	0.22	1.52	0.1735721	0.4121632	-5.44	FALSE
264850_at	unknown protein similar to F5J6.	---	AT2G17340	-1.18	-0.24	-1.52	0.1736442	0.4121632	-5.44	FALSE
255536_at	Expressed protein ; supported by	---	AT4G01575	1.33	0.41	1.52	0.173796	0.4124739	-5.44	TRUE
260556_at	putative endochitinase	---	AT2G43620	2.78	1.48	1.52	0.1738382	0.4125096	-5.44	FALSE
260583_x_a	putative polyribonucleotide phos	---	AT2G47220	-1.27	-0.34	-1.52	0.1738472	0.4125096	-5.44	FALSE
266601_at	hypothetical protein predicted by	---	AT2G46060	-1.34	-0.43	-1.52	0.1738771	0.4125222	-5.44	FALSE
267112_at	putative adenosine phosphosulfa	APK	AT2G14750	1.45	0.54	1.52	0.1738887	0.4125222	-5.44	FALSE
253068_at	putative protein Kaposi's sarcom	---	AT4G37820	-1.18	-0.24	-1.52	0.1739228	0.4125526	-5.44	FALSE
263005_at	hypothetical protein predicted by	---	AT1G54540	-1.34	-0.42	-1.52	0.1739377	0.4125526	-5.44	FALSE
263905_at	putative beta-fructofuranosidase	AtcwINV4	AT2G36190	1.28	0.36	1.52	0.1739866	0.4126258	-5.44	FALSE
267015_at	unknown protein	---	AT2G39340	1.23	0.30	1.52	0.174037	0.4127023	-5.44	FALSE
261655_at	hypothetical protein predicted by	---	AT1G01940	-1.27	-0.35	-1.52	0.1740578	0.4127075	-5.44	FALSE
254531_at	putative protein predicted protei	---	AT4G19650	-1.27	-0.34	-1.52	0.1740754	0.4127075	-5.44	FALSE
253590_at	putative protein various predicte	HHP2	AT4G30850	1.27	0.34	1.52	0.174098	0.4127184	-5.44	TRUE
245673_at	hypothetical protein similar to put	---	AT1G56690	-1.22	-0.28	-1.52	0.1741415	0.4127785	-5.44	FALSE

259265_at	hypothetical protein predicted by	---	AT3G01250	1.16	0.21	1.52	0.1742089	0.4128954	-5.44	FALSE
262049_at	unknown protein ;supported by fu	---	AT1G80180	-1.21	-0.28	-1.52	0.1742685	0.4129107	-5.44	FALSE
256155_at	MYB-family transcription factor,	MYB83	AT3G08500	1.16	0.21	1.52	0.1742981	0.4129107	-5.44	FALSE
255653_at	Similar to receptor kinase	---	AT4G00960	-1.15	-0.21	-1.52	0.1743002	0.4129107	-5.44	FALSE
266512_at	unknown protein	---	AT2G47690	-1.15	-0.20	-1.52	0.1742412	0.4129107	-5.44	FALSE
262896_at	chromaffin granule ATPase II ho	ALA3	AT1G59820	1.22	0.29	1.52	0.1743059	0.4129107	-5.44	FALSE
262747_at	hypothetical protein predicted by	---	AT1G28540	-1.16	-0.22	-1.52	0.1744448	0.4131969	-5.44	FALSE
262265_at	hypothetical protein predicted by	---	---	1.27	0.34	1.52	0.1745394	0.4133781	-5.44	FALSE
251303_at	NAM-like protein no apical meris	ANAC066	AT3G61910	1.16	0.21	1.52	0.1746065	0.413494	-5.45	FALSE
246948_at	cytochrome P450-like protein CY	CYP71B12	AT5G25130	1.16	0.21	1.52	0.1748303	0.4138952	-5.45	FALSE
260064_at	ethylene-insensitive3-like3 (EIL3	EIL3	AT1G73730	1.25	0.33	1.52	0.1748012	0.4138952	-5.45	FALSE
252029_s_a	putative RNA binding protein he	---	AT3G52660 ///	-1.16	-0.21	-1.52	0.1748176	0.4138952	-5.45	FALSE
249452_at	Sec7/gnom -like protein GNOM,	---	AT5G39500	-1.18	-0.24	-1.52	0.1748942	0.4139604	-5.45	FALSE
252172_at	putative protein predicted protei	---	AT3G50640	1.18	0.24	1.52	0.1748776	0.4139604	-5.45	FALSE
251064_at	putative zinc finger protein sever	---	AT5G01860	1.19	0.26	1.52	0.1749657	0.4140583	-5.45	FALSE
264447_at	hypothetical protein predicted by	---	AT1G27300	1.45	0.53	1.52	0.1749719	0.4140583	-5.45	FALSE
250656_at	putative protein contains similarit	---	AT5G06970	-1.27	-0.35	-1.52	0.1750327	0.4141163	-5.45	TRUE
251928_at	putative protein hypothetical pro	---	AT3G53980	1.72	0.78	1.52	0.1750287	0.4141163	-5.45	FALSE
253835_at	putative beta-glucosidase beta-g	BGLU9	AT4G27820	-1.21	-0.28	-1.52	0.1750809	0.4141875	-5.45	TRUE
267445_at	hypothetical protein predicted by	---	AT2G33680	-1.21	-0.27	-1.52	0.1751499	0.4141897	-5.45	FALSE
259026_at	putative protein kinase similar to	---	AT3G09240	1.21	0.27	1.52	0.1751672	0.4141897	-5.45	FALSE
251296_at	putative protein paladin - Mus m	---	AT3G62010	1.20	0.26	1.52	0.1751678	0.4141897	-5.45	FALSE
245666_at	hypothetical protein predicted by	---	AT1G28280	1.41	0.50	1.52	0.1751727	0.4141897	-5.45	FALSE
244964_at	PSII cytochrome b559	---	---	-1.13	-0.18	-1.52	0.175113	0.4141897	-5.45	FALSE
263758_s_a	putative NADPH dependent man	---	AT2G21250 ///	-1.17	-0.22	-1.52	0.1752234	0.4142669	-5.45	FALSE
251539_at	serine/threonine-specific protein	---	AT3G58690	-1.25	-0.32	-1.51	0.1753103	0.4144032	-5.45	FALSE
264060_at	hypothetical protein predicted by	---	AT2G27980	-1.16	-0.22	-1.51	0.1753356	0.4144032	-5.45	FALSE
266146_at	En/Spm-like transposon protein r	---	---	1.15	0.20	1.51	0.1753296	0.4144032	-5.45	FALSE
257561_at	hypothetical protein predicted by	APUM25	AT3G24270	1.19	0.26	1.51	0.1754667	0.4146052	-5.45	FALSE
257213_at	mitochondrial NAD-dependent m	---	AT3G15020	1.35	0.43	1.51	0.1754608	0.4146052	-5.45	FALSE
253525_at	predicted protein ; supported by	---	AT4G31330	-1.21	-0.27	-1.51	0.1754756	0.4146052	-5.45	FALSE
256151_at	multispanning membrane protei	---	AT1G55130	-1.28	-0.35	-1.51	0.1755455	0.4147274	-5.45	FALSE
250818_at	Expressed protein ; supported by	ALA1	AT5G04930	1.27	0.34	1.51	0.1756122	0.414842	-5.45	FALSE
254225_at	putative major latex protein majo	---	AT4G23670	2.13	1.09	1.51	0.1756843	0.4149693	-5.45	FALSE
249991_at	zinc finger -like protein zinc finge	---	AT5G18550	1.18	0.24	1.51	0.1757823	0.4150466	-5.45	FALSE

250774_at	ATP-dependent RNA helicase-lik	---	AT5G05450	-1.27	-0.34	-1.51	0.1758344	0.4150466	-5.45	FALSE
245132_at	hypothetical protein predicted by	---	AT2G45320	-1.29	-0.37	-1.51	0.1758444	0.4150466	-5.45	FALSE
247985_at	putative protein contains similarit	---	AT5G56790	-1.22	-0.28	-1.51	0.1758115	0.4150466	-5.45	FALSE
261180_at	hypothetical protein predicted by	---	---	1.18	0.24	1.51	0.1758162	0.4150466	-5.45	FALSE
267505_at	putative cytochrome P450 ;supp	CYP76C1	AT2G45560	-1.22	-0.29	-1.51	0.1758209	0.4150466	-5.45	FALSE
253893_at	putative protein hypothetical pro	---	AT4G27390	-1.27	-0.34	-1.51	0.1758327	0.4150466	-5.45	FALSE
253512_at	putative protein protein phospha	WIN2	AT4G31750	1.19	0.25	1.51	0.1758948	0.4150798	-5.45	FALSE
266420_at	putative RNA-binding protein ; s	---	AT2G38610	-1.15	-0.20	-1.51	0.1758911	0.4150798	-5.45	FALSE
259420_at	hypothetical protein similar to put	---	AT1G13900	1.13	0.18	1.51	0.1760706	0.4150855	-5.45	FALSE
247856_at	receptor-like protein kinase	---	AT5G58300	-1.27	-0.34	-1.51	0.1759383	0.4150855	-5.45	FALSE
250764_at	putative protein similar to unknov	---	AT5G05960	3.65	1.87	1.51	0.1760489	0.4150855	-5.45	FALSE
251716_at	anthranilate synthase alpha-1 ch	---	AT3G55870	1.17	0.23	1.51	0.1759801	0.4150855	-5.45	FALSE
251904_at	Machado-Joseph disease MJD1	---	AT3G54130	1.26	0.33	1.51	0.1760789	0.4150855	-5.45	FALSE
250587_at	putative protein contains similarit	---	AT5G07640	1.17	0.23	1.51	0.1760507	0.4150855	-5.45	FALSE
255234_at	contains similarity to Medicago tr	---	AT4G05500	1.19	0.25	1.51	0.1760644	0.4150855	-5.45	FALSE
249060_at	putative protein similar to unknov	VPS2.2	AT5G44560	-1.16	-0.21	-1.51	0.1760792	0.4150855	-5.45	FALSE
263088_at	putative replication protein A1	---	---	-1.17	-0.22	-1.51	0.1760063	0.4150855	-5.45	FALSE
256540_at	polyprotein, putative similar to p	---	---	-1.15	-0.21	-1.51	0.1759276	0.4150855	-5.45	FALSE
258393_at	unknown protein similar to unkno	---	AT3G15480	-1.32	-0.40	-1.51	0.1761207	0.4150974	-5.45	FALSE
254635_at	extensin-like protein extensin-lik	---	AT4G18670	1.21	0.28	1.51	0.176109	0.4150974	-5.45	TRUE
250810_at	putative protein contains similarit	---	AT5G05090	-1.33	-0.42	-1.51	0.176168	0.4151661	-5.45	FALSE
262342_at	unknown protein similar to hypot	---	AT1G64150	-1.34	-0.43	-1.51	0.176246	0.4153069	-5.45	FALSE
246238_at	sugar transporter like protein	---	AT4G36670	1.55	0.63	1.51	0.1763003	0.415392	-5.45	FALSE
254406_at	putative transposable element re	---	---	1.16	0.21	1.51	0.176395	0.4155635	-5.45	FALSE
263762_at	putative kinesin heavy chain ; su	---	AT2G21380	-1.32	-0.40	-1.51	0.1764095	0.4155635	-5.45	FALSE
250792_at	unknown protein ;supported by f	---	AT5G05520	-1.19	-0.25	-1.51	0.1766668	0.4161249	-5.46	FALSE
255816_at	unknown protein ;supported by f	GLTP1	AT2G33470	-1.15	-0.21	-1.51	0.1767026	0.4161249	-5.46	FALSE
249662_s_a	putative protein hypothetical prot	---	AT5G36680 /	1.14	0.19	1.51	0.1766917	0.4161249	-5.46	FALSE
266174_at	hypothetical protein predicted by	---	AT2G02440	1.14	0.19	1.51	0.1767209	0.416125	-5.46	FALSE
247878_at	unknown protein	---	AT5G57760	-4.24	-2.08	-1.51	0.176747	0.4161435	-5.46	FALSE
250349_at	putative receptor - like kinase re	---	AT5G12000	1.20	0.26	1.51	0.1768067	0.4161669	-5.46	FALSE
248983_at	ras-related GTP-binding protein I	RHA1	AT5G45130	1.17	0.22	1.51	0.1768117	0.4161669	-5.46	FALSE
249425_at	putative protein 5'-AMP-ACTIVA	---	AT5G39790	-1.42	-0.50	-1.51	0.1768038	0.4161669	-5.46	FALSE
257797_at	hypothetical protein contains Pfa	---	AT3G15940	1.21	0.27	1.51	0.1768632	0.4162452	-5.46	FALSE
252855_at	putative protein alpha-amino-ep	AGT2	AT4G39660	-1.24	-0.31	-1.51	0.176985	0.4164521	-5.46	FALSE

248169_at	ankyrin-repeat-containing protein	ANK	AT5G54610	2.99	1.58	1.51	0.1769876	0.4164521	-5.46	FALSE
265893_at	putative disease resistance prote	---	AT2G15040 ///	1.57	0.65	1.51	0.1770853	0.4166339	-5.46	FALSE
246678_at	putative protein predicted replica	---	---	-1.20	-0.27	-1.51	0.1771014	0.4166339	-5.46	FALSE
261843_at	unknown protein	---	AT1G16180	1.17	0.22	1.51	0.1771225	0.4166406	-5.46	FALSE
249332_at	putative protein similar to unknov	---	AT5G40980	1.22	0.29	1.51	0.1771437	0.4166476	-5.46	FALSE
253247_at	Homeodomain - like protein simi	BLH6	AT4G34610	1.35	0.43	1.51	0.1772002	0.4166514	-5.46	FALSE
251957_at	putative protein predicted protein	---	AT3G53690	-1.20	-0.27	-1.51	0.1771951	0.4166514	-5.46	FALSE
265077_at	hypothetical protein similar to RI	---	AT1G55530	1.28	0.36	1.51	0.1771656	0.4166514	-5.46	FALSE
255808_at	putative protein predicted protein	---	AT4G10280	-1.20	-0.26	-1.51	0.1773356	0.4169269	-5.46	FALSE
266846_at	unknown protein	---	AT2G25970	-1.16	-0.22	-1.51	0.177507	0.4172655	-5.46	FALSE
260953_at	transcriptional activator RF2a, p	---	AT1G06070	-1.20	-0.26	-1.51	0.1775162	0.4172655	-5.46	FALSE
250319_at	putative protein strong similarity	---	AT5G12120	-1.15	-0.20	-1.51	0.1775389	0.4172759	-5.46	FALSE
260353_at	putative nitrilase-associated prot	SP1L2	AT1G69230	1.22	0.29	1.51	0.1775608	0.4172843	-5.46	FALSE
246014_at	putative protein	---	AT5G10680	1.18	0.24	1.51	0.1776788	0.4173895	-5.46	FALSE
257958_at	unknown protein similar to diseas	---	AT3G25510	1.21	0.28	1.51	0.177663	0.4173895	-5.46	FALSE
248769_at	putative protein strong similarity	---	AT5G47730	1.78	0.83	1.51	0.1776602	0.4173895	-5.46	FALSE
260452_at	putative SRF-type transcription fa	---	AT1G72350	1.30	0.38	1.51	0.1776392	0.4173895	-5.46	FALSE
249985_at	Ser/Thr specific protein kinase -	---	AT5G18500	1.23	0.30	1.51	0.1776989	0.4173939	-5.46	TRUE
251878_at	putative protein predicted protein	---	AT3G54310	1.15	0.20	1.50	0.177808	0.4175368	-5.46	FALSE
253770_at	protein kinase ADK1-like protein	CKL6	AT4G28540	1.16	0.22	1.50	0.1778253	0.4175368	-5.46	FALSE
256344_at	C2H2-type zinc finger protein, p	TFIIIA	AT1G72050	-1.22	-0.29	-1.50	0.177833	0.4175368	-5.46	FALSE
264754_at	receptor kinase, putative similar	---	AT1G61400	1.21	0.27	1.50	0.1777983	0.4175368	-5.46	FALSE
257905_at	unknown protein	---	---	1.21	0.28	1.50	0.1778927	0.417634	-5.46	FALSE
251927_at	hypothetical protein ER6 protein	---	AT3G53990	1.17	0.22	1.50	0.1779395	0.4176791	-5.46	FALSE
255497_at	hypothetical protein similar to A.	UNE12	AT4G02590	1.18	0.24	1.50	0.1779485	0.4176791	-5.46	FALSE
250835_at	putative protein various predicte	DME	AT5G04560	1.22	0.29	1.50	0.1780587	0.4178603	-5.46	FALSE
255503_at	contains similarity to a protein ki	---	AT4G02420	1.83	0.87	1.50	0.1780624	0.4178603	-5.46	FALSE
250316_at	cystatin (emb|CAA03929.1) ; su	ATCYS1	AT5G12140	1.18	0.24	1.50	0.1781575	0.418015	-5.46	FALSE
250416_at	putative protein predicted protein	---	AT5G11220	1.18	0.24	1.50	0.1781649	0.418015	-5.46	FALSE
266086_at	putative Na+-dependent inorgani	PHT4;2	AT2G38060	1.19	0.26	1.50	0.178189	0.4180269	-5.46	FALSE
256388_at	unknown protein	---	AT3G06180	-1.19	-0.25	-1.50	0.1782174	0.4180269	-5.46	FALSE
246698_at	putative protein	---	---	1.16	0.22	1.50	0.178225	0.4180269	-5.46	FALSE
253864_at	hypothetical protein	---	AT4G27460	1.23	0.30	1.50	0.1782922	0.4181416	-5.46	FALSE
262705_at	putative wall-associated kinase s	---	AT1G16260	1.86	0.89	1.50	0.1783485	0.4182307	-5.46	FALSE
266613_at	similar to gibberellin-regulated pr	---	AT2G14900	4.86	2.28	1.50	0.1783845	0.418272	-5.46	FALSE

247293_at	putative protein similar to unknov	---	AT5G64510	1.77	0.83	1.50	0.1785023	0.4185053	-5.47	FALSE
255929_at	hypothetical protein predicted by	---	AT1G12650	-1.22	-0.28	-1.50	0.1786659	0.4187189	-5.47	FALSE
261560_at	acyl CoA thioesterase, putative	---	AT1G01710	1.15	0.20	1.50	0.1786124	0.4187189	-5.47	FALSE
252390_at	Expressed protein ; supported by	---	AT3G47836	-1.21	-0.28	-1.50	0.1786668	0.4187189	-5.47	FALSE
260907_at	hypothetical protein predicted by	---	AT1G02570	-1.16	-0.22	-1.50	0.1786497	0.4187189	-5.47	FALSE
247182_at	putative protein contains similarit	HB25	AT5G65410	-1.22	-0.28	-1.50	0.1787177	0.4187243	-5.47	FALSE
257408_at	unknown protein similar to A. tha	SON1	AT2G17310	1.21	0.27	1.50	0.1786904	0.4187243	-5.47	FALSE
263895_at	hypothetical protein predicted by	---	AT2G21920	1.14	0.20	1.50	0.1787242	0.4187243	-5.47	FALSE
252389_at	Expressed protein ; supported by	---	AT3G47833	1.38	0.46	1.50	0.1788007	0.4188605	-5.47	FALSE
261222_at	anter-specific proline-rich protei	---	AT1G20120	-1.17	-0.22	-1.50	0.1788281	0.4188815	-5.47	FALSE
263421_at	unknown protein ;supported by f	EXL5	AT2G17230	1.49	0.58	1.50	0.1788815	0.4189637	-5.47	TRUE
263987_at	putative lipase ; supported by cD	---	AT2G42690	-1.27	-0.34	-1.50	0.1789254	0.4189804	-5.47	FALSE
261029_at	unknown protein	---	AT1G17330	1.25	0.32	1.50	0.1789087	0.4189804	-5.47	FALSE
261367_at	protein kinase, putative similar t	---	AT1G53080	2.48	1.31	1.50	0.1790751	0.4192414	-5.47	FALSE
260117_at	AIG1-like protein similar to AIG1	---	AT1G33950	1.13	0.18	1.50	0.1790738	0.4192414	-5.47	FALSE
245446_at	enoyl-CoA hydratase	---	AT4G16800	-1.19	-0.25	-1.50	0.179092	0.4192414	-5.47	FALSE
259135_at	hypothetical protein predicted by	RAD9	AT3G05480	1.28	0.36	1.50	0.1791659	0.4193715	-5.47	FALSE
258670_at	unknown protein	---	AT3G08810	1.23	0.30	1.50	0.1792108	0.4194335	-5.47	FALSE
253625_at	signal recognition particle recep	---	AT4G30600	1.16	0.22	1.50	0.1792536	0.4194905	-5.47	FALSE
248436_at	putative protein contains similarit	---	AT5G51220	-1.18	-0.23	-1.50	0.1794289	0.4198578	-5.47	FALSE
262761_at	unknown protein ESTs gb|AA39	---	AT1G10720	1.27	0.35	1.50	0.179466	0.4199015	-5.47	FALSE
251945_at	dTDP-glucose 4-6-dehydratase	UXS1	AT3G53520	1.18	0.24	1.50	0.1796147	0.4199497	-5.47	FALSE
259321_at	unknown protein	GAUT13	AT3G01040	1.26	0.33	1.50	0.1796547	0.4199497	-5.47	FALSE
265375_at	unknown protein ;supported by f	VPS2.1	AT2G06530	1.24	0.31	1.50	0.1796201	0.4199497	-5.47	FALSE
257080_at	unknown protein	---	AT3G15240	1.14	0.19	1.50	0.1796436	0.4199497	-5.47	FALSE
250466_at	putative protein TETRATRICOP	---	AT5G10090	1.16	0.21	1.50	0.1796891	0.4199497	-5.47	FALSE
259391_s_a	delta 9 desaturase, putative sim	---	AT1G06350 ///	1.19	0.24	1.50	0.1795455	0.4199497	-5.47	FALSE
260670_at	Expressed protein ; supported by	NFD5	AT1G19520	-1.30	-0.38	-1.50	0.1796578	0.4199497	-5.47	FALSE
256493_at	hypothetical protein predicted by	---	AT1G31600	-1.22	-0.29	-1.50	0.179575	0.4199497	-5.47	FALSE
258382_at	hypothetical protein	UBC25	AT3G15355	1.25	0.32	1.50	0.1796236	0.4199497	-5.47	FALSE
263549_at	unknown protein	MEE3	AT2G21650	-2.04	-1.03	-1.50	0.1796869	0.4199497	-5.47	FALSE
265064_at	hypothetical protein contains sim	ENT7	AT1G61630	1.30	0.38	1.50	0.1796736	0.4199497	-5.47	FALSE
260958_at	unknown protein identical to unkr	---	AT1G06060	-1.21	-0.27	-1.50	0.1798033	0.4201734	-5.47	FALSE
246315_at	hypothetical protein	---	AT3G56870	-1.32	-0.40	-1.50	0.1798502	0.4202401	-5.47	FALSE
252491_at	disease resistance protein RPP8	---	AT3G46730	-1.15	-0.20	-1.50	0.1798961	0.4203042	-5.47	FALSE

259991_at	putative S-adenosyl-L-methionin	---	AT1G68040	1.18	0.24	1.50	0.1799233	0.4203248	-5.47	FALSE
249793_at	putative protein contains similarit	---	AT5G23680	-1.28	-0.35	-1.50	0.1799913	0.4203692	-5.47	FALSE
245032_at	En/Spm-like transposon protein r	---	---	1.29	0.36	1.50	0.1800055	0.4203692	-5.47	FALSE
262460_s_a	fructokinase, putative similar to f	---	AT1G06030 /A	-1.17	-0.22	-1.50	0.1799796	0.4203692	-5.47	FALSE
263367_at	putative retroelement pol polypro	---	---	1.21	0.27	1.50	0.1800161	0.4203692	-5.47	FALSE
261882_at	GTP-binding protein, putative sir	PDE318	AT1G80770	-1.18	-0.24	-1.50	0.1800629	0.4204356	-5.47	FALSE
260878_at	scarecrow-like 1 identical to scar	SCL1	AT1G21450	1.27	0.35	1.50	0.1802288	0.4207798	-5.47	FALSE
247722_at	GTP-binding protein rab11 - like	ATRABA2D	AT5G59150	1.19	0.25	1.49	0.1803067	0.4209187	-5.47	FALSE
261959_s_a	polyprotein, putative similar to p	---	---	1.21	0.28	1.49	0.1803962	0.4210846	-5.47	FALSE
249248_at	unknown protein	---	AT5G42320	1.21	0.28	1.49	0.1804958	0.4211876	-5.47	FALSE
261171_at	unknown protein	---	AT1G04880	1.18	0.23	1.49	0.1804878	0.4211876	-5.47	FALSE
263227_at	Expressed protein ; supported by	---	AT1G30750	1.22	0.28	1.49	0.1804828	0.4211876	-5.47	FALSE
247454_at	unknown protein	---	AT5G62440	-1.39	-0.47	-1.49	0.1805154	0.4211903	-5.48	FALSE
245650_at	F5A9.20 similar to S-adenosyl-L-	---	AT1G24735	1.21	0.27	1.49	0.180622	0.4212767	-5.48	FALSE
247373_at	unknown protein ;supported by f	---	AT5G63150	-1.22	-0.29	-1.49	0.1805758	0.4212767	-5.48	FALSE
265146_at	putative glucosyl transferase	---	AT1G51210	1.38	0.46	1.49	0.1806263	0.4212767	-5.48	FALSE
258005_at	cysteine proteinase contains sim	---	AT3G19390	1.95	0.96	1.49	0.1805955	0.4212767	-5.48	FALSE
253148_at	cyclin 2b protein	CYCB2;2	AT4G35620	1.22	0.28	1.49	0.1807023	0.4214108	-5.48	FALSE
246212_at	putative protein ; supported by cl	SPT	AT4G36930	-1.68	-0.75	-1.49	0.1807589	0.4214137	-5.48	TRUE
263291_at	unknown protein	---	AT2G10920	-1.18	-0.24	-1.49	0.1807445	0.4214137	-5.48	FALSE
254197_at	trehalase - like protein trehalase	TRE1	AT4G24040	1.29	0.37	1.49	0.1807549	0.4214137	-5.48	FALSE
245238_at	putative protein similarity to cyto	ACYB-2	AT4G25570	-1.23	-0.30	-1.49	0.1807976	0.4214598	-5.48	FALSE
254494_at	putative protein C65DMY30S	QRT3	AT4G20050	1.16	0.21	1.49	0.1808157	0.4214598	-5.48	FALSE
263541_at	unknown protein ; supported by	---	AT2G24860	1.18	0.24	1.49	0.1809017	0.4214842	-5.48	FALSE
265275_at	En/Spm-like transposon protein r	---	AT2G28440	1.35	0.43	1.49	0.1808782	0.4214842	-5.48	FALSE
254853_at	putative DNA-binding protein AT	---	AT4G12080	-1.25	-0.32	-1.49	0.1808866	0.4214842	-5.48	FALSE
261990_at	unknown protein	---	AT1G33660	1.18	0.24	1.49	0.1809185	0.4214842	-5.48	FALSE
264762_at	receptor kinase, putative similar	---	AT1G61460	1.21	0.28	1.49	0.1809082	0.4214842	-5.48	FALSE
258932_at	hypothetical protein predicted by	PAP16	AT3G10150	1.17	0.23	1.49	0.1809414	0.4214945	-5.48	FALSE
255072_at	outer envelope membrane prote	TOC75-IV	AT4G09080	-1.21	-0.28	-1.49	0.1810712	0.4217537	-5.48	FALSE
259270_at	putative porin similar to outer mit	VDAC1	AT3G01280	1.21	0.28	1.49	0.1810916	0.4217581	-5.48	FALSE
256715_at	hypothetical protein predicted by	MEE18	AT2G34090	1.29	0.37	1.49	0.1811427	0.421791	-5.48	FALSE
262702_at	putative protein phosphatase 2C	---	AT1G16220	1.20	0.26	1.49	0.1811293	0.421791	-5.48	FALSE
260087_at	hypothetical protein predicted by	---	AT1G73200	1.26	0.33	1.49	0.1811819	0.4218331	-5.48	FALSE
262903_at	NADPH-dependent codeinone r	---	AT1G59950	-2.02	-1.02	-1.49	0.1812348	0.4218331	-5.48	FALSE

253986_at	putative protein predicted protei	---	AT4G26210	-1.34	-0.42	-1.49	0.1812039	0.4218331	-5.48	FALSE
250964_at	putative protein various predicte	---	AT5G03010	1.23	0.30	1.49	0.1812204	0.4218331	-5.48	FALSE
254260_at	hypothetical protein	---	AT4G23440	1.30	0.38	1.49	0.1813534	0.4220537	-5.48	TRUE
266053_at	unknown protein	---	AT2G40730	1.20	0.26	1.49	0.1813918	0.4220537	-5.48	FALSE
252195_at	putative protein various predicte	---	AT3G50190	1.21	0.28	1.49	0.1814035	0.4220537	-5.48	FALSE
264595_at	putative vesicle-associated mem	VAMP721	AT1G04750	-1.26	-0.33	-1.49	0.1813837	0.4220537	-5.48	FALSE
256083_at	hypothetical protein predicted by	---	AT1G20730	1.14	0.20	1.49	0.181483	0.422126	-5.48	FALSE
257596_at	unknown protein	---	AT3G24760	-1.21	-0.27	-1.49	0.1815052	0.422126	-5.48	FALSE
249319_s_a	putative protein similar to unknov	---	AT5G40880 ///	1.22	0.28	1.49	0.1815086	0.422126	-5.48	FALSE
258958_at	vacuolar membrane ATPase sub	VMA10	AT3G01390	-1.27	-0.35	-1.49	0.1815038	0.422126	-5.48	FALSE
254492_at	endomembrane-associated prote	PCAP1	AT4G20260	-1.20	-0.26	-1.49	0.1815572	0.4221436	-5.48	FALSE
264490_at	putative protein import receptor	TOM20-2	AT1G27390	-1.33	-0.41	-1.49	0.1815717	0.4221436	-5.48	FALSE
265881_at	hypothetical protein predicted by	---	AT2G42480	1.20	0.27	1.49	0.1815621	0.4221436	-5.48	FALSE
261129_at	tubulin alpha-2/alpha-4 chain ide	TUA4	AT1G04820	1.55	0.63	1.49	0.1818445	0.4222884	-5.48	TRUE
253480_at	putative protein ENOD16, Medic	---	AT4G31840	-1.17	-0.23	-1.49	0.1817648	0.4222884	-5.48	FALSE
247854_at	contains similarity to phosphoest	---	AT5G58200	-1.20	-0.26	-1.49	0.1819179	0.4222884	-5.48	FALSE
250216_at	unknown protein	---	AT5G14090	1.24	0.31	1.49	0.1818787	0.4222884	-5.48	FALSE
255810_at	hypothetical protein ; supported b	---	AT4G10140	1.18	0.24	1.49	0.1818771	0.4222884	-5.48	FALSE
250918_at	putative protein proline-rich prot	---	AT5G03610	2.10	1.07	1.49	0.181743	0.4222884	-5.48	FALSE
250648_at	late embryogenesis abundant pro	---	AT5G06760	1.20	0.26	1.49	0.1816783	0.4222884	-5.48	FALSE
256743_at	Expressed protein ; supported by	---	AT3G29370	-1.61	-0.69	-1.49	0.1818748	0.4222884	-5.48	FALSE
263425_at	putative preprotein translocase S	EMB2289	AT2G31530	-1.21	-0.28	-1.49	0.1816901	0.4222884	-5.48	FALSE
257978_at	putative serine/threonine protein	ATNEK5	AT3G20860	1.73	0.79	1.49	0.1817933	0.4222884	-5.48	FALSE
267002_s_a	putative photosystem II type I chl	LHB1B1	AT2G34420 ///	-1.14	-0.19	-1.49	0.1819487	0.4222884	-5.48	FALSE
249305_at	putative protein strong similarity t	---	AT5G41490	1.21	0.28	1.49	0.1817307	0.4222884	-5.48	FALSE
259926_at	putative DNA-3-methyladenine g	---	AT1G75090	-1.14	-0.19	-1.49	0.181946	0.4222884	-5.48	FALSE
258288_at	unknown protein	LSH4	---	1.42	0.50	1.49	0.1818879	0.4222884	-5.48	FALSE
261797_at	cation-chloride co-transporter, p	---	AT1G30455	-1.19	-0.26	-1.49	0.1819074	0.4222884	-5.48	FALSE
245493_at	hypothetical protein	---	---	-1.16	-0.21	-1.49	0.181814	0.4222884	-5.48	FALSE
252429_at	H-protein promoter binding factor	CDF3	AT3G47500	-1.30	-0.38	-1.49	0.1817907	0.4222884	-5.48	FALSE
250446_at	nucleoid DNA-binding protein cr	---	AT5G10770	1.37	0.45	1.49	0.1819847	0.4223289	-5.48	FALSE
255225_at	U3 snoRNP-associated -like pro	---	AT4G05410	-1.47	-0.56	-1.49	0.182069	0.4224815	-5.48	TRUE
246644_at	putative protein	---	AT5G35100	-1.28	-0.36	-1.49	0.1821416	0.4226071	-5.48	FALSE
266901_at	hypothetical protein predicted by	JAZ7	AT2G34600	1.66	0.73	1.49	0.1821946	0.422687	-5.48	FALSE
257226_at	hypothetical protein predicted by	---	AT3G27880	-1.56	-0.64	-1.49	0.1822674	0.422813	-5.48	FALSE

255652_at	putative protein	MEE47	AT4G00950	-1.69	-0.76	-1.49	0.1824263	0.4231384	-5.48	FALSE
246138_at	putative protein predicted protein	---	AT5G19870	1.14	0.19	1.49	0.1824534	0.4231582	-5.48	FALSE
259852_at	disulfide bond formation protein,	AERO1	AT1G72280	1.46	0.54	1.49	0.1825213	0.4232542	-5.48	FALSE
252513_at	putative protein KIAA0776 prote	---	AT3G46220	-1.18	-0.24	-1.49	0.1825493	0.4232542	-5.49	FALSE
253503_at	cytochrome P450-like protein cy	CYP82C3	AT4G31950	1.36	0.44	1.49	0.1825504	0.4232542	-5.49	FALSE
250031_at	transfactor-like protein ; support	MYR1	AT5G18240	-1.27	-0.35	-1.49	0.1826662	0.4234632	-5.49	FALSE
265106_s_a	putative membrane-associated s	---	AT1G62590 ///	1.15	0.20	1.49	0.1826962	0.4234632	-5.49	FALSE
266217_at	unknown protein	AT2G28830	---	1.16	0.22	1.49	0.1826948	0.4234632	-5.49	FALSE
258983_at	putative aminotransferase simila	---	AT3G08860	-1.71	-0.77	-1.48	0.1828317	0.4236265	-5.49	FALSE
250252_at	transporter-like protein ;supporte	ZIFL1	AT5G13750	1.80	0.85	1.48	0.1828376	0.4236265	-5.49	FALSE
252860_at	putative protein bZIP protein, Ar	---	AT4G39790	1.15	0.20	1.48	0.1828671	0.4236265	-5.49	FALSE
254308_at	putative protein snRNP assembl	---	AT4G22410	-1.18	-0.23	-1.48	0.182851	0.4236265	-5.49	FALSE
252250_at	putative protein predicted protei	---	AT3G49790	1.30	0.38	1.48	0.1828709	0.4236265	-5.49	FALSE
249013_at	receptor-like protein kinase	GSO2	AT5G44700	-1.14	-0.19	-1.48	0.1828781	0.4236265	-5.49	FALSE
255496_at	putative protein similar to plant n	BZO2H1	AT4G02640	-1.26	-0.34	-1.48	0.1829403	0.4237275	-5.49	FALSE
266425_at	putative strictosidine synthase	---	AT2G41300	1.20	0.26	1.48	0.1829626	0.4237361	-5.49	FALSE
263294_at	hypothetical protein predicted by	---	---	1.25	0.32	1.48	0.1829987	0.4237519	-5.49	FALSE
257375_at	unknown protein	---	AT2G38640	1.64	0.71	1.48	0.1830066	0.4237519	-5.49	FALSE
259023_at	unknown protein ; supported by	---	AT3G07510	-1.32	-0.41	-1.48	0.1830865	0.4238136	-5.49	FALSE
257752_at	hypothetical protein predicted by	---	AT3G18720	1.19	0.25	1.48	0.1830702	0.4238136	-5.49	FALSE
249516_s_a	myrosinase binding protein-like;	---	AT5G38540 ///	1.20	0.26	1.48	0.183089	0.4238136	-5.49	FALSE
245749_at	proline-rich protein, putative sim	---	AT1G51090	-1.67	-0.74	-1.48	0.1831654	0.4238186	-5.49	TRUE
247664_at	APETALA2 protein - like APETA	TOE2	AT5G60120	-1.18	-0.24	-1.48	0.1831353	0.4238186	-5.49	FALSE
258520_at	hypothetical protein predicted by	---	AT3G06710	-1.26	-0.33	-1.48	0.1831497	0.4238186	-5.49	FALSE
256362_at	hypothetical protein	---	AT1G66450	1.19	0.25	1.48	0.1831212	0.4238186	-5.49	FALSE
259448_at	hypothetical protein similar to tra	---	AT1G13790	-1.21	-0.27	-1.48	0.1831961	0.4238464	-5.49	FALSE
262926_s_a	receptor kinase, putative similar	ARK1	AT1G65790 ///	1.59	0.67	1.48	0.1832241	0.4238583	-5.49	TRUE
255643_at	hypothetical protein	---	AT4G00840	-1.17	-0.23	-1.48	0.1832383	0.4238583	-5.49	FALSE
260363_at	unknown protein similar to hypot	---	AT1G70550	-1.23	-0.30	-1.48	0.1832907	0.4239364	-5.49	FALSE
258792_at	hypothetical protein predicted by	---	AT3G04640	1.75	0.81	1.48	0.183315	0.4239497	-5.49	FALSE
245080_at	putative receptor-like protein kina	---	AT2G23300	1.26	0.34	1.48	0.1833404	0.4239653	-5.49	FALSE
257154_at	unknown protein ; supported by	---	AT3G27210	-1.24	-0.31	-1.48	0.1833869	0.423985	-5.49	TRUE
251742_at	putative protein kinase serine th	---	AT3G56050	-1.17	-0.23	-1.48	0.1834046	0.423985	-5.49	FALSE
245163_at	putative flavin-containing monoo	---	AT2G33230	1.23	0.30	1.48	0.183403	0.423985	-5.49	FALSE
247021_at	putative protein similar to unknov	---	AT5G67040	1.19	0.25	1.48	0.1834601	0.4240701	-5.49	FALSE

256390_at	putative MAP kinase similar to M	ATMKK8	AT3G06230	1.16	0.21	1.48	0.1834913	0.4240995	-5.49	FALSE
255673_at	Similar to receptor-like protein ki	RLK4	AT4G00340	1.18	0.24	1.48	0.1836814	0.4244528	-5.49	FALSE
264176_at	bZIP-like protein similar to bZIP	---	AT1G02110	-1.32	-0.40	-1.48	0.1836786	0.4244528	-5.49	FALSE
264692_at	DNA binding protein MybSt1, pu	---	AT1G70000	-1.23	-0.30	-1.48	0.1837331	0.4244862	-5.49	FALSE
254653_at	polygalacturonase-like protein e	---	AT4G18180	-1.13	-0.18	-1.48	0.1837151	0.4244862	-5.49	FALSE
252681_at	NAC domain -like protein Tobac	anac061	AT3G44350	1.22	0.28	1.48	0.1837697	0.4245278	-5.49	FALSE
254404_at	hypothetical protein	B70	AT4G21340	1.13	0.18	1.48	0.1838016	0.4245441	-5.49	FALSE
263943_at	putative mitochondrial carrier pro	---	AT2G35800	-1.22	-0.28	-1.48	0.183814	0.4245441	-5.49	FALSE
258164_at	surfeit 1 identical to GB:AAF196(	SURF1	AT3G17910	-1.30	-0.38	-1.48	0.1839483	0.4248112	-5.49	FALSE
248970_at	urea active transporter-like prote	---	AT5G45380	1.50	0.58	1.48	0.1840007	0.4248427	-5.49	FALSE
248693_at	regulator of chromosome conder	---	AT5G48330	-1.28	-0.36	-1.48	0.1840396	0.4248427	-5.49	FALSE
248682_at	cytochrome b5 (dbj|BAA74840.1	CB5-D	AT5G48810	-1.17	-0.23	-1.48	0.184055	0.4248427	-5.49	FALSE
252233_at	AtMYB84 ;supported by full-leng	MYB84	AT3G49690	-1.20	-0.27	-1.48	0.1840497	0.4248427	-5.49	FALSE
252062_at	hypothetical protein KIAA0253 p	---	AT3G52640	-1.25	-0.33	-1.48	0.1840009	0.4248427	-5.49	FALSE
255589_s_a	hypothetical protein	---	AT4G01590 ///	-1.28	-0.35	-1.48	0.184119	0.4249472	-5.49	FALSE
257084_at	unknown protein	---	AT3G20620	1.30	0.38	1.48	0.1841842	0.4250548	-5.49	FALSE
256379_at	hypothetical protein predicted by	---	AT1G66840	-1.27	-0.34	-1.48	0.1842318	0.4251217	-5.49	FALSE
251313_at	putative protein several hypothet	---	AT3G61360	-1.19	-0.25	-1.48	0.184314	0.4252665	-5.49	FALSE
267343_at	hypothetical protein predicted by	---	AT2G44260	2.32	1.21	1.48	0.1843319	0.4252665	-5.49	FALSE
264674_at	Expressed protein ; supported by	POLD4	AT1G09815	1.20	0.26	1.48	0.1844191	0.4253817	-5.49	FALSE
265925_at	hypothetical protein predicted by	---	AT2G18610	1.17	0.23	1.48	0.1844066	0.4253817	-5.49	FALSE
247031_at	UDP-glucuronyltransferase-like p	---	AT5G67230	-1.28	-0.35	-1.48	0.1844426	0.425386	-5.49	FALSE
261143_at	unknown protein	ATPUP14	AT1G19770	1.36	0.44	1.48	0.1844583	0.425386	-5.49	FALSE
256308_s_a	ABC transporter, putative contai	ATMRP13	AT1G30410 ///	-1.33	-0.41	-1.48	0.1845201	0.4254268	-5.49	FALSE
257742_at	hypothetical protein predicted by	SDH2-1	AT3G27380	1.18	0.24	1.48	0.1845506	0.4254268	-5.49	FALSE
256291_at	protein kinase, putative contains	AtNek7	AT3G12200	-1.21	-0.28	-1.48	0.184506	0.4254268	-5.49	FALSE
253686_at	putative protein predicted protei	---	AT4G29750	-1.21	-0.28	-1.48	0.184544	0.4254268	-5.49	FALSE
247737_at	putative protein various predicte	---	AT5G59200	-1.13	-0.18	-1.48	0.1845734	0.4254366	-5.49	FALSE
252152_at	putative protein several hypothet	---	AT3G51350	1.17	0.22	1.48	0.1846262	0.4254722	-5.50	FALSE
252570_at	isovaleryl-CoA-dehydrogenase p	IVD	AT3G45300	1.44	0.53	1.48	0.1846118	0.4254722	-5.50	FALSE
255339_at	hypothetical protein similar to A.	---	AT4G04480	1.38	0.47	1.48	0.1846738	0.425539	-5.50	FALSE
265283_at	unknown protein predicted by ge	MUR3	AT2G20370	1.28	0.36	1.48	0.1848412	0.4258387	-5.50	FALSE
258035_at	putative Ca2+-transporting ATPa	ACA9	AT3G21180	1.20	0.27	1.48	0.1848256	0.4258387	-5.50	FALSE
267238_at	unknown protein ;supported by f	---	AT2G44130	2.02	1.01	1.48	0.1849094	0.4259527	-5.50	FALSE
261516_at	hypoxanthine ribosyl transferase	---	AT1G71750	-1.17	-0.22	-1.48	0.1850215	0.4261679	-5.50	FALSE

255103_at	putative phosphoglyceride trans	---	AT4G08690	1.17	0.23	1.48	0.1851428	0.4262752	-5.50	FALSE
251724_at	putative protein	---	AT3G56250	-1.19	-0.25	-1.48	0.1851354	0.4262752	-5.50	FALSE
252928_at	putative protein more than 30 pr	---	AT4G38940	1.40	0.49	1.48	0.1851151	0.4262752	-5.50	FALSE
266972_at	40S ribosomal protein S15A	---	AT2G39590	-1.16	-0.22	-1.48	0.1851159	0.4262752	-5.50	FALSE
252038_at	gamma response I protein ; sup	---	AT3G52120	1.25	0.32	1.48	0.1851661	0.4262856	-5.50	FALSE
263290_at	unknown protein	---	AT2G10930	1.14	0.19	1.48	0.1852102	0.4263442	-5.50	FALSE
253120_at	putative protein phospholipase D	PLDDELTA	AT4G35790	-1.25	-0.32	-1.48	0.1853509	0.4266251	-5.50	FALSE
259323_at	unknown protein	---	AT3G05280	-1.13	-0.18	-1.48	0.1853914	0.4266751	-5.50	FALSE
256281_at	myb-family transcription factor, p	TRFL9	AT3G12560	1.23	0.29	1.47	0.1854771	0.4266904	-5.50	FALSE
267507_at	putative ribosomal protein S27 ;	---	AT2G45710	-1.29	-0.37	-1.47	0.1854804	0.4266904	-5.50	FALSE
258977_s_a	putative aspartate kinase similar	AK3	AT3G02020 /	-1.30	-0.38	-1.47	0.1854613	0.4266904	-5.50	FALSE
249085_at	putative protein similar to unknov	---	AT5G44170	-1.20	-0.26	-1.47	0.1854915	0.4266904	-5.50	FALSE
256762_at	Expressed protein ; supported by	IDL1	AT3G25655	2.37	1.25	1.47	0.1854727	0.4266904	-5.50	FALSE
256734_at	unknown protein	RIK	AT3G29390	1.17	0.22	1.47	0.1855566	0.4267539	-5.50	FALSE
265339_at	putative inorganic pyrophosphata	AtPPa2	AT2G18230	-1.34	-0.42	-1.47	0.1855459	0.4267539	-5.50	FALSE
245632_at	unknown protein contains similar	ATRBL10	AT1G25290	-1.18	-0.24	-1.47	0.1856216	0.4268398	-5.50	FALSE
262143_at	unknown protein	---	AT1G52630	-1.19	-0.26	-1.47	0.1856408	0.4268398	-5.50	FALSE
249453_at	v-SNARE AtVTI1a	SGR4	AT5G39510	-1.15	-0.20	-1.47	0.1856501	0.4268398	-5.50	FALSE
253383_at	putative protein ;supported by fu	---	AT4G32900	-1.28	-0.35	-1.47	0.1856941	0.4268981	-5.50	FALSE
253265_at	putative protein RING-finger pro	---	AT4G34040	-1.15	-0.20	-1.47	0.1857428	0.4269331	-5.50	FALSE
265420_s_a	hypothetical protein predicted by	BRX	AT1G31880 /	-1.26	-0.33	-1.47	0.1857468	0.4269331	-5.50	FALSE
262731_at	hypothetical protein similar to gb	MC8	AT1G16420	3.40	1.77	1.47	0.1857963	0.426961	-5.50	FALSE
245282_at	hypothetical protein ; supported b	---	AT4G14990	1.24	0.31	1.47	0.1857908	0.426961	-5.50	FALSE
265662_at	putative C2H2-type zinc finger pr	FZF	AT2G24500	-1.25	-0.32	-1.47	0.1858204	0.4269732	-5.50	FALSE
264658_at	hypothetical protein similar to LG	---	AT1G09910	-1.19	-0.25	-1.47	0.1858403	0.426976	-5.50	FALSE
267440_at	putative anthranilate N-hydroxyc	SHT	AT2G19070	-1.18	-0.24	-1.47	0.1859026	0.4270761	-5.50	FALSE
251201_at	putative protein predicted protei	---	AT3G63020	1.14	0.19	1.47	0.1859252	0.4270849	-5.50	FALSE
262326_at	hypothetical protein similar to put	---	AT1G64140 /	1.16	0.21	1.47	0.1860268	0.4271524	-5.50	FALSE
248228_at	unknown protein ;supported by f	---	AT5G53800	-1.25	-0.32	-1.47	0.1859932	0.4271524	-5.50	FALSE
265263_at	putative DNA binding protein	---	AT2G42940	1.17	0.23	1.47	0.1860052	0.4271524	-5.50	FALSE
255439_at	putative phospho-ser/thr phospha	BSL1	AT4G03080	-1.17	-0.22	-1.47	0.1860295	0.4271524	-5.50	FALSE
258437_at	unknown protein contains protein	---	AT3G16560	-1.30	-0.38	-1.47	0.1860503	0.4271573	-5.50	FALSE
248021_at	RuBisCO subunit binding-protein	---	AT5G56500	-1.37	-0.45	-1.47	0.1860893	0.4272038	-5.50	TRUE
265626_at	unknown protein ;supported by f	---	AT2G27260	1.20	0.26	1.47	0.1861644	0.4273331	-5.50	FALSE
246514_at	DNA-directed RNA polymerase (	---	AT5G15700	-1.30	-0.38	-1.47	0.1861891	0.4273468	-5.50	FALSE

252572_at	putative protein Mlo-h1 protein -	MLO3	AT3G45290	1.34	0.42	1.47	0.1863039	0.4273591	-5.50	TRUE
262031_x_a	hypothetical protein similar to put	---	---	1.18	0.24	1.47	0.186283	0.4273591	-5.50	FALSE
255001_at	AIG1-like protein AIG1 - Arabido	---	AT4G09930	1.24	0.30	1.47	0.1862459	0.4273591	-5.50	FALSE
257465_at	hypothetical protein predicted by	---	AT1G13040	-1.14	-0.19	-1.47	0.1862377	0.4273591	-5.50	FALSE
257349_at	unknown protein	---	AT2G30630	1.17	0.23	1.47	0.1863068	0.4273591	-5.50	FALSE
265327_at	unknown protein	---	AT2G18210	2.35	1.23	1.47	0.1862913	0.4273591	-5.50	FALSE
261745_at	unknown protein identical to unk	---	AT1G08500	1.53	0.61	1.47	0.1863266	0.4273616	-5.50	FALSE
260863_at	hypothetical protein predicted by	---	---	1.28	0.36	1.47	0.186373	0.4274249	-5.50	FALSE
254365_at	putative protein hypothetical pro	---	AT4G22030	1.18	0.23	1.47	0.1864535	0.4275666	-5.50	FALSE
259227_at	putative 3 exoribonuclease conta	---	AT3G07750	-1.56	-0.64	-1.47	0.1865607	0.4275974	-5.50	TRUE
248784_at	putative protein similar to unknov	---	AT5G47380	1.29	0.36	1.47	0.1865198	0.4275974	-5.50	FALSE
246234_at	putative protein	---	AT4G37280	-1.21	-0.27	-1.47	0.1865429	0.4275974	-5.50	FALSE
260333_at	putative polygalacturonase simila	---	AT1G70500	1.29	0.37	1.47	0.1865328	0.4275974	-5.50	FALSE
259637_at	protein disulfide isomerase prec	ATPDIL1-5	AT1G52260	-1.25	-0.33	-1.47	0.1865197	0.4275974	-5.50	FALSE
246719_at	homology to many predicted put	---	---	1.15	0.20	1.47	0.1866146	0.4276779	-5.50	FALSE
266426_x_a	hypothetical protein predicted by	---	AT2G07140	-1.35	-0.43	-1.47	0.1866377	0.4276867	-5.50	FALSE
248936_at	heat shock transcription factor	RHA1	AT5G45710	1.27	0.34	1.47	0.1866559	0.4276867	-5.50	FALSE
255444_at	LUMINIDEPENDENS protein ; s	LD	AT4G02560	-1.17	-0.23	-1.47	0.1867284	0.4277746	-5.51	FALSE
265121_at	similar to flavin-containing mono	FMO GS-O	AT1G62560	-1.36	-0.44	-1.47	0.1867318	0.4277746	-5.51	FALSE
252283_at	60S ribosomal protein L13 (BBC	---	AT3G48960	-1.18	-0.24	-1.47	0.1867546	0.4277839	-5.51	FALSE
261005_at	hypothetical protein similar to ret	---	AT1G26420	1.60	0.68	1.47	0.1867849	0.4278063	-5.51	TRUE
257966_at	unknown protein ;supported by f	---	AT3G19800	-1.27	-0.35	-1.47	0.1868019	0.4278063	-5.51	FALSE
264597_at	unknown protein	---	AT1G04620	-1.25	-0.32	-1.47	0.1868622	0.4279015	-5.51	FALSE
256047_at	hypothetical protein predicted by	---	AT1G07060	1.22	0.28	1.47	0.1868918	0.4279262	-5.51	FALSE
261070_at	disease resistance protein, puta	AtRLP1	AT1G07390	-1.23	-0.30	-1.47	0.1870002	0.4280976	-5.51	TRUE
249973_at	GPAA1 - like protein glycosylph	---	AT5G19130	-1.20	-0.27	-1.47	0.1870042	0.4280976	-5.51	FALSE
261450_s_a	O-methyltransferase, putative si	---	AT1G21110 //	3.40	1.77	1.47	0.1870273	0.4281075	-5.51	FALSE
244939_at	ribosomal protein S12 (trans-spli	---	---	-1.32	-0.40	-1.47	0.1872124	0.4284401	-5.51	FALSE
246047_at	putative protein predicted protei	---	---	1.18	0.24	1.47	0.1871977	0.4284401	-5.51	FALSE
264879_at	cotton fiber expressed protein, p	---	AT1G61260	1.48	0.56	1.47	0.1872289	0.4284401	-5.51	FALSE
265685_at	NAM (no apical meristem)-like pr	ANAC038	AT2G24430	1.22	0.29	1.47	0.1872936	0.4285452	-5.51	FALSE
248527_at	putative protein contains similarit	---	AT5G50740	-1.19	-0.25	-1.47	0.1873921	0.4287275	-5.51	FALSE
260787_at	Ring3-like bromodomain protein	GTE4	AT1G06230	-1.19	-0.25	-1.47	0.1874141	0.4287349	-5.51	FALSE
258964_at	putative 3-phosphoinositide-depe	---	AT3G10540	1.18	0.24	1.47	0.1875138	0.4287567	-5.51	FALSE
260463_at	DNA helicase isolog	RECQ4A	AT1G10930	1.14	0.19	1.47	0.1875634	0.4287567	-5.51	FALSE

258391_at	hypothetical protein predicted by	---	AT3G15420	-1.29	-0.37	-1.47	0.1875039	0.4287567	-5.51	FALSE
261802_at	hypothetical protein similar to hyp	---	AT1G30550	-1.19	-0.25	-1.47	0.187565	0.4287567	-5.51	FALSE
254908_at	putative protein other hypothetica	---	---	1.20	0.27	1.47	0.1874903	0.4287567	-5.51	FALSE
259048_at	DegP protease contains similarity	DegP7	AT3G03380	1.18	0.24	1.47	0.1874835	0.4287567	-5.51	FALSE
248567_at	putative protein contains similarit	---	AT5G49750	1.16	0.22	1.47	0.187574	0.4287567	-5.51	FALSE
265642_at	putative nitrilase ;supported by f	NLP1	AT2G27450	1.24	0.31	1.47	0.1875525	0.4287567	-5.51	FALSE
261411_at	histone H2B identical to GB:CAA	HTB1	AT1G07790	-1.29	-0.36	-1.47	0.187604	0.4287736	-5.51	FALSE
250456_at	26S proteasome p55 protein-like	EMB2107	AT5G09900	-1.25	-0.33	-1.47	0.187619	0.4287736	-5.51	FALSE
258481_at	putative phosphatidate phosphoh	LPP3	AT3G02600	-1.25	-0.32	-1.47	0.1876662	0.4288377	-5.51	FALSE
246716_s_a	putative protein	---	AT5G28910 ///	-1.14	-0.19	-1.47	0.1876847	0.4288377	-5.51	FALSE
260398_at	putative RNA-binding domain co	APUM23	AT1G72320	-1.29	-0.37	-1.47	0.1879168	0.4292822	-5.51	FALSE
258581_at	hypothetical protein predicted by	---	AT3G04160	-1.17	-0.22	-1.47	0.1879096	0.4292822	-5.51	FALSE
250299_at	putative esterase - like protein c	---	AT5G11910	-1.19	-0.25	-1.47	0.1880001	0.4293434	-5.51	FALSE
245843_at	unknown protein	---	AT1G26180	-1.20	-0.27	-1.47	0.1879824	0.4293434	-5.51	FALSE
248296_at	protochlorophyllide reductase; ox	---	AT5G53090	-1.24	-0.31	-1.47	0.1879649	0.4293434	-5.51	FALSE
266300_at	putative auxin transport protein ;	PIN4	AT2G01420	-1.78	-0.83	-1.46	0.1881055	0.4294847	-5.51	FALSE
257668_at	sugar transporter, putative simila	---	AT3G20460	1.27	0.35	1.46	0.1881091	0.4294847	-5.51	FALSE
257953_at	predicted protein supported by fu	PEX22	AT3G21865	-1.31	-0.39	-1.46	0.1881184	0.4294847	-5.51	FALSE
265012_at	putative b-keto acyl reductase si	KCR2	AT1G24470	1.18	0.24	1.46	0.1881853	0.4295514	-5.51	FALSE
248677_at	unknown protein	---	AT5G48860	1.19	0.25	1.46	0.1881694	0.4295514	-5.51	FALSE
259891_at	putative Eukaryotic initiation fact	---	AT1G72730	1.21	0.28	1.46	0.1883617	0.4298249	-5.51	FALSE
252299_at	putative protein various predicte	---	AT3G49150	1.21	0.28	1.46	0.1883365	0.4298249	-5.51	FALSE
259679_at	putative protein kinase Pfam HM	---	AT1G77720	-1.14	-0.19	-1.46	0.1883521	0.4298249	-5.51	FALSE
258897_at	unknown protein	---	AT3G05730	-3.10	-1.63	-1.46	0.1883957	0.4298499	-5.51	FALSE
252645_at	bZIP transcription factor -like pro	DPBF2	AT3G44460	1.19	0.25	1.46	0.1884103	0.4298499	-5.51	FALSE
245697_at	latex-abundant protein - like ;sup	AtMC9	AT5G04200	2.13	1.09	1.46	0.1884522	0.4299024	-5.51	FALSE
257357_at	hypothetical protein predicted by	---	AT2G41050	1.17	0.23	1.46	0.1884805	0.429924	-5.51	FALSE
246369_at	light repressible receptor protein	---	AT1G51910	1.23	0.30	1.46	0.1886727	0.4302334	-5.51	FALSE
247753_at	hexosyltransferase - like protein	---	AT5G59070	1.54	0.62	1.46	0.1886623	0.4302334	-5.51	FALSE
254662_at	putative protein phospho-N-acet	TRANS11	AT4G18270	-1.29	-0.37	-1.46	0.1886506	0.4302334	-5.51	FALSE
254088_at	putative protein snurportin1 m3(	---	AT4G24880	-1.26	-0.33	-1.46	0.1887305	0.430279	-5.51	FALSE
257957_at	wall-associated serine/threonine	---	AT3G25490	1.27	0.34	1.46	0.1887162	0.430279	-5.51	FALSE
255283_at	putative symbiosis-related protei	ATG8B	AT4G04620	-1.28	-0.36	-1.46	0.1888154	0.4303867	-5.51	TRUE
259868_at	thioredoxin-like protein similar to	ATY1	AT1G76760	1.17	0.22	1.46	0.1888127	0.4303867	-5.51	FALSE
259309_at	putative cyclin-dependent protein	---	AT3G05050	1.25	0.32	1.46	0.188873	0.4304626	-5.52	FALSE

257238_at	unknown protein ; supported by	---	AT3G17430	-1.26	-0.33	-1.46	0.1888963	0.4304626	-5.52	FALSE
258206_at	hypothetical protein predicted by	CID4	AT3G14010	-1.18	-0.24	-1.46	0.1889242	0.4304626	-5.52	FALSE
250872_at	putative protein SF16 protein, c	IQD12	AT5G03960	-1.17	-0.23	-1.46	0.1889072	0.4304626	-5.52	FALSE
247269_at	alternative oxidase 2 (sp|O22049	AOX2	AT5G64210	1.16	0.22	1.46	0.1889888	0.4305667	-5.52	FALSE
245865_at	hypothetical protein contains sim	---	AT1G58025	-1.17	-0.23	-1.46	0.189028	0.4306131	-5.52	FALSE
254273_at	glycoprotein endopeptidase - lik	---	AT4G22720	-1.28	-0.35	-1.46	0.1890472	0.4306138	-5.52	FALSE
263831_at	putative ferritin	ATFER4	AT2G40300	-1.30	-0.38	-1.46	0.1890867	0.4306607	-5.52	FALSE
263980_at	hypothetical protein predicted by	---	AT2G42770	-1.23	-0.30	-1.46	0.1891098	0.4306703	-5.52	FALSE
251524_at	3-isopropylmalate dehydratase-l	---	AT3G58980 /	-1.44	-0.53	-1.46	0.1891511	0.4307124	-5.52	FALSE
262528_at	H+-transporting ATPase AHA10	AHA10	AT1G17260	1.23	0.29	1.46	0.189166	0.4307124	-5.52	FALSE
247380_at	4-coumarate-CoA ligase-like pro	---	AT5G63380	-1.24	-0.31	-1.46	0.1893292	0.43074	-5.52	FALSE
247830_at	putative protein predicted protei	---	AT5G58530	-1.30	-0.38	-1.46	0.1892839	0.43074	-5.52	FALSE
245814_at	mitotic checkpoint protein, putati	---	AT1G49910	1.22	0.29	1.46	0.1892387	0.43074	-5.52	FALSE
265690_at	hypothetical protein predicted by	---	AT2G24320	1.23	0.29	1.46	0.1892918	0.43074	-5.52	FALSE
254903_at	H+-transporting ATPase chain E	TUF	AT4G11150	1.21	0.27	1.46	0.1892346	0.43074	-5.52	FALSE
249490_s_a	germin -like protein germin -like	---	AT5G39110 /	1.61	0.69	1.46	0.1893119	0.43074	-5.52	FALSE
253907_at	putative protein dihydrokaempfe	---	AT4G27250	1.25	0.32	1.46	0.1892521	0.43074	-5.52	FALSE
262317_at	unknown protein ;supported by f	EDA4	AT2G48140	-1.38	-0.46	-1.46	0.1893132	0.43074	-5.52	FALSE
262540_at	hypothetical protein predicted by	---	AT1G34260	1.31	0.39	1.46	0.1893621	0.430772	-5.52	FALSE
265861_at	hypothetical protein predicted by	---	AT2G01790	1.18	0.24	1.46	0.189444	0.4309151	-5.52	FALSE
263807_at	putative indole-3-glycerol phosph	---	AT2G04400	2.11	1.08	1.46	0.1896086	0.4312466	-5.52	FALSE
259662_at	Expressed protein ; supported by	HUB2	AT1G55250	-1.25	-0.32	-1.46	0.1896964	0.4314027	-5.52	FALSE
255534_at	CHP-rich hypothetical protein sin	---	AT4G02190	1.17	0.22	1.46	0.1897151	0.4314027	-5.52	FALSE
266689_at	hypothetical protein predicted by	---	AT2G19930	-1.33	-0.41	-1.46	0.189749	0.4314368	-5.52	FALSE
265238_s_a	hypothetical protein	---	AT2G07696	1.28	0.35	1.46	0.1898275	0.4315722	-5.52	FALSE
262234_at	putative G protein coupled recep	GCR1	AT1G48270	1.27	0.34	1.46	0.1898482	0.4315763	-5.52	FALSE
250182_at	putative protein predicted protei	---	AT5G14470	1.61	0.68	1.46	0.189886	0.4316193	-5.52	FALSE
253462_at	synaptobrevin-like protein synap	ATVAMP71	AT4G32150	-1.22	-0.28	-1.46	0.1901135	0.4320331	-5.52	FALSE
261790_at	unknown protein ; supported by f	---	AT1G16000	-1.29	-0.37	-1.46	0.1901249	0.4320331	-5.52	FALSE
252006_at	purple acid phosphatase-like pr	PAP22	AT3G52820	2.14	1.10	1.46	0.1901012	0.4320331	-5.52	FALSE
245079_at	putative retroelement pol polypro	---	---	1.15	0.20	1.46	0.1901876	0.4321287	-5.52	FALSE
260154_at	putative histone H2A similar to hi	HTA9	AT1G52740	-1.26	-0.34	-1.46	0.1902238	0.4321287	-5.52	FALSE
263473_at	putative glucosyltransferase ; su	UGT74D1	AT2G31750	-1.57	-0.65	-1.46	0.1902155	0.4321287	-5.52	FALSE
253149_at	NAD+ dependent isocitrate dehy	---	AT4G35650	1.19	0.25	1.46	0.1902718	0.4321947	-5.52	FALSE
265260_at	NAM (no apical meristem)-like pr	anac042	AT2G43000	2.29	1.19	1.46	0.1904645	0.4323312	-5.52	FALSE

261975_at	unknown protein	---	AT1G64640	1.64	0.71	1.46	0.1903766	0.4323312	-5.52	FALSE
262989_at	F28C11.5 similar to INNER NO	INO	AT1G23420	1.21	0.28	1.46	0.190463	0.4323312	-5.52	FALSE
251433_at	putative protein SERINE/THREO	---	AT3G59830	1.14	0.19	1.46	0.1904005	0.4323312	-5.52	FALSE
246289_at	putative protein predicted protei	---	AT3G56880	1.36	0.44	1.46	0.1903639	0.4323312	-5.52	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=M651	---	---	-1.16	-0.21	-1.46	0.1904123	0.4323312	-5.52	FALSE
266757_at	unknown protein	---	AT2G46940	1.35	0.43	1.46	0.1904427	0.4323312	-5.52	FALSE
267568_at	hypothetical protein predicted by	---	AT2G30780	-1.19	-0.25	-1.46	0.1904929	0.4323524	-5.52	FALSE
248834_at	unknown protein ;supported by f	---	AT5G47090	-1.18	-0.24	-1.46	0.1905145	0.4323585	-5.52	FALSE
258691_at	unknown protein	---	AT3G08630	1.56	0.64	1.46	0.1906337	0.4325859	-5.52	FALSE
251867_at	SKP1 interacting partner 5 (SKIP	SKIP5	AT3G54480	1.16	0.21	1.45	0.1907599	0.4328046	-5.52	FALSE
248464_at	putative protein similar to unknov	---	AT5G51160	1.26	0.33	1.45	0.190768	0.4328046	-5.52	FALSE
263563_at	putative retroelement pol polypro	---	---	1.18	0.24	1.45	0.190908	0.4330792	-5.52	FALSE
255184_at	putative athila transposon protein	---	---	1.14	0.19	1.45	0.1910221	0.4332147	-5.53	FALSE
259146_at	putative glycerol-3-phosphate de	SDP6	AT3G10370	1.24	0.31	1.45	0.1910437	0.4332147	-5.53	FALSE
245343_at	hypothetical protein ;supported b	---	AT4G15830	-1.15	-0.20	-1.45	0.1910366	0.4332147	-5.53	FALSE
264629_at	hypothetical protein similar to hyp	---	AT1G65540	1.22	0.29	1.45	0.1909976	0.4332147	-5.53	FALSE
265547_at	hypothetical protein similar to hyp	---	AT2G28305	1.41	0.50	1.45	0.1911781	0.4334764	-5.53	FALSE
261438_at	metallothionein-like protein identi	---	AT1G07590 ///	1.15	0.21	1.45	0.1913618	0.4338498	-5.53	FALSE
255847_at	putative thioredoxin	ACHT3	AT2G33270	1.14	0.19	1.45	0.1914536	0.4339717	-5.53	FALSE
258108_at	unknown protein contains Pfam p	---	AT3G23570	1.61	0.69	1.45	0.1914505	0.4339717	-5.53	FALSE
261711_at	unknown protein similar to hypot	---	AT1G32700	-1.19	-0.25	-1.45	0.1915138	0.4340219	-5.53	FALSE
264331_at	hypothetical protein contains nor	---	AT1G04130	-1.18	-0.24	-1.45	0.1914949	0.4340219	-5.53	FALSE
265982_at	putative retroelement pol polypro	---	---	1.14	0.19	1.45	0.1915684	0.4341024	-5.53	FALSE
247781_at	dehydrodolichyl diphosphate syr	---	AT5G58784	1.25	0.32	1.45	0.1916456	0.4342342	-5.53	FALSE
250951_at	putative protein	---	AT5G03550	1.50	0.59	1.45	0.1917195	0.4343154	-5.53	FALSE
253242_at	isoflavone reductase - like prote	CIB1	AT4G34530 ///	-1.34	-0.43	-1.45	0.1917138	0.4343154	-5.53	FALSE
261130_at	unknown protein ; supported by c	PRMT10	AT1G04870	-1.37	-0.45	-1.45	0.1917989	0.4344522	-5.53	FALSE
262641_at	unknown protein ;supported by fu	---	AT1G62730	-1.13	-0.17	-1.45	0.191935	0.4347171	-5.53	FALSE
246967_at	FPF1 protein	FPF1	AT5G24860	1.32	0.40	1.45	0.1919624	0.4347361	-5.53	FALSE
260896_at	flower pigmentation protein ATAI	---	AT1G29310	1.38	0.46	1.45	0.1920559	0.4349048	-5.53	FALSE
249529_at	putative protein predicted protei	---	AT5G38730	-1.28	-0.35	-1.45	0.1921451	0.4350024	-5.53	FALSE
255059_at	putative protein downy mildew re	---	AT4G09420	-1.47	-0.56	-1.45	0.1921441	0.4350024	-5.53	FALSE
262915_at	response regulator 3 identical to	ARR3	AT1G59940	1.21	0.28	1.45	0.1922092	0.4350024	-5.53	FALSE
250434_at	histone H3 - like protein histone	---	AT5G10390	-2.05	-1.03	-1.45	0.1921748	0.4350024	-5.53	FALSE
251691_at	putative protein hypothetical pro	---	AT3G56520	1.21	0.28	1.45	0.1922166	0.4350024	-5.53	FALSE

245167_s_a	putative synaptobrevin ;supporte	ATVAMP72	AT2G33110 /.	1.15	0.20	1.45	0.1922325	0.4350024	-5.53	FALSE
245554_at	cytochrome P450 like protein	CYP705A4	AT4G15380	1.14	0.19	1.45	0.1921817	0.4350024	-5.53	FALSE
245848_at	putative protein predicted protein	FY	AT5G13480	-1.17	-0.23	-1.45	0.1922917	0.4350932	-5.53	FALSE
254307_at	putative protein various predicte	---	AT4G22400	1.30	0.38	1.45	0.1923463	0.4351304	-5.53	FALSE
254702_at	putative protein predicted protei	---	AT4G17940	1.20	0.26	1.45	0.1923463	0.4351304	-5.53	FALSE
261650_at	envelope Ca2+-ATPase identica	ACA1	AT1G27770	1.35	0.43	1.45	0.1923999	0.4352085	-5.53	FALSE
259230_at	unknown protein ; supported by	OBE1	AT3G07780	1.23	0.30	1.45	0.192451	0.4352809	-5.53	FALSE
256127_at	small GTP-binding protein (RAB	AtRABA6b	AT1G18200	1.21	0.27	1.45	0.19255	0.4354616	-5.53	FALSE
263567_at	hypothetical protein predicted by	---	AT2G15440	1.21	0.27	1.45	0.1925872	0.4355026	-5.53	FALSE
251406_at	putative protein various predicte	---	AT3G60260	1.35	0.43	1.45	0.1926466	0.4355937	-5.53	TRUE
250166_at	putative protein many predicted	---	AT5G15300	-1.16	-0.22	-1.45	0.1926805	0.4356271	-5.53	FALSE
262422_at	hypothetical protein similar to hy	---	AT1G23440	1.21	0.28	1.45	0.1927208	0.4356752	-5.53	FALSE
262291_at	zinc finger and C2 domain prote	---	AT1G70790	-1.16	-0.21	-1.45	0.1927415	0.4356786	-5.53	TRUE
245258_at	lupeol synthase like protein ; sup	ATPEN1	AT4G15340	1.19	0.25	1.45	0.1927831	0.4357296	-5.53	FALSE
256766_at	Expressed protein ; supported by	PCC1	AT3G22231	5.11	2.35	1.45	0.1928032	0.4357318	-5.53	FALSE
261699_at	hypothetical protein identical to h	---	AT1G32660	1.19	0.26	1.45	0.1928526	0.4358004	-5.53	FALSE
261080_at	proliferating cellular nuclear antig	PCNA1	AT1G07370	-1.91	-0.94	-1.45	0.192913	0.4358936	-5.53	FALSE
261969_at	hypothetical protein contains sim	---	AT1G65950	-1.16	-0.21	-1.45	0.1929646	0.4359669	-5.53	FALSE
258052_at	putative hydrolase predicted by g	---	AT3G16190	-1.20	-0.26	-1.45	0.1929929	0.4359877	-5.53	FALSE
251651_at	putative protein transcription init	---	AT3G57370	-1.13	-0.18	-1.45	0.1930285	0.436025	-5.53	FALSE
254195_at	putative protein various predicte	NLP7	AT4G24020	1.17	0.23	1.45	0.1930616	0.4360565	-5.53	FALSE
255400_at	hypothetical protein	---	---	1.20	0.26	1.45	0.1931079	0.436118	-5.53	FALSE
262269_at	hypothetical protein predicted by	---	---	1.15	0.21	1.45	0.1931432	0.4361545	-5.54	FALSE
260218_at	putative RING zinc finger protein	---	AT1G74620	1.14	0.18	1.45	0.193182	0.436199	-5.54	FALSE
259163_at	putative protein kinase similar to	---	AT3G01490	-1.23	-0.30	-1.45	0.193225	0.4362227	-5.54	FALSE
262888_at	RNA-directed RNA polymerase,	RDR1	AT1G14790	-1.49	-0.57	-1.45	0.1932499	0.4362227	-5.54	FALSE
263630_at	Expressed protein ; supported by	---	AT2G04845	-1.16	-0.21	-1.45	0.1932386	0.4362227	-5.54	FALSE
267029_at	unknown protein	ATIREG1	AT2G38460	-1.21	-0.28	-1.45	0.1932793	0.4362458	-5.54	FALSE
265499_at	putative glucosyltransferase	UGT73B5	AT2G15480	1.85	0.89	1.45	0.1932988	0.4362467	-5.54	TRUE
257192_at	unknown protein ;supported by f	EMB2769	AT3G13200	-1.20	-0.26	-1.44	0.1934306	0.4365009	-5.54	FALSE
253369_at	F-box protein family, AtFBL15 c	---	AT4G33210	-1.13	-0.18	-1.44	0.1934687	0.4365437	-5.54	FALSE
259597_at	ATP-dependent RNA helicase, p	---	AT1G27900	-1.20	-0.26	-1.44	0.1934983	0.4365674	-5.54	FALSE
265950_s_a	putative protein kinase contains a	---	AT2G18530 /.	1.18	0.24	1.44	0.1935746	0.4366963	-5.54	FALSE
251644_at	putative protein putative DNA bi	---	AT3G57540	1.37	0.46	1.44	0.1937524	0.4369073	-5.54	FALSE
265852_at	putative RING zinc finger protein	---	AT2G42350	1.34	0.43	1.44	0.1937412	0.4369073	-5.54	FALSE

266506_at	unknown protein	---	AT2G47850	-1.16	-0.22	-1.44	0.1937205	0.4369073	-5.54	FALSE
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gl	---	---	1.55	0.63	1.44	0.1937639	0.4369073	-5.54	FALSE
263746_at	putative retroelement pol polypro	---	---	-1.16	-0.22	-1.44	0.1937138	0.4369073	-5.54	FALSE
266441_at	hypothetical protein predicted by	---	AT2G43250	-1.17	-0.23	-1.44	0.1938136	0.4369762	-5.54	FALSE
246771_at	putative protein putative replicati	---	---	1.15	0.20	1.44	0.1938697	0.4370163	-5.54	FALSE
250707_at	putative protein similar to unknov	MEE60	AT5G05950	-1.26	-0.33	-1.44	0.1938591	0.4370163	-5.54	FALSE
256528_at	C2H2-type zinc finger protein, p	ZFP4	AT1G66140	-1.28	-0.36	-1.44	0.1940304	0.4372203	-5.54	FALSE
264379_at	hypothetical protein predicted by	---	AT2G25200	-1.37	-0.45	-1.44	0.1940369	0.4372203	-5.54	FALSE
248351_at	unknown protein ; supported by	---	AT5G52200	1.30	0.38	1.44	0.1939821	0.4372203	-5.54	FALSE
246532_at	putative protein beta-glucan-elic	---	AT5G15870	1.93	0.95	1.44	0.1940078	0.4372203	-5.54	FALSE
267528_at	MADS-box protein (AGL6) ; sup	AGL6	AT2G45650	1.17	0.23	1.44	0.1940774	0.437246	-5.54	FALSE
263832_at	putative polygalacturonase	---	AT2G40310	1.13	0.18	1.44	0.1940866	0.437246	-5.54	FALSE
262272_at	unknown protein ; supported by	---	AT1G42440	-1.14	-0.19	-1.44	0.1941124	0.4372609	-5.54	FALSE
248239_at	ribosomal protein L11 methyltran	---	AT5G53920	-1.28	-0.36	-1.44	0.1941387	0.4372769	-5.54	FALSE
258731_at	unknown protein ; supported by	---	AT3G11880	1.17	0.23	1.44	0.1941659	0.4372951	-5.54	FALSE
255312_at	putative transposon protein	---	---	-1.17	-0.22	-1.44	0.194255	0.4374526	-5.54	FALSE
262865_at	cytochrome p450, putative simil	CYP89A7	AT1G64930	1.19	0.25	1.44	0.1942872	0.4374819	-5.54	FALSE
251252_at	putative protein several hypothet	---	AT3G62230	1.17	0.22	1.44	0.1943897	0.4376695	-5.54	FALSE
259016_at	unknown protein HMM hit: 2Fe-2	---	AT3G07480	1.24	0.31	1.44	0.1944481	0.4377577	-5.54	FALSE
262779_at	putative cytochrome P450 mono	---	AT1G13070	1.14	0.19	1.44	0.1945194	0.4378749	-5.54	FALSE
251105_at	putative protein unknown protei	ATSCAR4	AT5G01730	1.44	0.53	1.44	0.194676	0.437908	-5.54	TRUE
264396_at	fumarylacetoacetate hydrolase-l	---	AT1G12050	-1.15	-0.21	-1.44	0.1947405	0.437908	-5.54	FALSE
247134_at	putative protein similar to unknov	---	AT5G66230	1.17	0.22	1.44	0.1946668	0.437908	-5.54	FALSE
262050_at	unknown protein ;supported by fu	---	AT1G80130	-2.01	-1.01	-1.44	0.1947408	0.437908	-5.54	FALSE
247762_at	cell wall protein	---	AT5G59170	1.47	0.55	1.44	0.194662	0.437908	-5.54	FALSE
264963_at	hypothetical protein predicted by	ABC4	AT1G60600	-1.28	-0.35	-1.44	0.1946333	0.437908	-5.54	FALSE
261048_at	flavonol 3-o-glucosyltransferase	UGT72B3	AT1G01420	-1.21	-0.27	-1.44	0.1945826	0.437908	-5.54	FALSE
262724_s_a	PC-MYB2, putative similar to PC	---	AT1G43330 /	1.15	0.20	1.44	0.1946204	0.437908	-5.54	FALSE
248992_at	disease resistance protein RPS4	---	AT5G45230	1.18	0.24	1.44	0.1946645	0.437908	-5.54	FALSE
267252_at	hypothetical protein predicted by	---	AT2G23100	-1.17	-0.23	-1.44	0.1947644	0.437908	-5.54	FALSE
261515_at	cleavage stimulation factor, puta	---	AT1G71800	1.16	0.21	1.44	0.1947493	0.437908	-5.54	FALSE
247782_at	putative protein predicted RNA b	---	AT5G58790	-1.15	-0.20	-1.44	0.1947274	0.437908	-5.54	FALSE
261855_at	unknown protein	---	AT1G50510	-1.22	-0.29	-1.44	0.1948987	0.4381667	-5.54	FALSE
251816_at	Expressed protein ; supported by	TON1B	AT3G55005	-1.25	-0.32	-1.44	0.1950528	0.438254	-5.54	FALSE
249989_at	putative protein FACTOR ASSO	---	AT5G18525	-1.20	-0.26	-1.44	0.1950217	0.438254	-5.54	FALSE

246757_at	Expressed protein ; supported by	WPP3	AT5G27940	1.14	0.19	1.44	0.1950355	0.438254	-5.54	FALSE
252610_x_a	putative protein putative MuDR p	---	---	1.13	0.18	1.44	0.1949612	0.438254	-5.54	FALSE
261580_at	unknown protein ;supported by fu	IQD18	AT1G01110	1.29	0.37	1.44	0.195032	0.438254	-5.54	FALSE
249343_at	succinate dehydrogenase iron-p	SDH2-2	AT5G40650	1.24	0.31	1.44	0.1950442	0.438254	-5.54	FALSE
263381_at	putative MADS-box protein	AGL48	AT2G40210	1.16	0.21	1.44	0.1950755	0.4382617	-5.54	FALSE
254281_at	predicted protein ileal sodium-de	---	AT4G22840	-1.66	-0.73	-1.44	0.1951383	0.4382735	-5.54	FALSE
247093_at	zinc finger protein SHI-like ; sup	SHI	AT5G66350	-1.25	-0.33	-1.44	0.1951021	0.4382735	-5.54	FALSE
267630_at	unknown protein predicted by ge	---	AT2G42130	-1.23	-0.30	-1.44	0.1951341	0.4382735	-5.54	FALSE
260379_at	putative glucosyltransferase simi	UGT89B1	AT1G73880 ///	1.25	0.32	1.44	0.1951872	0.43834	-5.54	FALSE
263199_at	hypothetical protein Similar to he	HEXO2	AT1G05590	-1.24	-0.31	-1.44	0.1953007	0.4384223	-5.54	FALSE
256653_at	hypothetical protein predicted by	---	AT3G18870	-1.18	-0.24	-1.44	0.1952737	0.4384223	-5.54	FALSE
263654_at	unknown protein	---	AT1G04300	-1.18	-0.24	-1.44	0.1952947	0.4384223	-5.54	FALSE
266136_at	unknown protein ;supported by f	---	AT2G45060	-1.13	-0.18	-1.44	0.1952879	0.4384223	-5.54	FALSE
262468_at	alanine--tRNA ligase, putative si	ALATS	AT1G50200	-1.25	-0.32	-1.44	0.19545	0.438568	-5.55	FALSE
245971_at	putative protein ; supported by c	NPH4	AT5G20730	1.17	0.23	1.44	0.1953889	0.438568	-5.55	FALSE
245233_at	putative protein similarity to low-	---	AT4G25580	1.19	0.26	1.44	0.1954493	0.438568	-5.55	FALSE
262226_at	Expressed protein ; supported by	---	AT1G53885 ///	1.55	0.63	1.44	0.1954617	0.438568	-5.55	FALSE
254251_at	serine/threonine kinase - like pro	---	AT4G23300	-1.22	-0.29	-1.44	0.1954078	0.438568	-5.55	FALSE
253950_at	putative dihydrolipoamide succin	---	AT4G26910	1.32	0.40	1.44	0.1955456	0.4387012	-5.55	FALSE
264353_at	hypothetical protein predicted by	---	AT1G03260	-1.17	-0.23	-1.44	0.1955723	0.4387012	-5.55	FALSE
256010_at	auxin response factor, putative s	ARF19	AT1G19220	1.20	0.26	1.44	0.1955788	0.4387012	-5.55	FALSE
260247_at	putative disease resistance prote	AtRLP16	AT1G74200	1.15	0.20	1.44	0.1956465	0.43881	-5.55	FALSE
249004_at	unknown protein	---	AT5G44570	1.23	0.30	1.44	0.1957412	0.4389791	-5.55	FALSE
255564_s_a	hypothetical protein T15B16.8	RGXT2	AT4G01750 ///	-1.19	-0.25	-1.44	0.1958249	0.4391236	-5.55	FALSE
262944_at	phosphoglycerate kinase, putati	PGK	AT1G79550	1.26	0.33	1.44	0.1958606	0.4391606	-5.55	FALSE
267428_at	putative coatomer epsilon subun	---	AT2G34840	-1.19	-0.25	-1.44	0.1959064	0.43922	-5.55	FALSE
255709_at	putative YABBY3 axial regulator	YAB3	AT4G00180	-1.21	-0.28	-1.44	0.1960131	0.4394162	-5.55	TRUE
261665_at	beta-glucan-elicitor receptor, put	---	AT1G18310	-1.16	-0.21	-1.44	0.1960804	0.4395238	-5.55	FALSE
260784_at	MYB-related protein identical to	ATMYB13	AT1G06180	1.40	0.48	1.43	0.1963203	0.4395569	-5.55	TRUE
261594_at	DNA-binding factor, putative sim	AT-GTL1	AT1G33240	-1.20	-0.26	-1.43	0.1963767	0.4395569	-5.55	TRUE
267279_at	hypothetical protein predicted by	---	AT2G19460	1.42	0.51	1.43	0.1964753	0.4395569	-5.55	TRUE
259431_at	plasma membrane intrinsic prote	PIP1C	AT1G01620	1.91	0.93	1.43	0.1962614	0.4395569	-5.55	TRUE
257293_at	unknown protein similar to symbi	APG8H	AT3G15580	-1.26	-0.34	-1.43	0.1963264	0.4395569	-5.55	FALSE
248816_at	prematurely terminated mRNA d	LBA1	AT5G47010	-1.16	-0.21	-1.43	0.1961829	0.4395569	-5.55	FALSE
247644_s_a	translation elongation factor eEF	---	AT1G07920 ///	-1.17	-0.23	-1.43	0.1964377	0.4395569	-5.55	FALSE

263097_at	hypothetical protein predicted by	PDV2	AT2G16070	-1.23	-0.29	-1.43	0.1964036	0.4395569	-5.55	FALSE
248379_at	RAR1 (gb|AAF18433.1) non-con	PBS2	AT5G51700	-1.18	-0.24	-1.43	0.1962322	0.4395569	-5.55	FALSE
246027_at	homoserine dehydrogenase-like	---	AT5G21060	-1.29	-0.37	-1.43	0.196472	0.4395569	-5.55	FALSE
263339_at	Mutator-like transposase similar	---	---	-1.13	-0.18	-1.43	0.1963478	0.4395569	-5.55	FALSE
246025_at	zwille/pinhead-like protein GERp	---	AT5G21150	1.23	0.29	1.43	0.1964727	0.4395569	-5.55	FALSE
251695_at	putative protein hypothetical prot	---	AT3G56590	-1.31	-0.39	-1.43	0.1962701	0.4395569	-5.55	FALSE
259073_at	unknown protein contains zinc fi	---	AT3G02290	1.36	0.44	1.43	0.1964806	0.4395569	-5.55	FALSE
249399_at	putative protein intracellular prot	---	AT5G40290	1.13	0.18	1.43	0.1963679	0.4395569	-5.55	FALSE
248281_at	unknown protein	---	AT5G52980	1.15	0.20	1.43	0.196261	0.4395569	-5.55	FALSE
248414_at	50S ribosomal protein L11-like	---	AT5G51610	-1.19	-0.25	-1.43	0.1961639	0.4395569	-5.55	FALSE
255337_at	putative DNA-binding protein sin	WRKY42	AT4G04450	1.24	0.31	1.43	0.1962968	0.4395569	-5.55	FALSE
256651_at	hypothetical protein predicted by	---	AT3G18840	1.22	0.28	1.43	0.1961413	0.4395569	-5.55	FALSE
254743_at	potassium transporter - like prot	HAK5	AT4G13420	3.11	1.64	1.43	0.1961578	0.4395569	-5.55	FALSE
257729_at	histone deacetylase, putative co	HDA15	AT3G18520	-1.26	-0.34	-1.43	0.196555	0.4396372	-5.55	FALSE
258102_at	unknown protein contains Pfam p	---	AT3G23600	1.23	0.30	1.43	0.1965386	0.4396372	-5.55	FALSE
254352_at	hypothetical protein	---	AT4G22320	1.15	0.20	1.43	0.1966871	0.4398895	-5.55	FALSE
257639_at	hypothetical protein	---	AT3G25720	1.19	0.25	1.43	0.1968038	0.4401073	-5.55	FALSE
264461_s_a	hypothetical protein	---	AT1G10190 ///	1.13	0.18	1.43	0.1968514	0.4401275	-5.55	FALSE
249106_at	protein transport protein SEC23	---	AT5G43670	-1.27	-0.35	-1.43	0.1968418	0.4401275	-5.55	FALSE
253579_at	SERINE CARBOXYPEPTIDASE	BRS1	AT4G30610	-1.48	-0.57	-1.43	0.1970437	0.4405142	-5.55	FALSE
248417_at	unknown protein	---	AT5G51650	1.14	0.18	1.43	0.1971594	0.4406948	-5.55	FALSE
253924_at	putative protein other hypothetic	COBL11	AT4G27110	1.20	0.26	1.43	0.1971631	0.4406948	-5.55	FALSE
260930_at	GTP-binding protein Sar1, putat	---	AT1G02620	-1.38	-0.47	-1.43	0.1973306	0.4407673	-5.55	TRUE
253935_at	putative aspartate-tRNA ligase a	---	AT4G26870	-1.47	-0.55	-1.43	0.1972192	0.4407673	-5.55	FALSE
253509_at	putative protein kainate receptor	GLR2.4	AT4G31710	1.18	0.24	1.43	0.197279	0.4407673	-5.55	FALSE
247479_at	NAC - like protein OsNAC7, Ory	ANAC101	AT5G62380	-1.15	-0.20	-1.43	0.1973308	0.4407673	-5.55	FALSE
247494_at	calnexin - like protein calnexin h	CNX1	AT5G61790	1.64	0.72	1.43	0.1972606	0.4407673	-5.55	FALSE
255323_at	putative transposon protein	---	---	-1.14	-0.19	-1.43	0.1973285	0.4407673	-5.55	FALSE
266173_at	unknown protein	---	AT2G02410	-1.15	-0.20	-1.43	0.1972391	0.4407673	-5.55	FALSE
249808_at	unknown protein	---	AT5G23890	-1.37	-0.45	-1.43	0.197404	0.4408876	-5.55	FALSE
255064_at	putative phi-1-like phosphate-ind	EXO	AT4G08950	1.88	0.91	1.43	0.1974351	0.4409139	-5.55	TRUE
248905_at	putative protein contains similarit	---	AT5G46250	-1.17	-0.23	-1.43	0.1975688	0.4410015	-5.55	FALSE
264825_at	hypothetical protein predicted by	---	AT1G03720	1.19	0.25	1.43	0.1976057	0.4410015	-5.56	FALSE
250730_at	C3HC4-type RING zinc finger pr	---	AT5G06490	1.18	0.24	1.43	0.1976097	0.4410015	-5.56	FALSE
262924_s_a	vacuolar ATP synthase, putative	AVA-P4	AT1G19910 ///	-1.21	-0.27	-1.43	0.1975056	0.4410015	-5.55	FALSE

266720_s_a	hypothetical protein predicted by	APRR9	AT2G46670 /.	-1.38	-0.46	-1.43	0.197601	0.4410015	-5.56	FALSE
260483_at	Barley Mlo protein isolog ; suppo	MLO4	AT1G11000	-1.26	-0.33	-1.43	0.1975321	0.4410015	-5.55	FALSE
264328_at	putative IAA1 protein Match to IA	IAA10	AT1G04100	1.27	0.34	1.43	0.1975448	0.4410015	-5.55	FALSE
260325_at	putative monodehydroascorbate	MDAR6	AT1G63940	-1.24	-0.31	-1.43	0.1976326	0.4410096	-5.56	FALSE
247135_at	auxin-induced protein-like	---	AT5G66260	1.14	0.18	1.43	0.197656	0.4410185	-5.56	FALSE
252678_s_a	nitrilase 2 ;supported by full-leng	NIT2	AT3G44300 /.	1.16	0.21	1.43	0.197752	0.4411897	-5.56	FALSE
245385_at	hypothetical protein ;supported b	---	AT4G14020	1.27	0.34	1.43	0.1977954	0.4412001	-5.56	TRUE
248953_at	serine/threonine-protein kinase M	---	AT5G45428 /.	1.16	0.22	1.43	0.1977902	0.4412001	-5.56	FALSE
251229_at	beta-glucosidase-like protein sev	BGLU7	AT3G62740	1.15	0.20	1.43	0.1978544	0.4412454	-5.56	FALSE
263900_at	unknown protein ;supported by f	---	AT2G36290	-1.23	-0.29	-1.43	0.1978525	0.4412454	-5.56	FALSE
259785_at	unknown protein ;supported by fu	---	AT1G29490	-1.21	-0.28	-1.43	0.1978765	0.4412516	-5.56	FALSE
247432_at	microtubule-associated protein E	ATEB1B	AT5G62500	1.19	0.25	1.43	0.1979586	0.4413915	-5.56	FALSE
247591_at	high-affinity nitrate transporter A	NRT2.4	AT5G60770	1.16	0.21	1.43	0.1980145	0.4414731	-5.56	FALSE
260626_at	storage protein, putative similar	---	AT1G08040	-1.20	-0.26	-1.43	0.1980496	0.4415081	-5.56	FALSE
261703_at	OsNAC7 protein, putative simila	ANAC012	AT1G32770	1.15	0.21	1.43	0.1981105	0.4416008	-5.56	FALSE
254178_at	hypothetical protein	---	AT4G23880	-1.95	-0.96	-1.43	0.1982194	0.4417994	-5.56	FALSE
262386_at	hypothetical protein predicted by	---	AT1G49370	1.23	0.30	1.43	0.1982384	0.4417994	-5.56	FALSE
264439_at	adenine phosphoribosyltransfera	APT1	AT1G27450	-1.18	-0.24	-1.43	0.1982814	0.4418522	-5.56	FALSE
249104_at	sucrose transporter protein	ATSUC6	AT5G43610	-1.17	-0.22	-1.43	0.1983881	0.4419002	-5.56	FALSE
265084_at	hypothetical protein contains Cys	SOM	AT1G03790	1.17	0.23	1.43	0.1983998	0.4419002	-5.56	FALSE
247159_at	1-aminocyclopropane-1-carboxyl	ACS5	AT5G65800	-1.14	-0.19	-1.43	0.1983964	0.4419002	-5.56	FALSE
260488_at	flowering protein CONSTANS, p	TIFY2A	AT1G51600	-1.22	-0.29	-1.43	0.1983962	0.4419002	-5.56	FALSE
257222_at	DegP protease almost identical	DEGP1	AT3G27925	-1.23	-0.30	-1.43	0.1983511	0.4419002	-5.56	FALSE
250636_at	glycine-rich protein atGRP	GRP18	AT5G07520	1.18	0.24	1.43	0.1984829	0.442042	-5.56	FALSE
245833_at	transposon protein, putative sim	---	---	1.19	0.25	1.43	0.1985217	0.4420853	-5.56	FALSE
251827_at	chalcone isomerase ;supported	TT5	AT3G55120	-1.26	-0.33	-1.43	0.1986509	0.4422762	-5.56	FALSE
264681_s_a	permease 1-like protein permea	---	AT1G65550 /.	1.21	0.28	1.43	0.1986656	0.4422762	-5.56	FALSE
248788_at	DNA-binding protein-like	---	AT5G47430	1.15	0.20	1.43	0.1986285	0.4422762	-5.56	FALSE
258523_at	pectin methylesterase, putative s	---	AT3G06830	1.13	0.18	1.43	0.1986895	0.4422863	-5.56	FALSE
264420_at	hypothetical protein predicted by	---	AT1G43320	1.15	0.20	1.43	0.1987448	0.442323	-5.56	FALSE
255986_x_a	putative protein predicted protei	---	---	1.13	0.18	1.43	0.1987304	0.442323	-5.56	FALSE
255419_at	putative receptor kinase	---	AT4G03230	1.19	0.25	1.43	0.198778	0.4423538	-5.56	FALSE
254370_at	L1 specific homeobox gene ATM	ATML1	AT4G21750	1.23	0.30	1.42	0.198894	0.4425688	-5.56	TRUE
255969_at	Expressed protein ; supported by	---	AT1G22330	1.39	0.47	1.42	0.1990277	0.4427316	-5.56	TRUE
245427_at	putative protein	---	AT4G17550	-1.25	-0.32	-1.42	0.1990448	0.4427316	-5.56	FALSE

248960_at	subtilisin-like protease	---	AT5G45640	-1.26	-0.33	-1.42	0.1990331	0.4427316	-5.56	FALSE
266326_at	putative cytochrome b5 ;support	CB5-C	AT2G46650	1.79	0.84	1.42	0.1990395	0.4427316	-5.56	FALSE
251106_at	putative protein peroxisomal Ca	---	AT5G01500	1.76	0.81	1.42	0.1991141	0.4428425	-5.56	FALSE
256570_at	unknown protein ; supported by	---	AT3G19540	1.14	0.19	1.42	0.1992528	0.4431077	-5.56	FALSE
265315_at	hypothetical protein predicted by	CLASP	AT2G20190	1.17	0.23	1.42	0.1992853	0.4431369	-5.56	FALSE
255632_at	putative actin-depolymerizing fac	ADF8	AT4G00680	1.14	0.19	1.42	0.1994045	0.4433587	-5.56	FALSE
260031_at	putative nuclear matrix constitue	LINC3	AT1G68790	-1.19	-0.25	-1.42	0.1995102	0.4435505	-5.56	FALSE
247606_at	RNA helicase	---	AT5G61000	-1.58	-0.66	-1.42	0.199536	0.4435588	-5.56	FALSE
250931_at	putative protein various predicte	---	AT5G03200	1.55	0.64	1.42	0.1995529	0.4435588	-5.56	FALSE
251454_at	putative protein COP1-interactin	---	AT3G60080	1.23	0.30	1.42	0.1995936	0.4436062	-5.56	FALSE
252363_at	lipase - like protein lipase Arab-	---	AT3G48460	1.64	0.71	1.42	0.1997676	0.443647	-5.56	TRUE
263472_at	molybdopterin synthase (CNX2)	CNX2	AT2G31955	1.22	0.29	1.42	0.1996962	0.443647	-5.56	FALSE
246924_at	putative protein KIAA0332 - Hon	---	AT5G25060	-1.14	-0.19	-1.42	0.1997555	0.443647	-5.56	FALSE
262717_s_a	putative cytochrome P450 simila	CYP79F2	AT1G16400 //	-1.28	-0.35	-1.42	0.1996815	0.443647	-5.56	FALSE
254291_at	putative protein UDP-galactose	UTR2	AT4G23010	1.29	0.36	1.42	0.1997093	0.443647	-5.56	FALSE
252538_at	putative transporter protein pept	---	AT3G45720	1.15	0.20	1.42	0.1996837	0.443647	-5.56	FALSE
267340_at	unknown protein	ACD11	AT2G34690	-1.16	-0.21	-1.42	0.19975	0.443647	-5.56	FALSE
259814_at	zinc finger protein ATZF1, putati	---	AT1G49900	1.31	0.39	1.42	0.1996784	0.443647	-5.56	FALSE
245708_at	pectate lyase-like protein	---	AT5G04310	1.21	0.28	1.42	0.1998858	0.4438663	-5.57	FALSE
258788_at	unknown protein ;supported by f	---	AT3G11780	-1.18	-0.24	-1.42	0.1999301	0.4439215	-5.57	FALSE
251615_at	putative protein hypothetical pro	---	AT3G57980	1.28	0.36	1.42	0.1999756	0.4439361	-5.57	FALSE
253718_at	serine/threonine-specific recepto	---	AT4G29450	1.19	0.25	1.42	0.1999731	0.4439361	-5.57	FALSE
261053_at	hypothetical protein predicted by	---	AT1G01320	-1.24	-0.31	-1.42	0.2000323	0.4440187	-5.57	FALSE
252207_at	putative protein mRNA of unkno	---	AT3G50370	-1.18	-0.24	-1.42	0.20014	0.4441696	-5.57	FALSE
263748_at	putative protein kinase contains a	---	AT2G21480	1.19	0.25	1.42	0.2001476	0.4441696	-5.57	FALSE
255211_at	may be a pseudogene	---	---	1.14	0.19	1.42	0.2001587	0.4441696	-5.57	FALSE
264282_at	hypothetical protein similar to hyp	---	AT1G61840	1.19	0.25	1.42	0.2002211	0.4442649	-5.57	FALSE
247329_at	putative protein similar to unknov	---	AT5G64150	-1.34	-0.42	-1.42	0.200277	0.4443457	-5.57	FALSE
262749_at	lipase, putative contains Pfam p	---	AT1G28580	1.17	0.23	1.42	0.2003363	0.4444341	-5.57	FALSE
260541_at	putative trypsin inhibitor	---	AT2G43530	1.68	0.75	1.42	0.200392	0.4445019	-5.57	FALSE
248699_at	putative protein similar to unknov	ATZIP4	AT5G48390	1.24	0.31	1.42	0.2004059	0.4445019	-5.57	FALSE
251244_at	pectinacetylesterase precursor-l	---	AT3G62060	-1.19	-0.25	-1.42	0.2004272	0.4445061	-5.57	FALSE
245353_at	hypothetical protein ;supported b	---	AT4G16000	-1.36	-0.44	-1.42	0.2004742	0.444567	-5.57	FALSE
264219_at	unknown protein contains similar	---	AT1G60420	-1.27	-0.35	-1.42	0.2005524	0.444654	-5.57	FALSE
251156_at	putative protein ZCF61, Arabido	EDL3	AT3G63060	1.22	0.29	1.42	0.2005436	0.444654	-5.57	FALSE

254417_at	putative protein	ATFMN/FH	AT4G21470	1.27	0.35	1.42	0.2005925	0.4446997	-5.57	TRUE
265702_at	putative purple acid phosphatase	PAP9	AT2G03450	-1.19	-0.26	-1.42	0.2006829	0.4448402	-5.57	FALSE
251522_at	hypothetical protein	---	AT3G59430	-1.19	-0.25	-1.42	0.2006949	0.4448402	-5.57	FALSE
258501_at	hypothetical protein predicted by	---	AT3G06780	1.27	0.35	1.42	0.2007365	0.4448445	-5.57	FALSE
245151_at	putative pectinesterase ;support	---	AT2G47550	2.65	1.41	1.42	0.2007319	0.4448445	-5.57	FALSE
263512_at	hypothetical protein predicted by	---	---	-1.16	-0.21	-1.42	0.2007553	0.4448445	-5.57	FALSE
247399_at	putative protein similar to unknov	---	AT5G62960	1.35	0.43	1.42	0.2007906	0.4448794	-5.57	TRUE
255443_at	sulfate transporter protein similar	SULTR3;2	AT4G02700	1.20	0.27	1.42	0.2009342	0.4451111	-5.57	FALSE
245903_at	CLB1 - like protein CLB1 protein	SYTD	AT5G11100	1.18	0.23	1.42	0.2009342	0.4451111	-5.57	FALSE
249344_at	prohibitin (gb AAC49691.1) ;supp	ATPHB3	AT5G40770	-1.33	-0.41	-1.42	0.2009564	0.445117	-5.57	FALSE
254785_at	putative pollen surface protein e	FLA2	AT4G12730	1.98	0.99	1.42	0.2010757	0.445122	-5.57	TRUE
264894_at	unknown protein Location of EST	---	AT1G23040	-1.21	-0.27	-1.42	0.2010377	0.445122	-5.57	FALSE
245206_at	putative protein similarity to NCA	DGS1	AT5G12290	-1.19	-0.26	-1.42	0.20101	0.445122	-5.57	FALSE
251824_at	ABC transporter - like protein AT	---	AT3G55090	1.18	0.24	1.42	0.2010311	0.445122	-5.57	FALSE
264263_at	Expressed protein ; supported by	AtPP2-B15	AT1G09155	-1.17	-0.23	-1.42	0.2010495	0.445122	-5.57	FALSE
265695_at	putative replication protein A1 ;s	RPA2	AT2G24490	-1.55	-0.63	-1.42	0.2010721	0.445122	-5.57	FALSE
265741_at	putative membrane transporter ;	---	AT2G01320	-1.36	-0.44	-1.42	0.2011778	0.4453047	-5.57	FALSE
245485_at	proline-rich, APG like protein	---	AT4G16230	1.19	0.25	1.42	0.2012076	0.4453201	-5.57	FALSE
253621_at	putative protein component of ar	---	AT4G30540	1.18	0.24	1.42	0.2012238	0.4453201	-5.57	FALSE
267461_at	putative auxin-regulated protein	---	AT2G33830	-1.21	-0.28	-1.42	0.2012694	0.4453779	-5.57	FALSE
248046_at	receptor protein kinase-like prote	---	AT5G56040	-1.24	-0.32	-1.42	0.2012978	0.4453856	-5.57	TRUE
251029_at	putative protein gene product of	---	AT5G02050	-1.40	-0.48	-1.42	0.2013326	0.4453856	-5.57	FALSE
245351_at	casein kinase II beta chain CKB2	CKB2	AT4G17640	-1.18	-0.24	-1.42	0.20139	0.4453856	-5.57	FALSE
252332_at	putative protein	---	AT3G48810	1.25	0.32	1.42	0.2013668	0.4453856	-5.57	FALSE
255092_s_a	putative protein various predicted	---	---	1.16	0.22	1.42	0.2013816	0.4453856	-5.57	FALSE
246399_at	bZIP transcription factor similar t	---	AT1G58110	1.19	0.25	1.42	0.2013884	0.4453856	-5.57	FALSE
257873_at	P-glycoprotein, putative similar t	PGP17	AT3G28380	1.21	0.28	1.42	0.2014351	0.445442	-5.57	FALSE
255372_at	putative reverse transcriptase	---	---	1.29	0.36	1.42	0.2014889	0.4455179	-5.57	FALSE
267032_at	putative protein kinase contains a	CIPK22	AT2G38490	1.29	0.37	1.42	0.2015576	0.4456265	-5.57	FALSE
246708_at	putative protein various predicte	---	AT5G28150	-1.23	-0.29	-1.41	0.201657	0.4456831	-5.57	FALSE
262037_at	hypothetical protein predicted by	---	---	1.17	0.23	1.41	0.2016613	0.4456831	-5.57	FALSE
246079_at	putative protein unconventional	---	AT5G20450	-1.22	-0.28	-1.41	0.2016603	0.4456831	-5.57	FALSE
265426_at	hypothetical protein predicted by	---	AT2G20740	-1.19	-0.25	-1.41	0.2016443	0.4456831	-5.57	FALSE
261956_at	oxidoreductase, putative similar	---	AT1G64590	1.33	0.41	1.41	0.2017022	0.445695	-5.57	FALSE
261396_at	hypothetical protein contains sim	---	AT1G79800	1.18	0.24	1.41	0.2017613	0.445695	-5.57	FALSE

260048_at	unknown protein contains Pfam p	---	AT1G73750	1.76	0.82	1.41	0.2017644	0.445695	-5.57	FALSE
259425_at	4,5 PIP kinase, putative similar t	PIPK11	AT1G01460	-1.15	-0.21	-1.41	0.2017417	0.445695	-5.57	FALSE
260631_at	hypothetical protein predicted by	---	AT1G62350	-1.20	-0.26	-1.41	0.2017188	0.445695	-5.57	FALSE
262891_at	ent-kaurene synthase, putative s	GA2	AT1G79460	1.30	0.38	1.41	0.2018631	0.4457834	-5.57	TRUE
246773_at	protein kinase-like protein MAP3	---	AT5G27510	1.25	0.32	1.41	0.2018548	0.4457834	-5.57	FALSE
252027_at	Spot 3 protein and vacuolar sorti	VSR1	AT3G52850	1.15	0.20	1.41	0.2018557	0.4457834	-5.57	FALSE
267240_at	hypothetical protein predicted by	---	AT2G02680	1.19	0.26	1.41	0.2019354	0.4458999	-5.57	FALSE
264904_s_a	putative thioredoxin reductase	NTRA	AT2G17420 ///	1.24	0.31	1.41	0.20198	0.4459553	-5.57	FALSE
253025_at	hypothetical protein	---	AT4G38120	-1.27	-0.35	-1.41	0.2020733	0.4460316	-5.57	FALSE
252059_at	E2, ubiquitin-conjugating enzym	UEV1D-4	AT3G52560	-1.16	-0.22	-1.41	0.2020598	0.4460316	-5.57	FALSE
252315_at	putative protein PrMC3 - Pinus r	CXE12	AT3G48690	1.22	0.28	1.41	0.2020592	0.4460316	-5.57	FALSE
265875_at	unknown protein ; supported by	---	AT2G01690	1.22	0.29	1.41	0.202165	0.446191	-5.58	FALSE
255932_at	mutator-like transposase, putativ	---	---	1.17	0.22	1.41	0.2021967	0.4462178	-5.58	FALSE
255043_at	putative protein several hypothet	---	AT4G09640	-1.32	-0.41	-1.41	0.2022923	0.4462632	-5.58	FALSE
247226_at	putative protein contains similarit	---	AT5G65100	1.14	0.19	1.41	0.2022955	0.4462632	-5.58	FALSE
256264_at	unknown protein ; supported by f	---	AT3G12210	-1.25	-0.33	-1.41	0.2022608	0.4462632	-5.58	FALSE
262018_at	hypothetical protein predicted by	---	AT1G35617	-1.20	-0.27	-1.41	0.2022915	0.4462632	-5.58	FALSE
253497_at	putative protein microtubule-ass	---	AT4G31880	-1.20	-0.26	-1.41	0.202353	0.4463469	-5.58	FALSE
258739_s_a	unknown protein similar to hypot	---	AT1G54300 ///	1.15	0.20	1.41	0.2023996	0.4464064	-5.58	FALSE
253086_at	hypothetical protein	---	AT4G36370	1.14	0.19	1.41	0.2024688	0.4465159	-5.58	FALSE
253072_at	putative protein ;supported by fu	---	AT4G37830	-1.14	-0.20	-1.41	0.2026246	0.446773	-5.58	FALSE
249097_at	putative protein strong similarity t	---	AT5G43520	-1.20	-0.26	-1.41	0.2026156	0.446773	-5.58	FALSE
263329_at	hypothetical protein contains C3H	---	AT2G15260	-1.16	-0.21	-1.41	0.2026446	0.4467741	-5.58	FALSE
260396_at	putative heme oxygenase similar	ho3	AT1G69720	1.31	0.39	1.41	0.2026744	0.4467964	-5.58	FALSE
256046_at	unknown protein	---	AT1G07135	1.89	0.92	1.41	0.2027123	0.4468368	-5.58	FALSE
261131_at	unknown protein	---	AT1G19835	-1.33	-0.41	-1.41	0.2027895	0.446859	-5.58	TRUE
246133_at	aldehyde oxidase AAO1 ; suppo	AAO1	AT5G20960	1.60	0.68	1.41	0.2028007	0.446859	-5.58	TRUE
245766_at	En/Spm-like transposon protein,	---	---	1.17	0.22	1.41	0.2028001	0.446859	-5.58	FALSE
252658_at	hypothetical protein	---	AT3G44800	1.22	0.29	1.41	0.2027678	0.446859	-5.58	FALSE
253841_at	putative beta-glucosidase beta-g	BGLU10	AT4G27830	1.26	0.34	1.41	0.2028884	0.4469659	-5.58	TRUE
252830_at	putative protein 70K peroxisoma	PXA1	AT4G39850	1.14	0.19	1.41	0.2028874	0.4469659	-5.58	FALSE
255508_at	putative zinc finger protein identi	---	AT4G02220	-1.20	-0.26	-1.41	0.2029303	0.4470151	-5.58	FALSE
251996_at	beta-galactosidase precursor - li	BGAL2	AT3G52840	-1.21	-0.27	-1.41	0.2029797	0.4470472	-5.58	TRUE
266629_at	putative serpin	---	AT2G35590	1.17	0.23	1.41	0.2029841	0.4470472	-5.58	FALSE
253820_at	hypothetical protein	---	AT4G28370	1.17	0.22	1.41	0.2030267	0.4470547	-5.58	FALSE

257348_at	hypothetical protein predicted by	---	AT2G42140	1.33	0.41	1.41	0.2030073	0.4470547	-5.58	FALSE
251482_s_a	receptor lectin kinase 3	---	AT3G59740 /	1.20	0.26	1.41	0.2030624	0.44709	-5.58	FALSE
267067_at	unknown protein	---	AT2G41020	-1.24	-0.31	-1.41	0.2030994	0.4471283	-5.58	FALSE
259057_at	unknown protein ; supported by	---	AT3G03310	1.23	0.30	1.41	0.2033098	0.4475483	-5.58	TRUE
245366_at	Expressed protein ; supported by	AtMAPR4	AT4G14965	-1.15	-0.20	-1.41	0.2033869	0.4476749	-5.58	FALSE
264236_at	hypothetical protein predicted by	---	AT1G54680	-1.18	-0.24	-1.41	0.2034259	0.4477175	-5.58	FALSE
266068_at	putative geranylgeranyl pyrophos	GGPS4	AT2G18640	1.21	0.27	1.41	0.203446	0.4477187	-5.58	FALSE
252799_at	putative protein various predicte	---	---	-1.13	-0.17	-1.41	0.2034691	0.4477262	-5.58	FALSE
259569_at	hypothetical protein	---	AT1G20480	1.20	0.26	1.41	0.203494	0.4477378	-5.58	FALSE
245608_at	protein kinase	---	AT4G14350	1.26	0.33	1.41	0.2035392	0.4477941	-5.58	FALSE
257851_at	unknown protein	---	AT3G12940	1.18	0.24	1.41	0.2036114	0.4479098	-5.58	FALSE
247601_at	zinc finger protein OBP4 - like zi	OBP4	AT5G60850	-1.27	-0.35	-1.41	0.2036394	0.4479282	-5.58	FALSE
250184_at	putative protein various predicte	---	AT5G14240	-1.16	-0.21	-1.41	0.2037128	0.4480463	-5.58	FALSE
258602_at	putative protein phosphatase-2C	---	AT3G02750	1.14	0.19	1.41	0.203777	0.4481444	-5.58	FALSE
247570_at	putative protein heparanase, Ho	AtGUS1	AT5G61250	1.49	0.58	1.41	0.2038524	0.4482669	-5.58	FALSE
252060_at	putative protein other hypothetica	PAD4	AT3G52430	1.73	0.79	1.41	0.2039739	0.4484908	-5.58	FALSE
267194_s_a	putative ARP2/3 protein complex	ARPC1A	AT2G30910 /	-1.18	-0.23	-1.41	0.2040709	0.4486608	-5.58	FALSE
247242_at	unknown protein	---	AT5G64690	1.14	0.19	1.41	0.2042055	0.4488864	-5.58	FALSE
252398_at	putative protein RING-H2 finger	---	AT3G47990	-1.17	-0.23	-1.41	0.2042522	0.4488864	-5.58	FALSE
264006_at	homeodomain transcription facto	ATHB6	AT2G22430	-1.27	-0.34	-1.41	0.2042251	0.4488864	-5.58	FALSE
247605_at	DNA binding protein - like putati	TCP5	AT5G60970	-1.21	-0.27	-1.41	0.2042514	0.4488864	-5.58	FALSE
248435_at	oleosin-like	OLEO3	AT5G51210	1.21	0.27	1.41	0.2043502	0.4490585	-5.58	FALSE
263015_at	hypothetical protein similar to hyp	---	AT1G23440	1.19	0.25	1.41	0.2044242	0.4491481	-5.58	FALSE
254468_at	UDP-glucose 4-epimerase - like	---	AT4G20460	1.17	0.23	1.41	0.2044303	0.4491481	-5.58	FALSE
246854_at	mitochondrial carrier - like protei	---	AT5G26200	-1.19	-0.25	-1.40	0.2044801	0.449171	-5.59	FALSE
256726_at	unknown protein	---	AT3G52210	1.24	0.32	1.40	0.204471	0.449171	-5.59	FALSE
246210_at	ribosomal protein ; supported by	---	AT4G36420	-1.27	-0.34	-1.40	0.2045719	0.4493293	-5.59	FALSE
261961_at	hypothetical protein predicted by	---	AT1G36510	1.20	0.26	1.40	0.2046089	0.4493674	-5.59	FALSE
249389_at	disease resistence like - protein	---	AT5G40100	1.22	0.28	1.40	0.2046624	0.4494415	-5.59	FALSE
259128_at	unknown protein similar to pushc	BIG	AT3G02260	-1.28	-0.35	-1.40	0.2047459	0.4495817	-5.59	FALSE
253968_at	putative calcineurin B-like protei	CBL7	AT4G26560	1.16	0.21	1.40	0.2049103	0.4498993	-5.59	FALSE
267336_at	putative small heat shock protein	---	AT2G19310	-1.26	-0.33	-1.40	0.2050198	0.4500551	-5.59	FALSE
256313_s_a	RNA-binding protein, putative co	APUM17	AT1G35850 /	-1.14	-0.19	-1.40	0.2050275	0.4500551	-5.59	FALSE
258195_at	myb protein(myb26) contains my	ATMYB26	AT3G13890	-1.18	-0.24	-1.40	0.2050404	0.4500551	-5.59	FALSE
258308_at	putative reverse transcriptase sir	---	---	1.35	0.43	1.40	0.2051108	0.4501662	-5.59	FALSE

262547_at	hypothetical protein predicted by	---	AT1G31270	1.13	0.18	1.40	0.205131	0.4501673	-5.59	FALSE
267632_at	hypothetical protein predicted by	---	AT2G42160	-1.27	-0.34	-1.40	0.2051931	0.4502601	-5.59	FALSE
263793_at	putative glucosyltransferase	ATCSLC08	AT2G24630	-1.39	-0.47	-1.40	0.2053117	0.4503904	-5.59	FALSE
262214_at	germin subunit, putative similar t	---	AT1G74820	1.16	0.21	1.40	0.2053076	0.4503904	-5.59	FALSE
256917_at	unknown protein contains Pfam	---	AT3G18930	1.15	0.20	1.40	0.2052904	0.4503904	-5.59	FALSE
247240_at	putative protein strong similarity t	CMPG2	AT5G64660	2.29	1.19	1.40	0.2053366	0.4504017	-5.59	FALSE
263146_at	lipase, putative similar to lipase	GLIP2	AT1G53940	1.20	0.27	1.40	0.2053631	0.4504166	-5.59	FALSE
247639_s_a	undecaprenyl diphosphate synth	---	AT5G60500 ///	1.13	0.17	1.40	0.2054466	0.450513	-5.59	FALSE
267151_at	aspartate aminotransferase (AAT	ASP1	AT2G30970	1.24	0.32	1.40	0.2054424	0.450513	-5.59	FALSE
246581_at	hypothetical protein predicted by	---	AT1G31760	-1.17	-0.23	-1.40	0.2054794	0.4505417	-5.59	FALSE
255165_at	putative protein putative centron	---	---	1.32	0.40	1.40	0.2055215	0.4505906	-5.59	FALSE
247765_at	cytochrome P450 CYP86A1	CYP86A1	AT5G58860	-1.36	-0.44	-1.40	0.2055911	0.4507	-5.59	FALSE
256402_at	hypothetical protein ; supported	---	AT3G06130	1.40	0.48	1.40	0.2056829	0.4508579	-5.59	FALSE
260233_at	putative cytochrome P450 simila	CYP98A9	AT1G74550	1.30	0.37	1.40	0.2057525	0.450967	-5.59	FALSE
251145_at	putative protein predicted protei	---	AT3G63500	1.20	0.27	1.40	0.2058168	0.450978	-5.59	FALSE
245748_at	unknown protein contains similar	---	AT1G51140	1.36	0.45	1.40	0.2057976	0.450978	-5.59	FALSE
246444_at	putative protein predicted protei	---	AT5G17570	-1.27	-0.35	-1.40	0.2058133	0.450978	-5.59	FALSE
262430_s_a	unknown protein	---	AT1G47550 ///	-1.18	-0.23	-1.40	0.2058451	0.4509968	-5.59	FALSE
263702_at	hypothetical protein identical to h	---	AT1G31240	1.17	0.22	1.40	0.2059635	0.4511695	-5.59	FALSE
257176_s_a	cyclopropane-fatty-acyl-phospho	---	AT3G23510 ///	1.70	0.77	1.40	0.2059615	0.4511695	-5.59	FALSE
247054_at	zinc finger protein	---	AT5G66730	1.18	0.24	1.40	0.2060795	0.4513802	-5.59	FALSE
248966_at	unknown protein ;supported by fu	---	AT5G45360	-1.18	-0.24	-1.40	0.2061536	0.4514992	-5.59	FALSE
256898_at	abscisic acid-insensitive protein	ABI3	AT3G24650	1.15	0.20	1.40	0.2061903	0.4515361	-5.59	FALSE
255553_at	predicted protein of unknown fun	---	AT4G01960	-1.25	-0.32	-1.40	0.2062196	0.4515396	-5.59	FALSE
254276_at	predicted protein PVPR3 protein	---	AT4G22820	1.39	0.47	1.40	0.2062315	0.4515396	-5.59	FALSE
256853_at	hypothetical protein predicted by	---	AT3G18640	-1.16	-0.21	-1.40	0.2063078	0.4516041	-5.59	FALSE
264226_at	hypothetical protein similar to put	---	AT1G67510	-1.18	-0.23	-1.40	0.2063452	0.4516041	-5.59	FALSE
245478_at	galactokinase like protein	ARA1	AT4G16130	-1.44	-0.53	-1.40	0.2063599	0.4516041	-5.59	FALSE
251921_at	40S ribosomal protein S21 homo	---	AT3G53890	-1.46	-0.55	-1.40	0.2063254	0.4516041	-5.59	FALSE
260507_at	unknown protein contains similar	WPP2	AT1G47200	-1.23	-0.30	-1.40	0.2063407	0.4516041	-5.59	FALSE
267119_at	putative cellulose synthase	ATCSLB01	AT2G32610	1.14	0.18	1.40	0.2064997	0.4518666	-5.59	FALSE
248073_at	pectate lyase	---	AT5G55720	1.17	0.22	1.40	0.2065709	0.451979	-5.59	FALSE
250395_at	putative protein cylicin II, bovine	---	AT5G10950	-1.28	-0.35	-1.40	0.2066009	0.4520014	-5.59	FALSE
248263_at	pectinesterase ; supported by cI	PMEPCRF	AT5G53370	1.38	0.47	1.40	0.2066301	0.4520218	-5.59	FALSE
260695_at	RNA helicase, putative similar to	ESP3	AT1G32490	-1.13	-0.18	-1.40	0.2067081	0.4521493	-5.59	FALSE

261568_at	DNA-binding protein, putative si	NGA3	AT1G01030	1.17	0.23	1.40	0.2068265	0.4523538	-5.60	FALSE
266496_at	putative zinc finger protein	---	---	1.19	0.25	1.40	0.2068413	0.4523538	-5.60	FALSE
253794_at	putative protein dimethylaniline r	---	AT4G28720	-1.57	-0.65	-1.40	0.2068988	0.4524157	-5.60	TRUE
258669_at	hypothetical protein predicted by	---	AT3G08800	-1.15	-0.20	-1.40	0.2069093	0.4524157	-5.60	FALSE
267372_at	putative protein kinase contains a	ARSK1	AT2G26290	1.77	0.83	1.40	0.2071039	0.4527978	-5.60	FALSE
267502_at	putative cytochrome P450	CYP76C4	AT2G45550	1.15	0.21	1.40	0.2071633	0.4528302	-5.60	FALSE
262389_at	hypothetical protein contains sim	---	AT1G49270	1.16	0.22	1.40	0.2071557	0.4528302	-5.60	FALSE
251378_at	putative protein	---	AT3G60660	-1.16	-0.22	-1.40	0.2071783	0.4528302	-5.60	FALSE
248556_at	unknown protein	---	AT5G50350	1.21	0.28	1.40	0.207204	0.452843	-5.60	FALSE
250865_at	putative protein predicted protei	---	AT5G03900	-1.26	-0.33	-1.40	0.2072342	0.4528657	-5.60	FALSE
263962_at	putative protein kinase contains a	---	AT2G36350	-1.26	-0.33	-1.40	0.2073211	0.4529687	-5.60	TRUE
264984_at	unknown protein ;supported by fu	---	AT1G27000	1.14	0.19	1.40	0.2073139	0.4529687	-5.60	FALSE
251123_at	putative protein predicted protei	---	AT5G01030	-1.15	-0.20	-1.39	0.2073561	0.4530018	-5.60	FALSE
249420_at	NAC domain/ NAM like protein N	anac094	AT5G39820	1.16	0.22	1.39	0.2073906	0.453034	-5.60	FALSE
251618_at	putative protein unknown protei	---	AT3G58020	-1.28	-0.35	-1.39	0.2074249	0.4530654	-5.60	FALSE
257654_at	DnaJ protein, putative contains I	---	AT3G13310	1.65	0.73	1.39	0.2075144	0.4531308	-5.60	FALSE
247785_at	subtilisin-like serine protease cor	---	AT5G58820	1.13	0.18	1.39	0.2075125	0.4531308	-5.60	FALSE
248269_at	putative protein contains similarit	ACBP1	AT5G53470	-1.21	-0.28	-1.39	0.2074953	0.4531308	-5.60	FALSE
245983_at	5-formyltetrahydrofolate cyclo-lig	5-FCL	AT5G13050	-1.16	-0.22	-1.39	0.2075895	0.4532079	-5.60	FALSE
263431_at	unknown protein ;supported by f	---	AT2G22170	2.75	1.46	1.39	0.2075827	0.4532079	-5.60	FALSE
264830_at	hypothetical protein predicted by	---	AT1G03710	1.20	0.26	1.39	0.2076226	0.4532368	-5.60	FALSE
267133_at	unknown protein	---	AT2G23440	1.18	0.24	1.39	0.2076953	0.4533521	-5.60	FALSE
251009_at	putative protein predicted protei	---	AT5G02640	1.40	0.48	1.39	0.2078169	0.4535309	-5.60	FALSE
258638_at	unknown protein ;supported by f	---	AT3G07950	-1.16	-0.21	-1.39	0.2078124	0.4535309	-5.60	FALSE
245803_at	cysteine proteinase RD21A ident	RD21	AT1G47128	1.22	0.29	1.39	0.2078992	0.4535391	-5.60	FALSE
262923_at	Dhp1-like protein similar to Dhp1	XRN3	AT1G75660	-1.17	-0.22	-1.39	0.2079003	0.4535391	-5.60	FALSE
264483_at	unknown protein	---	AT1G77230	-1.22	-0.29	-1.39	0.2078994	0.4535391	-5.60	FALSE
247799_at	subtilisin-like serine protease cor	---	AT5G58840	1.25	0.32	1.39	0.2078498	0.4535391	-5.60	FALSE
245100_at	ubiquitin-specific protease 5 (UB	UBP5	AT2G40930	-1.16	-0.22	-1.39	0.2079382	0.4535706	-5.60	FALSE
259401_at	hypothetical protein contains sim	CSTF77	AT1G17760	-1.31	-0.39	-1.39	0.2079545	0.4535706	-5.60	FALSE
264252_at	putative GTP-binding protein, SA	ATSARA1A	AT1G09180	1.17	0.22	1.39	0.2080894	0.4538215	-5.60	FALSE
267345_at	unknown protein ; supported by	---	AT2G44240	1.62	0.69	1.39	0.208137	0.4538818	-5.60	FALSE
263553_at	putative purple acid phosphatase	PAP10	AT2G16430	1.21	0.27	1.39	0.2083297	0.4541686	-5.60	TRUE
254859_at	putative protein Arabidopsis thal	---	AT4G12060	-1.22	-0.29	-1.39	0.2083486	0.4541686	-5.60	FALSE
246360_at	hypothetical protein	---	---	1.16	0.22	1.39	0.2084271	0.4541686	-5.60	FALSE

259279_at	putative cystathionine gamma-sy	MTO1	AT3G01120	1.16	0.22	1.39	0.2084476	0.4541686	-5.60	FALSE
261510_at	hypothetical protein predicted by	---	AT1G71760	-1.17	-0.22	-1.39	0.20835	0.4541686	-5.60	FALSE
249486_at	receptor protein kinase - like pro	---	AT5G39030	1.20	0.26	1.39	0.2083589	0.4541686	-5.60	FALSE
255744_at	hypothetical protein predicted by	---	---	-1.13	-0.17	-1.39	0.2084441	0.4541686	-5.60	FALSE
259341_at	unknown protein similar to hypot	ATBPM4	AT3G03740	1.15	0.20	1.39	0.2084014	0.4541686	-5.60	FALSE
264434_at	hypothetical protein predicted by	---	AT1G10340	1.71	0.77	1.39	0.2084476	0.4541686	-5.60	FALSE
250711_at	cell division related protein-like	---	AT5G06110	-1.17	-0.22	-1.39	0.2085666	0.4542888	-5.60	FALSE
262479_at	leucine-rich repeat transmembra	SUB	AT1G11130	1.14	0.19	1.39	0.208545	0.4542888	-5.60	FALSE
265176_at	OBP32pep protein, putative ider	---	AT1G23520	1.16	0.21	1.39	0.2085471	0.4542888	-5.60	FALSE
260540_at	hypothetical protein predicted by	---	AT2G43500	1.14	0.19	1.39	0.2085825	0.4542888	-5.60	FALSE
256058_at	UDP-glucose glucosyltransferas	UGT71C5	AT1G07240	1.23	0.30	1.39	0.2086358	0.4543615	-5.60	FALSE
246433_at	glutamine-rich protein predicted	---	AT5G17510	-1.26	-0.33	-1.39	0.2087495	0.4544356	-5.60	FALSE
246166_at	putative protein	---	---	1.17	0.23	1.39	0.2087099	0.4544356	-5.60	FALSE
252640_at	acyl CoA reductase -like protein	FAR8	AT3G44560	1.15	0.20	1.39	0.2087025	0.4544356	-5.60	FALSE
257762_at	hypothetical protein	XRCC4	AT3G23100	-1.16	-0.22	-1.39	0.2087472	0.4544356	-5.60	FALSE
263261_at	putative pre-mRNA splicing facto	---	AT1G10580	1.12	0.17	1.39	0.2087723	0.4544419	-5.60	FALSE
251617_at	putative protein hypothetical pro	---	AT3G58000	1.15	0.21	1.39	0.2088708	0.4545551	-5.60	FALSE
250026_at	putative protein similar to unknov	---	AT5G18090	1.19	0.25	1.39	0.208866	0.4545551	-5.60	FALSE
265504_at	putative Ta11-like non-LTR retro	---	---	1.18	0.24	1.39	0.2089638	0.4545551	-5.60	FALSE
246695_at	putative protein	---	---	1.23	0.30	1.39	0.2089465	0.4545551	-5.60	FALSE
257902_at	receptor kinase, putative similar	---	AT3G28450	1.29	0.37	1.39	0.2089577	0.4545551	-5.60	FALSE
254317_at	hypothetical protein	---	AT4G22510	1.14	0.18	1.39	0.2089469	0.4545551	-5.60	FALSE
266243_at	hypothetical protein predicted by	---	AT2G27750	1.15	0.20	1.39	0.2089042	0.4545551	-5.60	FALSE
263193_at	acetyl-CoA carboxylase, putative	---	AT1G36050	1.16	0.21	1.39	0.2091293	0.4546254	-5.60	FALSE
260377_at	unknown protein	---	AT1G73930	1.13	0.18	1.39	0.2090511	0.4546254	-5.60	FALSE
251650_at	hypothetical protein	---	AT3G57360	-1.25	-0.32	-1.39	0.2090681	0.4546254	-5.60	FALSE
259938_at	hypothetical protein predicted by	---	AT1G71310	-1.18	-0.24	-1.39	0.2091143	0.4546254	-5.60	FALSE
264393_at	unknown protein Contains simila	---	AT1G11880	-1.17	-0.23	-1.39	0.2091357	0.4546254	-5.60	FALSE
249879_at	serine/threonine protein kinase-li	---	AT5G23170	1.17	0.22	1.39	0.2091255	0.4546254	-5.60	FALSE
265362_at	putative retroelement pol polypro	---	---	-1.15	-0.21	-1.39	0.2090203	0.4546254	-5.60	FALSE
245892_at	putative lipid transfer protein lipi	---	AT5G09370	1.25	0.32	1.39	0.2092614	0.4547253	-5.61	FALSE
248213_at	putative protein similar to unknov	AtGRF7	AT5G53660	1.18	0.24	1.39	0.2092253	0.4547253	-5.61	FALSE
258494_at	cell division protein FtsH-like pro	---	AT3G02450	-1.21	-0.28	-1.39	0.2092561	0.4547253	-5.61	FALSE
252695_s_a	hypothetical protein predicted pr	---	---	-1.12	-0.17	-1.39	0.2092329	0.4547253	-5.61	FALSE
264844_at	putative glycosylation enzyme ;	---	AT1G03520	-1.23	-0.30	-1.39	0.209303	0.4547725	-5.61	FALSE

247095_at	dehydrin RAB18-like protein (sp	RAB18	AT5G66400	1.46	0.55	1.39	0.2094377	0.4550218	-5.61	FALSE
253535_at	putaive DNA-binding protein DN	WRKY11	AT4G31550	1.81	0.85	1.39	0.2094897	0.4550884	-5.61	FALSE
253448_at	putative protein mRNA for KIAA(	---	AT4G32640	1.14	0.19	1.39	0.2095083	0.4550884	-5.61	FALSE
258817_at	hypothetical protein similar to hy	---	AT3G04750	-1.14	-0.19	-1.39	0.2095359	0.4550899	-5.61	FALSE
254067_at	hypothetical protein	NAP8	AT4G25450	1.15	0.20	1.39	0.2095657	0.4550899	-5.61	FALSE
263959_at	hypothetical protein predicted by	---	AT2G36210	1.15	0.21	1.39	0.2095688	0.4550899	-5.61	FALSE
260557_at	putative endochitinase	---	AT2G43610	1.13	0.18	1.39	0.2096313	0.4551822	-5.61	FALSE
258515_at	ATP citrate lyase, putative simila	ACLB-1	AT3G06650	-1.15	-0.21	-1.39	0.2097899	0.4553966	-5.61	TRUE
246794_s_a	putative protein predicted protei	---	AT5G06350 /,	-1.36	-0.44	-1.39	0.2097864	0.4553966	-5.61	FALSE
259122_at	unknown protein similar to putat	COBL1	AT3G02210	1.20	0.27	1.39	0.2097782	0.4553966	-5.61	FALSE
259402_at	developmental protein, putative	VPS46.1	AT1G17730	-1.15	-0.21	-1.39	0.2098195	0.4554176	-5.61	FALSE
254343_at	PRH26 protein ;supported by ful	אפר-03	AT4G21990	1.63	0.71	1.39	0.2098635	0.4554696	-5.61	TRUE
254989_at	retrotransposon like protein copi	---	---	1.19	0.25	1.39	0.2099342	0.4554932	-5.61	FALSE
261456_at	hypothetical protein predicted by	---	AT1G21050	-2.12	-1.09	-1.39	0.209933	0.4554932	-5.61	FALSE
256233_at	ankyrin-like protein contains Pfar	ITN1	AT3G12360	1.14	0.19	1.39	0.2099269	0.4554932	-5.61	FALSE
263811_at	putative acyl-CoA synthetase ; su	---	AT2G04350	1.18	0.24	1.39	0.2099981	0.4555885	-5.61	FALSE
254947_at	putative retrotransposon polypro	---	---	1.27	0.35	1.39	0.2100615	0.4555959	-5.61	FALSE
267124_at	putative acetone-cyanohydrin lya	MES19	AT2G23570	-1.19	-0.25	-1.39	0.2100527	0.4555959	-5.61	FALSE
253334_at	putative protein dihydrokaempfe	---	AT4G33360	1.28	0.35	1.39	0.2100529	0.4555959	-5.61	FALSE
248535_at	putative protein contains similarit	---	AT5G50120	1.21	0.28	1.39	0.2101606	0.4557675	-5.61	FALSE
245115_at	putative esterase D ;supported b	SFGH	AT2G41530	-1.29	-0.37	-1.39	0.2102131	0.4558382	-5.61	FALSE
248196_at	putative protein similar to unknov	---	AT5G54150	1.15	0.20	1.38	0.2103859	0.4561694	-5.61	FALSE
255742_at	DNA-binding protein RAV2, puta	TEM1	AT1G25560	1.15	0.21	1.38	0.2104741	0.4562555	-5.61	FALSE
245439_at	hypothetical protein	---	AT4G16670	1.39	0.47	1.38	0.2104856	0.4562555	-5.61	FALSE
255597_at	hypothetical protein	---	AT4G01730	1.18	0.24	1.38	0.2104799	0.4562555	-5.61	FALSE
265189_at	unknown protein ; supported by	---	AT1G23840	1.40	0.49	1.38	0.2105385	0.4563268	-5.61	FALSE
256865_at	NAD dependent epimerase, puta	GAE6	AT3G23820	-1.35	-0.44	-1.38	0.2106867	0.4564053	-5.61	TRUE
257495_at	unknown protein	ATPDIL5-1	AT1G07960	-1.19	-0.25	-1.38	0.210642	0.4564053	-5.61	FALSE
245994_at	putative protein various predicte	---	---	1.19	0.25	1.38	0.2106142	0.4564053	-5.61	FALSE
260558_at	putative endochitinase	---	AT2G43600	1.22	0.29	1.38	0.2106502	0.4564053	-5.61	FALSE
265212_at	putative sugar transporter protein	---	AT1G05030	-1.17	-0.22	-1.38	0.2106862	0.4564053	-5.61	FALSE
252749_at	putative protein several hypothet	---	---	1.17	0.22	1.38	0.2106948	0.4564053	-5.61	FALSE
250092_at	putative protein	---	AT5G17360	-1.13	-0.18	-1.38	0.2107742	0.4565341	-5.61	FALSE
253307_at	putative protein auxin-induced p	---	AT4G33670	-1.19	-0.26	-1.38	0.2108267	0.4566044	-5.61	FALSE
265644_at	hypothetical protein predicted by	ATEPR1	AT2G27380	1.15	0.21	1.38	0.2109237	0.4566411	-5.61	FALSE

248596_at	putative protein contains similarit	AtMYB111	AT5G49330	-1.44	-0.53	-1.38	0.2108873	0.4566411	-5.61	FALSE
249874_at	putative protein contains similarit	---	AT5G23070	-1.32	-0.40	-1.38	0.2109087	0.4566411	-5.61	FALSE
245420_at	hypothetical protein	---	AT4G17410	1.18	0.24	1.38	0.210893	0.4566411	-5.61	FALSE
259581_at	RING zinc finger protein, putativ	---	AT1G28040	1.19	0.25	1.38	0.2110108	0.4567863	-5.61	FALSE
245319_at	Expressed protein ; supported by	---	AT4G16146	1.32	0.40	1.38	0.211187	0.4568207	-5.61	FALSE
254607_at	hypothetical protein ;supported b	---	AT4G18920	1.15	0.21	1.38	0.2111781	0.4568207	-5.61	FALSE
259595_at	CONSTANS family zinc finger p	---	AT1G28050	1.27	0.34	1.38	0.2110591	0.4568207	-5.61	FALSE
261542_at	unknown protein contains Pfam p	---	AT1G63560	1.19	0.26	1.38	0.21111	0.4568207	-5.61	FALSE
255900_at	hypothetical protein predicted by	---	AT1G17830 ///	1.56	0.64	1.38	0.2111727	0.4568207	-5.61	FALSE
257443_at	hypothetical protein predicted by	---	AT2G22050	-1.15	-0.21	-1.38	0.211154	0.4568207	-5.61	FALSE
256960_at	unknown protein ;supported by f	---	AT3G13510	-1.23	-0.30	-1.38	0.2111476	0.4568207	-5.61	FALSE
254807_at	putative protein	---	AT4G12700	-1.24	-0.31	-1.38	0.2111568	0.4568207	-5.61	FALSE
246389_at	amino acid carrier, putative simil	AAP3	AT1G77380	1.25	0.32	1.38	0.2112497	0.4568264	-5.61	TRUE
265231_s_a	hypothetical protein	---	AT2G07713	1.16	0.21	1.38	0.2112423	0.4568264	-5.61	FALSE
248316_at	putative protein similar to unknov	---	AT5G52670	1.23	0.30	1.38	0.2112443	0.4568264	-5.61	FALSE
244911_at	hypothetical protein	---	---	-1.18	-0.24	-1.38	0.2112713	0.45683	-5.61	FALSE
251754_at	beta-1,3-glucanase - like protein	---	AT3G55780	1.19	0.25	1.38	0.2113133	0.4568454	-5.61	FALSE
259576_at	RING zinc finger protein, putativ	---	AT1G35330	1.24	0.31	1.38	0.2113185	0.4568454	-5.61	FALSE
259393_at	trehalose-6-phosphate synthase	ATTPS7	AT1G06410	1.18	0.24	1.38	0.2114062	0.4568998	-5.61	TRUE
245307_at	gibberellin oxidase-like protein n	---	AT4G16770	-1.20	-0.26	-1.38	0.2114238	0.4568998	-5.61	FALSE
256866_at	unknown protein similar to alpha	---	AT3G26380	-1.23	-0.30	-1.38	0.2114148	0.4568998	-5.61	FALSE
262333_at	hypothetical protein similar to put	---	AT1G64020	-1.18	-0.24	-1.38	0.2113975	0.4568998	-5.61	FALSE
252805_at	putative protein	---	AT3G42380	1.14	0.19	1.38	0.2115707	0.457174	-5.61	FALSE
249108_at	steroid sulfotransferase-like	---	AT5G43690	1.13	0.17	1.38	0.2117388	0.4574773	-5.62	FALSE
263933_s_a	putative harpin-induced protein	---	AT2G35970 ///	1.17	0.23	1.38	0.2117521	0.4574773	-5.62	FALSE
250814_at	E2, ubiquitin-conjugating enzym	UBC22	AT5G05080	-1.20	-0.26	-1.38	0.2117713	0.4574773	-5.62	FALSE
255683_at	putative malate oxidoreductase	---	AT4G00570	1.20	0.26	1.38	0.211845	0.4575933	-5.62	FALSE
245649_at	F5A9.21 unknown protein; simila	---	AT1G24706	-1.20	-0.27	-1.38	0.2119725	0.4577819	-5.62	FALSE
261167_at	disulfide isomerase-related prote	ATPDIL2-2	AT1G04980	1.66	0.73	1.38	0.2119713	0.4577819	-5.62	FALSE
266825_at	unknown protein	---	AT2G22890	1.37	0.46	1.38	0.2120339	0.4578279	-5.62	FALSE
265248_at	unknown protein ; supported by	PIF4	AT2G43010	-1.31	-0.39	-1.38	0.2120149	0.4578279	-5.62	FALSE
264401_at	dihydroflavonol 4-reductase, put	BAN	AT1G61720	1.13	0.18	1.38	0.2120574	0.4578353	-5.62	FALSE
253474_at	hypothetical protein	---	AT4G32270	-1.20	-0.27	-1.38	0.2121798	0.4580367	-5.62	FALSE
253810_at	putative NADH dehydrogenase I	NDB1	AT4G28220	-1.49	-0.58	-1.38	0.2121909	0.4580367	-5.62	FALSE
256488_at	hypothetical protein	NFD4	AT1G31470	1.16	0.22	1.38	0.2122398	0.4580989	-5.62	FALSE

262544_at	hypothetical protein predicted by	---	AT1G15420	-1.20	-0.26	-1.38	0.2122929	0.4581092	-5.62	FALSE
253604_at	hypothetical protein	---	AT4G30970	1.14	0.19	1.38	0.2122786	0.4581092	-5.62	FALSE
256168_at	receptor protein kinase, putative	---	AT1G51805	1.44	0.52	1.38	0.2123048	0.4581092	-5.62	FALSE
245014_at	ATPase beta subunit	---	---	-1.13	-0.18	-1.38	0.212371	0.4582087	-5.62	FALSE
247690_at	putative protein	MBD7	AT5G59800	-1.34	-0.42	-1.38	0.2123988	0.4582253	-5.62	FALSE
245670_at	mitochondrial protein (AtJ1), put	ATJ1	AT1G28210	1.36	0.44	1.38	0.2124732	0.4583426	-5.62	FALSE
259046_at	calmodulin-like protein similar to	---	AT3G03400	1.17	0.23	1.38	0.2125181	0.4583961	-5.62	FALSE
261799_at	unknown protein contains similar	---	AT1G30473	1.24	0.31	1.38	0.2125942	0.4585168	-5.62	FALSE
245929_at	alcohol dehydrogenase - like pro	---	AT5G24760	1.61	0.69	1.38	0.2126502	0.4585941	-5.62	TRUE
263182_at	Expressed protein ; supported by	---	AT1G05575	2.72	1.44	1.38	0.2127524	0.4586846	-5.62	FALSE
246220_at	putative protein ; supported by cl	---	AT4G37210	-1.15	-0.20	-1.38	0.2127234	0.4586846	-5.62	FALSE
266324_at	putative rac GTPase activating p	---	AT2G46710	-1.74	-0.80	-1.38	0.2127374	0.4586846	-5.62	FALSE
251592_at	zinc finger - like protein finger pr	NTT	AT3G57670	1.15	0.20	1.38	0.2128315	0.4588117	-5.62	FALSE
250460_at	putative protein similar to unknov	---	AT5G09850	1.15	0.20	1.38	0.2130421	0.4591573	-5.62	FALSE
AFFX-BioC	E. coli /GEN=bioC /DB_XREF=g	---	---	1.44	0.52	1.38	0.2130307	0.4591573	-5.62	FALSE
261081_at	transformer-SR ribonucleoprotei	---	AT1G07350	-1.28	-0.36	-1.38	0.2130522	0.4591573	-5.62	FALSE
262824_at	putative DNA binding protein sin	RBP45B	AT1G11650	-1.13	-0.18	-1.38	0.2130793	0.4591723	-5.62	FALSE
263514_at	putative poly(ADP-ribose) glycoh	---	AT2G31860	1.17	0.22	1.37	0.2131649	0.459289	-5.62	FALSE
266544_at	similar to late embryogenesis ab	---	AT2G35300	1.14	0.19	1.37	0.2131737	0.459289	-5.62	FALSE
253111_at	putative protein glutamic acid-ric	---	AT4G35940	1.24	0.32	1.37	0.2132827	0.459437	-5.62	FALSE
266625_at	putative peroxidase	---	AT2G35380	1.17	0.23	1.37	0.2132784	0.459437	-5.62	FALSE
260923_at	glycine-rich RNA-binding protein	---	AT1G21570	1.18	0.24	1.37	0.2134094	0.459439	-5.62	FALSE
259212_at	hypothetical protein predicted by	---	AT3G09180	-1.18	-0.24	-1.37	0.2134448	0.459439	-5.62	FALSE
246742_at	TOPP8 serine/threonine protein	TOPP8	AT5G27840	1.13	0.17	1.37	0.213396	0.459439	-5.62	FALSE
254253_at	serine/threonine kinase - like pro	---	AT4G23320	1.61	0.69	1.37	0.2133297	0.459439	-5.62	FALSE
264905_at	putative Mlo protein	MLO7	AT2G17430	1.16	0.21	1.37	0.2133138	0.459439	-5.62	FALSE
261621_at	hypothetical protein similar to gu	EDA10	AT1G01960	-1.16	-0.21	-1.37	0.2133918	0.459439	-5.62	FALSE
254939_at	putative protein predicted protei	---	AT4G10800	-1.27	-0.34	-1.37	0.2134331	0.459439	-5.62	FALSE
250053_at	potassium-dependent sodium-ca	---	AT5G17850	1.20	0.26	1.37	0.21344	0.459439	-5.62	FALSE
245013_at	ATPase epsilon subunit	---	---	-1.13	-0.18	-1.37	0.2134698	0.4594496	-5.62	FALSE
251272_at	homeobox-leucine zipper protein	ATHB-12	AT3G61890	1.56	0.64	1.37	0.2135853	0.459499	-5.62	TRUE
262769_at	actin-like protein strong similarity	DIS1	AT1G13180	1.20	0.26	1.37	0.2136007	0.459499	-5.62	TRUE
259367_at	hypothetical protein predicted by	---	AT1G69070	-1.28	-0.35	-1.37	0.213593	0.459499	-5.62	FALSE
255672_at	hypothetical protein ; supported	EDA8	AT4G00310	1.19	0.25	1.37	0.2136338	0.459499	-5.62	FALSE
262129_at	mutM homologue-1 identical to m	ATMMH-1	AT1G52500	-1.21	-0.28	-1.37	0.2135939	0.459499	-5.62	FALSE

260983_at	hypothetical protein predicted by	---	AT1G53560	1.33	0.41	1.37	0.2136195	0.459499	-5.62	FALSE
255896_at	basic blue protein, putative simil	---	AT1G17800	1.14	0.19	1.37	0.2135543	0.459499	-5.62	FALSE
261810_at	ligase I, putative similar to ligase	ATLIG1	AT1G08130	-1.35	-0.44	-1.37	0.2136807	0.4595566	-5.62	FALSE
259553_x_a	hypothetical protein	ATEXT3	AT1G21310	1.48	0.56	1.37	0.2138047	0.4596608	-5.62	TRUE
246907_at	AtBgamma - like protein B' regu	---	AT5G25510	1.21	0.27	1.37	0.2137733	0.4596608	-5.62	FALSE
267046_at	hypothetical protein	---	AT2G34360	1.25	0.32	1.37	0.2138098	0.4596608	-5.62	FALSE
249458_at	putative protein predicted protei	---	AT5G39560	1.15	0.21	1.37	0.2138044	0.4596608	-5.62	FALSE
262497_at	putative 20S proteasome beta s	PBC1	AT1G21720	-1.17	-0.23	-1.37	0.2138432	0.4596893	-5.62	FALSE
249652_at	putative protein hypothetical prot	---	AT5G37070	1.22	0.28	1.37	0.2139056	0.4597801	-5.62	FALSE
266465_at	putative auxin-responsive protein	GH3.9	AT2G47750	1.18	0.24	1.37	0.2139608	0.4598122	-5.62	FALSE
261791_at	unknown protein ; supported by f	---	AT1G16170	-1.43	-0.52	-1.37	0.2139458	0.4598122	-5.62	FALSE
255631_at	hypothetical protein	BSK3	AT4G00710	-1.14	-0.18	-1.37	0.2140098	0.4598656	-5.62	FALSE
255762_at	unknown protein contains Pfam p	HAC12	AT1G16710	1.17	0.23	1.37	0.2140663	0.4598656	-5.62	FALSE
253166_at	putative protein putative ligand-g	GLUR2	AT4G35290	-1.28	-0.35	-1.37	0.214045	0.4598656	-5.62	FALSE
256339_at	hypothetical protein	---	AT1G72080	1.16	0.21	1.37	0.2140614	0.4598656	-5.62	FALSE
266736_at	putative cytochrome P450 ; supp	CYP709B1	AT2G46960	1.15	0.20	1.37	0.214095	0.4598839	-5.63	FALSE
247994_at	RNA-binding protein-like	---	AT5G56140	-1.20	-0.26	-1.37	0.2142014	0.4600692	-5.63	FALSE
254602_at	hypothetical protein	EDR2	AT4G19040	1.16	0.22	1.37	0.2142862	0.4601913	-5.63	FALSE
262793_at	putative cytochrome P450 monc	CYP71B7	AT1G13110	1.44	0.53	1.37	0.2142986	0.4601913	-5.63	FALSE
263408_at	predicted protein	---	AT2G04060	1.15	0.20	1.37	0.2144246	0.460387	-5.63	FALSE
252035_at	beta-ketoacyl-CoA synthase like	KCS15	AT3G52160	1.20	0.26	1.37	0.2144301	0.460387	-5.63	FALSE
249610_at	putative protein	---	AT5G37360	-1.38	-0.46	-1.37	0.2145201	0.46045	-5.63	TRUE
266428_at	putative protein kinase contains a	---	AT2G07180	-1.21	-0.28	-1.37	0.2145198	0.46045	-5.63	FALSE
248821_at	protein serine threonine kinase-li	---	AT5G47070	1.42	0.50	1.37	0.2144824	0.46045	-5.63	FALSE
263847_at	putative glucosyltransferase ; su	---	AT2G36970	-1.78	-0.83	-1.37	0.2145538	0.4604792	-5.63	TRUE
262486_at	putative bzip-like transcription fa	---	AT1G21740	1.25	0.33	1.37	0.2146546	0.4606088	-5.63	FALSE
256616_at	hypothetical protein similar to unl	---	AT3G22260	1.27	0.35	1.37	0.2146492	0.4606088	-5.63	FALSE
250624_at	putative protein	---	AT5G07330	1.18	0.24	1.37	0.214741	0.4607507	-5.63	FALSE
267287_at	putative pectinesterase	sks16	AT2G23630	1.14	0.19	1.37	0.2147874	0.4608072	-5.63	FALSE
256990_at	hypothetical protein predicted by	---	AT3G28590	1.25	0.32	1.37	0.2149069	0.4609582	-5.63	FALSE
261228_at	C-8,7 sterol isomerase identical	HYD1	AT1G20050	-1.21	-0.27	-1.37	0.2149185	0.4609582	-5.63	FALSE
249418_at	putative protein predicted protei	---	AT5G39785	1.14	0.19	1.37	0.2148861	0.4609582	-5.63	FALSE
254021_at	putative protein cell death suppr	ACD1-LIKE	AT4G25650	-1.20	-0.27	-1.37	0.2150245	0.4611422	-5.63	FALSE
249763_at	receptor-protein kinase-like prote	---	AT5G24010	-1.29	-0.37	-1.37	0.2150885	0.4612362	-5.63	FALSE
260481_at	ferredoxin precusor isolog ;supp	ATFD1	AT1G10960	-1.32	-0.40	-1.37	0.2151301	0.461282	-5.63	FALSE

265693_at	putative poly(A) binding protein	---	AT2G24350	-1.18	-0.24	-1.37	0.2151755	0.461336	-5.63	FALSE
261947_at	ubiquitin, putative similar to poly	---	AT1G64470	1.21	0.27	1.37	0.2152278	0.4614047	-5.63	FALSE
244973_at	PSII T protein	---	---	-1.43	-0.52	-1.37	0.2152953	0.4615061	-5.63	FALSE
266048_at	putative thioredoxin H contains a	ATCXXS2	AT2G40790	1.18	0.24	1.37	0.2153441	0.4615674	-5.63	FALSE
250274_at	putative protein predicted protei	---	AT5G13020	-1.19	-0.25	-1.37	0.2153927	0.4615693	-5.63	FALSE
258941_at	putative monodehydroascorbate	MDHAR	AT3G09940	3.23	1.69	1.37	0.2154057	0.4615693	-5.63	FALSE
259329_at	putative two-component phosph	AHP4	AT3G16360	-1.48	-0.57	-1.37	0.2153834	0.4615693	-5.63	FALSE
246421_at	TOM (target of myb1) -like prote	---	AT5G16880	1.20	0.26	1.37	0.2154516	0.4616242	-5.63	FALSE
257234_at	hypothetical protein predicted by	---	AT3G14880	1.23	0.29	1.37	0.215561	0.4618153	-5.63	FALSE
254081_at	putative protein various predicte	---	AT4G25660	1.20	0.26	1.37	0.2155947	0.4618439	-5.63	FALSE
262137_at	transcription factor, putative sim	---	AT1G77920	-1.16	-0.21	-1.37	0.215618	0.4618506	-5.63	TRUE
255034_at	putative protein Phaseolus vulga	---	---	1.15	0.20	1.37	0.2157351	0.4620579	-5.63	FALSE
257690_at	unknown protein contains similar	---	AT3G12830	-1.51	-0.59	-1.37	0.2158015	0.4621109	-5.63	FALSE
259695_at	hypothetical protein predicted by	---	AT1G63170	1.20	0.26	1.37	0.2158164	0.4621109	-5.63	FALSE
267418_at	putative RING zinc finger protein	---	AT2G35000	1.20	0.27	1.37	0.2158206	0.4621109	-5.63	FALSE
264151_at	hypothetical protein predicted b	---	AT1G02070	1.18	0.24	1.37	0.215899	0.4622355	-5.63	FALSE
250375_at	putative protein L-gulono-gamm	---	AT5G11540	-1.17	-0.22	-1.37	0.2159355	0.4622367	-5.63	FALSE
256844_s_a	En/Spm transposon protein, puta	---	---	1.16	0.21	1.37	0.2159401	0.4622367	-5.63	FALSE
249144_at	squamosa promoter binding prot	SPL2	AT5G43270	-1.18	-0.23	-1.37	0.2159923	0.462272	-5.63	FALSE
253749_at	phytochrome-associated protein	PAP2	AT4G29080	2.17	1.12	1.37	0.2159972	0.462272	-5.63	FALSE
251178_at	cytokinin oxidase -like protein cy	CKX6	AT3G63440	1.42	0.50	1.37	0.2160247	0.4622876	-5.63	TRUE
254270_at	gamma-glutamylcysteine synthet	GSH1	AT4G23100	1.49	0.57	1.37	0.2160636	0.4623275	-5.63	FALSE
247621_at	putative protein predicted protei	---	AT5G60340	1.15	0.21	1.37	0.21609	0.4623406	-5.63	FALSE
246277_at	hypothetical protein	---	AT4G36460	-1.18	-0.24	-1.37	0.2161119	0.4623441	-5.63	FALSE
257378_s_a	hypothetical protein predicted by	---	AT2G02290 /	1.18	0.24	1.36	0.2162246	0.4625419	-5.63	FALSE
249482_at	putative protein ;supported by fu	---	AT5G38980	-1.44	-0.53	-1.36	0.2162785	0.4625704	-5.63	FALSE
264368_at	hypothetical protein Contains sir	---	AT1G03280	-1.16	-0.21	-1.36	0.2162583	0.4625704	-5.63	FALSE
245073_at	putative glucosyltransferase	---	AT2G23210	1.17	0.22	1.36	0.2163533	0.4626434	-5.63	FALSE
245889_at	PEE-rich protein ;supported by f	---	AT5G09480	-1.38	-0.46	-1.36	0.2163426	0.4626434	-5.63	FALSE
251078_at	putative protein hypothetical prot	---	AT5G01990	-1.28	-0.35	-1.36	0.2163969	0.4626933	-5.63	FALSE
265633_at	F-box protein family, AtFBL6 cor	EBF1	AT2G25490	1.20	0.27	1.36	0.2165555	0.4629891	-5.63	FALSE
251768_at	phosphoinositide-specific phosp	---	AT3G55940	1.34	0.42	1.36	0.2165961	0.4630313	-5.64	TRUE
257750_at	unknown protein ;supported by f	---	AT3G18800	-1.20	-0.26	-1.36	0.2166158	0.4630313	-5.64	FALSE
249794_at	putative protein contains similarit	AtCXE18	AT5G23530	1.13	0.18	1.36	0.2167206	0.4631194	-5.64	FALSE
247052_at	homeodomain transcription facto	HB53	AT5G66700	1.18	0.24	1.36	0.2167468	0.4631194	-5.64	FALSE

251263_at	putative protein DNAJ PROTEIN	---	AT3G62190	-1.16	-0.22	-1.36	0.2167585	0.4631194	-5.64	FALSE
248965_at	nodulin-like protein	---	AT5G45370	1.22	0.28	1.36	0.2167451	0.4631194	-5.64	FALSE
262321_at	hypothetical protein predicted by	---	AT1G27570	1.16	0.22	1.36	0.2167121	0.4631194	-5.64	FALSE
252506_at	putative protein UDP-galactose	UTR5	AT3G46180	-1.18	-0.24	-1.36	0.2168001	0.4631647	-5.64	FALSE
264232_at	putative protein kinase Pfam HM	---	AT1G67470	1.69	0.76	1.36	0.2169258	0.4633898	-5.64	FALSE
250889_at	putative protein exostose-relate	---	AT5G04500	1.17	0.22	1.36	0.2169471	0.463392	-5.64	FALSE
250105_at	putative protein contains similarit	RAD4	AT5G16630	-1.33	-0.42	-1.36	0.2169852	0.4634301	-5.64	FALSE
266316_at	unknown protein ; supported by	---	AT2G27080	2.13	1.09	1.36	0.2170253	0.4634722	-5.64	FALSE
256456_at	unknown protein ; supported by f	---	AT1G75180	1.34	0.42	1.36	0.2172347	0.4636155	-5.64	TRUE
263130_at	hypothetical protein predicted by	POLD3	AT1G78650	-1.33	-0.41	-1.36	0.2172117	0.4636155	-5.64	FALSE
264412_at	hypothetical protein similar to put	---	AT1G43260	1.15	0.20	1.36	0.2171521	0.4636155	-5.64	FALSE
258819_at	unknown protein similar to putat	---	AT3G04590	-1.21	-0.27	-1.36	0.2172265	0.4636155	-5.64	FALSE
266733_at	similar to axi 1 protein from Nicot	---	AT2G03280	-1.17	-0.22	-1.36	0.2171191	0.4636155	-5.64	FALSE
253502_at	Cytochrome P450-like protein cy	CYP82C4	AT4G31940	1.15	0.20	1.36	0.217225	0.4636155	-5.64	FALSE
251869_at	putative protein	---	AT3G54500	-1.30	-0.38	-1.36	0.2172293	0.4636155	-5.64	FALSE
254230_at	polyprenyltransferase like protei	AtPPT1	AT4G23660	-1.17	-0.22	-1.36	0.217271	0.4636497	-5.64	FALSE
247499_at	predicted protein	---	AT5G61865	-1.17	-0.22	-1.36	0.2173484	0.4637714	-5.64	FALSE
263698_at	hypothetical protein similar to a	---	---	1.21	0.28	1.36	0.2173692	0.4637724	-5.64	FALSE
252690_at	putative protein	---	---	1.22	0.29	1.36	0.2174122	0.4638208	-5.64	FALSE
260509_at	natural resistance-associated ma	NRAMP2	AT1G47240	1.13	0.18	1.36	0.2175172	0.4639319	-5.64	FALSE
246686_at	putative protein predicted protein	---	---	1.22	0.29	1.36	0.2175235	0.4639319	-5.64	FALSE
253677_at	cytidine deaminase - like protein	---	AT4G29580	1.20	0.26	1.36	0.2175253	0.4639319	-5.64	FALSE
250401_at	putative protein HSPC184, Hom	---	AT5G10780	-1.14	-0.19	-1.36	0.2175701	0.463984	-5.64	FALSE
262199_at	unknown protein ; supported by	---	AT1G53800	-1.23	-0.30	-1.36	0.2176177	0.4640423	-5.64	FALSE
251038_at	putative protein unknown protein	---	AT5G02240	-1.15	-0.20	-1.36	0.2176758	0.4641227	-5.64	FALSE
254848_at	putative protein hypothetical pro	PGRL1B	AT4G11960	-1.17	-0.22	-1.36	0.2177893	0.4641628	-5.64	FALSE
257806_at	hypothetical protein predicted by	---	AT3G18670	1.16	0.21	1.36	0.2178929	0.4641628	-5.64	FALSE
247580_at	putative protein traube, Mus mus	---	AT5G61330	-1.19	-0.26	-1.36	0.2178	0.4641628	-5.64	FALSE
265373_at	putative replication protein A1	RPA1A	AT2G06510	-1.34	-0.42	-1.36	0.2177867	0.4641628	-5.64	FALSE
249888_s_a	zinc finger protein-like ; supporte	---	AT5G22480 //	-1.17	-0.23	-1.36	0.2178015	0.4641628	-5.64	FALSE
253961_at	putative protein SPF1 protein, Ip	WRKY34	AT4G26440	1.14	0.19	1.36	0.2177353	0.4641628	-5.64	FALSE
247649_at	KED - like protein KED, Nicotian	---	AT5G60030	-1.18	-0.24	-1.36	0.2178371	0.4641628	-5.64	FALSE
250368_at	putative protein ; supported by c	---	AT5G11280	-1.20	-0.26	-1.36	0.2178822	0.4641628	-5.64	FALSE
262076_at	hypothetical protein identical to G	ATMPK2	AT1G59580	-1.21	-0.28	-1.36	0.2178869	0.4641628	-5.64	FALSE
246160_at	putative protein predicted protei	FBX2	AT5G21040	-1.15	-0.20	-1.36	0.2178981	0.4641628	-5.64	FALSE

250917_at	fructose-bisphosphate aldolase	---	AT5G03690	1.21	0.27	1.36	0.2179603	0.4642521	-5.64	FALSE
260853_at	hypothetical protein predicted by	---	AT1G21950	1.26	0.33	1.36	0.2180107	0.464316	-5.64	FALSE
267409_at	hypothetical protein predicted by	---	AT2G34910	1.13	0.18	1.36	0.2183429	0.4644927	-5.64	FALSE
248976_at	putative protein strong similarity t	ARAD2	AT5G44930	-1.21	-0.28	-1.36	0.2183325	0.4644927	-5.64	FALSE
265479_at	hypothetical protein ;supported b	---	AT2G15760	2.01	1.01	1.36	0.2181962	0.4644927	-5.64	FALSE
246941_at	putative protein several hypothet	---	AT5G25415	1.16	0.21	1.36	0.2182396	0.4644927	-5.64	FALSE
253651_at	putative protein nucleoid DNA-b	---	AT4G30030	1.20	0.26	1.36	0.2183482	0.4644927	-5.64	FALSE
263771_at	putative Athila retroelement ORF	---	---	1.13	0.17	1.36	0.218121	0.4644927	-5.64	FALSE
256663_at	unknown protein ;supported by fu	---	AT3G12050	1.28	0.35	1.36	0.2183584	0.4644927	-5.64	FALSE
248139_at	putative protein similar to unknov	---	AT5G54970	-2.82	-1.50	-1.36	0.2181998	0.4644927	-5.64	FALSE
252251_at	hypothetical protein	---	AT3G49820	1.14	0.19	1.36	0.2182488	0.4644927	-5.64	FALSE
257392_at	hypothetical protein	FLA3	AT2G24450	1.17	0.22	1.36	0.2183376	0.4644927	-5.64	FALSE
251216_at	putative protein hypothetical pro	---	---	1.15	0.20	1.36	0.2183424	0.4644927	-5.64	FALSE
246539_at	putative protein geranylgeranyla	MUB2	AT5G15460	-1.13	-0.18	-1.36	0.218246	0.4644927	-5.64	FALSE
256817_at	F-box protein family, AtFBW1 co	---	AT3G21410	-1.19	-0.25	-1.36	0.2181744	0.4644927	-5.64	FALSE
248180_at	unknown protein ;supported by f	AGD5	AT5G54310	1.13	0.18	1.36	0.2184346	0.4645681	-5.64	FALSE
263437_at	putative disease resistance respo	---	AT2G28670	1.19	0.25	1.36	0.2184238	0.4645681	-5.64	FALSE
257227_at	monodehydroascorbate reductas	MDAR4	AT3G27820	-1.17	-0.23	-1.36	0.2184822	0.4645989	-5.64	FALSE
263669_at	putative cryptochrome 2 apoprot	CRY2	AT1G04400	-1.15	-0.20	-1.36	0.2184898	0.4645989	-5.64	FALSE
256396_at	unknown protein	---	AT3G06150	-1.31	-0.39	-1.36	0.2185928	0.4646868	-5.64	TRUE
249566_at	cytochrome P450-like protein	CYP735A1	AT5G38450	1.16	0.21	1.36	0.2186126	0.4646868	-5.64	FALSE
259195_at	hypothetical protein predicted by	---	AT3G01730	1.18	0.24	1.36	0.2185659	0.4646868	-5.64	FALSE
248454_at	receptor protein kinase-like	---	AT5G51350	-1.27	-0.34	-1.36	0.2185748	0.4646868	-5.64	FALSE
259366_at	allene oxide cyclase, putative sir	AOC4	AT1G13280	1.26	0.33	1.36	0.2186797	0.4647428	-5.64	FALSE
251832_at	putative protein tomato leucine z	ATEXO70H	AT3G55150	1.53	0.61	1.36	0.2186669	0.4647428	-5.64	FALSE
256455_at	unknown protein ;supported by fu	---	AT1G75190	1.16	0.22	1.36	0.2187628	0.4648327	-5.64	FALSE
247163_at	Expressed protein ; supported by	---	AT5G65685	-1.20	-0.26	-1.36	0.2187598	0.4648327	-5.64	FALSE
254440_at	putative protein desiccation-rela	---	AT4G21020	1.15	0.20	1.36	0.2188166	0.4648605	-5.64	FALSE
245051_at	putative WRKY-type DNA-bindin	WRKY15	AT2G23320	1.43	0.52	1.36	0.2188107	0.4648605	-5.64	FALSE
245237_at	putative protein similarity to ALR	SLK1	AT4G25520	-1.15	-0.20	-1.36	0.2188769	0.4649439	-5.64	FALSE
260737_at	receptor-like serine threonine kir	---	AT1G17540	-1.19	-0.26	-1.36	0.2188966	0.4649439	-5.64	FALSE
247041_at	floral homeotic protein apetala2-l	TOE3	AT5G67180	1.19	0.25	1.36	0.2189716	0.4650599	-5.64	FALSE
249647_at	putative protein hypothetical prot	---	AT5G37040	1.21	0.28	1.36	0.2189932	0.4650625	-5.64	FALSE
247234_at	putative protein similar to unknov	---	AT5G64980	-1.15	-0.20	-1.36	0.2190194	0.4650748	-5.64	FALSE
248080_at	wax synthase-like protein	---	AT5G55380	1.22	0.28	1.35	0.2192153	0.4654473	-5.65	FALSE

252159_at	hypothetical protein	---	AT3G50540	1.15	0.21	1.35	0.2192596	0.4654548	-5.65	FALSE
248973_at	disease resistance protein-like	TTR1	AT5G45050	1.13	0.18	1.35	0.219248	0.4654548	-5.65	FALSE
249250_at	arm repeat containing protein	---	AT5G42340	1.14	0.19	1.35	0.2193349	0.4655713	-5.65	FALSE
245806_at	light-harvesting complex protein	LHCA5	AT1G45474	-1.30	-0.38	-1.35	0.2193906	0.4655774	-5.65	FALSE
262178_at	membrane protein, putative simi	KOM	AT1G77860	1.24	0.31	1.35	0.219399	0.4655774	-5.65	FALSE
266437_at	unknown protein	---	AT2G43160	1.19	0.25	1.35	0.2193705	0.4655774	-5.65	FALSE
261339_at	protein kinase, putative similar t	---	AT1G35710	1.32	0.40	1.35	0.2194282	0.4655961	-5.65	FALSE
264123_at	unknown protein ; supported by	---	AT1G02270	-1.19	-0.25	-1.35	0.2194963	0.4656972	-5.65	FALSE
251788_at	putative protein	---	AT3G55420	1.43	0.52	1.35	0.2195933	0.4657279	-5.65	FALSE
251981_at	putative protein BETA-GALACT	---	AT3G53080	1.16	0.22	1.35	0.2196129	0.4657279	-5.65	FALSE
248115_at	putative protein strong similarity	---	AT5G54870	1.32	0.40	1.35	0.2195753	0.4657279	-5.65	FALSE
252308_at	putative protein sugar transporte	---	AT3G49310	-1.16	-0.21	-1.35	0.2196056	0.4657279	-5.65	FALSE
263869_at	unknown protein	PROPEP6	AT2G22000	-1.13	-0.18	-1.35	0.2195974	0.4657279	-5.65	FALSE
247461_at	putative protein various predicte	ATBAG2	AT5G62100	1.22	0.28	1.35	0.2196671	0.4657996	-5.65	TRUE
251109_at	ferritin 1 precursor ;supported by	FER1	AT5G01600	-1.39	-0.47	-1.35	0.2196926	0.4658105	-5.65	TRUE
261478_at	unknown protein	MIOX1	AT1G14520	1.25	0.33	1.35	0.219815	0.4660267	-5.65	FALSE
265651_at	hypothetical protein predicted by	---	AT2G13900	-1.15	-0.20	-1.35	0.2199397	0.4661718	-5.65	FALSE
255790_at	hypothetical protein predicted by	---	AT2G33560	1.17	0.23	1.35	0.2199448	0.4661718	-5.65	FALSE
260013_at	putative annexin similar to annex	ANN5	AT1G68090	1.14	0.18	1.35	0.2199099	0.4661718	-5.65	FALSE
261755_at	histone H2B, putative similar to	---	AT1G08170	1.22	0.29	1.35	0.2202028	0.4666753	-5.65	FALSE
245596_at	hypothetical protein	AtPRD1	AT4G14180	-1.16	-0.22	-1.35	0.2202702	0.4667747	-5.65	FALSE
248819_at	putative protein contains similarit	---	AT5G47050	-1.31	-0.39	-1.35	0.2202943	0.4667825	-5.65	TRUE
259144_at	putative kinesin-like centromere	---	AT3G10180	1.16	0.21	1.35	0.2203573	0.4668727	-5.65	FALSE
256205_at	hypothetical protein	---	AT1G50890	-1.16	-0.21	-1.35	0.2203896	0.4668976	-5.65	FALSE
249487_at	ABC transporter -like protein TA	TAP2	AT5G39040	1.33	0.41	1.35	0.2205066	0.467102	-5.65	FALSE
265507_s_a	Ac-like transposase related to Ac	---	---	-1.16	-0.21	-1.35	0.2205393	0.4671281	-5.65	FALSE
261174_at	26S proteasome regulatory subu	---	AT1G04810	-1.20	-0.26	-1.35	0.2206253	0.4672668	-5.65	FALSE
267601_at	hypothetical protein predicted by	---	AT2G32980	-1.17	-0.23	-1.35	0.2207184	0.4672903	-5.65	FALSE
258998_at	putative adenylate kinase similar	---	AT3G01820	1.20	0.27	1.35	0.2206724	0.4672903	-5.65	FALSE
256193_at	hypothetical protein similar to hy	---	AT1G30200	-1.15	-0.20	-1.35	0.2206794	0.4672903	-5.65	FALSE
253751_at	hypothetical protein ;supported b	---	AT4G29070	-1.34	-0.42	-1.35	0.2207115	0.4672903	-5.65	FALSE
259741_at	unknown protein	---	AT1G71020	1.24	0.31	1.35	0.220793	0.4673276	-5.65	TRUE
259018_at	unknown protein similar to unkno	AIR12	AT3G07390	1.66	0.73	1.35	0.2207974	0.4673276	-5.65	FALSE
255654_at	Similar to receptor kinase	---	AT4G00970	1.61	0.69	1.35	0.2207682	0.4673276	-5.65	FALSE
261720_at	hypothetical protein similar to hy	HDA08	AT1G08460	-1.30	-0.38	-1.35	0.2209477	0.4676022	-5.65	FALSE

249734_at	putative protein strong similarity t	IRE1-1	AT5G24360	1.13	0.18	1.35	0.2210275	0.4676843	-5.65	FALSE
248484_at	carbonyl reductase-like protein	---	AT5G51030	-1.13	-0.17	-1.35	0.221016	0.4676843	-5.65	FALSE
245887_at	putative protein CD2 cytoplasmi	---	AT5G09390	-1.12	-0.16	-1.35	0.2211084	0.4678121	-5.65	FALSE
264788_at	putative DnaJ protein ;supported	---	AT2G17880	-1.58	-0.66	-1.35	0.2212127	0.467946	-5.65	TRUE
260475_at	Serine carboxypeptidase isolog	scpl31	AT1G11080	1.38	0.47	1.35	0.2211982	0.467946	-5.65	FALSE
250518_at	Expressed protein ; supported by	---	AT5G08139	-1.14	-0.19	-1.35	0.2213569	0.4680339	-5.65	FALSE
257153_at	unknown protein ; supported by	---	AT3G27220	-1.25	-0.32	-1.35	0.2212778	0.4680339	-5.65	FALSE
258159_at	receptor kinase, putative similar	RLK902	AT3G17840	1.35	0.44	1.35	0.2213249	0.4680339	-5.65	FALSE
254426_at	putative protein predicted protei	---	AT4G21240	1.16	0.21	1.35	0.2213489	0.4680339	-5.65	FALSE
254731_at	hypothetical protein	---	AT4G13750	-1.19	-0.25	-1.35	0.2213177	0.4680339	-5.65	FALSE
251628_at	translation initiation factor 3 -like	EIF3E	AT3G57290	-1.19	-0.25	-1.35	0.2214598	0.4682081	-5.65	FALSE
265164_at	putative OBP32pep protein	---	AT1G23600	1.15	0.20	1.35	0.2215252	0.468243	-5.65	FALSE
263520_at	putative protein kinase contains a	---	AT2G42640	-1.16	-0.21	-1.35	0.2215568	0.468243	-5.65	FALSE
248415_at	unknown protein	---	AT5G51620	-1.15	-0.20	-1.35	0.2215523	0.468243	-5.65	FALSE
254055_at	hypothetical protein	---	AT4G25330	1.15	0.20	1.35	0.2215584	0.468243	-5.65	FALSE
247633_at	putative zinc finger protein finge	---	AT5G60470	1.28	0.36	1.35	0.2215956	0.4682783	-5.65	FALSE
258033_at	unknown protein similar to MRP-	MRP6	AT3G21250	1.32	0.40	1.35	0.2216687	0.4683288	-5.66	TRUE
253429_at	putative protein CDC28/cdc2-like	---	AT4G32420	-1.16	-0.21	-1.35	0.2217016	0.4683288	-5.66	FALSE
267626_at	putative cytochrome P450	CYP712A1	AT2G42250	1.28	0.36	1.35	0.2216549	0.4683288	-5.66	FALSE
266021_at	unknown protein	---	AT2G05910	1.27	0.34	1.35	0.2216929	0.4683288	-5.66	FALSE
246889_at	putative protein various predicte	---	AT5G25470	1.20	0.26	1.35	0.221749	0.4683422	-5.66	FALSE
256088_at	putative FKBP-type peptidyl-proly	---	AT1G20810	-1.26	-0.33	-1.35	0.2217378	0.4683422	-5.66	FALSE
263552_x_a	unknown protein proline, tyrosin	---	AT2G24980	1.24	0.31	1.35	0.221847	0.4684622	-5.66	FALSE
248866_s_a	putative protein contains similarit	---	AT5G46810 ///	-1.14	-0.19	-1.35	0.2218414	0.4684622	-5.66	FALSE
246920_at	phytocyanin-related protein-like	---	AT5G25090	1.14	0.19	1.35	0.2219626	0.4686631	-5.66	FALSE
265102_at	putative peroxidase similar to cat	---	AT1G30870	1.18	0.24	1.35	0.2220569	0.4687667	-5.66	FALSE
247146_at	unknown protein	---	AT5G65610	-1.27	-0.35	-1.35	0.2221144	0.4687667	-5.66	FALSE
256341_at	deoxyguanosine kinase, putative	---	AT1G72040	-1.34	-0.42	-1.35	0.2220813	0.4687667	-5.66	FALSE
260468_at	transcription factor RUSH-1alpha	---	AT1G11100	1.24	0.31	1.35	0.2221002	0.4687667	-5.66	FALSE
245402_at	putative protein	---	AT4G17585	-1.18	-0.24	-1.35	0.222076	0.4687667	-5.66	FALSE
261471_at	hypothetical protein contains sim	---	AT1G14460	-1.29	-0.37	-1.34	0.222185	0.4688642	-5.66	FALSE
257866_at	dihydroxyacetone kinase, putativ	---	AT3G17770	1.43	0.52	1.34	0.2222017	0.4688642	-5.66	FALSE
264548_at	unknown protein ; supported by c	---	AT1G55680	-1.16	-0.22	-1.34	0.2222811	0.4689883	-5.66	FALSE
256126_at	hypothetical protein similar to Mu	---	AT1G18050	1.24	0.31	1.34	0.2223682	0.4691286	-5.66	FALSE
245330_at	hypothetical protein ;supported b	---	AT4G14930	1.21	0.27	1.34	0.2224551	0.4692471	-5.66	FALSE

247202_at	GTP-binding protein ; supported	AtRABA4a	AT5G65270	1.19	0.25	1.34	0.2224655	0.4692471	-5.66	FALSE
247223_at	MADS box transcription factor-lik	MAF4	AT5G65070	1.13	0.17	1.34	0.2225435	0.4693682	-5.66	FALSE
249050_at	cyclin-dependent protein kinase-	---	AT5G44290	1.18	0.24	1.34	0.2225995	0.4694429	-5.66	FALSE
254522_at	hypothetical protein	---	AT4G19980	1.13	0.17	1.34	0.2227542	0.4697257	-5.66	FALSE
257865_at	protein kinase, putative contains	---	AT3G17750	-1.13	-0.18	-1.34	0.2229138	0.4699792	-5.66	FALSE
256491_at	hypothetical protein contains sim	---	AT1G31500	-1.18	-0.24	-1.34	0.2229156	0.4699792	-5.66	FALSE
263581_at	hypothetical protein identical to h	---	AT2G17160	1.20	0.26	1.34	0.2229488	0.4700058	-5.66	FALSE
257480_at	hypothetical protein similar to put	---	AT1G15640	1.33	0.41	1.34	0.2229949	0.4700595	-5.66	FALSE
265906_at	hypothetical protein predicted by	---	AT2G25565	1.17	0.23	1.34	0.2230279	0.4700857	-5.66	FALSE
260967_at	unknown protein contains similar	---	AT1G12230	-1.21	-0.28	-1.34	0.2230639	0.470118	-5.66	FALSE
261313_at	hypothetical protein predicted by	---	AT1G52970	1.13	0.18	1.34	0.2232753	0.4702524	-5.66	FALSE
260596_at	unknown protein	TIM50	AT1G55900	-1.29	-0.37	-1.34	0.2231776	0.4702524	-5.66	FALSE
260162_at	unknown protein	GC5	AT1G79830	-1.13	-0.17	-1.34	0.223218	0.4702524	-5.66	FALSE
266269_at	putative glutathione S-transferas	ATGSTU2	AT2G29480	1.54	0.63	1.34	0.2233006	0.4702524	-5.66	FALSE
258340_at	hypothetical protein predicted by	---	AT3G22770	1.13	0.18	1.34	0.2232391	0.4702524	-5.66	FALSE
266030_x_a	hypothetical protein predicted by	---	---	1.19	0.25	1.34	0.2233132	0.4702524	-5.66	FALSE
255377_at	hypothetical protein	---	AT4G03500	1.19	0.25	1.34	0.2232892	0.4702524	-5.66	FALSE
251822_at	centromere protein - like centron	---	AT3G55060	1.15	0.20	1.34	0.2232251	0.4702524	-5.66	FALSE
260668_at	unknown protein ;supported by fu	---	AT1G19530	1.96	0.97	1.34	0.2233106	0.4702524	-5.66	FALSE
255009_at	putative DNA-directed RNA poly	---	AT4G10070	-1.25	-0.32	-1.34	0.2233818	0.4702666	-5.66	FALSE
255461_at	ent-kaurene synthetase A - like p	GA1	AT4G02780	1.17	0.23	1.34	0.2233683	0.4702666	-5.66	FALSE
257781_at	spastin protein, putative similar t	---	AT3G27120	1.13	0.18	1.34	0.2233794	0.4702666	-5.66	FALSE
247274_at	putative protein similar to unknov	---	AT5G64360	-1.20	-0.27	-1.34	0.2234543	0.4703758	-5.66	FALSE
247542_at	autophagocytosis protein - like a	ATG3	AT5G61500	-1.20	-0.26	-1.34	0.2235003	0.4704293	-5.66	FALSE
247257_at	proteasome regulatory subunit-lik	RPN5B	AT5G64760	-1.38	-0.46	-1.34	0.2235737	0.4705403	-5.66	FALSE
250321_at	zinc finger transcription factor -li	---	AT5G12850	1.17	0.23	1.34	0.223654	0.470562	-5.66	FALSE
254248_at	serine/threonine kinase serine/th	---	AT4G23270	1.32	0.40	1.34	0.2236165	0.470562	-5.66	FALSE
266009_at	putative kinesin heavy chain	---	AT2G37420	1.16	0.22	1.34	0.22367	0.470562	-5.66	FALSE
251668_at	putative protein strictosidine synt	---	AT3G57010	1.40	0.48	1.34	0.223714	0.470562	-5.66	FALSE
263792_at	putative retroelement pol polypro	---	---	1.21	0.28	1.34	0.2236717	0.470562	-5.66	FALSE
259968_at	unknown protein	---	AT1G76530	1.17	0.23	1.34	0.2237329	0.470562	-5.66	FALSE
248293_at	unknown protein	---	AT5G53050	1.28	0.36	1.34	0.223749	0.470562	-5.66	FALSE
246089_at	ring-box protein - like ring-box p	RBX1	AT5G20570	-1.12	-0.17	-1.34	0.2237131	0.470562	-5.66	FALSE
247553_at	MAD box containing protein NAF	AGL8	AT5G60910	-1.34	-0.42	-1.34	0.2237876	0.4705672	-5.66	FALSE
253574_at	putative protein	---	AT4G31030	-1.24	-0.32	-1.34	0.2237927	0.4705672	-5.66	FALSE

258084_at	putative B regulatory subunit of p	---	AT3G26020	1.27	0.34	1.34	0.2238604	0.470666	-5.66	FALSE
265416_at	unknown protein ; supported by	---	AT2G37120	-1.43	-0.51	-1.34	0.2239399	0.4707464	-5.66	FALSE
254411_at	hypothetical protein	---	---	1.18	0.24	1.34	0.2239276	0.4707464	-5.66	FALSE
253394_at	putative protein predicted protei	VTE1	AT4G32770	1.33	0.41	1.34	0.2239875	0.4708031	-5.66	TRUE
265442_at	hypothetical protein predicted by	---	AT2G20940	-1.34	-0.42	-1.34	0.2240172	0.470822	-5.66	FALSE
254362_at	Expressed protein ; supported by	---	AT4G22160	1.23	0.30	1.34	0.2240754	0.4708263	-5.66	FALSE
252262_at	putative protein several hypothet	---	AT3G49510	1.13	0.18	1.34	0.2240497	0.4708263	-5.66	FALSE
252656_at	hypothetical protein	---	AT3G44770	1.23	0.29	1.34	0.2240811	0.4708263	-5.66	FALSE
247895_at	putative protein bHLH transcripti	---	AT5G58010	1.16	0.21	1.34	0.2241188	0.4708324	-5.66	FALSE
248077_at	putative protein contains similarit	---	AT5G55770	-1.15	-0.20	-1.34	0.2241259	0.4708324	-5.66	FALSE
248824_at	putative protein contains similarit	---	AT5G46940	5.55	2.47	1.34	0.2241459	0.4708324	-5.66	FALSE
257028_at	hypothetical protein predicted by	---	AT3G19230	1.30	0.38	1.34	0.2242584	0.4708751	-5.67	FALSE
265229_s_a	hypothetical protein	---	AT2G07701	1.15	0.20	1.34	0.2242695	0.4708751	-5.67	FALSE
264949_at	unknown protein contains similar	MAF1	AT1G77080	-1.14	-0.18	-1.34	0.2242194	0.4708751	-5.66	FALSE
246281_at	hypothetical protein	NAPRT1	AT4G36940	-1.27	-0.34	-1.34	0.2242314	0.4708751	-5.67	FALSE
251274_at	putative protein hypothetical pro	---	AT3G61700	-1.29	-0.37	-1.34	0.224258	0.4708751	-5.67	FALSE
260827_at	mudrA-like protein similar to Mu	AT1G0675(	---	-1.25	-0.32	-1.34	0.2243056	0.4709075	-5.67	FALSE
248337_at	low-temperature-induced protein	LTI78	AT5G52310	-2.16	-1.11	-1.34	0.2244246	0.4711094	-5.67	FALSE
250620_at	embryo-specific protein 3 (ATS3)	ATS3	AT5G07190	1.15	0.21	1.34	0.224443	0.4711094	-5.67	FALSE
245394_at	hypothetical protein ;supported b	---	AT4G16450	-1.22	-0.29	-1.34	0.2245252	0.4712384	-5.67	FALSE
267554_at	E2, ubiquitin-conjugating enzym	---	AT2G32790	1.20	0.26	1.34	0.2246213	0.47131	-5.67	FALSE
255740_at	wall-associated kinase, putative	---	AT1G25390	1.48	0.57	1.34	0.2245868	0.47131	-5.67	FALSE
259973_at	hypothetical protein contains Pfa	---	AT1G76630	-1.28	-0.36	-1.34	0.2246206	0.47131	-5.67	FALSE
253246_at	putative protein	---	AT4G34600	-1.20	-0.26	-1.34	0.2246527	0.4713282	-5.67	FALSE
260835_at	protein kinase interactor, putativ	---	AT1G06700	-1.16	-0.21	-1.34	0.2246712	0.4713282	-5.67	FALSE
257202_at	receptor-like kinase, putative sin	---	AT3G23750	1.20	0.27	1.34	0.2247936	0.4715414	-5.67	TRUE
245339_at	hypothetical protein ;supported b	COBL7	AT4G16120	1.32	0.40	1.34	0.2248541	0.4716059	-5.67	TRUE
262949_at	pectinesterase, putative similar t	sks18	AT1G75790	1.16	0.22	1.34	0.2248656	0.4716059	-5.67	FALSE
265787_at	Mutator-like transposase similar	---	---	1.22	0.29	1.34	0.2249503	0.4717401	-5.67	FALSE
251266_at	putative protein hypothetical pro	---	AT3G62320	1.20	0.26	1.34	0.2250348	0.4718677	-5.67	FALSE
266664_at	hypothetical protein predicted by	---	AT2G29800	1.16	0.22	1.34	0.2250526	0.4718677	-5.67	FALSE
248384_at	mandelonitrile lyase-like protein	---	AT5G51930	1.15	0.20	1.34	0.2251088	0.4719423	-5.67	FALSE
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gi	---	---	1.34	0.42	1.34	0.2251515	0.4719885	-5.67	FALSE
248719_at	respiratory burst oxidase protein	RBOHD	AT5G47910	1.68	0.75	1.33	0.2254135	0.4721038	-5.67	TRUE
259487_at	hypothetical protein contains sim	TRFL5	AT1G15720	1.12	0.17	1.34	0.2252434	0.4721038	-5.67	FALSE

265160_at	unknown protein similar to EST g	---	AT1G31050	1.20	0.27	1.33	0.2253709	0.4721038	-5.67	FALSE
254454_at	hypothetical protein	EMB2271	AT4G21130	1.17	0.22	1.33	0.2253444	0.4721038	-5.67	FALSE
259946_at	putative TINY similar to TINY GB	---	AT1G71450	1.12	0.17	1.33	0.2253953	0.4721038	-5.67	FALSE
259155_at	transcription initiation factor IIB (T	---	AT3G10330	-1.21	-0.27	-1.33	0.2253114	0.4721038	-5.67	FALSE
247153_at	receptor protein kinase-like prote	BAM1	AT5G65700	-1.37	-0.45	-1.33	0.2253921	0.4721038	-5.67	FALSE
252323_at	putative protein probable transcr	KING1	AT3G48530	-1.26	-0.34	-1.33	0.2253134	0.4721038	-5.67	FALSE
263694_at	putative reverse transcriptase str	---	---	1.13	0.18	1.33	0.2254075	0.4721038	-5.67	FALSE
259907_at	GCN4-complementing protein, p	AGD2	AT1G60860	-1.31	-0.38	-1.33	0.22532	0.4721038	-5.67	FALSE
259185_at	putative phosphate/phosphoenol	PPT2	AT3G01550	1.81	0.86	1.33	0.2254397	0.4721153	-5.67	TRUE
257437_s_a	hypothetical protein predicted by	---	AT2G16290 /A	-1.15	-0.21	-1.33	0.2255459	0.4722075	-5.67	FALSE
246202_at	methionyl aminopeptidase-like pr	MAP1D	AT4G37040	-1.25	-0.32	-1.33	0.2255212	0.4722075	-5.67	FALSE
264477_at	amp-binding protein, putative sir	---	AT1G77240	1.24	0.31	1.33	0.2255401	0.4722075	-5.67	FALSE
256288_at	arginine N-methyltransferase 3,	PRMT3	AT3G12270	-1.40	-0.49	-1.33	0.2257001	0.4723863	-5.67	FALSE
266421_at	putative nonspecific lipid-transfer	LP1	AT2G38540	1.67	0.74	1.33	0.2257175	0.4723863	-5.67	FALSE
255287_at	see T10M13.1 (GB:AF001308) s	---	AT4G04660	1.17	0.23	1.33	0.2257348	0.4723863	-5.67	FALSE
262358_at	mandelonitrile lyase, putative sir	---	AT1G73050	1.19	0.25	1.33	0.2256999	0.4723863	-5.67	FALSE
245379_at	heat shock transcription factor HS	HSF1	AT4G17750	-1.20	-0.26	-1.33	0.2257148	0.4723863	-5.67	FALSE
264165_at	hypothetical protein contains sim	ATNAP11	AT1G65410	-1.14	-0.19	-1.33	0.2258117	0.4725039	-5.67	FALSE
258733_at	unknown protein	---	---	1.14	0.19	1.33	0.225942	0.4727332	-5.67	FALSE
262565_at	hypothetical protein predicted by	---	AT1G34320	-1.17	-0.22	-1.33	0.2260009	0.4727696	-5.67	FALSE
249407_at	putative protein predicted protei	---	AT5G40320	1.14	0.19	1.33	0.2259855	0.4727696	-5.67	FALSE
259470_at	unknown protein	---	AT1G19110	-1.13	-0.17	-1.33	0.2260506	0.4728302	-5.67	FALSE
266394_at	Ras-related GTP-binding protein	ARA4	AT2G43130	-1.16	-0.22	-1.33	0.2261112	0.4728782	-5.67	FALSE
257695_at	hypothetical protein contains Pfa	HUA1	AT3G12680	-1.17	-0.23	-1.33	0.226115	0.4728782	-5.67	FALSE
265564_s_a	hypothetical protein predicted by	---	---	1.16	0.22	1.33	0.2261702	0.4729504	-5.67	FALSE
258421_at	MtN3-like protein similar to MtN3	---	AT3G16690	1.36	0.44	1.33	0.2262262	0.4730241	-5.67	TRUE
254122_at	CER2 ;supported by full-length c	CER2	AT4G24510	2.38	1.25	1.33	0.2262509	0.4730324	-5.67	TRUE
259681_at	nitrate reductase 1 (NR1) identic	NIA1	AT1G77760	2.97	1.57	1.33	0.2263212	0.473054	-5.67	FALSE
257549_at	hypothetical protein predicted by	agl103	AT3G18650	1.21	0.28	1.33	0.2262989	0.473054	-5.67	FALSE
251792_at	probable serine/threonine-specif	---	AT3G55550	-1.16	-0.22	-1.33	0.2263235	0.473054	-5.67	FALSE
249019_at	unknown protein	---	AT5G44780	-1.44	-0.52	-1.33	0.226348	0.473062	-5.67	FALSE
264942_at	unknown protein ; supported by c	---	AT1G67340	-1.22	-0.29	-1.33	0.2264275	0.4731848	-5.67	FALSE
255761_at	hypothetical protein predicted by	---	AT1G16770	1.16	0.22	1.33	0.2264973	0.4732438	-5.67	FALSE
265477_at	hypothetical protein predicted by	GAUT2	AT2G46480	1.17	0.23	1.33	0.2264899	0.4732438	-5.67	FALSE
249601_at	quinone oxidoreductase -like pro	---	AT5G37980	1.22	0.28	1.33	0.2266984	0.4735773	-5.67	FALSE

253823_at	putative protein ;supported by fu	---	AT4G28030	-1.13	-0.18	-1.33	0.2266799	0.4735773	-5.67	FALSE
258652_at	putative Ras-like GTP-binding pr	ATRABC2E	AT3G09910	1.32	0.40	1.33	0.2268139	0.4737114	-5.67	FALSE
246073_at	ribosomal protein L36-like ribosc	---	AT5G20180	-1.18	-0.24	-1.33	0.2268106	0.4737114	-5.67	FALSE
256198_at	Myb-family transcription factor, p	---	AT1G58220	-1.23	-0.30	-1.33	0.2268457	0.4737114	-5.67	FALSE
252829_at	homeodomain - like protein ; sup	ATHB16	AT4G40060	-1.20	-0.27	-1.33	0.2268303	0.4737114	-5.67	FALSE
265630_at	unknown protein similar to ovaria	---	AT2G27350	1.14	0.18	1.33	0.226967	0.4739214	-5.68	FALSE
248062_at	unknown protein ;supported by f	---	AT5G55450	-3.58	-1.84	-1.33	0.2270353	0.4740206	-5.68	FALSE
246911_at	transcription factor TINY	tny	AT5G25810	1.45	0.53	1.33	0.2270947	0.4741012	-5.68	TRUE
266934_at	unknown protein	---	AT2G18900	-1.19	-0.25	-1.33	0.2272546	0.47438	-5.68	FALSE
245599_at	RING-H2 finger protein RHF1a	RHF1A	AT4G14220	1.27	0.34	1.33	0.2272838	0.47438	-5.68	FALSE
264533_s_a	H+/Ca2+ antiporter, putative sim	CAX5	AT1G55720 /.	1.16	0.22	1.33	0.2272906	0.47438	-5.68	FALSE
249428_at	putative protein predicted protei	---	AT5G39870	1.13	0.17	1.33	0.2273341	0.4744274	-5.68	FALSE
259970_at	putative chlorophyll A-B binding p	---	AT1G76570	-1.28	-0.36	-1.33	0.2274668	0.4746354	-5.68	TRUE
266414_at	mevalonate diphosphate decarbo	MVD1	AT2G38700	1.17	0.23	1.33	0.2274754	0.4746354	-5.68	FALSE
245832_at	chorismate synthase, putative si	EMB1144	AT1G48850	1.57	0.65	1.33	0.2275731	0.4747958	-5.68	FALSE
247952_at	salt-inducible protein-like	CYP71B10	AT5G57250 /.	-1.17	-0.23	-1.33	0.2276151	0.47484	-5.68	FALSE
250866_at	Expressed protein ; supported by	---	AT5G03905	1.17	0.23	1.33	0.2276695	0.4748623	-5.68	FALSE
262785_at	putative carboxyl-terminal peptid	---	AT1G10750	1.26	0.34	1.33	0.227704	0.4748623	-5.68	FALSE
259312_at	putative RING-H2 zinc finger pro	ATL6	AT3G05200	1.53	0.61	1.33	0.2277091	0.4748623	-5.68	FALSE
257913_at	unknown protein ; supported by	LAG1	AT3G25540	-1.17	-0.22	-1.33	0.2276536	0.4748623	-5.68	FALSE
266899_at	hypothetical protein predicted by	---	AT2G34620	-1.46	-0.55	-1.33	0.2277719	0.4749065	-5.68	TRUE
245963_at	putative protein HPt phosphotra	---	AT5G19710	1.13	0.18	1.33	0.2277716	0.4749065	-5.68	FALSE
259998_at	hypothetical protein similar to unl	BPC3	AT1G68120	1.24	0.31	1.33	0.2278361	0.4749102	-5.68	FALSE
265261_at	putative APG isolog protein	---	AT2G42990	-1.62	-0.69	-1.33	0.2278204	0.4749102	-5.68	FALSE
258463_at	putative protein kinase similar to	---	AT3G17410	1.20	0.26	1.33	0.2277953	0.4749102	-5.68	FALSE
248437_at	putative protein similar to unknov	EMF2	AT5G51230	1.23	0.29	1.33	0.2278629	0.4749226	-5.68	FALSE
252847_at	putative transposase hypothetic	---	AT3G42170	-1.18	-0.24	-1.33	0.2279071	0.4749713	-5.68	FALSE
256695_at	unknown protein	---	AT3G32090	1.18	0.24	1.33	0.2279588	0.4750356	-5.68	FALSE
254556_at	putative protein various predicte	---	AT4G19220	-1.24	-0.31	-1.33	0.2280484	0.4751789	-5.68	FALSE
259980_at	unknown protein ;supported by f	---	AT1G76520	1.36	0.44	1.33	0.2281501	0.4753041	-5.68	TRUE
246515_at	putative protein unusual floral or	---	AT5G15710	-1.12	-0.17	-1.33	0.2281351	0.4753041	-5.68	FALSE
249308_at	unknown protein ; supported by	---	AT5G41350	1.14	0.18	1.33	0.2281961	0.4753129	-5.68	FALSE
258527_at	branched chain alpha-keto acid	BCE2	AT3G06850	1.64	0.72	1.33	0.2281952	0.4753129	-5.68	FALSE
265062_at	receptor kinase, putative similar	---	AT1G61550	1.30	0.38	1.33	0.228258	0.4753986	-5.68	FALSE
250778_at	unknown protein ;supported by fu	---	AT5G05500	1.16	0.21	1.33	0.2283018	0.4754463	-5.68	FALSE

258598_at	hypothetical protein predicted by	---	AT3G04410	1.22	0.28	1.32	0.2284054	0.4755319	-5.68	FALSE
262252_at	RING-H2 zinc finger protein ATL	---	AT1G53820	1.15	0.20	1.32	0.228394	0.4755319	-5.68	FALSE
267397_at	hypothetical protein predicted by	---	AT1G76170	-1.31	-0.39	-1.33	0.2283685	0.4755319	-5.68	FALSE
249965_at	putative protein predicted protei	---	AT5G19020	-1.12	-0.16	-1.32	0.2286529	0.4758838	-5.68	FALSE
250070_at	phosphoribosylanthranilate trans	---	AT5G17980	1.30	0.38	1.32	0.2286787	0.4758838	-5.68	FALSE
256321_at	lipoxygenase, putative similar to	LOX1	AT1G55020	1.94	0.96	1.32	0.2286287	0.4758838	-5.68	FALSE
245540_at	ABC transporter like protein	PDR2	AT4G15230	1.61	0.68	1.32	0.2286143	0.4758838	-5.68	FALSE
247574_at	putative protein predicted protei	---	AT5G61228 /	-1.17	-0.22	-1.32	0.228665	0.4758838	-5.68	FALSE
259971_at	unknown protein similar to SPL1	---	AT1G76580	-1.25	-0.32	-1.32	0.2288401	0.4761762	-5.68	FALSE
245908_at	laccase-like protein laccase - Ac	LAC14	AT5G09360	1.27	0.34	1.32	0.2289462	0.4763328	-5.68	FALSE
249583_at	CALMODULIN-RELATED PROT	TCH2	AT5G37770	1.71	0.78	1.32	0.2289571	0.4763328	-5.68	FALSE
252478_at	putative protein mitotic phospho	---	AT3G46540	-1.29	-0.36	-1.32	0.2290205	0.4763342	-5.68	FALSE
265133_s_a	unknown protein similar to hypotl	---	AT1G51240 /	-1.13	-0.18	-1.32	0.2289827	0.4763342	-5.68	FALSE
256409_at	hypothetical protein	---	AT1G66620	-1.19	-0.25	-1.32	0.2290129	0.4763342	-5.68	FALSE
258750_at	putative pectinacetylesterase sim	---	AT3G05910	1.44	0.52	1.32	0.2290937	0.476434	-5.68	TRUE
264032_at	unknown protein	GEK1	AT2G03800	1.17	0.23	1.32	0.2291102	0.476434	-5.68	FALSE
254084_at	ubiquitin activating enzyme - like	SAE1A	AT4G24940	-1.30	-0.38	-1.32	0.2291449	0.4764627	-5.68	FALSE
246880_s_a	myrosinase TGG2 ; supported b	TGG2	AT5G25980 /	1.61	0.69	1.32	0.2292606	0.4765816	-5.68	TRUE
266172_at	putative aquaporin (water channe	PIP2E	AT2G39010	-1.38	-0.47	-1.32	0.2292648	0.4765816	-5.68	TRUE
250602_s_a	unknown protein	---	AT5G07940 /	-1.16	-0.21	-1.32	0.2292544	0.4765816	-5.68	FALSE
262534_at	unknown protein contains Pfam p	SHA	AT1G17040	-1.23	-0.29	-1.32	0.2293883	0.4765826	-5.68	FALSE
258143_at	hypothetical protein	---	AT3G18170	1.27	0.34	1.32	0.2293749	0.4765826	-5.68	FALSE
254782_at	putative calmodulin calmodulin -	UNE14	AT4G12860	1.18	0.24	1.32	0.2293906	0.4765826	-5.68	FALSE
267325_at	unknown protein predicted by ge	---	AT2G19360	1.17	0.23	1.32	0.2293611	0.4765826	-5.68	FALSE
255311_at	putative protein	---	---	-1.14	-0.19	-1.32	0.2293385	0.4765826	-5.68	FALSE
263030_at	hypothetical protein predicted by	---	AT1G24060	-1.13	-0.17	-1.32	0.229344	0.4765826	-5.68	FALSE
252019_at	late embryogenesis abundant pr	---	AT3G53040	1.13	0.17	1.32	0.2294488	0.47666	-5.68	FALSE
256666_at	histone H2A, putative similar to I	HTA13	AT3G20670	-1.39	-0.47	-1.32	0.2295413	0.4767654	-5.69	FALSE
267152_at	hypothetical protein predicted by	---	AT2G31040	-1.24	-0.31	-1.32	0.2295295	0.4767654	-5.69	FALSE
255834_at	putative RNA-binding protein	---	AT2G33410	1.12	0.17	1.32	0.2296044	0.476853	-5.69	FALSE
257610_at	zinc finger protein, putative simil	AtIDD11	AT3G13810	-1.42	-0.51	-1.32	0.2296541	0.4768841	-5.69	FALSE
247485_at	putative protein ARR1, Arabidop	ARR23	AT5G62120	1.13	0.17	1.32	0.2296664	0.4768841	-5.69	FALSE
260075_at	putative integral membrane prote	---	AT1G73700	-1.21	-0.28	-1.32	0.2296821	0.4768841	-5.69	FALSE
260302_at	putative sulfate transporter conta	---	AT1G80310 /	1.22	0.29	1.32	0.2297255	0.4769309	-5.69	FALSE
258342_at	hypothetical protein similar to ext	---	AT3G22800	1.33	0.41	1.32	0.2298716	0.4771907	-5.69	FALSE

249584_s_a	Membrane integral protein (MIP	NIP4;1	AT5G37810 /.	1.19	0.25	1.32	0.2299753	0.4773625	-5.69	FALSE
247107_at	senescence-associated protein a	STR16	AT5G66040	1.28	0.35	1.32	0.2300587	0.4774695	-5.69	FALSE
265072_at	hypothetical protein predicted by	LAS	AT1G55580	1.22	0.29	1.32	0.2300687	0.4774695	-5.69	FALSE
245751_s_a	hypothetical protein contains sim	---	AT1G25682 /.	1.31	0.39	1.32	0.2301039	0.477499	-5.69	FALSE
247790_at	putative PRL1 associated protein	---	AT5G58720	1.18	0.24	1.32	0.2301412	0.477533	-5.69	FALSE
250897_at	putative protein ; supported by c	---	AT5G03430	-1.16	-0.21	-1.32	0.2302648	0.4776592	-5.69	FALSE
263505_s_a	hypothetical protein	---	AT2G07678	1.34	0.42	1.32	0.2302421	0.4776592	-5.69	FALSE
256795_at	20S proteasome subunit PAC1 i	PAC1	AT3G22110	-1.13	-0.18	-1.32	0.2302524	0.4776592	-5.69	FALSE
264131_at	unknown protein	---	AT1G79150	-1.25	-0.33	-1.32	0.2303552	0.4777212	-5.69	FALSE
246356_x_a	hypothetical protein, 5' partial	---	---	1.14	0.19	1.32	0.2303568	0.4777212	-5.69	FALSE
259917_at	hypothetical protein predicted by	---	AT1G72580	-1.15	-0.21	-1.32	0.2303576	0.4777212	-5.69	FALSE
267101_at	putative peroxidase	---	AT2G41480	-1.23	-0.30	-1.32	0.2303839	0.4777324	-5.69	FALSE
247118_at	uridylyl transferases-like ; suppo	ACR1	AT5G65890	1.28	0.36	1.32	0.2304472	0.4777708	-5.69	FALSE
267025_at	unknown protein predicted by ge	---	AT2G38350	1.12	0.17	1.32	0.2304652	0.4777708	-5.69	FALSE
260876_at	hypothetical protein contains sim	---	AT1G21460	1.25	0.33	1.32	0.2304338	0.4777708	-5.69	FALSE
246733_at	serine protease-like protein serir	---	AT5G27660	-1.18	-0.24	-1.32	0.2307364	0.4780575	-5.69	FALSE
254472_at	putative protein predicted protei	---	---	1.13	0.17	1.32	0.2307215	0.4780575	-5.69	FALSE
260831_at	glutaredoxin, putative similar to	---	AT1G06830	-2.25	-1.17	-1.32	0.2306506	0.4780575	-5.69	FALSE
259400_at	receptor-like protein kinase, puta	---	AT1G17750	1.94	0.96	1.32	0.2307502	0.4780575	-5.69	FALSE
249745_at	phloem-specific lectin-like protein	AtPP2-B12	AT5G24560	1.19	0.25	1.32	0.2307328	0.4780575	-5.69	FALSE
256729_at	hypothetical protein predicted by	---	AT3G25680	-1.17	-0.22	-1.32	0.2307309	0.4780575	-5.69	FALSE
264345_at	Expressed protein ; supported by	---	AT1G11915	1.21	0.28	1.32	0.2307409	0.4780575	-5.69	FALSE
261113_at	hypothetical protein predicted by	---	AT1G75400	-1.22	-0.28	-1.32	0.2308546	0.4781435	-5.69	FALSE
263738_at	hypothetical protein predicted by	---	AT1G60060	1.51	0.60	1.32	0.2308365	0.4781435	-5.69	FALSE
245767_at	hypothetical protein similar to put	---	AT1G33610	1.12	0.16	1.32	0.2308171	0.4781435	-5.69	FALSE
261250_at	unknown protein	---	AT1G05890	-1.15	-0.21	-1.32	0.2309029	0.4781524	-5.69	TRUE
249054_at	unknown protein	---	AT5G02870 /.	-1.19	-0.25	-1.32	0.2309847	0.4781524	-5.69	FALSE
265038_at	putative protein kinase highly sir	---	AT1G03920	1.16	0.22	1.32	0.2309642	0.4781524	-5.69	FALSE
267327_at	putative protein kinase contains a	---	AT2G19410	1.14	0.19	1.32	0.2309495	0.4781524	-5.69	FALSE
262096_at	NAC1 identical to NAC1 GB:AAF	NAC1	AT1G56010	-1.39	-0.48	-1.32	0.2309098	0.4781524	-5.69	FALSE
250067_at	unknown protein	---	AT5G17950	1.13	0.17	1.32	0.230942	0.4781524	-5.69	FALSE
260191_at	putative protein kinase Pfam HM	---	AT1G67580	-1.14	-0.19	-1.32	0.2310558	0.4782561	-5.69	FALSE
258790_at	putative RNA-binding protein sim	FLK	AT3G04610	-1.13	-0.17	-1.32	0.2311182	0.478342	-5.69	FALSE
245581_at	hypothetical protein	---	AT4G14840	1.19	0.25	1.32	0.2311581	0.478381	-5.69	FALSE
259103_at	unknown protein ; supported by	---	AT3G11690	1.43	0.52	1.32	0.2312274	0.4783878	-5.69	TRUE

266175_at	NAM (no apical meristem)-like pr	ANAC035	AT2G02450	-1.15	-0.21	-1.32	0.2312208	0.4783878	-5.69	FALSE
258828_at	putative purple acid phosphatase	PAP15	AT3G07130	1.18	0.24	1.32	0.2312452	0.4783878	-5.69	FALSE
250203_at	alpha-mannosidase	---	AT5G13980	-1.27	-0.35	-1.32	0.2312017	0.4783878	-5.69	FALSE
260728_at	Pto kinase interactor 1, putative	---	AT1G48210	1.35	0.43	1.32	0.2313096	0.4784691	-5.69	FALSE
AFFX-DapX	B. subtilis /GEN=dapB, jojF /DB_	---	---	-1.28	-0.35	-1.32	0.2313265	0.4784691	-5.69	FALSE
267622_at	hypothetical protein predicted by	---	AT2G39690	1.16	0.21	1.32	0.2313914	0.47856	-5.69	FALSE
265905_at	putative transcription elongation	---	AT2G25640	1.13	0.18	1.32	0.2314168	0.4785691	-5.69	FALSE
266050_at	putative SNF2/SWI2 family trans	---	AT2G40770	-1.14	-0.19	-1.31	0.2315479	0.4787969	-5.69	FALSE
260808_at	polyprotein, putative similar to p	---	---	1.14	0.18	1.31	0.231628	0.478919	-5.69	FALSE
253769_at	putative protein (fragment) prote	RIC7	AT4G28560	1.20	0.27	1.31	0.2316598	0.4789413	-5.69	FALSE
254285_at	putative cdc2 kinase homolog c	---	AT4G22940	-1.21	-0.27	-1.31	0.2317687	0.4791231	-5.69	FALSE
267260_at	putative proline-rich protein ; sup	AGP17	AT2G23130	-1.48	-0.56	-1.31	0.2318156	0.47916	-5.69	TRUE
265455_at	hypothetical protein predicted by	---	AT2G46560	-1.15	-0.20	-1.31	0.2318286	0.47916	-5.69	FALSE
263589_at	hypothetical protein predicted by	---	AT2G25280	-1.13	-0.18	-1.31	0.2318547	0.4791705	-5.69	FALSE
248912_at	GDSL-motif lipase/hydrolase-like	---	AT5G45670	1.21	0.27	1.31	0.2318857	0.4791912	-5.69	FALSE
262078_at	hypothetical protein predicted by	CW7	AT1G59520	-1.13	-0.18	-1.31	0.2319425	0.4792652	-5.69	FALSE
254441_at	prolamin box binding protein - lik	---	AT4G21050	1.13	0.18	1.31	0.2319957	0.4792883	-5.69	FALSE
265280_at	Expressed protein ; supported by	LCR5	AT2G28355	1.15	0.20	1.31	0.2319892	0.4792883	-5.69	FALSE
251594_at	putative protein DOC4, Mus mus	---	AT3G57630	1.58	0.66	1.31	0.2320436	0.4793439	-5.69	FALSE
246182_at	beta-1,3-glucanase - like protein	---	AT5G20870	1.20	0.26	1.31	0.2321802	0.4794141	-5.69	FALSE
261027_at	cyclic nucleotide and calmodulin	ATCNGC10	AT1G01340	1.55	0.63	1.31	0.2322002	0.4794141	-5.69	FALSE
248260_at	putative protein similar to unknov	---	AT5G53240	1.15	0.20	1.31	0.2321727	0.4794141	-5.69	FALSE
259480_at	hypothetical protein predicted by	---	AT1G19010	1.23	0.30	1.31	0.2322006	0.4794141	-5.69	FALSE
258740_at	Lon protease, putative similar to	LON3	AT3G05780	1.22	0.29	1.31	0.2321574	0.4794141	-5.69	FALSE
AFFX-r2-Bs	B. subtilis /GEN=dapB /DB_XRE	---	---	-1.36	-0.44	-1.31	0.2322037	0.4794141	-5.69	FALSE
255894_at	nuclear poly(A) polymerase, put	---	AT1G17980	-1.16	-0.22	-1.31	0.232268	0.4795033	-5.70	FALSE
AFFX-r2-Bs	B. subtilis /GEN=thrB /DB_XREF	---	---	-1.28	-0.35	-1.31	0.2323275	0.4795828	-5.70	FALSE
246198_at	geranylgeranyl pyrophosphate sy	GGPS1	AT4G36810	-1.22	-0.29	-1.31	0.2323847	0.4796159	-5.70	FALSE
259362_s_a	serin threonin-kinase, putative s	---	AT1G13350 ///	-1.18	-0.24	-1.31	0.2323856	0.4796159	-5.70	FALSE
246226_at	thiol-disulfide interchange like pr	HCF164	AT4G37200	-1.23	-0.30	-1.31	0.2324476	0.4797006	-5.70	FALSE
247184_at	putative protein contains similarit	UBP17	AT5G65450	-1.21	-0.27	-1.31	0.2324876	0.4797397	-5.70	FALSE
260096_at	hypothetical protein predicted by	---	AT1G73240	-1.20	-0.26	-1.31	0.2326192	0.4797542	-5.70	FALSE
256311_at	auxin response factor 6 (ARF6)	ARF6	AT1G30330	1.29	0.37	1.31	0.2325827	0.4797542	-5.70	FALSE
257452_at	hypothetical protein predicted by	---	AT1G05740	1.14	0.18	1.31	0.2326138	0.4797542	-5.70	FALSE
248524_s_a	putative protein contains similarit	---	AT5G50570 ///	1.65	0.73	1.31	0.2325613	0.4797542	-5.70	FALSE

264007_at	putative proline-rich protein	ATPRP2	AT2G21140	-2.40	-1.26	-1.31	0.2326015	0.4797542	-5.70	FALSE
264554_at	putative cinnamyl alcohol dehyd	---	AT1G09510	1.21	0.28	1.31	0.2326208	0.4797542	-5.70	FALSE
246878_at	putative protein self-incompatibil	---	AT5G26060	1.21	0.27	1.31	0.2327253	0.4799262	-5.70	FALSE
265266_at	putative RNA-binding protein ; s	AML2	AT2G42890	1.20	0.26	1.31	0.2328055	0.4800483	-5.70	FALSE
250188_at	putative protein COP9 complex	COP13	AT5G14250	-1.15	-0.21	-1.31	0.23285	0.4800531	-5.70	FALSE
254254_at	hypothetical protein	---	AT4G23330	-1.19	-0.25	-1.31	0.2328492	0.4800531	-5.70	FALSE
260267_at	very-long-chain fatty acid conde	KCS6	AT1G68530	1.39	0.47	1.31	0.2330355	0.4803488	-5.70	FALSE
265764_at	hypothetical protein predicted by	---	AT2G48060	1.19	0.25	1.31	0.2330225	0.4803488	-5.70	FALSE
261854_at	unknown protein	---	AT1G50670	1.12	0.17	1.31	0.2331159	0.4804125	-5.70	FALSE
246122_at	putative protein brain specific Na	PHT4;5	AT5G20380	-1.18	-0.24	-1.31	0.2331296	0.4804125	-5.70	FALSE
250689_at	putative protein similar to unknov	---	AT5G06610	-1.46	-0.55	-1.31	0.2330887	0.4804125	-5.70	FALSE
255430_at	putative chloroplast protein impo	tic20-IV	AT4G03320	-1.35	-0.43	-1.31	0.2331866	0.4804866	-5.70	TRUE
259830_at	hypothetical protein predicted by	---	AT1G80630	-1.17	-0.23	-1.31	0.2332311	0.4805221	-5.70	FALSE
246898_at	putative protein	---	AT5G25580	-1.13	-0.17	-1.31	0.233246	0.4805221	-5.70	FALSE
251094_at	putative protein ;supported by fu	---	AT5G01350	-1.18	-0.24	-1.31	0.2332795	0.4805478	-5.70	FALSE
265042_at	unknown protein Similar to acid	---	AT1G04040	-1.57	-0.65	-1.31	0.2333315	0.4806114	-5.70	TRUE
256883_at	unknown protein ; supported by	---	AT3G26440	1.57	0.65	1.31	0.233437	0.4806164	-5.70	TRUE
255216_s_a	putative peptidase	---	AT4G07670 /	-1.33	-0.41	-1.31	0.2334392	0.4806164	-5.70	FALSE
261905_at	hypothetical protein contains sim	---	AT1G65070	-1.16	-0.21	-1.31	0.2334313	0.4806164	-5.70	FALSE
256861_at	beta-amylase, putative similar to	BAM1	AT3G23920	1.32	0.40	1.31	0.2333678	0.4806164	-5.70	FALSE
255828_at	hypothetical protein predicted by	---	AT2G40630	-1.14	-0.19	-1.31	0.2334239	0.4806164	-5.70	FALSE
251989_at	RNA helicase -like protein RNA	LOS4	AT3G53110	-1.17	-0.23	-1.31	0.2336602	0.4810278	-5.70	FALSE
258600_at	putative protein kinase contains I	---	AT3G02810	-1.16	-0.21	-1.31	0.2337304	0.4811289	-5.70	FALSE
247005_at	adenylylsulfate kinase-like protei	---	AT5G67520	1.22	0.29	1.31	0.2337938	0.4811293	-5.70	TRUE
252825_at	small GTP-binding protein - like	AtRABH1c	AT4G39890	1.41	0.49	1.31	0.233783	0.4811293	-5.70	FALSE
252397_at	hypothetical protein	---	AT3G47980	1.25	0.32	1.31	0.2337664	0.4811293	-5.70	FALSE
245147_at	putative RAD51C-like DNA repai	ATRAD51C	AT2G45280	-1.33	-0.41	-1.31	0.23389	0.481197	-5.70	FALSE
255320_at	putative transposon protein	---	---	1.12	0.17	1.31	0.2338814	0.481197	-5.70	FALSE
262831_at	cytochrome B561, putative simil	---	AT1G14730	1.30	0.38	1.31	0.2338605	0.481197	-5.70	FALSE
245853_at	putative protein predicted protei	---	AT5G13500	1.22	0.28	1.31	0.2340171	0.4814151	-5.70	FALSE
267592_at	unknown protein similar to GP 22	---	AT2G39710	-1.13	-0.18	-1.31	0.2340867	0.481428	-5.70	TRUE
260913_at	s-adenosylmethionine synthetase	SAM1	AT1G02500	1.29	0.36	1.31	0.2340796	0.481428	-5.70	FALSE
248184_at	CHP-rich zinc finger protein-like	---	AT5G54050	-1.13	-0.18	-1.31	0.2340693	0.481428	-5.70	FALSE
251104_at	F-box protein family, AtFBL3 co	---	AT5G01720	1.21	0.28	1.31	0.2342853	0.4817495	-5.70	FALSE
264374_at	putative two-component respons	ARR12	AT2G25180	-1.16	-0.22	-1.31	0.2342667	0.4817495	-5.70	FALSE

260829_s_a	chloroplast thylakoidal processin	---	AT1G06870 /.	-1.24	-0.30	-1.31	0.2344549	0.4820549	-5.70	FALSE
252435_at	putative protein several hypothet	---	---	1.18	0.23	1.31	0.2344761	0.482055	-5.70	FALSE
247585_at	putative protein predicted protei	---	AT5G60680	-1.21	-0.28	-1.31	0.2346092	0.4821113	-5.70	FALSE
252537_at	putative transporter protein pept	---	AT3G45710	1.16	0.22	1.31	0.2345467	0.4821113	-5.70	FALSE
253348_at	putative protein SMT4 protein - S	---	AT4G33620	-1.13	-0.17	-1.31	0.2346031	0.4821113	-5.70	FALSE
260040_at	Expressed protein ; supported by	IDA	AT1G68765	1.99	0.99	1.31	0.2345327	0.4821113	-5.70	FALSE
254313_at	extensin like protein extensin lik	---	AT4G22460	1.18	0.24	1.31	0.2345757	0.4821113	-5.70	FALSE
255428_at	putative LRR receptor-like prote	SRF3	AT4G03390	1.15	0.21	1.30	0.234816	0.4824928	-5.70	TRUE
263220_at	hypothetical protein predicted by	emb2279	AT1G30610	-1.21	-0.27	-1.30	0.2349592	0.4827436	-5.70	FALSE
248783_at	putative protein contains similarit	---	AT5G47360	-1.28	-0.36	-1.30	0.2350282	0.4828419	-5.71	FALSE
253281_at	predicted protein	UGT73B1	AT4G34138	-1.38	-0.47	-1.30	0.2351222	0.4829444	-5.71	TRUE
245103_at	putative Ta11-like non-LTR retro	---	AT2G41590	1.14	0.19	1.30	0.2351185	0.4829444	-5.71	FALSE
253845_at	putative protein myosin heavy ch	---	AT4G27980	1.12	0.16	1.30	0.2351628	0.4829444	-5.71	FALSE
260421_at	acid phosphatase, putative simil	SBH1	AT1G69640	-1.16	-0.21	-1.30	0.2351542	0.4829444	-5.71	FALSE
251516_s_a	putative protein hypothetical pro	---	AT3G59310 /.	-1.17	-0.23	-1.30	0.2352257	0.4830301	-5.71	TRUE
259456_s_a	unknown protein similar to putati	---	---	1.17	0.22	1.30	0.2352938	0.4830505	-5.71	FALSE
251585_at	putative protein hypothetical pro	---	AT3G58630	-1.29	-0.37	-1.30	0.2352992	0.4830505	-5.71	FALSE
246101_at	putative protein	---	---	1.17	0.23	1.30	0.2352983	0.4830505	-5.71	FALSE
262581_at	unknown protein ESTs gb|T225(	---	AT1G15370	-1.13	-0.17	-1.30	0.2353578	0.4831274	-5.71	FALSE
249480_s_a	protein kinase - like protein rece	---	AT5G38990 /.	1.43	0.52	1.30	0.2354176	0.483178	-5.71	FALSE
254587_at	resistance protein RPP5 - like d	---	AT4G19520	1.18	0.24	1.30	0.2354248	0.483178	-5.71	FALSE
249597_at	putative protein probable quinon	---	AT5G37960	1.12	0.17	1.30	0.2354605	0.4832078	-5.71	FALSE
257473_at	unknown protein	---	AT1G33840	1.22	0.29	1.30	0.2356882	0.4836315	-5.71	FALSE
254351_at	putative protein probable membr	SOBER1	AT4G22300	-1.19	-0.25	-1.30	0.2357522	0.4837193	-5.71	FALSE
265405_at	putative protein kinase contains a	---	AT2G16750	-1.31	-0.39	-1.30	0.2360469	0.4841933	-5.71	TRUE
251980_at	putative protein endopeptidase C	---	AT3G53270	-1.13	-0.17	-1.30	0.2360284	0.4841933	-5.71	FALSE
254277_at	myb-like protein myb-related tra	MYB85	AT4G22680	1.61	0.68	1.30	0.2360172	0.4841933	-5.71	FALSE
257173_at	S-adenosyl-L-homocysteinas, pu	SAHH2	AT3G23810	1.77	0.82	1.30	0.2361575	0.4842739	-5.71	TRUE
246461_at	putative protein AAA family prote	---	AT5G16930	-1.46	-0.54	-1.30	0.2361756	0.4842739	-5.71	FALSE
265580_at	putative protein phosphatase 2C	---	AT2G20050	1.20	0.26	1.30	0.2361432	0.4842739	-5.71	FALSE
257435_at	putative RSZp22 splicing factor	---	AT2G24590	-1.22	-0.28	-1.30	0.2361227	0.4842739	-5.71	FALSE
254863_at	putative protein predicted protei	ATNUDX14	AT4G11980	-1.18	-0.24	-1.30	0.2361924	0.4842739	-5.71	FALSE
259467_at	hypothetical protein predicted by	---	AT1G19060	1.12	0.16	1.30	0.2362196	0.4842863	-5.71	FALSE
245023_at	PSII I protein	---	---	-1.29	-0.37	-1.30	0.2363309	0.4844709	-5.71	FALSE
252514_at	GTP-binding protein ara-3 ; supp	ATRAB8A	AT3G46060	-1.14	-0.18	-1.30	0.2364189	0.4846037	-5.71	FALSE

247909_at	unknown protein ; supported by	---	AT5G57370	-1.18	-0.24	-1.30	0.2364382	0.4846037	-5.71	FALSE
259943_at	unknown protein	---	AT1G71480	-1.26	-0.34	-1.30	0.2365522	0.4847939	-5.71	FALSE
251125_at	putative protein - kinase protein	---	AT5G01060	-1.13	-0.18	-1.30	0.2366162	0.4848814	-5.71	FALSE
266355_at	hypothetical protein predicted by	---	AT2G01400	-1.33	-0.41	-1.30	0.2367174	0.4850452	-5.71	FALSE
262067_at	hypothetical protein predicted by	---	AT1G80060	1.19	0.26	1.30	0.2367857	0.4851417	-5.71	FALSE
261499_at	cytochrome P450 (CYP93A1), p	CYP705A2	AT1G28430	1.17	0.23	1.30	0.2368251	0.4851788	-5.71	FALSE
245720_at	RNA binding protein - like	---	AT5G04210	1.15	0.20	1.30	0.2368872	0.4852624	-5.71	FALSE
246293_at	SigA binding protein ; supported	SIB1	AT3G56710	1.92	0.94	1.30	0.2369708	0.4853901	-5.71	FALSE
266735_at	putative pectinesterase ; suppor	---	AT2G46930	1.21	0.27	1.30	0.2371235	0.4856247	-5.71	TRUE
246599_at	putative protein ATP-dependent	---	AT5G14900	1.13	0.17	1.30	0.2371492	0.4856247	-5.71	FALSE
258077_at	unknown protein ;supported by f	---	AT3G26110	1.19	0.25	1.30	0.2371447	0.4856247	-5.71	FALSE
253098_at	cytochrome P450-like protein	CYP81D3	AT4G37340	1.18	0.24	1.30	0.2372725	0.4858335	-5.71	FALSE
247210_at	annexin ;supported by full-length	ANNAT2	AT5G65020	1.35	0.44	1.30	0.2374627	0.4858871	-5.71	TRUE
265599_at	unknown protein	AT2G14255	---	1.15	0.21	1.30	0.2373714	0.4858871	-5.71	FALSE
265056_at	mitochondrial processing peptid	---	AT1G51980	1.21	0.28	1.30	0.2374818	0.4858871	-5.71	FALSE
255060_at	putative protein TMV resistance	---	AT4G09430	1.18	0.24	1.30	0.2373296	0.4858871	-5.71	FALSE
266709_at	unknown protein ;supported by f	ATSPP	AT2G03120	1.23	0.30	1.30	0.2374904	0.4858871	-5.71	FALSE
245937_at	putative protein 22kDa peroxiso	---	AT5G19750	-1.30	-0.38	-1.30	0.2373782	0.4858871	-5.71	FALSE
263744_at	Mutator-like transposase similar	---	AT2G21420	1.16	0.22	1.30	0.2374241	0.4858871	-5.71	FALSE
250063_at	disease resistance protein - like	CSA1	AT5G17880	1.21	0.27	1.30	0.2374358	0.4858871	-5.71	FALSE
247496_at	putative protein predicted protei	GUT1	AT5G61840	-1.14	-0.19	-1.30	0.2374821	0.4858871	-5.71	FALSE
254603_at	putative protein hypothetical pro	---	AT4G19045 /	1.18	0.23	1.30	0.2375839	0.4859815	-5.71	FALSE
266545_at	hypothetical protein predicted by	---	AT2G35290	1.32	0.40	1.30	0.2376004	0.4859815	-5.71	FALSE
247683_at	serine/threonine-specific protein	---	AT5G59660	1.19	0.25	1.30	0.2375609	0.4859815	-5.71	FALSE
259489_at	unknown protein	---	AT1G15790	-1.31	-0.38	-1.30	0.2376415	0.4860219	-5.71	FALSE
266103_at	putative VAMP-associated protei	PVA12	AT2G45140	1.16	0.22	1.30	0.2376801	0.4860573	-5.71	FALSE
250225_at	Expressed protein ; supported by	---	AT5G14105	-1.21	-0.28	-1.30	0.237781	0.4861861	-5.72	FALSE
246082_at	receptor protein kinase - like pro	EFR	AT5G20480	1.53	0.61	1.30	0.2377857	0.4861861	-5.72	FALSE
253287_at	putative protein dJ69E11.3, Hon	---	AT4G34270	-1.13	-0.18	-1.30	0.2379252	0.4864276	-5.72	FALSE
254455_at	hypothetical protein	---	AT4G21140	-1.26	-0.33	-1.29	0.2379819	0.4865	-5.72	FALSE
262928_at	hypothetical protein	---	AT1G65760	1.18	0.24	1.29	0.2381024	0.4867026	-5.72	FALSE
264701_at	hypothetical protein similar to hy	---	AT1G70160	-1.17	-0.23	-1.29	0.2381564	0.4867259	-5.72	FALSE
249290_at	putative protein strong similarity	---	AT5G41060	-1.29	-0.37	-1.29	0.2381421	0.4867259	-5.72	FALSE
245844_at	hypothetical protein predicted by	---	AT1G26170	-1.16	-0.21	-1.29	0.2382311	0.486819	-5.72	FALSE
252910_at	putative protein various predicte	---	AT4G39590	-1.13	-0.17	-1.29	0.2382447	0.486819	-5.72	FALSE

260036_at	putative protein kinase Pfam HM	STN7	AT1G68830	-1.19	-0.25	-1.29	0.2383281	0.4869458	-5.72	FALSE
256372_at	cell division protein kinase, puta	CAK4	AT1G66750	-1.22	-0.29	-1.29	0.2383736	0.4869953	-5.72	FALSE
252067_at	protein phosphatase 2C -like pro	---	AT3G51370	-1.18	-0.24	-1.29	0.2384019	0.4870095	-5.72	FALSE
260800_at	unknown protein	TSD2	AT1G78240	1.24	0.30	1.29	0.2385222	0.4872115	-5.72	FALSE
250682_x_a	putative protein similar to unknov	---	AT5G06630	1.41	0.50	1.29	0.2386331	0.4873945	-5.72	FALSE
266511_at	putative ATP-dependent RNA he	---	AT2G47680	-1.19	-0.25	-1.29	0.2386796	0.4874125	-5.72	FALSE
258013_at	unknown protein	---	AT3G19320	1.21	0.27	1.29	0.2386847	0.4874125	-5.72	FALSE
265496_at	copia-like retroelement pol polyp	---	---	-1.12	-0.16	-1.29	0.2387727	0.4875485	-5.72	FALSE
260278_at	hypothetical protein predicted by	WRKY66	AT1G80590	1.27	0.34	1.29	0.238953	0.4878731	-5.72	FALSE
266912_at	hypothetical protein predicted by	---	AT2G45900	-1.70	-0.76	-1.29	0.2390502	0.4880278	-5.72	FALSE
262529_at	putative receptor protein kinase A	AtRLP3	AT1G17250	-1.20	-0.26	-1.29	0.2392068	0.4883037	-5.72	FALSE
255827_at	unknown protein ; supported by	---	AT2G40600	1.18	0.24	1.29	0.2393559	0.4885645	-5.72	FALSE
247147_at	putative protein contains similarit	GTE7	AT5G65630	1.22	0.29	1.29	0.239385	0.4885802	-5.72	FALSE
266389_s_a	unknown protein	---	AT2G31580 ///	1.14	0.18	1.29	0.2394407	0.4886501	-5.72	FALSE
264137_at	lupeol synthase, putative similar	ATLUP2	AT1G78960	-1.26	-0.33	-1.29	0.2395226	0.4886861	-5.72	FALSE
249083_at	prohibitin non-consensus TT acc	ATPHB7	AT5G44140	-1.15	-0.20	-1.29	0.2394991	0.4886861	-5.72	FALSE
245055_at	hypothetical protein predicted by	---	AT2G26470	-1.18	-0.24	-1.29	0.2395147	0.4886861	-5.72	FALSE
254709_at	Expressed protein ; supported by	AGD8	AT4G17890	1.20	0.26	1.29	0.2395599	0.4887185	-5.72	TRUE
246969_at	glutamic acid-rich protein other g	---	AT5G24880	1.17	0.23	1.29	0.2396452	0.4888488	-5.72	FALSE
254390_at	calcium-dependent protein kinas	CPK15	AT4G21940	1.16	0.21	1.29	0.2397375	0.4889933	-5.72	FALSE
251182_at	putative protein HIRA interacting	ATERDJ3B	AT3G62600	1.60	0.68	1.29	0.2398058	0.489089	-5.72	FALSE
254003_at	hypothetical protein	---	AT4G26290	1.17	0.22	1.29	0.2398989	0.489235	-5.72	FALSE
253322_at	putative protein ;supported by fu	---	AT4G33980	-1.21	-0.28	-1.29	0.2399503	0.4892866	-5.72	FALSE
248743_at	unknown protein	---	AT5G48240	-1.27	-0.34	-1.29	0.2399671	0.4892866	-5.72	FALSE
247370_at	putative protein similar to unknov	---	AT5G63320	1.32	0.40	1.29	0.2400414	0.4893944	-5.72	FALSE
251710_at	putative protein several hypothet	---	AT3G56930	1.33	0.41	1.29	0.2401017	0.4894735	-5.72	TRUE
245216_at	Expressed protein non-consensu	IMPA-2	AT4G16143	-1.12	-0.16	-1.29	0.2401374	0.4894768	-5.72	FALSE
246790_at	putative protein unknown protein	---	AT5G27610	1.22	0.28	1.29	0.2401462	0.4894768	-5.72	FALSE
253112_at	putative ascorbate peroxidase a	APX5	AT4G35970	1.25	0.32	1.29	0.2401801	0.4894809	-5.72	FALSE
249107_at	unknown protein	---	AT5G43680	-1.15	-0.21	-1.29	0.2401911	0.4894809	-5.72	FALSE
254548_at	putative protein various predicte	---	AT4G19865	-1.30	-0.38	-1.29	0.2402154	0.4894866	-5.72	FALSE
251571_at	putative protein several hypothet	---	AT3G58330	1.14	0.19	1.29	0.2402429	0.4894989	-5.72	FALSE
263704_at	unknown protein similar to unkn	---	AT1G31130	1.19	0.25	1.29	0.2402661	0.4895025	-5.72	FALSE
251032_at	putative homeodomain protein se	RPL	AT5G02030	-1.43	-0.52	-1.29	0.2403006	0.4895291	-5.72	FALSE
250410_at	putative protein putative ATP/G	---	AT5G11010	-1.25	-0.32	-1.29	0.2404221	0.4897241	-5.72	FALSE

265148_at	unknown protein	---	AT1G51160	-1.16	-0.21	-1.29	0.2404393	0.4897241	-5.72	FALSE
256406_at	unknown protein	---	AT1G50710	1.17	0.23	1.29	0.2404885	0.4897267	-5.72	FALSE
250195_at	putative protein	---	AT5G14560	-1.12	-0.16	-1.29	0.240505	0.4897267	-5.72	FALSE
247727_at	putative ripening-related protein	---	AT5G59490	1.21	0.28	1.29	0.240476	0.4897267	-5.72	FALSE
261528_at	pectate lyase, putative similar to	AT59	AT1G14420	1.16	0.22	1.29	0.2405665	0.4897943	-5.73	FALSE
261508_at	unknown protein	---	AT1G71730	-1.17	-0.22	-1.29	0.2405811	0.4897943	-5.73	FALSE
259229_at	unknown protein similar to transc	ADA2A	AT3G07740	-1.20	-0.27	-1.29	0.240862	0.490235	-5.73	FALSE
256838_at	ADP-ribosylation factor, putative	ATARFC1	AT3G22950	1.18	0.24	1.29	0.2408618	0.490235	-5.73	FALSE
249392_at	peroxidase ATP26a	---	AT5G40150	-1.18	-0.24	-1.29	0.2408247	0.490235	-5.73	FALSE
263121_at	receptor protein kinase, putative	---	AT1G78530	1.19	0.25	1.29	0.2409159	0.4903009	-5.73	FALSE
252349_at	cell division cycle protein 23 hon	APC8	AT3G48150	-1.26	-0.34	-1.29	0.2409631	0.4903095	-5.73	FALSE
257309_at	hypothetical protein predicted by	---	AT3G28150	-1.12	-0.16	-1.29	0.2409425	0.4903095	-5.73	FALSE
260700_at	hypothetical protein identical to h	---	AT1G32260	-1.18	-0.24	-1.29	0.2410871	0.4905179	-5.73	FALSE
262987_at	conserved hypothetical protein p	---	AT1G23240	1.25	0.32	1.29	0.2411497	0.4906015	-5.73	FALSE
256221_at	DnaJ protein, putative contains l	---	AT1G56300	-1.14	-0.19	-1.29	0.2412273	0.4907156	-5.73	FALSE
255236_at	score=11.7, E=0.66,N=1	ATEHD2	AT4G05520	-1.27	-0.35	-1.28	0.2412825	0.4907842	-5.73	FALSE
247276_at	putative protein contains similarit	HEN4	AT5G64390	1.27	0.35	1.28	0.2413651	0.4908942	-5.73	FALSE
266861_at	putative choline kinase ;supporte	emb1187	AT2G26830	-1.18	-0.24	-1.28	0.2413796	0.4908942	-5.73	FALSE
260313_at	putative disease resistance prote	---	AT1G63870	1.20	0.26	1.28	0.2414384	0.4909699	-5.73	FALSE
250770_at	laccase (diphenol oxidase)	LAC12	AT5G05390	1.23	0.29	1.28	0.2414726	0.4909894	-5.73	FALSE
263806_at	hypothetical protein predicted by	---	AT2G04305	1.38	0.47	1.28	0.241491	0.4909894	-5.73	FALSE
257247_at	helix-loop-helix DNA-binding prot	FMA	AT3G24140	1.22	0.29	1.28	0.2415962	0.4911596	-5.73	FALSE
267475_at	expressed protein ; supported by	---	AT2G02730	1.19	0.25	1.28	0.2417109	0.4913489	-5.73	FALSE
253044_at	hypothetical protein ;supported b	---	AT4G37290	2.38	1.25	1.28	0.2417578	0.4914004	-5.73	TRUE
255735_at	transmembrane protein, putative	---	AT1G25520	-1.31	-0.39	-1.28	0.2418226	0.4914318	-5.73	TRUE
249858_at	myb-related transcription factor-li	MYB37	AT5G23000	1.21	0.28	1.28	0.2418094	0.4914318	-5.73	FALSE
248599_at	putative protein contains similarit	---	AT5G49380	1.26	0.33	1.28	0.2418379	0.4914318	-5.73	FALSE
258315_at	Expressed protein ; supported by	---	AT3G16175	-1.17	-0.22	-1.28	0.2419132	0.491541	-5.73	FALSE
246837_at	pectin acetylesterase precursor	---	AT5G26670	1.29	0.36	1.28	0.2420223	0.4916751	-5.73	FALSE
250590_at	exonuclease-like protein	---	AT5G07710	-1.14	-0.19	-1.28	0.2420031	0.4916751	-5.73	FALSE
256539_at	hypothetical protein predicted by	---	---	1.14	0.18	1.28	0.2420574	0.4917027	-5.73	FALSE
247137_at	calcium-dependent protein kinas	CPK28	AT5G66210	1.40	0.49	1.28	0.2420973	0.4917399	-5.73	FALSE
255346_at	hypothetical protein	---	---	1.11	0.15	1.28	0.2421577	0.4918105	-5.73	FALSE
262030_s_a	mutator-like transposase, putativ	---	---	1.17	0.22	1.28	0.2421752	0.4918105	-5.73	FALSE
263399_at	unknown protein ; supported by f	---	AT2G31490	-1.15	-0.21	-1.28	0.2423709	0.4921641	-5.73	FALSE

250387_at	putative protein predicted protei	---	AT5G11290	1.13	0.17	1.28	0.2424253	0.4922307	-5.73	FALSE
260139_at	Myb-related transcription factor,	MYB114	AT1G66380	1.14	0.19	1.28	0.2425081	0.492355	-5.73	FALSE
266814_at	homeodomain transcription facto	ATHB4	AT2G44910	1.12	0.16	1.28	0.2425327	0.4923613	-5.73	FALSE
263253_at	bZIP transcription factor (POSF2	---	AT2G31370	1.20	0.26	1.28	0.2425989	0.4924465	-5.73	FALSE
257254_at	salicylic acid carboxyl methyltrar	---	AT3G21950	1.15	0.20	1.28	0.2426179	0.4924465	-5.73	FALSE
248275_at	isp4 protein	ATOPT8	AT5G53520	1.13	0.18	1.28	0.2427345	0.4926394	-5.73	FALSE
266807_at	hypothetical protein	---	AT2G29920	1.19	0.25	1.28	0.2427739	0.4926756	-5.73	FALSE
256668_at	hypothetical protein similar to hyp	---	AT3G32190	1.18	0.23	1.28	0.2428115	0.492708	-5.73	FALSE
253928_at	phosphoprotein phosphatase (PF	PPX1	AT4G26720	-1.16	-0.21	-1.28	0.2428719	0.4927428	-5.73	FALSE
246874_at	arabinosidase - like protein arab	ASD2	AT5G26120	1.16	0.22	1.28	0.2428654	0.4927428	-5.73	FALSE
259424_at	hypothetical protein contains sim	---	AT1G13830	1.24	0.31	1.28	0.2428951	0.4927462	-5.73	FALSE
252271_s_a	putative protein CGI-141 protein	---	AT3G49420 ///	-1.13	-0.18	-1.28	0.2429427	0.4927989	-5.73	FALSE
250954_at	putative protein ;supported by fu	ATRAB8C	AT5G03520	-1.21	-0.28	-1.28	0.2430059	0.4928552	-5.73	TRUE
259812_at	unknown protein	---	AT1G49840	-1.24	-0.31	-1.28	0.2430137	0.4928552	-5.73	FALSE
259626_at	bZIP transcription factor, putativ	ATBZIP60	AT1G42990	1.70	0.76	1.28	0.2430678	0.4928943	-5.73	FALSE
257760_s_a	putative AC-like transposase sim	---	---	1.15	0.20	1.28	0.2430762	0.4928943	-5.73	FALSE
253305_at	Expressed protein ; supported by	---	AT4G33666	1.45	0.54	1.28	0.2432472	0.4929001	-5.73	FALSE
249974_at	putative protein predicted protei	---	AT5G18780	1.34	0.42	1.28	0.2431858	0.4929001	-5.73	FALSE
252331_s_a	serine palmitoyltransferase-like p	SPT1	AT3G48780 ///	1.17	0.23	1.28	0.243166	0.4929001	-5.73	FALSE
261326_s_a	aminoacylase, putative similar to	---	AT1G44180 ///	-1.25	-0.32	-1.28	0.2431964	0.4929001	-5.73	FALSE
257910_at	hypothetical protein similar to hyp	---	AT3G25580	-1.18	-0.24	-1.28	0.2431333	0.4929001	-5.73	FALSE
265519_at	hypothetical protein	---	AT2G06040	-1.15	-0.20	-1.28	0.2431468	0.4929001	-5.73	FALSE
261001_at	hypothetical protein similar to hyp	---	AT1G26530	-1.19	-0.25	-1.28	0.2432519	0.4929001	-5.73	FALSE
246665_s_a	putative protein predicted protein	---	---	1.16	0.22	1.28	0.2432172	0.4929001	-5.73	FALSE
263961_at	F-box protein family, AtFBL11 co	---	AT2G36370	-1.20	-0.26	-1.28	0.2432793	0.4929118	-5.73	FALSE
261328_at	unknown protein	---	AT1G44835	-1.17	-0.23	-1.28	0.2433009	0.4929118	-5.73	FALSE
251282_at	putative protein transcription fac	CRF6	AT3G61630	-1.42	-0.50	-1.28	0.243348	0.4929634	-5.73	TRUE
264333_at	hypothetical protein similar to put	AtTLP4	AT1G61940	1.14	0.19	1.28	0.2434008	0.4929639	-5.73	FALSE
245135_at	putative non-LTR retroelement re	---	---	1.17	0.23	1.28	0.2434131	0.4929639	-5.73	FALSE
253252_at	amidophosphoribosyltransferase	ATASE2	AT4G34740	-1.25	-0.33	-1.28	0.2434096	0.4929639	-5.73	FALSE
249961_at	putative protein predicted protei	---	AT5G18770	-1.18	-0.23	-1.28	0.2434813	0.4930582	-5.74	FALSE
264397_at	hypothetical protein	---	AT1G11820	1.23	0.30	1.28	0.2435899	0.4932345	-5.74	FALSE
257485_at	hypothetical protein contains Pfa	---	AT1G63580	1.35	0.43	1.28	0.2436427	0.4932976	-5.74	FALSE
249713_at	putative protein contains similarit	---	AT5G35690	1.19	0.25	1.28	0.2437711	0.4934805	-5.74	FALSE
245586_at	hypothetical protein	---	AT4G14980	1.15	0.20	1.28	0.2437763	0.4934805	-5.74	FALSE

254800_at	putative protein several hypothet	---	AT4G13070	-1.25	-0.33	-1.28	0.2438386	0.4935627	-5.74	FALSE
248160_at	putative protein similar to unknov	---	AT5G54470	1.23	0.30	1.28	0.243872	0.4935866	-5.74	FALSE
259997_at	unknown protein similar to N-ace	---	AT1G67880	1.37	0.46	1.28	0.2439164	0.4936326	-5.74	FALSE
256506_at	unknown protein	---	AT1G75160	1.18	0.24	1.28	0.2439949	0.4937211	-5.74	FALSE
251681_at	putative protein hypothetical pro	---	AT3G57100	1.18	0.24	1.28	0.2440034	0.4937211	-5.74	FALSE
257692_at	hypothetical protein contains sim	---	AT3G12840	1.14	0.19	1.28	0.2440565	0.4937846	-5.74	FALSE
258392_at	anther development protein, AT/	ATA20	AT3G15400	1.21	0.27	1.28	0.2441423	0.4938707	-5.74	FALSE
254581_at	putative protein membrane-asso	---	AT4G19440	1.22	0.29	1.28	0.2441324	0.4938707	-5.74	FALSE
245468_at	pectinesterase like protein	---	AT4G15980	1.14	0.19	1.28	0.2442149	0.4939738	-5.74	FALSE
256737_at	farnesyltranstransferase, putativ	---	AT3G29420	1.14	0.18	1.28	0.2443182	0.4940512	-5.74	FALSE
247675_at	putative protein large number of	---	AT5G59940	1.21	0.27	1.28	0.2442977	0.4940512	-5.74	FALSE
259525_at	hypothetical protein	ATEXPA7	AT1G12560	-1.14	-0.19	-1.28	0.2443084	0.4940512	-5.74	FALSE
255490_at	putative protein lysosomal traffic	---	AT4G02660	-1.15	-0.20	-1.28	0.2443876	0.4941478	-5.74	FALSE
245193_at	F12A21.6 hypothetical protein	SUFE2	AT1G67810	1.70	0.76	1.28	0.2444151	0.4941573	-5.74	TRUE
256218_at	hypothetical protein predicted by	---	AT1G56270	1.19	0.25	1.28	0.2444357	0.4941573	-5.74	FALSE
259771_at	unknown protein	---	AT1G29470	-1.24	-0.31	-1.28	0.2445184	0.494237	-5.74	FALSE
259640_at	beta-glucosidase, putative identi	BGLU18	AT1G52400	1.38	0.46	1.28	0.2445016	0.494237	-5.74	FALSE
245825_at	protein kinase, putative similar t	ATSK42	AT1G57870	-1.16	-0.21	-1.27	0.2446804	0.4945028	-5.74	FALSE
250153_at	putative protein TMV response-r	WRKY72	AT5G15130	1.43	0.51	1.27	0.2446933	0.4945028	-5.74	FALSE
253162_at	phosphoserine aminotransferase	PSAT	AT4G35630	1.72	0.78	1.27	0.2447376	0.4945035	-5.74	FALSE
247294_at	putative protein similar to unknov	XRCC2	AT5G64520	1.14	0.19	1.27	0.2447466	0.4945035	-5.74	FALSE
259052_at	unknown protein	PEX19-1	AT3G03490	1.15	0.20	1.27	0.2447586	0.4945035	-5.74	FALSE
253853_at	putative diacylglycerol kinase (fr	---	AT4G28130	1.14	0.20	1.27	0.2448311	0.4945622	-5.74	FALSE
257757_at	hypothetical protein predicted by	PGSIP1	AT3G18660	-1.14	-0.19	-1.27	0.2448277	0.4945622	-5.74	FALSE
264267_at	hypothetical protein contains sim	---	AT1G60200	1.17	0.23	1.27	0.2448671	0.4945913	-5.74	FALSE
255432_at	SYR1-like syntaxin ;supported b	SYP123	AT4G03330	1.14	0.19	1.27	0.2449038	0.4946216	-5.74	FALSE
248121_at	putative protein contains similarit	GAUT12	AT5G54690	1.24	0.31	1.27	0.2449533	0.4946778	-5.74	FALSE
246225_at	putative protein ;supported by ful	LEJ2	AT4G36910	-1.20	-0.27	-1.27	0.2449832	0.4946944	-5.74	FALSE
267146_at	hypothetical protein predicted by	---	AT2G38160	1.14	0.19	1.27	0.2450099	0.4947044	-5.74	FALSE
249000_at	putative protein contains similarit	---	AT5G44980	1.16	0.22	1.27	0.2451017	0.4948461	-5.74	FALSE
259025_at	hypothetical protein predicted by	---	---	1.21	0.27	1.27	0.2452188	0.4949646	-5.74	FALSE
260417_at	putative chromomethylase simila	CMT3	AT1G69770	-1.34	-0.43	-1.27	0.2452256	0.4949646	-5.74	FALSE
266624_s_a	phosphoribosyl pyrophosphate s	---	AT1G32380 /	1.39	0.47	1.27	0.2452182	0.4949646	-5.74	FALSE
258940_at	putative lipase acylhydrolase cor	---	AT3G09930	1.12	0.16	1.27	0.2453677	0.495164	-5.74	FALSE
249294_at	unknown protein	---	AT5G41270	-1.25	-0.33	-1.27	0.2453482	0.495164	-5.74	FALSE

258529_at	hypothetical protein predicted by	---	AT3G06740	-1.22	-0.28	-1.27	0.2454496	0.4952711	-5.74	FALSE
264792_at	hypothetical protein similar to hyp	---	AT1G08620	1.15	0.20	1.27	0.2454643	0.4952711	-5.74	FALSE
261110_at	E2, ubiquitin-conjugating enzym	UBC16	AT1G75440	1.22	0.29	1.27	0.2455617	0.4953954	-5.74	FALSE
258759_at	putative bZIP transcription factor	BZIP28	AT3G10800	1.13	0.18	1.27	0.2455693	0.4953954	-5.74	FALSE
250270_at	putative protein FL10, EGF resp	---	AT5G12980	-1.19	-0.25	-1.27	0.2456294	0.4954729	-5.74	FALSE
264683_at	unknown protein similar to putati	FRA3	AT1G65580	1.12	0.17	1.27	0.2456624	0.4954956	-5.74	FALSE
251049_at	putative protein rab11 binding pr	---	AT5G02430	1.17	0.22	1.27	0.2457113	0.4955091	-5.74	FALSE
253034_at	calcium-dependent protein kinas	CPK26	AT4G38230	-1.16	-0.22	-1.27	0.2457125	0.4955091	-5.74	FALSE
246137_at	putative protein predicted protei	LSH1	AT5G28490	1.45	0.54	1.27	0.2457933	0.4956281	-5.74	FALSE
258875_at	unknown protein ;supported by f	---	AT3G03160	1.22	0.29	1.27	0.2458749	0.4957489	-5.74	FALSE
257072_at	myrosinase-associated protein,	---	AT3G14220	1.32	0.40	1.27	0.2460639	0.4959243	-5.74	FALSE
252234_at	putative protein ; supported by fu	ATPSK4	AT3G49780	1.76	0.81	1.27	0.2460839	0.4959243	-5.74	FALSE
248489_at	unknown protein	---	AT5G51090	1.13	0.18	1.27	0.2459922	0.4959243	-5.74	FALSE
251887_at	FKBP12 interacting protein (FIP3	ATFIP37	AT3G54170	-1.24	-0.31	-1.27	0.2460422	0.4959243	-5.74	FALSE
246397_at	hypothetical protein contains sim	AtRLP9	AT1G58190	1.13	0.18	1.27	0.2460271	0.4959243	-5.74	FALSE
246096_at	beta-1,3-glucanase bg4 ;suppor	BETAG4	AT5G20330	-1.17	-0.23	-1.27	0.2460924	0.4959243	-5.74	FALSE
262966_at	ER lumen protein retaining rece	---	AT1G75760	-1.15	-0.20	-1.27	0.2461586	0.49601	-5.74	FALSE
265131_at	putative polygalacuronase isoenz	JP630	AT1G23760	1.40	0.49	1.27	0.2461784	0.49601	-5.74	FALSE
253772_at	Expressed protein ; supported by	A7	AT4G28395	1.12	0.17	1.27	0.2462161	0.4960421	-5.74	FALSE
262145_at	unknown protein contains similar	---	AT1G52730	-1.19	-0.25	-1.27	0.2462704	0.496064	-5.74	FALSE
256550_at	En/Spm-like transposon protein,	---	---	1.13	0.17	1.27	0.246269	0.496064	-5.74	FALSE
251992_at	putative protein myosin heavy ch	---	AT3G53350	-1.22	-0.29	-1.27	0.2463268	0.4961337	-5.75	FALSE
249166_at	CHP-rich zinc finger protein-like	---	AT5G42840	-1.16	-0.22	-1.27	0.2464386	0.4962701	-5.75	FALSE
265613_at	putative DnaJ protein ; supporte	---	AT2G25560	-1.19	-0.25	-1.27	0.2464208	0.4962701	-5.75	FALSE
265639_at	putative reverse transcriptase	---	---	1.15	0.20	1.27	0.2464598	0.4962701	-5.75	FALSE
261076_at	unknown protein ;supported by fu	SMO2-1	AT1G07420	-1.13	-0.18	-1.27	0.2465094	0.4963261	-5.75	FALSE
255911_at	receptor-like kinase, putative sim	---	AT1G66930	-1.13	-0.17	-1.27	0.2466474	0.4965164	-5.75	FALSE
257722_at	putative chloroplast nucleoid DN	---	AT3G18490	-1.29	-0.37	-1.27	0.2466296	0.4965164	-5.75	FALSE
248208_at	unknown protein	ATHB52	AT5G53980	1.23	0.29	1.27	0.246675	0.4965281	-5.75	FALSE
254293_at	putative protein SF16 protein, H	IQD22	AT4G23060	1.32	0.40	1.27	0.2468518	0.4965773	-5.75	TRUE
264633_at	step II splicing factor, putative si	SMP1	AT1G65660	-1.16	-0.21	-1.27	0.2467815	0.4965773	-5.75	FALSE
254967_at	putative protein various predicte	---	AT4G10410	1.15	0.20	1.27	0.2468314	0.4965773	-5.75	FALSE
257649_at	predicted protein	ARR1	AT3G16857	1.14	0.19	1.27	0.2468324	0.4965773	-5.75	FALSE
253416_at	pyruvate decarboxylase-1 (Pdc1)	---	AT4G33070	1.22	0.28	1.27	0.246791	0.4965773	-5.75	FALSE
251765_at	putative protein	---	---	1.16	0.21	1.27	0.2468176	0.4965773	-5.75	FALSE

244960_at	ribosomal protein L32	---	---	-1.38	-0.47	-1.27	0.2467505	0.4965773	-5.75	FALSE
246284_at	putative protein	---	AT4G36780	-1.17	-0.22	-1.27	0.2470527	0.4967623	-5.75	TRUE
247077_at	putative protein similar to unknov	---	AT5G66420	-1.18	-0.24	-1.27	0.2470182	0.4967623	-5.75	FALSE
264297_at	hypothetical protein similar to hyp	---	AT1G78710	1.11	0.16	1.27	0.2470045	0.4967623	-5.75	FALSE
255996_s_a	receptor-like serine threonine kir	---	AT1G29730 /	1.19	0.25	1.27	0.2469798	0.4967623	-5.75	FALSE
252811_at	putative protein several hypothet	---	---	1.16	0.22	1.27	0.2470355	0.4967623	-5.75	FALSE
257082_at	hypothetical protein	COBL10	AT3G20580	1.14	0.19	1.27	0.2471582	0.4969306	-5.75	FALSE
249964_at	MAP kinase -like protein ATMPK	MPK16	AT5G19010	-1.15	-0.20	-1.27	0.2472836	0.4970513	-5.75	FALSE
253079_s_a	putative protein F56F10.1, Caen	---	AT4G36190 /	-1.21	-0.28	-1.27	0.2472553	0.4970513	-5.75	FALSE
263897_at	putative shikimate kinase precurs	---	AT2G21940	1.27	0.35	1.27	0.2472677	0.4970513	-5.75	FALSE
260423_at	unknown protein	ATEXO70D	AT1G72470	1.40	0.48	1.27	0.2474158	0.4972339	-5.75	FALSE
252828_at	DnaJ - like protein DnaJ-like pro	---	AT4G39960	-1.17	-0.23	-1.27	0.2474398	0.4972339	-5.75	FALSE
251871_at	hypothetical protein	---	AT3G54520	1.12	0.16	1.27	0.2474287	0.4972339	-5.75	FALSE
261675_at	hypothetical protein predicted by	---	AT1G18290	1.16	0.21	1.27	0.2475078	0.4973267	-5.75	FALSE
253339_at	metal-transporting P-type ATPas	PAA1	AT4G33520	1.25	0.32	1.27	0.2476431	0.4975548	-5.75	FALSE
246761_at	embryonic abundant protein - lik	---	AT5G27980	1.14	0.19	1.27	0.2476778	0.4975806	-5.75	FALSE
260820_at	receptor protein kinase, putative	---	AT1G06840	-1.31	-0.39	-1.27	0.2477307	0.497643	-5.75	TRUE
256684_at	geranylgeranyl pyrophosphate s	---	AT3G32040	1.20	0.27	1.27	0.2477574	0.497653	-5.75	FALSE
252352_at	Expressed protein ; supported by	---	AT3G48185	-1.20	-0.27	-1.26	0.2480646	0.4979635	-5.75	FALSE
251431_at	protein synthesis initiation factor	EIF4G	AT3G60240	-1.13	-0.17	-1.26	0.2479886	0.4979635	-5.75	FALSE
251237_at	bZIP transcription factor-like pro	CPuORF3	AT3G62420 /	1.16	0.21	1.26	0.2480648	0.4979635	-5.75	FALSE
265977_at	putative retroelement pol polypro	---	---	-1.13	-0.18	-1.26	0.2480572	0.4979635	-5.75	FALSE
257095_at	unknown protein ; supported by	ATPDIL5-3	AT3G20560	-1.20	-0.26	-1.26	0.2479511	0.4979635	-5.75	FALSE
263029_at	unknown protein	---	AT1G24050	-1.11	-0.15	-1.26	0.2480232	0.4979635	-5.75	FALSE
263276_at	putative cytochrome P450	CYP705A1	AT2G14100	1.15	0.20	1.26	0.2480157	0.4979635	-5.75	FALSE
247103_at	putative protein similar to unknov	DAR7	AT5G66610	1.14	0.19	1.26	0.2481077	0.4980057	-5.75	FALSE
252895_at	hypothetical protein	---	AT4G39450	-1.14	-0.19	-1.26	0.2481687	0.4980067	-5.75	FALSE
252883_at	GTP-binding - like protein GTP-l	---	AT4G39520	-1.21	-0.27	-1.26	0.2481737	0.4980067	-5.75	FALSE
255406_at	hypothetical protein similar to hy	---	AT4G03450	1.49	0.57	1.26	0.2481384	0.4980067	-5.75	FALSE
262935_at	hypothetical protein similar to put	AtOCT5	AT1G79410	1.51	0.59	1.26	0.2482768	0.4980195	-5.75	TRUE
260441_at	unknown protein ;supported by f	---	AT1G68260	1.39	0.48	1.26	0.2482369	0.4980195	-5.75	FALSE
264310_at	hypothetical protein similar to hyp	---	AT1G62030	-1.18	-0.23	-1.26	0.2482301	0.4980195	-5.75	FALSE
249825_at	putative protein similar to unknov	---	AT5G23390	-1.15	-0.20	-1.26	0.2482892	0.4980195	-5.75	FALSE
255666_at	putative protein ;supported by fu	---	AT4G00390	-1.18	-0.24	-1.26	0.2482863	0.4980195	-5.75	FALSE
261368_at	protein kinase, putative similar to	---	AT1G53070	1.21	0.27	1.26	0.2483121	0.4980215	-5.75	FALSE

253970_at	putative uracil phosphoribosyl tra	---	AT4G26510	-1.16	-0.21	-1.26	0.248362	0.4980777	-5.75	FALSE
259547_at	gypsy/Ty3 element polyprotein,	---	---	1.15	0.20	1.26	0.2484142	0.4981386	-5.75	FALSE
265835_at	putative retroelement pol polypro	---	---	1.19	0.25	1.26	0.2484651	0.498197	-5.75	FALSE
252851_at	putative protein CLATHRIN COA	---	AT4G40080	1.44	0.53	1.26	0.2488538	0.4988887	-5.75	FALSE
256621_at	unknown protein ; supported by	---	AT3G24450	1.16	0.22	1.26	0.2488403	0.4988887	-5.75	FALSE
252549_at	protein kinase - like receptor-like	---	AT3G45860	1.43	0.52	1.26	0.2491641	0.4990891	-5.75	TRUE
264501_at	putative lipase Similar to nodulin	---	AT1G09390	-1.50	-0.59	-1.26	0.2491399	0.4990891	-5.75	FALSE
255582_at	putative DNA-binding protein sim	NGA4	AT4G01500	1.14	0.18	1.26	0.2491172	0.4990891	-5.75	FALSE
251322_at	cysteine synthase AtcysC1 ;sup	CYSC1	AT3G61440	-1.42	-0.51	-1.26	0.2492141	0.4990891	-5.75	FALSE
247517_at	100 kDa coactivator - like protein	---	AT5G61780	1.19	0.25	1.26	0.2491189	0.4990891	-5.75	FALSE
264486_at	hypothetical protein contains sim	---	AT1G77180	-1.18	-0.24	-1.26	0.2492164	0.4990891	-5.75	FALSE
258990_at	unknown protein ;supported by f	---	AT3G08840	-1.26	-0.34	-1.26	0.2491138	0.4990891	-5.75	FALSE
261749_at	dehydrin, putative similar to deh	ERD14	AT1G76180	1.14	0.19	1.26	0.2490136	0.4990891	-5.75	FALSE
247133_at	chalcone isomerase-like protein	---	AT5G66220	1.30	0.38	1.26	0.2491507	0.4990891	-5.75	FALSE
254625_at	Expressed protein ; supported by	SNI1	AT4G18470	1.17	0.23	1.26	0.2490245	0.4990891	-5.75	FALSE
264969_at	hypothetical protein contains sim	---	AT1G67320	-1.39	-0.47	-1.26	0.2491678	0.4990891	-5.75	FALSE
249639_at	disease resistance like protein T	---	AT5G36930	-1.14	-0.19	-1.26	0.2492101	0.4990891	-5.75	FALSE
256371_at	hypothetical protein	---	AT1G66770	1.15	0.20	1.26	0.2492428	0.4990982	-5.75	FALSE
261404_at	alpha galactosyltransferase, put	---	AT1G18690	-1.28	-0.35	-1.26	0.2492723	0.4991135	-5.76	FALSE
264883_s_a	secretory carrier membrane prote	---	AT1G11180 ///	-1.15	-0.20	-1.26	0.2493219	0.499169	-5.76	FALSE
246999_at	photoreceptor-interacting protein	NPY3	AT5G67440	-1.31	-0.39	-1.26	0.2493487	0.4991789	-5.76	FALSE
265927_at	hypothetical protein	---	AT2G18590	1.19	0.25	1.26	0.2493898	0.4992173	-5.76	FALSE
261777_at	hypothetical protein predicted by	---	AT1G76210	1.15	0.20	1.26	0.2494556	0.4993051	-5.76	FALSE
264084_at	putative kinesin light chain	---	AT2G31240	-1.15	-0.21	-1.26	0.2496674	0.4996853	-5.76	FALSE
264805_at	unknown protein similar to putati	ATRX	AT1G08600	1.16	0.21	1.26	0.249697	0.4997006	-5.76	FALSE
258094_at	putative cytochrome P450 simila	CYP72A15	AT3G14690	-1.16	-0.22	-1.26	0.2497607	0.4997844	-5.76	FALSE
245704_at	glycine-rich protein	KTF1	AT5G04290	-1.13	-0.17	-1.26	0.2498391	0.4998535	-5.76	FALSE
266248_at	hypothetical protein predicted by	---	AT2G27650	1.11	0.16	1.26	0.2498262	0.4998535	-5.76	FALSE
248391_at	putative protein similar to unknov	---	AT5G52030	-1.16	-0.22	-1.26	0.2499333	0.4999177	-5.76	FALSE
258063_at	putative cytochrome P450 simila	CYP72A8	AT3G14620	1.55	0.63	1.26	0.2499369	0.4999177	-5.76	FALSE
253618_at	nodulin-like protein MtN21 gene	---	AT4G30420	-1.12	-0.16	-1.26	0.2499114	0.4999177	-5.76	FALSE
251490_at	putative protein	---	AT3G59490	-1.20	-0.26	-1.26	0.2499982	0.4999526	-5.76	FALSE
252607_at	xyloglucan endo-transglycosylas	XTR8	AT3G44990	1.32	0.40	1.26	0.2499767	0.4999526	-5.76	FALSE
264569_at	unknown protein EST gb|ATTS1	---	---	1.13	0.18	1.26	0.2500612	0.5000348	-5.76	FALSE
246833_at	putative protein	---	AT5G26620	-1.12	-0.16	-1.26	0.2500969	0.5000622	-5.76	FALSE

248632_at	unknown protein	SLD5	AT5G49010	-1.35	-0.43	-1.26	0.2501462	0.500117	-5.76	FALSE
256808_at	unknown protein	ALY3	AT3G21430	-1.13	-0.17	-1.26	0.2501686	0.500118	-5.76	FALSE
262781_s_a	proteasome epsilon chain precur	PBE1	AT1G13060 ///	-1.19	-0.25	-1.26	0.250296	0.500285	-5.76	FALSE
247445_at	putative protein similar to unknov	---	AT5G62640	1.16	0.21	1.26	0.2502952	0.500285	-5.76	FALSE
250585_at	putative protein contains similarit	---	AT5G07620	1.37	0.45	1.26	0.2504027	0.5003918	-5.76	FALSE
251126_at	putative protein various predicte	---	AT5G01070	1.14	0.18	1.26	0.2504261	0.5003918	-5.76	FALSE
257546_s_a	hypothetical protein predicted by	---	AT3G28410 ///	-1.12	-0.16	-1.26	0.2504271	0.5003918	-5.76	FALSE
256827_at	hypothetical protein contains sim	---	AT3G18570	1.12	0.17	1.26	0.2504372	0.5003918	-5.76	FALSE
261492_at	acid phosphatase, putative simil	SBH2	AT1G14290	1.21	0.27	1.26	0.2505322	0.500494	-5.76	TRUE
247331_at	putative protein contains similarit	FP3	AT5G63530	1.33	0.41	1.26	0.2505288	0.500494	-5.76	FALSE
247625_at	zinc finger protein - like dof6 zin	---	AT5G60200	1.21	0.28	1.26	0.2506232	0.5005575	-5.76	FALSE
263629_at	hypothetical protein predicted by	---	AT2G04850	-1.26	-0.34	-1.26	0.2507176	0.5005575	-5.76	FALSE
246059_at	putative protein KED, Nicotiana	---	AT5G08450	-1.14	-0.19	-1.26	0.2506796	0.5005575	-5.76	FALSE
246325_at	hypothetical protein contains sim	ABA3	AT1G16540	1.41	0.50	1.26	0.2507114	0.5005575	-5.76	FALSE
262861_at	hypothetical protein similar to hy	---	AT1G64820	1.15	0.21	1.26	0.250667	0.5005575	-5.76	FALSE
251016_at	pathogenesis related protein - lik	---	AT5G02730	1.27	0.34	1.26	0.250668	0.5005575	-5.76	FALSE
261245_at	anter-specific proline-rich protein	---	AT1G20130 ///	-1.13	-0.18	-1.26	0.2505887	0.5005575	-5.76	FALSE
259032_at	hypothetical protein similar to hy	---	AT3G09380	1.12	0.17	1.26	0.2507613	0.5006009	-5.76	FALSE
263129_at	unknown protein ;supported by fu	---	AT1G78620	1.15	0.20	1.26	0.2508402	0.5007146	-5.76	FALSE
264389_at	unknown protein similar to hypot	---	AT1G11960	1.27	0.35	1.26	0.2509621	0.5008738	-5.76	TRUE
262643_at	unknown protein ;supported by fu	---	AT1G62770	1.29	0.37	1.26	0.2509639	0.5008738	-5.76	FALSE
260182_at	unknown protein similar to IFA-bi	---	AT1G70750	1.17	0.22	1.26	0.251021	0.5008855	-5.76	FALSE
247820_at	serine/threonine protein kinase ;	SIP1	AT5G58380	1.21	0.27	1.26	0.2509932	0.5008855	-5.76	FALSE
252712_at	glutathione transferase-like prote	ATGSTU27	AT3G43800	-1.29	-0.37	-1.26	0.2510357	0.5008855	-5.76	FALSE
259951_at	unknown protein	---	AT1G71490	1.14	0.18	1.26	0.2510795	0.5009292	-5.76	FALSE
249894_at	unknown protein ; supported by	---	AT5G22580	6.61	2.73	1.26	0.2511307	0.5009876	-5.76	FALSE
252887_at	putative protein various predicte	---	AT4G39240	-1.12	-0.16	-1.26	0.2512592	0.5011793	-5.76	FALSE
259196_at	putative ribosomal protein S2 sim	RPS2	AT3G03600	-1.22	-0.29	-1.26	0.2512708	0.5011793	-5.76	FALSE
267575_at	unknown protein predicted by ge	---	AT2G30690	1.16	0.21	1.25	0.2513645	0.5013224	-5.76	FALSE
264747_at	unknown protein	---	AT1G70150	-1.20	-0.27	-1.25	0.2513991	0.5013475	-5.76	FALSE
253038_at	homeobox protein HAT22 ;supp	HAT22	AT4G37790	1.29	0.37	1.25	0.2514308	0.5013669	-5.76	FALSE
246523_at	CONSTANS-like 1	COL1	AT5G15850	-1.26	-0.33	-1.25	0.2516436	0.5017475	-5.76	FALSE
260589_at	hypothetical protein predicted by	---	AT1G53400	-1.12	-0.17	-1.25	0.2517113	0.5017947	-5.76	FALSE
252087_at	putative protein putative Na+/H+	chx28	AT3G52080	1.14	0.19	1.25	0.2516964	0.5017947	-5.76	FALSE
253713_at	putative protein several hypothet	---	AT4G29370	1.14	0.19	1.25	0.2518	0.5019277	-5.76	FALSE

251458_at	putative protein several retrotran	---	---	1.14	0.19	1.25	0.2518465	0.5019764	-5.76	FALSE
251269_at	putative protein Pm5 protein - H	---	AT3G62360	-1.19	-0.25	-1.25	0.2520778	0.5023935	-5.76	FALSE
250481_at	putative protein	---	AT5G10310	-1.15	-0.20	-1.25	0.2521071	0.502408	-5.76	FALSE
247495_at	putative protein predicted protei	IPK2BETA	AT5G61760	-1.19	-0.25	-1.25	0.252261	0.5026694	-5.77	FALSE
259134_at	hypothetical protein predicted by	---	AT3G05390	1.56	0.64	1.25	0.2522823	0.5026694	-5.77	FALSE
255922_at	trehalose-6-phosphate phospha	---	AT1G22210	1.14	0.19	1.25	0.2523484	0.5027571	-5.77	FALSE
249645_at	thionin Thi2.2 ;supported by full-	THI2.2	AT5G36910	1.22	0.28	1.25	0.2524199	0.5028118	-5.77	FALSE
250302_at	fructosidase - like protein fructos	AtcwINV6	AT5G11920	2.02	1.02	1.25	0.2524008	0.5028118	-5.77	FALSE
257023_at	RNA helicase, putative similar to	---	AT3G19760	-1.15	-0.20	-1.25	0.2524641	0.502856	-5.77	FALSE
254023_at	putative protein hypothetical pro	---	AT4G25770	1.18	0.24	1.25	0.2526402	0.5031352	-5.77	FALSE
264440_at	unknown protein similar to fim p	---	AT1G27340	-1.13	-0.18	-1.25	0.2526484	0.5031352	-5.77	FALSE
256430_at	DREB2B transcription factor ider	DREB2B	AT3G11020	-1.15	-0.20	-1.25	0.2527286	0.5032508	-5.77	FALSE
263076_at	putative protein kinase/endoribor	IRE1A	AT2G17520	1.15	0.20	1.25	0.2528149	0.5032688	-5.77	FALSE
261634_at	ATP-dependent Clp protease pro	CLPR1	AT1G49970	-1.20	-0.27	-1.25	0.2527828	0.5032688	-5.77	FALSE
258974_at	unknown protein similar to brahr	---	AT3G01890	-1.17	-0.22	-1.25	0.2527713	0.5032688	-5.77	FALSE
255980_at	hypothetical protein ;supported b	---	AT1G33970	-1.17	-0.22	-1.25	0.2529453	0.5032688	-5.77	FALSE
246080_at	putative protein	---	AT5G20460	-1.14	-0.19	-1.25	0.2528502	0.5032688	-5.77	FALSE
247663_at	putative protein predicted protei	APUM18	AT5G60110	-1.13	-0.17	-1.25	0.2529086	0.5032688	-5.77	FALSE
263546_at	putative dihydrofolate reductase-	---	AT2G21550	-1.19	-0.25	-1.25	0.2528324	0.5032688	-5.77	FALSE
252756_s_a	putative protein hypothetical prot	---	AT1G58520 ///	1.14	0.19	1.25	0.2529583	0.5032688	-5.77	FALSE
260212_at	hypothetical protein predicted by	---	AT1G74480	1.12	0.17	1.25	0.2529722	0.5032688	-5.77	FALSE
252836_at	putative protein predicted polypr	---	---	1.13	0.18	1.25	0.2529803	0.5032688	-5.77	FALSE
262520_at	putative polygalacturonase After	---	AT1G17150	1.19	0.25	1.25	0.2529721	0.5032688	-5.77	FALSE
250717_at	putative protein similar to unknov	---	AT5G06200	1.20	0.26	1.25	0.2530595	0.5032948	-5.77	FALSE
264719_at	receptor-like kinase, putative sin	---	AT1G70110	1.23	0.29	1.25	0.2530441	0.5032948	-5.77	FALSE
259181_at	unknown protein similar to putati	---	AT3G01690	-1.22	-0.28	-1.25	0.2530418	0.5032948	-5.77	FALSE
261219_at	hypothetical protein predicted by	---	AT1G19980	1.18	0.23	1.25	0.2532021	0.5034145	-5.77	FALSE
254330_at	predicted protein predicted gene	LBD32	AT4G22700	1.14	0.19	1.25	0.253208	0.5034145	-5.77	FALSE
265173_at	unknown protein	---	AT1G23530	1.14	0.19	1.25	0.2531547	0.5034145	-5.77	FALSE
245717_at	Expressed protein ; supported by	---	AT5G33390	1.16	0.21	1.25	0.2531883	0.5034145	-5.77	FALSE
257237_at	DNA nick sensor, putative conta	---	AT3G14890	-1.45	-0.54	-1.25	0.2532632	0.5034365	-5.77	FALSE
256194_at	unknown protein	---	---	-1.21	-0.27	-1.25	0.2532481	0.5034365	-5.77	FALSE
257770_at	unknown protein ;supported by f	LFR	AT3G22990	-1.16	-0.22	-1.25	0.2533145	0.5034552	-5.77	FALSE
252205_at	hypothetical protein various prec	---	AT3G50350	-1.20	-0.27	-1.25	0.2533609	0.5034552	-5.77	FALSE
264787_at	putative senescence-associated	ERD7	AT2G17840	-1.29	-0.36	-1.25	0.2533239	0.5034552	-5.77	FALSE

253245_at	bZIP transcription factor ATB2	GBF6	AT4G34588 /	-1.45	-0.53	-1.25	0.2533458	0.5034552	-5.77	FALSE
256840_x_a	unknown protein similar to putati	---	---	-1.12	-0.16	-1.25	0.2534403	0.503569	-5.77	FALSE
263341_at	hypothetical protein predicted by	---	---	1.16	0.22	1.25	0.2534807	0.5036055	-5.77	FALSE
257396_at	predicted protein	EPF1	AT2G20875	1.20	0.26	1.25	0.2535325	0.5036645	-5.77	FALSE
262014_at	unknown protein	---	AT1G35660	-1.30	-0.38	-1.25	0.2536244	0.5037464	-5.77	FALSE
264740_at	unknown protein	---	AT1G62070	1.15	0.20	1.25	0.2536043	0.5037464	-5.77	FALSE
264184_at	early nodule-specific protein, pu	---	AT1G54790	-1.15	-0.21	-1.25	0.25364	0.5037464	-5.77	FALSE
254926_at	ACC synthase (AtACS-6) ; supp	ACS6	AT4G11280	2.10	1.07	1.25	0.2536896	0.503801	-5.77	FALSE
265774_at	hypothetical protein predicted by	---	AT2G07240	1.21	0.27	1.25	0.2538107	0.5039978	-5.77	FALSE
255424_at	putative glycosylation enzyme si	---	AT4G03340	1.15	0.20	1.25	0.2538474	0.5040267	-5.77	FALSE
259610_at	bZIP protein, putative similar to	---	AT1G52320	-1.13	-0.18	-1.25	0.2539702	0.5041165	-5.77	FALSE
260505_at	Cyclin, putative similar to GB:CA	CYCA3;4	AT1G47230	-1.14	-0.18	-1.25	0.253981	0.5041165	-5.77	FALSE
263982_at	hypothetical protein predicted by	---	AT2G42860	1.19	0.26	1.25	0.2539487	0.5041165	-5.77	FALSE
250120_at	putative protein similar to unknov	RIC4	AT5G16490	1.25	0.32	1.25	0.2539181	0.5041165	-5.77	FALSE
250970_at	putative protein ; supported by c	---	AT5G02770	-1.14	-0.18	-1.25	0.2540072	0.5041246	-5.77	FALSE
255153_at	putative protein several hypothet	---	AT4G08210	1.19	0.25	1.25	0.2540594	0.5041844	-5.77	FALSE
262298_at	unknown protein Similar to gb|AF	---	AT1G27530	-1.12	-0.17	-1.25	0.2541297	0.504186	-5.77	FALSE
261254_at	Expressed protein ; supported by	---	AT1G05805	-1.16	-0.22	-1.25	0.2541851	0.504186	-5.77	FALSE
258820_at	putative tryptophanyl-tRNA synth	---	AT3G04600	-1.13	-0.18	-1.25	0.2542262	0.504186	-5.77	FALSE
265885_at	hypothetical protein predicted by	---	AT2G42330	1.21	0.28	1.25	0.2542563	0.504186	-5.77	FALSE
267292_at	hypothetical protein predicted by	---	AT2G23740	1.15	0.21	1.25	0.2541902	0.504186	-5.77	FALSE
AFFX-BioD	E. coli /GEN=bioD /DB_XREF=g	---	---	1.40	0.49	1.25	0.2541541	0.504186	-5.77	FALSE
253051_at	cyclin cyc1 ; supported by cDNA	CYCB1;1	AT4G37490	1.21	0.27	1.25	0.2543034	0.504186	-5.77	FALSE
262621_at	hypothetical protein	---	AT1G06530	-1.15	-0.20	-1.25	0.2542756	0.504186	-5.77	FALSE
248250_at	cyclic nucleotide-regulated ion ch	CNGC1	AT5G53130	-1.34	-0.42	-1.25	0.2542494	0.504186	-5.77	FALSE
247993_at	putative protein similar to unknov	---	AT5G56130	-1.19	-0.25	-1.25	0.2541742	0.504186	-5.77	FALSE
245536_at	hypothetical protein	SDG2	AT4G15180	1.14	0.19	1.25	0.2542911	0.504186	-5.77	FALSE
249595_at	putative protein SIAH1 protein, E	---	AT5G37930	-1.21	-0.27	-1.25	0.2543411	0.5042169	-5.77	FALSE
250354_at	putative protein predicted protei	---	AT5G11640	-1.15	-0.20	-1.25	0.2545233	0.5043608	-5.77	FALSE
253075_at	putative disease resistance prot	---	AT4G36150	-1.13	-0.18	-1.25	0.2545906	0.5043608	-5.77	FALSE
257123_at	hypothetical protein	---	AT3G20030	1.12	0.16	1.25	0.2545239	0.5043608	-5.77	FALSE
254935_at	putative disease resistance prot	---	AT4G10780	1.18	0.24	1.25	0.2545841	0.5043608	-5.77	FALSE
249156_s_a	putative protein similar to unknov	---	AT5G43490 /	1.12	0.17	1.25	0.2545876	0.5043608	-5.77	FALSE
249068_at	putative protein similar to unknov	PDLP1	AT5G43980	1.14	0.19	1.25	0.2544955	0.5043608	-5.77	FALSE
263317_s_a	similar to mammalian MHC III re	SUVH7	AT1G17770 /	1.23	0.30	1.25	0.2545609	0.5043608	-5.77	FALSE

265604_s_a	hypothetical protein predicted by	---	---	-1.16	-0.21	-1.25	0.2545453	0.5043608	-5.77	FALSE
263498_at	unknown protein ; supported by	LSH10	AT2G42610	1.96	0.97	1.25	0.2546525	0.5044397	-5.77	FALSE
251793_at	regulator of chromosome conde	---	AT3G55580	1.12	0.16	1.24	0.2547505	0.504566	-5.77	FALSE
258628_at	unknown protein	---	AT3G02890	-1.32	-0.40	-1.24	0.2547688	0.504566	-5.77	FALSE
247551_at	ras-GTPase-activating protein S	---	AT5G60980	-1.12	-0.16	-1.24	0.2547826	0.504566	-5.77	FALSE
245699_at	putative protein ;supported by ful	---	AT5G04250	1.29	0.37	1.24	0.2548691	0.5046934	-5.77	FALSE
264159_at	unknown protein ;supported by fu	---	AT1G65270	-1.12	-0.17	-1.24	0.2549098	0.5047302	-5.77	FALSE
255913_at	kinase, putative similar to leaf ru	---	AT1G66980	1.12	0.16	1.24	0.2549886	0.5048038	-5.77	FALSE
255519_at	hypothetical protein	---	AT4G02310	1.12	0.16	1.24	0.2549912	0.5048038	-5.77	FALSE
251047_at	putative protein mature-parasite	---	AT5G02390	1.17	0.23	1.24	0.2551411	0.5050568	-5.77	FALSE
261046_at	flavonol 3-o-glucosyltransferase	---	AT1G01390	-1.24	-0.31	-1.24	0.2552049	0.5050953	-5.77	FALSE
248333_at	photoassimilate-responsive prote	---	AT5G52390	1.90	0.92	1.24	0.25519	0.5050953	-5.77	FALSE
267257_at	putative casein kinase II catalytic	---	AT2G23080	-1.11	-0.15	-1.24	0.2552644	0.5051693	-5.77	FALSE
263942_at	unknown protein	FLA16	AT2G35860	2.21	1.15	1.24	0.2553675	0.5052419	-5.78	TRUE
264308_at	hypothetical protein similar to hy	---	AT1G61990	-1.11	-0.15	-1.24	0.2553512	0.5052419	-5.78	FALSE
247388_s_a	transcription factor Hap5a-like pr	NF-YC1	AT3G48590 /	-1.33	-0.41	-1.24	0.2553322	0.5052419	-5.78	FALSE
264738_at	unknown protein contains similar	---	AT1G62250	-1.19	-0.25	-1.24	0.2554965	0.5054531	-5.78	FALSE
267611_at	unknown protein	SPX2	AT2G26660	-1.29	-0.37	-1.24	0.2556218	0.5055968	-5.78	TRUE
250097_at	putative protein similar to unknov	---	AT5G17280	1.18	0.24	1.24	0.2556356	0.5055968	-5.78	FALSE
262010_at	hypothetical protein predicted by	---	---	1.16	0.22	1.24	0.2556128	0.5055968	-5.78	FALSE
254176_at	hypothetical protein hypothetical	---	AT4G24200	1.14	0.19	1.24	0.2556758	0.5056053	-5.78	FALSE
246544_at	auxin transport protein - like aux	PIN8	AT5G15100	1.13	0.17	1.24	0.2556842	0.5056053	-5.78	FALSE
265742_at	putative ribose 5-phosphate isom	---	AT2G01290	1.23	0.30	1.24	0.2559407	0.5057741	-5.78	FALSE
252110_at	disease resistance-like protein T	---	AT3G51560	1.13	0.18	1.24	0.2559166	0.5057741	-5.78	FALSE
258439_at	lipoamide dehydrogenase precur	mtLPD2	AT3G17240	1.24	0.31	1.24	0.2558525	0.5057741	-5.78	FALSE
250489_s_a	putative protein predicted protei	---	AT5G09710 /	-1.18	-0.24	-1.24	0.2558593	0.5057741	-5.78	FALSE
263270_at	putative replication protein A1	---	---	1.14	0.18	1.24	0.2559099	0.5057741	-5.78	FALSE
257801_at	mitogen activated protein kinase	WNK6	AT3G18750	-1.16	-0.22	-1.24	0.255947	0.5057741	-5.78	FALSE
254025_at	putative pathogenesis-related pr	---	AT4G25790	1.12	0.16	1.24	0.2558323	0.5057741	-5.78	FALSE
265081_at	hypothetical protein contains Zir	MGP	AT1G03840	1.15	0.21	1.24	0.2558513	0.5057741	-5.78	FALSE
245754_at	hypothetical protein predicted by	---	AT1G35183	-1.13	-0.18	-1.24	0.2560316	0.5058976	-5.78	FALSE
248064_at	unknown protein	---	AT5G55570	-1.42	-0.51	-1.24	0.2561253	0.5060388	-5.78	FALSE
249153_s_a	putative protein strong similarity t	---	AT5G43390 /	1.16	0.22	1.24	0.2562413	0.5061803	-5.78	FALSE
256553_at	hypothetical protein contains sim	---	---	1.15	0.20	1.24	0.2562333	0.5061803	-5.78	FALSE
253050_at	putative protein probable arabin	AGP18	AT4G37450	1.57	0.65	1.24	0.256535	0.5062392	-5.78	TRUE

262654_at	putative mandelonitrile lyase sim	---	AT1G14180	1.20	0.27	1.24	0.2565374	0.5062392	-5.78	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U849	---	---	1.12	0.16	1.24	0.2563263	0.5062392	-5.78	FALSE
262646_at	aspartate aminotransferase nea	ASP4	AT1G62800	1.33	0.41	1.24	0.256527	0.5062392	-5.78	FALSE
251902_at	uncoupling protein (ucp/PUMP)	PUMP1	AT3G54110	1.39	0.48	1.24	0.2565089	0.5062392	-5.78	FALSE
260437_at	hypothetical protein predicted by	---	AT1G68380	1.15	0.20	1.24	0.2565261	0.5062392	-5.78	FALSE
253859_at	Expressed protein ; supported by	---	AT4G27657	2.53	1.34	1.24	0.2564649	0.5062392	-5.78	FALSE
248887_at	Expressed protein ; supported by	---	AT5G46115	1.16	0.22	1.24	0.2563614	0.5062392	-5.78	FALSE
257328_s_a	hypothetical protein	---	---	1.21	0.27	1.24	0.2565232	0.5062392	-5.78	FALSE
266497_at	putative retroelement pol polypro	---	---	1.16	0.22	1.24	0.2564841	0.5062392	-5.78	FALSE
253801_at	hypothetical protein	---	AT4G28170	1.15	0.20	1.24	0.2564385	0.5062392	-5.78	FALSE
252091_at	putative protein NADH dehydrog	---	AT3G51390	-1.13	-0.17	-1.24	0.2564977	0.5062392	-5.78	FALSE
262986_at	unknown protein similar to hypot	---	AT1G23390	-1.31	-0.39	-1.24	0.2566258	0.5063697	-5.78	FALSE
258385_at	putative jasmonic acid regulatory	ATNAC2	AT3G15510	-1.23	-0.30	-1.24	0.2566758	0.5064247	-5.78	FALSE
251736_at	putative protein acetyl-CoA carb	---	AT3G56130	-1.28	-0.36	-1.24	0.2567655	0.5065579	-5.78	FALSE
262390_at	hypothetical protein predicted by	---	AT1G49260	1.17	0.23	1.24	0.2568014	0.5065849	-5.78	FALSE
255754_at	auxin-induced protein, putative s	---	AT1G43040	1.11	0.15	1.24	0.2568454	0.5066044	-5.78	FALSE
258603_at	putative heat shock transcription	ATHSFA1E	AT3G02990	-1.22	-0.28	-1.24	0.2568558	0.5066044	-5.78	FALSE
262091_at	Myb-family transcription factor, p	MYB72	AT1G56160	1.14	0.19	1.24	0.2569068	0.5066612	-5.78	FALSE
256261_at	ras-related GTP-binding protein (	RABA4D	AT3G12160	1.15	0.20	1.24	0.2570721	0.5069434	-5.78	FALSE
248004_at	putative protein similar to unknov	PRA1.G2	AT5G56230	1.33	0.41	1.24	0.2571041	0.5069626	-5.78	FALSE
253895_at	NWMU3 - 2S albumin 3 precurso	AT2S3	AT4G27160	1.13	0.17	1.24	0.2571814	0.5070713	-5.78	FALSE
244944_s_a	ribosomal protein L16	---	---	-1.23	-0.29	-1.24	0.2572251	0.5071136	-5.78	FALSE
263246_at	hypothetical protein predicted by	---	AT2G31460	1.18	0.24	1.24	0.2572636	0.5071457	-5.78	FALSE
263971_at	hypothetical protein predicted by	AtRLP29	AT2G42800	1.19	0.25	1.24	0.2573101	0.5071936	-5.78	FALSE
267301_at	ubiquitin activating enzyme 1 (UB	ATUBA1	AT2G30110	-1.15	-0.20	-1.24	0.2573756	0.5072788	-5.78	FALSE
257107_at	transmembrane trafficking prote	---	AT3G29070	1.16	0.22	1.24	0.257463	0.5074072	-5.78	FALSE
246474_at	putative protein predicted protei	---	AT5G17150	1.15	0.20	1.24	0.2575203	0.5074422	-5.78	FALSE
265874_at	hypothetical protein predicted by	---	AT2G01640	-1.17	-0.23	-1.24	0.2575277	0.5074422	-5.78	FALSE
267168_at	putative alcohol dehydrogenase	---	AT2G37770	2.35	1.23	1.24	0.2575475	0.5074422	-5.78	FALSE
249852_at	monosaccharide transporter	STP11	AT5G23270	1.16	0.21	1.24	0.2575804	0.5074632	-5.78	FALSE
250806_at	putative protein similar to unknov	---	AT5G05070	1.14	0.19	1.24	0.2577287	0.5077116	-5.78	FALSE
266161_at	hypothetical protein	ATCHX7	AT2G28170	1.20	0.27	1.24	0.2577753	0.5077594	-5.78	FALSE
254851_at	putative disease resistance prot	---	AT4G12010	-1.29	-0.37	-1.24	0.2578247	0.5078128	-5.78	FALSE
251890_at	SCARECROW1 ; supported by (	SCR	AT3G54220	-1.15	-0.20	-1.24	0.2578677	0.5078538	-5.78	FALSE
261930_at	alcohol dehydrogenase ADH, pu	---	AT1G22440	1.22	0.29	1.24	0.2580147	0.5080981	-5.78	FALSE

254646_at	putative protein	---	AT4G18530	-1.20	-0.27	-1.24	0.2580363	0.5080981	-5.78	FALSE
251397_at	putative protein cim1 protein, Gl	ATEXPB5	AT3G60570	1.20	0.27	1.23	0.258275	0.5084048	-5.78	FALSE
260469_at	BRCA1-associated RING domai	AGD4	AT1G10870	-1.19	-0.25	-1.23	0.2582812	0.5084048	-5.78	FALSE
263313_at	14-3-3 protein (grf15), putative c	---	AT2G10450	1.15	0.20	1.23	0.2582262	0.5084048	-5.78	FALSE
259939_s_a	ARE1-like protein similar to ARE	---	AT1G71270 ///	-1.19	-0.25	-1.23	0.2582605	0.5084048	-5.78	FALSE
260594_at	hypothetical protein predicted by	---	AT1G55880	-1.12	-0.16	-1.23	0.2583629	0.5085217	-5.79	FALSE
264124_at	hypothetical protein predicted by	ATOCT2	AT1G79360	1.16	0.22	1.23	0.2584929	0.5087336	-5.79	FALSE
254217_at	putative protein other hypothetic	---	AT4G23720	1.12	0.17	1.23	0.2585573	0.5087725	-5.79	FALSE
251005_at	putative protein various predicte	---	AT5G02590	-1.47	-0.55	-1.23	0.2585379	0.5087725	-5.79	FALSE
266234_at	SKP1 interacting partner 3 (SKI	SKIP3	AT2G02350	1.17	0.22	1.23	0.258713	0.5090163	-5.79	FALSE
267613_at	putative second messenger-depe	PID2	AT2G26700	-1.15	-0.20	-1.23	0.2587258	0.5090163	-5.79	FALSE
254425_at	putative membrane associated p	---	AT4G21450	-1.12	-0.17	-1.23	0.2587998	0.5090408	-5.79	FALSE
260628_at	hypothetical protein predicted by	---	AT1G62320	1.13	0.18	1.23	0.2588052	0.5090408	-5.79	FALSE
258537_at	putative disease resistance prote	---	AT3G04210	1.71	0.77	1.23	0.2588003	0.5090408	-5.79	FALSE
252457_at	zinc-finger protein-like protein D	---	AT3G47180	1.13	0.18	1.23	0.2588727	0.5090419	-5.79	FALSE
250201_at	ankyrin - like protein 270 kDa ar	---	AT5G14230	1.42	0.50	1.23	0.2588668	0.5090419	-5.79	FALSE
249397_at	putative protein MtN21, Medicag	---	AT5G40230	1.21	0.28	1.23	0.2588623	0.5090419	-5.79	FALSE
255330_s_a	putative polyprotein	---	---	1.12	0.16	1.23	0.2589174	0.5090859	-5.79	FALSE
245240_at	polyprotein, putative similar to p	---	---	1.18	0.23	1.23	0.2589537	0.5091134	-5.79	FALSE
252265_at	putative protein SRG1 protein -	DIN11	AT3G49620	1.77	0.83	1.23	0.2589843	0.5091297	-5.79	TRUE
247483_at	aldose reductase-like protein	---	AT5G62420	1.19	0.25	1.23	0.2590451	0.5092015	-5.79	FALSE
247946_at	putative protein similar to unknov	CIA2	AT5G57180	-1.45	-0.53	-1.23	0.2590655	0.5092015	-5.79	FALSE
259056_at	hypothetical protein similar to Ku	---	AT3G03420	-1.19	-0.25	-1.23	0.259205	0.5092561	-5.79	FALSE
253619_at	glycine-rich protein glycine-rich c	---	AT4G30460	1.22	0.29	1.23	0.2591868	0.5092561	-5.79	FALSE
254112_at	putative protein KIAA0136 gene	---	AT4G24970	1.15	0.20	1.23	0.2591498	0.5092561	-5.79	FALSE
246786_at	putative amino acid aminotransf	---	AT5G27410	-1.17	-0.23	-1.23	0.2591958	0.5092561	-5.79	FALSE
260445_at	ARG1 protein (Altered Response	ARG1	AT1G68370	1.18	0.23	1.23	0.2591684	0.5092561	-5.79	FALSE
263724_at	putative Ta11-like non-LTR retro	---	AT2G13510	1.14	0.18	1.23	0.2592272	0.5092561	-5.79	FALSE
257499_at	hypothetical protein similar to hy	---	AT1G63850	-1.31	-0.39	-1.23	0.259289	0.5093337	-5.79	FALSE
250397_at	histon H3 protein HISTONE H3.	---	AT5G10980	-1.11	-0.15	-1.23	0.2593993	0.5094302	-5.79	FALSE
247761_at	phosphoprotein phosphatase 1 c	TOPP2	AT5G59160	1.15	0.21	1.23	0.2593916	0.5094302	-5.79	FALSE
250907_at	putative protein predicted protei	---	AT5G03670	1.13	0.18	1.23	0.2594176	0.5094302	-5.79	FALSE
254685_at	SAUR-AC - like protein (small au	---	AT4G13790	1.43	0.52	1.23	0.2594275	0.5094302	-5.79	FALSE
264081_at	putative RING zinc finger transcr	---	AT2G28540	1.18	0.24	1.23	0.2594824	0.5094941	-5.79	FALSE
257701_at	unknown protein contains similar	---	AT3G12710	1.78	0.83	1.23	0.2595359	0.5095554	-5.79	FALSE

246323_at	hypothetical protein predicted by	---	AT1G16690	1.18	0.24	1.23	0.2595638	0.5095662	-5.79	FALSE
258684_at	putative protein kinase contains	---	AT3G08680	-1.20	-0.27	-1.23	0.2596002	0.5095939	-5.79	TRUE
252556_at	putative protein step II splicing fa	---	AT3G45950	-1.11	-0.15	-1.23	0.2596288	0.5096061	-5.79	FALSE
256090_at	predicted protein	---	AT1G20816	-1.18	-0.24	-1.23	0.2597173	0.509736	-5.79	FALSE
265524_at	hypothetical protein	---	---	1.12	0.16	1.23	0.2597877	0.5098302	-5.79	FALSE
254015_at	putative beta-galactosidase beta	BGAL12	AT4G26140	-1.24	-0.31	-1.23	0.2598256	0.509838	-5.79	FALSE
252361_at	hypothetical protein	---	AT3G48490	-1.34	-0.42	-1.23	0.2598364	0.509838	-5.79	FALSE
263455_at	hypothetical protein predicted by	---	AT2G22320	1.26	0.33	1.23	0.2598691	0.5098584	-5.79	FALSE
260213_at	putative protein kinase similar to	---	AT1G74490	-1.12	-0.17	-1.23	0.2599283	0.5099064	-5.79	FALSE
245658_at	hypothetical protein predicted by	RALFL4	AT1G28270	-1.14	-0.18	-1.23	0.2599383	0.5099064	-5.79	FALSE
257224_at	P-type ATPase, putative similar	---	AT3G27870	1.17	0.23	1.23	0.2599967	0.5099772	-5.79	FALSE
248419_at	putative protein similar to unknov	EXL3	AT5G51550	1.29	0.37	1.23	0.2601205	0.5099971	-5.79	TRUE
246959_at	unknown protein	---	AT5G24690	-1.33	-0.41	-1.23	0.2601854	0.5099971	-5.79	FALSE
252492_at	chloroplast import-associated ch	TOC75-III	AT3G46740	-1.17	-0.23	-1.23	0.2601857	0.5099971	-5.79	FALSE
261294_at	dihydroxyacetone kinase, putativ	---	AT1G48430	-1.22	-0.28	-1.23	0.2600539	0.5099971	-5.79	FALSE
255750_at	hypothetical protein predicted by	---	AT1G31960	1.14	0.19	1.23	0.2601417	0.5099971	-5.79	FALSE
264129_at	hypothetical protein predicted by	---	AT1G79170	1.17	0.22	1.23	0.260109	0.5099971	-5.79	FALSE
265204_at	hypothetical protein predicted by	---	AT2G36650	1.12	0.16	1.23	0.2601204	0.5099971	-5.79	FALSE
255486_at	AtMlo-h1-like protein	MLO1	AT4G02600	-1.15	-0.21	-1.23	0.2600891	0.5099971	-5.79	FALSE
265145_at	unknown protein similar to GB:C/	PLT2	AT1G51190	1.16	0.21	1.23	0.2602567	0.5100897	-5.79	FALSE
256759_at	hypothetical protein predicted by	---	AT3G25640	1.20	0.27	1.23	0.2602969	0.5100897	-5.79	FALSE
259059_at	hypothetical protein	---	AT3G07300	-1.15	-0.20	-1.23	0.2603119	0.5100897	-5.79	FALSE
258028_at	hypothetical protein	---	AT3G27473	1.11	0.15	1.23	0.2603224	0.5100897	-5.79	FALSE
255451_at	putative protein similar to T5J8.1	---	AT4G02860	-1.18	-0.24	-1.23	0.2604377	0.510115	-5.79	FALSE
266701_at	profilin 1 ; supported by cDNA: g	PRF1	AT2G19760	1.12	0.16	1.23	0.2603691	0.510115	-5.79	FALSE
262644_at	beta-VPE nearly identical to beta	BETA-VPE	AT1G62710	1.15	0.21	1.23	0.2604297	0.510115	-5.79	FALSE
258309_at	putative transposase related prot	---	---	1.13	0.18	1.23	0.2604132	0.510115	-5.79	FALSE
261811_at	DNA polymerase epsilon catalyt	TIL1	AT1G08260	-1.23	-0.30	-1.23	0.2604472	0.510115	-5.79	FALSE
266848_at	unknown protein ;supported by f	---	AT2G25950	-1.21	-0.28	-1.23	0.2605026	0.5101798	-5.79	FALSE
263103_at	putative Ta11-like non-LTR retro	---	---	1.15	0.20	1.23	0.2605412	0.5102117	-5.79	FALSE
254789_at	blue copper-binding protein, 15k	---	AT4G12880	2.26	1.18	1.23	0.2606369	0.5103108	-5.79	FALSE
250178_at	putative protein various unknow	---	AT5G14430	-1.13	-0.17	-1.23	0.260659	0.5103108	-5.79	FALSE
248801_at	homeobox-leucine zipper protein	HAT2	AT5G47370	-1.52	-0.60	-1.23	0.2606465	0.5103108	-5.79	FALSE
262052_at	hypothetical protein identical to h	---	---	-1.16	-0.21	-1.23	0.2607454	0.5103925	-5.79	FALSE
263675_x_a	En/Spm-like transposon protein r	---	---	1.22	0.29	1.23	0.2607351	0.5103925	-5.79	FALSE

248206_at	unknown protein	---	AT5G54350	1.18	0.24	1.23	0.2608143	0.5104835	-5.79	FALSE
261039_at	Expressed protein ; supported by	ELF4-L4	AT1G17455	-1.24	-0.31	-1.23	0.2608859	0.5105483	-5.79	FALSE
245943_at	putative protein permease family	---	AT5G19500	-1.20	-0.26	-1.23	0.2608922	0.5105483	-5.79	FALSE
250745_at	putative protein strong similarity t	---	AT5G05850	1.24	0.31	1.23	0.2609638	0.5106446	-5.79	FALSE
253987_at	pyrophosphate-dependent phos	PFK3	AT4G26270	1.37	0.45	1.23	0.2610329	0.5107359	-5.79	FALSE
258312_at	putative long-chain acyl-CoA syn	---	AT3G16170	-1.22	-0.29	-1.23	0.2611685	0.5109574	-5.79	FALSE
264803_at	hypothetical protein predicted by	---	AT1G08580	-1.22	-0.29	-1.23	0.2612406	0.5110187	-5.79	FALSE
245462_at	transcription factor like protein	---	AT4G17020	1.16	0.21	1.23	0.2612446	0.5110187	-5.79	FALSE
262961_at	exonuclease, putative similar to	XRN4	AT1G54490	1.15	0.20	1.23	0.261294	0.5110277	-5.79	FALSE
249084_at	unknown protein	---	AT5G44150	-1.16	-0.21	-1.23	0.2612849	0.5110277	-5.79	FALSE
245771_at	hypothetical protein predicted by	---	AT1G30250	2.08	1.06	1.23	0.2613399	0.5110712	-5.79	FALSE
245156_at	calcium-dependent protein kinas	CPK7	AT5G12480	1.15	0.21	1.23	0.2613651	0.5110712	-5.79	FALSE
252951_at	disease resistance response like	---	AT4G38700	-1.25	-0.33	-1.23	0.2614289	0.5110712	-5.79	FALSE
254899_at	serine/threonine kinase-like prot	---	AT4G11490	1.20	0.26	1.23	0.2614201	0.5110712	-5.79	FALSE
256460_at	60S ribosomal protein L30, puta	---	AT1G36240	-1.16	-0.22	-1.23	0.2614507	0.5110712	-5.79	FALSE
265624_at	CLAVATA3 CLE family of protein	CLV3	AT2G27250	-1.17	-0.22	-1.23	0.2613862	0.5110712	-5.79	FALSE
263733_at	polyprotein, putative similar to p	---	---	-1.11	-0.15	-1.23	0.2615188	0.5110734	-5.80	FALSE
250815_s_a	putative protein similar to unknov	---	AT5G05040 /	1.20	0.26	1.23	0.2614998	0.5110734	-5.80	FALSE
250333_at	membrane translocase - like pro	TIM17-3	AT5G11690	-1.30	-0.38	-1.23	0.261519	0.5110734	-5.80	FALSE
253915_at	putative protein centrin, Marsilea	---	AT4G27280	1.89	0.92	1.23	0.2616905	0.5113647	-5.80	FALSE
248650_at	putative protein similar to unknov	---	AT5G49250	-1.20	-0.27	-1.22	0.2617175	0.5113737	-5.80	FALSE
246452_at	putative protein predicted protein	BPA1	AT5G16840	-1.14	-0.19	-1.22	0.2617534	0.5114	-5.80	FALSE
253269_at	hypothetical protein	---	AT4G34140	1.14	0.18	1.22	0.2618022	0.5114514	-5.80	FALSE
251479_at	serine/threonine-specific kinase	ATHLECRK	AT3G59700	1.45	0.53	1.22	0.2619382	0.5114817	-5.80	TRUE
254131_at	protein kinase (AFC2) ; supporte	AFC2	AT4G24740	-1.17	-0.22	-1.22	0.2619113	0.5114817	-5.80	FALSE
246525_at	CONSTANS ;supported by full-l	CO	AT5G15840	-1.16	-0.21	-1.22	0.2619522	0.5114817	-5.80	FALSE
264847_at	clathrin assembly protein AP19,	AP19	AT2G17380	-1.11	-0.15	-1.22	0.261922	0.5114817	-5.80	FALSE
266665_at	unknown protein	---	AT2G29790	1.16	0.21	1.22	0.2618462	0.5114817	-5.80	FALSE
248995_at	disease resistance protein-like	RRS1	AT5G45260	1.14	0.19	1.22	0.2618939	0.5114817	-5.80	FALSE
266770_at	putative expansin Experimental e	ATEXPA15	AT2G03090	1.25	0.33	1.22	0.2620292	0.5115883	-5.80	FALSE
259847_at	unknown protein	---	AT1G72170	-1.18	-0.23	-1.22	0.2621052	0.5116928	-5.80	FALSE
254016_at	putative transcription factor Arab	CGA1	AT4G26150	1.29	0.37	1.22	0.2623787	0.512132	-5.80	TRUE
265720_at	unknown protein	---	AT2G40110	1.34	0.42	1.22	0.2623998	0.512132	-5.80	TRUE
249947_at	FVT1 - like protein follicular lymp	---	AT5G19200	1.13	0.17	1.22	0.262547	0.512132	-5.80	FALSE
266205_s_a	putative dTDP-glucose 4-6-dehy	AXS2	AT1G08200 /	1.17	0.23	1.22	0.2623856	0.512132	-5.80	FALSE

256400_at	putative RING zinc finger protein	---	AT3G06140	-1.20	-0.26	-1.22	0.2626165	0.512132	-5.80	FALSE
259068_at	unknown protein	PEX13	AT3G07560	-1.16	-0.21	-1.22	0.2626332	0.512132	-5.80	FALSE
258556_at	UDP-glucose:sterol glucosyltrans	---	AT3G07020	-1.17	-0.22	-1.22	0.2625534	0.512132	-5.80	FALSE
247055_at	putative protein similar to unknov	---	AT5G66740	1.18	0.24	1.22	0.2624309	0.512132	-5.80	FALSE
247900_at	60S acidic ribosomal protein P3	---	AT5G57290	-1.33	-0.41	-1.22	0.2626161	0.512132	-5.80	FALSE
247260_at	putative protein contains similarit	---	AT5G64500	-1.22	-0.28	-1.22	0.2625628	0.512132	-5.80	FALSE
249241_at	serine carboxypeptidase-II like	scpl41	AT5G42230	1.13	0.18	1.22	0.2625151	0.512132	-5.80	FALSE
265751_at	putative retroelement pol polypro	---	---	1.13	0.17	1.22	0.2625256	0.512132	-5.80	FALSE
256370_at	MATE efflux family protein, puta	---	AT1G66780	1.14	0.19	1.22	0.2626445	0.512132	-5.80	FALSE
255823_at	unknown protein ;supported by f	LBD15	AT2G40470	1.48	0.57	1.22	0.2625727	0.512132	-5.80	FALSE
267161_at	hypothetical protein predicted by	---	AT2G37680	-1.13	-0.17	-1.22	0.2626775	0.5121526	-5.80	FALSE
246801_at	threonyl-tRNA synthetase ; supp	---	AT5G26830	-1.14	-0.19	-1.22	0.2627129	0.5121778	-5.80	FALSE
254252_at	serine/threonine kinase - like pro	---	AT4G23310	1.22	0.28	1.22	0.2627396	0.5121862	-5.80	FALSE
262875_at	gamma-tocopherol methyltransfe	G-TMT	AT1G64970	-1.17	-0.23	-1.22	0.2627871	0.5121961	-5.80	FALSE
259893_at	putative disease resistance prote	AtRLP11	AT1G71390	1.16	0.22	1.22	0.2627896	0.5121961	-5.80	FALSE
257152_at	Expressed protein ; supported by	PUX1	AT3G27310	-1.13	-0.17	-1.22	0.2628323	0.5122355	-5.80	FALSE
265973_at	putative non-LTR retroelement re	---	---	1.12	0.16	1.22	0.2629089	0.512341	-5.80	FALSE
265556_at	putative Athila retroelement ORF	---	---	1.15	0.21	1.22	0.2629598	0.5123527	-5.80	FALSE
264912_at	auxin-induced protein, putative s	---	AT1G60750	1.15	0.20	1.22	0.2629456	0.5123527	-5.80	FALSE
249822_at	unknown protein	---	AT5G23710	-1.16	-0.21	-1.22	0.2630168	0.5124199	-5.80	FALSE
249896_at	unknown protein ; supported by	---	AT5G22530	1.18	0.24	1.22	0.2630545	0.5124498	-5.80	FALSE
257804_at	protein kinase, putative similar t	---	AT3G18810	1.13	0.18	1.22	0.2630982	0.5124911	-5.80	FALSE
252503_at	putative protein hypothetical pro	---	AT3G46910	1.16	0.21	1.22	0.2631487	0.5125456	-5.80	FALSE
262110_at	SF2/ASF-like splicing modulator	SR1	AT1G02840	-1.19	-0.25	-1.22	0.2632075	0.5125725	-5.80	FALSE
264861_at	putative glucosidase similar to a	---	AT1G24320	1.12	0.17	1.22	0.2631973	0.5125725	-5.80	FALSE
260090_at	putative serine carboxypeptidas	scpl4	AT1G73310	-1.12	-0.16	-1.22	0.2632439	0.5125997	-5.80	FALSE
254408_at	serine/threonine kinase - like pro	B120	AT4G21390	2.25	1.17	1.22	0.2633075	0.5126393	-5.80	TRUE
256164_at	terpene cyclase, putative similar	---	AT1G48800	-1.12	-0.17	-1.22	0.2633092	0.5126393	-5.80	FALSE
248542_at	putative protein similar to unknov	AT5G5019(	---	1.13	0.18	1.22	0.263378	0.5127093	-5.80	FALSE
249616_s_a	contains similarity to DnaJ protei	---	AT5G37440 ///	-1.13	-0.18	-1.22	0.2633901	0.5127093	-5.80	FALSE
257982_at	unknown protein similar to TYPE	ATTOP6B	AT3G20780	1.19	0.25	1.22	0.2634959	0.5128696	-5.80	FALSE
253523_at	putative protein myosin heavy ch	---	AT4G31340	1.15	0.20	1.22	0.2635174	0.5128696	-5.80	FALSE
249410_at	receptor-like protein kinase rece	---	AT5G40380	-1.31	-0.39	-1.22	0.2635944	0.5129757	-5.80	TRUE
262971_at	receptor-like protein kinase, puta	---	AT1G75640	1.21	0.27	1.22	0.2637216	0.5131796	-5.80	FALSE
261116_at	sec14 cytosolic factor, putative s	---	AT1G75370	-1.14	-0.19	-1.22	0.2637708	0.5132315	-5.80	FALSE

265750_x_a	putative Athila retroelement ORF	---	---	1.23	0.30	1.22	0.2637964	0.5132375	-5.80	FALSE
257562_at	hypothetical protein	---	---	1.18	0.23	1.22	0.2638475	0.513293	-5.80	FALSE
260208_s_a	unknown protein similar to Ca+2-	---	AT1G70670 /A	1.31	0.39	1.22	0.263901	0.5133097	-5.80	FALSE
266436_at	putative clathrin binding protein (	---	AT2G43160	1.29	0.37	1.22	0.2638899	0.5133097	-5.80	FALSE
262895_at	hypothetical protein predicted by	---	AT1G59800	1.18	0.24	1.22	0.2639711	0.5134022	-5.80	FALSE
251102_at	putative transporter protein Na+/	CHX27	AT5G01690	1.23	0.30	1.22	0.2640885	0.5135868	-5.80	FALSE
248614_at	putative protein similar to unknov	---	AT5G49560	-1.14	-0.19	-1.22	0.2641388	0.5136408	-5.80	FALSE
254718_at	putative protein disease resistan	---	AT4G13580	1.15	0.20	1.22	0.2642403	0.5137942	-5.80	FALSE
252896_at	cytochrome P450 - like protein c	CYP96A9	AT4G39480	1.13	0.17	1.22	0.2643548	0.5139732	-5.80	FALSE
261519_at	unknown protein ; supported by c	---	AT1G71810	-1.22	-0.29	-1.22	0.2645004	0.5141686	-5.80	FALSE
248806_at	putative protein contains similarit	---	AT5G47490	-1.13	-0.18	-1.22	0.2644995	0.5141686	-5.80	FALSE
262656_at	unknown protein location of EST	---	AT1G14200	1.15	0.21	1.22	0.2646846	0.5144391	-5.81	TRUE
264567_s_a	putative peroxidase ATP12a Stro	---	AT1G05240 /A	1.17	0.22	1.22	0.264673	0.5144391	-5.81	FALSE
257162_s_a	ammonium transporter, putative	AMT1;3	AT3G24290 /A	1.13	0.18	1.22	0.2647119	0.5144482	-5.81	FALSE
252427_at	hypothetical protein	---	AT3G47640	1.33	0.41	1.22	0.2648051	0.5145854	-5.81	FALSE
AFFX-r2-Bs	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.52	-0.61	-1.22	0.2648963	0.5147188	-5.81	FALSE
252718_at	putative protein predicted protei	---	AT3G43940	1.16	0.22	1.22	0.2649356	0.5147365	-5.81	FALSE
246715_at	putative protein glucose-6-phosp	---	AT5G28230	1.20	0.26	1.22	0.2649505	0.5147365	-5.81	FALSE
255999_at	DNA-binding protein, putative si	WRKY71	AT1G29860	1.41	0.49	1.22	0.2650579	0.514738	-5.81	TRUE
266356_at	putative uclacyanin I identical to	UCC1	AT2G32300	1.12	0.16	1.22	0.2650273	0.514738	-5.81	FALSE
246502_at	stearoyl-acyl carrier protein desa	---	AT5G16240	-1.22	-0.28	-1.22	0.2650641	0.514738	-5.81	FALSE
257612_at	unknown protein	ARO4	AT3G26600	1.40	0.49	1.22	0.2650483	0.514738	-5.81	FALSE
253279_at	putative protein B subunit of pro	MCCB	AT4G34030	1.31	0.38	1.22	0.2649884	0.514738	-5.81	FALSE
260785_at	hypothetical protein predicted by	---	AT1G06200	-1.14	-0.19	-1.22	0.2651681	0.5148262	-5.81	FALSE
266569_at	unknown protein	---	AT2G24080	1.13	0.18	1.22	0.2651564	0.5148262	-5.81	FALSE
257145_at	esterase, putative similar to este	---	AT3G27320	-1.20	-0.26	-1.22	0.2651772	0.5148262	-5.81	FALSE
248612_at	putative protein contains similarit	---	AT5G49530	1.24	0.31	1.22	0.2652101	0.5148462	-5.81	FALSE
262494_at	myosin-like protein similar to myo	---	AT1G21810	1.19	0.25	1.21	0.2653139	0.5149781	-5.81	FALSE
253217_at	actin depolymerizing factor - like	ADF9	AT4G34970	1.38	0.46	1.21	0.2653232	0.5149781	-5.81	FALSE
258498_at	unknown protein similar to pollen	---	AT3G02480	1.37	0.45	1.21	0.2654308	0.5150116	-5.81	FALSE
246217_at	APETALA2 protein ; supported b	AP2	AT4G36920	1.29	0.36	1.21	0.2653765	0.5150116	-5.81	FALSE
254509_at	terpene cyclase like protein 5-ep	---	AT4G20200	-1.13	-0.18	-1.21	0.2654025	0.5150116	-5.81	FALSE
248723_at	acetyl-CoA:benzylalcohol acetylt	---	AT5G47950	1.16	0.21	1.21	0.2654207	0.5150116	-5.81	FALSE
250574_at	putative protein putative transcri	---	AT5G08230	-1.13	-0.18	-1.21	0.2655147	0.5151306	-5.81	FALSE
265381_at	putative non-LTR retroelement re	---	---	1.21	0.27	1.21	0.2657375	0.5154613	-5.81	FALSE

245491_at	hypothetical protein	LDL3	---	1.18	0.23	1.21	0.2657258	0.5154613	-5.81	FALSE
262462_at	hypothetical protein predicted by	---	AT1G50350	1.13	0.17	1.21	0.265753	0.5154613	-5.81	FALSE
259918_at	putative AP2 domain transcriptio	---	AT1G72570	1.13	0.17	1.21	0.2657765	0.5154632	-5.81	FALSE
265551_at	putative replication protein A1	---	---	1.13	0.18	1.21	0.265911	0.5156802	-5.81	FALSE
248003_at	putative protein contains similarit	---	AT5G56220	-1.61	-0.68	-1.21	0.2660841	0.5159719	-5.81	FALSE
245777_at	unknown protein contains similar	atnudt21	AT1G73540	1.85	0.88	1.21	0.2661134	0.5159849	-5.81	FALSE
260395_at	homeobox gene 13 protein identi	ATHB13	AT1G69780	1.37	0.45	1.21	0.2661656	0.5159961	-5.81	FALSE
249221_at	serine/threonine protein kinase-li	---	AT5G42440	1.19	0.25	1.21	0.2661444	0.5159961	-5.81	FALSE
247973_at	putative protein contains similarit	---	AT5G56770	1.14	0.18	1.21	0.266187	0.5159961	-5.81	FALSE
265459_at	unknown protein ; supported by	---	AT2G46540	-1.13	-0.18	-1.21	0.2663644	0.516296	-5.81	FALSE
263186_at	lectin receptor kinase, putative s	---	---	1.21	0.28	1.21	0.2664017	0.5163245	-5.81	FALSE
259463_at	hypothetical protein predicted by	---	AT1G18950	-1.27	-0.34	-1.21	0.2664507	0.516352	-5.81	FALSE
250520_at	putative protein contains similarit	PEX1	AT5G08470	-1.12	-0.16	-1.21	0.2664612	0.516352	-5.81	FALSE
262525_at	putative cytochrome P450 41% i	CYP72C1	AT1G17060	1.27	0.34	1.21	0.2665509	0.5164548	-5.81	FALSE
263093_at	putative replication protein A1	---	---	1.13	0.18	1.21	0.2665822	0.5164548	-5.81	FALSE
267248_at	hypothetical protein predicted by	---	AT2G30120	-1.19	-0.25	-1.21	0.266572	0.5164548	-5.81	FALSE
260534_at	hypothetical protein predicted by	---	---	-1.13	-0.18	-1.21	0.266635	0.5165133	-5.81	FALSE
251281_at	putative protein hypothetical pro	AGP20	AT3G61640	1.42	0.51	1.21	0.2667463	0.5166851	-5.81	TRUE
254373_at	hypothetical protein ;supported b	---	AT4G21730	1.13	0.18	1.21	0.2667997	0.5167446	-5.81	FALSE
250596_at	putative protein contains similarit	---	AT5G07780	1.22	0.29	1.21	0.2668276	0.5167548	-5.81	FALSE
252795_at	putative protein predicted protei	---	---	1.14	0.19	1.21	0.266852	0.5167582	-5.81	FALSE
253370_at	pectinesterase - like protein pec	---	AT4G33230	-1.19	-0.25	-1.21	0.2668905	0.5167888	-5.81	FALSE
246468_at	UDP glucose:flavonoid 3-o-gluc	UGT78D2	AT5G17050	1.28	0.36	1.21	0.2669188	0.5167998	-5.81	FALSE
251610_at	putative protein hypothetical pro	---	AT3G57930	-1.53	-0.61	-1.21	0.2669803	0.5168352	-5.81	FALSE
254395_at	subtilisin-like protease subtilisin-	---	AT4G21640	1.12	0.16	1.21	0.2669824	0.5168352	-5.81	FALSE
259188_at	unknown protein ;supported by f	---	AT3G01510	-1.22	-0.28	-1.21	0.2670397	0.5168463	-5.81	FALSE
267198_at	putative gibberellin-regulated pro	---	AT2G30810	-1.12	-0.16	-1.21	0.2670561	0.5168463	-5.81	FALSE
250048_s_a	BCS1 - like protein h-bcs1, Hom	---	AT5G17740 /	1.14	0.19	1.21	0.2670541	0.5168463	-5.81	FALSE
261393_at	NAM (no apical meristem)-like p	SMB	AT1G79580	1.13	0.17	1.21	0.2671121	0.5169108	-5.81	FALSE
259369_s_a	hypothetical protein similar to put	---	AT1G69150 /	1.14	0.19	1.21	0.2673089	0.5172478	-5.81	FALSE
255086_at	putative protein chromosome I B	---	AT4G09300	1.16	0.22	1.21	0.2674258	0.5173861	-5.81	FALSE
256806_at	CCAAT-binding factor B chain, p	NF-YA9	AT3G20910	-1.16	-0.22	-1.21	0.2674156	0.5173861	-5.81	FALSE
251503_at	ABC transporter-like protein puta	ATMRP14	AT3G59140	-1.28	-0.35	-1.21	0.2674635	0.5174152	-5.81	TRUE
261676_at	Expressed protein ; supported by	---	AT1G18480	1.18	0.24	1.21	0.2676177	0.5176696	-5.81	FALSE
260322_at	unknown protein	---	AT1G63900	-1.15	-0.20	-1.21	0.2676829	0.5177518	-5.81	FALSE

258738_at	hypothetical protein similar to hyp	---	AT3G05750	-1.18	-0.24	-1.21	0.2677796	0.5178949	-5.81	FALSE
247898_at	F-box protein ZTL/LFK1/ADO1,	ZTL	AT5G57360	-1.15	-0.20	-1.21	0.2678049	0.5178999	-5.81	FALSE
261470_at	ethylene-responsive element bir	ERF11	AT1G28370	1.90	0.93	1.21	0.2679078	0.5179672	-5.82	FALSE
258205_at	unknown protein	---	AT3G13965	1.14	0.19	1.21	0.2678855	0.5179672	-5.82	FALSE
262694_at	unknown protein	---	AT1G62790	1.34	0.43	1.21	0.2679051	0.5179672	-5.82	FALSE
245864_at	hypothetical protein predicted by	---	AT1G58070	-1.26	-0.34	-1.21	0.2679328	0.5179716	-5.82	FALSE
259739_at	unknown protein supported by cD	SEH1H	AT1G64350	-1.15	-0.20	-1.21	0.2679692	0.5179981	-5.82	FALSE
254510_at	cadinene synthase like protein (	---	AT4G20210	1.19	0.25	1.21	0.2679956	0.5180052	-5.82	FALSE
261375_at	transcription factor, putative sim	SPL4	AT1G53160	-1.77	-0.83	-1.21	0.2682589	0.5184577	-5.82	TRUE
264446_at	putative nuclear transport factor	NTF2A	AT1G27310	-1.15	-0.21	-1.21	0.2682752	0.5184577	-5.82	FALSE
265879_at	hypothetical protein predicted by	---	AT2G42450	-1.13	-0.17	-1.21	0.2683226	0.5185055	-5.82	FALSE
259562_at	hypothetical protein ; supported b	---	AT1G21200	-1.15	-0.20	-1.21	0.2683883	0.5185743	-5.82	FALSE
259275_at	unknown protin ;supported by fu	---	AT3G01060	-1.27	-0.35	-1.21	0.2684037	0.5185743	-5.82	FALSE
252256_at	PRE-MRNA SPLICING FACTOR	SRp34a	AT3G49430	-1.19	-0.25	-1.21	0.2684415	0.5186034	-5.82	FALSE
256081_at	hypothetical protein contains Pfa	WOX14	AT1G20700	1.16	0.22	1.21	0.2685142	0.5186902	-5.82	FALSE
248978_at	putative protein contains similarit	AtPP2-A8	AT5G45070	1.20	0.26	1.21	0.2685319	0.5186902	-5.82	FALSE
266681_at	copia-like retroelement pol polyp	---	---	1.11	0.15	1.21	0.2685976	0.5187732	-5.82	FALSE
257715_at	putative zinc transporter identica	ZIP1	AT3G12750	1.30	0.38	1.21	0.2687252	0.5189756	-5.82	FALSE
257017_at	beta-xylosidase, putative similar	---	AT3G19620	1.14	0.19	1.21	0.2688455	0.5190212	-5.82	FALSE
265194_at	1-aminocyclopropane-1-carboxy	EFE	AT1G05010	1.38	0.47	1.20	0.2688865	0.5190212	-5.82	FALSE
256942_at	hypothetical protein similar to unl	LSH4	AT3G23290	1.49	0.57	1.20	0.2688833	0.5190212	-5.82	FALSE
264127_at	serine/threonine protein kinase,	AGC1.7	AT1G79250	1.11	0.15	1.20	0.2689236	0.5190212	-5.82	FALSE
245404_at	putative protein	---	AT4G17610	-1.19	-0.25	-1.21	0.2688296	0.5190212	-5.82	FALSE
264215_at	cytochrome P450, putative simil	CYP96A3	AT1G65340	1.13	0.17	1.21	0.2688042	0.5190212	-5.82	FALSE
246752_at	putative protein predicted protei	---	AT5G27890	1.15	0.20	1.20	0.2689308	0.5190212	-5.82	FALSE
258951_at	putative phosphatidylinositolglyca	---	AT3G01380	-1.15	-0.21	-1.20	0.2688841	0.5190212	-5.82	FALSE
253844_at	hypothetical protein	---	AT4G27930	1.16	0.22	1.20	0.2690106	0.5191312	-5.82	FALSE
262822_at	putative membrane-associated s	---	AT1G11630	-1.15	-0.20	-1.20	0.2691087	0.5192328	-5.82	FALSE
247693_at	putative protein leucine zipper-c	ATEXO70H	AT5G59730	1.53	0.61	1.20	0.2691055	0.5192328	-5.82	FALSE
250524_at	putative protein contains similarit	---	AT5G08520	-1.13	-0.18	-1.20	0.2691393	0.5192479	-5.82	FALSE
248264_at	putative protein similar to unknov	---	AT5G53310	-1.16	-0.22	-1.20	0.2691959	0.5192869	-5.82	FALSE
258469_at	unknown protein contains Pfam p	PRXIIF	AT3G06050	1.13	0.18	1.20	0.2692051	0.5192869	-5.82	FALSE
254881_at	hypothetical protein	---	AT4G11700	1.12	0.17	1.20	0.2692975	0.5194213	-5.82	FALSE
265733_at	unknown protein ;supported by f	---	AT2G01190	1.17	0.22	1.20	0.2693451	0.5194691	-5.82	FALSE
247396_at	putative protein predicted protei	---	AT5G62930	-1.13	-0.17	-1.20	0.269387	0.519506	-5.82	FALSE

258622_at	unknown protein contains Pfam p	---	AT3G02720	-1.14	-0.19	-1.20	0.2694613	0.5195667	-5.82	FALSE
246394_at	myrosinase binding protein, puta	---	AT1G58160	1.12	0.17	1.20	0.269464	0.5195667	-5.82	FALSE
257585_at	hypothetical protein predicted by	---	AT3G12420	1.15	0.20	1.20	0.2695708	0.5197287	-5.82	FALSE
264777_at	unknown protein similar to L-allo	THA1	AT1G08630	1.74	0.80	1.20	0.2696773	0.51989	-5.82	TRUE
255925_at	unknown protein ;supported by fu	---	AT1G22200	-1.19	-0.25	-1.20	0.2697303	0.5199043	-5.82	FALSE
251347_at	putative protein ferritin 1 precurs	---	AT3G61010	-1.26	-0.33	-1.20	0.2697121	0.5199043	-5.82	FALSE
248209_at	flavonol 3-O-glucosyltransferase-	---	AT5G53990	1.20	0.27	1.20	0.2698726	0.5201347	-5.82	FALSE
265448_at	putative DOF zinc finger protein	DAG2	AT2G46590	-1.19	-0.24	-1.20	0.2699089	0.5201606	-5.82	FALSE
250576_at	cytochrome P450-like protein sev	---	AT5G08250	1.15	0.20	1.20	0.2699478	0.5201918	-5.82	FALSE
258814_at	putative short-chain type dehydro	---	AT3G03980	-1.17	-0.22	-1.20	0.2700096	0.5202159	-5.82	FALSE
263659_at	unknown protein EST gb|ATTS5(	---	AT1G04470	1.15	0.20	1.20	0.2700287	0.5202159	-5.82	FALSE
255476_at	hypothetical protein similar to re	---	---	1.16	0.22	1.20	0.2700288	0.5202159	-5.82	FALSE
249218_at	pitrilysin	---	AT5G42390	-1.21	-0.27	-1.20	0.270204	0.5202953	-5.82	FALSE
260991_at	hypothetical protein predicted by	---	AT1G12160	-1.12	-0.17	-1.20	0.2701774	0.5202953	-5.82	FALSE
261391_at	hypothetical protein similar to hyp	---	AT1G35030	1.16	0.21	1.20	0.270201	0.5202953	-5.82	FALSE
255007_at	putative oxidoreductase 11beta-	AtHSD5	AT4G10020	-1.13	-0.18	-1.20	0.2701696	0.5202953	-5.82	FALSE
257482_x_a	hypothetical protein contains sim	---	AT1G27820	1.22	0.28	1.20	0.2701081	0.5202953	-5.82	FALSE
257120_at	protein kinase, putative contains	---	AT3G20200	-1.15	-0.20	-1.20	0.2702069	0.5202953	-5.82	FALSE
258791_at	hevein-like protein precursor (PF	PR4	AT3G04720	-1.45	-0.54	-1.20	0.2702578	0.5203496	-5.82	TRUE
250998_at	ankyrin - like protein ankyrin G1	---	AT5G02620	1.22	0.29	1.20	0.2703709	0.5204511	-5.82	FALSE
246693_at	putative protein	---	AT5G29070	1.13	0.18	1.20	0.270379	0.5204511	-5.82	FALSE
261485_at	unknown protein ;supported by fu	UTR3	AT1G14360	1.44	0.52	1.20	0.2703754	0.5204511	-5.82	FALSE
244929_at	NADH dehydrogenase subunit 4	---	---	-1.24	-0.31	-1.20	0.2708095	0.5208098	-5.82	FALSE
248274_at	isp4 protein	ATOPT9	AT5G53510	1.13	0.18	1.20	0.2707648	0.5208098	-5.82	FALSE
263757_at	cysteine proteinase similar to cy	---	AT2G21430	1.24	0.31	1.20	0.2707899	0.5208098	-5.82	FALSE
265331_at	similar to gibberellin-regulated pr	---	AT2G18420	1.14	0.19	1.20	0.2706899	0.5208098	-5.82	FALSE
256423_at	serine carboxypeptidase, putativ	scpl18	AT1G33540	1.11	0.16	1.20	0.2706508	0.5208098	-5.82	FALSE
267560_at	putative cytochrome P450	CYP76C3	AT2G45580	1.16	0.21	1.20	0.270664	0.5208098	-5.82	FALSE
265752_at	putative Athila retroelement ORF	---	---	1.13	0.18	1.20	0.2706375	0.5208098	-5.82	FALSE
254245_at	serine/threonine kinase - like pro	---	AT4G23240	1.13	0.18	1.20	0.2707917	0.5208098	-5.82	FALSE
264985_at	unknown protein ;supported by fu	---	AT1G27150	-1.27	-0.35	-1.20	0.2707111	0.5208098	-5.82	FALSE
251523_at	putative protein several hypothet	---	AT3G58975	-1.15	-0.20	-1.20	0.2708165	0.5208098	-5.82	FALSE
258619_at	isopentenyl diphosphate:dimethy	IPP2	AT3G02780	-1.18	-0.24	-1.20	0.2705928	0.5208098	-5.82	FALSE
255919_at	putative protein	---	---	1.15	0.20	1.20	0.2709835	0.5209992	-5.82	FALSE
267227_at	hypothetical protein predicted by	---	AT2G44030	1.19	0.25	1.20	0.2709793	0.5209992	-5.82	FALSE

255559_at	putative NAK-like ser/thr protein	---	AT4G02010	-1.19	-0.25	-1.20	0.270954	0.5209992	-5.82	FALSE
246587_at	putative protein predicted protei	---	---	1.15	0.21	1.20	0.2711862	0.5213449	-5.83	FALSE
266332_at	hypothetical protein predicted by	---	AT2G32415	1.15	0.20	1.20	0.2713069	0.521533	-5.83	FALSE
265068_at	hypothetical protein Similar to Ki	---	AT1G55550	-1.12	-0.17	-1.20	0.2713559	0.5215833	-5.83	FALSE
254034_at	P-glycoprotein-2 (pgp2)	PGP2	AT4G25960	-1.22	-0.29	-1.20	0.2714163	0.5216432	-5.83	TRUE
260030_at	putative bZIP transcription factor	AtbZIP	AT1G68880	1.14	0.19	1.20	0.2714328	0.5216432	-5.83	FALSE
251423_at	regulatory protein - like regulato	CYCP3;2	AT3G60550	1.18	0.24	1.20	0.2714748	0.5216798	-5.83	FALSE
246697_at	putative protein	---	AT5G29210	1.16	0.21	1.20	0.2715023	0.5216888	-5.83	FALSE
247442_s_a	tubulin beta-2/beta-3 chain (sp|P	TUB2	AT5G62690 /	-1.26	-0.34	-1.20	0.2716011	0.5217907	-5.83	FALSE
255694_at	putative transcriptional regulator	UNE10	AT4G00050	-1.19	-0.25	-1.20	0.2715992	0.5217907	-5.83	FALSE
254098_at	superoxide dismutase (EC 1.15.1	FSD1	AT4G25100	-1.19	-0.25	-1.20	0.2716402	0.5218219	-5.83	FALSE
251805_at	putative protein RING-H2 finger	SDIR1	AT3G55530	1.13	0.18	1.20	0.2716825	0.5218592	-5.83	FALSE
251906_at	putative protein several hypothet	ATCHX20	AT3G53720	1.20	0.26	1.20	0.2717609	0.5219659	-5.83	TRUE
254533_at	putative protein ARI protein - Dr	---	AT4G19670	1.22	0.29	1.20	0.2718042	0.522005	-5.83	FALSE
247934_at	putative protein similar to unknov	---	AT5G57000	-1.15	-0.20	-1.20	0.2718407	0.5220311	-5.83	TRUE
263870_at	unknown protein	RKP	AT2G22010	1.16	0.21	1.20	0.2719813	0.5222132	-5.83	FALSE
253499_at	putative protein zinc-finger helic	---	AT4G31900	1.13	0.18	1.20	0.2719596	0.5222132	-5.83	FALSE
263513_at	unknown protein	---	AT2G12400	1.26	0.33	1.20	0.2721233	0.5222933	-5.83	TRUE
267645_at	putative beta-glucosidase	BGLU33	AT2G32860	-1.46	-0.55	-1.20	0.2721964	0.5222933	-5.83	TRUE
265900_at	unknown protein	---	AT2G25730	-1.11	-0.15	-1.20	0.272229	0.5222933	-5.83	FALSE
249398_at	RING finger -like protein RING-H	---	AT5G40250	-1.16	-0.22	-1.20	0.2721353	0.5222933	-5.83	FALSE
249279_at	SCARECROW gene regulator-lik	---	AT5G41920	-1.12	-0.16	-1.20	0.2722173	0.5222933	-5.83	FALSE
259283_at	putative transcription factor simil	MYB65	AT3G11440	1.15	0.20	1.20	0.2721862	0.5222933	-5.83	FALSE
245215_at	F12A21.4 similar to iEP4 gb|AAD	ATFXG1	AT1G67830	-1.35	-0.43	-1.20	0.2721998	0.5222933	-5.83	FALSE
260964_at	E2, ubiquitin-conjugating enzym	ATUBC2-1	AT1G45050	-1.12	-0.16	-1.20	0.2721186	0.5222933	-5.83	FALSE
246403_at	pectinacetylesterase precursor,	---	AT1G57590	1.23	0.30	1.20	0.272135	0.5222933	-5.83	FALSE
261252_at	RAS-related protein ARA-1 ident	RABA5E	AT1G05810	-1.19	-0.25	-1.20	0.2722727	0.522333	-5.83	TRUE
259093_at	unknown protein similar to putati	---	AT3G04860	-1.30	-0.38	-1.20	0.272431	0.5225928	-5.83	FALSE
265593_s_a	unknown protein ;supported by f	LCV1	AT2G20120 /	-1.13	-0.18	-1.20	0.2724807	0.5226436	-5.83	FALSE
260962_at	pectin methylesterase, putative	PME7	AT1G44980	-1.15	-0.20	-1.19	0.2725033	0.5226436	-5.83	FALSE
251030_at	putative protein kinesin light cha	NDP1	AT5G02130	-1.22	-0.29	-1.19	0.2726553	0.5228471	-5.83	FALSE
259678_at	putative 30S ribosomal protein S	---	AT1G77750	-1.22	-0.29	-1.19	0.2726388	0.5228471	-5.83	FALSE
263932_at	unknown protein	---	AT2G35990	1.13	0.17	1.19	0.2728494	0.5231755	-5.83	FALSE
247667_at	putative protein predicted protei	---	AT5G60150	1.16	0.22	1.19	0.2728764	0.5231832	-5.83	FALSE
245196_at	F12A21.12 similar to pectate lya	---	AT1G67750	1.37	0.46	1.19	0.2729351	0.5231958	-5.83	FALSE

262382_at	virus resistance protein, putative	---	AT1G72920	1.97	0.98	1.19	0.2729747	0.5231958	-5.83	FALSE
252817_at	putative protein hypothetical prot	---	---	1.17	0.23	1.19	0.2729589	0.5231958	-5.83	FALSE
262841_at	aspartate-semialdehyde dehydr	---	AT1G14810	-1.23	-0.29	-1.19	0.2729386	0.5231958	-5.83	FALSE
253724_at	Expressed protein ; supported by	LCR24	AT4G29285	1.12	0.17	1.19	0.2730003	0.5232009	-5.83	FALSE
267095_at	putative AMP deaminase ; supp	FAC1	AT2G38280	-1.17	-0.22	-1.19	0.2731164	0.5233107	-5.83	FALSE
263709_at	unknown protein ESTs gb|T205	---	AT1G09310	2.05	1.04	1.19	0.273088	0.5233107	-5.83	FALSE
264732_at	serpin, putative similar to serpin	---	AT1G62160	1.12	0.16	1.19	0.2731264	0.5233107	-5.83	FALSE
249871_at	putative protein similar to unknov	---	AT5G23110	-1.21	-0.28	-1.19	0.2732638	0.5235299	-5.83	FALSE
259214_at	Expressed protein ; supported by	---	AT3G09085	1.15	0.20	1.19	0.2733265	0.523606	-5.83	FALSE
260660_at	hypothetical protein contains Pfa	---	AT1G19485	-1.18	-0.24	-1.19	0.2735745	0.5239932	-5.83	FALSE
256131_at	bZIP transcription factor, putativ	AtbZIP58	AT1G13600	1.18	0.24	1.19	0.2735726	0.5239932	-5.83	FALSE
266233_at	putative phloem-specific lectin	AtPP2-B8	AT2G02340	1.12	0.16	1.19	0.2736124	0.5240218	-5.83	FALSE
258190_at	hypothetical protein predicted by	---	AT3G29080	1.13	0.18	1.19	0.2736838	0.5241145	-5.83	FALSE
259310_s_a	Expressed protein ; supported by	---	AT3G05160 //	1.18	0.24	1.19	0.2737497	0.5241967	-5.83	FALSE
256857_at	NAM-like protein similar to NAM	CUC1	AT3G15170	1.11	0.15	1.19	0.2738488	0.5243425	-5.83	FALSE
257506_at	auxin-induced protein, putative s	---	AT1G29440	-1.63	-0.71	-1.19	0.2739078	0.5243947	-5.83	TRUE
254471_s_a	putative protein parts of other pr	---	---	1.13	0.18	1.19	0.2739221	0.5243947	-5.83	FALSE
264266_at	putative protein phosphatase 2C	---	AT1G09160	-1.21	-0.28	-1.19	0.2740979	0.5245112	-5.83	TRUE
259462_at	hypothetical protein contains sim	---	AT1G18940	1.21	0.27	1.19	0.2740397	0.5245112	-5.83	FALSE
264038_at	putative ubiquinone biosynthesis	---	AT2G03690	1.19	0.25	1.19	0.274083	0.5245112	-5.83	FALSE
263840_at	Expressed protein ; supported by	---	AT2G36885	1.22	0.29	1.19	0.2740526	0.5245112	-5.83	FALSE
260293_at	unknown protein predicted by ge	---	AT1G63670	-1.18	-0.23	-1.19	0.2740591	0.5245112	-5.83	FALSE
255130_at	hypothetical protein ; supported	---	AT4G08240	1.16	0.22	1.19	0.2741287	0.5245261	-5.83	FALSE
266312_at	20S proteasome subunit C8 (PA	PAG1	AT2G27020	-1.16	-0.22	-1.19	0.2741722	0.5245652	-5.83	FALSE
247588_at	protein disulfide isomerase prec	ATPDIL1-4	AT5G60640	-1.15	-0.20	-1.19	0.2742498	0.5246259	-5.83	FALSE
261890_at	hypothetical protein predicted by	---	AT1G80970	1.27	0.34	1.19	0.2742269	0.5246259	-5.83	FALSE
252184_at	steroid 22-alpha-hydroxylase (D	DWF4	AT3G50660	-1.20	-0.26	-1.19	0.2743577	0.5246562	-5.83	TRUE
264429_at	hypothetical protein similar to me	---	AT1G61670	-1.12	-0.17	-1.19	0.274338	0.5246562	-5.83	FALSE
249768_at	receptor-like protein kinase	---	AT5G24100	1.18	0.24	1.19	0.2743378	0.5246562	-5.83	FALSE
266250_at	putative reverse transcriptase	---	---	1.14	0.19	1.19	0.2742948	0.5246562	-5.83	FALSE
262434_at	lysine and histidine specific trans	---	AT1G47670	-1.29	-0.37	-1.19	0.2744826	0.5248438	-5.84	FALSE
262676_at	SKP1/ASK1 (At1) identical to Sk	SKP1	AT1G75950	1.11	0.15	1.19	0.2745018	0.5248438	-5.84	FALSE
250761_at	ankyrin-like protein	---	AT5G06050	-1.16	-0.21	-1.19	0.2746192	0.5250242	-5.84	FALSE
257819_at	Expressed protein ; supported by	RALFL25	AT3G25165	1.13	0.18	1.19	0.2746591	0.5250565	-5.84	FALSE
251086_at	putative protein hypothetical pro	---	AT5G01450	1.20	0.26	1.19	0.2747613	0.5252079	-5.84	FALSE

260851_at	nodulin-like protein similar to Mt	---	AT1G21890	1.15	0.20	1.19	0.2747913	0.5252212	-5.84	FALSE
245719_at	DNA gyrase subunit B - like prote	---	AT5G04110	-1.14	-0.18	-1.19	0.274879	0.5253226	-5.84	FALSE
251911_at	putative C2H2-type zinc finger pr	---	AT3G53820	1.14	0.19	1.19	0.2749048	0.5253226	-5.84	FALSE
262545_at	prolin rich protein, putative simil	---	AT1G31250	-1.14	-0.19	-1.19	0.2749134	0.5253226	-5.84	FALSE
250088_at	APG5 (autophagy 5)-like protein	APG5	AT5G17290	1.14	0.19	1.19	0.2749624	0.5253721	-5.84	FALSE
266751_at	putative peptide chain release fa	---	AT2G47020	-1.14	-0.18	-1.19	0.275004	0.5254076	-5.84	FALSE
252779_at	putative protein	---	AT3G42990	1.14	0.18	1.19	0.2750813	0.5255112	-5.84	FALSE
252586_at	dof6 zinc finger protein	---	AT3G45610	1.15	0.21	1.19	0.2751135	0.5255288	-5.84	FALSE
262602_at	unknown protein ESTs gb|AA65	---	AT1G15270	-1.12	-0.16	-1.19	0.2751848	0.5256209	-5.84	FALSE
245656_at	hypothetical protein predicted by	---	AT1G56620	1.14	0.19	1.19	0.2753125	0.5258209	-5.84	FALSE
264491_at	hypothetical protein predicted by	---	AT1G27410	-1.14	-0.18	-1.19	0.2754514	0.5259979	-5.84	FALSE
263944_at	hypothetical protein predicted by	---	---	1.12	0.17	1.19	0.2754441	0.5259979	-5.84	FALSE
256360_at	hypothetical protein	---	AT1G66440	1.20	0.27	1.19	0.2754945	0.5260363	-5.84	FALSE
259410_at	hypothetical protein predicted by	---	AT1G13340	-1.41	-0.50	-1.19	0.2756931	0.5262687	-5.84	TRUE
247947_at	auxin transport protein EIR1 (gb|	EIR1	AT5G57090	1.18	0.23	1.19	0.2758008	0.5262687	-5.84	FALSE
246143_at	lipophosphoglycan biosynthetic	---	AT5G19980	1.21	0.28	1.19	0.2757413	0.5262687	-5.84	FALSE
257945_at	SKP1/ASK1 (At10), putative sim	ASK10	AT3G21860	1.14	0.19	1.19	0.2757765	0.5262687	-5.84	FALSE
251553_at	DNA-binding WRKY - like protei	WRKY69	AT3G58710	1.18	0.24	1.19	0.2757125	0.5262687	-5.84	FALSE
245527_at	putative epoxide hydrolase	---	AT4G15955	1.19	0.25	1.19	0.2757999	0.5262687	-5.84	FALSE
266369_at	hypothetical protein predicted by	BOP2	AT2G41370	1.22	0.28	1.19	0.2756475	0.5262687	-5.84	FALSE
246486_at	putative protein ;supported by fu	---	AT5G15910	-1.15	-0.20	-1.19	0.2757102	0.5262687	-5.84	FALSE
254995_at	putative protein	---	AT4G10370	1.17	0.23	1.19	0.2758387	0.526297	-5.84	FALSE
261853_at	unknown protein	---	AT1G50660	-1.20	-0.26	-1.19	0.2759091	0.5263873	-5.84	FALSE
246862_at	E2, ubiquitin-conjugating enzym	PEX4	AT5G25760	-1.13	-0.18	-1.19	0.2759354	0.5263935	-5.84	FALSE
251624_at	hypothetical protein ;supported b	---	AT3G57280	1.18	0.24	1.19	0.2759987	0.5264701	-5.84	FALSE
259106_at	unknown protein ;supported by f	RALFL22	AT3G05490	1.38	0.47	1.19	0.2760872	0.5264829	-5.84	TRUE
254384_at	heat shock protein - like heat sh	---	AT4G21870	-1.50	-0.59	-1.19	0.2760977	0.5264829	-5.84	FALSE
257308_at	unknown protein	---	AT3G28120	1.11	0.15	1.19	0.2760515	0.5264829	-5.84	FALSE
251514_at	pirin-like protein pirin - Lycopers	---	AT3G59260	1.15	0.21	1.19	0.2760923	0.5264829	-5.84	FALSE
245148_at	putative pectinesterase ; suppor	---	AT2G45220	1.83	0.87	1.19	0.2761443	0.5265277	-5.84	TRUE
258099_at	unknown protein similar to hypot	---	AT3G23540	1.14	0.19	1.18	0.276179	0.5265483	-5.84	FALSE
257570_at	dirigent protein, putative similar	---	AT3G13662	1.14	0.18	1.18	0.2762043	0.5265483	-5.84	FALSE
265351_at	putative MADS-box protein AGL1	AGL17	AT2G22630	1.15	0.21	1.18	0.2762244	0.5265483	-5.84	FALSE
256053_at	UDP-glucose glucosyltransferas	UGT71C3	AT1G07260	-1.51	-0.59	-1.18	0.2762617	0.5265755	-5.84	FALSE
265791_at	putative transcription factor	MEE65	AT2G01280	1.17	0.22	1.18	0.2763387	0.5266782	-5.84	FALSE

267527_at	unknown protein	---	AT2G45610	-1.17	-0.22	-1.18	0.2763633	0.5266812	-5.84	FALSE
265126_s_a	hypothetical protein similar to hyp	---	AT1G55380 ///	1.15	0.20	1.18	0.2765454	0.5269842	-5.84	FALSE
255639_at	putative protein	APRR8	AT4G00760	-1.18	-0.24	-1.18	0.2766328	0.5271068	-5.84	FALSE
260499_at	unknown protein ; supported by	---	AT2G41760	-1.13	-0.17	-1.18	0.2767445	0.5272755	-5.84	FALSE
246207_at	RNA-binding like protein non-cor	---	AT4G36960	1.13	0.18	1.18	0.2767871	0.5273126	-5.84	FALSE
248517_at	St12p protein	---	AT5G50550 ///	-1.14	-0.19	-1.18	0.2769276	0.5275362	-5.84	FALSE
255963_at	unknown protein	MBD8	AT1G22310	-1.14	-0.19	-1.18	0.276961	0.5275557	-5.84	FALSE
260665_at	unknown protein ;supported by fu	---	AT1G19360	-1.15	-0.21	-1.18	0.2771662	0.5275902	-5.84	FALSE
261559_at	LIM domain protein, putative sim	---	AT1G01780	1.16	0.22	1.18	0.2772659	0.5275902	-5.84	FALSE
252186_at	putative protein	---	AT3G50810	-1.17	-0.23	-1.18	0.277326	0.5275902	-5.84	FALSE
246139_at	putative protein predicted protei	---	AT5G19900	-1.17	-0.23	-1.18	0.2772151	0.5275902	-5.84	FALSE
266655_at	putative protein kinase contains a	AtAUR2	AT2G25880	1.19	0.25	1.18	0.2772529	0.5275902	-5.84	FALSE
261072_at	hexose transporter, putative sim	ATSTP2	AT1G07340	1.17	0.23	1.18	0.2772669	0.5275902	-5.84	FALSE
248215_at	putative protein contains similarit	---	AT5G53680	1.22	0.28	1.18	0.2771446	0.5275902	-5.84	FALSE
247986_at	unknown protein	---	AT5G56880	1.17	0.23	1.18	0.2770827	0.5275902	-5.84	FALSE
263071_at	putative retroelement pol polypro	---	---	1.13	0.18	1.18	0.2771065	0.5275902	-5.84	FALSE
256764_at	hypothetical protein predicted by	---	AT3G29310	-1.18	-0.24	-1.18	0.2772054	0.5275902	-5.84	FALSE
250544_at	syntaxin-like protein syntaxin-rel	SYP132	AT5G08080	-1.18	-0.24	-1.18	0.2771555	0.5275902	-5.84	FALSE
257208_at	hypothetical protein predicted by	---	AT3G14910	-1.21	-0.28	-1.18	0.2772975	0.5275902	-5.84	FALSE
267167_at	putative C2H2-type zinc finger pr	ZFP10	AT2G37740	1.14	0.19	1.18	0.2773223	0.5275902	-5.84	FALSE
AFFX-CreX	Bacteriophage P1 /GEN=cre /DB	---	---	1.33	0.41	1.18	0.277019	0.5275902	-5.84	FALSE
256940_at	unknown protein	QQS	AT3G30720	-1.17	-0.23	-1.18	0.2772744	0.5275902	-5.84	FALSE
247352_at	serine/threonine-protein kinase ;	SNRK2.5	AT5G63650	1.41	0.50	1.18	0.2774343	0.5277522	-5.84	FALSE
253027_at	putative protein leaf protein (Pn(	---	AT4G38150	-1.25	-0.32	-1.18	0.2774711	0.5277608	-5.84	FALSE
264456_at	unknown protein similar to T cell	---	AT1G10390	-1.14	-0.19	-1.18	0.2775776	0.5277608	-5.84	FALSE
254429_at	Expressed protein ; supported by	---	AT4G21105	-1.14	-0.19	-1.18	0.2775548	0.5277608	-5.84	FALSE
253221_at	peptidylprolyl isomerase (cyclophi	ROC5	AT4G34870	-1.19	-0.25	-1.18	0.277486	0.5277608	-5.84	FALSE
256259_at	hypothetical protein predicted by	---	AT3G12460	1.19	0.26	1.18	0.2775439	0.5277608	-5.84	FALSE
251913_at	putative protein several malat de	---	AT3G53910	1.13	0.18	1.18	0.2775164	0.5277608	-5.84	FALSE
265337_at	putative ADP-ribosylation factor	TTN5	AT2G18390	-1.23	-0.29	-1.18	0.2777417	0.5280286	-5.84	FALSE
246744_at	putative protein predicted protei	---	AT5G27760	1.54	0.63	1.18	0.2779241	0.5283315	-5.85	FALSE
258836_at	hypothetical protein predicted us	---	AT3G07210	-1.21	-0.28	-1.18	0.277955	0.5283462	-5.85	TRUE
248883_at	putative protein strong similarity t	---	AT5G46190	-1.13	-0.18	-1.18	0.2781276	0.5286173	-5.85	FALSE
252089_at	putative protein	---	AT3G52110	1.21	0.27	1.18	0.278144	0.5286173	-5.85	FALSE
246859_at	putative protein various predicte	---	AT5G25950	1.14	0.19	1.18	0.2781829	0.5286472	-5.85	FALSE

267347_at	hypothetical protein predicted by	---	AT2G39950	-1.13	-0.18	-1.18	0.278304	0.5288333	-5.85	FALSE
253737_at	Expressed protein ; supported by	---	AT4G28703	1.47	0.55	1.18	0.2784444	0.529056	-5.85	FALSE
265987_at	unknown protein	---	AT2G24240	-1.23	-0.30	-1.18	0.2785755	0.5290846	-5.85	FALSE
259055_at	unknown protein ;supported by f	UNE6	AT3G03340	-1.14	-0.18	-1.18	0.2785583	0.5290846	-5.85	FALSE
246359_x_a	hypothetical protein	---	---	1.19	0.25	1.18	0.2785717	0.5290846	-5.85	FALSE
255577_at	putative hypoersensitive respons	---	AT4G01410	1.59	0.67	1.18	0.2785022	0.5290846	-5.85	FALSE
259953_at	putative anion exchanger contair	BOR5	AT1G74810	-1.21	-0.27	-1.18	0.2785253	0.5290846	-5.85	FALSE
245252_at	ethylene responsive element bin	ATERF-1	AT4G17500	1.52	0.60	1.18	0.2786056	0.5290977	-5.85	TRUE
256765_at	aminotransferase, putative simil	POP2	AT3G22200	1.19	0.25	1.18	0.2786844	0.5292034	-5.85	FALSE
263038_at	conserved hypothetical protein p	---	AT1G23270	1.13	0.18	1.18	0.2787885	0.5292725	-5.85	FALSE
257536_at	unknown protein	---	AT3G02800	1.94	0.95	1.18	0.2787466	0.5292725	-5.85	FALSE
259913_at	putative GTP-binding protein sim	---	AT1G72660	1.11	0.15	1.18	0.2787904	0.5292725	-5.85	FALSE
247425_at	unknown protein	---	AT5G62550	1.12	0.16	1.18	0.2788846	0.5293193	-5.85	FALSE
248251_at	unknown protein	---	AT5G53220	-1.13	-0.17	-1.18	0.2788725	0.5293193	-5.85	FALSE
255345_at	putative aspartic protease ; supp	---	AT4G04460	1.62	0.69	1.18	0.2788762	0.5293193	-5.85	FALSE
261610_at	hypothetical protein predicted by	---	AT1G49560	-1.25	-0.32	-1.18	0.2790235	0.5294946	-5.85	FALSE
265360_s_a	putative Athila retroelement ORF	---	---	1.14	0.19	1.18	0.2790188	0.5294946	-5.85	FALSE
263707_at	hypothetical protein Similar to gi	---	AT1G09300	-1.22	-0.29	-1.18	0.2790647	0.5295288	-5.85	FALSE
267330_at	unknown protein	---	AT2G19270	-1.10	-0.14	-1.18	0.2791311	0.5295667	-5.85	FALSE
264909_at	unknown protein	---	AT2G17300	-1.15	-0.20	-1.18	0.279114	0.5295667	-5.85	FALSE
245731_at	MAP kinase, putative similar to M	MKK9	AT1G73500	1.32	0.40	1.18	0.2792024	0.529658	-5.85	FALSE
255926_at	AP2 domain containing protein R	---	AT1G22190	1.33	0.41	1.18	0.2792749	0.5297074	-5.85	TRUE
255301_at	putative protein similar to transcr	ATMSRB3	AT4G04800	1.28	0.36	1.18	0.2792547	0.5297074	-5.85	FALSE
258244_at	unknown protein ; supported by	---	AT3G27770	-1.13	-0.18	-1.18	0.2793405	0.5297551	-5.85	FALSE
254329_at	putative protein oxysterol-bindin	ORP2A	AT4G22540	1.15	0.21	1.18	0.279393	0.5297551	-5.85	FALSE
259051_at	unknown protein similar to CGI-8	---	AT3G03330	-1.15	-0.20	-1.18	0.279381	0.5297551	-5.85	FALSE
249588_at	protein kinase - like protein Pto k	---	AT5G37790	-1.20	-0.27	-1.18	0.2793742	0.5297551	-5.85	FALSE
265402_at	hypothetical protein predicted by	---	AT2G10950	-1.14	-0.19	-1.18	0.2794229	0.5297678	-5.85	FALSE
252497_at	putative protein several putative	---	AT3G46800	-1.12	-0.16	-1.18	0.2794937	0.529858	-5.85	FALSE
246181_at	pectinesterase - like protein prob	---	AT5G20860	1.12	0.16	1.18	0.2796327	0.5299375	-5.85	FALSE
250419_at	RPP1 disease resistance protein	---	AT5G11250	1.21	0.27	1.18	0.2796512	0.5299375	-5.85	FALSE
245166_at	putative receptor-like protein kina	---	AT2G33170	1.16	0.21	1.18	0.2796518	0.5299375	-5.85	FALSE
259200_at	unknown protein similar to hypot	---	AT3G09070	1.14	0.19	1.18	0.279632	0.5299375	-5.85	FALSE
258293_at	unknown protein	PHO1	AT3G23430	1.66	0.73	1.18	0.2796108	0.5299375	-5.85	FALSE
259794_at	unknown protein	---	AT1G64330	-1.16	-0.21	-1.18	0.2797987	0.5301717	-5.85	FALSE

266287_at	putative tropinone reductase	---	AT2G29150	1.17	0.23	1.17	0.2799117	0.5303419	-5.85	FALSE
264592_at	putative prolyl 4-hydroxylase, al	---	AT2G17720	1.41	0.50	1.17	0.2799527	0.5303754	-5.85	FALSE
256601_s_a	At14a-1 protein identical to At14	AT14A	AT3G28290 /	1.13	0.18	1.17	0.28002	0.530459	-5.85	FALSE
258491_at	unknown protein ;supported by f	---	AT3G02700	1.22	0.29	1.17	0.2800459	0.5304639	-5.85	FALSE
257933_at	aminoalcoholphosphotransferas	AAPT2	AT3G25585	-1.25	-0.32	-1.17	0.2800727	0.5304707	-5.85	TRUE
266292_at	putative tropinone reductase ;su	SAG13	AT2G29350	2.36	1.24	1.17	0.2801059	0.5304895	-5.85	TRUE
257166_at	hypothetical protein similar to put	---	AT3G24710	1.14	0.19	1.17	0.2801925	0.5306026	-5.85	FALSE
252630_at	putative protein	---	AT3G44980	-1.13	-0.17	-1.17	0.2802121	0.5306026	-5.85	FALSE
249643_at	putative transposase putative tra	---	---	1.17	0.23	1.17	0.2802644	0.5306531	-5.85	FALSE
257467_at	hypothetical protein similar to hyp	LBD4	AT1G31320	-1.26	-0.33	-1.17	0.2802853	0.5306531	-5.85	FALSE
250772_at	putative protein contains similarit	---	AT5G05420	-1.23	-0.30	-1.17	0.2803279	0.5306896	-5.85	FALSE
250896_at	putative protein ; supported by c	---	AT5G03560	-1.21	-0.28	-1.17	0.2804463	0.53075	-5.85	FALSE
245505_at	glutaredoxin	---	AT4G15690	-1.43	-0.52	-1.17	0.2804471	0.53075	-5.85	FALSE
259887_at	putative protein kinase similar to	---	AT1G76360	1.15	0.20	1.17	0.2804528	0.53075	-5.85	FALSE
257377_at	unknown protein	PLL4	AT2G28890	1.33	0.41	1.17	0.2803936	0.53075	-5.85	FALSE
254513_at	cytochrome p450 like protein cyt	CYP71A27	AT4G20240	1.12	0.16	1.17	0.2804928	0.5307815	-5.85	FALSE
254912_at	respiratory burst oxidase homol	---	AT4G11230	1.14	0.19	1.17	0.2806206	0.5308912	-5.85	FALSE
258895_at	putative epoxide hydrolase simila	---	AT3G05600	1.11	0.16	1.17	0.2806138	0.5308912	-5.85	FALSE
257579_at	hypothetical protein predicted by	---	AT3G11000	1.15	0.21	1.17	0.280615	0.5308912	-5.85	FALSE
256265_at	serine carboxypeptidase, putativ	scpl16	---	1.18	0.24	1.17	0.2806647	0.5309307	-5.85	FALSE
248190_at	unknown protein	---	AT5G54130	-1.14	-0.19	-1.17	0.280779	0.5309855	-5.85	FALSE
254689_at	putative pectate lyase A11 ; sup	---	AT4G13710	1.21	0.27	1.17	0.2807584	0.5309855	-5.85	FALSE
253141_at	putative protein hypothetical pro	---	AT4G35430 /	-1.16	-0.21	-1.17	0.2808101	0.5309855	-5.85	FALSE
248539_at	ribitol dehydrogenase-like ; supp	---	AT5G50130	-1.18	-0.24	-1.17	0.2807894	0.5309855	-5.85	FALSE
264744_at	hypothetical protein predicted by	---	AT1G62050	1.27	0.35	1.17	0.2807828	0.5309855	-5.85	FALSE
266477_at	CLE4 CLAVATA3/ESR-Related 4	CLE6	AT2G31085	1.17	0.23	1.17	0.2808996	0.5309914	-5.85	FALSE
265537_at	putative retroelement pol polypro	---	---	1.16	0.22	1.17	0.2808668	0.5309914	-5.85	FALSE
259710_at	putative aminotransferase simila	---	AT1G77670	-1.42	-0.50	-1.17	0.2809063	0.5309914	-5.85	FALSE
262446_at	hypothetical protein predicted by	---	AT1G49310	-1.40	-0.49	-1.17	0.2808594	0.5309914	-5.85	FALSE
265550_at	hypothetical protein predicted by	---	---	1.14	0.19	1.17	0.2811094	0.5312871	-5.85	FALSE
265251_at	unknown protein predicted by ge	TET14	AT2G01960	1.14	0.19	1.17	0.2811008	0.5312871	-5.85	FALSE
248809_at	GTP-binding protein-like	AtRABA5a	AT5G47520	-1.16	-0.22	-1.17	0.2811562	0.5313316	-5.85	FALSE
245604_at	hypothetical protein	---	AT4G14290	-1.15	-0.21	-1.17	0.2811913	0.5313539	-5.86	FALSE
265143_at	unknown protein	NFU5	AT1G51390	-1.17	-0.22	-1.17	0.2812294	0.531382	-5.86	FALSE
248092_at	ubiquitin-like protein	SUMO3	AT5G55170	1.51	0.59	1.17	0.2813446	0.5315556	-5.86	FALSE

265481_at	unknown protein ; supported by	---	AT2G15960	-1.15	-0.20	-1.17	0.2813824	0.5315644	-5.86	FALSE
265329_at	putative succinate dehydrogenas	SDH1-2	AT2G18450	1.15	0.20	1.17	0.2814093	0.5315644	-5.86	FALSE
260709_at	hypothetical protein predicted by	ATNAP6	AT1G32500	-1.16	-0.21	-1.17	0.2814192	0.5315644	-5.86	FALSE
266851_at	similar to avrRpt2-induced protei	ATPP2-A3	AT2G26820	1.11	0.15	1.17	0.2814808	0.5316368	-5.86	FALSE
263606_at	putative beta-ketoacyl-CoA synth	KCS9	AT2G16280	1.22	0.29	1.17	0.2815283	0.531662	-5.86	TRUE
251809_at	putative protein predicted protei	---	AT3G55600	-1.15	-0.20	-1.17	0.2815408	0.531662	-5.86	FALSE
264884_at	unknown protein ;supported by fu	---	AT1G61170	1.31	0.39	1.17	0.2816061	0.5316972	-5.86	FALSE
249042_at	ethylene-regulated nuclear prote	---	AT5G44350	1.34	0.42	1.17	0.2815916	0.5316972	-5.86	FALSE
245480_at	transcription factor like protein	---	AT4G16150	-1.11	-0.15	-1.17	0.2816869	0.5318059	-5.86	FALSE
252342_at	endo-polygalacturonase - like pr	---	AT3G48950	1.10	0.14	1.17	0.2817403	0.5318626	-5.86	FALSE
246072_at	PISTILLATA ; supported by full-l	PI	AT5G20240	1.12	0.17	1.17	0.2818455	0.5320172	-5.86	FALSE
249679_at	unknown protein	---	AT5G35980	-1.10	-0.14	-1.17	0.2819398	0.5321511	-5.86	FALSE
255479_at	coded for by A. thaliana cDNA T	SAG21	AT4G02380	-1.70	-0.77	-1.17	0.282048	0.5321875	-5.86	TRUE
251394_at	endosperm specific protein - like	FLA10	AT3G60900	1.18	0.24	1.17	0.2820153	0.5321875	-5.86	FALSE
255915_at	putative protein	---	AT5G28620	1.14	0.19	1.17	0.282049	0.5321875	-5.86	FALSE
250015_at	N-acetylglucosamine-phosphate	DRT101	AT5G18070	1.29	0.37	1.17	0.2820524	0.5321875	-5.86	FALSE
262700_at	unknown protein	---	AT1G76020	1.19	0.25	1.17	0.2821335	0.5322525	-5.86	FALSE
262413_at	hypothetical protein contains sim	ATAPRL4	AT1G34780	-1.18	-0.24	-1.17	0.2821145	0.5322525	-5.86	FALSE
250073_at	unknown protein ; supported by	ENH1	AT5G17170	-1.32	-0.40	-1.17	0.2823103	0.5325421	-5.86	FALSE
256057_at	unknown protein contains similar	NDA1	AT1G07180	-1.33	-0.42	-1.17	0.2823637	0.5325987	-5.86	TRUE
261352_at	DNA repair protein RAD23, puta	RAD23	AT1G79650	1.15	0.20	1.17	0.2824109	0.5326436	-5.86	FALSE
254984_s_a	putative protein Homo sapiens c	UBP10	AT4G10570 ///	1.10	0.14	1.17	0.2825011	0.5326816	-5.86	FALSE
259120_at	unknown protein	---	AT3G02240	2.27	1.18	1.17	0.2824676	0.5326816	-5.86	FALSE
248903_at	3-oxoacyl-[acyl-carrier-protein] sy	KAS I	AT5G46290	-1.27	-0.35	-1.17	0.2824868	0.5326816	-5.86	FALSE
252164_at	hypothetical protein nodH - Rhiz	---	AT3G50620	1.33	0.41	1.17	0.2825588	0.5327023	-5.86	FALSE
255373_s_a	putative protein	---	---	1.15	0.21	1.17	0.2825515	0.5327023	-5.86	FALSE
260317_at	E2, ubiquitin-conjugating enzym	UBC5	AT1G63800	-1.25	-0.32	-1.17	0.2825913	0.5327197	-5.86	FALSE
263579_at	hypothetical protein similar to hyp	---	AT2G17030	-1.20	-0.26	-1.17	0.2826203	0.5327303	-5.86	FALSE
248120_at	putative protein similar to unknov	---	AT5G54540	-1.15	-0.21	-1.17	0.2826611	0.5327631	-5.86	FALSE
247806_at	ABC transporter-like protein ; sup	STA1	AT5G58270	-1.13	-0.18	-1.17	0.2826963	0.5327855	-5.86	FALSE
261497_x_a	hypothetical protein contains sim	AGL59	AT1G28460	-1.15	-0.20	-1.17	0.2827289	0.5328029	-5.86	FALSE
260603_at	membrane related protein CP5,	---	AT1G55960	1.23	0.29	1.17	0.2827771	0.5328497	-5.86	FALSE
251729_at	alpha-galactosidase-like protein	---	AT3G56310	1.27	0.35	1.17	0.2828746	0.5329894	-5.86	FALSE
263880_at	unknown protein ;supported by f	---	AT2G21960	-1.20	-0.27	-1.17	0.2829215	0.5329897	-5.86	FALSE
250514_at	GDP dissociation inhibitor GDP	---	AT5G09550	1.13	0.17	1.17	0.2829206	0.5329897	-5.86	FALSE

247313_at	3(2),5-bisphosphate nucleotidas	SAL1	AT5G63980	1.21	0.28	1.17	0.2829535	0.5330061	-5.86	FALSE
251211_s_a	putative protein several hypothet	---	AT3G62470 ///	-1.32	-0.41	-1.17	0.2830304	0.5330627	-5.86	FALSE
256719_at	En/Spm-like transposon protein r	---	---	1.13	0.18	1.17	0.2830194	0.5330627	-5.86	FALSE
250916_at	monodehydroascorbate reducta	ATMDAR2	AT5G03630	1.51	0.60	1.17	0.2831173	0.5331385	-5.86	TRUE
246438_at	putative protein non-phototropic	---	AT5G17580	-1.11	-0.15	-1.17	0.2831141	0.5331385	-5.86	FALSE
263025_at	reverse transcriptase, putative s	---	---	-1.14	-0.19	-1.17	0.2831943	0.5332393	-5.86	FALSE
261866_at	scarecrow-like 3 identical to GB:	SCL3	AT1G50420	-1.69	-0.76	-1.17	0.2833321	0.5334548	-5.86	FALSE
249351_at	MAP kinase kinase 3 (ATMKK3)	ATMKK3	AT5G40440	-1.15	-0.20	-1.17	0.2833768	0.5334949	-5.86	FALSE
255423_at	putative calmodulin	---	AT4G03290	1.13	0.18	1.17	0.2834052	0.5335043	-5.86	FALSE
266483_at	unknown protein ;supported by f	CRR6	AT2G47910	-1.17	-0.22	-1.17	0.2834433	0.5335321	-5.86	FALSE
257030_at	unknown protein	---	---	1.13	0.18	1.17	0.283614	0.5338093	-5.86	FALSE
266877_at	putative glucanase	AtGH9B12	AT2G44570	1.14	0.19	1.16	0.2836786	0.5338538	-5.86	FALSE
256821_at	hypothetical protein predicted by	---	AT3G22180	1.22	0.29	1.16	0.2836975	0.5338538	-5.86	FALSE
256907_at	hydoxyethylthiazole kinase, puta	---	AT3G24030	-1.22	-0.29	-1.16	0.2837131	0.5338538	-5.86	FALSE
247544_at	putative protein ;supported by fu	---	AT5G61670	1.20	0.27	1.16	0.2837313	0.5338538	-5.86	FALSE
250099_at	unknown protein ; supported by	---	AT5G17300	1.18	0.23	1.16	0.2838108	0.5339594	-5.86	FALSE
257602_at	hydrolase, putative similar to Me	---	AT3G13800	-1.14	-0.19	-1.16	0.2838422	0.5339685	-5.86	FALSE
253157_at	putative protein DNA helicase T	RecQl3	AT4G35740	-1.17	-0.22	-1.16	0.2838624	0.5339685	-5.86	FALSE
252622_at	cysteine proteinase AALP, putat	---	AT3G45310	-1.15	-0.21	-1.16	0.2840916	0.5342296	-5.86	FALSE
256227_at	unknown protein ; supported by	---	AT1G56290	-1.12	-0.17	-1.16	0.2841652	0.5342296	-5.86	FALSE
245437_at	RNA helicase like protein	---	AT4G16630	-1.22	-0.29	-1.16	0.284055	0.5342296	-5.86	FALSE
263643_at	unknown protein predicted by ge	---	AT2G04740	-1.22	-0.29	-1.16	0.2841263	0.5342296	-5.86	FALSE
254405_at	putative protein arm repeat cont	PUB8	AT4G21350	-1.22	-0.29	-1.16	0.2841514	0.5342296	-5.86	FALSE
261095_at	unknown protein	---	AT1G62930	-1.16	-0.21	-1.16	0.2841256	0.5342296	-5.86	FALSE
267432_at	putative UDP-N-acetylglucosami	---	AT2G35020	-1.24	-0.31	-1.16	0.2841506	0.5342296	-5.86	FALSE
255665_at	hypothetical protein	CRP	AT4G00450	-1.13	-0.17	-1.16	0.2842308	0.5343089	-5.86	FALSE
254257_s_a	putative protein predicted protei	---	AT4G23350 ///	-1.13	-0.18	-1.16	0.2842983	0.5343917	-5.86	FALSE
265246_at	putative pectinesterase	ATPMEPCI	AT2G43050	1.17	0.22	1.16	0.2843966	0.5344059	-5.86	FALSE
246351_at	unknown protein contains simila	---	AT1G16570	-1.13	-0.18	-1.16	0.2843846	0.5344059	-5.86	FALSE
251933_at	putative protein mucin MUC3, H	---	AT3G54060	1.17	0.23	1.16	0.2844393	0.5344059	-5.86	FALSE
255909_at	cdc2+/CDC28-related protein kir	CDKD1;3	AT1G18040	1.24	0.31	1.16	0.2844	0.5344059	-5.86	FALSE
262281_at	peptide transporter, putative sim	---	AT1G68570	-1.41	-0.50	-1.16	0.284425	0.5344059	-5.86	FALSE
267413_at	putative amino acid transporter	CAT5	AT2G34960	1.24	0.31	1.16	0.2844464	0.5344059	-5.86	FALSE
255190_x_a	may be a pseudogene similar to	---	---	1.11	0.15	1.16	0.2845374	0.5344449	-5.86	FALSE
249592_at	putative protein SIAH1 protein, E	---	AT5G37890	-1.17	-0.22	-1.16	0.2845182	0.5344449	-5.86	FALSE

264500_at	hypothetical protein predicted by	---	AT1G09370	1.11	0.15	1.16	0.284534	0.5344449	-5.86	FALSE
255865_at	unknown protein	---	AT2G30330	-1.11	-0.15	-1.16	0.2846347	0.5345836	-5.86	FALSE
255170_at	hypothetical protein similar to A.	---	---	1.13	0.18	1.16	0.284764	0.5347824	-5.87	FALSE
261563_at	polyphosphoinositide binding pr	---	AT1G01630	1.16	0.21	1.16	0.2848503	0.5348564	-5.87	TRUE
266159_at	putative chloroplast nucleoid DN	---	AT2G28030	1.12	0.16	1.16	0.2848453	0.5348564	-5.87	FALSE
256036_at	fructose-2,6-bisphosphatase, pu	F2KP	AT1G07110	-1.14	-0.19	-1.16	0.2848883	0.5348836	-5.87	FALSE
251603_at	putative protein wall-associated	---	AT3G57760	1.40	0.48	1.16	0.2850021	0.5350533	-5.87	FALSE
267370_at	unknown protein ;supported by f	---	AT2G44525	-1.11	-0.15	-1.16	0.2850421	0.5350844	-5.87	FALSE
250564_at	putative protein sigma factor F ir	---	AT5G08060	-1.11	-0.15	-1.16	0.2851132	0.5351298	-5.87	FALSE
265892_at	hypothetical protein predicted by	---	AT2G15020	1.28	0.36	1.16	0.2850964	0.5351298	-5.87	FALSE
264947_at	heat shock protein DnaJ, putativ	---	AT1G77020	1.18	0.24	1.16	0.2852088	0.5352651	-5.87	FALSE
263207_at	putative endoxyloglucan transfer	XTH33	AT1G10550	-1.72	-0.78	-1.16	0.2854911	0.5355971	-5.87	TRUE
248012_at	putative protein strong similarity t	---	AT5G56310	-1.18	-0.24	-1.16	0.2854093	0.5355971	-5.87	FALSE
252544_at	respiratory burst oxidase - like p	---	AT3G45810	1.17	0.22	1.16	0.2855031	0.5355971	-5.87	FALSE
256903_at	hypothetical protein	---	AT3G23960	1.14	0.19	1.16	0.2854834	0.5355971	-5.87	FALSE
262481_at	unknown protein Location of est	---	AT1G17080	1.15	0.20	1.16	0.2854959	0.5355971	-5.87	FALSE
265936_at	putative potassium/proton antipo	ATKEA4	AT2G19600	1.17	0.22	1.16	0.2855586	0.5356572	-5.87	FALSE
259234_at	unknown protein similar to unkno	---	AT3G11620	1.15	0.20	1.16	0.2857863	0.5358359	-5.87	FALSE
262797_at	putative sugar transporter protei	TMT1	AT1G20840	1.26	0.34	1.16	0.285792	0.5358359	-5.87	FALSE
261217_at	hypothetical protein contains sim	UBP11	AT1G32850	1.11	0.16	1.16	0.2857445	0.5358359	-5.87	FALSE
260255_at	putative protein kinase similar to	---	AT1G74330	1.27	0.35	1.16	0.2858164	0.5358359	-5.87	FALSE
247512_at	putative protein predicted protei	---	AT5G61720	1.12	0.16	1.16	0.2858183	0.5358359	-5.87	FALSE
263022_s_a	gamma-adaptin, putative similar	---	AT1G23900 /	1.20	0.26	1.16	0.2857307	0.5358359	-5.87	FALSE
256780_at	RNase L inhibitor, putative simila	ATRLI1	AT3G13640	-1.14	-0.19	-1.16	0.2856834	0.5358359	-5.87	FALSE
252135_at	putative cold acclimation protein	COR413-PI	AT3G50830	-1.20	-0.27	-1.16	0.2858757	0.5358553	-5.87	FALSE
252125_at	putative protein hypothetical pro	RTH	AT3G51040	-1.14	-0.19	-1.16	0.2858596	0.5358553	-5.87	FALSE
256939_at	multicatalytic endopeptidase cor	PBD1	AT3G22630	-1.21	-0.27	-1.16	0.2860196	0.5360696	-5.87	FALSE
257908_at	unknown protein contains Pfam p	---	AT3G25410	-1.15	-0.21	-1.16	0.286037	0.5360696	-5.87	FALSE
247405_at	Arac10 ; supported by cDNA: gi_	ARAC10	AT5G62880	-1.15	-0.20	-1.16	0.2861259	0.5361922	-5.87	FALSE
247264_at	putative protein contains similarit	XND1	AT5G64530	1.37	0.45	1.16	0.2862418	0.5363654	-5.87	FALSE
261733_at	clathrin coat assembly protein A	---	AT1G47830	-1.12	-0.16	-1.16	0.2863872	0.5365938	-5.87	FALSE
255275_at	putative protein various ubiquitin	---	AT4G05310	1.10	0.14	1.16	0.2865377	0.5367435	-5.87	FALSE
258961_at	hypothetical protein similar to m	---	AT3G10580	-1.11	-0.15	-1.16	0.2865187	0.5367435	-5.87	FALSE
259069_at	lysyl-tRNA synthetase identical t	ATKRS-1	AT3G11710	-1.18	-0.23	-1.16	0.286516	0.5367435	-5.87	FALSE
253240_at	putative ketoacyl-CoA synthase	KCS17	AT4G34510	1.12	0.16	1.16	0.2866274	0.5368233	-5.87	FALSE

250331_at	putative protein self-incompatibil	---	AT5G11820	1.15	0.20	1.16	0.2866178	0.5368233	-5.87	FALSE
260476_at	unknown protein	---	AT1G11060	1.18	0.24	1.16	0.286698	0.5368674	-5.87	FALSE
264502_at	putative 12-oxophytodienoate re	---	AT1G09400	1.17	0.23	1.16	0.2866779	0.5368674	-5.87	FALSE
258410_at	putative ribosomal protein similar	---	AT3G16780	-1.38	-0.46	-1.16	0.286753	0.5368919	-5.87	FALSE
264565_at	hypothetical protein Similar to hy	---	AT1G05280	1.18	0.24	1.16	0.2867582	0.5368919	-5.87	FALSE
251918_at	photoassimilate-responsive prot	---	AT3G54040	1.13	0.17	1.16	0.2868416	0.53696	-5.87	FALSE
263487_at	hypothetical protein predicted by	---	AT2G31850	1.13	0.17	1.16	0.2868347	0.53696	-5.87	FALSE
262371_at	putative glycosyl transferase con	---	AT1G73160	1.12	0.17	1.16	0.2869356	0.5370478	-5.87	FALSE
255958_at	high affinity sulphate transporter	SULTR1;3	AT1G22150	-1.17	-0.22	-1.16	0.2869199	0.5370478	-5.87	FALSE
249207_at	C2H2-type zinc finger protein-like	---	AT5G42640	1.14	0.19	1.16	0.2870001	0.5370859	-5.87	FALSE
254914_at	peroxidase ATP19a	---	AT4G11290	1.82	0.86	1.16	0.287003	0.5370859	-5.87	FALSE
247807_at	similar to unknown protein (gb|A	OFP3	AT5G58360	-1.16	-0.21	-1.16	0.2870448	0.53712	-5.87	FALSE
261175_at	unknown protein	---	AT1G04800	1.14	0.19	1.16	0.2873695	0.537395	-5.87	FALSE
257102_at	endoxyloglucan transferase, put	XTH3	AT3G25050	1.11	0.15	1.16	0.2872869	0.537395	-5.87	FALSE
265902_at	hypothetical protein predicted by	---	AT2G25590	1.14	0.19	1.16	0.2872291	0.537395	-5.87	FALSE
251222_at	putative membrane protein clone	---	AT3G62580	1.25	0.32	1.16	0.2872406	0.537395	-5.87	FALSE
249373_at	putative protein vanilloid recepto	---	AT5G40670	1.15	0.20	1.16	0.2874274	0.537395	-5.87	FALSE
264093_at	hypothetical protein predicted by	---	AT1G79220	-1.14	-0.18	-1.16	0.2874183	0.537395	-5.87	FALSE
249744_at	beta-glucosidase	BGLU32	AT5G24550	1.19	0.25	1.16	0.2873331	0.537395	-5.87	FALSE
252720_at	putative protein predicted protein	---	AT3G43970	-1.16	-0.22	-1.16	0.2872892	0.537395	-5.87	FALSE
254793_at	hypothetical protein	---	AT4G12930	1.14	0.19	1.16	0.2874138	0.537395	-5.87	FALSE
260253_at	disease resistance protein, puta	AtRLP15	AT1G74190	1.12	0.16	1.16	0.2873822	0.537395	-5.87	FALSE
257538_at	hypothetical protein predicted by	---	AT3G16160	1.12	0.16	1.15	0.2874659	0.5374229	-5.87	FALSE
256329_at	unknown protein	SEC5A	AT1G76850	1.11	0.15	1.15	0.2875415	0.5375203	-5.87	FALSE
258330_at	unknown protein	ROPGEF13	AT3G16130	1.15	0.20	1.15	0.2875925	0.5375715	-5.87	FALSE
256822_at	unknown protein contains PF006	IQD5	AT3G22190	-1.16	-0.21	-1.15	0.2877329	0.5377458	-5.87	FALSE
261874_at	ethylene responsive element bin	ERF3	AT1G50640	1.17	0.23	1.15	0.2877185	0.5377458	-5.87	FALSE
254953_at	Expressed protein ; supported by	---	AT4G10925	-1.14	-0.19	-1.15	0.2878353	0.5378931	-5.87	FALSE
264231_at	hypothetical protein similar to hyp	---	AT1G67450	1.11	0.15	1.15	0.2878917	0.5379545	-5.87	FALSE
267478_at	hypothetical protein predicted by	---	AT2G02700	1.11	0.16	1.15	0.2879613	0.5380404	-5.87	FALSE
262289_at	unknown protein identical to unkn	---	AT1G70770	1.12	0.17	1.15	0.2880389	0.5381414	-5.87	FALSE
265929_s_a	putative flavonol 3-O-glucosyltran	---	AT2G18560 //	-1.26	-0.34	-1.15	0.2880846	0.5381827	-5.87	FALSE
261038_at	unknown protein ; supported by f	---	AT1G17490	-1.17	-0.23	-1.15	0.2881303	0.538224	-5.87	FALSE
263657_at	putative casein kinase I similar to	CKL13	AT1G04440	1.28	0.35	1.15	0.2881922	0.5382954	-5.88	FALSE
267120_at	hypothetical protein predicted by	---	AT2G23530	-1.16	-0.22	-1.15	0.2882646	0.5383866	-5.88	FALSE

265207_at	unknown protein	---	AT2G36680	1.12	0.17	1.15	0.288317	0.5383963	-5.88	FALSE
254206_at	thaumatin-like protein thaumatin	---	AT4G24180	-1.16	-0.21	-1.15	0.2883152	0.5383963	-5.88	FALSE
253840_at	putative acyl-CoA binding protei	ACBP2	AT4G27780	1.18	0.24	1.15	0.2883621	0.5384364	-5.88	FALSE
248051_at	Atmyb103 (gb|AAD40692.1)	ATMYB103	AT5G56110	1.14	0.19	1.15	0.2884045	0.5384521	-5.88	FALSE
256580_s_a	hypothetical protein	---	AT3G28810 /	1.12	0.16	1.15	0.2884177	0.5384521	-5.88	FALSE
265099_at	unknown protein Location of ES	---	AT1G03990	1.40	0.49	1.15	0.2884596	0.5384863	-5.88	FALSE
250457_at	splicing factor-like protein ; supp	---	AT5G09880	-1.15	-0.20	-1.15	0.2886801	0.538795	-5.88	FALSE
251707_at	protein kinase C inhibitor-like pr	---	AT3G56490	-1.15	-0.20	-1.15	0.2886615	0.538795	-5.88	FALSE
252884_at	SEC14 - like protein phosphatidy	---	AT4G39170	-1.16	-0.22	-1.15	0.2886958	0.538795	-5.88	FALSE
259892_at	germin-like protein similar to gerr	GER1	AT1G72610	1.80	0.85	1.15	0.2887833	0.5388036	-5.88	TRUE
262782_at	Expressed protein ; supported by	---	AT1G13195	1.13	0.17	1.15	0.2887718	0.5388036	-5.88	FALSE
252765_at	putative protein hypothetical prot	---	AT3G42800	1.28	0.35	1.15	0.288795	0.5388036	-5.88	FALSE
257521_at	hypothetical protein predicted by	---	AT3G09140	1.12	0.16	1.15	0.2887839	0.5388036	-5.88	FALSE
264765_at	receptor kinase, putative similar	---	AT1G61430	1.15	0.21	1.15	0.2888257	0.538817	-5.88	FALSE
255171_at	hypothetical protein	---	AT4G07990	1.13	0.17	1.15	0.288933	0.5389288	-5.88	FALSE
248066_at	putative protein contains similarit	QRT1	AT5G55590	1.15	0.20	1.15	0.288926	0.5389288	-5.88	FALSE
247069_at	pectinesterase like protein ;supp	sks17	AT5G66920	-1.39	-0.48	-1.15	0.2890269	0.5389719	-5.88	TRUE
259083_at	putative kinase similar to NIMA-r	ATNEK2	AT3G04810	-1.13	-0.18	-1.15	0.2890201	0.5389719	-5.88	FALSE
247867_at	SNF1 related protein kinase-like	CIPK21	AT5G57630	1.25	0.32	1.15	0.2890016	0.5389719	-5.88	FALSE
261395_at	unknown protein similar to putati	---	AT1G79700	1.38	0.46	1.15	0.2891944	0.5391989	-5.88	TRUE
261737_at	hypothetical protein similar to put	---	AT1G47885	-1.16	-0.21	-1.15	0.2892196	0.5391989	-5.88	FALSE
250652_at	putative protein similar to unknov	FLA21	AT5G06920	1.13	0.18	1.15	0.2892111	0.5391989	-5.88	FALSE
266537_at	Expressed protein ; supported by	---	AT2G16860	-1.14	-0.19	-1.15	0.2892891	0.5392844	-5.88	FALSE
260201_at	F12A21.27 hypothetical protein;s	---	AT1G67600	-1.31	-0.39	-1.15	0.2893364	0.5392845	-5.88	TRUE
262969_at	unknown protein	---	AT1G75710	-1.20	-0.26	-1.15	0.2893149	0.5392845	-5.88	FALSE
261356_at	predicted protein	---	AT1G79660	-1.21	-0.27	-1.15	0.2893818	0.5393249	-5.88	TRUE
249281_at	GTPase activator protein of Rab-	---	AT2G36460 /	1.14	0.19	1.15	0.2894795	0.539463	-5.88	FALSE
250600_at	dimethylaniline monooxygenase-	---	AT5G07800	1.13	0.18	1.15	0.2895318	0.5394952	-5.88	FALSE
249805_at	putative protein similar to unknov	---	AT5G23800	1.13	0.18	1.15	0.2895441	0.5394952	-5.88	FALSE
261463_at	hypothetical protein predicted by	---	AT1G07730 /	-1.12	-0.16	-1.15	0.2895727	0.5395045	-5.88	FALSE
244959_s_a	hypothetical protein	---	AT2G07708	-1.19	-0.25	-1.15	0.2896922	0.539683	-5.88	FALSE
260744_at	hypothetical protein predicted by	---	AT1G15010	1.79	0.84	1.15	0.2897323	0.5397136	-5.88	TRUE
255945_at	putative protein	---	AT5G28610	1.18	0.23	1.15	0.2897943	0.5397851	-5.88	FALSE
248908_at	receptor kinase-like protein	MEE62	AT5G45800	1.46	0.55	1.15	0.2899505	0.5399664	-5.88	TRUE
251042_at	eceriferum3 (CER3)	PRT6	AT5G02310	-1.13	-0.17	-1.15	0.2899627	0.5399664	-5.88	FALSE

266584_s_a	putative steroid sulfotransferase	ST4C	AT1G13430 ///	-1.10	-0.14	-1.15	0.2899543	0.5399664	-5.88	FALSE
264269_at	hypothetical protein predicted by	---	AT1G60240	1.17	0.22	1.15	0.2900709	0.5400358	-5.88	FALSE
248089_at	salt stress inducible small GTP b	AtRAN4	AT5G55080	1.15	0.20	1.15	0.2900499	0.5400358	-5.88	FALSE
245835_at	hypothetical protein similar to put	---	AT1G42190	1.13	0.17	1.15	0.2900493	0.5400358	-5.88	FALSE
247498_at	peroxisomal Ca-dependent solu	---	AT5G61810	1.18	0.24	1.15	0.2901829	0.540106	-5.88	FALSE
248686_at	33 kDa secretory protein-like ; s	---	AT5G48540	1.57	0.65	1.15	0.2902489	0.540106	-5.88	FALSE
265108_s_a	similar to flavin-binding monooxy	---	AT1G62620 ///	1.17	0.23	1.15	0.290233	0.540106	-5.88	FALSE
256968_at	unknown protein	NADK1	AT3G21070	1.87	0.90	1.15	0.2901771	0.540106	-5.88	FALSE
258279_at	putative self-incompatibility prote	---	AT3G26870	-1.10	-0.14	-1.15	0.2901937	0.540106	-5.88	FALSE
248570_at	receptor protein kinase-like	---	AT5G49780	1.13	0.17	1.15	0.2902508	0.540106	-5.88	FALSE
248451_at	putative protein similar to unknov	---	AT5G51180	-1.11	-0.15	-1.15	0.2903303	0.54021	-5.88	FALSE
246871_at	extensin - like protein pAP8 prot	---	AT5G26070	1.12	0.16	1.15	0.2903763	0.5402516	-5.88	FALSE
264699_at	unknown protein ;supported by fu	---	AT1G69980 ///	-1.11	-0.15	-1.15	0.2905199	0.5404578	-5.88	FALSE
262383_at	disease resistance protein, puta	---	AT1G72940	1.88	0.91	1.15	0.2905346	0.5404578	-5.88	FALSE
249056_at	putative protein similar to unknov	---	AT5G44470	1.13	0.17	1.15	0.2907381	0.5407923	-5.88	FALSE
255528_at	hypothetical protein	---	AT4G02090	1.12	0.17	1.15	0.2907625	0.5407936	-5.88	FALSE
245859_at	serine (threonine) protein kinase	ATNEK3	AT5G28290	1.23	0.30	1.15	0.2908385	0.5408468	-5.88	TRUE
247046_at	unknown protein ; supported by	---	AT5G66540	-1.15	-0.20	-1.15	0.290816	0.5408468	-5.88	FALSE
267212_at	similar to late embryogenesis ab	---	AT2G44060	-1.12	-0.17	-1.15	0.2910458	0.5410494	-5.88	TRUE
248871_at	putative protein strong similarity t	---	AT5G46680	-1.15	-0.20	-1.15	0.2910563	0.5410494	-5.88	FALSE
263174_at	jasmonate inducible protein, put	ESP	AT1G54040	1.42	0.50	1.15	0.2910661	0.5410494	-5.88	FALSE
258348_at	unknown protein ;supported by f	---	AT3G17710	1.14	0.19	1.15	0.2910548	0.5410494	-5.88	FALSE
245724_at	hypothetical protein predicted by	---	AT1G73390	1.24	0.31	1.15	0.2909824	0.5410494	-5.88	FALSE
251639_at	acetylglutamate kinase-like prote	---	AT3G57560	-1.18	-0.23	-1.15	0.2911799	0.5410544	-5.88	FALSE
248009_at	transcription factor-like; similar to	CSN6A	AT5G56280	-1.14	-0.18	-1.15	0.2911469	0.5410544	-5.88	FALSE
250313_at	Rab geranylgeranyltransferase,	---	AT5G12210	-1.17	-0.23	-1.15	0.2911422	0.5410544	-5.88	FALSE
262404_at	transposon-like ORF, putative si	---	---	1.14	0.18	1.15	0.2912087	0.5410544	-5.88	FALSE
257778_at	hypothetical protein predicted by	---	---	1.15	0.20	1.15	0.2912111	0.5410544	-5.88	FALSE
250681_at	unknown protein	---	AT5G06590	-1.12	-0.16	-1.15	0.2911844	0.5410544	-5.88	FALSE
265103_at	UDP-N-acetylglucosamine pyrop	---	AT1G31070	-1.18	-0.23	-1.15	0.291249	0.5410807	-5.88	FALSE
260521_at	putative villin 2	VLN2	AT2G41740	1.22	0.29	1.14	0.2912982	0.5411281	-5.88	FALSE
263717_at	malate oxidoreductase (malic en	---	AT2G13560	1.11	0.15	1.14	0.2913613	0.5412013	-5.88	FALSE
250888_at	putative protein trichohyalin, Ory	---	AT5G04460	1.23	0.29	1.14	0.291462	0.5413443	-5.88	FALSE
263223_at	coatomer-like protein, epsilon su	---	AT1G30630	1.15	0.21	1.14	0.2914998	0.5413704	-5.88	FALSE
264690_at	hypothetical protein similar to hy	SNL4	AT1G70060	1.18	0.23	1.14	0.2915526	0.5413948	-5.88	FALSE

265307_at	hypothetical protein predicted by	RIN13	AT2G20310	-1.15	-0.21	-1.14	0.2916074	0.5413948	-5.88	FALSE
261764_at	receptor lectin kinase, putative s	---	AT1G15530	1.15	0.21	1.14	0.2916069	0.5413948	-5.88	FALSE
254295_at	putative protein predicted protei	---	AT4G23080	1.11	0.15	1.14	0.2916079	0.5413948	-5.88	FALSE
266214_at	putative retroelement integrase	---	---	1.11	0.15	1.14	0.2916602	0.5414479	-5.88	FALSE
247710_at	receptor-like protein kinase rece	---	AT5G59260	1.11	0.15	1.14	0.2917055	0.5414878	-5.88	FALSE
260773_at	gibberellin 2- oxidase identical to	ATGA2OX1	AT1G78440	1.16	0.21	1.14	0.2917531	0.5415322	-5.89	FALSE
251428_at	beta-glucosidase-like protein sev	DIN2	AT3G60140	2.45	1.29	1.14	0.2918998	0.5415516	-5.89	TRUE
250572_at	putative protein	MIR834A	---	-1.19	-0.25	-1.14	0.2919373	0.5415516	-5.89	FALSE
253934_at	putative beta-1,3-glucanase beta	---	AT4G26830	1.13	0.17	1.14	0.2919099	0.5415516	-5.89	FALSE
246939_at	AP2 domain containing protein A	SHN2	AT5G25390	1.14	0.19	1.14	0.2918128	0.5415516	-5.89	FALSE
250115_at	salt-inducible protein-like	---	AT5G16420	-1.21	-0.28	-1.14	0.2919266	0.5415516	-5.89	FALSE
267414_at	putative berberine bridge enzyme	MEE23	AT2G34790	1.25	0.33	1.14	0.2918192	0.5415516	-5.89	FALSE
253214_at	putative protein karyopherin alph	ARO1	AT4G34940	-1.12	-0.17	-1.14	0.2919535	0.5415516	-5.89	FALSE
251687_at	quinone reductase-like protein z	---	AT3G56460	-1.12	-0.17	-1.14	0.2919028	0.5415516	-5.89	FALSE
260996_at	NBS/LRR disease resistance pro	RFL1	AT1G12210	1.19	0.25	1.14	0.2922342	0.5416758	-5.89	FALSE
253789_at	putative protein predicted protei	---	AT4G28570	1.17	0.23	1.14	0.2922156	0.5416758	-5.89	FALSE
246094_at	putative protein predicted protei	---	AT5G19300	-1.24	-0.31	-1.14	0.2921126	0.5416758	-5.89	FALSE
247977_at	putative protein similar to unknov	---	AT5G56850	-1.20	-0.26	-1.14	0.2921229	0.5416758	-5.89	FALSE
248897_at	KCO-like protein 3 (emb|CAB403	KCO3	AT5G46360	1.15	0.20	1.14	0.2921014	0.5416758	-5.89	FALSE
262657_at	ribonuclease contains similarity t	---	AT1G14210	-1.36	-0.45	-1.14	0.2922076	0.5416758	-5.89	FALSE
250488_at	beta-glucosidase - like protein b	---	AT5G09700	1.14	0.18	1.14	0.2921578	0.5416758	-5.89	FALSE
254530_at	small GTP-binding protein - like	ARA7	AT4G19640	1.12	0.17	1.14	0.2922271	0.5416758	-5.89	FALSE
249384_at	putative protein hypothetical pro	---	AT5G39890	1.12	0.16	1.14	0.2921583	0.5416758	-5.89	FALSE
250930_at	putative protein P58 protein, Bos	ATP58IPK	AT5G03160	1.33	0.41	1.14	0.2922588	0.5416774	-5.89	FALSE
253226_at	beta-galactosidase - like protein	BGAL11	AT4G35010	-1.13	-0.17	-1.14	0.2923427	0.5417889	-5.89	FALSE
249803_at	putative protein similar to unknov	---	AT5G23780	1.14	0.19	1.14	0.2924779	0.5419954	-5.89	FALSE
264489_at	putative squamosa-promoter bin	---	AT1G27370	-1.30	-0.37	-1.14	0.2925026	0.5419971	-5.89	FALSE
247480_at	KED - like protein KED, Nicotian	ATBAG7	AT5G62390	1.18	0.24	1.14	0.2926022	0.5421377	-5.89	TRUE
259598_at	sphingosine-1-phosphate lyase,	DPL1	AT1G27980	-1.16	-0.22	-1.14	0.2926352	0.5421547	-5.89	TRUE
247659_at	DNA-directed RNA polymerase	NRPC1	AT5G60040	-1.37	-0.45	-1.14	0.2927736	0.542279	-5.89	TRUE
254284_at	putative fizzy-related protein fizz	FZR2	AT4G22910	1.21	0.28	1.14	0.2927282	0.542279	-5.89	FALSE
254283_s_a	anthocyanidin synthase - like pro	---	AT4G22870 /.	1.18	0.24	1.14	0.2927662	0.542279	-5.89	FALSE
248708_at	putative protein contains similarit	---	AT5G48560	-1.33	-0.41	-1.14	0.2929022	0.542429	-5.89	FALSE
258024_at	hypothetical protein predicted by	---	AT3G19360	-1.28	-0.36	-1.14	0.2928957	0.542429	-5.89	FALSE
252375_at	rac GTP binding protein Arac8 ;	ROP10	AT3G48040	-1.15	-0.20	-1.14	0.2930977	0.5426942	-5.89	FALSE

244921_s_a	hypothetical protein	---	AT2G07674 /.	-1.21	-0.28	-1.14	0.2931167	0.5426942	-5.89	FALSE
255841_at	putative tyrosine-specific transpo	---	AT2G33260	1.20	0.27	1.14	0.2931163	0.5426942	-5.89	FALSE
265177_at	OBP32pep protein, putative ider	---	AT1G23640	1.12	0.17	1.14	0.2931726	0.5427535	-5.89	FALSE
256582_at	unknown protein	---	AT3G28840	1.13	0.18	1.14	0.2932244	0.5428054	-5.89	FALSE
251684_at	putative protein	---	AT3G56410	1.25	0.32	1.14	0.2932745	0.54281	-5.89	FALSE
246687_at	putative protein proline-rich prote	---	AT5G33370	1.18	0.24	1.14	0.2932536	0.54281	-5.89	FALSE
267085_at	putative cellulose synthase	ATCSLB02	AT2G32620	-1.11	-0.15	-1.14	0.2933038	0.5428202	-5.89	FALSE
262239_at	unknown protein similar to putati	---	AT1G48230	-1.21	-0.28	-1.14	0.2933443	0.5428511	-5.89	FALSE
245087_at	hypothetical protein predicted by	DAR2	AT2G39830	1.21	0.28	1.14	0.2933993	0.542909	-5.89	FALSE
256970_at	ABC transporter, putative simila	---	AT3G21090	1.15	0.20	1.14	0.2934399	0.54294	-5.89	FALSE
266988_at	putative myrosinase-binding prot	JAL22	AT2G39310	1.23	0.29	1.14	0.2934909	0.5429903	-5.89	FALSE
264077_at	putative RAD51B-like DNA repai	RAD51B	AT2G28560	1.13	0.18	1.14	0.293546	0.5430482	-5.89	FALSE
261671_at	hypothetical protein similar to hyp	---	AT1G18340	-1.24	-0.31	-1.14	0.2936703	0.543234	-5.89	FALSE
253811_at	hypothetical protein ;supported b	ULT1	AT4G28190	-1.30	-0.38	-1.14	0.2937041	0.5432412	-5.89	TRUE
265566_at	hypothetical protein predicted by	---	AT2G05600	1.15	0.20	1.14	0.2937218	0.5432412	-5.89	FALSE
265542_at	putative SNF2 subfamily transcri	SYD	AT2G28290	-1.12	-0.16	-1.14	0.2937866	0.5433171	-5.89	FALSE
259071_at	unknown protein similar to hin1 C	NHL2	AT3G11650	1.24	0.32	1.14	0.2938821	0.5433504	-5.89	FALSE
253560_at	putative protein KIAA0800 prote	DCAF1	AT4G31160	-1.15	-0.20	-1.14	0.2938361	0.5433504	-5.89	FALSE
251069_at	(1-4)-beta-mannan endohydrola	---	AT5G01930	-1.33	-0.42	-1.14	0.2939058	0.5433504	-5.89	FALSE
245114_at	transcription factor IIB (TFIIB) ide	TFIIB	AT2G41630	-1.25	-0.32	-1.14	0.2938592	0.5433504	-5.89	FALSE
247109_at	putative protein similar to unknov	ATPSK5	AT5G65870	1.32	0.40	1.14	0.2939463	0.5433504	-5.89	FALSE
252989_at	putative pectinesterase pectines	sks9	AT4G38420	-1.69	-0.75	-1.14	0.2939476	0.5433504	-5.89	FALSE
248366_at	SCARECROW transcriptional reg	---	AT5G52510	-1.16	-0.22	-1.14	0.2941171	0.5435756	-5.89	TRUE
258097_at	transport protein, putative simila	---	AT3G23660	1.11	0.16	1.14	0.2941058	0.5435756	-5.89	FALSE
251075_at	putative protein leucine-rich rece	---	AT5G01890	-1.32	-0.40	-1.14	0.2942746	0.5438226	-5.89	FALSE
263151_at	hypothetical protein predicted by	---	AT1G54120	-1.39	-0.47	-1.14	0.2944312	0.544068	-5.89	FALSE
259247_at	unknown protein predicted by ge	---	AT3G07570	1.18	0.24	1.14	0.2945276	0.544202	-5.89	FALSE
259621_at	unknown protein	---	AT1G42710	1.11	0.16	1.14	0.2946598	0.5443582	-5.89	FALSE
254885_at	putative protein various predicte	---	AT4G11745	1.18	0.23	1.14	0.294643	0.5443582	-5.89	FALSE
252148_at	MS5-like protein	---	AT3G51280	-1.15	-0.20	-1.14	0.2946971	0.5443829	-5.89	FALSE
248279_at	putative protein similar to unknov	ATIM	AT5G52910	-1.33	-0.41	-1.14	0.2947405	0.5444191	-5.89	FALSE
253555_at	putative protein predicted proete	---	AT4G31080	-1.21	-0.27	-1.14	0.2949004	0.5446703	-5.89	FALSE
250090_at	glutamate decarboxylase 1 (GAD	GAD	AT5G17330	1.80	0.85	1.14	0.2950175	0.5447983	-5.89	TRUE
254119_at	putative pectate lyase pectate ly	---	AT4G24780	1.67	0.74	1.14	0.2950167	0.5447983	-5.89	FALSE
251508_at	putative protein mitochondrial R	---	AT3G58970	-1.17	-0.23	-1.14	0.2950939	0.5448952	-5.89	FALSE

257674_at	translational inhibitor protein, pu	---	AT3G20390	1.13	0.17	1.13	0.2952192	0.5450826	-5.89	FALSE
250285_at	putative protein GCN4-complem	SFC	AT5G13300	-1.23	-0.29	-1.13	0.2953416	0.5452644	-5.89	FALSE
246661_at	putative protein various predicte	---	---	-1.12	-0.16	-1.13	0.295407	0.545341	-5.90	FALSE
261329_at	hypothetical protein predicted by	---	AT1G44890	1.15	0.20	1.13	0.2954682	0.5454099	-5.90	FALSE
257646_at	methionine aminopeptidase, put	MAP1B	AT3G25740	-1.28	-0.36	-1.13	0.2955468	0.5455108	-5.90	FALSE
266362_at	unknown protein	---	AT2G32430	1.17	0.22	1.13	0.2960465	0.5463889	-5.90	FALSE
262605_at	hypothetical protein Strong simila	---	AT1G15170	-1.52	-0.60	-1.13	0.2960945	0.5464333	-5.90	FALSE
254110_at	putative protein pectinesterase -	---	AT4G25260	1.38	0.46	1.13	0.2961636	0.5464727	-5.90	TRUE
253894_at	NWMU2 - 2S albumin 2 precurso	---	AT4G27150	-1.12	-0.16	-1.13	0.2961637	0.5464727	-5.90	FALSE
254445_at	3-hydroxyisobutyrate dehydroge	---	AT4G20930	1.14	0.19	1.13	0.2962344	0.5465589	-5.90	TRUE
252839_at	putative protein PIF1 protein - C	---	---	1.19	0.25	1.13	0.2962762	0.5465918	-5.90	FALSE
248486_at	respiratory burst oxidase protein	RHD2	AT5G51060	1.11	0.15	1.13	0.2963679	0.5467167	-5.90	FALSE
260554_at	putative zinc protease member o	---	AT2G41790	1.11	0.15	1.13	0.2965424	0.5469944	-5.90	FALSE
253623_at	GDP-mannose pyrophosphoryla	---	AT4G30570	1.14	0.19	1.13	0.2966235	0.5470378	-5.90	FALSE
263611_at	hypothetical protein predicted by	---	AT2G16450	1.11	0.15	1.13	0.2966379	0.5470378	-5.90	FALSE
264015_at	putative XAP-5 protein [Homo sa	XCT	AT2G21150	1.13	0.18	1.13	0.2965931	0.5470378	-5.90	FALSE
250101_at	putative protein contains similarit	BGLU2	AT5G16580	1.27	0.34	1.13	0.2967955	0.5471515	-5.90	FALSE
265363_at	hypothetical protein predicted by	---	---	1.11	0.15	1.13	0.2967643	0.5471515	-5.90	FALSE
256473_at	unknown protein	---	---	1.14	0.18	1.13	0.2967284	0.5471515	-5.90	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U849	---	---	1.15	0.20	1.13	0.2967839	0.5471515	-5.90	FALSE
249485_at	receptor protein kinase - like pro	---	AT5G39020	1.44	0.53	1.13	0.2968506	0.5472089	-5.90	TRUE
259208_at	hypothetical protein similar to GE	---	AT3G09060	-1.14	-0.18	-1.13	0.2969333	0.5473171	-5.90	FALSE
258219_at	thioredoxin, putative similar to T	ATTDX	AT3G17880	-1.13	-0.18	-1.13	0.297032	0.5474105	-5.90	FALSE
266982_at	unknown protein ; supported by	---	AT2G39500	-1.18	-0.23	-1.13	0.2970099	0.5474105	-5.90	FALSE
259542_at	Expressed protein ; supported by	---	AT1G20575	-1.14	-0.18	-1.13	0.2970868	0.5474672	-5.90	FALSE
250199_at	putative protein contains similarit	MPL1	AT5G14180	-1.56	-0.64	-1.13	0.2972085	0.5474704	-5.90	FALSE
246852_at	putative protein various predicted	---	AT5G26880	-1.12	-0.17	-1.13	0.2972019	0.5474704	-5.90	FALSE
250922_at	Expressed protein ; supported by	---	AT5G03345	-1.14	-0.18	-1.13	0.2971714	0.5474704	-5.90	FALSE
264428_at	hypothetical protein predicted by	---	AT1G61790	-1.22	-0.29	-1.13	0.2971414	0.5474704	-5.90	FALSE
261729_s_a	hexokinase, putative similar to h	HXK3	AT1G47840	1.11	0.15	1.13	0.2971553	0.5474704	-5.90	FALSE
249936_at	putative protein similar to unknov	---	AT5G22450	1.16	0.21	1.13	0.2972891	0.5475747	-5.90	FALSE
257438_at	hypothetical protein similarity to p	---	AT2G15325	1.11	0.15	1.13	0.297376	0.5476906	-5.90	FALSE
254827_at	putative protein KIAA0255 gene	---	AT4G12650	1.14	0.19	1.13	0.2975159	0.5477269	-5.90	FALSE
257832_at	light regulated protein, putative s	CCL	AT3G26740	-1.13	-0.17	-1.13	0.2974802	0.5477269	-5.90	FALSE
252439_at	pectinesterase-like protein pecti	---	AT3G47400	1.11	0.15	1.13	0.2975012	0.5477269	-5.90	FALSE

253225_at	Rho1Ps homolog Rac-like prote	ARAC3	AT4G35020	-1.16	-0.21	-1.13	0.2974957	0.5477269	-5.90	FALSE
251373_at	GATA transcription factor 4 ; sup	---	AT3G60530	-1.54	-0.62	-1.13	0.2975099	0.5477269	-5.90	FALSE
257881_at	putative serine carboxypeptidase	scpl33	AT3G17180	1.17	0.23	1.13	0.297556	0.5477566	-5.90	FALSE
250921_at	Expressed protein ; supported by	---	AT5G03460	-1.18	-0.24	-1.13	0.297678	0.5478347	-5.90	FALSE
264943_at	hypothetical protein predicted by	---	AT1G76910	1.17	0.22	1.13	0.2976945	0.5478347	-5.90	FALSE
261360_at	hypothetical protein predicted by	---	---	1.14	0.19	1.13	0.2976543	0.5478347	-5.90	FALSE
249358_at	sucrose cleavage protein -like su	---	AT5G40510	1.15	0.20	1.13	0.2976276	0.5478347	-5.90	FALSE
251352_at	putative protein hypothetical pro	PEX11E	AT3G61070	1.18	0.24	1.13	0.2977621	0.5479149	-5.90	FALSE
264002_at	putative DnaJ protein ;supported	---	AT2G22360	1.19	0.25	1.13	0.2978053	0.5479501	-5.90	FALSE
252664_at	putative protein several hypothet	---	AT3G44080	-1.11	-0.15	-1.13	0.2978764	0.5480368	-5.90	FALSE
258277_at	putative cytochrome P450 simila	PAD3	AT3G26830	2.53	1.34	1.13	0.2979064	0.5480478	-5.90	TRUE
246653_at	putative protein clathrin assemb	---	AT5G35200	1.14	0.19	1.13	0.2979846	0.5481033	-5.90	FALSE
247042_at	putative protein similar to unknov	---	AT5G67220	1.12	0.17	1.13	0.2979842	0.5481033	-5.90	FALSE
255197_x_a	contains similarity to Oryza sativa	---	---	1.15	0.21	1.13	0.2980346	0.5481113	-5.90	FALSE
266698_at	copia-like retroelement pol polyp	SNF7.2	AT2G19830	-1.14	-0.19	-1.13	0.298037	0.5481113	-5.90	FALSE
259449_at	hypothetical protein similar to put	---	AT1G13800	-1.16	-0.22	-1.13	0.298168	0.5483079	-5.90	FALSE
245591_at	hypothetical protein	---	AT4G14530	1.11	0.14	1.13	0.2982086	0.5483384	-5.90	FALSE
251781_at	P-glycoprotein - like P-glycoprot	PGP20	AT3G55320	1.14	0.19	1.13	0.2982414	0.5483546	-5.90	FALSE
266788_at	putative receptor-like protein kina	---	AT2G29000	-1.11	-0.14	-1.13	0.2983222	0.5484147	-5.90	FALSE
246840_at	putative protein ;supported by fu	---	AT5G26610	-1.11	-0.15	-1.13	0.298318	0.5484147	-5.90	FALSE
255555_at	putative protein transport factor	---	AT4G01810	1.16	0.21	1.13	0.2984353	0.5485784	-5.90	FALSE
249864_at	putative protein similar to unknov	ATMGT10	AT5G22830	-1.11	-0.15	-1.13	0.2984889	0.5485885	-5.90	FALSE
249587_at	putative protein copper homeost	---	AT5G37860	-1.11	-0.15	-1.13	0.2984824	0.5485885	-5.90	FALSE
257231_at	DegP protease contains similarity	DEGP12	AT3G16550	1.11	0.16	1.13	0.2985761	0.5487046	-5.90	FALSE
253725_at	profilin 3 ;supported by full-lengt	PRF4	AT4G29340	1.13	0.18	1.13	0.2986216	0.5487439	-5.90	FALSE
253922_at	putative protein ; supported by c	VTC2	AT4G26850	1.22	0.29	1.13	0.2986913	0.5487836	-5.90	FALSE
266106_at	putative microtubule-associated	ATATG8E	AT2G45170	1.23	0.30	1.13	0.2987635	0.5487836	-5.90	FALSE
253403_at	putative serine/threonine protein	AtAUR1	AT4G32830	1.16	0.22	1.13	0.2987178	0.5487836	-5.90	FALSE
262938_at	hypothetical protein predicted by	---	AT1G79540	-1.15	-0.20	-1.13	0.2987412	0.5487836	-5.90	FALSE
252966_at	putative protein various predicte	---	AT4G38870	-1.15	-0.20	-1.13	0.2987543	0.5487836	-5.90	FALSE
265486_at	unknown protein predicted by ge	---	AT2G15560	-1.17	-0.23	-1.13	0.2988419	0.5488798	-5.90	FALSE
249091_at	AtCLH2 (gb|AAF27046.1) ; supp	CLH2	AT5G43860	-1.14	-0.19	-1.13	0.298864	0.5488798	-5.90	FALSE
263742_at	predicted protein	---	AT2G20625	1.12	0.16	1.13	0.2990267	0.5489693	-5.90	FALSE
258834_at	GTP cyclohydrolase I similar to G	---	AT3G07270	-1.17	-0.22	-1.13	0.2989931	0.5489693	-5.90	FALSE
245058_at	hypothetical protein predicted by	---	AT2G39790	1.13	0.17	1.13	0.2990157	0.5489693	-5.90	FALSE

259506_at	protein phosphatase type 2C, pu	---	AT1G43900	1.13	0.18	1.13	0.299033	0.5489693	-5.90	FALSE
249440_at	protein kinase -like protein proba	---	AT5G40030	1.13	0.18	1.13	0.2989793	0.5489693	-5.90	FALSE
248466_at	putative protein similar to unknov	HVA22E	AT5G50720	1.25	0.33	1.13	0.299091	0.5490315	-5.91	TRUE
253464_at	putative protein ; supported by fu	---	AT4G32030	1.18	0.24	1.12	0.2992942	0.5492459	-5.91	FALSE
247403_at	putative protein hypersensitive-i	---	AT5G62740	-1.13	-0.18	-1.12	0.2993183	0.5492459	-5.91	FALSE
250684_at	zinc finger-like protein	GIS2	AT5G06650	1.14	0.19	1.12	0.299316	0.5492459	-5.91	FALSE
262959_at	protein translation factor Sui1 ho	---	AT1G54290	1.15	0.21	1.12	0.2992394	0.5492459	-5.91	FALSE
247923_at	porin-like protein ;supported by f	VDAC4	AT5G57490	1.15	0.21	1.12	0.2993282	0.5492459	-5.91	FALSE
253150_at	putative protein predicted protei	---	AT4G35660	1.10	0.14	1.12	0.299403	0.5492893	-5.91	FALSE
260550_at	putative sterol dehydrogenase ;	---	AT2G43420	1.20	0.26	1.12	0.2993962	0.5492893	-5.91	FALSE
254304_at	hypothetical protein ; supported	---	AT4G22270	1.17	0.22	1.12	0.2994241	0.5492893	-5.91	FALSE
262557_at	photosystem I subunit III precurs	---	AT1G31330 ///	-1.14	-0.19	-1.12	0.2995066	0.5493964	-5.91	FALSE
256938_at	LEA protein, putative similar to L	ATECP31	AT3G22500	1.15	0.20	1.12	0.2995638	0.5494572	-5.91	FALSE
259089_at	hypothetical protein similar to GE	---	AT3G04960	-1.13	-0.18	-1.12	0.2996185	0.5495134	-5.91	FALSE
252697_at	nodulin - like protein nodulin-21,	---	AT3G43660	-1.15	-0.20	-1.12	0.2997028	0.5496238	-5.91	FALSE
251730_at	N2,N2-dimethylguanosine tRNA	---	AT3G56330	-1.17	-0.23	-1.12	0.2997826	0.549726	-5.91	FALSE
256566_at	hypothetical protein	---	AT3G19530	1.12	0.17	1.12	0.2998989	0.549895	-5.91	FALSE
245958_at	GNOM-like protein pattern-forma	---	AT5G19610	1.12	0.17	1.12	0.2999238	0.5498965	-5.91	FALSE
249719_at	Expressed protein ; supported by	---	AT5G35735	1.45	0.54	1.12	0.3000237	0.5500354	-5.91	FALSE
255879_at	receptor-like kinase, putative sin	---	AT1G67000	1.34	0.42	1.12	0.3000959	0.5500361	-5.91	TRUE
248540_at	FRO1 and FRO2-like protein	FRO8	AT5G50160	-1.11	-0.15	-1.12	0.3000964	0.5500361	-5.91	FALSE
263141_at	hypothetical protein similar to unl	---	AT1G65210	1.12	0.16	1.12	0.3000598	0.5500361	-5.91	FALSE
257597_at	protein kinase, putative similar to	---	AT3G24790	1.12	0.16	1.12	0.3002613	0.5501712	-5.91	FALSE
264462_at	putative transcription factor simil	WLIM1	AT1G10200	-1.22	-0.29	-1.12	0.3002576	0.5501712	-5.91	FALSE
249338_at	putative protein similar to unknov	anac095	AT5G41090	1.10	0.14	1.12	0.3002515	0.5501712	-5.91	FALSE
247413_at	NBS/LRR disease resistance pro	---	AT5G63020	-1.17	-0.22	-1.12	0.3002666	0.5501712	-5.91	FALSE
252599_at	receptor-like protein kinase rece	---	AT3G45390	1.18	0.24	1.12	0.3003415	0.5502379	-5.91	FALSE
266346_at	putative homeodomain transcript	ATHB17	AT2G01430	-1.17	-0.23	-1.12	0.3003513	0.5502379	-5.91	FALSE
265531_at	hypothetical protein predicted by	AtGRF6	AT2G06200	1.14	0.18	1.12	0.3004514	0.5503481	-5.91	FALSE
253071_at	putative protein various predicted	---	AT4G37880	1.13	0.18	1.12	0.3004597	0.5503481	-5.91	FALSE
255262_at	putative protein equilibrative nuc	---	AT4G05140	1.13	0.17	1.12	0.3005549	0.5504569	-5.91	FALSE
250824_at	putative protein contains similarit	---	AT5G05200	-1.18	-0.24	-1.12	0.3005673	0.5504569	-5.91	FALSE
260828_at	unknown protein	---	AT1G06750	-1.13	-0.17	-1.12	0.3006014	0.5504751	-5.91	FALSE
245533_at	putative phosphocholine cytidylyl	CCT2	AT4G15130	1.38	0.46	1.12	0.3006548	0.5504845	-5.91	FALSE
248154_at	putative protein strong similarity t	---	AT5G54400	1.61	0.69	1.12	0.3006358	0.5504845	-5.91	FALSE

264522_at	putative xylan endohydrolase sir	---	AT1G10050	-1.16	-0.22	-1.12	0.3009614	0.5509575	-5.91	FALSE
267398_at	putative glucanase	AtGH9B11	AT2G44560	1.15	0.21	1.12	0.3009375	0.5509575	-5.91	FALSE
265701_at	unknown protein related to uncha	---	AT2G03460	1.12	0.17	1.12	0.3010213	0.5510229	-5.91	FALSE
251620_at	putative protein hypothetical pro	---	AT3G58060	1.17	0.23	1.12	0.3010626	0.5510542	-5.91	FALSE
266459_at	unknown protein supported by fu	---	AT2G47970	1.13	0.18	1.12	0.3011015	0.5510812	-5.91	FALSE
258038_at	unknown protein ;supported by f	---	AT3G21260	-1.25	-0.32	-1.12	0.3011427	0.5511124	-5.91	FALSE
251899_at	nucleoid DNA-binding - like prot	---	AT3G54400	-1.85	-0.89	-1.12	0.3012999	0.5512208	-5.91	TRUE
256747_at	unknown protein similar to CW14	---	AT3G29180	-1.15	-0.20	-1.12	0.3012807	0.5512208	-5.91	FALSE
258265_at	putative beta-1,3-glucanase pre	---	AT3G15800	1.14	0.19	1.12	0.3012277	0.5512208	-5.91	FALSE
264791_at	predicted protein	---	AT2G17845	-1.11	-0.15	-1.12	0.3013228	0.5512208	-5.91	FALSE
266160_at	hypothetical protein	ATCHX8	AT2G28180	1.17	0.22	1.12	0.3012848	0.5512208	-5.91	FALSE
248619_at	amino acid permease 6 (emb CA	AAP6	AT5G49630	-1.19	-0.25	-1.12	0.3014572	0.5514225	-5.91	FALSE
253278_at	receptor protein kinase - like pro	---	AT4G34220	-1.51	-0.59	-1.12	0.3016305	0.5515184	-5.91	FALSE
254240_at	Expressed protein ; supported by	SP1L5	AT4G23496	1.13	0.18	1.12	0.3016138	0.5515184	-5.91	FALSE
251430_at	putative protein hypothetical pro	---	AT3G60110	1.15	0.20	1.12	0.3016147	0.5515184	-5.91	FALSE
262436_at	En/Spm-like transposon protein,	---	AT1G47610	-1.28	-0.35	-1.12	0.3015649	0.5515184	-5.91	FALSE
250064_at	disease resistance protein - like	DAR4	AT5G17890	-1.18	-0.24	-1.12	0.3016014	0.5515184	-5.91	FALSE
265796_at	Expressed protein ; supported by	---	AT2G35730	1.99	0.99	1.12	0.3017419	0.5516473	-5.91	FALSE
250908_at	GT2 -like protein GT2, Arabidop	PTL	AT5G03680	1.13	0.17	1.12	0.3017494	0.5516473	-5.91	FALSE
266116_at	unknown protein ;supported by f	TOM3	AT2G02180	1.18	0.24	1.12	0.3019444	0.5517836	-5.91	FALSE
255258_at	contains similarity to Arabidopsis	---	AT4G05060	1.15	0.20	1.12	0.3019412	0.5517836	-5.91	FALSE
248498_at	selenium-binding protein-like	---	AT5G50390	-1.13	-0.18	-1.12	0.3019173	0.5517836	-5.91	FALSE
251674_at	hypothetical protein	---	AT3G57250	1.13	0.18	1.12	0.3019441	0.5517836	-5.91	FALSE
262691_at	TPR-repeat protein contains mul	---	AT1G62740	1.19	0.25	1.12	0.3019449	0.5517836	-5.91	FALSE
264170_at	hypothetical protein	---	AT1G02260	1.14	0.19	1.12	0.3020122	0.5518624	-5.91	FALSE
260654_at	hypothetical protein predicted by	---	AT1G19290	-1.18	-0.24	-1.12	0.3021111	0.5519127	-5.91	FALSE
253563_at	putative protein predicted protei	---	AT4G31150	-1.18	-0.24	-1.12	0.3021123	0.5519127	-5.91	FALSE
260609_at	putative receptor protein kinase	---	AT2G43690	1.13	0.17	1.12	0.302082	0.5519127	-5.91	FALSE
248928_at	Rac-like gtp binding protein ARA	ARAC2	AT5G45970	1.10	0.14	1.12	0.3022083	0.5520438	-5.91	FALSE
256445_at	hypothetical protein predicted by	---	AT3G11160	1.14	0.19	1.12	0.3022474	0.5520711	-5.91	FALSE
256214_x_a	hypothetical protein predicted by	---	AT1G51000	1.13	0.18	1.12	0.3022935	0.5520856	-5.91	FALSE
261400_at	protein phosphatase-2C, putativ	---	AT1G79630	-1.20	-0.27	-1.12	0.302328	0.5520856	-5.91	FALSE
266820_at	putative AP2 domain transcriptio	---	AT2G44940	-1.40	-0.49	-1.12	0.3023119	0.5520856	-5.91	FALSE
245868_at	hypothetical protein	CAT2	AT1G58030	-1.16	-0.22	-1.12	0.3024227	0.5522143	-5.91	FALSE
249952_at	putative protein predicted protei	---	AT5G18950	-1.15	-0.20	-1.12	0.3024966	0.5523051	-5.91	FALSE

260502_at	putative Tub family protein conta	AtTLP6	AT1G47270	-1.15	-0.20	-1.12	0.3025236	0.5523102	-5.91	FALSE
248060_at	putative protein contains similarit	---	AT5G55560	1.14	0.18	1.12	0.3025614	0.552335	-5.91	TRUE
254876_at	putative phosphoribosylanthrani	---	AT4G11610	1.17	0.23	1.12	0.3026	0.5523613	-5.91	FALSE
254725_at	putative protein various predicte	---	AT4G13650	-1.16	-0.21	-1.12	0.3026761	0.552456	-5.91	FALSE
249696_at	copia-like retrotransposable elem	---	---	-1.11	-0.15	-1.12	0.3027698	0.5525827	-5.91	FALSE
248752_at	unknown protein	---	AT5G47600	1.12	0.17	1.12	0.3028528	0.55269	-5.92	FALSE
245661_at	purine permease, putative simila	ATPUP3	AT1G28220	1.15	0.20	1.12	0.3029263	0.5526915	-5.92	FALSE
258053_at	unknown protein similar to CGI-1	---	AT3G16230	1.11	0.15	1.12	0.3028885	0.5526915	-5.92	FALSE
248483_at	putative protein contains similarit	---	AT5G50990	-1.19	-0.25	-1.12	0.3029203	0.5526915	-5.92	FALSE
248445_at	unknown protein ;supported by f	---	AT5G51170	-1.17	-0.23	-1.12	0.3029975	0.5527772	-5.92	FALSE
258196_at	hypothetical protein predicted by	---	AT3G13980	1.47	0.55	1.11	0.3031134	0.5527879	-5.92	FALSE
259241_at	unknown protein similar to unkno	---	AT3G33530	-1.11	-0.15	-1.11	0.3031558	0.5527879	-5.92	FALSE
256760_at	SKP1/ASK1 (At15), putative sim	ASK15	AT3G25650	1.10	0.14	1.11	0.303173	0.5527879	-5.92	FALSE
251171_at	putative protein several hypothet	---	AT3G63220	1.11	0.15	1.11	0.3031089	0.5527879	-5.92	FALSE
252109_at	putative protein mucin 5AC, Hor	---	AT3G51540	1.32	0.41	1.12	0.30303	0.5527879	-5.92	FALSE
264091_at	hypothetical protein predicted by	---	AT1G79110	-1.35	-0.43	-1.11	0.3031421	0.5527879	-5.92	FALSE
263523_at	hypothetical protein predicted by	---	---	-1.12	-0.16	-1.11	0.3031165	0.5527879	-5.92	FALSE
255506_at	predicted glycosyl transferase si	GATL6	AT4G02130	-1.29	-0.37	-1.11	0.3032598	0.5529019	-5.92	TRUE
263671_at	hypothetical protein predicted by	---	AT2G04830	1.13	0.17	1.11	0.3033044	0.552939	-5.92	FALSE
245727_at	hypothetical protein contains sim	---	AT1G73350	-1.16	-0.21	-1.11	0.3033696	0.5530138	-5.92	FALSE
246039_at	putative protein serine-arginine-l	---	AT5G19480	1.12	0.17	1.11	0.3035249	0.5532525	-5.92	FALSE
250455_at	unknown protein ; supported by	PROPEP4	AT5G09980	1.20	0.26	1.11	0.3036475	0.5533434	-5.92	FALSE
254242_at	serine /threonine kinase - like pr	---	AT4G23200	1.51	0.60	1.11	0.3036101	0.5533434	-5.92	FALSE
265379_at	similar to late embryogenesis abu	---	AT2G18340	1.12	0.16	1.11	0.3036438	0.5533434	-5.92	FALSE
245423_at	putative protein	---	AT4G17483	1.16	0.21	1.11	0.3036723	0.5533444	-5.92	FALSE
254474_at	putative protein predicted protei	---	AT4G20390	1.20	0.26	1.11	0.3037806	0.5534534	-5.92	FALSE
253350_at	hypothetical protein	---	AT4G33690	-1.12	-0.17	-1.11	0.3037663	0.5534534	-5.92	FALSE
266480_at	unknown protein ; supported by	---	AT2G31130	-1.11	-0.16	-1.11	0.3039129	0.5536485	-5.92	TRUE
257825_at	protein kinase, putative contains	---	AT3G26700	1.14	0.19	1.11	0.3039363	0.5536485	-5.92	TRUE
254886_at	putative protein bp4A protein, Br	LCR17	AT4G11760	1.14	0.19	1.11	0.3040344	0.5537831	-5.92	FALSE
259858_at	putative receptor kinase similar t	---	AT1G68400	1.27	0.34	1.11	0.3042036	0.5540469	-5.92	TRUE
267604_at	hypothetical protein predicted by	ZFN2	AT2G32930	1.29	0.37	1.11	0.3042541	0.5540947	-5.92	FALSE
265786_at	putative replication protein A1	---	---	-1.10	-0.14	-1.11	0.3042946	0.5541241	-5.92	FALSE
245324_at	lactate dehydrogenase (LDH1) ;s	---	AT4G17260	1.35	0.44	1.11	0.3044585	0.554359	-5.92	FALSE
245965_at	pectin methylesterase-like prote	---	AT5G19730	1.26	0.33	1.11	0.3044721	0.554359	-5.92	FALSE

261553_at	hypothetical protein	---	AT1G63420	-1.15	-0.21	-1.11	0.3045546	0.5543765	-5.92	FALSE
262048_at	cytochrome c oxidase subunit, p	---	AT1G80230	1.15	0.20	1.11	0.3045128	0.5543765	-5.92	FALSE
254768_at	hypothetical protein	---	AT4G13320	1.15	0.20	1.11	0.3045366	0.5543765	-5.92	FALSE
250038_at	disease resistance protein -like	---	AT5G18360	1.20	0.26	1.11	0.3046215	0.5543801	-5.92	FALSE
266653_at	hypothetical protein predicted by	---	AT2G25740	-1.15	-0.20	-1.11	0.3046296	0.5543801	-5.92	FALSE
248480_at	ATP-dependent Clp protease AT	CLPC1	AT5G50920	-1.13	-0.17	-1.11	0.3046109	0.5543801	-5.92	FALSE
266167_at	unknown protein ;supported by f	YLS5	AT2G38860	1.54	0.62	1.11	0.304752	0.5545145	-5.92	TRUE
248349_at	progesterone-binding protein-like	MSBP1	AT5G52240	1.19	0.25	1.11	0.3047373	0.5545145	-5.92	FALSE
261760_at	hypothetical protein similar to put	---	AT1G15600	1.19	0.25	1.11	0.304791	0.5545411	-5.92	FALSE
254950_at	putative protein ;supported by fu	---	AT4G10810	-1.11	-0.15	-1.11	0.3048835	0.5546653	-5.92	FALSE
262810_at	putative salt-inducible protein sim	---	AT1G11710	-1.21	-0.28	-1.11	0.3049229	0.5546927	-5.92	FALSE
267565_at	putative cytochrome P450	CYP71A12	AT2G30750	1.69	0.75	1.11	0.304989	0.5547102	-5.92	TRUE
262846_at	endomembrane protein, putative	---	AT1G14670	1.14	0.19	1.11	0.3050055	0.5547102	-5.92	FALSE
255395_at	hypothetical protein	---	---	-1.12	-0.16	-1.11	0.3049691	0.5547102	-5.92	FALSE
265451_at	unknown protein	---	AT2G46490	1.11	0.15	1.11	0.3051406	0.5547993	-5.92	FALSE
263480_at	putative root iron transporter prot	ZIP7	AT2G04032	1.15	0.21	1.11	0.3051344	0.5547993	-5.92	FALSE
250708_at	Expressed protein ; supported by	RBE	AT5G06070	1.12	0.17	1.11	0.3051113	0.5547993	-5.92	FALSE
264347_at	putative extensin strong similarity	LRX1	AT1G12040	1.10	0.14	1.11	0.3051518	0.5547993	-5.92	FALSE
254871_at	Srw1 -like protein WD repeat pro	CCS52A2	AT4G11920	-1.10	-0.14	-1.11	0.3052043	0.5548506	-5.92	FALSE
257941_at	putative UDP-glucose glucosyltra	UGT71B8	AT3G21800	1.12	0.17	1.11	0.3052717	0.5549288	-5.92	FALSE
262316_at	pale cress protein identical to GB	PAC	AT2G48120	-1.20	-0.27	-1.11	0.3053011	0.5549381	-5.92	FALSE
249255_at	Na+/H+ antiporter-like protein	CHX18	AT5G41610	-1.16	-0.21	-1.11	0.305375	0.5550282	-5.92	FALSE
258251_at	unknown protein ; supported by	---	AT3G15810	1.14	0.19	1.11	0.3054018	0.5550327	-5.92	FALSE
266379_at	1,4-beta-xylan endohydrolase	---	AT2G14690	1.14	0.19	1.11	0.3055101	0.5551852	-5.92	FALSE
245139_at	putative AT-hook DNA-binding pr	---	AT2G45430	1.14	0.19	1.11	0.3055553	0.5552232	-5.92	FALSE
252670_at	dnaJ protein homolog atj3 ;supp	ATJ3	AT3G44110	1.16	0.22	1.11	0.3056234	0.5553027	-5.92	FALSE
246756_at	protein phosphatase - like protei	---	AT5G27930	-1.17	-0.23	-1.11	0.305682	0.5553649	-5.92	FALSE
260147_at	putative oxidoreductase similar to	---	AT1G52790	-1.12	-0.17	-1.11	0.3057688	0.5554783	-5.92	FALSE
259398_at	hypothetical protein predicted by	PRA1.F1	AT1G17700	1.45	0.54	1.11	0.3058004	0.5554915	-5.92	FALSE
260927_at	hypothetical protein predicted by	CAT9	AT1G05940	-1.16	-0.22	-1.11	0.3058755	0.5555836	-5.92	FALSE
252742_at	putative protein glyceraldehyde-	---	AT3G43290	1.17	0.23	1.11	0.3059245	0.5555843	-5.92	FALSE
261871_at	similar to serine/threonine protein	---	AT1G11440	-1.16	-0.21	-1.11	0.3059186	0.5555843	-5.92	FALSE
247784_at	subtilisin-like serine protease cor	---	AT5G58810	1.12	0.17	1.11	0.3060032	0.5556828	-5.92	FALSE
264197_at	unknown protein Similar to hypot	ATSAC1	AT1G22620	-1.11	-0.15	-1.11	0.3060601	0.5557419	-5.92	FALSE
265766_at	unknown protein	---	AT2G48080	1.18	0.24	1.11	0.3061181	0.5558031	-5.92	FALSE

249478_at	germin - like protein GLP6 germ	---	AT5G38950	1.13	0.18	1.11	0.3061518	0.55582	-5.92	FALSE
267204_at	putative blue copper-binding prot	---	AT2G31050	1.14	0.19	1.11	0.3062434	0.5559257	-5.92	FALSE
263484_at	putative presenilin	---	AT2G29900	-1.11	-0.15	-1.11	0.3062588	0.5559257	-5.92	FALSE
247858_at	similar to unknown protein (pir||T	TTL	AT5G58220	-1.15	-0.20	-1.11	0.3062861	0.5559311	-5.92	FALSE
256256_at	unknown protein ; supported by f	---	AT3G11230	1.14	0.19	1.11	0.3063542	0.5560105	-5.92	FALSE
245872_at	hypothetical protein contains sim	---	AT1G26300	-1.14	-0.18	-1.11	0.3064042	0.556057	-5.92	FALSE
264809_at	superoxidase dismutase identica	CSD1	AT1G08830	1.51	0.59	1.11	0.3064684	0.5561293	-5.92	FALSE
254118_at	DNA polymerase III like protein l	---	AT4G24790	-1.12	-0.16	-1.11	0.3065439	0.556222	-5.92	FALSE
250267_at	putative protein predicted protein	---	AT5G12930	1.67	0.74	1.11	0.3066268	0.5562654	-5.93	TRUE
266204_at	hypothetical protein predicted by	---	AT2G02410	-1.19	-0.25	-1.11	0.3067059	0.5562654	-5.93	FALSE
246416_at	putative protein predicted protei	---	AT5G16920	1.13	0.18	1.11	0.3066698	0.5562654	-5.93	FALSE
262122_at	polygalacturonase, putative simi	PGA4	AT1G02790	1.14	0.19	1.11	0.3067142	0.5562654	-5.93	FALSE
260658_at	hypothetical protein predicted by	---	AT1G19410	1.16	0.21	1.11	0.3066412	0.5562654	-5.93	FALSE
248602_s_a	MADS-box protein-like	---	AT5G38620 //	1.11	0.15	1.11	0.3066179	0.5562654	-5.92	FALSE
263888_at	unknown protein	---	AT2G37000	1.18	0.24	1.11	0.3067741	0.5563299	-5.93	FALSE
250175_at	putative protein CGI-67, Homo s	---	AT5G14390	-1.26	-0.33	-1.11	0.3068239	0.556376	-5.93	FALSE
260185_at	hypothetical protein similar to hy	---	AT1G36030	1.10	0.14	1.11	0.3068893	0.5564504	-5.93	FALSE
263984_at	hypothetical protein predicted by	---	AT2G42670	-1.14	-0.18	-1.10	0.3071146	0.5564626	-5.93	FALSE
262472_at	hypothetical protein similar to put	---	AT1G50160	1.13	0.17	1.10	0.3070999	0.5564626	-5.93	FALSE
265135_at	unknown protein similar to unkno	---	AT1G51270	1.13	0.18	1.11	0.3070434	0.5564626	-5.93	FALSE
266740_at	hypothetical protein predicted by	---	AT2G46840	1.14	0.19	1.11	0.3069421	0.5564626	-5.93	FALSE
249413_at	ras - related GTP binding protei	AtRABG1	AT5G39620	1.12	0.16	1.11	0.3070714	0.5564626	-5.93	FALSE
254988_at	putative protein Ran GTPase ac	GTC2	AT4G10670	1.14	0.18	1.11	0.3069781	0.5564626	-5.93	FALSE
252917_at	putative zinc finger protein zinc f	---	AT4G38960	1.19	0.25	1.11	0.306966	0.5564626	-5.93	FALSE
266499_at	hypothetical protein predicted by	---	---	1.19	0.25	1.11	0.3070574	0.5564626	-5.93	FALSE
264530_at	hypothetical protein	---	AT1G30780	-1.16	-0.22	-1.10	0.3071157	0.5564626	-5.93	FALSE
249791_at	amino acid transporter ; support	AAP7	AT5G23810	-1.23	-0.30	-1.10	0.3071757	0.5565273	-5.93	FALSE
250047_at	BCS1 - like protein h-bcs1, Hom	---	AT5G17730	1.15	0.21	1.10	0.3072582	0.5565566	-5.93	FALSE
249260_at	Pto kinase interactor 1-like prote	---	AT5G41680	1.14	0.19	1.10	0.307258	0.5565566	-5.93	FALSE
246412_at	phosphoglucomutase-like protei	---	AT5G17530	-1.24	-0.31	-1.10	0.3072651	0.5565566	-5.93	FALSE
247327_at	peroxidase (emb|CAA67551.1) ;	---	AT5G64120	1.74	0.80	1.10	0.3073486	0.5566637	-5.93	TRUE
262447_at	hypothetical protein contains sim	---	AT1G49250	1.13	0.17	1.10	0.3075255	0.5569398	-5.93	FALSE
253023_at	hypothetical protein	---	AT4G38070	1.18	0.24	1.10	0.3075721	0.55698	-5.93	FALSE
255246_at	putative protein hypothetical pro	---	---	1.16	0.21	1.10	0.3076922	0.5571533	-5.93	FALSE
258345_at	unknown protein	---	AT3G22845	-1.12	-0.17	-1.10	0.3079413	0.5572505	-5.93	FALSE

252395_at	H+-transporting ATPase - like pr	AHA4	AT3G47950	-1.21	-0.28	-1.10	0.3078029	0.5572505	-5.93	FALSE
262792_at	hypothetical protein predicted by	---	AT1G10710	1.13	0.18	1.10	0.3078687	0.5572505	-5.93	FALSE
249733_at	6-phosphogluconolactonase-like	emb2024	AT5G24400	-1.13	-0.18	-1.10	0.3077852	0.5572505	-5.93	FALSE
261064_at	unknown protein	ftsh10	AT1G07510	1.16	0.22	1.10	0.3079179	0.5572505	-5.93	FALSE
260226_at	hypothetical protein predicted by	MIF1	AT1G74660	-1.16	-0.22	-1.10	0.3078252	0.5572505	-5.93	FALSE
267303_at	hookless1-like protein	---	AT2G30090	-1.10	-0.13	-1.10	0.3079062	0.5572505	-5.93	FALSE
254220_at	putative protein Arabidopsis hypo	---	AT4G23780	1.12	0.16	1.10	0.3078589	0.5572505	-5.93	FALSE
245915_s_a	tubulin alpha-5 chain-like protein	TUA3	AT5G19770 ///	-1.14	-0.18	-1.10	0.3080948	0.5573616	-5.93	TRUE
251930_at	putative protein several hypothet	ATRBL4	AT3G53780	1.16	0.22	1.10	0.3081052	0.5573616	-5.93	FALSE
250519_at	GDSL-motif lipase/acylhydrolase	---	AT5G08460	1.15	0.20	1.10	0.3081982	0.5573616	-5.93	FALSE
261384_at	hypothetical protein predicted by	---	AT1G05440	1.13	0.18	1.10	0.3081387	0.5573616	-5.93	FALSE
266444_at	putative extensin	---	AT2G43150	-1.17	-0.22	-1.10	0.3081495	0.5573616	-5.93	FALSE
261444_at	hypothetical protein predicted by	SYP61	AT1G28490	-1.13	-0.17	-1.10	0.3080954	0.5573616	-5.93	FALSE
254920_at	putative protein 24 kDa seed ma	BTI2	AT4G11220	1.16	0.21	1.10	0.308102	0.5573616	-5.93	FALSE
255308_at	putative component of vesicle-m	NSF	AT4G04910	-1.15	-0.21	-1.10	0.3081951	0.5573616	-5.93	FALSE
259911_at	putative cinnamyl-alcohol dehydr	CAD1	AT1G72680	1.20	0.27	1.10	0.3082872	0.5574341	-5.93	TRUE
254314_at	extensin - like protein hybrid pro	---	AT4G22470	2.36	1.24	1.10	0.3082868	0.5574341	-5.93	FALSE
252594_at	putative transporter protein pept	---	AT3G45680	1.24	0.30	1.10	0.3083316	0.5574702	-5.93	FALSE
263060_s_a	hypothetical protein	---	AT2G07679 ///	1.20	0.26	1.10	0.3083681	0.5574921	-5.93	FALSE
249323_at	unknown protein	FLA20	AT5G40940	1.13	0.18	1.10	0.308404	0.5575127	-5.93	FALSE
265467_at	putative receptor-like protein kina	---	AT2G37050	-1.20	-0.27	-1.10	0.3084968	0.5575699	-5.93	FALSE
257160_at	hypothetical protein predicted by	---	---	1.21	0.27	1.10	0.3084631	0.5575699	-5.93	FALSE
264785_at	putative non-LTR retroelement re	---	---	1.13	0.18	1.10	0.308509	0.5575699	-5.93	FALSE
246540_at	nitrilase associated protein-like r	SP1L4	AT5G15600	-1.20	-0.26	-1.10	0.3085353	0.5575733	-5.93	FALSE
252170_at	hypothetical protein ; supported	HR4	AT3G26560 ///	1.17	0.22	1.10	0.308598	0.5576425	-5.93	FALSE
246714_at	putative protein predicted protei	---	AT5G28220	1.11	0.15	1.10	0.3086909	0.5577661	-5.93	FALSE
250131_at	unknown protein ; supported by	---	AT5G16550	-1.22	-0.28	-1.10	0.3087237	0.5577812	-5.93	FALSE
264321_at	unknown protein Contains simila	---	AT1G04200	1.19	0.25	1.10	0.308795	0.5578659	-5.93	TRUE
262421_at	hypothetical protein predicted by	---	AT1G50290	-1.20	-0.26	-1.10	0.3090285	0.5581992	-5.93	FALSE
255613_at	putative RING zinc finger protein	---	AT4G01270	-1.15	-0.21	-1.10	0.3090067	0.5581992	-5.93	FALSE
261199_at	unknown protein	---	AT1G12950	1.11	0.15	1.10	0.3091969	0.5584591	-5.93	FALSE
AFFX-BioD	E. coli /GEN=bioD /DB_XREF=g	---	---	1.33	0.42	1.10	0.30928	0.5585651	-5.93	FALSE
256158_at	hypothetical protein contains sim	ATPSK1	AT1G13590	1.12	0.17	1.10	0.3093469	0.5586416	-5.93	FALSE
262444_at	hypothetical protein similar to put	---	AT1G47480	1.26	0.33	1.10	0.3094167	0.5587234	-5.93	FALSE
254238_at	putative protein probable membr	---	AT4G23540	1.17	0.23	1.10	0.3096743	0.5591002	-5.93	FALSE

259784_at	auxin-induced protein, putative s	---	AT1G29450	-1.30	-0.38	-1.10	0.3096499	0.5591002	-5.93	FALSE
262128_at	late embryogenesis-abundant pr	---	AT1G52690	2.16	1.11	1.10	0.3097157	0.5591306	-5.93	FALSE
251494_at	protein kinase-like protein Pto ki	---	AT3G59350	1.34	0.43	1.10	0.3098055	0.5592484	-5.93	TRUE
262647_at	putative growth regulator protein	---	AT1G14020	1.20	0.26	1.10	0.3098552	0.5592939	-5.93	FALSE
256930_at	O-acetylserine(thiol) lyase, putat	OASA2	AT3G22460	1.16	0.22	1.10	0.3100417	0.5595862	-5.93	TRUE
248780_at	4-nitrophenylphosphatase-like pr	ATPGLP2	AT5G47760	1.13	0.18	1.10	0.310081	0.5596129	-5.93	FALSE
266503_at	unknown protein	---	AT2G47780	-1.29	-0.37	-1.10	0.3102832	0.5597468	-5.93	TRUE
263009_at	hypothetical protein contains sim	NHX5	AT1G54370	-1.12	-0.17	-1.10	0.3103282	0.5597468	-5.93	FALSE
255637_at	hypothetical protein	---	AT4G00750	-1.20	-0.27	-1.10	0.3103037	0.5597468	-5.93	FALSE
251489_at	putative protein putative proteins	---	AT3G59460	1.15	0.20	1.10	0.3103488	0.5597468	-5.93	FALSE
265801_at	fertilization-independent seed 2 p	FIS2	AT2G35670	1.13	0.18	1.10	0.3103365	0.5597468	-5.93	FALSE
255629_at	stress-induced protein OZI1 prec	ATOZI1	AT4G00860	1.21	0.28	1.10	0.3103234	0.5597468	-5.93	FALSE
257822_at	rotamase FKBP (ROF1) identica	ROF1	AT3G25230	1.37	0.46	1.10	0.3102766	0.5597468	-5.93	FALSE
252580_at	putative protein putative proteins	---	AT3G45490	1.12	0.16	1.10	0.3103515	0.5597468	-5.93	FALSE
264962_at	auxin transport protein EIR1, pu	PIN6	AT1G77110	1.18	0.24	1.10	0.3104246	0.5598343	-5.93	FALSE
267253_at	putative serine carboxypeptidase	---	AT2G22960	1.11	0.15	1.10	0.3105516	0.5599222	-5.94	FALSE
264937_at	hypothetical protein contains sim	SCPL32	AT1G61130	1.13	0.18	1.10	0.3105715	0.5599222	-5.94	FALSE
249196_at	unknown protein supported by fu	---	AT5G42560	1.13	0.18	1.10	0.3105252	0.5599222	-5.94	FALSE
263734_at	permease, putative similar to pe	NAT7	AT1G60030	1.19	0.25	1.10	0.310561	0.5599222	-5.94	FALSE
262576_at	unknown protein ESTs gb|R903	---	AT1G15280	-1.11	-0.15	-1.10	0.3106614	0.5600185	-5.94	FALSE
265856_at	hypothetical protein predicted by	LBD16	AT2G42430	-1.19	-0.25	-1.10	0.310674	0.5600185	-5.94	FALSE
248666_at	cyclin C-like protein ;supported b	---	AT5G48630	-1.17	-0.23	-1.10	0.3107001	0.5600213	-5.94	FALSE
248273_at	putative protein contains similarit	---	AT5G53500	-1.26	-0.33	-1.10	0.3111342	0.5600346	-5.94	TRUE
254051_at	putative protein other Arabidopsi	---	AT4G25270	1.13	0.18	1.10	0.3110541	0.5600346	-5.94	FALSE
251860_at	Gluthatione reductase, chloropla	GR	AT3G54660	-1.10	-0.14	-1.10	0.3111027	0.5600346	-5.94	FALSE
257621_at	calmodulin-domain protein kinas	CPK9	AT3G20410	1.26	0.33	1.10	0.3111169	0.5600346	-5.94	FALSE
245881_at	putative protein	---	AT5G09460 //	-1.21	-0.28	-1.09	0.3111746	0.5600346	-5.94	FALSE
260840_at	hypothetical protein similar to hyp	---	AT1G29050	1.17	0.22	1.10	0.3107637	0.5600346	-5.94	FALSE
254801_at	endoxyloglucan transferase-like	---	AT4G13080	1.10	0.14	1.09	0.3112476	0.5600346	-5.94	FALSE
253819_at	receptor protein kinase like prote	---	AT4G28350	1.89	0.91	1.10	0.3109199	0.5600346	-5.94	FALSE
267564_at	putative protein kinase contains a	---	AT2G30740	1.15	0.20	1.10	0.3109309	0.5600346	-5.94	FALSE
259689_x_a	unknown protein	---	AT1G63130	-1.24	-0.31	-1.09	0.3112348	0.5600346	-5.94	FALSE
250765_at	unknown protein ;supported by f	---	AT5G05930	1.20	0.27	1.10	0.3109114	0.5600346	-5.94	FALSE
251826_at	ABC transporter - like protein AT	---	AT3G55110	1.15	0.20	1.10	0.3110245	0.5600346	-5.94	FALSE
254786_at	putative protein gamma-interferc	---	AT4G12890	1.14	0.19	1.10	0.3109317	0.5600346	-5.94	FALSE

264272_at	hypothetical protein contains sim	ANAC023	AT1G60280	1.11	0.15	1.10	0.3107757	0.5600346	-5.94	FALSE
257673_at	unknown protein similar to GB:B	---	AT3G20370	1.17	0.22	1.09	0.3112014	0.5600346	-5.94	FALSE
267255_at	putative Ca2+-ATPase	---	AT2G22950	1.17	0.23	1.10	0.3110731	0.5600346	-5.94	FALSE
246875_at	pathogenesis-related protein - li	---	AT5G26130	1.13	0.17	1.10	0.3110741	0.5600346	-5.94	FALSE
263688_at	unknown protein Location of ES	---	AT1G26920	-1.50	-0.59	-1.10	0.3108574	0.5600346	-5.94	FALSE
259699_at	hypothetical protein predicted by	---	AT1G68940	1.11	0.15	1.10	0.3109622	0.5600346	-5.94	FALSE
247096_at	S-adenosyl-L-methionine:salicyli	---	AT5G66430	-1.10	-0.13	-1.10	0.3110146	0.5600346	-5.94	FALSE
251999_at	hypothetical protein teichoic acid	---	AT3G52700	1.12	0.16	1.09	0.3111568	0.5600346	-5.94	FALSE
249562_at	disease resistance protein-like	---	AT5G38350	-1.13	-0.18	-1.10	0.3108219	0.5600346	-5.94	FALSE
251597_at	protein kinase - like protein wall-	---	AT3G57750	1.31	0.39	1.09	0.311316	0.5601135	-5.94	FALSE
265743_s_a	En/Spm-like transposon protein r	---	---	1.11	0.15	1.09	0.3113557	0.5601406	-5.94	FALSE
264064_at	hypothetical protein predicted by	---	AT2G27900	1.12	0.17	1.09	0.3114097	0.5601936	-5.94	FALSE
246619_at	transmembrane protein FT27/PF	---	AT5G36290	-1.11	-0.15	-1.09	0.3114365	0.5601976	-5.94	FALSE
251638_at	40S ribosomal protein S2 homol	---	AT3G57490	-1.28	-0.36	-1.09	0.3114821	0.5602354	-5.94	FALSE
263202_at	putative inositol 1,4,5-trisphosph	5PTASE13	AT1G05630	1.35	0.44	1.09	0.3115186	0.560257	-5.94	FALSE
255748_at	hypothetical protein predicted by	---	AT1G32000	1.10	0.14	1.09	0.3116044	0.5603671	-5.94	FALSE
267186_at	unknown protein ; supported by	---	AT2G44090	1.13	0.17	1.09	0.3116641	0.5604074	-5.94	FALSE
250605_at	glycine/proline-rich protein flagell	---	AT5G07570	1.15	0.20	1.09	0.3116759	0.5604074	-5.94	FALSE
259580_at	oxidoreductase, putative contain	---	AT1G28030	1.17	0.22	1.09	0.3117047	0.560415	-5.94	FALSE
261786_at	cyclic nucleotide and calmodulin	ATCNGC7	AT1G15990	1.13	0.17	1.09	0.3120479	0.5609118	-5.94	FALSE
252696_at	hypothetical protein predicted tra	---	---	1.10	0.14	1.09	0.3120145	0.5609118	-5.94	FALSE
245457_s_a	disease resistance RPP5 like pro	---	AT4G16940 /A	1.13	0.18	1.09	0.3120548	0.5609118	-5.94	FALSE
248470_at	unknown protein	---	AT5G50830	1.13	0.18	1.09	0.3122014	0.5611311	-5.94	FALSE
265424_at	putative sugar transporter	---	AT2G20780	1.15	0.20	1.09	0.3122284	0.5611353	-5.94	FALSE
249225_at	TMV resistance protein-like	---	AT5G42140	1.21	0.28	1.09	0.3123685	0.5613429	-5.94	FALSE
259877_at	unknown protein C-terminal porti	SDG26	AT1G76710	-1.17	-0.22	-1.09	0.3125249	0.5615797	-5.94	FALSE
259972_at	unknown protein N-term similar t	CUC3	AT1G76420	-1.22	-0.28	-1.09	0.3125849	0.5616433	-5.94	FALSE
262763_at	hypothetical protein	---	AT1G28690	-1.18	-0.24	-1.09	0.3126283	0.5616771	-5.94	FALSE
256665_at	hypothetical protein predicted by	---	AT3G20700	-1.17	-0.23	-1.09	0.3126767	0.5617198	-5.94	FALSE
259440_at	hypothetical protein predicted by	BPS1	AT1G01550	1.12	0.17	1.09	0.3127061	0.5617283	-5.94	FALSE
265637_at	unknown protein	ATCOAE	AT2G27490	-1.13	-0.18	-1.09	0.3127618	0.5617585	-5.94	FALSE
253231_at	Nonclathrin coat protein gamma	---	AT4G34450	-1.14	-0.19	-1.09	0.3127722	0.5617585	-5.94	FALSE
246121_at	putative protein motif in PGPS/D	---	AT5G20370	1.14	0.19	1.09	0.3128183	0.5617972	-5.94	FALSE
265440_at	pEARLI 4 protein Same as GB: L	pEARLI4	AT2G20960	1.25	0.33	1.09	0.3129464	0.561806	-5.94	FALSE
262900_at	hypothetical protein contains sim	SNL5	AT1G59890	1.16	0.21	1.09	0.3128889	0.561806	-5.94	FALSE

248551_at	putative protein similar to unknov	WR3	AT5G50200	1.42	0.51	1.09	0.3129	0.561806	-5.94	FALSE
259386_at	hypothetical protein contains sim	NUB	AT1G13400	1.14	0.19	1.09	0.3128794	0.561806	-5.94	FALSE
250631_at	pectin methyl-esterase-like prote	---	AT5G07430	1.11	0.15	1.09	0.3129344	0.561806	-5.94	FALSE
256033_at	UDP-glucose glucosyltransferas	UGT71C4	AT1G07250	1.13	0.17	1.09	0.3130238	0.5618566	-5.94	FALSE
248584_at	putative protein similar to unknov	---	AT5G49960	-1.21	-0.28	-1.09	0.3130195	0.5618566	-5.94	FALSE
246828_at	putative protein hypothetical pro	---	---	-1.13	-0.17	-1.09	0.3130747	0.5619037	-5.94	FALSE
252225_at	ADP-RIBOSYLATION FACTOR	ATARLA1C	AT3G49870	-1.12	-0.16	-1.09	0.3131122	0.5619268	-5.94	FALSE
260936_at	hypothetical protein predicted by	---	AT1G45150	1.14	0.19	1.09	0.3131828	0.5620093	-5.94	FALSE
258772_at	putative ubiquinol-cytochrome C	---	AT3G10860	-1.16	-0.21	-1.09	0.3132374	0.5620173	-5.94	FALSE
249080_at	putative protein strong similarity t	SUVR2	AT5G43990	1.18	0.24	1.09	0.3132612	0.5620173	-5.94	FALSE
260277_at	hypothetical protein predicted by	---	AT1G80520	1.29	0.37	1.09	0.3132557	0.5620173	-5.94	FALSE
255441_at	putative cullin-like 1 protein simil	ATCUL1	AT4G02570	1.12	0.17	1.09	0.3133241	0.562086	-5.94	FALSE
264344_at	putative aspartic proteinase simil	---	AT1G11910	-1.10	-0.14	-1.09	0.3135127	0.5623801	-5.94	TRUE
246013_at	vacuolar calcium binding protein	---	AT5G10660	1.12	0.16	1.09	0.3135961	0.5624853	-5.94	FALSE
258708_at	putative oxidoreductase similar to	---	AT3G09580	-1.21	-0.28	-1.09	0.3136993	0.5626262	-5.94	TRUE
257329_at	hypothetical protein	---	---	1.21	0.28	1.09	0.3137452	0.5626643	-5.94	FALSE
258835_at	putative RNA-binding protein co	---	AT3G07250	1.15	0.20	1.09	0.3139019	0.5629012	-5.94	FALSE
262759_at	unknown protein	---	AT1G10800	1.12	0.16	1.09	0.3139324	0.5629116	-5.94	FALSE
247361_at	unknown protein ;supported by f	---	AT5G63480	-1.17	-0.23	-1.09	0.3139805	0.5629127	-5.94	FALSE
249147_at	cytosolic malate dehydrogenase	---	AT5G43330	-1.17	-0.23	-1.09	0.3139824	0.5629127	-5.94	FALSE
263559_at	putative non-LTR retroelement re	---	---	1.12	0.17	1.09	0.3142488	0.563346	-5.94	FALSE
247835_at	putative protein similar to unknov	---	AT5G57910	1.28	0.35	1.09	0.3143392	0.5634638	-5.94	FALSE
259723_at	putative iron-regulated transporte	IRT3	AT1G60960	-1.31	-0.39	-1.09	0.3146951	0.5634819	-5.95	FALSE
264138_at	beta-Amyrin Synthase, putative	---	AT1G78950	1.15	0.20	1.09	0.3145226	0.5634819	-5.95	FALSE
263274_at	putative protein kinase contains a	CRCK3	AT2G11520	1.15	0.20	1.09	0.3145953	0.5634819	-5.95	FALSE
254811_at	putative protein 2-hydroxy-6-oxo	---	AT4G12230	-1.14	-0.19	-1.09	0.3146492	0.5634819	-5.95	FALSE
266850_at	unknown protein	---	AT2G26850	1.11	0.15	1.09	0.3144832	0.5634819	-5.95	FALSE
262201_at	unknown protein	ORC4	AT2G01120	-1.11	-0.16	-1.09	0.3145978	0.5634819	-5.95	FALSE
267074_s_a	hypothetical protein predicted by	---	AT2G40955 /.	-1.12	-0.17	-1.09	0.3145491	0.5634819	-5.95	FALSE
261293_at	unknown protein ; supported by c	---	AT1G36980	-1.11	-0.15	-1.09	0.3146141	0.5634819	-5.95	FALSE
258188_at	unknown protein ;supported by f	---	AT3G17800	-1.16	-0.22	-1.09	0.3146566	0.5634819	-5.95	FALSE
246321_at	unknown protein	---	AT1G16640	1.14	0.19	1.09	0.3146791	0.5634819	-5.95	FALSE
265696_at	putative molybdopterin biosynthe	CNX2	AT2G31955	1.25	0.32	1.09	0.3146635	0.5634819	-5.95	FALSE
248372_at	putative protein similar to unknov	---	AT5G51850	-1.11	-0.15	-1.09	0.3146033	0.5634819	-5.95	FALSE
245371_at	hypothetical protein ;supported b	---	AT4G15750	-1.15	-0.20	-1.09	0.3145425	0.5634819	-5.95	FALSE

257981_at	ethylene-insensitive 3 (EIN3) ide	EIN3	AT3G20770	-1.13	-0.17	-1.09	0.3145039	0.5634819	-5.95	FALSE
259652_at	unknown protein	HUB2	AT1G55250	-1.19	-0.25	-1.09	0.314725	0.5634911	-5.95	FALSE
263403_at	hypothetical protein similar to hy	TX1	AT2G04040	1.90	0.93	1.09	0.3149649	0.5638765	-5.95	FALSE
246937_at	phospholipase D1-like protein pl	PLDALPHA	AT5G25370	-1.12	-0.16	-1.09	0.315039	0.5639647	-5.95	FALSE
251580_at	putative protein ethylene-respon	---	AT3G58450	1.20	0.26	1.09	0.3150705	0.5639769	-5.95	FALSE
252553_at	putative protein	---	AT3G45910	-1.12	-0.17	-1.09	0.3151943	0.5641543	-5.95	FALSE
246334_at	putative protein serine kinase SI	---	AT3G44850	-1.20	-0.27	-1.08	0.3152692	0.5641998	-5.95	FALSE
254477_at	zinc-finger protein Lsd1 ;support	---	AT4G20380	1.17	0.23	1.09	0.315251	0.5641998	-5.95	FALSE
253591_at	putative protein hypothetical pro	MUS81	AT4G30870	-1.19	-0.25	-1.08	0.3153429	0.5642875	-5.95	FALSE
265218_at	putative transcription factor	GTF2H2	AT1G05055	-1.11	-0.15	-1.08	0.3155034	0.5644861	-5.95	FALSE
267542_at	hypothetical protein predicted by	---	AT2G32740	1.11	0.15	1.08	0.3154969	0.5644861	-5.95	FALSE
250984_at	protein kinase - like protein kina	---	AT5G02800	-1.11	-0.15	-1.08	0.3156098	0.564614	-5.95	FALSE
252802_at	putative protein	---	---	-1.10	-0.13	-1.08	0.3156492	0.564614	-5.95	FALSE
263919_at	unknown protein ;supported by f	---	AT2G36470	-1.49	-0.58	-1.08	0.3156413	0.564614	-5.95	FALSE
264617_at	unknown protein	---	AT2G17660	1.27	0.34	1.08	0.3157145	0.5646866	-5.95	FALSE
261892_at	transcription factor, putative sim	WRKY40	AT1G80840	2.15	1.10	1.08	0.3157642	0.5646869	-5.95	FALSE
255398_at	hypothetical protein	---	AT4G03740	1.13	0.17	1.08	0.3157544	0.5646869	-5.95	FALSE
261042_at	GTP-binding protein, putative si	ATRABA3	AT1G01200	1.15	0.20	1.08	0.3158071	0.5647193	-5.95	FALSE
263230_at	putative indole-3-acetate beta-glu	---	AT1G05670	1.26	0.33	1.08	0.3158504	0.5647524	-5.95	FALSE
252433_at	putative protein putative hydroly	---	AT3G47560	-1.21	-0.27	-1.08	0.3159243	0.564796	-5.95	TRUE
249366_at	dihydroxyacetone 3-phosphate re	---	AT5G40610	-1.41	-0.49	-1.08	0.3159044	0.564796	-5.95	FALSE
261985_at	terpene synthase, putative simil	---	AT1G33750	1.11	0.15	1.08	0.3160205	0.5648368	-5.95	FALSE
263460_at	putative acetolactate synthase	---	AT2G31810	-1.18	-0.24	-1.08	0.3160213	0.5648368	-5.95	FALSE
266797_at	unknown protein	AtGRF1	AT2G22840	-1.32	-0.40	-1.08	0.3160125	0.5648368	-5.95	FALSE
262246_at	leaf development protein Argona	AGO1	AT1G48410	-1.15	-0.20	-1.08	0.3160633	0.5648675	-5.95	FALSE
250297_at	putative protein predicted protei	---	AT5G11980	1.15	0.20	1.08	0.3161205	0.5649156	-5.95	FALSE
245271_at	transcription factor like protein ; s	---	AT4G16430	-1.11	-0.15	-1.08	0.3161397	0.5649156	-5.95	FALSE
266965_at	nodulin-like protein	---	AT2G39510	1.13	0.17	1.08	0.3161986	0.5649322	-5.95	FALSE
245110_at	hypothetical protein predicted by	---	AT2G41550	-1.11	-0.15	-1.08	0.3161876	0.5649322	-5.95	FALSE
264846_at	senescence-associated protein c	---	AT2G17850	1.13	0.18	1.08	0.3162518	0.564983	-5.95	FALSE
255253_at	contains similarity to S. cerevisia	VPS28-2	AT4G05000	-1.12	-0.17	-1.08	0.3162845	0.5649973	-5.95	FALSE
252168_at	putative protein pir7a protein - C	MES10	AT3G50440	1.48	0.56	1.08	0.3163343	0.5650419	-5.95	FALSE
261073_at	hypothetical protein predicted by	---	AT1G07300	-1.13	-0.18	-1.08	0.3164282	0.5651654	-5.95	TRUE
251424_at	putative protein 04.05.01.01	---	AT3G60560	1.10	0.14	1.08	0.3164741	0.5652031	-5.95	FALSE
263162_at	hypothetical protein predicted by	---	AT1G54150	-1.11	-0.15	-1.08	0.3165038	0.5652119	-5.95	FALSE

265413_s_a	hypothetical protein predicted by	---	AT2G16650 ///	-1.14	-0.19	-1.08	0.3165375	0.5652278	-5.95	FALSE
253596_s_a	hypothetical protein ; supported	---	AT4G30730 ///	-1.20	-0.27	-1.08	0.3166379	0.5653629	-5.95	FALSE
251606_at	hypothetical protein	---	AT3G57840	1.16	0.22	1.08	0.3166958	0.565422	-5.95	FALSE
256952_at	mannosidase, putative similar to	---	AT3G21160	-1.16	-0.21	-1.08	0.3167581	0.565489	-5.95	FALSE
264903_at	putative phosphoglucomutase si	---	AT1G23190	1.15	0.20	1.08	0.3168261	0.5655217	-5.95	FALSE
247583_at	putative protein predicted protei	---	AT5G60750	1.12	0.17	1.08	0.3168163	0.5655217	-5.95	FALSE
252000_at	hypothetical protein predicted pr	---	AT3G52710	-1.17	-0.22	-1.08	0.3171421	0.5659771	-5.95	TRUE
265079_at	hypothetical protein contains sim	---	AT1G55460	-1.11	-0.16	-1.08	0.3171216	0.5659771	-5.95	FALSE
264404_at	putative cytochrome P450	CYP82F1	AT2G25160	1.17	0.22	1.08	0.3172301	0.5659771	-5.95	FALSE
245171_at	hypothetical protein predicted by	---	AT2G47560	-1.14	-0.19	-1.08	0.3171927	0.5659771	-5.95	FALSE
254824_s_a	origin recognition complex subu	ORC1B	AT4G12620 ///	-1.19	-0.25	-1.08	0.3171969	0.5659771	-5.95	FALSE
266674_at	hypothetical protein predicted by	---	AT2G29620	1.11	0.15	1.08	0.3172284	0.5659771	-5.95	FALSE
256392_at	putative glycosyl transferase con	GATL4	AT3G06260	1.14	0.19	1.08	0.3172904	0.5659963	-5.95	FALSE
258023_at	cinnamyl alcohol dehydrogenase	ATCAD4	AT3G19450	-1.36	-0.44	-1.08	0.317274	0.5659963	-5.95	FALSE
257021_at	branched-chain amino acid amir	BCAT4	AT3G19710	-1.31	-0.39	-1.08	0.3173882	0.5660741	-5.95	FALSE
248081_at	putative protein similar to unknov	EDM2	AT5G55390	-1.11	-0.15	-1.08	0.3174333	0.5660741	-5.95	FALSE
245582_at	hypothetical protein	LOI1	AT4G14850	-1.19	-0.25	-1.08	0.3174109	0.5660741	-5.95	FALSE
261099_at	expansin At-EXP6, putative simi	ATEXPA18	AT1G62980	1.16	0.22	1.08	0.3174251	0.5660741	-5.95	FALSE
265313_at	unknown protein	---	AT2G20210	-1.15	-0.20	-1.08	0.3175428	0.566225	-5.95	FALSE
261663_at	hypothetical protein similar to hy	EPR1	AT1G18330 ///	-1.45	-0.53	-1.08	0.3175767	0.5662413	-5.95	TRUE
251506_at	putative protein ; supported by c	---	AT3G59090	1.10	0.14	1.08	0.3177706	0.5664107	-5.95	FALSE
265367_at	hypothetical protein predicted by	---	---	-1.10	-0.14	-1.08	0.3177591	0.5664107	-5.95	FALSE
261022_at	unknown protein similar to NAM	ANAC007	AT1G12260	1.13	0.18	1.08	0.3177396	0.5664107	-5.95	FALSE
252387_at	aldose 1-epimerase - like protei	---	AT3G47800	1.19	0.25	1.08	0.317771	0.5664107	-5.95	FALSE
250521_at	selenium-binding protein-like	---	AT5G08490	1.12	0.17	1.08	0.3178347	0.5664396	-5.95	FALSE
256775_at	hypothetical protein predicted by	---	AT3G13770	-1.22	-0.29	-1.08	0.3178369	0.5664396	-5.95	FALSE
257925_at	unknown protein ;supported by f	---	AT3G23170	1.79	0.84	1.08	0.3179156	0.5665075	-5.95	TRUE
255412_at	auxin-binding protein 1 precurso	ABP1	AT4G02980	-1.13	-0.18	-1.08	0.3180489	0.5665075	-5.95	FALSE
263240_s_a	unknown protein ; supported by	---	AT1G72590 ///	-1.20	-0.26	-1.08	0.3180423	0.5665075	-5.95	FALSE
248616_at	putative protein contains similarit	---	AT5G49580	-1.18	-0.23	-1.08	0.3180148	0.5665075	-5.95	FALSE
260717_at	serine/threonine phosphatase P	---	AT1G48120	-1.17	-0.23	-1.08	0.3180222	0.5665075	-5.95	FALSE
256095_at	hypothetical protein contains Pfa	---	AT1G13630	-1.26	-0.33	-1.08	0.3179702	0.5665075	-5.95	FALSE
252814_at	putative protein several hypothet	---	---	1.14	0.19	1.08	0.3179712	0.5665075	-5.95	FALSE
251505_at	putative protein polyamine oxida	CPuORF18	AT3G59050 ///	1.22	0.29	1.08	0.3182081	0.5666141	-5.95	FALSE
252201_at	putative protein anthranilate N-h	---	AT3G50295	1.11	0.15	1.08	0.3181776	0.5666141	-5.95	FALSE

265152_s_a	hypothetical protein predicted by	---	AT1G30935 /.	1.11	0.15	1.08	0.3181786	0.5666141	-5.95	FALSE
249545_at	putative transmembrane protein	---	AT5G38030	-1.11	-0.15	-1.08	0.3181848	0.5666141	-5.95	FALSE
266433_at	unknown protein	---	AT2G07110	1.11	0.15	1.08	0.3182698	0.5666681	-5.95	FALSE
263768_x_a	putative Athila retroelement ORF	---	---	1.10	0.13	1.08	0.3182881	0.5666681	-5.95	FALSE
257532_at	hypothetical protein similar to hyp	---	AT3G04700	1.57	0.65	1.08	0.3183745	0.5667423	-5.95	FALSE
247343_at	unknown protein	---	AT5G63740	1.12	0.16	1.08	0.3183794	0.5667423	-5.95	FALSE
260440_at	hypothetical protein predicted by	---	AT1G68160	-1.12	-0.17	-1.08	0.3185932	0.5668131	-5.96	FALSE
258657_at	hypothetical protein predicted by	---	AT3G09890	-1.20	-0.26	-1.08	0.3184751	0.5668131	-5.96	FALSE
254180_at	putative protein hin1 protein hon	---	AT4G23930	-1.23	-0.29	-1.08	0.3185748	0.5668131	-5.96	FALSE
257629_at	cellulase, putative contains Pfan	---	AT3G26140	1.14	0.19	1.08	0.3185187	0.5668131	-5.96	FALSE
257018_at	unknown protein	---	AT3G19630	-1.13	-0.18	-1.08	0.3184744	0.5668131	-5.96	FALSE
261988_at	single-strand nucleic acid-bindin	---	AT1G33680	-1.19	-0.25	-1.08	0.3185127	0.5668131	-5.96	FALSE
263217_at	putative reticuline oxidase-like p	---	AT1G30740	1.12	0.16	1.08	0.3185851	0.5668131	-5.96	FALSE
253133_at	DNA-directed RNA polymerase (	NRPB1	AT4G35800	-1.13	-0.18	-1.08	0.31865	0.5668343	-5.96	FALSE
265891_at	putative thionin	---	AT2G15010	1.12	0.17	1.08	0.3186548	0.5668343	-5.96	FALSE
254286_at	putative MADS Box / AGL protei	AGL19	AT4G22950	-1.24	-0.31	-1.08	0.318687	0.5668474	-5.96	FALSE
264921_at	RNA binding protein, putative sir	---	AT1G60650	-1.14	-0.19	-1.08	0.3187369	0.5668919	-5.96	FALSE
257411_s_a	hypothetical protein predicted by	---	AT1G61320 /.	1.10	0.14	1.08	0.3188091	0.5669761	-5.96	FALSE
253956_at	fimbrin-like protein (ATFIM1) ; su	FIM1	AT4G26700	-1.23	-0.30	-1.08	0.3189034	0.5670996	-5.96	FALSE
259848_at	leucine-rich receptor-like protein	---	AT1G72180	-1.17	-0.22	-1.08	0.3189759	0.5671401	-5.96	TRUE
252074_at	putative protein DNA helicase ho	---	AT3G51700	-1.13	-0.18	-1.08	0.3189553	0.5671401	-5.96	FALSE
257175_s_a	cyclopropane-fatty-acyl-phospho	---	AT3G23470 /.	-1.14	-0.18	-1.08	0.3190303	0.5671926	-5.96	FALSE
264119_at	myb-related protein, putative sim	MYB63	AT1G79180	1.10	0.14	1.08	0.3191493	0.56736	-5.96	FALSE
256063_at	Expressed protein ; supported by	STN1	AT1G07130	-1.14	-0.19	-1.08	0.3191986	0.5674033	-5.96	FALSE
249245_at	putative protein contains similarit	---	AT5G42280	1.19	0.25	1.08	0.3192439	0.5674397	-5.96	FALSE
248153_at	cyclic nucleotide and calmodulin-	ATCNGC4	AT5G54250	1.14	0.19	1.08	0.3192926	0.5674798	-5.96	TRUE
250992_at	expansin precursor - like protein	ATEXPA9	AT5G02260	1.35	0.44	1.08	0.3193162	0.5674798	-5.96	FALSE
245824_at	hypothetical protein predicted by	ATPUP17	AT1G57943	1.20	0.27	1.07	0.3195977	0.5679357	-5.96	FALSE
250950_at	putative protein	ATEXO70A	AT5G03540 /.	-1.16	-0.22	-1.07	0.3197001	0.5680419	-5.96	FALSE
247225_at	inositol-1, 4, 5-trisphosphate 5-p	BST1	AT5G65090	-1.15	-0.20	-1.07	0.3197072	0.5680419	-5.96	FALSE
263479_x_a	hypothetical protein predicted by	---	---	1.12	0.16	1.07	0.3198085	0.5681775	-5.96	FALSE
251350_at	cytochrome P450 monooxygena	CYP76C7	AT3G61040	1.21	0.28	1.07	0.3199109	0.5682382	-5.96	FALSE
266943_at	putative reverse transcriptase	---	---	1.20	0.26	1.07	0.3199173	0.5682382	-5.96	FALSE
252486_at	arm repeat containing protein ho	PUB13	AT3G46510	1.14	0.19	1.07	0.3199009	0.5682382	-5.96	FALSE
249511_at	putative protein contains similarit	---	AT5G38500	1.12	0.16	1.07	0.3199686	0.568285	-5.96	FALSE

247151_at	unknown protein ;supported by f	bHLH093	AT5G65640	1.23	0.30	1.07	0.3200172	0.568327	-5.96	FALSE
263321_at	ADP-ribosylation factor 1 ;suppo	ARF1A1C	AT2G47170	1.13	0.17	1.07	0.3201203	0.5684658	-5.96	FALSE
249553_at	receptor serine/threonine protein	---	AT5G38260	1.19	0.25	1.07	0.3206412	0.5689802	-5.96	FALSE
255864_at	putative pseudouridine synthase	---	AT2G30320	-1.15	-0.20	-1.07	0.3206161	0.5689802	-5.96	FALSE
251721_s_a	alpha-soluble NSF attachment pr	ALPHA-SN	AT3G56190 /	-1.15	-0.20	-1.07	0.3205979	0.5689802	-5.96	FALSE
246772_at	putative protein unknown protein	---	AT5G27490	-1.26	-0.33	-1.07	0.3205699	0.5689802	-5.96	FALSE
254521_at	putative protein similar to unknov	---	AT5G44820	1.13	0.18	1.07	0.3204393	0.5689802	-5.96	FALSE
249712_at	eIF4Eiso protein (emb|CAA7157	LSP1	AT5G35620	-1.19	-0.25	-1.07	0.3204675	0.5689802	-5.96	FALSE
252499_s_a	subtilisin-like serine protease co	---	AT3G46840 /	-1.13	-0.18	-1.07	0.3206076	0.5689802	-5.96	FALSE
252739_at	putative protein mRNA, Homo sa	---	AT3G43250	1.13	0.18	1.07	0.320574	0.5689802	-5.96	FALSE
260330_at	putative RING zinc finger protein	---	AT1G80400	-1.13	-0.17	-1.07	0.320621	0.5689802	-5.96	FALSE
265191_at	hypothetical protein Similar to Sa	---	AT1G05120	1.13	0.17	1.07	0.3206594	0.5689802	-5.96	FALSE
251065_at	lipid-transfer protein-like lipid-tra	---	AT5G01870	1.16	0.21	1.07	0.3206996	0.5690074	-5.96	FALSE
249692_s_a	putative protein strong similarity t	---	AT5G36670 /	1.15	0.20	1.07	0.3207266	0.5690109	-5.96	FALSE
264798_at	putative myosin MYA1, class V (	XIC	AT1G08730	1.12	0.17	1.07	0.3209229	0.569315	-5.96	FALSE
254241_at	serine/threonine kinase - like pro	CRK11	AT4G23190	1.53	0.61	1.07	0.321131	0.5695069	-5.96	FALSE
257297_at	unknown protein contains Pfam	---	AT3G28040	-1.35	-0.43	-1.07	0.3210736	0.5695069	-5.96	FALSE
264082_at	unknown protein ;supported by f	---	AT2G28570	1.13	0.17	1.07	0.321096	0.5695069	-5.96	FALSE
259478_at	germin, putative similar to germi	---	AT1G18980	2.08	1.05	1.07	0.3211072	0.5695069	-5.96	FALSE
260042_at	hypothetical protein C-term simila	---	AT1G68820	1.23	0.29	1.07	0.3212234	0.5696264	-5.96	FALSE
247763_at	RNA polymerase II	NRPB7	AT5G59180	-1.13	-0.17	-1.07	0.3212529	0.5696346	-5.96	FALSE
247199_at	DNA binding protein TGA1a hom	TGA1	AT5G65210	1.27	0.35	1.07	0.3213134	0.5696975	-5.96	TRUE
249674_at	unknown protein	---	AT5G35930	-1.11	-0.15	-1.07	0.3214655	0.5699162	-5.96	FALSE
265128_at	hypothetical protein predicted by	---	AT1G30860	1.17	0.22	1.07	0.3214867	0.5699162	-5.96	FALSE
264316_at	unknown protein ; supported by c	ENT1,AT	AT1G70330	1.16	0.21	1.07	0.3215933	0.5699723	-5.96	FALSE
257032_at	zinc finger protein, putative simil	---	AT3G19140	1.10	0.14	1.07	0.3215836	0.5699723	-5.96	FALSE
263395_at	putative mitochondrial inner mem	ATTIM44-1	AT2G20500 /	1.12	0.16	1.07	0.3215924	0.5699723	-5.96	FALSE
262474_at	hypothetical protein identical to h	FU	AT1G50240	1.14	0.19	1.07	0.3216456	0.5700206	-5.96	FALSE
255563_at	putative CHP-rich zinc finger pro	---	AT4G01740	-1.12	-0.16	-1.07	0.321835	0.570312	-5.96	FALSE
249049_at	tubulin beta-4 chain (sp|P24636)	TUB4	AT5G44340	1.20	0.26	1.07	0.3218923	0.5703295	-5.96	FALSE
261462_at	hypothetical protein predicted by	---	AT1G07850	1.15	0.20	1.07	0.3218949	0.5703295	-5.96	FALSE
263105_at	putative N-acetylglucosaminyltra	---	AT2G05320	-1.11	-0.15	-1.07	0.3220524	0.5704756	-5.96	FALSE
259821_at	subtilisin-like serine protease cor	---	AT1G66220	1.17	0.23	1.07	0.3220483	0.5704756	-5.96	FALSE
246285_at	putative protein	---	AT4G36980	-1.11	-0.15	-1.07	0.3220231	0.5704756	-5.96	FALSE
253280_at	poly(A)-binding protein non-cons	PAB2	AT4G34110	-1.11	-0.15	-1.07	0.3221151	0.5705424	-5.96	FALSE

259824_at	copper homeostasis factor, puta	ATX1	AT1G66240	-1.12	-0.16	-1.07	0.3221567	0.5705588	-5.96	FALSE
262353_at	hypothetical protein similar to hy	---	AT1G64210	1.10	0.14	1.07	0.3221757	0.5705588	-5.96	FALSE
260640_at	viral resistance protein, putative	---	AT1G53350	-1.31	-0.39	-1.07	0.322223	0.5705588	-5.96	FALSE
257179_at	topoisomerase VIA (SPO11 gen	---	AT3G13160 /	1.10	0.14	1.07	0.3222408	0.5705588	-5.96	FALSE
253182_at	putative protein ctf, Mycobacteri	---	AT4G35190	1.23	0.30	1.07	0.3222494	0.5705588	-5.96	FALSE
245800_at	heat shock transcription factor, p	HSFB4	AT1G46264	1.12	0.17	1.07	0.3223268	0.5706275	-5.96	FALSE
259336_at	hypothetical protein C-term portic	SDG20	AT3G03750	-1.21	-0.28	-1.07	0.3223426	0.5706275	-5.96	FALSE
266826_at	putative amino acid acetyltransfe	---	AT2G22910	-1.29	-0.37	-1.07	0.3223633	0.5706275	-5.96	FALSE
264724_at	putative JUN kinase activator pr	CSN5A	AT1G22920	-1.11	-0.15	-1.07	0.3224099	0.5706658	-5.96	FALSE
252338_at	putative progesterone-binding pr	MAPR3	AT3G48890	1.49	0.58	1.07	0.3225865	0.5708455	-5.97	TRUE
266983_at	putative phospholipase ; suppor	---	AT2G39400	-1.21	-0.27	-1.07	0.3225509	0.5708455	-5.97	TRUE
245504_at	glutaredoxin	---	AT4G15660	-1.22	-0.29	-1.07	0.3225702	0.5708455	-5.97	FALSE
257031_at	fucosyltransferase, putative simi	FUT11	AT3G19280	-1.13	-0.18	-1.07	0.3226513	0.5709159	-5.97	FALSE
251504_at	putative protein putative multidru	TT12	AT3G59030	1.14	0.19	1.07	0.3226859	0.5709328	-5.97	FALSE
246946_at	putative protein	---	AT5G25070	-1.11	-0.15	-1.07	0.3227516	0.5710047	-5.97	FALSE
251310_at	homeobox protein Anthocyaninle	HDG1	AT3G61150	-1.17	-0.23	-1.07	0.322854	0.5710972	-5.97	FALSE
255254_at	hypothetical protein	---	AT4G05030	1.17	0.23	1.07	0.3228306	0.5710972	-5.97	FALSE
259586_at	unknown protein	---	AT1G28100	-1.12	-0.17	-1.07	0.3229794	0.5711664	-5.97	TRUE
265310_at	hypothetical protein predicted by	---	AT2G20280	-1.12	-0.16	-1.07	0.3229615	0.5711664	-5.97	FALSE
261133_at	DYW7 protein identical to DYW7	---	AT1G19715	-1.21	-0.27	-1.07	0.3229908	0.5711664	-5.97	FALSE
260121_at	AIG1-like protein similar to AIG1	---	AT1G33910	1.10	0.14	1.07	0.3229932	0.5711664	-5.97	FALSE
252330_at	hypothetical protein	---	AT3G48770	1.18	0.24	1.07	0.3232008	0.5714006	-5.97	FALSE
262102_at	hypothetical protein contains sim	CUL2	AT1G02980	1.11	0.14	1.07	0.3231915	0.5714006	-5.97	FALSE
261643_at	hypothetical protein similar to hy	TAF4B	AT1G27720	1.18	0.24	1.07	0.3231732	0.5714006	-5.97	FALSE
246519_at	proline-rich protein other proline-	---	AT3G23750 /	1.93	0.94	1.07	0.3232272	0.5714029	-5.97	FALSE
264757_at	receptor protein kinase (IRK1), p	---	AT1G61360	1.68	0.75	1.07	0.3233445	0.5714402	-5.97	TRUE
260813_at	VirE2-interacting protein VIP1 ide	VIP1	AT1G43700	-1.19	-0.25	-1.07	0.3233037	0.5714402	-5.97	FALSE
256918_s_a	hypothetical protein similar to hy	---	AT3G18960 /	1.18	0.23	1.07	0.3232765	0.5714402	-5.97	FALSE
250553_at	putative protein PTD008, Homo	---	AT5G07960	-1.15	-0.21	-1.07	0.3233485	0.5714402	-5.97	FALSE
265515_at	hypothetical protein predicted by	---	---	1.12	0.17	1.07	0.3234185	0.5715197	-5.97	FALSE
247880_at	putative protein similar to unknov	---	AT5G57780	-1.55	-0.63	-1.07	0.3234901	0.5715577	-5.97	FALSE
264713_at	hypothetical protein Similar to N.	---	AT1G09820	-1.14	-0.18	-1.07	0.323489	0.5715577	-5.97	FALSE
259915_at	unknown protein	---	AT1G72790	1.35	0.43	1.06	0.3237716	0.5718275	-5.97	TRUE
251374_at	homeobox-leucine zipper protein	HAT3	AT3G60390	-1.28	-0.36	-1.06	0.3237932	0.5718275	-5.97	FALSE
256008_s_a	allinase, putative similar to allina	---	AT1G34040 /	-1.13	-0.17	-1.06	0.3237478	0.5718275	-5.97	FALSE

252822_at	Expressed protein ; supported by	---	AT4G39955	-1.15	-0.20	-1.06	0.3237408	0.5718275	-5.97	FALSE
258698_at	unknown protein	---	AT3G09690	1.14	0.19	1.06	0.323763	0.5718275	-5.97	FALSE
261962_s_a	hypothetical protein predicted by	---	---	1.13	0.18	1.06	0.3237045	0.5718275	-5.97	FALSE
261968_at	disease resistance protein RPP1	---	AT1G65850	1.10	0.14	1.06	0.3238767	0.5719305	-5.97	FALSE
265784_at	hypothetical protein predicted by	---	AT2G07280	-1.12	-0.16	-1.06	0.3239065	0.5719389	-5.97	FALSE
254898_at	serine/threonine kinase-like prot	---	AT4G11480	1.61	0.69	1.06	0.3239501	0.5719717	-5.97	FALSE
257232_at	phytochrome-associated protein	PAP1	AT3G16500	-1.16	-0.21	-1.06	0.3239881	0.5719946	-5.97	FALSE
259568_at	hypothetical protein	---	AT1G20490	-1.12	-0.16	-1.06	0.3240549	0.5720682	-5.97	FALSE
263535_at	hypothetical protein predicted by	---	AT2G24970	-1.15	-0.21	-1.06	0.3241689	0.5722251	-5.97	FALSE
262673_at	unknown protein	EMB1793	AT1G76060	1.13	0.17	1.06	0.324252	0.5723275	-5.97	FALSE
255185_at	hypothetical protein	---	AT4G07740	1.13	0.17	1.06	0.3243262	0.5724141	-5.97	FALSE
252944_at	hypothetical protein ;supported b	---	AT4G39320	1.12	0.16	1.06	0.3243777	0.5724164	-5.97	FALSE
257126_at	E2, ubiquitin-conjugating enzym	UBC19	AT3G20060	1.17	0.22	1.06	0.3243724	0.5724164	-5.97	FALSE
266835_at	putative NADH dehydrogenase (	NDA2	AT2G29990	1.40	0.49	1.06	0.3244629	0.5724783	-5.97	FALSE
253154_at	putative protein predicted protei	---	AT4G35710	1.14	0.19	1.06	0.3244462	0.5724783	-5.97	FALSE
AFFX-PheX	B. subtilis /GEN=pheB /DB_XRE	---	---	-1.21	-0.27	-1.06	0.3246025	0.5726802	-5.97	FALSE
262560_at	hypothetical protein predicted by	---	AT1G34280	1.14	0.20	1.06	0.3247409	0.5728801	-5.97	FALSE
250237_at	putative protein strong similarity t	---	AT5G13560	1.16	0.21	1.06	0.3248194	0.5729152	-5.97	FALSE
255994_at	hypothetical protein predicted by	---	AT1G29760	1.11	0.16	1.06	0.3248552	0.5729152	-5.97	FALSE
260131_at	unknown protein contains Pfam p	---	AT1G66310	-1.12	-0.17	-1.06	0.3247918	0.5729152	-5.97	FALSE
259353_at	putative branched-chain amino a	---	AT3G05190	-1.11	-0.15	-1.06	0.3248612	0.5729152	-5.97	FALSE
250767_at	putative protein contains similarit	ATNFXL2	AT5G05660	1.11	0.15	1.06	0.3250047	0.5730529	-5.97	TRUE
252208_at	putative protein hypothetical pro	---	AT3G50380	-1.20	-0.26	-1.06	0.3250147	0.5730529	-5.97	FALSE
266833_at	hypothetical protein predicted by	---	---	-1.09	-0.13	-1.06	0.3249727	0.5730529	-5.97	FALSE
261472_at	hypothetical protein predicted by	---	AT1G14470	-1.09	-0.13	-1.06	0.3252822	0.5734801	-5.97	FALSE
262566_at	auxin response factor 1, putative	ARF12	AT1G34310	1.19	0.26	1.06	0.3253129	0.57349	-5.97	TRUE
253617_at	hypothetical protein	---	AT4G30410	-1.38	-0.47	-1.06	0.3254816	0.5735214	-5.97	TRUE
260634_at	initiation factor isozyme 4F p82 s	---	AT1G62410	-1.13	-0.18	-1.06	0.3254308	0.5735214	-5.97	FALSE
258473_s_a	putative stearoyl-acyl carrier prot	---	AT3G02610 ///	-1.21	-0.27	-1.06	0.3254474	0.5735214	-5.97	FALSE
258960_at	hypothetical protein similar to m	---	AT3G10590	1.12	0.17	1.06	0.3253701	0.5735214	-5.97	FALSE
259537_at	hypothetical protein ; supported b	PHR1	AT1G12370	-1.15	-0.21	-1.06	0.3254786	0.5735214	-5.97	FALSE
254676_at	putative protein Hypothetical prot	---	AT4G18460	-1.16	-0.21	-1.06	0.3254343	0.5735214	-5.97	FALSE
248277_at	ABC transporter-like protein	---	AT5G52860	1.16	0.21	1.06	0.3255555	0.5736074	-5.97	FALSE
266775_at	putative SCARECROW gene reg	---	AT2G29060	1.28	0.36	1.06	0.3256174	0.5736721	-5.97	TRUE
255214_at	hypothetical protein	---	---	1.10	0.14	1.06	0.3257836	0.5738934	-5.97	FALSE

257223_at	50S ribosomal protein L12-B ide	RPL12-B	AT3G27840	1.15	0.20	1.06	0.3257933	0.5738934	-5.97	FALSE
258679_at	putative 2,3-bisphosphoglycerat	---	AT3G08590	1.27	0.34	1.06	0.3258546	0.573957	-5.97	TRUE
251389_at	putative protein	---	AT3G60850	-1.11	-0.16	-1.06	0.3259922	0.5741108	-5.97	FALSE
256647_at	unknown protein contains similar	---	AT3G13610	2.69	1.43	1.06	0.3259685	0.5741108	-5.97	FALSE
249624_at	putative protein predicted protei	---	AT5G37570	-1.17	-0.23	-1.06	0.3260789	0.5742058	-5.97	FALSE
260743_at	unknown protein	---	AT1G15030	1.26	0.33	1.06	0.3260965	0.5742058	-5.97	FALSE
248367_at	actin depolymerizing factor-like ;	ADF10	AT5G52360	1.15	0.21	1.06	0.3261371	0.5742329	-5.97	FALSE
254866_at	putative protein other predicted	---	AT4G12220	-1.10	-0.13	-1.06	0.3263469	0.5745514	-5.97	FALSE
258422_at	hypothetical protein predicted by	---	AT3G16710	1.12	0.16	1.06	0.3263684	0.5745514	-5.97	FALSE
263917_at	putative AP2 domain transcriptio	HRD	AT2G36450	1.19	0.25	1.06	0.3264453	0.5746021	-5.97	FALSE
245659_at	hypothetical protein predicted by	---	AT1G28260	-1.25	-0.33	-1.06	0.3264693	0.5746021	-5.97	FALSE
249708_at	unknown protein	---	AT5G35660	1.26	0.33	1.06	0.3264727	0.5746021	-5.97	FALSE
264583_at	putative AVR9 elicitor response p	---	AT1G05170	1.16	0.22	1.06	0.326576	0.5746508	-5.97	FALSE
265359_at	putative MYB family transcription	MYB7	AT2G16720	1.39	0.47	1.06	0.3265578	0.5746508	-5.97	FALSE
255453_at	hypothetical protein similar to A.	---	AT4G02900	-1.17	-0.23	-1.06	0.326556	0.5746508	-5.97	FALSE
256448_s_a	unknown protein	MED21	AT4G04780 /	1.12	0.16	1.06	0.3267376	0.5748022	-5.98	FALSE
257640_at	hypothetical protein	---	AT3G25750	1.16	0.21	1.06	0.3267057	0.5748022	-5.98	FALSE
246471_s_a	putative protein predicted protei	---	AT5G17100 /	-1.11	-0.15	-1.06	0.3267307	0.5748022	-5.98	FALSE
256114_at	unknown protein ; supported by c	---	AT1G16850	1.47	0.56	1.06	0.3267961	0.5748164	-5.98	TRUE
266448_s_a	unknown protein ;supported by f	---	AT2G43210	-1.12	-0.16	-1.06	0.3267949	0.5748164	-5.98	FALSE
253361_at	putative protein various predicted	---	AT4G33100	-1.23	-0.30	-1.06	0.3268455	0.574859	-5.98	FALSE
254061_at	putative protein several hypothet	---	AT4G25360	1.13	0.17	1.06	0.3269271	0.5749582	-5.98	FALSE
260049_at	DNA-directed RNA polymerase :	NRPA2	AT1G29940	-1.26	-0.34	-1.06	0.3269685	0.5749866	-5.98	FALSE
262511_at	syntaxin-related protein At-SYR1	SYP125	AT1G11250	1.16	0.22	1.06	0.3270402	0.575024	-5.98	FALSE
261889_at	unknown protein	---	AT1G80810	-1.14	-0.19	-1.06	0.3270232	0.575024	-5.98	FALSE
258986_at	putative heat shock protein simil	---	AT3G08910	1.13	0.18	1.06	0.3270814	0.5750522	-5.98	FALSE
266815_at	F-box protein family, AtFBX5 co	---	AT2G44900	-1.15	-0.20	-1.06	0.3271393	0.5751096	-5.98	FALSE
248393_at	putative protein contains similarit	ATBAG1	AT5G52060	1.22	0.29	1.06	0.3275518	0.5754183	-5.98	TRUE
246595_at	formate dehydrogenase (FDH) ;	FDH	AT5G14780	-1.12	-0.17	-1.06	0.3274375	0.5754183	-5.98	TRUE
258700_at	putative SF16 protein similar to S	IQD1	AT3G09710	1.12	0.17	1.06	0.3274728	0.5754183	-5.98	FALSE
262921_at	transfactor, putative similar to tra	APL	AT1G79430	-1.13	-0.17	-1.06	0.3275665	0.5754183	-5.98	FALSE
247299_at	putative protein contains similarit	---	AT5G63900	1.11	0.15	1.06	0.3274674	0.5754183	-5.98	FALSE
252879_at	putative protein predicted protei	NST-K1	AT4G39390	1.36	0.44	1.06	0.3275494	0.5754183	-5.98	FALSE
261537_at	carbonyl reductase, putative sim	---	AT1G01800	-1.10	-0.14	-1.06	0.327516	0.5754183	-5.98	FALSE
259350_at	putative serine/threonine protein	RBK2	AT3G05140	1.14	0.19	1.06	0.3275451	0.5754183	-5.98	FALSE

248837_at	putative protein similar to unknov	---	AT5G47260	-1.10	-0.13	-1.06	0.3275672	0.5754183	-5.98	FALSE
252541_at	putative protein hypothetical pro	---	AT3G45750	-1.12	-0.16	-1.06	0.3273788	0.5754183	-5.98	FALSE
257622_at	hypothetical protein contains Pfa	---	AT3G20280	-1.19	-0.25	-1.06	0.3276237	0.5754733	-5.98	FALSE
250736_s_a	putative protein contains similarit	---	AT1G01350 ///	-1.18	-0.24	-1.06	0.3277105	0.5755371	-5.98	FALSE
264817_at	hypothetical protein similar to me	---	AT1G03540	1.11	0.15	1.06	0.327705	0.5755371	-5.98	FALSE
245953_at	myrosinase - binding protein - lik	---	AT5G28520	1.19	0.25	1.06	0.3277411	0.5755467	-5.98	FALSE
260945_at	hypothetical protein predicted by	---	AT1G05950	1.14	0.19	1.06	0.327768	0.5755496	-5.98	FALSE
249963_at	putative protein SPECKLE-TYPI	ATBPM1	AT5G19000	1.15	0.21	1.05	0.3278649	0.5756753	-5.98	FALSE
267006_at	putative membrane transporter ;	---	AT2G34190	1.14	0.19	1.05	0.3279202	0.5757281	-5.98	FALSE
257501_at	hypothetical protein predicted by	---	---	-1.09	-0.13	-1.05	0.3279496	0.5757354	-5.98	FALSE
262633_at	Expressed protein ; supported by	---	AT1G06630	-1.11	-0.15	-1.05	0.3282018	0.5759718	-5.98	FALSE
260034_at	putative DNA-binding protein Pfa	---	AT1G68810	-1.41	-0.49	-1.05	0.3281353	0.5759718	-5.98	FALSE
267113_at	hypothetical protein predicted by	---	AT2G14850	1.11	0.15	1.05	0.328145	0.5759718	-5.98	FALSE
247568_at	putative protein predicted protei	---	AT5G61260	1.27	0.35	1.05	0.3282105	0.5759718	-5.98	FALSE
262352_at	hypothetical protein similar to hyp	---	---	1.23	0.30	1.05	0.328194	0.5759718	-5.98	FALSE
266367_s_a	unknown protein	---	AT2G41390 ///	1.11	0.15	1.05	0.3283301	0.5761374	-5.98	FALSE
258484_at	sterol-C5-desaturase identical to	STE1	AT3G02580	-1.13	-0.18	-1.05	0.3284594	0.5762141	-5.98	TRUE
260295_at	putative aminopeptidase similar t	---	AT1G63770	-1.15	-0.21	-1.05	0.3284368	0.5762141	-5.98	FALSE
259755_at	unknown protein similar to glucos	---	AT1G71070	1.15	0.20	1.05	0.3285394	0.5762141	-5.98	FALSE
257572_at	hypothetical protein predicted by	---	AT3G16880	1.15	0.20	1.05	0.3285018	0.5762141	-5.98	FALSE
266657_at	unknown protein ;supported by f	---	AT2G25910	1.10	0.13	1.05	0.3284717	0.5762141	-5.98	FALSE
255609_s_a	hypothetical protein	---	AT4G01180 ///	1.10	0.14	1.05	0.3284773	0.5762141	-5.98	FALSE
263445_at	unknown protein	---	AT2G31590	1.11	0.15	1.05	0.3285506	0.5762141	-5.98	FALSE
245568_at	hypothetical protein	---	AT4G14650	1.17	0.23	1.05	0.3286935	0.576376	-5.98	FALSE
252494_at	receptor-like protein kinase rece	---	AT3G46760	1.13	0.18	1.05	0.3286738	0.576376	-5.98	FALSE
259613_at	hypothetical protein predicted by	---	AT1G48010	1.11	0.15	1.05	0.3287409	0.5764147	-5.98	FALSE
246151_at	putative protein predicted protein	---	AT5G19950	-1.14	-0.19	-1.05	0.3288265	0.5765205	-5.98	FALSE
248458_at	putative protein contains similarit	EYE	AT5G51430	-1.12	-0.16	-1.05	0.3289395	0.576631	-5.98	FALSE
257921_at	hypothetical protein contains Pfa	---	AT3G23270	1.10	0.14	1.05	0.32894	0.576631	-5.98	FALSE
262500_at	unknown protein Contains PF|00	FBP7	AT1G21760	-1.12	-0.16	-1.05	0.3290867	0.5768189	-5.98	FALSE
252471_at	phosphoprotein phosphatase ;su	TOPP5	AT3G46820	1.14	0.19	1.05	0.3291216	0.5768189	-5.98	FALSE
256800_at	hypothetical protein predicted by	---	AT3G20900	1.14	0.19	1.05	0.3291231	0.5768189	-5.98	FALSE
265151_at	hypothetical protein similar to hyp	---	AT1G51340	1.16	0.22	1.05	0.3292353	0.5769712	-5.98	TRUE
259159_at	unknown protein contains Pfam p	ACBP4	AT3G05420	1.18	0.23	1.05	0.3293262	0.5769974	-5.98	FALSE
262698_at	AMP-binding protein, putative co	---	AT1G75960	1.33	0.42	1.05	0.3293514	0.5769974	-5.98	FALSE

263376_at	putative surface protein ; suppor	FLA6	AT2G20520	1.10	0.14	1.05	0.3292835	0.5769974	-5.98	FALSE
253670_at	putative protein ; supported by fu	---	AT4G30010	1.13	0.18	1.05	0.3293362	0.5769974	-5.98	FALSE
264343_at	unknown protein ; supported by	---	AT1G11850	1.21	0.28	1.05	0.3295364	0.5772327	-5.98	FALSE
256777_at	hypothetical protein predicted by	---	AT3G13780	-1.12	-0.16	-1.05	0.3295325	0.5772327	-5.98	FALSE
253407_at	putative protein	---	AT4G32920	-1.14	-0.18	-1.05	0.3295678	0.5772435	-5.98	TRUE
251939_at	putative protein MICRONUCLEA	---	AT3G53440	-1.19	-0.26	-1.05	0.3297917	0.5775913	-5.98	FALSE
266140_at	nodulin-like protein ; supported b	---	AT2G28120	1.18	0.24	1.05	0.32996	0.5778416	-5.98	TRUE
266911_at	putative protein kinase contains a	---	AT2G45910	-1.17	-0.23	-1.05	0.3300269	0.5779145	-5.98	FALSE
262124_at	nucleoporin 98-like protein simila	---	AT1G59660	-1.10	-0.14	-1.05	0.3300651	0.5779369	-5.98	FALSE
264579_at	Expressed protein ; supported by	---	AT1G05205	-1.18	-0.24	-1.05	0.3301395	0.5779786	-5.98	FALSE
266708_at	putative chloroplast nucleoid DN	---	AT2G03200	1.18	0.24	1.05	0.3301256	0.5779786	-5.98	FALSE
250351_at	heat shock protein 17.6A	AT-HSP17.	AT5G12030	1.39	0.48	1.05	0.3301989	0.5779801	-5.98	TRUE
267242_at	hypothetical protein predicted by	---	AT2G02670	-1.12	-0.17	-1.05	0.3302124	0.5779801	-5.98	FALSE
253243_at	putative protein	---	AT4G34560	-1.59	-0.67	-1.05	0.3302164	0.5779801	-5.98	FALSE
250496_at	inorganic pyrophosphatase - like	AtPPa6	AT5G09650	-1.37	-0.46	-1.05	0.3302864	0.5780582	-5.98	FALSE
253637_at	putative protein ; supported by fu	---	AT4G30390	1.21	0.27	1.05	0.3303692	0.5781588	-5.98	FALSE
265372_at	Ac-like transposase related to Ac	---	AT2G06500	1.14	0.19	1.05	0.3305328	0.5784006	-5.98	FALSE
263640_at	hypothetical protein predicted by	---	AT2G25270	-1.12	-0.16	-1.05	0.3305693	0.5784203	-5.98	FALSE
255303_at	predicted protein of unknown fun	DER2.2	AT4G04860	-1.13	-0.17	-1.05	0.3306937	0.5785935	-5.98	FALSE
247546_at	Expressed protein ; supported by	---	AT5G61605	1.13	0.18	1.05	0.3308746	0.5788657	-5.99	FALSE
262945_at	unknown protein ;supported by fu	---	AT1G79510	-1.25	-0.32	-1.05	0.3309245	0.5789085	-5.99	FALSE
254511_at	hypothetical protein	---	AT4G20220	1.12	0.16	1.05	0.3309529	0.5789138	-5.99	FALSE
259729_at	hypothetical protein predicted by	---	AT1G77640	-1.41	-0.50	-1.05	0.3310011	0.5789538	-5.99	TRUE
250690_at	ABC transporter-like protein ; su	---	AT5G06530	-1.20	-0.27	-1.05	0.3310317	0.5789629	-5.99	TRUE
265161_at	putative vacuolar sorting recepto	---	AT1G30900	1.61	0.68	1.05	0.3310644	0.5789757	-5.99	FALSE
251070_at	translation initiation factor eIF-2	---	AT5G01940	-1.23	-0.30	-1.05	0.3311665	0.5791098	-5.99	FALSE
265703_at	putative ankyrin	---	AT2G03430	-1.16	-0.21	-1.05	0.3311986	0.5791215	-5.99	FALSE
259960_at	cell division control protein, puta	---	AT1G53710	1.16	0.22	1.05	0.3312241	0.5791217	-5.99	FALSE
254507_at	Glu-rich protein mature-parasite	---	AT4G20160	-1.11	-0.15	-1.05	0.3312546	0.5791307	-5.99	FALSE
260418_s_a	hypothetical protein predicted by	COX19-1	AT1G66590 //	-1.33	-0.41	-1.05	0.3314875	0.5794933	-5.99	FALSE
250915_at	homeodomain -like protein home	HB51	AT5G03790	1.21	0.28	1.05	0.3315408	0.579524	-5.99	FALSE
252988_at	putative cold-regulated protein c	---	AT4G38410	-1.26	-0.33	-1.05	0.3315558	0.579524	-5.99	FALSE
247676_at	putative protein RNaseP protein	---	AT5G59980	-1.23	-0.30	-1.05	0.3316234	0.5795976	-5.99	FALSE
267483_at	unknown protein ;supported by f	UTR1	AT2G02810	1.51	0.60	1.05	0.3316984	0.5796719	-5.99	FALSE
265382_at	putative gluconokinase ;support	---	AT2G16790	1.24	0.31	1.05	0.3317167	0.5796719	-5.99	FALSE

264112_at	putative 1,3-beta-D-glucan synth	CALS5	AT2G13680	1.14	0.19	1.05	0.3318912	0.5799324	-5.99	FALSE
246846_at	putative protein	---	AT5G26760	-1.11	-0.15	-1.05	0.3319381	0.5799701	-5.99	FALSE
265053_at	myrosinase binding protein, puta	---	AT1G52000	1.26	0.34	1.05	0.3319723	0.5799853	-5.99	FALSE
252935_at	dnaJ-like protein CAJ1 protein, S	---	AT4G39150	-1.11	-0.16	-1.05	0.3320072	0.5800018	-5.99	FALSE
253500_at	predicted protein RegA gene, Di	ARR10	AT4G31920	-1.20	-0.26	-1.05	0.3320454	0.5800242	-5.99	FALSE
248271_at	putative protein similar to unknov	---	AT5G53420	1.32	0.40	1.05	0.3320986	0.5800728	-5.99	FALSE
250233_at	putative protein weak homology	IQD11	AT5G13460	1.50	0.59	1.04	0.3322734	0.5803336	-5.99	TRUE
261403_at	unknown protein ;supported by fu	SYP52	AT1G79590	-1.11	-0.15	-1.04	0.3323073	0.5803483	-5.99	FALSE
261465_at	unknown protein	---	AT1G07705	1.11	0.15	1.04	0.3323926	0.5804529	-5.99	FALSE
256502_at	Eukaryotic translation initiation fa	---	AT1G36730 ///	-1.18	-0.24	-1.04	0.3324759	0.5804651	-5.99	FALSE
250280_at	putative protein many predicted	---	AT5G13230	-1.15	-0.20	-1.04	0.3324348	0.5804651	-5.99	FALSE
258209_at	expressed protein supported by c	GAPC1	AT3G04120 ///	1.33	0.41	1.04	0.3324548	0.5804651	-5.99	FALSE
262171_at	unknown protein ;supported by fu	TIFY10B	AT1G74950	1.21	0.28	1.04	0.3327307	0.5808654	-5.99	FALSE
260973_at	hypothetical protein predicted by	---	AT1G53490	1.11	0.15	1.04	0.3328643	0.5810542	-5.99	FALSE
260782_at	unknown protein ; supported by c	---	AT1G14570	-1.11	-0.15	-1.04	0.3329194	0.5811058	-5.99	FALSE
257852_at	unknown protein	---	AT3G12950	1.16	0.21	1.04	0.3329842	0.5811745	-5.99	FALSE
261051_at	cytochrome P450, putative simil	CYP703A2	AT1G01280	1.12	0.16	1.04	0.3330181	0.5811893	-5.99	FALSE
250123_at	putative protein contains similarit	PIN5	AT5G16530	-1.15	-0.20	-1.04	0.3331126	0.5812526	-5.99	FALSE
257302_at	hypothetical protein predicted by	---	AT3G30220	1.11	0.14	1.04	0.3331195	0.5812526	-5.99	FALSE
250919_at	putative protein myosin heavy ch	---	AT5G03660	-1.15	-0.20	-1.04	0.3331818	0.5812526	-5.99	FALSE
250179_at	putative protein	---	AT5G14440	-1.15	-0.20	-1.04	0.3331687	0.5812526	-5.99	FALSE
247937_at	Ca2+-transporting ATPase-like p	ACA8	AT5G57110	-1.25	-0.32	-1.04	0.3331674	0.5812526	-5.99	FALSE
260107_at	fructokinase, putative similar to f	---	AT1G66430	-1.57	-0.65	-1.04	0.3333533	0.5815073	-5.99	FALSE
259743_at	hypothetical protein predicted by	---	AT1G71140	1.59	0.67	1.04	0.3333943	0.5815342	-5.99	TRUE
253035_at	glycosyltransferase like protein a	CGL1	AT4G38240	-1.11	-0.15	-1.04	0.3334333	0.5815404	-5.99	FALSE
266910_at	unknown protein	---	AT2G45920	1.32	0.40	1.04	0.3334488	0.5815404	-5.99	FALSE
256984_at	hypothetical protein predicted by	---	AT3G13480	-1.14	-0.19	-1.04	0.333493	0.5815731	-5.99	FALSE
260839_at	unknown protein	---	AT1G43690	1.10	0.14	1.04	0.3335421	0.5816142	-5.99	FALSE
260691_s_a	hypothetical protein predicted by	---	---	1.13	0.17	1.04	0.3335685	0.5816159	-5.99	FALSE
247561_at	putative protein	---	AT5G61110	1.11	0.16	1.04	0.3336729	0.5817534	-5.99	FALSE
249272_at	geranylgeranyl transferase alpha	---	AT5G41820	1.19	0.25	1.04	0.3337825	0.581811	-5.99	FALSE
249072_at	putative protein similar to unknov	---	AT5G44060	1.46	0.55	1.04	0.3337709	0.581811	-5.99	FALSE
260788_at	cysteine proteinase contains sim	---	AT1G06260	1.12	0.16	1.04	0.3337646	0.581811	-5.99	FALSE
247630_at	putative protein	SIZ1	AT5G60410	1.14	0.19	1.04	0.3339286	0.5819275	-5.99	FALSE
262073_at	unknown protein ;supported by fu	ZCW32	AT1G59640	1.26	0.33	1.04	0.333925	0.5819275	-5.99	FALSE

251401_at	stellacyanin (uclacyanin 3) - like	---	AT3G60270	1.16	0.21	1.04	0.3339514	0.5819275	-5.99	FALSE
263767_at	putative retroelement pol polypro	---	---	1.10	0.14	1.04	0.3339487	0.5819275	-5.99	FALSE
262006_at	hypothetical protein predicted by	---	AT1G64570	1.12	0.17	1.04	0.3340056	0.5819775	-5.99	FALSE
252939_at	NAD(P)H oxidoreductase, isofla	---	AT4G39230	1.50	0.59	1.04	0.3340571	0.5819996	-5.99	TRUE
250756_at	putative protein strong similarity t	ROPGEF5	AT5G05940	1.13	0.18	1.04	0.3340919	0.5819996	-5.99	FALSE
254998_at	choline kinase GmCK2p -like pr	---	AT4G09760	-1.25	-0.32	-1.04	0.3340948	0.5819996	-5.99	FALSE
262685_at	unknown protein ; supported by	---	AT1G76010	-1.19	-0.25	-1.04	0.334206	0.5821489	-5.99	FALSE
257431_at	unknown protein	---	AT2G36360	1.13	0.17	1.04	0.3342758	0.5821815	-5.99	FALSE
264876_at	hypothetical protein	---	AT2G17410	1.13	0.18	1.04	0.334265	0.5821815	-5.99	FALSE
261451_at	unknown protein	---	AT1G21060	-1.42	-0.51	-1.04	0.3343634	0.5822895	-5.99	TRUE
245783_s_a	hypothetical protein similar to hy	---	AT1G35170 //	-1.39	-0.48	-1.04	0.3344533	0.5824017	-5.99	FALSE
267511_at	unknown protein	---	AT2G45670	1.12	0.16	1.04	0.3345356	0.582456	-5.99	FALSE
245620_at	hypothetical protein	---	AT4G14050	-1.14	-0.19	-1.04	0.3345273	0.582456	-5.99	FALSE
245413_at	asparagine--tRNA ligase	NS1	AT4G17300	-1.12	-0.17	-1.04	0.3346205	0.5824705	-5.99	FALSE
264606_at	unknown protein ;supported by f	---	AT1G04660	1.18	0.24	1.04	0.3345768	0.5824705	-5.99	FALSE
253760_at	putative protein (fragment) predi	AT4G28815	---	1.16	0.21	1.04	0.3346064	0.5824705	-5.99	FALSE
256032_at	polyprotein, putative similar to p	---	---	1.09	0.12	1.04	0.334702	0.5825308	-5.99	FALSE
254900_at	hypothetical protein	RALFL28	AT4G11510	1.10	0.14	1.04	0.3347062	0.5825308	-5.99	FALSE
249693_at	histidine kinase-like protein ; sup	AHK2	AT5G35750	-1.22	-0.29	-1.04	0.3347882	0.5825845	-5.99	TRUE
252396_at	hypothetical protein	---	AT3G47980	-1.11	-0.15	-1.04	0.3347877	0.5825845	-5.99	FALSE
254359_at	putative protein hypothetical pro	---	AT4G22360	-1.14	-0.19	-1.04	0.3350628	0.5829291	-5.99	FALSE
260450_at	hypothetical protein predicted by	---	AT1G72390	1.19	0.25	1.04	0.3350493	0.5829291	-5.99	FALSE
247695_at	putative protein Not2p, Homo sa	VIP2	AT5G59710	-1.11	-0.15	-1.04	0.3350327	0.5829291	-5.99	FALSE
263303_at	unknown protein ;supported by f	---	AT2G15240	-1.15	-0.20	-1.04	0.3351046	0.5829573	-5.99	FALSE
257895_at	dihydrolipoamide dehydrogenas	LPD1	AT3G16950	-1.26	-0.34	-1.04	0.3351534	0.5829977	-6.00	FALSE
265054_x_a	mutator-like transposase, putativ	---	---	1.16	0.22	1.04	0.3352031	0.5830397	-6.00	FALSE
248025_at	NOI protein, nitrate-induced	NOI	AT5G55850	1.15	0.20	1.04	0.3352322	0.5830458	-6.00	FALSE
263565_at	unknown protein	FUT4	AT2G15390	1.48	0.57	1.04	0.3353371	0.5831838	-6.00	TRUE
260921_at	amp-binding protein, putative sir	---	AT1G21540	-1.20	-0.27	-1.04	0.3354184	0.5831983	-6.00	FALSE
258169_at	hypothetical protein	---	AT3G21590	1.13	0.18	1.04	0.3354055	0.5831983	-6.00	FALSE
255376_x_a	putative athila-like protein	---	---	1.18	0.23	1.04	0.3354221	0.5831983	-6.00	FALSE
253913_at	myosin heavy chain - like protei	VIIIB	AT4G27370	1.11	0.15	1.04	0.3355805	0.5834208	-6.00	FALSE
255085_at	putative protein several hypothet	---	---	-1.12	-0.17	-1.04	0.3356012	0.5834208	-6.00	FALSE
257931_at	hypothetical protein predicted by	---	AT3G17030	-1.12	-0.16	-1.04	0.3356274	0.5834218	-6.00	FALSE
246413_at	unknown protein	---	AT1G77310	-1.13	-0.18	-1.04	0.3357877	0.5836112	-6.00	FALSE

267144_at	unknown protein	GPAT6	AT2G38110	-1.32	-0.41	-1.04	0.3357843	0.5836112	-6.00	FALSE
263613_at	unknown protein	---	AT2G25250	1.27	0.35	1.04	0.3358131	0.5836112	-6.00	FALSE
266406_at	hypothetical protein predicted by	---	AT2G38570	-1.15	-0.20	-1.04	0.3361287	0.5841151	-6.00	FALSE
250228_at	cell cycle switch protein	FZR3	AT5G13840	1.15	0.20	1.04	0.3361704	0.5841432	-6.00	FALSE
260675_at	unknown protein ; supported by	---	AT1G19430	-1.16	-0.21	-1.04	0.3361963	0.5841437	-6.00	FALSE
253660_at	putative protein proline-rich prot	---	AT4G30140	1.11	0.16	1.04	0.3362266	0.5841517	-6.00	FALSE
265928_at	Ac-like transposase related to Ac	---	---	1.15	0.20	1.04	0.3362866	0.5842115	-6.00	FALSE
255584_at	putative reverse transcriptase-lik	---	---	1.11	0.15	1.04	0.3363835	0.5842464	-6.00	FALSE
263124_at	beta-Amyrin Synthase, putative	---	AT1G78480	-1.17	-0.23	-1.04	0.3363343	0.5842464	-6.00	FALSE
256018_at	plastid heme oxygenase, putativ	ho4	AT1G58300	-1.21	-0.27	-1.04	0.3363663	0.5842464	-6.00	FALSE
250347_at	putative protein	---	AT5G11960	1.12	0.16	1.03	0.3364929	0.5843918	-6.00	FALSE
255106_at	putative protein hypothetical prot	---	---	1.10	0.14	1.03	0.3365319	0.5844151	-6.00	FALSE
263324_at	hypothetical protein predicted by	---	AT2G04220	1.11	0.15	1.03	0.3367638	0.5847733	-6.00	FALSE
258773_at	hypothetical protein predicted by	---	AT3G10730	1.09	0.13	1.03	0.3368513	0.5848096	-6.00	FALSE
265452_at	putative bHLH transcription facto	ATAIB	AT2G46510	1.45	0.54	1.03	0.3368616	0.5848096	-6.00	FALSE
249730_at	calcium dependent protein kinas	---	AT5G24430	1.28	0.35	1.03	0.3368203	0.5848096	-6.00	FALSE
250344_at	glutaredoxin - like protein glutare	---	AT5G11930	1.25	0.32	1.03	0.336918	0.5848629	-6.00	FALSE
262141_s_a	hypothetical protein predicted by	---	AT1G52440 /	-1.09	-0.13	-1.03	0.3369578	0.5848876	-6.00	FALSE
252046_at	putative protein extensin -Nicotia	---	AT3G52460	1.14	0.19	1.03	0.3369982	0.5849131	-6.00	FALSE
262883_at	ammonium transporter, puitative	ATAMT1;2	AT1G64780	-1.23	-0.29	-1.03	0.337118	0.5849415	-6.00	FALSE
262742_at	GTP-binding protein, putative si	AtRABA1i	AT1G28550	1.11	0.16	1.03	0.3371428	0.5849415	-6.00	FALSE
264590_at	unknown protein ;supported by f	---	AT2G17710	-1.70	-0.77	-1.03	0.3370448	0.5849415	-6.00	FALSE
263364_at	unknown protein predicted by ge	---	AT2G20540	-1.10	-0.14	-1.03	0.3371266	0.5849415	-6.00	FALSE
250528_at	putative protein strong similarity t	---	AT5G08600	-1.10	-0.13	-1.03	0.3371021	0.5849415	-6.00	FALSE
266434_s_a	unknown protein	---	AT2G07120 /	1.11	0.15	1.03	0.3372006	0.5849973	-6.00	FALSE
262331_at	unknown protein	---	AT1G64050	1.10	0.13	1.03	0.3372859	0.5851009	-6.00	FALSE
261421_at	hypothetical protein similar to unl	IQD30	AT1G18840	-1.32	-0.40	-1.03	0.3374201	0.5852473	-6.00	TRUE
245898_at	ser/thr specific protein kinase-lik	---	AT5G11020	-1.16	-0.21	-1.03	0.3374217	0.5852473	-6.00	FALSE
258389_at	hypothetical protein predicted by	SDE5	AT3G15390	1.16	0.21	1.03	0.3375091	0.58531	-6.00	FALSE
258444_at	expressed protein supported by	TIC	AT3G22380	-1.12	-0.17	-1.03	0.3374976	0.58531	-6.00	FALSE
257754_at	GTP binding protein, putative si	ATRAB7B	AT3G18820	-1.11	-0.15	-1.03	0.3375529	0.5853415	-6.00	FALSE
255463_at	putative polyprotein of LTR trans	---	---	1.13	0.17	1.03	0.3376049	0.5853872	-6.00	FALSE
245939_at	oxoglutarate/malate translocator	---	AT5G19760	-1.13	-0.17	-1.03	0.3378129	0.5854808	-6.00	FALSE
254761_at	Expressed protein ; supported by	CLE44	AT4G13195	1.18	0.24	1.03	0.3377997	0.5854808	-6.00	FALSE
262466_at	hypothetical protein similar to hy	NTMC2T5.	AT1G50260	1.16	0.22	1.03	0.3377306	0.5854808	-6.00	FALSE

263790_at	hypothetical protein predicted by	---	AT2G24530	-1.16	-0.22	-1.03	0.3377738	0.5854808	-6.00	FALSE
257379_x_a	Mutator-like transposase similar	---	---	1.12	0.16	1.03	0.3377614	0.5854808	-6.00	FALSE
251101_at	putative transporter protein Na+/	CHX26	AT5G01680	1.10	0.13	1.03	0.3377036	0.5854808	-6.00	FALSE
259878_at	putative catechol O-methyltransf	---	AT1G76790	1.30	0.38	1.03	0.3379994	0.5857595	-6.00	TRUE
253586_s_a	putative protein hypothetical pro	---	AT4G30710 /	-1.22	-0.28	-1.03	0.3380376	0.5857812	-6.00	FALSE
265217_s_a	unknown protein ESTs gb|H7659	---	AT1G05090 /	-1.19	-0.25	-1.03	0.3380691	0.5857912	-6.00	FALSE
264737_at	unknown protein	---	AT1G62210	1.17	0.23	1.03	0.3382539	0.586067	-6.00	FALSE
265141_at	hypothetical protein predicted by	---	AT1G51350	1.13	0.17	1.03	0.3383112	0.5860771	-6.00	FALSE
253204_at	GTP binding protein beta subunit	AGB1	AT4G34460	1.10	0.14	1.03	0.3383103	0.5860771	-6.00	FALSE
258512_at	beta-glucosidase, putative simila	---	AT3G06510 /	1.09	0.13	1.03	0.3383944	0.586104	-6.00	FALSE
251726_at	protein kinase NPK1-related pro	---	AT3G56280	1.09	0.13	1.03	0.3384175	0.586104	-6.00	FALSE
262675_at	anter-specific proline-rich -like pr	EXL6	AT1G75930	1.14	0.18	1.03	0.3384438	0.586104	-6.00	FALSE
257675_at	ethylene responsive element bir	ERF7	AT3G20310	-1.15	-0.21	-1.03	0.3385579	0.586104	-6.00	FALSE
257665_at	unknown protein	---	AT3G20430	-1.11	-0.15	-1.03	0.3385348	0.586104	-6.00	FALSE
252232_at	bZIP transcription factor - like pr	AtbZIP5	AT3G49760	1.10	0.14	1.03	0.3384499	0.586104	-6.00	FALSE
266976_at	putative phospholipase	---	AT2G39410	1.20	0.26	1.03	0.3385409	0.586104	-6.00	FALSE
255122_at	putative athila-like protein	---	---	-1.17	-0.22	-1.03	0.3385235	0.586104	-6.00	FALSE
254772_at	extensin-like protein extensin cla	---	AT4G13390	-1.09	-0.12	-1.03	0.3385545	0.586104	-6.00	FALSE
263965_at	putative retroelement pol polypro	---	---	1.13	0.17	1.03	0.3385862	0.5861084	-6.00	FALSE
252275_at	ubiquitin-specific protease 26 (U	UBP26	AT3G49600	1.18	0.24	1.03	0.3386809	0.5862279	-6.00	FALSE
257645_at	unknown protein ;supported by f	---	AT3G25790	1.16	0.21	1.03	0.3389915	0.5866765	-6.00	FALSE
245522_at	hypothetical protein	---	AT4G15890	1.11	0.15	1.03	0.3389846	0.5866765	-6.00	FALSE
265603_at	hypothetical protein predicted by	---	---	-1.13	-0.18	-1.03	0.339044	0.5867228	-6.00	FALSE
261972_at	hypothetical protein predicted by	---	AT1G64600	-1.22	-0.29	-1.03	0.3392583	0.5869601	-6.00	TRUE
253846_at	putative protein MSP1, Sacchar	---	AT4G28000	1.10	0.14	1.03	0.3392514	0.5869601	-6.00	FALSE
257898_s_a	hypothetical protein predicted by	---	---	-1.09	-0.13	-1.03	0.3392363	0.5869601	-6.00	FALSE
258676_at	hypothetical protein predicted by	---	AT3G08600	-1.15	-0.20	-1.03	0.3393642	0.5870098	-6.00	TRUE
250393_at	serine/threonine protein phospha	---	AT5G10900	1.13	0.18	1.03	0.3393401	0.5870098	-6.00	FALSE
257453_at	hypothetical protein predicted by	---	AT1G65130	1.14	0.19	1.03	0.339347	0.5870098	-6.00	FALSE
256087_at	hypothetical protein predicted by	---	AT1G20800	1.12	0.16	1.03	0.339433	0.5870842	-6.00	FALSE
258891_at	unknown protein	EMB2016	AT3G05680	-1.11	-0.15	-1.03	0.3395361	0.587218	-6.01	FALSE
265503_at	putative non-LTR retroelement re	---	---	1.16	0.21	1.03	0.33957	0.5872321	-6.01	FALSE
263465_at	hypothetical protein predicted by	---	AT2G31940	1.15	0.21	1.03	0.3396436	0.5873149	-6.01	FALSE
248245_at	MtN3 protein-like	---	AT5G53190	1.15	0.20	1.03	0.3396894	0.5873495	-6.01	FALSE
260524_at	unknown protein	---	AT2G47230	1.12	0.16	1.03	0.3398959	0.5876621	-6.01	FALSE

265811_at	unknown protein possibly related	EDA2	AT2G18080	1.12	0.16	1.03	0.3399543	0.5877185	-6.01	FALSE
259628_at	hypothetical protein contains Pfa	---	AT1G56440	-1.18	-0.24	-1.03	0.3400108	0.5877716	-6.01	FALSE
267042_at	putative non-LTR retroelement re	---	AT2G34320	1.12	0.16	1.03	0.3401442	0.5879577	-6.01	FALSE
266026_at	putative non-LTR retroelement re	---	---	1.13	0.18	1.03	0.3402193	0.5879983	-6.01	FALSE
247473_at	putative protein AT-hook protein	---	AT5G62260	1.17	0.22	1.03	0.3401987	0.5879983	-6.01	FALSE
259709_at	Expressed protein ; supported by	---	AT1G77655	1.14	0.19	1.03	0.3402705	0.5880021	-6.01	FALSE
263309_at	putative replication protein A1	---	---	1.18	0.24	1.03	0.340273	0.5880021	-6.01	FALSE
257116_at	arginine methyltransferase, puta	PRMT6	AT3G20020	-1.14	-0.19	-1.03	0.3403475	0.5880862	-6.01	FALSE
247321_s_a	phosphatidylinositol 4-kinase (en	PI-4KBETA	AT5G09350 ///	-1.17	-0.22	-1.03	0.3403975	0.5881023	-6.01	FALSE
260346_at	hypothetical protein predicted by	CLE10	AT1G69320 ///	1.15	0.20	1.03	0.3404084	0.5881023	-6.01	FALSE
265677_at	putative purine-rich single-strand	PUR ALPH	AT2G32080	1.11	0.15	1.03	0.3404862	0.5881032	-6.01	FALSE
263111_s_a	hypothetical protein contains sim	---	AT1G65190 ///	1.18	0.24	1.03	0.3404755	0.5881032	-6.01	FALSE
255195_at	may be a pseudogene	---	---	1.11	0.15	1.03	0.3404766	0.5881032	-6.01	FALSE
254506_at	leucine rich repeat-like protein C	GSO1	AT4G20140	-1.17	-0.22	-1.03	0.3405502	0.5881691	-6.01	FALSE
246953_at	unknown protein ;supported by f	VPS60.2	AT5G04850	-1.12	-0.16	-1.03	0.340737	0.5884027	-6.01	FALSE
263518_at	Expressed protein ; supported by	---	AT2G21655	1.12	0.16	1.03	0.3407125	0.5884027	-6.01	FALSE
261974_at	protein kinase, putative similar to	CPuORF57	AT1G64628 ///	-1.12	-0.16	-1.03	0.3407782	0.5884063	-6.01	FALSE
258761_at	unknown protein	---	AT3G10760	-1.20	-0.26	-1.02	0.3407907	0.5884063	-6.01	FALSE
262315_at	unknown protein ;supported by fu	---	AT1G70990	1.28	0.36	1.02	0.3408953	0.5885424	-6.01	FALSE
252276_at	hypothetical protein ; supported	---	AT3G49490	1.14	0.19	1.02	0.341002	0.5886374	-6.01	FALSE
265234_at	hypothetical protein	---	AT2G07721	1.14	0.19	1.02	0.3409899	0.5886374	-6.01	FALSE
254041_at	Expressed protein ; supported by	---	AT4G25830	1.46	0.55	1.02	0.3411078	0.5886864	-6.01	TRUE
260111_at	hypothetical protein similar to unl	---	AT1G63320	-1.10	-0.13	-1.02	0.3411073	0.5886864	-6.01	FALSE
262004_at	calcineurin B-like protein similar t	CBL8	AT1G64480	1.18	0.23	1.02	0.3411042	0.5886864	-6.01	FALSE
262572_at	unknown protein Contains a PF|	---	AT1G15140	1.16	0.21	1.02	0.3411445	0.5887052	-6.01	FALSE
249505_at	putative protein	---	---	1.26	0.34	1.02	0.3412132	0.5887793	-6.01	FALSE
266762_at	putative alcohol dehydrogenase	---	AT2G47120	-1.11	-0.15	-1.02	0.3412459	0.5887911	-6.01	FALSE
264108_at	hypothetical protein predicted by	CALS5	AT2G13680	1.11	0.15	1.02	0.3413973	0.5889996	-6.01	FALSE
254341_at	serine/threonine protein kinase l	SRF8	AT4G22130	1.36	0.45	1.02	0.34143	0.5889996	-6.01	FALSE
265180_at	putative OBP32pep protein ;sup	---	AT1G23590	1.09	0.12	1.02	0.3414442	0.5889996	-6.01	FALSE
264637_at	allyl alcohol dehydrogenase, put	---	AT1G65560	-1.19	-0.25	-1.02	0.3414723	0.5890036	-6.01	FALSE
266574_at	hypothetical protein predicted by	---	AT2G23890	-1.27	-0.34	-1.02	0.3415766	0.5890943	-6.01	FALSE
259004_at	putative protein kinase C-termin	---	AT3G01840	1.12	0.16	1.02	0.3415583	0.5890943	-6.01	FALSE
263780_at	hypothetical protein predicted by	SPA1	AT2G46340	1.23	0.30	1.02	0.3416514	0.5891789	-6.01	FALSE
247518_at	putative protein many predicted	---	AT5G61800	-1.14	-0.19	-1.02	0.341688	0.5891975	-6.01	FALSE

263252_at	putative CONSTANS-like B-box	STH	AT2G31380	-1.21	-0.28	-1.02	0.3417188	0.589206	-6.01	FALSE
250894_s_a	putative protein proline-rich prot	---	AT5G03810 /	1.13	0.18	1.02	0.3418049	0.5892695	-6.01	FALSE
264620_at	putative bZIP transcription factor	ATBZIP27	AT2G17770	1.15	0.20	1.02	0.3418073	0.5892695	-6.01	FALSE
266764_at	putative pectinesterase ;support	---	AT2G47050	1.13	0.18	1.02	0.34195	0.5894709	-6.01	FALSE
263020_at	unknown protein	---	AT1G23880	-1.11	-0.16	-1.02	0.3421504	0.5897719	-6.01	FALSE
258131_at	protein kinase, putative similar t	---	AT3G24540	1.17	0.23	1.02	0.3422043	0.5898201	-6.01	FALSE
253641_at	hypothetical protein ;supported b	---	AT4G29980	1.14	0.19	1.02	0.3422685	0.5898862	-6.01	FALSE
259020_at	unknown protein ; supported by	---	AT3G07470	-1.15	-0.20	-1.02	0.342402	0.590016	-6.01	TRUE
246815_at	putative protein integrin analogu	---	AT5G27220	-1.10	-0.14	-1.02	0.3424214	0.590016	-6.01	FALSE
253326_at	putative protein polygalacturona	---	AT4G33440	-1.13	-0.17	-1.02	0.3424189	0.590016	-6.01	FALSE
261561_at	unknown protein ;supported by fu	---	AT1G01730	-1.18	-0.24	-1.02	0.3424575	0.5900337	-6.01	FALSE
266936_at	hypothetical protein predicted by	---	AT2G18920	1.10	0.14	1.02	0.3425	0.5900624	-6.01	FALSE
245251_at	calcineurin B-like protein 1 ; supp	CBL1	AT4G17615	1.41	0.49	1.02	0.3425503	0.5901044	-6.01	TRUE
256210_at	hypothetical protein	---	AT1G50950	-1.40	-0.49	-1.02	0.3425821	0.5901145	-6.01	FALSE
261020_at	hypothetical protein similar to ret	---	AT1G26390	-1.38	-0.46	-1.02	0.3426397	0.5901693	-6.01	TRUE
253918_at	putative protein ; supported by fu	PHOS34	AT4G27320	-1.13	-0.17	-1.02	0.3427775	0.590362	-6.01	FALSE
260198_at	F12A21.23 hypothetical protein	---	AT1G67635	1.10	0.14	1.02	0.3428908	0.5905126	-6.01	FALSE
265462_at	putative vetispiradiene synthase	---	AT2G37140	1.13	0.18	1.02	0.3429222	0.5905221	-6.01	FALSE
249465_at	AIG2 - like protein AIG2, Arabid	AIG2L	AT5G39720	1.13	0.18	1.02	0.3429607	0.5905438	-6.01	FALSE
257413_at	putative RNA-binding protein co	---	AT1G22910	1.19	0.25	1.02	0.3430782	0.5906661	-6.01	FALSE
258197_at	hypothetical protein predicted by	ATBRXL2	AT3G14000	-1.14	-0.19	-1.02	0.3430835	0.5906661	-6.01	FALSE
258904_at	putative ATPase (ISW2-like) sim	CHR11	AT3G06400	-1.13	-0.18	-1.02	0.3431512	0.5906934	-6.01	FALSE
266898_at	unknown protein ; supported by	---	AT2G45990	-1.15	-0.20	-1.02	0.343144	0.5906934	-6.01	FALSE
261021_at	hypothetical protein similar to ret	---	AT1G26380	1.70	0.77	1.02	0.3432531	0.5907797	-6.01	TRUE
265292_s_a	hypothetical protein predicted by	---	---	-1.10	-0.14	-1.02	0.3432448	0.5907797	-6.01	FALSE
258578_at	germin-like protein contains Pfam	---	AT3G04200	1.20	0.26	1.02	0.3435272	0.5908985	-6.01	FALSE
254006_at	putative protein various predicte	---	AT4G26340	1.12	0.16	1.02	0.3433752	0.5908985	-6.01	FALSE
265522_at	putative TPR repeat nuclear pho	ELF8	AT2G06210	-1.14	-0.18	-1.02	0.3434344	0.5908985	-6.01	FALSE
256373_at	hypothetical protein	SGA2	AT1G66740	1.16	0.22	1.02	0.3434367	0.5908985	-6.01	FALSE
263190_at	mutator-like transposase, putativ	---	---	1.10	0.13	1.02	0.3433542	0.5908985	-6.01	FALSE
252447_at	beta-D-glucan exohydrolase - lik	---	AT3G47040	1.12	0.16	1.02	0.3435294	0.5908985	-6.01	FALSE
247811_at	leucine zipper-containing protein	ATEXO70B	AT5G58430	1.32	0.40	1.02	0.3434809	0.5908985	-6.01	FALSE
245615_at	reverse transcriptase like protein	---	---	1.11	0.15	1.02	0.3434818	0.5908985	-6.01	FALSE
246760_at	putative protein predicted protei	---	AT5G27970	1.11	0.15	1.02	0.3435862	0.5909145	-6.01	FALSE
250431_at	cyclin protein - like cyclin D2.1 p	CYCD4;2	AT5G10440	1.12	0.16	1.02	0.3435905	0.5909145	-6.01	FALSE

264823_at	putative serine/threonine protein	BSU1	AT1G03445	1.17	0.23	1.02	0.3437036	0.5910296	-6.01	FALSE
263383_at	putative protein kinase contains a	---	AT2G40120	1.14	0.19	1.02	0.3437092	0.5910296	-6.01	FALSE
250236_at	delta subunit of mitochondrial F1	---	AT5G13450	1.14	0.19	1.02	0.3438736	0.5912676	-6.01	FALSE
253093_at	putative protein SPINDLY protei	SRFR1	AT4G37460	-1.12	-0.16	-1.02	0.343909	0.5912839	-6.02	FALSE
260577_at	hypothetical protein predicted by	---	AT2G47340	1.12	0.16	1.02	0.3440181	0.591427	-6.02	FALSE
250674_at	laccase-like protein laccase - Pc	LAC13	AT5G07130	1.21	0.27	1.02	0.3440723	0.5914755	-6.02	FALSE
256712_at	unknown protein similar to T14G	---	AT2G34020	1.10	0.13	1.02	0.3441226	0.5915175	-6.02	FALSE
252875_at	GTP-binding protein GB3 ;suppo	RABA4B	AT4G39990	-1.11	-0.15	-1.02	0.3441822	0.5915297	-6.02	FALSE
267304_at	putative Fe(II) transport protein	ZIP6	AT2G30080	-1.16	-0.21	-1.02	0.3442075	0.5915297	-6.02	FALSE
259736_at	endo-beta-1,4-glucanase, putati	AtGH9C2	AT1G64390	1.82	0.86	1.02	0.3441759	0.5915297	-6.02	FALSE
257409_at	unknown protein predicted by ge	---	AT2G17470	1.14	0.18	1.02	0.3442435	0.5915408	-6.02	FALSE
266383_at	putative pathogenesis related-1 (	ATPRB1	AT2G14580	-1.19	-0.25	-1.02	0.3442658	0.5915408	-6.02	FALSE
262043_at	unknown protein	PSF1	AT1G80190	-1.17	-0.22	-1.02	0.344371	0.5916768	-6.02	FALSE
256483_at	hypothetical protein	---	AT1G31410	-1.15	-0.21	-1.02	0.3444435	0.5917569	-6.02	FALSE
245648_at	F5A9.12 hypothetical protein	---	---	1.12	0.16	1.02	0.3445325	0.5917761	-6.02	FALSE
AFFX-r2-At-	Arabidopsis thaliana /REF=U37	---	---	-1.10	-0.14	-1.02	0.3445109	0.5917761	-6.02	FALSE
246362_at	hypothetical protein	---	---	-1.09	-0.13	-1.02	0.3444991	0.5917761	-6.02	FALSE
250850_at	putative protein ; supported by c	---	AT5G04550	1.15	0.20	1.02	0.3446042	0.5918547	-6.02	FALSE
263673_at	unknown protein	---	AT2G04800	1.20	0.26	1.02	0.3446498	0.5918801	-6.02	FALSE
259931_at	hypothetical protein predicted by	---	AT1G34400	1.13	0.17	1.02	0.3446709	0.5918801	-6.02	FALSE
245515_at	hypothetical protein	---	AT4G15810	-1.23	-0.30	-1.02	0.3447303	0.5919375	-6.02	FALSE
264588_at	unknown protein contains similar	---	AT2G17730	-1.28	-0.35	-1.02	0.344794	0.5920023	-6.02	FALSE
248071_at	unknown protein	---	AT5G55670	-1.12	-0.17	-1.02	0.3448845	0.5921132	-6.02	FALSE
248350_at	putative protein similar to unknov	---	AT5G52160	1.11	0.15	1.02	0.344947	0.5921759	-6.02	FALSE
264808_at	unknown protein similar to EST g	PRA1.E	AT1G08770	1.11	0.16	1.02	0.344991	0.5922037	-6.02	FALSE
247590_at	putative protein predicted protei	---	AT5G60720	1.14	0.19	1.02	0.3450151	0.5922037	-6.02	FALSE
252869_at	putative protein	---	AT4G39930	1.12	0.16	1.01	0.345242	0.5924481	-6.02	FALSE
253599_at	putative protein ash1 protein, Dr	SDG4	AT4G30860	1.19	0.25	1.01	0.3452259	0.5924481	-6.02	FALSE
253565_at	predicted protein DAN26, Homo	---	AT4G31200	-1.16	-0.21	-1.01	0.3452545	0.5924481	-6.02	FALSE
251067_at	hypothetical protein	---	AT5G01910	-1.18	-0.24	-1.01	0.3452614	0.5924481	-6.02	FALSE
257373_at	hypothetical protein predicted by	---	AT2G43140	1.16	0.21	1.01	0.3453607	0.5924849	-6.02	FALSE
265105_s_a	unknown protein contains similar	---	AT1G62580 ///	1.10	0.13	1.01	0.3453215	0.5924849	-6.02	FALSE
265124_at	hypothetical protein similar to put	---	AT1G55430	-1.14	-0.19	-1.01	0.3453423	0.5924849	-6.02	FALSE
245218_s_a	viral resistance protein, putative	---	AT1G58848 ///	1.10	0.13	1.01	0.3454205	0.5924982	-6.02	FALSE
249921_at	reverse-transcriptase - like protei	---	AT5G19270	1.11	0.16	1.01	0.3454189	0.5924982	-6.02	FALSE

249131_at	putative protein contains similarit	APUM14	AT5G43110	-1.10	-0.14	-1.01	0.345458	0.592518	-6.02	FALSE
253778_at	heat-shock protein heat-shock p	---	AT4G28480	1.15	0.20	1.01	0.3455651	0.5926352	-6.02	FALSE
248029_at	beta-amylase ; supported by cD	BAM4	AT5G55700	-1.13	-0.18	-1.01	0.3455783	0.5926352	-6.02	FALSE
249531_at	putative protein predicted protei	AtGDU7	AT5G38770	1.11	0.15	1.01	0.3456281	0.5926761	-6.02	FALSE
255814_at	unknown protein	---	AT1G19900	1.11	0.15	1.01	0.3459118	0.5929842	-6.02	FALSE
250812_at	putative protein similar to unknov	---	AT5G04900	-1.11	-0.15	-1.01	0.3459029	0.5929842	-6.02	FALSE
260756_at	hypothetical protein contains sin	---	AT1G48970	1.10	0.14	1.01	0.345867	0.5929842	-6.02	FALSE
252551_at	phospholipase - like protein cyto	---	AT3G45880	-1.17	-0.22	-1.01	0.345875	0.5929842	-6.02	FALSE
246968_at	RING finger-like protein RING-H	---	AT5G24870	-1.17	-0.22	-1.01	0.3459503	0.5930057	-6.02	TRUE
245164_at	mitochondrial chaperonin (HSP6	HSP60-2	AT2G33210	-1.32	-0.40	-1.01	0.3461064	0.5931841	-6.02	FALSE
257200_at	hypothetical protein predicted by	---	---	-1.10	-0.13	-1.01	0.3460873	0.5931841	-6.02	FALSE
248958_at	unknown protein ; supported by	---	AT5G45590	-1.18	-0.23	-1.01	0.3461799	0.5932655	-6.02	FALSE
248291_at	putative protein similar to unknov	---	AT5G53020	1.13	0.17	1.01	0.3462745	0.593383	-6.02	FALSE
251323_at	delta-8 sphingolipid desaturase	---	AT3G61580	1.13	0.18	1.01	0.346372	0.5934291	-6.02	TRUE
245053_at	putative pectinesterase	---	AT2G26450	1.17	0.23	1.01	0.3463795	0.5934291	-6.02	FALSE
254316_at	putative protein glycine-rich cell	---	---	1.13	0.17	1.01	0.3463413	0.5934291	-6.02	FALSE
257604_s_a	hypothetical protein predicted by	---	AT1G11810 /	-1.11	-0.15	-1.01	0.3464353	0.5934802	-6.02	FALSE
262516_at	putative glutathione transferase (	ATGSTU26	AT1G17190	1.13	0.17	1.01	0.3466116	0.5936533	-6.02	FALSE
256477_at	unknown protein	---	---	1.12	0.16	1.01	0.3465626	0.5936533	-6.02	FALSE
266123_at	unknown protein identical to GB:	---	AT2G45180	-1.09	-0.13	-1.01	0.3466144	0.5936533	-6.02	FALSE
258641_at	unknown protein ;supported by f	---	AT3G08030	-1.49	-0.57	-1.01	0.346995	0.5939811	-6.02	TRUE
267416_at	putative phosphatidylinositol-glyc	SETH1	AT2G34980	1.11	0.15	1.01	0.3470586	0.5939811	-6.02	FALSE
262149_at	hypothetical protein predicted by	---	AT1G52530	-1.16	-0.22	-1.01	0.347109	0.5939811	-6.02	FALSE
266990_at	putative ABC transporter	ATATH8	AT2G39190	-1.25	-0.32	-1.01	0.3469566	0.5939811	-6.02	FALSE
263089_at	putative retroelement pol polypro	---	---	1.15	0.21	1.01	0.3469551	0.5939811	-6.02	FALSE
249239_at	MAP kinase ; supported by cDN	CPuORF58	AT5G41990 /	1.11	0.15	1.01	0.3471661	0.5939811	-6.02	FALSE
265468_at	hypothetical protein predicted by	---	AT2G37210	1.12	0.17	1.01	0.3469379	0.5939811	-6.02	FALSE
254925_at	beta-adaptin - like protein beta-a	---	AT4G11380	-1.14	-0.19	-1.01	0.3471704	0.5939811	-6.02	FALSE
264444_at	putative squamosa-promoter bin	---	AT1G27360	1.12	0.16	1.01	0.3471616	0.5939811	-6.02	FALSE
257557_at	terpene synthase-related protein	---	AT3G14490	1.16	0.21	1.01	0.3470041	0.5939811	-6.02	FALSE
253963_at	putative protein probable calciun	---	AT4G26470	1.24	0.31	1.01	0.3471696	0.5939811	-6.02	FALSE
256150_at	beta-fructofuranosidase identical	ATFRUCT5	AT1G55120	1.29	0.36	1.01	0.3470676	0.5939811	-6.02	FALSE
253990_at	putative thioredoxin thioredoxin	ACHT1	AT4G26160	-1.23	-0.29	-1.01	0.3469323	0.5939811	-6.02	FALSE
263409_at	predicted protein	---	AT2G04063	-1.12	-0.16	-1.01	0.3471535	0.5939811	-6.02	FALSE
261595_at	hypothetical protein predicted by	---	AT1G33070	1.09	0.13	1.01	0.3473183	0.5940233	-6.02	FALSE

260555_at	hypothetical protein predicted by	---	AT2G41780	1.37	0.45	1.01	0.3473299	0.5940233	-6.02	FALSE
256132_at	hypothetical protein similar to hyp	---	AT1G13610	1.12	0.16	1.01	0.3472874	0.5940233	-6.02	FALSE
265748_at	putative Athila retroelement ORF	---	---	1.12	0.17	1.01	0.347347	0.5940233	-6.02	FALSE
247893_at	RNA polymerase I, II and III 24.3	RPB5C	AT5G57980	1.16	0.21	1.01	0.3473428	0.5940233	-6.02	FALSE
250499_at	beta-xylosidase - like protein bet	BXL3	AT5G09730	-1.12	-0.16	-1.01	0.3473513	0.5940233	-6.02	FALSE
251194_at	putative protein	---	AT3G62920	-1.20	-0.27	-1.01	0.3474455	0.5940954	-6.02	FALSE
253170_at	putative protein various predicte	---	AT4G35130	1.10	0.14	1.01	0.3474302	0.5940954	-6.02	FALSE
252431_at	putative protein	MAG2	AT3G47700	1.19	0.26	1.01	0.3475233	0.5941838	-6.02	FALSE
259503_at	unknown protein ; supported by c	---	AT1G15870	-1.18	-0.24	-1.01	0.347615	0.5942532	-6.02	FALSE
252150_at	vacuolar sorting protein 35 homo	VPS35C	AT3G51310	1.11	0.14	1.01	0.347616	0.5942532	-6.02	FALSE
258842_at	unknown protein similar to putati	CLPS3	AT3G04680	-1.16	-0.22	-1.01	0.3477684	0.5943801	-6.02	FALSE
263990_at	putative phosphoprotein phospha	PP5.2	AT2G42810	-1.12	-0.16	-1.01	0.3477608	0.5943801	-6.02	FALSE
266658_at	Expressed protein ; supported by	---	AT2G25735	1.80	0.84	1.01	0.3477263	0.5943801	-6.02	FALSE
261486_at	nucleic acid binding protein (alfi	AL7	AT1G14510	-1.13	-0.17	-1.01	0.3479544	0.5946536	-6.02	FALSE
252565_at	actin depolymerizing factor 2 (AD	ADF2	AT3G46000	-1.10	-0.14	-1.01	0.3479827	0.5946573	-6.02	FALSE
247714_at	wuschel protein - like wuschel pr	WOX2	AT5G59340	1.22	0.28	1.01	0.3481118	0.5948333	-6.02	FALSE
252624_at	Expressed protein ; supported by	PSK1	AT3G44735	1.29	0.37	1.01	0.3482355	0.594911	-6.02	TRUE
264116_at	putative poly (ADP-ribose) polym	PARP2	AT2G31320	-1.24	-0.31	-1.01	0.348235	0.594911	-6.02	FALSE
252777_at	hypothetical protein	---	AT3G42970	1.11	0.15	1.01	0.3482326	0.594911	-6.02	FALSE
253940_at	putative protein other Arabidopsi	---	AT4G26950	-1.14	-0.19	-1.01	0.3483965	0.5951005	-6.03	FALSE
261389_s_a	hypothetical protein identical to h	---	---	-1.10	-0.14	-1.01	0.3483986	0.5951005	-6.03	FALSE
251481_at	receptor lectin kinase-like protei	---	AT3G59730	1.09	0.13	1.01	0.3484259	0.5951025	-6.03	FALSE
247460_at	AtOXA1 ;supported by full-length	OXA1	AT5G62050	-1.09	-0.12	-1.01	0.348505	0.5951931	-6.03	FALSE
257426_at	hypothetical protein contains sim	---	AT1G54850	-1.16	-0.21	-1.01	0.3485628	0.5952472	-6.03	FALSE
263385_at	ABA-regulated gene (ATEM6) ;	GEA6	AT2G40170	1.15	0.20	1.01	0.3487725	0.5955607	-6.03	FALSE
258689_at	putative GTPase activating prote	---	AT3G07940	-1.11	-0.14	-1.01	0.3488289	0.595568	-6.03	FALSE
257417_at	hypothetical protein predicted by	---	AT1G10110	1.13	0.17	1.01	0.3488104	0.595568	-6.03	FALSE
261861_at	hypothetical protein predicted by	---	AT1G50450	-1.27	-0.35	-1.01	0.3489853	0.5957233	-6.03	FALSE
256961_at	transcription initiation factor TFIII	TBP1	AT3G13445	-1.13	-0.17	-1.01	0.3490244	0.5957233	-6.03	FALSE
266242_at	hypothetical protein predicted by	---	AT2G27790	-1.11	-0.15	-1.01	0.3489624	0.5957233	-6.03	FALSE
246983_at	receptor protein kinase-like prote	---	AT5G67200	-1.18	-0.24	-1.01	0.3490024	0.5957233	-6.03	FALSE
267201_at	putative protein kinase contains a	---	AT2G31010	1.23	0.30	1.01	0.3491268	0.5957887	-6.03	TRUE
261794_at	hypothetical protein contains sim	---	AT1G16060	1.15	0.20	1.01	0.3491654	0.5957887	-6.03	FALSE
266231_at	putative protein kinase	PSKR1	AT2G02220	1.46	0.54	1.01	0.3491672	0.5957887	-6.03	FALSE
262125_at	heat shock protein, putative simi	EDA1	AT1G59680	1.12	0.17	1.01	0.3491274	0.5957887	-6.03	FALSE

261227_at	proteasome regulatory subunit S	EMB2719	AT1G20200	-1.11	-0.14	-1.01	0.3492054	0.5958094	-6.03	FALSE
248592_at	unknown protein ;supported by f	---	AT5G49280	1.33	0.41	1.01	0.3492797	0.595847	-6.03	FALSE
252033_at	putative protein ;supported by fu	---	AT3G51950	-1.22	-0.29	-1.01	0.3492756	0.595847	-6.03	FALSE
262293_at	heat-shock protein 90, putative i	---	AT1G27640	1.18	0.24	1.01	0.3495491	0.5962174	-6.03	FALSE
251671_at	putative protein hypothetical pro	---	AT3G57210	1.12	0.16	1.01	0.3495397	0.5962174	-6.03	FALSE
264756_at	receptor protein kinase (IRK1), p	---	AT1G61370	1.52	0.61	1.01	0.3496526	0.5962601	-6.03	TRUE
253010_at	ovule development protein ainteg	ANT	AT4G37750	1.13	0.18	1.01	0.349617	0.5962601	-6.03	FALSE
247521_at	putative protein ATP/GTP nucle	---	AT5G61450	1.13	0.18	1.01	0.3496302	0.5962601	-6.03	FALSE
257104_at	ER lumen retaining receptor (HD	---	AT3G25040	-1.12	-0.16	-1.00	0.349763	0.5962926	-6.03	FALSE
251332_at	putative protein putative protein	---	AT3G61670	-1.18	-0.24	-1.00	0.3497762	0.5962926	-6.03	FALSE
246119_at	ankyrin-repeat protein patsas pr	TIP1	AT5G20350	-1.14	-0.19	-1.00	0.3497498	0.5962926	-6.03	FALSE
248550_at	putative protein similar to unknov	QS	AT5G50210	1.20	0.27	1.00	0.349757	0.5962926	-6.03	FALSE
245048_at	orf within trnK intron orf within trn	---	---	-1.17	-0.23	-1.00	0.3498596	0.5963457	-6.03	FALSE
261856_at	hypothetical protein	---	AT1G50530	-1.14	-0.19	-1.00	0.3498485	0.5963457	-6.03	FALSE
262940_at	unknown protein	---	AT1G79520	-1.19	-0.25	-1.00	0.3501093	0.5963489	-6.03	FALSE
260053_at	hypothetical protein similar to un	---	AT1G78120	1.15	0.21	1.00	0.3501287	0.5963489	-6.03	FALSE
251563_at	anthranilate phosphoribosyltrans	---	AT3G57880	1.23	0.30	1.00	0.3501491	0.5963489	-6.03	FALSE
267434_at	3-beta-hydroxysteroid dehydroge	AT3BETAH	AT2G26260	1.14	0.19	1.00	0.3500422	0.5963489	-6.03	FALSE
256705_at	cytochrome P450, putative simil	CYP702A8	AT3G30290	1.14	0.19	1.00	0.3500561	0.5963489	-6.03	FALSE
253132_at	NAM / CUC2 -like protein nap ge	NTL9	AT4G35580	-1.15	-0.20	-1.00	0.3500203	0.5963489	-6.03	FALSE
246560_at	putative protein hypothetical prot	---	AT5G15560	1.11	0.15	1.00	0.3498924	0.5963489	-6.03	FALSE
252495_at	putative protein hypothetical prot	---	AT3G46770	1.13	0.17	1.00	0.3501026	0.5963489	-6.03	FALSE
259339_at	putative adenylylsulfate kinase si	---	AT3G03900	1.16	0.21	1.00	0.3499461	0.5963489	-6.03	FALSE
251673_at	beta-1,3-glucanase	BG3	AT3G57240	-2.97	-1.57	-1.00	0.3501401	0.5963489	-6.03	FALSE
246641_s_a	Expressed protein ; supported by	---	AT5G34883 /,	1.12	0.17	1.00	0.3499196	0.5963489	-6.03	FALSE
253577_at	putative protein	---	AT4G31080	-1.21	-0.28	-1.00	0.3502617	0.5964008	-6.03	FALSE
258653_at	hypothetical protein similar to au	---	AT3G09870	1.15	0.20	1.00	0.3502797	0.5964008	-6.03	FALSE
257877_at	hypothetical protein	---	AT3G17140	1.12	0.17	1.00	0.3503103	0.5964008	-6.03	FALSE
252731_at	putative protein predicted protei	---	---	1.16	0.22	1.00	0.3502669	0.5964008	-6.03	FALSE
265769_at	unknown protein weak similarity t	---	AT2G48090	1.13	0.18	1.00	0.3503098	0.5964008	-6.03	FALSE
265971_at	putative retroelement pol polypro	---	---	1.11	0.15	1.00	0.3503443	0.5964142	-6.03	FALSE
256149_at	zinc finger protein, putative simil	AtIDD7	AT1G55110	-1.17	-0.23	-1.00	0.3505152	0.5964184	-6.03	FALSE
263090_at	hypothetical protein predicted by	---	AT2G16190	1.11	0.15	1.00	0.3505241	0.5964184	-6.03	FALSE
247439_at	plasma membrane proton ATPas	AHA11	AT5G62670	-1.26	-0.34	-1.00	0.3503764	0.5964184	-6.03	FALSE
245298_at	hypothetical protein ; supported b	---	AT4G15010	1.11	0.15	1.00	0.350495	0.5964184	-6.03	FALSE

259600_at	hypothetical protein predicted by	---	AT1G35220	1.16	0.21	1.00	0.3505298	0.5964184	-6.03	FALSE
249170_at	abscisic acid responsive element	---	AT5G42910	1.11	0.15	1.00	0.3505246	0.5964184	-6.03	FALSE
245733_at	hypothetical protein predicted by	---	AT1G73380	-1.19	-0.25	-1.00	0.3504218	0.5964184	-6.03	FALSE
266823_at	hypothetical protein predicted by	---	AT2G44930	1.12	0.16	1.00	0.3506332	0.5965498	-6.03	FALSE
266970_at	hypothetical protein predicted by	---	AT2G39560	1.12	0.17	1.00	0.3507797	0.5967545	-6.03	FALSE
263940_at	putative calcium-dependent prote	CPK25	AT2G35890	1.10	0.14	1.00	0.3508273	0.5967692	-6.03	FALSE
267391_at	putative beta-glucosidase	BGLU17	AT2G44480	1.18	0.24	1.00	0.3508406	0.5967692	-6.03	FALSE
254840_at	hypothetical protein	---	AT4G11930	1.17	0.23	1.00	0.3509241	0.5967777	-6.03	FALSE
257777_x_a	hypothetical protein	---	---	1.13	0.18	1.00	0.3509046	0.5967777	-6.03	FALSE
263446_at	putative SET-domain transcriptio	ATX1	AT2G31650	-1.13	-0.18	-1.00	0.3508916	0.5967777	-6.03	FALSE
246685_at	putative protein nucleoid DNA-b	---	AT5G33350	1.23	0.30	1.00	0.3510351	0.5968434	-6.03	FALSE
247948_at	putative protein strong similarity	---	AT5G57130	1.14	0.19	1.00	0.3510438	0.5968434	-6.03	FALSE
263233_at	hypothetical protein similar to Na	---	AT1G05577	1.10	0.13	1.00	0.351054	0.5968434	-6.03	FALSE
249890_at	putative protein contains similarit	WRKY38	AT5G22570	2.07	1.05	1.00	0.3510674	0.5968434	-6.03	FALSE
262898_at	hypothetical protein predicted by	---	AT1G59850	1.13	0.18	1.00	0.3511765	0.5968953	-6.03	FALSE
262187_at	hypothetical protein	---	AT1G77960	-1.11	-0.15	-1.00	0.3511437	0.5968953	-6.03	FALSE
263890_at	putative auxin-induced protein	---	AT2G37030	-1.17	-0.23	-1.00	0.3511731	0.5968953	-6.03	FALSE
253306_at	dynamin-like protein ADL2	DRP3A	AT4G33650	-1.11	-0.15	-1.00	0.3512175	0.5969206	-6.03	FALSE
260366_at	putative protein kinase similar to	---	AT1G70460	-1.11	-0.15	-1.00	0.3512767	0.5969767	-6.03	FALSE
264816_at	hypothetical protein similar to me	---	AT1G03560	-1.32	-0.40	-1.00	0.3513046	0.5969797	-6.03	FALSE
257368_at	hypothetical protein predicted by	---	AT2G29860	1.11	0.15	1.00	0.3513916	0.5970223	-6.03	FALSE
246930_at	KNAT3 homeodomain protein ;s	KNAT3	AT5G25220	-1.15	-0.20	-1.00	0.3513722	0.5970223	-6.03	FALSE
246578_at	MADS-box protein, putative simi	AGL86	AT1G31630	1.10	0.14	1.00	0.3514082	0.5970223	-6.03	FALSE
255416_at	hypothetical protein	---	AT4G03170	-1.10	-0.13	-1.00	0.3515502	0.5971301	-6.03	FALSE
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=g	---	---	1.34	0.42	1.00	0.3515377	0.5971301	-6.03	FALSE
254697_at	putative protein predicted protei	---	AT4G17970	1.10	0.14	1.00	0.3515458	0.5971301	-6.03	FALSE
261714_at	hypothetical protein similar to hy	TET16	AT1G18510	1.17	0.23	1.00	0.3516523	0.597259	-6.03	FALSE
257203_at	xyloglucan endotransglycosylas	---	AT3G23730	1.11	0.15	1.00	0.3517518	0.597311	-6.03	TRUE
260995_at	unknown protein	---	AT1G12120	-1.12	-0.16	-1.00	0.3517165	0.597311	-6.03	FALSE
248222_at	GTPase activator protein of Rab-	---	AT5G53570	1.15	0.21	1.00	0.3517614	0.597311	-6.03	FALSE
255031_at	putative proteins various hypothe	---	AT4G09490	-1.16	-0.21	-1.00	0.3518453	0.5973844	-6.03	FALSE
247417_at	putative protein similar to unknov	---	AT5G63040	-1.11	-0.15	-1.00	0.3518571	0.5973844	-6.03	FALSE
258734_at	putative DNA-binding protein sim	---	AT3G05860	1.10	0.14	1.00	0.3519076	0.5974258	-6.03	FALSE
258492_at	unknown protein	---	AT3G02390	-1.11	-0.15	-1.00	0.3519443	0.5974436	-6.03	FALSE
249518_at	putative protein similar to unknov	---	AT5G38610	1.12	0.16	1.00	0.3520466	0.5975727	-6.03	FALSE

256656_at	hypothetical protein similar to hyp	---	AT3G18900	1.11	0.15	1.00	0.3523006	0.5979595	-6.03	FALSE
257182_s_a	crn-like protein similar to crn GB:	---	AT3G13210 ///	-1.17	-0.22	-1.00	0.3523577	0.5980119	-6.03	FALSE
253346_at	hypothetical protein	---	AT4G33600	1.11	0.15	1.00	0.3524867	0.5981863	-6.03	FALSE
258301_at	hypothetical protein predicted by	---	---	1.09	0.13	1.00	0.3525653	0.5982751	-6.03	FALSE
247315_at	unknown protein	---	AT5G64010	-1.12	-0.16	-1.00	0.352615	0.598315	-6.03	FALSE
263389_at	putative retroelement pol polypro	---	---	1.11	0.15	1.00	0.352684	0.598343	-6.03	FALSE
247689_at	putative protein protein tyrosine	---	AT5G59770	-1.17	-0.22	-1.00	0.3526674	0.598343	-6.03	FALSE
247418_at	glutaredoxin-like protein ; suppo	---	AT5G63030	-1.16	-0.21	-1.00	0.3528619	0.5986004	-6.03	FALSE
248799_at	ethylene responsive element bin	ERF5	AT5G47230	1.82	0.87	1.00	0.3531742	0.598952	-6.04	FALSE
266969_at	similar to gibberellin-regulated pr	---	AT2G39540	1.14	0.20	1.00	0.3531459	0.598952	-6.04	FALSE
252051_at	putative protein similarity hypoth	---	AT3G52570	-1.11	-0.15	-1.00	0.3531611	0.598952	-6.04	FALSE
248761_at	Expressed protein ; supported by	---	AT5G47635	1.21	0.28	1.00	0.353123	0.598952	-6.04	FALSE
260146_at	putative non-phototropic hypocot	---	AT1G52770	-1.36	-0.44	-1.00	0.353224	0.5989918	-6.04	FALSE
245728_at	steroid 22-alpha-hydroxylase, pu	---	AT1G73340	1.15	0.20	1.00	0.3532672	0.5990203	-6.04	FALSE
263561_at	unknown protein	---	AT2G15360	1.09	0.12	1.00	0.3532933	0.5990203	-6.04	FALSE
262512_at	Expressed protein ; supported by	---	AT1G17145	-1.29	-0.36	-1.00	0.3533427	0.5990595	-6.04	FALSE
263285_at	unknown protein	DOT1	AT2G36120	1.23	0.30	1.00	0.3534111	0.5991309	-6.04	FALSE
261221_at	hypothetical protein predicted by	---	AT1G19960	2.19	1.13	1.00	0.3534999	0.5991925	-6.04	FALSE
252381_s_a	ABC-type transport protein-like p	ABCA4	AT3G47750 ///	1.13	0.18	1.00	0.3534949	0.5991925	-6.04	FALSE
267520_at	putative integral membrane prote	---	AT2G30460	-1.21	-0.27	-1.00	0.3535305	0.5991997	-6.04	FALSE
246349_at	Expressed protein ; supported by	---	AT1G51915	1.36	0.44	1.00	0.3535787	0.5992369	-6.04	FALSE
250002_at	proline-richh protein predicted pr	AGP25	AT5G18690	-1.41	-0.49	-1.00	0.3536367	0.5992906	-6.04	FALSE
259648_at	hypothetical protein predicted by	---	---	1.10	0.13	1.00	0.3538535	0.5994354	-6.04	FALSE
259706_at	unknown protein similar to GB:A/	---	AT1G77540	-1.14	-0.19	-1.00	0.3537742	0.5994354	-6.04	FALSE
253377_at	putative protein NBS/LRR disea	ADR1-L1	AT4G33300	1.13	0.18	1.00	0.3538509	0.5994354	-6.04	FALSE
259315_at	unknown protein	AtRP2	AT3G01200	1.10	0.13	1.00	0.3538446	0.5994354	-6.04	FALSE
254018_at	putative mitochondrial carrier pro	---	AT4G26180	-1.13	-0.17	-1.00	0.3537917	0.5994354	-6.04	FALSE
259202_at	putative mRNA capping enzyme	---	AT3G09100	-1.13	-0.17	-1.00	0.3538891	0.5994512	-6.04	FALSE
247708_at	putative protein COP1-interactin	---	AT5G59550	1.53	0.62	1.00	0.3539364	0.5994868	-6.04	FALSE
262054_s_a	putative heat-shock protein cont	---	AT1G79920 ///	1.16	0.22	1.00	0.3539716	0.5995019	-6.04	FALSE
258968_at	hypothetical protein similar to hyp	---	AT3G10460	-1.12	-0.16	-1.00	0.3540351	0.599565	-6.04	FALSE
253026_at	hypothetical protein	---	AT4G38120	1.17	0.23	1.00	0.3541089	0.5996455	-6.04	FALSE
247045_at	putative protein similar to unknov	---	AT5G66930	-1.15	-0.20	-0.99	0.3541719	0.5997076	-6.04	FALSE
260920_at	amp-binding protein, putative sir	---	AT1G21530	1.10	0.14	0.99	0.3543583	0.5999787	-6.04	FALSE
264284_at	protein kinase, putative similar to	---	AT1G61860	1.12	0.17	0.99	0.3544803	0.6001407	-6.04	FALSE

245291_at	Expressed protein ; supported by	---	AT4G16155	-1.12	-0.16	-0.99	0.3545685	0.6002455	-6.04	FALSE
255914_at	hypothetical protein predicted by	---	AT1G20290	1.14	0.19	0.99	0.3546833	0.6003953	-6.04	FALSE
259168_at	unknown protein similar to hypotl	---	AT3G03570	1.13	0.18	0.99	0.3547708	0.6004989	-6.04	FALSE
266864_at	putative hydroxymethylglutaryl-C	---	AT2G26800	1.16	0.21	0.99	0.3548276	0.6005463	-6.04	FALSE
256886_at	hypothetical protein contains Pfa	---	AT3G15130	-1.09	-0.12	-0.99	0.3548515	0.6005463	-6.04	FALSE
245809_at	squalene monooxygenase, puta	XF1	AT1G58440	-1.14	-0.19	-0.99	0.354994	0.6007429	-6.04	TRUE
263349_at	putative chromodomain-helicase	CHR5	AT2G13370	1.16	0.21	0.99	0.3550363	0.6007698	-6.04	FALSE
249701_at	putative protein similar to unknov	---	AT5G35460	-1.11	-0.15	-0.99	0.3550732	0.6007878	-6.04	FALSE
258756_at	hypothetical protein similar to hy	---	AT3G11960	-1.13	-0.17	-0.99	0.3551779	0.6008584	-6.04	FALSE
252655_at	hypothetical protein with predicte	---	AT3G44760	1.10	0.14	0.99	0.3551856	0.6008584	-6.04	FALSE
267516_at	unknown protein	RPT2	AT2G30520	-1.14	-0.19	-0.99	0.355194	0.6008584	-6.04	FALSE
248561_at	unknown protein	---	AT5G49680	1.16	0.22	0.99	0.3552356	0.6008843	-6.04	FALSE
250293_s_a	auxin reponsive - like protein Nt-	---	AT5G13360 /.	1.30	0.38	0.99	0.3553689	0.600903	-6.04	TRUE
247691_at	heat shock protein 18 ;supporte	HSP18.2	AT5G59720	1.12	0.17	0.99	0.3553027	0.600903	-6.04	FALSE
267455_at	hypothetical protein predicted by	---	AT2G33760	-1.15	-0.21	-0.99	0.3553054	0.600903	-6.04	FALSE
253289_at	putative protein F10M10_100, A	---	AT4G34320	-1.12	-0.16	-0.99	0.3553784	0.600903	-6.04	FALSE
248848_at	disease resistance protein-like	---	AT5G46520	1.09	0.12	0.99	0.3553748	0.600903	-6.04	FALSE
254211_at	phosphatase like protein phosph	SGT1A	AT4G23570	-1.20	-0.26	-0.99	0.3555037	0.6010704	-6.04	FALSE
257791_at	unknown protein contains Pfam p	---	AT3G27110	1.16	0.22	0.99	0.3556251	0.6011419	-6.04	FALSE
264643_at	unknown protein	PGSIP5	AT1G08990	1.10	0.14	0.99	0.355624	0.6011419	-6.04	FALSE
250352_at	beta-adaptin-like protein A ; sup	---	AT5G11490	-1.10	-0.13	-0.99	0.3556055	0.6011419	-6.04	FALSE
253174_at	catalase ; supported by cDNA: g	CAT2	AT4G35090	-1.14	-0.19	-0.99	0.3557382	0.6011755	-6.04	FALSE
246112_at	putative protein predicted protein	---	AT5G20200	-1.14	-0.19	-0.99	0.3557504	0.6011755	-6.04	FALSE
252909_at	putative protein	---	AT4G39680	-1.10	-0.14	-0.99	0.355677	0.6011755	-6.04	FALSE
263069_at	unknown protein	---	AT2G17590	1.24	0.31	0.99	0.355702	0.6011755	-6.04	FALSE
256710_at	hypothetical protein predicted by	---	AT3G30350	1.21	0.28	0.99	0.3557816	0.6011837	-6.04	FALSE
251080_at	putative protein hypothetical prot	ROPGEF7	AT5G02010	-1.31	-0.38	-0.99	0.3558202	0.6012044	-6.04	FALSE
249781_at	unknown protein	---	AT5G24250	1.14	0.19	0.99	0.3558634	0.6012328	-6.04	FALSE
252452_at	receptor protein kinase - like pro	---	AT3G47110	1.09	0.13	0.99	0.3560027	0.6014236	-6.04	FALSE
265740_at	RING-H2 finger protein RHA2b ic	RHA2B	AT2G01150	1.30	0.38	0.99	0.3561607	0.6016459	-6.04	TRUE
248041_at	unknown protein ;supported by f	emb2731	AT5G55940	-1.10	-0.13	-0.99	0.3563535	0.6019271	-6.04	FALSE
250124_at	putative protein contains similarit	---	AT5G16480	-1.13	-0.18	-0.99	0.3563896	0.6019435	-6.04	FALSE
AFFX-r2-Ec	E. coli /GEN=bioB /DB_XREF=gi	---	---	1.32	0.40	0.99	0.3564681	0.6020315	-6.04	FALSE
258230_s_a	hypothetical protein similar to hy	ARI13	AT3G27710 /.	1.10	0.14	0.99	0.3565006	0.6020379	-6.04	FALSE
259337_at	putative cationic amino acid trans	CAT4	AT3G03720	1.11	0.15	0.99	0.3565511	0.6020379	-6.04	FALSE

260482_at	endomembrane protein EMP70 p	---	AT1G10950	-1.11	-0.16	-0.99	0.3565249	0.6020379	-6.04	FALSE
258678_at	E2, ubiquitin-conjugating enzym	UBC11	AT3G08690	1.16	0.21	0.99	0.3566915	0.6021858	-6.04	FALSE
266015_at	putative carbonyl reductase	---	AT2G24190	-1.13	-0.18	-0.99	0.3566904	0.6021858	-6.04	FALSE
266474_at	hypothetical protein predicted by	---	AT2G31110	-1.40	-0.49	-0.99	0.3567905	0.6023083	-6.04	FALSE
247510_at	putative protein predicted protei	---	AT5G62030	-1.15	-0.20	-0.99	0.3569145	0.6024732	-6.04	FALSE
244999_at	RNA polymerase beta subunit	---	---	-1.20	-0.26	-0.99	0.3569581	0.6025021	-6.04	FALSE
250007_at	beta-amylase-like proten beta-a	BMY3	AT5G18670	1.56	0.64	0.99	0.3570506	0.6026136	-6.04	FALSE
251488_at	calmodulin-like protein calcium-b	---	AT3G59440	1.09	0.12	0.99	0.3572721	0.602943	-6.04	FALSE
260074_at	putative ras-related GTP-binding	AtRABA6a	AT1G73640	1.11	0.15	0.99	0.3573797	0.6030799	-6.04	FALSE
250308_at	calcium-dependent protein kinas	CPK17	AT5G12180	1.15	0.20	0.99	0.3574599	0.6031706	-6.04	FALSE
249368_at	putative protein predicted protei	---	AT5G40640	-1.16	-0.22	-0.99	0.3575817	0.6032144	-6.04	FALSE
262322_at	hypothetical protein similar to hy	---	AT1G27590	1.14	0.19	0.99	0.35752	0.6032144	-6.04	FALSE
250926_at	Expressed protein ; supported by	---	AT5G03555	-1.28	-0.36	-0.99	0.3575499	0.6032144	-6.04	FALSE
262816_at	alkylation repair-like protein	---	AT1G11780	-1.17	-0.23	-0.99	0.3575916	0.6032144	-6.04	FALSE
254155_at	putative protein kinase putative	---	AT4G24480	1.14	0.18	0.99	0.3576443	0.6032587	-6.05	FALSE
251688_at	putative protein hypothetical pro	---	AT3G56480	1.28	0.35	0.99	0.3577575	0.6033603	-6.05	TRUE
264608_at	putative acetyl-CoA acyltransfera	PKT4	AT1G04710	1.12	0.16	0.99	0.3577424	0.6033603	-6.05	FALSE
253939_at	putative myb-related protein myl	MYB97	AT4G26930	1.17	0.22	0.99	0.3578176	0.6033725	-6.05	FALSE
254348_at	putative protein p47 - Homo sap	PUX3	AT4G22150	-1.10	-0.14	-0.99	0.3578118	0.6033725	-6.05	FALSE
250502_at	heat shock protein 70 (Hsc70-5)	MTHSC70-	AT5G09590	1.28	0.36	0.99	0.3578703	0.6034168	-6.05	FALSE
263822_at	hypothetical protein predicted by	---	AT2G40240	-1.15	-0.21	-0.99	0.3579978	0.6035871	-6.05	FALSE
251432_at	putative protein leucine zipper-E	---	AT3G59820	-1.19	-0.25	-0.99	0.3581437	0.6036785	-6.05	FALSE
248725_at	acetyl-CoA:benzylalcohol acetylt	---	AT5G47980	1.12	0.17	0.99	0.3581063	0.6036785	-6.05	FALSE
260092_at	putative serine carboxypeptidas	scpl3	AT1G73280	1.10	0.14	0.99	0.3581844	0.6036785	-6.05	FALSE
255162_at	putative transposon protein	---	---	1.09	0.12	0.99	0.3581205	0.6036785	-6.05	FALSE
259549_at	unknown protein ;supported by fu	---	AT1G35290	-1.11	-0.16	-0.99	0.3581655	0.6036785	-6.05	FALSE
246189_at	ABI3-interacting protein 2 ;suppo	---	AT5G20910	1.17	0.22	0.99	0.3582755	0.6037429	-6.05	FALSE
256791_at	hypothetical protein predicted by	---	---	1.16	0.22	0.99	0.3582613	0.6037429	-6.05	FALSE
250991_at	metallothionein 2b ; supported b	MT2B	AT5G02380	1.13	0.17	0.99	0.3584141	0.6039044	-6.05	FALSE
250363_at	putative protein predicted protei	---	AT5G11390	-1.22	-0.29	-0.99	0.3584243	0.6039044	-6.05	FALSE
248890_at	disease resistance protein-like	---	AT5G46270	-1.11	-0.15	-0.99	0.3586828	0.6039385	-6.05	FALSE
256904_at	unknown protein	---	AT3G23980	1.09	0.13	0.99	0.3586247	0.6039385	-6.05	FALSE
259454_at	unknown protein similar to hypot	---	AT1G44050	1.13	0.18	0.99	0.3586064	0.6039385	-6.05	FALSE
245406_at	GTP-binding RAB2A like protein	ATRABB1A	AT4G17160	1.10	0.14	0.99	0.3585397	0.6039385	-6.05	FALSE
246481_s_a	cold and ABA inducible protein k	KIN1	AT5G15960 ///	-1.82	-0.86	-0.99	0.3586579	0.6039385	-6.05	FALSE

249560_at	putative protein	LCR80	AT5G38330	1.19	0.25	0.99	0.3584869	0.6039385	-6.05	FALSE
252801_at	putative protein various predicte	---	---	1.10	0.14	0.99	0.3585173	0.6039385	-6.05	FALSE
257709_at	unknown protein similar to negat	---	AT3G27325	1.18	0.24	0.99	0.3586474	0.6039385	-6.05	FALSE
249627_at	NADH dehydrogenase (ubiquinc	EMB1467	AT5G37510	1.14	0.19	0.99	0.3586156	0.6039385	-6.05	FALSE
265710_at	unknown protein	---	AT2G03370	1.10	0.14	0.98	0.3587216	0.6039592	-6.05	FALSE
266746_s_a	putative glutathione S-transferas	ATGSTF3	AT2G02930 ///	-1.62	-0.70	-0.98	0.3587868	0.6039799	-6.05	FALSE
255558_at	P II nitrogen sensing protein GLE	GLB1	AT4G01900	-1.13	-0.18	-0.98	0.358765	0.6039799	-6.05	FALSE
265572_at	putative carbonic anhydrase	ATACA2	AT2G28210	2.01	1.01	0.98	0.3589079	0.6040981	-6.05	TRUE
266423_at	putative DNA-directed RNA polyı	RPB5D	AT2G41340	-1.15	-0.20	-0.98	0.35891	0.6040981	-6.05	FALSE
267342_at	putative heme A:farnesyltransfer	COX10	AT2G44520	1.19	0.25	0.98	0.3591896	0.604524	-6.05	FALSE
255934_at	cytochrome P450, putative simil	CYP87A2	AT1G12740	1.11	0.15	0.98	0.359331	0.6045916	-6.05	FALSE
249541_at	anthranilate N-benzoyltransferas	---	AT5G38130	1.13	0.17	0.98	0.3592933	0.6045916	-6.05	FALSE
261176_at	hypothetical protein predicted by	---	AT1G04780	1.10	0.14	0.98	0.3592668	0.6045916	-6.05	FALSE
266255_at	putative selenium-binding protein	---	AT2G27610	-1.11	-0.15	-0.98	0.3593357	0.6045916	-6.05	FALSE
250307_at	putative protein similar to unknov	---	AT5G12170	1.22	0.29	0.98	0.3594378	0.6047065	-6.05	FALSE
258833_at	unknown protein	---	---	-1.14	-0.18	-0.98	0.359457	0.6047065	-6.05	FALSE
252558_at	actin depolymerising like protein	---	AT3G45990	1.11	0.15	0.98	0.3594959	0.6047273	-6.05	FALSE
259387_at	histone H3 protein, putative simi	---	AT1G13370	-1.10	-0.14	-0.98	0.3595579	0.604787	-6.05	FALSE
264859_at	glucose-6-phosphate 1-dehydro	G6PD3	AT1G24280	-1.42	-0.50	-0.98	0.3596967	0.6048372	-6.05	FALSE
263854_at	putative mutT domain protein	atnudt5	AT2G04430	1.11	0.15	0.98	0.359677	0.6048372	-6.05	FALSE
259601_s_a	CACTA-element transposase, p	---	---	-1.11	-0.14	-0.98	0.3596869	0.6048372	-6.05	FALSE
265278_at	hypothetical protein predicted by	---	AT2G28330	-1.15	-0.21	-0.98	0.3596338	0.6048372	-6.05	FALSE
245507_at	hypothetical protein	---	AT4G15710	-1.16	-0.21	-0.98	0.3597204	0.6048372	-6.05	FALSE
246845_at	glutamyl-tRNA synthetase ; supp	---	AT5G26710	-1.10	-0.13	-0.98	0.3597963	0.6049202	-6.05	FALSE
266954_at	hypothetical protein predicted by	---	AT2G34530	1.10	0.14	0.98	0.3598445	0.6049567	-6.05	FALSE
266415_at	putative nonspecific lipid-transfer	LTP2	AT2G38530	1.70	0.76	0.98	0.3602292	0.6055589	-6.05	FALSE
266075_s_a	unknown protein	---	AT2G40710 ///	-1.15	-0.20	-0.98	0.3604521	0.6058649	-6.05	FALSE
264863_at	putative peroxidase similar to pe	---	AT1G24110	1.13	0.18	0.98	0.3604644	0.6058649	-6.05	FALSE
255822_at	putative expansin ;supported by	ATEXPA8	AT2G40610	-2.42	-1.27	-0.98	0.3605383	0.6059446	-6.05	FALSE
262615_at	initiation factor 5A-4 identical to i	ELF5A-1	AT1G13950	-1.14	-0.19	-0.98	0.3607137	0.6061946	-6.05	FALSE
267638_at	unknown protein ; supported by	OEP16-3	AT2G42210	-1.09	-0.13	-0.98	0.3607441	0.606201	-6.05	FALSE
263391_at	putative monogalactosyldiacylgly	MGDC	AT2G11810	1.22	0.29	0.98	0.360881	0.6063864	-6.05	TRUE
263573_at	unknown protein similar to A. tha	---	AT2G17150	-1.17	-0.22	-0.98	0.3609478	0.6064093	-6.05	FALSE
253929_s_a	putative protein H+-transporting	---	AT2G16030 ///	1.13	0.17	0.98	0.3609386	0.6064093	-6.05	FALSE
246500_at	putative protein HR21spA protei	SYN4	AT5G16270	-1.13	-0.17	-0.98	0.361018	0.6064826	-6.05	FALSE

248306_at	unknown protein ; supported by	WRKY27	AT5G52830	1.20	0.26	0.98	0.3610746	0.6065252	-6.05	FALSE
260241_at	putative cytochrome P450 simila	CYP86A7	AT1G63710	-1.17	-0.22	-0.98	0.3610965	0.6065252	-6.05	FALSE
257048_at	hypothetical protein predicted by	---	AT3G19740	1.10	0.14	0.98	0.3612927	0.6068099	-6.05	FALSE
264666_at	hypothetical protein Similar to N.	---	AT1G09680	-1.15	-0.20	-0.98	0.3613405	0.6068221	-6.05	FALSE
255014_at	MADS-box protein AGL11 ; supp	STK	AT4G09960	-1.10	-0.14	-0.98	0.3613531	0.6068221	-6.05	FALSE
257924_at	unknown protein	---	AT3G23190	1.16	0.22	0.98	0.3614023	0.60686	-6.05	FALSE
251855_at	sugar-phosphate isomerase - lik	---	AT3G54690	1.25	0.33	0.98	0.3615961	0.6070066	-6.05	TRUE
262982_at	unknown protein ;supported by fu	ING2	AT1G54390	1.10	0.14	0.98	0.361578	0.6070066	-6.05	FALSE
247036_at	putative protein contains similarit	---	AT5G67130	-1.17	-0.22	-0.98	0.3615934	0.6070066	-6.05	FALSE
264311_at	hypothetical protein similar to hyp	---	AT1G70400	1.10	0.13	0.98	0.3615903	0.6070066	-6.05	FALSE
246955_at	calcium-dependent protein kinas	CPK1	AT5G04870	1.31	0.39	0.98	0.3617312	0.6070807	-6.05	FALSE
261265_at	hypothetical protein predicted by	---	AT1G26800	-1.22	-0.29	-0.98	0.3617352	0.6070807	-6.05	FALSE
252425_at	putative protein auxin-induced b	AtTCP14	AT3G47620	-1.19	-0.25	-0.98	0.3617466	0.6070807	-6.05	FALSE
264180_at	hypothetical protein contains sim	---	AT1G02190	1.11	0.15	0.98	0.3616979	0.6070807	-6.05	FALSE
255917_at	putative protein	---	AT5G28560	1.09	0.13	0.98	0.3617814	0.6070943	-6.05	FALSE
254599_at	putative protein hypothetical pro	---	AT4G19000	1.13	0.17	0.98	0.3618639	0.6071881	-6.05	FALSE
251978_at	CYTOCHROME P450 - like prot	CYP71B30	AT3G53290	1.14	0.19	0.98	0.3619446	0.6072789	-6.05	FALSE
248656_at	fimbrin 2 (gb|AAB97844.1) ; sup	---	AT5G48460	-1.37	-0.46	-0.98	0.3620242	0.6073533	-6.05	TRUE
249878_at	TATA-binding protein-associated	NF-YB13	AT5G23090	-1.15	-0.20	-0.98	0.3620422	0.6073533	-6.05	FALSE
257112_at	cytochrome P450, putative conta	CYP705A2	AT3G20120	-1.12	-0.17	-0.98	0.3621109	0.6074239	-6.05	FALSE
255855_at	ABC transporter, putative simila	PDR11	AT1G66950	1.16	0.21	0.98	0.3621717	0.6074813	-6.05	FALSE
264178_at	latex-abundant protein, putative	AMC1	AT1G02170	1.13	0.18	0.98	0.3622081	0.6074976	-6.05	FALSE
264729_at	putative metal-binding protein hig	---	AT1G22990	-1.22	-0.28	-0.98	0.3622557	0.6075327	-6.05	FALSE
255306_at	putative calcium dependent prote	CPK23	AT4G04740	1.18	0.24	0.98	0.3623043	0.6075696	-6.05	FALSE
264338_at	potassium transporter, putative s	KUP6	AT1G70300	-1.19	-0.25	-0.98	0.3623541	0.6076083	-6.05	TRUE
245558_at	hypothetical protein	---	AT4G15430	1.10	0.13	0.98	0.362431	0.607648	-6.06	FALSE
254107_at	putative protein putative glycero	---	AT4G25220	1.15	0.20	0.98	0.3624093	0.607648	-6.06	FALSE
254414_at	hypothetical protein	HSA32	AT4G21320	1.15	0.20	0.98	0.3625053	0.6077278	-6.06	FALSE
255099_at	hypothetical protein	---	---	1.10	0.14	0.98	0.3625371	0.6077365	-6.06	FALSE
249833_at	putative protein contains similarit	---	AT5G23430	1.14	0.20	0.98	0.3626022	0.607801	-6.06	FALSE
266291_at	putative tropinone reductase ;su	---	AT2G29320	-1.24	-0.31	-0.98	0.3627654	0.6078782	-6.06	TRUE
260547_at	putative trypsin inhibitor ;suppor	---	AT2G43550	1.48	0.56	0.98	0.3627103	0.6078782	-6.06	FALSE
259414_at	hypothetical protein contains Pfa	---	AT1G02420	-1.14	-0.19	-0.98	0.3627587	0.6078782	-6.06	FALSE
263402_at	hypothetical protein similar to hyp	---	AT2G04050	1.54	0.62	0.98	0.3627815	0.6078782	-6.06	FALSE
262256_at	hypothetical protein similar to put	---	---	1.13	0.17	0.98	0.3626993	0.6078782	-6.06	FALSE

251777_s_a	pyruvate kinase - like protein pyr	---	AT3G55650 /.	-1.13	-0.18	-0.98	0.3629839	0.6081727	-6.06	FALSE
247463_at	embryo-specific protein - like em	---	AT5G62210	1.13	0.17	0.98	0.3631004	0.6083231	-6.06	FALSE
257432_at	unknown protein	---	AT2G21850	1.14	0.19	0.98	0.363279	0.6085777	-6.06	FALSE
254842_at	putative protein other hypothetica	---	AT4G11950	1.15	0.20	0.97	0.3634355	0.608684	-6.06	FALSE
261155_at	unknown protein ;supported by fu	---	AT1G04960	1.14	0.18	0.97	0.3633748	0.608684	-6.06	FALSE
254083_at	PROTEIN TRANSPORT PROTE	---	AT4G24920	1.17	0.23	0.97	0.3634304	0.608684	-6.06	FALSE
266008_at	hypothetical protein predicted by	---	AT2G37390	-1.14	-0.19	-0.97	0.3634492	0.608684	-6.06	FALSE
257339_s_a	ATP synthase subunit 9	---	AT2G07671	1.19	0.25	0.97	0.3635347	0.6086882	-6.06	TRUE
252385_at	putative protein Vps29, Schizosa	MAG1	AT3G47810	-1.10	-0.14	-0.97	0.363506	0.6086882	-6.06	FALSE
245989_s_a	polyubiquitin (UBQ4) identical to	UBQ4	AT5G20620	-1.13	-0.17	-0.97	0.3636118	0.6086882	-6.06	FALSE
246085_at	putative protein predicted protei	ATBRXL4	AT5G20540	1.14	0.19	0.97	0.363599	0.6086882	-6.06	FALSE
262465_at	hypothetical protein similar to hy	---	AT1G50270	-1.10	-0.14	-0.97	0.3635702	0.6086882	-6.06	FALSE
264578_at	hypothetical protein predicted by	---	AT1G05370	1.09	0.13	0.97	0.3635545	0.6086882	-6.06	FALSE
247773_at	putative protein	---	AT5G58630	1.11	0.16	0.97	0.3636848	0.6087657	-6.06	FALSE
251831_at	pectate lyase -like protein pectat	---	AT3G55140	-1.09	-0.13	-0.97	0.3637422	0.6087908	-6.06	FALSE
264640_at	pollen allergen, putative similar t	ATEXPB2	AT1G65680	1.19	0.25	0.97	0.3637531	0.6087908	-6.06	FALSE
252930_at	putative endo-1,4-beta-glucanas	AtGH9B18	AT4G39010	1.14	0.20	0.97	0.363835	0.608883	-6.06	FALSE
247679_at	1-aminocyclopropane-1-carboxy	---	AT5G59540	-1.26	-0.34	-0.97	0.3639032	0.6089526	-6.06	FALSE
262939_s_a	glyceraldehyde-3-phosphate del	GAPCP-2	AT1G16300 /.	1.57	0.65	0.97	0.3639418	0.6089725	-6.06	FALSE
256908_at	hypothetical protein similar to mu	---	AT3G24040	-1.13	-0.17	-0.97	0.3640191	0.6089793	-6.06	FALSE
246167_at	putative protein	---	---	1.14	0.19	0.97	0.3640045	0.6089793	-6.06	FALSE
264503_at	hypothetical protein Similar to A	---	AT1G09410	1.10	0.14	0.97	0.3640447	0.6089793	-6.06	FALSE
257959_at	somatic embryogenesis recepto	NIK2	AT3G25560	-1.25	-0.32	-0.97	0.3640527	0.6089793	-6.06	FALSE
246131_at	MOLYBDOPTERIN BIOSYNTHE	B73	AT5G20990	1.10	0.14	0.97	0.3641258	0.609057	-6.06	FALSE
266922_s_a	SKP1/ASK1-related, putative sir	ASK20	AT2G45950 /.	-1.21	-0.28	-0.97	0.3641529	0.6090575	-6.06	FALSE
263314_at	putative membrane transporter	---	AT2G05760	1.09	0.13	0.97	0.3641808	0.6090596	-6.06	FALSE
263898_at	SKP1 interacting partner 6 (SKIF	SKIP6	AT2G21950	-1.12	-0.17	-0.97	0.3642394	0.609113	-6.06	FALSE
254086_at	putative proteasome regulatory s	---	AT4G24820	1.09	0.13	0.97	0.364472	0.6094425	-6.06	FALSE
250362_at	1-D-deoxyxylulose 5-phosphate	DXPS3	AT5G11380	-1.10	-0.14	-0.97	0.3644899	0.6094425	-6.06	FALSE
256563_at	unknown protein	RALFL27	AT3G29780	1.12	0.16	0.97	0.3645462	0.6094511	-6.06	FALSE
257450_at	unknown protein similar to gb|AA	---	AT1G10530	1.14	0.19	0.97	0.3645485	0.6094511	-6.06	FALSE
261518_at	peroxidase ATP4a identical to G	---	AT1G71695	-1.14	-0.19	-0.97	0.3650489	0.6102037	-6.06	FALSE
255304_at	putative potassium transporter s	KEA3	AT4G04850	-1.20	-0.27	-0.97	0.3650522	0.6102037	-6.06	FALSE
248186_at	unknown protein ;supported by f	---	AT5G53880	-1.55	-0.63	-0.97	0.3651198	0.6102424	-6.06	FALSE
266180_at	putative PHD-type zinc finger pro	AL6	AT2G02470	-1.15	-0.21	-0.97	0.3651288	0.6102424	-6.06	FALSE

264568_at	putative O-GlcNAc transferase si	---	AT1G05150	-1.15	-0.20	-0.97	0.3651601	0.6102501	-6.06	FALSE
256639_at	hypothetical protein predicted by	---	---	1.14	0.19	0.97	0.3651886	0.610253	-6.06	FALSE
258831_at	putative integral membrane prote	---	AT3G07080	-1.09	-0.13	-0.97	0.365224	0.6102673	-6.06	FALSE
265646_at	putative lipase	---	AT2G27360	1.13	0.17	0.97	0.3652649	0.610291	-6.06	FALSE
253253_at	putative protein auxin-regulated	---	AT4G34750	-1.11	-0.16	-0.97	0.3653411	0.6103543	-6.06	TRUE
246766_at	hypothetical protein	---	AT5G27340	1.18	0.24	0.97	0.3653563	0.6103543	-6.06	FALSE
258148_s_a	DNA-directed RNA polymerase	NRPD2B	AT3G18090 //	-1.21	-0.27	-0.97	0.3654284	0.6103905	-6.06	FALSE
259691_at	hypothetical protein predicted by	---	AT1G63200	1.17	0.23	0.97	0.3654315	0.6103905	-6.06	FALSE
256086_at	hypothetical protein predicted by	---	AT1G20770	-1.12	-0.16	-0.97	0.3655193	0.6104925	-6.06	FALSE
247503_at	GCN4-complementing protein -	AGD1	AT5G61980	1.13	0.18	0.97	0.3656309	0.6105	-6.06	FALSE
254490_at	CTP synthase like protein CTP s	---	AT4G20320	1.19	0.25	0.97	0.3655917	0.6105	-6.06	FALSE
264727_at	putative cytochrome C strong sin	CYTC-1	AT1G22840	1.27	0.34	0.97	0.3656187	0.6105	-6.06	FALSE
265052_at	caffeic acid O-methyltransferase	---	AT1G51990	1.10	0.13	0.97	0.3656234	0.6105	-6.06	FALSE
247038_at	anthranilate N-hydroxycinnamoyl	EPS1	AT5G67160	1.16	0.22	0.97	0.3656676	0.6105166	-6.06	FALSE
261781_at	far-red impaired response protei	FRS4	AT1G76320	-1.14	-0.19	-0.97	0.3657481	0.6106064	-6.06	FALSE
249109_at	auxin-induced protein AUX2-11 (	ATAUX2-11	AT5G43700	-1.47	-0.55	-0.97	0.365836	0.6107084	-6.06	FALSE
265717_at	unknown protein ;supported by f	---	AT2G03510	-1.15	-0.20	-0.97	0.365929	0.6107296	-6.06	FALSE
263955_at	putative E2F5 family transcriptior	E2F3	AT2G36010	1.18	0.24	0.97	0.3659052	0.6107296	-6.06	FALSE
261376_at	hypothetical protein contains sim	---	AT1G18660	-1.12	-0.17	-0.97	0.3659279	0.6107296	-6.06	FALSE
265809_at	unknown protein	---	AT2G18100	1.13	0.18	0.97	0.366035	0.6108618	-6.06	FALSE
255150_at	putative xylan endohydrolase	---	AT4G08160	-1.21	-0.27	-0.97	0.3661982	0.6110335	-6.06	FALSE
266565_at	putative serine carboxypeptidase	scpl23	AT2G24010	1.13	0.17	0.97	0.3662183	0.6110335	-6.06	FALSE
255198_at	contains similarity to an Arabido	---	---	1.10	0.14	0.97	0.3662081	0.6110335	-6.06	FALSE
259533_at	hypothetical protein	---	AT1G12530	-1.09	-0.12	-0.97	0.3663206	0.6111196	-6.06	FALSE
264703_at	serine threonine protein phospha	PP2A	AT1G69960	1.10	0.13	0.97	0.3663235	0.6111196	-6.06	FALSE
262013_s_a	mudrA-like protein similar to Mu t	---	---	-1.15	-0.20	-0.97	0.3664456	0.6112787	-6.06	FALSE
261168_at	unknown protein	---	AT1G04940 //	-1.22	-0.29	-0.97	0.3666868	0.6116363	-6.06	TRUE
254000_at	galactinol synthase WSI76 prote	AtGolS6	AT4G26250	-1.09	-0.12	-0.97	0.3667455	0.6116894	-6.06	FALSE
245756_at	hyoscyamine 6-dioxygenase hyd	---	AT1G35190	1.17	0.23	0.97	0.3670199	0.6120927	-6.06	FALSE
247702_at	putative protein ;supported by fu	---	AT5G59500	-1.12	-0.17	-0.97	0.3670409	0.6120927	-6.06	FALSE
249619_at	stelar K+ outward rectifying char	GORK	AT5G37500	-1.18	-0.24	-0.97	0.3671237	0.6121412	-6.06	FALSE
245028_at	unknown protein	---	AT2G26570	1.17	0.23	0.97	0.3671138	0.6121412	-6.06	FALSE
246305_at	putative protein protein At2g400	---	AT3G51890	1.14	0.19	0.97	0.3671511	0.6121422	-6.06	FALSE
255381_at	RMA1 RING zinc finger protein id	RMA1	AT4G03510	-1.24	-0.31	-0.97	0.3672556	0.6122716	-6.07	FALSE
267377_at	beta-ketoacyl-CoA synthase (FID	KCS10	AT2G26250	1.26	0.34	0.97	0.3672887	0.612282	-6.07	TRUE

257826_at	RING zinc finger protein, putativ	---	AT3G26730	-1.11	-0.15	-0.97	0.3673167	0.612284	-6.07	FALSE
262809_at	putative glycogen synthase stron	ATSS3	AT1G11720	-1.32	-0.40	-0.97	0.3675423	0.6126153	-6.07	FALSE
249073_at	vegetative storage protein-like ;s	---	AT5G44020	1.34	0.42	0.97	0.3675878	0.6126463	-6.07	TRUE
263813_s_a	putative TNP1-like transposon pr	---	---	1.11	0.15	0.97	0.3677037	0.6127947	-6.07	FALSE
247317_at	putative protein contains similarit	anac103	AT5G64060	1.13	0.17	0.97	0.3678306	0.6129167	-6.07	FALSE
246890_at	Expressed protein ; supported by	---	AT5G25410	1.13	0.17	0.97	0.3678096	0.6129167	-6.07	FALSE
251441_at	SKP1/ASK1 (At5), putative simil	ASK5	AT3G60020	-1.10	-0.14	-0.97	0.3678647	0.6129287	-6.07	FALSE
256610_at	hypothetical protein predicted by	---	AT3G30845	-1.09	-0.13	-0.96	0.3680008	0.6131106	-6.07	FALSE
249501_s_a	expansin-like protein expansin -	ATEXP26	AT5G39270 ///	1.09	0.13	0.96	0.3682553	0.6133555	-6.07	FALSE
267487_at	putative non-LTR retroelement re	---	---	1.13	0.17	0.96	0.3682226	0.6133555	-6.07	FALSE
245945_at	putative protein various predicte	ROPGEF10	AT5G19560	1.09	0.13	0.96	0.3682324	0.6133555	-6.07	FALSE
262097_at	hypothetical protein predicted by	---	AT1G55990	1.11	0.15	0.96	0.368235	0.6133555	-6.07	FALSE
266693_at	unknown protein predicted by ge	MIOX2	AT2G19800	1.79	0.84	0.96	0.3686113	0.6139037	-6.07	FALSE
252380_at	ABC-type transport protein-like p	ATH2	AT3G47740	1.11	0.15	0.96	0.3687652	0.614115	-6.07	FALSE
249496_s_a	putative protein predicted protein	---	AT5G39140 ///	1.11	0.15	0.96	0.3688172	0.6141568	-6.07	FALSE
261687_at	hypothetical protein predicted by	---	AT1G47280	1.11	0.15	0.96	0.3688499	0.6141664	-6.07	FALSE
256989_at	hypothetical protein predicted by	---	AT3G28580	1.89	0.92	0.96	0.3688809	0.6141732	-6.07	FALSE
252530_at	putative protein several oxidase	---	AT3G46500	1.12	0.16	0.96	0.3689133	0.6141808	-6.07	FALSE
263165_at	putataive transport protein Simil	---	AT1G03060	1.09	0.13	0.96	0.3689393	0.6141808	-6.07	FALSE
252354_at	betaine aldehyde dehydrogenas	ALDH10A9	AT3G48170	1.10	0.14	0.96	0.3691131	0.6144253	-6.07	FALSE
262450_at	hypothetical protein identical to h	---	AT1G11320	-1.14	-0.18	-0.96	0.3691633	0.614464	-6.07	FALSE
262678_at	hypothetical protein ;supported b	---	AT1G75810	-1.16	-0.21	-0.96	0.3693253	0.614528	-6.07	TRUE
265799_at	unknown protein ; supported by	---	AT2G35680	-1.13	-0.17	-0.96	0.3693744	0.614528	-6.07	FALSE
259423_at	unknown protein similar to putati	---	AT1G13880	-1.16	-0.21	-0.96	0.3692839	0.614528	-6.07	FALSE
252369_at	putative protein deoxycytidylate	---	AT3G48540	1.11	0.15	0.96	0.3692383	0.614528	-6.07	FALSE
255499_at	putative WD-repeat protein simil	---	AT4G02730	1.10	0.14	0.96	0.3692952	0.614528	-6.07	FALSE
249180_at	26S proteasome AAA-ATPase su	RPT4A	AT5G43010	-1.16	-0.21	-0.96	0.3693811	0.614528	-6.07	FALSE
260807_at	hypothetical protein predicted by	---	AT1G78310	1.09	0.12	0.96	0.3693903	0.614528	-6.07	FALSE
252914_at	putative protein dehydrin, Glycin	---	AT4G39130	1.15	0.20	0.96	0.3694579	0.6145957	-6.07	FALSE
254235_at	putative Ap2 domain protein DN	CRF2	AT4G23750	1.11	0.15	0.96	0.3695479	0.6147004	-6.07	FALSE
251257_at	ADP-ribosylation factor-like prot	ATARFA1E	AT3G62290	-1.17	-0.22	-0.96	0.3695756	0.6147017	-6.07	FALSE
260723_at	unknown protein	---	AT1G48070	1.10	0.14	0.96	0.36989	0.6151798	-6.07	FALSE
245689_at	phosphoglycerate mutase - like p	---	AT5G04120	1.12	0.16	0.96	0.369938	0.6152148	-6.07	FALSE
250820_at	receptor-like protein kinase	---	AT5G05160	1.14	0.18	0.96	0.3699987	0.6152353	-6.07	FALSE
258088_at	hypothetical protein predicted by	---	AT3G14580	-1.11	-0.15	-0.96	0.3700313	0.6152353	-6.07	FALSE

264534_at	hypothetical protein predicted by	---	AT1G55700	1.16	0.22	0.96	0.3700198	0.6152353	-6.07	FALSE
250642_at	receptor-like protein kinase seve	ERL2	AT5G07180	-1.09	-0.13	-0.96	0.3700677	0.6152511	-6.07	FALSE
245740_at	amino acid permease, putative a	AAP5	AT1G44100	1.15	0.20	0.96	0.3701699	0.6153761	-6.07	TRUE
249760_at	(+)-delta-cadinene synthase (d-c	TPS21	AT5G23960	1.09	0.13	0.96	0.3702728	0.61547	-6.07	FALSE
263725_at	unknown protein	---	AT2G13550	-1.09	-0.13	-0.96	0.3702804	0.61547	-6.07	FALSE
261575_at	hypothetical protein contains sim	---	AT1G01130	1.19	0.25	0.96	0.3704043	0.6154966	-6.07	FALSE
263358_x_a	hypothetical protein similar to hy	---	---	1.12	0.16	0.96	0.3703703	0.6154966	-6.07	FALSE
257527_at	hypothetical protein similar to hy	---	AT3G01880	1.11	0.15	0.96	0.3703783	0.6154966	-6.07	FALSE
247980_at	putative protein similar to unknov	GNC	AT5G56860	-1.35	-0.44	-0.96	0.3703951	0.6154966	-6.07	FALSE
258630_at	putative CCHC-type zinc finger p	---	AT3G02820	-1.18	-0.24	-0.96	0.3705067	0.615622	-6.07	FALSE
256916_at	GATA transcription factor 1 (AtG	---	AT3G24050	1.15	0.20	0.96	0.3706199	0.6157203	-6.07	FALSE
259049_at	unknown protein	---	AT3G03370	-1.14	-0.19	-0.96	0.3706168	0.6157203	-6.07	FALSE
258779_at	putative protein kinase contains I	---	AT3G11870	1.09	0.13	0.96	0.3707106	0.6157978	-6.07	FALSE
262725_at	hypothetical protein predicted by	---	AT1G43580	-1.22	-0.29	-0.96	0.3707205	0.6157978	-6.07	FALSE
247792_at	Expressed protein ; supported by	---	AT5G58787	-1.20	-0.27	-0.96	0.3708519	0.6159705	-6.07	FALSE
257574_at	hypothetical protein predicted by	---	AT3G20710	1.12	0.17	0.96	0.3708883	0.6159705	-6.07	FALSE
249686_at	putative protein contains similarit	CYP716A2	AT5G36140	1.09	0.12	0.96	0.3709055	0.6159705	-6.07	FALSE
264073_at	putative replication protein A1	---	---	-1.13	-0.17	-0.96	0.3709697	0.6160322	-6.07	FALSE
244919_at	cytochrome c biogenesis orf203	---	AT2G07768 ///	1.12	0.16	0.96	0.3710953	0.616196	-6.07	FALSE
263834_at	hypothetical protein	---	AT2G40316	-1.13	-0.17	-0.96	0.3711706	0.6162762	-6.07	FALSE
245243_at	hypothetical protein predicted by	---	AT1G44414	-1.10	-0.14	-0.96	0.371294	0.6164362	-6.07	FALSE
251908_at	putative protein late embryogeni	---	AT3G53770	1.12	0.16	0.96	0.3714019	0.6165255	-6.07	FALSE
247404_at	permease 1 - like protein perme	---	AT5G62890	-1.26	-0.33	-0.96	0.3713837	0.6165255	-6.07	FALSE
257242_at	9-cis-epoxycarotenoid dioxygena	NCED6	AT3G24220	-1.11	-0.15	-0.96	0.3714793	0.6166091	-6.07	FALSE
261447_at	transcription factor, putative sim	---	AT1G21160	1.11	0.15	0.96	0.3716402	0.6166968	-6.07	FALSE
252405_at	putative protein RNA helicase H	---	AT3G48120	-1.14	-0.18	-0.96	0.3715719	0.6166968	-6.07	FALSE
255098_at	hypothetical protein	---	AT4G08640	1.09	0.12	0.96	0.3716275	0.6166968	-6.07	FALSE
248546_at	putative protein similar to unknov	---	AT5G50270	-1.09	-0.12	-0.96	0.3716236	0.6166968	-6.07	FALSE
266011_at	unknown protein	---	AT2G37440	1.11	0.16	0.96	0.3716728	0.616706	-6.07	FALSE
255003_at	AIG1-like protein AIG1 - Arabido	---	AT4G09950	1.10	0.14	0.96	0.3717182	0.6167363	-6.07	FALSE
249172_at	putative protein similar to unknov	---	AT5G42950	-1.12	-0.17	-0.96	0.3717782	0.616791	-6.07	FALSE
264693_at	hypothetical protein predicted by	CLE26	AT1G69970	-1.11	-0.15	-0.96	0.3718672	0.6168682	-6.07	FALSE
267000_at	Expressed protein ; supported by	---	AT2G34310	-1.22	-0.29	-0.96	0.3719203	0.6168682	-6.07	FALSE
267348_at	unknown protein	---	AT2G39960	-1.10	-0.14	-0.96	0.3719328	0.6168682	-6.07	FALSE
261243_at	hypothetical protein predicted by	---	AT1G20180	1.35	0.44	0.96	0.3718882	0.6168682	-6.07	FALSE

251159_at	hypothetical protein	---	AT3G63230	-1.16	-0.21	-0.96	0.3719722	0.6168886	-6.07	FALSE
261949_at	hypothetical protein predicted by	BDG1	AT1G64670	1.31	0.39	0.96	0.3720159	0.6169163	-6.07	TRUE
254306_at	putative protein ; supported by c	ATCES1	AT4G22330	1.09	0.13	0.96	0.3722177	0.6171985	-6.08	FALSE
265155_at	putative major latex protein type	---	AT1G30990	1.12	0.16	0.96	0.3722402	0.6171985	-6.08	FALSE
247250_at	FAS2 (dbj|BAA77766.1) ; suppo	FAS2	AT5G64630	-1.19	-0.25	-0.96	0.3722819	0.6172228	-6.08	FALSE
259396_at	shaggy-like kinase, putative sim	GSK1	AT1G06390	-1.10	-0.13	-0.96	0.3723811	0.6173423	-6.08	FALSE
265005_at	Expressed protein ; supported by	---	AT1G61667	-1.21	-0.28	-0.96	0.3725999	0.6174565	-6.08	FALSE
256545_at	hypothetical protein predicted by	---	---	-1.12	-0.16	-0.96	0.3725768	0.6174565	-6.08	FALSE
247288_at	non-phototropic hypocotyl 3 (gb|	NPH3	AT5G64330	-1.41	-0.50	-0.96	0.3725899	0.6174565	-6.08	FALSE
260462_at	ZIP4, a putative zinc transporter	ZIP4	AT1G10970	-1.22	-0.29	-0.96	0.3725103	0.6174565	-6.08	FALSE
267501_at	unknown protein	---	AT2G45540	-1.15	-0.20	-0.96	0.3725793	0.6174565	-6.08	FALSE
252192_at	CASEIN KINASE II, ALPHA CH	CKA2	AT3G50000	-1.09	-0.13	-0.96	0.3726124	0.6174565	-6.08	FALSE
258014_at	hypothetical protein predicted by	---	AT3G19330	-1.17	-0.23	-0.95	0.372699	0.6175103	-6.08	FALSE
250871_at	putative protein	---	AT5G03930	1.13	0.18	0.95	0.3726829	0.6175103	-6.08	FALSE
255334_at	putative transposon protein	---	---	1.09	0.12	0.95	0.3727422	0.617537	-6.08	FALSE
257005_at	hypothetical protein predicted by	---	AT3G14190	-1.14	-0.18	-0.95	0.3727711	0.61754	-6.08	FALSE
262630_at	unknown protein ;supported by fu	GPAT1	AT1G06520	1.48	0.57	0.95	0.3727993	0.6175418	-6.08	FALSE
256243_at	basic chitinase identical to basic	ATHCHIB	AT3G12500	-1.45	-0.54	-0.95	0.3729362	0.6176414	-6.08	TRUE
248536_at	ankyrin-like protein	---	AT5G50140	1.11	0.15	0.95	0.3729677	0.6176414	-6.08	FALSE
267581_at	putative RING zinc finger protein	---	AT2G41980	-1.20	-0.27	-0.95	0.3729346	0.6176414	-6.08	FALSE
263627_at	Expressed protein ; supported by	---	AT2G04675	1.12	0.17	0.95	0.3729555	0.6176414	-6.08	FALSE
247668_at	pseudo-response regulator - like	APRR3	AT5G60100	-1.09	-0.13	-0.95	0.3730616	0.6177521	-6.08	FALSE
266464_at	glutathione-conjugate transporter	ATMRP4	AT2G47800	1.73	0.79	0.95	0.3731077	0.6177835	-6.08	TRUE
266573_at	unknown protein	---	AT2G23860	1.16	0.21	0.95	0.3731661	0.6178354	-6.08	FALSE
267127_at	putative acetone-cyanohydrin lya	MES3	AT2G23610	1.12	0.17	0.95	0.3732526	0.6179109	-6.08	TRUE
257545_at	hypothetical protein predicted by	---	AT3G23200	-1.17	-0.23	-0.95	0.3732659	0.6179109	-6.08	FALSE
252193_at	R2R3-MYB transcription factor ;	MYB77	AT3G50060	1.34	0.43	0.95	0.3735033	0.6180431	-6.08	TRUE
254141_at	glucose-6-phosphate isomerase	PGI1	AT4G24620	-1.11	-0.15	-0.95	0.3735325	0.6180431	-6.08	FALSE
256686_at	non-LTR reverse transcriptase,	---	---	-1.09	-0.12	-0.95	0.3735354	0.6180431	-6.08	FALSE
248022_at	putative protein contains similarit	APUM12	AT5G56510	1.09	0.12	0.95	0.3734645	0.6180431	-6.08	FALSE
260171_at	hypothetical protein predicted by	---	AT1G71910	1.31	0.38	0.95	0.3734988	0.6180431	-6.08	FALSE
256212_at	hypothetical protein	---	AT1G50970	1.13	0.18	0.95	0.3734354	0.6180431	-6.08	FALSE
253450_at	putative protein MUS308 gene,	---	AT4G32700	-1.10	-0.13	-0.95	0.3734999	0.6180431	-6.08	FALSE
250829_at	disease resistance - like protein	ADR1-L2	AT5G04720	-1.14	-0.18	-0.95	0.3737586	0.6182601	-6.08	FALSE
256510_at	ATP-dependent Clp protease AT	---	AT1G33360	1.13	0.17	0.95	0.3737655	0.6182601	-6.08	FALSE

248909_at	serine threonine protein kinase ;	CIPK19	AT5G45810	1.16	0.22	0.95	0.3737266	0.6182601	-6.08	FALSE
255149_at	KNAT1 homeobox-like protein	KNAT1	AT4G08150	1.13	0.17	0.95	0.373775	0.6182601	-6.08	FALSE
262651_at	hypothetical protein One of a clu	FUT9	AT1G14100 /	1.13	0.17	0.95	0.3738617	0.618314	-6.08	FALSE
251498_at	putative protein hypothetical prot	---	AT3G59070	-1.13	-0.18	-0.95	0.3738389	0.618314	-6.08	FALSE
254288_at	putative protein Human mRNA f	AESP	AT4G22970	1.09	0.12	0.95	0.3739476	0.6184112	-6.08	FALSE
251453_at	putative protein hypothetical pro	---	AT3G60070	1.12	0.16	0.95	0.3740108	0.6184707	-6.08	FALSE
262867_at	hypothetical protein predicted by	---	AT1G64960	-1.12	-0.16	-0.95	0.3740728	0.6184988	-6.08	FALSE
267275_at	putative Na H antiporter	ATCHX13	AT2G30240	1.15	0.20	0.95	0.3741091	0.6184988	-6.08	FALSE
266080_at	hypothetical protein predicted by	---	AT2G37840	-1.09	-0.12	-0.95	0.3740875	0.6184988	-6.08	FALSE
262153_at	unknown protein	---	AT1G52710	1.09	0.13	0.95	0.374283	0.6187414	-6.08	FALSE
259656_at	protein kinase, putative contains	---	AT1G55200	-1.11	-0.15	-0.95	0.3743359	0.6187842	-6.08	FALSE
257098_at	hypothetical protein	---	---	1.10	0.14	0.95	0.3743754	0.6188045	-6.08	FALSE
253040_at	endo-xyloglucan transferase - lik	---	AT4G37800	-1.45	-0.54	-0.95	0.3745222	0.6188103	-6.08	TRUE
247002_at	putative protein strong similarity t	HOS15	AT5G67320	-1.13	-0.18	-0.95	0.3745416	0.6188103	-6.08	FALSE
262185_at	MADS box transcription factor, p	AGL67	AT1G77950	1.09	0.12	0.95	0.3744737	0.6188103	-6.08	FALSE
248462_at	nucleotide-binding protein ; supp	NBP35	AT5G50960	1.13	0.18	0.95	0.3744974	0.6188103	-6.08	FALSE
266469_at	myb-related protein	MYB14	AT2G31180	1.11	0.16	0.95	0.3745352	0.6188103	-6.08	FALSE
261936_at	seed maturation protein PM27, p	---	AT1G22600	1.16	0.22	0.95	0.3744103	0.6188103	-6.08	FALSE
267558_at	unknown protein ; supported by	LUH	AT2G32700	-1.10	-0.14	-0.95	0.3747908	0.6191771	-6.08	FALSE
252635_at	putative protein predicted protei	---	AT3G44510	1.13	0.18	0.95	0.3748513	0.6192322	-6.08	FALSE
245042_at	hypothetical protein predicted by	HEMD	AT2G26540	1.21	0.28	0.95	0.3750028	0.6193031	-6.08	TRUE
250470_at	(3R)-hydroxymyristoyl-[acyl carr	---	AT5G10160	-1.14	-0.19	-0.95	0.3749586	0.6193031	-6.08	FALSE
248324_at	putative protein similar to unknov	---	AT5G52790	-1.13	-0.18	-0.95	0.3749531	0.6193031	-6.08	FALSE
252700_at	hypothetical protein envelope-lik	---	---	1.12	0.17	0.95	0.3749941	0.6193031	-6.08	FALSE
254884_at	H+-transporting ATPase - like pr	---	AT4G11730	1.09	0.12	0.95	0.375093	0.6194072	-6.08	FALSE
263046_at	unknown protein ; supported by	GRP3S	AT2G05380	-1.24	-0.31	-0.95	0.3751958	0.6194872	-6.08	FALSE
246844_at	transcription factor ATMYB4 ; su	ATMYB86	AT5G26660	1.13	0.18	0.95	0.375175	0.6194872	-6.08	FALSE
258685_at	putative polygalacturonase simila	---	AT3G07830	1.15	0.20	0.95	0.3752572	0.6195438	-6.08	FALSE
258997_at	hypothetical protein similar to un	---	AT3G01810	-1.21	-0.27	-0.95	0.3752957	0.6195625	-6.08	TRUE
255937_at	transcriptional activator CBF1, p	DDF1	AT1G12610	1.25	0.33	0.95	0.3753818	0.619615	-6.08	FALSE
256374_at	DNA ligase I, putative similar to	---	AT1G66730	-1.13	-0.18	-0.95	0.3753668	0.619615	-6.08	FALSE
247090_at	putative protein similar to unknov	---	AT5G66370	1.11	0.15	0.95	0.3754875	0.6196835	-6.08	FALSE
263354_at	hypothetical protein predicted by	---	AT2G22060	1.09	0.12	0.95	0.3755048	0.6196835	-6.08	FALSE
267468_at	unknown protein ; supported by	---	AT2G30530	1.13	0.18	0.95	0.3754791	0.6196835	-6.08	FALSE
265962_at	nodulin-like protein ;supported b	---	AT2G37460	-1.34	-0.42	-0.95	0.3755351	0.6196886	-6.08	FALSE

266440_at	unknown protein	---	AT2G43235 /.	1.11	0.15	0.95	0.3756695	0.6198655	-6.08	FALSE
267450_at	hypothetical protein predicted by	---	AT2G33720	1.17	0.23	0.95	0.3757145	0.619895	-6.08	FALSE
261842_at	hypothetical protein contains sim	WAKL5	AT1G16160	1.15	0.20	0.95	0.3757727	0.6199462	-6.08	FALSE
261530_at	unknown protein contains Pfam p	---	AT1G63460	-1.15	-0.20	-0.95	0.3758292	0.6199945	-6.08	FALSE
248192_at	IAA-amino acid hydrolase homol	ILL3	AT5G54140	1.11	0.15	0.95	0.375896	0.620014	-6.08	FALSE
256599_at	hypothetical protein predicted by	---	AT3G14760	1.10	0.14	0.95	0.3759562	0.620014	-6.08	FALSE
252567_at	zinc finger -like protein zinc finge	---	AT3G46070	1.10	0.14	0.95	0.375977	0.620014	-6.08	FALSE
246201_at	minor allergen ;supported by full-	---	AT4G36750	-1.09	-0.13	-0.95	0.3759376	0.620014	-6.08	FALSE
249021_at	putative protein similar to unknov	---	AT5G44820	1.20	0.26	0.95	0.3759042	0.620014	-6.08	FALSE
253351_at	putative protein hemolysin, 38K,	---	AT4G33700	-1.12	-0.16	-0.95	0.3760418	0.6200314	-6.08	FALSE
264982_at	hypothetical protein predicted by	---	AT1G27220	1.13	0.17	0.95	0.3760299	0.6200314	-6.08	FALSE
248188_at	putative protein contains similarit	HSFA9	AT5G54070	-1.09	-0.12	-0.95	0.3761368	0.6201431	-6.08	FALSE
251835_at	lipase -like protein monoglyceric	---	AT3G55180	1.10	0.14	0.95	0.3762047	0.6202091	-6.08	FALSE
265980_at	hypothetical protein predicted by	---	---	1.12	0.16	0.95	0.3762312	0.6202091	-6.08	FALSE
246529_at	serine/threonine-specific protein	---	AT5G15730	1.28	0.35	0.95	0.3763346	0.6203348	-6.08	FALSE
257267_at	unknown protein similar to TCP3	TCP4	AT3G15030	-1.13	-0.17	-0.95	0.3764447	0.6204348	-6.08	FALSE
252105_at	protein phosphatase 2C-like pro	---	AT3G51470	-1.14	-0.19	-0.95	0.3764851	0.6204348	-6.08	FALSE
260461_at	membrane protein PTM1 precurs	---	AT1G10980	1.12	0.16	0.95	0.3764973	0.6204348	-6.08	FALSE
255736_at	unknown protein contains similar	---	AT1G25380	1.12	0.16	0.95	0.3765041	0.6204348	-6.08	FALSE
251748_at	putative protein predicted protei	---	AT3G55680	1.14	0.19	0.95	0.3766703	0.6206639	-6.08	FALSE
251738_at	PROBABLE EUKARYOTIC TRA	EIF3C	AT3G56150	-1.10	-0.14	-0.95	0.3768569	0.6207471	-6.08	FALSE
265242_at	hypothetical protein	---	AT2G07705	1.21	0.27	0.95	0.3768549	0.6207471	-6.08	FALSE
253892_at	hypothetical protein ;supported b	---	AT4G27620	-1.11	-0.15	-0.95	0.3768192	0.6207471	-6.08	FALSE
248013_at	putative protein contains similarit	ACA8	AT5G56330	1.16	0.22	0.95	0.3768297	0.6207471	-6.08	FALSE
246365_at	hypothetical protein	---	---	1.12	0.16	0.95	0.3767945	0.6207471	-6.08	FALSE
256920_at	hypothetical protein predicted by	---	AT3G18980	-1.09	-0.13	-0.95	0.3770121	0.6208955	-6.08	FALSE
259061_at	putative GTP-binding protein sin	AtRABA5b	AT3G07410	-1.24	-0.31	-0.95	0.3770287	0.6208955	-6.08	FALSE
251708_at	Expressed protein ; supported by	---	AT3G56580	-1.15	-0.20	-0.95	0.3769978	0.6208955	-6.08	FALSE
258356_at	unknown protein	---	AT3G14340	-1.14	-0.18	-0.95	0.3771145	0.6209921	-6.08	FALSE
264741_at	aspartic protease, putative simila	---	AT1G62290	1.40	0.49	0.95	0.3772133	0.62111	-6.09	FALSE
246425_at	cellulose synthase catalytic subu	IRX3	AT5G17420	-1.27	-0.35	-0.95	0.3773106	0.6211862	-6.09	FALSE
257678_at	RNA helicase, putative contains	RTL2	AT3G20420	-1.14	-0.18	-0.95	0.3773141	0.6211862	-6.09	FALSE
265324_at	hypothetical protein predicted by	ATCOAD	AT2G18250	-1.13	-0.18	-0.94	0.3773957	0.6212756	-6.09	FALSE
262963_at	dihydrolipoamide S-acetyltransfe	---	AT1G54220	1.10	0.14	0.94	0.3774773	0.6213645	-6.09	FALSE
263827_at	unknown protein	---	AT2G40420	1.19	0.25	0.94	0.3775041	0.6213645	-6.09	FALSE

262181_at	xylosidase, putative similar to xy	---	AT1G78060	-1.32	-0.40	-0.94	0.3776236	0.6215162	-6.09	FALSE
259715_at	hypothetical protein predicted by	---	AT1G60990	-1.14	-0.19	-0.94	0.377694	0.6215729	-6.09	FALSE
252846_at	putative protein several pectin m	---	AT3G42160	-1.09	-0.13	-0.94	0.3777125	0.6215729	-6.09	FALSE
255366_x_a	putative transposon protein	---	---	1.11	0.16	0.94	0.3777745	0.6216301	-6.09	FALSE
266223_at	putative thaumatin ;supported by	---	AT2G28790	1.48	0.56	0.94	0.3778343	0.6216837	-6.09	FALSE
260608_at	putative polygalacturonase	---	AT2G43870	2.37	1.24	0.94	0.3778969	0.6216969	-6.09	FALSE
257767_at	hypothetical protein predicted by	---	AT3G23040	-1.14	-0.19	-0.94	0.3778773	0.6216969	-6.09	FALSE
254396_at	peptide transporter - like protein	---	AT4G21680	-1.74	-0.80	-0.94	0.3779839	0.6217504	-6.09	FALSE
248038_at	unknown protein	---	AT5G55980	-1.10	-0.14	-0.94	0.3779839	0.6217504	-6.09	FALSE
248475_at	unknown protein	---	AT5G50880	-1.09	-0.12	-0.94	0.3780979	0.6218931	-6.09	FALSE
266193_at	unknown protein	---	AT2G39080	-1.13	-0.18	-0.94	0.3781318	0.621904	-6.09	FALSE
257011_at	predicted protein	CAX9	AT3G14070	1.26	0.33	0.94	0.3781827	0.6219428	-6.09	FALSE
264736_at	oligopeptide transporter, putative	---	AT1G62200	1.15	0.21	0.94	0.3783609	0.6221747	-6.09	FALSE
261586_at	hypothetical protein predicted by	---	AT1G01640	-1.26	-0.34	-0.94	0.3783782	0.6221747	-6.09	FALSE
260230_at	putative DNA-binding protein con	---	AT1G74500	1.11	0.15	0.94	0.3784309	0.6222164	-6.09	FALSE
266844_at	hypothetical protein predicted by	---	AT2G26120	-1.12	-0.17	-0.94	0.3785493	0.6223662	-6.09	FALSE
248718_at	farnesyl diphosphate synthase p	FPS1	AT5G47770	-1.19	-0.25	-0.94	0.3786977	0.6224297	-6.09	FALSE
266391_at	putative strictosidine synthase id	---	AT2G41290	-1.15	-0.20	-0.94	0.3786674	0.6224297	-6.09	FALSE
255273_at	putative protein various predicte	---	---	1.09	0.13	0.94	0.3787516	0.6224297	-6.09	FALSE
265765_at	hypothetical protein predicted by	---	AT2G48060	-1.12	-0.17	-0.94	0.3786929	0.6224297	-6.09	FALSE
262743_at	unknown protein similar to unkno	---	AT1G29020	1.12	0.16	0.94	0.378677	0.6224297	-6.09	FALSE
257383_at	hypothetical protein predicted by	---	AT2G19630	-1.10	-0.14	-0.94	0.3787355	0.6224297	-6.09	FALSE
251403_at	putative protein RING finger pro	---	AT3G60300	-1.16	-0.22	-0.94	0.3790188	0.6225778	-6.09	FALSE
256588_at	unknown protein	---	AT3G28790	1.13	0.18	0.94	0.3790135	0.6225778	-6.09	FALSE
251208_at	putative protein amino acid sele	ATOEP16-4	AT3G62880	-1.11	-0.15	-0.94	0.3789317	0.6225778	-6.09	FALSE
255940_at	prolyl endopeptidase, putative si	---	AT1G20380	1.09	0.13	0.94	0.378956	0.6225778	-6.09	FALSE
254459_at	gibberellin 20-oxidase - like prot	GA2OX8	AT4G21200	-1.09	-0.13	-0.94	0.3790601	0.6225778	-6.09	FALSE
252714_x_a	putative protein p97 homologous	---	AT3G43880	1.09	0.12	0.94	0.3790333	0.6225778	-6.09	FALSE
248622_at	xylosidase	---	AT5G01980 ///	1.30	0.37	0.94	0.3790403	0.6225778	-6.09	FALSE
263234_at	hypothetical protein predicted by	---	AT1G10417	-1.10	-0.14	-0.94	0.3788927	0.6225778	-6.09	FALSE
258633_at	putative serine carboxypeptidase	SCPL27	AT3G07990	-1.25	-0.32	-0.94	0.3791486	0.6225988	-6.09	TRUE
254832_at	pEARLI 1-like protein Arabidops	---	AT4G12490	-1.89	-0.92	-0.94	0.3791792	0.6225988	-6.09	FALSE
261735_at	hypothetical protein similar to hy	---	AT1G47765	1.12	0.16	0.94	0.379182	0.6225988	-6.09	FALSE
256005_at	hypothetical protein similar to put	---	---	1.11	0.15	0.94	0.3791388	0.6225988	-6.09	FALSE
256926_at	hypothetical protein predicted by	---	AT3G22540	1.16	0.21	0.94	0.3793158	0.6227736	-6.09	FALSE

255172_x_a	putative transposon protein simil	---	---	1.15	0.20	0.94	0.3793603	0.6228018	-6.09	FALSE
260694_at	NAD+ dependent isocitrate dehy	---	AT1G32480	-1.09	-0.13	-0.94	0.3794454	0.6228967	-6.09	FALSE
249415_at	promoter-binding protein like as	CDF2	AT5G39660	-1.21	-0.27	-0.94	0.379502	0.6229448	-6.09	FALSE
265183_at	unknown protein ;supported by f	---	AT1G23750	-1.20	-0.26	-0.94	0.3796489	0.6230752	-6.09	TRUE
252612_at	hypothetical protein	---	AT3G45160	1.73	0.79	0.94	0.3796842	0.6230752	-6.09	FALSE
259197_at	putative peroxidase similar to per	---	AT3G03670	1.48	0.57	0.94	0.3796907	0.6230752	-6.09	FALSE
263925_at	putative glycine-rich RNA binding	---	AT2G21690	-1.09	-0.12	-0.94	0.3796129	0.6230752	-6.09	FALSE
249756_at	Expressed protein ; supported by	---	AT5G24313	1.10	0.14	0.94	0.3797349	0.6231029	-6.09	FALSE
251820_at	putative protein In2-1 protein, Ze	GSTL2	AT3G55040	-1.25	-0.32	-0.94	0.3797657	0.6231087	-6.09	FALSE
253531_at	putative protein tomato leucine z	ATEXO70G	AT4G31540	-1.11	-0.14	-0.94	0.3798214	0.6231552	-6.09	FALSE
252023_at	putative protein various predicte	---	AT3G52920	-1.30	-0.38	-0.94	0.3799007	0.6232405	-6.09	FALSE
246816_at	putative protein	---	AT5G27230	-1.10	-0.14	-0.94	0.3799411	0.6232619	-6.09	FALSE
262837_at	dynamin, putative similar to dyna	ADL1C	AT1G14830	1.12	0.16	0.94	0.3800711	0.6233661	-6.09	FALSE
265297_at	putative disease resistance prote	---	AT2G14080	1.10	0.13	0.94	0.3801463	0.6233661	-6.09	FALSE
250838_at	cytochrome P450 - like protein c	CYP77A9	AT5G04630	1.09	0.12	0.94	0.3801623	0.6233661	-6.09	FALSE
260562_at	putative protein kinase contains a	---	AT2G43850	-1.16	-0.21	-0.94	0.3801574	0.6233661	-6.09	FALSE
255393_at	hypothetical protein	---	---	-1.08	-0.12	-0.94	0.3801686	0.6233661	-6.09	FALSE
246795_at	putative protein	---	AT5G27020	1.11	0.15	0.94	0.3801451	0.6233661	-6.09	FALSE
248460_at	Expressed protein ; supported by	---	AT5G50915	-1.47	-0.56	-0.94	0.3801998	0.6233725	-6.09	TRUE
257500_s_a	putative serine carboxypeptidas	scpl2	AT1G73300 ///	1.09	0.12	0.94	0.3802449	0.6234016	-6.09	FALSE
257710_at	unknown protein ;supported by f	---	AT3G27350	-1.12	-0.16	-0.94	0.3802895	0.6234299	-6.09	FALSE
253230_at	putative protein ; supported by fu	---	AT4G34700	-1.11	-0.15	-0.94	0.380321	0.6234367	-6.09	FALSE
264098_at	hypothetical protein predicted by	---	AT1G79260	-1.20	-0.26	-0.94	0.3804119	0.6235343	-6.09	FALSE
267324_at	hypothetical protein predicted by	---	AT2G19360	1.09	0.13	0.94	0.3804352	0.6235343	-6.09	FALSE
251584_at	putative protein At2g42580 - Ara	TTL4	AT3G58620	-1.30	-0.38	-0.94	0.3805508	0.6235894	-6.09	TRUE
267063_at	hypothetical protein predicted by	---	AT2G41120	-1.15	-0.21	-0.94	0.3805388	0.6235894	-6.09	FALSE
AFFX-ThrX-	B. subtilis /GEN=thrC, thrB /DB_	---	---	-1.27	-0.34	-0.94	0.3805233	0.6235894	-6.09	FALSE
250864_at	putative protein predicted protei	---	AT5G03870	1.12	0.16	0.94	0.3807048	0.6237247	-6.09	FALSE
257142_at	cytochrome P450, putative conta	CYP705A1	AT3G20090	-1.15	-0.20	-0.94	0.3807154	0.6237247	-6.09	FALSE
256927_at	unknown protein	---	AT3G22550	1.10	0.14	0.94	0.380666	0.6237247	-6.09	FALSE
256778_at	nucleosome assembly protein, p	NAP1;4	AT3G13782	1.10	0.14	0.94	0.3808083	0.623832	-6.09	FALSE
248252_at	putative protein similar to unknov	AGP22	AT5G53250	-1.36	-0.44	-0.94	0.3809975	0.6238857	-6.09	TRUE
256444_at	hypothetical protein predicted by	---	AT3G11060	1.10	0.13	0.94	0.3810734	0.6238857	-6.09	FALSE
262439_at	hypothetical protein identical to h	---	AT1G47730	1.09	0.12	0.94	0.3810664	0.6238857	-6.09	FALSE
250639_at	oleosin-like protein oleosin - Bra	GRP20	AT5G07560	1.13	0.17	0.94	0.3810872	0.6238857	-6.09	FALSE

253786_at	receptor protein kinase-like prote	---	AT4G28650	1.11	0.15	0.94	0.3810569	0.6238857	-6.09	FALSE
260910_at	importin alpha, putative similar t	IMPA-6	AT1G02690	-1.18	-0.23	-0.94	0.3809781	0.6238857	-6.09	FALSE
AFFX-TrpnX	B. subtilis /GEN=trpD, trpC /DB_	---	---	1.10	0.13	0.94	0.3808982	0.6238857	-6.09	FALSE
257554_at	synaptobrevin, putative similar t	VAMP728	AT3G24890	-1.11	-0.15	-0.94	0.3808918	0.6238857	-6.09	FALSE
246679_at	putative protein replication prote	---	---	-1.10	-0.14	-0.94	0.3809288	0.6238857	-6.09	FALSE
261193_at	unknown protein ; supported by c	---	AT1G32920	1.37	0.45	0.94	0.3812875	0.6241325	-6.09	FALSE
265137_at	F-box protein family, AtFBX10 c	---	AT1G51290	1.11	0.15	0.94	0.3813146	0.6241325	-6.09	FALSE
247296_at	unknown protein ;supported by f	---	AT5G64160	1.15	0.20	0.94	0.38132	0.6241325	-6.09	FALSE
245467_at	hypothetical protein	---	AT4G16610	1.18	0.24	0.94	0.3813739	0.6241758	-6.09	FALSE
259330_at	hypothetical protein gene model	---	AT3G16270	1.13	0.18	0.94	0.3814971	0.6242579	-6.09	FALSE
249731_at	RNA-binding protein-like	CID13	AT5G24440	1.15	0.20	0.94	0.3815061	0.6242579	-6.09	FALSE
262100_s_a	hypothetical protein similar to hyp	---	AT1G59550 ///	1.15	0.20	0.94	0.3815051	0.6242579	-6.09	FALSE
254422_at	putative protein hypothetical pro	VPS28-1	AT4G21560	1.22	0.29	0.94	0.3815474	0.6242807	-6.09	FALSE
246934_at	putative protein several hypothet	---	AT5G25290	-1.14	-0.18	-0.94	0.381599	0.6243203	-6.09	FALSE
256275_at	actin 11 (ACT11) identical to acti	ACT11	AT3G12110	-1.17	-0.23	-0.94	0.3816505	0.6243377	-6.09	TRUE
260949_at	F-box protein family contains sim	SKIP16	AT1G06110	-1.11	-0.15	-0.94	0.3817192	0.6243377	-6.09	FALSE
256416_at	ferritin subunit, putative similar t	ATFER2	AT3G11050	1.13	0.18	0.94	0.3816964	0.6243377	-6.09	FALSE
258614_at	putative S-adenosylmethionine:2	---	AT3G02770	-1.20	-0.26	-0.94	0.3816983	0.6243377	-6.09	FALSE
250404_at	CCR4-ASSOCIATED FACTOR	---	AT5G10960	-1.09	-0.13	-0.94	0.3817932	0.6243693	-6.09	FALSE
262601_at	hypothetical protein similar to GE	ATHSRP54	AT1G15310	1.16	0.21	0.94	0.3817688	0.6243693	-6.09	FALSE
254959_at	predicted protein	UGE5	AT4G10955 ///	1.18	0.24	0.94	0.3819461	0.6245745	-6.09	FALSE
264143_at	latex-abundant protein, putative	ATMC5	AT1G79330	1.11	0.15	0.94	0.3821104	0.6247984	-6.09	FALSE
254114_at	putative protein (fragment) MtN2	---	AT4G24980	1.14	0.19	0.93	0.3822062	0.6249102	-6.09	FALSE
255016_at	sucrose-phosphate synthase - li	ATSPS4F	AT4G10120	-1.18	-0.24	-0.93	0.3824796	0.6250436	-6.10	TRUE
258200_at	putative ATPase similar to ATPa	---	AT3G13900	1.13	0.18	0.93	0.3823612	0.6250436	-6.10	FALSE
246430_at	calmodulin-like protein calmodul	---	AT5G17470	1.10	0.14	0.93	0.382446	0.6250436	-6.10	FALSE
264604_at	hypothetical protein predicted by	---	AT1G04650	-1.15	-0.21	-0.93	0.3824628	0.6250436	-6.10	FALSE
247458_at	putative protein PrMC3, Pinus ra	AtCXE20	AT5G62180	1.22	0.28	0.93	0.3824055	0.6250436	-6.10	FALSE
265562_at	hypothetical protein predicted by	---	AT2G05500	1.08	0.11	0.93	0.3823786	0.6250436	-6.10	FALSE
252730_at	putative protein	---	AT3G43110	1.16	0.21	0.93	0.3824232	0.6250436	-6.10	FALSE
260254_at	putative glycerophosphodiester p	---	AT1G74210	1.11	0.15	0.93	0.382536	0.625091	-6.10	TRUE
257619_at	unknown protein	ICK3	AT3G24810	-1.13	-0.17	-0.93	0.3826596	0.6252232	-6.10	FALSE
249976_at	Serine/arginine rich protein - like	SCL28	AT5G18810	1.11	0.16	0.93	0.3826717	0.6252232	-6.10	FALSE
245192_at	F12A21.9 hypothetical protein	---	AT1G67780	-1.10	-0.13	-0.93	0.382742	0.6252485	-6.10	FALSE
254747_at	serine/threonine-specific protein	MHK	AT4G13020	-1.11	-0.16	-0.93	0.382736	0.6252485	-6.10	FALSE

255681_at	predicted protein of unknown fun	DGD2	AT4G00550	-1.13	-0.18	-0.93	0.3828463	0.6253741	-6.10	FALSE
246770_at	putative protein DNA-binding pro	---	AT5G27460	-1.15	-0.20	-0.93	0.3828829	0.625389	-6.10	FALSE
265431_at	(1-4)-beta-mannan endohydrolas	---	AT2G20680	-1.11	-0.15	-0.93	0.3829783	0.6254699	-6.10	FALSE
258517_at	galactose kinase identical to GB	GALK	AT3G06580	1.11	0.16	0.93	0.3830103	0.6254699	-6.10	FALSE
255091_at	putative protein various predicted	---	---	1.09	0.13	0.93	0.3830146	0.6254699	-6.10	FALSE
264194_at	putative wall-associated kinase d	---	AT1G22720	1.11	0.15	0.93	0.3830799	0.6255317	-6.10	FALSE
253433_s_a	nodulin - like protein nodulin (clo	---	AT4G28365 ///	1.13	0.18	0.93	0.3831786	0.6256481	-6.10	FALSE
253003_s_a	putative protein tapetum specific	---	AT4G38300 ///	-1.12	-0.17	-0.93	0.3832137	0.6256606	-6.10	FALSE
258659_at	B' regulatory subunit of PP2A (A	ATB' BETA	AT3G09880	-1.11	-0.15	-0.93	0.3832519	0.6256782	-6.10	FALSE
252589_s_a	putative protein different transpo	NAXT1	AT3G45650 ///	1.32	0.40	0.93	0.3833066	0.6257228	-6.10	FALSE
252758_at	putative protein several hypothet	---	---	1.12	0.16	0.93	0.3834082	0.6258438	-6.10	FALSE
261178_at	synaptobrevin 7B, putative simila	ATVAMP72	AT1G04760	-1.10	-0.13	-0.93	0.3835169	0.6259765	-6.10	FALSE
248793_at	mutT domain protein-like ;suppo	atnudt8	AT5G47240	1.28	0.36	0.93	0.3837412	0.6262805	-6.10	FALSE
255159_at	putative polyprotein	---	---	1.14	0.19	0.93	0.3837581	0.6262805	-6.10	FALSE
246843_at	putative protein various predicte	---	AT5G26740	-1.10	-0.14	-0.93	0.3838939	0.6263676	-6.10	TRUE
264734_at	hypothetical protein predicted by	SLAH1	AT1G62280	1.11	0.14	0.93	0.3838466	0.6263676	-6.10	FALSE
259722_at	putative DNA helicase similar to /	ATRECQ4B	AT1G60930	1.08	0.11	0.93	0.3838883	0.6263676	-6.10	FALSE
260889_at	hypothetical protein predicted by	---	AT1G29120	-1.10	-0.14	-0.93	0.3839575	0.6264266	-6.10	FALSE
245254_at	ATP-sulfurylase ; supported by c	APS3	AT4G14680	1.53	0.61	0.93	0.3840043	0.6264582	-6.10	FALSE
260305_at	putative ADP-ribosylation factor	ARFA1D	AT1G70490	-1.13	-0.18	-0.93	0.3844364	0.6271182	-6.10	FALSE
265418_at	AP2 domain transcription factor	---	AT2G20880	1.47	0.56	0.93	0.3844708	0.6271295	-6.10	FALSE
260621_at	carbonic anhydrase, putative	ACA5	AT1G08065	-1.12	-0.16	-0.93	0.3845603	0.6272307	-6.10	FALSE
262589_s_a	hypothetical protein Strong simila	---	AT1G15150 ///	-1.11	-0.14	-0.93	0.3847413	0.6274231	-6.10	FALSE
264008_at	unknown protein	---	AT2G21120	1.15	0.20	0.93	0.3847608	0.6274231	-6.10	FALSE
263554_at	putative Ta11-like non-LTR retro	---	---	1.20	0.27	0.93	0.3847567	0.6274231	-6.10	FALSE
245411_at	hypothetical protein	---	AT4G17240	-1.20	-0.27	-0.93	0.3848897	0.6275022	-6.10	FALSE
266088_at	hypothetical protein predicted by	---	AT2G37780	1.14	0.19	0.93	0.3848669	0.6275022	-6.10	FALSE
245074_at	putative protein kinase contains a	---	AT2G23200	1.44	0.53	0.93	0.3848918	0.6275022	-6.10	FALSE
266462_at	unknown protein ; supported by	---	AT2G47770	1.37	0.45	0.93	0.3849729	0.6275447	-6.10	FALSE
267222_at	putative polygalacturonase	---	AT2G43880	1.10	0.13	0.93	0.3849625	0.6275447	-6.10	FALSE
262826_at	putative cytochrome P450 mono	CYP71B2	AT1G13080	1.26	0.33	0.93	0.3850011	0.6275457	-6.10	FALSE
257324_at	hypothetical protein	---	---	-1.34	-0.43	-0.93	0.3852629	0.6278326	-6.10	TRUE
259985_at	unknown protein ; supported by	---	AT1G76620	1.11	0.15	0.93	0.3852743	0.6278326	-6.10	FALSE
263951_at	putative harpin-induced protein ;	NHL12	AT2G35960	-1.43	-0.52	-0.93	0.3852352	0.6278326	-6.10	FALSE
256166_at	hypothetical protein	---	AT1G36920	-1.09	-0.12	-0.93	0.3852872	0.6278326	-6.10	FALSE

256518_at	hypothetical protein	---	AT1G66080	-1.13	-0.18	-0.93	0.3853355	0.6278364	-6.10	FALSE
251560_at	squamosa promoter-binding pro	SPL15	AT3G57920	1.15	0.20	0.93	0.3853711	0.6278364	-6.10	FALSE
260256_at	putative type II intron maturase c	---	AT1G74350	1.13	0.17	0.93	0.3853721	0.6278364	-6.10	FALSE
260094_at	GDP-4-keto-6-deoxy-D-mannos	GER1	AT1G73250	1.14	0.19	0.93	0.3854839	0.6279527	-6.10	FALSE
266488_at	putative pectinesterase ; suppor	---	AT2G47670	1.18	0.24	0.93	0.3855532	0.6279527	-6.10	FALSE
258036_at	unknown protein	---	AT3G21210	1.09	0.13	0.93	0.3855466	0.6279527	-6.10	FALSE
258411_at	hypothetical protein predicted by	---	AT3G17280	1.10	0.14	0.93	0.3855536	0.6279527	-6.10	FALSE
250261_at	peptide transporter - like protein	---	AT5G13400	1.25	0.32	0.93	0.3858819	0.6279588	-6.10	TRUE
257093_at	hypothetical protein ;supported b	---	AT3G20570	-1.20	-0.26	-0.93	0.3857232	0.6279588	-6.10	TRUE
251733_at	copper homeostasis factor ;supp	CCH	AT3G56240	-1.12	-0.16	-0.93	0.385693	0.6279588	-6.10	FALSE
260671_at	unknown protein ;supported by fu	---	AT1G19310	1.13	0.18	0.93	0.3856206	0.6279588	-6.10	FALSE
248202_at	unknown protein	---	AT5G54220	1.16	0.21	0.93	0.3857937	0.6279588	-6.10	FALSE
245488_at	peroxidase like protein	---	AT4G16270	1.11	0.15	0.93	0.385848	0.6279588	-6.10	FALSE
258328_at	putative zinc finger protein simila	---	AT3G16090	1.09	0.12	0.93	0.3857406	0.6279588	-6.10	FALSE
264710_at	putative phytochelatin synthetase	COBL6	AT1G09790	-1.11	-0.15	-0.93	0.385879	0.6279588	-6.10	FALSE
257870_at	prolyl 4-hydroxylase, putative sir	---	AT3G28490	1.08	0.12	0.93	0.3857345	0.6279588	-6.10	FALSE
254175_at	putative protein CGI-82 protein -	---	AT4G24050	-1.11	-0.15	-0.93	0.3858164	0.6279588	-6.10	FALSE
263506_s_a	hypothetical protein	---	---	1.14	0.19	0.93	0.3858877	0.6279588	-6.10	FALSE
258081_at	Expressed protein ; supported by	---	AT3G26085	-1.11	-0.15	-0.93	0.3858357	0.6279588	-6.10	FALSE
257634_s_a	cytochrome P450, putative simil	CYP71B19	AT3G26170 ///	1.24	0.30	0.93	0.3861149	0.628239	-6.10	TRUE
249565_at	contains similarity to S1 self-inco	---	AT5G38440	1.11	0.15	0.93	0.3860933	0.628239	-6.10	FALSE
257616_at	hypothetical protein contains Pfa	---	AT3G26540	-1.14	-0.19	-0.93	0.3862378	0.6283492	-6.10	FALSE
263836_at	unknown protein ;supported by f	---	AT2G40330	-1.42	-0.51	-0.93	0.3862309	0.6283492	-6.10	FALSE
249573_at	ubiquitin-like protein (UBQ9), pu	UBQ9	AT5G37640	1.10	0.14	0.93	0.3863757	0.6285287	-6.10	FALSE
260599_at	cytochrome P450, putative simil	CYP708A1	AT1G55940	-1.09	-0.12	-0.93	0.3864051	0.6285317	-6.10	FALSE
257731_at	unknown protein similar to CAL0	---	AT3G18430	1.10	0.14	0.93	0.3864645	0.6285835	-6.10	FALSE
248141_at	unknown protein	---	AT5G55010	-1.10	-0.14	-0.93	0.386605	0.6287673	-6.10	FALSE
247017_at	putative protein similar to unknov	---	AT5G66980	1.09	0.12	0.93	0.3866331	0.6287681	-6.10	FALSE
260568_at	endochitinase isolog	---	AT2G43570	2.25	1.17	0.93	0.3867575	0.6288597	-6.10	TRUE
264551_at	unknown protein similar to beta-	---	AT1G09460	1.22	0.29	0.93	0.3867997	0.6288597	-6.10	FALSE
254193_at	putative protein predicted protei	---	AT4G23870	-1.36	-0.45	-0.93	0.3867977	0.6288597	-6.10	FALSE
257511_at	hypothetical protein	---	AT1G43000	1.12	0.16	0.93	0.3867177	0.6288597	-6.10	FALSE
251205_at	glutathione peroxidase -like prot	ATGPX5	AT3G63080	1.14	0.19	0.92	0.387085	0.6290889	-6.10	FALSE
247713_at	putative protein nonspecific lipid	---	AT5G59330	1.11	0.15	0.92	0.3871338	0.6290889	-6.10	FALSE
247892_at	putative protein contains similarit	---	AT5G57970	1.19	0.25	0.92	0.3869986	0.6290889	-6.10	FALSE

255343_at	hypothetical protein	---	---	1.08	0.11	0.92	0.3870446	0.6290889	-6.10	FALSE
266654_at	putative oleosin protein	---	AT2G25890	1.15	0.20	0.92	0.387116	0.6290889	-6.10	FALSE
246980_at	peptidylprolyl isomerase (cyclophi	---	AT5G67530	-1.10	-0.14	-0.92	0.3870376	0.6290889	-6.10	FALSE
253699_at	putative protein patatin-like prote	PLP8	AT4G29800	-1.11	-0.14	-0.92	0.3871332	0.6290889	-6.10	FALSE
255284_at	5-adenylylsulfate reductase ;sup	אפר-01	AT4G04610	1.42	0.50	0.92	0.3871783	0.6291165	-6.10	FALSE
253024_at	putative protein	---	AT4G38080	-1.60	-0.68	-0.92	0.3872345	0.6291629	-6.10	FALSE
263353_at	hypothetical protein predicted by	---	AT2G22070	-1.11	-0.15	-0.92	0.3872765	0.6291852	-6.10	FALSE
262335_at	hypothetical protein predicted by	SPO11-2	AT1G63990	1.08	0.12	0.92	0.3873305	0.6291852	-6.10	FALSE
264764_at	receptor kinase, putative similar	---	AT1G61440	1.09	0.13	0.92	0.3873309	0.6291852	-6.10	FALSE
259534_at	hypothetical protein	---	AT1G12290	1.13	0.18	0.92	0.3874023	0.6291856	-6.10	FALSE
254834_at	flavonoid 3,5-hydroxylase -like p	CYP706A4	AT4G12300	-1.15	-0.20	-0.92	0.3874139	0.6291856	-6.10	FALSE
253411_at	homeobox gene ATH1	ATH1	AT4G32980	-1.23	-0.30	-0.92	0.387368	0.6291856	-6.10	FALSE
257683_at	hypothetical protein predicted by	---	AT3G13280	1.10	0.14	0.92	0.3876268	0.6294864	-6.11	FALSE
262152_s_a	hypothetical protein predicted by	---	AT1G52430 ///	-1.10	-0.14	-0.92	0.3877873	0.6296331	-6.11	FALSE
250697_at	putative protein contains similarit	---	AT5G06800	-1.13	-0.18	-0.92	0.3877779	0.6296331	-6.11	FALSE
254420_at	hypothetical protein	---	AT4G21500	-1.14	-0.19	-0.92	0.3877999	0.6296331	-6.11	FALSE
256516_at	receptor protein kinase (TMK1),	TMK1	AT1G66150	-1.19	-0.25	-0.92	0.3878944	0.6296643	-6.11	FALSE
261262_at	hypothetical protein predicted by	SDG35	AT1G26760	1.09	0.13	0.92	0.3879202	0.6296643	-6.11	FALSE
265171_at	hypothetical protein	---	AT1G23790	-1.08	-0.11	-0.92	0.3879258	0.6296643	-6.11	FALSE
265862_at	putative S-locus glycoprotein	---	AT2G01780	-1.12	-0.16	-0.92	0.3879295	0.6296643	-6.11	FALSE
253640_at	putative protein ;supported by fu	---	AT4G30630	-1.09	-0.13	-0.92	0.388026	0.6297761	-6.11	FALSE
250959_at	F-box protein family, AtFBL25 co	---	AT5G02920	1.11	0.15	0.92	0.3880746	0.6298102	-6.11	FALSE
245792_at	pinoresinol-lariciresinol reductas	PRR1	AT1G32100	1.38	0.47	0.92	0.3881247	0.6298308	-6.11	FALSE
258774_at	putative alpha-L-arabinofuranosi	ASD1	AT3G10740	1.36	0.45	0.92	0.3881425	0.6298308	-6.11	FALSE
251462_at	mitogen-activated protein kinase	ATMPK10	AT3G59790	1.13	0.18	0.92	0.3881745	0.6298378	-6.11	FALSE
264504_at	unknown protein similar to ATP-	ACLA-3	AT1G09430	1.10	0.14	0.92	0.3882177	0.6298632	-6.11	FALSE
257295_at	serine/threonine protein kinase,	GPK1	AT3G17420	1.20	0.26	0.92	0.3883021	0.6299553	-6.11	FALSE
253355_at	putative protein	---	AT4G33380	-1.09	-0.13	-0.92	0.3883322	0.6299593	-6.11	FALSE
260574_at	hypothetical protein predicted by	---	AT2G47300	1.12	0.17	0.92	0.3884123	0.6300443	-6.11	FALSE
256333_at	Sm-like protein contains Pfam pr	---	AT1G76860	-1.18	-0.24	-0.92	0.3886043	0.6302809	-6.11	FALSE
259313_at	hypothetical protein predicted by	---	AT3G05090	-1.13	-0.17	-0.92	0.3886183	0.6302809	-6.11	FALSE
246712_at	putative protein various predicte	---	---	1.09	0.12	0.92	0.3886772	0.6302809	-6.11	FALSE
248117_at	FH protein interacting protein FIF	FIP2	AT5G55000	-1.14	-0.19	-0.92	0.3887054	0.6302809	-6.11	FALSE
256733_at	hypothetical protein predicted by	---	AT3G30370	1.11	0.15	0.92	0.3887239	0.6302809	-6.11	FALSE
264995_at	mutator-like transposase, putativ	---	---	1.15	0.20	0.92	0.3887006	0.6302809	-6.11	FALSE

249498_at	putative protein motif in transcrip	---	AT5G39230	1.11	0.15	0.92	0.3888345	0.6303706	-6.11	FALSE
256399_at	hypothetical protein predicted by	---	AT3G06240	-1.11	-0.15	-0.92	0.3888284	0.6303706	-6.11	FALSE
246861_at	putative protein phytochrome-as	IAA28	AT5G25890	1.11	0.15	0.92	0.388961	0.6303995	-6.11	FALSE
267277_at	putative protein transport protein	---	AT2G30050	1.11	0.15	0.92	0.3889387	0.6303995	-6.11	FALSE
249539_at	putative protein AtPP - Brassica	---	AT5G38100	1.13	0.18	0.92	0.3889629	0.6303995	-6.11	FALSE
263394_at	hypothetical protein predicted by	---	---	1.11	0.15	0.92	0.3889291	0.6303995	-6.11	FALSE
257412_at	unknown protein	---	AT1G22980	-1.11	-0.15	-0.92	0.3891239	0.6305853	-6.11	FALSE
250018_at	putative protein similar to unknov	---	AT5G18150	1.38	0.47	0.92	0.3891328	0.6305853	-6.11	FALSE
266649_at	putative aquaporin (tonoplast intr	TIP4;1	AT2G25810	1.10	0.13	0.92	0.3891852	0.6306254	-6.11	FALSE
248534_at	putative protein contains similarit	---	AT5G50030	1.10	0.14	0.92	0.3893738	0.6306655	-6.11	FALSE
247289_at	2-oxoglutarate/malate translocat	DIT2.1	AT5G64290	-1.14	-0.19	-0.92	0.3892934	0.6306655	-6.11	FALSE
263197_at	polyubiquitin, putative similar to	---	AT1G53930	1.12	0.17	0.92	0.3894035	0.6306655	-6.11	FALSE
265871_at	unknown protein ;supported by f	---	AT2G01680	-1.15	-0.20	-0.92	0.3893591	0.6306655	-6.11	FALSE
261726_at	putative auxin-independent grow	---	AT1G76270	1.20	0.26	0.92	0.3893875	0.6306655	-6.11	FALSE
245838_at	disease resistance protein, puta	---	AT1G58410	1.11	0.15	0.92	0.3893949	0.6306655	-6.11	FALSE
260169_at	hypothetical protein predicted b	FUT13	AT1G71990	-1.21	-0.27	-0.92	0.389279	0.6306655	-6.11	FALSE
251758_at	transcription factor L2 ;supporte	---	AT3G55770	-1.12	-0.16	-0.92	0.3894846	0.6307522	-6.11	FALSE
254574_at	expressed protein supported by	---	AT4G19430	-1.52	-0.61	-0.92	0.389548	0.63081	-6.11	FALSE
265178_at	Pto kinase interactor, putative si	---	AT1G23540	1.11	0.16	0.92	0.3896069	0.6308606	-6.11	FALSE
247616_at	putative protein various predicte	---	AT5G60260	1.11	0.15	0.92	0.3896908	0.6309374	-6.11	FALSE
248667_at	putative protein contains similarit	---	AT5G48710	1.08	0.11	0.92	0.3897096	0.6309374	-6.11	FALSE
253156_at	putative protein mRNA for KIAA	---	AT4G35730	-1.12	-0.17	-0.92	0.3897655	0.6309382	-6.11	FALSE
258058_at	unknown protein	---	AT3G28980	1.11	0.15	0.92	0.3897454	0.6309382	-6.11	FALSE
266382_at	hypothetical protein predicted by	---	---	1.09	0.12	0.92	0.3898025	0.6309534	-6.11	FALSE
264934_at	hypothetical protein predicted by	---	AT1G61090	-1.10	-0.14	-0.92	0.3898396	0.6309687	-6.11	FALSE
249031_at	putative protein contains similarit	---	AT5G44900	1.12	0.17	0.92	0.389966	0.6310389	-6.11	FALSE
263123_at	beta-Amyrin Synthase, putative	---	AT1G78500	1.11	0.15	0.92	0.3899658	0.6310389	-6.11	FALSE
249681_s_a	putative protein strong similarity t	---	---	1.14	0.19	0.92	0.3899283	0.6310389	-6.11	FALSE
256673_at	unknown protein	FLA15	AT3G52370	1.51	0.60	0.92	0.3900075	0.6310574	-6.11	TRUE
256260_at	hypothetical protein	---	AT3G12440	-1.09	-0.13	-0.92	0.3900328	0.6310574	-6.11	FALSE
251410_at	uclacyanin 3 ; supported by cDN	UCC3	AT3G60280	1.10	0.13	0.92	0.3902104	0.6313	-6.11	FALSE
264405_at	putative mitogen-activated prote	ATMPK1	AT1G10210	-1.23	-0.30	-0.92	0.3904307	0.6315669	-6.11	FALSE
245584_at	amine oxidase like protein	ATAO1	AT4G14940	1.09	0.12	0.92	0.3904238	0.6315669	-6.11	FALSE
247083_at	unknown protein	---	AT5G66290	-1.10	-0.14	-0.92	0.3904724	0.6315895	-6.11	FALSE
262292_at	hypothetical protein similar to hyp	---	AT1G27595	1.12	0.16	0.92	0.390522	0.631625	-6.11	FALSE

263189_at	hypothetical protein similar to hyp	---	AT1G36100	-1.10	-0.14	-0.92	0.3905614	0.6316438	-6.11	FALSE
249962_at	pectin methyl esterase -like prot	---	AT5G18990	1.18	0.24	0.92	0.3908455	0.6320318	-6.11	FALSE
245226_at	gene_id:K17E7.15~unknown pro	---	AT3G29970	1.62	0.70	0.92	0.3908567	0.6320318	-6.11	FALSE
252877_at	hypothetical protein supported by	---	AT4G39630	-1.12	-0.16	-0.92	0.3909012	0.6320591	-6.11	FALSE
255664_at	putative protein	---	AT4G00440	1.09	0.13	0.92	0.390951	0.6320947	-6.11	FALSE
252037_at	putative calmodulin calmodulin -	CAM9	AT3G51920	1.18	0.24	0.92	0.3911841	0.6324106	-6.11	FALSE
251003_at	putative protein	---	AT5G02690	1.11	0.16	0.92	0.3912018	0.6324106	-6.11	FALSE
258565_at	unknown protein ; supported by	---	AT3G04350	-1.17	-0.23	-0.92	0.3913528	0.6324474	-6.11	TRUE
253413_at	putative protein Fe(II) transport p	ZIP9	AT4G33020	-1.08	-0.11	-0.92	0.391301	0.6324474	-6.11	FALSE
263361_at	putative senescence-associated	TET13	AT2G03840	1.11	0.15	0.92	0.3913632	0.6324474	-6.11	FALSE
253161_at	senescence-associated protein s	SEN1	AT4G35770	1.32	0.40	0.92	0.3913516	0.6324474	-6.11	FALSE
245571_at	light induced protein like	---	AT4G14695	-1.14	-0.19	-0.92	0.3913572	0.6324474	-6.11	FALSE
253372_at	pectinesterase - like protein pec	PME44	AT4G33220	1.31	0.39	0.92	0.3915323	0.632631	-6.11	TRUE
259659_at	hypothetical protein contains sim	---	AT1G55170	1.16	0.21	0.92	0.3915233	0.632631	-6.11	FALSE
251581_at	putative protein CARBON CATA	---	AT3G58560	-1.13	-0.18	-0.92	0.3915971	0.6326909	-6.11	FALSE
263467_at	unknown protein	---	AT2G31730	-1.25	-0.33	-0.92	0.3917493	0.6327522	-6.11	TRUE
248919_at	putative protein contains similarit	---	AT5G45920	1.12	0.16	0.92	0.3917074	0.6327522	-6.11	FALSE
258636_at	putative GTPase activator protei	---	AT3G07890	1.11	0.16	0.92	0.3917738	0.6327522	-6.11	FALSE
263187_at	athila ORF 1, putative similar to	---	---	-1.08	-0.11	-0.92	0.3917515	0.6327522	-6.11	FALSE
258768_at	hypothetical protein predicted by	---	AT3G10880	-1.09	-0.12	-0.92	0.3917148	0.6327522	-6.11	FALSE
245688_at	prolin-rich protein, putative simil	AGP31	AT1G28290	1.74	0.80	0.91	0.391982	0.6329279	-6.11	FALSE
259647_at	acetyl-CoA synthetase, putative	---	AT1G55325	-1.13	-0.17	-0.91	0.3919509	0.6329279	-6.11	FALSE
247318_at	3(2),5-bisphosphate nucleotidas	---	AT5G63990	1.31	0.39	0.91	0.3919936	0.6329279	-6.11	FALSE
249362_at	putative protein predicted protei	---	AT5G40550	-1.30	-0.37	-0.91	0.3919685	0.6329279	-6.11	FALSE
261292_at	hypothetical protein predicted by	---	AT1G36940	-1.13	-0.17	-0.91	0.3921921	0.6331153	-6.11	TRUE
266489_at	unknown protein ; supported by	NPSN11	AT2G35190	-1.19	-0.25	-0.91	0.3922154	0.6331153	-6.11	TRUE
254636_at	putative protein kinase ; support	CIPK12	AT4G18700	-1.10	-0.13	-0.91	0.3921576	0.6331153	-6.11	FALSE
267623_at	unknown protein	---	AT2G39650	1.54	0.62	0.91	0.3922206	0.6331153	-6.11	FALSE
253378_at	hypothetical protein	---	AT4G33310	1.09	0.13	0.91	0.3922621	0.6331375	-6.11	FALSE
251515_at	putative protein several hypothet	---	AT3G59270	-1.08	-0.11	-0.91	0.3925079	0.6334894	-6.11	FALSE
257209_at	hypothetical protein	---	AT3G14920	1.09	0.12	0.91	0.3925532	0.6335177	-6.11	FALSE
263152_at	hypothetical protein predicted by	ASIL1	AT1G54060	-1.16	-0.22	-0.91	0.3925901	0.6335324	-6.11	FALSE
254310_at	putative protein predicted protei	---	AT4G22430	1.08	0.11	0.91	0.3927479	0.6337422	-6.11	FALSE
258122_at	hypothetical protein contains sim	ATGSL04	AT3G14570	1.20	0.26	0.91	0.3927761	0.6337428	-6.11	FALSE
258608_at	unknown protein ;supported by f	---	AT3G03020	-1.23	-0.30	-0.91	0.3928572	0.6338289	-6.12	FALSE

256608_at	hypothetical protein predicted by	---	AT3G30840	1.08	0.11	0.91	0.3929104	0.6338699	-6.12	FALSE
246032_s_a	putative protein	---	---	1.12	0.16	0.91	0.393011	0.6339425	-6.12	FALSE
248841_at	ubiquitin-specific protease 21 (UI	UBP21	AT5G46740	1.17	0.23	0.91	0.3930027	0.6339425	-6.12	FALSE
245483_at	cysteine proteinase contains sim	---	AT4G16190	-1.09	-0.13	-0.91	0.3930562	0.6339705	-6.12	FALSE
255946_at	glycine hydroxymethyltransferas	SHM6	AT1G22020	1.08	0.11	0.91	0.3932437	0.6341385	-6.12	FALSE
249990_at	hypothetical protein	---	AT5G18540	-1.10	-0.14	-0.91	0.3932403	0.6341385	-6.12	FALSE
246000_at	putative protein predicted protei	---	AT5G20820	1.21	0.27	0.91	0.3932431	0.6341385	-6.12	FALSE
265757_x_a	putative PttA2-like transposon pr	---	---	-1.14	-0.19	-0.91	0.3932925	0.6341723	-6.12	FALSE
252888_at	glucose-1-phosphate adenylyltra	APL3	AT4G39210	-1.29	-0.37	-0.91	0.3934148	0.6343246	-6.12	FALSE
263952_s_a	unknown protein ;supported by f	---	AT2G35810 ///	-1.11	-0.14	-0.91	0.3935581	0.6345108	-6.12	FALSE
266890_at	acyl carrier protein identical to G	MTACP-1	AT2G44620	-1.14	-0.19	-0.91	0.3936438	0.6346041	-6.12	FALSE
256709_at	hypothetical protein predicted by	---	---	-1.10	-0.13	-0.91	0.3936913	0.634636	-6.12	FALSE
267106_s_a	putative vacuolar sorting recepto	ATVSR3	AT2G14720 ///	1.14	0.19	0.91	0.3937769	0.6347291	-6.12	FALSE
255006_at	putative protein kinase M.sativa	---	AT4G10010	-1.10	-0.13	-0.91	0.3938773	0.634846	-6.12	FALSE
266927_at	aquaporin (plasma membrane in	PIP1B	AT2G45960	-1.14	-0.19	-0.91	0.3939819	0.6349614	-6.12	FALSE
254744_at	Expressed protein ; supported by	MEE55	AT4G13345	1.16	0.22	0.91	0.3940045	0.6349614	-6.12	FALSE
248258_at	putative protein contains similarit	---	AT5G53400	-1.23	-0.30	-0.91	0.3941086	0.6350628	-6.12	FALSE
255297_x_a	hypothetical protein	---	---	1.13	0.17	0.91	0.3941231	0.6350628	-6.12	FALSE
252788_at	putative protein several hypothet	---	---	1.10	0.14	0.91	0.3942334	0.6351524	-6.12	FALSE
251405_at	plasma membrane H+-ATPase -	AHA7	AT3G60330	1.09	0.13	0.91	0.3942344	0.6351524	-6.12	FALSE
265721_at	putative ABC1 protein identical t	ATATH9	AT2G40090	1.16	0.21	0.91	0.3943014	0.6352154	-6.12	FALSE
264157_at	xyloglucan endotransglycosylas	XTH17	AT1G65310	1.21	0.28	0.91	0.3944139	0.6353415	-6.12	FALSE
256361_at	formyl transferase, putative cont	pde194	AT1G66520	-1.14	-0.19	-0.91	0.3944354	0.6353415	-6.12	FALSE
250731_at	putative protein contains similarit	AGL96	AT5G06500	1.09	0.13	0.91	0.3946589	0.6356566	-6.12	FALSE
253129_at	glycine-rich protein glycine-rich	CSDP1	AT4G36020	-1.16	-0.22	-0.91	0.3947594	0.6357571	-6.12	FALSE
252820_at	plasma membrane H+-ATPase-	AHA8	AT3G42640	-1.18	-0.24	-0.91	0.394777	0.6357571	-6.12	FALSE
258384_at	hypothetical protein predicted by	---	AT3G15490	1.10	0.14	0.91	0.394913	0.6359312	-6.12	FALSE
246598_at	dolichyl-phosphate-mannose--gl	---	AT5G14850	-1.14	-0.19	-0.91	0.394965	0.63597	-6.12	FALSE
263765_at	putative phosphatidylinositol pho	SFH3	AT2G21540	1.39	0.48	0.91	0.3950662	0.6360881	-6.12	FALSE
248114_at	wax synthase-like protein	---	AT5G55370	1.11	0.15	0.91	0.3951293	0.6361448	-6.12	FALSE
259216_at	hypothetical protein ; supported b	---	AT3G09000	1.24	0.31	0.91	0.3953619	0.6364744	-6.12	FALSE
246668_at	putative protein	---	---	1.10	0.14	0.91	0.3954446	0.6365625	-6.12	FALSE
259131_at	unknown protein similar to hypot	SP1L3	AT3G02180	-1.10	-0.14	-0.91	0.3954832	0.6365798	-6.12	FALSE
262568_at	hypothetical protein contains sim	AtRLP5	AT1G34290	1.12	0.17	0.91	0.3955883	0.6366723	-6.12	FALSE
263602_at	40S ribosomal protein S25	---	AT2G16360	-1.10	-0.14	-0.91	0.3955965	0.6366723	-6.12	FALSE

244941_at	hypothetical protein	---	---	1.13	0.17	0.91	0.3956677	0.6367419	-6.12	FALSE
264229_at	unknown protein	---	AT1G67480	1.18	0.24	0.91	0.3957098	0.6367647	-6.12	FALSE
261611_at	hypothetical protein predicted by	---	AT1G49730	-1.22	-0.28	-0.91	0.3958351	0.6368766	-6.12	TRUE
252024_at	monodehydroascorbate reducta	ATMDAR1	AT3G52880	-1.14	-0.19	-0.91	0.3958164	0.6368766	-6.12	FALSE
257550_at	hypothetical protein similar to GE	---	AT3G18460	1.13	0.18	0.91	0.3958726	0.636892	-6.12	FALSE
246933_at	ZFP3 zinc finger protein ; suppo	ZFP3	AT5G25160	1.08	0.11	0.91	0.395962	0.6369909	-6.12	FALSE
266998_at	hypothetical protein predicted by	---	AT2G34400	-1.11	-0.15	-0.91	0.3960192	0.637038	-6.12	FALSE
261202_at	flower pigmentation protein ATA	ATAN11	AT1G12910	-1.11	-0.16	-0.91	0.3961878	0.6371293	-6.12	FALSE
266354_at	putative homeodomain transcript	PFS2	AT2G01500	1.11	0.15	0.91	0.3961346	0.6371293	-6.12	FALSE
251604_at	putative protein 60S RIBOSOMA	---	AT3G57820	1.09	0.13	0.91	0.3961748	0.6371293	-6.12	FALSE
248216_at	unknown protein	---	AT5G53690	-1.10	-0.13	-0.91	0.3961198	0.6371293	-6.12	FALSE
246567_at	alpha-mannosidase -like protein	GMII	AT5G14950	1.09	0.12	0.91	0.3963213	0.6372992	-6.12	FALSE
260006_at	phosphatidylinositol synthase (PI	ATPIS1	AT1G68000	1.08	0.12	0.91	0.3964257	0.6373322	-6.12	FALSE
261654_at	hypothetical protein contains sin	---	AT1G01920	-1.15	-0.20	-0.91	0.3964062	0.6373322	-6.12	FALSE
262325_at	dirigent protein, putative similar	---	AT1G64160	-1.25	-0.32	-0.91	0.3963894	0.6373322	-6.12	FALSE
266016_at	putative RING zinc finger protein	---	AT2G18670 /	-1.11	-0.16	-0.91	0.3966608	0.6376576	-6.12	FALSE
246118_at	beta-1,3-glucanase bg5	BG5	AT5G20340	1.12	0.16	0.91	0.396684	0.6376576	-6.12	FALSE
263538_at	hypothetical protein predicted by	---	AT2G25010	-1.16	-0.21	-0.90	0.3967434	0.6376632	-6.12	FALSE
253652_at	putative protein nucleoid DNA-b	---	AT4G30040	1.08	0.12	0.90	0.396723	0.6376632	-6.12	FALSE
261710_at	hypothetical protein identical to h	---	AT1G32730	-1.12	-0.17	-0.90	0.3967895	0.6376924	-6.12	FALSE
245320_at	Expressed protein ; supported by	---	AT4G16444	-1.10	-0.14	-0.90	0.396841	0.6377302	-6.12	FALSE
245577_at	kinase like protein	---	AT4G14780	-1.12	-0.17	-0.90	0.3968918	0.637767	-6.12	FALSE
260115_at	AIG1-like protein similar to AIG1	---	AT1G33870	1.13	0.17	0.90	0.3970751	0.6380166	-6.12	FALSE
259987_at	thaumatin-like protein (PR-5) sim	ATLP-3	AT1G75030	1.14	0.19	0.90	0.3971431	0.6380359	-6.12	FALSE
266386_at	putative homeodomain transcript	HDG3	AT2G32370	1.12	0.17	0.90	0.3971192	0.6380359	-6.12	FALSE
256206_at	hypothetical protein predicted by	---	AT1G50910	1.15	0.20	0.90	0.3971966	0.6380769	-6.12	FALSE
246355_at	hypothetical protein	---	---	1.22	0.29	0.90	0.3973351	0.6382434	-6.12	FALSE
267283_at	Mutator-like transposase similar	---	---	-1.08	-0.11	-0.90	0.3973562	0.6382434	-6.12	FALSE
261688_at	unknown protein contains similar	---	AT1G47380	1.35	0.44	0.90	0.397421	0.6382576	-6.12	TRUE
256316_at	hypothetical protein	---	AT1G35890	1.09	0.12	0.90	0.3974052	0.6382576	-6.12	FALSE
249175_at	COP8 (constitutive photomorpho	COP8	AT5G42970	1.10	0.13	0.90	0.3974506	0.6382603	-6.12	FALSE
257246_at	pectinesterase, putative contains	---	AT3G24130	1.10	0.14	0.90	0.3974998	0.6382942	-6.12	FALSE
260674_at	unknown protein ; supported by	---	AT1G19370	1.11	0.15	0.90	0.3975898	0.6383938	-6.12	FALSE
252165_at	hypothetical protein ;supported b	---	AT3G50550	-1.13	-0.17	-0.90	0.397716	0.6384834	-6.12	FALSE
266306_at	hypothetical protein predicted by	---	AT2G26970	-1.12	-0.16	-0.90	0.3977459	0.6384834	-6.12	FALSE

253103_at	putative auxin-induced protein h	---	AT4G36110	1.64	0.72	0.90	0.3977014	0.6384834	-6.12	FALSE
257026_at	hypothetical protein predicted by	---	AT3G19200	1.11	0.15	0.90	0.3977575	0.6384834	-6.12	FALSE
251812_at	hypothetical protein ;supported b	---	AT3G54970	1.15	0.20	0.90	0.3978074	0.6385186	-6.12	FALSE
260721_at	hypothetical protein predicted by	---	AT1G48060	-1.10	-0.14	-0.90	0.3979423	0.6386902	-6.12	FALSE
247632_at	protein transport protein subunit	---	AT5G60460	-1.12	-0.17	-0.90	0.3979703	0.6386902	-6.12	FALSE
245424_at	putative protein	---	AT4G17505	1.10	0.14	0.90	0.3980056	0.6387019	-6.12	FALSE
245546_at	cellulose synthase like protein	ATCSLB05	AT4G15290	1.17	0.23	0.90	0.398194	0.6389592	-6.12	FALSE
247564_at	RNA helicase - like protein RNA	---	AT5G61140	-1.11	-0.16	-0.90	0.3983539	0.6389911	-6.13	FALSE
247962_at	protein kinase MEK1 homolog	MKK6	AT5G56580	1.10	0.14	0.90	0.3983069	0.6389911	-6.13	FALSE
260975_at	receptor-like serine/threonine kir	---	AT1G53430	1.31	0.39	0.90	0.3983496	0.6389911	-6.13	FALSE
258803_at	unknown protein similar to elicito	WRKY39	AT3G04670	1.11	0.15	0.90	0.3982518	0.6389911	-6.13	FALSE
267395_at	unknown protein	---	AT2G44250	1.09	0.12	0.90	0.3983274	0.6389911	-6.13	FALSE
263826_at	hypothetical protein predicted by	---	AT2G40410	1.15	0.20	0.90	0.3984925	0.6390785	-6.13	FALSE
265806_at	putative auxin-regulated protein	---	AT2G18010	-1.37	-0.45	-0.90	0.3984736	0.6390785	-6.13	FALSE
263057_at	hypothetical protein predicted by	---	AT2G09840	1.15	0.20	0.90	0.3984675	0.6390785	-6.13	FALSE
258732_at	putative alkaline/neutral invertase	---	AT3G05820	1.11	0.15	0.90	0.3985377	0.639106	-6.13	FALSE
261958_at	peptide transporter, putative pre	---	AT1G64500	-1.23	-0.30	-0.90	0.3987134	0.6392082	-6.13	FALSE
246376_at	auxin regulated protein IAA18, p	IAA18	AT1G51950	-1.15	-0.20	-0.90	0.3986884	0.6392082	-6.13	FALSE
254171_at	PsRT17-1 like protein PsRT17-1	---	AT4G24530	-1.09	-0.13	-0.90	0.3986717	0.6392082	-6.13	FALSE
260917_at	unknown protein similar to hypott	---	AT1G02700	1.12	0.17	0.90	0.3986594	0.6392082	-6.13	FALSE
258402_at	unknown protein very similar to u	---	AT3G15450	1.28	0.35	0.90	0.3987857	0.639279	-6.13	FALSE
266000_at	putative cytochrome P450 identic	CYP71B6	AT2G24180	1.23	0.30	0.90	0.398834	0.6393051	-6.13	TRUE
253032_at	guanine nucleotide-exchange pr	---	AT4G38200	1.10	0.13	0.90	0.398858	0.6393051	-6.13	FALSE
255525_at	coded for by A. thaliana cDNA T	---	AT4G02340	1.12	0.16	0.90	0.3989531	0.639359	-6.13	FALSE
249590_at	putative protein SIAH1, Brassica	---	AT5G37870	-1.09	-0.13	-0.90	0.39895	0.639359	-6.13	FALSE
265095_at	putative cruciferin 12S seed stor	CRU2	AT1G03880	1.11	0.15	0.90	0.3989757	0.639359	-6.13	FALSE
251575_at	putative protein basic leucine zip	BZIP61	AT3G58120	1.33	0.41	0.90	0.3990148	0.6393768	-6.13	TRUE
255327_at	putative malonyl-CoA decarboxy	---	AT4G04320	1.09	0.12	0.90	0.3990997	0.6394679	-6.13	FALSE
248638_at	fatty acid elongase; beta-ketoacy	KCS21	AT5G49070	1.08	0.11	0.90	0.3991616	0.6394772	-6.13	FALSE
253395_at	protein kinase AME3 ; supported	AME3	AT4G32660	-1.09	-0.12	-0.90	0.3991427	0.6394772	-6.13	FALSE
258417_at	Expressed protein ; supported by	---	AT3G17365	-1.14	-0.19	-0.90	0.3992429	0.6395626	-6.13	FALSE
256534_at	unknown protein	---	AT1G33270	-1.10	-0.14	-0.90	0.399385	0.6396008	-6.13	FALSE
248818_at	Lon protease homolog 1 precurs	LON2	AT5G47040	-1.14	-0.19	-0.90	0.3994078	0.6396008	-6.13	FALSE
263422_s_a	putative ubiquitin-like protein ; su	---	AT2G17190 //	-1.09	-0.13	-0.90	0.3993277	0.6396008	-6.13	FALSE
245499_at	membrane transporter like protei	INT4	AT4G16480	1.10	0.13	0.90	0.3994694	0.6396008	-6.13	FALSE

262301_at	ripening-induced protein, putativ	---	AT1G70880	1.11	0.16	0.90	0.3994407	0.6396008	-6.13	FALSE
259107_at	hypothetical protein predicted by	---	AT3G05460	1.09	0.12	0.90	0.3994911	0.6396008	-6.13	FALSE
265975_at	putative citrate synthetase	---	AT2G11270	1.14	0.19	0.90	0.3993439	0.6396008	-6.13	FALSE
255576_at	predicted protein of unknown fur	---	AT4G01440	-1.19	-0.25	-0.90	0.3994111	0.6396008	-6.13	FALSE
265138_at	hypothetical protein predicted by	---	AT1G51300	-1.15	-0.20	-0.90	0.3995368	0.6396291	-6.13	FALSE
251418_at	putative protein prib5, Ribes nigr	---	AT3G60440	-1.20	-0.26	-0.90	0.3996086	0.6396991	-6.13	FALSE
262023_at	hypothetical protein predicted by	---	AT1G35500	1.11	0.15	0.90	0.3996728	0.6397569	-6.13	FALSE
265213_at	clathrin protein family Similar to	---	AT1G05020	-1.16	-0.21	-0.90	0.3997977	0.6399121	-6.13	FALSE
262715_at	putative myb-related transcriptior	MYB58	AT1G16490	1.08	0.11	0.90	0.3999449	0.6400683	-6.13	FALSE
245518_at	ATP-dependent RNA helicase lik	ATRH1	AT4G15850	-1.18	-0.24	-0.90	0.3999795	0.6400683	-6.13	FALSE
261529_at	hypothetical protein contains sim	---	AT1G14430	-1.10	-0.13	-0.90	0.3999542	0.6400683	-6.13	FALSE
248265_at	putative protein contains similarit	SDG29	AT5G53430	-1.15	-0.20	-0.90	0.4001955	0.6403591	-6.13	FALSE
256974_at	unknown protein similar to putativ	---	---	1.09	0.12	0.90	0.4002174	0.6403591	-6.13	FALSE
258635_at	unknown protein	---	AT3G08020	-1.09	-0.12	-0.90	0.4003009	0.6404214	-6.13	FALSE
267401_at	unknown protein	---	AT2G26210	-1.10	-0.14	-0.90	0.4003139	0.6404214	-6.13	FALSE
248831_at	putative protein contains similarit	---	AT5G47160	-1.12	-0.16	-0.90	0.4003697	0.6404214	-6.13	FALSE
265437_at	hypothetical protein predicted by	MCM10	AT2G20980	1.11	0.15	0.90	0.4003967	0.6404214	-6.13	FALSE
256120_at	hypothetical protein contains sim	---	AT1G18130	1.09	0.12	0.90	0.400371	0.6404214	-6.13	FALSE
263021_at	hypothetical protein predicted by	---	AT1G23910	1.08	0.12	0.90	0.4005271	0.640585	-6.13	FALSE
249633_at	sucrose synthase-like protein su	SUS5	AT5G37180	-1.10	-0.13	-0.90	0.4006973	0.6408123	-6.13	FALSE
267024_s_a	putative aquaporin (plasma mem	NIP2;1	AT2G29870 ///	1.13	0.17	0.90	0.4007341	0.6408262	-6.13	FALSE
245190_at	F12A21.16 hypothetical protein	---	AT1G67690	-1.15	-0.20	-0.90	0.4007783	0.640852	-6.13	FALSE
259809_at	hypothetical protein predicted by	---	AT1G49800	1.16	0.22	0.90	0.4008907	0.6409867	-6.13	FALSE
249911_at	glucosyltransferase-like protein	CSLA02	AT5G22740	1.45	0.54	0.90	0.400992	0.6410588	-6.13	FALSE
259572_at	hypothetical protein	---	AT1G20400	1.12	0.17	0.90	0.4009666	0.6410588	-6.13	FALSE
261624_at	nucleotide sugar epimerase, put	GAE2	AT1G02000	1.20	0.26	0.90	0.4010635	0.6411282	-6.13	FALSE
246627_s_a	5-enolpyruvylshikimate-3-phosp	---	AT1G48860 ///	1.30	0.37	0.90	0.4011194	0.6411341	-6.13	FALSE
262652_at	hypothetical protein One of a clu	FUT9	AT1G14110	1.10	0.13	0.90	0.4011234	0.6411341	-6.13	FALSE
256522_at	unknown protein ;supported by fu	CMPG1	AT1G66160	1.69	0.76	0.90	0.4011986	0.6412094	-6.13	FALSE
263692_at	unknown protein Location of EST	---	AT1G26850	1.11	0.14	0.90	0.4012894	0.6412897	-6.13	FALSE
254869_at	protein kinase - like protein KI de	---	AT4G11890	1.27	0.34	0.90	0.4014002	0.6412897	-6.13	FALSE
248509_at	Expressed protein ; supported by	---	AT5G50335	2.65	1.41	0.90	0.4014176	0.6412897	-6.13	FALSE
262196_at	ubiquitin-fusion protein, putative	MUB5	AT1G77870	-1.23	-0.30	-0.90	0.4013468	0.6412897	-6.13	FALSE
259156_at	hypothetical protein predicted by	SEC8	AT3G10380	1.10	0.14	0.90	0.4013889	0.6412897	-6.13	FALSE
266446_at	hypothetical protein predicted by	---	AT2G43310	-1.09	-0.13	-0.90	0.4013281	0.6412897	-6.13	FALSE

262309_at	phosphoglucomutase, putative s	---	AT1G70820	-1.23	-0.30	-0.90	0.4016274	0.6414004	-6.13	TRUE
251756_at	putative protein	---	AT3G55820	1.09	0.13	0.90	0.4016145	0.6414004	-6.13	FALSE
255711_at	putative WD repeat membrane p	---	AT4G00090	-1.13	-0.17	-0.90	0.4015517	0.6414004	-6.13	FALSE
245537_at	hypothetical protein	---	AT4G15200	1.09	0.12	0.90	0.4015742	0.6414004	-6.13	FALSE
265954_at	putative WRKY-type DNA bindin	TTG2	AT2G37260	-1.10	-0.14	-0.90	0.4015354	0.6414004	-6.13	FALSE
260192_at	putative DNA polymerase alpha	POLA2	AT1G67630	-1.34	-0.42	-0.89	0.401711	0.6414889	-6.13	FALSE
264915_at	hypothetical protein predicted by	---	AT1G60790	-1.08	-0.12	-0.89	0.4017995	0.6415853	-6.13	FALSE
264622_at	putative vacuolar sorting protein	VPS35A	AT2G17790	1.12	0.16	0.89	0.4019191	0.6417314	-6.13	FALSE
256345_at	hypothetical protein similar to hy	---	AT1G55030	1.10	0.14	0.89	0.4020527	0.6418998	-6.13	FALSE
257736_at	hypothetical protein predicted by	---	AT3G27410	-1.11	-0.15	-0.89	0.402157	0.6420214	-6.13	FALSE
267219_at	putative transport protein ;suppo	---	AT2G02590	-1.15	-0.20	-0.89	0.4021904	0.6420298	-6.13	FALSE
264114_at	hypothetical protein predicted by	CDT1A	AT2G31270	-1.26	-0.34	-0.89	0.4022202	0.6420324	-6.13	FALSE
261914_at	dirigent protein, putative similar	---	AT1G65870	1.16	0.21	0.89	0.4023059	0.6421041	-6.13	FALSE
260643_at	hypothetical protein contains sim	---	AT1G53270	1.10	0.13	0.89	0.4023214	0.6421041	-6.13	FALSE
264204_at	putative sucrose transport protei	SUC2	AT1G22710	-1.16	-0.21	-0.89	0.4024078	0.642197	-6.13	FALSE
257605_at	hypothetical protein predicted by	---	AT3G13840	1.08	0.12	0.89	0.4024424	0.6422074	-6.13	FALSE
263065_at	MAP kinase (ATMPK7) identical	ATMPK7	AT2G18170	-1.19	-0.25	-0.89	0.4026135	0.6424	-6.13	FALSE
251542_at	putative protein protein-tyrosine	---	AT3G58760	-1.14	-0.18	-0.89	0.4026195	0.6424	-6.13	FALSE
247117_at	3-hydroxyisobutyryl-coenzyme A	CHY1	AT5G65940	-1.15	-0.20	-0.89	0.4027196	0.6425149	-6.13	FALSE
250332_at	putative protein predicted protei	---	AT5G11680	1.13	0.17	0.89	0.4028455	0.6426707	-6.13	FALSE
255854_at	unknown protein ;supported by fu	---	AT1G67050	-1.31	-0.39	-0.89	0.402927	0.6427558	-6.13	FALSE
250379_at	transcription factor like protein tr	TINY2	AT5G11590	1.10	0.13	0.89	0.402977	0.6427906	-6.13	FALSE
252617_at	n-acetylglucosaminyl-phosphati	SETH2	AT3G45100	-1.09	-0.13	-0.89	0.4030764	0.6428227	-6.13	FALSE
251002_at	putative protein predicted protei	---	AT5G02680	1.09	0.12	0.89	0.4030313	0.6428227	-6.13	FALSE
258262_at	hypothetical protein	---	AT3G15770	-1.13	-0.18	-0.89	0.4030817	0.6428227	-6.13	FALSE
251549_at	putative protein predicted protei	---	AT3G58890	1.10	0.13	0.89	0.4031424	0.6428746	-6.13	FALSE
264216_at	hypothetical protein similar to hy	---	AT1G60180	1.09	0.13	0.89	0.4031731	0.6428786	-6.13	FALSE
246010_at	putative protein predicted protei	---	AT5G08440	-1.09	-0.12	-0.89	0.4033979	0.6431594	-6.13	FALSE
264457_at	puative glucosyl transferase simi	---	AT1G10400	1.11	0.15	0.89	0.4034056	0.6431594	-6.13	FALSE
248309_at	putative protein contains similarit	---	AT5G52540	1.33	0.41	0.89	0.4034771	0.6432284	-6.13	FALSE
254913_at	putative protein beta-transducin	---	AT4G11270	-1.10	-0.14	-0.89	0.4035065	0.6432303	-6.13	FALSE
255893_at	threonyl-tRNA synthetase, putat	---	AT1G17960	1.20	0.26	0.89	0.4035791	0.6433011	-6.13	FALSE
250096_at	putative protein similar to unknov	---	AT5G17190	-1.11	-0.15	-0.89	0.4037166	0.6434753	-6.13	FALSE
265252_at	putative Na+/H+ antiporter	SOS1	AT2G01980	1.09	0.12	0.89	0.4037773	0.6435272	-6.14	FALSE
247615_at	putative protein various predicte	---	AT5G60250	1.09	0.12	0.89	0.4038061	0.6435281	-6.14	FALSE

252711_at	lipid-transfer protein-like protein	---	AT3G43720	1.40	0.49	0.89	0.4038926	0.6435311	-6.14	TRUE
254595_at	floral homeotic protein agamous	AG	AT4G18960	1.09	0.12	0.89	0.4038609	0.6435311	-6.14	FALSE
255797_at	putative steroid dehydrogenase	---	AT2G33630	1.16	0.22	0.89	0.4038887	0.6435311	-6.14	FALSE
252161_at	proline-rich protein	---	AT3G50580	1.08	0.11	0.89	0.4040059	0.6435738	-6.14	FALSE
250291_at	aspartate kinase ;supported by f	AK-LYS1	AT5G13280	-1.17	-0.22	-0.89	0.4040323	0.6435738	-6.14	FALSE
262079_at	unknown protein ; supported by c	ZCW7	AT1G59600	-1.16	-0.21	-0.89	0.4040288	0.6435738	-6.14	FALSE
263660_at	unknown protein ESTs gb|N657	MPI7	AT1G04260	-1.10	-0.14	-0.89	0.4039525	0.6435738	-6.14	FALSE
261977_at	hypothetical protein contains sim	---	---	1.09	0.13	0.89	0.404118	0.6436203	-6.14	FALSE
246078_s_a	putative protein probable mitosis	---	AT5G20430 ///	1.17	0.23	0.89	0.4041117	0.6436203	-6.14	FALSE
256358_at	unknown protein	---	AT1G66470	-1.12	-0.17	-0.89	0.404219	0.6437364	-6.14	FALSE
260994_at	hypothetical protein contains sim	---	AT1G12130	-1.12	-0.16	-0.89	0.4043832	0.6439308	-6.14	FALSE
263595_at	putative purple acid phosphatase	PAP8	AT2G01890	2.61	1.38	0.89	0.4043976	0.6439308	-6.14	FALSE
246981_at	unknown protein	---	AT5G04840	-1.15	-0.20	-0.89	0.4044594	0.6439393	-6.14	FALSE
260188_at	Mutator-like transposase similar	---	---	1.09	0.12	0.89	0.4044489	0.6439393	-6.14	FALSE
262088_at	unknown protein	---	AT1G56020	1.10	0.14	0.89	0.4045546	0.644001	-6.14	FALSE
245904_at	sucrose-phosphate synthase -lik	ATSPS2F	AT5G11110	-1.13	-0.17	-0.89	0.4045381	0.644001	-6.14	FALSE
261030_at	unknown protein contains similar	---	AT1G17410	-1.12	-0.17	-0.89	0.4045982	0.6440134	-6.14	FALSE
250377_at	putative protein predicted protei	---	AT5G11560	1.14	0.19	0.89	0.4046188	0.6440134	-6.14	FALSE
256424_at	unknown protein ;supported by fu	---	AT1G33490	-1.10	-0.14	-0.89	0.4047313	0.6440438	-6.14	FALSE
250986_at	putative protein	---	AT5G02850	-1.10	-0.14	-0.89	0.4047791	0.6440438	-6.14	FALSE
251910_at	serine/threonine-specific kinase	---	AT3G53810	1.46	0.55	0.89	0.4047558	0.6440438	-6.14	FALSE
264547_at	unknown protein ; supported by c	CLC-F	AT1G55620	-1.16	-0.22	-0.89	0.4046957	0.6440438	-6.14	FALSE
264304_at	Expressed protein ; supported by	---	AT1G78895	-1.13	-0.18	-0.89	0.4046772	0.6440438	-6.14	FALSE
247513_at	quinone oxidoreductase - like pr	---	AT5G61510	-1.15	-0.20	-0.89	0.404946	0.6442644	-6.14	FALSE
256446_at	RING zinc finger protein contain	---	AT3G11110	-1.19	-0.25	-0.89	0.4050374	0.6442898	-6.14	FALSE
259394_at	hypothetical protein predicted by	---	AT1G06420	1.09	0.12	0.89	0.4050442	0.6442898	-6.14	FALSE
249263_at	putative protein contains similarit	---	AT5G41730	1.09	0.13	0.89	0.4050467	0.6442898	-6.14	FALSE
248119_at	serine/threonine-specific protein	---	AT5G54590	1.15	0.20	0.89	0.4051764	0.6444512	-6.14	FALSE
246034_at	putative protein FH protein intera	---	AT5G08350	1.19	0.25	0.89	0.4052511	0.6445249	-6.14	TRUE
264435_at	putative glutathione S-transferas	ATGSTU18	AT1G10360	-1.20	-0.26	-0.89	0.4053081	0.6445708	-6.14	FALSE
265553_at	putative retroelement pol polypro	---	---	-1.10	-0.14	-0.89	0.4053508	0.6445937	-6.14	FALSE
266445_at	unknown protein	---	AT2G43070	1.14	0.19	0.89	0.4054327	0.6446789	-6.14	FALSE
264598_at	putative dimethylaniline monooxy	---	AT1G04610	1.09	0.13	0.89	0.4054612	0.6446793	-6.14	FALSE
265404_at	putative beta-galactosidase	BGAL13	AT2G16730	1.15	0.20	0.89	0.4055216	0.6447304	-6.14	FALSE
262105_at	pectin esterase, putative similar	---	AT1G02810	1.14	0.19	0.89	0.405796	0.6451217	-6.14	FALSE

256118_at	hypothetical protein predicted by	KU70	AT1G16970	-1.13	-0.18	-0.89	0.4058571	0.6451289	-6.14	FALSE
247336_at	putative protein similar to unknov	---	AT5G63640	-1.14	-0.18	-0.89	0.4058456	0.6451289	-6.14	FALSE
258212_at	unknown protein contains Pfam p	---	AT3G17920	-1.08	-0.11	-0.89	0.4059642	0.6452361	-6.14	FALSE
265094_at	putative cruciferin 12S seed stor	---	AT1G03890	1.09	0.12	0.89	0.4059811	0.6452361	-6.14	FALSE
252522_at	hypothetical protein	---	AT1G32337 /	1.10	0.13	0.89	0.4060197	0.6452526	-6.14	FALSE
266281_at	putative protein kinase contains a	---	AT2G29250	1.12	0.16	0.89	0.4062276	0.6455379	-6.14	FALSE
260687_at	inner mitochondrial membrane p	ATTIM23-1	AT1G17530	-1.17	-0.22	-0.89	0.4063156	0.6455824	-6.14	FALSE
247044_at	MAP protein kinase ; supported	MAPKKK5	AT5G66850	1.14	0.19	0.89	0.406375	0.6455824	-6.14	FALSE
256851_at	hypothetical protein predicted by	---	AT3G27930	1.09	0.12	0.89	0.4063043	0.6455824	-6.14	FALSE
249978_at	putative protein	---	AT5G18850	-1.11	-0.16	-0.89	0.4063853	0.6455824	-6.14	FALSE
255084_s_a	putative protein same aa sequen	---	AT4G09220 /	-1.10	-0.13	-0.89	0.4063971	0.6455824	-6.14	FALSE
266961_at	Athila retroelement ORF1-like pr	---	---	1.12	0.17	0.89	0.4065509	0.6457818	-6.14	FALSE
257109_s_a	hypothetical protein	---	---	1.09	0.12	0.89	0.4066199	0.6458015	-6.14	FALSE
247358_at	flavonol synthase	FLS2	AT5G63580	-1.13	-0.18	-0.89	0.4066023	0.6458015	-6.14	FALSE
263631_at	unknown protein ; supported by	---	AT2G04900	-1.09	-0.12	-0.88	0.4068265	0.6460626	-6.14	FALSE
263368_at	putative protein kinase contains a	---	AT2G20470	1.13	0.18	0.88	0.4068693	0.6460626	-6.14	FALSE
254407_at	receptor kinase - like protein rec	---	AT4G21370	1.11	0.15	0.88	0.4068461	0.6460626	-6.14	FALSE
248487_at	ATP-dependent Clp protease AT	ERD1	AT5G51070	1.12	0.16	0.88	0.4069657	0.6460802	-6.14	TRUE
250811_at	cysteine proteinase inhibitor-like	---	AT5G05110	-1.20	-0.27	-0.88	0.4069866	0.6460802	-6.14	FALSE
263634_at	putative retroelement gag/pol pol	---	---	1.10	0.14	0.88	0.4069875	0.6460802	-6.14	FALSE
260478_at	DnaJ isolog	---	AT1G11040	1.10	0.13	0.88	0.4070486	0.6460802	-6.14	FALSE
262508_at	serine/threonine kinase, putative	---	AT1G11300	-1.26	-0.34	-0.88	0.4070259	0.6460802	-6.14	FALSE
267235_at	unknown protein	---	AT2G43945	-1.08	-0.11	-0.88	0.4070503	0.6460802	-6.14	FALSE
260826_at	hypothetical protein predicted by	---	AT1G06710	-1.10	-0.14	-0.88	0.4073075	0.6464434	-6.14	FALSE
260123_at	AIG1-like protein similar to AIG1	---	AT1G33890	-1.10	-0.14	-0.88	0.4073922	0.6465329	-6.14	FALSE
252845_at	vacuolar H(+)-ATPase subunit-li	---	AT3G42050	-1.09	-0.13	-0.88	0.4075051	0.646667	-6.14	FALSE
260623_at	high-affinity nitrate transporter NI	ATNRT2:1	AT1G08090	-1.12	-0.17	-0.88	0.4075853	0.6467435	-6.14	FALSE
253435_at	adenylate translocator (brittle-1)	SHS1	AT4G32400	1.16	0.22	0.88	0.40761	0.6467435	-6.14	FALSE
253501_at	predicted protein predicted prote	HSL1	AT4G32010	1.11	0.15	0.88	0.4076418	0.6467489	-6.14	FALSE
260637_at	ACC oxidase, putative similar to	ACO2	AT1G62380	1.35	0.44	0.88	0.4077945	0.6469013	-6.14	FALSE
265378_at	putative GATA-type zinc finger tr	---	AT2G18380	-1.10	-0.14	-0.88	0.4077941	0.6469013	-6.14	FALSE
263551_at	hypothetical protein contains NLS	---	AT2G17110	-1.23	-0.30	-0.88	0.4078854	0.6469765	-6.14	FALSE
250432_at	putative protein various predicte	---	AT5G10420	-1.10	-0.13	-0.88	0.4078987	0.6469765	-6.14	FALSE
266156_at	hypothetical protein predicted by	FRA8	AT2G28110	-1.39	-0.47	-0.88	0.4080083	0.6470902	-6.14	FALSE
257121_at	hypothetical protein similar to aux	---	AT3G20220	-1.11	-0.15	-0.88	0.4080271	0.6470902	-6.14	FALSE

248407_at	pectinesterase	---	AT5G51500	-1.10	-0.13	-0.88	0.4080753	0.6471217	-6.14	FALSE
248935_at	salt-inducible protein-like	---	AT5G46100	-1.12	-0.16	-0.88	0.4082438	0.6473439	-6.14	FALSE
246721_at	putative protein glycine-rich prot	---	---	-1.09	-0.12	-0.88	0.4083256	0.6474286	-6.14	FALSE
245770_at	hypothetical protein predicted by	---	AT1G30240	-1.19	-0.25	-0.88	0.4084444	0.6475719	-6.14	FALSE
249098_at	DNA repair protein-like	---	AT5G43530	-1.10	-0.13	-0.88	0.4085303	0.6476631	-6.14	FALSE
250012_x_a	auxin-induced protein-like	---	AT5G18060	-1.70	-0.77	-0.88	0.4085794	0.6476959	-6.14	FALSE
261825_at	endo-xyloglucan transferase, pu	---	AT1G11545	-1.78	-0.83	-0.88	0.4086389	0.6477453	-6.14	FALSE
247983_at	pyrophosphate-dependent phosp	PFK7	AT5G56630	1.30	0.38	0.88	0.4087042	0.647795	-6.14	TRUE
246857_at	putative protein	---	AT5G25920	1.11	0.15	0.88	0.4087303	0.647795	-6.14	FALSE
259284_at	putative cell division related prote	---	AT3G11450	1.12	0.16	0.88	0.4087556	0.647795	-6.14	FALSE
263516_at	AtRer1B ;supported by full-lengt	ATRER1B	AT2G21600	-1.11	-0.16	-0.88	0.4087973	0.6478162	-6.14	FALSE
259072_at	unknown protein similar to unkno	FLA18	AT3G11700	1.15	0.20	0.88	0.4089592	0.6478289	-6.14	TRUE
262107_at	hypothetical protein predicted by	---	AT1G02750	-1.09	-0.13	-0.88	0.4089728	0.6478289	-6.14	FALSE
259255_at	putative glycerol-3-phosphate de	---	AT3G07690	-1.20	-0.27	-0.88	0.4089904	0.6478289	-6.14	FALSE
259301_at	hypothetical protein predicted by	---	AT3G05110	-1.15	-0.20	-0.88	0.408957	0.6478289	-6.14	FALSE
262881_at	unknown protein ; supported by c	---	AT1G64890	-1.20	-0.26	-0.88	0.4089808	0.6478289	-6.14	FALSE
252545_at	putative protein	---	AT3G45820	-1.12	-0.16	-0.88	0.4090042	0.6478289	-6.14	FALSE
245684_at	Expressed protein ; supported by	RHF2A	AT5G22000	1.09	0.13	0.88	0.4089832	0.6478289	-6.14	FALSE
254224_at	calcium-dependent protein kinas	CDPK6	AT4G23650	-1.09	-0.13	-0.88	0.409119	0.6478866	-6.14	FALSE
253575_at	putative protein TINY, Arabidops	---	AT4G31060	-1.10	-0.14	-0.88	0.4090907	0.6478866	-6.14	FALSE
265430_at	hypothetical protein predicted by	---	AT2G20700	1.19	0.25	0.88	0.4091412	0.6478866	-6.14	FALSE
260825_at	hypothetical protein predicted by	---	AT1G06810	1.10	0.14	0.88	0.4091542	0.6478866	-6.14	FALSE
260371_at	unknown protein ; supported by	---	AT1G69690	1.30	0.37	0.88	0.4092898	0.6479665	-6.14	TRUE
253570_at	hypothetical protein	---	AT4G31260	1.13	0.17	0.88	0.409237	0.6479665	-6.14	FALSE
252717_at	putative protein predicted protei	---	AT3G43930	1.20	0.27	0.88	0.4092752	0.6479665	-6.14	FALSE
253187_at	putative zinc-finger protein PETh	---	AT4G35280	1.09	0.12	0.88	0.4094278	0.6481399	-6.15	FALSE
262551_at	putative heat shock transcription	RUB1	AT1G31340	-1.14	-0.19	-0.88	0.4094924	0.6481972	-6.15	FALSE
257323_at	hypothetical protein	---	AT2G07698	-1.31	-0.39	-0.88	0.4097093	0.6484474	-6.15	TRUE
265117_at	putative proline-rich cell wall pro	---	AT1G62500	1.16	0.21	0.88	0.4096885	0.6484474	-6.15	FALSE
262905_at	thioredoxin, putative similar to th	ATH7	AT1G59730	1.09	0.12	0.88	0.4097358	0.6484474	-6.15	FALSE
246017_at	putative protein predicted protein	---	AT5G10730	1.09	0.13	0.88	0.4099209	0.6486954	-6.15	FALSE
259558_at	hypothetical protein	WAK5	AT1G21230	-1.11	-0.15	-0.88	0.4100147	0.6487726	-6.15	FALSE
263101_s_a	hypothetical protein predicted by	---	AT2G05230 ///	-1.10	-0.14	-0.88	0.4100266	0.6487726	-6.15	FALSE
246876_at	putative protein various predicte	---	AT5G26140	-1.09	-0.13	-0.88	0.4102262	0.6490435	-6.15	FALSE
250744_at	putative protein strong similarity t	---	AT5G05840	1.13	0.17	0.88	0.4102701	0.6490679	-6.15	FALSE

245750_at	histone H2A, putative similar to	HTA10	AT1G51060	-1.23	-0.30	-0.88	0.4103328	0.6490731	-6.15	FALSE
248247_at	putative protein contains similarit	SPCH	AT5G53210	1.10	0.13	0.88	0.4103349	0.6490731	-6.15	FALSE
250251_at	putative protein contains similarit	---	AT5G13670	-1.10	-0.14	-0.88	0.4103587	0.6490731	-6.15	FALSE
245331_at	hypothetical protein ;supported b	---	AT4G14410	1.10	0.14	0.88	0.4104298	0.6491405	-6.15	FALSE
247368_at	putative protein contains similarit	---	AT5G63320	1.13	0.17	0.88	0.4105541	0.649247	-6.15	FALSE
251495_at	putative protein RanBP7/importi	---	AT3G59020	-1.14	-0.19	-0.88	0.4105318	0.649247	-6.15	FALSE
254439_s_a	carbonic anhydrase -like protein	ACA6	AT4G20990 /	1.08	0.11	0.88	0.4106024	0.6492783	-6.15	FALSE
264916_at	ATP citrate-lyase, putative simila	ACLA-2	AT1G60810	-1.15	-0.20	-0.88	0.4106314	0.6492792	-6.15	TRUE
265761_at	putative stress protein	---	AT2G01330	1.10	0.14	0.88	0.4107115	0.6493159	-6.15	FALSE
257871_at	hypothetical protein predicted by	---	AT3G28350	1.09	0.12	0.88	0.410689	0.6493159	-6.15	FALSE
261601_at	ARP protein, putative similar to A	NQR	AT1G49670	1.10	0.13	0.88	0.4107728	0.6493678	-6.15	FALSE
260591_at	predicted protein	---	AT1G53325	1.08	0.12	0.88	0.4109049	0.6495316	-6.15	FALSE
267608_at	hypothetical protein predicted by	---	AT2G26770	1.11	0.15	0.88	0.411103	0.6497997	-6.15	FALSE
252393_at	putative protein predicted protei	---	AT3G47910	1.12	0.16	0.88	0.4111762	0.6498704	-6.15	FALSE
255544_at	predicted protein of unknown fun	---	AT4G01880	-1.14	-0.18	-0.88	0.411266	0.6499353	-6.15	FALSE
249075_at	putative protein similar to unknov	---	AT5G44000	-1.14	-0.19	-0.88	0.4113146	0.6499353	-6.15	FALSE
266632_at	putative serpin	---	AT2G35570	1.11	0.15	0.88	0.4113313	0.6499353	-6.15	FALSE
257974_at	unknown protein similar to NA-D/	---	AT3G20820	1.37	0.45	0.88	0.4112986	0.6499353	-6.15	FALSE
264492_at	unknown protein similar to unkn	---	AT1G27430	-1.08	-0.11	-0.88	0.4114889	0.6501393	-6.15	FALSE
253031_at	putative protein cellulose syntha	CSLD4	AT4G38190	1.11	0.15	0.88	0.4116042	0.6502562	-6.15	FALSE
265781_at	putative Athila retroelement ORF	---	---	1.09	0.13	0.88	0.4116199	0.6502562	-6.15	FALSE
245609_at	disease resistance N like protein	---	AT4G14368 /	1.12	0.16	0.87	0.4117303	0.6503857	-6.15	FALSE
246588_at	putative protein predicted protei	---	AT3G06433 /	1.08	0.11	0.87	0.4118254	0.6504909	-6.15	FALSE
267518_at	unknown protein	---	AT2G30500	1.32	0.40	0.87	0.4118892	0.6504957	-6.15	FALSE
262734_at	lipase, putative similar to lipase	---	AT1G28640	1.09	0.13	0.87	0.4119091	0.6504957	-6.15	FALSE
254897_at	serine/threonine kinase-like prot	---	AT4G11470	1.34	0.42	0.87	0.4119348	0.6504957	-6.15	FALSE
255192_at	hypothetical protein	---	AT4G07380	-1.10	-0.13	-0.87	0.4119426	0.6504957	-6.15	FALSE
250558_at	flavonoid 3-hydroxylase - like pr	TT7	AT5G07990	1.12	0.17	0.87	0.4120635	0.6505516	-6.15	FALSE
248368_at	mandelonitrile lyase-like protein	---	AT5G51950	-1.10	-0.13	-0.87	0.4120568	0.6505516	-6.15	FALSE
251434_at	polygalacturonase-like protein p	---	AT3G59850	1.10	0.14	0.87	0.4120564	0.6505516	-6.15	FALSE
262381_at	virus resistance protein, putative	---	AT1G72900	1.50	0.58	0.87	0.4121304	0.6505633	-6.15	TRUE
262120_at	glutathione-S-transferase, putati	ATGSTF4	AT1G02950	-1.14	-0.19	-0.87	0.4122711	0.6505633	-6.15	FALSE
255888_at	hypothetical protein contains sim	---	AT1G20300	-1.31	-0.39	-0.87	0.4122458	0.6505633	-6.15	FALSE
259813_at	glutathione S-transferase, putati	ATGSTF14	AT1G49860	1.11	0.15	0.87	0.4122991	0.6505633	-6.15	FALSE
266759_at	unknown protein predicted by ge	---	AT2G46915	1.10	0.14	0.87	0.4121313	0.6505633	-6.15	FALSE

256636_at	S-locus related protein SLR1 hor	---	AT3G12000	1.10	0.13	0.87	0.4121954	0.6505633	-6.15	FALSE
AFFX-LysX	B. subtilis /GEN=lys /DB_XREF=	---	---	-1.18	-0.24	-0.87	0.4122193	0.6505633	-6.15	FALSE
248830_at	putative protein contains similarit	---	AT5G47150	1.11	0.15	0.87	0.4122027	0.6505633	-6.15	FALSE
264529_at	CTP synthase-like protein simila	---	AT1G30820	-1.26	-0.33	-0.87	0.4123979	0.6506741	-6.15	FALSE
254202_at	putative protein hydroxymuconic	---	AT4G24140	-1.18	-0.23	-0.87	0.4124472	0.6506828	-6.15	FALSE
263764_at	putative vacuolar proton-ATPase	VHA-A2	AT2G21410	-1.13	-0.17	-0.87	0.4124605	0.6506828	-6.15	FALSE
254136_at	putative protein various predicte	---	AT4G24860	1.10	0.14	0.87	0.4125363	0.6507575	-6.15	FALSE
262294_at	hypothetical protein identical to h	---	AT1G27610	1.10	0.13	0.87	0.4126891	0.6509535	-6.15	FALSE
260368_at	AtHVA22c identical to AtHVA22c	ATHVA22C	AT1G69700	-1.37	-0.45	-0.87	0.4128334	0.6510463	-6.15	TRUE
262451_at	receptor-associated kinase isolog	SUB	AT1G11130	1.19	0.25	0.87	0.4127873	0.6510463	-6.15	FALSE
246557_at	putative protein hypothetical pro	---	AT5G15510	-1.10	-0.13	-0.87	0.4128336	0.6510463	-6.15	FALSE
255575_at	predicted protein of unknown fur	---	AT4G01430	-1.32	-0.40	-0.87	0.4128766	0.6510692	-6.15	TRUE
251801_at	cytosolic triosephosphatisomeras	TPI	AT3G55440	-1.08	-0.11	-0.87	0.4129087	0.6510741	-6.15	FALSE
249543_at	Expressed protein ; supported by	---	---	-1.11	-0.16	-0.87	0.4129369	0.6510741	-6.15	FALSE
266377_at	Mutator-like transposase similar	---	---	1.08	0.11	0.87	0.4130818	0.6512576	-6.15	FALSE
250743_at	phosphate/phosphoenolpyruvate	---	AT5G05820	1.11	0.16	0.87	0.4133428	0.6513297	-6.15	TRUE
256122_at	hypothetical protein predicted by	---	AT1G18180	1.11	0.15	0.87	0.4133845	0.6513297	-6.15	FALSE
258660_at	hypothetical protein predicted by	---	AT3G09850	1.12	0.16	0.87	0.4133775	0.6513297	-6.15	FALSE
265878_at	putative SUPERMAN-like C2H2	ZFP11	AT2G42410	-1.09	-0.12	-0.87	0.4132256	0.6513297	-6.15	FALSE
258080_at	unknown protein ;supported by f	---	AT3G25930	1.08	0.11	0.87	0.4132875	0.6513297	-6.15	FALSE
246735_at	histone H2A-like protein histone	HTA7	AT5G27670	-1.12	-0.16	-0.87	0.4132268	0.6513297	-6.15	FALSE
259298_at	putative disease resistance prote	AtRLP31	AT3G05370	1.51	0.59	0.87	0.4133145	0.6513297	-6.15	FALSE
267122_at	putative acetone-cyanohydrin lya	MES6	AT2G23550	-1.10	-0.13	-0.87	0.4133787	0.6513297	-6.15	FALSE
256519_at	hypothetical protein predicted by	---	AT1G66110	1.15	0.20	0.87	0.4132072	0.6513297	-6.15	FALSE
267339_at	unknown protein ; supported by	---	AT2G39870	1.20	0.26	0.87	0.4135611	0.6513857	-6.15	TRUE
248839_at	putative protein contains similarit	bHLH071	AT5G46690	1.30	0.37	0.87	0.4136125	0.6513857	-6.15	FALSE
261538_at	unknown protein ; supported by c	---	AT1G01830	-1.23	-0.30	-0.87	0.4137026	0.6513857	-6.15	FALSE
258446_at	hypothetical protein predicted by	---	AT3G22430	-1.10	-0.13	-0.87	0.4137087	0.6513857	-6.15	FALSE
254146_at	endo-1,4-beta-glucanase like pr	ATGH9A3	AT4G24260	1.12	0.17	0.87	0.4136915	0.6513857	-6.15	FALSE
258886_at	putative importin alpha similar to	IMPA-7	AT3G05720	1.10	0.14	0.87	0.4134965	0.6513857	-6.15	FALSE
247951_at	oxysterol-binding protein-like	ORP4C	AT5G57240	-1.10	-0.13	-0.87	0.4135465	0.6513857	-6.15	FALSE
254691_at	hypothetical protein ; supported	---	AT4G17840	1.18	0.23	0.87	0.4135362	0.6513857	-6.15	FALSE
250771_at	NBS/LRR disease resistance pro	---	AT5G05400	-1.10	-0.14	-0.87	0.4137341	0.6513857	-6.15	FALSE
248617_at	putative protein similar to unknov	---	AT5G49590	1.09	0.13	0.87	0.4136048	0.6513857	-6.15	FALSE
259317_at	hypothetical protein identical to h	HYP1	AT3G01100	1.11	0.15	0.87	0.4136375	0.6513857	-6.15	FALSE

255270_at	putative protein (ubiquitin like) to	---	AT4G05250	1.08	0.12	0.87	0.4137649	0.6513891	-6.15	FALSE
257410_at	hypothetical protein similar to pol	emb2421	AT1G24340	-1.15	-0.20	-0.87	0.4138423	0.6514661	-6.15	FALSE
253267_at	putative protein TEB4 protein, H	---	AT4G34100	-1.12	-0.16	-0.87	0.4139296	0.6515586	-6.15	FALSE
249946_at	putative protein predicted protei	---	AT5G19170	1.23	0.30	0.87	0.4139818	0.6515958	-6.15	FALSE
246149_at	peroxidase ATP N ;supported by	---	AT5G19890	-1.69	-0.76	-0.87	0.4141721	0.6518053	-6.15	FALSE
249620_at	putative protein predicted protei	---	AT5G37520	1.09	0.13	0.87	0.4141467	0.6518053	-6.15	FALSE
251588_at	putative protein several putative	---	AT3G58090	-1.12	-0.17	-0.87	0.4143429	0.6520291	-6.15	FALSE
258724_at	unknown protein	---	AT3G09600	-1.08	-0.12	-0.87	0.4144281	0.652093	-6.15	FALSE
262423_at	hypothetical protein predicted by	---	AT1G23450	1.10	0.13	0.87	0.4144407	0.652093	-6.15	FALSE
253399_at	putative poly(A) polymerase poly	nPAP	AT4G32850	-1.09	-0.13	-0.87	0.4145992	0.6522054	-6.15	FALSE
256276_at	geranylgeranyl transferase type	---	AT3G12070	-1.11	-0.15	-0.87	0.4147312	0.6522054	-6.15	FALSE
266260_at	putative ATPase skd1 family; sup	SKD1	AT2G27600	1.09	0.12	0.87	0.4148245	0.6522054	-6.15	FALSE
254294_at	putative membrane protein mem	ATRBL7	AT4G23070	1.20	0.26	0.87	0.4147807	0.6522054	-6.15	FALSE
261805_at	hypothetical protein almost identi	---	AT1G30540	1.11	0.14	0.87	0.4148552	0.6522054	-6.15	FALSE
263974_at	hypothetical protein predicted by	---	AT2G42720	1.10	0.14	0.87	0.4148172	0.6522054	-6.15	FALSE
251609_at	putative protein hypothetical pro	---	AT3G57900	1.08	0.11	0.87	0.4146224	0.6522054	-6.15	FALSE
245344_at	F-box protein family, AtFBL4 cor	---	AT4G15475	-1.12	-0.17	-0.87	0.4148224	0.6522054	-6.15	FALSE
248317_at	unknown protein	---	AT5G52680	1.10	0.14	0.87	0.4147884	0.6522054	-6.15	FALSE
248130_at	unknown protein	---	AT5G54790	-1.09	-0.13	-0.87	0.414726	0.6522054	-6.15	FALSE
259328_at	putative lectin contains Pfam pro	ATMLP-300	AT3G16440	1.12	0.17	0.87	0.4148456	0.6522054	-6.15	FALSE
259692_at	unknown protein	---	AT1G63080	-1.10	-0.14	-0.87	0.4148101	0.6522054	-6.15	FALSE
255775_at	hypothetical protein predicted by	RBL12	AT1G18600	1.10	0.14	0.87	0.4149785	0.6522674	-6.15	FALSE
259532_at	hypothetical protein	---	AT1G12470	1.08	0.12	0.87	0.4149279	0.6522674	-6.15	FALSE
253415_at	putative protein peptidyl-prolyl ci	---	AT4G33060	-1.16	-0.21	-0.87	0.4149805	0.6522674	-6.15	FALSE
AFFX-r2-Bs	B. subtilis /GEN=pheA /DB_XRE	---	---	-1.24	-0.31	-0.87	0.4150715	0.6523655	-6.15	FALSE
248623_at	putative protein similar to unknov	---	AT5G49170	-1.39	-0.47	-0.87	0.4151108	0.6523824	-6.15	FALSE
258249_s_a	unknown protein ; supported by	---	AT3G15820 //	-1.16	-0.21	-0.87	0.415196	0.6524712	-6.16	FALSE
264966_at	hypothetical protein predicted by	---	AT1G60570	1.14	0.19	0.87	0.4152408	0.6524967	-6.16	FALSE
261232_at	unknown protein ; supported by c	---	AT1G20220	1.10	0.14	0.87	0.4152822	0.6525169	-6.16	FALSE
252316_at	putative protein PrMC3 - Pinus r	ATCXE13	AT3G48700	1.10	0.13	0.87	0.4153466	0.6525601	-6.16	FALSE
253179_at	putative protein various predicte	---	AT4G35200	-1.08	-0.11	-0.87	0.4153669	0.6525601	-6.16	FALSE
248846_at	putative protein similar to unknov	---	AT5G46500	1.09	0.13	0.87	0.4155673	0.6528299	-6.16	FALSE
256535_at	unknown protein	ANAC015	AT1G33280	1.13	0.18	0.87	0.4156749	0.652954	-6.16	FALSE
245940_at	putative protein predicted protein	---	AT5G19630	-1.12	-0.17	-0.87	0.4157381	0.6529632	-6.16	FALSE
251111_at	putative protein different hypothe	---	AT5G01310	1.11	0.16	0.87	0.4157211	0.6529632	-6.16	FALSE

248514_s_a	unknown protein	---	AT5G50510 /.	1.09	0.12	0.87	0.4157964	0.6529861	-6.16	FALSE
247905_at	unknown protein	---	AT5G57400	1.08	0.11	0.87	0.4158099	0.6529861	-6.16	FALSE
267137_at	hypothetical protein predicted by	ACPT	AT2G23410	-1.09	-0.12	-0.87	0.4159252	0.6531222	-6.16	FALSE
257169_at	Expressed protein ; supported by	AtSec20	AT3G24315	-1.12	-0.16	-0.87	0.4159929	0.6531837	-6.16	FALSE
266222_at	hypothetical protein predicted by	---	AT2G28780	1.10	0.13	0.87	0.4161025	0.6532536	-6.16	FALSE
256790_at	ARR1 protein, putative similar to	ARR1	AT3G16857	-1.11	-0.14	-0.87	0.4161234	0.6532536	-6.16	FALSE
256142_at	hypothetical protein predicted by	---	AT1G48790	-1.11	-0.15	-0.87	0.4161134	0.6532536	-6.16	FALSE
252648_at	disease resistance protein homo	---	AT3G44630	1.10	0.14	0.87	0.416285	0.6534623	-6.16	FALSE
258813_at	NAM-like protein (no apical meris	anac046	AT3G04060	1.15	0.20	0.87	0.4163505	0.6535201	-6.16	TRUE
263600_at	hypothetical protein predicted by	DRD1	AT2G16390	1.11	0.16	0.87	0.4164918	0.653697	-6.16	FALSE
258946_at	hypothetical protein predicted by	---	AT3G10650	-1.12	-0.17	-0.87	0.4166292	0.6538197	-6.16	FALSE
253941_at	putative protein	---	AT4G26980	-1.09	-0.13	-0.87	0.416656	0.6538197	-6.16	FALSE
265622_at	unknown protein	---	AT2G27280	1.09	0.12	0.87	0.4166113	0.6538197	-6.16	FALSE
254120_at	putative mitochondrial uncouplin	DIC2	AT4G24570	1.98	0.98	0.87	0.4167015	0.6538461	-6.16	FALSE
257885_at	S1 self-incompatibility protein, p	---	AT3G16970	1.09	0.13	0.87	0.4167747	0.6539161	-6.16	FALSE
259774_at	plasma membrane associated p	---	AT1G29520	-1.16	-0.21	-0.86	0.4168828	0.6540407	-6.16	FALSE
257331_at	hypothetical protein	---	---	-1.12	-0.17	-0.86	0.4170048	0.654187	-6.16	FALSE
257263_at	unknown protein ;supported by f	---	AT3G22070	-1.19	-0.25	-0.86	0.417077	0.6542553	-6.16	FALSE
261103_s_a	O-methyltransferase 1, putative	---	AT1G62900 /.	1.11	0.15	0.86	0.417119	0.6542763	-6.16	FALSE
254895_at	hypothetical protein	---	AT4G11870	-1.13	-0.18	-0.86	0.4173323	0.6544428	-6.16	FALSE
248657_at	peptidylprolyl isomerase	ROF2	AT5G48570	1.88	0.91	0.86	0.4173687	0.6544428	-6.16	FALSE
263050_at	unknown protein ; supported by	ATVPS11	AT2G05170	1.10	0.14	0.86	0.4173408	0.6544428	-6.16	FALSE
266350_at	putative protein transport protein	STL2P	AT2G01470	-1.15	-0.20	-0.86	0.4173074	0.6544428	-6.16	FALSE
250241_at	photoreceptor-interacting protein	---	AT5G13600	-1.13	-0.18	-0.86	0.4173073	0.6544428	-6.16	FALSE
254227_at	putative protein chS-Rex-b - Ga	BTI1	AT4G23630	1.15	0.20	0.86	0.4174233	0.6544835	-6.16	FALSE
246586_at	putative protein predicted protei	---	AT5G14770	-1.14	-0.19	-0.86	0.4174949	0.6545508	-6.16	FALSE
252694_at	nodulin -like protein nodulin-21,	---	AT3G43630	-1.10	-0.14	-0.86	0.4175818	0.654597	-6.16	FALSE
246467_at	UDP glucose:flavonoid 3-o-gluc	---	AT5G17040	1.16	0.21	0.86	0.4175775	0.654597	-6.16	FALSE
255626_at	coded for by A. thaliana cDNA T	---	AT4G00780	1.12	0.16	0.86	0.4178372	0.6546918	-6.16	TRUE
262297_at	hypothetical protein similar to hy	---	AT1G27600	1.08	0.12	0.86	0.4178395	0.6546918	-6.16	FALSE
247744_at	putative protein various predicte	---	AT5G59020	1.14	0.19	0.86	0.4178121	0.6546918	-6.16	FALSE
245687_at	unknown protein	DEG15	AT1G28320	-1.08	-0.11	-0.86	0.4178143	0.6546918	-6.16	FALSE
256363_at	unknown protein ; supported by	---	AT1G66510	-1.20	-0.27	-0.86	0.4178432	0.6546918	-6.16	FALSE
257256_at	hypothetical protein contains Pfa	---	AT3G21970	1.08	0.11	0.86	0.4177331	0.6546918	-6.16	FALSE
249752_at	putative protein similar to unknov	LSU2	AT5G24660	1.13	0.17	0.86	0.4178089	0.6546918	-6.16	FALSE

261226_at	expansin S2 precursor, putative	ATEXPA11	AT1G20190	1.89	0.92	0.86	0.4179177	0.6547185	-6.16	FALSE
257566_x_a	hypothetical protein predicted by	---	---	1.09	0.12	0.86	0.4179057	0.6547185	-6.16	FALSE
254508_at	putative protein gene F4P9.34 c	---	AT4G20170	-1.12	-0.17	-0.86	0.4183235	0.6551438	-6.16	FALSE
255953_at	transcription factor identical to tra	TGA3	AT1G22070	-1.14	-0.19	-0.86	0.4183328	0.6551438	-6.16	FALSE
249819_at	unknown protein	---	AT5G23640	-1.09	-0.12	-0.86	0.4183218	0.6551438	-6.16	FALSE
256475_s_a	myosin heavy chain ATM2, puta	---	AT1G42680 /.	1.10	0.14	0.86	0.4182527	0.6551438	-6.16	FALSE
260439_at	hypothetical protein predicted by	---	AT1G68340	1.21	0.28	0.86	0.4183192	0.6551438	-6.16	FALSE
258061_at	unknown protein ; supported by	---	AT3G25910	-1.10	-0.14	-0.86	0.41846	0.6552532	-6.16	FALSE
261437_at	hypothetical protein predicted by	RAD51D	AT1G07745	-1.11	-0.15	-0.86	0.4184464	0.6552532	-6.16	FALSE
245397_at	auxin-responsive protein IAA1 ;s	IAA1	AT4G14560	-1.32	-0.40	-0.86	0.4186626	0.6552573	-6.16	FALSE
255362_at	putative reverse transcriptase	---	---	1.09	0.12	0.86	0.4186637	0.6552573	-6.16	FALSE
253070_at	putative protein symbiotic ammo	---	AT4G37850	1.11	0.15	0.86	0.4185359	0.6552573	-6.16	FALSE
255218_at	putative athila transposon protein	---	---	1.08	0.11	0.86	0.4186442	0.6552573	-6.16	FALSE
254046_at	hypothetical protein	---	AT4G26020	1.09	0.12	0.86	0.4185889	0.6552573	-6.16	FALSE
258016_at	hypothetical protein similar to pol	MPC	AT3G19350	1.10	0.13	0.86	0.4185369	0.6552573	-6.16	FALSE
247203_at	unknown protein ; supported by	---	AT5G65180	-1.10	-0.13	-0.86	0.4186549	0.6552573	-6.16	FALSE
257592_at	leucine-rich repeat disease resis	---	AT3G24982	1.10	0.14	0.86	0.4187531	0.6553521	-6.16	FALSE
249934_at	peroxidase ATP14a homolog	---	AT5G22410	1.08	0.12	0.86	0.4187849	0.655357	-6.16	FALSE
251492_at	putative protein CGI-136 protein	TXR1	AT3G59280	1.08	0.11	0.86	0.4188467	0.6554088	-6.16	FALSE
246088_at	putative protein	---	AT5G20600	-1.15	-0.20	-0.86	0.4189841	0.6555337	-6.16	FALSE
259500_at	unknown protein ; supported by c	---	AT1G15740	-1.14	-0.19	-0.86	0.4189577	0.6555337	-6.16	FALSE
266373_x_a	putative retroelement pol polypro	---	---	1.12	0.16	0.86	0.4190188	0.6555432	-6.16	FALSE
249189_at	putative protein similar to unknov	AtHB27	AT5G42780	1.15	0.21	0.86	0.4190767	0.6555888	-6.16	FALSE
258992_at	unknown protein similar to unkno	---	AT3G08930	1.08	0.11	0.86	0.4191751	0.6556195	-6.16	FALSE
257235_at	ras-related GTP-binding protein c	AtRABA1g	AT3G15060	1.41	0.50	0.86	0.4192282	0.6556195	-6.16	TRUE
245054_at	unknown protein	---	AT2G26460	-1.12	-0.16	-0.86	0.4192401	0.6556195	-6.16	FALSE
247674_at	putative protein large number of	---	AT5G59930	1.14	0.19	0.86	0.4192298	0.6556195	-6.16	FALSE
246328_at	putative protein hexamer-binding	---	AT3G43590	-1.10	-0.14	-0.86	0.419198	0.6556195	-6.16	FALSE
249061_at	putative protein similar to unknov	---	AT5G44550	1.10	0.13	0.86	0.4193652	0.6557703	-6.16	FALSE
262111_at	hypothetical protein predicted by	---	AT1G02960	-1.10	-0.13	-0.86	0.4194196	0.6557834	-6.16	FALSE
267249_at	hypothetical protein predicted by	---	AT2G23040	1.09	0.12	0.86	0.4194311	0.6557834	-6.16	FALSE
248853_at	protein kinase-like protein	BSK2	AT5G46570	-1.13	-0.18	-0.86	0.4194893	0.6558294	-6.16	FALSE
265527_at	putative Athila retroelement ORF	---	---	-1.08	-0.12	-0.86	0.419524	0.6558388	-6.16	FALSE
249846_at	cation-transporting ATPase	---	AT5G23630	1.08	0.12	0.86	0.4195696	0.655865	-6.16	FALSE
253310_at	hypothetical protein ; supported	EX1	AT4G33630	-1.09	-0.13	-0.86	0.4196817	0.6559953	-6.16	FALSE

257667_at	1,4-alpha-glucan branching enzy	EMB2729	AT3G20440	-1.17	-0.22	-0.86	0.4197356	0.6560345	-6.16	FALSE
257867_at	unknown protein	---	AT3G17780	1.12	0.16	0.86	0.4199137	0.6562679	-6.16	FALSE
246482_at	plant adhesion molecule 1 (PAM	PAM1	AT5G15930	1.10	0.14	0.86	0.4200173	0.6563002	-6.16	TRUE
262432_at	unknown protein	---	AT1G47530	1.20	0.27	0.86	0.4200781	0.6563002	-6.16	FALSE
249830_at	dihydroorotate dehydrogenase p	PYRD	AT5G23300	-1.21	-0.27	-0.86	0.4200681	0.6563002	-6.16	FALSE
256049_at	unknown protein	---	AT1G07010	-1.14	-0.18	-0.86	0.4200535	0.6563002	-6.16	FALSE
245583_at	hypothetical protein	---	AT4G14920	-1.10	-0.14	-0.86	0.4200727	0.6563002	-6.16	FALSE
263699_at	putative potassium transporter si	KUP10	AT1G31120	-1.16	-0.21	-0.86	0.4202025	0.6564494	-6.16	FALSE
252419_at	putative protein	---	AT3G47510	-1.24	-0.31	-0.86	0.420345	0.6565822	-6.16	FALSE
260093_at	putative serine carboxypeptidas	scpl6	AT1G73270	1.09	0.13	0.86	0.4203375	0.6565822	-6.16	FALSE
257588_x_a	En/Spm-like transposon protein,	---	---	1.15	0.20	0.86	0.4204138	0.6566447	-6.16	FALSE
261836_at	hypothetical protein contains sim	WAKL7	AT1G16090	1.45	0.53	0.86	0.4204958	0.6567106	-6.16	FALSE
266378_at	hypothetical protein predicted by	---	AT2G14700	1.12	0.17	0.86	0.4205136	0.6567106	-6.16	FALSE
252833_at	Expressed protein ; supported by	AGP3	AT4G40090	1.09	0.13	0.86	0.4207462	0.6568544	-6.16	FALSE
255300_at	putative phosphatidylglycerotran	CLS	AT4G04870	1.15	0.20	0.86	0.4207126	0.6568544	-6.16	FALSE
254512_at	terpene cyclase like protein vetis	---	AT4G20230	-1.11	-0.15	-0.86	0.4207496	0.6568544	-6.16	FALSE
257784_at	geranylgeranylated protein, puta	MUB4	AT3G26980	1.35	0.43	0.86	0.4206569	0.6568544	-6.16	FALSE
245920_at	putative protein	---	---	1.08	0.11	0.86	0.4207495	0.6568544	-6.16	FALSE
260716_at	peroxiredoxin identical to SP:O04	ATPER1	AT1G48130	1.13	0.17	0.86	0.4208644	0.6569497	-6.16	FALSE
263299_s_a	hypothetical protein predicted by	---	AT2G11570	1.10	0.13	0.86	0.4208722	0.6569497	-6.16	FALSE
253347_at	putative protein	---	AT4G33610	1.09	0.13	0.86	0.4209497	0.6569497	-6.16	FALSE
265285_at	hypothetical protein predicted by	---	AT2G20410	1.12	0.16	0.86	0.4209547	0.6569497	-6.16	FALSE
264193_at	CRK1 protein, putative similar to	---	AT1G54610	-1.08	-0.11	-0.86	0.4209533	0.6569497	-6.16	FALSE
254729_at	putative protein purple acid phos	PAP23	AT4G13700	1.11	0.16	0.86	0.4209914	0.6569621	-6.16	FALSE
255145_at	hypothetical protein	---	---	1.12	0.16	0.86	0.4210918	0.6570738	-6.17	FALSE
258091_at	hypothetical protein predicted by	---	AT3G14560	1.35	0.44	0.86	0.4211484	0.657117	-6.17	FALSE
256699_at	hypothetical protein predicted by	---	AT3G20690	1.12	0.16	0.86	0.4212258	0.6571479	-6.17	FALSE
261096_at	4-coumarate:coenzyme A ligase	ACOS5	AT1G62940	1.10	0.14	0.86	0.4212184	0.6571479	-6.17	FALSE
249755_at	unknown protein ;supported by f	---	AT5G24580	-1.34	-0.42	-0.86	0.4213569	0.6572963	-6.17	TRUE
251772_at	cyclophilin-like protein ROC7, cy	---	AT3G55920	1.13	0.17	0.86	0.4216	0.6572963	-6.17	FALSE
247435_at	glutathione S-transferase-like pro	ATGSTU9	AT5G62480	1.74	0.80	0.86	0.4215656	0.6572963	-6.17	FALSE
250263_at	putative protein	---	AT5G13470	-1.12	-0.17	-0.86	0.4216147	0.6572963	-6.17	FALSE
252099_at	putative protein senescence-ass	---	AT3G51250	1.12	0.17	0.86	0.4216379	0.6572963	-6.17	FALSE
254916_at	putative protein hypothetical pro	---	AT4G11340	1.10	0.14	0.86	0.4213883	0.6572963	-6.17	FALSE
255464_s_a	putative protein similar to T4I9.17	AT7SL-1	AT4G02970 /	1.09	0.12	0.86	0.42163	0.6572963	-6.17	FALSE

245447_at	triacylglycerol lipase like protein	---	AT4G16820	1.36	0.44	0.86	0.4215914	0.6572963	-6.17	FALSE
248715_at	ATFP4, putative	---	AT5G48290	1.15	0.20	0.86	0.4215377	0.6572963	-6.17	FALSE
254172_at	clathrin coat assembly like prote	---	AT4G24550	-1.09	-0.12	-0.86	0.4214829	0.6572963	-6.17	FALSE
261774_at	unknown protein	---	AT1G76260	-1.19	-0.25	-0.86	0.4215176	0.6572963	-6.17	FALSE
252856_at	putative protein ; supported by cI	---	AT4G39690	-1.09	-0.12	-0.86	0.42172	0.6573735	-6.17	FALSE
266973_at	hypothetical protein predicted by	---	AT2G39620	-1.11	-0.15	-0.86	0.421745	0.6573735	-6.17	FALSE
261223_at	hypothetical protein predicted by	HVA22H	AT1G19950	1.08	0.11	0.86	0.4218305	0.6574618	-6.17	FALSE
255538_at	putative transcription factor ; sup	MYB55	AT4G01680	1.30	0.37	0.86	0.4218633	0.6574681	-6.17	FALSE
248627_at	putative protein similar to unknov	---	AT5G48950	1.14	0.18	0.85	0.4219853	0.6575683	-6.17	FALSE
265142_at	unknown protein	DABB1	AT1G51360	-1.09	-0.12	-0.85	0.4219834	0.6575683	-6.17	FALSE
253402_at	HD-zip transcription factor (athb-	ATHB-8	AT4G32880	1.17	0.23	0.85	0.4221334	0.6576194	-6.17	FALSE
260714_at	chaperonin CPN10 identical to S	CPN10	AT1G14980	-1.20	-0.26	-0.85	0.4221171	0.6576194	-6.17	FALSE
262339_at	WRKY DNA binding protein, put	WRKY56	AT1G64000	-1.09	-0.12	-0.85	0.4221086	0.6576194	-6.17	FALSE
254424_at	hypothetical protein ;supported b	---	AT4G21510	-1.18	-0.24	-0.85	0.4220952	0.6576194	-6.17	FALSE
248042_at	putative protein similar to unknov	---	AT5G55960	1.13	0.17	0.85	0.4222703	0.6577877	-6.17	FALSE
255703_at	putative chalcone synthase simil	---	AT4G00040	1.17	0.22	0.85	0.4223277	0.6577879	-6.17	FALSE
252719_at	putative protein predicted protei	---	AT3G43950	1.10	0.14	0.85	0.4223281	0.6577879	-6.17	FALSE
260758_at	endo-beta-1,4-glucanase, putati	AtGH9C1	AT1G48930	1.13	0.18	0.85	0.4224152	0.6578787	-6.17	FALSE
256027_at	putative protein	---	AT1G34160	-1.08	-0.11	-0.85	0.4225308	0.6579913	-6.17	FALSE
254216_at	V-ATPase subunit G (vag2 gene	VAG2	AT4G23710	1.21	0.27	0.85	0.4225452	0.6579913	-6.17	FALSE
257590_s_a	hypothetical protein predicted by	---	AT3G24870 ///	-1.13	-0.17	-0.85	0.4225763	0.6579948	-6.17	FALSE
261648_at	salt-tolerance zinc finger protein	STZ	AT1G27730	1.50	0.58	0.85	0.4227452	0.6581547	-6.17	FALSE
247997_at	putative protein contains similarit	ATARP8	AT5G56180	1.12	0.16	0.85	0.4227322	0.6581547	-6.17	FALSE
259385_at	hypothetical protein predicted by	---	AT1G13470	1.99	0.99	0.85	0.4227656	0.6581547	-6.17	FALSE
267642_at	unknown protein	---	AT2G32905 ///	-1.08	-0.11	-0.85	0.4230726	0.6585877	-6.17	FALSE
258191_at	putative vesicle transport protein	VTI13	AT3G29100	-1.08	-0.12	-0.85	0.423106	0.6585948	-6.17	FALSE
267400_at	unknown protein	---	AT2G26240	-1.13	-0.18	-0.85	0.4231724	0.6586533	-6.17	FALSE
254077_at	putative protein NorM, Vibrio par	---	AT4G25640	1.13	0.17	0.85	0.4232904	0.658792	-6.17	TRUE
261364_at	dynamin-like protein similar to GI	---	AT1G53140	1.11	0.15	0.85	0.4234178	0.6589451	-6.17	FALSE
250597_at	NAM (no apical meristem)-like pr	ANAC080	AT5G07680	-1.22	-0.28	-0.85	0.4235577	0.6590699	-6.17	FALSE
248751_at	putative protein similar to unknov	---	AT5G47540	-1.11	-0.15	-0.85	0.4235517	0.6590699	-6.17	FALSE
254059_at	Arabidopsis mitochondrion-locali	ATHSP23.6	AT4G25200	1.13	0.18	0.85	0.4235846	0.6590699	-6.17	FALSE
263414_at	putative bZIP transcription factor	---	AT2G21230	-1.10	-0.13	-0.85	0.4237519	0.6591815	-6.17	FALSE
260061_at	cell division protein kinase simila	CDKD1;1	AT1G73690	1.16	0.21	0.85	0.4237229	0.6591815	-6.17	FALSE
262577_at	unknown protein ESTs gb|F2011	---	AT1G15290	-1.14	-0.19	-0.85	0.4237719	0.6591815	-6.17	FALSE

267543_at	26S proteasome regulatory subu	---	AT2G32730	-1.08	-0.11	-0.85	0.4237126	0.6591815	-6.17	FALSE
250658_at	C3HC4-type RING zinc finger pr	---	AT5G07040	1.12	0.16	0.85	0.4238551	0.6592109	-6.17	FALSE
251364_at	anthranilate phosphoribosyltrans	---	AT3G61300	1.11	0.14	0.85	0.4238807	0.6592109	-6.17	FALSE
251121_at	putative protein ; supported by c	AGG1	AT3G63420	-1.15	-0.20	-0.85	0.4239064	0.6592109	-6.17	FALSE
255971_at	transposon related protein simila	---	---	1.08	0.11	0.85	0.4238798	0.6592109	-6.17	FALSE
253616_at	blight-associated protein homolo	EXLB2	AT4G30380	1.09	0.12	0.85	0.4239455	0.6592267	-6.17	FALSE
245455_at	disease resistance RPP5 like pro	---	AT4G16930	1.10	0.13	0.85	0.4241098	0.6593756	-6.17	FALSE
252715_x_a	putative protein predicted protei	---	AT3G43900	1.12	0.16	0.85	0.4241028	0.6593756	-6.17	FALSE
265561_s_a	putative glycine-rich protein	---	AT1G47480 ///	1.14	0.19	0.85	0.424128	0.6593756	-6.17	FALSE
261417_at	Expressed protein ; supported by	---	AT1G07700	1.10	0.13	0.85	0.4242758	0.6595605	-6.17	FALSE
253532_at	putative protein centromere prot	---	AT4G31570	-1.10	-0.13	-0.85	0.4243275	0.659596	-6.17	FALSE
267583_at	unknown protein	---	AT2G41960	-1.08	-0.11	-0.85	0.4244734	0.6597396	-6.17	FALSE
248439_at	putative protein similar to unknov	---	AT5G51250	1.09	0.13	0.85	0.4245012	0.6597396	-6.17	FALSE
250275_at	putative protein mRNA, Moritella	---	AT5G13030	1.14	0.19	0.85	0.4245357	0.6597396	-6.17	FALSE
264260_at	putative calcium-binding protein	---	AT1G09210	1.27	0.35	0.85	0.4245144	0.6597396	-6.17	FALSE
258748_at	germin-like protein similar to gerr	GLP8	AT3G05930	1.11	0.16	0.85	0.4245651	0.6597405	-6.17	FALSE
260885_at	protein kinase PK4, putative sim	CIPK18	AT1G29230	1.12	0.17	0.85	0.4248129	0.6600806	-6.17	FALSE
254904_at	putative translation initiation fact	---	AT4G11160	-1.15	-0.20	-0.85	0.4248432	0.6600826	-6.17	FALSE
253542_at	putative protein deubiquitinating	UBP18	AT4G31670	-1.10	-0.13	-0.85	0.4249308	0.6601737	-6.17	FALSE
248648_at	putative protein similar to unknov	---	AT5G49220	-1.11	-0.15	-0.85	0.4250364	0.6602928	-6.17	FALSE
246012_at	Pspzf zinc finger protein - like D	---	AT5G10650	-1.16	-0.21	-0.85	0.4251232	0.6603776	-6.17	FALSE
263254_x_a	hypothetical protein similar to hyp	---	---	1.14	0.19	0.85	0.4251488	0.6603776	-6.17	FALSE
258066_at	hypothetical protein predicted by	---	AT3G25970	1.08	0.11	0.85	0.4252146	0.6604348	-6.17	FALSE
262461_at	myosin, putative similar to myos	VIIIA	AT1G50360	1.19	0.25	0.85	0.4253063	0.6605323	-6.17	FALSE
262885_at	alpha-tubulin, putative similar to	TUA1	AT1G64740	1.11	0.16	0.85	0.4254153	0.6606565	-6.17	FALSE
246187_at	putative protein	AT5G21020	---	1.14	0.18	0.85	0.4255663	0.660846	-6.17	FALSE
258271_at	hypothetical protein predicted by	---	AT3G15605	1.11	0.15	0.85	0.4256066	0.6608637	-6.17	FALSE
266001_at	hypothetical protein predicted by	HHP3	AT2G24150	-1.09	-0.12	-0.85	0.4257754	0.6609213	-6.17	FALSE
260471_at	hypothetical protein predicted by	---	AT1G11070	1.09	0.12	0.85	0.4257755	0.6609213	-6.17	FALSE
247309_at	putative protein contains similarit	---	AT5G63940	1.15	0.21	0.85	0.425693	0.6609213	-6.17	FALSE
256507_at	hypothetical protein predicted by	---	AT1G75150	1.12	0.16	0.85	0.4257886	0.6609213	-6.17	FALSE
265334_at	putative lipid transfer protein ; su	---	AT2G18370	-1.23	-0.30	-0.85	0.4257797	0.6609213	-6.17	FALSE
252647_at	protein-tyrosine-phosphatase-lik	---	AT3G44620	-1.17	-0.22	-0.85	0.4259719	0.6609311	-6.17	FALSE
246785_at	glutathione synthetase gsh2 nor	GSH2	AT5G27380	-1.21	-0.27	-0.85	0.4259126	0.6609311	-6.17	FALSE
247617_at	receptor like protein kinase rece	---	AT5G60270	1.25	0.32	0.85	0.4259556	0.6609311	-6.17	FALSE

252367_at	putative protein MEL-26, Caeno	BT2	AT3G48360	1.37	0.45	0.85	0.4260023	0.6609311	-6.17	FALSE
255868_at	putative MYB family transcription	---	AT2G30380	1.12	0.16	0.85	0.425934	0.6609311	-6.17	FALSE
261010_at	hypothetical protein predicted by	---	AT1G26350	-1.10	-0.13	-0.85	0.425945	0.6609311	-6.17	FALSE
266729_at	50S ribosomal protein L7/L12	---	AT2G03130	1.10	0.13	0.85	0.4258263	0.6609311	-6.17	FALSE
254139_at	hypothetical protein	---	AT4G24600	1.12	0.16	0.85	0.4260267	0.6609311	-6.17	FALSE
264370_at	hybrid proline-rich protein, putati	---	AT1G12100	1.10	0.14	0.85	0.4261744	0.6611152	-6.17	FALSE
259876_at	putative DnaJ protein similar to	---	AT1G76700	1.19	0.26	0.85	0.4262258	0.66115	-6.17	FALSE
258705_at	hypothetical protein predicted by	---	AT3G09470	-1.10	-0.14	-0.85	0.426263	0.6611627	-6.17	FALSE
256312_x_a	hypothetical protein	---	AT1G35820	1.09	0.12	0.85	0.4263361	0.6612311	-6.17	FALSE
249024_at	putative protein strong similarity t	---	AT5G44860	-1.10	-0.13	-0.85	0.4263759	0.6612479	-6.17	FALSE
266748_at	putative squamosa-promoter bin	SPL1	AT2G47070	1.17	0.22	0.85	0.4264566	0.6612934	-6.17	FALSE
255390_at	hypothetical protein similar to A.	---	---	1.10	0.13	0.85	0.4264632	0.6612934	-6.17	FALSE
262250_at	Expressed protein predicted by g	---	AT1G48280	-1.38	-0.46	-0.85	0.426587	0.6614217	-6.17	FALSE
249363_at	DegP protease contains similarity	DegP13	AT5G40560	1.08	0.11	0.85	0.426633	0.6614217	-6.17	FALSE
249044_at	Na+-dependent inorganic phospl	PHT4;6	AT5G44370	1.15	0.20	0.85	0.4266065	0.6614217	-6.17	FALSE
266827_at	putative serine carboxypeptidase	SCPL12	AT2G22920	1.09	0.12	0.85	0.4267078	0.6614928	-6.17	FALSE
266525_at	putative tetracycline transporter p	MEE15	AT2G16970	1.12	0.16	0.85	0.4267823	0.6615634	-6.17	FALSE
263079_at	putative retroelement pol polypro	---	---	1.09	0.12	0.85	0.4268434	0.661613	-6.17	FALSE
249113_at	putative protein similar to unknov	---	AT5G43790	1.14	0.19	0.85	0.4268995	0.661655	-6.17	FALSE
255378_at	putative glucan synthase compo	ATGSL05	AT4G03550	1.09	0.13	0.85	0.4271152	0.6617358	-6.18	FALSE
250109_at	GASA4 ; supported by cDNA: gi	GASA4	AT5G15230	1.75	0.80	0.85	0.4269962	0.6617358	-6.17	FALSE
248356_at	putative protein strong similarity t	ATEXO70A	AT5G52350	-1.08	-0.12	-0.85	0.4270216	0.6617358	-6.17	FALSE
265055_at	hypothetical protein similar to hyp	---	---	1.10	0.14	0.85	0.4270674	0.6617358	-6.18	FALSE
266305_at	putative DNA polymerase epsilon	TIL2	AT2G27120	1.10	0.14	0.85	0.4271013	0.6617358	-6.18	FALSE
264919_at	hypothetical protein contains sim	---	AT1G60540	1.10	0.14	0.85	0.4271257	0.6617358	-6.18	FALSE
250967_at	putative protein In2, Zea mays,	---	AT5G02790	1.14	0.19	0.84	0.4272281	0.6618496	-6.18	FALSE
246291_at	hypothetical protein ; supported	---	AT3G56820	-1.11	-0.15	-0.84	0.4274441	0.6619547	-6.18	FALSE
253675_at	hypothetical protein	---	AT4G29560	-1.09	-0.13	-0.84	0.4274701	0.6619547	-6.18	FALSE
254069_at	putative protein similarity to antis	ATNUDT10	AT4G25434	1.14	0.19	0.84	0.4274494	0.6619547	-6.18	FALSE
253930_at	embryo-specific protein 1 (ATS1)	ATS1	AT4G26740	1.10	0.14	0.84	0.4274634	0.6619547	-6.18	FALSE
250082_at	polygalacturonase-like protein	---	AT5G17200	1.12	0.17	0.84	0.4274344	0.6619547	-6.18	FALSE
255533_at	putative CHP-rich zinc finger pro	---	AT4G02180	1.09	0.12	0.84	0.4273363	0.6619547	-6.18	FALSE
263805_at	unknown protein ; supported by	---	AT2G40400	-1.08	-0.11	-0.84	0.4275101	0.6619717	-6.18	FALSE
260028_at	unknown protein ; supported by	---	AT1G29980	1.47	0.55	0.84	0.4275902	0.6620508	-6.18	TRUE
247127_at	putative protein similar to unknov	---	AT5G66100	1.09	0.13	0.84	0.4277968	0.6622185	-6.18	FALSE

246135_at	putative protein non-consensus	---	AT5G20885	-1.21	-0.27	-0.84	0.4277767	0.6622185	-6.18	FALSE
265523_at	putative Ty3-gypsy-like retroelem	---	---	1.08	0.12	0.84	0.4278437	0.6622185	-6.18	FALSE
265482_at	hypothetical protein contains a d	---	AT2G15780	2.09	1.06	0.84	0.4277698	0.6622185	-6.18	FALSE
249495_at	germin - like protein GLP6 exon	GLP6	AT5G39100	1.11	0.16	0.84	0.4278268	0.6622185	-6.18	FALSE
253065_at	putative protein predicted protei	AtGRF2	AT4G37740	-1.14	-0.19	-0.84	0.4280383	0.6624299	-6.18	FALSE
254100_at	hypothetical protein ;supported b	---	AT4G25020	1.20	0.26	0.84	0.428029	0.6624299	-6.18	FALSE
253456_at	putative protein norbin, Rattus n	---	AT4G32050	-1.13	-0.17	-0.84	0.4281161	0.6625053	-6.18	FALSE
264363_at	hypothetical protein predicted by	---	AT1G03170	1.11	0.15	0.84	0.4282074	0.6626016	-6.18	FALSE
257258_at	hypothetical protein contains Pfa	---	AT3G22040	-1.15	-0.20	-0.84	0.4283608	0.6627941	-6.18	FALSE
254434_at	ethylene-regulated transcript 2 (E	---	AT4G20880	-1.09	-0.13	-0.84	0.4284774	0.6628395	-6.18	TRUE
262495_at	unknown protein Contains simila	---	AT1G21780	-1.15	-0.20	-0.84	0.4284537	0.6628395	-6.18	FALSE
265290_at	putative anthocyanidin-3-glucosi	---	AT2G22590	1.09	0.12	0.84	0.4284654	0.6628395	-6.18	FALSE
252794_at	putative protein predicted protei	---	---	1.08	0.12	0.84	0.4285186	0.6628584	-6.18	FALSE
245695_at	rec - like protein	---	AT5G04270	-1.10	-0.14	-0.84	0.4286295	0.6629849	-6.18	FALSE
256211_at	gibberellin 20-oxidase, putative	GA2OX7	AT1G50960	1.08	0.11	0.84	0.428678	0.663015	-6.18	FALSE
253434_at	potassium channel - protein	AKT5	AT4G32500	1.10	0.13	0.84	0.4287353	0.6630477	-6.18	FALSE
255876_at	hypothetical protein	---	AT2G40480	-1.23	-0.29	-0.84	0.4287575	0.6630477	-6.18	FALSE
254733_at	putative polygalacturonase polyg	---	AT4G13760	1.09	0.12	0.84	0.4287863	0.6630477	-6.18	FALSE
250737_at	putative protein similar to unknov	---	AT5G06370	-1.14	-0.19	-0.84	0.4288599	0.6631165	-6.18	FALSE
262387_s_a	hypothetical protein contains sim	---	AT1G49340 ///	-1.10	-0.14	-0.84	0.4290061	0.6632975	-6.18	FALSE
246408_at	hypothetical protein predicted by	---	AT1G57680	-1.13	-0.18	-0.84	0.429209	0.6634144	-6.18	TRUE
245960_at	subtilisin-like protein subtilisin/ke	S1P	AT5G19660	-1.08	-0.11	-0.84	0.4292049	0.6634144	-6.18	FALSE
256153_at	ubiquitin-like (UBQ12), putative	UBQ12	AT1G55060	1.12	0.16	0.84	0.4291807	0.6634144	-6.18	FALSE
259941_s_a	putative DEAD/DEAH box helica	---	AT1G71280 ///	1.09	0.13	0.84	0.4292271	0.6634144	-6.18	FALSE
AFFX-CreX	Bacteriophage P1 /GEN=cre /DB	---	---	1.22	0.29	0.84	0.4291128	0.6634144	-6.18	FALSE
256254_at	hypothetical protein predicted by	---	AT3G11290	-1.13	-0.17	-0.84	0.4293328	0.6635328	-6.18	FALSE
252898_at	cytochrome P450 -like protein si	CYP96A11	AT4G39500	1.08	0.11	0.84	0.4294311	0.6636398	-6.18	FALSE
261712_at	alcohol dehydrogenase, putative	---	AT1G32780	-1.11	-0.15	-0.84	0.429462	0.6636426	-6.18	FALSE
245088_at	subtilisin-like serine protease cor	---	AT2G39850	1.24	0.31	0.84	0.4295243	0.6636939	-6.18	FALSE
256578_at	peroxidase, putative similar to p	---	AT3G28200	-1.21	-0.27	-0.84	0.4295551	0.6636965	-6.18	TRUE
258978_at	unknown protein ; supported by	---	AT3G09320	-1.09	-0.12	-0.84	0.4297322	0.6638552	-6.18	FALSE
266413_at	unknown protein ;supported by f	---	AT2G38740	-1.11	-0.15	-0.84	0.4297451	0.6638552	-6.18	FALSE
246710_at	putative protein predicted protei	---	---	-1.08	-0.11	-0.84	0.4296875	0.6638552	-6.18	FALSE
255477_at	coded for by A. thaliana cDNA R	---	AT4G02370	-1.13	-0.18	-0.84	0.4298566	0.6639825	-6.18	FALSE
246200_at	putative protein ;supported by ful	---	AT4G37240	1.20	0.26	0.84	0.4299865	0.6641381	-6.18	TRUE

254828_at	putative cell wall-plasma membra	AIR1	AT4G12550	1.09	0.13	0.84	0.4301	0.6642234	-6.18	FALSE
256560_s_a	vetispiradiene synthase, putative	---	AT3G31415 /.	-1.09	-0.13	-0.84	0.430099	0.6642234	-6.18	FALSE
252932_at	putative proton pump vacuolar p	VHA-A3	AT4G39080	1.10	0.14	0.84	0.4302294	0.6642784	-6.18	FALSE
259810_at	Na+/H+ antiporter, putative simil	ATNHD2	AT1G49810	1.08	0.12	0.84	0.4302398	0.6642784	-6.18	FALSE
246579_at	hypothetical protein predicted by	---	AT1G31620	1.12	0.16	0.84	0.4301995	0.6642784	-6.18	FALSE
256354_at	dormancy related protein, putativ	---	AT1G54870	-1.13	-0.18	-0.84	0.4302521	0.6642784	-6.18	FALSE
255042_at	putative protein hypothetical pro	---	AT4G09630	1.10	0.13	0.84	0.4302835	0.664282	-6.18	FALSE
260375_at	unknown protein	---	AT1G73950	-1.10	-0.14	-0.84	0.4305749	0.6646868	-6.18	FALSE
245294_at	casein kinase I ; supported by cD	CKI1	AT4G14340	1.10	0.13	0.84	0.4306472	0.6647085	-6.18	FALSE
249520_at	putative protein similar to unknov	---	AT5G38670	1.08	0.11	0.84	0.4306354	0.6647085	-6.18	FALSE
245685_at	Expressed protein ; supported by	E2F1	AT5G22220	1.08	0.11	0.84	0.4308954	0.6647168	-6.18	FALSE
260311_at	hypothetical protein predicted by	---	AT1G70570	-1.08	-0.11	-0.84	0.4307956	0.6647168	-6.18	FALSE
253213_at	RNA helicase (RH16)	---	AT4G34910	1.10	0.14	0.84	0.4308776	0.6647168	-6.18	FALSE
257255_at	hypothetical protein contains Pfa	---	AT3G21960	1.10	0.14	0.84	0.4308696	0.6647168	-6.18	FALSE
256123_at	hypothetical protein predicted by	GC2	AT1G18190	1.08	0.11	0.84	0.4308912	0.6647168	-6.18	FALSE
257261_s_a	hypothetical protein contains Pfa	---	AT3G21920 /.	1.08	0.11	0.84	0.4307419	0.6647168	-6.18	FALSE
252629_at	cytochrome P450 - like protein c	---	AT3G44970	-1.08	-0.12	-0.84	0.430944	0.6647168	-6.18	FALSE
263387_at	unknown protein ; supported by	---	AT2G40160	-1.11	-0.15	-0.84	0.4308266	0.6647168	-6.18	FALSE
263269_at	En/Spm-like transposon protein r	---	---	-1.09	-0.13	-0.84	0.4309234	0.6647168	-6.18	FALSE
261690_at	branched-chain amino acid amir	---	AT1G50090	1.09	0.13	0.84	0.4308741	0.6647168	-6.18	FALSE
252987_at	putative growth regulator protein	---	AT4G38390	1.12	0.16	0.84	0.4312751	0.6651826	-6.18	FALSE
251199_at	transport inhibitor response 1 (T	TIR1	AT3G62980	1.18	0.23	0.84	0.4314111	0.6653023	-6.18	FALSE
245541_at	hypothetical protein	---	AT4G15240	-1.15	-0.20	-0.84	0.4313989	0.6653023	-6.18	FALSE
262222_at	unknown protein	TRZ1	AT1G74700	-1.10	-0.14	-0.84	0.4314507	0.6653185	-6.18	FALSE
250437_at	AtAGP4 ; supported by cDNA: g	AGP4	AT5G10430	1.47	0.55	0.84	0.4315314	0.6653529	-6.18	FALSE
264795_at	unknown protein similar to ESTs	ZIGA4	AT1G08680	-1.21	-0.27	-0.84	0.4315133	0.6653529	-6.18	FALSE
264080_at	putative vacuolar proton-ATPase	VHA-A1	AT2G28520	-1.08	-0.11	-0.84	0.4317238	0.6656046	-6.18	FALSE
250629_at	respiratory burst oxidase protein	ATRBOHA	AT5G07390	1.10	0.14	0.84	0.4317943	0.6656683	-6.18	FALSE
252241_at	putative protein CND41, chlorop	---	AT3G50050	-1.10	-0.14	-0.84	0.4319028	0.6657905	-6.18	FALSE
254174_at	putative protein various predicted	YSL1	AT4G24120	-1.16	-0.22	-0.84	0.4319415	0.6657991	-6.18	TRUE
262414_at	acyl CoA synthetase, putative si	LACS2	AT1G49430	1.45	0.53	0.84	0.4319667	0.6657991	-6.18	TRUE
251679_at	putative protein strictosidine synt	---	AT3G57030	-1.20	-0.26	-0.84	0.4320315	0.6658539	-6.18	FALSE
255156_at	putative athila transposon protein	---	---	1.07	0.10	0.84	0.4320993	0.6659134	-6.18	FALSE
261212_at	hypothetical protein predicted by	atnudt12	AT1G12880	-1.16	-0.21	-0.84	0.4321779	0.6659896	-6.18	FALSE
267329_at	hypothetical protein	---	AT2G19250	-1.10	-0.13	-0.84	0.4322176	0.6660057	-6.18	FALSE

263815_at	hypothetical protein predicted by	---	AT2G10020	1.16	0.21	0.84	0.4322522	0.6660141	-6.18	FALSE
252667_at	protein kinase-like protein MSTK	NEK6	AT3G44200	1.13	0.18	0.83	0.4326082	0.6664647	-6.18	FALSE
254845_at	hydroxymethylglutaryl-CoA synth	MVA1	AT4G11820	1.13	0.18	0.83	0.4326323	0.6664647	-6.18	FALSE
252086_at	hypothetical protein	---	AT3G52030	-1.10	-0.14	-0.83	0.4326101	0.6664647	-6.18	FALSE
245854_at	adenosine nucleotide translocato	AAC2	AT5G13490	1.61	0.69	0.83	0.4328049	0.6666855	-6.18	FALSE
246971_at	Protein phosphatase 2C-like pro	---	AT5G24940	1.09	0.12	0.83	0.4329735	0.6669003	-6.18	FALSE
247092_at	putative protein contains similarit	ATFOLT1	AT5G66380	1.12	0.16	0.83	0.4331647	0.6671496	-6.18	FALSE
258344_at	hypothetical protein similar to hyp	CEG	AT3G22650	1.10	0.13	0.83	0.4333384	0.6673722	-6.19	FALSE
254279_at	Expressed protein ; supported by	---	AT4G22750	-1.10	-0.14	-0.83	0.4333772	0.6673869	-6.19	FALSE
262009_at	hypothetical protein predicted by	---	AT1G35610	1.12	0.16	0.83	0.4334608	0.6674705	-6.19	FALSE
251512_at	putative protein several hypothet	---	AT3G59190	-1.09	-0.13	-0.83	0.4335141	0.6675075	-6.19	FALSE
259561_at	hypothetical protein ; supported b	WAK1	AT1G21250	1.68	0.75	0.83	0.4335817	0.6675665	-6.19	FALSE
265546_at	putative proline/hydroxyproline-ri	---	AT2G28240	-1.10	-0.14	-0.83	0.4336841	0.6676792	-6.19	FALSE
AFFX-r2-Ec	E. coli /GEN=bioD /DB_XREF=g	---	---	1.25	0.32	0.83	0.4337614	0.6677531	-6.19	FALSE
256353_at	unknown protein ; supported by f	---	AT1G55000	-1.10	-0.14	-0.83	0.4338264	0.6678081	-6.19	FALSE
252682_at	putative protein AtOXA1, Arabid	---	AT3G44370	1.12	0.16	0.83	0.4338767	0.6678404	-6.19	FALSE
255115_at	putative protein probable regulat	APUM11	AT4G08840	1.09	0.12	0.83	0.4339892	0.6679685	-6.19	FALSE
260242_at	putative transcription factor simil	EGL3	AT1G63650	1.10	0.13	0.83	0.4340229	0.6679753	-6.19	FALSE
261154_at	unknown protein ;supported by fu	---	AT1G04970	1.13	0.18	0.83	0.4341033	0.668054	-6.19	FALSE
258639_at	polygalacturonase (PGA3) ident	---	AT3G07820	-1.07	-0.10	-0.83	0.4341454	0.6680737	-6.19	FALSE
252969_at	putative protein vsf-1 protein, Ly	---	AT4G38900	-1.09	-0.13	-0.83	0.4343218	0.6682551	-6.19	FALSE
245628_at	anthocyanin2, putative similar to	PAP1	AT1G56650	1.16	0.21	0.83	0.4343137	0.6682551	-6.19	FALSE
262877_at	unknown protein ;supported by fu	---	AT1G64850	-1.13	-0.17	-0.83	0.4343757	0.6682929	-6.19	FALSE
255737_at	unknown protein ;supported by fu	---	AT1G25420	-1.11	-0.14	-0.83	0.4346387	0.6685094	-6.19	FALSE
247650_at	putative protein ;supported by fu	---	AT5G59960	-1.17	-0.23	-0.83	0.434663	0.6685094	-6.19	FALSE
260204_at	hypothetical protein predicted by	---	AT1G52900	1.10	0.13	0.83	0.434641	0.6685094	-6.19	FALSE
255076_at	putative protein RING-H2 zinc fi	---	AT4G09130	-1.09	-0.12	-0.83	0.4345741	0.6685094	-6.19	FALSE
253661_at	putative protein bZIP protein - A	---	AT4G30130	1.10	0.14	0.83	0.4346149	0.6685094	-6.19	FALSE
244910_s_a	hypothetical protein	---	---	1.10	0.14	0.83	0.4347424	0.6685865	-6.19	FALSE
260944_at	beta-galactosidase, putative sim	BGAL5	AT1G45130	1.77	0.82	0.83	0.4348595	0.6686292	-6.19	FALSE
249326_at	unknown protein ; supported by	SYN2	AT5G40840	-1.10	-0.14	-0.83	0.4349461	0.6686292	-6.19	FALSE
250334_at	NADH dehydrogenase (ubiquino	---	AT5G11770	1.10	0.13	0.83	0.4348899	0.6686292	-6.19	FALSE
263008_at	unknown protein	RPP27	AT1G54470	1.08	0.12	0.83	0.4349148	0.6686292	-6.19	FALSE
248808_at	putative protein contains similarit	---	AT5G47510	1.08	0.11	0.83	0.4349214	0.6686292	-6.19	FALSE
253194_s_a	hypothetical protein	---	---	1.10	0.14	0.83	0.4348456	0.6686292	-6.19	FALSE

267417_at	putative RING zinc finger protein	---	AT2G34990	1.08	0.12	0.83	0.4351917	0.6689166	-6.19	FALSE
251564_at	myosin heavy chain MYA3	XIJ	AT3G58160	-1.10	-0.14	-0.83	0.4351874	0.6689166	-6.19	FALSE
246092_at	glutaredoxin ;supported by full-le	---	AT5G20500	-1.11	-0.15	-0.83	0.4352521	0.6689643	-6.19	FALSE
248870_at	putative protein similar to unknov	---	AT5G46710	-1.37	-0.45	-0.83	0.4353524	0.6690735	-6.19	FALSE
245105_at	hypothetical protein predicted by	---	AT2G41610	1.17	0.23	0.83	0.435484	0.6691405	-6.19	FALSE
244957_at	hypothetical protein	AT2G07835	---	1.10	0.14	0.83	0.4354624	0.6691405	-6.19	FALSE
266619_at	similar to harpin-induced protein	---	AT2G35460	-1.13	-0.17	-0.83	0.4354812	0.6691405	-6.19	FALSE
263461_at	putative protein kinase contains a	---	AT2G31800	-1.12	-0.16	-0.83	0.4355507	0.6691978	-6.19	FALSE
259104_at	unknown protein ;supported by f	LNG2	AT3G02170	1.18	0.24	0.83	0.4356297	0.6692668	-6.19	TRUE
254097_at	putative Ser/Thr protein kinase s	---	AT4G25160	-1.08	-0.11	-0.83	0.4356542	0.6692668	-6.19	FALSE
257469_at	hypothetical protein predicted by	---	AT1G49290	-1.07	-0.10	-0.83	0.4357181	0.6693198	-6.19	FALSE
255818_at	hypothetical protein predicted by	---	AT2G33570	-1.31	-0.39	-0.83	0.4358436	0.6693773	-6.19	TRUE
245454_at	disease resistance RPP5 like pro	---	AT4G16920	-1.08	-0.11	-0.83	0.4358027	0.6693773	-6.19	FALSE
262427_s_a	thioglucosidase, putative similar	BGLU34	AT1G47600 //	-1.09	-0.12	-0.83	0.4358339	0.6693773	-6.19	FALSE
249212_at	putative protein strong similarity t	---	AT5G42690	1.10	0.14	0.83	0.4358997	0.6694185	-6.19	FALSE
261244_at	subtilisin-like serine protease sim	---	AT1G20150	1.07	0.10	0.83	0.4359309	0.6694213	-6.19	FALSE
252512_at	receptor protein kinase -like rece	---	AT3G46290	1.10	0.13	0.83	0.4360643	0.6694825	-6.19	FALSE
254106_at	geranylgeranylated protein ATGP	ATGP4	AT4G24990	-1.12	-0.16	-0.83	0.4360813	0.6694825	-6.19	FALSE
263865_at	putative ABC transporter related	ABCB1	AT2G36910	-1.15	-0.20	-0.83	0.4360641	0.6694825	-6.19	FALSE
266364_at	unknown protein	---	AT2G41230	1.50	0.58	0.83	0.4360882	0.6694825	-6.19	FALSE
261661_at	lysophospholipase homolog, put	---	AT1G18360	-1.16	-0.22	-0.83	0.4362941	0.6697536	-6.19	FALSE
263106_at	hypothetical protein predicted by	---	AT2G05160	1.12	0.17	0.83	0.4365695	0.6699246	-6.19	FALSE
247636_at	putative protein predicted protein	---	AT5G60570	1.10	0.13	0.83	0.4365106	0.6699246	-6.19	FALSE
262040_at	receptor protein kinase, putative	TMM	AT1G80080	1.10	0.14	0.83	0.4365603	0.6699246	-6.19	FALSE
262755_at	unknown protein	---	AT1G16360	-1.10	-0.13	-0.83	0.4365193	0.6699246	-6.19	FALSE
267071_at	unknown protein	---	AT2G40980	1.09	0.12	0.83	0.4364472	0.6699246	-6.19	FALSE
263211_at	germin-like oxalate oxidase simil	GLP7	AT1G10460	-1.13	-0.17	-0.83	0.4365817	0.6699246	-6.19	FALSE
263052_at	unknown protein	---	AT2G13430	-1.09	-0.12	-0.83	0.4366151	0.6699308	-6.19	FALSE
256625_at	uteroglobin promoter-binding pro	---	AT3G20010	-1.17	-0.23	-0.83	0.436704	0.6699991	-6.19	FALSE
265687_s_a	hypothetical protein predicted by	---	AT2G24470 //	1.09	0.12	0.83	0.4367184	0.6699991	-6.19	FALSE
258139_at	heat shock transcription factor H	HSFC1	AT3G24520	-1.13	-0.17	-0.83	0.4368051	0.6700871	-6.19	FALSE
259823_at	beta-1,3-glucanase precursor, p	---	AT1G66250	-1.12	-0.16	-0.83	0.436947	0.6702597	-6.19	FALSE
254957_at	putative protein ; supported by fu	---	AT4G10970	-1.11	-0.15	-0.83	0.4369915	0.6702829	-6.19	FALSE
262271_x_a	hypothetical protein predicted by	---	---	1.17	0.22	0.83	0.4370369	0.6703074	-6.19	FALSE
256108_at	hypothetical protein predicted by	---	AT1G16940	1.14	0.19	0.83	0.4372076	0.6705241	-6.19	FALSE

264992_at	integral membrane protein, puta	---	AT1G67300	-1.12	-0.17	-0.83	0.4372418	0.6705314	-6.19	FALSE
259007_at	putative MYB family transcription	MYB3R-3	AT3G09370	1.13	0.17	0.83	0.4373293	0.6705921	-6.19	FALSE
248740_at	putative protein contains similarit	---	AT5G48130	1.13	0.18	0.83	0.4373401	0.6705921	-6.19	FALSE
249243_s_a	beta-glucosidase	BGLU13	AT5G42260 ///	-1.08	-0.12	-0.83	0.4375658	0.670893	-6.19	FALSE
254282_at	hypothetical protein	---	AT4G22860	-1.09	-0.12	-0.83	0.4376302	0.6709467	-6.19	FALSE
256077_at	hypothetical protein contains sim	---	AT1G18090	-1.12	-0.17	-0.82	0.4376915	0.6709956	-6.19	FALSE
252999_at	putative protein other Arabidopsi	---	AT4G38500	-1.10	-0.14	-0.82	0.4378227	0.6711065	-6.19	FALSE
257454_at	hypothetical protein predicted by	---	AT1G65170	1.13	0.17	0.82	0.4377938	0.6711065	-6.19	FALSE
245614_at	retrovirus-related like polyprotein	---	---	1.11	0.15	0.82	0.4379422	0.6712446	-6.19	FALSE
266858_at	unknown protein	GRV2	AT2G26890	-1.09	-0.13	-0.82	0.4380965	0.671436	-6.19	FALSE
254549_at	putative protein various predicted	---	AT4G19880	1.14	0.19	0.82	0.4384016	0.6718583	-6.19	FALSE
247783_at	light harvesting pigment - like pr	---	AT5G58800	1.20	0.26	0.82	0.4384369	0.6718674	-6.19	FALSE
247369_at	unknown protein	---	AT5G63340	-1.11	-0.15	-0.82	0.4384695	0.6718722	-6.19	FALSE
246622_at	protein phosphatase-2C PP2C-li	---	AT5G36250	-1.08	-0.11	-0.82	0.4386178	0.6718737	-6.19	FALSE
248702_at	unknown protein	---	AT5G48420	-1.09	-0.12	-0.82	0.4385014	0.6718737	-6.19	FALSE
254302_at	hypothetical protein	---	AT4G22800	-1.07	-0.10	-0.82	0.4385821	0.6718737	-6.19	FALSE
248851_s_a	disease resistance protein-like ;	---	AT5G46260 ///	-1.10	-0.14	-0.82	0.4386066	0.6718737	-6.19	FALSE
258702_at	hypothetical protein predicted by	---	AT3G09730	-1.14	-0.19	-0.82	0.438617	0.6718737	-6.19	FALSE
263265_at	hypothetical protein predicted by	---	AT2G38820	1.16	0.22	0.82	0.4387634	0.6720517	-6.19	FALSE
248063_at	RNA-binding protein-like ; suppo	---	AT5G55550	1.09	0.13	0.82	0.4387936	0.6720528	-6.19	FALSE
264559_at	unknown protein similar to hypot	---	AT1G09610	-1.07	-0.10	-0.82	0.4389158	0.6721496	-6.19	FALSE
262470_at	disease resistance protein, puta	---	AT1G50180	1.10	0.14	0.82	0.4389158	0.6721496	-6.19	FALSE
248166_at	putative protein contains similarit	---	AT5G54520	-1.08	-0.12	-0.82	0.4389722	0.672191	-6.19	FALSE
257170_at	beta-1,3-glucanase, putative sim	---	AT3G23770	-1.14	-0.19	-0.82	0.4390442	0.672256	-6.19	FALSE
254500_at	vacuolar sorting receptor-like pr	---	AT4G20110	1.23	0.30	0.82	0.4391758	0.6723673	-6.19	TRUE
251562_at	putative protein hypothetical pro	---	AT3G57890	1.09	0.13	0.82	0.4391698	0.6723673	-6.19	FALSE
245979_at	putative protein leucine zipper-c	ATEXO70C	AT5G13150	1.08	0.11	0.82	0.4392093	0.6723734	-6.19	FALSE
260009_at	unknown protein ;supported by f	---	AT1G67950	-1.15	-0.20	-0.82	0.4395743	0.6724998	-6.20	TRUE
266854_at	putative C2H2-type zinc finger pr	---	AT2G26940	1.13	0.17	0.82	0.4393792	0.6724998	-6.19	FALSE
245812_at	hypothetical protein predicted by	---	---	1.09	0.12	0.82	0.4394127	0.6724998	-6.19	FALSE
250754_at	arginine-tRNA-protein transferas	ATE1	AT5G05700	1.09	0.12	0.82	0.4395027	0.6724998	-6.20	FALSE
254436_at	putative protein receptor kinase-	---	AT4G20940	1.08	0.12	0.82	0.4395045	0.6724998	-6.20	FALSE
252771_at	receptor protein kinase -like prot	---	AT3G42880	1.10	0.14	0.82	0.4395715	0.6724998	-6.20	FALSE
266692_at	Ac-like transposase related to Ac	---	AT2G19960	-1.09	-0.13	-0.82	0.4395316	0.6724998	-6.20	FALSE
251290_at	transcription factor BBFa	DAG1	AT3G61850	1.11	0.15	0.82	0.4394334	0.6724998	-6.19	FALSE

249450_at	serine/threonine-specific protein	SnRK1.3	AT5G39440	-1.09	-0.13	-0.82	0.4394662	0.6724998	-6.20	FALSE
251099_at	putative protein KIAA0132 - Hor	---	AT5G01660	-1.09	-0.13	-0.82	0.4395867	0.6724998	-6.20	FALSE
261361_at	hypothetical protein predicted by	---	---	-1.11	-0.15	-0.82	0.4397589	0.6727182	-6.20	FALSE
258563_at	putative long-chain-fatty-acid--Co	LACS6	AT3G05970	1.10	0.14	0.82	0.4399669	0.6729913	-6.20	FALSE
265041_at	unknown protein Contains simila	TOM22-I	AT1G04070	-1.16	-0.21	-0.82	0.4400676	0.6730584	-6.20	FALSE
255516_at	hypothetical protein similar to ex	---	AT4G02270	1.15	0.20	0.82	0.4400698	0.6730584	-6.20	FALSE
260229_at	putative RING zinc finger protein	---	AT1G74370	-1.13	-0.17	-0.82	0.4401151	0.6730826	-6.20	FALSE
267602_at	unknown protein ; supported by	---	AT2G32970	1.14	0.18	0.82	0.4401731	0.6731261	-6.20	TRUE
247769_at	laccase precursor - like protein l	LAC16	AT5G58910	1.09	0.12	0.82	0.4403317	0.6732529	-6.20	FALSE
252209_at	putative protein RXF26, Arabido	---	AT3G50400	-1.19	-0.25	-0.82	0.4402869	0.6732529	-6.20	FALSE
254060_at	putative protein polytropic murin	SHB1	AT4G25350	1.19	0.25	0.82	0.4403446	0.6732529	-6.20	FALSE
259545_at	hypothetical protein ; supported b	AAE1	AT1G20560	1.10	0.14	0.82	0.4404974	0.6733274	-6.20	FALSE
255483_at	putative glycosyltransferase sim	XT2	AT4G02500	-1.14	-0.20	-0.82	0.4405114	0.6733274	-6.20	FALSE
264256_at	putative importin alpha similar to	IMPA-4	AT1G09270	1.08	0.12	0.82	0.4404707	0.6733274	-6.20	FALSE
249431_at	polygalacturonase-like protein p	---	AT5G39910	1.16	0.21	0.82	0.4404612	0.6733274	-6.20	FALSE
257434_at	hypothetical protein predicted by	---	AT2G21740	1.08	0.11	0.82	0.4406953	0.6735633	-6.20	FALSE
245692_at	myc - like protein	BHLH101	AT5G04150	1.14	0.19	0.82	0.441063	0.6737642	-6.20	TRUE
266183_at	unknown protein	ATPT2	AT2G38940	1.12	0.17	0.82	0.4410458	0.6737642	-6.20	FALSE
265357_at	E2, ubiquitin-conjugating enzym	UBC29	AT2G16740	1.14	0.19	0.82	0.4410285	0.6737642	-6.20	FALSE
247896_at	26S proteasome regulatory subu	---	AT5G57950	-1.08	-0.11	-0.82	0.4410231	0.6737642	-6.20	FALSE
264684_at	unknown protein	HEXO3	AT1G65590	1.20	0.27	0.82	0.4408662	0.6737642	-6.20	FALSE
249673_at	cytochrome P450-like	CYP79A4P	AT5G35920	1.07	0.10	0.82	0.4409208	0.6737642	-6.20	FALSE
256606_at	hypothetical protein	---	AT3G32960	1.09	0.12	0.82	0.4410392	0.6737642	-6.20	FALSE
262053_at	putative DnaJ protein contains F	ATERDJ2A	AT1G79940	1.11	0.15	0.82	0.4409454	0.6737642	-6.20	FALSE
249302_at	putative protein similar to unknov	---	AT5G41450	1.12	0.16	0.82	0.4411683	0.6738798	-6.20	FALSE
252643_at	acidic ribosomal protein P2 -like	---	AT3G44590	-1.25	-0.32	-0.82	0.4413379	0.6740939	-6.20	FALSE
259260_at	unknown protein similar to unkno	---	AT3G11370	1.11	0.14	0.82	0.441474	0.6742566	-6.20	FALSE
245821_at	hypothetical protein similar to put	---	AT1G26270	1.12	0.17	0.82	0.4417166	0.6745368	-6.20	FALSE
265239_s_a	hypothetical protein	---	AT2G07692	1.11	0.15	0.82	0.4417094	0.6745368	-6.20	FALSE
259015_at	unknown protein similar to hypot	---	AT3G07350	1.27	0.34	0.82	0.4418329	0.6746181	-6.20	FALSE
246593_at	putative protein predicted protein	---	AT5G14790	1.14	0.19	0.82	0.4419717	0.6746181	-6.20	TRUE
257504_at	dynein light chain, putative simil	ROPGEF11	AT1G52240	1.20	0.27	0.82	0.4419232	0.6746181	-6.20	FALSE
260730_at	lipoamide dehydrogenase precur	mtLPD1	AT1G48030	-1.13	-0.18	-0.82	0.4419675	0.6746181	-6.20	FALSE
250010_at	AP2-domain DNA-binding protei	---	AT5G18450	1.13	0.18	0.82	0.4419005	0.6746181	-6.20	FALSE
266429_at	hypothetical protein predicted by	---	AT2G07190	1.10	0.14	0.82	0.4418022	0.6746181	-6.20	FALSE

262660_at	putative protein kinase	VIK	AT1G14000	1.10	0.13	0.82	0.4419769	0.6746181	-6.20	FALSE
256101_at	hypothetical protein predicted by	---	AT1G13760	1.09	0.13	0.82	0.4420077	0.67462	-6.20	FALSE
260817_at	unknown protein	---	AT1G06900	-1.10	-0.14	-0.82	0.4420462	0.6746336	-6.20	FALSE
254867_at	hypothetical proteins	---	AT4G12240	-1.14	-0.19	-0.82	0.4420908	0.6746565	-6.20	FALSE
264524_at	tat-binding protein, putative High	ATBCAT-2	AT1G10070	1.48	0.56	0.82	0.442277	0.674746	-6.20	TRUE
254927_at	putative protein hypothetical pro	---	AT4G11400	1.11	0.16	0.82	0.4422925	0.674746	-6.20	FALSE
258227_at	6-4 photolyase (UVR3) identical	UVR3	AT3G15620	-1.41	-0.50	-0.82	0.4422973	0.674746	-6.20	FALSE
261194_at	unknown protein contains Pfam	---	AT1G12770 ///	-1.07	-0.10	-0.82	0.4422922	0.674746	-6.20	FALSE
255222_at	putative protein Mitochondrial AT	---	AT4G05340	1.07	0.10	0.82	0.442211	0.674746	-6.20	FALSE
264281_at	hypothetical protein similar to put	---	AT1G61830	1.11	0.16	0.82	0.4423975	0.6748204	-6.20	FALSE
254836_at	flavonoid 3,5-hydroxylase like pr	CYP706A7	AT4G12330	1.08	0.11	0.82	0.4424053	0.6748204	-6.20	FALSE
261814_at	unknown protein	---	AT1G08310	1.55	0.63	0.82	0.4424416	0.6748306	-6.20	TRUE
264507_at	Expressed protein ; supported by	NIMIN-3	AT1G09415	-1.13	-0.18	-0.82	0.4425359	0.6748843	-6.20	FALSE
252807_at	putative replication protein vario	---	---	-1.07	-0.10	-0.82	0.4425358	0.6748843	-6.20	FALSE
258434_at	AP2 domain containing protein R	ATEBP	AT3G16770	-1.15	-0.20	-0.82	0.4427401	0.6751054	-6.20	TRUE
263263_at	putative guanylate binding protei	---	AT2G38840	1.12	0.17	0.82	0.4427237	0.6751054	-6.20	FALSE
245313_at	UFD1 like protein ; supported by	---	AT4G15420	1.11	0.16	0.82	0.4428232	0.675187	-6.20	FALSE
254047_at	hypothetical protein	---	AT4G26040	1.12	0.17	0.82	0.4429407	0.6753209	-6.20	FALSE
261011_at	cytochrome b5 similar to cytochr	CB5-A	AT1G26340	-1.11	-0.15	-0.81	0.4430124	0.6753401	-6.20	FALSE
260563_at	putative glucosyltransferase	UGT74F1	AT2G43840	1.11	0.16	0.81	0.4430092	0.6753401	-6.20	FALSE
253571_at	putative calmodulin-binding prot	---	AT4G31000	1.34	0.43	0.81	0.4431836	0.6754614	-6.20	TRUE
248553_at	putative protein strong similarity t	---	AT5G50170	1.21	0.27	0.81	0.4431558	0.6754614	-6.20	FALSE
245441_at	decarboxylase like protein	PSD1	AT4G16700	-1.13	-0.17	-0.81	0.4431813	0.6754614	-6.20	FALSE
251164_s_a	putative protein protein phospha	---	AT3G63320 ///	-1.11	-0.15	-0.81	0.4432382	0.6754614	-6.20	FALSE
257899_at	P-glycoprotein, putative similar t	---	AT3G28345	-1.08	-0.12	-0.81	0.4432401	0.6754614	-6.20	FALSE
267373_at	unknown protein	CID7	AT2G26280	1.10	0.14	0.81	0.4432995	0.6755068	-6.20	FALSE
254010_at	putative protein ;supported by fu	---	AT1G72125 ///	1.09	0.12	0.81	0.4434499	0.6756909	-6.20	FALSE
263522_at	hypothetical protein	---	AT2G24950	1.08	0.11	0.81	0.4434866	0.6757016	-6.20	FALSE
262746_at	Expressed protein ; supported by	ATNUDX15	AT1G28960	-1.08	-0.11	-0.81	0.4436068	0.6757493	-6.20	FALSE
257889_at	S1 self-incompatibility protein, p	---	AT3G17080	1.12	0.16	0.81	0.4435689	0.6757493	-6.20	FALSE
252153_at	putative protein several hypothet	---	AT3G51360	1.13	0.17	0.81	0.4435949	0.6757493	-6.20	FALSE
251623_at	MADS transcription factor-like pr	AGL18	AT3G57390	-1.08	-0.11	-0.81	0.4436589	0.6757646	-6.20	FALSE
257424_at	hypothetical protein predicted by	---	AT1G78840	1.14	0.18	0.81	0.4436761	0.6757646	-6.20	FALSE
260510_at	hypothetical protein predicted by	---	AT1G51580	-1.17	-0.23	-0.81	0.4437239	0.6757924	-6.20	FALSE
259740_at	phytochrome, putative similar to	---	AT1G64300	-1.14	-0.20	-0.81	0.4438825	0.6759817	-6.20	FALSE

261593_at	unknown protein	---	AT1G33170	-1.70	-0.77	-0.81	0.4439075	0.6759817	-6.20	FALSE
253263_at	abscisic acid responsive element	ABF3	AT4G34000	-1.23	-0.30	-0.81	0.4442102	0.6762621	-6.20	TRUE
253747_at	serine threonine-specific kinase	---	AT4G29050	1.19	0.26	0.81	0.444137	0.6762621	-6.20	TRUE
266904_at	putative pyruvate dehydrogenase	---	AT2G34590	1.20	0.26	0.81	0.444198	0.6762621	-6.20	FALSE
263855_at	putative non-LTR retrolelement r	---	AT2G04420	1.10	0.13	0.81	0.4442012	0.6762621	-6.20	FALSE
264223_s_a	receptor kinase, putative similar	---	AT1G67520 /	1.26	0.34	0.81	0.4443693	0.6764268	-6.20	TRUE
250928_at	putative protein	EIN2	AT5G03280	-1.09	-0.12	-0.81	0.4444132	0.6764268	-6.20	FALSE
265888_at	putative cleavage and polyadeny	RIE1	AT2G01735	1.08	0.11	0.81	0.4445557	0.6764268	-6.20	FALSE
262503_at	hypothetical protein predicted by	---	AT1G21670	1.21	0.27	0.81	0.4444645	0.6764268	-6.20	FALSE
247084_at	NAM (no apical meristem)-like pr	NAC105	AT5G66300	-1.09	-0.12	-0.81	0.4443887	0.6764268	-6.20	FALSE
260066_at	putative lipase/acylhydrolase cor	---	AT1G73610	1.24	0.31	0.81	0.4445317	0.6764268	-6.20	FALSE
265629_at	unknown protein ; supported by	LHW	AT2G27228 /	1.16	0.21	0.81	0.4445051	0.6764268	-6.20	FALSE
248671_at	putative protein strong similarity t	---	AT5G48750	1.08	0.11	0.81	0.4445092	0.6764268	-6.20	FALSE
265545_at	putative protein kinase contains a	NCRK	AT2G28250	1.11	0.15	0.81	0.4448357	0.6767174	-6.20	FALSE
247715_at	putative protein predicted protei	---	AT5G59360	1.15	0.21	0.81	0.4448213	0.6767174	-6.20	FALSE
249578_at	putative protein predicted protei	---	AT5G37730	-1.07	-0.10	-0.81	0.4448003	0.6767174	-6.20	FALSE
258291_at	putative protein kinase similar to	---	AT3G23310	-1.11	-0.15	-0.81	0.4449139	0.6767913	-6.20	FALSE
266683_at	hypothetical protein predicted by	GC1	AT2G19950	1.09	0.13	0.81	0.4449557	0.6768098	-6.20	FALSE
261026_at	hypothetical protein predicted by	---	AT1G01240	-1.12	-0.16	-0.81	0.4451352	0.6770377	-6.20	FALSE
258030_at	hypothetical protein predicted by	---	AT3G27590	1.11	0.15	0.81	0.4451778	0.6770574	-6.20	FALSE
261276_at	v-SNARE protein AtVTI1b, putat	VTI1B	AT1G26670	-1.14	-0.19	-0.81	0.4452083	0.6770586	-6.20	FALSE
246899_at	putative protein various predicte	---	AT5G25590	1.09	0.13	0.81	0.4452499	0.6770766	-6.20	FALSE
258383_at	hypothetical protein predicted by	---	AT3G15440	-1.23	-0.29	-0.81	0.4452903	0.677093	-6.20	FALSE
254994_at	putative methyltransferase	MTA	AT4G10760	-1.18	-0.24	-0.81	0.445342	0.6771264	-6.20	FALSE
251223_at	putative transcription factor MYB	ATMYB11	AT3G62610	1.08	0.11	0.81	0.44541	0.6771847	-6.20	FALSE
257633_at	hypothetical protein	CYP86C2	AT3G26125	-1.09	-0.12	-0.81	0.4455017	0.677279	-6.20	FALSE
261083_at	unknown protein ; supported by c	---	AT1G07310	1.11	0.15	0.81	0.4455392	0.6772909	-6.20	FALSE
247423_at	putative protein predicted protei	---	AT5G62830	1.08	0.11	0.81	0.4457682	0.6775708	-6.20	FALSE
265395_at	putative LRR receptor protein kir	SRF1	AT2G20850	-1.14	-0.18	-0.81	0.4457828	0.6775708	-6.20	FALSE
266723_at	SKP1/ASK1 (At16), putative sim	ASK16	AT2G03190	1.08	0.11	0.81	0.44582	0.6775822	-6.20	FALSE
262123_at	hypothetical protein predicted by	---	AT1G59630	1.11	0.15	0.81	0.4460742	0.6779048	-6.21	FALSE
266644_at	unknown protein ;supported by f	---	AT2G29660	-1.12	-0.17	-0.81	0.446099	0.6779048	-6.21	FALSE
245513_at	SYBL1 like protein	ATVAMP72	AT4G15780	-1.19	-0.25	-0.81	0.4461214	0.6779048	-6.21	FALSE
253461_at	cytochrome p450 - like protein c	CYP96A2	AT4G32170	1.08	0.12	0.81	0.4462016	0.6779816	-6.21	FALSE
261619_x_a	hypothetical protein	---	---	-1.09	-0.12	-0.81	0.446309	0.6780995	-6.21	FALSE

245520_at	delta-cadinene synthase like prot	ATTS1	AT4G15870	1.10	0.13	0.81	0.4464259	0.678232	-6.21	FALSE
256305_at	glutathione S-conjugate transpor	MRP1	AT1G30400	1.15	0.20	0.81	0.4465364	0.6782867	-6.21	TRUE
260479_at	hypothetical protein predicted by	---	AT1G11020	-1.08	-0.11	-0.81	0.4465512	0.6782867	-6.21	FALSE
267402_at	putative SF16 protein {Helianthus	IQD6	AT2G26180	1.13	0.18	0.81	0.4465022	0.6782867	-6.21	FALSE
266221_at	putative nucleotide-sugar dehydr	UXS6	AT2G28760	1.52	0.60	0.81	0.4466049	0.6783232	-6.21	FALSE
260803_at	glutathione transferase, putative	ATGSTU22	AT1G78340	-1.09	-0.12	-0.81	0.446741	0.6784847	-6.21	FALSE
258488_at	unknown protein ;supported by f	---	AT3G02420	-1.10	-0.14	-0.81	0.4468304	0.6785364	-6.21	FALSE
245601_at	hypothetical protein	---	AT4G14240	-1.11	-0.15	-0.81	0.4468345	0.6785364	-6.21	FALSE
247231_at	transcription factor-like protein	AtMYB53	AT5G65230	1.09	0.13	0.81	0.4468839	0.6785662	-6.21	FALSE
247791_at	cyclophilin ROC7 ;supported by	ROC7	AT5G58710	-1.13	-0.18	-0.81	0.4469619	0.6785943	-6.21	FALSE
246505_at	putative protein hypothetical pro	---	AT5G16250	1.18	0.24	0.81	0.446934	0.6785943	-6.21	FALSE
261410_at	metallothionein-like protein identi	MT1C	AT1G07610	1.32	0.40	0.81	0.4471248	0.6787965	-6.21	FALSE
259620_s_a	Tam3-like transposon protein sir	---	---	1.14	0.19	0.81	0.4471673	0.6788157	-6.21	FALSE
248312_at	unknown protein	---	AT5G52580	1.11	0.14	0.81	0.4473534	0.6788556	-6.21	FALSE
252710_at	cellulase-like protein cellulase, S	AtGH9A4	AT3G43860	1.09	0.12	0.81	0.4473002	0.6788556	-6.21	FALSE
255815_at	histone H3, putative similar to hi	MGH3	AT1G19890	1.11	0.15	0.81	0.4473721	0.6788556	-6.21	FALSE
265821_at	putative homeodomain transcrip	WUS	AT2G17950	-1.14	-0.19	-0.81	0.4473212	0.6788556	-6.21	FALSE
267098_at	hypothetical protein predicted by	---	AT2G41451	1.12	0.16	0.81	0.4473662	0.6788556	-6.21	FALSE
245548_at	cytochrome P450 like protein	CYP702A3	AT4G15310	1.08	0.11	0.81	0.4472712	0.6788556	-6.21	FALSE
264667_s_a	hypothetical protein identical to h	ZW18	AT1G09980 ///	-1.09	-0.12	-0.81	0.447404	0.6788588	-6.21	FALSE
256297_at	cytochrome P450, putative conta	---	AT1G69500	-1.11	-0.16	-0.81	0.4474589	0.678897	-6.21	FALSE
263179_at	unknown protein similar to unkno	---	AT1G05710	1.19	0.25	0.81	0.4475576	0.6789292	-6.21	FALSE
248018_at	putative protein strong similarity t	---	AT5G56470	1.11	0.15	0.81	0.4475694	0.6789292	-6.21	FALSE
259066_at	hypothetical protein predicted by	---	AT3G07530	-1.13	-0.18	-0.81	0.4475677	0.6789292	-6.21	FALSE
248957_at	26S proteasome subunit-like pro	---	AT5G45620	-1.09	-0.13	-0.81	0.4477364	0.6791373	-6.21	FALSE
262261_at	CLE17, putative CLAVATA3/ES	CLE17	AT1G70895	1.11	0.16	0.81	0.4477826	0.6791622	-6.21	FALSE
258587_at	hypothetical protein predicted by	---	AT3G04310	-1.19	-0.25	-0.81	0.4479751	0.6793502	-6.21	FALSE
253300_at	carbonate dehydratase - like pro	BCA5	AT4G33580	-1.15	-0.21	-0.81	0.447942	0.6793502	-6.21	FALSE
261509_at	hypothetical protein predicted by	---	AT1G71740	1.14	0.19	0.81	0.4479959	0.6793502	-6.21	FALSE
248286_at	putative protein similar to unknov	---	AT5G52870	1.23	0.30	0.81	0.448033	0.6793614	-6.21	FALSE
252488_at	glucuronosyl transferase-like pro	---	AT3G46700	1.09	0.12	0.81	0.4481061	0.6793818	-6.21	FALSE
267022_at	hypothetical protein predicted by	---	AT2G34230	1.07	0.10	0.81	0.4480872	0.6793818	-6.21	FALSE
257304_at	hypothetical protein predicted by	---	---	1.08	0.11	0.81	0.4481816	0.6794511	-6.21	FALSE
258039_at	unknown protein ;supported by f	---	AT3G21200	-1.09	-0.13	-0.81	0.4483002	0.6795858	-6.21	FALSE
262357_at	jacalin, putative similar to jacalin	---	AT1G73040	1.33	0.41	0.80	0.4484407	0.6797031	-6.21	TRUE

260289_at	CAD ATPase (AAA1) identical to	ERH3	AT1G80350	-1.07	-0.10	-0.80	0.4484918	0.6797031	-6.21	FALSE
249003_at	putative protein contains similarit	---	AT5G44500	-1.11	-0.14	-0.80	0.448446	0.6797031	-6.21	FALSE
245566_at	disease resistance RPS2 like pro	---	AT4G14610	1.10	0.14	0.80	0.4484968	0.6797031	-6.21	FALSE
262359_at	disease resistance protein, puta	---	AT1G73060 /	1.10	0.14	0.80	0.4485328	0.6797126	-6.21	FALSE
258004_at	unknown protein similar to putati	MYB110	AT3G29020	1.10	0.13	0.80	0.4488988	0.680222	-6.21	FALSE
252160_at	proline-rich protein	---	AT3G50570	1.13	0.17	0.80	0.4489308	0.6802253	-6.21	FALSE
250618_at	putative protein hypothetical prot	ATBAG3	AT5G07220	1.09	0.12	0.80	0.4491467	0.6803071	-6.21	TRUE
265352_at	cytosolic cyclophilin (ROC3) ;su	ROC3	AT2G16600	-1.10	-0.14	-0.80	0.449193	0.6803071	-6.21	FALSE
256711_at	unknown protein contains Pfam p	---	AT3G30390	1.16	0.21	0.80	0.449113	0.6803071	-6.21	FALSE
267352_at	hypothetical protein predicted by	---	AT2G40050	1.08	0.11	0.80	0.4491905	0.6803071	-6.21	FALSE
264671_at	unknown protein ; supported by	---	AT1G09920	1.11	0.15	0.80	0.4491652	0.6803071	-6.21	FALSE
256893_x_a	unknown protein	---	---	-1.08	-0.11	-0.80	0.4491936	0.6803071	-6.21	FALSE
262101_at	hypothetical protein identical to h	---	AT1G59535	1.08	0.11	0.80	0.4491661	0.6803071	-6.21	FALSE
261807_at	Expressed protein ; supported by	---	AT1G30515	-1.09	-0.12	-0.80	0.4493035	0.6804285	-6.21	FALSE
253379_at	putative protein glycogenin gluc	PGSIP3	AT4G33330	-1.09	-0.12	-0.80	0.449365	0.6804764	-6.21	FALSE
256619_at	hypothetical protein predicted by	---	AT3G24460	1.09	0.12	0.80	0.4494212	0.6805163	-6.21	FALSE
262480_at	receptor kinase, putative similar	---	AT1G11340	-1.19	-0.25	-0.80	0.4495511	0.6806678	-6.21	FALSE
261837_s_a	transcriptional regulator, putative	---	AT1G15910 /	-1.13	-0.17	-0.80	0.4496645	0.6807502	-6.21	FALSE
252753_at	hypothetical protein	---	AT3G43500	1.10	0.14	0.80	0.449695	0.6807502	-6.21	FALSE
265443_at	beta-expansin ;supported by full	ATEXPB1	AT2G20750	-1.13	-0.18	-0.80	0.449691	0.6807502	-6.21	FALSE
264382_at	unknown protein similarity to str	SDF2	AT2G25110	1.17	0.22	0.80	0.4497795	0.6808328	-6.21	FALSE
249173_at	unknown protein	---	AT5G43000	1.12	0.16	0.80	0.4498374	0.6808752	-6.21	FALSE
263206_at	unknown protein similar to ESTs	---	AT1G10590	-1.07	-0.10	-0.80	0.4498978	0.6809216	-6.21	FALSE
263930_at	hypothetical protein predicted by	---	AT2G36300	1.10	0.13	0.80	0.4500496	0.6810785	-6.21	FALSE
264594_at	hypothetical protein ; supported b	ATSERAT3	AT2G17640	-1.10	-0.14	-0.80	0.4501806	0.6810785	-6.21	FALSE
261104_at	unknown protein	---	AT1G62910	1.11	0.14	0.80	0.4501468	0.6810785	-6.21	FALSE
254024_at	putative pathogenesis-related pr	---	AT4G25780	-1.16	-0.21	-0.80	0.4501749	0.6810785	-6.21	FALSE
256137_at	auxin-regulated protein, putative	---	AT1G48690	-1.08	-0.11	-0.80	0.4500761	0.6810785	-6.21	FALSE
255054_s_a	cellulase-like protein cellulase (E	AtGH9B15	AT4G09740 /	-1.10	-0.13	-0.80	0.4501464	0.6810785	-6.21	FALSE
252706_at	putative protein predicted protei	---	---	1.07	0.10	0.80	0.4503046	0.6812209	-6.21	FALSE
263318_at	Expressed protein ; supported by	AtGDU4	AT2G24762	-1.49	-0.58	-0.80	0.4504418	0.6812477	-6.21	FALSE
247167_at	unknown protein	---	AT5G65850	-1.12	-0.16	-0.80	0.4504171	0.6812477	-6.21	FALSE
256234_at	50S ribosomal protein L10, puta	---	AT3G12370	-1.09	-0.13	-0.80	0.4503945	0.6812477	-6.21	FALSE
255048_at	gibberellin-regulated protein GAS	GASA3	AT4G09600	-1.08	-0.11	-0.80	0.450393	0.6812477	-6.21	FALSE
257314_at	integral membrane protein, puta	---	AT3G26590	1.26	0.33	0.80	0.4505656	0.6813267	-6.21	TRUE

245796_at	unknown protein similar to unknc	RCD1	AT1G32230	1.10	0.13	0.80	0.4505836	0.6813267	-6.21	FALSE
255579_at	putative bHLH DNA-binding prote	---	AT4G01460	-1.21	-0.28	-0.80	0.4505312	0.6813267	-6.21	FALSE
253047_at	Expressed protein ; supported by	---	AT4G37295	1.18	0.24	0.80	0.4507017	0.6814601	-6.21	FALSE
264189_s_a	hypothetical protein similar to acy	ACP3	AT1G54580 ///	-1.13	-0.18	-0.80	0.4508123	0.6815821	-6.21	FALSE
250830_at	putative protein similar to unknov	---	AT5G04910	-1.13	-0.17	-0.80	0.4510071	0.6818314	-6.21	FALSE
246346_at	hypothetical protein	---	AT3G56810	-1.15	-0.20	-0.80	0.451042	0.681839	-6.21	FALSE
249411_at	raffinose synthase -like protein r	SIP1	AT5G40390	1.27	0.34	0.80	0.4511833	0.6820074	-6.21	FALSE
256955_at	L-ascorbate oxidase precursor,	sks11	AT3G13390	1.14	0.19	0.80	0.451262	0.6820812	-6.21	FALSE
259790_s_a	auxin-induced protein, putative s	---	AT1G29430 ///	-1.33	-0.41	-0.80	0.4514004	0.6822451	-6.21	TRUE
264704_at	unknown protein similar to putati	LGT8	AT1G70090	1.17	0.22	0.80	0.4515588	0.6823037	-6.21	TRUE
257252_at	glutathione reductase, cytosolic	ATGR1	AT3G24170	1.19	0.25	0.80	0.4515245	0.6823037	-6.21	FALSE
250568_at	putative protein several putative	---	AT5G08110	-1.10	-0.13	-0.80	0.4515588	0.6823037	-6.21	FALSE
250551_at	SNAP25 - like protein SNAP25A	SNAP29	AT5G07880	1.10	0.14	0.80	0.4514866	0.6823037	-6.21	FALSE
255335_at	putative transposon protein	---	---	-1.10	-0.13	-0.80	0.4516651	0.6823058	-6.21	FALSE
260532_at	putative ATP-dependent RNA he	---	AT2G47330	-1.08	-0.11	-0.80	0.4516112	0.6823058	-6.21	FALSE
260227_at	unknown protein similar to hypot	---	AT1G74450	1.27	0.34	0.80	0.451653	0.6823058	-6.21	FALSE
260032_at	putative phosphoenolpyruvate ca	ATPPC4	AT1G68750	1.10	0.13	0.80	0.4516799	0.6823058	-6.21	FALSE
252535_at	hypothetical protein	---	AT3G46150	-1.18	-0.24	-0.80	0.4517466	0.6823614	-6.21	FALSE
245578_at	RNA helicase like protein	ATSUV3	AT4G14790	-1.12	-0.16	-0.80	0.4517867	0.6823768	-6.21	FALSE
249374_at	20S proteasome beta subunit PE	PBB2	AT5G40580	-1.10	-0.14	-0.80	0.4518616	0.6824448	-6.21	FALSE
255409_at	NDX1 homeobox protein homolo	---	AT4G03090	-1.07	-0.10	-0.80	0.4519686	0.6825611	-6.21	FALSE
248779_at	acetoacyl-CoA-thiolase ;support	---	AT5G47720	-1.17	-0.23	-0.80	0.4522405	0.6826637	-6.21	FALSE
262804_at	putative RNA-binding protein sir	---	AT1G20880	1.12	0.16	0.80	0.4520717	0.6826637	-6.21	FALSE
251802_at	E2, ubiquitin-conjugating enzym	UBC14	AT3G55380	-1.08	-0.12	-0.80	0.4521755	0.6826637	-6.21	FALSE
245293_at	HSP like protein ; supported by c	---	AT4G16660	1.32	0.40	0.80	0.4522079	0.6826637	-6.21	FALSE
264902_at	unknown protein Location of EST	---	AT1G23060	1.21	0.27	0.80	0.4521122	0.6826637	-6.21	FALSE
257693_at	hypothetical protein predicted by	---	AT3G12850	1.16	0.22	0.80	0.452246	0.6826637	-6.21	FALSE
246979_s_a	putative protein hypothetical prot	---	AT5G24990 ///	1.12	0.17	0.80	0.4521335	0.6826637	-6.21	FALSE
262219_at	hypothetical protein predicted by	---	AT1G74750	1.16	0.21	0.80	0.4524446	0.6827657	-6.22	FALSE
256994_s_a	limonene cyclase, putative simila	ATTPS-CIN	AT3G25820 ///	1.09	0.12	0.80	0.4524004	0.6827657	-6.22	FALSE
250478_at	non-phototropic hypocotyl 3-like	DOT3	AT5G10250	-1.12	-0.16	-0.80	0.4524526	0.6827657	-6.22	FALSE
251426_at	URIDYLATE KINASE-like protei	---	AT3G60180	-1.10	-0.14	-0.80	0.4523819	0.6827657	-6.21	FALSE
261342_at	putative replication protein simila	---	AT1G52950	1.08	0.11	0.80	0.4524632	0.6827657	-6.22	FALSE
266321_at	putative cytochrome P450	CYP78A6	AT2G46660	-1.13	-0.17	-0.80	0.4525223	0.6828096	-6.22	FALSE
254891_at	putative protein Fly Fas-associa	SAY1	AT4G11740	-1.08	-0.11	-0.80	0.4526811	0.6829589	-6.22	FALSE

261549_at	DNA-binding protein, putative co	---	AT1G63470	1.12	0.16	0.80	0.4526725	0.6829589	-6.22	FALSE
256467_at	copia-type polyprotein, putative	---	---	1.09	0.12	0.80	0.4527132	0.6829622	-6.22	FALSE
252584_at	putative protein several hypothet	---	AT3G45560	1.09	0.12	0.80	0.4527597	0.6829872	-6.22	FALSE
252685_at	disease resistence - like protein	---	AT3G44410	1.17	0.23	0.80	0.4529506	0.6831847	-6.22	FALSE
247018_at	AP2 domain transcription factor-l	---	AT5G67000	1.07	0.10	0.80	0.4529333	0.6831847	-6.22	FALSE
259060_at	hypothetical protein predicted by	---	AT3G07400	-1.13	-0.17	-0.80	0.4530155	0.6832335	-6.22	FALSE
246324_at	arginine/serine-rich protein, puta	SR45	AT1G16610	1.09	0.12	0.80	0.4530728	0.6832335	-6.22	FALSE
245955_at	hypothetical protein	BGLU24	AT5G28510	1.09	0.12	0.80	0.4530723	0.6832335	-6.22	FALSE
254268_at	putative protein FAF1, Mus mus	---	AT4G23040	1.11	0.15	0.80	0.4531144	0.6832511	-6.22	FALSE
265923_at	putative protein kinase contains a	---	AT2G18470	-1.08	-0.11	-0.80	0.4531831	0.6833096	-6.22	FALSE
250193_at	putative protein proline-rich prot	---	AT5G14540	1.10	0.13	0.80	0.453346	0.6834051	-6.22	FALSE
257821_at	Expressed protein ; supported by	RALFL26	AT3G25170	1.08	0.11	0.80	0.4533663	0.6834051	-6.22	FALSE
267491_at	unknown protein predicted by ge	---	---	1.12	0.17	0.80	0.4533482	0.6834051	-6.22	FALSE
258971_at	unknown protein similar to uridyl	ACR6	AT3G01990	1.25	0.32	0.80	0.4533503	0.6834051	-6.22	FALSE
262324_at	hypothetical protein similar to hyp	ATCHX16	AT1G64170	-1.58	-0.66	-0.80	0.4534025	0.6834145	-6.22	TRUE
251162_at	putative protein hypothetical prot	---	AT3G63300	-1.09	-0.12	-0.80	0.4534678	0.6834678	-6.22	FALSE
264944_at	hypothetical protein similar to hyp	---	AT1G76940	1.13	0.18	0.80	0.4536099	0.6836117	-6.22	FALSE
246163_at	putative protein predicted protei	---	---	-1.11	-0.16	-0.80	0.4536233	0.6836117	-6.22	FALSE
261935_at	phosphoribosylanthranilate trans	---	AT1G22610	1.08	0.11	0.80	0.4537033	0.6836871	-6.22	FALSE
262665_at	xyloglucan fucosyltransferase, p	FUT7	AT1G14070	-1.27	-0.35	-0.79	0.4539348	0.6838292	-6.22	TRUE
257087_at	purple acid phosphatase, putativ	PAP18	AT3G20500	1.11	0.15	0.79	0.4539293	0.6838292	-6.22	FALSE
263056_at	Mutator-like transposase similar	---	---	1.07	0.10	0.79	0.4539475	0.6838292	-6.22	FALSE
245589_at	subtilisin-like serine protease cor	---	AT4G15040	1.14	0.19	0.79	0.4538751	0.6838292	-6.22	FALSE
251808_at	AP3-complex beta-3A adaptin s	---	AT3G55480	-1.10	-0.14	-0.79	0.4539215	0.6838292	-6.22	FALSE
254057_at	putative protein ;supported by fu	---	AT4G25170	1.18	0.24	0.79	0.4540589	0.6838728	-6.22	FALSE
250024_at	NAM (no apical meristem)-like pr	ANAC087	AT5G18270	1.16	0.21	0.79	0.4540663	0.6838728	-6.22	FALSE
262843_at	Expressed protein ; supported by	AtHB32	AT1G14687	-1.15	-0.20	-0.79	0.4540083	0.6838728	-6.22	FALSE
264972_at	meiotic asynaptic mutant asy1, p	ASY1	AT1G67370	-1.15	-0.20	-0.79	0.4541136	0.6838989	-6.22	FALSE
267572_at	3-hydroxyisobutyryl-coenzyme A	---	AT2G30660	1.09	0.13	0.79	0.4543185	0.6841287	-6.22	FALSE
249509_at	strong similarity to unknown prot	---	AT5G38390	1.07	0.10	0.79	0.454372	0.6841287	-6.22	FALSE
261657_at	pathogenesis-related protein 1b	---	AT1G50050	-1.10	-0.13	-0.79	0.4543313	0.6841287	-6.22	FALSE
247883_at	unknown protein	---	AT5G57790	1.13	0.18	0.79	0.4543862	0.6841287	-6.22	FALSE
252408_at	putative transcription factor MYB	ATMYB94	AT3G47600	1.08	0.11	0.79	0.4544281	0.6841308	-6.22	FALSE
261477_at	unknown protein	---	AT1G14310	-1.12	-0.17	-0.79	0.4544476	0.6841308	-6.22	FALSE
262606_at	hypothetical protein predicted by	---	AT1G15190	1.12	0.16	0.79	0.4545271	0.6842053	-6.22	FALSE

259977_at	unknown protein ;supported by f	---	AT1G76590	-1.26	-0.33	-0.79	0.4547372	0.6843971	-6.22	FALSE
244945_at	cytochrome c biogenesis orf206	---	---	1.12	0.16	0.79	0.4548782	0.6843971	-6.22	FALSE
247470_at	putative protein various predicte	---	AT5G62220	-1.33	-0.41	-0.79	0.4547992	0.6843971	-6.22	FALSE
249249_at	unknown protein	---	AT5G42330	-1.10	-0.14	-0.79	0.4547726	0.6843971	-6.22	FALSE
263968_s_a	PttA-like transposon protein no A	---	---	1.10	0.14	0.79	0.4548643	0.6843971	-6.22	FALSE
251239_at	putative protein several hypothet	---	AT3G62440	1.13	0.17	0.79	0.4547408	0.6843971	-6.22	FALSE
249321_at	disease resistance protein-like	---	AT5G40920	1.13	0.18	0.79	0.45481	0.6843971	-6.22	FALSE
264815_at	hypothetical protein similar to hyp	---	AT1G03620	-1.21	-0.27	-0.79	0.4548945	0.6843971	-6.22	FALSE
256185_at	dof zinc finger protein identical to	ADOF1	AT1G51700	1.31	0.39	0.79	0.4551068	0.6844592	-6.22	TRUE
259245_at	unknown protein predicted by ge	---	AT3G07660	-1.11	-0.15	-0.79	0.4550848	0.6844592	-6.22	FALSE
255813_at	hypothetical protein contains Pfa	---	AT1G19930	1.10	0.13	0.79	0.4550134	0.6844592	-6.22	FALSE
256941_at	hypothetical protein	---	---	1.11	0.15	0.79	0.4550347	0.6844592	-6.22	FALSE
246616_at	aspartyl protease-like	---	AT5G36260	1.15	0.21	0.79	0.4551158	0.6844592	-6.22	FALSE
265031_at	serine/threonine protein kinase,	---	AT1G61590	-1.08	-0.11	-0.79	0.4550008	0.6844592	-6.22	FALSE
267271_at	hypothetical protein predicted by	ATHB21	AT2G02540	1.09	0.12	0.79	0.4554144	0.684863	-6.22	FALSE
260022_at	unknown protein	---	AT1G30020	1.09	0.13	0.79	0.4554884	0.6849291	-6.22	FALSE
256426_at	hypothetical protein predicted by	---	AT1G33420	-1.26	-0.34	-0.79	0.4555404	0.6849622	-6.22	FALSE
250911_at	SERINE/THREONINE-PROTEIN	CTR1	AT5G03730	1.13	0.17	0.79	0.4556862	0.6851363	-6.22	FALSE
249515_at	tryptophan synthase beta chain	---	AT5G38530	1.36	0.44	0.79	0.4557249	0.6851493	-6.22	TRUE
265298_s_a	putative retroelement pol polypro	---	---	-1.08	-0.11	-0.79	0.4558302	0.6852625	-6.22	FALSE
258137_at	Expressed protein ; supported by	UBC37	AT3G24515	-1.08	-0.11	-0.79	0.4558935	0.6853124	-6.22	FALSE
246633_at	hypothetical protein ; supported b	---	AT1G29720	-1.30	-0.38	-0.79	0.4559801	0.6853142	-6.22	FALSE
266805_at	hypothetical protein ;supported b	---	AT2G30010	1.72	0.78	0.79	0.4559848	0.6853142	-6.22	FALSE
249667_at	unknown protein	---	---	1.07	0.10	0.79	0.4559316	0.6853142	-6.22	FALSE
263920_at	unknown protein ;supported by f	---	AT2G36410	-1.12	-0.16	-0.79	0.4561822	0.6855174	-6.22	FALSE
248268_at	importin beta	---	AT5G53480	1.11	0.15	0.79	0.456287	0.6855174	-6.22	FALSE
266309_at	unknown protein ;supported by f	---	AT2G27140	-1.13	-0.18	-0.79	0.4562318	0.6855174	-6.22	FALSE
246992_at	N-acetyltransferase hookless1-lik	---	AT5G67430	1.09	0.13	0.79	0.4562726	0.6855174	-6.22	FALSE
258865_at	NAM-like protein (no apical meris	anac045	AT3G03200	-1.08	-0.10	-0.79	0.4562097	0.6855174	-6.22	FALSE
264632_at	DegP protease contains similarity	DegP4	AT1G65640	-1.08	-0.11	-0.79	0.4563003	0.6855174	-6.22	FALSE
253629_at	glycine-rich protein glycine-rich	---	AT4G30450	1.12	0.16	0.79	0.4564064	0.6855864	-6.22	FALSE
261645_at	hypothetical protein similar to hyp	---	---	-1.09	-0.12	-0.79	0.4564024	0.6855864	-6.22	FALSE
248833_at	Bax inhibitor-1 like ;supported by	ATBI1	AT5G47120	1.11	0.16	0.79	0.4565092	0.6856957	-6.22	FALSE
248047_at	putative protein similar to unknov	---	AT5G56070	1.09	0.12	0.79	0.4565411	0.6856985	-6.22	FALSE
258438_at	hypothetical protein predicted by	---	AT3G17230	1.07	0.10	0.79	0.4566485	0.6857309	-6.22	FALSE

263188_at	hypothetical protein predicted by	---	AT1G36095	1.10	0.13	0.79	0.4566529	0.6857309	-6.22	FALSE
260918_at	hypothetical protein predicted by	---	AT1G21510	1.08	0.12	0.79	0.4566394	0.6857309	-6.22	FALSE
252957_at	glycine-rich protein 2 (GRP2) ; s	GRP2	AT4G38680	1.19	0.25	0.79	0.4570337	0.6862576	-6.22	FALSE
265606_s_a	putative non-LTR retroelement re	---	AT3G09510	1.08	0.12	0.79	0.4571967	0.6864572	-6.22	FALSE
252075_at	putative protein saposin precurs	---	AT3G51730	1.13	0.18	0.79	0.4574752	0.686789	-6.22	FALSE
252974_at	putative protein ; supported by c	MTN1	AT4G38800	1.09	0.12	0.79	0.4575382	0.686789	-6.22	FALSE
262550_at	hypothetical protein similar to hy	---	AT1G31310	1.09	0.12	0.79	0.4575257	0.686789	-6.22	FALSE
264342_at	unknown protein ; supported by f	---	AT1G12080	-1.49	-0.57	-0.79	0.4574854	0.686789	-6.22	FALSE
251735_at	putative protein ferritin 2 precurs	ATFER3	AT3G56090	-1.23	-0.30	-0.79	0.4576758	0.6869213	-6.22	FALSE
260419_at	putative protein kinase contains l	---	AT1G69730	1.26	0.33	0.79	0.4576865	0.6869213	-6.22	FALSE
266994_at	MADS-box protein (AGL29)	AGL29	AT2G34440	1.11	0.14	0.79	0.4577886	0.6870293	-6.22	FALSE
263302_at	hypothetical protein predicted by	---	---	-1.07	-0.10	-0.79	0.4578666	0.6871012	-6.22	FALSE
261343_s_a	putative protein hypothetical prot	---	---	1.08	0.11	0.79	0.4579251	0.6871438	-6.22	FALSE
251586_at	zinc finger-like protein several zi	GIS	AT3G58070	1.12	0.17	0.79	0.4580805	0.6873317	-6.22	FALSE
260763_at	RING-H2 finger protein RHA3a,	---	AT1G49220	-1.07	-0.10	-0.79	0.4581141	0.6873368	-6.22	FALSE
250320_at	CCAAT box binding factor/ trans	NF-YA1	AT5G12840	-1.10	-0.13	-0.79	0.458154	0.6873516	-6.22	FALSE
256029_at	integral membrane protein, puta	STT3B	AT1G34130	-1.19	-0.26	-0.79	0.4581982	0.6873726	-6.22	FALSE
259897_at	putative beta-glucanase similar t	ATCEL3	AT1G71380	1.09	0.12	0.79	0.4582419	0.687393	-6.22	FALSE
261557_at	kinesin-like protein C-terminal re	---	AT1G63640	-1.13	-0.18	-0.79	0.4583079	0.6874468	-6.22	FALSE
263081_at	putative homeodomain transcript	BLH5	AT2G27220	1.07	0.10	0.79	0.4583483	0.6874622	-6.22	FALSE
257137_at	P-glycoprotein, putative similar t	ABCB19	AT3G28860	-1.36	-0.44	-0.79	0.4584405	0.6875552	-6.22	TRUE
267364_at	unknown protein ;supported by f	ELF4	AT2G40080	-1.11	-0.16	-0.79	0.458533	0.6875584	-6.22	TRUE
261149_s_a	GSH-dependent dehydroascorb	DHAR1	AT1G19550 ///	1.16	0.22	0.79	0.4585134	0.6875584	-6.22	FALSE
247350_at	unknown protein	---	AT5G63830	-1.10	-0.14	-0.79	0.4585152	0.6875584	-6.22	FALSE
246551_at	putative protein predicted protei	---	AT5G15070	1.10	0.14	0.79	0.4585866	0.6875935	-6.22	FALSE
252327_at	MTN3-like protein MtN3 gene pr	---	AT3G48740	-1.14	-0.19	-0.79	0.4586988	0.6875992	-6.22	FALSE
247852_at	ATGP1 ; supported by cDNA: gi	YKT61	AT5G58060	-1.09	-0.12	-0.79	0.458651	0.6875992	-6.22	FALSE
261467_at	unknown protein	VOZ1	AT1G28520	1.14	0.19	0.79	0.4587411	0.6875992	-6.22	FALSE
266550_s_a	Expressed protein ; supported by	---	AT2G35070 ///	-1.36	-0.44	-0.79	0.4586802	0.6875992	-6.22	FALSE
250841_at	putative protein CGI-01 protein,	---	AT5G04610	-1.17	-0.22	-0.79	0.4587235	0.6875992	-6.22	FALSE
251676_at	hypothetical protein	---	AT3G57320	-1.14	-0.19	-0.79	0.4588605	0.6876573	-6.22	FALSE
253822_at	hypothetical protein	---	AT4G28410	1.08	0.12	0.79	0.4588703	0.6876573	-6.22	FALSE
246100_at	putative protein predicted protei	---	---	1.09	0.13	0.79	0.4588277	0.6876573	-6.22	FALSE
250855_at	putative protein predicted protei	---	AT5G04730	1.09	0.12	0.79	0.4589311	0.6877033	-6.22	FALSE
249261_at	putative protein similar to unknov	---	---	1.12	0.17	0.79	0.4589904	0.6877469	-6.22	FALSE

262814_at	putative heat-shock protein stron	---	AT1G11660	-1.08	-0.12	-0.79	0.4590759	0.6878298	-6.22	FALSE
249810_at	unknown protein	---	AT5G23920	-1.15	-0.20	-0.79	0.4591299	0.687848	-6.23	FALSE
265843_at	putative acyl-CoA oxidase possib	ACX5	AT2G35690	-1.10	-0.13	-0.79	0.4591483	0.687848	-6.23	FALSE
253756_at	Cdk-activating kinase CAK1At ; s	CAK1AT	AT4G28980	1.07	0.10	0.78	0.4592079	0.687892	-6.23	FALSE
246297_at	putative protein hypothetical pro	---	AT3G51760	-1.14	-0.18	-0.78	0.4592755	0.687903	-6.23	FALSE
260561_at	putative endochitinase	---	AT2G43580	1.12	0.16	0.78	0.4592519	0.687903	-6.23	FALSE
250779_at	eukaryotic translation initiation fa	EIF2 ALPH	AT5G05470	-1.15	-0.20	-0.78	0.4593903	0.6879204	-6.23	FALSE
251720_at	putative protein	---	AT3G56160	1.19	0.26	0.78	0.4593997	0.6879204	-6.23	FALSE
257539_at	hypothetical protein predicted by	---	AT3G29150	1.08	0.11	0.78	0.4593817	0.6879204	-6.23	FALSE
266139_at	Expressed protein ; supported by	---	AT2G28085	1.20	0.27	0.78	0.4594078	0.6879204	-6.23	FALSE
257140_at	MYB family transcription factor (	MYB30	AT3G28910	-1.22	-0.28	-0.78	0.4595896	0.6881474	-6.23	FALSE
253184_at	putative protein protein kinase A	BSK1	AT4G35230	1.10	0.13	0.78	0.4597391	0.6883261	-6.23	FALSE
246233_at	putative protein	---	AT4G36550	-1.27	-0.34	-0.78	0.4598309	0.6884185	-6.23	TRUE
264167_at	unknown protein Location of EST	---	AT1G02060	-1.13	-0.18	-0.78	0.4599891	0.6885992	-6.23	FALSE
255755_s_a	polygalacturonase, putative simi	---	AT1G43050 /	1.10	0.13	0.78	0.460012	0.6885992	-6.23	FALSE
247875_at	putative protein similar to unknov	---	AT5G57720	-1.10	-0.14	-0.78	0.4600598	0.6886255	-6.23	FALSE
249502_s_a	expansin-like protein expansin -	ATEXPA23	AT5G39280 /	1.11	0.15	0.78	0.4601286	0.6886832	-6.23	FALSE
250294_at	auxin reponsive - like protein Nt-	---	AT5G13380	1.09	0.12	0.78	0.4602594	0.6888339	-6.23	FALSE
251177_at	cyclophylin -like protein CDC28/	---	AT3G63400	-1.11	-0.16	-0.78	0.460323	0.6888652	-6.23	FALSE
257135_at	hypothetical protein similar to oxi	---	AT3G12900	1.12	0.16	0.78	0.4603408	0.6888652	-6.23	FALSE
266311_at	hypothetical protein predicted by	---	AT2G27130	-1.32	-0.40	-0.78	0.4604456	0.6889624	-6.23	TRUE
248867_at	bHLH transcription factor	---	AT5G46830	1.09	0.12	0.78	0.4604912	0.6889624	-6.23	FALSE
263852_at	putative mutT domain protein	ATNUDT6	AT2G04450	-1.57	-0.65	-0.78	0.4604963	0.6889624	-6.23	FALSE
245288_at	transcriptional adaptor like protei	ADA2B	AT4G16420	-1.09	-0.12	-0.78	0.460544	0.6889862	-6.23	FALSE
258106_at	ribonucleoside-diphosphate redu	RNR2A	AT3G23580	-1.11	-0.16	-0.78	0.4606312	0.6889862	-6.23	FALSE
262204_at	unknown protein ; supported by	---	AT2G01100	-1.09	-0.12	-0.78	0.460633	0.6889862	-6.23	FALSE
256377_at	hypothetical protein	---	AT1G66650	1.07	0.10	0.78	0.4606238	0.6889862	-6.23	FALSE
260911_at	hypothetical protein predicted by	---	AT1G02490	-1.09	-0.12	-0.78	0.4608351	0.6892433	-6.23	FALSE
266776_at	putative ubiquitin fusion-degrada	---	AT2G29070	-1.11	-0.15	-0.78	0.4611562	0.6892756	-6.23	FALSE
267060_at	unknown protein ; supported by	---	AT2G32580	-1.15	-0.20	-0.78	0.4611224	0.6892756	-6.23	FALSE
260832_at	unknown protein ; supported by c	GAUT6	AT1G06780	-1.10	-0.14	-0.78	0.4609511	0.6892756	-6.23	FALSE
260727_at	polygalacturonase PG1, putative	---	AT1G48100	1.12	0.17	0.78	0.4611809	0.6892756	-6.23	FALSE
246749_at	putative protein ; supported by c	---	AT5G27830	-1.13	-0.18	-0.78	0.4609083	0.6892756	-6.23	FALSE
265494_at	putative calmodulin-like protein	---	AT2G15680	-1.12	-0.17	-0.78	0.4609415	0.6892756	-6.23	FALSE
259594_at	unknown protein contains similar	---	AT1G28140	-1.09	-0.12	-0.78	0.4611429	0.6892756	-6.23	FALSE

247402_at	putative protein predicted protei	---	AT5G62750	1.08	0.11	0.78	0.4611891	0.6892756	-6.23	FALSE
256871_at	WD-repeat protein, putative con	---	AT3G26480	1.18	0.24	0.78	0.461035	0.6892756	-6.23	FALSE
254378_at	putative protein NADH oxidored	DER2.1	AT4G21810	-1.18	-0.24	-0.78	0.461091	0.6892756	-6.23	FALSE
249737_at	putative protein similar to unknov	---	AT5G24480	1.10	0.14	0.78	0.4610189	0.6892756	-6.23	FALSE
258239_at	putative chlorophyll A-B binding	LHCB2.3	AT3G27690	-1.52	-0.60	-0.78	0.4612412	0.6893082	-6.23	TRUE
263690_at	putative DNA-binding protein Sir	AtHB23	AT1G26960	1.17	0.23	0.78	0.4613605	0.6894414	-6.23	FALSE
263370_at	hypothetical protein predicted by	---	AT2G20500	1.19	0.25	0.78	0.4614213	0.6894419	-6.23	FALSE
245448_at	disease resistance RPP5 like pro	RPP4	AT4G16860	-1.10	-0.14	-0.78	0.461398	0.6894419	-6.23	FALSE
263424_at	putative RING zinc finger protein	---	AT2G31510	-1.09	-0.13	-0.78	0.4615384	0.6895429	-6.23	FALSE
248031_at	unknown protein ; supported by	---	AT5G55640	1.07	0.10	0.78	0.4615494	0.6895429	-6.23	FALSE
263268_at	unknown protein	---	---	-1.09	-0.13	-0.78	0.4616047	0.6895512	-6.23	FALSE
260011_at	hypothetical protein similar to hy	---	AT1G68110	-1.11	-0.16	-0.78	0.461672	0.6895512	-6.23	FALSE
257512_at	unknown protein	---	AT1G35250	1.08	0.11	0.78	0.4616758	0.6895512	-6.23	FALSE
245978_at	putative protein MORC microrch	---	AT5G13130	1.10	0.14	0.78	0.4616329	0.6895512	-6.23	FALSE
252762_at	putative protein hypothetical pro	---	AT3G42780	1.13	0.17	0.78	0.4617271	0.6895826	-6.23	FALSE
245651_s_a	F5A9.18 unknown protein; simila	---	AT1G24793 /.	1.13	0.18	0.78	0.4618398	0.6897057	-6.23	FALSE
260661_at	hypothetical protein predicted by	---	AT1G19500	1.11	0.15	0.78	0.461922	0.6897833	-6.23	FALSE
256934_at	unknown protein contains Pfam p	---	AT3G22530	1.11	0.15	0.78	0.4619537	0.6897856	-6.23	FALSE
254594_at	putative protein	---	AT4G18930	-1.15	-0.21	-0.78	0.4625601	0.6901489	-6.23	FALSE
259590_at	hypothetical protein contains sim	---	AT1G28160	1.10	0.14	0.78	0.4623393	0.6901489	-6.23	FALSE
264973_at	nitrate transporter, putative nitra	---	AT1G27040	1.11	0.16	0.78	0.46241	0.6901489	-6.23	FALSE
258888_at	putative pectinesterase similar to	---	AT3G05620	1.16	0.22	0.78	0.4622902	0.6901489	-6.23	FALSE
254233_at	98b like protein 98b - Daucus ca	---	AT4G23800	1.16	0.21	0.78	0.4625434	0.6901489	-6.23	FALSE
252709_at	putative protein predicted protei	---	AT3G43840	1.07	0.10	0.78	0.4624125	0.6901489	-6.23	FALSE
245516_at	hypothetical protein	---	AT4G15820	-1.11	-0.16	-0.78	0.4625146	0.6901489	-6.23	FALSE
246542_at	transcriptional regulatory - like p	SNL2	AT5G15020	-1.12	-0.16	-0.78	0.4625368	0.6901489	-6.23	FALSE
260428_at	putative translation initiation fact	---	AT1G72340	-1.13	-0.18	-0.78	0.4623371	0.6901489	-6.23	FALSE
245563_at	SNF1 like protein kinase ; suppo	CIPK4	AT4G14580	-1.28	-0.35	-0.78	0.4624901	0.6901489	-6.23	FALSE
253104_at	thaumatin-like protein thaumatin	---	AT4G36010	1.36	0.44	0.78	0.4624721	0.6901489	-6.23	FALSE
255181_at	predicted protein of unknown fun	---	---	1.10	0.14	0.78	0.4623964	0.6901489	-6.23	FALSE
254402_at	putative protein predicted protei	---	AT4G21310	1.15	0.20	0.78	0.4626973	0.6902757	-6.23	FALSE
265017_at	unknown protein similar to EST e	---	AT1G24390	1.09	0.13	0.78	0.4627359	0.6902757	-6.23	FALSE
246022_at	putative protein predicted protei	---	AT5G21110	-1.09	-0.12	-0.78	0.4627343	0.6902757	-6.23	FALSE
265600_at	hypothetical protein predicted by	---	---	-1.08	-0.12	-0.78	0.4627714	0.6902835	-6.23	FALSE
266875_at	putative flavonol synthase	---	AT2G44800	1.11	0.15	0.78	0.4628188	0.6903091	-6.23	FALSE

257589_at	hypothetical protein predicted by	---	AT1G55050	-1.12	-0.16	-0.78	0.4628948	0.6903322	-6.23	FALSE
249567_at	SAMT-like protein S-adenosyl-L	---	AT5G38020	1.07	0.10	0.78	0.4628712	0.6903322	-6.23	FALSE
258663_at	hypothetical protein	---	AT3G08670	1.08	0.11	0.78	0.4631844	0.6907189	-6.23	FALSE
263393_at	hypothetical protein similar to hyp	---	---	1.08	0.11	0.78	0.4632268	0.6907369	-6.23	FALSE
263213_at	unknown protein Strong similarity	---	AT1G30560	1.10	0.14	0.78	0.4633123	0.6908192	-6.23	FALSE
250490_at	pectin methylesterase - like prot	---	AT5G09760	-1.22	-0.28	-0.78	0.4634597	0.6909939	-6.23	TRUE
250311_at	unknown protein	---	AT5G12240	1.07	0.10	0.78	0.4634921	0.6909971	-6.23	FALSE
267020_at	hypothetical protein predicted by	---	AT2G39320	1.09	0.13	0.78	0.4635634	0.6910582	-6.23	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U372	---	---	1.11	0.15	0.78	0.463744	0.6911296	-6.23	FALSE
260402_at	putative gamma-glutamyltransfe	GGT3	AT1G69820	1.12	0.17	0.78	0.4637679	0.6911296	-6.23	FALSE
252434_s_a	putative protein mudrA protein -	---	---	1.10	0.13	0.78	0.4636614	0.6911296	-6.23	FALSE
253528_s_a	putative protein bcop gene prod	---	AT4G31480 /	-1.08	-0.11	-0.78	0.4638448	0.6911296	-6.23	FALSE
267389_at	putative beta-glucosidase	BGLU28	AT2G44460	-2.20	-1.14	-0.78	0.4638537	0.6911296	-6.23	FALSE
248577_at	myrosinase binding protein-like ;	---	AT5G49870	1.08	0.10	0.78	0.4638419	0.6911296	-6.23	FALSE
251307_at	putative protein ;supported by fu	---	AT3G61200	1.11	0.15	0.78	0.4638319	0.6911296	-6.23	FALSE
255256_at	see GB:AC003952 similar to a fa	---	AT4G05080	-1.11	-0.15	-0.78	0.4637182	0.6911296	-6.23	FALSE
253102_at	Expressed protein ; supported by	---	AT4G36105	1.13	0.18	0.78	0.464087	0.6913869	-6.23	FALSE
246046_at	putative protein predicted protei	---	---	-1.10	-0.14	-0.78	0.4640792	0.6913869	-6.23	FALSE
255965_at	14-3-3 protein (grf14), putative s	---	AT1G22290	1.08	0.12	0.78	0.4641827	0.6914843	-6.23	FALSE
262833_at	cyclin, putative contains Pfam pr	SDS	AT1G14750	1.07	0.10	0.78	0.4642189	0.691493	-6.23	FALSE
265578_at	unknown protein	---	AT2G20100	1.11	0.15	0.78	0.4642704	0.6915159	-6.23	FALSE
255324_s_a	putative reverse transcriptase	---	---	1.07	0.10	0.78	0.4642949	0.6915159	-6.23	FALSE
248521_s_a	nodulin-like protein ; supported b	---	AT5G50520 /	-1.09	-0.13	-0.78	0.4644246	0.6916264	-6.23	FALSE
262242_at	hypothetical protein predicted by	---	AT1G48360	1.11	0.16	0.78	0.4644297	0.6916264	-6.23	FALSE
256848_at	hypothetical protein similar to hyp	---	AT3G27960	1.31	0.39	0.78	0.4645321	0.6916569	-6.23	TRUE
251619_at	putative protein hypothetical pro	---	AT3G58050	-1.07	-0.10	-0.78	0.4645411	0.6916569	-6.23	FALSE
255998_at	hypothetical protein contains sim	---	AT1G29780	-1.08	-0.11	-0.78	0.4645388	0.6916569	-6.23	FALSE
262336_at	hypothetical protein predicted be	TOM7-2	AT1G64220	-1.07	-0.10	-0.78	0.4646042	0.6917057	-6.23	FALSE
245739_at	mitotic cyclin a2-type, putative s	CYCA1;1	AT1G44110	-1.08	-0.11	-0.78	0.4646499	0.6917285	-6.23	FALSE
254457_at	putative protein various predicte	---	AT4G21170	-1.12	-0.17	-0.77	0.4647188	0.691786	-6.23	FALSE
247142_at	putative protein strong similarity t	---	AT5G65570	-1.10	-0.13	-0.77	0.4648153	0.6918844	-6.23	FALSE
254491_at	putative protein hypothetical prot	---	AT4G20300	1.13	0.18	0.77	0.464852	0.6918938	-6.23	FALSE
265409_at	unknown protein	PIP2;8	AT2G16830 /	1.10	0.13	0.77	0.4649531	0.6919992	-6.23	FALSE
249214_at	beta-1,3-glucanase-like protein	---	AT5G42720	1.19	0.25	0.77	0.4651126	0.6921915	-6.23	FALSE
257971_at	unknown protein similar to hypot	GC6	AT3G27530	-1.15	-0.20	-0.77	0.4652454	0.6923438	-6.23	FALSE

258489_at	14-3-3 protein GF14nu (grf7) ide	GRF7	AT3G02520	-1.08	-0.11	-0.77	0.4653901	0.6923778	-6.23	FALSE
265192_at	hypothetical protein predicted by	---	AT1G05060	1.12	0.16	0.77	0.4653894	0.6923778	-6.23	FALSE
247138_at	3-dehydroquinate synthase-like p	---	AT5G66120	1.14	0.19	0.77	0.4653296	0.6923778	-6.23	FALSE
260739_at	serine carboxypeptidase precurs	scpl50	AT1G15000	-1.19	-0.26	-0.77	0.4653914	0.6923778	-6.23	FALSE
245496_at	LET1 like protein	---	AT4G16440	1.09	0.12	0.77	0.4654199	0.6923778	-6.23	FALSE
248879_at	ornithine aminotransferase	DELTA-OA	AT5G46180	-1.12	-0.16	-0.77	0.4656214	0.692542	-6.23	TRUE
265772_at	putative protein kinase contains a	RKF3	AT2G48010	1.12	0.16	0.77	0.4656206	0.692542	-6.23	FALSE
256357_at	hypothetical protein	---	AT1G66490	-1.07	-0.09	-0.77	0.4656164	0.692542	-6.23	FALSE
253357_at	Dem -like protein Dem (defective	---	AT4G33400	-1.09	-0.12	-0.77	0.4657437	0.6926777	-6.23	FALSE
253642_at	hypothetical protein ;supported b	---	AT4G29960	-1.11	-0.15	-0.77	0.4657734	0.6926777	-6.23	FALSE
253376_at	hypothetical protein Arabidopsis	---	AT4G33290	1.07	0.10	0.77	0.4658942	0.6928122	-6.23	FALSE
265347_at	similar to mammalian MHC III reg	SUVH6	AT2G22740	-1.07	-0.10	-0.77	0.4659407	0.6928363	-6.23	FALSE
246383_at	hypothetical protein predicted by	---	AT1G77360	-1.16	-0.22	-0.77	0.4663187	0.693353	-6.24	FALSE
267484_at	E2, ubiquitin-conjugating enzym	ATUBC2	AT2G02760	-1.09	-0.12	-0.77	0.4663736	0.6933895	-6.24	FALSE
262951_at	nodulin-like protein similar to Mt	---	AT1G75500	-1.12	-0.16	-0.77	0.4665039	0.6934476	-6.24	FALSE
259259_at	spindly (gibberellin signal transdu	SPY	AT3G11540	-1.09	-0.13	-0.77	0.4665001	0.6934476	-6.24	FALSE
248254_at	receptor protein kinase-like prote	---	AT5G53320	-1.12	-0.16	-0.77	0.4665022	0.6934476	-6.24	FALSE
258575_at	putative O-linked GlcNAc transfe	SEC	AT3G04240	1.08	0.12	0.77	0.4665982	0.6934522	-6.24	FALSE
245286_at	cytosolic O-acetylserine(thiol)lyas	OASA1	AT4G14880	1.09	0.13	0.77	0.4665474	0.6934522	-6.24	FALSE
264423_at	hypothetical protein predicted by	---	AT1G61690	-1.11	-0.15	-0.77	0.4665893	0.6934522	-6.24	FALSE
264964_at	hypothetical protein predicted by	---	AT1G60460	1.11	0.15	0.77	0.466637	0.6934648	-6.24	FALSE
245993_at	putative protein predicted protei	---	AT5G20700	-1.15	-0.20	-0.77	0.4666913	0.6935003	-6.24	FALSE
246798_at	putative protein various predicte	---	AT5G26930	1.08	0.11	0.77	0.4667678	0.6935688	-6.24	FALSE
254196_at	putative protein	---	AT4G24030	1.12	0.16	0.77	0.466854	0.6935854	-6.24	FALSE
260802_at	exopolygalacturonase, putative s	---	AT1G78400	1.07	0.10	0.77	0.4668702	0.6935854	-6.24	FALSE
264110_at	unknown protein	---	---	-1.07	-0.10	-0.77	0.4668108	0.6935854	-6.24	FALSE
266056_at	hypothetical protein predicted by	ATATG18C	AT2G40810	-1.08	-0.11	-0.77	0.4669178	0.6936109	-6.24	FALSE
266546_at	putative AT-hook DNA-binding pr	---	AT2G35270	1.08	0.11	0.77	0.467181	0.6939566	-6.24	FALSE
248397_at	unknown protein	---	AT5G52140	1.09	0.13	0.77	0.4673291	0.6939603	-6.24	FALSE
251925_at	hypothetical protein ;supported b	---	AT3G54000	1.15	0.20	0.77	0.4674225	0.6939603	-6.24	FALSE
254243_at	serine/threonine kinase - like pro	CRK13	AT4G23210	1.49	0.58	0.77	0.4674423	0.6939603	-6.24	FALSE
262179_at	hypothetical protein predicted by	AGL66	AT1G77980	1.11	0.15	0.77	0.4675174	0.6939603	-6.24	FALSE
258083_at	Expressed protein ; supported by	---	AT3G25855	-1.10	-0.14	-0.77	0.4674729	0.6939603	-6.24	FALSE
265001_at	hypothetical protein contains sim	---	AT1G67350	-1.09	-0.12	-0.77	0.4673782	0.6939603	-6.24	FALSE
247337_at	putative protein similar to unknov	PDF2.5	AT5G63660	-1.07	-0.10	-0.77	0.4675628	0.6939603	-6.24	FALSE

252139_at	putative protein hypothetical pro	---	AT3G51050	-1.09	-0.12	-0.77	0.4673273	0.6939603	-6.24	FALSE
246938_at	cyclin 3a	CYCA2;1	AT5G25380	1.11	0.15	0.77	0.467579	0.6939603	-6.24	FALSE
260474_at	lysophospholipase isolog	---	AT1G11090	-1.10	-0.14	-0.77	0.4675575	0.6939603	-6.24	FALSE
264979_s_a	disease resistance protein, puta	---	AT1G27170 ///	1.11	0.15	0.77	0.4673943	0.6939603	-6.24	FALSE
245538_at	p140mDia like protein	---	AT4G15200	-1.09	-0.13	-0.77	0.4673909	0.6939603	-6.24	FALSE
258864_at	unknown protein	---	AT3G03210	-1.12	-0.16	-0.77	0.4673982	0.6939603	-6.24	FALSE
263281_at	putative glycine-rich RNA-bindin	---	AT2G14160	1.09	0.12	0.77	0.4676233	0.693981	-6.24	FALSE
265222_at	putative endosomal protein ; sup	---	AT2G01970	1.07	0.10	0.77	0.4676868	0.693985	-6.24	FALSE
246639_x_a	adenylate kinase -like protein pr	---	---	1.09	0.13	0.77	0.4676669	0.693985	-6.24	FALSE
262457_at	hypothetical protein similar to hy	---	AT1G11200	1.16	0.22	0.77	0.4678522	0.6940911	-6.24	FALSE
249262_at	putative protein similar to unknov	---	AT5G41720	1.09	0.12	0.77	0.4678586	0.6940911	-6.24	FALSE
249185_at	CHP-rich zinc finger protein-like	---	AT5G43030	1.09	0.13	0.77	0.4678671	0.6940911	-6.24	FALSE
257711_at	20S proteasome beta subunit (P	PBB1	AT3G27430	1.10	0.13	0.77	0.4678801	0.6940911	-6.24	FALSE
245600_at	hypothetical protein	---	AT4G14230	-1.12	-0.16	-0.77	0.4679726	0.6941381	-6.24	FALSE
262424_at	hypothetical protein predicted by	---	AT1G47680	-1.08	-0.11	-0.77	0.4679586	0.6941381	-6.24	FALSE
247359_at	acyltransferase-like protein ;supp	---	AT5G63560	1.11	0.15	0.77	0.4680393	0.6941918	-6.24	FALSE
248781_at	putative protein similar to unknov	---	AT5G47870	1.21	0.27	0.77	0.4681541	0.6942718	-6.24	FALSE
259803_at	cytosolic factor, putative similar	PATL1	AT1G72150	-1.09	-0.12	-0.77	0.4681281	0.6942718	-6.24	FALSE
248787_at	putative protein similar to unknov	---	AT5G47420	1.14	0.19	0.77	0.4682601	0.6943838	-6.24	FALSE
244958_at	hypothetical protein	---	---	1.08	0.11	0.77	0.4683116	0.694415	-6.24	FALSE
249869_at	acetyl-CoA synthetase-like prote	AAE17	AT5G23050	1.14	0.19	0.77	0.4684155	0.6944338	-6.24	FALSE
259781_at	reverse transcriptase, putative s	---	---	1.10	0.14	0.77	0.4683991	0.6944338	-6.24	FALSE
253774_at	NAM / CUC2 -like protein No ap	anac074	AT4G28530	1.16	0.22	0.77	0.4683562	0.6944338	-6.24	FALSE
251249_at	putative protein 10-deacetylbac	---	AT3G62160	-1.10	-0.13	-0.77	0.4686966	0.6947151	-6.24	FALSE
251420_at	transcription factor - like protein	---	AT3G60490	1.13	0.17	0.77	0.4686921	0.6947151	-6.24	FALSE
254090_at	MtN3 - like protein MtN3 (induce	---	AT4G25010	1.11	0.15	0.77	0.4686552	0.6947151	-6.24	FALSE
265497_at	putative non-LTR retroelement re	---	---	1.22	0.29	0.77	0.4688125	0.6948417	-6.24	FALSE
265859_at	hypothetical protein predicted by	---	---	-1.09	-0.12	-0.77	0.4689611	0.6950167	-6.24	FALSE
249787_at	putative protein contains similarit	---	AT5G24320	-1.08	-0.11	-0.77	0.4690809	0.6950347	-6.24	FALSE
261111_at	homeodomain protein BELL1, p	BLH11	AT1G75430	1.07	0.10	0.77	0.4691125	0.6950347	-6.24	FALSE
264498_at	Expressed protein ; supported by	DIS2	AT1G30825	-1.10	-0.14	-0.77	0.4691197	0.6950347	-6.24	FALSE
247062_at	putative protein similar to unknov	---	AT5G66810	-1.19	-0.25	-0.77	0.4691256	0.6950347	-6.24	FALSE
259413_at	hypothetical protein contains sim	---	AT1G02320	-1.08	-0.12	-0.77	0.4690673	0.6950347	-6.24	FALSE
249094_at	dimethylaniline monooxygenase-	YUC5	AT5G43890	1.11	0.15	0.77	0.4692295	0.6951435	-6.24	FALSE
251436_at	putative protein hypothetical pro	ARGOS	AT3G59900	-1.51	-0.60	-0.77	0.4694036	0.6953562	-6.24	FALSE

255892_at	hypothetical protein contains sim	---	AT1G17910	1.08	0.11	0.77	0.4694623	0.6953981	-6.24	FALSE
246244_at	receptor kinase-like protein	---	AT4G37250	1.08	0.12	0.77	0.4695105	0.6954219	-6.24	FALSE
256868_at	eukaryotic translation initiation fa	EIF4B1	AT3G26400	1.16	0.22	0.77	0.4695394	0.6954219	-6.24	FALSE
246541_at	ubiquitin-fusion degradation prot	---	AT5G15400	-1.09	-0.12	-0.77	0.4696533	0.6955327	-6.24	FALSE
250940_at	putative protein	---	AT5G03310	1.08	0.11	0.77	0.4696751	0.6955327	-6.24	FALSE
264526_at	putative calcium ATPase very si	ECA3	AT1G10130	-1.10	-0.14	-0.77	0.469949	0.6957011	-6.24	FALSE
255056_at	putative protein helix-loop-helix	TT8	AT4G09820	1.07	0.10	0.77	0.4699909	0.6957011	-6.24	FALSE
257384_at	unknown protein	---	AT2G15110	1.09	0.12	0.77	0.4699513	0.6957011	-6.24	FALSE
263894_at	putative cytochrome P450	CYP96A5	AT2G21910	-1.10	-0.13	-0.77	0.469898	0.6957011	-6.24	FALSE
260099_at	unknown protein ;supported by f	---	AT1G73180	-1.08	-0.11	-0.77	0.4699184	0.6957011	-6.24	FALSE
261215_at	subtilase, putative similar to sub	---	AT1G32970	1.08	0.11	0.77	0.4700329	0.6957011	-6.24	FALSE
249349_at	putative transcription factor MYB	MYB24	AT5G40350	1.09	0.12	0.77	0.4700212	0.6957011	-6.24	FALSE
262469_s_a	hypothetical protein identical to h	---	AT1G50190 /	-1.08	-0.11	-0.77	0.4699395	0.6957011	-6.24	FALSE
257519_at	unknown protein	---	AT3G01210	-1.10	-0.14	-0.77	0.470081	0.6957272	-6.24	FALSE
263067_at	hypothetical protein predicted by	---	AT2G17550	-1.16	-0.21	-0.77	0.4701321	0.6957357	-6.24	FALSE
256543_at	unknown protein supported by fu	---	AT1G42480	-1.10	-0.14	-0.77	0.4701477	0.6957357	-6.24	FALSE
252063_at	lipid transfer protein-like protein	LTP12	AT3G51590	1.09	0.13	0.77	0.4701817	0.6957408	-6.24	FALSE
257110_x_a	hypothetical protein	---	---	1.11	0.15	0.76	0.4702449	0.6957441	-6.24	FALSE
264497_at	hypothetical protein predicted by	ATPUP4	AT1G30840	1.13	0.18	0.77	0.4702355	0.6957441	-6.24	FALSE
245414_at	hypothetical protein	---	AT4G17310	-1.11	-0.15	-0.76	0.4703842	0.695905	-6.24	FALSE
247451_at	MYB99 ; supported by cDNA: gi	ATMYB99	AT5G62320	-1.10	-0.14	-0.76	0.4705758	0.6961434	-6.24	FALSE
261682_at	unknown protein similar to hypot	---	AT1G47330	-1.11	-0.15	-0.76	0.4706513	0.6961648	-6.24	FALSE
259633_at	hypothetical protein	---	AT1G56500	-1.12	-0.16	-0.76	0.4706433	0.6961648	-6.24	FALSE
259446_at	hypothetical protein contains sim	---	AT1G02410	1.12	0.16	0.76	0.4706871	0.6961725	-6.24	FALSE
258360_at	hypothetical protein predicted by	---	AT3G14250	1.09	0.12	0.76	0.4707346	0.6961976	-6.24	FALSE
257427_at	hypothetical protein predicted by	---	AT1G79060	1.15	0.21	0.76	0.4708789	0.6962466	-6.24	FALSE
253851_at	putative transcription factor MYB	AtMYB41	AT4G28110	1.11	0.14	0.76	0.4708535	0.6962466	-6.24	FALSE
260184_s_a	putative protein predicted protei	---	---	1.07	0.10	0.76	0.4708898	0.6962466	-6.24	FALSE
246333_at	proteinkinase AtPP -like protein	---	AT3G44840	1.09	0.13	0.76	0.4708885	0.6962466	-6.24	FALSE
254042_at	xyloglucan endo-1,4-beta-D-gluc	XTR6	AT4G25810	1.50	0.59	0.76	0.4709493	0.6962895	-6.24	FALSE
264450_s_a	unknown protein similar to hypot	SNL6	AT1G10250 /	-1.15	-0.20	-0.76	0.4710147	0.6962959	-6.24	FALSE
250661_at	nucleoid DNA-binding-like protei	---	AT5G07030	1.68	0.75	0.76	0.4710017	0.6962959	-6.24	FALSE
246571_at	putative protein	---	AT5G15000	1.07	0.09	0.76	0.4711113	0.6963033	-6.24	FALSE
264626_at	unknown protein	AS2	AT1G65620	1.14	0.19	0.76	0.4710583	0.6963033	-6.24	FALSE
258938_at	germin-like protein similar to gerr	---	AT3G10080	-1.47	-0.55	-0.76	0.4711033	0.6963033	-6.24	FALSE

261461_at	hypothetical protein predicted by	---	AT1G07860	1.10	0.14	0.76	0.4712683	0.6964615	-6.24	FALSE
253134_at	putative protein procollagen-pro	---	AT4G35820	1.08	0.11	0.76	0.4712794	0.6964615	-6.24	FALSE
252864_at	putative protein regulatory prote	---	AT4G39740	-1.17	-0.23	-0.76	0.4713778	0.6965567	-6.24	FALSE
245858_at	CER1-like protein CER1-like, A.	---	AT5G28280	-1.10	-0.13	-0.76	0.4714049	0.6965567	-6.24	FALSE
260866_at	polyprotein, putative similar to p	---	---	1.10	0.13	0.76	0.4714675	0.6966041	-6.24	FALSE
256431_s_a	putative disease resistance prote	AtRLP34	AT3G11010 /	1.19	0.25	0.76	0.471677	0.6968684	-6.24	FALSE
250113_at	putative protein similar to unknov	FRL1	AT5G16320	1.09	0.12	0.76	0.4719574	0.6972375	-6.24	FALSE
254231_at	putative protein AR411 - Arabido	WRKY53	AT4G23810	1.61	0.69	0.76	0.471988	0.6972376	-6.24	FALSE
262562_at	hypothetical protein predicted by	---	AT1G34220	-1.08	-0.11	-0.76	0.4723025	0.6976571	-6.24	FALSE
267230_at	unknown protein	ARL	AT2G44080	-1.57	-0.65	-0.76	0.4723771	0.6977167	-6.24	FALSE
247424_at	LIM7 - like protein LIM7, Lilium l	AtVEX1	AT5G62850	1.09	0.13	0.76	0.4724041	0.6977167	-6.24	FALSE
264288_at	Expressed protein ; supported by	---	AT1G62045	-1.09	-0.12	-0.76	0.4724766	0.6977787	-6.24	FALSE
266144_at	hypothetical protein	---	AT2G12170	-1.08	-0.11	-0.76	0.472692	0.6980515	-6.24	FALSE
262186_at	hypothetical protein	---	AT1G77960	1.20	0.27	0.76	0.4727263	0.698057	-6.24	FALSE
247022_at	unknown protein	---	AT5G67050	-1.08	-0.11	-0.76	0.4728235	0.6981554	-6.24	FALSE
244991_s_a	NADH dehydrogenase ND2	---	---	-1.09	-0.12	-0.76	0.4729418	0.698242	-6.24	FALSE
259886_at	putative protein kinase similar to	---	AT1G76370	1.08	0.11	0.76	0.4729434	0.698242	-6.24	FALSE
249052_at	antifungal protein-like (PDF1.2)	PDF1.2	AT5G44420	-1.45	-0.54	-0.76	0.4730943	0.6983319	-6.25	TRUE
260392_at	putative enolase similar to ENOL	---	AT1G74030	1.58	0.66	0.76	0.4730961	0.6983319	-6.25	FALSE
251635_at	endo-polygalacturonase	ADPG1	AT3G57510	1.11	0.16	0.76	0.4730841	0.6983319	-6.25	FALSE
249684_s_a	cytochrome P450-like	---	AT5G36110 /	1.08	0.11	0.76	0.4731421	0.6983546	-6.25	FALSE
247874_at	101 kDa heat shock protein; HSF	---	AT5G57710	1.14	0.19	0.76	0.4734129	0.6986187	-6.25	FALSE
255237_at	hypothetical protein	---	---	1.08	0.10	0.76	0.4734053	0.6986187	-6.25	FALSE
251587_at	hypothetical protein	---	AT3G58080	1.15	0.20	0.76	0.4733727	0.6986187	-6.25	FALSE
254099_at	protein-methionine-S-oxide reduc	---	AT4G25130	-1.14	-0.18	-0.76	0.4735105	0.6986723	-6.25	FALSE
262384_at	disease resistance protein, puta	---	AT1G72950	-1.12	-0.17	-0.76	0.4734877	0.6986723	-6.25	FALSE
267449_at	hypothetical protein predicted by	---	AT2G33690	1.07	0.10	0.76	0.4735416	0.698673	-6.25	FALSE
261117_at	unknown protein	AUL1	AT1G75310	1.15	0.20	0.76	0.4739409	0.6987386	-6.25	TRUE
262634_at	unknown protein ; supported by c	---	AT1G06690	-1.25	-0.32	-0.76	0.4737765	0.6987386	-6.25	TRUE
259950_at	hypothetical protein predicted by	---	AT1G71410	1.10	0.13	0.76	0.4737064	0.6987386	-6.25	FALSE
249088_at	selenium-binding protein-like	---	AT5G44230	-1.13	-0.17	-0.76	0.4739182	0.6987386	-6.25	FALSE
254053_s_a	SRG1-like protein strong homolo	---	AT4G25300 /	-1.17	-0.23	-0.76	0.4737991	0.6987386	-6.25	FALSE
260389_at	Expressed protein ; supported by	---	AT1G74055	-1.14	-0.19	-0.76	0.4740068	0.6987386	-6.25	FALSE
249969_at	putative protein glycine-rich prot	---	AT5G19090	-1.17	-0.23	-0.76	0.4739763	0.6987386	-6.25	FALSE
267150_at	putative anthranilate N-hydroxyc	SDT	AT2G23510	-1.07	-0.10	-0.76	0.4738141	0.6987386	-6.25	FALSE

262045_at	hypothetical protein predicted by	---	AT1G80240 /	-1.15	-0.20	-0.76	0.4737027	0.6987386	-6.25	FALSE
256947_at	hypothetical protein contains Pfa	POK2	AT3G19050	-1.07	-0.10	-0.76	0.473839	0.6987386	-6.25	FALSE
256359_at	protein kinase, putative contains	---	AT1G66460	1.08	0.10	0.76	0.4737571	0.6987386	-6.25	FALSE
246692_at	putative protein predicted protei	---	---	1.11	0.15	0.76	0.4739202	0.6987386	-6.25	FALSE
259870_at	putative heat shock protein predi	---	AT1G76780	-1.07	-0.10	-0.76	0.4739163	0.6987386	-6.25	FALSE
257947_at	putative isocitrate lyase similar to	ICL	AT3G21720	-1.12	-0.16	-0.76	0.4740149	0.6987386	-6.25	FALSE
249484_at	cytochrome P450 - like protein c	BR6OX1	AT5G38970	-1.08	-0.11	-0.76	0.4740792	0.698743	-6.25	FALSE
266975_at	hypothetical protein predicted by	ATEXO70H	AT2G39380	1.22	0.28	0.76	0.4740777	0.698743	-6.25	FALSE
249725_at	unknown protein	---	AT5G35470	-1.08	-0.11	-0.76	0.4741609	0.6988182	-6.25	FALSE
264564_at	hypothetical protein predicted by	---	AT1G05290	-1.07	-0.09	-0.76	0.4742503	0.6989049	-6.25	FALSE
256531_at	cystathionine gamma-synthase,	---	AT1G33320	1.08	0.11	0.76	0.4743306	0.698978	-6.25	FALSE
263993_at	hypothetical protein predicted by	---	---	1.10	0.14	0.76	0.4744138	0.6990103	-6.25	FALSE
252050_at	hypothetical protein	---	AT3G52550	1.11	0.15	0.76	0.4743857	0.6990103	-6.25	FALSE
255901_at	GDP-L-fucose synthetase, putat	GER2	AT1G17890	1.14	0.19	0.76	0.4745023	0.6990955	-6.25	FALSE
248618_at	myb-related transcription factor	AtMYB78	AT5G49620	1.10	0.14	0.76	0.4745417	0.6991085	-6.25	FALSE
257841_at	nitrate transporter, putative simil	---	AT3G25260	1.08	0.11	0.76	0.4746595	0.6992368	-6.25	FALSE
249267_at	putative protein contains similarit	BTI3	AT5G41600	-1.15	-0.20	-0.76	0.4748561	0.6994812	-6.25	FALSE
251351_s_a	CaLB protein	NTMC2T4	AT3G60950 /	-1.09	-0.13	-0.76	0.4749349	0.6995522	-6.25	FALSE
248323_at	unknown protein	---	AT5G52770	1.07	0.09	0.76	0.4750097	0.6996172	-6.25	FALSE
265322_at	hypothetical protein predicted by	---	AT2G18270	-1.07	-0.10	-0.76	0.4751562	0.6997685	-6.25	FALSE
257992_at	hypothetical protein similar to hy	---	AT3G19880	-1.12	-0.16	-0.76	0.4751738	0.6997685	-6.25	FALSE
257766_at	auxin-inducible gene (IAA2) iden	IAA2	AT3G23030	-1.15	-0.20	-0.76	0.4754369	0.7000203	-6.25	TRUE
251051_at	putative zinc finger protein zinc f	---	AT5G02460	-1.10	-0.13	-0.76	0.4754332	0.7000203	-6.25	FALSE
251977_at	putative protein auxin-induced p	---	AT3G53250	1.07	0.10	0.76	0.475401	0.7000203	-6.25	FALSE
264399_at	postsynaptic protein CRIPT, put	---	AT1G61780	-1.07	-0.09	-0.76	0.4755924	0.7001783	-6.25	FALSE
254456_at	putative protein ribophorin II pre	HAP6	AT4G21150	-1.11	-0.15	-0.76	0.4756055	0.7001783	-6.25	FALSE
252151_at	putative protein several hypothet	---	AT3G51320	-1.07	-0.10	-0.76	0.4757177	0.7002983	-6.25	FALSE
250846_at	sulphite reductase ; supported b	SIR	AT5G04590	-1.18	-0.23	-0.75	0.4758811	0.700461	-6.25	FALSE
257156_at	hypothetical protein predicted by	---	AT3G24260	-1.08	-0.11	-0.75	0.4758897	0.700461	-6.25	FALSE
246157_at	cytochrome-b5 reductase - like p	---	AT5G20080	1.12	0.16	0.75	0.4760098	0.7005925	-6.25	FALSE
249855_at	unknown protein	---	AT5G22970	1.09	0.12	0.75	0.4760644	0.7006277	-6.25	FALSE
245012_at	NADH dehydrogenase D3	---	---	-1.12	-0.16	-0.75	0.4762044	0.700733	-6.25	FALSE
266276_at	putative tropinone reductase	TRI	AT2G29330	-1.07	-0.10	-0.75	0.4762177	0.700733	-6.25	FALSE
252382_at	ABC-type transport protein-like p	ATH5	AT3G47770	-1.07	-0.10	-0.75	0.4762281	0.700733	-6.25	FALSE
262211_at	AP2 domain containing protein,	ORA47	AT1G74930	1.38	0.46	0.75	0.4763472	0.7008178	-6.25	FALSE

245523_at	drought-induced protein like	ATDI21	AT4G15910	1.13	0.17	0.75	0.4763377	0.7008178	-6.25	FALSE
252379_at	ABC-type transport protein-like p	ATH1	AT3G47730	1.09	0.13	0.75	0.4764726	0.7009077	-6.25	FALSE
252892_at	hypothetical protein	---	AT4G39420	1.08	0.10	0.75	0.4764495	0.7009077	-6.25	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=U372	---	---	-1.08	-0.11	-0.75	0.4765005	0.7009077	-6.25	FALSE
265387_at	unknown protein ;supported by f	---	AT2G20670	1.26	0.33	0.75	0.4765922	0.7009975	-6.25	FALSE
260194_at	hypothetical protein similar to hyp	---	AT1G67530	-1.17	-0.23	-0.75	0.4767705	0.7012145	-6.25	FALSE
261315_at	AP2 domain containing protein,	ERF8	AT1G53170	1.20	0.27	0.75	0.4768776	0.7012364	-6.25	TRUE
260776_at	zinc finger protein, putative simil	---	AT1G14580	-1.23	-0.29	-0.75	0.4768426	0.7012364	-6.25	FALSE
254450_at	putative protein prolamin box bir	---	AT4G21080	1.09	0.12	0.75	0.4768615	0.7012364	-6.25	FALSE
250219_at	putative protein similar to unknov	MPL1	AT5G14180	-1.23	-0.30	-0.75	0.4769419	0.7012857	-6.25	FALSE
261434_at	receptor-like serine/threonine kir	---	AT1G07650	1.14	0.19	0.75	0.4770688	0.701356	-6.25	FALSE
251566_at	putative protein several hypothet	---	AT3G58210	1.07	0.10	0.75	0.4770296	0.701356	-6.25	FALSE
258913_at	unknown protein similar to putat	---	AT3G06450	-1.13	-0.17	-0.75	0.477082	0.701356	-6.25	FALSE
260433_at	MtN21-like protein similar to MtN	---	AT1G68170	-1.10	-0.13	-0.75	0.4773958	0.7017721	-6.25	FALSE
245629_at	hypothetical protein predicted by	---	AT1G56580	-1.12	-0.16	-0.75	0.4779253	0.7019661	-6.25	TRUE
263126_at	hypothetical protein predicted by	---	AT1G78460	-1.33	-0.41	-0.75	0.477737	0.7019661	-6.25	TRUE
263449_at	unknown protein	AtRABA5d	AT2G31670 ///	1.08	0.11	0.75	0.4778544	0.7019661	-6.25	FALSE
247075_at	putative protein contains similarit	PLP3b	AT5G66410	-1.10	-0.14	-0.75	0.4779445	0.7019661	-6.25	FALSE
258924_at	putative diadenosine 5',5'''-P1,P	ATNUDX26	AT3G10620	-1.08	-0.11	-0.75	0.4777683	0.7019661	-6.25	FALSE
249957_at	putative protein predicted protei	---	AT5G18900	-1.11	-0.15	-0.75	0.4778072	0.7019661	-6.25	FALSE
266607_at	hypothetical protein predicted by	---	AT2G46300	1.10	0.14	0.75	0.4779384	0.7019661	-6.25	FALSE
266301_at	putative MYB family transcription	AtMYB81	AT2G26960	1.13	0.18	0.75	0.4777476	0.7019661	-6.25	FALSE
260304_at	unknown protein identical to mos	---	AT1G70480	1.15	0.20	0.75	0.4779382	0.7019661	-6.25	FALSE
255845_at	putative cinnamoyl-CoA reductas	---	AT2G33600	-1.14	-0.19	-0.75	0.4778737	0.7019661	-6.25	FALSE
264145_at	latex-abundant protein, putative	AtMC7	AT1G79310	1.07	0.10	0.75	0.4777971	0.7019661	-6.25	FALSE
246081_s_a	myosin-like protein unconventior	---	AT5G20470 ///	1.14	0.19	0.75	0.4779586	0.7019661	-6.25	FALSE
259894_at	hypothetical protein predicted by	---	AT1G71430	-1.10	-0.14	-0.75	0.4775854	0.7019661	-6.25	FALSE
265616_at	hypothetical protein predicted by	---	AT2G25500	1.07	0.10	0.75	0.4776117	0.7019661	-6.25	FALSE
248888_at	potassium channel protein KAT1	KAT1	AT5G46240	1.24	0.32	0.75	0.4780296	0.7020251	-6.25	FALSE
251058_at	putative protein	---	AT5G01790	1.35	0.43	0.75	0.4783945	0.7020748	-6.25	FALSE
253013_at	heat shock protein 70 like protei	mtHsc70-1	AT4G37910	-1.18	-0.24	-0.75	0.4784266	0.7020748	-6.25	TRUE
252416_at	chromosome assembly protein h	ATSMC2	AT3G47460	1.07	0.09	0.75	0.4782255	0.7020748	-6.25	FALSE
263769_at	5S ribosomal RNA	---	---	1.10	0.14	0.75	0.4783401	0.7020748	-6.25	FALSE
257684_s_a	unknown protein contains Pfam	VCS	AT3G13290 ///	-1.10	-0.14	-0.75	0.4782186	0.7020748	-6.25	FALSE
246358_x_a	hypothetical protein	---	AT2G06570	1.09	0.13	0.75	0.4784219	0.7020748	-6.25	FALSE

264478_at	hypothetical protein predicted by	---	AT1G77270	1.08	0.11	0.75	0.4784327	0.7020748	-6.25	FALSE
246972_s_a	cytochrome P-450-like protein cy	CYP71A14	AT5G24950 /,	-1.20	-0.27	-0.75	0.47825	0.7020748	-6.25	FALSE
245564_at	hypothetical protein	emb2739	AT4G14590	1.10	0.14	0.75	0.4783782	0.7020748	-6.25	FALSE
249437_at	putative protein predicted protein	---	AT5G39990	1.11	0.15	0.75	0.4783306	0.7020748	-6.25	FALSE
253081_at	putative protein F35D11.3, Caen	---	AT4G36210	1.11	0.15	0.75	0.4782886	0.7020748	-6.25	FALSE
244994_at	NADH dehydrogenase ND5	---	---	-1.11	-0.15	-0.75	0.4781169	0.7020748	-6.25	FALSE
254954_at	hypothetical protein ;supported b	---	AT4G10910	-1.27	-0.34	-0.75	0.4786059	0.70226	-6.25	TRUE
261184_at	pol polyprotein, putative similar t	---	---	1.10	0.14	0.75	0.4786205	0.70226	-6.25	FALSE
264033_at	hypothetical protein predicted by	---	AT2G03580	1.10	0.14	0.75	0.4787305	0.7023762	-6.25	FALSE
259201_at	hypothetical protein predicted us	---	AT3G09080	1.13	0.17	0.75	0.4788682	0.702498	-6.25	FALSE
245189_at	F12A21.18 hypothetical protein	---	AT1G67670	1.07	0.10	0.75	0.4788751	0.702498	-6.25	FALSE
249471_at	putative protein predicted protein	EDL2	AT5G39360	1.13	0.17	0.75	0.4789095	0.7025033	-6.25	FALSE
258433_at	translationally controlled tumor p	TCTP	AT3G16640	-1.11	-0.14	-0.75	0.4792305	0.7026667	-6.25	FALSE
249059_at	subtilisin-like serine protease cor	---	AT5G44530	1.15	0.20	0.75	0.4792441	0.7026667	-6.25	FALSE
248310_at	putative protein similar to unknov	CPuORF14	AT5G52550 /,	-1.08	-0.11	-0.75	0.4791767	0.7026667	-6.25	FALSE
246720_at	putative protein predicted protein	---	AT5G28950	1.06	0.09	0.75	0.4791996	0.7026667	-6.25	FALSE
263360_at	unknown protein	---	AT2G03830	-1.09	-0.12	-0.75	0.4792801	0.7026667	-6.25	FALSE
265598_at	putative protein phosphatase 2C	---	AT2G14270	1.09	0.12	0.75	0.4790664	0.7026667	-6.25	FALSE
246648_at	putative protein predicted protein	---	---	1.09	0.12	0.75	0.4792478	0.7026667	-6.25	FALSE
260864_at	hypothetical protein predicted by	---	---	-1.09	-0.13	-0.75	0.4791452	0.7026667	-6.25	FALSE
253211_at	amidase - like protein amidase,	---	AT4G34880	1.08	0.11	0.75	0.4792981	0.7026667	-6.25	FALSE
251301_at	cytochrome p450 (CYP78A9) ;s	CYP78A9	AT3G61880	1.10	0.14	0.75	0.479373	0.7026838	-6.25	FALSE
247305_at	Expressed protein ; supported by	---	AT5G63905	1.26	0.33	0.75	0.4794585	0.7026838	-6.25	FALSE
248052_at	putative protein contains similarit	---	AT5G55800	1.09	0.13	0.75	0.4794947	0.7026838	-6.25	FALSE
265565_at	putative retroelement pol polypro	---	---	1.09	0.12	0.75	0.4794746	0.7026838	-6.25	FALSE
263176_at	UDP-glucose:indole-3-acetate b	UGT75B2	AT1G05530	1.08	0.12	0.75	0.4794867	0.7026838	-6.25	FALSE
253454_at	Expressed protein ; supported by	---	AT4G31875	1.16	0.21	0.75	0.4794505	0.7026838	-6.25	FALSE
260024_at	beta-1,3-glucanase precursor, p	---	AT1G30080	-1.07	-0.10	-0.75	0.4795378	0.7027019	-6.25	FALSE
251017_at	protein phosphatase - like protei	---	AT5G02760	-1.66	-0.73	-0.75	0.4795992	0.7027159	-6.25	TRUE
265308_at	putative protein kinase contains a	ALE2	AT2G20300	-1.07	-0.10	-0.75	0.479609	0.7027159	-6.25	FALSE
257934_at	serine carboxypeptidase, putativ	scpl21	AT3G25420	1.13	0.18	0.75	0.4797759	0.7028732	-6.25	FALSE
254397_at	gibberellin 3 beta-hydroxylase -	GA3OX3	AT4G21690	1.16	0.22	0.75	0.4797779	0.7028732	-6.25	FALSE
259855_at	putative asparaginyl-tRNA synthe	---	AT1G68420	-1.09	-0.12	-0.75	0.4798918	0.7029948	-6.25	FALSE
255314_at	putative transposon protein	---	---	-1.10	-0.14	-0.75	0.4799645	0.7030561	-6.25	FALSE
249559_at	putative protein	---	AT5G38320	-1.13	-0.17	-0.75	0.4800721	0.7031686	-6.25	FALSE

265915_at	En/Spm-like transposon protein r	---	---	-1.08	-0.10	-0.75	0.4801365	0.7032166	-6.25	FALSE
247308_at	receptor-like protein kinase	---	AT5G63930	1.09	0.12	0.75	0.4801665	0.7032166	-6.26	FALSE
266680_s_a	hypothetical protein predicted by	---	AT2G19850 ///	1.07	0.10	0.75	0.4803459	0.703389	-6.26	FALSE
259807_at	hypothetical protein predicted by	---	AT1G47920	1.08	0.11	0.75	0.4803383	0.703389	-6.26	FALSE
265872_at	unknown protein ;supported by f	atnudt17	AT2G01670	-1.13	-0.18	-0.75	0.4804673	0.7035215	-6.26	FALSE
263677_at	unknown protein	PDLP2	AT1G04520	1.09	0.13	0.75	0.480659	0.7037188	-6.26	FALSE
245429_at	Bax inhibitor-1-like protein	---	AT4G17580	1.07	0.10	0.75	0.4806945	0.7037188	-6.26	FALSE
260711_at	myosin, putative similar to myos	MYA1	AT1G17580	-1.10	-0.14	-0.75	0.4806825	0.7037188	-6.26	FALSE
264994_at	hypothetical protein contains sim	---	AT1G67270	1.08	0.11	0.75	0.4807556	0.7037238	-6.26	FALSE
248485_at	calcium-binding transporter-like p	---	AT5G51050	1.13	0.18	0.75	0.4807839	0.7037238	-6.26	FALSE
252258_at	putative protein several hypothet	---	AT3G49450	1.11	0.15	0.75	0.4807905	0.7037238	-6.26	FALSE
267570_at	putative RNA helicase A identica	HVT1	AT2G30800	-1.10	-0.14	-0.75	0.4808372	0.7037469	-6.26	FALSE
255271_at	putative protein (ubiquitin like) to	---	AT4G05260	1.09	0.13	0.75	0.4809537	0.7038724	-6.26	FALSE
255921_at	hypothetical protein contains Pfa	APUM8	AT1G22240	1.09	0.12	0.75	0.4810492	0.703967	-6.26	FALSE
252669_at	putative protein hypothetical pro	---	AT3G44100	-1.09	-0.12	-0.75	0.4810825	0.7039704	-6.26	FALSE
261944_at	unknown protein	---	AT1G64650	-1.12	-0.16	-0.75	0.4811383	0.704007	-6.26	FALSE
264005_at	unknown protein ; supported by	AGP2	AT2G22470	1.59	0.67	0.75	0.4811794	0.7040219	-6.26	FALSE
262227_s_a	26S proteasome ATPase subun	---	AT1G53750 ///	-1.08	-0.11	-0.75	0.4812544	0.7040413	-6.26	FALSE
257850_at	putative protein kinase leucine-ri	SRF4	AT3G13065	-1.08	-0.11	-0.75	0.48123	0.7040413	-6.26	FALSE
255417_at	F-box protein GRR1-like protein	GRH1	AT4G03190	1.39	0.47	0.75	0.4813241	0.7040981	-6.26	FALSE
259473_at	hypothetical protein predicted by	---	AT1G19025	-1.11	-0.15	-0.75	0.4814691	0.7042005	-6.26	FALSE
263417_at	putative C2H2-type zinc finger pr	---	AT2G17180	1.12	0.16	0.74	0.4814866	0.7042005	-6.26	FALSE
258892_at	unknown protein	---	AT3G05670	-1.08	-0.11	-0.75	0.4814454	0.7042005	-6.26	FALSE
250561_at	glycerophosphodiester phospho	---	AT5G08030	-1.11	-0.15	-0.74	0.4815241	0.70421	-6.26	FALSE
258509_at	protein kinase, putative similar t	---	AT3G06620	-1.15	-0.20	-0.74	0.4816144	0.7042861	-6.26	FALSE
261976_at	hypothetical protein predicted by	---	---	-1.10	-0.13	-0.74	0.4816379	0.7042861	-6.26	FALSE
257785_at	geranylgeranylated protein, puta	MUB4	AT3G26980	1.34	0.42	0.74	0.4817813	0.7042981	-6.26	FALSE
265617_at	putative phosphate/phosphoenol	---	AT2G25520	1.17	0.23	0.74	0.481733	0.7042981	-6.26	FALSE
250281_at	putative protein prdeicted protei	---	AT5G13240	-1.12	-0.17	-0.74	0.4818313	0.7042981	-6.26	FALSE
249812_at	putative protein similar to unknov	---	AT5G23830	1.12	0.16	0.74	0.4818194	0.7042981	-6.26	FALSE
252842_at	putative protein hypothetical prot	---	---	-1.10	-0.14	-0.74	0.4817932	0.7042981	-6.26	FALSE
250592_at	putative protein contains similarit	---	AT5G07740	1.10	0.14	0.74	0.4817347	0.7042981	-6.26	FALSE
264246_at	trehalose-6-phosphate synthase	ATTPS10	AT1G60140	1.28	0.36	0.74	0.4818694	0.7043086	-6.26	FALSE
257593_at	phosphatidylinositol transfer pro	---	AT3G24840	1.08	0.11	0.74	0.4819057	0.7043166	-6.26	FALSE
263058_at	putative non-LTR retrolelement r	---	---	1.09	0.12	0.74	0.4820423	0.7044712	-6.26	FALSE

252550_at	putative protein MtN21, Medicag	---	AT3G45870	1.10	0.14	0.74	0.4821468	0.7045787	-6.26	FALSE
255169_x_a	hypothetical protein	---	AT4G07940	-1.08	-0.11	-0.74	0.4823763	0.7048689	-6.26	FALSE
245021_at	PSII component	---	---	-1.11	-0.16	-0.74	0.4826372	0.7052049	-6.26	FALSE
247964_at	profilin-like protein ; supported by	PRF3	AT5G56600	-1.13	-0.18	-0.74	0.4827559	0.7053332	-6.26	FALSE
253719_at	putative protein, fragment prolid	---	AT4G29490	1.07	0.10	0.74	0.4828719	0.7054575	-6.26	FALSE
258119_at	putative MAP kinase similar to G	MPK19	AT3G14720	1.10	0.14	0.74	0.482966	0.7055498	-6.26	FALSE
262981_at	unknown protein ;supported by fu	---	AT1G75590	1.12	0.16	0.74	0.4830124	0.7055724	-6.26	FALSE
246902_at	putative protein	---	AT5G25640	-1.07	-0.10	-0.74	0.4830703	0.7056117	-6.26	FALSE
256564_at	alpha/beta hydrolase, putative c	MES11	AT3G29770	1.23	0.30	0.74	0.4831138	0.7056302	-6.26	FALSE
261590_at	hypothetical protein predicted by	ROPGEF2	AT1G01700	-1.08	-0.11	-0.74	0.4831661	0.7056613	-6.26	FALSE
247907_at	unknown protein	---	AT5G57460	1.08	0.11	0.74	0.4832872	0.7057458	-6.26	FALSE
253299_at	hypothetical protein ;supported b	---	AT4G33800	-1.10	-0.13	-0.74	0.4832709	0.7057458	-6.26	FALSE
255618_at	hypothetical protein	---	AT4G01340	1.07	0.09	0.74	0.4833168	0.7057458	-6.26	FALSE
246062_at	putative protein VAC8 protein, S	---	AT5G19330	1.08	0.11	0.74	0.4833802	0.7057932	-6.26	FALSE
267157_at	putative MYB family transcription	AS1	AT2G37630	-1.14	-0.19	-0.74	0.4834423	0.7057936	-6.26	FALSE
262873_at	hypothetical protein predicted by	---	AT1G64700	-1.09	-0.12	-0.74	0.4834319	0.7057936	-6.26	FALSE
AFFX-r2-Bs	B. subtilis /GEN=thrC /DB_XREF	---	---	-1.20	-0.27	-0.74	0.4835032	0.7058373	-6.26	FALSE
260336_at	putative protease IV similar to pr	SPPA	AT1G73990	1.10	0.14	0.74	0.4835811	0.7059058	-6.26	FALSE
259497_at	unknown protein	---	AT1G15860	1.07	0.10	0.74	0.4837403	0.7059968	-6.26	FALSE
250968_at	putative protein ;supported by fu	---	AT5G02890	1.22	0.28	0.74	0.4837149	0.7059968	-6.26	FALSE
248142_at	putative protein similar to unknov	---	AT5G55040	1.08	0.11	0.74	0.4841073	0.7059968	-6.26	FALSE
257735_at	pectate lyase, putative similar to	---	AT3G27400	1.16	0.21	0.74	0.4839583	0.7059968	-6.26	FALSE
250819_at	putative protein strong similarity t	---	AT5G05100	-1.10	-0.14	-0.74	0.4841077	0.7059968	-6.26	FALSE
244923_s_a	orf153b orf153b	---	AT2G07674	1.15	0.20	0.74	0.4839547	0.7059968	-6.26	FALSE
263139_at	hypothetical protein similar to hyp	---	AT1G65110	1.07	0.10	0.74	0.4837693	0.7059968	-6.26	FALSE
251147_at	kinesin heavy chain - like protein	---	AT3G63480	1.09	0.12	0.74	0.4839607	0.7059968	-6.26	FALSE
246065_at	calcium-dependent protein kinas	CPK34	AT5G19360	1.09	0.12	0.74	0.4838457	0.7059968	-6.26	FALSE
263308_at	hypothetical protein predicted by	---	---	1.08	0.11	0.74	0.4839636	0.7059968	-6.26	FALSE
252003_at	hypothetical protein emm32, Str	ZPR3	AT3G52770	1.08	0.12	0.74	0.4839003	0.7059968	-6.26	FALSE
249749_at	unknown protein	BIN4	AT5G24630	1.10	0.14	0.74	0.4840582	0.7059968	-6.26	FALSE
AFFX-ThrX	B. subtilis /GEN=thrB /DB_XREF	---	---	-1.15	-0.21	-0.74	0.4840726	0.7059968	-6.26	FALSE
248017_at	protein kinase-like protein	---	AT5G56460	1.15	0.20	0.74	0.4840289	0.7059968	-6.26	FALSE
249132_at	putative protein contains similarit	---	AT5G43120	-1.09	-0.13	-0.74	0.483725	0.7059968	-6.26	FALSE
264148_at	NAM (no apical meristem)-like p	ANAC003	AT1G02220	2.01	1.01	0.74	0.4842015	0.7060092	-6.26	FALSE
246615_at	putative protein similar to unknov	---	---	1.09	0.13	0.74	0.48424	0.7060092	-6.26	FALSE

265127_at	hypothetical protein similar to pol	sks14	AT1G55560	-1.08	-0.11	-0.74	0.4841769	0.7060092	-6.26	FALSE
262842_at	xyloglucan endo-transglycosylas	XTR2	AT1G14720	-1.19	-0.25	-0.74	0.4842313	0.7060092	-6.26	FALSE
251466_at	putative protein hypothetical pro	---	AT3G59340	1.10	0.14	0.74	0.4843321	0.7060307	-6.26	FALSE
260080_at	putative RNA-binding protein co	APUM7	AT1G78160	1.07	0.10	0.74	0.4843131	0.7060307	-6.26	FALSE
267086_at	putative salt-inducible protein	---	AT2G32630	-1.11	-0.15	-0.74	0.4843476	0.7060307	-6.26	FALSE
251648_at	protein kinase - like protein S-re	---	AT3G57720	1.12	0.16	0.74	0.4844397	0.7061198	-6.26	FALSE
245089_at	putative transketolase precursor	---	AT2G45290	1.48	0.57	0.74	0.4847546	0.7065337	-6.26	FALSE
248175_at	histone H2A (gb|AAF64418.1) ;	RAT5	AT5G54640	-1.09	-0.13	-0.74	0.4848159	0.7065778	-6.26	FALSE
251362_at	DEAD box RNA helicase RH12	---	AT3G61240	-1.09	-0.12	-0.74	0.485185	0.7070707	-6.26	FALSE
265922_at	putative sugar transporter	---	AT2G18480	1.08	0.11	0.74	0.4853104	0.7071179	-6.26	FALSE
267495_at	myb-like protein isolog	ETC2	AT2G30420	-1.18	-0.24	-0.74	0.4852625	0.7071179	-6.26	FALSE
252666_at	putative protein hypothetical prot	---	AT3G44180	1.09	0.13	0.74	0.4852847	0.7071179	-6.26	FALSE
262438_at	hypothetical protein identical to h	---	AT1G47410	-1.17	-0.23	-0.74	0.4853958	0.7071971	-6.26	FALSE
259031_at	putative transcription factor simil	---	AT3G09360	-1.12	-0.16	-0.74	0.4854501	0.7072111	-6.26	FALSE
257360_at	unknown protein	---	AT2G39240	1.08	0.11	0.74	0.4854917	0.7072111	-6.26	FALSE
267334_at	hypothetical protein predicted by	---	AT2G19420	1.09	0.13	0.74	0.4854984	0.7072111	-6.26	FALSE
245475_at	hypothetical protein	---	AT4G16080	1.08	0.11	0.74	0.4856558	0.7073953	-6.26	FALSE
257347_at	pseudogene, gene_id:K17E7.6	---	---	1.07	0.10	0.74	0.485706	0.7073979	-6.26	FALSE
247803_at	similar to unknown protein (gb|A	---	AT5G58340	1.07	0.09	0.74	0.4857233	0.7073979	-6.26	FALSE
265528_at	hypothetical protein predicted by	---	---	1.07	0.09	0.74	0.4857507	0.7073979	-6.26	FALSE
253165_at	putative protein predicted protei	---	AT4G35320	1.20	0.27	0.74	0.4857932	0.7073994	-6.26	TRUE
245170_at	60S ribosomal protein L18, 5'pa	---	AT2G47570	1.09	0.12	0.74	0.4858551	0.7073994	-6.26	FALSE
260285_at	putative 3-isopropylmalate dehyd	---	AT1G80560	-1.11	-0.15	-0.74	0.4858758	0.7073994	-6.26	FALSE
263481_at	predicted protein	---	AT2G04025	1.07	0.10	0.74	0.4858686	0.7073994	-6.26	FALSE
253601_at	hypothetical protein	---	AT4G30900	-1.07	-0.10	-0.74	0.4859145	0.7074106	-6.26	FALSE
246589_at	glucosyltransferase -like protein	---	AT5G14860	1.08	0.12	0.74	0.4859945	0.7074819	-6.26	FALSE
254809_at	putative protein auxin-induced p	---	AT4G12410	1.13	0.18	0.74	0.4860469	0.707513	-6.26	FALSE
250227_at	FtsJ (dbj|BAA83750.1)	---	AT5G13830	1.10	0.14	0.74	0.4861294	0.707588	-6.26	FALSE
256133_at	hypothetical protein predicted by	---	AT1G13570	-1.16	-0.21	-0.74	0.4861846	0.7076232	-6.26	FALSE
257576_at	hypothetical protein predicted by	---	AT3G28280	1.09	0.12	0.74	0.4862242	0.7076357	-6.26	FALSE
256352_at	proline-rich protein, putative sim	ATPRP1	AT1G54970	1.11	0.15	0.74	0.486331	0.7077459	-6.26	FALSE
255852_at	unknown protein	SVL2	AT1G66970	1.26	0.33	0.74	0.4865251	0.7079833	-6.26	FALSE
260888_at	hypothetical protein similar to alle	---	AT1G29140	1.08	0.11	0.74	0.4865826	0.7080218	-6.26	FALSE
254391_at	putative bifunctional nuclease bi	ENDO3	AT4G21590	1.08	0.11	0.74	0.4871121	0.7087471	-6.26	FALSE
266593_at	hypothetical protein predicted by	---	AT2G46200	-1.09	-0.12	-0.73	0.4871782	0.708798	-6.26	FALSE

251333_at	putative protein putative protein	---	AT3G61690	-1.07	-0.09	-0.73	0.4872564	0.7088666	-6.26	FALSE
251487_at	cysteine synthase	OASC	AT3G59760	1.18	0.24	0.73	0.4873998	0.708956	-6.26	FALSE
252221_at	RuvB DNA helicase - like protein	---	AT3G49830	1.09	0.13	0.73	0.4874111	0.708956	-6.26	FALSE
261237_at	hypothetical protein contains sim	---	AT1G32980	1.08	0.12	0.73	0.4873602	0.708956	-6.26	FALSE
252088_at	putative protein	---	AT3G52100 /	-1.11	-0.15	-0.73	0.4875032	0.7090447	-6.26	FALSE
264494_at	hypothetical protein predicted by	---	AT1G27461	1.13	0.17	0.73	0.487578	0.7091082	-6.27	FALSE
261883_at	protein kinase, putative similar t	---	AT1G80870	-1.09	-0.13	-0.73	0.4877518	0.7092122	-6.27	FALSE
263256_at	unknown protein similar to ESTs	ATCPISCA	AT1G10500	1.11	0.16	0.73	0.4877925	0.7092122	-6.27	FALSE
257493_at	unknown protein	---	AT1G48180	1.14	0.19	0.73	0.4878049	0.7092122	-6.27	FALSE
246375_at	light repressible receptor protein	---	AT1G51830	-1.13	-0.17	-0.73	0.4877769	0.7092122	-6.27	FALSE
264369_at	Ste-20 related kinase SPAK, put	---	AT1G70430	1.09	0.12	0.73	0.4877661	0.7092122	-6.27	FALSE
256463_s_a	unknown protein	---	---	1.08	0.12	0.73	0.4879041	0.7093111	-6.27	FALSE
261823_at	hypothetical protein predicted by	PYM	AT1G11400	1.09	0.12	0.73	0.4879781	0.7093735	-6.27	FALSE
246887_at	hexose transporter - like protein	---	AT5G26250	1.09	0.12	0.73	0.4880709	0.7093774	-6.27	FALSE
255410_at	putative rac GTPase activating p	---	AT4G03100	-1.09	-0.12	-0.73	0.4880696	0.7093774	-6.27	FALSE
267097_at	unknown protein predicted by ge	---	AT2G41440	1.07	0.10	0.73	0.488074	0.7093774	-6.27	FALSE
254880_at	putative protein Crp1, Zea mays	---	AT4G11690	1.11	0.15	0.73	0.4881162	0.7093935	-6.27	FALSE
261581_at	serine/threonine kinase, putative	CIPK9	AT1G01140	-1.12	-0.17	-0.73	0.488156	0.7094061	-6.27	FALSE
266831_at	putative squalene epoxidase	SQE2	AT2G22830	-1.28	-0.36	-0.73	0.48851	0.7098301	-6.27	TRUE
260166_at	homeobox protein (GLABRA2) id	GL2	AT1G79840	1.07	0.10	0.73	0.488508	0.7098301	-6.27	FALSE
255005_at	putative protein putative proteins	---	AT4G09990	1.10	0.13	0.73	0.4886593	0.7099113	-6.27	FALSE
255570_at	putative carrier protein similar to	ADNT1	AT4G01100	-1.09	-0.13	-0.73	0.4886305	0.7099113	-6.27	FALSE
258944_at	hypothetical protein similar to hy	FLD	AT3G10390	1.11	0.15	0.73	0.488614	0.7099113	-6.27	FALSE
258568_at	unknown protein contains Pfam p	---	AT3G04470	-1.09	-0.12	-0.73	0.4887322	0.7099275	-6.27	FALSE
253486_at	putative protein KIAA0260 gene	---	AT4G31600	-1.09	-0.12	-0.73	0.4887327	0.7099275	-6.27	FALSE
247416_at	40S ribosomal protein S15-like p	---	AT5G63070	1.10	0.13	0.73	0.4888399	0.7100381	-6.27	FALSE
253255_at	putative auxin-regulated protein	---	AT4G34760	-1.38	-0.47	-0.73	0.4889725	0.7101479	-6.27	TRUE
260300_at	gibberellin 3 beta-hydroxylase id	GA3OX2	AT1G80340	-1.15	-0.21	-0.73	0.4889778	0.7101479	-6.27	FALSE
245194_at	F12A21.5 similar to protein phos	---	AT1G67820	-1.16	-0.22	-0.73	0.4891203	0.7103041	-6.27	FALSE
258294_at	hypothetical protein predicted by	---	AT3G23350	1.08	0.12	0.73	0.4892631	0.7103041	-6.27	FALSE
265166_at	putative OBP32pep protein	---	AT1G23640	-1.07	-0.10	-0.73	0.4892722	0.7103041	-6.27	FALSE
247019_at	AP2 domain transcription factor-l	---	AT5G67010	1.09	0.12	0.73	0.4891886	0.7103041	-6.27	FALSE
251963_at	protein kinase (AME2/AFC1) ; s	AFC1	AT3G53570	-1.08	-0.11	-0.73	0.4892518	0.7103041	-6.27	FALSE
263447_s_a	putative PHD-type zinc finger pro	ATX2	AT1G05830 /	1.19	0.25	0.73	0.4891585	0.7103041	-6.27	FALSE
246810_at	putative protein many predicted	---	---	1.08	0.11	0.73	0.4893282	0.7103402	-6.27	FALSE

257303_at	hypothetical protein predicted by	---	AT3G30230	1.08	0.12	0.73	0.4893913	0.7103866	-6.27	FALSE
261334_at	unknown protein	---	AT1G44960	1.09	0.12	0.73	0.4894959	0.7103898	-6.27	FALSE
252012_at	ubiquinol--cytochrome-c reducta	---	AT3G52730	-1.08	-0.11	-0.73	0.4895181	0.7103898	-6.27	FALSE
255448_at	hypothetical protein	---	AT4G02810	1.11	0.15	0.73	0.4894568	0.7103898	-6.27	FALSE
247774_at	putative protein fruit ripening exp	---	AT5G58660	1.08	0.11	0.73	0.4894483	0.7103898	-6.27	FALSE
253519_at	predicted protein red-1 gene, M.	---	AT4G31240	-1.18	-0.24	-0.73	0.4897278	0.7106037	-6.27	TRUE
263397_s_a	putative GDSL-motif lipase/hydro	---	AT2G31540 //	1.06	0.09	0.73	0.489703	0.7106037	-6.27	FALSE
260812_at	nodulin-like protein similar to Mt	---	AT1G43650	-1.15	-0.20	-0.73	0.4898859	0.7107879	-6.27	TRUE
248496_at	MtN3-like protein ;supported by	---	AT5G50790	1.11	0.14	0.73	0.4899513	0.7107945	-6.27	FALSE
251844_at	putative protein retinoblastoma-a	---	AT3G54630	1.10	0.13	0.73	0.4899527	0.7107945	-6.27	FALSE
266987_at	unknown protein	---	AT2G39280	-1.07	-0.10	-0.73	0.4900833	0.7109387	-6.27	FALSE
246380_at	cytochrome P450, putative simil	CYP96A15	AT1G57750	1.12	0.17	0.73	0.4901256	0.7109548	-6.27	FALSE
248863_at	zinc finger protein Glo3-like	AGD9	AT5G46750	-1.07	-0.10	-0.73	0.4901666	0.7109692	-6.27	FALSE
261513_at	unknown protein contains Pfam	---	AT1G71840	-1.10	-0.13	-0.73	0.4902124	0.7109903	-6.27	FALSE
266588_at	putative proline-rich protein ; sup	AGP9	AT2G14890	1.55	0.63	0.73	0.4902807	0.7110442	-6.27	FALSE
252650_at	putative protein	---	AT3G44690	-1.08	-0.11	-0.73	0.49038	0.7110525	-6.27	FALSE
257694_at	nucleolar protein, putative nucle	---	AT3G12860	-1.08	-0.11	-0.73	0.4903307	0.7110525	-6.27	FALSE
252388_at	putative protein ;supported by fu	---	AT3G47850	-1.09	-0.13	-0.73	0.4903694	0.7110525	-6.27	FALSE
249868_at	senescence-associated protein 5	TET12	AT5G23030	1.09	0.12	0.73	0.4904168	0.7110607	-6.27	FALSE
259936_at	putative UDP-glucose:glycoprote	EBS1	AT1G71220	-1.08	-0.11	-0.73	0.4906445	0.7113457	-6.27	FALSE
252257_at	putative protein several hypothet	---	AT3G49440	1.07	0.10	0.73	0.4907186	0.7113791	-6.27	FALSE
248993_at	putative protein contains similarit	---	AT5G45240	1.09	0.12	0.73	0.4907611	0.7113791	-6.27	FALSE
255316_at	putative protein	---	---	1.07	0.10	0.73	0.4907398	0.7113791	-6.27	FALSE
246741_at	glycine rich protein - like glycine	emb1644	AT5G27720	-1.10	-0.14	-0.73	0.4909477	0.7116043	-6.27	FALSE
267539_at	putative RING zinc finger protein	---	AT2G42030	-1.10	-0.13	-0.73	0.4910996	0.7116556	-6.27	FALSE
248637_at	DNAJ-like protein	---	AT5G49060	-1.08	-0.11	-0.73	0.4911079	0.7116556	-6.27	FALSE
262355_at	unknown protein	---	AT1G72820	-1.12	-0.16	-0.73	0.491055	0.7116556	-6.27	FALSE
251558_at	putative protein ;supported by fu	---	AT3G57810	-1.17	-0.22	-0.73	0.4910815	0.7116556	-6.27	FALSE
256490_at	unknown protein ;supported by fu	---	AT1G31460	-1.12	-0.17	-0.73	0.491257	0.7118265	-6.27	FALSE
257448_s_a	putative protein various predicted	---	AT2G11620 //	1.08	0.12	0.73	0.4913477	0.7119127	-6.27	FALSE
252247_at	putative protein various predicted	---	AT3G49740	-1.08	-0.11	-0.73	0.4915213	0.712119	-6.27	FALSE
259832_at	transfactor, putative similar to G	---	AT1G69580	1.23	0.30	0.73	0.4916503	0.7121702	-6.27	FALSE
250556_at	diacylglycerol kinase (ATDGK1)	DGK1	AT5G07920	1.19	0.25	0.73	0.4916311	0.7121702	-6.27	FALSE
256004_at	retroelement pol polyprotein, put	---	---	-1.07	-0.10	-0.73	0.4916016	0.7121702	-6.27	FALSE
258799_at	putative 40S ribosomal protein id	RPSAb	AT3G04770	-1.12	-0.16	-0.73	0.4917753	0.712306	-6.27	FALSE

249163_at	glucose-6-phosphate isomerase	---	AT5G42740	1.12	0.16	0.73	0.4921756	0.7128405	-6.27	FALSE
259169_at	unknown protein similar to unkno	---	AT3G03520	-1.29	-0.37	-0.73	0.4922585	0.7129154	-6.27	FALSE
261366_at	unknown protein	---	AT1G53100	1.25	0.32	0.73	0.492388	0.7129218	-6.27	TRUE
261041_at	hypothetical protein contains sim	EER4	AT1G17440	-1.09	-0.12	-0.73	0.4923421	0.7129218	-6.27	FALSE
254096_at	acid phosphatase - like protein a	---	AT4G25150	1.09	0.13	0.73	0.4923643	0.7129218	-6.27	FALSE
250230_at	putative protein similar to unknov	---	AT5G13900	1.15	0.20	0.73	0.4923273	0.7129218	-6.27	FALSE
257712_at	hypothetical protein predicted by	---	AT3G27420	1.07	0.09	0.73	0.4926923	0.7130379	-6.27	FALSE
258496_at	putative plant adhesion molecule	---	AT3G02460	1.13	0.17	0.73	0.4926597	0.7130379	-6.27	FALSE
261533_at	hypothetical protein predicted by	---	AT1G71690	1.11	0.15	0.73	0.4925748	0.7130379	-6.27	FALSE
256750_at	unknown protein contains Pfam p	---	AT3G27150	1.11	0.15	0.73	0.4927172	0.7130379	-6.27	FALSE
264049_at	putative GTP-binding protein	---	AT2G22390	-1.13	-0.17	-0.73	0.4927033	0.7130379	-6.27	FALSE
254039_at	putative protein Human GS1 (pr	GPP1	AT4G25840	-1.11	-0.15	-0.73	0.4925552	0.7130379	-6.27	FALSE
264715_at	hypothetical protein contains sim	---	AT1G70180	1.09	0.12	0.73	0.4927183	0.7130379	-6.27	FALSE
257523_at	hypothetical protein similar to pu	---	AT3G01620	1.08	0.11	0.73	0.4926514	0.7130379	-6.27	FALSE
246853_at	putative protein	---	AT5G26890	1.08	0.11	0.73	0.4928231	0.7131443	-6.27	FALSE
247531_at	putative protein protein kinase 1	---	AT5G61550	1.10	0.13	0.72	0.4929547	0.7132896	-6.27	FALSE
246177_at	putative protein predicted protein	---	AT5G28420	1.07	0.10	0.72	0.4931067	0.7134219	-6.27	FALSE
248600_at	putative protein contains similarit	---	AT5G49390	-1.10	-0.13	-0.72	0.4931087	0.7134219	-6.27	FALSE
265153_at	unusual floral organ (UFO), AtF	UFO	AT1G30950	-1.09	-0.13	-0.72	0.4932507	0.7135368	-6.27	FALSE
258450_at	hypothetical protein predicted by	---	---	1.08	0.12	0.72	0.4932309	0.7135368	-6.27	FALSE
266066_at	putative xyloglucan endo-transgl	XTH21	AT2G18800	1.12	0.16	0.72	0.4934872	0.7137885	-6.27	FALSE
248986_at	putative protein similar to unknov	---	AT5G45170	-1.11	-0.15	-0.72	0.49347	0.7137885	-6.27	FALSE
245669_at	hypothetical protein contains sim	LEC2	AT1G28300	1.10	0.14	0.72	0.493567	0.7138586	-6.27	FALSE
258436_at	putative RING zinc finger protein	ATL2	AT3G16720	1.26	0.33	0.72	0.4936636	0.7139529	-6.27	FALSE
258221_at	Snf1-related protein kinase KIN1	AKIN11	AT3G29160	-1.16	-0.21	-0.72	0.4937479	0.7140296	-6.27	FALSE
245927_at	sterol glucosyltransferase - like p	---	AT5G24750	1.06	0.09	0.72	0.4938652	0.7141088	-6.27	FALSE
252865_at	Expressed protein ; supported by	---	AT4G39753	1.12	0.16	0.72	0.4938552	0.7141088	-6.27	FALSE
265611_at	unknown protein ;supported by f	---	AT2G25510	1.16	0.22	0.72	0.4940158	0.7142812	-6.27	FALSE
254829_at	AIR1A-like protein putative cell v	---	AT4G12530	1.08	0.11	0.72	0.4940492	0.7142842	-6.27	FALSE
263379_at	putative CCCH-type zinc finger p	CZF1	AT2G40140	1.40	0.49	0.72	0.4941396	0.7143697	-6.27	FALSE
251343_at	phosphatidate cytidylyltransferas	---	AT3G60620	-1.16	-0.22	-0.72	0.4942891	0.7145405	-6.27	FALSE
252563_at	putative protein cim1 induced all	ATEXLA1	AT3G45970	1.29	0.37	0.72	0.4943449	0.7145758	-6.27	TRUE
261504_at	MADS-box protein identical to G	AGL12	AT1G71692	-1.11	-0.15	-0.72	0.4943914	0.7145978	-6.27	FALSE
253478_at	putative protein trichohyalin - hu	---	AT4G32350	-1.15	-0.20	-0.72	0.4946663	0.7149499	-6.27	TRUE
254421_at	VP1 like protein transcription act	VAL3	AT4G21550	-1.13	-0.17	-0.72	0.4949199	0.7150899	-6.27	FALSE

251054_at	receptor like protein kinase rece	LECRKA4.1	AT5G01540	1.47	0.55	0.72	0.4949017	0.7150899	-6.27	FALSE
245667_at	FH protein interacting protein FIF	FIP1	AT1G28200	-1.08	-0.11	-0.72	0.4948809	0.7150899	-6.27	FALSE
254823_at	putative protein predicted protein	---	AT4G12580	-1.07	-0.10	-0.72	0.4948557	0.7150899	-6.27	FALSE
245948_at	putative protein ;supported by fu	---	AT5G19540	1.13	0.17	0.72	0.4949088	0.7150899	-6.27	FALSE
266357_at	putative beta-amylase	BAM6	AT2G32290	-1.27	-0.34	-0.72	0.4949729	0.7151211	-6.27	FALSE
245186_at	F12A21.15 hypothetical protein	ARR11	AT1G67710	1.21	0.27	0.72	0.4951128	0.715278	-6.28	FALSE
259645_at	putative DNA-binding protein pre	BIM2	AT1G69010	-1.12	-0.16	-0.72	0.4954397	0.7154647	-6.28	TRUE
256380_at	pheromone receptor, putative (A	AR401	AT1G66680	-1.10	-0.14	-0.72	0.495304	0.7154647	-6.28	FALSE
253746_at	putative protein hypothetical pro	---	AT4G29100	1.18	0.24	0.72	0.4953541	0.7154647	-6.28	FALSE
245638_s_a	F5A9.10 unknown protein; simila	---	AT1G24822 ///	1.09	0.12	0.72	0.495444	0.7154647	-6.28	FALSE
253128_at	Calcium-dependent serine/threo	CPK18	AT4G36070	1.07	0.10	0.72	0.4955171	0.7154647	-6.28	FALSE
252745_at	putative protein Sh3yl1 mRNA, I	---	AT3G43230	1.09	0.12	0.72	0.4955244	0.7154647	-6.28	FALSE
265003_at	protein kinase, putative similar t	---	AT1G26970	1.06	0.09	0.72	0.495458	0.7154647	-6.28	FALSE
267480_at	putative retroelement pol polypro	---	---	-1.07	-0.10	-0.72	0.4954658	0.7154647	-6.28	FALSE
253007_at	putative protein hypothetical pro	---	AT4G38090	-1.10	-0.14	-0.72	0.4954273	0.7154647	-6.28	FALSE
263560_s_a	unknown protein	FUT5	AT2G15350 ///	-1.09	-0.13	-0.72	0.4956854	0.7155159	-6.28	FALSE
253884_at	heat shock protein 21	HSP21	AT4G27670	1.10	0.13	0.72	0.4956814	0.7155159	-6.28	FALSE
255648_at	coded for by A. thaliana cDNA T2	---	AT4G00910	-1.07	-0.10	-0.72	0.495644	0.7155159	-6.28	FALSE
262276_at	hypothetical protein predicted by	---	AT1G68700	1.09	0.12	0.72	0.495631	0.7155159	-6.28	FALSE
265746_at	hypothetical protein predicted by	---	---	-1.08	-0.12	-0.72	0.4957254	0.7155284	-6.28	FALSE
245906_at	putative protein ;supported by fu	---	AT5G11070	1.21	0.27	0.72	0.4958472	0.715659	-6.28	TRUE
260934_at	hypothetical protein predicted by	---	AT1G45100	-1.07	-0.09	-0.72	0.4959387	0.7157299	-6.28	FALSE
259459_at	En/Spm-like transposon protein,	---	---	1.08	0.11	0.72	0.4959591	0.7157299	-6.28	FALSE
261182_at	hypothetical protein predicted by	---	AT1G34575	-1.07	-0.10	-0.72	0.4961668	0.7159391	-6.28	FALSE
265380_at	putative retroelement pol polypro	---	---	1.08	0.12	0.72	0.4961423	0.7159391	-6.28	FALSE
267433_at	putative peroxisome assembly pr	PEX10	AT2G26350	-1.09	-0.12	-0.72	0.4962428	0.7159638	-6.28	FALSE
254297_at	hypothetical protein	---	AT4G23110	-1.07	-0.10	-0.72	0.4962467	0.7159638	-6.28	FALSE
266176_at	lectin-like protein	AtPP2-B2	AT2G02250	1.12	0.16	0.72	0.4963342	0.7160447	-6.28	FALSE
267041_at	unknown protein	---	AT2G34315	1.07	0.09	0.72	0.496386	0.7160722	-6.28	FALSE
262519_at	putative ribokinase Except for fir	---	AT1G17160	1.14	0.19	0.72	0.496416	0.7160722	-6.28	FALSE
253466_at	homeodomain containing protein	KNAT5	AT4G32040	-1.10	-0.14	-0.72	0.4964664	0.7160996	-6.28	FALSE
252311_at	calcium dependent protein kinas	---	AT3G49370	1.21	0.28	0.72	0.4965154	0.7161249	-6.28	FALSE
245655_at	hypothetical protein predicted by	---	AT1G56530	1.07	0.10	0.72	0.4965716	0.7161608	-6.28	FALSE
259688_at	membrane protein, putative simi	ATRBL2	AT1G63120	-1.13	-0.18	-0.72	0.4966744	0.716216	-6.28	FALSE
264668_at	putative 2,3-bisphosphoglycerat	---	AT1G09780	-1.11	-0.15	-0.72	0.4966614	0.716216	-6.28	FALSE

246306_at	putative protein hypothetical pro	ATBAG4	AT3G51780	-1.06	-0.09	-0.72	0.4967041	0.716216	-6.28	FALSE
248423_at	putative protein contains similarit	---	AT5G51670	-1.14	-0.18	-0.72	0.4967677	0.7162625	-6.28	FALSE
250933_at	arabinogalactan protein - like ara	FLA11	AT5G03170	-1.20	-0.27	-0.72	0.4968151	0.7162855	-6.28	FALSE
249659_s_a	putative protein similar to unknov	---	AT5G36710 ///	-1.11	-0.16	-0.72	0.4969375	0.7163714	-6.28	FALSE
249547_at	lipid transfer - like protein P48h-	---	AT5G38160	1.11	0.15	0.72	0.4969137	0.7163714	-6.28	FALSE
253425_at	putative protein myosin heavy ch	---	AT4G32190	-1.15	-0.20	-0.72	0.4970829	0.7164101	-6.28	FALSE
256295_at	hypothetical protein	---	AT1G69470	1.08	0.11	0.72	0.4970788	0.7164101	-6.28	FALSE
249663_s_a	unknown protein	---	---	1.10	0.14	0.72	0.49709	0.7164101	-6.28	FALSE
244987_s_a	ribosomal protein L2	---	---	-1.07	-0.09	-0.72	0.497025	0.7164101	-6.28	FALSE
245951_at	aspartate aminotransferase Asp2	ASP2	AT5G19550	1.15	0.21	0.72	0.497268	0.7165308	-6.28	FALSE
266855_at	unknown protein	---	AT2G26920	1.10	0.13	0.72	0.497217	0.7165308	-6.28	FALSE
262626_at	FtsH protease, putative similar to	FTSH8	AT1G06430	-1.11	-0.15	-0.72	0.4972602	0.7165308	-6.28	FALSE
254495_at	hypothetical protein	EMB1895	AT4G20060	-1.13	-0.18	-0.72	0.4973198	0.7165602	-6.28	FALSE
264871_at	pyruvate dehydrogenase E1 alph	IAR4	AT1G24180	1.15	0.21	0.72	0.4973864	0.716584	-6.28	FALSE
261738_s_a	hypothetical protein identical to h	---	AT1G47813 ///	-1.14	-0.19	-0.72	0.4973991	0.716584	-6.28	FALSE
250892_at	putative protein beta-(1-3)-gluco	ATCSLA09	AT5G03760	1.74	0.80	0.72	0.4975137	0.7166564	-6.28	TRUE
253833_at	putative calcium binding protein	---	AT4G27790	-1.14	-0.19	-0.72	0.4975559	0.7166564	-6.28	FALSE
260282_at	putative N-terminal acetyltransfer	EMB2753	AT1G80410	-1.08	-0.11	-0.72	0.4975222	0.7166564	-6.28	FALSE
265783_at	putative Athila retroelement ORF	---	---	1.10	0.13	0.72	0.4975751	0.7166564	-6.28	FALSE
267243_at	hypothetical protein predicted by	---	AT2G02660	-1.07	-0.09	-0.72	0.497632	0.7166932	-6.28	FALSE
255427_at	hypothetical protein	---	AT4G03380	-1.06	-0.09	-0.72	0.4977018	0.7167484	-6.28	FALSE
246553_at	putative protein hypothetical pro	EDL1	AT5G15440	-1.09	-0.13	-0.72	0.4977499	0.7167724	-6.28	FALSE
260893_at	hypothetical protein similar to hyp	---	AT1G29180	1.08	0.11	0.72	0.4978255	0.7168361	-6.28	FALSE
245962_at	putative protein predicted protein	---	AT5G19700	1.09	0.12	0.72	0.4979464	0.7169649	-6.28	FALSE
252100_at	crooked neck-like protein crooke	---	AT3G51110	-1.16	-0.21	-0.72	0.4979901	0.7169826	-6.28	FALSE
254726_at	isoflavone reductase-like protein	PRR2	AT4G13660	1.22	0.29	0.72	0.4980617	0.7170404	-6.28	TRUE
245435_at	hypothetical protein	AT4G17140	---	-1.07	-0.09	-0.72	0.4983364	0.7173906	-6.28	FALSE
262191_at	hypothetical protein contains sim	---	---	1.09	0.12	0.72	0.4983735	0.7173987	-6.28	FALSE
257968_at	hypothetical protein predicted by	---	AT3G27550	-1.13	-0.18	-0.72	0.4985044	0.7175418	-6.28	FALSE
264647_at	putative respiratory burst oxidase	ATRBOHB	AT1G09090	1.09	0.13	0.72	0.4985887	0.7176179	-6.28	FALSE
266567_at	putative eukaryotic initiation fact	---	AT2G24050	-1.12	-0.17	-0.71	0.4986725	0.7176932	-6.28	FALSE
257343_s_a	pseudogene, polyprotein similar	---	---	1.06	0.09	0.71	0.4987867	0.7178122	-6.28	FALSE
245947_at	spermine synthase (ACL5) ;supp	ACL5	AT5G19530	-1.15	-0.20	-0.71	0.4989688	0.7179735	-6.28	TRUE
257029_at	dem-like protein similar to dem	---	AT3G19240	-1.08	-0.12	-0.71	0.4989931	0.7179735	-6.28	FALSE
258692_at	unknown protein	---	AT3G08640	1.16	0.21	0.71	0.4989531	0.7179735	-6.28	FALSE

252950_at	putative protein phospholipase C	---	AT4G38690	-1.20	-0.26	-0.71	0.499191	0.7181905	-6.28	TRUE
266920_at	hypothetical protein predicted by	---	AT2G45750	1.10	0.13	0.71	0.4992069	0.7181905	-6.28	FALSE
261779_at	hypothetical protein predicted by	---	AT1G76230	-1.07	-0.09	-0.71	0.4993404	0.7183372	-6.28	FALSE
254846_at	Expressed protein ; supported by	PLDGAMM	AT4G11830	-1.11	-0.14	-0.71	0.4994216	0.7183455	-6.28	FALSE
253805_at	putative protein	---	AT4G28260	-1.10	-0.14	-0.71	0.4994407	0.7183455	-6.28	FALSE
249364_at	putative protein predicted protei	---	AT5G40590	1.08	0.11	0.71	0.4994318	0.7183455	-6.28	FALSE
260021_at	unknown protein	---	AT1G30010	1.15	0.20	0.71	0.4994793	0.7183558	-6.28	FALSE
255470_at	hypothetical protein	---	AT4G03040	1.09	0.13	0.71	0.4995319	0.7183861	-6.28	FALSE
254808_at	adenine DNA glycosylase like pr	---	AT4G12740	1.07	0.10	0.71	0.4996662	0.718534	-6.28	FALSE
259271_at	Expressed protein ; supported by	---	AT3G01170	1.09	0.13	0.71	0.4998092	0.7186943	-6.28	FALSE
260246_at	hypothetical protein similar to GB	---	AT1G74220	1.08	0.11	0.71	0.4998568	0.7187175	-6.28	FALSE
247282_at	putative protein strong similarity t	AtMC3	AT5G64240	1.09	0.13	0.71	0.499926	0.7187182	-6.28	FALSE
265208_at	putative giberellin beta-hydroxyla	---	AT2G36690	1.25	0.33	0.71	0.4999295	0.7187182	-6.28	FALSE
251112_s_a	pyruvate decarboxylase-like pro	PDC3	AT5G01320 ///	-1.12	-0.17	-0.71	0.4999519	0.7187182	-6.28	FALSE
255445_at	hypothetical protein	---	AT4G02740	1.09	0.13	0.71	0.5000067	0.71873	-6.28	FALSE
258310_at	unknown protein	ICE1	AT3G26744	-1.09	-0.12	-0.71	0.5000546	0.71873	-6.28	FALSE
263175_at	hypothetical protein similar to unl	---	AT1G05510	1.07	0.10	0.71	0.5000248	0.71873	-6.28	FALSE
259888_at	hypothetical protein similar to no	---	AT1G76350	-1.24	-0.30	-0.71	0.5001536	0.718827	-6.28	FALSE
262435_at	cytochrome P450, putative simil	CYP96A8	AT1G47620	1.06	0.09	0.71	0.5002059	0.7188569	-6.28	FALSE
251491_at	fructokinase-like protein fructoki	---	AT3G59480	1.13	0.17	0.71	0.5002651	0.7188967	-6.28	FALSE
250389_at	putative protein probable flavin-c	YUC4	AT5G11320	1.07	0.10	0.71	0.5003043	0.7189077	-6.28	FALSE
260159_at	putative helicase similar to helica	---	AT1G79890	1.08	0.12	0.71	0.5003437	0.7189191	-6.28	FALSE
261425_at	peptide transporter, putative sim	---	AT1G18880	-1.19	-0.25	-0.71	0.5004431	0.718926	-6.28	TRUE
266397_at	unknown protein	---	AT2G38690	1.07	0.10	0.71	0.5004142	0.718926	-6.28	FALSE
266385_at	pathogenesis-related PR-1-like p	PR1	AT2G14610	-2.99	-1.58	-0.71	0.5004347	0.718926	-6.28	FALSE
248100_at	beta-1,3-glucanase-like protein	---	AT5G55180	-1.27	-0.35	-0.71	0.5006697	0.7191222	-6.28	TRUE
257606_at	root hair defective 3 (RHD3) ide	RHD3	AT3G13870	1.10	0.14	0.71	0.5006671	0.7191222	-6.28	FALSE
265085_at	hypothetical protein predicted by	TPX2	AT1G03780	1.12	0.17	0.71	0.5006743	0.7191222	-6.28	FALSE
264058_at	F-box protein family, AtFBX7 co	---	AT2G03560	1.08	0.10	0.71	0.5007196	0.7191421	-6.28	FALSE
267636_at	hypothetical protein predicted by	---	AT2G42110	1.07	0.10	0.71	0.5007801	0.7191837	-6.28	FALSE
265996_at	putative leucine aminopeptidase	---	AT2G24200	1.19	0.25	0.71	0.5009699	0.7192172	-6.28	FALSE
251298_at	hypothetical protein contains nor	---	AT3G62040	-1.19	-0.25	-0.71	0.5009793	0.7192172	-6.28	FALSE
258278_at	putative self-incompatibility prote	---	AT3G26860	1.08	0.11	0.71	0.501052	0.7192172	-6.28	FALSE
265199_s_a	putative glucosyl transferase	---	AT2G36770 ///	1.14	0.19	0.71	0.5008609	0.7192172	-6.28	FALSE
266334_at	hypothetical protein predicted by	---	AT2G32380	1.14	0.19	0.71	0.5008818	0.7192172	-6.28	FALSE

260891_at	cysteine protease contains simila	---	AT1G29080	1.09	0.12	0.71	0.5010557	0.7192172	-6.28	FALSE
258898_at	putative DNA helicase	RECQI1	AT3G05740	-1.15	-0.20	-0.71	0.5009574	0.7192172	-6.28	FALSE
262296_at	putative cyclin similar to cyclin G	CYCT1;3	AT1G27630	-1.08	-0.11	-0.71	0.5010207	0.7192172	-6.28	FALSE
258928_at	unknown protein similar to hypot	TAF12	AT3G10070	-1.11	-0.15	-0.71	0.5011471	0.719235	-6.28	FALSE
267600_at	mitochondrial F1-ATPase, gamn	---	AT2G33040	1.13	0.18	0.71	0.5011627	0.719235	-6.28	FALSE
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB	---	---	1.15	0.20	0.71	0.5011007	0.719235	-6.28	FALSE
246004_at	germin-like protein ; supported b	GER3	AT5G20630	-2.11	-1.08	-0.71	0.5013766	0.7194967	-6.28	FALSE
257883_at	calmodulin-binding protein, puta	---	AT3G16940	-1.11	-0.15	-0.71	0.5014136	0.7195045	-6.28	FALSE
250805_at	unknown protein	---	AT5G05050	1.07	0.10	0.71	0.5014718	0.7195427	-6.28	FALSE
248150_at	kinesin-like protein ; supported b	ATK3	AT5G54670	1.21	0.27	0.71	0.5015835	0.7196577	-6.28	FALSE
246126_at	putative protein predicted protei	ATNUDX19	AT5G20070	-1.18	-0.24	-0.71	0.501764	0.7198716	-6.28	FALSE
259605_at	unknown protein	PUB45	AT1G27910	-1.16	-0.21	-0.71	0.5018996	0.7199754	-6.28	FALSE
253353_at	pathogenesis-related protein - lil	---	AT4G33730	1.07	0.10	0.71	0.5018931	0.7199754	-6.28	FALSE
247772_at	putative protein various predicte	---	AT5G58610	1.10	0.13	0.71	0.5019516	0.7200047	-6.28	FALSE
256679_at	putative protein similar to ATP sy	ATPQ	AT3G52300	-1.09	-0.12	-0.71	0.5020627	0.7201112	-6.28	FALSE
252804_at	putative protein	---	---	1.07	0.09	0.71	0.502089	0.7201112	-6.28	FALSE
267323_at	unknown protein	---	AT2G19340	-1.08	-0.11	-0.71	0.5021639	0.7201735	-6.28	FALSE
266533_s_a	putative plasma membrane intrin	PIP2;8	AT2G16850 /	1.12	0.17	0.71	0.5022929	0.7202116	-6.28	TRUE
264709_at	putative DNA-binding protein, M	ATCDC5	AT1G09770	-1.14	-0.19	-0.71	0.5023168	0.7202116	-6.28	FALSE
263307_at	hypothetical protein similar to my	---	---	-1.09	-0.12	-0.71	0.502247	0.7202116	-6.28	FALSE
267574_at	hypothetical protein predicted by	---	AT2G30680	1.12	0.16	0.71	0.5023108	0.7202116	-6.28	FALSE
255599_at	cyclic nucleotide gated channel	ATCNGC13	AT4G01010	1.18	0.23	0.71	0.5024542	0.7202222	-6.28	FALSE
245220_at	hypothetical protein contains sim	---	AT1G59171	-1.07	-0.10	-0.71	0.5024807	0.7202222	-6.28	FALSE
263782_at	hypothetical protein predicted by	---	AT2G46380	1.09	0.12	0.71	0.5024821	0.7202222	-6.28	FALSE
248381_at	fructokinase 1 ; supported by cD	---	AT5G51830	1.18	0.24	0.71	0.5024088	0.7202222	-6.28	FALSE
266177_at	putative phloem-specific lectin	ATPP2-B3	AT2G02270	1.11	0.15	0.71	0.5024757	0.7202222	-6.28	FALSE
258070_at	hypothetical protein predicted by	---	AT3G26040	1.11	0.15	0.71	0.5025368	0.7202554	-6.28	FALSE
248087_at	unknown protein	---	AT5G55060	1.06	0.09	0.71	0.5026107	0.7202707	-6.28	FALSE
266358_at	hypothetical protein predicted by	---	AT2G32280	-1.20	-0.26	-0.71	0.5025795	0.7202707	-6.28	FALSE
261074_at	hypothetical protein predicted by	---	AT1G07290	1.08	0.11	0.71	0.5027191	0.7203809	-6.28	FALSE
262740_at	lipase, putative contains Pfam p	---	AT1G28590	-1.08	-0.11	-0.71	0.5028374	0.7205051	-6.28	FALSE
261635_at	tubulin alpha-6 chain, putative ic	---	AT1G50020	1.11	0.15	0.71	0.5028893	0.7205288	-6.29	FALSE
248412_at	putative protein contains similarit	---	AT5G51590	1.09	0.12	0.71	0.5029171	0.7205288	-6.29	FALSE
267121_at	putative GDSL-motif lipase/hydro	---	AT2G23540	-1.16	-0.22	-0.71	0.5030426	0.7206634	-6.29	FALSE
245765_at	hypothetical protein similar to put	---	AT1G33600	1.29	0.37	0.71	0.5032228	0.7207492	-6.29	FALSE

252792_at	hypothetical protein	---	---	1.10	0.14	0.71	0.5031734	0.7207492	-6.29	FALSE
259923_at	putative protein kinase contains	---	AT1G72760	-1.07	-0.10	-0.71	0.503229	0.7207492	-6.29	FALSE
246049_at	putative protein predicted protei	---	---	1.09	0.13	0.71	0.5032107	0.7207492	-6.29	FALSE
245911_at	oligosaccharyl transferase STT3	STT3A	AT5G19690	-1.07	-0.10	-0.71	0.5034723	0.7210524	-6.29	FALSE
264852_at	similar to Mlo proteins from H. vu	MLO8	AT2G17480	1.22	0.28	0.71	0.5035134	0.7210661	-6.29	FALSE
260084_at	chromatin structure regulator, pu	---	AT1G63210	1.09	0.13	0.71	0.5035626	0.7210912	-6.29	FALSE
256501_at	hypothetical protein predicted by	---	AT1G36756	1.08	0.11	0.71	0.5036527	0.721175	-6.29	FALSE
259726_at	Expressed protein ; supported by	SCRL6	AT1G60985	-1.07	-0.10	-0.71	0.5037096	0.7212112	-6.29	FALSE
261584_at	CAF protein identical to RNA hel	DCL1	AT1G01040	-1.12	-0.17	-0.71	0.5038714	0.7213523	-6.29	FALSE
259582_at	hypothetical protein	---	AT1G28060	-1.10	-0.14	-0.71	0.5038484	0.7213523	-6.29	FALSE
260214_at	hypothetical protein contains Pfa	---	AT1G74510	1.08	0.11	0.71	0.5039523	0.7214229	-6.29	FALSE
246287_at	unknown protein	---	AT1G31870	1.08	0.11	0.71	0.504055	0.7215247	-6.29	FALSE
260879_at	hypothetical protein predicted by	---	AT1G21480	-1.09	-0.12	-0.71	0.5041259	0.7215809	-6.29	FALSE
257034_at	hypothetical protein predicted by	---	AT3G19184	1.07	0.10	0.71	0.5041844	0.7216193	-6.29	FALSE
250525_at	putative protein contains similarit	ILP1	AT5G08550	-1.08	-0.11	-0.71	0.5042693	0.7216955	-6.29	FALSE
248385_at	putative protein contains similarit	---	AT5G51910	-1.10	-0.14	-0.71	0.5044165	0.721725	-6.29	FALSE
265400_at	unknown protein ;supported by f	---	AT2G10940	3.08	1.62	0.71	0.5043783	0.721725	-6.29	FALSE
264166_at	unknown protein ; supported by c	---	AT1G65370	1.09	0.12	0.71	0.5043387	0.721725	-6.29	FALSE
259901_at	disease resistance protein, puta	AtRLP14	AT1G74180	-1.11	-0.15	-0.71	0.5043979	0.721725	-6.29	FALSE
256605_at	hypothetical protein predicted by	---	AT3G32940	-1.09	-0.12	-0.71	0.5044618	0.7217446	-6.29	FALSE
267310_at	unknown protein	AIR9	AT2G34680	1.24	0.31	0.70	0.5045738	0.7217899	-6.29	FALSE
245716_at	Expressed protein ; supported by	NDC1	AT5G08740	-1.15	-0.20	-0.70	0.5045884	0.7217899	-6.29	FALSE
260715_at	hypothetical protein predicted by	---	AT1G48200	-1.16	-0.22	-0.70	0.5045395	0.7217899	-6.29	FALSE
266249_at	hypothetical protein predicted by	---	AT2G27630	-1.07	-0.10	-0.70	0.5046281	0.7218013	-6.29	FALSE
263739_at	putative CONSTANS-like B-box	---	AT2G21320	-1.17	-0.22	-0.70	0.5046898	0.7218444	-6.29	FALSE
245099_at	unknown protein ; supported by	RHC1A	AT2G40830	1.13	0.18	0.70	0.5048186	0.7219833	-6.29	FALSE
266749_at	putative protein kinase contains	---	AT2G47060	1.18	0.24	0.70	0.5048868	0.7220357	-6.29	FALSE
251828_at	putative protein unnamed seque	---	AT3G55070	1.09	0.12	0.70	0.5050531	0.7222281	-6.29	FALSE
256197_at	hypothetical protein	---	---	1.12	0.16	0.70	0.5050938	0.722241	-6.29	FALSE
263749_at	putative phosphatidylinositol/pho	---	AT2G21520	1.09	0.12	0.70	0.5051877	0.72233	-6.29	FALSE
252264_at	putative protein hypothetical pro	---	AT3G49590	1.08	0.11	0.70	0.5053153	0.7224672	-6.29	FALSE
261321_at	hypothetical protein predicted by	---	AT1G44740	1.09	0.12	0.70	0.5053905	0.7225294	-6.29	FALSE
261440_at	hypothetical protein predicted by	---	AT1G28510	1.08	0.11	0.70	0.5054768	0.7226075	-6.29	FALSE
253483_at	putative protein anthranilate N-h	---	AT4G31910	1.15	0.21	0.70	0.5057055	0.7228892	-6.29	FALSE
265970_at	Mutator-like transposase similar	---	---	1.07	0.10	0.70	0.5057395	0.7228925	-6.29	FALSE

262561_at	late embryogenesis abundant pr	---	AT1G34340	1.08	0.12	0.70	0.5060181	0.7231095	-6.29	FALSE
256330_at	hypothetical protein predicted by	---	AT1G76870	-1.11	-0.15	-0.70	0.5059899	0.7231095	-6.29	FALSE
266187_at	putative retroelement pol polypro	---	AT2G38970	-1.14	-0.19	-0.70	0.5059309	0.7231095	-6.29	FALSE
246881_at	putative protein histone deacety	HDA2	AT5G26040	-1.14	-0.19	-0.70	0.5059939	0.7231095	-6.29	FALSE
260701_at	heat shock transcription factor H	ATHSFA1D	AT1G32330	-1.10	-0.14	-0.70	0.5061029	0.7231853	-6.29	FALSE
261704_at	hypothetical protein identical to h	---	AT1G32600	-1.07	-0.10	-0.70	0.5061608	0.7232228	-6.29	FALSE
263132_at	unknown protein ;supported by fu	---	AT1G78560	-1.07	-0.10	-0.70	0.5063038	0.7233817	-6.29	FALSE
265110_at	hypothetical protein predicted by	---	AT1G62490	1.11	0.15	0.70	0.5063802	0.7234455	-6.29	FALSE
257249_at	unknown protein	---	AT3G24180	1.12	0.17	0.70	0.5064755	0.7235364	-6.29	FALSE
260862_at	unknown protein	SEU	AT1G43850	-1.08	-0.11	-0.70	0.5066695	0.7237613	-6.29	FALSE
258303_at	hypothetical protein predicted by	---	---	1.07	0.10	0.70	0.5067281	0.7237613	-6.29	FALSE
252628_at	putative protein	---	AT3G44960	-1.06	-0.09	-0.70	0.5066979	0.7237613	-6.29	FALSE
254737_at	fatty acid elongase - like protein	---	AT4G13840	-1.24	-0.31	-0.70	0.5068082	0.7237937	-6.29	TRUE
259959_at	hypothetical protein predicted by	CYP59	AT1G53720	-1.10	-0.13	-0.70	0.5068307	0.7237937	-6.29	FALSE
245576_at	hypothetical protein	TCX2	AT4G14770	1.12	0.17	0.70	0.506846	0.7237937	-6.29	FALSE
247157_at	nuclear matrix constituent protein	LINC4	AT5G65770	-1.08	-0.11	-0.70	0.5070576	0.7240053	-6.29	FALSE
248318_at	unknown protein	---	AT5G52690	-1.07	-0.10	-0.70	0.5070432	0.7240053	-6.29	FALSE
267646_at	putative phosphate transporter	PHT5	AT2G32830	1.13	0.18	0.70	0.5072584	0.7242369	-6.29	FALSE
264416_at	hypothetical protein similar to put	---	AT1G43140	-1.09	-0.12	-0.70	0.5072834	0.7242369	-6.29	FALSE
264826_at	putative 1-aminocyclopropane-1	2A6	AT1G03410	-1.11	-0.15	-0.70	0.5073493	0.7242756	-6.29	FALSE
253902_at	NWMU4 - 2S albumin 4 precurso	---	AT4G27170	1.07	0.10	0.70	0.5073739	0.7242756	-6.29	FALSE
266714_at	NAM (no apical meristem)-like pr	EMB2301	AT2G46770	1.09	0.12	0.70	0.5074365	0.7243196	-6.29	FALSE
256200_at	hypothetical protein predicted by	EMB1674	AT1G58210	-1.09	-0.12	-0.70	0.5075283	0.7244052	-6.29	FALSE
261741_at	transcription factor, putative sim	ATE2F2	AT1G47870	1.08	0.12	0.70	0.5075952	0.7244555	-6.29	FALSE
251665_at	responce reactor 4 ; supported b	ARR9	AT3G57040	1.24	0.30	0.70	0.5077092	0.7245728	-6.29	TRUE
264040_at	putative uridylyl transferase ; su	ACR5	AT2G03730	1.06	0.09	0.70	0.5079584	0.724883	-6.29	FALSE
249703_at	putative protein strong similarity t	---	AT5G35560	-1.07	-0.10	-0.70	0.5080546	0.7249435	-6.29	FALSE
254036_at	putative peroxidase peroxidase	---	AT4G25980	1.08	0.11	0.70	0.5080643	0.7249435	-6.29	FALSE
262028_at	DNA binding protein, putative sir	---	AT1G35560	-1.08	-0.11	-0.70	0.5081725	0.7250072	-6.29	FALSE
248940_at	replication protein A1-like	---	AT5G45400	-1.09	-0.13	-0.70	0.5081472	0.7250072	-6.29	FALSE
257014_at	hypothetical protein predicted by	---	AT3G26930	-1.11	-0.15	-0.70	0.5082639	0.7250922	-6.29	FALSE
257365_x_a	putative antifungal protein	PDF1.2b	AT2G26020	-1.50	-0.59	-0.70	0.5083231	0.7251313	-6.29	FALSE
255142_at	stromal ascorbate peroxidase ; s	SAPX	AT4G08390	1.35	0.44	0.70	0.5084362	0.7252473	-6.29	FALSE
260015_at	putative S-adenosyl-L-methionin	CCOAMT	AT1G67980	1.37	0.46	0.70	0.5085183	0.7252737	-6.29	TRUE
246419_at	UDP glucose:flavonoid 3-o-gluc	UGT78D3	AT5G17030	1.07	0.10	0.70	0.5084883	0.7252737	-6.29	FALSE

254882_s_a	putative protein various predicte	---	---	1.07	0.10	0.70	0.5086143	0.7252746	-6.29	FALSE
258336_at	putative ethylene-inducible prote	PDX1.2	AT3G16050	-1.18	-0.24	-0.70	0.5085909	0.7252746	-6.29	FALSE
246663_at	putative protein	---	AT5G35300	1.08	0.11	0.70	0.5086095	0.7252746	-6.29	FALSE
256391_at	hypothetical protein predicted by	---	AT3G06090	1.06	0.09	0.70	0.5087874	0.7254761	-6.29	FALSE
250116_at	putative protein similar to unknov	---	AT5G16430	1.11	0.15	0.70	0.5090005	0.7256408	-6.29	FALSE
256427_at	hypothetical protein predicted by	LBD21	AT3G11090	-1.17	-0.22	-0.70	0.5090302	0.7256408	-6.29	FALSE
263682_at	hypothetical protein similar to rev	AT5G49590	---	-1.07	-0.09	-0.70	0.5089544	0.7256408	-6.29	FALSE
264051_at	hypothetical protein predicted by	---	AT2G22340	-1.08	-0.11	-0.70	0.5089703	0.7256408	-6.29	FALSE
258276_at	putative signal peptidase 21kDa	---	AT3G15710	1.10	0.14	0.70	0.5090993	0.7256486	-6.29	FALSE
251589_at	putative protein SINA2p zinc fing	SINAT2	AT3G58040	-1.08	-0.11	-0.70	0.5090752	0.7256486	-6.29	FALSE
247365_at	putative protein similar to unknov	---	AT5G63220	-1.10	-0.13	-0.70	0.5091671	0.7256999	-6.29	FALSE
259065_at	unknown protein similar to putati	GLR1.4	AT3G07520	-1.15	-0.20	-0.70	0.5092702	0.7258015	-6.29	FALSE
264085_at	putative glutamyl tRNA reductase	HEMA3	AT2G31250	1.07	0.10	0.70	0.5093339	0.7258469	-6.29	FALSE
257262_at	zinc finger protein, putative cont	---	AT3G21890	1.16	0.21	0.70	0.5093888	0.7258663	-6.29	FALSE
246569_at	lysophospholipase -like protein l	---	AT5G14980	-1.07	-0.10	-0.70	0.5094111	0.7258663	-6.29	FALSE
252560_at	histone H2B -like protein histone	HTB11	AT3G46030	-1.07	-0.10	-0.70	0.5095407	0.7259602	-6.29	FALSE
248455_at	unknown protein	---	AT5G51360	1.07	0.10	0.70	0.5095143	0.7259602	-6.29	FALSE
259801_at	blue copper protein, putative sim	---	AT1G72230	-1.22	-0.28	-0.70	0.5096294	0.7260413	-6.29	FALSE
261963_at	hypothetical protein predicted by	---	---	-1.09	-0.13	-0.70	0.5096983	0.7260941	-6.29	FALSE
257359_x_a	putative protein kinase contains a	---	AT2G34290	-1.07	-0.10	-0.70	0.5097384	0.7261058	-6.29	FALSE
255266_at	receptor protein kinase - like pro	---	AT4G05200	-1.08	-0.11	-0.70	0.5098552	0.7262269	-6.29	FALSE
254190_at	Expressed protein ; supported by	---	AT4G23885	-1.13	-0.18	-0.70	0.5099625	0.7263343	-6.29	FALSE
247113_at	unknown protein ;supported by fu	---	AT5G65960	-1.08	-0.11	-0.70	0.5100147	0.7263633	-6.29	FALSE
254648_at	lipase-like protein Pn47p, Ipomo	---	AT4G18550	1.08	0.11	0.70	0.5100958	0.7264335	-6.29	FALSE
266971_at	unknown protein	---	AT2G39580	1.18	0.23	0.70	0.5101863	0.7264586	-6.29	TRUE
258561_at	putative hexose transporter simil	STP6	AT3G05960	-1.11	-0.15	-0.70	0.5101589	0.7264586	-6.29	FALSE
249937_at	putative protein seed maturation	---	AT5G22470	1.11	0.15	0.70	0.510209	0.7264586	-6.29	FALSE
264866_at	putative metalloproteinase simila	---	AT1G24140	1.55	0.63	0.70	0.5102817	0.7265168	-6.29	FALSE
265517_at	putative S1 self-incompatibility pr	---	AT2G06090	1.07	0.10	0.69	0.5104159	0.7266625	-6.29	FALSE
261291_at	hypothetical protein predicted by	---	AT1G36970	1.13	0.18	0.69	0.5104838	0.7267138	-6.29	FALSE
252963_at	putative protein	---	AT4G38820	1.07	0.10	0.69	0.5105495	0.726762	-6.29	FALSE
261012_at	CLE9, putative CLAVATA3/ESR	CLE9	AT1G26600	1.06	0.09	0.69	0.5107124	0.7268601	-6.29	FALSE
264103_at	unknown protein	---	AT2G13660	-1.09	-0.12	-0.69	0.510681	0.7268601	-6.29	FALSE
262409_at	hypothetical protein predicted by	---	---	1.10	0.14	0.69	0.5107605	0.7268601	-6.29	FALSE
249611_at	putative protein unnamed ORF,	ATSRL1	AT5G37370	1.10	0.13	0.69	0.5107882	0.7268601	-6.29	FALSE

265832_at	putative replication protein A1	---	---	1.07	0.10	0.69	0.5108096	0.7268601	-6.29	FALSE
266603_at	hypothetical protein predicted by	---	AT2G46040	-1.08	-0.11	-0.69	0.5107646	0.7268601	-6.29	FALSE
260684_at	transcription factor, putative sim	NF-YA8	AT1G17590	-1.12	-0.16	-0.69	0.5109363	0.726995	-6.30	FALSE
266933_at	putative Ta11-like non-LTR retro	---	AT2G07760	1.10	0.14	0.69	0.5110447	0.7270585	-6.30	FALSE
264991_s_a	putative protein hypothetical prot	---	AT1G67400 /	1.12	0.17	0.69	0.5110281	0.7270585	-6.30	FALSE
264910_at	resistance protein, putative simil	---	AT1G61100	1.18	0.24	0.69	0.5111412	0.7271268	-6.30	TRUE
247382_at	adenylate kinase ;supported by f	ADK1	AT5G63400	-1.11	-0.15	-0.69	0.5111564	0.7271268	-6.30	FALSE
258394_at	unknown protein ;supported by f	---	AT3G15530	1.16	0.22	0.69	0.5113247	0.7272174	-6.30	TRUE
253691_at	putative protein predicted protei	EMB2752	AT4G29660	-1.06	-0.09	-0.69	0.5113462	0.7272174	-6.30	FALSE
252490_at	glucuronosyl transferase-like pro	---	AT3G46720	1.08	0.11	0.69	0.5113795	0.7272174	-6.30	FALSE
247991_at	expansin ;supported by full-leng	ATEXPA14	AT5G56320	1.07	0.09	0.69	0.5113654	0.7272174	-6.30	FALSE
256739_s_a	hypothetical protein similar to put	---	---	-1.06	-0.09	-0.69	0.5113151	0.7272174	-6.30	FALSE
253610_at	putative protein ; supported by c	VEL1	AT4G30200	-1.09	-0.13	-0.69	0.5116795	0.7275532	-6.30	FALSE
263036_at	hypothetical protein predicted by	---	AT1G23890	1.09	0.13	0.69	0.5116495	0.7275532	-6.30	FALSE
264074_at	putative retroelement pol polypro	---	---	-1.08	-0.11	-0.69	0.5117295	0.727579	-6.30	FALSE
246388_at	hypothetical protein predicted by	---	AT1G77405	1.11	0.15	0.69	0.5117845	0.7276119	-6.30	FALSE
260257_at	putative dolichyl-phosphate man	---	AT1G74340	-1.07	-0.10	-0.69	0.5119606	0.7278169	-6.30	FALSE
253215_at	putative protein AT.I.24-7, Arabi	---	AT4G34950	1.23	0.30	0.69	0.5120686	0.7279251	-6.30	TRUE
252881_at	putative protein predicted protei	---	AT4G39610	1.12	0.16	0.69	0.5121127	0.7279423	-6.30	FALSE
246787_s_a	cdc20-like protein putative cdc20	---	AT5G27570 /	1.07	0.09	0.69	0.5122114	0.7280373	-6.30	FALSE
261543_at	unknown protein contains Pfam p	---	AT1G63550	1.10	0.14	0.69	0.5122767	0.7280394	-6.30	FALSE
246751_at	pectin methyl-esterase - like pro	---	AT5G27870	1.06	0.09	0.69	0.5122665	0.7280394	-6.30	FALSE
258826_at	putative glucan synthase similar	ATGSL10	AT3G07160	1.06	0.09	0.69	0.5125563	0.7283913	-6.30	FALSE
251093_at	putative protein several hypothet	---	AT5G01360	1.14	0.19	0.69	0.5126284	0.7284031	-6.30	FALSE
256749_at	hypothetical protein similar to put	---	---	-1.07	-0.10	-0.69	0.5126274	0.7284031	-6.30	FALSE
251973_at	nodulin / glutamate-ammonia lig	---	AT3G53180	1.15	0.20	0.69	0.512861	0.7284638	-6.30	TRUE
261627_at	arsA homolog (hASNA-I), putativ	---	AT1G01910	1.07	0.10	0.69	0.512855	0.7284638	-6.30	FALSE
257720_at	hypothetical protein similar to GE	---	AT3G18450	1.09	0.12	0.69	0.5129905	0.7284638	-6.30	FALSE
253084_at	putative protein lateral root prim	STY2	AT4G36260	1.13	0.17	0.69	0.5129494	0.7284638	-6.30	FALSE
256596_at	hypothetical protein predicted by	---	AT3G28540	1.16	0.21	0.69	0.5129648	0.7284638	-6.30	FALSE
257476_at	unknown protein	---	AT1G80960	1.07	0.09	0.69	0.512818	0.7284638	-6.30	FALSE
257927_at	ethylene response factor 1 (ERF	ERF1	AT3G23240	1.82	0.86	0.69	0.5129674	0.7284638	-6.30	FALSE
264196_at	putative RING zinc finger protein	---	AT1G22670	-1.07	-0.10	-0.69	0.5129029	0.7284638	-6.30	FALSE
259509_at	mutator-like transposase, putativ	---	---	1.07	0.10	0.69	0.5127035	0.7284638	-6.30	FALSE
267522_at	hypothetical protein predicted by	---	AT2G30430	1.09	0.12	0.69	0.5129901	0.7284638	-6.30	FALSE

256098_at	unknown protein similar to 6-pho	---	AT1G13700	1.17	0.22	0.69	0.513118	0.7285994	-6.30	TRUE
248346_at	GTP-binding protein-like ;suppo	ATGB1	AT5G52210	1.14	0.19	0.69	0.5133472	0.7287434	-6.30	FALSE
258566_at	putative glutamate receptor (GLF	GLR1.1	AT3G04110	1.15	0.20	0.69	0.5132633	0.7287434	-6.30	FALSE
261884_at	myrosinase precursor, putative	---	AT1G80910	1.09	0.12	0.69	0.513284	0.7287434	-6.30	FALSE
249280_at	unknown protein	---	AT5G41940	1.11	0.14	0.69	0.5133392	0.7287434	-6.30	FALSE
255173_at	putative transposon protein simi	---	---	1.09	0.13	0.69	0.5133981	0.7287704	-6.30	FALSE
249512_at	DNA repair protein RAD23 homo	---	AT5G38470	-1.06	-0.09	-0.69	0.5135344	0.7289184	-6.30	FALSE
250472_at	putative protein	---	AT5G10210	1.11	0.15	0.69	0.5136129	0.7289845	-6.30	FALSE
265365_at	En/Spm-like transposon protein r	---	---	1.07	0.10	0.69	0.5136827	0.7289929	-6.30	FALSE
247804_at	strong similarity to unknown prot	SVL5	AT5G58170	1.08	0.11	0.69	0.5136619	0.7289929	-6.30	FALSE
265959_at	unknown protein ;supported by f	---	AT2G37240	-1.18	-0.24	-0.69	0.5137309	0.7290159	-6.30	FALSE
264940_at	galactinol synthase, putative sim	AtGolS4	AT1G60470	1.28	0.36	0.69	0.5137872	0.7290505	-6.30	FALSE
262832_s_a	unknown protein	---	AT1G14870 /.	-1.98	-0.99	-0.69	0.5138863	0.7291458	-6.30	FALSE
258032_at	hypothetical protein predicted by	---	AT3G21170	1.12	0.16	0.69	0.5139724	0.7292137	-6.30	FALSE
247539_at	putative protein predicted protei	---	AT5G61710	-1.07	-0.10	-0.69	0.5139982	0.7292137	-6.30	FALSE
259986_at	thaumatin-like protein similar to t	---	AT1G75050	1.09	0.12	0.69	0.5141888	0.7294388	-6.30	FALSE
249352_at	putative transcription factor MYB	MYB22	AT5G40430	-1.07	-0.09	-0.69	0.5142838	0.7295282	-6.30	FALSE
247196_at	putative protein similar to unknov	AIL7	AT5G65510	-1.07	-0.09	-0.69	0.5143628	0.7295949	-6.30	FALSE
247728_at	putative protein	---	---	-1.08	-0.11	-0.69	0.5144569	0.729683	-6.30	FALSE
245664_at	hypothetical protein predicted by	---	AT1G28327	1.07	0.10	0.69	0.5145839	0.7298177	-6.30	FALSE
256561_s_a	hypothetical protein similar to put	---	---	-1.07	-0.10	-0.69	0.5149499	0.7302837	-6.30	FALSE
261067_at	lectin, putative contains Pfam pr	---	AT1G07460	-1.08	-0.11	-0.69	0.5149765	0.7302837	-6.30	FALSE
265184_at	unknown protein ;supported by f	---	AT1G23710	1.35	0.44	0.69	0.5150227	0.7303039	-6.30	FALSE
263456_at	unknown protein	---	AT2G22125	-1.11	-0.15	-0.69	0.5152028	0.7304249	-6.30	TRUE
258111_at	putative cytochrome P450 simila	CYP72A9	AT3G14630	1.10	0.14	0.69	0.5152105	0.7304249	-6.30	FALSE
248822_at	peroxidase ;supported by full-ler	---	AT5G47000	1.07	0.10	0.69	0.5151552	0.7304249	-6.30	FALSE
254771_at	hypothetical protein	MEE56	AT4G13380	1.07	0.10	0.69	0.5152361	0.7304249	-6.30	FALSE
255307_at	hypothetical protein similar to A.	RIC10	AT4G04900	1.09	0.12	0.69	0.5152717	0.7304299	-6.30	FALSE
264644_at	hypothetical protein Similar to Ca	CAX11	AT1G08960	1.09	0.13	0.69	0.5153255	0.7304607	-6.30	FALSE
263591_at	unknown protein	ATMAP65-(	AT2G01910	1.31	0.39	0.69	0.5153684	0.730469	-6.30	TRUE
258959_at	putative amino acid transporter s	CAT7	AT3G10600	1.08	0.11	0.69	0.5153954	0.730469	-6.30	FALSE
250439_at	14-3-3 protein GF14lambda (grf6	GRF6	AT5G10450	1.08	0.12	0.69	0.5154567	0.7305106	-6.30	FALSE
254183_at	putative protein predicted protei	---	AT4G23960	1.09	0.12	0.69	0.5155034	0.7305314	-6.30	FALSE
260140_at	Myb-related transcription factor,	MYB90	AT1G66390	1.09	0.13	0.69	0.515552	0.7305548	-6.30	FALSE
263201_at	putative ADP-glucose pyrophos	APS2	AT1G05610	1.08	0.12	0.69	0.5155984	0.7305752	-6.30	FALSE

266610_at	Ac-like transposase related to Ac	---	---	-1.07	-0.09	-0.69	0.5156536	0.7306081	-6.30	FALSE
253330_at	putative potassium transporter A	KUP5	AT4G33530	1.08	0.11	0.69	0.5157673	0.7306783	-6.30	TRUE
250839_at	MADS-box protein - like SLM3 M	AGL99	AT5G04640	1.07	0.09	0.69	0.5157615	0.7306783	-6.30	FALSE
251829_at	putative protein KIAA0882 prote	---	AT3G55020	-1.19	-0.25	-0.69	0.5158021	0.7306823	-6.30	FALSE
263116_s_a	unknown protein Similar to gb|U5	---	AT1G03140 ///	-1.09	-0.13	-0.69	0.5159401	0.7308324	-6.30	FALSE
262394_at	unknown protein	emb1273	AT1G49510	-1.13	-0.18	-0.69	0.5160051	0.7308791	-6.30	FALSE
245860_at	putative protein predicted protei	---	AT5G28310	1.09	0.12	0.69	0.5160749	0.7309326	-6.30	FALSE
255571_at	hypothetical protein ; supported	---	AT4G01220	-1.14	-0.18	-0.69	0.5161465	0.7309885	-6.30	TRUE
264528_at	hypothetical protein similar to Hu	---	AT1G30810	1.06	0.09	0.68	0.5162508	0.7310325	-6.30	FALSE
254462_at	putative protein ;supported by fu	---	AT4G20150	-1.06	-0.09	-0.68	0.5162737	0.7310325	-6.30	FALSE
249762_at	putative protein contains similarit	---	AT5G24000	-1.07	-0.10	-0.68	0.5162353	0.7310325	-6.30	FALSE
253382_at	putative protein AT.I.24, Arabido	---	AT4G33040	1.10	0.14	0.68	0.5164786	0.7311542	-6.30	TRUE
252080_at	putative protein polyphosphoino	---	AT3G51670	1.14	0.19	0.68	0.5164507	0.7311542	-6.30	FALSE
251076_at	putative protein putative protein	---	AT5G01970	1.13	0.18	0.68	0.5164282	0.7311542	-6.30	FALSE
266153_at	hypothetical protein	---	---	1.07	0.09	0.68	0.5164878	0.7311542	-6.30	FALSE
252144_at	ribosomal protein L8 homolog rib	---	AT3G51190	-1.07	-0.10	-0.68	0.5165457	0.7311907	-6.30	FALSE
248308_at	putative protein similar to unknov	---	AT5G52530	1.07	0.10	0.68	0.5165987	0.7312203	-6.30	FALSE
263928_at	hypothetical protein predicted by	---	AT2G36330	1.12	0.16	0.68	0.5168115	0.7314763	-6.30	FALSE
259964_at	glutathione transferase, putative	ATGSTU28	AT1G53680	1.08	0.11	0.68	0.5168969	0.7315516	-6.30	FALSE
257520_at	hypothetical protein	---	AT3G07710	1.09	0.13	0.68	0.5169847	0.7316306	-6.30	FALSE
257148_at	cytochrome c, putative similar to	---	AT3G27240	1.14	0.18	0.68	0.5170844	0.7316355	-6.30	FALSE
258304_at	hypothetical protein predicted by	---	---	1.06	0.09	0.68	0.5170261	0.7316355	-6.30	FALSE
266282_at	putative protein kinase contains a	---	AT2G29220	1.07	0.09	0.68	0.5170821	0.7316355	-6.30	FALSE
253153_at	hypothetical protein	---	AT4G35700	-1.08	-0.11	-0.68	0.5171516	0.7316852	-6.30	FALSE
261272_at	Expressed protein ; supported by	---	AT1G26665	-1.17	-0.23	-0.68	0.5177622	0.7322925	-6.30	TRUE
258649_at	putative transitional endoplasmic	CDC48	AT3G09840	-1.06	-0.09	-0.68	0.5177086	0.7322925	-6.30	FALSE
254694_at	putative protein	---	AT4G17900	-1.11	-0.16	-0.68	0.5178125	0.7322925	-6.30	FALSE
252040_at	putative protein hypothetical pro	---	AT3G52060	1.19	0.25	0.68	0.5178111	0.7322925	-6.30	FALSE
265429_at	hypothetical protein predicted by	---	AT2G20710	-1.10	-0.14	-0.68	0.5177667	0.7322925	-6.30	FALSE
247236_at	putative protein similar to unknov	---	AT5G64590	1.08	0.12	0.68	0.5178377	0.7322925	-6.30	FALSE
266586_s_a	putative protein	---	---	1.06	0.08	0.68	0.5177447	0.7322925	-6.30	FALSE
251202_at	putative protein predicted protei	---	AT3G63040	1.07	0.09	0.68	0.5177663	0.7322925	-6.30	FALSE
251719_at	putative protein PUTATIVE PRO	---	AT3G56140	-1.10	-0.13	-0.68	0.5179429	0.7323124	-6.30	FALSE
267367_at	unknown protein ;supported by f	---	AT2G44210	-1.12	-0.16	-0.68	0.5178847	0.7323124	-6.30	FALSE
256634_s_a	hypothetical protein predicted by	---	---	-1.07	-0.09	-0.68	0.5179481	0.7323124	-6.30	FALSE

249273_at	unknown protein	---	AT5G41850	-1.10	-0.13	-0.68	0.5180812	0.7323644	-6.30	FALSE
264801_at	hypothetical protein gene overlap	emb2411	AT1G08840	1.08	0.11	0.68	0.518068	0.7323644	-6.30	FALSE
265456_at	Expressed protein ; supported by	SDH4	AT2G46505	1.07	0.10	0.68	0.5180337	0.7323644	-6.30	FALSE
248575_at	ATP-dependent Clp protease AT	---	AT5G49840	-1.07	-0.10	-0.68	0.5181904	0.7324734	-6.30	FALSE
264090_at	cytochrome P-450, putative simi	CYP79C1	AT1G79370	1.08	0.11	0.68	0.5183036	0.732588	-6.30	FALSE
248467_at	MtN3-like protein ;supported by f	---	AT5G50800	1.23	0.30	0.68	0.5183831	0.732655	-6.30	FALSE
263776_s_a	putative cyclic nucleotide-regulat	ATCNGC3	AT2G46430 /A	1.41	0.50	0.68	0.5185936	0.732907	-6.30	FALSE
251071_at	putative protein receptor protein	---	AT5G01950	1.14	0.19	0.68	0.5187017	0.7330145	-6.30	FALSE
264249_at	vacuolar-type H+-translocating in	AVP2	AT1G78920	1.09	0.12	0.68	0.5187863	0.7330885	-6.30	FALSE
256635_at	hypothetical protein predicted by	---	AT3G28260	-1.06	-0.09	-0.68	0.5188199	0.7330907	-6.30	FALSE
257955_at	unknown protein ; supported by	---	AT3G21810	1.17	0.23	0.68	0.5188822	0.7331332	-6.30	FALSE
266752_at	putative ABC transporter related	ABCB4	AT2G47000	1.54	0.62	0.68	0.5189392	0.7331679	-6.30	TRUE
265399_at	hypothetical protein predicted by	---	AT2G11010	1.17	0.23	0.68	0.518971	0.7331679	-6.30	FALSE
252190_at	putative protein various predicte	---	AT3G50170	-1.07	-0.10	-0.68	0.5191428	0.7333651	-6.31	FALSE
265868_at	unknown protein ;supported by f	PUX2	AT2G01650	1.11	0.15	0.68	0.5192245	0.7334351	-6.31	FALSE
266670_at	putative flavonol 3-O-glucosyltran	UGT71C2	AT2G29740	-1.10	-0.13	-0.68	0.519285	0.7334752	-6.31	FALSE
250549_at	N-hydroxycinnamoyl benzoyltran	---	AT5G07860	1.13	0.18	0.68	0.5194591	0.7335848	-6.31	TRUE
245737_at	hypothetical protein similar to put	---	AT1G44160	-1.12	-0.17	-0.68	0.5193951	0.7335848	-6.31	FALSE
254022_at	putative membrane transporter E	---	AT4G25750	-1.09	-0.12	-0.68	0.5194458	0.7335848	-6.31	FALSE
261534_at	unknown protein ;supported by fu	PEX11C	AT1G01820	-1.07	-0.09	-0.68	0.5195115	0.7336134	-6.31	FALSE
266594_at	hypothetical protein	---	AT2G46190	-1.06	-0.08	-0.68	0.5196663	0.7337866	-6.31	FALSE
264630_at	hypothetical protein predicted by	FAS1	AT1G65470	1.10	0.14	0.68	0.5197349	0.7338381	-6.31	FALSE
249025_at	putative protein contains similarit	---	AT5G44720	1.15	0.21	0.68	0.5200699	0.7342655	-6.31	FALSE
247124_at	prolyl 4-hydroxylase, alpha subu	---	AT5G66060	-1.07	-0.10	-0.68	0.5201506	0.7342885	-6.31	FALSE
254714_at	myb-like protein snapdragon my	AtMYB79	AT4G13480	1.07	0.10	0.68	0.5201378	0.7342885	-6.31	FALSE
248774_at	unknown protein	---	AT5G47830	-1.07	-0.10	-0.68	0.5202093	0.7343261	-6.31	FALSE
267540_at	hypothetical protein predicted by	---	AT2G32760	1.07	0.10	0.68	0.5203411	0.7344211	-6.31	FALSE
247945_at	putative protein contains similarit	---	AT5G57150	1.26	0.33	0.68	0.520324	0.7344211	-6.31	FALSE
249958_at	plasma membrane associated p	---	AT5G18970	1.11	0.15	0.68	0.5204272	0.7344972	-6.31	FALSE
262027_at	DNA-binding protein, putative si	HOS10	AT1G35515	1.15	0.21	0.68	0.5204701	0.7345123	-6.31	FALSE
245662_at	hypothetical protein predicted by	---	AT1G28190	1.34	0.42	0.68	0.5207759	0.7348947	-6.31	TRUE
260113_at	hypothetical protein predicted by	---	AT1G63300	1.06	0.09	0.68	0.5208293	0.7348947	-6.31	FALSE
263568_at	hypothetical protein predicted by	---	AT2G27160	1.10	0.14	0.68	0.5208377	0.7348947	-6.31	FALSE
260797_at	neoxanthin cleavage enzyme, p	NCED9	AT1G78390	1.09	0.12	0.68	0.5209539	0.7350132	-6.31	FALSE
252451_at	hypothetical protein	---	AT3G47100	1.07	0.10	0.68	0.5210625	0.7351209	-6.31	FALSE

250025_at	putative protein similar to unknov	SIP1;2	AT5G18290	1.11	0.15	0.68	0.5210997	0.7351279	-6.31	FALSE
257318_at	hypothetical protein	---	AT2G07777	-1.07	-0.10	-0.68	0.5212442	0.7352863	-6.31	FALSE
251072_at	putative protein wound-inducible	---	AT5G01740	1.17	0.23	0.68	0.5214413	0.735337	-6.31	TRUE
267135_at	cyclin-dependent kinase inhibitor	ICK1	AT2G23430	-1.16	-0.22	-0.68	0.5214197	0.735337	-6.31	FALSE
255478_at	putative protein ;supported by fu	EID1	AT4G02440	-1.09	-0.12	-0.68	0.5213215	0.735337	-6.31	FALSE
266390_at	hypothetical protein predicted by	---	AT2G32310	1.07	0.10	0.68	0.5213522	0.735337	-6.31	FALSE
255375_at	putative athila-like protein	---	---	1.07	0.10	0.68	0.5214245	0.735337	-6.31	FALSE
261523_at	protein tyrosine phosphatase ide	PTP1	AT1G71860	1.08	0.11	0.68	0.5215249	0.7354094	-6.31	FALSE
256575_at	dTDP-glucose 4,6-dehydratase,	RHM3	AT3G14790	-1.11	-0.16	-0.68	0.5215817	0.735444	-6.31	FALSE
251700_at	putative protein exocyst complex	---	AT3G56640	-1.14	-0.19	-0.68	0.5217515	0.735638	-6.31	FALSE
245900_at	putative protein predicted protei	---	AT5G11040	-1.09	-0.13	-0.68	0.5218965	0.735797	-6.31	FALSE
256307_at	pectate lyase, putative contains	---	AT1G30350	-1.06	-0.09	-0.68	0.5220878	0.7360212	-6.31	FALSE
252321_at	hypothetical protein ;supported b	---	AT3G48510	1.09	0.12	0.68	0.5221289	0.7360336	-6.31	FALSE
252609_at	putative protein	---	AT3G45110	1.08	0.11	0.67	0.5222851	0.7362084	-6.31	FALSE
250253_at	putative protein contains similarit	PDAT	AT5G13640	-1.09	-0.13	-0.67	0.5223511	0.7362558	-6.31	FALSE
255057_at	hypothetical protein	---	AT4G09840	-1.06	-0.09	-0.67	0.5224312	0.7363232	-6.31	FALSE
254338_s_a	pectate lyase like protein pectate	---	AT4G22080 //	1.06	0.09	0.67	0.522479	0.7363451	-6.31	FALSE
252317_at	putative protein hypersensitivity-	---	AT3G48720	1.33	0.42	0.67	0.5228151	0.7366994	-6.31	TRUE
248681_at	pectate lyase non-consensus AG	---	AT5G48900	1.86	0.89	0.67	0.5228272	0.7366994	-6.31	FALSE
265498_at	putative C2H2-type zinc finger pr	---	AT2G15740	1.07	0.09	0.67	0.52277	0.7366994	-6.31	FALSE
256802_at	cytochrome P450, putative simil	CYP705A3	AT3G20950	1.07	0.09	0.67	0.5229681	0.7367613	-6.31	FALSE
267272_at	hypothetical protein predicted by	---	---	-1.07	-0.10	-0.67	0.5229516	0.7367613	-6.31	FALSE
260854_at	CCAAT-box binding factor HAP3	LEC1	AT1G21970	-1.11	-0.15	-0.67	0.5229053	0.7367613	-6.31	FALSE
259180_at	unknown protein	---	AT3G01680	1.24	0.31	0.67	0.5231528	0.7369759	-6.31	TRUE
245030_at	putative polygalacturonase	---	AT2G26620	1.06	0.08	0.67	0.5233262	0.7371748	-6.31	FALSE
260409_at	Expressed protein ; supported by	SHW1	AT1G69935	-1.14	-0.19	-0.67	0.523671	0.7374351	-6.31	FALSE
253978_at	putative protein probable kinesin	---	AT4G26660	1.10	0.13	0.67	0.5236338	0.7374351	-6.31	FALSE
245434_at	hypothetical protein	---	AT4G17140	1.07	0.10	0.67	0.5236727	0.7374351	-6.31	FALSE
250997_at	putative protein histone H2B-2, t	---	AT5G02570	-1.08	-0.11	-0.67	0.5236424	0.7374351	-6.31	FALSE
260861_at	hypothetical protein predicted by	---	---	1.08	0.11	0.67	0.5236339	0.7374351	-6.31	FALSE
258325_at	putative heat shock protein simila	HSFA6B	AT3G22830	1.08	0.11	0.67	0.5240082	0.7378297	-6.31	FALSE
258266_at	hypothetical protein predicted by	---	AT3G15860	1.10	0.14	0.67	0.5240176	0.7378297	-6.31	FALSE
252973_s_a	peptidylprolyl isomerase ROC1 ;	ROC1	AT4G38740	1.12	0.16	0.67	0.5240932	0.7378906	-6.31	FALSE
261759_at	hypothetical protein similar to put	---	AT1G15590	-1.08	-0.11	-0.67	0.5242416	0.738054	-6.31	FALSE
248573_at	cellulase homolog OR16pep pred	ATGH9A1	AT5G49720	1.09	0.12	0.67	0.5243858	0.7382114	-6.31	FALSE

250315_at	putative protein contains similarit	PDE149	AT5G12130	-1.15	-0.20	-0.67	0.5244207	0.738215	-6.31	FALSE
256956_at	expressed protein supported by	---	AT3G13410	-1.07	-0.10	-0.67	0.5245772	0.7383898	-6.31	FALSE
263887_at	hypothetical protein predicted by	---	AT2G36980	-1.10	-0.14	-0.67	0.5246544	0.7384529	-6.31	FALSE
246600_at	putative protein disease resistan	SAG101	AT5G14930	1.16	0.21	0.67	0.5248635	0.7384891	-6.31	FALSE
255036_at	putative protein similarity RING	---	AT4G09560	1.14	0.19	0.67	0.5249716	0.7384891	-6.31	FALSE
246312_at	G-protein, putative contains Pfa	XLG3	AT1G31930	1.19	0.25	0.67	0.5248886	0.7384891	-6.31	FALSE
251569_at	putative protein several hypothet	---	AT3G58290	1.09	0.13	0.67	0.5247849	0.7384891	-6.31	FALSE
263830_at	hypothetical protein predicted by	---	AT2G40260	1.08	0.11	0.67	0.5248279	0.7384891	-6.31	FALSE
263620_at	hypothetical protein predicted by	---	---	1.07	0.10	0.67	0.52484	0.7384891	-6.31	FALSE
265698_at	hypothetical protein predicted by	---	AT2G32160	-1.08	-0.11	-0.67	0.5249258	0.7384891	-6.31	FALSE
263576_at	hypothetical protein similar to hy	---	AT2G17080	1.06	0.09	0.67	0.5248039	0.7384891	-6.31	FALSE
263084_at	hypothetical protein predicted by	---	AT2G27180	1.08	0.11	0.67	0.5249644	0.7384891	-6.31	FALSE
245396_at	hypothetical protein ;supported b	---	AT4G14870	-1.14	-0.19	-0.67	0.5250603	0.7384896	-6.31	FALSE
256209_at	electron transport flavoprotein, p	ETFALPHA	AT1G50940	1.08	0.11	0.67	0.525069	0.7384896	-6.31	FALSE
254792_at	putative protein nucleoid DNA-b	---	AT4G12920	1.08	0.11	0.67	0.5250187	0.7384896	-6.31	FALSE
265590_at	SKP1/ASK1 (At17), putative sim	MEO	AT2G20160	1.07	0.10	0.67	0.5252047	0.7385956	-6.31	FALSE
251761_at	glucuronosyl transferase - like p	---	AT3G55700	-1.11	-0.15	-0.67	0.5252091	0.7385956	-6.31	FALSE
248406_at	pectinesterase	---	AT5G51490	1.11	0.16	0.67	0.5254183	0.7388441	-6.31	FALSE
264244_at	pantothenate kinase, putative si	ATPANK1	AT1G60440	1.08	0.11	0.67	0.5255487	0.7389819	-6.31	FALSE
245069_at	putative glucosyltransferase	UGT84B2	AT2G23250	1.08	0.11	0.67	0.5256198	0.7390363	-6.31	FALSE
250050_at	putative protein predicted protei	VAR3	AT5G17790	-1.08	-0.12	-0.67	0.525745	0.7391315	-6.31	FALSE
251180_at	putative protein hypothetical pro	---	AT3G62640	-1.13	-0.17	-0.67	0.5257801	0.7391315	-6.31	FALSE
265924_at	putative geranylgeranyl pyrophos	---	AT2G18620	1.06	0.08	0.67	0.5258056	0.7391315	-6.31	FALSE
261288_at	hypothetical protein predicted by	---	AT1G37010	-1.08	-0.11	-0.67	0.5258171	0.7391315	-6.31	FALSE
249837_at	Expressed protein ; supported by	---	AT5G23480	1.08	0.11	0.67	0.5258644	0.7391525	-6.31	FALSE
245335_at	pore protein homolog ;supported	ATOEP16-2	AT4G16160	1.10	0.13	0.67	0.5260276	0.7393363	-6.31	FALSE
256803_at	cytochrome P450, putative simil	CYP705A3	AT3G20960	1.07	0.10	0.67	0.5261049	0.739359	-6.31	FALSE
253556_at	serine/threonine-specific protein	---	AT4G31100	1.06	0.09	0.67	0.5261085	0.739359	-6.31	FALSE
262968_at	hypothetical protein predicted by	---	AT1G75720	1.08	0.11	0.67	0.5263282	0.7395832	-6.31	FALSE
260681_at	hypothetical protein predicted by	AT1G0803(	---	1.07	0.10	0.67	0.5264175	0.7395832	-6.31	FALSE
253304_at	putative protein ;supported by fu	---	AT4G33640	-1.09	-0.12	-0.67	0.5263677	0.7395832	-6.31	FALSE
251253_at	putative zinc-finger protein zinc-	---	AT3G62240	1.13	0.18	0.67	0.5264302	0.7395832	-6.31	FALSE
256136_s_a	lectin receptor kinase, putative s	---	AT1G48720	-1.06	-0.09	-0.67	0.5264235	0.7395832	-6.31	FALSE
265609_at	hypothetical protein predicted by	---	AT2G25420	-1.13	-0.17	-0.67	0.5265951	0.7397694	-6.31	FALSE
261517_at	unknown protein ; supported by f	---	AT1G71780	1.09	0.12	0.67	0.5267543	0.7399474	-6.31	FALSE

266047_at	unknown protein	---	AT2G40800	-1.10	-0.13	-0.67	0.5268756	0.7399902	-6.31	FALSE
262077_at	dynamin-like protein similar to dy	ADL3	AT1G59610	-1.07	-0.10	-0.67	0.5268687	0.7399902	-6.31	FALSE
248930_at	unknown protein	---	AT5G46010	1.08	0.11	0.67	0.5268821	0.7399902	-6.31	FALSE
260217_at	hypothetical protein contains Pfa	---	AT1G74600	-1.07	-0.09	-0.67	0.5269387	0.7400242	-6.31	FALSE
251306_at	putative DNA-binding protein DN	---	AT3G61260	-1.10	-0.14	-0.67	0.5271814	0.7401959	-6.31	FALSE
259992_at	putative heat shock transcription	HSFA8	AT1G67970	-1.14	-0.18	-0.67	0.5271064	0.7401959	-6.31	FALSE
245419_at	putative protein	MSH4	AT4G17380	-1.07	-0.09	-0.67	0.5271658	0.7401959	-6.31	FALSE
263555_at	unknown protein ;supported by f	---	AT2G16460	1.07	0.10	0.67	0.5271908	0.7401959	-6.31	FALSE
256997_at	subtilisin-like serine protease, pu	---	AT3G14067	-1.13	-0.17	-0.67	0.5272233	0.740196	-6.31	FALSE
259657_at	phospholipase D alpha, putative	PLDEPSIL(	AT1G55180	1.07	0.10	0.67	0.5273286	0.7402649	-6.31	FALSE
262922_at	hypothetical protein predicted by	---	AT1G79420	1.10	0.14	0.67	0.5273455	0.7402649	-6.31	FALSE
266548_at	unknown protein ;supported by f	RPA	AT2G35210	-1.12	-0.16	-0.67	0.5274671	0.7402649	-6.32	FALSE
244918_at	hypothetical protein	AT2G0774	---	1.08	0.11	0.67	0.5274666	0.7402649	-6.32	FALSE
253356_at	putative protein myosin II heavy	---	AT4G33390	1.07	0.10	0.67	0.5274225	0.7402649	-6.31	FALSE
250032_at	glutamate dehydrogenase (EC 1	GDH1	AT5G18170	-1.26	-0.34	-0.67	0.5274656	0.7402649	-6.32	FALSE
246855_at	putative protein various predicte	---	AT5G26280	-1.23	-0.30	-0.67	0.5275484	0.7402878	-6.32	FALSE
255726_at	lysine and histidine specific trans	---	AT1G25530	1.29	0.37	0.67	0.5275232	0.7402878	-6.32	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=X523	---	---	1.11	0.15	0.67	0.5276294	0.7403559	-6.32	FALSE
250579_at	putative protein terminal ear1, Z	MCT2	AT5G07930	1.07	0.10	0.67	0.527712	0.7404263	-6.32	FALSE
249416_at	putative protein DNA DAMAGE-	---	AT5G39570	-1.08	-0.11	-0.67	0.5278161	0.7405269	-6.32	FALSE
254878_at	heat shock transcription factor -	AT-HSFB2I	AT4G11660	-1.14	-0.19	-0.67	0.5280035	0.740553	-6.32	FALSE
264901_at	putative sulphate transporter pro	AST91	AT1G23090	1.27	0.34	0.67	0.5280175	0.740553	-6.32	FALSE
267180_at	unknown protein ; supported by	SLT1	AT2G37570	1.08	0.11	0.67	0.5279905	0.740553	-6.32	FALSE
259869_at	putative heat shock protein predi	---	AT1G76770	1.08	0.11	0.67	0.5280295	0.740553	-6.32	FALSE
246629_at	unknown protein similar to hypot	---	AT1G50750	-1.10	-0.14	-0.67	0.5279911	0.740553	-6.32	FALSE
249209_at	major surface glycoprotein-like ;	---	AT5G42620	1.08	0.11	0.67	0.5280243	0.740553	-6.32	FALSE
251745_at	putative protein zinc finger trans	SZF1	AT3G55980	1.51	0.60	0.66	0.5282092	0.7407594	-6.32	FALSE
262442_at	unknown protein identical to hypo	---	AT1G47420	-1.07	-0.10	-0.66	0.5282996	0.7407618	-6.32	FALSE
259115_at	hypothetical protein predicted by	---	AT3G01360	-1.09	-0.13	-0.66	0.5283252	0.7407618	-6.32	FALSE
249390_at	60S RIBOSOMAL PROTEIN L5	---	AT5G40130	-1.07	-0.09	-0.66	0.5283175	0.7407618	-6.32	FALSE
261061_at	DNA-binding protein, putative co	TRFL2	AT1G07540	1.08	0.11	0.66	0.5283408	0.7407618	-6.32	FALSE
262523_at	ubiquitin-specific protease 15 (U	UBP15	AT1G17110	-1.06	-0.09	-0.66	0.5284219	0.74083	-6.32	FALSE
259728_at	putative coatomer zeta subunit s	---	AT1G60970	1.07	0.10	0.66	0.5284788	0.7408643	-6.32	FALSE
267605_at	putative protein disulfide isomera	ATPDIL2-3	AT2G32920	-1.10	-0.14	-0.66	0.5285993	0.7409875	-6.32	FALSE
255863_s_a	putative GDSL-motif lipase/hydro	---	AT2G30220 /.	1.07	0.09	0.66	0.5287104	0.7410522	-6.32	FALSE

246520_at	putative protein RING-H2 finger	---	AT5G15790	-1.07	-0.09	-0.66	0.5286928	0.7410522	-6.32	FALSE
261031_at	hypothetical protein predicted by	---	AT1G17360	-1.16	-0.21	-0.66	0.5288499	0.7411774	-6.32	FALSE
257560_at	galactosyltransferase, putative c	---	AT3G14960	1.06	0.09	0.66	0.5288972	0.7411774	-6.32	FALSE
263245_at	hypothetical protein predicted by	---	AT2G31470	-1.06	-0.09	-0.66	0.5288706	0.7411774	-6.32	FALSE
259501_at	unknown protein ; supported by c	TPL	AT1G15750	-1.09	-0.13	-0.66	0.5291101	0.7414302	-6.32	FALSE
258930_at	unknown protein predicted by ge	---	AT3G10040	-1.07	-0.10	-0.66	0.5294527	0.7418486	-6.32	FALSE
259182_at	hypothetical protein predicted by	---	AT3G01750	-1.14	-0.19	-0.66	0.5294737	0.7418486	-6.32	FALSE
261991_at	hypothetical protein predicted by	---	AT1G33700	-1.10	-0.14	-0.66	0.5296439	0.7419347	-6.32	FALSE
263614_at	putative serpin	---	AT2G25240	1.10	0.14	0.66	0.5295896	0.7419347	-6.32	FALSE
AFFX-DapX	B. subtilis /GEN=dapB /DB_XRE	---	---	-1.17	-0.23	-0.66	0.5296653	0.7419347	-6.32	FALSE
267313_at	putative protein phosphatase 2C	---	AT2G34740	-1.10	-0.14	-0.66	0.5296034	0.7419347	-6.32	FALSE
245977_at	glucose-6-phosphate 1-dehydrog	G6PD2	AT5G13110	1.16	0.21	0.66	0.5297874	0.7420147	-6.32	FALSE
252206_at	centrin	ATCEN2	AT3G50360	1.08	0.11	0.66	0.5297699	0.7420147	-6.32	FALSE
266230_at	hypothetical protein predicted by	---	AT2G28830	-1.16	-0.21	-0.66	0.5298294	0.7420243	-6.32	FALSE
257330_at	hypothetical protein	---	---	1.07	0.10	0.66	0.5298593	0.7420243	-6.32	FALSE
255574_at	putative calcium-regulated prote	CBL5	AT4G01420	-1.08	-0.11	-0.66	0.5300898	0.7420763	-6.32	FALSE
245231_at	hypothetical protein	---	AT4G25600	-1.09	-0.13	-0.66	0.5299744	0.7420763	-6.32	FALSE
251189_at	putative protein putative mitocho	---	AT3G62650	-1.11	-0.15	-0.66	0.5300237	0.7420763	-6.32	FALSE
246618_at	putative protein similar to unknov	---	AT5G36280	1.07	0.09	0.66	0.530039	0.7420763	-6.32	FALSE
253315_at	putative protein various predicte	---	AT4G33900	1.08	0.11	0.66	0.5300917	0.7420763	-6.32	FALSE
250675_at	putative protein contains similarit	---	AT5G06260	1.07	0.09	0.66	0.5299467	0.7420763	-6.32	FALSE
266947_at	hypothetical protein predicted by	---	AT2G18830	1.09	0.13	0.66	0.5301516	0.7421146	-6.32	FALSE
263816_at	putative CCHC-type zinc finger p	---	---	1.09	0.13	0.66	0.5301991	0.7421356	-6.32	FALSE
263474_at	hypothetical protein predicted by	---	AT2G31725	-1.10	-0.14	-0.66	0.530357	0.7422766	-6.32	FALSE
247035_at	putative protein similar to unknov	ALC	AT5G67110	-1.07	-0.10	-0.66	0.5303649	0.7422766	-6.32	FALSE
247582_at	putative protein various predicte	---	AT5G60760	1.09	0.12	0.66	0.5304672	0.7423361	-6.32	FALSE
245177_at	annexin-like protein genmodel s	---	AT5G12380	1.08	0.11	0.66	0.5304725	0.7423361	-6.32	FALSE
257526_s_a	hypothetical protein similar to put	---	AT3G09330 ///	1.07	0.09	0.66	0.5305808	0.742351	-6.32	FALSE
265406_at	En/Spm-like transposon protein r	---	---	1.06	0.08	0.66	0.5305445	0.742351	-6.32	FALSE
253471_at	hypothetical protein	---	---	1.08	0.11	0.66	0.530557	0.742351	-6.32	FALSE
261558_at	unknown protein	---	AT1G01770	-1.13	-0.18	-0.66	0.5306888	0.7423655	-6.32	FALSE
267537_at	putative guanylate kinase ; supp	GK-1	AT2G41880	-1.25	-0.32	-0.66	0.5306535	0.7423655	-6.32	FALSE
251329_at	putative protein hypothetical pro	SYP73	AT3G61450	1.11	0.15	0.66	0.5306886	0.7423655	-6.32	FALSE
251672_at	MADS-box transcription factor-li	AGL16	AT3G57230	1.07	0.10	0.66	0.5307607	0.742375	-6.32	FALSE
264610_at	Expressed protein ; supported by	---	AT1G04645	-1.08	-0.11	-0.66	0.5307528	0.742375	-6.32	FALSE

255228_at	F-box protein family, AtFBL21 c	---	AT4G05470	-1.07	-0.10	-0.66	0.5309203	0.7424705	-6.32	FALSE
255605_at	hypothetical protein	---	AT4G01090	1.13	0.18	0.66	0.5309266	0.7424705	-6.32	FALSE
259866_at	putative calmodulin similar to cal	---	AT1G76640	1.25	0.32	0.66	0.5309067	0.7424705	-6.32	FALSE
248697_at	putative protein contains similarit	---	AT5G48370	-1.15	-0.20	-0.66	0.5310367	0.7425334	-6.32	FALSE
255747_s_a	hypothetical protein predicted by	---	AT1G32010 /,	1.07	0.10	0.66	0.5310197	0.7425334	-6.32	FALSE
249277_at	GDSL-motif lipase/hydrolase-like	---	AT5G41890	-1.23	-0.29	-0.66	0.5311963	0.7426655	-6.32	FALSE
267593_at	similar to disease resistance prot	AtRLP25	AT2G33030	1.07	0.09	0.66	0.5311953	0.7426655	-6.32	FALSE
262042_at	polygalacturonase, putative simi	---	AT1G80140	-1.08	-0.11	-0.66	0.5312299	0.742667	-6.32	FALSE
248055_at	serine/threonine-specific kinase l	---	AT5G55830	1.08	0.11	0.66	0.5312969	0.7427151	-6.32	FALSE
265894_at	putative lipid transfer protein	LTP	AT2G15050	1.23	0.30	0.66	0.5313627	0.7427615	-6.32	FALSE
262510_at	hypothetical protein similar to hyp	---	AT1G11270	-1.09	-0.12	-0.66	0.5314531	0.7428424	-6.32	FALSE
245895_at	SIR2-family protein sirtuin type 4	SRT2	AT5G09230	1.08	0.11	0.66	0.5314869	0.7428441	-6.32	FALSE
257998_at	hypothetical protein similar to hyp	---	AT3G27510	1.06	0.09	0.66	0.5315212	0.7428466	-6.32	FALSE
254169_at	putative protein ; supported by c	---	AT4G24290	1.10	0.14	0.66	0.5315714	0.7428713	-6.32	FALSE
266228_at	unknown protein ; supported by	CXIP4	AT2G28910	-1.09	-0.13	-0.66	0.5316463	0.7428848	-6.32	FALSE
257594_at	unknown protein	---	AT3G24740	1.09	0.13	0.66	0.5316362	0.7428848	-6.32	FALSE
258275_at	unknown protein ;supported by f	---	AT3G15760	1.14	0.19	0.66	0.5317541	0.7429586	-6.32	FALSE
244903_at	hypothetical protein	---	---	1.22	0.29	0.66	0.5317642	0.7429586	-6.32	FALSE
266697_at	profilin 4 ; supported by full-leng	PRF5	AT2G19770	1.10	0.14	0.66	0.531823	0.7429952	-6.32	FALSE
252268_at	kinesin-like protein several kines	---	AT3G49650	-1.11	-0.15	-0.66	0.5318772	0.7430255	-6.32	FALSE
248280_at	putative protein similar to unknov	---	AT5G52950	1.08	0.11	0.66	0.5320288	0.7431462	-6.32	FALSE
252614_at	serpin-like protein serpin - Horde	---	AT3G45220	1.06	0.08	0.66	0.532026	0.7431462	-6.32	FALSE
253653_at	hypothetical protein	---	AT4G30050	1.08	0.11	0.66	0.532231	0.743383	-6.32	FALSE
260038_at	Expressed protein ; supported by	---	AT1G68875	-1.07	-0.09	-0.66	0.5325165	0.743707	-6.32	FALSE
267521_at	hypothetical protein predicted by	---	AT2G30480	1.10	0.14	0.66	0.5325281	0.743707	-6.32	FALSE
260988_at	MAP3K alpha protein kinase, pu	MAP3KA	AT1G53570	1.12	0.16	0.66	0.532671	0.7438093	-6.32	FALSE
262391_at	geranyl geranyl pyrophosphate s	GGPS6	AT1G49530	-1.08	-0.11	-0.66	0.5326992	0.7438093	-6.32	FALSE
248024_at	putative protein contains similarit	---	AT5G55840	-1.10	-0.13	-0.66	0.5326578	0.7438093	-6.32	FALSE
247850_at	receptor-like protein kinase	---	AT5G58150	1.27	0.35	0.66	0.5328663	0.7439617	-6.32	FALSE
248413_at	putative protein strong similarity t	PLE	AT5G51600	-1.08	-0.11	-0.66	0.5328736	0.7439617	-6.32	FALSE
259158_at	hypothetical protein predicted by	---	AT3G05430	1.06	0.09	0.66	0.5329516	0.7439795	-6.32	FALSE
247756_at	subtilisin-like serine protease cor	---	AT5G59100	1.07	0.10	0.66	0.5329458	0.7439795	-6.32	FALSE
263504_s_a	hypothetical protein	---	AT2G07677	-1.07	-0.10	-0.66	0.5330087	0.7440137	-6.32	FALSE
265214_at	unkown protein ESTs gb|H3624	---	AT1G05000	1.19	0.25	0.66	0.5331361	0.7440857	-6.32	TRUE
264540_at	hypothetical protein predicted by	---	AT1G55630	-1.08	-0.11	-0.66	0.533124	0.7440857	-6.32	FALSE

257085_at	ubiquitin-specific protease 14 (U	UBP14	AT3G20630	-1.13	-0.18	-0.66	0.5331581	0.7440857	-6.32	FALSE
260451_at	putative AP2 domain transcriptio	---	AT1G72360	1.31	0.38	0.66	0.5331932	0.7440892	-6.32	FALSE
252203_at	hypothetical protein	---	AT3G50320	1.07	0.09	0.66	0.5332651	0.7441439	-6.32	FALSE
255065_s_a	putative arginase similar to argir	---	AT4G08870 ///	1.30	0.38	0.66	0.5333983	0.744221	-6.32	FALSE
257335_at	hypothetical protein	---	---	1.07	0.10	0.66	0.5333896	0.744221	-6.32	FALSE
246545_at	pectate lyase -like protein pectat	---	AT5G15110	1.07	0.09	0.66	0.5334508	0.744221	-6.32	FALSE
266580_at	unknown protein ;supported by f	---	AT2G46260	1.08	0.11	0.66	0.5334377	0.744221	-6.32	FALSE
248410_at	putative protein similar to unknov	---	AT5G51570	1.07	0.10	0.66	0.533611	0.7442624	-6.32	FALSE
253681_at	cytidine deaminase 3 (CDA3)	---	AT4G29630	1.08	0.11	0.66	0.5335667	0.7442624	-6.32	FALSE
249784_at	putative protein similar to unknov	---	AT5G24280	-1.11	-0.15	-0.66	0.5335792	0.7442624	-6.32	FALSE
251517_at	putative protein hypothetical pro	---	AT3G59370	1.06	0.08	0.66	0.5335386	0.7442624	-6.32	FALSE
245715_s_a	Expressed protein ; supported by	---	AT5G08670 ///	-1.09	-0.12	-0.66	0.5336543	0.7442772	-6.32	FALSE
261809_at	rac GTPase activating protein, p	---	AT1G08340	1.11	0.16	0.66	0.5337036	0.7443006	-6.32	FALSE
259261_at	unknown protein similar to unkno	---	AT3G11390	1.09	0.13	0.66	0.533782	0.7443644	-6.32	FALSE
248722_at	pyrophosphate-fructose-6-phosp	PFK2	AT5G47810	1.06	0.08	0.66	0.5338658	0.7444357	-6.32	FALSE
249571_at	putative protein predicted protei	---	AT5G37620	-1.07	-0.09	-0.66	0.5339236	0.7444708	-6.32	FALSE
256906_at	hypothetical protein contains Pfa	---	AT3G24000	-1.10	-0.13	-0.66	0.5340503	0.7446019	-6.32	FALSE
266507_at	unknown protein EST matches c	---	AT2G47860	1.07	0.10	0.65	0.5343592	0.7449871	-6.32	FALSE
267261_at	unknown protein ;supported by f	---	AT2G23120	1.15	0.20	0.65	0.5346725	0.7449983	-6.32	TRUE
264616_at	unknown protein	---	AT2G17740	-1.54	-0.63	-0.65	0.5344939	0.7449983	-6.32	FALSE
251309_at	putative protein carbonyl reducta	---	AT3G61220	-1.09	-0.13	-0.65	0.5347265	0.7449983	-6.32	FALSE
254087_at	brefeldin A-sensitive Golgi prote	---	AT4G24840	1.06	0.09	0.65	0.5347138	0.7449983	-6.32	FALSE
252524_at	putative protein mitochondrial AT	---	AT3G46430	-1.09	-0.12	-0.65	0.5347019	0.7449983	-6.32	FALSE
249391_at	putative protein predicted protei	---	AT5G40140	-1.11	-0.15	-0.65	0.534521	0.7449983	-6.32	FALSE
256547_at	receptor-like serine/threonine kir	---	AT3G14840	1.17	0.22	0.65	0.53463	0.7449983	-6.32	FALSE
264305_at	Expressed protein ; supported by	LSH7	AT1G78815	1.07	0.09	0.65	0.5347208	0.7449983	-6.32	FALSE
249521_at	putative protein strong similarity t	---	AT5G38690	-1.07	-0.10	-0.65	0.5344736	0.7449983	-6.32	FALSE
246475_at	putative protein IFA-binding prot	---	AT5G16720	-1.10	-0.14	-0.65	0.53465	0.7449983	-6.32	FALSE
250773_at	putative protein similar to unknov	---	AT5G05430	-1.13	-0.18	-0.65	0.5345142	0.7449983	-6.32	FALSE
267034_at	unknown protein ;supported by f	---	AT2G38310	-1.25	-0.32	-0.65	0.5348064	0.7450291	-6.32	TRUE
260002_at	putative ABC transporter similar	ATNAP3	AT1G67940	-1.13	-0.17	-0.65	0.534814	0.7450291	-6.32	FALSE
258187_at	HSC70-interacting protein, putat	ATTDX	AT3G17880	-1.07	-0.10	-0.65	0.5348977	0.7451003	-6.32	FALSE
249555_at	putative protein predicted protei	---	AT5G38300	1.08	0.11	0.65	0.5349967	0.7451927	-6.32	FALSE
261717_at	helix-loop-helix protein homolog	BEE1	AT1G18400	1.31	0.39	0.65	0.5351138	0.7452803	-6.32	TRUE
253498_at	putative protein various predicted	---	AT4G31890	1.17	0.23	0.65	0.5351577	0.7452803	-6.32	FALSE

249766_at	peroxidase-like protein	---	AT5G24070	1.08	0.11	0.65	0.5351392	0.7452803	-6.32	FALSE
254354_at	hypothetical protein	---	AT4G22370	1.06	0.08	0.65	0.5352501	0.745318	-6.32	FALSE
262264_at	Niemann-Pick C disease protein-	---	AT1G42470	1.21	0.28	0.65	0.5352232	0.745318	-6.32	FALSE
AFFX-r2-At-	Arabidopsis thaliana /REF=M64	---	---	1.21	0.27	0.65	0.5354068	0.7454907	-6.32	TRUE
250983_at	putative protein In2, Zea mays, I	---	AT5G02780	1.33	0.41	0.65	0.5355846	0.7456353	-6.32	TRUE
262280_at	unknown protein	---	AT1G68580	-1.15	-0.21	-0.65	0.5356741	0.7456353	-6.32	FALSE
250956_at	putative protein	---	AT5G03210	1.12	0.16	0.65	0.535656	0.7456353	-6.32	FALSE
252748_at	putative protein putative proteins	---	---	-1.07	-0.09	-0.65	0.5356377	0.7456353	-6.32	FALSE
248211_at	flavonol 3-O-glucosyltransferase-	---	AT5G54010	1.06	0.08	0.65	0.5355885	0.7456353	-6.32	FALSE
260444_at	unknown protein ;supported by f	---	AT1G68300	1.08	0.12	0.65	0.5357169	0.7456494	-6.32	FALSE
257128_at	cytochrome P450, putative conta	CYP705A1	AT3G20080	-1.10	-0.14	-0.65	0.5358183	0.745745	-6.32	FALSE
256810_at	adenyl cyclase, putative similar f	---	AT3G21465	-1.09	-0.12	-0.65	0.5359025	0.7458167	-6.32	FALSE
252417_at	putative calcium-binding protein	---	AT3G47480	-1.45	-0.53	-0.65	0.5360877	0.7459834	-6.32	FALSE
261615_at	unknown protein	---	AT1G33050	1.08	0.12	0.65	0.5360862	0.7459834	-6.32	FALSE
256524_at	glutamine synthetase, putative s	ATGSR2	AT1G66200	1.08	0.11	0.65	0.5362448	0.746111	-6.33	FALSE
249370_at	zinc finger - like protein predicte	---	AT5G40710	-1.06	-0.08	-0.65	0.5362229	0.746111	-6.33	FALSE
258695_at	putative ascorbate peroxidase st	APX2	AT3G09640	1.09	0.13	0.65	0.5363362	0.7461927	-6.33	FALSE
255611_at	hypothetical protein	---	AT4G01210	1.07	0.09	0.65	0.5364335	0.746237	-6.33	FALSE
247796_at	Expressed protein ;supported by	---	AT5G58782	-1.08	-0.11	-0.65	0.5364327	0.746237	-6.33	FALSE
255800_at	putative protein transposase, Ipo	---	AT4G10200	1.07	0.09	0.65	0.536542	0.7463425	-6.33	FALSE
246583_at	protein kinase -like protein Ste-2	---	AT5G14720	1.09	0.13	0.65	0.536593	0.7463678	-6.33	FALSE
263574_at	putative tetracycline transporter p	---	AT2G16990	1.07	0.09	0.65	0.5368524	0.7464104	-6.33	FALSE
260795_at	CLE3, putative CLAVATA3/ESR	CLE3	AT1G06225	1.07	0.10	0.65	0.536868	0.7464104	-6.33	FALSE
244947_at	hypothetical protein	---	---	1.10	0.13	0.65	0.5368694	0.7464104	-6.33	FALSE
246873_at	putative protein	---	AT5G26100	-1.07	-0.10	-0.65	0.5368149	0.7464104	-6.33	FALSE
246585_at	myb transcription factor werewolf	ATMYB66	AT5G14750	-1.07	-0.09	-0.65	0.5368998	0.7464104	-6.33	FALSE
263998_at	unknown protein	---	AT2G22510	-1.17	-0.23	-0.65	0.5369181	0.7464104	-6.33	FALSE
266375_at	En/Spm-like transposon protein r	---	---	1.08	0.11	0.65	0.5367951	0.7464104	-6.33	FALSE
261000_at	hypothetical protein predicted by	---	AT1G26540	-1.07	-0.09	-0.65	0.5369097	0.7464104	-6.33	FALSE
265505_at	putative RING zinc finger protein	---	AT2G15530	1.07	0.09	0.65	0.536684	0.7464104	-6.33	FALSE
259557_at	hypothetical protein	WAK4	AT1G21210	-1.07	-0.09	-0.65	0.5369526	0.7464129	-6.33	FALSE
245039_at	putative beta-1,3-glucanase ;su	---	AT2G26600	-1.08	-0.11	-0.65	0.536994	0.7464249	-6.33	FALSE
252460_at	putative protein predicted protei	---	---	-1.06	-0.08	-0.65	0.5370707	0.7464406	-6.33	FALSE
245552_at	cytochrome P450 like protein	CYP705A3	AT4G15360	1.07	0.10	0.65	0.5370406	0.7464406	-6.33	FALSE
255949_at	hypothetical protein predicted by	---	AT1G22080	1.06	0.08	0.65	0.5371136	0.7464547	-6.33	FALSE

245436_at	membrane protein homolog	---	AT4G16620	1.08	0.11	0.65	0.5372351	0.7465054	-6.33	FALSE
255144_at	putative protein predicted protein	---	---	-1.06	-0.08	-0.65	0.5372482	0.7465054	-6.33	FALSE
263458_at	putative GTP-binding protein	ATRABH1D	AT2G22290	-1.09	-0.12	-0.65	0.5372237	0.7465054	-6.33	FALSE
252938_at	hypothetical protein	---	AT4G39190	-1.25	-0.32	-0.65	0.5373473	0.7465975	-6.33	FALSE
265364_at	putative retroelement pol polypro	---	---	-1.07	-0.09	-0.65	0.5374088	0.7466375	-6.33	FALSE
253219_at	MYB-like protein myb-related pr	AtMYB32	AT4G34990	-1.14	-0.19	-0.65	0.5375753	0.7468234	-6.33	FALSE
258441_at	hypothetical protein predicted by	AT3G17265	---	1.07	0.10	0.65	0.5376621	0.7468985	-6.33	FALSE
262407_at	hypothetical protein predicted by	---	AT1G34630	-1.14	-0.19	-0.65	0.5377462	0.746918	-6.33	FALSE
246996_at	putative protein similar to unknov	LBD37	AT5G67420	-1.13	-0.18	-0.65	0.5377153	0.746918	-6.33	FALSE
254336_at	aspartic proteinase like protein c	---	AT4G22050	1.10	0.13	0.65	0.5378072	0.746918	-6.33	FALSE
261453_at	O-methyltransferase, putative si	---	AT1G21130	1.19	0.25	0.65	0.5377747	0.746918	-6.33	FALSE
246431_at	calcium-binding protein calcium	APC1	AT5G17480	-1.06	-0.08	-0.65	0.5378462	0.7469267	-6.33	FALSE
258399_at	early auxin-induced protein, IAA	IAA19	AT3G15540	-1.30	-0.38	-0.65	0.5380207	0.7469569	-6.33	TRUE
245095_at	putative protein kinase contains a	---	AT2G40860	-1.11	-0.15	-0.65	0.5380236	0.7469569	-6.33	FALSE
262328_at	hypothetical protein similar to hyp	---	AT1G64100	1.06	0.08	0.65	0.5380161	0.7469569	-6.33	FALSE
263128_at	zinc finger protein, putative simil	LZF1	AT1G78600	-1.14	-0.19	-0.65	0.5380462	0.7469569	-6.33	FALSE
255408_at	hypothetical protein similar to A.	---	AT4G03490	1.13	0.18	0.65	0.5380644	0.7469569	-6.33	FALSE
249614_at	putative protein predicted protei	WSD1	AT5G37300	1.06	0.08	0.65	0.5379626	0.7469569	-6.33	FALSE
254584_at	putative protein probable membr	VPS54	AT4G19490	-1.07	-0.09	-0.65	0.5381491	0.7469858	-6.33	FALSE
258624_at	unknown protein ; supported by	---	AT3G02950	-1.09	-0.12	-0.65	0.5381507	0.7469858	-6.33	FALSE
245430_at	hypothetical protein	FIP2	AT4G17060	1.06	0.08	0.65	0.5382242	0.7470134	-6.33	FALSE
252288_at	hypothetical protein	---	AT3G49080	-1.11	-0.15	-0.65	0.5382361	0.7470134	-6.33	FALSE
250296_at	heat shock protein 17.6-II ;suppo	HSP17.6II	AT5G12020	1.18	0.24	0.65	0.5382977	0.7470534	-6.33	FALSE
255849_at	hypothetical protein predicted by	---	AT2G33320	1.07	0.10	0.65	0.5383513	0.7470823	-6.33	FALSE
267331_at	putative salt-inducible protein	---	AT2G19280	1.09	0.13	0.65	0.538399	0.7471031	-6.33	FALSE
246617_at	GSH-dependent dehydroascorba	---	AT5G36270	1.08	0.11	0.65	0.5385655	0.7471766	-6.33	FALSE
257244_at	receptor kinase, putative similar	---	AT3G24240	1.15	0.20	0.65	0.538525	0.7471766	-6.33	FALSE
259314_at	putative glucose and ribitol dehyd	---	AT3G05260	1.12	0.17	0.65	0.5385774	0.7471766	-6.33	FALSE
249950_at	protein kinase - like protein Pto k	---	AT5G18910	1.06	0.09	0.65	0.538583	0.7471766	-6.33	FALSE
262593_at	putative ubiquinol--cytochrome-c	---	AT1G15120	-1.12	-0.17	-0.65	0.5387457	0.7473435	-6.33	FALSE
262757_at	putative Na/H antiporter similar to	ATCHX1	AT1G16380	1.08	0.11	0.65	0.5387688	0.7473435	-6.33	FALSE
255094_at	putative zinc finger protein	ORTHL	AT4G08590	1.13	0.18	0.65	0.5388242	0.7473748	-6.33	FALSE
263663_at	putative malate dehydrogenase s	---	AT1G04410	-1.07	-0.10	-0.65	0.5391067	0.7477213	-6.33	FALSE
253529_at	putative protein hypothetical pro	---	AT4G31520	1.06	0.09	0.65	0.5392611	0.7478899	-6.33	FALSE
255329_at	hypothetical protein	---	AT4G04370	-1.06	-0.09	-0.65	0.539302	0.7479012	-6.33	FALSE

253297_at	beta-xylan endohydrolase -like p	---	AT4G33810	-1.07	-0.10	-0.65	0.5394122	0.7480086	-6.33	FALSE
266416_at	unknown protein ; supported by	---	AT2G38710	1.11	0.15	0.65	0.5395581	0.7481199	-6.33	FALSE
265645_at	unknown protein	---	AT2G27370	1.07	0.10	0.65	0.5395387	0.7481199	-6.33	FALSE
256707_at	hypothetical protein predicted by	---	---	-1.06	-0.09	-0.65	0.5397419	0.7482725	-6.33	FALSE
245370_at	Expressed protein ; supported by	---	AT4G16840	-1.15	-0.20	-0.65	0.5397666	0.7482725	-6.33	FALSE
262750_at	unknown protein ; supported by	---	AT1G28710	-1.09	-0.12	-0.65	0.539722	0.7482725	-6.33	FALSE
266577_at	predicted protein	---	AT2G23945	-1.08	-0.11	-0.65	0.5399664	0.7484585	-6.33	FALSE
266798_at	putative embryo-abundant protei	AtbZIP6	AT2G22850	1.15	0.21	0.65	0.5399498	0.7484585	-6.33	FALSE
245839_at	disease resistance protein, puta	---	AT1G58390	1.06	0.09	0.65	0.5400572	0.748539	-6.33	FALSE
249203_at	cytochrome P450	CYP71A16	AT5G42590	1.08	0.11	0.65	0.5401776	0.7486603	-6.33	FALSE
245992_at	receptor protein kinase - like rec	---	AT5G20690	1.06	0.08	0.64	0.5403907	0.7486827	-6.33	FALSE
257245_at	hypothetical protein contains Pfa	---	AT3G24110	1.09	0.13	0.64	0.540356	0.7486827	-6.33	FALSE
257714_at	histone H3, putative similar to hi	---	AT3G27360	-1.09	-0.12	-0.65	0.5402777	0.7486827	-6.33	FALSE
248929_at	myrosinase-binding protein-like;	---	AT5G46000	1.08	0.11	0.64	0.5403743	0.7486827	-6.33	FALSE
255108_at	hypothetical protein	---	AT4G08740	1.10	0.14	0.64	0.5403656	0.7486827	-6.33	FALSE
265686_at	hypothetical protein predicted by	---	AT2G24460	1.06	0.09	0.65	0.540264	0.7486827	-6.33	FALSE
264406_at	putative phragmoplastin similar	ADL6	AT1G10290	1.08	0.12	0.64	0.5405929	0.7488323	-6.33	FALSE
256031_at	choline kinase (GmCK2p), putat	---	AT1G34100	-1.07	-0.10	-0.64	0.5405888	0.7488323	-6.33	FALSE
255361_at	hypothetical protein	---	---	1.06	0.08	0.64	0.5405972	0.7488323	-6.33	FALSE
267454_at	putative U5 small nuclear ribonu	---	AT2G33730	-1.07	-0.10	-0.64	0.5407164	0.7489088	-6.33	FALSE
267551_at	ubiquitin-specific protease 1 (UB	UBP1	AT2G32780	1.09	0.13	0.64	0.5407181	0.7489088	-6.33	FALSE
267307_at	putative laccase	LAC3	AT2G30210	1.10	0.14	0.64	0.5409648	0.7491808	-6.33	FALSE
265509_at	putative retroelement pol polypro	---	---	1.10	0.14	0.64	0.5409801	0.7491808	-6.33	FALSE
254659_at	starch synthase-like protein bac	SS4	AT4G18240	-1.13	-0.17	-0.64	0.5410658	0.7492539	-6.33	FALSE
245133_at	putative nucleotide sugar epimer	GAE4	AT2G45310	-1.12	-0.17	-0.64	0.5411374	0.749262	-6.33	FALSE
259151_at	kinesin-like protein similar to carb	---	AT3G10310	-1.10	-0.14	-0.64	0.5411104	0.749262	-6.33	FALSE
254578_at	putative pectinacetylesterase pr	---	AT4G19400 /	-1.12	-0.17	-0.64	0.5413807	0.7494694	-6.33	FALSE
251026_at	hypothetical protein	FHL	AT5G02200	-1.32	-0.40	-0.64	0.5413362	0.7494694	-6.33	FALSE
259930_at	hypothetical protein predicted by	---	AT1G34355	1.08	0.11	0.64	0.5413857	0.7494694	-6.33	FALSE
259382_s_a	jasmonate inducible protein isolo	JAL31	AT3G16420 /	1.43	0.52	0.64	0.5414619	0.7495294	-6.33	FALSE
247204_at	GTP binding protein-like	AtRABH1a	AT5G64990	1.08	0.11	0.64	0.5415486	0.7496039	-6.33	FALSE
249114_at	putative protein similar to unknov	---	---	-1.10	-0.13	-0.64	0.5415835	0.7496068	-6.33	FALSE
255663_at	hypothetical protein	---	AT4G00420	-1.08	-0.11	-0.64	0.5416316	0.7496279	-6.33	FALSE
259412_at	DNA binding protein GT-1, putat	---	AT1G13450	-1.07	-0.10	-0.64	0.5417807	0.7497455	-6.33	FALSE
263779_at	putative photomorphogenesis re	SPA1	AT2G46340	-1.09	-0.12	-0.64	0.5417823	0.7497455	-6.33	FALSE

264030_at	putative steroid sulfotransferase	---	AT2G03770	-1.09	-0.13	-0.64	0.5418472	0.7497898	-6.33	FALSE
250206_at	mitochondrial phosphate translo	---	AT5G14040	1.14	0.19	0.64	0.5418885	0.7498014	-6.33	FALSE
255970_s_a	hypothetical protein predicted by	---	---	1.06	0.09	0.64	0.5419613	0.7498567	-6.33	FALSE
266199_at	putative calcium-dependent prot	CPK20	AT2G38910	1.07	0.10	0.64	0.5420761	0.7499701	-6.33	FALSE
245517_at	hypothetical protein	---	AT4G15840	-1.06	-0.08	-0.64	0.5421394	0.7500121	-6.33	FALSE
246117_at	CAF-like protein CAF protein - A	DCL4	AT5G20320	-1.11	-0.16	-0.64	0.542381	0.7502978	-6.33	FALSE
267473_at	hypothetical protein predicted by	---	AT2G02750	1.08	0.10	0.64	0.5424117	0.7502978	-6.33	FALSE
257547_at	hypothetical protein predicted by	---	AT3G13000	-1.22	-0.28	-0.64	0.5424691	0.7503317	-6.33	TRUE
261198_at	nitrate transporter, putative simil	ATNRT2.5	AT1G12940	1.06	0.09	0.64	0.5425464	0.7503931	-6.33	FALSE
264218_at	unknown protein	---	AT1G60200	1.06	0.09	0.64	0.5427827	0.7505417	-6.33	FALSE
259619_at	hypothetical protein	---	AT1G42980	-1.09	-0.12	-0.64	0.5427866	0.7505417	-6.33	FALSE
260725_at	Expressed protein ; supported by	---	AT1G48170	-1.08	-0.11	-0.64	0.5428167	0.7505417	-6.33	FALSE
AFFX-r2-P1	Bacteriophage P1 /GEN=cre /DB	---	---	1.13	0.18	0.64	0.542738	0.7505417	-6.33	FALSE
248056_at	unknown protein ; supported by	XYLT	AT5G55500	1.06	0.08	0.64	0.5428183	0.7505417	-6.33	FALSE
267128_at	putative acetone-cyanohydrin lya	MES1	AT2G23620	1.09	0.13	0.64	0.542924	0.7506423	-6.33	FALSE
265771_at	unknown protein ;supported by f	---	AT2G48030	1.09	0.13	0.64	0.5429625	0.75065	-6.33	TRUE
247556_at	putative protein predicted protei	---	AT5G61040	-1.10	-0.13	-0.64	0.543239	0.7508631	-6.33	FALSE
252216_at	putative protein several hypothet	---	AT3G50420	-1.09	-0.13	-0.64	0.5432483	0.7508631	-6.33	FALSE
247823_at	putative protein predicted protei	---	AT5G58450	-1.06	-0.08	-0.64	0.5432285	0.7508631	-6.33	FALSE
261599_at	hypothetical protein similar to hy	---	AT1G49700	1.08	0.11	0.64	0.5432024	0.7508631	-6.33	FALSE
263999_at	hypothetical protein predicted by	---	AT2G22370	-1.08	-0.11	-0.64	0.5433267	0.750926	-6.33	FALSE
264519_at	putative reverse transcriptase sir	---	AT1G10000	1.09	0.13	0.64	0.5434945	0.7511124	-6.33	FALSE
266754_at	hypothetical protein	---	AT2G46980	1.10	0.14	0.64	0.5435307	0.7511168	-6.33	FALSE
250512_at	Expressed protein ; supported by	---	AT5G09995	1.09	0.12	0.64	0.5435951	0.7511603	-6.33	FALSE
252521_at	hypothetical protein	---	AT3G46380	-1.12	-0.16	-0.64	0.5436725	0.7512218	-6.33	FALSE
253711_at	hypothetical protein	DER1	---	1.07	0.10	0.64	0.5437725	0.751269	-6.33	FALSE
245763_at	transposon protein, putative sim	---	AT1G27850	1.06	0.09	0.64	0.5437575	0.751269	-6.33	FALSE
247996_at	putative protein contains similarit	---	AT5G56170	1.14	0.18	0.64	0.5439696	0.7514047	-6.33	FALSE
247415_at	unknown protein	---	AT5G63060	-1.15	-0.20	-0.64	0.5439406	0.7514047	-6.33	FALSE
250614_at	putative protein homeodomain p	---	AT5G07260	-1.05	-0.08	-0.64	0.5439087	0.7514047	-6.33	FALSE
253077_at	hypothetical protein	---	AT4G36170	-1.06	-0.09	-0.64	0.5440571	0.7514801	-6.33	FALSE
263921_at	putative fructose bisphosphate a	---	AT2G36460	-1.10	-0.13	-0.64	0.5442986	0.7517681	-6.33	FALSE
245954_at	far-red impaired response protei	FRS10	AT5G28530	-1.08	-0.11	-0.64	0.5443361	0.7517744	-6.33	FALSE
253442_at	H+-transporting ATPase - like pr	---	AT4G32530	1.07	0.09	0.64	0.5443775	0.7517861	-6.33	FALSE
251905_at	putative protein zinc finger prote	GAPB	AT1G42970 ///	1.08	0.12	0.64	0.544489	0.7518491	-6.33	FALSE

258572_at	hypothetical protein	---	AT3G04270	-1.06	-0.08	-0.64	0.5444589	0.7518491	-6.33	FALSE
256905_at	mitochondrial chaperonin hsp60	HSP60	AT3G23990	-1.19	-0.25	-0.64	0.5445696	0.7519106	-6.33	FALSE
252347_at	ribosomal protein L13 homolog r	---	AT3G48130	1.08	0.11	0.64	0.5445995	0.7519106	-6.33	FALSE
263215_at	putative reticuline oxidase-like p	---	AT1G30710	1.08	0.11	0.64	0.5446782	0.7519738	-6.33	FALSE
254854_at	putative protein hypothetical pro	---	AT4G12130	1.10	0.14	0.64	0.5448023	0.7520084	-6.33	FALSE
248972_at	putative protein similar to unknov	ATDSS1(V)	AT5G45010	-1.13	-0.17	-0.64	0.5447418	0.7520084	-6.33	FALSE
267052_at	unknown protein	---	AT2G38410	1.08	0.11	0.64	0.544801	0.7520084	-6.33	FALSE
265536_at	unknown protein contains a dom	---	AT2G15880	-1.18	-0.24	-0.64	0.5448616	0.7520448	-6.33	FALSE
247557_at	putative protein	---	AT5G61050	1.06	0.08	0.64	0.5449363	0.7521024	-6.33	FALSE
257733_at	unknown protein ; supported by	---	AT3G18350	1.08	0.11	0.64	0.5451549	0.7523159	-6.34	FALSE
252302_at	putative protein hypothetical pro	---	AT3G49190	-1.06	-0.09	-0.64	0.545157	0.7523159	-6.34	FALSE
259614_at	dioxygenase, putative similar to	ATGA2OX4	AT1G47990	1.08	0.11	0.64	0.5452178	0.7523267	-6.34	FALSE
253896_at	putative protein NBS/LRR disea	---	AT4G27190	1.08	0.11	0.64	0.5452307	0.7523267	-6.34	FALSE
250506_at	ABC transporter, ATP-binding p	GCN2	AT5G09930	1.08	0.11	0.64	0.545332	0.752421	-6.34	FALSE
256304_at	Expressed protein ; supported by	---	AT1G69523	-1.14	-0.18	-0.64	0.5454309	0.7525119	-6.34	FALSE
264581_at	hypothetical protein predicted by	---	AT1G05210	-1.17	-0.22	-0.64	0.545509	0.7525286	-6.34	FALSE
260435_at	putative transcription factor simil	MYB62	AT1G68320	1.19	0.25	0.64	0.5455054	0.7525286	-6.34	FALSE
258926_s_a	unknown protein N-terminus simi	anac052	AT3G10480 /	1.10	0.14	0.64	0.5455479	0.7525367	-6.34	FALSE
259064_at	putative calmodulin similar to ca	AGD11	AT3G07490	1.08	0.11	0.64	0.5456354	0.7526119	-6.34	FALSE
260477_at	Ser/Thr protein kinase isolog	---	AT1G11050	1.34	0.42	0.64	0.5459204	0.7526692	-6.34	TRUE
257403_at	hypothetical protein similar to hy	---	AT1G62520	1.07	0.10	0.64	0.5459064	0.7526692	-6.34	FALSE
263918_at	putative proline transporter ;sup	ProT3	AT2G36590	1.30	0.38	0.64	0.5459739	0.7526692	-6.34	FALSE
246292_at	putative protein hnRNP A/B rela	UBA2A	AT3G56860	1.09	0.12	0.64	0.5457817	0.7526692	-6.34	FALSE
249992_at	AP2 domain -like protein AP2/E	PUCHI	AT5G18560	1.08	0.11	0.64	0.5459583	0.7526692	-6.34	FALSE
246827_at	copper binding - like protein mav	---	AT5G26330	-1.09	-0.12	-0.64	0.545901	0.7526692	-6.34	FALSE
255712_at	hypothetical protein similar to A.	---	AT4G00280	-1.07	-0.10	-0.64	0.5458617	0.7526692	-6.34	FALSE
254735_at	putative disease resistance prot	AtRLP47	AT4G13810	1.08	0.12	0.64	0.5457508	0.7526692	-6.34	FALSE
267045_at	putative protein kinase contains a	CIPK13	AT2G34180	-1.07	-0.09	-0.64	0.5459465	0.7526692	-6.34	FALSE
248430_at	putative protein similar to unknov	---	AT5G51800	-1.08	-0.11	-0.64	0.5460237	0.7526923	-6.34	FALSE
253472_at	hypothetical protein	---	AT4G32230	1.07	0.10	0.64	0.5462101	0.7529039	-6.34	FALSE
247344_at	ARI-like RING zinc finger protein	---	AT5G63750	1.08	0.12	0.64	0.5463074	0.7529924	-6.34	FALSE
266639_at	defender against cell death prote	DAD2	AT2G35520	-1.07	-0.10	-0.64	0.5463876	0.7530119	-6.34	FALSE
262613_at	putative DNA-binding protein sim	WRKY4	AT1G13960	1.07	0.10	0.64	0.5463754	0.7530119	-6.34	FALSE
259837_at	aquaporin, putative similar to de	---	AT1G52180	1.12	0.16	0.63	0.546523	0.7530426	-6.34	FALSE
254223_at	putative protein Pennisetum cilia	---	AT4G23730	-1.06	-0.09	-0.63	0.5464975	0.7530426	-6.34	FALSE

253730_at	putative protein hypothetical pro	---	AT4G29480	-1.13	-0.18	-0.63	0.5464694	0.7530426	-6.34	FALSE
257380_at	hypothetical protein predicted by	---	AT2G28090	1.09	0.12	0.63	0.5465779	0.7530426	-6.34	FALSE
256320_at	DnaJ protein, putative contains l	---	AT3G12170	1.09	0.12	0.63	0.5465589	0.7530426	-6.34	FALSE
257118_at	hypothetical protein	---	AT3G20180	-1.06	-0.09	-0.63	0.5466079	0.7530426	-6.34	FALSE
264024_at	hypothetical protein predicted by	---	AT2G21180	-1.15	-0.20	-0.63	0.5467523	0.7530945	-6.34	FALSE
262504_at	putative protein disulfide isomer	ATPDIL1-1	AT1G21750	-1.12	-0.16	-0.63	0.5468106	0.7530945	-6.34	FALSE
255263_at	4-coumarate--CoA ligase - like p	---	AT4G05160	1.06	0.09	0.63	0.5467246	0.7530945	-6.34	FALSE
259898_at	hypothetical protein predicted by	---	AT1G71200	1.07	0.10	0.63	0.5468005	0.7530945	-6.34	FALSE
250699_at	receptor-like protein kinase	SRF2	AT5G06820	1.08	0.11	0.63	0.5467355	0.7530945	-6.34	FALSE
245259_at	kinesin like protein ; supported b	PAKRP1	AT4G14150	1.07	0.09	0.63	0.5470134	0.7533282	-6.34	FALSE
260010_at	putative trehalose-6-phosphate s	ATTPS6	AT1G68020	1.12	0.17	0.63	0.5471819	0.7534239	-6.34	FALSE
246255_at	transcription initiation factor like	ATPBRP	AT4G36650	1.08	0.11	0.63	0.547129	0.7534239	-6.34	FALSE
267316_at	homeodomain transcription facto	PHB	AT2G34710	-1.13	-0.18	-0.63	0.5471632	0.7534239	-6.34	FALSE
252527_at	dTDP-glucose 4-6-dehydratases	UXS5	AT3G46440	1.09	0.12	0.63	0.5473243	0.7535502	-6.34	FALSE
257864_at	hypothetical protein predicted by	---	AT3G17740	-1.11	-0.15	-0.63	0.5474554	0.7535502	-6.34	FALSE
257221_at	MYB family transcription factor (	ATMYB0	AT3G27920	1.10	0.13	0.63	0.5474719	0.7535502	-6.34	FALSE
257415_at	hypothetical protein similar to hy	---	AT1G70040	1.08	0.11	0.63	0.5473994	0.7535502	-6.34	FALSE
260992_at	hypothetical protein predicted by	---	AT1G12150	-1.06	-0.09	-0.63	0.5473984	0.7535502	-6.34	FALSE
244908_at	hypothetical protein	---	---	1.12	0.17	0.63	0.5474439	0.7535502	-6.34	FALSE
249622_at	putative protein	---	AT5G37550	1.11	0.15	0.63	0.5475964	0.7535851	-6.34	FALSE
245553_at	lupeol synthase like protein	BARS1	AT4G15370	1.06	0.08	0.63	0.5475458	0.7535851	-6.34	FALSE
260673_at	unknown protein ; supported by f	---	AT1G19330	-1.14	-0.19	-0.63	0.5475928	0.7535851	-6.34	FALSE
245296_at	isp4 like protein ; supported by c	ATOPT3	AT4G16370	1.14	0.19	0.63	0.5478256	0.7538551	-6.34	FALSE
245172_at	hypothetical protein predicted by	---	AT2G47540	1.06	0.08	0.63	0.5478659	0.7538651	-6.34	FALSE
246851_at	putative protein various predicte	AGL26	AT5G26870	1.06	0.08	0.63	0.5479693	0.7539619	-6.34	FALSE
259044_at	pollen allergen Bra r II identical t	---	AT3G03430	1.07	0.09	0.63	0.5480661	0.7540495	-6.34	FALSE
249854_at	putative protein contains similarit	---	AT5G22960	-1.09	-0.12	-0.63	0.5482164	0.7542109	-6.34	FALSE
257057_at	hypothetical protein predicted by	---	---	1.05	0.08	0.63	0.5484473	0.7543465	-6.34	FALSE
256175_at	unknown protein	---	AT1G51670	-1.07	-0.09	-0.63	0.548399	0.7543465	-6.34	FALSE
247227_at	putative protein contains similarit	---	AT5G65130	1.07	0.10	0.63	0.5484181	0.7543465	-6.34	FALSE
245918_at	putative protein various predicte	---	---	-1.06	-0.08	-0.63	0.5484114	0.7543465	-6.34	FALSE
258620_at	putative MYB family transcription	MYB107	AT3G02940	1.05	0.08	0.63	0.5486372	0.7543803	-6.34	FALSE
260750_at	light repressible receptor protein	---	AT1G49100	-1.07	-0.10	-0.63	0.5485265	0.7543803	-6.34	FALSE
261209_at	unknown protein ; supported by c	---	AT1G12810	1.10	0.14	0.63	0.5485491	0.7543803	-6.34	FALSE
261965_at	athila ORF 1, putative similar to	---	---	1.06	0.08	0.63	0.548575	0.7543803	-6.34	FALSE

257479_at	hypothetical protein contains sim	WAKL4	AT1G16150	1.12	0.17	0.63	0.5486336	0.7543803	-6.34	FALSE
266549_at	Expressed protein ; supported by	EXL1	AT2G35150	1.08	0.11	0.63	0.5487384	0.7544284	-6.34	FALSE
266107_at	hypothetical protein predicted by	---	AT2G37910	1.12	0.16	0.63	0.5487228	0.7544284	-6.34	FALSE
258043_at	unknown protein ; supported by	---	AT3G21290	-1.06	-0.08	-0.63	0.5487773	0.7544365	-6.34	FALSE
249920_at	putative protein various predicted	---	AT5G19260	-1.21	-0.27	-0.63	0.5488373	0.7544735	-6.34	FALSE
245561_at	indole-3-acetate beta-glucosyltra	UGT84A4	AT4G15500	1.09	0.13	0.63	0.5488732	0.7544774	-6.34	FALSE
265837_at	unknown protein	LURP1	AT2G14560	1.70	0.77	0.63	0.5489631	0.7545554	-6.34	FALSE
264378_at	hypothetical protein predicted by	---	AT2G25220	1.22	0.28	0.63	0.5490135	0.7545644	-6.34	FALSE
267354_at	putative MYB family transcription	MYB25	AT2G39880	1.12	0.16	0.63	0.5490513	0.7545644	-6.34	FALSE
258105_at	Expressed protein ; supported by	---	AT3G23605	-1.15	-0.20	-0.63	0.5491019	0.7545644	-6.34	FALSE
254143_at	putative protein histidine-rich ca	---	AT4G24680	1.06	0.08	0.63	0.5490965	0.7545644	-6.34	FALSE
257251_at	type 1 membrane protein, putati	PMP	AT3G24160	1.07	0.10	0.63	0.5492409	0.7546076	-6.34	FALSE
250134_at	Expressed protein ; supported by	---	---	-1.09	-0.12	-0.63	0.5492472	0.7546076	-6.34	FALSE
259585_at	hypothetical protein contains sim	---	AT1G28090	-1.07	-0.10	-0.63	0.5494641	0.7546076	-6.34	FALSE
264682_at	polygalacturonase, putative simi	---	AT1G65570	1.06	0.09	0.63	0.5493321	0.7546076	-6.34	FALSE
264742_at	hypothetical protein similar to hy	---	AT1G62130	1.09	0.13	0.63	0.5493501	0.7546076	-6.34	FALSE
247749_at	myb-related protein - like myb-re	MYB119	AT5G58850	1.09	0.13	0.63	0.5494438	0.7546076	-6.34	FALSE
251891_at	aintegumaenta-like protein ovule	WRI1	AT3G54320	-1.06	-0.09	-0.63	0.5493335	0.7546076	-6.34	FALSE
265533_at	putative replication protein A1	---	---	1.06	0.08	0.63	0.549412	0.7546076	-6.34	FALSE
255024_at	hypothetical protein	---	AT4G09860	1.06	0.08	0.63	0.5494448	0.7546076	-6.34	FALSE
250052_at	putative protein predicted protei	---	AT5G17830	-1.09	-0.12	-0.63	0.5492184	0.7546076	-6.34	FALSE
257972_at	putative protein kinase, ATN1 al	ATN1	AT3G27560	-1.08	-0.11	-0.63	0.549501	0.7546128	-6.34	FALSE
249848_at	putative protein similar to unknov	NIC3	AT5G23220	-1.08	-0.11	-0.63	0.54973	0.7548818	-6.34	FALSE
250469_at	pollen allergen -like protein SAH	---	AT5G10130	-1.10	-0.13	-0.63	0.5498254	0.7549219	-6.34	FALSE
245001_at	PSII low MW protein	---	---	-1.08	-0.11	-0.63	0.549812	0.7549219	-6.34	FALSE
259348_at	hypothetical protein may contain	---	AT3G03770	1.13	0.17	0.63	0.5499473	0.7549984	-6.34	FALSE
248827_at	calcium sensor protein, calcineu	CBL9	AT5G47100	-1.12	-0.16	-0.63	0.549942	0.7549984	-6.34	FALSE
247356_at	beta-galactosidase (emb|CAB64	MUM2	AT5G63800	1.15	0.20	0.63	0.5501	0.7551626	-6.34	FALSE
260857_at	unknown protein contains Pfam p	LYM1	AT1G21880	-1.18	-0.24	-0.63	0.5502202	0.755208	-6.34	FALSE
245250_at	ethylene responsive element bin	ATERF6	AT4G17490	1.49	0.58	0.63	0.5502324	0.755208	-6.34	TRUE
251443_at	putative protein unknown protein	---	AT3G59940	-1.15	-0.20	-0.63	0.5501871	0.755208	-6.34	FALSE
246755_at	F-box protein family contains sim	---	AT5G27920	1.17	0.23	0.63	0.5502699	0.755214	-6.34	FALSE
267597_at	putative leucine-rich repeat disea	AtRLP24	AT2G33020	1.14	0.19	0.63	0.5503135	0.7552284	-6.34	FALSE
249636_at	beta-glucosidase -like protein pr	BGLU42	AT5G36890	1.08	0.10	0.63	0.550488	0.7554224	-6.34	FALSE
249011_at	putative protein strong similarity	---	AT5G44670	-1.18	-0.24	-0.63	0.5505522	0.7554651	-6.34	FALSE

251779_at	putative protein various predicte	---	---	1.07	0.10	0.63	0.5505957	0.7554792	-6.34	FALSE
259845_at	auxin transporter splice variant b	PIN1	AT1G73590	1.11	0.15	0.63	0.550717	0.7556003	-6.34	FALSE
249870_at	unknown protein	TGH	AT5G23080	-1.18	-0.24	-0.63	0.5507867	0.7556051	-6.34	FALSE
248469_at	putative protein similar to unknov	anac097	AT5G50820	1.10	0.13	0.63	0.5507807	0.7556051	-6.34	FALSE
265203_at	unknown protein	---	AT2G36630	1.09	0.12	0.63	0.5510113	0.7558223	-6.34	FALSE
264842_at	hypothetical protein predicted by	---	AT1G03700	1.06	0.08	0.63	0.5509965	0.7558223	-6.34	FALSE
247684_at	serine/threonine-specific protein	---	AT5G59670	1.54	0.62	0.63	0.5511458	0.7559612	-6.34	FALSE
AFFX-PheX	B. subtilis /GEN=pheA /DB_XRE	---	---	-1.17	-0.23	-0.63	0.5512271	0.7560273	-6.34	FALSE
263723_at	putative Ta11-like non-LTR retro	---	AT2G13500	1.07	0.10	0.63	0.551285	0.7560613	-6.34	FALSE
263590_at	putative receptor-like protein kina	---	AT2G01820	-1.07	-0.09	-0.63	0.5514567	0.7562011	-6.34	FALSE
255860_at	putative protein heparanase, Ho	AtGUS3	AT5G34940	1.66	0.73	0.63	0.5514744	0.7562011	-6.34	FALSE
265782_at	putative two-component respons	---	AT2G07440	1.08	0.11	0.63	0.5514864	0.7562011	-6.34	FALSE
257772_at	unknown protein C-term similar t	---	AT3G23080	-1.09	-0.12	-0.63	0.551856	0.7566421	-6.34	TRUE
254499_at	putative protein probable membr	---	AT4G20100	1.07	0.10	0.63	0.5519075	0.7566421	-6.34	FALSE
265555_at	putative Mutator-like transposase	---	---	-1.05	-0.07	-0.63	0.5518983	0.7566421	-6.34	FALSE
266381_at	putative sucrose-proton symporte	ATSUC8	AT2G14670	1.07	0.09	0.63	0.5520109	0.7567383	-6.34	FALSE
261877_at	putative indole-3-acetate beta-glu	---	AT1G50580	1.07	0.10	0.63	0.5520461	0.7567411	-6.34	FALSE
259529_at	hypothetical protein	---	AT1G12400	-1.07	-0.09	-0.63	0.5521556	0.7568458	-6.34	FALSE
257387_s_a	putative receptor-like protein kina	---	AT2G14440 ///	-1.08	-0.12	-0.63	0.5522317	0.7569045	-6.34	FALSE
257114_at	cytochrome P450, putative conta	CYP705A2	AT3G20140	1.10	0.13	0.63	0.5524086	0.7570758	-6.34	FALSE
252889_at	hypothetical protein	---	AT4G39380	-1.09	-0.12	-0.63	0.5524231	0.7570758	-6.34	FALSE
249154_at	Nicotiana EREBP-3 like	---	AT5G43410	1.35	0.44	0.62	0.5526456	0.7572443	-6.34	FALSE
250693_at	ubiquitin-specific protease 12 (U	UBP12	AT5G06600	1.07	0.09	0.62	0.5525931	0.7572443	-6.34	FALSE
263617_at	putative retroelement pol polypro	---	---	1.08	0.12	0.62	0.5526362	0.7572443	-6.34	FALSE
256515_at	terpene synthase, putative conta	---	AT1G66020	1.07	0.10	0.62	0.5527123	0.7572903	-6.34	FALSE
261506_at	choline kinase, putative similar t	ATCK1	AT1G71697	1.15	0.20	0.62	0.5527854	0.7573449	-6.34	FALSE
252011_at	carbonic anhydrase (CAH1) ; su	ACA1	AT3G52720	-1.11	-0.15	-0.62	0.5529379	0.7575083	-6.34	FALSE
252722_at	putative protein hypothetical pro	---	---	1.06	0.08	0.62	0.5529956	0.7575419	-6.34	FALSE
261257_at	tat-binding protein, putative simi	---	AT1G05910	1.09	0.13	0.62	0.5531297	0.7575436	-6.34	FALSE
251276_at	putative protein hypothetical pro	SDG14	AT3G61740	-1.07	-0.09	-0.62	0.5531254	0.7575436	-6.34	FALSE
254780_s_a	auxilin-like protein auxilin - bovir	---	AT4G12770	1.12	0.16	0.62	0.5530667	0.7575436	-6.34	FALSE
247395_at	putative protein predicted protei	---	AT5G62910	-1.08	-0.11	-0.62	0.5530851	0.7575436	-6.34	FALSE
263996_at	unknown protein	---	AT2G22530	1.08	0.12	0.62	0.5531778	0.757564	-6.34	FALSE
253873_at	hypothetical protein ;supported b	PRA1.H	AT4G27540	1.07	0.10	0.62	0.5533032	0.757611	-6.34	FALSE
263216_s_a	putative reticuline oxidase-like p	---	AT1G30720 ///	1.45	0.54	0.62	0.5532516	0.757611	-6.34	FALSE

247950_at	unknown protein	---	AT5G57230	1.07	0.10	0.62	0.5533118	0.757611	-6.34	FALSE
259513_at	hypothetical protein ; supported b	ARK3	AT1G12430	1.08	0.11	0.62	0.553384	0.7576407	-6.34	FALSE
267467_at	putative C3HC4 zinc finger prote	DRIP2	AT2G30580	1.08	0.11	0.62	0.5534331	0.7576407	-6.34	FALSE
254552_at	putative protein several hypothet	---	AT4G19900	-1.07	-0.10	-0.62	0.5534139	0.7576407	-6.34	FALSE
248036_at	nucleolar protein-like	OLI2	AT5G55920	-1.11	-0.15	-0.62	0.5535433	0.7577461	-6.34	FALSE
264517_at	hypothetical protein predicted by	---	AT1G10120	-1.10	-0.14	-0.62	0.5536257	0.7578134	-6.34	FALSE
246783_at	sugar transporter-like protein pu	SFP2	AT5G27360	1.25	0.32	0.62	0.5536637	0.7578199	-6.34	FALSE
250939_at	putative protein various predicte	iqd2	AT5G03040	1.12	0.16	0.62	0.5537983	0.7579586	-6.34	TRUE
251135_at	putative protein proteophosphog	---	AT5G01280	-1.07	-0.10	-0.62	0.5538464	0.757979	-6.34	FALSE
262713_at	unknown protein	---	AT1G16520	-1.14	-0.19	-0.62	0.5540182	0.7581686	-6.34	FALSE
261251_at	hypothetical protein predicted by	---	AT1G05920	1.11	0.16	0.62	0.5540649	0.758187	-6.34	FALSE
252581_at	hypothetical protein	---	AT3G45500	1.08	0.11	0.62	0.5542945	0.7584557	-6.35	FALSE
259523_at	hypothetical protein	---	AT1G12500	1.13	0.18	0.62	0.5545119	0.7586586	-6.35	TRUE
246427_at	ADP/ATP translocase-like protei	ER-ANT1	AT5G17400	1.09	0.12	0.62	0.5545045	0.7586586	-6.35	FALSE
263791_at	putative plasma membrane proto	AHA5	AT2G24520	-1.12	-0.16	-0.62	0.5545425	0.7586586	-6.35	FALSE
251006_at	putative protein predicted protei	---	AT5G02600	-1.08	-0.11	-0.62	0.5547314	0.7588715	-6.35	FALSE
245657_at	unknown protein similar to recep	---	AT1G56720	1.21	0.27	0.62	0.5549348	0.7589089	-6.35	TRUE
249345_at	putative protein ; supported by c	---	AT5G40740	-1.08	-0.11	-0.62	0.5548614	0.7589089	-6.35	FALSE
245395_at	hypothetical protein ;supported b	---	AT4G17420	-1.09	-0.12	-0.62	0.5549584	0.7589089	-6.35	FALSE
266869_at	putative glucosyltransferase	---	AT2G44660	1.12	0.16	0.62	0.554837	0.7589089	-6.35	FALSE
267438_at	putative GDSL-motif lipase/hydro	---	AT2G19050	1.11	0.16	0.62	0.5548988	0.7589089	-6.35	FALSE
252900_at	shikimate kinase - like protein sh	---	AT4G39540	-1.10	-0.14	-0.62	0.5548749	0.7589089	-6.35	FALSE
254303_at	predicted protein	---	AT4G22830	1.07	0.10	0.62	0.5550146	0.7589322	-6.35	FALSE
253954_at	putative aconitase Pumpkin mR	---	AT4G26970	1.12	0.16	0.62	0.5551358	0.7589322	-6.35	FALSE
249340_at	putative protein contains similarit	---	AT5G41140	1.09	0.12	0.62	0.5551154	0.7589322	-6.35	FALSE
258306_at	putative transcription factor simil	ATBZIP42	AT3G30530	1.06	0.08	0.62	0.5551751	0.7589322	-6.35	FALSE
262950_at	transcription initiation factor, put	---	AT1G75510	1.06	0.08	0.62	0.5551536	0.7589322	-6.35	FALSE
257354_x_a	hypothetical protein predicted by	---	---	-1.08	-0.11	-0.62	0.5551269	0.7589322	-6.35	FALSE
252837_at	putative protein hypothetical prot	---	---	1.06	0.08	0.62	0.5552515	0.7589912	-6.35	FALSE
266208_at	putative tRNA isopentenylpyroph	ATIPT2	AT2G27760	-1.12	-0.17	-0.62	0.555442	0.7592062	-6.35	FALSE
250364_at	putative protein serine threonine	---	AT5G11400	1.08	0.11	0.62	0.5554856	0.7592202	-6.35	FALSE
257113_at	cytochrome P450, putative conta	CYP705A2	AT3G20130	1.16	0.21	0.62	0.5556599	0.7592541	-6.35	TRUE
255012_at	putative protein ;supported by fu	---	AT4G10030	-1.13	-0.18	-0.62	0.5556841	0.7592541	-6.35	FALSE
257904_at	myb transcription factor, putative	TDF1	AT3G28470	-1.06	-0.08	-0.62	0.5556121	0.7592541	-6.35	FALSE
255530_at	hypothetical protein	---	AT4G02140	1.07	0.10	0.62	0.5557433	0.7592541	-6.35	FALSE

250799_at	putative protein strong similarity t	---	AT5G05350	-1.07	-0.10	-0.62	0.5557176	0.7592541	-6.35	FALSE
266900_at	hypothetical protein predicted by	---	AT2G34610	1.06	0.08	0.62	0.5557421	0.7592541	-6.35	FALSE
250979_at	putative protein	---	AT5G03090	1.10	0.14	0.62	0.5557434	0.7592541	-6.35	FALSE
249609_at	putative protein predicted protei	---	---	-1.06	-0.09	-0.62	0.5559112	0.7594379	-6.35	FALSE
254177_at	putative protein gene T22C1.1, (	---	AT4G23860	-1.10	-0.14	-0.62	0.5559698	0.7594724	-6.35	FALSE
257552_at	cellulase, putative contains Pfan	---	AT3G26130	1.06	0.09	0.62	0.5560893	0.7595903	-6.35	FALSE
263802_at	unknown protein ;supported by f	---	AT2G40430	-1.13	-0.18	-0.62	0.5561754	0.7596623	-6.35	FALSE
259902_at	disease resistance protein, puta	AtRLP13	AT1G74170	1.17	0.22	0.62	0.5564245	0.7598869	-6.35	FALSE
262146_at	membrane protein, putative simi	ATRBL5	AT1G52580	1.13	0.18	0.62	0.5564257	0.7598869	-6.35	FALSE
255655_at	contains similarity to gag protein	---	AT4G00980	-1.12	-0.17	-0.62	0.5564398	0.7598869	-6.35	FALSE
262070_at	far-red impaired response protei	FRS8	AT1G80010	1.07	0.09	0.62	0.5565252	0.7599581	-6.35	FALSE
265083_at	hypothetical protein predicted by	---	AT1G03820	-1.15	-0.21	-0.62	0.5566394	0.7600041	-6.35	FALSE
254756_at	putative protein late embryogene	EDA21	AT4G13235	1.07	0.10	0.62	0.5566589	0.7600041	-6.35	FALSE
265516_at	putative Athila retroelement ORF	---	---	-1.07	-0.10	-0.62	0.5566442	0.7600041	-6.35	FALSE
255473_at	putative protein similar to severa	---	AT4G02450	-1.06	-0.09	-0.62	0.5567863	0.7601325	-6.35	FALSE
245199_at	Expressed protein ; supported by	KCR1	AT1G67730	1.09	0.12	0.62	0.5570194	0.7603986	-6.35	FALSE
262113_at	late embryogenis abundant prot	---	AT1G02820	-1.16	-0.21	-0.62	0.5570478	0.7603986	-6.35	FALSE
258362_at	unknown protein	---	AT3G14280	-1.31	-0.40	-0.62	0.5570934	0.7604153	-6.35	FALSE
260546_at	putative trypsin inhibitor ;suppor	ATTI2	AT2G43520	1.32	0.40	0.62	0.5574531	0.7608308	-6.35	FALSE
260272_at	F-box protein family, AtFBL14 c	---	AT1G80570	-1.10	-0.14	-0.62	0.5574645	0.7608308	-6.35	FALSE
259686_at	transcription factor SCARECRO	---	AT1G63100	1.11	0.15	0.62	0.5575237	0.7608661	-6.35	FALSE
255189_at	hypothetical protein	---	AT4G07350	1.06	0.09	0.62	0.5575959	0.760919	-6.35	FALSE
263580_at	hypothetical protein similar to hyp	---	AT2G17140	-1.08	-0.11	-0.62	0.5577004	0.7609251	-6.35	FALSE
263916_at	hypothetical protein predicted by	---	AT2G36440	1.08	0.11	0.62	0.5576753	0.7609251	-6.35	FALSE
252240_at	putative protein several hypothet	---	AT3G50010	-1.08	-0.11	-0.62	0.5576382	0.7609251	-6.35	FALSE
252204_at	putative protein predicted protei	---	AT3G50340	-1.22	-0.29	-0.62	0.5578005	0.7609706	-6.35	FALSE
248168_at	beta-glucosidase	BGLU41	AT5G54570	1.07	0.10	0.62	0.5577831	0.7609706	-6.35	FALSE
246654_s_a	putative protein predicted protein	EGY1	AT5G35210 /	-1.06	-0.08	-0.62	0.5579124	0.7610777	-6.35	FALSE
262801_at	unknown protein ;supported by f	---	AT1G21010	1.19	0.26	0.62	0.5579668	0.7611065	-6.35	FALSE
250325_s_a	putative protein contains similarit	---	AT5G12060 /	1.06	0.08	0.62	0.5582104	0.7611876	-6.35	FALSE
262752_at	putative mitotic cyclin similar to g	CYCB3;1	AT1G16330	1.09	0.12	0.62	0.5581417	0.7611876	-6.35	FALSE
255202_at	putative polyprotein	---	---	1.07	0.09	0.62	0.5581343	0.7611876	-6.35	FALSE
266870_at	putative heterogeneous nuclear r	---	AT2G44710	-1.11	-0.15	-0.62	0.5581652	0.7611876	-6.35	FALSE
251227_at	ABC transporter-like protein glut	ATMRP10	AT3G62700	-1.13	-0.18	-0.62	0.558111	0.7611876	-6.35	FALSE
245703_at	S-adenosyl-L-methionine:salicylic	---	AT5G04380	1.07	0.09	0.62	0.5582265	0.7611876	-6.35	FALSE

247682_at	serine/threonine-specific protein	---	AT5G59650	1.08	0.11	0.62	0.5584285	0.7613868	-6.35	FALSE
247767_at	putative protein various predicte	AGL82	AT5G58890	1.06	0.09	0.62	0.5584393	0.7613868	-6.35	FALSE
259217_at	unknown protein similar to F16N	---	AT3G03620	-1.07	-0.10	-0.62	0.5586091	0.7615728	-6.35	FALSE
256683_at	unknown protein ; supported by c	---	AT3G52220	1.06	0.08	0.62	0.558668	0.7616059	-6.35	FALSE
260901_at	flavin-containing monooxygenas	YUC11	AT1G21430	1.09	0.13	0.62	0.5587002	0.7616059	-6.35	FALSE
263960_at	putative kinesin-related cytokines	---	AT2G36200	-1.07	-0.10	-0.61	0.558856	0.7617273	-6.35	FALSE
264874_at	unknown protein Location of EST	---	AT1G24240	-1.06	-0.09	-0.61	0.5588481	0.7617273	-6.35	FALSE
251238_at	putative protein several hypothet	---	AT3G62430	-1.08	-0.11	-0.61	0.5590401	0.7619074	-6.35	FALSE
245762_at	ATP-dependent DNA helicase R	---	AT1G27880	1.06	0.08	0.61	0.559055	0.7619074	-6.35	FALSE
259053_at	unknown protein similar to hypot	---	AT3G03320	-1.08	-0.11	-0.61	0.5594022	0.7623022	-6.35	FALSE
255391_at	hypothetical protein similar to T6	---	---	-1.06	-0.08	-0.61	0.5594115	0.7623022	-6.35	FALSE
251677_at	putative protein hypothetical pro	BHLH039	AT3G56980	1.25	0.32	0.61	0.5595188	0.762319	-6.35	FALSE
267154_at	glutathione S-transferase identic	GSTF10	AT2G30870	1.24	0.31	0.61	0.5595241	0.762319	-6.35	FALSE
249329_at	putative protein similar to unknov	---	AT5G40960	1.10	0.13	0.61	0.5595108	0.762319	-6.35	FALSE
249716_at	sterile apetala (emb|CAA11128.1	SAP	AT5G35770	1.07	0.10	0.61	0.5596624	0.7623282	-6.35	FALSE
247559_at	histone deacetylase - like GR AF	HDA18	AT5G61070	1.06	0.09	0.61	0.5595835	0.7623282	-6.35	FALSE
267190_at	putative N-myristoyltransferase	NMT2	AT2G44170	-1.07	-0.10	-0.61	0.5596979	0.7623282	-6.35	FALSE
255751_at	terpene synthase family protein,	---	AT1G31950	-1.08	-0.12	-0.61	0.5596775	0.7623282	-6.35	FALSE
265240_s_a	hypothetical protein	---	AT2G07691	-1.08	-0.12	-0.61	0.5596959	0.7623282	-6.35	FALSE
247197_at	receptor-like protein kinase	---	AT5G65240	-1.17	-0.23	-0.61	0.5598204	0.7624039	-6.35	FALSE
263183_at	putative glucan synthase Highly s	CALS1	AT1G05570	-1.23	-0.30	-0.61	0.5598024	0.7624039	-6.35	FALSE
267187_s_a	putative methylenetetrahydrofola	MTHFR2	AT2G44160 ///	1.11	0.15	0.61	0.5599181	0.7624863	-6.35	FALSE
246304_at	acyl-coA dehydrogenase Mus mu	ACX4	AT3G51840	1.10	0.14	0.61	0.5599477	0.7624863	-6.35	FALSE
250205_at	unknown protein	---	AT5G14020	1.07	0.09	0.61	0.5600102	0.7625259	-6.35	FALSE
247548_at	putative protein various predicte	---	AT5G61400	-1.10	-0.13	-0.61	0.5600501	0.7625347	-6.35	FALSE
255895_at	12-oxophytodienoate reductase,	---	AT1G17990 ///	-1.28	-0.36	-0.61	0.5601249	0.7625455	-6.35	FALSE
255450_at	putative protein similar to T5J8.1	---	AT4G02850	-1.07	-0.10	-0.61	0.5600989	0.7625455	-6.35	FALSE
255959_at	phosphatidylinositol-4-phosphat	ATPIP5K1	AT1G21980	-1.28	-0.36	-0.61	0.5602353	0.7626047	-6.35	FALSE
264843_at	putative 1-aminocyclopropane-1	---	AT1G03400	1.13	0.17	0.61	0.5602276	0.7626047	-6.35	FALSE
256469_at	zinc-finger protein, putative simi	LOL1	AT1G32540	1.12	0.17	0.61	0.5602822	0.7626231	-6.35	FALSE
247484_at	putative protein predicted protei	---	AT5G62110	1.07	0.09	0.61	0.5603968	0.7626919	-6.35	FALSE
255678_at	predicted protein with unknown f	AT4G00520	---	1.08	0.11	0.61	0.5603997	0.7626919	-6.35	FALSE
267366_at	unknown protein ;supported by f	---	AT2G44310 ///	-1.07	-0.10	-0.61	0.5605359	0.7628318	-6.35	FALSE
245514_at	OEP8 like protein	---	AT4G15810	1.11	0.15	0.61	0.5605975	0.7628701	-6.35	FALSE
248373_at	MADS box transcription factor-lik	---	AT5G51860	-1.09	-0.13	-0.61	0.5606425	0.7628858	-6.35	FALSE

249287_at	putative protein strong similarity t	---	AT5G41250	1.08	0.11	0.61	0.5607777	0.7630243	-6.35	FALSE
261290_at	hypothetical protein predicted by	---	AT1G36990	1.11	0.15	0.61	0.5608496	0.7630311	-6.35	FALSE
262788_at	unknown protein ESTs gb|T7561	---	AT1G10690	-1.10	-0.14	-0.61	0.5608251	0.7630311	-6.35	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=M641	GAPC1	---	-1.10	-0.14	-0.61	0.560972	0.7631521	-6.35	TRUE
256471_at	hypothetical protein predicted by	---	---	1.06	0.09	0.61	0.5611267	0.7632739	-6.35	FALSE
263859_at	hypothetical protein predicted by	---	AT2G04360	-1.11	-0.15	-0.61	0.5611613	0.7632739	-6.35	FALSE
255083_s_a	hypothetical protein	---	---	1.09	0.12	0.61	0.561184	0.7632739	-6.35	FALSE
247085_at	kinesin heavy chain DNA binding	---	AT5G66310	-1.07	-0.10	-0.61	0.5611954	0.7632739	-6.35	FALSE
245264_at	Expressed protein ; supported by	---	AT4G17245	-1.23	-0.30	-0.61	0.561252	0.7633054	-6.35	FALSE
249030_at	putative protein similar to unknov	---	---	1.06	0.09	0.61	0.5613202	0.7633526	-6.35	FALSE
253457_at	putative protein C56A3.6,Caeno	---	AT4G32060	1.08	0.11	0.61	0.5614377	0.7634214	-6.35	FALSE
266638_at	putative fibrillin ;supported by ful	---	AT2G35490	-1.08	-0.11	-0.61	0.5614072	0.7634214	-6.35	FALSE
257915_at	superman protein identical to sup	SUP	AT3G23130	1.08	0.11	0.61	0.5615833	0.7635574	-6.35	FALSE
255964_at	hypothetical protein predicted by	ZYP1b	AT1G22275	-1.07	-0.09	-0.61	0.5616046	0.7635574	-6.35	FALSE
249493_at	acyltransferase -like protein Antl	---	AT5G39080	1.12	0.16	0.61	0.5617045	0.7636477	-6.35	TRUE
257829_at	unknown protein	SNM1	AT3G26680	1.13	0.18	0.61	0.5622744	0.763938	-6.35	FALSE
256689_at	hypothetical protein predicted by	---	AT3G32150	1.06	0.09	0.61	0.5622865	0.763938	-6.35	FALSE
250612_s_a	putative protein ARR2 protein - A	ARR13	AT2G27070 /A	1.10	0.13	0.61	0.5621877	0.763938	-6.35	FALSE
254364_at	glycine-rich protein glycine-rich c	---	AT4G22020	1.08	0.12	0.61	0.5620722	0.763938	-6.35	FALSE
267232_at	hypothetical protein predicted by	EDE1	AT2G44190	1.08	0.10	0.61	0.5620927	0.763938	-6.35	FALSE
262266_at	mudrA-like protein similar to mud	---	---	-1.08	-0.10	-0.61	0.5622157	0.763938	-6.35	FALSE
265408_at	Mutator-like transposase similar t	---	---	1.06	0.08	0.61	0.5621307	0.763938	-6.35	FALSE
252403_at	hypothetical protein	---	AT3G48080	1.06	0.08	0.61	0.5622083	0.763938	-6.35	FALSE
257429_at	putative RING zinc finger protein	---	AT2G27940	-1.11	-0.15	-0.61	0.5621558	0.763938	-6.35	FALSE
263991_at	putative retroelement pol polypro	---	---	1.10	0.14	0.61	0.5622523	0.763938	-6.35	FALSE
256950_at	hypothetical protein similar to hyp	---	AT3G19080	-1.15	-0.20	-0.61	0.5620832	0.763938	-6.35	FALSE
265396_at	predicted protein	---	AT2G21040	1.11	0.15	0.61	0.5625472	0.7641228	-6.35	FALSE
261531_at	RB-binding protein -like similar to	---	AT1G63490	1.11	0.15	0.61	0.56259	0.7641228	-6.35	FALSE
245725_at	sucrose synthase, putative simil	SUS6	AT1G73370	1.16	0.21	0.61	0.5625408	0.7641228	-6.35	FALSE
257289_at	hypothetical protein	---	AT3G29690	1.06	0.09	0.61	0.562569	0.7641228	-6.35	FALSE
248733_at	unknown protein	ELP1	---	1.08	0.11	0.61	0.5625078	0.7641228	-6.35	FALSE
253241_at	fatty acid elongase 1	KCS18	AT4G34520	1.10	0.14	0.61	0.5626381	0.7641426	-6.35	FALSE
258851_at	glutathione S-transferase identica	ATGSTF11	AT3G03190	1.17	0.23	0.61	0.5626959	0.7641756	-6.35	FALSE
263331_at	unknown protein ; supported by	---	AT2G15270	-1.07	-0.09	-0.61	0.5628618	0.7643554	-6.35	FALSE
258704_at	putative protein kinase similar to	CCR1	AT3G09780	1.10	0.14	0.61	0.56292	0.7643557	-6.35	FALSE

262563_at	somatic embryogenesis recepto	SERK2	AT1G34210	1.09	0.13	0.61	0.562929	0.7643557	-6.35	FALSE
266191_at	putative peroxidase	---	AT2G39040	1.07	0.10	0.61	0.5629899	0.7643928	-6.35	FALSE
256135_at	hypothetical protein predicted by	---	AT1G48730	1.08	0.11	0.61	0.5630546	0.764417	-6.35	FALSE
256346_s_a	unknown protein	---	AT2G15040	-1.05	-0.07	-0.61	0.5630747	0.764417	-6.35	FALSE
260422_at	hypothetical protein predicted by	---	AT1G69630	1.07	0.09	0.61	0.5632339	0.7645876	-6.35	FALSE
258765_at	putative pectinesterase contains	---	AT3G10710	-1.07	-0.10	-0.61	0.5633845	0.7647465	-6.35	FALSE
246994_at	putative protein similar to unknov	---	AT5G67460	1.18	0.24	0.61	0.5634293	0.7647618	-6.35	FALSE
267523_at	unknown protein	---	AT2G30600	1.08	0.11	0.61	0.5635016	0.7647704	-6.35	FALSE
265956_at	hypothetical protein predicted by	---	AT2G37290	1.05	0.08	0.61	0.5635026	0.7647704	-6.35	FALSE
245270_at	tubulin alpha-6 chain (TUA6) ; su	TUA6	AT4G14960	-1.14	-0.19	-0.61	0.5637268	0.765021	-6.35	FALSE
248583_at	putative protein strong similarity t	emb1441	AT5G49930	1.08	0.12	0.61	0.5637544	0.765021	-6.35	FALSE
256966_at	pollen specific protein, putative s	sks13	AT3G13400	-1.06	-0.08	-0.61	0.5638142	0.7650566	-6.36	FALSE
260161_at	hypothetical protein similar to put	ROPGEF12	AT1G79860	-1.06	-0.08	-0.61	0.5639289	0.7651212	-6.36	FALSE
258007_at	putative tyrosine phosphatase sir	ATPEN2	AT3G19420	-1.10	-0.14	-0.61	0.5639007	0.7651212	-6.36	FALSE
262774_at	chloroplast nucleoid DNA bindin	---	AT1G13230	1.06	0.08	0.61	0.5639848	0.7651516	-6.36	FALSE
255158_s_a	hypothetical protein	---	---	-1.06	-0.09	-0.61	0.5640493	0.7651936	-6.36	FALSE
259873_s_a	putative translation initiation facto	---	AT1G76720 ///	-1.10	-0.13	-0.61	0.5642026	0.7652273	-6.36	FALSE
246649_at	putative protein predicted protein	---	---	1.06	0.09	0.61	0.5642084	0.7652273	-6.36	FALSE
259222_at	putative phosphoribosylanthranil	---	AT3G03680	1.09	0.12	0.61	0.5641457	0.7652273	-6.36	FALSE
254707_at	putative protein inositol polypho	AT5PTASE	AT4G18010	1.19	0.25	0.61	0.564207	0.7652273	-6.36	FALSE
246669_at	galactinol synthase, putative	---	AT5G30500	1.09	0.13	0.61	0.5643817	0.7654169	-6.36	FALSE
263330_at	putative leucine-rich repeat disea	---	AT2G15320	-1.15	-0.21	-0.61	0.5645696	0.7655807	-6.36	FALSE
266974_at	unknown protein	---	AT2G39370	1.06	0.08	0.61	0.5645457	0.7655807	-6.36	FALSE
255126_at	putative protein hypothetical pro	---	AT4G08270	1.06	0.08	0.61	0.5646158	0.7655979	-6.36	FALSE
267192_at	hypothetical protein predicted by	---	AT2G30890	1.09	0.12	0.61	0.5647576	0.7656991	-6.36	FALSE
266919_at	hypothetical protein predicted by	AT2G45780	---	1.06	0.09	0.61	0.5647367	0.7656991	-6.36	FALSE
257749_at	actin 2 identical to GB:AAB3709	ACT2	AT3G18780	1.06	0.09	0.61	0.5648306	0.765707	-6.36	FALSE
265466_at	putative CCAAT-box binding tran	NF-YB8	AT2G37060	1.09	0.13	0.61	0.5648155	0.765707	-6.36	FALSE
248125_at	2S storage protein-like	---	AT5G54740	1.07	0.10	0.61	0.5648997	0.7657145	-6.36	FALSE
267295_at	pregeranylgeranyl pyrophospha	GGPS2	AT2G23800	1.06	0.09	0.61	0.5649256	0.7657145	-6.36	FALSE
245381_at	MYB transcription factor like prot	MYB39	AT4G17785	1.06	0.09	0.61	0.5649369	0.7657145	-6.36	FALSE
255935_at	hypothetical protein contains Pfa	---	AT1G12700	-1.08	-0.11	-0.61	0.5650095	0.7657675	-6.36	FALSE
253824_at	putative protein protein kinase L	MTM1	AT4G27940	-1.26	-0.33	-0.60	0.5651452	0.7659059	-6.36	FALSE
247801_at	putative protein ; supported by fu	---	AT5G58560	-1.07	-0.10	-0.60	0.5652227	0.76592	-6.36	FALSE
259028_at	putative C2H2-type zinc finger p	TAC1	AT3G09290	1.08	0.11	0.60	0.5652206	0.76592	-6.36	FALSE

255239_at	contains similarity to Arabidopsis	---	---	1.05	0.07	0.60	0.5653263	0.7659237	-6.36	FALSE
250541_at	putative proline-rich protein surfa	---	AT5G09520	-1.13	-0.18	-0.60	0.5653198	0.7659237	-6.36	FALSE
259565_at	hypothetical protein	---	AT1G20530	-1.05	-0.07	-0.60	0.5653224	0.7659237	-6.36	FALSE
259983_at	3-hydroxy-3-methylglutaryl CoA	HMG1	AT1G76490	-1.08	-0.11	-0.60	0.5653899	0.7659644	-6.36	FALSE
252138_at	peroxidase-like protein peroxida	---	AT3G50990	-1.08	-0.12	-0.60	0.5659273	0.766556	-6.36	FALSE
256687_x_a	hypothetical protein predicted by	---	AT3G32120	1.06	0.09	0.60	0.5659036	0.766556	-6.36	FALSE
266024_at	En/Spm-like transposon protein r	---	---	-1.06	-0.08	-0.60	0.5659202	0.766556	-6.36	FALSE
264463_at	unknown protein similar to ESTs	---	AT1G10150	-1.09	-0.13	-0.60	0.5659897	0.7665949	-6.36	FALSE
257353_at	hypothetical protein predicted by	NPY4	AT2G23050	1.07	0.10	0.60	0.5660266	0.7665994	-6.36	FALSE
262205_at	hypothetical protein predicted by	---	AT2G01080	1.07	0.10	0.60	0.5661097	0.7666664	-6.36	FALSE
257364_at	hypothetical protein predicted by	---	AT2G45940	-1.06	-0.08	-0.60	0.5661729	0.7667065	-6.36	FALSE
267217_at	hypothetical protein	---	AT2G02610	1.06	0.08	0.60	0.5662255	0.7667322	-6.36	FALSE
255889_at	ABC transporter, putative similar	WBC11	AT1G17840	-1.10	-0.14	-0.60	0.5663131	0.766805	-6.36	TRUE
246056_at	katanin p80 subunit - like protein	---	AT5G08390	1.08	0.12	0.60	0.5663465	0.766805	-6.36	FALSE
252322_at	putative protein putative zinc-fin	---	AT3G48550	1.16	0.21	0.60	0.5664196	0.766853	-6.36	FALSE
263728_at	gamma-adaptin, putative similar	---	AT1G60070	-1.07	-0.10	-0.60	0.5664538	0.766853	-6.36	FALSE
260348_at	PPR-repeat protein, putative cor	---	AT1G69350	-1.10	-0.14	-0.60	0.5664828	0.766853	-6.36	FALSE
248636_at	putative protein similar to unknov	---	---	-1.07	-0.10	-0.60	0.5665658	0.7669198	-6.36	FALSE
248078_at	putative protein contains similarit	---	AT5G55780	1.06	0.09	0.60	0.5666982	0.7670535	-6.36	FALSE
260035_at	peroxidase ATP23a identical to p	---	AT1G68850	-1.13	-0.17	-0.60	0.5667358	0.7670589	-6.36	FALSE
260000_at	unknown protein similar to C-ter	ATMAP70-	AT1G68060	-1.09	-0.13	-0.60	0.5668286	0.7670935	-6.36	TRUE
256877_at	unknown protein ;supported by f	---	AT3G26470	1.20	0.27	0.60	0.5668167	0.7670935	-6.36	FALSE
247086_at	GATA-binding transcription facto	---	AT5G66320	1.32	0.40	0.60	0.5670023	0.767283	-6.36	FALSE
254366_s_a	LTR retrotransposon like protein	---	---	-1.06	-0.08	-0.60	0.5671462	0.7673867	-6.36	FALSE
245322_at	Expressed protein ; supported by	---	AT4G14815	1.15	0.20	0.60	0.5671165	0.7673867	-6.36	FALSE
260884_at	unknown protein similar to unkno	---	AT1G29240	1.18	0.24	0.60	0.5672548	0.7674881	-6.36	FALSE
256464_at	late-embryogenesis abundant pr	---	AT1G32560	1.20	0.27	0.60	0.5673081	0.7675147	-6.36	FALSE
266351_at	unknown protein ;supported by f	---	AT2G01490	-1.08	-0.11	-0.60	0.5676256	0.7676444	-6.36	FALSE
262173_at	betaine aldehyde dehydrogenas	ALDH10A8	AT1G74920	1.08	0.10	0.60	0.5675667	0.7676444	-6.36	FALSE
265253_at	putative peptide/amino acid trans	---	AT2G02020	-1.06	-0.09	-0.60	0.5675853	0.7676444	-6.36	FALSE
263684_at	hypothetical protein predicted by	---	AT1G26900	-1.07	-0.10	-0.60	0.5676155	0.7676444	-6.36	FALSE
250399_at	putative protein predicted protein	---	AT5G10750	1.09	0.13	0.60	0.5675582	0.7676444	-6.36	FALSE
263273_x_a	En/Spm-like transposon protein r	---	---	1.07	0.10	0.60	0.5675847	0.7676444	-6.36	FALSE
255105_at	putative sulfate transporter ; sup	SULTR1;1	AT4G08620	-1.08	-0.10	-0.60	0.5676396	0.7676444	-6.36	FALSE
265401_at	hypothetical protein predicted by	---	AT2G10970	1.07	0.09	0.60	0.5676862	0.767662	-6.36	FALSE

253354_at	putative protein RNA helicase D	---	AT4G33370	-1.13	-0.17	-0.60	0.5677804	0.7677438	-6.36	FALSE
246105_at	putative protein predicted helica	---	---	1.05	0.07	0.60	0.5678659	0.7678139	-6.36	FALSE
253855_at	senescence-associated protein -	TET7	AT4G28050	-1.20	-0.26	-0.60	0.5679042	0.7678202	-6.36	TRUE
254674_at	EREBP - like protein EREBP-1 (	---	AT4G18450	1.06	0.08	0.60	0.5679669	0.7678215	-6.36	FALSE
262405_at	hypothetical protein contains sim	HDG10	AT1G34650	-1.08	-0.11	-0.60	0.5680062	0.7678215	-6.36	FALSE
253036_at	putative protein other predicted p	---	AT4G38340	1.09	0.12	0.60	0.5679798	0.7678215	-6.36	FALSE
267318_at	fatty acid hydroxylase (FAH1) ide	FAH1	AT2G34770	-1.08	-0.11	-0.60	0.5684366	0.767919	-6.36	TRUE
259786_at	lipase/hydrolase, putative contai	---	AT1G29660	1.79	0.84	0.60	0.5681946	0.767919	-6.36	FALSE
259588_at	unknown protein ;supported by fu	---	AT1G27930	-1.05	-0.08	-0.60	0.5682666	0.767919	-6.36	FALSE
252894_at	hypothetical protein	---	AT4G39440	1.08	0.11	0.60	0.5683067	0.767919	-6.36	FALSE
252519_at	hypothetical protein	---	AT3G46360	1.07	0.10	0.60	0.5682895	0.767919	-6.36	FALSE
263462_at	similar to Ariadne protein from D	ARI11	AT2G31780	1.07	0.09	0.60	0.5684314	0.767919	-6.36	FALSE
252903_at	putative protein various predicte	---	AT4G39570	-1.12	-0.16	-0.60	0.5684277	0.767919	-6.36	FALSE
251877_at	synaptobrevin -like protein vesic	ATVAMP72	AT3G54300	1.08	0.11	0.60	0.5684486	0.767919	-6.36	FALSE
252791_at	transposase - like protein putativ	---	---	1.06	0.09	0.60	0.5684088	0.767919	-6.36	FALSE
249274_at	unknown protein	---	AT5G41860	1.10	0.14	0.60	0.5682901	0.767919	-6.36	FALSE
250567_at	hypothetical protein	---	AT5G08090	-1.08	-0.11	-0.60	0.568175	0.767919	-6.36	FALSE
246834_at	putative protein homeotic protein	---	AT5G26630	1.07	0.10	0.60	0.5685532	0.7679239	-6.36	FALSE
255166_at	putative protein putative centron	---	---	1.06	0.09	0.60	0.5685478	0.7679239	-6.36	FALSE
254261_at	beta adaptin - like protein beta-a	---	AT4G23460	1.06	0.09	0.60	0.5685515	0.7679239	-6.36	FALSE
262257_at	hypothetical protein predicted by	---	AT1G53860	1.07	0.10	0.60	0.5688958	0.7682957	-6.36	FALSE
256867_at	hypothetical protein predicted by	---	AT3G26390	1.06	0.08	0.60	0.5688672	0.7682957	-6.36	FALSE
246561_at	putative protein hypothetical pro	---	AT5G15570	-1.07	-0.10	-0.60	0.5689407	0.7683108	-6.36	FALSE
256242_at	actin-like protein contains Pfam p	ATARP5	AT3G12380	-1.09	-0.13	-0.60	0.5690081	0.7683564	-6.36	FALSE
265512_at	hypothetical protein predicted by	---	AT2G05590	-1.09	-0.12	-0.60	0.5692574	0.7686475	-6.36	FALSE
248645_at	unknown protein	GEX2	AT5G49150	1.08	0.11	0.60	0.5693165	0.7686817	-6.36	FALSE
261512_at	actin capping protein beta-2, put	---	AT1G71790	-1.11	-0.15	-0.60	0.5694207	0.768777	-6.36	FALSE
245470_at	retrotransposon like protein	---	---	1.09	0.12	0.60	0.5698076	0.7692538	-6.36	FALSE
263312_at	putative replication protein A1	---	---	-1.07	-0.09	-0.60	0.5698601	0.769279	-6.36	FALSE
252400_at	hypothetical protein	---	AT3G48020	1.16	0.21	0.60	0.5700629	0.7695073	-6.36	TRUE
251320_at	3-methyl-2-oxobutanoate hydrox	PANB2	AT3G61530	-1.06	-0.08	-0.60	0.5701104	0.7695258	-6.36	FALSE
261065_at	hypothetical protein predicted by	---	AT1G07500	1.09	0.13	0.60	0.5701972	0.7695975	-6.36	FALSE
246300_at	putative transmembrane protein	SAC8	AT3G51830	-1.06	-0.09	-0.60	0.570293	0.7696405	-6.36	FALSE
250276_at	putative protein mRNA, Moritella	---	AT5G13030	-1.07	-0.10	-0.60	0.5702966	0.7696405	-6.36	FALSE
248789_at	putative protein strong similarity t	---	AT5G47440	-1.10	-0.14	-0.60	0.570384	0.76971	-6.36	FALSE

265436_at	putative retroelement pol polypro	---	---	-1.06	-0.08	-0.60	0.5704155	0.76971	-6.36	FALSE
258762_at	hypothetical protein	---	AT3G10750	1.09	0.13	0.60	0.5705563	0.7698544	-6.36	FALSE
266398_at	hypothetical protein predicted by	---	AT2G38680	-1.16	-0.22	-0.60	0.5706126	0.7698848	-6.36	FALSE
253494_at	putative protein	---	AT4G31830	1.07	0.10	0.60	0.5708313	0.7700926	-6.36	FALSE
249492_at	germin-like protein (GLP2a) copy	GER2	AT5G39130 /	1.06	0.09	0.60	0.5708341	0.7700926	-6.36	FALSE
266304_at	hypothetical protein	---	AT2G27090	1.07	0.09	0.60	0.57091	0.7701106	-6.36	FALSE
257567_at	hypothetical protein predicted by	---	AT3G23930	-1.05	-0.07	-0.60	0.570915	0.7701106	-6.36	FALSE
261298_at	cytochrome c oxidase assembly	---	AT1G48510	1.06	0.09	0.60	0.5710109	0.7701945	-6.36	FALSE
255471_at	putative oxidoreductase similar t	AOP3	AT4G03050	1.07	0.10	0.60	0.5711785	0.7703293	-6.36	FALSE
265866_at	unknown protein ;supported by f	---	AT2G01710	-1.08	-0.11	-0.60	0.5711509	0.7703293	-6.36	FALSE
264577_at	putative peroxidase Strong simila	RCI3	AT1G05260	1.06	0.08	0.60	0.5712122	0.7703293	-6.36	FALSE
261024_at	hypothetical protein predicted by	---	AT1G12190	1.06	0.08	0.60	0.5712716	0.7703639	-6.36	FALSE
252229_at	putative protein lea32, Arabidop	---	AT3G49890	1.09	0.12	0.59	0.5714533	0.7705178	-6.36	FALSE
254070_at	hypothetical protein	---	AT4G25430	1.10	0.14	0.59	0.5714464	0.7705178	-6.36	FALSE
253603_at	putative protein SP8 binding pro	WRKY32	AT4G30935	1.06	0.08	0.59	0.5715322	0.7705786	-6.36	FALSE
247929_at	apospory-associated protein C	---	AT5G57330	-1.09	-0.12	-0.59	0.5716048	0.770631	-6.36	FALSE
251473_at	putative protein myrosinase-bind	---	AT3G59610	1.10	0.14	0.59	0.571725	0.7707475	-6.36	FALSE
256097_at	unknown protein	---	AT1G13670	-1.06	-0.08	-0.59	0.5718072	0.7708127	-6.36	FALSE
264062_at	unknown protein	---	AT2G27950	1.07	0.10	0.59	0.5719946	0.7710197	-6.36	FALSE
265473_at	Expressed protein ; supported by	LCR10	AT2G15535	1.07	0.10	0.59	0.5720332	0.7710263	-6.36	FALSE
261960_at	hypothetical protein similar to put	---	---	-1.05	-0.07	-0.59	0.5720948	0.7710637	-6.36	FALSE
252891_at	putative WRKY DNA-binding pro	WRKY13	AT4G39410	1.10	0.13	0.59	0.572157	0.771102	-6.36	FALSE
252248_at	putative protein resistance gene	AtRLP44	AT3G49750	-1.13	-0.17	-0.59	0.5722607	0.7711506	-6.36	FALSE
258042_at	hypothetical protein similar to hyp	---	AT3G21310	1.06	0.08	0.59	0.5722338	0.7711506	-6.36	FALSE
257143_at	cytochrome P450, putative conta	CYP705A2(	AT3G20110	-1.08	-0.11	-0.59	0.5723297	0.7711525	-6.36	FALSE
246978_at	cytochrome P450-like protein fat	CYP714A1	AT5G24910	1.12	0.17	0.59	0.5723288	0.7711525	-6.36	FALSE
262590_at	putative RING-H2 zinc finger pro	RHA2A	AT1G15100	-1.08	-0.11	-0.59	0.5723857	0.7711824	-6.36	FALSE
264751_at	putative superoxide-generating I	FRO3	AT1G23020	1.25	0.32	0.59	0.5726359	0.7714738	-6.36	FALSE
262417_at	hypothetical protein similar to hyp	ATSIRB	AT1G50170	-1.05	-0.08	-0.59	0.5728652	0.7717372	-6.36	FALSE
253522_at	predicted protein cation transpor	---	AT4G31290	1.21	0.27	0.59	0.5729014	0.7717404	-6.36	FALSE
263283_at	hypothetical protein predicted by	---	AT2G36090	-1.07	-0.09	-0.59	0.5730253	0.7718162	-6.36	FALSE
253877_at	Expressed protein ; supported by	---	AT4G27435	1.15	0.20	0.59	0.5730064	0.7718162	-6.36	FALSE
264020_at	putative signal sequence recept	---	AT2G21160	-1.09	-0.13	-0.59	0.5731894	0.7719916	-6.36	FALSE
264028_at	putative nitrilase-associated prot	SPR1	AT2G03680	-1.12	-0.17	-0.59	0.5733131	0.7721126	-6.36	FALSE
256442_at	hypothetical protein predicted by	---	AT3G10930	1.40	0.49	0.59	0.5734296	0.7721328	-6.36	TRUE

249111_at	unknown protein	---	AT5G43770	1.06	0.08	0.59	0.5734148	0.7721328	-6.36	FALSE
259916_at	hypothetical protein predicted by	---	AT1G72600	-1.05	-0.08	-0.59	0.5733731	0.7721328	-6.36	FALSE
248490_at	putative protein similar to unknov	---	AT5G50940	1.19	0.25	0.59	0.5736137	0.7721984	-6.36	FALSE
265597_at	Expressed protein ; supported by	---	AT2G20142	-1.24	-0.31	-0.59	0.5736003	0.7721984	-6.36	FALSE
256846_at	pectin methylesterase, putative	---	AT3G27980	-1.06	-0.08	-0.59	0.5736016	0.7721984	-6.36	FALSE
245202_at	F12A21.14 similar to receptor pr	---	AT1G67720	-1.09	-0.12	-0.59	0.5735832	0.7721984	-6.36	FALSE
255769_at	hypothetical protein predicted by	---	AT1G18610	-1.07	-0.09	-0.59	0.5737314	0.7723112	-6.37	FALSE
266660_at	hypothetical protein predicted by	---	AT2G25920	-1.11	-0.16	-0.59	0.5738128	0.7723752	-6.37	FALSE
253732_at	putative protein several hypothet	---	AT4G29140	1.07	0.10	0.59	0.5739555	0.7723947	-6.37	FALSE
248429_at	putative protein contains similarit	---	AT5G51770	1.15	0.20	0.59	0.5738816	0.7723947	-6.37	FALSE
254929_at	putative protein mitochondrial ca	---	AT4G11440	1.07	0.10	0.59	0.5739198	0.7723947	-6.37	FALSE
255112_at	casein kinase I - Arabidopsis tha	---	AT4G08800	-1.07	-0.10	-0.59	0.5739628	0.7723947	-6.37	FALSE
263149_at	unknown protein	---	AT1G53970	1.07	0.09	0.59	0.5740462	0.7724614	-6.37	FALSE
251090_at	putative protein ACR1-protein -	---	AT5G01340	1.22	0.28	0.59	0.5741175	0.7725118	-6.37	FALSE
261050_at	transcription factor MYC7E, puta	---	AT1G01260	-1.11	-0.16	-0.59	0.5742161	0.772599	-6.37	FALSE
249500_at	expansin-like protein expansin -	ATEXPA21	AT5G39260	1.11	0.15	0.59	0.574263	0.7726164	-6.37	FALSE
261873_at	serine/threonine kinase, putative	SD1-13	AT1G11350	1.12	0.16	0.59	0.5743034	0.7726253	-6.37	FALSE
263109_at	hypothetical protein similar to put	---	AT1G65180	-1.08	-0.11	-0.59	0.5743388	0.7726273	-6.37	FALSE
248506_at	adenylate kinase ;supported by	---	AT5G50370	1.19	0.25	0.59	0.5745066	0.7727629	-6.37	FALSE
254325_at	putative protein various predicte	---	AT4G22650	1.10	0.14	0.59	0.5745074	0.7727629	-6.37	FALSE
260306_at	hypothetical protein predicted by	EDA24	AT1G70540	1.07	0.10	0.59	0.5746776	0.7729463	-6.37	FALSE
256751_at	CLC-b chloride channel protein	CLC-B	AT3G27170	1.15	0.20	0.59	0.5747614	0.7730135	-6.37	TRUE
266856_at	putative ABC transporter related	PDR4	AT2G26910	-1.14	-0.19	-0.59	0.5748422	0.7730262	-6.37	FALSE
248673_at	putative protein contains similarit	---	AT5G48780	-1.06	-0.08	-0.59	0.574878	0.7730262	-6.37	FALSE
247070_at	Expressed protein ; supported by	---	AT5G66815	1.07	0.10	0.59	0.5748742	0.7730262	-6.37	FALSE
255274_at	putative protein various predicte	---	---	-1.08	-0.11	-0.59	0.5749065	0.7730262	-6.37	FALSE
256999_at	hypothetical protein predicted by	---	AT3G14200	-1.07	-0.09	-0.59	0.5750772	0.7731728	-6.37	TRUE
262262_at	unknown protein identical to unkr	---	AT1G70780 /	1.12	0.16	0.59	0.575151	0.7731728	-6.37	FALSE
250583_at	zinc finger transcription factor ; s	PEI1	AT5G07500	1.06	0.09	0.59	0.5751489	0.7731728	-6.37	FALSE
248554_at	putative protein contains similarit	---	AT5G50330	1.09	0.13	0.59	0.5750948	0.7731728	-6.37	FALSE
261964_at	hypothetical protein similar to en	---	---	1.05	0.08	0.59	0.5753496	0.7733941	-6.37	FALSE
262109_at	hypothetical protein similar to cel	ATCSLD5	AT1G02730	1.14	0.18	0.59	0.5754552	0.7734904	-6.37	FALSE
254717_at	histone H2A.F/Z - like protein his	HTA4	AT4G13570	1.08	0.12	0.59	0.5755188	0.7735304	-6.37	FALSE
260765_at	actin 8 almost identical to actin 8	ACT8	AT1G49240	-1.16	-0.21	-0.59	0.5755981	0.7735459	-6.37	FALSE
252651_at	putative protein several hypothet	---	AT3G44700	1.08	0.11	0.59	0.5755886	0.7735459	-6.37	FALSE

265049_at	jasmonate inducible protein, put	---	AT1G52060	1.06	0.08	0.59	0.5758038	0.7737766	-6.37	FALSE
257103_at	hypothetical protein contains Pfa	---	AT3G25060	-1.08	-0.11	-0.59	0.5759811	0.7739444	-6.37	FALSE
265665_at	cysteine proteinase contains sim	---	AT2G27420	-1.06	-0.09	-0.59	0.5759965	0.7739444	-6.37	FALSE
259742_at	putative proline-rich APG protein	GLIP6	AT1G71120	1.10	0.14	0.59	0.5760374	0.7739538	-6.37	FALSE
250860_at	amino acid transport - like protei	CAT6	AT5G04770	1.15	0.21	0.59	0.576073	0.7739561	-6.37	FALSE
253237_at	putative aldehyde dehydrogenas	ALDH3I1	AT4G34240	1.11	0.15	0.59	0.5762689	0.774128	-6.37	FALSE
248647_at	sucrose synthase	SUS2	AT5G49190	1.06	0.08	0.59	0.5762369	0.774128	-6.37	FALSE
254033_at	V-ATPase G-subunit like protein	VATG3	AT4G25950	1.05	0.07	0.59	0.5763286	0.7741626	-6.37	FALSE
261263_at	H-protein promoter binding facto	---	AT1G26790	1.06	0.08	0.59	0.5763962	0.7741699	-6.37	FALSE
254152_at	hypothetical protein	---	AT4G24410	1.06	0.09	0.59	0.5764019	0.7741699	-6.37	FALSE
252621_at	putative protein Ac-like transposa	---	---	-1.07	-0.10	-0.59	0.576499	0.7742548	-6.37	FALSE
266114_at	hypothetical protein predicted by	---	AT2G02150	-1.05	-0.08	-0.59	0.5765605	0.7742727	-6.37	FALSE
254344_at	alcohol dehydrogenase like prot	---	AT4G22110	1.11	0.15	0.59	0.5765803	0.7742727	-6.37	FALSE
253088_at	ferulate-5-hydroxylase (FAH1) ;	FAH1	AT4G36220	1.16	0.21	0.59	0.5766996	0.7743417	-6.37	TRUE
258307_x_a	hypothetical protein predicted by	---	---	1.07	0.10	0.59	0.5766812	0.7743417	-6.37	FALSE
259788_at	lipase/hydrolase, putative contai	---	AT1G29670	1.31	0.39	0.59	0.576735	0.7743437	-6.37	TRUE
254561_at	putative protein ; supported by c	---	AT4G19160	1.11	0.15	0.59	0.5767724	0.7743483	-6.37	FALSE
261426_at	unknown protein contains similar	---	AT1G18680	-1.06	-0.09	-0.59	0.5769715	0.7743959	-6.37	FALSE
249533_at	putative protein predicted protei	---	AT5G38790	1.07	0.10	0.59	0.5769767	0.7743959	-6.37	FALSE
267087_at	putative MYB family transcription	MYB101	AT2G32460	-1.10	-0.14	-0.59	0.5768902	0.7743959	-6.37	FALSE
263891_at	putative glucan synthase	GSL8	AT2G36850	-1.06	-0.09	-0.59	0.5769185	0.7743959	-6.37	FALSE
255073_at	beta-1,3-glucanase-like protein p	---	AT4G09090	-1.06	-0.08	-0.59	0.5769776	0.7743959	-6.37	FALSE
253039_at	squalene epoxidase - like protei	SQE3	AT4G37760	-1.15	-0.20	-0.59	0.5771218	0.7745194	-6.37	TRUE
265745_at	hypothetical protein predicted by	---	---	1.06	0.08	0.59	0.5771995	0.7745194	-6.37	FALSE
254762_at	Expressed protein ; supported by	---	AT4G13230	-1.07	-0.10	-0.59	0.5771628	0.7745194	-6.37	FALSE
246381_at	hypothetical protein	---	---	1.12	0.16	0.59	0.5772054	0.7745194	-6.37	FALSE
265502_at	putative poly(A) binding protein	---	AT2G15500	1.08	0.11	0.59	0.5772467	0.7745293	-6.37	FALSE
266721_at	unknown protein	FT1	AT2G03220	-1.09	-0.13	-0.59	0.5774781	0.7747942	-6.37	TRUE
267460_at	putative squamosa-promoter bin	SPL3	AT2G33810	1.27	0.34	0.59	0.5775351	0.7748251	-6.37	FALSE
256184_at	epsilon subunit of mitochondrial I	---	AT1G51650	-1.10	-0.14	-0.59	0.5776134	0.7748845	-6.37	FALSE
248322_at	putative protein similar to unknov	---	AT5G52760	1.67	0.74	0.58	0.5778362	0.7751378	-6.37	FALSE
257868_at	unknown protein	RIN4	AT3G25070	1.09	0.13	0.58	0.578326	0.775162	-6.37	FALSE
255397_at	putative transposon protein	---	---	1.09	0.12	0.58	0.5782697	0.775162	-6.37	FALSE
266853_at	putative salt-inducible protein	---	AT2G26790	-1.06	-0.09	-0.58	0.5782814	0.775162	-6.37	FALSE
257878_at	hypothetical protein predicted by	---	AT3G17150	1.07	0.09	0.58	0.577912	0.775162	-6.37	FALSE

265202_at	unknown protein	AT2G3681(	---	1.07	0.10	0.58	0.578398	0.775162	-6.37	FALSE
264988_at	glutathione transferase, putative	ATGSTU14	AT1G27140	1.10	0.13	0.58	0.5782665	0.775162	-6.37	FALSE
258204_at	hypothetical protein predicted by	AtGRF5	AT3G13960	1.08	0.11	0.58	0.5780698	0.775162	-6.37	FALSE
245829_at	hypothetical protein predicted by	---	AT1G57780	-1.07	-0.10	-0.58	0.5779301	0.775162	-6.37	FALSE
247587_at	putative protein predicted protei	---	AT5G60620	1.07	0.10	0.58	0.5781798	0.775162	-6.37	FALSE
265744_at	putative CENP-B/ARS binding pr	---	---	-1.05	-0.07	-0.58	0.5780644	0.775162	-6.37	FALSE
261545_at	unknown protein	---	AT1G63530	1.07	0.10	0.58	0.5779767	0.775162	-6.37	FALSE
266200_at	hypothetical protein predicted by	---	AT2G38920	1.11	0.16	0.58	0.5779936	0.775162	-6.37	FALSE
258427_at	putative DNA-binding protein sir	---	AT3G16600	-1.06	-0.08	-0.58	0.5783362	0.775162	-6.37	FALSE
261776_at	hypothetical protein similar to put	---	AT1G76190	-1.09	-0.13	-0.58	0.5781374	0.775162	-6.37	FALSE
247631_at	putative MADS box protein varic	AGL62	AT5G60440	-1.05	-0.07	-0.58	0.5783764	0.775162	-6.37	FALSE
263362_at	putative selenium-binding protein	---	AT2G03880	-1.06	-0.08	-0.58	0.5782534	0.775162	-6.37	FALSE
255405_s_a	hypothetical protein similar to A.	---	AT4G03440 ///	1.09	0.12	0.58	0.5785442	0.7753125	-6.37	FALSE
256462_at	hypothetical protein predicted by	---	AT1G36230	1.07	0.10	0.58	0.5786555	0.7754161	-6.37	FALSE
254946_at	putative protein proline-rich prot	---	AT4G10950	-1.07	-0.09	-0.58	0.5787154	0.7754508	-6.37	FALSE
248488_at	putative protein contains similarit	---	AT5G51080	-1.07	-0.10	-0.58	0.5787632	0.7754692	-6.37	FALSE
263510_s_a	hypothetical protein	---	AT2G07681 ///	-1.06	-0.08	-0.58	0.5788079	0.7754835	-6.37	FALSE
256231_at	unknown protein ; supported by f	---	AT3G12630	-1.06	-0.09	-0.58	0.5788864	0.7755398	-6.37	FALSE
266342_at	hypothetical protein predicted by	---	AT2G01540	1.10	0.13	0.58	0.5789179	0.7755398	-6.37	FALSE
258471_at	NPK1-related protein kinase 3 ic	ANP3	AT3G06030	1.07	0.10	0.58	0.5789866	0.7755863	-6.37	FALSE
264603_at	hypothetical protein predicted by	---	AT1G04670	1.05	0.08	0.58	0.5790824	0.7756235	-6.37	FALSE
257728_at	hypothetical protein predicted by	---	AT3G18295	1.09	0.12	0.58	0.579077	0.7756235	-6.37	FALSE
266871_at	unknown protein	---	AT2G44710	1.05	0.07	0.58	0.5791828	0.775667	-6.37	FALSE
265097_at	unknown protein	BARD1	AT1G04020	-1.11	-0.15	-0.58	0.5791815	0.775667	-6.37	FALSE
264460_at	hypothetical protein similar to tra	ATNFXL1	AT1G10170	1.09	0.12	0.58	0.5792523	0.7757144	-6.37	FALSE
267567_at	putative cytochrome P450	CYP71A13	AT2G30770	1.78	0.83	0.58	0.5794225	0.7757264	-6.37	TRUE
249640_at	cationic amino acid transporter -	CAT3	AT5G36940	-1.11	-0.15	-0.58	0.5793503	0.7757264	-6.37	FALSE
258723_at	putative MYB-related protein sim	---	AT3G09600	-1.07	-0.09	-0.58	0.5794038	0.7757264	-6.37	FALSE
246271_at	photosystem II oxygen-evolving c	---	AT4G37230	1.07	0.10	0.58	0.5793011	0.7757264	-6.37	FALSE
246208_at	hypothetical protein ; supported b	SFH12	AT4G36490	1.07	0.10	0.58	0.5794312	0.7757264	-6.37	FALSE
250425_at	lectin-like protein kinase - like le	---	AT5G10530	-1.06	-0.08	-0.58	0.5794971	0.775769	-6.37	FALSE
262554_at	hypothetical protein similar to hy	---	AT1G31380	1.06	0.08	0.58	0.5796313	0.7759032	-6.37	FALSE
261921_at	hypothetical protein predicted by	---	AT1G65900	-1.13	-0.17	-0.58	0.5797446	0.7760093	-6.37	FALSE
253755_at	26S proteasome subunit 4-like p	RPT2a	AT4G29040	-1.07	-0.10	-0.58	0.5799052	0.7761331	-6.37	FALSE
255646_at	hypothetical protein	---	AT4G00890	1.07	0.10	0.58	0.579879	0.7761331	-6.37	FALSE

265014_at	hypothetical protein similar to de	---	AT1G24430	1.10	0.14	0.58	0.5800924	0.7763102	-6.37	FALSE
249561_at	disease resistance - like protein	---	AT5G38340	1.07	0.10	0.58	0.5801056	0.7763102	-6.37	FALSE
266085_at	hypothetical protein	---	AT2G37800	-1.08	-0.11	-0.58	0.5801881	0.7763751	-6.37	FALSE
261158_at	hypothetical protein predicted by	---	AT1G34500	-1.06	-0.09	-0.58	0.5803983	0.7765652	-6.37	FALSE
260197_at	F12A21.25 hypothetical protein	---	AT1G67623	1.06	0.09	0.58	0.5803749	0.7765652	-6.37	FALSE
249671_at	putative protein similar to unknov	LBD35	AT5G35900	1.07	0.10	0.58	0.580517	0.776587	-6.37	FALSE
251633_at	putative protein metalloendopep	---	AT3G57460	1.14	0.19	0.58	0.5805507	0.776587	-6.37	FALSE
246216_at	cytochrome P450 like protein ; su	ROT3	AT4G36380	-1.10	-0.14	-0.58	0.5804815	0.776587	-6.37	FALSE
260571_at	MAP kinase (ATMPK6) identical	ATMPK6	AT2G43790	-1.06	-0.08	-0.58	0.5805204	0.776587	-6.37	FALSE
263365_at	putative heat shock protein	---	AT2G20550	1.11	0.15	0.58	0.5806505	0.776675	-6.37	FALSE
259319_at	Snf1-related protein kinase KIN1	AKIN10	AT3G01090	-1.05	-0.08	-0.58	0.5807213	0.7767241	-6.37	FALSE
262535_at	trehalose-6-phosphate synthase	ATTPS3	AT1G17000	1.05	0.07	0.58	0.5808927	0.7769078	-6.37	FALSE
262197_at	AP2 domain containing protein,	RAP2.12	AT1G53910	1.12	0.16	0.58	0.5810947	0.777049	-6.37	FALSE
262787_at	putative clathrin-coat assembly p	---	AT1G10730	-1.11	-0.15	-0.58	0.5810536	0.777049	-6.37	FALSE
265557_at	unknown protein	---	---	1.08	0.10	0.58	0.5811345	0.777049	-6.37	FALSE
252812_at	putative protein hypothetical prot	---	---	-1.06	-0.08	-0.58	0.5811006	0.777049	-6.37	FALSE
252994_at	putative protein gene PC326 pro	---	AT4G38480	1.17	0.23	0.58	0.5812336	0.7771359	-6.37	FALSE
247466_at	putative protein predicted protei	---	AT5G62090	-1.10	-0.14	-0.58	0.5813301	0.7772193	-6.37	FALSE
259041_at	unknown protein similar to putati	ATCSLC6	AT3G07330	1.10	0.14	0.58	0.5814698	0.7773606	-6.37	FALSE
252242_at	F-box protein family, AtFBL16 c	VFB2	AT3G50080	1.07	0.10	0.58	0.581545	0.7774155	-6.37	FALSE
250664_at	putative protein 10-deacetylbac	---	AT5G07080	1.16	0.21	0.58	0.5817185	0.7775752	-6.37	FALSE
262650_at	lipoamide dehydrogenase, putat	---	AT1G14090	-1.05	-0.07	-0.58	0.5817326	0.7775752	-6.37	FALSE
265282_at	unknown protein	---	AT2G20380	1.07	0.09	0.58	0.581823	0.7776505	-6.37	FALSE
267228_at	putative polygalacturonase	---	AT2G43890	1.06	0.08	0.58	0.5819373	0.7776693	-6.37	FALSE
252961_at	putative protein KIAA0169 gene	---	AT4G38760	-1.08	-0.11	-0.58	0.5819223	0.7776693	-6.37	FALSE
247562_at	putative protein	---	AT5G61120	-1.06	-0.08	-0.58	0.5819394	0.7776693	-6.37	FALSE
261929_at	hypothetical protein similar to axi	---	AT1G22460	1.08	0.11	0.58	0.581979	0.7776766	-6.37	FALSE
250766_at	putative protein similar to unknov	---	AT5G05550	1.08	0.11	0.58	0.5820422	0.7777156	-6.37	FALSE
247817_at	Expressed protein ; supported by	---	AT5G58375	1.08	0.11	0.58	0.5822552	0.7777713	-6.37	TRUE
246251_at	cold acclimation protein homolog	---	AT4G37220	-1.19	-0.25	-0.58	0.5822959	0.7777713	-6.37	TRUE
250655_at	transcription factor HBP-1b (gb|A	OBF5	AT5G06960	1.06	0.08	0.58	0.5823226	0.7777713	-6.37	FALSE
245503_at	kinase like protein	---	AT4G15650	1.06	0.08	0.58	0.5821733	0.7777713	-6.37	FALSE
266539_at	similar to mammalian MHC III re	SUVH5	AT2G35160	1.07	0.10	0.58	0.5822574	0.7777713	-6.37	FALSE
255282_at	putative polyprotein	---	---	1.06	0.08	0.58	0.5822461	0.7777713	-6.37	FALSE
249053_at	berberine bridge enzyme-like pro	---	AT5G44440	-1.08	-0.11	-0.58	0.5822542	0.7777713	-6.37	FALSE

245753_at	hypothetical protein similar to put	---	---	1.06	0.08	0.58	0.5824106	0.7778433	-6.37	FALSE
264676_at	unknown protein EST gb|R64758	---	AT1G09870	-1.06	-0.08	-0.58	0.5826723	0.7781018	-6.37	FALSE
249069_at	unknown protein	---	AT5G44010	-1.15	-0.21	-0.58	0.5826627	0.7781018	-6.37	FALSE
251718_at	putative protein hypothetical prot	MRLK	AT3G56100	1.09	0.12	0.58	0.5829324	0.7783917	-6.37	FALSE
262524_at	tuftelin-interacting-like protein Sir	---	AT1G17070	-1.05	-0.08	-0.58	0.5829577	0.7783917	-6.37	FALSE
246215_at	putative cytoskeletal protein ; sup	---	AT4G37180	1.17	0.23	0.58	0.5832222	0.7786537	-6.37	FALSE
254379_at	putative protein calmodulin-bind	---	AT4G21820	-1.05	-0.08	-0.58	0.5832122	0.7786537	-6.37	FALSE
257336_at	hypothetical protein	---	---	1.06	0.08	0.58	0.5832725	0.7786752	-6.37	FALSE
245980_at	putative protein ;supported by fu	---	AT5G13140	1.56	0.64	0.58	0.5834063	0.7787555	-6.37	FALSE
247220_at	cdc2-like protein kinase ; suppor	CDKC2	AT5G64960	-1.07	-0.09	-0.58	0.5834663	0.7787555	-6.37	FALSE
267576_at	putative Mutator-like transposase	---	---	-1.09	-0.12	-0.58	0.5834691	0.7787555	-6.37	FALSE
245917_at	putative protein HCNP, Homo sa	---	AT5G28740	-1.07	-0.10	-0.58	0.5834032	0.7787555	-6.37	FALSE
254164_at	putative protein ;supported by fu	TIFY1	AT4G24470	1.07	0.10	0.58	0.5835584	0.778829	-6.37	FALSE
245871_at	hypothetical protein predicted by	---	AT1G26290	-1.09	-0.12	-0.58	0.5837656	0.7790599	-6.37	FALSE
249972_at	tRNA isopentenyltransferase -lik	IPT5	AT5G19040	1.07	0.09	0.58	0.5838282	0.7790979	-6.38	FALSE
247121_at	putative protein contains similarit	---	AT5G66010	-1.08	-0.11	-0.58	0.5839394	0.7791551	-6.38	FALSE
246836_s_a	putative protein MADS box prote	---	AT5G26650 //	-1.05	-0.08	-0.58	0.5839052	0.7791551	-6.38	FALSE
258220_at	DnaJ, putative similar to DnaJ G	---	AT3G17830	-1.09	-0.13	-0.57	0.584143	0.7793812	-6.38	FALSE
261813_at	hypothetical protein contains sim	---	AT1G08280	1.10	0.14	0.57	0.5842525	0.7794818	-6.38	FALSE
263267_at	putative vacuolar proton-ATPase	---	AT2G16510	1.07	0.10	0.57	0.5843952	0.7796265	-6.38	FALSE
267314_at	putative myosin heavy chain	---	AT2G34730	1.09	0.13	0.57	0.5845788	0.7796373	-6.38	FALSE
248898_at	outward rectifying potassium cha	KCO2	AT5G46370	1.08	0.11	0.57	0.5846084	0.7796373	-6.38	FALSE
249006_at	putative protein similar to unknov	---	AT5G44650 //	-1.10	-0.14	-0.57	0.584514	0.7796373	-6.38	FALSE
256878_at	major latex protein, putative sim	---	AT3G26460	-1.08	-0.12	-0.57	0.5844959	0.7796373	-6.38	FALSE
260314_at	unknown protein similar to putati	---	AT1G63830	1.12	0.16	0.57	0.5846072	0.7796373	-6.38	FALSE
248902_at	unknown protein	---	AT5G46440	1.07	0.09	0.57	0.5844927	0.7796373	-6.38	FALSE
252072_at	putative protein protein kinase P	---	AT3G51710	1.07	0.09	0.57	0.5847018	0.7797163	-6.38	FALSE
267250_at	similar to hookless1 (HLS1)	---	AT2G23060	1.06	0.08	0.57	0.5847491	0.7797339	-6.38	FALSE
253780_at	protein phosphatase 2C-like pro	---	AT4G28400	-1.16	-0.21	-0.57	0.5848273	0.7797518	-6.38	FALSE
260926_at	unknown protein	GLTP2	AT1G21360	1.07	0.09	0.57	0.5848309	0.7797518	-6.38	FALSE
254713_at	hypothetical protein	---	AT4G18090	1.09	0.13	0.57	0.585045	0.7799609	-6.38	FALSE
260319_at	hypothetical protein predicted by	---	AT1G63950	1.08	0.11	0.57	0.5850562	0.7799609	-6.38	FALSE
247890_at	cyclic nucleotide and calmodulin-	ATCNGC5	AT5G57940	-1.08	-0.11	-0.57	0.585219	0.7800868	-6.38	FALSE
267111_s_a	hypothetical protein predicted by	---	---	1.08	0.12	0.57	0.585211	0.7800868	-6.38	FALSE
263947_at	unknown protein ;supported by f	---	AT2G35820	-1.13	-0.17	-0.57	0.5854798	0.7803889	-6.38	TRUE

266508_at	hypothetical protein predicted by	---	AT2G47920	-1.08	-0.12	-0.57	0.585516	0.7803914	-6.38	FALSE
256073_at	terminal Flower 1 (TFL1), putativ	E12A11	AT1G18100	1.08	0.11	0.57	0.5855684	0.7804157	-6.38	FALSE
248572_at	unknown protein	---	AT5G49800	-1.07	-0.10	-0.57	0.5856435	0.7804703	-6.38	FALSE
245393_at	beta-1,3-glucanase class I precu	---	AT4G16260	-1.15	-0.20	-0.57	0.5858281	0.7806188	-6.38	TRUE
250138_at	DRH1 DEAD box protein - like D	---	AT5G14610	1.06	0.09	0.57	0.5858217	0.7806188	-6.38	FALSE
248565_at	putative protein similar to unknov	---	AT5G49710	-1.10	-0.13	-0.57	0.5858577	0.7806188	-6.38	FALSE
249709_at	putative protein similar to unknov	iqd33	AT5G35670	-1.08	-0.11	-0.57	0.5860781	0.7808669	-6.38	FALSE
252997_at	putative pollen allergen pollen al	ATEXLA2	AT4G38400	1.19	0.25	0.57	0.5863181	0.7810922	-6.38	TRUE
264086_at	unknown protein ;supported by f	---	AT2G31190	-1.09	-0.12	-0.57	0.5865896	0.7810922	-6.38	FALSE
245092_at	putative TGACG-sequence-spec	BZIP17	AT2G40950	-1.08	-0.11	-0.57	0.5863631	0.7810922	-6.38	FALSE
249232_at	dynamin-like protein (pir||S59558	ADL1	AT5G42080	-1.10	-0.13	-0.57	0.5864426	0.7810922	-6.38	FALSE
245495_at	hypothetical protein	---	AT4G16400	1.05	0.07	0.57	0.5865345	0.7810922	-6.38	FALSE
255634_at	hypothetical protein ; supported	FRI	AT4G00650	1.05	0.08	0.57	0.5864865	0.7810922	-6.38	FALSE
249504_at	disease resistance protein - like	---	AT5G38850	-1.14	-0.19	-0.57	0.5865789	0.7810922	-6.38	FALSE
256236_at	hypothetical protein predicted by	---	AT3G12350	-1.08	-0.11	-0.57	0.5863935	0.7810922	-6.38	FALSE
262858_at	major latex protein type3 identica	---	AT1G14940	1.07	0.09	0.57	0.5865203	0.7810922	-6.38	FALSE
248817_at	putative protein strong similarity f	---	AT5G47020	-1.08	-0.11	-0.57	0.5865274	0.7810922	-6.38	FALSE
252507_at	putative protein predicted protei	aTNUDT9	AT3G46200	-1.10	-0.14	-0.57	0.5866986	0.7811918	-6.38	FALSE
246179_at	putative protein hypothetical pro	---	AT5G28440	1.09	0.12	0.57	0.5867506	0.7812154	-6.38	FALSE
263796_at	unknown protein ;supported by f	AFR	AT2G24540	-1.12	-0.16	-0.57	0.5871049	0.7816313	-6.38	FALSE
254467_at	receptor protein kinase - like pro	---	AT4G20450	1.08	0.11	0.57	0.5871315	0.7816313	-6.38	FALSE
252597_at	putative protein several hypothet	---	---	1.08	0.11	0.57	0.5872721	0.7817728	-6.38	FALSE
246230_at	SCARECROW-like protein	---	AT4G36710	1.06	0.09	0.57	0.5873769	0.7818	-6.38	FALSE
255612_at	hypothetical protein	---	AT4G01240	1.09	0.12	0.57	0.5873464	0.7818	-6.38	FALSE
260646_at	hypothetical protein similar to CH	---	AT1G53340	-1.10	-0.14	-0.57	0.5873954	0.7818	-6.38	FALSE
262184_at	hypothetical protein contains sim	---	AT1G77910	1.05	0.08	0.57	0.5875402	0.7819471	-6.38	FALSE
260952_at	hypothetical protein predicted by	---	AT1G06140	-1.09	-0.13	-0.57	0.5876345	0.7819814	-6.38	FALSE
249892_at	unknown protein	---	AT5G22600	1.06	0.08	0.57	0.5876032	0.7819814	-6.38	FALSE
250537_at	Expressed protein ; supported by	---	AT5G08565	1.11	0.15	0.57	0.5877216	0.7820517	-6.38	FALSE
251937_at	putative protein predicted protei	CPuORF46	AT3G53400 //	1.23	0.30	0.57	0.5878665	0.7821989	-6.38	FALSE
262920_at	2-dehydro-3-deoxyphosphoocto	---	AT1G79500	-1.16	-0.21	-0.57	0.5883686	0.7822185	-6.38	FALSE
254259_s_a	putative protein rape mRNA, Bra	---	AT4G23420 //	1.10	0.14	0.57	0.5882478	0.7822185	-6.38	FALSE
246499_at	putative protein Tat-SF1 - Homo	---	AT5G16260	-1.08	-0.12	-0.57	0.5883722	0.7822185	-6.38	FALSE
260880_at	hypothetical protein similar to un	---	AT1G21380	1.07	0.09	0.57	0.5882452	0.7822185	-6.38	FALSE
248939_at	tyrosine-specific protein phospha	---	AT5G45790	-1.07	-0.10	-0.57	0.5882219	0.7822185	-6.38	FALSE

262349_at	unknown protein ;supported by f	---	AT2G48130	-1.10	-0.13	-0.57	0.588285	0.7822185	-6.38	FALSE
251271_at	hypothetical protein ; supported b	---	AT3G62050	1.09	0.13	0.57	0.5881323	0.7822185	-6.38	FALSE
254138_at	hypothetical protein	---	AT4G24950	1.06	0.09	0.57	0.58843	0.7822185	-6.38	FALSE
249213_at	unknown protein	---	AT5G42700	-1.06	-0.09	-0.57	0.588247	0.7822185	-6.38	FALSE
256643_at	unknown protein similar to putati	---	---	-1.07	-0.09	-0.57	0.5882369	0.7822185	-6.38	FALSE
262537_s_a	putative ubiquitin-conjugating en	UBC34	AT1G17280 /	-1.10	-0.14	-0.57	0.588061	0.7822185	-6.38	FALSE
248203_at	Myb-related transcription factor-l	MYB49	AT5G54230	1.05	0.07	0.57	0.5881474	0.7822185	-6.38	FALSE
262674_at	anter-specific proline-rich -like pr	EXL4	AT1G75910	1.08	0.11	0.57	0.5883959	0.7822185	-6.38	FALSE
257631_at	cytochrome P450, putative simil	CYP71B17	AT3G26160	1.10	0.14	0.57	0.5883278	0.7822185	-6.38	FALSE
257342_at	pseudogene, putative polyprotei	---	---	1.11	0.15	0.57	0.588252	0.7822185	-6.38	FALSE
259716_at	unknown protein	---	AT1G60995 /	-1.09	-0.13	-0.57	0.5882327	0.7822185	-6.38	FALSE
255729_at	hypothetical protein similar to put	---	AT1G25470 /	-1.07	-0.09	-0.57	0.5888479	0.7827285	-6.38	FALSE
246501_at	putative protein KIAA1012 prote	---	AT5G16280	-1.06	-0.09	-0.57	0.5888919	0.7827413	-6.38	FALSE
256788_at	cytochrome P450, putative simil	CYP90D1	AT3G13730	-1.29	-0.37	-0.57	0.5889744	0.7827598	-6.38	FALSE
246940_at	expressed protein glucose-6-pho	---	AT5G25400	-1.07	-0.10	-0.57	0.5889531	0.7827598	-6.38	FALSE
249506_at	putative protein	---	AT5G38880	-1.07	-0.10	-0.57	0.5890746	0.782767	-6.38	FALSE
256387_at	hypothetical protein	---	AT3G06170	-1.09	-0.12	-0.57	0.5890828	0.782767	-6.38	FALSE
265976_at	putative Athila retroelement ORF	---	---	-1.06	-0.09	-0.57	0.5890779	0.782767	-6.38	FALSE
265972_at	putative retroelement pol polypro	---	---	1.05	0.08	0.57	0.5891303	0.7827845	-6.38	FALSE
254007_s_a	putative protein RNA-directed D	---	AT1G60720	1.06	0.08	0.57	0.5892974	0.782961	-6.38	FALSE
247829_at	protein kinase - like protein kina	---	AT5G58520	-1.09	-0.13	-0.57	0.58942	0.7830783	-6.38	FALSE
254893_at	putative phospholipase D-gamm	PLDGAMM	AT4G11830	-1.12	-0.16	-0.57	0.5896301	0.7833096	-6.38	FALSE
250240_at	unknown protein	---	AT5G13590	-1.10	-0.14	-0.57	0.5896628	0.7833096	-6.38	FALSE
251859_at	putative protein proteophosphog	---	AT3G54680	1.07	0.10	0.57	0.5897715	0.7833935	-6.38	FALSE
265223_at	putative pectinesterase	---	AT2G36700	1.05	0.07	0.57	0.5897947	0.7833935	-6.38	FALSE
259281_at	putative Myb-related transcriptior	MYB106	AT3G01140	1.07	0.10	0.57	0.5898675	0.7834446	-6.38	FALSE
257682_at	hypothetical protein predicted by	---	AT3G13240	-1.05	-0.08	-0.57	0.589904	0.7834475	-6.38	FALSE
266538_at	hypothetical protein predicted by	---	AT2G35230	-1.06	-0.09	-0.57	0.5899829	0.783466	-6.38	FALSE
247190_at	D-type cyclin (emb|CAB41347.1)	CYCD4;1	AT5G65420	-1.07	-0.10	-0.57	0.590005	0.783466	-6.38	FALSE
258680_at	adenylate translocator identical t	AAC1	AT3G08580	1.11	0.15	0.57	0.590021	0.783466	-6.38	FALSE
255233_at	putative protein ADRENODOXIN	MFDX1	AT4G05450	1.07	0.10	0.57	0.5900838	0.7835037	-6.38	FALSE
251291_at	putative protein auxin-induced p	---	AT3G61900	-1.06	-0.09	-0.56	0.5905876	0.7839952	-6.38	FALSE
248672_at	disease resistance protein	---	AT5G48770	1.07	0.10	0.56	0.5905633	0.7839952	-6.38	FALSE
249897_at	putative protein strong similarity t	---	AT5G22550	1.07	0.09	0.56	0.5905914	0.7839952	-6.38	FALSE
255245_at	hypothetical protein	---	AT4G05630	-1.06	-0.09	-0.56	0.5905548	0.7839952	-6.38	FALSE

248478_at	ubiquitin-conjugating enzyme-like	UBC27	AT5G50870	-1.05	-0.08	-0.56	0.5907798	0.7840172	-6.38	FALSE
252979_at	Expressed protein ; supported by	---	AT4G38225	-1.11	-0.15	-0.56	0.5907695	0.7840172	-6.38	FALSE
248610_at	SRP54 (signal recognition particl	---	AT5G49500	-1.06	-0.08	-0.56	0.5906863	0.7840172	-6.38	FALSE
266734_at	hypothetical protein predicted by	---	AT2G46900	-1.08	-0.11	-0.56	0.5907029	0.7840172	-6.38	FALSE
254741_s_a	putative disease resistance prot	AtRLP49	AT4G13900 /	-1.05	-0.08	-0.56	0.5907423	0.7840172	-6.38	FALSE
267387_at	hypothetical protein predicted by	---	AT2G44440	1.05	0.07	0.56	0.5908498	0.7840645	-6.38	FALSE
255842_at	putative serine carboxypeptidase	scpl46	AT2G33530	1.17	0.23	0.56	0.5913103	0.7844473	-6.38	TRUE
262158_at	somatic embryogenesis recepto	---	AT1G52540	1.10	0.14	0.56	0.5912719	0.7844473	-6.38	FALSE
249251_at	putative protein similar to unknov	---	AT5G42000	-1.08	-0.12	-0.56	0.5912891	0.7844473	-6.38	FALSE
265933_at	putative esterase contains estera	---	AT2G19550	1.07	0.10	0.56	0.5911888	0.7844473	-6.38	FALSE
254651_at	potassium channel - like protein	KCO6	AT4G18160	1.08	0.12	0.56	0.5913064	0.7844473	-6.38	FALSE
265635_at	hypothetical protein predicted by	---	AT2G25360	1.05	0.08	0.56	0.5915271	0.7846894	-6.38	FALSE
249522_at	putative protein similar to unknov	---	AT5G38700	1.06	0.09	0.56	0.591683	0.7848505	-6.38	FALSE
250861_at	putative protein predicted protei	---	AT5G04740	1.08	0.10	0.56	0.5920423	0.7849163	-6.38	FALSE
248388_at	putative protein contains similarit	---	AT5G51980	-1.07	-0.10	-0.56	0.5921218	0.7849163	-6.38	FALSE
264914_at	clathrin adaptor medium chain p	HAP13	AT1G60780	1.07	0.10	0.56	0.5921452	0.7849163	-6.38	FALSE
253419_at	putative protein predicted protei	---	AT4G32780	1.08	0.11	0.56	0.5921227	0.7849163	-6.38	FALSE
249913_at	GDSL-motif lipase/hydrolase-like	---	AT5G22810	1.07	0.10	0.56	0.5920762	0.7849163	-6.38	FALSE
256171_s_a	hypothetical protein similar to rev	---	---	1.07	0.10	0.56	0.5919824	0.7849163	-6.38	FALSE
258216_at	unknown protein contains Pfam p	---	AT3G17980	1.08	0.12	0.56	0.5919295	0.7849163	-6.38	FALSE
259833_at	MYB-family transcription factor,	MYB105	AT1G69560	1.06	0.08	0.56	0.5921719	0.7849163	-6.38	FALSE
247452_at	H-protein promoter binding factor	CDF1	AT5G62430	1.10	0.14	0.56	0.5917675	0.7849163	-6.38	FALSE
253676_at	cytidine deaminase - like protein	---	AT4G29570	-1.08	-0.11	-0.56	0.5919458	0.7849163	-6.38	FALSE
248653_at	disease resistance protein-like	---	AT5G49290	1.06	0.09	0.56	0.5919346	0.7849163	-6.38	FALSE
252052_at	beta-fructofuranosidase	AtcwINV2	AT3G52600	1.06	0.08	0.56	0.5921799	0.7849163	-6.38	FALSE
256718_at	hypothetical protein predicted by	---	AT2G34120	1.07	0.09	0.56	0.5921527	0.7849163	-6.38	FALSE
264570_at	unknown protein Similar to Caen	---	AT1G05350	1.08	0.11	0.56	0.5922298	0.7849368	-6.38	FALSE
260519_at	unknown protein	---	AT1G51540	1.05	0.08	0.56	0.5924523	0.7851025	-6.38	FALSE
252469_at	protein kinase - like protein Raf	---	AT3G46920	1.09	0.12	0.56	0.5924925	0.7851025	-6.38	FALSE
254992_at	putative transcriptional regulator	SPT16	AT4G10710	-1.09	-0.13	-0.56	0.5924652	0.7851025	-6.38	FALSE
258408_at	unknown protein similar to putati	ATCHX19	AT3G17630	-1.06	-0.08	-0.56	0.5924544	0.7851025	-6.38	FALSE
263710_at	unknown protein ;supported by f	---	AT1G09330	1.07	0.09	0.56	0.5925971	0.7851955	-6.38	FALSE
257837_at	hypothetical protein predicted by	---	AT3G25200	1.07	0.10	0.56	0.5926676	0.7852432	-6.38	FALSE
258311_at	transport inhibitor response 1 (T	AFB2	AT3G26810	1.07	0.10	0.56	0.5927344	0.7852861	-6.38	FALSE
254481_at	hypothetical protein ; supported	---	AT4G20480	-1.10	-0.14	-0.56	0.5929284	0.7853607	-6.38	FALSE

252155_at	putative protein	---	AT3G50920	-1.09	-0.12	-0.56	0.5929267	0.7853607	-6.38	FALSE
247363_at	unknown protein	---	AT5G63200	-1.07	-0.09	-0.56	0.5928659	0.7853607	-6.38	FALSE
257119_at	receptor kinase protein, putative	---	AT3G20190	1.06	0.08	0.56	0.59285	0.7853607	-6.38	FALSE
246508_at	sugar transporter-like protein pu	PGLCT	AT5G16150	1.08	0.11	0.56	0.5930002	0.7854102	-6.38	FALSE
251796_at	synaptic glycoprotein SC2-like p	---	AT3G55360	-1.11	-0.15	-0.56	0.5931937	0.7855752	-6.38	TRUE
246066_at	putative protein predicted protei	SMG7	AT5G19400	1.07	0.10	0.56	0.593181	0.7855752	-6.38	FALSE
266645_at	hypothetical protein	---	AT2G29880	1.06	0.08	0.56	0.5932739	0.7856358	-6.38	FALSE
250479_at	GTP-binding protein GTP-bindin	AtRABH1e	AT5G10260	-1.07	-0.09	-0.56	0.5934015	0.7857592	-6.38	FALSE
259110_at	unknown protein	---	AT3G05570	-1.09	-0.13	-0.56	0.5934898	0.7857849	-6.38	FALSE
263452_at	putative trehalose-6-phosphate p	---	AT2G22190	-1.13	-0.18	-0.56	0.5934643	0.7857849	-6.38	FALSE
252705_at	putative protein predicted protei	---	---	1.08	0.12	0.56	0.5936311	0.7858851	-6.38	FALSE
254541_at	putative LTR retrotransposon Br	---	---	1.05	0.08	0.56	0.5936344	0.7858851	-6.38	FALSE
251339_at	putative protein various predicte	---	AT3G60780	1.08	0.12	0.56	0.5937002	0.7859266	-6.38	FALSE
250078_at	putative protein	ORC3	AT5G16690	-1.08	-0.10	-0.56	0.5937401	0.7859338	-6.38	FALSE
252351_at	putative protein ;supported by fu	---	AT3G48210	-1.08	-0.12	-0.56	0.5938731	0.7860642	-6.38	FALSE
267076_at	calcium binding protein (CaBP-2	---	AT2G41090	1.37	0.46	0.56	0.5940156	0.7862073	-6.38	FALSE
265899_s_a	SKP1/ASK1 (At3), putative simil	ASK4	AT1G20140 /	-1.07	-0.10	-0.56	0.5940684	0.7862315	-6.38	FALSE
251136_at	mRNA capping enzyme - like pr	---	AT5G01290	1.05	0.08	0.56	0.5942858	0.7864736	-6.38	FALSE
262854_at	unknown protein	---	AT1G20870	1.06	0.09	0.56	0.5943774	0.7865491	-6.39	FALSE
260767_s_a	unknown protein ; supported by f	---	AT1G49140 /	-1.06	-0.09	-0.56	0.5944471	0.7865958	-6.39	FALSE
246813_at	putative protein various predicte	---	---	1.06	0.08	0.56	0.5944952	0.7866138	-6.39	FALSE
249016_at	putative protein contains similarit	REV1	AT5G44750	1.09	0.12	0.56	0.5945509	0.7866419	-6.39	FALSE
267472_at	putative basic blue protein (plant	ARPN	AT2G02850	1.07	0.10	0.56	0.5946351	0.7867076	-6.39	FALSE
255608_at	hypothetical protein	---	AT4G01140	1.09	0.12	0.56	0.5948135	0.7868903	-6.39	FALSE
250051_at	MYB56 R2R3-MYB factor family	AtMYB56	AT5G17800	1.09	0.12	0.56	0.5948422	0.7868903	-6.39	FALSE
247930_at	putative protein similar to unknov	---	AT5G57060	-1.10	-0.14	-0.56	0.5949545	0.7869476	-6.39	FALSE
263837_at	unknown protein	---	AT2G04500	-1.05	-0.07	-0.56	0.5949294	0.7869476	-6.39	FALSE
256287_at	hypothetical protein	---	AT3G12190	1.06	0.09	0.56	0.5949938	0.786954	-6.39	FALSE
245445_at	apetala2 domain TINY like protei	---	AT4G16750	-1.17	-0.23	-0.56	0.595034	0.7869616	-6.39	FALSE
261625_at	hypothetical protein predicted by	---	AT1G01930	-1.05	-0.08	-0.56	0.5952347	0.7871814	-6.39	FALSE
246353_s_a	hypothetical protein	---	---	1.06	0.08	0.56	0.5953413	0.7872766	-6.39	FALSE
256544_at	Mlo-like protein similar to Mlo [H	MLO9	AT1G42560	1.07	0.10	0.56	0.5954114	0.7872899	-6.39	FALSE
259674_at	thaumatin-like protein similar to t	---	AT1G77700	1.07	0.10	0.56	0.5954315	0.7872899	-6.39	FALSE
251311_at	FUSCA PROTEIN FUS6 ; suppo	FUS6	AT3G61140	1.06	0.09	0.56	0.59546	0.7872899	-6.39	FALSE
260699_at	MAP kinase, putative similar to M	ATMKK10	AT1G32320	-1.06	-0.08	-0.56	0.5954894	0.7872899	-6.39	FALSE

246185_at	5-methyltetrahydropteroyltrigluta	ATMS3	AT5G20980	-1.05	-0.07	-0.56	0.5956215	0.7874189	-6.39	FALSE
247736_at	actin 4 ;supported by full-length	ACT4	AT5G59370	-1.06	-0.08	-0.56	0.595693	0.7874679	-6.39	FALSE
255704_at	putative proline-rich protein ;sup	---	AT4G00170	1.05	0.07	0.56	0.5957684	0.7875218	-6.39	FALSE
249237_at	putative protein similar to unknov	---	AT5G42050	1.10	0.14	0.56	0.5959055	0.787564	-6.39	FALSE
258714_at	putative RING zinc finger protein	---	AT3G09770	-1.10	-0.13	-0.56	0.5959729	0.787564	-6.39	FALSE
256642_at	hypothetical protein similar to hyp	---	AT3G32280	1.06	0.08	0.56	0.5959137	0.787564	-6.39	FALSE
257492_at	hypothetical protein contains sim	ARR19	AT1G49190	-1.05	-0.07	-0.56	0.5958848	0.787564	-6.39	FALSE
258096_at	hypothetical protein similar to put	---	AT3G23650	-1.07	-0.09	-0.56	0.5959577	0.787564	-6.39	FALSE
255212_at	putative athila transposon protein	---	---	1.05	0.08	0.56	0.5960218	0.7875829	-6.39	FALSE
252485_at	disease resistance protein RPP1	RPP13	AT3G46530	-1.07	-0.09	-0.56	0.5960602	0.7875881	-6.39	FALSE
266536_at	hypothetical protein predicted by	---	AT2G16900	1.21	0.27	0.56	0.5962192	0.7876157	-6.39	TRUE
256415_at	unknown protein ; supported by f	---	AT3G11210	-1.20	-0.27	-0.56	0.5961972	0.7876157	-6.39	FALSE
250790_at	putative protein similar to unknov	---	AT5G05640	1.10	0.13	0.56	0.596175	0.7876157	-6.39	FALSE
246229_at	pectinesterase like protein	sks15	AT4G37160	-1.06	-0.08	-0.56	0.5962111	0.7876157	-6.39	FALSE
260867_at	hypothetical protein predicted by	TED6	AT1G43790	1.23	0.30	0.56	0.5964957	0.7878454	-6.39	TRUE
247533_at	putative protein kinase-like trans	---	AT5G61570	1.16	0.22	0.56	0.5964968	0.7878454	-6.39	FALSE
249058_at	disease resistance protein-like	TAO1	AT5G44510	1.07	0.10	0.56	0.5964671	0.7878454	-6.39	FALSE
250443_at	Pto kinase interactor - like protei	RBK1	AT5G10520	-1.35	-0.43	-0.56	0.5965829	0.7879136	-6.39	TRUE
253869_at	hypothetical protein	---	AT4G27510	-1.08	-0.11	-0.56	0.5966875	0.7880061	-6.39	FALSE
254327_at	RCc3- like protein RCc3 protein	---	AT4G22490	1.15	0.20	0.56	0.5967842	0.7880426	-6.39	FALSE
257551_at	hypothetical protein contains sim	---	---	1.07	0.10	0.56	0.5967516	0.7880426	-6.39	FALSE
260221_at	GAST1-like protein similar to GA	---	AT1G74670	1.36	0.44	0.55	0.5968732	0.7880891	-6.39	TRUE
258644_at	putative RNA-binding protein co	---	AT3G07810	1.05	0.07	0.55	0.5968885	0.7880891	-6.39	FALSE
257810_at	TOM20, putative similar to TOM	TOM20-1	AT3G27070	-1.07	-0.09	-0.55	0.5970426	0.7882469	-6.39	FALSE
256945_at	hypothetical protein similar to ext	---	AT3G19020	1.06	0.09	0.55	0.5971802	0.7883373	-6.39	FALSE
252085_s_a	serine-type carboxypeptidase lik	scpl37	AT3G52000 /.	1.05	0.07	0.55	0.5971505	0.7883373	-6.39	FALSE
260870_at	GTP-binding protein(RAB1Y), pu	ATRAB18	AT1G43890	-1.08	-0.11	-0.55	0.5972683	0.788408	-6.39	FALSE
250118_at	putative protein similar to unknov	---	AT5G16460	1.07	0.10	0.55	0.5974251	0.7884781	-6.39	FALSE
263616_at	unknown protein	---	AT2G04680	1.07	0.10	0.55	0.5974109	0.7884781	-6.39	FALSE
257394_at	hypothetical protein predicted by	---	---	-1.08	-0.11	-0.55	0.5973948	0.7884781	-6.39	FALSE
252798_at	putative protein	---	AT3G42310	-1.06	-0.08	-0.55	0.5975292	0.7885698	-6.39	FALSE
257292_s_a	hypothetical protein contains Pfa	---	---	1.05	0.07	0.55	0.5977571	0.788825	-6.39	FALSE
254074_at	transcriptional activator CBF1 C	CBF1	AT4G25490	-1.15	-0.20	-0.55	0.5978045	0.7888418	-6.39	FALSE
255354_at	putative transposon protein	---	---	-1.05	-0.07	-0.55	0.5980762	0.7891547	-6.39	FALSE
249526_at	putative protein contains similarit	---	AT5G38560	1.08	0.11	0.55	0.598127	0.7891761	-6.39	FALSE

247955_at	nucleosome assembly protein	NAP1;3	AT5G56950	-1.08	-0.11	-0.55	0.598162	0.7891767	-6.39	FALSE
246274_at	transcription factor like protein	---	AT4G36620	1.08	0.11	0.55	0.5982991	0.7893119	-6.39	FALSE
247501_at	putative protein predicted protei	---	AT5G61920	-1.05	-0.07	-0.55	0.5983418	0.7893226	-6.39	FALSE
261211_at	uridine diphosphate glucose epi	UGE1	AT1G12780	1.12	0.16	0.55	0.5984222	0.7893829	-6.39	FALSE
256783_at	casein kinase, putative similar to	---	AT3G13670	1.05	0.07	0.55	0.5985343	0.7894852	-6.39	FALSE
251317_at	putative protein polygalacturona	---	AT3G61490	-1.10	-0.14	-0.55	0.5986204	0.7895167	-6.39	FALSE
245944_at	putative protein various predicte	MSL9	AT5G19520	-1.06	-0.09	-0.55	0.5986274	0.7895167	-6.39	FALSE
260933_at	hypothetical protein contains nor	---	AT1G02470	1.27	0.34	0.55	0.5987083	0.7895777	-6.39	TRUE
258933_at	unknown protein similar to unkn	---	AT3G09980	-1.07	-0.09	-0.55	0.5990286	0.789936	-6.39	FALSE
256632_at	hypothetical protein	---	AT3G28330	1.08	0.10	0.55	0.5990493	0.789936	-6.39	FALSE
255532_at	hypothetical protein similar to or	---	AT4G02170	1.09	0.12	0.55	0.5991264	0.7899921	-6.39	FALSE
267141_at	putative MYB family transcription	---	AT2G38090	-1.09	-0.12	-0.55	0.5991996	0.790043	-6.39	FALSE
264562_at	hypothetical protein predicted by	---	AT1G55760	-1.13	-0.18	-0.55	0.5992542	0.7900693	-6.39	FALSE
253807_at	putative GPI-anchored protein G	---	AT4G28280	1.09	0.12	0.55	0.5993844	0.790108	-6.39	FALSE
245159_at	putative cellulose synthase	ATCSLD1	AT2G33100	-1.08	-0.11	-0.55	0.5993809	0.790108	-6.39	FALSE
252778_at	putative protein replication prote	---	---	1.06	0.08	0.55	0.5993875	0.790108	-6.39	FALSE
245444_at	limonene cyclase like protein	ATTPS03	AT4G16740	1.08	0.12	0.55	0.5995714	0.7903047	-6.39	FALSE
251218_at	CP12 protein precursor-like prot	CP12-2	AT3G62410	-1.09	-0.12	-0.55	0.5998808	0.790562	-6.39	FALSE
259822_at	myb-related transcription factor,	MYB20	AT1G66230	-1.13	-0.17	-0.55	0.5999685	0.790562	-6.39	FALSE
257584_at	hypothetical protein similar to put	---	---	-1.10	-0.14	-0.55	0.5999745	0.790562	-6.39	FALSE
245587_at	putative protein	---	AT4G15020	-1.12	-0.16	-0.55	0.5998193	0.790562	-6.39	FALSE
251382_at	pectinesterase - like protein pec	---	AT3G60730	1.05	0.08	0.55	0.5999069	0.790562	-6.39	FALSE
265060_at	HD-Zip protein, putative similar t	ATHB-15	AT1G52150	1.15	0.21	0.55	0.5999141	0.790562	-6.39	FALSE
247969_at	putative protein similar to unknov	---	AT5G56700	-1.11	-0.15	-0.55	0.6000776	0.7906521	-6.39	FALSE
250163_at	putative protein various predicte	---	AT5G15270	-1.07	-0.10	-0.55	0.6001198	0.790662	-6.39	FALSE
246580_at	ABC transporter, putative contai	---	AT1G31770	-1.08	-0.11	-0.55	0.6001766	0.790674	-6.39	FALSE
254558_at	Expressed protein ; supported by	---	AT4G19185	1.06	0.08	0.55	0.6002198	0.790674	-6.39	FALSE
265822_at	putative SEC1 family transport p	ATSLY1	AT2G17980	-1.06	-0.09	-0.55	0.6002414	0.790674	-6.39	FALSE
258044_at	Dof zinc finger protein identical to	ADOF2	AT3G21270	-1.14	-0.19	-0.55	0.6002675	0.790674	-6.39	FALSE
252054_at	hypothetical protein ;supported b	OFP18	AT3G52540	1.07	0.10	0.55	0.6003246	0.7907036	-6.39	FALSE
257611_at	unknown protein	---	AT3G26580	-1.09	-0.12	-0.55	0.6004711	0.7908509	-6.39	FALSE
266006_at	putative ABC transporter	---	AT2G37360	1.08	0.12	0.55	0.6005254	0.7908767	-6.39	FALSE
252432_at	hypothetical protein	---	AT3G47675 /	1.05	0.07	0.55	0.6005867	0.7909118	-6.39	FALSE
256174_at	NADP-specific glutatamate dehy	---	AT1G51720	1.06	0.09	0.55	0.6006225	0.7909133	-6.39	FALSE
252962_at	splicing factor - like protein splic	---	AT4G38780	1.07	0.09	0.55	0.6006668	0.7909259	-6.39	FALSE

249371_at	hypothetical protein	---	AT5G40750	1.05	0.07	0.55	0.6008541	0.7911268	-6.39	FALSE
254745_at	putative protein G9A protein, Mu	SUVH9	AT4G13460	-1.05	-0.07	-0.55	0.6009757	0.7912414	-6.39	FALSE
256338_at	hypothetical protein similar to see	---	AT1G72100	1.06	0.09	0.55	0.6011788	0.791463	-6.39	FALSE
264535_at	Phosphatidylinositol Transfer Pr	---	AT1G55690	1.17	0.23	0.55	0.6013205	0.7915256	-6.39	FALSE
258222_at	putative zinc finger protein conta	---	AT3G15680	-1.12	-0.17	-0.55	0.6013197	0.7915256	-6.39	FALSE
256830_at	eukaryotic translation initiation fa	TIF3C2	AT3G22860	1.08	0.11	0.55	0.6013304	0.7915256	-6.39	FALSE
261740_at	hypothetical protein similar to unl	---	AT1G47740	-1.09	-0.13	-0.55	0.6014917	0.7915442	-6.39	TRUE
248947_at	putative protein similar to unknov	---	AT5G45540	1.08	0.12	0.55	0.6015181	0.7915442	-6.39	FALSE
266897_at	remorin identical to GB:M25268	---	AT2G45820	-1.11	-0.15	-0.55	0.6014152	0.7915442	-6.39	FALSE
247656_at	actin depolymerizing factor 4 - li	ADF4	AT5G59890	1.08	0.11	0.55	0.6014622	0.7915442	-6.39	FALSE
259187_at	putative transcription factor simil	AtMYB57	AT3G01530	-1.08	-0.11	-0.55	0.6014558	0.7915442	-6.39	FALSE
256854_at	hypothetical protein predicted by	---	AT3G15180	1.06	0.08	0.55	0.6015779	0.7915749	-6.39	FALSE
256208_at	hypothetical protein predicted by	---	AT1G50930	1.05	0.07	0.55	0.6016108	0.7915749	-6.39	FALSE
262237_at	hypothetical protein predicted by	---	AT1G48320	1.12	0.17	0.55	0.601947	0.7916062	-6.39	TRUE
264796_at	unknown protein similar to ESTs	ZIGA4	AT1G08680	-1.06	-0.09	-0.55	0.6017734	0.7916062	-6.39	FALSE
245988_at	putative protein predicted protei	---	AT5G20610	1.09	0.12	0.55	0.6018725	0.7916062	-6.39	FALSE
248516_at	unknown protein	---	AT5G50540 ///	-1.08	-0.11	-0.55	0.6018272	0.7916062	-6.39	FALSE
255897_at	mutator-like transposase, putativ	---	---	1.05	0.07	0.55	0.6017903	0.7916062	-6.39	FALSE
259589_at	unknown protein	---	AT1G28135	-1.08	-0.11	-0.55	0.6017325	0.7916062	-6.39	FALSE
252531_at	actin 12	ACT12	AT3G46520	-1.06	-0.08	-0.55	0.6018599	0.7916062	-6.39	FALSE
262869_s_a	putative protein predicted protei	GTG1	AT1G64990 ///	-1.08	-0.11	-0.55	0.6019182	0.7916062	-6.39	FALSE
252838_at	hypothetical protein	---	---	1.05	0.07	0.55	0.6019068	0.7916062	-6.39	FALSE
253303_at	putative protein ; supported by fu	---	AT4G33780	1.07	0.09	0.55	0.6022116	0.791667	-6.39	FALSE
267634_at	putative actin	---	AT2G42100	1.05	0.08	0.55	0.6022361	0.791667	-6.39	FALSE
262156_at	hypothetical protein contains sim	---	AT1G52680	1.07	0.10	0.55	0.6021953	0.791667	-6.39	FALSE
246377_at	low-temperature-specific protein	---	AT1G57550	-1.10	-0.14	-0.55	0.6020709	0.791667	-6.39	FALSE
256937_at	hypothetical protein predicted by	---	AT3G22620	1.52	0.60	0.55	0.6021077	0.791667	-6.39	FALSE
261449_at	putative ATPase similar to GB:AA	---	AT1G21120	1.11	0.16	0.55	0.6022142	0.791667	-6.39	FALSE
258808_at	putative pyruvate kinase similar	---	AT3G04050	-1.06	-0.08	-0.55	0.6021243	0.791667	-6.39	FALSE
251521_at	putative protein receptor kinase	ACR4	AT3G59420	-1.08	-0.11	-0.55	0.6022755	0.7916731	-6.39	FALSE
256953_at	flavonol 3-O-Glucosyltransferase	---	AT3G29630	1.09	0.12	0.55	0.6023224	0.7916892	-6.39	FALSE
264730_at	hypothetical protein similar to put	---	AT1G62085	-1.06	-0.09	-0.55	0.6024349	0.7917914	-6.39	FALSE
257790_at	gda-1, putative similar to gda-1 (	---	AT3G27090	1.08	0.11	0.55	0.6024902	0.7918184	-6.39	FALSE
250235_s_a	ubiquinol--cytochrome-c reducta	---	AT5G13430 ///	-1.05	-0.08	-0.55	0.6027206	0.7918475	-6.39	FALSE
248526_at	putative protein contains similarit	---	AT5G50740	1.09	0.13	0.55	0.6026823	0.7918475	-6.39	FALSE

253580_at	putative protein RING-H2 finger	---	AT4G30400	1.15	0.20	0.55	0.6026221	0.7918475	-6.39	FALSE
259969_at	putative pyrophosphate-depende	---	AT1G76550	1.15	0.20	0.55	0.6026809	0.7918475	-6.39	FALSE
249638_at	acetyl-CoA synthetase ; support	---	AT5G36880	1.17	0.23	0.55	0.6026889	0.7918475	-6.39	FALSE
247848_at	resistance protein - like disease	---	AT5G58120	1.08	0.11	0.55	0.6026126	0.7918475	-6.39	FALSE
260070_at	putative helix-loop-helix DNA-bin	BEE3	AT1G73830	-1.32	-0.40	-0.55	0.6027844	0.7918484	-6.39	FALSE
256141_at	lysine and histidine specific trans	---	AT1G48640	1.05	0.07	0.55	0.6027907	0.7918484	-6.39	FALSE
259773_at	auxin-induced protein, putative s	---	AT1G29500	-1.25	-0.32	-0.55	0.6029108	0.791915	-6.39	TRUE
250840_at	putative protein predicted protei	---	---	1.09	0.12	0.55	0.6028976	0.791915	-6.39	FALSE
250804_at	putative protein contains similarit	---	AT5G05030	1.07	0.10	0.55	0.6030832	0.7920959	-6.39	FALSE
251165_at	putative protein different MAP kir	---	AT3G63330	1.08	0.11	0.55	0.6032212	0.7922315	-6.39	FALSE
249926_at	E1, ubiquitin-like activating enzy	ECR1	AT5G19180	-1.08	-0.11	-0.54	0.6034581	0.7924513	-6.39	FALSE
254005_at	subtilisin-like serine protease co	UNE17	AT4G26330	-1.09	-0.12	-0.54	0.603432	0.7924513	-6.39	FALSE
263078_at	hypothetical protein predicted by	---	AT2G05350	1.07	0.10	0.54	0.6036226	0.7926217	-6.39	FALSE
246496_at	putative protein KIAA1468 - Hon	---	AT5G16210	1.07	0.10	0.54	0.6037586	0.7927488	-6.39	FALSE
258794_at	ankyrin-like protein similar to ank	---	AT3G04710	-1.15	-0.20	-0.54	0.6037889	0.7927488	-6.39	FALSE
258550_at	putative mudrA protein similar to	---	---	1.07	0.10	0.54	0.6040518	0.792925	-6.39	FALSE
251723_at	putative protein speckle-type pro	---	AT3G56230	1.08	0.11	0.54	0.6042098	0.792925	-6.39	FALSE
258214_at	amidase, putative similar to amid	atToc64-III	AT3G17970	-1.12	-0.16	-0.54	0.6041464	0.792925	-6.39	FALSE
246456_at	telomerase reverse transcriptase	ATTERT	AT5G16850	1.06	0.08	0.54	0.6040789	0.792925	-6.39	FALSE
259268_at	putative lamin similar to blue cop	---	AT3G01070	1.05	0.07	0.54	0.6041709	0.792925	-6.39	FALSE
253936_at	STIG1 like protein STIG1 protein	---	AT4G26880	1.06	0.09	0.54	0.6042387	0.792925	-6.39	FALSE
250211_at	unknown protein ; supported by	---	AT5G13880	-1.06	-0.09	-0.54	0.6041456	0.792925	-6.39	FALSE
252244_at	putative protein some putative pr	---	AT3G50130	1.07	0.10	0.54	0.603969	0.792925	-6.39	FALSE
257446_at	hypothetical protein predicted by	---	AT2G10440	-1.05	-0.07	-0.54	0.6040501	0.792925	-6.39	FALSE
266393_at	late embryogenesis abundant M1	M17	AT2G41260	-1.05	-0.07	-0.54	0.6042707	0.792925	-6.39	FALSE
256437_s_a	putative clathrin heavy chain sim	---	AT3G08530 ///	1.05	0.07	0.54	0.6043759	0.7930174	-6.39	FALSE
255199_at	coded for by A. thaliana cDNA N	---	AT4G07390	1.06	0.08	0.54	0.6045126	0.7931055	-6.39	FALSE
256541_at	ligand-gated ion channel, putativ	GLR3.3	AT1G42540	-1.09	-0.12	-0.54	0.6045025	0.7931055	-6.39	FALSE
261630_at	hypothetical protein predicted by	---	AT1G50080	1.05	0.08	0.54	0.6045989	0.7931317	-6.39	FALSE
263040_at	conserved hypothetical protein p	---	AT1G23300	-1.06	-0.08	-0.54	0.6046021	0.7931317	-6.39	FALSE
254883_at	putative protein histidine-rich gly	HAP2	AT4G11720	1.08	0.11	0.54	0.6047034	0.793195	-6.39	FALSE
247482_at	chromosomal protein - like chron	SMC2	AT5G62410	1.07	0.10	0.54	0.6047199	0.793195	-6.39	FALSE
253551_at	Expressed protein ; supported by	---	AT4G30996	1.07	0.10	0.54	0.6051593	0.7932485	-6.39	TRUE
265157_at	putative reverse transcriptase sir	---	---	1.06	0.09	0.54	0.605093	0.7932485	-6.39	FALSE
265348_at	putative RNA-binding protein	---	AT2G22600	1.07	0.09	0.54	0.6052454	0.7932485	-6.39	FALSE

246535_at	putative protein several hypothet	---	AT5G15900	1.09	0.12	0.54	0.6051239	0.7932485	-6.39	FALSE
264707_at	unknown protein	---	AT1G09730	-1.06	-0.08	-0.54	0.6050174	0.7932485	-6.39	FALSE
245890_at	ribosomal protein S15-like ribos	---	AT5G09490	1.05	0.07	0.54	0.605001	0.7932485	-6.39	FALSE
252191_at	putative protein various predicte	---	AT3G50180	1.07	0.10	0.54	0.6051907	0.7932485	-6.39	FALSE
265532_at	hypothetical protein predicted by	---	---	1.07	0.09	0.54	0.6052476	0.7932485	-6.39	FALSE
251509_at	pectinesterase precursor-like pr	---	AT3G59010	-1.19	-0.25	-0.54	0.6050182	0.7932485	-6.39	FALSE
245384_at	glycoprotein homolog ;supported	---	AT4G16790	1.11	0.14	0.54	0.6049848	0.7932485	-6.39	FALSE
263651_at	unknown protein Similar to Nicot	---	AT1G04340	1.08	0.12	0.54	0.6051121	0.7932485	-6.39	FALSE
245102_at	putative non-LTR retroelement re	---	---	-1.09	-0.13	-0.54	0.6050343	0.7932485	-6.39	FALSE
248033_s_a	putative protein similar to unknov	---	AT5G54330 /	1.06	0.08	0.54	0.6049713	0.7932485	-6.39	FALSE
265491_s_a	putative retroelement pol polypro	---	---	1.05	0.07	0.54	0.6051552	0.7932485	-6.39	FALSE
258470_at	Expressed protein ; supported by	---	AT3G06035	1.36	0.44	0.54	0.6053013	0.7932644	-6.39	TRUE
251557_at	v-ATPase subunit D (vATPD) ; s	---	AT3G58730	1.06	0.09	0.54	0.6053532	0.7932644	-6.40	FALSE
264775_at	putative endo-1,4-beta-D-glucar	CEL5	AT1G22880	1.08	0.11	0.54	0.605364	0.7932644	-6.40	FALSE
262142_at	hypothetical protein predicted by	---	AT1G52640	-1.07	-0.10	-0.54	0.6054949	0.793323	-6.40	FALSE
267138_s_a	similar to SOR1 from the fungus	PDX1.1	AT2G38210 /	1.15	0.21	0.54	0.6054994	0.793323	-6.40	FALSE
260224_at	hypothetical protein contains Pfa	---	AT1G74400	-1.05	-0.07	-0.54	0.6055131	0.793323	-6.40	FALSE
252757_at	putative protein several hypothet	---	---	1.07	0.10	0.54	0.6057059	0.7935301	-6.40	FALSE
250645_at	putative protein strong similarity t	---	AT5G06700	-1.12	-0.16	-0.54	0.6058388	0.7935958	-6.40	TRUE
259304_at	putative nucleotide repair protein	ERCC1	AT3G05210	1.06	0.09	0.54	0.6058605	0.7935958	-6.40	FALSE
262669_at	hypothetical protein	---	AT1G62850	-1.06	-0.09	-0.54	0.6058065	0.7935958	-6.40	FALSE
264057_at	putative AP2 domain transcriptio	RAP2.7	AT2G28550	-1.10	-0.14	-0.54	0.6061665	0.793951	-6.40	FALSE
260385_at	putative flavonol sulfotransferase	SOT18	AT1G74090	-1.08	-0.11	-0.54	0.606282	0.7940568	-6.40	FALSE
266430_at	unknown protein	---	AT2G07200	1.05	0.07	0.54	0.6064001	0.7941658	-6.40	FALSE
249932_at	unknown protein	---	AT5G22390	1.18	0.24	0.54	0.6065335	0.7941833	-6.40	TRUE
256222_at	hypothetical protein predicted by	---	AT1G56210	-1.10	-0.14	-0.54	0.6065513	0.7941833	-6.40	FALSE
249851_at	MADS-box transcription factor-lik	TT16	AT5G23260	1.05	0.07	0.54	0.6064514	0.7941833	-6.40	FALSE
247286_at	2-oxoglutarate/malate translocat	DiT2.2	AT5G64280	1.06	0.09	0.54	0.6065527	0.7941833	-6.40	FALSE
245460_at	disease resistance RPP5 like pro	RLM3	AT4G16990	-1.13	-0.17	-0.54	0.6065909	0.7941878	-6.40	TRUE
264957_at	F-box protein family, AtFBL5 cor	SKP2B	AT1G77000	1.11	0.16	0.54	0.6067013	0.7942866	-6.40	FALSE
250713_at	putative protein similar to unknov	---	AT5G06130	-1.07	-0.10	-0.54	0.6069232	0.7944995	-6.40	FALSE
250468_at	transcription factor TEIL/ethylen	---	AT5G10120	1.05	0.07	0.54	0.6069335	0.7944995	-6.40	FALSE
259510_at	hypothetical protein predicted by	---	AT1G43970	1.05	0.07	0.54	0.6069826	0.7945181	-6.40	FALSE
259322_at	unknown protein	---	AT3G05270	1.08	0.11	0.54	0.6071438	0.7946836	-6.40	FALSE
256774_at	hypothetical protein predicted by	---	AT3G13760	1.05	0.07	0.54	0.6072342	0.7947562	-6.40	FALSE

246630_at	hypothetical protein predicted by	---	AT1G50730	-1.11	-0.15	-0.54	0.6074183	0.7947761	-6.40	FALSE
261304_at	unknown protein ;supported by fu	---	AT1G48440	-1.05	-0.07	-0.54	0.6073815	0.7947761	-6.40	FALSE
259492_at	hypothetical protein predicted by	---	AT1G15830	1.10	0.14	0.54	0.6075038	0.7947761	-6.40	FALSE
250155_at	putative protein predicted protei	---	AT5G15160	1.17	0.22	0.54	0.607287	0.7947761	-6.40	FALSE
263398_at	putative RAS superfamily GTP-b	AtRABA5d	AT2G31680	1.07	0.09	0.54	0.6075539	0.7947761	-6.40	FALSE
261493_at	DNA-binding protein p24, putativ	WHY1	AT1G14410	-1.09	-0.13	-0.54	0.6075161	0.7947761	-6.40	FALSE
266498_at	1-aminocyclopropane-1-carboxyl	---	AT2G06960	1.06	0.08	0.54	0.6075629	0.7947761	-6.40	FALSE
245207_at	RING finger-like protein similarit	---	AT5G12310	1.06	0.09	0.54	0.6075628	0.7947761	-6.40	FALSE
245878_at	hypothetical protein contains sim	---	AT1G26190	-1.07	-0.10	-0.54	0.6073729	0.7947761	-6.40	FALSE
245360_at	naringenin 3-dioxygenase like pr	---	AT4G16330	-1.06	-0.09	-0.54	0.6076955	0.7948697	-6.40	FALSE
257555_at	hypothetical protein predicted by	---	AT3G24780	1.09	0.12	0.54	0.6077042	0.7948697	-6.40	FALSE
257844_at	prolyl 4-hydroxylase, putative sir	---	AT3G28480	1.09	0.12	0.54	0.6078585	0.795026	-6.40	FALSE
248185_at	flavonol 3-O-glucosyltransferase-	UF3GT	AT5G54060	1.06	0.08	0.54	0.6079826	0.795097	-6.40	FALSE
266597_at	putative WRKY-type DNA bindin	WRKY43	AT2G46130	-1.05	-0.07	-0.54	0.6079782	0.795097	-6.40	FALSE
252852_at	hypothetical protein ;supported b	---	AT4G39900	-1.14	-0.19	-0.54	0.6081084	0.795216	-6.40	TRUE
252834_at	putative protein RING-H2 zinc fi	---	AT4G40070	1.13	0.18	0.54	0.608212	0.7953059	-6.40	TRUE
247915_at	putative protein similar to unknov	---	AT5G57570	1.06	0.08	0.54	0.6082882	0.7953599	-6.40	FALSE
264582_at	putative ovule-specific homeotic	HDG2	AT1G05230	1.06	0.09	0.54	0.6083697	0.7954209	-6.40	FALSE
262611_at	Expressed protein ; supported by	---	AT1G14060	1.11	0.15	0.54	0.6084897	0.7955322	-6.40	FALSE
254361_at	Expressed protein ; supported by	---	AT4G22212	1.08	0.11	0.54	0.6086439	0.7956882	-6.40	FALSE
262115_at	Expressed protein ; supported by	---	AT1G02813	1.06	0.09	0.54	0.608892	0.7959213	-6.40	FALSE
257307_at	myb-like transcription factor, put	MYB121	AT3G30210	1.09	0.12	0.54	0.6088588	0.7959213	-6.40	FALSE
260222_at	putative alpha galactosyltransfer	XXT5	AT1G74380	1.13	0.17	0.54	0.6089645	0.7959704	-6.40	TRUE
248714_at	polygalacturonase ;supported by	---	AT5G48140	-1.05	-0.07	-0.54	0.6090706	0.7960635	-6.40	FALSE
265417_at	unknown protein	---	AT2G20920	-1.11	-0.15	-0.54	0.6092356	0.7962335	-6.40	FALSE
259516_at	hypothetical protein ; supported b	ERD10	AT1G20450	-1.13	-0.18	-0.54	0.6093558	0.7963169	-6.40	TRUE
254403_at	subtilisin-like serine protease cor	---	AT4G21323	1.05	0.07	0.54	0.6093692	0.7963169	-6.40	FALSE
249683_x_a	putative protein similar to unknov	---	---	-1.07	-0.10	-0.54	0.609484	0.7964213	-6.40	FALSE
245856_at	putative protein predicted protei	---	---	1.09	0.12	0.54	0.6095449	0.7964553	-6.40	FALSE
264544_s_a	unknown protein	---	AT1G55790 //	1.06	0.08	0.54	0.6096189	0.7964606	-6.40	FALSE
246361_s_a	hypothetical protein	---	---	1.05	0.08	0.54	0.6096155	0.7964606	-6.40	FALSE
257404_at	hypothetical protein predicted by	SUVR1	AT1G04050	1.06	0.09	0.54	0.6097465	0.7965529	-6.40	FALSE
256439_at	putative [Mn] superoxide dismuta	MSD1	AT3G10920	-1.07	-0.10	-0.54	0.6097594	0.7965529	-6.40	FALSE
253750_at	putative transcription factor legh	---	AT4G29000	1.09	0.12	0.53	0.6098952	0.7966848	-6.40	FALSE
264414_s_a	putative protein several hypothet	---	---	-1.11	-0.15	-0.53	0.6099839	0.796755	-6.40	FALSE

267641_at	Argonaute (AGO1)-like protein	AGO6	AT2G32940	1.05	0.07	0.53	0.6101354	0.7967705	-6.40	FALSE
265753_at	putative Athila retroelement ORF	---	---	-1.05	-0.07	-0.53	0.6101307	0.7967705	-6.40	FALSE
246945_s_a	putative membrane protein hypo	---	AT5G25040 /	1.07	0.09	0.53	0.6101262	0.7967705	-6.40	FALSE
255313_at	putative transposon protein	---	---	-1.07	-0.09	-0.53	0.610111	0.7967705	-6.40	FALSE
258893_at	putative disease resistance prote	AtRLP33	AT3G05660	-1.24	-0.31	-0.53	0.6102648	0.7968937	-6.40	FALSE
264767_at	hypothetical protein similar to put	SD1-29	AT1G61380	1.17	0.23	0.53	0.6103193	0.7969193	-6.40	FALSE
263672_at	putative retroelement pol polypro	---	---	1.05	0.07	0.53	0.6105414	0.7971637	-6.40	FALSE
258912_at	unknown protein similar to hypot	---	AT3G06460	1.09	0.13	0.53	0.6106165	0.7972161	-6.40	FALSE
254461_at	receptor kinase - like protein SR	---	AT4G21230	1.09	0.12	0.53	0.6107259	0.7973133	-6.40	FALSE
265159_at	unknown protein similar to EST g	---	AT1G31060	1.07	0.10	0.53	0.6108306	0.7973587	-6.40	FALSE
266605_at	putative SNF2 subfamily transcri	BRM	AT2G46020	1.06	0.08	0.53	0.6108064	0.7973587	-6.40	FALSE
266028_at	hypothetical protein predicted by	---	AT2G06000	-1.09	-0.12	-0.53	0.6109463	0.7973811	-6.40	FALSE
264245_at	galactinol synthase, putative sim	AtGolS7	AT1G60450	-1.06	-0.08	-0.53	0.6109421	0.7973811	-6.40	FALSE
257664_at	hypothetical protein predicted by	EMB2743	AT3G20400	1.08	0.11	0.53	0.6109526	0.7973811	-6.40	FALSE
252231_at	hypothetical protein ;supported b	---	AT3G49720	1.07	0.10	0.53	0.6111138	0.7975458	-6.40	TRUE
260506_at	Cyclin, putative similar to GB:CA	CYCA3;2	AT1G47210	-1.13	-0.17	-0.53	0.611199	0.7976113	-6.40	FALSE
255955_at	hypothetical protein predicted by	---	AT1G22030	-1.12	-0.16	-0.53	0.611235	0.7976128	-6.40	FALSE
248852_at	unknown protein	---	AT5G46560	1.05	0.07	0.53	0.6114889	0.797867	-6.40	FALSE
265758_at	hypothetical protein similar to my	---	---	1.05	0.07	0.53	0.6114998	0.797867	-6.40	FALSE
247671_at	putative protein slow myosin hea	---	AT5G60210	-1.05	-0.07	-0.53	0.6116197	0.7979777	-6.40	FALSE
253734_at	putative serine/threonine-specifi	---	AT4G29180	1.06	0.09	0.53	0.611761	0.7981164	-6.40	FALSE
247391_at	unknown protein	---	AT5G63540	1.05	0.07	0.53	0.6117984	0.7981197	-6.40	FALSE
254583_at	hypothetical protein	---	AT4G19480	-1.06	-0.08	-0.53	0.6118508	0.7981423	-6.40	FALSE
264774_at	unknown protein	---	AT1G22890	1.17	0.22	0.53	0.6119296	0.7981547	-6.40	TRUE
255160_at	putative pathogenesis-related pr	---	AT4G07820	-1.05	-0.07	-0.53	0.6119303	0.7981547	-6.40	FALSE
259617_at	hypothetical protein predicted by	---	AT1G47970	-1.07	-0.10	-0.53	0.6120047	0.7982062	-6.40	FALSE
266407_at	putative elongation factor	TFIIS	AT2G38560	-1.06	-0.08	-0.53	0.6121028	0.7982428	-6.40	FALSE
252348_at	B12D-like protein B12D protein -	---	AT3G48140	1.06	0.08	0.53	0.6120701	0.7982428	-6.40	FALSE
265458_at	unknown protein ;supported by f	---	AT2G46580	-1.07	-0.10	-0.53	0.6124105	0.7985071	-6.40	FALSE
246624_at	flavin-containing monooxygenas	YUC10	AT1G48910	-1.07	-0.09	-0.53	0.6123948	0.7985071	-6.40	FALSE
247778_at	wounding stress induced protein	---	AT5G58750	-1.05	-0.07	-0.53	0.6123899	0.7985071	-6.40	FALSE
247023_at	putative protein similar to unknov	HEC1	AT5G67060	1.09	0.12	0.53	0.6124841	0.7985469	-6.40	FALSE
257586_at	hypothetical protein predicted by	---	AT1G50760	-1.05	-0.07	-0.53	0.6125111	0.7985469	-6.40	FALSE
247379_at	unknown protein	---	---	1.08	0.12	0.53	0.6125807	0.7985591	-6.40	FALSE
262732_at	putative protein kinase similar to	---	AT1G16440	1.07	0.10	0.53	0.6125904	0.7985591	-6.40	FALSE

257216_at	4-methyl-5(b-hydroxyethyl)-thiaz	---	AT3G14990	1.14	0.19	0.53	0.6129106	0.798868	-6.40	TRUE
248692_s_a	hypothetical protein	---	AT4G15070 /	-1.06	-0.09	-0.53	0.6129325	0.798868	-6.40	FALSE
262973_at	histone H3, putative similar to H	---	AT1G75600	1.06	0.08	0.53	0.612878	0.798868	-6.40	FALSE
262567_at	hypothetical protein contains sim	---	AT1G34300	-1.10	-0.14	-0.53	0.6129787	0.7988682	-6.40	FALSE
246395_at	dirigent protein, putative similar	---	AT1G58170	-1.06	-0.08	-0.53	0.6130026	0.7988682	-6.40	FALSE
265735_at	putative aldolase ;supported by	---	AT2G01140	1.09	0.13	0.53	0.6130616	0.7988994	-6.40	FALSE
262367_at	hypothetical protein contains sim	VPS46.2	AT1G73030	-1.08	-0.11	-0.53	0.6131539	0.798974	-6.40	FALSE
252774_at	putative protein predicted protei	---	---	1.08	0.11	0.53	0.6134323	0.7992912	-6.40	FALSE
244948_at	hypothetical protein	---	---	-1.05	-0.08	-0.53	0.6135081	0.7993295	-6.40	FALSE
260899_at	hypothetical protein predicted by	---	AT1G21370	1.08	0.11	0.53	0.6135318	0.7993295	-6.40	FALSE
261834_at	polygalacturonase PG1, putative	---	AT1G10640	1.05	0.08	0.53	0.6135771	0.7993429	-6.40	FALSE
251898_at	floral homeotic protein APETALA	AP3	AT3G54340	-1.05	-0.07	-0.53	0.6137061	0.7994652	-6.40	FALSE
250785_at	unknown protein	---	AT5G05510	1.08	0.12	0.53	0.6137541	0.7994821	-6.40	FALSE
266642_at	putative chloroplast RNA binding	---	AT2G35410	-1.06	-0.09	-0.53	0.6140466	0.7995578	-6.40	FALSE
255178_at	may be a pseudogene	---	---	1.05	0.07	0.53	0.6140518	0.7995578	-6.40	FALSE
246161_at	putative protein predicted protei	JAZ12	AT5G20900	1.09	0.12	0.53	0.6138737	0.7995578	-6.40	FALSE
263903_at	putative touch-induced calmoduli	---	AT2G36180	-1.05	-0.08	-0.53	0.6140574	0.7995578	-6.40	FALSE
267443_at	hypothetical protein predicted by	---	AT2G19000	1.05	0.07	0.53	0.6140576	0.7995578	-6.40	FALSE
AFFX-TrpnX	B. subtilis /GEN=trpC, trpF /DB_	---	---	1.05	0.07	0.53	0.6139885	0.7995578	-6.40	FALSE
247672_at	senescence-associated protein -	TET4	AT5G60220	-1.05	-0.07	-0.53	0.6139007	0.7995578	-6.40	FALSE
255358_at	hypothetical protein	---	AT4G03940	-1.05	-0.07	-0.53	0.6143756	0.7999262	-6.40	FALSE
254078_at	putative protein various predicte	---	AT4G25710	1.07	0.09	0.53	0.6144794	0.7999703	-6.40	FALSE
253244_at	putative protein SEC14 protein,	COW1	AT4G34580	-1.08	-0.12	-0.53	0.6144796	0.7999703	-6.40	FALSE
257627_at	cytochrome P450, putative conta	CYP71B25	AT3G26270	-1.07	-0.09	-0.53	0.6145197	0.7999769	-6.40	FALSE
255573_at	hypothetical protein	---	AT4G01400	1.05	0.07	0.53	0.6145874	0.8000193	-6.40	FALSE
245219_at	viral resistance protein, putative	---	AT1G58807 /	1.06	0.08	0.53	0.6147574	0.800182	-6.40	FALSE
248101_at	chaperone GrpE-like protein ;su	---	AT5G55200	1.15	0.20	0.53	0.6147825	0.800182	-6.40	FALSE
259375_at	putative APG protein similar to a	---	AT3G16370	1.75	0.81	0.53	0.6148996	0.8002431	-6.40	FALSE
254392_at	endonuclease, putative ; suppor	ENDO5	AT4G21600	-1.06	-0.09	-0.53	0.6148662	0.8002431	-6.40	FALSE
251680_at	putative protein 13S condensin	---	AT3G57060	-1.06	-0.08	-0.53	0.6149906	0.8003158	-6.40	FALSE
260794_at	unknown protein ; supported by	---	AT1G06210	1.07	0.09	0.53	0.6151315	0.8003166	-6.40	FALSE
258022_at	hypothetical protein predicted by	---	AT3G19460	1.05	0.07	0.53	0.6150794	0.8003166	-6.40	FALSE
266722_at	unknown protein	FUT2	AT2G03210	-1.07	-0.09	-0.53	0.6151121	0.8003166	-6.40	FALSE
255363_x_a	hypothetical protein	---	---	1.09	0.12	0.53	0.6150911	0.8003166	-6.40	FALSE
249328_at	AtRAD3 (dbj|BAA92828.1) ; sup	ATR	AT5G40820	1.07	0.10	0.53	0.6152514	0.8003863	-6.40	FALSE

246819_at	WD-repeat protein - like WD-rep	---	AT5G26900	-1.06	-0.09	-0.53	0.6152553	0.8003863	-6.40	FALSE
253343_at	putative protein	---	AT4G33540	1.17	0.22	0.53	0.6155014	0.8006607	-6.40	TRUE
246849_at	putative protein various predicte	---	AT5G26850	1.15	0.20	0.53	0.6155829	0.8007211	-6.40	FALSE
254631_at	putative protein predicted protei	LSH9	AT4G18610	1.14	0.19	0.53	0.6158088	0.8009236	-6.40	FALSE
246128_at	putative protein predicted protei	---	---	-1.07	-0.09	-0.53	0.6158056	0.8009236	-6.40	FALSE
247475_at	IRE (root hair elongation)	IRE	AT5G62310	1.06	0.08	0.53	0.6159473	0.8010581	-6.40	FALSE
260868_at	unknown protein ;supported by fu	---	AT1G43860	-1.08	-0.11	-0.53	0.616053	0.8010599	-6.40	FALSE
255163_at	putative polyprotein	---	---	-1.06	-0.08	-0.53	0.6160835	0.8010599	-6.40	FALSE
264646_at	hypothetical protein Similar to Hc	BON3	AT1G08860	1.06	0.08	0.53	0.6160892	0.8010599	-6.40	FALSE
263747_at	putative ubiquitin activating enzy	SAE2	AT2G21470	1.05	0.07	0.53	0.6160485	0.8010599	-6.40	FALSE
245510_at	hypothetical protein	---	AT4G15740	1.10	0.14	0.53	0.6161802	0.8011326	-6.40	FALSE
256335_at	hypothetical protein predicted by	---	AT1G72110	1.07	0.10	0.52	0.6165255	0.8014706	-6.40	FALSE
257439_at	hypothetical protein similar to hyp	---	AT2G17000	1.05	0.07	0.52	0.6165456	0.8014706	-6.40	FALSE
261636_at	branched-chain amino acid amir	---	AT1G50110	-1.07	-0.09	-0.52	0.616511	0.8014706	-6.40	FALSE
246797_at	putative protein ;supported by fu	---	AT5G26790	1.05	0.07	0.52	0.6167655	0.8017108	-6.41	FALSE
245899_at	putative protein	ALF4	AT5G11030	-1.06	-0.09	-0.52	0.6170736	0.8018875	-6.41	FALSE
266164_at	putative salt-inducible protein	---	AT2G28050	1.10	0.14	0.52	0.6170757	0.8018875	-6.41	FALSE
250755_at	DnaJ-like protein ; supported by	---	AT5G05750	-1.08	-0.10	-0.52	0.6169945	0.8018875	-6.41	FALSE
265196_at	hypothetical protein predicted by	SWC2	AT2G36740	1.08	0.11	0.52	0.6170772	0.8018875	-6.41	FALSE
266690_at	malate oxidoreductase (malic en	ATNADP-M	AT2G19900	-1.06	-0.08	-0.52	0.6170369	0.8018875	-6.41	FALSE
259703_at	putative endo-1,3-beta-glucanas	---	AT1G77790	1.06	0.08	0.52	0.6172688	0.8020907	-6.41	FALSE
250782_at	SYN1 splice variant 1 (gb AAF08	SYN1	AT5G05490	1.06	0.09	0.52	0.6174131	0.8021995	-6.41	FALSE
255765_at	protein kinase, putative contains	---	AT1G16760	-1.04	-0.06	-0.52	0.6174228	0.8021995	-6.41	FALSE
260919_at	hypothetical protein predicted by	---	AT1G21520 /	-1.25	-0.32	-0.52	0.617552	0.8022302	-6.41	TRUE
256554_at	hypothetical protein similar to put	---	---	-1.08	-0.11	-0.52	0.6174901	0.8022302	-6.41	FALSE
258629_at	stelar K+ outward rectifying chan	SKOR	AT3G02850	1.05	0.07	0.52	0.6175225	0.8022302	-6.41	FALSE
256146_at	delta-adaptin, putative similar to	delta-ADR	AT1G48760	-1.06	-0.08	-0.52	0.6176021	0.8022496	-6.41	FALSE
257371_at	putative CCAAT-box binding tran	NF-YB5	AT2G47810	1.07	0.10	0.52	0.6178232	0.8024911	-6.41	FALSE
261040_at	oligouridylate binding protein, pu	UBP1B	AT1G17370	1.06	0.08	0.52	0.6180345	0.8026893	-6.41	FALSE
245086_at	putative translation initiation facto	---	AT2G39820	-1.06	-0.08	-0.52	0.6180662	0.8026893	-6.41	FALSE
248856_at	putative protein similar to unknov	---	AT5G46620	-1.05	-0.08	-0.52	0.6180813	0.8026893	-6.41	FALSE
264601_at	hypothetical protein similar to hyp	---	AT1G04540	1.06	0.09	0.52	0.6183269	0.8027489	-6.41	FALSE
254222_at	hypothetical protein	---	AT4G23840	1.07	0.09	0.52	0.6182703	0.8027489	-6.41	FALSE
255038_at	neutral invertase like protein Da	CINV2	AT4G09510	-1.14	-0.19	-0.52	0.618205	0.8027489	-6.41	FALSE
253515_at	auxin induced like-protein auxin-	---	AT4G31320	1.08	0.11	0.52	0.6182902	0.8027489	-6.41	FALSE

258948_at	putative sulfite oxidase similar to	SOX	AT3G01910	1.05	0.07	0.52	0.6181921	0.8027489	-6.41	FALSE
264117_at	hypothetical protein predicted by	---	AT2G31210	1.05	0.07	0.52	0.6183384	0.8027489	-6.41	FALSE
249462_at	putative protein predicted protei	EMB2744	AT5G39680	1.07	0.09	0.52	0.618478	0.8027539	-6.41	FALSE
262323_at	6-phosphogluconate dehydroge	---	AT1G64190	-1.05	-0.07	-0.52	0.6184481	0.8027539	-6.41	FALSE
245970_at	beta-galactosidase ; supported b	BGAL7	AT5G20710	1.07	0.10	0.52	0.618483	0.8027539	-6.41	FALSE
258841_at	hypothetical protein similar to hy	---	AT3G04660	-1.06	-0.08	-0.52	0.618387	0.8027539	-6.41	FALSE
256809_at	hypothetical protein predicted by	ALY3	AT3G21430	1.07	0.10	0.52	0.6186552	0.8029318	-6.41	FALSE
252489_at	disease resistance protein RPP8	---	AT3G46710	1.07	0.10	0.52	0.6187455	0.8030033	-6.41	FALSE
265371_at	putative PttA-like transposon pro	---	---	1.05	0.07	0.52	0.618827	0.8030633	-6.41	FALSE
264986_at	glutathione transferase, putative	ATGSTU13	AT1G27130	1.26	0.34	0.52	0.6188874	0.803096	-6.41	FALSE
255861_at	putative vacuolar sorting recepto	---	AT2G30290	-1.05	-0.07	-0.52	0.6189417	0.8031208	-6.41	FALSE
258056_at	hypothetical protein similar to GE	---	AT3G29010	1.08	0.11	0.52	0.6189922	0.8031406	-6.41	FALSE
249872_at	unknown protein	---	AT5G23130	-1.19	-0.26	-0.52	0.6191449	0.8032474	-6.41	TRUE
262150_at	hypothetical protein contains sim	FRS6	AT1G52520	-1.07	-0.10	-0.52	0.6191417	0.8032474	-6.41	FALSE
247814_at	polyneuridine aldehyde esterase	MES18	AT5G58310	1.29	0.36	0.52	0.6192293	0.803276	-6.41	FALSE
246530_at	Expressed protein ; supported by	---	AT5G15725	1.06	0.08	0.52	0.6192374	0.803276	-6.41	FALSE
250601_at	putative protein contains similarit	---	AT5G07810	1.05	0.07	0.52	0.6193927	0.8034317	-6.41	FALSE
254633_at	putative protein (fragment)	MRH1	AT4G18640	-1.10	-0.13	-0.52	0.6195124	0.8035414	-6.41	FALSE
263939_at	hypothetical protein predicted by	ATTIM44-2	AT2G36070	-1.06	-0.08	-0.52	0.6197563	0.8036749	-6.41	FALSE
264697_at	cyclin, putative similar to cyclin D	CYCD1;1	AT1G70210	-1.30	-0.38	-0.52	0.6197099	0.8036749	-6.41	FALSE
252518_at	receptor-like protein kinase hom	---	AT3G46350	-1.06	-0.08	-0.52	0.6197182	0.8036749	-6.41	FALSE
246848_at	putative protein	---	AT5G26840	-1.06	-0.09	-0.52	0.6197431	0.8036749	-6.41	FALSE
255191_at	may be a pseudogene	---	---	1.05	0.07	0.52	0.6199279	0.8038101	-6.41	FALSE
246869_at	putative protein various predicte	---	---	1.05	0.07	0.52	0.619931	0.8038101	-6.41	FALSE
250698_at	putative protein similar to unknov	---	AT5G06810	1.05	0.08	0.52	0.6202176	0.8039363	-6.41	FALSE
248529_at	protein kinase ;supported by full-	---	AT5G50000	-1.09	-0.12	-0.52	0.6201611	0.8039363	-6.41	FALSE
257542_at	hypothetical protein predicted by	---	AT3G26050	-1.05	-0.07	-0.52	0.6201455	0.8039363	-6.41	FALSE
259376_at	unknown protein C-terminus simi	CDC27a	AT3G16320	1.06	0.08	0.52	0.6202399	0.8039363	-6.41	FALSE
248742_at	unknown protein	---	AT5G48200	-1.07	-0.10	-0.52	0.6201719	0.8039363	-6.41	FALSE
249435_at	putative protein tail-specific thyr	---	AT5G39970	-1.05	-0.07	-0.52	0.6202193	0.8039363	-6.41	FALSE
262791_at	unknown protein EST gb|F13926	---	AT1G10830	-1.07	-0.10	-0.52	0.6203085	0.8039797	-6.41	FALSE
256969_at	unknown protein	---	AT3G21080	-1.23	-0.29	-0.52	0.6203869	0.8040355	-6.41	FALSE
261632_at	hypothetical protein predicted by	---	AT1G50120	-1.07	-0.10	-0.52	0.620445	0.8040651	-6.41	FALSE
266372_at	putative two-component respons	ATRR3	AT2G41310	-1.07	-0.10	-0.52	0.6205606	0.8041173	-6.41	FALSE
252578_at	putative protein Ariadne protein	---	AT3G45480	1.05	0.07	0.52	0.620591	0.8041173	-6.41	FALSE

265683_at	putative auxin-regulated protein	---	AT2G24400	-1.07	-0.09	-0.52	0.6205394	0.8041173	-6.41	FALSE
262215_at	hypothetical protein contains sim	---	AT1G74790	1.14	0.19	0.52	0.620702	0.8041697	-6.41	FALSE
249476_at	germin - like protein probable ge	---	AT5G38910	1.07	0.10	0.52	0.620698	0.8041697	-6.41	FALSE
263628_at	unknown protein ;supported by f	FLA7	AT2G04780	1.24	0.31	0.52	0.6208682	0.8043393	-6.41	TRUE
AFFX-TrpnX	B. subtilis /GEN=trpE, trpD /DB_	---	---	1.06	0.09	0.52	0.6209191	0.8043596	-6.41	FALSE
266727_at	putative calmodulin	emb1579	AT2G03150	-1.07	-0.10	-0.52	0.6210779	0.8045196	-6.41	FALSE
257165_at	beta-1,3-glucanase, putative sim	---	AT3G24330	1.09	0.12	0.52	0.6212482	0.8046945	-6.41	FALSE
246298_at	putative protein sequence in Ger	ETO1	AT3G51770	1.05	0.07	0.52	0.6213112	0.8047273	-6.41	FALSE
262083_at	hypothetical protein predicted by	---	AT1G56100	-1.06	-0.09	-0.52	0.6213793	0.8047273	-6.41	FALSE
246147_s_a	26S proteasome AAA-ATPase s	RPT6A	AT5G19990 ///	1.07	0.09	0.52	0.6213528	0.8047273	-6.41	FALSE
261757_at	hypothetical protein similar to put	---	AT1G08210	-1.09	-0.13	-0.52	0.6214602	0.8047864	-6.41	FALSE
250172_at	putative protein	---	AT5G14330	1.08	0.12	0.52	0.6216106	0.804874	-6.41	FALSE
245826_at	disease resistance protein RPS4	---	AT1G57850	1.07	0.09	0.52	0.6216104	0.804874	-6.41	FALSE
253345_at	putative protein	BCA5	AT4G33580	1.08	0.11	0.52	0.6216337	0.804874	-6.41	FALSE
253131_at	homeodomain - like protein seve	WOX13	AT4G35550	1.07	0.10	0.52	0.6217837	0.8048845	-6.41	FALSE
257965_at	unknown protein ;supported by f	---	AT3G19900	1.09	0.13	0.52	0.621779	0.8048845	-6.41	FALSE
250497_at	putative protein predicted protei	---	AT5G09630	-1.08	-0.11	-0.52	0.6217601	0.8048845	-6.41	FALSE
247097_at	mannan endo-1,4-beta-mannosi	---	AT5G66460	-1.09	-0.12	-0.52	0.6218533	0.8048845	-6.41	FALSE
252230_at	putative protein various predicte	---	AT3G49810	1.21	0.28	0.52	0.6218481	0.8048845	-6.41	FALSE
258346_at	hypothetical protein predicted by	---	AT3G22690	-1.07	-0.10	-0.52	0.6218536	0.8048845	-6.41	FALSE
250990_at	serine/threonine-specific protein	NAK	AT5G02290	-1.12	-0.16	-0.52	0.6218934	0.8048905	-6.41	FALSE
251636_at	calcium-dependent protein kinas	CPK32	AT3G57530	1.21	0.28	0.52	0.6220366	0.8049882	-6.41	FALSE
246132_at	Rad51-like protein ; supported b	ATRAD51	AT5G20850	1.05	0.07	0.52	0.6220395	0.8049882	-6.41	FALSE
256263_at	5,10-methylenetetrahydrofolate	---	AT3G12290	1.06	0.09	0.52	0.6222719	0.8052433	-6.41	FALSE
249117_at	heat shock transcription factor-lik	AT-HSFA6A	AT5G43840	-1.05	-0.08	-0.52	0.6223255	0.8052669	-6.41	FALSE
256592_at	hypothetical protein predicted by	---	---	-1.05	-0.07	-0.52	0.6224205	0.8053441	-6.41	FALSE
250853_s_a	putative protein prtedicted prtein	---	AT5G04680 ///	-1.05	-0.07	-0.52	0.6225875	0.8055145	-6.41	FALSE
257705_at	unknown protein ; supported by	---	AT3G12760	1.04	0.06	0.52	0.6227153	0.8056342	-6.41	FALSE
254518_at	downy mildew resistance-like pr	---	AT4G19910	1.06	0.09	0.52	0.6229719	0.8059204	-6.41	FALSE
249422_at	putative protein predicted protei	AtHB23	AT5G39760	-1.07	-0.10	-0.51	0.6231446	0.8060981	-6.41	FALSE
257445_x_a	hypothetical protein predicted by	---	---	1.05	0.07	0.51	0.6232255	0.8061571	-6.41	FALSE
262007_at	hypothetical protein predicted by	---	AT1G64580	1.06	0.08	0.51	0.6235873	0.8065794	-6.41	FALSE
253318_at	extensin-like protein extensin-lik	---	AT4G33970	-1.05	-0.07	-0.51	0.6236502	0.8066149	-6.41	FALSE
249099_at	putative protein similar to unknov	---	AT5G43550	-1.04	-0.06	-0.51	0.6236882	0.8066184	-6.41	FALSE
264010_at	putative disease resistance resp	---	AT2G21100	-1.10	-0.14	-0.51	0.6237526	0.8066559	-6.41	FALSE

257338_s_a	NADH dehydrogenase subunit 5	---	AT2G07711 /.	1.09	0.12	0.51	0.6239547	0.8066586	-6.41	TRUE
256007_at	allinase, putative similar to allina	SAMC2	AT1G34065	-1.08	-0.11	-0.51	0.623861	0.8066586	-6.41	FALSE
253634_at	putative protein ENOD20 gene p	---	AT4G30590	1.05	0.07	0.51	0.6239036	0.8066586	-6.41	FALSE
249503_at	expansin-like protein expansin -	ATEXPA24	AT5G39310	-1.06	-0.08	-0.51	0.6238998	0.8066586	-6.41	FALSE
256163_at	terpene cyclase, putative similar	---	AT1G48820	-1.05	-0.07	-0.51	0.6239669	0.8066586	-6.41	FALSE
266058_at	glycerol-3-phosphate dehydroge	GLY1	AT2G40690	-1.08	-0.11	-0.51	0.6237901	0.8066586	-6.41	FALSE
245149_at	putative SWI/SNF family transcri	ATSWI3A	AT2G47620	-1.06	-0.09	-0.51	0.6241341	0.8067813	-6.41	FALSE
266479_at	unknown protein ; supported by	LSH3	AT2G31160	1.22	0.29	0.51	0.6241588	0.8067813	-6.41	FALSE
263257_at	putative DNA polymerase Beta s	---	AT1G10520	-1.08	-0.12	-0.51	0.6241679	0.8067813	-6.41	FALSE
258967_at	hypothetical protein predicted by	---	AT3G10470	-1.07	-0.09	-0.51	0.6242257	0.8068104	-6.41	FALSE
261348_at	hypothetical protein contains sim	TED3	AT1G79810	-1.05	-0.07	-0.51	0.6243196	0.806886	-6.41	FALSE
255125_at	putative protein SCARECROW -	---	AT4G08250	-1.07	-0.09	-0.51	0.6243941	0.8069204	-6.41	FALSE
263648_at	hypothetical protein predicted by	---	AT1G04390	-1.07	-0.10	-0.51	0.624417	0.8069204	-6.41	FALSE
250154_at	putative aldose 1-epimerase - lik	---	AT5G15140	1.05	0.07	0.51	0.6245485	0.8070446	-6.41	FALSE
260914_at	beta-xylosidase, putative similar	BXL2	AT1G02640	1.16	0.22	0.51	0.6246526	0.8070877	-6.41	TRUE
262893_at	hypothetical protein contains sim	---	AT1G59790	1.05	0.07	0.51	0.6246415	0.8070877	-6.41	FALSE
252296_at	putative protein GMFP7 isopren	---	AT3G48970	1.10	0.14	0.51	0.6247414	0.8071194	-6.41	FALSE
255204_at	putative myosin-like protein	---	---	1.08	0.11	0.51	0.6247479	0.8071194	-6.41	FALSE
264939_at	receptor kinase, putative similar	---	AT1G60630	-1.06	-0.09	-0.51	0.6247909	0.8071292	-6.41	FALSE
267529_at	putative protein kinase contains a	AtAUR3	AT2G45490	1.08	0.10	0.51	0.6249019	0.8071818	-6.41	FALSE
262976_at	unknown protein	SRS5	AT1G75520	1.08	0.10	0.51	0.6249024	0.8071818	-6.41	FALSE
266111_at	unknown protein	---	AT2G02060 /.	-1.06	-0.08	-0.51	0.6249992	0.8072611	-6.41	FALSE
264248_at	hypothetical protein predicted by	---	AT1G78700	-1.08	-0.12	-0.51	0.6251509	0.8072742	-6.41	FALSE
262662_at	hypothetical protein similar to hyp	---	AT1G13920	1.07	0.10	0.51	0.6250619	0.8072742	-6.41	FALSE
258743_s_a	shaggy related protein kinase, A	ATSK12	AT3G05840 /.	1.07	0.09	0.51	0.625146	0.8072742	-6.41	FALSE
253488_at	putative protein reproductive me	REM1	AT4G31610	1.07	0.10	0.51	0.6251011	0.8072742	-6.41	FALSE
252211_at	putative protein predicted protei	---	AT3G50220	1.06	0.08	0.51	0.6252382	0.8073412	-6.41	FALSE
259125_at	unknown protein Pfam HMM hit:	---	AT3G02300	1.05	0.07	0.51	0.6253318	0.8074164	-6.41	FALSE
259757_at	putative thioredoxin similar to pro	ATPDIL1-2	AT1G77510	1.21	0.27	0.51	0.625377	0.8074291	-6.41	TRUE
256203_at	hypothetical protein	---	AT1G50800	-1.06	-0.09	-0.51	0.6255051	0.8075488	-6.41	FALSE
265898_at	hypothetical protein predicted by	---	AT2G25690	1.11	0.15	0.51	0.6257437	0.8078111	-6.41	FALSE
266686_at	hypothetical protein	---	AT2G19700	1.06	0.09	0.51	0.6258447	0.80785	-6.41	FALSE
264035_at	hypothetical protein predicted by	---	AT2G03630	-1.07	-0.09	-0.51	0.6258372	0.80785	-6.41	FALSE
261402_at	wall-associated kinase 4, putativ	RFO1	AT1G79670	1.11	0.15	0.51	0.6260933	0.8080794	-6.41	FALSE
250650_at	anthranilate phosphoribosyltrans	---	AT5G06850	-1.10	-0.13	-0.51	0.6260752	0.8080794	-6.41	FALSE

253611_at	RNase L inhibitor-like protein rib	NAP15	AT4G30300	1.06	0.09	0.51	0.6261669	0.8081287	-6.41	FALSE
266524_at	putative importin, beta subunit	---	AT2G16960	1.06	0.09	0.51	0.6262527	0.8081937	-6.41	FALSE
266564_at	putative serine carboxypeptidase	scpl22	AT2G24000	1.08	0.11	0.51	0.6264033	0.8083423	-6.41	FALSE
266333_at	putative ubiquitin activating enzy	AXL	AT2G32410	-1.07	-0.10	-0.51	0.6266088	0.8084992	-6.41	FALSE
246142_at	putative protein	---	AT5G19970	1.05	0.07	0.51	0.6266027	0.8084992	-6.41	FALSE
249022_s_a	polygalacturonase-like protein	---	AT5G44830 ///	1.06	0.08	0.51	0.6266312	0.8084992	-6.41	FALSE
254803_at	putative protein several hypothet	---	AT4G13100	-1.09	-0.13	-0.51	0.6268694	0.8085322	-6.41	FALSE
245964_at	putative protein C-terminus of gl	---	AT5G19720	-1.07	-0.10	-0.51	0.626852	0.8085322	-6.41	FALSE
253085_s_a	putative protein hypothetical pro	---	AT4G36270 ///	-1.10	-0.14	-0.51	0.6267201	0.8085322	-6.41	FALSE
263615_at	putative MYB family transcription	MYB100	AT2G25230	-1.05	-0.06	-0.51	0.6267597	0.8085322	-6.41	FALSE
248763_at	putative protein similar to unknov	---	AT5G47550	-1.51	-0.60	-0.51	0.6268426	0.8085322	-6.41	FALSE
260105_at	hypothetical protein predicted by	---	---	-1.05	-0.07	-0.51	0.6268672	0.8085322	-6.41	FALSE
246638_at	putative protein predicted protei	---	---	1.06	0.08	0.51	0.6269578	0.8085777	-6.41	FALSE
265063_at	receptor kinase, putative similar	---	AT1G61500	-1.08	-0.11	-0.51	0.6269756	0.8085777	-6.41	FALSE
255972_at	hypothetical protein similar to hyp	---	---	-1.05	-0.06	-0.51	0.627034	0.8086072	-6.41	FALSE
252660_at	putative protein	---	AT3G44440	1.05	0.07	0.51	0.6271074	0.8086106	-6.41	FALSE
250619_at	A9 ;supported by full-length cDN	---	AT5G07230	1.04	0.06	0.51	0.6271064	0.8086106	-6.41	FALSE
245310_at	hypothetical protein ;supported b	RALFL31	AT4G13950	1.15	0.20	0.51	0.6273273	0.8086655	-6.41	FALSE
260234_at	putative lipase/acylhydrolase cor	---	AT1G74460	1.08	0.11	0.51	0.6272601	0.8086655	-6.41	FALSE
264036_at	hypothetical protein similar to hyp	---	AT2G03810	-1.08	-0.12	-0.51	0.6273157	0.8086655	-6.41	FALSE
256030_at	hypothetical protein contains sim	---	AT1G34110	-1.06	-0.09	-0.51	0.6272179	0.8086655	-6.41	FALSE
256382_at	unknown protein ;supported by fu	---	AT1G66860	1.16	0.22	0.51	0.6272342	0.8086655	-6.41	FALSE
257090_at	protein kinase, putative contains	---	AT3G20530	-1.06	-0.09	-0.51	0.6274572	0.8087415	-6.41	FALSE
259262_at	unknown protein similar to nifU-li	ISU2	AT3G01020	-1.05	-0.07	-0.51	0.6274441	0.8087415	-6.41	FALSE
250223_at	glutaredoxin-like protein ;suppor	ROXY2	AT5G14070	1.06	0.08	0.51	0.6277118	0.8090028	-6.41	FALSE
256271_at	unknown protein	---	AT3G12140	-1.08	-0.12	-0.51	0.6277379	0.8090028	-6.41	FALSE
255374_at	hypothetical protein	---	---	1.05	0.07	0.51	0.6277663	0.8090028	-6.41	FALSE
250849_at	putative protein NAC2, Arabidop	NAC2	AT5G04410	1.06	0.08	0.51	0.6278144	0.8090191	-6.41	FALSE
247366_at	putative protein contains similarit	---	AT5G63260	1.07	0.10	0.51	0.6278643	0.8090376	-6.41	FALSE
267013_at	putative protein kinase contains a	CCR2	AT2G39180	1.06	0.09	0.51	0.62795	0.8090566	-6.41	FALSE
247872_at	putative protein similar to unknov	---	AT5G57670	1.08	0.12	0.51	0.6279328	0.8090566	-6.41	FALSE
261047_at	hypothetical protein predicted by	APUM22	AT1G01410	1.10	0.14	0.51	0.6279955	0.8090696	-6.41	FALSE
254615_at	RNase L inhibitor-like protein RN	RLI2	AT4G19210	-1.06	-0.08	-0.51	0.6281221	0.809187	-6.41	FALSE
255369_at	putative NifU-like metallocluster a	ISU3	AT4G04080	1.06	0.09	0.51	0.6281723	0.809206	-6.41	FALSE
260183_at	hypothetical protein similar to DN	---	---	-1.05	-0.06	-0.51	0.6282251	0.8092283	-6.41	FALSE

250828_at	unknown protein ; supported by c	---	AT5G05250	-1.36	-0.45	-0.51	0.628285	0.8092597	-6.41	FALSE
256804_at	hypothetical protein predicted by	---	AT3G20920	1.04	0.06	0.51	0.6283597	0.8093102	-6.41	FALSE
253799_at	putative DNA-binding protein AF	---	AT4G28140	1.40	0.49	0.51	0.6286016	0.8095382	-6.42	FALSE
259940_at	hypothetical protein	---	AT1G71290	1.05	0.07	0.51	0.6286076	0.8095382	-6.42	FALSE
265046_s_a	mutator-like transposase, putativ	---	---	1.06	0.08	0.51	0.6288089	0.8097516	-6.42	FALSE
257325_at	hypothetical protein	---	AT2G07798	-1.15	-0.20	-0.51	0.629135	0.8097602	-6.42	TRUE
256624_at	hypothetical protein predicted by	---	AT3G19990	1.05	0.08	0.51	0.628932	0.8097602	-6.42	FALSE
267030_at	unknown protein	SCAR2	AT2G38440	-1.05	-0.08	-0.51	0.6289313	0.8097602	-6.42	FALSE
267143_at	putative peptide/amino acid trans	---	AT2G38100	1.06	0.09	0.51	0.6291037	0.8097602	-6.42	FALSE
258844_at	hypothetical protein predicted by	SWP	AT3G04740	-1.05	-0.07	-0.51	0.6291289	0.8097602	-6.42	FALSE
266408_at	putative retroelement pol polypro	---	---	1.07	0.10	0.51	0.6290617	0.8097602	-6.42	FALSE
266837_x_a	unknown protein	---	AT2G25990	-1.05	-0.07	-0.51	0.6289224	0.8097602	-6.42	FALSE
246184_at	beta-D-glucan exohydrolase - lik	---	AT5G20950	1.10	0.13	0.51	0.629112	0.8097602	-6.42	FALSE
251043_s_a	putative protein various predicte	---	AT5G02330 ///	-1.06	-0.08	-0.51	0.6290676	0.8097602	-6.42	FALSE
265833_at	Mutator-like transposase similar t	---	---	1.05	0.07	0.51	0.629201	0.8097995	-6.42	FALSE
256716_at	hypothetical protein predicted by	---	AT2G34100	1.06	0.09	0.51	0.6294344	0.8100542	-6.42	FALSE
259147_at	putative RNA binding protein sim	APUM4	AT3G10360	1.10	0.14	0.51	0.6295546	0.8101631	-6.42	FALSE
263860_at	hypothetical protein predicted by	---	---	1.05	0.07	0.51	0.6296425	0.8102305	-6.42	FALSE
265850_at	putative DnaJ protein	---	AT2G35720	-1.08	-0.11	-0.50	0.6297673	0.8102539	-6.42	FALSE
253957_at	putative protein ; supported by c	AGP13	AT4G26320	1.09	0.12	0.50	0.6297136	0.8102539	-6.42	FALSE
263262_at	unknown protein	---	AT2G38830	1.06	0.08	0.50	0.6297615	0.8102539	-6.42	FALSE
252423_at	putative protein putative hydroly	---	AT3G47590	1.05	0.08	0.50	0.6300154	0.8104417	-6.42	FALSE
253409_at	putative protein	---	AT4G32960	-1.05	-0.07	-0.50	0.629976	0.8104417	-6.42	FALSE
263070_at	unknown protein	---	AT2G17600	1.06	0.08	0.50	0.6300198	0.8104417	-6.42	FALSE
252634_x_a	putative protein predicted protei	---	---	1.07	0.09	0.50	0.6301173	0.8105214	-6.42	FALSE
263892_at	putative MYB family transcription	RAX2	AT2G36890	1.05	0.06	0.50	0.6302667	0.8106678	-6.42	FALSE
249306_at	RING zinc finger protein-like ;su	---	AT5G41400	1.16	0.21	0.50	0.6303867	0.8107765	-6.42	TRUE
249717_at	unknown protein ;supported by f	---	AT5G35730	1.06	0.08	0.50	0.6304486	0.8107807	-6.42	FALSE
252448_at	beta-D-glucan exohydrolase - lik	---	AT3G47050	-1.06	-0.09	-0.50	0.6304611	0.8107807	-6.42	FALSE
250760_at	unknown protein	---	AT5G06040	-1.06	-0.08	-0.50	0.6305199	0.8108106	-6.42	FALSE
254324_at	putative protein various predicte	---	AT4G22640	-1.07	-0.10	-0.50	0.6306293	0.8108599	-6.42	FALSE
263140_at	hypothetical protein predicted by	---	AT1G65120	-1.05	-0.06	-0.50	0.6305954	0.8108599	-6.42	FALSE
265979_at	putative replication protein A1	---	---	-1.06	-0.09	-0.50	0.6307667	0.8109908	-6.42	FALSE
260181_at	endo-1,4-beta-glucanase identic	ATGH9B1	AT1G70710	-1.14	-0.19	-0.50	0.6308093	0.8109998	-6.42	FALSE
259142_at	unknown protein similar to ankyri	---	AT3G10200	1.06	0.09	0.50	0.6308951	0.8110644	-6.42	FALSE

261739_at	hypothetical protein similar to hyp	PEX11A	AT1G47750	1.05	0.07	0.50	0.6309395	0.8110758	-6.42	FALSE
245178_at	putative protein similarity to cDNA	FIS1B	AT5G12390	1.05	0.07	0.50	0.6310285	0.8110874	-6.42	FALSE
266836_at	hypothetical protein predicted by	---	AT2G26000	-1.08	-0.11	-0.50	0.6311199	0.8110874	-6.42	FALSE
263751_at	putative kinesin heavy chain	---	AT2G21300	-1.10	-0.14	-0.50	0.6310592	0.8110874	-6.42	FALSE
246672_at	putative protein	---	---	-1.05	-0.07	-0.50	0.6311263	0.8110874	-6.42	FALSE
249155_at	unknown protein	---	AT5G43480	1.05	0.06	0.50	0.6310359	0.8110874	-6.42	FALSE
249802_at	putative protein similar to unknov	---	AT5G23770	-1.05	-0.07	-0.50	0.6312277	0.811172	-6.42	FALSE
247354_at	flavonol synthase ;supported by	FLS3	AT5G63590	1.05	0.07	0.50	0.6312957	0.8112137	-6.42	FALSE
255753_at	myb factor, putative similar to m	MYB51	AT1G18570	1.37	0.46	0.50	0.6314189	0.8113264	-6.42	TRUE
253817_at	hypothetical protein ;supported b	---	AT4G28310	-1.17	-0.22	-0.50	0.6315198	0.8113809	-6.42	FALSE
258541_at	hypothetical protein	---	AT3G07000	1.05	0.06	0.50	0.6315325	0.8113809	-6.42	FALSE
261214_at	Mutator-like protein similar to ma	---	---	1.08	0.11	0.50	0.6316232	0.8114517	-6.42	FALSE
265209_at	putative DNA binding protein with	ATHB22	AT2G36610	1.05	0.07	0.50	0.6317046	0.8115106	-6.42	FALSE
246002_at	ripening-related protein - like gri	---	AT5G20740	1.13	0.18	0.50	0.631857	0.8116606	-6.42	FALSE
246386_at	beta-galactosidase, putative sim	BGAL16	AT1G77410	1.07	0.10	0.50	0.6319498	0.8117341	-6.42	FALSE
255992_at	unknown protein	---	AT1G29790	-1.07	-0.09	-0.50	0.6320219	0.8117811	-6.42	FALSE
246164_at	putative protein predicted protein	---	---	1.06	0.08	0.50	0.6322612	0.8118969	-6.42	FALSE
253887_at	putative protein isp4 protein, Sch	OPT6	AT4G27730	-1.15	-0.20	-0.50	0.6321777	0.8118969	-6.42	FALSE
265846_at	putative serine carboxypeptidase	scpl28	AT2G35770	-1.06	-0.09	-0.50	0.6322901	0.8118969	-6.42	FALSE
249623_at	putative protein Ariadne-2 protei	---	AT5G37560	1.04	0.06	0.50	0.6322415	0.8118969	-6.42	FALSE
245236_at	putative DNA mismatch repair p	MSH3	AT4G25540	-1.05	-0.07	-0.50	0.6322862	0.8118969	-6.42	FALSE
265130_at	unknown protein similar to ESTs	---	AT1G30890	1.04	0.06	0.50	0.6324057	0.8119539	-6.42	FALSE
266558_at	putative polygalacturonase	---	AT2G23900	-1.05	-0.07	-0.50	0.6323968	0.8119539	-6.42	FALSE
267459_at	unknown protein ;supported by f	---	AT2G33850	-1.05	-0.07	-0.50	0.6324609	0.8119791	-6.42	FALSE
267426_at	hypothetical protein predicted by	---	AT2G34820	1.05	0.08	0.50	0.6325036	0.8119883	-6.42	FALSE
248400_at	putative protein contains similarit	---	AT5G52020	1.08	0.10	0.50	0.6325688	0.8120263	-6.42	FALSE
246263_at	unknown protein	---	AT1G31780	-1.08	-0.10	-0.50	0.6328514	0.8122518	-6.42	FALSE
247576_at	putative protein predicted protein	---	AT5G61280	-1.05	-0.06	-0.50	0.6328302	0.8122518	-6.42	FALSE
251044_at	putative protein various predicte	---	AT5G02350	-1.05	-0.07	-0.50	0.6327852	0.8122518	-6.42	FALSE
247780_at	dehydrodolichyl diphosphate - lik	---	AT5G58770	1.17	0.23	0.50	0.6329159	0.812282	-6.42	FALSE
262437_at	hypothetical protein	---	---	1.07	0.09	0.50	0.6329461	0.812282	-6.42	FALSE
249168_at	putative protein strong similarity t	---	AT5G42870	1.07	0.09	0.50	0.6331321	0.8124293	-6.42	FALSE
253784_at	putative protein WREBP-1, Nico	PHR1	AT4G28610	1.06	0.09	0.50	0.6331303	0.8124293	-6.42	FALSE
254960_at	predicted protein	---	AT4G10845	1.06	0.09	0.50	0.6332661	0.8124999	-6.42	FALSE
251534_at	ATP-dependent RNA helicase-li	---	AT3G58510	1.10	0.14	0.50	0.63335	0.8124999	-6.42	FALSE

253540_at	putative protein various predicte	---	AT4G31615	1.05	0.08	0.50	0.6333652	0.8124999	-6.42	FALSE
259563_s_a	hypothetical protein	---	AT1G20590 /.	-1.05	-0.07	-0.50	0.6332613	0.8124999	-6.42	FALSE
247619_at	putative protein	---	AT5G60290	-1.08	-0.11	-0.50	0.6333602	0.8124999	-6.42	FALSE
260401_at	unknown protein similar to hypot	---	AT1G69840	1.07	0.10	0.50	0.633565	0.8125413	-6.42	FALSE
256270_at	unknown protein ; supported by c	---	AT3G12300	1.06	0.08	0.50	0.6335095	0.8125413	-6.42	FALSE
245131_s_a	unknown protein	emb1067	AT2G45330 /.	1.05	0.07	0.50	0.6336112	0.8125413	-6.42	FALSE
250654_at	receptor protein kinase-like prote	---	AT5G06940	-1.06	-0.09	-0.50	0.6335611	0.8125413	-6.42	FALSE
248218_at	unknown protein ;supported by fu	---	AT5G53710	-1.08	-0.11	-0.50	0.6336013	0.8125413	-6.42	FALSE
254802_at	endoxyloglucan transferase-like	---	AT4G13090	-1.07	-0.10	-0.50	0.6335914	0.8125413	-6.42	FALSE
245373_s_a	Expressed protein ; supported by	ATARD2	AT4G14710 /.	-1.06	-0.08	-0.50	0.6337026	0.8125671	-6.42	FALSE
252692_at	cysteine proteinase contains sim	---	AT3G43960	1.14	0.19	0.50	0.6336914	0.8125671	-6.42	FALSE
266956_at	unknown protein	---	AT2G34510	1.16	0.21	0.50	0.6338119	0.8126403	-6.42	TRUE
247377_at	pectate lyase ; supported by cDI	---	AT5G63180	-1.54	-0.62	-0.50	0.633831	0.8126403	-6.42	FALSE
267311_at	hypothetical protein	---	AT2G34670	-1.05	-0.07	-0.50	0.6340357	0.812828	-6.42	FALSE
248776_at	unknown protein	---	AT5G47900	1.06	0.08	0.50	0.6340532	0.812828	-6.42	FALSE
246811_at	putative protein	---	AT5G27170	-1.06	-0.08	-0.50	0.6340842	0.812828	-6.42	FALSE
262476_at	phosphoprotein phosphatase ide	---	AT1G50370	1.05	0.08	0.50	0.6343792	0.8129807	-6.42	FALSE
258165_at	unknown protein ; supported by	---	AT3G17900	-1.06	-0.08	-0.50	0.6342827	0.8129807	-6.42	FALSE
253536_at	RSZp22 splicing factor ;supporte	SRZ-22	AT4G31580	-1.05	-0.06	-0.50	0.6342928	0.8129807	-6.42	FALSE
246278_at	tubulin-like protein	---	AT4G37190	1.13	0.17	0.50	0.6343816	0.8129807	-6.42	FALSE
260270_at	putative disease resistance prote	---	AT1G63730	-1.06	-0.08	-0.50	0.6343382	0.8129807	-6.42	FALSE
264479_at	hypothetical protein similar to rec	---	AT1G77280	1.07	0.09	0.50	0.6344689	0.8130013	-6.42	TRUE
247524_at	thioredoxin-like 3 ; supported by	ACHT5	AT5G61440	1.19	0.25	0.50	0.6344651	0.8130013	-6.42	FALSE
255684_at	putative glycosylasparaginase	---	AT4G00590	1.09	0.12	0.50	0.6346393	0.8131739	-6.42	FALSE
260705_at	unknown protein ;supported by fu	TOM2A	AT1G32400	1.05	0.07	0.50	0.6348058	0.8133417	-6.42	FALSE
245309_at	putative protein ; supported by cI	---	AT4G15140	1.10	0.14	0.50	0.6348934	0.8133625	-6.42	FALSE
262138_at	NBS/LRR disease resistance pr	---	AT1G52660	1.07	0.09	0.50	0.6348578	0.8133625	-6.42	FALSE
248874_at	putative protein strong similarity t	---	AT5G46460	1.09	0.12	0.50	0.6352392	0.8136493	-6.42	FALSE
261097_at	protein kinase, putative contains	---	AT1G62950	1.09	0.12	0.50	0.6351654	0.8136493	-6.42	FALSE
266025_at	putative retroelement pol polypro	---	---	-1.06	-0.08	-0.50	0.6353989	0.8136493	-6.42	FALSE
266322_at	putative auxin-regulated protein	---	AT2G46690	-1.12	-0.16	-0.50	0.6353536	0.8136493	-6.42	FALSE
260615_at	mitochondrial NAD-dependent m	---	AT1G53240	-1.12	-0.17	-0.50	0.635339	0.8136493	-6.42	FALSE
262958_at	water stress-induced protein, pu	---	AT1G54410	-1.07	-0.09	-0.50	0.6352226	0.8136493	-6.42	FALSE
256119_at	guanine nucleotide regulatory pr	---	AT1G18070	1.06	0.08	0.50	0.6353805	0.8136493	-6.42	FALSE
251747_at	putative protein various predicte	---	AT3G55670	1.05	0.07	0.50	0.6354027	0.8136493	-6.42	FALSE

266834_s_a	putative protein phosphatase 2C	---	AT2G05050 /	1.32	0.40	0.50	0.635678	0.8137277	-6.42	TRUE
245681_at	alkaline/neutral invertase, putati	---	AT1G56560	1.05	0.07	0.50	0.6356672	0.8137277	-6.42	FALSE
265567_at	unknown protein predicted by ge	---	AT2G05580	1.07	0.09	0.50	0.635586	0.8137277	-6.42	FALSE
258010_at	unknown protein similar to recep	---	AT3G19300	-1.05	-0.07	-0.50	0.6356746	0.8137277	-6.42	FALSE
251158_at	rac-GTP binding protein -like RA	MIRO2	AT3G63150	-1.05	-0.08	-0.50	0.6355476	0.8137277	-6.42	FALSE
265719_at	unknown protein related to putati	---	AT2G03500	-1.05	-0.07	-0.50	0.6355259	0.8137277	-6.42	FALSE
249286_at	transcription factor-like protein	---	AT5G41580	-1.06	-0.08	-0.50	0.6358237	0.8138626	-6.42	FALSE
254142_at	putative protein other predicted	---	AT4G24630	-1.06	-0.08	-0.50	0.6359038	0.8138626	-6.42	FALSE
259573_at	hypothetical protein	---	---	1.05	0.08	0.50	0.6360022	0.8138626	-6.42	FALSE
256001_at	unknown protein contains similar	---	AT1G29850	1.08	0.11	0.50	0.6359888	0.8138626	-6.42	FALSE
255347_at	putative retrotransposon protein	---	---	-1.05	-0.07	-0.50	0.6359477	0.8138626	-6.42	FALSE
260838_at	hypothetical protein predicted by	---	AT1G43680	1.05	0.07	0.50	0.6359396	0.8138626	-6.42	FALSE
259798_at	hypothetical protein predicted by	---	AT1G64310	1.08	0.11	0.50	0.6360331	0.8138626	-6.42	FALSE
261094_at	hypothetical protein predicted by	---	AT1G62920	1.09	0.12	0.50	0.6361847	0.8140109	-6.42	FALSE
256167_at	hypothetical protein similar to put	---	---	-1.05	-0.07	-0.50	0.636261	0.8140629	-6.42	FALSE
253600_at	SERINE CARBOXYPEPTIDASE	scpl29	AT4G30810	-1.06	-0.08	-0.49	0.6364512	0.8142605	-6.42	FALSE
251036_at	putative protein ; supported by c	---	AT5G02160	-1.06	-0.09	-0.49	0.6365126	0.8142934	-6.42	TRUE
263534_at	putative steroid binding protein ;	AtMAPR2	AT2G24940 /	-1.06	-0.09	-0.49	0.6365707	0.8143221	-6.42	FALSE
266695_at	putative CCCH-type zinc finger p	---	AT2G19810	1.14	0.19	0.49	0.6367715	0.8144629	-6.42	FALSE
267176_at	putative zinc finger protein	---	AT2G37730	1.06	0.09	0.49	0.6367878	0.8144629	-6.42	FALSE
245185_at	F12A21.11 similar to T-Complex	---	AT1G67760	-1.08	-0.10	-0.49	0.6367402	0.8144629	-6.42	FALSE
261120_at	homeodomain protein BELL1, p	BLH3	AT1G75410	-1.09	-0.12	-0.49	0.6369227	0.8145088	-6.42	FALSE
249955_at	sugar transporter - like protein p	---	AT5G18840	1.15	0.20	0.49	0.6369301	0.8145088	-6.42	FALSE
259299_at	unknown protein	---	AT3G05080	-1.08	-0.11	-0.49	0.6369309	0.8145088	-6.42	FALSE
260544_at	unknown protein predicted by ge	---	AT2G43540	-1.09	-0.12	-0.49	0.6370173	0.814528	-6.42	FALSE
259035_at	hypothetical protein predicted by	---	AT3G09430	1.05	0.07	0.49	0.6369997	0.814528	-6.42	FALSE
248756_at	sodium-dicarboxylate cotranspor	TDT	AT5G47560	-1.12	-0.16	-0.49	0.6372734	0.814681	-6.42	TRUE
253825_at	Expressed protein ; supported by	---	AT4G28025	1.08	0.11	0.49	0.6371915	0.814681	-6.42	FALSE
259629_at	disease resistance protein contai	WRR4	AT1G56510	1.08	0.11	0.49	0.6372798	0.814681	-6.42	FALSE
259635_at	purple acid phosphatase, putativ	PAP6	AT1G56360	1.06	0.09	0.49	0.6372206	0.814681	-6.42	FALSE
246491_at	hypothetical protein	---	AT5G16100	-1.05	-0.07	-0.49	0.6374695	0.8148748	-6.42	FALSE
254094_at	putative protein ATP-dependent	---	AT4G25120	-1.07	-0.10	-0.49	0.6375029	0.8148748	-6.42	FALSE
265775_at	Mutator-like transposase similar	---	---	1.09	0.12	0.49	0.6377507	0.8151052	-6.42	FALSE
263346_at	En/Spm-like transposon protein r	---	---	1.05	0.07	0.49	0.6377546	0.8151052	-6.42	FALSE
251840_at	protein disulfide-isomerase-like	ATPDIL1-3	AT3G54960	1.12	0.16	0.49	0.6379541	0.8151336	-6.42	FALSE

258727_at	ethylene-responsive protein, put	---	AT3G11930	1.07	0.09	0.49	0.6379424	0.8151336	-6.42	FALSE
246962_s_a	transcription factor-like protein li	BZIP9	AT5G24800	1.11	0.15	0.49	0.6379552	0.8151336	-6.42	FALSE
264784_s_a	unknown protein similar to Arabi	---	AT2G17830 /.	-1.06	-0.08	-0.49	0.6378579	0.8151336	-6.42	FALSE
255757_at	putative protein	ROPGEF3	AT4G00460	-1.05	-0.07	-0.49	0.6379555	0.8151336	-6.42	FALSE
265585_at	CDC27/NUC2-like protein TPR-r	HBT	AT2G20000	-1.07	-0.10	-0.49	0.6380537	0.8152134	-6.42	FALSE
266650_at	unknown protein	---	AT2G25800	-1.07	-0.10	-0.49	0.6381623	0.8153065	-6.42	TRUE
260455_at	hypothetical protein predicted by	---	AT1G72500	1.15	0.20	0.49	0.638227	0.8153249	-6.42	FALSE
265490_s_a	putative polygalacturonase	---	AT2G15450 /.	1.05	0.08	0.49	0.6382702	0.8153249	-6.42	FALSE
249629_at	kinesin -like protein Krm protein,	---	AT5G37590	1.08	0.11	0.49	0.638284	0.8153249	-6.42	FALSE
264574_at	putative zinc transporter Similar t	ZIP5	AT1G05300	-1.12	-0.17	-0.49	0.6386143	0.815464	-6.42	TRUE
253627_at	low temperature and salt respon	---	AT4G30650	-1.38	-0.47	-0.49	0.6385067	0.815464	-6.42	TRUE
254624_at	hypothetical protein ;supported b	---	AT4G18580	-1.06	-0.08	-0.49	0.6385739	0.815464	-6.42	FALSE
259498_at	unknown protein similar to putati	GOS11	AT1G15880	-1.05	-0.08	-0.49	0.6385054	0.815464	-6.42	FALSE
264813_at	putative Ca2+-dependent ser/thr	CPK16	AT2G17890	1.08	0.11	0.49	0.6385532	0.815464	-6.42	FALSE
254278_at	Expressed protein ; supported by	---	AT4G22740	-1.06	-0.09	-0.49	0.6386431	0.815464	-6.42	FALSE
260504_at	Cyclin similar to GB:CAB77269 f	CYCA3;3	AT1G47220	1.06	0.09	0.49	0.638447	0.815464	-6.42	FALSE
265608_at	hypothetical protein predicted by	---	AT2G25380	1.04	0.06	0.49	0.6387864	0.8156013	-6.42	FALSE
249637_at	hypothetical protein	---	AT5G36900	1.05	0.08	0.49	0.6388969	0.8156611	-6.42	FALSE
254394_at	subtilisin-like serine protease cor	---	AT4G21630	1.04	0.06	0.49	0.6389762	0.8156611	-6.42	FALSE
252453_at	putative RNA-binding protein var	---	AT3G47120	1.05	0.07	0.49	0.6389179	0.8156611	-6.42	FALSE
256604_at	hypothetical protein predicted by	---	---	1.05	0.07	0.49	0.6389616	0.8156611	-6.42	FALSE
251998_at	putative protein KIAA0010 prote	UPL7	AT3G53090	-1.06	-0.08	-0.49	0.6390505	0.8157011	-6.42	FALSE
252653_at	putative kinesin-like protein simi	---	AT3G44730	-1.06	-0.09	-0.49	0.6390791	0.8157011	-6.42	FALSE
257290_at	hypothetical protein predicted by	---	AT3G15550	1.05	0.07	0.49	0.63922	0.8157142	-6.42	FALSE
263872_at	putative cellulose synthase catal	CESA9	AT2G21770	1.07	0.09	0.49	0.6392278	0.8157142	-6.42	FALSE
250145_at	putative protein predicted protei	---	AT5G14690	1.08	0.11	0.49	0.6392324	0.8157142	-6.42	FALSE
263915_at	hypothetical protein predicted by	---	AT2G36430	1.18	0.23	0.49	0.6391831	0.8157142	-6.42	FALSE
256327_at	unknown protein ;supported by fu	GAUT9	AT3G02350	-1.07	-0.10	-0.49	0.6393926	0.8157149	-6.42	TRUE
254547_at	putative protein	---	AT4G19860	-1.09	-0.12	-0.49	0.6393593	0.8157149	-6.42	FALSE
260449_at	unknown protein	---	AT1G72390	1.05	0.06	0.49	0.6394117	0.8157149	-6.42	FALSE
265265_at	unknown protein	---	AT2G42900	1.09	0.12	0.49	0.6392753	0.8157149	-6.42	FALSE
256085_at	hypothetical protein predicted by	---	AT1G20760	-1.05	-0.07	-0.49	0.6393471	0.8157149	-6.42	FALSE
265640_at	putative cysteine proteinase	---	AT2G27395	-1.05	-0.06	-0.49	0.6394489	0.8157167	-6.42	FALSE
265377_at	putative beta-1,3-glucanase	---	AT2G05790	1.32	0.40	0.49	0.6395201	0.8157618	-6.42	TRUE
254799_at	putative protein various predicted	---	AT4G13060	-1.06	-0.09	-0.49	0.6395668	0.8157758	-6.42	FALSE

260265_at	hypothetical protein similar to hy	LBD42	AT1G68510	-1.07	-0.09	-0.49	0.6398115	0.8160423	-6.42	FALSE
262608_at	dioxygenase-like protein very sir	---	AT1G14120	1.06	0.09	0.49	0.6398921	0.8160995	-6.42	FALSE
249439_at	thaumatin-like protein thaumatin	---	AT5G40020	1.12	0.16	0.49	0.6400052	0.8161958	-6.42	FALSE
254618_at	cellulose synthase - like protein	IRX1	AT4G18780	-1.10	-0.14	-0.49	0.6400473	0.8161958	-6.42	FALSE
259957_at	putative protein kinase C-termina	---	AT1G67890	-1.11	-0.15	-0.49	0.640103	0.8161958	-6.42	FALSE
261358_s_a	hypothetical protein predicted by	---	AT1G41920 /.	1.06	0.08	0.49	0.6401107	0.8161958	-6.42	FALSE
254757_at	putative protein other putative or	ROPGEF9	AT4G13240	1.06	0.08	0.49	0.6402688	0.8163061	-6.42	FALSE
249680_s_a	putative protein strong similarity t	---	AT3G61730 /.	1.04	0.06	0.49	0.6402654	0.8163061	-6.42	FALSE
256283_at	hypothetical protein	---	AT3G12540	1.05	0.07	0.49	0.6403594	0.8163759	-6.42	FALSE
247859_at	unknown protein	---	AT5G58410	1.04	0.06	0.49	0.6404201	0.8163805	-6.42	FALSE
257529_at	hypothetical protein predicted by	---	AT3G03290	1.05	0.08	0.49	0.6404346	0.8163805	-6.42	FALSE
264510_at	putative phytochrome-associated	PIF3	AT1G09530	-1.11	-0.15	-0.49	0.6405998	0.8165008	-6.42	FALSE
253055_at	putative protein cyclin delta-1, A	CYCD5;1	AT4G37630	1.08	0.11	0.49	0.6406006	0.8165008	-6.42	FALSE
247857_at	peroxidase	---	AT5G58400	1.06	0.09	0.49	0.6406685	0.8165418	-6.42	FALSE
266559_at	unknown protein	---	AT2G23920	1.06	0.08	0.49	0.6407336	0.8165791	-6.42	FALSE
251550_at	putative protein proline-rich prot	---	AT3G58800	-1.06	-0.08	-0.49	0.6407932	0.8166095	-6.42	FALSE
264385_at	unknown protein	---	AT1G12020	-1.09	-0.12	-0.49	0.6412107	0.8170176	-6.43	FALSE
263649_at	putative 1-aminocyclopropane-1-	---	AT1G04380	1.05	0.07	0.49	0.6411638	0.8170176	-6.43	FALSE
255425_s_a	putative protein	---	AT4G02950 /.	1.07	0.09	0.49	0.6412209	0.8170176	-6.43	FALSE
263433_at	putative myo-inositol 1-phosphat	MIPS2	AT2G22240	-1.09	-0.12	-0.49	0.6413993	0.8170237	-6.43	TRUE
249953_at	FAR1 - like protein far-red impai	FRS12	AT5G18960	-1.06	-0.09	-0.49	0.6414048	0.8170237	-6.43	FALSE
261943_at	plasma membrane ATPase, puta	AHA9	AT1G80660	1.06	0.08	0.49	0.6413213	0.8170237	-6.43	FALSE
253910_at	putative receptor like kinase rec	---	AT4G27290	1.05	0.07	0.49	0.6412888	0.8170237	-6.43	FALSE
260301_at	hypothetical protein ;supported b	---	AT1G80290	1.06	0.09	0.49	0.6413394	0.8170237	-6.43	FALSE
245698_at	phosphate/phosphoenolpyruvate	---	AT5G04160	1.10	0.14	0.49	0.6415817	0.8170637	-6.43	TRUE
245884_at	branched-chain alpha keto-acid	---	AT5G09300	-1.08	-0.12	-0.49	0.6415565	0.8170637	-6.43	FALSE
249240_at	putative protein similar to unknov	---	AT5G42220	-1.07	-0.10	-0.49	0.6415604	0.8170637	-6.43	FALSE
250271_at	putative protein predicted protei	CLE40	AT5G12990	-1.05	-0.07	-0.49	0.6416061	0.8170637	-6.43	FALSE
261246_at	unknown protein	SYTB	AT1G20080	1.06	0.08	0.49	0.6416153	0.8170637	-6.43	FALSE
259783_at	auxin-induced protein, putative s	SAUR68	AT1G29510	1.30	0.38	0.49	0.6417905	0.8172298	-6.43	TRUE
256517_at	PHD-finger protein, putative con	MMD1	AT1G66170	1.05	0.06	0.49	0.6418257	0.8172298	-6.43	FALSE
253069_at	hexokinase - like protein hexokir	HKL3	AT4G37840	1.05	0.08	0.49	0.6418532	0.8172298	-6.43	FALSE
255392_at	hypothetical protein	---	---	1.04	0.06	0.49	0.6418929	0.8172347	-6.43	FALSE
251280_at	putative protein beta-1,3-glucana	---	AT3G61810	1.05	0.08	0.49	0.6419555	0.8172688	-6.43	FALSE
249417_at	calcium-binding protein - like cbp	---	AT5G39670	1.38	0.46	0.49	0.6422064	0.817369	-6.43	FALSE

262165_at	putative acyl-CoA:1-acylglycerol-	LPAT4	AT1G75020	1.10	0.13	0.49	0.6421524	0.817369	-6.43	FALSE
250068_at	CHP-rich zinc finger protein-like	---	AT5G17960	1.07	0.10	0.49	0.6421508	0.817369	-6.43	FALSE
246534_at	putative protein several hypothet	---	AT5G15890	1.07	0.10	0.49	0.6421855	0.817369	-6.43	FALSE
248513_at	unknown protein	---	AT5G50500	1.05	0.07	0.49	0.6422134	0.817369	-6.43	FALSE
256849_at	hypothetical protein similar to hy	---	---	1.06	0.09	0.49	0.6422934	0.8174253	-6.43	FALSE
260858_at	hypothetical protein predicted by	---	AT1G43770	1.06	0.08	0.49	0.6423361	0.817434	-6.43	FALSE
266888_s_a	putative thiamin pyrophosphokin	TPK1	AT1G02880 ///	-1.05	-0.07	-0.49	0.6424769	0.8175219	-6.43	FALSE
261325_at	hypothetical protein predicted by	---	AT1G44780	-1.04	-0.06	-0.49	0.6424629	0.8175219	-6.43	FALSE
247949_at	cytochrome P450	CYP81F2	AT5G57220	1.29	0.37	0.49	0.642652	0.8175657	-6.43	TRUE
258584_at	hypothetical protein predicted by	SIP1A	AT3G04090	-1.04	-0.06	-0.49	0.6426547	0.8175657	-6.43	FALSE
254644_at	CLE2, putative CLAVATA3/ESR	CLE2	AT4G18510	-1.06	-0.09	-0.49	0.642613	0.8175657	-6.43	FALSE
249772_at	unknown protein	---	AT5G24130	1.10	0.14	0.49	0.6426367	0.8175657	-6.43	FALSE
257436_s_a	hypothetical protein predicted by	---	AT2G24650 ///	-1.07	-0.10	-0.49	0.642745	0.8176351	-6.43	FALSE
266522_at	putative ubiquitin-conjugating en	UBC23	AT2G16920	-1.06	-0.09	-0.49	0.6427933	0.8176508	-6.43	FALSE
261881_at	nodulin-like protein similar to noc	NIP6;1	AT1G80760	-1.10	-0.13	-0.49	0.6428879	0.8176801	-6.43	FALSE
255269_at	putative protein various predicte	---	AT4G05240	1.06	0.08	0.49	0.6428737	0.8176801	-6.43	FALSE
247462_at	A9 protein precursor - like A9 pr	---	AT5G62080	1.06	0.09	0.49	0.6430546	0.8178464	-6.43	FALSE
264755_at	receptor kinase, putative similar	---	AT1G61390	-1.06	-0.08	-0.48	0.6432118	0.8179551	-6.43	FALSE
248444_at	putative protein similar to unknov	---	---	1.05	0.07	0.48	0.643202	0.8179551	-6.43	FALSE
250204_at	leucine zipper protein-like	ATEXO70C	AT5G13990	1.06	0.09	0.48	0.6433363	0.8180678	-6.43	FALSE
262087_at	hypothetical protein predicted by	---	AT1G56030	1.05	0.08	0.48	0.6434853	0.8182116	-6.43	FALSE
245239_at	putative homeodomain-protein s	FWA	AT4G25530	-1.06	-0.08	-0.48	0.6435407	0.8182365	-6.43	FALSE
253690_at	putative protein various predicte	---	AT4G29550	1.08	0.11	0.48	0.6436515	0.8183318	-6.43	FALSE
254170_at	LG27/30-like gene LG27/30 gen	---	AT4G24430	-1.05	-0.07	-0.48	0.6437026	0.8183511	-6.43	FALSE
247552_at	phytochelatin synthetase - like p	COB	AT5G60920	-1.10	-0.14	-0.48	0.6438263	0.8183716	-6.43	TRUE
258970_at	putative serine carboxypeptidase	scpl49	AT3G10410	1.08	0.11	0.48	0.6438126	0.8183716	-6.43	FALSE
259464_at	hypothetical protein predicted by	---	AT1G18990	-1.05	-0.08	-0.48	0.6437792	0.8183716	-6.43	FALSE
245222_at	contains similarity to En/Spm tra	---	---	-1.05	-0.07	-0.48	0.643899	0.8184183	-6.43	FALSE
247003_at	putative protein similar to unknov	---	AT5G67550	1.07	0.10	0.48	0.6440502	0.8185193	-6.43	FALSE
251596_at	1-acylcerol-3-phosphate acyltran	LPAT2	AT3G57650	1.04	0.06	0.48	0.6440262	0.8185193	-6.43	FALSE
257732_at	unknown protein contains Pfam p	AtCASP	AT3G18480	-1.06	-0.08	-0.48	0.6442607	0.8187412	-6.43	FALSE
251582_at	putative protein CARBON CATA	---	AT3G58580	1.05	0.08	0.48	0.6443518	0.8188059	-6.43	FALSE
261907_at	4-coumarate:CoA ligase 3 identic	4CL3	AT1G65060	1.16	0.22	0.48	0.6443834	0.8188059	-6.43	FALSE
251346_at	putative protein hypothetical pro	---	AT3G60980	-1.06	-0.08	-0.48	0.6444884	0.8188937	-6.43	FALSE
250339_at	NADP dependent malic enzyme	ATNADP-M	AT5G11670	-1.08	-0.11	-0.48	0.6447881	0.8189096	-6.43	FALSE

255442_at	predicted NADH dehydrogenase	---	AT4G02580	-1.05	-0.07	-0.48	0.6447162	0.8189096	-6.43	FALSE
254400_at	kinesin-related protein katA ; sup	ATK1	AT4G21270	1.05	0.06	0.48	0.6447047	0.8189096	-6.43	FALSE
249789_at	putative protein similar to unknov	---	AT5G24340	-1.07	-0.09	-0.48	0.6445967	0.8189096	-6.43	FALSE
266337_at	putative ligand-gated ion channe	ATGLR3.5	AT2G32390	1.05	0.07	0.48	0.644643	0.8189096	-6.43	FALSE
251419_at	putative protein various predicte	---	AT3G60470	-1.05	-0.07	-0.48	0.6446352	0.8189096	-6.43	FALSE
265937_at	putative RING zinc finger protein	---	AT2G19610	1.06	0.09	0.48	0.6447374	0.8189096	-6.43	FALSE
250491_at	putative protein predicted protei	---	AT5G09780	-1.08	-0.11	-0.48	0.6447606	0.8189096	-6.43	FALSE
257096_at	hypothetical protein	---	AT3G30820	1.05	0.07	0.48	0.6449024	0.8189636	-6.43	FALSE
250086_at	NAM (no apical meristem)-like pr	anac086	AT5G17260	-1.06	-0.08	-0.48	0.6448755	0.8189636	-6.43	FALSE
255168_at	putative protein hypothetical pro	---	---	1.06	0.09	0.48	0.6451202	0.8191946	-6.43	FALSE
249158_at	electron transfer flavoprotein bet	ETFBETA	AT5G43430	1.05	0.07	0.48	0.6452372	0.8192519	-6.43	FALSE
256465_at	hypothetical protein predicted by	---	AT1G32570	1.08	0.11	0.48	0.6452183	0.8192519	-6.43	FALSE
261503_at	hypothetical protein predicted by	---	AT1G71691	-1.06	-0.09	-0.48	0.6454323	0.819454	-6.43	FALSE
264136_at	leucine-rich repeat transmembra	SRF5	AT1G78980	1.08	0.11	0.48	0.6455518	0.8194909	-6.43	FALSE
261172_at	hypothetical protein predicted by	---	AT1G04840	-1.06	-0.09	-0.48	0.6455582	0.8194909	-6.43	FALSE
246705_x_a	putative protein predicted resista	---	---	1.06	0.08	0.48	0.6455691	0.8194909	-6.43	FALSE
245526_at	putative protein	NRPD4	AT4G15950	-1.05	-0.06	-0.48	0.6457265	0.8196451	-6.43	FALSE
247877_at	putative protein contains similarit	XBAT32	AT5G57740	1.10	0.13	0.48	0.6458088	0.8197039	-6.43	FALSE
260400_at	putative peptide transporter simil	---	AT1G69860	-1.05	-0.06	-0.48	0.6460813	0.8200042	-6.43	FALSE
250402_at	putative protein unnamed ORF	---	AT5G10940	-1.05	-0.07	-0.48	0.6461398	0.8200327	-6.43	FALSE
265000_at	hypothetical protein predicted by	---	AT1G67410	-1.06	-0.08	-0.48	0.6464141	0.820107	-6.43	FALSE
256224_at	GTP-binding protein (SAR1B) ide	ATSAR1B	AT1G56330	1.08	0.11	0.48	0.6462721	0.820107	-6.43	FALSE
253177_s_a	O-methyltransferase - like protei	---	AT4G35150 /	1.09	0.12	0.48	0.6462925	0.820107	-6.43	FALSE
259780_at	exonuclease, putative similar to	---	AT1G29630	-1.05	-0.07	-0.48	0.6464003	0.820107	-6.43	FALSE
255984_at	inositol polyphosphate 5-phosph	IP5PI	AT1G34120	-1.06	-0.08	-0.48	0.6463657	0.820107	-6.43	FALSE
259518_at	hypothetical protein ; supported b	OPCL1	AT1G20510	1.16	0.22	0.48	0.6463834	0.820107	-6.43	FALSE
253982_at	calcineurin B-like protein 3 ;supp	ATCBL3	AT4G26570	1.09	0.12	0.48	0.6465212	0.8201351	-6.43	FALSE
264139_at	hypothetical protein contains sim	---	AT1G78940	-1.05	-0.08	-0.48	0.64658	0.8201351	-6.43	FALSE
257117_at	geranyl geranyl pyrophosphate s	---	AT3G20160	-1.05	-0.07	-0.48	0.6465443	0.8201351	-6.43	FALSE
245085_at	putative poly(A) binding protein	PAB4	AT2G23350	1.07	0.10	0.48	0.6464874	0.8201351	-6.43	FALSE
253352_at	pathogenesis-related protein 1 p	---	AT4G33710	1.07	0.09	0.48	0.6466557	0.8201856	-6.43	FALSE
246127_s_a	putative protein	---	---	-1.04	-0.06	-0.48	0.6467145	0.8202146	-6.43	FALSE
266481_at	unknown protein ; supported by	TCP10	AT2G31070	-1.08	-0.11	-0.48	0.6468567	0.8202217	-6.43	TRUE
259164_at	hypothetical protein contains bro	ATBET10	AT3G01770	-1.08	-0.11	-0.48	0.6469544	0.8202217	-6.43	FALSE
248148_at	putative protein similar to unknov	---	AT5G54930	1.09	0.12	0.48	0.6470079	0.8202217	-6.43	FALSE

251131_at	laccase - like protein laccase pre	LAC10	AT5G01190	-1.04	-0.06	-0.48	0.6469503	0.8202217	-6.43	FALSE
254864_at	putative reverse transcriptase oth	---	---	1.04	0.06	0.48	0.6467983	0.8202217	-6.43	FALSE
247894_at	putative protein similar to unknov	CPL4	AT5G58000 /	-1.10	-0.13	-0.48	0.6469776	0.8202217	-6.43	FALSE
253636_at	putative protein predicted protei	---	AT4G30500	1.26	0.33	0.48	0.6468825	0.8202217	-6.43	FALSE
256674_at	unknown protein ;supported by fu	---	AT3G52360	-1.09	-0.12	-0.48	0.6468226	0.8202217	-6.43	FALSE
263819_x_a	putative TNP2-like transposon pr	---	---	1.04	0.06	0.48	0.6471059	0.8203004	-6.43	FALSE
257027_at	DNA repair protein, putative sim	ATRAD54	AT3G19210	-1.05	-0.07	-0.48	0.6471437	0.8203027	-6.43	FALSE
253362_s_a	putative protein cyclopropane-fa	---	AT4G33110 /	-1.08	-0.11	-0.48	0.6472254	0.8203522	-6.43	FALSE
255032_at	putative protein anthocyanin rha	---	AT4G09500	1.07	0.10	0.48	0.6472936	0.8203522	-6.43	FALSE
257457_at	hypothetical protein predicted by	---	AT2G05430	1.05	0.07	0.48	0.6472559	0.8203522	-6.43	FALSE
256798_at	uracil-DNA glycosylase, putative	---	AT3G18630	-1.07	-0.10	-0.48	0.6473266	0.8203522	-6.43	FALSE
247975_at	putative protein similar to unknov	---	AT5G56800	1.05	0.07	0.48	0.6473958	0.8203944	-6.43	FALSE
253874_at	putative protein stem-specific pr	---	AT4G27450	-1.14	-0.19	-0.48	0.6476971	0.8207305	-6.43	FALSE
246028_at	AKIN beta1 ; supported by full-le	---	AT5G21170	1.09	0.12	0.48	0.647834	0.8208197	-6.43	FALSE
262449_at	hypothetical protein similar to hyp	---	AT1G11160	1.04	0.06	0.48	0.6478394	0.8208197	-6.43	FALSE
254520_at	potassium transporter-like protei	---	AT4G19960	1.08	0.11	0.48	0.6480849	0.820952	-6.43	TRUE
265926_at	RUB1-conjugating enzyme, puta	---	AT2G18600	-1.09	-0.12	-0.48	0.6481005	0.820952	-6.43	FALSE
249949_at	SAE1-S9-protein - like SAE1-S9	---	AT5G18880	-1.05	-0.08	-0.48	0.6480262	0.820952	-6.43	FALSE
250780_at	expansin At-EXP2 (gb|AAB3807	ATEXPA2	AT5G05290	-1.08	-0.11	-0.48	0.6480449	0.820952	-6.43	FALSE
245072_s_a	putative cytochrome P450	CYP81D7	AT2G23190 /	-1.06	-0.09	-0.48	0.6481238	0.820952	-6.43	FALSE
266189_at	unknown protein	---	AT2G39020	1.04	0.06	0.48	0.6484391	0.8213058	-6.43	FALSE
258194_at	unknown protein ; supported by	---	AT3G29170	-1.08	-0.11	-0.48	0.6486391	0.8214691	-6.43	FALSE
250628_at	hypothetical protein	---	AT5G07380	-1.07	-0.10	-0.48	0.6486401	0.8214691	-6.43	FALSE
252642_at	putative protein predicted protei	---	AT3G44580	-1.04	-0.06	-0.48	0.6487173	0.8215213	-6.43	FALSE
267358_at	proline transporter 1 ;supported	PROT1	AT2G39890	-1.07	-0.09	-0.48	0.6489589	0.821736	-6.43	FALSE
251449_at	Rab GDP dissociation inhibitor ;	ATGDI2	AT3G59920	-1.07	-0.10	-0.48	0.6489275	0.821736	-6.43	FALSE
253729_at	beta-1,3-glucanase-like protein I	---	AT4G29360	1.07	0.09	0.48	0.6490635	0.8218229	-6.43	FALSE
246998_at	putative protein similar to unknov	---	AT5G67370	1.11	0.15	0.48	0.6491136	0.8218407	-6.43	FALSE
263497_at	cold-regulated protein cor15a pre	COR15A	AT2G42540	-1.34	-0.43	-0.48	0.6492999	0.8220308	-6.43	TRUE
266238_at	phosphoprotein phosphatase, ty	TOPP1	AT2G29400	-1.09	-0.12	-0.48	0.6493826	0.8220744	-6.43	FALSE
250160_at	putative protein various predicte	ATHB30	AT5G15210	-1.14	-0.18	-0.48	0.6494063	0.8220744	-6.43	FALSE
257946_at	hypothetical protein predicted by	---	AT3G21710	-1.05	-0.07	-0.48	0.6494831	0.822126	-6.43	FALSE
258972_at	hypothetical protein predicted by	---	AT3G01920	1.09	0.12	0.48	0.6495892	0.8222146	-6.43	FALSE
259432_at	myb-related protein, putative sim	---	AT1G01520	1.07	0.10	0.48	0.649759	0.8223535	-6.43	FALSE
247010_at	60S ribosomal protein L26 ;supp	---	AT5G67510	-1.14	-0.18	-0.48	0.649771	0.8223535	-6.43	FALSE

253108_at	putative bZIP transcription factor	FD	AT4G35900	-1.11	-0.14	-0.47	0.6498614	0.8224222	-6.43	FALSE
253513_at	peroxidase - like protein peroxid	---	AT4G31760	-1.05	-0.07	-0.47	0.6499724	0.8224714	-6.43	FALSE
245598_at	hypothetical protein	---	AT4G14200	1.08	0.11	0.47	0.6499533	0.8224714	-6.43	FALSE
267607_s_a	epoxide hydrolase (ATsEH) iden	ATSEH	AT2G26740 /	-1.10	-0.14	-0.47	0.6502886	0.8225881	-6.43	TRUE
248838_at	carnitine/acylcarnitine translocas	BOU	AT5G46800	1.10	0.13	0.47	0.6502259	0.8225881	-6.43	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=M641	GAPC1	---	1.11	0.16	0.47	0.6502953	0.8225881	-6.43	FALSE
254568_x_a	hypothtetical protein	---	---	1.06	0.09	0.47	0.6501111	0.8225881	-6.43	FALSE
248288_at	unknown protein ; supported by	---	AT5G52840	-1.07	-0.10	-0.47	0.6502075	0.8225881	-6.43	FALSE
254322_at	hypothetical protein	---	AT4G22600	1.08	0.12	0.47	0.650317	0.8225881	-6.43	FALSE
261587_at	hypothetical protein predicted by	---	AT1G01660	1.05	0.07	0.47	0.6502678	0.8225881	-6.43	FALSE
255594_at	putative ABC transporter	ATABC1	AT4G01660	1.05	0.07	0.47	0.650492	0.8227309	-6.43	FALSE
259779_s_a	hypothetical protein predicted by	---	AT1G29620 /	-1.06	-0.08	-0.47	0.650502	0.8227309	-6.43	FALSE
261146_at	hypothetical protein predicted by	---	AT1G19620	1.07	0.10	0.47	0.6506158	0.8228291	-6.43	FALSE
258176_at	B regulatory subunit of PP2A, pu	---	AT3G21650	-1.11	-0.15	-0.47	0.6507053	0.8228967	-6.43	FALSE
252871_at	proliferating-cell nucleolar antige	---	AT4G40000	1.05	0.07	0.47	0.6509029	0.8230792	-6.43	FALSE
256977_at	hypothetical protein predicted by	---	---	1.06	0.08	0.47	0.6509218	0.8230792	-6.43	FALSE
250164_at	putative protein various predicte	---	AT5G15280	-1.07	-0.10	-0.47	0.6511597	0.8233344	-6.43	FALSE
258146_at	putative WD-repeat protein (WD	---	AT3G18060	-1.06	-0.09	-0.47	0.6513378	0.8234556	-6.43	FALSE
255203_at	hypothetical protein	---	---	1.07	0.10	0.47	0.6513972	0.8234556	-6.43	FALSE
248363_at	nodulin-like protein	---	AT5G52480	1.05	0.07	0.47	0.6513999	0.8234556	-6.43	FALSE
248805_at	putative protein similar to unknov	---	AT5G47480	1.05	0.07	0.47	0.6513622	0.8234556	-6.43	FALSE
257257_at	hypothetical protein contains Pfa	---	AT3G22020	1.04	0.06	0.47	0.6516407	0.8237143	-6.43	FALSE
265123_at	hypothetical protein similar to put	---	AT1G55440	1.05	0.07	0.47	0.651949	0.823721	-6.43	FALSE
249859_at	serine protein kinase-like protein	---	AT5G22840 /	-1.10	-0.14	-0.47	0.651848	0.823721	-6.43	FALSE
265061_at	hypothetical protein contains sim	---	AT1G61640	1.13	0.18	0.47	0.6517801	0.823721	-6.43	FALSE
252636_at	putative protein triacylglycerol lip	---	AT3G44510	1.06	0.08	0.47	0.6518702	0.823721	-6.43	FALSE
253735_at	putative protein SNF7 protein - S	SNF7.1	AT4G29160	-1.05	-0.08	-0.47	0.6517815	0.823721	-6.43	FALSE
255223_at	putative protein predicted protei	---	AT4G05370	1.04	0.06	0.47	0.6518821	0.823721	-6.43	FALSE
262735_at	hypothetical protein	---	AT1G28630	1.05	0.08	0.47	0.65181	0.823721	-6.43	FALSE
253145_at	hypothetical protein	---	AT4G35560	-1.11	-0.15	-0.47	0.6519236	0.823721	-6.43	FALSE
265731_at	putative RNA helicase A 3' end c	---	AT2G01130	1.04	0.06	0.47	0.651971	0.823721	-6.43	FALSE
249654_at	putative protein hypothetical prot	---	---	1.05	0.07	0.47	0.6520314	0.8237517	-6.43	FALSE
AFFX-r2-At	Arabidopsis thaliana /REF=U372	---	---	1.04	0.06	0.47	0.6520723	0.8237577	-6.43	FALSE
266958_at	putative trans-prenyltransferase	GPS1	AT2G34630	1.08	0.11	0.47	0.6521329	0.8237886	-6.43	FALSE
253460_at	hypothetical protein	---	AT4G32130	-1.07	-0.09	-0.47	0.652245	0.8238178	-6.43	FALSE

251404_at	putative protein	---	AT3G60310	-1.06	-0.08	-0.47	0.6523005	0.8238178	-6.43	FALSE
258258_at	transcriptional regulator (FUSCA	FUS3	AT3G26790	1.05	0.07	0.47	0.6522731	0.8238178	-6.43	FALSE
257559_at	hypothetical protein contains Pfa	---	AT3G22050	1.06	0.08	0.47	0.6522516	0.8238178	-6.43	FALSE
255796_at	similar to mammalian MHC III re	SUVH2	AT2G33290	-1.06	-0.08	-0.47	0.6523849	0.8238332	-6.43	FALSE
253568_at	putative protein receptor-like kin	---	AT4G31230	1.06	0.08	0.47	0.65235	0.8238332	-6.43	FALSE
255285_at	putative protein A. thaliana hypo	---	AT4G04630	-1.18	-0.24	-0.47	0.6524336	0.8238491	-6.43	FALSE
263588_s_a	unknown protein	---	AT2G25320 ///	1.05	0.08	0.47	0.6526376	0.8239499	-6.43	FALSE
261867_at	unknown protein ; supported by c	---	AT1G50575	-1.06	-0.09	-0.47	0.6526579	0.8239499	-6.43	FALSE
247273_at	unknown protein	CPuORF40	AT5G64340 ///	-1.09	-0.12	-0.47	0.6526161	0.8239499	-6.43	FALSE
252631_s_a	putative protein predicted protei	---	---	-1.04	-0.06	-0.47	0.6525758	0.8239499	-6.43	FALSE
247013_at	putative protein strong similarity t	BT4	AT5G67480	1.10	0.14	0.47	0.6527486	0.8240188	-6.43	FALSE
266041_s_a	hypothetical protein	---	---	-1.06	-0.08	-0.47	0.652841	0.8240343	-6.43	FALSE
263062_at	putative phosphatidylinositol/pho	---	AT2G18180	1.06	0.08	0.47	0.6528185	0.8240343	-6.43	FALSE
248893_at	unknown protein	---	AT5G46310	-1.06	-0.09	-0.47	0.6528693	0.8240343	-6.43	FALSE
245066_at	putative serine/threonine protein	TOPP4	AT2G39840	1.06	0.08	0.47	0.6529355	0.8240723	-6.43	FALSE
263355_at	putative RNA-binding protein ;su	---	AT2G22100	-1.07	-0.10	-0.47	0.6530456	0.8241657	-6.43	FALSE
249254_at	unknown protein	---	AT5G42110	1.06	0.08	0.47	0.6531599	0.8242186	-6.43	FALSE
255873_at	hypothetical protein predicted by	LBD13	AT2G30340	1.06	0.08	0.47	0.6531568	0.8242186	-6.43	FALSE
264413_s_a	hypothetical protein similar to hy	---	---	1.07	0.10	0.47	0.6532238	0.8242538	-6.43	FALSE
249474_s_a	germin-like protein (GLP2a) copy	GER2	AT5G39130 ///	-1.06	-0.09	-0.47	0.6533043	0.8243097	-6.43	FALSE
264075_at	envelope-like protein identical to	---	---	1.07	0.10	0.47	0.6533468	0.8243178	-6.43	FALSE
260132_s_a	hypothetical protein	---	AT1G66320 ///	1.04	0.06	0.47	0.6533855	0.824321	-6.43	FALSE
246750_at	putative protein predicted protei	AT5G27860	---	-1.09	-0.13	-0.47	0.6535161	0.8244402	-6.43	FALSE
250343_at	putative protein density regulate	---	AT5G11900	1.05	0.07	0.47	0.6535983	0.8244527	-6.43	FALSE
246259_at	amino acid permease, putative c	---	AT1G31830	1.06	0.09	0.47	0.65357	0.8244527	-6.43	FALSE
252980_at	putative protein Human multiple	---	AT4G38040	-1.04	-0.06	-0.47	0.6537007	0.8245363	-6.43	FALSE
252284_at	putative protein various predicte	---	AT3G49020	1.06	0.08	0.47	0.6537636	0.82457	-6.43	FALSE
254488_at	putative protein receptor-like pro	---	AT4G20790	-1.04	-0.06	-0.47	0.6539721	0.8247873	-6.44	FALSE
266504_at	hypothetical protein predicted by	---	AT2G47820	1.06	0.09	0.47	0.6541701	0.8249459	-6.44	FALSE
248842_at	unknown protein	---	AT5G46850	-1.07	-0.09	-0.47	0.654136	0.8249459	-6.44	FALSE
253196_at	NAD+ dependent isocitrate dehy	IDH1	AT4G35260	1.07	0.10	0.47	0.654209	0.8249492	-6.44	FALSE
261876_at	pirin-like protein similar to pirin G	---	AT1G50590	-1.15	-0.20	-0.47	0.6543027	0.8250218	-6.44	FALSE
257740_at	hypothetical protein predicted by	---	AT3G27330	1.04	0.06	0.47	0.6543715	0.8250629	-6.44	FALSE
256292_at	unknown protein	---	AT1G69430	1.06	0.09	0.47	0.6544781	0.8251135	-6.44	FALSE
250517_at	serine-type carboxypeptidase II-	scpl35	AT5G08260	-1.16	-0.21	-0.47	0.6544839	0.8251135	-6.44	FALSE

245742_at	aldehyde dehydrogenase, putati	ALDH3H1	AT1G44170	-1.09	-0.12	-0.47	0.6545735	0.8251808	-6.44	TRUE
263924_at	enolase (2-phospho-D-glycerate	LOS2	AT2G36530	1.13	0.17	0.47	0.6546799	0.8252693	-6.44	FALSE
256408_at	hypothetical protein	---	AT1G66610	1.06	0.09	0.47	0.6547255	0.8252812	-6.44	FALSE
260466_at	phosphatidylinositol-4-phosphate	---	AT1G10900	-1.12	-0.17	-0.47	0.6549521	0.8255212	-6.44	FALSE
247734_at	putative protein predicted protei	---	AT5G59400	-1.06	-0.08	-0.47	0.6552395	0.8256098	-6.44	FALSE
248108_at	molybdopterin synthase sulphury	CNX5	AT5G55130	-1.06	-0.08	-0.47	0.6552241	0.8256098	-6.44	FALSE
252835_at	putative protein several hypothet	---	AT3G42060	1.06	0.09	0.47	0.6551142	0.8256098	-6.44	FALSE
256162_at	hypothetical protein similar to hyp	---	AT1G55390	1.04	0.06	0.47	0.6551814	0.8256098	-6.44	FALSE
249735_at	putative protein contains similari	---	AT5G24450	1.07	0.10	0.47	0.6551798	0.8256098	-6.44	FALSE
249912_at	putative protein similar to unknov	RER1	AT5G22790	1.12	0.17	0.47	0.6550796	0.8256098	-6.44	FALSE
250942_at	putative protein	---	AT5G03350	1.58	0.66	0.47	0.6554313	0.8258058	-6.44	FALSE
259282_at	unknown protein similar to unkno	GPAT5	AT3G11430	1.07	0.10	0.47	0.6555657	0.8259295	-6.44	FALSE
245912_at	putative protein sulfate transport	SULTR3;5	AT5G19600	1.15	0.20	0.47	0.6556232	0.8259563	-6.44	FALSE
261658_at	hypothetical protein predicted by	---	AT1G50040	1.16	0.22	0.47	0.6558936	0.8260918	-6.44	TRUE
258540_at	hypothetical protein predicted by	---	AT3G06990	1.05	0.07	0.47	0.6559481	0.8260918	-6.44	FALSE
251048_at	putative protein potassium chan	---	AT5G02410	-1.06	-0.09	-0.47	0.6557852	0.8260918	-6.44	FALSE
246718_at	putative protein various predicte	---	---	1.06	0.08	0.47	0.6558327	0.8260918	-6.44	FALSE
259758_s_a	putative caffeic acid 3-O-methyltr	---	AT1G77520 ///	1.05	0.07	0.47	0.6559445	0.8260918	-6.44	FALSE
249688_at	putative protein tyrosine aminotra	---	AT5G36160	1.07	0.10	0.47	0.6558762	0.8260918	-6.44	FALSE
248355_at	putative protein strong similarity t	ATEXO70A	AT5G52340	1.05	0.07	0.47	0.656025	0.8260976	-6.44	FALSE
251554_at	putative protein predicted protei	---	AT3G58670	-1.06	-0.09	-0.47	0.6560053	0.8260976	-6.44	FALSE
249141_at	putative protein similar to unknov	---	AT5G43200	-1.05	-0.07	-0.47	0.6560953	0.8261404	-6.44	FALSE
249536_at	pollen coat -like protein pollen co	---	AT5G38760	1.04	0.06	0.47	0.6561539	0.8261687	-6.44	FALSE
259676_at	hypothetical protein similar to put	---	AT1G77730	1.05	0.07	0.47	0.6563516	0.8263719	-6.44	FALSE
251527_at	putative protein hypothetical pro	---	AT3G58650	1.05	0.07	0.47	0.6564812	0.8264737	-6.44	FALSE
258397_at	Expressed protein ; supported by	---	AT3G15357	-1.05	-0.07	-0.47	0.6565049	0.8264737	-6.44	FALSE
259608_at	unknown protein	ECT9	AT1G27960	-1.06	-0.08	-0.46	0.6567792	0.82675	-6.44	FALSE
261994_at	hypothetical protein contains sim	---	AT1G33640	-1.05	-0.07	-0.46	0.656815	0.82675	-6.44	FALSE
248872_at	Expressed protein ; supported by	MSP2	AT5G46795	1.06	0.08	0.46	0.6568331	0.82675	-6.44	FALSE
263500_s_a	hypothetical protein	---	AT2G07672	-1.06	-0.09	-0.46	0.6569345	0.826832	-6.44	FALSE
253142_at	putative protein methyl-directed	MLH3	AT4G35520	-1.05	-0.07	-0.46	0.6573513	0.8272652	-6.44	FALSE
259575_at	unknown protein	---	AT1G35320	1.05	0.07	0.46	0.6573158	0.8272652	-6.44	FALSE
247981_at	putative protein similar to unknov	MIOX5	AT5G56640	1.05	0.07	0.46	0.6573881	0.827266	-6.44	FALSE
266150_s_a	hypothetical protein	---	AT2G12290 ///	-1.17	-0.22	-0.46	0.6574831	0.8273299	-6.44	TRUE
249917_at	putative protein strong similarity t	---	AT5G22460	-1.30	-0.37	-0.46	0.6575114	0.8273299	-6.44	FALSE

265540_at	Mutator-like transposase similar	---	---	1.05	0.06	0.46	0.6575595	0.8273447	-6.44	FALSE
264250_at	gamma glutamyl hydrolase, puta	ATGGH2	AT1G78680	1.06	0.09	0.46	0.657625	0.8273814	-6.44	FALSE
245334_at	Expressed protein ; supported by	RALFL33	AT4G15800	-1.12	-0.16	-0.46	0.6577516	0.8274951	-6.44	TRUE
267424_at	hypothetical protein predicted by	---	AT2G34800	1.04	0.06	0.46	0.6578353	0.8275548	-6.44	FALSE
257389_at	hypothetical protein predicted by	---	AT2G17970	-1.05	-0.07	-0.46	0.6580724	0.8278074	-6.44	FALSE
255770_at	hypothetical protein predicted by	---	AT1G18560	1.05	0.07	0.46	0.6581988	0.8279208	-6.44	FALSE
253678_at	cytidine deaminase 7	---	AT4G29600	-1.05	-0.07	-0.46	0.6583724	0.8280934	-6.44	FALSE
249460_at	v-SNARE - like protein v-SNARE	---	AT5G39630	1.06	0.08	0.46	0.6584751	0.8281416	-6.44	FALSE
256537_at	unknown protein	---	AT1G33340	-1.15	-0.20	-0.46	0.6584833	0.8281416	-6.44	FALSE
263241_at	arginine decarboxylase identical	ADC1	AT2G16500	1.18	0.24	0.46	0.6588339	0.8285369	-6.44	FALSE
260103_at	unknown protein	---	AT1G35430	-1.05	-0.07	-0.46	0.6589574	0.8286465	-6.44	FALSE
245934_at	putative protein NAC1 - Medicag	anac082	AT5G09330	-1.07	-0.10	-0.46	0.659249	0.8288234	-6.44	FALSE
260722_at	protein phosphatase-2C, putativ	---	AT1G48040	1.09	0.13	0.46	0.6592235	0.8288234	-6.44	FALSE
257101_at	disease resistance protein, puta	AtRLP42	AT3G25020	-1.05	-0.08	-0.46	0.6591961	0.8288234	-6.44	FALSE
246739_at	putative protein predicted protei	---	AT5G27800	1.05	0.07	0.46	0.6593161	0.8288234	-6.44	FALSE
262817_at	putative reticuline oxidase strong	---	AT1G11770	1.06	0.08	0.46	0.659265	0.8288234	-6.44	FALSE
253931_at	putative CDP-diacylglycerol synt	---	AT4G26770	-1.06	-0.08	-0.46	0.6592932	0.8288234	-6.44	FALSE
265125_at	hypothetical protein similar to put	---	AT1G55410	1.04	0.06	0.46	0.6594856	0.8289907	-6.44	FALSE
248138_at	pyruvate decarboxylase (gb|AAB	PDC2	AT5G54960	-1.07	-0.10	-0.46	0.6595736	0.8290557	-6.44	TRUE
267514_at	putative glycerate dehydrogenas	---	AT2G45630	1.15	0.20	0.46	0.6596701	0.8291057	-6.44	FALSE
254719_at	putative protein beta 1,3-glucana	---	AT4G13600	1.06	0.08	0.46	0.6596861	0.8291057	-6.44	FALSE
249783_at	calcium sensor homolog (gb|AAC	SOS3	AT5G24270	1.12	0.16	0.46	0.6597433	0.8291319	-6.44	TRUE
248943_s_a	putative protein similar to unknov	---	AT5G45440 /	1.12	0.17	0.46	0.6597838	0.8291372	-6.44	TRUE
248194_at	Expressed protein ; supported by	---	AT5G54095	-1.04	-0.06	-0.46	0.659834	0.8291546	-6.44	FALSE
265163_at	putative OBP32pep protein	---	AT1G23580	-1.04	-0.06	-0.46	0.6598737	0.8291588	-6.44	FALSE
263954_at	unknown protein ; supported by	---	AT2G35840	-1.07	-0.09	-0.46	0.6601666	0.8294811	-6.44	FALSE
246385_at	mitotic cyclin a2-type, putative s	CYCA1;2	AT1G77390	1.14	0.18	0.46	0.6602369	0.8295237	-6.44	FALSE
253286_at	hypothetical protein	FUC95A	AT4G34260	1.23	0.30	0.46	0.6603604	0.8296333	-6.44	TRUE
245706_at	putative protein	---	AT5G04310	1.05	0.08	0.46	0.6604535	0.8297044	-6.44	FALSE
250150_at	putative protein ;supported by ful	---	AT5G14710	1.08	0.11	0.46	0.6604984	0.8297152	-6.44	FALSE
266892_at	putative glycine dehydrogenase	AtGLDP2	AT2G26080	-1.07	-0.10	-0.46	0.6606346	0.829751	-6.44	TRUE
247275_at	beta-ureidopropionase	BETA-UP	AT5G64370	1.09	0.13	0.46	0.6606637	0.829751	-6.44	FALSE
253176_at	putative protein Human (H326) r	---	AT4G35140	-1.08	-0.12	-0.46	0.6606724	0.829751	-6.44	FALSE
248297_at	protochlorophyllide reductase; ox	---	AT5G53100	1.04	0.06	0.46	0.6605929	0.829751	-6.44	FALSE
267297_at	putative RING zinc finger protein	---	AT2G23780	1.06	0.08	0.46	0.6607241	0.8297702	-6.44	FALSE

250366_at	putative protein predicted protei	---	AT5G11420	-1.39	-0.47	-0.46	0.6608935	0.8298459	-6.44	FALSE
251412_at	RING-H2 zinc finger protein ATL	ATL4	AT3G60220	1.13	0.17	0.46	0.6608839	0.8298459	-6.44	FALSE
249909_s_a	alpha-adaptin	---	AT5G22770 /	1.06	0.09	0.46	0.6608507	0.8298459	-6.44	FALSE
264362_at	unknown protein ESTs gb|H369	---	AT1G03290	1.08	0.11	0.46	0.6609343	0.8298514	-6.44	FALSE
253700_at	threonine synthase	MTO2	AT4G29840	1.08	0.11	0.46	0.6610302	0.8299262	-6.44	FALSE
259777_at	zinc finger protein, putative simil	---	AT1G29570	1.05	0.07	0.46	0.6610723	0.8299334	-6.44	FALSE
245957_at	putative protein predicted protein	---	AT5G19590	-1.04	-0.06	-0.46	0.6612826	0.8300982	-6.44	FALSE
246546_at	voltage-dependent anion-selectiv	VDAC3	AT5G15090	-1.08	-0.11	-0.46	0.6612741	0.8300982	-6.44	FALSE
261997_at	hypothetical protein similar C-ter	---	---	1.05	0.06	0.46	0.6613502	0.8300982	-6.44	FALSE
246093_at	ethylene-forming-enzyme-like di	---	AT5G20550	-1.05	-0.08	-0.46	0.6613137	0.8300982	-6.44	FALSE
257136_at	hypothetical protein predicted by	ASML2	AT3G12890	1.06	0.08	0.46	0.6613856	0.8300982	-6.44	FALSE
252267_at	putative protein NITROGEN RE	---	AT3G49640	-1.08	-0.11	-0.46	0.66149	0.8301836	-6.44	FALSE
266647_at	hypothetical protein predicted by	---	AT2G25870	-1.07	-0.10	-0.46	0.661628	0.8302638	-6.44	FALSE
260196_at	hypothetical protein similar to hy	---	AT1G67570	-1.04	-0.06	-0.46	0.6616556	0.8302638	-6.44	FALSE
265793_at	unknown protein	---	AT2G01220	1.07	0.10	0.46	0.6616631	0.8302638	-6.44	FALSE
248344_at	hyaluronan mediated motility rec	---	AT5G52280	-1.10	-0.14	-0.46	0.6618689	0.8302869	-6.44	TRUE
250800_at	ubiquinol-cytochrome C reductas	HPR	AT1G68010 /	1.12	0.17	0.46	0.6620455	0.8302869	-6.44	FALSE
247711_at	receptor-like protein kinase rece	---	AT5G59270	1.05	0.08	0.46	0.6618574	0.8302869	-6.44	FALSE
252735_at	putative protein predicted protei	---	AT3G43170	-1.05	-0.07	-0.46	0.6619891	0.8302869	-6.44	FALSE
262849_at	unknown protein ; supported by c	---	AT1G14710	-1.14	-0.19	-0.46	0.6620363	0.8302869	-6.44	FALSE
260512_at	unknown protein	---	AT1G51520	-1.07	-0.10	-0.46	0.6619602	0.8302869	-6.44	FALSE
251081_at	putative protein kinase wall-assc	---	AT5G02070	1.07	0.10	0.46	0.6617988	0.8302869	-6.44	FALSE
265514_s_a	Mutator-like transposase similar	---	---	-1.05	-0.07	-0.46	0.6618	0.8302869	-6.44	FALSE
256109_at	hypothetical protein predicted by	---	AT1G16950	1.10	0.13	0.46	0.6618507	0.8302869	-6.44	FALSE
261316_at	MAP kinase BnMAP4K alpha1,	ATMAP4K /	AT1G53165	-1.05	-0.07	-0.46	0.6620237	0.8302869	-6.44	FALSE
255243_at	putative protein hypothetical pro	---	AT4G05590	-1.05	-0.07	-0.46	0.6622888	0.8303153	-6.44	TRUE
256117_at	unknown protein ; supported by c	---	AT1G16840	-1.05	-0.06	-0.46	0.6623263	0.8303153	-6.44	FALSE
246590_at	cyclic nucleotide and calmodulin	CNGC18	AT5G14870	-1.04	-0.06	-0.46	0.6623255	0.8303153	-6.44	FALSE
261152_at	hypothetical protein predicted by	---	AT1G04930	-1.08	-0.11	-0.46	0.6623594	0.8303153	-6.44	FALSE
246963_at	putative protein nucleoid DNA-b	---	AT5G24820	-1.06	-0.09	-0.46	0.6623123	0.8303153	-6.44	FALSE
259624_at	hypothetical protein similar to un	---	AT1G43020	1.06	0.09	0.46	0.6621826	0.8303153	-6.44	FALSE
254906_at	putative disease resistance resp	---	AT4G11180	1.05	0.07	0.46	0.6622165	0.8303153	-6.44	FALSE
246256_at	glucosyltransferase-like protein	---	AT4G36770	1.09	0.12	0.46	0.6623233	0.8303153	-6.44	FALSE
266914_at	putative beta-amylase	BAM7	AT2G45880	-1.10	-0.14	-0.46	0.6624452	0.8303773	-6.44	FALSE
256557_at	hypothetical protein similar to hy	---	---	1.05	0.07	0.46	0.6625094	0.8304121	-6.44	FALSE

250847_at	putative protein predicted protei	---	AT5G04480	1.11	0.15	0.46	0.662645	0.8304141	-6.44	TRUE
262690_at	PPR-repeat protein contains mul	---	AT1G62720	-1.05	-0.07	-0.46	0.6626566	0.8304141	-6.44	FALSE
246409_at	CRK1 protein, putative similar to	---	AT1G57700	-1.08	-0.10	-0.46	0.6626234	0.8304141	-6.44	FALSE
250474_at	annexin -like protein annexin (A	ANNAT7	AT5G10230	1.04	0.06	0.46	0.6625772	0.8304141	-6.44	FALSE
266963_at	unknown protein	MTP11	AT2G39450	-1.06	-0.08	-0.46	0.6628493	0.8305284	-6.44	TRUE
261052_at	hypothetical protein similar to hy	---	AT1G01440	-1.07	-0.09	-0.46	0.6628124	0.8305284	-6.44	FALSE
259276_at	putative peroxidase very similar	---	AT3G01190	-1.05	-0.06	-0.46	0.6628571	0.8305284	-6.44	FALSE
259080_at	putative mitogen activated protei	WNK1	AT3G04910	1.06	0.09	0.46	0.662944	0.8305461	-6.44	FALSE
261849_at	pectin methylesterase, putative	---	AT1G11370	1.06	0.08	0.46	0.6629339	0.8305461	-6.44	FALSE
255633_at	Expressed protein ; supported by	---	AT4G00585	-1.05	-0.08	-0.46	0.6629979	0.830551	-6.44	FALSE
247088_at	unknown protein	---	AT5G66340	-1.05	-0.08	-0.46	0.6630207	0.830551	-6.44	FALSE
254526_at	putative protein cyclin C homolo	CYCT1;4	AT4G19600	-1.05	-0.07	-0.46	0.6631389	0.8305874	-6.44	FALSE
250726_at	putative protein similar to unknov	---	AT5G06410	-1.07	-0.09	-0.46	0.6631254	0.8305874	-6.44	FALSE
256586_at	hypothetical protein	---	AT3G28770	1.04	0.06	0.46	0.6631591	0.8305874	-6.44	FALSE
258172_at	unknown protein similar to HYP1	---	AT3G21620	-1.05	-0.06	-0.46	0.663207	0.8306018	-6.44	FALSE
253342_at	Expressed protein ; supported by	PAA1	AT4G33520	-1.13	-0.17	-0.46	0.6633296	0.8306642	-6.44	FALSE
258522_at	hypothetical protein predicted by	---	AT3G06660	-1.08	-0.11	-0.46	0.6633143	0.8306642	-6.44	FALSE
247906_at	putative protein similar to unknov	IAA33	AT5G57420	-1.07	-0.10	-0.46	0.6634095	0.8306731	-6.44	FALSE
264312_at	putative protein kinase similar to	---	AT1G70450	1.05	0.07	0.46	0.6633752	0.8306731	-6.44	FALSE
256300_at	unknown protein similar to N-terr	NAP	AT1G69490	1.21	0.27	0.45	0.6635431	0.8307554	-6.44	TRUE
246806_at	putative cdc20 protein	---	AT5G27080	-1.05	-0.07	-0.45	0.6635481	0.8307554	-6.44	FALSE
262318_at	putative hypersensitivity-related	---	AT1G27620	-1.05	-0.08	-0.45	0.6636485	0.8308354	-6.44	FALSE
263619_at	putative GDP-mannose pyropho	---	AT2G04650	1.05	0.07	0.45	0.6637044	0.8308599	-6.44	FALSE
248432_at	putative protein similar to unknov	---	AT5G51390	1.13	0.17	0.45	0.6637877	0.8308646	-6.44	FALSE
266244_at	unknown protein	---	AT2G27740	-1.15	-0.20	-0.45	0.663776	0.8308646	-6.44	FALSE
260811_s_a	hypothetical protein predicted by	---	---	-1.04	-0.06	-0.45	0.6638174	0.8308646	-6.44	FALSE
258116_at	hypothetical protein similar to ter	---	AT3G14520	1.06	0.09	0.45	0.6638748	0.8308908	-6.44	FALSE
266777_at	putative AAA-type ATPase	ftsh3	AT2G29080	1.05	0.07	0.45	0.6639358	0.8309215	-6.44	FALSE
247884_at	lipid transfer protein; glossy1 hor	CER3	AT5G57800	1.15	0.20	0.45	0.6639878	0.830941	-6.44	TRUE
259405_at	Expressed protein ; supported by	---	AT1G17744	1.08	0.11	0.45	0.664192	0.8311305	-6.44	FALSE
258942_at	unknown protein predicted by ge	---	AT3G09960	1.05	0.08	0.45	0.6642121	0.8311305	-6.44	FALSE
250127_at	putative protein similar to unknov	---	AT5G16380	-1.07	-0.09	-0.45	0.6642567	0.8311407	-6.44	FALSE
249229_at	putative protein similar to unknov	---	AT5G42090	-1.05	-0.08	-0.45	0.6644507	0.8313378	-6.44	FALSE
265932_at	hypothetical protein predicted by	LBD8	AT2G19510	1.04	0.06	0.45	0.6644994	0.8313531	-6.44	FALSE
257796_at	hypothetical protein predicted by	---	AT3G15930	-1.06	-0.08	-0.45	0.6646202	0.8314132	-6.44	FALSE

249714_at	unknown protein	---	---	1.07	0.10	0.45	0.6645991	0.8314132	-6.44	FALSE
244924_at	hypothetical protein	---	---	-1.06	-0.08	-0.45	0.6647218	0.8314491	-6.44	FALSE
256381_at	lipid transfer protein, putative co	---	AT1G66850	-1.06	-0.08	-0.45	0.6646915	0.8314491	-6.44	FALSE
256660_at	hypothetical protein similar to hyp	---	AT3G12060	1.06	0.08	0.45	0.6648088	0.8315122	-6.44	FALSE
260495_at	unknown protein similar to T11A(	---	AT2G41810	1.07	0.10	0.45	0.6649394	0.83163	-6.44	FALSE
251949_at	receptor protein kinase -like prot	---	AT3G53590	1.07	0.09	0.45	0.6651767	0.8318812	-6.44	FALSE
250062_at	BCS1 - like protein h-bcs1, Hom	---	AT5G17760	-1.09	-0.13	-0.45	0.6652656	0.831883	-6.44	TRUE
260472_at	hypothetical protein predicted by	---	AT1G10990	1.35	0.43	0.45	0.6652876	0.831883	-6.44	FALSE
253328_at	putative protein ABC-type transp	ATNAP13	AT4G33460	1.05	0.07	0.45	0.6652838	0.831883	-6.44	FALSE
254451_at	adrenodoxin - like protein adren	---	AT4G21090	-1.04	-0.06	-0.45	0.665348	0.831913	-6.44	FALSE
258425_at	unknown protein	---	AT3G16760	1.04	0.06	0.45	0.6655983	0.8321802	-6.44	FALSE
255952_at	MADS-box protein (ZAP1), puta	AGL104	AT1G22130	-1.04	-0.06	-0.45	0.6657568	0.8323329	-6.44	FALSE
249773_at	squalene monooxygenase 2 (squ	SQP2	AT5G24140	1.05	0.07	0.45	0.6658365	0.8323868	-6.44	FALSE
250054_at	potassium-dependent sodium-ca	CAX7	AT5G17860	1.15	0.20	0.45	0.6661955	0.8324707	-6.44	TRUE
248032_at	myosin heavy chain-like	---	AT5G55860	-1.07	-0.09	-0.45	0.6661206	0.8324707	-6.44	FALSE
266257_at	putative chorismate mutase/prep	PD1	AT2G27820	1.07	0.10	0.45	0.6661818	0.8324707	-6.44	FALSE
261895_at	metal ion transporter identical to	NRAMP1	AT1G80830	-1.13	-0.18	-0.45	0.666126	0.8324707	-6.44	FALSE
245187_s_a	F12A21.17 similar to signal recog	---	AT1G67650 /	-1.05	-0.07	-0.45	0.6661105	0.8324707	-6.44	FALSE
265321_at	putative Tub family protein	AtTLP2	AT2G18280	1.04	0.06	0.45	0.666062	0.8324707	-6.44	FALSE
258686_at	putative polygalacturonase simil	---	AT3G07840	-1.04	-0.06	-0.45	0.6660092	0.8324707	-6.44	FALSE
256995_at	protein kinase, putative contains	---	AT3G25840	-1.06	-0.08	-0.45	0.6659535	0.8324707	-6.44	FALSE
266460_at	unknown protein ; supported by c	AGP26	AT2G47930	1.41	0.50	0.45	0.6662725	0.8324757	-6.44	FALSE
265341_at	hypothetical protein predicted by	---	AT2G18360	1.07	0.10	0.45	0.6662696	0.8324757	-6.44	FALSE
254149_at	putative protein hypothetical pro	---	AT4G24300	1.07	0.10	0.45	0.6664469	0.8325568	-6.44	FALSE
249557_at	receptor serine/threonine kinase	PR5K	AT5G38280	1.10	0.13	0.45	0.6664194	0.8325568	-6.44	FALSE
251294_at	zinc transporter-like protein zinc	MTPA1	AT3G61940	-1.05	-0.07	-0.45	0.6664394	0.8325568	-6.44	FALSE
261753_at	unknown protein	---	AT1G76340	-1.06	-0.08	-0.45	0.6665054	0.8325843	-6.44	FALSE
263544_at	putative ADP-glucose pyrophosp	APL4	AT2G21590	1.06	0.09	0.45	0.6665503	0.8325947	-6.44	FALSE
263243_at	putative glyoxalase II	GLX2-5	AT2G31350	1.06	0.08	0.45	0.6666755	0.83266	-6.44	FALSE
259815_at	hypothetical protein predicted by	---	AT1G49870	1.05	0.07	0.45	0.6666548	0.83266	-6.44	FALSE
255422_at	putative D-type cyclin	CYCD6;1	AT4G03270	-1.05	-0.07	-0.45	0.6667714	0.8327341	-6.44	FALSE
255299_at	putative adenosine deaminase si	---	AT4G04880	-1.06	-0.08	-0.45	0.6668884	0.8328347	-6.44	FALSE
264537_at	receptor kinase, putative similar	BRL1	AT1G55610	1.08	0.11	0.45	0.6669545	0.8328716	-6.44	FALSE
249043_at	berberine bridge enzyme	---	AT5G44360	-1.04	-0.06	-0.45	0.6670856	0.832944	-6.44	FALSE
259651_at	unknown protein	---	AT1G55280	-1.12	-0.17	-0.45	0.6670501	0.832944	-6.44	FALSE

262664_at	hypothetical protein predicted by	---	AT1G13970	-1.05	-0.07	-0.45	0.6671239	0.8329463	-6.44	FALSE
248472_at	cyclin-dependent protein kinase-	---	AT5G50860	-1.06	-0.08	-0.45	0.6671646	0.8329515	-6.44	FALSE
249574_at	putative protein embryonic abun	PDLP7	AT5G37660	-1.05	-0.08	-0.45	0.6672113	0.8329642	-6.44	FALSE
266062_at	putative diacylglycerol kinase	---	AT2G18730	-1.04	-0.06	-0.45	0.6672565	0.832975	-6.44	FALSE
265817_at	histone H1 ;supported by full-ler	HIS1-3	AT2G18050	-1.15	-0.20	-0.45	0.6673697	0.8330708	-6.44	TRUE
253800_at	putative protein probable cell wa	---	AT4G28160	1.06	0.09	0.45	0.6674378	0.8331103	-6.44	FALSE
247627_at	cysteine proteinase AALP identic	AALP	AT5G60360	1.05	0.06	0.45	0.6675335	0.8331385	-6.44	FALSE
250055_at	NADH-cytochrome b5 reductase	ATCBR	AT5G17770	1.13	0.18	0.45	0.6675069	0.8331385	-6.44	FALSE
263055_at	unknown protein	---	---	-1.05	-0.06	-0.45	0.6676896	0.8332762	-6.45	FALSE
252605_s_a	sulfotransferase-like protein FLA	---	AT3G45070 ///	-1.04	-0.06	-0.45	0.6677169	0.8332762	-6.45	FALSE
264726_at	Expressed protein ; supported by	---	AT1G22985	1.07	0.10	0.45	0.667831	0.8332972	-6.45	FALSE
266492_at	putative protein kinase contains a	---	AT2G07020	1.06	0.08	0.45	0.6677751	0.8332972	-6.45	FALSE
263884_at	hypothetical protein predicted by	---	AT2G36920	-1.04	-0.06	-0.45	0.6678799	0.8332972	-6.45	FALSE
260906_at	hypothetical protein predicted by	---	AT1G02540	-1.05	-0.07	-0.45	0.667874	0.8332972	-6.45	FALSE
246211_at	G-box-binding factor 1 ; supporte	GBF1	AT4G36730	1.10	0.14	0.45	0.6679964	0.8333295	-6.45	FALSE
248916_at	receptor protein kinase-like prote	---	AT5G45840	-1.13	-0.18	-0.45	0.6680638	0.8333295	-6.45	FALSE
247087_at	putative protein contains similarit	---	AT5G66330	-1.10	-0.13	-0.45	0.6680884	0.8333295	-6.45	FALSE
265790_at	putative amino acid or GABA per	BAT1	AT2G01170	1.07	0.10	0.45	0.6680165	0.8333295	-6.45	FALSE
266145_at	putative TNP2-like transposon pr	---	---	-1.04	-0.06	-0.45	0.668088	0.8333295	-6.45	FALSE
246180_at	putative protein predicted protei	---	AT5G20840	1.05	0.07	0.45	0.6681911	0.833412	-6.45	FALSE
261689_at	hypothetical protein contains sim	---	AT1G50140	-1.07	-0.10	-0.45	0.6682853	0.8334839	-6.45	FALSE
255033_at	putative protein phosphonopyruv	---	AT4G09520	-1.06	-0.09	-0.45	0.6685823	0.8337631	-6.45	FALSE
261380_at	hypothetical protein predicted by	---	AT1G05400	1.07	0.10	0.45	0.6685636	0.8337631	-6.45	FALSE
249356_at	putative protein predicted protei	---	AT5G40520	-1.09	-0.12	-0.45	0.6686566	0.8337716	-6.45	FALSE
263430_at	unknown protein ;supported by f	---	AT2G22270	-1.06	-0.09	-0.45	0.6686622	0.8337716	-6.45	FALSE
264433_at	beta-glucosidase, putative simila	BGLU45	AT1G61810	1.27	0.35	0.45	0.6687483	0.8338156	-6.45	TRUE
266600_at	putative mitogen-activated protei	MPK12	AT2G46070	-1.09	-0.12	-0.45	0.6687706	0.8338156	-6.45	FALSE
260136_at	hypothetical protein predicted by	---	AT1G66360	-1.05	-0.07	-0.45	0.6689846	0.8340369	-6.45	FALSE
245062_at	hypothetical protein predicted by	BPM3	AT2G39760	1.04	0.06	0.45	0.6690457	0.8340675	-6.45	FALSE
254332_at	leucine rich repeat receptor kina	---	AT4G22730	1.08	0.11	0.45	0.6691866	0.834151	-6.45	TRUE
260320_at	hypothetical protein similar to put	---	AT1G63930	1.07	0.10	0.45	0.6692208	0.834151	-6.45	FALSE
245959_at	peptide transport protein-like pe	---	AT5G19640	1.05	0.07	0.45	0.6692224	0.834151	-6.45	FALSE
264797_at	unknown protein similar to ESTs	---	AT1G08710	-1.06	-0.08	-0.45	0.6695081	0.8341942	-6.45	FALSE
249702_at	axi 1 (auxin-independent growth	---	AT5G35570	1.14	0.18	0.45	0.6695497	0.8341942	-6.45	FALSE
260367_at	unknown protein ;supported by f	---	AT1G69760	-1.15	-0.21	-0.45	0.6695259	0.8341942	-6.45	FALSE

266618_at	unknown protein	---	AT2G35480	1.13	0.17	0.45	0.6694377	0.8341942	-6.45	FALSE
248949_at	putative protein strong similarity t	---	AT5G45570	-1.04	-0.06	-0.45	0.6693797	0.8341942	-6.45	FALSE
249313_at	unknown protein	---	AT5G41560	1.05	0.06	0.45	0.6694725	0.8341942	-6.45	FALSE
255348_at	hypothetical protein	---	AT4G03820	-1.05	-0.08	-0.45	0.6694832	0.8341942	-6.45	FALSE
245469_at	reverse transcriptase like protein	---	---	1.04	0.06	0.45	0.6694387	0.8341942	-6.45	FALSE
254044_at	putative xyloglucan endo-1,4-be	XTR9	AT4G25820	1.05	0.07	0.45	0.6697379	0.8343832	-6.45	FALSE
265574_at	putative replication protein A1	---	---	-1.05	-0.07	-0.45	0.669843	0.8344685	-6.45	FALSE
267571_at	3-hydroxyisobutyryl-coenzyme A	---	AT2G30650	1.05	0.06	0.45	0.6698921	0.8344841	-6.45	FALSE
246822_at	putative protein predicted protei	---	AT5G26960	-1.06	-0.08	-0.45	0.6699638	0.8344894	-6.45	FALSE
246248_at	hypothetical protein	---	AT4G36560	-1.04	-0.06	-0.45	0.6699695	0.8344894	-6.45	FALSE
256839_at	calmodulin, putative similar to ca	---	AT3G22930	-1.06	-0.08	-0.45	0.6701064	0.8346143	-6.45	FALSE
244989_s_a	hypothetical protein	---	---	1.07	0.10	0.45	0.6701885	0.8346711	-6.45	FALSE
245191_at	F12A21.10 similar to terminal ea	TEL2	AT1G67770	1.08	0.11	0.45	0.6702684	0.8347249	-6.45	FALSE
248294_at	RNA-binding protein-like	---	AT5G53060	1.06	0.08	0.44	0.6704102	0.8348367	-6.45	FALSE
261205_at	hypothetical protein predicted by	---	AT1G12790	-1.09	-0.12	-0.44	0.6704313	0.8348367	-6.45	FALSE
247719_at	Expressed protein ; supported by	---	AT5G59305	1.05	0.08	0.44	0.6704817	0.8348538	-6.45	FALSE
257045_at	dynamin-like protein similar to ph	ARC5	AT3G19720	-1.09	-0.12	-0.44	0.6705677	0.8348698	-6.45	TRUE
244922_s_a	hypothetical protein	---	AT2G07674	-1.06	-0.09	-0.44	0.6705611	0.8348698	-6.45	FALSE
250453_at	putative protein predicted protei	---	AT5G10620	1.07	0.09	0.44	0.6706954	0.8349377	-6.45	FALSE
251613_at	hypothetical protein	---	AT3G57960	1.06	0.09	0.44	0.670689	0.8349377	-6.45	FALSE
265241_at	hypothetical protein	---	---	1.06	0.08	0.44	0.67083	0.8350596	-6.45	FALSE
245941_at	putative protein karyopherin beta	emb2734	AT5G19820	1.06	0.08	0.44	0.6711789	0.8352171	-6.45	FALSE
260138_at	calmodulin-4 identical to GB:Q0	CAM4	AT1G66410	-1.06	-0.09	-0.44	0.6712495	0.8352171	-6.45	FALSE
261004_at	hypothetical protein similar to pu	---	AT1G26450	1.08	0.12	0.44	0.6710992	0.8352171	-6.45	FALSE
264445_at	unknown protein similar to ESTs	---	AT1G27290	1.09	0.13	0.44	0.6712342	0.8352171	-6.45	FALSE
254856_at	putative ribosomal protein (fragn	---	AT4G12160	-1.05	-0.07	-0.44	0.6710292	0.8352171	-6.45	FALSE
257575_at	hypothetical protein similar to hy	---	---	1.05	0.07	0.44	0.6710803	0.8352171	-6.45	FALSE
264889_at	unknown protein	---	AT1G23050	-1.06	-0.08	-0.44	0.6712446	0.8352171	-6.45	FALSE
247091_at	peroxidase (emb CAA66964.1)	---	AT5G66390	1.06	0.08	0.44	0.6711819	0.8352171	-6.45	FALSE
259246_s_a	hypothetical protein predicted by	---	AT3G07730 //	-1.07	-0.09	-0.44	0.6713532	0.8353007	-6.45	FALSE
246477_at	putative transcription factor (MYB	AtMYB9	AT5G16770	1.09	0.13	0.44	0.6715376	0.8354845	-6.45	FALSE
248727_at	cytochrome P450	CYP705A5	AT5G47990	1.04	0.06	0.44	0.6716932	0.8356326	-6.45	FALSE
266786_at	putative non-LTR retroelement re	---	---	-1.05	-0.06	-0.44	0.6718193	0.8357437	-6.45	FALSE
265988_at	hypothetical protein predicted by	---	AT2G24255	1.05	0.07	0.44	0.6718595	0.8357483	-6.45	FALSE
255794_at	putative NAM (no apical meriste	ANAC041	AT2G33480	-1.12	-0.17	-0.44	0.6719457	0.8358099	-6.45	TRUE

260625_at	storage protein, putative similar	MOM	AT1G08060	-1.04	-0.06	-0.44	0.6720609	0.8359076	-6.45	FALSE
255933_at	membrane protein, putative simi	ATRBL6	AT1G12750	-1.08	-0.12	-0.44	0.6721412	0.8359619	-6.45	FALSE
253583_at	translation initiation factor-like pr	---	AT4G30680	1.07	0.09	0.44	0.6723225	0.836005	-6.45	FALSE
258255_at	hypothetical protein predicted by	---	AT3G26800	-1.05	-0.06	-0.44	0.6722186	0.836005	-6.45	FALSE
249534_at	bZIP transcription factor - like pr	AtbZIP43	AT5G38800	1.04	0.06	0.44	0.6723071	0.836005	-6.45	FALSE
248840_at	unknown protein ; supported by	---	AT5G46770	1.06	0.09	0.44	0.6723022	0.836005	-6.45	FALSE
254301_at	predicted protein predicted prote	---	AT4G22790	-1.08	-0.11	-0.44	0.6723808	0.8360319	-6.45	FALSE
264780_at	putative protein kinase similar to	EDR1	AT1G08720	1.06	0.09	0.44	0.6724431	0.8360639	-6.45	FALSE
247126_at	protein phosphatase 2C-like prot	---	AT5G66080	-1.08	-0.11	-0.44	0.6725871	0.8361973	-6.45	TRUE
264672_at	hypothetical protein predicted by	---	AT1G09750	1.52	0.61	0.44	0.6727718	0.8363814	-6.45	FALSE
257397_at	hypothetical protein predicted by	RIC6	AT2G20430	-1.07	-0.10	-0.44	0.6730052	0.8366259	-6.45	FALSE
246635_at	hypothetical protein predicted by	---	AT1G31720	-1.08	-0.11	-0.44	0.6730892	0.8366847	-6.45	FALSE
262836_at	hypothetical protein predicted by	---	AT1G14680	1.04	0.06	0.44	0.6731843	0.8367573	-6.45	FALSE
248504_at	transcription factor Hap5a-like	NF-YC6	AT5G50480	1.08	0.11	0.44	0.6732608	0.8367676	-6.45	FALSE
253152_at	putative protein predicted protei	---	AT4G35690	-1.06	-0.09	-0.44	0.6732659	0.8367676	-6.45	FALSE
260942_s_a	hypothetical protein contains sim	---	AT1G45190 ///	-1.05	-0.07	-0.44	0.6734486	0.8369491	-6.45	FALSE
266527_at	hypothetical protein predicted by	---	---	1.06	0.09	0.44	0.6735393	0.8370162	-6.45	FALSE
254201_at	putative protein predicted protein	---	AT4G24130	1.07	0.10	0.44	0.6735879	0.8370309	-6.45	FALSE
262927_at	hypothetical protein shares simila	---	AT1G65810	-1.05	-0.07	-0.44	0.6736644	0.8370804	-6.45	FALSE
261721_at	unknown protein ; supported by c	---	AT1G08480	-1.05	-0.06	-0.44	0.6738777	0.8372542	-6.45	FALSE
254699_at	putative protein predicted protei	---	AT4G17990	1.05	0.07	0.44	0.6738752	0.8372542	-6.45	FALSE
265625_at	hypothetical protein predicted by	---	AT2G27240	1.06	0.09	0.44	0.6739258	0.8372684	-6.45	FALSE
261234_x_a	hypothetical protein predicted by	---	---	1.05	0.07	0.44	0.6740206	0.8373405	-6.45	FALSE
261766_at	auxin-induced protein IAA5, puta	IAA5	AT1G15580	-1.16	-0.21	-0.44	0.6740831	0.8373726	-6.45	FALSE
266467_at	Not56-like protein ; supported by	ALG3	AT2G47760	1.06	0.08	0.44	0.6745595	0.8376578	-6.45	FALSE
252401_at	putative protein predicted protei	---	AT3G48030	1.06	0.08	0.44	0.6744781	0.8376578	-6.45	FALSE
248463_at	putative protein contains similarit	---	AT5G51130	-1.12	-0.17	-0.44	0.6744832	0.8376578	-6.45	FALSE
266251_s_a	unknown protein	---	AT2G18320 ///	-1.04	-0.06	-0.44	0.6745544	0.8376578	-6.45	FALSE
261349_at	Expressed protein ; supported by	AT1G7961(	---	1.04	0.06	0.44	0.6745522	0.8376578	-6.45	FALSE
256562_at	Ty1/Copia-type retroelement poly	---	---	-1.05	-0.07	-0.44	0.6745697	0.8376578	-6.45	FALSE
245279_at	putative protein ; supported by cI	---	AT4G17270	-1.05	-0.07	-0.44	0.6744134	0.8376578	-6.45	FALSE
266014_s_a	hypothetical protein	---	AT2G07722	1.11	0.15	0.44	0.6747586	0.8377061	-6.45	TRUE
252188_at	putative clathrin coat assembly p	---	AT3G50860	1.09	0.12	0.44	0.6747624	0.8377061	-6.45	FALSE
251328_at	putative protein putative protein	ATPOB1	AT3G61600	1.04	0.06	0.44	0.674682	0.8377061	-6.45	FALSE
247838_at	ubiquitin-specific protease 23 (U	UBP23	AT5G57990	-1.09	-0.13	-0.44	0.6747923	0.8377061	-6.45	FALSE

248321_at	putative protein similar to unknov	---	AT5G52740	1.05	0.07	0.44	0.6746939	0.8377061	-6.45	FALSE
257008_at	myrosinase-associated protein,	ESM1	AT3G14210	-1.26	-0.33	-0.44	0.675055	0.8378043	-6.45	TRUE
261397_at	hexose transporter, putative sim	SGB1	AT1G79820	1.09	0.13	0.44	0.6749631	0.8378043	-6.45	FALSE
250710_at	MYB family transcription factor-li	MYB33	AT5G06100	-1.05	-0.07	-0.44	0.6749642	0.8378043	-6.45	FALSE
266997_at	hypothetical protein predicted by	---	AT2G34410	1.08	0.11	0.44	0.675031	0.8378043	-6.45	FALSE
263310_s_a	hypothetical protein	---	---	1.04	0.06	0.44	0.6750065	0.8378043	-6.45	FALSE
250958_at	laccase precursor - like laccase	LAC11	AT5G03260	-1.17	-0.23	-0.44	0.6752338	0.8379349	-6.45	FALSE
248750_at	putative protein similar to unknov	---	AT5G47530	1.08	0.11	0.44	0.675225	0.8379349	-6.45	FALSE
247444_at	putative protein strong similarity t	HIPL2	AT5G62630	1.13	0.18	0.44	0.6755418	0.8379497	-6.45	TRUE
250609_at	peptide methionine sulfoxide red	PMSR3	AT5G07470	1.05	0.06	0.44	0.6755036	0.8379497	-6.45	FALSE
258480_at	unknown protein ;supported by f	---	AT3G02640	1.05	0.08	0.44	0.6756865	0.8379497	-6.45	FALSE
256626_at	hypothetical protein, 5' partial	---	AT3G20015	-1.13	-0.18	-0.44	0.6756639	0.8379497	-6.45	FALSE
248860_at	putative protein contains similarit	---	AT5G46670	1.05	0.07	0.44	0.6756496	0.8379497	-6.45	FALSE
266755_at	putative alcohol dehydrogenase	---	AT2G47150	-1.06	-0.08	-0.44	0.6755549	0.8379497	-6.45	FALSE
264234_at	hypothetical protein contains sim	---	AT1G54720	1.04	0.06	0.44	0.6754237	0.8379497	-6.45	FALSE
264749_at	hypothetical protein Contains sim	---	AT1G22830	-1.09	-0.12	-0.44	0.6753879	0.8379497	-6.45	FALSE
248724_at	putative protein strong similarity t	---	AT5G47970	-1.09	-0.12	-0.44	0.6754728	0.8379497	-6.45	FALSE
265355_at	hypothetical protein predicted by	---	AT2G16760	1.08	0.12	0.44	0.6753631	0.8379497	-6.45	FALSE
253292_at	Expressed protein ; supported by	---	AT4G33985	1.08	0.11	0.44	0.6756404	0.8379497	-6.45	FALSE
263340_at	hypothetical protein predicted by	---	---	1.05	0.06	0.44	0.6754503	0.8379497	-6.45	FALSE
262536_at	SOUL-like protein Similar to SO	---	AT1G17100	-1.11	-0.15	-0.44	0.6757874	0.8380293	-6.45	FALSE
257047_at	hypothetical protein predicted by	---	AT3G19570	-1.07	-0.10	-0.44	0.6759002	0.8380441	-6.45	FALSE
249615_x_a	contains similarity to unknown pr	AGL105	AT5G37420	1.05	0.07	0.44	0.6759535	0.8380441	-6.45	FALSE
255200_at	hypothetical protein	---	---	1.05	0.08	0.44	0.6759413	0.8380441	-6.45	FALSE
245990_at	putative protein predicted protei	---	AT5G20640	1.07	0.10	0.44	0.6759649	0.8380441	-6.45	FALSE
245461_at	hypothetical protein	---	AT4G17000	-1.05	-0.07	-0.44	0.675983	0.8380441	-6.45	FALSE
263485_at	putative villin ; supported by cDN	VLN1	AT2G29890	1.05	0.07	0.44	0.6761195	0.8381677	-6.45	FALSE
257157_at	syntaxin-like protein similar to sy	SYP32	AT3G24350	1.07	0.10	0.44	0.6762129	0.8381972	-6.45	TRUE
265727_at	putative DNA topoisomerase III b	---	AT2G32000	-1.05	-0.07	-0.44	0.6762167	0.8381972	-6.45	FALSE
252177_at	protein kinase ATN1 - like protei	---	AT3G50730	1.06	0.08	0.44	0.6762764	0.8382255	-6.45	FALSE
253539_at	putative protein RING-finger pro	---	AT4G31450	-1.05	-0.08	-0.44	0.6764375	0.8382915	-6.45	FALSE
265376_at	hypothetical protein predicted by	---	AT2G05810	-1.05	-0.08	-0.44	0.6764221	0.8382915	-6.45	FALSE
248707_at	putative protein similar to unknov	---	AT5G48550	-1.05	-0.08	-0.44	0.6764399	0.8382915	-6.45	FALSE
266753_at	auxin-induced protein (IAA20) ide	IAA20	AT2G46990	1.05	0.07	0.44	0.6765359	0.8383194	-6.45	FALSE
246009_at	Expressed protein ; supported by	ATSTE14B	AT5G08335	1.07	0.10	0.44	0.6765014	0.8383194	-6.45	FALSE

251235_at	putative protein lysophospholipa	---	AT3G62860	-1.09	-0.13	-0.44	0.6767733	0.8385681	-6.45	FALSE
249820_at	putative protein contains similarit	---	AT5G23650	1.08	0.11	0.44	0.67684	0.8386051	-6.45	FALSE
267195_at	putative protein kinase contains a	---	AT2G30940	1.07	0.10	0.44	0.6769485	0.8386608	-6.45	FALSE
264453_at	putative GTP-binding protein sin	---	AT1G10300	-1.04	-0.05	-0.44	0.6769585	0.8386608	-6.45	FALSE
246280_at	hypothetical protein	---	AT4G36660	-1.11	-0.15	-0.44	0.6771441	0.838663	-6.45	FALSE
257643_at	AP2 domain transcription factor	---	AT3G25730	1.14	0.19	0.44	0.6770268	0.838663	-6.45	FALSE
246974_at	putative protein	---	AT5G24980	-1.06	-0.09	-0.44	0.677081	0.838663	-6.45	FALSE
246936_at	putative protein hypothetical pro	---	AT5G25360	1.05	0.07	0.44	0.6771212	0.838663	-6.45	FALSE
254677_at	chloroplast protein cs/ch-42	---	AT4G18490	-1.06	-0.08	-0.44	0.6770566	0.838663	-6.45	FALSE
263986_at	putative citrate synthase ;suppo	CSY3	AT2G42790	1.07	0.10	0.43	0.677222	0.8387139	-6.45	FALSE
257455_s_a	hypothetical protein	---	AT1G27870 ///	1.04	0.06	0.43	0.6774104	0.8387485	-6.45	FALSE
263464_at	putative ARI-like RING zinc finge	---	AT2G31760	-1.05	-0.08	-0.43	0.6774705	0.8387485	-6.45	FALSE
266926_at	unknown protein predicted by ge	---	AT2G46000	1.07	0.09	0.43	0.6773313	0.8387485	-6.45	FALSE
266667_at	hypothetical protein predicted by	---	AT2G29770	1.04	0.06	0.43	0.6773129	0.8387485	-6.45	FALSE
256662_at	male sterility protein 2 (MS2) nea	MS2	AT3G11980	-1.04	-0.06	-0.43	0.6773986	0.8387485	-6.45	FALSE
248345_at	unknown protein	SHOC1	AT5G52290	1.04	0.06	0.43	0.677456	0.8387485	-6.45	FALSE
260244_at	putative choline kinase similar to	---	AT1G74320	1.05	0.07	0.43	0.6777783	0.8390841	-6.45	FALSE
256985_at	myb-related protein 5 identical to	ATMYB5	AT3G13540	1.07	0.09	0.43	0.6779681	0.8392734	-6.45	FALSE
267264_at	putative serine carboxypeptidase	SCPL11	AT2G22970	-1.15	-0.20	-0.43	0.6780131	0.8392835	-6.45	FALSE
247397_at	Dof zinc finger protein - like Dof	---	AT5G62940	1.09	0.12	0.43	0.6780524	0.8392866	-6.45	FALSE
258075_at	homocysteine S-methyltransfera	HMT-1	AT3G25900	1.26	0.33	0.43	0.6783386	0.8395954	-6.45	FALSE
257528_at	hypothetical protein predicted by	---	AT3G02125	1.05	0.06	0.43	0.6784123	0.8396411	-6.45	FALSE
252021_at	putative protein predicted protei	---	AT3G53070	1.06	0.08	0.43	0.6785105	0.8396475	-6.45	FALSE
246667_at	putative protein hypothetical prot	---	---	1.05	0.07	0.43	0.6785636	0.8396475	-6.45	FALSE
262696_at	hypothetical protein	---	AT1G75870	-1.05	-0.07	-0.43	0.6785507	0.8396475	-6.45	FALSE
260485_at	putative amp-binding protein sim	---	AT1G68270	-1.05	-0.07	-0.43	0.6785648	0.8396475	-6.45	FALSE
246753_at	putative protein	---	---	1.06	0.08	0.43	0.6787035	0.8397736	-6.45	FALSE
263989_at	putative MAP kinase ; supported	ATMPK20	AT2G42880	1.08	0.11	0.43	0.6788407	0.8398523	-6.45	TRUE
250608_at	pectin methyl-esterase-like prote	---	AT5G07420	1.04	0.06	0.43	0.6788083	0.8398523	-6.45	FALSE
249968_at	putative protein predicted protei	---	AT5G19070	1.11	0.15	0.43	0.6790658	0.8399308	-6.45	FALSE
257298_at	hypothetical protein predicted by	---	AT3G28155	-1.07	-0.09	-0.43	0.6790085	0.8399308	-6.45	FALSE
257286_s_a	transposase, putative similar to t	---	AT1G19260 ///	-1.06	-0.08	-0.43	0.6790008	0.8399308	-6.45	FALSE
261840_at	hypothetical protein contains sim	AtTLP8	AT1G16070	1.05	0.06	0.43	0.6790882	0.8399308	-6.45	FALSE
266245_at	putative translation initiation facto	---	AT2G27700	1.05	0.07	0.43	0.6790299	0.8399308	-6.45	FALSE
254311_at	hypothetical protein	---	AT4G22440	1.06	0.08	0.43	0.6791683	0.8399842	-6.45	FALSE

252738_at	putative protein predicted protei	---	AT3G43240	1.05	0.06	0.43	0.6793115	0.8401158	-6.45	FALSE
253235_at	putative protein hypothetical pro	HDR	AT4G34350	1.10	0.14	0.43	0.6793702	0.8401429	-6.45	FALSE
255835_at	unknown protein	---	AT2G33420	1.05	0.07	0.43	0.6795974	0.8403349	-6.45	FALSE
245182_at	putative protein similarity to TET	---	AT5G12430	-1.07	-0.10	-0.43	0.6796729	0.8403349	-6.45	FALSE
245267_at	major latex protein like ; supporte	---	AT4G14060	1.05	0.07	0.43	0.6796488	0.8403349	-6.45	FALSE
262063_at	unknown protein identical to unkı	---	AT1G80000	-1.06	-0.08	-0.43	0.6796607	0.8403349	-6.45	FALSE
250187_at	putative protein predicted protei	---	AT5G14370	-1.09	-0.13	-0.43	0.6798346	0.8404438	-6.45	FALSE
249564_at	unknown protein	---	AT5G38400	1.06	0.08	0.43	0.6798234	0.8404438	-6.45	FALSE
260076_at	putative calmodulin similar to cal	---	AT1G73630	-1.08	-0.11	-0.43	0.6801554	0.8407397	-6.45	FALSE
258533_at	hypothetical protein	---	AT3G06670	1.05	0.08	0.43	0.6801149	0.8407397	-6.45	FALSE
248996_at	unknown protein	RRS1	AT5G45260	-1.08	-0.11	-0.43	0.6801846	0.8407397	-6.45	FALSE
260393_at	putative lipase similar to lipase G	---	AT1G73920	1.07	0.09	0.43	0.6803536	0.8408641	-6.45	FALSE
252810_at	putative protein several hypothet	---	---	1.06	0.08	0.43	0.680359	0.8408641	-6.45	FALSE
250550_at	N-hydroxycinnamoyl benzoyltrar	---	AT5G07870	1.11	0.15	0.43	0.6808269	0.8410459	-6.45	FALSE
248896_at	putative protein contains similarit	WRKY8	AT5G46350	1.19	0.25	0.43	0.6808698	0.8410459	-6.45	FALSE
258289_at	hypothetical protein predicted by	---	AT3G23450	-1.04	-0.06	-0.43	0.6808824	0.8410459	-6.45	FALSE
262514_at	NAM(no apical meristem) protei	anac017	AT1G34190	1.04	0.06	0.43	0.6807897	0.8410459	-6.45	FALSE
262253_s_a	unknown protein contains similar	---	AT1G53880 ///	-1.06	-0.08	-0.43	0.6807349	0.8410459	-6.45	FALSE
267399_at	hypothetical protein predicted by	---	AT2G44195	-1.04	-0.06	-0.43	0.6806474	0.8410459	-6.45	FALSE
266830_at	1-aminocyclopropane-1-carboxyl	ACS4	AT2G22810	-1.21	-0.27	-0.43	0.6809854	0.8410459	-6.45	FALSE
252386_at	putative protein various predicte	---	AT3G47840	-1.06	-0.09	-0.43	0.6806184	0.8410459	-6.45	FALSE
257502_at	unknown protein	---	AT1G78110	1.11	0.15	0.43	0.6809505	0.8410459	-6.45	FALSE
255293_at	putative zinc finger protein	---	AT4G04730	-1.05	-0.07	-0.43	0.6807221	0.8410459	-6.45	FALSE
252767_at	ring-box protein-like ring-box pro	---	AT3G42830	-1.05	-0.07	-0.43	0.6809315	0.8410459	-6.45	FALSE
259632_at	nicotianamine synathase, putati	NAS4	AT1G56430	-1.13	-0.18	-0.43	0.6805519	0.8410459	-6.45	FALSE
255708_at	predicted protein	---	AT4G00232	1.05	0.08	0.43	0.6808762	0.8410459	-6.45	FALSE
245721_s_a	hypothetical protein similar to Se	---	AT1G73450 ///	-1.07	-0.10	-0.43	0.6810976	0.841098	-6.45	FALSE
259078_at	unknown protein predicted by ge	HST	AT3G05040	-1.04	-0.06	-0.43	0.6811013	0.841098	-6.45	FALSE
260856_at	TINY-like protein similar to TINY	---	AT1G21910	1.22	0.29	0.43	0.6812061	0.8411819	-6.45	TRUE
266966_at	hypothetical protein predicted by	---	AT2G39520	1.04	0.05	0.43	0.6814269	0.8414089	-6.45	FALSE
261858_at	Expressed protein ; supported by	---	AT1G50570	-1.04	-0.06	-0.43	0.6817809	0.8415402	-6.45	FALSE
264448_at	putative sensory transduction his	AHK3	AT1G27320	1.04	0.06	0.43	0.6817914	0.8415402	-6.45	FALSE
245627_at	water stress-induced protein, pu	AtGolS2	AT1G56600	-1.11	-0.15	-0.43	0.6816254	0.8415402	-6.45	FALSE
265439_at	senescence-associated protein d	---	AT2G21045	-1.21	-0.28	-0.43	0.6817211	0.8415402	-6.45	FALSE
264306_at	unknown protein predicted by ge	---	AT1G78890	-1.06	-0.08	-0.43	0.681743	0.8415402	-6.45	FALSE

250171_at	prohibitin - like protein prohibitin	ATPHB5	AT5G14300	1.05	0.07	0.43	0.6816167	0.8415402	-6.45	FALSE
257745_at	unknown protein ;supported by f	---	AT3G29240	1.15	0.20	0.43	0.681709	0.8415402	-6.45	FALSE
250508_at	selenium-binding protein-like	---	AT5G09950	-1.05	-0.07	-0.43	0.6819615	0.8416135	-6.46	FALSE
258745_at	unknown protein ; supported by f	---	AT3G05920	-1.05	-0.07	-0.43	0.6819465	0.8416135	-6.46	FALSE
249202_at	cytochrome P450	CYP705A1	AT5G42580	-1.04	-0.06	-0.43	0.6819021	0.8416135	-6.45	FALSE
265309_at	putative myosin heavy chain	XIG	AT2G20290	1.07	0.10	0.43	0.6820587	0.8416233	-6.46	FALSE
261327_at	transcription factor, putative con	---	AT1G44830	1.32	0.40	0.43	0.6820898	0.8416233	-6.46	FALSE
252546_at	DNA-binding protein - like DNA	---	AT3G45830	-1.05	-0.07	-0.43	0.6820711	0.8416233	-6.46	FALSE
257146_at	unknown protein contains Pfam p	GTE8	AT3G27260	1.04	0.06	0.43	0.6821171	0.8416233	-6.46	FALSE
260627_at	hypothetical protein predicted by	---	AT1G62310	1.08	0.11	0.43	0.6824406	0.841781	-6.46	FALSE
AFFX-r2-At	Arabidopsis thaliana /REF=M64	---	---	1.10	0.14	0.43	0.6827246	0.841781	-6.46	FALSE
257214_at	hypothetical protein ;supported b	---	AT3G15040	1.06	0.08	0.43	0.682327	0.841781	-6.46	FALSE
260344_at	polyneuridine aldehyde esterase	MES15	AT1G69240	1.05	0.07	0.43	0.6825826	0.841781	-6.46	FALSE
255836_at	putative splicing factor U2AF larg	---	AT2G33440	1.07	0.10	0.43	0.6824767	0.841781	-6.46	FALSE
244976_at	cytochrome B6	---	---	-1.04	-0.06	-0.43	0.6826672	0.841781	-6.46	FALSE
254523_at	putative protein hypothetical pro	FRS1	AT4G19990	1.07	0.10	0.43	0.6823231	0.841781	-6.46	FALSE
253667_at	peroxidase ATP8a ;supported by	---	AT4G30170	1.05	0.07	0.43	0.6824229	0.841781	-6.46	FALSE
254478_at	putative protein TRANSCRIPTIC	---	AT4G20330	-1.07	-0.09	-0.43	0.6825306	0.841781	-6.46	FALSE
250712_at	human RAN binding protein 16-li	---	AT5G06120	1.05	0.08	0.43	0.6827123	0.841781	-6.46	FALSE
251212_at	putative protein hypothetical pro	---	---	-1.05	-0.07	-0.43	0.6826888	0.841781	-6.46	FALSE
260050_at	hypothetical protein predicted by	AGL64	AT1G29960 /	1.06	0.08	0.43	0.6826261	0.841781	-6.46	FALSE
264095_at	mercaptopyruvate sulfurtransfera	MST1	AT1G79230	-1.04	-0.06	-0.43	0.682673	0.841781	-6.46	FALSE
247537_s_a	ABC transport protein - like ABC	ATH15	AT5G61690 /	-1.05	-0.07	-0.43	0.6827842	0.8418089	-6.46	FALSE
256620_at	disease resistance protein, puta	---	AT3G24480	1.09	0.12	0.43	0.682952	0.8419397	-6.46	FALSE
265759_at	putative membrane transporter	---	AT2G13100	-1.04	-0.06	-0.43	0.6829641	0.8419397	-6.46	FALSE
245111_at	putative Ta11-like non-LTR retro	---	---	1.05	0.07	0.43	0.6832344	0.8422274	-6.46	FALSE
259993_at	unknown protein	---	AT1G67960	-1.05	-0.08	-0.43	0.6834048	0.842392	-6.46	FALSE
245176_at	unknown protein similar to GP|21	---	AT2G47440	1.13	0.17	0.43	0.6837673	0.8424381	-6.46	TRUE
262798_at	putative SPL1-related protein sir	SPL14	AT1G20980	1.05	0.07	0.43	0.6835086	0.8424381	-6.46	FALSE
255824_at	hypothetical protein predicted by	---	AT2G40530	-1.15	-0.21	-0.43	0.6836346	0.8424381	-6.46	FALSE
263612_at	putative CDC21 protein	MCM4	AT2G16440	-1.17	-0.23	-0.43	0.6836429	0.8424381	-6.46	FALSE
262972_at	unknown protein	---	AT1G75620	-1.05	-0.07	-0.43	0.6837746	0.8424381	-6.46	FALSE
265427_at	unknown protein	---	AT2G20740	-1.06	-0.09	-0.43	0.6836849	0.8424381	-6.46	FALSE
246986_at	receptor-like protein kinase ;sup	RLK	AT5G67280	1.16	0.21	0.43	0.6837067	0.8424381	-6.46	FALSE
260326_at	putative MYB family transcription	AtMYB103	AT1G63910	1.06	0.08	0.43	0.6835611	0.8424381	-6.46	FALSE

248892_at	unknown protein	---	AT5G46300	1.04	0.06	0.43	0.6836377	0.8424381	-6.46	FALSE
253406_at	putative protein GATA transcript	---	AT4G32890	1.09	0.13	0.43	0.6838403	0.8424735	-6.46	FALSE
264854_at	putative RING zinc finger protein	RHA3A	AT2G17450	-1.06	-0.08	-0.43	0.6838784	0.842475	-6.46	FALSE
265684_at	unknown protein	---	AT2G24410	-1.04	-0.05	-0.43	0.6840489	0.8426395	-6.46	FALSE
256551_at	unknown protein	---	---	-1.05	-0.07	-0.42	0.6841225	0.8426846	-6.46	FALSE
264324_at	myosin heavy chain MYA2 Stron	XIB	AT1G04160	-1.10	-0.14	-0.42	0.6842166	0.842755	-6.46	TRUE
261573_at	hypothetical protein identical to h	---	AT1G01180	1.04	0.06	0.42	0.6843186	0.8428352	-6.46	FALSE
245398_at	hydroxyproline-rich glycoprotein	---	AT4G14900	1.08	0.11	0.42	0.684465	0.8428357	-6.46	TRUE
265086_at	hypothetical protein contains Zir	RING1B	AT1G03770	-1.07	-0.10	-0.42	0.6844254	0.8428357	-6.46	FALSE
249419_s_a	putative protein MADS-box prote	AGL98	AT5G39750 /	-1.04	-0.06	-0.42	0.6844668	0.8428357	-6.46	FALSE
256074_at	unknown protein ; supported by c	---	AT1G18260	1.06	0.08	0.42	0.6844292	0.8428357	-6.46	FALSE
244977_at	cytochrome b/f	---	---	-1.10	-0.14	-0.42	0.684542	0.8428372	-6.46	FALSE
252782_at	putative protein predicted protein	---	---	1.04	0.06	0.42	0.6845175	0.8428372	-6.46	FALSE
247810_at	26S proteasome AAA-ATPase su	RPT3	AT5G58290	-1.04	-0.06	-0.42	0.6848469	0.8428638	-6.46	FALSE
248342_at	unknown protein	MBD13	AT5G52230	-1.04	-0.06	-0.42	0.6847396	0.8428638	-6.46	FALSE
256825_at	unknown protein similar to cell w	CWLP	AT3G22120	1.46	0.55	0.42	0.6847709	0.8428638	-6.46	FALSE
257872_at	P-glycoprotein, putative similar t	PGP16	AT3G28360	-1.04	-0.05	-0.42	0.68462	0.8428638	-6.46	FALSE
257568_s_a	hypothetical protein	---	AT3G23950 /	1.06	0.09	0.42	0.6848337	0.8428638	-6.46	FALSE
245440_at	RNA helicase	---	AT4G16680	1.04	0.06	0.42	0.6848592	0.8428638	-6.46	FALSE
256395_at	putative helix-loop-helix DNA-bin	MUTE	AT3G06120	1.05	0.07	0.42	0.6847882	0.8428638	-6.46	FALSE
245542_at	CONSTANS like protein	---	AT4G15250	1.05	0.07	0.42	0.6847516	0.8428638	-6.46	FALSE
249668_at	putative protein similar to unknov	---	AT5G35870	-1.06	-0.08	-0.42	0.6849425	0.8429208	-6.46	FALSE
247509_at	heat shock factor 6	HSFB2A	AT5G62020	-1.06	-0.08	-0.42	0.6850597	0.8430196	-6.46	FALSE
254941_s_a	putative protein various reverse t	---	---	1.05	0.07	0.42	0.6852765	0.8432409	-6.46	FALSE
246805_at	putative protein various predicte	AGL101	AT5G27050	-1.04	-0.06	-0.42	0.6853979	0.8433448	-6.46	FALSE
255606_at	hypothetical protein similar to T3	---	AT4G01110	-1.07	-0.09	-0.42	0.6854416	0.843353	-6.46	FALSE
256277_at	omega-6 fatty acid desaturase, e	FAD2	AT3G12120	1.09	0.12	0.42	0.6855518	0.8434432	-6.46	FALSE
257089_at	hypothetical protein	SVL3	AT3G20520	-1.05	-0.07	-0.42	0.6856227	0.8434849	-6.46	FALSE
259469_at	hypothetical protein predicted by	---	AT1G19100	-1.05	-0.06	-0.42	0.6857787	0.8435763	-6.46	FALSE
260376_at	putative cytochrome P-450 simila	CYP78A10	AT1G74110	-1.05	-0.07	-0.42	0.685808	0.8435763	-6.46	FALSE
263527_at	putative thaumatin-like pathogen	---	AT2G24810	-1.08	-0.11	-0.42	0.6857538	0.8435763	-6.46	FALSE
267489_s_a	putative DNA2-NAM7 helicase fa	---	AT2G19120 /	-1.08	-0.10	-0.42	0.6859126	0.8436596	-6.46	FALSE
246367_at	light repressible receptor protein	---	AT1G51880	-1.05	-0.07	-0.42	0.6860375	0.8437269	-6.46	FALSE
258115_at	hypothetical protein predicted by	---	AT3G14670	1.05	0.07	0.42	0.6860413	0.8437269	-6.46	FALSE
248405_at	putative protein pectinesterase-li	SKS2	AT5G51480	1.25	0.33	0.42	0.6862314	0.8437786	-6.46	TRUE

262249_at	root hairless 1 (RHL1) similar to	RHL1	AT1G48380	1.05	0.07	0.42	0.6862139	0.8437786	-6.46	FALSE
257718_at	organ separation protein, putativ	anac058	AT3G18400	1.05	0.07	0.42	0.6861692	0.8437786	-6.46	FALSE
265870_at	hypothetical protein predicted by	PDLP6	AT2G01660	-1.04	-0.06	-0.42	0.6862024	0.8437786	-6.46	FALSE
248255_at	ATP-dependent Clp protease AT	CLPX	AT5G53350	1.05	0.08	0.42	0.6864166	0.8438751	-6.46	FALSE
248361_at	putative protein similar to unknov	EDA41	AT5G52460	1.05	0.07	0.42	0.6864386	0.8438751	-6.46	FALSE
258597_x_a	hypothetical protein predicted by	---	AT3G04390	1.04	0.06	0.42	0.6864578	0.8438751	-6.46	FALSE
249350_at	MYB -like protein MYB22, Arabi	MYB115	AT5G40360	-1.05	-0.07	-0.42	0.6863512	0.8438751	-6.46	FALSE
251167_at	putative protein proteinase inhib	---	AT3G63360	1.04	0.06	0.42	0.6866977	0.8439168	-6.46	FALSE
246690_at	hypothetical protein	---	---	1.05	0.07	0.42	0.6866901	0.8439168	-6.46	FALSE
248137_at	putative protein contains similarit	---	AT5G54950	-1.05	-0.07	-0.42	0.6866653	0.8439168	-6.46	FALSE
256574_at	hypothetical protein similar to cal	---	AT3G14780	1.09	0.12	0.42	0.6867137	0.8439168	-6.46	FALSE
265912_at	hypothetical protein predicted by	---	AT2G25565 /	-1.05	-0.07	-0.42	0.6865341	0.8439168	-6.46	FALSE
247051_at	At14a protein-like	---	AT5G66670	-1.05	-0.07	-0.42	0.6867059	0.8439168	-6.46	FALSE
245873_at	bHLH transcription factor GBOF	CIB5	AT1G26260	-1.06	-0.09	-0.42	0.686765	0.8439343	-6.46	FALSE
265877_at	unknown protein ; supported by	BZIP34	AT2G42380	1.09	0.13	0.42	0.6869789	0.8439699	-6.46	TRUE
260697_at	unknown protein	---	AT1G32530	1.08	0.11	0.42	0.6869612	0.8439699	-6.46	FALSE
248811_at	putative protein contains similarit	---	AT5G47310	1.05	0.07	0.42	0.6868445	0.8439699	-6.46	FALSE
250242_at	putative protein similar to unknov	---	AT5G13620	1.05	0.06	0.42	0.6869306	0.8439699	-6.46	FALSE
262834_at	hypothetical protein predicted by	MAP65-7	AT1G14690	-1.05	-0.07	-0.42	0.6869468	0.8439699	-6.46	FALSE
260528_at	putative WRKY-type DNA bindin	WRKY23	AT2G47260	1.12	0.16	0.42	0.6870282	0.843985	-6.46	FALSE
251776_at	eukaryotic translation initiation fa	emb1624	AT3G55620	-1.07	-0.09	-0.42	0.6872272	0.8441632	-6.46	FALSE
254127_at	NADPH-ferrihemoprotein reducta	ATR1	AT4G24520	-1.06	-0.08	-0.42	0.6872843	0.8441632	-6.46	FALSE
245891_at	amino acid transport protein AAF	AAP2	AT5G09220	-1.14	-0.18	-0.42	0.6872713	0.8441632	-6.46	FALSE
245045_at	unknown protein similar to glycop	---	AT2G26590	-1.04	-0.06	-0.42	0.6873476	0.8441861	-6.46	FALSE
248732_at	xyloglucan endo-1,4-beta-D-gluc	XTH20	AT5G48070	-1.06	-0.09	-0.42	0.6874067	0.8441861	-6.46	FALSE
252082_at	putative protein	---	AT3G51940	-1.04	-0.06	-0.42	0.687451	0.8441861	-6.46	FALSE
251460_at	hypothetical protein	SAC9	AT3G59770	1.04	0.06	0.42	0.6874381	0.8441861	-6.46	FALSE
255732_at	fatty acid condensing enzyme C	KCS5	AT1G25450 /	-1.14	-0.19	-0.42	0.6875769	0.8442222	-6.46	TRUE
245935_at	hypothetical protein	---	AT5G19840	1.04	0.06	0.42	0.6875914	0.8442222	-6.46	FALSE
266220_at	putative dTDP-glucose 4-6-dehy	---	AT2G28755	1.06	0.09	0.42	0.6875681	0.8442222	-6.46	FALSE
262089_s_a	hypothetical protein predicted by	---	AT1G55980 /	-1.07	-0.09	-0.42	0.6876959	0.8443051	-6.46	FALSE
263609_at	putative LRR receptor protein kir	---	AT2G16250	-1.05	-0.06	-0.42	0.6878067	0.8443219	-6.46	FALSE
257625_at	cytochrome P450, putative conta	CYP71B24	AT3G26230	-1.26	-0.34	-0.42	0.6878551	0.8443219	-6.46	FALSE
248270_at	putative protein similar to unknov	ORG1	AT5G53450	1.11	0.15	0.42	0.6878564	0.8443219	-6.46	FALSE
260576_at	putative FCA-related protein	---	AT2G47310	-1.06	-0.09	-0.42	0.6880028	0.8443219	-6.46	FALSE

260514_at	hypothetical protein predicted by	---	AT1G51480	1.05	0.07	0.42	0.6879428	0.8443219	-6.46	FALSE
245772_at	hypothetical protein similar to put	---	AT1G30300	1.08	0.11	0.42	0.6878879	0.8443219	-6.46	FALSE
267109_at	hypothetical protein predicted by	---	AT2G14810	1.05	0.08	0.42	0.6879028	0.8443219	-6.46	FALSE
256850_at	hypothetical protein similar to hyp	---	---	-1.04	-0.05	-0.42	0.6880057	0.8443219	-6.46	FALSE
250501_at	carboxypeptidase - like protein (	SCPL19	AT5G09640	-1.05	-0.06	-0.42	0.6883868	0.8447441	-6.46	FALSE
245154_at	putative protein similarity to pred	---	AT5G12460	1.05	0.07	0.42	0.6885798	0.8449354	-6.46	FALSE
267092_at	unknown protein ;supported by f	AUX1	AT2G38120	1.12	0.16	0.42	0.688639	0.8449626	-6.46	FALSE
264511_at	putative galactinol synthase simil	AtGolS3	AT1G09350	1.17	0.22	0.42	0.6887381	0.8449933	-6.46	TRUE
263874_at	putative ATP synthase ;supporte	---	AT2G21870	1.07	0.09	0.42	0.6887179	0.8449933	-6.46	FALSE
252399_at	putative cyclic nucleotide-gated	CNGC16	AT3G48010	1.04	0.06	0.42	0.688786	0.8450066	-6.46	FALSE
266730_at	putative RNA-binding protein	---	AT2G03110	1.05	0.07	0.42	0.6890387	0.8452258	-6.46	FALSE
248143_at	putative protein similar to unknov	---	AT5G55040	-1.05	-0.06	-0.42	0.6890269	0.8452258	-6.46	FALSE
259602_at	disease resistance protein, puta	---	AT1G56520	1.04	0.06	0.42	0.6891232	0.8452789	-6.46	FALSE
258510_at	hypothetical protein predicted by	---	AT3G06600	-1.05	-0.07	-0.42	0.6891827	0.8452789	-6.46	FALSE
257996_at	unknown protein	---	AT3G19950	1.04	0.06	0.42	0.6891932	0.8452789	-6.46	FALSE
246823_at	putative protein	---	AT5G26970	1.04	0.05	0.42	0.6896844	0.8457558	-6.46	FALSE
267066_at	hypothetical protein predicted by	---	AT2G41040	-1.07	-0.10	-0.42	0.6896679	0.8457558	-6.46	FALSE
261878_at	cytochrome P450, putative simil	CYP705A2	AT1G50560	-1.05	-0.06	-0.42	0.6896932	0.8457558	-6.46	FALSE
251297_at	germin-like protein (GLP10)	GLP10	AT3G62020	-1.13	-0.18	-0.42	0.689732	0.8457579	-6.46	FALSE
265181_at	putative OBP32pep protein ;sup	---	AT1G23510	1.06	0.08	0.42	0.6897837	0.8457758	-6.46	FALSE
253995_at	Col-0 casein kinase I-like protein	CK1	AT4G26100	1.06	0.09	0.42	0.6901114	0.8461321	-6.46	FALSE
251661_at	putative protein NODULIN-26 - (	SIP2;1	AT3G56950	-1.06	-0.09	-0.42	0.6902461	0.8462518	-6.46	TRUE
259355_at	hypothetical protein predicted by	---	AT3G05240	-1.05	-0.07	-0.42	0.6903037	0.8462768	-6.46	FALSE
254458_at	putative protein heat shock prote	ATERDJ2B	AT4G21180	-1.08	-0.11	-0.42	0.6903592	0.8462994	-6.46	FALSE
249367_at	putative protein predicted protei	---	AT5G40630	1.05	0.07	0.42	0.6904828	0.8463988	-6.46	FALSE
248876_at	putative protein similar to unknov	---	---	1.04	0.05	0.42	0.6905324	0.8463988	-6.46	FALSE
266646_at	unknown protein ;supported by f	ATPH1	AT2G29700	1.05	0.07	0.42	0.6905515	0.8463988	-6.46	FALSE
248911_at	tumor-related protein-like	DOG1	AT5G45830	-1.07	-0.09	-0.42	0.6906123	0.8464228	-6.46	FALSE
263489_at	putative inositol polyphosphate 5	---	AT2G31830	1.05	0.07	0.42	0.6906454	0.8464228	-6.46	FALSE
245849_at	leukotriene-A4 hydrolase-like pr	---	AT5G13520	-1.11	-0.14	-0.42	0.6906946	0.8464377	-6.46	FALSE
255052_at	rab7 -like protein rab7 protein -V	ATRABG3A	AT4G09720	1.05	0.08	0.42	0.6908854	0.8465805	-6.46	FALSE
255930_at	hypothetical protein predicted by	---	AT1G12660	1.04	0.06	0.42	0.6908852	0.8465805	-6.46	FALSE
246696_at	putative protein predicted protei	---	---	1.05	0.07	0.42	0.6909807	0.8466063	-6.46	FALSE
259925_at	thaumatin-like protein similar to t	PR5	AT1G75040	1.68	0.75	0.42	0.6909741	0.8466063	-6.46	FALSE
247195_at	putative protein contains similarit	---	AT5G65500	1.06	0.08	0.42	0.6910274	0.846618	-6.46	FALSE

255552_at	S-adenosylmethionine synthase	SAM-2	AT4G01850	1.05	0.07	0.41	0.6911374	0.8466382	-6.46	TRUE
262148_at	chloroplast-localized small heat	---	AT1G52560	1.11	0.15	0.41	0.6913763	0.8466382	-6.46	FALSE
255560_at	hypothetical protein similar to C.	---	AT4G02030	-1.04	-0.06	-0.41	0.6912145	0.8466382	-6.46	FALSE
253752_at	putative protein ;supported by fu	---	AT4G28910	1.06	0.09	0.41	0.691354	0.8466382	-6.46	FALSE
258228_at	unknown protein similar to unkno	---	AT3G27610	1.04	0.06	0.41	0.6913124	0.8466382	-6.46	FALSE
266209_at	similar to terminal flower ; suppo	ATC	AT2G27550	1.08	0.11	0.41	0.6911628	0.8466382	-6.46	FALSE
264079_at	putative seed storage protein (vic	---	AT2G28490	1.05	0.06	0.41	0.6912603	0.8466382	-6.46	FALSE
247581_at	receptor-like protein kinase prec	---	AT5G61350	-1.04	-0.06	-0.41	0.6910877	0.8466382	-6.46	FALSE
256323_at	unknown protein ; supported by c	---	AT1G54920	-1.06	-0.09	-0.41	0.6913779	0.8466382	-6.46	FALSE
253526_at	putative zinc finger protein hypo	---	AT4G31420	1.05	0.06	0.41	0.6914876	0.8467271	-6.46	FALSE
245471_at	probable ribosomal protein	---	AT4G16030	1.04	0.06	0.41	0.6915522	0.8467607	-6.46	FALSE
263023_at	unknown protein	---	AT1G23960	1.10	0.13	0.41	0.6916434	0.846827	-6.46	FALSE
257099_s_a	disease resistance protein, putat	---	AT3G24982 /.	-1.04	-0.05	-0.41	0.691703	0.8468545	-6.46	FALSE
254690_at	N-acetylornithine deacetylase-lik	---	AT4G17830	1.04	0.05	0.41	0.6918109	0.8468957	-6.46	FALSE
255002_at	AIG1-like protein AIG1 - Arabido	---	AT4G09940	1.05	0.07	0.41	0.691776	0.8468957	-6.46	FALSE
248609_at	unknown protein ; supported by	---	AT5G49440	1.05	0.07	0.41	0.6919048	0.8469651	-6.46	FALSE
252219_at	putative protein some putative pr	---	AT3G50160	1.06	0.08	0.41	0.6921359	0.8471571	-6.46	FALSE
255101_at	putative lipid transfer protein sim	---	AT4G08670	1.06	0.09	0.41	0.6921326	0.8471571	-6.46	FALSE
252280_at	SF16 -like protein SF16 protein,	iqd21	AT3G49260	-1.13	-0.17	-0.41	0.692175	0.8471595	-6.46	TRUE
248360_at	putative protein contains similarit	---	AT5G52430	-1.07	-0.10	-0.41	0.6923615	0.8472871	-6.46	FALSE
254319_at	putative protein predicted protei	---	AT4G22560	1.07	0.09	0.41	0.6923218	0.8472871	-6.46	FALSE
250963_at	putative protein various predicte	---	AT5G03000	1.06	0.09	0.41	0.6923907	0.8472871	-6.46	FALSE
261822_at	unknown protein ;supported by fu	---	AT1G11380	-1.09	-0.13	-0.41	0.6925276	0.8473278	-6.46	TRUE
249110_at	disease resistance protein	---	AT5G43730	1.04	0.05	0.41	0.6925958	0.8473278	-6.46	FALSE
251348_at	putative protein hypothetical pro	---	AT3G61010	-1.07	-0.10	-0.41	0.6925688	0.8473278	-6.46	FALSE
253256_at	putative protein endothelin conv	---	AT4G34360	1.06	0.09	0.41	0.6926445	0.8473278	-6.46	FALSE
267531_at	putative calcium-dependent prote	CPK14	AT2G41860	1.04	0.06	0.41	0.6925072	0.8473278	-6.46	FALSE
258839_at	unknown protein ; supported by	---	AT3G07170	-1.04	-0.06	-0.41	0.6926468	0.8473278	-6.46	FALSE
264802_at	putative syntaxin-related protein	SYP111	AT1G08560	-1.10	-0.14	-0.41	0.6927671	0.847384	-6.46	FALSE
257942_at	SKP1/ASK1 (At8), putative simil	ASK8	AT3G21830	1.06	0.08	0.41	0.6927326	0.847384	-6.46	FALSE
266540_at	hypothetical protein predicted by	---	AT2G35310	1.04	0.06	0.41	0.6929973	0.847514	-6.46	FALSE
257617_at	hypothetical protein	---	AT3G26550	1.04	0.06	0.41	0.6929298	0.847514	-6.46	FALSE
262041_at	HPt phosphotransmitter, putative	AHP6	AT1G80100	-1.06	-0.08	-0.41	0.693022	0.847514	-6.46	FALSE
252140_at	putative protein several hypothet	---	AT3G51070	1.04	0.05	0.41	0.6929715	0.847514	-6.46	FALSE
261585_at	NAC domain protein, putative si	ANAC001	AT1G01010	-1.08	-0.11	-0.41	0.6931432	0.8475714	-6.46	TRUE

252882_at	Expressed protein ; supported by	---	AT4G39675	1.04	0.05	0.41	0.6931295	0.8475714	-6.46	FALSE
259451_at	synaptosomal associated protei	SNAP30	AT1G13890	1.04	0.06	0.41	0.6932415	0.8476461	-6.46	FALSE
258078_at	unknown protein ;supported by f	---	AT3G25870	1.10	0.14	0.41	0.6933069	0.8476807	-6.46	FALSE
263577_at	putative protein kinase identical t	SSP	AT2G17090	1.06	0.08	0.41	0.693704	0.8480415	-6.46	FALSE
247927_at	unknown protein	---	AT5G57310	1.05	0.07	0.41	0.6936559	0.8480415	-6.46	FALSE
260752_at	unknown protein contains similar	---	AT1G49030	-1.06	-0.08	-0.41	0.6937136	0.8480415	-6.46	FALSE
264021_at	putative auxin-regulated protein	---	AT2G21200	1.11	0.16	0.41	0.6938446	0.8481531	-6.46	FALSE
262909_at	serine/threonine protein phospha	PP2A-1	AT1G59830	-1.05	-0.07	-0.41	0.6938792	0.8481531	-6.46	FALSE
253125_at	DnaJ-like protein DnaJ-like prote	---	AT4G36040	-1.06	-0.09	-0.41	0.6939215	0.8481557	-6.46	FALSE
263721_at	hypothetical protein predicted by	---	AT2G13630	1.05	0.07	0.41	0.6939557	0.8481557	-6.46	FALSE
255437_at	putative oxidoreductase similar t	AOP2	AT4G03060	1.15	0.20	0.41	0.6946587	0.8485878	-6.46	TRUE
255615_at	hypothetical protein	---	AT4G01290	-1.04	-0.05	-0.41	0.694501	0.8485878	-6.46	FALSE
264687_at	cysteine protease XBCP3 identic	XBCP3	AT1G09850	1.04	0.06	0.41	0.6944434	0.8485878	-6.46	FALSE
266121_at	unknown protein ; supported by	---	AT2G02160	-1.06	-0.09	-0.41	0.6944047	0.8485878	-6.46	FALSE
250085_at	unknown protein	---	AT5G17250	-1.06	-0.09	-0.41	0.6945447	0.8485878	-6.46	FALSE
262815_at	putative cytochrome P450 strong	CYP71A18	AT1G11610	1.09	0.13	0.41	0.6946671	0.8485878	-6.46	FALSE
259713_at	unknown protein similar to phos	---	AT1G77610	1.07	0.10	0.41	0.6944541	0.8485878	-6.46	FALSE
256896_at	hypothetical protein predicted by	---	AT3G24630	1.10	0.13	0.41	0.6946813	0.8485878	-6.46	FALSE
249935_at	acyl CoA reductase-like protein	FAR7	AT5G22420	1.04	0.06	0.41	0.6945138	0.8485878	-6.46	FALSE
257936_at	hypothetical protein contains sim	---	---	-1.06	-0.08	-0.41	0.6945792	0.8485878	-6.46	FALSE
256278_at	unknown protein ; supported by f	---	AT3G12130	-1.04	-0.06	-0.41	0.6948417	0.8487383	-6.46	FALSE
246886_at	CLC-d chloride channel protein	CLC-D	AT5G26240	1.05	0.07	0.41	0.6950862	0.8489915	-6.46	FALSE
252414_at	putative protein sn-glycerol-3-ph	---	AT3G47420	-1.07	-0.10	-0.41	0.6952869	0.8490659	-6.46	TRUE
247881_at	putative protein similar to unknov	---	AT5G57700	-1.12	-0.16	-0.41	0.6952817	0.8490659	-6.46	TRUE
267453_at	putative homeodomain transcript	HB-3	AT2G33880	-1.07	-0.10	-0.41	0.6954077	0.8490659	-6.46	FALSE
245403_at	putative protein	---	AT4G17590	1.04	0.06	0.41	0.6953912	0.8490659	-6.46	FALSE
249593_at	putative protein SIAH1 protein, E	---	AT5G37900	1.04	0.06	0.41	0.6953464	0.8490659	-6.46	FALSE
247028_at	DNA polymerase alpha 1	ICU2	AT5G67100	-1.11	-0.15	-0.41	0.6952526	0.8490659	-6.46	FALSE
251715_at	putative protein putative WRKY-	---	AT3G56390	-1.04	-0.06	-0.41	0.695321	0.8490659	-6.46	FALSE
259388_at	steroid sulfotransferase, putative	ST4B	AT1G13420	-1.05	-0.07	-0.41	0.6954635	0.8490886	-6.46	FALSE
254550_at	Fe(II) transport protein ;supporte	IRT1	AT4G19690	-1.04	-0.05	-0.41	0.6955864	0.8491253	-6.46	FALSE
265004_at	polyprotein, putative similar to p	---	---	-1.06	-0.08	-0.41	0.695552	0.8491253	-6.46	FALSE
260742_at	putative glycerol kinase identica	IAA34	AT1G15050	-1.04	-0.06	-0.41	0.6956053	0.8491253	-6.46	FALSE
244932_at	PSI 9KDa protein	---	---	-1.05	-0.08	-0.41	0.6957116	0.8491643	-6.46	FALSE
251465_at	transporter-like protein UDP-gal	UTR6	AT3G59360	-1.04	-0.05	-0.41	0.6956774	0.8491643	-6.46	FALSE

260860_at	hypothetical protein predicted by	---	AT1G43810	1.05	0.07	0.41	0.6958128	0.8492423	-6.46	FALSE
249182_at	putative protein similar to unknov	---	AT5G42960	1.04	0.06	0.41	0.6960089	0.8494362	-6.46	FALSE
260690_at	RING finger protein, putative sin	NHL8	AT1G32340	-1.04	-0.05	-0.41	0.6960958	0.8494968	-6.46	FALSE
254210_at	putative protein zinc finger prote	---	AT4G23450	1.10	0.13	0.41	0.6965967	0.8496116	-6.46	TRUE
251663_at	putative protein hypothetical pro	---	AT3G57070	-1.05	-0.07	-0.41	0.6967968	0.8496116	-6.46	FALSE
259685_at	unknown protein	AtPP2-A11	AT1G63090	1.08	0.11	0.41	0.6968513	0.8496116	-6.46	FALSE
264240_at	protein kinase, putative Simisimi	---	AT1G54820	1.20	0.27	0.41	0.6968573	0.8496116	-6.46	FALSE
263429_at	putative aspartate aminotransfer	AAT	AT2G22250	1.17	0.23	0.41	0.6967881	0.8496116	-6.46	FALSE
257399_at	putative OBP32pep protein	---	AT1G23690	-1.03	-0.05	-0.41	0.6964723	0.8496116	-6.46	FALSE
267293_at	hypothetical protein	TET8	AT2G23810	1.09	0.12	0.41	0.6967464	0.8496116	-6.46	FALSE
258487_at	unknown protein ;supported by f	LBD41	AT3G02550	1.21	0.27	0.41	0.6964018	0.8496116	-6.46	FALSE
265935_at	putative senescence-associated	TET2	AT2G19580	1.08	0.11	0.41	0.6964992	0.8496116	-6.46	FALSE
246647_at	putative protein predicted protein	---	---	1.04	0.06	0.41	0.6963178	0.8496116	-6.46	FALSE
250084_at	unknown protein	SDG40	AT5G17240	-1.07	-0.10	-0.41	0.6966789	0.8496116	-6.46	FALSE
266307_at	putative cytochrome P450	CYP705A8	AT2G27000	-1.05	-0.07	-0.41	0.6965209	0.8496116	-6.46	FALSE
256701_at	transcription initiation factor IIF,	---	AT3G52270	-1.05	-0.07	-0.41	0.6964724	0.8496116	-6.46	FALSE
260977_at	hypothetical protein predicted by	---	AT1G53420	1.05	0.06	0.41	0.6968603	0.8496116	-6.46	FALSE
257490_x_a	Myb homolog (CPC), putative si	ETC1	AT1G01380	-1.03	-0.05	-0.41	0.6962321	0.8496116	-6.46	FALSE
258363_at	putative pectin methylesterase si	ATPMEPCI	AT3G14300	1.05	0.07	0.41	0.6963095	0.8496116	-6.46	FALSE
255404_at	predicted protein	---	AT4G03153	1.05	0.07	0.41	0.6965338	0.8496116	-6.46	FALSE
256847_at	early nodule-specific protein, pu	---	AT3G27950	-1.05	-0.07	-0.41	0.6967144	0.8496116	-6.46	FALSE
244931_at	hypothetical protein	---	---	1.07	0.10	0.41	0.6970682	0.8498197	-6.46	FALSE
260108_at	hypothetical protein similar to put	---	AT1G63280	1.05	0.07	0.41	0.6973035	0.850061	-6.47	FALSE
250373_at	putative protein	---	AT5G11470	1.04	0.05	0.41	0.6974009	0.8501343	-6.47	FALSE
253206_at	putative squalene synthase non-	SQS1	AT4G34640	-1.05	-0.07	-0.41	0.6974393	0.8501358	-6.47	FALSE
257385_at	hypothetical protein predicted by	---	AT2G01800	-1.05	-0.07	-0.41	0.6974825	0.850143	-6.47	FALSE
248479_at	unknown protein	---	AT5G50910	1.04	0.05	0.41	0.6976062	0.8502483	-6.47	FALSE
248300_at	PP2A regulatory subunit ;suppor	TAP46	AT5G53000	1.06	0.09	0.40	0.6980569	0.8507068	-6.47	FALSE
266443_at	putative myb-related transcription	---	AT2G43270	-1.04	-0.05	-0.41	0.6980253	0.8507068	-6.47	#VALUE!
246424_at	Exportin1 (XPO1) protein ; supp	XPO1A	AT5G17020	-1.05	-0.08	-0.40	0.6983079	0.8507379	-6.47	FALSE
261370_at	cell division-related protein, puta	---	AT1G53050	-1.04	-0.06	-0.40	0.6982479	0.8507379	-6.47	FALSE
262609_at	unknown protein ;supported by fu	---	AT1G13930	-1.05	-0.08	-0.40	0.6983183	0.8507379	-6.47	FALSE
265808_at	hypothetical protein predicted by	---	AT2G17960	1.04	0.06	0.40	0.6981847	0.8507379	-6.47	FALSE
257503_at	DAG-like protein similar to DAG	---	AT1G72530	-1.06	-0.09	-0.40	0.6983436	0.8507379	-6.47	FALSE
255592_s_a	hypothetical protein	---	AT2G34280 ///	-1.05	-0.08	-0.40	0.6982599	0.8507379	-6.47	FALSE

264631_at	DegP protease contains similarity	DegP3	AT1G65630	-1.05	-0.07	-0.40	0.6981601	0.8507379	-6.47	FALSE
256500_at	Ty1/copia-element polyprotein	---	---	1.05	0.07	0.40	0.6984197	0.8507397	-6.47	FALSE
255705_at	hypothetical protein ;supported b	---	AT4G00160	-1.04	-0.06	-0.40	0.698387	0.8507397	-6.47	FALSE
249093_at	putative protein similar to unknov	---	AT5G43880	-1.04	-0.06	-0.40	0.6985076	0.8508014	-6.47	TRUE
250870_at	hypothetical protein	---	AT5G03920	-1.05	-0.06	-0.40	0.6985546	0.8508133	-6.47	FALSE
263656_at	putative auxin-induced protein AU	SHY2	AT1G04240	-1.26	-0.33	-0.40	0.6986754	0.8509149	-6.47	TRUE
256376_s_a	unknown protein	PXMT1	AT1G66690 ///	-1.16	-0.21	-0.40	0.6987573	0.8509238	-6.47	TRUE
250924_at	putative protein ;supported by fu	---	AT5G03440	1.05	0.07	0.40	0.6987343	0.8509238	-6.47	FALSE
244954_s_a	hypothetical protein	---	AT2G07732	1.10	0.14	0.40	0.6989668	0.85106	-6.47	FALSE
254748_at	unknown protein	---	---	-1.04	-0.06	-0.40	0.6989424	0.85106	-6.47	FALSE
259949_at	hypothetical protein predicted by	---	AT1G71420	1.05	0.07	0.40	0.6989811	0.85106	-6.47	FALSE
258000_at	AIG2-like protein similar to AIG2	---	AT3G28940	1.09	0.12	0.40	0.6992448	0.8513302	-6.47	TRUE
255179_at	putative transposon protein	---	---	1.03	0.05	0.40	0.6992776	0.8513302	-6.47	FALSE
266542_at	unknown protein	ARAD1	AT2G35100	1.04	0.06	0.40	0.6993567	0.851381	-6.47	FALSE
254374_at	hypothetical protein ;supported b	---	AT4G21780	1.04	0.06	0.40	0.6994024	0.8513913	-6.47	FALSE
262894_at	disease resistance protein, puta	---	AT1G59780	-1.05	-0.07	-0.40	0.6995123	0.8514659	-6.47	FALSE
247840_at	putative protein protein x 0001, l	---	AT5G58020	1.04	0.05	0.40	0.6995384	0.8514659	-6.47	FALSE
254781_at	putative protein putative protein	---	AT4G12840	1.04	0.06	0.40	0.6996207	0.8515206	-6.47	FALSE
261917_at	hypothetical protein similar to TM	---	AT1G65920	-1.10	-0.14	-0.40	0.6997735	0.8515993	-6.47	FALSE
252755_at	putative protein hypothetical prot	---	---	1.05	0.07	0.40	0.6997974	0.8515993	-6.47	FALSE
258020_at	unknown protein ;supported by f	NHD1	AT3G19490	-1.05	-0.07	-0.40	0.6997749	0.8515993	-6.47	FALSE
255127_at	nodulin-like protein nodulin gene	---	AT4G08300	-1.18	-0.24	-0.40	0.7000055	0.8517035	-6.47	TRUE
261013_at	fatty acid elongase 3-ketoacyl-Co	ATUPS5	AT1G26440	1.07	0.09	0.40	0.7000181	0.8517035	-6.47	FALSE
252761_at	putative protein several hypothet	---	AT3G42770	1.08	0.10	0.40	0.6999542	0.8517035	-6.47	FALSE
262681_at	anter-specific proline-rich -like pr	---	AT1G75890	1.04	0.05	0.40	0.7000323	0.8517035	-6.47	FALSE
260587_at	unknown protein ; supported by c	---	AT1G53210	-1.05	-0.07	-0.40	0.7002975	0.8517535	-6.47	FALSE
255882_x_a	hypothetical protein contains sim	---	AT1G20280	-1.05	-0.07	-0.40	0.7001829	0.8517535	-6.47	FALSE
248988_at	putative protein contains similarit	---	AT5G45190	-1.05	-0.07	-0.40	0.7001479	0.8517535	-6.47	FALSE
250445_at	nucleoid DNA-binding protein cn	---	AT5G10760	-1.37	-0.46	-0.40	0.700216	0.8517535	-6.47	FALSE
260130_s_a	beta-glucosidase, putative simila	BGLU21	AT1G66270 ///	-1.04	-0.05	-0.40	0.7002752	0.8517535	-6.47	FALSE
261028_at	hypothetical protein predicted by	---	AT1G26620	1.05	0.06	0.40	0.7002309	0.8517535	-6.47	FALSE
262210_at	hypothetical protein predicted by	IQD31	AT1G74690	-1.11	-0.15	-0.40	0.7004156	0.8518063	-6.47	TRUE
255746_at	heat shock transcription factor, p	---	AT1G32020	-1.04	-0.06	-0.40	0.7003846	0.8518063	-6.47	FALSE
260490_at	ATP-dependent transmembrane	CER5	AT1G51500	-1.09	-0.13	-0.40	0.7005169	0.8518842	-6.47	TRUE
256925_at	hypothetical protein predicted by	---	---	1.04	0.06	0.40	0.7006242	0.8519692	-6.47	FALSE

252243_at	putative protein some putative pr	---	AT3G50120	-1.10	-0.14	-0.40	0.7007369	0.8520608	-6.47	FALSE
248604_at	protein kinase	---	AT5G49470	-1.08	-0.11	-0.40	0.701	0.8523352	-6.47	FALSE
250680_at	putative protein similar to unknov	---	AT5G06570	-1.11	-0.15	-0.40	0.7011461	0.8524604	-6.47	TRUE
246882_at	putative protein predicted protei	---	AT5G26180	-1.04	-0.06	-0.40	0.7013102	0.8524604	-6.47	FALSE
260436_at	unknown protein	---	AT1G68140	1.06	0.08	0.40	0.7012738	0.8524604	-6.47	FALSE
257886_at	pectinesterase, putative similar t	---	AT3G17060	1.05	0.07	0.40	0.7013271	0.8524604	-6.47	FALSE
248396_at	unknown protein	---	AT5G52130	1.05	0.07	0.40	0.7012307	0.8524604	-6.47	FALSE
254706_at	putative protein DNA-binding pro	---	AT4G17950	-1.06	-0.09	-0.40	0.7012704	0.8524604	-6.47	FALSE
262035_at	polyprotein, putative similar to p	---	---	1.04	0.06	0.40	0.7013733	0.8524711	-6.47	FALSE
254572_at	putative protein predicted protei	---	AT4G19380	-1.04	-0.06	-0.40	0.70143	0.8524946	-6.47	FALSE
256702_at	unknown protein contains Pfam p	---	AT3G30380	1.07	0.10	0.40	0.7016389	0.8527031	-6.47	FALSE
265303_at	hypothetical protein	---	---	1.04	0.06	0.40	0.7017069	0.8527402	-6.47	FALSE
248802_at	Expressed protein ; supported by	---	AT5G47435	-1.05	-0.07	-0.40	0.7019635	0.8528255	-6.47	FALSE
256988_s_a	adenosine triphosphatase, putat	---	AT3G28710 ///	-1.04	-0.05	-0.40	0.7019746	0.8528255	-6.47	FALSE
254156_at	Rab geranylgeranyl transferase	---	AT4G24490	-1.06	-0.09	-0.40	0.7019452	0.8528255	-6.47	FALSE
251050_at	putative protein	---	AT5G02440	1.05	0.07	0.40	0.7019691	0.8528255	-6.47	FALSE
245820_at	allyl alcohol dehydrogenase, put	---	AT1G26320	1.04	0.06	0.40	0.7018278	0.8528255	-6.47	FALSE
261082_at	unknown protein ; supported by c	---	AT1G07360	-1.04	-0.05	-0.40	0.7020014	0.8528255	-6.47	FALSE
259211_at	unknown protein identical to GB:	---	AT3G09020	1.18	0.23	0.40	0.7020809	0.8528767	-6.47	TRUE
245764_s_a	hypothetical protein contains sim	ATCSA-1	AT1G19750 ///	-1.04	-0.06	-0.40	0.7021232	0.8528826	-6.47	FALSE
248008_at	transcription factor NtWRKY4-lik	WRKY2	AT5G56270	-1.07	-0.10	-0.40	0.702519	0.8530502	-6.47	FALSE
266273_at	putative zinc transporter	MTPB1	AT2G29410	1.18	0.24	0.40	0.702523	0.8530502	-6.47	FALSE
262765_at	putative cytochrome P450 mono	CYP86C4	AT1G13150	1.05	0.07	0.40	0.7025229	0.8530502	-6.47	FALSE
247233_at	mitochondrial carrier protein-like	---	AT5G64970	-1.05	-0.07	-0.40	0.7023679	0.8530502	-6.47	FALSE
250882_at	putative protein ;supported by fu	---	AT5G04000	-1.04	-0.06	-0.40	0.7023893	0.8530502	-6.47	FALSE
257197_at	selenium binding protein, putativ	SBP3	AT3G23800	1.04	0.06	0.40	0.702414	0.8530502	-6.47	FALSE
263741_at	hypothetical protein predicted by	---	AT2G20620	1.06	0.08	0.40	0.7024518	0.8530502	-6.47	FALSE
250807_at	helicase-like transcription factor-	---	AT5G05130	-1.06	-0.08	-0.40	0.7028852	0.853417	-6.47	FALSE
249980_at	putative protein	---	AT5G18870	-1.05	-0.07	-0.40	0.7028999	0.853417	-6.47	FALSE
251863_at	kinesin-like protein kinesin, Syn	MRH2	AT3G54870	1.04	0.05	0.40	0.7029471	0.853429	-6.47	FALSE
249556_at	Expressed protein ; supported by	---	AT5G38195	-1.04	-0.06	-0.40	0.7030276	0.8534359	-6.47	FALSE
255386_at	hypothetical protein	---	AT4G03620	-1.04	-0.06	-0.40	0.703003	0.8534359	-6.47	FALSE
263604_s_a	putative replication protein A1	---	---	-1.03	-0.05	-0.40	0.7030655	0.8534365	-6.47	FALSE
262827_at	putative cytochrome P450 mono	CYP71B29	AT1G13100	1.10	0.13	0.40	0.7032693	0.8536384	-6.47	FALSE
248646_at	unknown protein ;supported by f	---	AT5G49100	1.10	0.13	0.40	0.703417	0.8537268	-6.47	FALSE

266491_at	putative retroelement pol polypro	---	---	-1.04	-0.06	-0.40	0.7033806	0.8537268	-6.47	FALSE
258552_at	putative pectate lyase similar to p	---	AT3G07010	1.30	0.38	0.40	0.7034611	0.8537291	-6.47	FALSE
248319_at	unknown protein	---	AT5G52710	1.04	0.06	0.40	0.7034938	0.8537291	-6.47	FALSE
259177_at	hypothetical protein similar to put	---	AT3G01630	1.04	0.06	0.40	0.7035954	0.8537617	-6.47	FALSE
258118_at	unknown protein	---	AT3G14710	1.06	0.08	0.40	0.7035927	0.8537617	-6.47	FALSE
252927_at	cysteine proteinase RD19A iden	RD19	AT4G39090	-1.04	-0.06	-0.40	0.7038655	0.853955	-6.47	FALSE
264654_s_a	putative sugar transport protein,	---	AT1G08890 /A	-1.08	-0.11	-0.40	0.7038671	0.853955	-6.47	FALSE
248703_at	dermal glycoprotein precursor, e	---	AT5G48430	1.40	0.48	0.40	0.7038393	0.853955	-6.47	FALSE
254962_at	putative glucanase endo-beta-1,	AtGH9C3	AT4G11050	1.05	0.07	0.40	0.7039625	0.85398	-6.47	FALSE
249665_at	unknown protein	---	AT5G35830	1.05	0.07	0.40	0.7039579	0.85398	-6.47	FALSE
262002_at	hypothetical protein predicted by	---	AT1G64450	1.04	0.05	0.40	0.7041581	0.8541717	-6.47	FALSE
261983_at	protein kinase, putative similar t	---	AT1G33770	1.08	0.11	0.40	0.7042715	0.8542566	-6.47	FALSE
247471_at	putative protein receptor-like pro	ERL1	AT5G62230	1.05	0.07	0.40	0.704345	0.8542566	-6.47	FALSE
253870_at	putative protein	---	AT4G27530	1.05	0.07	0.40	0.7043628	0.8542566	-6.47	FALSE
258571_at	hypothetical protein predicted by	anac048	AT3G04420	1.05	0.07	0.40	0.7043778	0.8542566	-6.47	FALSE
256347_at	unknown protein similar to putati	---	---	-1.05	-0.07	-0.40	0.7045465	0.8544158	-6.47	FALSE
253408_at	putative protein phosphoprotein	---	AT4G32950	1.04	0.05	0.40	0.7046579	0.8544768	-6.47	FALSE
247888_at	phytocyanin/early nodulin-like pr	---	AT5G57920	-1.05	-0.07	-0.40	0.7046718	0.8544768	-6.47	FALSE
263278_at	dynamin-like protein	DRP3B	AT2G14120	-1.05	-0.07	-0.40	0.704895	0.8546812	-6.47	FALSE
259737_at	acyl-CoA synthetase, putative si	---	AT1G64400	1.15	0.20	0.40	0.7049153	0.8546812	-6.47	FALSE
256776_at	multispanning membrane protei	---	AT3G13772	1.04	0.06	0.39	0.7052587	0.855017	-6.47	FALSE
264029_at	unknown protein	MRH6	AT2G03720	1.05	0.06	0.39	0.7052672	0.855017	-6.47	FALSE
255590_at	cathepsin B-like cysteine protea	---	AT4G01610	-1.06	-0.08	-0.39	0.7053719	0.8550248	-6.47	TRUE
263879_at	hypothetical protein predicted by	---	AT2G22030	1.04	0.06	0.39	0.7053861	0.8550248	-6.47	FALSE
253510_at	hypothetical protein	GDU1	AT4G31730	1.10	0.14	0.39	0.7053813	0.8550248	-6.47	FALSE
262020_at	polyprotein, putative similar to g	---	---	-1.04	-0.06	-0.39	0.7055371	0.8551624	-6.47	FALSE
260710_at	protein phosphatase 2C, putativ	---	AT1G17545	1.04	0.06	0.39	0.7056635	0.8552701	-6.47	FALSE
262695_at	vacuolor sorting protein 35, puta	VPS35B	AT1G75850	1.04	0.06	0.39	0.7059634	0.8555551	-6.47	FALSE
250947_at	putative protein	---	AT5G03450	-1.06	-0.08	-0.39	0.7059736	0.8555551	-6.47	FALSE
247768_at	I-box binding factor - like protein	---	AT5G58900	-1.14	-0.19	-0.39	0.7061073	0.8555808	-6.47	TRUE
245675_at	hypothetical protein similar to put	---	---	1.07	0.09	0.39	0.7060922	0.8555808	-6.47	FALSE
257591_at	leucine-rich repeat disease resis	AtRLP39	AT3G24900	1.03	0.05	0.39	0.7060383	0.8555808	-6.47	FALSE
249995_at	protein kinase -like protein prote	---	AT5G18610	-1.04	-0.05	-0.39	0.7063244	0.8557983	-6.47	FALSE
255157_at	hypothetical protein	---	---	1.03	0.05	0.39	0.7063992	0.8558435	-6.47	FALSE
257923_at	hypothetical protein predicted by	---	AT3G23160	1.12	0.17	0.39	0.7064454	0.8558541	-6.47	TRUE

260905_at	hypothetical protein predicted by	---	AT1G02710	1.03	0.05	0.39	0.706557	0.8558796	-6.47	FALSE
262144_at	hypothetical protein predicted by	---	AT1G52620	1.04	0.06	0.39	0.7065554	0.8558796	-6.47	FALSE
265995_at	hypothetical protein predicted by	---	AT2G24140	1.04	0.06	0.39	0.7065791	0.8558796	-6.47	FALSE
248782_at	palmitoyl-protein thioesterase pre	---	AT5G47340	1.05	0.06	0.39	0.7066268	0.8558919	-6.47	FALSE
249174_at	putative protein similar to unknov	---	AT5G42900	1.09	0.12	0.39	0.706792	0.855956	-6.47	FALSE
255772_at	calmodulin, putative similar to ca	---	AT1G18530	-1.05	-0.07	-0.39	0.7067272	0.855956	-6.47	FALSE
245203_at	hypothetical protein similar to pro	---	---	1.04	0.05	0.39	0.7067922	0.855956	-6.47	FALSE
244956_s_a	hypothetical protein	---	---	1.05	0.07	0.39	0.7069623	0.8561164	-6.47	FALSE
262034_at	hypothetical protein predicted by	---	---	1.04	0.06	0.39	0.7071084	0.8562475	-6.47	FALSE
248123_at	putative protein similar to unknov	---	AT5G54720	1.04	0.06	0.39	0.7071455	0.8562475	-6.47	FALSE
262871_at	hypothetical protein predicted by	---	AT1G65010	-1.15	-0.20	-0.39	0.7072603	0.8562852	-6.47	TRUE
250355_at	putative protein predicted protei	---	AT5G11700	1.05	0.08	0.39	0.7072894	0.8562852	-6.47	FALSE
247221_at	Expressed protein ; supported by	LIP1	AT5G64813	1.04	0.05	0.39	0.7072442	0.8562852	-6.47	FALSE
264829_at	hypothetical protein predicted by	ANAC006	AT1G03490	-1.04	-0.05	-0.39	0.7073608	0.8563263	-6.47	FALSE
266163_at	hypothetical protein predicted by	---	AT2G28130	-1.07	-0.10	-0.39	0.7075368	0.8564126	-6.47	TRUE
264172_at	unknown protein	VAD1	AT1G02120	1.07	0.09	0.39	0.7075483	0.8564126	-6.47	FALSE
248569_at	receptor protein kinase-like	---	AT5G49770	-1.05	-0.07	-0.39	0.7075823	0.8564126	-6.47	FALSE
250435_at	putative protein various predicte	RING1	AT5G10380	1.10	0.14	0.39	0.7075491	0.8564126	-6.47	FALSE
256104_at	trehalose-6-phosphate synthase	ATTPS2	AT1G16980	1.04	0.06	0.39	0.7076477	0.8564186	-6.47	FALSE
255209_at	see GB:AF077408	---	---	1.05	0.07	0.39	0.7076999	0.8564186	-6.47	FALSE
249206_at	putative protein similar to unknov	ATS	AT5G42630	-1.06	-0.08	-0.39	0.7076643	0.8564186	-6.47	FALSE
247426_at	putative protein contains similarit	---	AT5G62570	1.09	0.12	0.39	0.7077457	0.8564286	-6.47	FALSE
251115_at	putative protein symplekin - Hon	ESP4	AT5G01400	-1.05	-0.06	-0.39	0.7079754	0.8566612	-6.47	FALSE
262337_at	hypothetical protein similar to hyp	---	AT1G64260	1.05	0.07	0.39	0.7080661	0.8567255	-6.47	FALSE
254309_s_a	putative protein predicted protei	---	AT4G22390 /	-1.05	-0.08	-0.39	0.7082104	0.8568545	-6.47	FALSE
253164_at	Expressed protein ; supported by	---	AT4G35725	1.04	0.06	0.39	0.708281	0.8568946	-6.47	FALSE
245361_at	hypothetical protein ;supported b	---	AT4G17790	1.09	0.12	0.39	0.7084225	0.8570203	-6.47	FALSE
259725_at	Expressed protein ; supported by	---	AT1G61065	-1.07	-0.10	-0.39	0.7085925	0.8571252	-6.47	FALSE
259421_at	disease resistance protein, puta	---	AT1G13910	1.06	0.08	0.39	0.7086242	0.8571252	-6.47	FALSE
266133_at	putative C2H2-type zinc finger pr	---	AT2G45120	1.04	0.06	0.39	0.7086596	0.8571252	-6.47	FALSE
256623_at	myosin identical to myosin GB:C/	ATM1	AT3G19960	1.05	0.07	0.39	0.708583	0.8571252	-6.47	FALSE
248794_at	ethylene responsive element bin	ERF2	AT5G47220	-1.24	-0.31	-0.39	0.7089068	0.8572425	-6.47	FALSE
246242_at	putative protein	---	AT4G36600	1.07	0.09	0.39	0.7088477	0.8572425	-6.47	FALSE
257483_at	hypothetical protein contains sim	ICK5	AT1G49620	1.04	0.06	0.39	0.708883	0.8572425	-6.47	FALSE
258103_at	hypothetical protein contains Pfa	IPT7	AT3G23630	-1.06	-0.08	-0.39	0.7088351	0.8572425	-6.47	FALSE

263028_at	protein kinase, putative similar t	---	AT1G24030	1.06	0.09	0.39	0.7090225	0.8572666	-6.47	FALSE
259560_at	hypothetical protein	WAK2	AT1G21270	1.15	0.20	0.39	0.7089698	0.8572666	-6.47	FALSE
263282_at	Expressed protein ; supported by	---	AT2G14095	1.04	0.06	0.39	0.7090395	0.8572666	-6.47	FALSE
260216_at	hypothetical protein contains Pfa	---	AT1G74580	-1.04	-0.06	-0.39	0.7091683	0.8573768	-6.47	FALSE
266278_at	putative tropinone reductase	---	AT2G29300	-1.12	-0.17	-0.39	0.7092078	0.8573791	-6.47	FALSE
246835_at	putative protein putative APC11	---	AT5G26640	1.05	0.08	0.39	0.7092655	0.8574035	-6.47	FALSE
249642_at	putative protein	---	AT5G36960	-1.05	-0.07	-0.39	0.7093863	0.8575041	-6.47	FALSE
261727_at	S-adenosyl-methionine-sterol-C	SMT3	AT1G76090	1.09	0.12	0.39	0.7098069	0.8575624	-6.47	TRUE
263548_at	glycine-rich RNA binding protein	CCR2	AT2G21660 /	1.05	0.07	0.39	0.7099923	0.8575624	-6.47	FALSE
267208_at	putative shaggy-like protein kinas	ASKdZeta	AT2G30980	1.04	0.05	0.39	0.7098351	0.8575624	-6.47	FALSE
258238_at	unknown protein	RST1	AT3G27670	-1.04	-0.05	-0.39	0.7099579	0.8575624	-6.47	FALSE
266859_at	putative MADS-box protein	AGL41	AT2G26880	1.05	0.07	0.39	0.7098956	0.8575624	-6.47	FALSE
266135_at	putative transcription factor IIIB 7	---	AT2G45100	-1.08	-0.11	-0.39	0.7096885	0.8575624	-6.47	FALSE
265144_at	putative serine/threonine protein	---	AT1G51170	-1.06	-0.09	-0.39	0.7096906	0.8575624	-6.47	FALSE
265493_at	unknown protein predicted by ge	---	AT2G15670	1.04	0.06	0.39	0.7098073	0.8575624	-6.47	FALSE
255642_at	hypothetical protein	iqd17	AT4G00820	-1.08	-0.11	-0.39	0.7100361	0.8575624	-6.47	FALSE
264182_at	MADS-box protein, putative simi	AGL23	AT1G65360	-1.04	-0.06	-0.39	0.7097795	0.8575624	-6.47	FALSE
266849_at	putative vacuolar processing enz	ALPHA-VP	AT2G25940	1.04	0.06	0.39	0.7098329	0.8575624	-6.47	FALSE
256768_at	hypothetical protein predicted by	LDL2	AT3G13682	-1.04	-0.05	-0.39	0.7096298	0.8575624	-6.47	FALSE
261862_at	DNA-binding protein, putative si	---	AT1G50410	-1.06	-0.08	-0.39	0.7100098	0.8575624	-6.47	FALSE
257316_at	hypothetical protein predicted by	---	---	1.04	0.06	0.39	0.709945	0.8575624	-6.47	FALSE
265421_s_a	predicted protein	---	AT2G20616 /	1.05	0.07	0.39	0.7097976	0.8575624	-6.47	FALSE
250121_at	protein kinase-like protein	---	AT5G16500	1.04	0.05	0.39	0.7099433	0.8575624	-6.47	FALSE
250298_at	putative protein NLI-interacting f	---	AT5G11860	1.05	0.07	0.39	0.7102838	0.8577876	-6.47	FALSE
258548_at	hypothetical protein	ULP1A	AT3G06910	-1.06	-0.08	-0.39	0.7103252	0.8577876	-6.47	FALSE
257015_at	hypothetical protein predicted by	---	AT3G28680	1.05	0.07	0.39	0.7103354	0.8577876	-6.47	FALSE
267038_at	expressed protein supported by c	---	AT2G38480	1.12	0.16	0.39	0.7105736	0.8580298	-6.47	TRUE
254795_at	putative protein	---	AT4G12990	1.04	0.06	0.39	0.7106325	0.8580556	-6.47	FALSE
249038_at	putative protein contains similarit	RING1A	AT5G44280	1.05	0.07	0.39	0.710756	0.8581592	-6.47	FALSE
248097_at	protein phosphatase X isoform 2	PPX2	AT5G55260	-1.05	-0.07	-0.39	0.7109847	0.8581759	-6.47	FALSE
254577_at	putative protein ;supported by fu	---	AT4G19450	-1.07	-0.09	-0.39	0.71102	0.8581759	-6.47	FALSE
251886_at	putative protein various predicte	---	AT3G54260	-1.08	-0.10	-0.39	0.7108192	0.8581759	-6.47	FALSE
251459_at	putative protein hypothetical pro	---	AT3G60200	1.13	0.18	0.39	0.7110036	0.8581759	-6.47	FALSE
261347_at	unknown protein	ELF7	AT1G79730	1.05	0.07	0.39	0.7109813	0.8581759	-6.47	FALSE
248512_at	protein translocation complex Se	SIG2	AT1G08540 /	1.09	0.13	0.39	0.7110332	0.8581759	-6.47	FALSE

252098_at	putative protein several hypothet	---	AT3G51330	1.16	0.22	0.39	0.7108508	0.8581759	-6.47	FALSE
256891_at	hypothetical protein contains sim	---	AT3G19030	1.06	0.08	0.39	0.711291	0.858382	-6.47	TRUE
258859_at	Expressed protein ; supported by	---	AT3G02120	-1.03	-0.05	-0.39	0.7114297	0.858382	-6.47	FALSE
249943_at	putative protein similar to unknov	---	AT5G22280	-1.09	-0.13	-0.39	0.7113884	0.858382	-6.47	FALSE
255350_at	putative transposon protein simil	---	---	-1.04	-0.05	-0.39	0.7114024	0.858382	-6.47	FALSE
251435_at	putative protein hypothetical prot	---	---	-1.04	-0.06	-0.39	0.7112826	0.858382	-6.47	FALSE
255758_at	hypothetical protein predicted by	---	AT1G16800	1.04	0.06	0.39	0.7114287	0.858382	-6.47	FALSE
267229_s_a	putative translation initiation facto	---	AT2G44070 /	-1.09	-0.13	-0.39	0.7116014	0.8585006	-6.47	FALSE
255114_at	putative protein various putative	---	---	1.06	0.09	0.39	0.7116033	0.8585006	-6.47	FALSE
261778_at	hypothetical protein predicted by	---	AT1G76220	1.03	0.05	0.39	0.7116956	0.8585666	-6.47	FALSE
264769_at	hypothetical protein predicted by	---	AT1G61350	-1.10	-0.14	-0.39	0.7117731	0.8586146	-6.47	FALSE
259559_at	hypothetical protein	WAK3	AT1G21240	-1.07	-0.10	-0.39	0.7119236	0.858646	-6.47	FALSE
264961_at	unknown protein contains similar	PRAF1	AT1G76950	-1.09	-0.13	-0.39	0.7119081	0.858646	-6.47	FALSE
267546_at	putative disease resistance prote	AtRLP23	AT2G32680	1.24	0.31	0.39	0.7119393	0.858646	-6.47	FALSE
256368_at	cinnamyl alcohol dehydrogenase	---	AT1G66800	-1.04	-0.06	-0.39	0.7119496	0.858646	-6.47	FALSE
246516_at	putative protein auxin-independe	---	AT5G15740	-1.16	-0.22	-0.39	0.7119918	0.8586514	-6.47	FALSE
262081_at	kinesin motor protein (kin2), puta	ZCF125	AT1G59540	-1.05	-0.07	-0.39	0.7120759	0.8587074	-6.47	FALSE
252335_at	putative protein putative protein	---	AT3G48860	-1.05	-0.07	-0.38	0.7123167	0.8587972	-6.47	FALSE
259672_at	DNA-directed RNA polymerase	---	AT1G68990	-1.12	-0.16	-0.38	0.7123242	0.8587972	-6.47	FALSE
245524_at	cytochrome c oxidoreductase like	---	AT4G15920	-1.13	-0.18	-0.38	0.7123762	0.8587972	-6.47	FALSE
262723_at	hypothetical protein predicted by	---	AT1G43630	1.06	0.08	0.38	0.7123579	0.8587972	-6.47	FALSE
264135_at	S-locus protein, putative similar	---	AT1G79030	-1.04	-0.06	-0.38	0.7122431	0.8587972	-6.47	FALSE
257388_at	putative non-LTR retroelement re	---	---	1.03	0.05	0.38	0.7123666	0.8587972	-6.47	FALSE
264625_at	hypothetical protein Contains sim	SNF4	AT1G09020	1.04	0.06	0.38	0.7126055	0.8589374	-6.47	FALSE
254470_at	putative protein other hypothetica	---	---	1.06	0.08	0.38	0.7125315	0.8589374	-6.47	FALSE
259223_at	hypothetical protein	WOX11	AT3G03660	1.04	0.06	0.38	0.7125935	0.8589374	-6.47	FALSE
263043_at	conserved hypothetical protein p	---	AT1G23350	1.05	0.07	0.38	0.7126676	0.8589669	-6.47	FALSE
265349_at	putative kinesin heavy chain	---	AT2G22610	1.05	0.07	0.38	0.7129211	0.8590896	-6.47	FALSE
245214_at	F12A21.1 hypothetical protein	---	AT1G67855	-1.04	-0.06	-0.38	0.7129508	0.8590896	-6.47	FALSE
262139_at	mutator-like transposase, putativ	AT1G52615	---	-1.04	-0.05	-0.38	0.7128323	0.8590896	-6.47	FALSE
249881_at	cytochrome P450-like protein	CYP86B1	AT5G23190	1.04	0.05	0.38	0.7129577	0.8590896	-6.47	FALSE
248734_at	putative protein similar to unknov	ELP1	AT5G48090	-1.06	-0.09	-0.38	0.7128879	0.8590896	-6.47	FALSE
249523_at	cytochrome b-561 (gb|AAD4558	ACYB-1	AT5G38630	-1.04	-0.06	-0.38	0.7131188	0.8592113	-6.47	FALSE
249776_at	unknown protein	---	AT5G24170	1.06	0.08	0.38	0.713134	0.8592113	-6.47	FALSE
263296_at	unknown protein	---	AT2G38800	1.09	0.13	0.38	0.7133264	0.8593976	-6.47	FALSE

254888_at	putative protein predicted protei	---	AT4G11780	-1.04	-0.06	-0.38	0.7135746	0.8595604	-6.48	FALSE
254538_at	putative protein chitinase / lysoz	---	AT4G19740	-1.04	-0.06	-0.38	0.7135564	0.8595604	-6.48	FALSE
251027_at	putative protein hypothetical pro	---	AT5G02210	-1.03	-0.05	-0.38	0.713572	0.8595604	-6.48	FALSE
257783_at	unknown protein	---	AT3G26950	-1.04	-0.06	-0.38	0.7137317	0.8595652	-6.48	FALSE
263556_at	hypothetical protein predicted by	---	AT2G16365	1.05	0.07	0.38	0.7138008	0.8595652	-6.48	FALSE
261612_at	fucosyltransferase c3 protein, pu	FUT12	AT1G49710	-1.04	-0.06	-0.38	0.7138046	0.8595652	-6.48	FALSE
255671_at	Expressed protein ; supported by	---	AT4G00355	-1.05	-0.07	-0.38	0.7138043	0.8595652	-6.48	FALSE
258112_at	putative cytochrome P450 simila	CYP72A10	AT3G14640	1.05	0.06	0.38	0.7137786	0.8595652	-6.48	FALSE
254843_at	putative protein TAK1 binding pr	---	AT4G11860	1.04	0.05	0.38	0.7137451	0.8595652	-6.48	FALSE
257091_at	DNA polymerase, putative C-ter	POLGAMM	AT3G20540	1.06	0.09	0.38	0.7138618	0.8595886	-6.48	FALSE
256258_at	unknown protein	NF-YC11	AT3G12480	1.04	0.05	0.38	0.7139945	0.859703	-6.48	FALSE
247079_at	Expressed protein ; supported by	AKRP	AT5G66055	-1.07	-0.09	-0.38	0.7141339	0.8598114	-6.48	TRUE
261188_at	hypothetical protein contains sim	---	---	1.05	0.07	0.38	0.7141599	0.8598114	-6.48	FALSE
249303_at	putative protein strong similarity t	---	AT5G41460	-1.07	-0.10	-0.38	0.7143274	0.8599678	-6.48	FALSE
262796_at	cysteine proteinase XCP2 identic	XCP2	AT1G20850	-1.12	-0.17	-0.38	0.714592	0.8601714	-6.48	TRUE
251113_at	hypothetical protein	---	AT5G01370	-1.05	-0.08	-0.38	0.7146368	0.8601714	-6.48	FALSE
248857_at	putative protein contains similarit	---	AT5G46640	-1.09	-0.12	-0.38	0.7145903	0.8601714	-6.48	FALSE
245511_at	hypothetical protein	---	AT4G15755	1.04	0.05	0.38	0.7146474	0.8601714	-6.48	FALSE
257815_at	unknown protein	---	AT3G25130	-1.04	-0.06	-0.38	0.7147691	0.860227	-6.48	FALSE
255489_at	predicted protein destination fac	---	AT4G02650 ///	1.06	0.08	0.38	0.7147451	0.860227	-6.48	FALSE
245637_at	hypothetical protein similar to put	---	AT1G25230	1.14	0.18	0.38	0.7149133	0.8603552	-6.48	FALSE
266790_at	expansin AtEx6 identical to GB U	ATEXPA6	AT2G28950	1.22	0.29	0.38	0.7150185	0.860391	-6.48	FALSE
267369_at	unknown protein ;supported by f	---	AT2G44420	1.05	0.07	0.38	0.7150078	0.860391	-6.48	FALSE
246115_at	putative protein chloroplast oute	---	AT5G20300	-1.05	-0.07	-0.38	0.7150693	0.8604068	-6.48	FALSE
251656_at	putative protein N-ACETYLGLU	---	AT3G57170	-1.05	-0.06	-0.38	0.715232	0.860425	-6.48	FALSE
247832_at	putative protein predicted protei	EOL2	AT5G58550	-1.05	-0.07	-0.38	0.7152354	0.860425	-6.48	FALSE
253914_at	putative protein late embryogene	---	AT4G27400	1.07	0.09	0.38	0.7151536	0.860425	-6.48	FALSE
258130_at	unknown protein	---	AT3G24510	-1.04	-0.06	-0.38	0.715229	0.860425	-6.48	FALSE
251660_at	Expressed protein ; supported by	---	AT3G57160	1.06	0.09	0.38	0.7153353	0.8604999	-6.48	FALSE
260847_s_a	alanine aminotransferase, putati	AlaAT1	AT1G17290 ///	1.04	0.06	0.38	0.7153881	0.860505	-6.48	FALSE
265666_at	putative rac GTPase activating p	---	AT2G27440	-1.03	-0.05	-0.38	0.7154151	0.860505	-6.48	FALSE
247314_at	3(2),5-bisphosphate nucleotidas	SAL2	AT5G64000	-1.12	-0.17	-0.38	0.7155087	0.8605723	-6.48	TRUE
255562_at	G/T DNA mismatch repair enzym	MSH6	AT4G02070	-1.06	-0.08	-0.38	0.7155646	0.8605872	-6.48	FALSE
264827_at	hypothetical protein similar to ant	---	AT1G03390	-1.04	-0.06	-0.38	0.7155965	0.8605872	-6.48	FALSE
246314_at	promoter-binding factor-like prot	AREB3	AT3G56850	-1.05	-0.07	-0.38	0.7156979	0.8606637	-6.48	FALSE

264977_at	unknown protein	---	AT1G27090	1.07	0.10	0.38	0.7157948	0.8607093	-6.48	FALSE
251764_at	putative protein exostose-relatec	EPC1	AT3G55830	1.05	0.07	0.38	0.7158113	0.8607093	-6.48	FALSE
254066_at	transcriptional activator CBF1-lik	DREB1A	AT4G25480	-1.13	-0.18	-0.38	0.715951	0.8607411	-6.48	TRUE
254163_s_a	putative protein storage protein -	---	AT4G24340 ///	1.20	0.26	0.38	0.7159162	0.8607411	-6.48	FALSE
247290_at	putative protein similar to unknov	---	AT5G64450	-1.09	-0.12	-0.38	0.7158802	0.8607411	-6.48	FALSE
257020_at	mitotic checkpoint protein, putati	---	AT3G19590	-1.05	-0.07	-0.38	0.7160333	0.8607947	-6.48	FALSE
259143_at	calmodulin-like protein similar to	---	AT3G10190	1.06	0.09	0.38	0.7161995	0.8608444	-6.48	TRUE
250239_at	ABC transporter-like protein	---	AT5G13580	-1.06	-0.09	-0.38	0.7165136	0.8608444	-6.48	FALSE
265098_at	unknown protein	---	AT1G04010	1.09	0.13	0.38	0.7162364	0.8608444	-6.48	FALSE
259511_at	unknown protein contains similar	ATCCS	AT1G12520	1.14	0.19	0.38	0.7162555	0.8608444	-6.48	FALSE
263740_at	hypothetical protein predicted by	RALFL14	AT2G20660	-1.05	-0.07	-0.38	0.7164265	0.8608444	-6.48	FALSE
264536_at	hypothetical protein predicted by	PRA1.G1	AT1G55640	1.07	0.10	0.38	0.7164706	0.8608444	-6.48	FALSE
263578_at	F-box protein family, AtFBL10 co	---	AT2G17020	1.04	0.06	0.38	0.7163204	0.8608444	-6.48	FALSE
247700_at	RNA-binding protein - like cold-ir	---	AT5G59860	-1.03	-0.05	-0.38	0.7165275	0.8608444	-6.48	FALSE
253430_at	putative protein	---	AT4G32430	1.05	0.07	0.38	0.7161588	0.8608444	-6.48	FALSE
245245_at	delta-aminolevulinic acid dehydr	hemb2	AT1G44318	-1.04	-0.06	-0.38	0.7164921	0.8608444	-6.48	FALSE
248210_at	ethylene-forming-enzyme-like dio	---	AT5G54000	1.04	0.06	0.38	0.7165015	0.8608444	-6.48	FALSE
246048_at	putative protein	---	---	-1.05	-0.06	-0.38	0.716412	0.8608444	-6.48	FALSE
256452_at	hypothetical protein predicted by	AtHB33	AT1G75240	1.16	0.22	0.38	0.7165967	0.8608615	-6.48	FALSE
265951_at	hypothetical protein predicted by	OFP7	AT2G18500	1.07	0.10	0.38	0.7166172	0.8608615	-6.48	FALSE
254909_at	putative disease resistance resp	---	AT4G11210	-1.05	-0.07	-0.38	0.7166962	0.8609111	-6.48	FALSE
265568_s_a	hypothetical protein predicted by	---	---	-1.05	-0.08	-0.38	0.7167679	0.8609519	-6.48	FALSE
245459_at	hypothetical protein	---	---	1.07	0.09	0.38	0.7169507	0.8610021	-6.48	FALSE
250686_at	gamma-tubulin interacting protein	SPC98	AT5G06680	-1.07	-0.09	-0.38	0.7169384	0.8610021	-6.48	FALSE
257704_at	myb-related transcription factor,	ATMYB67	AT3G12720	1.03	0.05	0.38	0.7169026	0.8610021	-6.48	FALSE
266380_at	unknown protein	MEE13	AT2G14680	-1.05	-0.06	-0.38	0.7169607	0.8610021	-6.48	FALSE
258092_at	Expressed protein ; supported by	---	AT3G14595	-1.07	-0.10	-0.38	0.7170858	0.8610688	-6.48	FALSE
254978_at	subtilisin-like serine protease cor	---	AT4G10540	-1.04	-0.05	-0.38	0.7170918	0.8610688	-6.48	FALSE
251717_at	putative protein EXOENZYMES	LAF3	AT3G55850	-1.06	-0.08	-0.38	0.7172816	0.8612125	-6.48	FALSE
267125_at	putative acetone-cyanohydrin lya	MES4	AT2G23580	-1.04	-0.05	-0.38	0.7172869	0.8612125	-6.48	FALSE
254001_at	putative protein PRE87 mRNA, I	MIOX4	AT4G26260	1.14	0.19	0.38	0.7173705	0.8612675	-6.48	FALSE
265485_at	putative Ta11-like non-LTR retro	---	---	1.07	0.09	0.38	0.7174773	0.8613051	-6.48	FALSE
252047_at	putative protein heat shock prote	---	AT3G52490	1.05	0.07	0.38	0.7174428	0.8613051	-6.48	FALSE
245573_at	hypothetical protein	---	AT4G14730	-1.04	-0.05	-0.38	0.717546	0.8613422	-6.48	FALSE
262863_at	rhamnosyltransferase, putative s	---	AT1G64910	1.05	0.06	0.38	0.7176243	0.8613491	-6.48	FALSE

252407_at	chloroplast NAD-dependent mala	MDH	AT3G47520	-1.06	-0.08	-0.38	0.7176651	0.8613491	-6.48	FALSE
254091_at	hypothetical protein	---	AT4G25070	1.08	0.11	0.38	0.7176439	0.8613491	-6.48	FALSE
258829_at	putative Sec24-like COPII protein	---	AT3G07100	-1.03	-0.05	-0.38	0.7178113	0.8614219	-6.48	FALSE
264432_at	hypothetical protein similar to hyp	---	AT1G61710	-1.04	-0.06	-0.38	0.717839	0.8614219	-6.48	FALSE
248212_at	CHP-rich zinc finger protein-like	---	AT5G54020	-1.05	-0.07	-0.38	0.7178272	0.8614219	-6.48	FALSE
265342_at	hypothetical protein predicted by	---	AT2G18300	-1.08	-0.12	-0.38	0.717979	0.8614992	-6.48	TRUE
252849_at	Histon H3 ;supported by full-leng	---	AT4G40040	-1.04	-0.06	-0.38	0.7179468	0.8614992	-6.48	FALSE
259538_at	putative serine/threonine kinase	---	AT1G12310	1.05	0.07	0.38	0.7180804	0.8615303	-6.48	FALSE
264759_at	receptor protein kinase (IRK1), p	---	AT1G61480	-1.05	-0.06	-0.38	0.7180454	0.8615303	-6.48	FALSE
261566_at	unknown protein ;supported by fu	---	AT1G33230	-1.06	-0.08	-0.38	0.7181946	0.8615582	-6.48	FALSE
250816_at	coatomer delta subunit (delta-coa	---	AT5G05010	-1.06	-0.08	-0.38	0.7182417	0.8615582	-6.48	FALSE
253709_at	pyrophosphate-dependent phos	PFK1	AT4G29220	1.06	0.08	0.38	0.7182548	0.8615582	-6.48	FALSE
265543_at	unknown protein	---	AT2G28270	-1.03	-0.05	-0.38	0.7181451	0.8615582	-6.48	FALSE
260012_at	Expressed protein ; supported by	---	AT1G67865	1.09	0.12	0.38	0.7183473	0.8616239	-6.48	FALSE
258002_at	AIG2-like protein similar to AIG2	AIG2	AT3G28930	1.24	0.31	0.38	0.7186172	0.8617433	-6.48	FALSE
252616_at	serine threonine-protein kinase-	GRIK1	AT3G45240 /	1.05	0.08	0.38	0.718713	0.8617433	-6.48	FALSE
254698_at	NAM (no apical meristem) - like p	anac071	AT4G17980	1.03	0.05	0.38	0.7186584	0.8617433	-6.48	FALSE
252686_at	putative protein predicted protei	---	---	1.04	0.05	0.38	0.7186713	0.8617433	-6.48	FALSE
247165_at	transcription factor-like protein ;	MYB68	AT5G65790	1.04	0.05	0.38	0.7187491	0.8617433	-6.48	FALSE
247742_at	random slug protein - like rando	---	AT5G58980	1.05	0.07	0.38	0.7185335	0.8617433	-6.48	FALSE
255853_at	hypothetical protein predicted by	---	AT1G67020	-1.04	-0.05	-0.38	0.7185312	0.8617433	-6.48	FALSE
264789_at	putative glycine-rich, zinc-finger	---	AT2G17870	-1.04	-0.05	-0.38	0.7186743	0.8617433	-6.48	FALSE
260088_at	tonoplast intrinsic protein, alpha	TIP3;1	AT1G73190	1.05	0.07	0.38	0.7189094	0.8617652	-6.48	FALSE
263562_at	hypothetical protein predicted by	---	AT2G15420	-1.04	-0.05	-0.38	0.7188341	0.8617652	-6.48	FALSE
251452_at	putative protein male sterility pro	---	AT3G60060	1.03	0.05	0.38	0.7189185	0.8617652	-6.48	FALSE
259333_at	putative auxin-independent grow	EDA30	AT3G03810	-1.05	-0.07	-0.38	0.718868	0.8617652	-6.48	FALSE
251091_at	pyridoxine biosynthesis protein -	RSR4	AT5G01410	-1.10	-0.14	-0.38	0.7189854	0.8618001	-6.48	FALSE
245175_at	putative protein disulfide-isomera	UNE5	AT2G47470	1.08	0.11	0.38	0.7190243	0.8618015	-6.48	FALSE
259486_at	embryo abundance protein (EMI	---	AT1G15710	1.05	0.07	0.37	0.7192384	0.861956	-6.48	FALSE
266630_at	putative serpin	---	AT2G35580	1.04	0.05	0.37	0.7192355	0.861956	-6.48	FALSE
263530_at	HSP100/ClpB, putative similar to	---	AT2G25030 /	1.04	0.06	0.37	0.7192666	0.861956	-6.48	FALSE
257229_at	putative calmodulin-binding prote	IQD26	AT3G16490	1.06	0.08	0.37	0.7194818	0.8621234	-6.48	FALSE
255322_at	putative protein	---	---	1.03	0.05	0.37	0.719452	0.8621234	-6.48	FALSE
255774_at	unknown protein	---	AT1G18620	-1.10	-0.14	-0.37	0.7197865	0.8621262	-6.48	TRUE
263160_at	oligouridylate binding protein, pu	UBP1A	AT1G54080	1.05	0.06	0.37	0.7197498	0.8621262	-6.48	FALSE

254188_at	UDPglucose 4-epimerase - like	UGE2	AT4G23920	-1.10	-0.13	-0.37	0.7197425	0.8621262	-6.48	FALSE
260980_at	hypothetical protein predicted by	---	AT1G53600	1.06	0.08	0.37	0.7196526	0.8621262	-6.48	FALSE
265981_s_a	putative replication protein A1	---	---	1.06	0.08	0.37	0.7195624	0.8621262	-6.48	FALSE
260662_at	2-hydroxyisoflavone reductase,	---	AT1G19540	1.05	0.07	0.37	0.7195616	0.8621262	-6.48	FALSE
246707_at	putative protein	---	---	-1.04	-0.06	-0.37	0.7197363	0.8621262	-6.48	FALSE
245433_at	hypothetical protein	---	AT4G17140	-1.04	-0.06	-0.37	0.719763	0.8621262	-6.48	FALSE
258295_at	unknown protein ;supported by f	---	AT3G23400	-1.07	-0.09	-0.37	0.7200214	0.8623622	-6.48	FALSE
252020_at	SKP1/ASK1 (At6), putative simil	ASK6	AT3G53060	-1.03	-0.04	-0.37	0.7200639	0.8623678	-6.48	FALSE
263881_at	unknown protein ; supported by	---	AT2G21820	1.04	0.06	0.37	0.7203109	0.8624111	-6.48	FALSE
257922_at	ethylene receptor, putative (ETR	ETR2	AT3G23150	1.09	0.12	0.37	0.7203294	0.8624111	-6.48	FALSE
265994_at	putative multispanning membran	---	AT2G24170	-1.10	-0.13	-0.37	0.7203647	0.8624111	-6.48	FALSE
260019_at	polyprotein, putative simlar to G	---	---	-1.04	-0.05	-0.37	0.7203448	0.8624111	-6.48	FALSE
259828_at	RING-H2 zinc finger protein ATL	---	AT1G72220	-1.05	-0.07	-0.37	0.720306	0.8624111	-6.48	FALSE
257441_at	putative GDSL-motif lipase/hydro	---	AT2G04020	-1.05	-0.07	-0.37	0.7201992	0.8624111	-6.48	FALSE
247543_at	DNA binding protein - like DNA b	---	AT5G61600	1.14	0.19	0.37	0.7201895	0.8624111	-6.48	FALSE
260345_at	receptor protein kinase, putative	RPK1	AT1G69270	-1.07	-0.09	-0.37	0.7206154	0.8624957	-6.48	FALSE
252713_at	calmodulin 7 ; supported by full-	CAM7	AT3G43810	-1.05	-0.06	-0.37	0.7206158	0.8624957	-6.48	FALSE
266032_x_a	putative replication protein A1	---	---	1.04	0.06	0.37	0.7205696	0.8624957	-6.48	FALSE
251974_at	myb protein(MYB27) contains my	AtMYB27	AT3G53200	1.03	0.05	0.37	0.7204931	0.8624957	-6.48	FALSE
262008_s_a	CACTA-element, putative simila	---	---	-1.05	-0.07	-0.37	0.7206244	0.8624957	-6.48	FALSE
266219_at	putative para-aminobenzoate sy	emb1997	AT2G28880	-1.04	-0.06	-0.37	0.7207639	0.8626174	-6.48	FALSE
249121_at	aluminum-induced protein-like ;	---	AT5G43830	-1.04	-0.06	-0.37	0.7212322	0.8627709	-6.48	FALSE
255724_at	hypothetical protein	BRCA2(IV)	AT4G00020	1.04	0.05	0.37	0.7213336	0.8627709	-6.48	FALSE
251345_at	putative protein hypothetical prot	---	AT3G60940	-1.04	-0.06	-0.37	0.7210439	0.8627709	-6.48	FALSE
258242_at	hypothetical protein predicted by	---	AT3G27640	-1.04	-0.06	-0.37	0.7214217	0.8627709	-6.48	FALSE
266007_at	unknown protein	---	AT2G37380	-1.05	-0.07	-0.37	0.7210549	0.8627709	-6.48	FALSE
245217_at	retroelement pol polyprotein, put	---	---	1.06	0.08	0.37	0.7213714	0.8627709	-6.48	FALSE
252576_s_a	clpC-like protein AtClpC - Arabid	---	AT3G45450 /	1.07	0.10	0.37	0.7210035	0.8627709	-6.48	FALSE
260016_at	Athila ORF 1, putative simlar to	---	---	-1.04	-0.05	-0.37	0.7211507	0.8627709	-6.48	FALSE
246123_at	beta-1,3-glucanase-like protein b	---	AT5G20390	-1.03	-0.05	-0.37	0.7211386	0.8627709	-6.48	FALSE
250093_at	hypothetical protein	---	AT5G17370	1.04	0.05	0.37	0.7211405	0.8627709	-6.48	FALSE
251046_at	kinesin -like protein kinesin, Xen	---	AT5G02370	1.04	0.05	0.37	0.721319	0.8627709	-6.48	FALSE
249724_at	disease resistance protein	---	AT5G35450	1.03	0.05	0.37	0.7213102	0.8627709	-6.48	FALSE
260604_at	polyphosphoinositide binding pr	---	AT1G55840	1.06	0.08	0.37	0.72117	0.8627709	-6.48	FALSE
245779_at	hypothetical protein predicted by	---	AT1G73510	-1.04	-0.05	-0.37	0.7213952	0.8627709	-6.48	FALSE

245097_at	Expressed protein ; supported by	---	AT2G40935	-1.03	-0.05	-0.37	0.7218113	0.8631915	-6.48	FALSE
265019_at	putative myosin heavy chain sim	---	AT1G24560	1.04	0.05	0.37	0.7219628	0.8633275	-6.48	FALSE
267498_at	unknown protein	---	AT2G45720	-1.06	-0.08	-0.37	0.7221036	0.8634171	-6.48	FALSE
255187_s_a	putative transposon protein	---	---	1.04	0.06	0.37	0.7221135	0.8634171	-6.48	FALSE
264499_at	Expressed protein ; supported by	---	AT1G30795	1.05	0.07	0.37	0.7222046	0.8634808	-6.48	FALSE
249811_at	unknown protein ;supported by f	---	AT5G23760	-1.04	-0.05	-0.37	0.7224067	0.8634962	-6.48	FALSE
256322_at	unknown protein ; supported by	AXR4	AT1G54990	-1.09	-0.12	-0.37	0.7222578	0.8634962	-6.48	FALSE
257859_at	Expressed protein ; supported by	---	AT3G12955	1.05	0.07	0.37	0.7223972	0.8634962	-6.48	FALSE
252783_at	putative protein predicted protei	---	---	1.04	0.05	0.37	0.7223824	0.8634962	-6.48	FALSE
266724_at	hypothetical protein predicted by	---	AT2G03180	1.04	0.05	0.37	0.7223587	0.8634962	-6.48	FALSE
246023_at	ethylene-insensitive3-like2 (EIL2	EIL2	AT5G21120	1.04	0.06	0.37	0.7224853	0.8635448	-6.48	FALSE
246174_s_a	putative protein hypothetical pro	---	AT5G28340 /	-1.04	-0.05	-0.37	0.7227283	0.86379	-6.48	FALSE
266034_at	Expressed protein ; supported by	FIP1	AT2G06005	-1.04	-0.05	-0.37	0.7228946	0.863865	-6.48	FALSE
267422_at	putative protein kinase contains a	---	AT2G35050	-1.04	-0.05	-0.37	0.7229046	0.863865	-6.48	FALSE
262458_at	serine/threonine kinase, putative	---	AT1G11280	-1.04	-0.06	-0.37	0.722884	0.863865	-6.48	FALSE
256787_at	beta-fructofuranosidase 1 identic	ATBFRUCT	AT3G13790	-1.09	-0.12	-0.37	0.7234826	0.8639051	-6.48	TRUE
256948_at	unknown protein	---	AT3G18930	1.04	0.06	0.37	0.7233876	0.8639051	-6.48	FALSE
260579_at	putative cytochrome c oxidase V	---	AT2G47380	1.05	0.06	0.37	0.7231445	0.8639051	-6.48	FALSE
245401_at	hypothetical protein ;supported b	---	AT4G17670	-1.12	-0.16	-0.37	0.7233059	0.8639051	-6.48	FALSE
262278_at	transcription factor PERIANTHIA	PAN	AT1G68640	-1.05	-0.07	-0.37	0.7230258	0.8639051	-6.48	FALSE
258040_at	unknown protein ;supported by f	---	AT3G21190	1.25	0.32	0.37	0.7234504	0.8639051	-6.48	FALSE
263115_at	Expressed protein ; supported by	---	AT1G03055	1.08	0.11	0.37	0.7234694	0.8639051	-6.48	FALSE
250077_at	putative protein	---	AT5G16680	1.04	0.05	0.37	0.7235442	0.8639051	-6.48	FALSE
266384_at	hypothetical protein predicted by	---	AT2G14660	-1.05	-0.07	-0.37	0.7233797	0.8639051	-6.48	FALSE
256748_x_a	En/Spm transposon protein, puta	---	---	-1.04	-0.06	-0.37	0.7234175	0.8639051	-6.48	FALSE
254654_at	translation initiation factor eIF4E	EIF4E	AT4G18040	-1.04	-0.06	-0.37	0.723336	0.8639051	-6.48	FALSE
264496_at	putative polyprotein similar to GB	---	---	1.05	0.07	0.37	0.7230124	0.8639051	-6.48	FALSE
255382_at	putative pre-mRNA splicing facto	EMB2770	AT4G03430	1.03	0.05	0.37	0.7232955	0.8639051	-6.48	FALSE
267049_at	putative transcription elongation	---	AT2G34210	1.08	0.11	0.37	0.7233172	0.8639051	-6.48	FALSE
259427_at	MADS-box transcription factor, p	AGL28	AT1G01530	1.04	0.05	0.37	0.7233231	0.8639051	-6.48	FALSE
261332_s_a	hypothetical protein contains sim	---	---	-1.03	-0.05	-0.37	0.7235197	0.8639051	-6.48	FALSE
259721_at	putative phosphatidylinositol-4-ph	---	AT1G60890	-1.06	-0.09	-0.37	0.723704	0.8640054	-6.48	FALSE
250317_at	tubulin beta-6 chain (sp|P29514)	TUB6	AT5G12250	-1.13	-0.18	-0.37	0.7236669	0.8640054	-6.48	FALSE
260060_at	feebly-like protein similar to feebl	---	AT1G73680	1.05	0.08	0.37	0.7238832	0.864047	-6.48	FALSE
250859_at	cytochrom P450 - like protein cy	CYP77A4	AT5G04660	1.03	0.05	0.37	0.7238904	0.864047	-6.48	FALSE

251210_at	hypothetical protein ;supported b	---	AT3G62810	1.05	0.07	0.37	0.7238145	0.864047	-6.48	FALSE
256128_at	laccase, putative similar to high-	LAC1	AT1G18140	-1.05	-0.07	-0.37	0.7238401	0.864047	-6.48	FALSE
255152_at	Rab-like protein Rab11 protein -	---	AT4G08190	1.03	0.05	0.37	0.7240084	0.8640975	-6.48	FALSE
259022_at	putative asparaginyl-tRNA synth	NS2	AT3G07420	-1.07	-0.09	-0.37	0.7239927	0.8640975	-6.48	FALSE
266315_at	unknown protein ; supported by	SE	AT2G27100	-1.04	-0.05	-0.37	0.7242813	0.8641345	-6.48	FALSE
246676_at	putative protein	---	---	1.03	0.05	0.37	0.7243046	0.8641345	-6.48	FALSE
250277_at	putative protein DRT100 protein	---	AT5G12940	-1.24	-0.32	-0.37	0.7242309	0.8641345	-6.48	FALSE
264417_at	hypothetical protein contains sim	---	---	1.07	0.09	0.37	0.7242349	0.8641345	-6.48	FALSE
256202_s_a	hypothetical protein	---	AT1G48150 /A	-1.04	-0.05	-0.37	0.7242687	0.8641345	-6.48	FALSE
246688_at	putative protein predicted protein	---	---	1.04	0.05	0.37	0.7241503	0.8641345	-6.48	FALSE
254964_at	98b like protein 98b - Daucus ca	---	AT4G11080	1.05	0.07	0.37	0.7240975	0.8641345	-6.48	FALSE
265849_at	hypothetical protein predicted by	---	AT2G35736	-1.06	-0.09	-0.37	0.7243446	0.864137	-6.48	FALSE
256099_at	cytochrome P450, putative simil	CYP78A5	AT1G13710	1.07	0.09	0.37	0.7244604	0.8641848	-6.48	FALSE
245603_at	hypothetical protein	---	AT4G14280	1.05	0.07	0.37	0.7244547	0.8641848	-6.48	FALSE
257155_at	hypothetical protein predicted by	---	AT3G27290	1.05	0.07	0.37	0.7246259	0.864337	-6.48	FALSE
262767_at	putative oxysterol-binding protein	ORP1D	AT1G13170	-1.09	-0.13	-0.37	0.724927	0.8644903	-6.48	FALSE
252360_at	putative protein predicted protei	---	AT3G48480	-1.05	-0.07	-0.37	0.7249029	0.8644903	-6.48	FALSE
262241_at	hypothetical protein predicted by	---	AT1G48390	-1.03	-0.05	-0.37	0.7249299	0.8644903	-6.48	FALSE
259145_at	hypothetical protein predicted by	---	AT3G10180	-1.03	-0.05	-0.37	0.7248661	0.8644903	-6.48	FALSE
259095_at	acyl carrier protein 1 precursor (A	ACP1	AT3G05020	-1.11	-0.14	-0.37	0.7249439	0.8644903	-6.48	FALSE
263781_at	hypothetical protein predicted by	---	AT2G46360	-1.03	-0.05	-0.37	0.7250649	0.8645894	-6.48	FALSE
245416_at	putative protein	---	AT4G17350	-1.05	-0.07	-0.37	0.7252181	0.8647269	-6.48	FALSE
260650_at	Expressed protein ; supported by	TOM2B	AT1G32370	1.04	0.05	0.37	0.7254381	0.8649406	-6.48	FALSE
248301_at	DnaJ protein-like	---	AT5G53150	1.04	0.05	0.37	0.7254732	0.8649406	-6.48	FALSE
267028_at	putative WRKY-type DNA bindin	WRKY33	AT2G38470	-1.24	-0.31	-0.37	0.7256707	0.8650404	-6.48	TRUE
257277_at	disease resistance protein, puta	---	AT3G14470	1.05	0.07	0.37	0.7255951	0.8650404	-6.48	FALSE
255640_at	hypothetical protein	---	AT4G00800	-1.06	-0.08	-0.37	0.7256513	0.8650404	-6.48	FALSE
257184_at	ABC transporter, putative simila	ATMRP8	AT3G13090	1.04	0.05	0.37	0.7257564	0.8650974	-6.48	FALSE
258057_at	unknown protein	AAR3	AT3G28970	-1.04	-0.05	-0.37	0.7260023	0.8653	-6.48	FALSE
263697_at	hypothetical protein contains sim	---	AT1G31080	-1.05	-0.07	-0.37	0.7259938	0.8653	-6.48	FALSE
263475_at	Expressed protein ; supported by	---	AT2G31945	-1.05	-0.07	-0.37	0.72605	0.8653117	-6.48	TRUE
257986_at	Expressed protein ; supported by	AGP40	AT3G20865	-1.07	-0.09	-0.37	0.7261698	0.8654093	-6.48	FALSE
260296_at	putative disease resistance prote	---	AT1G63750	1.15	0.20	0.36	0.7263868	0.8656227	-6.48	FALSE
251528_at	putative protein hypothetical pro	---	AT3G58600	1.05	0.07	0.36	0.7265387	0.8657133	-6.48	FALSE
245909_at	putative protein DNA-directed R	---	AT5G09380	1.05	0.07	0.36	0.7265191	0.8657133	-6.48	FALSE

265279_at	hypothetical protein predicted by	---	AT2G28460	-1.06	-0.09	-0.36	0.7265988	0.8657395	-6.48	FALSE
255620_at	putative copper-containing glyco	---	AT4G01380	1.04	0.05	0.36	0.7266601	0.8657673	-6.48	FALSE
255561_at	putative hexose transporter simil	---	AT4G02050	1.07	0.09	0.36	0.7271481	0.8658084	-6.48	TRUE
267569_at	putative photosystem II oxygen-e	PSBP-2	AT2G30790	-1.07	-0.10	-0.36	0.7272011	0.8658084	-6.48	FALSE
254692_at	putative protein predicted protei	---	AT4G17860	1.04	0.06	0.36	0.7267475	0.8658084	-6.48	FALSE
253880_at	Expressed protein ;supported by	---	AT4G27590	-1.05	-0.07	-0.36	0.7270234	0.8658084	-6.48	FALSE
247011_at	putative protein contains similarit	FRO1	AT5G67590	1.07	0.10	0.36	0.7268914	0.8658084	-6.48	FALSE
248665_at	Expressed protein ; supported by	---	AT5G48655	1.04	0.05	0.36	0.7269153	0.8658084	-6.48	FALSE
245535_at	cell wall protein like	---	AT4G15160	-1.05	-0.07	-0.36	0.7269364	0.8658084	-6.48	FALSE
261297_at	hypothetical protein predicted by	JAZ4	AT1G48500	-1.04	-0.05	-0.36	0.7272259	0.8658084	-6.48	FALSE
257836_at	hypothetical protein	---	---	1.04	0.06	0.36	0.7270317	0.8658084	-6.48	FALSE
250365_at	putative protein serine threonine	---	AT5G11410	1.07	0.10	0.36	0.7271305	0.8658084	-6.48	FALSE
252668_at	hypothetical protein	---	AT3G44210	1.03	0.05	0.36	0.7270116	0.8658084	-6.48	FALSE
263670_at	hypothetical protein predicted by	---	AT2G04840	-1.04	-0.05	-0.36	0.7270978	0.8658084	-6.48	FALSE
245815_at	unknown protein	---	AT1G26090	-1.05	-0.07	-0.36	0.726861	0.8658084	-6.48	FALSE
266392_at	late embryogenesis abundant M1	M10	AT2G41280	1.03	0.05	0.36	0.727165	0.8658084	-6.48	FALSE
263001_at	hypothetical protein contains sim	TAF6B4	AT1G54360	-1.08	-0.10	-0.36	0.7272797	0.8658273	-6.48	FALSE
263386_at	unknown protein ; supported by	---	AT2G40150	1.09	0.12	0.36	0.7273545	0.865871	-6.48	TRUE
245570_at	heat shock protein 101 (HSP101	CLPB2	AT4G14670	-1.04	-0.06	-0.36	0.7275371	0.8659981	-6.48	FALSE
256470_at	hypothetical protein predicted by	---	AT1G42570	1.04	0.05	0.36	0.7275087	0.8659981	-6.48	FALSE
249840_at	unknown protein ; supported by	ATLCBK1	AT5G23450	1.03	0.05	0.36	0.7275868	0.8660121	-6.48	FALSE
263323_at	putative receptor-like protein kina	---	AT2G04300	-1.04	-0.06	-0.36	0.7277575	0.86617	-6.48	FALSE
265778_at	unknown protein	---	AT2G07360	1.04	0.05	0.36	0.7279043	0.8662995	-6.48	FALSE
256216_at	calreticulin (crt1) identical to calr	CRT1	AT1G56340 ///	1.09	0.12	0.36	0.7281287	0.8664664	-6.48	FALSE
250890_at	3-oxoacyl-[acyl-carrier-protein] s	---	AT5G04520	1.04	0.05	0.36	0.7281585	0.8664664	-6.48	FALSE
252237_at	putative protein lateral suppress	---	AT3G49950	-1.05	-0.07	-0.36	0.7280916	0.8664664	-6.48	FALSE
247207_at	putative protein similar to unknov	---	AT5G65000	-1.03	-0.05	-0.36	0.728361	0.8665944	-6.48	FALSE
266449_at	hypothetical protein predicted by	AT-P4H-1	AT2G43080	1.05	0.07	0.36	0.728327	0.8665944	-6.48	FALSE
266405_at	hypothetical protein predicted by	---	AT2G38580	1.08	0.11	0.36	0.72838	0.8665944	-6.48	FALSE
253037_at	putative protein other predicted A	GAUT3	AT4G38270	-1.04	-0.06	-0.36	0.7284347	0.866607	-6.48	FALSE
245643_at	myb-related transcription factor (	MYB116	AT1G25340	1.04	0.06	0.36	0.7285046	0.866607	-6.48	FALSE
260098_at	tumor-related protein, putative s	---	AT1G73320	-1.08	-0.11	-0.36	0.7284883	0.866607	-6.48	FALSE
254448_at	fatty acid hydroxylase - like prote	FAH2	AT4G20870	1.13	0.17	0.36	0.7286062	0.8666827	-6.48	FALSE
256987_at	hypothetical protein predicted by	---	AT3G28560	-1.04	-0.05	-0.36	0.7288061	0.86683	-6.48	FALSE
251954_at	putative protein predicted protei	CPuORF51	AT3G53668 ///	1.10	0.13	0.36	0.7288011	0.86683	-6.48	FALSE

265836_at	Mutator-like transposase similar	---	---	-1.04	-0.06	-0.36	0.7288468	0.8668332	-6.48	FALSE
267485_at	putative MYB family transcription	MYB88	AT2G02820	1.05	0.07	0.36	0.7291095	0.8668745	-6.48	FALSE
258801_at	unknown protein predicted by ge	---	AT3G04560	-1.03	-0.05	-0.36	0.7290186	0.8668745	-6.48	FALSE
254536_at	putative protein chitinase / lysoz	---	AT4G19720	1.04	0.06	0.36	0.7290387	0.8668745	-6.48	FALSE
264532_at	seed imbibition protein, putative	AtSIP1	AT1G55740	1.04	0.06	0.36	0.7289219	0.8668745	-6.48	FALSE
255407_at	hypothetical protein similar to A.	---	AT4G03480	1.06	0.08	0.36	0.729056	0.8668745	-6.48	FALSE
265358_at	putative HesB-like protein ; supp	---	AT2G16710	-1.06	-0.08	-0.36	0.729104	0.8668745	-6.48	FALSE
264783_at	putative calcium-dependent prot	PPCK1	AT1G08650	1.09	0.12	0.36	0.7291668	0.8668975	-6.48	FALSE
264237_at	hypothetical protein predicted by	---	AT1G54700	-1.03	-0.05	-0.36	0.7293014	0.8669671	-6.48	FALSE
264149_at	NAM (no apical meristem)-like p	anac005	AT1G02250	1.04	0.06	0.36	0.7292759	0.8669671	-6.48	FALSE
249361_at	protein kinase - like protein prote	---	AT5G40540	-1.09	-0.12	-0.36	0.7294948	0.8670827	-6.48	TRUE
265813_at	putative NAM (no apical meriste	VND1	AT2G18060	-1.04	-0.05	-0.36	0.7295127	0.8670827	-6.48	FALSE
263575_at	hypothetical protein similar to hy	---	AT2G17070	-1.04	-0.05	-0.36	0.7294977	0.8670827	-6.48	FALSE
262642_at	hypothetical protein predicted by	---	AT1G62690	1.04	0.06	0.36	0.729621	0.8671663	-6.48	FALSE
254082_at	glutamine cyclotransferase prec	QC	AT4G25720	1.09	0.12	0.36	0.7298317	0.8673714	-6.48	FALSE
263392_at	putative PttA-like transposon pro	---	---	-1.03	-0.05	-0.36	0.7298822	0.8673863	-6.48	FALSE
260644_at	hypothetical protein contains sim	---	AT1G53290	-1.05	-0.07	-0.36	0.7300307	0.8674272	-6.48	FALSE
267182_at	unknown protein	---	AT2G23360	1.05	0.07	0.36	0.7300036	0.8674272	-6.48	FALSE
257240_at	monooxygenase, putatve contai	---	AT3G24200	1.04	0.06	0.36	0.7300105	0.8674272	-6.48	FALSE
261574_at	cytochrome P450, putative simil	CYP78A8	AT1G01190	1.09	0.12	0.36	0.7301104	0.8674768	-6.48	FALSE
256618_at	hypothetical protein	VRN5	AT3G24440	1.09	0.13	0.36	0.7301753	0.8675087	-6.48	FALSE
256349_at	late embryogenesis protein, puta	---	AT1G54890	1.43	0.51	0.36	0.7303686	0.8676931	-6.48	FALSE
263042_at	conserved hypothetical protein p	---	AT1G23340	1.05	0.07	0.36	0.7305191	0.8678267	-6.48	FALSE
264016_at	putative auxin-regulated protein	---	AT2G21220	1.04	0.06	0.36	0.7306778	0.8679248	-6.48	FALSE
258326_at	unknown protein similar to putati	SOL1	AT3G22760	-1.06	-0.08	-0.36	0.7306404	0.8679248	-6.48	FALSE
266432_s_a	putative gag-protease polyprotei	---	---	-1.04	-0.05	-0.36	0.730724	0.8679346	-6.49	FALSE
251565_at	putative protein several hypothet	LBD29	AT3G58190	-1.04	-0.05	-0.36	0.7308441	0.8680319	-6.49	FALSE
263661_at	unknown protein EST gb|T45093	---	AT1G04290	1.07	0.10	0.36	0.7310159	0.8681908	-6.49	FALSE
248259_at	proline-rich cell wall protein-like	---	AT5G53330	-1.04	-0.06	-0.36	0.7310979	0.8681978	-6.49	FALSE
246683_at	putative protein chromokinesin k	---	AT5G33300	-1.04	-0.06	-0.36	0.7310756	0.8681978	-6.49	FALSE
254497_at	Phosphoribosylanthranilate trans	---	AT4G20080	-1.06	-0.09	-0.36	0.731183	0.8682536	-6.49	FALSE
260018_at	hypothetical protein predicted by	---	AT1G41820	-1.04	-0.06	-0.36	0.7313077	0.8683566	-6.49	FALSE
259524_at	hypothetical protein	---	AT1G12550	1.06	0.08	0.36	0.7315609	0.868386	-6.49	FALSE
247914_at	xyloglucan endotransglycosylase	---	AT5G57540	1.05	0.06	0.36	0.7314931	0.868386	-6.49	FALSE
251338_at	putative protein VAP27, Nicotian	VAP	AT3G60600 /	-1.04	-0.05	-0.36	0.731558	0.868386	-6.49	FALSE

258793_at	hypothetical protein supported by	---	AT3G04780	1.04	0.06	0.36	0.731432	0.868386	-6.49	FALSE
261880_at	unknown protein	HIT1	AT1G50500	-1.05	-0.06	-0.36	0.7314906	0.868386	-6.49	FALSE
263571_at	putative disease resistance prote	---	AT2G17050	1.03	0.05	0.36	0.7314382	0.868386	-6.49	FALSE
260143_at	sucrose transport protein SUC1 i	SUC1	AT1G71880	1.10	0.14	0.36	0.7317519	0.8684172	-6.49	FALSE
262799_at	hypothetical protein predicted by	---	AT1G20970	1.07	0.09	0.36	0.7317889	0.8684172	-6.49	FALSE
263812_at	putative replication protein A1	---	---	-1.03	-0.05	-0.36	0.7318157	0.8684172	-6.49	FALSE
250044_at	disease resistance protein RPP1	---	AT5G17680	-1.06	-0.09	-0.36	0.7316894	0.8684172	-6.49	FALSE
264488_s_a	unknown protein similar to EST g	---	AT1G27330 ///	1.07	0.10	0.36	0.7317598	0.8684172	-6.49	FALSE
254534_at	putative Fe(II) transport protein I	IRT2	AT4G19680	1.03	0.04	0.36	0.7316667	0.8684172	-6.49	FALSE
258535_at	unknown protein ; supported by	---	AT3G06750	-1.08	-0.11	-0.36	0.7318556	0.8684194	-6.49	FALSE
250273_at	pre-mRNA splicing factor ATP-d	EMB3011	AT5G13010	1.04	0.05	0.36	0.7319348	0.8684682	-6.49	FALSE
252936_at	putative protein transcription init	---	AT4G39160	1.06	0.09	0.36	0.7320301	0.8684943	-6.49	FALSE
251608_at	putative protein hypothetical pro	UVI4-LIKE	AT3G57860	1.05	0.07	0.36	0.7321372	0.8684943	-6.49	FALSE
252897_at	cytochrome P450 - like protein c	CYP96A9	AT4G39480 ///	1.04	0.06	0.36	0.7320426	0.8684943	-6.49	FALSE
244955_at	hypothetical protein	---	---	1.06	0.09	0.36	0.732172	0.8684943	-6.49	FALSE
265654_s_a	En/Spm-like transposon protein r	---	---	1.04	0.05	0.36	0.7321216	0.8684943	-6.49	FALSE
255201_at	putative transposon protein	---	---	1.03	0.04	0.36	0.7321852	0.8684943	-6.49	FALSE
261832_at	S-ribonuclease binding protein S	---	AT1G10650	1.07	0.09	0.36	0.7322234	0.8684944	-6.49	FALSE
258613_at	putative myo-inositol monophosp	VTC4	AT3G02870	1.08	0.11	0.36	0.7324074	0.868514	-6.49	FALSE
256421_at	hypothetical protein predicted by	---	AT1G33500	1.04	0.05	0.36	0.7322866	0.868514	-6.49	FALSE
254767_s_a	cytochrome p450 - like protein c	CYP71A19	AT4G13290 ///	-1.03	-0.05	-0.36	0.7323738	0.868514	-6.49	FALSE
253656_at	putative protein hypothetical pro	emb1353	AT4G30090	-1.04	-0.05	-0.36	0.7324261	0.868514	-6.49	FALSE
249402_at	Expressed protein ; supported by	---	AT5G40155	1.04	0.06	0.36	0.7324956	0.868514	-6.49	FALSE
254516_at	putative protein	---	AT4G20290	-1.05	-0.07	-0.36	0.7324312	0.868514	-6.49	FALSE
261302_at	hypothetical protein predicted by	---	AT1G48580	-1.04	-0.06	-0.36	0.7325065	0.868514	-6.49	FALSE
250330_at	putative protein	---	AT5G11810	-1.05	-0.06	-0.36	0.732772	0.8685931	-6.49	FALSE
250060_at	chromo domain protein polycom	TFL2	AT5G17690	-1.05	-0.07	-0.36	0.7328398	0.8685931	-6.49	FALSE
258189_at	unknown protein ;supported by f	JAZ3	AT3G17860	1.08	0.11	0.36	0.7327052	0.8685931	-6.49	FALSE
256664_at	DNA-3-methlyadenine glycosylas	---	AT3G12040	-1.05	-0.08	-0.36	0.7326294	0.8685931	-6.49	FALSE
263159_at	RSH3 (RelA/SpoT homolog) ider	RSH3	AT1G54130	1.05	0.08	0.36	0.7328089	0.8685931	-6.49	FALSE
251477_at	putative protein	---	AT3G59680	-1.03	-0.05	-0.36	0.7328078	0.8685931	-6.49	FALSE
247180_at	histone H3	---	AT5G65350 ///	1.03	0.05	0.36	0.7327919	0.8685931	-6.49	FALSE
250001_at	tub family-like protein tubby-like	AtTLP11	AT5G18680	-1.07	-0.09	-0.36	0.7329786	0.8687126	-6.49	FALSE
252564_at	actin depolymerizing factor 1 (AD	ADF1	AT3G46010	1.04	0.06	0.36	0.7330255	0.868723	-6.49	FALSE
260180_at	E2, ubiquitin-conjugating enzym	MMZ2	AT1G70660	-1.06	-0.08	-0.36	0.7330793	0.8687416	-6.49	FALSE

265990_at	putative prolylcarboxypeptidase	---	AT2G24280	-1.07	-0.09	-0.36	0.7332731	0.8687972	-6.49	FALSE
254346_at	symbiosis-related like protein sy	APG8A	AT4G21980	1.07	0.10	0.35	0.733469	0.8687972	-6.49	FALSE
260966_at	NBS/LRR disease resistance pr	RPS5	AT1G12220	-1.04	-0.06	-0.36	0.7333141	0.8687972	-6.49	FALSE
267139_s_a	hypothetical protein predicted by	---	AT2G38195 /	1.03	0.05	0.36	0.7333914	0.8687972	-6.49	FALSE
257564_at	unknown protein	---	AT3G28610	1.06	0.08	0.35	0.7334686	0.8687972	-6.49	FALSE
248159_at	unknown protein	---	AT5G54460	1.03	0.05	0.36	0.7333781	0.8687972	-6.49	FALSE
257416_at	unknown protein	---	AT2G17750	-1.05	-0.07	-0.36	0.7333638	0.8687972	-6.49	FALSE
258280_at	putative self-incompatibility prote	---	AT3G26880	1.03	0.05	0.36	0.7333884	0.8687972	-6.49	FALSE
255351_x_a	putative transposon protein simil	---	---	-1.04	-0.06	-0.36	0.7334295	0.8687972	-6.49	FALSE
246784_at	signal peptidase ; supported by	---	AT5G27430	-1.03	-0.05	-0.35	0.7335297	0.868824	-6.49	FALSE
263468_at	hypothetical protein predicted by	---	AT2G31930	-1.05	-0.07	-0.35	0.7335772	0.8688352	-6.49	FALSE
254922_at	RING-H2 finger protein RHA1a -	RHA1A	AT4G11370	1.27	0.34	0.35	0.7337751	0.8689792	-6.49	FALSE
256028_at	poly(A)-binding protein, putative	PAB1	AT1G34140	1.05	0.08	0.35	0.7337533	0.8689792	-6.49	FALSE
256692_at	hypothetical protein predicted by	---	AT3G32050	1.03	0.05	0.35	0.7338249	0.8689931	-6.49	FALSE
266944_at	unknown protein predicted by ge	---	AT2G18870 /	1.04	0.06	0.35	0.7340736	0.8692426	-6.49	FALSE
246607_at	receptor-like protein kinase - like	---	AT5G35370	1.10	0.13	0.35	0.7342257	0.8692844	-6.49	TRUE
248327_at	putative protein similar to unknov	---	AT5G52750	-1.26	-0.34	-0.35	0.7342614	0.8692844	-6.49	TRUE
247322_at	unknown protein	---	AT5G64090	1.04	0.06	0.35	0.7342436	0.8692844	-6.49	FALSE
255235_at	contains similarity to transposase	---	---	1.05	0.07	0.35	0.7341698	0.8692844	-6.49	FALSE
248829_at	putative protein contains similarit	---	AT5G47130	1.06	0.09	0.35	0.7343359	0.8693274	-6.49	FALSE
265785_at	hypothetical protein predicted by	---	AT2G07290	1.03	0.05	0.35	0.734409	0.8693688	-6.49	FALSE
245781_at	S-ribonuclease binding protein S	SBP1	AT1G45976	-1.05	-0.07	-0.35	0.7346429	0.8696006	-6.49	FALSE
254740_s_a	glycine hydroxymethyltransferas	---	AT2G42450 /	1.13	0.18	0.35	0.7347036	0.8696039	-6.49	FALSE
252638_at	acyl CoA reductase - protein acy	FAR4	AT3G44540	-1.05	-0.07	-0.35	0.7347219	0.8696039	-6.49	FALSE
255493_at	putative glutamate-/aspartate-bi	---	AT4G02690	1.04	0.05	0.35	0.7348409	0.8696873	-6.49	FALSE
259854_at	RING-H2 zinc finger protein ATL	---	AT1G72200	1.06	0.08	0.35	0.7348686	0.8696873	-6.49	FALSE
264253_at	putative kinesin similar to GB:AA	---	AT1G09170	1.06	0.09	0.35	0.7349241	0.8697079	-6.49	FALSE
264198_at	unknown protein ESTs gb|Z340	---	AT1G22800	1.06	0.08	0.35	0.735168	0.8699446	-6.49	FALSE
264097_s_a	NADH dehydrogenase, putative	---	AT1G16700 /	-1.04	-0.06	-0.35	0.7352004	0.8699446	-6.49	FALSE
246299_at	embryonic abundant protein AtE	EM1	AT3G51810	-1.03	-0.04	-0.35	0.7352499	0.869958	-6.49	FALSE
245160_at	putative leucine-rich repeat disea	AtRLP28	AT2G33080	1.03	0.05	0.35	0.7353794	0.8699759	-6.49	FALSE
256508_at	unknown protein	---	AT1G75140	-1.04	-0.05	-0.35	0.7353191	0.8699759	-6.49	FALSE
261702_at	unknown protein similar to hypot	---	AT1G32760	-1.04	-0.06	-0.35	0.7353713	0.8699759	-6.49	FALSE
265434_at	predicted protein	---	AT2G20805	1.03	0.05	0.35	0.7354787	0.8700309	-6.49	FALSE
265830_at	putative helicase	---	---	1.05	0.07	0.35	0.7355022	0.8700309	-6.49	FALSE

261156_s_a	hypothetical protein predicted by	---	AT1G34490 /.	1.04	0.05	0.35	0.7355988	0.8701	-6.49	FALSE
266765_at	putative inorganic pyrophosphata	AtPPa3	AT2G46860	-1.04	-0.05	-0.35	0.735873	0.8703792	-6.49	FALSE
264599_at	putative myosin heavy chain sim	XIA	AT1G04600	1.04	0.05	0.35	0.7359225	0.8703927	-6.49	FALSE
250304_at	elongation factor 1B alpha-subur	---	AT5G12110	1.13	0.18	0.35	0.7360803	0.8705341	-6.49	FALSE
257210_at	hypothetical protein	TTL2	AT3G14950	1.03	0.05	0.35	0.7362149	0.870603	-6.49	FALSE
259264_at	putative aldose 1-epimerase sho	---	AT3G01260	1.05	0.07	0.35	0.7361919	0.870603	-6.49	FALSE
252721_at	putative protein predicted protei	---	AT3G43990	1.05	0.08	0.35	0.7364312	0.8708137	-6.49	FALSE
258562_at	unknown protein ;supported by f	---	AT3G05980	1.03	0.05	0.35	0.7365528	0.8709123	-6.49	FALSE
257811_at	nitrate transporter, putative simil	---	AT3G25280	1.03	0.05	0.35	0.7367996	0.8711589	-6.49	FALSE
264037_at	putative steroid sulfotransferase	---	AT2G03750	-1.05	-0.07	-0.35	0.7368974	0.8712112	-6.49	FALSE
254553_at	TMV resistance protein N - like	---	AT4G19530	1.08	0.11	0.35	0.7370107	0.8712112	-6.49	FALSE
260775_at	14-3-3 protein GF14omega (grf2	GRF2	AT1G78300	1.05	0.07	0.35	0.7370344	0.8712112	-6.49	FALSE
263753_at	putative dehydrin ;supported by	LEA	AT2G21490	1.03	0.04	0.35	0.7370694	0.8712112	-6.49	FALSE
248562_at	putative protein strong similarity t	---	AT5G49680	1.10	0.13	0.35	0.737073	0.8712112	-6.49	FALSE
245210_at	putative protein similarity to UVE	---	AT5G12350	1.03	0.05	0.35	0.7369538	0.8712112	-6.49	FALSE
259745_at	unknown protein	SAG18	AT1G71190	1.04	0.06	0.35	0.7372285	0.87135	-6.49	FALSE
261767_s_a	adenine nucleotide translocase,	NTT1	AT1G15500 /.	-1.05	-0.07	-0.35	0.7373993	0.8714588	-6.49	TRUE
250039_at	disease resistance protein -like	---	AT5G18370	-1.05	-0.07	-0.35	0.7374036	0.8714588	-6.49	FALSE
247793_at	putative protein ; supported by c	PSY1	AT5G58650	1.06	0.08	0.35	0.7374353	0.8714588	-6.49	FALSE
263427_at	hypothetical protein predicted by	---	AT2G22260	-1.03	-0.05	-0.35	0.7375681	0.8715707	-6.49	FALSE
261993_at	unknown protein	---	AT1G33860	1.04	0.05	0.35	0.7376144	0.8715802	-6.49	FALSE
263981_at	unknown protein ;supported by f	PAR1	AT2G42870	-1.14	-0.19	-0.35	0.7377109	0.8716491	-6.49	TRUE
261865_at	sterol delta7 reductase identical t	DWF5	AT1G50430	1.07	0.09	0.35	0.7378344	0.8717106	-6.49	FALSE
248662_at	unknown protein	---	AT5G48690	-1.04	-0.06	-0.35	0.7378394	0.8717106	-6.49	FALSE
256913_at	unknown protein	---	AT3G23870	-1.07	-0.10	-0.35	0.7380197	0.8718785	-6.49	FALSE
260026_at	60S ribosomal protein L18A, put	RPL18AA	AT1G29970	-1.04	-0.06	-0.35	0.7380887	0.8719148	-6.49	FALSE
250398_at	putative protein predicted protei	---	AT5G11000	1.08	0.11	0.35	0.7382275	0.8720336	-6.49	FALSE
248790_at	membrane channel protein-like; a	TIP2;3	AT5G47450	1.06	0.08	0.35	0.7384551	0.8722121	-6.49	FALSE
251361_at	LIM domain protein LIM domain	---	AT3G61230	1.05	0.07	0.35	0.7384308	0.8722121	-6.49	FALSE
255196_x_a	see GB:AF058826	---	---	1.04	0.05	0.35	0.7385018	0.8722221	-6.49	FALSE
246932_at	ethylene-responsive element - li	---	AT5G25190	1.10	0.13	0.35	0.7385585	0.8722439	-6.49	TRUE
254944_at	putative protein proliferation pot	---	AT4G10930	1.03	0.04	0.35	0.738683	0.8723458	-6.49	FALSE
256993_at	unknown protein ; supported by	---	AT3G28670	-1.03	-0.05	-0.35	0.7389057	0.8725637	-6.49	FALSE
256859_at	hypothetical protein	---	AT3G22940	1.05	0.07	0.35	0.7390109	0.8726427	-6.49	FALSE
262011_at	hypothetical protein predicted by	---	AT1G35614	1.05	0.08	0.35	0.7391388	0.8727485	-6.49	FALSE

251236_at	putative protein hypothetical prot	---	AT3G62380	-1.03	-0.04	-0.35	0.7393051	0.8728997	-6.49	FALSE
258476_at	hypothetical protein predicted by	---	AT3G02400	-1.05	-0.08	-0.35	0.7394132	0.8729821	-6.49	FALSE
262051_at	putative coatomer protein compl	---	AT1G79990	1.05	0.07	0.35	0.739464	0.872997	-6.49	FALSE
254064_at	putative protein hypothetical pro	---	AT4G25410	-1.03	-0.05	-0.35	0.7396229	0.8731393	-6.49	FALSE
256923_at	hypothetical protein	---	AT3G29635	-1.05	-0.07	-0.35	0.7397315	0.8731771	-6.49	FALSE
260007_at	unknown protein contains non-co	---	AT1G67870	-1.08	-0.11	-0.35	0.7397312	0.8731771	-6.49	FALSE
260005_at	unknown protein ;supported by f	---	AT1G67920	-1.14	-0.19	-0.35	0.739976	0.8732681	-6.49	TRUE
266880_at	hypothetical protein predicted by	---	AT2G44770	-1.05	-0.07	-0.35	0.7400382	0.8732681	-6.49	FALSE
251219_at	putative protein several hypothet	---	AT3G62390	-1.08	-0.11	-0.35	0.7399432	0.8732681	-6.49	FALSE
260998_at	CAF protein similar to C2H2 zinc	---	AT1G26590	1.04	0.06	0.35	0.7400338	0.8732681	-6.49	FALSE
253127_at	putative Myc-type transcription f	---	AT4G36060	1.04	0.05	0.35	0.7399366	0.8732681	-6.49	FALSE
259698_at	hypothetical protein similar to hy	---	AT1G68930	-1.05	-0.07	-0.35	0.7399592	0.8732681	-6.49	FALSE
257514_at	hypothetical protein similar to put	---	---	1.06	0.08	0.35	0.7403037	0.8735362	-6.49	FALSE
257058_at	Expressed protein ; supported by	COX17	AT3G15352	1.16	0.21	0.35	0.7405395	0.8737692	-6.49	FALSE
262001_at	myrosinase binding protein, puta	---	AT1G33790	1.04	0.06	0.35	0.7405895	0.873783	-6.49	FALSE
256420_at	unknown protein	---	AT1G33475 /	1.05	0.07	0.34	0.7407388	0.8739139	-6.49	FALSE
258987_at	putative SCO1 protein similar to	---	AT3G08950	-1.08	-0.11	-0.34	0.7410096	0.8740465	-6.49	FALSE
266388_at	hypothetical protein predicted by	---	AT2G32340	1.05	0.07	0.34	0.7411577	0.8740465	-6.49	FALSE
255687_at	hypothetical protein	KEA2	AT4G00630	1.08	0.11	0.34	0.7411445	0.8740465	-6.49	FALSE
246318_at	putative protein predicted protei	---	AT3G56740	1.05	0.07	0.34	0.7411452	0.8740465	-6.49	FALSE
245232_at	actin depolymerizing factor-like p	ADF7	AT4G25590	-1.04	-0.06	-0.34	0.7409927	0.8740465	-6.49	FALSE
259374_at	putative AP2 domain transcriptio	---	AT3G16280	-1.05	-0.08	-0.34	0.7411087	0.8740465	-6.49	FALSE
251775_s_a	delta-1-pyrroline-5-carboxylate sy	P5CS1	AT2G39800 /	1.09	0.12	0.34	0.74093	0.8740465	-6.49	FALSE
258465_at	unknown protein	PMEI2	AT3G17220	-1.05	-0.07	-0.34	0.7410046	0.8740465	-6.49	FALSE
258110_at	putative cytochrome P450 simila	CYP72A7	AT3G14610	1.05	0.07	0.34	0.7413778	0.8741705	-6.49	FALSE
258347_at	unknown protein identical to LEA	---	AT3G17520	1.04	0.06	0.34	0.7413696	0.8741705	-6.49	FALSE
262655_s_a	putative mandelonitrile lyase sim	---	AT1G14185 /	-1.03	-0.05	-0.34	0.7413619	0.8741705	-6.49	FALSE
261613_at	abscisic acid responsive element	ABF1	AT1G49720	-1.06	-0.09	-0.34	0.7415132	0.874241	-6.49	FALSE
259694_at	uridine diphosphate glucose epi	UGE3	AT1G63180	1.12	0.16	0.34	0.7415909	0.874241	-6.49	FALSE
252227_at	putative protein various predicte	---	AT3G49900	1.04	0.05	0.34	0.7415565	0.874241	-6.49	FALSE
253787_at	serine/threonine kinase-like prot	---	AT4G28670	1.04	0.06	0.34	0.7415427	0.874241	-6.49	FALSE
256179_at	ubiquitin-specific protease 6 (UB	UBP6	AT1G51710	1.03	0.05	0.34	0.7416734	0.874293	-6.49	FALSE
251601_at	Expressed protein ; supported by	---	AT3G57800	-1.07	-0.09	-0.34	0.7420357	0.8746749	-6.49	TRUE
258845_at	unknown protein ; supported by	---	AT3G03150	-1.04	-0.06	-0.34	0.7422536	0.8748865	-6.49	FALSE
251572_at	pelota-like protein pelota PEL1 -	---	AT3G58390	-1.04	-0.05	-0.34	0.7423649	0.8749725	-6.49	FALSE

267319_at	ABC transporter (AtMRP2) identi	ATMRP2	AT2G34660	-1.06	-0.08	-0.34	0.7425021	0.875089	-6.49	TRUE
258015_at	unknown protein	---	AT3G19340	-1.04	-0.06	-0.34	0.7426416	0.8752082	-6.49	FALSE
250157_at	prx10 peroxidase - like protein p	---	AT5G15180	-1.04	-0.06	-0.34	0.7429616	0.8755401	-6.49	FALSE
257013_at	hypothetical protein contains Pfa	---	AT3G26920 /	1.04	0.06	0.34	0.743082	0.8756367	-6.49	FALSE
258558_at	hypothetical protein predicted by	---	AT3G06000	1.03	0.04	0.34	0.7431953	0.875725	-6.49	FALSE
265655_at	unknown protein contains weak F	---	AT2G13920	1.04	0.06	0.34	0.7433417	0.8757822	-6.49	FALSE
261185_at	cytochrome p450, putative simil	CYP94D1	AT1G34540	-1.04	-0.05	-0.34	0.7433974	0.8757822	-6.49	FALSE
257669_at	DNA mismatch repair protein, pu	MSH5	AT3G20475	1.03	0.05	0.34	0.7433967	0.8757822	-6.49	FALSE
267555_at	Expressed protein ; supported by	SUMO5	AT2G32765	1.04	0.06	0.34	0.7432843	0.8757822	-6.49	FALSE
246804_at	putative protein	---	---	-1.03	-0.05	-0.34	0.7436913	0.8760832	-6.49	FALSE
261256_at	disease resistance protein RTM	RTM1	AT1G05760	1.05	0.07	0.34	0.7440175	0.8763699	-6.49	FALSE
251931_at	putative protein glyoxal oxidase	---	AT3G53950	1.07	0.09	0.34	0.7441268	0.8763699	-6.49	FALSE
255467_at	putative leucine-rich repeat prot	---	AT4G03010	-1.04	-0.06	-0.34	0.7440969	0.8763699	-6.49	FALSE
253014_at	MADS-box protein AGL17 -like p	AGL21	AT4G37940	1.03	0.04	0.34	0.7440735	0.8763699	-6.49	FALSE
246605_at	putative protein predicted protei	---	---	1.04	0.06	0.34	0.7440106	0.8763699	-6.49	FALSE
259702_at	putative endo-1,3-beta-glucanas	---	AT1G77780	1.04	0.05	0.34	0.744233	0.8764119	-6.49	FALSE
259445_at	dioxygenase, putative similar to	GA2OX6	AT1G02400	1.25	0.33	0.34	0.7442646	0.8764119	-6.49	FALSE
245883_at	ribosomal protein S15-like ribos	---	AT5G09500	1.03	0.05	0.34	0.7443437	0.8764119	-6.49	FALSE
247661_at	protein kinase - like protein kina	---	AT5G60080	1.03	0.05	0.34	0.744393	0.8764119	-6.49	FALSE
257603_at	unknown protein	---	AT3G13820	1.03	0.04	0.34	0.7442808	0.8764119	-6.49	FALSE
255123_at	putative lipid transfer protein	---	AT4G08530	-1.04	-0.05	-0.34	0.744365	0.8764119	-6.49	FALSE
245862_at	putative protein	---	AT5G01010	1.04	0.06	0.34	0.7444372	0.8764187	-6.49	FALSE
265919_at	putative retroelement pol polypro	---	---	1.04	0.06	0.34	0.7445239	0.876431	-6.49	FALSE
266454_at	putative bHLH transcription facto	---	AT2G22750	1.04	0.06	0.34	0.7445245	0.876431	-6.49	FALSE
254443_at	putative protein (fragment) BRC	BRCA1	AT4G21070	1.04	0.05	0.34	0.7446627	0.8765485	-6.49	FALSE
260543_at	putative membrane transporter	INT1	AT2G43330	1.06	0.09	0.34	0.7448277	0.8765617	-6.49	FALSE
246125_at	Expressed protein ; supported by	---	AT5G19875	1.13	0.18	0.34	0.7447975	0.8765617	-6.49	FALSE
252683_at	putative protein predicted protei	---	AT3G44380	-1.05	-0.07	-0.34	0.7447406	0.8765617	-6.49	FALSE
262979_s_a	unknown protein similar to histon	---	AT1G13370 /	-1.04	-0.06	-0.34	0.7447977	0.8765617	-6.49	FALSE
245487_at	phytochrome D	PHYD	AT4G16250	-1.05	-0.07	-0.34	0.744891	0.8765911	-6.49	FALSE
253437_at	putative protein mRNAs from Ri	---	AT4G32460	-1.11	-0.15	-0.34	0.7449623	0.8766297	-6.49	FALSE
260240_at	putative tRNA isopentenyl transf	ATIPT1	AT1G68460	-1.03	-0.05	-0.34	0.7451042	0.8767231	-6.49	FALSE
248443_at	gibberellin 20-oxidase-like protei	---	AT5G51310	-1.03	-0.05	-0.34	0.7451186	0.8767231	-6.49	FALSE
255240_at	coded for by A. thaliana cDNA Z	IBR1	AT4G05530	1.04	0.05	0.34	0.7452213	0.8767988	-6.49	FALSE
252826_at	hypothetical protein ; supported	---	AT4G40050	-1.04	-0.06	-0.34	0.7452799	0.8768225	-6.49	FALSE

261142_at	cyclic nucleotide and calmodulin	ATCNGC8	AT1G19780	-1.03	-0.04	-0.34	0.7453681	0.8768811	-6.49	FALSE
250638_at	glycine-rich protein atGRP-6	GRP16	AT5G07540	-1.05	-0.07	-0.34	0.7455098	0.8770025	-6.49	FALSE
245228_at	phytochelatin synthetase-like pro	COBL2	AT3G29810	-1.09	-0.13	-0.34	0.7457786	0.8770474	-6.49	FALSE
254150_at	putative protein storage protein -	---	AT4G24350	1.22	0.29	0.34	0.745777	0.8770474	-6.49	FALSE
254769_at	hypothetical protein	---	AT4G13330	-1.08	-0.11	-0.34	0.7457779	0.8770474	-6.49	FALSE
266039_s_a	hypothetical protein	---	AT2G07739	1.05	0.06	0.34	0.7457221	0.8770474	-6.49	FALSE
245802_at	hypothetical protein similar to hyp	---	AT1G46840	-1.03	-0.04	-0.34	0.7456854	0.8770474	-6.49	FALSE
249438_at	putative protein BCS1 nuclear g	AATP1	AT5G40010	1.05	0.07	0.34	0.7456394	0.8770474	-6.49	FALSE
266802_at	Expressed protein ; supported by	---	AT2G22900	1.18	0.24	0.34	0.7459373	0.8770982	-6.49	FALSE
247567_at	putative protein various predicte	---	AT5G61190	1.05	0.07	0.34	0.7458735	0.8770982	-6.49	FALSE
255973_at	hypothetical protein predicted by	---	AT3G32400	-1.03	-0.04	-0.34	0.7459192	0.8770982	-6.49	FALSE
250167_at	myb-related protein - like myb-re	ATMYB16	AT5G15310	-1.06	-0.08	-0.34	0.7460996	0.8771986	-6.49	TRUE
250610_at	glycine-rich protein PUTG1 ;sup	GRP19	AT5G07550	1.06	0.09	0.34	0.7460941	0.8771986	-6.49	FALSE
264247_at	potassium transporter, putative s	---	AT1G60160	-1.08	-0.12	-0.34	0.7461905	0.8772603	-6.49	FALSE
246106_at	receptor-like protein kinase prec	---	AT5G28680	1.03	0.04	0.34	0.7462368	0.8772696	-6.49	FALSE
252577_at	putative protein putative proteins	---	AT3G45460	1.03	0.04	0.34	0.7463708	0.8773819	-6.49	FALSE
261679_at	polyprotein, putative similar to p	---	---	-1.03	-0.04	-0.34	0.7464874	0.8774738	-6.49	FALSE
264354_s_a	unknown protein similar to Lamb	---	AT1G03200 ///	-1.04	-0.06	-0.34	0.7466541	0.8775746	-6.49	FALSE
260777_at	mitochondrial carrier protein, put	---	AT1G14560	1.04	0.06	0.34	0.7466142	0.8775746	-6.49	FALSE
251079_at	hypothetical protein	---	AT5G02000	1.03	0.05	0.34	0.7467271	0.8775746	-6.49	FALSE
255096_at	hypothetical protein similar to T2	---	---	1.04	0.05	0.34	0.7467256	0.8775746	-6.49	FALSE
257620_at	hypothetical protein predicted by	---	AT3G24850	-1.04	-0.06	-0.34	0.746813	0.8775851	-6.49	FALSE
262192_at	hypothetical protein predicted by	---	AT1G77830	1.03	0.05	0.34	0.7468088	0.8775851	-6.49	FALSE
260327_at	putative RING zinc finger protein	---	AT1G63840	-1.07	-0.09	-0.34	0.7469647	0.8776749	-6.49	TRUE
255916_at	putative protein	---	AT5G28550	1.05	0.06	0.34	0.7470049	0.8776749	-6.49	FALSE
258757_at	putative RING zinc finger protein	---	AT3G10910 ///	1.07	0.09	0.34	0.7469999	0.8776749	-6.49	FALSE
247999_at	E2, ubiquitin-conjugating enzym	UBC30	AT5G56150	1.04	0.06	0.34	0.7471523	0.8777577	-6.49	FALSE
258688_at	putative eukaryotic translation ini	---	AT3G07920	-1.03	-0.04	-0.34	0.7471308	0.8777577	-6.49	FALSE
249386_at	disease resistance -like protein c	---	AT5G40060	-1.04	-0.05	-0.34	0.7472424	0.8778184	-6.49	FALSE
263592_at	putative non-LTR retroelement re	---	---	-1.06	-0.09	-0.34	0.7474595	0.8780282	-6.49	FALSE
245382_at	hypothetical protein	---	AT4G17800	1.04	0.05	0.34	0.7475465	0.8780852	-6.49	FALSE
259461_at	unknown protein	---	AT1G18900	1.06	0.09	0.33	0.7478604	0.878273	-6.49	FALSE
255979_at	hypothetical protein	UPF3	AT1G33980	-1.04	-0.05	-0.34	0.7477588	0.878273	-6.49	FALSE
265312_at	unknown protein	---	AT2G20240	1.08	0.11	0.33	0.7478359	0.878273	-6.49	FALSE
254287_at	putative protein similaritry to hyp	---	AT4G22960	1.03	0.05	0.33	0.7478593	0.878273	-6.49	FALSE

258183_at	unknown protein ;supported by f	---	AT3G21550	1.13	0.18	0.33	0.7479646	0.8783501	-6.49	TRUE
250573_at	putative protein	---	AT5G08220 ///	1.05	0.06	0.33	0.7481801	0.878377	-6.49	FALSE
245205_at	putative protein similarity to splic	---	AT5G12280	1.05	0.07	0.33	0.7481775	0.878377	-6.49	FALSE
251279_at	hypothetical protein	---	AT3G61800	1.06	0.09	0.33	0.7480774	0.878377	-6.49	FALSE
247143_at	unknown protein	---	AT5G65580	-1.07	-0.09	-0.33	0.7480918	0.878377	-6.49	FALSE
263011_at	conserved hypothetical protein p	---	AT1G23250	1.04	0.05	0.33	0.748106	0.878377	-6.49	FALSE
262978_at	tubulin beta-1 chain identical to	TUB1	AT1G75780	1.27	0.34	0.33	0.7483705	0.878465	-6.49	FALSE
256326_at	RING zinc-finger protein, putativ	---	AT3G02340	-1.05	-0.07	-0.33	0.7483618	0.878465	-6.49	FALSE
256035_at	Ran-binding protein (atranbp1a)	SIRANBP	AT1G07140	1.04	0.06	0.33	0.7482979	0.878465	-6.49	FALSE
264104_at	En/Spm-like transposon protein r	---	---	-1.04	-0.06	-0.33	0.7484669	0.8785329	-6.49	FALSE
256176_at	hypothetical protein predicted by	ATEXO70G	AT1G51640	1.04	0.05	0.33	0.7485544	0.8785905	-6.49	FALSE
256864_at	topoisomerase II identical to top	TOPII	AT3G23890	1.05	0.07	0.33	0.7487389	0.8787618	-6.49	FALSE
254239_at	water channel - like protein plas	PIP1;5	AT4G23400	-1.07	-0.09	-0.33	0.7488054	0.8787767	-6.49	FALSE
256895_at	zinc-finger protein, putative almo	---	---	1.04	0.05	0.33	0.7488287	0.8787767	-6.49	FALSE
260669_at	hypothetical protein predicted by	---	AT1G19340	1.04	0.05	0.33	0.7489234	0.8788006	-6.49	FALSE
267091_at	Expressed protein ; supported by	---	AT2G38185	-1.06	-0.08	-0.33	0.7489261	0.8788006	-6.49	FALSE
256933_at	unknown protein contains Pfam p	---	AT3G22600	1.32	0.40	0.33	0.7489983	0.8788016	-6.49	TRUE
262683_at	anter-specific proline-rich -like pr	---	AT1G75920	1.03	0.05	0.33	0.749004	0.8788016	-6.49	FALSE
248448_at	putative protein contains similarit	---	AT5G51190	-1.19	-0.25	-0.33	0.749174	0.8788195	-6.49	TRUE
251944_at	ABC transporter -like protein bre	---	AT3G53510	1.05	0.07	0.33	0.7492119	0.8788195	-6.49	FALSE
245707_at	NAC2-like protein	anac077	AT5G04400	1.04	0.06	0.33	0.7491184	0.8788195	-6.49	FALSE
252005_at	purple acid phosphatase-like pro	PAP21	AT3G52810	1.05	0.07	0.33	0.7491144	0.8788195	-6.49	FALSE
260071_at	putative proline-rich protein precu	ESP1	AT1G73840	-1.03	-0.05	-0.33	0.7491791	0.8788195	-6.49	FALSE
265289_at	unknown protein predicted by ge	---	AT2G22690	1.03	0.04	0.33	0.7493043	0.8788827	-6.49	FALSE
252095_at	epoxide hydrolase-like protein e	---	AT3G51000	-1.05	-0.07	-0.33	0.7495263	0.8790527	-6.50	FALSE
249491_at	germin - like protein germin-like	---	AT5G39130	-1.04	-0.05	-0.33	0.7495223	0.8790527	-6.50	FALSE
262311_at	homeodomain leucine zipper pro	ATHB18	AT1G70920	1.04	0.06	0.33	0.7495733	0.8790625	-6.50	FALSE
263499_at	unknown protein ; supported by	TTL3	AT2G42580	-1.06	-0.09	-0.33	0.7497042	0.8791257	-6.50	TRUE
247161_at	putative protein similar to unknov	---	AT5G65810	1.05	0.07	0.33	0.7496806	0.8791257	-6.50	TRUE
264772_at	unknown protein location of EST	---	AT1G22930	-1.04	-0.06	-0.33	0.7499732	0.8793959	-6.50	TRUE
249707_at	putative protein similar to unknov	---	AT5G35640	-1.06	-0.08	-0.33	0.7500897	0.8794538	-6.50	FALSE
245412_at	hypothetical protein	---	AT4G17280	1.06	0.09	0.33	0.7500997	0.8794538	-6.50	FALSE
248261_at	putative protein similar to unknov	PDV1	AT5G53280	-1.04	-0.05	-0.33	0.750204	0.8795309	-6.50	FALSE
259252_at	hypothetical protein similar to hy	IBM1	AT3G07610	1.03	0.05	0.33	0.7502615	0.8795532	-6.50	FALSE
254555_at	putative protein curved DNA-bin	---	AT4G19570	-1.04	-0.05	-0.33	0.7503656	0.87963	-6.50	FALSE

248796_at	VAMP (vesicle-associated memb	---	AT5G47180	-1.06	-0.09	-0.33	0.7505282	0.8797267	-6.50	FALSE
251510_at	putative protein several hypothet	---	AT3G59170	1.03	0.04	0.33	0.7505639	0.8797267	-6.50	FALSE
248963_at	unknown protein	---	AT5G45700	-1.04	-0.06	-0.33	0.7505033	0.8797267	-6.50	FALSE
254775_at	hypothetical protein	---	AT4G13450	-1.03	-0.04	-0.33	0.750639	0.8797696	-6.50	FALSE
265175_at	hypothetical protein similar to put	ATCSLA03	AT1G23480	-1.06	-0.09	-0.33	0.7509472	0.8798292	-6.50	TRUE
260274_at	putative glycerol kinase similar to	NHO1	AT1G80460	1.05	0.07	0.33	0.7508282	0.8798292	-6.50	FALSE
267482_s_a	unknown protein	---	AT2G02770 //	1.10	0.14	0.33	0.7508585	0.8798292	-6.50	FALSE
265113_at	hypothetical protein	---	---	-1.04	-0.05	-0.33	0.7507919	0.8798292	-6.50	FALSE
248745_at	unknown protein	---	AT5G48250	1.05	0.07	0.33	0.7509599	0.8798292	-6.50	FALSE
263007_at	hypothetical protein contains sim	---	AT1G54260	-1.04	-0.05	-0.33	0.7508874	0.8798292	-6.50	FALSE
258337_at	hypothetical protein predicted by	---	AT3G16040	-1.06	-0.08	-0.33	0.7509376	0.8798292	-6.50	FALSE
267625_at	putative RNA-binding protein	---	AT2G42240	-1.04	-0.05	-0.33	0.751069	0.8799118	-6.50	FALSE
253159_at	HMG delta protein ;supported by	HMGB5	AT4G35570	-1.03	-0.05	-0.33	0.7511635	0.8799773	-6.50	FALSE
245477_at	hypothetical protein	ARR2	AT4G16110	-1.04	-0.06	-0.33	0.7515066	0.8802287	-6.50	FALSE
249023_at	putative protein strong similarity t	---	AT5G44850	1.08	0.12	0.33	0.7515355	0.8802287	-6.50	FALSE
267019_at	hypothetical protein predicted by	---	AT2G39130	1.04	0.06	0.33	0.751571	0.8802287	-6.50	FALSE
267104_at	ERD15 protein identical to GB D	ERD15	AT2G41430	1.04	0.06	0.33	0.7514631	0.8802287	-6.50	FALSE
259157_at	hypothetical protein predicted by	---	AT3G05440	-1.03	-0.04	-0.33	0.7515474	0.8802287	-6.50	FALSE
258464_at	kinesin-like protein similar to KLP	POK1	AT3G17360	1.03	0.04	0.33	0.7516104	0.8802297	-6.50	FALSE
253798_at	predicted protein CUC2 (involve	ANAC073	AT4G28500	1.04	0.06	0.33	0.7517155	0.8802865	-6.50	FALSE
246723_at	putative protein various predicte	---	AT5G29030	-1.04	-0.05	-0.33	0.7517361	0.8802865	-6.50	FALSE
264083_at	ethylene reponse factor-like AP2	ATERF15	AT2G31230	1.15	0.20	0.33	0.7518647	0.8803919	-6.50	TRUE
250282_at	putative protein predicted protei	---	AT5G13260	-1.05	-0.08	-0.33	0.7519561	0.8804085	-6.50	FALSE
262857_at	major latex homologue type2 ide	---	AT1G14930	-1.03	-0.05	-0.33	0.751941	0.8804085	-6.50	FALSE
264688_at	hypothetical protein similar to LG	---	AT1G09890	1.05	0.08	0.33	0.7521199	0.880555	-6.50	FALSE
259508_at	hypothetical protein predicted by	---	---	1.06	0.08	0.33	0.7522324	0.8806416	-6.50	FALSE
267639_at	putative squamosa-promoter bin	SPL9	AT2G42200	-1.03	-0.05	-0.33	0.7523937	0.88074	-6.50	FALSE
249300_at	putative protein similar to unknov	---	AT5G41380	1.04	0.05	0.33	0.7523916	0.88074	-6.50	FALSE
265291_at	unknown protein predicted by ge	---	AT2G22720	1.04	0.06	0.33	0.7524822	0.8807985	-6.50	FALSE
251903_at	putative protein 24 kDa seed ma	---	AT3G54120	-1.09	-0.13	-0.33	0.7525267	0.8808053	-6.50	FALSE
265558_at	putative non-LTR retroelement re	---	---	-1.03	-0.04	-0.33	0.7525676	0.8808079	-6.50	FALSE
254334_at	predicted protein	---	AT4G22760	-1.04	-0.06	-0.33	0.7526144	0.8808175	-6.50	FALSE
264398_at	unknown protein similar to hypot	---	AT1G61730	-1.04	-0.05	-0.33	0.7526543	0.8808191	-6.50	FALSE
264315_at	aromatic rich glycoprotein, putat	---	AT1G70370	1.14	0.19	0.33	0.7528482	0.8809126	-6.50	TRUE
251335_at	1-aminocyclopropane-1-carboxy	---	AT3G61400	1.06	0.08	0.33	0.7528501	0.8809126	-6.50	FALSE

246893_at	PHD finger protein - like PHD fin	---	AT5G25520	-1.03	-0.04	-0.33	0.7528401	0.8809126	-6.50	FALSE
262223_at	hypothetical protein predicted by	---	AT1G74680	-1.06	-0.09	-0.33	0.7529633	0.8809999	-6.50	FALSE
260869_at	stearoyl acyl carrier protein desa	---	AT1G43800	1.03	0.05	0.33	0.753065	0.8810286	-6.50	FALSE
266902_at	hypothetical protein predicted by	---	AT2G34580	1.03	0.05	0.33	0.7530279	0.8810286	-6.50	FALSE
248116_at	putative protein contains similarit	MYB120	AT5G55020	1.05	0.07	0.33	0.7536202	0.8816328	-6.50	FALSE
258857_at	putative serine carboxypeptidase	scpl25	AT3G02110	-1.14	-0.18	-0.33	0.7537404	0.8817283	-6.50	FALSE
256093_at	predicted protein ; supported by	---	AT1G20823	1.13	0.18	0.33	0.7540461	0.8819377	-6.50	TRUE
265513_at	hypothetical protein	---	---	1.03	0.04	0.33	0.7540741	0.8819377	-6.50	FALSE
255022_at	NAM/NAP like protein nap gene	ANAC070	AT4G10350	1.03	0.05	0.33	0.7540504	0.8819377	-6.50	FALSE
262995_s_a	hypothetical protein predicted by	---	---	-1.03	-0.04	-0.33	0.7540381	0.8819377	-6.50	FALSE
259088_at	unknown protein, contains TNFR	---	AT3G04970	1.06	0.08	0.33	0.7541551	0.8819872	-6.50	FALSE
266677_at	hypothetical protein predicted by	---	AT2G29820	1.05	0.06	0.33	0.7541954	0.8819891	-6.50	FALSE
258462_at	unknown protein	---	AT3G17350	-1.09	-0.12	-0.33	0.7542524	0.8820105	-6.50	FALSE
244930_at	hypothetical protein	---	AT2G07809	-1.03	-0.05	-0.33	0.7542928	0.8820126	-6.50	FALSE
258923_at	putative glucose acyltransferase	SCPL7	AT3G10450	-1.08	-0.12	-0.33	0.7543381	0.8820203	-6.50	TRUE
266470_at	putative non-LTR retroelement re	---	---	1.07	0.09	0.33	0.7545595	0.882234	-6.50	FALSE
249449_at	unknown protein	---	AT5G39430	-1.03	-0.04	-0.33	0.7546145	0.8822531	-6.50	FALSE
252555_at	putative protein alpha-xylosidase	---	AT3G45940	1.03	0.04	0.33	0.7546786	0.8822827	-6.50	FALSE
244967_at	PSI J protein	---	---	1.08	0.11	0.33	0.7547281	0.8822954	-6.50	FALSE
255119_at	hypothetical protein	---	---	-1.03	-0.05	-0.33	0.7547921	0.882325	-6.50	FALSE
253875_at	putative protein ENOD20 gene,	---	AT4G27520	1.08	0.11	0.33	0.7548701	0.8823426	-6.50	TRUE
264146_at	hypothetical protein contains sim	CER1	AT1G02205	1.41	0.50	0.33	0.7548845	0.8823426	-6.50	TRUE
248374_at	MADS box transcription factor-lik	AGL71	AT5G51870	1.03	0.04	0.33	0.7550229	0.8824592	-6.50	FALSE
262019_s_a	hypothetical protein predicted by	---	---	-1.04	-0.05	-0.32	0.7550747	0.8824744	-6.50	FALSE
257346_at	pseudogene, putative retroelem	---	---	1.04	0.05	0.32	0.7551701	0.8825408	-6.50	FALSE
246150_at	putative protein predicted protein	---	AT5G19930	-1.07	-0.09	-0.32	0.7552834	0.8826279	-6.50	FALSE
261920_at	isocitrate dehydrogenase, putati	---	AT1G65930	1.04	0.06	0.32	0.7553422	0.8826514	-6.50	FALSE
262848_at	unknown protein ; supported by	BPC2	AT1G14685	-1.04	-0.05	-0.32	0.755462	0.8827046	-6.50	FALSE
266810_at	hypothetical protein predicted by	---	AT2G44880	1.03	0.05	0.32	0.7554651	0.8827046	-6.50	FALSE
248631_at	putative protein strong similarity	---	AT5G49000	-1.04	-0.06	-0.32	0.7555126	0.8827149	-6.50	FALSE
252885_at	glycine-rich protein (clone AtGRP	GR-RBP8	AT4G39260	-1.06	-0.08	-0.32	0.7558498	0.88294	-6.50	TRUE
249814_at	putative protein similar to unknov	---	AT5G23840	-1.03	-0.05	-0.32	0.7557514	0.88294	-6.50	FALSE
249675_at	putative protein myrosinase-bind	---	AT5G35940	1.03	0.04	0.32	0.7558283	0.88294	-6.50	FALSE
257040_at	unknown protein ; supported by	SCO2	AT3G19220	-1.06	-0.08	-0.32	0.7558601	0.88294	-6.50	FALSE
255702_at	subtilisin-like serine protease XS	XSP1	AT4G00230	-1.06	-0.08	-0.32	0.7560296	0.8830023	-6.50	FALSE

264899_at	unknown protein similar to ripen	---	AT1G23130	1.08	0.11	0.32	0.7560053	0.8830023	-6.50	FALSE
266196_at	putative protein kinase contains a	---	AT2G39110	-1.04	-0.05	-0.32	0.7560094	0.8830023	-6.50	FALSE
256262_at	unknown protein	---	AT3G12150	1.05	0.07	0.32	0.7560725	0.8830039	-6.50	FALSE
251915_at	putative protein peroxisomal Ca	---	AT3G53940	-1.05	-0.07	-0.32	0.7561083	0.8830039	-6.50	FALSE
245529_at	SEN1 like protein	MAA3	AT4G15570	-1.07	-0.09	-0.32	0.7562106	0.8830781	-6.50	FALSE
262808_at	Avr9 elicitor response-like protein	---	AT1G11730	1.04	0.05	0.32	0.7564474	0.8832846	-6.50	FALSE
249451_s_a	hypothetical protein	---	AT5G39480 ///	1.03	0.04	0.32	0.7564649	0.8832846	-6.50	FALSE
253748_at	putative protein RNA-binding pro	---	AT4G28990	1.05	0.07	0.32	0.7567861	0.8836144	-6.50	FALSE
261311_at	disease resistance protein RTM	---	AT1G05770	1.05	0.08	0.32	0.7569302	0.8836469	-6.50	FALSE
258781_at	hypothetical protein predicted by	---	AT3G11740	1.03	0.04	0.32	0.7568739	0.8836469	-6.50	FALSE
265763_at	unknown protein	---	AT2G48060	-1.03	-0.04	-0.32	0.7569268	0.8836469	-6.50	FALSE
260909_at	hypothetical protein predicted by	---	AT1G02670	-1.04	-0.06	-0.32	0.7571797	0.883893	-6.50	FALSE
253967_at	putative protein probable membr	---	AT4G26550	1.06	0.08	0.32	0.7573084	0.8839589	-6.50	FALSE
250750_at	glucuronosyl transferase-like pro	UGT76C2	AT5G05860 ///	1.04	0.05	0.32	0.7573137	0.8839589	-6.50	FALSE
245125_at	putative histidine kinase identical	CKI1	AT2G47430	1.04	0.06	0.32	0.7574936	0.8841006	-6.50	FALSE
254825_at	putative protein Pad-1, Neurosp	---	AT4G12640	-1.05	-0.07	-0.32	0.7575126	0.8841006	-6.50	FALSE
249983_at	putative protein S-receptor kinas	---	AT5G18470	-1.27	-0.35	-0.32	0.7578413	0.8843032	-6.50	TRUE
247904_at	putative protein contains similarit	AIL5	AT5G57390	1.05	0.07	0.32	0.7577661	0.8843032	-6.50	FALSE
249278_at	putative protein strong similarity t	---	AT5G41900	1.27	0.35	0.32	0.7578271	0.8843032	-6.50	FALSE
254305_at	potassium channel protein AKT3	AKT2/3	AT4G22200	1.03	0.04	0.32	0.757726	0.8843032	-6.50	FALSE
256411_at	ATP-dependent Clp protease pro	CLPP3	AT1G66670	-1.06	-0.09	-0.32	0.7579848	0.8844254	-6.50	TRUE
253096_at	cytochrome P450-like protein	CYP81D4	AT4G37330	-1.04	-0.06	-0.32	0.7581379	0.8845589	-6.50	FALSE
252028_at	hypothetical protein	---	AT3G52640	-1.06	-0.09	-0.32	0.7582261	0.8846165	-6.50	FALSE
246124_at	putative protein acyl-protein thio	---	AT5G20060	1.03	0.04	0.32	0.7584443	0.8847155	-6.50	FALSE
246341_x_a	putative protein predicted protein	---	AT3G43150	1.05	0.07	0.32	0.7584661	0.8847155	-6.50	FALSE
249412_at	putative protein predicted protein	---	AT5G40410	1.04	0.06	0.32	0.7583941	0.8847155	-6.50	FALSE
256845_x_a	hypothetical protein similar to put	---	---	1.04	0.05	0.32	0.75844	0.8847155	-6.50	FALSE
263809_at	putative GDSL-motif lipase/hydro	---	AT2G04570	1.09	0.12	0.32	0.7588127	0.8847608	-6.50	TRUE
254144_at	putative protein	---	AT4G24690	-1.04	-0.05	-0.32	0.7587935	0.8847608	-6.50	FALSE
266860_at	putative phospholipase C	---	AT2G26870	1.07	0.10	0.32	0.7585607	0.8847608	-6.50	FALSE
253671_at	serine threonine-specific recepto	---	AT4G29990	-1.05	-0.07	-0.32	0.7588152	0.8847608	-6.50	FALSE
254627_at	Expressed protein ; supported by	---	AT4G18395	1.03	0.05	0.32	0.758778	0.8847608	-6.50	FALSE
262904_at	chaperone, putative similar to ch	---	AT1G59725	-1.04	-0.06	-0.32	0.7586045	0.8847608	-6.50	FALSE
245482_at	hypothetical protein	---	AT4G16180	1.05	0.07	0.32	0.7586698	0.8847608	-6.50	FALSE
257259_at	hypothetical protein predicted by	---	AT3G22090	1.03	0.04	0.32	0.7586449	0.8847608	-6.50	FALSE

249292_at	repair endonuclease (gb|AAF012	UVH1	AT5G41150	-1.03	-0.05	-0.32	0.7591484	0.885104	-6.50	FALSE
258170_at	unknown protein similar to senes	---	AT3G21600	1.09	0.12	0.32	0.7593764	0.8853246	-6.50	FALSE
255230_at	ferredoxin--NADP+ reductase - I	ATRFNR1	AT4G05390	1.14	0.19	0.32	0.7595341	0.8854244	-6.50	TRUE
254062_at	putative protein zinc finger prote	---	AT4G25380	1.13	0.18	0.32	0.7596173	0.8854244	-6.50	FALSE
256492_at	hypothetical protein contains sim	---	AT1G31490	-1.04	-0.06	-0.32	0.7595967	0.8854244	-6.50	FALSE
248944_at	putative protein similar to unknov	---	AT5G45500	-1.05	-0.07	-0.32	0.759588	0.8854244	-6.50	FALSE
254812_at	nucleotide sugar epimerase -like	GAE5	AT4G12250	-1.09	-0.12	-0.32	0.7597592	0.8855446	-6.50	FALSE
255353_at	putative transposon protein simil	---	---	1.03	0.04	0.32	0.7599182	0.8856847	-6.50	FALSE
258019_at	hypothetical protein predicted by	---	AT3G19470	-1.03	-0.05	-0.32	0.760102	0.8858083	-6.50	FALSE
249863_at	putative protein contains similarit	VPS24.1	AT5G22950	1.03	0.04	0.32	0.7600726	0.8858083	-6.50	FALSE
252573_at	zinc finger protein zinc finger pro	---	AT3G45260	-1.04	-0.05	-0.32	0.7602826	0.8858972	-6.50	FALSE
245969_at	putative protein nuclear gene for	---	AT5G19830	-1.07	-0.09	-0.32	0.7602947	0.8858972	-6.50	FALSE
258580_at	germin-like protein contains Pfam	---	AT3G04170	-1.04	-0.05	-0.32	0.7602879	0.8858972	-6.50	FALSE
255676_at	putative beta-amylase similar to	BAM2	AT4G00490	-1.09	-0.12	-0.32	0.7603742	0.8859445	-6.50	TRUE
264896_at	Hypothetical protein similar to en	AtGH9B6	AT1G23210	1.04	0.05	0.32	0.7604559	0.8859609	-6.50	FALSE
248571_at	putative protein similar to unknov	---	---	1.03	0.04	0.32	0.7604659	0.8859609	-6.50	FALSE
258371_at	hypothetical protein contains sim	---	AT3G14410	-1.04	-0.06	-0.32	0.7606652	0.8859741	-6.50	TRUE
251055_at	putative protein putative protein	---	AT5G01710 ///	1.03	0.05	0.32	0.7607297	0.8859741	-6.50	FALSE
255079_s_a	14-3-3 protein GF14chi (grf1) ide	GF14 PHI	AT1G35160 ///	-1.03	-0.04	-0.32	0.7606587	0.8859741	-6.50	FALSE
247384_at	protein kinase ; supported by cD	---	AT5G63370	1.06	0.09	0.32	0.7606987	0.8859741	-6.50	FALSE
264235_at	myosin, putative similar to myos	XIE	AT1G54560	1.04	0.06	0.32	0.7607285	0.8859741	-6.50	FALSE
267326_at	putative RNA-binding protein	---	AT2G19380	1.04	0.06	0.32	0.7607492	0.8859741	-6.50	FALSE
257278_at	hypothetical protein predicted by	---	AT3G14480	-1.05	-0.07	-0.32	0.7605686	0.8859741	-6.50	FALSE
257191_at	Expressed protein ; supported by	---	AT3G13175	-1.04	-0.06	-0.32	0.7608474	0.8860433	-6.50	FALSE
248179_at	receptor-protein kinase-like prote	THE1	AT5G54380	-1.09	-0.12	-0.32	0.7609323	0.8860969	-6.50	TRUE
255109_s_a	hypothetical protein	---	AT4G08760	1.03	0.04	0.32	0.7610155	0.8861486	-6.50	FALSE
249217_at	ubiquitin-like protein ; supported	UBL5	AT5G42300	1.03	0.04	0.32	0.7612412	0.8862914	-6.50	FALSE
249461_at	putative protein predicted protei	---	AT5G39640	1.04	0.05	0.32	0.7612525	0.8862914	-6.50	FALSE
267258_at	hypothetical protein predicted by	---	AT2G23140	1.03	0.05	0.32	0.7612548	0.8862914	-6.50	FALSE
248494_at	putative protein contains similarit	AtHSD6	AT5G50770	-1.04	-0.05	-0.32	0.7613723	0.8863377	-6.50	FALSE
267012_at	similar to latex allergen from Hev	PLP6	AT2G39220	-1.10	-0.14	-0.32	0.7613681	0.8863377	-6.50	FALSE
252171_at	hypothetical protein ; supported	---	AT3G50590	-1.04	-0.05	-0.32	0.7615918	0.8865236	-6.50	FALSE
265812_at	hypothetical protein predicted by	---	AT2G18070	1.04	0.06	0.32	0.7616097	0.8865236	-6.50	FALSE
253195_at	putative protein dihydroflavonol-	---	AT4G35420	-1.04	-0.06	-0.32	0.761807	0.8867081	-6.50	FALSE
251795_at	putative protein MtN24, Medicag	---	AT3G55390	1.06	0.08	0.32	0.7619186	0.8867474	-6.50	FALSE

247067_at	putative protein strong similarity t	---	AT5G66950	-1.05	-0.07	-0.32	0.7618877	0.8867474	-6.50	FALSE
267643_at	hypothetical protein predicted by	RALFL17	AT2G32890	-1.03	-0.04	-0.32	0.7620222	0.8868227	-6.50	FALSE
267603_at	unknown protein ; supported by	ATZW10	AT2G32900	-1.04	-0.06	-0.32	0.7620803	0.8868451	-6.50	FALSE
265535_at	hypothetical protein predicted by	---	AT2G15900	1.03	0.05	0.31	0.7624278	0.8870368	-6.50	FALSE
253906_at	putative protein disease resistan	---	AT4G27220	-1.05	-0.07	-0.31	0.7624711	0.8870368	-6.50	FALSE
260842_at	19S proteosome subunit 9, puta	ATS9	AT1G29150	-1.04	-0.05	-0.31	0.7623527	0.8870368	-6.50	FALSE
257656_at	Expressed protein ; supported by	---	AT3G13228	1.03	0.04	0.31	0.7624783	0.8870368	-6.50	FALSE
265692_at	hypothetical protein predicted by	---	AT2G24340	1.03	0.05	0.31	0.7624576	0.8870368	-6.50	FALSE
261967_at	En/Spm-like transposon protein,	---	---	1.05	0.07	0.31	0.7624278	0.8870368	-6.50	FALSE
254031_at	putative protein other hypothetica	---	AT4G25920	-1.03	-0.05	-0.31	0.7625233	0.8870438	-6.50	FALSE
258181_at	nitrate transporter identical to nitr	---	AT3G21670	1.06	0.08	0.31	0.7626413	0.8870454	-6.50	FALSE
249721_at	Expressed protein ; supported by	LSU4	AT5G24655	-1.03	-0.04	-0.31	0.7626168	0.8870454	-6.50	FALSE
256924_at	Anthocyanin 5-aromatic acyltran	AT5MAT	AT3G29590	1.04	0.05	0.31	0.7626046	0.8870454	-6.50	FALSE
249481_at	frnE protein - like frnE protein, D	---	AT5G38900	1.15	0.20	0.31	0.7629539	0.8872772	-6.50	TRUE
259184_at	unknown protein ;supported by f	---	AT3G01520	1.04	0.05	0.31	0.7629573	0.8872772	-6.50	FALSE
246338_s_a	putative protein putative integral	ATCHX10	AT3G44920 ///	1.03	0.04	0.31	0.7629166	0.8872772	-6.50	FALSE
264641_at	ATP-dependent Clp protease pr	---	AT1G09130	-1.04	-0.06	-0.31	0.7630907	0.8873871	-6.50	FALSE
265548_s_a	putative helicase	---	---	-1.03	-0.04	-0.31	0.7631605	0.8874231	-6.50	FALSE
264836_at	unknown protein similar to hypot	---	AT1G03610	1.06	0.08	0.31	0.7632494	0.8874812	-6.50	TRUE
246847_at	putative protein ferroportin1, Mu	ATIREG3	AT5G26820	-1.06	-0.09	-0.31	0.7633729	0.8875385	-6.50	FALSE
246077_at	putative protein XNP-1, Caenorh	CHR42	AT5G20420	1.05	0.08	0.31	0.7633765	0.8875385	-6.50	FALSE
266946_at	putative protein kinase contains a	---	AT2G18890	1.04	0.06	0.31	0.7634766	0.8875644	-6.50	TRUE
251324_at	plasma membrane intrinsic prote	PIP1A	AT3G61430	-1.04	-0.06	-0.31	0.7634604	0.8875644	-6.50	FALSE
245916_at	putative protein	---	AT5G28720	-1.04	-0.06	-0.31	0.7635706	0.8876284	-6.50	FALSE
258290_at	hypothetical protein predicted by	---	AT3G23460	-1.03	-0.04	-0.31	0.7636874	0.887719	-6.50	FALSE
257400_s_a	hypothetical protein	---	AT1G23810 ///	-1.03	-0.04	-0.31	0.7637644	0.8877632	-6.50	FALSE
259206_at	hypothetical protein similar to put	---	AT3G09040	-1.04	-0.06	-0.31	0.7639548	0.8878753	-6.50	FALSE
264220_at	unknown protein similar to putati	ARPC3	AT1G60430	1.03	0.05	0.31	0.7640064	0.8878753	-6.50	FALSE
250640_at	putative protein protein kinase X	---	AT5G07150	1.07	0.10	0.31	0.7639183	0.8878753	-6.50	FALSE
262012_s_a	integral membrane protein, puta	---	AT1G35625 ///	-1.03	-0.05	-0.31	0.7640289	0.8878753	-6.50	FALSE
252536_at	putative transporter protein pept	---	AT3G45700	1.04	0.06	0.31	0.7640555	0.8878753	-6.50	FALSE
259465_at	hypothetical protein similar to put	---	AT1G19025	1.04	0.06	0.31	0.7641035	0.8878859	-6.50	FALSE
266043_at	hypothetical protein	---	AT2G07724	-1.05	-0.07	-0.31	0.7643899	0.888083	-6.50	FALSE
265035_at	hypothetical protein contains Pfa	---	AT1G61620	-1.04	-0.05	-0.31	0.7643379	0.888083	-6.50	FALSE
264723_at	putative salt-inducible protein sim	---	AT1G22960	1.03	0.05	0.31	0.7643889	0.888083	-6.50	FALSE

256670_at	Athila ORF 1, putative similar to	---	---	1.03	0.05	0.31	0.7645286	0.888199	-6.50	FALSE
250781_at	DREB2A (dbj|BAA33794.1) ; su	DREB2A	AT5G05410	1.07	0.10	0.31	0.7646663	0.8883137	-6.50	FALSE
247970_at	cytosolic malate dehydrogenase	---	AT5G56720	-1.03	-0.05	-0.31	0.7647802	0.8883192	-6.50	FALSE
264950_at	peroxidase, putative similar to p	---	AT1G77100	1.04	0.05	0.31	0.7648269	0.8883192	-6.50	FALSE
254449_at	putative protein predicted protei	HEN1	AT4G20910	-1.05	-0.07	-0.31	0.7648094	0.8883192	-6.50	FALSE
245801_at	hypothetical protein similar to hy	---	AT1G46912	1.04	0.05	0.31	0.7647393	0.8883192	-6.50	FALSE
263017_at	putative cyclin 2	CYCB2;1	AT2G17620	1.03	0.05	0.31	0.7648922	0.8883499	-6.50	FALSE
267465_at	subtilisin-like serine protease cor	SLP3	AT2G19170	1.09	0.12	0.31	0.7652244	0.8884474	-6.50	FALSE
258429_at	putative GTP-binding protein sim	TOC120	AT3G16620	-1.04	-0.05	-0.31	0.7652006	0.8884474	-6.50	FALSE
250962_at	putative protein various predicte	---	AT5G02990	-1.04	-0.05	-0.31	0.7651393	0.8884474	-6.50	FALSE
245931_at	major pollen allergen-like protei	---	AT5G09280	-1.05	-0.07	-0.31	0.7651004	0.8884474	-6.50	FALSE
245380_at	hypothetical protein	---	AT4G17760	1.05	0.07	0.31	0.7652488	0.8884474	-6.50	FALSE
248431_at	auxin-responsive GH3-like protei	---	AT5G51470	-1.04	-0.05	-0.31	0.765246	0.8884474	-6.50	FALSE
245212_at	hypothetical protein predicted by	AT1G4422	---	-1.05	-0.07	-0.31	0.7650733	0.8884474	-6.50	FALSE
251881_at	DIPHOSPHOMEVALONATE DE	---	AT3G54250	1.07	0.10	0.31	0.765386	0.8885042	-6.50	TRUE
264373_at	putative vesicle transport protein	SEC22	AT1G11890	-1.05	-0.07	-0.31	0.7653438	0.8885042	-6.50	FALSE
248050_at	unknown protein	---	AT5G56100	-1.07	-0.10	-0.31	0.7654926	0.8885042	-6.50	FALSE
257716_at	hypothetical protein predicted by	---	AT3G18300	1.04	0.05	0.31	0.7654344	0.8885042	-6.50	FALSE
253927_at	putative protein	---	AT4G26710	-1.04	-0.06	-0.31	0.7654555	0.8885042	-6.50	FALSE
252623_at	hypothetical protein	---	AT3G45320	1.04	0.05	0.31	0.7658515	0.8888757	-6.50	FALSE
263024_at	hypothetical protein predicted by	---	AT1G23980	-1.05	-0.06	-0.31	0.765992	0.8889588	-6.50	FALSE
245846_at	P-type transporting ATPase, put	---	AT1G26130	1.05	0.07	0.31	0.7660011	0.8889588	-6.50	FALSE
260597_at	hypothetical protein predicted by	---	AT1G55915	-1.05	-0.08	-0.31	0.76613	0.8890421	-6.50	FALSE
254437_s_a	putative protein	---	AT3G06433	-1.06	-0.08	-0.31	0.7661508	0.8890421	-6.50	FALSE
254191_at	hypothetical protein ;supported b	---	AT4G23900	1.04	0.06	0.31	0.7662023	0.8890566	-6.50	FALSE
266935_at	F-box protein LKP2/ADO2, AtFB	LKP2	AT2G18915	-1.03	-0.05	-0.31	0.7662825	0.8891044	-6.50	FALSE
249469_at	UDP-glucose dehydrogenase-lik	---	AT5G39320	1.09	0.12	0.31	0.7665385	0.8893104	-6.50	TRUE
267360_at	unknown protein ;supported by f	---	AT2G40060	1.04	0.06	0.31	0.7665661	0.8893104	-6.50	FALSE
246726_at	putative protein predicted protei	---	AT5G29050	-1.03	-0.04	-0.31	0.766577	0.8893104	-6.50	FALSE
261092_at	unknown protein	---	AT1G62870	1.03	0.04	0.31	0.7666874	0.8893899	-6.50	FALSE
255141_at	putative protein several hypothet	---	---	-1.03	-0.04	-0.31	0.7667235	0.8893899	-6.50	FALSE
259574_at	hypothetical protein	MLP168	AT1G35310	1.03	0.04	0.31	0.7669049	0.8895098	-6.50	FALSE
255213_at	putative athila transposon protei	---	---	1.03	0.04	0.31	0.7669043	0.8895098	-6.50	FALSE
256949_at	hypothetical protein predicted by	---	AT3G19070	-1.03	-0.04	-0.31	0.7670192	0.8895971	-6.50	FALSE
262744_at	anthranilate N-hydroxycinnamoy	---	AT1G28680	-1.06	-0.09	-0.31	0.7671715	0.8896895	-6.50	TRUE

254048_at	putative protein various predicte	---	AT4G25680	1.06	0.08	0.31	0.7676592	0.8896895	-6.50	FALSE
255485_at	predicted protein of unknown fur	---	AT4G02550	-1.03	-0.05	-0.31	0.7676125	0.8896895	-6.50	FALSE
245879_at	putative subunit of TOC complex	ATTOC64-V	AT5G09420	-1.10	-0.13	-0.31	0.767916	0.8896895	-6.50	FALSE
253444_at	putative protein ring finger prote	---	AT4G32600	-1.03	-0.04	-0.31	0.7671797	0.8896895	-6.50	FALSE
261179_at	unknown protein	---	AT1G04985	-1.04	-0.06	-0.31	0.7677564	0.8896895	-6.50	FALSE
263002_at	hypothetical protein predicted by	---	AT1G54200	1.08	0.12	0.31	0.7675216	0.8896895	-6.50	FALSE
249806_at	putative protein contains similarit	---	AT5G23850	1.08	0.11	0.31	0.7673633	0.8896895	-6.50	FALSE
246219_at	aminopeptidase-like protein ; sup	APP1	AT4G36760	1.05	0.07	0.31	0.7678657	0.8896895	-6.50	FALSE
265587_at	putative pathogenesis-related pr	---	AT2G19980	-1.04	-0.05	-0.31	0.7676794	0.8896895	-6.50	FALSE
249051_at	berberine bridge enzyme-like pro	---	AT5G44390	-1.04	-0.06	-0.31	0.7672603	0.8896895	-6.50	FALSE
267618_at	putative cyclin ; supported by cD	CYCB1;4	AT2G26760	-1.04	-0.06	-0.31	0.7674553	0.8896895	-6.50	FALSE
257341_at	pseudogene, Mutator-like transp	---	---	1.03	0.04	0.31	0.7676786	0.8896895	-6.50	FALSE
248778_at	unknown protein	---	AT5G47940	-1.04	-0.05	-0.31	0.7675346	0.8896895	-6.50	FALSE
248598_at	putative protein contains similarit	---	AT5G49370	1.04	0.06	0.31	0.7677753	0.8896895	-6.50	FALSE
252588_at	putative protein potential transcr	---	AT3G45630	-1.03	-0.05	-0.31	0.7677726	0.8896895	-6.50	FALSE
257440_at	unknown protein	---	AT2G24880	-1.03	-0.04	-0.31	0.7674614	0.8896895	-6.50	FALSE
249105_at	40S ribosomal protein S15	---	AT5G43640	1.03	0.05	0.31	0.7678222	0.8896895	-6.50	FALSE
252708_at	putative protein amine oxidase,	---	AT3G43820	1.04	0.06	0.31	0.7675276	0.8896895	-6.50	FALSE
257049_at	hypothetical protein predicted by	---	AT3G15250	1.05	0.07	0.31	0.7673417	0.8896895	-6.50	FALSE
245153_at	putative protein similarity to prec	---	AT5G12450	-1.03	-0.04	-0.31	0.7679178	0.8896895	-6.50	FALSE
264898_at	Unknown protein ; supported by	---	AT1G23205	-1.06	-0.08	-0.31	0.7681772	0.8898544	-6.50	FALSE
266785_at	putative receptor-like protein kina	---	AT2G28970	1.04	0.05	0.31	0.7681597	0.8898544	-6.50	FALSE
264174_s_a	hypothetical protein	ANAC004	AT1G02230	-1.05	-0.07	-0.31	0.7681416	0.8898544	-6.50	FALSE
262103_at	glutathione S-transferase, putati	GSTF5	AT1G02940	1.06	0.08	0.31	0.7682801	0.8898831	-6.50	FALSE
265156_at	hypothetical protein predicted by	---	AT1G31000	-1.04	-0.05	-0.31	0.7682467	0.8898831	-6.50	FALSE
262416_at	flavonol synthase, putative simil	---	AT1G49390	-1.03	-0.05	-0.31	0.7684685	0.8900562	-6.50	FALSE
248989_at	disease resistance protein RPS4	---	AT5G45200	-1.04	-0.06	-0.31	0.7685145	0.8900643	-6.50	FALSE
247472_at	cytokinesis regulating protein - li	MAP65-9	AT5G62250	-1.03	-0.04	-0.31	0.7686786	0.8902091	-6.50	FALSE
252740_at	pectinesterase -like protein PEC	---	AT3G43270	-1.06	-0.08	-0.31	0.7687237	0.8902162	-6.50	TRUE
264649_at	hypothetical protein Similar to Vi	---	AT1G09060	-1.04	-0.06	-0.31	0.7689566	0.8902214	-6.50	FALSE
249018_at	CHP-rich zinc finger protein-like	---	AT5G44770	1.05	0.08	0.31	0.7688345	0.8902214	-6.50	FALSE
260762_at	I-box binding factor, putative sim	---	AT1G49015	1.03	0.05	0.31	0.7687887	0.8902214	-6.50	FALSE
262874_at	hypothetical protein predicted by	---	AT1G65020	-1.04	-0.06	-0.31	0.7688808	0.8902214	-6.50	FALSE
262585_at	hypothetical protein Is a member	BOR4	AT1G15460	1.05	0.07	0.31	0.7689624	0.8902214	-6.50	FALSE
265827_at	hypothetical protein predicted by	VOZ2	AT2G42400	1.03	0.04	0.31	0.7689172	0.8902214	-6.50	FALSE

258694_at	putative non-phototropic hypocot	---	AT3G08660	-1.07	-0.10	-0.31	0.7690943	0.8903219	-6.50	FALSE
253180_at	putative protein various predicte	---	AT4G35210	-1.03	-0.04	-0.31	0.7691273	0.8903219	-6.50	FALSE
256457_at	3-methyladenine DNA glycosyla	---	AT1G75230	1.07	0.10	0.31	0.7692522	0.8904213	-6.50	FALSE
246490_at	S-adenosylmethionine decarboxy	CPuORF10	AT5G15948 /	-1.05	-0.07	-0.31	0.7694474	0.8904723	-6.50	FALSE
264141_at	hypothetical protein predicted by	---	AT1G79090	-1.03	-0.04	-0.31	0.7694413	0.8904723	-6.50	FALSE
252372_at	aldehyde dehydrogenase (NAD-	ALDH2B4	AT3G48000	1.05	0.07	0.31	0.7694914	0.8904723	-6.50	FALSE
248545_at	cysteine proteinase similar to cys	---	AT5G50260	1.03	0.05	0.31	0.7694578	0.8904723	-6.50	FALSE
265168_at	putative Ser/Thr protein kinase	---	AT1G23700	1.04	0.05	0.31	0.7694504	0.8904723	-6.50	FALSE
265325_at	putative integral membrane prote	---	AT2G18240	1.05	0.06	0.30	0.7696036	0.890557	-6.50	FALSE
261089_at	protein kinase APK1A identical to	APK1A	AT1G07570	1.06	0.08	0.30	0.7698156	0.8907372	-6.50	FALSE
256638_at	RNA-binding protein, putative si	---	AT3G19090	1.05	0.07	0.30	0.7698375	0.8907372	-6.50	FALSE
255781_at	unknown protein	---	AT1G19880	1.03	0.04	0.30	0.7699246	0.8907928	-6.50	FALSE
251535_at	hypothetical protein ;supported b	---	AT3G58540	1.05	0.07	0.30	0.7701264	0.8909811	-6.51	FALSE
264464_at	putative heat-shock protein simila	---	AT1G10350	-1.04	-0.05	-0.30	0.7702568	0.8910868	-6.51	FALSE
254476_at	putative protein gamma-SNAP p	GSNAP	AT4G20410	-1.03	-0.05	-0.30	0.7703205	0.8911072	-6.51	FALSE
262597_at	unknown protein Strong similarit	---	AT1G15470	-1.05	-0.07	-0.30	0.7703526	0.8911072	-6.51	FALSE
252727_s_a	putative protein predicted protei	---	---	-1.03	-0.04	-0.30	0.7704211	0.8911412	-6.51	FALSE
245925_at	bZIP transcription factor family p	BZO2H3	AT5G28770	1.05	0.07	0.30	0.7704618	0.8911431	-6.51	FALSE
263784_at	Expressed protein ; supported by	---	AT2G46375	-1.03	-0.05	-0.30	0.77067	0.8913388	-6.51	FALSE
247407_at	putative protein predicted protei	---	AT5G62900	1.05	0.06	0.30	0.7708979	0.8915119	-6.51	FALSE
254862_at	putative transport protein Na(+)	---	AT4G12030	-1.06	-0.09	-0.30	0.7708815	0.8915119	-6.51	FALSE
246175_s_a	putative protein hypothetical pro	---	AT5G28320 /	1.03	0.05	0.30	0.7710115	0.8915555	-6.51	FALSE
250534_at	NADH dehydrogenase ;supporte	CI51	AT5G08530	1.03	0.05	0.30	0.7710137	0.8915555	-6.51	FALSE
251247_at	hypothetical protein	---	AT3G62140	1.04	0.06	0.30	0.7710968	0.8916064	-6.51	FALSE
247166_at	unknown protein	---	AT5G65840	1.07	0.10	0.30	0.7714057	0.8917929	-6.51	FALSE
250348_at	putative protein	---	AT5G11990	1.04	0.06	0.30	0.7717664	0.8917929	-6.51	FALSE
263293_x_a	hypothetical protein similar to hy	---	---	-1.03	-0.04	-0.30	0.7714992	0.8917929	-6.51	FALSE
255944_at	putative protein	---	---	1.04	0.05	0.30	0.771531	0.8917929	-6.51	FALSE
266134_s_a	putative beta-expansin	---	AT1G65680 /	-1.03	-0.05	-0.30	0.7713604	0.8917929	-6.51	FALSE
262429_at	polyprotein, putative similar to p	---	---	1.04	0.06	0.30	0.771472	0.8917929	-6.51	FALSE
253298_at	putative protein ;supported by fu	---	AT4G33560	1.04	0.05	0.30	0.7716538	0.8917929	-6.51	FALSE
246470_at	putative protein predicted protei	---	AT5G17080	1.03	0.05	0.30	0.7717233	0.8917929	-6.51	FALSE
263418_at	putative selenium-binding protein	---	AT2G17210	1.03	0.05	0.30	0.7717425	0.8917929	-6.51	FALSE
251084_at	putative protein putative proteins	---	AT5G01520	-1.07	-0.10	-0.30	0.7716432	0.8917929	-6.51	FALSE
257920_at	hypothetical protein predicted by	---	AT3G23260	1.03	0.04	0.30	0.771715	0.8917929	-6.51	FALSE

263441_at	putative kinesin-like spindle prote	---	AT2G28620	-1.03	-0.04	-0.30	0.7715457	0.8917929	-6.51	FALSE
253030_at	hypothetical protein	FRS5	AT4G38180	-1.03	-0.04	-0.30	0.7715205	0.8917929	-6.51	FALSE
252793_at	hypothetical protein	---	---	1.03	0.04	0.30	0.7718949	0.8918962	-6.51	FALSE
267376_at	putative receptor-like protein kin	ER	AT2G26330	1.15	0.20	0.30	0.7719406	0.8919038	-6.51	FALSE
248987_at	dimethylaniline monooxygenase	---	AT5G45180	1.03	0.04	0.30	0.7721018	0.8919815	-6.51	FALSE
251450_at	squamosa promoter binding prot	SPL12	AT3G60030	-1.04	-0.06	-0.30	0.7722033	0.8919815	-6.51	FALSE
257569_at	hypothetical protein	---	AT3G26350	-1.05	-0.07	-0.30	0.7721435	0.8919815	-6.51	FALSE
255698_at	scarecrow-like 6 (SCL6)	---	AT4G00150	-1.05	-0.06	-0.30	0.7721843	0.8919815	-6.51	FALSE
249939_at	unknown protein ;supported by f	---	AT5G22430	1.04	0.06	0.30	0.7720756	0.8919815	-6.51	FALSE
262960_at	unknown protein ; supported by c	---	AT1G54320	1.03	0.05	0.30	0.7724531	0.8921796	-6.51	FALSE
256703_at	MADS-box transcription factor s	AGL79	AT3G30260	-1.03	-0.04	-0.30	0.7724325	0.8921796	-6.51	FALSE
252587_at	putative protein Human (H326) t	---	AT3G45620	1.07	0.09	0.30	0.7725753	0.8922303	-6.51	FALSE
250037_at	disease resistance protein -like c	---	AT5G18350	1.05	0.06	0.30	0.7725452	0.8922303	-6.51	FALSE
267423_at	putative potassium transporter	KUP11	AT2G35060	1.06	0.09	0.30	0.7726559	0.8922784	-6.51	FALSE
262913_at	NADPH-dependent codeinone r	---	AT1G59960	-1.10	-0.14	-0.30	0.7729542	0.892489	-6.51	FALSE
247752_at	putative protein	---	AT5G59060	1.03	0.04	0.30	0.7729949	0.892489	-6.51	FALSE
266609_at	unknown protein ; supported by	SRO1	AT2G35510	1.05	0.07	0.30	0.7729181	0.892489	-6.51	FALSE
258305_at	hypothetical protein predicted by	---	---	1.03	0.04	0.30	0.7729803	0.892489	-6.51	FALSE
254815_at	putative pollen-specific protein p	SKU5	AT4G12420	1.06	0.09	0.30	0.7732045	0.8925143	-6.51	TRUE
259008_at	metallothionein-like protein simila	MT2A	AT3G09390	-1.04	-0.05	-0.30	0.773103	0.8925143	-6.51	TRUE
252026_at	serine protein kinase - like serin	SRPK4	AT3G53030	-1.04	-0.05	-0.30	0.7732027	0.8925143	-6.51	FALSE
254123_at	Bnm1 like protein pollen-specific	APPB1	AT4G24640	1.03	0.05	0.30	0.7732124	0.8925143	-6.51	FALSE
251359_at	putative protein several hypothet	---	AT3G61170	-1.03	-0.04	-0.30	0.7732114	0.8925143	-6.51	FALSE
258343_at	unknown protein similar to hypot	---	AT3G22810	1.04	0.05	0.30	0.773311	0.8925829	-6.51	FALSE
267207_at	putative dioxygenase	---	AT2G30840	-1.09	-0.12	-0.30	0.773519	0.8927649	-6.51	TRUE
246680_at	putative protein predicted protein	---	---	1.04	0.05	0.30	0.7735837	0.8927649	-6.51	FALSE
247421_at	SIAH1 - like protein SIAH1, Bras	---	AT5G62800	1.04	0.06	0.30	0.773586	0.8927649	-6.51	FALSE
246067_at	membrane transporter - like prot	---	AT5G19410	-1.03	-0.04	-0.30	0.7736833	0.8928319	-6.51	FALSE
255399_at	hypothetical protein	---	---	1.04	0.06	0.30	0.7737357	0.8928473	-6.51	FALSE
263608_at	putative glycine-rich RNA-binding	---	---	1.04	0.06	0.30	0.7737751	0.8928475	-6.51	FALSE
253468_at	putative protein predicted gene 1	---	AT4G32160	-1.04	-0.06	-0.30	0.7739564	0.8929508	-6.51	FALSE
258300_at	putative casein kinase I similar to	ckl10	AT3G23340	-1.05	-0.07	-0.30	0.7739683	0.8929508	-6.51	FALSE
247477_at	putative protein 21K protein prec	---	AT5G62340	1.05	0.07	0.30	0.7740212	0.8929508	-6.51	FALSE
249873_at	ATP-dependent Clp protease pr	NCLPP7	AT5G23140	-1.04	-0.05	-0.30	0.7739931	0.8929508	-6.51	FALSE
248684_at	Expressed protein ; supported by	DIR1	AT5G48485	-1.10	-0.14	-0.30	0.7741825	0.8930917	-6.51	FALSE

253262_at	putative serine threonine protein	---	AT4G34440	-1.03	-0.05	-0.30	0.7743566	0.8932475	-6.51	FALSE
266029_at	putative serine carboxypeptidase	scpl38	AT2G05850	1.04	0.05	0.30	0.7744168	0.8932716	-6.51	FALSE
246923_at	putative multispanning membrar	---	AT5G25100	-1.04	-0.06	-0.30	0.7746058	0.8933541	-6.51	FALSE
257268_at	unknown protein	---	AT3G17450	-1.05	-0.07	-0.30	0.7745813	0.8933541	-6.51	FALSE
262689_at	unknown protein	ANAC026	AT1G62700	-1.04	-0.05	-0.30	0.7745676	0.8933541	-6.51	FALSE
245625_at	transport protein	---	AT4G14160	1.03	0.05	0.30	0.7748826	0.8936282	-6.51	FALSE
254608_at	major intrinsic protein (MIP)- like	NIP1;2	AT4G18910	1.08	0.12	0.30	0.7749511	0.8936621	-6.51	FALSE
263745_at	hypothetical protein predicted by	CHR34	AT2G21450	1.03	0.04	0.30	0.7749936	0.8936659	-6.51	FALSE
249982_at	putative protein predicted protei	---	AT5G18520	-1.03	-0.05	-0.30	0.7751145	0.89376	-6.51	FALSE
261331_at	hypothetical protein predicted by	---	---	-1.04	-0.05	-0.30	0.7752087	0.8938236	-6.51	FALSE
255722_at	hypothetical protein	---	AT3G29570	-1.04	-0.05	-0.30	0.7752781	0.8938584	-6.51	FALSE
261025_at	Expressed protein ; supported by	---	AT1G01225	1.06	0.09	0.30	0.7754717	0.8940216	-6.51	TRUE
255502_at	contains similarity to a protein ki	---	AT4G02410	1.14	0.19	0.30	0.7755718	0.8940216	-6.51	TRUE
257984_at	putative cell differentiation prote	---	AT3G20800	-1.05	-0.06	-0.30	0.7755765	0.8940216	-6.51	FALSE
263158_at	CCAAT-binding factor B subunit	NF-YA5	AT1G54160	-1.03	-0.05	-0.30	0.7755457	0.8940216	-6.51	FALSE
262679_at	unknown protein ; supported by c	LCR67	AT1G75830	1.04	0.06	0.30	0.7756255	0.8940329	-6.51	FALSE
250003_at	hypothetical protein predicted pr	---	AT5G18710	1.03	0.04	0.30	0.7757102	0.8940854	-6.51	FALSE
261514_at	hypothetical protein predicted by	---	AT1G71870	-1.05	-0.07	-0.30	0.7757552	0.8940921	-6.51	FALSE
245913_at	predicted protein	---	AT5G19860	-1.04	-0.05	-0.30	0.7758081	0.8941079	-6.51	FALSE
255943_at	UDP-glucose glucosyltransferas	AtUGT85A5	AT1G22370	-1.11	-0.15	-0.30	0.7758827	0.8941487	-6.51	FALSE
249697_at	unknown protein	---	AT5G35510	-1.03	-0.05	-0.30	0.7759825	0.8942185	-6.51	FALSE
256549_at	hypothetical protein predicted by	---	---	1.03	0.04	0.30	0.7761114	0.8943219	-6.51	FALSE
256051_at	hypothetical protein similar to put	CHX14	AT1G06970	1.04	0.06	0.30	0.776161	0.8943338	-6.51	FALSE
256240_at	unknown protein ; supported by c	atnudt16	AT3G12600	1.04	0.05	0.30	0.7765158	0.8946781	-6.51	FALSE
264856_at	3-hydroxy-3-methylglutaryl-coen	HMG2	AT2G17370	1.05	0.07	0.30	0.7765775	0.8946781	-6.51	FALSE
261800_at	HD-Zip protein identical to HD-Zi	PHV	AT1G30490	1.04	0.06	0.30	0.776562	0.8946781	-6.51	FALSE
253316_s_a	putative protein hyphally regulat	---	AT4G33930 ///	-1.06	-0.08	-0.30	0.7766357	0.8947	-6.51	FALSE
257497_at	hypothetical protein predicted by	---	AT1G51430	-1.05	-0.08	-0.30	0.7766854	0.8947121	-6.51	FALSE
260350_at	Eukaryotic initiation factor 5A , p	ELF5A-3	AT1G69410	1.05	0.07	0.30	0.776789	0.8947411	-6.51	FALSE
253250_at	hypothetical protein	---	AT4G34690	1.03	0.04	0.30	0.7767851	0.8947411	-6.51	FALSE
256105_at	hypothetical protein predicted by	LSH8	AT1G16910	1.04	0.05	0.30	0.7768299	0.8947429	-6.51	FALSE
259002_at	putative glutaredoxin similar to gl	ROXY1	AT3G02000	1.05	0.07	0.29	0.7771945	0.8950725	-6.51	FALSE
257558_s_a	hypothetical protein contains Pfa	---	AT3G22000 ///	1.03	0.05	0.29	0.7771696	0.8950725	-6.51	FALSE
250530_at	unknown protein	---	AT5G08630	1.04	0.05	0.29	0.7772946	0.8950974	-6.51	FALSE
246168_at	meristem protein - like reproduct	---	AT5G32460	1.05	0.07	0.29	0.7772917	0.8950974	-6.51	FALSE

264078_at	putative beta-galactosidase	BGAL8	AT2G28470	-1.12	-0.16	-0.29	0.7775377	0.8952869	-6.51	TRUE
257563_at	hypothetical protein predicted by	---	AT3G19610	-1.03	-0.04	-0.29	0.7775152	0.8952869	-6.51	FALSE
262484_at	putative transcriptional regulator	ATSWI3C	AT1G21700	1.03	0.04	0.29	0.777595	0.8953078	-6.51	FALSE
261459_at	O-methyltransferase, putative si	---	AT1G21100	-1.19	-0.25	-0.29	0.7777923	0.895309	-6.51	TRUE
258667_at	hypothetical protein	---	AT3G08750	1.03	0.05	0.29	0.777743	0.895309	-6.51	FALSE
264771_at	phosphomethylpyrimidine kinase	TH1	AT1G22940	-1.03	-0.04	-0.29	0.7777042	0.895309	-6.51	FALSE
248113_at	wax synthase-like protein	---	AT5G55360	1.04	0.05	0.29	0.7777822	0.895309	-6.51	FALSE
267386_at	unknown protein	---	AT2G44430	-1.05	-0.07	-0.29	0.7777387	0.895309	-6.51	FALSE
261995_at	unknown protein similar to N-terr	---	AT1G33850 ///	-1.03	-0.04	-0.29	0.7778987	0.8953863	-6.51	FALSE
256302_at	Expressed protein ; supported by	---	AT1G69526	1.04	0.06	0.29	0.7779677	0.8954205	-6.51	FALSE
246140_at	SOH1 - like protein SOH1, Sacc	---	AT5G19910	-1.03	-0.04	-0.29	0.7780154	0.8954302	-6.51	FALSE
263338_at	hypothetical protein predicted by	---	---	-1.04	-0.05	-0.29	0.7781433	0.8955323	-6.51	FALSE
250422_at	putative protein KIAA0255 gene	---	AT5G10840	1.06	0.08	0.29	0.7783861	0.8956624	-6.51	FALSE
257491_at	hypothetical protein predicted by	---	AT1G06170	1.03	0.04	0.29	0.7784266	0.8956624	-6.51	FALSE
259356_at	unknown protein	---	AT3G05250	-1.03	-0.04	-0.29	0.778476	0.8956624	-6.51	FALSE
254542_s_a	putative LTR retrotransposon Br	---	---	1.03	0.04	0.29	0.7783513	0.8956624	-6.51	FALSE
254712_at	hypothetical protein	---	AT4G18080	1.03	0.04	0.29	0.7783819	0.8956624	-6.51	FALSE
254968_at	putative protein various predicte	---	AT4G10420	1.03	0.04	0.29	0.778492	0.8956624	-6.51	FALSE
256911_at	glutamine:fructose-6-phosphate	---	AT3G24090	1.12	0.17	0.29	0.7786278	0.8957735	-6.51	FALSE
252916_at	kinesin like protein kinesin-relate	---	AT4G38950	1.03	0.05	0.29	0.7787212	0.8958357	-6.51	FALSE
258855_at	unknown protein	---	AT3G02070	1.06	0.08	0.29	0.7789117	0.8959444	-6.51	FALSE
266622_at	hypothetical protein predicted by	---	AT2G35430	-1.04	-0.06	-0.29	0.7789335	0.8959444	-6.51	FALSE
259359_at	B regulatory subunit of protein p	---	AT1G13460	1.04	0.05	0.29	0.7789261	0.8959444	-6.51	FALSE
250413_at	adenine phosphoribosyltransfera	APT5	AT5G11160	-1.05	-0.07	-0.29	0.7790768	0.8959811	-6.51	TRUE
248408_at	ripening-related protein-like	---	AT5G51520	-1.03	-0.04	-0.29	0.7790496	0.8959811	-6.51	FALSE
247244_at	putative protein similar to unknov	---	AT5G64710	1.03	0.04	0.29	0.7790832	0.8959811	-6.51	FALSE
261662_at	MAP kinase kinase 5, putative s	ATMKK7	AT1G18350	1.03	0.04	0.29	0.7791443	0.8960061	-6.51	FALSE
246504_at	hypothetical protein ;supported b	---	AT5G16160	1.03	0.04	0.29	0.7792016	0.8960269	-6.51	FALSE
265028_at	hypothetical protein predicted by	---	AT1G24530	-1.12	-0.16	-0.29	0.7792461	0.8960329	-6.51	TRUE
261868_s_a	hypothetical protein contains sim	---	AT1G11450 ///	1.02	0.03	0.29	0.779287	0.8960347	-6.51	FALSE
252066_at	receptor-protein kinase-like prot	FER	AT3G51550	1.05	0.07	0.29	0.7793396	0.8960501	-6.51	TRUE
266773_at	hypothetical protein predicted by	---	AT2G29040	-1.03	-0.04	-0.29	0.7793997	0.8960621	-6.51	FALSE
249357_at	ribonucleoprotein -like ribonucle	---	AT5G40490	1.04	0.06	0.29	0.7794287	0.8960621	-6.51	FALSE
257405_at	putative calmodulin similar to ES	---	AT1G24620	-1.03	-0.04	-0.29	0.7795322	0.8961359	-6.51	FALSE
251380_at	putative protein	---	AT3G60700	1.03	0.04	0.29	0.7796161	0.8961377	-6.51	FALSE

266872_at	unknown protein	---	AT2G44730	1.04	0.05	0.29	0.779617	0.8961377	-6.51	FALSE
258873_at	hypothetical protein similar to unl	---	AT3G03240	1.04	0.06	0.29	0.7796516	0.8961377	-6.51	FALSE
267407_at	unknown protein	MEE27	AT2G34880	1.04	0.05	0.29	0.7797259	0.8961454	-6.51	FALSE
264034_s_a	unknown protein	ATUPS1	AT2G03590 ///	1.03	0.05	0.29	0.7797368	0.8961454	-6.51	FALSE
249774_at	squalene monooxygenase	SQP1	AT5G24150	1.06	0.08	0.29	0.7799012	0.8961988	-6.51	FALSE
245818_at	cytochrome b561, putative simila	---	AT1G26100	1.06	0.09	0.29	0.779865	0.8961988	-6.51	FALSE
255875_s_a	putative protein kinase contains a	---	AT2G40500 ///	-1.04	-0.05	-0.29	0.7798428	0.8961988	-6.51	FALSE
245268_at	hypothetical protein ; supported b	PRMT7	AT4G16570	1.06	0.09	0.29	0.7803444	0.8964574	-6.51	FALSE
266949_s_a	unknown protein ;supported by fu	---	AT2G18840 ///	-1.04	-0.06	-0.29	0.7803509	0.8964574	-6.51	FALSE
259190_at	unknown protein est hit, predicte	TPLATE	AT3G01780	-1.05	-0.07	-0.29	0.780255	0.8964574	-6.51	FALSE
264132_at	hypothetical protein predicted by	---	AT1G79100	1.04	0.06	0.29	0.780362	0.8964574	-6.51	FALSE
245997_at	putative protein saur1 protein, Z	---	AT5G20810	1.05	0.07	0.29	0.7802758	0.8964574	-6.51	FALSE
252684_at	disease resistence - like protein	---	AT3G44400	1.03	0.05	0.29	0.7802521	0.8964574	-6.51	FALSE
250322_at	putative transcription factor (MYB	MYB46	AT5G12870	1.03	0.04	0.29	0.7804509	0.8965044	-6.51	FALSE
259680_at	putative AUX1-like permease sir	LAX3	AT1G77690	1.16	0.21	0.29	0.7804816	0.8965044	-6.51	FALSE
251533_at	putative protein several hypothet	ATRBL15	AT3G58460	1.03	0.04	0.29	0.7806453	0.8965401	-6.51	FALSE
258626_at	transfactor, putative similar to tra	---	AT3G04450	-1.04	-0.05	-0.29	0.7806026	0.8965401	-6.51	FALSE
245836_at	hypothetical protein similar to hyp	---	---	-1.03	-0.04	-0.29	0.7807092	0.8965401	-6.51	FALSE
262845_at	unknown protein ; supported by c	---	AT1G14740	1.06	0.09	0.29	0.7805702	0.8965401	-6.51	FALSE
255137_at	extensin-like protein extensin pre	---	AT4G08370	-1.04	-0.05	-0.29	0.7806848	0.8965401	-6.51	FALSE
258320_at	hypothetical protein predicted by	---	AT3G22710	1.03	0.04	0.29	0.7807809	0.8965773	-6.51	FALSE
265526_x_a	putative Athila retroelement ORF	---	---	-1.03	-0.04	-0.29	0.7808766	0.8965969	-6.51	FALSE
267245_at	hypothetical protein	---	AT2G02640	1.03	0.04	0.29	0.7808587	0.8965969	-6.51	FALSE
250391_at	putative protein predicted protein	---	---	-1.04	-0.05	-0.29	0.7809273	0.8966101	-6.51	FALSE
266124_at	putative PREG1-like negative reg	cycp3;1	AT2G45080	-1.04	-0.05	-0.29	0.7809676	0.8966112	-6.51	FALSE
265249_at	putative C2H2-type zinc finger pr	SGR5	AT2G01940	-1.09	-0.12	-0.29	0.7810563	0.8966427	-6.51	FALSE
267582_at	putative protein kinase contains a	---	AT2G41970	-1.03	-0.04	-0.29	0.7811456	0.8966427	-6.51	FALSE
260881_at	unknown protein contains similar	---	AT1G21550	1.16	0.22	0.29	0.7811523	0.8966427	-6.51	FALSE
261848_at	pectin methylesterase, putative s	---	AT1G11590	-1.04	-0.05	-0.29	0.7810811	0.8966427	-6.51	FALSE
266060_at	unknown protein unusual splice s	---	AT2G18630	1.05	0.06	0.29	0.7812374	0.8966709	-6.51	FALSE
256201_at	hypothetical protein predicted by	---	AT1G58230	1.03	0.05	0.29	0.7812555	0.8966709	-6.51	FALSE
265755_at	En/Spm transposon hypothetical	---	---	1.03	0.04	0.29	0.7813453	0.8967289	-6.51	FALSE
259606_at	hypothetical protein predicted by	MAP65-8	AT1G27920	1.03	0.04	0.29	0.7818311	0.8969705	-6.51	FALSE
256189_at	hypothetical protein predicted by	---	AT1G30140	1.03	0.04	0.29	0.7816701	0.8969705	-6.51	FALSE
247887_at	unknown protein	---	AT5G57880	-1.03	-0.04	-0.29	0.7818131	0.8969705	-6.51	FALSE

256429_at	unknown protein	---	AT3G11040	1.04	0.06	0.29	0.7817881	0.8969705	-6.51	FALSE
254591_at	heat shock transcription factor -	---	AT4G18870	1.02	0.03	0.29	0.7817608	0.8969705	-6.51	FALSE
257284_at	TNP1-like protein similar to TNP	---	---	-1.02	-0.03	-0.29	0.7817515	0.8969705	-6.51	FALSE
249893_at	Expressed protein ; supported by	---	AT5G22555	-1.03	-0.05	-0.29	0.7818102	0.8969705	-6.51	FALSE
262716_at	multicatalytic endopeptidase ide	PAB1	AT1G16470	-1.04	-0.06	-0.29	0.781878	0.8969792	-6.51	FALSE
259165_at	homeobox-leucine zipper protein	ATHB-1	AT3G01470 /	1.07	0.10	0.29	0.7820778	0.8971585	-6.51	FALSE
263569_at	putative chromosome associated	TTN7	AT2G27170	-1.05	-0.07	-0.29	0.7821523	0.8971585	-6.51	FALSE
263789_at	putative GDSL-motif lipase/hydro	---	AT2G24560	-1.05	-0.07	-0.29	0.7821426	0.8971585	-6.51	FALSE
258029_at	serine/threonine-protein kinase,	ATPK7	AT3G27580	-1.03	-0.04	-0.29	0.7822317	0.8972044	-6.51	FALSE
261598_at	unknown protein contains similar	---	AT1G49750	1.16	0.21	0.29	0.7823834	0.8972882	-6.51	FALSE
247928_at	villin	---	AT5G57320	1.04	0.06	0.29	0.7823654	0.8972882	-6.51	FALSE
259263_at	putative UDP-glucose 6-dehydro	---	AT3G01010	1.03	0.05	0.29	0.7826414	0.897539	-6.51	FALSE
250777_at	putative protein similar to unknov	---	AT5G05440	1.14	0.19	0.29	0.7828734	0.8977148	-6.51	TRUE
262692_at	hypothetical protein predicted by	---	---	1.03	0.05	0.29	0.7828714	0.8977148	-6.51	FALSE
248438_at	putative protein contains similarit	EMF2	AT5G51230	-1.05	-0.07	-0.29	0.7829935	0.8978074	-6.51	FALSE
252145_at	putative protein several putative	---	AT3G51200	-1.03	-0.04	-0.29	0.7831832	0.8979797	-6.51	FALSE
260432_at	putative DNA binding protein sim	WRKY9	AT1G68150	1.04	0.06	0.29	0.7832256	0.8979832	-6.51	FALSE
253662_at	transcription factor-like protein A	ARF16	AT4G30080	-1.03	-0.05	-0.29	0.7833209	0.8980474	-6.51	FALSE
256451_s_a	unknown protein	---	AT1G75170 /	1.09	0.13	0.29	0.7837582	0.898082	-6.51	TRUE
258588_s_a	glyceraldehyde-3-phosphate del	GAPC1	AT3G04120	1.07	0.10	0.29	0.7834959	0.898082	-6.51	FALSE
263774_at	unknown protein ; supported by	---	AT2G40280	1.03	0.04	0.29	0.7836573	0.898082	-6.51	FALSE
253453_at	protein phosphatase 2C - like pr	---	AT4G31860	1.03	0.04	0.29	0.7837709	0.898082	-6.51	FALSE
258372_at	ubiquitin-specific protease 25 (U	UBP25	AT3G14400	1.03	0.04	0.29	0.7838439	0.898082	-6.51	FALSE
246740_at	putative protein	---	AT5G27810	1.03	0.04	0.29	0.7836586	0.898082	-6.51	FALSE
261520_at	unknown protein ; supported by	SEC6	AT1G71820	-1.03	-0.04	-0.29	0.783863	0.898082	-6.51	FALSE
259599_at	serine carboxypeptidase II, puta	SCPL45	AT1G28110	1.11	0.15	0.29	0.7836959	0.898082	-6.51	FALSE
245677_at	hypothetical protein predicted by	---	AT1G56660	1.03	0.04	0.29	0.7837797	0.898082	-6.51	FALSE
245391_at	symbiosis-related like protein ;su	ATG8F	AT4G16520	-1.05	-0.07	-0.29	0.783748	0.898082	-6.51	FALSE
246556_at	putative protein hypothetical pro	---	AT5G15480	1.04	0.05	0.29	0.7834618	0.898082	-6.51	FALSE
260054_at	putative transporter contains Pfa	UNE2	AT1G78130	-1.06	-0.08	-0.29	0.7838173	0.898082	-6.51	FALSE
250378_at	putative oligopeptide transporter	---	AT5G11570	1.04	0.05	0.29	0.783738	0.898082	-6.51	FALSE
255938_at	hypothetical protein contains Pfa	---	AT1G12620	1.04	0.06	0.29	0.7839272	0.8981105	-6.51	FALSE
258513_at	protein kinase, putative contains	---	AT3G06630	-1.03	-0.04	-0.29	0.7840896	0.8982515	-6.51	FALSE
252841_at	putative protein replication prote	---	---	1.04	0.06	0.29	0.7841869	0.8982726	-6.51	FALSE
261283_s_a	hypothetical protein predicted by	---	---	-1.03	-0.04	-0.29	0.7841507	0.8982726	-6.51	FALSE

263772_at	Expressed protein ; supported by	ELF4-L3	AT2G06255	-1.06	-0.08	-0.28	0.7842793	0.8983235	-6.51	FALSE
264600_at	hypothetical protein predicted by	---	AT1G04730	-1.05	-0.07	-0.28	0.7843101	0.8983235	-6.51	FALSE
249032_at	putative protein contains similarit	---	AT5G44910	1.14	0.19	0.28	0.7843926	0.8983729	-6.51	FALSE
264102_at	hypothetical protein predicted by	ECT8	AT1G79270	1.05	0.06	0.28	0.7845832	0.8985461	-6.51	TRUE
260539_at	putative peroxidase	---	AT2G43480	1.03	0.04	0.28	0.7846278	0.8985521	-6.51	FALSE
258351_at	hypothetical protein contains sim	CNBT1	AT3G17700	1.05	0.07	0.28	0.7848667	0.8985574	-6.51	TRUE
257069_at	hypothetical protein predicted by	---	AT3G28170	1.03	0.04	0.28	0.7847899	0.8985574	-6.51	FALSE
246903_at	putative protein	---	AT5G25750	1.04	0.05	0.28	0.7848657	0.8985574	-6.51	FALSE
265652_x_a	hypothetical protein predicted by	---	---	-1.04	-0.05	-0.28	0.7846767	0.8985574	-6.51	FALSE
247678_at	putative zinc transporter ZIP2 - li	ZIP2	AT5G59520	1.06	0.09	0.28	0.7848688	0.8985574	-6.51	FALSE
261562_at	actin depolymerizing factor, puta	ADF11	AT1G01750	-1.04	-0.06	-0.28	0.7848588	0.8985574	-6.51	FALSE
260037_at	putative DNA-binding protein (RA	RAV2	AT1G68840	1.13	0.18	0.28	0.7849638	0.8986211	-6.51	FALSE
261945_at	unknown protein	---	AT1G64530	-1.06	-0.08	-0.28	0.7850177	0.8986376	-6.51	FALSE
259074_at	putative protein kinase contains I	RPK2	AT3G02130	-1.05	-0.07	-0.28	0.7850618	0.898643	-6.51	FALSE
262902_x_a	hypothetical protein similar to put	---	AT1G59930	1.05	0.08	0.28	0.7851958	0.8987513	-6.51	TRUE
262541_at	hypothetical protein contains sim	---	---	1.03	0.04	0.28	0.7852726	0.8987941	-6.51	FALSE
263315_at	Expressed protein ; supported by	---	AT2G05755	1.03	0.04	0.28	0.7853618	0.898806	-6.51	FALSE
251166_at	heat shock transcription factor-li	AT-HSFA7I	AT3G63350	1.03	0.05	0.28	0.7853265	0.898806	-6.51	FALSE
267170_at	putative RING zinc finger protein	---	AT2G37585	-1.06	-0.08	-0.28	0.7855276	0.8989129	-6.51	TRUE
252579_at	putative protein hypothetical pro	---	AT3G45510	1.03	0.04	0.28	0.7855735	0.8989129	-6.51	FALSE
251568_at	putative protein several hypothet	---	AT3G58280	1.04	0.05	0.28	0.785558	0.8989129	-6.51	FALSE
261045_at	pathogenesis related protein, pu	---	AT1G01310	-1.03	-0.04	-0.28	0.7856552	0.8989364	-6.51	FALSE
257320_at	hypothetical protein	---	AT2G07749	-1.04	-0.05	-0.28	0.7856728	0.8989364	-6.51	FALSE
260882_at	DNA binding protein, putative sir	WRKY65	AT1G29280	1.06	0.09	0.28	0.7858259	0.8990512	-6.51	TRUE
262829_at	auxin-independent growth prom	---	AT1G14970	1.06	0.08	0.28	0.785852	0.8990512	-6.51	FALSE
244953_s_a	NADH dehydrogenase subunit 6	---	AT2G07731	1.05	0.07	0.28	0.7861248	0.8992043	-6.51	TRUE
266581_at	putative desiccation related prote	---	AT2G46140	1.16	0.21	0.28	0.7862223	0.8992043	-6.51	TRUE
252472_at	GTP-binding protein Rab11 ; su	ATRABA2C	AT3G46830	-1.04	-0.05	-0.28	0.7861701	0.8992043	-6.51	FALSE
247066_at	DNA binding protein-like	---	AT5G66940	1.03	0.04	0.28	0.7862129	0.8992043	-6.51	FALSE
267589_at	hypothetical protein	---	---	-1.03	-0.04	-0.28	0.7862186	0.8992043	-6.51	FALSE
253960_at	putative protein various predicte	GAMT1	AT4G26420	1.04	0.05	0.28	0.7862104	0.8992043	-6.51	FALSE
247764_at	subtilisin-like serine protease cor	---	AT5G59190	-1.03	-0.05	-0.28	0.7864096	0.8992382	-6.51	FALSE
249632_at	caffeic acid O-methyltransferase	---	AT5G37170	1.03	0.04	0.28	0.7863209	0.8992382	-6.51	FALSE
255745_at	hypothetical protein predicted by	---	AT1G32030	-1.02	-0.03	-0.28	0.7863461	0.8992382	-6.51	FALSE
266879_at	putative phragmoplastin	ADL1D	AT2G44590	1.04	0.05	0.28	0.7864089	0.8992382	-6.51	FALSE

264290_at	hypothetical protein predicted by	---	AT1G78810	1.04	0.06	0.28	0.7865182	0.8993173	-6.51	FALSE
253712_at	putative protein putative NADH (	DER1	AT4G29330	-1.03	-0.05	-0.28	0.7865672	0.8993282	-6.51	FALSE
247346_at	diacylglycerol kinase	ATDGK2	AT5G63770	1.05	0.07	0.28	0.7867154	0.8993611	-6.51	FALSE
257677_at	unknown protein contains Pfam p	ATEHD1	AT3G20290	1.04	0.05	0.28	0.7867931	0.8993611	-6.51	FALSE
256187_at	55 kDa B regulatory subunit of pl	ATB ALPHA	AT1G51690	-1.04	-0.05	-0.28	0.7866417	0.8993611	-6.51	FALSE
261091_at	protein kinase, putative contains	---	AT1G07550	-1.03	-0.04	-0.28	0.786759	0.8993611	-6.51	FALSE
254489_at	putative protein berberine bridge	---	AT4G20800	1.03	0.04	0.28	0.7867307	0.8993611	-6.51	FALSE
263825_at	putative laccase (diphenol oxidas	LAC5	AT2G40370	1.08	0.11	0.28	0.786845	0.8993754	-6.51	FALSE
253057_at	putative protein amino-acid N-ac	---	AT4G37670	1.09	0.13	0.28	0.7869402	0.8994073	-6.51	FALSE
252880_at	putative protein ;supported by ful	---	AT4G39730	1.06	0.08	0.28	0.7869518	0.8994073	-6.51	FALSE
245539_at	ABC transporter homolog	PDR2	AT4G15230	1.04	0.06	0.28	0.7870468	0.8994659	-6.51	FALSE
256801_at	cytochrome P450, putative simil	CYP705A3(	AT3G20940	-1.03	-0.04	-0.28	0.787082	0.8994659	-6.51	FALSE
256461_s_a	adenylosuccinate lyase - like pro	---	AT1G36280 ///	1.10	0.14	0.28	0.7874693	0.8996636	-6.51	TRUE
262361_at	unknown protein contains similar	GTE3	AT1G73150	-1.03	-0.04	-0.28	0.7875269	0.8996636	-6.51	FALSE
246156_at	putative protein predicted protein	---	AT5G20090	-1.04	-0.05	-0.28	0.7874817	0.8996636	-6.51	FALSE
256731_at	hypothetical protein contains Pfa	---	AT3G30340	1.03	0.04	0.28	0.7875705	0.8996636	-6.51	FALSE
245534_at	hypothetical protein	---	AT4G15150	1.03	0.05	0.28	0.7875576	0.8996636	-6.51	FALSE
247961_at	putative protein similar to unknov	---	AT5G56570	1.03	0.04	0.28	0.7873769	0.8996636	-6.51	FALSE
254312_s_a	hypothetical protein	---	---	-1.04	-0.05	-0.28	0.787414	0.8996636	-6.51	FALSE
259929_at	transcription factor, putative sim	---	AT1G34360	-1.03	-0.05	-0.28	0.7875409	0.8996636	-6.51	FALSE
256650_at	hypothetical protein contains sim	---	AT3G13620	1.04	0.05	0.28	0.7878211	0.8999048	-6.51	FALSE
267259_at	Expressed protein ; supported by	---	AT2G23090 ///	1.03	0.05	0.28	0.7878756	0.899922	-6.51	FALSE
251872_at	putative protein predicted protein	---	AT3G54570	-1.03	-0.04	-0.28	0.7879828	0.8999994	-6.51	FALSE
247828_at	putative protein KIAA0066, Hom	---	AT5G58510	1.03	0.04	0.28	0.7881363	0.9001297	-6.51	FALSE
260057_at	putative protein phosphatase 2C	---	AT1G78200	-1.03	-0.04	-0.28	0.7884009	0.9003023	-6.51	FALSE
259836_at	unknown protein	ROPGEF11	AT1G52240	1.03	0.04	0.28	0.7884059	0.9003023	-6.51	FALSE
262771_at	hypothetical protein predicted by	---	AT1G13200	1.04	0.05	0.28	0.788344	0.9003023	-6.51	FALSE
247251_at	cellulose synthase catalytic subu	CESA6	AT5G64740	-1.05	-0.07	-0.28	0.7886501	0.900514	-6.51	TRUE
254335_at	putative protein alternative oxida	IM	AT4G22260	1.03	0.04	0.28	0.7886702	0.900514	-6.51	FALSE
249135_at	putative protein similar to unknov	---	AT5G43160	1.06	0.09	0.28	0.7887582	0.9005243	-6.51	FALSE
244913_at	hypothetical protein	---	---	-1.03	-0.05	-0.28	0.7887275	0.9005243	-6.51	FALSE
265211_at	late embryogenesis abundant pro	ATECP63	AT2G36640	1.03	0.04	0.28	0.7888519	0.9005862	-6.51	FALSE
251818_at	vacuolar protein sorting protein 3	ATVPS33	AT3G54860	-1.03	-0.05	-0.28	0.7889199	0.9006187	-6.51	FALSE
247879_at	unknown protein	---	AT5G57770	-1.03	-0.04	-0.28	0.7890084	0.9006364	-6.51	FALSE
266612_at	22 kDa peroxisomal membrane p	---	AT2G14860	-1.03	-0.04	-0.28	0.7890143	0.9006364	-6.51	FALSE

258508_at	protein kinase, putative similar t	---	AT3G06640	-1.03	-0.04	-0.28	0.7891183	0.900662	-6.51	FALSE
254065_at	gibberellin 20-oxidase - Arabidop	GA20OX1	AT4G25420	1.08	0.12	0.28	0.7891552	0.900662	-6.51	FALSE
263486_at	AP2 domain transcription factor	---	AT2G22200	1.03	0.04	0.28	0.789086	0.900662	-6.51	FALSE
248754_at	putative protein contains similarit	NF-YB6	AT5G47670	1.03	0.04	0.28	0.7892674	0.9007449	-6.51	FALSE
258728_at	unknown protein ; supported by	---	AT3G11800	-1.03	-0.04	-0.28	0.7894269	0.9008819	-6.51	FALSE
253720_at	acid phosphatase-like protein a	---	AT4G29270	1.03	0.04	0.28	0.7895375	0.9009631	-6.51	FALSE
247599_at	putative protein	---	AT5G60880	1.06	0.09	0.28	0.7896575	0.9010549	-6.51	FALSE
254614_at	putatative protein various predic	---	AT4G19191	1.04	0.06	0.28	0.7896986	0.9010567	-6.51	FALSE
255075_at	putative protein RING-H2 zinc fi	---	AT4G09110	-1.02	-0.03	-0.28	0.7898696	0.9012068	-6.51	FALSE
258749_at	hypothetical protein predicted by	---	AT3G05760	-1.04	-0.05	-0.28	0.7900634	0.9013828	-6.51	FALSE
244925_at	NADH dehydrogenase subunit 7	---	---	1.04	0.06	0.28	0.7901037	0.9013837	-6.51	FALSE
249296_at	kinesin-like protein	---	AT5G41310	1.03	0.05	0.28	0.7902561	0.9015125	-6.51	FALSE
261494_at	homeobox transcription factor H	HB-1	AT1G28420	1.04	0.05	0.28	0.790342	0.9015336	-6.51	FALSE
248917_at	putative protein similar to unknov	---	AT5G45850	1.02	0.03	0.28	0.7903537	0.9015336	-6.51	FALSE
257498_at	hypothetical protein predicted by	---	AT1G69660	1.03	0.04	0.28	0.7905459	0.9017077	-6.51	FALSE
249649_at	putative transporter protein Na+	CHX24	AT5G37060	1.02	0.03	0.28	0.7906251	0.9017531	-6.51	FALSE
257355_at	hypothetical protein predicted by	---	AT2G38150	-1.03	-0.04	-0.28	0.7906778	0.901768	-6.51	FALSE
262277_at	transmembrane protein, putative	---	AT1G68650	-1.07	-0.10	-0.28	0.7909597	0.9018213	-6.51	FALSE
255833_at	unknown protein	---	AT2G33390	-1.04	-0.05	-0.28	0.7910408	0.9018213	-6.51	FALSE
253882_at	pelota (PEL1)	PEL1	AT4G27650	1.04	0.05	0.28	0.7908467	0.9018213	-6.51	FALSE
246562_at	putative protein unknown protein	LNG1	AT5G15580	1.19	0.25	0.28	0.7908941	0.9018213	-6.51	FALSE
263477_at	putative glucosyltransferase ; su	---	AT2G31790	-1.05	-0.07	-0.28	0.7908841	0.9018213	-6.51	FALSE
249761_at	acetyl-CoA:benzylalcohol acetylt	---	AT5G23970	1.04	0.06	0.28	0.7910053	0.9018213	-6.51	FALSE
263862_at	putative protein phosphatase	IBR5	AT2G04550	-1.03	-0.04	-0.28	0.7908646	0.9018213	-6.51	FALSE
256963_at	lysyl-tRNA synthetase, putative	OVA5	AT3G13490	-1.05	-0.07	-0.28	0.7910339	0.9018213	-6.51	FALSE
267114_at	Expressed protein ; supported by	---	AT2G14835	1.03	0.04	0.28	0.791115	0.9018391	-6.51	FALSE
249062_at	putative protein contains similarit	---	AT5G44270	1.03	0.05	0.28	0.7911355	0.9018391	-6.51	FALSE
251838_at	cysteine proteinase non-consens	---	AT3G54940	1.04	0.05	0.28	0.7911811	0.9018461	-6.51	FALSE
267276_at	hypothetical protein predicted by	ASL5	AT2G30130	-1.03	-0.04	-0.28	0.7912268	0.9018531	-6.51	FALSE
267541_at	hypothetical protein predicted by	---	AT2G32750	1.04	0.05	0.28	0.7913016	0.9018724	-6.51	FALSE
267117_at	unknown protein	---	AT2G32560	1.03	0.04	0.28	0.7913229	0.9018724	-6.51	FALSE
258226_at	putative phospholipase D simila	PLDALPHA	AT3G15730	-1.03	-0.05	-0.28	0.7915391	0.9019424	-6.51	FALSE
254375_at	putative protein (fragment) ATP(	QQT2	AT4G21800	-1.03	-0.04	-0.28	0.7915424	0.9019424	-6.51	FALSE
246659_at	putative protein predicted protein	---	---	-1.03	-0.04	-0.28	0.7914606	0.9019424	-6.51	FALSE
249179_at	Expressed protein ; supported by	---	AT5G42955	-1.04	-0.05	-0.28	0.7915186	0.9019424	-6.51	FALSE

265636_at	putative calcium binding protein	---	AT2G27480	-1.04	-0.05	-0.27	0.7916863	0.9020163	-6.51	FALSE
264067_x_a	putative chloroplast nucleoid DN/	---	AT2G28010	-1.04	-0.05	-0.27	0.7916833	0.9020163	-6.51	FALSE
247624_at	aspartyl aminopeptidase - like pr	---	AT5G60160	-1.02	-0.04	-0.27	0.7918695	0.9020503	-6.51	FALSE
248076_at	unknown protein	---	AT5G55750	-1.03	-0.04	-0.27	0.791914	0.9020503	-6.51	FALSE
252763_at	Expressed protein ; supported by	---	AT3G42725	1.03	0.05	0.27	0.7918973	0.9020503	-6.51	FALSE
256434_at	putative 60S ribosomal protein L1	---	AT3G10950	-1.03	-0.04	-0.27	0.791837	0.9020503	-6.51	FALSE
263531_s_a	hypothetical protein predicted by	---	AT2G25020 ///	-1.03	-0.04	-0.27	0.7917912	0.9020503	-6.51	FALSE
261238_at	hypothetical protein predicted by	---	AT1G32810	-1.03	-0.05	-0.27	0.7919867	0.9020881	-6.51	FALSE
254300_at	Translation factor EF-1 alpha - li	ACR7	AT4G22780	-1.05	-0.07	-0.27	0.7920429	0.902107	-6.51	TRUE
248352_at	low-temperature-induced 65 kD p	LTI65	AT5G52300	1.11	0.15	0.27	0.7922024	0.9021987	-6.51	FALSE
254479_at	putative protein hypothetical pro	---	AT4G20350	-1.04	-0.05	-0.27	0.7921632	0.9021987	-6.51	FALSE
248744_at	putative protein contains similarit	---	AT5G48250	-1.04	-0.06	-0.27	0.7923559	0.9022491	-6.51	FALSE
252998_at	probable H+-transporting ATPas	---	AT4G38510	1.03	0.05	0.27	0.792373	0.9022491	-6.51	FALSE
255851_at	hypothetical protein predicted by	---	AT1G67040	-1.04	-0.05	-0.27	0.7924049	0.9022491	-6.51	FALSE
266842_at	FtsH protease, putative contains	ftsh4	AT2G26140	1.04	0.05	0.27	0.7924043	0.9022491	-6.51	FALSE
248382_at	peroxidase	---	AT5G51890	-1.12	-0.16	-0.27	0.7924773	0.9022865	-6.51	TRUE
265938_at	putative SF21 protein {Helianthu	---	AT2G19620	-1.09	-0.12	-0.27	0.7926569	0.9023279	-6.51	TRUE
261910_at	zinc finger protein identical to GB	ZFP1	AT1G80730	-1.03	-0.04	-0.27	0.7925608	0.9023279	-6.51	FALSE
264275_at	hypothetical protein predicted by	anac024	AT1G60350	-1.02	-0.03	-0.27	0.792639	0.9023279	-6.51	FALSE
249902_at	unknown protein	---	AT5G22680	1.05	0.06	0.27	0.7926719	0.9023279	-6.51	FALSE
257484_at	unknown protein	---	AT1G01650	1.03	0.04	0.27	0.7931041	0.9027748	-6.52	FALSE
261068_at	tropinone reductase-I, putative s	---	AT1G07450	1.03	0.04	0.27	0.7934419	0.9028547	-6.52	FALSE
255777_at	glycine-rich RNA-binding protein	GR-RBP6	AT1G18630	-1.04	-0.06	-0.27	0.7934512	0.9028547	-6.52	FALSE
260263_at	hypothetical protein predicted by	JAG	AT1G68480	1.03	0.04	0.27	0.7933231	0.9028547	-6.52	FALSE
250623_at	peroxisomal Ca-dependent solu	---	AT5G07320	1.03	0.04	0.27	0.7932202	0.9028547	-6.52	FALSE
259228_at	unknown protein similar to hypot	---	AT3G07720	-1.04	-0.05	-0.27	0.7932813	0.9028547	-6.52	FALSE
252569_at	receptor-like protein kinase rece	---	AT3G45420	-1.03	-0.05	-0.27	0.7934055	0.9028547	-6.52	FALSE
267427_at	putative WRKY-type DNA bindin	WRKY35	AT2G34830	-1.03	-0.04	-0.27	0.7934513	0.9028547	-6.52	FALSE
256770_at	hypothetical protein predicted by	---	AT3G13700 ///	-1.04	-0.06	-0.27	0.793546	0.9028602	-6.52	FALSE
266157_at	unknown protein	ATFUC1	AT2G28100	-1.02	-0.03	-0.27	0.7935958	0.9028602	-6.52	FALSE
246691_at	putative protein predicted protein	---	---	-1.03	-0.04	-0.27	0.7936051	0.9028602	-6.52	FALSE
247392_at	glutamate-1-semialdehyde 2,1-a	GSA1	AT5G63570	1.05	0.07	0.27	0.7936145	0.9028602	-6.52	FALSE
263094_at	hypothetical protein predicted by	---	AT2G16020	-1.03	-0.05	-0.27	0.7937639	0.9029851	-6.52	FALSE
262864_at	anthocyanidin-3-glucoside rham	---	AT1G64920	-1.03	-0.05	-0.27	0.7938504	0.9030385	-6.52	FALSE
257769_at	indoleacetic acid (IAA)-inducible	IAA7	AT3G23050	1.22	0.28	0.27	0.7939752	0.9031048	-6.52	FALSE

260836_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.27	0.7939879	0.9031048	-6.52	FALSE
251694_s_a	putative protein NAM (no apical	anac063	AT3G55210 ///	1.03	0.04	0.27	0.7940853	0.9031705	-6.52	FALSE
251387_at	putative protein	---	AT3G60810	-1.05	-0.07	-0.27	0.7941296	0.9031759	-6.52	TRUE
246336_at	putative protein putative integral	ATCHX4	AT3G44900	1.03	0.04	0.27	0.7943886	0.9034255	-6.52	FALSE
263835_at	putative eukaryotic translation in	---	AT2G40290	-1.03	-0.04	-0.27	0.7945824	0.9035709	-6.52	FALSE
254582_at	putative protein TMV resistance	---	AT4G19470	-1.03	-0.04	-0.27	0.7945958	0.9035709	-6.52	FALSE
249414_at	putative transcription factor MYB	MYB89	AT5G39700	-1.03	-0.05	-0.27	0.7947671	0.9037208	-6.52	FALSE
265650_at	hypothetical protein predicted by	---	AT2G27460	-1.03	-0.04	-0.27	0.7948376	0.9037558	-6.52	FALSE
259839_at	peptide transporter, putative sim	---	AT1G52190	-1.18	-0.24	-0.27	0.794885	0.9037646	-6.52	FALSE
267263_at	similar to late embryogenesis ab	---	AT2G23110	1.16	0.21	0.27	0.7950025	0.9038532	-6.52	FALSE
249215_at	dihydroflavonol 4-reductase	DFR	AT5G42800	-1.05	-0.07	-0.27	0.7950829	0.9038577	-6.52	FALSE
262388_at	unknown protein	---	AT1G49320	-1.03	-0.05	-0.27	0.7950857	0.9038577	-6.52	FALSE
256646_at	hypothetical protein predicted by	---	AT3G13590	-1.03	-0.05	-0.27	0.7952097	0.9039536	-6.52	FALSE
259358_at	hypothetical protein similar to put	GATL3	AT1G13250	1.10	0.14	0.27	0.7956883	0.9040922	-6.52	TRUE
247550_at	putative protein many predicted p	---	AT5G61370	1.03	0.04	0.27	0.7956728	0.9040922	-6.52	FALSE
248974_at	disease resistance protein-like	---	AT5G45060	1.03	0.04	0.27	0.7955841	0.9040922	-6.52	FALSE
260152_at	putative IAA6 protein similar to IA	IAA6	AT1G52830	1.07	0.10	0.27	0.7955577	0.9040922	-6.52	FALSE
265661_at	putative protein kinase contains a	---	AT2G24360	-1.04	-0.05	-0.27	0.7954823	0.9040922	-6.52	FALSE
255802_s_a	putative protein RING-H2 finger	---	AT4G10150 ///	-1.03	-0.04	-0.27	0.7955526	0.9040922	-6.52	FALSE
265886_at	putative protein phosphatase 2C	---	AT2G25610 ///	-1.06	-0.09	-0.27	0.7956722	0.9040922	-6.52	FALSE
250899_at	putative protein ; supported by c	---	AT5G03340	1.04	0.06	0.27	0.7955955	0.9040922	-6.52	FALSE
248178_at	root cap protein 2-like protein	---	AT5G54370	1.04	0.06	0.27	0.7956076	0.9040922	-6.52	FALSE
250360_at	putative protein probable serine/	---	AT5G11360	1.03	0.04	0.27	0.7957829	0.9041096	-6.52	FALSE
253521_at	multicatalytic endopeptidase cor	PBA1	AT4G31300	-1.05	-0.07	-0.27	0.7957808	0.9041096	-6.52	FALSE
254085_at	abscisic acid-induced - like prote	HVA22D	AT4G24960	1.07	0.09	0.27	0.7958769	0.9041263	-6.52	TRUE
250535_at	putative protein similar to unknov	---	AT5G08480	1.03	0.05	0.27	0.7958618	0.9041263	-6.52	FALSE
262708_at	UV-sensitive rad23, putative sim	---	AT1G16190	1.03	0.04	0.27	0.7959361	0.9041485	-6.52	FALSE
249884_at	Na+/H+ antiporter-like protein	CHX9	AT5G22910	1.03	0.05	0.27	0.7961102	0.9042466	-6.52	FALSE
267234_x_a	putative protein kinase contains a	---	AT2G43930	-1.03	-0.05	-0.27	0.7961371	0.9042466	-6.52	FALSE
261177_at	hypothetical protein predicted by	---	AT1G04770	-1.05	-0.08	-0.27	0.7961413	0.9042466	-6.52	FALSE
246016_at	histidine kinase - like protein ser	AHK5	AT5G10720	-1.03	-0.05	-0.27	0.796248	0.9043226	-6.52	FALSE
263596_at	putative inositol polyphosphate-5	---	AT2G01900	-1.03	-0.04	-0.27	0.7962944	0.9043303	-6.52	FALSE
250043_at	putative protein proline-rich prot	---	AT5G18430	1.04	0.05	0.27	0.7963659	0.9043665	-6.52	FALSE
246942_at	anion exchanger-like protein chl	---	AT5G25430	-1.03	-0.05	-0.27	0.796421	0.9043841	-6.52	FALSE
247334_at	cdc2-like protein kinase-like prote	CDKE;1	AT5G63610	1.02	0.03	0.27	0.7966373	0.9045846	-6.52	FALSE

266791_at	unknown protein	---	AT2G02960	-1.03	-0.04	-0.27	0.7967552	0.9046285	-6.52	TRUE
255367_at	putative transposon protein	---	---	1.03	0.04	0.27	0.7967329	0.9046285	-6.52	FALSE
266095_at	3-oxo-5-alpha-steroid 4-dehydro	DET2	AT2G38050	1.04	0.06	0.27	0.7968498	0.9046909	-6.52	FALSE
255856_at	unknown protein identical to unk	---	AT1G66940	1.13	0.18	0.27	0.7969695	0.9047817	-6.52	TRUE
267236_at	GDP dissociation inhibitor identic	ATGDI1	AT2G44100	-1.03	-0.04	-0.27	0.7971047	0.9048901	-6.52	FALSE
249317_at	glutathione transferase	ATGSTT2	AT5G41240	1.03	0.04	0.27	0.7972219	0.9049782	-6.52	FALSE
266473_at	unknown protein	---	AT2G31110	1.09	0.13	0.27	0.7976117	0.9052855	-6.52	FALSE
246227_at	hypothetical protein	---	AT4G36510	1.03	0.05	0.27	0.7976101	0.9052855	-6.52	FALSE
251045_s_a	putative protein various predicte	---	AT2G13910 ///	1.02	0.03	0.27	0.7975961	0.9052855	-6.52	FALSE
253392_at	potassium channel protein AtKC	ATKC1	AT4G32650	-1.10	-0.14	-0.27	0.7978173	0.9054287	-6.52	FALSE
252137_at	dehydrin-like protein dehydrin X	XERO1	AT3G50980	-1.04	-0.05	-0.27	0.7978093	0.9054287	-6.52	FALSE
262445_at	Expressed protein ; supported by	---	AT1G47485	1.03	0.04	0.27	0.7979405	0.9055235	-6.52	FALSE
257486_at	unknown protein	---	AT1G63590	1.03	0.04	0.27	0.7980716	0.9055512	-6.52	FALSE
247757_at	putative protein	---	AT5G59105 ///	1.03	0.04	0.27	0.7980329	0.9055512	-6.52	FALSE
250357_at	putative protein various predicte	---	AT5G11730	1.03	0.05	0.27	0.7981083	0.9055512	-6.52	FALSE
266178_at	putative phloem-specific lectin	AtPP2-B4	AT2G02280	1.03	0.05	0.27	0.7981237	0.9055512	-6.52	FALSE
253587_at	hypothetical protein	---	AT4G30770	1.03	0.05	0.27	0.7981757	0.9055651	-6.52	FALSE
262812_at	hypothetical protein predicted by	---	AT1G11690	-1.02	-0.03	-0.27	0.7982315	0.9055834	-6.52	FALSE
257812_at	hypothetical protein	---	AT3G25090	1.04	0.05	0.27	0.7983305	0.9056505	-6.52	FALSE
250372_at	putative protein various predicte	---	AT5G11460	-1.04	-0.05	-0.27	0.79837	0.9056505	-6.52	FALSE
246275_at	putative protein ; supported by fu	BEE2	AT4G36540	1.17	0.22	0.27	0.7985023	0.9056861	-6.52	TRUE
259003_at	hypothetical protein similar to hy	---	AT3G02010	-1.05	-0.07	-0.27	0.798521	0.9056861	-6.52	FALSE
261812_at	hypothetical protein contains sim	---	AT1G08270	1.02	0.03	0.27	0.7985004	0.9056861	-6.52	FALSE
264419_s_a	hypothetical protein contains sim	---	AT1G43310 ///	-1.08	-0.11	-0.27	0.7985602	0.9056861	-6.52	FALSE
253905_s_a	putative protein retrotransposon	---	---	1.02	0.03	0.27	0.7986179	0.9057065	-6.52	FALSE
261261_at	putative aldehyde oxidase	---	AT1G26730	1.12	0.16	0.27	0.7987505	0.9058118	-6.52	FALSE
267488_at	putative cadmium-transporting A	HMA4	AT2G19110	-1.04	-0.06	-0.27	0.7988527	0.9058827	-6.52	FALSE
260151_at	unknown protein ;supported by f	---	AT1G52910	-1.11	-0.15	-0.26	0.798956	0.9059548	-6.52	FALSE
260649_at	storage protein, putative similar	ACA7	AT1G08080	1.03	0.04	0.26	0.7990652	0.9060336	-6.52	FALSE
254966_at	COP1 like protein photomorpho	SPA2	AT4G11110	-1.02	-0.03	-0.26	0.7992229	0.9061195	-6.52	FALSE
252476_at	glucosyltransferase-like protein	---	AT3G46650	1.04	0.06	0.26	0.7992999	0.9061195	-6.52	FALSE
253056_at	SHORT-ROOT (SHR)	SHR	AT4G37650	-1.05	-0.08	-0.26	0.7992786	0.9061195	-6.52	FALSE
252270_at	putative protein ;supported by fu	---	AT3G49560	-1.03	-0.05	-0.26	0.7992849	0.9061195	-6.52	FALSE
257130_at	vacuolar processing enzyme/asp	DELTA-VPE	AT3G20210	1.02	0.03	0.26	0.7993699	0.9061538	-6.52	FALSE
249165_at	putative protein similar to unknov	ATIPK1	AT5G42810	1.04	0.06	0.26	0.7998778	0.9065855	-6.52	FALSE

250008_at	triacylglycerol lipase-like protein	---	AT5G18630	1.06	0.09	0.26	0.7998447	0.9065855	-6.52	FALSE
264241_at	hypothetical protein contains sim	---	AT1G54840	-1.02	-0.03	-0.26	0.7998666	0.9065855	-6.52	FALSE
264493_at	unknown protein similar to multi	GUT2	AT1G27440	-1.06	-0.08	-0.26	0.7999494	0.9065855	-6.52	FALSE
245683_at	ubiquitin-specific protease 8 (UB	UBP8	AT5G22030	-1.03	-0.04	-0.26	0.7999225	0.9065855	-6.52	FALSE
255624_at	MAP kinase 4 (MPK4) ;supporte	ATMPK4	AT4G01370	1.04	0.06	0.26	0.8001219	0.906736	-6.52	FALSE
259787_at	auxin-induced protein, putative s	---	AT1G29460	-1.10	-0.13	-0.26	0.8001623	0.9067366	-6.52	TRUE
251682_s_a	hypothetical protein	---	AT3G57110 ///	-1.04	-0.05	-0.26	0.8005456	0.9071259	-6.52	FALSE
261385_at	lipid-transfer protein, putative sir	---	AT1G05450	1.03	0.04	0.26	0.8005966	0.9071387	-6.52	FALSE
257973_at	unknown protein	---	AT3G20720	-1.04	-0.05	-0.26	0.8009437	0.9072616	-6.52	FALSE
264352_at	unknown protein Strong similarity	---	AT1G03270	1.05	0.07	0.26	0.8009106	0.9072616	-6.52	FALSE
256691_at	hypothetical protein predicted by	---	---	1.02	0.03	0.26	0.8008608	0.9072616	-6.52	FALSE
246102_at	putative protein various predicte	---	AT5G32590	-1.03	-0.04	-0.26	0.8009062	0.9072616	-6.52	FALSE
255383_at	hypothetical protein	---	AT4G03570	1.02	0.03	0.26	0.8008393	0.9072616	-6.52	FALSE
245230_at	hypothetical protein Contains Zi	---	AT4G25610	-1.04	-0.05	-0.26	0.8008285	0.9072616	-6.52	FALSE
261649_at	putative clathrin-coat assembly p	---	AT1G27700	1.03	0.04	0.26	0.801066	0.90731	-6.52	FALSE
260052_at	14-3-3 protein (grf13), putative c	GRF13	AT1G78220	1.03	0.04	0.26	0.8010607	0.90731	-6.52	FALSE
248416_at	putative protein disease resistan	---	AT5G51630	-1.03	-0.05	-0.26	0.80117	0.9073376	-6.52	FALSE
254435_at	putative protein	MS5	AT4G20900	-1.03	-0.04	-0.26	0.8011358	0.9073376	-6.52	FALSE
255717_at	coded for by A. thaliana cDNA H	---	AT4G00350	-1.03	-0.04	-0.26	0.801286	0.907424	-6.52	FALSE
265390_at	unknown protein ; supported by	---	AT2G20820	-1.03	-0.04	-0.26	0.8014361	0.9075038	-6.52	FALSE
263051_s_a	En/Spm-like transposon protein r	---	---	1.03	0.04	0.26	0.8014126	0.9075038	-6.52	FALSE
259054_at	putative hypersensitivity-related g	CHAT	AT3G03480	1.18	0.23	0.26	0.8015806	0.9076187	-6.52	FALSE
245549_at	cellulose synthase like protein	ATCSLB06	AT4G15320	-1.03	-0.04	-0.26	0.8016171	0.9076187	-6.52	FALSE
249960_at	squamosa promoter binding prot	SPL7	AT5G18830	-1.03	-0.04	-0.26	0.8017669	0.9077433	-6.52	FALSE
267631_at	hypothetical protein predicted by	---	AT2G42150	-1.03	-0.04	-0.26	0.8018491	0.9077462	-6.52	FALSE
253436_at	ubiquinol-cytochrome c reductas	---	AT4G32470	1.03	0.04	0.26	0.8018192	0.9077462	-6.52	FALSE
252128_at	transcription factor-like protein A	MNP	AT3G50870	1.03	0.04	0.26	0.801943	0.9078074	-6.52	FALSE
245290_at	hypothetical protein ; supported b	---	AT4G16490	-1.04	-0.06	-0.26	0.8021697	0.908019	-6.52	FALSE
263107_at	putative cytochrome P450	CYP705A6	AT2G05180	-1.03	-0.04	-0.26	0.8024618	0.9081408	-6.52	FALSE
253123_at	thaumatin-like protein thaumatin	---	AT4G36000	1.03	0.05	0.26	0.8023589	0.9081408	-6.52	FALSE
265080_at	overlap with bases 100,099-109	sks12	AT1G55570	1.04	0.06	0.26	0.8024617	0.9081408	-6.52	FALSE
259042_at	RGA1-like protein similar to RGA	RGL2	AT3G03450	-1.04	-0.06	-0.26	0.8023812	0.9081408	-6.52	FALSE
260280_at	unknown protein contains AP2 D	---	AT1G80580	1.05	0.06	0.26	0.8024764	0.9081408	-6.52	FALSE
257206_at	putative lectin similar to lectin SP	---	AT3G16530	1.16	0.21	0.26	0.8027356	0.9081821	-6.52	TRUE
257671_at	hypothetical protein predicted by	---	AT3G20450	1.03	0.05	0.26	0.8027517	0.9081821	-6.52	FALSE

254787_at	putative protein hypothetical prot	---	AT4G12690	-1.05	-0.07	-0.26	0.8026137	0.9081821	-6.52	FALSE
261260_at	hypothetical protein predicted by	---	AT1G26680	1.03	0.04	0.26	0.8026043	0.9081821	-6.52	FALSE
259890_at	inner mitochondrial membrane pr	ATTIM23-2	AT1G72750	1.05	0.07	0.26	0.8026702	0.9081821	-6.52	FALSE
250901_at	putative protein ; supported by c	RABC2A	AT5G03530	-1.10	-0.14	-0.26	0.8026872	0.9081821	-6.52	FALSE
248626_at	receptor protein kinase-like prote	---	AT5G48940	-1.03	-0.04	-0.26	0.8028083	0.908201	-6.52	FALSE
249941_at	putative protein similar to unknov	---	AT5G22270	-1.04	-0.06	-0.26	0.8031165	0.9082343	-6.52	TRUE
253066_at	1-aminocyclopropane-1-carboxy	ACS8	AT4G37770	1.14	0.19	0.26	0.8031121	0.9082343	-6.52	TRUE
265419_at	putative secretory carrier-associa	---	AT2G20840	-1.04	-0.05	-0.26	0.8028959	0.9082343	-6.52	FALSE
266494_at	putative receptor-like protein kina	PRK2A	AT2G07040	-1.03	-0.04	-0.26	0.803032	0.9082343	-6.52	FALSE
255768_at	Expressed protein ; supported by	---	AT1G16705	1.03	0.04	0.26	0.8029466	0.9082343	-6.52	FALSE
252703_at	leucine-rich repeat protein LRP -	---	AT3G43740	-1.03	-0.04	-0.26	0.8030688	0.9082343	-6.52	FALSE
258595_at	unknown protein contains Pfam p	---	AT3G04500	-1.03	-0.04	-0.26	0.8029996	0.9082343	-6.52	FALSE
250565_at	putative protein various predicte	E13L3	AT5G08000	1.04	0.05	0.26	0.8032556	0.9083466	-6.52	FALSE
265789_at	putative receptor-like protein kina	---	AT2G01210	-1.03	-0.04	-0.26	0.8033073	0.90836	-6.52	FALSE
253239_at	putative serine/threonine protein	---	AT4G34500	1.05	0.07	0.26	0.8034609	0.908415	-6.52	FALSE
262251_at	hypothetical protein predicted by	---	AT1G53760	1.05	0.08	0.26	0.8035152	0.908415	-6.52	FALSE
265407_at	F-box protein family, AtFBX8 co	---	AT2G16810	1.04	0.06	0.26	0.8034115	0.908415	-6.52	FALSE
260310_at	hypothetical protein predicted by	---	AT1G70590	-1.04	-0.06	-0.26	0.8035095	0.908415	-6.52	FALSE
263861_at	hypothetical protein	---	AT2G04560	-1.04	-0.06	-0.26	0.8035846	0.9084484	-6.52	FALSE
254701_at	putative protein predicted protei	---	AT4G18030	-1.06	-0.08	-0.26	0.8036509	0.9084784	-6.52	TRUE
263171_at	unknown protein	CCX4	AT1G54115	-1.03	-0.04	-0.26	0.8038455	0.9086083	-6.52	FALSE
251468_at	epsin-like protein Af10-protein -	---	AT3G59290	-1.03	-0.04	-0.26	0.8038223	0.9086083	-6.52	FALSE
260124_at	E2, ubiquitin-conjugating enzym	UBC31	AT1G36340	1.03	0.04	0.26	0.803996	0.9087334	-6.52	FALSE
248926_at	Ole e I (main olive allergen)-like	---	AT5G45880	1.05	0.08	0.26	0.8040373	0.908735	-6.52	FALSE
250552_at	putative protein microtubule bind	---	AT5G07890	1.03	0.04	0.26	0.8042017	0.9088122	-6.52	FALSE
257212_at	zinc-binding dehydrogenase, pu	---	AT3G15090	1.04	0.06	0.26	0.8042251	0.9088122	-6.52	FALSE
250934_at	DNAJ protein - like DNAJ domai	---	AT5G03030	-1.05	-0.07	-0.26	0.8042163	0.9088122	-6.52	FALSE
246203_at	putative protein ; supported by fu	---	AT4G36610	1.06	0.08	0.26	0.8042904	0.908841	-6.52	FALSE
244943_at	NADH dehydrogenase subunit 9	---	ATMG00070	1.04	0.06	0.26	0.804389	0.9088624	-6.52	TRUE
256693_at	hypothetical protein predicted by	---	---	1.02	0.03	0.26	0.8043873	0.9088624	-6.52	FALSE
247965_at	putative protein similar to unknov	AGP14	AT5G56540	1.05	0.07	0.26	0.8044764	0.908916	-6.52	FALSE
246728_at	putative protein various predicte	---	AT5G28040	-1.02	-0.03	-0.26	0.8045163	0.9089162	-6.52	FALSE
251962_at	plasma membrane intrinsic prote	PIP2A	AT3G53420	1.05	0.08	0.26	0.8045715	0.9089268	-6.52	TRUE
245636_at	hypothetical protein similar to hy	---	AT1G25240	1.04	0.05	0.26	0.8046453	0.9089268	-6.52	FALSE
248525_s_a	unknown protein	---	AT5G50610 ///	-1.03	-0.04	-0.26	0.8046445	0.9089268	-6.52	FALSE

251763_at	MYB transcription factor - like pr	MYB109	AT3G55730	1.03	0.05	0.26	0.8048123	0.9089804	-6.52	FALSE
261692_at	calreticulin, putative similar to ca	CRT3	AT1G08450	-1.06	-0.08	-0.26	0.8047989	0.9089804	-6.52	FALSE
265518_at	hypothetical protein predicted by	---	AT2G06040	-1.05	-0.06	-0.26	0.8047904	0.9089804	-6.52	FALSE
259119_at	transport protein SEC13, putativ	---	AT3G01340	-1.02	-0.04	-0.26	0.8049787	0.9091233	-6.52	FALSE
257281_s_a	hypothetical protein predicted by	---	AT3G29680 ///	-1.03	-0.05	-0.26	0.8050789	0.9091914	-6.52	FALSE
260647_at	hypothetical protein predicted by	---	AT1G08030	1.04	0.05	0.26	0.8052527	0.9092025	-6.52	FALSE
267100_at	unknown protein	---	AT2G41470	1.03	0.04	0.26	0.8052516	0.9092025	-6.52	FALSE
264017_s_a	putative ER lumen protein retaini	---	AT2G21190 ///	-1.03	-0.04	-0.26	0.8052879	0.9092025	-6.52	FALSE
259963_at	phosphate/phosphoenolpyruvate	---	AT1G53660	1.03	0.04	0.26	0.805257	0.9092025	-6.52	FALSE
249079_at	putative protein contains similarit	---	AT5G43930	1.04	0.06	0.26	0.8052018	0.9092025	-6.52	FALSE
267437_at	hypothetical protein predicted by	---	AT2G19200	1.03	0.04	0.26	0.8055505	0.9094539	-6.52	FALSE
246777_at	RING-H2 zinc finger protein-like	---	AT5G27420	1.15	0.20	0.26	0.8059389	0.9094553	-6.52	TRUE
266363_at	hypothetical protein predicted by	---	AT2G41250	-1.05	-0.08	-0.26	0.8056039	0.9094553	-6.52	TRUE
259994_at	putative C2H2-type zinc finger p	AtIDD14	AT1G68130 ///	-1.05	-0.07	-0.25	0.8063887	0.9094553	-6.52	FALSE
256533_at	unknown protein	---	AT1G33250	-1.04	-0.06	-0.26	0.8061444	0.9094553	-6.52	FALSE
259450_at	hypothetical protein predicted by	DRL1	AT1G13870	-1.03	-0.05	-0.26	0.8062639	0.9094553	-6.52	FALSE
248994_at	disease resistance protein-like	RPS4	AT5G45250	-1.04	-0.05	-0.26	0.8060131	0.9094553	-6.52	FALSE
253365_at	putative protein various predicte	---	AT4G33170	1.03	0.04	0.26	0.8062701	0.9094553	-6.52	FALSE
252746_at	sucrose synthase -like protein S	SUS4	AT3G43190	-1.03	-0.04	-0.25	0.8066742	0.9094553	-6.52	FALSE
248425_at	ACC synthase; 1-aminocycloprop	ACS12	AT5G51690	1.04	0.05	0.26	0.8057259	0.9094553	-6.52	FALSE
267563_at	putative protein kinase contains a	---	AT2G30730	1.03	0.04	0.25	0.8066196	0.9094553	-6.52	FALSE
267328_at	putative receptor-like protein kina	---	AT2G19230	-1.03	-0.05	-0.25	0.8065847	0.9094553	-6.52	FALSE
257077_at	PR-1 protein, putative similar to	---	AT3G19690	-1.04	-0.06	-0.25	0.8064617	0.9094553	-6.52	FALSE
259744_at	putative ketoacyl-CoA synthase s	KCS7	AT1G71160	1.03	0.04	0.26	0.8057617	0.9094553	-6.52	FALSE
254565_at	replication A protein-like replicat	---	AT4G19130	1.02	0.03	0.26	0.8060787	0.9094553	-6.52	FALSE
250392_at	putative protein multifunctional a	---	AT5G10880	1.02	0.04	0.25	0.8065016	0.9094553	-6.52	FALSE
263801_at	putative Athila retroelement ORF	---	---	-1.03	-0.04	-0.26	0.8063189	0.9094553	-6.52	FALSE
262515_at	unknown protein ; supported by c	---	AT1G34200	1.04	0.06	0.26	0.8061186	0.9094553	-6.52	FALSE
261285_at	Ca2+-dependent membrane-binc	ANNAT1	AT1G35720	1.08	0.11	0.26	0.8061184	0.9094553	-6.52	FALSE
254678_at	hypothetical protein	---	AT4G18500	1.03	0.04	0.25	0.806708	0.9094553	-6.52	FALSE
255174_at	putative Athila-like protein	---	---	1.02	0.03	0.25	0.8064215	0.9094553	-6.52	FALSE
260473_at	hypothetical protein predicted by	---	AT1G10880	-1.03	-0.04	-0.26	0.8060537	0.9094553	-6.52	FALSE
246592_at	putative protein predicted protei	---	AT5G14890	1.04	0.05	0.26	0.8061768	0.9094553	-6.52	FALSE
265361_at	putative retroelement pol polypro	---	---	1.03	0.04	0.25	0.8063769	0.9094553	-6.52	FALSE
262564_at	anionic peroxidase, putative sim	---	AT1G34330	1.03	0.04	0.26	0.8058873	0.9094553	-6.52	FALSE

254949_at	hypothetical protein	---	AT4G11020	1.03	0.04	0.26	0.8059413	0.9094553	-6.52	FALSE
247040_at	anthranilate N-hydroxycinnamoyl	---	AT5G67150	1.04	0.05	0.25	0.806612	0.9094553	-6.52	FALSE
261121_at	hypothetical protein predicted by	---	AT1G75340	-1.02	-0.03	-0.26	0.8060503	0.9094553	-6.52	FALSE
263266_at	hypothetical protein predicted by	---	AT2G16520	1.03	0.04	0.25	0.8066589	0.9094553	-6.52	FALSE
265667_at	putative CCAAT-binding transcri	NF-YB11	AT2G27470	1.02	0.04	0.26	0.805767	0.9094553	-6.52	FALSE
254965_at	putative protein other hypothetica	---	AT4G11090	-1.03	-0.04	-0.25	0.8068202	0.9095044	-6.52	FALSE
246896_at	extensin - like protein Pex1 exte	---	AT5G25550	1.03	0.05	0.25	0.8068313	0.9095044	-6.52	FALSE
247065_s_a	disease resistance protein-like	---	AT5G66900 /	-1.04	-0.05	-0.25	0.8069118	0.9095503	-6.52	FALSE
257105_at	unknown protein	---	AT3G15300	1.04	0.06	0.25	0.8069582	0.9095576	-6.52	FALSE
262872_at	hypothetical protein predicted by	---	AT1G64690	1.04	0.06	0.25	0.807001	0.9095609	-6.52	FALSE
254764_at	putative protein ; supported by c	---	AT4G13250	-1.07	-0.09	-0.25	0.8071141	0.9095988	-6.52	TRUE
256066_at	hypothetical protein similar to hyp	---	AT1G06980	1.08	0.12	0.25	0.8071144	0.9095988	-6.52	FALSE
261225_at	unknown protein ;supported by fu	---	AT1G20100	1.03	0.04	0.25	0.8072485	0.9096853	-6.52	FALSE
250023_at	beta-1,3-glucanase-like protein	---	AT5G18220	1.03	0.05	0.25	0.8073108	0.9096853	-6.52	FALSE
264326_at	unknown protein	---	AT1G04230	-1.03	-0.05	-0.25	0.8072736	0.9096853	-6.52	FALSE
265219_at	unknown protein ; supported by	---	AT2G02050	1.04	0.05	0.25	0.8073571	0.9096926	-6.52	FALSE
246913_at	GATA transcription factor - like (	---	AT5G25830	1.04	0.05	0.25	0.8075316	0.9098442	-6.52	FALSE
245349_at	cyanohydrin lyase like protein ;su	MES16	AT4G16690	-1.07	-0.09	-0.25	0.8078718	0.9100404	-6.52	TRUE
245665_at	unknown protein ;supported by fu	---	AT1G28250	1.03	0.04	0.25	0.8079407	0.9100404	-6.52	FALSE
264001_at	putative peroxidase ;supported b	---	AT2G22420	1.06	0.08	0.25	0.8078269	0.9100404	-6.52	FALSE
258129_at	hypothetical protein predicted by	ROPGEF8	AT3G24620	-1.03	-0.04	-0.25	0.8079547	0.9100404	-6.52	FALSE
256103_at	hypothetical protein similar to hyp	---	AT1G13540	1.02	0.03	0.25	0.807985	0.9100404	-6.52	FALSE
252157_at	hypothetical protein	---	AT3G50430	-1.03	-0.04	-0.25	0.8078683	0.9100404	-6.52	FALSE
248354_at	putative protein contains similarit	---	AT5G52330	-1.03	-0.04	-0.25	0.8078947	0.9100404	-6.52	FALSE
248377_at	unknown protein ; supported by	---	AT5G51720	-1.06	-0.09	-0.25	0.808165	0.9101397	-6.52	FALSE
246512_at	putative phytochelatin synthetas	IRX6	AT5G15630	1.04	0.05	0.25	0.8083126	0.9101397	-6.52	FALSE
248859_at	putative protein contains similarit	---	AT5G46660	-1.03	-0.05	-0.25	0.808286	0.9101397	-6.52	FALSE
261744_at	nitrogen fixation protein (nifS), p	CPNIFS	AT1G08490	1.03	0.04	0.25	0.8082245	0.9101397	-6.52	FALSE
249548_at	lipid transfer - like protein lipid tr	---	AT5G38170	-1.03	-0.04	-0.25	0.8082353	0.9101397	-6.52	FALSE
249455_s_a	putative protein predicted protei	---	AT1G50870 /	1.02	0.03	0.25	0.8082728	0.9101397	-6.52	FALSE
266925_at	unknown protein ;supported by f	PEX11D	AT2G45740	-1.03	-0.04	-0.25	0.8084518	0.9102335	-6.52	FALSE
266169_at	putative protease inhibitor ;supp	---	AT2G38900	-1.03	-0.04	-0.25	0.8084757	0.9102335	-6.52	FALSE
261203_at	Expressed protein ; supported by	---	AT1G12845	1.12	0.16	0.25	0.8085389	0.9102597	-6.52	FALSE
265224_at	putative pectinesterase	---	AT2G36710	1.03	0.04	0.25	0.8086766	0.9103348	-6.52	FALSE
250995_at	dnaK-type molecular chaperone	HSC70-1	AT5G02500	1.04	0.06	0.25	0.8086854	0.9103348	-6.52	FALSE

252867_at	putative protein hypothetical pro	---	AT4G39870	1.03	0.05	0.25	0.8088776	0.9104164	-6.52	FALSE
264872_at	putative floral homeotic protein,	sepa-03	AT1G24260	-1.04	-0.06	-0.25	0.8088738	0.9104164	-6.52	FALSE
266027_at	En/Spm-like transposon protein r	---	---	1.02	0.03	0.25	0.8088172	0.9104164	-6.52	FALSE
257814_at	acyl-(acyl carrier protein) thioest	AtFaTA	AT3G25110	-1.06	-0.09	-0.25	0.8089762	0.9104374	-6.52	FALSE
263885_at	unknown protein	---	AT2G36940	-1.03	-0.04	-0.25	0.8089595	0.9104374	-6.52	FALSE
265623_at	hypothetical protein predicted by	---	AT2G27270	-1.03	-0.05	-0.25	0.8090364	0.9104603	-6.52	FALSE
261894_at	unknown protein ;supported by fu	MGT1	AT1G80900	1.03	0.04	0.25	0.8091601	0.9105546	-6.52	FALSE
249813_at	acyltransferase ; supported by fu	EMB3009	AT5G23940	-1.02	-0.03	-0.25	0.8094175	0.9107994	-6.52	FALSE
255326_at	hypothetical protein	---	---	-1.02	-0.03	-0.25	0.8095033	0.9108509	-6.52	FALSE
258703_at	unknown protein	---	AT3G09750	-1.03	-0.05	-0.25	0.8096876	0.9110134	-6.52	FALSE
252785_at	putative protein AND-1 protein -	---	AT3G42660	1.05	0.08	0.25	0.8097526	0.9110416	-6.52	FALSE
261007_at	hypothetical protein similar to ret	---	AT1G26400	1.02	0.03	0.25	0.8099421	0.9110751	-6.52	FALSE
248520_at	11-beta-hydroxysteroid dehydrog	AtHSD1	AT5G50600 ///	1.04	0.06	0.25	0.8099302	0.9110751	-6.52	FALSE
251629_at	villin 3 fragment ; supported by c	VLN3	AT3G57410	1.04	0.05	0.25	0.8099234	0.9110751	-6.52	FALSE
255015_at	putative protein m6A methyltran	EMB1691	AT4G09980	-1.05	-0.06	-0.25	0.8098317	0.9110751	-6.52	FALSE
260859_at	serine carboxypeptidase II, puta	scpl44	AT1G43780	1.04	0.05	0.25	0.8101767	0.9111373	-6.52	FALSE
255210_at	may be a pseudogene	---	---	-1.02	-0.03	-0.25	0.8101972	0.9111373	-6.52	FALSE
266115_at	protease inhibitor II ;supported b	LCR72	AT2G02140	-1.05	-0.07	-0.25	0.8101475	0.9111373	-6.52	FALSE
266190_at	unknown protein	---	AT2G38840	1.03	0.04	0.25	0.8101205	0.9111373	-6.52	FALSE
257167_at	hypothetical protein predicted by	chr40	AT3G24340	1.02	0.04	0.25	0.8101508	0.9111373	-6.52	FALSE
265713_at	putative integral membrane prote	UPS2	AT2G03530	1.09	0.12	0.25	0.8104586	0.9113863	-6.52	FALSE
249669_at	putative protein similar to unknov	---	---	1.03	0.04	0.25	0.8106584	0.9114762	-6.52	FALSE
252627_at	putative protein	---	AT3G44950	-1.03	-0.05	-0.25	0.8106151	0.9114762	-6.52	FALSE
257813_at	Cdc45-like protein similar to Cdc	CDC45	AT3G25100	1.03	0.04	0.25	0.8106536	0.9114762	-6.52	FALSE
252662_at	putative protein Sec24A protein,	CEF	AT3G44340	-1.03	-0.04	-0.25	0.8108489	0.9115107	-6.52	FALSE
257195_at	hypothetical protein predicted by	---	AT3G23680	1.03	0.04	0.25	0.8107763	0.9115107	-6.52	FALSE
263244_at	hypothetical protein predicted by	---	AT2G31480	1.03	0.04	0.25	0.8108384	0.9115107	-6.52	FALSE
250797_at	unknown protein	---	AT5G05310	1.03	0.05	0.25	0.8107467	0.9115107	-6.52	FALSE
254109_at	Pollen-specific protein precursor	SKS1	AT4G25240	1.03	0.04	0.25	0.8109118	0.9115205	-6.52	FALSE
246606_at	putative protein	---	---	-1.02	-0.03	-0.25	0.8109376	0.9115205	-6.52	FALSE
254068_at	putative protein similarity to mult	NAP8	AT4G25450	-1.03	-0.04	-0.25	0.8110542	0.9116067	-6.52	FALSE
253838_at	putative zinc finger protein zinc f	---	AT4G27880	-1.04	-0.06	-0.25	0.811177	0.9116818	-6.52	FALSE
253865_at	putative RING zinc finger protein	---	AT4G27470	1.04	0.06	0.25	0.8112409	0.9116818	-6.52	FALSE
257688_at	Snf2-related CBP activator prote	PIE1	AT3G12810	1.02	0.03	0.25	0.811211	0.9116818	-6.52	FALSE
249765_at	putative protein contains similarit	SLAH3	AT5G24030	1.10	0.13	0.25	0.812088	0.9117359	-6.52	TRUE

254601_at	putative protein DNA (cytosine-5	CMT2	AT4G19020	-1.04	-0.06	-0.25	0.8113769	0.9117359	-6.52	TRUE
264309_at	coatomer alpha subunit, putative	---	AT1G62020	-1.02	-0.03	-0.25	0.8113699	0.9117359	-6.52	FALSE
266059_at	predicted protein ;supported by c	---	AT2G40765	1.06	0.08	0.25	0.8119436	0.9117359	-6.52	FALSE
252484_at	glucuronosyl transferase-like pro	---	AT3G46690	1.03	0.05	0.25	0.8117678	0.9117359	-6.52	FALSE
249198_s_a	putative protein similar to unknov	---	AT5G42350 ///	1.03	0.04	0.25	0.8118395	0.9117359	-6.52	FALSE
266012_s_a	predicted protein	---	AT2G07699 ///	1.06	0.08	0.25	0.8117404	0.9117359	-6.52	FALSE
247527_at	leucine-rich receptor-like protein	---	AT5G61480	-1.04	-0.06	-0.25	0.8120813	0.9117359	-6.52	FALSE
266931_at	putative non-LTR retroelement re	---	---	1.03	0.04	0.25	0.8119198	0.9117359	-6.52	FALSE
253613_at	PR-1-like protein gene PR-1 pro	---	AT4G30320	-1.03	-0.05	-0.25	0.8117324	0.9117359	-6.52	FALSE
253261_at	putative protein mRNA, partial c	CHB3	AT4G34430	-1.03	-0.04	-0.25	0.8120885	0.9117359	-6.52	FALSE
265762_at	hypothetical protein	---	AT2G01240	1.04	0.06	0.25	0.8115091	0.9117359	-6.52	FALSE
260759_at	hypothetical protein contains sim	---	AT1G49180	-1.05	-0.07	-0.25	0.8117306	0.9117359	-6.52	FALSE
252840_at	putative protein various predicte	---	---	1.03	0.04	0.25	0.8115643	0.9117359	-6.52	FALSE
263795_at	putative cyclic nucleotide-regulat	ATCNGC14	AT2G24610	1.03	0.04	0.25	0.8118411	0.9117359	-6.52	FALSE
253439_at	dimethylaniline monooxygenase	YUC1	AT4G32540	1.03	0.04	0.25	0.8119704	0.9117359	-6.52	FALSE
262983_at	hypothetical protein similar to un	---	AT1G54550	1.03	0.04	0.25	0.8120318	0.9117359	-6.52	FALSE
247751_at	putative protein	---	AT5G59050	-1.06	-0.08	-0.25	0.8120328	0.9117359	-6.52	FALSE
265559_at	putative glycine-rich protein	---	AT2G05530	1.03	0.05	0.25	0.8118584	0.9117359	-6.52	FALSE
252554_s_a	protein kinase - like receptor-like	MEE39	AT3G45920 ///	1.02	0.03	0.25	0.8119749	0.9117359	-6.52	FALSE
245325_at	xyloglucan endotransglycosylase	XTR7	AT4G14130	-1.14	-0.19	-0.25	0.8126547	0.9117882	-6.52	TRUE
259769_at	RNA-binding protein MEI2, puta	AML5	AT1G29400	-1.04	-0.06	-0.25	0.8124933	0.9117882	-6.52	FALSE
254056_at	putative protein Group I Pectines	---	AT4G25250	1.03	0.04	0.25	0.8122767	0.9117882	-6.52	FALSE
250162_at	FtsH protease, putative similar t	FTSH6	AT5G15250	1.02	0.03	0.25	0.8126196	0.9117882	-6.52	FALSE
249297_at	unknown protein	---	AT5G41320	1.03	0.04	0.25	0.8124714	0.9117882	-6.52	FALSE
260740_at	thioredoxin, putative contains Pf	ATQSOX1	AT1G15020	1.02	0.03	0.25	0.8126475	0.9117882	-6.52	FALSE
263185_at	transport protein, putative simila	---	AT1G05520	1.02	0.03	0.25	0.8124466	0.9117882	-6.52	FALSE
262543_at	Expressed protein ; supported by	---	AT1G34245	1.03	0.04	0.25	0.8125115	0.9117882	-6.52	FALSE
263976_at	unknown protein	---	AT2G42700	-1.03	-0.05	-0.25	0.8125723	0.9117882	-6.52	FALSE
261186_at	hypothetical protein predicted by	---	---	1.02	0.03	0.25	0.8125065	0.9117882	-6.52	FALSE
252728_at	putative protein various predicte	---	---	-1.03	-0.04	-0.25	0.8126429	0.9117882	-6.52	FALSE
254173_at	putative protein Kaposi's sarcom	REN1	AT4G24580	1.02	0.03	0.25	0.8124688	0.9117882	-6.52	FALSE
267149_s_a	Mutator-like transposase similar t	---	---	1.04	0.05	0.25	0.8124118	0.9117882	-6.52	FALSE
266422_at	hypothetical protein predicted by	GAUT7	AT2G38650	1.03	0.04	0.25	0.8129141	0.9119426	-6.52	FALSE
264339_at	trehalose-6-phosphate synthase	TPS8	AT1G70290	1.04	0.06	0.25	0.8131521	0.9119426	-6.52	FALSE
247255_at	putative protein similar to unknov	---	AT5G64780	1.05	0.08	0.25	0.8128942	0.9119426	-6.52	FALSE

250834_at	putative protein various predicte	DME	AT5G04560	1.04	0.05	0.25	0.8129685	0.9119426	-6.52	FALSE
259045_at	calmodulin-like protein similar to	---	AT3G03410	-1.03	-0.04	-0.25	0.8130272	0.9119426	-6.52	FALSE
256875_at	cytochrome P450, putative conta	CYP71B37	AT3G26330	1.03	0.04	0.25	0.8131363	0.9119426	-6.52	FALSE
267332_at	hypothetical protein predicted by	---	AT2G19290	-1.02	-0.03	-0.25	0.8130635	0.9119426	-6.52	FALSE
253228_at	putative protein ;supported by fu	---	AT4G34630	1.08	0.12	0.25	0.8131365	0.9119426	-6.52	FALSE
261680_at	hypothetical protein similar to hyp	---	AT1G47350	1.02	0.03	0.25	0.8129106	0.9119426	-6.52	FALSE
266666_at	hypothetical protein predicted by	---	AT2G29780	-1.03	-0.04	-0.25	0.8132159	0.9119693	-6.52	FALSE
248083_at	unknown protein	---	AT5G55420	-1.10	-0.13	-0.25	0.8133188	0.9120254	-6.52	FALSE
247332_at	unknown protein ; supported by	---	AT5G63440	-1.04	-0.05	-0.25	0.813346	0.9120254	-6.52	FALSE
254875_at	putative protein various predicte	---	AT4G11590	1.03	0.04	0.25	0.8134019	0.9120433	-6.52	FALSE
246458_at	putative protein various predicte	---	AT5G16860	-1.03	-0.05	-0.25	0.813571	0.9121547	-6.52	FALSE
255355_at	hypothetical protein	---	---	-1.03	-0.04	-0.25	0.8135812	0.9121547	-6.52	FALSE
247766_at	FtsH protease, putative contains	ftsh9	AT5G58870	-1.03	-0.04	-0.24	0.8138041	0.9123598	-6.52	FALSE
259291_at	unknown protein similar to unkno	---	AT3G11550	1.03	0.05	0.24	0.8140245	0.9125298	-6.52	FALSE
244975_at	PSII 10KDa phosphoprotein	---	---	-1.03	-0.04	-0.24	0.8140358	0.9125298	-6.52	FALSE
247306_at	ser/thr protein phosphatase catal	PP7	AT5G63870	-1.03	-0.05	-0.24	0.8141361	0.9125974	-6.52	FALSE
248157_at	putative protein similar to unknov	---	AT5G54420	1.03	0.04	0.24	0.8142507	0.912681	-6.52	FALSE
263026_at	hypothetical protein predicted by	---	AT1G24000	1.02	0.04	0.24	0.8143223	0.9127164	-6.52	FALSE
249464_at	putative protein crp1, Zea mays,	EMB2745	AT5G39710	-1.07	-0.10	-0.24	0.8144329	0.9127955	-6.52	FALSE
262047_at	hypothetical protein predicted by	---	AT1G80160	1.12	0.16	0.24	0.814872	0.9128499	-6.52	TRUE
264147_at	receptor-like protein glossy1 (gl1	CER1	AT1G02205	1.23	0.30	0.24	0.8149217	0.9128499	-6.52	FALSE
259760_at	hypothetical protein similar to GE	---	AT1G77580	1.02	0.03	0.24	0.8148325	0.9128499	-6.52	FALSE
265901_at	putative selenium-binding protein	---	AT2G25580	-1.03	-0.05	-0.24	0.8146076	0.9128499	-6.52	FALSE
264518_at	unknown protein	---	AT1G09980	1.04	0.05	0.24	0.8149176	0.9128499	-6.52	FALSE
251366_at	putative protein several hypothet	---	AT3G61340	-1.03	-0.04	-0.24	0.8147423	0.9128499	-6.52	FALSE
255102_s_a	putative MuDR-A-like transposon	---	---	1.03	0.04	0.24	0.8147977	0.9128499	-6.52	FALSE
258543_at	unknown protein	---	AT3G06870	1.03	0.05	0.24	0.8147047	0.9128499	-6.52	FALSE
246717_at	putative protein	---	AT5G28920	-1.03	-0.04	-0.24	0.8147472	0.9128499	-6.52	FALSE
256880_at	major latex protein, putative sim	---	AT3G26450	1.05	0.07	0.24	0.8148713	0.9128499	-6.52	FALSE
257944_at	SKP1/ASK1 (At9), putative simil	ASK9	AT3G21850	1.03	0.04	0.24	0.8147012	0.9128499	-6.52	FALSE
262559_at	unknown protein similar to hypot	---	AT1G31300	-1.03	-0.04	-0.24	0.8151278	0.9129912	-6.52	FALSE
261706_at	hypothetical protein similar to hyp	---	---	1.02	0.03	0.24	0.8151022	0.9129912	-6.52	FALSE
256786_at	unknown protein ;supported by f	---	AT3G13740	1.04	0.05	0.24	0.8156407	0.9132626	-6.52	FALSE
264822_at	putative ribonucleoprotein	---	AT1G03457	1.05	0.07	0.24	0.8160279	0.9132626	-6.52	FALSE
260875_at	hypothetical protein predicted by	SKP2A	AT1G21410	-1.06	-0.08	-0.24	0.8159654	0.9132626	-6.52	FALSE

259806_at	mysoin-like protein similar to GI:	---	AT1G47900	-1.04	-0.06	-0.24	0.8158447	0.9132626	-6.52	FALSE
265244_at	putative amine oxidase	ATPAO2	AT2G43018 /	1.05	0.08	0.24	0.8159551	0.9132626	-6.52	FALSE
259136_at	unknown protein	---	AT3G05470	-1.04	-0.06	-0.24	0.8157707	0.9132626	-6.52	FALSE
256888_at	hypothetical protein predicted by	---	AT3G15160	1.03	0.04	0.24	0.8158567	0.9132626	-6.52	FALSE
254369_at	putative protein	---	AT4G21720	-1.04	-0.05	-0.24	0.8160908	0.9132626	-6.52	FALSE
266640_at	Expressed protein ; supported by	---	AT2G35585	-1.03	-0.05	-0.24	0.8160637	0.9132626	-6.52	FALSE
264427_at	hypothetical protein predicted by	---	AT1G61770	-1.03	-0.04	-0.24	0.8159176	0.9132626	-6.52	FALSE
245585_at	hypothetical	---	AT4G14970	-1.03	-0.04	-0.24	0.8160614	0.9132626	-6.52	FALSE
267155_at	CLE7, putative CLAVATA3/ESR	---	AT2G30925	1.03	0.05	0.24	0.8158704	0.9132626	-6.52	FALSE
255148_at	putative mitogen-activated protei	MAPKKK1(	AT4G08470	1.07	0.10	0.24	0.816087	0.9132626	-6.52	FALSE
260456_at	hypothetical protein	---	AT1G72490	1.03	0.05	0.24	0.8157287	0.9132626	-6.52	FALSE
258767_at	putative (1-4)-beta-mannan endo	---	AT3G10890	1.03	0.04	0.24	0.8157613	0.9132626	-6.52	FALSE
249194_at	kinesin heavy chain-like protein	---	AT5G42490	-1.02	-0.03	-0.24	0.8157489	0.9132626	-6.52	FALSE
252532_at	glucosidase-like protein GLUCA	---	AT3G46570	-1.04	-0.06	-0.24	0.8156051	0.9132626	-6.52	FALSE
263652_at	unknown protein EST gb|H7641	---	AT1G04330	-1.02	-0.03	-0.24	0.815535	0.9132626	-6.52	FALSE
248907_at	putative protein contains similarit	---	AT5G46340	-1.03	-0.04	-0.24	0.8162882	0.9132672	-6.52	FALSE
257598_at	PRT1 identical to GB:CAA11891	PRT1	AT3G24800	1.04	0.05	0.24	0.8162197	0.9132672	-6.52	FALSE
260702_at	calmodulin, putative similar to ca	---	AT1G32250	1.03	0.04	0.24	0.8166555	0.9132672	-6.52	FALSE
256694_at	hypothetical protein predicted ge	---	---	1.03	0.04	0.24	0.8164795	0.9132672	-6.52	FALSE
257183_at	ABC transporter contains Pfam p	---	AT3G13220	-1.03	-0.04	-0.24	0.8165502	0.9132672	-6.52	FALSE
266376_at	putative endoxyloglucan glycosyl	---	AT2G14620	1.04	0.05	0.24	0.8164677	0.9132672	-6.52	FALSE
257653_at	hypothetical protein	---	AT3G13225	-1.03	-0.05	-0.24	0.8164277	0.9132672	-6.52	FALSE
260850_at	glucose 6 phosphate/phosphate	---	AT1G21870	-1.03	-0.05	-0.24	0.8165197	0.9132672	-6.52	FALSE
264745_at	5'-adenylylphosphosulfate reduc	אפר-02	AT1G62180	1.05	0.07	0.24	0.8165701	0.9132672	-6.52	FALSE
252266_at	putative protein ethylene-forming	---	AT3G49630	-1.04	-0.06	-0.24	0.8162154	0.9132672	-6.52	FALSE
253680_at	cytidine deaminase 2 (CDA2)	---	AT4G29620	-1.03	-0.04	-0.24	0.81642	0.9132672	-6.52	FALSE
254554_at	hypothetical protein	---	AT4G19550	1.03	0.04	0.24	0.8164094	0.9132672	-6.52	FALSE
245837_at	peptidylprolyl isomerase, putativ	---	AT1G58450	1.02	0.03	0.24	0.8166143	0.9132672	-6.52	FALSE
256481_at	elicitor response protein, putativ	---	AT1G33430	-1.02	-0.03	-0.24	0.8166546	0.9132672	-6.52	FALSE
256139_at	Nt-gh3 deduced protein, putative	---	AT1G48660	-1.03	-0.04	-0.24	0.8167283	0.913272	-6.52	FALSE
245653_at	heat shock transcription factor lik	FBD1	AT4G13985	-1.03	-0.04	-0.24	0.8168191	0.913272	-6.52	FALSE
248389_at	AP2 domain transcription factor-l	CBF4	AT5G51990	1.03	0.04	0.24	0.81686	0.913272	-6.52	FALSE
247647_at	respiratory burst oxidase protein	---	AT5G60010	1.03	0.04	0.24	0.8168354	0.913272	-6.52	FALSE
261691_at	branched-chain amino acid amir	---	AT1G50060	1.02	0.03	0.24	0.8168397	0.913272	-6.52	FALSE
266179_at	putative phloem-specific lectin	AtPP2-B5	AT2G02300	1.02	0.03	0.24	0.816955	0.9133335	-6.52	FALSE

249063_at	NBD-like protein (gb|AAD20643.	POP1	AT5G44110	1.04	0.05	0.24	0.8171343	0.9134444	-6.52	FALSE
251782_at	beta-N-acetylhexosaminidase -lik	HEXO1	AT3G55260	-1.04	-0.06	-0.24	0.8171269	0.9134444	-6.52	FALSE
261835_at	hypothetical protein contains sim	---	AT1G16040	-1.03	-0.04	-0.24	0.817548	0.9137766	-6.52	FALSE
252781_at	polygalacturonase -like protein p	---	AT3G42950	-1.03	-0.04	-0.24	0.8175917	0.9137766	-6.52	FALSE
265997_at	Expressed protein ; supported by	---	AT2G24250	1.03	0.04	0.24	0.8175818	0.9137766	-6.52	FALSE
255241_at	putative protein hypothetical pro	---	---	1.02	0.03	0.24	0.8174779	0.9137766	-6.52	FALSE
256555_at	hypothetical protein similar to put	---	---	1.02	0.03	0.24	0.8177046	0.9138581	-6.52	FALSE
260976_at	hypothetical protein	CID8	AT1G53650	-1.04	-0.06	-0.24	0.8178247	0.9139167	-6.52	FALSE
245046_at	putative membrane transporter ;	PDE135	AT2G26510	1.03	0.04	0.24	0.8178373	0.9139167	-6.52	FALSE
259189_at	unknown protein	AGP11	AT3G01700	1.03	0.05	0.24	0.8179052	0.9139478	-6.52	FALSE
261255_at	hypothetical protein contains sim	ATNTH2	AT1G05900	1.03	0.04	0.24	0.8181141	0.9141365	-6.52	FALSE
247697_at	subtilisin-like protease - like prot	SBT5.4	AT5G59810	-1.03	-0.05	-0.24	0.8181879	0.9141742	-6.52	FALSE
262372_at	hypothetical protein predicted by	---	AT1G73130	-1.05	-0.07	-0.24	0.8182739	0.9142249	-6.52	FALSE
252149_at	putative protein hypothetical pro	---	AT3G51290	1.02	0.03	0.24	0.8183134	0.9142249	-6.52	FALSE
252699_at	hypothetical protein predicted pr	---	---	1.05	0.07	0.24	0.8186502	0.9143772	-6.52	FALSE
249535_at	transporter -like protein N syster	---	AT5G38820	1.03	0.05	0.24	0.8185638	0.9143772	-6.52	FALSE
254983_at	putative protein other hypothetica	MEE53	AT4G10560	-1.02	-0.03	-0.24	0.8185978	0.9143772	-6.52	FALSE
247622_at	putative protein	---	AT5G60350	1.03	0.04	0.24	0.8186155	0.9143772	-6.52	FALSE
249445_at	putative protein predicted protei	---	AT5G39380	-1.03	-0.05	-0.24	0.8185029	0.9143772	-6.52	FALSE
253274_at	Phosphoglycerate dehydrogena	EDA9	AT4G34200	1.17	0.22	0.24	0.8187423	0.9144257	-6.52	TRUE
257215_at	RING zinc finger protein, putativ	---	AT3G15070	1.03	0.04	0.24	0.8188038	0.9144257	-6.52	FALSE
250069_at	disease resistance protein-like	---	AT5G17970	1.03	0.04	0.24	0.8188139	0.9144257	-6.52	FALSE
254774_at	hypothetical protein	---	AT4G13440	1.05	0.07	0.24	0.8188852	0.9144605	-6.53	FALSE
251308_at	putative protein several hypothet	GAUT1	AT3G61130	-1.03	-0.04	-0.24	0.8189685	0.9144783	-6.53	FALSE
249670_at	unknown protein	---	AT5G35890	-1.03	-0.04	-0.24	0.8189813	0.9144783	-6.53	FALSE
247253_at	beta-1,3-glucanase	---	AT5G64790	-1.08	-0.11	-0.24	0.8190545	0.9144998	-6.53	FALSE
264958_at	unknown protein ; supported by	---	AT1G76960	1.04	0.06	0.24	0.8190807	0.9144998	-6.53	FALSE
261427_at	protein kinase, putative similar t	IBS1	AT1G18670	1.05	0.07	0.24	0.819504	0.9148597	-6.53	FALSE
264560_at	hypothetical protein predicted by	---	AT1G55820	1.02	0.03	0.24	0.819509	0.9148597	-6.53	FALSE
251965_at	putative protein variety of predic	---	AT3G53360	-1.03	-0.04	-0.24	0.819764	0.9148597	-6.53	FALSE
249959_at	NADH:ubiquinone oxidoreductas	---	AT5G18800	-1.03	-0.05	-0.24	0.8196857	0.9148597	-6.53	FALSE
256630_at	unknown protein	---	AT3G28230	-1.03	-0.04	-0.24	0.8197576	0.9148597	-6.53	FALSE
264892_at	GH3-like auxin-regulated protein	---	AT1G23160	-1.03	-0.04	-0.24	0.8197374	0.9148597	-6.53	FALSE
260219_at	hypothetical protein contains Pfa	---	AT1G74630	1.03	0.04	0.24	0.819711	0.9148597	-6.53	FALSE
259667_at	unknown protein ; supported by	---	AT1G55270	-1.03	-0.04	-0.24	0.8195655	0.9148597	-6.53	FALSE

254567_s_a	hypothetical protein	---	AT4G19260 /.	1.02	0.03	0.24	0.8195639	0.9148597	-6.53	FALSE
257068_at	non-LTR reverse transcriptase, (	---	---	-1.02	-0.03	-0.24	0.8198299	0.9148885	-6.53	FALSE
252220_at	putative protein hypothetical pro	LBD38	AT3G49940	1.05	0.06	0.24	0.8199202	0.9148997	-6.53	FALSE
246964_at	putative protein crp1 protein - Ze	---	AT5G24830	-1.03	-0.04	-0.24	0.8198925	0.9148997	-6.53	FALSE
250734_at	putative protein similar to unknov	---	AT5G06270	1.07	0.10	0.24	0.8201895	0.9151106	-6.53	FALSE
247490_at	LFY floral meristem identity contr	LFY	AT5G61850	1.02	0.04	0.24	0.8201556	0.9151106	-6.53	FALSE
257054_at	Expressed protein ; supported by	MT3	AT3G15353	1.02	0.03	0.24	0.8204666	0.9151463	-6.53	FALSE
245081_at	unknown protein overlap with T2	---	---	1.04	0.06	0.24	0.8204164	0.9151463	-6.53	FALSE
251856_at	Peptidase - like protein ileal pep	AMP1	AT3G54720	1.05	0.06	0.24	0.8205153	0.9151463	-6.53	FALSE
254115_at	putative protein binding protein I	---	AT4G24710	1.03	0.04	0.24	0.8204238	0.9151463	-6.53	FALSE
247433_at	E2, ubiquitin-conjugating enzym	UBC3	AT5G62540	-1.04	-0.06	-0.24	0.8205866	0.9151463	-6.53	FALSE
253741_at	putative protein various hypothet	---	AT4G28890	-1.02	-0.03	-0.24	0.8206226	0.9151463	-6.53	FALSE
249499_at	hypothetical protein	---	AT5G39250	1.03	0.04	0.24	0.820386	0.9151463	-6.53	FALSE
267281_at	putative protein kinase contains a	---	AT2G19400	1.03	0.05	0.24	0.8206176	0.9151463	-6.53	FALSE
263272_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.24	0.8204151	0.9151463	-6.53	FALSE
262268_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.24	0.8204019	0.9151463	-6.53	FALSE
260957_at	delta 9 desaturase identical to de	ADS1	AT1G06080	1.05	0.07	0.24	0.820845	0.9153495	-6.53	FALSE
254611_at	Expressed protein ; supported by	---	AT4G19095	1.02	0.04	0.24	0.8210314	0.9155127	-6.53	FALSE
245973_at	putative protein predicted protei	---	---	1.02	0.03	0.24	0.8211155	0.9155168	-6.53	FALSE
257386_at	hypothetical protein predicted by	---	AT2G42440	1.02	0.03	0.24	0.8211092	0.9155168	-6.53	FALSE
260083_at	putative elicitor-responsive gene	---	AT1G63220	1.10	0.13	0.23	0.8212061	0.9155732	-6.53	FALSE
245280_at	Expressed protein ; supported by	VRN2	AT4G16845	1.03	0.04	0.23	0.8212648	0.9155938	-6.53	FALSE
261913_at	flavin-containing monooxygenas	FMO GS-O	AT1G65860	-1.06	-0.09	-0.23	0.8213828	0.9156359	-6.53	TRUE
257181_at	hypothetical protein	---	AT3G13190	-1.03	-0.05	-0.23	0.8213777	0.9156359	-6.53	FALSE
265286_at	putative NADH-ubiquinone oxire	---	AT2G20360	1.03	0.04	0.23	0.8214782	0.9156975	-6.53	FALSE
256102_at	unknown protein	---	AT1G13680	-1.02	-0.03	-0.23	0.8216853	0.9158389	-6.53	FALSE
252101_at	rac-like GTP binding protein Arac	ROP1	AT3G51300	1.03	0.04	0.23	0.8216744	0.9158389	-6.53	FALSE
245119_at	unknown protein ; supported by	---	AT2G41640	1.13	0.18	0.23	0.8218844	0.9159583	-6.53	FALSE
256983_at	chaperonin 60 beta, putative ver	---	AT3G13470	1.07	0.09	0.23	0.8218895	0.9159583	-6.53	FALSE
266216_at	putative DOF zinc finger protein	---	AT2G28810	-1.03	-0.04	-0.23	0.8220378	0.9159583	-6.53	FALSE
263814_at	putative TNP2-like transposon pr	---	---	-1.03	-0.04	-0.23	0.8220314	0.9159583	-6.53	FALSE
254855_s_a	putative protein other predicted (	---	AT4G12140 /.	1.03	0.05	0.23	0.8220736	0.9159583	-6.53	FALSE
252729_at	putative protein replication prote	---	---	1.02	0.03	0.23	0.8220111	0.9159583	-6.53	FALSE
249657_at	sen1-like protein SEN1 - Saccha	---	AT5G37140	-1.02	-0.03	-0.23	0.8220088	0.9159583	-6.53	FALSE
253985_at	caffeoyl-CoA O-methyltransferas	---	AT4G26220	-1.03	-0.04	-0.23	0.8221601	0.9159911	-6.53	FALSE

258769_at	putative alpha-hydroxynitrile lyas	MES17	AT3G10870	1.05	0.07	0.23	0.8221833	0.9159911	-6.53	FALSE
253302_at	Expressed protein ; supported by	---	AT4G33660	1.04	0.05	0.23	0.8223049	0.9160237	-6.53	FALSE
252955_at	multiubiquitin chain binding prote	RPN10	AT4G38630	1.02	0.03	0.23	0.8223306	0.9160237	-6.53	FALSE
260810_s_a	retroelement protein, putative si	---	---	-1.03	-0.04	-0.23	0.822333	0.9160237	-6.53	FALSE
260618_at	flower development protein cycl	TCP3	AT1G53230	-1.03	-0.05	-0.23	0.8225311	0.9160757	-6.53	FALSE
257681_at	hypothetical protein predicted by	---	AT3G13370	1.02	0.03	0.23	0.8225172	0.9160757	-6.53	FALSE
246497_at	putative protein hypothetical prot	---	AT5G16220	-1.05	-0.07	-0.23	0.8225076	0.9160757	-6.53	FALSE
256124_at	hypothetical protein predicted by	ATPUP9	AT1G18220	-1.02	-0.03	-0.23	0.8225404	0.9160757	-6.53	FALSE
260630_at	subtilisin-like serine protease cor	ALE1	AT1G62340	1.04	0.05	0.23	0.8225887	0.9160847	-6.53	FALSE
261919_at	type 2 peroxiredoxin, putative si	TPX1	AT1G65980	-1.03	-0.04	-0.23	0.8226831	0.9161005	-6.53	FALSE
253689_at	hypothetical protein ;supported b	---	AT4G29770	-1.03	-0.04	-0.23	0.8226514	0.9161005	-6.53	FALSE
256100_at	unknown protein	---	AT1G13750	1.08	0.12	0.23	0.8227614	0.9161429	-6.53	FALSE
250858_at	I-box binding factor - like protein	---	AT5G04760	1.04	0.06	0.23	0.8229159	0.9162702	-6.53	FALSE
249220_at	putative protein strong similarity t	---	AT5G42420	1.03	0.04	0.23	0.8229868	0.9163044	-6.53	FALSE
259825_at	RNA and export factor binding p	---	AT1G66260	-1.03	-0.05	-0.23	0.8232895	0.916552	-6.53	FALSE
253826_s_a	E2, ubiquitin-conjugating enzym	UBC9	AT4G27960 /	-1.02	-0.03	-0.23	0.8232819	0.916552	-6.53	FALSE
245109_at	hypothetical protein predicted by	---	AT2G41520	1.03	0.04	0.23	0.8235949	0.9168472	-6.53	FALSE
248499_at	putative protein contains similarit	PAP27	AT5G50400	-1.02	-0.03	-0.23	0.8236389	0.9168514	-6.53	FALSE
246989_at	unknown protein	---	AT5G67350	1.07	0.10	0.23	0.8237004	0.9168751	-6.53	FALSE
263100_at	hypothetical protein predicted by	AtPOT1a	AT2G05210	-1.04	-0.05	-0.23	0.8237684	0.9169061	-6.53	FALSE
255175_at	putative glucosyltransferase ;su	ATCSLC12	AT4G07960	-1.03	-0.04	-0.23	0.8238405	0.9169148	-6.53	FALSE
255090_at	putative protein disease resistan	---	AT4G09360	-1.03	-0.04	-0.23	0.8238566	0.9169148	-6.53	FALSE
245059_at	unknown protein ;supported by f	RHC2A	AT2G39720	-1.02	-0.03	-0.23	0.8240087	0.9169947	-6.53	FALSE
254159_at	putative DNA-binding protein DN	WRKY7	AT4G24240	-1.06	-0.08	-0.23	0.823976	0.9169947	-6.53	FALSE
247732_at	putative protein various predicte	---	AT5G59600	1.02	0.03	0.23	0.824177	0.9170477	-6.53	FALSE
246664_at	putative protein predicted protein	---	---	-1.03	-0.04	-0.23	0.8241642	0.9170477	-6.53	FALSE
250802_at	pectinesterase	---	AT5G04970	1.03	0.04	0.23	0.8241555	0.9170477	-6.53	FALSE
255727_at	hypothetical protein similar to unl	---	AT1G25510	1.03	0.04	0.23	0.8243217	0.9170744	-6.53	FALSE
264004_at	Expressed protein ; supported by	---	AT2G22425	1.03	0.04	0.23	0.8242833	0.9170744	-6.53	FALSE
254887_at	putative protein various predicte	---	AT4G11770	1.03	0.04	0.23	0.8242852	0.9170744	-6.53	FALSE
250176_at	putative protein cytochrome P45	CYP724A1	AT5G14400	-1.04	-0.05	-0.23	0.8244558	0.9170786	-6.53	FALSE
263927_s_a	putative cinnamyl-alcohol dehydr	CAD2	AT2G21730 /	-1.03	-0.05	-0.23	0.8243841	0.9170786	-6.53	FALSE
261128_at	ubiquitin-specific protease 2 (UB	UBP2	AT1G04860	-1.03	-0.04	-0.23	0.824479	0.9170786	-6.53	FALSE
247911_at	putative protein contains similarit	XRCC3	AT5G57450	1.03	0.04	0.23	0.8244863	0.9170786	-6.53	FALSE
252333_at	putative protein N-terminus: sev	---	AT3G48830	1.02	0.03	0.23	0.8245843	0.917143	-6.53	FALSE

264291_at	hypothetical protein contains sim	---	AT1G78800	-1.03	-0.04	-0.23	0.8249484	0.9175032	-6.53	FALSE
260116_at	AIG1 identical to AIG1 (exhibits	AIG1	AT1G33960	-1.02	-0.03	-0.23	0.8250909	0.9176169	-6.53	FALSE
265433_at	unknown protein	---	AT2G20950	-1.04	-0.05	-0.23	0.825219	0.9176321	-6.53	TRUE
259988_at	Athila ORF 1, putative simlar to	---	---	-1.02	-0.03	-0.23	0.8252252	0.9176321	-6.53	FALSE
244907_at	hypothetical protein	---	---	1.02	0.03	0.23	0.8251951	0.9176321	-6.53	FALSE
263752_at	putative retroelement pol polypro	---	---	1.03	0.05	0.23	0.825477	0.9178225	-6.53	FALSE
248904_at	Expressed protein ; supported by	---	AT5G46295	1.03	0.04	0.23	0.8254663	0.9178225	-6.53	FALSE
252007_at	hypothetical protein MobA, Pseu	---	AT3G52830	-1.03	-0.05	-0.23	0.8255723	0.9178839	-6.53	FALSE
257930_at	hypothetical protein	---	AT3G17010	-1.04	-0.05	-0.23	0.825632	0.9179054	-6.53	FALSE
256558_at	hypothetical protein predicted by	---	---	1.02	0.03	0.23	0.8257588	0.9180017	-6.53	FALSE
259132_at	putative auxin-independent grow	---	AT3G02250	-1.04	-0.06	-0.23	0.8259117	0.9181269	-6.53	TRUE
257952_at	putative peroxidase almost identi	---	AT3G21770	1.04	0.06	0.23	0.8260151	0.9181523	-6.53	FALSE
254569_s_a	hypothetical protein	---	---	1.02	0.03	0.23	0.8259875	0.9181523	-6.53	FALSE
256317_at	hypothetical protein predicted by	---	AT1G35900	1.04	0.06	0.23	0.8261269	0.9182014	-6.53	FALSE
246634_at	epsilon-adaptin, putative similar	---	AT1G31730	1.02	0.03	0.23	0.8261397	0.9182014	-6.53	FALSE
261383_at	hypothetical protein predicted by	---	AT1G05380	1.03	0.04	0.23	0.8262344	0.9182172	-6.53	FALSE
263492_at	putative seed maturation protein	---	AT2G42560	-1.03	-0.04	-0.23	0.8262223	0.9182172	-6.53	FALSE
264451_s_a	putative lectin receptor kinase ve	---	---	1.03	0.04	0.23	0.8263487	0.9182772	-6.53	FALSE
258370_at	Expressed protein ; supported by	---	AT3G14395	1.03	0.04	0.23	0.826369	0.9182772	-6.53	FALSE
245693_at	thioredoxin - like protein	WCRKC2	AT5G04260	1.03	0.04	0.23	0.8265348	0.9184167	-6.53	FALSE
255357_at	putative pectinesterase	---	AT4G03930	-1.02	-0.03	-0.23	0.8270162	0.9188174	-6.53	FALSE
256685_at	hypothetical protein predicted by	---	AT3G32100	1.03	0.04	0.23	0.8269947	0.9188174	-6.53	FALSE
265756_at	putative bZIP transcription factor	---	AT2G13150	-1.02	-0.03	-0.23	0.8269961	0.9188174	-6.53	FALSE
253766_at	putative protein ;supported by fu	---	AT4G28770	1.03	0.04	0.23	0.8271833	0.9189582	-6.53	FALSE
253533_at	putative protein cellulose syntha	ATCSLC5	AT4G31590	-1.09	-0.12	-0.23	0.827229	0.9189643	-6.53	FALSE
249408_at	myb-related protein	MYB23	AT5G40330	-1.03	-0.04	-0.23	0.8272826	0.918979	-6.53	FALSE
254194_at	auxin response factor 9 (ARF9)	ARF9	AT4G23980	-1.04	-0.06	-0.23	0.8274847	0.9191588	-6.53	FALSE
262889_at	hypothetical protein	---	AT1G14800	1.04	0.05	0.23	0.8275268	0.9191608	-6.53	FALSE
257641_s_a	hypothetical protein	AOC1	AT3G25760 ///	-1.05	-0.07	-0.23	0.8276131	0.9191905	-6.53	FALSE
260657_at	wall-associated kinase 2, putativ	---	AT1G19390	1.03	0.04	0.23	0.8276342	0.9191905	-6.53	FALSE
255368_at	hypothetical protein	---	---	-1.02	-0.03	-0.23	0.8281224	0.919688	-6.53	FALSE
250400_at	protein phosphatase 2C -like pro	---	AT5G10740	-1.04	-0.06	-0.23	0.8284539	0.9198561	-6.53	FALSE
254339_at	glucosidase like protein furostan	BGLU3	AT4G22100	1.02	0.03	0.23	0.8284071	0.9198561	-6.53	FALSE
248716_at	unknown protein ;supported by f	---	AT5G48210	1.03	0.05	0.23	0.8283979	0.9198561	-6.53	FALSE
265839_at	putative serpin	---	AT2G14540	1.03	0.04	0.23	0.8285373	0.9198561	-6.53	FALSE

265549_at	hypothetical protein predicted by	---	---	1.03	0.04	0.23	0.8285451	0.9198561	-6.53	FALSE
263147_at	polyubiquitin, putative similar to	---	AT1G53980	-1.02	-0.03	-0.23	0.8285561	0.9198561	-6.53	FALSE
254017_at	putative transcription factor	---	AT4G26170	1.02	0.03	0.23	0.8285346	0.9198561	-6.53	FALSE
259306_at	unknown protein ;supported by f	PNC1	AT3G05290	1.02	0.04	0.23	0.8286111	0.9198725	-6.53	FALSE
261716_at	kinesin-related protein, putative	---	AT1G18410	1.02	0.03	0.22	0.8287659	0.9199996	-6.53	FALSE
251197_at	glutaredoxin -like protein glutare	---	AT3G62960	-1.05	-0.08	-0.22	0.8288308	0.9200268	-6.53	FALSE
255869_at	unknown protein	---	AT2G30270	1.03	0.04	0.22	0.8289349	0.9200976	-6.53	FALSE
256971_at	unknown protein contains Pfam p	---	AT3G21100	-1.04	-0.05	-0.22	0.8290964	0.9201464	-6.53	FALSE
247707_at	scarecrow-like 11 - like scarecro	---	AT5G59450	1.11	0.16	0.22	0.8290644	0.9201464	-6.53	FALSE
261637_at	DNA-binding protein PcMYB1, p	TRB1	AT1G49950	1.03	0.05	0.22	0.8290999	0.9201464	-6.53	FALSE
247129_at	alpha-mannosidase	---	AT5G66150	1.04	0.06	0.22	0.8291963	0.9202086	-6.53	FALSE
253441_at	putative protein Fidipidine, Dros	---	AT4G32560	-1.03	-0.04	-0.22	0.8292534	0.9202272	-6.53	FALSE
262917_at	hypothetical protein contains sim	---	AT1G64800	-1.03	-0.04	-0.22	0.8294579	0.9202381	-6.53	FALSE
264935_at	hypothetical protein predicted by	---	AT1G61150	-1.04	-0.06	-0.22	0.829465	0.9202381	-6.53	FALSE
265018_s_a	hypothetical protein predicted by	---	AT2G13770	-1.02	-0.03	-0.22	0.8294516	0.9202381	-6.53	FALSE
259100_at	DNA-damage-repair/toleration pr	DRT102	AT3G04880	-1.03	-0.04	-0.22	0.8294586	0.9202381	-6.53	FALSE
257282_at	TNP2-like transposon protein, p	---	---	-1.03	-0.04	-0.22	0.8293948	0.9202381	-6.53	FALSE
246170_at	putative protein various predicte	---	AT5G32450	-1.03	-0.04	-0.22	0.8295928	0.9202904	-6.53	FALSE
244952_at	hypothetical protein	---	---	1.03	0.04	0.22	0.8295581	0.9202904	-6.53	FALSE
248428_at	protein phosphatase-2C; PP2C-l	AHG1	AT5G51760	1.02	0.03	0.22	0.8297068	0.9203721	-6.53	FALSE
251649_at	Ca2+-transporting ATPase-like p	ACA11	AT3G57330	1.04	0.06	0.22	0.829767	0.9203828	-6.53	FALSE
258869_at	hypothetical protein similar to xyl	AtVGT1	AT3G03090	-1.03	-0.04	-0.22	0.8298373	0.9203828	-6.53	FALSE
248325_at	unknown protein	---	AT5G52800	-1.02	-0.03	-0.22	0.8298375	0.9203828	-6.53	FALSE
260122_at	AIG1-like protein similar to AIG1	---	AT1G33900	1.03	0.04	0.22	0.8299973	0.9205153	-6.53	FALSE
264409_s_a	hypothetical protein similar to hy	---	---	-1.03	-0.05	-0.22	0.830086	0.9205689	-6.53	FALSE
265823_at	hypothetical protein predicted by	---	AT2G35760	-1.03	-0.04	-0.22	0.8304252	0.9207632	-6.53	TRUE
258648_at	putative auxin-independent grow	---	AT3G07900	-1.04	-0.06	-0.22	0.8303416	0.9207632	-6.53	FALSE
262320_at	hypothetical protein predicted by	---	AT1G27550	-1.02	-0.04	-0.22	0.8303589	0.9207632	-6.53	FALSE
254589_at	hypothetical protein	---	AT4G18850	1.03	0.04	0.22	0.8304343	0.9207632	-6.53	FALSE
264877_at	putative obtusifoliol 14-alpha der	CYP51G2	AT2G17330	1.02	0.03	0.22	0.830463	0.9207632	-6.53	FALSE
265411_at	unknown protein	---	AT2G16630	1.09	0.13	0.22	0.8305361	0.9207995	-6.53	TRUE
248328_at	putative protein contains similarit	---	AT5G52660	1.02	0.03	0.22	0.8306239	0.920852	-6.53	FALSE
264431_at	RNA polymerase II subunit (hsR	---	AT1G61700	-1.03	-0.04	-0.22	0.8307248	0.9209191	-6.53	FALSE
251463_at	hypothetical protein	---	AT3G59800	1.03	0.04	0.22	0.8308169	0.9209419	-6.53	FALSE
261829_at	P-glycoprotein, putative similar t	PGP10	AT1G10680	1.03	0.04	0.22	0.830826	0.9209419	-6.53	FALSE

248375_at	potassium/proton antiporter-like	KEA5	AT5G51710	-1.02	-0.03	-0.22	0.8309905	0.9210347	-6.53	FALSE
254465_at	tapetum-specific A3 like protein	---	AT4G20420	-1.03	-0.04	-0.22	0.8309573	0.9210347	-6.53	FALSE
264109_at	unknown protein	---	AT2G13720	-1.02	-0.03	-0.22	0.8311582	0.9211758	-6.53	FALSE
257067_at	unknown protein contains Pfam	CYP77A5P	AT3G18270	-1.03	-0.04	-0.22	0.8312425	0.9212244	-6.53	FALSE
262032_at	biotin holocarboxylase synthetas	HCS2	AT1G37150	1.02	0.03	0.22	0.8313619	0.921312	-6.53	FALSE
260871_at	hypothetical protein predicted by	---	AT1G29040	-1.02	-0.03	-0.22	0.8315009	0.9214213	-6.53	FALSE
252440_at	aquaporin-like protein aquaporin	TIP5;1	AT3G47440	1.02	0.03	0.22	0.8317613	0.9215285	-6.53	FALSE
248229_at	caffeic acid 3-O-methyltransferas	---	AT5G53810	1.03	0.04	0.22	0.8318401	0.9215285	-6.53	FALSE
246448_at	putative protein putative N-acetl	---	AT5G16800	1.03	0.04	0.22	0.831771	0.9215285	-6.53	FALSE
253517_at	predicted protein hypothetical pr	---	AT4G31390	-1.03	-0.05	-0.22	0.8317234	0.9215285	-6.53	FALSE
266678_at	hypothetical protein predicted by	---	AT2G25870	-1.02	-0.03	-0.22	0.8317833	0.9215285	-6.53	FALSE
248873_at	disease resistance protein-like	---	AT5G46450	1.08	0.11	0.22	0.831829	0.9215285	-6.53	FALSE
245302_at	Expressed protein ; supported by	KAN3	AT4G17695	1.04	0.06	0.22	0.8322539	0.9218655	-6.53	FALSE
258387_at	hypothetical protein predicted by	---	AT3G15550	-1.03	-0.04	-0.22	0.8322655	0.9218655	-6.53	FALSE
265669_at	unknown protein ;supported by f	---	AT2G32040	-1.04	-0.06	-0.22	0.8322406	0.9218655	-6.53	FALSE
256039_at	hypothetical protein contains sim	---	AT1G19190	-1.03	-0.04	-0.22	0.8323167	0.9218774	-6.53	FALSE
254822_at	polyubiquitin-like protein polyubi	UPL5	AT4G12570	1.02	0.03	0.22	0.8324823	0.921971	-6.53	FALSE
258718_at	unknown protein ; supported by	---	AT3G09760	-1.03	-0.04	-0.22	0.832536	0.921971	-6.53	FALSE
249664_at	putative protein histone stem-loo	---	AT5G36722 /	-1.02	-0.03	-0.22	0.8326487	0.921971	-6.53	FALSE
254544_at	putative chitinase chitinase (EC	---	AT4G19820	1.03	0.04	0.22	0.832588	0.921971	-6.53	FALSE
247547_at	putative protein	---	AT5G61360	1.04	0.06	0.22	0.8326841	0.921971	-6.53	FALSE
266602_at	hypothetical protein predicted by	---	AT2G46050	1.02	0.03	0.22	0.8324794	0.921971	-6.53	FALSE
250594_at	putative protein contains similarit	---	AT5G07760	1.03	0.04	0.22	0.8326641	0.921971	-6.53	FALSE
248067_at	unknown protein	---	AT5G55600	1.03	0.04	0.22	0.8329221	0.9221522	-6.53	FALSE
256389_at	hypothetical protein predicted by	---	AT3G06220	-1.03	-0.04	-0.22	0.8329286	0.9221522	-6.53	FALSE
252141_at	putative protein	---	AT3G51100	1.02	0.03	0.22	0.833057	0.9221693	-6.53	FALSE
252306_at	hypothetical protein	---	AT3G49270	1.02	0.03	0.22	0.8330627	0.9221693	-6.53	FALSE
263388_at	En/Spm-like transposon protein r	---	---	1.03	0.04	0.22	0.8330654	0.9221693	-6.53	FALSE
249715_at	putative protein similar to unknov	---	AT5G35760	1.03	0.04	0.22	0.8331356	0.9222023	-6.53	FALSE
250042_at	putative protein non-consensus	---	AT5G18420	1.02	0.04	0.22	0.8331769	0.9222033	-6.53	FALSE
259522_at	hypothetical protein	---	AT1G12490	-1.02	-0.03	-0.22	0.8333764	0.9223794	-6.53	FALSE
257464_at	hypothetical protein predicted by	---	AT1G20940	1.02	0.03	0.22	0.8334255	0.922389	-6.53	FALSE
258420_at	putative RNA polymerase simila	---	AT3G16680	1.02	0.03	0.22	0.8334831	0.9224079	-6.53	FALSE
249070_at	cellulose synthase catalytic subu	CESA4	AT5G44030	1.03	0.04	0.22	0.8337066	0.9226105	-6.53	FALSE
257912_at	formin-like protein AHF1 identica	AFH1	AT3G25500	-1.06	-0.08	-0.22	0.8338135	0.9226841	-6.53	TRUE

256761_at	hypothetical protein predicted by	---	AT3G25670	-1.03	-0.05	-0.22	0.8339681	0.9228103	-6.53	FALSE
251188_at	putative protein DESSICATION-	---	AT3G62730	-1.03	-0.04	-0.22	0.8341648	0.9229833	-6.53	FALSE
254930_at	putative protein hypothetical pro	---	AT4G11450	1.05	0.07	0.22	0.8342894	0.9230463	-6.53	FALSE
263012_at	homeotic protein, putative simila	KNAT6	AT1G23380	-1.02	-0.03	-0.22	0.8343372	0.9230463	-6.53	FALSE
256355_at	hypothetical protein predicted by	---	AT1G55040	-1.03	-0.04	-0.22	0.8343432	0.9230463	-6.53	FALSE
252859_at	putative protein AP2 domain cor	---	AT4G39780	-1.04	-0.06	-0.22	0.8348511	0.9231605	-6.53	TRUE
262578_at	hypothetical protein Similar to gi|	---	---	1.03	0.04	0.22	0.8347248	0.9231605	-6.53	FALSE
246537_at	putative protein protochlorophyll	---	AT5G15940	1.03	0.04	0.22	0.8347513	0.9231605	-6.53	FALSE
248257_at	putative protein similar to unknov	---	AT5G53410	-1.03	-0.05	-0.22	0.834655	0.9231605	-6.53	FALSE
250692_at	putative protein strong similarity t	---	AT5G06560	-1.03	-0.04	-0.22	0.8347884	0.9231605	-6.53	FALSE
263208_at	zinc finger protein 5, ZFP5 poss	ZFP5	AT1G10480	1.03	0.04	0.22	0.8347635	0.9231605	-6.53	FALSE
264812_at	putative thaumatin-like pathogen	---	AT2G17860	1.02	0.03	0.22	0.8348049	0.9231605	-6.53	FALSE
246626_at	hypothetical protein contains sim	---	AT1G48870	-1.04	-0.05	-0.22	0.8348041	0.9231605	-6.53	FALSE
262080_at	unknown protein ; supported by c	CW14	AT1G59650	1.03	0.05	0.22	0.8346285	0.9231605	-6.53	FALSE
247411_at	putative protein contains similarit	---	AT5G63000	-1.03	-0.04	-0.22	0.8348311	0.9231605	-6.53	FALSE
250337_at	putative protein SF21 protein, H	---	AT5G11790	1.08	0.11	0.22	0.8353187	0.9232727	-6.53	FALSE
260372_at	unknown protein contains a regic	---	AT1G73980	1.02	0.03	0.22	0.8352563	0.9232727	-6.53	FALSE
245084_at	putative MYB family transcription	AtMYB70	AT2G23290	1.04	0.06	0.22	0.8352319	0.9232727	-6.53	TRUE
247642_at	putative protein various predicted	---	AT5G60590	-1.02	-0.03	-0.22	0.8353574	0.9232727	-6.53	FALSE
245040_at	hypothetical protein predicted by	---	AT2G26520	1.03	0.04	0.22	0.8352783	0.9232727	-6.53	FALSE
257817_at	putative RNA-binding protein co	---	AT3G25150	1.02	0.03	0.22	0.8351244	0.9232727	-6.53	FALSE
262499_at	unknown protein EST gb|T41993	---	AT1G21770	1.03	0.05	0.22	0.8351572	0.9232727	-6.53	FALSE
260855_at	phosphatidylinositol-4-phosphat	---	AT1G21920	-1.04	-0.05	-0.22	0.8351946	0.9232727	-6.53	FALSE
258589_at	putative GDSL-motif lipase/acylh	LTL1	AT3G04290	-1.03	-0.04	-0.22	0.8351498	0.9232727	-6.53	FALSE
248803_at	selenium-binding protein-like	---	AT5G47460	-1.03	-0.04	-0.22	0.8352613	0.9232727	-6.53	FALSE
258401_at	unknown protein ; supported by	---	AT3G15430	-1.03	-0.04	-0.22	0.8354638	0.9233455	-6.53	FALSE
248826_at	casein kinase II beta chain ; supp	CKB1	AT5G47080	-1.03	-0.04	-0.22	0.8356897	0.9235057	-6.53	FALSE
250450_at	putative transcription factor MYB	ATMYB92	AT5G10280	-1.02	-0.03	-0.22	0.8356696	0.9235057	-6.53	FALSE
255402_at	Expressed protein	hemf2	AT4G03205	-1.05	-0.07	-0.22	0.8358837	0.923661	-6.53	FALSE
263508_s_a	hypothetical protein	---	---	1.03	0.05	0.22	0.8359418	0.923661	-6.53	FALSE
247827_at	putative protein various predicte	LSH5	AT5G58500	1.03	0.04	0.22	0.8359517	0.923661	-6.53	FALSE
265845_at	unknown protein	---	AT2G35610	-1.02	-0.03	-0.21	0.8361606	0.9238297	-6.53	FALSE
255325_at	putative membrane trafficking fac	PUX4	AT4G04210	1.02	0.03	0.21	0.8362632	0.9238297	-6.53	FALSE
261233_at	hypothetical protein similar to hyp	---	AT1G32810	1.03	0.04	0.21	0.8362664	0.9238297	-6.53	FALSE
246495_at	putative protein hypothetical pro	---	AT5G16200	-1.09	-0.12	-0.21	0.8362323	0.9238297	-6.53	FALSE

245337_at	Expressed protein ; supported by	---	AT4G16566	1.02	0.03	0.21	0.8364244	0.92387	-6.53	FALSE
250091_at	unknown protein	---	AT5G17340	1.02	0.03	0.21	0.8363876	0.92387	-6.53	FALSE
264278_at	myrosinase binding protein, puta	---	AT1G60130	-1.02	-0.03	-0.21	0.8363869	0.92387	-6.53	FALSE
249146_at	putative protein contains similarit	---	AT5G43310	1.02	0.03	0.21	0.8365823	0.9239102	-6.53	FALSE
251168_at	putative protein several hypothet	---	AT3G63370	1.03	0.04	0.21	0.8365385	0.9239102	-6.53	FALSE
250606_s_a	pectin methyl-esterase-like prote	PPME1	AT1G69940 /.	-1.02	-0.03	-0.21	0.8365774	0.9239102	-6.53	FALSE
252945_at	putative protein ;supported by fu	---	AT4G39140	-1.03	-0.04	-0.21	0.8371183	0.9241333	-6.53	TRUE
261597_at	hypothetical protein predicted by	PUB26	AT1G49780	-1.09	-0.13	-0.21	0.837026	0.9241333	-6.53	FALSE
258428_at	unknown protein	---	AT3G16610	-1.02	-0.04	-0.21	0.8368505	0.9241333	-6.53	FALSE
257326_s_a	hypothetical protein	---	---	1.03	0.04	0.21	0.8371894	0.9241333	-6.53	FALSE
246466_at	sugar transporter - like protein D	---	AT5G17010	1.04	0.05	0.21	0.8370961	0.9241333	-6.53	FALSE
259634_at	hypothetical protein	---	AT1G56380	1.02	0.03	0.21	0.8371891	0.9241333	-6.53	FALSE
264088_at	unknown protein	emb1381	AT2G31340	1.03	0.04	0.21	0.8371889	0.9241333	-6.53	FALSE
257481_at	hypothetical protein identical to h	ALMT1	AT1G08430	-1.02	-0.03	-0.21	0.8369705	0.9241333	-6.53	FALSE
263436_at	hypothetical protein	---	AT2G28690	1.03	0.04	0.21	0.8369481	0.9241333	-6.53	FALSE
267404_at	hypothetical protein predicted by	atnudt22	AT2G33980	-1.02	-0.04	-0.21	0.8369427	0.9241333	-6.53	FALSE
260707_s_a	Expressed protein ; supported by	---	AT1G32410	1.03	0.04	0.21	0.8375114	0.92444	-6.53	FALSE
246802_at	kinesin-like heavy chain non-con	ATK4	AT5G27000	1.03	0.04	0.21	0.8375483	0.92444	-6.53	FALSE
261926_at	unknown protein	PATL2	AT1G22530	-1.03	-0.04	-0.21	0.8376367	0.9244481	-6.53	TRUE
253449_at	putative protein hypothetical pro	---	AT4G32700	1.02	0.03	0.21	0.8376325	0.9244481	-6.53	FALSE
256393_at	hypothetical protein	---	AT3G06280	1.02	0.03	0.21	0.8376994	0.9244726	-6.53	FALSE
249850_at	putative protein similar to unknov	---	AT5G23240	1.02	0.03	0.21	0.8379422	0.924651	-6.53	TRUE
250405_at	ubiquitin-specific protease 22 (U	UBP22	AT5G10790	-1.04	-0.05	-0.21	0.8379305	0.924651	-6.53	FALSE
246931_at	putative protein apoptosis-relate	---	AT5G25170	1.08	0.11	0.21	0.8380827	0.9247613	-6.53	FALSE
254722_at	putative protein predicted protei	---	AT4G13530	-1.05	-0.06	-0.21	0.8382504	0.9249017	-6.53	FALSE
254770_at	extensin-like protein extensin-lik	---	AT4G13340	1.06	0.09	0.21	0.8383441	0.9249156	-6.53	TRUE
249550_at	protein kinase - like protein wall-	---	AT5G38210	1.05	0.07	0.21	0.838315	0.9249156	-6.53	TRUE
266845_at	unknown protein	---	AT2G26110	1.04	0.06	0.21	0.8384989	0.9249521	-6.53	TRUE
263301_x_a	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.21	0.8384936	0.9249521	-6.53	FALSE
249488_at	putative protein putative transpo	---	---	-1.02	-0.03	-0.21	0.8384325	0.9249521	-6.53	FALSE
247653_at	transcriptional coactivator - like	---	AT5G59950	-1.02	-0.03	-0.21	0.8386093	0.9250291	-6.53	FALSE
256738_at	geranylgeranyl pyrophosphate s	---	AT3G29430	-1.03	-0.04	-0.21	0.8386776	0.9250598	-6.53	FALSE
245787_at	unknown protein	---	AT1G32130	-1.03	-0.04	-0.21	0.8387418	0.9250858	-6.53	FALSE
256454_at	NADPH oxidoreductase, putative	---	AT1G75280	-1.07	-0.09	-0.21	0.838826	0.925134	-6.53	FALSE
267059_at	putative carboxymethylenebuten	---	AT2G32520	1.02	0.03	0.21	0.8389773	0.9252561	-6.53	FALSE

253554_at	putative protein predicted protei	---	AT4G30940	1.04	0.05	0.21	0.8392339	0.9254944	-6.53	FALSE
249369_at	putative protein Kelch motif cont	---	AT5G40680	1.02	0.03	0.21	0.8393384	0.9255649	-6.53	FALSE
253198_at	putative protein various predicted	---	AT4G35360	1.02	0.03	0.21	0.8395704	0.9257759	-6.53	FALSE
260252_at	putative mitochondrial carrier pro	---	AT1G74240	-1.03	-0.05	-0.21	0.8396787	0.9258506	-6.53	FALSE
266611_at	putative auxin-regulated protein	GH3.1	AT2G14960	1.02	0.03	0.21	0.8397421	0.9258758	-6.53	FALSE
257269_at	unknown protein contains Pfam p	NPSN13	AT3G17440	1.04	0.05	0.21	0.8399471	0.9259303	-6.53	FALSE
257340_at	pseudogene, retroelement pol p	---	---	-1.03	-0.04	-0.21	0.8398673	0.9259303	-6.53	FALSE
250103_at	transcription factor (gb|AAD5309	MYB43	AT5G16600	-1.02	-0.03	-0.21	0.839954	0.9259303	-6.53	FALSE
264720_at	hypothetical protein similar to vet	---	AT1G70080	1.03	0.04	0.21	0.8399084	0.9259303	-6.53	FALSE
267209_at	unknown protein ;supported by f	---	AT2G30930	-1.03	-0.04	-0.21	0.8400929	0.9260121	-6.53	TRUE
261705_at	hypothetical protein predicted by	---	AT1G32670	1.02	0.03	0.21	0.8401093	0.9260121	-6.53	FALSE
245229_at	putative protein contains EST gb	---	AT4G25620	-1.04	-0.06	-0.21	0.840281	0.9261492	-6.53	FALSE
248305_at	putative protein similar to unknov	ATUSP	AT5G52560	-1.03	-0.04	-0.21	0.8403957	0.9261492	-6.53	FALSE
258352_at	putative auxin-induced protein si	IAA31	AT3G17600	1.03	0.04	0.21	0.8403604	0.9261492	-6.53	FALSE
260751_at	unknown protein	SCD1	AT1G49040	1.04	0.05	0.21	0.8403961	0.9261492	-6.53	FALSE
248233_at	F-box protein family, AtFBL13 c	---	AT5G53840	-1.02	-0.03	-0.21	0.8405853	0.9263129	-6.53	FALSE
245098_at	ethylene response sensor (ERS)	ERS1	AT2G40940	-1.05	-0.08	-0.21	0.8407391	0.9264376	-6.53	FALSE
258376_at	hypothetical protein similar to GE	---	AT3G17680	1.02	0.03	0.21	0.8408605	0.9264819	-6.53	FALSE
260072_at	unknown protein supported by cl	---	AT1G73650	1.03	0.04	0.21	0.8408242	0.9264819	-6.53	FALSE
251304_at	putative protein several O-methy	---	AT3G61990	1.08	0.12	0.21	0.8409951	0.9265855	-6.53	TRUE
266212_at	putative retroelement pol polypro	---	---	1.03	0.04	0.21	0.8412432	0.9266851	-6.53	FALSE
262773_at	putative nuclear matrix constitue	LINC2	AT1G13220	-1.03	-0.04	-0.21	0.8411452	0.9266851	-6.53	FALSE
247262_at	putative protein contains similarit	AtFAAH	AT5G64440	-1.02	-0.04	-0.21	0.8411866	0.9266851	-6.53	FALSE
263966_s_a	putative TNP2-like transposon pr	---	---	-1.02	-0.03	-0.21	0.8412481	0.9266851	-6.53	FALSE
263096_at	class 1 non-symbiotic hemoglobi	AHB1	AT2G16060	1.06	0.09	0.21	0.8413561	0.9267594	-6.53	FALSE
249723_at	putative protein similar to unknov	---	AT5G35430	1.02	0.03	0.21	0.8413971	0.9267598	-6.53	FALSE
256019_at	cytochrome P-450, putative simi	---	AT1G58260 ///	1.02	0.03	0.21	0.8415548	0.9267687	-6.53	FALSE
251909_at	putative protein initiator-binding	TRFL4	AT3G53790	1.03	0.04	0.21	0.8415677	0.9267687	-6.53	FALSE
250059_at	peroxidase ATP13a ; supported	---	AT5G17820	1.02	0.03	0.21	0.841553	0.9267687	-6.53	FALSE
251709_at	response regulator-like protein r	ARR17	AT3G56380	-1.02	-0.03	-0.21	0.8414466	0.9267687	-6.53	FALSE
258144_at	hypothetical protein	---	AT3G18180	1.02	0.03	0.21	0.84166	0.9268256	-6.53	FALSE
248642_at	putative protein similar to unknov	---	AT5G49120	-1.02	-0.03	-0.21	0.8417107	0.9268366	-6.53	FALSE
247114_at	unknown protein ; supported by	---	AT5G65910	1.03	0.04	0.21	0.8418445	0.9268652	-6.53	FALSE
253314_at	hypothetical protein	---	AT4G33890	-1.02	-0.03	-0.21	0.8418179	0.9268652	-6.53	FALSE
245070_at	metallothionein-like protein identi	---	AT2G23240	1.03	0.04	0.21	0.8418585	0.9268652	-6.53	FALSE

263923_at	Expressed protein ; supported by	---	AT2G36485	1.03	0.05	0.21	0.8419378	0.9269077	-6.53	FALSE
257565_at	hypothetical protein predicted by	---	AT3G28620	1.02	0.03	0.21	0.8419986	0.9269299	-6.53	FALSE
245550_at	cytochrome P450 like protein	CYP705A1	AT4G15330	-1.02	-0.03	-0.21	0.8422678	0.9271816	-6.53	FALSE
267159_at	putative SCARECROW gene reg	---	AT2G37650	1.02	0.03	0.21	0.8429026	0.9272079	-6.53	FALSE
264821_at	hypothetical protein predicted by	---	AT1G03470	-1.04	-0.06	-0.21	0.8430182	0.9272079	-6.53	FALSE
265544_at	putative cyclic nucleotide and ca	ATCNGC15	AT2G28260	-1.03	-0.05	-0.21	0.8425952	0.9272079	-6.53	FALSE
253270_at	cyclin delta-3	CYCD3;1	AT4G34160	-1.04	-0.05	-0.21	0.8429179	0.9272079	-6.53	FALSE
250143_at	ADP-ribosylation factor - like pro	ATARFA1B	AT5G14670	-1.02	-0.03	-0.21	0.8425295	0.9272079	-6.53	FALSE
264302_at	ATPase 70 kDa subunit, putative	VHA-A	AT1G78900	1.03	0.04	0.21	0.8428968	0.9272079	-6.53	FALSE
251767_at	putative protein U4/U6 small nuc	---	AT3G55930	1.02	0.03	0.21	0.8425014	0.9272079	-6.53	FALSE
253848_at	putative protein regulator protein	---	AT4G28020	-1.03	-0.05	-0.21	0.8426946	0.9272079	-6.53	FALSE
256054_at	unknown protein	---	AT1G07120	-1.02	-0.03	-0.21	0.842821	0.9272079	-6.53	FALSE
250417_at	putative protein predicted protein	---	AT5G11230	1.03	0.04	0.21	0.8424857	0.9272079	-6.53	FALSE
264473_at	hypothetical protein predicted by	---	AT1G67180	1.05	0.06	0.21	0.8428377	0.9272079	-6.53	FALSE
256727_at	hypothetical protein	---	AT3G52240	1.03	0.04	0.21	0.8426865	0.9272079	-6.53	FALSE
248182_at	putative protein contains similarit	---	AT5G54030	1.02	0.03	0.21	0.84283	0.9272079	-6.53	FALSE
264287_at	hypothetical protein similar to hyp	---	AT1G61930	1.03	0.04	0.21	0.8427509	0.9272079	-6.53	FALSE
255164_at	hypothetical protein	---	---	1.02	0.03	0.21	0.8430234	0.9272079	-6.53	FALSE
250411_at	putative protein	---	AT5G11120	-1.02	-0.03	-0.21	0.8425064	0.9272079	-6.53	FALSE
265749_at	putative retroelement pol polypro	---	---	1.02	0.04	0.21	0.8429924	0.9272079	-6.53	FALSE
266339_s_a	hypothetical protein predicted by	---	AT2G01360 ///	1.03	0.04	0.21	0.842771	0.9272079	-6.53	FALSE
252547_at	putative protein many predicted	---	AT3G45840	1.03	0.04	0.21	0.8430901	0.9272365	-6.53	FALSE
265807_at	unknown protein	---	AT2G17990	-1.02	-0.04	-0.21	0.8432789	0.9273994	-6.53	FALSE
251300_at	hypothetical protein ;supported b	---	AT3G61980	-1.03	-0.05	-0.21	0.843375	0.9274604	-6.53	FALSE
246570_at	putative protein nonmuscle myo	---	AT5G14990	1.02	0.03	0.21	0.8434477	0.9274956	-6.53	FALSE
265414_at	nodulin-like protein	---	AT2G16660	1.06	0.09	0.21	0.8435287	0.9275399	-6.53	TRUE
249517_at	putative protein similar to unknov	---	AT5G38580	1.02	0.03	0.20	0.8436457	0.9276239	-6.53	FALSE
260572_at	putative molybdopterin synthase	---	AT2G43760	-1.02	-0.03	-0.20	0.8438676	0.9278232	-6.53	FALSE
251631_at	putative protein several hypothet	---	AT3G57430	-1.03	-0.04	-0.20	0.8439955	0.9278265	-6.53	FALSE
262739_at	lipase, putative contains Pfam p	---	AT1G28650	1.04	0.06	0.20	0.844074	0.9278265	-6.53	FALSE
264711_at	hypothetical protein predicted by	---	AT1G09800	-1.02	-0.03	-0.20	0.843968	0.9278265	-6.53	FALSE
263988_at	floral homeodomain transcription	SHP2	AT2G42830	-1.02	-0.03	-0.20	0.8439642	0.9278265	-6.53	FALSE
257470_at	hypothetical protein predicted by	---	AT1G53770	-1.03	-0.04	-0.20	0.8440607	0.9278265	-6.53	FALSE
247186_at	putative protein contains similarit	---	AT5G65470	-1.04	-0.06	-0.20	0.844132	0.9278456	-6.53	TRUE
260549_at	Expressed protein ; supported by	---	AT2G43535	-1.07	-0.10	-0.20	0.844346	0.928036	-6.53	FALSE

262167_at	putative RING zinc finger protein	---	AT1G74990	-1.03	-0.04	-0.20	0.8446177	0.9282899	-6.53	FALSE
248588_at	unknown protein ; supported by	---	AT5G49540	1.02	0.03	0.20	0.8447484	0.9283888	-6.53	FALSE
254979_at	subtilisin-like serine protease cor	---	AT4G10550	-1.02	-0.03	-0.20	0.8449876	0.9284284	-6.53	FALSE
248755_at	putative protein strong similarity t	---	AT5G47690	1.03	0.05	0.20	0.845048	0.9284284	-6.53	FALSE
249270_at	putative protein similar to unknov	---	AT5G41780	1.02	0.03	0.20	0.8450692	0.9284284	-6.53	FALSE
263818_at	putative retroelement pol polypro	---	---	-1.02	-0.02	-0.20	0.8449936	0.9284284	-6.53	FALSE
251128_at	putative protein crp1 protein, Ze	---	AT5G01110	-1.02	-0.03	-0.20	0.8449066	0.9284284	-6.53	FALSE
261157_at	peroxidase ATP13a, putative sir	---	AT1G34510	-1.02	-0.03	-0.20	0.845007	0.9284284	-6.53	FALSE
265009_at	putative protein kinase similar to	---	AT1G24650	1.02	0.03	0.20	0.8449862	0.9284284	-6.53	FALSE
245555_at	HSR201 like protein	---	AT4G15390	-1.02	-0.03	-0.20	0.8452094	0.9285376	-6.53	FALSE
263019_at	trehalose 6-phosphate synthase	ATTPS9	AT1G23870	1.07	0.10	0.20	0.8453209	0.928597	-6.53	FALSE
265631_at	putative helicase	---	---	1.02	0.03	0.20	0.8453449	0.928597	-6.53	FALSE
257296_at	hypothetical protein predicted by	---	AT3G28020	1.02	0.03	0.20	0.845585	0.9288161	-6.53	FALSE
265412_at	putative chloroplast outer membr	TOC132	AT2G16640	1.02	0.03	0.20	0.8456697	0.9288643	-6.53	FALSE
245676_at	nodule-specific protein, putative	---	AT1G56670	-1.02	-0.03	-0.20	0.8457251	0.9288805	-6.53	FALSE
265820_at	hypothetical protein predicted by	---	AT2G17940	1.03	0.04	0.20	0.8458591	0.9289381	-6.53	FALSE
251053_at	Ca2+/H+ exchanger-like protein	CAX4	AT5G01490	-1.04	-0.06	-0.20	0.8458546	0.9289381	-6.53	FALSE
260552_at	putative glyoxalase II ; supporte	GLX2-1	AT2G43430	-1.02	-0.03	-0.20	0.8459583	0.9290024	-6.53	FALSE
252954_at	putative thaumatin-like protein th	---	AT4G38660	-1.08	-0.12	-0.20	0.8461272	0.9291432	-6.53	FALSE
247530_at	glycosylasparaginase - like prote	---	AT5G61540	-1.03	-0.05	-0.20	0.8462173	0.9291973	-6.53	FALSE
252986_at	putative protein T19C21.18 Arab	---	AT4G38380	1.02	0.02	0.20	0.8463428	0.9292685	-6.53	FALSE
250943_at	putative protein	---	AT5G03360	-1.02	-0.03	-0.20	0.8463947	0.9292685	-6.53	FALSE
247662_at	protein kinase - like protein kina	---	AT5G60090	1.03	0.05	0.20	0.8464043	0.9292685	-6.53	FALSE
245169_at	unknown protein predicted by ge	---	AT2G33220	-1.02	-0.03	-0.20	0.8464527	0.9292769	-6.53	FALSE
265389_at	putative riboflavin synthase alpha	---	AT2G20690	-1.03	-0.04	-0.20	0.8466893	0.9293143	-6.53	FALSE
247141_at	putative protein strong similarity t	---	AT5G65560	-1.03	-0.05	-0.20	0.8467128	0.9293143	-6.53	FALSE
259554_at	hypothetical protein	---	---	-1.03	-0.04	-0.20	0.8466479	0.9293143	-6.53	FALSE
258795_at	hypothetical protein similar to pu	---	AT3G04570	1.03	0.04	0.20	0.846772	0.9293143	-6.53	FALSE
256946_at	hypothetical protein contains Pfa	HAF2	AT3G19040	1.04	0.05	0.20	0.8465897	0.9293143	-6.53	FALSE
247579_at	cytochrome P450 - like protein c	CYP89A3	AT5G61320	-1.02	-0.03	-0.20	0.8467675	0.9293143	-6.53	FALSE
261730_s_a	mutator-like transposase, putativ	---	---	-1.02	-0.03	-0.20	0.8466798	0.9293143	-6.53	FALSE
255315_at	hypothetical protein	---	---	1.02	0.03	0.20	0.8468485	0.9293536	-6.53	FALSE
253360_at	aminopeptidase- like protein am	APM1	AT4G33090	1.03	0.04	0.20	0.846949	0.9294192	-6.53	FALSE
261093_at	non-LTR reverse transcriptase,	AT1G6288(	---	1.03	0.04	0.20	0.8470999	0.9295025	-6.53	FALSE
258954_at	unknown protein contains Pfam p	---	AT3G01400	-1.02	-0.03	-0.20	0.8471064	0.9295025	-6.53	FALSE

252819_at	putative protein several hypothet	---	---	1.02	0.03	0.20	0.8471949	0.9295548	-6.53	FALSE
263476_at	putative poly(ADP-ribose) glycoh	TEJ	AT2G31870	-1.02	-0.03	-0.20	0.8473054	0.9296314	-6.53	FALSE
246711_at	putative protein	---	AT5G28190	1.02	0.03	0.20	0.8474282	0.9296766	-6.53	FALSE
246172_s_a	fragment of 1-aminocyclopropar	ACS1	AT3G61510 /	1.03	0.04	0.20	0.8474019	0.9296766	-6.53	FALSE
255217_s_a	hypothetical protein	---	---	-1.03	-0.05	-0.20	0.8474915	0.9297014	-6.53	FALSE
265734_at	predicted by genscan and genefi	---	AT2G01260	-1.02	-0.03	-0.20	0.847828	0.9300258	-6.53	FALSE
246737_at	putative protein	---	AT5G27710	-1.04	-0.06	-0.20	0.8479417	0.9301058	-6.53	FALSE
250560_at	replication factor A - like protein	RPA70B	AT5G08020	-1.04	-0.06	-0.20	0.8480936	0.9302277	-6.53	FALSE
246506_at	putative protein hypothetical pro	---	AT5G16110	-1.03	-0.04	-0.20	0.8482222	0.9302793	-6.53	FALSE
258031_s_a	hypothetical protein similar to hyp	---	AT3G27480 /	1.03	0.04	0.20	0.8481958	0.9302793	-6.53	FALSE
259636_at	RNA pseudouridylate synthase,	---	AT1G56345	-1.05	-0.07	-0.20	0.8483375	0.930361	-6.53	FALSE
257747_at	hypothetical protein predicted by	---	AT3G18700	1.02	0.03	0.20	0.8484633	0.9304542	-6.53	FALSE
248284_at	Expressed protein ; supported by	---	AT5G52975	-1.03	-0.04	-0.20	0.8485793	0.9305157	-6.53	FALSE
256190_at	9-cis-epoxycarotenoid dioxygena	NCED5	AT1G30100	-1.02	-0.03	-0.20	0.8486322	0.9305157	-6.53	FALSE
265955_at	putative ABC transporter	PDR5	AT2G37280	-1.02	-0.03	-0.20	0.8486417	0.9305157	-6.53	FALSE
251979_at	caffeic acid O-methyltransferase	LUT1	AT3G53130 /	-1.02	-0.03	-0.20	0.8488037	0.9306198	-6.53	FALSE
259646_at	n-calpain-1 large subunit, putativ	DEK1	AT1G55350	-1.02	-0.03	-0.20	0.8488183	0.9306198	-6.53	FALSE
265834_at	hypothetical protein predicted by	---	AT2G14410	1.02	0.03	0.20	0.848976	0.930748	-6.53	FALSE
266387_at	hypothetical protein predicted by	---	AT2G32360	-1.02	-0.03	-0.20	0.849029	0.9307613	-6.53	FALSE
248420_at	receptor-like protein kinase ;sup	---	AT5G51560	-1.06	-0.09	-0.20	0.8492687	0.9307899	-6.53	TRUE
261697_at	hypothetical protein identical to h	---	AT1G32610	1.04	0.05	0.20	0.8492999	0.9307899	-6.53	FALSE
264552_at	hypothetical protein predicted by	---	AT1G09470	-1.04	-0.05	-0.20	0.8491811	0.9307899	-6.53	FALSE
245857_at	putative protein various predicte	---	---	1.03	0.04	0.20	0.8492035	0.9307899	-6.53	FALSE
256532_at	PPR-repeat protein, putative cor	---	AT1G33350	1.03	0.05	0.20	0.8492616	0.9307899	-6.53	FALSE
257943_at	SKP1/ASK1 (At7), putative simil	ASK7	AT3G21840	-1.02	-0.04	-0.20	0.8492825	0.9307899	-6.53	FALSE
246652_at	extensin -like protein extensin, s	---	AT5G35190	-1.02	-0.03	-0.20	0.8493672	0.930819	-6.53	FALSE
264181_at	ubiquitin, putative similar to ubiq	UBQ13	AT1G65350	-1.02	-0.03	-0.20	0.8495629	0.9309448	-6.53	FALSE
251698_at	putative protein	---	AT3G56610	1.02	0.03	0.20	0.8495636	0.9309448	-6.53	FALSE
250132_at	putative protein similar to unknov	KAN	AT5G16560	-1.04	-0.06	-0.20	0.8496938	0.9309532	-6.54	TRUE
255675_at	MYC1 transcription factor	ATMYC1	AT4G00480	1.02	0.03	0.20	0.8496688	0.9309532	-6.54	FALSE
250100_at	Expressed protein ; supported by	GLN1;4	AT5G16570	1.06	0.09	0.20	0.8496264	0.9309532	-6.53	FALSE
254433_at	putative protein tripeptidyl-peptic	TPP2	AT4G20850	1.02	0.03	0.20	0.8499276	0.9311105	-6.54	FALSE
255905_at	tonoplast intrinsic protein, putativ	BETA-TIP	AT1G17810	-1.04	-0.06	-0.20	0.8499598	0.9311105	-6.54	FALSE
261275_at	Mlo protein, putative similar to G	MLO14	AT1G26700	1.02	0.03	0.20	0.8499024	0.9311105	-6.54	FALSE
247341_at	unknown protein	---	AT5G63720	-1.02	-0.03	-0.20	0.8500194	0.9311311	-6.54	FALSE

246731_at	putative protein RING finger rng	ACBP5	AT5G27630	1.02	0.03	0.20	0.8501212	0.9311979	-6.54	FALSE
249706_at	histone deacetylase	HDA7	AT5G35600	1.02	0.03	0.20	0.8502068	0.9312469	-6.54	FALSE
263075_at	hypothetical protein predicted by	---	AT2G17570	1.03	0.05	0.20	0.8505115	0.9312676	-6.54	FALSE
262990_at	E2, ubiquitin-conjugating enzym	MMZ1	AT1G23260	1.02	0.03	0.20	0.8504252	0.9312676	-6.54	FALSE
248057_at	putative protein strong similarity t	---	AT5G55520	1.02	0.03	0.20	0.8504322	0.9312676	-6.54	FALSE
254600_at	4-coumarate-CoA ligase - like 4-	---	AT4G19010	-1.04	-0.06	-0.20	0.8504026	0.9312676	-6.54	FALSE
266403_at	putative acid phosphatase contai	---	AT2G38600	1.03	0.04	0.20	0.850497	0.9312676	-6.54	FALSE
256594_at	hypothetical protein similar to put	---	AT3G28520	-1.02	-0.03	-0.20	0.8503932	0.9312676	-6.54	FALSE
253059_s_a	putative protein other predicted p	HHP5	AT4G37680 /,	1.04	0.05	0.20	0.8504227	0.9312676	-6.54	FALSE
251923_at	reductase-like protein abscisic a	---	AT3G53880	1.05	0.07	0.20	0.8506176	0.9313391	-6.54	FALSE
266745_at	unknown protein ; supported by	PKS1	AT2G02950	1.06	0.08	0.20	0.8507704	0.9314617	-6.54	TRUE
262768_at	putative beta-1,4-N-acetylglucos	---	AT1G12990	1.05	0.07	0.20	0.8508962	0.9315547	-6.54	FALSE
253363_at	hypothetical protein	---	AT4G33130	-1.02	-0.03	-0.20	0.8509786	0.9316002	-6.54	FALSE
244920_s_a	NADH dehydrogenase subunit 3	---	AT2G07751	1.02	0.04	0.20	0.8510713	0.931657	-6.54	FALSE
245808_at	RNA binding protein identical to I	ATRBP1	AT1G58470	1.03	0.04	0.19	0.8511559	0.9317048	-6.54	FALSE
253989_at	uncharacterized protein ;support	---	AT4G26130	1.04	0.05	0.19	0.8512108	0.9317202	-6.54	FALSE
249037_at	putative protein contains similarit	FLA13	AT5G44130	1.08	0.11	0.19	0.851253	0.9317217	-6.54	TRUE
249178_at	putative protein similar to unknov	SCP2	AT5G42890	1.02	0.03	0.19	0.8514741	0.9318479	-6.54	FALSE
249017_at	C2 domain-containing protein-like	---	AT5G44760	-1.03	-0.04	-0.19	0.8514908	0.9318479	-6.54	FALSE
AFFX-r2-Bs	B. subtilis /GEN=thrC, thrB /DB_	---	---	-1.05	-0.06	-0.19	0.8514844	0.9318479	-6.54	FALSE
244937_at	NADH dehydrogenase 49KDa pr	---	---	1.04	0.06	0.19	0.8517177	0.9319679	-6.54	TRUE
251630_at	putative protein unknown protein	---	AT3G57420	1.02	0.03	0.19	0.8516587	0.9319679	-6.54	FALSE
262330_at	disease resistance protein, puta	RLM1	AT1G64070	-1.02	-0.03	-0.19	0.851723	0.9319679	-6.54	FALSE
252117_at	mucin -like protein hemomucin,	YLS2	AT3G51430	1.04	0.05	0.19	0.8517942	0.932001	-6.54	TRUE
264976_at	peptide transporter, putative sim	NRT1.6	AT1G27080	-1.03	-0.04	-0.19	0.8518874	0.9320583	-6.54	FALSE
256385_at	60S ribosomal protein L10, puta	---	AT1G66580	-1.04	-0.06	-0.19	0.8520279	0.9321673	-6.54	TRUE
255370_at	putative protein	---	---	1.02	0.03	0.19	0.8520909	0.9321916	-6.54	FALSE
260508_at	Unknown protein ; supported by	GAMMA CA	AT1G47260	1.02	0.03	0.19	0.8521572	0.9322194	-6.54	FALSE
254009_at	pyruvate kinase like protein pyru	---	AT4G26390	1.04	0.05	0.19	0.852331	0.93232	-6.54	FALSE
258098_at	hypothetical protein similar to kin	KINESIN-12	AT3G23670	-1.03	-0.05	-0.19	0.8523209	0.93232	-6.54	FALSE
261371_at	ubiquitin-conjugating enzyme, p	UBC26	AT1G53020	1.02	0.03	0.19	0.8523832	0.9323324	-6.54	FALSE
255739_at	unknown protein similar to hypot	ANAC008	AT1G25580	-1.03	-0.04	-0.19	0.852548	0.9323339	-6.54	FALSE
267156_at	hypothetical protein predicted by	---	AT2G37610	-1.02	-0.03	-0.19	0.8525262	0.9323339	-6.54	FALSE
264426_at	hypothetical protein similar to hyp	---	AT1G61760	-1.02	-0.04	-0.19	0.8524776	0.9323339	-6.54	FALSE
254367_at	hypothetical protein	---	AT4G21700	1.03	0.04	0.19	0.852453	0.9323339	-6.54	FALSE

246488_at	steroid 5alpha-reductase-like pr	---	AT5G16010	1.04	0.06	0.19	0.8528826	0.9324652	-6.54	TRUE
254592_at	heat shock transcription factor -	HSF A4A	AT4G18880	-1.07	-0.10	-0.19	0.8527839	0.9324652	-6.54	TRUE
257884_at	hypothetical protein predicted by	---	AT3G16960	1.02	0.03	0.19	0.8531178	0.9324652	-6.54	FALSE
247191_at	homeobox-leucine zipper protein	ATHB5	AT5G65310	1.04	0.05	0.19	0.8530042	0.9324652	-6.54	FALSE
263626_at	transcription factor ZAP1 identica	ZAP1	AT2G04880	-1.02	-0.03	-0.19	0.8530141	0.9324652	-6.54	FALSE
253169_at	putative protein various predicte	---	AT4G35120	1.02	0.03	0.19	0.8528549	0.9324652	-6.54	FALSE
251248_at	P-glycoprotein-like proetin P-gly	PGP21	AT3G62150	-1.10	-0.14	-0.19	0.852972	0.9324652	-6.54	FALSE
259857_at	hypothetical protein predicted by	---	AT1G68430	-1.02	-0.03	-0.19	0.852813	0.9324652	-6.54	FALSE
255206_at	putative transposon protein	---	---	-1.02	-0.02	-0.19	0.8527897	0.9324652	-6.54	FALSE
258785_at	unknown protein	---	---	-1.03	-0.04	-0.19	0.8530635	0.9324652	-6.54	FALSE
262475_at	hypothetical protein predicted by	---	AT1G50340	1.02	0.03	0.19	0.8530916	0.9324652	-6.54	FALSE
263450_at	putative calcium-dependent prote	CPK24	AT2G31500	-1.02	-0.03	-0.19	0.8531662	0.9324735	-6.54	FALSE
261464_at	disease resistance response pro	---	AT1G07730 /	-1.02	-0.04	-0.19	0.8534012	0.9326856	-6.54	FALSE
245407_at	GTP-binding RAB2A like protein	RABB1C	AT4G17170	-1.02	-0.03	-0.19	0.8535357	0.9327794	-6.54	FALSE
256900_at	pectate lyase, putative similar to	---	AT3G24670	1.03	0.04	0.19	0.8536085	0.9327794	-6.54	FALSE
255251_at	see GB:U95973 similar to a fami	---	AT4G04980	1.02	0.03	0.19	0.8536506	0.9327794	-6.54	FALSE
266793_at	homeotic protein AGL30	AGL30	AT2G03060	-1.04	-0.05	-0.19	0.8536113	0.9327794	-6.54	FALSE
248110_at	wax synthase-like protein	---	AT5G55320	-1.02	-0.03	-0.19	0.8537565	0.9327802	-6.54	FALSE
263113_at	unknown protein Belongs to PF|	---	AT1G03150	-1.02	-0.03	-0.19	0.8536945	0.9327802	-6.54	FALSE
262216_at	hypothetical protein contains sim	---	AT1G74780	1.03	0.04	0.19	0.853774	0.9327802	-6.54	FALSE
259408_at	protein phosphatase 2A 65 kDa	PP2AA2	AT3G25800	1.02	0.03	0.19	0.8538438	0.9328118	-6.54	FALSE
253595_at	putative protein M1 protein, Stre	---	AT4G30830	-1.02	-0.03	-0.19	0.8539872	0.9329237	-6.54	FALSE
260149_at	putative oxidoreductase similar t	---	AT1G52810	-1.05	-0.07	-0.19	0.8540507	0.9329484	-6.54	FALSE
253977_at	putative protein various Caenorh	---	AT4G26630	1.03	0.05	0.19	0.8542434	0.9329802	-6.54	FALSE
245234_at	myb-like protein similarity to ATI	AtMYB18	AT4G25560	-1.02	-0.04	-0.19	0.8541357	0.9329802	-6.54	FALSE
252371_at	putative protein finger protein SI	---	AT3G48070	1.02	0.03	0.19	0.8542117	0.9329802	-6.54	FALSE
264695_at	lipid transfer protein, putative sir	---	AT1G70250	-1.03	-0.04	-0.19	0.8541942	0.9329802	-6.54	FALSE
259494_at	mitotic checkpoint protein, putati	---	AT1G15850	1.03	0.04	0.19	0.8543314	0.9330317	-6.54	FALSE
265883_at	unknown protein	---	AT2G42310	-1.02	-0.03	-0.19	0.8543914	0.9330525	-6.54	FALSE
263713_at	Expressed protein ; supported by	---	AT2G20595	1.02	0.04	0.19	0.8544819	0.9331057	-6.54	FALSE
258720_at	putative ankyrin similar to ankyri	---	AT3G09550	1.03	0.04	0.19	0.8545219	0.9331057	-6.54	FALSE
254221_at	putative polygalacturonase poly	---	AT4G23820	-1.09	-0.12	-0.19	0.8546372	0.9331869	-6.54	TRUE
248193_at	homogentisate 1,2-dioxygenase	HGO	AT5G54080	-1.04	-0.06	-0.19	0.854755	0.9332709	-6.54	FALSE
253022_at	putative protein	---	AT4G38060	1.04	0.06	0.19	0.8550706	0.9334089	-6.54	TRUE
259257_at	unknown protein ;supported by f	---	AT3G07760	-1.02	-0.04	-0.19	0.8550861	0.9334089	-6.54	FALSE

256820_at	far-red impaired response protei	FHY3	AT3G22170	1.02	0.03	0.19	0.8550044	0.9334089	-6.54	FALSE
253016_at	putative protein partial LG127/3(	---	AT4G37950	1.02	0.02	0.19	0.854945	0.9334089	-6.54	FALSE
251947_at	putative protein various predicte	---	AT3G53550	-1.02	-0.03	-0.19	0.8550686	0.9334089	-6.54	FALSE
258381_at	kinesin-like protein similar to mitc	KINESIN-1	AT3G16630	-1.02	-0.03	-0.19	0.8552162	0.9335063	-6.54	FALSE
246036_at	alpha-galactosidase - like protei	AtAGAL2	AT5G08370	-1.05	-0.07	-0.19	0.8553585	0.9335723	-6.54	FALSE
258754_at	hypothetical protein similar to hyp	---	AT3G11920	1.02	0.03	0.19	0.8553511	0.9335723	-6.54	FALSE
258871_at	putative 26S proteosome regulat	---	AT3G03060	1.05	0.07	0.19	0.8554474	0.9336061	-6.54	FALSE
252868_at	putative protein tubulin-folding c	POR	AT4G39920	-1.02	-0.03	-0.19	0.8555888	0.9336061	-6.54	FALSE
251312_at	MADS-box protein AGL13 ; supp	AGL13	AT3G61120	1.02	0.03	0.19	0.8556347	0.9336061	-6.54	FALSE
249967_at	putative protein	---	AT5G19050	1.02	0.03	0.19	0.855676	0.9336061	-6.54	FALSE
259827_at	hypothetical protein	---	AT1G72270	1.02	0.03	0.19	0.855503	0.9336061	-6.54	FALSE
258261_at	putative RING zinc finger protein	---	AT3G15740	1.04	0.05	0.19	0.8556586	0.9336061	-6.54	FALSE
250427_at	putative protein myosin heavy ch	---	AT5G10500	-1.02	-0.03	-0.19	0.8555169	0.9336061	-6.54	FALSE
247686_at	receptor-like protein kinase prec	---	AT5G59700	1.07	0.09	0.19	0.8559135	0.9337969	-6.54	FALSE
246577_at	MADS box transcription factor, p	AGL92	AT1G31640	1.02	0.03	0.19	0.8559327	0.9337969	-6.54	FALSE
255715_s_a	hypothetical protein	---	AT4G00320 ///	1.02	0.03	0.19	0.8562549	0.9340591	-6.54	FALSE
257961_at	unknown protein	---	AT3G19780	1.02	0.03	0.19	0.8562317	0.9340591	-6.54	FALSE
264171_at	hypothetical protein predicted by	---	AT1G02100	-1.03	-0.04	-0.19	0.85636	0.934129	-6.54	FALSE
261455_at	unknown protein ;supported by fu	---	AT1G21070	-1.04	-0.05	-0.19	0.8564518	0.9341398	-6.54	FALSE
261683_at	hypothetical protein similar to hyp	---	AT1G47300	-1.02	-0.03	-0.19	0.85642	0.9341398	-6.54	FALSE
260281_at	unknown protein	---	AT1G80500	-1.02	-0.03	-0.19	0.8566348	0.93425	-6.54	FALSE
252049_at	putative protein putative and hyp	---	AT3G52510	-1.02	-0.03	-0.19	0.8566082	0.93425	-6.54	FALSE
244909_at	hypothetical protein	---	---	1.02	0.03	0.19	0.856714	0.9342917	-6.54	FALSE
250328_at	putative protein	---	AT5G11780	1.02	0.03	0.19	0.8568622	0.9343442	-6.54	FALSE
267439_at	putative GDSL-motif lipase/hydro	---	AT2G19060	1.02	0.03	0.19	0.8568347	0.9343442	-6.54	FALSE
248133_at	unknown protein	---	AT5G54850	-1.03	-0.04	-0.19	0.856885	0.9343442	-6.54	FALSE
258252_at	putative polygalacturonase simila	---	AT3G15720	1.04	0.06	0.19	0.8571039	0.9344936	-6.54	FALSE
251543_at	putative protein	---	AT3G58770	1.02	0.03	0.19	0.8570655	0.9344936	-6.54	FALSE
261833_at	ATP citrate-lyase, putative simila	ACLA-1	AT1G10670	-1.02	-0.03	-0.19	0.8572759	0.934604	-6.54	FALSE
250902_at	putative protein predicted protei	---	AT5G03590	-1.03	-0.04	-0.19	0.8572871	0.934604	-6.54	FALSE
249010_at	unknown protein ; supported by	---	AT5G44580	1.04	0.05	0.19	0.8576027	0.9349033	-6.54	FALSE
263337_at	hypothetical protein predicted by	---	---	1.02	0.02	0.19	0.8577498	0.935019	-6.54	FALSE
248696_at	putative protein similar to unknov	---	AT5G48360	1.02	0.03	0.19	0.8579009	0.935139	-6.54	FALSE
266502_at	hypothetical protein predicted by	---	AT2G47720 ///	1.02	0.03	0.19	0.8580003	0.9352027	-6.54	FALSE
252592_at	mitogen-activated protein kinase	NAXT1	AT3G45640 ///	-1.06	-0.09	-0.19	0.8581768	0.9352987	-6.54	FALSE

247012_at	putative protein contains similarit	TRB2	AT5G67580	-1.02	-0.03	-0.19	0.8582524	0.9352987	-6.54	FALSE
260104_x_a	hypothetical protein predicted by	---	AT1G35410	-1.02	-0.03	-0.19	0.8582135	0.9352987	-6.54	FALSE
247953_at	cytochrome P450	CYP71B10	AT5G57260	-1.02	-0.02	-0.19	0.8582099	0.9352987	-6.54	FALSE
252528_at	E2, ubiquitin-conjugating enzym	UBC13	AT3G46460	1.02	0.03	0.19	0.858403	0.9353849	-6.54	FALSE
261831_at	ADP-ribosylation factor, putative	ATARFA1F	AT1G10630	1.03	0.04	0.19	0.8584545	0.9353849	-6.54	FALSE
261642_at	ADP-glucose pyrophosphorylase	APL2	AT1G27680	1.03	0.05	0.19	0.8584512	0.9353849	-6.54	FALSE
265281_at	unknown protein ; supported by	---	AT2G28370	-1.03	-0.04	-0.18	0.8587195	0.9355593	-6.54	FALSE
260515_at	ATP-dependent transmembrane	---	AT1G51460	-1.02	-0.03	-0.18	0.8587347	0.9355593	-6.54	FALSE
260778_at	splicing factor, putative similar to	---	AT1G14640	1.03	0.04	0.18	0.8587376	0.9355593	-6.54	FALSE
255215_at	putative athila transposon protein	---	---	1.02	0.02	0.18	0.858856	0.9356435	-6.54	FALSE
248471_at	unknown protein	---	AT5G50840	-1.03	-0.04	-0.18	0.8589537	0.9357053	-6.54	FALSE
258323_at	unknown protein similar to putativ	---	AT3G22750	-1.03	-0.04	-0.18	0.8591063	0.9357184	-6.54	FALSE
257081_at	RING zinc finger protein contain	---	AT3G30460	-1.02	-0.03	-0.18	0.8591201	0.9357184	-6.54	FALSE
249832_at	disease resistance protein-like	---	AT5G23400	-1.03	-0.04	-0.18	0.8590492	0.9357184	-6.54	FALSE
255396_at	hypothetical protein	---	---	1.02	0.03	0.18	0.8591708	0.9357184	-6.54	FALSE
256318_s_a	hypothetical protein	---	---	1.02	0.02	0.18	0.8591533	0.9357184	-6.54	FALSE
264978_at	unknown protein contains Pfam p	---	AT1G27120	1.04	0.06	0.18	0.8592169	0.9357239	-6.54	FALSE
256637_at	unknown protein similar to membr	---	AT3G12030	1.03	0.04	0.18	0.8593138	0.9357401	-6.54	FALSE
257159_at	protein kinase, putative similar to	---	AT3G24400	1.03	0.05	0.18	0.8593122	0.9357401	-6.54	FALSE
262639_at	calmodulin, putative similar to ca	---	AT1G62820	-1.03	-0.05	-0.18	0.8593734	0.9357603	-6.54	FALSE
257976_at	putative transcription factor cont	PLT1	AT3G20840	1.02	0.03	0.18	0.859495	0.935848	-6.54	FALSE
255966_at	14-3-3 protein GF14epsilon (grf1	GRF10	AT1G22300	-1.02	-0.04	-0.18	0.8596121	0.9359309	-6.54	FALSE
260086_at	hypothetical protein predicted by	---	AT1G63240	-1.03	-0.04	-0.18	0.8598165	0.9360908	-6.54	FALSE
247868_at	Myb-related transcription factor-li	MYB36	AT5G57620	-1.02	-0.03	-0.18	0.8598411	0.9360908	-6.54	FALSE
252815_at	hypothetical protein	---	---	-1.02	-0.04	-0.18	0.8599126	0.936124	-6.54	FALSE
257929_at	RNA Polymerase II subunit 14.5	NRPB9A	AT3G16980	-1.02	-0.03	-0.18	0.8601156	0.936211	-6.54	FALSE
257358_at	unknown protein predicted by ge	---	AT2G40990	1.03	0.05	0.18	0.8600829	0.936211	-6.54	FALSE
262319_s_a	unknown protein similar to unkno	---	AT1G27540 /	-1.04	-0.05	-0.18	0.860038	0.936211	-6.54	FALSE
253414_at	putative protein	EDA39	AT4G33050	-1.11	-0.15	-0.18	0.8604194	0.9364209	-6.54	FALSE
248537_at	putative protein similar to unknov	---	AT5G50100	-1.03	-0.04	-0.18	0.8604316	0.9364209	-6.54	FALSE
262999_at	NAM protein, putative similar to	ANAC020	AT1G54330	-1.03	-0.04	-0.18	0.8604022	0.9364209	-6.54	FALSE
247120_at	amino acid transporter protein-lik	---	AT5G65990	1.02	0.03	0.18	0.8604809	0.9364299	-6.54	FALSE
253380_at	hypothetical protein hypothetical	PGSIP3	AT4G33330	-1.02	-0.03	-0.18	0.8605703	0.9364825	-6.54	FALSE
259661_at	Expressed protein ; supported by	---	AT1G55265	1.03	0.04	0.18	0.8606403	0.9365139	-6.54	TRUE
252733_at	putative protein INDOLE-3-ACE	---	AT3G43120	-1.02	-0.03	-0.18	0.8606882	0.9365214	-6.54	FALSE

251803_at	putative protein predicted protei	---	AT3G55350	1.03	0.04	0.18	0.8607859	0.9365603	-6.54	TRUE
258299_at	unknown protein contains GMC	---	AT3G23410	-1.03	-0.04	-0.18	0.8608061	0.9365603	-6.54	TRUE
248901_at	putative protein contains similarit	---	AT5G46410	-1.02	-0.04	-0.18	0.8609883	0.9366692	-6.54	FALSE
255097_at	predicted transposon protein sin	---	---	-1.03	-0.04	-0.18	0.860972	0.9366692	-6.54	FALSE
255840_at	unknown protein	---	AT2G33520	1.03	0.04	0.18	0.8611076	0.9367543	-6.54	FALSE
261345_at	hypothetical protein predicted by	DTA4	AT1G79760	-1.02	-0.04	-0.18	0.861159	0.9367656	-6.54	FALSE
267321_at	hypothetical protein predicted by	---	AT2G19320	-1.02	-0.03	-0.18	0.8612314	0.9367996	-6.54	FALSE
252691_at	kinesin -like protein KLP2 protei	---	AT3G44050	-1.02	-0.03	-0.18	0.8613385	0.9368714	-6.54	FALSE
251817_at	small GTP-binding protein - like	ARA6	AT3G54840	1.02	0.03	0.18	0.8614809	0.936937	-6.54	FALSE
261274_at	myb-related protein, putative sin	MYB117	AT1G26780	-1.02	-0.02	-0.18	0.8614728	0.936937	-6.54	FALSE
257508_at	bZIP transcription factor, putativ	---	AT1G64320	-1.02	-0.03	-0.18	0.8615698	0.936989	-6.54	FALSE
251591_at	carboxyl terminal protease - like	---	AT3G57680	1.04	0.05	0.18	0.861838	0.937236	-6.54	FALSE
265410_at	putative protein kinase contains	---	AT2G16620	-1.02	-0.03	-0.18	0.8619581	0.9373219	-6.54	FALSE
264768_at	hypothetical protein similar to put	---	AT1G61410	1.02	0.03	0.18	0.862151	0.9374422	-6.54	FALSE
246729_at	putative protein	---	AT5G28070	-1.02	-0.03	-0.18	0.8621171	0.9374422	-6.54	FALSE
246970_at	cytochrome P450-like protein fat	CYP714A2	AT5G24900	1.03	0.05	0.18	0.8623291	0.9375525	-6.54	FALSE
249447_at	PTEN -like protein PTEN/MMAC	PTEN1	AT5G39400	-1.03	-0.04	-0.18	0.8623346	0.9375525	-6.54	FALSE
253324_at	Expressed protein ; supported by	---	AT4G33940	1.02	0.03	0.18	0.8623885	0.9375664	-6.54	FALSE
260231_at	putative RING zinc finger protein	---	AT1G74410	-1.03	-0.04	-0.18	0.8625943	0.9376122	-6.54	FALSE
263336_x_a	hypothetical protein predicted by	---	---	1.02	0.03	0.18	0.8625266	0.9376122	-6.54	FALSE
257808_at	unknown protein, putative conta	---	AT3G26935	-1.02	-0.03	-0.18	0.8625763	0.9376122	-6.54	FALSE
249660_at	putative protein similar to unknov	---	AT5G36720 ///	1.03	0.04	0.18	0.862595	0.9376122	-6.54	FALSE
256730_at	floral homeotic protein AGL8, pu	AGL79	AT3G30260	-1.02	-0.02	-0.18	0.8627864	0.9377755	-6.54	FALSE
256403_at	unknown protein similar to SPOF	BPM2	AT3G06190	-1.02	-0.03	-0.18	0.8629724	0.937933	-6.54	FALSE
263540_at	unknown protein	---	AT2G24780	-1.02	-0.03	-0.18	0.8630367	0.9379582	-6.54	FALSE
263726_at	putative ABC transporter ;suppo	---	AT2G13610	1.09	0.13	0.18	0.8631111	0.9379944	-6.54	FALSE
246914_at	putative protein various predicte	---	AT5G25860	1.03	0.04	0.18	0.8632844	0.9381051	-6.54	FALSE
266328_at	unknown protein ; supported by	---	AT2G01600	1.02	0.02	0.18	0.8632952	0.9381051	-6.54	FALSE
245075_at	putative cytochrome P450	CYP96A1	AT2G23180	1.02	0.03	0.18	0.8634244	0.9381148	-6.54	FALSE
261818_at	similar to hypethetical 62.8 KD p	---	AT1G11390	1.02	0.03	0.18	0.8634276	0.9381148	-6.54	FALSE
267183_at	hypothetical protein predicted by	---	AT2G44020	-1.02	-0.03	-0.18	0.8634077	0.9381148	-6.54	FALSE
247534_at	pyrophosphate-dependent phos	PFK4	AT5G61580	1.02	0.02	0.18	0.8635572	0.9381962	-6.54	FALSE
246222_at	TINY-like protein ; supported by	RAP2.10	AT4G36900	-1.04	-0.06	-0.18	0.8635847	0.9381962	-6.54	FALSE
264238_at	hypothetical protein predicted by	---	AT1G54740	1.05	0.07	0.18	0.8636671	0.9381999	-6.54	FALSE
267420_at	hypothetical protein predicted by	---	AT2G35030	1.04	0.06	0.18	0.8636704	0.9381999	-6.54	FALSE

259457_at	auxin response factor 1, putative	ARF23	AT1G43950	1.02	0.03	0.18	0.8637428	0.9382339	-6.54	FALSE
265621_at	NAM (no apical meristem)-like pr	NTL8	AT2G27300	-1.02	-0.03	-0.18	0.8638496	0.9383052	-6.54	FALSE
245005_at	ribosomal protein S14	---	---	1.03	0.05	0.18	0.8638969	0.9383119	-6.54	FALSE
261247_at	hypothetical protein predicted by	---	AT1G20070	1.08	0.11	0.18	0.8640625	0.9384326	-6.54	TRUE
254940_at	putative protein predicted protei	---	AT4G10820	1.02	0.03	0.18	0.8640903	0.9384326	-6.54	FALSE
250909_at	S-receptor kinase - like protein S	---	AT5G03700	-1.07	-0.10	-0.18	0.8641741	0.9384358	-6.54	FALSE
256351_at	NPK1-related protein kinase, pu	ANP2	AT1G54960	-1.02	-0.03	-0.18	0.8641756	0.9384358	-6.54	FALSE
251087_at	putative protein unknown protei	---	AT5G01460	1.02	0.03	0.18	0.8642458	0.938466	-6.54	FALSE
252911_at	cytochrome P450 -like protein cy	CYP96A12	AT4G39510	1.06	0.08	0.18	0.8645325	0.938466	-6.54	FALSE
252212_at	protein kinase -like protein NTPI	MAPKKK20	AT3G50310	-1.05	-0.07	-0.18	0.864319	0.938466	-6.54	FALSE
249532_at	AtPP - like protein AtPP protein,	---	AT5G38780	-1.05	-0.07	-0.18	0.8645174	0.938466	-6.54	FALSE
247252_at	unknown protein	---	AT5G64770	1.08	0.11	0.18	0.8643747	0.938466	-6.54	FALSE
267615_at	putative phytocyanin	---	AT2G26720	1.03	0.04	0.18	0.864482	0.938466	-6.54	FALSE
252438_at	putative protein riboflavin biosyn	---	AT3G47390	-1.02	-0.02	-0.18	0.8644046	0.938466	-6.54	FALSE
263006_at	hypothetical protein contains sim	---	AT1G54240	1.02	0.03	0.18	0.8644322	0.938466	-6.54	FALSE
256697_at	hypothetical protein contains sim	AtOCT4	AT3G20660	-1.04	-0.06	-0.18	0.8647886	0.9386576	-6.54	FALSE
245634_at	MtN21 nodulin protein, putative	---	AT1G25270	1.02	0.03	0.18	0.8647913	0.9386576	-6.54	FALSE
258854_at	putative UDP-glucosyl transfera	---	AT3G02100	-1.02	-0.03	-0.18	0.8650853	0.9387141	-6.54	FALSE
251417_at	putative protein prib5, Ribes nig	AT3G6042(	---	1.02	0.02	0.18	0.8650903	0.9387141	-6.54	FALSE
246331_at	non-phototropic hypocotyl 3-like	---	AT3G44820	-1.02	-0.03	-0.18	0.8649754	0.9387141	-6.54	FALSE
252832_at	ubiquitin-specific protease 3 (UB	ATUBP3	AT4G39910	1.02	0.02	0.18	0.8650554	0.9387141	-6.54	FALSE
258268_at	putative WD-repeat protein cont	WSIP2	AT3G15880	-1.03	-0.04	-0.18	0.8648968	0.9387141	-6.54	FALSE
251894_at	putative protein predicted protei	---	AT3G54380	-1.02	-0.03	-0.18	0.8649813	0.9387141	-6.54	FALSE
247596_at	putative protein predicted protei	---	AT5G60840	1.04	0.05	0.18	0.8651834	0.9387705	-6.54	TRUE
265350_at	unknown protein predicted by ge	---	AT2G22620	-1.02	-0.03	-0.18	0.8652369	0.9387839	-6.54	FALSE
246671_at	putative protein	---	---	-1.02	-0.02	-0.18	0.8652785	0.9387843	-6.54	FALSE
267610_at	K+ transporter, AKT1 identical to	AKT1	AT2G26650	-1.05	-0.08	-0.18	0.8653602	0.9388283	-6.54	TRUE
258101_at	unknown protein	RFR1	AT3G23590	-1.04	-0.06	-0.18	0.8654411	0.9388715	-6.54	FALSE
261355_at	putative malate oxidoreductase s	ATNADP-M	AT1G79750	1.02	0.03	0.18	0.8655788	0.9389762	-6.54	FALSE
251191_at	putative protein putative protein	---	AT3G62590	-1.04	-0.06	-0.18	0.8659084	0.9391241	-6.54	TRUE
260590_at	phosphoenolpyruvate carboxyla	ATPPC1	AT1G53310	-1.03	-0.04	-0.18	0.8659995	0.9391241	-6.54	FALSE
262710_at	unknown protein ESTs gb|T0435	---	AT1G16210	-1.02	-0.03	-0.18	0.8659498	0.9391241	-6.54	FALSE
263743_at	coatomer alpha subunit	---	AT2G21390	1.02	0.02	0.18	0.8657623	0.9391241	-6.54	FALSE
258017_at	unknown protein	---	AT3G19370	-1.04	-0.06	-0.18	0.8659497	0.9391241	-6.54	FALSE
248048_at	nicotianamine synthase	NAS2	AT5G56080	1.02	0.03	0.18	0.8659923	0.9391241	-6.54	FALSE

247104_at	putative protein similar to unknov	DAR6	AT5G66620	1.03	0.04	0.18	0.8660034	0.9391241	-6.54	FALSE
250949_at	putative protein	---	AT5G03510	-1.02	-0.03	-0.18	0.8660943	0.9391781	-6.54	FALSE
261937_at	peptide transporter, putative sim	---	AT1G22570	1.05	0.07	0.18	0.8662026	0.9392509	-6.54	FALSE
259693_at	hypothetical protein predicted by	---	AT1G63060	1.02	0.03	0.17	0.8662558	0.9392639	-6.54	FALSE
253491_at	RNA lariat debranching enzyme	---	AT4G31770	1.04	0.05	0.17	0.8663156	0.9392841	-6.54	FALSE
247016_at	putative protein contains similarit	---	AT5G66970	1.02	0.03	0.17	0.8664185	0.9393063	-6.54	FALSE
263775_at	putative MYB family transcription	CPC	AT2G46410	1.02	0.03	0.17	0.8664077	0.9393063	-6.54	FALSE
249613_at	putative protein mDj10, Mus mu	---	AT5G37380	-1.02	-0.04	-0.17	0.8666334	0.9393103	-6.54	FALSE
255498_at	putative vacuolar ATPase simila	---	AT4G02620	-1.01	-0.02	-0.17	0.8666692	0.9393103	-6.54	FALSE
257322_at	hypothetical protein	AT2G0766	---	1.02	0.03	0.17	0.8666394	0.9393103	-6.54	FALSE
261452_s_a	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.17	0.8665674	0.9393103	-6.54	FALSE
259796_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.17	0.8666555	0.9393103	-6.54	FALSE
265992_at	putative receptor-like protein kina	---	AT2G24130	1.02	0.03	0.17	0.8664904	0.9393103	-6.54	FALSE
255050_at	putative protein hypothetical pro	---	---	1.03	0.04	0.17	0.8667839	0.93939	-6.54	FALSE
257858_at	hypothetical protein predicted by	---	AT3G12920	1.04	0.05	0.17	0.8674193	0.9398265	-6.54	TRUE
258468_at	unknown protein predicted by ge	---	AT3G06070	-1.05	-0.07	-0.17	0.8672979	0.9398265	-6.54	TRUE
256116_at	unknown protein contains similar	CPuORF55	AT1G16858 //	1.02	0.03	0.17	0.8675163	0.9398265	-6.54	TRUE
246384_at	glutaredoxin, putative similar to	---	AT1G77370	1.02	0.02	0.17	0.8673779	0.9398265	-6.54	FALSE
250581_at	copine-like protein copine VII pr	BON2	AT5G07300	-1.02	-0.03	-0.17	0.8672929	0.9398265	-6.54	FALSE
252462_at	putative protein various predicte	---	AT3G47250	1.02	0.03	0.17	0.8674972	0.9398265	-6.54	FALSE
245580_at	hypothetical protein	---	AT4G14820	1.03	0.04	0.17	0.8674594	0.9398265	-6.54	FALSE
252582_at	putative protein several hypothet	---	AT3G45530	-1.02	-0.03	-0.17	0.8674536	0.9398265	-6.54	FALSE
259010_at	unknown protein contains helix-lo	---	AT3G07340	1.03	0.05	0.17	0.8676447	0.9399209	-6.54	TRUE
257186_at	hypothetical protein predicted by	---	AT3G13130	1.02	0.03	0.17	0.8678994	0.9401522	-6.54	FALSE
262274_at	deaminase, putative similar to cy	TADA	AT1G68720	1.02	0.02	0.17	0.8679965	0.9402128	-6.54	FALSE
266094_at	Expressed protein ; supported by	---	AT2G37975	-1.02	-0.03	-0.17	0.8680727	0.9402507	-6.54	FALSE
257488_s_a	putative RING-finger protein	---	AT1G36950 //	1.01	0.02	0.17	0.868256	0.9404045	-6.54	FALSE
256682_at	putative protein dihydrolipoamide	LTA3	AT3G52200	1.02	0.02	0.17	0.8684604	0.9405366	-6.54	FALSE
257161_at	hypothetical protein predicted by	SMAP2	AT3G24280	-1.02	-0.03	-0.17	0.8684409	0.9405366	-6.54	FALSE
257265_at	PHD-finger protein, putative con	---	AT3G14980	1.02	0.03	0.17	0.8686131	0.9406573	-6.54	FALSE
253673_at	putative protein putative phosph	---	AT4G29530	1.02	0.03	0.17	0.8687461	0.9406673	-6.54	FALSE
258341_at	unknown protein similar to centro	---	AT3G22790	-1.06	-0.09	-0.17	0.8687067	0.9406673	-6.54	FALSE
249388_at	putative protein downy mildew re	---	AT5G40090	-1.02	-0.03	-0.17	0.868668	0.9406673	-6.54	FALSE
261685_at	3-beta-hydroxysteroid dehydrog	AT3BETAH	AT1G47290	-1.04	-0.06	-0.17	0.8688009	0.940682	-6.54	FALSE
263695_at	putative phosphoribosylglycinam	---	AT1G31220	-1.02	-0.03	-0.17	0.8688542	0.9406951	-6.54	FALSE

259623_at	hypothetical protein predicted by	---	AT1G42700	1.02	0.03	0.17	0.8689473	0.9407512	-6.54	FALSE
261312_at	putative NPK1-related protein kir	---	AT1G05790	1.02	0.03	0.17	0.8690806	0.9408509	-6.54	FALSE
258060_at	protein phosphatase 2A regulato	ATB' DELT	AT3G26030	1.02	0.02	0.17	0.8695392	0.9413027	-6.54	FALSE
262119_s_a	glutathione S-transferase, putati	ATGSTF6	AT1G02920 /	-1.07	-0.09	-0.17	0.8697714	0.9413809	-6.54	TRUE
263275_at	putative methylmalonate semi-al	ALDH6B2	AT2G14170	1.03	0.04	0.17	0.870097	0.9413809	-6.54	FALSE
258980_at	putative reversibly glycosylatable	RGP3	AT3G08900	1.02	0.03	0.17	0.869752	0.9413809	-6.54	FALSE
253938_at	putative homeodomain protein h	---	AT4G26920	1.02	0.03	0.17	0.8699181	0.9413809	-6.54	FALSE
263623_at	hypothetical protein predicted by	---	AT2G04860	-1.02	-0.02	-0.17	0.8698763	0.9413809	-6.54	FALSE
254874_at	putative protein beta-phosphogl	---	AT4G11570	1.03	0.04	0.17	0.8700958	0.9413809	-6.54	FALSE
252704_at	putative protein KIAA0161 gene	---	AT3G43750	1.02	0.03	0.17	0.8698055	0.9413809	-6.54	FALSE
258506_at	hypothetical protein predicted by	---	AT3G06520	-1.03	-0.04	-0.17	0.8701067	0.9413809	-6.54	FALSE
254124_at	hypothetical protein ; supported	---	AT4G24500	-1.02	-0.03	-0.17	0.8698249	0.9413809	-6.54	FALSE
259731_at	unknown protein similar to unkno	---	AT1G77460	1.04	0.06	0.17	0.8697241	0.9413809	-6.54	FALSE
248825_at	ATP synthase delta chain, mitoc	---	AT5G47030	-1.02	-0.03	-0.17	0.8700366	0.9413809	-6.54	FALSE
248090_at	putative protein contains similarit	MAPKKK15	AT5G55090	1.01	0.02	0.17	0.8699914	0.9413809	-6.54	FALSE
247954_at	beta-galactosidase (emb|CAB64	BGAL4	AT5G56870	-1.02	-0.03	-0.17	0.8702357	0.9413865	-6.54	TRUE
264945_at	MADS-box protein (MADS2), pu	MAF1	AT1G77080	-1.04	-0.06	-0.17	0.8702087	0.9413865	-6.54	FALSE
257997_at	hypothetical protein similar to hy	---	AT3G27500	1.02	0.02	0.17	0.8701568	0.9413865	-6.54	FALSE
246778_at	mevalonate kinase supported by	MK	AT5G27450	1.02	0.03	0.17	0.8705883	0.9414872	-6.54	FALSE
254340_at	putative protein hypothetical pro	---	AT4G22120	1.04	0.06	0.17	0.8705042	0.9414872	-6.54	FALSE
265754_x_a	En/Spm transposon protein (mos	---	---	1.02	0.02	0.17	0.8705766	0.9414872	-6.54	FALSE
257657_at	Expressed protein ; supported by	---	AT3G13235	-1.02	-0.02	-0.17	0.8706403	0.9414872	-6.54	FALSE
254896_at	MADS-box protein AGL14	AGL14	AT4G11880	1.02	0.02	0.17	0.8706142	0.9414872	-6.54	FALSE
247920_at	putative protein contains similarit	---	AT5G57670	-1.02	-0.03	-0.17	0.870659	0.9414872	-6.54	FALSE
254165_at	putative protein hypothetical pro	---	AT4G24330	-1.03	-0.04	-0.17	0.8704829	0.9414872	-6.54	FALSE
246658_at	putative protein predicted protei	---	---	1.02	0.03	0.17	0.8705541	0.9414872	-6.54	FALSE
266769_s_a	putative reverse transcriptase	---	---	-1.02	-0.03	-0.17	0.8708491	0.9416481	-6.54	FALSE
261605_at	CDPK-related protein kinase, pu	---	AT1G49580	-1.02	-0.03	-0.17	0.8710176	0.9416518	-6.54	FALSE
252194_at	putative tyrosine phosphatase p	ATPEN3	AT3G50110	-1.02	-0.03	-0.17	0.870948	0.9416518	-6.54	FALSE
254246_at	protein kinase - like protein rece	EMB1290	AT4G23250	1.02	0.02	0.17	0.8710087	0.9416518	-6.54	FALSE
259183_at	hypothetical protein similar to put	---	AT3G01580	-1.03	-0.04	-0.17	0.8709	0.9416518	-6.54	FALSE
263547_at	hypothetical protein predicted by	---	AT2G21680	1.02	0.03	0.17	0.8710971	0.9416522	-6.54	FALSE
257496_s_a	hypothetical protein predicted by	---	AT2G43730 /	1.02	0.03	0.17	0.8711005	0.9416522	-6.54	FALSE
251344_at	putative protein beige-like protei	---	AT3G60920	1.02	0.03	0.17	0.8712613	0.9417368	-6.54	FALSE
258237_at	myb protein identical to ATMYB3	ATMYB21	AT3G27810	1.02	0.03	0.17	0.8712419	0.9417368	-6.54	FALSE

256369_at	hypothetical protein predicted by	---	AT1G66790 /	1.01	0.02	0.17	0.8713919	0.9418332	-6.54	FALSE
264650_at	putative transcription factor Simil	NF-YC9	AT1G08970	-1.02	-0.03	-0.17	0.8716436	0.9419714	-6.54	FALSE
265302_at	Mutator-like transposase similar	---	---	1.02	0.02	0.17	0.8716074	0.9419714	-6.54	FALSE
249157_at	unknown protein	---	AT5G43510 /	1.02	0.02	0.17	0.8715877	0.9419714	-6.54	FALSE
257595_at	hypothetical protein predicted by	---	AT3G24750	1.02	0.03	0.17	0.8717948	0.9420901	-6.54	FALSE
254517_at	putative protein conserved hypo	---	AT4G20310	-1.02	-0.03	-0.17	0.871929	0.9421459	-6.54	FALSE
264303_s_a	E2, ubiquitin-conjugating enzym	UBC35	AT1G16890 /	1.02	0.03	0.17	0.8719055	0.9421459	-6.54	FALSE
248011_at	S-adenosyl-L-methionine:salicyli	GAMT2	AT5G56300	1.01	0.02	0.17	0.8719709	0.9421466	-6.54	FALSE
253109_at	putative protein predicted protei	MCA1	AT4G35920	-1.04	-0.05	-0.17	0.8720774	0.9422081	-6.54	TRUE
258783_at	unknown protein	---	AT3G11760	-1.02	-0.03	-0.17	0.8723541	0.9422081	-6.54	FALSE
260459_at	hypothetical protein predicted by	---	AT1G68240	1.02	0.03	0.17	0.8722496	0.9422081	-6.54	FALSE
263941_at	unknown protein	---	---	-1.02	-0.03	-0.17	0.8721184	0.9422081	-6.54	FALSE
255272_at	putative protein (ubiquitin like) to	---	AT4G05270	-1.02	-0.02	-0.17	0.8721761	0.9422081	-6.54	FALSE
258579_s_a	germin-like protein contains Pfam	---	AT3G04180 /	1.02	0.02	0.17	0.8723583	0.9422081	-6.54	FALSE
252772_at	hypothetical protein	---	---	1.02	0.03	0.17	0.8723397	0.9422081	-6.54	FALSE
262255_at	hypothetical protein similar to hy	---	AT1G53790	-1.02	-0.02	-0.17	0.8722975	0.9422081	-6.54	FALSE
267566_at	unknown protein predicted by ge	---	AT2G30760	1.01	0.02	0.17	0.8728567	0.942434	-6.54	FALSE
244942_at	hypothetical protein	---	---	1.02	0.02	0.17	0.8728422	0.942434	-6.54	FALSE
260170_at	putative sucrose transport protei	SUC5	AT1G71890	1.03	0.04	0.17	0.8726979	0.942434	-6.54	FALSE
258208_at	putative acetyltransferase similar	---	AT3G13930	1.03	0.04	0.17	0.8728096	0.942434	-6.54	FALSE
263777_at	putative cyclic nucleotide-regulat	ATCNGC12	AT2G46450	-1.08	-0.11	-0.17	0.8727303	0.942434	-6.54	FALSE
246165_at	putative protein	---	---	1.02	0.02	0.17	0.8727771	0.942434	-6.54	FALSE
247200_at	unknown protein ;supported by f	---	AT5G65120	1.02	0.03	0.17	0.8727303	0.942434	-6.54	FALSE
261183_at	hypothetical protein predicted by	EMB2756	AT1G34550	-1.02	-0.03	-0.17	0.8730367	0.9425426	-6.54	FALSE
249205_at	cycloartenol synthase	MRN1	AT5G42600	1.03	0.05	0.17	0.8730399	0.9425426	-6.54	FALSE
257830_at	MutT-like protein contains Pfam	ATNUDX13	AT3G26690	-1.04	-0.05	-0.17	0.8730855	0.9425472	-6.54	FALSE
262300_at	ripening-induced protein, putativ	---	AT1G70870	-1.01	-0.02	-0.17	0.873141	0.9425625	-6.54	FALSE
248608_at	ATP citrate lyase ; supported by	ACLB-2	AT5G49460	-1.02	-0.03	-0.17	0.8732208	0.9425989	-6.54	TRUE
257037_at	nuclear acid binding protein, put	ATRBP47B	AT3G19130	-1.04	-0.05	-0.17	0.8732574	0.9425989	-6.54	FALSE
255743_at	unknown protein ; supported by	---	AT1G25375	-1.02	-0.03	-0.17	0.8734901	0.9428055	-6.54	FALSE
261939_at	cytochrome c oxidase subunit, p	COX6B	AT1G22450	-1.03	-0.04	-0.17	0.8735641	0.9428408	-6.54	FALSE
252970_at	small auxin up RNA (SAUR-AC1	SAUR15	AT4G38850	-1.03	-0.05	-0.17	0.8736842	0.9429257	-6.54	TRUE
245000_at	hypothetical protein	---	---	1.02	0.03	0.16	0.8738329	0.942997	-6.54	FALSE
249005_at	terpene cyclase/synthase	---	AT5G44630	-1.01	-0.02	-0.16	0.873817	0.942997	-6.54	FALSE
246378_at	integral membrane protein, puta	---	AT1G57620	-1.02	-0.02	-0.16	0.8739757	0.9431066	-6.54	FALSE

246763_at	NHE1 Na+/H+ exchanger ; supp	NHX1	AT5G27150	1.03	0.04	0.16	0.8740873	0.9431824	-6.54	FALSE
250913_at	3-deoxy-D-manno-octulosonic a	---	AT5G03770	-1.02	-0.02	-0.16	0.8741878	0.9432462	-6.54	FALSE
266873_at	putative PREG1-like negative re	CYCP4;1	AT2G44740	1.07	0.09	0.16	0.8747552	0.9432778	-6.54	TRUE
261363_at	pectinesterase, putative similar	SKS6	AT1G41830	1.12	0.17	0.16	0.8747076	0.9432778	-6.54	FALSE
257444_at	hypothetical protein predicted by	---	AT2G12550	-1.02	-0.03	-0.16	0.874842	0.9432778	-6.54	FALSE
260680_s_a	GATA transcription factor 3, puta	---	AT1G08000 /	-1.02	-0.02	-0.16	0.8743461	0.9432778	-6.54	FALSE
256165_at	hypothetical protein predicted by	---	AT1G48780	-1.02	-0.03	-0.16	0.8743693	0.9432778	-6.54	FALSE
257420_at	hypothetical protein predicted by	---	AT1G77250	-1.02	-0.03	-0.16	0.8745852	0.9432778	-6.54	FALSE
266915_at	hypothetical protein predicted by	---	AT2G45870	-1.02	-0.02	-0.16	0.8749377	0.9432778	-6.54	FALSE
266096_at	putative vacuolar protein sorting-	VCL1	AT2G38020	1.02	0.02	0.16	0.8742889	0.9432778	-6.54	FALSE
258145_at	integral membrane protein, puta	---	AT3G18200	-1.02	-0.03	-0.16	0.8749544	0.9432778	-6.54	FALSE
263195_at	non-specific lipid transfer protein	---	AT1G36150	1.03	0.04	0.16	0.8749341	0.9432778	-6.54	FALSE
262069_at	hypothetical protein similar to SN	---	AT1G80090	-1.02	-0.03	-0.16	0.8748725	0.9432778	-6.54	FALSE
248131_at	unknown protein	---	AT5G54830	-1.04	-0.05	-0.16	0.8749338	0.9432778	-6.54	FALSE
259153_at	unknown protein ;supported by f	---	AT3G10250	-1.02	-0.03	-0.16	0.8745295	0.9432778	-6.54	FALSE
245519_at	retrotransposon like protein	---	---	-1.01	-0.02	-0.16	0.8749615	0.9432778	-6.54	FALSE
252196_at	putative protein predicted protein	---	AT3G50200	1.02	0.04	0.16	0.8744487	0.9432778	-6.54	FALSE
248214_at	putative protein similar to unknov	---	AT5G53670	1.03	0.04	0.16	0.8743843	0.9432778	-6.54	FALSE
249226_at	GDSL-motif lipase/hydrolase-like	---	AT5G42170	-1.02	-0.02	-0.16	0.8747486	0.9432778	-6.54	FALSE
245157_at	putative polygalacturonase	---	AT2G33160	-1.02	-0.02	-0.16	0.8747146	0.9432778	-6.54	FALSE
245834_at	transposon protein, putative sim	---	---	-1.02	-0.02	-0.16	0.8750682	0.9433482	-6.54	FALSE
246469_at	putative protein predicted protein	---	AT5G17070	1.02	0.02	0.16	0.8751749	0.9434187	-6.54	FALSE
263642_at	putative fimbrin	---	AT2G04750	-1.02	-0.02	-0.16	0.8754231	0.9435457	-6.54	FALSE
250295_at	putative protein	NEF1	AT5G13390	-1.02	-0.03	-0.16	0.875471	0.9435457	-6.54	FALSE
257995_at	putative monosaccharide transp	---	AT3G19940	-1.02	-0.03	-0.16	0.8754608	0.9435457	-6.54	FALSE
255954_at	hypothetical protein predicted by	emb2204	AT1G22090	-1.02	-0.03	-0.16	0.8754797	0.9435457	-6.54	FALSE
246320_at	unknown protein	---	AT1G16560	-1.03	-0.04	-0.16	0.8754995	0.9435457	-6.54	FALSE
252517_at	receptor-like protein kinase hom	---	AT3G46340	1.02	0.03	0.16	0.8756831	0.9436989	-6.54	FALSE
245077_at	hypothetical protein predicted by	---	AT2G23160	1.03	0.04	0.16	0.8757695	0.9437137	-6.54	FALSE
267390_at	putative beta-glucosidase	BGLU29	AT2G44470	-1.02	-0.02	-0.16	0.8757796	0.9437137	-6.54	FALSE
261743_s_a	protein serine/threonine phospha	BSL2	AT1G08420 /	-1.02	-0.03	-0.16	0.8758317	0.9437253	-6.54	FALSE
250876_at	hypothetical protein	---	AT5G04030	-1.02	-0.02	-0.16	0.8759743	0.9437452	-6.54	FALSE
266659_at	putative poly(A) polymerase ; su	---	AT2G25850	1.02	0.03	0.16	0.8759418	0.9437452	-6.54	FALSE
258870_at	putative NADP-dependent oxidor	---	AT3G03080	-1.02	-0.03	-0.16	0.8759647	0.9437452	-6.54	FALSE
256523_at	unknown protein ;supported by fu	---	AT1G66070	-1.02	-0.03	-0.16	0.8760313	0.9437621	-6.54	FALSE

262218_at	hypothetical protein contains sim	---	AT1G74770	1.03	0.04	0.16	0.8761308	0.9438247	-6.54	FALSE
258339_at	putative dynein light chain protei	---	AT3G16120	-1.01	-0.02	-0.16	0.8762198	0.9438314	-6.54	FALSE
259850_at	hypothetical protein predicted by	---	AT1G72240	-1.03	-0.04	-0.16	0.8761871	0.9438314	-6.54	FALSE
263586_at	unknown protein predicted by ge	---	AT2G25350	1.03	0.04	0.16	0.8763572	0.9439349	-6.54	FALSE
261850_at	hypothetical protein predicted by	---	AT1G50470	-1.03	-0.04	-0.16	0.8765242	0.9440701	-6.54	FALSE
252933_at	putative receptor-like protein kin	---	AT4G39110	-1.02	-0.03	-0.16	0.8767104	0.9441369	-6.54	FALSE
257630_at	cytochrome P450, putative simil	CYP71B16	AT3G26150	1.02	0.02	0.16	0.8766512	0.9441369	-6.54	FALSE
257916_at	unknown protein similar to hypot	---	AT3G23210	1.03	0.04	0.16	0.876692	0.9441369	-6.54	FALSE
246863_at	nodulin - like protein early nodul	---	AT5G25940	1.04	0.06	0.16	0.8772779	0.944273	-6.54	FALSE
250795_at	RING zinc finger protein-like	CPuORF64	AT5G05280 /	-1.02	-0.03	-0.16	0.8772433	0.944273	-6.54	FALSE
264539_at	hypothetical protein predicted by	---	AT1G55590	1.02	0.03	0.16	0.8770186	0.944273	-6.54	FALSE
254579_at	hypothetical protein ;supported b	---	AT4G19400	1.02	0.03	0.16	0.877276	0.944273	-6.54	FALSE
250183_at	putative protein various predicte	---	AT5G14510	-1.03	-0.04	-0.16	0.8769237	0.944273	-6.54	FALSE
267486_at	putative protein kinase contains a	APK2B	AT2G02800	1.03	0.04	0.16	0.8771141	0.944273	-6.54	FALSE
263820_at	hypothetical protein predicted by	---	---	-1.03	-0.04	-0.16	0.8772274	0.944273	-6.54	FALSE
255039_at	calmodulin-domain protein kinas	CPK4	AT4G09570	1.02	0.03	0.16	0.8772392	0.944273	-6.54	FALSE
256658_at	unknown protein	---	AT3G12010 /	1.02	0.02	0.16	0.8772921	0.944273	-6.54	FALSE
265201_at	unknown protein	---	AT2G36810	1.01	0.02	0.16	0.8772688	0.944273	-6.54	FALSE
261382_at	hypothetical protein contains sim	CVP2	AT1G05470	1.02	0.03	0.16	0.8769784	0.944273	-6.54	FALSE
249429_at	putative protein	---	AT5G39880	-1.01	-0.02	-0.16	0.8774833	0.9443897	-6.54	FALSE
250169_at	putative protein many predicted	---	AT5G15340	1.03	0.04	0.16	0.877469	0.9443897	-6.54	FALSE
260447_at	hypothetical protein similar to N-t	---	AT1G72410	1.02	0.02	0.16	0.8775804	0.9444495	-6.54	FALSE
256713_at	putative peroxidase	---	AT2G34060	-1.03	-0.04	-0.16	0.8776781	0.9445102	-6.54	TRUE
259995_at	putative golgi transport complex	---	AT1G67930	-1.02	-0.03	-0.16	0.877814	0.9445712	-6.54	TRUE
253333_at	2-dehydro-3-deoxyphosphohepto	DHS2	AT4G33510	1.02	0.03	0.16	0.8778591	0.9445712	-6.54	FALSE
262212_at	response regulator 7, putative si	ARR15	AT1G74890	-1.02	-0.04	-0.16	0.8778352	0.9445712	-6.54	FALSE
263382_at	putative anthranilate N-hydroxyc	---	AT2G40230	1.02	0.03	0.16	0.8779018	0.9445727	-6.54	TRUE
257241_at	hypothetical protein contains Pfa	---	AT3G24210	-1.02	-0.03	-0.16	0.8780565	0.9446946	-6.54	FALSE
256732_at	hypothetical protein predicted by	---	---	1.02	0.02	0.16	0.8780997	0.9446964	-6.54	FALSE
255265_at	kinesin - like protein kinesin like	ATK5	AT4G05190	-1.02	-0.03	-0.16	0.8782727	0.944838	-6.54	FALSE
261941_at	hypothetical protein contains sim	---	AT1G22490	-1.04	-0.06	-0.16	0.878355	0.944882	-6.54	FALSE
261210_at	vacuolar ATP synthase subunit (	DET3	AT1G12840	-1.01	-0.02	-0.16	0.8784046	0.9448908	-6.54	FALSE
246178_s_a	putative protein predicted protein	---	---	-1.02	-0.03	-0.16	0.8785543	0.9450072	-6.54	FALSE
258872_at	hypothetical protein similar to L1	HDG8	AT3G03260	-1.03	-0.04	-0.16	0.8787525	0.9451758	-6.54	FALSE
258443_at	unknown protein	---	AT3G22290	1.02	0.03	0.16	0.87887	0.9452577	-6.54	FALSE

260703_at	syntaxin, putative similar to synt	ATSYP24	AT1G32270	1.01	0.02	0.16	0.8789147	0.9452612	-6.54	FALSE
251728_at	cysteine-tRNA ligase-like protein	---	AT3G56300	-1.02	-0.03	-0.16	0.8789683	0.9452743	-6.54	FALSE
247515_at	ABC family transporter - like pro	ATH14	AT5G61740	1.01	0.02	0.16	0.8790475	0.9453149	-6.54	FALSE
245174_at	putative kinesin heavy chain	---	AT2G47500	-1.03	-0.05	-0.16	0.8791306	0.9453596	-6.54	FALSE
247179_at	putative protein contains similarit	---	AT5G65320	-1.02	-0.02	-0.16	0.8791989	0.9453885	-6.54	FALSE
266628_at	unknown protein	---	AT2G35330	-1.02	-0.02	-0.16	0.8795159	0.9456402	-6.54	FALSE
261870_at	nuclear transport factor 2, putati	NTL	AT1G11570	-1.02	-0.03	-0.16	0.8794952	0.9456402	-6.54	FALSE
251967_at	putative protein DMR-N9 PROT	---	AT3G53390	1.02	0.02	0.16	0.8795716	0.9456555	-6.54	FALSE
251215_at	putative protein region within dis	---	AT3G62510	1.02	0.03	0.16	0.8796241	0.9456674	-6.54	FALSE
262870_at	alcohol dehydrogenase, putative	---	AT1G64710	-1.07	-0.09	-0.16	0.8797456	0.9457142	-6.54	FALSE
267075_at	putative bZIP transcription factor	EEL	AT2G41070	1.02	0.02	0.16	0.8797506	0.9457142	-6.54	FALSE
249394_at	putative protein predicted protei	---	AT5G40180	1.01	0.02	0.16	0.8798175	0.9457416	-6.54	FALSE
259904_at	hypothetical protein predicted by	---	AT1G74150	-1.02	-0.03	-0.16	0.8798703	0.9457538	-6.54	FALSE
256526_at	disease resistance protein, puta	---	AT1G66090	-1.02	-0.03	-0.16	0.8799713	0.9457733	-6.54	FALSE
266118_at	protease inhibitor II ; supported	LCR68	AT2G02130	1.05	0.07	0.16	0.8799536	0.9457733	-6.54	FALSE
253685_at	putative protein nucleotide pyrop	---	AT4G29710	-1.02	-0.02	-0.16	0.8800303	0.945792	-6.54	FALSE
256082_at	hypothetical protein predicted by	---	AT1G20720	1.03	0.05	0.16	0.8801015	0.9458241	-6.54	FALSE
267169_at	putative oxidoreductase	---	AT2G37540	1.04	0.05	0.16	0.8802522	0.9458339	-6.54	TRUE
245938_at	putative protein protein phospha	---	AT5G19680	-1.02	-0.03	-0.16	0.8802814	0.9458339	-6.54	FALSE
261466_at	hypothetical protein predicted by	---	AT1G07690	1.02	0.03	0.16	0.8803059	0.9458339	-6.54	FALSE
246129_at	putative protein predicted protei	---	---	-1.01	-0.02	-0.16	0.880318	0.9458339	-6.54	FALSE
262243_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.16	0.8802057	0.9458339	-6.54	FALSE
252641_at	putative protein predicted protei	---	AT3G44570	1.02	0.02	0.16	0.8803978	0.9458751	-6.54	FALSE
264395_at	putative GDP-dissociation inhibit	---	AT1G12070	1.02	0.03	0.16	0.8804439	0.94588	-6.54	FALSE
247049_at	putative protein similar to unknov	---	AT5G66440	-1.08	-0.12	-0.16	0.8806735	0.9460822	-6.54	FALSE
255780_at	hypothetical protein contains Pfa	GAUT11	AT1G18580	1.02	0.03	0.16	0.8807172	0.9460845	-6.54	FALSE
265065_at	putative phytochelatin synthase	ATPCS2	AT1G03980	-1.02	-0.02	-0.16	0.8808127	0.9461425	-6.54	FALSE
262174_at	putative GDP-mannose pyrophos	---	AT1G74910	-1.02	-0.03	-0.16	0.8809007	0.9461926	-6.54	TRUE
260761_at	hypothetical protein predicted by	---	AT1G49150	1.03	0.04	0.16	0.8809568	0.946208	-6.54	FALSE
252384_at	ABC-type transport protein-like p	ATH7	AT3G47790	-1.01	-0.02	-0.16	0.880998	0.946208	-6.54	FALSE
256378_at	receptor protein kinase, putative	---	AT1G66830	1.02	0.02	0.16	0.8810493	0.9462185	-6.54	FALSE
249551_at	putative protein predicted protei	---	AT5G38220	-1.02	-0.03	-0.16	0.8811778	0.9462312	-6.54	FALSE
252260_at	putative protein several hypothet	---	AT3G49480	1.02	0.04	0.16	0.8811856	0.9462312	-6.54	FALSE
266637_at	hypothetical protein ;supported b	BRXL1	AT2G35600	1.03	0.04	0.16	0.8811135	0.9462312	-6.54	FALSE
262649_at	unknown protein contains similar	---	AT1G14040	1.05	0.07	0.16	0.8813596	0.9462931	-6.54	TRUE

257970_at	putative sucrose cleavage protei	---	AT3G27570	1.02	0.03	0.15	0.8813705	0.9462931	-6.54	FALSE
262997_at	disease resistance protein, puta	RPP27	AT1G54470	-1.01	-0.02	-0.15	0.8814092	0.9462931	-6.54	FALSE
265607_at	hypothetical protein predicted by	---	AT2G25370	-1.02	-0.02	-0.16	0.8813501	0.9462931	-6.54	FALSE
259954_at	cytochrome P450, putative simil	CYP721A1	AT1G75130	-1.03	-0.04	-0.15	0.8814688	0.9463126	-6.54	FALSE
255061_at	putative protein disulfide isomera	ATAPRL6	AT4G08930	-1.01	-0.02	-0.15	0.8815424	0.9463471	-6.54	FALSE
249689_at	putative protein similar to unknov	---	AT5G36190	-1.01	-0.02	-0.15	0.8816118	0.946377	-6.54	FALSE
258100_at	unknown protein	---	AT3G23550	1.09	0.13	0.15	0.881659	0.9463831	-6.54	FALSE
249538_at	kanadaptin - like protein unname	---	AT5G38840	1.02	0.02	0.15	0.8819604	0.946436	-6.54	FALSE
250152_at	putative protein predicted protei	---	AT5G15120	-1.02	-0.02	-0.15	0.882121	0.946436	-6.54	FALSE
255517_at	putative endo-1,4-beta glucanas	AtGH9B13	AT4G02290	-1.02	-0.03	-0.15	0.8820425	0.946436	-6.54	FALSE
263178_at	hypothetical protein predicted by	---	AT1G05550	-1.02	-0.03	-0.15	0.8818982	0.946436	-6.54	FALSE
252259_at	putative protein acidic ribosomal	---	AT3G49460	-1.03	-0.04	-0.15	0.8821189	0.946436	-6.54	FALSE
249882_at	putative protein contains similarit	---	AT5G22890	-1.01	-0.02	-0.15	0.8819475	0.946436	-6.54	FALSE
253375_at	hypothetical protein	---	AT4G33280	-1.02	-0.02	-0.15	0.8821232	0.946436	-6.54	FALSE
255229_at	F-box protein family, AtFBL22 co	---	AT4G05490	-1.01	-0.02	-0.15	0.8819646	0.946436	-6.54	FALSE
266090_at	unknown protein	---	AT2G38000	1.02	0.03	0.15	0.8819753	0.946436	-6.54	FALSE
253078_at	putative receptor protein kinase	---	AT4G36180	1.03	0.04	0.15	0.8820882	0.946436	-6.54	FALSE
256841_x_a	hypothetical protein predicted by	---	---	1.03	0.04	0.15	0.8822286	0.9465046	-6.54	FALSE
258073_at	putative auxin-resistance protein	---	AT3G25880	-1.02	-0.02	-0.15	0.882425	0.9466052	-6.54	FALSE
255515_at	putative pistil-specific protein sin	---	AT4G02250	1.02	0.02	0.15	0.8825624	0.9466052	-6.54	FALSE
258567_at	apyrase (Atapy1) identical to apy	ATAPY1	AT3G04080	-1.02	-0.03	-0.15	0.8825706	0.9466052	-6.54	FALSE
246526_at	putative protein RXF26 - Arabido	GLIP7	AT5G15720	1.02	0.02	0.15	0.8824733	0.9466052	-6.54	FALSE
257581_s_a	RAV-like DNA-binding protein, p	---	AT1G50680 ///	-1.01	-0.02	-0.15	0.8825714	0.9466052	-6.54	FALSE
265851_at	hypothetical protein predicted by	---	AT2G42340	-1.02	-0.03	-0.15	0.8823904	0.9466052	-6.54	FALSE
260059_at	trehalose-6-phosphate phospha	ATTPPB	AT1G78090	1.03	0.04	0.15	0.8826445	0.9466391	-6.54	FALSE
266939_at	plasma membrane proton ATPas	AHA1	AT2G18960	-1.01	-0.02	-0.15	0.8827761	0.9466467	-6.54	FALSE
267479_at	hypothetical protein	---	AT2G02690	-1.01	-0.02	-0.15	0.8827374	0.9466467	-6.54	FALSE
248086_at	putative protein similar to unknov	GEX1	AT5G55490	-1.01	-0.02	-0.15	0.8827211	0.9466467	-6.54	FALSE
253891_at	putative protein ;supported by fu	---	AT4G27720	-1.04	-0.05	-0.15	0.8832244	0.9467003	-6.54	TRUE
258719_at	putative pectate lyase simliar to p	---	AT3G09540	-1.04	-0.06	-0.15	0.8829445	0.9467003	-6.54	TRUE
260501_at	unknown protein ; supported by	---	AT2G41770	-1.02	-0.03	-0.15	0.8830807	0.9467003	-6.54	TRUE
256112_at	guanine nucleotide regulatory pr	ATRABA1B	AT1G16920	1.05	0.07	0.15	0.8832411	0.9467003	-6.54	TRUE
246918_at	putative protein hypothetical pro	---	AT5G25340	1.02	0.03	0.15	0.8829553	0.9467003	-6.54	FALSE
264576_at	unknown protein Similar to Arabi	---	AT1G05360	-1.02	-0.02	-0.15	0.8831964	0.9467003	-6.54	FALSE
264348_at	putative NPK1-related protein kir	NRT1.1	AT1G12110	1.10	0.14	0.15	0.8831889	0.9467003	-6.54	FALSE

249599_at	putative protein AtPP protein, Br	---	AT5G37990	1.02	0.03	0.15	0.8832178	0.9467003	-6.54	FALSE
255295_at	putative sugar transporter	---	AT4G04760	1.02	0.02	0.15	0.8830514	0.9467003	-6.54	FALSE
255049_at	gibberellin-regulated protein GAS	GASA2	AT4G09610	1.01	0.02	0.15	0.8830735	0.9467003	-6.54	FALSE
266069_at	putative RING zinc finger protein	MEE16	AT2G18650	-1.03	-0.04	-0.15	0.8834723	0.9468796	-6.54	FALSE
265918_at	putative fatty acid elongase	KCS8	AT2G15090	-1.07	-0.10	-0.15	0.8834914	0.9468796	-6.54	FALSE
253367_at	hypothetical protein	---	AT4G33180	-1.03	-0.04	-0.15	0.8835695	0.9469188	-6.54	FALSE
254590_at	hypothetical protein	---	AT4G18860	1.02	0.02	0.15	0.8836572	0.9469683	-6.54	FALSE
261200_at	60S ribosomal protein L27a, put	---	AT1G12960	1.02	0.02	0.15	0.8837575	0.9470313	-6.54	FALSE
245224_at	gene_id:K17E7.8~unknown prote	---	AT3G29796	-1.01	-0.02	-0.15	0.8838367	0.9470717	-6.54	FALSE
259325_at	unknown protein	---	AT3G05320	-1.11	-0.15	-0.15	0.8840587	0.9472206	-6.54	FALSE
256474_at	unknown protein	---	---	1.02	0.03	0.15	0.8840395	0.9472206	-6.54	FALSE
258217_at	unknown protein contains Pfam p	XPL1	AT3G17998 /	-1.03	-0.04	-0.15	0.8841171	0.9472387	-6.54	FALSE
261666_at	hypothetical protein contains sim	---	AT1G18440	1.02	0.03	0.15	0.8844698	0.9475721	-6.54	FALSE
256884_at	hypothetical protein contains Pfa	---	AT3G15200	-1.03	-0.04	-0.15	0.8845671	0.9476318	-6.54	FALSE
257556_at	hypothetical protein predicted by	---	AT3G28100	1.04	0.06	0.15	0.8847318	0.9477192	-6.54	TRUE
257421_at	hypothetical protein predicted by	---	AT1G12030	1.03	0.04	0.15	0.8847244	0.9477192	-6.54	FALSE
261105_at	unknown protein ;supported by fu	NRS/ER	AT1G63000	-1.02	-0.03	-0.15	0.8848524	0.9477333	-6.54	FALSE
254130_at	MADS-box protein AGL24 ; supp	AGL24	AT4G24540	-1.03	-0.04	-0.15	0.8848259	0.9477333	-6.54	FALSE
264691_s_a	putative reverse transcriptase	---	---	1.02	0.02	0.15	0.8848696	0.9477333	-6.54	FALSE
263983_at	unknown protein ;supported by f	---	AT2G42780	-1.01	-0.02	-0.15	0.8849358	0.9477545	-6.54	FALSE
263444_at	putative MADS-box protein	AGL46	AT2G28700	1.02	0.03	0.15	0.8849725	0.9477545	-6.54	FALSE
252132_at	putative LEA protein Picea glauc	---	AT3G50790	1.03	0.05	0.15	0.8852598	0.9479287	-6.54	FALSE
248865_at	putative protein similar to unknov	---	AT5G46790	-1.02	-0.03	-0.15	0.8852386	0.9479287	-6.54	FALSE
267469_at	unknown protein ; supported by	WRKY21	AT2G30590	-1.02	-0.03	-0.15	0.8851977	0.9479287	-6.54	FALSE
246044_at	calcium-dependent protein kinas	CDPK19	AT5G19450	-1.02	-0.03	-0.15	0.8853124	0.9479405	-6.54	FALSE
254484_at	hypothetical protein	---	AT4G20760	-1.02	-0.02	-0.15	0.8853733	0.9479612	-6.54	TRUE
263080_at	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.15	0.8854501	0.9479989	-6.54	FALSE
264126_at	hypothetical protein predicted by	NUA	AT1G79280	1.01	0.02	0.15	0.8855923	0.9481067	-6.54	FALSE
258717_at	unknown protein ; supported by	SYP71	AT3G09740	-1.01	-0.02	-0.15	0.8856479	0.9481217	-6.54	FALSE
258178_at	hypothetical protein predicted by	---	AT3G21680	-1.01	-0.02	-0.15	0.8857761	0.9482145	-6.54	FALSE
255232_at	putative protein phosphatidylinos	AGD13	AT4G05330	1.02	0.03	0.15	0.8859486	0.9482326	-6.54	TRUE
263033_s_a	unknown protein ; supported by f	---	AT1G23950 /	-1.03	-0.04	-0.15	0.8859283	0.9482326	-6.54	FALSE
258231_at	hypothetical protein contains Pfa	RCK	AT3G27730	1.01	0.02	0.15	0.8859594	0.9482326	-6.54	FALSE
264068_at	putative homeodomain transcript	BLH8	AT2G27990	-1.03	-0.05	-0.15	0.8859375	0.9482326	-6.54	FALSE
254290_at	hypothetical protein	---	AT4G23000	-1.02	-0.04	-0.15	0.8860356	0.9482697	-6.54	FALSE

255413_at	putative alcohol dehydrogenase	---	AT4G03140	-1.02	-0.03	-0.15	0.8861577	0.9483446	-6.54	FALSE
267375_at	G protein alpha subunit 1 (GPA1	GP ALPHA	AT2G26300	-1.02	-0.03	-0.15	0.8861888	0.9483446	-6.54	FALSE
267290_at	putative SET-domain transcriptio	---	AT2G23740	1.02	0.03	0.15	0.8866386	0.9486931	-6.54	FALSE
263194_at	AP2 domain transcription factor,	---	AT1G36060	-1.03	-0.04	-0.15	0.8865652	0.9486931	-6.54	FALSE
262036_at	ATP-dependent RNA helicase, p	---	AT1G35530	-1.02	-0.03	-0.15	0.8866392	0.9486931	-6.54	FALSE
247841_at	putative protein predicted protei	ATFIP1[V]	AT5G58040	1.02	0.03	0.15	0.8868206	0.9488427	-6.54	FALSE
251968_at	putative protein proline-rich prot	---	AT3G53100	1.02	0.03	0.15	0.887162	0.9489025	-6.54	FALSE
248006_at	unknown protein	HAP8	AT5G56250	1.02	0.02	0.15	0.8872287	0.9489025	-6.54	FALSE
252618_at	lipoxygenase AtLOX2 ; supporte	LOX2	AT3G45140	-1.02	-0.03	-0.15	0.8869613	0.9489025	-6.54	FALSE
248376_at	unknown protein ; supported by f	---	AT5G51880	-1.02	-0.02	-0.15	0.8869518	0.9489025	-6.54	FALSE
260470_at	hypothetical protein predicted by	---	AT1G11120	-1.02	-0.03	-0.15	0.8872483	0.9489025	-6.54	FALSE
253687_at	putative protein ;supported by fu	---	AT4G29520	1.08	0.11	0.15	0.8870428	0.9489025	-6.54	FALSE
246670_at	putative protein	---	AT5G30520	1.02	0.03	0.15	0.8871865	0.9489025	-6.54	FALSE
259243_at	unknown protein similar to unkn	---	AT3G07565	1.01	0.02	0.15	0.8871996	0.9489025	-6.54	FALSE
264739_at	hypothetical protein predicted by	---	AT1G62260	1.02	0.03	0.15	0.8872509	0.9489025	-6.54	FALSE
257283_at	hypothetical protein predicted by	---	AT3G29750	1.01	0.02	0.15	0.8876133	0.9492011	-6.54	FALSE
257582_at	hypothetical protein	---	AT1G50720	-1.01	-0.02	-0.15	0.8875995	0.9492011	-6.54	FALSE
259067_at	F-box protein family, AtFBL12 c	---	AT3G07550	-1.01	-0.02	-0.15	0.8877006	0.9492322	-6.54	FALSE
257390_x_a	hypothetical protein predicted by	---	---	-1.02	-0.03	-0.15	0.8877256	0.9492322	-6.54	FALSE
248040_at	putative protein contains similarit	---	AT5G55970	-1.04	-0.05	-0.15	0.887795	0.9492619	-6.54	TRUE
267463_at	Expressed protein ; supported by	---	AT2G33845	-1.03	-0.04	-0.15	0.8878969	0.9493264	-6.54	FALSE
264888_at	hypothetical protein	---	AT1G23070	1.02	0.02	0.15	0.8880452	0.9494404	-6.54	FALSE
266424_at	unknown protein	---	AT2G41330	1.03	0.04	0.15	0.8883023	0.9494483	-6.54	TRUE
247436_at	dehydrogenase ; supported by c	ALDH12A1	AT5G62530	1.02	0.03	0.15	0.8882507	0.9494483	-6.54	FALSE
245726_at	homeobox protein, putative simi	HDG11	AT1G73360	1.02	0.02	0.15	0.8880968	0.9494483	-6.54	FALSE
254586_at	TMV resistance protein N-like T	---	AT4G19510	-1.02	-0.03	-0.15	0.8882875	0.9494483	-6.54	FALSE
254028_s_a	putative protein N.crassa mRNA	ORP4B	AT4G25850 /	-1.02	-0.02	-0.15	0.8882375	0.9494483	-6.54	FALSE
253311_s_a	putative protein xylan endohydro	---	AT4G33830 /	-1.01	-0.02	-0.15	0.8881722	0.9494483	-6.54	FALSE
250635_at	glycine-rich protein glycine-rich	GRP14	AT5G07510	-1.02	-0.03	-0.15	0.888411	0.9494754	-6.54	FALSE
254934_at	putative Ap2 domain protein DN	CRF1	AT4G11140	1.02	0.03	0.15	0.8884044	0.9494754	-6.54	FALSE
246609_at	putative receptor-like protein kin	---	AT5G35390	-1.01	-0.02	-0.15	0.8885632	0.9495856	-6.54	FALSE
261723_at	unknown protein ; supported by f	---	AT1G76200	-1.02	-0.02	-0.15	0.8885973	0.9495856	-6.54	FALSE
262722_at	sterol glucosyltransferase, putat	---	AT1G43620	-1.02	-0.02	-0.15	0.8886828	0.9496325	-6.54	FALSE
260645_at	hypothetical protein predicted by	TTL1	AT1G53300	-1.03	-0.04	-0.15	0.8888389	0.9496639	-6.54	FALSE
250929_at	putative protein ; supported by c	---	AT5G03290	-1.03	-0.04	-0.15	0.8888329	0.9496639	-6.54	FALSE

262334_at	hypothetical protein similar to put	---	AT1G64010	1.02	0.02	0.15	0.8888368	0.9496639	-6.54	FALSE
252750_at	putative protein hypothetical pro	---	AT3G43420	-1.01	-0.02	-0.15	0.8888787	0.9496639	-6.54	FALSE
248084_at	sodium proton exchanger	NHX3	AT5G55470	-1.02	-0.03	-0.14	0.889115	0.9498555	-6.54	FALSE
246706_at	putative protein predicted protei	---	---	1.03	0.04	0.14	0.8891497	0.9498555	-6.55	FALSE
258234_at	hypothetical protein similar to my	MYB118	AT3G27785	-1.02	-0.02	-0.14	0.889183	0.9498555	-6.55	FALSE
254868_at	copper amine oxidase like prote	---	AT4G12270	1.02	0.03	0.14	0.8893013	0.9498929	-6.55	FALSE
253130_at	putative protein ;supported by fu	---	AT4G35510	-1.03	-0.04	-0.14	0.8892624	0.9498929	-6.55	FALSE
265986_at	putative receptor-like protein kina	---	AT2G24230	1.02	0.03	0.14	0.8894741	0.9500225	-6.55	FALSE
262994_at	hypothetical protein predicted by	---	AT1G54420	1.01	0.02	0.14	0.8895247	0.9500225	-6.55	FALSE
248772_at	photoreceptor-interacting protein	---	AT5G47800	-1.04	-0.05	-0.14	0.8895476	0.9500225	-6.55	FALSE
263406_at	subtilisin-like serine protease AI	AIR3	AT2G04160	1.05	0.07	0.14	0.8898021	0.9501922	-6.55	FALSE
255418_at	predicted protein of unknown fun	---	AT4G03200	-1.02	-0.03	-0.14	0.8898731	0.9501922	-6.55	FALSE
265047_at	hypothetical protein similar to unl	IQD27	AT1G51960	-1.02	-0.03	-0.14	0.8898559	0.9501922	-6.55	FALSE
263817_at	hypothetical protein predicted by	---	---	1.02	0.03	0.14	0.8898695	0.9501922	-6.55	FALSE
256954_at	E2, ubiquitin-conjugating enzym	FUS9	AT3G13550	1.02	0.03	0.14	0.8900747	0.9503629	-6.55	FALSE
265069_at	awaiting functional assignment s	---	AT1G55545	1.02	0.02	0.14	0.8901313	0.9503789	-6.55	FALSE
262478_at	hypothetical protein similar to hy	---	AT1G11170	1.02	0.03	0.14	0.8903176	0.9504262	-6.55	FALSE
262527_at	SRG1-like protein Strong homol	---	AT1G17010	-1.02	-0.02	-0.14	0.8903423	0.9504262	-6.55	FALSE
263850_at	hypothetical protein predicted by	---	AT2G04480	-1.03	-0.04	-0.14	0.8902981	0.9504262	-6.55	FALSE
251398_at	zinc finger protein - like ZPT3-3,	---	AT3G60580	1.02	0.03	0.14	0.8902238	0.9504262	-6.55	FALSE
252339_at	hypothetical protein	---	AT3G48900	1.01	0.02	0.14	0.8905342	0.9505866	-6.55	FALSE
266750_s_a	putative pectinesterase	VGDH1	AT2G47030 ///	-1.01	-0.02	-0.14	0.8908376	0.950862	-6.55	FALSE
266128_at	hypothetical protein predicted by	EMB2766	---	-1.02	-0.02	-0.14	0.8908756	0.950862	-6.55	FALSE
247578_at	putative protein predicted protei	---	AT5G61300	1.02	0.03	0.14	0.8909617	0.9509095	-6.55	FALSE
255193_at	score=10.1, E=1.2, N=1 contain	VFB3	AT4G07400	1.02	0.03	0.14	0.8911169	0.9510138	-6.55	FALSE
264411_at	mutator-like transposase, putativ	---	---	-1.01	-0.02	-0.14	0.8911428	0.9510138	-6.55	FALSE
258797_at	auxin-induced protein identical to	IAA16	AT3G04730	1.02	0.03	0.14	0.8914564	0.9510814	-6.55	FALSE
256040_at	hypothetical protein similar to put	---	AT1G07270	1.01	0.02	0.14	0.891375	0.9510814	-6.55	FALSE
259475_at	unknown protein ;supported by fu	---	AT1G19140	-1.03	-0.04	-0.14	0.8913932	0.9510814	-6.55	FALSE
248016_at	putative protein similar to unknov	---	AT5G56380	-1.02	-0.03	-0.14	0.8914397	0.9510814	-6.55	FALSE
254528_at	hypothetical protein	---	AT4G19620	1.02	0.02	0.14	0.8914094	0.9510814	-6.55	FALSE
255124_at	putative self-incompatability RNA	APUM15	AT4G08560	1.02	0.03	0.14	0.8913413	0.9510814	-6.55	FALSE
247798_at	subtilisin-like serine protease cor	---	AT5G58830	-1.01	-0.02	-0.14	0.8915189	0.9511036	-6.55	FALSE
256160_at	pyruvate dehydrogenase E1 bet	PDH-E1 BE	AT1G30120	1.02	0.03	0.14	0.8919808	0.9515418	-6.55	FALSE
257577_at	hypothetical protein predicted by	---	---	-1.02	-0.02	-0.14	0.8920548	0.9515418	-6.55	FALSE

250376_at	putative protein	---	AT5G11550	1.03	0.04	0.14	0.8920202	0.9515418	-6.55	FALSE
251421_at	enoyl-CoA-hydratase - like prote	---	AT3G60510	-1.02	-0.02	-0.14	0.8923276	0.9516548	-6.55	FALSE
247508_at	auxin response factor - like prote	ARF2	AT5G62000	1.02	0.03	0.14	0.892283	0.9516548	-6.55	FALSE
262403_s_a	mutator-like transposase, putativ	---	---	-1.01	-0.02	-0.14	0.8922744	0.9516548	-6.55	FALSE
256975_at	unknown protein similar to putativ	---	AT3G21000	-1.02	-0.03	-0.14	0.8923059	0.9516548	-6.55	FALSE
262934_s_a	hypothetical protein contains sim	---	AT1G16270 ///	1.02	0.03	0.14	0.8923775	0.9516635	-6.55	FALSE
254328_at	adenine phosphoribosyltransfera	APT3	AT4G22570	1.03	0.05	0.14	0.8926925	0.9517369	-6.55	TRUE
267552_at	putative purple acid phosphatase	PAP13	AT2G32770	1.01	0.02	0.14	0.8929249	0.9517369	-6.55	FALSE
261656_at	unknown protein similar to kinesi	ARK2	AT1G01950	-1.04	-0.06	-0.14	0.8928892	0.9517369	-6.55	FALSE
266783_at	putative laccase (diphenol oxidas	LAC2	AT2G29130	-1.02	-0.03	-0.14	0.8928463	0.9517369	-6.55	FALSE
260318_at	hypothetical protein predicted by	---	AT1G63960	-1.02	-0.03	-0.14	0.8924978	0.9517369	-6.55	FALSE
252498_at	putative protein several hypothet	---	AT3G46810	-1.01	-0.02	-0.14	0.8929554	0.9517369	-6.55	FALSE
260612_at	hypothetical protein similar to hyp	---	AT1G53360	1.01	0.02	0.14	0.8926192	0.9517369	-6.55	FALSE
247245_at	putative protein similar to unknov	---	AT5G64720	-1.01	-0.02	-0.14	0.8928097	0.9517369	-6.55	FALSE
251385_at	putative protein various predicte	---	AT3G60790	-1.02	-0.02	-0.14	0.8927322	0.9517369	-6.55	FALSE
258802_at	unknown protein predicted by ge	---	AT3G04650	1.02	0.03	0.14	0.8929887	0.9517369	-6.55	FALSE
261548_at	DNA-binding protein, putative co	---	AT1G63480	-1.02	-0.03	-0.14	0.892862	0.9517369	-6.55	FALSE
260659_s_a	hypothetical protein predicted by	---	AT1G19460 ///	1.01	0.02	0.14	0.8927477	0.9517369	-6.55	FALSE
263977_at	hypothetical protein predicted by	---	AT2G42660	-1.02	-0.03	-0.14	0.8927494	0.9517369	-6.55	FALSE
255697_at	hypothetical protein	---	AT4G00130	1.02	0.03	0.14	0.8932153	0.951756	-6.55	FALSE
267408_at	putative CTP synthase	---	AT2G34890	1.01	0.02	0.14	0.8932022	0.951756	-6.55	FALSE
263258_at	putative permease similar to puta	---	AT1G10540	1.02	0.03	0.14	0.8931946	0.951756	-6.55	FALSE
264403_at	unknown protein similarity to HS	---	AT2G25150	-1.01	-0.02	-0.14	0.8931076	0.951756	-6.55	FALSE
249857_at	C2H2-type zinc finger protein-like	---	AT5G22990	-1.02	-0.03	-0.14	0.8930995	0.951756	-6.55	FALSE
267561_at	putative protein kinase contains a	---	AT2G45590	1.03	0.04	0.14	0.8934198	0.9517961	-6.55	FALSE
254128_at	ubiquitin-specific protease 16 (U	UBP16	AT4G24560	1.01	0.02	0.14	0.8933859	0.9517961	-6.55	FALSE
253151_at	putative polygalacturonase polyg	---	AT4G35670	-1.01	-0.02	-0.14	0.8934103	0.9517961	-6.55	FALSE
260354_at	unknown protein ;supported by f	---	AT1G69330	-1.02	-0.03	-0.14	0.8933145	0.9517961	-6.55	FALSE
246734_at	putative protein WRN (Werner s	RECQSIM	AT5G27680	-1.01	-0.02	-0.14	0.8934617	0.9517963	-6.55	FALSE
266151_x_a	En/Spm transposon protein (mos	---	---	1.02	0.02	0.14	0.893564	0.9518163	-6.55	FALSE
246531_at	MADS box protein AGL2 ; suppo	סמס-01	AT5G15800	-1.02	-0.03	-0.14	0.8935368	0.9518163	-6.55	FALSE
247729_at	1-aminocyclopropane-1-carboxy	---	AT5G59530	1.03	0.04	0.14	0.8936793	0.9518502	-6.55	TRUE
252523_at	putative protein light repressible	---	AT3G46400	-1.02	-0.03	-0.14	0.8936465	0.9518502	-6.55	FALSE
250972_at	putative protein various Myb rela	LCL1	AT5G02840	-1.03	-0.04	-0.14	0.8938019	0.9519364	-6.55	FALSE
265045_s_a	putative protein kinase, ADK1 du	ADK1	AT1G03930 ///	-1.03	-0.04	-0.14	0.8939066	0.9519618	-6.55	FALSE

252142_at	putative protein hypothetical pro	---	AT3G51120	-1.02	-0.03	-0.14	0.8939092	0.9519618	-6.55	FALSE
252598_at	putative protein putative proteins	---	---	1.01	0.02	0.14	0.8940342	0.952006	-6.55	FALSE
261918_at	hypothetical protein	---	AT1G65940	1.01	0.02	0.14	0.8940296	0.952006	-6.55	FALSE
266817_at	hypothetical protein similar to hy	HUB1	AT2G44950	1.02	0.03	0.14	0.8940785	0.9520087	-6.55	FALSE
248426_at	putative protein contains similarit	---	AT5G51740	1.01	0.02	0.14	0.8941968	0.9520902	-6.55	FALSE
255752_at	secretory carrier membrane prot	---	AT1G32050	-1.02	-0.03	-0.14	0.8943788	0.9520997	-6.55	FALSE
251693_at	putative protein several hypothet	---	AT3G56550	-1.02	-0.02	-0.14	0.8944065	0.9520997	-6.55	FALSE
249387_at	putative protein predicted protei	---	AT5G40070	1.02	0.03	0.14	0.8944144	0.9520997	-6.55	FALSE
245901_at	HOMEOBOX PROTEIN KNOTTI	KNAT4	AT5G11060	1.02	0.03	0.14	0.8943842	0.9520997	-6.55	FALSE
267047_at	putative selenium-binding protein	---	AT2G34370	1.02	0.02	0.14	0.8942747	0.9520997	-6.55	FALSE
251100_at	aldose reductase-like protein ald	---	AT5G01670	1.03	0.04	0.14	0.8945103	0.9521129	-6.55	TRUE
267021_at	hypothetical protein predicted by	---	AT2G39300	1.01	0.02	0.14	0.8944729	0.9521129	-6.55	FALSE
249996_at	glutaredoxin -like protein glutare	---	AT5G18600	1.03	0.05	0.14	0.8945629	0.9521245	-6.55	FALSE
257319_at	hypothetical protein	---	---	-1.02	-0.03	-0.14	0.8946994	0.9522253	-6.55	FALSE
265254_at	unknown protein ; supported by	DRB2	AT2G28380	1.02	0.02	0.14	0.8949058	0.9523525	-6.55	FALSE
245221_s_a	polyprotein, putative similar to p	---	---	-1.01	-0.02	-0.14	0.8949442	0.9523525	-6.55	FALSE
262604_at	unknown protein similar to unkn	---	AT1G15060	-1.01	-0.02	-0.14	0.8948696	0.9523525	-6.55	FALSE
247162_at	xyloglucan endo-transglycosylas	---	AT5G65730	-1.04	-0.06	-0.14	0.8951131	0.9524508	-6.55	TRUE
246646_at	putative protein ;supported by fu	---	AT5G35090	1.02	0.02	0.14	0.89512	0.9524508	-6.55	FALSE
255289_at	score=11/3, E=0.23, N=1 contai	---	AT4G04690	1.02	0.02	0.14	0.8951816	0.9524673	-6.55	FALSE
250260_at	putative protein contains similarit	---	AT5G13810	-1.02	-0.02	-0.14	0.8952191	0.9524673	-6.55	FALSE
264853_at	putative ligand-gated ion channe	GLR2	AT2G17260 /	-1.02	-0.03	-0.14	0.8953407	0.9524918	-6.55	FALSE
255182_at	hypothetical protein	---	---	1.01	0.02	0.14	0.8953674	0.9524918	-6.55	FALSE
265428_at	hypothetical protein predicted by	---	AT2G20720	1.03	0.05	0.14	0.895292	0.9524918	-6.55	FALSE
254621_at	gene 11-1 protein - like gene 11	WAVE5	AT4G18600	-1.01	-0.02	-0.14	0.8954517	0.9525371	-6.55	FALSE
251836_at	lipase -like protein monoglyceric	---	AT3G55190	-1.01	-0.02	-0.14	0.8954996	0.9525437	-6.55	FALSE
253427_at	putative protein phosphate/phos	---	AT4G32390	-1.01	-0.02	-0.14	0.8956191	0.9526264	-6.55	FALSE
249919_at	putative protein predicted protei	---	AT5G19250	1.02	0.03	0.14	0.8956849	0.9526519	-6.55	FALSE
249605_at	putative protein predicted protei	---	AT5G37240	-1.02	-0.02	-0.14	0.8957885	0.9527177	-6.55	FALSE
249045_at	berberine bridge enzyme-like pro	---	AT5G44380	1.05	0.08	0.14	0.8959683	0.9527928	-6.55	TRUE
259415_at	hypothetical protein contains sim	---	AT1G02330	-1.02	-0.03	-0.14	0.8959845	0.9527928	-6.55	FALSE
258763_s_a	putative beta-mannan endohydro	---	AT3G10900 /	1.01	0.02	0.14	0.8959656	0.9527928	-6.55	FALSE
260747_at	unknown protein ; supported by	---	AT1G78420	1.01	0.02	0.14	0.8961672	0.9528554	-6.55	FALSE
257853_at	hypothetical protein predicted by	---	AT3G12960	-1.02	-0.02	-0.14	0.8961686	0.9528554	-6.55	FALSE
263068_at	putative poly(A) polymerase	---	AT2G17580	1.02	0.03	0.14	0.896142	0.9528554	-6.55	FALSE

248456_at	putative protein similar to unknov	---	AT5G51380	1.01	0.02	0.14	0.8962962	0.9529466	-6.55	FALSE
259395_at	GTP-binding protein(RAB11D),	ARA-2	AT1G06400	1.01	0.02	0.14	0.8964599	0.9529739	-6.55	FALSE
263668_at	putative 1-aminocyclopropane-1-	---	AT1G04350	1.02	0.03	0.14	0.8965268	0.9529739	-6.55	FALSE
253615_at	cyclic nucleotide and calmodulin	CNGC17	AT4G30360	1.02	0.03	0.14	0.8964435	0.9529739	-6.55	FALSE
263214_at	hypothetical protein predicted by	---	AT1G30660	-1.02	-0.03	-0.14	0.8965139	0.9529739	-6.55	FALSE
247669_at	putative protein transcriptional re	---	AT5G60170	-1.02	-0.03	-0.13	0.8965726	0.9529739	-6.55	FALSE
245646_x_a	F5A9.9 hypothetical protein	---	AT1G24851 /	1.01	0.02	0.14	0.8965507	0.9529739	-6.55	FALSE
251316_s_a	putative protein putative protein	---	AT3G61480 /	-1.02	-0.02	-0.13	0.8967204	0.9530866	-6.55	FALSE
253006_at	putative amino acid transport pr	---	AT4G38250	-1.02	-0.03	-0.13	0.8968739	0.953161	-6.55	FALSE
246239_at	putative protein	---	AT4G36790	1.01	0.02	0.13	0.8968646	0.953161	-6.55	FALSE
257039_at	tRNA isopentenyl transferase, p	ATIPT8	AT3G19160	-1.02	-0.02	-0.13	0.897156	0.9534164	-6.55	FALSE
256079_at	hypothetical protein predicted by	---	AT1G20680	1.01	0.02	0.13	0.8972628	0.953441	-6.55	FALSE
246363_at	hypothetical protein	---	AT1G40390	-1.02	-0.02	-0.13	0.8972496	0.953441	-6.55	FALSE
265300_at	unknown protein contains weak	---	AT2G13950	1.02	0.03	0.13	0.8973154	0.9534525	-6.55	FALSE
257133_at	hypothetical protein predicted by	---	AT3G17190	-1.01	-0.02	-0.13	0.8974479	0.9535488	-6.55	FALSE
251862_at	putative protein arm repeat cont	PUB14	AT3G54850	1.01	0.02	0.13	0.8975841	0.9536491	-6.55	FALSE
250102_at	receptor-like protein kinase	LRR1	AT5G16590	-1.02	-0.03	-0.13	0.8977855	0.9537298	-6.55	TRUE
251960_at	GTPase AtRAB8 ;supported by	HEMB1	AT1G69740 /	1.02	0.02	0.13	0.8977055	0.9537298	-6.55	FALSE
247750_at	protein kinase 6 - like protein kin	---	AT5G58950	-1.02	-0.02	-0.13	0.8977711	0.9537298	-6.55	FALSE
252687_at	putative protein predicted protei	---	---	-1.02	-0.03	-0.13	0.897841	0.9537444	-6.55	FALSE
256228_at	phosphoglycerate kinase, putati	---	AT1G56190	-1.02	-0.03	-0.13	0.8980641	0.9537876	-6.55	TRUE
267294_at	hypothetical protein predicted by	YCF37	AT2G23670	-1.02	-0.03	-0.13	0.8980783	0.9537876	-6.55	FALSE
254412_at	putative protein chloroplast DNA	B160	AT4G21430	-1.02	-0.04	-0.13	0.8980908	0.9537876	-6.55	FALSE
256631_at	At14a-like protein similar to At14	---	AT3G28320	1.03	0.04	0.13	0.8979785	0.9537876	-6.55	FALSE
253883_at	hypothetical protein	---	AT4G27660	1.02	0.02	0.13	0.8980831	0.9537876	-6.55	FALSE
255030_at	putative protein retrovirus-relate	---	---	-1.01	-0.02	-0.13	0.8981946	0.9538535	-6.55	FALSE
262522_at	putative amino acid transporter V	CAT8	AT1G17120	1.02	0.02	0.13	0.8984361	0.9538901	-6.55	FALSE
254695_at	putative protein predicted protei	ATL4H	AT4G17905 /	1.02	0.02	0.13	0.89848	0.9538901	-6.55	FALSE
253327_at	putative transcription factor	MYB69	AT4G33450	-1.02	-0.03	-0.13	0.8983525	0.9538901	-6.55	FALSE
260883_at	hypothetical protein predicted by	---	AT1G29270	-1.01	-0.02	-0.13	0.8984143	0.9538901	-6.55	FALSE
265591_at	hypothetical protein predicted by	---	AT2G20150	1.02	0.03	0.13	0.898478	0.9538901	-6.55	FALSE
261631_at	unknown protein contains similar	---	AT1G49940	-1.01	-0.02	-0.13	0.8984404	0.9538901	-6.55	FALSE
252048_at	expressed protein supported by	---	AT3G52500	1.02	0.03	0.13	0.8985676	0.9539387	-6.55	TRUE
256115_at	unknown protein ; supported by	---	AT1G16880	-1.02	-0.03	-0.13	0.8986355	0.9539664	-6.55	FALSE
255546_at	putative CHP-rich zinc finger pro	---	AT4G01910	-1.04	-0.05	-0.13	0.8987518	0.9540454	-6.55	TRUE

263501_s_a	hypothetical protein	---	AT2G07673	-1.02	-0.02	-0.13	0.8987994	0.9540516	-6.55	FALSE
256441_at	unknown protein ;supported by f	---	AT3G10940	-1.03	-0.04	-0.13	0.8990295	0.9540905	-6.55	TRUE
262093_at	receptor protein kinase, putative	---	AT1G56145	1.02	0.03	0.13	0.8990683	0.9540905	-6.55	TRUE
262025_at	growth regulator, putative simila	---	AT1G35510	-1.02	-0.02	-0.13	0.8992478	0.9540905	-6.55	FALSE
249314_at	receptor kinase-like protein	---	AT5G41180	-1.02	-0.03	-0.13	0.8992271	0.9540905	-6.55	FALSE
261600_x_a	hypothetical protein similar to hyp	---	AT1G49680 /.	1.01	0.02	0.13	0.8989552	0.9540905	-6.55	FALSE
247211_at	unknown protein ; supported by	---	AT5G64880	1.03	0.04	0.13	0.8992543	0.9540905	-6.55	FALSE
246812_at	putative protein predicted protei	---	---	1.01	0.02	0.13	0.8992278	0.9540905	-6.55	FALSE
264721_at	hypothetical protein predicted by	---	AT1G23000	-1.02	-0.02	-0.13	0.8989151	0.9540905	-6.55	FALSE
263169_at	hypothetical protein similar to unl	---	AT1G03010	1.02	0.03	0.13	0.8991878	0.9540905	-6.55	FALSE
266829_at	hypothetical protein predicted by	---	AT2G22940	-1.01	-0.02	-0.13	0.8989742	0.9540905	-6.55	FALSE
248502_at	putative protein strong similarity t	---	AT5G50450	-1.02	-0.03	-0.13	0.8994052	0.9541378	-6.55	FALSE
255352_at	putative transposon protein simila	---	---	-1.02	-0.02	-0.13	0.8993584	0.9541378	-6.55	FALSE
253655_at	Expressed protein ;supported by	LCR59	AT4G30070	-1.01	-0.02	-0.13	0.8994244	0.9541378	-6.55	FALSE
245786_at	G-Box binding protein, putative s	---	AT1G32150	1.01	0.02	0.13	0.8995688	0.9542144	-6.55	FALSE
263997_at	hypothetical protein predicted by	---	AT2G22520	-1.01	-0.02	-0.13	0.8995803	0.9542144	-6.55	FALSE
245272_at	hypothetical protein ; supported b	---	AT4G17250	-1.03	-0.04	-0.13	0.8996329	0.9542258	-6.55	FALSE
266472_at	unknown protein	---	AT2G31150	-1.01	-0.02	-0.13	0.8999678	0.9542995	-6.55	FALSE
258931_at	hypothetical protein similar to hy	DML2	AT3G10010	1.03	0.04	0.13	0.8998946	0.9542995	-6.55	FALSE
261677_at	unknown protein ;supported by fu	---	AT1G18470	-1.02	-0.03	-0.13	0.8998032	0.9542995	-6.55	FALSE
AFFX-ThrX-	B. subtilis /GEN=thrC /DB_XREF	---	---	-1.03	-0.04	-0.13	0.8999486	0.9542995	-6.55	FALSE
255858_at	zinc finger protein (ZFP6) identic	ZFP6	AT1G67030	-1.02	-0.03	-0.13	0.8997583	0.9542995	-6.55	FALSE
262090_at	CREB-binding protein, putative s	HAC4	AT1G55970	1.01	0.02	0.13	0.8999953	0.9542995	-6.55	FALSE
265653_at	hypothetical protein	---	---	-1.01	-0.02	-0.13	0.8998354	0.9542995	-6.55	FALSE
265838_at	putative spliceosome associated	---	AT2G14550	-1.01	-0.02	-0.13	0.900165	0.9544351	-6.55	FALSE
253714_at	putative protein adaptor protein	---	AT4G29380	1.01	0.02	0.13	0.9003008	0.9545348	-6.55	FALSE
250310_at	unknown protein	---	AT5G12230	-1.02	-0.03	-0.13	0.9004481	0.9546023	-6.55	FALSE
251912_at	protein kinase-like protein wall-a	---	AT3G53840	1.02	0.02	0.13	0.9004363	0.9546023	-6.55	FALSE
251077_at	putative protein COP1-interactin	---	AT5G01980	1.01	0.02	0.13	0.9009232	0.9549038	-6.55	FALSE
261546_at	hypothetical protein	---	AT1G63520	1.01	0.02	0.13	0.9009452	0.9549038	-6.55	FALSE
257425_at	hypothetical protein similar to he	---	AT1G60400	1.02	0.03	0.13	0.9009837	0.9549038	-6.55	FALSE
252078_at	putative protein brassinosteroid-	IMK2	AT3G51740	-1.01	-0.02	-0.13	0.9008631	0.9549038	-6.55	FALSE
255067_at	putative phosphotyrosyl phospha	---	AT4G08960	-1.01	-0.02	-0.13	0.900848	0.9549038	-6.55	FALSE
264144_at	latex-abundant protein, putative	AtMC6	AT1G79320	1.01	0.02	0.13	0.900781	0.9549038	-6.55	FALSE
254858_at	putative protein other predicted	---	AT4G12070	-1.01	-0.02	-0.13	0.9010826	0.954942	-6.55	FALSE

265423_at	unknown protein	---	AT2G20790	-1.02	-0.04	-0.13	0.9012288	0.954942	-6.55	FALSE
250033_at	eukaryotic cap-binding protein (g	NCBP	AT5G18110	-1.01	-0.02	-0.13	0.9011843	0.954942	-6.55	FALSE
254525_at	putative protein predicted protei	---	AT4G19580	-1.02	-0.02	-0.13	0.9011662	0.954942	-6.55	FALSE
260713_at	disease resistance protein RPP1	---	AT1G17615	1.01	0.02	0.13	0.9012292	0.954942	-6.55	FALSE
259406_at	hypothetical protein predicted by	---	AT1G17690	1.01	0.02	0.13	0.9013707	0.9549929	-6.55	FALSE
265074_at	hypothetical protein ; supported b	emb1011	AT1G55540	-1.02	-0.02	-0.13	0.9014446	0.9549929	-6.55	FALSE
261915_at	amp-binding protein, putative sir	BZO1	AT1G65880	-1.01	-0.02	-0.13	0.9014178	0.9549929	-6.55	FALSE
264998_at	unknown protein similar to hypotl	---	AT1G67330	1.05	0.07	0.13	0.9014085	0.9549929	-6.55	FALSE
247353_at	alcohol dehydrogenase-like prote	---	AT5G63620	1.02	0.03	0.13	0.9015418	0.9550325	-6.55	FALSE
254071_at	hypothetical protein	---	AT4G25510	-1.01	-0.02	-0.13	0.9015657	0.9550325	-6.55	FALSE
259342_at	unknown protein ;supported by f	---	AT3G03890	1.02	0.03	0.13	0.9017184	0.9551499	-6.55	FALSE
253889_at	forever young gene (FEY)	FEY	AT4G27760	-1.01	-0.02	-0.13	0.9022862	0.9552184	-6.55	FALSE
264474_s_a	ribulose-bisphosphate carboxyla	RBCS1A	AT1G06820 /	1.01	0.02	0.13	0.9023297	0.9552184	-6.55	FALSE
250220_at	receptor protein kinase-like prote	---	AT5G14210	-1.03	-0.05	-0.13	0.9022902	0.9552184	-6.55	FALSE
256025_at	xylan endohydrolase, putative si	RXF12	AT1G58370	1.02	0.03	0.13	0.9023694	0.9552184	-6.55	FALSE
253135_at	cytoplasmatic aconitate hydratas	---	AT4G35830	-1.02	-0.03	-0.13	0.9023051	0.9552184	-6.55	FALSE
248621_at	putative protein similar to unknov	---	AT5G49350	1.01	0.02	0.13	0.9020114	0.9552184	-6.55	FALSE
247481_at	putative protein predicted protei	---	AT5G62400	-1.01	-0.02	-0.13	0.9022896	0.9552184	-6.55	FALSE
265747_s_a	hypothetical protein predicted by	---	AT2G06570 /	1.02	0.02	0.13	0.9023021	0.9552184	-6.55	FALSE
249603_at	putative protein predicted protei	---	AT5G37210	1.01	0.02	0.13	0.901905	0.9552184	-6.55	FALSE
252301_at	putative protein various predicte	EMB2261	---	-1.02	-0.03	-0.13	0.9021462	0.9552184	-6.55	FALSE
248557_at	transport inhibitor response 1 (T	AFB5	AT5G49980	-1.02	-0.02	-0.13	0.9020151	0.9552184	-6.55	FALSE
246657_at	putative protein predicted protei	---	---	1.01	0.02	0.13	0.9021388	0.9552184	-6.55	FALSE
258711_at	ubiquitin-like protein (UBQ8) ide	UBQ8	AT3G09790	-1.01	-0.02	-0.13	0.9019134	0.9552184	-6.55	FALSE
256026_at	auxin response factor 1, putative	---	AT1G34170	1.01	0.02	0.13	0.9021376	0.9552184	-6.55	FALSE
256447_at	nitrate transporter NTL1, putativ	---	AT1G33440	1.02	0.03	0.13	0.9024576	0.9552674	-6.55	FALSE
256413_at	hypothetical protein predicted by	---	AT3G11100	-1.02	-0.02	-0.13	0.902835	0.9553244	-6.55	FALSE
254850_at	putative protein predicted protein	---	AT4G12000	1.02	0.03	0.13	0.902762	0.9553244	-6.55	FALSE
267587_at	unknown protein	---	AT2G42080	1.02	0.03	0.13	0.9026089	0.9553244	-6.55	FALSE
265023_at	unknown protein weak similarity t	---	AT1G24440	1.02	0.03	0.13	0.9027971	0.9553244	-6.55	FALSE
261953_at	UDP-galactose 4-epimerase, pu	RHD1	AT1G64440	-1.03	-0.04	-0.13	0.9028024	0.9553244	-6.55	FALSE
256931_at	LEA protein, putative similar to L	---	AT3G22490	-1.01	-0.02	-0.13	0.9025606	0.9553244	-6.55	FALSE
263357_s_a	Mutator-like transposase similar t	---	---	-1.01	-0.02	-0.13	0.9027848	0.9553244	-6.55	FALSE
252803_at	putative protein various predicte	---	---	-1.02	-0.02	-0.13	0.9028465	0.9553244	-6.55	FALSE
247638_at	arabinogalactan protein - like ara	FLA12	AT5G60490	1.03	0.05	0.13	0.9031636	0.9554384	-6.55	FALSE

264366_at	unknown protein EST gb|N96383	---	AT1G03250	1.02	0.03	0.13	0.9030828	0.9554384	-6.55	FALSE
265525_at	putative Ty3-gypsy-like retroelem	---	---	1.02	0.02	0.13	0.9030643	0.9554384	-6.55	FALSE
266165_at	putative copper/zinc superoxide d	CSD2	AT2G28190	-1.08	-0.11	-0.13	0.9030204	0.9554384	-6.55	FALSE
246037_at	putative protein predicted chrom	---	AT5G19420	1.02	0.02	0.13	0.9031586	0.9554384	-6.55	FALSE
247514_at	peptide methionine sulfoxide red	PMSR1	AT5G61640	1.02	0.03	0.13	0.9033072	0.955546	-6.55	FALSE
254777_at	putative protein hypothetical pro	---	AT4G12960	-1.02	-0.03	-0.13	0.9033625	0.9555601	-6.55	FALSE
249507_at	similar to unknown protein (pir||T	---	AT5G38370	-1.01	-0.02	-0.13	0.9034377	0.9555954	-6.55	FALSE
257985_at	hypothetical protein predicted by	---	AT3G20810	1.02	0.03	0.13	0.9035798	0.9556828	-6.55	TRUE
253962_at	hypothetical protein	---	AT4G26460	1.01	0.02	0.13	0.9036041	0.9556828	-6.55	FALSE
256736_at	terpene synthase, putative simila	---	AT3G29410	1.01	0.02	0.13	0.9036525	0.9556896	-6.55	FALSE
264561_at	uracil phosphoribosyltransferase	---	AT1G55810	-1.02	-0.03	-0.13	0.9039676	0.9558633	-6.55	FALSE
260712_at	protein phosphatase 2C, putativ	HAB2	AT1G17550	1.02	0.03	0.12	0.9042777	0.9558633	-6.55	FALSE
259416_at	Expressed protein ; supported by	---	AT1G02305	1.02	0.03	0.13	0.9038692	0.9558633	-6.55	FALSE
259649_at	Serine/arginine-rich protein, puta	TAF7	AT1G55300	1.01	0.02	0.12	0.9042004	0.9558633	-6.55	FALSE
265257_at	succinyl-CoA ligase beta subunit	---	AT2G20420	1.03	0.04	0.12	0.9042728	0.9558633	-6.55	FALSE
254410_at	serine/threonine kinase - like pro	---	AT4G21410	1.04	0.06	0.13	0.9040946	0.9558633	-6.55	FALSE
252370_at	putative protein	---	AT3G48600	-1.03	-0.04	-0.13	0.9040299	0.9558633	-6.55	FALSE
254274_at	putative DNA binding protein DN	---	AT4G22770	-1.02	-0.03	-0.12	0.9042532	0.9558633	-6.55	FALSE
257882_at	hypothetical protein predicted by	---	AT3G16930	-1.02	-0.02	-0.13	0.9040392	0.9558633	-6.55	FALSE
248641_at	unknown protein	---	AT5G49110	-1.01	-0.02	-0.12	0.9041842	0.9558633	-6.55	FALSE
248054_at	unknown protein	---	AT5G55820	1.02	0.03	0.13	0.9040182	0.9558633	-6.55	FALSE
254987_s_a	hypothetical protein	---	AT4G10660 ///	-1.01	-0.02	-0.12	0.9044748	0.9559484	-6.55	FALSE
260342_at	hypothetical protein predicted by	---	AT1G69280	1.02	0.02	0.12	0.9045258	0.9559484	-6.55	FALSE
252926_at	H+-transporting ATPase 16K ch	ATVHA-C3	AT4G38920	-1.02	-0.02	-0.12	0.904453	0.9559484	-6.55	FALSE
263059_at	putative non-LTR retrolelement r	---	---	1.01	0.02	0.12	0.9045222	0.9559484	-6.55	FALSE
263198_at	lipase, putative similar to lipase	GLIP3	AT1G53990	1.02	0.03	0.12	0.9046019	0.9559845	-6.55	FALSE
267579_at	metallothionein-like protein	---	AT2G42000	-1.01	-0.02	-0.12	0.9046535	0.9559947	-6.55	FALSE
260928_at	hypothetical protein similar to put	GATL5	AT1G02720	-1.01	-0.02	-0.12	0.9048873	0.9561898	-6.55	FALSE
246650_at	putative protein p76, Homo sapi	---	AT5G35160	-1.01	-0.02	-0.12	0.9051323	0.9561898	-6.55	FALSE
260636_at	hypothetical protein contains sim	ATCDS1	AT1G62430	1.03	0.04	0.12	0.9051735	0.9561898	-6.55	FALSE
264468_at	unknown protein similar to daunc	---	AT1G10310	-1.02	-0.03	-0.12	0.9050206	0.9561898	-6.55	FALSE
251982_at	pectate lyase -like protein pectat	---	AT3G53190	-1.02	-0.03	-0.12	0.9050338	0.9561898	-6.55	FALSE
255713_s_a	predicted protein	---	AT4G00234 ///	-1.01	-0.02	-0.12	0.9049858	0.9561898	-6.55	FALSE
250641_at	putative bZIP protein bZIP prote	---	AT5G07160	-1.02	-0.02	-0.12	0.9051613	0.9561898	-6.55	FALSE
263280_x_a	hypothetical protein predicted by	---	---	1.01	0.02	0.12	0.9051579	0.9561898	-6.55	FALSE

265978_at	putative retroelement pol polypro	---	---	1.01	0.02	0.12	0.9052525	0.956229	-6.55	FALSE
246919_at	putative protein hypothetical pro	---	AT5G25460	1.11	0.15	0.12	0.9054952	0.956409	-6.55	TRUE
263653_at	putative ethylene receptor (ERS2	ERS2	AT1G04310	1.02	0.03	0.12	0.9055067	0.956409	-6.55	FALSE
258916_at	putative ABC transporter ATPase	ATNAP7	AT3G10670	-1.01	-0.02	-0.12	0.9055785	0.9564405	-6.55	FALSE
249191_at	putative protein similar to unknov	---	AT5G42760	-1.02	-0.03	-0.12	0.9057473	0.9565303	-6.55	FALSE
247603_at	microtubule-associated motor - l	---	AT5G60930	1.02	0.03	0.12	0.9057419	0.9565303	-6.55	FALSE
265320_at	unknown protein predicted by ge	---	AT2G18320	1.01	0.02	0.12	0.9059041	0.9566515	-6.55	FALSE
245265_at	hypothetical protein ; supported b	ACD6	AT4G14400	1.09	0.13	0.12	0.9061806	0.9568992	-6.55	FALSE
252800_at	putative protein	---	---	-1.01	-0.02	-0.12	0.9062551	0.9569336	-6.55	FALSE
260633_at	protein kinase, putative similar t	HT1	AT1G62400	1.01	0.02	0.12	0.9063118	0.9569492	-6.55	FALSE
250476_at	MADS box protein FLOWERING	FLC	AT5G10140	1.01	0.02	0.12	0.9063574	0.956953	-6.55	FALSE
246035_at	succinyl-CoA-ligase alpha subun	---	AT5G08300	1.03	0.05	0.12	0.9064118	0.9569661	-6.55	FALSE
260043_at	hypothetical protein predicted by	---	---	-1.02	-0.02	-0.12	0.9067305	0.9572583	-6.55	FALSE
262363_at	disease resistance protein, puta	---	AT1G72850	1.01	0.02	0.12	0.9068709	0.957332	-6.55	FALSE
246709_s_a	putative protein many predicted	---	AT5G28160 ///	-1.01	-0.02	-0.12	0.9068843	0.957332	-6.55	FALSE
246155_at	putative protein predicted protei	---	AT5G20030	1.01	0.02	0.12	0.9069883	0.9573675	-6.55	FALSE
247565_at	putative protein Atu, Drosophila	VIP4	AT5G61150	1.01	0.02	0.12	0.9070018	0.9573675	-6.55	FALSE
252525_at	putative protein hypothetical prot	---	AT3G46450	1.01	0.02	0.12	0.9072724	0.9576088	-6.55	FALSE
248864_at	bHLH protein-like	---	AT5G46760	-1.01	-0.02	-0.12	0.9073589	0.9576558	-6.55	FALSE
267627_at	putative ATP-dependent RNA he	---	AT2G42270	1.03	0.04	0.12	0.9074268	0.9576832	-6.55	FALSE
259767_s_a	unknown protein	---	AT1G29350 ///	-1.01	-0.02	-0.12	0.9075385	0.9577341	-6.55	FALSE
263849_at	putative retroelement pol polypro	---	---	-1.02	-0.02	-0.12	0.9075591	0.9577341	-6.55	FALSE
247478_at	DC1.2 homologue - like protein l	---	AT5G62360	-1.04	-0.06	-0.12	0.907727	0.9578321	-6.55	TRUE
258969_at	hypothetical protein predicted by	---	AT3G10680	1.01	0.02	0.12	0.907736	0.9578321	-6.55	FALSE
261783_at	vacuolar assembly protein vps4	---	AT1G08190	-1.02	-0.02	-0.12	0.9078763	0.9579359	-6.55	FALSE
265230_s_a	hypothetical protein	---	AT2G07707	-1.02	-0.03	-0.12	0.9083562	0.9580923	-6.55	FALSE
253552_at	ubiquitin-specific protease 24 (U	UBP24	AT4G30890	1.01	0.02	0.12	0.9083474	0.9580923	-6.55	FALSE
246675_at	putative protein	---	AT5G30420	1.01	0.02	0.12	0.9081115	0.9580923	-6.55	FALSE
257703_at	unknown protein ; supported by f	---	AT3G12640	-1.01	-0.02	-0.12	0.9083605	0.9580923	-6.55	FALSE
258668_at	hypothetical protein predicted by	---	AT3G08780	1.01	0.02	0.12	0.9082575	0.9580923	-6.55	FALSE
255238_at	see GB:AL022580)	---	---	-1.01	-0.01	-0.12	0.908152	0.9580923	-6.55	FALSE
247897_at	unknown protein ;supported by f	TET15	AT5G57810	1.01	0.02	0.12	0.9081186	0.9580923	-6.55	FALSE
263316_s_a	putative ligand-gated ion channe	ATGLR2.3	AT2G24710 ///	1.01	0.02	0.12	0.9082341	0.9580923	-6.55	FALSE
266044_s_a	hypothetical protein	---	AT2G07725	1.03	0.04	0.12	0.9084545	0.9581201	-6.55	TRUE
252185_at	putative protein	---	AT3G50780	1.02	0.03	0.12	0.908513	0.9581201	-6.55	FALSE

249448_at	cdc2-like protein	cdc2cAt	AT5G39420	1.02	0.03	0.12	0.9085109	0.9581201	-6.55	FALSE
258902_at	putative pyruvate dehydrogenas	PDK	AT3G06483	-1.01	-0.02	-0.12	0.9085977	0.9581209	-6.55	FALSE
264881_s_a	lysine and histidine specific trans	---	AT1G61270 ///	-1.01	-0.01	-0.12	0.9085922	0.9581209	-6.55	FALSE
251917_at	putative protein	---	AT3G53970	1.01	0.02	0.12	0.9087838	0.9582286	-6.55	FALSE
265534_at	En/Spm-like transposon protein r	---	---	1.01	0.01	0.12	0.9087734	0.9582286	-6.55	FALSE
249432_at	putative ATP/GTP-binding prote	CLPS5	AT5G39930	1.01	0.02	0.12	0.90883	0.958233	-6.55	FALSE
267080_at	unknown protein ; supported by	---	AT2G41190	-1.04	-0.05	-0.12	0.9089933	0.9583608	-6.55	FALSE
251704_at	putative protein unknown protein	---	AT3G56360	1.03	0.05	0.12	0.9091613	0.9584743	-6.55	FALSE
251731_at	manganese superoxide dismuta	---	AT3G56350	-1.02	-0.02	-0.12	0.9091849	0.9584743	-6.55	FALSE
265942_at	putative casein kinase I ;support	ckl5	AT2G19470	-1.01	-0.02	-0.12	0.9093344	0.9585875	-6.55	FALSE
262022_at	hypothetical protein predicted by	---	AT1G35490	-1.02	-0.02	-0.12	0.9093778	0.958589	-6.55	FALSE
254539_s_a	chitinase - like protein chitinase	---	AT4G19750 ///	-1.01	-0.02	-0.12	0.9094428	0.9586133	-6.55	FALSE
245851_at	putative protein HERC2 - Homo	KEG	AT5G13530	-1.01	-0.02	-0.12	0.9095257	0.9586413	-6.55	FALSE
259851_at	kinesin, putative	---	AT1G72250	-1.01	-0.02	-0.12	0.9095535	0.9586413	-6.55	FALSE
252600_at	putative protein unknown protein	VPS24.2	AT3G45000	-1.02	-0.02	-0.12	0.9096448	0.958649	-6.55	FALSE
247387_at	unknown protein	---	AT5G63460	1.01	0.02	0.12	0.909635	0.958649	-6.55	FALSE
252127_at	putative protein ATP binding pro	PLP3a	AT3G50960	-1.02	-0.03	-0.12	0.9097353	0.958659	-6.55	FALSE
248068_at	unknown protein	---	AT5G55610	1.02	0.03	0.12	0.9097384	0.958659	-6.55	FALSE
251190_at	RING-H2 zinc finger protein ATL	ATL5	AT3G62690	-1.03	-0.04	-0.12	0.9098806	0.9587202	-6.55	FALSE
244963_at	PSII cytochrome b559	---	---	-1.01	-0.01	-0.12	0.9098688	0.9587202	-6.55	FALSE
265115_at	rho GDP-dissociation inhibitor, p	---	AT1G62450	1.01	0.02	0.12	0.9099732	0.9587735	-6.55	FALSE
260493_at	hypothetical protein predicted by	---	AT2G41830	-1.02	-0.03	-0.12	0.9102598	0.9588541	-6.55	TRUE
245822_at	unknown protein ; supported by c	---	AT1G26110	1.02	0.02	0.12	0.9102352	0.9588541	-6.55	FALSE
259468_at	unknown protein	TTN10	AT1G19080 ///	-1.02	-0.02	-0.12	0.9102019	0.9588541	-6.55	FALSE
246765_at	glutamic acid-rich protein hypoth	---	AT5G27330	-1.01	-0.02	-0.12	0.9101815	0.9588541	-6.55	FALSE
264634_at	cytochrome P450, putative	CYP702A1	AT1G65670	1.01	0.01	0.12	0.9101021	0.9588541	-6.55	FALSE
255415_at	hypothetical protein	---	AT4G03160	1.01	0.01	0.12	0.9104512	0.9590114	-6.55	FALSE
259765_at	unknown protein ;supported by fu	---	AT1G64370	1.02	0.03	0.12	0.9106471	0.9591734	-6.55	FALSE
249208_at	allene oxide synthase (emb CAA	AOS	AT5G42650	1.04	0.05	0.12	0.9107594	0.9592475	-6.55	FALSE
258123_at	putative MAP kinase similar to bl	MPK9	AT3G18040	1.03	0.04	0.12	0.9110922	0.9594795	-6.55	TRUE
264402_at	HSP100/ClpB, putative similar to	CLPB4	AT2G25140	1.03	0.04	0.12	0.9113202	0.9594795	-6.55	TRUE
249233_at	putative protein contains similarit	---	AT5G42150	-1.04	-0.05	-0.12	0.9113341	0.9594795	-6.55	FALSE
250588_at	SMC-like protein	---	AT5G07660	1.01	0.02	0.12	0.9111596	0.9594795	-6.55	FALSE
259407_at	protein phosphatase 2A regulato	PP2AA3	AT1G13320	-1.01	-0.02	-0.12	0.9113583	0.9594795	-6.55	FALSE
264779_at	putative thioredoxin similar to ES	ACHT4	AT1G08570	-1.03	-0.04	-0.12	0.9112929	0.9594795	-6.55	FALSE

246645_at	putative protein ;supported by fu	---	AT5G35080	-1.02	-0.02	-0.12	0.9110789	0.9594795	-6.55	FALSE
250759_at	unknown protein	---	AT5G06020	-1.01	-0.02	-0.12	0.9113353	0.9594795	-6.55	FALSE
267403_at	MADS-box protein (AGL33)	AGL33	AT2G26320	1.01	0.01	0.12	0.9113506	0.9594795	-6.55	FALSE
257243_at	pectate lyase, putative similar to	---	AT3G24230	-1.01	-0.01	-0.12	0.9114013	0.9594805	-6.55	FALSE
265705_at	unknown protein related to MO25	---	AT2G03410	1.04	0.05	0.12	0.9114754	0.9595143	-6.55	FALSE
261442_at	Expressed protein ; supported by	---	AT1G28375	1.01	0.02	0.12	0.9117857	0.9597966	-6.55	FALSE
256059_at	hypothetical protein contains sim	---	AT1G06990	1.02	0.02	0.11	0.9119636	0.9599287	-6.55	FALSE
266067_s_a	hypothetical protein predicted by	---	AT2G18810 ///	1.01	0.01	0.11	0.9119993	0.9599287	-6.55	FALSE
259778_at	hypothetical protein predicted by	---	AT1G29610	-1.01	-0.02	-0.11	0.9120375	0.9599287	-6.55	FALSE
257938_at	cell elongation protein, Dwarf1 ic	DWF1	AT3G19820	1.06	0.08	0.11	0.9121249	0.9599764	-6.55	FALSE
255177_at	strong similarity to 1-aminocyclop	ACS11	AT4G08040	1.04	0.06	0.11	0.9121898	0.9599995	-6.55	TRUE
254331_s_a	cytochrome P450 - like protein fl	CYP706A2	AT4G22690 ///	1.04	0.05	0.11	0.912231	0.9599995	-6.55	FALSE
265255_at	unknown protein ; supported by	---	AT2G28420	-1.02	-0.03	-0.11	0.9123499	0.9600361	-6.55	FALSE
262147_at	phospholipase D1, putative simil	PLDALPHA	AT1G52570	1.01	0.02	0.11	0.9123196	0.9600361	-6.55	FALSE
263439_at	hypothetical protein predicted by	ATEXO70H	AT2G28650	1.01	0.02	0.11	0.9124555	0.9601029	-6.55	FALSE
260724_at	unknown protein ;supported by fu	---	AT1G48140	-1.01	-0.02	-0.11	0.9127045	0.9602921	-6.55	FALSE
248543_at	putative protein similar to unknov	---	AT5G50230	1.01	0.01	0.11	0.9127599	0.9602921	-6.55	FALSE
253158_at	putative protein protein kinase 6	---	AT4G35780	-1.02	-0.02	-0.11	0.9127616	0.9602921	-6.55	FALSE
258272_at	unknown protein similar to serin	---	AT3G15610	1.02	0.03	0.11	0.9129195	0.9604139	-6.55	FALSE
260349_at	mitotic checkpoint protein, putati	---	AT1G69400	-1.01	-0.02	-0.11	0.9131823	0.9605575	-6.55	FALSE
262217_at	hypothetical protein predicted by	---	AT1G74770	-1.01	-0.01	-0.11	0.9131552	0.9605575	-6.55	FALSE
251625_at	beta-1,3-glucanase 2 (BG2) (PR	BGL2	AT3G57260	1.17	0.23	0.11	0.9131064	0.9605575	-6.55	FALSE
258996_at	putative ribosome recycling facto	---	AT3G01800	-1.02	-0.02	-0.11	0.9133592	0.9605664	-6.55	FALSE
250615_at	putative protein ankyrins - differe	---	AT5G07270	-1.02	-0.02	-0.11	0.9133211	0.9605664	-6.55	FALSE
251799_at	putative protein P59 PROTEIN (	---	AT3G55520	1.02	0.02	0.11	0.9133456	0.9605664	-6.55	FALSE
252309_at	cysteine protease contains simila	---	AT3G49340	-1.01	-0.02	-0.11	0.9133375	0.9605664	-6.55	FALSE
261365_at	proton pump interactor, putative	---	AT1G53110	1.03	0.05	0.11	0.9134428	0.96061	-6.55	FALSE
264669_at	putative RAS-related protein, RA	ATRAB11C	AT1G09630	1.02	0.03	0.11	0.9139394	0.961088	-6.55	FALSE
256237_at	leucine rich repeat protein, putat	DRT100	AT3G12610	1.14	0.19	0.11	0.9140174	0.9610918	-6.55	FALSE
260698_at	unknown protein contains similar	---	AT1G32300	-1.01	-0.01	-0.11	0.9140273	0.9610918	-6.55	FALSE
249796_at	26S proteasome, non-ATPase r	---	AT5G23540	1.01	0.02	0.11	0.9141881	0.9612165	-6.55	FALSE
245128_at	unknown protein similar to gi234	---	AT2G45380	1.01	0.02	0.11	0.9143398	0.9613317	-6.55	FALSE
249885_at	putative protein strong similarity t	F8H	AT5G22940	-1.02	-0.03	-0.11	0.9144685	0.9613581	-6.55	FALSE
260489_at	hypothetical protein ; supported b	---	AT1G51610	-1.01	-0.02	-0.11	0.9144907	0.9613581	-6.55	FALSE
244912_at	cytochrome c biogenesis orf382	---	AT2G07783	1.02	0.03	0.11	0.9144914	0.9613581	-6.55	FALSE

266412_at	hypothetical protein predicted by	MAP65-5	AT2G38720	1.01	0.02	0.11	0.9145998	0.9614141	-6.55	FALSE
252111_at	propable disease resistance pro	---	AT3G51570	-1.02	-0.03	-0.11	0.9146289	0.9614141	-6.55	FALSE
248847_at	disease resistance protein-like	---	AT5G46510	1.01	0.02	0.11	0.9147583	0.9615058	-6.55	FALSE
256721_at	hypothetical protein predicted by	WAVE1	AT2G34150	1.02	0.02	0.11	0.9148239	0.9615304	-6.55	FALSE
261423_at	homeodomain transcription facto	AGL65	AT1G18750	-1.02	-0.02	-0.11	0.9150872	0.9616868	-6.55	FALSE
247658_at	actin depolymerizing factor 3 - li	ADF3	AT5G59880	-1.01	-0.02	-0.11	0.9150992	0.9616868	-6.55	FALSE
265904_at	putative beta-glucosidase	BGLU14	AT2G25630	-1.01	-0.02	-0.11	0.9150201	0.9616868	-6.55	FALSE
257571_at	hypothetical protein predicted by	---	AT3G16870	-1.02	-0.03	-0.11	0.9153161	0.9618303	-6.55	FALSE
252224_at	putative protein various ADP-RIB	ATARLA1B	AT3G49860	-1.01	-0.02	-0.11	0.9153201	0.9618303	-6.55	FALSE
259029_at	putative oxysterol-binding protein	ORP3B	AT3G09300	-1.01	-0.02	-0.11	0.9155811	0.9620603	-6.55	FALSE
257204_at	Expressed protein ; supported by	RALFL24	AT3G23805	1.03	0.05	0.11	0.9156649	0.962104	-6.55	TRUE
245760_s_a	receptor serine/threonine kinase	---	AT1G66910 ///	-1.03	-0.04	-0.11	0.915892	0.962194	-6.55	TRUE
258611_at	unknown protein ;supported by f	---	AT3G02860	-1.01	-0.02	-0.11	0.9159192	0.962194	-6.55	FALSE
249655_at	putative helicase PIF1 protein -	---	---	1.01	0.02	0.11	0.9158775	0.962194	-6.55	FALSE
248660_at	RNA-binding protein-like	---	AT5G48650	1.02	0.02	0.11	0.9159148	0.962194	-6.55	FALSE
262670_s_a	transposase [Escherichia coli] m	---	---	-1.01	-0.02	-0.11	0.9162143	0.9624596	-6.55	FALSE
267280_at	diacylglycerol O-acyltransferase	TAG1	AT2G19450	1.02	0.02	0.11	0.9163405	0.9625479	-6.55	FALSE
266891_at	putative GTP-binding protein ; s	ARAC9	AT2G44690	-1.01	-0.02	-0.11	0.9164273	0.9625947	-6.55	FALSE
263503_s_a	hypothetical protein	---	AT2G07676	-1.01	-0.02	-0.11	0.9165564	0.9626416	-6.55	FALSE
248246_at	putative protein contains similarit	TRY	AT5G53200	1.01	0.02	0.11	0.9165195	0.9626416	-6.55	FALSE
261901_at	J8-like protein similar to DnaJ ho	J8	AT1G80920	1.01	0.02	0.11	0.9166341	0.9626789	-6.55	FALSE
246414_at	hypothetical protein similar to hy	---	AT1G77340	-1.01	-0.02	-0.11	0.9168965	0.9629102	-6.55	FALSE
261785_at	hypothetical protein contains sim	---	AT1G08230	-1.01	-0.02	-0.11	0.9171613	0.9630995	-6.55	TRUE
245559_at	glycine-rich protein like	---	AT4G15460	1.01	0.02	0.11	0.9171561	0.9630995	-6.55	FALSE
264974_at	unknown protein contains Pfam p	ATHB54	AT1G27050	-1.01	-0.02	-0.11	0.9172248	0.9631219	-6.55	FALSE
258874_at	hypothetical protein similar to un	---	AT3G03230	-1.02	-0.02	-0.11	0.9173687	0.9631534	-6.55	FALSE
257967_at	hypothetical protein predicted by	---	AT3G19910	1.01	0.02	0.11	0.9174133	0.9631534	-6.55	FALSE
264386_at	putative pyrophosphate-fructose	---	AT1G12000	-1.03	-0.04	-0.11	0.9173978	0.9631534	-6.55	FALSE
255336_at	putative transposon protein	---	---	1.01	0.01	0.11	0.9174237	0.9631534	-6.55	FALSE
262587_at	unknown protein Contains PF|00	---	AT1G15490	-1.02	-0.03	-0.11	0.9174865	0.9631751	-6.55	FALSE
264611_at	putative pectate lyase A11 simila	---	AT1G04680	-1.05	-0.07	-0.11	0.9179639	0.963557	-6.55	TRUE
252025_at	putative protein chromosome as	---	AT3G52900	1.01	0.02	0.11	0.9179692	0.963557	-6.55	FALSE
262851_at	putative RNA helicase Contains	---	AT1G20920	1.01	0.02	0.11	0.9179771	0.963557	-6.55	FALSE
261820_at	hypothetical protein predicted by	---	AT1G11420	-1.02	-0.02	-0.11	0.9181764	0.9637219	-6.55	FALSE
263969_at	putative VSF-1-like b-ZIP transcr	UNE4	AT2G12940	1.01	0.02	0.11	0.9182422	0.9637466	-6.55	FALSE

246793_at	putative protein seven transmem	---	AT5G27210	-1.01	-0.02	-0.11	0.9183117	0.9637717	-6.55	FALSE
251160_at	inositol-1,4,5-trisphosphate 5-Ph	---	AT3G63240	1.01	0.02	0.11	0.9183506	0.9637717	-6.55	FALSE
253744_s_a	putative protein hypothetical pro	---	---	-1.01	-0.02	-0.11	0.9185661	0.9639534	-6.55	FALSE
256640_at	hypothetical protein predicted by	---	AT3G32260	1.01	0.02	0.11	0.918734	0.9640853	-6.55	FALSE
263896_at	hypothetical protein predicted by	---	AT2G21930	1.01	0.02	0.11	0.9188781	0.9641921	-6.55	FALSE
259474_at	unknown protein ;supported by fu	---	AT1G19130	-1.03	-0.04	-0.11	0.9189678	0.964242	-6.55	FALSE
259483_at	hypothetical protein predicted by	---	AT1G43980	-1.01	-0.02	-0.11	0.9190725	0.9642551	-6.55	FALSE
257418_at	hypothetical protein predicted by	---	AT1G30850	1.02	0.02	0.11	0.9190719	0.9642551	-6.55	FALSE
250747_at	glucuronosyl transferase-like pro	---	AT5G05900	1.01	0.02	0.11	0.9191072	0.9642551	-6.55	FALSE
255529_at	CTP synthase - like protein	---	AT4G02120	1.01	0.02	0.10	0.919458	0.9645788	-6.55	FALSE
245184_at	F12A21.8 hypothetical protein	---	AT1G67790	1.01	0.02	0.10	0.9195033	0.964582	-6.55	FALSE
249353_at	oleosin ; supported by cDNA: gi_	OLEO2	AT5G40420	1.01	0.02	0.10	0.9195946	0.964598	-6.55	FALSE
264469_at	hypothetical protein similar to hy	LBD40	AT1G67100	-1.01	-0.02	-0.10	0.9196032	0.964598	-6.55	FALSE
258415_at	putative s-adenosylmethionine sy	MTO3	AT3G17390	-1.03	-0.04	-0.10	0.9198449	0.9646134	-6.55	FALSE
258707_at	putative histone H2B similar to hi	---	AT3G09480	1.02	0.02	0.10	0.9198494	0.9646134	-6.55	FALSE
266323_at	putative calcium-dependent prote	CRK3	AT2G46700	1.01	0.02	0.10	0.9198716	0.9646134	-6.55	FALSE
255710_at	predicted protein of unknown fun	---	AT4G00030 ///	-1.02	-0.03	-0.10	0.9198474	0.9646134	-6.55	FALSE
245647_at	F5A9.22 hypothetical protein	---	AT1G24706	-1.01	-0.01	-0.10	0.9197582	0.9646134	-6.55	FALSE
248544_at	putative protein contains similarit	PIMT2	AT5G50240	-1.02	-0.03	-0.10	0.9198318	0.9646134	-6.55	FALSE
248383_at	putative protein contains similarit	---	AT5G51900	1.01	0.02	0.10	0.9200482	0.9647099	-6.55	FALSE
261468_s_a	hypothetical protein predicted by	---	AT1G27860 ///	-1.02	-0.02	-0.10	0.9200149	0.9647099	-6.55	FALSE
261035_at	hypothetical protein contains Pfa	---	---	-1.01	-0.01	-0.10	0.9203833	0.9650169	-6.55	FALSE
267267_at	putative cytochrome P450	CYP71B9	AT2G02580	-1.01	-0.02	-0.10	0.9206501	0.9652079	-6.55	FALSE
265463_at	unknown protein	IRX9	AT2G37090	-1.02	-0.03	-0.10	0.9206482	0.9652079	-6.55	FALSE
255110_at	peroxidase C2 precursor like pro	---	AT4G08770	-1.06	-0.08	-0.10	0.9209111	0.9653928	-6.55	TRUE
257305_at	hypothetical protein predicted by	---	---	-1.01	-0.02	-0.10	0.9209017	0.9653928	-6.55	FALSE
258777_at	hypothetical protein predicted by	---	AT3G11850	1.02	0.02	0.10	0.9211967	0.9656478	-6.55	FALSE
265167_at	putative OBP32pep protein	---	AT1G23680	1.01	0.02	0.10	0.9213375	0.965751	-6.55	FALSE
260974_at	receptor-like serine/threonine kir	---	AT1G53440	-1.02	-0.04	-0.10	0.92138	0.9657512	-6.55	FALSE
245305_at	Expressed protein ; supported by	---	AT4G17215	1.04	0.06	0.10	0.9215147	0.9658037	-6.55	FALSE
262302_at	hypothetical protein predicted by	---	AT1G70910	1.01	0.02	0.10	0.9214927	0.9658037	-6.55	FALSE
245626_at	unknown protein ;supported by fu	---	AT1G56700	1.02	0.02	0.10	0.9218013	0.9660152	-6.55	FALSE
260990_at	hypothetical protein predicted by	---	AT1G12180	1.02	0.02	0.10	0.9217937	0.9660152	-6.55	FALSE
245975_at	putative protein CGI-107 protein	---	AT5G13070	1.01	0.02	0.10	0.9218518	0.9660237	-6.55	FALSE
263348_at	cytoplasmic aconitate hydratase	---	AT2G05710	1.02	0.02	0.10	0.9221833	0.9662516	-6.55	TRUE

252343_at	putative protein hypothetical pro	---	AT3G48610	1.04	0.05	0.10	0.9222174	0.9662516	-6.55	FALSE
265170_at	putative carbonic anhydrase	BCA3	AT1G23730	-1.07	-0.09	-0.10	0.922281	0.9662516	-6.55	FALSE
254841_at	putative protein predicted protein	---	AT4G11940	1.01	0.02	0.10	0.9221205	0.9662516	-6.55	FALSE
246643_s_a	putative protein various predicte	---	---	-1.01	-0.01	-0.10	0.9222704	0.9662516	-6.55	FALSE
255941_at	mitochondrial inner membrane t	ATTIM17-1	AT1G20350	-1.02	-0.03	-0.10	0.9224114	0.9663438	-6.55	FALSE
258021_at	hypothetical protein predicted ge	PUB25	AT3G19380	-1.04	-0.05	-0.10	0.9225771	0.9663842	-6.55	FALSE
249695_at	putative protein similar to unknov	---	---	-1.01	-0.02	-0.10	0.9225711	0.9663842	-6.55	FALSE
267254_at	putative protein kinase contains a	SNRK2.9	AT2G23030	-1.04	-0.05	-0.10	0.9225325	0.9663842	-6.55	FALSE
261473_at	hypothetical protein similar to put	---	AT1G14490	1.02	0.03	0.10	0.9226787	0.9664463	-6.55	FALSE
262697_at	beta-glucosidase, putative simila	ATA27	AT1G75940	-1.01	-0.01	-0.10	0.9227823	0.9665104	-6.55	FALSE
258274_at	putative cytochrome c oxidase su	---	AT3G15640	1.01	0.02	0.10	0.9228275	0.9665134	-6.55	FALSE
253470_s_a	putative protein dnaK-type mole	SDH3-2	AT4G32210 /	-1.01	-0.01	-0.10	0.9228992	0.9665441	-6.55	FALSE
261306_at	regulatory protein HAL3B similar	---	AT1G48610	-1.01	-0.02	-0.10	0.9230596	0.9665535	-6.55	FALSE
262932_at	glutathione-s-transferase, putativ	---	AT1G65820	-1.02	-0.02	-0.10	0.9229793	0.9665535	-6.55	FALSE
245700_at	carbonate dehydratase - like prot	ACA3	AT5G04180	1.01	0.01	0.10	0.92312	0.9665535	-6.55	FALSE
249923_at	conglutin gamma - like protein c	---	AT5G19120	-1.02	-0.03	-0.10	0.923083	0.9665535	-6.55	FALSE
262688_at	PPR-repeat protein contains mul	---	AT1G62680	1.01	0.01	0.10	0.9230583	0.9665535	-6.55	FALSE
253707_at	hypothetical protein	---	AT4G29200	-1.01	-0.01	-0.10	0.9232415	0.9666364	-6.55	FALSE
248574_at	putative protein strong similarity t	---	AT5G49830	1.01	0.01	0.10	0.9233885	0.9667458	-6.55	FALSE
247733_at	putative protein heat shock prote	---	AT5G59610	-1.02	-0.02	-0.10	0.9234726	0.9667895	-6.55	FALSE
265691_at	unknown protein predicted by ge	---	AT2G24330	1.02	0.03	0.10	0.9235666	0.9667991	-6.55	FALSE
267251_at	putative casein kinase II catalytic	---	AT2G23070	-1.01	-0.01	-0.10	0.9235616	0.9667991	-6.55	FALSE
266236_at	putative glutathione S-transferas	ATGSTZ2	AT2G02380	-1.01	-0.02	-0.10	0.9238484	0.9670054	-6.55	FALSE
255460_at	hypothetical protein similar to A.	---	AT4G02800	-1.01	-0.01	-0.10	0.9238427	0.9670054	-6.55	FALSE
245274_at	ankyrin like protein ; supported b	---	AT4G14360	1.01	0.02	0.10	0.9242296	0.9671825	-6.55	TRUE
247532_at	putative protein disease resistan	---	AT5G61560	1.03	0.05	0.10	0.9242196	0.9671825	-6.55	FALSE
261555_s_a	hypothetical protein predicted by	---	AT1G63230 /	1.01	0.01	0.10	0.9241944	0.9671825	-6.55	FALSE
261123_at	hypothetical protein predicted by	---	AT1G62860	-1.02	-0.02	-0.10	0.9242126	0.9671825	-6.55	FALSE
265552_at	putative plasma membrane proto	AHA6	AT2G07560	1.01	0.02	0.10	0.9242144	0.9671825	-6.55	FALSE
254551_at	lectin like protein lectin phloem p	ATPP2-A1	AT4G19840	-1.01	-0.02	-0.10	0.9245557	0.967435	-6.55	FALSE
267282_at	unknown protein ; supported by	---	AT2G19390	1.01	0.02	0.10	0.9245231	0.967435	-6.55	FALSE
265824_at	putative glucosyltransferase ;sup	ATCSLA07	AT2G35650	1.02	0.02	0.10	0.9248315	0.9674765	-6.55	TRUE
260362_at	putative protein kinase similar to	---	AT1G70530	1.03	0.04	0.10	0.9246548	0.9674765	-6.55	FALSE
259484_at	calcium-dependent protein kinas	PEPKR1	AT1G12580	-1.01	-0.02	-0.10	0.9250891	0.9674765	-6.55	FALSE
262876_at	unknown protein ;supported by fu	ATDSS1(I)	AT1G64750	-1.01	-0.02	-0.10	0.9251233	0.9674765	-6.55	FALSE

262538_at	Expressed protein ; supported by	---	AT1G17140	1.02	0.03	0.10	0.9251605	0.9674765	-6.55	FALSE
267043_at	unknown protein	---	AT2G34330	-1.01	-0.02	-0.10	0.9251497	0.9674765	-6.55	FALSE
245691_at	zinc finger protein - like	ELF6	AT5G04240	1.02	0.02	0.10	0.9251601	0.9674765	-6.55	FALSE
249569_at	putative protein Pit1 - Arabidops	---	AT5G38070	1.01	0.02	0.10	0.9249799	0.9674765	-6.55	FALSE
256546_at	hypothetical protein contains sim	---	AT3G14820	-1.01	-0.01	-0.10	0.9249128	0.9674765	-6.55	FALSE
266195_at	putative RING zinc finger protein	---	AT2G39100	1.01	0.01	0.10	0.9248725	0.9674765	-6.55	FALSE
260516_at	unknown protein	---	AT1G51450	-1.01	-0.02	-0.10	0.9251656	0.9674765	-6.55	FALSE
256498_at	hypothetical protein	---	---	-1.01	-0.01	-0.10	0.9250098	0.9674765	-6.55	FALSE
253727_at	profilin 2 ; supported by full-leng	PFN2	AT4G29350	-1.01	-0.02	-0.10	0.9251507	0.9674765	-6.55	FALSE
248240_at	CUC2 (dbj|BAA19529.1)	CUC2	AT5G53950	-1.01	-0.02	-0.10	0.9251891	0.9674765	-6.55	FALSE
261647_at	hypothetical protein similar to hy	---	AT1G27740	1.01	0.02	0.10	0.9252455	0.9674911	-6.55	FALSE
247064_at	putative protein contains similarit	---	AT5G66890	1.02	0.03	0.10	0.9253288	0.9675338	-6.55	FALSE
250111_at	acetolactate synthase-like protei	---	AT5G16290	1.02	0.02	0.10	0.9255529	0.9675907	-6.55	FALSE
251567_at	putative protein several hypothet	---	AT3G58230	1.01	0.02	0.10	0.9255376	0.9675907	-6.55	FALSE
248652_at	putative protein contains similarit	SHV2	AT5G49270	1.02	0.02	0.10	0.9254924	0.9675907	-6.55	FALSE
248441_at	putative protein contains similarit	---	AT5G51270	-1.01	-0.01	-0.10	0.9255278	0.9675907	-6.55	FALSE
249904_at	unknown protein	---	AT5G22700	1.01	0.01	0.10	0.9256776	0.9676324	-6.55	FALSE
266953_at	hypothetical protein predicted by	---	AT2G34540	1.01	0.02	0.10	0.9256762	0.9676324	-6.55	FALSE
259530_at	hypothetical protein	---	AT1G12450	1.02	0.03	0.10	0.9258017	0.9677178	-6.55	TRUE
245622_at	A6 anther-specific protein	MEE48	AT4G14080	-1.01	-0.02	-0.10	0.9259338	0.9678115	-6.55	FALSE
263936_at	putative ATP-dependent RNA he	---	AT2G35920	1.01	0.02	0.10	0.9259791	0.9678145	-6.55	FALSE
250447_at	putative protein KIAA0332 gene	---	AT5G10800	1.01	0.01	0.10	0.926109	0.9678483	-6.55	FALSE
264612_at	unknown protein similar to GB:A	---	AT1G04560	-1.01	-0.02	-0.10	0.9261388	0.9678483	-6.55	FALSE
264346_at	putative amino-cyclopropane-car	---	AT1G12010	1.01	0.02	0.10	0.9260956	0.9678483	-6.55	FALSE
253704_at	X-Pro dipeptidase - like protein (	---	AT4G29490	-1.01	-0.02	-0.10	0.9263628	0.9679991	-6.55	FALSE
266186_at	unknown protein	AERO2	AT2G38960	-1.01	-0.01	-0.10	0.9264107	0.9679991	-6.55	FALSE
253146_at	putative protein predicted protei	---	AT4G35590	-1.01	-0.02	-0.10	0.9264952	0.9679991	-6.55	FALSE
252816_at	putative protein several putative	---	AT3G42550	1.01	0.01	0.10	0.9264082	0.9679991	-6.55	FALSE
249617_at	receptor protein kinase-like prote	---	AT5G37450	-1.01	-0.02	-0.10	0.9264865	0.9679991	-6.55	FALSE
262748_at	lipase, putative contains Pfam p	---	AT1G28610	1.02	0.03	0.10	0.926747	0.9682058	-6.55	FALSE
250643_at	putative protein similar to unknov	---	AT5G06780	-1.01	-0.01	-0.10	0.926778	0.9682058	-6.55	FALSE
255252_at	contains similarity to Gossypium	---	AT4G04990	1.01	0.01	0.10	0.9268946	0.9682623	-6.55	FALSE
247140_at	putative protein similar to unknov	---	AT5G66250	1.01	0.01	0.10	0.9269594	0.9682623	-6.55	FALSE
250269_at	anthranilate phosphoribosyltrans	---	AT5G12970	-1.01	-0.02	-0.10	0.9269386	0.9682623	-6.55	FALSE
266984_at	unknown protein ; supported by	---	AT2G39570	1.02	0.03	0.09	0.9271167	0.9682698	-6.55	TRUE

260458_at	unknown protein	---	AT1G68250	1.01	0.02	0.09	0.9271558	0.9682698	-6.55	FALSE
254604_at	cadmium-induced protein	---	AT4G19070	1.01	0.02	0.09	0.9271788	0.9682698	-6.55	FALSE
267189_at	putative methionine aminopeptid	MAP2A	AT2G44180	-1.02	-0.03	-0.09	0.9270917	0.9682698	-6.55	FALSE
266996_at	putative cytochrome P450 ;supp	CYP710A2	AT2G34490	1.06	0.09	0.10	0.927033	0.9682698	-6.55	FALSE
266937_at	hypothetical protein predicted by	---	AT2G18930	-1.01	-0.02	-0.09	0.9272836	0.9683349	-6.55	FALSE
247916_at	adenosylmethionine-8-amino-7-c	BIO1	AT5G57590	-1.01	-0.02	-0.09	0.9273479	0.9683577	-6.55	FALSE
252967_at	amidophosphoribosyltransferase	ATASE3	AT4G38880	-1.01	-0.02	-0.09	0.9275491	0.9685234	-6.55	FALSE
257531_at	putative RNA-binding protein co	---	AT3G07250	1.01	0.01	0.09	0.9275951	0.9685272	-6.55	FALSE
257880_at	AMP-binding protein, putative c	AAE7	AT3G16910	-1.02	-0.03	-0.09	0.9278327	0.9685994	-6.55	TRUE
258267_at	putative delta 9 desaturase simil	---	AT3G15870	-1.01	-0.01	-0.09	0.9278766	0.9685994	-6.55	FALSE
259040_at	putative glutathione transferase s	ATGSTU8	AT3G09270	1.05	0.07	0.09	0.9278041	0.9685994	-6.55	FALSE
264334_at	calcium-dependent protein kinas	CPK19	AT1G61950	1.01	0.01	0.09	0.9278762	0.9685994	-6.55	FALSE
255167_at	putative protein hypothetical pr	---	---	-1.01	-0.01	-0.09	0.9278452	0.9685994	-6.55	FALSE
246582_at	hypothetical protein predicted by	---	AT1G31750	1.02	0.04	0.09	0.9279977	0.9686815	-6.55	FALSE
247039_at	putative protein contains similarit	ATEB1C	AT5G67270	1.01	0.02	0.09	0.9282079	0.9687679	-6.55	FALSE
263238_at	putative auxin-induced protein	---	AT2G16580	-1.01	-0.01	-0.09	0.9281923	0.9687679	-6.55	FALSE
249656_at	putative protein hypothetical prot	---	AT5G37130	1.01	0.01	0.09	0.9281573	0.9687679	-6.55	FALSE
248290_at	Ca2+-transporting ATPase-like p	---	AT5G53010	1.01	0.02	0.09	0.9283927	0.9689165	-6.55	FALSE
251314_at	putative protein several hypothet	---	AT3G61180	-1.01	-0.01	-0.09	0.9285098	0.9689943	-6.55	FALSE
246900_at	putative protein flavin-containing	YUC6	AT5G25620	1.01	0.02	0.09	0.9287393	0.9691008	-6.55	FALSE
255661_at	hypothetical protein	ULP1B	AT4G00690	-1.01	-0.01	-0.09	0.9286769	0.9691008	-6.55	FALSE
250046_at	putative protein predicted protei	---	AT5G17720	-1.01	-0.02	-0.09	0.9287084	0.9691008	-6.55	FALSE
254942_at	putative protein predicted protei	---	AT4G10880	1.01	0.01	0.09	0.9287834	0.9691025	-6.55	FALSE
254902_at	putative protein several hypothet	---	AT4G11550	-1.01	-0.01	-0.09	0.9288969	0.9691766	-6.55	FALSE
259800_at	Expressed protein ; supported by	---	AT1G72175	-1.01	-0.02	-0.09	0.929012	0.9692524	-6.55	TRUE
246393_at	phosphoglycerate kinase, putati	---	AT1G58150	1.01	0.02	0.09	0.9290646	0.9692629	-6.55	FALSE
266286_at	putative tropinone reductase	---	AT2G29160 //	1.01	0.02	0.09	0.9291557	0.9692692	-6.55	FALSE
264387_at	putative growth regulator protein	---	AT1G11990	1.01	0.02	0.09	0.9291288	0.9692692	-6.55	FALSE
258590_at	putative response regulator prot	ARR22	AT3G04280	-1.01	-0.01	-0.09	0.9292762	0.9693304	-6.55	FALSE
252726_at	putative protein predicted protei	---	---	-1.02	-0.02	-0.09	0.9292993	0.9693304	-6.55	FALSE
248122_at	unknown protein	---	AT5G54700	1.01	0.01	0.09	0.9293802	0.9693705	-6.55	FALSE
256811_at	serine/threonine-specific protein	---	AT3G21340	1.01	0.01	0.09	0.9294801	0.9693939	-6.55	FALSE
248370_at	homeodomain transcription facto	HDG7	AT5G52170	1.01	0.02	0.09	0.9295171	0.9693939	-6.55	FALSE
263163_at	fructokinase, putative predicted	FZL	AT1G03160	1.02	0.03	0.09	0.9295302	0.9693939	-6.55	FALSE
248059_at	putative protein similar to unknov	TRN1	AT5G55540	-1.02	-0.03	-0.09	0.9296146	0.9694376	-6.55	FALSE

251376_at	scarecrow - like protein scarecrc	---	AT3G60630	-1.02	-0.02	-0.09	0.9298617	0.9694493	-6.55	FALSE
249711_at	putative protein contains similarit	---	AT5G35680	-1.01	-0.02	-0.09	0.929708	0.9694493	-6.55	FALSE
246473_at	putative protein cathepsin L-like	---	AT5G17140	-1.01	-0.02	-0.09	0.9298193	0.9694493	-6.55	FALSE
261267_at	unknown protein ;supported by fu	---	AT1G26750	-1.01	-0.02	-0.09	0.9297242	0.9694493	-6.55	FALSE
247181_at	putative protein similar to unknov	---	AT5G65370	-1.01	-0.01	-0.09	0.9298672	0.9694493	-6.55	FALSE
266676_s_a	hypothetical protein predicted by	---	AT2G29605 ///	1.01	0.01	0.09	0.9298808	0.9694493	-6.55	FALSE
245996_at	putative protein predicted non-LT	---	---	-1.01	-0.01	-0.09	0.9299808	0.969465	-6.55	FALSE
266143_at	Expressed protein ; supported by	---	AT2G38905	1.01	0.02	0.09	0.9299624	0.969465	-6.55	FALSE
251555_at	shatterproof 1 (SHP1)/ agamous	SHP1	AT3G58780	1.01	0.01	0.09	0.9300738	0.9695176	-6.55	FALSE
254498_at	membrane-associated salt-induc	EMB1025	AT4G20090	-1.02	-0.02	-0.09	0.9301814	0.9695411	-6.55	FALSE
253771_at	hypothetical protein ;supported b	---	AT4G28430	-1.01	-0.02	-0.09	0.9301672	0.9695411	-6.55	FALSE
266940_at	unknown protein	---	AT2G18970	-1.01	-0.02	-0.09	0.9302822	0.9696018	-6.55	FALSE
259570_at	hypothetical protein	COR47	AT1G20440	1.02	0.03	0.09	0.9305511	0.9696321	-6.55	FALSE
257894_at	unknown protein ; supported by c	---	AT3G17100	1.02	0.03	0.09	0.9306088	0.9696321	-6.55	FALSE
246410_at	hypothetical protein predicted by	---	AT1G57760	-1.01	-0.01	-0.09	0.9304045	0.9696321	-6.55	FALSE
263829_at	unknown protein	---	AT2G40435	1.03	0.04	0.09	0.9305673	0.9696321	-6.55	FALSE
248979_at	putative protein contains similarit	AtPP2-A6	AT5G45080	-1.01	-0.02	-0.09	0.9305283	0.9696321	-6.55	FALSE
259867_at	hypothetical protein predicted by	---	AT1G76740	1.01	0.01	0.09	0.9304194	0.9696321	-6.55	FALSE
259797_at	unknown protein	---	---	1.01	0.02	0.09	0.9305927	0.9696321	-6.55	FALSE
261916_at	jasmonic acid, putative similar to	anac028	AT1G65910	-1.01	-0.02	-0.09	0.9306716	0.9696533	-6.55	FALSE
252604_at	high-affinity nitrate transporter -	NRT2.6	AT3G45060	-1.03	-0.05	-0.09	0.9308012	0.969728	-6.55	TRUE
263095_at	Ac-like transposase related to Ac	---	AT2G16040	1.01	0.01	0.09	0.9308708	0.969728	-6.55	FALSE
247301_at	DNA topoisomerase III	---	AT5G63920	1.02	0.02	0.09	0.9308655	0.969728	-6.55	FALSE
246411_at	hypothetical protein contains sim	---	AT1G57770	-1.02	-0.03	-0.09	0.9310901	0.9697584	-6.55	TRUE
246891_at	putative protein various predicte	---	AT5G25490	1.01	0.01	0.09	0.9310073	0.9697584	-6.55	FALSE
253933_at	hypothetical protein	---	AT4G26820	1.01	0.02	0.09	0.9310239	0.9697584	-6.55	FALSE
251001_at	putative protein	---	AT5G02670	1.01	0.02	0.09	0.9311552	0.9697584	-6.55	FALSE
253904_at	NWMU1 - 2S albumin 1 precurso	---	AT4G27140	-1.01	-0.01	-0.09	0.9311143	0.9697584	-6.55	FALSE
252568_at	receptor-like protein kinase rece	---	AT3G45410	1.02	0.02	0.09	0.9310339	0.9697584	-6.55	FALSE
249477_s_a	germin - like protein probable ge	---	AT5G38930 ///	1.01	0.01	0.09	0.9312403	0.9698028	-6.55	FALSE
265294_at	Mutator-like transposase similar t	---	---	1.01	0.02	0.09	0.9313865	0.9699108	-6.55	FALSE
245630_at	hypothetical protein similar to put	---	AT1G25360	1.01	0.01	0.09	0.9316278	0.9700292	-6.55	FALSE
259905_s_a	hypothetical protein predicted by	---	AT1G74130 ///	1.01	0.01	0.09	0.9316081	0.9700292	-6.55	FALSE
250630_at	hypothetical protein	---	AT5G07400	-1.01	-0.02	-0.09	0.9316067	0.9700292	-6.55	FALSE
259772_at	hypothetical protein predicted by	---	AT1G29480	1.01	0.01	0.09	0.9316826	0.970042	-6.55	FALSE

249823_s_a	putative protein contains similarit	---	AT5G23350 /.	1.01	0.02	0.09	0.9318219	0.9700543	-6.55	TRUE
249922_at	aluminium-induced protein - like	AILP1	AT5G19140	-1.01	-0.01	-0.09	0.9318023	0.9700543	-6.55	FALSE
247837_at	N-hydroxycinnamoyl/benzoyltran	---	AT5G57840	1.01	0.02	0.09	0.931822	0.9700543	-6.55	FALSE
258368_at	subtilisin-like serine protease cor	---	AT3G14240	-1.02	-0.03	-0.09	0.932097	0.970252	-6.55	TRUE
265277_at	unknown protein ;supported by f	---	AT2G28410	-1.03	-0.04	-0.09	0.9320966	0.970252	-6.55	FALSE
246109_at	hypothetical protein (fragment?)	---	AT5G20120	-1.01	-0.02	-0.09	0.9321521	0.9702651	-6.55	FALSE
245336_at	Expressed protein ; supported by	---	AT4G16515	1.04	0.06	0.09	0.9322963	0.9703709	-6.55	TRUE
248378_at	unknown protein ;supported by f	---	AT5G51840	1.01	0.01	0.09	0.9323829	0.9704168	-6.55	FALSE
250467_at	trehalose-6-phosphate phospha	---	AT5G10100	1.01	0.01	0.09	0.9324265	0.9704179	-6.55	FALSE
261374_at	hypothetical protein contains thio	---	AT1G52990	1.01	0.01	0.09	0.9325316	0.9704667	-6.55	FALSE
263908_at	hypothetical protein predicted by	---	AT2G36480	-1.01	-0.01	-0.09	0.9325837	0.9704667	-6.55	FALSE
246254_at	MAP kinase like protein	ATMPK14	AT4G36450	-1.02	-0.02	-0.09	0.9326011	0.9704667	-6.55	FALSE
249887_at	putative protein similar to unknov	---	AT5G22310	-1.03	-0.04	-0.09	0.9328263	0.9705542	-6.55	FALSE
252732_at	putative protein predicted protei	---	---	1.01	0.01	0.09	0.9328554	0.9705542	-6.55	FALSE
261137_at	auxin-induced protein, putative s	---	AT1G19830	1.01	0.01	0.09	0.9327968	0.9705542	-6.55	FALSE
260340_at	putative dihydropterin pyrophosp	---	AT1G69190	1.01	0.01	0.09	0.9328193	0.9705542	-6.55	FALSE
258950_at	unknown protein contains Pfam p	MBD9	AT3G01460	1.01	0.01	0.09	0.9329499	0.9705641	-6.55	FALSE
263964_at	putative CCHC-type zinc finger p	---	AT2G12880	-1.01	-0.02	-0.09	0.9329438	0.9705641	-6.55	FALSE
252702_at	putative protein predicted protei	---	---	-1.01	-0.01	-0.09	0.9330285	0.9706016	-6.55	FALSE
255985_at	putative protein contains similarit	---	AT1G34150	1.01	0.01	0.09	0.9330993	0.9706309	-6.55	FALSE
262929_at	hypothetical protein ;supported b	---	AT1G65720	-1.01	-0.02	-0.09	0.9332808	0.9707754	-6.55	FALSE
AFFX-Athal	Arabidopsis thaliana /REF=M641	GAPC1	---	1.02	0.02	0.09	0.9333257	0.9707779	-6.55	TRUE
248601_at	putative protein contains similarit	---	AT5G49400	1.01	0.01	0.09	0.9333905	0.9708011	-6.55	FALSE
264087_at	hypothetical protein predicted by	emb1381	AT2G31340	-1.01	-0.01	-0.09	0.9335706	0.9708555	-6.55	FALSE
256037_at	hypothetical protein predicted by	---	AT1G19160	-1.01	-0.02	-0.09	0.9335597	0.9708555	-6.55	FALSE
266023_at	copia-like retroelement pol polyp	---	---	1.01	0.01	0.09	0.9335483	0.9708555	-6.55	FALSE
254596_at	putative protein proline-rich prot	---	AT4G18975	-1.01	-0.01	-0.09	0.9336806	0.9709257	-6.55	FALSE
256325_at	hypothetical protein	---	AT3G02330	-1.01	-0.02	-0.09	0.9337808	0.9709466	-6.55	FALSE
265921_at	putative C2H2-type zinc finger pr	---	AT2G18490	-1.01	-0.01	-0.09	0.9337859	0.9709466	-6.55	FALSE
257534_at	hypothetical protein predicted by	---	AT3G09670	1.01	0.01	0.09	0.9342592	0.9711679	-6.55	FALSE
256282_at	unknown protein	---	AT3G12550	-1.01	-0.02	-0.09	0.9342116	0.9711679	-6.55	FALSE
264541_at	hypothetical protein predicted by	---	AT1G55660	1.01	0.02	0.09	0.934161	0.9711679	-6.55	FALSE
246054_at	putative protein predicted protei	---	AT5G08360	1.01	0.01	0.09	0.9340875	0.9711679	-6.55	FALSE
245090_at	putative integral membrane prote	---	AT2G40900	-1.01	-0.02	-0.09	0.9342793	0.9711679	-6.55	FALSE
267351_at	unknown protein	NRPD1B	AT2G40030	1.01	0.01	0.09	0.9342967	0.9711679	-6.55	FALSE

256418_at	hypothetical protein	---	AT3G06160	-1.01	-0.01	-0.09	0.9341233	0.9711679	-6.55	FALSE
260529_at	putative chloroplast protein CP12	CP12-1	AT2G47400	1.01	0.01	0.09	0.9343396	0.9711682	-6.55	FALSE
259865_at	putative casein kinase I similar to	CKL2	AT1G72710	-1.01	-0.02	-0.09	0.9343898	0.9711762	-6.55	FALSE
261830_at	protein kinase, putative similar to	---	AT1G10620	-1.01	-0.01	-0.09	0.9345213	0.9712686	-6.55	FALSE
250254_at	24-sterol C-methyltransferase ; s	SMT1	AT5G13710	-1.01	-0.02	-0.09	0.9345787	0.9712839	-6.55	TRUE
267394_s_a	putative cellulase	AtGH9B9	AT2G44540 /	1.01	0.01	0.09	0.9346963	0.9713177	-6.55	FALSE
251946_at	putative protein predicted protein	---	AT3G53540	-1.04	-0.05	-0.09	0.934687	0.9713177	-6.55	FALSE
258846_at	unknown protein ; supported by	---	AT3G03070	-1.01	-0.01	-0.08	0.9348376	0.9714202	-6.55	FALSE
245619_at	hypothetical protein	---	AT4G13990	1.01	0.02	0.08	0.9349704	0.9714697	-6.55	FALSE
253639_at	putative protein component of ar	---	AT4G30550	-1.01	-0.02	-0.08	0.93495	0.9714697	-6.55	FALSE
245869_at	hypothetical protein predicted by	---	AT1G26330	-1.01	-0.01	-0.08	0.9350756	0.9715348	-6.55	FALSE
260175_at	neutral invertase, putative simila	---	AT1G72000	1.01	0.01	0.08	0.9351303	0.9715474	-6.55	FALSE
257151_at	blue copper protein, putative sim	---	AT3G27200	1.01	0.02	0.08	0.9355054	0.9718928	-6.55	FALSE
265910_at	putative vacuolar ATP synthase	---	AT2G25610	1.01	0.01	0.08	0.9359871	0.9723047	-6.55	FALSE
249444_at	putative protein S-locus-specific	---	AT5G39370	1.01	0.01	0.08	0.9359466	0.9723047	-6.55	FALSE
246241_at	patatin-like protein	PLP4	AT4G37050	1.01	0.02	0.08	0.9361032	0.9723367	-6.55	FALSE
247535_at	transcriptional activator - like pro	---	AT5G61620	1.01	0.02	0.08	0.9360644	0.9723367	-6.55	FALSE
251284_at	hypothetical protein	---	AT3G61840	-1.01	-0.02	-0.08	0.9362039	0.972397	-6.55	FALSE
253493_at	putative protein various predicted	ENP	AT4G31820	1.02	0.02	0.08	0.9364242	0.9725372	-6.55	TRUE
246839_at	putative protein	---	AT5G26720	-1.01	-0.01	-0.08	0.9363991	0.9725372	-6.55	FALSE
259269_at	putative pectate lyase similar to p	---	AT3G01270	1.01	0.01	0.08	0.9364879	0.9725592	-6.55	FALSE
267163_at	unknown protein	---	AT2G37520	-1.01	-0.02	-0.08	0.9367252	0.9726134	-6.55	FALSE
258536_at	Rab escort protein, putative simi	---	AT3G06540	-1.01	-0.02	-0.08	0.9366064	0.9726134	-6.55	FALSE
258177_at	ubiquitin-regulatory protein, puta	---	AT3G21660	-1.01	-0.01	-0.08	0.9367182	0.9726134	-6.55	FALSE
261441_at	NAM protein, putative similar to	ANAC010	AT1G28470	1.02	0.02	0.08	0.9367533	0.9726134	-6.55	FALSE
249382_at	putative protein predicted protein	---	AT5G40050	-1.01	-0.01	-0.08	0.9367352	0.9726134	-6.55	FALSE
245257_at	calmodulin ; supported by cDNA:	CAM8	AT4G14640	-1.01	-0.01	-0.08	0.9368691	0.972645	-6.55	FALSE
251381_at	secretory protein - like 33 kDa s	PDLP8	AT3G60720 /	-1.02	-0.03	-0.08	0.9368678	0.972645	-6.55	FALSE
266130_at	putative transcription activator	---	AT2G44980	1.01	0.02	0.08	0.9370044	0.9727413	-6.55	FALSE
248343_at	putative protein contains similarit	AtMYB19	AT5G52260	-1.01	-0.01	-0.08	0.9370512	0.9727455	-6.55	FALSE
249483_at	Expressed protein ; supported by	---	AT5G38895	-1.01	-0.02	-0.08	0.9371888	0.9728118	-6.55	FALSE
263886_at	hypothetical protein predicted by	TKI1	AT2G36960	-1.01	-0.01	-0.08	0.9372111	0.9728118	-6.55	FALSE
251577_at	putative protein several hypothet	---	AT3G58350	1.01	0.02	0.08	0.937243	0.9728118	-6.55	FALSE
261058_at	histone, putative similar to histor	HTR12	AT1G01370	1.01	0.01	0.08	0.9375087	0.972954	-6.55	FALSE
246608_at	putative protein various predicte	---	AT5G35380	1.01	0.02	0.08	0.937451	0.972954	-6.55	FALSE

258121_s_a	putative geranylgeranyl pyrophos	GGPS3	AT3G14530 /.	1.01	0.02	0.08	0.9375506	0.972954	-6.55	FALSE
251377_at	putative protein	---	AT3G60650	-1.01	-0.01	-0.08	0.9375448	0.972954	-6.55	FALSE
258741_at	Lon protease, putative similar to	LON4	AT3G05790	-1.01	-0.01	-0.08	0.9376533	0.9730163	-6.55	FALSE
253418_at	putative protein tom-1B protein,	---	AT4G32760	1.01	0.01	0.08	0.9377945	0.9731185	-6.55	FALSE
257419_at	hypothetical protein predicted by	---	AT1G30800	1.01	0.01	0.08	0.9379767	0.9732634	-6.55	FALSE
257134_at	hypothetical protein similar to oxi	---	AT3G12870	1.01	0.02	0.08	0.9381919	0.973361	-6.55	FALSE
257993_at	hypothetical protein similar to hy	---	AT3G19890	-1.01	-0.01	-0.08	0.9381454	0.973361	-6.55	FALSE
246872_at	extensin - like protein hydroxypr	---	AT5G26080	1.01	0.02	0.08	0.9381989	0.973361	-6.55	FALSE
259567_at	hypothetical protein	---	AT1G20500	1.01	0.01	0.08	0.938339	0.9734622	-6.55	FALSE
260559_at	putative polygalacturonase	---	AT2G43860	-1.01	-0.02	-0.08	0.9384347	0.9734874	-6.55	FALSE
262638_at	oxidoreductase, putative contain	---	AT1G06650	-1.01	-0.01	-0.08	0.938534	0.9734874	-6.55	FALSE
245241_at	hypothetical protein contains sim	---	AT1G44478	1.01	0.01	0.08	0.9384926	0.9734874	-6.55	FALSE
264225_at	hypothetical protein predicted by	---	AT1G67420	-1.01	-0.02	-0.08	0.9384663	0.9734874	-6.55	FALSE
253033_at	putative protein aminoacylase I	---	AT4G38220	-1.01	-0.01	-0.08	0.9386718	0.973586	-6.55	FALSE
259397_at	hypothetical protein predicted by	---	AT1G17680	-1.01	-0.01	-0.08	0.9387857	0.9736156	-6.55	FALSE
253508_at	putative protein various predicte	---	AT4G31680	-1.01	-0.01	-0.08	0.9387459	0.9736156	-6.55	FALSE
262240_at	Pto kinase interactor 1, putative	---	AT1G48220	-1.01	-0.01	-0.08	0.9389864	0.9737795	-6.55	FALSE
267009_at	unknown protein	---	AT2G39260	-1.01	-0.01	-0.08	0.9392674	0.973809	-6.55	FALSE
259331_at	putative auxin-induced protein si	---	AT3G03840	1.01	0.02	0.08	0.939271	0.973809	-6.55	FALSE
253888_at	hypothetical protein	ISI1	AT4G27750	-1.01	-0.01	-0.08	0.9392416	0.973809	-6.55	FALSE
249378_at	putative protein microtubule-ass	---	AT5G40450	-1.01	-0.02	-0.08	0.9391909	0.973809	-6.55	FALSE
248593_at	pectin methylesterase ;supporte	---	AT5G49180	1.01	0.02	0.08	0.9391651	0.973809	-6.55	FALSE
260578_at	unknown protein predicted by ge	---	AT2G47350	-1.01	-0.01	-0.08	0.9390789	0.973809	-6.55	FALSE
264555_at	hypothetical protein predicted by	---	AT1G09360	-1.01	-0.01	-0.08	0.9393164	0.9738118	-6.55	FALSE
261430_at	hypothetical protein predicted by	---	AT1G18830	-1.01	-0.02	-0.08	0.9394999	0.9738575	-6.55	FALSE
262936_at	hypothetical protein similar to put	ATCHX2	AT1G79400	-1.01	-0.02	-0.08	0.9395305	0.9738575	-6.55	FALSE
260382_at	unknown protein	---	AT1G73850	-1.01	-0.02	-0.08	0.9395312	0.9738575	-6.55	FALSE
263524_x_a	hypothetical protein predicted by	---	---	-1.01	-0.02	-0.08	0.9394566	0.9738575	-6.55	FALSE
255771_at	hypothetical protein contains sim	---	AT1G18550	-1.01	-0.01	-0.08	0.9396885	0.973963	-6.55	FALSE
267191_at	similar to Mlo proteins from H. vu	MLO15	AT2G44110	-1.01	-0.02	-0.08	0.9397185	0.973963	-6.55	FALSE
258074_at	unknown protein	---	AT3G25890	-1.02	-0.03	-0.08	0.939794	0.9739828	-6.55	TRUE
262556_at	hypothetical protein	---	AT1G31370	1.01	0.01	0.08	0.939823	0.9739828	-6.55	FALSE
261340_at	hypothetical protein predicted by	APUM9	AT1G35730	1.01	0.01	0.08	0.9398768	0.9739944	-6.55	FALSE
248276_at	EspB-like protein	YSL3	AT5G53550	1.01	0.02	0.08	0.9400827	0.9740308	-6.55	TRUE
263112_at	unknown protein Strong similarity	---	AT1G03080	-1.01	-0.01	-0.08	0.9400549	0.9740308	-6.55	FALSE

251675_at	helicase-like protein DNA helica	INO80	AT3G57300	1.01	0.01	0.08	0.9399877	0.9740308	-6.55	FALSE
246357_x_a	hypothetical protein	---	---	-1.01	-0.01	-0.08	0.9400699	0.9740308	-6.55	FALSE
266427_at	hypothetical protein predicted by	---	AT2G07170	-1.01	-0.02	-0.08	0.9403707	0.9742849	-6.55	FALSE
264041_at	MADS-box protein (AGL3) ; sup	ספט-04	AT2G03710	-1.02	-0.03	-0.08	0.9405261	0.9744016	-6.55	FALSE
250677_at	putative protein similar to unknov	---	AT5G06520	1.01	0.01	0.08	0.9405855	0.9744189	-6.55	FALSE
258877_at	putative expansin precursor simil	ATEXPA13	AT3G03220	1.02	0.03	0.08	0.9408879	0.9745109	-6.55	TRUE
267341_at	hypothetical protein predicted by	---	AT2G44200	-1.01	-0.02	-0.08	0.940797	0.9745109	-6.55	FALSE
261847_at	hypothetical protein predicted by	---	AT1G11560	-1.01	-0.02	-0.08	0.9408029	0.9745109	-6.55	FALSE
259843_at	hypothetical protein predicted by	---	AT1G73570	1.01	0.02	0.08	0.9407781	0.9745109	-6.55	FALSE
249169_at	putative protein strong similarity t	---	AT5G42880	1.01	0.01	0.08	0.9408828	0.9745109	-6.55	FALSE
261399_at	receptor protein kinase, putative	---	AT1G79620	1.01	0.01	0.08	0.9410369	0.9745936	-6.55	FALSE
254514_at	hypothetical protein	---	AT4G20250	-1.01	-0.02	-0.08	0.9410533	0.9745936	-6.55	FALSE
257472_at	hypothetical protein predicted by	---	AT1G56040	1.01	0.01	0.08	0.9412159	0.9747178	-6.55	FALSE
251092_at	putative protein ;supported by fu	---	AT5G01470	-1.01	-0.01	-0.08	0.9412804	0.9747403	-6.55	FALSE
261063_at	transcription factor scarecrow-lik	---	AT1G07520	1.03	0.05	0.08	0.9413469	0.9747649	-6.55	FALSE
248146_at	translation initiation factor-like pr	---	AT5G54940	1.01	0.01	0.08	0.9414673	0.9748453	-6.55	FALSE
253045_at	Expressed protein ; supported by	---	AT4G37445	1.01	0.02	0.08	0.9417066	0.9750489	-6.55	FALSE
245827_at	disease resistance protein RPS4	---	AT1G57830	1.01	0.01	0.08	0.9418879	0.9750596	-6.55	FALSE
257158_at	3-hydroxyisobutyryl-coenzyme A	---	AT3G24360	1.01	0.01	0.08	0.941834	0.9750596	-6.55	FALSE
248661_at	putative protein contains similarit	AGL80	AT5G48670	1.01	0.02	0.08	0.9418563	0.9750596	-6.55	FALSE
264425_at	serine/threonine protein kinase,	---	AT1G61750	1.01	0.01	0.08	0.9417847	0.9750596	-6.55	FALSE
246584_at	putative protein predicted protei	---	AT5G14730	-1.03	-0.04	-0.07	0.9429967	0.9751453	-6.55	TRUE
258298_at	unknown protein ; supported by	---	AT3G23300	1.01	0.02	0.07	0.9426859	0.9751453	-6.55	FALSE
255077_at	putative protein	---	AT4G09150	1.01	0.02	0.08	0.9421284	0.9751453	-6.55	FALSE
260176_at	unknown protein similar to Pi sta	---	AT1G71950	1.01	0.01	0.08	0.9423239	0.9751453	-6.55	FALSE
263526_at	hypothetical protein predicted by	---	AT2G24830	1.01	0.01	0.08	0.9423871	0.9751453	-6.55	FALSE
263037_at	conserved hypothetical protein	---	AT1G23230	-1.01	-0.01	-0.07	0.9428182	0.9751453	-6.55	FALSE
252769_at	arabinose kinase - like protein p	---	AT3G42850	1.01	0.01	0.07	0.9429403	0.9751453	-6.55	FALSE
254993_at	putative protein kinase	---	AT4G10730	-1.01	-0.01	-0.07	0.9424522	0.9751453	-6.55	FALSE
267544_at	putative cytochrome b5	CB5-B	AT2G32720	-1.02	-0.03	-0.08	0.9422467	0.9751453	-6.55	FALSE
247941_at	putative protein strong similarity t	---	AT5G57200	-1.01	-0.01	-0.07	0.9429494	0.9751453	-6.55	FALSE
246382_at	hypothetical protein	---	---	1.01	0.01	0.08	0.9421747	0.9751453	-6.55	FALSE
262548_at	unknown protein contains similar	AGO2	AT1G31280	1.01	0.01	0.07	0.9428874	0.9751453	-6.55	FALSE
254161_at	hypothetical protein ;supported b	---	AT4G24370	1.01	0.01	0.08	0.9422196	0.9751453	-6.55	FALSE
248262_at	Avr9 elicitor response protein-like	---	AT5G53340	1.01	0.02	0.07	0.94275	0.9751453	-6.55	FALSE

267053_s_a	peroxidase	---	AT2G38380 /.	-1.02	-0.03	-0.07	0.9429577	0.9751453	-6.55	FALSE
245208_at	lateral root primordia (LRP1)	LRP1	AT5G12330	-1.01	-0.01	-0.07	0.942505	0.9751453	-6.55	FALSE
249853_at	farnesyl cysteine carboxyl methy	ATSTE14A	AT5G23320	-1.01	-0.01	-0.07	0.9424314	0.9751453	-6.55	FALSE
260611_at	putative beta-1,3-glucanase, C t	---	AT2G43670	1.01	0.01	0.07	0.9428461	0.9751453	-6.55	FALSE
263343_at	putative replication protein A1	---	---	-1.01	-0.01	-0.07	0.9424669	0.9751453	-6.55	FALSE
258246_s_a	hypothetical protein similar to put	---	---	-1.01	-0.01	-0.07	0.9429453	0.9751453	-6.55	FALSE
259820_at	subtilisin-like serine protease cor	---	AT1G66210	1.01	0.01	0.07	0.9426471	0.9751453	-6.55	FALSE
252809_at	putative protein various predicte	---	---	1.01	0.01	0.08	0.9422064	0.9751453	-6.55	FALSE
263277_at	hypothetical protein predicted by	---	AT2G14110	-1.01	-0.01	-0.07	0.9427607	0.9751453	-6.55	FALSE
246276_at	Cu2+-transporting ATPase-like p	HMA1	AT4G37270	1.01	0.01	0.07	0.9429324	0.9751453	-6.55	FALSE
261114_at	bZIP transcription factor ATB2, p	AtbZIP44	AT1G75388 /.	-1.05	-0.07	-0.07	0.9430437	0.9751497	-6.55	FALSE
259437_at	protein serine/threonine kinase,	---	AT1G01540	-1.02	-0.02	-0.07	0.9434353	0.9754219	-6.55	TRUE
247000_at	casein kinase II alpha subunit ; s	CKA1	AT5G67380	1.01	0.01	0.07	0.9434116	0.9754219	-6.55	FALSE
251732_at	putative protein prenylated Rab	PRA1.B1	AT3G56110	-1.01	-0.01	-0.07	0.9433884	0.9754219	-6.55	FALSE
253209_at	putative protein membrane-asso	---	AT4G34830	-1.01	-0.02	-0.07	0.943563	0.9754656	-6.55	FALSE
259203_at	hypothetical protein predicted by	---	AT3G09130	-1.01	-0.01	-0.07	0.94353	0.9754656	-6.55	FALSE
262709_at	unknown protein ESTs gb|F154	SYP51	AT1G16240	-1.01	-0.01	-0.07	0.9438971	0.9757225	-6.55	FALSE
249102_at	patatin-like protein	---	AT5G43590	1.01	0.01	0.07	0.9438656	0.9757225	-6.55	FALSE
251273_at	serine/threonine-protein kinase-	---	AT3G61960	-1.01	-0.02	-0.07	0.944074	0.9757772	-6.55	FALSE
255104_at	Expressed protein ; supported by	SAH7	AT4G08685	-1.03	-0.04	-0.07	0.9440126	0.9757772	-6.55	FALSE
246866_at	putative protein various predicte	---	AT5G25960	1.01	0.01	0.07	0.9440784	0.9757772	-6.55	FALSE
256003_at	Ta11 non-LTR retroelement prot	---	AT3G31430	1.01	0.01	0.07	0.944236	0.9758331	-6.55	FALSE
255831_at	hypothetical protein predicted by	---	AT2G33350	-1.01	-0.01	-0.07	0.9442608	0.9758331	-6.55	FALSE
257845_at	unknown protein GC donor splice	---	AT3G28430	1.01	0.01	0.07	0.944252	0.9758331	-6.55	FALSE
264089_at	actin depolymerizing factor 6 ;su	ADF6	AT2G31200	-1.01	-0.02	-0.07	0.9443158	0.9758458	-6.55	FALSE
249758_at	putative protein similar to unknov	---	AT5G24350	1.01	0.02	0.07	0.9443886	0.9758768	-6.55	FALSE
252776_at	putative protein predicted protei	---	AT3G42940	1.01	0.01	0.07	0.9448131	0.97623	-6.55	FALSE
257272_at	unknown protein ; supported by	---	AT3G28130	1.01	0.01	0.07	0.9448161	0.97623	-6.55	FALSE
246342_at	putative protein male sterility pro	FAR6	AT3G56700	1.01	0.01	0.07	0.9448712	0.9762428	-6.55	FALSE
252096_at	hypothetical protein ; supported	---	AT3G51180	-1.01	-0.02	-0.07	0.9450355	0.9762785	-6.55	FALSE
265116_at	unknown protein ; supported by f	---	AT1G62480	1.04	0.06	0.07	0.9450779	0.9762785	-6.55	FALSE
249771_at	receptor-like protein kinase ; sup	---	AT5G24080	1.01	0.02	0.07	0.9449738	0.9762785	-6.55	FALSE
264273_s_a	hypothetical protein contains sim	---	AT1G60300 /.	1.01	0.02	0.07	0.9451198	0.9762785	-6.55	FALSE
252992_at	putative protein phosphatase-2c	---	AT4G38520	-1.01	-0.02	-0.07	0.9450517	0.9762785	-6.55	FALSE
259638_at	coatomer complex subunit, puta	---	AT1G52360	-1.01	-0.01	-0.07	0.9452484	0.9763231	-6.55	FALSE

247116_at	Mlo protein-like ; supported by cI	MLO10	AT5G65970	1.01	0.01	0.07	0.9452486	0.9763231	-6.55	FALSE
267549_at	hypothetical protein predicted by	---	AT2G32640	1.02	0.03	0.07	0.9455412	0.9764939	-6.55	TRUE
264602_at	putative Ser/Thr protein kinase s	---	AT1G04700	1.01	0.01	0.07	0.9455116	0.9764939	-6.55	FALSE
259101_at	hypothetical protein predicted by	---	AT3G11640	1.01	0.01	0.07	0.9455692	0.9764939	-6.55	FALSE
248156_at	unknown protein	---	AT5G54410	1.01	0.01	0.07	0.9455852	0.9764939	-6.55	FALSE
257962_at	hypothetical protein predicted by	---	AT3G19790	1.01	0.02	0.07	0.9460214	0.9769002	-6.55	FALSE
258407_at	unknown protein similar to unkno	---	AT3G17620	1.01	0.02	0.07	0.9461413	0.9769398	-6.55	FALSE
263719_at	hypothetical protein predicted by	---	AT2G13600	1.01	0.01	0.07	0.9461454	0.9769398	-6.55	FALSE
262194_at	hypothetical protein similar to put	---	AT1G77930	1.01	0.02	0.07	0.9462119	0.9769642	-6.55	FALSE
248895_at	receptor protein kinase	FLS2	AT5G46330	-1.02	-0.03	-0.07	0.9464094	0.9771184	-6.55	TRUE
260114_at	AIG1-like protein similar to AIG1	---	AT1G33880	-1.01	-0.01	-0.07	0.9464897	0.9771184	-6.55	FALSE
261908_at	stig1-like protein similar to Stig1	---	AT1G50650	1.01	0.01	0.07	0.9464529	0.9771184	-6.55	FALSE
253076_at	NAM like protein P.hybrida NAM	ANAC076	AT4G36160	-1.01	-0.01	-0.07	0.9465453	0.9771315	-6.55	FALSE
263909_at	hypothetical protein predicted by	DML1	AT2G36490	-1.01	-0.02	-0.07	0.9467778	0.9772698	-6.55	FALSE
263219_at	putative serine proteinase Strong	---	AT1G30600	-1.01	-0.02	-0.07	0.9468078	0.9772698	-6.55	FALSE
251153_at	putative protein predicted protei	NPL41	AT3G63000	1.01	0.01	0.07	0.9467895	0.9772698	-6.55	FALSE
258062_at	unknown protein ; supported by	---	AT3G26000	-1.01	-0.02	-0.07	0.9470707	0.9773779	-6.55	FALSE
252008_at	hypothetical protein ; supported b	---	AT3G52610	1.01	0.01	0.07	0.947067	0.9773779	-6.55	FALSE
266263_at	putative flavonol sulfotransferase	---	AT2G27570	-1.01	-0.01	-0.07	0.9469663	0.9773779	-6.55	FALSE
256080_at	high mobility group protein (HMG	---	AT1G20690	-1.01	-0.01	-0.07	0.9470839	0.9773779	-6.55	FALSE
250473_at	annexin -like protein annexin (An	ANN6	AT5G10220	1.01	0.01	0.07	0.9471573	0.9774095	-6.55	FALSE
246724_at	putative protein CDPK substrate	---	AT5G29000	1.01	0.01	0.07	0.9475337	0.9776251	-6.55	TRUE
265316_at	unknown protein	---	AT2G20400	1.01	0.02	0.07	0.9475378	0.9776251	-6.55	FALSE
246337_at	putative protein putative integral	CHX12	AT3G44910	-1.01	-0.02	-0.07	0.94748	0.9776251	-6.55	FALSE
261079_s_a	transcription factor IIA large subu	---	AT1G07470 ///	1.01	0.01	0.07	0.9475275	0.9776251	-6.55	FALSE
260003_at	unknown protein ;supported by f	IAR1	AT1G68100	1.01	0.01	0.07	0.9476782	0.9777258	-6.55	FALSE
250374_at	putative protein	EMF1	AT5G11530	1.01	0.02	0.07	0.9478737	0.9778225	-6.55	FALSE
248643_at	putative protein strong similarity t	---	AT5G49130	1.01	0.01	0.07	0.9479434	0.9778225	-6.55	FALSE
250945_at	putative protein	---	AT5G03400	1.01	0.01	0.07	0.9478451	0.9778225	-6.55	FALSE
262720_s_a	hypothetical protein similar to hyp	---	AT1G43600 ///	1.01	0.01	0.07	0.9479276	0.9778225	-6.55	FALSE
256157_at	longevity assurance protein, put	LAG13	AT1G13580	1.01	0.01	0.07	0.9484829	0.9781823	-6.55	FALSE
245847_at	MYB DNA-binding - like protein	MYB64	AT5G11050	-1.01	-0.01	-0.07	0.9485896	0.9781823	-6.55	FALSE
255721_at	unknown protein ;supported by fu	---	AT1G31940	-1.01	-0.01	-0.07	0.9484379	0.9781823	-6.55	FALSE
253106_at	putative protein predicted protei	---	AT4G35870	1.01	0.01	0.07	0.9484887	0.9781823	-6.55	FALSE
247802_at	putative protein RING-H2 zinc fi	ATL63	AT5G58580	-1.01	-0.01	-0.07	0.948429	0.9781823	-6.55	FALSE

247371_at	histone deacetylase ;supported	HDA6	AT5G63110	-1.01	-0.01	-0.07	0.9485743	0.9781823	-6.55	FALSE
255514_s_a	hypothetical protein similar to MN	AGL78	AT5G65330	-1.01	-0.01	-0.07	0.9485924	0.9781823	-6.55	FALSE
250165_at	putative protein many predicted	---	AT5G15290	-1.01	-0.01	-0.07	0.9488156	0.9783683	-6.55	FALSE
248474_at	pyruvate dehydrogenase E1 cor	MAB1	AT5G50850	1.01	0.01	0.07	0.9489803	0.978422	-6.55	FALSE
258135_at	Expressed protein ; supported by	---	AT3G24506	1.01	0.01	0.07	0.948959	0.978422	-6.55	FALSE
248481_at	putative protein similar to unknov	---	AT5G50930	1.01	0.01	0.07	0.9489964	0.978422	-6.55	FALSE
255146_at	putative protein disease resistar	---	AT4G08450	-1.01	-0.01	-0.07	0.9490574	0.9784407	-6.55	FALSE
262627_at	hypothetical protein	---	AT1G06580	-1.01	-0.01	-0.07	0.9491798	0.9784784	-6.55	FALSE
249634_at	putative protein several hypothet	---	---	-1.01	-0.01	-0.07	0.9491748	0.9784784	-6.55	FALSE
265560_at	putative glycine-rich protein	GRP-3	AT2G05520	-1.01	-0.01	-0.07	0.9492438	0.9784974	-6.55	FALSE
256814_at	beta-glucosidase, putative simila	BGLU19	AT3G21370	1.01	0.02	0.07	0.9492841	0.9784974	-6.55	FALSE
267619_at	putative receptor-like protein kina	---	AT2G26730	-1.01	-0.02	-0.07	0.9493378	0.9785086	-6.55	TRUE
245464_at	hypothetical protein	UGLYAH	AT4G17050	-1.01	-0.01	-0.07	0.9495618	0.9786952	-6.55	FALSE
245318_at	Expressed protein ; supported by	---	AT4G16980	-1.05	-0.06	-0.07	0.9496175	0.9787059	-6.55	FALSE
264786_at	putative Ta11-like non-LTR retro	---	AT2G17920	1.01	0.01	0.07	0.9496579	0.9787059	-6.55	FALSE
258925_at	unknown protein similar to hypot	---	AT3G10420	1.01	0.01	0.07	0.9497423	0.9787341	-6.55	FALSE
252461_at	putative protein predicted protei	---	---	1.01	0.01	0.07	0.9497711	0.9787341	-6.55	FALSE
249136_at	putative protein similar to unknov	---	AT5G43180	1.01	0.02	0.07	0.9498778	0.9787556	-6.55	FALSE
262016_at	unknown protein	---	---	1.01	0.01	0.07	0.9498727	0.9787556	-6.55	FALSE
257954_at	putative UDP-glucose glucosyltra	---	AT3G21760	1.01	0.01	0.06	0.9501739	0.9788885	-6.55	FALSE
249041_at	male sterility MS5; pollenless3	---	AT5G44330	-1.01	-0.01	-0.06	0.9500873	0.9788885	-6.55	FALSE
259266_at	hypothetical protein predicted by	---	AT3G01240	1.01	0.01	0.06	0.9501785	0.9788885	-6.55	FALSE
249621_at	putative protein predicted protei	---	AT5G37530	1.01	0.01	0.06	0.950106	0.9788885	-6.55	FALSE
257273_at	hypothetical protein contains Pfa	UVH3	AT3G28030	-1.01	-0.01	-0.06	0.9502262	0.9788935	-6.55	FALSE
253008_at	expansin -like protein expansin (	ATEXPA20	AT4G38210	-1.01	-0.02	-0.06	0.9503042	0.9789297	-6.55	FALSE
251966_at	receptor lectin kinase -like prote	---	AT3G53380	-1.01	-0.01	-0.06	0.9505074	0.9790947	-6.55	FALSE
264066_at	Argonaute (AGO1)-like protein	AGO5	AT2G27880	-1.01	-0.01	-0.06	0.9506042	0.9791502	-6.55	FALSE
254037_at	hypothetical protein hypothetical	ATGDU2	AT4G25760	-1.01	-0.01	-0.06	0.950666	0.9791696	-6.55	FALSE
258431_at	hypothetical protein predicted by	---	AT3G16580	1.01	0.01	0.06	0.9508384	0.9792967	-6.55	FALSE
249336_at	putative protein similar to unknov	DRB5	AT5G41070	1.01	0.02	0.06	0.9508994	0.9792967	-6.55	FALSE
258546_at	hypothetical protein predicted by	emb1974	AT3G07060	-1.01	-0.01	-0.06	0.9509182	0.9792967	-6.55	FALSE
245374_at	hypothetical protein	---	AT4G17620	-1.01	-0.01	-0.06	0.9511223	0.9793382	-6.55	FALSE
259170_at	hypothetical protein similar to put	---	AT3G03510	-1.01	-0.01	-0.06	0.9510834	0.9793382	-6.55	FALSE
264459_at	putative reverse transcriptase sir	---	---	1.01	0.02	0.06	0.9511301	0.9793382	-6.55	FALSE
246628_at	signal recognition particle 54 kD	---	AT1G48900	1.01	0.01	0.06	0.9510763	0.9793382	-6.55	FALSE

246995_at	formin-like protein	---	AT5G67470	1.01	0.02	0.06	0.9512298	0.9793482	-6.55	TRUE
252253_at	Expressed protein ; supported by	---	AT3G49300	1.01	0.01	0.06	0.9512687	0.9793482	-6.55	FALSE
255349_at	hypothetical protein	---	AT4G03830	-1.01	-0.01	-0.06	0.9512567	0.9793482	-6.55	FALSE
247995_at	putative protein contains similarit	---	AT5G56160	-1.01	-0.01	-0.06	0.9513364	0.9793737	-6.55	FALSE
258666_at	hypothetical protein	KOB1	AT3G08550	-1.01	-0.01	-0.06	0.9514946	0.9794924	-6.55	FALSE
260101_at	putative trypsin inhibitor similar to	---	AT1G73260	1.01	0.01	0.06	0.9519404	0.979901	-6.55	TRUE
261999_at	hypothetical protein predicted by	---	AT1G33800	-1.01	-0.01	-0.06	0.9519775	0.979901	-6.55	FALSE
257285_at	unknown protein	---	AT3G29760	1.01	0.01	0.06	0.9521674	0.9800522	-6.55	FALSE
266921_at	putative cytochrome P450	CYP86A8	AT2G45970	-1.02	-0.03	-0.06	0.9522522	0.9800954	-6.55	FALSE
255787_at	putative cinnamoyl-CoA reductas	---	AT2G33590	-1.01	-0.01	-0.06	0.9523723	0.9801747	-6.55	FALSE
259622_at	hypothetical protein predicted by	---	AT1G43010	-1.01	-0.01	-0.06	0.952632	0.9803978	-6.55	FALSE
265066_at	unknown protein location of EST	FLA9	AT1G03870	-1.01	-0.02	-0.06	0.9529649	0.9805032	-6.55	TRUE
261279_at	class I chitinase, putative similar	POM1	AT1G05850	1.03	0.05	0.06	0.9530611	0.9805032	-6.55	TRUE
250011_at	putative protein crp1 protein, ma	---	AT5G18475	1.01	0.01	0.06	0.9530989	0.9805032	-6.55	FALSE
248731_at	phosphoribosylanthranilate trans	---	AT5G48060	1.01	0.01	0.06	0.9531354	0.9805032	-6.55	FALSE
251789_at	serine/threonine-specific protein	---	AT3G55450	1.01	0.01	0.06	0.9529184	0.9805032	-6.55	FALSE
255659_at	Expressed protein ; supported by	---	AT4G00895	1.01	0.02	0.06	0.9531643	0.9805032	-6.55	FALSE
255912_at	2,3-oxidosqualene-triterpenoid c	---	AT1G66960	1.01	0.01	0.06	0.952795	0.9805032	-6.55	FALSE
247809_at	unknown protein	---	AT5G58280	-1.01	-0.01	-0.06	0.9530398	0.9805032	-6.55	FALSE
263102_at	unknown protein	---	AT2G05270	-1.01	-0.01	-0.06	0.9530782	0.9805032	-6.55	FALSE
247712_at	E2, ubiquitin-conjugating enzym	UBC7	AT5G59300	1.01	0.01	0.06	0.9531157	0.9805032	-6.55	FALSE
261407_at	unknown protein ;supported by fu	---	AT1G18810	1.01	0.02	0.06	0.953497	0.9806913	-6.55	TRUE
257129_at	cytochrome P450, putative conta	CYP705A1	AT3G20100	1.01	0.02	0.06	0.9535191	0.9806913	-6.55	TRUE
246273_at	globulin-like protein	---	AT4G36700	-1.01	-0.01	-0.06	0.953478	0.9806913	-6.55	FALSE
245223_at	gene_id:K17E7.5~unknown prote	---	AT3G29791	-1.01	-0.01	-0.06	0.9534166	0.9806913	-6.55	FALSE
264515_at	hypothetical protein similar to hyp	---	AT1G10090	-1.01	-0.01	-0.06	0.9539442	0.9806965	-6.55	FALSE
248495_at	putative protein strong similarity t	---	AT5G50780	1.01	0.01	0.06	0.9538205	0.9806965	-6.55	FALSE
267158_at	putative expansin	EXP3	AT2G37640	1.04	0.05	0.06	0.9538527	0.9806965	-6.55	FALSE
267216_at	hypothetical protein	---	AT2G02620	-1.01	-0.01	-0.06	0.9536024	0.9806965	-6.55	FALSE
255804_at	putative protein IB1C3-1 protein	---	AT4G10220	1.01	0.01	0.06	0.9538873	0.9806965	-6.55	FALSE
251020_at	ABC transporter -like protein NB	NAP9	AT5G02270	1.02	0.03	0.06	0.9539814	0.9806965	-6.55	FALSE
258618_at	Expressed protein ; supported by	GASA5	AT3G02885	1.01	0.01	0.06	0.9536551	0.9806965	-6.55	FALSE
265111_at	similar to 14KD proline-rich prote	---	AT1G62510	-1.04	-0.05	-0.06	0.9539971	0.9806965	-6.55	FALSE
249289_at	N-hydroxycinnamoyl/benzoyltran	---	AT5G41040	1.03	0.04	0.06	0.9536822	0.9806965	-6.55	FALSE
256084_at	hypothetical protein predicted by	---	AT1G20750	1.01	0.01	0.06	0.9539813	0.9806965	-6.55	FALSE

260186_at	hypothetical protein predicted by	---	AT1G36020	1.01	0.01	0.06	0.9538097	0.9806965	-6.55	FALSE
246171_at	putative protein centrosomal Ne	---	AT5G32440	-1.01	-0.01	-0.06	0.9540454	0.9807019	-6.55	FALSE
263232_at	putative light repressible recepto	---	AT1G05700	-1.01	-0.01	-0.06	0.9541259	0.9807404	-6.55	FALSE
250566_at	putative helix-loop-helix DNA bir	TCP17	AT5G08070	-1.01	-0.01	-0.06	0.9542732	0.9808476	-6.55	FALSE
257991_at	unknown protein	---	AT3G19870	1.01	0.01	0.06	0.9543892	0.9808785	-6.55	FALSE
251154_at	tRNA isopentenyl transferase -li	ATIPT3	AT3G63110	-1.02	-0.03	-0.06	0.9543497	0.9808785	-6.55	FALSE
257001_at	Sm protein, putative similar to G	---	AT3G14080	1.01	0.01	0.06	0.954516	0.9808811	-6.55	FALSE
258224_at	LEA76 homologue type2 identica	---	AT3G15670	1.01	0.01	0.06	0.9545637	0.9808811	-6.55	FALSE
262190_at	unknown protein	---	AT1G78030	1.01	0.01	0.06	0.9545359	0.9808811	-6.55	FALSE
254974_at	putative flavanone 3-beta-hydro	---	AT4G10490	-1.01	-0.01	-0.06	0.9545595	0.9808811	-6.55	FALSE
248711_at	putative protein similar to unknov	---	AT5G48270	1.01	0.01	0.06	0.9549278	0.981211	-6.55	FALSE
248198_at	putative protein contains similarit	---	AT5G54200	-1.01	-0.02	-0.06	0.9552914	0.981298	-6.55	TRUE
262195_at	allergen, putative similar to aller	---	AT1G78040	1.02	0.02	0.06	0.9553997	0.981298	-6.55	FALSE
263730_at	beta-glucosidase, putative simila	BGLU4	AT1G60090	1.01	0.01	0.06	0.9551135	0.981298	-6.55	FALSE
256272_at	unknown protein	---	AT3G12100	1.01	0.01	0.06	0.9553795	0.981298	-6.55	FALSE
257474_at	DNA-3-methyladenine glycosida	---	AT1G80850	1.01	0.01	0.06	0.9551946	0.981298	-6.55	FALSE
246029_at	leucine-rich repeat protein ; supp	---	AT5G21090	-1.01	-0.01	-0.06	0.9552408	0.981298	-6.55	FALSE
262406_at	myb-related protein, putative sin	AtMYB93	AT1G34670	-1.01	-0.01	-0.06	0.955354	0.981298	-6.55	FALSE
246905_at	putative protein ;supported by fu	---	AT5G25570	-1.01	-0.02	-0.06	0.9551561	0.981298	-6.55	FALSE
254519_at	putative protein W15DMY30S	---	AT4G19940	-1.01	-0.01	-0.06	0.9551715	0.981298	-6.55	FALSE
253321_at	putative protein prolyl 4-hydroxy	---	AT4G33910	-1.01	-0.01	-0.06	0.9555308	0.9813127	-6.55	FALSE
249956_at	putative protein CGI-66 protein,	---	AT5G18940	1.01	0.01	0.06	0.955543	0.9813127	-6.55	FALSE
245617_at	hypothetical protein	---	AT4G14490	-1.01	-0.01	-0.06	0.9555262	0.9813127	-6.55	FALSE
253100_at	cytochrome P450 monooxygena	CYP81F3	AT4G37400	-1.02	-0.03	-0.06	0.9558445	0.9815782	-6.55	FALSE
250318_at	dihydropyrimidinase ; supported	---	AT5G12200	1.01	0.01	0.06	0.9559753	0.9816014	-6.55	FALSE
253649_at	putative protein predicted protei	---	AT4G29790	1.01	0.02	0.06	0.9559427	0.9816014	-6.55	FALSE
259844_at	lipid transfer protein, putative sir	---	AT1G73560	1.01	0.01	0.06	0.9559963	0.9816014	-6.55	FALSE
265788_at	putative auxin-induced protein	IAA32	AT2G01200	-1.01	-0.01	-0.06	0.956054	0.9816165	-6.55	FALSE
250570_at	putative protein hypothetical bac	EMB1873	AT5G08170	1.01	0.01	0.06	0.9562096	0.9816442	-6.55	FALSE
258889_at	putative pectinesterase similar to	---	AT3G05610	-1.01	-0.01	-0.06	0.9561957	0.9816442	-6.55	FALSE
262332_at	hypothetical protein similar to put	---	AT1G64030	-1.01	-0.01	-0.06	0.9562101	0.9816442	-6.55	FALSE
248005_at	unknown protein	---	AT5G56240	1.01	0.01	0.06	0.9565061	0.9819039	-6.55	FALSE
263470_at	putative unconventional myosin	XIF	AT2G31900	-1.01	-0.01	-0.06	0.956784	0.9820974	-6.56	FALSE
249788_at	putative protein contains similarit	ATXR6	AT5G24330	1.01	0.01	0.06	0.9568355	0.9820974	-6.56	FALSE
265829_at	unknown protein	---	AT2G14490	1.01	0.01	0.06	0.9567937	0.9820974	-6.56	FALSE

257428_at	hypothetical protein predicted by	---	AT1G78990	-1.01	-0.01	-0.06	0.9568669	0.9820974	-6.56	FALSE
259472_at	hypothetical protein contains sim	---	AT1G18910	1.01	0.01	0.06	0.9570735	0.9822653	-6.56	FALSE
267070_at	putative DnaJ protein	---	AT2G41000	-1.01	-0.01	-0.06	0.957119	0.9822678	-6.56	FALSE
245735_at	myb-like transcription factor, put	MYB54	AT1G73410	-1.00	-0.01	-0.06	0.9572849	0.9823938	-6.56	FALSE
257623_at	cytochrome P450, putative conta	CYP71B23	AT3G26210	-1.02	-0.03	-0.06	0.9574902	0.9824278	-6.56	TRUE
249602_at	porin -like protein porin, Prunus	---	AT5G37610	-1.01	-0.01	-0.06	0.9574113	0.9824278	-6.56	FALSE
262998_at	hypothetical protein predicted by	---	AT1G54280	1.00	0.01	0.06	0.9574556	0.9824278	-6.56	FALSE
248482_at	unknown protein	---	AT5G50970	1.01	0.01	0.06	0.957461	0.9824278	-6.56	FALSE
259531_at	hypothetical protein	---	AT1G12460	-1.01	-0.01	-0.06	0.9576928	0.9825915	-6.56	FALSE
245071_at	putative vetispiradiene synthase	---	AT2G23230	-1.01	-0.01	-0.05	0.9578879	0.9827474	-6.56	FALSE
254428_at	putative protein Human mRNA f	ZAC	AT4G21160	-1.01	-0.01	-0.05	0.9579802	0.9827973	-6.56	FALSE
254473_s_a	putative protein kinase like prote	---	AT4G20520 ///	-1.01	-0.01	-0.05	0.9580227	0.9827973	-6.56	FALSE
254266_at	protein kinase - like protein serin	CRK5	AT4G23130	1.02	0.03	0.05	0.9581242	0.9828572	-6.56	FALSE
257847_at	hypothetical protein predicted by	---	AT3G13020	1.01	0.01	0.05	0.958204	0.9828948	-6.56	FALSE
248497_at	putative protein strong similarity t	ATEXO70F	AT5G50380	1.01	0.01	0.05	0.9583783	0.9829852	-6.56	FALSE
259332_at	putative auxin-induced protein si	---	AT3G03830	-1.01	-0.01	-0.05	0.9583647	0.9829852	-6.56	FALSE
263335_x_a	hypothetical protein	---	---	1.01	0.01	0.05	0.9584786	0.9830439	-6.56	FALSE
256671_at	unknown protein	IQD3	AT3G52290	1.01	0.01	0.05	0.9585953	0.9830534	-6.56	FALSE
246169_at	putative protein predicted protei	---	AT5G32470	-1.01	-0.01	-0.05	0.9586171	0.9830534	-6.56	FALSE
250976_at	putative protein various predicte	---	AT5G03060	-1.01	-0.01	-0.05	0.9585847	0.9830534	-6.56	FALSE
267349_at	60S acidic ribosomal protein P0	---	AT2G40010	1.01	0.01	0.05	0.9586616	0.9830548	-6.56	FALSE
249986_at	putative protein predicted protei	---	AT5G18460	-1.01	-0.02	-0.05	0.9587639	0.9830784	-6.56	TRUE
257070_at	hypothetical protein predicted by	---	AT3G28190	-1.01	-0.01	-0.05	0.9587708	0.9830784	-6.56	FALSE
247224_at	MADS box transcription factor-lik	MAF5	AT5G65080	1.01	0.01	0.05	0.9588182	0.9830828	-6.56	FALSE
263453_at	hypothetical protein predicted by	---	AT2G22180	-1.00	-0.01	-0.05	0.9590124	0.9832377	-6.56	FALSE
259752_at	spore coat protein-like protein sir	LPR2	AT1G71040	1.01	0.01	0.05	0.9591567	0.9832844	-6.56	FALSE
254154_at	hypothetical protein	---	AT4G24460	-1.01	-0.01	-0.05	0.9593151	0.9832844	-6.56	FALSE
249598_at	putative protein AtPP protein, Br	---	AT5G37970	-1.01	-0.01	-0.05	0.9592264	0.9832844	-6.56	FALSE
266343_at	putative non-LTR retroelement re	---	---	1.01	0.01	0.05	0.9593208	0.9832844	-6.56	FALSE
248844_s_a	extA (emb CAA47807.1)	---	AT5G46890 ///	1.01	0.01	0.05	0.9592359	0.9832844	-6.56	FALSE
264206_at	putative topoisomerase strong si	---	AT1G22730	1.01	0.01	0.05	0.9593597	0.9832844	-6.56	FALSE
261978_at	Athila retroelment ORF 1, putati	---	---	1.00	0.01	0.05	0.9592718	0.9832844	-6.56	FALSE
259546_at	unknown protein	---	AT1G35350	-1.02	-0.02	-0.05	0.9595641	0.9833824	-6.56	FALSE
262684_s_a	vacuolar ATP synthase subunit E	---	AT1G20260 ///	-1.01	-0.01	-0.05	0.9595846	0.9833824	-6.56	FALSE
263910_at	hypothetical protein predicted by	---	AT2G36550	-1.01	-0.01	-0.05	0.9595715	0.9833824	-6.56	FALSE

251395_at	unknown protein ;supported by f	FLA8	AT2G45470	-1.04	-0.06	-0.05	0.9596448	0.9833848	-6.56	FALSE
254166_at	HSP90-like protein HSP90 hom	SHD	AT4G24190	1.02	0.03	0.05	0.9596987	0.9833848	-6.56	FALSE
263091_at	unknown protein	---	AT2G16200	-1.01	-0.01	-0.05	0.9597164	0.9833848	-6.56	FALSE
258632_s_a	putative MAP3K epsilon protein	MAPKKK7	AT3G07980 ///	-1.01	-0.01	-0.05	0.9599536	0.9833881	-6.56	TRUE
247824_at	putative protein Na+/H+-exchan	CHX25	AT5G58460	1.01	0.01	0.05	0.9600644	0.9833881	-6.56	FALSE
255205_at	putative transposon protein	---	---	1.00	0.01	0.05	0.9599573	0.9833881	-6.56	FALSE
254381_at	putative protein membrane-asso	---	AT4G21880	1.01	0.01	0.05	0.959801	0.9833881	-6.56	FALSE
252857_at	putative protein various predicte	---	AT4G39756	1.01	0.01	0.05	0.9599407	0.9833881	-6.56	FALSE
257462_at	hypothetical protein	---	AT1G65740	-1.01	-0.01	-0.05	0.9600638	0.9833881	-6.56	FALSE
258248_at	hypothetical protein predicted by	---	AT3G29140	1.01	0.01	0.05	0.9600066	0.9833881	-6.56	FALSE
266669_at	putative flavonol 3-O-glucosyltran	UGT71C1	AT2G29750	-1.01	-0.01	-0.05	0.9598573	0.9833881	-6.56	FALSE
258472_at	unknown protein identical to unkn	---	AT3G06080	1.01	0.01	0.05	0.9606904	0.983411	-6.56	TRUE
258662_at	unknown protein	---	AT3G02900	1.01	0.02	0.05	0.9604166	0.983411	-6.56	TRUE
250851_at	putative protein rngB protein, Di	---	AT5G04420	-1.01	-0.01	-0.05	0.9603019	0.983411	-6.56	FALSE
263756_at	putative ubiquitin fusion-degrada	---	AT2G21270	1.00	0.01	0.05	0.9605706	0.983411	-6.56	FALSE
258500_at	S-adenosylmethionine decarboxy	CPuORF9	AT3G02468 ///	-1.01	-0.01	-0.05	0.9606675	0.983411	-6.56	FALSE
259697_at	putative DNA-binding protein sim	---	AT1G68920	-1.01	-0.01	-0.05	0.9603934	0.983411	-6.56	FALSE
267431_at	unknown protein ;supported by f	MEE26	AT2G34870	1.01	0.01	0.05	0.9604065	0.983411	-6.56	FALSE
266082_at	hypothetical protein predicted by	---	AT2G37830	1.01	0.01	0.05	0.9606167	0.983411	-6.56	FALSE
245782_at	60S ribosomal protein (fragment	---	AT1G35200	1.01	0.01	0.05	0.9604588	0.983411	-6.56	FALSE
257842_at	P-glycoprotein, putative similar t	PGP18	AT3G28390	1.01	0.01	0.05	0.960641	0.983411	-6.56	FALSE
256571_at	hypothetical protein predicted by	---	AT3G30730	-1.00	-0.01	-0.05	0.9605399	0.983411	-6.56	FALSE
252768_at	putative protein hypothetical prot	---	---	1.00	0.01	0.05	0.9604742	0.983411	-6.56	FALSE
258564_at	poly(A) polymerase, putative sim	---	AT3G06560	1.01	0.01	0.05	0.9603045	0.983411	-6.56	FALSE
254766_at	putative protein predicted protein	TPS12	AT4G13280	1.00	0.01	0.05	0.9606828	0.983411	-6.56	FALSE
263191_at	polyprotein, putative similar to p	---	---	-1.01	-0.01	-0.05	0.9608754	0.9835563	-6.56	FALSE
253446_at	putative protein predicted protein	---	AT4G32620	-1.01	-0.01	-0.05	0.9609821	0.9835665	-6.56	FALSE
264618_at	hypothetical protein predicted by	---	AT2G17680	-1.01	-0.01	-0.05	0.9610148	0.9835665	-6.56	FALSE
250775_at	putative protein contains similarit	---	AT5G05460	1.01	0.02	0.05	0.9609779	0.9835665	-6.56	FALSE
263342_at	putative helicase	---	---	-1.00	-0.01	-0.05	0.9611168	0.9836268	-6.56	FALSE
257264_at	hypothetical protein contains Pfa	---	AT3G22060	1.02	0.03	0.05	0.9612628	0.9836648	-6.56	TRUE
255596_at	putative DNA-binding protein sim	WRKY47	AT4G01720	-1.01	-0.02	-0.05	0.9612833	0.9836648	-6.56	FALSE
267306_at	Ran binding protein (AtRanBP1b	---	AT2G30060	-1.01	-0.01	-0.05	0.9612648	0.9836648	-6.56	FALSE
260560_at	putative endochitinase	---	AT2G43590	-1.01	-0.01	-0.05	0.9615505	0.9838941	-6.56	FALSE
260077_at	thaumatin-like protein contains P	---	AT1G73620	1.01	0.01	0.05	0.9616361	0.9839375	-6.56	FALSE

246928_at	putative protein Scythe protein -	---	AT5G25270	-1.01	-0.01	-0.05	0.9617774	0.9839588	-6.56	FALSE
257776_at	terpene synthase-related protein	---	AT3G29190	-1.01	-0.01	-0.05	0.9617006	0.9839588	-6.56	FALSE
247666_at	putative protein various predicte	---	AT5G60140	-1.00	-0.01	-0.05	0.9617863	0.9839588	-6.56	FALSE
263443_at	putative fatty acid elongase ;sup	KCS12	AT2G28630	-1.02	-0.03	-0.05	0.9619439	0.9840759	-6.56	FALSE
256472_at	unknown protein	---	---	-1.01	-0.01	-0.05	0.962039	0.9841291	-6.56	FALSE
258127_at	unknown protein	---	AT3G24570	-1.00	-0.01	-0.05	0.9623595	0.9843245	-6.56	FALSE
262057_at	unknown protein ;supported by fu	---	AT1G80040	-1.01	-0.01	-0.05	0.9622949	0.9843245	-6.56	FALSE
265890_s_a	En/Spm-like transposon protein r	---	---	-1.00	-0.01	-0.05	0.9623526	0.9843245	-6.56	FALSE
255267_at	putative protein LpxD gene, Bru	---	AT4G05210	1.00	0.01	0.05	0.9624995	0.9843744	-6.56	FALSE
266070_at	hypothetical protein predicted by	EXLB3	AT2G18660	-1.06	-0.09	-0.05	0.9624796	0.9843744	-6.56	FALSE
245741_at	hypothetical protein similar to unl	---	AT1G44120	1.01	0.01	0.05	0.9625378	0.9843744	-6.56	FALSE
257983_at	unknown protein	---	AT3G20790	-1.01	-0.02	-0.05	0.9626277	0.9843997	-6.56	TRUE
266651_at	putative casein kinase I	---	AT2G25760	-1.01	-0.01	-0.05	0.9626678	0.9843997	-6.56	FALSE
248244_at	heat shock transcription factor HS	---	AT5G53640	1.01	0.01	0.05	0.962692	0.9843997	-6.56	FALSE
263841_at	putative xyloglucan endo-transgly	---	AT2G36870	-1.04	-0.05	-0.05	0.9628874	0.9844242	-6.56	FALSE
260837_at	fructose 1,6-bisphosphatase, pu	---	AT1G43670	-1.01	-0.01	-0.05	0.9628495	0.9844242	-6.56	FALSE
257230_at	DegP protease contains similarity	DegP11	AT3G16540	1.00	0.01	0.05	0.9628886	0.9844242	-6.56	FALSE
263970_at	putative cytochrome P450	CYP718	AT2G42850	1.01	0.01	0.05	0.9628476	0.9844242	-6.56	FALSE
254660_at	receptor serine/threonine kinase	---	AT4G18250	1.01	0.01	0.05	0.962973	0.9844664	-6.56	FALSE
267050_at	putative RNA-binding protein ; s	---	AT2G41060	-1.01	-0.01	-0.05	0.963167	0.9846206	-6.56	FALSE
265447_at	putative laccase (diphenol oxidas	LAC6	AT2G46570	-1.01	-0.01	-0.05	0.9634117	0.9846501	-6.56	FALSE
262443_at	Expressed protein ; supported by	---	AT1G47655	1.01	0.01	0.05	0.9634115	0.9846501	-6.56	FALSE
256303_at	disease resistance protein, puta	---	AT1G69550	-1.01	-0.01	-0.05	0.9633377	0.9846501	-6.56	FALSE
255658_at	hypothetical protein ;supported b	---	AT4G00770	1.01	0.01	0.05	0.9633694	0.9846501	-6.56	FALSE
260517_at	unknown protein	SPP1	AT1G51420	-1.00	-0.01	-0.05	0.9633996	0.9846501	-6.56	FALSE
265043_at	Expressed protein ; supported by	ATNAP4	AT1G03900	-1.01	-0.01	-0.05	0.9636374	0.9848367	-6.56	FALSE
256565_at	hypothetical protein	AT3G19515	---	-1.01	-0.01	-0.05	0.9636934	0.9848497	-6.56	FALSE
267118_at	hypothetical protein	---	AT2G32590	-1.01	-0.01	-0.05	0.9637882	0.9849025	-6.56	FALSE
247839_at	eukaryotic initiation factor 4, eIF-	---	AT5G57870	1.01	0.01	0.05	0.9640079	0.9849337	-6.56	FALSE
251773_at	putative protein HSPC058, Hom	---	AT3G55960	-1.01	-0.01	-0.05	0.964108	0.9849337	-6.56	FALSE
261153_at	unknown protein ;supported by fu	---	AT1G04850	1.01	0.01	0.05	0.9641047	0.9849337	-6.56	FALSE
251390_at	guanine nucleotide exchange fa	---	AT3G60860	1.01	0.01	0.05	0.964121	0.9849337	-6.56	FALSE
255388_at	hypothetical protein similar to A.	---	---	-1.00	-0.01	-0.05	0.9640496	0.9849337	-6.56	FALSE
258634_at	putative RNA-binding protein co	---	AT3G08000	-1.01	-0.01	-0.05	0.9640157	0.9849337	-6.56	FALSE
252620_at	hypothetical protein	---	---	1.00	0.01	0.05	0.9639142	0.9849337	-6.56	FALSE

245752_at	hypothetical protein similar to Ac	---	AT1G35150	1.00	0.01	0.05	0.964184	0.9849539	-6.56	FALSE
254749_at	putative protein various predicte	---	AT4G13130	1.00	0.01	0.05	0.964376	0.9850096	-6.56	FALSE
256688_at	non-LTR reverse transcriptase,	---	AT3G32130	1.00	0.01	0.05	0.964284	0.9850096	-6.56	FALSE
261980_at	hypothetical protein predicted by	---	AT1G33820	1.00	0.01	0.05	0.9643841	0.9850096	-6.56	FALSE
259127_at	putative translation initiation facto	---	AT3G02270	1.01	0.01	0.05	0.9644306	0.9850096	-6.56	FALSE
260202_at	hypothetical protein predicted by	---	---	1.00	0.01	0.05	0.9644544	0.9850096	-6.56	FALSE
257789_at	unknown protein ;supported by f	YSL6	AT3G27020	-1.01	-0.01	-0.05	0.96467	0.9851679	-6.56	FALSE
249728_at	GTPase activator-like protein of I	---	AT5G24390	-1.01	-0.01	-0.05	0.9646957	0.9851679	-6.56	FALSE
247861_at	strong similarity to unknown prot	---	AT5G58160	1.01	0.01	0.05	0.9648686	0.9852294	-6.56	FALSE
253371_at	putative protein FAB1 protein, S	---	AT4G33240	-1.01	-0.01	-0.05	0.9648277	0.9852294	-6.56	FALSE
246825_at	putative protein various predicte	---	AT5G26260	1.00	0.01	0.05	0.9648855	0.9852294	-6.56	FALSE
250660_at	RNA-binding protein-like	---	AT5G07060	-1.00	-0.01	-0.05	0.9649491	0.9852501	-6.56	FALSE
261008_at	hypothetical protein contains sim	---	AT1G26370	-1.01	-0.01	-0.05	0.9650162	0.9852746	-6.56	FALSE
260997_at	zinc-finger protein (ZPT4-4), put	---	AT1G26610	-1.00	-0.01	-0.05	0.9650807	0.9852964	-6.56	FALSE
260332_at	hypothetical protein predicted by	---	AT1G70470	-1.00	-0.01	-0.05	0.9651452	0.9853181	-6.56	FALSE
264449_at	hypothetical protein predicted by	NPGR1	AT1G27460	-1.01	-0.01	-0.04	0.9654145	0.9854286	-6.56	TRUE
257651_at	polygalacturonase, putative simi	---	AT3G16850	1.01	0.01	0.05	0.9653706	0.9854286	-6.56	FALSE
245340_at	elicitor like protein ; supported by	---	AT4G14420	1.01	0.01	0.05	0.9653505	0.9854286	-6.56	FALSE
252493_at	hypothetical protein	---	AT3G46750	-1.01	-0.01	-0.04	0.9654263	0.9854286	-6.56	FALSE
255545_at	putative polygalacturonidase sim	---	AT4G01890	-1.00	-0.01	-0.04	0.9654902	0.9854498	-6.56	FALSE
260588_at	unknown protein contains similar	AtTLP7	AT1G53320	-1.01	-0.01	-0.04	0.9656694	0.9855886	-6.56	FALSE
250361_at	putative protein various predicte	---	AT5G11370	-1.00	-0.01	-0.04	0.9657927	0.9856703	-6.56	FALSE
256869_at	nodulin, putative similar to nodul	---	AT3G26420 /	1.01	0.01	0.04	0.9658428	0.9856774	-6.56	FALSE
254973_at	putative retrotransposon Oryza a	---	---	-1.01	-0.01	-0.04	0.9659108	0.9857026	-6.56	FALSE
260924_at	hypothetical protein similar to Pto	---	AT1G21590	1.01	0.01	0.04	0.9661542	0.985795	-6.56	TRUE
266194_at	unknown protein	---	AT2G39090	-1.00	-0.01	-0.04	0.9662115	0.985795	-6.56	FALSE
247595_at	ring finger protein - like ring finge	---	AT5G60820	-1.01	-0.01	-0.04	0.9660473	0.985795	-6.56	FALSE
266411_at	putative peptidyl-prolyl cis-trans i	---	AT2G38730	1.01	0.01	0.04	0.9662877	0.985795	-6.56	FALSE
264418_at	nuclear ribonucleoprotein, putati	---	AT1G43190	-1.01	-0.01	-0.04	0.9663331	0.985795	-6.56	FALSE
252340_at	myb-like protein	AtMYB45	AT3G48920	1.01	0.01	0.04	0.9661922	0.985795	-6.56	FALSE
251268_at	putative protein hypothetical prot	---	AT3G62350	-1.01	-0.01	-0.04	0.966347	0.985795	-6.56	FALSE
246107_at	putative protein various predicte	---	---	-1.00	-0.01	-0.04	0.9662202	0.985795	-6.56	FALSE
245278_at	syntaxin ; supported by cDNA: gi	SYP23	AT4G17730	-1.01	-0.01	-0.04	0.9664599	0.9858219	-6.56	FALSE
246991_at	peroxidase (emb|CAA66967.1)	---	AT5G67400	-1.00	-0.01	-0.04	0.9664326	0.9858219	-6.56	FALSE
251655_at	hypothetical protein	AT3G5715	---	-1.01	-0.01	-0.04	0.9665707	0.9858908	-6.56	FALSE

248341_at	unknown protein	---	AT5G52220	1.01	0.01	0.04	0.9667169	0.9859959	-6.56	FALSE
264593_at	putative GTP-binding protein ; s	ARAC1	AT2G17800	1.00	0.01	0.04	0.9667913	0.9860277	-6.56	FALSE
264807_at	putative presenilin similar to pres	---	AT1G08700	1.01	0.01	0.04	0.9668977	0.9860335	-6.56	FALSE
252238_at	peroxidase ATP21a	---	AT3G49960	1.01	0.01	0.04	0.9669267	0.9860335	-6.56	FALSE
263528_at	putative peroxidase	---	AT2G24800	-1.01	-0.01	-0.04	0.9668589	0.9860335	-6.56	FALSE
254570_s_a	puatative protein various predict	---	AT4G19250 /.	1.01	0.01	0.04	0.9670021	0.9860663	-6.56	FALSE
250647_at	putative protein contains similarit	---	AT5G06770	1.00	0.01	0.04	0.9671383	0.986117	-6.56	FALSE
250507_at	putative protein similar to unknov	---	AT5G09940	1.00	0.01	0.04	0.9671271	0.986117	-6.56	FALSE
263992_at	putative retroelement pol polypro	---	---	1.00	0.01	0.04	0.9673513	0.9862901	-6.56	FALSE
260809_at	hypothetical protein predicted by	---	AT1G43730	1.00	0.01	0.04	0.9675407	0.9862985	-6.56	FALSE
262677_at	unknown protein	---	AT1G75860	-1.01	-0.01	-0.04	0.967549	0.9862985	-6.56	FALSE
254637_at	putative protein KIAA0244 gene	---	AT4G18720	-1.00	-0.01	-0.04	0.9675476	0.9862985	-6.56	FALSE
249738_at	60s acidic ribosomal protein P1	---	AT5G24510	1.00	0.01	0.04	0.9675452	0.9862985	-6.56	FALSE
263967_at	En/Spm-like transposon protein	---	---	1.00	0.01	0.04	0.9675757	0.9862985	-6.56	FALSE
257312_at	Expressed protein ; supported by	AT3G26590	---	1.00	0.01	0.04	0.9677522	0.986424	-6.56	FALSE
266341_at	hypothetical protein predicted by	---	AT2G01510	1.00	0.01	0.04	0.9677853	0.986424	-6.56	FALSE
261192_at	NAM protein, putative similar to	ANAC13	AT1G32870	1.01	0.01	0.04	0.968077	0.9864576	-6.56	TRUE
246290_at	calmodulin-3 ;supported by full-l	CAM3	AT3G56800	1.00	0.01	0.04	0.9679559	0.9864576	-6.56	FALSE
264380_at	unknown protein predicted by ge	---	AT2G25190	-1.00	-0.01	-0.04	0.9680413	0.9864576	-6.56	FALSE
258627_at	unknown protein similar to perox	PEX12	AT3G04460	1.01	0.01	0.04	0.9679259	0.9864576	-6.56	FALSE
253015_at	hypothetical protein	---	AT4G37950	1.00	0.01	0.04	0.9680777	0.9864576	-6.56	FALSE
255504_at	drought-induced-19-like 1 simila	---	AT4G02200	-1.02	-0.02	-0.04	0.968004	0.9864576	-6.56	FALSE
255906_at	hypothetical protein similar to RI	---	AT1G17790	-1.00	-0.01	-0.04	0.9681724	0.98651	-6.56	FALSE
259224_at	putative thymidine kinase similar	---	AT3G07800	1.01	0.01	0.04	0.9682901	0.9865858	-6.56	FALSE
261284_at	hypothetical protein predicted by	---	---	1.00	0.01	0.04	0.9683925	0.9866461	-6.56	FALSE
248899_at	carboxy-terminal proteinase D1-l	---	AT5G46390	1.00	0.01	0.04	0.9684528	0.9866634	-6.56	FALSE
254951_at	putative protein various kinesin li	---	AT4G10840	1.00	0.01	0.04	0.9685653	0.986734	-6.56	FALSE
251600_at	protein kinase - like protein wall-	---	AT3G57710	-1.00	-0.01	-0.04	0.9688065	0.9869357	-6.56	FALSE
256538_x_a	hypothetical protein predicted by	---	---	1.00	0.01	0.04	0.9689607	0.9870046	-6.56	FALSE
257266_at	RNA-binding protein contains Pf	---	AT3G15010	1.00	0.01	0.04	0.9689206	0.9870046	-6.56	FALSE
260736_at	hypothetical protein predicted by	---	AT1G17630	-1.00	-0.01	-0.04	0.9692765	0.9872822	-6.56	FALSE
248266_at	putative protein similar to unknov	---	AT5G53440	1.00	0.01	0.04	0.9693719	0.9872941	-6.56	FALSE
255903_at	myb-like protein, putative similar	MYB52	AT1G17950	1.00	0.01	0.04	0.9693747	0.9872941	-6.56	FALSE
258843_at	putative protein kinase similar to	---	AT3G04690	1.00	0.01	0.04	0.9694791	0.9873563	-6.56	FALSE
260091_at	putative serine carboxypeptidas	scpl5	AT1G73290	-1.00	-0.01	-0.04	0.9696733	0.9875099	-6.56	FALSE

258737_at	unknown protein similar to unkno	---	AT3G05940	-1.00	-0.01	-0.04	0.9697667	0.9875202	-6.56	FALSE
261527_at	hypothetical protein similar to put	---	AT1G14390	-1.01	-0.01	-0.04	0.9697699	0.9875202	-6.56	FALSE
249409_at	putative protein KED, Nicotiana	---	AT5G40340	1.01	0.02	0.04	0.9698333	0.9875407	-6.56	FALSE
253155_at	putative protein predicted protei	---	AT4G35720	1.00	0.01	0.04	0.9699806	0.9876465	-6.56	FALSE
262061_at	hypothetical protein contains sim	ATPP2-B11	AT1G80110	-1.00	-0.01	-0.04	0.9700512	0.9876744	-6.56	FALSE
254632_at	putative protein predicted protei	---	AT4G18630	1.00	0.01	0.04	0.9701141	0.9876943	-6.56	FALSE
249651_at	auxin response factor 8 (ARF8)	ARF8	AT5G37020	1.01	0.01	0.04	0.970249	0.9877875	-6.56	FALSE
259496_at	hypothetical protein predicted by	---	AT1G15900	1.00	0.01	0.04	0.9703911	0.9878232	-6.56	FALSE
258867_at	hypothetical protein predicted by	---	AT3G03130	-1.00	-0.01	-0.04	0.970414	0.9878232	-6.56	FALSE
258962_at	putative cytochrome P450 simila	CYP77A6	AT3G10570	-1.02	-0.03	-0.04	0.9703353	0.9878232	-6.56	FALSE
258840_at	unknown protein similar to unkno	---	AT3G04620	-1.00	-0.01	-0.04	0.9707013	0.9880275	-6.56	FALSE
248606_at	putative protein contains similarit	CPuORF4	AT5G49448 /	1.01	0.01	0.04	0.9706614	0.9880275	-6.56	FALSE
266458_at	unknown protein ;supported by f	---	AT2G47710	1.00	0.01	0.04	0.9708747	0.9880397	-6.56	FALSE
254918_at	putative protein phosphatase like	SGT1B	AT4G11260	-1.00	-0.01	-0.04	0.9708865	0.9880397	-6.56	FALSE
254585_at	resistence protein - like downy n	---	AT4G19500	-1.00	-0.01	-0.04	0.9708087	0.9880397	-6.56	FALSE
258530_at	hypothetical protein predicted by	---	AT3G06840	-1.00	-0.01	-0.04	0.970849	0.9880397	-6.56	FALSE
248706_at	unknown protein	---	AT5G48530	1.00	0.01	0.04	0.9711003	0.9882132	-6.56	FALSE
253207_at	putative protein small auxin up-r	---	AT4G34770	-1.01	-0.02	-0.04	0.9712375	0.9882599	-6.56	TRUE
256226_at	unknown protein ; supported by c	ATDI19	AT1G56280	-1.01	-0.01	-0.04	0.9713109	0.9882599	-6.56	FALSE
267037_at	hypothetical protein ; supported	---	AT2G38320	1.00	0.01	0.04	0.9713196	0.9882599	-6.56	FALSE
266688_at	hypothetical protein	---	AT2G19660	-1.00	0.00	-0.04	0.9712789	0.9882599	-6.56	FALSE
248654_at	importin alpha	IMPA-5	AT5G49310	1.00	0.01	0.04	0.971417	0.9883082	-6.56	FALSE
254296_at	hypothetical protein	---	AT4G23090	1.01	0.01	0.04	0.9714537	0.9883082	-6.56	FALSE
264025_at	AUX1-like amino acid permease	---	AT2G21050	1.01	0.02	0.04	0.9715311	0.9883429	-6.56	FALSE
251607_at	hypothetical protein	---	AT3G57850	-1.00	-0.01	-0.04	0.9716384	0.988408	-6.56	FALSE
249082_at	legumin-like protein	CRA1	AT5G44120	1.00	0.01	0.04	0.9717954	0.9885236	-6.56	FALSE
254616_at	shaggy-like protein kinase etha (	BIN2	AT4G18710	-1.00	-0.01	-0.04	0.971855	0.9885402	-6.56	FALSE
245805_at	hypothetical protein predicted by	---	AT1G46336	-1.00	0.00	-0.04	0.9721296	0.9887754	-6.56	FALSE
256021_at	unknown protein contains Pfam p	ZW9	AT1G58270	-1.01	-0.01	-0.04	0.9722507	0.9888544	-6.56	FALSE
263204_at	hypothetical protein contains sim	chr31	AT1G05490	-1.00	0.00	-0.04	0.9723668	0.9889059	-6.56	FALSE
245922_at	putative protein predicted protei	---	AT5G28810	1.00	0.01	0.04	0.972388	0.9889059	-6.56	FALSE
247246_at	invertase inhibitor homolog (emb	C/VIF2	AT5G64620	-1.01	-0.01	-0.04	0.972503	0.9889788	-6.56	TRUE
265089_at	hypothetical protein similar to hy	SUVR1	AT1G04050	1.00	0.01	0.04	0.9729816	0.9894214	-6.56	FALSE
266087_at	putative alcohol dehydrogenase	---	AT2G37790	1.00	0.01	0.04	0.9730921	0.9894455	-6.56	FALSE
246990_at	subtilisin-like serine protease AR	ARA12	AT5G67360	1.01	0.01	0.04	0.9730721	0.9894455	-6.56	FALSE

250611_at	gibberellin 20-oxidase	GA20OX3	AT5G07200	-1.01	-0.01	-0.03	0.9732323	0.9894781	-6.56	TRUE
255385_at	putative hydrolase	---	AT4G03610	-1.01	-0.01	-0.03	0.9732543	0.9894781	-6.56	FALSE
246550_at	putative protein predicted protei	---	AT5G14920	1.02	0.02	0.03	0.9731807	0.9894781	-6.56	FALSE
266843_at	hypothetical protein predicted by	---	AT2G26135	1.00	0.01	0.03	0.9734443	0.9895155	-6.56	FALSE
267457_at	putative proline-rich protein	AGP30	AT2G33790	-1.00	-0.01	-0.03	0.9733763	0.9895155	-6.56	FALSE
253082_at	putative glycine-rich cell wall pro	---	AT4G36230	1.01	0.01	0.03	0.973394	0.9895155	-6.56	FALSE
249646_at	SEN1-like protein SEN1 - Sacch	---	AT5G37030	-1.00	0.00	-0.03	0.9734646	0.9895155	-6.56	FALSE
247687_at	protein serine /threonine kinase	---	AT5G59740	-1.00	-0.01	-0.03	0.973826	0.9898388	-6.56	FALSE
246116_at	putative protein predicted protein	---	AT5G20310	1.00	0.01	0.03	0.9739474	0.9899037	-6.56	FALSE
251384_at	putative protein	---	AT3G60760	1.00	0.00	0.03	0.9739768	0.9899037	-6.56	FALSE
256567_at	amino acid permease, putative c	---	AT3G19553	1.00	0.01	0.03	0.9740836	0.9899682	-6.56	FALSE
247657_at	Expressed protein ; supported by	---	AT5G59845	-1.00	-0.01	-0.03	0.9741388	0.9899802	-6.56	FALSE
253723_at	extensin-like protein ;supported	---	AT4G29240	1.00	0.01	0.03	0.9742022	0.9900006	-6.56	FALSE
259166_at	unknown protein ; supported by	---	AT3G01670	1.01	0.02	0.03	0.9746275	0.9900803	-6.56	TRUE
246864_at	cytochrome P450 GA3 ; supporte	GA3	AT5G25900	1.01	0.01	0.03	0.9743438	0.9900803	-6.56	FALSE
264735_s_a	hypothetical protein similar to hyp	---	AT1G62000 /	-1.00	-0.01	-0.03	0.9744435	0.9900803	-6.56	FALSE
260960_at	calcium-binding protein, putative	---	AT1G05990	1.00	0.01	0.03	0.9745766	0.9900803	-6.56	FALSE
248858_at	AP47 50p (gb|AAB88283.1) ; sup	---	AT5G46630	-1.00	-0.01	-0.03	0.9745454	0.9900803	-6.56	FALSE
250200_at	peroxidase ATP20a (emb|CAA67	---	AT5G14130	1.00	0.01	0.03	0.9746279	0.9900803	-6.56	FALSE
259556_at	hypothetical protein	---	---	1.00	0.00	0.03	0.9743743	0.9900803	-6.56	FALSE
263507_s_a	hypothetical protein	---	---	-1.01	-0.01	-0.03	0.9745828	0.9900803	-6.56	FALSE
266656_at	putative CCCH-type zinc finger p	ATCTH	AT2G25900	-1.01	-0.01	-0.03	0.9747556	0.9901338	-6.56	FALSE
245718_at	putative protein	---	AT5G04110	1.00	0.01	0.03	0.9747674	0.9901338	-6.56	FALSE
257337_at	NADH dehydrogenase subunit 5	---	---	-1.01	-0.01	-0.03	0.9752245	0.9902211	-6.56	TRUE
264301_at	hypothetical protein contains sim	---	AT1G78780	1.01	0.01	0.03	0.9752225	0.9902211	-6.56	TRUE
251445_at	putative protein hypothetical pro	---	AT3G59870	-1.00	0.00	-0.03	0.9751742	0.9902211	-6.56	FALSE
253431_at	putative protein predicted protei	---	AT4G32440	-1.00	-0.01	-0.03	0.9753743	0.9902211	-6.56	FALSE
263086_at	putative non-LTR retrolelement r	---	AT2G16110	1.00	0.01	0.03	0.9753246	0.9902211	-6.56	FALSE
247998_at	unknown protein	---	AT5G56200	-1.01	-0.01	-0.03	0.9752161	0.9902211	-6.56	FALSE
257115_at	kinesin-like protein contains Pfar	---	AT3G20150	1.00	0.01	0.03	0.9752045	0.9902211	-6.56	FALSE
257614_at	putative non-LTR retroelement re	---	---	-1.00	-0.01	-0.03	0.9752706	0.9902211	-6.56	FALSE
258594_at	hypothetical protein predicted by	---	AT3G04490	-1.00	-0.01	-0.03	0.9751777	0.9902211	-6.56	FALSE
244905_at	hypothetical protein	---	---	-1.00	-0.01	-0.03	0.9753577	0.9902211	-6.56	FALSE
251231_at	Glutathione transferase III-like p	ATGSTF13	AT3G62760	-1.00	-0.01	-0.03	0.9751789	0.9902211	-6.56	FALSE
250977_at	importin alpha - like protein impo	IMPA-9	AT5G03070	1.00	0.01	0.03	0.9749936	0.9902211	-6.56	FALSE

246041_at	phospholipase - like protein varic	---	AT5G19290	-1.00	0.00	-0.03	0.9755522	0.9902614	-6.56	FALSE
255677_at	putative calmodulin-binding heat	---	AT4G00500	-1.01	-0.01	-0.03	0.9757265	0.9902614	-6.56	FALSE
259544_at	hypothetical protein ; supported b	CAT3	AT1G20620	-1.00	0.00	-0.03	0.975678	0.9902614	-6.56	FALSE
260601_at	Expressed protein ; supported by	ZIP11	AT1G55910	-1.01	-0.01	-0.03	0.9757763	0.9902614	-6.56	FALSE
256075_at	mitogen-activated protein kinase	ATMPK8	AT1G18150	-1.00	-0.01	-0.03	0.9757542	0.9902614	-6.56	FALSE
261181_at	monosaccharide transporter, put	---	AT1G34580	1.00	0.01	0.03	0.9758284	0.9902614	-6.56	FALSE
259978_at	putative cell division control prote	CDKB2;1	AT1G76540	1.01	0.01	0.03	0.9755622	0.9902614	-6.56	FALSE
253110_at	hypothetical protein	---	AT4G35930	1.01	0.01	0.03	0.9757079	0.9902614	-6.56	FALSE
254386_at	peroxidase prxr1 ;supported by f	PRXR1	AT4G21960	-1.01	-0.01	-0.03	0.9758482	0.9902614	-6.56	FALSE
252341_at	remorin -like protein remorin, So	---	AT3G48940	-1.00	0.00	-0.03	0.9755278	0.9902614	-6.56	FALSE
247254_at	CLE21, putative CLAVATA3/ES	CLE21	AT5G64800	1.01	0.01	0.03	0.9759149	0.9902851	-6.56	FALSE
255741_at	tRNA isopentenyl transferase, p	ATIPT6	AT1G25410	1.00	0.01	0.03	0.9760176	0.9903452	-6.56	FALSE
259730_at	unknown protein similar to hypot	---	AT1G77660	1.01	0.01	0.03	0.9766799	0.9909732	-6.56	TRUE
267039_at	hypothetical protein predicted by	---	AT2G34270	-1.00	0.00	-0.03	0.9767584	0.9910087	-6.56	FALSE
256556_at	mutator-like transposase, putativ	---	---	1.00	0.00	0.03	0.9768132	0.9910203	-6.56	FALSE
255129_at	nodulin-like protein nodulin gene	---	AT4G08290	-1.01	-0.01	-0.03	0.9769691	0.9910319	-6.56	FALSE
250632_at	putative protein cyclin 2 - Trypar	CYCP4;3	AT5G07450	-1.00	-0.01	-0.03	0.977001	0.9910319	-6.56	FALSE
253899_at	putative protein protein disulfide	ATPDIL5-4	AT4G27080	1.00	0.01	0.03	0.9770419	0.9910319	-6.56	FALSE
263901_at	unknown protein ;supported by f	---	AT2G36320	1.00	0.01	0.03	0.977033	0.9910319	-6.56	FALSE
256559_at	Athila ORF 1, putative similar to	---	---	-1.00	0.00	-0.03	0.9769311	0.9910319	-6.56	FALSE
245588_at	putative protein	---	AT4G15030	-1.00	-0.01	-0.03	0.9771308	0.9910781	-6.56	FALSE
253260_at	hypothetical protein	---	AT4G34420 ///	1.00	0.01	0.03	0.9772594	0.9911323	-6.56	FALSE
249880_at	putative protein similar to unknov	---	AT5G23180	-1.00	0.00	-0.03	0.9772712	0.9911323	-6.56	FALSE
259853_at	leucine-rich receptor-like protein	---	AT1G72300	1.00	0.01	0.03	0.9775358	0.9912508	-6.56	FALSE
261359_at	hypothetical protein predicted by	---	---	-1.00	0.00	-0.03	0.9777054	0.9912508	-6.56	FALSE
258909_at	putative DnaJ protein Pfam HMM	---	AT3G06340	-1.00	0.00	-0.03	0.9775828	0.9912508	-6.56	FALSE
264997_at	hypothetical protein contains sim	HAC2	AT1G67220	1.00	0.01	0.03	0.9776245	0.9912508	-6.56	FALSE
258593_at	unknown protein	---	AT3G04480	1.00	0.01	0.03	0.9778661	0.9912508	-6.56	FALSE
259205_at	hypothetical protein similar to put	---	AT3G09030	1.00	0.01	0.03	0.9777231	0.9912508	-6.56	FALSE
266063_at	putative SNF2/RAD54 family DN	CHR8	AT2G18760	-1.00	0.00	-0.03	0.9775889	0.9912508	-6.56	FALSE
266485_at	putative phospholipase ;support	---	AT2G47630	1.01	0.01	0.03	0.9775561	0.9912508	-6.56	FALSE
253018_at	putative protein Zn finger protein	---	AT4G38000	-1.00	0.00	-0.03	0.9778596	0.9912508	-6.56	FALSE
259684_at	unknown protein	---	AT1G63070	-1.00	0.00	-0.03	0.9777787	0.9912508	-6.56	FALSE
257662_at	low affinity calcium antiporter CA	CAX2	AT3G13320	-1.00	0.00	-0.03	0.9778309	0.9912508	-6.56	FALSE
251213_at	putative protein hypothetical prot	---	---	-1.00	0.00	-0.03	0.9779682	0.9912662	-6.56	FALSE

264495_at	hypothetical protein predicted by	RIC2	AT1G27380	-1.00	0.00	-0.03	0.9779575	0.9912662	-6.56	FALSE
259011_s_a	unknown protein similar to putati	---	AT3G07380 /	-1.00	0.00	-0.03	0.9780544	0.9913096	-6.56	FALSE
263622_at	hypothetical protein predicted by	---	AT2G04870	-1.00	0.00	-0.03	0.9781014	0.9913131	-6.56	FALSE
251896_at	putative protein predicted protei	---	AT3G54390	1.00	0.01	0.03	0.9781562	0.9913246	-6.56	FALSE
255220_at	polyubiquitin (UBQ10) identical t	UBQ10	AT4G05320	1.00	0.01	0.03	0.9782237	0.9913489	-6.56	FALSE
247189_at	unknown protein ;supported by f	AGP7	AT5G65390	1.01	0.01	0.03	0.9784459	0.9914482	-6.56	FALSE
264840_at	unknown protein similar to leucin	---	AT1G03440	1.00	0.00	0.03	0.978462	0.9914482	-6.56	FALSE
267094_at	putative diphenol oxidase ; supp	IRX12	AT2G38080	-1.01	-0.02	-0.03	0.9785021	0.9914482	-6.56	FALSE
249176_at	thioredoxin (clone GIF1) (pir||S5	ATTRX3	AT5G42980	1.00	0.00	0.03	0.978539	0.9914482	-6.56	FALSE
265107_s_a	similar to glucose 1-dehydrogena	---	AT1G62610 /	1.00	0.00	0.03	0.978505	0.9914482	-6.56	FALSE
257896_at	basic chitinase, putative similar t	---	AT3G16920	1.01	0.02	0.03	0.9786809	0.991548	-6.56	FALSE
251133_at	LAX1 / AUX1 -like permease	---	AT5G01240	-1.00	-0.01	-0.03	0.9787299	0.9915536	-6.56	FALSE
250988_at	putative protein thyroid receptor	UPL4	AT5G02880	-1.00	0.00	-0.03	0.9790052	0.9915784	-6.56	FALSE
266572_at	unknown protein	---	AT2G23840	1.00	0.01	0.03	0.9790152	0.9915784	-6.56	FALSE
264050_at	putative non-LTR retroelement re	---	---	1.00	0.01	0.03	0.9789081	0.9915784	-6.56	FALSE
259220_at	expressed protein predicted by g	---	AT3G03550	1.00	0.01	0.03	0.9790051	0.9915784	-6.56	FALSE
251897_at	RING finger - like protein DNA-b	---	AT3G54360	-1.00	-0.01	-0.03	0.9789191	0.9915784	-6.56	FALSE
251287_at	putative protein nucleoid DNA-b	---	AT3G61820	-1.01	-0.01	-0.03	0.9788943	0.9915784	-6.56	FALSE
266726_at	SKP1/ASK1 (At19), putative sim	ASK19	AT2G03160	-1.00	-0.01	-0.03	0.979079	0.991599	-6.56	FALSE
249865_at	unknown protein ; supported by	---	AT5G22820	-1.00	-0.01	-0.03	0.9791298	0.9916064	-6.56	FALSE
253631_at	nucleotide sugar epimerase-like	GAE1	AT4G30440	-1.00	-0.01	-0.03	0.9793616	0.9917971	-6.56	TRUE
251797_at	putative protein AT-hook protein	AGF2	AT3G55560	1.00	0.01	0.03	0.9794264	0.9918187	-6.56	FALSE
245458_at	kinase like protein	---	AT4G16970	1.00	0.00	0.03	0.9795867	0.9918768	-6.56	FALSE
246144_at	dynein light chain - like protein d	---	AT5G20110	-1.01	-0.01	-0.03	0.9795503	0.9918768	-6.56	FALSE
258605_at	phi-1-like protein similar to phi-1	EXL6	AT3G02970	-1.00	0.00	-0.03	0.9796199	0.9918768	-6.56	FALSE
266840_at	hypothetical protein predicted by	---	AT2G26160	-1.00	0.00	-0.03	0.9796578	0.9918768	-6.56	FALSE
266571_at	unknown protein	---	AT2G23830	1.01	0.01	0.03	0.9797925	0.9919692	-6.56	FALSE
257548_s_a	hypothetical protein	LBD23	AT3G26620 /	1.00	0.00	0.03	0.9799583	0.992093	-6.56	FALSE
259117_at	unknown protein similar to hypot	SNL1	AT3G01320	-1.00	0.00	-0.03	0.9802193	0.9920931	-6.56	FALSE
248741_at	putative protein similar to unknov	SLY2	AT5G48170	1.00	0.01	0.03	0.9800773	0.9920931	-6.56	FALSE
254205_at	putative protein kinesin heavy ch	---	AT4G24170	-1.00	0.00	-0.03	0.9801457	0.9920931	-6.56	FALSE
263641_at	putative non-LTR retroelement re	---	---	-1.00	0.00	-0.03	0.9800139	0.9920931	-6.56	FALSE
264706_at	hypothetical protein predicted by	---	AT1G09720	-1.00	0.00	-0.03	0.9801082	0.9920931	-6.56	FALSE
255180_at	putative polyprotein	---	---	-1.00	0.00	-0.03	0.9802191	0.9920931	-6.56	FALSE
260081_at	unknown protein	---	AT1G78170	1.01	0.02	0.03	0.980357	0.9921223	-6.56	FALSE

267160_at	putative WD-40 repeat protein	---	AT2G37670	-1.00	0.00	-0.03	0.9803469	0.9921223	-6.56	FALSE
263463_at	putative ARI-like RING zinc finge	---	AT2G31770	-1.00	0.00	-0.03	0.9803786	0.9921223	-6.56	FALSE
249081_at	protein phosphatase 2A 62 kDa l	---	AT5G44090	1.00	0.00	0.03	0.9805062	0.9921633	-6.56	FALSE
257696_at	protein kinase, putative similar t	AGC1.5	AT3G12690	-1.00	-0.01	-0.03	0.9805008	0.9921633	-6.56	FALSE
254652_at	DNA binding-like protein SPF1 p	WRKY28	AT4G18170	-1.01	-0.02	-0.03	0.9805818	0.9921958	-6.56	FALSE
249549_at	lipid transfer - like protein lipid tr	---	AT5G38180	-1.00	0.00	-0.03	0.9806425	0.9922132	-6.56	FALSE
261066_at	hypothetical protein predicted by	---	AT1G07485	1.00	0.00	0.03	0.9807528	0.9922808	-6.56	FALSE
254232_at	tyrosine transaminase like prote	CORI3	AT4G23600	1.01	0.01	0.02	0.9808751	0.9923605	-6.56	TRUE
256280_at	unknown protein	---	AT3G12590	1.00	0.00	0.02	0.9810661	0.9924883	-6.56	FALSE
259019_at	hypothetical protein similar to ser	CHIP	AT3G07370	1.00	0.00	0.02	0.9810975	0.9924883	-6.56	FALSE
262546_at	iron-regulated transporter protei	ZIP10	AT1G31260	1.01	0.01	0.02	0.9811319	0.9924883	-6.56	FALSE
266409_at	hypothetical protein predicted by	---	AT2G38510	1.00	0.00	0.02	0.9814813	0.9927977	-6.56	FALSE
245923_at	putative protein predicted protei	---	AT5G28820	1.00	0.00	0.02	0.9815272	0.9928001	-6.56	FALSE
252307_at	putative protein SAE1-S9-protei	---	---	1.00	0.00	0.02	0.9815847	0.9928142	-6.56	FALSE
266905_at	putative katanin ;supported by fu	---	AT2G34560	-1.00	-0.01	-0.02	0.9816733	0.9928598	-6.56	TRUE
261608_at	unknown protein similar to putati	---	AT1G49650	1.00	0.00	0.02	0.9817355	0.9928644	-6.56	FALSE
256832_at	meiotic recombination protein (A	DMC1	AT3G22880	-1.00	-0.01	-0.02	0.9817649	0.9928644	-6.56	FALSE
256342_at	unknown protein ; supported by f	---	AT1G72020	1.00	0.00	0.02	0.9820105	0.9930688	-6.56	FALSE
249653_at	putative protein REPLICATION	---	---	-1.00	0.00	-0.02	0.9822022	0.9932187	-6.56	FALSE
248311_at	beta-carotene hydroxylase	BETA-OHA	AT5G52570	-1.00	-0.01	-0.02	0.9824829	0.9933496	-6.56	TRUE
260355_at	transcription factor CRC identica	CRC	AT1G69180	1.00	0.00	0.02	0.982506	0.9933496	-6.56	FALSE
245819_at	cauliflower identical to CAULIFL	CAL	AT1G26310	1.00	0.00	0.02	0.9824643	0.9933496	-6.56	FALSE
247758_at	subtilisin-like serine protease cor	ATSBT4.13	AT5G59120	1.00	0.00	0.02	0.9824607	0.9933496	-6.56	FALSE
262686_at	proteasome regulatory subunit S	---	AT1G75990	-1.00	0.00	-0.02	0.9825977	0.9933983	-6.56	FALSE
249580_at	putative protein predicted protei	---	AT5G37740	1.00	0.00	0.02	0.9828408	0.9935561	-6.56	FALSE
246264_at	hypothetical protein	FRL2	AT1G31814	1.00	0.00	0.02	0.9828356	0.9935561	-6.56	FALSE
259507_at	unknown protein	---	AT1G43910	1.01	0.01	0.02	0.9828879	0.9935596	-6.56	TRUE
267617_at	heme oxygenase 1 (HO1) identic	TED4	AT2G26670	-1.00	-0.01	-0.02	0.9830011	0.9935981	-6.56	FALSE
252585_s_a	putative protein UbcH 7-binding	---	AT3G45570 //	-1.00	0.00	-0.02	0.9830131	0.9935981	-6.56	FALSE
245489_at	FCA gamma protein	FCA	AT4G16280	-1.00	0.00	-0.02	0.9830933	0.9936351	-6.56	FALSE
259249_at	hypothetical protein predicted by	---	AT3G07790	1.00	0.01	0.02	0.983318	0.9937896	-6.56	FALSE
263229_s_a	putative polygalacturonase simila	---	AT1G05650 //	1.00	0.00	0.02	0.9834012	0.9937896	-6.56	FALSE
260307_at	unknown protein similar to unkno	---	AT1G70620	1.00	0.00	0.02	0.9834203	0.9937896	-6.56	FALSE
260503_at	proteasome, 30 kda subunit (ec	PAF2	AT1G47250	-1.00	0.00	-0.02	0.9834154	0.9937896	-6.56	FALSE
255188_at	contains similarity to Xenopus la	---	---	1.00	0.00	0.02	0.9835412	0.9938677	-6.56	FALSE

245356_at	adenosylhomocysteinase ;suppo	MEE58	AT4G13940	-1.00	-0.01	-0.02	0.9836357	0.9938738	-6.56	FALSE
261780_at	cyclin, putative similar to B-like c	CYCB2;4	AT1G76310	-1.00	0.00	-0.02	0.9837025	0.9938738	-6.56	FALSE
266906_at	Expressed protein ; supported by	---	AT2G34585	1.00	0.00	0.02	0.9837215	0.9938738	-6.56	FALSE
256495_at	hypothetical protein contains sim	---	AT1G31530	1.00	0.00	0.02	0.9835993	0.9938738	-6.56	FALSE
262492_at	unknown protein Contains simila	---	AT1G21630	1.00	0.00	0.02	0.9839061	0.9938919	-6.56	FALSE
255454_at	hypothetical protein	---	AT4G02910	-1.00	0.00	-0.02	0.9839161	0.9938919	-6.56	FALSE
248220_at	26S proteasome regulatory parti	---	AT5G53540	1.00	0.00	0.02	0.9838997	0.9938919	-6.56	FALSE
264596_at	unknown protein similar to polyga	---	AT1G04625	1.00	0.00	0.02	0.984001	0.9938919	-6.56	FALSE
249661_x_a	putative protein similar to unknov	---	---	1.00	0.00	0.02	0.9839666	0.9938919	-6.56	FALSE
267221_at	similar to prokaryotic DNA polym	STI	AT2G02480	-1.00	0.00	-0.02	0.9839543	0.9938919	-6.56	FALSE
248447_at	putative protein contains similarit	PABN1	AT5G51120	1.00	0.00	0.02	0.9841016	0.9939496	-6.56	FALSE
246950_at	transcription initiation factor IID-	TAF5	AT5G25150	1.00	0.00	0.02	0.9841741	0.9939788	-6.56	FALSE
263587_at	putative synaptobrevin	ATVAMP71	AT2G25340	-1.00	0.00	-0.02	0.9842971	0.994015	-6.56	FALSE
260845_at	transcription factor, putative sim	---	AT1G17310	-1.00	0.00	-0.02	0.984294	0.994015	-6.56	FALSE
246120_at	tetratricopeptide repeat protein t	---	AT5G20360	-1.00	0.00	-0.02	0.9843885	0.9940633	-6.56	FALSE
261144_s_a	unknown protein ;supported by fu	---	AT1G19660 ///	1.00	0.00	0.02	0.9845823	0.9940885	-6.56	FALSE
257524_at	hypothetical protein similar to put	DEL3	AT3G01330	-1.00	0.00	-0.02	0.984673	0.9940885	-6.56	FALSE
258991_at	unknown protein contains Pfam p	---	AT3G08820	-1.00	0.00	-0.02	0.9846536	0.9940885	-6.56	FALSE
261125_at	zinc finger protein 2, putative sir	---	AT1G04990	1.00	0.01	0.02	0.9848493	0.9940885	-6.56	FALSE
245140_at	unknown protein predicted by ge	LBD18	AT2G45420	1.00	0.00	0.02	0.9846851	0.9940885	-6.56	FALSE
265393_at	unknown protein ; supported by	---	AT2G20830	-1.00	-0.01	-0.02	0.9847708	0.9940885	-6.56	FALSE
253210_at	putative protein predicted protei	MTN2	AT4G34840	-1.00	0.00	-0.02	0.9848358	0.9940885	-6.56	FALSE
262015_at	hypothetical protein predicted by	---	---	-1.00	0.00	-0.02	0.9844889	0.9940885	-6.56	FALSE
247604_at	putative phytochelatin synthetas	COBL5	AT5G60950	-1.01	-0.02	-0.02	0.9848354	0.9940885	-6.56	FALSE
260865_at	reverse transcriptase, putative s	---	AT1G43760	-1.00	0.00	-0.02	0.9847098	0.9940885	-6.56	FALSE
265344_at	unknown protein predicted by ge	---	AT2G22660	-1.00	0.00	-0.02	0.9849005	0.9940962	-6.56	FALSE
262623_at	integral membrane protein, puta	---	AT1G06470	-1.00	0.00	-0.02	0.9853051	0.9941937	-6.56	FALSE
258878_at	hypothetical protein predicted by	---	AT3G03170	1.00	0.00	0.02	0.9853458	0.9941937	-6.56	FALSE
259630_at	peptide chain release factor 2, p	---	AT1G56350	1.00	0.00	0.02	0.9851169	0.9941937	-6.56	FALSE
248924_at	GDSL-motif lipase/hydrolase-like	---	AT5G45960	1.00	0.00	0.02	0.9853152	0.9941937	-6.56	FALSE
257334_at	hypothetical protein	---	---	-1.01	-0.01	-0.02	0.9851556	0.9941937	-6.56	FALSE
254113_at	hypothetical protein	---	AT4G24900	1.00	0.00	0.02	0.9851763	0.9941937	-6.56	FALSE
245452_at	retrotransposon like protein	---	---	1.00	0.00	0.02	0.9852636	0.9941937	-6.56	FALSE
258361_at	unknown protein similar to hypot	---	AT3G14270	-1.00	-0.01	-0.02	0.9850411	0.9941937	-6.56	FALSE
262819_at	putative cytochrome P450 strong	CYP77B1	AT1G11600	1.00	0.00	0.02	0.9854942	0.9942555	-6.56	FALSE

257543_at	hypothetical protein predicted by	---	AT3G28960	-1.00	0.00	-0.02	0.9854618	0.9942555	-6.56	FALSE
263110_at	unknown protein ;supported by fu	---	AT1G65220	-1.00	0.00	-0.02	0.9855556	0.9942735	-6.56	FALSE
248689_at	SCARECROW gene regulator-lik	PAT1	AT5G48150	-1.00	0.00	-0.02	0.9857004	0.9943325	-6.56	FALSE
246104_at	DNA-binding protein - like DNA-	WRKY74	AT5G28650	-1.00	0.00	-0.02	0.9857013	0.9943325	-6.56	FALSE
264355_at	unknown protein similar to PHZF	---	AT1G03210	-1.00	0.00	-0.02	0.9857699	0.9943577	-6.56	FALSE
265802_at	predicted protein	---	AT2G35733	-1.00	0.00	-0.02	0.9859526	0.9944981	-6.56	FALSE
250923_at	putative protein ; supported by fu	CDC25	AT5G03455	1.00	0.00	0.02	0.9863384	0.9946286	-6.56	FALSE
252313_at	RNA-binding - like protein RNA-	CID10	AT3G49390	-1.00	-0.01	-0.02	0.9863381	0.9946286	-6.56	FALSE
259294_at	hypothetical protein predicted by	ATN	AT3G05330	1.00	0.00	0.02	0.9863873	0.9946286	-6.56	FALSE
267265_at	putative serine carboxypeptidase	SCPL13	AT2G22980	1.00	0.00	0.02	0.986381	0.9946286	-6.56	FALSE
252119_at	thioredoxin h ;supported by full-l	ATTRX1	AT3G51030	-1.00	-0.01	-0.02	0.9862139	0.9946286	-6.56	FALSE
263235_at	serine/threonine protein phospha	PP2A-2	AT1G10430	-1.00	0.00	-0.02	0.9861264	0.9946286	-6.56	FALSE
245823_at	hypothetical protein predicted by	---	AT1G57906	-1.00	0.00	-0.02	0.9862352	0.9946286	-6.56	FALSE
247323_at	putative protein similar to unknov	---	AT5G64170	1.00	0.00	0.02	0.9865148	0.9947132	-6.56	FALSE
266125_at	putative GATA-type zinc finger tr	---	AT2G45050	-1.00	0.00	-0.02	0.9866477	0.9947601	-6.56	FALSE
259086_at	hypothetical protein predicted by	---	AT3G04990	-1.00	0.00	-0.02	0.9866485	0.9947601	-6.56	FALSE
248519_at	11-beta-hydroxysteroid dehydrog	AtHSD7	AT5G50590 //	-1.00	0.00	-0.02	0.9867711	0.9948047	-6.56	FALSE
251547_at	putative protein predicted protei	---	AT3G58860	1.00	0.00	0.02	0.98678	0.9948047	-6.56	FALSE
250021_at	casein kinase-like protein	---	AT5G18190	-1.00	0.00	-0.02	0.9868899	0.9948715	-6.56	FALSE
264521_at	unknown protein Location of EST	---	AT1G10020	-1.00	-0.01	-0.02	0.9871388	0.9949471	-6.56	TRUE
259944_at	hypothetical protein predicted by	---	AT1G71470	1.00	0.00	0.02	0.987131	0.9949471	-6.56	FALSE
258236_at	hypothetical protein predicted by	---	AT3G27800	1.00	0.00	0.02	0.9871394	0.9949471	-6.56	FALSE
259324_at	unknown protein	MIRO3	AT3G05310	-1.00	0.00	-0.02	0.9870987	0.9949471	-6.56	FALSE
264009_at	putative disease resistance respo	---	AT2G21110	-1.00	0.00	-0.02	0.9873117	0.9949889	-6.56	FALSE
246186_at	PINHEAD - like protein PINHEA	---	AT5G21030	-1.00	0.00	-0.02	0.9872833	0.9949889	-6.56	FALSE
257471_at	G-box binding factor, putative sir	ATBZIP4	AT1G59530	1.00	0.00	0.02	0.9872589	0.9949889	-6.56	FALSE
256332_at	trihelix DNA-binding protein (GT	GT2	AT1G76890	1.00	0.01	0.02	0.9873566	0.9949903	-6.56	FALSE
266865_at	omega-3 fatty acid desaturase id	FAD3	AT2G29980	-1.02	-0.02	-0.02	0.9875845	0.9951759	-6.56	FALSE
256375_at	unknown protein	---	AT1G66720	1.00	0.00	0.02	0.9878923	0.9954244	-6.56	FALSE
261875_at	receptor-like protein kinase, puta	---	AT1G50610	1.00	0.00	0.02	0.9879183	0.9954244	-6.56	FALSE
264954_at	carboxyphosphonoenolpyruvate	---	AT1G77060	-1.00	0.00	-0.01	0.9885231	0.9955049	-6.56	TRUE
267609_at	unknown protein similar to GP|52	---	AT2G26780	1.00	0.00	0.01	0.9884854	0.9955049	-6.56	FALSE
246136_at	peptide transporter - like protein	---	AT5G28470	-1.00	0.00	-0.02	0.9882131	0.9955049	-6.56	FALSE
257361_at	putative Ta11-like non-LTR retro	---	---	-1.00	0.00	-0.02	0.9880611	0.9955049	-6.56	FALSE
254423_at	Lsd1 like protein zinc-finger prot	LOL2	AT4G21610	-1.00	0.00	-0.01	0.9885344	0.9955049	-6.56	FALSE

254838_at	hypothetical protein	---	AT4G12380	-1.00	0.00	-0.01	0.9885656	0.9955049	-6.56	FALSE
252744_at	putative protein hypothetical pro	---	AT3G43310	-1.00	0.00	-0.02	0.9882344	0.9955049	-6.56	FALSE
252279_at	1-aminocyclopropane-1-carboxy	ACS9	AT3G49700	-1.00	0.00	-0.01	0.9884745	0.9955049	-6.56	FALSE
257301_at	hypothetical protein predicted by	---	---	-1.00	0.00	-0.02	0.9884406	0.9955049	-6.56	FALSE
259842_at	phosphoethanolamine N-methyl	CPuORF32	AT1G73600 /	1.01	0.02	0.01	0.9884941	0.9955049	-6.56	FALSE
255649_at	contains region of similarity to m	---	AT4G00920	1.00	0.00	0.02	0.9883904	0.9955049	-6.56	FALSE
260187_at	hypothetical protein	LBD5	AT1G36000	-1.00	0.00	-0.02	0.9884127	0.9955049	-6.56	FALSE
249246_at	unknown protein	---	AT5G42290	1.00	0.00	0.02	0.9880928	0.9955049	-6.56	FALSE
260745_at	2,4-D inducible glutathione S-tra	ATGSTU20	AT1G78370	1.00	0.01	0.01	0.9887686	0.995648	-6.56	TRUE
250878_at	maturase -like protein gene cob	---	AT5G04050	-1.00	0.00	-0.01	0.9887951	0.995648	-6.56	FALSE
262707_at	hypothetical protein	---	AT1G16290	-1.00	0.00	-0.01	0.9888518	0.9956612	-6.56	FALSE
263041_at	putative alliinase similar to alliina	TAR1	AT1G23320	-1.00	0.00	-0.01	0.9888984	0.9956642	-6.56	FALSE
251811_at	APETALA2 - like protein APETA	SMZ	AT3G54990	1.00	0.00	0.01	0.9889858	0.9957082	-6.56	FALSE
249027_at	ATP dependent copper transport	RAN1	AT5G44790	-1.00	0.00	-0.01	0.989321	0.995723	-6.56	TRUE
258658_at	putative adenosine kinase simila	ADK1	AT3G09820	-1.00	-0.01	-0.01	0.9892009	0.995723	-6.56	FALSE
249236_at	putative protein similar to unknov	---	AT5G41950	-1.00	0.00	-0.01	0.9892434	0.995723	-6.56	FALSE
265930_at	putative spliceosome associated	emb2444	AT2G18510	1.00	0.00	0.01	0.9893556	0.995723	-6.56	FALSE
257917_at	ethylene responsive element bir	---	AT3G23220	-1.00	0.00	-0.01	0.9893871	0.995723	-6.56	FALSE
254540_s_a	putative protein chitinase / lysoz	---	AT4G19770 /	1.00	0.00	0.01	0.9892429	0.995723	-6.56	FALSE
248736_at	terpene synthase	---	AT5G48110	1.00	0.00	0.01	0.9891684	0.995723	-6.56	FALSE
250142_at	polygalacturonase - like protein	---	AT5G14650	-1.00	0.00	-0.01	0.9890781	0.995723	-6.56	FALSE
258442_at	hypothetical protein predicted by	---	AT3G01015	1.00	0.00	0.01	0.9893933	0.995723	-6.56	FALSE
264814_at	putative SET-domain transcriptio	SDG37	AT2G17900	-1.00	0.00	-0.01	0.9896176	0.9959048	-6.56	FALSE
266706_at	hypothetical protein predicted by	---	AT2G03320	-1.00	0.00	-0.01	0.9898074	0.9960079	-6.56	FALSE
247646_at	putative protein various predicte	---	AT5G59990	1.00	0.00	0.01	0.9898002	0.9960079	-6.56	FALSE
253742_at	putative protein retrofit - Oryza l	---	---	1.00	0.00	0.01	0.9900656	0.9962238	-6.56	FALSE
265256_at	hypothetical protein predicted by	---	AT2G28390	1.00	0.00	0.01	0.9901924	0.9962602	-6.56	FALSE
250081_at	unknown protein	---	AT5G17180	1.00	0.00	0.01	0.9902329	0.9962602	-6.56	FALSE
260720_at	hypothetical protein predicted by	---	AT1G48095	1.00	0.00	0.01	0.9901919	0.9962602	-6.56	FALSE
250844_at	putative protein ;supported by fu	SIM	AT5G04470	-1.00	0.00	-0.01	0.9903767	0.996361	-6.56	FALSE
259829_at	oligopeptide transporter, putative	---	---	-1.00	0.00	-0.01	0.9904484	0.9963892	-6.56	FALSE
257734_at	unknown protein contains Pfam p	ATSYTF	AT3G18370	1.00	0.00	0.01	0.9906368	0.9964678	-6.56	FALSE
246209_at	BEL1-like homeobox 2 protein (E	BLH2	AT4G36870	1.00	0.00	0.01	0.9906092	0.9964678	-6.56	FALSE
245162_at	putative myosin heavy chain	XID	AT2G33240	1.00	0.00	0.01	0.9906577	0.9964678	-6.56	FALSE
251440_at	SKP1/ASK1 (At13), putative sim	ASK13	AT3G60010	-1.00	0.00	-0.01	0.9907192	0.9964858	-6.56	FALSE

257980_at	hypothetical protein predicted by	---	AT3G20760	1.00	0.00	0.01	0.9908574	0.996493	-6.56	FALSE
249804_at	galactinol synthase	AtGolS5	AT5G23790	1.00	0.00	0.01	0.9908407	0.996493	-6.56	FALSE
254580_at	putative protein ; supported by c	---	AT4G19390	-1.00	0.00	-0.01	0.9908519	0.996493	-6.56	FALSE
254199_at	putative protein Ste-20 related k	---	AT4G24100	-1.00	0.00	-0.01	0.9910354	0.9966281	-6.56	FALSE
249442_at	putative protein ; supported by c	---	AT5G39590	1.00	0.00	0.01	0.9912764	0.9967826	-6.56	FALSE
257737_at	uridine kinase/uracil phosphorib	---	AT3G27440	1.00	0.00	0.01	0.9912418	0.9967826	-6.56	FALSE
261863_at	unknown protein ; supported by c	---	AT1G50630	-1.00	0.00	-0.01	0.9913702	0.9968329	-6.56	FALSE
260067_at	putative lipid transfer protein sim	---	AT1G73780	1.00	0.00	0.01	0.9914733	0.9968501	-6.56	FALSE
259663_at	hypothetical protein predicted by	PRA7	AT1G55190	-1.00	0.00	-0.01	0.9914747	0.9968501	-6.56	FALSE
253476_at	S-receptor kinase -like protein s	SD2-5	AT4G32300	-1.00	0.00	-0.01	0.9916022	0.9968738	-6.56	FALSE
256915_at	unknown protein	---	AT3G23900	1.00	0.00	0.01	0.9916294	0.9968738	-6.56	FALSE
257306_at	hypothetical protein contains reg	---	AT3G30200	-1.00	0.00	-0.01	0.9915556	0.9968738	-6.56	FALSE
251220_at	cytochrome c oxidase subunit 5c	---	AT3G62400	1.00	0.00	0.01	0.9917145	0.9969155	-6.56	FALSE
253083_at	aldehyde dehydrogenase like pr	ALDH3F1	AT4G36250	1.00	0.00	0.01	0.9918217	0.9969792	-6.56	FALSE
248501_at	golgi SNARE protein	MEMB12	AT5G50440	-1.00	0.00	-0.01	0.9918666	0.9969805	-6.56	FALSE
255111_at	peroxidase C2 precursor like pro	---	AT4G08780	-1.01	-0.01	-0.01	0.9924595	0.9970742	-6.56	TRUE
253397_at	putative protein kinase protein k	---	AT4G32710	1.00	0.00	0.01	0.9922114	0.9970742	-6.56	FALSE
264179_at	hypothetical protein predicted by	---	AT1G02180	-1.00	0.00	-0.01	0.992423	0.9970742	-6.56	FALSE
255693_s_a	putative BRCA2 homolog	BRCA2(IV)	AT4G00020 ///	1.00	0.00	0.01	0.992431	0.9970742	-6.56	FALSE
253650_at	EST GB:N37377 spans last intro	---	AT4G30020	-1.01	-0.01	-0.01	0.9920375	0.9970742	-6.56	FALSE
255484_at	putative protein similar to A. thal	---	AT4G02540	-1.00	0.00	-0.01	0.9923096	0.9970742	-6.56	FALSE
265882_at	putative copper amine oxidase	---	AT2G42490	-1.00	0.00	-0.01	0.9923813	0.9970742	-6.56	FALSE
254151_at	F-box protein family, AtFBX14 s	---	AT4G24390	1.00	0.00	0.01	0.9921996	0.9970742	-6.56	FALSE
265489_at	hypothetical protein predicted by	---	AT2G15640	-1.00	0.00	-0.01	0.9924844	0.9970742	-6.56	FALSE
258418_at	unknown protein	---	AT3G16660	1.00	0.01	0.01	0.9922507	0.9970742	-6.56	FALSE
252674_at	cytochrome P450-like protein CY	CYP71B38	AT3G44250	1.00	0.00	0.01	0.9924609	0.9970742	-6.56	FALSE
256527_at	thionin, putative similar to thionir	---	AT1G66100	-1.00	0.00	-0.01	0.9922157	0.9970742	-6.56	FALSE
267081_at	putative phosphatidylinositol-4-pl	PIP5K5	AT2G41210	1.00	0.00	0.01	0.99258	0.9970824	-6.56	FALSE
248670_at	receptor protein kinase-like prote	---	AT5G48740	-1.00	0.00	-0.01	0.9925735	0.9970824	-6.56	FALSE
261541_at	unknown protein contains Pfam p	---	AT1G63600	1.00	0.00	0.01	0.9927269	0.9971861	-6.56	FALSE
261431_at	Myb-related transcription factor	AtMYB47	AT1G18710	1.00	0.00	0.01	0.9929344	0.9973505	-6.56	TRUE
261032_at	unknown protein ;supported by fu	---	AT1G17430	-1.00	0.00	-0.01	0.9931669	0.9973889	-6.56	TRUE
250072_at	putative protein similar to unknov	---	AT5G17210	-1.00	0.00	-0.01	0.9931772	0.9973889	-6.56	FALSE
260378_at	putative actin similar to actin GB	ATARP4A	AT1G73910	-1.00	0.00	-0.01	0.993175	0.9973889	-6.56	FALSE
247938_at	putative protein similar to unknov	---	AT5G57140 ///	1.00	0.00	0.01	0.9930515	0.9973889	-6.56	FALSE

253514_at	putative protein DNA-binding pro	---	AT4G31805	-1.00	0.00	-0.01	0.9931912	0.9973889	-6.56	FALSE
263662_at	ankyrin-like protein EST gb|ATTS	---	AT1G04430	-1.00	0.00	-0.01	0.9933145	0.9974688	-6.56	TRUE
247860_at	bis(5'-adenosyl)-triphosphatase-l	---	AT5G58240	-1.00	0.00	-0.01	0.9933695	0.9974801	-6.56	FALSE
267116_at	unknown protein	---	AT2G32560	1.00	0.00	0.01	0.9934572	0.9974803	-6.56	TRUE
261641_at	hypothetical protein similar to hyp	---	AT1G27670	1.00	0.00	0.01	0.9934196	0.9974803	-6.56	FALSE
246309_at	putative transmembrane protein	ATG1	AT3G51790	-1.00	0.00	-0.01	0.9935118	0.9974913	-6.56	FALSE
264044_at	putative pyrophosphate--fructose	PFK5	AT2G22480	-1.00	0.00	-0.01	0.9938905	0.9977837	-6.56	FALSE
257138_at	hypothetical protein predicted by	---	AT3G28870	-1.00	0.00	-0.01	0.9938523	0.9977837	-6.56	FALSE
264261_at	putative nicotianamine synthase	NAS3	AT1G09240	-1.00	-0.01	-0.01	0.9939573	0.9978068	-6.56	FALSE
258894_at	putative disease resistance prote	AtRLP32	AT3G05650	1.00	0.00	0.01	0.9940808	0.9978808	-6.56	FALSE
251988_at	CYTOCHROME P450-like prote	CYP71B31	AT3G53300	-1.00	0.00	-0.01	0.9941185	0.9978808	-6.56	FALSE
260338_at	putative RNA-binding protein sim	---	AT1G69250	1.00	0.00	0.01	0.9941874	0.997906	-6.56	FALSE
257287_at	hypothetical protein predicted by	---	---	-1.00	0.00	-0.01	0.9942603	0.9979353	-6.56	FALSE
264349_at	putative Proline synthetase asso	---	AT1G11930	1.00	0.00	0.01	0.9943554	0.9979869	-6.56	FALSE
263904_at	putative ABC transporter related	PDR6	AT2G36380	-1.00	0.00	-0.01	0.9944537	0.9980416	-6.56	FALSE
262980_at	endo-beta-1,4-glucanase, putati	AtGH9B7	AT1G75680	1.00	0.00	0.01	0.9946785	0.9980963	-6.56	TRUE
245369_at	Expressed protein ; supported by	---	AT4G15975	1.00	0.00	0.01	0.9947539	0.9980963	-6.56	FALSE
265700_at	putative MYB family transcription	---	AT2G03470	1.00	0.00	0.01	0.9947668	0.9980963	-6.56	FALSE
263457_at	unknown protein	SR1	AT2G22300	1.00	0.00	0.01	0.9947708	0.9980963	-6.56	FALSE
262553_at	hypothetical protein similar to hyp	RECQL2	AT1G31360	-1.00	0.00	-0.01	0.99457	0.9980963	-6.56	FALSE
254672_at	hypothetical protein	---	---	-1.00	0.00	-0.01	0.9947167	0.9980963	-6.56	FALSE
258631_at	putative polygalacturonase simila	QRT2	AT3G07970	-1.00	0.00	-0.01	0.9948607	0.9980991	-6.56	FALSE
249184_at	receptor kinase-like protein	---	AT5G43020	1.00	0.00	0.01	0.9948611	0.9980991	-6.56	FALSE
254383_at	hypothetical protein	---	AT4G21950	-1.00	0.00	-0.01	0.9951075	0.9982491	-6.56	FALSE
251873_at	putative protein KIAA0122 gene	---	AT3G54230	1.00	0.00	0.01	0.9950576	0.9982491	-6.56	FALSE
248658_at	chromosome condensation prote	ATSMC3	AT5G48600	1.00	0.00	0.01	0.9951418	0.9982491	-6.56	FALSE
259488_at	hypothetical protein preedicted b	---	AT1G15780	-1.00	0.00	-0.01	0.9953957	0.9982842	-6.56	FALSE
267173_at	origin recognition complex protei	ORC2	AT2G37560	1.00	0.00	0.01	0.9953407	0.9982842	-6.56	FALSE
261115_at	hypothetical protein predicted by	---	AT1G75360	-1.00	0.00	-0.01	0.995328	0.9982842	-6.56	FALSE
261924_at	peptide transporter, putative sim	---	AT1G22550	1.00	0.00	0.01	0.99526	0.9982842	-6.56	FALSE
256138_at	Nt-gh3 deduced protein, putative	---	AT1G48670	1.00	0.00	0.01	0.9953918	0.9982842	-6.56	FALSE
264125_at	hypothetical protein predicted by	EMB1135	AT1G79350	-1.00	0.00	-0.01	0.9955398	0.9983848	-6.56	FALSE
257624_at	cytochrome P450 monooxygena	CYP71B3	AT3G26220	-1.00	0.00	0.00	0.9965276	0.9984573	-6.56	TRUE
265150_at	unknown protein ; supported by	---	AT1G51200	1.00	0.00	0.00	0.9964615	0.9984573	-6.56	FALSE
249718_at	putative protein contains similari	---	AT5G35740	1.00	0.00	0.00	0.9965	0.9984573	-6.56	FALSE

251714_at	putative protein leucine-rich rece	---	AT3G56370	1.00	0.00	0.00	0.9965026	0.9984573	-6.56	FALSE
261460_at	MAP kinase, putative similar to (	ATMPK13	AT1G07880	1.00	0.00	0.01	0.9958501	0.9984573	-6.56	FALSE
250539_at	WD-repeat protein-like ; support	---	AT5G08560	-1.00	0.00	0.00	0.9961689	0.9984573	-6.56	FALSE
265343_at	unknown protein ; supported by f	NIC1	AT2G22570	-1.00	0.00	-0.01	0.9957218	0.9984573	-6.56	FALSE
262628_at	glucan synthase, putative simila	ATGSL07	AT1G06490	-1.00	0.00	0.00	0.9965313	0.9984573	-6.56	FALSE
249915_at	putative protein similar to unknov	---	AT5G22870	-1.00	0.00	0.00	0.9965308	0.9984573	-6.56	FALSE
252402_s_a	putative protein predicted protei	---	AT3G48050 ///	-1.00	0.00	-0.01	0.996119	0.9984573	-6.56	FALSE
258349_at	Expressed protein ; supported by	HYH	AT3G17609	-1.00	0.00	-0.01	0.9960867	0.9984573	-6.56	FALSE
246894_at	heat-shock protein - like heat-sh	---	AT5G25530	-1.00	0.00	0.00	0.9964521	0.9984573	-6.56	FALSE
258770_at	hypothetical protein	---	AT3G10830	1.00	0.00	0.01	0.9960565	0.9984573	-6.56	FALSE
265165_at	putative OBP32pep protein	---	AT1G23610	-1.00	0.00	0.00	0.996306	0.9984573	-6.56	FALSE
266517_at	glycine decarboxylase complex H	---	AT2G35120	-1.00	0.00	0.00	0.9964266	0.9984573	-6.56	FALSE
253290_at	putative protein predicted protei	---	AT4G34330	1.00	0.00	0.01	0.996065	0.9984573	-6.56	FALSE
251692_s_a	serine carboxypeptidase-like pro	---	AT3G52020 ///	-1.00	0.00	0.00	0.996343	0.9984573	-6.56	FALSE
253658_at	cadmium-transporting ATPase-li	HMA3	AT4G30120	-1.00	0.00	-0.01	0.9961444	0.9984573	-6.56	FALSE
251014_at	putative protein fimbriae-associa	---	AT5G02520	1.00	0.00	0.01	0.9960707	0.9984573	-6.56	FALSE
265368_at	hypothetical protein identical to h	---	AT2G13350	-1.00	0.00	0.00	0.996443	0.9984573	-6.56	FALSE
265134_at	putative acyl-CoA : 1-acylglycero	LPAT3	AT1G51260	1.00	0.00	0.00	0.996436	0.9984573	-6.56	FALSE
255565_at	putative CHP-rich zinc finger pro	---	AT4G01760	-1.00	0.00	0.00	0.9966851	0.9985675	-6.56	FALSE
251526_at	putative protein several serine/th	---	AT3G58640	1.00	0.00	0.00	0.996839	0.9986779	-6.56	FALSE
249883_at	Na+/H+ antiporter-like protein	CHX3	AT5G22900	-1.00	0.00	0.00	0.9968934	0.9986885	-6.56	FALSE
265198_at	putative glucosyl transferase	UGT73C2	AT2G36760	1.00	0.00	0.00	0.9972523	0.9987424	-6.56	FALSE
262106_at	hypothetical protein similar to We	WEE1	AT1G02970	1.00	0.00	0.00	0.9972719	0.9987424	-6.56	FALSE
250346_at	lysine decarboxylase - like prote	---	AT5G11950	-1.00	0.00	0.00	0.997131	0.9987424	-6.56	FALSE
253781_at	putative protein predicted protei	---	AT4G28580	-1.00	0.00	0.00	0.9972975	0.9987424	-6.56	FALSE
261940_at	hypothetical protein predicted by	---	AT1G22520	1.00	0.00	0.00	0.9971384	0.9987424	-6.56	FALSE
245450_at	disease resistance RPP5 like pro	---	AT4G16880	1.00	0.00	0.00	0.997201	0.9987424	-6.56	FALSE
248712_at	unknown protein	---	AT5G48280	-1.00	0.00	0.00	0.9970929	0.9987424	-6.56	FALSE
252169_at	putative protein several bacterial	---	AT3G50520	1.00	0.00	0.00	0.9972354	0.9987424	-6.56	FALSE
249740_at	unknown protein	---	AT5G24500	1.00	0.00	0.00	0.9974116	0.9988129	-6.56	FALSE
265520_at	hypothetical protein predicted by	---	AT2G06020	-1.00	0.00	0.00	0.9974697	0.9988271	-6.56	FALSE
266404_at	hypothetical protein predicted by	---	AT2G38590	-1.00	0.00	0.00	0.997639	0.9989529	-6.56	FALSE
252689_at	putative protein predicted protei	---	AT3G44030	-1.00	0.00	0.00	0.9977683	0.9989946	-6.56	FALSE
263454_at	putative cysteine proteinase	---	AT2G22160	-1.00	0.00	0.00	0.9977602	0.9989946	-6.56	FALSE
266122_at	putative helicase ; supported by	ETL1	AT2G02090	1.00	0.00	0.00	0.9983493	0.9992785	-6.56	FALSE

250946_at	putative protein	---	AT5G03420	1.00	0.00	0.00	0.9983668	0.9992785	-6.56	FALSE
267148_at	hypothetical protein predicted by	---	AT2G23470	-1.00	0.00	0.00	0.9984004	0.9992785	-6.56	FALSE
267203_at	hypothetical protein predicted by	---	AT2G31035	1.00	0.00	0.00	0.9984133	0.9992785	-6.56	FALSE
260312_at	putative disease resistance prote	---	AT1G63880	1.00	0.00	0.00	0.9983518	0.9992785	-6.56	FALSE
258746_at	germin-like protein similar to gerr	---	AT3G05950	-1.00	0.00	0.00	0.9982902	0.9992785	-6.56	FALSE
264207_at	unknown protein strong similarity	---	AT1G22750	-1.00	0.00	0.00	0.9984151	0.9992785	-6.56	FALSE
264358_at	hypothetical protein predicted by	---	AT1G03180	1.00	0.00	0.00	0.9982338	0.9992785	-6.56	FALSE
256758_at	hypothetical protein similar to Ath	---	---	-1.00	0.00	0.00	0.9984461	0.9992785	-6.56	FALSE
255063_at	putative transposon protein simila	---	---	-1.00	0.00	0.00	0.9985124	0.999301	-6.56	FALSE
257800_at	unknown protein ;supported by f	---	AT3G15900	-1.00	0.00	0.00	0.9986245	0.9993693	-6.56	FALSE
260804_at	hypothetical protein predicted by	---	AT1G78410	1.00	0.00	0.00	0.9987566	0.99937	-6.56	TRUE
263328_at	hypothetical protein similar to hyp	---	AT2G15280	1.00	0.00	0.00	0.9986707	0.99937	-6.56	FALSE
252743_at	guanine nucleotide-exchange - I	ATMIN7	AT3G43300	1.00	0.00	0.00	0.9987399	0.99937	-6.56	FALSE
266599_at	unknown protein	---	AT2G46100	-1.00	0.00	0.00	0.9989683	0.9993792	-6.56	FALSE
265958_at	putative adenylate kinase ;suppo	ADK	AT2G37250	1.00	0.00	0.00	0.9990287	0.9993792	-6.56	FALSE
246883_at	putative protein many predicted	---	AT5G26190	-1.00	0.00	0.00	0.998943	0.9993792	-6.56	FALSE
251363_at	putative transcription factor (MYB	AtMYB17	AT3G61250	1.00	0.00	0.00	0.9989935	0.9993792	-6.56	FALSE
267003_at	hypothetical protein predicted by	---	AT2G34340	1.00	0.00	0.00	0.9990036	0.9993792	-6.56	FALSE
265487_at	hypothetical protein	---	---	1.00	0.00	0.00	0.9989945	0.9993792	-6.56	FALSE
250591_at	alpha galactosyltransferase prote	---	AT5G07720	-1.00	0.00	0.00	0.9991333	0.99944	-6.56	FALSE
265140_at	F-box protein family, AtFBX11 c	---	AT1G51320	-1.00	0.00	0.00	0.9991841	0.999447	-6.56	FALSE
260347_at	DHHC-type zinc finger protein, p	---	AT1G69420	1.00	0.00	0.00	0.9995616	0.9997063	-6.56	TRUE
258142_at	unknown protein	---	AT3G18120	-1.00	0.00	0.00	0.9995099	0.9997063	-6.56	FALSE
262267_at	hypothetical protein predicted by	---	---	1.00	0.00	0.00	0.9995748	0.9997063	-6.56	FALSE
255898_at	hypothetical protein similar to hyp	---	AT1G17930	-1.00	0.00	0.00	0.9997856	0.9998733	-6.56	FALSE
247739_at	40S ribosomal protein S8 - like 4	---	AT5G59240	-1.00	0.00	0.00	0.9998973	0.9998973	-6.56	FALSE
252483_at	scarecrow-like protein scarecrov	---	AT3G46600	1.00	0.00	0.00	0.9998778	0.9998973	-6.56	FALSE